Iron and Manganese Homeostasis in Marine Bacteria

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Abstract

Using a mixture of bioinformatic analyses, microarrays on cells that were grown in media that were either replete or depleted for manganese or for iron, and by making targeted mutations and reporter fusions, several important observations were made on the mechanisms of Mn and Fe homeostasis in the marine α -proteobacterium *Ruegeria pomeroyi* (the main species studied here), and in other important marine bacteria.

R. pomeroyi lacks most of the known Fe uptake systems, including TonB and outer-membrane receptors, but has a predicted, but incomplete iron uptake ABC-class transporter operon, whose expression is much enhanced in Fe-depleted conditions, although a strain lacking these genes was unaffected in growth. The Fe-specific regulatory network of *R. pomeroyi* was found to involve the Irr transcriptional regulator, which controlled the expression of several genes. Microarrays revealed many other genes whose expression was enhanced or diminished in Fe-replete conditions, providing material for future work on the iron regulon of this bacterium,

Turning to manganese, here too the expression of many genes was affected (up or down) by Mn availability. These included an operon corresponding to *sitABCD*, an effective ABC-type Mn²⁺ transporter in many other bacteria. This was confirmed, directly, to be the case for *Ruegeria*. Bioinformatic analyses showed that some other Roseobacter strains lacked any previously known Mn²⁺ transporter, but instead, had a gene that likely encoded an inner membrane protein and was preceded by a motif (MRS box) that was known to be recognised by the Mn²⁺ -responsive transcriptional regulator Mur. It was confirmed that this gene, termed *mntX*, did indeed encode a manganese transporter and that MntX orthologues occurred in several other, unrelated marine bacteria, notably most strains of the pathogenic genus *Vibrio* (including *V. cholerae*) and some of the most abundant bacteria in the oceans, namely the SAR11 clade (*Pelagibacter*).

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Chapter 1 - General Introduction

1.1 Iron

On Earth, iron is the second most common metal, and the fourth most plentiful element in the Earth's crust (Emsley 2001). It predominantly exists in two oxidised states, the extremely water-soluble ferrous iron (Fe²⁺) and the extremely insoluble ferric iron (Fe³⁺) (Crichton and Boelaert 2001). Fe found in seawater is nearly all in the ferric form, due to the oxic and slightly alkaline conditions.

1.1.1 Dependence of bacteria on iron

Iron (Fe) is required for growth of almost all microorganisms. It is used as a catalytic cofactor in many biological processes including photosynthesis, respiration, the citric acid cycle of central metabolism, gene regulation and DNA biosynthesis (Andrews *et al.* 2003). There are some examples of bacteria that do not require iron; these include *Lactobacillus*, which uses manganese and cobalt in place of iron (Archibald 1983; Pandey *et al.* 1994), *Borrelia burgdorferi*, a genome-reduced endosymbiotic parasite that utilises its host's metabolism to replace its own iron dependency (Posey and Gherardini 2000) and some species of Streptococci that can grow in the absence of Fe (Niven *et al.* 1999; Spatafora and Moore 1998). All bacteria that do not require Fe for growth have an absolute requirement for Mn (Jakubovics and Jenkinson 2001).

1.1.2 Iron chemistry

The coordination stereochemistry of both Fe²⁺ and Fe³⁺ means that they are often found as octahedral complexes in nature. Dependent on the associated ligand, a coordinated iron atom can exist in a high or low spin state. Weak field ligands such as F⁻ or OH⁻ increase the frequency of paired electrons in the iron-ligand interaction and are described as a low spin complex, whereas strong field ligands such as CO or CN⁻ maximise unpaired electrons and cause high spin complexes (Crichton and Boelaert 2001). Both the ferric and ferrous forms of iron are Lewis acids, the ferric state being stronger than the ferrous (Crichton and Boelaert 2001). The range of redox potential of both Fe²⁺ and Fe³⁺ is huge, and can be fine-tuned by various ligands. The iron site of any molecule or complex can

almost span the entire range of biologically relevant redox potentials, from -0.5 V to +0.6 V (Crichton and Boelaert 2001). Furthermore, iron complexes can catalyse electron transfer and acid-base reactions, making iron a hugely important and adaptable element for many physiological processes.

All these chemical properties make iron the ideal cofactor for many enzymes (Andrews *et al.* 2003), and the near-ubiquitous iron-dependency of all living things suggests that this has been the case since life evolved (Beinert *et al.* 1997) and may even have contributed to the emergence of life (Wachtershauser 2000).

Molecular oxygen was not present on Earth when life emerged, so all the iron present was in the reduced form. This iron was soluble, and easily accessible to all forms of emerging life. As early cyanobacteria 'breathed' oxygen into our atmosphere, the great majority of the dissolved iron became oxidised and precipitated out of the oceans, leaving huge deposits of iron hydroxides in the Precambrian fossil layer (Crichton and Boelaert 2001).

1.1.3 Iron catalyses the formation of oxygen free-radicals

Ferrous iron can participate in the heterolytic fission of the dioxygen bond in hydrogen peroxide (H_2O_2) leading to the generation of a hydroxyl radical and a hydroxide ion. This process involves both Fenton chemistry and the Haber-Weiss reaction, as shown below:

Fenton chemistry (Fenton 1894).

$$Fe^{2+} + H_2O_2 \longrightarrow Fe^{3+} + \cdot OH + OH^{-}$$

Iron can also catalyse the formation of a hydroxyl radical through the Haber-Weiss reaction (Haber and Weiss 1932):

$$O_2^- + H_2O_2 \longrightarrow O_2 + \cdot OH + OH^-$$

The lone unpaired electron in the hydroxyl radical makes it highly reactive, and this hydroxyl species can damage proteins, carbohydrates, lipids and nucleic acids, so it is genotoxic, and mildly mutagenic (Sies 1993). This means that this essential metal can also be lethal. It follows that Fe homoeostasis in bacteria (and, indeed, all organisms) is tightly regulated, so that cells have neither too little, nor too much Fe.

1.2 Manganese

Manganese is the twelfth most common element in the Earth's crust (Emsley 2001), and exists in a range of oxidised states (+1 - +7), the most common being Mn^{4+} in MnO_2 (pyrolusite). Manganese in sea water is found in the soluble state Mn^{2+} , although it also occurs as the insoluble oxides Mn^{3+} and Mn^{4+} (Stumm and Morgan 1981). In the oceans, soluble Mn oxides are reduced to Mn^{2+} by sunlight (Sunda *et al.* 1998), making them biologically available. Dissolved Mn levels are in the low nanomolar range in surface waters of the ocean (Landing and Bruland 1987; Middag *et al.* 2011).

1.2.1 Dependence of Bacteria on Manganese

Manganese (Mn) is also an essential metal, being critical for photosynthesis, gluconeogenesis, glycolysis, amino acid and aromatic acid metabolism, peptide cleavage, nucleic acid degradation, signal transduction and the stringency and oxidative stress responses in a variety of bacteria (Jakubovics and Jenkinson 2001). In bacteria, there is a clear biological, as well as a chemical, link between the two very similar transition metals Mn and Fe. Thus, Mn can regulate intracellular levels of Fe in *Bradyrhizobium japonicum* (Puri *et al.* 2010) and the expression of Mn uptake systems is under the control of Fe and Mn in *Escherichia coli* (Patzer and Hantke 2001), *Salmonella enterica* serovar Typhimurium (Kehres *et al.* 2002) and *Bacillus subtilis* (Que and Helmann 2000).

1.2.2 Manganese chemistry

Mn(II) has an ionic radius of 0.8Å, which is very similar to that of Fe²⁺ (0.76Å), and indeed other transition metals such as calcium and magnesium (Jakubovics and Jenkinson 2001). Because of this size similarity, Mn will often substitute for Fe in the metal-binding sites of proteins; Mn also commonly incorporates into Mg-specific ligands due to their similar binding properties (Jakubovics and Jenkinson 2001).

Mn has a major role in biological systems by catalysing redox reactions. These Mn-containing enzymes can have 1, 2 or 4 Mn atoms to facilitate redox chemistry. Mononuclear Mn containing enzymes include the Mn-containing superoxide dismutase, Mn-dependent peroxidase, and Mn-

dioxygenase. Bacterial catalase and Mn-ribonucleotide reductase enzymes utilise a binuclear Mn redox site, and the oxygenic catalytic centre of photosystem II has 4 Mn atoms (Law *et al.* 1998).

1.2.3 Manganese helps protect cells from oxidative damage

In contrast to iron, the reactions between Mn^{2+} and O_2 , H_2O_2 or OH do not form hydroxyl radicals (Cheton and Archibald 1988; Stadtman *et al.* 1990). Indeed, being a co-factor in the Mn-superoxide dismutase SodA, Mn is essential in detoxifying reactive oxygen species (Keele *et al.* 1970), and several groups of lactic acid bacteria use millimolar levels of intracellular Mn^{2+} to "mop up" and detoxify superoxides (Archibald 1986).

1.3 The ocean environment

1.3.1 Ocean Geochemical Cycles

Cycling of organic molecules within the epipelagic zone (<200 m) occurs readily by mixing due to wind action, thermohaline current (Millero 2006), and through the abundant aquatic microbes (Whitman *et al.* 1998) constituting the 'biological pump' (Buesseler and Boyd 2009). Below the epipelagic, the mesopelagic (< 1000m) zone contains water that remains in place for decades, yet bacteria and archeae (Karner *et al.* 2001; Kirchman *et al.* 2007), protists (Peter *et al.* 2007) and nanoflagellates (Hideki *et al.* 2007) found here contribute extensively to ocean metabolism (Aristegui *et al.* 2009). Further down still, the bathypelagic (1000–4000-m depth) and abyssal zones (>4000 m) contain extremely high pressure water which remains *in situ* for centuries (Aristegui *et al.* 2009). In these ecosystems, very little is known about the biology, although a study by Sogin *et al.* (Sogin *et al.* 2006), revealed that 80% of mesopelagic and bathypelagic organisms were from uncharacterised genera. Movement of nutrients, metabolites and sequestered compounds down the water column is also caused by gravity – in the form of marine snow.

1.3.2 Marine Snow

Marine snow consists of organic material, excreted waste and inorganic solids falling from the densely populated euphotic zone, settling on the ocean floor in benthic sludge depositions. Phytoplankton, bacteria, flagellates and protozoans form part of clumping snow particles, which can measure many centimetres across, and are considered an important part of nutrient cycling in the water column (Alldredge and Silver 1988). Bacteria can reach densities of $10^8 - 10^9$ per ml of marine snow (Alldredge *et al.* 1986). These break down organic material, releasing plumes of small molecules and ions from the snow particles (Azam and Malfatti 2007; Kioerboe and Jackson 2001). These plumes play a major role in recycling iron, phosphate and nitrates back to the higher water column (Kioerboe and Jackson 2001), and also lead to a net loss of carbon from the upper ocean compared to these compounds; refer to figure 1.1 (Azam and Malfatti 2007).

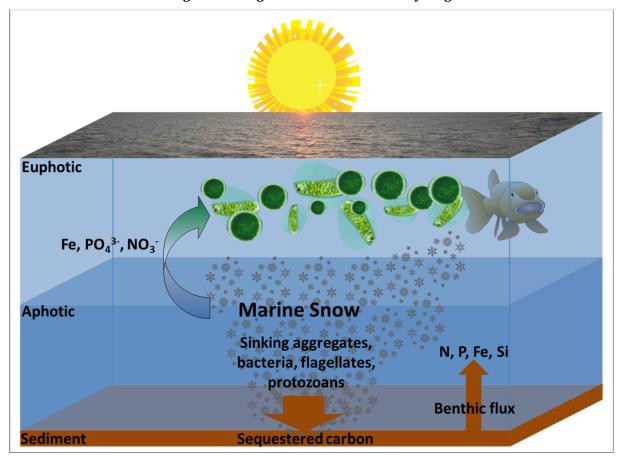


Figure 1.1 Diagram of marine nutrient cycling

Marine snow falling from the euphotic zone is colonised by microorganisms which contribute to the flux of nutrients. Plumes of nutrients, Fe, $PO_4^{3\cdot}$ and NO_3 , are released by grazing bacteria, flagellates and protozoans from marine snow. These are recycled back into the phytoplankton rich euphotic zone; the remaining snow falls through the aphotic zone where it is sequestered into the benthic sediment. Over time, elemental nitrogen, phosphorus, iron and silicon are reabsorbed by the water column where they re-join the cycle. Also, a net loss of carbon occurs from the water as marine snow enters the sediment (Azam and Malfatti 2007).

1.3.3 Input of metals into the ocean

The influx of Fe and Mn into the oceans is mainly from erosion of sediments, which are washed into terrestrial waterways (Johnson *et al.* 1997), and the metal laced dust that is carried around in the atmosphere (Coale *et al.* 1996; Duce and Tindale 1991). Dust is considered to be the major pathway of marine iron input (Jickells *et al.* 2005), only 10 % of which is soluble in seawater (Zhuang *et al.* 1990). However, Mn concentrations in surface seawater are nearly entirely due to dust deposition

(Mendez *et al.* 2010). There are extremely low levels of Fe and Mn in the Southern Oceans due to a lack of dust input into this body of water (Martin *et al.* 1990).

Global iron deposition into the oceans is estimated to be between 131 and 487 x 10^9 mol yr⁻¹ (Duce and Tindale 1991; Mahowald *et al.* 1999; Tegen and Fung 1995), fuelling blooms of life in both coastal and offshore waters (Archer and Johnson 2000). Iron availability in the oceans contributes directly to both the strength of the biological pump, and the amount of dissolved CO_2 (Archer and Johnson 2000), both of which are vital to a stable climate (Sunda 2010).

The global input of Mn into the oceans has not been determined, but some initial estimates for the flux of Mn to the Southern Ocean indicate that that ~2 μ mol Mn m⁻²·yr⁻¹ of Mn is deposited by dust, which is less than the estimate of Mn flux from marine and land sediments into the same water system - 3.3 μ mol Mn m⁻²·yr⁻¹ (Middag *et al.* 2011)

Iron cycling within oceans is complex. Fe(III) is almost entirely bound to organic ligands (Gledhill and van den Berg 1994; Rue and Bruland 1995; Rue and Bruland 1997; van den Berg 1995; Wu and Luther 1995). The precise makeup of these Fe-containing materials is poorly understood; thus Hopkinson (2009) states that the ligand pool 'is likely to be a mixture of siderophores, organic exudates and humic material'. Any Fe(II) is either used by bacteria and phytoplankton, or falls to the ocean floor in marine snow, where benthic flux slowly returns metals to the water by diffusion (Azam and Malfatti 2007). The mechanical stirring of water via waves, and currents such as the Gulf Stream, and transport of iron via feeding and migrating macroscopic life leads to its movement both horizontally and vertically around the water column, so both physical and biological factors impact on the distribution of this metal (Morel and Price 2003).

The iron cycle is directly linked to the 'biological pump': 25 % of all CO_2 released into the atmosphere is absorbed into the oceans (Feely *et al.* 2009), causing a decrease in pH (Sunda 2010). By the end of the century, current trends show that the global pH of seawater will drop from 8.2 to 7.7 (Feely *et al.* 2009; Millero *et al.* 2009). Increasing acidification of surface water will decrease the bioavailable (Fe(II)) iron, less phytoplankton will grow, and less CO_2 will be fixed, with real potential for increasing global warming further – a dangerous feedback loop (Shi *et al.* 2010).

1.3.4 Iron and manganese availability in the ocean

Total dissolved iron concentrations in the oceans range from 20 pM to 1 nM in pelagic, offshore zones (Bruland *et al.* 1994; Gordon *et al.* 1982; Martin *et al.* 1991), and 100 pM to 10 nM around the coastlines (Gordon *et al.* 1982; Wu and Luther 1995). Iron availability is sensitive to pH, a particularly relevant factor, given the increasing atmospheric CO₂, and consequent acidification of the oceans (Shi *et al.* 2010). Modelled increases in irradiation or decreases in temperature were both shown to enhance levels of Fe(II) (Tagliabue *et al.* 2009), the biologically available form of iron. More than 99% of dissolved iron is in complex with unidentified ligands (Gledhill and van den Berg 1994; Rue and Bruland 1995; Rue and Bruland 1997; van den Berg 1995; Wu and Luther 1995), thereby reducing free iron concentration to low picomolar quantities (Bruland *et al.* 1994; Gordon *et al.* 1982; Martin *et al.* 1991; Wu and Luther 1995), although there is ongoing debate about iron availability in seawater (Hutchins *et al.* 1999; Wells *et al.* 1995). It is strongly suggested that the ligands responsible for most of the iron chelation are bacterial siderophore pools (Granger and Price 1999; Haygood *et al.* 1993; Hutchins *et al.* 1999; Rue and Bruland 1995; Tortell *et al.* 1999; Wilhelm *et al.* 1998).

Even though Mn is, overall, an abundant element on Earth, it only exists in low nanomolar concentrations in seawater - < 1nM in the Southern Ocean, though somewhat higher (~ 20 nM) in the Arctic Ocean (Middag *et al.* 2011a). Mn is found as both insoluble Mn oxides, and soluble Mn ions, which are rapidly lost from the upper water column by sinking, and by uptake by cells (Sunda and Huntsman 1994). Therefore, Mn concentrations fall with increasing depth (Middag *et al.* 2011).

1.3.5 Iron limitation for life in the ocean

Bacterial communities in the euphotic zone are hugely abundant (Hobbie *et al.* 1977; Whitman *et al.* 1998) and diversity is rich (Rusch *et al.* 2007; Shaw *et al.* 2008). Competition for nutrients, including iron (Measures *et al.* 2008), is therefore extremely high (Hutchins *et al.* 1999), as has been extensively modelled by Moore *et al.* (2001). Iron limits growth of bacteria in certain parts of the oceans (Martin *et al.* 1991; Moore *et al.* 2001), as graphically revealed by the iron fertilisation experiments, IRONEX I and II (Coale *et al.* 1996; Martin *et al.* 1994). In IRONEX I, Martin *et al.* (1994) increased iron concentration 2-fold (to around 4 nM) over a 64 km² area in the equatorial Pacific. Subsequently, IRONEX II (Coale *et al.* 1996) expanded this work by using three separate iron fertilisation events (2 nM, then two subsequent additions of 1 nM) over a 7 day period. Both studies

produced large-scale blooms of phytoplankton, with a 27-fold increase in chlorophyll concentration in the case of IRONEX II. Recent research in the eastern Pacific (Boyd *et al.* 2004; Tsuda *et al.* 2003) and the Southern Ocean (Blain *et al.* 2007; Boyd *et al.* 2000; Coale *et al.* 2004; Pollard *et al.* 2009) showed massive variation in this phenomenon: persistence of blooms lasted from 2 – 50 days, and sequestered carbon levels were inconsistent. None of the studies purported to discover the fate of sequestered carbon but are considered good early studies into the principle of iron fertilisation (Güssow *et al.* 2010). The amount of iron chelation by organic ligands increased by an average of 4-fold after iron fertilisation, suggesting that these molecules are biological in origin (Rue and Bruland 1997). This increase in organic ligand production is likely due to the increase in bacterial numbers.

Since iron is so poorly available, various physiological strategies have evolved to acquire this limited nutrient. Morphological adaption to low iron conditions is exemplified by a very small cell size in the abundant cyanobacterium, *Synechococcus* (Rueter and Unsworth 1991) and in the highly abundant SAR11 (Morris *et al.* 2002). Furthermore, a 20-50 % decrease in cell volume, in response to low Fe, was reported in both coastal (*Thalassiosira weissflogii, T. pseudonana, Prorocentrum minimum*) and offshore species (*Emiliania huxleyi, Pelagomonas calceolata, T. oceanica* (Sunda and Huntsman 1995)) of eukaryotic phytoplankton.

Bactivory by the phytoplankton *Ochromonas* was shown by (Maranger *et al.* 1998) to be a major source of this flagellate's iron requirements: 'let someone else do the hard work...'.

On a molecular level, several species of phytoplankton and bacteria show adaptations in metalloprotein use under low iron conditions, replacing the photosynthetic electron transfer chain component cytochrome c-553 with a copper-containing plastocyanin, for example (Wood 1978). In the cyanobacterium *Synechocystis* 6803, this switch is regulated by the availability of copper (Zhang *et al.* 1992).

Another Fe-S-containing protein, ferredoxin, was shown to be replaced *in vivo* with flavodoxin in cyanobacteria (Lin *et al.* 2009; Mitsui and Arnon 1971; Smillie 1965), in diatoms (Pankowski and McMinn 2009; Roche *et al.* 1995), and other phytoplankton (Doucette *et al.* 1996; Entsch *et al.* 1983; Erdner *et al.* 1999; Sandmann *et al.* 1990). This phenomenon is also found in terrestrial bacteria, demonstrating that the ability of bacteria to adapt to Fe availability is clearly well conserved and likely very important.

1.4 Bacterial Iron Uptake Systems

As a result, bacteria have evolved a variety of iron acquisition strategies. Most of what we know about Fe uptake is from a number of mostly terrestrial bacteria, most notably *E. coli* and the enterics, though with others as well. These include high affinity transporters, employment of iron chelating molecules and reduction of ferric iron to the ferrous form.

1.4.1 Feo

In anaerobic conditions, iron is found in the reduced ferrous form. Obligate and facultative anaerobic species of bacteria can use Fe²⁺-specific transporters to obtain this iron (Schroder *et al.* 2003). Bacteria such as *E. coli*, *Salmonella*, and *Shigella*, which can reside in the micro-oxic conditions of the gut, use the Feo polypeptide transporters to obtain ferrous iron. The *feo* locus consists of three genes, *feoABC*. Deletion mutants in *feoB* causes lower survival rates in a mouse colon in both *Salmonella typhimurium* (Tsolis *et al.* 1996) and *E. coli* (Stojiljkovic *et al.* 1993).

The C-terminal domain of FeoB is a helix rich transmembrane domain thought to be the permease for ferrous iron transport. The N-terminus is homologous to a GTP-binding G-protein, which is proposed to provide the active transport energy (Cartron *et al.* 2006). The functions of FeoA and FeoC are unresolved, but are not required for expression of *feoB*, but are needed for iron transport functionality. FeoA interacts directly with FeoB in *Salmonella enterica* (Kim *et al.* 2012), and is homologous to the C-terminal domain of the DtxR regulator (Braun and Killmann 1999; Kammler *et al.* 1993). The sequence of FeoA is predicted to be a GTPase activating protein, and is possibly an Fedependant transcriptional regulator (Cartron *et al.* 2006). FeoC is homologous to a winged-helix domain protein, only found in the γ -proteobacteria. An alignment of FeoC proteins found 4 conserved cysteine residues, which are believed to be involved in iron-sulphur cluster binding (Cartron *et al.* 2006).

1.4.2 Ferric reductases

In aerobic conditions, the availability of ferrous iron is too low to support optimal growth of bacteria (Andrews *et al.* 2003). Bacteria can use ferric reductases to convert the relatively insoluble ferric iron

into highly soluble and more easily transported ferrous iron. All bacteria (except some *Lactobacilli*) contain iron assimilatory pathways, of which ferric reductases are a component (Schroder *et al.* 2003). All bacterial assimilatory ferric reductases are flavin reductases, using either flavin mononucleotide (FMN), flavin adenine nucleotide (FAD) or riboflavin as a cofactor. They use NADH or NADPH as an electron donor to reduce ferric iron to the ferrous form (Schroder *et al.* 2003). The localisation of the ferric reductase in the bacterial cell is linked to the assimilatory function. For the reduction of ferric iron and subsequent uptake, reductases are located on the outer membrane, or even secreted, such as in *Mycobacterium paratuberculosis* (Homuth *et al.* 1998).

Thus, a wide range of bacterial species can reduce extracellular Fe³⁺ to Fe²⁺, which they can then transport into the cytoplasm (see below). Several pathogenic bacteria (such as *E. coli, Salmonella typhimurium, Listeria* spp. and *Pseudomonas aeroginosa*), use ferric reductases to liberate Fe²⁺ from chelates such as haemoglobin and lactoferrin, enabling them to scavenge iron from their hosts during infection (Deneer *et al.* 1995; Vartivarian and Cowart 1999) and see review by (Schroder *et al.* 2003).

1.4.3 Siderophores

A commonly utilised bacterial iron acquisition strategy is *via* the secretion and uptake of siderophores. These are low molecular weight iron chelating compounds that bind strongly to Fe(III) (Braun *et al.* 1998). They were first isolated and characterised in 1952 (Neilands), and these molecules were initially called siderochromes, due to their spectroscopic properties when in complex with Fe. The exhibit significant structural diversity, but can be classified into three major groups:

The hydroxamates, these contain N-hydroxamated amide bonds and bind to iron with a hydroxamic acid functional group. This family includes desferrioxamine B, which is used as a drug to treat any iron surplus following a blood transfusion (Fernandes 2012). Hydroxamate siderophores have been shown to be produced by several marine γ -proteobacteria (Armstrong and Van Baalen 1979; Trick 1989).

<u>The catechols</u> which form co-ordinate bonds with iron using catecholate hydroxyl groups. These include the major siderophore of *E. coli*, enterobactin (Pollack and Neilands 1970)

Both types above have been shown to be produced in response to low iron conditions in many bacteria (Lewis *et al.*, 1995; Wilhelm *et al.*, 1998; Trick, 1989; Reid & Butler, 1991; Haygood *et al.*, 1993).

<u>The carboxylates</u>, which are based on the structure of citric acid, and bind to iron with carboxy- or hydroxy-groups. Examples include Rhizobactin, produced by *Rhizobium meliloti* (Smith *et al.* 1985), Staphyloferrin, produced by Staphylococcus (Drechsel *et al.* 1993) and a fungal equivalent, Rhizoferrin (Drechsel *et al.* 1995), which is the main siderophore of the Zygomycetes.

Despite their variation in structure, all siderophores bind to Fe (III) with six co-ordinate bonds with very high stability. The biosynthesis of siderophores involves several enzyme catalysed steps, and usually begins with a non-ribosomal peptide synthetase, from a variety of different non-protein amino acids (Wandersman and Delepelaire 2004). For a review of the structure and biosynthesis of siderophores see Crosa and Walsh (Crosa and Walsh 2002).

1.3.4 Other bacterial sources of iron

ferric citrate

Citrate forms the basis of most hydroxamate-type siderophores, but can also act as an iron chelator. Bacteria secrete citrate, and then use active transport systems to recover the chelated Fe (III)-citrate complex. This transport is mediated by the products of the *fec* genes in *E. coli*. Here, FecA is an outer membrane receptor which binds and internalises citrate, and FecBCDE make an inner membrane complex responsible for the inner membrane transport of the Fe-citrate (Harle *et al.* 1995).

haeme-containing proteins

Haeme uptake is best studied in pathogenic bacteria, but can also be found in bacteria which dwell in the soil, such as *Rhizobium* (Noya *et al.* 1997) and *Bradyrhizobium* (Nienaber *et al.* 2001). Pathogenic bacteria require iron to cause infection, and have a vast amount of Fe available to them in the form of haeme, which they can obtain from host haemoglobin or haemopexin (Tong and Guo

2009). Haeme can be imported in the same way as citrate, via a cognate outer membrane receptor, such as HmbR of *Neisseria* (Stojiljkovic *et al.* 1996) or HasR of *Serratia marcescens* (*Letoffe et al.* 1994). The latter produces a haeme-binding hemophore (Cescau *et al.* 2007), which is secreted out of the cell, where it scavenges haeme, and can be taken up by the bacterium using HasR. This has also been demonstrated in *Haemophilus influenza*, which produces a haemophore, HxuA, which leaves the cell, binds haemopexin, and in returned inside the bacterium using an outer membrane receptor HxuC (Cope *et al.* 1995).

transferrin, lactoferrin and ferritin

In addition to haeme, bacterial pathogens can obtain host Fe from transferrin, lactoferrin and ferritin, all host Fe-storage molecules (Cornelissen and Sparling 1994). In *Neisseria*, receptors for the uptake of transferrin and lactoferrin have been identified, and are known to remove Fe at the outer membrane, before transporting it into the cell (Legrain *et al.* 1993; Schryvers and Morris 1988).

1.3.5 Outer membrane receptors

The outer membrane of gram-negative bacteria contains various porins, which allow passive transport of small molecules (<600 Daltons). However, to transport molecules against a concentration gradient, or for molecules >600 Da in size, active transport must take place. In the case of ferric iron uptake an outer membrane receptor binds to a Fe-associated molecule, requiring physical association of the receptor and Fe. Once bound, the Fe-ligand is internalised into the periplasm, through the internal barrel structure of the receptor, using the proton motive force present on the inner membrane. This coupling of proton motive force from the inner to outer membrane requires the action of a protein called TonB (see below). These TonB dependent, outer membrane receptors (TBDR) are well conserved throughout gram negative bacteria, and are responsible for transporting a wide range of substrates – including haem, siderophores, vitamin B₁₂ (Noinaj *et al.* 2010) and even some carbohydrates such as sucrose (Schauer *et al.* 2008).

The biosynthesis of TBDR is tightly regulated, to enable a fast response to varied ligand concentrations in the environment (Noinaj *et al.* 2010).

Structurally, all TBDR's are similar, they all possess a 22-stranded β -barrel transmembrane domain, which is closed by a plug domain. The N-terminus of the TBDR has a peptide sequence which has been identified as a point of TonB interaction – the Ton box (see below) (Noinaj *et al.* 2010).

1.3.6 TonB

The proton motive force of the inner membrane in gram-negative bacteria is used to power the active transport of siderophores and other iron complexes through the outer membrane. Here, a multimeric complex consisting of 1-2 copies of TonB, and many copies of two other proteins, ExbB and ExbD, assemble on the inner membrane, but with the C-terminus of TonB extending into the periplasm (see Figure 1.1). Higgs $et\ al.$ (2002) showed that in $E.\ coli$, the exact proportion of TonB:ExbB:ExbD in each cell was 1:7:2, although this \underline{may} not be indicative of the actual conformation of the TonB:ExbBD complex. When a TBDT is loaded with its substrate, a signal is tranduced across the membrane, where a conformational change occurs in 5 periplasmic residues of the TBDR – the Ton box. This signal induces the binding by β -sheet pairing of the C-terminus of TonB to the N-terminus of the TBDR, at the site of the Ton box (Noinaj $et\ al.$ 2010). However, the exact mechanism of how energy is transduced into the TBDT is still unresolved.

The TonB of *E. coli* provides energy for all known TBDT expressed in this species, however, some bacteria have multiple copies of TonB, each of which is specific for a subset of their TBDT's (Gresock *et al.* 2011). We have noted, though, that TonB is also extremely poorly conserved across bacterial genera and much still needs to be done on this important protein in non-model bacteria (see Chapter 2).

1.3.7 ABC Transporters

Once iron, or iron chelates, are in the periplasm, bacteria use cognate Fe/Fe-complex-binding protein dependent ABC-class transporters to import the iron into the cytoplasm (Köster 2001). Such systems include Fbp (*Neisseria* spp.); Hit (*Haemophilus influenza*); Yfu (*Yersinia* spp.); Afu (*Actinobacillus pleuropneumoniae*); Piu (*Streptococcus pneumoniae*); and Sit (*S. typhimurium*) (Adhikari *et al.* 1996; Adhikari *et al.* 1995; Berish *et al.* 1990; Chin *et al.* 1996; Rakin and Heesemann 1995; Tai *et al.* 2003; Zhou *et al.* 1999). The *Salmonella* iron transporter SitABCD has since been

shown to have a far higher affinity for manganese and is likely the inner membrane transporter for this metal (Kehres *et al.* 2002).

During inner membrane transport, a specific periplasmic binding protein binds to either free ferrous Fe, or to the Fe-ligand complex, and delivers them to a cognate ABC-class transporter. Here, the ligand is transported through a dimer of transmembrane permease proteins (sometimes comprising a single "intra-molecular" dimer), powered by the hydrolysis of ATP via a specific nucleotide binding protein – see figure 1.2.

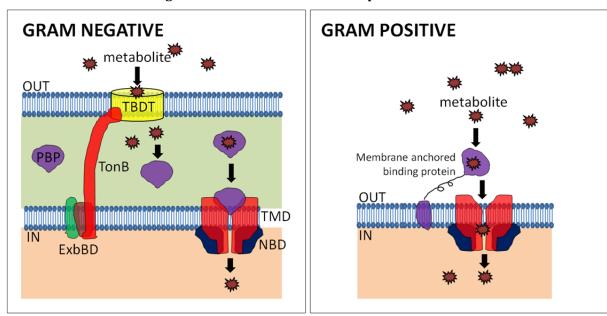


Figure 1.2 Mechanism of iron transport in bacteria

Fe, (star) is transported into a Gram-negative bacterial cell via a TonB-dependent outer membrane transporter (TBDT), powered by the proton motive force of the inner membrane, which is coupled to the TBDT by TonB and ExbBD. Once in the periplasm, the method of iron import into the cytoplasm is similar in both Gram negative and Gram-positive bacteria. Here, a cognate binding protein binds to iron (PBP), and delivers it to a permease – (a transmembrane domain protein – TMD). This internalises the iron using the energy from ATP hydrolysis via a nucleotide-binding domain protein – NBD. The entire inner membrane transport complex is known as an ABC class transporter.

In *E. coli*, the transport of Fe-siderophore complexes through the cytoplasmic membrane is performed by three different ABC-class transporters, namely Fhu, Fec and Fep, with each system comprising its cognate periplasmic binding protein, trans-membrane transporter and ATPase, and

each system having specificity to the cognate class of siderophore/Fe-ligand. The genes *fhuDCB* encode an ABC-class transporter which has specificity for aerobactin and ferrichrome uptake; The Fep transporter encoded by *fepBDGC* is specific for enterobactin (there are two genes which make up the peremease domain of this transporter) and the Fec transporter, encoded by *fecBCDE* has specificity for ferric citrate uptake.

There are examples of ABC class transporters which are capable of TonB-independent iron uptake, iron deficient growth of an *E. coli* TonB⁻ EntF⁻ strain (ARM100) was enhanced when the cloned *Vibrio fbpABC* genes were introduced (Wyckoff *et al.* 2006). This is especially interesting given that another FbpA homologue in *Neisseria shayeganii* 871 is possibly extracellular, meaning some bacteria <u>may</u> have the capacity to import iron through both membranes without the need for TonB – indeed this is the case for the Feo system.

1.3.8 Marine siderophores

The production and uptake of siderophores has been described in some heterotrophic marine bacteria, such as *Alteromonas luteoviolacea*, *Halomonas aquamarina* and *Marinobacter* sp. strains (Granger and Price 1999; Hopkinson and Morel 2009; Martinez *et al.* 2000; Reid *et al.* 1993); the lab of Alison Butler has been instrumental in furthering our understanding of siderophore production in the marine environment.

Siderophore production in the turbulent environment of the ocean is an expensive strategy for bacteria (Hutchins *et al.* 1991) and especially for smaller cells, as modelled by Völker and Wolf-Gladrow (1999). However, siderophore production increases under iron limitation (Buck and Bruland 2007); the concentration of a specific ferroxamine siderophore was found to correlate exactly with increasing bacterial abundance (Mawji *et al.* 2008), showing that bacteria do choose to use this seemingly wasteful strategy.

Interestingly, many marine siderophores are amphiphillic (Butler and Theisen 2010), containing an Fe³⁺-binding head group attached to a series of fatty acids. These include the aquachelins (Martinez *et al.* 2000), the loihichelins from the γ-proteobacteria *Halomonas* (Homann *et al.* 2009) and marinobactins from Marinobacter (Martinez *et al.* 2000), synechobactins from the cyanobacteria *Synechococcus* (Ito and Butler 2005) and ochrobactin from the rhizobiales species - *Ochrobactrum* (Martin *et al.* 2006). Intriguingly, Marinobactins can form micelles, which become compacted when bound to Fe (III). Both marinobactins and aquachelins are structurally similar to mycobactin and

exochelin siderophores produced by terrestrial mycobacteria; all have a fatty acid tail, although in the mycobacteria, these remain associated with the bacterial membrane, serving as an anchor (Martinez *et al.* 2000) – refer to Figure 1.3.

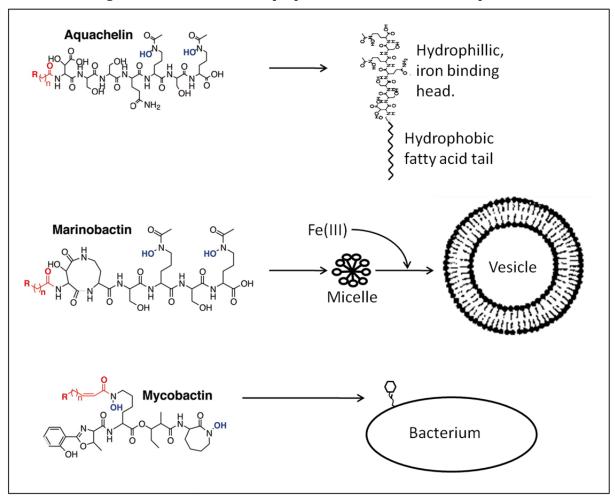


Figure 1.3 The structure and properties of three marine siderophores.

Aquachelin and marinobactin have long fatty acid tail moieties, which in the latter, can form micelles. These can aggregate in the presence of iron, to form vesicles containing large amounts of iron. Of similar structure, mycobactin contains a lipid membrane-bound fatty acid tail (shown in red) which anchors it to the cell surface. Adapted from (Martinez et al. 2000).

Remarkably, multiple Fe(III)-marinobactin complexes can aggregate into multimellular vesicles, enhanced through addition of Zn(II), Cd(II), or La(III) to Fe(III) (Butler 2005). Whether these chemical properties occur in the oceanic bacterial communities is unknown, but the phenomenon of concentrating siderophores into discrete bundles of metals for passing bacteria is intriguing.

Many marine siderophores contain a photoreactive α -hydroxy-carboxylic acid when bound to Fe(III), so that near-UV light can cause the release of CO_2 and the reduction of Fe(III) to Fe(II) (Butler and Theisen 2010), thus contributing to iron cycling in the euphotic zone (Martin *et al.* 2006).

As far as is known, it is uncommon for marine cyanobacteria to produce siderophores, and there have been no reported examples of siderophores made by eukaryotic phytoplankton (Hopkinson and Morel 2009). Siderophore uptake in gram negative bacteria has evolved to require an analogue of the TonB protein (Faraldo-Gomez and Sansom 2003), but many offshore marine cyanobacteria lack this polypeptide (Palenik *et al.* 2003; Palenik *et al.* 2006; Webb *et al.* 2001), as does the subject of this work, *Ruegeria pomeroyi* (see chapter 2). Even though these bacteria are predicted to lack the ability to transport iron-siderophore complexes, they may still acquire iron from siderophores – possibly by reducing the bound Fe(III) to Fe(II) on the cell surface as is the case in *Trichodesmium erythraeum* (Hopkinson and Morel 2009) – or these species may use a TonB independent system for siderophore uptake.

1.4 Iron storage

Bacteria cannot survive with high levels of 'free' intracellular iron, and so have evolved methods of iron storage, thus preventing iron from participating in toxic reactions. These are detailed below.

1.4.1 Ferritins

One such class of storage molecule are ferritins, which are called bacterioferritins if they contain haeme *B* (Andrews 1998; Carrondo 2003). Ferritins are multimeric cage-like structures usually comprising 12 or 24 individual subunits (Arosio *et al.* 2009), which can store up to 4500 Fe ions within a central cavity (Carrondo 2003). Ferritins can supply the cell with iron when uptake is insufficient, and can also help to buffer against oxidative damage by sequestering iron (Carrondo 2003).

In *E. coli*, a strain which contains a bacterial ferritin FtnA was shown to grow better in iron limited conditions that a strain which lacked FtnA (Abdul-Tehrani *et al.* 1999). Although, it has also been reported that many ferritin deletion mutations have no growth phenotype (Arosio *et al.* 2009).

The controlled release of Fe from the cental core of ferritins is poorly understood, but is likely to involve both reduction, and chelation of the Fe (III) contained within the ferritin. In *E. coli* bacterioferritin haeme functions as a redox centre during the release of iron (Yasmin *et al.* 2011).

1.4.2 Fe-S

Iron sulphur clusters - [Fe-S] are one of the most common protein prosthetic groups in polypeptides and serve many functions (Beinert 2000). They consist of multinuclear Fe and sulphur atoms, and are variously capable of catalysing electron transfer, enzymatic activity, proton transfer, and are also used as a sulphur donor and as a regulatory sensor for iron availability (Beinert 2000). Since both free Fe and S are toxic, the biosynthesis of [Fe-S] is carefully coordinated *in vivo* (Ayala-Castro *et al.* 2008). The biosynthesis of [Fe-S] occurs via the Suf pathway, or the Isc pathway in *E. coli*.

Here, a sulphur source (cysteine) is used to generate sulphur by a desulphurase enzyme, which cleaves cysteine to form alanine. This sulphur is delivered to the scaffold proteins (either IscA and IscU, or SufA and SufB). Next, Fe is generated from an iron source, bought to the scaffold by a chaperone protein, and both Fe and S are coordinated in the scaffold complex. This generates an [Fe-S] cluster, most commonly either [2Fe-2S] or [4Fe-4S], ready to be integrated into the apo form of an enzyme (Fontecave and Ollagnier-de-Choudens 2008; Peters and Broderick 2012).

Regulation of the [Fe-S] synthesis operon *suf* and *isc* in *E. coli* is well characterised, and has been shown to be mediated by the Rrf2 family transcriptional regulator IscR, which is in the same operon as the structural [Fe-S] biosynthesis genes; IscR binds to [2Fe-2S] and can repress the *iscRSUA* operon. This causes a negative feedback loop where *iscR* is repressed by IscR, thus limiting further repression (Ayala-Castro *et al.* 2008). However, it has been shown that apo-IscR can *induce* the *suf* [Fe-S] biosynthetic genes in response to oxidative stress. Thus, *E. coli* uses both [Fe-S] operons under different conditions; *isc* is for homeostasis of a nominal level of [Fe-S], whereas the *suf* operon is used in response to oxidative stress. Furthermore, in *E. coli*, both the *isc* and *suf* operons are

controlled by the global iron regulator Fur in response to cellular iron levels. The *suf* promoter is a binding site for Fur, so the *suf* operon is repressed in high iron conditions.

1.5 Manganese uptake

Studies on Mn import in a range of different terrestrial bacteria have revealed two, widely used, but very different transporters, termed MntH and SitABCD, with some bacteria (e.g. *Salmonella*) harbouring both systems (Boyer *et al.* 2002).

1.5.1 MntH

The Nramp family (Natural resistance-associated macrophage proteins) of transporters transports metals, with particular affinity for Fe and Mn, in many eukaryotic species. MntH-like proteins exist in bacteria, where they are termed MntH (Makui *et al.* 2000). In gram-negative bacteria, MntH homologues are responsible for high affinity Mn uptake through the inner membrane, but can also transport iron with lower efficiency (Kehres *et al.* 2000; Makui *et al.* 2000). In the α -proteobacteria *Bradyrhizobium japonicum*, a homologue of MntH was shown to be required for Mn²⁺ uptake, and is essential for growth in Mn-limited conditions (Hohle and O'Brian 2009). The gene encoding MntH was shown to be regulated by Mn via the Mur transcriptional regulator (see below). In contrast, MntH from *Bacillus subtilis* is also required for growth in Mn limited media (Que and Helmann 2002) and is regulated by Mn availability, but via a different transcriptional regulator – MntR (see below).

1.5.2 SitABCD

SitABCD is an ABC-transporter type system (see above), initially thought to be involved in iron uptake - hence its somewhat misleading acronym of <u>Salmonella</u> iron transporter (Zhou *et al.*, 1999). Expression of *sit* genes is strongly repressed by Mn in the α -proteobacteria *Sinorhizobium meliloti* (Platero *et al.* 2004), and *Rhizobium leguminosarum* (Diaz-Mireles *et al.* 2004) but by both Fe and Mn in the γ -proteobacteria *Shigella flexerii* (Runyen-Janecky *et al.* 2006) and *E. coli* (Sabri *et al.* 2006). In

the α -proteobacteria, this Mn-dependant regulation is mediated by a Fur homologue – Mur (see below).

1.5.3 MnoP

Hohle *et al.* (2011) recently described a novel outer membrane ion channel, MnoP, which facilitates Mn²⁺ transport across the outer membrane of *Bradyrhizobium japonicum*. Here, they showed that growth of an MnoP mutant strain required the addition of extra Mn²⁺ to the medium, although the mutant was not as severely compromised for growth in low levels of Mn as was an MntH⁻ mutant.

1.6 Iron and manganese -responsive regulatory systems

The importance of regulating iron uptake is paramount for bacteria; too little and the cells are starved of an essential metal, too much and they run the risk of oxidative and/or free radical damage. Here I will describe several examples of transcriptional regulators which mediate this balance.

1.6.1 Fur

The paradigm system of iron-responsive regulation in many bacteria is that of the <u>Ferric uptake</u> regulator (Fur), which has been characterised in many bacterial phyla, including the γ - and β -proteobacteria, bacilli and cyanobacteria, actinomycetes (Alahari *et al.* 2006; Delany *et al.* 2001; Fuangthong and Helmann 2003; Grifantini *et al.* 2003; Hantke 2001; Hernandez *et al.* 2004; Parker *et al.* 2005; Quatrini *et al.* 2005; Rodionov *et al.* 2006; Wan *et al.* 2004; Zhou *et al.* 2006).

Fur exists *in vivo* as a dimer, with each monomer binding to one Zn²⁺ and one regulatory Fe²⁺ ion (Cornelis and Andrews 2010). Once bound to Fe, Fur will recognise and bind to a well conserved DNA sequence— the Fur box (Escolar *et al.* 1999). Fe(II)-Fur dimers bind to a conserved 19bp sequence consisting of 3 identical and adjacent 6 bp regions. It is thought that 2 Fe(II)-Fur dimers bind to each Fur box in a 'tandem head-to-tail fashion' (Cornelis *et al.* 2009; Oeffelen *et al.* 2008; Pohl *et al.* 2003).

Fur boxes are usually found overlapping the promoter sequences of a gene, so when Fur is present, it blocks RNA polymerase therefore repressing expression of that gene (Cornelis *et al.* 2009).

The primary role of Fur is therefore that of an <u>iron-responsive</u> transcriptional repressor. The list of genes found to be Fur-repressed is usually large in any given bacterial strain and so Fur is known as the global iron-uptake regulator in these species. The genes found to be Fur-repressed usually include siderophore biosynthesis and Fe-uptake systems, acid and oxidative stress responses, energy metabolism and virulence, all of which are therefore activated in low iron conditions (Bijlsma *et al.* 2002; Cornelis and Andrews 2010; Hassett *et al.* 1996; Ochsner and Vasil 1996).

Fur can also act indirectly, by repressing secondary regulators. These include sigma factors, two component sensors, AraC-type regulators and small regulatory RNA molecules (Cornelis and Andrews 2010), and so Fur can act as an indirect <u>activator</u> of iron-responsive genes.

In *E.coli*, several genes were found to be positively regulated by Fur, including those encoding bacteroferritin and SodB (Andrews *et al.* 2003). These genes are post-transcriptionally regulated by a small RNA called RyhB, which is Fur repressed (Cornelis and Andrews 2010; Masse and Gottesman 2002). RyhB is a 90 nucleotide RNA, which can bind to complementary sequences in mRNA targets, this binding requires Hfq. RyhB has been shown to act both positively and negatively on the regulation of target genes, either by causing RNAse E mediated degradation, or stabilisation of the transcript (Masse and Gottesman 2002).

There are other known examples of metal responsive Fur-superfamily regulators: Zinc – Zur (Patzer and Hantke 1998);Mn – Mur (see below), Nickel – Nur (Ahn *et al.* 2006), peroxidase - PerR, and Fe again by Irr (see below), showing that this protein family has a key role in metal metabolism across many genera of bacteria.

1.6.2 DtxR

Some members of the DtxR-like (<u>Diphtheria toxin repressor</u>) proteins have been shown to be global iron-responsive regulators, acting much like Fur in *E. coli*, but do not have any sequence similarity. These include DtxR of *Corynebacterium*, and IdeR of *Mycobacterium tuberculosis*. DtxR of *Corynebacterium diphtheria* has been shown to regulate the expression of the diphtheria toxin, but also biosynthesis and export of siderophores, iron uptake, and haem utilisation genes (Brune et al.

2006). Similarly, IdeR was found to regulate genes involved in siderophore biosynthesis and iron storage (Rodriguez *et al.* 2002).

1.7 Iron and manganese gene regulation in the α -proteobacteria

Recently, the α -proteobacteria have been shown to be dramatically different in their Fe homeostasis, compared to the canonical systems that have been described for *E. coli*, and other taxa. These differences are introduced below.

1.7.1 Fur

There are homologues of Fur found throughout the α -proteobacteria, however, it has become apparent that *Rhizobium*, *Sinorhizobium* and *Bradyrhizobium* Fur homologues are responsible for regulation of manganese uptake (Chao *et al.* 2004; Diaz-Mireles *et al.* 2004; Diaz-Mireles *et al.* 2005; Hohle and O'Brian 2009), even though these proteins are capable of binding to Fur boxes, and complimenting Fur mutants in *E. coli* (Wexler *et al.* 2003).

These so-called Mur regulators are introduced below.

In the Rhizobiales, the role of Fur is performed by two other regulators, the Fur-family protein Irr (Iron response regulator) and the Rrf2 family protein RirA (Rhizobial iron regulator).

1.7.2 Irr

Irr was originally identified as the repressor of haeme biosynthesis gene *hemB* during iron limitation in *B. japonicum* (Hamza *et al.* 1998). Since its discovery, Irr has been studied in other α -proteobacteria, firstly in Rhizobium (Singleton *et al.* 2010; Todd *et al.* 2005; Todd *et al.* 2006; White *et al.* 2011). In *Rhizobium*, Irr binds to Fe (III)-haeme at two sites. This causes an allosteric shift in the protein which prevents it binding to DNA. Irr binds to specific sequences upstream of genes, called ICE boxes - Iron Control Element (Singleton *et al.* 2010). The deduced regulon of Irr in *Rhizobium*

includes the membrane-bound ferritin gene *mbfA*, the haeme biosynthesis gene *hemA*, and the [Fe-S] biosynthesis *suf* genes (Todd *et al.* 2006).

Secondly, Irr of *Agrobacterium* has been shown to repress Fe utilisation genes in low Fe conditions, via binding to ICE boxes and repressing the upstream genes (Hibbing and Fuqua 2011). This Irr protein also binds to two haeme molecules (Yang *et al.* 2005), thus sensing the intracellular concentration of haeme to determine iron availability.

Thirdly, Irr in *Brucella abortis* has also been shown to bind to haeme, and to regulate haeme uptake (Anderson *et al.* 2011; Martinez *et al.* 2005). However, this Irr protein appears to be unstable, and degrades in the presence of haeme, therefore alleviating repression of its target genes (Martinez *et al.* 2005).

Finally, Irr of *B. japonicum* has also been shown to be degraded when interacting with haeme (Qi and O'Brian 2002; Yang *et al.* 2005). This protein recognises ICE boxes, and represses haeme biosynthesis and iron storage genes under iron sufficient conditions (Rudolph *et al.* 2006). In addition, this Irr protein has been shown to positively regulate siderophore biosynthesis in *B. japonicum*, under iron depleted conditions (Small *et al.* 2009).

Irr appears to be a signature regulator of the α -proteobacteria, with ICE box motifs found in the genomes of many different genera (Rodionov *et al.* 2006). However, another iron responsive regulator is found within the Rhizobiales – RirA.

1.7.3 RirA

In a complex complementary set-up, Rhizobium has a copy of an Rrf2 family protein – RirA (Todd *et al.* 2002). This essentially has the function of Fur, but is absolutely not related in sequence. RirA is a transcriptional repressor of iron uptake genes in *Rhizobium* and *Sinorhizobium* (Chao *et al.* 2005; Todd *et al.* 2002). The RirA protein binds to [Fe-S] clusters and so can sense the availability of iron (Johnston *et al.* 2007). The extent of the RirA regulon in these bacteria has been shown by transcriptomic (Chao *et al.* 2005) and proteomic analyses (Todd *et al.* 2005). These revealed that, in high Fe conditions, RirA represses many genes, including those involved in [Fe-S] biosynthesis (*suf*), and siderophore and haem uptake.

The DNA sequence which is recognised by RirA was termed the IRO (Iron Responsive Operator) box (Yeoman *et al.* 2004). This is very different from the Fur box described earlier, and is shown in more detail in chapter 3.

Bioinformatic analysis of potential IRO boxes found upstream of genes revealed that there are likely many RirA regulated genes found in strains of *Agrobacterium, Brucella, Bartonella, Mesorhizobium, Rhizobium* and *Sinorhizobium*. However, the range of bacteria is limited since there were no IRO box homologues found in *Bradyrhizobium* (Johnston *et al.* 2007; Rodionov *et al.* 2006) – and indeed this strain lacks a copy of RirA (Rodionov *et al.* 2006).

Together, Irr and RirA act to regulate homeostasis of Fe uptake, and usage. Irr is active under low Fe conditions, whereas RirA is active under high Fe conditions. Together, these iron-responsive repressors can respond to the level of iron in a highly controlled and sensitive fashion.

1.7.4 *IscR*

The regulation of [Fe-S] biosynthesis (see above) in bacteria has been shown to be mediated by IscR, an Rrf-2 family transcriptional regulator (Schwartz *et al.* 2001). IscR has been shown to be an [Fe-S] containing protein, which, when in complex with this co-factor, can bind to target sequences. Homologues of IscR are found throughout the eubacteria, and form part of the [Fe-S] biosynthetic *suf* operon in the Rhodobacterales, Rhodospirillales, Sphingomonadales, Rickettsiales, and Caulobacterales (Rodionov *et al.* 2006). However, despite there being *suf* homologues in the Rhizobiales, these genes are regulated by Irr and RirA (Rodionov *et al.* 2006; Todd *et al.* 2005) and not by IscR.

1.7.5 Mur

The regulation of iron uptake and utilisation in the α -proteobacteria is vastly different from that of *E. coli* – Fur has become a manganese responsive regulator and is termed Mur.

The Mur of *Rhizobium* and *Sinorhizobium* regulates the expression of SitABCD, a Mn²⁺ specific transporter (Chao *et al.* 2004; Diaz-Mireles *et al.* 2004; Diaz-Mireles *et al.* 2005), and is not involved

in the regulation of iron uptake. The promoter of sitABCD contains a binding sequence for Mur – The MRS box (Mur Recognition Sequence) (Diaz-Mireles et~al.~2005). Homologous sequences to the MRS box are found upstream of another gene in Rhizobium – the manganese transporter MntH (see below). Furthermore, MRS motifs are found in the promoter regions of sitABCD/mntH in many other members of the Rhizobiaceae and Rhodobacterales. The prevalence of Mur, and MRS boxes has been predicted by Rodionov et~al.~(2006), and shows that Mn-responsive regulation via Mur likely extends further, to the Roseobacters, a taxonomically distinct group of marine~a-proteobacteria.

Finally, *Bradyrhizobium* sp. BTAi1 has a copy of both Mur, and another class of Mn-responsive regulators – MntR (see below) (Rodionov *et al.* 2006).

1.7.6 MntR

A member of the DtxR family of transcriptional regulators, MntR was found to regulate Mn uptake in response to Mn availability. In *Bacillus subtilis*, MntR is a Mn²⁺ dependent repressor of *mntH*, and therefore Mn uptake via this transporter (Que and Helmann 2002). Furthermore, repression of both SitABCD and MntH in the enterobacteria is mediated by MntR in response to high Mn levels (Kehres *et al.* 2002; Patzer and Hantke 2001). Contrastingly, MntR can also act as a positive regulator of the expression of MntABCD under Mn limitation (Sabri *et al.* 2006).

In the α -proteobacteria, there are few homologues of MntR, but there are several interesting exceptions.

Both *Rhodobacter capsulatus* and *Mesorhizobium loti* lack Mur, and instead have a homologue of MntR, unlike the other sequences strains within those genera (Rodionov *et al.* 2006). Here, the copies of MntR are found next to a copy of MntH – and the bioinformatic searches performed in Rodionov *et al.*, (2006) have shown the presence of MntR boxes, homologous to those found in the enterobacteria, upstream of MntH in these strains.

1.8 Marine metagenomics

1.8.1 The GOS dataset

The recent metagenomic studies produced by the Venter institute's GOS (Global Ocean Sampling) expeditions and others have produced a staggering amount of data on microbial diversity, gene frequency and indeed species and gene discovery in the marine environment (Rusch *et al.* 2007; Venter *et al.* 2004; Yooseph *et al.* 2007). The Venter institute has created a compendium of sequence data, species identification and protein families called CAMERA (Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis) (available online at: http://camera.calit2.net/), which prove extremely useful in producing data about the abundance, and diversity of marine iron transport systems. These data are easily searchable using a nucleotide, or peptide query, and the resultant homologous genes/proteins returned are accompanied by data about the sampling site location, depth, temperature and other features. This really is an amazing resource to have when studying marine bacterial genetics.

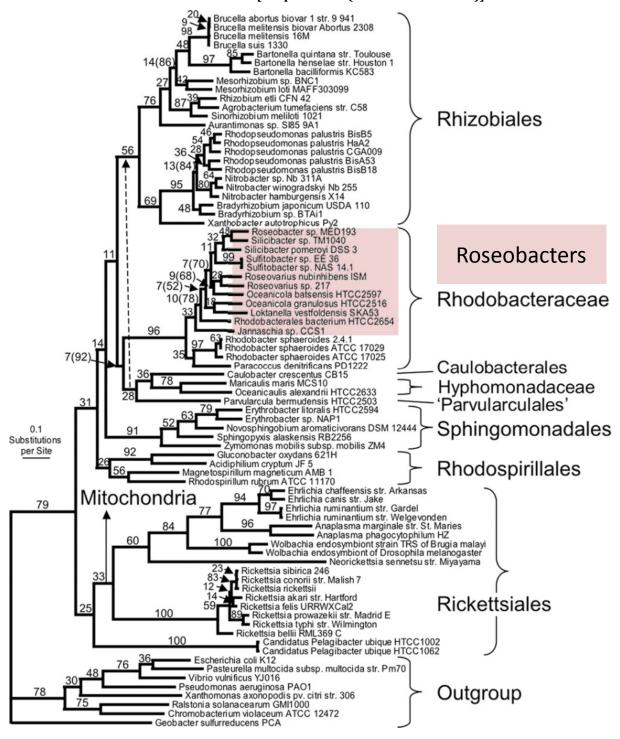
1.9 The model Roseobacters

1.9.1 The Roseobacter Clade

A subset of the α -proteobacterial Rhodobacteriaceae (refer to figure 1.4) were found to be abundant in the coastal waters of south-eastern USA (Gonzalez and Moran 1997); up to 28% of all isolated 16S ribosomal DNA sequences were identified as belonging to this group, consequently named the **Roseobacters** (Gonzalez *et al.* 1999).

The genomes of many of the Roseobacters have been fully sequenced (available at http://www.roseobase.org/), and many are easily culturable (Gonzalez *et al.* 1999; Gonzalez *et al.* 2000), making this group amenable to *in vivo* and *in silico* research. The Roseobacters are therefore a model group of marine α -proteobacteria for the study of marine iron and manganese uptake and regulation.

Figure 1.4 Tree of selected members of the α -proteobacteria, to show the taxanomic distribution of the Roseobacters [adapted from (Williams et al. 2007)].



Phylogenetic tree adapted from Williams et al., (2007) showing the taxonomic relationship of selected Rosoeobacters to a selection of the α -proteobacteria.

1.9.2 The Ruegeria and Silicibacter Genera

Members of the *Ruegeria* genus was originally classified as *Agrobacterium*, but 16S DNA sequence analysis, chemotaxonomic, morphological, and physiological studies suggested that these marine species were significantly different and were reassigned (Uchino *et al.* 1998). The phylogeny of the *Ruegeria* genus is shown below:

Bacteria → Proteobacteria → Alphaproteobacteria → Rhodobacterales → Rhodobacteraceae → Ruegeria

The main focus of this study, *Ruegeria pomeroyi* was isolated in 2003 (Gonzalez *et al.*) from seawater collected off the coast of Georgia. Originally termed *Silicibacter pomeroyi* it was the first member of the Roseobacters to have its genome sequenced (Moran *et al.* 2004), prior to its allocation to the genus *Ruegeria*, in 2007 (Yi *et al.*). Since then it has become something of a model for the genetic and genomic studies of the Roseobacters, with much of this work having been done in the Moran lab at the University of Georgia and here in Norwich. Indeed, several for the tools that were to be used for the planned work on the metallo-ome of this strain were already in place at UEA.

The closely related *Silicibacter* genus (refer to figure 1.4) includes *Silicibacter* sp. TM1040, 96% identity in 16S rDNA sequence to *R. pomeroyi* (Moran *et al.* 2007). Isolated from the dinoflagellate *Pfiesteria piscicida*, cultures of *P. piscicida* require *Silicibacter* sp.TM1040 to survive (Alavi *et al.* 2001; Miller and Belas 2004).

Despite their natural abundance in the oceans, the metal acquisition systems of the Roseobacters and SAR11 are yet to be investigated using functional genetic techniques. The deduced proteome of *Ruegeria pomeroyi* reveals has no identifiable iron transport systems other than *fbpAB* and there are no TonB homologues or any recognisable siderophore biosynthetic pathways (Rodionov *et al.* 2006). The following work sets out to identify how *R. pomeroyi* acquires Fe and Mn, and how the homeostasis of these metals is regulated.

1.10 Thesis aims

- To conduct a full study of potential iron and manganese uptake and regulatory genes in the Roseobacters using homology based searches.
- To study the predicted iron and manganese regulated genes in the Roseobacter *Ruegeria* pomeroyi.
- To elucidate the regulatory networks controlling iron and manganese uptake in R. pomeroyi.
- To analyse the transcriptional response to both iron and manganese limitation in *R. pomeroyi*.

Chapter 2 - Iron Uptake in the Roseobacters - A Bioinformatic Approach

2.0 Introduction

There has been remarkably little direct study of iron uptake genes in marine bacteria, with two, very recent, exceptions being on *Pelagibacter ubique* (Smith *et al.* 2010) and *Rhodobacter sphaeroides* (Peuser *et al.* 2011). A small scale bioinformatically-based study was performed by Hopkinson and Barbeau (2012) on the diversity of bacterial iron uptake genes in the oceans.

The work of Rodionov *et al.* (2006) provided a useful background to the work set out in this chapter, which uses bioinformatic approaches to infer some information on iron homeostasis in the Roseobacter clade of marine bacteria, Rodionov *et* al identified a range of *cis*-acting DNA regulatory motifs upstream of genes involved in iron homeostasis in the alpha-proteobacteria, including several examples of the Roseobacters. That paper also helped to expand the range of genes shown to be involved in iron homeostasis through *in silico* identification of the iron-responsive regulon of many alpha-proteobacteria.

2.1.1 Comparative genomics - bioinformatic analysis of iron uptake systems in the Roseobacters

The genes/polypeptides that were examined were in the following general classes:

Regulatory: including, Irr (iron-response regulator), Fur (Ferric uptake regulator) and RirA (Rhizobial iron regulator).

Receptors for siderophores, haem and haem-containing molecules, citrate and vitamin B₁₂.

Siderophore biosynthetic genes, including those for enterobactin (Ent), vicibactin (Vbs), aerobactin (Iuc), rhodochellin (Rhc) and vibriobactin (Vib).

TonB and ExbBD - energy-transducing proteins.

Ferrous uptake (Feo) and ferric reductase (Mtr and Fer) polypeptides.

Others, which include the 'iron regulated protein' IrpA.

These are presented and described in more detail, below. Note that a similar survey was presented by Hopkinson and Barbeau (2012) but with much less scope and detail as far as the Roseobacters are concerned.

Table 2.1. Bioinformatic study of iron uptake genes in the Roseobacters

The protein-coding sequences of each gene listed were used to interrogate the Roseobase BLAST database for each of the organisms shown in the table. The resultant 'E-value' output was used to populate the table, and colour-coded according to the level of homology: red for "poor", yellow for "moderate", and green for "good".

	Дахэ	16.19	46.22	65.18	1E16 6E04 6E04	4E19	3533	76.18	6E-17	3E16 6E15	55-16	SE-19	1616	85.17	2E-19 SE-04 1E-03	\$6.17	SE 19	75.21	16.19	7E-18	16.17	76.21	3£.16	3E-40 6E-21
sfer	gqxə	16.28	45.28	1627	SE-31	16-26	35.57	2E-31 6E-13	16-33	3E-31 6E-31	36-31	0E-36	2E-30 7E-13	SE-30 3E-13	4E-30 3E-14	SE-33	25-27	1E-29	36-31	2627	1627	6E-28	2531	5E59 4E28
Energy Transfer	anot	26-10	2E-24 1E-11 2E-10	16-14	46-14	3E-28 8E-12 5E-11	1E-10	26-12	4611	26-11		2E-23 3E-10 4E-10	3631	1631	3E-10			16:14	SE-10	3E-12 SE-10	76.40	16-10	1E-10	36-21
rgy	Dlot	4.00E-58	4.00E-55 3.00E-10	7.005-58	4.000.59	8.000.61	5.006.27	1,006-62	2.000-60	4.006-59	1.006-57	2,006-59	1,000.40 9,000.10	100E-60 900E-10	3,006-61	\$.000.63	4.00E-60	8.005-61	S.00E-60	\$.00E-56	1.00E-56	1.00£-57	3.00E-58	2.00E-59 9.00E-28 5.00E-10
Ene	Rlot	1006-37	4.00E-32 2.00E-04	1.005.30	2.00E33	7.00E28	2.005.30	1.00E32	100£31	600E34 200E31	3.00E-29	6.00 £ 29	2005-04	1.005.04	200E04 400E04	3.00E32	9.00E33	200534	8.00E.34	3.00E-30	100530	2.00E-28	3.00F.33	100E35 200E18 0006
	Alot	7.00E.21	2005-15	1.005-14	1001-19	2.005-20	7.006.17	1006-16	100518	2005-09	1.000.09	\$2006-20 1006-12 1006-11 2006-08	3006-16	2005.16	4005:14	3.00£-14	3.005.09	3.00E-13 8.00E-12	4.006-19	2.005.10	600615	S.00E.17	\$ 00E.17	2.00£14
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educ	graf	9E34 6E20 2E02	16.15	45.14	7E15 SE06	1E19 7E07 2E04	SE03	2E.18 3E.04	35.02	SE14	75.18	16.18 16.02	36.12	4614	76.15	6E-15	76.13		35-03	26-13	36.12	46.12	88-17	4E13 7E13
ricR	A19	25-20	36.36	26-22	46-32	16:39	1E-39		26-41			1642	2E-38 8E-33 6E-25	7E39 2E33	3E-36 1E-26	36.37	16:37	36-18	9E-34	8E-43 4E-37	2E-41 1E-37		46-33	26.32
프	Нірү	2E-39 4E-19 1E-00		35.02	\$6.01	1E-22 2E-03 2E-03		2E-19 2E-16 1E-00	6E-01 6E-01			46.23	3E-20 3E-04 8E-01	SE-20 6E-04 1E-00	96-19	3£-23		35.20	16:00			16-01		46-01
	Inmi	8.00E-81 1.00E-07 1.00E-05 6.00E-04	1005.80	8005.88	3,000:72	6005.84			5000	0.002		8.00E-48 1.00E-13 2.00E-05	7,000-05	7.006.05					7.006.07	2005.86		8 005-09	4 0 0 6 0 5	3000.04
	Auty	15.28	35.25	95.28	6522	2E28	75.28	4E-28 1E-14	1518	15-28 95-23 55-16	2E-26 8E-26	6£29	2E-28 2E-12	25-28	2631	35-22	6532	35.26	45.26	8E-29 8E-16 2E-14	36.14	6E-27	25-24	7E14
10)dqf	9E-71 2E-70 SE-69		95-88				46.85	26-71	4E-69		3£-73 5£-73 6£-71 4£-69			16-69	8E-73	16-72 26-72 16-71	1E-103 1E-70 SE-69	16:70	35.98	15.68	SE-75 7E-69	96-71	69-36
orten	gdqf	26.23		0E:00			76.26	46-52	26.20	3E-54 7E-28	25-32	21:38	6F.30 SE-2S	46.24	26-32			36-41	46-27	0E+00 7E-53 4E-21	3E.32 SE.21		28-19	16-25
nspo	Addt	1E-15 1E-11 2E-08 SE-08	46.08	15107		8E-41	75.07	SE34	36.22	15-19 45-08	35.06	25-08 15-06	8E-17 2E-09	26.09	16.06			15.109	25-09	7E-13 7E-18 8E-09 2E-07	1E-114 1E-09 1E-07			SE-08
ABC Transporters	₽dəĮ	15-41 8 5-41	3534	4E-41 1E-40 SE-35	SE37	6E41 2E38		3533	46-42	35.40		2634 2634	26-51	76-53	15-48				76.39	9E39 7E34		26.38	8F41 1E33	9E37
AB(Qq9{	3E-56 1E-45 2E-41	76.37	3£41 7£39	16-39	2E-48 2E-42 8E-38		3£66	36-52	36.42		7£-44 1£-40	32.54	36 <u>86</u>	SE-35					4£40		1E-42	3£-57	76-45
	⊃dəĮ	26.74 76.43 16.41	1E-35	96-54		46.55		9E-78 4E-45	26:33	46:37		2E-47 3E-43 7E-41	SE-38	4E-79 2E-34	16-37					16-33	36.36	3£-36	1E-68 2E-33	
	gdəf	35-05 25-03 55-03 15-02		75.09	6£02 7£01 1500	66-07		25.03	2E-04			70 30 E	1E-03 3E-01 9E-01	35-01	3E-02	25:00			96-01	SE-01	45.01	36-01	26-02	26-02
	ฎทพบุ	100566 100510 100507	00E-127	005-148	00E-154	100E72		1.00E-12		005.174		1006-25 1006-22 1006-07	1006-08	0005-06	100611					100564			1	
	Z6TZ_uppM	0.002	000E-12	-	90500	6000	2006.21	1006-35	9700	0000		0022	000:42	100 44	1006.34					6000	022			\$000.00 \$000.00 \$000.00
	Auių	7E-16 1E-11 7 6E-09 1E-06 3E-04	2E-08 2	80-35	46-16 2		45.04	25.00		76:10		1E-25 5E-09 1E-05 2E-03	25.08	26.09 86.09	36-08					36-12				3E31 8 6E28 8
	Anda	55.32 25.27 65.22 25.08	26.23 36.14	SE-61	8E-55	3£34		25-23 26-15 26-15		15.64		5£40 4£28 9£21 2£18 1£14	9E-32 2E-09	46.32 26.09						0E+00				4521
STS	рагу	5E-12 4E-06 8E-05	25.39 25.08	36-23	3£27	SE-11	36.0 <u>3</u>	26-14		16-31		2£-47 2£-14 3£-13 2£-05 6£-05	46-15	38.47						8F40				85-08 15-05
eptc	Auvt	4£-20 4£-11 2£-06 6£-06 8£-06	90 39	36-14	16:06		16.04	26.05		80 35		76-15 66-12 26-09 16-08	16.09	76-10	1E-04					SE-10				6E-11 4E-09 9E-07
e rec	Avql	16-117 16-107 36-10 16-04	1E-15 1E-05 6E-05	26-06	36-08		26-23	46.83		76.07		16-104 16-06 16-06 96-06 26-04	06-35 35	25.91	46-91	\$6.01				9£-07				1E-23 8E-18 4E-13
bran	Atql	26-33 26-22 36-04	15.04 85.03 35.02	26.02	90-99		15.13	98.37	2602	2501		45.08 45.07 25.06	7E36	26.36	1E35 2E01				75.02	26.03				SE 18 2E-06 SE-03
nem	Ліду/иі}	8E-43 8E-06 1E-03	1508	16.05	36.08		8+36	7£.04		66-11		7£39 3£04 2£03	1E-2 S	SE 27	35.2.5					1603				0£+00 6£-09 6£-08
ıterı	Buiv	1E-15 1E-13 2E-00 8E-00		46-73		1E-72 2E-07		1E-14	86-23			1E-15 3E-00	26-13	36-13	2E-14	16.06	00-38	25.74		85.400	16-01	46.00		35:400
nt or	Auiv	3E-12 3E-03 5E-06 3E-04	4E.06 2E.03	15.04	45-08		90 36	80-36 80-36		3£.07		96-19 26-11 36-05 16-02	36.08	36.08	25.05					16.00	_			2E-10 4E-10 2E-02
suda	Aqət	1519 9518 2617 1511 7610	46.13	36.05	SE08	16.07	5095	16.11		1610		36.76 26.23 46.09 16.07	46.07	4607	16.06					1E-13				66-25 16-21 16-06
debe	Asel	1E-144 3E-71 1E-09 2E-02	25.09	26-05	25-17		38.25	2E-03 6E-01		6038		3E-68 4E-10 8E-09	16-91	1501	16.87					76.08				1E-23 1E-13 8E-06
TonB dependant outer membrane receptors	Ario	16-19 96-18 26-17 16-11 76-10	46.13	36-05	\$6.08	16-07	50 35	26.06		16-10		3E-76 2E-23 4E-09 1E-07	10 at	46.07	16.06					16-13				6£-25 1£-21 1£-06
	Опшч	16-114	16-56	16.112	16.117	15103				96-56		1651 1651 1651	1655	1E5S	16.53				16-50	16-56	2E-56	46-56	SE-55	2E-56 SE-52
	Butd	45.67 25.09 15.08 85.07 35.06	\$6.12 \$6.04		3502		2602	95.04 SF.01		1674		35.25 15.06 35.06 15.01	75.04	1603	35.03	16:01				7607		35.02		2E-80 SE-41 4E-04
	∃nųf	1E-33 3E-30 3E-05 7E-05 1E-02	26.04	16-04			16.22	36.25	86.02	36.03		1E-32 9E-08 5E-06 1E-05 7E-03 9E-03	46.35	1E3S	26.32									2E-18 SE-10 SE-03
	Auft	1E-107 2E-91 3E-10 1E-04	1E-15 1E-05 6E-05	26.06	35-08		26.23	46.81		76-07		16-18 16-18 16-06 96-06 26-04	06-35	26-91	46-91	10-35				20-36				16-23 8E-18 4E-13
	/					4										33	0.	55						
	Gene Name Species	Citreicella SE45	Dinoroseobacter shibae DFL 12	Jannaschia sp. CCS1	Loktanella vestfoldensis SKA53	Maritimibacter alkaliphilus HTCC2654	Oceanibulbus indolifex HEL45	Oceanicola batsensis HTCC2597	Oceanicola granulosus HTCC2516	Octadecabacter antarcticus 307	Octadecabacter arcticus 238	o Pelagibaca bermudensis HTCC2601	Phaeobacter gallaeciensis 2.10	Phaeobacter gallaeciensis BS107	Phaeobacter sp. Y41	Rhodobacterales bacterium HTCC2083	Rhodobacterales bacterium HTCC2150	Rhodobacterales bacterium HTCC2255	Rhodobacterales bacterium KLH11	Roseobacter denitrificans OCh 114	Roseobacter litoralis Och 149	Roseobacter sp. AzwK-3b	Roseobacter sp. CCS2	Roseobacter sp. GAI101
	Spec	Сй	Dinoroseo	Jann	Loktanella	Maritimibacte	Oceanibu	Oceanicole	Oceanicola	Octadecab	Octadeco	Pelagibaca l 8	Phaeobact	Phaeobact	Phae	Rhodobactera	Rhodobactera	Rhodobactera	Rhodobacte	Roseobacte	Roseobac	Roseob	Rosec	

	Дdхэ	2E-19	16-19	4E-19	2E-20 2E-05	16-21	26-19	SE-19	2E-17 5E-04	15-19	1E-19 5E-04	1E-37 5E-19	4E-41 7E-21	4E-41 7E-21	16-17
fer	вахэ	1E-30 3E-14	9E-30 7E-14	4E-27	2E-27	2E-26	3E-30	7E-30	6E-31	8E-31	4E-31 7E-14	ZE-57 7E-30	7E-56 6E-29	2E-57 6E-29	2E-30
rans	anot	45:30	6E-28 4E-13	2E-15 7E-13	3E-15 9E-10	8E-12	1E-10	5E-14 1E-11	76-10	4E-13	2E30 5E-13		4E-13	4E-12	8E-17
Energy Transfer	Dlo 1	2.00E-61	1.00E-60	7.00E-S2	1.00E-57	7.00E-57	2.006-59	1,005-61	2.00E-60	5.00E-60	S.00E-60	6.00E-62 3.00E-28	6.00E-59	3.006-27	2.00E-60
Ene	Riot	2.00E-29	2.00E-30	1.00E-27	1,00E-33	5.00E-34	5.00E-34	1.00E-35	5.00E-33	1.00E-31	1.00E-31	2.00E-38	1.00E-33 2.00E-19	1.00E-33 2.00E-19	1.00E-30
	Alot	S00E-18	2.00E-16	5.00E-15 2.00E-08	3.00E-20 1.00E-10 1.00E-08	S00E-18	2.00E-18	200E-26	3.00E-13	2.00E-16	2005-17	4005-17	1.00E-16 2.00E-08	2.00E-16 2.00E-08	7.00E-16
v	Brtm	3.1	6	3.1			S								
tase	Artm				3.6		0.017	1.2							
onpa	gr9{		2E-17	2E-14	65:12	16-12	35-13	15.17	46-15	35.16	4E-23 1E-16	8E-33 7E-13 2E-06	4E-02	4E-02	1E-17
Ferric Reductases	A19₹	2E-37 6E-28	7E36 3E-25				66-35	2E-22	2E-42 8E-32	26-35	2635	3E43 1E21 7E20	2E-33	3633	46.34
Fer	Н[рү	3E-15	SE-12		3E-22 7E-02	26-01	8E-17	16-01	8E-30		1E-14	3E-01 8E-01	3E-08	2E-08 1E+00	1E-16 1E-12
	Inmy	.006-71	00E-76 00E-06 00E-04	006-08	.00E-80	006-80			.00E-78	0.024	5.00E-86 1.00E-09 0.001 0.011	.006-08	008-86	0.024	1E-136 0.024
	Autγ	1627	66.26	2E-27 S	16-30	16:30	6E-24 6E-13	2E-27	2E-29	8E-27	8626	1E29 1 6E14 1	8E-27	2627	7E-30
)dat		35.70	1E-70	1E-77 9E-74 2E-71	3E-76 3E-72	1E-101	2E-71 6E-70		45-70	2E-75 4E-72	1E-106 1E-71			
ABC Transporters	gdqf	3E-29 4E-23	ZE 37				0E+00	2E-25	9E-24	SE-29	2E-56 2E-33 5E-30 5E-25 8E-20	0E+00 4E-46 1E-21	2E-29 3E-25	SE-29 3E-25	
odsı	Aqdt	4E-18 3E-12		2607	3506		E-115	45.09	7507	5E-21 5E-10	26-21 46-18 16-12 16-08	F-133	1E-19 3E-09	4E-20 2E-09	2F.08
Tran		2E-48 3E-38	1E-47 2E-38	16.33	35-41	1E-39 2E-39	3E-48		1F-38 2F-33	1E30	9E-53 4E-45 4E-39 1E-37	2E-40 3E-35	2E-37 1E-35	5E-37 3E-36	4E-44 5E-40
ABC	5d9f	2E-49 2 3E-42 3	6E-51 1 8E-43 2 9E-37	2E-40	SE-43	2E-42 1 4E-37 2	4E-47		2E-41 1	3E-38	2E-47 4 6E-40 4 8E-40 1 4E-37	7E-42 3	3E-46 2 1E-39 1	6E-46 S	3E-42 4 2E-41 5 2E-40
	□ də}	2E-75 21 1E-41 31 4E-37 8E-34	9E-43 81	3E-39 21 3E-37	SE-46	4E-34 21	6.76		4E-34 28		35-78 11 88-76 21 15-41 66 25-40 88 6F-36 44	E35	9E-38 31 4E-35 18	1E-37 6i 4E-34 4i	9E-38 31 4E-35 21
) dəf	11 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	10	38	20:	4	200		q	10-3	3E-08 3E 2E-02 8E 5E-02 1E 1E-01 2E 4E-01 6E	£0.	010	10.01	9 4
	aga€	15 2E	81 6E 15 7E 14	22 22 22	89	69	39 38		22	62 2E	20 26 20 26 19 56 13 16 07 46	32 25	77 11	75 1E	0
	ฎทพบุ	3.00E 3.00E 3.00E	42 3.00E 02 7.00E 49 2.00E	1.00E 4.00E 8.00E	100E	7.00E	0 88		5.006	2.005	28 3.00E 28 3.00E 25 6.00E 04 5.00E 07 2.00E	25 2.00E	27 8.00E	34 8.00E	8
	Maqu_2192	8 2.00E 4	0 400E-4	<u> </u>	9 e00E→		7.00E-		q.	9	2 2.00E-31 9 1.00E-28 8 1.00E-25 6 3.00E-04 4 0.076	3 2.00E-	2 3.00E-3 9 1.00E-2 4 1.00E-2	5 8.00E-3 0 7.00E-2 M 9.00E-2	9 7.00E-(
	Anių	36.0	3 3E-05 6 1E-02	2 2 2 5 6 6	SEC		3E.(SEC	8 SEC	65-17 5 2E-05 7 3E-06 8 3E-04	166	5 5E-0	3E-15 3E-10 5E-04	SEC
	Anys	1E-20 1E-20 3E-17	6E-41 4E-23 1E-16	2E-44 4E-32	35-3	2E-37			8E-3	2E-3	5E-40 1E-35 6E-34 9E-24 7E-08	2E-0	7E-10	5E-3	45.6
tors	уагу	2E-13 6E-03 1E-01	4E-15 3E-17 4E-08	2E-16 4E-14 1E-13	4E-20	16-18			2E-1	16-18	2E-58 3E-10 7E-00	4E-0	2E-1; 3E-0; 4E-0!	2E-00	3E-3(
dese	Auyl	6E-12 4E-05 1E-04	8E-09 1E-07	1E-08 2E-06	4E-11 2E-07	16.08	9039		8E06	SE06	4E-18 7E-18 2E-09	2607	7E-10 3E-09 4E-06 1E-04	6E-11 3E-09 4E-05 1E-04	60-39
ne r	Avqt	35-89	3E-11	16.04	1E-101 6E-05		1E-100		65.08		1E-109 2E-78 3E-76 7E-07	4E-20 5E-01 5E-01 5E-01	1E-106 1E-73 4E-27 2E-01	1E-108 6E-74 7E-28	1E-09
nbra	Atqt	3E-33 4E-02	1E-35 7E-02	6E-03	2E-36		1E-27	9E-02	ZE:01		2E-31 2E-24 1E-19	1E-16 6E-04 2E-02 2E-02	1E-38 2E-23 8E-19	1E-39 2E-23 2E-18	4E-02
men	Jidy/uñ	3E-26 2E-03	1E-26 1E-03	2E-07 6E-05	4E-30 SE-07	1E09 8E05	3E24		1E08		4E33 2E-27 1E-23 5E-05	0E+00	7E-34 1E-18 5E-05	0E+00 1E-32 5E-19 5E-05	25.07
uter	Buiv	2E-10 8E+00	8E-10 1E-00		1E-12 3E+00	8E+00	2E-10		76-89	3E+00	2E-07 4E+00		3E+00	3E+00	3E-78 1E-52 7E-08
int o	Auiv	4E-09 4E-05 2E-04 SE-04	2E-08 6E-06 4E-03	3E-14 7E-11			4E-10		16-10		9E-13 2E-12 1E-08 8E-04 7E-03		1E-11 6E-10	6E-10 9E-08	8E-07
enda	Aqəl	2608	2508	3E06 1E05 4E05	2E-13		15.06		7607	4605	16-12 36-09 46-08 26-06 16-05 26-04	46.07	9E-16 4E-07 3E-06 5E-06	2E-14 4E-07 2E-06 4E-05	15.08
deb	Asst	3E-86 4E-02	15-86	20-39	2E-73 1E-05	35.02	16-78		7E-02	SE-04	05-00 7E-77 2E-54 1E-10 8E-01	2F-20	7E-69 5E-61 5E-29	1E-70 1E-62 9E-29	2E-06
TonB dependant outer membrane receptors	Ario	25-08	25-08	3E-06 1E-05 4E-05	2E-13		1E-06		7E-07	4E-05	1E-12 3E-09 4E-08 2E-06 1E-05 2E-04	45-07	9E-16 4E-07 3E-06 5E-06	2E-14 4E-07 2E-06 4E-05	1E-08
	Дпш ү	3E-50	2E-512 2E-53 4E-51	6E-53	1E-109	1E-106 7E-56			1E-108 7E-56	1E-108	4E-57 6E-52 6E-52	6E-55 1E-54	1E-109 8E-57 SE-52	1E-109 6E-57 SE-52	1E-118 4E-55
	Butd	35-04	2E-04 7E-04 5E-01	6E-03	SE-07		2E-04	2E+00	15.04		2E-11 1E-07 7E-05 2E-05 4E-01	35-07	3E-08 8E-05 1E-02	3E-08 8E-05 7E-03	35.04
	3nyf	7E-35 3E-04 3E-02	2E-33 1E-06 6E-02 8E-02	3E-06	4E-37		6E-34				4E-35 1E-32 4E-25 4E-06 1E-04	26-24	5E-40 8E-31 7E-21 3E-03	5E-39 8E-31 6E-20	8E-10
	Andt	3E89 1E02	35-11	15.04	6E-05		1E-100		80-39		1E-109 2E-78 3E-76 7E-07	4E-20 SE-01 SE-01 SE-01	1E-106 1E-73 4E-27 7F-01	1E-108 6E-74 7E-28	1E-09
	/														
	Gene Name Species	Roseobacter sp. MED193	Roseobacter sp. SK209-2-6	Roseovarius nubinhibens ISM	Roseovarius sp. 217	Roseovarius sp. TM1035	Ruegeria lacuscaerulensis ITI-1157	Ruegeria pomeroyi DSS-3	Ruegeria sp. R11	Ruegeria sp. TM1040	Ruegeria sp. Trich CH4B	Sagittula stellata E-37	Sulfitobacter NAS-14.1	Sulfitobacter sp. EE-36	Thalassiobium R2A62
				<u> </u>		49	Rue								

					ιΣ	dero	phore	Bio.	synth	esis	/Tra	Siderophore Biosynthesis / Transport	t							<u> </u>	Iron Responsive	pons	ive		ō	Other	
			主	HYDROXAMATES	KAM	MES							CATECHOLATES	8	A	S					Kegulators	ator	ın.				
Gene Name Species	Dsdv Dsdv	Asdv	Asui G.	Boui	Osui 	gnųf	2nuf	anuf	крсв	ошл	∃div	Adiv	Stn9 / Abdy	Atns	gjuə	Эţиə	Q tuə	3ju9	∃tn∋	Arir	ınm	Rosi	ınş	Aqri	8q7i	Aoəł	Boəł
Citreicella SE45	200E04 0.13 0.37 0.62		8			0.21 3.00E-34 0.21 3.00E-33 2.4 6.00E-32	E34 1.00E-52 E33 3.00E-42 E32 7.00E-38	42 42	300E33 \$00E32	23 S S S S S S S S S S S S S S S S S S S	1 0E+00 3 2E-50 9 2E-47	65.28	26-24	4E-30 5E-28 6E-28 8E-28	26.08 26.06 16.05 46.04	36-18	26-24	1E-133 7E-37 6E-36	06-00 8E-53 6E-43	2£25 2£20 1£12 2£07	9E.29 7	2 t 20 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	1 F 0 7	F31 161 200 200 200 200 200 200 200 200 200 20	8 8	8 9 1 s	4006
Dinoroseobacter shibae DFL 12	0019					3009	E34 2.00E	2	22	vi	8637	3627		2633	10 39	25:18	26.07	2E-36 SE-34	26.36	25-26	2605	# E 30	8507 1	E41 1E4 E06 2E4	2 2 00	m	3005
Jannaschia sp. CCS1	4.005.04	9				4.00E-3	E-40 S.00E	46 00	06 800E:	2 5	3 SE42		36-14		35.03	15:16			16.33		25.49	26.30	1662 2	6.45 1E.1	73 0.01	4 00	1 2006
Loktanella vestfoldensis SKA53						800	F:32					2625	25.07		35.04	25:16		1E:34			45.48	76.32	\$ 29	643		90	3,0000
Maritimibacter alkaliphilus HTCC2654	0.043			15	3.2	0.62 1.00E-3 0.62 5.00E-3 6.9	E41 6.00E	00	3006	1	2 2 5 3 7	16-28	\$6.63	3E-29	16-03	46-18		3E-32 3E-32 1E-31	16-33	2E-16	4E36 9E03	SE 32 1E 06	3 5 5 3	E33 1E4 E05 3E	3000	2 3	3 4 000
Oceanibulbus indolifex HEL45						2.4			4006	20 S	86.58		06-24 36-12 96-12 16-10			26-18	2E:34		2£49		65-44	1631	25.66	E-05 2E-	00 1	2 2	3 1006
Oceanicola batsensis HTCC2597	0.48					0.001 7.001 0.005 0.0073 0.28	6.000	5 S	21 6 0 0 F	2	et 19	1F28 2F28 2F26		\$E:30 3E:29 1E:27	SE-04	46-16		1E48 2E38 8E36 2E35 4E32		45.16	SE-40	16.28	1564	F3			3006
Oceanicola granulosus HTCC2516	530		<u>7.8</u>			24 200	1.000:36	37	8 3			1627	16-10	9E-31 2E-29 2E-28 8E-28	76.05	26-17		<mark>36-32</mark>			4E-44 8E-05	1E33 4	1E-58	F41 F03	20	8	1005
Octadecabacter antarcticus 307			77			200	5300	41	\$ 00E.	8 8	3 8E-4C	26.2.4	66-10		76.06	SE-17		56-37	66-36	86-19	3E-45 3E-24 1E-06 SE-05	5E33 7E22 2	2E-57 11	E-44 1E-1 E-23 1E-1 E-07 3E-	99	8 8 1	2 10054
Octadecabacter arcticus 238	7			2.5						5.		8526		25-27	80-36	26-17					4E-45 a	1633	2E.59 9	E-43 1E-1	69 1	3 0.6	1 2.005-4
Pelagibaca bermudensis HTCC2601	0000					021 021 800 021	F32 8005-34 2.005-37	6006 42 87	2006 2006	8 8	26-40 26-40	35.26	9E-23 4E-08	26-38 66-28 86-28	8	35-14	700	1E 43	26-55 40 40-55 40 40-55 40 40-55 40 40-55 40 40-55 40 40-55 40 40 40 40 40 40 40 40 40 40 40 40 40	26-21 16-19 16-07		2 2 2 2 3 3 3 3 3 3 3 3 3 3	3	25. 25. 25.	8 8 8	•	8 4 4 3 8 8
Phaeobacter gallaeciensis 2.10	0.16	3 3	1000:19	* 9	006.48	100	1.00E-38 1.00E-51 1.00E-31 6.00E-39 8.00E-39	38 38	\$00E-99 \$00E-34 700E-37 \$00E-34 100E-30	0 4 6 4 O	2E54 2E41 3E39	3£26	36-14	26.28	15.04	96-15	21.65		4£85 1E-48 0E-35 2E-33 1E-31	8E-25 2E-15 3E-14	<u>9€44</u>	1630	9	[42	22	1	3005
Phaeobacter gallaeciensis BS107	0.28	4 K	7006.11	2 2	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4000	E-38 600E-52 E-32 100E-39 700E-36	38	42 200E97 400E53 200E35 800E35	2 2 9 10	2E90 4E53 3E41 4E39	1625	1E-14 8E-10	16-27		46-16	31.66	16-33	8E-34 8E-34 8E-34 2E-32	8E-25 4E-14	7E-44	1630	7 E 68	E41	**		\$00E
Phaeobacter sp. Y41	0.001 0.074 0.096		33		32	2006	E36 S00E	444	300E3	55	8E56 2E36 1E34	76.25	7£-14 1£-09 3£-08	46.28		16-17	16:00	7E-45	3E.55 3E.35	3£26	2E-46		25-62	E-42 1E-1	24		\$ 000 E
Rhodobacterales bacterium HTCC2083	0.043			43					6.00E-1	7. % 3. 3.	3549	\$£.25 7E.25	36.40	6E-28	16.08	16.17	16.21	16:31	26-50	7E-15 6E-14	86-43	\$ 203	16.30	E-40 1E-1	8 8		1,000
Rhodobacterales bacterium HTCC2150										2									Tr. Or					16.	SS		
Rhodobacterales bacterium HTCC2255		•										16.28	26-74					26-32			45-42	36.29	35-56	£43			10064
Rhodobacterales bacterium KLH11	037		11		9.4 6.0	2003			3005	2 2	38-49	\$6.25		5E-31 5E-28	46.09	26.16	26-00 36-00 56-00	and a	SE-60 3E-44	6F-22	2E-44		1E-79	16-4	28	~	3 30054
Roseobacter denitrificans OCh 114	0011	82				200E-34 200E-32 800E-32	F34 800E	42	•	000	E 00.4	16.25	46.09	16-29	16-01	SE-17		1E-42 SE-32		3£24 1£16	6E-46	3 E 31	3506	16.	8	s	2005
Roseobacter litoralis Och 149	910					800	1006	9			4 4	16.25	76.09	26-38	7£ 06 4£ 05 6£ 05	26-17		36-42		3E10	16-45	£ 3	25.06 25.06	<u>2</u>	8 6	vo so vol	1001
Roseobacter sp. AzwK-3b	2.00E.04 0.043			H		100	E-31					15.26	45.09			26-18		2E-34	96:33	76.21	1E-46 8E-06	15.31	15:67 4	E-42	000	8	3 2006-0
Roseobacter sp. CCS2			8.7			300	E-33 2.00E	9 8	1006		66-97		36-13			7536		06:33	88-33 88-33	8014	35-46 	07 -37	000	\$ 1	o e	2 7 6	2
Roseobacter sp. GAI101									2.00E-4 2.00E-4	S 0 4	9 16.57 66.56 9 26.48	26.27	26-23	2E-30 SE-28	26-22 96-11 16-04 16-04	96:47		7E-40 1E-31	2E-57 9E-52 7E-43	1623	86-24 86-24	35.31 2 35.10 4	5 6 64 1 5 08	25 JE	8006-5	S S	2 2006
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Jer		Aoəŧ	23		2.3	1.8	0.47	1.8		3	2.3	5.2		2.3	2.3	
Other		Bqri	7.005-85	2005-86	13	6.00E-48 0.78	3.005-49		0		3.9	23 23 5	13	1.00E-21 2.00E-13 0.07	2.00E-56 0.2 0.78	0.16
		Aqri	1E-174	16-172	15-176	1E-161 1E+00 2E+00	1E-160	16-170	0E+00 2E-01 4E-01	16-177	16-173	25.1.31	1E-179	1E167 2E+00	1E-168 2E+00	1E-168
a		ınf	3E-41	9E-43	16-42	9E-41	2E-41 1E-04	25-43	3E-42	8E-42 2E-04	1E-39	1E-40	2E-41	2E-32 6E-05	1E-22 6E-05	7E-43 SE-06
onsiv		Assi	45-70	25-68	3E-64	2E-64	2E-66 9E-06 2E-05	6E-74	16-71	\$E-62	2E-68	1991	2E-65	15-65	99-34	99-39
n Responsi Regulators	,	irr	9E-32 1E-06	3E-31 1E-06	56-30	6E-31 1E-06	2E-31 1E-07	6E-31 2E-07	3E-31	1E-29 2E-07	1E-31	76-37	2E-27	4E-31 4E-10	4E-31 3E-10	2E-31
Iron Responsive Regulators		ınıı	8E-46	3E-44 4E-05	16-45	3E-45	2E-45 2E-05	1E-44	3E-46	1E-44	1E-42	6E-43	9E-45	6E-25	3E-25	4E-45
=		Arir	2E-23	1E24 7E16		15-18 75-18 35-17 15-15	8E-25 5E-19 5E-16 2E-09	16-25	35-25 6E-15 6E-07	15-18	2E-26	85.25	3E-22 2E-19 8E-17	15.24		
		₹uə	25-81 35-73 15-45 15-33	46-51	7E-47 5E-32	9E-57 1E-31	36-59		2E-50 2E-36	2E-48	3E-47	7E-51	6E-50 7E-41			3E-31
		Эtnэ	1E-40 9E-34	7E-42	3E-34	3E-34			2E-40 4E-35 2E-32		16-35	1E-31	<u>6E-39</u>	8E-41 2E-33 3E-32	1E-39 8E-33 4E-32	3E-38 4E-32
		Qins	6E-61	1E-69	5E-43 6E-00	3E-36	35:33		16-45	3E-64 8E+00	1E-136 2E+00	16-39	4E-20 6E+00 6E+00			ZE+0.0
	S	Эţиə	7E-17 4E-16	2E-18 6E-14	1E-17 3E-14	2E-18	3E-19	3E-17 4E-14	1E-17 5E-16	1E-16 7E-15	4E-17	3E-17 1E-13	SE-18	75-17	7E-17	2E-17
보	САТЕСНОГАТЕ	Bins	3E-06	6E-02 8E-02		6E-09	3E-08 2E-01	90-39	6E-07 1E-04 SE-04			5E-04	3E-07 SE-06 SE-06	2E-04	6E-10 7E-05 7E-05	1E-04
nuspc	윉	Ajnə	76-29	46-27	4E-42 2E-29 4E-29 6E-29	4E30 5E28 5E28	26-29	16-27	1E-29	6E-28 2E-27			26-29 26-28 36-28 36-28			
Siderophore Biosynthesis and Transport	A P	Stn9 \ Abdy		16-14		1E-30 1E-13 1E-12 2E-09	16-26	1E-09	1E-16 2E-08	3E-11 2E-08	2E-11 1E-08	1E-10 9E-09	5E-18 1E-07	SE-12	4E-08	
is an		Adiv	4E-27 7E-27 4E-25	ZE-26	1E-142 8E-28 1E-26	ZE-27	4E-28	1E-25	SE-26	3E-26	1E-25 2E-25	25-24	3E-29 5E-27 ZE-26			28-25
thesi		Adiv	2E-91 1E-79 3E-43 3E-40	2E50 7E36	5E-48 7E-38	16-55	8E-59 9E-41		1E54 5E39	3E50 1E37	26-52	55-35	7E54 2E46			
ukso		ошл	3.1	53		4	69	3.1			5.3	53	0.21	6.9	3.1	0.62
e Bi		Boda	1,00E-82 1,00E-67 1,00E-56	2.00E-54	5.00E-49	3.00E-59 9.00E-34	3.00E-31		7.00E-60 5.00E-34 1.00E-33	8.00E-54	5.00E-53	7.00E-55 1.00E-30	6.00E-54			
ohdo		Qu ult	0.055	6.00E-04	5.00E-05 0.008 5.1	2,006-25	3	0.21	5.1 6.7 8.8	5.1		0.006	1.4	2.00E-21	2.00E-21 5.1	9.00E-05
iderc		ϽnųͿ	9,00E-54 1,00E-41 8,00E-37	1,00E-52 6,00E-45	2.00E-42 3.00E-40 3.00E-32	4.006-75		1.00E-57		3.00E-40	3.00E-34	1,00E-56 3,00E-48 2,00E-42 7,00E-40 9,00E-35		\$.00E-63	7,00E-64 2,00E-41	1.00E.36 3.00E.36
	S	gnųſ	3.00E-33 2.00E-32	2.00E-35 2.00E-34 2.00E-33	2.005-31	1.00E-114	4.00E-32	3.00E-32		2.00E-35		3.00E-34 3.00E-33 4.00E-33	2.00E-31	1.00E-123	1.00E-124 3.00E-31	6.00E-41 3.00E-32 8.00E-32
	OXAMATES	Gɔni	14	0.21				0011	0009				0.21			
	OXA	Joui	8.6										5.5			
	HYDR	Boui	26								4.3					
	٦	Asui	V L				9.7					7.4				
		Asdv						7.8	7.8	7.8		9	4.6			
		9sq _V												68	6.8	
		Ssdv	0.019	0.21	0000			2.00E-04	0025	0.056	1.00E-04 0.096 0.37	0.002	0.62	0000	0000	
		Gene Name Species	Roseobacter sp. MED193	Roseobacter sp. SK209-2-6	Roseovarius nubinhibens ISM	Roseovarius sp. 217	Roseovarius sp. TM1035	Ruegeria lacuscaerulensis ITI-1157	Ruegeria pomeroyi DSS-3	Ruegeria sp. R11	Ruegeria sp. TM1040	Ruegeria sp. Trich CH4B	Sagittula stellata E-37	Sulfitobacter NAS-14.1	Sulfitobacter sp. EE-36	Thalassiobium R2A62

Table 2.2 Functions and genbank identities of all peptides used in Table 2.1

Gene	Genbank Accession	Function	Gene	Genbank Accession	Function
fhuA	NP_414692	ferrichrome	vbsC	CAK12032	
fhuE	ACI36233	ferric-rhodotorulic acid, ferric siderophores coprogen and ferrioxamine B	vbsG	CAC48061	<i>Rhizobium</i> vicibactin
btuB	AAA23524	vitamin B12, E colicins	vbsA	CAC48060	
Unmy	AAC64869	heme/haemoglobin receptor	iucA	AAK71631.1	
cirA	NP_416660	ferric iron-ca techolate - colicins	iucB	AAK71632.1	the section of the se
fecA	ACT45941	ferriccitrate	iucC	AAK71633.1	aefobactin syntnesis - <i>snigelid boydii</i>
fepA	YP_002269216.1	Ferrienterobactin permease	iucD	AAK71634.1	
viuA	AET27297	vibriobactin receptor	fhuB	YP_406700.1	
viuB	AET27296	ferric vibriobactin utilization	fhuC	YP_406698.1	ae robactin uptake
fiu/ybiL	NP_415326	believed to facilitate the uptake of the siderophore dihydroxybenzoylserine	Gnuf	YP_406699.1	
fptA	AAC43213	pyochelin receptor - P <i>seudomonas aeruginosa</i>	rhcB	ABG94125.1	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;
fpvA	AAO17439	ferri c pyoverdine receptor	rmo	YP_704660.1	rnod ocneiin syntnesis <i>- knod ococcus Josti i</i>
fyuA	EGT69989	Yersinia bactin receptor	vibF	YP_001217726	vibriobactin synthesis
hasR	CAE46936	Serratia marcescens heme receptor	vibA	ACP08808	1st step in vibriobactin synthesis
ShuA	AAC27809	heme/hemoglobin receptor - Shigella dysenteriae	ybdA / entS	YP_003076595	Enterobactin exporter
yiuR	ADV99409	catecholate siderophores - <i>Yersinia pestis</i>	entA	NP_415128.1	Enterobactin biosynthesis
Maqu_2192	ABM19271.1	Marinobactin receptor - <i>Marinobacter</i>	entB	NP_286322	Enterobactin biosynthesis
hmuR	ABX87333	TonB-de pendent he me/hemoglobin uptake - <i>Yersinia pestis</i>	entC	ACI36818	Enterobactin biosynthesis
fepB	EGT66731	Ferrienterobactin-binding periplasmic protein	entD	ACI36635.1	Enterobactin biosynthesis
fepC	ACI38323	ATPase	entE	YP_002269228	Enterobactin biosynthesis
Gdəf	CAA42043	Ferrienterobactin transporter, permease	entF	YP_002269220	Enterobactin biosynthesis
S def	CAA40708	Ferrienterobactin transporter, permease	rirA	YP_766387	Rihizobial iron regulator
fbpA	NP_286103	Ferric iron permease	mur	CAK05888	Manganese uptake regulator
fbpB	YP_002400786	Ferric iron periplasmic binding protein	irr	AAC3 2183	Iron responsive regulator
fbpC	YP_003076376	ATPase	iscR	EGT66035	Iron sulphur clusters
yfuA	NP_668846.1	iron(III)-binding periplasmic protein	fur	AAR12905	Ferric uptake regulator
hmuT	AAC64868	hemin periplasmic binding protein	irpA	98000dS	Iron regulated protein
yajH	NP_417541	ferric reductase	irpB	AAV93418.1	Iron regulated protein
ferA	YP_913877	Paracoccus denitrificans ferric reductase	feoA	CAA50386.1	ferrous iron transporter
ferB	YP_917833	P. denitrificans ferric reductase	feoB	YP_001732246.1	ferrous iron transporter
mtrA	NP_717386	Shewanella iron reduction			
mtrB	NP_717385	Shewanella iron reduction			
tolA	YP_769548				
tolR	YP_002977283				
tolQ	YP_769550	Couples proton motive force from inner to outer membrane for energising transport			
tonB	YP_001730249	into periplasm			
expB	AAA69173 -				
Gqxa	AAA69172				

2.1.2 The distribution of TonB-dependent outer membrane receptors in the Roseobacters

As presented in the Introduction, many iron-containing compounds are imported via an active transport process, whose initial step involves the recognition and uptake of the Fe-ligand across the outer membrane via a receptor that has a highly conserved basic structure, comprising a beta barrel. Such systems are used to import many siderophores, ferric-citrate complexes and haem, either alone, or complexed in carrier proteins, such as hemoglobin. This process also requires energy, which is transduced via the TonB/ExbBD polypeptides, so are termed, collectively "TonB-dependent outer membrane receptors" (TBDR).

A glance at Table 2.1 shows that there are few close homologues to the various receptors.

However, it is apparent that there are significant matches to members of this super-family, but at a low level of similarity. Importantly, too, there are remarkable differences in the portfolios of different strains and even in the numbers that they have.

To infer function based on homology would be unwise given the significant diversity of the TBDR peptides; when a FhuA homologue is shown to be present in any given Roseobacter in Table 2.1, this does not mean we know the identity of the molecule which it likely imports.

As shown in Table 2.1, there is a remarkable diversity in the distribution of the types and numbers of TBDRs in the different Roseobacters. Thus, as shown in the histogram in Figure 2.1, the numbers range from zero (in eight different strains) to ten (in *Ruegeria* sp. Trich CH4B), but with only a minority of strains (10 out of 37) having four or more polypeptides in this family.

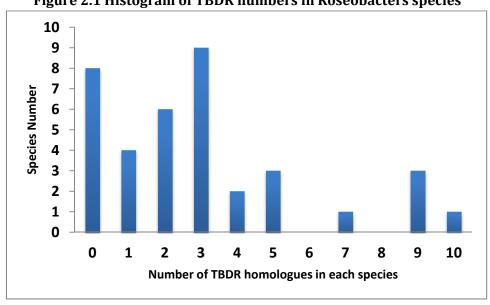


Figure 2.1 Histogram of TBDR numbers in Roseobacters species

Histogram of the numbers of TBDR gene homologues found in genome sequenced Roseobacters, as shown in Table 2.1.

The list below sets out the names of the strains with their total numbers of receptors and of the types that they <u>most closely resemble</u> shown in brackets: (C = citrate; H = haem; S = siderophore and B = vitamin B₁₂) are as follows: Only those with close homologues, i.e. shown as green in Table 2.1, were used for these analyses.

0 receptors: Oceanicola granulosus HTCC2516, Octadecabacter arcticus 238, Rhodobacterales bacterium HTCC2150, Rhodobacterales bacterium KLH11, Roseobacter litoralis Och 149, Roseobacter sp. AzwK-3b, Roseobacter sp. CCS2 and Ruegeria pomeroyi DSS-3.

One receptor: Oceanibulbus indolifex HEL45 (S), Rhodobacterales bacterium HTCC2083 (S), Rhodobacterales bacterium HTCC2255 (S), Sagittula stellata E-37 (S),

Two receptors Dinoroseobacter shibae DFL 12 (H), Loktanella vestfoldensis SKA53 (H), Roseobacter sp. GAI101 (SB), Roseovarius nubinhibens ISM (H), Roseovarius sp. TM1035 (H), Ruegeria sp. R11 (SH) and Ruegeria sp. TM1040 (H).

Three receptors: Maritimibacter alkaliphilus HTCC2654 (HS), Oceanicola batsensis HTCC2597 (S), Phaeobacter gallaeciensis 2.10 (S), Phaeobacter gallaeciensis BS107 (S), Phaeobacter sp. Y41 (S), Roseobacter denitrificans OCh 114 (H), Ruegeria lacuscaerulensis ITI-1157 (S)

Four receptors: Jannaschia sp. CCS1 (HS), Octadecabacter antarcticus 307 (HB) and Thalassiobium R2A62 (SH).

Five receptors: Roseobacter sp. MED193 (SH), Roseobacter sp. SK209-2-6 (SH) and Roseovarius sp.

217 (SH).

Seven receptors: Sulfitobacter sp. EE-36 (CHS).

Nine receptors: Citreicella SE45 (CHSB), Pelagibaca bermudensis HTCC2601 (CHSB) and Sulfitobacter

NAS-14.1 (CHS).

Ten receptors: Ruegeria sp. Trich CH4B (CHS).

Indeed, some species possess a wide complement of receptors, such as Citreicella SE45, which has two copies of both "fhuA" and "fpvA" and single copies of btuB-, hmuU- and hmuR-like genes in its genome (see Table 2.1). Ruegeria sp. Trich CH4B also has a large complement of homologues to iron specific receptors - fhuA, hmuU, fecA, fpvA and hmuR, but this is surpassed by Sulfitobacter NAS-14.1 and Sulfitobacter EE36, both of which also have a homologue of fiu, an enterochelin breakdown-product receptor. But, the TBDR record-holder, to date, is Pelagibaca bermudensis HTCC2601 which has homologues of fhuA, hmuU, fecA, fpvA, btuB and two catecholate siderophore

In contrast, several Roseobacters lack homologues to any known TBDRs; these are R. pomeroyi DSS-3, Oceanicola granulosus HTCC2516, Octadecabacter arcticus 238 and Rhodobacterales bacterium HTCC2150. Several other Roseobacters lack all TBDR genes, except a weak homologue to hmuU.

2.1.3 The search for TonB

receptors - cirA and yiuR.

The presence of TBDRs at least in some Roseobacters, points, not unreasonably to the need for a TonB polypeptide in such strains. However, using the bone fide TonB of Rhizobium leguminosarum as the BLASTP probe, none of the Roseobacter proteomes yielded a convincing homologue ($e < 10^{25}$). But, given the hyper-variability of TonBs in bacteria, I decided to search for TonB in the Roseobacters using a different approach.

I used the sequence of the TonB peptides of E. coli, Rhizobium leguminosarum and Rhodobacter sphaeroides as probes to interrogate all Roseobacter genomes, and discovered a homologue in

56

Roseovarius nubinhibens – the product of the ISM_04245 gene (30% ID to TonB of Rhizobium leguminosarum). Although not a bone fide TonB gene, ISM-04245 is next to putative haem uptake genes hmuR and a putative exbB gene, so I added the ISM_04245 gene product to the in silico probes used for my TonB search.

I used all the TonB probes against the proteomes of all the Roseobacters. The resulting matches are shown in table 2.3. Since each putative TonB polypeptide is targeted by four probes (four different colours), any gene locus with analogous to **most** of the probes was considered to be a *bona fide* TonB. Even with this approach, none of the TonBs was >45% identical to any of the probes, except, of course for *R. nubinhibens* itself. Although this approach may have indeed identified TonBs in the Roseobacters, further direct experimentation will be needed to ratify this (for example, by examining the iron uptake abilities of strains with mutations in these genes).

However, several Roseobacters did not contain a gene homologous to more than two of the probe sequences, and therefore **may** not possess a copy of TonB. These were: <u>Octadecabacter antarcticus 238</u>, <u>Oceanibulbus indolifex HEL-45</u>, <u>Rhodobacterales bacterium HTCC2255</u>, <u>Roseobacter sp. AzwK3b</u>, <u>Rhodobacterales bacterium HTCC2083</u>, <u>Rhodobacterales bacterium HTCC2150</u>, <u>Roseobacter sp. CCS2</u>, <u>Roseobacter denitrificans Och114</u>, <u>Roseobacter litoralis Och 149</u>, <u>Loktanella vestfoldensis SKA53</u> and <u>Ruegeria lacuscaerulensis ITI-1157</u>.

Crucially, of these **eleven** strains that lack TonB, **five** did not have not appear to have any TBDR polypeptides (underlined above and shown in Table 2.1). Two of the other strains that had no detectable TBDR polypeptides (*Ruegeria pomeroyi* DSS-3 and *Oceanicola granulosus* HTCC2516) also had very poor homologues of TonB, which were of questionable validity (E values > 5E⁻¹⁰). Therefore, there is some correlation between the lack of TonB and the absence of a TBDR in the same strain. This observation warrants further investigation.

The concept of bacterial species lacking TonB has received some attention - *Francisella tularensis* imports a rhizoferrin-like carboxylate siderophore via the outer membrane receptor FsIE , albeit still in an energy dependent process (Ramakrishnan *et al.* 2008; 2012). *Legionella pneumophila* produces a siderophore (legiobactin) which is imported via a receptor termed LbtU, which is also supposedly TonB independent. The authors report that LbtU is a 16 stranded β -barrel, distinct from 22-stranded normal TBDRs (Chatfield *et al.* 2011).

Of course, there were also strains which do have homologues of TBDRs, and yet do not appear to have TonB. Again, without further work these questions remain unanswered, but fascinating.

Table 2.3 Presence of TonB Homologues in Genome-Sequenced Strains of the Roseobacter Clade

Gene Tag	Genome	Percentage ID	Expect value
<u>CH4B_21510</u>	<i>Ruegeria</i> sp. Trich CH4B	38	4.00E ⁻⁴⁷
CH4B 21510	Ruegeria sp. Trich CH4B	27	1.00E ⁻²⁰
CH4B 21510	Ruegeria sp. Trich CH4B	24	1.00E ⁻¹³
<u>CH4B_45730</u>	Ruegeria sp. Trich CH4B	36	8.00E ⁻²⁸
<u>CH4B_45730</u>	Ruegeria sp. Trich CH4B	30	5.00E ⁻¹⁶
<u>CH4B_45730</u>	Ruegeria sp. Trich CH4B	27	3.00E ⁻¹³
<u>CH4B 45730</u>	<i>Ruegeria</i> sp. Trich CH4B	26	3.00E ⁻⁰⁸
<u>Dshi 0567</u>	Dinoroseobacter shibae DFL12	38	7.00E ⁻²⁴
<u>Dshi_0567</u>	Dinoroseobacter shibae DFL12	29	3.00E ⁻¹³
<u>Dshi 0567</u>	Dinoroseobacter shibae DFL12	28	6.00E ⁻¹²
<u>Dshi 1110</u>	Dinoroseobacter shibae DFL12	34	1.00E ⁻¹³
<u>Dshi 1110</u>	Dinoroseobacter shibae DFL12	37	3.00E ⁻¹⁰
<u>Dshi 1110</u>	Dinoroseobacter shibae DFL12	26	3.00E ⁻⁰⁷
<u>Dshi 2367</u>	Dinoroseobacter shibae DFL12	29	2.00E ⁻⁰⁶
<u>Dshi 2725</u>	Dinoroseobacter shibae DFL12	29	8.00E ⁻⁰⁹
<u>EE36_09740</u>	Sulfitobacter sp. EE-36	31	2.00E ⁻⁰⁹
<u>EE36 09740</u>	Sulfitobacter sp. EE-36	32	3.00E ⁻⁰⁹
<u>EE36_09740</u>	Sulfitobacter sp. EE-36	26	6.00E ⁻⁰⁷
<u>EE36_10430</u>	Sulfitobacter sp. EE-36	29	3.00E ⁻¹⁰
EE36 13013	Sulfitobacter sp. EE-36	42	3.00E ⁻⁵³
EE36 13013	Sulfitobacter sp. EE-36	29	5.00E ⁻²⁵
EE36 13013	Sulfitobacter sp. EE-36	28	5.00E ⁻¹⁴
EE36 15637	Sulfitobacter sp. EE-36	32	3.00E ⁻⁰⁹
<u>EE36_15637</u>	Sulfitobacter sp. EE-36	30	2.00E ⁻⁰⁷
<u>ISM_03305</u>	Roseovarius nubinhibens ISM	27	4.00E ⁻⁰⁷

<u>ISM_04245</u>	Roseovarius nubinhibens ISM	100	1.00E ⁻¹⁷⁴
<u>ISM 04245</u>	Roseovarius nubinhibens ISM	30	4.00E ⁻²⁴
<u>ISM 04245</u>	Roseovarius nubinhibens ISM	28	3.00E ⁻¹⁶
<u>ISM 06055</u>	Roseovarius nubinhibens ISM	34	1.00E ⁻¹³
<u>ISM 06055</u>	Roseovarius nubinhibens ISM	29	6.00E ⁻⁰⁶
<u>ISM 16395</u>	Roseovarius nubinhibens ISM	32	4.00E ⁻¹⁰
<u>ISM_16395</u>	Roseovarius nubinhibens ISM	32	8.00E ⁻⁰⁷
<u>Jann_0972</u>	Jannaschia sp. CCS1	28	1.00E ⁻⁰⁶
<u>Jann_1616</u>	Jannaschia sp. CCS1	32	2.00E ⁻⁰⁶
<u>Jann_2127</u>	Jannaschia sp. CCS1	36	2.00E ⁻⁴¹
<u>Jann_2127</u>	Jannaschia sp. CCS1	29	4.00E ⁻²⁰
<u>Jann_2127</u>	Jannaschia sp. CCS1	28	4.00E ⁻¹³
<u>KLH11_10350</u>	Rhodobacterales bacterium KLH11	27	6.00E ⁻⁰⁶
<u>KLH11_13530</u>	Rhodobacterales bacterium KLH11	26	2.00E ⁻⁰⁹
<u>KLH11_14940</u>	Rhodobacterales bacterium KLH11	30	2.00E ⁻²²
<u>KLH11_14940</u>	Rhodobacterales bacterium KLH11	27	6.00E ⁻¹⁷
<u>KLH11_14940</u>	Rhodobacterales bacterium KLH11	24	7.00E ⁻¹⁰
MED193 17529	<i>Roseobacter</i> sp MED193	35	6.00E ⁻⁴²
MED193 17529	Roseobacter sp MED193	30	3.00E ⁻²³
MED193_17529	Roseobacter sp MED193	26	3.00E ⁻¹⁷
MED193_22036	Roseobacter sp MED193	38	5.00E ⁻²⁹
MED193_22036	<i>Roseobacter</i> sp MED193	31	2.00E ⁻¹⁹
MED193 22036	Roseobacter sp MED193	27	7.00E ⁻¹⁶
MED193_22036	Roseobacter sp MED193	27	3.00E ⁻¹¹
NAS141_05758	Sulfitobacter sp. NAS-14.1	31	8.00E ⁻⁰⁸
NAS141_06398	Sulfitobacter sp. NAS-14.1	29	1.00E ⁻⁰⁶
NAS141_06398	Sulfitobacter sp. NAS-14.1	30	3.00E ⁻⁰⁶

NAS141_14753	Sulfitobacter sp. NAS-14.1	31	8.00E ⁻¹⁰
NAS141 14753	Sulfitobacter sp. NAS-14.1	25	6.00E ⁻⁰⁹
NAS141 14753	Sulfitobacter sp. NAS-14.1	26	1.00E ⁻⁰⁶
NAS141_15333	Sulfitobacter sp. NAS-14.1	29	3.00E ⁻¹⁰
NAS141_18179	Sulfitobacter sp. NAS-14.1	43	9.00E ⁻⁵⁴
NAS141_18179	Sulfitobacter sp. NAS-14.1	31	6.00E ⁻²³
NAS141_18179	Sulfitobacter sp. NAS-14.1	28	1.00E ⁻¹³
NAS141_18179	Sulfitobacter sp. NAS-14.1	23	2.00E ⁻⁰⁷
<u>OA238_811</u>	Octadecabacter antarcticus 238	29	3.00E ⁻⁰⁹
<u>OA307_2153</u>	Octadecabacter antarcticus 307	32	9.00E ⁻³²
OA307_2153	Octadecabacter antarcticus 307	25	1.00E ⁻¹⁶
<u>OA307_2153</u>	Octadecabacter antarcticus 307	26	2.00E ⁻¹¹
<u>OB2597_05450</u>	Oceanicola batsensis HTCC2597	36	2.00E ⁻⁵⁰
<u>OB2597_05450</u>	Oceanicola batsensis HTCC2597	29	6.00E ⁻¹⁸
<u>OB2597_05450</u>	Oceanicola batsensis HTCC2597	28	4.00E ⁻¹⁵
<u>OB2597_05450</u>	Oceanicola batsensis HTCC2597	24	3.00E ⁻⁰⁶
OB2597_15655	Oceanicola batsensis HTCC2597	24	1.00E ⁻⁰⁶
OB2597_15655	Oceanicola batsensis HTCC2597	26	2.00E ⁻⁰⁶
OG2516_01015	Oceanicola granulosus HTCC2516	30	5.00E ⁻⁰⁶
OG2516_12444	Oceanicola granulosus HTCC2516	32	5.00E ⁻¹⁰
OG2516_12444	Oceanicola granulosus HTCC2516	23	2.00E ⁻⁰⁷
OG2516_12444	Oceanicola granulosus HTCC2516	24	5.00E ⁻⁰⁷
<u>OIHEL45_09568</u>	Oceanibulbus indolifex HEL-45	25	2.00E ⁻¹⁰
<u>OIHEL45_09568</u>	Oceanibulbus indolifex HEL-45	31	5.00E ⁻⁰⁷
<u>OIHEL45_15869</u>	Oceanibulbus indolifex HEL-45	25	7.00E ⁻¹⁰
<u>OIHEL45_15869</u>	Oceanibulbus indolifex HEL-45	24	8.00E ⁻⁰⁷
OM2255_13534	Rhodobacterales bacterium HTCC2255	38	6.00E ⁻¹²

OM2255_13534	Rhodobacterales bacterium HTCC2255	37	7.00E ⁻¹²
<u>R2601_11699</u>	Pelagibaca bermudensis HTCC2601	25	1.00E ⁻⁰⁶
R2601 12453	Pelagibaca bermudensis HTCC2601	29	4.00E ⁻¹¹
R2601_12453	Pelagibaca bermudensis HTCC2601	38	2.00E ⁻¹⁰
<u>R2601_12453</u>	Pelagibaca bermudensis HTCC2601	23	2.00E ⁻⁰⁹
<u>R2601_12453</u>	Pelagibaca bermudensis HTCC2601	25	3.00E ⁻⁰⁷
<u>R2601_21051</u>	Pelagibaca bermudensis HTCC2601	33	8.00E ⁻¹¹
R2601 26191	Pelagibaca bermudensis HTCC2601	25	9.00E ⁻⁰⁸
R2601 27243	Pelagibaca bermudensis HTCC2601	42	1.00E ⁻⁶⁵
R2601 27243	Pelagibaca bermudensis HTCC2601	31	3.00E ⁻²⁹
R2601 27243	Pelagibaca bermudensis HTCC2601	31	6.00E ⁻²²
R2A62 18510	Thalassiobium sp. R2A62	26	4.00E ⁻⁰⁶
R2A62 19050	Thalassiobium sp. R2A62	32	3.00E ⁻³⁵
R2A62 19050	Thalassiobium sp. R2A62	28	3.00E ⁻¹⁹
R2A62 19050	Thalassiobium sp. R2A62	27	3.00E ⁻¹⁵
R2A62 29000	Thalassiobium sp. R2A62	21	3.00E ⁻⁰⁶
RAZWK3B 06677	<i>Roseobacter</i> sp. AzwK3b	26	5.00E ⁻¹¹
RAZWK3B 20566	<i>Roseobacter</i> sp. AzwK3b	42	2.00E ⁻⁰⁹
RB2083 2039	Rhodobacterales bacterium HTCC2083	35	7.00E ⁻⁰⁷
RB2150_04948	Rhodobacterales bacterium HTCC2150	26	2.00E ⁻⁰⁸
RB2150 05338	Rhodobacterales bacterium HTCC2150	36	8.00E ⁻¹¹
RB2654 05647	Maritimibacter alkaliphilus HTCC2654	31	1.00E ⁻¹⁰
RB2654_05647	Maritimibacter alkaliphilus HTCC2654	27	1.00E ⁻⁰⁷
RB2654 05647	Maritimibacter alkaliphilus HTCC2654	28	5.00E ⁻⁰⁷
RB2654 15821	Maritimibacter alkaliphilus HTCC2654	35	3.00E ⁻²⁷
RB2654_15821	Maritimibacter alkaliphilus HTCC2654	29	5.00E ⁻¹⁹
RB2654_15821	Maritimibacter alkaliphilus HTCC2654	26	4.00E ⁻¹²

RB2654_18448	Maritimibacter alkaliphilus HTCC2654	28	2.00E ⁻⁰⁶
<u>RB2654_19658</u>	Maritimibacter alkaliphilus HTCC2654	33	2.00E ⁻¹²
<u>RBY41_2464</u>	Phaeobacter sp. Y4I	31	2.00E ⁻⁰⁹
<u>RBY4I_2464</u>	Phaeobacter sp. Y4I	25	1.00E ⁻⁰⁶
<u>RBY4I_2464</u>	Phaeobacter sp. Y4I	34	3.00E ⁻⁰⁶
<u>RBY4I_4149</u>	Phaeobacter sp. Y4I	34	1.00E ⁻²⁶
<u>RBY4I_4149</u>	Phaeobacter sp. Y4I	30	6.00E ⁻¹⁸
<u>RBY4I_4149</u>	Phaeobacter sp. Y4I	28	2.00E ⁻¹³
RCCS2_05544	Roseobacter sp. CCS2	24	4.00E ⁻⁰⁷
RCCS2_05544	Roseobacter sp. CCS2	25	2.00E ⁻⁰⁶
<u>RD1_1932</u>	Roseobacter denitrificans Och114	34	2.00E ⁻¹²
<u>RD1_1932</u>	Roseobacter denitrificans Och114	31	2.00E ⁻¹⁰
<u>RD1_3158</u>	Roseobacter denitrificans Och114	33	3.00E ⁻¹²
<u>RD1_4199</u>	Roseobacter denitrificans Och114	37	2.00E ⁻³⁸
<u>RD1_4199</u>	Roseobacter denitrificans Och114	30	4.00E ⁻²¹
<u>RG210_03453</u>	Phaeobacter gallaeciensis 2.10	22	2.00E ⁻⁰⁶
<u>RG210_11773</u>	Phaeobacter gallaeciensis 2.10	37	7.00E ⁻³¹
<u>RG210_11773</u>	Phaeobacter gallaeciensis 2.10	28	3.00E ⁻¹⁸
<u>RG210_11773</u>	Phaeobacter gallaeciensis 2.10	26	3.00E ⁻¹⁰
<u>RG210_11773</u>	Phaeobacter gallaeciensis 2.10	24	8.00E ⁻⁰⁸
<u>RGAI101_1183</u>	Roseobacter sp. GAI101	31	1.00E ⁻⁰⁹
RGAI101_1183	Roseobacter sp. GAI101	35	1.00E ⁻⁰⁹
RGAI101_1183	Roseobacter sp. GAI101	32	3.00E ⁻⁰⁷
RGAI101_1183	Roseobacter sp. GAI101	26	2.00E ⁻⁰⁶
RGAI101_2719	Roseobacter sp. GAI101	30	3.00E ⁻²¹
RGAI101_2719	Roseobacter sp. GAI101	31	1.00E ⁻¹⁶
RGAI101_2719	Roseobacter sp. GAI101	28	2.00E ⁻¹³

RGAI101_3387	Roseobacter sp. GAI101	28	1.00E ⁻⁰⁶
<u>RGAI101_4137</u>	Roseobacter sp. GAI101	29	2.00E ⁻¹¹
RGBS107_01618	Phaeobacter gallaeciensis BS107	36	3.00E ⁻³⁰
RGBS107_01618	Phaeobacter gallaeciensis BS107	28	6.00E ⁻¹⁸
<u>RGBS107_01618</u>	Phaeobacter gallaeciensis BS107	27	7.00E ⁻¹³
RGBS107_01618	Phaeobacter gallaeciensis BS107	25	3.00E ⁻⁰⁶
RLO149_00770	Roseobacter litoralis Och 149	30	1.00E ⁻⁰⁶
RLO149_16723	Roseobacter litoralis Och 149	36	5.00E ⁻⁰⁸
RLO149_22885	Roseobacter litoralis Och 149	28	3.00E ⁻⁰⁷
ROS217_05079	Roseovarius sp 217	34	1.00E ⁻¹¹
ROS217_08174	Roseovarius sp 217	28	2.00E ⁻⁰⁷
ROS217_17015	Roseovarius sp 217	30	5.00E ⁻⁰⁶
ROS217_22847	Roseovarius sp 217	43	1.00E ⁻⁵³
ROS217_22847	Roseovarius sp 217	28	9.00E ⁻¹⁹
ROS217_22847	Roseovarius sp 217	29	6.00E ⁻¹⁷
<u>RR11_3124</u>	Ruegeria sp. R11	27	2.00E ⁻⁰⁶
<u>RR11_420</u>	<i>Ruegeria</i> sp. R11	28	1.00E ⁻⁰⁶
<u>RR11_420</u>	Ruegeria sp. R11	24	1.00E ⁻⁰⁶
<u>RR11_420</u>	Ruegeria sp. R11	27	3.00E ⁻⁰⁶
<u>RR11_89</u>	<i>Ruegeria</i> sp. R11	38	6.00E ⁻⁴⁴
<u>RR11_89</u>	Ruegeria sp. R11	34	5.00E ⁻¹⁵
<u>RR11_89</u>	Ruegeria sp. R11	26	1.00E ⁻¹⁰
RSK20926_04157	Roseobacter sp. SK20926	26	1.00E ⁻⁰⁷
RSK20926_04157	Roseobacter sp. SK20926	37	5.00E ⁻⁰⁶
<u>RSK20926_10619</u>	Roseobacter sp. SK20926	35	2.00E ⁻³⁷
RSK20926_10619	Roseobacter sp. SK20926	26	7.00E ⁻²²
RSK20926_10619	<i>Roseobacter</i> sp. SK20926	27	1.00E ⁻¹³

RSK20926_15376	Roseobacter sp. SK20926	35	4.00E ⁻²⁹
RSK20926 15376	Roseobacter sp. SK20926	31	2.00E ⁻¹⁷
RSK20926 15376	Roseobacter sp. SK20926	26	1.00E ⁻¹⁴
RSK20926 15376	Roseobacter sp. SK20926	26	9.00E ⁻¹⁰
RSK20926 17927	Roseobacter sp. SK20926	32	5.00E ⁻⁰⁷
RTM1035_05560	Roseovarius sp. TM1035	41	4.00E ⁻⁵¹
RTM1035_05560	Roseovarius sp. TM1035	26	4.00E ⁻¹⁷
RTM1035_05560	Roseovarius sp. TM1035	24	2.00E ⁻¹²
RTM1035_06468	Roseovarius sp. TM1035	27	5.00E ⁻⁰⁶
RTM1035_18951	Roseovarius sp. TM1035	30	1.00E ⁻¹⁰
RTM1035_18951	Roseovarius sp. TM1035	26	8.00E ⁻⁰⁷
<u>SE45_29970</u>	Citreicella sp. SE45	29	5.00E ⁻⁰⁹
<u>SE45_44320</u>	Citreicella sp. SE45	28	3.00E ⁻⁰⁷
<u>SE45_44420</u>	Citreicella sp. SE45	45	1.00E ⁻⁶⁵
<u>SE45_44420</u>	Citreicella sp. SE45	34	8.00E ⁻²⁷
<u>SE45_44420</u>	Citreicella sp. SE45	30	2.00E ⁻²⁴
<u>SE45_44420</u>	Citreicella sp. SE45	21	6.00E ⁻⁰⁶
<u>SE45_53730</u>	Citreicella sp. SE45	29	2.00E ⁻⁰⁹
<u>SE45_53730</u>	Citreicella sp. SE45	22	3.00E ⁻⁰⁶
<u>SKA53_03031</u>	Loktanella vestfoldensis SKA53	31	7.00E ⁻¹⁰
SKA53_05955	Loktanella vestfoldensis SKA53	43	4.00E ⁻⁰⁷
SKA53_06392	Loktanella vestfoldensis SKA53	33	4.00E ⁻³¹
SKA53_06392	Loktanella vestfoldensis SKA53	31	6.00E ⁻¹⁹
SKA53_06392	Loktanella vestfoldensis SKA53	31	9.00E ⁻¹⁶
<u>SKA53_08576</u>	Loktanella vestfoldensis SKA53	28	5.00E ⁻⁰⁸
<u>SL1157_14710</u>	Ruegeria lacuscaerulensis ITI-1157	33	3.00E ⁻⁰⁹
<u>SPO0227</u>	Ruegeria pomeroyi DSS-3	38	7.00E ⁻¹²

<u>SPO2336</u>	Ruegeria pomeroyi DSS-3	28	2.00E ⁻⁰⁶
<u>SPO3110</u>	Ruegeria pomeroyi DSS-3	32	3.00E ⁻¹²
<u>SPO3110</u>	Ruegeria pomeroyi DSS-3	32	2.00E ⁻¹¹
<u>SPO3110</u>	Ruegeria pomeroyi DSS-3	28	8.00E ⁻⁰⁷
<u>SSE37_01135</u>	Sagittula stellata E-37	25	3.00E ⁻¹⁰
<u>SSE37_01135</u>	Sagittula stellata E-37	27	1.00E ⁻⁰⁶
<u>SSE37_20382</u>	Sagittula stellata E-37	34	3.00E ⁻⁰⁹
<u>SSE37_20382</u>	Sagittula stellata E-37	29	3.00E ⁻⁰⁷
<u>SSE37_20382</u>	Sagittula stellata E-37	23	8.00E ⁻⁰⁷
<u>TM1040_0352</u>	<i>Ruegeria</i> sp. TM1040	41	4.00E ⁻⁵²
TM1040_0352	Ruegeria sp. TM1040	27	5.00E ⁻²⁰
TM1040_0352	Ruegeria sp. TM1040	26	2.00E ⁻¹³
<u>TM1040_0352</u>	Ruegeria sp. TM1040	22	5.00E ⁻⁰⁶

Four probe sequences corresponding to TonB polypeptides were used to interrogate the sequenced Roseobacter genomes. The probes were from E. coli (Orange), Rhizobium leguminosarum (Green), Roseovarius nubinhibens (Yellow) and Rhodobacter sphaeroides (Blue). For each of the Roseobacter clade gene locus tags, the target with the closest similarity is colour coded and the similarity is indicated by the %age identities of the polypeptides and the Expect values.

2.1.4 Haeme and Ferrous iron ABC-class transporters are poorly conserved in the Roseobacters

Most of the known TBDRs have cognate ABC transporters that comprise the corresponding periplasmic binding protein that receive, (for example) the Fe-hydroxamate complex that has been transported through the FhuA surface-membrane receptor, which is then transported through the inner membrane via a transporter polypeptide, with the energy being delivered via the ATPase polypeptide component of the FbpABC transporter. Furthermore, there is at least one system variously known as Fbp (and there are many others in, for example, *Yersinia* and *Vibrio*) in which the ABC transporter may deliver the Fe³⁺ without the need of a corresponding OM receptor.

Table 2.1 shows that the different Roseobacters contain a variety of combinations of these types of ABC transporter, but mostly, there are no very close homologues.

The four main ABC-class transporters tested in this section of table 2.1 were Fep, the ferrienterobactin transporter from *E. coli*, Fbp and YfuA, both ferric iron specific from *E. coli* and *Yersinia pestis* respectively, and HmuT a periplasmic haemin binding-domain also of *Y. pestis*.

None of the Roseobacters has a homologue of FepB, the periplasmic binding-protein for enterobactin, but 11 species have homologues of FepC and FepD, the ATPase and permease components of this ABC-class transporter. Interestingly, *Pelagibaca bermudensis* HTCC2601 has a good homologue of FepA, the only member of the Roseobacters to possess this protein.

FbpA and FbpB were poorly conserved in the Roseobacters, with just 6 species containing a homologue of these particular proteins. However the ATPase, FbpC was well conserved with 25 of the 37 Roseobacters having at least one homologue with an E-value $> 1E^{-69}$. It is likely that just the conservation of peptide sequence of FbpA and FbpB is poor, and may not be representative of the actual conservation of function throughout the Roseobacters.

None of the Roseobacter strains had a peptide in their deduced proteome homologous to YfuA, although most (29 out of the 37 sequenced strains) had a weaker homologue (shown as yellow in Table 2.1).

Finally, the most common ABC-class transporter homologue shown in this table was HmuT; there are 18 strains which possess a homologue (E-value of between 1E⁻⁷⁰ and 1E⁻¹⁵⁸).

This list is far from exhaustive in terms of potential iron specific ABC transporters found in bacteria, but an in-depth study into the full range found in the Roseobacters was outside the scope of this work.

2.2 Siderophore biosynthetic genes in the Roseobacters

There is remarkably little known about the genes encoding siderophores synthesised by marine bacteria. To our knowledge, there are no studies, of any type, on the biosynthesis of siderophores in the marine Roseobacters. This made the prediction of any possible siderophore biosynthetic genes in these bacteria tenuous at best.

Known genes from biosynthetic pathways for both catecholate- and hydroxamate-type siderophores were used to interrogate the products of the all the sequenced genomes of the Roseobacters, these are detailed in Table 2.2.

2.2.1 Homologues of vicibactin and aerobactin biosynthesis genes in the Roseobacters

Vicibactin of *Rhizobium leguminosarum* is a hydroxamate-type siderophore, and is synthesised from ornithine in a pathway of dedicated enzymatic steps (Heemstra *et al.* 2009). The translated protein products of the genes *vbsC*, *vbsG* and *vbsA* of *Rhizobium*, were each used to interrogate the Roseobacters, but no species contained even a moderate (<E⁻²⁵) homologue. Similarly, aerobactin synthetic enzymes (encoded by the genes *iucABCD*) from *Shigella boydii* yielded no homologues in the Roseobacters, with the exception of *Phaeobacter gallaeciensis* BS107, which had moderate homologues (2e⁻⁴⁸ and 4e⁻⁴⁸) to IucA and IucC respectively. A single homologue (3e⁻³⁸) of *Shigella boydii* IucC was present in a different strain (*P. gallaeciensis* 2.10) of the same species.

2.2.2 Vibriobactin biosynthetic genes in the Roseobacters

Vibriobactin is produced by *Vibrio cholerae* during iron deficiency. Mutants in the biosynthetic pathway can no longer produce vibriobactin and show increased sensitivity to EDDA, as it removes any available iron from the growth medium (Wyckoff *et al.* 1997). The first dedicated step in vibriobactin biosynthesis in *V. cholerae* is the catalysis of 2,3-dihydro-2,3-dihydroxybenzoate to 2,3-dihydroxybenzoate by a vibriobactin-specific 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, VibA. The final step in the vibriobactin biosynthetic pathway is catalysed by a non-ribosomal peptide synthetase, VibF. This step forms the complete vibriobactin from dihydroxyphenyl-5-methyloxazoline-norspermidine-2,3-dihydroxybenzoate and dihydroxyphenyl-5-methyloxazoline bound to VibF (Crosa and Walsh 2002). The protein sequences encoded by genes *vibA* and *vibF* of *V. cholerae* 0395 were used to interrogate all Roseobacter genomes as before, refer to Table 2.1.

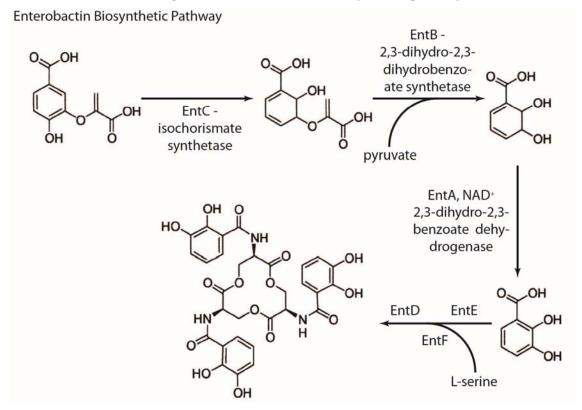
The closest homologue of *V. cholerae* 0395 VibF in the Rhodobacteraceae ($4e^{-53}$) was the Citreicella SE45 gene CSE45_4536, which is annotated as being 'enterobactin synthetase component-F'. A good homologue of this gene is found in four other Roseobacter genomes - *Phaeobacter gallaeciensis* 2.10 ($1E^{-91}$), *Phaeobacter gallaeciensis* BS107 ($2E^{-90}$), *Phaeobacter* sp. Y4I ($6E^{-69}$) and *Roseobacter* sp. MED193, which has two good homologues ($2E^{-91}$ and E^{-79}). There are 19 other Roseobacters genomes which encode moderate ($1E^{-30} - 1E^{-60}$) homologues of VibF of *Citreicella* SE45 (refer to Table 2.1).

Furthermore, the closest homologue of *V. cholerae* 0395 VibA in the Rhodobacteraceae was found in *Roseovarius nubinhibens* ISM (1e⁻⁴⁴), and is indeed predicted to be a 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase as expected. The Roseobacters were found to have 16 members which encode homologues of this gene, although not particularly well conserved – all were between 1E⁻²⁵ and 1E⁻²⁹. Crucially, of those 16 Roseobacters which have a homologue of VibA, 15 also had VibF, perhaps validating the presence of this, or at least a related, biosynthetic pathway in those strains.

2.2.3 Enterobactin biosynthesis genes in the Roseobacters

The iron-scavenging siderophore produced by *E. coli* and *Salmonella* is the catecholate enterobactin, also called enterochelin (O'Brien and Gibson 1970; Pollack and Neilands 1970). The biosynthesis requires several steps, beginning with the aromatic amino acid precursor chorismic acid (see Figure 2.2). This is converted to isochorismate by EntC, and then into 2,3-dihydro-2,3-dihydroxybenzoate by EntB, and finally into 2,3-dihydroxybenzoic acid (DHB) by EntA. A DHB moiety is joined with an amide linkage to a serine molecule by EntD, EntE, EntF and EntB, then three DHB-lysine molecules cyclise to form *iso*-enterobactin (Raymond *et al.* 2003).

Figure 2.2 The enterochelin biosynthetic pathway



The biosynthetic pathway of enterobactin, adapted from (Raymond et al. 2003).

The protein sequences of EntA, EntB, EntC, EntD, EntE and EntF of *E. coli* K-12 were used to interrogate the Rhodobacteriaceae, and the sequence of the most similar protein was used as a query in the Roseobacter genomes.

There is a homologue of EntA in *Paracoccus* sp. TRP (9e⁻⁵⁹), and when this was used, in turn, as a probe, homologues were found in 23 different strains of the Roseobacters, the most similar being in *Roseovarius nubinhibens* ISM (1E⁻⁴²). There were no homologues of EntB or EntC found in any of the Roseobacters, when searched either directly, or using *Paracoccus* species homologues as queries. In contrast, the presence of an EntD homologue was shown in several Roseobacters.

The putative translated products of both *entE* and *entF* were extremely well conserved in the Rhodobacteraceae, with the genome of *Paracoccus denitrificans* PD1222 encoding an EntE homologue (E-value of 0, gene locus: Pden_2386), and *Paracoccus* sp. TRP encoding an EntF homologue (E-value of 0, gene locus: PaTRP_010100004572). Given the conservation of these *E. coli* protein-coding genes in the Rhodobacteraceae, the resultant data from homology based searches of the Roseobacters was unparalleled when compared to the rest of this bioinformatic study. The

genome of *Citreicella* sp. SE45 has good homologues to both *entE* (1E⁻¹³³) and *entF* (E-value of 0) and also contains a homologue of *entA*, but lacks homologues to the *entB*, *entC* and *entD*.

2.3 Siderophore export and uptake in the Roseobacters

2.3.1 Enterobactin export genes in the Roseobacters

Export of enterobactin into the periplasm is facilitated by the protein EntS, which is a member of the major facilitator superfamily (MFS) of transporters. The closest homologue of this gene product in the Rhodobacteraceae is in *Jannaschia* sp. CCS1 (3e⁻¹⁴), which although poorly conserved, is predicted to be a MFS-family protein. Homologues to this peptide sequence are only found in few Roseobacters - *Maritimibacter alkaliphilus* HTCC2654 (5E⁻⁶³), *Rhodobacterales bacterium* HTCC2255 (2E⁻⁷⁴), *Roseobacter denitrificans* OCh 114 (2E⁻³¹), *Roseovarius* sp. 217 (1E⁻³⁰) and *Roseovarius* sp. TM1035 (1E⁻²⁶) – and it is certainly not impossible that these MFS polypeptides have function(s) other than siderophore export.

2.3.2 Aerobactin uptake genes in the Roseobacters

The uptake of iron-bound aerobactin, and indeed other hydroxamate-type siderophores by *E. coli* is mediated by a TonB dependent outer membrane receptor – FhuA, and then by the cognate ABC-type transporter FhuCDB (Forman *et al.* 2007). The translated products of the permease gene *fhuB* and ATPase gene *fhuC* have 'moderate' homologues (1E⁻³¹ - 1E⁻⁶⁰) in 21 of the Roseobacter strains, and indeed many of these strains (12) have multiple homologues to each of these genes (refer to Table 2.1). Four Roseobacter strains have 'good' homologues (>1E⁻⁶⁰) to both FhuB and FhuC, namely *Roseovarius* sp. 217, *Sulfitobacter* NAS-14.1, *Sulfitobacter* EE36 and *Pelagibaca bermudensis* HTCC2601, the latter of which is the only Roseobacter to also have a copy of the periplasmic binding protein gene *fhuD* (6E⁻³¹).

2.3.3 Rhodochellin uptake genes in the Roseobacters

The Actinomycete *Rhodococcus jostii* RHA1 is known to synthesise a mixed catecholate-hydroxamate siderophore, rhodochellin. The biosynthetic genes for this siderophore have been described by Bosello *et al.* (2011). The first step from I-ornithine into I- δ -N-hydroxyornithine is catalysed by the monooxygenase, Rmo (Bosello *et al.* 2012), and a secondary structural pathway mediated by RhcB later adds the final module to complete the siderophore molecule (Bosello *et al.* 2011). The products of each of these two genes, *rmo*, and *rhcB*, were used to interrogate the Roseobacter genome sequences. Only homologues to RhcB were found in the Roseobacters, with 19 species having moderate ($1E^{-30} - 1E^{-60}$) homologues, and 6 species, namely, *Citreicella* SE45, *Phaeobacter gallaeciensis* 2.10, *Phaeobacter gallaeciensis* BS107, *Roseobacter* sp. GAI101, *Roseobacter* sp. MED193 and *Roseovarius* sp. TM1035, having good homologues ($7E^{-63} - 1E^{-135}$). *Roseobacter* sp. MED193 was found to have two well conserved homologues of RhcB ($1E^{-82}$ and $1E^{-67}$), although the best conservation was that observed for *Citreicella* SE45, with an E value of $1E^{-135}$.

2.4 Iron responsive regulators in the Roseobacters

To examine the presence of *known* iron-responsive transcriptional regulators in the Roseobacters, several, well characterised examples were used as queries.

2.4.1 Mur

Fur is the global <u>Ferric uptake regulator</u> originally identified in *E. coli* (Hantke 1981), and since shown to control iron homeostasis in a wide range of bacterial phyla. However, in the rhizobiales, Fur has become a "Mur", and regulates genes in response to Mn availability (see Introduction).

Two well-studied Mur peptides are those of *Bradyrhizobium japonicum*, and of *Rhizobium leguminosarum*. These probes revealed the presence of convincing Mur homologues in the great majority of Roseobacter strains (Table 2.1). These are considered in more detail in Chapter 6, as are those (which are of more interest) that *lack* a Mur-like regulator.

2.4.2 Irr and RirA

Rhizobium does regulate ferric iron and haem uptake, and to do so, it uses the antagonistic action of two transcriptional regulators; the Fur-family Iron responsive regulator, Irr and the RRF-2 family Rhizobial iron regulator, RirA (Todd *et al.* 2002). Irr represses genes in Fe-depleted conditions and, conversely, RirA negatively regulates genes in the presence of iron (again, refer to Introduction). Consequently, the amino acid sequences of both RirA of *R. leguminosarum*, and Irr of *B. japonicum* were each used to search for homologues in the Roseobacters.

No Roseobacter genome contains a homologue of the protein coding sequence of *Rhizobium rirA* with a cut-off value < E⁻²⁷. In contrast, all but three of the Roseobacter genomes had a close homologue of Irr, these being *Phaeobacter* sp. Y4I, *Rhodobacterales bacterium* HTCC2083 and *Rhodobacterales bacterium* KLH11, the last of which also lacked a homologue of Fur/Mur and RirA.

2.4.3 IscR

The final Fe-responsive regulator examined in Table 2.1 was the <u>Iron sulphur cluster Regulator</u>, IscR, which regulates the biosynthesis of iron sulphur cluster in *E. coli* (Schwartz *et al.* 2001), and whose encoding gene is found directly 5' of the Fe-S biosynthesis *suf* genes in the α -proteobacteria - refer to the Introduction for more detail.

However, IscR has been lost in the Rhizobiales (Rodionov *et al.* 2006), and although the *suf* genes remain, these are regulated by RirA and Irr (Todd *et al.* 2005). When the translated peptide sequence of *iscR* of *E. coli* O104:H4 was used to interrogate the *Rhodobacteraceae* proteomes, the closest homologue was found in *Rhodobacteraceae bacterium* KLH11 (9E⁻³⁹). This protein was found to be well conserved in the Roseobacters, and most homologues were annotated as IscR, and were found upstream of the *suf* genes, as occurs in other bacteria. All the sequenced Roseobacters had a homologue of IscR of *Rhodobacteraceae bacterium* KLH11 at an E-value of between 1E⁻⁵⁰ and 1E⁻⁷⁵.

2.4.4 The Roseobacters likely do not use ferric reductases

There were no homologues found in any Roseobacter genome to any known characterised ferric reductase (the products of the *ferA*, *ferB* / *mtrA* and *mtrB* genes of *Paracoccus denitrificans*

/Shewanella oneidensis). However, YqjH, a possible ferric reductase from *E. coli* - see Miethke *et al.* (Miethke *et al.* 2011), was found in only one Roseobacter genome - *Oceanicola granulosus* HTCC2516 (gene locus OG2516_12819, 38% ID to YqjH). However, even using this *Oceanicola* polypeptide as a probe, no other convincing homologues were found in the Roseobacters.

2.4.5 The Roseobacters may not import ferrous iron

Table 2.1 also includes two characterised ferrous iron transporter genes, *feoA* and *feoB* from *E. coli* K-12. Ferrous iron transport in *E. coli* is switched on in response to anaerobic growth, to facilitate iron uptake during infection (Cartron *et al.* 2006). Strikingly, there were no close homologues of the FeoA and FeoB gene products in any sequenced Roseobacter genome. This may indicate that the Roseobacters always live aerobically and do not have access to ferrous iron; indeed, there are no reports of anaerobic growth of Roseobacters.

2.4.6 Other genes linked to iron

Also shown in table 2.1 are the genes *irpA* and *irpB* of *R. pomeroyi* DSS-3 (refer to Chapter 3 for a detailed discussion of these genes). Both appear to be under the control of a strongly iron repressed promoter in *R. pomeroyi* and so their distribution among the Roseobacters was of interest. As table 2.1 shows, the IrpA polypeptide exhibited a clear "present or absent" pattern, with 30 strains having very close homologues (<1e⁻¹⁵⁰) to IrpA of R. pomeroyi (SPO0086), with the remaining 7 strains lacking a polypeptide with a detectable IrpA-like polypeptide. The *irpB* (*SPO0087*) gene of *R. pomeroyi* encodes a putative membrane protein. Homologues to this peptide were found only in *Sulfitobacter* sp. EE-36 (2E⁻⁵⁶), *Roseovarius* sp. 217 (6E⁻⁴⁸), *Roseovarius* sp. TM1035 (3E⁻⁴⁹), *Roseobacter* sp. GAI101 (8E⁻⁵⁶), *Roseobacter* sp. MED193 (7E⁻⁸⁵) and *Roseobacter* sp. SK209-2-6 (2E⁻⁸⁶), and in all cases the corresponding gene was very close to the *irpA* gene.

2.7 Discussion

This bioinformatic study of the iron homeostasis genes in the Roseobacters has revealed both the diversity of genes present, and the striking differences between species.

The Roseobacters are a taxonomically distinct group of the Rhodobacteraceae, so it may be expected that they share some features in their ability to acquire and respond to iron. However, this survey has shown that different strains and species may use very distinct portfolios of genes for the import of this metal, probably as a result of repeated acquisition of genes by horizontal gene transfer and/or loss of genes, and crucially demonstrates that the Roseobacters are a collection of very different bacteria, from many different genera.

The distribution of the TBDR proteins with specificity for iron-bound molecules appears to reveal three evolutionary strategies within the Roseobacters, the generalist strategy, where some species have many TBDR homologues; the specialist strategy, where only one or two TBDR homologues are present; and the "unknown strategy" group, which appear to lack any TBDR homologues. These organisms may have iron receptors which fall into a yet uncharacterised class of TBDR proteins, or simply lack TonB-mediated transport, and therefore use an entirely new method of outer membrane translocation of iron. It would be of great interest to study the function of TonB homologues in the Roseobacters to help identify these proteins definitively. Furthermore, those strains which appear to not have TonB could use a novel TonB independent iron import system.

Synthesis of siderophores is an expensive process for bacteria, especially so if they do not recover these siderophores. However, if enough marine bacteria synthesise these molecules, and indeed enough iron-bound chelating molecules leach into the oceans from the land, then a strategy of having receptors for a wide range of these iron-chelators would be advantageous; just as having a receptor with high promiscuity for various iron-chelates would be advantageous.

However, if a bacterium were to remove iron from a chelator at the outer membrane, then transport the iron in a ferrous form, this would negate the requirement for a complex and presumably substrate limiting receptor. We see such a 'reduction linked uptake strategy' in Synechocystis sp. PCC 6803, where Fe-siderophore complexes are reduced at the outer membrane interface, allowing uptake of biologically available iron into the cell (Kranzler *et al.* 2011). Nevertheless, we do see several genes that may encode siderophore biosynthesis and indeed uptake in the Roseobacters, but the lack of functionally verified genes from marine bacteria, for either uptake or biosynthesis of siderophores demonstrates the clear gap in knowledge here which unfortunately limits this analysis.

The distribution of RirA and Irr is interesting, and may be indicative of the loss of function of RirA in particular within most Roseobacters – indeed this gene is not conserved across the α -proteobacteria. Irr was conserved in nearly all Roseobacters, and indeed the function of this peptide is examined directly in *R. pomeroyi* in Chapter 5.

IscR is highly conserved throughout the Roseobacters, and is likely the functional regulator of iron-sulfur clusters across this group —always being found upstream of the *suf* genes.

It is very clear that all bioinformatic predictions here will require direct work to validate them. The following chapters do go some way towards this, with regards to Fe and Mn uptake in *R. pomeroyi*, and indeed go further afield to the Roseobacters and beyond when looking at Mn uptake systems (see Chapter 6).

Chapter 3 - *in silico* study of putative iron regulated genes of *R. pomeroyi*

3.0 Introduction

The previous chapter described an *in silico* survey of all the genome-sequenced strains of the Roseobacter clade for their types of iron uptake systems, as deduced by the presence of genes whose products were known to be involved in Fe homeostasis in other types of bacteria.

In this chapter, and in those that follow, attention is focussed on one particular strain of the Roseobacters, namely *Ruegeria pomeroyi* DSS-3 (see Introduction). From the survey conducted above, *R. pomeroyi* DSS-3 was one of the unusual strains in that it lacked any discernible siderophore production systems and also had no genes that were predicted to encode an outer-membrane TonB-dependent receptor. Indeed, this was one of those 30 Roseobacter strains that appeared to lack a version of TonB itself. Therefore, it was of interest to determine how this strain obtained its iron.

Before embarking on direct experimental work on this topic in *R. pomeroyi* DSS-3, its genome was subjected to another round of *in silico* analyses, but this time with the focus being on *cis*-acting regulatory sequences which by comparison with known regulatory motifs, were likely to be the binding sites for iron-responsive transcriptional regulators.

As before, Rodionov *et al.* (2006) set the stage for these studies, having already predicted some of these motifs and their downstream target genes. As described in the Introduction, the mechanisms of iron homeostasis in the alpha proteobacteria are very different from those in many other bacterial phyla, including those that harbour such model bacteria as *E. coli, Bacillus, Pseudomonas* and many others, in which the Ferric uptake Regulator, Fur, is the pivotal global Fe-responsive transcriptional regulator (Stojiljkovic *et al.* 1994; Vassinova and Kozyrev 2000). Instead a limited number of labbased studies, mainly on the Rhizobia, *Agrobactreium* and *Brucella* coupled with the *ab initio* bioinformatic predictions have shown the one of the key Fe-responsive regulators in the α-proteobacteria is Irr, which, although a member of the Fur super-family, is very different from Fur, *sensu stricto*, refer to the Introduction and (Hamza *et al.* 1998). In addition, some of the Rhizobia and their close relatives also have the transcriptional regulator RirA, which is a member of the Rrf2-

superfamily of regulators, very different in all ways from Fur, except in its overall role, which is to repress several genes involved in Fe acquisition in Fe-replete conditions (Todd *et al.* 2002).

Here we describe the distribution of two of these predicted regulatory, *cis* acting sequences in *Ruegeria pomeroyi*. These are (a) the ICE motifs, recognised by the Irr regulator and (b) the Iron-Rhodo (IR) boxes, whose corresponding transcriptional regulator has not been identified.

3.1.1 Irr and its target ICE sequences and genes in Ruegeria pomeroyi

Under Fe-depleted conditions (usually) the Irr polypeptide of several α -proteobacteria has been shown to bind to "iron control elements", repressing transcription of the downstream genes. These ICE boxes have a canonical sequence whose particular version in the Rhodobacteraceae is shown in Figure 3.1.

ICE box (Rhodobacteraceae)

Figure 3.1 Logos of iron responsive regulator binding sites in Ruegeria pomeroyi

Logo of predicted iron responsive regulator binding motif, the ICE box. Reproduced from Rodoionov et al. (2006).

Inspection of the genome of *R. pomeroyi* DSS-3 revealed four convincing ICE motifs, situated near the predicted promoters of the genes that would be regulated by Irr (summarized in table 3.1). Significantly, several of these resemble those that have been shown to be Fe/Irr-regulated in other bacteria and are as follows.

Table 3.1 Genes with ICE boxes

Those genes with a predicted ICE motif are shown. Detailed are their predicted function, locus and name. The sequence and position relative to the translational start codon of each ICE motif are also shown.

Gene locus / name	Predicted function	ICE box sequence	Position
SPO3842 mbfA	membrane-bound ferritin	AtcTTgGAATCATTCTAAAtT	-33 bp
SPO0382 fssA	hypothetical Fe-S scaffold protein	tcTTTAGAAcCgTTCcAAAgT	-75 bp
SPO2025 iscR-sufSBCD	Fe-S cluster assembly	AtcTTAGAATGgTTCTAAgtc	-102 bp
SPO0330 ccpA	cytochrome c peroxidase	AtgTTAGAATGATTCTAAtCg	-73 bp

3.1.2 SP03842, MbfA

This 324 amino acid polypeptide is ~70% identical to the corresponding gene product in the rhizobia, where it was first identified (Rudolph *et al.* 2006; Todd *et al.* 2005). The *mbfA* gene has been shown to be expressed at higher level in Fe-replete conditions, under the control of Irr in *Rhizobium*, *Brucellla*, *Bradyrhizobium* and, very recently, in *Rhodobacter sphaeroides*, the first published example in the Rhodobacterales (Peuser *et al.* 2012). MbfA has an unusual domain constitution – an N-terminal half with a ferritin-like fold within a domain that resembles a Rubrerythin electron transporter and a C-terminal half that is strongly predicted to be in the inner membrane – hence the term membrane-bound ferritin. A similar C-terminal domain is found in the CCC1 protein of yeast, where it also has a link with iron, being a trans-membrane protein that is required to accumulate manganese and iron in the vacuole of this fungus (Li *et al.* 2001).

MbfA is very much a signature polypeptide for the α -proteobacteria, being found in nearly all genome-sequenced strains of this sub-phylum, but only very rarely in other clades.

3.1.3 SP00382 FssA

A second *Ruegeria pomeroyi* gene that has an ICE box in its promoter region is *SPO0382*, whose product is 63% identical to FssA (iron sulfur scaffold) of *Rhizobium leguminosarum*. This was first described by Todd *et al.* (Todd *et al.* 2006) who noted that is very similar (48% identical) to a eukaryotic protein, which is termed Nfu1 in yeast and HIRIP5 (<u>HIRA-interacting protein 5</u>, the HirA protein being a transcriptional regulator of histone gene transcription) in mammals. These two eukaryotic proteins HIRIP5 act as scaffolds to transfer FeS clusters to different acceptor proteins (Lorain *et al.* 2001). As with MbfA, predicted orthologues of FssA protein are confined to the α -proteobacteria, although there is lower-level sequence similarity to parts of the NifU protein, another scaffold protein that delivers FeS clusters to nitrogenase (Agar *et al.* 2000).

3.1.4 SP00330; CcpA

CcpA is a widely distributed cytochrome-c peroxidase enzyme (pfam03150), which contain two haem groups, using the iron centres as cofactors to reduce H_2O_2 to water (reviewed by Torres and Ayala, 2010). Predicted orthologues (at least 70% identical) occur in a wide range of Proteobacteria, and in some cases, the regulation of the corresponding gene has been studied. For example, *ccpA* of *Pseudomonas stutzerei*, it was found to be under the control of Fnr, an O_2 -sensing transcriptional regulator (Vollack *et al.* 1999). Homologues of *ccpA* in the Rhizobiaceae and Rhodobacteraceae were shown to likely be under the control of Irr (Rodionov *et al.* 2006).

3.1.5 SPO2025–SPO2014; – *the* iscR-suf *operon*

As shown in Figure 3.2, the *Ruegeria pomeroyi* genome has a group of 12 contiguous genes that are preceded by an ICE motif. Based on detailed studies in several other bacteria, these are the *suf* genes, which are responsible for the synthesis of FeS clusters, plus the promoter-proximal gene, *iscR*, which encodes a transcriptional regulator of the Rrf2 family that regulates this operon in response to iron availability (Bandyopadhyay *et al.* 2008). The *suf* operon of several α -proteobacteria have ICE boxes in their *cis*-acting regulatory DNA (Rodionov *et al.* 2006) and it had been shown directly that the *suf* operon of *Rhizobium leguminosarum* is regulated by Irr, in response to Fe availability.

It was noted by Rodionov *et al.* (2006) that there was another potential regulatory motif, termed an IR box, which was predicted to be the site at which the IscR regulator bound. Interestingly the *suf* operon of *Rhizobium* is also under dual control, being repressed under Fe-depleted conditions, but, when the cells were grown with Fe sufficiency, the RirA regulator exerted a level of repression, due to its interaction with its cognate binding (IRO) motif that was immediately downstream of the ICE box (Todd *et al.*, 2006).

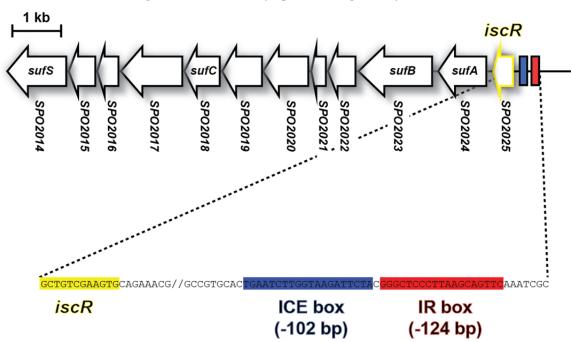


Figure 3.2 The iscR-suf operon of R. pomeroyi

Representation of the R. pomeroyi iscR-suf genes (SPO2014-SPO2025). Zoomed region shows position of IR (red) and ICE (blue) boxes 5' of iscR, whose 5' coding sequence is shown in yellow.

3.2.1 Iron-Rhodo (IR) boxes

The second set of conserved, potential cis acting regulatory sequences that might respond to Fe availability were termed Iron-Rhodo (IR) boxes by Rodionov et~al. (2006). The consensus IR box had some similarity to that of the IRO box recognition site of the previously identified RirA transcriptional regulator in the rhizobia and, to a lesser extent, to the motif termed IscR $^{\alpha}$ -box-I, which is the predicted IscR-binding site for the IscR of the Rhodobacterales (see Figure 3.3).

a) IRO box

b) IR box

cruck a final content of the
Figure 3.3 Logos of iron responsive regulator binding sites in *Ruegeria pomeroyi*

Logo representations of predicted iron responsive regulator binding motifs. a) IRO box, predicted binding motif of RirA, generated from DNA loci found in four Rhizobiaceae, two Mesorhizobium species, Brucella, and Bartonella. b) Iron-Rhodo box found in the Rhodobacteraceae, and c) IscR box from the Rhodobacteraceae. Reproduced from Rodoionov et al. (2006).

A total of six transcriptional units, together with their predicted IR sequences are listed in Table 3.2, and are as follows:

Table 3.2 Ruegeria pomeroyi genes with predicted IR motifs

Those genes with a predicted IR motif are shown. Detailed are their predicted function, locus and name. The sequence and position relative to the translational start codon of each IR motif is also shown.

Gene locus / name	Predicted function	IR box sequence	Position
SPO0086 irpA	iron-regulated protein A	aCTGACaAATTTAGTCAGA	-89 bp
SPO3139	similar to truncated hemoglobins	TCcGACTttAacAGTCgGA	-32 bp
SPO3287 fbpA	periplasmic binding protein	cCcGACTgAAaTAaTCAGt	-74 bp -25 bp
SPO0789 hemP	haemin uptake	ggcGACaAAAaTAGTCAGg	-100 bp
*SPO2025 iscR -sufSBCD	Fe-S cluster assembly	ctTGACgAATTcccTCgGg	-141 bp
*SPO3288 fbpB	permease	TCcGACTAAAcTgGTCgat	-39 bp

3.2.2 SP00086 - irpA

The *SPO0086* gene is the promoter proximal gene of a strongly predicted 5 gene operon, *SPO0086* – *SPO0090* shown in Figure 3.4 below. Of the polypeptides that are similar in sequence to the *SPO0086* gene product, the one that is, *a priori*, of most interest is that of *Synechococcus elongatus* PCC6301 (previously strain PCC7942) gene locus: syc0095_d (34% identical; 1e⁻⁵³). This polypeptide had been termed IrpA, because it was shown to be an <u>iron-regulated-protein</u>, mediated by the Fur transcriptional regulator and which was involved in iron uptake in these cyanobacteria (Reddy *et al.* 1988).

More broadly, the IrpA polypeptides are membrane-bound members of the M75 family of peptidases (Pfam cl09159), as first identified in *Pseudomonas aeruginosa* (Fricke *et al.* 1999). The IrpA-like polypeptide from *P. aeruginosa* PA4370 can cleave radiolabelled insulin, and was therefore

the founding member of the M75 family of proteins - the insulin cleaving metallopeptidases (ICMP), or imelysins, which were thought to bind to zinc. A functional and structural study of two groups of imelysin-like proteins was performed by Xu *et al.* (2011) who suggested that these proteins may act as a scaffold for iron uptake complexes to form on the outer membrane. Recently, a novel iron transporter EfeUOB was identified and characterised (Cao *et al.* 2007; Rajasekaran *et al.* 2009; Rajasekaran *et al.* 2010). Interestingly the 250 C-teminal residues of the EfeO protein was shown to contain an imelysin-like domain, the other half of this protein being a putative iron binding cupredoxin domain, which might bind iron (Rajasekaran *et al.* 2010).

SP00086 SP00087 SP00088 SP00089 SP00090

28 3 2 4

Figure 3.4 SPO0086-SPO0090 Operon Map

The SP00086-SP00090 genes of R. pomeroyi (arrows) likely form a single transcriptional unit, with small intergenic gaps shown as circled numbers of base pairs. Scale is indicated by 1 kb bar.

Close homologues of the IrpA of *Ruegeria* pomeroyi (termed IrpA^{RP}) are found throughout all divisions of the proteobacteria, with >250 homolgues with greater than 50% identity. Perhaps significantly, the first ~25 amino acids is sometimes absent from homologues of IrpA^{RP} when aligned (not shown). Indeed, when the IrpA^{RP} sequence was used as a query with SignalP [available at: http://www.cbs.dtu.dk/services/SignalP/] (Petersen *et al.* 2011), this program strongly predicted (90% chance) an N-terminal signal peptide that would be cleaved at position 22.

Furthermore, Irp^{RP} is strongly predicted to be localised in the outer membrane when analysed with psortb [available at: http://www.psort.org/psortb/index.html] (Yu *et al.* 2010), with a score of 9.93 (a value >7.5 is the cut-off value with this tool). The predicted topology was examined, using the trans-membrane domain prediction software Pred-TMBB [http://biophysics.biol.uoa.gr/PRED-TMBB/] (Bagos *et al.* 2004), which indicated that IrpARP has an extracellular loop, flanked by two transmembrane domains. It is unclear why a usually soluble M75 protein would be present in the outer membrane, but IrpARP may represent a significant evolution away from the canonical examples

of this peptide family. Furthermore, IrpA^{RP} does contain a putative metal binding site – HxxE, at position 182 of the amino acid sequence.

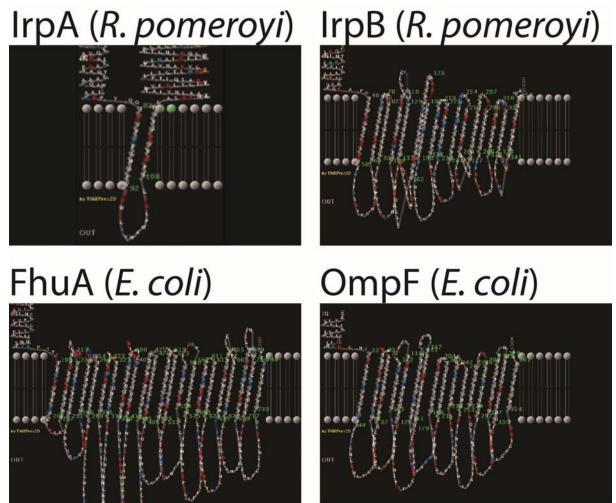
Of those imelysin-type proteins that have been functionally linked to iron uptake, the imelysin homologue in *Pseudomonas aeruginosa*, IcmP (gene locus - PA4370) was Fur-regulated (Cornelis *et al.* 2009). There is also a homologue of IrpA^{RP} in *Vibrio cholerae* VC1264, which has two Fur boxes in its promoter region, and is highly regulated by both Fur and iron (Mey *et al.* 2005). And, of course, the eponymous, original, IrpA of *Synechococcus* was identified on the basis of its response to Fe availability.

3.2.3 SPO0087 - irpB

The *SPO0087* gene product has no known domains and its function is unknown. In contrast to the very widespread range of IrpA homologues in the NCBI data base, there are very few (14) homologues of the SPO0087 gene product, even when a relaxed threshold (<4e⁻⁰⁸) was used, with seven of these being in other Roseobacter strains. (See table 2.1). It is also extremely poorly represented in the GOS marine metagenome data base, with only 5 homologues with E values < 0.01. It was noted, though, that the gene *MICA_2042* from the predatory 'vampire' bacterium *Micavibrio aeruginosavorus* ARL-13 (Wang *et al.* 2011) encodes a homologue of IrpB (30% identity, 8e⁻²¹) and that this gene may encode the periplasmic protein of a suggested manganese transporter.

The IrpB of *R. pomeroyi* is predicted to be in the outer membrane (psortb, >7.5), and to have a signal peptide (SignalP). Furthermore, Pred-TMBB predicts 16 trans-membrane helices, and a cytoplasmic, n-terminal 'plug' domain as shown in Figure 3.5 below. Indeed, IrpB is not dissimilar to the classical beta-barrels of the TonB-dependent receptors (Locher *et al.* 1998) or the outer membrane porin OmpF (both shown in Figure 3.5 below). However the IrpB polypeptide has no sequence similarity to either of these types of outer membrane polypeptides, so, if this general function has any validity, IrpB would have to represent a wholly new class of porin molecules.

Figure 3.5 IrpA, IrpB, OmpF and FhuA modelled in the outer membrane



The membrane architecture of IrpA and IrpB, of Ruegeria pomeroyi and FhuA and OmpF of E. coli DH1 as predicted using Pred-TMBB (Bagos et al., 2004).

3.2.4 SP00088

This gene encodes a hypothetical protein, with 2 cytochrome C-like domains (DUF1111 [pfam06537]), but It is predicted to localise to the cytoplasmic membrane (10.0 in psortb). There are close homologues in many alpha-Proteobacteria (including 33 of the Roseobacter strains) where for example, the *RSKD131_2939* of *Rhodobacter sphaeroides* KD131 (61% identity, E-value = 0), is adjacent to 2 bacterioferritin genes and an M75 imelysin homologue of IrpA^{RP}.

3.2.5 SP00089

The *SPO0089* gene product is also a member of the imelysin group of M75 family peptidases and, indeed, is 31% identical to the *SPO0086* product (see above) and 25% identical to the experimentally characterised IrpA of *Synechoccus*. Its closest match (56%) was to a gene (*SL1157_1932*) in *Silicibacter lacuscaerulensis* ITI-1157, and most of the genome-sequenced Roseobacter strains contain homologues with ~50% identity to the *SPO0089* gene product.

3.2.6 SP00090

Finally, in this operon, the product of *SPO0090* is also a domain of unknown function, although it is strongly predicted {by tatP: (Bendtsen *et al.* 2005)} to contain a TAT export signal (see review by Palmer and Berks 2012), with the mature protein being located in the membrane.

When the layout of the genes in other bacteria that encoded homologues of the *Ruegeria pomeroyi SPO0086 – SPO0090* was examined, it was striking how similar was their synteny, even in distantly related bacterial strains. Thus, very similar arrangements were seen in members of the Alteromonadales (28 taxa), Vibrionacaea (14 taxa), Pseudomonadales (29 taxa), Oceanospiralles (4 taxa) {all gamma-proteobacteria}, Comamonadaceae (10 taxa) {betas}. And, outside the Proteobacteria, homologues of both *SPO0086* and *SPO0088* are found as adjacent genes in several strains of the Cyanobacteria (37 taxa), the Bacteroides/Chlorobi (36 taxa, the Spirochaetales (18 taxa) and finally the Chlamydiae/Verrucamicrobia (18 taxa).

It was noted that the γ -proteobacterium *Vesicomyosocius okutanii*, an intracellular endosymbiont of the deep-sea clam, and which has a small (<1.1 Mb) genome, has a predicted operon that comprises, in order from the promoter: a homologue of *SPO0086*, then *SPO0088*, followed by two hypothetical genes, then a multicopper oxidase, and finally, an iron ABC transporter, including a homologue (36 % identical) of *SPO3288*; this points to a role in Fe transport for this operon.

Furthermore, all sequenced genomes of the Rhizobiales, and both *Rhodobacter sphaeroides*, and *Ruegeria* TM1040 contain all but one (*SPO0087*) of the members of the *SPO0086 - SPO0090* operon. However, these all have one or more genes in the position occupied by *SPO0087 in Ruegeria pomeroyi*; in the Rhizobiales there is a single gene that encodes a multicopper oxidase, and in both

Rhodobacter and Ruegeria TM1040, there are two genes which encode bacterioferritin (reviewed in Andrews 1998; Carrondo 2003).

We also noted that the genome of *Roseobacter denitrificans* contains a homologue (74 % identical at the amino acid level) of *SPO0086*. Perhaps significantly, this is adjacent to a gene that encodes a predicted, FbpB-type (see below), permease of an ABC transporter for Fe uptake.

Taken together, the *SPO0086 – SPO0090* operon of *Ruegeria* appears to have several suggested and ratified links as judged by the predicted functions of the homologues of the various gene products. It is also striking that several of the gene products are associated with the bacterial membrane(s), again pointing to a possible role in Fe transport.

The preservation of this cluster of genes in a range of bacteria suggests that their products function co-ordinately, though the role of the special case of *SPO0087* is certainly not clear.

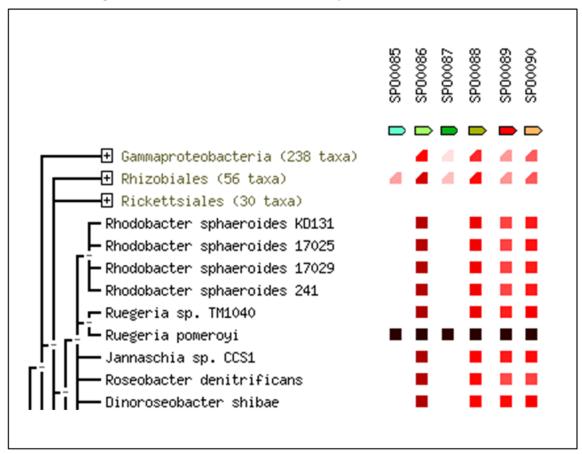


Figure 3.6 STRING 9.0 Co-occurance analysis of SPO0086-SPO0090

Co-occurrence analysis of SP00086 to SP00090 reveals the presence of a homologue of SP00085 in those species and taxa shown. The darkness of squares indicated the quality of similarity, black being 100%, fading from dark red to light pink as similarity diminishes. Analysis was performed using STRING 9.0 [http://www.string-db.org/].

3.2.7 SPO3139 – A truncated haemoglobin protein

The product of the gene *SPO3139* is a member of the family of O_2 -binding homo-dimers that are widespread in bacteria and eukaryotes, but its function is unknown. Significant homologues (>30 % identity) are found in most other Roseobacters. The function of this gene is not known in any of the bacteria in which it has been found, though its general predicted function, as a polypeptide that binds O_2 is consistent with its being regulated in response to Fe availability.

3.2.8 SP00789- hemP

This gene encodes a very small (50 amino acids) polypeptide, that resembles the HemP polypeptide of *Escherichia coli*, which had been shown to be required for the uptake of haeme in that species, and to be regulated by Fur, in response to Fe availability (Stojiljkovic and Hantke 1992). There is a motif homologous to an IR box located 100 bp upstream of the *hemP* translational start. The *hemP* gene in *R. pomeroyi* is found as part of a two gene (predicted) operon, the other member, *SPO0790*, encodes a hypothetical protein found in a few Roseobacter genomes. However, *hemP* is only present in *R. pomeroyi*, and not in any other Roseobacters. A close homologue of HemP was found in *Rhodobacter sphaeroides* (64 % identity), where a recent microarray study showed that this gene was ~5-fold induced by low iron, and deregulated (~15-fold) in a Fur background (Peuser *et al.* 2011). This Fur homologue is described as a Fur/Mur, regulating both Fe and Mn uptake in *Rhodobacter* (Peuser *et al.* 2011).

3.2.9 Components of an iron specific ABC-class transporter – FbpA and FbpB

There are two adjacent, convergent transcribed genes, *SPO3287* and *SPO3288*, each of which is preceded by a convincing IR sequence (Figure 3.7). These two genes are strongly predicted to encode the periplasmic binding protein and the permease of an ABC-type transporter, each of these polypeptides being particularly similar to those that are involved in iron uptake in many other bacteria – hence their names of ferrous binding proteins (Fbp). Close homologues of these two gene products not only occur in all the Roseobacters (see Table 2.1) but in a very wide range of other bacteria many different phyla (proteobacteria, Firmicutes, Cyanobacteria, for example). Not unexpectedly for Fe uptake polypeptides, the expression of the *fbp* genes has been shown to be repressed in Fe-replete bacteria (for example *Vibrio cholerae* (Mey *et al.* 2005), *Sinorhizobium meliloti* (Chao *et al.* 2005) and *Rhizobium leguminosarum* (Todd *et al.* 2005; Todd *et al.* 2002)), and this has been shown to be mediated by the Fur transcriptional regulator in *V. cholerae*, and by RirA in *Rhizobium* and *Sinorhizobium*.

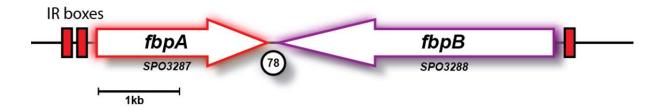
The genome of one species, *Vibrio cholerae* O1 biovar El Tor str. N16961, encodes good homologues of *fbpA* (40% identity) and fbpB (41% identity), plus *SPO2689* (40% identity). These three genes, *VC0608*, *VC0609* and *VC0610*, are all transcribed unidirectionally, and are identified as *fbpABC* in this strain. There is a sequence homologous to the canonical Fur box upstream of *fbpA*, and indeed this

gene has been shown to be negatively regulated by both iron, and Fur (Mey *et al.* 2005). The subsequent genes *fbpBC* must be transcribed from a second promoter, as their expression was unaffected by iron or Fur (Mey *et al.* 2005). The function of these genes were verified by Wyckoff *et al.* (2006), where they showed that cloned *V. cholerae fbpABC* is able to complement the growth defect of an iron uptake deficient strain *S. flexneri* (strain SM193w). Wyckoff and colleagues also showed that the uptake of ⁵⁹Fe into SM193w cells increased 6-fold when the cloned *fbpABC* genes were present. Intriguingly, they also show that iron deficient growth of an *E. coli* TonB⁻ EntF⁻ strain (ARM100) was enhanced when the cloned *Vibrio fbpABC* genes were introduced (Wyckoff *et al.* 2006). This is especially interesting given that another FbpA homologue in *Neisseria shayeganii* 871¹ (locus *HMPREF9371_0466*, 39% identity to FbpA of *R. pomeroyi*) is possibly extracellular. Homologues of FbpA are present in all pathogenic strains of *Neisseria* (Ferreiros *et al.* 1999) and have been shown to bind to iron (Zhu *et al.* 2003). Ferreiros *et al.* (1999) also show that FbpA is antigenic and subsequently that parts of the protein have an extracellular presence through the outer membrane.

Although *R. pomeroyi* FbpA and FbpB are similar in sequence to other Fbp polypeptides, they have two rather unusual features, compared to the canonical arrangement of the *fbp* genes elsewhere. In most bacteria the genes that encode all three components of the Fbp transporter are contiguous and co-transcribed. Clearly this is not the case here, where *fbpA* and *fbpB* are both in single gene transcriptional units. Furthermore, there is no nearby gene that corresponds to *fbpC*, which encodes the ATPase cassette that is a signature of ABC transporters.

¹ misannotated as an ATPase of the FbpABC transporter. The translated product of *HMPREF9371_0466* has an E-value of 0 to the characterised FbpA of *Neisseria weaveri* ATCC51223 and *Neisseria weaveri* LMG5135.

Figure 3.7 Arrangement of fbpA and fbpB genes in R. pomeroyi



Arrangement of the genes SP03287 (fbpA) and SP03288 (fbpB) in the genome of R. pomeroyi; the positions of IR boxes are shown as red squares. The intergenic gap of 78 bp is indicated, and scale is shown by the bar marked 1kb.

In an attempt to identify the cognate ATPase of this transporter in *Ruegeria pomeroyi*, the amino acid sequence of a *bona fide* FbpC was used to interrogate the deduced proteome of this strain. The closest matches were to *SPO2689*.

Furthermore, STRING 9.0 neighbourhood analysis was performed using FbpA and FbpB of *R. pomeroyi* as query proteins. This analysis confirmed the presence of FbpAB arranged as a potential transcriptional unit in many phyla of bacteria. In many species, homologues of genes encoding FbpA and FbpB had a third gene present, *fbpC*. This gene was in the same orientation as *fbpA* and *fbpB* indicating that it may be part of the same transcriptional unit. This pattern was observed throughout the proteobacteria, and even extended further from this taxonomic group, although with decreasing certainty as the similarity between proteins decreased with evolutionary distance; this gene was always predicted to be homologous to *SPO2689* of *R. pomeroyi*.

3.3.1 Concluding comments

These *in silico* searches of the *Ruegeria pomeroyi* have extended those of Rodionov et al (2006). We can conclude that many of those genes predicted to be under the control of iron responsive regulatory motifs are indeed likely to be involved in Fe uptake and/or metabolism or are at least deduced to be so. The likely iron homeostasis system of *R. pomeroyi* involves a large set of genes, including probably transporters, iron storage proteins and transcriptional regulators. However, some of the genes discussed above remain a mystery, such as the *irp* genes, and the seemingly incomplete

fbp transporter. Indeed, homologues of many of the predicted iron-regulated genes discussed above have been shown to be regulated by iron in other bacteria, either via unknown means, or by cognate iron responsive regulators such as Fur and RirA and Irr.

Although useful, bioinformatic studies need to be confirmed, or otherwise, by direct experimental work. Such is the material in the remainder of this thesis, in which the roles and regulation of some selected genes is described and, at the end, by a pan-genomic, microarray investigation of *R. pomeroyi*.

Chapter 4 - *in vivo* studies on iron uptake in *R.*pomeroyi

4.0.1 Introduction

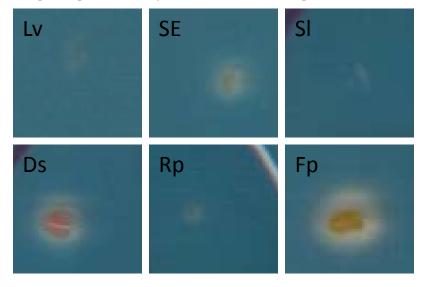
As shown previously, several potential iron homeostasis genes were identified, *in silico*, for *R. pomeroyi*. However, this strain appears to lack any known outer membrane transport system for iron, and does not appear to be able to synthesise siderophores. Also, the *fbp* genes of *R. pomeroyi* appear to be incomplete and are arranged in an unusual orientation. The following experimental work explores these facets of this marine bacterium.

4.1.1. R. pomeroyi does not produce siderophores

The bioinformatic interrogations in Table 2.1 predicted that *R. pomeroyi* DSS-3 does not appear to be able to synthesise siderophores, nor does it possess the necessary receptors for siderophore uptake or the energy conduit TonB. This was tested directly, using the chrome azurol sulphonate (CAS) assay for siderophore production (Schwyn and Neilands 1987). When complexed with Fe³⁺, CAS agar is blue in colour, but this turns orange when the iron is chelated by a molecule with higher affinity than CAS, such as a siderophore. Importantly, this assay is independent of the chemical class of siderophore and can be readily adapted to microbes growing on solid media, in which case, colonies of siderophore-producing strains are surrounded by orange halos.

As seen in Figure 4.1, *Ruegeria pomeroyi* DSS-3 failed to make such an orange halo, nor did some other Roseobacter strains (Petursdottir and Kristjansson 1997; Van Trappen *et al.* 2004) that were also examined (Figure 4.1). In contrast, *Fulvimarina pelagi* strain HTCC2506, which is in the closely related Rhizobiales family of α -Proteobacteria, did make a pronounced orange halo on CAS medium. Another strain of the Rhizobiales, *Dinoroseobacter shibae* DFL-12 (Biebl *et al.* 2005) also produced a small CAS halo.

Figure 4.1 Siderophore production by different strains and species of the Roseobacter clade



Cells from single colonies of a selection of Roseobacter strains were picked to MBM minimal medium with CAS and 5mM FeCl₃ and incubated at 28° C for 4 days before scoring for the orange halo that indicates siderophore production. Lv = Loktanella vestfoldensis SKA53, SE = Sulfitobacter EE36, SI = Silicibacter lacuscaerulensis ITI-1157, Ds = Dinoroseobacter shibae DFL-12, Rp = Ruegeria pomeroyi DSS-3, Fp = Fulvimarina pelagi.

4.1.2 Iron deficiency limits growth of R. pomeroyi

Since *R. pomeroyi* does not produce siderophores, and appears to lack an identifiable means of outer membrane iron transport, it was of interest to examine its iron requirement for growth, something that had not been previously done for *R. pomeroyi* or indeed, any strains of Roseobacters. Therefore, *R. pomeroyi* DSS-3 (a rifampicin resistant derivative of strain J470) was grown in minimal MBM media, containing 500 nM or 20 µM FeCl₃ respectively, and in MBM with no added iron.

As shown in Figure 4.2, R. pomeroyi has an absolute requirement for Fe for growth and responds to levels as high as 20 μ M. Higher concentrations did not enhance growth rate or final cell density (data not shown). In comparative experiments with another bacterium, Rhizobium leguminosarum, whose Fe homeostasis has been studied in detail (summarised in Crosa et al. 2004), a similar pattern was seen. Thus, R. pomeroyi is not exceptional in terms of its need for a supply of Fe for its ability to grow and must therefore have an effective system for capture of this metal.

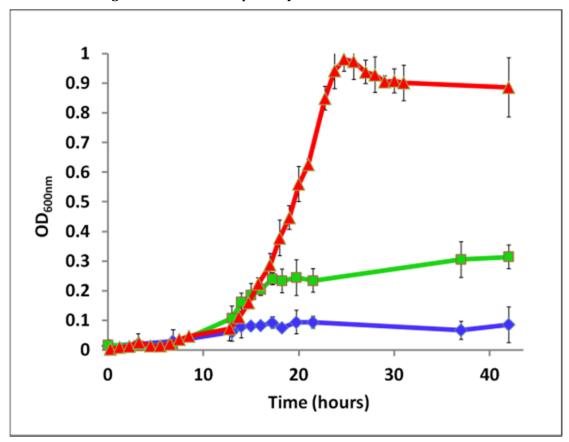


Figure 4.2 Growth of *R. pomeroyi* in MBM with iron limitation

R. pomeroyi cells were grown in MBM with no added iron (BLUE line), with 0.5 μ M FeCl₃ (GREEN line) or 20 μ M FeCl₃ (RED line). Triplicate cultures were incubated at 28°C, shaking at 200 rpm. OD_{600nm} values with standard errors are shown.

4.1.3 The fbp *iron transport genes of* R. pomeroyi

The only genes that were strongly predicted *in silico* in the *R. pomeroyi* genome sequence were the adjacent *SPO3287* and *SPO3288*, whose products were similar to two of the key components that form Fbp iron ABC-type transporters, found in many other bacteria (see Table 2.1 and Figure 3.7). The product of *SPO3287* and *SPO3288* gene products closely resemble the periplasmic binding protein and the trans-membrane transporter respectively. As mentioned above, the convergently transcribed arrangement of *fbpA* and *fbpB* is unusual, as is the lack of a nearby *fbpC* gene, encoding the ATPase.

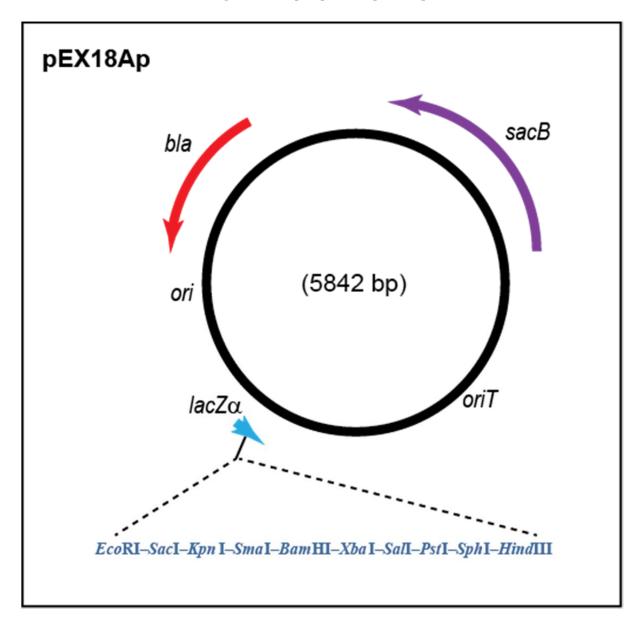
The sections below describe attempts to show if these genes do indeed, encode Fe transporters and to determine if and how they are subject to Fe-responsive regulation.

4.1.4 Disruption of the fbpAB genes does not affect growth of R. pomeroyi

To make a genomic mutation in *fbpA* and *fbpB* of *R. pomeroyi* DSS-3 (J470), most of the coding region of both genes was deleted and was replaced with a selectable marker. To do this, the "suicide" plasmid pEX18Ap (Hoang *et al.* 1998) was used. This is a wide host-range plasmid that encodes ampicillin resistance (via its *bla* gene) and can be mobilised from *E. coli* to many different proteobacteria, but it fails to replicate in such hosts (Figure 4.3 PLASMID MAP). It also contains a polylinker cloning region and a *sacB* gene, which encodes a levan-sucrase that cleaves sucrose into glucose plus fructose, the latter being polymerised to levan, a toxin for most bacteria (Bollen *et al.* 1979; Gay *et al.* 1985).

A 5011bp region of DNA that spans both fbpA and fbpB was amplified by PCR, using oligonucleotides **FbpABflankF** and **FbpABflankR** and *R. pomeroyi* genomic DNA as a template. This PCR product was cut using EcoRI and HindIII and ligated into pEX18Ap, cut with the same enzymes. The ligated products were used to transform competent $E.\ coli$ JM101 cells (a $IacZ\alpha - \omega + \text{strain}$) which were spread onto LB agar plates containing ampicillin to select for transformants. The resultant colonies were screened for plasmids with the correct insert by restriction endonuclease analysis of plasmids that were isolated from a selection of these transformants (Figure 4.4). Two recombinant plasmids (pBIO2103 and pBIO2104) containing a band of the correct size - 5011bp, were confirmed by sequencing.

Figure 4.3 Map of plasmid pEX18Ap



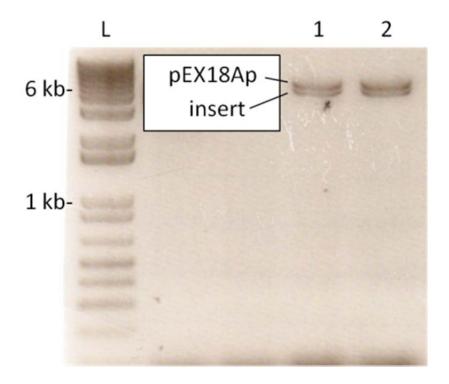
Key features of plasmid vector pEX18Ap showing positions of the origins of replication (ori), and of transfer (oriT), the sucrose inducible sacB gene, the ampicillin resistance gene (bla) and the lacZ α gene, containing multiple cloning sites, indicated with dotted lines.

One of these plasmids, pBIO2103 was then used for further manipulations in which most of the *fbpA* and *fbpB* genes were removed and were replaced with a a spectinomycin resistance (Spc^R) cassette. There are two *Pst*I sites, one located within *fbpA* and one within *fbpB*, such that most of the coding sequence of the genes could be deleted by cutting with *Pst*I, and replaced with the SPEC^R cassette which was obtained by PCR using oligonucleotides **SpecPstIF** and **SpecPstIR** on DNA of another plasmid, R100, as the template (see Figure 4.5). Both pBIO2103 and the SPEC^R cassette DNA were

digested with *Pst*I, ligated together, and used to transform *E. coli* JM101 as described before, selecting ampicillin and spectinomycin resistance. This resulted in pBIO2105, shown in panel 3 of Figure 4.5.

Plasmid pBIO2104 was transferred from *E. coli* to *R. pomeroyi* cells via a tri-parental conjugation, selecting for Amp^R/Spc^R transconjugants. Since pBIO2104 is a derivative of pEX18Ap, the only surviving cells should be those that had undergone a single recombination (SCO) event between the chromosome and the incoming plasmid, in the homologous region flanking *fbpA* or *fbpB* (refer to Figure 4.5 below). Cultures from three such transconjugants were grown overnight in non-selective complete HY medium, to allow for a second, intra-molecular crossover event that would remove the majority of the plasmid DNA, including the *sacB* gene, but would retain the insertion of the Spc^R cassette in the *fbpAB* genes. These were detected by examining single colonies derived from the overnight cultures for those that were Spc^R and sucrose resistant, but had lost their resistance to ampicillin; three such derivatives were retained for further study. Approximately 30% of the colonies derived from the initial cross proved to be correct as judged by their resistance patterns.

Figure 4.4 pBIO2103, and pBIO2104

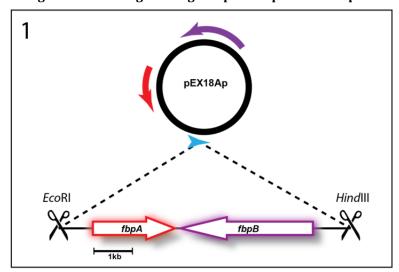


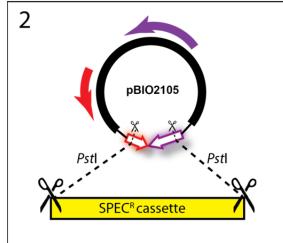
Two independent derivatives of pEX18Ap, into which a 5011bp fragment spanning fbpA and fbpB of R. pomeroyi was cloned, were digested with EcoRI and HindIII and the resultant fragments were visualised following electrophoresis on a 1% agarose gel. Lanes 1 (pBIO2103) and 2 (pBIO2104) both show two distinct bands at the appropriate size for both pEX18Ap (5842bp) and the 5011bp cloned fragment (labelled as insert). Size marker ladder (L).

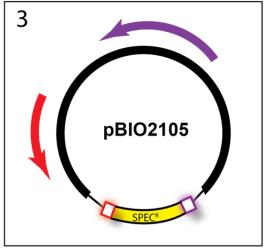
To check that these were genuine replacement mutants, genomic DNA was obtained from each of these three strains and was used as template for PCR amplification using two sets of primers, whose ability to produce amplicons of particular sizes should provide diagnostic evidence for the veracity of the intended mutational events.

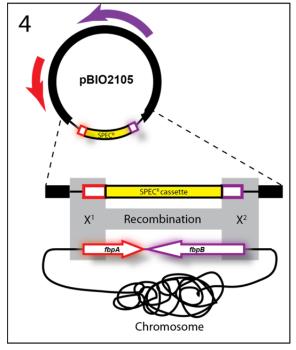
Thus, primers **P1** and **P2** should yield a product of 2316 bps if the SPEC^R cassette has inserted as intended but should give no product if not (e.g. if the cassette had inserted elsewhere in the genome). Primers **P1** and **P3** would show that a size difference would occur for the deletion of a 1880 bp *Pst*I fragment within *fbpA* and *fbpB*, and the insertion of a 1700 bp Spc^R cassette – the wild type product was expected to be 2800 bps, and the mutant strain should yield 2620 bps. This 180 bps difference is clearly visible in the lower right panel of Figure 4.6, for samples 2 and 3 compared to the wild type. These two sample strains were renamed J531 and J532.

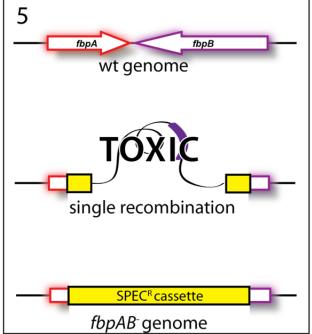
Figure 4.5 Creating a mutagenic pEX18Ap derivative pBIO2105











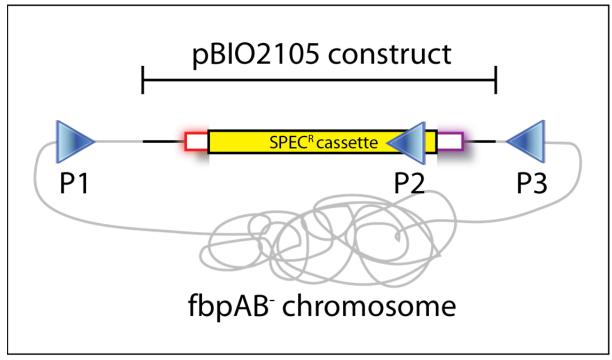
Panel 1. A 5011 bp region of R. pomeroyi genome was amplified and cloned into pEX18Ap using EcoRI and HindIII (panel 1), yielding pBIO2103

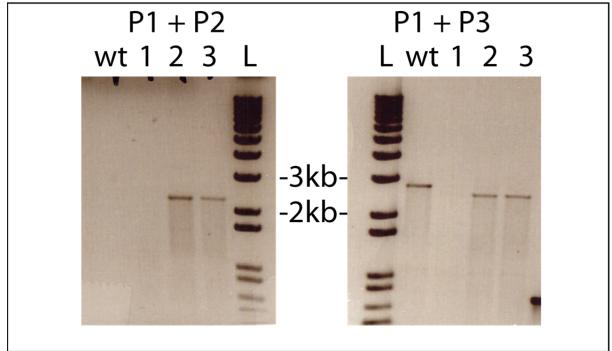
Panels 2 and 3. The DNA between the PstI sites in fbpA and fbpB was removed and was replaced with a SPEC^R fragment, also cleaved with PstI, to form plasmid pBIO2105.

Panel 4. Plasmid pBIO2105 was transferred to R. pomeroyi cells via conjugation, a host in which this plasmid cannot replicate. Homologous recombination events within the regions of homology between the genomic DNA and pBIO2105 occur at locations shown as X^1 and X^2 .

Panel 5. Addition of sucrose ensures that the incoming plasmid pBIO2105 is lost, by selecting against single recombination mutants, which will express the lethal sacB gene expressed from the pEX18Ap plasmid DNA. The final product is a strain in which the cassette has replaced the majority of the fbpAB DNA.

Figure 4.6 Screening FbpAB strains of R. pomeroyi using PCR





Upper panel depicts the position of oligonucleotide priming sites for screening potential fbpAB strains of R. pomeroyi. The sites are located within the SPECR cassette (P2), and upstream of the region 5' of fbpA used to generate pBIO2105 (P1). Used in a standard colony PCR reaction (see Materials and Methods) these oligonucleotides would fail to generate a product in the wt strain, but could amplify the region shown between P1 and P2 to generate a 2400bp PCR product. As shown in the lower panel, a band at 2400bp is visible for samples 2 and 3, but not in the wt, verifying the mutagenesis for samples 2 and 3. Furthermore, primers P1 and P3 used together allowed the visualisation of the change in size of the fbp region following the replacement of a 1880 bp PstI fragment by a 1700 bp SPECR cassette. Lane 1 did not produce a PCR product with either set of primers and so this strain was discarded.

4.1.5 Growth phenotype of the $\Delta FbpAB$ strain of R. pomeroyi

To test the effects of deleting the *fbpAB* genes in strains J531 and J532 the growth rates of these two mutants in Fe-replete and Fe-depleted MBM media were compared with the wild type. As shown in Figure 4.7, the $\Delta fbpAB$ mutation had no detectable effect on the growth either in the presence (20 μ M) or absence of added FeCl₃. Thus, this putative FbpAB transporter was not critical for iron uptake in *Ruegeria*. In addition to the data shown in figure 4.7 below, an intermediate level of FeCl₃ was tested (500 nM); however, the FbpAB⁻ strains were unchanged in growth compared to the wt at this intermediate iron concentration and so it was omitted.

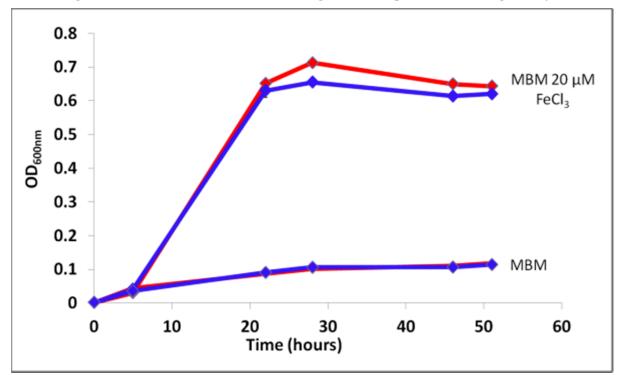


Figure 4.7 The effect of iron limitation on growth of FbpAB strains of R. pomeroyi

R. pomeroyi wt (red lines) and FbpAB⁻ (blue lines) were grown in MBM with no added iron (- FeCl₃) or supplemented with 20 μ M FeCl₃ (+ FeCl₃). Cultures were incubated at 28°C, shaking at 200 rpm. Data shown are the mean OD_{600nm} values of three replicate cultures of each mutant strain (J531 and J532) with the standard deviation shown as error bars.

4.1.6 Analysis of fbpA-lacZ and fbpB-lacZ transcriptional fusions

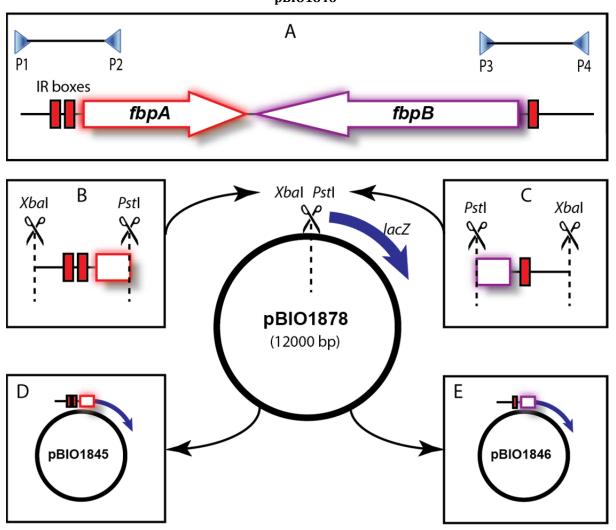
The genes *fbpA* and *fbpB* were predicted to be under the control of a putative *cis*-acting regulatory motif, the IR box (described earlier), suggesting that their transcription would vary, according to the availability of Fe in the medium, through the action of an as-yet unknown transcriptional regulator. To test directly if the expression of *fbpA* and/or *fbpB* was affected by Fe availability, transcriptional fusions to each of these genes were made, and assayed, as follows.

The transcriptional fusion vector pBIO1878 (Todd *et al.* 2011) was used as the basis for the construction of these *lac* fusions. Plasmid pBIO1878 is derived from pMP220, which has a wide host-range in gram negative bacteria, a polylinker 5' of its promoter-less *lacZ* reporter and a gene that confers tetracycline resistance (Spaink 1987). However, the Tet^R phenotype is expressed rather poorly in *Ruegeria* and other Roseobacters, so a more suitable selectable *spc* gene marker, which

confers resistance to spectinomycin, had been cloned into the *Sph*I site of its poly-cloning site (Todd *et al.* 2011).

To generate the *fbpA-lacZ* and *fbpB-lacZ* fusion plasmids, their individual promoter regions were each amplified from *R. pomeroyi* genomic DNA using primers **fbpAfwd** and **fbpArev** for the *fbpA* promoter (**P1** and **P2** in Figure 4.8) and primers **fbpBfwd** and **fbpBrev**,(**P4** and **P3** in Figure 4.8) for the *fbpB* promoter. These fragments were each purified from gels, cloned into pBIO1878 such that the *lacZ* reporter would be under the control of the *fbpA* (pBIO1845) or *fbpB* (pBIO1846) promoter. The constructs were verified by sequencing. Details of the steps involved are shown in Figure 4.8.

Figure 4.8 Generation of wide host range fbpA- and fbpB-lacZ fusion plasmids pBIO1845 and pBIO1846



Locations of the primers used to amplify the promoter regions of fbpA (P1 and P2) and of fbpB (P3 and P4) are shown in panel A. Note that these primers contain XbaI and PstI restriction sites used for subsequent cloning steps (see Panels B and C). Each PCR fragment was cleaved with XbaI plus PstI and ligated to pBIO1878, digested with the same enzymes. These manipulations produced plasmids pBIO1845 and pBIO1846 in which the reporter lacZ would be controlled by the fbpA and fbpB promoters respectively (Panels D and E). The two IR boxes preceding fbpA gene and the one preceding fbpB are indicated.

To measure the transcription of fbpA and fbpB, plasmids pBIO1845 and pBIO1846 were each mobilised by conjugation into R. pomeroyi strain J470.Transconjugants were selected on HY agar plates containing 50 μ g/ml rifampicin and 200 μ g/ml spectinomycin. For each cross, three separate, purified transconjugants were assayed for β -galactosidase activity (detailed in Materials and

Methods) following growth in MBM minimal media that either contained (20 μ M) or lacked added FeCl₃.

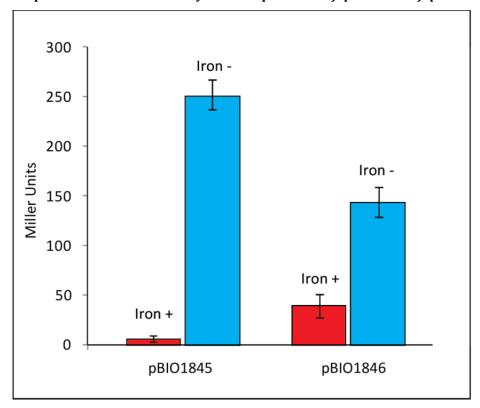


Figure 4.9 Expression of iron availability on the expression of fbpA-lacZ and fbpB-lacZ fusions.

Ruegeria pomeroyi containing either the fbpA- or fbpB-lacZ fusion plasmids (pBIO1845 and pBIO1846 respectively) were grown in minimal medium (MBM) either supplemented with 20 μ M FeCl₃ (Iron +) or not (Iron -) and assayed for β -galactosidase activity, expressed in Miller units. Error bars represent the standard deviation of 2 biological, and three technical replicates.

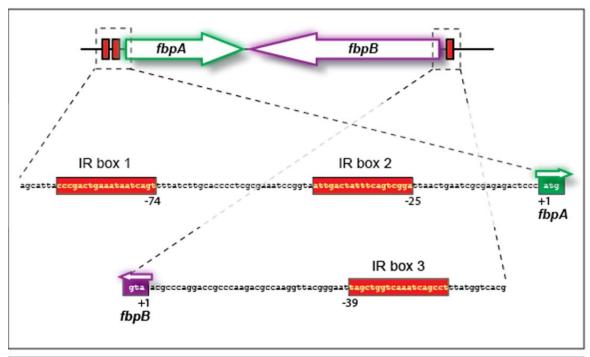
Both the *fbpA-lacZ* and *fbpB-lacZ* fusions were expressed at much higher levels in Fe-depleted than Fe-replete media, ~41-fold for *fbpA-lacZ* and rather less (3.5-fold), for *fbpB*.

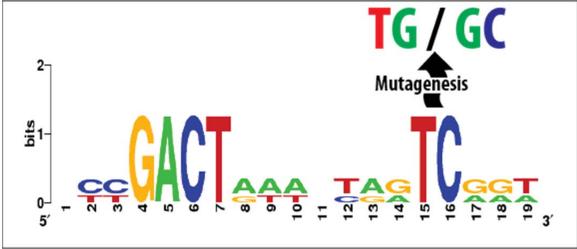
4.1.7 IR motifs preceding fbpA and fbpB are important for their Fe-responsive transcription

As predicted by Rodionov and colleagues (2006), and discussed in Chapter 3, both *fbpA* and *fbpB* have regions of dyad symmetry upstream of their transcriptional start codons, which are resemble

the motifs found upstream of many putative iron-responsive genes in the Rhodobacteraceae. These "IR boxes", their sequences and positions are shown in Figure 4.10 below.						

Figure 4.10 The IR boxes upstream of fbpA and fbpB of R. pomeroyi





Upper panel shows the R. pomeroyi genomic fbp region, with sequences 5' of fbpA and fbpB shown in the zoomed boxes, dotted lines. The locations of the two IR motifs (boxes 1 and 2) upstream region of fbpA and the single IR 5' of fbpB (box 3) are shown in red. The numbers on the DNA sequences denote the distances from the corresponding "A" of the ATG translational starts of fbpA (green highlight) and fbpB (purple highlight).

Lower panel shows the consensus sequence for all three IR boxes generated using WEBLOGO. The conserved TC motif was used as a target for subsequent site-directed mutagenesis, and was changed to both a TG and GC motif for all three boxes.

The *lacZ*-fusion plasmids pBIO1845 and pBIO1846 contained the promoter regions of *fbpA* and *fbpB* respectively, including all perceived IR boxes, and so were used as templates to generate site directed mutations in these putative regulatory motifs. To do this, the mutagenic primers shown in Table 4.1 were used to alter the conserved TC motif shown in Figure 4.10. Both the T and C bases were mutated to a G for each of the three IR boxes (6 mutants in total). Since *fbpA* has two IR boxes, a seventh mutant was constructed, where the T nucleotide of the conserved TC motif in each IR box was changed to a G. Care was taken to not disrupt the putative -10 and -35 promoter sequences, which were predicted to overlap the 3' end of the IR boxes, hence the selection of bases at the 5' end of the IR boxes for mutagenesis.

Table 4.1 Oligonucleotide primer sequences for IR box site directed mutagenesis

Oligonucleotide primers used to mutate the bases of IR boxes 1-3 as shown in Figure 4.10, of fbpA (boxes 1 and 2) and fbpB (box 3) of R. pomeroyi. The primer names, sequence and nucleotide target for mutagenesis are shown along with the resultant mutagenised plasmid name. All bases listed as a target were mutated to a G.

Oligo Name	Sequence	Target	Plasmid
fbpA51TtoGFWD	GCGACAGCATTACCCGACTGAAATAAGCAGTTTTATCTTGC	IR box 1 'T'	pBIO2106
fbpA51TtoGREV	GCAAGATAAAACTGCTTATTTCAGTCGGGTAATGCTGTCGC		
fbpA51CtoGFWD	GCGACAGCATTACCCGACTGAAATAATGAGTTTTATCTTGC	IR box 1 'C'	pBIO2107
fbpA51CtoGREV	GCAAGATAAAACTCATTATTTCAGTCGGGTAATGCTGTCGC		
fbpA2TtoGFWD	GCGAAATCCGGTAATTGACTATTTCAGGCGGATTAACTGAATCG	IR box 2 'T'	pBIO2108
fbpA2TtoGREV	CGATTCAGTTAATCCGCCTGAAATAGTCAATTACCGGATTTCGC		
fbpA2CtoGFWD	GCGAAATCCGGTAATTGACTATTTCAGTGGGATTAACTGAATCG	IR box 2 'C'	pBIO2109
fbpA2CtoGREV	CGATTCAGTTAATCCCACTGAAATAGTCAATTACCGGATTTCGC		
fbpBTtoGFWD	TCAGGCACTGGTATTTCCGACTAAACTGGGCGATTAAGGGCATTGGAACC	IR box 3 'T'	pBIO2110
fbpBTtoGREV	GGTTCCAATGCCCTTAATCGCCCAGTTTAGTCGGAAATACCAGTGCCTGA		
fbpBCtoGFWD	TCAGGCACTGGTATTTCCGACTAAACTGGTGGATTAAGGGCATTGGAACC	IR box 3 'C'	pBIO2111
fbpBCtoGREV	GGTTCCAATGCCCTTAATCCACCAGTTTAGTCGGAAATACCAGTGCCTGA	IN SOX 3 C	P5.02111
fbpA51TtoG	Both sets of primers used sequentially.	IR box 1	nDIO2112
fbpA2TtoG	Both sets of primers used sequentially.	and 2 'T'	pBIO2112

Each mutagenic reaction was performed, as detailed in Materials and Methods, and the mutated plasmid DNA was used to transform $\it E.~coli~XL10-GOLD~cells$. Transformants were selected on LB agar with spectinomycin added at 200 $\mu g/ml$. Plasmids containing the correct mutations were assigned pBIO numbers shown in Table 4.1 above.

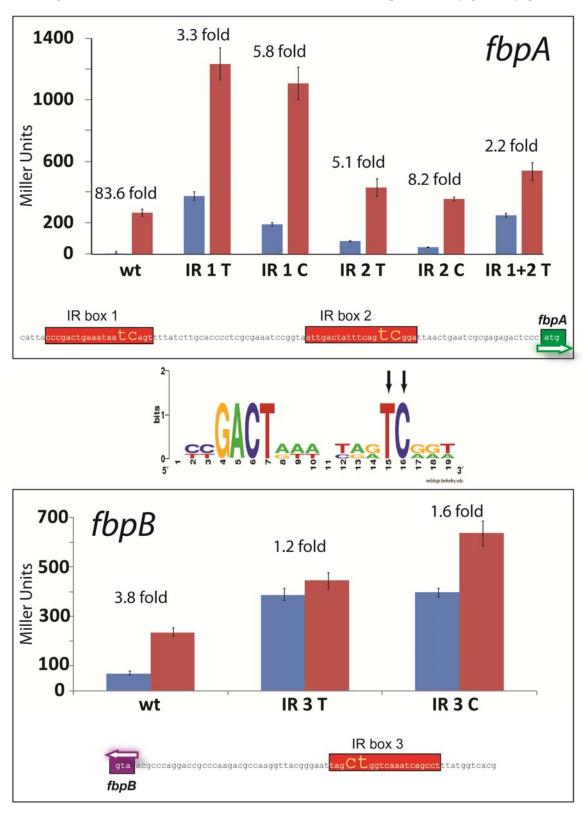
Having generated, and sequence verified, a suite of single base-pair mutations in the IR boxes of fbpA and fbpB, each of the mutant plasmids was mobilised into R. pomeroyi and the transconjugants were assayed for β -galactosidase activities after growth in Fe-depleted and Fe-replete conditions.

As shown in Figure 4.11, all of the mutations resulted in an increase in the level of expression of the corresponding fusion, though there were differences in the details of this deregulation in the individual mutations.

Thus for *fbpA-lacZ*, both mutations (refered to here as T and C) in IR box 1 greatly increased the expression of the fusion both in +Fe: 4.6- (T) and 4.2-fold (C) compared to wild type, and –Fe: 118- (T) and 60.1-fold (C) when compared to wild type. Mutations in IR box 2 also enhanced the transcription of *fbpA-lacZ*, in both media, though not to the same extent as those in box 1: 1.6- (T) and 1.3-fold (C) in the +Fe media, and 26.5- (T) and 13.7-fold (C) in the –Fe media, compared to the wild type. Perhaps surprisingly, the mutant plasmid pBIO2112, which had mutations in both IR box 1 and IR box 2 behaved similarly to pBIO2110, which had mutations only in IR box 2.

Turning to the *fbpB-lacZ* fusion, its expression was also enhanced by each of the mutations in the IR box 3. The "T" mutation led to an enhanced constitutive expression, in which the transcription of the fusion was similar in both –Fe and +Fe media. When the "C" was mutated, though, there was even higher expression in the –Fe than the +Fe media (Figure 4.11).

Figure 4.11 Effects of mutations in the IR boxes on the expression of fbpA and fbpB



The fbpA-lacZ and fbpB-lacZ fusion plasmids pBIO1845 and pBIO1846 respectively were used to generate IR box mutants. The highly conserved TC motif in the IR boxes of fbpA and fbpB (arrowed in middle panel) was mutated, so that each base became a G nucleotide, separately, in 6 different mutant plasmids. In a seventh mutant, the conserved T bases in both fbpA IR boxes were mutated to G. Expression of the lacZ fusions in R. pomeroyi containing the various mutant plasmids after growth in MBM with 20 μ M FeCl₃ (BLUE BARS) or none added (RED BARS) and is shown in Miller units in the upper and lower panels, for fbpA and fbpB respectively. Wild type fusion is labelled wt. All data are the average of 3 biological and two technical replicates.

4.1.8 'The "Irp" operon of Ruegeria pomeroyi.

Of the transcriptional units that were preceded by IR motifs, located in their predicted regulatory regions, another one whose gene products were implicated in Fe uptake was the 5-gene operon comprising *SPO0086 – SPO0090*, in which the product of the promoter-proximal gene, *SPO0086* was very similar to IrpA in other bacteria. The location and sequence of this IR motif is shown in Figure 4.12.

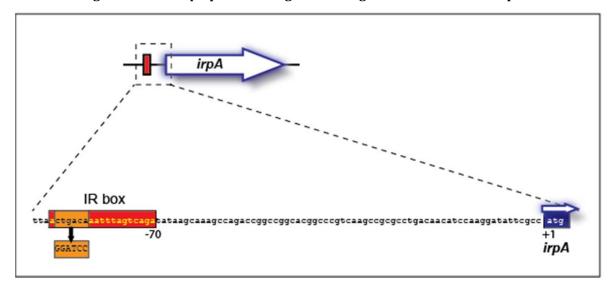


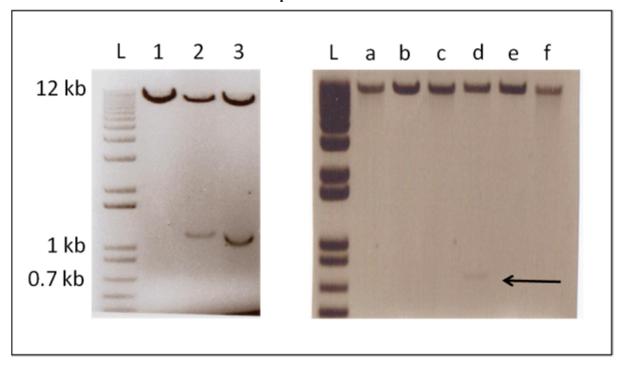
Figure 4.12 The irpA promoter region showing IR box location and sequence

The sequence 5' of irpA is shown, including the IR box (red box) 70bp upstream of the ATG start of irpA. The sequence in orange was subject to SDM, from ctgaca to ggatcc, creating a BamHI site.

4.1.9 Expression of irpA is repressed by iron in R. pomeroyi

To study the expression of the *irp* operon, a transcriptional fusion plasmid, pBIO1847, was constructed by cloning a 1016bp region spanning the 5' upstream region of *irpA* of *R. pomeroyi* into pBIO1878, following amplification by PCR using primers **irpAfwd** and **irpArev** and *R. pomeroyi* genomic DNA as the template. DNA from plasmid pBIO1847 was also used as a template for site-directed mutagenesis (SDM) of the IR motif upstream region of *irpA*. Briefly, primers **IrpABamHIFWD** and **IrpABamHIREV** were used to substitute the CTGACA (which includes the adjacent, highly conserved GA – see figure 3.3b) to GGATCC, which represents a *Bam*HI site to facilitate screening of potential mutants (see Figure 4.13).

Figure 4.13 Gel photos of clone, and site-directed mutant clone, of the promoter region of *irpA* into pBIO1878



The left panel shows the restriction digest pattern of the DNA of three potential recombinant plasmids, containing the irpA promoter region cloned into pBIO1878, and digested with XbaI plus PstI, and separated on a 1% agarose gel. A fragment of the correct size (1016 bp) is seen in Lanes 1 and 2. The plasmid in Lane 2 was used as the template for SDM, where a BamHI site was made in the IR motif, 744 bp downstream of the PstI site. The right panel shows the DNA of 6 potential mutant derivatives of pBIO1847, digested with PstI and BamHI. Sample 'd' liberated a fragment of the correct size (see arrow). Following sequence verification, this mutated plasmid was named pBIO2115.

The plasmids pBIO1847 and pBIO2115 were introduced by conjugation into *R. pomeroyi* J470. For each plasmid, three different transconjugants were grown in MBM minimal medium either containing 20 μ M FeCl₃ or with no added Fe, before assaying β -galactosidase activities.

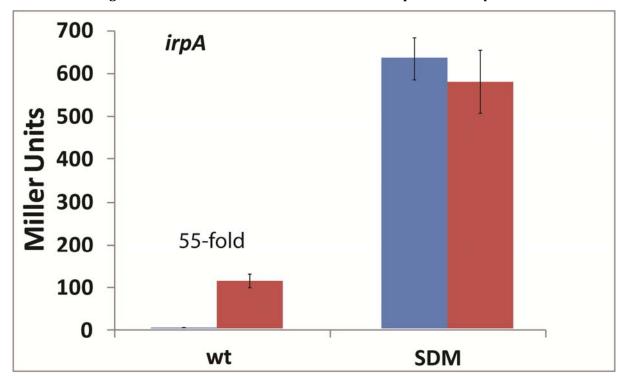


Figure 4.14 Effects of Fe and the IR motif on the expression of irpA-lacZ

Plasmids pBIO1847 (wt irpA-lacZ) and pBIO2115 (SDM irpA-lacZ) in R. pomeroyi were assayed for 6-galactosidase activity following growth in MBM either containing 20μ M FeCl₃ (blue bars) or no added iron (red bars). Data are in Miller units (y-axis) and represent the average of three biological replicates.

As shown in (Figure 4.14), the expression of the wild type version of the *irpA-lacZ* fusion (in plasmid pBIO1847) was much higher (55-fold) in the Fe-depleted than the Fe-replete media. Furthermore, the removal of the IR box in the mutated plasmid pBIO2115 resulted in greatly increased expression, both in the absence and even more dramatically (313-fold compared to the wild-type) in the presence of added Fe. Thus, the *irpA* operon is regulated in response to Fe and this requires a functional IR box motif.

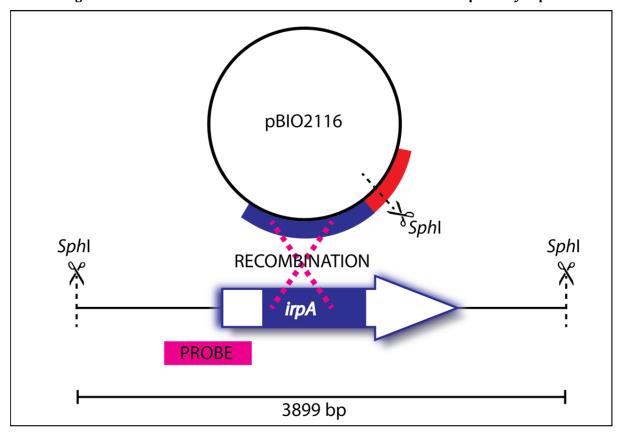
4.1.10 Construction of an IrpA- strain of R. pomeroyi

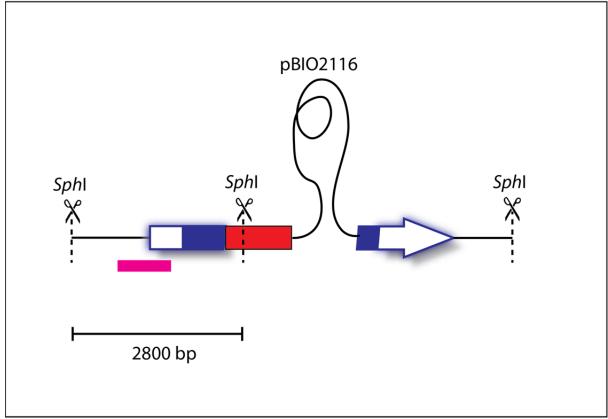
Mutations in *irpA* of *Synechococcus elongatus* PCC 7942 had been shown to be deficient in their growth in low-Fe media (Reddy *et al.* 1988). To examine the effects of mutating the homologous gene in *Ruegeria*, an IrpA⁻ strain was made, as follows. The vector used to construct this mutant, pBIO1879, was derived from the wide host-range "suicide" plasmid pK19mob (Schafer *et al.* 1994),

and has a spectinomycin resistance cassette cloned into the PCS, and so confers resistance to both spectinomycin and kanamycin (Todd *et al.* 2011). The chosen method of mutagenesis involves the cloning of an internal fragment of the targeted gene into pBIO1879, followed by the introduction of the resulting plasmid in a recipient bacterium (in this case *Ruegeria* pomeroyi) in which it cannot replicate. Therefore, by plating on selective media containing spectinomycin plus kanamycin, insertional mutants, generated by homologous recombination between the cloned internal fragment and the target gene can be obtained (see Figure 4.15).

An internal fragment of *irpA* was amplified using PCR, using primers **IrpApk19fwd** and **IrpApk19rev**, using *R. pomeroyi* genomic DNA as a template. This 740 bp PCR product was purified and digested with *Eco*RI and *Xba*I, ligated into pBIO1879, then transformed into *E. coli*, a host species in which the plasmid can replicate normally. Plasmid DNA was isolated from a selection of the transformants and one, termed pBIO2116, that contained the correct insert (as checked by restriction digests and sequencing) was retained for further use.

Figure 4.15 Insertion and ratification of insertion mutation into *R. pomeroyi irpA*





The pK19mob derived suicide vector pBIO2116 integrates into irpA of the R. pomeroyi genome, via a single recombination event with the cloned internal irpA DNA, shown in blue. The dimensions of the DNA used as the probe in the Southern blots are shown in pink. As shown, this would hybridise to a 3899 bp fragment in the wild type, and a 2,800 bp fragment if pBIO2116 has inserted into irpA.

This plasmid was then mobilised into *R. pomeroyi* J470 by conjugation, selecting transconjugants on HY medium containing rifampicin (to kill the donor *E. coli*) plus spectinomycin and kanamycin (conferred by the incoming plasmid). Colonies arose at a frequency of $^{\sim}10^{-2}$, and several of these were purified and checked for insertions into *irpA*, as follows.

First, a 'colony-PCR' based approach was used, with primers **irpA1F1** and **irpA2R2**, which are located to either side of the *irpA* gene. These would amplify a 1751bp region if presented with wild type template DNA, but if there was a large insertion within the gene, no PCR product would be made. Of 6 colonies that were examined, one failed to generate a PCR product, so likely contained an insertion in *irpA*. This was confirmed by a Southern blot, in which genomic DNA was isolated from this putative mutant and probed with a DIG-labelled DNA fragment that spanned the 5' end of the *irpA* gene. This would reveal a ~4 kb (exact size is 3899 bp) band in a Southern blot with the wild type DNA, but if the plasmid pBIO2116 had inserted into *irpA*, the predicted size of the hybridising band would be smaller, since pBIO2116 contains a *SphI* site within the spectinomycin resistance cassette. The DNA from the putative IrpA- mutant did indeed, lead to the production of a hybridising fragment of the expected size for an insertional mutation, as shown in Figure 4.16 below. This IrpA- mutant was named J533.

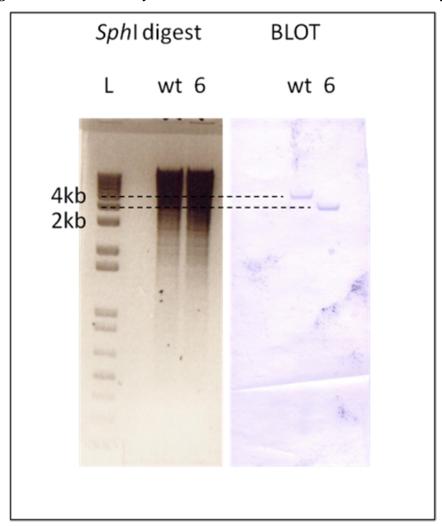


Figure 4.16 Verification by Southern blot of an insertional mutation into irpA

Genomic preps of wild type R. pomeroyi (wt) and putative IrpA· strain (6) digested with SphI and separated on a 1% agarose gel (left-hand panel), were blotted and probed with DIG-labelled DNA corresponding to the 5' end of irpA. The sizes of the hybridising bands are indicated. The size marker is shown as L.

4.1.11 Phenotypic analysis of the IrpA- strain of R. pomeroyi

Although the IrpA⁻ strain of *Synechococcus* grew poorly on iron deficient media compared to the wild type strain (Reddy *et al.* 1988), no such defect was seen when the IrpA⁻ mutant strain J533 of *R. pomeroyi* was cultured in MBM minimal medium to which no FeCl₃ had been added.

There was no detectable difference between the wild type and IrpA strain after 60 hours of growth. To see if there was an effect of residual iron from the starter culture, the MBM cultures were subcultured into MBM containing iron or not as before. These cultures were still identical for growth in both iron-depleted and -replete MBM after another 70 hours. It is therefore unlikely that IrpA alone is required for iron uptake or storage, as suggested by Reddy et al. (1988) for the *Synechococcus* IrpA protein.

4.1.12 Iron-responsive expression of the hemP *and* iscR *genes of* R. pomeroyi

As described in Chapter 3, two other *Ruegeria pomeroyi* genes, namely *hemP* and *iscR* are preceded by predicted IR boxes, these two genes being predicted to encode, respectively, a polypeptide involved in haem uptake and in the regulation of the complex operon that includes *iscR* itself, plus the downstream *suf* genes (Table 3.2).

To examine the expression of *hemP* and of *iscR*, transcriptional *lacZ* fusions to each gene were constructed, using the same general approach as described above for the *fbp* genes. For *hemP*, a 546 bp spanning its promoter region was amplified, using primers **SPO0789XbaIF1** and **SPO0789PstIR1**. For *iscR*, an 840 bp region spanning its 5' upstream region was amplified, using primers *iscRpS4F* and *iscRpS4R*. The resultant products were each purified, digested with *XbaI* plus *PstI*, and cloned, separately, into pBIO1878. The sequence verified *hemP-lacZ* and *iscR-lacZ* fusion plasmids were named pBIO2117 and pBIO2118 respectively. These plasmids were crossed into *R. pomeroyi* by triparental conjugation as described earlier and the transconjugants were assayed for β-galactosidase after growth in Fe-depleted and Fe-replete MBM minimal medium.

As shown in Figure 4.17, both the *hemP*- and *iscR-lacZ* fusions were expressed at significantly higher level in the Fe-depleted medium than in the medium to which 20 μ M FeCl₂ had been added. However, the factors of increase were much less than had been seen with the *fbp-lacZ* fusions, especially for *hemP*, where the *hemP* fusion was expressed <2-fold more in the –Fe than in the + Fe medium. This was due, largely, to the higher expression of both these fusions in the Fe-replete medium. Note that the absolute levels of expression were considerably greater for the *hemP*- than the *iscR-lacZ* fusion.

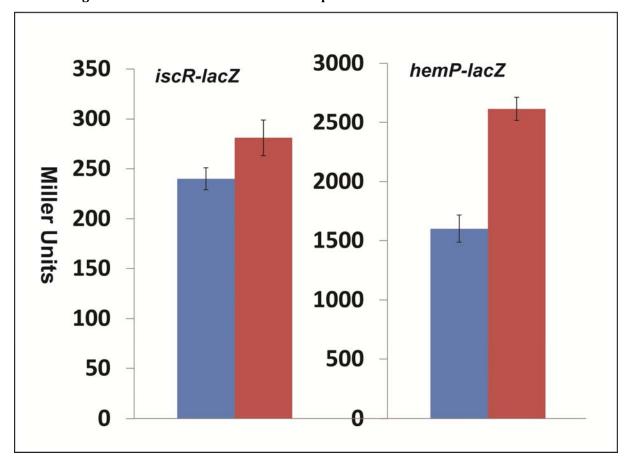


Figure 4.17 Effect of iron limitation on expression of hemP- and iscR-lacZ fusions

Assays were performed on R. pomeroyi containing the iscR-lacZ and hemP-lacZ fusion plasmids pBIO2118 and pBIO2117 respectively, after pre-growth in MBM containing 20 μM FeCl₃ (RED BARS) or no added iron (BLUE BARS). Results are averages of three biological and two technical replicates.

4.2 Discussion

The *fbp* genes of *R. pomeroyi* are expressed separately, immediately obvious due to the convergent transcription of each gene. Although the *fbpABC* genes are arranged contiguously in *Vibrio*, the genes still have very different expression patterns, as the RNA levels of each gene differ significantly, *fbpA* is expressed at a much greater level than *fbpB* (Wyckoff *et al.* 2006). This was also clearly true of *R. pomeroyi*, shown via the expression of *lacZ*-fusions. The regulation of each of these two genes was also different, with *fbpA* far more inducible by low iron conditions than *fbpB*.

It is possible that FbpA is capable of binding to extracellular iron and facilitate transport across the outer membrane without the need for a TBDR, as the evidence of (Ferreiros *et al.* 1999) in *Neisseria* show.

However, mutations in the *fbp* genes of *R. pomeroyi* have shown that there must be at least one other system of iron uptake encoded on the *Ruegeria* genome. The bioinformatics predictions made in this work and in (Rodionov *et al.* 2006) did not give any insight into the identity of this transporter.

R. pomeroyi is predicted to lack TonB, or any TBDR. Given that FbpABC of V. cholerae is able to enhance growth of TonB⁻ E. coli in low iron conditions (Wyckoff et al. 2006), it is possible that iron is transported into the cell in ferrous form – possibly via a ferric reductase, where it is internalised through a porin, much like the predicted product of irpB (SPO0087). Indeed, the bioinformatics study on the irp operon of R. pomeroyi alludes to fascinating future data on the role of these genes in iron uptake and homeostasis.

The expression of several iron uptake genes - those with an IR box motif upstream, was not completely deregulated in response to site directed mutations made in these motifs. This phenotype must mean another regulator – or regulatory system is controlling these genes. Whether this is via an uncharacterised transcriptional regulator, or a small RNA such as in the case of RyhB (Massé *et al.* 2005), remains unresolved.

The expression of *fbpA* and *irpA* in particular appeared to be highly inducible by low iron, something which was not so apparent from the expression of the *lacZ*-fusions for *fbpB*, *hemP* and *iscR*, although all these genes also had an IR box motif. Perhaps the cognate regulator of these IR boxes has highly specific binding properties, and has simply lost the ability to control these boxes. Bioinformatic searches for such motifs does risk finding 'pseudo-motifs' - relics of iron regulation in an ancestral strain.

Chapter 5 - Iron-Responsive transcriptional regulators in *R. pomeroyi* DSS-3

5.1 Introduction

As shown in Chapter 4, two potential (though not ratified) iron uptake systems in *R. pomeroyi* are tightly controlled, and have been shown to be expressed in Fe-depleted condition. This regulation was shown to require IR boxes, as shown by the effects of disrupting these *cis*-acting sequences. As mentioned before, the canonical IR box sequences are similar to those of the "IRO box" which are the target of an Rrf2 family transcriptional regulator, RirA.

A second Fe-responsive transcriptional regulator that is characteristic of the α -Proteobacteria is Irr, which can bind to very different motifs, known as ICE boxes (see above).

The genome of *Ruegeria pomeroyi* has several genes with products in the Rrf2 family of transcriptional regulators plus one gene that resembles *irr*. This observation, coupled with the fact that this bacterium has motifs that correspond to ICE boxes and to IR boxes, underpins the work described in this chapter, in which evidence was sought to define the roles, if any, of these regulators in iron homeostasis in *Ruegeria*.

5.2 in vivo analysis of iron responsive regulators of R. pomeroyi

5.2.1 The Rrf2 family of proteins in Ruegeria pomeroyi and the Roseobacters

A BLASTp search of the proteins encoded by the genome of *R. pomeroyi*, using the *Rhizobium leguminosarum* RirA amino acid sequence (gene locus *RL_0777*) as the probe revealed five members of the Rrf2 family proteins, encoded by the genes *SPO0432*, *SPOA0186*, *SPO1393*, *SPO3722* and *SPO2025*. To show the relationship between the five Rrf2 family proteins and several characterised examples of Rrf2 family transcriptional regulators a phylogenetic tree was made.

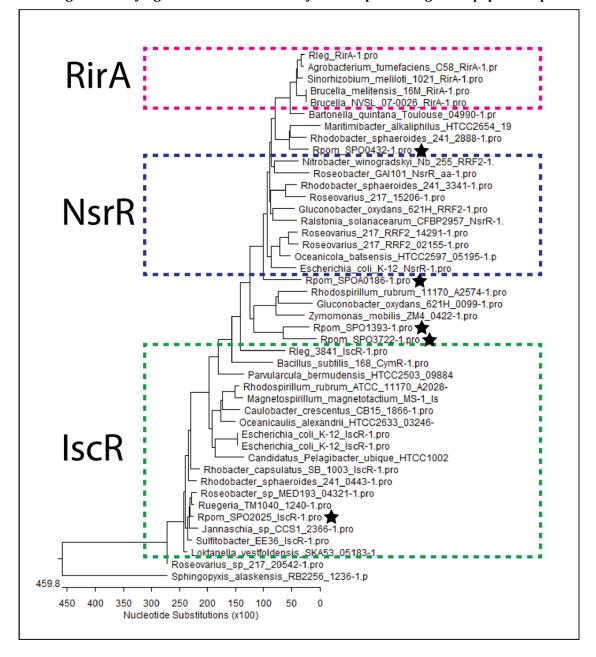


Figure 5.1 Phylogenetic tree of Rrf2 family transcriptional regulator peptide sequences

Phylogenetic tree generated using an alignment of peptide sequences of Rrf2 family proteins. Those with a functional annotation are labelled accordingly – RirA, IscR and NsrR (<u>N</u>itrosative <u>s</u>tress <u>r</u>esponse <u>R</u>egulator). Marked with a star are the 5 Rrf2 peptides found in the deduced proteome of R. pomeroyi.

As shown in Figure 5.1 and in Rodionov *et al.*, (2006), none of these *Ruegeria* Rrf2 family proteins cluster with the characterised examples of RirA. However, there is a likely candidate for an NsrR-type regulator, the product of *SPOA0186*, and a likely candidate for an IscR-type regulator, the product of

SPO2025. Interestingly, two Rrf2 family proteins (the products of *SPO1393* and *SPO3722*) are not very similar to each other (42% identical), but form something of an out-group of the Rrf2 superfamily in this bacterium.

As table 5.1 below shows, only SPO2025 is present in all the Roseobacter genomes. The next most common and indeed the most similar to RirA of *Rhizobium* was *SPO0432*. Proteins homologous to both *SPO1393* and *SPO3722* were only found in *Ruegeria pomeroyi*.

Table 5.1 Prevalence of Rrf2 gene homologues of Ruegeria in the Roseobacters

Gene	No. of hits in Roseobacters <1E ⁻²⁰
SPO0432	26
SPOA0186	10
SPO1393	1
SPO3722	1
SPO2025	38

5.2.2 Construction and analysis of mutations in genes for Rrf2-family proteins in Ruegeria

Since there was no obvious candidate that matched RirA *sensu stricto*, it was decided to make insertional mutations in all five genes that encode Rrf2-family proteins and determine if these have any effects on the expression of one or more genes that contain IR motifs. The approach taken was the same as that used to make the *irpA* mutation, above. Thus, fragments internal to each of the five genes were cloned into the suicide plasmid pBIO1879 and these were used to generate insertional mutations into the corresponding chromosomal gene following the introduction of the various mutagenic plasmids into *Ruegeria pomeroyi* J470. The particular primers used to generate the insert fragments for this set of constructions are shown in Table 5.2 below.

Table 5.2 Primer sequences used to generate mutant strains of *R. pomeroyi*.

Primer	Sequence	Plasmid	Mutant
SPO0432EcoF	ATCGGAATTCGCATTACCAAGCGCACAAAT	pBIO2119	J534
SPO0432XbaR	ACGTTCTAGATTATCACAGACCAGCGCATC		
SPO3722F	CACCGAAGGACTGGAATGG	pBIO2120	J535
SPO3722R	ACGTTCTAGATGAGAGCTTTTCCTGAAACCA		
SPO1393F	AGTCGAATTCATTGGGTGACGGGGTAGAG	pBIO2121	J536
SPO1393R	TACGTCTAGAGCCTGGAGATTCTCAAATCC		
SPO2025F	TGACGAATTCGTCGACAAAGGGGCGCTAT	pBIO2122	J537
SPO2025R	AGTCTCTAGATCTTCACCACATCCGAAAGC		
SPOA0186F	ACGTGAATTCCTCCAAGTTCTCCGACTATGC	pBIO2123	J538
SPOA0186R	GACTTCTAGACCGGATCGTATTTTGACCTG		

Each of the five recombinant plasmids was ratified by verifying the correct insert, and then crossed into *R. pomeroyi* J470 by tri-parental conjugation. Mutants were selected for using spectinomycin, kanamycin and rifampicin as detailed earlier. Each mutant was checked using Southern blots and/or PCR. The mutant strains with ratified insertions in the five *SPO* genes were named as follows: SPO1393⁻ = J536, SPO3722⁻ = J535, SPO0432⁻ = J534, SPOA0186⁻ = J538, SPO2025⁻ = J537.

Then, into each of these mutants was introduced each of the two transcriptional fusion plasmids containing fbpA-lacZ (pBIO1845) and irpA-lacZ (pBIO1847). The array of transconjugants were then grown in Fe-depleted and Fe-replete media as described above and assayed for β -galactosidase activity. In no case was the behaviour of either fusion, in either of the growth media markedly different from the case when the wild type strain harboured these plasmids (not shown). Thus, it appears that neither irpB nor fbpA is under the control of any of the Rrf2 family proteins examined here.

5.2.3 Ruegeria pomeroyi Irr – a global iron-responsive regulator in other α -proteobacteria

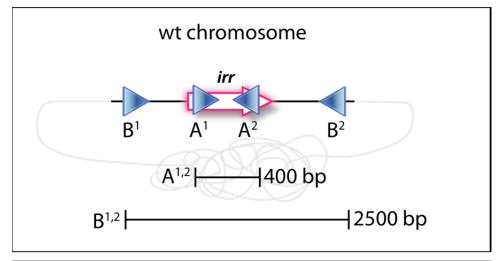
The second, "global" iron-responsive transcriptional regulator that is found in alpha-Proteobacteria is the iron responsive regulator, Irr. *R. pomeroyi* has a predicted *irr* gene *SPOA0445*, on its large resident plasmid whose translated product is 57% identical to *Rhizobium* Irr. Furthermore, there are ICE boxes in the promoter regions of several genes that are Irr-regulated in other bacteria. This

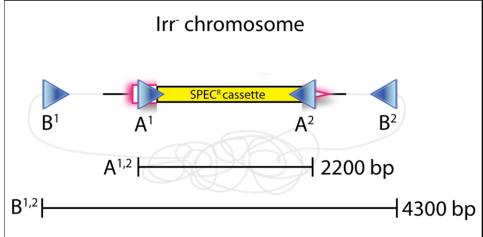
section examines if *SPOA0455* does indeed encode a functional Irr regulator that acts on these ICE boxes.

Therefore, an Irr mutant strain was made, using the pEX18Ap delivery system (see Chapter 4, and Material and Methods for the pEX18Ap procedure) to create an insertion into *SPOA0455*. Briefly, a 2.2 kb region that flanked the *irr* coding sequence was amplified from *R. pomeroyi* genomic DNA using standard PCR protocols, and primers *irrflankEcoFWD* and *irrflankHindIIIREV*. This product was digested with *EcoR*1 and *HindIII*, and ligated into pEX18Ap, cut using the same enzymes. The ligation products were used to transform *E. coli* 803 competent cells, selecting transformants by their ampicillin resistance. After screening the plasmids from several transformants, one (termed pBIO2113) was confirmed by sequencing to have the correct insert. Into this plasmid was then introduced the 1.8 kb spectinomycin cassette (as detailed in chapter 4) cloned into a *Pst*1 site that is internal to *irr*, 220 bp downstream of its start codon. Following ligation, transformants of *E. coli* 803 were selected on media containing ampicillin and spectinomycin. Following the usual ratification procedures, one recombinant plasmid, named pBIO2114, was confirmed to have the correct constitution. This plasmid was then mobilised into *R. pomeroyi* and recombinants that were resistant to spectinomycin, but sensitive to ampicillin, were chosen as candidates in which the spectinomycin cassette had recombined into the genomic version of *irr*.

Several potential mutants were tested using two sets of primers that flanked the *irr* gene **Irrflank1F** and **Irrflank2R** (labelled primer set B in Figure 5.2, which amplify a 2.5 kb region in the wild type) and primers which flanked the *Pst*I site within the *irr* gene **IrrcheckF** and **IrrcheckR** (labelled primer set A in Figure 5.2, which amplify a 400 bp region in the wild type). Of ten mutants screened, three were correct in both primer sets, and did not make any secondary products. The Irr⁻ discussed in this work relates to sample 13 in Figure 5.3, and was renamed J539.

Figure 5.2 Map of Irr recombinant mutant





Map of irr locus in wild type and Irr strain of R. pomeroyi showing position of primers used to screen for successful mutation, and showing predicted sizes of amplified products using these primers.

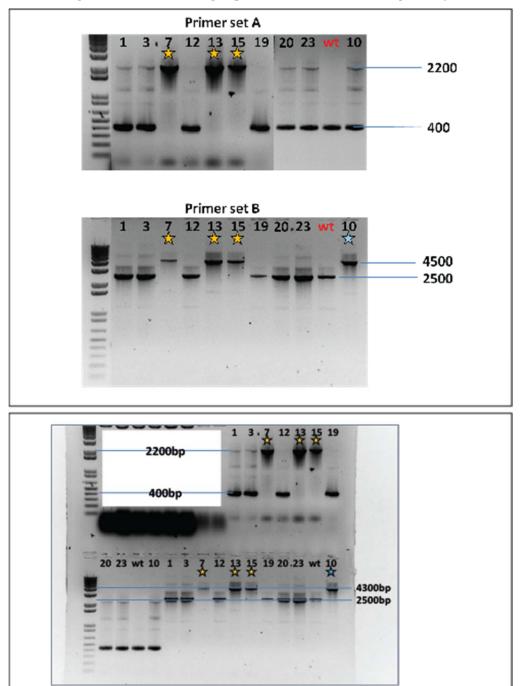


Figure 5.3 PCR screening of potential Irr mutants of R. pomeroyi

Upper panel shows the results of electrophoretic separation (1% agarose gel) of PCR products generated using primers which flank a PstI site within the irr gene of R. pomeroyi (primer set A), and primers which anneal either side of the irr gene (primer set B). These primers were used in colony PCR reactions on potential Irr mutants of R. pomeroyi (numbered) and the wild type R. pomeroyi (wt). Colonies which generated a mutant PCR product without a wild type product are shown with a gold star. The blue star indicates a colony which did not produce a mutant product with both primer sets. The lower panel shows the agarose gel photo without any editing.

5.2.4 Phenotype of Irr- mutant of R. pomeroyi

It was immediately obvious that colonies and liquid cultures of the Irr mutant strain of *R. pomeroyi* J539 were pigmented, with a brick-red colour. This was particularly pronounced under conditions of iron deficiency, in which the chelating agent dipyridyl (30 μ M) was added to HY rich medium and was abolished by adding extra (100 μ M) FeCl₃ into HY rich medium.

Previous work in both *Rhizobium leguminosarum* and *Bradyrhizobium japonicum* (Hamza *et al.* 1998) had shown that an Irr⁻ strain accumulates Protoporphyrin IX (PPIX), due to constitutive expression of HemB, likely due to an uncoupling of the haem biosynthetic pathway from iron availability.

However, in *R. pomeroyi*, the pigment produced by the Irr strain did not fluoresce under UV light, making it unlikely to be PPIX. Furthermore, attempts to isolate the pigment using acetone (Yeoman *et al.* 1997) were also unsuccessful. The pigment appeared to be a precipitate which was separate from the cell pellet. In support of the red pigment being unrelated to PPIX, the expression of *Rhodobacter sphaeroides hemB* was shown to be unchanged in an Irr mutant (Peuser *et al.* 2012). Furthermore, in a microarray study performed as part of this work (see chapter 7) expression of *hemB* of *Ruegeria* {*SPO2076*} was shown to be unchanged in an Irr strain.

5.2.5 Expression of mbfA *in the Irr-strain of* R. pomeroyi

The gene *SPO0382* (*mbfA*) was predicted to be preceded with an ICE box, and, indeed, a homologue of this gene had been shown to be regulated by Irr, in other alpha-proteobacteria, namely *Rhizobium leguminosarum*, *Bradyrhizobium japonicum*, *Agrobacterium tumefaciens* and *Brucella abortus* in Irr repressed *mbfA* in Fe-depleted conditions (Martinez *et al.* 2005; Rudolph *et al.* 2006; Todd *et al.* 2006; Ruangkiattikul *et al.* 2012). Furthermore, a homologue of *mbfA* has been shown to be Irrregulated in *Rhodobacter* (Peuser *et al.* 2011).

To test the expression of mbfA in R. pomeroyi, a fusion of its promoter to the lacZ gene in pBIO1878 was made. The primers MbfApXba1fwd and MbfApPst1rev were used to amplify a 759 bp region that spanned the upstream region of mbfA, this was digested with XbaI and PstI, and cloned into pBIO1878, to generate pBIO1929. This fusion plasmid was crossed into R. pomeroyi by conjugation, and single colonies of purified transconjugants were used to make starter cultures for β -galactosidase assays. As shown in Figure 5.4, in the wild type background, the expression of the

mbfA-lacZ fusion is considerably higher (~5-fold) in the +Fe than the –Fe medium. Strikingly though, in the Irr⁻ mutant, expression of the fusion was greatly enhanced in both sets of media – indeed, in the absence of Irr, the expression is *greater* in the Fe-depleted than the Fe-replete media. This suggests that the mbfA promoter is subject to another, as yet unknown, Fe-responsive regulator, whose action is normally masked by the opposing regulatory action of Irr.

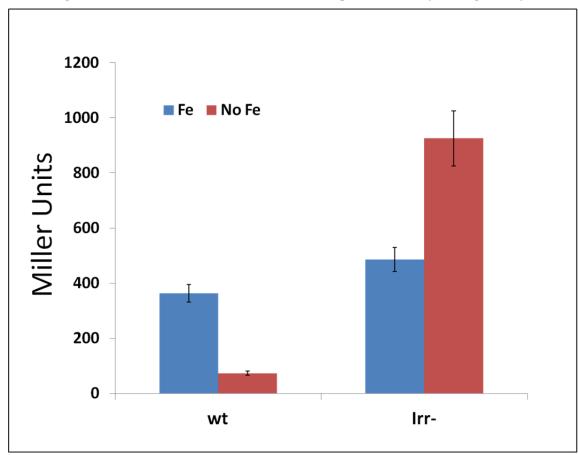


Figure 5.4 Effect of iron limitation and irr on expression of mbfA in R. pomeroyi

Ruegeria pomeroyi containing the mbfA-lacZ fusion plasmid (pBIO1929) were grown in minimal medium (MBM) either supplemented with 20 μ M FeCl₃ (Fe) or not (No Fe) and assayed for β -galactosidase activity, expressed in Miller units. Error bars represent the standard deviation of 2 biological, and three technical replicates.

To confirm that the mutation in *irr* was indeed responsible for the altered expression of the *mbfA-lacZ* fusion, the effects of introducing a wild-type version of *irr* were determined. To do this, a fragment of DNA that contained the entire *irr* gene plus its upstream regulatory sequence was generated by PCR from genomic DNA using the primers **irrCOMPFWD** and **irrCOMPREV**. This

fragment was then cloned (using Xbal) into pOT2, another, wide host-range plasmid, which confers resistance to gentamicin and is compatible with pBIO1845, the lacZ fusion plasmid. The resulting plasmid, called pBIO1928, was mobilised into the R. pomeroyi Irr^- mutant that harboured the mbfA-lacZ fusion plasmid pBIO1929. The expression pattern of β -galactosidase activities were restored to normal, being higher in +Fe than \neg Fe media, conforming that the mutation in irr was indeed responsible for the altered expression of the mbfA-lacZ fusion.

5.2.6 Expression of iscR *in the Irr-strain of* R. pomeroyi

IscR is predicted to regulate the biosynthesis of Fe-S clusters, and indeed is found as part of a *suf* gene cluster in *R. pomeroyi* (see chapter 3 for details).

The potential regulation of IscR in *R. pomeroyi* is intriguing, and leads us to believe that the regulation of the Fe-S synthesis pathway in *R. pomeroyi* is of particular importance to the Fe-homeostasis in this bacterium. There is a motif homologous to the IR box, and a motif homologous to the ICE boxes discussed earlier (see Figure 3.3). This feature has been identified in several proteobacteria (Rodionov *et al.* 2006).

A fusion was made to *iscR* (*SPO2025*) of *R. pomeroyi* described in chapter 4 – pBIO2118. This fusion was crossed into the *R. pomeroyi* strain J470 and the Irr⁻ strain J539.

Here, shown in figure 5.5, the expression of *iscR* is clearly hugely deregulated in the Irr⁻ background, but is still clearly Fe regulated (~2-fold Fe-repressed).

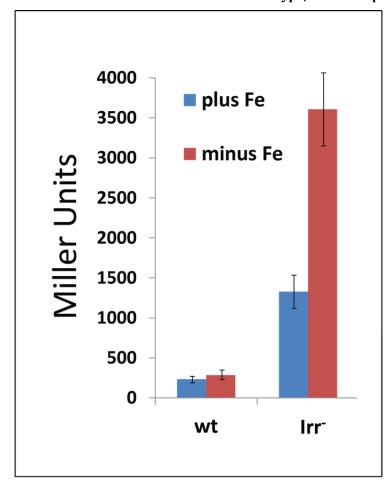


Figure 5.5 Effect of Fe on a iscR fusion in both wild type, and Irr R. pomeroyi

Ruegeria pomeroyi containing either the iscR-lacZ fusion plasmid (pBIO2118) was grown in minimal medium (MBM) either supplemented with 20 μ M FeCl₃ (Iron +) or not (Iron -) and assayed for β -galactosidase activity, expressed in Miller units. Error bars represent the standard deviation of 2 biological, and three technical replicates.

5.3 Discussion

It was clear that Irr, one of the recognised global Fe-responsive gene regulators in the alphaproteobacteria behaves in a conventional way in *Ruegeria pomeroyi* as expected from the canonical systems of the rhizobiales. Further characterisation would be required to ascertain if this Irr behaves more like that of *Rhizobium*, or *Bradyrhizobium* in response to haem binding.

The expression of *mbfA* and *iscR* is likely controlled by the recognition of the ICE boxes that precede these genes by Irr in Fe-depleted conditions. It would be surprising if the other genes *fssA* and *ccpA*

(SPO0382 and SPO0330) (see Table 3.1) with a conserved ICE box did not respond in a similar way, though this was not examined directly.

Peuser *et al.* (2012) performed a microarray study in the well characterised α -proteobacteria *Rhodobacter sphaeroides*, and showed that repression of *mbfA* in this strain was mediated by Irr under low iron conditions. Conversely, a homologue of *iscR* in *Rhodobacter* (*RSP_0443*) was not regulated by Irr under high or low iron conditions. This related bacterial species would likely use Irr in a similar way to Ruegeria, especially as it is likely that Rhodobacter was isolated from a marine environment. To further investigate the transcriptome of Ruegeria, a transcriptomic experiment was performed as part of this work, including the Irr strain, which adds to this interesting story (see chapter 7).

In contrast, the picture is much less clear concerning the identity of a regulator or regulators that *repress* genes under Fe-replete conditions. As shown in Chapter 4, there are at least some genes whose expression is massively increased in low-Fe media, including some of those that are predicted – though not confirmed – to be involved in the import of Fe. In most bacterial taxa, these are the types of gene that are repressed by Fur and, in the special case of at least some members of the alpha-proteobacteria, by a very different transcriptional regulator, RirA.

However, close homologues of RirA are confined to *Rhizobium*, and a few close relatives, namely *Sinorhizobium*, *Mesorhizobium*, *Agrobacterium*, *Brucella* and *Bartonella*, so the identity of any analogous regulator in other, alpha-proteobacteria is not immediately obvious. However, the "ironrhodo" boxes that precede several genes that are expected, *a priori*, to be involved in iron uptake and therefore repressed under +Fe conditions has a similar sequence to that of the IRO box recognition site for the RirA regulator (see Figure 3.3). Given the experimentally confirmed importance (see Chapter 4) of the IR boxes, this provides circumstantial, though not cast-iron evidence that the IR boxes are also recognition sites for transcriptional regulators that are in the Rrf2 family and so would have some similarity to RirA. However, this was not supported by the evidence described in this chapter; none of the mutant strains, with insertions in each of the genes that encode Rrf2-family proteins in *Ruegeria pomeroyi* was altered in the Fe-dependent repression of those genes (*fbpA* and *irpA*) that have IR regulatory sequences.

Taken together, these findings mean that *R. pomeroyi* may use a novel Fe-responsive transcriptional regulator to regulate genes under the control of *cis*-acting IR boxes. In time, a library of transposon mutants could be created for *R. pomeroyi*, allowing the potential identification of candidate regulators of the IR box, as was performed in Rhizobium to identify RirA (Todd *et al.* 2002). Here, the authors utilised both an iron regulated promoter-gfp fusion to identify a Tn5 mutant which was

deregulated for *gfp* expression in high iron conditions. This mutant was also shown to produce ~3-fold more vicibactin. Both phenotypes were corrected by using a gene library of *Rhizobium leguminosarum*, and the correcting clone was mapped to finally identify the RirA gene locus.

Of course, there could be functional redundancy in this regulatory network of *Ruegeria*, which would make identifying the regulator of IR boxes a lot more difficult. This may be evident in both the lack of complete deregulation of several of the site-directed mutants in IR boxes, and the lack of phenotype for any single Rrf2 family mutant in *Ruegeria*.

It would be expected that there would be reasonable conservation of the IR box-binding transcriptional regulator in those closely related marine species — the Roseobacters, so a more complete and detailed analysis of potential transcriptional regulators could provide more targets for testing.

These negative results show that the classical-type Fe-responsive transcriptional regulator(s) that represses Fe-uptake genes remain(s) elusive. It is clearly not an Rrf2-type (unless, of course there is redundancy between the five Rrf2 family proteins in *Ruegeria*). We assumed that the regulator would be an Rrf2-type given the similarity of IR and IRO boxes, but this may have been an oversight, there is great similarity between IR, IRO and IscR boxes in the α -proteobacteria, but all have very different and distinct regulons.

Furthermore, the IR boxes are not recognised by the γ -proteobacterial global iron regulator "Fur", which is actually a Mur – see chapter 6, for Mn responsive regulation.

Without any further target genes identifiable, this work is left for future projects, and would be of great interest, potentially identifying a novel iron-responsive regulator in marine α -proteobacteria. The difference between the RirA-mediated IRO box regulation in *Rhizobium* and what we observe in *R. pomeroyi* is also very exciting. The shift away from the Fur paradigm of *E. coli*, to the Irr/RirA system of *Rhizobium* was an abrupt change in our understanding of iron uptake, and the potential for another such shift is clearly possible here in the marine α -proteobacteria.

Chapter 6_a - Manganese Uptake and Regulation in *R. pomeroyi*

6.1 Introduction

Like iron, manganese is largely biologically unavailable in the marine environment. Bacteria have therefore evolved highly specific transport systems to import this physiologically important metal. Somewhat less studied than iron uptake systems in bacteria, Mn transport has been shown to be tightly regulated in response to both Mn availability and to oxidative stress. Here, I will examine the Mn responsive regulation and uptake of this metal in *Ruegeria*, and further afield.

6.1.1 Ruegeria pomeroyi has a homologue of the SitABCD manganese transporter

Inspection of the *R. pomeroyi* DSS-3 genome identified at least two sets of genes with a likely role in Mn uptake (Rodionov *et al.* 2006). One of these comprised the consecutive chromosomal genes *SPO3366, SPO3365, SPO3364* and *SPO3363,* which are predicted to encode the individual polypeptides that comprise the ABC-class Mn²⁺ -transporter SitABCD (Figure 6.1) on the basis of the striking similarity with the corresponding gene products in other bacteria – see below; *sitA* encodes the periplasmic binding protein, *sitB* the ATPase and *sitC* and *sitD* the two inner membrane permease polypeptides. These genes are likely expressed as a single operon from a single promoter upstream of *sitA*. We confirmed that *Ruegeria pomeroyi sitABCD* are indeed involved in Mn uptake as follows.

Figure 6.1 Map of the sit locus of R. pomeroyi

The operon structure of R. pomeroyi sitABCD is shown, with the sizes of the intergenic gaps indicated, in base pairs, in circles between genes. The "-4" between sitC and sitD denotes overlap between these two genes, suggestive of translational coupling. The positions of two MRS boxes are shown upstream of sitA. The sequence of this upstream region is shown as the zoomed (dotted lines) region. Bases targeted for site-directed mutagenesis in the two MRS boxes are shaded black. The start codon of sitA is shown in blue, and underlined. The inset shows the dimensions of the 1086 bp cloned DNA in the sitA-lacZ fusion plasmid pBIO2050.

6.1.2 The expression of sitABCD responds to manganese levels

In order to study the regulation of *sitABCD*, a 1086 bp region spanning the predicted regulatory region of this operon, and extending into *sitA* itself was cloned into the wide host-range *lacZ* transcriptional fusion plasmid pBIO1878, generating pBIO2050 (Figure 6.1). To do this, oligonucleotide primers **SitAF2** and **SitAR2** were used to amplify the insert DNA, using *R. pomeroyi* gDNA as a template in a standard PCR reaction. This PCR product was purified and digested using *Xbal* and *PstI*, as was the vector pBIO1878. These were ligated together and used to transform *E. coli* 803 competent cells. Transformants were purified on selective LB agar medium (containing

spectinomycin and tetracycline as detailed before). A single transformant was used to purify the recombinant plasmid, which was checked for the presence of an insert and sequence-verified.

The resultant plasmid, pBIO2050, was crossed into *R. pomeroyi* by conjugation and the purified transconjugant strain was used to conduct β -galactosidase assays. The cells were grown in MBM or in MBM to which extra MnCl₂ (20 μ M) had been added. In both media, the fusion was expressed at barely detectable levels, which was surprising, since it had been anticipated that the *sitABCD* promoter would be expressed at higher levels in the Mn-deficient medium, not least because there were two convincing MRS regulatory sequences upstream of *sitA*.

It was then realised that a component of MBM is a proprietary blend of sea salts from Sigma, the recipe of which is unavailable. It was plausible that these sea salts contained sufficient levels of Mn to repress *sitABCD*, even with no addition of MnCl₂. Therefore, a new, defined "sea salts" cocktail, termed Rob's Sea Salts (RSS), was devised. It was designed to comprise a mix of magnesium, calcium, sodium and potassium that resembled those in natural seawater, with the exception of manganese, which was deliberately omitted. The constitution of RSS is shown in the Materials and Methods (Chapter 9).

The experiment above was therefore repeated, but this time using RSS as the background medium, to which extra $MnCl_2$ was added, or not. In this case, it was found that the expression of the *sitA-lacZ* fusion was 16-fold higher in the cultures that lacked Mn (789 Miller Units) than when 20 μ M MnCl₂ was present (42 Miller Units), shown in Figure 6.4. Thus the expression of *sitABCD* was repressed in Mn-replete conditions, as expected by the precedents seen in other bacteria that contain these genes (Diaz-Mireles *et al.* 2004; Platero *et al.* 2004).

6.1.3 A SitA- strain of R. pomeroyi requires manganese for growth

The wild type *R. pomeroyi* DSS-3 does not show any growth limitation when Mn is excluded from the medium, as shown in Figure 6.2. If SitABCD is the only Mn-specific transporter encoded by the *R. pomeroyi* genome, as predicted bioinformatically, and by Rodionov and colleagues (2006), then a deletion mutant should have a growth phenotype during Mn limitation. To test this, a SitA mutant was made using the pK19mob derivative pBIO1879, into which a fragment of SitA, >100bp from each end of the coding sequence was cloned into pBIO1879, generating pBIO2124. This was sequence verified and crossed into *R. pomeroyi* J470 by conjugation. Successful single recombinant mutants

were screened as detailed before, selecting for Spec^R and Kan^R colonies. These were purified and checked by PCR.

Cultures of wild type *R. pomeroyi* and J529 were grown at 28°C for two days before being diluted 1:100 into RSS medium with or without added Mn (as with MBM minimal medium experiments, succinate was added at 10 mM, and vitamin solution {1:1000} was added to all cultures, refer to Material and Methods, chapter 9). As shown in Figure 6.2, growth of the SitA strain J529 was deficient in growth without added Mn.

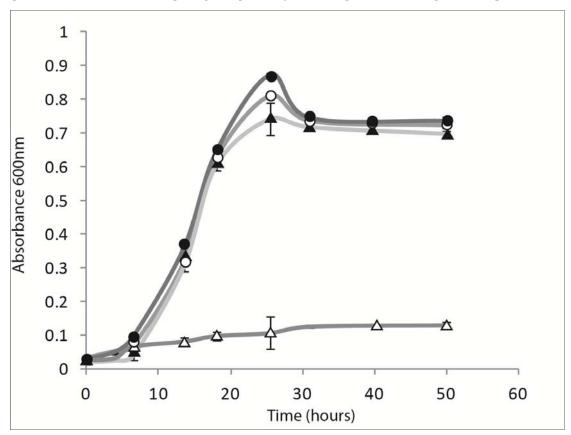


Figure 6.2 Effects of mutating Ruegeria pomeroyi sitA on growth in manganese-depleted media

Cultures of R. pomeroyi DSS-3 wild-type (circles) or the SitA⁻ mutant J529 (triangles) were diluted, in triplicate, into RSS minimal media that either lacked (open symbols) or contained (filled symbols) added 20µM MnCl₂. Growth at 28°C, with shaking, was monitored by measuring absorbance at 600nm.

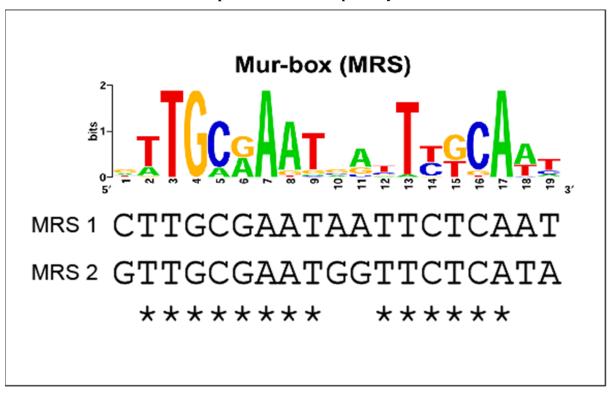
As shown in Figure 6.2 above, the SitA $^-$ strain J529 was unable to grow well without added Mn, but addition of 20 μ M MnCl $_2$ restored growth to that of the wild type, which grew well irrespective of

the addition of extra MnCl₂. Thus, the SitABCD polypeptides do indeed appear to constitute a very effective manganese import system.

6.1.4 Two cis-acting motifs regulate expression of sitABCD

Rodionov *et al.* (2006) identified canonical target sequences upstream of predicted and ratified Mn-regulated genes in various α -Proteobacteria, including several members of the Rhodobacteraceae, including *R. pomeroyi* DSS-3. These 19 bp "Mur recognition sequences" (MRS) have dyad symmetry, and are the targets for the Mn²⁺⁻responsive transcriptional regulator Mur (Figure 6.3).

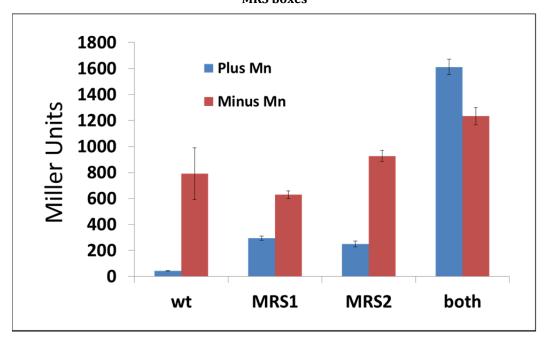
Figure 6.3 Mur-box (MRS) of the Rhodobacteraceae and an alignment of the two MRS boxes upstream of *sitA* in *R. pomeroyi*



Top: logo of the Rhodobacteraceae MRS consensus sequence (Rodionov et al., 2006). Below: sequences found 5' of sitA of R. pomeroyi. Identical bases in the two MRS motifs are marked with a star.

There are two such MRS boxes centred 75 and 45 bps upstream of the ATG translational start of R. pomeroyi sitA, termed MRS1 and MRS2 respectively (Figures 6.1, and 6.3). To establish the effects (if any) of these potential cis-acting elements on transcription of sitA, site-directed mutants within each of them were constructed. To do this, the highly conserved TG motif, found at position 3 and 4 within the 19 bp MRS box, and highlighted in Figure 6.1, was replaced with AA, using the Agilent Quikchange lightening mutagenesis kit. Briefly, the plasmid pBIO2050 was used as a template for mutagenesis, and the mutagenic primers MRS1sdmF, MRS1sdmR, MRS2sdmF and MRS2sdmR were used to mutate both boxes separately, and then to create a plasmid in which both boxes contained the TG \rightarrow AA mutation. Following sequence verification, three new plasmids were named: MRS1 mutant, pBIO2100, MRS2 mutant pBIO2101 and both, pBIO2102. These were each crossed into R. pomeroyi J470 by conjugation and the resultant transconjugants were assayed for β -galactosidase activity in both Mn replete (20 μ M) and Mn limited (no addition) conditions in RSS minimal medium. The results of these assays are shown in Figure 6.4.

Figure 6.4 β -galactosidase activity of sitA-lacZ fusion in R. pomeroyi and the effect of mutating the MRS boxes



The wild type sitA-lacZ fusion plasmid pBIO2050, or derivatives (respectively pBIO2100, pBIO2101 and pBIO2102) containing mutations in the MRS1 or MRS2 or in both regulatory sequences were introduced into wild type R. pomeroyi DSS-3. The transconjugants were grown in RSS minimal medium either without Mn or with 20μ M MnCl₂ added. Data shown represent two biological and three technical replicates.

Compared to the wild type fusion, the mutation in the upstream MRS1 caused a ~7-fold increase in β -galactosidase activity in Mn-replete conditions, but was little changed under Mn-limitation. Similarly, the mutation in MRS2 caused a ~6-fold higher expression of β -galactosidase than the wild type in Mn-replete conditions (Figure 6.4). The fusion plasmid with mutations in both MRS1 and MRS2 was deregulated even further, under both Mn replete (38-fold) and Mn-depleted (1.5-fold) conditions. Thus, both MRS1 and MRS2 contribute to the Mn-responsive, Mur-dependent repression of the *sitABCD* operon, as had been seen in other bacteria, such as *Rhizobium leguminosarum* (Diaz-Mireles *et al.* 2004).

6.1.5 Mur regulates sitABCD in Ruegeria pomeroyi

The predicted regulator of MRS boxes is the Fur-family transcriptional regulator Mur. There is a good Mur homologue in R. pomeroyi, encoded by the gene SPO2477, whose product is 67% identical to Mur of Rhizobium leguminosarum, which has been shown to regulate sitA in that species (Diaz-Mireles et al. 2004; Diaz-Mireles et al. 2005). To demonstrate the effects of R. pomeroyi Mur on the expression of sitA, an insertion mutant in the mur gene was made, using single recombination of the pK19mob-derived pBIO1879 into the mur locus. Briefly (see Figure 4.15 for the procedure used), primers FURFwd and FURRev were used to generate a PCR product that was internal to the coding sequence of mur of R. pomeroyi. This 231 bp fragment was ligated into pBIO1879 following digestion with Xbal and BamHI. The resultant recombinant plasmid was purified, sequence-verified, and named pBIO1861. This was crossed into R. pomeroyi J470 by conjugation, and derivatives in which pBIO1861 had inserted into mur via a single resultant single recombination mutant colonies were selected using rifampicin, spectinomycin and kanamycin as described earlier and in Materials and Methods. The insertion into the mur gene was verified by Southern blot, performed as detailed earlier and the Mur mutant strain was named J528. The sitA-lacZ fusion plasmid pBIO2050 was then crossed into the Mur⁻ R. pomeroyi strain J528 and β-galactosidase assays were performed in cultures grown in Mn, or without, as detailed earlier.

Table 6.1 The effect of a Mur mutation on the expression of a sitA-lacZ fusion.

	WT	Mur
	sitA-lacZ	sitA-lacZ
Plus Mn	42±1	1736±178
Minus Mn	791±30	1817±204

The wild type sitA-lacZ fusion plasmid pBI02050 was introduced into wild type and Mur-mutant Ruegeria pomeroyi DSS-3 recipients. Transconjugants were grown in media that either did or did not have added MnCl₂ before assaying β -galactosidase in triplicate. Activities are shown in Miller Units, with standard errors.

As shown in table 6.1, the Mn-dependent repression of the *sitA-lacZ* fusion was completely abolished in the Mur⁻ background, just as was noted when the two MRS boxes had been mutated, in plasmid pBIO2102 (see above). Thus, Mur is required for the Mn-dependent repression of *sitA* in *R. pomeroyi*.

6.1.6 Mur regulates another Fur-family transcriptional regulator, irr in R. pomeroyi

There is a predicted *irr* gene (*SPOA0445*) on the large plasmid of *Ruegeria pomeroyi*. Interestingly, this gene has a predicted MRS sequence (Rodionov *et al.* 2006), suggesting that it might be regulated in response to Mn²⁺ availability, via the action of the Mur regulator. Both these predictions were verified as follows. An *irr-lacZ* transcriptional fusion was made, using a 198 bps DNA fragment that spanned the predicted transcriptional start of the *irr* gene, and covered the entire intergenic region upstream of *irr*. This amplified region was cloned into the promoter-probe plasmid pBIO1878. The resultant *irr-lacZ* fusion plasmid was sequence-verified and named pBIO2125. It was then crossed into *R. pomeroyi* J470, and into the Mur strain J528 as described before, and single colonies of transconjugants were used to inoculate RSS medium either lacking Mn, or containing 20 μ M as detailed earlier. These cultures were assayed for β -galactosidase activity. As shown in Figure 6.5 the *irr-lacZ* fusion is repressed ~2-fold by growth in the presence of added 20 μ M MnCl₂. in the wild type

background. However, this Mn-dependent repression was completely absent in the Murbackground, with constitutive expression of *irr-lacZ* in both Mn conditions.

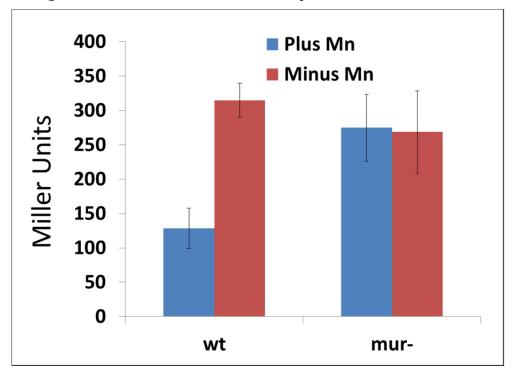


Figure 6.5 Effects of Mn-limitation of the expression of the irr-lacZ fusion

The irr-lacZ fusion plasmid pBIO2125 was crossed into both the wild type and the Mur R. pomeroyi strains. Transconjugants were grown in RSS medium with or without added 20μ M MnCl₂. The β -galactosidase levels were assayed and shown as the means of two biological and three technical replicates.

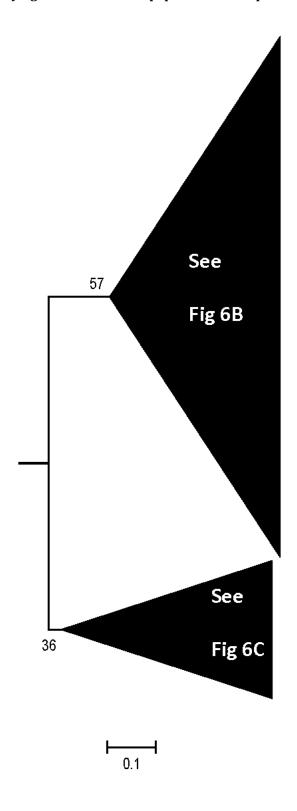
Chapter 6_b - Manganese uptake in other Marine Bacteria

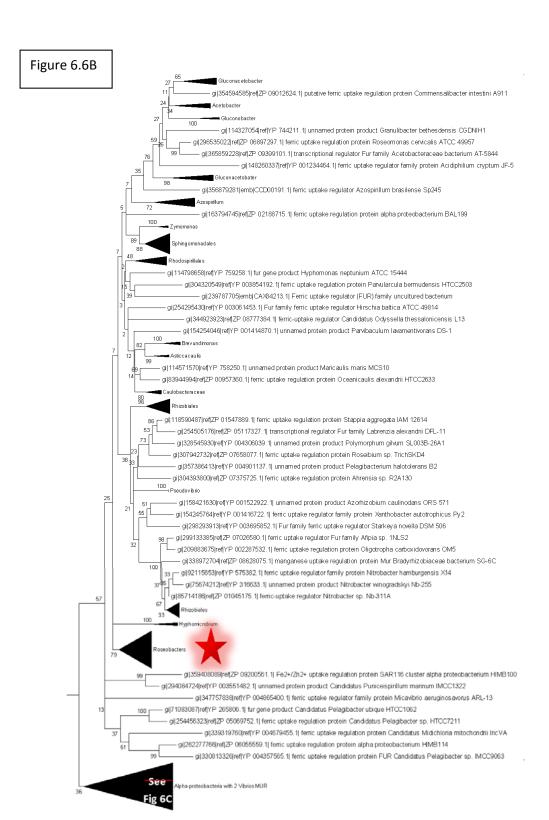
6.2 Diversity of *mur*, *sitABCD* and other genes involved in Mn uptake and sensing in the Roseobacters

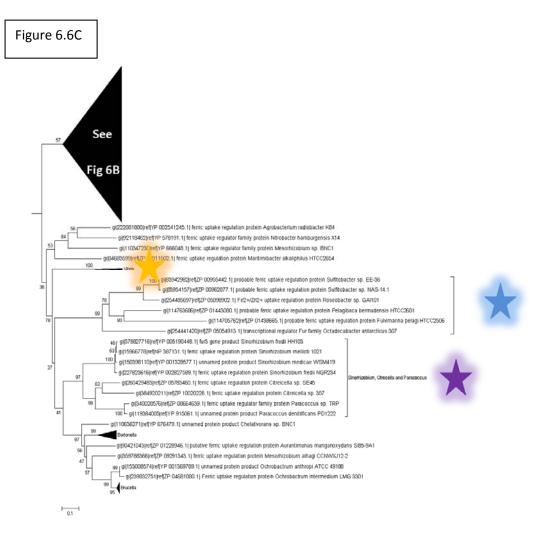
6.2.1 Mur

Inspection of the genomes of 37 other Roseobacters showed that none of them contained a MntR-type transcriptional regulator, but that all of them contained at least one gene whose product was within the Mur branch of the Fur super-family. However, we discerned different sub-types of these Mur polypeptides, judged by their sequences in different strains and species (Table 6.2). In most Roseobacter strains, the Mur polypeptide closely resembles (>70% identical) that of *R. pomeroyi* DSS-3 (above). However, those of *Sulfitobacter*, *Citreicella*, *Pelagibaca*, and one strain (GAI101) of *Roseobacter* are only ~40% identical to that of *R. pomeroyi*, with those of *Sulfitobacter*, *Pelagibaca bermudensis* and *Roseobacter* GAI101 being very similar to each other. *Citreicella* Mur is very similar (65% identical) to that of *Sinorhizobium meliloti*, a ratified manganese-responsive regulator in that species (Platero *et al.* 2007). Finally, one Roseobacter strain, *Octadecabacter antarcticus* 307, had two Mur polypeptides; one resembled that in *Ruegeria pomeroyi* and the other is of the *Sulfitobacter/Roseobacter* GA101 type. These different sub-types of Mur are seen in a relatedness tree, which also includes Mur polypeptides from other bacteria (Figure 6.6).

Figure 6.6 Phylogenetic tree of Mur peptides in the $\alpha\text{-proteobacteria}$







Mega 5 was used to construct a neighbour-joining tree of the Mur polypeptides of the alphaproteobacteria.

Figure 6a) shows that there are two sub-groups, which are shown in detail in 6b and 6c.

- 6b) the triangle marked with the red star includes Mur of Ruegeria pomeroyi and contains the other closely related polypeptides.
- 6c) the close relationship of the Murs of Citreicella to those of Sinorhizobium is demonstrated (purple star), these being also similar to Mur of Roseobacter sp GA101, Pelagibaca bermudensis HTCC2601, Sulfitobacter and one of those in Octadecabacter antarcticus 307 (blue stars). Note, too, the two Mur-like polypeptides in Vibrio strains Vibrio sinaloensis DSM 21326 and Vibrio caribbenthicus ATCC BAA-2122 (Orange star).

6.2.2 SitABCD

This ABC-type transporter is also widespread in the Roseobacters, with all but four strains (see below) containing the corresponding four genes, arranged contiguously (Table 6.2). Closer examination of the sequences of SitA, SitB, SitC and SitD showed that in most strains, these closely resemble (~70% identical) those in R. pomeroyi DSS-3 itself (Table 6.2). Several other Roseobacters contained a somewhat distinct version of the SitABCD polypeptides, which were very similar to each other in the different strains (~77% identity) but less so (40-50% identity) to those of the R. pomeroyi group (Table 6.2). This second sub-class of Roseobacter SitABCD polypeptides closely resembled (~75 % identical) those of various strains of Rhizobium, Sinorhizobium and Agrobacterium, and other bacteria, whose function as manganese transporters has been ratified (Davies and Walker 2007; Diaz-Mireles et al. 2004). Finally, the SitABCD polypeptides of Loktanella vestfoldensis SKA53 are somewhat divergent from those homologues in all the other Roseobacters and more closely resembles deduced SitA-like polypeptides in two other species of marine bacteria, Halomonas elongata and Pelagibacterium halotolerans. A phylogenetic tree was drawn, using an alignment of SitA peptides closely homologous to both the Rhizobium type, and the Ruegeria type, and is shown in Figure 6.7. Peptide sequences homologous to SitB, SitC and SitD always showed very similar phylogenetic relationships.

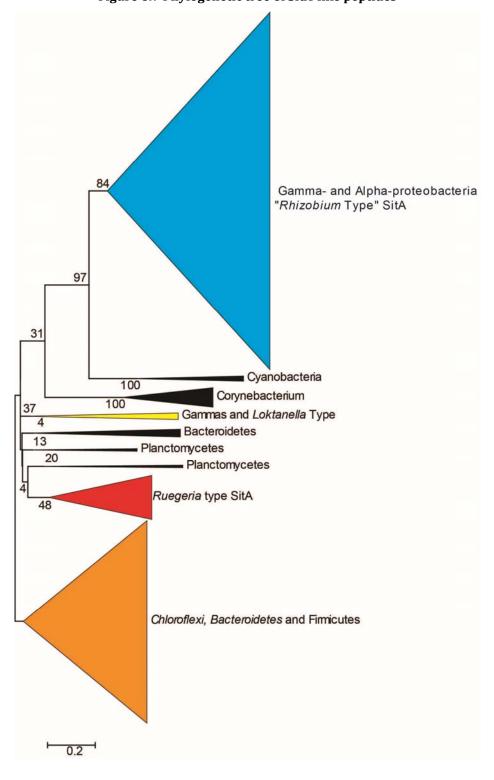


Figure 6.7 Phylogenetic tree of SitA-like peptides

Using Mega5, a tree of SitA peptides, identified due to their homology to peptides from Ruegeria pomeroyi and from Rhizobium leguminosarum was constructed using the neighbour-joining method, bootstrap values are shown for 500 replicates performed.

It was noted that all those Roseobacter strains that had a form of the Mur polypeptide that did not closely resemble that of *Ruegeria pomeroyi* (see above) also had SitABCD polypeptides that were somewhat divergent from those in that species (Table 6.2). However, some strains with the "non–*R. pomeroyi*" version of SitABCD (*e.g. Dinoroseobacter shibae*) did have the "conventional" form of Mur that resembles that of *R. pomeroyi* (Table 6.2).

Although the SitA polypeptides may be of different sub-classes, all the corresponding *sitA* genes are preceded by sequences that strongly resemble MRS motifs, indicating that they are regulated in a similar fashion, via the Mur transcriptional regulator (Figure 6.8).

Figure 6.8 Comparison of MRS sequences that precede the *sitA* and *mntX* genes of selected Roseobacter strains

Ruegeria pomeroyi DSS-3	sitA MRS1	700 000 000 000 000 000 000 000 000 000		CTŤĠĊĠÅATAATŤCTĊÅAT GTŤĠĊĠÅATGGTŤCTĊÅTA	
Citreicella SE45	sitA MRS1	-119 bp	CACATCGA	aatĠċ <mark>Ġ</mark> åct <mark>gag</mark> ttgċått	TGTCAACT
	sitA MRS2			CTTGCAAGTCATTTGCAAC	
Roseobacter denitrificans OCh 114	sitA MRS1			ATŤĠĊĠĂATGCTŤCĠĊĂAC	
	sitA MRS2			CTTGCGAACGATTCTCAAT	
Loktanella vestfoldensis SKA53	sitA MRS			GTTGCGAACGCTTCTCATT	
Roseovarius nubinhibens ISM	mntX MRS			ATŤĠĊĠĂATTATŤCTĊĂAT	
Oceanicola granulosis HTCC2516	mntX MRS			ATŤĠĊĠÅATTATŤCĠĊÅAT	
Rhodobacterales bacterium HTCC2255	mntX MRS	-37 bp	AATTTCTA	CTTGCGAATAGTTCTCACT	TGCATTAG

The sequences of the ratified MRS1 and MRS2 motifs of Ruegeria pomeroyi were compared, using MEME (Bailey and Elkan 1994), with those that preceded different sub-classes (see Table 6.2) of the sitA and mntX genes in a selection of Roseobacter strains. Conserved bases in these motifs are denoted by asterisks. Distances, in base pairs, from the gene-proximal end of the MRS box to the corresponding ATG start codons are shown.

6.2.3 The Mn²⁺ specific transporter MnH is also found in the Roseobacters

Two Roseobacter strains, *Ruegeria* sp. TrichCH4B and *Citreicella* sp. 357, contain a gene (SCH4B_0376 and C357_18417 respectively) whose product resembles MntH, a very different Mn^{2+} transporter, being ~50% (E value $1e^{-120}$) identical to *E. coli* MntH.. These two *mntH* genes were both preceded by convincing MRS boxes, strongly suggesting that they, too, are regulated by Mur, in response to Mn^{2+} availability (Figure 6.8). Note that *Ruegeria* sp. TrichCH4B contains both MntH *and*

SitABCD, whereas in *Citreicella sp.* 357, MntH is its *only* recognisable manganese transporter (Table 6.2).

Table 6.2 Distribution of sub-types of the SitA, MntX, MntH and Mur polypeptides in genome-sequenced Roseobacter strains

In-fills with the same colours represent polypeptides that closely resemble each other. In the case of the SitA, B, C and D polypeptides, all four components of this transport system showed a coherent relatedness pattern; thus all four polypeptides of (e.g.) Sulfitobacter were most similar to those in strains (e.g. Octadecabacter) with the same in-fill pattern. Empty boxes represent absence of the corresponding polypeptide. Note that Octadecabacter antarcticus 307 has two Mur sequences, one resembling that in most of the Roseobacters (Including Ruegeria pomeroyi) and one that is similar to those in Sulfitobacter, Pelagibaca and Roseobacter GAI101.

Gene Name Species	sitABCD	mntX	mntH	mur
Species	٠,			
Citreicella SE45				
Citreicella sp. 357				
Dinoroseobacter shibae DFL 12				
Jannaschia sp. CCS1				
Loktanella vestfoldensis SKA53				
Maritimibacter alkaliphilus HTCC2654				
Oceanibulbus indolifex HEL45				
Oceanicola batsensis HTCC2597				
Oceanicola granulosus HTCC2516				
Octadecabacter antarcticus 307				
Octadecabacter arcticus 238				
Pelagibaca bermudensis HTCC2601				
Phaeobacter gallaeciensis 2.10				
Phaeobacter gallaeciensis BS107				
Phaeobacter sp. Y4I				
Rhodobacterales bacterium HTCC2083				
Rhodobacterales bacterium HTCC2150				
Rhodobacterales bacterium HTCC2255				
Rhodobacterales bacterium KLH11				
Roseobacter denitrificans OCh 114				
Roseobacter litoralis Och 149				
Roseobacter sp. AzwK-3b				
Roseobacter sp. CCS2				
Roseobacter sp. GAI101				
Roseobacter sp. MED193				
Roseobacter sp. SK209-2-6				
Roseovarius nubinhibens ISM				
Roseovarius sp. 217				
Roseovarius sp. TM1035				
Ruegeria lacuscaerulensis ITI-1157				
Ruegeria pomeroyi DSS-3				
Ruegeria sp. R11				
Ruegeria sp. TM1040				
Ruegeria sp. Trich CH4B				
Sagittula stellata E-37				
Sulfitobacter NAS-14.1 Sulfitobacter sp. EE-36 Thalassiobium R2A62				

6.2.4 A novel class of Marine Mn uptake systems, MntX

We noted that three members, namly *Roseovarius nubinhibens* ISM, *Oceanicola granulosus* HTCC2516 and *Rhodobacterales* strain HTCC22 of the Roseobacter group lack homologues of both MntH and SitABCD and contained no known manganese transporter. However, these three strains, and *only* these three were found to have a predicted MRS motif that preceded a gene whose product was likely to be an inner membrane polypeptide, and therefore was a possible candidate to be a novel Mn²⁺ transporter. This MRS motif was first noted by Rodionov *et al.* (2006) in *Roseovarius nubinhibens* ISM and *Oceanicola granulosus* HTCC2516, who termed the corresponding gene *mntX*. The MntX polypeptides are ~400 amino acids in length (e.g. 387 for *Roseovarius nubinhibens* ISM_02005 gene product) and are categorised as "function unknown", with their C-terminal 300 amino acids corresponding to a domain of unknown function (DUF2899 [pfam11449]). They have predicted trans-membrane helices, as shown in Figure 6.10. {This MntX has no similarity to a hydrophobic Mn exporter, also termed MntX, described in *Neisseria meningitides* by Veyrier *et al.* (2011).}

Confirmation of that MntX is indeed a Mn²⁺ transporter and that *mntX* is regulated by Mur in response to Mn availability forms the subject matter of the following sections.

6.2.5 Expression of mntX of Roseovarius nubinhibens is regulated by Mn levels via the Mur transcriptional regulator

To study the regulation of *mntX* of *Roseovarius nubinhibens* ISM, a *lacZ* transcriptional fusion to this gene was made. This comprised a 569 bp fragment that spanned its predicted promoter, plus its predicted MRS *cis*-acting regulatory sequence, and extended into the first 180 bps of the *mntX* structural gene, cloned into the promoter-probe plasmid pBIO1628, forming pBIO2067. This plasmid was mobilised by conjugation into wild type *Roseovarius nubinhibens* and into two strains of *Ruegeria pomeroyi*, namely the wild type J470 and the Mur- mutant J528. For both wild type versions of these two species, the β-galactosidase activities were ~16-fold greater when transconjugants were grown in Mn-depleted than in Mn-replete medium, with respectively, 1607 and 94 Miller Units. However, in the Mur⁻ mutant of *Ruegeria pomeroyi*, the fusion was expressed at high level in both +Mn and –Mn media (1861 and 1889 Miller Units respectively). Thus, the *mntX* gene of one Roseobacter strain (*Roseovarius nubinhibens*) is indeed regulated by Mur in response to

Mn²⁺, even if the regulatory gene is supplied by a different species (namely *Ruegeria pomeroyi*). This is consistent with the similarity of the MRS box sequences in the different Roseobacters, as shown in Figure 6.8.

6.2.6 Cloning and complementation of mntX of R. nubinhibens

To confirm that this predicted transporter gene really is involved in Mn transport, a functional complementation test was used, in an attempt to restore the mutant phenotype of the SitA mutant of *Ruegeria pomeroyi*. This was done, initially, with the *mntX* gene of *Roseovarius nubinhibens*, from whose genomic DNA a 1574 bp fragment that included the *mntX* gene (*ISM_02005*) plus upstream regulatory sequences was amplified and cloned into the wide host-range vector pOT2, forming the recombinant plasmid pBIO2066. This was mobilised into the SitA strain J529 of *R. pomeroyi* by conjugation. The growth of J529 with pBIO2066 was restored to wild type levels without added Mn – refer to Figure 6.11 below. Thus, MntX of *Roseovarius nubinhibens* is able to complement the growth of a Mn transporter mutant, in a heterologous bacterial strain.

6.2.7 The distribution of MntX in other bacteria

We found that there are many significant MntX homologues, in addition to those in the three Roseobacter strains. These homologues were restricted to a few genera in the Orders Vibrionales, Altermonadales and Oceanospirillales of γ -proteobacteria and in two α -proteobacterial clades, namely SAR11 and SAR116. Significantly, all these taxa are sea-dwelling and are considered individually as follows.

6.2.8 The y-proteobacterial MntX

Vibrionales

Among this Order of marine bacteria, there are genome-sequenced strains in the genera *Aliivibrio* (*A. salmonicida*), *Photobacterium* (five species, six strains) and *Vibrio* itself (20 species, 99 strains). The single *Aliivibrio*, and three *Photobacterium* strains contain MntX homologues (E values <e⁻⁷⁵) as do all

but four of the total of the 99 sequenced strains of *Vibrio* itself, the exceptions being the strains of *V. campbelii, V. caribbenthicus, V. nigripulchritudo* and *V. sinaloensis*. Strikingly, all these strains that lacked *mntX* contained at least one other known Mn²⁺ transporter, either SitABCD alone (*V. caribbenthicus, V. sinaloensis, V. nigripulchritudo*) or both SitABCD plus MntH (three *Photobacterium* strains and *V. campbellii* DS40M4). Furthermore, the *sitABCD* operon of *V. caribbenthicus* and *V. sinaloensis* abut a gene that encodes a Mur-like polypeptide whose sequence resembled those of *Citreicella, Sulfitobacter* and a few other Roseobacters (Figure 6.6). Finally, some *Vibrio* and *Photobacterium* strains contain MntH and MntX, but no SitABCD transporters (Table 6.3). (The available genomes of all those strains that had no known Mn transporters and were in draft form were not included here.)

<u>Altermonadales</u>

MntX homologues occur in some strains of *Colwellia, Alteromonas, Pseudoalteromonas,* all of which are in the Altermonadales Order of γ -proteobacteria. As in other clades, there is diversity even within a single genus; thus, *Alteromonas macleodii* ATCC 27126 contains *mntX* but strain "Deep ecotype" does not (Table 6.3).

Oceanospirillales

Within the Order Oceanospirillales, too, some strains of a given genus, namely *Marinomonas*, harbour *mntX* (*M. mediterranea MMB-1* and *M. posidonica* IVIA-Po-181), but strain MWYL1 lacks the gene (Table 6.3).

Table 6.3 Distribution of manganese transporters in α -proteobacterial genera that have at least one strain with a homologue of MntX

Names of the genome-sequenced strains in those genera with at least one MntX homologue are shown in the left-hand column. The presence of a close homologue of the Mn²⁺ transporters MntX, SitA or MntH is denoted by a coloured box, containing the E value in comparison to the corresponding polypeptide in Roseovarius nubinhibens (MntX), Ruegeria pomeroyi (SitA) or E. coli (MntH). Those strains whose deduced proteomes lacked any of these polypeptides, and whose genome was only available in draft form are not included.

Genome-sequenced strains in genera with at least one MntX homologue	MntX	SitA	MntH	
Aliivibrio salmonicida LFI1238	1.00E-74			
Alteromonadales bacterium TW7	2.00E-83			
Alteromonas macleodii ATCC 27126	4.00E-75			
Alteromonas macleodii str. 'Deep ecotype'				
Colwellia psychrerythraea 34H	2.00E-71			
Marinomonas mediterranea MMB-1	2.00E-73	2E-35 ¹		
Marinomonas sp. MWYL1				
Marinomonas posidonica IVIA-Po-181	5.00E-78	3E-48 ¹		
Photobacterium angustum S14		2.00E-154	3.00E-169	
Photobacterium damselae subsp. damselae CIP 102761	6.00E-76		0	
Photobacterium leiognathi subsp. mandapamensis svers.1.1		8.00E-153	5.00E-167	
Photobacterium profundum 3TCK	4.00E-80			
Photobacterium profundum SS9	3.00E-78			
Photobacterium sp. SKA34		4.00E-154	3.00E-168	
Pseudoalteromonas atlantica T6c		4		
Pseudoalteromonas haloplanktis TAC125	3.00E-84			
Pseudoalteromonas sp BSi20311	7.00E-82			
Pseudoalteromonas sp BSi20429	4.00E-87			
Pseudoalteromonas sp BSi20439	7.00E-82			
Pseudoalteromonas sp BSi20480	1.00E-82			
Pseudoalteromonas sp BSi20495	4.00E-84			
Pseudoalteromonas sp BSi20652	2.00E-83			
Pseudoalteromonas sp SM9913	3.00E-84			
Pseudoalteromonas tunicata D2	1.00E-78			
Vibrio alginolyticus 12G01	2.00E-76			
Vibrio alginolyticus 40B	1.00E-76			
Vibrio brasiliensis LMG	3.00E-77			
Vibrio campbellii DS40M4		2.00E-159	6.00E-178	
Vibrio caribbenthicus ATCC BAA-2122		2.00E-137		

Genome-sequenced strains in genera with at least one MntX homologue	MntX	SitA	MntH
Vibrio cholerae 12129(1)	3.00E-75		
Vibrio cholerae 1587	7.00E-76		
Vibrio cholerae 2740-80	5.00E-76		
Vibrio cholerae 623-39	7.00E-76		
Vibrio cholerae AM-19226	7.00E-76		
Vibrio cholerae B33	5.00E-76		
Vibrio cholerae BJG-01	7.00E-76		
Vibrio cholerae bv. albensis VL426	4.00E-76		
Vibrio cholerae BX 330286	5.00E-76		
Vibrio cholerae CIRS101	3.00E-76		
Vibrio cholerae CT 5369-93	7.00E-76		
Vibrio cholerae HC-02A1	1.00E-73		
Vibrio cholerae HC-06A1	3.00E-76		
Vibrio cholerae HC-19A1	5.00E-76		
Vibrio cholerae HC-21A1	3.00E-76		
Vibrio cholerae HC-22A1	3.00E-76		
Vibrio cholerae HC-23A1	3.00E-76		
Vibrio cholerae HC-28A1	3.00E-76		
Vibrio cholerae HC-32A1	3.00E-76		
Vibrio cholerae HC-33A2	3.00E-76		
Vibrio cholerae HC-38A1	3.00E-76		
Vibrio cholerae HC-40A1	5.00E-76		
Vibrio cholerae HC-43A1	3.00E-76		
Vibrio cholerae HC-48A1	3.00E-76		
Vibrio cholerae HC-48B2	5.00E-76		
Vibrio cholerae HC-49A2	5.00E-76		
Vibrio cholerae HC-61A1	3.00E-76		
Vibrio cholerae HC-70A1	3.00E-76		
Vibrio cholerae HCUF01	3.00E-76		
Vibrio cholerae HE-09	6.00E-76		
Vibrio cholerae HE39	1.00E-74		
Vibrio cholerae HE48	1.00E-74		
Vibrio cholerae HFU-02	5.00E-76		
Vibrio cholerae IEC224	3.00E-76		
Vibrio cholerae INDRE 91/1	5.00E-76		

Genome-sequenced strains in genera with at least one MntX homologue	MntX	SitA	MntH
Vibrio cholerae M66-2	5.00E-76		
Vibrio cholerae MAK 757	5.00E-76		
Vibrio cholerae MJ-1236	5.00E-76		
Vibrio cholerae MO10	5.00E-76		
Vibrio cholerae MZO-2	3.00E-75		
Vibrio cholerae MZO-3	6.00E-76		
Vibrio cholerae NCTC 8457	5.00E-76		
Vibrio cholerae O1 biovar El Tor str. N16961	5.00E-76		
Vibrio cholerae O1 str. 2010EL-1786	5.00E-76		
Vibrio cholerae O395	4.00E-76		
Vibrio cholerae RC27	4.00E-76		
Vibrio cholerae RC385	6.00E-76		
Vibrio cholerae RC9	5.00E-76		
Vibrio cholerae TM 11079-80	1.00E-75		
Vibrio cholerae TMA 21	6.00E-76		
Vibrio cholerae V51	7.00E-76		
Vibrio cholerae V52	7.00E-76		
Vibrio coralliilyticus ATCC BAA450	4.00E-70		
Vibrio fischeri ES114	5.00E-77		
Vibrio fischeri MJ11	2.00E-77		
Vibrio fischeri SR5	1.00E-77		
Vibrio furnissii CIP 102972	1.00E-72		5.00E-164
Vibrio furnissii NCTC 11218	4.00E-73		6.00E-164
Vibrio harveyi 1DA3	2.00E-76		1.00E-178
Vibrio harveyi ATCC BAA1116	4.00E-79		1.00E-178
Vibrio harveyi HY01	2.00E-79		2.00E-179
Vibrio ichthyoenteri ATCC 700023	1.00E-77		
Vibrio mimicus MB451	3.00E-76		
Vibrio mimicus SX4	5.00E-76		
Vibrio mimicus VM223	1.00E-76		
Vibrio mimicus VM573	2.00E-75		
Vibrio mimicus VM603	3.00E-76		
Vibrio nigripulchritudo ATCC 27043		6.00E-146	
Vibrio orientalis CIP 102891	4.00E-78		

Genome-sequenced strains in genera with at least one MntX homologue	MntX	SitA	MntH
Vibrio parahaemolyticus 10329	5.00E-79		
Vibrio parahaemolyticus 16	4.00E-81		
Vibrio parahaemolyticus AN5034	4.00E-80		
Vibrio parahaemolyticus AQ3810	1.00E-80		
Vibrio parahaemolyticus AQ4037	1.00E-80		
Vibrio parahaemolyticus K5030	4.00E-80		
Vibrio parahaemolyticus Peru466	4.00E-80		
Vibrio parahaemolyticus RIMD 2210633	4.00E-80		
Vibrio rotiferianus DAT722	3.00E-80		8.00E-178
Vibrio scophthalmi LMG 19158	5.00E-78		
Vibrio shilonii AK1	2.00E-63		7.00E-178
Vibrio sinaloensis DSM 21326		3.00E-139	
Vibrio sp AND4	4.00E-81		
Vibrio sp EJY3	3.00E-76		
Vibrio sp Ex25	2.00E-75		
Vibrio sp MED222	6.00E-71		
Vibrio sp N418	1.00E-74		1.00E-163
Vibrio splendidus 12B01	1.00E-73		
Vibrio splendidus ATCC 33789	2.00E-70		
Vibrio splendidus LGP32	6.00E-71		
Vibrio tubiashii ATCC 19109	5.00E-76		
Vibrio vulnificus CMCP6	8.00E-73		
Vibrio vulnificus MO624/O	9.00E-73		
Vibrio vulnificus YJ016	7.00E-72		

 $^{^1}$ These genes are similar to Zn and Mn periplasmic binding proteins from ABC-class transporters, including RL1049 from R. leguminosarum.

6.2.9 The α -proteobacterial MntX

In addition to the few Roseobacter strains described above, two other taxa of important marine α -Proteobacteria contain mntX genes. These two clades, SAR11 (*Candidatus* Pelagibacter ubique) and SAR116 (*Candidatus* Puniceispirillum marinum) were initially detected by culture-independent analysis of bacterial DNA sequence samples from the <u>Sargasso Sea</u> (Rappe *et al.* 2002; Stingl *et al.* 2007), but both were subsequently grown in pure culture and some strains have been genome-sequenced.

SAR11

These bacteria are the most abundant on Earth (Morris *et al.* 2002). Of four sequenced strains, one, *Candidatus* Pelagibacter sp. IMCC9063, encodes a homologue of MntX (gene tag *SAR11G3_00277*), which is 39% identical to that of *R. nubinhibens*. Interestingly, this *mntX*-like gene is adjacent to a divergently transcribed gene (SAR11G3_00278) whose product is predicted to be in the MntR family, being 50% identical to the *E. coli* version of this manganese-responsive transcriptional repressor. Strain IMCC9063 is in *Pelagibacter* subgroup 3, rather distantly related to other genome-sequenced strains (HTCC7211, HTCC1062 and HTCC1002) (Oh *et al.* 2011), all of which lack MntX. Indeed, these three strains lack genes for any known Mn²⁺ transporters.

SAR116

SAR116 bacteria are also widespread throughout the oceans, although they are not as abundant as the SAR11 group (Morris *et al.* 2012). The only genome-sequenced SAR116 strain, *Candidatus* Puniceispirillum marinum IMCC1322 (Oh *et al.* 2010) contains a gene, SAR116_1166, whose product is 46% identical to MntX of *R. nubinhibens*. The draft genome sequence of the SAR116 cluster alpha proteobacterium sp. HIMB100 also has a gene (HIMB100_00004540), whose product is 44% identical to MntX of *R. nubinhibens*.

6.2.10 MntX in the GOS

To identify all the MntX peptides possible, we interrogated the CAMERA database for the Global Oceanic Survey (GOS) in addition to the NCBI peptide records using *R. nubinhibens* MntX as a query sequence.

All resulting MntX polypeptides fell into 6 sub-classes, each being associated with one the above

bacterial lineages (Figure 6.9), as described below. One set of sequences did not cluster with any described taxanomic group. Closer examination of these peptide sequences revealed that they had a very low GC content; often below 30% (refer to Appendix 2). This unidentified clade of sequences, and presumably strains which harbour these peptides was named clade X in figure 6.9. These peptides could be indicative of a novel, and widespread new clade of bacteria, analogous to SAR11. Individual phylogenetic trees were constructed for each of the 5 distinct groups of MntX peptides shown in Figure 6.9 and these are included as Appendix 1. In addition, some basic information about each of the MntX peptides shown in figure 6.9 is included as Appendix 2.

γ-proteobacteria 2 GOS sequences 71 SAR116 59 GOS sequences 91 93 Χ 59 GOS sequences 97 Roseobacters 27 GOS sequences Pelagibacter 35 GOS sequences Outgroup

Figure 6.9 Phylogenetic tree of all MntX peptides

Using Mega5, a tree of the MntX homologues in the bacteria described in the text and in the GOS marine metagenome was constructed using the neighbour-joining method; bootstrap values are shown for 500 replicates performed. The MntX homologues were of five sub-classes as indicated, each corresponding to those found in the bacterial clade that is shown. Group "X", shown in blue, corresponds to those in the GOS that were not close homologues of a polypeptide in any known bacterium. The numbers of GOS sequences found in each of the five groups are indicated. Accession numbers of the individual GOS sequences are in Appendix 2.

6.2.11 Structural predictions for mntX

The translated products of *mntX* from *R. nubinhibens, Vibrio cholerae*, and from Pelagibacter IMCC9063 are predicted to be localised in the cytoplasmic membrane, as judged by the program pSORTB 3.0 (Yu *et al.* 2010). It was also possible to predict the presence of hydrophobic regions of these polypeptide sequences, which may indicate the trans-membrane (TM) parts of the protein that are embedded in the membrane *in vivo*. The presence of possible TM domains in any given peptide sequence can be evaluated using SPLIT4 {http://split4.pmfst.hr/split/4/ (Juretic *et al.* 2002)}, which predicted that MntX of *R. nubinhibens, V. cholerae*, and *Pelagibacter* all have ~10 TM domains, with a similar overall profile to that of another Mn²⁺ transporter, namely MntH of *E. coli* (Figure 6.10).

MntX Pelagibacter MntX R. nubinhibens IMCC9063 (SAR11G3_00277) (ISM_02005) MntX V. cholerge 0395 MntH E. coli (NP_754813) (YP_001217237) 3.5 150 200 250 300 400 450 100 350

Figure 6.10 Prediction of TM domains in MntX proteins, with MntH for reference

SPLIT4 (Juretic et al. 2002) output for three MntX peptide sequences show the presence of hydrophobic regions of the peptide sequence (red lines). These are used to predict possible TM regions (purple boxes). The peptide sequence of E. coli MntH was included for reference.

6.2.12 Correction of the SitA- mutant of Ruegeria pomeroyi DSS-3 with the cloned mntX genes of Candidatus Pelagibacter sp. IMCC9063 and of Vibrio cholerae

Although the MntX homologues were very similar to those in the various bacterial clades described above, it was important to confirm that these were functional Mn transporters by direct experimentation. It was decided to do this for two examples, namely *Candidatus* Pelagibacter sp.

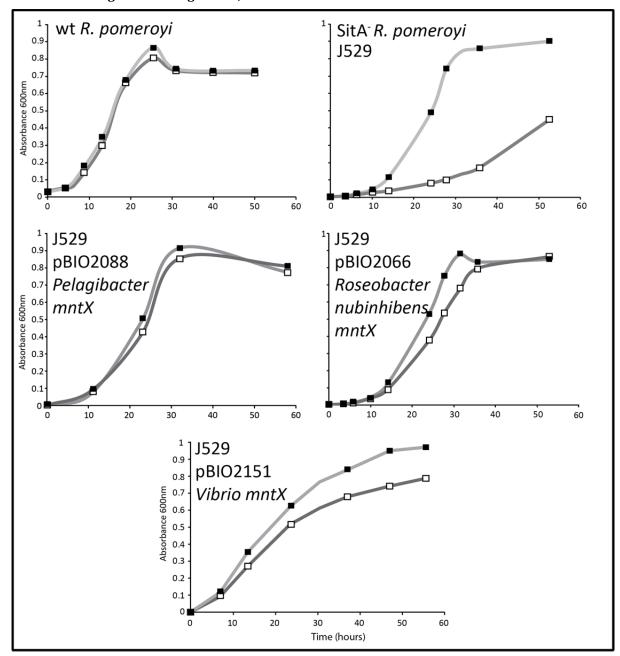
IMCC9063 and *Vibrio cholerae*, because these are (a) in different sub-phyla of the Proteobacteria and (b) because, in their different ways, they are very important bacteria, at a global level.

For *Candidatus* Pelagibacter sp. IMCC9063 we purchased (from GenScript) a 1345 bp fragment that contained its intact *mntX* gene (*SAR11G3_00277*), in a form whose codon usage was optimised {using OPTIMIZER (Puigbo *et al.* 2007)} for expression in the Roseobacters (whose GC content is ~60%, compared to ~30% in Pelagibacter). This *mntX*-like gene was sub-cloned into pRK415 (Keen *et al.* 1988) and the resulting plasmid (pBIO2088) was conjugated into the *Ruegeria pomeroyi* DSS-3 SitA mutant J529.

For Vibrio *cholerae*, we obtained a plasmid, VcCD00018495, from the DNASU Plasmid Repository. This plasmid contains the *mntX* gene (*VC1688*) of *Vibrio cholerae* O1 biovar ElTor str. N16961, cloned in the vector pDONR221 (Nakagawa *et al.* 2008). Using primers **VcXbamp1** and **VcXecop2**, this *mntX* gene was then amplified and ligated to pRK415 that had been cut with *BamH*I and *EcoR*I, forming pBIO2150. This plasmid was conjugated into the *Ruegeria pomeroyi* DSS-3 SitA⁻ mutant J529.

As shown in Figure 6.11, the cloned genes of both *V. cholera* and of Pelagibacter could complement the growth defect of the SitA mutant in Mn-depleted media, just as had been shown for the cloned *mntX* of *Roseovarius nubinhibens*.

Figure 6.11 Growth defect of the *R. pomeroyi* SitA⁻ strain J529 is corrected by the cloned *mntX* genes of Pelagibacter, *Roseovarius nubinhibens* and *Vibrio cholerae*.



Cultures of Ruegeria pomeroyi wild type, or the SitA- mutant J529 or J529 corrected with cloned mntX of Roseovarius nubinhibens (pBIO2066), Candidatus Pelagibacter ubique (pBIO2088) or Vibrio cholera (pBIO2151) were diluted into RSS minimal medium either lacking any added MnCl₂ (white squares), or supplemented with 10 μ M MnCl₂ (black squares). Cultures were grown, with shaking, at 28°C, and growth was measured by absorbance at 600 nm.

6.3 Discussion

To date there has been no research into manganese uptake and regulation in marine bacteria.

The work described here initially generated a series of conventional results, relating to Mn homeostasis in *Ruegeria pomeroyi*, but more novelty emerged from a comparative study of the portfolio of the relevant genes in the different strains of Roseobacters (Table 6.2).

- All contained Mur and no other known, dedicated Mn-responsive transcriptional regulator.
- There were two distinct families of SitA peptides
- Three strains lacked any known Mn uptake genes SitA or MntH
- These three strains all had a homologue of MntX a novel Mn transporter

It was fascinating to see that SitABCD was not well conserved across the Roseobacters, the distribution of this Mn transporter was clearly divided into three separate groups, that of *R. pomeroyi*, a group homologous to the Rhizobial SitA, and another group, most similar to *Loktanella vesfoldenesis*. This was surprising and perhaps highlights the potential for diversity in this group of taxonomically distinct bacteria; applied to the wider marine community, diversity of metal transporters within taxonomic groups may be the rule rather than the exception.

From this analysis of the diversity of Mn transporters in the Roseobacters came the identification of MntX. Only those Roseobacter strains which lacked homologues of either SitABCD or MntH contained a homologue of MntX. One strain, *Ruegeria* sp. Trich CH4B had a homologue of MntH and SitABCD, it would be interesting to see the effect of mutations in each Mn-uptake system of this strain.

In the Roseobacters, the *mntX* gene was always preceded by a MRS box; both protein and MRS box were well conserved between *Roseovarius nubinhibens* ISM, *Oceanicola granulosus* HTCC2516 and *Rhodobacterales* strain HTCC22. The MntX protein is structurally predicted to be similar to MntH, and is located in the inner membrane making a good candidate for being a functional Mn transporter. Indeed, we were able to show that the *R. nubinhibens mntX* gene encodes a functional Mn transporter, and that regulation of *mntX* is via Mur.

The MntX peptide is found in a limited number of orders of the Proteobacteria, namely in the Oceanospirillales, the Altermonadales, the Vibrionales, all in the γ -subphylum, and in the SAR11, SAR116 and Roseobacter clades of α -proteobacteria. MntX is not distributed throughout each genus which has a homologue to this Mn transporter, indicating that MntX may have been acquired by

horizontal gene transfer (HGT). Also, since none of the Roseobacters which have SitABCD or MntH also had MntX it may be that this system is more beneficial in the marine habitat.

It must be noted that nearly all sequenced strains of the Vibrionales contained MntX, and indeed all *Vibrio cholerae* strains have a homologue of MntX. This may either mean that these bacteria acquired mntX early in their evolution, or that it originated from these bacteria. The function of one of the *Vibrio cholerae mntX* genes was demonstrated, in the complementation of the SitA⁻ strain of *R. pomeroyi*. This gene is also likely regulated by MntR, and not Mur, since the γ -proteobacteria use MntR to regulate Mn homeostasis. Unfortunately, I was unable to identify any potential *cis*-acting motifs homologous to MntH-boxes upstream of the *Vibrio mntX* gene. It is of course pertinent to mention the potential for MntX to be a target for therapeutic research. *Vibrio cholerae* is still a very dangerous pathogen where water sanitation is insufficient, and since MntX is likely an inner membrane protein, it could represent a potential vaccine antigen.

MntX was also found in the abundant α -proteobacterial SAR11 and SAR116 groups, of which Candidatus Pelagibacter sp. IMCC9063 encoded another functional MntX protein, capable of complementing the SitA⁻ strain of *R. pomeroyi*.

Given the abundance of the Roseobacters, Vibrios and SAR11/116 in the oceans, it was unsurprising to find that MntX was 82% as abundant in the GOS samples as SitA, and ~4-fold more abundant than MntH. This surely makes MntX a hugely important component of the marine Mn cycle and indeed for the bioavailability of Mn globally.

Fascinatingly, the analysis of MntX peptides found in the GOS survey revealed the presence of an asyet unidentified group of bacteria, which harbour MntX (group X in the MntX phylogenetic tree, Figure 6.9). These bacteria likely have a very low genomic GC content, with all homologues of MntX being between 28 and 33% GC in this group. This is very comparable to the GC content of SAR11 bacteria, and perhaps is the first identification of a new large and abundant clade of bacteria related to SAR11. Further study into these bacteria would be extremely rewarding, perhaps using the novel group X MntX homologues as DNA probes to identify these previously uncharacterised bacteria.

Since MntX appears to be a solely marine Mn transporter, it would be of interest to perform biochemical studies on this transporter to show if the saline environment is of benefit to this transporter system, or perhaps it functions better than SitABCD/MntH when there is very low Mn concentration, as found in the oceans.

Finally, the fact that both SitA and MntX have been shown to be Mn-repressed means that these transporters are not always required either due to high levels of available Mn, such as in marine

sediments or algal blooms, or simply that these bacteria can simply shut down a lot of gene expression and wait for a better environment for growth. We already know that there are many strategies for survival in the oceans, such as the extreme minimalism of SAR11, and the extreme levels of iron uptake systems shown by some Roseobacters. All those in between can alter gene expression to suit a variety of conditions experienced by these bacteria in the variable habitat of the ocean.

Finally, this study identified bacterial strains which had no characterised systems for Mn uptake – most noteworthy in the SAR11 clade. These must have yet another novel Mn transporter, or could even have lost their requirement for this metal, in both cases; this would be an interesting study.

Chapter 7 - Microarray study of the Fe- and Mnresponsive transcriptome of *Ruegeria pomeroyi*

7.1 Introduction

The volume of data generated from a transcriptomics experiment is vast. The transcription of each of the >4000 genes of *R. pomeroyi* was measured using two conditions, and in two different mutant strains, so to go through all those genes whose expression went up or down in response to one or more of these parameters is not practical. Instead, only those genes of particular interest or whose on/off ratio in response to one or more of the conditions was truly out of the ordinary will be discussed here; also, this chapter will be presented with discussion forming part of the main text. The full data set is available at Appendix 3.

7.1.1 Methodology

A microarray chip was designed for *Ruegeria pomeroyi* DSS-3 using ArrayDesigner (Premier Biosoft). Here, each gene on both the main chromosome and the megaplasmid had a minimum of three oligonucleotides, each 60 nucleotides in length, designed, and randomised, before being printed in single spots on a glass slide by Agilent. Each array was printed eight separate times on a single glass slide. These eight arrays allowed the comparison of eight pairs of fluorescently labelled populations of cDNA, synthesised using total RNA extractions from different genotypes of *R. pomeroyi* cells that had been grown in our chosen conditions. The cDNA copies of a given gene would be labelled with two fluorescent dyes, which competitively bind to the oligonucleotide spot printed on the slide. If the gene is differentially expressed in one of the conditions, then the relative fluorescence will be higher for one colour than the other. The array is also, to a degree, quantitative, in that highly expressed genes will have a high level of fluorescence due to the higher level of cDNA copies of the mRNA; this does of course depend on the binding affinity of the individual oligo probes, and so is not truly quantitative.

I chose to use type I arrays (DeRisi *et al.* 1997), where RNA from two different conditions are compared on a single array. For example, two cultures of *R. pomeroyi*, one grown with added FeCl₃, and one without, would be used to prepare total RNA, which could then be compared on a single array. (In contrast, Type II arrays use labelled genomic DNA as a control on each array, to which RNA from a single condition can be compared.) Type II arrays can be compared to each other, but are less economical. For this work, we intended the arrays to be provide an overview of the transcriptional changes which occur during Fe and Mn limitation, hence our choice of type I arrays.

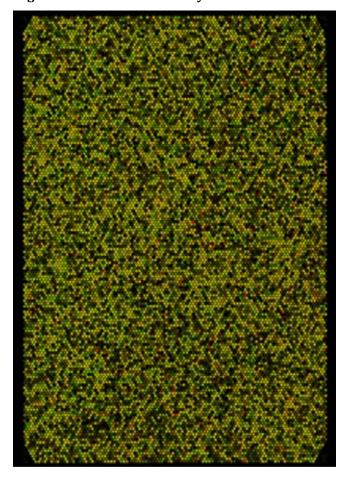
7.1.2 Performing the microarray

My array experiments consisted of the following comparisons:

- 1. Wild type R. pomeroyi grown in MBM with, or without extra, 20μM, FeCl₃.
- 2. Wild type R. pomeroyi grown in RSS with, or without extra, 20μM, MnCl₂.
- 3. Wild type R. pomeroyi and the Mur strain J528, both grown in RSS with $20\mu M$ FeCl₃ plus $20\mu M$ MnCl₂ added.
- 4. Wild type *R. pomeroyi* and the Irr strain J539 grown in MBM with 20μM FeCl₃ added.

Each comparison was performed in duplicate on cultures derived from single colonies of each of the strains that were used. The RNA was extracted from 100 ml cultures grown to early exponential phase (the RNA extraction and labelling method is detailed in Materials and Methods), which equated to around 14 hours of growth in each condition. At this point, the cultures in all the conditions tested were at a similar growth phase and optical densities (OD_{600nm} = 0.15). Total RNA was checked for quality and quantity and was labelled during reverse transcription using either Cy3 (green) or Cy5 (red) fluorescent residues. The cDNA samples were purified and hybridised to the array slide. Where RNA from each condition was in equal concentration, the hybridised probe would fluoresce yellow, and where either Cy3 or Cy5 labelled RNA proliferated, the probe would fluoresce red or green (see Figure 7.1).

Figure 7.1 Scanned microarray slide from this work



Scanned array showing both fluorescent channels together. Green or red spots indicate where a gene was expressed at different levels in the two conditions. Yellow spots indicated equal levels of binding of both fluorescently labelled cDNA samples.

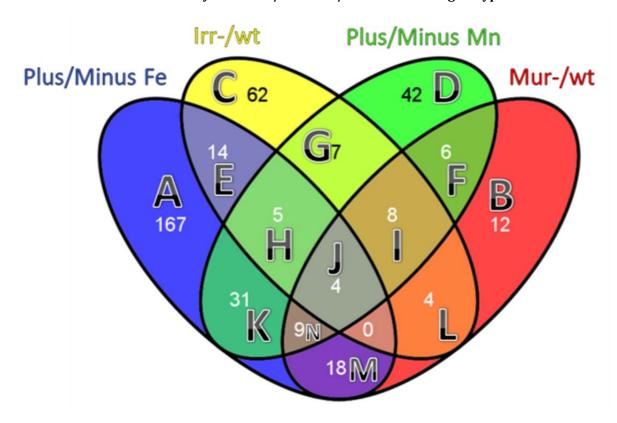
The relative fluorescence of each spot on each array was measured, and these data were normalised to eliminate any bias of the total fluorescence of each dye. These values of relative fluorescence were used to calculate a ratio for each probe, which could then be used to calculate the relative fold-change in expression for each gene, based on the three technical replicates of the three separate probes to each gene, and the two biological replicates of the two separate arrays. These values could then be assigned significance, to establish if they were statistically similar between all replicates, based on their p-value in a t-test of normalised values.

Large scale, batch analysis of groups of similarly behaving genes was performed first, to obtain a sense of the overall changes occurring across all arrays. These analyses are detailed in the following sections.

7.2.1 Venn diagrams of gene expression patterns

A selection of the genes whose expression changed in each condition was used to populate lists, as shown below. Only those genes that (a) behaved in a similar way in all the replicates (and which therefore had small errors associated with the measurements) and (b) had a significant—fold difference greater expression than the control condition, were used (see Figure 7.2 for different fold-change cut-off values used). These lists were compared using Venn diagrams, to see if any genes were co-regulated by the environmental conditions (+/- Mn and/or Fe), or genotype (Mur-, Irr-, wild type) wild type/mutant) as shown in Figure 7.2.

Figure 7.2 Venn diagram showing numbers of genes that were differentially expressed depending on availability of Mn and/or Fe and/or the *mur* or *irr* genotype



Venn diagram produced using Venny (Oliveros 2007). The integers in each of the areas represent the numbers of genes whose expression was of affected (either positively or negatively) by the particular environmental and genetic variables. Thus, for example, the expression of 42 genes (in Box D) was affected by the mur genotype but not by that of irr or the presence of added Mn or Fe. In contrast, expression of the 4 genes in Box J was affected by all four of these variables. The cut off values of the –fold differences were; 3-fold for Fe limitation, 1.5-fold for Irr vs. wild type, and 2-fold for both Mn limitation and for Mur vs. wild type. The letters A-N correspond to those used in the gene list in Table 7.1.

Table 7.1 Lists of Ruegeria pomeroyi genes in the categories in the Venn diagram in Figure 7.2

Α					3	С		D	D		
SP00021	SP00432	SPO1409	SPO2370	SP03230	SPO3770	SPO113		SP00185	SPO2014	SPO0162	SPO2994
SPO0045	SPO0692	SPO1419	SPO2450	SP03275	SP03882	SPO153		SPO0186	SPO2015	SPO0351	SPO3161
PO0050	SPO0759	SPO1548	SPO2508	SP03288	SPOA0037			SPO0274	SPO2016	SPO0459	SPO3284
P00051	SPO0789	SPO1557	SPO2516	SPO3329	SPOA0056			SPO0323	SPO2017	SPO0537	SPO3509
SPO0052	SPO0858	SPO1587	SP02567	SPO3354	SPOA0057			SPO0328	SPO2020	SPO0761	SPO3513
PO0071	SPC0909	SPO1689	SPO2580	SPO3355	SPOA0059			5PO0330	SPO2021	SPO0886	SPO3540
SPO0088	SPO0930	SPO1780	SP02614	SP03381	SPOA0061			SPO0608	SPO2022	SPO1226	SPO3671
SP00090	SPO0937	SPO1794	SP02615	SPO3409	SPOA0186	SP03590		SPO0609	SPO2025	SPO1317	SPO3823
SPO0112	SPO0943	SPO1796	SPO2619	SPO3410	SPOA0289			SPO0610	SPO2159	SPO1500	SPOA0337
SPO0115	SPO1017	SPO1799	SP02631	SPO3457	SPOA0315			5PO0611	SPO2163	SPO1507	SPOA0349
SPO0175	SPO1018	SPO1848	SP02632	SPO3459	SPOA0321		24	SPO0612	SPO2180	SPO1512	SPOA0410
SP00179	SPO1019	SPO1849	SPO2633	SP03460	SPOA0338			SP00613	SPO2236	SPO1516	
SPO0180 SPO0181	SPO1020 SPO1021	SPO1860 SPO1909	SPO2635 SPO2637	SPO3461 SPO3484		_		SPO0614	SPO2390	SPO1518 SPO1520	
SPO0181 SPO0192								SP00615	SPO2573 SPO2645		
SPO0192 SPO0197	SPO1060	SPO1938	SPO2802	SP03523	_	_		SP00628		SPO1521	
	SPO1063	SPO1983	SPO2804	SP03524	_	_		SP00646	SPO3065	SPO1524	
SPO0198 SPO0201	SPO1064	SPO2102 SPO2106	SPO2817 SPO2839	SP03525	_	_		SP00662	SPO3543	SPO1564 SPO1568	
SPO0201 SPO0202	SPO1089 SPO1177	SPO2106 SPO2130		SPO3526 SPO3527		_		SPO0671 SPO0718	SPO3589	SPO1568 SPO1569	
			SPO2846		_	_			SPO3685		
SPO0203 SPO0227	SPO1195 SPO1236	SPO2131 SPO2135	SPO2871 SPO2872	SPO3529 SPO3532	_			SPO0831 SPO0855	SPO3774 SPO3842	SPO1692 SPO1798	
SPO0227 SPO0254	SPO1256	SPO2135 SPO2222	SP02872 SP02876	SP03532 SP03547				SPO1054	SPO3842 SPO3843	SPO1798 SPO1840	
SPO0254 SPO0255	SPO1256 SPO1271	SP02222	SPO2876 SPO2930	SP03604	_			SPO1054 SPO1173	SPO3843 SPOA0104	SPO1840 SPO1878	_
SPO0255 SPO0307	SPO1271 SPO1281	SPO2240 SPO2241	SPO2930 SPO2932	SP03606		_		SPO11/3 SPO1405	SPOA0104 SPOA0152	SPO1929	
SPO0307 SPO0313	SPO1281 SPO13S1	SPO2241 SPO2242	SPO2962	SP03613	_	_		SP01405 SP01440	SPOA0152 SPOA0225	SPO1929 SPO1975	
SPO0313 SPO0314	SPO1351 SPO1366	SPOZZ4Z SPOZZ46	SPO2962 SPO3032	SPO3613 SPO3700	_			SPO1440 SPO1478	SPOA0225 SPOA0351	SPO2048	
SPO0314 SPO0363	SPO1366 SPO1376	SPO2246 SPO2247	SPO3032 SPO3078	SP03700 SP03701	_			SPO1478 SPO1718	SPOA0351 SPOA0388	SPO2048 SPO2107	_
SPO0383	SPO1376 SPO1387	SPO2295	SPO3078 SPO3095	SP03701		_		SPO1718 SPO1957	SPOA0388 SPOA0411	SPO2307 SPO2252	
SPO0382 SPO0388	SPO1387 SPO1392	SPO2395 SPO2324	SP03095 SP03103	SP03721 SP03722				SPO1957 SPO1973	SPOA0411	SPOZZSZ SPOZZS3	
SPO0390	SPO1392 SPO1393	SPO2324 SPO2335	SP03108 SP03118	SP03767				SPO1978	SPOA0444	SPO2255	
SPO0404	SPO1398	SPO2335 SPO2346	SP03118 SP03139	SP03767 SP03768	_			SPO19/8 SPO1999	SPOA0446	SPO2263	
3700104	3F-V1398	37-02346	3103139	3F-U3/68				3FU1999	SFUNDAME	3-02263	1
E	F	G		H	1	J		K	L	M	N
SPO0086	SPO0834	SPO0698	SPO02		055 SF	PO1216	SP00		SP00154	SPO0089	SPO0769
SPO0087	SPO0919	SPO1217	SPO070	1 SPO2	576 SF	PO2398	SPO1	1502	SPO1977	SPO0157	SPO0833
SPO0169	SPO0921	SPO1682	SPO156	S SPOA	0392 SI	PO2399	SPO1	1503	SPO2018	SPO0784	SPO1555
SPO0199	SPO1556	SPO1863	SPO18	SPOA	.0393 SF	POA0399	SPO1	1504	SPO2577	SPO0924	SPO1790
SPO0647	SPO1789	SPO2154	SPO22	4 SPOA	0395		SPO1	1508		SPO1015	SPO1791
SPO0790	SPO2331	SPO2396		SPOA	0396		SPO1	514		SPO1280	SPO3363
SPO2023		SPO2397		SPOA	0397		SPO1	1515		SPO1593	SPO3365
SPO2486				SPOA	0398		SPO1	517		SPO1795	SPO3366
SPO3014	1			2.01	-		SPO1			SP02568	
SPO3014 SPO3287							SPO1			SPO2586	_
			_				_				+
SPO3359	+				$\overline{}$		SPO2			SPO2706	
SPO3360	+						SPO2			SPO2867	
SPO3607							SPO2			SPO3027	
SPOA0445							SPO2	2289		SPO3081	
							SPO2	2371		SPO3445	
							SPO2	628		SPO3781	
							SPO2	2634		SPOA0273	
							SPO2	1636			
		ICE BOX					SPO3				
	1	IR BOX					SPO3				1
	_	MUR BOX			-		SPO3			_	_
	+				$\overline{}$						
		RRF-2			$\overline{}$		SPO3			_	_
		Operons						10339			
								A0340			
							SPOA	N0341			
							SPOA	10342			
							SPOA	A0343			
							-	N0345			
							SPOA	A0346	1	1	
								10346 10347			
							SPOA	A0346 A0347 A0348			

Each set of genes shown in Figure 7.2 had an associated letter. These letters are shown here, as lists of genes which populated each section of the Venn diagram. Any gene which has a predicted regulatory motif (ICE, IR, MUR, see Chapter 3) or was a predicted Rrf-2 family transcriptional regulator (Chapter 3), or was in a predicted operon of genes, is coloured according to the key shown in column G.

This analysis revealed some expected, and also some surprising findings. As expected, there were 13 genes which were altered in expression in response to both Irr and to Fe, consistent with the known responses of the Irr regulator to Fe availability. Similarly, 27 genes responded to both the *mur* genotype and to its cognate co-regulator Mn. However, 31 genes were altered in both Fe and Mur, and 24 in both Irr and Mn. Thus, there is still considerable cross-talk in the regulatory networks for Mn and Fe homeostasis. Indeed, Mur of *R. pomeroyi* was shown to repress the *irr* locus in response to Mn levels (chapter 4). The *mur* gene is thought to have evolved from the global iron regulator gene *fur*, and clearly still has potential to be involved (directly or indirectly) in the response to Fe availability.

No genes were regulated by Mur, Irr and by Fe above the cut-off values used in this analysis, but 9 genes were shown to be regulated by Mn, Fe and Irr. This may show that Mur plays a lesser role in the homeostasis of Mn and Fe than the levels of Fe and Mn themselves, and that Irr is the more important regulator. Indeed, the fact that Mur itself is regulated by Irr makes this regulatory hierarchy more probable.

A total of 12 genes changed in response to Mn independently of Mur, or Fe, or Irr, indicating the presence of a yet unidentified Mn-responsive transcriptional regulator. Similarly, a total of 31 genes responded to Fe AND Mn limitation, but to neither Mur nor Irr.

Although not shown in the Venn diagram, it was apparent that several adjacent, contiguous genes displayed the same pattern of differential expression, consistent with their being part of the same transcriptional units (operons), and also demonstrating the robustness of the data.

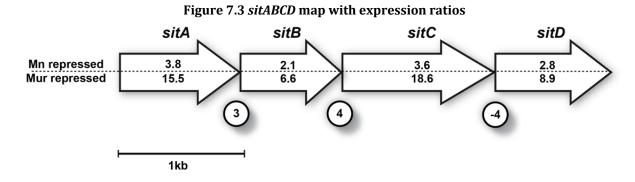
In what follows, some of the more interesting of these operons are described in more detail.

7.3.1 Effects of manganese availability and mutations in mur on the transcriptome of Ruegeria pomeroyi

The focus of this section is on those operons whose expression was markedly affected (>5-fold difference) by the *mur* genotype and/or the availability of Mn. These fell into one of four classes, depending on their response to Mn and to the *mur* genotype, as follows.

As shown in Table 7.1, a total of 12 genes, in just two clusters, behaved in a conventional way for those that are repressed by the Mur regulator, in cells grown in Mn-replete conditions.

SPO3366, SPO3365, SPO3364 and SPO3363 (sitABCD)



Scale map of the sitABCD locus of R. pomeroyi (SP03363-SP03366) including intergenic gaps (circled) and fold-change ratios for both +/- Mn and wt/mur microarray experiments (Mn repressed and Mur repressed).

Reassuringly, the *sitABCD* genes were among those whose expression was most strikingly repressed in the +Mn medium and this effect was dependent on a functional *mur* gene. The expression of *mur* itself was not affected significantly by the presence of added Mn in the medium. Here, the fold-change ratio of *sitA* expression shown in Figure 7.3 is lower (3.8-fold) to that obtained using a *sitA-lacZ* fusion (16-fold), but both show that *sitA* expression is repressed by Mn (see Chapter 6).

Interestingly, the *sit* genes appear to be induced by Fe (see Appendix 3, *sitA*, *sitC* and *sitD* all ~4-fold induced by Fe), although the mechanism of this regulation is unknown.

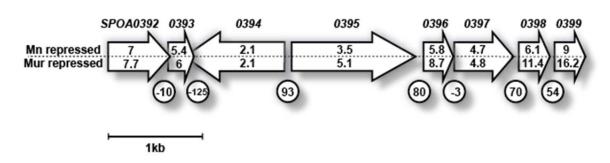


Figure 7.4 SPOA0392-SPOA0399 map with expression ratios

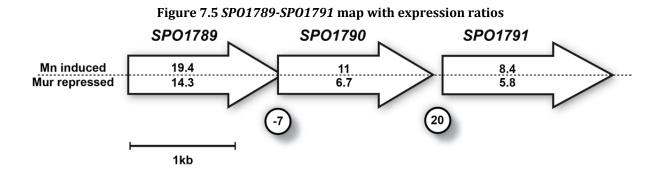
Scale map of the SPOA0392-SPOA0399 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for both +/- Mn and wt/mur microarray experiments (Mn repressed and Mur repressed).

R. pomeroyi DSS-3 has a resident, 491,611 bp, megaplasmid (Moran et al. 2004). It has a cluster of 8 contiguous genes, arranged in at least four predicted transcriptional units (Figure 7.4), whose expression was markedly reduced in cells grown in Mn-replete medium. This only occurred in the wild type strain, showing that Mur was required for this repression. The leftmost (as shown in Figure 7.4) of these genes, SPOA0392, encodes a polypeptide that is weakly predicted to be an RpoE-type or -factor of RNA polymerase, but the closest homologue, FecI of Pseudomonas, is only 34% identical to the SPOA0392 gene product. So, if this Ruegeria gene does indeed encode a σ -factor, it must be of a rather novel type and predictions of its function are not possible. Downstream of SPOA0392, and in the same orientation, is SPO0393, which encodes a small (99 amino acid) polypeptide with significant similarity to one of the components of refractile inclusion bodies (R-bodies), which are ribbon-like polypeptides associated with the ability of some bacteria to act as killers in endosymbiotic interactions with eukaryotes (Pond et al. 1989). At the other end of the cluster lie the adjacent genes SPOA0398 and SPOA0399, whose products are 78% identical to each other and less so (34%) to that of SPOA0393, with all three having significant identity to other R-body proteins in Caedibacter taeniospiralis, an obligate endosymbiont of Paramecium (Beier et al. 2002; Jeblick and Kusch 2005). I could find no links between manganese availability and R-bodies in the literature and the reason why the expression of these three genes should be elevated in Mn-deficient media, under the control of Mur, is unknown. Between the two sets of R-body genes are four other genes (SPOA0394 -SPOA0397), one of which, SPO0394 is in the opposite orientation and shows only a modest response to Mur and to Mn availability. The genes in this cluster do not occur in any other genome-sequenced Roseobacter species, their products have no known function, and they have no homologues in any known organism. However, the SPO0397 gene product has three significant matches in the Global Ocean Sampling metagenome (Sun *et al.* 2010), pointing to the presence of the corresponding gene in (unknown) marine organisms.

The *sitABCD* operon has two MRS motifs in its promoter region (see Chapter 6), but no such sequence was seen 5' of any of the genes in the *SPOA0392 – SPOA0399* cluster. It is not known, therefore, if Mur acts directly by binding to motifs that share only very limited similarity to the canonical MRS boxes or indirectly, perhaps by affecting the expression of another regulatory system that affects the transcription of these R-body genes.

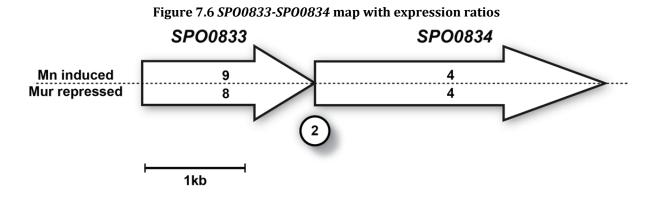
7.3.3 Class II – expression enhanced in Mn-replete medium, and enhanced in wild type, compared to Mur-mutant

There were several groups of different genes, in four separate regions of the *R. pomeroyi* genome, whose expression was enhanced in the +Mn medium in the wild type strain, but this induction was not seen in the Mur⁻ mutant (Table 7.2).



Scale map of the SP01789-SP01791 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for both +/- Mn and wt/mur microarray experiments (Mn induced and Mur repressed).

These three genes are strongly predicted to encode the components of an ABC transporter, respectively its permease, ATPase and periplasmic binding protein. Their expression was enhanced 19.4-, 11- and 8.4-fold respectively in the "+Mn" compared to the "-Mn" medium and by 14.3-, 6.7- and 5.8-fold respectively in the Mur⁺ wild type compared to the Mur⁻ mutant (see Figure 7.5 and Table 7.2). There are close homologues (> 60% identical) of all these gene products in many other Roseobacter strains, and also in bacteria in other sub-phyla of Proteobacteria. There were no close homologues to any transporter whose substrate specificity has been ratified, although the products of the *SPO1789* and *SPO1791* genes are classified as likely being involved in the import of tungstate or sulfate. However, this prediction needs to be ratified. Without knowing the identity of the substrate, and, indeed, without being certain if this transporter acts as an exporter or an importer, the adaptive advantage of its enhanced expression in Mn-rich medium is not clear.



Scale map of the SP00833-SP0834 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for both +/- Mn and wt/mur microarray experiments (Mn induced and Mur repressed).

The consecutive genes *SPO0833* and *SPO0834* are_in a predicted two-gene operon whose expression was much enhanced (9- and 4-fold) in the +Mn media and 8- and 4-fold higher in the in wild type strain, relative to the Mur⁻ mutant. Their corresponding products are highly conserved, not only in the Roseobacters, but in a wide range of other bacterial clades and, strikingly, in the products of two other, *SPO1555* and *SPO1556*, in *R. pomeroyi* DSS-3 itself (see below). Their products are strongly predicted to encode the two polypeptides of a family of NADH:ubiquinone reductases. The predicted sub-type of this family that most closely resembled the *SPO0833* and *SPO1555* gene products are the β-subunit of a molybdopterin-containing formate dehydrogenase and those of *SPO0834* and *SPO1556* correspond to the α-polypeptide of the same enzyme.

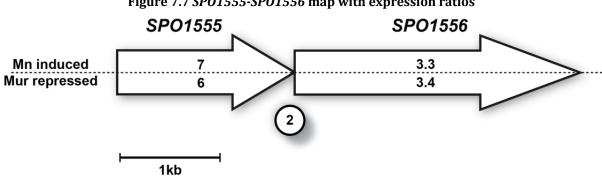


Figure 7.7 SP01555-SP01556 map with expression ratios

Scale map of the SPO1555-SPO1556 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for both +/- Mn and wt/mur microarray experiments (Mn induced and Mur repressed).

As mentioned above, SPO1555 and SPO1556 are two contiguous genes (see Figure 7.7) that respond similarly to SPO0833 and SPO0834 with regard to manganese availability and to the mur genotype. Not only are the gene products of SPO1555 and SPO1556 very similar (>98% identical) to those of SPO0833 and SPO0834 respectively, but so too were the corresponding DNA sequences of the genes. This was the only example in which these genes had been duplicated in any of the genomesequenced Roseobacters.

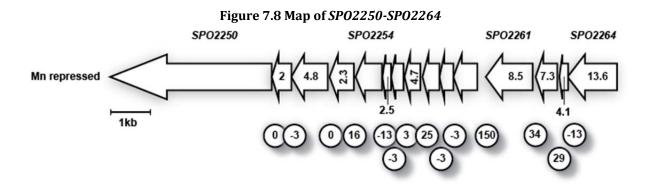
Perhaps coincidentally, at least some formate dehydrogenases contain tungsten, a metal that occurs in only a few metallo-enzymes. Furthermore, in Desulfovibrio vulgaris Hildenborough, the expression of the FdhAB formate dehydrogenase is induced by addition of tungstate (da Silva et al. 2011). Direct experiments are required to show if the purported formate dehydrogenases of Ruegeria (and other, related bacteria) do indeed contain tungsten. If so, it would provide a functional, though not mechanistic, explanation for the parallel induction of the two sets of genes that encode this enzyme plus a putative transport system for this metallic co-factor, encoded by the SPO1789, SPO1790, and SPO1791 genes (see above).

The SPO1216 gene forms a single-gene transcriptional unit that encodes a 239 amino acid polypeptide with no domains with known function. There is a near-identical homologue in just one other Roseobacter strain, namely *Dinoroseobacter shibae* DFL 12; other than that, there are no homologues in any known organism, or in any metagenomic data base.

These findings of genes whose expression is enhanced in Mn-replete media and which require a functional Mur regulator for this induction are novel for this particular regulator. However, other members of the Fur super-family, including Fur itself, have analogous properties. Thus, although Fur is an Fe-responsive repressor of genes involved in iron uptake, for example, it is required for the expression of some other genes (e.g., the sdh operon for succinate dehydrogenase in E. coli), giving Fur the initial appearance of acting as an activator. However, this is due to its ability to repress a repressor, in this case the small RNA ryhB, which can act post-transcriptionally to inhibit the expression of several target genes (including sdH). Since transcription of ryhB itself is repressed by Fur in Fe-replete media, the sdh (and several other) targets for the RyhB RNA will be expressed in these conditions. Conversely, in a Fur mutant, RyhB RNA is made constitutively, and so the expression of its targets will be lowered under all conditions (Massé et al. 2007). Since small RNAs have not (yet) been identified in Roseobacters, it is possible that an analogous mechanism exists here, but this would require further work to demonstrate a role for such molecules in this particular case. There are no conserved sequences in the vicinity of the promoters of any of the genes that displayed this form of regulation. Indeed, the regions immediately upstream of SPO0833 and SPO1555 had very little similarity to each other, despite the remarkable similarities of the genes themselves and their patterns of regulation (see above).

7.3.4 Class III – expression repressed in Mn-replete medium, independent of mur genotype

There was one transcriptional unit that appeared to be repressed by Mn, but, in contrast to the cases described above, this was unaffected by the genotype at the *mur* locus (Table 7.2).



Scale map of the SPO2250-SPO2264 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for +/- Mn microarray experiments (Mn repressed).

Gene Transfer Agents (GTAs) are very small, virus-like particles, first found in *Rhodobacter* (Marrs 1974), and then shown to be a feature of the Rhodobacterales family, including many strains of the Roseobacter clade (Biers *et al.* 2008). There are also homologues of the corresponding genes in other genera of alpha-proteobacteria, including *Agrobacterium, Brucella* and *Caulobacter*. In *R. pomeroyi* DSS-3, Biers *et al.* (2008) identified a cluster of ~15 genes whose products correspond to the various components required to make its GTA (shown Figure 7.8).

Within that cluster are four consecutive genes, *SPO2264 – SPO2261*, which are predicted to be in one operon. The expression of all four genes is much lower in the +Mn medium, with that of the promoter-proximal gene, *SPO2264* having the highest factor of reduction (11.4-fold). The promoter-proximal gene (*SPO2260*) of a downstream operon is also significantly repressed by Mn, as are some of the other genes in the cluster, though to a lesser degree (Table 7.2; Figure 7.8). I am unaware of any reports that describe any biochemical or functional connections between manganese and GTAs.

7.3.5 Class IV – expression enhanced in Mn-replete medium, independent of the mur genotype

There were at least three other gene clusters whose expression was greater, sometimes to a remarkable extent, in the +Mn medium, irrespective of the *mur* genotype. These are as follows.

<u>SPOA0343 –SPOA0339</u> and <u>SPOA0345-SPOA0347</u>

Mn induced SPOA0347 0346 0345 0344 0343 0342 0341 0340 0339 11.7 13.5 12.1 19.8 11.7 11.7 11.7 12.1 13.5 13.5 12.1 1

Figure 7.9 Map of *SPOA0339-SPOA0347*

Scale map of the SPOA0339-SPOA0347 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for + Mn microarray experiments (Mn induced).

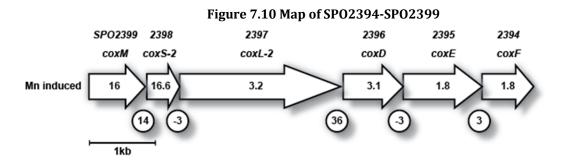
There is a cluster of nine closely linked genes, *SPOA0347 – SPOA0339* with a remarkable response to Mn availability. As shown in table 7.2, the expression of some of these was markedly *enhanced* (by factors as high as 20-fold) in Mn-replete medium, but this response was not mediated by Mur, since they displayed no differential expression in the Mur⁻ mutant and in the wild type strains. This cluster comprised two, divergently transcribed sets of genes, *SPOA0343 - SPOA0339* and *SPOA0345 - SPOA0347*, which were separated by *SPOA0344*, whose expression was unaffected by the availability of manganese or the *mur* genotype (Table 7.2; Figure 7.9).

Three of these Mn-induced genes, *SPOA0345-SPOA0347*, were contiguous and are likely in a single operon. The other five may be co-transcribed, or may comprise two operons, *SPOA0343-SPOA0342* and *SPOA0341-SPOA0339*, separated by 128 bps (see Figure 7.9). None of these eight gene products

had close similarity to polypeptides of known function, although those of *SPOA0339, SPOA0340, SPOA0342, SPOA0345, SPOA0346* and *SPOA0347* could be allocated to general polypeptide families (Table 7.2). But even taking these various gene products together did not predict their overall biochemical function. However, it was noted that the closest homologues (ranging from 30% – 50% identical) of all of the gene products in this cluster occurred in a limited number of bacterial strains, namely *Erwinia tasmaniensis* Et1/99, *Acinetobacter sp.* ATCC 27244, *Photorhabdus asybiotic,* and *Klebsiella oxytoca* KCTC 1686. And, in each of these strains, the corresponding genes that encoded the homologues were often clustered, as in *R. pomeroyi* DSS-3. Thus, even though these versions of the genes may have diverged very considerably in their sequences compared to those in *Ruegeria*, there has been long-term, concerted selection to maintain their linkage within the genomes of different bacteria, suggesting that the individual gene functions in these clusters operate coordinately towards similar biochemical purposes.

It is noteworthy that *SPOA0344*, which is located between the highly induced *SPOA0343* and *SPOA0345* but whose expression is not itself affected by the addition of MnCl₂, encodes a LysR-type regulatory (LTTR) protein. Members of this very widespread family normally activate their target gene(s) in response to a cognate small molecular weight co-inducer and are often autoregulatory, repressing their own transcription (Maddocks and Oyston 2008). There are no known members of the LTTR family that respond to Mn²⁺, but the location of *SPOA0344*, between two sets of genes whose expression is markedly enhanced by this metal makes this gene a strong candidate for encoding a regulator that does sense manganese. In that connection, it was noted that there is a motif with dyad symmetry (5'-TTTCC-N₆-GGAAA-3'), respectively 137 and 79 bps upstream of the ATG starts of both *SPOA0343* and of *SPOA0345*, which might represent binding sites for the SPOA0344 regulatory protein.

Cox cluster I



Scale map of the SP02394-SP02399 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for + Mn microarray experiments (Mn induced).

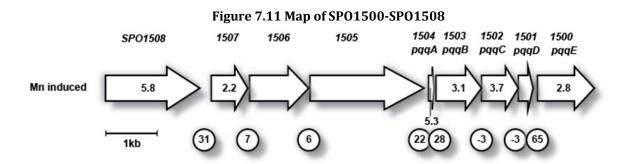
A feature of the Roseobacters is that most strains of this clade contain a group of *cox* genes (Cluster I – Figure 7.10), which are predicted to encode the enzyme carbon monoxide dehydrogenase, which catalyses the production of CO₂ from CO (Cunliffe 2011). Indeed, several strains, including *R. pomeroyi* DSS-3, have been shown to have CO oxidation activity (Cunliffe 2011), and it has very recently been shown in *Ruegeria pomeroyi* DSS-3 that these do indeed function on CO oxidation, since a mutation in one of them (*coxL-2 – SPO2397*) completely abolished this ability (Simone Payne and Michael Cunliffe, personal communication) though it has not been formally shown that this is due to their annotated *cox* genes. Furthermore, some Roseobacters , including *R. pomeroyi* DSS-3, contain another cluster (Cluster II) of genes whose products have some sequence similarity to the *bona fide* Cox polypeptides, but which may not function in CO oxidation (Simone Payne and Michael Cunliffe, personal communication) (Cunliffe, 2011).

The expression of several of the genes within both the Form I cluster (*SPO2394* – to *SPO2499* inclusive; Figure 7.10) and in the Form II cluster (*SPO1515* – *SPO1521*) was markedly enhanced in cells grown in +Mn medium, but that the *mur* genotype was not involved in this effect (Table 7.2). This enhanced expression is particularly pronounced with the consecutive and likely co-transcribed *coxM*, *coxS-2*, *coxL-2*, *coxD*, *coxE* and *coxG* genes in the Form I cluster; the signal for the promoter-proximal *coxM* gene is 16-fold greater in the Mn-grown cells. Several of the Form II genes show more

modestly enhanced expression in response to added Mn (Table 7.2). These include the consecutive genes *coxG*, *coxS-1*, *coxS-2* and *coxM*, plus two upstream genes *SPO1515* and *SPO1516*, which respectively encode a putative cytochrome c550 and a predicted periplasmic binding protein of an ABC transporter, though their functional link, if any, with carbon monoxide is unknown.

Although the CO dehydrogenase of *Oligotropha carboxidovorans* is a metallo-protein, with a very unusual metallo-cofactor, CuSMoO₂ (Resch *et al.* 2005), no functional links between manganese and the CO dehydrogenase enzyme have been reported in the literature.

SPO1508- SPO1500 region



Scale map of the SPO1500-SPO1508 locus of R. pomeroyi including intergenic gaps (circled) and fold-change ratios for + Mn microarray experiments (Mn induced).

Close to the Form II cluster of *cox* genes is another predicted operon, *SPO1504-SPO1500*, whose expression is enhanced by factors ranging from 1.6- to 5.3-fold for the different genes (Table 7.2). These five genes are predicted to encode components of the enzymes needed to make the bacterial redox active cofactor, pyrroloquinoline quinone (Puehringer et al. 2008). There is evidence that a quinone is a used as a cofactor in Mn(II) oxidase of a strain of the alpha-proteobacterium *Erythrobacter*, a genus that is closely related to the Roseobacters (Johnson and Tebo 2008). Although several Rosebacters do have Mn(II) oxidase activity, *R. pomeroyi* DSS-3 does not (Hansel and Francis 2006), so the significance of this observation in terms of the effect of Mn on the expression of this *pgg* operon is not known.

Not far upstream of SPO1504, is SPO1508 forming a predicted one gene operon that likely encodes

an ethanol dehydrogenase of a type that (perhaps significantly – see above) has PQQ as a co-factor. Though closely linked to *SPO1504-SPO1500* (Figure 7.11) it is not co-transcribed with these genes.

Table 7.2 Genes whose expression is affected by the Mur regulator and/or Mn²⁺ availability.

A. Class I genes; expression is reduced by Mn, and greater in Mur mutant than wild type.

^a Gene	^b Factor of reduction with added Mn ²⁺	^c Factor of increase in Mur ⁻ mutant	d Predicted general function
SPO3363	3.8 ± 0.1	15.5 ± 1.1	Permease of ABC transporter; SitD
SPO3364	2.0 ± 0.3	6.6 ± 0.7	Permease ABC transporter; SitC
SPO3365	3.6 ± 0.2	18.3 ± 2.6	ATPase of ABC transporter; SitB
SPO3366	2.8 ± 0.1	8.8 ± 1.6	Periplasmic binding protein of ABC transporter; SitA
SPOA0392	6.95 ± 0.6	7.7 ± 0.4	Weak homology to RpoE-type σ- factor
SPOA0393	5.4 ± 0.6	6 ± 0	R body protein RebB-like protein
SPOA0394	2.1 ± 0.2	2.1 ± 0.3	Hypothetical; no known domains
SPOA0395	3.5 ± 0	5.1 ± 1.0	Hypothetical; no known domains
SPOA0396	5.75 ± 0.1	8.65 ± 2.2	Hypothetical; no known domains
SPOA0397	4.7 ± 0.6	4.75 ± 0.9	Hypothetical; no known domains
SPOA0398	6.1 ± 0.1	11.4 ± 0.1	R body protein RebB-like protein
SPOA0399	9.0 ± 0.5	16.2 ± 0.5	R body protein RebB-like protein

B. Class II genes; expression is enhanced by Mn, and lower in Mur mutant than wild type.

^a Gene	^b Factor of increase with added Mn ²⁺	^c Factor of reduction in Mur ⁻ mutant	^d Predicted general function
SPO1789	19.35 ± 2.7	14.25 ± 0.4	Related to permease of sulfate/tungstate ABC-type- transporter
SPO1790	10.5 ± 2.8	6.65 ± 0.9	Related to ATPase of sulfate/tungstate ABC-type-transporter
SPO1791	O1791 8.4 ± 2.4 5.75 ± 0.5		Related to periplasmic binding protein of sulfate/tungstate ABC-type-transporter
SPO0833	8.8 ± 0.2	7.9 ± 0.3	β polypeptides, molybdopterin- containing formate dehydrogenase
SPO1555	7 ± 0.1	5.95 ± 0.1	β polypeptides, molybdopterin-
SPO0834	3.9 ± 0.0	3.85 ± 0.5	containing formate dehydrogenase α polypeptides, molybdopterincontaining formate dehydrogenase
SPO1556	3.25 ± 0.2	3.4 ± 0.2	lpha polypeptides, molybdopterin-
			containing formate dehydrogenase
SPO1216	10 ± 0.1	12.55 ± 2.1	Hypothetical; no known domains

C. Class III genes; expression is reduced by Mn, and is unaffected by *mur* genotype.

^a Gene	^b Factor of reduction with added Mn ²⁺	^d Predicted general function				
SPO2261	8.5 ± 1.4	GTA gene cluster; major capsid protein				
SPO2262	7.3± 0.5	GTA gene cluster; possible peptidase				
SPO2263	4.1 ± 1.0	GTA gene cluster; no known domains				
SPO2264	13.6 ± 2.2	GTA gene cluster; phage portal polypeptide				

D. Class IV genes; expression is enhanced by Mn, and is unaffected by *mur* genotype.

^a Gene	^b Factor of increase with added Mn ²⁺	^d Predicted general function			
SPOA0339	11.7± 0.5	Subfamily of haloacid dehalogenase superfamily of aspartate nucleophile hydrolases			
SPOA0340	11.6 ± 1.4	Related to 4-oxalocrotonate tautomerase			
SPOA0341	19.8 ± 0.6	Hypothetical; no known domains			
SPOA0342	12.1 ± 0.5	Related to AfsA family protein, involved in A-factor biosynthesis			
SPOA0343	13.5 ± 2.0	Hypothetical; no known domains			
SPOA0344	No change	LysR-type transcriptional regulator			
SPOA0345	7.1 ± 0.6	In superfamily of soluble NAD(P)(H) oxidoreductases			
SPOA0346	6.7 ± 0.4	Related to 4-carboxymuconolactone decarboxylase			
SPOA0347	4.8 ± 0.4	Low-level similarity to major facilitator subfamily (MFS) of transporters			
SPO2394	1.8± 0.15	Carbon monoxide dehydrogenase, CoxF subunit			
SPO2395	1.8 ± 0.0	Carbon monoxide dehydrogenase, CoxE subunit			
SPO2396	3.1 ± 0.1	Carbon monoxide dehydrogenase, CoxD subunit			
SPO2397	3.2 ± 0.2	Carbon monoxide dehydrogenase, CoxL-2 subunit			
SPO2398	16.6 ± 3.1	Carbon monoxide dehydrogenase, CoxS-2 subunit			
SPO2399	16.0 ± 1.3	Carbon monoxide dehydrogenase, CoxM subunit			
SPO1515	8.2 ± 0.5	Putative cytochrome <i>c550</i>			
SPO1516	2.3 ± 0.1	Periplasmic-binding protein of ABC transporter; substrate unknown			
SPO1517	6.5 ± 0.5	Membrane attachment for CoxG subunit (Form II) of CO dehydrogenase			

SPO1518	2.5 ± 0.4	S-I subunit of CO dehydrogenase
SPO1519	No change	L-I subunit of CO dehydrogenase
SPO1520	2.1 ± 0.1	Medium sub-unit CO dehydrogenase
SPO1504	5.3 ± 0.1	PqqA-like; coenzyme PQQ synthesis protein A
SPO1503	3.1 ± 0.0	PqqB-like; coenzyme PQQ synthesis protein B
SPO1502	3.7 ± 0.1	PqqC-like; coenzyme PQQ synthesis protein C
SPO1501	No change	PqqD-like; coenzyme PQQ synthesis protein D
SPO1500	2.8 ± 0.4	PqqE-like; coenzyme PQQ synthesis protein E
SPO1508	5.8 ± 0.1	Strongly predicted quinoprotein (PQQ-dependent type I alcohol dehydrogenase)

Tables 7.2: A, B, C and D respectively show the gene numbers in Classes I, II, III and IV, described in text. Column a ; Clusters of genes whose levels of expression are affected by Mn availability and/or mur genotype are grouped. Column b ; Mean ratios plus standard errors of increase or decrease in the microarray signals in "+" and "-" manganese media. Column c ; Mean ratios plus standard errors of increase or decrease in the microarray signals in wild type compared to the Mur mutant in Mn-replete medium. Column d ; Polypeptide family of gene product, where known, is indicated Bold typeface indicates RNA levels significantly reduced/increased (p <0.05).

7.4.1 Genes regulated by iron in Ruegeria pomeroyi

The expression of many *Ruegeria pomeroyi* genes was affected by the availability of Fe. In some cases, this appeared to be mediated by (or implicated) Irr or the Mur (or both) transcriptional regulators, but in other cases, neither of these was involved. Some examples of such genes are presented in the following section, note that these are given in much more abridged style than the Mn-regulated genes. The data generated in this experiment presented literally dozens of different combinations. So, I will restrict myself to those in which there is a really big difference irrespective of Irr and Mur and Mn.

7.4.2 Effects of iron availability and mutations in irr on the transcriptome of Ruegeria pomeroyi

There were 23 genes that were altered above the chosen cut-off points in their expression in both Fe limitation and in the Irr⁻ mutant (refer to Table 7.3). Of these, 10 had similar responses; repressed by Fe, and were expressed higher in the Irr⁻ background (see Table 7.1, sections E, H and J in Figure 7.2).

Table 7.3 Genes affected by both Fe limitation and the irr mutation

Venn			result in
box ^a	Gene ^b	result in Fe ^c	Irr ^d
E	SPO0086	49.7 ± 9.1	3.83 ± 0.15
E	SPO0087	56.25 ± 0.04	4.135 ± 0.4
E	SPO0169	4.53 ± 1.4	3.71 ± 1.4
Е	SPO0199	5.96 ± 0.5	1.615 ± 0.06
E	SPO0647	3.08 ± 0.02	1.56 ± 0.03
E	SPO0790	28 ± 0.4	2.31 ± 0.03
E	SPO2023	4.42 ± 0.2	2.3 ± 0
E	SPO2486	2.975 ± 0.4	3.04 ± 0.2
E	SPO3014	6.69 ± 0.4	2.235 ± 0.1
E	SPO3287	45.85 ± 5.1	1.995 ± 0.01
Е	SPO3359	16 ± 0.5	1.96 ± 0.03
E	SPO3360	13.25 ± 0.1	1.985 ± 0.04
Е	SPO3607	4.095 ± 0.03	1.7 ± 0.05
Е	SPOA0445	3.52 ± 0.04	n/a
Н	SPO0222	32.15 ± 1.2	5.8 ± 0.5
Н	SPO0701	13.85 ± 0.1	2.105 ± 0.02
Н	SPO1565	4.125 ± 0.2	1.55 ± 0.01
Н	SPO1861	3.085 ± 0.02	1.545 ± 0.04
Н	SPO2264	8.8 ± 0.4	2.145 ± 0.2
J	SPO1216	6.655 ± 0.4	13.7 ± 1
J	SPO2398	6.36 ± 0.6	3.38 ± 0.09
J	SPO2399	7.87 ± 0.3	3.44 ± 0.2
J	SPOA0399	3.205 ± 0.2	15.7 ± 1.2

(Column a) shows those genes from sections E and E and E and E and E of Venn diagram, Figure 7.2, their resultant expression (in fold change, E the standard deviation (Column b)). Red indicates that the gene was expressed higher in the absence of E than its presence (Column c) or that expression was higher in the Irr- mutant than in the wild type (Column d). The green boxes indicate the opposite ratio of expression.

Six genes had the opposite phenotype, being induced by iron, but expressed at lower levels in the Irr mutant than in the wild type. These genes include the *cox* genes *SPO2398* and *SPO2399* which are discussed above in relation to their responses to manganese. Another gene that displayed this pattern was *SPO1216*, which was expressed 6.6-fold higher when Fe was present in the medium, and 13.7-fold less in the Irr strain compared to the wild type. The translated product of *SPO1216* does not have any predicted function, and there is only one other homologous peptide found in the ncbi database – in *Dinoroseobacter shibae* DFL-12.

Finally, there were six genes that were shown to the repressed by Fe, and were expressed at higher levels in the Irr background. These genes may be under the control of a repressor in the Irr regulatory hierarchy, and would be good targets for further experiments to elucidate the Feregulatory networks in *R. pomeroyi*.

Four of these genes have predicted function, and two were adjacent to each other in the genome. These two genes, SPO3359 and SPO3360, were closely linked to the sitABCD operon, and were ~14-fold repressed by the added $FeCl_3$, and were 2-fold lower in the Irr^- background compared to the wild type. These two genes are predicted to encode an L-threonine 3-dehydrogenase and a 2-amino-3-ketobutyrate coenzyme A ligase respectively; these are both well conserved in the Roseobacters, and are closely related to peptides found in both α - and γ -proteobacteria.

Two other, unlinked genes, *SPO0222* and *SPO0701*, were significantly Fe repressed, 32- and 14-fold respectively, and were 5.8- and 2.1-fold lower in the Irr⁻ background. The translated product of *SPO0222* is predicted to be an alanine dehydrogenase, which is well conserved in the Roseobacters and indeed throughout the proteobacteria.

Finally, *SPO0701* is predicted to encode a Type 1 glyceraldehyde-3-phosphate dehydrogenase. It is difficult to assign any likely link to iron for these genes, other than these preliminary transcriptomic data.

In summary, there are clearly some interesting target genes here for further study into the role Irr plays in regulated iron uptake and usage in *R. pomeroyi*. Given that the genes presented in table 7.2 exhibit differential regulation in response to both Fe, and Irr, there must be other transcriptional regulatory elements which mediate this, and indeed this précis of the *R. pomeroyi* transcriptional response to Fe should allow a focussed approach into this future work. Note that 12 out of the 23 genes shown in table have no predicted function; there is therefore still much to learn about the "iron-ome" in this bacterium.

7.5.1 Genes that enhance the story already told in this thesis – regulation and uptake of Mn and Fe

So far, we have defined the system for Mn uptake, via SitABCD, and the regulation of this process, via Mur in *R. pomeroyi*, and this microarray analysis has verified our findings. However, the same cannot be said for Fe; an FbpAB⁻ strain of *R. pomeroyi* did not have a growth deficiency on low iron,

meaning there must be functional redundancy for inner membrane iron transport, or that these genes do not encode an iron-specific transporter. Also, Fe-responsive regulation has been demonstrated for Irr of *R. pomeroyi*, but the regulator of other iron-responsive genes – those with an IR box has not been identified. The following provides a walk-through of the transcriptional responses of genes already studied in this work, and provides further insight into the 'unknown' aspects of *Ruegeria* iron metabolism.

7.5.2 Irr

The transcription of Irr was *induced* ~3.5-fold by Fe. This agrees with findings in Rhizobium (Todd *et al.* 2002), but in *Brucella abortis, Bradyrhizobium japonicum* and *Rhodobacter sphaeroides,* Irr was not Fe-regulated at a transcriptional level (Martinez *et al.* 2005; Peuser *et al.* 2012; Qi *et al.* 1999). In these organisms, Irr is regulated at a post-transcriptional level. It would be of interest to study the effect of high/low Fe on Irr protein levels in *R. pomeroyi*, and also whether this protein has a haem binding capacity. As shown above, several genes were altered in expression in the Irr strain of *R. pomeroyi*.

7.5.3 *MbfA*

The expression of *mbfA* homologues have been shown to be regulated by Irr in *Rhizobium*, *Bradyrhizobium* and *Brucella* (Martinez *et al.* 2005; Qi *et al.* 1999; Todd *et al.* 2002).

In *Ruegeria*, *mbfA* expression was Fe induced, as shown by both *lacZ* fusion, and in the microarray study. This regulation is likely due to Irr, via an ICE box motif, as *mbfA* expression was significantly higher in the Irr⁻ background than in the wild type (13.5-fold), also in agreement with *lacZ* fusion data.

7.5.4 IscR

Another gene with a conserved ICE motif was the regulator of [Fe-S] biosynthesis, *iscR*. Indeed, it is likely that this gene forms part of a single transcriptional unit with the downstream *suf* genes. The expression of *iscR* was only significantly differently (2.5-fold) regulated in the Irr mutant compared to the wild type, and not by Fe levels. Furthermore, the downstream *suf* genes showed little regulation in response to either Irr, or Fe (all <2-fold). A *lacZ* fusion to *iscR* showed considerable deregulation in the Irr- strain, which is not apparent in the microarray data. It is clear that further work on the regulation of both *iscR* and the *suf* genes is required.

7.5.5 RRF-2 family proteins

It was hypothesised that the regulator of the IR boxes of *R. pomeroyi* may be an Rrf2 family protein, similar to RirA found in the rhizobiales. However, mutant strains lacking each individual Rrf2 family protein found in *R. pomeroyi* were not deregulated in expression of genes under the control of IR boxes (see Chapter 4). It was of interest to observe the transcriptional response of each Rrf2 gene in *R. pomeroyi*, to both Fe, and to Irr since RirA has been shown to be Irr and Fe regulated in *Rhizobium* (Todd *et al.* 2006; Todd *et al.* 2002).

Interestingly, four of the Rrf2 family genes were iron regulated:

SPO0432 - 7.8-fold Fe induced

SPO3722 - 5.4-fold Fe repressed

SPO1393 - 3.9-fold Fe repressed

SPOA0186 - 3.4-fold Fe repressed

And, as discussed, the fifth Rrf2 family gene, *iscR* (*SPO2025*) was not Fe regulated, but was Irr repressed.

This result would appear to show that there may well be functional redundancy between these regulators, and it is possible that multiple, clearly Fe-responsive regulators are responsible for the repression of genes under the control of IR boxes. Crucially, none of the Rrf2 family genes were altered in expression by either Mn or Mur.

7.5.6 The fbpAB genes

As shown in Chapter 4, the expression of *fbpA* and *fbpB* is Fe-repressed, mediated by IR boxes of which *fbpA* has two and *fbpB* just one. As discussed earlier, there is a lack of a cognate ATPase gene for this putative iron transporter, FbpAB, and it was proposed that *SPO2689* may encode a likely candidate (refer to Chapter 4).

The microarray data confirm that *fbpA* is highly Fe-repressed; indeed it is one of the most Ferepressed genes in the array data (~45-fold). However, and in agreement with *lacZ* fusion data, expression of *fbpB* is far less Fe-repressed (3.9-fold).

The expression of any potential ATPase peptide is less clear, the hypothesised *SPO2689* is poorly induced in low Fe conditions (<2-fold), and is unlikely to be the ATPase for the FbpAB transporter. Indeed, this transporter may not be required at all by *R. pomeroyi* as a functional mutant was unaffected in growth (Chapter 4). Furthermore, as shown in Table 7.4, there were no other ABC-class transporter genes induced >5-fold by Fe limitation in this microarray experiment.

7.5.7 The irp genes

The *irp* locus of *R. pomeroyi* is a fascinating prospect for a novel iron uptake mechanism (see Chapter 3). Here, the microarray study further emphasised this potential: As shown in Table 7.4, the genes *SPO0086-SPO0090* were all hugely Fe-repressed, and are therefore very likely to form a single transcriptional unit. Indeed *SPO0086* (*irpA*) was the single highest iron regulated gene in all replicates of these conditions. Furthermore, there were strong predictions of signal peptides, and localisation to the outer membrane for *SPO0086*, and other genes in this operon (Table 7.4).

In Chapter 4, irpA was shown to be Fe-repressed, and that this was mediated by a copy of an IR box.

The expression of both *SPO0086* and *SPO0087* were also shown to be Irr repressed, albeit by a low level compared to the level of Fe-repression (Appendix 3). This could be an artefact of the Fe status of an Irr strain compared to the wild type, or may represent a cross-over in regulation from Irr to the transcriptional regulator of IR boxes.

7.6.1 Genes highly regulated by iron and manganese limitation

A detailed predictive functional analysis was performed on all those genes whose expression was altered, >5-fold in the iron limitation experiment. This list of 98 genes was analysed using a variety of online predictive programs to gain an insight into the putative function, location and structure of all 98 proteins.

Table 7.4 *Ruegeria pomeroyi* genes whose expression was altered >5-fold in response to iron limitation; predicted function, cellular location, structural prediction and prevalence in the Roseobacters

Gene ID - operons shaded	Iron Array Result	Manganese Array Result	Function (if known)	Accession number	Localisation (pSORTB)	Signal Peptide (SIGNALP)	TAT signal (TATP)	Beta Barrel (MCMBB)	Pred TMBB	Presence in other Roseobacters (max 150)
SPO0086	56.3	1.48	lipoprotein, putative	YP 165360	OuterMembrane 9.93	YES		0.014	YES	33
SPO0087	58.8	1.245	hypothetical	YP 165361	Unknown	YES		0.052	YES	8
SPO0088	29.7	1.11	thiol oxidoreductase	YP 165362	CytoplasmicMembrane 9.82			-0.042	YES	33
SPO0089	11	1.9	Imelysin, Peptidase_M75	YP 165363	Unknown	YES		-0.018	YES	30
SPO0090	14.8	1.13	hypothetical	YP 165364	Unknown		YES	0.003	YES	32
SP00181	7.66	1.0375	Flagella rod protein FliC	YP_165451	Unknown MLS		YES (But no TA	0.009	NO	30
SPO0197	6.37	1.24	flagellar motor switch protein FliN	YP 165467	Extracellular 2.00			-0.004		20
SPO0198	6.2	1.08	ABC transporter ATP-binding protein, flagellar	YP 165468	Extracellular 0.26			-0.031		18
SPO0199	5.45	1.15	Flagella MS-ring protein	YP_165469	Extracellular 0.00			0.008	Possible	32
SPO0222	33.3	4.025	Alanine dehydrogenase [Amino acid transport and metabolism]	YP 165491	Periplasmic 0.01			-0.024		78
SPO0227	5.28	1.51	Peptidase M10 serralysin C terminal	YP 165496	Extracellular MLS* 10.00			-0.067		100
SPO0254	6.01	1.72	organic hydroperoxide resistance protein OsmC	YP 165518	Cytoplasmic 9.26			-0.001		11
SPO0313	9.97	1.425	Glyoxalase/Bleomycin resistance protein	YP 165576	Unknown			0.001	NO	23
SPO0390	5.5	1.23	glutamate/leucine/phenylalanine/valine dehydrogenase	YP 165653	Cytoplasmic 9.97			0		17
SPO0432	7.42	1.775	rirA' RRF-2 family transcriptional regulator	YP 165695	Cytoplasmic 8.96			-0.069		28
SPO0692	9.04	1.0005	Cytochrome C oxidase subunit II, periplasmic	YP 165947	Periplasmic 9.76		YES	-0.032		49
SP00701	13.7	4.02	glyceral dehyde-3-phosphate dehydrogenase	YP 165955	Cytoplasmic 9.97			-0.013		121
SPO0759	9.11	1.11	hypothetical	YP 166012	Unknown			-0.01		1
SP00784	12.8	1.585	chloramphenicol acetyltransferase	YP 166037	Unknown			-0.044		26
SP00789	18.8	1.0045	Hemin uptake protein hemP	YP 166042	Unknown			-0.024		1
SP00790	28.4	1.0605	hypothetical	YP 166043	Unknown			-0.087		21
SPO0858	13.9	1.155	MauG methylamine utilisation protein	YP 166111	Periplasmic 9.76	YES		-0.028		49
SPO0900	5.5	2.465	bifunctional sulfate adenylyltransferase 'sat'	YP 166153	Cytoplasmic 9.97			-0.058		38
SPO1018	5.93	1.535	branched-chain amino acid ABC transporter ATPase	YP 166270	Cytoplasmic MLS 9.12			-0.039		150
SPO1019	8.37	1.355	branched-chain amino acid ABC transporter permease	YP 166271	CytoplasmicMembrane 10.00			-0.023		150
SPO1020	7.33	1.385	branched-chain amino acid ABC transporter permease	YP 166272	CytoplasmicMembrane 10.00			-0.051		150
SPO1021	7.58	1.62	branched-chain amino acid ABC transporter substrate binding	YP 166273	Unknown	YES	YES	-0.002		39
SPO1177	9.85	1.06	hypothetical	YP 166424	Unknown			-0.006		1
SPO1216	7.05	9.985	hypothetical	YP 166463	CytoplasmicMembrane 10.00			-0.026		2
SPO1280	5.48	1.635	hypothetical	YP 166525	Cytoplasmic 8.96			-0.052		33
SPO1351	8.23	1.65	MetZ - O-succinylhomoserine sulfhydrylase - Methionine biosynthesis	YP 166593	Cytoplasmic 9.97			-0.01		135
SPO1366	5.41	1.11	ilvC ketol-acid reductoisomerase Isoleucine biosynthesis	YP 166608	Cytoplasmic 9.97			-0.064		37
SPO1387	7.65	1.215	cation efflux system protein	YP 166629	CytoplasmicMembrane 10.00			-0.075		40
SPO1409	5.28	1.265	rpoH heatr shock sigma factor	YP 166650	Cytoplasmic 9.97			-0.023		112
SPO1515	9.3	8.165	cytochrome c550	YP 166756	Unknown MLS	YES		-0.011		8
SPO1517	5.76	6.49	coxG carbon monoxide dehydrogenase operon G protein	YP 166758	Unknown			-0.034		52
SPO1593	5.49	1.82	zinc-dependent alcohol dehydrogenase	YP 166834	CytoplasmicMembrane 9.82			-0.022		100
SPO1689	12.1	1.0225	hypothetical	YP 166928	Unknown	YES		-0.018		3
SPO1795	12.6	1.15	HybA - formate dehydrogenase, iron-sulfur subunit	YP 167032	Cytoplasmic 9.97			-0.132		31
SPO1796	24.8	1.07	formate dehydrogenase subunit alpha	YP 167033	Periplasmic 9.76			-0.041		97
SPO1847	5.24	2.29	Long-chain acyl-CoA synthetases	YP 167084	CytoplasmicMembrane 7.88			-0.049		150
SPO1909	8.03	1.07	NTF2_like domain, hypothetical protein	YP 167145	Cytoplasmic 8.96			-0.03		8
SPO2130	6.47	1.755	alpha-isopropylmalate/homocitrate synthase	YP 167358	Cytoplasmic 9.97			-0.008		75
SPO2131	8.54	1.045	cysS - cysteinyl-tRNA synthetase	YP_167359	Cytoplasmic 3.37			-0.039		36
SPO2135	5.86	1.205	Hypothetical	YP 167363	Unknoyny	YES			Possible	2
SPO2222	5.51	1.055	dihydrolipoamide dehydrogenase	YP 167448	Cytoplasmic 9.97			-0.039	. 5551616	150
SPO2246	9.66	1.305	CysK - cysteine synthase A	YP 167472	Cytoplasmic 9.26			-0.008		56
SPO2261	10.8	8.44	HK97 family major capsid protein	YP 167486	Unknown			0.008	VES	34

Gene ID - operons shaded	Iron Array Result	Manganese Array Result	Function (if known)	Accession number	Localisation (pSORTB)	Signal Peptide (SIGNALP)	TAT signal (TATP)	Beta Barrel (MCMBB)	Pred TMBB	Presence in other Roseobacters (max 150)
SPO2262	7.83	7.23	HK97 family phage prohead protease	YP 167487	Unknown			0.02	YES	36
SPO2264	8.4	13.6	HK97 family portal protein	YP 167489	Unknown		YES	-0.011		33
SPO2398	5.74	16.55	coxS carbon monoxide dehydrogenase, small subunit	YP_167617	Cytoplasmic 9.97			-0.121		150
SPO2399	8.18	16	coxM carbon monoxide dehydrogenase, medium subunit	YP_167618	Cytoplasmic 9.97			-0.027		80
SPO2508	10.5	1.54	hypothetical	YP 167723	Unknown			-0.005		1
SPO2614	17.7	1.105	hypothetical	YP 167824	Cytoplasmic 8.96			-0.06		1
SPO2615	18.5	1.15	Oye family NADH-dependent flavin oxidoreductase	YP 167825	Cytoplasmic 9.97			0.017	YES	96
SPO2632	9.08	1.925	CobJ type uroporphyrin-III C-methyltransferase	YP_167842	Cytoplasmic 9.26			-0.01		100
SPO2633	8.67	1.675	hypothetical	YP 167843	Unknown			-0.011		33
SPO2634	10.8	2.43	CysI - sulfite reductase	YP 167844	Cytoplasmic 9.97			-0.031		37
SPO2636	8.25	2.225	hypothetical	YP 167846	Unknown			0.013	NO	37
SPO2637	5.43	1.565	ferredoxin-NADP reductase	YP 167847	Cytoplasmic 9.97			-0.049		46
SPO2686	5.84	1.515	LysM/M23/M37 peptidase	YP 167896	OuterMembrane 9.92	YES		0.016	YES	38
SPO2706	14.5	1.845	caiD-1 carnitinyl-CoA dehydratase	YP_167916	Cytoplasmic 9.97			-0.057		150
SPO2839	5.05	1.64	GlcB - malate synthase G	YP_168047	Cytoplasmic 9.97			-0.053		35
SPO2867	6.69	1.21	CobJ type precorrin-3B C(17)-methyltransferase	YP 168075	Cytoplasmic 9.97			-0.031		36
SPO2962	10.8	1.93	hypothetical	YP 168170	Unknown			-0.058		1
SPO3014	7.04	1.56	hypothetical	YP 168218	Unknown			-0.097		2
SPO3027	7.61	1.28	HisC - histidinol-phosphate aminotransferase	YP 168231	Periplasmic 9.80			-0.025		77
SPO3118	6.09	1.06	hypothetical	YP 168321	Unknown		YES	0.041	Possible	1
SPO3287	50.9	1.155	FbpA - ferric iron ABC transporter periplasmic binding protein	YP 168483	Periplasmic 9.76			0.01		41
SPO3355	5.34	1.93	SerA - serine biosynthesis D-3-phosphoglycerate dehydrogenase	YP 168551	Cytoplasmic 9.97			-0.02		150
SPO3359	15.5	1.3	L-threonine 3-dehydrogenase	YP_168555	Cytoplasmic 9.97			-0.035		57
SPO3360	13.2	1.695	2-amino-3-ketobutyrate CoA ligase	YP 168556	Cytoplasmic 9.97			-0.008		92
SPO3409	5.32	1.37	anti-anti-sigma factor	YP 168605	Unknown			0.01	NO	30
SPO3445	7.42	1.255	lpxK tetraacyldisaccharide 4'-kinase	YP 168641	Unknown			-0.016		37
SPO3523	5.68	1.18	CcoP cytochrome c oxidase, cbb3-type subunit III	YP 168718	Unknown			-0.01		37
SPO3524	6.68	1.3	CcoQ cytochrome c oxidase, cbb3-type subunit IV	YP 168719	CytoplasmicMembrane 9.82			-0.015		8
SPO3525	8.25	1.36	CcoO-1 cbb3-type cytochrome c oxidase subunit II	YP 168720	Unknown			-0.029		37
SPO3526	6.66	1.27	CcoN-1 cbb3-type cytochrome c oxidase subunit I	YP 168721	CytoplasmicMembrane 10.00			-0.04		39
SPO3529	5.97	1.155	serine hydroxymethyl transferase	YP 168724	Cytoplasmic 9.97			-0.022		61
SPO3547	8.45	1.89	hypothetical	YP 168742	Unknown			-0.074		6
SPO3606	5.28	1.215	mandelate racemase	YP 168801	Periplasmic 9.51			-0.026		37
SPO3613	5.7	1.1	LysE - amino acid transporter	YP 168808	CytoplasmicMembrane 10.00			-0.026		59
SP03721	7.17	1.46	hypothetical	YP 168915	CytoplasmicMembrane 10.00			-0.058		1
SPO3722	5.33	1.145	RRF2 family trascriptional regulator	YP 168916	Unknown			-0.053		2
SPO3770	5.24	1.585	GltD type oxidoreductase	YP_168965	Cytoplasmic 9.97			-0.039		73
SPOA0061	6.16	1.83	KatG - catalase/peroxidase HPI (heme binding site)	YP_164892	Cytoplasmic 9.26			-0.02		39
SPOA0273	8	1.355	PuuR - transcriptional repressor, putrescine degradation	YP 165102	Cytoplasmic 9.97			-0.017		11
SPOA0321	6.05	1.05	glyoxalase family protein	YP 165148	Unknown			-0.05		7
SPOA0339	149	11.65	HAD family hydrolase	YP 165166	Cytoplasmic 9.97			-0.015		1
SPOA0340	109	11.6	4-Oxalocrotonate Tautomerase	YP 165167	Unknown			-0.032		1
SPOA0341	164	19.8	hypothetical	YP 165168	Cytoplasmic 8.96			-0.05		1
SPOA0342	47.4	12.05	hypothetical	YP 165169	Cytoplasmic 8.96			-0.071		1
SPOA0343	86.5	13.5	hypothetical	YP 165170	Cytop 2605 ic 8.96			-0.002		1
SPOA0345	79.8	7.125	aldo/keto reductase family oxidoreductase	YP 165172	Cytoplasmic 9.97			-0.04		57
SPOA0346	91.2	6.665	carboxymuconolactone decarboxylase family protein	YP 165173	Unknown			-0.031		4
SPOA0347	29.8	4.745	MFS - secondary transporter superfamily	YP 165174	CytoplasmicMembrane 10.00			0.011	YES	13
SPOA0348	10.4	3.35	hypothetical	YP 165175	Unknown			-0.031		13
					*MLS means this protein may have	e multiple locali	sation sites	5.552		

The 97 genes with >5-fold difference in expression are listed in column 1, and the relative fold change in expression is shown for Fe limitation in column 2, and for Mn in column 3. The accession number of each protein is shown in column 4, and the predicted subcellular location as given by pSORTB (Yu et al. 2010) in column 5. Column 6 contains the prediction of a SEC signal peptide {SignalP, (Petersen et al. 2011)}, and column 7 contains a TAT signal peptide prediction {TATP, (Bendtsen et al. 2005)}. Columns 8 and 9 contain predictions for beta-barrel structure, and transmembrane beta-barrel structure respectively {PredTMBB, (Bagos et al. 2004)}. Each peptide sequence was used to interrogate the Roseobase database, and the relative numbers of homologues found were converted into a scale from 1, where there was only one homologue, to 150, where there were multiple homologues in many of the Roseobacter strains. These data are shown in column 10.

There are a few intriguing genes which were highly regulated by Fe limitation, referring to table 7.4. Given that the only homologue for an Fe-specific ABC-class transporter is incomplete (*fbpA* and *fbpB*), it was of interest to see that *SPO1018-SPO0121* were all induced >6-fold in the absence of iron. These genes encode a complete ABC-class transporter, an ATPase, 2 permease proteins and a substrate binding protein (respectively, *SPO1018-SPO1021*). These genes are annotated as a branched –chain amino acid transporter, but are <10% ID to FbpAB or SitABCD. However, given their induction by iron limitation, further work on these genes would be useful for our understanding of their possible role in Fe uptake.

The two genes of the transcriptional unit *SPO0789-SPO0790* were both highly induced (19- and 28-fold respectively) in the absence of Fe. Interestingly, the former is predicted to be a haemin uptake protein, HemP (pfam10636), but the *SPO0790* product has no predicted function. HemP has been shown to be required for haem uptake in *Yersinia enterocolitica*, where is serves as a haemin uptake system, and is Fur regulated (Stojiljkovic and Hantke 1992). *R. pomeroyi* is the only genome-sequenced Roseobacter that contains such a *hemP* like gene, unlike *SPO0790* which is present in >20 Roseobacter genomes.

A suite of cytochrome genes (*SPO3523-SPO3526*) were shown to be repressed in low Fe (5 to 8-fold). These four genes encode all four subunits of a Cbb3-class cytochrome C oxidase. This family of cytochromes are haem-copper oxidases, and catalyse the final step in aerobic respiration of dioxygen to water. It is interesting to see that a haem containing protein complex is repressed in low

Fe conditions, and could be an example of bacterial adaption to a low Fe environment, conserving the demand for the metal by down-regulating gene products which require Fe.

The Cox genes introduced above for their Mn-responsive expression also show a significant increase in expression by Fe, and that this is likely mediated by Irr. The expression of *coxL-2* (*SPO2399*) is ~5-fold induced by iron, and shows a ~3-fold induction by Irr.

Finally, and of note, a gene encoding a predicted anti-anti sigma factor (*SPO3409*) was 5.3-fold Ferepressed. The deduced protein of this gene is in the STAS and SulP families (pfam01740) which are proposed to be regulatory over anion transport – including sulphur, from where the SulP name is derived. Given that *SPO3409* was Fe-repressed, this gene product would therefore be in a higher concentration during Fe-limitation, and would be predicted to increase its binding to its cognate anti sigma factor, releasing the sigma factor which would, in turn, allow the expression of a suite of genes. Further microarray analysis of a mutant in this gene might be instructive in the analysis of such a regulatory circuit.

Chapter 8 - General Discussion

The work described in this thesis represents the first sortie into the genetics and genomics of manganese and of iron homeostasis in the Roseobacters and is one of very few studies on this subject in any marine bacteria. The recent work on *Rhodobacter* and *Pelagibacter* only appeared well into the project (Peuser *et al.*, 2011; Smith *et al.*, 2010).

In what follows, I summarise the major outcomes of the work in the form of a series of questions that address future challenges in these topics, and outline the sorts of experiments that could be used to answer these. The discussion deals separately with the two metals.

8.1 Iron - Bioinformatically based outcomes

8.1.1 Paucity of ferrous iron and Fe-reductase genes

One consistent observation of the deduced proteomes of the Roseobacters was that they lack the FeoA/B ferrous iron uptake system, although the *feoAB* genes are commonly found in other alphaproteobacteria, such as *Rhodobacter sphaeroides* and *Caulobacter crescentus*. This suggests that the Roseobacters may not use this reduced form of the metal, consistent with the fact that the surface waters of the oceans are fully oxygenated. Furthermore, there were no examples of any enzyme that resembled a flavo-reductase in the deduced proteomes of any Roseobacters. However, given that UV light has been shown to reduce Fe(II), the Roseobacters may simply not require a cognate reductase (Butler and Theisen 2010).

However, Roseobacters are also found in marine sediments (Wagner-Döbler and Biebl, 2006), where the O_2 tension would be lower, so the Roseobacters may be able to import Fe(II), but via an uncharacterised transporter. FeoAB mutants are deficient in Fe(II) uptake, shown by growth, and by final Fe content of cells. For growth experiments, Fe(II) can be produced by the addition of ascorbate to FeCl₃ (Kammler *et al.* 1993). To identify a potential Fe(II) uptake system, a Tn5 mutant library could be screened for increased expression of an iron-repressed reporter fusion during growth on Fe(II) supplemented media.

All Roseobacters lacked any known ferric reductases that correspond to the *ferAB* or *mtrAB* gene products. However, *Oceanicola granulosus* HTCC2516 was unusual in that it encodes a protein (*OG2516_12819*) that is 34% identical to YqjH of *E. coli* – a polypeptide that is implicated in ferric iron reduction from siderophores (Miethke *et al.* 2011). Indeed, the *Oceanicola* gene product is annotated as a siderophore-interacting protein. It would be interesting to see if *Oceanicola* can grow with only reduced Fe, and if so, to examine the effect of a mutation in the *OG2516_12819* gene.

It is possible that Roseobacters simply have no need to reduce Fe (III) and instead entirely rely on the uptake of Fe-chelates. It has been shown that Fe-siderophore complexes can be reduced by sunlight, which causes an increase in Fe uptake by marine microorganisms (Amin *et al.* 2009). This may make ferric reductases redundant in the case of the Roseobacters.

The status of Fe in the oxygenated open water is likely to be mostly fully oxidised. However, within other marine environments, such as marine snow, sediment and in large clusters of bacteria, it would be possible for areas of reduced Fe to exist, and would likely be a target for uptake by bacteria inhabiting such places.

To further study the Fe status of different habitats, and how this relates to the types of bacteria Fe uptake systems would require careful sampling of bacteria from such habitats, and then to study the presence of Fe(II) uptake genes in these strains. Currently, the Roseobacter strains that have available genome sequences were not sampled precisely from specific marine habitats. Although demanding, it might be instructive to examine the expression of genes, and indeed, genomes of the Roseobacters in more precisely defined niches, in which, for example, the O_2 levels were much lower than in the surface waters of the oceans. This might be done by high throughput metatranscriptomics, for example.

Another major outcome of the work in this thesis was the demonstration of the diversity of the predicted systems for the uptake of iron. There is a bewildering variety in the numbers and identities of the different, predicted mechanisms for the acquisition of this metal, with some strains being predicted to have multiple (the maximum predicted number, In *Ruegeria* sp. Trich CH4B, was ten) TonB-dependent receptors and others with none (see Chapters 2 and 6).

8.1.2 Marine siderophore production and uptake

Several strains of Roseobacter that contain TBDRs lack predicted siderophore synthesis genes (see Chapter 2). These strains are most probably siderophore 'pirates', being able to use siderophores that are made by other strains. This phenomenon is not unique to the Roseobacters and has been reported in many bacteria (Traxler *et al.* 2012).

However, this strategy may be expected to be more prevalent in marine bacteria since unattached siderophores will drift away from the bacterial cell that produced them. Alison Butler and colleagues have shown that marine bacteria can produce lipid-bound, amphiphilic siderophores that can form micelles, as described in Butler and Theisen (2010). However, there is no evidence that any Roseobacter siderophores have these properties, as there is no information about the siderophore biosynthetic genes for those molecules identified by Alison Butler's lab.

It was noted that several strains of Roseobacters have genes that are predicted to be involved in siderophore production – and other genes involved in uptake (see Chapter 2). This raises a pertinent question: Is it beneficial to synthesise a siderophore in a marine environment? The likelihood of a single cell ever synthesising, exporting and then recovering a siderophore seems highly unlikely.

Since very little is known about the biosynthetic genes of marine siderophores, bioinformatic predictions about the presence of siderophores in any Roseobacter should be treated with caution. The logical next step in this area of my work would be to screen all of the Roseobacter strains for siderophore production using CAS plate, or other assays (see Chapter 4). Those strains which do produce siderophores would be used to construct mutant libraries, and screened again for a CAS phenotype. This would function two-fold, firstly in the identification of any potential negative regulators of siderophore production (a larger CAS halo) and secondly to identify siderophore biosynthetic genes (no CAS halo). This would represent the first example of siderophore biosynthetic gene identification in marine bacteria.

Furthermore, and importantly to supplement the data generated in Chapter 2, would be to identify the cognate molecules taken up by each TBDR. One approach to achieve this would be to take those Roseobacters with a single, or small number of receptor genes, and to perform metabolic arrays, for growth on many different Fe-ligand sources. Once a potential Fe-ligand has been identified, the

cognate outer membrane receptors can be systematically mutated until the strain no-longer grows on that Fe source.

Since there is no exact information about the siderophores that may be produced by members of the Roseobacter clade, it would also be pertinent to perform siderophore purification, and structural analysis on these molecules. These novel siderophores could be used to identify their cognate receptors using metabolomics if a high enough concentration can be purified. This strategy would be particularly useful in those strains which appear to have both siderophore synthesis and uptake systems in their genome.

8.1.3 TonB

TonB is required for outer membrane transport of several Fe-bound compounds: siderophores, haem and vitamin B_{12} , for example It was therefore surprising to find that TonB was missing from many Roseobacter strains, as had been noted by Rodionov *et al.* (2006.) However, given the significant variation of TonB peptides (*E. coli* TonB is only ~30% identical to TonB of *Rhizobium* for example), it could be that a gene performing the function of TonB is present in these genomes, but is unidentifiable by means of homology-based searches. Importantly, some Roseobacters *do* have siderophore biosynthetic genes, and yet do not appear to have TonB.

It was also apparent that several Roseobacters lacked both a copy of TonB, and any identifiable TBDR's, and these species could indeed represent a class of bacteria which use a novel means of outer membrane iron transport. This may be via Fbp class transporters which can span the periplasm – such as may occur in *Vibrio* (Wyckoff *et al.* 2006), or even via the IrpA system, as described in chapter 3. In both cases, TonB-independent outer membrane Fe transport could be possible, and would be a significant change in our understanding of iron uptake by gram negative bacteria.

TonB functions to energise outer membrane transport with two other proteins – ExbB and ExbD. It should be noted that *R. pomeroyi* likely does not have functional ExbBD proteins. Indeed, the presence of *exbBD* genes in the Rosobacters is unresolved – there were no proteins with greater than 50 % identity to either ExbB or ExbD from *E. coli* K-12 encoded in any Roseobacter genome.

The lack of knowledge in marine metal uptake systems is exemplified by our observations in *R. pomeroyi*, a strain that apparently lacks any known TBDR, lacks TonB itself (see Chapter 2), does not require its FbpABC-type transporter for iron uptake, does not use RirA to regulate Fe uptake and yet

does regulate this process using motifs homologous to IRO boxes of *Rhizobium*. There are therefore some major unanswered questions even in this one "model" strain:

How does Ruegeria pomeroyi import iron complexes through the outer membrane?

Does R. pomeroyi really lack a TonB-type system and, if so, what, if anything, does it use in its place?

How does R. pomeroyi import iron from the periplasm to the cytoplasm?

What transcriptional regulator binds to IR boxes?

These questions extend further than just this species, as similar portfolios of genes exist in other Roseobacters. Indeed, the IR box may be present in many of the Rhodobacteraceae, as identified in Rodionov *et al.* (2006).

To answer these questions will take some careful and thorough experiments, as detailed below.

8.1.4 Iron transporters in R. pomeroyi

Fbp

Although a clear objective of this work was to identify the transporters responsible for Fe uptake in *R. pomeroyi*, this was unsuccessful, despite identifying a likely *a priori* candidate pair of genes, *fbpA* and *fbpB*, whose expression was markedly induced in lo-Fe and whose products comprised two of the polypeptide components of an ABC transporter that closely resembled those involved in Fe import in other bacteria. There were also no clear indications of a TonB-dependent uptake system for Fe-ligands, and indeed no alternative identified for the inner membrane transport of Fe. All we know is that growth of *R. pomeroyi* is limited when Fe is at, or < 0.5 μ M. There was an indication that another ABC-class transporter, encoded by the *SPO1018-SPO1021* genes, might be involved, since its expression was induced by Fe limitation. It would be interesting to mutate these genes, either alone, or in combination with a mutation in *fbpA* and examine its Fe uptake phenotype.

It would be expected that the further microarray experiments may generate more potential target genes for investigation. The regulon of the IR box regulator may indeed include the entire range of iron uptake genes, which our bioinformatic predictions are currently missing.

<u>IrpA</u>

A second set of gene products whose initial properties made them promising candidates for *the*, or at least "a" set of Fe transporters were those encoded by an operon that included the *irpA* gene plus *SPO0087-SPO0090*. However, this too did not come to fruition. Even though the IrpA is known in other bacteria to be an Fe transporter, and indeed this study confirmed that it was markedly induced in Fe-depleted conditions, it was a big disappointment when a mutation in the *irpA* gene was not deficient in growth on Fe limited media. Furthermore, the predictions made for IrpB were tantalising, but experimental work failed to produce any meaningful results.

The range of metal uptake strategies used by the Roseobacters could well reflect the niches that these bacteria occupy. Very little is known of the various strains that have been studied in the laboratory, which have been obtained almost randomly by sampling various coastal and far-ocean sites. Although some strains (e.g. *Dinoroseobacter shibae* DFL 12) were obtained from blooms of dinoflagillates (e.g. *Prorocentrum lima*) this does not necessarily mean that the particular isolate that was cultivated on a Petri dish in Georgia or in Braunschweig was necessarily adapted to life in association with that species of marine plankton. It may be, therefore, that a particular strategy for the acquisition of iron and/or manganese is linked to a particular lifestyle, but our lack of knowledge of their precise niches precludes such a judgment. And, of course, the bioinformatic insights presented the predicted functions of any given set of genes also pose many unanswered questions. Most notably, just because a strain has a TBDR that resembles (say) FhuA, this only suggests but does not prove that its function is to recognise hydroxamate-type siderophores and it certainly does not reveal the exact chemical structure of such a molecule. Similarly with manganese, the each of the different Mnt systems may be more suited to particular lifestyles.

And, as if the complexity revealed already were not enough, the few genome-sequenced strains of Roseobacters are but a tiny fraction of those that are in the oceans and even more diversity is yet to be uncovered.

8.2 Iron - Experimentally based outcomes

8.2.1 Regulation of the fbpAB genes of R. pomeroyi

Unusually, the *fbpA* and *fbpB* genes were not co-transcribed and were not near *fbpC*. This is not unique, though, where the transcription of *fbpA* of *Vibrio cholerae* is different from *fbpBC* (Mey *et al.* 2005).

A potential candidate for a complete Fe-ABC transporter in *R. pomeroyi* may be *SPO1018-SPO1021* predicted to be an ABC-class transporter, with binding protein, two permease proteins, and an ATPase; which were all ~7-fold Fe-repressed (Chapter 7). These genes are annotated as a branched chain amino acid transporter, but lack any functional characterisation.

Crucially, given the phenotype of the FbpAB⁻ strain, there must be another high-affinity Fe-specific, inner-membrane transport system in *R. pomeroyi*.

8.2.2 The IR box cognate regulator

The work on the IR box-containing promoters of *irpA*, *fbpA* and *fbpB* in Chapter 4 showed that these motifs are responsible for (or at least contribute to) the Fe-responsive regulation of these genes. Point mutations in the most conserved bases in the IR boxes caused deregulation of *lacZ* fusions, under Fe-repressed conditions. It should be noted that there is significant homology between IR boxes and IRO boxes of *Rhizobium*, as shown in Rodionov *et al.* (2006), and that the predicted IscR box and IR box of *Ruegeria* is actually the same motif. Given this similarity, it was anticipated that an Rrf2 family transcriptional repressor might be responsible for the regulation of IR boxes in *R. pomeroyi*. This was not the case, as shown in Chapter 5.

Perhaps this was to be not wholly unexpected, since none of the Rrf2 family proteins of *R. pomeroyi* closely resembled the RirA sub-group of this family (Chapter 5), the closest homologue to RirA of *Rhizobium* being just 30% identical to *SPO0432* of *Ruegeria*. Despite this, four of the five Rrf2 genes in *R. pomeroyi* were shown to be significantly regulated by Fe, but not at all by Mn (Chapter 7). Furthermore, the expression of the fifth Rrf2 gene, *iscR*, was confirmed, by the use of *a lacZ* fusion, to be Fe-regulated, and affected by the *irr* genotype. Given the differences we observe between *E*.

coli, Bradyrhizobium and Rhizobium, in terms of Fur, Irr and RirA mediated regulation, it is possible that their distant marine cousins use a wholly new, or significantly adapted system of Fe-regulation.

By far the most important missing detail in this work is the identity of the regulator which binds to IR boxes in *R. pomeroyi*. To this end, the first future project would entail the construction of a Tn5 mutant library of *R. pomeroyi*, with complete genome coverage. This could be achieved using the E-Z-Tn5 kit from Illumina, for example. Having generated such a library, the potential regulator of both *fbpA*, and *irpA* could be found. These genes both showed large induction by Fe-limitation, enough that a fluorescent fusion could be shown to be differentially expressed on an agar plate with varied Fe levels. Here, a *gfp*, or other fluorescent reporter gene could be fused to the promoter of either *fbpA* or *irpA*, and crossed into the complete set of the *R. pomeroyi* mutant library. The library could then be plated onto Fe-replete medium, to obtain many single colonies. Those that were deregulated in expression of the fusion should fluoresce brightly. These colonies may well have a mutation in the IR box regulator. By simply mapping the location of Tn5 in these strains, the identity of the regulator should be apparent.

8.2.3 The marine Irr story

The global Fe-responsive regulator Irr has been shown to be a repressor of iron storage and iron utilisation genes in *Rhizobium leguminosarum*, and as a repressor and activator of such genes in *Bradyrhizobium japonicum*. Irr binds to motifs known as ICE boxes, and these are well conserved in several α -proteobacteria (Rodionov *et al.*, 2006). Several ICE box-like motifs were identified in the genome of *R. pomeroyi*, upstream of genes known to be Fe-regulated in other α -proteobacteria – *mbfA*, *iscR*, *fssA* and *ccpA*. However, when analysing the transcriptional response of these genes, we found that *fssA* (*SPO0382*) was Fe-repressed, but was unchanged in expression in the Irr mutant. However, the converse was true for *mbfA*, *iscR* and *ccpA*, all were repressed by Irr, and not shown to be significantly Fe-regulated.

It should be said here, that the microarray conditions used to study Irr were not complete – Irr represses genes in low Fe conditions, and yet the mutant transcriptome was produced from high Fe cultures, where it was compared to the wild type, also from high Fe cultures. It was hoped that many genes would be significantly deregulated by the lack of Irr peptide, even in this Fe-replete state.

Therefore, it is possible that we are yet to show the full extent of the Irr-regulon in *R. pomeroyi*, or the extent to which the genes mentioned above are regulated.

Nevertheless, it is likely that Irr does function as a regulator of Fe storage in *R. pomeroyi*, as demonstrated by the expression of *mbfA*. Whether this is in tandem with another RirA-type repressor or not, remains to be shown.

It is interesting to note that some genes were shown to be positively regulated by Irr, such as *SPO1957*, which was ~16-fold higher in the wild type than in the Irr mutant, and that again, as with *mbfA* and friends, this was not mediated by Fe. Clearly, more work needs to be done to verify these results, and to study the Irr regulator in detail.

Finally, it would be of interest to observe if Irr binds to haem, as has been shown for other Irr peptides, and indeed if a haem-Irr complex is stable or degraded.

8.2.4 Pigment production by Irr- R. pomeroyi

Another 'loose-end' in this study is the red pigment produced by the Irr mutant strain of *R. pomeroyi*. Although the Irr mutants of *Rhizobium* and *Bradyrhizobium* have a coloured phenotype, due to protoporphyrin IX (PPIX) over-production, the pigment in the Irr⁻ *R. pomeroyi* mutant did not fluoresce under UV light, which is a property of PPIX. Attempts to isolate the pigment were unsuccessful (see Chapter 5), but it was noted that it was extracellular, because it formed a particulate layer on top of the pellet when cells were centrifuged. Finally, the red pigment was dark, brick red, not the light pink of PPIX.

Taken together, these observations suggest that Irr of *R. pomeroyi* represses the production of a highly pigmented, extracellular particle, or at least a particle that can be separated from the cells when grown in culture. The identity of this pigmented substance could be identified by careful physical separation and then further characterisation. Also, the identity of the genes responsible for the production of the substance in the Irr⁻ strain could become evident once more is known about the pigment itself, and once further microarrays are performed – see below.

8.3 Manganese - Bioinformatically based outcomes

8.3.1 MntX

Possibly the most surprising, and potentially the most important outcome of the work on manganese was the identification of a novel Mn-specific transporter, MntX. This peptide was found to in three Roseobacter species, namely *Oceanicola granulosis* HTCC2516, *Rhodobacterales bacterium* HTCC2255 and *Roseovarius nubinhibens* ISM, but was far more widespread than that, being present in several gamma proteobacterial genera, many other α -proteobacteria, and potentially in the Firmicutes and Archaea too (see Chapter 6). The MntX polypeptide was also present at every sampling site present in the GOS data, at a frequency similar to that of the SitABCD transporter, but was not represented in any other metagenomic data base. It is therefore a very important player in manganese uptake in the oceans, but it is not clear why it should be confined to bacteria, even very distantly related ones, that are mainly (e.g. *Vibrio*) or exclusively (e.g. the SAR11 and SAR116 clades, *Alteromonas*, and the Roseobacters) marine in origin.

8.3.2 Manganese uptake and regulation in the Roseobacters

In *Ruegeria pomeroyi* the priamry means of Mn uptake is via SitABCD. The expression of the *sit* genes is repressed by Mn, via the Mur transcriptional regulator, which likely binds to two MRS-like motifs found upstream of *sitA*. However, not all Roseobacters have the *sit* genes, and indeed those that do, are in two subclasses of peptides, one being similar to the version in *R. pomeroyi*, and the other closer to the Sit polypeptides in *Rhizobium* SitABCD – furthermore, it was shown that a third type was present, but found only in *Loktanella*. Thus the *sitABCD* genes were likely acquired, on more than one occasion by the different Roseobacter species. Either the acquisition of SitABCD in the Roseobacters happened on two separate occasions, or that significant evolution away from the Rhizobial type peptides has occurred.

Furthermore, one Roseobacter, *Ruegeria* sp. Trich CH4B lacked SitABCD altogether, and had a copy of MntH, and *Citreicella* sp. 357 had both SitABCD and MntH. These species clearly have either acquired these genes separately, or all the other Roseobacters have lost MntH during their evolution.

A final point of interest in this Mn-uptake story is that the hugely abundant SAR11 bacteria still do not appear to have a known Mn-specific transporter. Only one member of this clade was found to have MntX, the others lacked SitABCD, MntH and MntX. This either means that the non-MntX SAR11 strains do not have a requirement for Mn, or that they use another novel Mn transporter.

These data could be obtained by testing the Mn-requirement of the SAR11 strains, and then performing a full bioinformatic search of the genome sequences for potential MRS, or MntR regulatory motifs. It is expected that genes involved in uptake of Mn by these strains would be regulated by one of these Mn-responsive regulators, since they are the only two we have observed in the α -proteobacteria. Any potential transporter genes could be cloned, or synthesised and tested in the SitA strain of *R. pomeroyi*, as demonstrated for MntX in chapter 6.

8.4 Manganese - Experimentally based outcomes

8.4.1 SitABCD

The function and regulation of the ABC-class transporter SitABCD in *R. pomeroyi* was similar to that which had been found in other alpha-proteobacteria, notably the Rhizobia. It is the main Mn transporter of *R. pomeroyi*, as a mutant strain was unable to grow well without the addition of exogenous MnCl₂. There may be other non-specific, and/or low affinity transporters that import Mn when present at higher levels in the medium. The expression of *sitA* was shown to be repressed by Mn, most likely by the binding of Mur to the MRS motifs found upstream of *sitA*. Further, confirmatory work could include the exact mapping of the transcript start site(s) by 5' RACE, or by 5' transcriptome sequencing. Also, direct foot-printing of Mur protein to the MRS sequences would confirm the direct interaction between these two regulatory components.

8.4.2 MntX is a functional Mn transporter

The three strains of Roseobacters that lacked SitABCD led me to investigate the function of MntX, which was thought to be a likely Mn transporter because (a) it only occurred in the three strains of Roseobacter that lacked any known Mn transporters; (b) the *mntX* gene is preceded by a MRS motif

in all three strains of Roseobacter, and (c) MntX is predicted to be a membrane-spanning protein. This work showed that MntX of *Roseovarius nubinhibens* is indeed a functional Mn transporter, that can correct the Mn-deficient growth phenotype of a *Ruegeria pomeroyi* SitA⁻ mutant. Furthermore, this MntX was also regulated by Mur of *Ruegeria*, when a transcriptional fusion to *mntX* from *Roseovarius* was expressed in both the wild type and Mur⁻ *Ruegeria* strains.

One strain of Roseobacter, *Ruegeria* sp. Trich CH4B has both SitABCD and MntH Mn transporters, and it would be very interesting to make mutants in each gene to observe the relative importance of each system in this strain. Perhaps this strain uses each transporter in quite different environmental conditions – such as in different oxygen concentrations for example. This may show that this strain is adapted to take up Mn in different environmental niches within the ocean, or, it may just happen to have two Mn specific transporters.

Moving away from the Roseobacters, the MntX transporter was found in several orders of the Proteobacteria. Specifically, these are the Vibrionales, Oceanospirillales and Altermonadales, all in the γ -proteobacteria; and in the SAR11, SAR116 and Roseobacter clades of the α -proteobacteria, and in two cases, namely *Vibrio cholera* El Tor and of *Candidatus* Pelagibacter sp. IMCC9063, the MntX was shown directly to be a functional Mn transporter. Strikingly, all these bacteria live in marine or brackish habitats, showing that MntX is clearly an important Mn transporter in this habitat.

Cholera is a major disease, with 3–5 million cases and 100,000–120,000 deaths worldwide each year, and every single sequenced strain of *V. cholerae* encodes *mntX* in their genome. This makes MntX a potentially important component of *Vibrio* pathogenesis.

MntX occurs in several bacterial clades that are abundant in the oceans – namely SAR11, SAR116 and the Roseobacters. Subsequently it was not surprising to see large numbers of homologues in the GOS marine metagenome database. Furthermore, MntX homologues in the GOS metagenome were found to be 82% as abundant as SitABCD, and 373% compared to MntH (Green et al, 2012, in press). Of great interest was the group of bacteria which did not cluster with peptides from any known genus, when MntX was used to construct a neighbour-joining tree (see Chapter 6). This group of bacteria was shown to have ~30% GC content of the region surrounding, and including MntX, which is similar to the GC content of SAR11 strains. However, these MntX homologues may well be in a novel group of abundant and low GC organisms. It would be of great interest to attempt to culture these strains, or at least prove their existence by probing seawater samples using the identified *mntX* genes from this group.

Finally, these observations on MntX distribution have provided another interesting observation. Several strains of bacteria, including *Pelagibacter ubique*, lack SitABCD, MntH and MntX, and must therefore either not require Mn for growth, or must possess another novel Mn transporter.

8.5 The transcriptome of R. pomeroyi – some conclusions

An interesting aspect of the effects of the environment (high and low Fe; high and low Mn) or genotype (wild type, Mur-, Irr-) on the *R. pomeroyi* transcriptome was that the expression of many genes was affected by more than one of these parameters, and in some cases, by as many as 4. Thus, the transcriptional responses of *R. pomeroyi* to both Fe and Mn limitation are linked to some degree.

Regulatory interplay between these two metals has been seen in other alpha-proteobacteria. For example, Mn deficiency in *Bradyrhizobium japonicum* caused cells to be Fe deficient (Puri *et al.* 2010). This was likely due to a lack of Mn binding to Irr, which normally inhibits Irr-haem binding. Therefore in the absence of Mn, more Irr protein was degraded, thus affecting the global Fe status of the cell (Puri *et al.* 2010).

There were several very interesting clusters of genes that were significantly regulated in the microarray data, the importance of these will be discussed in the following:

Firstly, a completely uncharacterised gene cluster, likely comprising two separate operons – *SPOA0339-SPOA0347* was highly induced by both Fe and Mn. These genes had very little functional predictions available in the NCBI databases, but their regulation does present an interesting prospect. The gene product of *SPOA0344* encodes a LysR-type transcriptional regulator, not known for their metal responsive regulation. Additionally, a conserved, 16 bp motif was found upstream of both *SPOA0343* and *SPOA0345*, which could be the cognate binding site for this LysR regulator. Pending further investigation, this regulator may be a novel, and highly Fe- and Mn-responsive transcriptional regulator.

The *cox* cluster genes of *R. pomeroyi* also showed significant Mn- and Fe-responsive regulation, and this was independent of Mur, but not Irr. This could be a good example of the regulation of Feresponsive genes by Irr, which can be also mediated by a Mn deficiency.

Also, and very interestingly, a cluster of genes which encode components of GTAs, capable of disseminating genetic material of *R. pomeroyi*, possibly as a means of propagating beneficial traits to other *Ruegeria* cells. The exact cause and function of GTAs are not fully understood, but the idea that extreme stress, such as metal deficiency, could induce their production, in an attempt to form a natural 'library' of the genome, is an attractive thought. If such a strategy gave a selective advantage to the species as a whole, then it could certainly have been selected for in the evolution of *R. pomeroyi*, and indeed other bacteria that harbour GTA-like genes.

8.5.1 Future microarray studies

The microarrays performed as part of this study were always intended to be 'a first pass' at the transcriptional response of *R. pomeroyi* to Mn and Fe limitation, and the role that Irr and Mur played in this. As such, an important extension of this study has to be further microarray experiments. It would be immediately important to perform some Type II arrays, where all results can be compared between experiments, allowing more analysis of the transcriptional regulatory networks to be performed. Here, both Fe- and Mn-limited cultures would be used on arrays with a labelled gDNA sample as the control.

In addition, I would perform arrays on the Irr mutant, in both high and low Fe and Mn, to fully characterise the Irr-ome already alluded to in this study. Similarly, once the regulator of IR boxes was identified, microarray analysis of a mutant strain in this regulator would be fascinating – and would be performed in the same conditions used to analyse the response of the Irr strain, again using type II arrays.

Having completed these new transcriptomics experiments, there should be further scope for future work on the nature of iron uptake and regulation in *R. pomeroyi*.

8.5.2 Other targets for study

The array data already collected have provided numerous targets for further study, all of which would make very interesting, small projects. These include:

- The mechanisms and the functions of the metal-dependent regulation of the cox genes.
- The production of GTAs in response to metal (and other) limitations
- The potential predicted LysR transcriptional regulator SPOA0344 and its interactions with Fe and/or Mn.
- Finally, a study of the effects on the *R. pomeroyi* transcriptome of a mutation in the predicted anti-anti sigma factor gene *SPO3409*.

Chapter 9 - Materials and Methods

9.0 Media and General Growth Conditions

9.0.1 Luria-Bertani (LB) medium
Luria-Bertani (LB) medium (Maniatis et al. 1982) was used to maintain E. coli and comprises, per litre ddH_2O :
10 g Tryptone
5 g Yeast extract
5 g NaCl
1.5 g D-glucose
Adjusted to pH 7.2 using 1M HCl or 1M NaOH.
E. coli strains were routinely grown at 37°C with 200 rpm agitation.
9.0.2 Half-YTSS (HY) Medium
<i>R. pomeroyi</i> strains were maintained on half strength YTSS medium (Gonzalez <i>et al.</i> 1997) which comprises, per litre ddH_2O :
2 g Yeast extract
1.25 g Tryptone
20 g Sea salts (Sigma)

9.0.3 Marine Basal Medium (MBM)

R. pomeroyi was grown in defined medium MBM (Baumann and Baumann 1981) to analyse growth and gene expression during iron limitation. It comprises per litre of ddH₂O:

75 ml 1M Tris HCl pH 7.5 43 mg K₂HPO₄ 0.75 g NH₄Cl 20 g Sea salts (Sigma) Supplemented 1:1000 with vitamins solution from (Gonzalez et al. 1997) which comprises, per 100 ml of ddH₂O: 2 mg Biotin 2 mg Folic acid 10 mg Pyridoxine-HCl 5 mg Riboflavin 5 mg Thiamine 5 mg Nicotinic acid 5 mg Pantothenic acid 5 mg Cyanocobalamin 5 mg of p-Aminobenzoic acid

9.0.4 Rob's Sea Salts (RSS) Medium

The pH was adjusted to 7.

R. pomeroyi was grown in RSS to analyse growth and gene expression during manganese limitation using succinate at 10mM as carbon source, and vitamin solution added. RSS comprises per litre of ddH₂O:

75 ml 1M Tris HCl pH 7.5

43 mg K₂HPO₄

 $0.75 \text{ g NH}_4\text{Cl}$

17 g NaCl

1.5 g MgCl₂

0.75 g CaCl₂

0.75 g KCl

9.0.5 Growth experiments

All *R. pomeroyi* experiments were performed at 28°C, with 180 rpm of agitation. For all growth experiments, a starter culture in complete HY media with selective antibiotic(s) was inoculated using a single colony of the desired strain. This was incubated for two days, or until in stationary phase. This culture was diluted 1 in 200 into minimal medium: MBM for Fe limitation and RSS for Mn limitation. As appropriate, FeCl₃ or MnCl₂ was added to the media, along with vitamin solution and succinate as detailed above. Growth was measured as optical density at 600nm wavelength in a spectrophotometer.

9.1 Strain storage

9.1.1 Glycerol storage

Strains of *E. coli* were grown overnight at 28°C in LB with antibiotics. An aliquot (1 ml) of overnight culture was mixed with the same volume of 50% glycerol solution and frozen at -80°C.

9.1.2 DMSO storage

Cultures of *R. pomeroyi* strains were grown to stationary phase, then stored in 15% glycerol plus 15% DMSO at -80°C.

9.2 in vivo genetic manipulations

9.2.1 Bacterial Conjugations

Plasmids were transferred by conjugation from *E. coli* strains JM101 or 803 to *R. pomeroyi* strains using patch crosses (Johnston *et al.* 1978) or filter crosses (Beringer and Hopwood 1976) in triparental matings with *E. coli* 803 containing helper plasmid pRK2013 to mobilise the transfer of plasmids between strains.

9.2.2 Conjugation via patch crosses

R. pomeroyi and *E. coli* strains were cultured on HY and LB agar medium, respectively, prior to patch crossing. A sterile loop was used to transfer approximately a 3:1:1 ratio of donor:helper:recipient bacteria where they were mixed in a patch on an HY agar medium plate and incubated for 48 hours at 28°C. These patches were then streaked onto selective HY agar plates containing the appropriate antibiotics, incubated at 28°C for ~4 days, allowing single colony transconjugants to form.

9.2.3 Conjugation via filter crosses

Filter crosses were used when selecting for low frequency events, such as insertional mutations with pEX18Ap. *R. pomeroyi* strains were grown in HY medium overnight at 28°C, and the *E. coli* donor and helper strains were grown overnight at 37°C in LB medium, all **without** antibiotics. A 3:1:1 ratio of donor:helper:recipient was used, with 1.5 ml of the donor, and 0.5 ml of the other cultures mixed

and pelleted via centrifugation. These were resuspended in $200\mu l$ of HY and spread onto a sterile nitrocellulose filter (Whatman) positioned on a HY plate without any selective antibiotics. This was incubated for 48 hours at 28° C, after which the cells were washed off the filters using MBM medium and diluted sufficiently to obtain single colonies when $200~\mu l$ of the diluted cells were spread onto selective HY agar medium. The selective plates were incubated for around 4 days.

9.3 Methods of Nucleic Acid Purification

9.3.1 Purification of plasmid DNA using QIAGEN Miniprep kit

For small-scale ($< 5 \mu g$), high purity isolation of plasmids from *E. coli*, to use for restriction digest analyses, transformation, sequencing, and as PCR templates, Plasmid Miniprep kits (Qiagen) were used, which employ a protocol optimised from Birnboim and Doly (1979). Cells are lysed using an alkaline buffer and a silica gel column facilitates the purification of plasmid DNA. This was done (see below) according to manufacturer's specifications, using all the reagents supplied with the kit. All centrifugation steps, were performed at 16,000 x g in a 5415 D Microcentrifuge (Eppendorf).

- 1. A single colony of *E. coli* containing the required plasmid was inoculated into 5 ml LB liquid, containing the appropriate antibiotics, and incubated at 37 °C overnight.
- 2. Cells were pelleted (1.5 ml culture for high copy number plasmids; 3 ml for low copy number plasmids) by centrifugation in 1.5 ml microfuge tubes; the supernatant was removed.
- 3. Pelleted cells were resuspended in 250 μ l P1 resuspension buffer, containing 100 μ g ml⁻¹ RNase A to remove RNA, and incubated at room temperature for 5 minutes.
- 4. $250 \mu l$ P2 lysis buffer was added and mixed well by inversion. Samples were then incubated at room temperature for no more than 5 minutes.
- 5. 350 μ l P3 (stored at 4 °C) neutralisation buffer was added and mixed well by inversion. Samples were then incubated on ice for 5 minutes to precipitate protein, genomic DNA and cell debris.
- 6. Each tube was centrifuged for 15 minutes to clear precipitate.

- 7. The resultant supernatant was applied to a Qiaprep spin column and centrifuged for 1 minute. The pelleted precipitate was discarded.
- 8. The eluate was discarded and 500 μ l PB binding buffer was applied to the column and centrifuged for 1 minute. This step removes excess nuclease activity and high carbohydrate content from *endA* mutant strains such as JM101.
- 9. The eluate was discarded and 750 μ l PE wash buffer was applied to the column and centrifuged for 1 minute.
- 10. The eluate was discarded and the column and collection tube was centrifuged again for 1 minute to remove residual wash buffer from the column matrix.
- 11. Spin columns were transferred to clean, labelled 1.5 ml microfuge tubes and DNA was eluted by pipetting 50 μ l dH₂O onto the matrix and allowed to stand for 1 minute. This was then centrifuged for 1 minute; the spin column was discarded and the eluted DNA stored at -20 °C.

9.3.2 Mini-preparation of plasmid DNA by alkaline lysis and phenol-chloroform purification

To isolate and purify DNA of plasmids > 10 kb in size the following method was used, as the QIAGEN Miniprep spin column did not yield sufficient DNA. Buffers used here were from this kit however, as they still provided means of cell lysis. All centrifugation steps were performed at $16,000 \times g$ in a 5415 D Microcentrifuge (Eppendorf).

- 1. A single colony of *E. coli* containing the required plasmid was inoculated into 5 ml LB liquid, containing the appropriate antibiotics, and incubated at 37 °C overnight.
- 2. Cells were pelleted (total of 3 ml) by centrifugation in 1.5 ml microfuge tubes; the supernatant was completely removed.
- 3. Pelleted cells were resuspended in 250 μ l P1 resuspension buffer, containing 100 μ g ml⁻¹ RNase A to remove RNA, and incubated at room temperature for 5 minutes.
- 4. $250 \mu l$ P2 lysis buffer was added and mixed well by inversion. Samples were then incubated at room temperature for no more than 5 minutes.

- 5. 350 μ l P3 (stored at 4 °C) neutralisation buffer was added and mixed well by inversion. Samples were then incubated on ice for 5 minutes to precipitate protein, genomic DNA and cell debris.
- 6. Each tube was centrifuged for 15 minutes to clear precipitate.
- 7. The resultant supernatant was transferred to a clean 1.5 ml microfuge tube to which 400 μ l of phenol-chloroform (phenol:chloroform:isoamyl alcohol 25:24:1, Sigma) were added and mixed by vortexing for 10 seconds. Samples were then centrifuged for 2 minutes.
- 8. The upper aqueous layer was transferred to a clean 1.5 ml microfuge tube containing 700 μ l room temperature 100% ethanol to precipitate plasmid DNA. Samples were then centrifuged for 15 minutes.
- 9. The supernatant was then discarded and the resultant DNA pellet was washed in 500 μ l 70% (v/v) ethanol and centrifuged for 2 minutes.
- 10. The supernatant was then completely removed using a micropipette, and the DNA pellet was airdried for 10 minutes.
- 11. The pelleted DNA was resuspended in 30 μl dH₂O and stored at -20 °C.

9.3.3 Purification of plasmid DNA using QIAGEN Midi kit

The QIAGEN plasmid Midi Kit was used to purify high quality plasmid DNA in large quantities (~100 μg). This DNA was of sufficient quality for sequencing, cloning and site-directed mutagenesis.

The QIAGEN kit used alkaline lysis, optimised from Birnboim and Doly (1979), followed by column-based purification of plasmid DNA, and precipitation of the DNA using isoproponol. The procedure was performed according to manufacturer's specifications, using all the reagents supplied with the kit:

1. A single colony of *E. coli* containing the required plasmid was inoculated into 100 ml LB media, containing the appropriate antibiotic(s), and incubated at 37 °C, with 200 rpm of shaking for 16 hours.

- 2. The culture was used to fill a 50 ml centrifuge tube (Corning), and centrifuged to produce a pellet (9000 x g for 10 minutes in an Eppendorf Centrifuge, model 5804R).
- 3. This pellet was resuspended in 4 ml of P1 buffer (stored at 4 $^{\circ}$ C), containing 100 μ g ml-1 RNase A to remove RNA.
- 4. Then, 4 ml of P2 lysis buffer was added and inverted until a blue colour appeared (indicating alkaline pH); this was incubated at room temperature for 5 minutes.
- 5. To precipitate all cellular debris, 4 ml of neutralisation buffer N3 was added, mixed well by inversion and incubated on ice for 15 minutes.
- 6. Precipitates were pelleted by centrifugation for 15 minutes.
- 7. A column (supplied with the kit) was equilibrated by adding 4 ml QBT equilibration buffer, which was discarded after passing through the column by gravity.
- 8. The supernatant from Step 6 was applied to the column, allowing it to enter the column matrix by gravity flow. The eluate was discarded.
- 9. The DNA bound to the column matrix was washed by two separate additions of 10 ml of QC buffer to the column; again, the eluate was discarded.
- 10. Plasmid DNA was eluted from the matrix by adding 5 ml QF elution buffer, and the eluate was collected in a sterile 50 ml Falcon tube (Corning).
- 11. Eluted plasmid DNA was precipitated by adding 3.5 ml of 100% isopropanol, mixed by inversion and centrifuged at 9000 x g for 30 minutes to pellet precipitated plasmid DNA.
- 12. The DNA pellet was washed by adding 1 ml 70% ethanol and centrifuged as before for 2 minutes. The resultant supernatant was removed completely using a micropipette, and the DNA pellet was air-dried for 10 minutes.
- 13. The dried pellet was rehydrated in 80 μ l of Ultra-pure water (Sigma).

9.3.4 Purification of genomic DNA

A Wizard genomic DNA purification kit (Promega) was used to purify genomic DNA from *Ruegeria pomeroyi* strains and from *Roseovarius nubinhibens* ISM. This genomic DNA (gDNA) was used for PCR amplifications and Southern blot analyses.

- 1. A single colony of either *Ruegeria* or *Roseovarius* was inoculated into 5 ml HY media and grown for 2 days at 28°C.
- 2. Using a benchtop Eppendorf centrifuge, 1.5 ml of each culture was pelleted at 13,000 x g.
- 3. The supernatant was removed, and 600 μ l Nuclei lysis solution was added and used to resuspend the pellet. Cells were lysed by incubating at 80 °C for 5 minutes before cooling to room temperature.
- 4. To remove RNA from the samples, 3 μ l of RNase solution were added and mixed into the lysate; this was incubated at 37 °C for 1 hour.
- 5. To this, 200 μ l of Protein precipitation solution was added and mixed well; this mixture was incubated on ice for 5 minutes to precipitate all cellular debris.
- 6. The precipitate was removed by centrifugation for 3 minutes.
- 7. The DNA was precipitated from the supernatant using $600 \mu l$ of isoproponol. This was collected by centrifugation for 2 minutes; the supernatant was discarded.
- 8. The pelleted DNA was washed with 600 μ l room temperature 70% ethanol (v/v) and mixed by inversion. DNA was again pelleted by centrifugation for 2 minutes and the supernatant was removed carefully.
- 9. The DNA pellet was air-dried for 10 minutes.
- 10. Dried DNA pellets were then resuspended in 100 μ l Ultra-pure water (Sigma) and incubated for 1 hour at 65 °C. Genomic DNA preparations were always stored at -20 °C.

9.3.5 RNA purification for microarrays

The extraction of RNA from bacteria requires careful measures to ensure there is no degradation. A clean space was used, where all equipment was treated with RNaseZAP® (Ambion) and all plastics were autoclaved prior to use to ensure no contamination with RNase enzymes. TipOne® RNase-free filter tips (*StarLab*) were used when pipetting.

Firstly, a single colony of *Ruegeria pomeroyi* Rif^R strain J470 was used to inoculate HY broth with 20 µg/ml rifampicin; this was grown for 48 hours at 28°C with shaking.

For the experiments in which the effects of Fe were measured, this starter culture was diluted 1 in 200 into 100ml of MBM minimal medium, pre-warmed to 28° C and with vitamin solution added (1 in 1000 dilution) and succinate at 10 mM. In total 2 biological replicates were performed, with either $20 \, \mu$ M FeCl₃ or no iron added to each flask.

For Mn limitation experiments the cultures were diluted 1 in 200 into RSS media, pre-warmed to 28° C with 20 μ M FeCl₃, vitamins and succinate as in MBM. Here, 2 replicates were performed with $20 \,\mu$ M MnCl₂ or no manganese added to each flask.

For the "Irr $^-$ vs. wild type" microarray comparison experiment, both cultures were grown in 20 μ M FeCl $_3$ in MBM as detailed above.

For the "Mur vs. wild type" experiment, two replicates were performed, where both cultures were grown in RSS with 20 μ M MnCl₂ and 20 μ M FeCl₃ as detailed above.

To grow the cells and stabilise the RNA the following steps were performed:

- 1. All cultures were incubated in 250 ml conical flasks for exactly 16 hours at 28°C, with 180 rpm shaking.
- 2. Following growth, the cells were killed and their RNA was stabilised using a 1 in 5 addition of 10 % Phenol:Ethanol solution (Sigma), before being put on ice for 1 hour.

- 3. The cells were harvested by centrifugation (3200 \times g at 4 °C for 10 minutes in an Eppendorf Centrifuge, model 5804R); then, the supernatant was removed, and the cell pellet was resuspended in the residual liquid.
- 4. This was centrifuged again at 13000 x g for 30 seconds, and all residual supernatant was removed.
- 5. Each sample was frozen in dry ice pellets and stored overnight at -80°C.

To extract and purify the RNA, three cell lysis steps were used, since *R. pomeroyi* cells grown in minimal medium gave poor RNA yield when any of these three steps was omitted.

- 1. Treatment with lysozyme: 100 μ l RNase-free TE buffer (10 mM Tris, 1 mM EDTA, pH 8.0) containing 100 mg ml⁻¹ chicken egg white lysozyme (Sigma) was added to each sample, which was then incubated at 37°C for 30 minutes.
- 2. Five successive freeze-thaw cycles using dry ice were performed on each sample.
- 3. Mechanical shearing: 1 g of 0.1 μ M acid-washed glass beads (Sigma) were added to each sample, and were agitated in an MP Biomedicals FastPrep24 machine, on setting 6, for 40 seconds. Samples were all immediately cooled on ice. The resultant supernatant was removed following centrifugation (2 minutes at 13,200 x g).

Total RNA was purified from the resultant lysates using the Promega SV total RNA kit as per the manufacturer's protocol, as follows.

- 1. 75 µl Lysis Reagent were added and mixed by inversion.
- 2. 350 μ l RNA dilution buffer were then added and mixed by inversion, and samples were incubated for 3 minutes at 70 °C, before being centrifuged for 10 minutes at 13000 x g at 4 °C.
- 3. 200 μ l 100% ethanol were added and mixed by pipette.
- 4. A spin column was used to bind and clean the RNA, here, each sample was added to a column and centrifuged for 30 s at 13000 x g at $4 ^{\circ}\text{C}$, the flow through was discarded.

- 5. The RNA, bound to the column matrix, was washed using 600 μ l Wash buffer) and centrifuged for 30 s at 13000 x g at 4 °C, the flow through was discarded.
- 6. A DNase mix (see below) was prepared, and 50 μ l was added to the RNA in the each column. These were incubated at 37 °C for 40 minutes to remove any DNA contamination.

DNase mix comprised (all supplied with kit):

- a. $5 \mu l 90 \text{ mM MnCl}_2$
- b. 40 µl DNase core buffer
- c. 5 µl DNase solution
- 7. To inactivate the DNase, 200 μ l of DNase stop mix was added to each column and then removed by centrifugation for 30 s at 13000 x g at 4 °C. The flow through was discarded.
- 8. The RNA sample bound to the matrix in each spin column was washed twice by adding 600 μ l Wash Buffer and centrifuging for 30 s at 13000 x g at 4 °C. After each wash, the flow through was discarded.
- 9. The RNA was eluted into a clean microfuge tube by applying 80 μ l of Ultra-pure water (Sigma), incubating for 2 minutes at room temperature before being centrifuged for 2 minutes at 4500 x g.
- 10. To ensure there was no DNA in any sample, TURBO DNA-free (Ambion) was used, according to the protocol supplied, as follows:
- a. To each RNA sample, 0.1 volumes of 10 x Turbo buffer, and 1 μ l of Turbo DNase enzyme was added and incubated at 37 °C for 30 minutes.
- b. Following incubation, 0.1 volumes of DNase inactivation reagent were added, mixed well and incubated for 5 minutes at room temperature.
- c. This mixture was then centrifuged for 90 s at 13000 x g at 4°C to pellet any precipitate, and the supernatant was harvested into a clean microfuge tube.

The RNA was assayed for purity and lack of degradation using a Bioanalyser chip (Agilent 2100).

Here, the appearance of 16S and 23S ribosome bands were required to be bright and sharp, with no

smearing, as this would indicate RNA degradation.

The concentration of the RNA was determined using a Nanodrop Spectrophotometer NS-1000

(Thermo Scientific) and it was ensured that both the 260/280 and 260/230nm ratios were >2. All

RNA samples were stored at -80°C until required.

9.4 Microarrays

9.4.1 Performing microarray experiments

An 8 × 15K microarray slide (Agilent) specific for the genome of R. pomeroyi DSS-3 was used to

visualise relative mRNA levels between samples. An Affinity Script kit (GE Healthcare) was used to

produce cDNA, from each RNA sample, which was then labelled with single-stranded DNA containing

the Cy3 or Cy5 florescence marker as follows:

10 μg of RNA dried using a rotary vacuum, then resuspended in 7.7 μl of RNase free water.

Random priming reactions set up with:

7.7 μl of RNA sample (10 μg)

5 μg (1.7 μl) of random hexamers (Invitrogen)

These were incubated at 70°C for 5 mins then placed on ice for 10 mins before being briefly

centrifuged to collect any evaporated liquid.

To each tube, the following were added:

- a. 2 µl of 10 x RT buffer
- b. $2 \mu l$ of 0.1 M DTT
- c. 0.6 μ l of 50 x dNTPs (25 mM of dATP, dGTP, dTTP and 10 mM of dCTP, which was 25 μ l of dA, dG, dT and 10 μ l of dCTP from Amersham Pharmacia 100 mM stock dNTP kit.
- d. 2 μ l of Cy3 or Cy5-dCTP (1 mM stock from Amersham Pharmacia) and 4 μ l of reverse transcriptase (AffinityScript, Stratagene), total volume is 20 μ l.

These were pipette mixed, and incubated at 25°C for 10 mins, before being incubated overnight at 42°C.

In the morning, the RNA was degraded to leave only the labelled cDNA as follows:

- a. 15 μl of freshly made 0.1 M NaOH, to hydrolyse RNA. This was incubated at 70°C for 10 mins
- b. To this, 15 μ l of 0.1 M HCl was added to neutralise the NaOH.

Clean up (Invitrogen PureLink PCR Purification Kit):

- 1. 50 μ l of labelled RNA/gDNA reactions were added to 200 μ l of PureLink binding buffer B2 and mixed well by inversion.
- 2. Sample was added to a spin column and centrifuged at $10,000 \times g$ in a microcentrifuge for 1 minute.
- 3. The flow through was discarded, and column washed with 650 μ l of Wash Buffer, then spun as before.
- 4. The flow through discarded again, and the empty spin column was spun at full speed for 3 mins to remove all traces of wash buffer.

4. DNA was eluted using 50 uL DEPC-treated water and spun after incubating for 1 min at room temperature, elution was performed by centrifugation into a clean eppendorf for 2 minutes at maximum speed.

The labelled cDNA was mixed as per the design of experiments and hybridised to the microarray slide using the Agilent Hi-RPM Gene Expression Hybridization Kit according to the manufacturer's instructions, as follows:

- 1. Both conditions for each array were dried in a rotary vacuum, then resuspended in 10 μ l of DEPC-treated water, before being mixed.
- 2. To this 20 μ l sample, 25 μ l of hybridisation buffer (Agilent) and 5 μ l of blocking reagent (Agilent) were added, and boiled for 3 minutes before being cooled to room temperature.
- 3. 40 μ l of each sample was applied to a well on an Agilent hybridisation chamber, held in a clamp (Agilent). The array was carefully applied on top of the chamber, and clamped down firmly. This was incubated in a hybridisation oven at 65°C overnight.

Washing the hybridised arrays:

- 1. The hybridisation chamber and microarray, held in the clamp was disassembled in wash buffer 1 (Agilent) away from bright light.
- 2. The array was loaded into a foil covered 50 ml falcon tube filled with wash buffer 1 and rotated gently for 1 minute at room temperature.
- 3. The array slide was transferred to another falcon tube containing wash buffer 2, prewarmed to 37°C and rotated again for 2 minutes.
- 4. Finally, the array slide was dried by placing in acetonitrile and removing, then into stabilisation buffer, air dried and then stored in the dark before scanning.

Scanning:

The array slide was scanned using a GenePix 4000B scanner, and data acquired using GenePix 6.0 software.

9.4.2 Microarray analysis

DNA microarrays were scanned using an Axon GenePix 4000A microarray laser scanner (Axon Instruments) and the data from detected features were initially processed using the GenePix 3.0 software. Statistical analysis of the data was performed with Marray as described in Holmes *et al.* (2005).

All data were deposited in a large file (Appendix 3) where for each gene, the relative expression change was shown as a ratio for the pair of conditions under comparison, and the P-value for each gene is shown.

9.5 Manipulation and in vitro analysis of nucleic acids – DNA amplification and plasmid construction

9.5.1 Design of oligonucleotides used for PCR and SDM

DNA oligonucleotide primers were ordered from MWG Biotech, and designed using Primer3Plus (Untergasser *et al.* 2007) and ARTEMIS (Rutherford *et al.* 2000). Where appropriate, they had a GC content <60%, a melting temperature (Tm) of ~60 °C and a length of 18-22 base pairs. For those that incorporated a restriction site, this was placed to the 5' end of the primer, with a further 4 bases added upstream to ensure that the enzyme could clamp the DNA. Sequences and use of primers are listed in Table 10.1.

9.5.2 Polymerase chain reaction (PCR) amplification of DNA

A TC-512 Thermal cycler machine (Techne) was used to perform PCR to amplify fragments from genomic or plasmid DNA. Typically, Taq master mix (Roche) was used according to specifications of the manufacturer. Unless otherwise stated, standard PCR reactions were set up as follows:

1 μ l genomic DNA template (~ 50 ng / μ l)

22 μl dH₂O

1 μl Forward primer (20 pmol μl⁻¹)

1 μl Reverse primer (20 pmol μl⁻¹)

25 μl Taq Master Mix

Thermal cycling was always performed as follows: (30 cycles)

- 1. Denaturation was performed at 95°C for 2 minutes
- 2. Primer annealing was at 2°C below the melting temperature of the primer pair used.
- 3. Extension was at 72°C for 30 seconds per kb of DNA to be amplified, so for a 2 kb amplicon, a one minute extension time was used.
- 4. Finally, a 5 minute extension was performed, and this was quickly cooled to 10°C.

9.5.3 Colony PCR

A single colony was picked to a small PCR tube using a toothpick, with just enough cell material to see a trace on the side of the tube. These cells were mixed with 10 μ l of Ultra-pure water (Sigma), and vortexed to mix. The tube was heated to 99°C for 10 minutes in a TC-512 Thermal cycler machine (Techne) to lyse the cells. To use the released plasmid DNA as a template in a PCR reaction, the cell debris was pelleted by centrifugation at 13,000 x g for 2 minutes, and 1 μ l of the supernatant

was carefully transferred from the top of the 10 μ l sample to a fresh PCR tube. A normal PCR

reaction (see above) was then performed, using the 1 μ l of the colony preparation as the template.

9.5.4 Southern blot

Before the lab-based work, a virtual digest of the relevant DNA was performed using NEBcutter

(http://tools.neb.com/NEBcutter2/index.php). Here, the sites of restriction endonuclease cleavage

were visualised, to select an enzyme which would cut the genome either side of the target gene,

generating a genomic fragment that would be easily visualised on a gel (ideally, 3 - 10 kb).

The genomic DNA to be tested was purified using the Promega Wizard genomic DNA kit (see above)

and the resultant fragments were electrophoretically separated on a 1% agarose gel.

The agarose gel was treated using the following solutions, to allow DNA transfer onto a

nitrocellulose membrane:

Denaturation Solution (500ml)

0.5M NaOH (10g)

1.5M NaCl (43.75g)

Neutralising Solution (500ml)

1M Tris-HCl pH 8 (60.55g)

1.5M NaCl (45.75g)

Depurination Solution (500ml)

0.2M HCI (4.55ml)

240

20x SSC (in 2L)

346.6g NaCl

176.4g Tri Sodium Citrate pH 7

Method

- 1. A photo of the finished gel was produced with a ruler alongside to allow measurement of the migration of each band relative to the size marker (1kb Plus, Roche). The gel was carefully placed in a plastic box for subsequent treatment:
- 2. The gel was depurinated by soaking for 20 mins in Depurination Solution before being washed with dH_2O .
- 3. Next, the gel was immersed in Denaturation Solution for 20 minutes before being washed with dH₂O.
- 4. Finally, the gel was neutralised by immersion in Neutralising Solution for 20 mins, before a final wash with dH_2O .

The DNA could then be transferred from the gel to a nylon membrane (Hybond-N+, Amersham) by upward capillary action as in Sambrook *et al.* (1989). Once transferred, the DNA was fixed to the membrane by cross-linking using UV light (254nm wavelength for 20 seconds, using a UV Stratalinker 2400, Stratagene).

To label and hybridise a probe to the DNA on the nylon membrane, the following steps were performed, using reagents and protocols from the (Roche) DIG High Prime DNA Labelling and Detection kit:

1. To make the probe, 4 μ l of reagent 1 was added to 20 μ l of purified PCR product, and incubated at 37°C overnight.

(This procedure attaches a steroid isolated from digitalis plants, dixoxigenin (DIG), to the DNA probe.

A PCR product was used that would bind within the digested genomic DNA fragment containing the

suspected mutation).

2. The nylon filter was incubated in 20ml DIG-easy hybridisation solution (Roche) at 42°C, for 30

minutes (prehybridisation).

3. 5 µl of the DIG-labelled probe was heat denatured at 95°C for 10 minutes and added to 5ml of

DIG-easy hybridisation solution.

4. The nylon filter was removed from the prehybridisation solution and the probe-containing

hybridisation solution was added at a volume of 2.5 ml per 100cm² of membrane. This was

incubated overnight at 42°C, with gentle agitation.

5. The filter was washed to remove all remaining unbound probe, and the hybridisation solution:

a. 2 x 5 minutes with 50 ml of solution 1 (2x SSC, 0.1% SDS) at room temperature.

Then,

b. 2 x 15 minutes with solution 2 (0.1x SSC, 0.1% SDS) at 68°C.

The targeted genomic fragments were now bound by many copies of probe, which had DIG steroid

attached. To visualise the probe signals an anti-DIG antibody was bound to the membrane. This

required the following reagents:

Maleic Acid Buffer

0.1 M Maleic acid

0.15 M NaCl;

Adjusted to pH 7.5 with NaOH.

50 ml Blocking reagent (Roche) 450 ml Maleic Acid Buffer. **Detection Buffer** 0.1 M Tris-HCl 0.1 M NaCl 50 mM MgCl₂ Adjusted to pH 9.5. Method: 1. The membrane was immersed in Maleic Acid Buffer for 5 minutes, before being removed. 2. The membrane was incubated for 30 min in 100 ml of Blocking Solution at room temperature. 3. The Anti-DIG-AP-conjugate (Alkaline Phosphatase conjugated to the anti-DIG antibody) was diluted 1 in 10,000 in 5 ml of Blocking Solution and added to the membrane, this was incubated for 30 minutes at room temperature. 4. The membrane was washed for 15 minutes in 100 ml of Maleic Acid Buffer, then removed, and repeated with fresh buffer. 5. Following washing, the membrane was equilibrated for 5 minutes by incubation in Detection Buffer at room temperature.

Blocking Solution (500 ml)

6. Finally, 5 ml of a solution of 5-Bromo-4-chloro-3-indolyl phosphate, toluidine salt [BCIP] and Nitro

blue tetrazolium chloride [NBT] (Roche) was added to the membrane. Briefly, BCIP is dephosphorylated by the alkaline phosphatase enzyme, and then oxidised by NBT.

Dephosphorylated and oxidised BCIP is dark blue in colour, as is reduced NBT, providing an intense coloured band at the site of the probe.

9.5.5 Purification of PCR-amplified DNA

Following PCR amplification, DNA was purified using a High-Pure PCR purification kit (*Roche*) according to the supplied protocol as follows. All centrifugation steps were performed at 16,000 x g in a 5415 D Microcentrifuge (Eppendorf).

- 1. For each 50 μl PCR reaction, 500 μl Binding buffer was added and mixed using a pipette.
- 2. This was applied to a High Pure filter column and centrifuged for 1 minute; the eluate was discarded.
- 3. To the column, 500 μ l of Wash buffer was added, centrifuged for 1 minute and the eluate was discarded.
- 4. Here, 200 μ l of Wash buffer was added, and again centrifuged for 1 minute, discarding the eluate.
- 5. To collect the purified PCR product, the column was transferred to a 1.5 ml microfuge tube and 30 μ l of Ultra-pure water (Sigma) was added, allowed to stand for 2 minutes and then centrifuged for 1 minute. The resultant PCR products were routinely stored at -20°C.

9.5.6 Restriction enzyme digestion

DNA digestions were carried out using restriction enzymes supplied by *Roche* with their supplied buffers. Here, around 300 ng of plasmid DNA was cut in a 20 μ l reaction as follows:

2 μl of appropriate buffer solution

17 μl of Ultra-pure water containing 300 ng of plasmid DNA

1 μl (10 units) of the appropriate enzyme(s)

These reactions were always incubated at 37°C for 4 hours to ensure all DNA was cut. To inactivate the enzymes, samples were heated to 65°C for 10 minutes.

9.5.7 Dephosphorylation of plasmid DNA

To prevent religation of plasmid DNA when only cut with one enzyme, rAPID Alkaline Phosphatase (Roche) was used to dephosphorylate the 5' ends. To a typical 20 μ l digest reaction, 10 units of rAPID Alkaline Phosphatase was added, without any extra buffer or water. Reactions were incubated for 30 minutes at 37 °C, and were stopped by heating at 75 °C for 2 minutes.

9.5.8 Ligation of DNA fragments

Concentrations of vector and insert DNA were determined using a nanodrop spectrophotometer (Agilent), before being mixed in a 1:3 molar ratio of vector:insert, calculated using a ligation calculator (http://www.insilico.uni-duesseldorf.de/Lig_Input.html). The insert DNA was ligated to the vector using Roche T4 DNA ligase overnight at 11°C in a 10 μ l reaction, containing 0.5 μ l of enzyme, 1 μ l of 10 x ligase buffer (Roche), and the correct molar ratio of DNA in 8.5 μ l of Ultra-pure water (Sigma).

9.5.9 DNA gel electrophoresis

All separations of DNA performed used 1 % agarose dissolved in TBE buffer (45 mM Tris-borate, 1 mM EDTA, pH 8.0) containing ethidium bromide (500 ng /ml) to stain the DNA. Samples (5 μ ll) were mixed with loading buffer containing 0.25% bromophenol blue and 30% glycerol (v/v). Gels were run in SCIE-PLAS mini or midi horizontal gel tanks, with 1x TBE as running buffer, at 70-100 mV until desired separation had occurred. To measure the sizes of DNA fragments, a lane loaded with 1 kb+ DNA ladder (Invitrogen) was added to each gel prior to running.

9.5.10 Extraction of DNA from agarose gels

To extract digested DNA from agarose gels, a QIAquick Gel Extraction kit (Qiagen) was used, as per the supplied protocol.

- 1. A sterile scalpel was used to cut around and remove the desired DNA fragment.
- 2. To this, 300 μ l of QG buffer was added in a 1.5 ml microfuge tube. This was incubated for 10 minutes at 50 °C to melt the agarose.
- 3. This sample was decanted into a QIAquick spin column and centrifuged for 1 minute. The eluate was discarded.
- 4. The column was washed by adding 750 μ l PE buffer before centrifuging for 1 minute. The eluate was discarded.
- 5. The column was transferred to a clean 1.5 ml microfuge tube, and the DNA was eluted by adding 30 µl of Ultra-pure water (Sigma).

9.5.11 Site-directed mutagenesis (SDM)

Site directed mutagenesis was performed using an Agilent Quikchange Lightening kit. Mutagenesis of plasmids was achieved by using two primers, which are the reverse compliment of each other, which span the region targeted for mutagenesis. The nucleotides to be mutated are altered within the primer sequences, which are then used in a PCR reaction, with a long elongation cycle time to allow replication of the entire plasmid. New copies of the plasmid will contain the mutated bases, due to the incorporation of the primers into the PCR products. The newly synthesised DNA from a PCR reaction is not methylated, so the restriction endonuclease *DpnI* is used to cut the methylated template plasmids into small pieces (*DpnI* cuts at 5'-GATC-3' sites). The linear PCR products that contain the mutations are used to transform a strain of *E. coli* (XL10-GOLD) which can repair the nicked-DNA plasmids to generate functionally replicating mutated versions of the original template plasmid.

Reactions were set up as follows, using reagents supplied with the Agilent kit:

2.5 μl Reaction Buffer
62.5 ng of each oligonucleotide primer
25 ng of template plasmid DNA
0.5 μl of dNTP mix
0.75 μl of Quik Solution
0.5 μl Quikchange Enzyme
20.25 μl of Ultra Pure H ₂ O
The thermal cycles used to generate the site-directed mutants in this work were as follows:
2 minutes at 95°C, 1 cycle.
18 cycles of:
20 seconds at 95°C
10 seconds at 60°C
5 minutes at 68°C
Followed by:
5 minutes at 68°C
1. To each reaction, 2 μl of <i>Dpn</i> I was added, and incubated for 2 hours at 37°C.
2. 1 μ l of <i>DpnI</i> treated sample was used to transform <i>E. coli</i> XL10-Gold (Agilent) according to the manufacturer's specification.
3. Transformed XL10-Gold cells were selected by plating on LB containing the appropriate antibiotics.

9.6 Generation of genomic insertion mutants of R. pomeroyi

9.6.1 pK19 derivatives

Several of the insertional mutations that were made in this study were based on a suicide plasmid, pBIO1879 (Todd *et al.* 2011), which is a derivative of pK19*mob* (Schafer *et al.* 1994) into which a spectinomycin resistance (Spc^R) cassette was cloned into the polycloning site, and so confers resistance to both spectinomycin in addition to kanamycin, present on pK19*mob*.

Firstly, a fragment internal to the targeted gene was ligated into pBIO1879. The newly formed recombinant plasmid was then introduced into *Ruegeria* by tri-parental conjugation (see above). Since pK19*mob* and its derivatives cannot replicate outside the enteric bacteria, selection for Spc^R/Kan^R transconjugants can yield recombinants between the cloned internal fragment and the target gene, generating a targeted, insertional mutation. See Figure 4.15 in Chapter 4 for an illustration of this procedure.

9.6.2 pEX18Ap derivatives

pEX18Ap (Hoang *et al.* 1998) is a wide host range plasmid that encodes ampicillin resistance (via its *bla* gene) and can be mobilised from *E. coli* to many different proteobacteria, but it fails to replicate in such hosts. It also contains a polylinker cloning region and a *sacB* gene, which encodes a levan-sucrase that cleaves sucrose into glucose plus fructose, the latter being polymerised to levan, a toxin for most bacteria (Merlin *et al.* 2002). pEX18Ap is therefore a selectable, suicide vector that can be used to generate genomic mutants. This can be achieved by cloning a selectable marker between two regions of DNA that flank the gene that is targeted for mutagenesis, crossing this construct into the target strain, and then selecting for the cloned marker, usually spectinomycin resistance (200 μ g /ml), making sure that the resultant transconjugants are sucrose resistant and have therefore lost the pEX18Ap derivative.

9.7 Transformation of E. coli with plasmid DNA

9.7.1 Preparation of competent cells

Recipient E. coli cells for transformations were made competent using ice-cold CaCl₂ (Sambrook *et al.* 1989), as follows:

- 1. A single colony of the required *E. coli* strain was used to inoculate 5 ml LB media. This was incubated overnight at 37°C with 200 rpm of shaking.
- 2. This culture was then diluted 1 in 100 into 100 ml of LB media and incubated for \sim 1.5 hours until the OD_{600nm} value reached \sim 0.4.
- 3. The cultures were cooled on ice for 10 minutes, before harvesting the cells in two 50 ml centrifuge tubes (Corning) at 4500 x g for 10 minutes at 4 °C using an Eppendorf centrifuge, model 5804R.
- 4. The supernatant was quickly removed and the cells were resuspended in 15 ml of ice-cold 0.1M CaCl₂ and incubated for 30 minutes on ice.
- 5. The cells were pelleted by centrifugation as before, the supernatant discarded, and the cell pellet was resuspended, in 2 ml of ice-cold 0.1M CaCl₂. This was incubated on ice for at least 2 hours.
- 6. The now competent cells were used immediately or within 24 hours, if stored on ice.

9.7.2 Transformation of competent cells

- 1. Either 5 μ l of a ligation reaction, or 0.5 μ l of a plasmid preparation was added to 100 μ l of competent *E. coli* cells in an ice-cold microfuge tube.
- 2. These were incubated for 30 minutes on ice.
- 3. The tubes were transferred to a water bath at 42°C for 1 minute, and returned to ice for a further 2 minutes.
- 4. Then, 500 μ l pre-warmed LB broth (42°C) was added to each tube and incubated at 37°C for one hour, to allow expression of the introduced selectable marker..

5. Cells were plated onto selective LB medium containing the appropriate antibiotic(s) using a sterile

spreader. Transformants were screened following overnight incubation at 37°C.

9.7.3 DNA sequencing

Sequencing was carried out by Genome Enterprise Ltd., (John Innes Centre, UK) using an AbiPrism

3730 capillary sequencer. Plasmid DNA that was to be used as template for sequencing reactions

was isolated using the Qiagen Midiprep method as detailed earlier. For each sample, 5 µg of

template DNA was sent to be sequenced, using primers specific to the cloned fragment, or to the

vector, where appropriate, at a concentration of 1.5 pmol / μ l.

9.7.4 β-Galactosidase assays

The plasmid pBIO1878 is a derivative of the wide host-range promoter-probe plasmid vector

pMP220 derivative (Spaink 1987). It has an additional Spc^R cassette, cloned into the SphI site of

pMP220 in order to facilitate counter-selection when the plasmid was to be introduced into strains

of Ruegeria. The cloning sites in pBIO1878 are upstream of a lacZ gene, which has a ribosome

binding site derived from the chloramphenicol acetyl transferase gene of E. coli, but lacks any

promoter or operator sequence. Thus, a promoter from a gene of choice, cloned in the correct

orientation into the PCS of pBIO1878 will control the expression of β -galactosidase encoded by yhe

reporter *lacZ* .

The assay for β-galactosidase involves the cleavage of o-nitrophenyl-β-D-galactoside (ONPG) to o-

nitrophenol a yellow product that absorbs at 420nm and is measured in a spectrophotometer

(Genova spectrophotometer {Jenway}).

Reagents required:

Z-buffer - in 50 ml of dH₂O

3M Na₂HPO₄·7H₂O 1 ml

250

0.5 ml 4M NaHPO₄·7H₂O

0.5 ml 1M KCl

0.5 ml MgSO₄·7H₂O

175 μl β-mercaptoethanol

ONPG solution – per ml of dH₂O

4 mg O-nitrophenyl-β-D-galactopyranoside

- 1. *R. pomeroyi* strains were inoculated from single colonies into 5 ml HY medium containing appropriate antibiotics and grown for 2 days at 28°C.
- 2. These starter cultures were used to inoculate either MBM (for Fe limitation experiments) or RSS (for Mn limitation) containing 10 mM succinate and vitamin solution as described earlier.
- 3. These cultures were grown for \sim 15 hours or until the OD_{600nm} had reached at least 0.1. The cultures which lacked iron rarely grew above an OD_{600nm} value of 0.15.
- 4. From each culture, 500 μ l aliquots were added to a 2 ml microfuge tube containing 500 μ l Z-buffer.
- 5. Using a Pasteur pipette, 2 drops of chloroform and 1 drop of 0.1% SDS (w/v) were added to each microfuge tube and vortexed for 10 seconds. These were then incubated at 28° C for 5 minutes.
- 6. To each tube, 200 μl ONPG solution was added, before returning the tubes to 28°C.
- 7. When sufficient yellow colour had developed, the reactions were stopped using 500 μ l 1M sodium bicarbonate, and the length of incubation was recorded.
- 8. All tubes were centrifuged for 3 minutes at 13,200 x g to clear the cell debris.
- 9. A 1 ml aliquot from each tube was transferred to a 2 ml cuvette and the OD_{420nm} was recorded.
- 10. β -galactosidase activities, in Miller Units, were calculated using the following equation:

$$Miller Units = \frac{1000 \times OD420nm}{t \times V \times OD600nm}$$

Where,

t = time in minutes, and V = volume of culture

9.7.5 CAS assay plates

Chrome azural sulfonate (CAS) solution was made as follows:

60.5 mg CAS, dissolved in 50 ml dH₂O

10 ml 1 mM FeCl₃·6H₂O in 10 mM HCl

72.9 mg HDTMA (Hexadecyltrimethylammonium bromide) in 40 ml dH₂O.

These constituents were mixed and autoclaved. Then 20 ml of this CAS solution was added per 200 ml of MBM agar to make CAS plates.

9.8 in silico analyses

9.8.1 DNA sequence analysis

DNA sequences returned from TGAC were analysed using *BioEdit*. Sequences were compared to genomic and protein sequences available from the National Centre for Biotechnology Information (NCBI - www.ncbi.nlm.nih.gov) using the Basic Local Alignment Search Tool, BLAST (Altschul *et al.* 1997).

DNA sequence motifs were discovered, and logo graphics of these motifs generated using MEME (Bailey and Elkan 1994).

9.8.2 Sequence alignments and phylogenetic trees

Evolutionary analyses were conducted in MEGA5 (Tamura *et al.* 2011). Alignments were performed using the Neighbor-Joining method (Saitou and Nei 1987). Bootstrap consensus trees were inferred from 500 replicates and are taken to represent the evolutionary history of the taxa analyzed (Felsenstein 1985). Branches corresponding to partitions reproduced in fewer than 50% bootstrap replicates are collapsed. The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches (Felsenstein 1985). The trees are drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the JTT matrix-based method (Jones *et al.* 1992) and are in the units of the number of amino acid substitutions per site.

9.8.3 Database searches

Searches for homologous protein sequences in the NCBI non-redundant protein database were done using BLAST. Metagenomic databases were interrogated using BLAST, with input sequences obtained from NCBI, using the Community Cyberinfrastructure for Advanced Microbial Ecology Research and Analysis (CAMERA), described by Sun *et al.* (2010).

9.8.4 Other bioinformatic tools

Several online programmes were used to analyse peptide sequences where indicated in the text. They are available at the following websites:

- SignalP (Petersen et al. 2011) used to predict the presence of a SEC-signal peptide.
- TatP (Bendtsen et al. 2005) used to predict the presence of a TAT-signal peptide.
- iMembrane (Kelm *et al.* 2009) predicts putative tertiary / membrane structure of a protein based on closest homologue within the iMembrane database.
- String 9.0 (Szklarczyk *et al.* 2011) functional prediction / neighbourhood / co-occurance analysis of genes.

•	PredTM-BB (Bagos et al. 2004) – predicts whether a protein is likely found within a bacterial
	membrane, and can be used to draw the secondary structure of a protein integrated in a
	membrane.

Table 9.1 Details of Strains, Plasmids and Oligonucleotide primers used in this work

Strain Description Source	
Escherichia coli 803 Met; used as host for transformation with large plasmids Wood (1966) E. coli X110-Gold High transformation rate, used for site directed mutagenesis Stratagene E. coli JM101 Used as host for pUC18-based plasmids Messing (1979) Dinoroseobacter shibae DFL-12 Lab strain Biebl et al. (2005) Sulfitobacter IE36 Lab strain Gonzalez et al. (1996) Silicibacter locuscaerulensis ITI-1157 Lab strain Petursdutri and Kristjansson (1997) Fulvimarina pelagi HTCC2506 Lab strain Cho and Giovannoni (2003) Loktonello vestfoldensis SKA53 Lab strain Van Trappen et al. (2004) Id469 R. pomeroyi wild type strain Van Trappen et al. (2004) Id470 J469, Rif [®] González (2003) Id470 J469, Rif [®] Todd et al. (2011) I528 Mur strain of R. pomeroyi , generated using pBIO2161. Spec [®] Rif [®] Kan [®] This Work I531 FbpAB strain of R. pomeroyi , generated using pBIO2104. Spec [®] Rif [®] . This Work I533 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work	
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1470 J469, Rif [®] Todd et al. (2011) 1528 Mur' strain of R. pomeroyi , generated using pBIO1861. Spec [®] Rif [®] Kan [®] This Work 1529 SitA strain of R. pomeroyi , generated using pBIO2104. Spec [®] Rif [®] Kan [®] This Work 1531 FbpAB strain of R. pomeroyi , generated using pBIO2104. Spec [®] Rif [®] . This Work 1532 FbpAB strain of R. pomeroyi , generated using pBIO2104. Spec [®] Rif [®] . This Work 1533 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1533 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1539 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1530 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1531 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1532 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1532 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1532 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1533 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1534 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1535 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1536 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1536 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1537 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1537 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work 1537 IrpA strain of R. pomeroyi , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work	
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FbpAB strain of <i>R. pomeroyi</i> , generated using pBIO2104. Spec [®] Rif [®] . This Work	
1533 IrpA strain of <i>R. pomeroyi</i> , generated using pBIO2116. Spec [®] Rif [®] Kan [®] This Work	
J534 SPO0432 strain of <i>R. pomeroyi</i> , generated using pBIO2119. Spec [®] Rif [®] Kan [®] This Work	
SPO3722 strain of <i>R. pomeroyi</i> , generated using pBIO2120. Spec [®] Rif [®] Kan [®] This Work	
SPO1393 strain of <i>R. pomeroyi</i> , generated using pBIO2121. Spec [®] Rif [®] Kan [®] This Work	
J537 SPO2025' strain of <i>R. pomeroyi</i> , generated using pBIO2122. Spec [®] Rif [®] Kan [®] This Work	
J538 SPOA0186 strain of <i>R. pomeroyi</i> , generated using pBIO2123. Spec ^R Rif ^R Kan ^R This Work	
Irr- strain of R. pomeroyi , generated using pBIO2114. Rif ^R Amp ^R Spec ^R This Work	
	•
PRIMERS	
Oligo Name Sequence Restriction site / Function	Plasmid
Outgo name Sequence RESTITCTION SITE / FUNCTION fbpA fwd: SCYCTYARAGCATTACGTGCACGAGGGC Pstl / Wbal	. raamitu
Topa we. Scientification of the Control of the Cont	†
Topin to: Description Des	1
fbpB rev: cgtctagaccaccaagatcaagggc Psti /kbal	
irpA fwd: gctctxgacgcgatcgatcgcccg Psti / Xbal	
irpA rev: cggrcgccgctgcAgArAggcgcc Psti / Xbal	
rpApk19FWD ggtgaattectgggegg EcoRl	
rpApk19REV ccatctagacgttccggatacc Xbal	
mbfApXba1FWD gcgctctxgaccgctcggccxggc Amplifies mbfA promoter	
mbfApPst1REV gcgccTcatgcagcgctatcag Amplifies mbfA promoter	ļ
IrrCOMPFWD GCGCTCTAGAGGTCTCCTTGTCAAAGCTGC Amplifies irr and its promoter	ļ
IrrCOMPREV GCGCTCTAGACCGCGGGGGGCACAGGTC Amplifies irr and its promoter	
TopAS1TroGFWD GCGACAGCATTACCCGACTGAAATAAGCAGTTTTATCTTGC Mutagenesis of IR box 1 'T'	
fbpA51TtoGREV GCAAGATAAAACTGCTTATTTCAGTCGGGTAATGCTGCC fbpA51CtoGFWD GCGACAGCATTACCCGACTGAAATAATGAGTTTTATCTTGC	pBIO2106
fbpA51CtoGFWD GCGACAGCATTACCCGACTGAAATAATGAGTTTTATCTTGC Mutagenesis of IR box 1 'C' GCAAGATAAAACTCATTATTTCAGTCGGGTAATGCTGTCGC GCAAGATAAAACTCATTATTCAGTCGGGTAATGCTGTCGC Mutagenesis of IR box 1 'C' GCAAGATAAAACTCATTATTCAGTCGGGTAATGCTGTCGC GCAAGATAAAACTCATTATTCAGTCGGTGTATTCAGTCGGTATATATTCAGTCGGTGTGCGC GCAAGATAAAACTCATTATTCAGTCGGTATATTCAGTCGGTGTATTATTCAGTCGGTATATTCAGTCGGTGTGTGCC GCAAGATAAAACTCAGTGTGTGTGCGC GCAAGATAAAACTCAGTATTATTCAGTCGGTGTGTGCGC GCAAGATAAAAATAAAACTCAGTGTGTGTGTGTGTGTGTG	pBIO2107
fbnA7TroGEWD GCGAAATCGGTAATTGACTGATTACTGAATCG	pbiozior
TibpAZTIOGREV CGATTCAGTTAATCCGCCTGAAATAGTCAATTACCGGATTTCGC Mutagenesis of IR box 2 'T'	pBIO2108
TBPA2CLOGFWD GCGARATCGGGTAATTGACTATTTACTGGGGGTTAACTGGATCG Mutagenesis of IR box 2 °C'	
TOPAZCTOGREV CGATTCAGTTAATCCCACTGAAATAGTCAATTACCGGATTTCGC	pBIO2109
Teaggractggtatttccgactaaactgggggattaagggcattggaacc Mutagenesis of IR box 3 'T'	
TOPS I TO	pBIO2110
TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR	
fbpBCtoGREV GGTTCCAATGCCCTTAATCCACCAGTTTAGTCGGAAATACCAGTGCCTGA lrpABamHIFWD ATCGGTGTGATCGGGGTGTTGACTTAAGGATCCAATTTAGTCAGATATAAGCAAAGCCAG	pBIO2111
InpABamHiREV CREGATIVANTEGRACITATATTCGRACTATATTCGATCACACCCGAT Mutagenesis of IR box upstream of irpA	pBIO2115
SpecPstIF GCCCTGCAGATCGTGCCGAAT spec cassette amplification Pst I	pbioziis
Spec 43th Spec Cassette amplification 78t Spec 43th Spec Cassette amplification 78t	
P1 GCTGGTGCCGCTGGCC fbpAB mutant check primers	
P2 AGATCGCTTGGCCTCGCGCG fbpAB mutant check primers	
P3 CACCTCGGCCATCGCCGAGG fbpAB mutant check primers	
irpAIF1 GCATGGATCCCGTCGACGAGCGCTGTCGAACA irpA mutant check primers	
irpA2R2 GCTGAAAGTATCGTTGAACC irpA mutant check primers	
SPO0789XbalF1 GGACTCTAGACCTCGCATCAGTGTG SPO0789 promoter cloning	
SPO0789PstlR1 CGATCTGCAGGCAAGATTGCCGCCCTTGGT SP00789 promoter cloning	
SERPSAF TGCATCTAGAGTGTCCATGTGCTGGTTCTG ScR promoter cloning	
IscRp54R GCATCTGCAGTGCAGCGCGATATCGGTCAG IscR promoter cloning	ļ
SPO0432EcoF ATGGGATTGGGATTGCAAGGGGGCAAAAT pBIO1879 cloning to create mutagenic suicide plasmid	1
SPO0432XbaR ACGTTCTAGATTATCACAGACCAGCGCATC pBIO1879 cloning to create mutagenic suicide plasmid SPO3722F caccgaaggactggaatgg pBi01879 cloning to create mutagenic suicide plasmid	
SPO3722F caccgaaggacttggaatgg pBI01879 cloning to create mutagenic suicide plasmid SPO3722R acgtrctagatgaggcttttcctgaaacca pBI01879 cloning to create mutagenic suicide plasmid	+
SPU372ZR POLITIZARI GEOGRACIA PROLITIZARI GEOGRACIA PROLITIZARI PROLITIZARI GEOGRACIA PROLITIZARI PROLITIZI PROLIT	†
SP01393R TAGGETTAGAGCCTGGAGATTCTCAAATCC pB012879 cloning to create mutagenic suicide plasmid	1
SPO2025F TGACGACATCGTCGACAAAGGGGGGCTAT pBIO1879 cloning to create mutagenic suicide plasmid	İ
SPO2025R AGTOTAGATOTTCACCACATCCGAAAGC pBIO1879 cloning to create matagenic suicide plasmid	İ
SPOA0186F ACGTGAATTCCTCCAAGTTCTCCGACTATGC pBI01879 cloning to create mutagenic suicide plasmid	
SPOA0186R gacttctagaccggatcgtattttgacctg pBI01879 cloning to create mutagenic suicide plasmid	
irrflankEcoFWD CACTATGCCAGAAGACGGAAT irr flanking region amplification for pEX18Ap cloning	
irrflankHindllIREV GCGCAAGCTTGCAAGCCCTCTGTTCAAATCA irr flanking region amplification for pEX18Ap cloning	
Irrflank1F CACTATGCCAGAAGACGGAAT Irr mutant screening	
Irrflank2R GCGCAAGCTTGCAGGCCTCTGTTCAAATCA Irr mutant screening	ļ
IrrcheckF CAGGAAATCGCCACCGATTG Irr mutant screening	ļ
IrrcheckR CTTGCGGCGCAGCCGGATC Irr mutant screening	ļ
SitAF2 GCGCTCTMARACCGCGAGATCACGATTGGS sitA promoter cloning	-
SITARZ GCGACTGCAGCGAACTTGTCGGCATAATCG	!
MRS1sdmF TTTACCTTTCGGACAAAATTCACCTTTCTAACGAATAATTCTCCAATTGCGTT MRS box mutagenesis upstream of sitA MRS1sdmR AACGCAATTGAGAATTATTCGTTAGAAAGGTGAATTTTGTCCGAAAGGTAAA MRS box mutagenesis upstream of sitA	+
MRS1sdmR AACGCAATTGAGAATTATTCGTTAGAAAGGTGAATA MRS box mutagenesis upstream of sitA MRS2sdmF CTTGCGAATGATTCCAATTGCGTTAGACGAATGGTTCCATATT MRS box mutagenesis upstream of sitA	+
MRS250MF CHICAGATANTICIDANTICUTANTICUTIANCITACATTACCATACTACCATA MRS DOX mutagenesis upstream of strA MRS25dmR Antargagacatactatricatant	
FURFurd GCTCTAGACGGGTTCGAGAACTCG	+
FURREY GCGGATCCGATGTCGAGGAGCTGTATGC internal fragment of Mur for cloning into pBIO1879	
irroromfwd CTTGTCAAAGCTGCTCGGGT	†
Irr promoter GCGATTTCCTGAGAATTTGGCGT Irr promoter cloning	
VcXhamn1 GCGGATCCGAAGGAGATATACATATGTCGATAATATCTCATTCA	
VCKECOp2 GCGAATTCTACATTTCAAAATAACCAAAAAGT Cloning Vibrio mntX into pRK415	
Sit Ank 19F ACTGGATTCGCGATGGTGGTGTTGT	
STRAPKISR ATCGTCTAGAGTGGCAACCACCGGTATG internal fragment of sitA of R. pomeroyi	
MntXpF ACGTTCTAGAGTGGATCACCCCGGTTTC mntX of R nubinhibers promoter fusion	
MntXpR gcatctgcagcacataggcatcgaccatca mntx of k. nuplinibens promoter tusion	

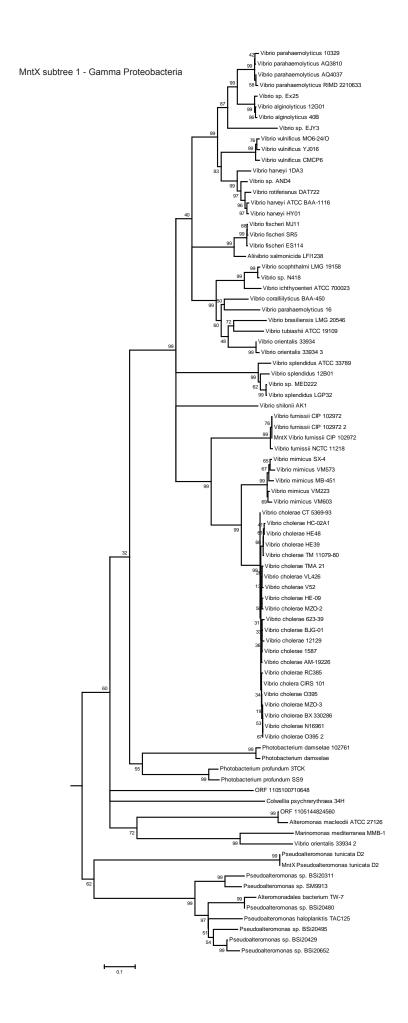
PLASMIDS

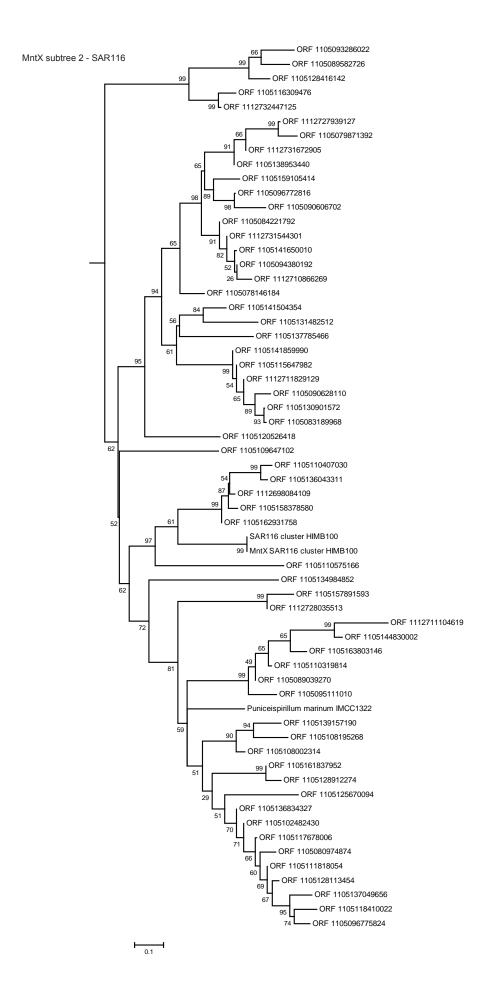
Vector	Function	Source	Marker Selection
pRK2013	Used as mobilising plasmid in tri-parental crosses	Figurski and Helinski (1979)	Kan ^R
pμP220	Wide host-range lacZ promoter probe vector	Spaink et al . (1987)	Tet ^R
pOT2	Broad host-range promoter probe vector with promoterless gfp gene	Allaway et al . (2001)	Gent ^R
	pK19mob::spec, Suicide insertion plasmid with a spectinomycin resistence cassette		
pBIO1879	F	Todd et al . (2011)	Spec ^R , Kan ^R
pRK415	Broad host-range expression vector	Keen et al . (1988)	Tet ^R
pDONR221	pUC origin Gateway vector	Nakagawa et al. (2008)	Kan ^R
poormeer	poe ongai datendy vector	Hanagana et al. (2000)	No.
pBIO1845	pBIO1878 with fbpA promoter from R. pomeroyi cloned in using Xba I and Bam HI	This Work	Spec ^R , Tet ^R
pb101043		IIIIS WOIK	Spec , Tet
pBIO1846	pBIO1878 with fbpB promoter from R. pomeroyi cloned in using Xba I and Bam HI	This Work	Spec ^R , Tet ^R
pBIO1040	DUIT TII	IIIIS WOIK	Spec , Tet
pBIO1847	pBIO1878 with irpA promoter from R. pomeroyi cloned in using Xba I and Bam HI	This Work	Spec ^R , Tet ^R
рыот647	psio1878 With IrpA promoter from R. pomeroyi cloned in using Xbb Fand Bam Hi	THIS WOLK	spec , Tet
	DIOAGTO with internal forwards of more discussion when I and Day III		Spec ^R , Kan ^R
pBIO1861	pBIO1879 with internal fragment of mur cloned in using Xba I and Bam HI	This Work	spec , kan
			. B B
pBIO1863	pBIO1879 with internal fragment of iscR cloned in using Xbal and EcoRI	This Work	Spec ^R , Kan ^R
			- P P
pBIO1864	pBIO1879 with internal fragment of rirA cloned in using XbaI and EcoRI	This Work	Spec ^R , Kan ^R
pBIO1928	Contains irr plus promoter of J470 in pOT2	This Work	Gent ^R
pBIO1929	Contains J470 mbfA promoter-LacZ fusion in pS4	This Work	Spec ^R , Tet ^R
pBIO2088	Candidatus Pelagibacter sp. IMCC9063 mntX gene cloned into pRK415	This Work	D D
pBIO2050	1086 bp promoter region of sitA cloned into pBIO1878	This Work	Spec ^R , Tet ^R
pBIO2100	MRS1 box mutation in pBIO2050	This Work	Spec ^R , Tet ^R
pBIO2101	MRS2 box mutation in pBIO2050	This Work	Spec ^R , Tet ^R
pBIO2102	MRS1 and MRS2 box mutation in pBIO2050	This Work	Spec ^R , Tet ^R
pBIO2103	5011bp region flanking fbpAB of R. pomeroyi in pEX18Ap	This Work	Amp ^R
pBIO2104	5011bp region flanking fbpAB of R. pomeroyi in pEX18Ap	This Work	Amp ^R
pBIO2105	pBIO2104 with a 1.8 kb Spec ^R cassette cloned into Pst I	This Work	Amp ^R , Spec ^R
pBIO2106	pBIO2104 with a 1.8 kb Spec ^R cassette cloned into Pst I	This Work	Amp ^R , Spec ^R
pBIO2107	pBIO1878 with mutation in IR box 1 T	This Work	Spec ^R , Tet ^R
pBIO2108	pBIO1878 with mutation in IR box 1 C	This Work	Spec ^R , Tet ^R
pBIO2109	pBIO1878 with mutation in IR box 2 T	This Work	Spec ^R , Tet ^R
pBIO2110	pBIO1878 with mutation in IR box 2 C	This Work	Spec ^R , Tet ^R
pBIO2111	pBIO1879 with mutation in IR box 3 T	This Work	Spec ^R , Tet ^R
pBIO2112	pBIO1879 with mutation in IR box 3 C	This Work	Spec ^R , Tet ^R
pBIO2112 pBIO2113	irr flanking region cloned into pEX18Ap	This Work	Amp ^R
	pBIO2113 with a 1.8 kb Spec ^R cassette cloned into <i>Pst</i> I		Amp ^R , Spec ^R
pBIO2114		This Work	
pBIO2115	pBIO1847 with mutation, IR box changed to Bam HI site	This Work	Spec ^R , Tet ^R
			. B B
pBIO2116	irpA internal fragment cloned into pBIO1879	This Work	Spec ^R , Kan ^R
pBIO2117	SPO0789 promoter cloned into pBIO1878	This Work	Spec ^R , Tet ^R
pBIO2118	iscR promoter cloned into pBIO1878	This Work	Spec ^K , Tet ^K
pBIO2119	SPO0432 internal fragment cloned into pBIO1879	This Work	Spec ^R , Kan ^R
pBIO2120	SPO3722 internal fragment cloned into pBIO1879	This Work	Spec ^R , Kan ^R
pBIO2121	SPO1393 internal fragment cloned into pBIO1879	This Work	Spec ^R , Kan ^R
pBIO2122	SPO2025 internal fragment cloned into pBIO1879	This Work	Spec ^R , Kan ^R
pBIO2123	SPOA0186 internal fragment cloned into pBIO1879	This Work	Spec ^R , Kan ^R
	· · · · · · · · · · · · · · · · · · ·		,
pBIO2124	sitA internal fragment cloned into pBIO1879	This Work	Spec ^R , Kan ^R
pBIO2125	irr promoter fusion cloned into pBIO1878	This Work	Spec ^R , Tet ^R

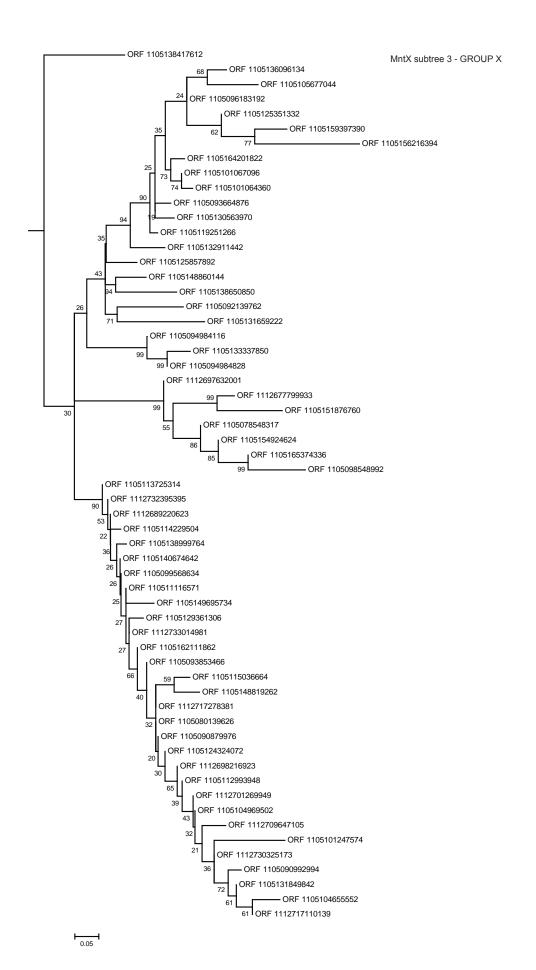
Appendix

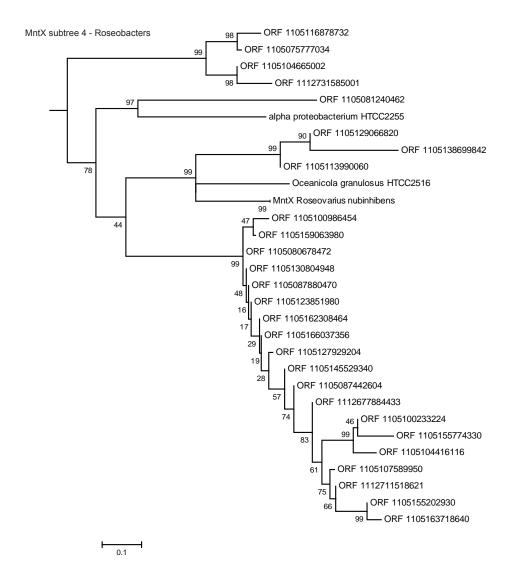
Appendix Figure 1. Blow-up of relatedness tree of MntX polypeptides

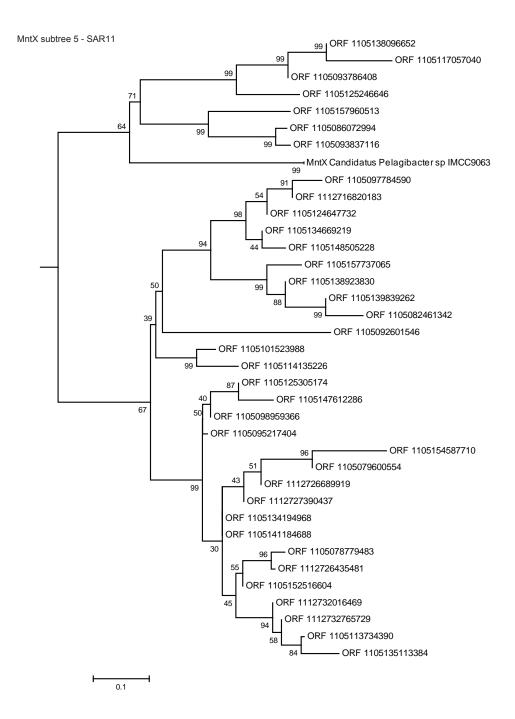
The individual sequences in each of the five sub-groups of MntX polypeptides in the relatedness tree in Figure 6.9 are shown in higher magnification. Those with the prefix "ORF" are from the GOS data base and are described further in Appendix Table 1. The MntX subtrees 1-5 contain the MntX sequences of the γ -proteobacterial, SAR116, Class X, Roseobacter and Pelagibacter types, respectively.











Appendix Table 1. Details of the MntX homologues in the GOS data base

The CAMERA data set "GOS: All ORF Peptides" was interrogated using MntX of *Roseovarius nubinhibens* (locus: *ISM_02005*). All GOS homologous sequences (in column ^a) with E-values <1E⁻²⁰, (values in column ^b) are shown, together with their geographic origin (column ^c) and habitat (column ^d). Column ^e lists the GOS homologues on the bases of the clusters shown in Figure 6.9 and Appendix Figure 1, using abbreviations: "116" = SAR116 group; "G" = gamma-proteobacteria; "P" = *Pelagibacter*; "R" = Roseobacters; "X" = the cluster that contains only GOS sequences. Those GOS homologues with insufficient coverage of the MntX polypeptide to be included in the neighborjoining trees are shown as "not used" in column ^e.

	E-			
Subject Name ^a	Value ^b	Sample Position ^c	Habitat ^d	Cluster ^e
JCVI_PEP_1105136834328	1.13E-52	Cape May, NJ	Coastal	116
JCVI_PEP_1105111818055	2.45E-50	Newport Harbor, RI	Coastal	116
JCVI_PEP_1105117678007	1.68E-49	Block Island, NY	Coastal	116
JCVI_PEP_1105102482431	1.03E-47	Block Island, NY	Coastal	116
JCVI_PEP_1105138953441	8.65E-47	250 miles from Panama City	Open Ocean Coastal	116
JCVI_PEP_1105078146185	2.08E-46	Upwelling, Fernandina Island	upwelling	116
JCVI_PEP_1105159105415	2.69E-46	Off Nags Head, NC	Coastal Coral Reef	116
JCVI_PEP_1105141859991	1.31E-45	Rangirora Atoll	Atoll	116
JCVI_PEP_1105162931759	7.76E-45	Wolf Island	Coastal	116
JCVI_PEP_1105115647983	6.74E-45	Hydrostation S	Open Ocean	116
JCVI_PEP_1105158378581	6.68E-44	Devil's Crown, Floreana Island	Coastal Coral Reef	116
JCVI_PEP_1105084221793	5.61E-44	Rangirora Atoll	Atoll Coastal	116
JCVI_PEP_1105128416143	2.10E-42	Upwelling, Fernandina Island	upwelling Coastal	116
JCVI_PEP_1105120526419	4.05E-42	Upwelling, Fernandina Island International water between	upwelling	116
JCVI_PEP_1112711829130	1.85E-41	Madagascar and South Africa	Open Ocean	116
JCVI_PEP_1105116309477	2.56E-41	Sargasso Station 13	Open Ocean	116
JCVI_PEP_1105095111011	1.16E-40	Cabo Marshall, Isabella Island	Coastal	116
JCVI_PEP_1105128113455	9.03E-40	Off Nags Head, NC	Coastal Coral Reef	116
JCVI_PEP_1105089039271	2.13E-39	Rangirora Atoll	Atoll	116
JCVI_PEP_1105109647103	2.79E-39	Hydrostation S	Open Ocean	116
JCVI_PEP_1105096772817	9.66E-39	Gulf of Maine	Coastal	116
JCVI_PEP_1112732447126	2.54E-38	Moorea, Outside Cooks Bay	Coastal	116
JCVI_PEP_1105094380193	2.50E-38	Devil's Crown, Floreana Island	Coastal	116
JCVI_PEP_1105141650011	4.27E-38	Coastal Floreana	Coastal	116
JCVI_PEP_1105093286023	6.98E-38	Coastal Floreana	Coastal	116
JCVI_PEP_1105161837953	1.98E-37	250 miles from Panama City	Open Ocean	116
JCVI_PEP_1105157891594	2.86E-37	Yucatan Channel	Open Ocean Coastal	116
JCVI_PEP_1112731544302	5.13E-37	St. Anne Island, Seychelles	sample	116
JCVI_PEP_1105110407031	8.46E-37	Wolf Island	Coastal	116
JCVI_PEP_1105080974875	7.40E-37	Off Nags Head, NC	Coastal	116
JCVI_PEP_1105128912275	1.13E-36	Northeast of Colon	Coastal	116
JCVI_PEP_1105130901573	2.19E-36	North James Bay, Santigo Island	Coastal	116
JCVI_PEP_1105083189969	3.67E-36	North James Bay, Santigo Island	Coastal	116
JCVI_PEP_1105136043312	2.38E-35	Wolf Island	Coastal	116
JCVI_PEP_1105139157191	2.93E-35	134 miles NE of Galapagos	Open Ocean Coastal	116
JCVI_PEP_1105110319815	2.28E-34	Upwelling, Fernandina Island	upwelling	116
JCVI_PEP_1112728035514	1.81E-33	Outside Seychelles, Indian Ocean	Open Ocean	116
JCVI_PEP_1105110575167	2.19E-33	Gulf of Panama	Coastal	116

JCVI_PEP_1105141504355	1.16E-32	Rosario Bank	Open Ocean	116
JCVI_PEP_1105108002315	1.16E-31	Devil's Crown, Floreana Island	Coastal	116
JCVI_PEP_1105131482513	1.93E-31	Sargasso Station 13	Open Ocean	116
JCVI_PEP_1112698084110	2.72E-31	Coccos Keeling, Inside Lagoon	Lagoon Reef	116
JCVI_PEP_1105090606703	4.61E-31	Devil's Crown, Floreana Island	Coastal	116
JCVI_PEP_1105137785467	1.77E-30	Sargasso Station 13	Open Ocean	116
JCVI_PEP_1105118410023	2.47E-30	Gulf of Maine	Coastal	116
JCVI_PEP_1105137049657	4.77E-30	Newport Harbor, RI	Coastal	116
ICVII DED 440E000E02727	7 105 20	Harralling Formanding Island	Coastal	116
JCVI_PEP_1105089582727	7.18E-29	Upwelling, Fernandina Island	upwelling	116
JCVI_PEP_1105125670095	4.21E-28	250 miles from Panama City	Open Ocean	116
JCVI_PEP_1105096775825	5.63E-28	Gulf of Maine	Coastal Coral Reef	110
JCVI_PEP_1105108195269	3.04E-27	Rangirora Atoll	Atoll	116
			Coastal	
JCVI_PEP_1112731672906	2.68E-26	St. Anne Island, Seychelles	sample	116
JCVI PEP 1105163803147	2.71E-26	Upwelling, Fernandina Island	Coastal upwelling	116
JCVI PEP 1105134984853	5.41E-26	Hydrostation S	Open Ocean	116
JCVI PEP 1112711104620	5.41E-26	Indian Ocean	Open Ocean	116
JCVI PEP 1112727939128	2.89E-25	Outside Seychelles, Indian Ocean	Open Ocean	116
JCVI PEP 1105079871393	1.42E-23	Northeast of Colon	Coastal	116
JCVI PEP 1105144830003	4.54E-23	Sargasso Station 13	Open Ocean	116
JCVI_PEP_1105090628111	5.50E-22	Sargasso Station 13	Open Ocean	116
JCVI_PEP_1112710866270	1.17E-20	Indian Ocean	Open Ocean	116
			Coastal	
JCVI_PEP_1105100710649	5.03E-42	Upwelling, Fernandina Island	upwelling	G
JCVI_PEP_1105144824561	3.79E-41	Sargasso Station 13	Open Ocean	G
JCVI_PEP_1105086072995	7.77E-44	Delaware Bay, NJ	Estuary	Р
JCVI_PEP_1105093837117	1.40E-43	Delaware Bay, NJ	Estuary	Р
JCVI_PEP_1105095217405	1.85E-42	Warm seep, Roca Redonda	Warm Seep	Р
JCVI_PEP_1105101523989	2.69E-42	Newport Harbor, RI	Coastal	Р
JCVI_PEP_1105152516605	3.67E-42	Warm seep, Roca Redonda	Warm Seep	Р
JCVI_PEP_1105134669220	3.24E-41	Sargasso Station 13	Open Ocean	P
JCVI_PEP_1105124647733	1.66E-39	Devil's Crown, Floreana Island	Coastal	Р
JCVI_PEP_1105114135227	2.03E-39	Off Nags Head, NC	Coastal	P
JCVI_PEP_1105078779484	4.26E-39	Warm seep, Roca Redonda	Warm Seep	P
JCVI_PEP_1105134194969	6.31E-39	North James Bay, Santigo Island	Coastal	P
JCVI_PEP_1105093786409	3.73E-38	Off Nags Head, NC	Coastal	P
JCVI_PEP_1105125305175	2.17E-37	Warm seep, Roca Redonda	Warm Seep	P
JCVI_PEP_1105125246647	2.26E-37	Gulf of Maine	Coastal	Р
JCVI_PEP_1105157960514	3.35E-37	Chesapeake Bay, MD	Estuary	Р
JCVI_PEP_1105154587711	4.34E-37	Warm seep, Roca Redonda	Warm Seep	Р
JCVI_PEP_1105098959367	6.70E-37	Warm seep, Roca Redonda	Warm Seep	Р
JCVI_PEP_1105079600555	6.64E-37	Warm seep, Roca Redonda East coast Zanzibar (Tanzania),	Warm Seep	Р
JCVI_PEP_1112727390438	1.73E-36	offshore Paje lagoon	Fringing Reef	Р
JCVI_PEP_1105147612287	2.32E-36	Warm seep, Roca Redonda	Warm Seep	P

JCVI_PEP_1105141184689	3.64E-35	North James Bay, Santigo Island West coast Zanzibar (Tanzania),	Coastal	Р
JCVI_PEP_1112726689920	2.25E-34	harbour region	Harbor	Р
JCVI_PEP_1105113734391	4.34E-33	Warm seep, Roca Redonda	Warm Seep	Р
JCVI_PEP_1105138923831	2.66E-32	Wolf Island	Coastal Coastal	Р
JCVI_PEP_1112732765730	9.44E-32	St. Anne Island, Seychelles	sample	Р
JCVI_PEP_1105138096653	5.68E-31	Chesapeake Bay, MD	Estuary	Р
JCVI_PEP_1105157737066	3.44E-30	Warm seep, Roca Redonda	Warm Seep	Р
JCVI_PEP_1105139839263	2.94E-28	Warm seep, Roca Redonda	Warm Seep	Р
JCVI_PEP_1105117057041	3.45E-27	Chesapeake Bay, MD	Estuary	Р
JCVI_PEP_1105092601547	9.86E-27	Coastal Floreana	Coastal	Р
IOVI DED 444272C42E402	C 425 2C	West coast Zanzibar (Tanzania),	Hankan	
JCVI_PEP_1112726435482	6.13E-26	harbour region	Harbor	Р
JCVI_PEP_1105097784591	3.53E-25	201 miles from F. Polynesia	Open Ocean	P
JCVI_PEP_1105082461343	1.17E-23	Warm seep, Roca Redonda	Warm Seep Coastal	р
JCVI PEP 1112732016470	1.64E-23	St. Anne Island, Seychelles	sample	Р
JCVI_PEP_1105135113385	2.78E-23	North James Bay, Santigo Island	Coastal	Р
JCVI PEP 1105148505229	2.62E-23	Sargasso Station 13	Open Ocean	Р
JCVI_PEP_1112716820184	6.14E-22	Indian Ocean	Open Ocean	Р
	5.79E-		i i	
JCVI_PEP_1105113990061	105	Bedford Basin, Nova Scotia	Embayment	R
JCVI_PEP_1105129066821	2.56E-95	Cape May, NJ	Coastal	R
JCVI_PEP_1105100986455	5.74E-82	Yucatan Channel	Open Ocean	R
JCVI_PEP_1105162308465	5.28E-79	North James Bay, Santigo Island	Coastal	R
JCVI_PEP_1105116878733	1.58E-78	134 miles NE of Galapagos	Open Ocean	R
JCVI_PEP_1105123851981	8.58E-73	Warm seep, Roca Redonda	Warm Seep	R
JCVI_PEP_1105087880471	2.24E-72	Warm seep, Roca Redonda	Warm Seep	R
JCVI_PEP_1105087442605	1.09E-68	Northeast of Colon	Coastal	R
JCVI_PEP_1105159063981	2.34E-68	Northeast of Colon	Coastal	R
JCVI_PEP_1105104665003	3.06E-66	134 miles NE of Galapagos	Open Ocean	R
JCVI_PEP_1105080678473	4.38E-65	Rosario Bank	Open Ocean	R
JCVI_PEP_1105075777035	6.43E-64	Yucatan Channel	Open Ocean	R
JCVI_PEP_1105127929205	6.37E-64	Warm seep, Roca Redonda	Warm Seep	R
JCVI_PEP_1105130804949	2.63E-63	Hydrostation S	Open Ocean	R
JCVI_PEP_1105138699843	5.86E-63	Newport Harbor, RI	Coastal	R
JCVI_PEP_1105145529341	3.65E-59	Warm seep, Roca Redonda	Warm Seep Coastal	R
JCVI_PEP_1105081240463	2.49E-56	Upwelling, Fernandina Island	upwelling	R
JCVI_PEP_1105104416117	3.62E-56	Wolf Island	Coastal	R
JCVI_PEP_1105166037357	4.07E-56	201 miles from F. Polynesia	Open Ocean	R
JCVI_PEP_1105107589951	7.48E-56	Yucatan Channel	Open Ocean	R
JCVI_PEP_1105100233225	9.00E-55	Coastal Floreana International water between	Coastal	R
JCVI_PEP_1112711518622	1.05E-51	Madagascar and South Africa 500 Miles west of the Seychelles in	Open Ocean	R
JCVI_PEP_1112677884434	4.66E-48	the Indian Ocean	Open Ocean	R
JCVI_PEP_1105155202931	8.65E-47	Off Key West, FL	Coastal	R

JCVI_PEP_1105163718641	1.19E-46	South of Charleston, SC	Coastal	R
JCVI_PEP_1105155774331	6.15E-43	North James Bay, Santigo Island	Coastal	R
101/1 DED 4442724505002	6 625 42		Coastal	n
JCVI_PEP_1112731585002	6.63E-43	St. Anne Island, Seychelles	sample	R X
JCVI_PEP_1105119251267	1.41E-58	Sargasso Stations 3	Open Ocean	
JCVI_PEP_1105090879977	2.23E-56	Warm seep, Roca Redonda	Warm Seep	X
JCVI_PEP_1105148860145	8.20E-56	Yucatan Channel	Open Ocean	X
JCVI_PEP_1105154924625	1.95E-54	Off Key West, FL	Coastal	X
JCVI_PEP_1105162111863	3.25E-54	Yucatan Channel	Open Ocean	X
JCVI_PEP_1105096183193	2.49E-53	Mangrove on Isabella Island	Mangrove Coastal	X
JCVI_PEP_1105132911443	1.02E-52	Upwelling, Fernandina Island	upwelling	X
JCVI_PEP_1105093664877	3.20E-52	Sargasso Stations 3	Open Ocean	Χ
JCVI_PEP_1105101067097	9.79E-50	Sargasso Station 13	Open Ocean	Χ
JCVI_PEP_1105129361307	1.09E-47	Warm seep, Roca Redonda	Warm Seep	Χ
JCVI_PEP_1105111165715	1.09E-47	Sargasso Station 13	Open Ocean	Χ
JCVI_PEP_1105099568635	1.63E-47	Sargasso Station 13	Open Ocean	Χ
JCVI_PEP_1105124324073	1.70E-47	Sargasso Stations 3	Open Ocean	Χ
JCVI_PEP_1105112993949	6.51E-47	Off Key West, FL	Coastal	Χ
JCVI_PEP_1105138999765	9.32E-47	Warm seep, Roca Redonda	Warm Seep	Χ
JCVI_PEP_1105092139763	5.33E-46	Sargasso Stations 3	Open Ocean	Χ
JCVI_PEP_1112732395396	9.89E-46	Moorea, Outside Cooks Bay	Coastal	Χ
JCVI_PEP_1105093853467	1.24E-45	Off Key West, FL	Coastal	Χ
JCVI_PEP_1105130563971	2.58E-45	Sargasso Stations 3	Open Ocean	Χ
JCVI_PEP_1105094984117	4.22E-45	Block Island, NY	Coastal	Χ
		500 Miles west of the Seychelles in		
JCVI_PEP_1112689220624	4.40E-45	the Indian Ocean	Open Ocean	X
JCVI_PEP_1105140674643	6.91E-45	Warm seep, Roca Redonda	Warm Seep	X
JCVI_PEP_1105113725315	1.07E-44	30 miles from Cocos Island	Open Ocean	X
JCVI_PEP_1105114229505	9.33E-44	Sargasso Station 13	Open Ocean	X
JCVI_PEP_1105115036665	9.81E-44	Warm seep, Roca Redonda	Warm Seep Coastal	X
JCVI_PEP_1105138417613	1.36E-43	Upwelling, Fernandina Island	upwelling	Χ
JCVI PEP 1105133337851	1.80E-43	Gulf of Maine	Coastal	X
JCVI PEP 1105101064361	1.36E-41	Sargasso Station 13	Open Ocean	Χ
JCVI PEP 1105149695735	1.61E-41	Sargasso Station 13	Open Ocean	Χ
JCVI_PEP_1105136096135	1.14E-40	Cabo Marshall, Isabella Island	Coastal	Χ
JCVI PEP 1105148819263	1.48E-40	Warm seep, Roca Redonda	Warm Seep	Χ
JCVI PEP 1112697632002	1.98E-40	Moorea, Cooks Bay	Coral Reef	Χ
JCVI PEP 1105078548318	2.05E-39	Sargasso Station 13	Open Ocean	Χ
JCVI_PEP_1105165374337	1.93E-39	Rosario Bank	Open Ocean	Χ
JCVI_PEP_1105104969503	2.91E-39	Warm seep, Roca Redonda	Warm Seep	X
JCVI_PEP_1105138650851	8.31E-39	North Seamore Island	Coastal	Χ
JCVI_PEP_1105125351333	1.20E-37	Sargasso Station 13	Open Ocean	X
JCVI_PEP_1105094984829	3.52E-37	Block Island, NY	Coastal	X
JCVI_PEP_1112701269950	1.25E-36	Indian Ocean	Open Ocean	X
JCVI_PEP_1105131659223	1.14E-36	Sargasso Stations 3	Open Ocean	Χ
JCVI_PEP_1105125857893	1.24E-36	Upwelling, Fernandina Island	Coastal	Χ

			upwelling	
JCVI_PEP_1105159397391	2.15E-36	Sargasso Stations 3	Open Ocean	Х
JCVI_PEP_1112698216924	2.54E-36	Coccos Keeling, Inside Lagoon	Lagoon Reef	X
JCVI_PEP_1105164201823	3.01E-36	Sargasso Station 13	Open Ocean	X
JCVI_PEP_1112733014982	2.70E-35	Moorea, Outside Cooks Bay	Coastal	X
JCVI_PEP_1112733014382 JCVI_PEP_1112717278382	2.70E-33 2.44E-34	Indian Ocean		X
			Open Ocean Coastal	X
JCVI_PEP_1105080139627	1.51E-32	Devil's Crown, Floreana Island		X
JCVI_PEP_1105156216395	2.82E-32	Mangrove on Isabella Island	Mangrove	X
JCVI_PEP_1105104655553	3.68E-32	Northeast of Colon	Coastal	X
JCVI_PEP_1105131849843	1.08E-30	Warm seep, Roca Redonda	Warm Seep	X
JCVI_PEP_1112717110140	1.71E-30	Indian Ocean	Open Ocean	
JCVI_PEP_1105098548993	9.29E-30	250 miles from Panama City 500 Miles west of the Seychelles in	Open Ocean	X
JCVI_PEP_1112677799934	1.16E-29	the Indian Ocean	Open Ocean	Χ
JCVI PEP 1105101247575	1.65E-29	Sargasso Station 13	Open Ocean	Χ
JCVI_PEP_1105090992995	4.07E-28	North Seamore Island	Coastal	Χ
		International Water Outside of		
JCVI_PEP_1112709647106	3.56E-28	Reunion Island	Open Ocean	X
JCVI_PEP_1112730325174	2.00E-27	St. Anne Island, Seychelles	Coastal sample	Х
JCVI_PEP_1105151876761	3.72E-22	30 miles from Cocos Island	Open Ocean	X
JCVI_PEP_1105131870701 JCVI_PEP_1105105677045	2.39E-21	Sargasso Stations 3	Open Ocean	X
JCVI_PEP_1105107514191	1.28E-75	Off Nags Head, NC	Coastal	Not used
	7.07E-52	Off Key West, FL	Coastal	Not used
JCVI_PEP_1105099089301		134 miles NE of Galapagos		Not used
JCVI_PEP_1105136338456	3.10E-50	500 Miles west of the Seychelles in	Open Ocean	Not used
JCVI_PEP_1112690003418	8.93E-50	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105116878665	6.45E-49	134 miles NE of Galapagos	Open Ocean	Not used
JCVI_PEP_1105143559379	2.97E-47	Newport Harbor, RI	Coastal	Not used
JCVI_PEP_1112700253728	2.76E-44	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1112727904146	3.73E-44	Outside Seychelles, Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105114026345	2.98E-42	Browns Bank, Gulf of Maine	Coastal	Not used
			Coastal	
JCVI_PEP_1112731465778	5.21E-42	St. Anne Island, Seychelles	sample	Not used
JCVI PEP 1105113025343	1.04E-39	Upwelling, Fernandina Island	Coastal upwelling	Not used
JCVI_PEP_11051159847901	1.32E-39	Hydrostation S	Open Ocean	Not used
JCVI_PEP_1105139847901	7.84E-39	South of Charleston, SC	Coastal	Not used
JCVI_PEP_1112727988980	8.67E-39	Outside Seychelles, Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105135357286	1.12E-38	South of Charleston, SC	Coastal	Not used
JCVI_FEF_1103133337280	1.121-30	500 Miles west of the Seychelles in	Coastai	NOT USEU
JCVI_PEP_1112689810654	1.28E-38	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105083323561	3.58E-38	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1112732711068	3.61E-38	Moorea, Outside Cooks Bay	Coastal	Not used
JCVI_PEP_1112700904284	6.81E-38	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105089169351	6.58E-38	North Seamore Island	Coastal	Not used
JCVI_PEP_1105147669289	1.30E-37	Hydrostation S	Open Ocean	Not used
JCVI_PEP_1105096718169	5.08E-37	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105106372949	7.04E-37	Sargasso Station 13	Open Ocean	Not used

		International waters between		
JCVI_PEP_1112715377066	1.07E-36	International waters between Madagascar and South Africa	Open Ocean Coastal	Not used
JCVI_PEP_1112732036080	1.15E-36	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1105113364519	1.01E-35	Warm seep, Roca Redonda International water between	Warm Seep	Not used
JCVI_PEP_1112736930156	1.53E-35	Madagascar and South Africa	Open Ocean	Not used
JCVI_PEP_1105114415063	8.61E-35	134 miles NE of Galapagos	Open Ocean	Not used
JCVI_PEP_1105111010569	1.69E-33	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105113630737	2.48E-33	Hydrostation S	Open Ocean	Not used
JCVI_PEP_1105104989057	3.01E-33	Hydrostation S	Open Ocean	Not used
JCVI_PEP_1105141522597	5.44E-33	Off Key West, FL	Coastal	Not used
JCVI_PEP_1105154687927	8.12E-33	Wolf Island	Coastal	Not used
JCVI_PEP_1112716329812	1.61E-32	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105106556727	1.43E-32	Northeast of Colon	Coastal	Not used
JCVI_PEP_1105113595619	1.39E-32	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105164191053	1.93E-32	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1105105072647	1.78E-32	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1105109654545	2.00E-32	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105086669349	1.97E-32	Cabo Marshall, Isabella Island	Coastal	Not used
JCVI_PEP_1112740668362	1.95E-32	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105154381661	2.40E-32	30 miles from Cocos Island	Open Ocean	Not used
JCVI_PEP_1105116215075	2.84E-32	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1112717206458	3.68E-32	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105095036641	3.24E-32	Off Key West, FL	Coastal	Not used
JCVI_PEP_1105119379713	2.96E-32	North Seamore Island	Coastal	Not used
JCVI_PEP_1105097618317	4.35E-32	Tropical South Pacific	Open Ocean	Not used
JCVI_PEP_1105145646771	4.13E-32	Rosario Bank	Open Ocean	Not used
JCVI_PEP_1105120406825	6.22E-32	Rosario Bank	Open Ocean Coastal	Not used
JCVI_PEP_1112732355738	5.87E-32	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1105166013885	5.97E-32	250 miles from Panama City 500 Miles west of the Seychelles in	Open Ocean	Not used
JCVI_PEP_1112677954140	5.97E-32	the Indian Ocean International water between	Open Ocean	Not used
JCVI_PEP_1112736829988	5.92E-32	Madagascar and South Africa	Open Ocean	Not used
JCVI_PEP_1105155324503	1.12E-31	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105091666459	1.24E-31	Sargasso Station 13 500 Miles west of the Seychelles in	Open Ocean	Not used
JCVI_PEP_1112701697274	1.32E-31	the Indian Ocean 500 Miles west of the Seychelles in	Open Ocean	Not used
JCVI_PEP_1112678137292	1.67E-31	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105096964981	1.61E-31	Coastal Floreana	Coastal	Not used
JCVI_PEP_1105165869551	2.27E-31	North James Bay, Santigo Island	Coastal	Not used
JCVI_PEP_1105082141787	1.87E-31	Hydrostation S	Open Ocean Coastal	Not used
JCVI_PEP_1105091831231	2.10E-31	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105110024891	1.92E-31	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1112697730458	2.68E-31	Moorea, Cooks Bay	Coral Reef	Not used

JCVI_PEP_1105117775409	2.79E-31	North James Bay, Santigo Island 500 Miles west of the Seychelles in	Coastal	Not used
JCVI_PEP_1112700762872	4.13E-31	the Indian Ocean International water between	Open Ocean	Not used
JCVI_PEP_1112711565750	5.40E-31	Madagascar and South Africa	Open Ocean	Not used
JCVI_PEP_1112730419344	5.58E-31	St. Anne Island, Seychelles	Coastal sample Coastal	Not used
JCVI_PEP_1105085284613	5.49E-31	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105103638901	1.10E-30	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105158948811	1.43E-30	Newport Harbor, RI	Coastal	Not used
JCVI_PEP_1105118294623	1.89E-30	Sargasso Station 13	Open Ocean Coastal	Not used
JCVI_PEP_1112732506124	2.64E-30	St. Anne Island, Seychelles	sample Coastal	Not used
JCVI_PEP_1105132253699	2.53E-30	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105145195751	3.30E-30	Northern Gulf of Maine	Coastal	Not used
JCVI_PEP_1112710545372	2.96E-30	Indian Ocean	Open Ocean	Not used
JCVI PEP 1112736597466	3.04E-30	International water between	Onen Osean	Not used
		Madagascar and South Africa Coastal Floreana	Open Ocean Coastal	Not used
JCVI_PEP_1105115884603	4.21E-30 5.49E-30	Coastal Floreana	Coastal	Not used
JCVI_PEP_1105104491509		Wolf Island		Not used
JCVI_PEP_1105144133381	4.69E-30	500 Miles west of the Seychelles in	Coastal	Not useu
JCVI_PEP_1112689265682	6.94E-30	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105150593617	7.17E-30	North James Bay, Santigo Island	Coastal	Not used
JCVI_PEP_1105084814695	8.99E-30	Devil's Crown, Floreana Island	Coastal	Not used
JCVI_PEP_1105118423279	1.08E-29	Gulf of Maine	Coastal	Not used
JCVI_PEP_1105085958526	1.47E-29	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105102055405	1.72E-29	Block Island, NY	Coastal	Not used
JCVI_PEP_1105143160005	1.40E-29	Browns Bank, Gulf of Maine	Coastal Coastal	Not used
JCVI_PEP_1112731010420	1.86E-29	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1105117204245	2.23E-29	North James Bay, Santigo Island 500 Miles west of the Seychelles in	Coastal	Not used
JCVI_PEP_1112677871538	2.73E-29	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105163551669	2.75E-29	Yucatan Channel	Open Ocean	Not used
JCVI_PEP_1105105202075	2.82E-29	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1105098197629	2.39E-29	North James Bay, Santigo Island	Coastal	Not used
JCVI_PEP_1105135289252	3.39E-29	Yucatan Channel	Open Ocean	Not used
JCVI_PEP_1105146897813	3.06E-29	Yucatan Channel	Open Ocean	Not used
JCVI_PEP_1105127980721	3.09E-29	201 miles from F. Polynesia	Open Ocean	Not used
JCVI_PEP_1105103115679	3.36E-29	Bay of Fundy, Nova Scotia	Estuary	Not used
JCVI_PEP_1105138603371	4.24E-29	Block Island, NY	Coastal	Not used
JCVI_PEP_1112701310826	4.24E-29	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105091541629	4.73E-29	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105124799295	5.97E-29	Bay of Fundy, Nova Scotia	Estuary	Not used
JCVI_PEP_1105126693923	8.00E-29	134 miles NE of Galapagos	Open Ocean	Not used
JCVI_PEP_1105129750425	6.88E-29	North Seamore Island	Coastal	Not used
JCVI_PEP_1105108274835	1.36E-28	Warm seep, Roca Redonda	Warm Seep	Not used

JCVI_PEP_1105158222097	1.77E-28	Northeast of Colon	Coastal	Not used
JCVI_PEP_1105147549529	1.55E-28	Sargasso Station 13	Open Ocean Coral Reef	Not used
JCVI_PEP_1105136237363	1.65E-28	Rangirora Atoll	Atoll	Not used
JCVI_PEP_1105140117765	1.48E-28	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105122641279	1.68E-28	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105125171135	1.59E-28	134 miles NE of Galapagos	Open Ocean Coastal	Not used
JCVI_PEP_1105143074023	2.12E-28	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105119959175	2.47E-28	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105146457801	2.41E-28	30 miles from Cocos Island	Open Ocean	Not used
JCVI_PEP_1105087623455	2.31E-28	Off Key West, FL	Coastal	Not used
JCVI_PEP_1105116097393	2.91E-28	Devil's Crown, Floreana Island	Coastal	Not used
JCVI_PEP_1105119057297	3.25E-28	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105126224171	2.51E-28	Wolf Island	Coastal	Not used
JCVI_PEP_1105158569931	2.53E-28	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105105227201	3.90E-28	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105113173947	3.30E-28	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1112700650814	3.68E-28	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105098554789	3.65E-28	250 miles from Panama City	Open Ocean	Not used
JCVI_PEP_1105092898513	3.59E-28	Cabo Marshall, Isabella Island	Coastal Coral Reef	Not used
JCVI_PEP_1105118401697	5.14E-28	Rangirora Atoll	Atoll	Not used
JCVI_PEP_1105092561319	6.55E-28	Mangrove on Isabella Island	Mangrove	Not used
JCVI_PEP_1105125434021	9.14E-28	Off Nags Head, NC	Coastal Coral Reef	Not used
JCVI_PEP_1105156491461	9.53E-28	Rangirora Atoll	Atoll	Not used
JCVI_PEP_1105092387615	1.18E-27	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1105162749005	1.59E-27	30 miles from Cocos Island International waters between	Open Ocean	Not used
JCVI_PEP_1112715898796	1.47E-27	Madagascar and South Africa International water between	Open Ocean	Not used
JCVI_PEP_1112736927170	1.64E-27	Madagascar and South Africa	Open Ocean Coastal	Not used
JCVI_PEP_1105105125543	1.77E-27	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105165471345	3.39E-27	North Seamore Island	Coastal	Not used
JCVI_PEP_1112710779374	3.28E-27	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105114874431	3.14E-27	Hydrostation S	Open Ocean Coastal	Not used
JCVI_PEP_1112731646012	3.84E-27	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1105080855761	6.08E-27	30 miles from Cocos Island	Open Ocean	Not used
JCVI_PEP_1105106333735	5.68E-27	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105141696121	5.59E-27	Devil's Crown, Floreana Island	Coastal	Not used
JCVI_PEP_1105120443141	7.74E-27	Delaware Bay, NJ	Estuary	Not used
JCVI_PEP_1105097461657	8.92E-27	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105081307505	8.70E-27	Yucatan Channel International water between	Open Ocean	Not used
JCVI_PEP_1112736226318	8.92E-27	Madagascar and South Africa	Open Ocean	Not used
JCVI_PEP_1105088248059	8.48E-27	Sargasso Station 13	Open Ocean	Not used

JCVI_PEP_1105165585411	9.38E-27	Delaware Bay, NJ	Estuary	Not used
JCVI_PEP_1105106739435	1.03E-26	Delaware Bay, NJ	Estuary Coastal	Not used
JCVI_PEP_1105152531997	1.25E-26	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105102340705	1.30E-26	Sargasso Station 13 International water between	Open Ocean	Not used
JCVI_PEP_1112736547410	1.46E-26	Madagascar and South Africa International waters between	Open Ocean	Not used
JCVI_PEP_1112715632406	2.16E-26	Madagascar and South Africa	Open Ocean	Not used
JCVI_PEP_1105108895531	2.33E-26	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105110703857	1.89E-26	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105100445535	3.09E-26	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1112697484856	4.58E-26	Moorea, Cooks Bay	Coral Reef	Not used
JCVI_PEP_1105139830403	5.64E-26	Off Key West, FL	Coastal	Not used
JCVI_PEP_1105162291717	8.41E-26	Newport Harbor, RI	Coastal	Not used
JCVI_PEP_1105095790659	1.16E-25	Bay of Fundy, Nova Scotia	Estuary	Not used
JCVI_PEP_1105161697585	1.18E-25	Chesapeake Bay, MD	Estuary	Not used
JCVI_PEP_1105133358451	1.86E-25	Yucatan Channel	Open Ocean	Not used
JCVI_PEP_1105157143905	2.00E-25	Chesapeake Bay, MD	Estuary Coral Reef	Not used
JCVI_PEP_1105135428984	2.55E-25	Rangirora Atoll	Atoll	Not used
JCVI_PEP_1105107383401	2.62E-25	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1105151220301	2.68E-25	Chesapeake Bay, MD	Estuary	Not used
JCVI_PEP_1105093949197	3.81E-25	Gulf of Panama	Coastal	Not used
JCVI_PEP_1105139459569	4.98E-25	Newport Harbor, RI 500 Miles west of the Seychelles in	Coastal	Not used
JCVI_PEP_1112689421410	7.43E-25	the Indian Ocean West coast Zanzibar (Tanzania),	Open Ocean	Not used
JCVI_PEP_1112726506970	7.68E-25	harbour region	Harbor	Not used
JCVI_PEP_1105145927877	9.54E-25	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105141881745	7.62E-25	Coastal Floreana	Coastal	Not used
JCVI_PEP_1105118643945	1.59E-24	Sargasso Station 13 International water between	Open Ocean	Not used
JCVI_PEP_1112736431814	1.45E-24	Madagascar and South Africa	Open Ocean	Not used
JCVI_PEP_1105139672153	1.53E-24	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105143724721	2.18E-24	Warm seep, Roca Redonda	Warm Seep Coastal	Not used
JCVI_PEP_1112730289950	2.13E-24	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1112732611676	2.53E-24	Moorea, Outside Cooks Bay	Coastal	Not used
JCVI_PEP_1105095212519	3.25E-24	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105142526283	4.50E-24	Sargasso Station 13 International water between	Open Ocean	Not used
JCVI_PEP_1112711765764	4.32E-24	Madagascar and South Africa	Open Ocean Coastal	Not used
JCVI_PEP_1112730564854	4.81E-24	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1105159007305	4.28E-24	134 miles NE of Galapagos 500 Miles west of the Seychelles in	Open Ocean	Not used
JCVI_PEP_1112701681448	4.01E-24	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105091810867	6.08E-24	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105124126853	5.46E-24	Newport Harbor, RI	Coastal	Not used

JCVI_PEP_1105141429891	8.08E-24	Off Key West, FL	Coastal	Not used
JCVI_PEP_1105125820711	7.94E-24	Northeast of Colon	Coastal	Not used
JCVI_PEP_1105125216765	8.71E-24	134 miles NE of Galapagos	Open Ocean	Not used
JCVI_PEP_1105119376039	1.18E-23	North Seamore Island	Coastal	Not used
JCVI_PEP_1105099708065	1.68E-23	Coastal Floreana	Coastal	Not used
JCVI_PEP_1105113485987	2.92E-23	Yucatan Channel	Open Ocean	Not used
JCVI_PEP_1105124122977	2.60E-23	Newport Harbor, RI	Coastal	Not used
JCVI_PEP_1105128061417	3.15E-23	250 miles from Panama City	Open Ocean	Not used
JCVI_PEP_1105127055507	2.69E-23	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105093675327	2.75E-23	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105165959985	3.88E-23	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105126736045	6.89E-23	Gulf of Panama	Coastal	Not used
JCVI_PEP_1105122405441	5.41E-23	134 miles NE of Galapagos	Open Ocean	Not used
JCVI_PEP_1112716859452	8.35E-23	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1112700318142	9.31E-23	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105106811677	1.39E-22	Cape May, NJ	Coastal	Not used
JCVI_PEP_1105147329807	1.83E-22	Sargasso Stations 3	Open Ocean	Not used
JCVI_PEP_1105127299435	1.74E-22	Yucatan Channel	Open Ocean Coastal	Not used
JCVI_PEP_1112730859118	1.86E-22	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1105098531181	2.14E-22	Gulf of Panama	Coastal	Not used
JCVI_PEP_1105142526493	2.09E-22	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105100740193	2.51E-22	Hydrostation S	Open Ocean	Not used
JCVI_PEP_1105140347375	3.12E-22	Coastal Floreana	Coastal	Not used
JCVI_PEP_1105155289873	2.85E-22	North Seamore Island	Coastal	Not used
JCVI_PEP_1112716468310	3.17E-22	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105135987488	2.99E-22	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105149886963	3.12E-22	134 miles NE of Galapagos	Open Ocean Coastal	Not used
JCVI_PEP_1105080298835	3.54E-22	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105091051111	5.41E-22	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105146303567	5.50E-22	Cabo Marshall, Isabella Island	Coastal	Not used
JCVI_PEP_1105086989417	4.86E-22	Gulf of Maine	Coastal	Not used
JCVI_PEP_1105131426975	6.90E-22	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105100950699	8.42E-22	Off Nags Head, NC	Coastal	Not used
JCVI_PEP_1105151211469	8.50E-22	Chesapeake Bay, MD	Estuary Coastal	Not used
JCVI_PEP_1105160660249	1.21E-21	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105129908865	1.28E-21	250 miles from Panama City	Open Ocean	Not used
JCVI_PEP_1105091806945	1.14E-21	Sargasso Station 13 West coast Zanzibar (Tanzania),	Open Ocean	Not used
JCVI_PEP_1112707080748	1.31E-21	harbour region	Harbor	Not used
JCVI_PEP_1105083202315	1.66E-21	Devil's Crown, Floreana Island	Coastal	Not used
JCVI_PEP_1105093948591	1.60E-21	Gulf of Panama	Coastal	Not used
JCVI_PEP_1105149813711	1.54E-21	Chesapeake Bay, MD	Estuary	Not used
JCVI_PEP_1105112940361	1.71E-21	Sargasso Station 13 International water between	Open Ocean	Not used
JCVI_PEP_1112736667600	1.64E-21	Madagascar and South Africa	Open Ocean	Not used

JCVI_PEP_1112701128738	1.96E-21	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105100457189	2.16E-21	Bay of Fundy, Nova Scotia	Estuary	Not used
JCVI PEP 1112726649886	1.74E-21	West coast Zanzibar (Tanzania), harbour region	Harbor	Not used
JCVI_PEP_1105134931704	1.83E-21	Sargasso Station 13	Open Ocean	Not used
JCVI PEP 1112728035934	2.53E-21	Outside Seychelles, Indian Ocean	Open Ocean	Not used
JCVI PEP 1105117730315	2.92E-21	North James Bay, Santigo Island	Coastal	Not used
JCVI_PEP_1105150508493	2.69E-21	Chesapeake Bay, MD	Estuary	Not used
		500 Miles west of the Seychelles in	,	
JCVI_PEP_1112689973594	3.81E-21	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105130457819	3.75E-21	Sargasso Station 13 500 Miles west of the Seychelles in	Open Ocean	Not used
JCVI_PEP_1112701696480	3.75E-21	the Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105092807081	3.60E-21	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105139938083	3.78E-21	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105156577609	3.81E-21	Chesapeake Bay, MD	Estuary	Not used
JCVI_PEP_1105081942563	3.15E-21	Sargasso Stations 3	Open Ocean	Not used
ICM DED 4442700272224	4 475 24	West coast Zanzibar (Tanzania),	Hawkan	Notused
JCVI_PEP_1112708273324	4.47E-21	harbour region	Harbor	Not used
JCVI_PEP_1105127048611	4.58E-21	Chesapeake Bay, MD	Estuary Coastal	Not used
JCVI_PEP_1112731372198	4.62E-21	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1112697229568	4.94E-21	Madagascar Waters	Open Ocean	Not used
JCVI_PEP_1112710167110	4.43E-21	Indian Ocean	Open Ocean Coastal	Not used
JCVI_PEP_1112731662020	4.01E-21	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1105096213641	6.45E-21	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105146521897	5.84E-21	Warm seep, Roca Redonda	Warm Seep Coral Reef	Not used
JCVI_PEP_1105104110707	5.15E-21	Rangirora Atoll	Atoll	Not used
JCVI_PEP_1105100076867	5.42E-21	Warm seep, Roca Redonda	Warm Seep	Not used
JCVI_PEP_1105158351529	5.65E-21	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105104652049	5.84E-21	Northeast of Colon	Coastal	Not used
JCVI_PEP_1105111584485	7.44E-21	Bay of Fundy, Nova Scotia	Estuary	Not used
JCVI_PEP_1105097457325	7.88E-21	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1112700722492	1.11E-20	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105154510997	9.63E-21	Warm seep, Roca Redonda	Warm Seep Coastal	Not used
JCVI_PEP_1105161925515	1.04E-20	Upwelling, Fernandina Island	upwelling	Not used
JCVI_PEP_1105108169439	1.02E-20	Coastal Floreana	Coastal	Not used
JCVI_PEP_1105160085301	9.71E-21	Sargasso Station 13	Open Ocean	Not used
JCVI PEP 1112736817690	1.43E-20	International water between Madagascar and South Africa	Open Ocean	Not used
JCVI_PEP_1105134803719	1.43E-20 1.24E-20	30 miles from Cocos Island	Open Ocean	Not used
JCVI_PEP_1105161199357	1.24E-20 1.17E-20	Off Key West, FL	Coastal	Not used
JCVI_PEP_1105141830183	1.17E-20 1.51E-20	Equatorial Pacific TAO Buoy	Open Ocean	Not used
2041 ⁻ 1 F1 ⁻ 1103141030103	1.J1L-2U	East coast Zanzibar (Tanzania),	Open Ocean	140t daca
JCVI_PEP_1112709099426	1.77E-20	offshore Paje lagoon International water between	Fringing Reef	Not used
JCVI_PEP_1112711357040	1.59E-20	Madagascar and South Africa	Open Ocean	Not used

			Coastal	
JCVI_PEP_1112729206852	1.76E-20	St. Anne Island, Seychelles	sample	Not used
JCVI_PEP_1112710886578	1.74E-20	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1112700685818	1.86E-20	Indian Ocean	Open Ocean	Not used
JCVI_PEP_1105156079629	1.64E-20	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105115760905	2.08E-20	North James Bay, Santigo Island	Coastal	Not used
			Coastal	
JCVI_PEP_1105161930303	2.13E-20	Upwelling, Fernandina Island	upwelling	Not used
JCVI PEP 1105157010119	2.20E-20	Upwelling, Fernandina Island	Coastal upwelling	Not used
JCVI PEP 1112709338490	3.00E-20	Madagascar Waters	Open Ocean	Not used
JCVI PEP 1105075560255	2.92E-20	North James Bay, Santigo Island	Coastal	Not used
	3.26E-20	· · ·		Not used
JCVI_PEP_1105158717777		Warm seep, Roca Redonda	Warm Seep	
JCVI_PEP_1105125545815	2.67E-20	Rosario Bank	Open Ocean	Not used
JCVI_PEP_1105108872723	2.87E-20	Coastal Floreana	Coastal	Not used
JCVI_PEP_1105122486497	3.69E-20	Rosario Bank	Open Ocean	Not used
JCVI_PEP_1105124317113	3.95E-20	Yucatan Channel	Open Ocean	Not used
JCVI_PEP_1105083261181	3.75E-20	Delaware Bay, NJ	Estuary	Not used
JCVI_PEP_1105149163675	4.82E-20	Cape May, NJ	Coastal	Not used
			Coral Reef	
JCVI_PEP_1105164402459	4.78E-20	Rangirora Atoll	Atoll	Not used
JCVI_PEP_1105086250205	4.58E-20	Newport Harbor, RI	Coastal	Not used
JCVI_PEP_1105097981111	8.36E-20	Sargasso Station 13	Open Ocean	Not used
JCVI_PEP_1105138279939	9.40E-20	Wolf Island	Coastal	Not used
JCVI_PEP_1105075079390	8.94E-20	30 miles from Cocos Island	Open Ocean	Not used
JCVI_PEP_1105127489175	8.36E-20	North Seamore Island	Coastal	Not used

Appendix Table 2. Full microarray dataset discussed in this work

	Mn 1 Ratio of			Mn 2			Mur 1			Mur 2			Fe 1			Fe 2			Irr 1			Irr 2	
Gene ID SPO0001	+Mn vs - Mn 1.16	p-value 0.051	Gene ID SPO0001	+Mn vs - Mn 1.23	p-value 0.106	Gene ID SPO0001	Ratio of wt vs Mur- 0.92	p-value 0.645	Gene ID SPO0001	Ratio of wt vs Mur- 0.85	p-value 0.059	Gene ID SPO0001	+Fe vs - Fe 1.86	p-value 0.000	Gene ID	+Fe vs - Fe 2.03	p-value 0.000	Gene ID SPO0001	Ratio of wt vs Irr- 1.09	p-value 0.416	Gene ID SPO0001	Ratio of wt vs Irr-	p-value 0.339
SPO0002 SPO0003 SPO0004	1.49 0.94 0.91	0.512 0.23	SPO0002 SPO0003 SPO0004	1.38 1.01 0.97	0.71	SPO0002 SPO0003 SPO0004	0.89 0.93 0.75	0.119 0.368	SPO0002 SPO0003 SPO0004	0.91 0.89 0.76	0.323 0.947 0.78	SPO0002 SPO0003 SPO0004	2.29 1.32 1.44	0.001 0.019 0.002	SPO0002 SPO0003 SPO0004	2.07 1.27 1.47	0.000 0.054 0.001	SPO0002 SPO0003 SPO0004	1.24 0.86 1.01	0.118 0.365	SPO0002 SPO0003 SPO0004	1.08 0.92 1.04	0.437 0.516 0.504
SPO0005 SPO0006	1.4 1.18	0.332 0.143	SPO0005 SPO0006	1.37 1.27	0.218 0.009	SPO0005 SPO0006	0.78 0.93	0.548 0.614	SPO0005 SPO0006	0.78 0.93	0.745	SPO0005 SPO0006	0.93 1.41	0.803 0.022	SPO0005 SPO0006	0.88 1.45	0.618 0.076	SPO0005 SPO0006	0.89 1.12	0.679 0.466	SPO0005 SPO0006	1.00 1.23	0.978 0.658
SPO0007 SPO0008 SPO0009	1.33 1.02 0.9	0.359 0.762 0.509	SPO0007 SPO0008 SPO0009	1.35 1.02 0.95	0.423	SPO0007 SPO0008 SPO0009	0.85 0.99 0.91		SPO0007 SPO0008 SPO0009	0.88 0.87 0.96	0.17 0.031 0.049	SPO0007 SPO0008 SPO0009	1.62 1.42 0.89	0.063 0.005 0.463	SPO0007 SPO0008 SPO0009	1.59 1.48 0.96	0.023 0.001 0.763	SPO0007 SPO0008 SPO0009	1.43 1.17 0.95	0.123	SPO0007 SPO0008 SPO0009	1.37 1.21 0.95	0.304 0.120 0.608
SP00010 SP00011 SP00012	1.28 1.33 1.83	0.052 0.001 0.062	SPO0010 SPO0011 SPO0012	1.15 1.19 1.52	0.02	SPO0010 SPO0011 SPO0012	0.74 0.98 0.97	0.082	SPO0010 SPO0011 SPO0012	0.65 1 0.96	0.459 0.274 0.325	SPO0010 SPO0011 SPO0012	0.84 1.23 0.82	0.429 0.135 0.370	SPO0010 SPO0011 SPO0012	0.89 1.24 0.79	0.921 0.009 0.000	SPO0010 SPO0011 SPO0012	1.20 0.99 1.26	0.805	SPO0010 SPO0011 SPO0012	1.14 1.01 1.21	0.477 1.000 0.039
SPO0013 SPO0014	1.36 0.74	0.375 0.013	SPO0013 SPO0014	1.41 0.77	0.255 0.007	SPO0013 SPO0014	0.98 0.99	0.583 0.989	SPO0013 SPO0014	1.01 0.9	0.709 0.198	SPO0013 SPO0014	1.22 0.33	0.564 0.000	SPO0013 SPO0014	1.18 0.35	0.559 0.000	SPO0013 SPO0014	1.06	0.863 0.960	SPO0013 SPO0014	1.11 0.95	0.778 0.517
SPO0015 SPO0016 SPO0017	1.18 1.33 1.47	0.009	SPO0015 SPO0016 SPO0017	1.03 1.17 1.47	0.068	SPO0015 SPO0016 SPO0017	0.93 0.88 0.93	0.347	SPO0015 SPO0016 SPO0017	0.82 0.96 0.79	0.482 0.601 0.562	SPO0015 SPO0016 SPO0017	0.93 0.68 1.06	0.350 0.068 0.677	SPO0015 SPO0016 SPO0017	1.06 0.64 0.96	0.003 0.934	SPO0015 SPO0016 SPO0017	1.06 0.80 0.99	0.037	SP00015 SP00016 SP00017	1.04 0.77 1.05	0.772 0.076 0.824
SPO0018 SPO0019 SPO0020	1.32 1.37 0.52	0.034	SPO0018 SPO0019 SPO0020	1.37 1.16 0.58		SPO0018 SPO0019 SPO0020	0.81 0.8 0.86	0.046	SPO0018 SPO0019 SPO0020	0.75 0.8 0.74	0.107 0.096 0.683	SPO0018 SPO0019 SPO0020	1.11 0.43 1.95		SPO0018 SPO0019 SPO0020	1.08 0.45 1.88	0.000	SPO0018 SPO0019 SPO0020	1.02 0.96 1.26	0.653	SPO0018 SPO0019 SPO0020	1.01 0.94 1.23	0.715 0.666 0.129
SPO0021 SPO0022 SPO0023	1.01 0.74 1.11	0.128	SPO0021 SPO0022 SPO0023	1.11 0.74 1.18	0.124	SPO0021 SPO0022 SPO0023	0.77 1 0.92	0.089	SPO0021 SPO0022 SPO0023	0.98 0.97 0.97	0.886 0.044 0.947	SPO0021 SPO0022 SPO0023	0.21 0.61 1.13	0.000 0.006 0.286	SPO0021 SPO0022 SPO0023	0.20 0.69 1.15	0.068	SPO0021 SPO0022 SPO0023	0.91 1.21 1.20	0.606	SPO0021 SPO0022 SPO0023	0.95 1.08 1.22	0.509 0.884 0.201
SPO0024 SPO0025	1.17 1.88	0.116 0.003	SPO0024 SPO0025	1.22 1.62	0.115 0.012	SPO0024 SPO0025	0.89 0.85	0.058 0.064	SPO0024 SPO0025	0.99 0.85	0.158 0.02	SPO0024 SPO0025	1.26 1.33	0.015 0.053	SPO0024 SPO0025	1.25 1.51	0.005	SPO0024 SPO0025	1.26 1.46	0.106 0.008	SPO0024 SPO0025	1.20 1.32	0.210 0.046
SPO0026 SPO0027 SPO0028	1.41 1.14 0.96	0.157 0.482 0.996	SPO0026 SPO0027 SPO0028	1.48 1.07 1.02	0.72	SPO0026 SPO0027 SPO0028	0.78 0.74 0.92		SPO0026 SPO0027 SPO0028	0.79 0.7 0.94	0.54 0.616 0.703	SPO0026 SPO0027 SPO0028	1.08 0.79 1.07	0.802 0.264 0.756	SPO0026 SPO0027 SPO0028	1.07 0.80 1.02	0.821 0.504 0.923	SPO0026 SPO0027 SPO0028	1.06 0.96 0.93	0.811	SPO0026 SPO0027 SPO0028	1.10 0.95 0.91	0.776 0.856 0.752
SPO0029 SPO0030 SPO0031	1.69 1.81 1.11	0.001 0.017 0.621	SPO0029 SPO0030 SPO0031	1.59 1.57 1.09	0.015	SPO0029 SPO0030 SPO0031	0.85 0.96 0.98	0.168	SPO0029 SPO0030 SPO0031	0.95 0.88 0.99	0.66 0.222 0.825	SPO0029 SPO0030 SPO0031	1.04 0.83 1.28	0.606 0.299 0.214	SPO0029 SPO0030 SPO0031	1.06 0.85 1.25	0.509 0.536 0.265	SPO0029 SPO0030 SPO0031	1.03 1.21 1.02	0.347	SPO0029 SPO0030 SPO0031	1.03 1.11 1.03	0.773 0.503 0.833
SPO0032 SPO0033 SPO0034	0.88 1.08 0.95	0.656 0.181 0.712	SPO0032 SPO0033 SPO0034	0.93 1.08 0.96	0.913 0.055	SPO0032 SPO0033 SPO0034	0.97 0.93 0.8	0.908 0.523	SPO0032 SPO0033 SPO0034	0.92 0.96 0.94	0.704 0.742 0.297	SPO0032 SPO0033 SPO0034	0.91 1.41 1.02	0.676 0.016 0.325	SPO0032 SPO0033	0.79 1.57 0.96	0.325 0.002 0.641	SPO0032 SPO0033 SPO0034	0.91 0.94 0.95	0.754 0.329	SPO0032 SPO0033 SPO0034	1.01 1.00 0.97	0.988 0.778 0.807
SPO0035 SPO0036	1.07 0.87	0.606 0.493	SPO0035 SPO0036	1.07 0.93	0.066 0.796	SPO0035 SPO0036	0.9 0.95	0.155 0.882	SPO0035 SPO0036	0.93 0.83	0.037 0.655	SPO0035 SPO0036	1.02 1.11	0.755 0.415	SPO0035 SPO0036	1.08 1.08	0.065	SPO0035 SPO0036	1.07 1.00	0.530 0.985	SPO0035 SPO0036	1.05 0.98	0.455 0.941
SPO0037 SPO0038 SPO0039	0.97 1.33 1.19	0.215 0.001	SPO0037 SPO0038 SPO0039	1.01 1.34 1.24	0.034	SPO0037 SPO0038 SPO0039	0.42 0.99 0.93	0.344	SPO0037 SPO0038 SPO0039	0.99 0.92 0.4	0.335 0.295 0.94	SPO0037 SPO0038 SPO0039	1.29 0.76 1.09	0.074 0.230 0.058	SPO0037 SPO0038 SPO0039	1.16 0.68 1.06	0.016	SPO0038 SPO0039	1.34 0.82 1.05	0.020 0.376	SPO0037 SPO0038 SPO0039	1.03 0.83 1.06	0.881 0.225 0.437
SPO0040 SPO0041 SPO0042	1.07 1.27 1.49	0.42	SPO0040 SPO0041 SPO0042	1.04 1.12 1.26	0.716	SPO0040 SPO0041 SPO0042	0.9 0.93	0.595	SPO0040 SPO0041 SPO0042	0.93 0.86 0.91	0.187 0.579 0.861	SPO0040 SPO0041 SPO0042	0.60 0.58 0.81	0.001 0.212 0.782	SPO0040 SPO0041 SPO0042	0.56 0.57 0.78	0.278	SPO0040 SPO0041 SPO0042	0.82 0.88 0.94	0.761	SPO0040 SPO0041 SPO0042	0.79 0.90 0.94	0.070 0.795 0.904
SPO0043 SPO0044 SPO0045	0.94 1.66 1.09	0.772 0.043	SPO0043 SPO0044 SPO0045	0.9 1.38 1.04	0.704 0.178	SPO0043 SPO0044 SPO0045	0.95 0.95 0.83	0.971 0.342	SPO0043 SPO0044 SPO0045	0.94 0.98 0.96	0.935 0.512 0.597	SPO0043 SPO0044 SPO0045	0.93 0.64	0.714 0.149 0.001	SPO0043 SPO0044 SPO0045	0.94 0.65	0.608	SPO0043 SPO0044 SPO0045	1.03 0.97 1.04	0.834 0.956	SPO0043 SPO0044 SPO0045	1.03 1.06 1.09	0.800 0.742 0.606
SPO0046.1	0.83 0.98	0.56 0.967	SPO0046 SPO0046.1	0.83 1.01	0.252 0.892	SPO0046.1	0.88 0.83	0.218 0.856	SPO0046 SPO0046.1	0.93 0.85	0.143 0.941	SPO0046.1	0.37	0.001 0.032	SPO0046.1	0.43	0.000	SPO0046.1	0.93 1.01	0.692 0.992	SPO0046 SPO0046.1	0.97 1.02	0.787 0.982
SPO0047 SPO0048 SPO0049	0.96 0.85 0.56	0.858 0.542 0.002	SPO0047 SPO0048 SPO0049	0.96 0.88 0.65	0.114	SPO0047 SPO0048 SPO0049	0.86 0.92	0.01	SPO0047 SPO0048 SPO0049	0.89 0.86 1.01	0.035 0.025 0.051	SPO0047 SPO0048 SPO0049	0.37 0.42 0.36	0.000 0.000 0.000	SPO0047 SPO0048 SPO0049	0.40 0.47 0.36	0.001 0.000 0.000	SPO0047 SPO0048 SPO0049	1.21 1.43 1.10	0.017	SPO0047 SPO0048 SPO0049	1.21 1.30 1.11	0.106 0.038 0.495
SPO0050 SPO0051 SPO0052	0.66 1.03 1.46	0.154 0.705 0.012	SPO0050 SPO0051 SPO0052	0.7 1.03 1.34	0.459	SPO0050 SPO0051 SPO0052	0.93 0.83	0.14 0.976 0.43	SPO0050 SPO0051 SPO0052	0.94 0.8 0.92	0.099 0.852 0.207	SPO0050 SPO0051 SPO0052	0.21 0.20 0.25	0.000 0.000 0.000	SPO0050 SPO0051 SPO0052	0.22 0.21 0.26	0.000 0.000 0.000	SPO0050 SPO0051 SPO0052	1.11 1.03 1.01	0.875	SPO0050 SPO0051 SPO0052	1.13 1.08 1.01	0.407 0.541 0.930
SPO0053 SPO0054 SPO0055	1.29 1.18 0.98	0.006 0.315 0.983	SPO0053 SPO0054 SPO0055	1.24 1.19 0.95	0.015 0.014	SPO0053 SPO0054 SPO0055	0.95 0.97 0.9	0.601 0.517	SPO0053 SPO0054 SPO0055	0.8 0.96 0.89	0.38 0.576 0.835	SPO0053 SPO0054 SPO0055	0.37 0.32 1.62	0.000 0.002 0.002	SPO0053 SPO0054 SPO0055	0.39 0.37 1.56	0.000 0.000 0.013	SPO0053 SPO0054 SPO0055	0.88 1.01 1.04	0.382 0.864	SPO0053 SPO0054 SPO0055	0.91 0.99 0.99	0.356 0.732 0.997
SPO0056 SPO0057	1.08 0.89	0.167 0.454	SPO0056 SPO0057	1.16 0.95	0.06 0.853	SPO0056 SPO0057	0.92 0.81	0.635 0.602	SPO0056 SPO0057	0.78 0.82	0.984 0.99	SPO0056 SPO0057	0.80 1.22	0.295 0.081	SPO0056 SPO0057	0.86 1.24	0.049	SPO0056 SPO0057	1.14	0.505 0.766	SPO0056 SPO0057	1.07 1.12	0.846 0.362
SPO0058 SPO0059 SPO0060	1.14 1.33 1.24	0.5 0.149 0.094		1.14 1.24 1.23	0.575 0.103 0.003	SPO0058 SPO0059 SPO0060	0.95 0.93 0.86	0.788 0.568 0.998	SPO0058 SPO0059 SPO0060	0.97 0.93 0.96	0.903 0.745 0.683	SPO0058 SPO0059 SPO0060	1.04 0.99 1.11	0.116 0.159 0.059	SPO0058 SPO0059 SPO0060	1.03 0.95 1.12	0.211 0.612 0.062	SPO0058 SPO0059 SPO0060	0.94 1.25 1.00	0.010	SPO0058 SPO0059 SPO0060	0.97 1.29 1.05	0.973 0.012 0.485
SPO0061 SPO0062 SPO0063	1.96 0.93 1.35	0.218 0.026	SPO0061 SPO0062 SPO0063	1.65 1.09 1.34	0.03	SPO0061 SPO0062 SPO0063	0.82 0.91 0.97	0.02	SPO0061 SPO0062 SPO0063	0.91 0.93 0.92	0.037 0.02 0.001	SPO0061 SPO0062 SPO0063	0.76 1.83 1.04	0.186 0.000 0.101	SPO0061 SPO0062 SPO0063	0.72 1.93 1.01	0.014 0.000 0.034	SPO0061 SPO0062 SPO0063	1.06 1.00 1.04	0.776	SPO0061 SPO0062 SPO0063	0.92 1.07 1.08	0.245 0.069 0.122
SPO0064 SPO0065 SPO0066	0.68 1.1 0.67	0.081 0.502	SPO0064 SPO0065 SPO0066	0.79 1.02 0.7	0.08 0.532	SPO0064 SPO0065 SPO0066	0.75 0.99	0.149 0.234	SPO0064 SPO0065 SPO0066	0.9 0.91 0.81	0.078 0.272 0.568	SPO0064 SPO0065 SPO0066	2.27 0.81 1.06	0.000 0.050 0.235	SPO0064 SPO0065 SPO0066	2.44 0.79 1.08	0.000 0.050	SPO0064 SPO0065 SPO0066	1.19 1.05 0.86	0.407 0.563	SPO0064 SPO0065 SPO0066	1.20 1.00 0.88	0.181 0.934 0.414
SPO0067 SPO0068	1.45	0 0.191	SPO0067 SPO0068	1.39 1.17	0.042	SPO0067 SPO0068	0.98 0.79	0.705 0.027	SPO0067 SPO0068	0.89 1	0.731 0.069	SPO0067 SPO0068	0.78 0.66	0.010 0.005	SPO0067 SPO0068	0.75 0.67	0.000	SPO0067 SPO0068	1.10 1.00	0.449 0.944	SPO0067 SPO0068	1.01 1.01	0.877 0.772
SPO0069 SPO0070 SPO0071	0.89 0.95	0.809 0.367 0.944	SPO0069 SPO0070 SPO0071	1.06 0.9 0.85		SPO0069 SPO0070 SPO0071	0.88 0.78 0.76	0.557	SPO0069 SPO0070 SPO0071	0.68 0.92 0.99	0.225 0.602 0.742	SPO0069 SPO0070 SPO0071	0.83 0.92 0.24	0.214 0.969 0.000	SPO0069 SPO0070 SPO0071	0.85 0.88 0.27	0.119 0.836 0.000	SPO0069 SPO0070 SPO0071	1.10 1.00 0.84	0.934 0.376	SPO0069 SPO0070 SPO0071	1.03 0.99 0.84	0.783 0.961 0.479
SPO0072 SPO0073 SPO0074	1.43 1.1 1.3	0.009 0.447 0.029	SPO0072 SPO0073 SPO0074	1.33 1.02 1.1		SPO0072 SPO0073 SPO0074	0.65 0.82 0.79		SPO0072 SPO0073 SPO0074	0.78 0.93 0.65	0.85 0.727 0.01	SPO0072 SPO0073 SPO0074	1.04 1.23 0.75	0.422 0.489 0.216	SPO0072 SPO0073 SPO0074	1.07 1.18 0.68	0.130 0.371 0.019	SPO0072 SPO0073 SPO0074	1.14 1.12 1.24	0.586	SPO0072 SPO0073 SPO0074	1.13 1.08 1.11	0.069 0.725 0.027
SP00075 SP00076 SP00077	0.81 1.65 0.99	0.022 0.002 0.926	SPO0075 SPO0076 SPO0077	0.77 1.43 0.98	0.016 0.008	SPO0075 SPO0076 SPO0077	0.99 1.01 0.93	0.626 0.02	SPO0075 SPO0076 SPO0077	0.83 0.68 0.76	0.967 0.022 0.171	SPO0075 SPO0076 SPO0077	0.96 0.59 0.93	0.205 0.005 0.320	SPO0075 SPO0076 SPO0077	0.97 0.61 0.90	0.146 0.001 0.512	SPO0075 SPO0076 SPO0077	0.93 1.02 0.99	0.744 0.736	SPO0075 SPO0076 SPO0077	0.95 0.98 0.97	0.738 0.981 0.999
SPO0078 SPO0079	0.8 1.21	0.008 0.172	SPO0078 SPO0079	0.89 1.17	0.337 0.027	SPO0078 SPO0079	0.87 0.91	0.138 0.982	SPO0078 SPO0079	0.8	0.125 0.63	SPO0078 SPO0079	0.79 1.36	0.350 0.013	SPO0078 SPO0079	0.69 1.39	0.120	SPO0078 SPO0079	0.99 1.27	0.564 0.038	SPO0078 SPO0079	0.99 1.27	0.697 0.088
SPO0080 SPO0081 SPO0082	1.42 0.86 1.24	0.04 0.035	SPO0080 SPO0081 SPO0082	1.35 0.91 1.23	0.259 0.012	SPO0080 SPO0081 SPO0082	0.94 0.86 0.96	0.533 0.777	SPO0080 SPO0081 SPO0082	0.89 0.79	0.022 0.322 0.991	SPO0080 SPO0081 SPO0082	0.83 1.17 0.93	0.342 0.035 0.867	SPO0080 SPO0081 SPO0082	0.89 1.24 0.97	0.002 0.450	SPO0080 SPO0081 SPO0082	1.18 1.12 1.17	0.102 0.038	SPO0080 SPO0081 SPO0082	1.13 1.17 1.18	0.137 0.044 0.138
SPO0083 SPO0084 SPO0085	1.03 0.95 0.57		SPO0083 SPO0084 SPO0085	1.07 1.04 0.63	0.216	SPO0083 SPO0084 SPO0085	0.78 0.97 0.84	0.017	SPO0083 SPO0084 SPO0085	0.92 0.93	0.294 0.11 0.873	SPO0083 SPO0084 SPO0085	0.85 2.08 0.67	0.690 0.001 0.050	SPO0083 SPO0084 SPO0085	0.83 1.86 0.63	0.505 0.000 0.018	SPO0083 SPO0084 SPO0085	1.23 0.98 1.11	0.745	SPO0083 SPO0084 SPO0085	1.21 0.96 1.27	0.001 0.524 0.086
SPO0086 SPO0087 SPO0088	0.69 0.76 0.91	0.368	SPO0086 SPO0087 SPO0088	0.66 0.85 0.89	0.763	SPO0086 SPO0087 SPO0088	0.99 0.86 0.94	0.809	SPO0086 SPO0087 SPO0088	0.78 0.95 0.76	0.528 0.629 0.831	SPO0086 SPO0087 SPO0088	0.02 0.02 0.03	0.000 0.000 0.000	SPO0086 SPO0087 SPO0088	0.02 0.02 0.03		SPO0086 SPO0087 SPO0088	0.25 0.22 0.66	0.000 0.001	SPO0086 SPO0087 SPO0088	0.27 0.27 0.71	0.000 0.000 0.341
SPO0089 SPO0090	0.47 0.86	0.003 0.86	SPO0089 SPO0090	0.6 0.91	0.02 0.945	SPO0089 SPO0090	0.93 0.96	0.006 0.991	SPO0089 SPO0090	0.98 0.88	0.001 0.973	SPO0089 SPO0090	0.10 0.07	0.000 0.001	SPO0089 SPO0090	0.09 0.07	0.000	SPO0089 SPO0090	1.38 0.69	0.297 0.599	SPO0089 SPO0090	1.51 0.73	0.075 0.633
SPO0091 SPO0092 SPO0093	1.53 1.14 0.93	0.706 0.896	SPO0091 SPO0092 SPO0093	1.47 1.31 0.95	0.537 0.994	SPO0091 SPO0092 SPO0093	0.57 0.92 0.89	0.845 0.066	SPO0091 SPO0092 SPO0093	0.97 0.92 0.56	0.365 0.819 0.046	SPO0091 SPO0092 SPO0093	1.10 1.67 0.63	0.276 0.162 0.009	SPO0091 SPO0092 SPO0093	1.24 1.55 0.67	0.146	SPO0091 SPO0092 SPO0093	1.14 1.35 1.07	0.468 0.566	SPO0091 SPO0092 SPO0093	1.15 1.16 1.01	0.049 0.699 0.786
SPO0094 SPO0095 SPO0096	1.11 1 1.11	0.949 0.755	SPO0094 SPO0095 SPO0096	1.12 1.03 1.03	0.609	SPO0094 SPO0095 SPO0096	0.74 0.98 0.72	0.803	SPO0094 SPO0095 SPO0096	0.97 0.97 0.91	0.509 0.926 0.783	SPO0094 SPO0095 SPO0096	0.20 1.13 0.89	0.054 0.352 0.688	SPO0094 SPO0095 SPO0096	0.36 1.13 0.91	0.015 0.188 0.926	SPO0094 SPO0095 SPO0096	0.92 0.95 0.87	0.912	SPO0094 SPO0095 SPO0096	1.02 0.96 0.97	0.982 0.901 0.953
SPO0097 SPO0098 SPO0099	0.98 1.04 0.91	0.973 0.803	SPO0097 SPO0098 SPO0099	1.01 1 0.92	0.775 0.814	SPO0097 SPO0098 SPO0099	0.8 0.86	0.851 0.525	SPO0097 SPO0098 SPO0099	0.79 0.72 0.98	0.513 0.058 0.135	SPO0097 SPO0098 SPO0099	0.69 0.88 0.73	0.106 0.763 0.028	SPO0097 SPO0098 SPO0099	0.70 0.88 0.78	0.114 0.275 0.094	SPO0097 SPO0098 SPO0099	1.11 1.04 1.01	0.912	SPO0097 SPO0098 SPO0099	1.03 0.93 1.04	0.874 0.330 0.723
SP00100 SP00101	0.93 0.71	0.762 0.124	SP00100 SP00101	0.97 0.77	0.846	SP00100 SP00101	0.93	0.431 0.662	SPO0100 SPO0101	0.93 0.88	0.186 0.653	SPO0100 SPO0101	0.78 0.44	0.029 0.001	SPO0100 SPO0101	0.78 0.43	0.034	SPO0100 SPO0101	1.01 0.83	0.947 0.626	SP00100 SP00101	1.14 0.83	0.192 0.494
SP00102 SP00103 SP00104	0.52 0.68 0.76		SPO0102 SPO0103 SPO0104	0.53 0.66 0.75	0.046	SPO0102 SPO0103 SPO0104	0.98 0.95 0.93	0.145	SP00102 SP00103 SP00104	0.91 0.98 0.94	0.006 0.094 0.571	SPO0102 SPO0103 SPO0104	2.65 2.25 1.15	0.000 0.009 0.320	SPO0102 SPO0103 SPO0104	2.68 1.87 1.18	0.000 0.007 0.019	SPO0102 SPO0103 SPO0104	1.04 1.02 0.75	0.855	SP00102 SP00103 SP00104	0.98 0.97 0.82	0.903 0.884 0.036
SPO0105 SPO0106 SPO0107	0.79 1.1 0.93	0.358	SP00105 SP00106 SP00107	0.79 1.03 0.91	0.45	SPO0105 SPO0106 SPO0107	0.94 0.93	0.441	SP00105 SP00106 SP00107	0.96 0.85	0.82 0.634 0.714	SPO0105 SPO0106 SPO0107	0.93 1.65	0.766 0.010 0.273	SPO0105 SPO0106 SPO0107	0.99 1.59	0.004	SPO0105 SPO0106 SPO0107	0.97 1.12 0.95	0.445	SPO0105 SPO0106 SPO0107	0.95 1.13 0.97	0.370 0.372 0.931
SPO0108 SPO0109 SPO0110	0.95 0.9 1.12		SP00108 SP00109 SP00110	1.06 0.88 1.05	0.55	SPO0108 SPO0109 SPO0110	0.83 0.96 0.94	0.181	SP00108 SP00109 SP00110	0.94 0.86 0.91	0.06 0.636 0.11	SPO0108 SPO0109 SPO0110	1.07 0.72 0.62	0.926 0.061 0.005	SPO0108 SPO0109 SPO0110	0.93 0.70 0.76	0.035 0.006 0.032	SPO0108 SPO0109 SPO0110	1.19 1.24 1.28	0.193	SPO0108 SPO0109 SPO0110	1.13 1.19 1.19	0.457 0.289 0.185
SP00111 SP00112	0.83 0.71	0.193 0.088	SP00111 SP00112	0.93 0.7	0.78 0.045	SP00111 SP00112	0.96 0.85	0.118 0.219	SP00111 SP00112	0.95 0.92	0.34 0.463	SPO0111 SPO0112	0.49 0.24	0.003 0.000	SPO0111 SPO0112	0.49 0.26	0.015	SPO0111 SPO0112	0.95	0.701 0.069	SP00111 SP00112	0.94 1.25	0.721 0.399
SPO0113 SPO0114 SPO0115	1.03 0.81 1.14	0.519	SP00113 SP00114 SP00115	0.98 0.92 1.12	0.867 0.184	SP00113 SP00114 SP00115	0.87 0.95 0.93	0.282 0.499	SP00113 SP00114 SP00115	0.89 0.85 0.93	0.726 0.508 0.607	SPO0113 SPO0114 SPO0115	0.38 0.48 0.26	0.004	SPO0113 SPO0114 SPO0115	0.42 0.44 0.27	0.000	SPO0113 SPO0114 SPO0115	1.05 0.99 1.05	0.799 0.861	SP00113 SP00114 SP00115	1.08 0.93 1.16	0.742 0.774 0.114
SP00116 SP00118 SP00119	1.18 0.69 0.85	0.089	SP00116 SP00118 SP00119	1.25 0.78 0.86	0.254	SP00116 SP00118 SP00119	0.99 0.9 0.52	0.785	SP00116 SP00118 SP00119	0.94 0.95 0.81	0.778 0.831 0.084	SPO0116 SPO0118 SPO0119	0.39 1.19 1.88	0.000 0.633 0.004	SP00116 SP00118 SP00119	1.30 1.98		SPO0116 SPO0118 SPO0119	1.30 1.25 1.19	0.404	SP00116 SP00118 SP00119	1.09 1.13 1.16	0.556 0.676 0.303
SPO0120 SPO0122	1.2 1.19 0.55	0.336 0.324	SPO0120 SPO0122	1.11 1.17 0.62	0.551 0.002	SPO0120 SPO0122	0.95 0.78	0.256 0.013	SP00120 SP00122	0.85 0.97	0.448	SPO0120 SPO0122	0.77 0.66	0.117 0.024	SPO0120 SPO0122	0.68 0.68	0.066	SPO0120 SPO0122	0.88 0.92 0.75	0.257 0.562	SPO0120 SPO0122	0.78 0.95 0.85	0.089 0.657 0.154
SPO0123 SPO0124 SPO0125	0.81 0.96	0.957	SP00123 SP00124 SP00125	0.88 1.02	0.245 0.66	SPO0123 SPO0124 SPO0125	0.88 0.96	0.233 0.218	SP00124 SP00125	0.93 0.96 0.99	0.1 0.122 0.72	SPO0123 SPO0124 SPO0125	1.21 0.87 1.24	0.005 0.771 0.025	SPO0123 SPO0124 SPO0125	0.87 1.46	0.001 0.864 0.087	SPO0123 SPO0124 SPO0125	0.96 1.15	0.931 0.472	SP00123 SP00124 SP00125	0.96 1.06	0.863 0.824
SP00126 SP00127 SP00128	1.6 0.99 0.7	0.01	SPO0126 SPO0127 SPO0128	1.2 1.02 0.8	0.527 0.019	SPO0126 SPO0127 SPO0128	0.97 0.97 0.9	0.337 0.697	SPO0126 SPO0127 SPO0128	0.9 0.98 0.56	0.597 0.452 0.583	SPO0126 SPO0127 SPO0128	0.85 1.04 0.99	0.890 0.428 0.545	SPO0126 SPO0127 SPO0128	1.13 1.23 0.93		SPO0127 SPO0128	1.03 1.09 0.96	0.335 0.934	SPO0126 SPO0127 SPO0128	1.06 1.02 1.06	0.856 0.800 0.293
SP00129 SP00130 SP00131	0.96 0.59 1.47	0	SP00129 SP00130 SP00131	0.97 0.74 1.28	0.782	SPO0129 SPO0130 SPO0131	0.96 0.96 0.97	0.518	SP00129 SP00130 SP00131	0.91 0.71 0.96	0.295 0.434 0.204	SPO0129 SPO0130 SPO0131	0.88 1.06 1.21	0.311 0.004 0.017	SPO0129 SPO0130 SPO0131	0.96 1.06 1.23	0.786 0.004 0.009		0.97 0.88 1.17	0.868 0.056	SP00129 SP00130 SP00131	0.93 0.92 1.15	0.664 0.410 0.050
SP00132 SP00133 SP00134	0.98 0.98 1.08	0.771 0.943	SPO0132 SPO0133 SPO0134	0.99 0.93 1.03	0.653 0.608	SPO0132 SPO0133 SPO0134	0.96 0.88 0.98	0.637 0.232	SP00132 SP00133 SP00134	0.87 0.98 0.99	0.953 0.024 0.659	SPO0131 SPO0133 SPO0134	0.64 0.68 0.74	0.022 0.018	SPO0132 SPO0133 SPO0134	0.69 0.61 0.76	0.020	SPO0131 SPO0132 SPO0133 SPO0134	1.02 1.07 0.97	0.802 0.418	SPO0131 SPO0133 SPO0134	0.98 0.99 1.00	0.841 0.998 0.951
SP00134 SP00135 SP00136	1.08 1.52 0.89	0.012	SPO0134 SPO0135 SPO0136	1.03 1.34 0.91	0.006	SP00134 SP00135 SP00136	0.98 0.74 0.88	0.648	SP00134 SP00135 SP00136	0.99 0.98 0.96	0.659 0.028 0.155	SPO0134 SPO0135 SPO0136	0.74 0.51 1.17	0.000	SPO0134 SPO0135 SPO0136	0.76 0.54 1.23	0.000	SPO0134 SPO0135 SPO0136	0.97 1.20 0.98	0.152	SP00134 SP00135 SP00136	1.00 1.10 1.01	0.485 0.899

SP00137 SP00138	1.02	0.311 S	PO0137 PO0138	1.01 1.04	0.248	SP00137 SP00138	0.88 0.93	0.892 SPO013 0.51 SPO013	0.81			1.11	0.461 0.116	SPO0137 SPO0138	1.10	0.047	SPO0137 SPO0138	1.27 0.98	0.159 0.856	SP00137 SP00138	1.16	0.133 0.778
SPO0139 SPO0140 SPO0141	0.68 1.3 0.85	0.078 SI 0.19 SI	PO0139 PO0140 PO0141	0.74 1.23 0.89	0.031	SPO0139 SPO0140 SPO0141	0.9 0.93 0.81	0.13 SPO0139 0.15 SPO0149 0.547 SPO014	0.95	0.671 0.033 0.995	SPO0139 SPO0140 SPO0141	0.97 0.68 0.62	0.116 0.003 0.007	SPO0140 SPO0141	0.95 0.76 0.65	0.007 0.021 0.008	SPO0139 SPO0140 SPO0141	0.83 1.05 0.98	0.011 0.562 0.882	SPO0139 SPO0140 SPO0141	0.87 1.02 1.02	0.028 0.788 0.839
SP00142 SP00143 SP00144	1.04 0.68 1.49	0.047 SI	PO0142 PO0143 PO0144	0.81 0.77 1.34		SP00142 SP00143 SP00144	0.93 0.97 0.99	0.403 SPO0142 0.804 SPO0142 0.231 SPO0144	0.68	0.18 0.665 0.233	SPO0142 SPO0143 SPO0144	1.98 1.18 0.63	0.000 0.140 0.003	SPO0143 SPO0144	1.92 1.18 0.54	0.000 0.265 0.001	SPO0142 SPO0143 SPO0144	1.20 1.01 0.98	0.103 0.978 0.847	SP00142 SP00143 SP00144	1.16 1.04 0.93	0.054 0.852 0.690
SPO0145 SPO0146 SPO0147	0.88 0.78 1.5	0.034 SI	PO0145 PO0146 PO0147	0.98 0.81 1.37	0.129	SPO0145 SPO0146 SPO0147	0.78 0.59 0.74	0.009 SPO0148 0.932 SPO0148 0.524 SPO0147	0.88 0.94 0.84	0.016 0.055 0.321	SPO0145 SPO0146 SPO0147	1.53 1.06 0.72	0.003 0.318 0.037	SPO0145 SPO0146 SPO0147	1.58 1.22 0.76	0.000 0.171 0.052	SPO0145 SPO0146 SPO0147	1.28 1.17 1.03	0.404 0.075 0.698	SP00145 SP00146 SP00147	1.25 1.19 0.88	0.155 0.188 0.338
SPO0148 SPO0149 SPO0150	1.16 1.05	0.813 SI	PO0148 PO0149 PO0150	1.34 0.95 1.41	0.906	SPO0148 SPO0149 SPO0150	0.99 0.93 0.87	0.623 SPO014 0.916 SPO014 0.025 SPO015		0.541 0.853 0.008		1.15 1.89 0.72	0.020 0.024 0.080	SPO0148 SPO0149 SPO0150	1.04 1.88 0.66	0.025 0.014 0.019	SPO0148 SPO0149 SPO0150	1.07 1.12 1.19	0.571	SPO0148 SPO0149 SPO0150	1.00 1.10 1.01	0.832 0.633 0.807
SP00151 SP00152 SP00153	1.35 1.28 1.32	0.292 S 0.392 S	PO0151 PO0152 PO0153	1.26 1.24 1.39	0.015 0.485	SPO0151 SPO0152 SPO0153	0.85 0.92 0.9	0.286 SPO015 0.533 SPO015 0.001 SPO015	0.98	0.114 0.525 0.001	SPO0151	1.28 0.88 0.83	0.017 0.807 0.088	SPO0151 SPO0152 SPO0153	1.39 0.92 0.78	0.001	SPO0151 SPO0152 SPO0153	1.15 0.81 0.71	0.277 0.519	SPO0151 SPO0152 SPO0153	1.12 0.80 0.68	0.330 0.308 0.023
SPO0154 SPO0155	1.25 1.06	0.058 SI 0.52 SI	PO0154 PO0155	1.26 1.09	0.043	SPO0154 SPO0155	0.99 0.99	0.002 SPO015 0.906 SPO015	0.56	0.198	SPO0154 SPO0155	1.34 1.43	0.019 0.007	SPO0154 SPO0155	1.41 1.48	0.000	SPO0154 SPO0155	0.41 0.87	0.000 0.260	SPO0154 SPO0155	0.46 0.95	0.000 0.765
SP00156 SP00157 SP00160	1.12 1.23 1.28	0.035 SI 0.017 SI	PO0156 PO0157 PO0160	1.08 1.2 1.27	0.005	SP00156 SP00157 SP00160	0.87 0.9 0.53	0.574 SPO0156 0 SPO015 0.004 SPO0166	0.92 0.95 0.83	0.001	SPO0156 SPO0157 SPO0160	1.25 0.31 0.64	0.412 0.000 0.000	SPO0156 SPO0157 SPO0160	0.33 0.71	0.000	SPO0156 SPO0157 SPO0160	1.31 1.31 1.07	0.042 0.694	SP00156 SP00157 SP00160	1.10 1.39 1.04	0.784 0.001 0.659
SP00161 SP00162 SP00163	0.83 0.23 0.75	0.15 Si 0 Si 0.203 Si	PO0161 PO0162 PO0163	0.88 0.25 0.76	0.525 0 0.185	SPO0161 SPO0162 SPO0163	0.99 0.96 0.95	0.066 SPO016 0.199 SPO016 0.44 SPO016	0.98 0.89	0.151 0.285 0.793	SPO0161 SPO0162 SPO0163	1.05 1.64 0.99	0.228 0.002 0.900	SPO0161 SPO0162 SPO0163	0.94 1.64 1.07	0.836 0.002 0.529	SPO0161 SPO0162 SPO0163	1.16 1.20 1.30	0.140 0.159 0.403	SP00161 SP00162 SP00163	1.14 1.12 1.28	0.108 0.319 0.505
SPO0164 SPO0165 SPO0166	0.97 1.13 0.85	0.866 SI 0.192 SI	PO0164 PO0165 PO0166	1.03 1.11 0.89	0.081	SP00164 SP00165 SP00166	0.89 0.81 0.87	0.71 SPO016 0.683 SPO016 0.138 SPO016	0.91 0.85	0.536 0.394 0.284	SPO0164 SPO0165 SPO0166	1.63 1.59 1.75	0.020 0.003 0.000	SPO0164 SPO0165 SPO0166	1.70 1.61 1.63	0.006 0.003	SPO0164 SPO0165 SPO0166	1.09 0.95 0.84		SP00164 SP00165 SP00166	0.97 0.86 0.82	0.608 0.258
SPO0167 SPO0168 SPO0169	0.66 1.17 1.02	0.005 SI 0.008 SI	PO0167 PO0168 PO0169	0.74 1.2 1.13	0.005	SP00167 SP00168 SP00170	0.91 0.95 0.98	0.034 SP0016 0.23 SP0016 0.933 SP00170	0.95 0.98 0.88	0.036 0.383 0.92	SPO0168	2.63 1.77	0.001	SPO0168 SPO0168	1.82	0.000 0.002 0.000	SPO0167 SPO0168 SPO0169	0.82	0.044	SPO0167 SPO0168 SPO0169	0.86	0.039
SP00170 SP00171 SP00172	1.08 1.16 0.99	0.697 SI 0.045 SI	PO0170 PO0171 PO0172	1.19 1.24 0.78	0.279 0.011	SPO0171 SPO0172 SPO0173	0.97 0.71 0.69	0.86 SP0017 0.032 SP0017 0.904 SP0017	0.85	0.32 0.002	SPO0170 SPO0171	0.71 0.75 1.05	0.068 0.017 0.863	SPO0170 SPO0171 SPO0172	0.76 0.98 1.00	0.013 0.106 0.371	SPO0170 SPO0171 SPO0172	1.09 0.93 1.02	0.807 0.405 0.894	SPO0170 SPO0171 SPO0172	1.06 0.83 0.93	0.916 0.016 0.552
SP00173 SP00174	1.04 1.21	0.324 S 0.067 S	PO0173 PO0174	1.05 1.19	0.015 0.003	SPO0174 SPO0175	0.96 0.7	0.246 SPO0174 0.981 SPO0175	0.95	0.243 0.842	SPO0173 SPO0174	0.89	0.503 0.002	SPO0173 SPO0174	0.88	0.112	SPO0173 SPO0174	1.01 1.01	0.888	SP00173 SP00174	1.09 0.96	0.617 0.670
SP00175 SP00176 SP00177	0.93 0.89	0.996 SI	PO0175 PO0176 PO0177	1.32 0.88 1.02	0.362	SP00176 SP00177 SP00178	0.98 0.96 0.72	0.132 SPO0170 0.681 SPO0170 0.914 SPO0170	0.91 0.69 0.81	0.175 0.664 0.964	SPO0175 SPO0176 SPO0177	0.28 0.28 0.58	0.000 0.000 0.011	SPO0175 SPO0176 SPO0177	0.32 0.35 0.61	0.000 0.000 0.014	SPO0175 SPO0176 SPO0177	0.93 1.02 0.91	0.954	SP00175 SP00176 SP00177	0.85 0.96 0.95	0.098 0.701 0.669
SPO0178 SPO0179 SPO0180	1.1 0.81 0.85		PO0178 PO0179 PO0180	1.12 0.85 0.92	0.0	SPO0179 SPO0180 SPO0181	0.75 0.93 0.94	0.033 SP00179 0.006 SP0018 0.576 SP0018	0.88 0.67 0.97	0.002 0.29 0.686		0.36 0.23 0.22	0.342 0.000 0.000	SPO0178 SPO0179 SPO0180	0.42 0.27 0.28	0.404 0.000 0.000	SPO0178 SPO0179 SPO0180	0.81 1.15 1.00		SP00178 SP00179 SP00180	1.05 1.12 1.13	0.974 0.446 0.250
SP00181 SP00182 SP00183	0.92 0.8 1.12	0.346 SI	PO0181 PO0182 PO0183	1.02 0.65 1.06	0.013	SPO0182 SPO0183 SPO0184	0.93 0.99 0.96	0.012 SPO018 0.68 SPO018 0.634 SPO018	0.94 0.98 0.94	0.109 0.613 0.694	SPO0181 SPO0182 SPO0183	0.14 0.33 0.60	0.000 0.000 0.269	SPO0181 SPO0182 SPO0183	0.13 0.37 0.56	0.000 0.000 0.221	SPO0181 SPO0182 SPO0183	1.03 1.05 0.77	0.924	SP00181 SP00182 SP00183	0.93 1.08 0.80	0.429 0.805 0.640
SP00184 SP00185 SP00186	1.14 1.34 0.95		PO0184 PO0185 PO0186	1.17 1.13 0.89	0.471 0.546 0.239	SPO0185 SPO0186 SPO0187	0.89 0.94 0.95	0.252 SP0018 0.011 SP0018 0.425 SP0018	0.74 0.79 0.88	0.196 0.087 0.842	SPO0184 SPO0185 SPO0186	0.78 0.93 0.68	0.411	SPO0184 SPO0185 SPO0186	0.77 1.04 0.70	0.311	SPO0184 SPO0185 SPO0186	1.20 1.50 1.51	0.492 0.046 0.060	SPO0184 SPO0185 SPO0186	1.22 1.56 1.54	0.436 0.022
SPO0187 SPO0188	0.8 1.22	0.259 SI 0.026 SI	PO0187 PO0188	0.99 1.16	0.933 0.047	SPO0188 SPO0189	1 0.98	0.058 SPO018 0.566 SPO018	0.93	0.089 0.536	SPO0187 SPO0188	0.56 0.62	0.050	SPO0187 SPO0188	0.63 0.63	0.291	SPO0187 SPO0188	0.72 0.97	0.227 0.221	SP00187 SP00188	0.78 0.95	0.280 0.565
SPO0189 SPO0190 SPO0191	1.02 0.97 1	0.789 SI 0.86 SI	PO0189 PO0190 PO0191	0.95 1.02 0.94	0.643 0.999	SPO0190 SPO0191 SPO0192	0.99 0.96 0.9	0.125 SPO019 0.995 SPO019 0.913 SPO019	0.97 0.88 0.93	0.369 0.959 0.598	SPO0189 SPO0190 SPO0191	0.79 0.70 0.54	0.183 0.155 0.053	SPO0189 SPO0190 SPO0191	0.88 0.70 0.55	0.015 0.038 0.023	SPO0189 SPO0190 SPO0191	0.95 0.89 0.87	0.656 0.590	SPO0189 SPO0190 SPO0191	0.99 0.86 0.84	0.876 0.561 0.421
SPO0192 SPO0193 SPO0194	0.86 1	0.733 SI	PO0192 PO0193 PO0194	0.94 1.05 0.93	0.963 0.643 0.989	SPO0193 SPO0194 SPO0195	0.93 0.98 0.67	0.853 SPO019 0.725 SPO019 0.832 SPO019	0.96	0.819 0.882 0.751	SPO0192 SPO0193 SPO0194	0.25 0.43 0.63	0.000 0.020 0.049	SPO0192 SPO0193 SPO0194	0.31 0.47 0.63	0.002 0.003 0.053	SPO0192 SPO0193 SPO0194	0.93 1.09 1.03	0.631 0.847 1.000	SPO0192 SPO0193 SPO0194	0.91 0.99 1.02	0.565 0.869 0.992
SPO0195 SPO0196 SPO0197	1.18 0.91 1.35	0.912 SI	PO0195 PO0196 PO0197	1.26 0.97 1.13	0.007 0.977 0.288	SPO0196 SPO0197 SPO0198	0.79 0.8 0.95	0.755 SPO019 0.822 SPO019 0.622 SPO019	0.91 0.96 0.9	0.725 0.316 0.74	SPO0195 SPO0196 SPO0197	0.74 0.74 0.12	0.017 0.498 0.000	SPO0195 SPO0196 SPO0197	1.03 0.72 0.16	0.122 0.448 0.000	SPO0195 SPO0196 SPO0197	1.00 0.90 1.11	0.780 0.842 0.862	SPO0195 SPO0196 SPO0197	0.97 1.01 0.87	0.501 0.992 0.463
SPO0198 SPO0199 SPO0200	0.99 1.22 0.71	0.033 SI	PO0198 PO0199 PO0200	1.08 1.08 0.88	0.695 0.178 0.876	SPO0199 SPO0200 SPO0201	0.96 0.75 0.91	0.693 SPO0199 0.406 SPO0209 0.939 SPO0209	0.93 0.95 0.93	0.706 0.82 0.749	SPO0199	0.15 0.15 0.38	0.002 0.001 0.031	SPO0198 SPO0199 SPO0200	0.16 0.18 0.38	0.001 0.000 0.000	SPO0198 SPO0199 SPO0200	0.94 0.60 1.00	0.726 0.142	SPO0198 SPO0199 SPO0200	0.98 0.65 1.11	0.851 0.114 0.805
SPO0201 SPO0202 SPO0203	0.97 0.99 1.03	0.773 SI	PO0201 PO0202 PO0203	1.06 0.9 1.14		SPO0202 SPO0203 SPO0204	0.83 0.87 0.78	0.036 SPO020 0.39 SPO020 0.93 SPO020	0.64	0.041 0.249 0.804	SPO0201	0.19 0.21 0.27	0.001 0.000	SPO0201 SPO0202	0.22 0.29 0.32	0.000	SPO0201 SPO0202 SPO0203	1.09 1.23	0.851	SPO0201 SPO0202 SPO0203	1.06 1.11 0.96	0.878 0.587 0.672
SPO0204 SPO0205	1.2 1.02	0.131 SI 0.55 SI	PO0204 PO0205	1.17 0.77	0.258	SPO0205 SPO0206	0.82 0.89	0.286 SPO020 0.393 SPO020	0.7	0.068 0.364	SPO0205	0.40 0.87	0.001	SPO0203 SPO0204 SPO0205	0.50 1.02	0.000	SPO0204 SPO0205	0.88 0.86	0.543 0.604	SPO0204 SPO0205	1.00 1.15	0.757 0.295
SPO0206 SPO0207 SPO0209	0.93 1.18 1.11	0.036 SI	PO0206 PO0207 PO0209	0.94 1.1 1.08	0.032 0.191	SPO0207 SPO0209 SPO0210	0.82 0.97 0.91	0.003 SPO0201 0.087 SPO0201 0.624 SPO0211	0.76 0.88 0.78	0.013 0.017 0.654	SPO0206 SPO0207 SPO0209	0.84 0.79 0.79	0.415 0.160 0.014	SPO0206 SPO0207 SPO0209	0.86 1.01 0.83	0.079 0.494 0.018	SPO0206 SPO0207 SPO0209	0.99 1.00 1.01	0.745 0.946	SPO0206 SPO0207 SPO0209	1.00 0.96 0.89	0.924 0.682 0.104
SPO0210 SPO0211 SPO0212	1.28 1.03 0.69	0.371 SI 0.241 SI	PO0210 PO0211 PO0212	1.31 1.05 0.76	0.001 0.134 0.464	SP00211 SP00212 SP00213	0.92 0.84 0.89	0.359 SPO021 0.985 SPO021 0.669 SPO021	0.83 0.88 0.78	0.096 0.988 0.67	SPO0210 SPO0211 SPO0212	0.81 1.47 0.90	0.115 0.056 0.360	SPO0210 SPO0211 SPO0212	0.72 1.61 1.05	0.025 0.004 0.990	SPO0210 SPO0211 SPO0212	1.17 1.01 0.94	0.011 0.735 0.663	SPO0210 SPO0211 SPO0212	1.08 1.00 1.03	0.140 0.808 0.926
SPO0213 SPO0214 SPO0215	0.99 1.2 1.73	0.278 SI	PO0213 PO0214 PO0215	0.85 1.14 1.58	0.715 0.304 0.005	SPO0214 SPO0215 SPO0216	0.88 0.93 0.94	0.053 SPO0214 0.35 SPO0215 0.108 SPO0216	0.91 0.83 0.93	0.153 0.792 0.336	SPO0213 SPO0214 SPO0215	1.24 1.17 0.70	0.315 0.212 0.014	SPO0213 SPO0214 SPO0215	1.24 1.19 0.68	0.520 0.183 0.012	SPO0213 SPO0214 SPO0215	1.01 0.88 1.17	0.973 0.435 0.164	SP00213 SP00214 SP00215	0.95 0.80 1.00	0.934 0.186 0.829
SP00216 SP00217 SP00218	1.34 0.8 1.07	0.293 SI	PO0216 PO0217 PO0218	1.46 0.74 1.03	0.175 0.172	SP00217 SP00218 SP00219	0.93 0.98 0.95	0.936 SPO021 0.013 SPO0218 0.003 SPO0219	0.91 0.93 0.89	0.69	SPO0216 SPO0217 SPO0218	0.99 1.10 0.75	0.398 0.848 0.001	SPO0216 SPO0217 SPO0218	0.88 1.20 0.74	0.774 0.530 0.000	SPO0216 SPO0217 SPO0218	1.06 0.53 0.88	0.674 0.349 0.120	SP00216 SP00217 SP00218	1.05 1.05 0.95	0.414 0.954 0.383
SPO0219 SPO0220 SPO0221	1.08 1.67 1.42	0.012 SI 0.002 SI	PO0219 PO0220 PO0221	1.11 1.57 1.26		SP00220 SP00221 SP00222	0.95 0.93 0.88	0.169 SPO022 0.629 SPO022 0.003 SPO022	0.89 0.98	0.529 0.826		0.97 1.11 1.25	0.007 0.010 0.262	SPO0219 SPO0220 SPO0221	1.01 1.14 1.20	0.000 0.295 0.482	SPO0219 SPO0220 SPO0221	1.07 1.09 1.23	0.025 0.442 0.499	SPO0219 SPO0220 SPO0221	1.01 1.08 1.16	0.561 0.734 0.596
SP00222 SP00223 SP00224	0.25 1.06 0.85	0 SI	PO0222 PO0223 PO0224	0.24 1.07 0.87	0.067	SPO0223 SPO0224 SPO0225	0.95 0.8 0.81	0.382 SPO022 0.96 SPO022 0.421 SPO022	0.93		SPO0222 SPO0223 SPO0224	0.03 1.58 1.12	0.000 0.003 0.192	SPO0222 SPO0223 SPO0224	0.03 1.65 1.02	0.000 0.000 0.218	SPO0222 SPO0223 SPO0224	6.31 0.97	0.002 0.781	SPO0222 SPO0223 SPO0224	5.29 0.99 1.04	0.000 0.888 0.738
SPO0225 SPO0226	0.97 1.53	0.791 SI 0.005 SI	PO0225 PO0226	1.14 1.52	0.041 0.019	SPO0226 SPO0227	0.7 0.9 0.85	0.419 SPO022 0.001 SPO022	0.81 1.02	0.634 0.067	SPO0225 SPO0226	1.32	0.137 0.165	SPO0225 SPO0226	1.22	0.291	SPO0225 SPO0226	1.23 1.12	0.388 0.750	SPO0225 SPO0226	1.16 0.96	0.567 0.712
SPO0227 SPO0228 SPO0229	0.88 1.22	0.826 SI 0.198 SI	PO0227 PO0228 PO0229	1.37 0.89 1.26	0.726	SPO0228 SPO0229 SPO0230	0.99 0.97	0.184 SPO0229 0.101 SPO023	0.65	0.04 0.008	SPO0228 SPO0229	0.86 1.08	0.000 0.276 0.000	SPO0227 SPO0228 SPO0229	0.70 0.91	0.000 0.023 0.029	SPO0227 SPO0228 SPO0229	1.00 0.70 1.07	0.040	SPO0227 SPO0228 SPO0229	0.96 0.65 0.96	0.992 0.101 0.993
SPO0230 SPO0231 SPO0232	0.93 1.63 0.76	0.002 SI 0.018 SI	PO0230 PO0231 PO0232	0.91 1.5 0.81	0.034	SP00231 SP00232 SP00233	0.93 0.58 0.86	0.144 SPO023 0.653 SPO023 0.872 SPO023	0.98	0.726 0.929	SPO0231	0.83 0.88	0.125 0.143 0.801	SPO0230 SPO0231 SPO0232	1.33 0.83 0.83	0.265 0.722	SPO0230 SPO0231 SPO0232	1.08 1.00 0.87	0.855 0.259	SPO0230 SPO0231 SPO0232	1.06 1.02 0.83	0.445 0.581 0.069
SPO0233 SPO0234 SPO0235	1.05 0.81 0.94	0.468 SI	PO0233 PO0234 PO0235	1.01 0.81 1.02	0.649	SPO0234 SPO0235 SPO0236	0.77 0.84 0.81	0.936 SPO023 0.255 SPO023 0.249 SPO023	0.94 0.99 0.53	0.872 0.162 0.48	SPO0233 SPO0234 SPO0235	1.40 0.36 0.49	0.103 0.005 0.037	SPO0233 SPO0234 SPO0235	1.35 0.39 0.52	0.088 0.017 0.058	SPO0233 SPO0234 SPO0235	0.85 0.94		SPO0233 SPO0234 SPO0235	1.17 0.86 0.91	0.094 0.566 0.574
SP00236 SP00237 SP00238	0.91 0.8 0.82	0.413 SI	PO0236 PO0237 PO0238	0.82 0.87 0.95	0.542 0.394 0.95	SPO0237 SPO0238 SPO0239	0.53 0.68 0.98	0.782 SPO023 0.869 SPO023 0.452 SPO023	0.98 0.85	0.406 0.975 0.726	SPO0237	1.07 1.22 1.31	0.796 0.186 0.191	SPO0236 SPO0237 SPO0238	1.08 1.37 1.36	0.869 0.065 0.144	SPO0236 SPO0237 SPO0238	1.10 0.91 0.98	0.876 0.748 0.833	SP00236 SP00237 SP00238	1.03 1.05 1.05	0.895 0.902 0.903
SPO0239 SPO0240 SPO0241	0.97 0.63	0.914 SI 0.002 SI	PO0239 PO0240 PO0241	0.98 0.69 1.03	0.891	SP00240 SP00241 SP00247	0.95 0.78 0.83	0.863 SPO024 0.925 SPO024 0.483 SPO024	0.81 0.85 0.52	0.168 0.896	SPO0239 SPO0240	1.07 1.35 1.14	0.908 0.002 0.791	SPO0239 SPO0240	1.06 1.35 1.06		SPO0239 SPO0240 SPO0241	0.89 0.84 0.94	0.496	SPO0239 SPO0240 SPO0241	0.88 0.94 0.93	0.510 0.543 0.829
SPO0247 SPO0248 SPO0249	1.07 1.22 1.08	0.452 SI 0.586 SI	PO0247 PO0248 PO0249	1.2 1.24 1.08	0.192 0.707	SPO0248 SPO0249 SPO0250	0.98 0.78 0.88	0.782 SPO024 0.436 SPO024 0.496 SPO025	0.65	0.78 0.588	SPO0247 SPO0248	1.59 0.88 0.96	0.081 0.883 0.647	SPO0247 SPO0248 SPO0249	1.37 0.85 0.98	0.263	SPO0247 SPO0248 SPO0249	0.89 1.05	0.189 0.892	SPO0247 SPO0248 SPO0249	0.95 1.06	0.801 0.861 0.844
SPO0250 SPO0251	0.89 0.74	0.53 SI 0.032 SI	PO0250 PO0251 PO0252	0.9 0.85	0.601 0.046	SPO0251 SPO0252 SPO0253	0.83 0.94 0.83	0.735 SPO025 0.322 SPO025 0.169 SPO025	0.81	0.862 0.346 0.316	SPO0250 SPO0251	1.00 1.07 0.57	0.739 0.295 0.002	SPO0250 SPO0251 SPO0252	1.06 1.04 0.56	0.382 0.473 0.000	SPO0250 SPO0251 SPO0252	0.90 0.90 0.79	0.495 0.566	SPO0250 SPO0251 SPO0252	0.93 0.89 0.84	0.610 0.445 0.258
SPO0252 SPO0253 SPO0254	1.03 1.1 0.56	0.19 SI	PO0253 PO0254	1.16 0.61	0.216 0.014	SPO0254 SPO0255	0.88 0.67	0.457 SPO025 0.092 SPO025	0.72	0.276 0.056	SPO0253 SPO0254	1.05 0.17	0.024 0.000	SPO0253 SPO0254	1.08 0.17	0.123 0.000	SPO0253 SPO0254	1.00 1.12	0.807 0.386	SPO0253 SPO0254	0.98 1.02	0.993 0.782
SPO0255 SPO0256 SPO0257	1.13 0.83 1.12	0.097 SI	PO0255 PO0256 PO0257	1.13 0.96 0.99	0.835	SP00256 SP00257 SP00258	0.85 0.85 0.93	0.905 SPO025 0.279 SPO025 0.953 SPO025	0.83	0.804 0.626 0.956	SPO0256	0.23 1.06 0.75	0.000 0.794 0.084	SPO0255 SPO0256 SPO0257	0.23 0.97 0.79	0.000 0.530 0.313	SPO0255 SPO0256 SPO0257	0.89 1.10 0.81	0.681	SPO0255 SPO0256 SPO0257	0.85 1.21 0.86	0.080 0.181 0.671
SPO0258 SPO0259 SPO0260	1.05 0.93 1.06	0.949 SI	PO0258 PO0259 PO0260	0.96 1.06 1.09	0.073	SPO0259 SPO0260 SPO0261	0.9 0.93 0.96	0.048 SPO0259 0.003 SPO0269 0.459 SPO026	0.61	0.071 0.015 0.99	SPO0259	0.88 1.53 1.72	0.834 0.091 0.007	SPO0258 SPO0259 SPO0260	0.88 1.44 1.70	0.879 0.011 0.001	SPO0258 SPO0259 SPO0260	0.99 1.51 0.92	0.033	SPO0258 SPO0259 SPO0260	1.05 1.28 0.85	0.801 0.029 0.054
SPO0261 SPO0262 SPO0263	1.37 1.19 1.17	0.039 SI	PO0261 PO0262 PO0263	1.31 1.12 1.05		SPO0262 SPO0263 SPO0264	0.98 1 0.85	0.594 SPO026 0.74 SPO026 0.115 SPO026		0.078 0.847 0.024	SPO0261 SPO0262 SPO0263	1.28 0.96 0.93	0.014 0.333 0.626	SPO0261 SPO0262 SPO0263	1.16 0.95 1.19		SPO0261 SPO0262 SPO0263	1.12 0.94 1.22	0.622	SP00261 SP00262 SP00263	1.07 0.91 1.03	0.661 0.229 0.986
SPO0264 SPO0265	1.3 1.55 1.42	0.292 SI 0.425 SI	PO0263 PO0264 PO0265 PO0266	1.32 1.49 1.34	0.003 0.354	SPO0265 SPO0266 SPO0267	0.83 0.82 0.9	0.977 SPO026 0.708 SPO026	0.87	0.916 0.377	SPO0264	0.60 0.84 0.92	0.000 0.656 0.331	SPO0264 SPO0265	0.57 0.89 0.99	0.000 0.721	SPO0264 SPO0265 SPO0266	1.07 1.15 0.94		SPO0264 SPO0265 SPO0266	1.05 1.06 0.91	0.494 0.933 0.588
SPO0266 SPO0267 SPO0268	0.93 0.87	0.289 SI 0.758 SI	PO0267 PO0268	1.03 0.98	0.394 0.916	SPO0268 SPO0269	0.98 0.71	0.998 SPO0269 0.49 SPO0269	0.99	0.886 0.324	SPO0267 SPO0268	1.25 1.04	0.055 0.840	SPO0266 SPO0267 SPO0268	1.16 1.01	0.083 0.949	SPO0267 SPO0268	0.95 1.05	0.615 0.889	SPO0267 SPO0268	1.04 0.97	0.515 0.890
SPO0269 SPO0270 SPO0271	0.98 1.03 0.91	0.334 SI 0.494 SI	PO0269 PO0270 PO0271	1.06 0.95 1.02	0.723	SP00270 SP00271 SP00272	0.94 0.93 0.53	0.323 SPO027 0.603 SPO027 0.095 SPO027	0.85		SPO0270 SPO0271	1.29 1.11 1.86	0.014 0.012 0.001	SPO0269 SPO0270 SPO0271	1.23 1.09 1.60	0.001	SPO0269 SPO0270 SPO0271	1.00 0.96 0.94	0.640 0.776	SPO0269 SPO0270 SPO0271	1.03 0.96 0.94	0.739 0.864 0.757
SP00272 SP00273 SP00274	1 1.78 0.74	0.011 Si 0.258 Si	PO0272 PO0273 PO0274	1.09 1.59 0.82	0.482	SP00273 SP00274 SP00275	0.93 0.97 0.87	0.336 SPO0273 0.575 SPO0274 0.001 SPO0275	1.01	0.34 0.221 0.005	SPO0273 SPO0274	1.45 0.93 0.79	0.000 0.682 0.164	SPO0272 SPO0273 SPO0274	1.37 1.02 0.93	0.001 0.378 0.167	SPO0272 SPO0273 SPO0274	0.80 1.02 0.61	0.644	SPO0272 SPO0273 SPO0274	0.89 1.04 0.63	0.300 0.675 0.012
SPO0275 SPO0276 SPO0277	1.1 1.35 1.15	0.183 SI	PO0275 PO0276 PO0277	1.08 1.18 1.24		SP00276 SP00277 SP00278	0.97 0.84 0.87	0.259 SPO0270 0.11 SPO0277 0.969 SPO0270	0.73	0.163 0.354 0.7	SPO0276	0.63 0.86 1.38	0.008 0.130 0.015	SP00275 SP00276 SP00277	0.68 0.82 1.36	0.007 0.002 0.003	SPO0275 SPO0276 SPO0277	0.84 0.95 1.12		SP00275 SP00276 SP00277	0.81 0.94 1.12	0.050 0.333 0.463
SPO0278 SPO0280 SPO0281	1.5 1.63 0.54	0.003 SI 0 SI	PO0278 PO0280 PO0281	1.47 1.56 0.58	0.003	SPO0280 SPO0281 SPO0282	0.94 0.74 0.71	0.001 SPO028 0.029 SPO028 0.309 SPO028	0.96	0.041 0.281 0.226	SPO0278	1.20 1.50 0.50	0.073 0.004 0.003	SPO0278 SPO0280 SPO0281	1.21 1.37 0.49	0.004 0.004 0.001	SPO0278 SPO0280 SPO0281	1.03 0.99 1.38	0.787 0.651	SPO0278 SPO0280 SPO0281	0.98 0.99 1.26	0.899 0.600 0.136
SPO0282 SPO0283	1.3 1.29 1.03	0.01 SI 0.364 SI	PO0282 PO0283	1.22 1.1	0.008 0.56	SPO0283 SPO0284	0.71 0.79 0.88 0.88	0.876 SPO028 0.326 SPO028	0.78	0.911 0.097	SPO0283	1.42 0.67	0.082 0.210	SPO0281 SPO0282 SPO0283	1.39 0.63	0.010 0.209	SPO0282 SPO0283	1.32 0.87	0.176 0.623	SPO0282 SPO0283	1.12 0.92	0.463 0.773
SPO0284	1.03	0.619 SI	PUU284	1.18	0.065	SPO0285	0.88	0.388 SPO028	0.84	0.368	SPO0284	1.27	0.007	SPO0284	1.26	0.000	SPO0284	1.07	0.455	SP00284	1.11	0.104

SPOUZET 1.62 0 SPOUZET 1.66 0 SPOUZET 1.66 SPOUZET 1.67 0 0.74 SPOUZET 1.06 0.74 0.327 SPOUZET 1.06 0.512 SPOUZET 1.06 0.512 SPOUZET 1.07 0.513 SPOUZET 1.07 0.513 SPOUZET 1.07 0.513 SPOUZET 0.513 S	0.90 0.620 0.83 0.756 1.06 0.381 1.05 0.639 1.01 0.962 1.02 0.942
SPO0282 1.09	1.01 0.962 1.02 0.942
SPO0295 1.32 0.38 SPO0295 1.25 0.08 SPO0295 0.71 0.387 SPO0295 0.97 0.372 SPO0295 0.61 0.002 SPO0295 0.60 0.000 SPO0295 0.75 0.311 SPO0295 0.61 0.057 SPO0295 0.61 0.055 SPO0297 0.99 0.60 SPO0295 0.61 0.057 SPO0295 0.61 0.055	
SPO0298 1.2 0.197 SPO0298 1.23 0.098 SPO0299 0.96 0.707 SPO0299 0.95 0.746 SPO0298 0.96 0.740 SPO0298 0.90 0.480 SPO0298 0.90 0.480 SPO0298 0.95 0.746 SPO0299 0.116 0.115 SPO0299 0.117 0.452 SPO0299 0.111 0.115	1.10 0.152 0.98 0.997 0.75 0.325
\$\begin{array}{cccccccccccccccccccccccccccccccccccc	1.00 0.961 0.88 0.384 1.00 0.932
\$\begin{array}{cccccccccccccccccccccccccccccccccccc	0.97 0.467 1.00 0.960 1.12 0.764
\$\text{SPO3097}\$ 0.81 0.731 \$\text{\$\$\$\$}}}\text{\$\$\text{\$\tex{\$\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\}\$\$\$}\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\e	1.04 0.133 1.02 0.875 0.99 0.974
SP00310 1.15 0.255 SP00310 0.99 0.82 SP00311 0.94 0.199 SP00311 0.83 0.293 SP00310 0.74 0.226 SP00310 0.73 0.147 SP00310 0.81 0.124 SP00310 SP00311 1.27 0.089 SP00311 1.23 0.14 SP00312 0.85 0.768 SP00312 0.75 0.911 SP00311 1.12 0.370 SP00311 1.12 0.370 SP00311 1.01 0.967 SP00311	1.01 0.813 0.91 0.899 1.08 0.367
	1.02 0.870 0.83 0.140 1.03 0.865
SPU0312 U.75 U.234 SPU0312 U.75 U.234 SPU0313 U.75 U.234 SPU0313 U.75 U.234 SPU0313 U.75 U.75 SPU0312 U.75 SPU0312 U.75 U.75 U.75 U.75 U.75 U.75 U.75 U.75	1.04 0.390 1.36 0.008 0.87 0.361
\$\text{SPO0315}\$ 0.61 \(\text{0.04} \) \$\text{SPO0315}\$ 0.67 \(\text{0.001} \) \$\text{SPO0316}\$ 0.95 \(\text{0.478} \) \$\text{SPO0316}\$ 0.78 \(\text{0.62} \) \$\text{SPO0315}\$ 0.72 \(\text{0.031} \) \$\text{SPO0315}\$ 0.73 \(\text{0.016} \) \$\text{SPO0315}\$ 0.96 \(\text{0.808} \) \$\text{SPO0315}\$ 0.78 \(\text{SPO0316} \) \$\text{0.72}\$ \$\text{SPO0316}\$ 0.78 \(\text{0.623} \) \$\text{SPO0315}\$ 0.78 \(\text{0.0315} \) \$\text{SPO0316}\$ 0.78 \(\text{0.0315} \) \$\text{SPO0316}\$ 0.78 \(\text{0.0315} \) \$\text{SPO0317}\$ 0.78 \(\text{SPO0316} \) \$\text{0.0315}\$ 0.79 \(\text{0.0315} \) \$\text{SPO0317}\$ 0.78 \(\text{SPO0316} \) \$\text{0.0315}\$ 0.78 \(\text{0.0315} \) \$\text{SPO0317}\$ 0.78 \(\text{SPO0316} \) \$\text{0.0315}\$ 0.78 \(\text{0.0315} \) \$\text{SPO0317}\$ 0.78 \(\text{SPO0316} \) \$\text{0.0315}\$ 0.78 \(\text{0.0315} \) \$0.031	0.93 0.514 0.93 0.738 0.98 0.931
\$P00318 1.3 0 \$P00318 1.28 0.001 \$P00319 0.97 0.064 \$P00320 0.93 0.17 \$P00318 1.13 0.019 \$P00318 1.13 0.052 \$P00318 0.92 0.402 \$P00318 \$P00319 1.44 0.003 \$P00319 1.47 0 \$P00320 0.94 0.903 \$P00320 0.94 0.903 \$P00320 0.91 0.903 \$P00320 1.92 0.018 \$P00320 1.92 0.018 \$P00320 1.92 0.918 \$P00320 1.92 0.	0.90 0.289 1.12 0.255 1.12 0.590
\$\overline{\text{SPO0321}}\$ 1.2 0.41 \begin{small} \text{SPO0321} & 1.19 0.246 \begin{small} \text{SPO0322} & 0.91 0.182 \begin{small} \text{SPO0322} & 0.98 0.063 \begin{small} \text{SPO0321} & 1.00 0.004 \begin{small} \text{SPO0321} & 1.03 0.516 \begin{small} \text{SPO0321} & 1.20 0.251 \begin{small} \text{SPO0322} & 0.96 0.024 \begin{small} \text{SPO0322} & 0.98 0.063 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0322} & 0.98 0.003 \begin{small} \text{SPO0323} & 0.98	1.09 0.539 0.76 0.010 1.63 0.005
SP00324 1.2 0.014 SP00324 1.16 0.006 SP00325 0.83 0.192 SP00325 0.94 0.116 SP00324 1.12 0.171 SP00324 1.14 0.111 SP00324 1.04 0.785 SP00324 SP00325 0.77 0.066 SP00325 0.75 0.016 SP00325 0.85 0.85 0.289 SP00326 0.81 0.308 SP00325 1.07 0.052 SP00325 1.00 0.088 SP00325 0.97 0.999 SP00325 0.999 0.999 SP00325 0.999 0.999 SP00325 0.999 0.999 SP00325 0.999 SP00325 0.999 0.999 SP00325 0.999 SP003	1.06 0.257 1.00 0.767 1.07 0.001
\$P00327 0.88 0.80 \$P00327 0.89 0.737 \$P00328 0.78 0.003 \$P00328 0.9 0.002 \$P00327 0.47 0.015 \$P00327 0.61 0.001 \$P00327 1.03 0.966 \$P00327 \$P00327 0.61 0.001 \$P00327 0.001 \$P00329 0.9 0.002 \$P00329 0.9 0.002 \$P00329 0.9 0.002 \$P00329 0.9 0.002 \$P00329 0.9 0.003 \$P000329 0.9 0.0	0.92 0.560 0.63 0.004 0.68 0.016
\$P00330 1.28 0.109 \$P00330 1.22 0.265 \$P00331 0.92 0.447 \$P00331 0.79 0.096 \$P00330 1.19 0.301 \$P00330 1.29 0.165 \$P00330 0.39 0.000 \$P00330 \$P00331 1.07 0.139 \$P00331 1.04 0.331 \$P00332 0.88 0.698 \$P00332 0.98 0.435 \$P00331 0.72 0.012 \$P00331 0.74 0.010 \$P00331 1.12 0.283 \$P00331 0.79 0.789 \$P00332 0.98 0.789 \$P0	0.33 0.004 1.10 0.176 1.04 0.497
SP00333 1.32 0.187 [SP00333 1.18 0.224 [SP00334 0.85 0.239 [SP00334 0.9 0.182 [SP00333 0.59 0.441 [SP00333 0.55 0.011 [SP00333 0.86 0.716 [SP00333 SP00334 1.2] 0.125 [SP00335 0.79 0.466 [SP00335 0.99 0.485 [SP00334 1.59 0.002 [SP00334 1.83 0.002 [SP00334 1.5] 0.002 [SP00334 1.5] 0.002 [SP00334 1.5] 0.002 [SP00334 1.5] 0.002 [SP00335 0.83 0.416 [SP00335 0.83 0.416 [SP00335 0.85] 0.85 0.35 [SP00335 0.85 0.85] 0.016 [SP00335 0.85 0.85 0.85 0.85] 0.016 [SP00335 0.85 0.85 0.85 0.85] 0.016 [SP00335 0.85 0.85 0.85 0.85] 0.016 [SP00335 0.85 0.85 0.85 0.85] 0.016 [SP00335 0.85 0.85 0.85] 0.016 [SP00335 0.85 0.85 0.85] 0.016 [SP00335 0.85 0.85] 0.016 [SP00335 0.85 0.85] 0.016 [SP00335 0.85 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00335 0.85] 0.016 [SP00355 0.85] 0.016 [0.86 0.596 1.26 0.032 0.97 0.913
\$P00336 1.08 0.142 \$P00336 1.05 0.286 \$P00337 0.81 0.847 \$P00337 0.95 0.877 \$P00336 0.89 0.643 \$P00336 0.88 0.575 \$P00336 1.00 0.801 \$P00338 \$P00337 1.37 0.001 \$P00337 1.24 0.104 \$P00338 0.72 0.689 \$P00338 0.85 0.335 \$P00337 0.97 0.676 \$P00337 0.94 0.773 \$P00337 1.10 0.217 \$P00337 1.10 0.217 \$P00337 0.94 0.773 \$P00337 0.94 0.773 \$P00337 0.94 0.773 \$P00337 0.94 0.774 0.204 \$P00338 0.85 0.229 \$P00338 0.72 0.000 \$P00338 0.84 0.941 \$P00338 0.79 0.056 \$P00338 0.72 0.000 \$P00338 0.79 0.945 \$P00338 0.945 \$P00338	1.03 0.063 1.13 0.094 0.88 0.340
\$P00339 1.6 0.00\$ \$P00339 1.44 0.02\$ \$P00340 0.69 0.479 \$P00340 0.78 0.271 \$P00339 0.66 0.079 \$P00339 0.70 0.130 \$P00339 0.90 0.452 \$P00339 0.70 0.130 \$P00339 0.90 0.452 \$P00339 0.70 0.130 \$P00339 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00339 0.70 0.130 \$P00340 0.90 0.452 \$P00340 0.90 0.90 0.452 \$P00340 0.90 0.90 0.452 \$P00340 0.90 0.90 0.452 \$P00340 0.90 0.90 0.452 \$P00340 0.90 0.90 0.452 \$P00340 0.90 0.90 0.452 \$P00340 0.90 0.90 0.90 0.452 \$P00340 0.90 0.90 0.90 0.90 0.90 0.90 0.90 0.	0.88 0.367 0.99 0.873 1.15 0.665
\$\overline{\text{SPO0342}} 0.87 0.116 \begin{array}{c} \overline{\text{SPO0342}} 0.87 0.16 \begin{array}{c} \overline{\text{SPO0342}} 0.81 0.729 \begin{array}{c} \overline{\text{SPO0343}} 0.9 0.86 \begin{array}{c} \overline{\text{SPO0342}} 0.85 0.97 0.005 \begin{array}{c} \overline{\text{SPO0344}} 0.85 0.97 0.005 \begin{array}{c} \overline{\text{SPO0344}} 0.87 0.8	0.75 0.079 0.97 0.949 1.15 0.011
\$P00345 1.01 0.924 \$P00345 1.04 0.865 \$P00346 0.92 0.034 \$P00346 0.82 0.063 \$P00345 0.89 0.91 \$P00345 0.90 0.668 \$P00345 0.88 0.450 \$P00345 \$P00345 0.90 0.668 \$P00345 0.89 0.450 \$P00345 0.90 0.668 \$P00345 0.89 0.450 \$P00345 0.90 0.668 \$P00345 0.89 0.450 \$P00345 0.90 0.668 \$P00345 0.89 0.450 \$P00345 0.90 0.668 \$P00345 0.90 0.90 0.668 \$P00345 0.90 0.668 \$P00345 0.90 0.90 0.668 \$P00345 0.90 0.90 0.668 \$P00345 0.90 0.90 0.668 \$P00345 0.90 0.90 0.668 \$P00345 0.90 0.90 0.90 0.90 0.90 0.90 0.90 0.9	0.94 0.740 1.00 0.812 0.88 0.343
5P00349 1.08 0.381 SP00349 1.28 0.228 SP00349 0.86 0.678 SP00359 0.86 0.678 SP00349 1.31 0.381 SP00349 1.30 0.00 SP00349 1.30 0.00 SP00349 1.30 0.00 SP00349 1.30 0.00 SP00349 1.30 0.381 SP00359 1.381	0.98 0.768 1.03 0.053 0.95 0.609
SP00351 0 SP00352 0.85 0.003 SP00352 0.61 0.007 SP00351 0.02 SP00351 0.02 SP00351 0.02 SP00351 0.02 SP00351 0.02 SP00351 0.00 SP00351 0.00 SP00351 0.00 SP00351 0.00 SP00351 0.00 SP00351 0.00 SP00351 0.00 SP00351 0.00 SP00352 0	0.93 0.732 1.03 0.496 1.01 0.783
SP00354 0.81 0.225 SP00354 0.88 0.014 SP00355 0.97 0.575 SP00355 0.75 0.63 SP00354 1.60 0.000 SP00354 1.54 0.000 SP00354 1.13 0.071 SP00355 SP00355 1.52 0.46 SP00355 1.31 0.338 SP00356 0.97 0.326 SP00355 0.94 0.488 SP00355 0.94 0.488 SP00355 0.99 0.797 SP00355 1.16 0.322 SP00355 0.94 0.488 SP00356 0.94 0.488 SP00356 0.99 0.797 SP00355 0.998 0.797 SP00355 0.998	1.19 0.147 1.05 0.729 0.82 0.361
\$P00357 0.75 0.496 \$P00357 0.81 0.414 \$P00358 0.98 0.167 \$P00358 0.88 0.133 \$P00357 0.96 0.976 \$P00357 0.90 0.750 \$P00357 0.97 0.908 \$P00357 \$P00358 1.13 0.314 \$P00358 1.13 0.314 \$P00358 1.13 0.314 \$P00359 0.98 0.115 \$P00359 0.98 0.115 \$P00359 0.78 0.78 \$P00359 0.98 0.78 0.78 \$P00359 0.98 0.98 0.99 0.99 0.99 0.99 0.99 0.9	0.92 0.778 0.93 0.564 1.03 0.466
\$P00360 0.81 0.122 \$P00360 0.95 0.576 \$P00361 0.82 0.23 \$P00361 0.9 0.113 \$P00360 3.15 0.000 \$P00360 2.80 0.000 \$P00360 0.96 0.994 \$P00360 \$P00361 1.15 0.376 \$P00361 0.98 0.977 \$P00362 0.96 0.571 \$P00362 0.96 0.571 \$P00362 0.97 0.071 \$P00362 0.97 0.071 \$P00361 0.98 0.971 \$P00361 0.99 0.96 0.948 \$P00381 0.98 0.994 \$P00363 0.98 0.994 \$P00363 0.98 0.994 \$P00362 0.99 0.995 \$P00362 0.99 0.995 \$P00362 0.99 0.995 \$P00362 0.99 0.995 \$P00362 0.99 0.995 \$P00362 0.99 0.995 \$P00362 0.99 0.995 \$P00362 0.995 \$P0036	1.00 0.812 0.89 0.549 0.93 0.593
\$P00383 0.74 0.071 \$P00383 0.86 0.466 \$P00364 0.98 0.963 \$P00364 0.81 0.996 \$P00383 0.01 \$P00383 0.18 0.000 \$P00383 0.93 0.843 \$P00383 \$P00384 0.91 0.92 \$P00384 0.91 0.92 \$P00384 0.91 0.92 \$P00385 0.99 0.065 \$P00385 0.92 0.045 \$P00385 0.92 0.045 \$P00384 1.03 0.815 \$P00384 1.03 0.815 \$P00384 1.09 0.841 \$P00384 0.91 0.91 \$P00385 0.91 \$P00385 0.91 \$P	0.98 0.936 1.09 0.796 0.90 0.279
\$P00366 1.47 0.006 \$P00366 1.55 0.003 \$P00367 0.92 0.600 \$P00368 1 0.034 \$P00368 1.42 0.007 \$P00366 1.16 0.022 \$P00366 0.76 0.105 \$P00367 \$P00367 1.32 0.334 \$P00367 1.41 0.174 \$P00368 0.88 0.126 \$P00368 0.99 0.055 \$P00367 1.74 0.000 \$P00368 1.30 0.00 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00367 0.76 0.004 \$P00368 0.99 0.76 \$P00368 0.99 0.99 0.76 \$P00368 0.99 0.99 0.76 \$P00368 0.99 0.99 0.76 \$P00368 0.99 0.99 0.76 \$P00368 0.99 0.99 0.76 \$P00368 0.99 0.99 0.76 \$P00368 0.99 0.99 0.99 0.99 0.99 0.99 0.99 0.9	0.72 0.045 0.81 0.178 0.92 0.515
\$\text{SPO0369} & 0.95 & 0.99 \text{\$PO0369} & 0.93 & 0.90 \text{\$PO0370} & 0.8 & 0.003 \text{\$PO0370} & 0.99 & 0.003 \text{\$PO0370} & 0.99 & 0.003 \text{\$PO0369} & 0.93 & 0.65 \text{\$PO0369} & 1.00 & 0.96 \text{\$PO0369} & 1.01 & 0.99 \text{\$PO0369} \text{\$PO0370} & 0.91 & 0.91 \text{\$PO0370} & 0.91 & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0371} & 0.91 \text{\$PO0372} & 0.91 \text{\$PO0371} & 0.91	0.85 0.822 0.91 0.281 0.73 0.198
\$\text{SP00372}\$ 1.44 0.096 \$\text{SP00372}\$ 1.36 0.005 \$\text{SP00373}\$ 0.96 0.051 \$\text{SP00373}\$ 0.97 0.01 \$\text{SP00372}\$ 0.59 0.012 \$\text{SP00372}\$ 0.75 0.003 \$\text{SP00372}\$ 1.13 0.877 \$\text{SP00373}\$ \$\text{SP00373}\$ 0.87 0.162 \$\text{SP00373}\$ 0.83 0.079 \$\text{SP00374}\$ 0.34 0.356 \$\text{SP00374}\$ 0.38 0.59 \$\text{SP00373}\$ 1.71 0.015 \$\text{SP00373}\$ 1.58 0.003 \$\text{SP00373}\$ 1.14 0.244 \$\text{SP00374}\$ \$\text{SP00374}\$ 1.14 0.214 \$\text{SP00374}\$ 1.15 0.256 \$\text{SP00375}\$ 0.87 0.737 \$\text{SP00374}\$ 1.10 0.15 \$\text{SP00375}\$ 1.10 0.85 \$\text{SP00375}\$ 0.87 0.87 \$\text{SP00375}\$ 1.10 0.256 \$\text{SP00375}\$ 0.87 0.87 \$\text{SP00375}\$ 1.10 0.87 \$\text{SP00375}\$ 0.87 0.87 \$\text{SP00375}\$ 1.10 0.87 \$\text{SP00375}\$ 0.87 0.87 0.87 \$\text{SP00375}\$ 0.87 0.87 0.87 0.87 0.87 0.87 0.87 0.87	0.99 0.775 1.11 0.302 0.93 0.850
\$\text{SP00375}\$ 1.46 0.335 \$\text{\$P00375}\$ 1.25 0.49 \$\text{\$P00376}\$ 0.99 0.222 \$\text{\$P00376}\$ 0.97 0.330 \$\text{\$P00375}\$ 0.99 0.817 \$\text{\$P00375}\$ 1.05 0.494 \$\text{\$P00375}\$ 0.99 0.995 \$\text{\$P00376}\$ \$\text{\$P00376}\$ 1.25 \$\text{\$P00376}\$ 0.101 \$\text{\$P00376}\$ 0.001 \$\text{\$P00377}\$ 0.85 0.04 \$\text{\$P00377}\$ 0.59 0.01 \$\text{\$P00377}\$ 0.59 0.01 \$\text{\$P00377}\$ 0.59 0.01 \$\text{\$P00377}\$ 0.59 0.001 \$\text{\$P00377}\$ 0.50 0.001 \$\text	1.03 0.876 0.93 0.741 0.98 0.942
\$\text{SPO3378}\$ 0.85 0.399 \$\text{\$\text{SPO3378}\$} 1 1 0.316 \$\text{\$\text{\$\text{\$\text{\$PO3379}\$}}\$ 0.99 1 0.9P03379 0.97 0.006 \$\$\text{\$\$\text{\$\tex{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\texi{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\texitex{\$\text{\$\text{	0.83 0.430 1.05 0.268 0.88 0.331
\$\text{SPO0381}\$ 1.21 0.802 \text{\$\text{SPO0381}\$ 1.24 0.78 \$\text{\$\text{\$\text{SPO0382}\$}\$ 0.33 0.18 \$\text{\$\text{\$\text{SPO0382}\$}\$ 0.88 0.107 \$\text{\$\text{\$\text{\$\text{\$\text{SPO0381}\$}\$}\$ 0.55 0.564 \$\text{\$\$\exitit{\$\text{\$\text{\$\text{\$\text{\$\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\$\text{\$\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\$\text{\$\$\text{\$\texit{\$\text{\$\$\}\$\$\text{\$\text{\$\text{\$\text{\$\text{\$\tex	0.79 0.771 0.69 0.003 0.83 0.189
SP00384 1.16 0.46 SP00384 1.172 0.546 SP00385 0.96 0.623 SP00385 0.93 0.347 SP00384 0.57 SP00384 0.30 0.455 SP00384 1.01 0.993 SP00385 SP00385 1.29 0.005 SP00385 1.16 0.25 SP00385 0.19 0.29 SP00385 0.57 0.006 SP00385 0.60 0.001 SP00385 1.001 SP003	1.01 0.978 0.94 0.665 0.92 0.600
\$\(\circ\)5\(\ci	1.13 0.368 0.88 0.259 1.12 0.473
SPO0390 0.79 0.789 (\$PO0390 0.84 0.87 (\$PO0391 0.98 0.055 (\$PO0391 0.92 0.152 (\$PO0390 0.91 0.91 0.915 (\$PO0390 0.91 0.915 (\$PO0391	0.96 0.959 0.95 0.761 1.05 0.309
\$P00393 1.24 0.04 \$P00393 1.12 0.107 \$P00394 0.89 0.474 \$P00394 0.93 0.601 \$P00393 0.76 0.091 \$P00393 0.77 0.032 \$P00393 0.81 0.096 \$P00393 0.81 0.096 \$P00394 0.88 0.686 \$P00394 1.02 0.924 \$P00395 0.99 0.982 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.99 0.992 \$P00395 0.992 \$P00395 0.99 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P00395 \$P00395 0.992 \$P00395 0.992 \$P00395 0.992 \$P000395 \$P00395 \$P00395 \$P00395 \$P00395 \$P00395 \$P00395 \$P00395 \$P00395 \$P00395 \$P0039	0.85 0.018 0.75 0.246 0.92 0.804
SP00398 1.38 0.004 [SP00396 12.6 0.144 [SP00397 0.86 0.722 [SP00397 0.77 0.672 [SP00396 0.8 0 0.652 [SP00396 0.8 0.340 [SP00398 0.9 0.612 [SP00397 0.9 0.8 0.7 0.9 0.8 0.7 0.9 0.8 0.7 0.9 0.8 0.8 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.94 0.806 0.96 0.792 1.06 0.185
\$\text{SPO399}\$ 1.12 0.085 \text{\$\subset{\$\cince{\since{\since{\subset{\$\su}\$}}}}}}}}} 1.05}} \simetimes \simetint{\sin}\sinms\}}} \simetimes \sinm\}} \eno	1.03 0.738 1.17 0.272 1.08 0.544
SPO0402 0.96 0.987 [SPO0402 0.97 0.974 [SPO0403 0.91 0.414 [SPO0403 0.94 0.26 [SPO0402 0.87 0.846 [SPO0402	1.04 0.968 1.14 0.306 1.12 0.667
\$\begin{array}{cccccccccccccccccccccccccccccccccccc	1.08 0.621 1.11 0.591 1.02 0.903
SPO0408 1.01 0.886 SPO0408 1 0.827 SPO0409 0.82 0.969 SPO0409 0.88 0.999 SPO0409 0.67 0.685 SPO0408 0.69 0.070 SPO0408 0.67 0.645 SPO0408 0.67 0.67 SPO0408 0.67 SPO0408 0.67 0.67 SPO0408 0.67 SPO0408 0.67 0.67 SPO0408 0.67 SPO0408 0.67 0.67 SPO0408 0.67 SPO0408 0.67 SPO0408 0.67 0.67 SPO0408	0.87 0.407 1.04 0.912 1.22 0.431
SPO0411 0.94 0.858 SPO0411 0.93 0.858 SPO0412 0.47 0.148 SPO0412 0.91 0.97 SPO0413 0.92 0.97 SPO0413 0.93 0.97 SPO	1.12 0.499 0.94 0.458 1.01 0.880
SPO0414 1.1e 0.135 [SPO0414 1.02 0.749 [SPO0415 0.93 0.223 [SPO0415 0.51 0.261 [SPO0414 0.47 0.07] [SPO0414 0.46 0.016 [SPO0414 0.90 0.556 [SPO0414 0.90 0.556 [SPO0414 0.90] [SPO0415 0.90] [SPO0415 0.90] [SPO0415 0.90] [SPO0415 0.90] [SPO0415 0.90] [SPO0415 0.90] [SPO0415 0.90] [SPO0415 0.90] [SPO0416 0.9	0.92 0.606 1.25 0.279 1.11 0.417
SPO0417 0.93 0.85 SPO0417 1.05 0.169 SPO0418 0.95 0.207 SPO0418 0.87 0.022 SPO0417 1.30 0.022 SPO0417 1.27 0.002 SPO0417 1.31 0.544 SPO0417 1.70 0.01 SPO0418 0.95 0.207 SPO0418 0.95 0.95 0.95 SPO0418 0.95 0.95 0.95 SPO0418 0.95 0.95 0.95 SPO0418 0.95 SPO0418 0.95 0.95 SPO0418 0.95 0.95 SPO0418 0.95 0.95 SPO0418 0.95	1.09 0.268 0.94 0.515 0.93 0.561
\$\text{SPO0420}\$ 1.06 0.366 \$\text{SPO0420}\$ 1.13 0.032 \$\text{SPO0421}\$ 0.96 0.713 \$\text{SPO0421}\$ 0.79 0.624 \$\text{SPO0420}\$ 1.51 0.000 \$\text{SPO0420}\$ 1.77 0.000 \$\text{SPO0420}\$ 1.05 0.374 \$\text{SPO0420}\$ 5.070 \$\text{SPO0421}\$ 0.99 0.72 \$\text{SPO0421}\$ 1.076 6.58 \$\text{SPO0422}\$ 1.05 0.95 \$\text{SPO0422}\$ 1.37 0.072 \$\text{SPO0421}\$ 1.48 0.091 \$\text{SPO0422}\$ 1.06 0.96 \$\text{SPO0422}\$ 1.05 0.96 \$\text{SPO0422}\$ 1.20 0.048 \$\text{SPO0422}\$ 1.20 0.048 \$\text{SPO0422}\$ 1.20 0.046 \$\text{SPO0422}\$ 1.20 0.046 \$\text{SPO0422}\$ 1.20 0.046 \$\text{SPO0422}\$ 1.20 0.046 \$\text{SPO0422}\$ 1.20 0.048 \$\text{SPO0422}\$ 1.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 0.20 0.20 \$\text{SPO0422}\$ 1.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20	1.06 0.072 1.08 0.723 0.98 0.924 1.00 0.978

SP00424 SP00425	1.05	0.169 SPO0424 0.041 SPO0425	0.83	0.183 SPO04 0.44 SPO04		0.701 SPO0425 0.4 SPO0426	0.33 0.97	0.256 0.206	SPO0424 SPO0425	1.35	0.087	SPO0424 SPO0425	1.21	0.047	SPO0424 SPO0425	1.02	0.896 0.128	SP00424 SP00425	0.99	0.766 0.097
SPO0426 SPO0427 SPO0428	1.11 1.37 1.05	0.042 SPO0426 0.024 SPO0427 0.312 SPO0428	1.15 1.32 0.98	0.08 SPO04 0.002 SPO04 0.923 SPO04	128 0.99	0.052 SPO0427 0.613 SPO0428 0.383 SPO0429	0.86 0.97	0.004 0.673 0.072	SPO0426 SPO0427 SPO0428	0.76 0.58 1.11	0.037 0.006 0.540	SPO0426 SPO0427 SPO0428	0.85 0.57	0.238 0.001 0.922	SPO0426 SPO0427 SPO0428	1.12 0.84 0.94	0.100 0.339 0.743	SPO0426 SPO0427 SPO0428	1.06 0.83 0.95	0.203 0.205 0.876
SPO0429 SPO0430 SPO0431	0.81 1.45 1.37	0.03 SP00429 0.001 SP00430 0.536 SP00431	0.75 1.33	0.084 SP004 0.001 SP004 0.468 SP004	0.84 131 0.94	0.422 SPO0430 0.83 SPO0431 0.004 SPO0432	0.99 0.96 0.94	0.328 0.717 0.001	SPO0429 SPO0430	0.72 1.03 0.86	0.002 0.137 0.704	SPO0429 SPO0430	0.77 1.08 0.90	0.003 0.052 0.763	SPO0429 SPO0430 SPO0431	1.20 1.10 1.04	0.064 0.292 0.982	SPO0429 SPO0430 SPO0431	1.14 1.07 0.88	0.362 0.271 0.787
SPO0432 SPO0433	0.57 1.25	0.004 SPO0432 0.604 SPO0433	0.55 1.24	0.007 SPO04 0.388 SPO04	0.98 134 0.97	0.559 SPO0433 0.003 SPO0434	0.89 0.95	0.497 0.007	SPO0432 SPO0433	8.19 0.92	0.000 0.669	SPO0432 SPO0433	7.42 0.93	0.000	SPO0432 SPO0433	1.30	0.030 0.549	SP00432 SP00433	1.39 1.20	0.010 0.375
SPO0434 SPO0435 SPO0436	1.01 1.11 1.03	0.945 SPO0434 0.1 SPO0435 0.379 SPO0436	1.08 0.94 1.05	0.14 SPO04 0.877 SPO04 0.139 SPO04	136 0.86	0.607 SPO0435 0.028 SPO0436 0.932 SPO0437	0.75 0.6 0.71	0.633 0.074 0.409	SPO0434 SPO0435 SPO0436	0.69 0.89 1.05	0.030 0.559 0.476	SPO0434 SPO0435 SPO0436	0.69 1.02 1.07	0.007 0.441 0.147	SPO0434 SPO0435 SPO0436	0.99 0.99 0.98	0.959	SP00434 SP00435 SP00436	0.99 0.94 0.99	0.869 0.634 0.718
SPO0437 SPO0438 SPO0439	1.16 0.76 0.83	0.326 SPO0437 0.026 SPO0438 0.373 SPO0439	0.99 0.78 0.96	0.976 SPO04 0.109 SPO04 0.939 SPO04	0.96	0.053 SPO0438 0.917 SPO0439 0.74 SPO0440	0.7 0.93 0.98	0.069 0.93 0.633	SPO0437 SPO0438 SPO0439	0.93 1.13 0.83	0.453 0.077 0.387	SPO0437 SPO0438 SPO0439	0.90 1.11 0.76	0.344 0.005 0.319	SPO0437 SPO0438 SPO0439	0.85 0.79 1.02	0.082	SP00437 SP00438 SP00439	0.98 0.83 1.03	0.804 0.082 0.882
SPO0440 SPO0441	1.01 0.83	0.461 SPO0440 0.73 SPO0441	0.97 0.95	0.827 SPO04 0.721 SPO04	0.84 142 0.76	0.288 SP00441 0.019 SP00442	0.99 0.93	0.062 0.005	SPO0440 SPO0441	0.94 1.08	0.421 0.641	SPO0440 SPO0441	0.92 0.95	0.402 0.532	SPO0440 SPO0441	1.25 1.12	0.318 0.839	SPO0440 SPO0441	1.27 1.17	0.067 0.528
SPO0442 SPO0443 SPO0444	1.28 1.09 0.89	0.029 SPO0442 0.538 SPO0443 0.614 SPO0444	1.21 1.15 0.85	0.025 SPO04 0.155 SPO04 0.679 SPO04	0.89 145 0.79	0.038 SP00443 0.44 SP00444 0.85 SP00445	0.81 0.85 0.99	0.026 0.463 0.889	SPO0443 SPO0444	0.60 0.58 1.39	0.000 0.047 0.234	SPO0442 SPO0443 SPO0444	0.62 0.56 1.29	0.000 0.004 0.289	SPO0442 SPO0443 SPO0444	0.98 0.90 0.99	0.741		1.05 0.87 0.93	0.560 0.318 0.776
SPO0445 SPO0446 SPO0447	1.14 0.95 0.88	0.644 SPO0445 0.642 SPO0446 0.582 SPO0447	1.51 1.02 0.98	0.456 SPO04 0.469 SPO04 0.175 SPO04	147 0.74	0.25 SP00446 0.633 SP00447 0.922 SP00448	0.93 0.93 0.87	0.35 0.326 0.929	SPO0445 SPO0446 SPO0447	0.50 1.11 2.32	0.019 0.027 0.000	SPO0445 SPO0446 SPO0447	0.52 1.16 2.35	0.006 0.007 0.000	SPO0445 SPO0446 SPO0447	0.83 1.01 1.27	0.482 0.882 0.050	SP00445 SP00446 SP00447	0.89 1.03 1.31	0.782 0.806 0.012
SPO0448 SPO0449 SPO0450	1 1.51 1.62	0.98 SPO0448 0.381 SPO0449 0.064 SPO0450	0.97 1.31 1.43	0.995 SPO04 0.524 SPO04 0.123 SPO04	150 0.89	0.629 SPO0449 0.508 SPO0450 0.159 SPO0451	0.9 0.93 0.93	0.645 0.541 0.144	SPO0448 SPO0449 SPO0450	0.71 0.74 0.68	0.769 0.636 0.056	SPO0448 SPO0449 SPO0450	0.74 0.79 0.73	0.832 0.747 0.156	SPO0448 SPO0449 SPO0450	0.81 0.93 1.07	0.809 0.907 0.834	SP00448 SP00449 SP00450	0.88 0.98 1.18	0.876 0.987 0.442
SPO0451 SPO0452	0.98 0.9	0.993 SPO0451 0.314 SPO0452	0.93 0.9	0.733 SPO04 0.304 SPO04	152 0.91 153 0.47	0.785 SPO0452 0.284 SPO0453	0.9 0.97	0.618 0.296	SPO0451 SPO0452 SPO0453	0.70 0.78	0.122 0.155	SPO0451 SPO0452 SPO0453	0.70 0.79	0.045 0.235	SPO0451 SPO0452	0.87 0.93	0.612 0.520	SPO0451 SPO0452	0.83 0.93	0.439 0.583
SPO0453 SPO0454 SPO0455	1.17 1.04 1.2	0.174 SPO0453 0.647 SPO0454 0.446 SPO0455	1.18 1.02 1.16	0.612 SPO04 0.694 SPO04	155 0.78 156 0.83	0.995 SPO0454 0.891 SPO0455 0.39 SPO0456	0.98 0.75 0.91	0.744 0.998 0.458	SPO0454 SPO0455	0.83 0.89 1.32	0.170 0.572 0.291	SPO0454 SPO0455	0.86 0.95 1.44	0.021 0.775 0.291	SPO0453 SPO0454 SPO0455	1.23 0.90 1.18	0.334 0.417 0.676	SPO0453 SPO0454 SPO0455	1.18 0.88 1.12	0.424 0.382 0.700
SPO0456 SPO0457 SPO0458	0.9 0.88 1.14	0.703 SPO0456 0.334 SPO0457 0.524 SPO0458	0.85 1.01 1.23	0.057 SPO04 0.668 SPO04 0.423 SPO04	158 0.91	0.97 SPO0457 0.227 SPO0458 0.596 SPO0459	0.72 0.65 0.89	0.953 0.469 0.605	SPO0456 SPO0457 SPO0458	0.79 0.91 0.82	0.028 0.800 0.260	SPO0456 SPO0457 SPO0458	0.82 0.87 0.75	0.108 0.660 0.221	SPO0456 SPO0457 SPO0458	0.93 1.16 0.94	0.359 0.296 0.682	SPO0456 SPO0457 SPO0458	0.92 1.13 0.81	0.504 0.280 0.443
SPO0459 SPO0460 SPO0461	1.38 0.73	0.048 SPO0459 0.018 SPO0460 0.011 SPO0461	2.43 1.19 0.81	0.002 SPO04 0.199 SPO04 0.033 SPO04	161 0.81	0.389 SPO0460 0.016 SPO0461 0.999 SPO0462	0.76 0.83 0.71	0.244 0.007 0.989	SPO0459 SPO0460	0.39 0.40 1.58	0.009 0.005 0.002	SPO0459 SPO0460	0.43 0.41 1.68	0.011 0.001 0.000	SPO0459 SPO0460 SPO0461	0.83 0.99 0.98	0.375 0.876 0.656	SPO0459 SPO0460 SPO0461	0.84 0.84 0.88	0.547
SPO0462 SPO0463	0.91 0.82	0.168 SPO0462 0.038 SPO0463	0.91 0.83	0.617 SPO04 0.007 SPO04	0.96 164 0.93	0.089 SPO0463 0.457 SPO0464	0.64 0.83	0.064 0.04	SPO0462 SPO0463	0.47 1.29	0.000	SPO0462 SPO0463	0.45 1.34	0.000	SPO0462 SPO0463	0.95 1.14	0.252 0.094	SP00462 SP00463 SP00464	0.92 1.12	0.370
SPO0464 SPO0465 SPO0466	0.78 1.02 1.03	0.052 SPO0464 0.12 SPO0465 0.844 SPO0466	0.82 0.98 0.96	0.022 SPO04 0.661 SPO04 0.927 SPO04	166 0.69 167 0.83	0.661 SPO0465 0.999 SPO0466 0.847 SPO0467	0.85 0.68 0.91	0.888 0.791 0.847	SPO0464 SPO0465 SPO0466	0.88 1.10 0.96	0.652 0.891 0.860	SPO0464 SPO0465 SPO0466	0.96 1.30 0.99		SPO0464 SPO0465 SPO0466	0.93 1.14 1.06	0.525 0.816	SP00465 SP00466	0.92 1.07 1.09	0.483 0.732 0.393
SPO0467 SPO0468 SPO0469	1.1 0.98 0.76	0.676 SPO0467 0.994 SPO0468 0.129 SPO0469	1.01 0.99 0.75	0.871 SPO04 0.976 SPO04 0.105 SPO04	169 0.39	0.926 SPO0468 0.93 SPO0469 0.988 SPO0470	0.99 0.46 0.92	0.947 0.877 0.383	SPO0468 SPO0469	1.11 0.80 1.06	0.868 0.874 0.797	SPO0467 SPO0468 SPO0469	1.13 0.85 0.93	0.850 0.922 0.544	SPO0467 SPO0468 SPO0469	0.85 0.89 0.94		SP00467 SP00468 SP00469	0.85 0.90 0.96	0.716 0.923 0.790
SP00470 SP00471 SP00472	0.69 0.93 0.93	0.008 SPO0470 0.844 SPO0471 0.903 SPO0472	0.84 0.98 0.89	0.226 SPO04 0.854 SPO04 0.295 SPO04	172 0.85	0.778 SPO0471 0.777 SPO0472 0.569 SPO0473	0.99 0.71 0.83	0.681 0.79 0.37	SPO0470 SPO0471 SPO0472	1.75 0.95 1.20	0.050 0.711 0.263	SPO0470 SPO0471 SPO0472	2.14 0.88 1.25	0.000 0.496 0.059	SPO0470 SPO0471 SPO0472	1.17 0.89 1.01	0.583 0.426 0.944	SPO0470 SPO0471 SPO0472	1.20 0.94 1.07	0.434 0.805 0.635
SPO0473 SPO0474 SPO0475	1.14 1.13 1.21	0.107 SPO0473 0.572 SPO0474 0.203 SPO0475	1.04 1.06 1.25	0.253 SPO04 0.653 SPO04 0.052 SPO04	175 0.97	0.669 SPO0474 0.646 SPO0475 0.85 SPO0476	0.85 1.02 0.78	0.547 0.575 0.789	SPO0473 SPO0474 SPO0475	1.19 0.83 1.06	0.390 0.555 0.703	SPO0473 SPO0474 SPO0475	1.44 0.88 1.12	0.024 0.584 0.137	SPO0473 SPO0474 SPO0475	0.99 0.87 1.25	0.583 0.686 0.116	SP00473 SP00474 SP00475	1.07 0.88 1.25	0.583 0.703 0.063
SPO0476 SPO0477	1.19 0.7	0.056 SPO0476 0.079 SPO0477	1.12 0.86	0.118 SPO04 0.056 SPO04	177 0.88 178 0.93	0.712 SPO0477 0.092 SPO0478	0.76 0.96	0.069 0.305	SPO0476 SPO0477	1.10 1.62	0.636 0.001	SPO0476 SPO0477	1.26 1.55	0.018	SPO0476 SPO0477	1.30 1.17	0.306	SPO0476 SPO0477	1.20 1.10	0.133 0.733
SPO0478 SPO0479 SPO0481	0.98 0.79 2.11	0.869 SPO0478 0.287 SPO0479 0 SPO0481	0.94 0.84 1.78	0.951 SPO04 0.262 SPO04 0 SPO04	181 0.88 182 0.93	0.85 SP00479 0.019 SP00481 0.24 SP00482	0.73 0.96 0.81	0.493 0.063 0.122	SPO0478 SPO0479 SPO0481	1.13 0.86 0.75	0.284 0.210 0.002	SPO0478 SPO0479 SPO0481	1.14 0.91 0.76	0.038 0.627 0.003	SPO0478 SPO0479 SPO0481	1.34 1.03 0.98	0.006 0.811 0.693	SP00478 SP00479 SP00481	1.25 1.09 0.89	0.043 0.529 0.127
SPO0482 SPO0483 SPO0484	1.25 1.74 0.9	0.02 SPO0482 0 SPO0483 0.153 SPO0484	1.16 1.81 1.08	0.012 SPO04 0 SPO04 0.599 SPO04	184 0.88	0 SPO0483 0.026 SPO0484 0.127 SPO0485	0.76 0.97 0.66	0.001 0 0.186	SPO0482 SPO0483 SPO0484	0.83 0.40 2.18	0.445 0.000 0.000	SPO0482 SPO0483 SPO0484	0.89 0.39	0.408 0.000 0.000	SPO0482 SPO0483 SPO0484	1.01 1.14 1.13	0.577 0.041 0.225	SPO0482 SPO0483 SPO0484	0.93 1.16 1.31	0.271 0.057 0.084
SPO0485 SPO0486 SPO0487	0.94 1.27 1.31	0.732 SPO0485 0.001 SPO0486 0.005 SPO0487	1.16 1.41 1.36	0.424 SPO04 0.01 SPO04 0.006 SPO04	186 0.93 187 0.93	0.376 SPO0486 0.112 SPO0487 0.01 SPO0488	0.81	0.781	SPO0485 SPO0486	2.15 1.36 1.53	0.002 0.004 0.000	SPO0485 SPO0486	1.91 1.26 1.42	0.003 0.000 0.000	SPO0485 SPO0486 SPO0487	1.14 1.06 1.15		SP00485 SP00486 SP00487	1.20 1.07 1.14	0.244
SPO0488 SPO0489	2.41 1.06	0 SPO0488 0.473 SPO0489	1.93 1.11	0.001 SPO04 0.548 SPO04	0.99 190 0.92	0.708 SPO0489 0.476 SPO0490	0.32 0.78 0.91	0.749 0.691	SPO0488 SPO0489	0.63 1.03	0.038	SPO0488 SPO0489	0.57 1.06	0.016 0.912	SPO0488 SPO0489	0.88 0.97	0.485 0.764	SPO0488 SPO0489	0.92 0.99	0.728 0.693
SPO0490 SPO0491 SPO0492	0.88 1.18 1.04	0.807 SPO0490 0.137 SPO0491 0.377 SPO0492	0.95 1.25 0.99	0.992 SPO04 0.098 SPO04 0.786 SPO04	192 0.7	0.021 SPO0491 0.261 SPO0492 0.032 SPO0493	0.83 0.74 0.92	0.013 0.474 0.002	SPO0490 SPO0491 SPO0492	0.34 1.89 0.68	0.013 0.000 0.007	SPO0490 SPO0491 SPO0492	0.35 1.94 0.74	0.010 0.000 0.002	SPO0490 SPO0491 SPO0492	0.75 1.34 0.94	0.004	SPO0490 SPO0491 SPO0492	0.78 1.30 0.95	0.476 0.097 0.553
SPO0493 SPO0494 SPO0495	0.88 1 1.16	0.015 SPO0493 0.722 SPO0494 0.073 SPO0495	0.93 1.06 1.15	0.546 SPO04 0.011 SPO04 0.002 SPO04	195 0.81	0 SPO0494 0.011 SPO0495 0.807 SPO0496	0.93 0.87 0.89	0.005 0.638	SPO0493 SPO0494 SPO0495	2.10 2.01 1.64	0.000 0.000 0.000	SPO0493 SPO0494 SPO0495	2.04 2.02 1.61	0.000 0.000 0.000	SPO0493 SPO0494 SPO0495	1.04 1.15 1.07	0.084 0.004 0.010	SPO0493 SPO0494 SPO0495	1.14 1.21 1.13	0.046 0.000 0.001
SPO0496 SPO0497 SPO0498	1.13 1.01 1.11	0.234 SPO0496 0.982 SPO0497 0.636 SPO0498	1.36 1.1 1.15	0.02 SPO04 0.44 SPO04 0.132 SPO04	198 0.9	0.077 SPO0497 0.033 SPO0498 0.024 SPO0499	0.97 0.92 0.93	0.138 0.03 0.103	SPO0496 SPO0497 SPO0498	1.39 2.44 1.79	0.000 0.001 0.001	SPO0496 SPO0497 SPO0498	1.28 2.13 1.71	0.000 0.003 0.001	SPO0496 SPO0497 SPO0498	0.99 0.92 1.00	0.464 0.771 0.906	SP00496 SP00497 SP00498	1.03 0.97 1.07	0.089 0.933 0.432
SPO0499 SPO0500 SPO0501	1.34 0.87 1.84	0.015 SPO0499 0.183 SPO0500 0.005 SPO0501	1.2 1 1.67	0.001 SPO05 0.959 SPO05 0 SPO05	0.95	0.019 SPO0500 0.719 SPO0501 0.91 SPO0502	0.9 0.83 0.88	0.071 0.661 0.861	SPO0499 SPO0500 SPO0501	1.34 1.79 1.16	0.000 0.000 0.021	SPO0499 SPO0500 SPO0501	1.32 1.65 1.05	0.001 0.003 0.012	SPO0499 SPO0500 SPO0501	1.08 1.15 1.01	0.208 0.106 0.757	SPO0499 SPO0500 SPO0501	1.19 1.28 1.00	0.004 0.000 0.624
SPO0502 SPO0503	1.57 1.82	0.017 SPO0502 0 SPO0503	1.58 1.75	0.005 SPO05 0 SPO05	0.99 04 0.89	0.086 SPO0503 0.811 SPO0504	0.98 0.88	0.015 0.641	SPO0502 SPO0503	1.20 0.99	0.013 0.277	SPO0502 SPO0503	1.19 1.04	0.002 0.015	SPO0502 SPO0503	0.88 0.85	0.336 0.218	SPO0502 SPO0503	0.93 0.83	0.604 0.010
SPO0504 SPO0505 SPO0506	1.19 1.82 1.03	0.065 SPO0504 0 SPO0505 0.553 SPO0506	1.39 1.7 1.06	0.002 SPO05 0 SPO05 0.226 SPO05	0.84 507 0.97	0.01 SPO0505 0.157 SPO0506 0.225 SPO0507	0.9 0.88 0.98	0.012 0.106 0.024	SPO0505 SPO0506	0.86 0.90 0.96	0.607 0.235 0.167	SPO0504 SPO0505 SPO0506	0.88 0.85 1.02	0.135 0.736 0.004	SPO0504 SPO0505 SPO0506	1.97 1.02 1.08	0.058 0.301 0.165	SPO0504 SPO0505 SPO0506	1.49 0.95 1.14	0.171 0.754 0.046
SPO0507 SPO0508 SPO0509	0.85 1.29 1.21	0.202 SPO0507 0.007 SPO0508 0.3 SPO0509	0.86 1.38 1.18	0.221 SPO05 0.005 SPO05 0.342 SPO05	0.88	0.115 SPO0508 0.308 SPO0509 0.045 SPO0510	0.77 0.94 0.7	0.588 0.408 0.124	SPO0507 SPO0508 SPO0509	1.34 1.28 0.95	0.016 0.050 0.451	SPO0507 SPO0508 SPO0509	1.37 1.28 0.91	0.006 0.048 0.466	SPO0507 SPO0508 SPO0509	1.26 1.39 0.90	0.087 0.020 0.753	SPO0507 SPO0508 SPO0509	1.21 1.30 0.93	0.101 0.197 0.862
SPO0510 SPO0511 SPO0512	1.38 1.23 1.95	0.001 SPO0510 0.003 SPO0511 0.14 SPO0512	1.37 1.26 1.85	0.01 SPO05 0 SPO05 0.146 SPO05	0.92	0.983 SPO0511 0.77 SPO0512 0.214 SPO0513	0.97 0.83 0.65	0.473 0.656 0.29	SPO0510 SPO0511 SPO0512	0.91 1.42 0.92	0.220 0.001 0.931	SPO0510 SPO0511 SPO0512	0.93 1.44 0.94	0.128 0.004 0.843	SPO0510 SPO0511 SPO0512	0.96 1.02 0.96	0.470	SP00510 SP00511 SP00512	0.98 1.06 0.94	0.597 0.075 0.931
SPO0513 SPO0514 SPO0515	1.18 1.36	0.128 SPO0513 0.024 SPO0514 0.101 SPO0515	0.99 1.34 1.33	0.872 SPO05 0.003 SPO05	0.97 515 0.97	0.818 SPO0514 0.562 SPO0515 0.648 SPO0516	0.97 0.98 0.9	0.875 0.379	SPO0513 SPO0514	0.94 0.72 0.78	0.590 0.011 0.328	SPO0514	0.94 0.74 0.74	0.594 0.010	SPO0513 SPO0514 SPO0515	1.07 1.07 0.93	0.466 0.385	SPO0513 SPO0514 SPO0515	1.07 1.07 0.90	0.424 0.390 0.449
SPO0516 SPO0517	1.6 1.16	0.01 SPO0516 0.469 SPO0517	1.45 1.23	0.018 SPO05 0.195 SPO05	0.41 0.88 0.88	0.732 SPO0517 0.584 SPO0518	1.02 0.93	0.529 0.492 0.548	SPO0515 SPO0516 SPO0517	1.38 2.01	0.044	SPO0515 SPO0516 SPO0517	1.41 1.95	0.019 0.047 0.011	SPO0516 SPO0517	1.24 1.08	0.271 0.710	SPO0516 SPO0517	1.14 1.10	0.399 0.577
SPO0518 SPO0519 SPO0520	1.22 0.88 1.13	0.267 SPO0518 0.089 SPO0519 0.382 SPO0520	1.24 0.85 1.14	0.191 SPO05 0.023 SPO05 0.203 SPO05	0.87	0.038 SPO0519 0.303 SPO0520 0.14 SPO0521	0.97 0.85	0.058 0.332 0.89	SPO0518 SPO0519 SPO0520	1.84 1.36 1.90	0.023 0.000 0.001	SPO0518 SPO0519 SPO0520	1.88 1.27 1.60	0.017 0.001 0.001	SPO0518 SPO0519 SPO0520	1.10 1.01 0.87	0.704 0.371 0.456	SPO0518 SPO0519 SPO0520	1.18 0.89 0.88	0.427 0.468 0.497
SPO0521 SPO0522 SPO0523	1.02 0.99	0.946 SPO0521 0.977 SPO0522 0.691 SPO0523	1.08 1.02	0.308 SPO05 0.87 SPO05 0.3 SPO05	0.91	0.868 SPO0522 0.005 SPO0523 0.896 SPO0524	0.83 0.94 0.86	0.882 0.152 0.865	SPO0521 SPO0522 SPO0523	2.17 2.16 0.66	0.000 0.021 0.004	SPO0521 SPO0522 SPO0523	1.94 2.04 0.68	0.001 0.037 0.028	SPO0521 SPO0522 SPO0523	0.91 0.98 0.89		SPO0521 SPO0522 SPO0523	0.98 0.95 0.91	0.908 0.941 0.268
SPO0524 SPO0525 SPO0526	0.91 1 1.46	0.772 SPO0524 0.77 SPO0525 0.056 SPO0526	0.96 1.03 1.29	0.961 SPO05 0.694 SPO05 0.036 SPO05	0.98 526 0.65	0.155 SPO0525 0.683 SPO0526 0.787 SPO0527	0.87 0.95 0.89	0.004 0.839 0.285	SPO0524 SPO0525 SPO0526	0.40 0.85 0.94	0.001 0.277 0.827	SPO0524 SPO0525 SPO0526	0.38 0.93 0.96		SPO0524 SPO0525 SPO0526	1.01 0.97 1.25	0.962 0.842	SPO0524 SPO0525 SPO0526	0.99 0.90 1.16	0.968 0.170 0.065
SPO0527 SPO0528	1.02 0.6	0.763 SPO0527 0 SPO0528	0.95 0.7	0.914 SPO05 0.066 SPO05	528 0.86 529 0.87	0.104 SPO0528 0.044 SPO0529	0.81 0.97	0.32 0.147	SPO0527 SPO0528	0.69 1.14	0.143 0.006	SPO0527 SPO0528	0.78 1.17	0.052 0.048	SPO0527 SPO0528	1.06 1.08	0.875 0.140	SPO0527 SPO0528	1.04 1.15	0.864 0.183
SPO0529 SPO0530 SPO0531	0.92 0.83 1.58	0.417 SPO0529 0.401 SPO0530 0.041 SPO0531	0.91 0.88 1.4	0.446 SPO05 0.631 SPO05 0.002 SPO05	0.97 0.86	0.606 SPO0530 0.34 SPO0531 0.614 SPO0532	0.91 0.81 0.44	0.982 0.626 0.641	SPO0529 SPO0530 SPO0531	0.77 0.83 0.97	0.075 0.560 0.910	SPO0529 SPO0530 SPO0531	0.79 1.05 1.14	0.737	SPO0529 SPO0530 SPO0531	1.07 1.04 1.16	0.839	SPO0529 SPO0530 SPO0531	0.97 1.05 1.14	0.857 0.829 0.747
SPO0532 SPO0533 SPO0534	1.55 1.27 1.61	0.066 SPO0532 0.282 SPO0533 0.003 SPO0534	1.44 1.12 1.59	0.076 SPO05 0.316 SPO05 0.002 SPO05	0.79	0.303 SPO0533 0.631 SPO0534 0.202 SPO0535	0.93 0.81 0.83	0.407 0.621 0.117	SPO0532 SPO0533 SPO0534	1.04 0.34 0.92	0.510 0.002 0.317	SPO0532 SPO0533 SPO0534	1.12 0.36 0.89	0.376 0.002 0.251	SPO0532 SPO0533 SPO0534	0.94 0.78 1.05	0.871 0.301 0.412	SPO0532 SPO0533 SPO0534	0.93 0.85 0.93	0.792 0.335 0.401
SPO0535 SPO0536 SPO0537	1.53	0.005 SPO0535 0.494 SPO0536 0 SPO0537	1.45	0.001 SPO05 0.49 SPO05 0 SPO05	0.67	0.548 SPO0536 0.029 SPO0537 0.112 SPO0538	0.85 0.71 0.88	0.499 0.005 0.103	SPO0535 SPO0536 SPO0537	1.02 0.66 1.04	0.981 0.168 0.261	SPO0535 SPO0536 SPO0537	1.03 0.65 1.13	0.994 0.078 0.098	SPO0535 SPO0536 SPO0537	1.04 1.14 1.20	0.710	SP00535 SP00536 SP00537	0.91 1.15 1.04	0.544 0.513 0.596
SPO0538 SPO0539	1.91	0.03 SPO0538 0.546 SPO0539	1.78	0.028 SPO05 0.863 SPO05	0.71 540 0.8	0.818 SPO0539 0.386 SPO0540	0.97 0.83	0.529 0.329	SPO0538 SPO0539	0.81 0.98	0.750 0.666	SPO0538 SPO0539	0.74 0.95	0.444	SPO0538 SPO0539	0.88 1.30	0.725 0.004	SPO0538 SPO0539	0.75 1.23	0.307 0.118
SPO0540 SPO0541 SPO0543	1.17 1.17 0.96	0.504 SPO0540 0.186 SPO0541 0.851 SPO0543	1.07 1.1 1.13	0.644 SPO05 0.256 SPO05 0.196 SPO05	543 0.87 544 0.97	0.111 SPO0543 0.345 SPO0544	0.95 0.91 0.81	0.514 0.028 0.261	SPO0540 SPO0541 SPO0543	0.83 0.85 0.97	0.554 0.200 0.620	SPO0540 SPO0541 SPO0543	0.87 0.94 0.94	0.750 0.284	SPO0540 SPO0541 SPO0543	0.93 1.16 0.98	0.627 0.695	SPO0540 SPO0541 SPO0543	0.88 1.11 1.02	0.506 0.625 0.964
SPO0544 SPO0545 SPO0546	0.92 0.72 0.74	0.621 SPO0544 0.128 SPO0545 0.279 SPO0546	1.09 0.7 0.75	0.075 SPO05 0.297 SPO05 0.218 SPO05	546 0.6	0.131 SPO0545 0.247 SPO0546 0.663 SPO0547	0.9 0.93 0.96	0.277 0.176 0.842	SPO0544 SPO0545 SPO0546	1.07 1.28 2.24	0.966 0.052 0.013	SPO0544 SPO0545 SPO0546	1.17 1.43 2.08		SPO0544 SPO0545 SPO0546	0.95 1.10 1.46	0.607 0.682 0.209	SP00544 SP00545 SP00546	0.99 1.08 1.35	0.747 0.754 0.089
SPO0547 SPO0548 SPO0549	1.35 1.06 1.31	0.15 SPO0547 0.573 SPO0548 0.012 SPO0549	1.24 1 1.25	0.254 SPO05 0.722 SPO05 0.248 SPO05	548 0.84 549 0.77	0.049 SPO0548 0.844 SPO0549 0.758 SPO0550	0.87 0.88 0.77	0.138 0.876 0.771	SPO0547 SPO0548 SPO0549	0.63 0.91 1.06	0.036 0.928 0.690	SPO0547 SPO0548 SPO0549	0.66 0.93 1.10		SPO0547 SPO0548 SPO0549	0.88 0.85 0.99	0.434 0.249	SPO0547 SPO0548 SPO0549	0.93 0.89 1.00	0.748 0.520 0.985
SPO0550 SPO0551 SPO0552	1.1 0.79 1.31	0.337 SPO0550 0.536 SPO0551 0.058 SPO0552	1.11 0.87 1.26	0.306 SPO05 0.506 SPO05 0.036 SPO05	551 0.66 552 0.71	0.009 SPO0551 0.483 SPO0552	0.74 0.74 0.74	0.206 0.366 0.823	SPO0550 SPO0551 SPO0552	1.26 1.35 1.08	0.412 0.414 0.382	SPO0550 SPO0551 SPO0552	1.10 0.98 1.09	0.597 0.623	SPO0550 SPO0551 SPO0552	0.93 0.95 0.87	0.767 0.962	SPO0550 SPO0551 SPO0552	0.95 1.07 0.93	0.766 0.877 0.587
SPO0553 SPO0554	1.3 1.41	0.115 SPO0553 0.009 SPO0554	1.35 1.38	0.197 SPO05 0.011 SPO05	0.79 0.97	0.631 SPO0554 0.023 SPO0555	0.72 0.74	0.499 0.006	SPO0553 SPO0554	1.45 1.71	0.123 0.014	SPO0553 SPO0554	1.57 1.81	0.107 0.005	SPO0553 SPO0554	1.00 1.22	0.909 0.269	SPO0553 SPO0554	1.07 1.06	0.735 0.780
SPO0555 SPO0556 SPO0557	1.25 0.81 0.83	0.135 SPO0555 0.243 SPO0556 0.347 SPO0557	1.32 0.94 0.87	0 SPO05 0.9 SPO05 0.601 SPO05	557 0.89 558 0.89	0.455 SPO0556 0.869 SPO0557 0.066 SPO0558	0.93 0.83 0.81	0.385 0.882 0.106	SPO0555 SPO0556 SPO0557	1.12 1.12 0.89	0.367 0.238 0.925	SPO0555 SPO0556 SPO0557	1.17 1.04 0.86	0.843	SPO0555 SPO0556 SPO0557	0.91 0.93 0.90	0.582 0.644	SPO0555 SPO0556 SPO0557	0.91 0.96 0.93	0.081 0.808 0.724
SPO0558 SPO0559 SPO0560	0.86 0.77 0.95	0.033 SPO0558 0.634 SPO0559 0.177 SPO0560	0.93 0.76 0.9	0.469 SPO05 0.724 SPO05 0.617 SPO05	660 0.09	0.854 SP00559 0.343 SP00560 0.313 SP00562	0.87 0.83 0.63	0.842 0.202 0.197	SPO0558 SPO0559 SPO0560	1.22 1.35 0.50	0.007 0.517 0.000	SPO0558 SPO0559 SPO0560	1.14 1.43 0.41	0.015 0.471 0.002	SPO0558 SPO0559 SPO0560	0.94 1.00 0.66	0.983	SPO0558 SPO0559 SPO0560	0.97 1.03 0.68	0.669 0.921 0.007
SPO0562 SPO0563 SPO0564	1.02 1.18 0.88	0.816 SPO0562 0.21 SPO0563 0.322 SPO0564	1.07 1.22 0.9	0.437 SPO05 0.004 SPO05 0.847 SPO05	663 0.8 664 0.87	0.933 SPO0563	0.63 0.83 0.79	0.877 0.967 0.715	SPO0562 SPO0563 SPO0564	1.32 1.02 1.45	0.003 0.791 0.009	SPO0562 SPO0563 SPO0564	1.28 1.08 1.63	0.043 0.369 0.089	SPO0562 SPO0563 SPO0564	1.12 0.97 0.95	0.231 0.663	SPO0562 SPO0563 SPO0564	1.10 1.01 0.93	0.478 0.983 0.799
SP00565	0.76	0.697 SPO0565	0.81	0.405 SPO05			0.65	0.618	SPO0565	1.04	0.772		0.99		SPO0565	0.86		SP00565	0.90	0.799

SP00566	0.75	0.017 SPO0566	0.81		SP00567	0.8		0.65	0.558	SPO0566	0.78	0.078 SPC	00566	0.76	0.013 Si		0.98		SP00566	0.99	0.889
SPO0567 SPO0568 SPO0569	1.26 1.12 0.99	0.138 SPO0567 0.326 SPO0568 0.611 SPO0569	1.14 0.95 1.02	0.852	SPO0568 SPO0569 SPO0570	0.81 0.95 0.98	0.245 SPO0568 0.728 SPO0569 0.137 SPO0570	0.74 0.88 0.79	0.227 0.932 0.23	SPO0567 SPO0568 SPO0569	0.88 0.81 0.93	0.030 SPC	00567 00568 00569	1.03 0.72 0.88	0.840 SI 0.099 SI 0.080 SI	PO0568	1.05 1.06 0.81	0.953	SPO0567 SPO0568 SPO0569	0.99 0.86 0.70	0.816 0.605 0.046
SPO0570 SPO0571 SPO0572	0.98 0.66 1.26	0.784 SPO0570 0.456 SPO0571 0.014 SPO0572	1.07 0.63 1.07	0.491	SP00571 SP00572 SP00573	0.92 0.93 0.85	0.368 SPO0571 0.711 SPO0572 0.069 SPO0573	0.94 0.78 0.82	0.305 0.711 0.015	SPO0570 SPO0571 SPO0572	0.96 3.38 0.87	0.015 SPC	00570 00571 00572	1.04 2.57 0.80	0.979 SI 0.133 SI 0.156 SI		1.25 1.19 0.93	0.748	SP00570 SP00571 SP00572	1.11 1.23 0.96	0.799 0.711 0.818
SPO0573 SPO0574	2.17 0.81 1.03	0.011 SPO0573 0.259 SPO0574	1.93 0.83 1.06	0.009	SPO0574 SPO0575 SPO0576	0.82 0.74 0.85	0.72 SPO0574 0.162 SPO0575	0.83	0.84 0.056 0.238	SPO0573 SPO0574	0.41 0.88 0.68	0.003 SPC 0.742 SPC	00573	0.40 0.99 0.61	0.000 SI 0.729 SI	PO0573 PO0574	1.17 0.97 0.76	0.323 0.879	SPO0573 SPO0574	1.06 0.88 0.74	0.568 0.381 0.160
SP00575 SP00576 SP00577	0.66 0.96	0.666 SPO0575 0.007 SPO0576 0.772 SPO0577	1.06 0.73 1.01	0.009	SP00576 SP00577 SP00578	0.85 0.93 0.78	0.124 SP00576 0.721 SP00577 0.03 SP00578	0.07 0.95 0.96	0.238 0.527 0.256	SPO0575 SPO0576 SPO0577	1.30 1.00	0.079 SPC	00575 00576 00577	1.33 0.89	0.063 SI	PO0575 PO0576 PO0577	0.76	0.859	SP00575 SP00576 SP00577	0.74 0.99 0.95	0.160 0.951 0.684
SPO0578 SPO0579 SPO0580	1.15 1.17 0.76	0.008 SPO0578 0.736 SPO0579 0.324 SPO0580	1.13 1.17 0.81	0.061 0.775 0.664	SP00580	0.88 0.89 0.91	0.904 SPO0579 0.823 SPO0580 0.391 SPO0581	0.93 1.02 0.81	0.926 0.966 0.557	SPO0578 SPO0579	0.85 0.90 0.67		00578	0.96 0.88 0.57	0.906 SI	PO0578 PO0579 PO0580	0.86 0.98 0.79	0.976	SPO0578 SPO0579 SPO0580	0.86 1.01 0.89	0.223 0.981 0.731
SPO0581 SPO0582	0.75 0.8	0.205 SPO0581 0.153 SPO0582	0.78 0.88	0.408	SPO0582 SPO0583	0.81 0.95	0.295 SPO0582 0.364 SPO0583	0.81 0.85	0.446 0.486	SPO0581 SPO0582	1.14 0.68	0.181 SPC 0.034 SPC	00581	1.09 0.75	0.301 SI 0.207 SI	PO0581 PO0582	0.88	0.332 0.086	SPO0581 SPO0582	0.91 0.83	0.625 0.241
SPO0583 SPO0584 SPO0585	0.77 1.15 1.19	0.296 SPO0583 0.089 SPO0584 0.52 SPO0585	0.72 1.16 1.17	0.072	SP00586	0.78 0.4 0.95	0.413 SPO0584 0.937 SPO0585 0.011 SPO0586	0.87 0.69 0.85	0.18 0.863 0.006	SPO0583 SPO0584 SPO0585	0.97 0.70 0.79	0.025 SPC 0.443 SPC	00583 00584 00585	0.89 0.64 0.88	0.017 SI 0.605 SI	PO0583 PO0584 PO0585	0.97 0.71 1.12	0.321 0.753	SPO0583 SPO0584 SPO0585	0.98 0.79 0.98	0.892 0.070 0.872
SPO0586 SPO0587 SPO0588	0.77 0.87 0.78	0.063 SPO0586 0.539 SPO0587 0.71 SPO0588	0.63 0.79 0.83		SPO0587 SPO0588 SPO0589	0.73 0.93 0.83	0.009 SPO0587 0.98 SPO0588 0.92 SPO0589	0.99 0.98 0.87	0.015 0.969 0.821	SPO0586 SPO0587 SPO0588	1.64 1.31 1.46		00586 00587 00588	1.63 1.58	0.006 SI	PO0586 PO0587 PO0588	0.88 0.88		SPO0586 SPO0587 SPO0588	1.05 0.93 1.02	0.691 0.742 0.991
SPO0589 SPO0590	0.81 1.55	0.554 SPO0589 0.049 SPO0590	0.86 1.55 1.05	0.013		0.93	0.055 SPO0590 0.011 SPO0591	0.86	0.387	SPO0589 SPO0590 SPO0591	0.93 1.05 1.85	0.993 SPC	00589 00590 00591	0.93 1.11 1.96	0.823 SI		0.98	0.385	SPO0589 SPO0590 SPO0591	0.94 1.03	0.465
SPO0591 SPO0592 SPO0593	0.92 0.99	0.262 SPO0591 0.883 SPO0592 0.813 SPO0593	0.98 1.08	0.981	SPO0594	0.74 0.72 0.99	0.188 SPO0594	0.69 0.84 0.97	0.161 0.971 0.024	SPO0592 SPO0593	0.93 1.18	0.885 SPC	00592	0.88 1.12	0.587 SI 0.790 SI	PO0593	0.91 1.01 0.88	0.932 0.366	SPO0592 SPO0593	0.91 1.05 0.84	0.141 0.821 0.014
SPO0594 SPO0595 SPO0596	0.85 1.09 0.85	0.547 SPO0594 0.168 SPO0595 0.387 SPO0596	0.96 1.09 0.95	0.025	SPO0595 SPO0596 SPO0597	0.92 0.85 0.99	0.204 SPO0596	0.94 0.74 0.86	0.083 0.002 0.807	SPO0594 SPO0595 SPO0596	1.77 1.55 1.86	0.243 SPC	00594 00595 00596	2.17 1.60 1.99	0.000 SI 0.011 SI 0.000 SI	PO0595	1.14 0.92 1.14	0.402	SPO0594 SPO0595 SPO0596	1.00 0.88 1.10	0.786 0.223 0.448
SPO0597 SPO0598 SPO0599	0.78 0.75 1.06	0.354 SPO0597 0.186 SPO0598 0.512 SPO0599	0.8 0.87 1.1	0.691	SPO0598 SPO0599 SPO0600	0.94 0.97 0.98	0.384 SPO0598 0.459 SPO0599 0.178 SPO0600	0.95 0.89 0.78	0.087 0.102 0.121	SPO0597 SPO0598 SPO0599	1.13 0.86 1.06	0.955 SPC	00597 00598 00599	0.87 0.83 1.11	0.893 SI	PO0597 PO0598 PO0599	0.92 0.93 1.14	0.928	SPO0597 SPO0598 SPO0599	0.93 1.03 1.15	0.748 0.768 0.207
SPO0600 SPO0601	0.62 0.85	0.036 SPO0600 0.03 SPO0601	0.53 0.88	0.037	SPO0601 SPO0602	0.98 0.9	0.035 SPO0601 0.172 SPO0602	0.76 0.38	0.071	SPO0600 SPO0601	2.08 1.09	0.036 SPC 0.051 SPC	00600 00601	2.24 1.10	0.010 SI 0.009 SI	PO0600 PO0601	1.13 1.10	0.727 0.120	SPO0600 SPO0601	1.16 1.10	0.674 0.188
SPO0602 SPO0603 SPO0604	0.81 0.75 0.68	0.027 SPO0602 0.136 SPO0603 0.001 SPO0604	0.84 0.83 0.67	0.061	SPO0603 SPO0604 SPO0605	0.96 0.83 0.96	0.698 SPO0603 0.84 SPO0604 0.067 SPO0605	0.98 0.97 0.75	0.56 0.097 0.177	SPO0602 SPO0603 SPO0604	1.63 1.77 1.48	0.035 SPC	00602 00603 00604	1.80 2.34 1.58	0.015 SI	PO0602 PO0603 PO0604	1.15 1.12 0.89	0.425 0.326	SPO0602 SPO0603 SPO0604	1.16 1.13 0.98	0.428 0.750 0.827
SPO0605 SPO0606 SPO0607	0.75 0.7 0.85	0.046 SPO0605 0.045 SPO0606 0.742 SPO0607	0.85 0.76 0.76		SPO0606 SPO0607 SPO0608	0.96 0.93 0.97	0.653 SPO0606 0.87 SPO0607 0.896 SPO0608	0.87 0.83 0.92	0.873 0.764 0.797	SPO0605 SPO0606 SPO0607	1.98 1.22 0.94		00605 00606 00607	1.71 1.31 0.99	0.244 SI	PO0605 PO0606 PO0607	0.90 0.99 0.94	0.879	SPO0605 SPO0606 SPO0607	0.97 0.97 1.00	0.622 0.755 0.996
SPO0608 SPO0609	0.94 0.97	0.985 SPO0608 0.818 SPO0609	0.86 0.96 0.89	0.714	SPO0609 SPO0610 SPO0611	0.98 0.95 0.93	0.725 SPO0609 0.957 SPO0610	0.9 0.72 0.67	0.953 0.838 0.959	SPO0608 SPO0609 SPO0610	3.01 1.06	0.002 SPC 0.976 SPC	00608	2.72 1.21 0.74	0.000 SI 0.476 SI	PO0608 PO0609	0.13 0.24	0.002 0.000	SPO0608 SPO0609	0.15 0.27 0.57	0.000 0.001 0.012
SPO0610 SPO0611 SPO0612	0.85 0.81 0.9	0.643 SPO0611 0.62 SPO0612	0.84 0.9	0.577	SPO0612 SPO0613	0.87 0.81	0.934 SPO0612 0.204 SPO0613	0.96 0.88	0.721 0.415	SPO0611 SPO0612	0.86 1.13 1.02	0.587 SPC 0.882 SPC	00611	1.07 0.94	0.970 SI 0.193 SI	PO0610 PO0611 PO0612	0.29	0.009	SPO0610 SPO0611 SPO0612	0.29 0.32	0.001
SP00613 SP00614 SP00615	1.06 0.86 1.14	0.356 SPO0613 0.155 SPO0614 0.022 SPO0615	1.03 0.84 0.99	0.224	SPO0614 SPO0615 SPO0616	0.63 0.92 0.88	0.027 SPO0614 0.001 SPO0615 0.873 SPO0616	0.87 0.95 0.9	0.035 0.002 0.505	SPO0613 SPO0614 SPO0615	0.96 0.56 0.54	0.001 SPC	00613 00614 00615	0.95 0.53 0.56	0.001 SI	PO0613 PO0614 PO0615	0.25 0.57 0.61		SP00613 SP00614 SP00615	0.26 0.57 0.61	0.000 0.002 0.001
SPO0616 SPO0618 SPO0619	1.25 0.67 1.1	0.005 SPO0616 0.264 SPO0618 0.6 SPO0619	1.06 0.72 1.12	0.259	SPO0618 SPO0619 SPO0620	0.76 0.98 0.93	0.415 SPO0618 0.691 SPO0619 0.279 SPO0620	0.96 0.97 0.78	0.666 0.548 0.344	SPO0616 SPO0618 SPO0619	0.56 0.79 0.99	0.351 SPC	00616 00618 00619	0.61 0.77 0.97	0.000 SI 0.383 SI	PO0616	1.00 0.81 0.96		SP00616 SP00618 SP00619	1.00 0.83 0.95	0.958 0.610 0.826
SPO0620 SPO0621	0.81 0.87	0.406 SPO0620 0.668 SPO0621	0.79 0.88	0.218	SPO0621 SPO0622	0.88 0.91	0.402 SPO0621 0.925 SPO0622	0.95 0.98	0.255 0.952	SPO0620 SPO0621	1.24 0.93	0.275 SPC 0.512 SPC	00620 00621	1.14 0.92	0.659 SI 0.309 SI	PO0620 PO0621	1.21 0.99	0.203 0.761	SPO0620 SPO0621	1.15 1.02	0.506 0.989
SPO0622 SPO0623 SPO0624	0.81 0.97 0.76	0.859 SPO0622 0.916 SPO0623 0.011 SPO0624	0.76 0.99 0.86		SPO0623 SPO0624 SPO0628	0.9 0.92 0.88	0.909 SPO0623 0.53 SPO0624 0.263 SPO0628	0.85 0.93 0.94	0.926 0.694 0.267	SPO0622 SPO0623 SPO0624	0.98 1.31 1.41	0.119 SPC	00622 00623 00624	0.88 1.31 1.42	0.157 SI	PO0622 PO0623 PO0624	0.90 1.17 1.01	0.298	SPO0622 SPO0623 SPO0624	0.98 1.14 0.98	0.987 0.527 0.918
SPO0628 SPO0629 SPO0631	0.99 0.63 0.66	0.774 SPO0628 0.001 SPO0629 0.013 SPO0631	1.17 0.71 0.74	0.461	SPO0629 SPO0631 SPO0632	0.92 0.93 1.01	0.802 SPO0629 0.001 SPO0631 0.319 SPO0632	0.89 0.95 0.88	0.657 0.002 0.399	SPO0628 SPO0629 SPO0631	0.55 1.22	0.004 SPC	00628 00629 00631	0.45 1.14	0.007 SI	PO0628 PO0629 PO0631	0.43 0.93 0.93	0.535	SPO0628 SPO0629 SPO0631	0.47 0.95 1.06	0.004 0.725 0.189
SPO0632 SPO0633	0.9 0.51	0.441 SPO0632 0.006 SPO0633	0.85 0.52	0.007	SPO0633 SPO0634	0.95 0.94	0.624 SPO0633 0.227 SPO0634	0.83 0.96	0.41 0.463	SPO0632 SPO0633	0.94 1.46	0.766 SPC	D0632 D0633	0.93 1.47	0.639 SI 0.000 SI	PO0632 PO0633	0.88	0.241 0.645	SPO0632 SPO0633	0.92 0.93	0.454 0.497
SPO0634 SPO0635 SPO0636	0.71 0.69 1.06	0.019 SPO0634 0.323 SPO0635 0.243 SPO0636	0.73 0.79 1.16	0.327	SPO0636 SPO0637	0.81 0.96 0.88	0.189 SPO0635 0.694 SPO0636 0.914 SPO0637	0.62 0.95 0.8	0.21 0.516 0.873	SPO0634 SPO0635 SPO0636	0.87 1.96 0.94	0.157 SPC 0.660 SPC	00634 00635 00636	0.88 2.04 1.23	0.128 SI 0.428 SI	PO0634 PO0635 PO0636	1.11 1.13 1.03	0.769 0.941	SPO0634 SPO0635 SPO0636	1.08 1.22 0.96	0.048 0.618 0.830
SPO0637 SPO0638 SPO0639	1.03 0.48 1.15	0.608 SPO0637 0.001 SPO0638 0.042 SPO0639	0.97 0.57 1.06	0.763	SPO0638 SPO0639 SPO0640	0.96 0.88 0.68	0.263 SPO0638 0.875 SPO0639 0.277 SPO0640	0.74 0.87 0.83	0.009 0.407 0.022	SPO0637 SPO0638 SPO0639	1.29 2.09 1.33	0.000 SPC	00637 00638 00639	1.35 2.10 1.54	0.000 SI	PO0637 PO0638 PO0639	1.31 1.11 1.02		SPO0637 SPO0638 SPO0639	1.26 1.31 1.03	0.367 0.019 0.882
SP00640 SP00641 SP00642	1.08 0.76 1.01	0.314 SPO0640 0.122 SPO0641 0.875 SPO0642	1.04 0.85 0.98	0.092	SPO0641 SPO0642 SPO0643	0.99 0.93	0.175 SPO0641 1 SPO0642 0.924 SPO0643	0.94 0.96 0.85	0.197 0.879 0.25	SPO0640 SPO0641 SPO0642	1.52 1.34 0.68	0.036 SPC	00640 00641	1.82 1.31 0.69	0.007 SI	PO0640 PO0641 PO0642	1.22 1.01 0.86	0.979	SPO0640	1.11 1.00 0.85	0.290 0.981 0.460
SPO0643 SPO0644	0.89	0.239 SPO0643 0.155 SPO0644	0.84 0.68	0.043	SPO0644 SPO0645	0.57 0.95	0.427 SPO0644 0.113 SPO0645	0.89	0.378	SPO0643 SPO0644	0.87 1.05	0.360 SPC 0.132 SPC	00643	0.90	0.753 SI 0.106 SI	PO0643 PO0644	0.98		SPO0643 SPO0644	1.00	0.952 0.624
SPO0645 SPO0646 SPO0647	1.17 0.88 0.57	0.023 SPO0645 0.082 SPO0646 0.022 SPO0647	0.98 0.89 0.6		SPO0646 SPO0647 SPO0648	0.86 0.83 0.84	0.004 SP00646 0.016 SP00647 0.816 SP00648	0.99 1 0.99	0.004 0.003 0.616	SPO0645 SPO0646 SPO0647	0.84 3.10 3.06	0.000 SPC	00645 00646 00647	0.84 2.92 3.10		PO0645 PO0646 PO0647	0.99 2.07 1.59	0.000	SP00645 SP00646 SP00647	0.99 1.91 1.53	0.973 0.001 0.066
SPO0648 SPO0649 SPO0650	0.68 0.51 0.93	0.004 SPO0648 0 SPO0649 0.37 SPO0650	0.74 0.55 0.92	0.011 0.001 0.532	SPO0649 SPO0650 SPO0651	0.98 0.89 0.93	0.015 SPO0649 0.221 SPO0650 0.78 SPO0651	0.88 0.87 0.97	0.002 0.061 0.766	SPO0648 SPO0649 SPO0650	1.48 2.07 0.88		00648 00649 00650	1.40 2.25 0.89		PO0648 PO0649 PO0650	1.01 1.05 1.06		SPO0648 SPO0649 SPO0650	1.00 1.11	0.630 0.038 0.081
SPO0651 SPO0652 SPO0653	0.82 0.77 0.89	0.011 SPO0651 0.016 SPO0652 0.581 SPO0653	0.87 0.79 0.81	0.452 0.121 0.141		0.93 0.98 0.86	0.29 SPO0652 0.344 SPO0653 0.741 SPO0654	0.85 0.89 0.84	0.009 0.932 0.413	SPO0652 SPO0652	0.83 1.28 0.81	0.012 SPC	00651 00652	0.83 1.40 0.88		PO0651 PO0652	0.86 1.13 0.88	0.550	SPO0651 SPO0652 SPO0653	0.98 1.18 0.86	0.965 0.241 0.471
SPO0654 SPO0655	0.75 1.24	0.024 SPO0654 0.318 SPO0655	0.78 1.15	0.017	SPO0655 SPO0656	0.96 0.77	0.825 SPO0655 0.023 SPO0656	0.91 0.93	0.81 0.081	SPO0654 SPO0655	1.37 0.81	0.029 SPC 0.324 SPC	00654	1.40 0.92	0.015 SI 0.605 SI	PO0654 PO0655	1.13 0.93	0.602 0.746	SPO0654 SPO0655	1.10 0.83	0.319 0.553
SPO0656 SPO0657 SPO0658	0.8 1.16 0.84	0.136 SPO0656 0.418 SPO0657 0.406 SPO0658	0.85 1.04 0.79		SPO0657 SPO0658 SPO0659	0.93 0.86 0.94	0.857 SPO0657 0.011 SPO0658 0.206 SPO0659	0.88 0.93 0.61	0.956 0.073 0.512	SPO0656 SPO0657 SPO0658	1.57 1.25 1.20	0.279 SPC	00656 00657 00658	1.66 1.14 1.13	0.546 SI	PO0656 PO0657 PO0658	1.09 1.18 1.03	0.446	SPO0656 SPO0657 SPO0658	1.03 1.16 1.00	0.726 0.442 0.875
SPO0659 SPO0660 SPO0661	0.83 0.8 1.04	0.125 SPO0659 0.324 SPO0660 0.482 SPO0661	0.74 0.82 0.86	0.353	SPO0660 SPO0661 SPO0662	0.87 0.78 0.93	0.827 SPO0660 0.382 SPO0661 0.481 SPO0662	0.67 0.92 0.83	0.694 0.873 0.897	SPO0659 SPO0660 SPO0661	0.88 1.22 1.28	0.134 SPC	00659 00660 00661	0.85 1.18 1.51	0.262 SI	PO0659 PO0660 PO0661	0.96 0.84 1.20	0.286	SPO0659 SPO0660 SPO0661	1.01 0.85 1.12	0.996 0.268 0.529
SPO0662 SPO0663 SPO0664	1.09 1.06 0.89	0.595 SPO0662 0.623 SPO0663 0.921 SPO0664	1.02 1.03 0.99	0.634	SP00663 SP00664 SP00665	0.92 0.93 0.88	0.383 SPO0663 0.941 SPO0664 0.843 SPO0665	0.88 0.83 0.93	0.275 0.975 0.752	SPO0662 SPO0663 SPO0664	0.85 0.74 0.93	0.147 SPC	00662 00663 00664	0.88 0.64 0.81	0.175 SI 0.071 SI	PO0662	0.64 0.72 1.17	0.048 0.313	SP00662 SP00663 SP00664	0.67 0.74 1.14	0.007 0.248 0.787
SPO0665 SPO0666	0.9 1.16	0.479 SPO0665 0.644 SPO0666	0.99 1.1	0.841	SPO0666 SPO0667	0.89 0.98	0.784 SPO0666 0.549 SPO0667	0.99 0.98	0.708 0.802	SPO0665 SPO0666	1.32 0.72	0.061 SPC 0.555 SPC	D0665 D0666	1.32 0.71	0.104 SI 0.514 SI	PO0665 PO0666	1.05 0.88	0.776 0.766	SPO0665 SPO0666	1.10 0.90	0.594 0.786
SPO0667 SPO0668 SPO0669	1.04 1.75 2.13	0.788 SPO0667 0 SPO0668 0 SPO0669	1.13 1.48 1.74	0.056	SPO0668 SPO0669 SPO0670	0.99 0.85 0.94		0.86 0.75 0.97	0.135 0.726 0.054	SPO0668 SPO0669	0.85 1.39 0.99		00667 00668 00669	0.72 1.45 1.02	0.207 Si 0.025 Si 0.263 Si	PO0668	0.93 1.22 1.05	0.045	SPO0667 SPO0668 SPO0669	0.92 1.18 1.03	0.776 0.381 0.701
SPO0670 SPO0671 SPO0672	0.56 0.6 0.54	0.127 SPO0670 0 SPO0671 0.001 SPO0672	0.64 0.64 0.59	0.153	SPO0671 SPO0672 SPO0673	0.97 0.81 0.98	0.034 SPO0671 0.022 SPO0672 0.01 SPO0673	0.95 0.74 0.95	0.04 0.002 0.1	SPO0670 SPO0671 SPO0672	1.29 1.99 1.58	0.005 SPC	00670 00671 00672	1.32 1.75 1.69	0.151 SI 0.003 SI 0.001 SI	PO0671	1.26 1.70 1.42	0.010	SPO0670 SPO0671 SPO0672	1.30 1.60	0.148 0.032 0.019
SPO0673 SPO0674 SPO0675	0.83 0.93 0.79	0.015 SPO0673 0.331 SPO0674 0.625 SPO0675	0.85 0.85 0.75	0.045	SP00674 SP00675 SP00676	0.9 0.95 0.79	0.07 SPO0674 0.708 SPO0675 0.007 SPO0676	0.87 0.98 0.75	0.247 0.444 0.113	SPO0673 SPO0674 SPO0675	0.73 1.09	0.117 SPC	00673 00674 00675	0.72 1.23 1.94	0.038 SI 0.007 SI 0.056 SI		0.88 1.10 1.23	0.501	SP00673 SP00674 SP00675	0.91 1.09 1.22	0.340 0.313 0.504
SP00676 SP00677	1.25 1.21	0.008 SPO0676 0.644 SPO0677	1.03 1.17	0.422	SPO0677 SPO0678	0.93 0.85	0.721 SPO0677 0.112 SPO0678	0.94 0.81	0.673 0.881	SPO0676 SPO0677	1.75	0.022 SPC 0.860 SPC	00676 00677	1.70 0.80	0.002 SI 0.776 SI	PO0676 PO0677	0.94 0.78	0.509 0.616	SP00676 SP00677	0.93 0.77	0.691 0.612
SPO0678 SPO0679 SPO0680	0.65 0.79 0.95	0.002 SPO0678 0.079 SPO0679 0.912 SPO0680	0.68 0.89 0.96		SPO0679 SPO0680 SPO0681	0.9 0.88 0.93	0.693 SPO0679 0.267 SPO0680 0.182 SPO0681	0.89 0.87 0.91	0.207 0.068 0.346	SPO0678 SPO0679 SPO0680	0.98 0.95 2.15	0.690 SPC	00678 00679 00680	0.99 0.89 2.13	0.215 SI	PO0678 PO0679 PO0680	1.00 0.97 1.17	0.780	SPO0678 SPO0679 SPO0680	0.99 1.01 1.19	0.952 0.992 0.118
SPO0681 SPO0682 SPO0683	0.72 0.98 0.85	0.189 SPO0681 0.994 SPO0682 0.291 SPO0683	0.78 0.96 0.88	0.982	SPO0682 SPO0683 SPO0684	0.88 0.9	0.529 SPO0682 0.27 SPO0683 0.018 SPO0684	0.89 0.9 0.87	0.96 0.237 0.002	SPO0681 SPO0682 SPO0683	1.76 0.83 1.38	0.729 SPC	00681 00682 00683	1.47 0.83 1.31	0.799 SI	PO0681 PO0682 PO0683	1.19 0.93 1.14	0.899	SPO0681 SPO0682 SPO0683	1.21 0.93 1.13	0.401 0.912 0.450
SPO0684 SPO0685	0.75 0.76	0.025 SPO0684 0.243 SPO0685	0.79 0.75	0.163	SPO0685 SPO0686	0.91	0.117 SPO0685 0.001 SPO0686	0.89 0.93	0.006 0.009	SPO0684 SPO0685	2.05 1.18	0.000 SPC 0.135 SPC	00684 00685	2.21 1.16	0.000 SI 0.063 SI	PO0684 PO0685	1.07 0.94	0.492 0.628	SPO0684 SPO0685	1.12 1.04	0.171 0.600
SPO0686 SPO0687 SPO0688	0.71 0.91 1.15	0.053 SPO0686 0.276 SPO0687 0.185 SPO0688	0.74 0.94 1.13	0.836	SPO0687 SPO0688 SPO0689	0.78 0.96 0.92	0.064 SPO0687 0.983 SPO0688 0.009 SPO0689	0.85 0.93 0.88	0.018 0.855 0.006	SPO0686 SPO0687 SPO0688	1.67 1.38 0.98	0.032 SPC 0.700 SPC	00686 00687 00688	1.67 1.43 1.02	0.020 SI 0.388 SI		1.09 1.08 1.10	0.654 0.462	SPO0686 SPO0687 SPO0688	1.13 1.13 1.10	0.088 0.263 0.517
SPO0689 SPO0690 SPO0691	1.77 2.04 1.13	0 SPO0689 0.001 SPO0690 0.468 SPO0691	1.47 1.83 1.3	0.002 0.002 0.131	SPO0690 SPO0691 SPO0692	0.93 0.94 0.9	0.654 SPO0690 0.419 SPO0691 0.915 SPO0692	0.99 0.81 0.85	0.457 0.535 0.86	SPO0689 SPO0690 SPO0691	1.54 1.09 1.44	0.860 SPC	00689 00690 00691	1.68 1.21 1.27		PO0689 PO0690 PO0691	1.13 1.18 1.09	0.553	SPO0689 SPO0690 SPO0691	0.91 1.10 1.09	0.177 0.483 0.633
SPO0692 SPO0693	0.99 1.98	0.816 SPO0692 0.002 SPO0693	1.01	0.039	SP00693 SP00694	0.97	0.809 SPO0694	0.93 1.01	0.002	SPO0692 SPO0693	0.11 0.83	0.078 SPC	00692	0.11	0.000 SI 0.713 SI	PO0693	1.08	0.761	SPO0692 SPO0693	0.85 0.88	0.570 0.310
SPO0694 SPO0695 SPO0697	1 1.26 1.66	0.901 SPO0694 0.004 SPO0695 0.088 SPO0697	1.01 1.23 1.43	0.003	SPO0695 SPO0697 SPO0698	0.99 0.78 0.95	0.002 SPO0698	0.94 0.94 0.97	0.843 0.62 0.004	SPO0694 SPO0695 SPO0697	0.91 0.95 1.87	0.886 SPC	00694 00695 00697	0.92 1.05 1.73	0.937 SI 0.146 SI 0.007 SI	PO0695 PO0697	1.10 1.06 0.83	0.580 0.327	SPO0694 SPO0695 SPO0697	1.04 1.07 0.78	0.833 0.297 0.190
SPO0698 SPO0699 SPO0700	3.5 1.87 0.99	0 SPO0698 0.09 SPO0699 0.928 SPO0700	2.72 1.75 1.07	0.231	SP00701	0.93 0.9 0.88	0.815 SPO0699 0.359 SPO0700 0.048 SPO0701	0.88 0.99 0.85	0.856 0.849 0.018	SPO0698 SPO0699 SPO0700	1.16 2.60 0.70	0.123 SPC 0.014 SPC		1.18 2.47 0.73	0.072 SI 0.123 SI 0.006 SI	PO0699	0.55 0.71 0.96	0.486 0.747	SPO0698 SPO0699 SPO0700	0.63 0.71 1.04	0.003 0.432 0.485
SP00701 SP00702 SP00703	4.31 0.93 0.87	0 SPO0701 0.851 SPO0702 0.364 SPO0703	3.73 0.93 0.81	0.914	SP00702 SP00703 SP00704	0.93 0.94 0.81	0.822 SPO0702 0.058 SPO0703 0.561 SPO0704	0.78 0.81 0.84	0.981 0.604 0.946	SPO0701 SPO0702 SPO0703	0.07 1.27 1.47	0.038 SPC	00701 00702 00703	0.07 1.35 1.48	0.123 SI	PO0701 PO0702 PO0703	1.03 1.11	0.969	SP00701 SP00702 SP00703	2.13 1.06 1.13	0.001 0.849 0.531
SPO0704 SPO0705	1.08 0.8	0.263 SPO0704 0.137 SPO0705	1.01 0.87	0.562	SP00705 SP00706	1 0.99	0.529 SPO0705 0.662 SPO0706	0.85 0.93	0.847 0.492	SPO0704 SPO0705	0.86 1.21	0.167 SPC 0.212 SPC	00704	0.79 1.27	0.105 SI 0.135 SI	PO0704 PO0705	0.99 1.10	0.840 0.728	SPO0704 SPO0705	0.97 0.97	0.756 0.916
SP00706 SP00707 SP00708	0.73 0.46 1.14	0.02 SPO0706 0 SPO0707 0.553 SPO0708	0.79 0.54 1.04		SPO0707 SPO0708 SPO0709	0.49 0.95 0.97	0.012 SPO0707 0.709 SPO0708 0.549 SPO0709	0.91 0.78 0.87	0.017 0.818 0.606	SPO0706 SPO0707 SPO0708	1.06 1.72 0.76	0.000 SPC 0.159 SPC	00706 00707 00708	0.95 1.76 0.65	0.000 SI 0.048 SI	PO0706 PO0707 PO0708	1.04 1.09 1.04	0.223 0.957	SPO0706 SPO0707 SPO0708	1.01 1.21 0.89	0.838 0.002 0.591
SP00709 SP00710	0.5 0.87	0.066 SPO0709 0.447 SPO0710	0.52 0.93		SP00710 SP00711	0.92 0.63	0.462 SPO0710 0.444 SPO0711	0.88	0.487 0.609	SPO0709 SPO0710	2.67 0.91		00709	2.71 0.89	0.016 SI 0.735 SI	PO0709 PO0710	1.28		SP00709 SP00710	1.17	0.546 0.594

SP00711 SP00712	1.15	0.14 SPO0 0.539 SPO0		1.13		SP00712 SP00713	0.78	0.592 SP00712 0.723 SP00713	0.84	0.897	SPO0711 SPO0712	0.86	0.804	SPO0711 SPO0712	0.91	0.934	SPO0711 SPO0712	0.90	0.421	SP00711 SP00712	0.86	0.567 0.958
SP00713 SP00714	1.17 0.54	0.364 SPO0 0 SPO0	713 714	1.2 0.66	0.215 0.002	SP00714 SP00715	0.93 0.78	0.51 SP00714 0.346 SP00715	0.84 0.88	0.024 0.418	SPO0713 SPO0714	1.24 1.42	0.155 0.001	SPO0713 SPO0714	1.31 1.38	0.094	SPO0713 SPO0714	1.15 0.95	0.500 0.649	SP00713 SP00714	1.14 1.06	0.480 0.483
SP00715 SP00716 SP00717	0.89 1.27 0.96	0.129 SPO0 0.277 SPO0 0.309 SPO0	716	0.96 1.29 0.88	0.27	SP00716 SP00717 SP00718	0.86 0.17 0.3	0.962 SP00716 0.232 SP00717 0.996 SP00718	0.93 0.96 0.93	0.865 0.284 0.789	SPO0715 SPO0716 SPO0717	1.07 1.02 0.95	0.167 0.706 0.647	SPO0715 SPO0716 SPO0717	1.04 0.98 1.03	0.155 0.719 0.241	SPO0715 SPO0716 SPO0717	1.02 1.06 0.97	0.695 0.842 0.845	SP00715 SP00716 SP00717	0.99 1.04 0.98	0.958 0.872 0.923
SPO0718 SPO0719 SPO0720	0.96 2.08 1.06	0.955 SPO0 0 SPO0 0.607 SPO0	719	1 1.74 1.07	0.911 S	SPO0719 SPO0720 SPO0721	0.71 0.93 0.75	0.175 SPO0719 0.08 SPO0720 0.206 SPO0721	0.69 0.99 1.01	0.853 0.031 0.26	SPO0718 SPO0719 SPO0720	0.56 0.87 1.18	0.306 0.864 0.001	SPO0718 SPO0719 SPO0720	0.48 0.85 1.27	0.125 0.444 0.001	SPO0718 SPO0719 SPO0720	0.53 1.16	0.204 0.235 0.036	SP00718 SP00719 SP00720	0.57 1.07 1.09	0.098 0.329 0.039
SPO0721 SPO0722	1.26 1.59	0.095 SPO0 0 SPO0	721 722	1.13 1.5	0.013 0.023	SPO0722 SPO0723	0.88 0.94	0.49 SPO0722 0.73 SPO0723	0.5 0.94	0.461 0.584	SPO0721 SPO0722	0.89 0.74	0.260 0.506	SPO0721 SPO0722	0.96 0.74	0.324 0.511	SPO0721 SPO0722	1.08 1.03	0.819 0.766	SP00721 SP00722	1.14 0.96	0.025 0.842
SPO0723 SPO0724 SPO0725	1.01 0.94 0.78	0.97 SPO0 0.901 SPO0 0.398 SPO0	724	0.89 0.98 0.78	0.931	SPO0724 SPO0725 SPO0726	0.97 0.96 0.99	0.917 SP00724 0.924 SP00725 0.559 SP00726	0.9 0.93 0.92	0.832 0.3 0.151	SPO0723 SPO0724 SPO0725	1.28 1.14 1.27	0.340 0.509 0.639	SPO0723 SPO0724 SPO0725	1.38 1.15 1.42	0.282 0.492 0.294	SPO0723 SPO0724 SPO0725	0.97 1.07 1.32	0.831	SP00723 SP00724 SP00725	0.97 1.01 1.05	0.999 0.959 0.935
SPO0726 SPO0727 SPO0728	1 1.08 1.13	0.948 SPO0 0.191 SPO0 0.624 SPO0	727	0.99 1.05 0.99	0.642	SP00727 SP00728 SP00729	0.9 0.92 0.72	0.03 SP00727 0.079 SP00728 0.584 SP00729	0.99 0.97	0.535 0.117 0.937	SPO0726 SPO0727 SPO0728	1.50 1.83 1.02	0.051 0.000 0.031	SPO0726 SPO0727 SPO0728	1.47 2.03 1.00	0.000 0.000 0.042	SPO0726 SPO0727 SPO0728	1.10 1.06 1.10	0.375	SP00726 SP00727 SP00728	1.07 1.06 1.19	0.405 0.626
SPO0729 SPO0731	1.58	0.001 SPO0 0.081 SPO0	729 731	1.37 1.27	0.003 0.002	SP00731 SP00732	0.8 0.93	0.289 SPO0731 0.466 SPO0732	0.98 0.61	0.744 0.413	SPO0729 SPO0731	1.07 1.83	0.244	SPO0729 SPO0731	1.08 2.03	0.124	SPO0729 SPO0731	0.83 1.10	0.040 0.743	SPO0729 SPO0731	0.93 1.00	0.555 0.931
SPO0732 SPO0733 SPO0734	1 1.08 0.93	0.829 SPO0 0.437 SPO0 0.621 SPO0	733	1.04 1.04 0.93	0.149	SPO0733 SPO0734 SPO0735	0.75 0.83 0.67	0.132 SP00733 0.748 SP00734 0.115 SP00735	0.78 0.85 1.01	0.067 0.794 0.443	SPO0732 SPO0733 SPO0734	1.10 0.64 0.72	0.386 0.010 0.120	SPO0732 SPO0733 SPO0734	1.20 0.69 0.77	0.031 0.004 0.109	SPO0732 SPO0733 SPO0734	0.89 1.01 1.04	0.884	SP00732 SP00733 SP00734	0.94 1.05 1.02	0.578 0.543 0.843
SPO0735 SPO0736	0.78 0.97 1.09	0.129 SPO0 0.988 SPO0 0.395 SPO0	736	0.81	0.38 S 0.956 S 0.541 S	SPO0736 SPO0737 SPO0738	0.67 0.76 0.8	0.877 SPO0736 0.953 SPO0737 0.41 SPO0738	0.97 0.78 0.96	0.892 0.477 0.129	SPO0735 SPO0736 SPO0737	1.13 0.89	0.627 0.919 0.491	SPO0735 SPO0736 SPO0737	0.98 0.80 0.98	0.561 0.825 0.233	SPO0735 SPO0736 SPO0737	1.02 0.77 0.98	0.996 0.796 0.783	SP00735 SP00736 SP00737	1.10 0.80 0.93	0.573 0.827 0.565
SP00737 SP00738 SP00739	0.79 0.7	0.256 SPO0 0.032 SPO0	738 739	0.82 0.81	0.09 S	SPO0739 SPO0740	0.89 0.93	0.787 SPO0739 0.736 SPO0740	0.17 0.29	0.749 0.806	SPO0738 SPO0739	1.22 1.70 1.20	0.057 0.753	SPO0738 SPO0739	1.57 0.98	0.015 0.849	SPO0738 SPO0739	1.08 0.87	0.696 0.596	SPO0738 SPO0739	1.11 0.96	0.512 0.879
SPO0740 SPO0741 SPO0742	0.83 0.62 0.67	0.711 SPO0 0.015 SPO0 0.013 SPO0	741	0.87 0.74 0.72		SPO0741 SPO0742 SPO0743	0.93 0.85 0.91	0.623 SP00741 0.236 SP00742 0.052 SP00743	0.72 0.91 0.75	0.738 0.096 0.274	SPO0740 SPO0741 SPO0742	0.74 0.88 0.93	0.533 0.498 0.806	SPO0740 SPO0741 SPO0742	0.75 0.88 1.05	0.488 0.608 0.162	SPO0740 SPO0741 SPO0742	0.75 0.77 1.05	0.422 0.055 0.797	SP00740 SP00741 SP00742	0.74 0.79 1.07	0.311 0.022 0.540
SPO0743 SPO0744 SPO0745	0.99 0.73 0.64	0.849 SPO0 0.316 SPO0 0.078 SPO0	743 744	1.02 0.78 0.68	0.425 0.147	SP00744 SP00745	0.77	0.109 SP00744 0.158 SP00745 0.019 SP00746	0.96 0.94 0.94	0.315 0.199 0.044	SPO0743 SPO0744 SPO0745	1.27 1.03 1.30	0.003 0.979 0.077	SPO0743 SPO0744 SPO0745	1.39 1.14 1.37	0.027 0.450 0.047	SPO0743 SPO0744 SPO0745	1.17 1.24 1.15	0.523 0.441 0.339	SP00743 SP00744 SP00745	1.13 1.17 1.14	0.576 0.529 0.471
SPO0746 SPO0747	0.6 0.81	0.014 SPO0 0.69 SPO0	746	0.66 0.99	0.001 0.678	SPO0746 SPO0747 SPO0748	0.88 0.34 0.61	0.27 SPO0747 0.835 SPO0748	0.82 0.93	0.143 0.778	SPO0745 SPO0746 SPO0747	1.23 0.88	0.082 0.185	SPO0745 SPO0746 SPO0747	1.26	0.011	SPO0746 SPO0747	0.95 0.91	0.610	SPO0746 SPO0747	1.05 0.93	0.733 0.431
SPO0748 SPO0749 SPO0750	0.81 1.05 0.99	0.834 SPO0 0.544 SPO0 0.977 SPO0	749	0.85 0.8 0.92	0.064	SPO0749 SPO0750 SPO0751	0.78 0.98 0.86	0.865 SPO0749 0.988 SPO0750 0.585 SPO0751	0.85 0.7 0.78	0.126 0.957 0.626	SPO0748 SPO0749 SPO0750	1.09 1.14 0.66	0.917 0.832 0.701	SPO0748 SPO0749 SPO0750	0.90 1.08 0.60	0.816 0.542 0.630	SPO0748 SPO0749 SPO0750	1.11 1.34 0.86	0.116	SP00748 SP00749 SP00750	0.93 0.96 0.87	0.910 0.699 0.862
SP00751 SP00752	1.28 1.01	0.418 SPO0 0.903 SPO0	751 752	1.03 0.99	0.827 0.955	SPO0752 SPO0753	0.98 0.85	0.304 SP00752 0.371 SP00753	0.97 0.76	0.278	SPO0751 SPO0752	1.17 0.90	0.516 0.892	SPO0751 SPO0752	1.07 0.89	0.718 0.889	SPO0751 SPO0752	1.12 1.26	0.804 0.416	SPO0751 SPO0752	1.08 1.26	0.821 0.476
SPO0753 SPO0754 SPO0755	0.76 0.6 0.75	0.518 SPO0 0.006 SPO0 0.531 SPO0	754	0.75 0.68 0.78		SPO0754 SPO0755 SPO0756	0.93 0.76 0.85	0.009 SP00754 0.616 SP00755 0.012 SP00756	0.83 0.7 0.64	0.009 0.662 0.033	SPO0754 SPO0755	0.75 1.04 0.88	0.466 0.761 0.894	SPO0753 SPO0754 SPO0755	0.74 1.13 0.81	0.392 0.259 0.771	SPO0753 SPO0754 SPO0755	0.98 1.23 1.13		SP00753 SP00754 SP00755	1.07 1.23 1.18	0.817 0.183 0.706
SP00756 SP00757 SP00758	0.82 0.62	0.143 SP00 0.005 SP00 0.913 SP00	757	0.81 0.67 0.94	0.006	SPO0757 SPO0758 SPO0759	0.95 0.85	0.171 SPO0757 0.722 SPO0758 0.604 SPO0759	0.81 0.99 0.96	0.011 0.782 0.402	SPO0756 SPO0757 SPO0758	0.88 0.85 0.58	0.516 0.324 0.033	SPO0756 SPO0757 SPO0758	0.89 0.81 0.65	0.341 0.191 0.028	SPO0756 SPO0757 SPO0758	1.12 0.99 0.86	0.902	SP00756 SP00757 SP00758	1.11 1.06 0.88	0.313 0.484 0.368
SPO0759 SPO0760	1.13 0.83	0.308 SPO0 0.557 SPO0	759 760	1.09	0.213	SPO0760 SPO0761	0.92 0.84	0.689 SP00760 0.151 SP00761	0.8 0.93	0.534 0.004	SPO0759 SPO0760	0.12 1.77	0.000 0.027	SPO0760	0.65 0.11 1.54	0.000	SPO0759 SPO0760	1.23 1.14	0.016 0.542	SPO0759 SPO0760	1.15 1.07	0.163 0.772
SP00761 SP00762 SP00763	0.41 1.16 0.76	0 SP00 0.09 SP00 0.117 SP00	762	0.45 1.11 0.87		SPO0763 SPO0764	0.99 0.85 0.91	0.134 SP00762 0.249 SP00763 0.157 SP00764	0.87 0.81 0.85	0.118 0.25 0.345	SPO0761 SPO0762 SPO0763	0.76 1.40	0.000 0.017 0.102	SPO0761 SPO0762 SPO0763	0.80 1.43	0.000 0.048 0.083	SPO0761 SPO0762 SPO0763	1.04 0.98 1.29	0.423 0.774 0.324	SP00761 SP00762 SP00763	1.16 0.93 1.15	0.005 0.328 0.641
SP00764 SP00765 SP00766	0.93 0.83 1.26	0.951 SPO0 0.102 SPO0 0.716 SPO0	765	0.91 0.78 1.13	0.057	SPO0765 SPO0766 SPO0767	0.93 0.77 0.97	0.017 SPO0765 0.94 SPO0766 0.881 SPO0767	0.58 0.88 0.9	0.009 0.911 0.957	SPO0764 SPO0765 SPO0766	1.29 1.44 0.92	0.065 0.014 0.829	SPO0764 SPO0765 SPO0766	1.35 1.48 1.13	0.001 0.001 0.906	SPO0764 SPO0765 SPO0766	1.08 1.19 1.14	0.159 0.307 0.925	SP00764 SP00765 SP00766	1.04 1.16 0.93	0.688 0.270 0.900
SP00767 SP00768	0.93 1.55	0.665 SPO0 0.022 SPO0	767 768	0.93 1.64	0.641 S	SPO0768 SPO0769	0.93 0.87	0.297 SPO0768 0 SPO0769	0.97 0.9	0.126 0.001	SPO0767 SPO0768	1.41	0.002 0.741	SPO0767 SPO0768	1.36	0.001	SPO0767 SPO0768	0.96 0.98	0.841 0.862	SPO0767 SPO0768	0.97 0.96	0.944
SP00769 SP00770 SP00771	0.37 0.8 1.07	0 SP00 0.165 SP00 0.32 SP00	770	0.4 0.78 0.95	0.353	SP00770 SP00771 SP00772	0.96 0.84 0.85	0.558 SP00770 0.661 SP00771 0.401 SP00772	0.35 1 0.64	0.227 0.782 0.34	SPO0769 SPO0770 SPO0771	1.69 1.39	0.000 0.044 0.153	SPO0769 SPO0770 SPO0771	1.39 1.44	0.000 0.188 0.127	SPO0769 SPO0770 SPO0771	1.09 0.98 0.97	0.579 0.857 0.853	SP00769 SP00770 SP00771	1.05 1.02 0.83	0.687 0.944 0.394
SP00772 SP00773 SP00774	0.9 0.61 0.74	0.645 SP00 0.034 SP00 0.002 SP00	773	0.85 0.61 0.75	0.043	SP00773 SP00774 SP00775	0.81 1.01 0.96	0.465 SP00773 0.246 SP00774 0.76 SP00775	0.84 0.95 0.99	0.572 0.081 0.998	SPO0772 SPO0773 SPO0774	0.85 0.96 1.79	0.467 0.740 0.000	SPO0772 SPO0773 SPO0774	0.88 0.98 1.90	0.591	SPO0772 SPO0773 SPO0774	0.85 0.88 0.87	0.573	SP00772 SP00773 SP00774	0.80 0.93 0.91	0.143 0.713 0.352
SP00775 SP00776	1.11 1.13	0.449 SPO0 0.341 SPO0	775 776	1.04 1.13	0.464 0.487	SP00776 SP00777	0.7 0.99	0.752 SP00776 0.923 SP00777	0.98 0.76	0.77 0.845	SPO0775 SPO0776	1.16 1.08	0.150 0.733	SPO0775 SPO0776	1.24 1.13	0.128 0.626	SPO0775 SPO0776	1.01 0.94	0.949 0.512	SP00775 SP00776	0.95 0.93	0.644
SP00777 SP00778 SP00779	0.95 0.94 1.31	0.955 SPO0 0.95 SPO0 0.063 SPO0	778	0.97 0.98 1.26	0.93	SPO0778 SPO0779 SPO0780	0.92 0.97 0.82	0.925 SP00778 0.597 SP00779 0.263 SP00780	0.78 0.88 0.74	0.957 0.21 0.813	SPO0777 SPO0778 SPO0779	0.76 1.14 1.02	0.850 0.547 0.489	SPO0777 SPO0778 SPO0779	0.76 1.21 1.07	0.859 0.423 0.011	SPO0777 SPO0778 SPO0779	0.76 0.92 1.14	0.692	SP00777 SP00778 SP00779	0.76 0.93 1.09	0.730 0.735 0.164
SPO0780 SPO0781 SPO0782	1 1.15 0.95	0.387 SPO0 0.177 SPO0 0.6 SPO0	781	0.99 1.06 1.05		SPO0781 SPO0782 SPO0783	0.88 0.85 0.93	0.652 SP00781 0.224 SP00782 0.221 SP00783	0.89 0.89	0.457 0.865 0.251	SPO0780 SPO0781 SPO0782	0.88 0.98 1.18	0.533 0.752 0.001	SPO0780 SPO0781	0.92 0.98 1.20	0.462 0.636 0.286	SPO0780 SPO0781 SPO0782	0.81 1.06 0.79	0.911	SP00780 SP00781 SP00782	0.81 0.97 0.89	0.213 0.749 0.707
SPO0783 SPO0784	0.94 0.55	0.955 SPO0 0.033 SPO0	783 784	0.86 0.74	0.736 S	SP00784 SP00785	0.83 0.96	0.001 SP00784 0.978 SP00785	0.98 0.93	0.001 0.965	SPO0783 SPO0784	1.67 12.60	0.073 0.000	SPO0783 SPO0784	1.67 12.80	0.087	SPO0783 SPO0784	0.99 0.95	0.969 0.960	SP00783 SP00784	1.01 0.97	0.963 0.995
SP00785 SP00786 SP00787	0.99 1.51 1.02	0.976 SPO0 0.002 SPO0 0.348 SPO0	786	1.06 1.4	0.001	SPO0786 SPO0787 SPO0788	0.91 0.78 0.83	0.356 SP00786 0.932 SP00787 0.737 SP00788	0.98 0.8 0.83	0.323 0.678 0.664	SPO0785 SPO0786 SPO0787	0.63 0.93 0.97	0.683 0.513 0.993	SPO0785 SPO0786 SPO0787	0.61 1.02 0.99	0.643 0.803 0.696	SPO0785 SPO0786 SPO0787	0.94 1.10 1.01	0.947 0.439 0.910	SP00785 SP00786 SP00787	0.93 1.04 0.98	0.933 0.704 0.703
SPO0788 SPO0789 SPO0790	0.78 1.02 1.13	0.195 SPO0 0.589 SPO0 0.291 SPO0	789	0.81 1.03 1.01		SPO0789 SPO0790 SPO0791	0.97 0.88 0.66	0.362 SPO0789 0.642 SPO0790 0.601 SPO0791	0.94 0.96	0.252 0.269 0.419	SPO0788 SPO0789 SPO0790	1.03 0.06 0.04	0.879 0.000 0.000	SPO0788 SPO0789 SPO0790	1.15 0.05 0.04	0.444 0.000 0.000	SPO0788 SPO0789 SPO0790	0.93 0.64 0.43	0.244 0.050 0.005	SP00788 SP00789 SP00790	0.94 0.67 0.44	0.662 0.005 0.001
SPO0791 SPO0792 SPO0793	1.06 1.19 0.83	0.31 SP00 0.028 SP00 0.241 SP00	791 792	1.11 1.05 0.88	0.045 0.218	SPO0792 SPO0793 SPO0794	0.99 0.91 0.93	0.362 SPO0792 0.925 SPO0793 0.349 SPO0794	0.97 0.97 0.89	0.838 0.756 0.597	SPO0791 SPO0792	0.57 0.68	0.000 0.003	SPO0791 SPO0792 SPO0793	0.58 0.65	0.000 0.006 0.002	SPO0791 SPO0792 SPO0793	1.05 1.01 0.99	0.636 0.670 0.885	SP00791 SP00792 SP00793	1.01 0.99 1.04	0.741 0.897 0.865
SPO0794 SPO0795	0.76 1.18	0.212 SPO0 0.152 SPO0	794 795	0.79	0.371 5	SPO0795 SPO0796	0.88	0.84 SPO0795 0.622 SPO0796	0.93	0.993	SPO0794 SPO0795	0.38	0.001 0.886	SPO0794 SPO0795	0.38	0.001	SPO0794 SPO0795	1.04	0.840	SPO0794 SPO0795	1.00	0.919 0.471
SP00796 SP00797 SP00798	1.19 1.19 0.86	0.096 SPO0 0.731 SPO0 0.795 SPO0	797	1.12 1.02 0.9	0.909	SPO0797 SPO0798 SPO0799	0.95 0.86 0.71	0.215 SP00797 0.768 SP00798 0.576 SP00799	0.9 0.78 0.92	0.916 0.826 0.747	SPO0796 SPO0797 SPO0798	1.18 0.92 1.20	0.432 0.981 0.744	SPO0796 SPO0797 SPO0798	1.11 0.85 1.17	0.818	SPO0796 SPO0797 SPO0798	0.99 1.02 0.89	0.964	SP00796 SP00797 SP00798	1.01 1.06 0.94	0.962 0.902 0.862
SPO0799 SPO0800 SPO0801	1.35 0.76 0.83	0.471 SPO0 0.173 SPO0 0.608 SPO0	800	1.36 0.71 0.88	0.111	SPO0800 SPO0801 SPO0802	0.81 0.85 0.92	0.108 SPO0800 0.509 SPO0801 0.354 SPO0802	0.99 0.92 0.81	0.054 0.504 0.218	SPO0799 SPO0800 SPO0801	0.90 1.39 0.81	0.665 0.214 0.471	SPO0799 SPO0800 SPO0801	0.94 1.37 0.81	0.688 0.016 0.362	SPO0799 SPO0800 SPO0801	0.91 1.23 0.84	0.091	SP00799 SP00800 SP00801	0.92 1.17 0.86	0.648 0.112 0.550
SPO0802 SPO0803	1.4 0.93	0.008 SPO0 0.758 SPO0	802 803	1.36 0.93	0.006 0.882	SPO0803 SPO0804	0.91 0.79	0.529 SPO0803 0.089 SPO0804	0.91 0.86	0.55 0.063	SPO0802 SPO0803	1.70 1.17	0.007 0.249	SPO0802 SPO0803	1.67 1.06	0.001 0.561	SPO0802 SPO0803	1.16 1.16	0.158 0.579	SPO0802 SPO0803	1.15 1.07	0.130 0.688
SPO0804 SPO0805 SPO0806	1.29 1.52 1.91	0.004 SP00 0.001 SP00 0.022 SP00	805	1.24 1.42 1.71	0.003	SPO0805 SPO0806 SPO0807	0.6 0.83 0.97	0.026 SPO0805 0.265 SPO0806 0.872 SPO0807	0.82 0.88 0.91	0.024 0.176 0.783	SPO0804 SPO0805 SPO0806	0.72 0.85 1.30	0.011 0.543 0.025	SPO0804 SPO0805 SPO0806	0.74 0.93 1.32	0.023 0.356 0.021	SPO0804 SPO0805 SPO0806	0.93 0.91 1.08	0.425	SPO0804 SPO0805 SPO0806	0.93 0.85 0.98	0.676 0.100 0.958
SPO0807 SPO0808 SPO0809	1.43 1.33 1.04	0.083 SPO0 0.214 SPO0 0.496 SPO0	808	1.4 1.35	0.361	SPO0808 SPO0809 SPO0810	0.69 0.91 0.69	0.817 SPO0808 0.471 SPO0809 0.896 SPO0810	0.81 0.96 0.88	0.862 0.17 0.979	SPO0807 SPO0808 SPO0809	0.57 1.06 0.88	0.012 0.508 0.375	SPO0807 SPO0808 SPO0809	0.66 1.17 0.90	0.006 0.362 0.303	SPO0807 SPO0808 SPO0809	1.08 0.97 0.99	0.999	SPO0807 SPO0808 SPO0809	1.03 0.88 0.95	0.967 0.652 0.603
SPO0810 SPO0811	0.85 1.11	0.753 SPO0 0.321 SPO0	810 811	0.89	0.342 S	SP00811 SP00812	0.75 0.65	0.391 SPO0811 0.005 SPO0812	0.83 0.72	0.098 0.002	SPO0810 SPO0811 SPO0812	0.68 1.15	0.091 0.148	SPO0810 SPO0811	0.64 1.18	0.039 0.013	SPO0810 SPO0811	0.88 0.96	0.665 0.596	SPO0810 SPO0811	0.95 0.99	0.549 0.914
SPO0812 SPO0813 SPO0814	1.75 0.85 0.99	0 SPO0 0.583 SPO0 0.576 SPO0	813 814	0.94 0.97	0.922 S	SPO0813 SPO0814 SPO0815	0.61 0.88 0.93	0.682 SPO0813 0.996 SPO0814 0.995 SPO0815	0.93 0.6 0.95	0.743 0.648 0.909	SPO0813 SPO0814	0.77 0.80 1.01	0.312 0.365 0.908	SPO0812 SPO0813 SPO0814	0.72 0.79 1.03	0.294	SPO0812 SPO0813 SPO0814	0.86 0.84 1.02	0.227 0.974	SP00812 SP00813 SP00814	0.84 0.83 1.01	0.081 0.282 0.956
SPO0815 SPO0816 SPO0817	1.33 0.99 1.29	0.166 SPO0 0.912 SPO0 0.255 SPO0	816	1.37 0.83 1.28	0.763	SPO0816 SPO0817 SPO0818	0.98 0.97 0.96	0.691 SPO0816 0.328 SPO0817 0.247 SPO0818	0.85 0.89 0.85	0.797 0.378 0.057	SPO0815 SPO0816 SPO0817	1.27 0.79 1.58	0.160 0.541 0.126	SPO0815 SPO0816 SPO0817	1.34 0.81 1.54	0.000 0.500 0.083	SPO0815 SPO0816 SPO0817	1.09 0.97 1.15		SPO0815 SPO0816 SPO0817	1.11 0.93 1.11	0.232 0.652 0.632
SPO0818 SPO0819 SPO0820	1.07 1.3 1.19	0.507 SPO0 0.02 SPO0 0.097 SPO0	819	1.05 1.29 1.16	0.011	SPO0819 SPO0820 SPO0821	0.59 0.84 0.95	0.468 SPO0819 0.404 SPO0820 0.75 SPO0821	0.92 0.93 0.83	0.166 0.424 0.956	SPO0818 SPO0819 SPO0820	1.66 0.92 1.34	0.000 0.569	SPO0818 SPO0819 SPO0820	1.68 1.05	0.002 0.932 0.003	SPO0818 SPO0819 SPO0820	1.23 0.83 1.18	0.101	SPO0818 SPO0819 SPO0820	1.32 0.80 1.12	0.087 0.033 0.442
SPO0821 SPO0822	1.6 1.06	0.103 SPO0 0.269 SPO0	821 822	1.49	0.361	SPO0822 SPO0823	0.95 0.88 0.96	0.593 SPO0822 0.899 SPO0823	0.72 0.75	0.930 0.321 0.543	SPO0821 SPO0822	0.78 1.30	0.674	SPO0821 SPO0822	0.82	0.827	SPO0821 SPO0822	0.99 1.06	0.989 0.820	SPO0821 SPO0822	0.95 1.04	0.914 0.837
SPO0823 SPO0824 SPO0825	1.22 1.66 0.74	0.321 SPO0 0.027 SPO0 0.03 SPO0	824	1.21 1.3 0.72	0.017	SPO0824 SPO0825 SPO0826	0.77 0.85 0.91	0.104 SPO0824 0.723 SPO0825 0.166 SPO0826	0.82 0.85 0.8	0.415 0.803 0.22	SPO0823 SPO0824 SPO0825	1.09 0.99 1.38	0.763 0.915 0.028	SPO0823 SPO0824 SPO0825	1.16 1.04 1.35	0.152 0.601 0.001	SPO0823 SPO0824 SPO0825	0.93 0.96 1.00	0.847	SPO0823 SPO0824 SPO0825	1.00 0.99 1.00	0.937 0.957 0.958
SPO0826 SPO0827	0.76 0.79	0.178 SPO0 0.246 SPO0	827	0.85	0.258 0.199	SPO0827 SPO0828	0.99	0.381 SPO0827 0.139 SPO0828	0.85 0.97	0.143	SPO0826 SPO0827 SPO0828	0.88 0.85	0.210	SPO0826 SPO0827 SPO0828	0.82 0.93	0.481	SPO0826 SPO0827	0.88	0.470	SPO0826 SPO0827	0.94 0.99	0.740 0.935
SPO0828 SPO0829 SPO0830	0.85 0.99 0.73	0.393 SPO0 0.902 SPO0 0.077 SPO0	829 830	0.88 1.03 0.88	0.479	SPO0829 SPO0830 SPO0831	0.82 0.74 0.96	0.977 SPO0829 0.698 SPO0830 0.253 SPO0831	0.61 0.99 0.86	0.953 0.651 0.415	SPO0829 SPO0830	1.24 0.84 1.18	0.448 0.477 0.449	SPO0829 SPO0830	1.22 0.86 0.98	0.703	SPO0828 SPO0829 SPO0830	1.10 0.92 1.04	0.725 0.914	SPO0828 SPO0829 SPO0830	1.10 0.93 0.98	0.710 0.778 0.753
SPO0831 SPO0832 SPO0833	0.97 1.58 0.11	0.931 SP00 0.023 SP00 0 SP00	832	1.03 1.29 0.12	0.29	SPO0832 SPO0833 SPO0834	0.78 0.88 0.93	0.168 SPO0832 0 SPO0833 0 SPO0834	0.89 0.93 0.7	0.466 0	SPO0831 SPO0832 SPO0833	0.63 0.76 0.27	0.009 0.188 0.000	SPO0831 SPO0832 SPO0833	0.61 0.95 0.28	0.041 0.605 0.000	SPO0831 SPO0832 SPO0833	0.53 0.91 1.06	0.006 0.439 0.288	SPO0831 SPO0832 SPO0833	0.50 0.77 1.10	0.004 0.217 0.104
SPO0834 SPO0835	0.26	0 SP00 0.001 SP00	834 835	0.26	0 S	SPO0835 SPO0836	0.5 0.88	0.012 SPO0835 0.283 SPO0836	0.91 0.71	0.016	SPO0835 SPO0835	0.42	0.000	SPO0835 SPO0835	0.40 0.76	0.000 0.036 0.042	SPO0834 SPO0835	1.07 1.08	0.539	SPO0834 SPO0835	1.12 1.13	0.318 0.152
SPO0836 SPO0837 SPO0838	0.68 1.1 1.46	0.333 SPO0 0.006 SPO0	837 838	0.68 1.13 1.46	0.051 S	SPO0837 SPO0838 SPO0839	0.97 0.99 0.87	0.083 SPO0837 0.003 SPO0838 0.08 SPO0839	0.94 0.96 0.71	0.003 0 0.048	SPO0836 SPO0837 SPO0838	0.76 0.81 0.65	0.293 0.105 0.130	SPO0836 SPO0837 SPO0838	0.74 0.88 0.80	0.107 0.024	SPO0836 SPO0837 SPO0838	0.99 1.08 1.33	0.626 0.086	SP00836 SP00837 SP00838	0.94 0.98 1.42	0.735 0.708 0.007
SPO0839 SPO0840 SPO0841	1.09 0.97 0.99	0.533 SPO0 0.91 SPO0 0.885 SPO0	840	1.1 1.03	0.265	SPO0840 SPO0841 SPO0842	0.98 0.07 0.14	0.004 SPO0840 0.005 SPO0841 0.181 SPO0842	0.69 0.68 1	0.005 0.049 0.045	SPO0839 SPO0840 SPO0841	0.65 0.83 0.90	0.014 0.110 0.747	SPO0839 SPO0840 SPO0841	0.74 0.85 0.93	0.016 0.233 0.755	SPO0839 SPO0840 SPO0841	1.20 0.90 0.90	0.389 0.378 0.527	SPO0839 SPO0840 SPO0841	1.25 0.88 0.82	0.218 0.153 0.303
SPO0842 SPO0843	1.14 1.5	0.444 SPO0 0.045 SPO0	842 843	1.31	0.01 S	SPO0843 SPO0844	0.16 0.87	0.088 SPO0843 0.925 SPO0844	0.97	0.3 0.526	SPO0842 SPO0843	0.92 1.00	0.358 0.957	SPO0842 SPO0843	0.93 0.94	0.409 0.589	SPO0842 SPO0843	1.05 1.09	0.935 0.764	SPO0842 SPO0843	0.96 1.02	0.724 0.966
SPO0844 SPO0845 SPO0846	1.01 0.88 0.99	0.497 SPO0 0.226 SPO0 0.964 SPO0	845 846	0.97 0.93 1.08	0.775 0.881	SPO0845 SPO0846 SPO0847	0.95 0.91 0.83	0.861 SPO0845 0.831 SPO0846 0.195 SPO0847	0.94 0.93 0.96	0.913 0.826 0.306	SPO0845 SPO0846	1.01 1.39 1.00	0.836 0.004 0.972	SPO0845 SPO0846	1.03 1.32 0.97	0.801 0.025 0.991	SPO0844 SPO0845 SPO0846	0.98 1.04 0.91	0.567 0.899	SP00844 SP00845 SP00846	0.97 1.08 1.05	0.776 0.597 0.940
SPO0847 SPO0848 SPO0849	0.75 0.84 0.96	0.671 SPO0 0.114 SPO0 0.901 SPO0	848	0.76 0.88 0.94	0.687	SPO0848 SPO0849 SPO0850	0.75 0.93	0.371 SPO0848 0.571 SPO0849 0.458 SPO0850	0.93 0.66 0.88	0.439 0.869 0.541	SPO0847 SPO0848 SPO0849	1.53 1.77 1.02	0.061 0.048 0.778	SPO0847 SPO0848 SPO0849	1.52 1.59 1.10	0.016 0.042 0.647	SPO0847 SPO0848 SPO0849	0.93 1.17 0.99	0.276	SP00847 SP00848 SP00849	1.05 1.16 1.02	0.762 0.336 0.931
SPO0850	0.87	0.889 SPO0		0.99		SPO0851	0.96	0.458 SPO0851	0.95	0.683		0.85	0.778	SPO0850	0.81		SPO0850	0.89		SP00850	0.93	0.870

SPO0851 SPO0852	1.63		0851 0852	1.46	0.375	SPO0852 SPO0853	0.88	0.391 SPO0852 0.23 SPO0853	0.9	0.41	SPO0851 SPO0852	0.80	0.714	SPO0851	0.79		SPO0851 SPO0852	0.91	0.861	SPO0851 SPO0852	0.92	0.891 0.266
SPO0853 SPO0854	0.81	0.017 SPO 0.69 SPO	0853 0854	0.85 1	0.605 0.27	SPO0854 SPO0855	0.87 0.97	0.146 SPO0854 0.972 SPO0855	0.98 0.88	0.446 0.732	SPO0853 SPO0854 SPO0855	1.58 1.41	0.066 0.049	SPO0853 SPO0854 SPO0855	1.47 1.45	0.064	SPO0853 SPO0854	1.10 1.20	0.541	SPO0853 SPO0854	1.04 1.24	0.880 0.110
SPO0855 SPO0856 SPO0857	0.74 0.86 1.02	0.875 SPO	0855 0856 0857	0.9 0.9 0.93	0.844 0.935 0.881	SPO0856 SPO0857 SPO0858	0.91 0.97 0.56	0.703 SPO0856 0.384 SPO0857 0.59 SPO0858	0.73 0.97 0.74	0.712 0.388 0.888	SPO0856 SPO0857	0.80 0.88 0.97	0.092 0.780 0.400	SPO0855 SPO0857	0.78 0.93 0.83	0.502 0.731 0.219	SPO0855 SPO0856 SPO0857	0.59 0.63 0.95	0.015 0.236 0.814	SP00855 SP00856 SP00857	0.53 0.67 0.85	0.122 0.394 0.490
SPO0858 SPO0859 SPO0860	0.84 0.85 0.99	0.186 SPO	0858 0859 0860	0.89 0.89 0.96	0.515 0.527 0.991	SPO0859 SPO0860 SPO0861	0.91 0.81 0.83	0.82 SPO0859 0.974 SPO0860 0.188 SPO0861	0.81 0.76 0.99	0.545 0.794 0.145	SPO0858 SPO0859 SPO0860	0.08 1.45 0.98	0.005 0.018 0.782	SPO0858 SPO0859 SPO0860	0.07 1.53 0.97	0.001 0.005 0.796	SPO0858 SPO0859 SPO0860	1.11 1.19 0.99	0.674 0.449 0.983	SPO0858 SPO0859 SPO0860	1.16 1.12 0.98	0.572 0.406 0.987
SPO0861 SPO0862	0.9 0.87	0.228 SPO	0861 0862	0.85 0.74	0.074	SPO0862 SPO0863	0.94 0.98	0.393 SPO0862 0.872 SPO0863	0.79 0.94	0.045 0.938	SPO0861 SPO0862	1.73 0.79	0.009 0.741	SPO0861 SPO0862 SPO0863	1.72 0.90	0.009	SPO0861 SPO0862	0.93 0.87	0.565	SPO0861 SPO0862	0.81	0.151 0.849
SPO0863 SPO0864 SPO0865	1.15 1.38 1.31	0.802 SPO 0.568 SPO	0863 0864 0865	1.08 1.32 1.14	0.75	SPO0865 SPO0866	0.93 0.97 0.9	0.981 SPO0864 0.933 SPO0865 0.27 SPO0866	0.76 0.85 0.98	0.986 0.855 0.382	SPO0863 SPO0864 SPO0865	1.17 1.45 0.84	0.409 0.760 0.753	SPO0864 SPO0865	1.21 1.44 0.94	0.417 0.751 0.888	SPO0863 SPO0864 SPO0865	0.92 1.10 0.84	0.963 0.714	SP00863 SP00864 SP00865	0.96 1.19 0.86	0.619 0.909 0.696
SPO0866 SPO0867 SPO0868	1.25 1.04	0.729 SPO	0866 0867 0868	1.26 1.09	0.157 0.045 0.486	SPO0867 SPO0868 SPO0869	0.96 0.74 0.86	0.024 SPO0867 0.934 SPO0868 0.883 SPO0869	0.82 0.85 0.57	0.038 0.89 0.903	SPO0866 SPO0867 SPO0868	1.11 0.97 0.84	0.367 0.880 0.457	SPO0866 SPO0867 SPO0868	1.31 0.98 0.83	0.036 0.299 0.087	SPO0866 SPO0867 SPO0868	1.23 1.14 1.01	0.033	SPO0866 SPO0867 SPO0868	1.09 1.08 0.97	0.615 0.661 0.861
SPO0869 SPO0870 SPO0871	0.85 1.2 0.88	0.017 SPO	0869 0870 0871	0.85 1.13 0.9		SP00870 SP00871 SP00872	0.93 0.85 0.83	0.538 SPO0870 0.976 SPO0871 0.95 SPO0872	0.93 0.93 0.85	0.562 0.852 0.895	SPO0869 SPO0870	0.86 0.97 1.09	0.891 0.967 0.775	SPO0869 SPO0870	0.97 0.95 1.12		SPO0869 SPO0870 SPO0871	0.91 0.91 1.02	0.602	SP00869 SP00870 SP00871	1.00 0.97 1.00	0.997 0.887 0.986
SPO0872 SPO0873	1.11 1.05	0.201 SPO 0.846 SPO	0872 0873	1.1	0.094 0.741	SPO0873 SPO0874	0.61 0.68	0.899 SPO0873 0.902 SPO0874	0.95 0.07	0.81 0.252	SPO0872 SPO0873	1.15 1.40	0.612 0.422	SPO0872 SPO0873	1.23 1.49	0.226	SPO0872 SPO0873	1.12 0.97	0.396 0.907	SPO0872 SPO0873	0.99 0.89	0.939 0.761
SPO0874 SPO0875 SPO0876	1.17 0.85 0.91	0.162 SPO	0874 0875 0876	1.25 0.85 1.03	0.003 0.084 0.408	SPO0875 SPO0876 SPO0877	0.79 0.82 0.9	0.051 SPO0875 0.144 SPO0876 0.371 SPO0877	0.17 0.19 0.89	0.068 0.16 0.488	SPO0874 SPO0875 SPO0876	1.37 1.22 0.76	0.146 0.020 0.041	SPO0874 SPO0875 SPO0876	1.16 1.26 0.75	0.301 0.023 0.072	SPO0874 SPO0875 SPO0876	0.97 1.17 1.18	0.935 0.090 0.134	SP00874 SP00875 SP00876	0.96 1.22 1.22	0.834 0.098 0.113
SPO0877 SPO0878 SPO0879	1.18 0.75 0.78	0.639 SPO	0877 0878 0879	1.09 0.75 0.76	0.59 0.477 0.123	SPO0878 SPO0879 SPO0880	0.93 0.88 0.7	0.989 SPO0878 0.154 SPO0879 0.404 SPO0880	0.98 0.99 0.87	0.975 0.169 0.315	SPO0877 SPO0878 SPO0879	0.74 0.61 0.74	0.377 0.423 0.144	SPO0877 SPO0878 SPO0879	0.81 0.59 0.71	0.423 0.376 0.087	SPO0877 SPO0878 SPO0879	0.92 0.91 0.90	0.716 0.894 0.491	SP00877 SP00878 SP00879	0.88 0.97 0.97	0.649 0.997 0.948
SPO0880 SPO0881	0.76 0.77	0.343 SPO 0.02 SPO	0880 0881	0.86 0.76	0.522 0.025	SPO0881 SPO0882	0.63 0.59	0.057 SPO0881 0.642 SPO0882	0.75 0.87	0.396 0.708	SPO0880 SPO0881	1.43 1.77	0.062 0.014	SPO0880 SPO0881	1.38 1.75	0.079	SPO0880 SPO0881	1.14 0.91	0.311 0.402	SPO0880 SPO0881	1.06 0.88	0.605 0.467
SPO0882 SPO0883 SPO0884	1.02 1.18 1.14	0.507 SPO 0.588 SPO	0882 0883 0884	0.91 1.06 1.08	0.961 0.322 0.572	SP00883 SP00884 SP00885	0.91 0.96 0.95	0.596 SPO0883 0.627 SPO0884 0.945 SPO0885	0.77 0.89 0.87	0.253 0.519 0.979	SPO0882 SPO0883 SPO0884	0.97 1.01 1.16	0.853 0.733 0.439	SPO0882 SPO0883 SPO0884	0.96 1.02 1.08	0.840 0.171 0.222	SPO0882 SPO0883 SPO0884	0.87 0.96	0.789 0.739 0.959	SP00882 SP00883 SP00884	1.14 0.85 0.93	0.849 0.065 0.646
SPO0885 SPO0886 SPO0887	0.97 0.26 0.79	0.003 SPO	0885 0886 0887	0.97 0.3 0.85	0.983 0 0.668	SPO0886 SPO0887 SPO0888	0.94 0.98 0.94	0.016 SPO0886 0.16 SPO0887 0.74 SPO0888	0.93 0.8 0.95	0.964 0.618	SPO0885 SPO0886 SPO0887	0.83 2.30 0.88	0.788 0.013 0.206	SPO0885 SPO0886 SPO0887	0.77 2.08 0.78	0.653 0.001 0.942	SPO0885 SPO0886 SPO0887	0.96 1.23 1.06		SPO0885 SPO0886 SPO0887	0.90 1.44 1.05	0.865 0.010 0.444
SPO0888 SPO0889	1.61 1.06	0.065 SPO 0.889 SPO	0888 0889	1.45 0.99	0.062 0.989	SPO0889 SPO0890	0.95 0.98	0.994 SPO0889 0.942 SPO0890 0.339 SPO0891	0.94 0.5	0.998 0.794	SPO0888 SPO0889 SPO0890	1.39 0.83	0.046 0.920	SPO0888 SPO0889 SPO0890	1.44 0.76	0.038	SPO0888 SPO0889 SPO0890	0.93 0.85	0.853	SP00888 SP00889	0.93 0.88	0.727 0.923
SPO0890 SPO0891 SPO0892	1.61 1.6 1.11	0.064 SPO 0.452 SPO	0890 0891 0892	1.77 1.64 1.12	0.012 0.446	SPO0891 SPO0892 SPO0893	0.88 0.89 0.84	0.409 SPO0892 0.125 SPO0893	0.93 0.96 0.89	0.371 0.234 0.677	SPO0891 SPO0892	1.10 1.57 1.22	0.689 0.028 0.020	SPO0891 SPO0892	1.13 1.53 1.24	0.119 0.008 0.106	SPO0891 SPO0892	1.00 1.43 1.14	0.099 0.037	SP00890 SP00891 SP00892	0.94 1.26 1.10	0.711 0.192 0.187
SPO0893 SPO0894 SPO0895	1.59 1.15 1.12	0.426 SPO	0893 0894 0895	1.54 1.13 1.09		SPO0894 SPO0895 SPO0896	0.88 0.97 0.99	0.66 SPO0894 0.236 SPO0895 0.72 SPO0896	0.93 0.89 0.94	0.231 0.109 0.902	SPO0893 SPO0894 SPO0895	1.31 0.77 0.59	0.026 0.188 0.057	SPO0893 SPO0894 SPO0895	1.17 0.73 0.59	0.013 0.056 0.070	SPO0893 SPO0894 SPO0895	1.31 1.06 1.16	0.612	SPO0893 SPO0894 SPO0895	1.17 1.04 1.14	0.365 0.722 0.216
SPO0896 SPO0897 SPO0898	1.25 1.55 1.17	0.079 SPO	0896 0897 0898	1.01 1.37 1.19	0.866 0.048 0.608	SPO0897 SPO0898 SPO0899	0.97 0.97 0.91	0.279 SPO0897 0.578 SPO0898 0.542 SPO0899	0.81 0.93 0.74	0.145 0.6 0.693	SPO0896 SPO0897 SPO0898	0.79 0.78 0.76	0.388 0.512 0.740	SPO0896 SPO0897 SPO0898	0.83 0.80 0.60	0.629 0.272 0.329	SPO0896 SPO0897 SPO0898	1.02 1.18 0.96		SP00896 SP00897 SP00898	1.10 1.13 0.93	0.292 0.656 0.827
SPO0899 SPO0900	0.81 2.56	0.675 SPO 0.025 SPO	0899 0900	0.78 2.37	0.596	SPO0900 SPO0901	0.93 0.83	0.23 SPO0900 0.039 SPO0901	0.85 0.98	0.261 0.411	SPO0899 SPO0900	0.70 0.18	0.448	SPO0900	0.76 0.18	0.638	SPO0899 SPO0900	0.92 0.97	0.852 0.998	SPO0899 SPO0900	0.88 0.92	0.753 0.811
SPO0901 SPO0902 SPO0903	0.92 1.36 1.22	0.523 SPO	0901 0902 0903	0.88 1.32 1.26	0.121 0.571 0.26	SPO0902 SPO0903 SPO0904	0.88 0.8 0.96	0.819 SPO0902 0.422 SPO0903 0.689 SPO0904	0.86 0.93 0.55	0.837 0.215 0.491	SPO0901 SPO0902 SPO0903	0.65 0.82 0.68	0.013 0.856 0.221	SPO0901 SPO0902 SPO0903	0.71 0.77 0.68	0.066 0.866 0.101	SPO0901 SPO0902 SPO0903	1.00 1.18 1.00	0.945 0.772 0.902	SP00901 SP00902 SP00903	0.97 1.08 1.05	0.732 0.909 0.710
SPO0904 SPO0905 SPO0906	1.59 1.24 1.15	0.168 SPO	0904 0905 0906	1.51 1.19 1.07	0.419 0.315 0.068	SPO0905 SPO0906 SPO0907	0.79 0.95 0.98	0.006 SPO0905 0.749 SPO0906 0.665 SPO0907	0.66 0.81 0.83	0.152 0.171 0.651	SPO0904 SPO0905 SPO0906	1.60 0.91 0.70	0.010 0.562 0.132	SPO0904 SPO0905 SPO0906	1.54 0.93 0.72	0.065 0.371 0.037	SPO0904 SPO0905 SPO0906	1.06 1.03 1.25	0.799 0.791 0.339	SPO0904 SPO0905 SPO0906	0.98 1.09 1.22	0.986 0.464 0.164
SPO0907 SPO0908 SPO0909	0.82 1.32 1.84	0.324 SPO 0.284 SPO	0907 0908 0909	0.9 1.21 1.27	0.336 0.327 0.576	SPO0908 SPO0909 SPO0910	0.88 0.76 0.77	0.217 SPO0908 0.457 SPO0909 0.009 SPO0910	0.93 0.93 0.93	0.068 0.671 0.035	SPO0907 SPO0908 SPO0909	0.86 0.69	0.677 0.356 0.067	SPO0907 SPO0908 SPO0909	0.76 0.73	0.237 0.216 0.153	SPO0907 SPO0908 SPO0909	0.88 1.04 0.86	0.290 0.835 0.491	SP00907 SP00908 SP00909	0.94 1.06 0.84	0.866 0.688 0.583
SPO0910 SPO0911	1.04	0.745 SPO 0.421 SPO	0910 0911	1.02 0.97	0.943	SPO0911 SPO0912	0.67 0.96	0.606 SPO0911 0.722 SPO0912	0.93 0.68	0.785 0.629	SPO0910 SPO0911	0.35 0.71	0.006 0.385	SPO0910 SPO0911	0.35 0.74	0.012 0.508	SPO0910 SPO0911	0.93	0.898 0.656	SPO0910 SPO0911	0.83 1.12	0.475 0.596
SPO0912 SPO0913 SPO0914	0.91 1.29 1.07	0.426 SPO	0912 0913 0914	0.93 1.22 1.06	0.63 0.024 0.437	SPO0913 SPO0914 SPO0915	0.85 0.89 0.72	0.044 SPO0913 0.192 SPO0914 0.057 SPO0915	0.58 0.6 0.94	0.282 0.171 0.081	SPO0912 SPO0913 SPO0914	0.88 0.84 1.91	0.125 0.338 0.012	SPO0912 SPO0913 SPO0914	0.88 0.90 1.90	0.603 0.891 0.009	SPO0912 SPO0913 SPO0914	1.03 0.99 1.11	0.919	SP00912 SP00913 SP00914	1.01 0.95 1.09	0.940 0.518 0.295
SPO0915 SPO0916 SPO0917	0.97 1.68 0.91	0.368 SPO	0915 0916 0917	1 1.52 0.97	0.722 0.358 0.692	SP00916 SP00917 SP00918	0.74 0.99 0.85	0.55 SPO0916 0.195 SPO0917 0.99 SPO0918	0.93 0.89 0.89	0.484 0.967 0.876	SPO0915 SPO0916 SPO0917	0.83 0.58 0.56	0.519 0.199	SPO0915 SPO0916	0.88 0.60 0.55	0.994	SPO0915 SPO0916 SPO0917	0.90 0.85 1.19		SP00915 SP00916 SP00917	0.97 0.83 1.15	0.897 0.598 0.454
SPO0918 SPO0919	0.69	0.043 SPO 0.004 SPO	0918 0919	0.78 2.84	0.054 0.006	SPO0919 SPO0920	0.95 0.77	0.043 SPO0919 0.161 SPO0920	0.96 0.98	0.001 0.12	SPO0918 SPO0919	1.84 0.74	0.018 0.018	SPO0918 SPO0919	1.84 0.67	0.010	SPO0918 SPO0919	0.91 0.76	0.458 0.057	SPO0918 SPO0919	0.93 0.72	0.596 0.110
SPO0920 SPO0921 SPO0922	3.23 0.55	0.003 SPO 0.013 SPO	0920 0921 0922	1.85 3.05 0.6	0.155 0.001 0.016	SPO0921 SPO0922 SPO0923	0.87 0.98 0.87	0.028 SPO0921 0.162 SPO0922 0.227 SPO0923	0.93 0.95 0.85	0.091 0.188 0.241	SPO0920 SPO0921 SPO0922	0.67 0.63 1.11	0.161 0.221 0.087	SPO0920 SPO0921 SPO0922	0.61 0.60 1.15	0.031 0.142	SPO0920 SPO0921 SPO0922	0.90 0.82 0.98	0.365 0.314 0.888	SP00920 SP00921 SP00922	0.88 0.80 0.99	0.660 0.427 0.993
SPO0923 SPO0924 SPO0925	1.18 1.23 1.32	0.104 SPO	0923 0924 0925	1.16 0.69 1.31	0.084 0.346 0.124	SPO0924 SPO0925 SPO0926	0.84 0.96 0.98	0.012 SPO0924 0.518 SPO0925 0.464 SPO0926	0.86 0.85 0.95	0.082 0.055 0.711	SPO0923 SPO0924 SPO0925	1.03 3.78 0.70	0.181 0.002 0.388	SPO0923 SPO0924 SPO0925	7.09 0.65	0.128 0.023 0.090	SPO0923 SPO0924 SPO0925	1.13 1.24 0.94	0.366 0.299 0.897	SPO0923 SPO0924 SPO0925	1.15 1.30 0.95	0.126 0.522 0.884
SPO0926 SPO0927 SPO0928	1.68 2.01 0.68	0.029 SPO 0.105 SPO	0926 0927 0928	1.56 1.81 0.76	0.009 0.085 0.059	SPO0927 SPO0928 SPO0929	0.84 0.93 0.83	0.977 SPO0927 0.253 SPO0928 0.295 SPO0929	0.92 0.94 0.85	0.752 0.184 0.089	SPO0926 SPO0927 SPO0928	0.98 1.02 1.50	0.646 0.824 0.096	SPO0926 SPO0927 SPO0928	1.06 1.09	0.347 0.406 0.037	SPO0926 SPO0927 SPO0928	1.19 1.11 1.19	0.034 0.869 0.784	SP00926 SP00927 SP00928	1.15 1.06 1.19	0.346 0.883 0.659
SPO0929 SPO0930	0.83 1.02	0.698 SPO 0.878 SPO	0929 0930	0.84 1.15	0.006 0.749	SPO0930 SPO0931	0.89 0.93	0.789 SPO0930 0.397 SPO0931	0.89 0.88	0.765 0.194	SPO0929 SPO0930	1.11	0.046 0.014	SPO0929 SPO0930	1.18	0.025	SPO0929 SPO0930	1.25 0.87	0.072 0.616	SPO0929 SPO0930	1.12 0.83	0.028 0.590
SPO0931 SPO0932 SPO0933	0.65 1.21 1.63	0.397 SPO	0931 0932 0933	0.63 1.28 1.46	0.066 0.294 0.084	SPO0932 SPO0933 SPO0934	0.95 0.95 0.97	0.936 SPO0932 0.595 SPO0933 0.538 SPO0934	0.8 0.82 0.78	0.835 0.3 0.767	SPO0931 SPO0932 SPO0933	0.85 1.02 0.79	0.911 0.097 0.095	SPO0931 SPO0932 SPO0933	1.20 1.01 0.80	0.398 0.169 0.153	SPO0931 SPO0932 SPO0933	1.03 1.10 1.17	0.973 0.257 0.242	SP00931 SP00932 SP00933	1.20 1.05 1.14	0.682 0.401 0.135
SPO0934 SPO0935 SPO0936	1.19 1.11 0.6		0934 0935 0936	1.03 1.19 0.68		SPO0935 SPO0936 SPO0937	0.96 0.95 0.96	0.051 SPO0935 0.835 SPO0936 0.501 SPO0937	0.86 0.97 0.98	0.06 0.965 0.479	SPO0934 SPO0935 SPO0936	0.69 0.67 0.80	0.473 0.240 0.164	SPO0934 SPO0935 SPO0936	0.68 0.67 0.80	0.474 0.126 0.271	SPO0934 SPO0935 SPO0936	1.07 1.28 1.05		SPO0934 SPO0935 SPO0936	1.10 1.28 1.00	0.748 0.422 0.983
SPO0937 SPO0938 SPO0939	1.37 0.61 0.81	0.044 SPO	0937 0938 0939	1.39 0.62 0.88	0.044	SPO0938 SPO0939 SPO0940	0.96 0.98 0.95	0.438 SPO0938 0.427 SPO0939 0.04 SPO0940	0.94 0.69 0.81	0.816 0.59 0.485	SPO0937 SPO0938 SPO0939	0.27 1.87 0.91	0.006 0.011 0.876	SPO0937 SPO0938 SPO0939	0.28 1.84 0.90	0.010 0.021 0.840	SPO0937 SPO0938 SPO0939	1.15 1.00 1.10	0.627	SP00937 SP00938 SP00939	1.06 0.88 1.06	0.558 0.428 0.592
SPO0940 SPO0941	1.39 1.18	0.191 SPO 0.196 SPO	0940 0941	1.3 1.14	0.326 0.073	SPO0941 SPO0942	0.77 0.85	0.885 SPO0941 0.944 SPO0942	0.63 0.93	0.742 0.759	SPO0940 SPO0941	0.65 1.90	0.300 0.067	SPO0940 SPO0941	0.62 1.66	0.386	SPO0940 SPO0941	0.85 1.30	0.216 0.361	SPO0940 SPO0941	0.80 1.18	0.214 0.335
SPO0942 SPO0943 SPO0944	1.05 0.82 1.28	0.333 SPO 0.411 SPO	0942 0943 0944	1.05 0.8 1.29		SPO0944 SPO0945	0.8 0.83 0.85	0.083 SPO0943 0.515 SPO0944 0.228 SPO0945	0.81 0.92 0.72	0.377 0.694 0.083	SPO0942 SPO0943 SPO0944	1.30 4.34 1.26	0.482 0.007 0.259	SPO0942 SPO0943 SPO0944	1.44 4.89 1.23		SPO0942 SPO0943 SPO0944	1.01 0.84 1.26	0.675	SP00942 SP00943 SP00944	1.08 0.79 1.19	0.608 0.514 0.636
SPO0945 SPO0946 SPO0947	0.88 1.48 0.92	0.103 SPO	0945 0946 0947	0.94 1.2 0.78	0.649 0.125 0.271	SPO0946 SPO0947 SPO0948	0.94 0.95 0.85	0.654 SPO0946 0.258 SPO0947 0.032 SPO0948	0.79 0.83 0.96	0.29 0.133 0.011	SPO0945 SPO0946 SPO0947	0.56 1.07 1.37	0.004 0.588 0.136	SPO0945 SPO0946 SPO0947	0.50 1.21 1.53	0.022 0.034 0.049	SPO0945 SPO0946 SPO0947	0.96 1.01 1.07	0.953	SP00945 SP00946 SP00947	0.95 0.93 1.21	0.851 0.525 0.209
SPO0948 SPO0949 SPO0950	0.74 0.57 0.98	0.401 SPO	0948 0949 0950	0.7 0.65 0.84		SPO0949 SPO0950 SPO0951	0.93 0.8 0.91	0.592 SPO0949 0.899 SPO0950 0.87 SPO0951	0.93 0.72 0.87	0.504 0.691 0.813	SPO0948 SPO0949 SPO0950	1.85 1.88 0.64	0.011 0.279 0.631	SPO0948 SPO0949	1.75 1.83 0.61	0.009 0.257 0.475	SPO0948 SPO0949 SPO0950	1.25 0.97 0.65	0.106 0.997 0.601	SPO0948 SPO0949 SPO0950	1.17 1.04 0.69	0.105 0.900 0.507
SPO0951 SPO0953	1.18 0.93 0.85	0.893 SPO 0.449 SPO	0951 0952	0.88 1.07 0.89	0.949	SPO0952 SPO0953	0.47 0.59 0.97	0 SPO0953 0.351 SPO0954	0.97 0.9 0.78	0.203 0.367 0.785	SPO0951 SPO0952 SPO0953	0.89 0.50 0.88	0.986	SPO0951 SPO0952	0.95 0.62 0.88	0.979 0.385	SPO0951 SPO0952	0.97 2.46 1.14		SPO0951 SPO0952 SPO0953	1.06 0.81 1.04	0.968 0.849 0.405
SPO0954 SPO0955 SPO0956	0.65 1.63	0.172 SPO 0.091 SPO	0953 0954 0955	0.76 0.67	0.184	SPO0954 SPO0955 SPO0956	0.97 0.84	0.945 SPO0955 0.701 SPO0956 0.097 SPO0957	0.94 0.99	0.022 0.247	SPO0954 SPO0955	0.37 0.59	0.097 0.051	SPO0953 SPO0954 SPO0955	0.42	0.029 0.017	SPO0953 SPO0954 SPO0955	0.88	0.746 0.956	SPO0954 SPO0955	0.88 0.94	0.427 0.543
SPO0957 SPO0958 SPO0959	1.8 0.83 1.19	0.321 SPO	0956 0957 0958	1.55 1.47 0.87	0.056	SPO0957 SPO0958 SPO0959	0.9 0.83 0.81	0.723 SPO0958 0.972 SPO0959 0.7 SPO0960	0.77 0.9 0.78	0.952 0.999 0.393	SPO0956 SPO0957 SPO0958	0.60 0.75 0.58	0.012 0.013 0.401	SPO0956 SPO0957 SPO0958	0.57 0.72 0.51	0.152 0.087 0.458	SPO0956 SPO0957 SPO0958	0.89 1.00 0.87	0.925	SPO0956 SPO0957 SPO0958	0.86 0.95 0.93	0.478 0.462 0.767
SPO0960 SPO0961 SPO0962	1.22 1.01	0.112 SPO 0.844 SPO	0959 0960 0961	1.11 1.13 0.96	0.54 0.299	SPO0960 SPO0961 SPO0962	0.94 0.79 0.62	0.275 SPO0961 0.898 SPO0962 0.307 SPO0963	0.91 0.96 0.95	0.863 0.586 0.984	SPO0959 SPO0960 SPO0961	0.79 0.84 0.68	0.193 0.282 0.214	SPO0959 SPO0960 SPO0961	0.76 0.93 0.63	0.276 0.703	SPO0959 SPO0960 SPO0961	1.12 0.98 1.10	0.847	SPO0959 SPO0960 SPO0961	1.12 0.88 0.99	0.720 0.374 0.960
SPO0963 SPO0964	0.96 0.76	0.941 SPO 0.725 SPO	0962 0963	0.96 1.02	0.956 0.923	SPO0963 SPO0964	0.81 0.95	0.911 SPO0964 0.83 SPO0965	0.94 1	0.419 0.944	SPO0962 SPO0963	0.92 0.78	0.926 0.575	SPO0962 SPO0963	0.87 0.82	0.366 0.860	SPO0962 SPO0963	1.01 1.03	0.881 0.850	SPO0962 SPO0963	1.00 1.05	0.928 0.881
SPO0965 SPO0966 SPO0967	1.35 0.93 1.69	0.781 SPO 0.029 SPO	0964 0965 0966	0.78 1.24 1.03	0.741	SPO0965 SPO0966 SPO0967	0.92 0.87 0.81	0.953 SPO0966 0.243 SPO0967 0.638 SPO0968	0.95 0.92 0.94	0.209 0.557 0.031	SPO0965 SPO0966	1.45 0.93 0.90	0.139 0.930 0.411	SPO0964 SPO0965 SPO0966	1.37 0.85 0.83	0.710 0.218	SPO0964 SPO0965 SPO0966	1.20 1.11 1.02	0.897 0.971	SP00964 SP00965 SP00966	1.13 0.89 1.04	0.668 0.796 0.821
SPO0968 SPO0970 SPO0971	0.81 0.81	0.136 SPO	0967 0968 0970	1.67 1.09 0.72	0.056 0.034 0.43	SPO0968 SPO0970 SPO0971	0.76 0.74 0.61	0.011 SPO0970 0.313 SPO0971 0.868 SPO0972	0.96 0.7 0.85	0.293 0.925 0.662	SPO0967 SPO0968 SPO0970	1.09 1.06 0.79	0.455 0.160 0.539	SPO0967 SPO0968 SPO0970	1.00 1.05 0.88		SPO0967 SPO0968 SPO0970	1.05 1.10 0.86	0.243	SPO0967 SPO0968 SPO0970	1.00 1.08 0.94	0.984 0.498 0.851
SPO0972 SPO0973 SPO0974	1.21 1.06	0.211 SPO 0.454 SPO	0971 0972 0973	0.81 1.29 1.03		SPO0972 SPO0973 SPO0974	0.53 0.49 0.9	0.889 SPO0973 0.915 SPO0974 0.462 SPO0975	0.74 0.82 0.85	0.522 0.494 0.315	SPO0971 SPO0972 SPO0973	0.81 1.23 0.93	0.497 0.132 0.917	SPO0971 SPO0972 SPO0973	0.90 1.08 0.95		SPO0971 SPO0972 SPO0973	0.87 1.03 0.94		SP00971 SP00972 SP00973	0.90 0.91 1.00	0.280 0.334 0.963
SPO0975 SPO0976	0.89 1.14	0.337 SPO 0.129 SPO	0974 0975	1.11	0.435 0.854	SPO0975 SPO0976	0.68 0.81	0.184 SPO0976 0.162 SPO0977	0.88 0.86	0.202 0.19	SPO0974 SPO0975	1.31 0.75	0.025	SP00973 SP00974 SP00975	1.24 0.65	0.059 0.150	SPO0974 SPO0975	1.08	0.149 0.337	SPO0974 SPO0975	1.01 1.15	0.754 0.370
SPO0977 SPO0978 SPO0979	0.88 0.91 0.94	0.8 SPO 0.907 SPO	0976 0977 0978	1.09 0.92 1	0.108 0.563 0.673	SPO0977 SPO0978 SPO0979	0.74 0.69 0.7	0.103 SPO0978 0.194 SPO0979 0.58 SPO0980	0.89 0.78 0.93	0.395 0.789 0.859	SPO0976 SPO0977 SPO0978	0.80 0.78 0.80	0.063 0.154 0.305	SP00976 SP00977 SP00978	0.76 0.73 0.77		SPO0976 SPO0977 SPO0978	1.23 0.78 0.84	0.489	SP00976 SP00977 SP00978	1.19 0.83 0.90	0.072 0.277 0.793
SPO0980 SPO0981 SPO0982	1.47 1.01 0.81	0.54 SPO 0.943 SPO	0979 0980 0981	0.83 1.3 1.26	0.351 0.374 0.762	SPO0980 SPO0981 SPO0982	0.87 0.9 0.81	0.802 SPO0981 0.952 SPO0982 0.594 SPO0983	0.39 0.49 0.91	0.95 0.767 0.761	SPO0979 SPO0980 SPO0981	1.01 0.84 0.79	0.815 0.851 0.796	SPO0979 SPO0980 SPO0981	1.09 0.88 0.83		SPO0979 SPO0980 SPO0981	0.97 1.12 0.80	0.787 0.890	SP00979 SP00980 SP00981	0.98 1.10 0.93	0.938 0.839 0.916
SPO0983 SPO0984	1.96 1.26	0.128 SPO 0.756 SPO	0982 0983	0.79 1.59	0.32	SPO0983 SPO0984	0.71 0.88	0.89 SPO0984 0.954 SPO0985	0.95 0.85	0.915 0.744	SPO0982 SPO0983	1.03 1.11	0.767 0.684	SPO0982 SPO0983	1.01	0.853 0.689	SPO0982 SPO0983	1.20 1.19	0.475 0.682	SPO0982 SPO0983	1.11 1.14	0.594 0.695
SPO0985 SPO0986 SPO0987	1.44 1.12 0.93	0.69 SPO 0.168 SPO	0984 0985 0986	1.32 1.37 1.11	0.056	SPO0985 SPO0986 SPO0987	0.99 0.85 0.89	0.776 SPO0986 0.835 SPO0987 0.203 SPO0988	0.96 0.98 0.77	0.864 0.031 0.435	SPO0984 SPO0985 SPO0986	0.98 1.53 1.51	0.991 0.444 0.313	SPO0984 SPO0985 SPO0986	0.98 2.04 1.32		SPO0984 SPO0985 SPO0986	1.09 1.52 1.19	0.058 0.688	SPO0984 SPO0985 SPO0986	1.10 1.40 1.11	0.891 0.259 0.447
SPO0988 SPO0989 SPO0990	1.35 1.44 0.89	0.161 SPO	0987 0988 0989	0.92 1.21 1.33	0.428	SPO0988 SPO0989 SPO0990	0.79 0.93 0.94	0.586 SPO0989 0.214 SPO0990 0.744 SPO0991	0.76 0.97 0.73	0.182 0.372 0.639	SPO0987 SPO0988 SPO0989	1.49 0.63 0.96	0.090 0.241 0.932	SPO0987 SPO0988 SPO0989	1.57 0.60 1.06	0.524	SPO0987 SPO0988 SPO0989	1.20 0.94 0.92	0.823	SPO0987 SPO0988 SPO0989	1.22 0.93 0.88	0.069 0.842 0.691
SPO0991	0.7		0990	0.93		SPO0991	0.93	0.595 SPO0992	0.7	0.224	SPO0990	1.19	0.323	SPO0990	1.46		SPO0990	1.13		SPO0990	1.08	0.656

SPO0992 SPO0993	0.53 0.67	0.059	SP00991 SP00992	0.79 0.57		SPO0992 SPO0993	0.92	0.229 SPO0993 0.097 SPO0994	0.79	0.053	SPO0991 SPO0992	0.64 1.65	0.399	SPO0991 SPO0992	0.57 1.75		SPO0991 SPO0992	0.66	0.465	SP00991 SP00992	0.79	0.699 0.672
SPO0994 SPO0995	0.79 0.69	0.572 0.277	SPO0993 SPO0994	0.74 0.85	0.082 0.616	SPO0994 SPO0995	0.8 0.94	0.735 SPO0995 0.509 SPO0996	0.92 0.91	0.193 0.102	SPO0993 SPO0994	2.72 1.34	0.157 0.315	SPO0993 SPO0994	2.57 1.21	0.087 0.558	SPO0993 SPO0994	1.13 0.93	0.787 0.821	SPO0993 SPO0994	1.22 1.08	0.557 0.656
SPO0996 SPO0997 SPO0998	0.89 0.66 0.64	0.339 0.072 0.157	SP00995 SP00996 SP00997	0.76 0.91 0.65	0.504 0.309 0.214	SPO0996 SPO0997 SPO0998	0.94 0.97 0.98	0.097 SPO0997 0.155 SPO0998 0.506 SPO0999	0.75 0.99 0.76	0.308 0.132 0.7	SPO0995 SPO0997	2.30 2.56 2.39	0.010 0.006 0.147	SPO0995 SPO0996 SPO0997	2.20 2.37 2.24	0.012 0.005 0.109	SPO0995 SPO0996 SPO0997	1.01 1.09 1.12	0.891 0.428 0.645	SP00995 SP00996 SP00997	1.11 1.09 1.10	0.531 0.163 0.792
SPO1000 SPO1001	0.88 0.79	0.486 0.046	SPO0998 SPO0999 SPO1000	0.71 0.92 0.81	0.06 0.911 0.106	SPO1000 SPO1001	0.79 0.82 0.81	0.324 SPO1000 0.052 SPO1001 0.093 SPO1002	0.75 0.63 0.55	0.264 0.028 0.923	SPO0998 SPO0999 SPO1000	1.92 1.52 1.53	0.041 0.048 0.057	SPO0998 SPO0999 SPO1000	1.75 1.63 1.65	0.068 0.274 0.018	SPO0998 SPO0999 SPO1000	1.09 1.07 0.98	0.450 0.889 0.715	SPO0998 SPO0999 SPO1000	1.16 1.07 1.03	0.506 0.690 0.769
SPO1002 SPO1003	0.86 0.65	0.858	SPO1001 SPO1002	1.11 0.92	0.963	SPO1002 SPO1003	0.83	0.837 SPO1003 0.227 SPO1004	0.48 0.82	0.28	SPO1001 SPO1002	2.54 0.84	0.011	SPO1001 SPO1002 SPO1003	2.35	0.005	SPO1001 SPO1002	1.06	0.999	SPO1001 SPO1002	1.14 0.99	0.275 0.989
SPO1004 SPO1005 SPO1006	1.18 0.88 1.22	0.33 0.231 0.028	SPO1003 SPO1004 SPO1005	0.69 1.11 0.88	0.048 0.367 0.361	SPO1004 SPO1005 SPO1006	0.79 0.92 0.98	0.197 SPO1005 0.182 SPO1006 0.015 SPO1007	0.67 0.82 0.74	0.197 0.05 0.107	SPO1003 SPO1004 SPO1005	1.12 0.45 1.13	0.077 0.028 0.125	SPO1003 SPO1004 SPO1005	1.11 0.45 1.15	0.109 0.027 0.034	SPO1003 SPO1004 SPO1005	0.93 0.93 0.97	0.828 0.991	SPO1003 SPO1004 SPO1005	0.92 0.85 1.01	0.702 0.248 0.692
SPO1007 SPO1008 SPO1009	1.4 1.74 1.56	0.066 0.035 0.062	SPO1006 SPO1007 SPO1008	1.18 1.28 1.64	0.052 0.01 0.032	SPO1007 SPO1008 SPO1009	0.87 0.91 0.86	0.09 SPO1008 0.101 SPO1009 0.901 SPO1010	0.66 0.65 0.86	0.124 0.385 0.985	SPO1006 SPO1007 SPO1008	0.84 0.82 0.68	0.415 0.343 0.172	SPO1006 SPO1007 SPO1008	0.88 0.81 0.67	0.473 0.681 0.219	SPO1006 SPO1007 SPO1008	0.98 1.05 0.89	0.219	SPO1006 SPO1007 SPO1008	0.93 0.97 0.88	0.713 0.934 0.452
SPO1010 SPO1011	1.83 0.92	0.608	SPO1009 SPO1010	1.58 1.56	0.023 0.023	SPO1010 SPO1011	0.93 0.93	0.997 SPO1011 0.636 SPO1012	0.86 0.84	0.961 0.96	SPO1009 SPO1010	1.24 1.07	0.301 0.176	SPO1009 SPO1010	1.18 1.15	0.255 0.037	SPO1009 SPO1010	1.05 1.01	0.743 0.442	SPO1009 SPO1010	0.98 0.95	0.889 0.788
SPO1012 SPO1013 SPO1014	0.77 0.49 0.47	0.549 0.009 0.043	SPO1011 SPO1012 SPO1013	0.98 0.79 0.52		SPO1012 SPO1013 SPO1014	0.94 0.87 0.32	0.913 SPO1013 0.931 SPO1014 0.808 SPO1015	0.96 0.84 0.81	0.798 0.456 0.285	SPO1011 SPO1013	1.29 0.83 1.16	0.090 0.805 0.313	SPO1011 SPO1012 SPO1013	1.24 0.86 1.28	0.048	SPO1011 SPO1012 SPO1013	1.08 0.91 1.24	0.235	SPO1011 SPO1012 SPO1013	1.13 0.93 1.27	0.223 0.834 0.170
SPO1015 SPO1016 SPO1017	0.49 1.01 0.71	0.456 0.654	SPO1014 SPO1015 SPO1016	0.52 0.58	0.136 0.17 0.471	SPO1015 SPO1016 SPO1017	0.96 0.97 0.96	0.046 SPO1016 0.188 SPO1017 0.287 SPO1018	0.95 0.82 0.94	0.063 0.535 0.639	SPO1014 SPO1015 SPO1016	1.72 6.02 0.74	0.029 0.020 0.042	SPO1014 SPO1015 SPO1016	1.74 4.91 0.72	0.021 0.048 0.060	SPO1014 SPO1015 SPO1016	1.39 1.15 0.88	0.244 0.887 0.265	SPO1014 SPO1015 SPO1016	1.36 1.17 0.89	0.162 0.877 0.350
SPO1018 SPO1019 SPO1020	0.62 0.76 0.71	0.41 0.524 0.624	SPO1017 SPO1018 SPO1019	0.71 0.69 0.72	0.138 0.479 0.209	SPO1018 SPO1019 SPO1020	0.93 0.96 0.63	0.812 SPO1019 0.62 SPO1020 0.396 SPO1021	0.8 0.91 0.91	0.28 0.664 0.339	SPO1017 SPO1018	0.22 0.17	0.002	SPO1017 SPO1018	0.24 0.17	0.006 0.011 0.004	SPO1017 SPO1018 SPO1019	1.16 0.93 1.07	0.607 0.805 0.908	SPO1017 SPO1018 SPO1019	1.28 0.89 0.91	0.065 0.735 0.447
SPO1021 SPO1022	0.63 1.34	0.142 0.129	SPO1020 SPO1021	0.74 0.6	0.573 0.156	SPO1021 SPO1022	0.76 0.7	0.738 SPO1022 0.246 SPO1023	0.98 0.93	0.129 0.725	SPO1020 SPO1021	0.10 0.14 0.13	0.003 0.019 0.003	SPO1020 SPO1021	0.12 0.14 0.13	0.022 0.012	SPO1020 SPO1021	0.84 1.00	0.623 0.955	SPO1020 SPO1021	0.86 1.05	0.710 0.780
SPO1023 SPO1024 SPO1025	1.1 1.31 1.07	0.875 0.653 0.53	SPO1022 SPO1023 SPO1024	1.37 1.05 1.27	0.056 0.924 0.083	SPO1023 SPO1024 SPO1025	0.87 0.84 0.88	0.88 SPO1024 0.153 SPO1025 0.72 SPO1026	0.93 0.69 0.91	0.305 0.816 0.484	SPO1022 SPO1023 SPO1024	0.32 0.69 0.63	0.004 0.672 0.092	SPO1022 SPO1023 SPO1024	0.35 0.62 0.68	0.016 0.579 0.114	SPO1022 SPO1023 SPO1024	0.97 0.97 0.88	0.471 0.993 0.226	SPO1022 SPO1023 SPO1024	0.93 0.94 0.97	0.637 0.926 0.885
SPO1026 SPO1027 SPO1028	1.1 1.1 0.95	0.348 0.41 0.97	SPO1025 SPO1026 SPO1027	1 1.13 1.18	0.691 0.486 0.191	SPO1026 SPO1027 SPO1028	0.81 0.79 0.91	0.417 SPO1027 0.928 SPO1028 0.934 SPO1029	0.93 0.98 0.92	0.957 0.953 0.647	SPO1025 SPO1026 SPO1027	0.89 0.39 0.92	0.295 0.010 0.656	SPO1025 SPO1026 SPO1027	1.32 0.40 0.94	0.515	SPO1025 SPO1026 SPO1027	0.97 0.79 1.02	0.239	SPO1025 SPO1026 SPO1027	0.87 0.85 1.05	0.360 0.168 0.370
SPO1029 SPO1030	1.11 0.8	0.466 0.612	SPO1028 SPO1029	0.93 1.01	0.97 0.538	SPO1029 SPO1030	0.91 0.9	0.733 SPO1030 0.613 SPO1031	0.71 0.79	0.517 0.315	SPO1028 SPO1029	0.83 0.78	0.963 0.412	SPO1028 SPO1029	0.83 0.76	0.969 0.101	SPO1028 SPO1029	0.80 1.00	0.880 0.994	SPO1028 SPO1029	0.81 0.96	0.878 0.885
SPO1031 SPO1032 SPO1033	0.45 1.69 1.73	0.152 0.003 0.414	SPO1030 SPO1031 SPO1032	0.83 0.5 1.42	0.407 0.148 0.082	SPO1031 SPO1032 SPO1033	0.86 0.85 0.88	0.456 SPO1032 0.625 SPO1033 0.634 SPO1034	0.83 0.78 0.91	0.761 0.609 0.369	SPO1030 SPO1031 SPO1032	1.00 2.22 0.94	0.836 0.082 0.894	SPO1030 SPO1031 SPO1032	0.94 2.17 0.93	0.940 0.074 0.489	SPO1030 SPO1031 SPO1032	0.88 1.03 1.16		SPO1030 SPO1031 SPO1032	0.93 1.17 1.12	0.585 0.566 0.540
SPO1034 SPO1036 SPO1037	1.25 0.73 0.67	0.371 0.702 0.131	SPO1033 SPO1034 SPO1036	1.65 1.27 0.78	0.305	SPO1034 SPO1036 SPO1037	0.97 0.63 0.55	0.357 SPO1036 0.821 SPO1037 0.421 SPO1038	0.92 0.76 0.96	0.823 0.221 0.84	SPO1033 SPO1034 SPO1036	0.72 0.84 1.35	0.562 0.620 0.688	SPO1033 SPO1034 SPO1036	0.74 0.81 1.23		SPO1033 SPO1034 SPO1036	1.02 0.87 1.02	0.400	SPO1033 SPO1034 SPO1036	0.88 0.85 1.07	0.797 0.246 0.912
SPO1038 SPO1039	1.07 0.74	0.574	SPO1037 SPO1038	0.68 1.08	0.06	SPO1038 SPO1039	0.85 0.87	0.648 SPO1039 0.598 SPO1040	0.98 0.98	0.723 0.615	SPO1037 SPO1038 SPO1039	1.20 0.83	0.239 0.136	SPO1037 SPO1038 SPO1039	1.20 0.96	0.063	SPO1037 SPO1038	1.08 1.18	0.628	SPO1037 SPO1038	1.08 1.15	0.485 0.606
SPO1040 SPO1041 SPO1042	0.76 0.7 0.6	0.269 0.77 0.014	SPO1039 SPO1040 SPO1041	0.98 0.59 0.84	0.944 0.264 0.93	SPO1040 SPO1041 SPO1042	0.89 0.97 0.9	0.036 SPO1041 0.855 SPO1042 0.515 SPO1043	0.83 0.94 0.91	0.975 0.057 0.911	SPO1049 SPO1041	1.22 1.65 1.03	0.662 0.609 0.982	SPO1039 SPO1040 SPO1041	1.21 1.32 1.06		SPO1039 SPO1040 SPO1041	1.58 1.20 0.88	0.603 0.864	SPO1039 SPO1040 SPO1041	1.30 1.19 0.93	0.700 0.792 0.899
SPO1043 SPO1044 SPO1045	1.13 0.85 0.81	0.423 0.804 0.33	SPO1042 SPO1043 SPO1044	0.64 0.97 0.79	0.032 0.764 0.391	SPO1043 SPO1044 SPO1045	0.91 0.89 0.87	0.945 SPO1044 0.864 SPO1045 0.659 SPO1046	0.93 0.89 0.91	0.376 1 0.995	SPO1042 SPO1043 SPO1044	1.87 1.35 1.11	0.123 0.140 0.895	SPO1042 SPO1043 SPO1044	1.67 0.92 1.07	0.054 0.416 0.866	SPO1042 SPO1043 SPO1044	1.24 1.13 0.94	0.672 0.832 0.613	SPO1042 SPO1043 SPO1044	1.27 1.25 1.00	0.520 0.633 0.911
SPO1046 SPO1047 SPO1048	0.74 0.76 0.62	0.381 0.093 0.056	SPO1045 SPO1046 SPO1047	0.77 0.72 0.76	0.149 0.383 0.012	SPO1046 SPO1047 SPO1048	0.77 0.91 0.6	0.863 SPO1047 0.288 SPO1048 0.674 SPO1049	0.9	0.896 0.987 0.008	SPO1045 SPO1046 SPO1047	0.91 1.13 1.15	0.813 0.583 0.111	SPO1045 SPO1046 SPO1047	0.94 1.13 1.19	0.567 0.513 0.053	SPO1045 SPO1046 SPO1047	0.97 0.93 0.93	0.962 0.895 0.734	SPO1045 SPO1046 SPO1047	1.02 0.93 0.93	0.713 0.876 0.518
SPO1049 SPO1050	0.46 0.98	0.009	SPO1048 SPO1049	0.65 0.52	0.066 0.01	SPO1049 SPO1050	0.98 0.72	0.216 SPO1050 0.871 SPO1051	0.95 0.99	0.952 0.412	SPO1047 SPO1048 SPO1049	1.67 2.15	0.070 0.010	SPO1048 SPO1049	1.61 2.02	0.032	SPO1048 SPO1049	1.10 1.20	0.663 0.056	SPO1048 SPO1049	1.10 1.20	0.459 0.024
SPO1051 SPO1053 SPO1054	0.64 0.93 0.49	0.351 0.885 0.162	SPO1050 SPO1051 SPO1053	1.21 0.72 0.91	0.405 0.443 0.751	SPO1051 SPO1053 SPO1054	0.65 0.95 0.99	0.71 SPO1053 0.37 SPO1054 0.096 SPO1055	0.93 0.96 0.7	0.295 0.345 0.01	SPO1050 SPO1051 SPO1052	0.76 1.12 1.35	0.042 0.872	SPO1050 SPO1051 SPO1052	0.74 0.95 1.04	0.267 0.766 0.548	SPO1050 SPO1051 SPO1052	0.97 1.11 0.96	0.705 0.959 0.625	SPO1050 SPO1051 SPO1052	0.94 1.40 1.04	0.533 0.649 0.991
SPO1055 SPO1056 SPO1057	0.33 0.62 1.02	0.034 0.144 0.838	SPO1054 SPO1055 SPO1056	0.64 0.36 0.71	0.271 0.012 0.337	SPO1055 SPO1056 SPO1057	0.91 0.88 0.87	0.059 SPO1056 0.198 SPO1057 0.775 SPO1058	0.65 0.9 0.82	0.449 0.547 0.058	SPO1053 SPO1054 SPO1055	1.33	0.242 0.316	SPO1053 SPO1054 SPO1055	1.37 2.78	0.103 0.219 0.036	SPO1053 SPO1054 SPO1055	1.30 1.55	0.152	SPO1053 SPO1054 SPO1055	1.20 2.01	0.573 0.016 0.008
SPO1058 SPO1059	1.01 1.13	0.405 0.227	SPO1057 SPO1058	1.03 1.14	0.684 0.703	SPO1058 SPO1059	0.88 0.95	0.037 SPO1059 0.908 SPO1060	0.96 0.89	0.875 0.087	SPO1056 SPO1057	1.06 1.15	0.747	SPO1056 SPO1057	0.84 1.20	0.636 0.213	SPO1056 SPO1057	1.03	0.942 0.141	SPO1056 SPO1057	1.16	0.509 0.621
SPO1060 SPO1061 SPO1062	0.79 0.98 0.89	0.305 0.824 0.713	SPO1059 SPO1060 SPO1061	0.79 0.89		SPO1060 SPO1061 SPO1062	0.99 0.98 0.97	0.098 SPO1061 0.106 SPO1062 0.813 SPO1063	0.78 0.79 0.93	0.109 0.7 0.203	SPO1058 SPO1059 SPO1060	1.77 1.68 3.95	0.049 0.034 0.002	SPO1058 SPO1059 SPO1060	1.57 1.58 3.29	0.012 0.010 0.001	SPO1058 SPO1059 SPO1060	1.06 0.80 0.91		SPO1058 SPO1059 SPO1060	1.06 0.83 0.95	0.515 0.278 0.701
SPO1063 SPO1064 SPO1065	0.95 1.02 1.41	0.642 0.956	SPO1062 SPO1063 SPO1064	0.93 0.99 1.06	0.821 0.917 0.823	SPO1063 SPO1064 SPO1065	0.96 0.94 0.69	0.207 SPO1064 0.674 SPO1065 0.724 SPO1066	0.92 0.94 0.93	0.691 0.76 0.297	SPO1061 SPO1062 SPO1063	2.30 1.97 3.26	0.004 0.107 0.009	SPO1061 SPO1062 SPO1063	2.29 1.96 3.08	0.001 0.138 0.005	SPO1061 SPO1062 SPO1063	0.90 0.88 0.86	0.481 0.774 0.511	SPO1061 SPO1062 SPO1063	0.92 0.90 0.92	0.381 0.789 0.711
SPO1066 SPO1067	1.85	0.001 0.886 0.232	SPO1065 SPO1066	1.21 1.58	0.046 0.044 0.796	SPO1066 SPO1067 SPO1068	0.88	0.469 SPO1067 0.819 SPO1068 0.43 SPO1069	0.88 0.62 0.7	0.825	SPO1064 SPO1065	3.97 1.99	0.013 0.019 0.643	SPO1064 SPO1065	4.19 1.96	0.038 0.008 0.365	SPO1064 SPO1065	0.98	0.973	SPO1064 SPO1065	0.94 0.88 1.16	0.934 0.192
SPO1068 SPO1069 SPO1070	1.13 0.88 0.7	0.623 0.082	SPO1067 SPO1068 SPO1069	1.09 1.16 1.02	0.332 0.898	SPO1069 SPO1070	0.87 1 0.96	0.717 SPO1070 0.286 SPO1071	0.87 0.9	0.902 0.555 0.522	SPO1066 SPO1068	0.97 1.06 2.39	0.728 0.026	SPO1066 SPO1068	1.01	0.779 0.021	SPO1066 SPO1067 SPO1068	1.07 1.00 1.15	0.761 0.956 0.337	SPO1066 SPO1067 SPO1068	1.04 1.15	0.051 0.899 0.280
SPO1071 SPO1072 SPO1073	1.85 1.18 0.94	0.021 0.37 0.933	SPO1070 SPO1071 SPO1072	0.69 1.56 1.15	0.331 0.031 0.606	SPO1071 SPO1072 SPO1073	0.83 0.86 0.67	0.667 SPO1072 0.513 SPO1073 0.327 SPO1074	0.86 0.88 0.94	0.148 0.601 0.891	SPO1069 SPO1070 SPO1071	2.49 1.78 1.03	0.098 0.031 0.675	SPO1069 SPO1070 SPO1071	2.46 1.91 1.10	0.090 0.109 0.128	SPO1069 SPO1070 SPO1071	0.99 0.88 1.15	0.954 0.147 0.342	SPO1069 SPO1070 SPO1071	0.97 0.92 1.02	0.988 0.672 0.859
SPO1074 SPO1075 SPO1076	1.12 1.22 1.29	0.502 0.597 0.77	SPO1073 SPO1074 SPO1075	0.99 1.05 1.07	0.886 0.833 0.725	SPO1074 SPO1075 SPO1076	0.94 0.93 0.66	0.652 SPO1075 0.83 SPO1076 0.608 SPO1077	0.91 0.88 0.9	0.998 0.227 0.623	SPO1072 SPO1073 SPO1074	1.24 1.13 0.68	0.097 0.666 0.236	SPO1072 SPO1073 SPO1074	1.27 1.01 0.68	0.041 0.992 0.415	SPO1072 SPO1073 SPO1074	1.09 0.88 0.78	0.225 0.466 0.478	SPO1072 SPO1073 SPO1074	1.14 0.90 0.79	0.189 0.760 0.521
SPO1077 SPO1078 SPO1079	1.02 1.05	0.799 0.642 0.573	SPO1076 SPO1077 SPO1078	1.05 1.05 0.98	0.507 0.757	SPO1077 SPO1078 SPO1079	0.94 0.95 0.94	0.516 SPO1078 0.418 SPO1079 0.853 SPO1080	0.73 0.95 0.94	0.66 0	SPO1075 SPO1076 SPO1077	1.57 0.65	0.338 0.311 0.702	SPO1075 SPO1076 SPO1077	1.36 0.71	0.366	SPO1075 SPO1076 SPO1077	1.02 1.02	0.906 0.949	SPO1075 SPO1076 SPO1077	0.88 0.93	0.685 0.524 0.595
SPO1080 SPO1081	1.24 1 1.07	0.991	SPO1079 SPO1080	1.2 1.11	0.186 0.942	SPO1080 SPO1081	0.87 0.93	0.974 SPO1081 0.052 SPO1082	0.63 0.93	0.255 0.832	SPO1078 SPO1079	1.13 0.85	0.654 0.067	SPO1078 SPO1079	1.10	0.758	SPO1078 SPO1079	0.90 0.88	0.499 0.702	SPO1078 SPO1079	1.12 1.03 0.76	0.808 0.178
SPO1082 SPO1083 SPO1084	0.92 0.98 1.44	0.783 0.971 0.021	SPO1081 SPO1082 SPO1083	1.21 0.95 0.95	1	SPO1082 SPO1083 SPO1084	0.94 0.72 0.87	0.657 SPO1083 0.849 SPO1084 0.175 SPO1085	0.66 0.65 0.92	0.832 0.351 0.445	SPO1080 SPO1081 SPO1082	0.85 1.00 1.29	0.964 0.929 0.110	SPO1080 SPO1081 SPO1082	0.79 0.93 1.31	0.235	SPO1080 SPO1081 SPO1082	0.91 1.06 1.00	0.677	SPO1080 SPO1081 SPO1082	0.93 0.97 1.02	0.953 0.635 0.716
SPO1085 SPO1086 SPO1087	1.06 1.04 0.84	0.36 0.9 0.52	SPO1084 SPO1085 SPO1086	1.53 1 1.05		SPO1085 SPO1086 SPO1087	0.98 0.79 0.83	0.978 SPO1086 0.024 SPO1087 0.885 SPO1088	0.92 0.93 0.88	0.236 0.261 0.685	SPO1083 SPO1084 SPO1085	1.32 0.60 0.57	0.226 0.084 0.031	SPO1083 SPO1084 SPO1085	1.27 0.61 0.55	0.179 0.057 0.033	SPO1083 SPO1084 SPO1085	1.02 1.16 1.01	0.703	SPO1083 SPO1084 SPO1085	1.01 1.20 1.00	0.924 0.432 0.819
SPO1088 SPO1089	1.06 0.55	0.436	SPO1087 SPO1088	0.9 1.02	0.747 0.857	SPO1088 SPO1089	0.85 0.77	0.936 SPO1089 0.012 SPO1090	0.9 0.89	0.019 0.589	SPO1086 SPO1087	0.79 1.43	0.300 0.094	SPO1086 SPO1087	0.76 1.14	0.175 0.399	SPO1086 SPO1087	0.86 0.79	0.083 0.358	SPO1086 SPO1087	0.86 0.99	0.252 0.904
SPO1090 SPO1091 SPO1092	1.01 0.83 1.13	0.838 0.63 0.84	SPO1089 SPO1090 SPO1091	0.58 0.95 1.01	0.756	SPO1090 SPO1091 SPO1092	0.88 0.93 0.94	0.826 SPO1091 0.485 SPO1092 0.936 SPO1093	0.85 0.96 0.9	0.763 0.959 0.902	SPO1088 SPO1089 SPO1090	0.91 4.13 0.72	0.540 0.036 0.237	SPO1088 SPO1089 SPO1090	1.02 3.49 0.70	0.004 0.162	SPO1088 SPO1089 SPO1090	0.65 1.27 0.86	0.074 0.239	SPO1088 SPO1089 SPO1090	0.70 1.15 0.85	0.194 0.110 0.441
SPO1093 SPO1094 SPO1095	1.32 0.83 1.31	0.023 0.203 0.083	SPO1092 SPO1093 SPO1094	1.09 1.15 0.87	0.929 0.322 0.32	SPO1093 SPO1094 SPO1095	0.83 0.92 0.94	0.402 SPO1094 0.297 SPO1095 0.263 SPO1096	0.98 0.91 0.63	0.804 0.059 0.68	SPO1091 SPO1092 SPO1093	0.70 0.74 0.70	0.058 0.783 0.078	SPO1091 SPO1092 SPO1093	0.75 0.75 0.77	0.436 0.855 0.027	SPO1091 SPO1092 SPO1093	0.52 0.87 0.96		SPO1091 SPO1092 SPO1093	0.74 0.94 1.00	0.287 0.943 0.990
SPO1096 SPO1097 SPO1098	1.15 1.36 0.82	0.038 0.443	SPO1095 SPO1096 SPO1097	1.36 0.88	0.171 0.157	SPO1096 SPO1097 SPO1098	0.87 0.88 0.91	0.246 SPO1097 0.93 SPO1098 0.93 SPO1099	0.83 0.88 0.94	0.871 0.924 0.797	SPO1094 SPO1095 SPO1096	0.33 0.38 1.29	0.025 0.001 0.006	SPO1094 SPO1095 SPO1096	0.34 0.43	0.002 0.017 0.004	SPO1094 SPO1095 SPO1096	1.03 1.32 1.27	0.930 0.043	SPO1094 SPO1095 SPO1096	1.11 1.15 1.09	0.392 0.076 0.131
SPO1099 SPO1100	1.29 0.83	0.141	SPO1098 SPO1099	0.9	0.957 0.644	SPO1099 SPO1100	0.85 0.95	0.512 SPO1100 0.991 SPO1101	1 0.93	0.881 0.265	SPO1097 SPO1098	0.66 0.72	0.708 0.814	SPO1097 SPO1098	0.65	0.517 0.766	SPO1097 SPO1098	0.96 0.72	0.976 0.752	SPO1097 SPO1098	0.94 0.82	0.911 0.840
SPO1101 SPO1102 SPO1103	1.37 1.4 0.84	0.426 0.562 0.119	SPO1100 SPO1101 SPO1102	0.9 1.23 1.38	0.707 0.449 0.49	SPO1101 SPO1102 SPO1103	0.87 0.97 0.88	0.402 SPO1102 0.923 SPO1103 0.026 SPO1104	0.94 0.72 0.97	0.938 0.218 0.172	SPO1099 SPO1100 SPO1101	1.21 3.01 0.71	0.415 0.001 0.331	SPO1099 SPO1100 SPO1101	1.31 2.63 0.67	0.516 0.013 0.340	SPO1099 SPO1100 SPO1101	1.05 0.75 1.14		SPO1099 SPO1100 SPO1101	0.97 0.72 1.18	0.953 0.202 0.392
SPO1104 SPO1105 SPO1106	0.64 1.12 0.91	0.025 0.342 0.764	SPO1103 SPO1104 SPO1105	0.91 0.7 1.13		SPO1104 SPO1105 SPO1106	0.88 0.6 1.01	0.036 SPO1105 0.164 SPO1106 0.414 SPO1107	0.91 0.66 1	0.569 0.307 0.754	SPO1102 SPO1103 SPO1104	0.61 0.69 1.63	0.282 0.130 0.066	SPO1102 SPO1103 SPO1104	0.65 0.69 1.54	0.330 0.154 0.057	SPO1102 SPO1103 SPO1104	1.11 0.95 1.14	0.761	SP01102 SP01103 SP01104	1.10 0.94 1.19	0.845 0.909 0.432
SPO1107 SPO1108	0.79 0.91 1.16	0.515 0.36	SPO1106 SPO1107	0.9 0.81 0.94	0.725 0.698	SPO1108 SPO1108 SPO1109	1.01 0.84 0.93	0.942 SPO1108 0.537 SPO1109 0.75 SPO1110	0.93 0.64 0.91	0.58 0.892	SPO1105 SPO1106	0.74 0.76 1.19	0.048 0.315 0.488	SPO1105 SPO1106	0.70 0.82 1.16	0.004	SPO1105 SPO1106 SPO1107	0.88 0.84 0.97	0.503 0.487	SPO1105 SPO1106 SPO1107	0.86 0.81 1.04	0.145 0.418 0.883
SPO1109 SPO1110 SPO1111	0.99 1.02	0.915	SPO1108 SPO1109 SPO1110	1.06 1.02	0.091 0.801	SPO1110 SPO1111	0.97 0.98	0.828 SPO1111 0.724 SPO1112	0.93 0.92	0.582 0.784 0.513	SPO1107 SPO1108 SPO1109	0.95 0.46	0.461 0.034	SPO1107 SPO1108 SPO1109	0.98 0.46	0.106	SPO1108 SPO1109	0.95 1.14	0.711 0.448	SPO1108 SPO1109	0.96 1.03	0.884 0.820
SPO1112 SPO1113 SPO1114	0.86 1.6 1.15	0.485 0.037 0.076	SPO1111 SPO1112 SPO1113	1.04 0.88 1.33	0.407 0.196 0.133	SP01112 SP01113 SP01114	0.78 0.76 0.9	0.763 SPO1113 0.805 SPO1114 0.081 SPO1115	0.93 0.99 0.96	0.871 0.313 0.12	SPO1110 SPO1111 SPO1112	0.94 0.56 0.42	0.881 0.089 0.010	SPO1110 SPO1111 SPO1112	0.95 0.56 0.48	0.856 0.045 0.004	SPO1110 SPO1111 SPO1112	1.05 0.76 0.93	0.588	SPO1110 SPO1111 SPO1112	0.88 1.02 0.90	0.668 0.992 0.300
SPO1115 SPO1116	1.19 0.88 0.87	0.258 0.314 0.719	SPO1114 SPO1115 SPO1116	1.13 1.07 0.89	0.087 0.18	SPO1115 SPO1116 SPO1117	0.89 0.86 0.93	0.811 SPO1116 0.011 SPO1117 0.947 SPO1118	0.96 0.7 0.82	0.004 0.839 0.063	SPO1113 SPO1114 SPO1115	0.76 0.58 0.65	0.118 0.017 0.013	SPO1113 SPO1114 SPO1115	0.76 0.59 0.78	0.253	SPO1113 SPO1114 SPO1115	1.09 0.89 1.20	0.670 0.570	SPO1113 SPO1114 SPO1115	1.03 0.87 1.05	0.932 0.399 0.549
SPO1117 SPO1118 SPO1119	1.13 1.47	0.058	SPO1117 SPO1118	0.98 1.17	0.948	SPO1118 SPO1119	0.78 0.94	0.397 SPO1119 0.355 SPO1120	0.94 0.92	0.521 0.969	SPO1116 SPO1117	0.42	0.001 0.584	SPO1116 SPO1117	0.42 0.81	0.004 0.280	SPO1116 SPO1117	0.89 0.96	0.145 0.901	SPO1116 SPO1117	0.85 1.02	0.036 0.886
SPO1120 SPO1121 SPO1122	1.01 0.97 1.14	0.771 0.976 0.359	SPO1119 SPO1120 SPO1121	1.26 0.99 1.01		SPO1120 SPO1121 SPO1122	0.81 0.88 0.98	0.996 SPO1121 0.522 SPO1122 0.048 SPO1123	0.8 0.77 0.8	0.431 0.314 0.676	SPO1118 SPO1119 SPO1120	1.97 0.68 1.17	0.004 0.126 0.629	SPO1118 SPO1119 SPO1120	1.96 0.72 1.26		SPO1118 SPO1119 SPO1120	1.04 1.00 1.08	0.967	SPO1118 SPO1119 SPO1120	1.10 1.02 1.03	0.179 0.676 0.970
SPO1123 SPO1124 SPO1125	1.05 1.2 1.33	0.802 0.363 0.188	SPO1122 SPO1123 SPO1124	1.1 1.09 1.16		SPO1123 SPO1124 SPO1125	0.84 0.7 0.97	0.691 SPO1124 0.899 SPO1125 0.383 SPO1126	0.9 0.83 0.74	0.805 0.504 0.028	SPO1121 SPO1122 SPO1123	1.34 0.85 1.18	0.404 0.502 0.200	SPO1121 SPO1122 SPO1123	1.24 0.79 1.11		SPO1121 SPO1122 SPO1123	0.96 0.88 0.94	0.768	SP01121 SP01122 SP01123	1.01 0.95 0.94	0.895 0.427 0.813
SPO1126 SPO1127	0.85 1.09	0.64 0.815	SPO1125 SPO1126	1.22 0.92	0.419 0.641	SPO1126 SPO1127	0.98 0.95	0.796 SPO1127 0.593 SPO1128	0.89 0.9	0.693 0.342	SPO1124 SPO1125	1.36 1.44	0.192 0.129	SPO1124 SPO1125	1.37	0.005 0.161	SPO1124 SPO1125	1.00 1.11	0.906 0.635	SPO1124 SPO1125	0.96 1.07	0.556 0.771
SPO1128 SPO1129 SPO1130	0.68 1.12 0.7	0.031 0.805 0.618	SPO1127 SPO1128 SPO1129	0.96 0.75 1.03	0.108 0.866	SPO1128 SPO1129 SPO1130	0.71 0.73 0.95	0.564 SPO1129 0.787 SPO1130 0.878 SPO1131	0.95 0.94 0.88	0.784 0.765 0.109	SPO1126 SPO1127 SPO1128	1.45 0.56 0.90	0.102 0.338 0.721	SPO1126 SPO1127 SPO1128	1.46 0.61 0.84	0.384 0.281	SPO1126 SPO1127 SPO1128	1.18 0.80 0.94	0.495 0.688	SPO1126 SPO1127 SPO1128	1.21 0.83 0.97	0.225 0.729 0.895
SPO1131 SPO1132	0.87 0.92	0.123	SPO1130 SPO1131	0.64 0.83		SPO1131 SPO1132	0.82 0.81	0.043 SPO1132 0.441 SPO1133	0.74 0.84	0.847 0.19	SPO1129 SPO1130	0.66 1.35	0.532 0.491	SPO1129 SPO1130	0.72 1.44		SPO1129 SPO1130	1.06 0.93		SPO1129 SPO1130	1.01	0.976 0.950

SPO1133 SPO1134	1.23	0.079	SPO1132 SPO1133	1.02	0.619	SPO1133 SPO1134	0.87	0.174 SPO1134 0.989 SPO1135	1.02	0.957	SPO1131 SPO1132	1.29	0.052	SPO1131 SPO1132	1.34	0.010	SPO1131 SPO1132	1.04	0.564	SPO1131 SPO1132	1.02	0.406
SPO1135 SPO1136	1.27 0.76	0.25 0.073	SPO1134 SPO1135	1.05 1.11	0.935 0.42	SPO1135 SPO1136	0.93 0.69	0.965 SPO1136 0.794 SPO1137	0.76 0.93	0.472 0.483	SPO1133 SPO1134 SPO1135	1.17	0.080 0.822	SPO1133 SPO1134 SPO1135	1.23 0.99	0.055 0.953	SPO1133 SPO1134	1.05 0.97	0.530 0.964	SPO1133 SPO1134	1.08 0.95	0.345 0.972
SPO1137 SPO1138 SPO1139	0.89 1.19 0.43	0.888 0.367 0.408	SPO1136 SPO1137 SPO1138	0.83 0.83 1.26	0.234 0.727 0.099	SPO1137 SPO1138 SPO1139	0.63 0.88 0.92	0.022 SPO1138 0.298 SPO1139 0.207 SPO1140	0.97 0.81 0.88	0.142 0.221 0.8	SPO1136 SPO1137	0.77 1.19 1.02	0.649 0.143 0.908	SPO1136 SPO1137	0.72 1.36 1.26	0.368 0.068 0.330	SPO1135 SPO1136 SPO1137	0.89 1.07 1.00	0.788 0.803 0.893	SPO1135 SPO1136 SPO1137	0.89 1.10 1.04	0.626 0.577 0.912
SPO1140 SPO1141 SPO1142	0.89 0.82 0.76	0.918 0.594 0.07	SPO1139 SPO1140 SPO1141	0.51 0.83 0.76	0.443 0.568 0.659	SPO1140 SPO1141 SPO1142	0.85 0.6 0.93	0.766 SPO1141 0.084 SPO1142 0.443 SPO1143	0.56 0.68 0.91	0.622 0.383 0.338	SPO1138 SPO1139 SPO1140	1.21 2.67 0.83	0.670 0.034 0.700	SPO1138 SPO1139 SPO1140	1.06 2.51 0.89	0.671 0.098 0.667	SPO1138 SPO1139 SPO1140	1.08 1.46 1.17	0.676 0.196 0.808	SPO1138 SPO1139 SPO1140	0.94 1.66 1.05	0.756 0.452 0.880
SPO1143 SPO1144	0.81 0.76	0.764 0.506	SPO1142 SPO1143	0.83 0.85	0.579 0.625	SPO1143 SPO1144	0.89 0.95	0.772 SPO1144 0.275 SPO1145	0.93 0.99	0.348 0.648	SPO1141 SPO1142	1.08 1.13	0.450 0.414	SPO1141 SPO1142	1.08 1.19	0.520 0.028	SPO1141 SPO1142	1.02 1.05	0.993 0.769	SPO1141 SPO1142	0.99 1.05	0.957 0.827
SPO1145 SPO1146 SPO1147	1.06 0.85 0.82	0.321 0.812 0.835	SPO1144 SPO1145 SPO1146	0.76 1.05 0.85	0.254 0.736 0.425	SPO1145 SPO1146 SPO1147	0.95 0.73 0.91	0.774 SPO1146 0.48 SPO1147 0.924 SPO1148	0.75 0.75 0.92	0.067 0.91 0.898	SPO1144 SPO1145	1.11 1.44 0.76	0.850 0.074 0.570	SPO1143 SPO1144 SPO1145	1.10 1.05 0.80	0.766 0.727 0.372	SPO1143 SPO1144 SPO1145	1.12 0.95 0.84	0.894	SPO1144 SPO1145	1.02 1.21 0.92	0.976 0.568 0.500
SPO1148 SPO1150 SPO1151	0.68 1.13 1.56	0.249 0.332 0.066	SPO1147 SPO1148 SPO1150	0.88 0.71 1.08	0.948 0.417 0.644	SPO1148 SPO1150 SPO1151	0.97 0.93 0.9	0.944 SPO1150 0.863 SPO1151 0.743 SPO1152	0.84 0.85 0.84	0.892 0.305 0.075	SPO1146 SPO1147 SPO1148	1.39 1.66 1.19	0.519 0.683 0.748	SPO1146 SPO1147 SPO1148	1.69 1.44 1.32	0.095 0.725 0.613	SPO1146 SPO1147 SPO1148	1.13 0.93 0.93	0.753 0.929	SPO1146 SPO1147 SPO1148	1.16 0.95 0.98	0.500 0.945 0.930
SPO1152 SPO1153	1.04 1.13	0.75 0.66	SPO1151 SPO1152	1.25 0.92	0.06 0.582	SPO1152 SPO1153	0.96 0.96	0.439 SPO1153 0.918 SPO1154	0.83 0.83	0.877 0.877	SPO1150 SPO1151	0.83 0.66	0.643 0.066	SPO1150 SPO1151	0.79 0.66	0.474	SPO1150 SPO1151	0.88 1.12	0.551 0.639	SPO1150 SPO1151	0.90 1.08	0.145 0.534
SPO1154 SPO1155 SPO1156	0.83 1.18 1.16	0.664 0.125 0.336	SPO1153 SPO1154 SPO1155	1.14 0.83 1.12	0.542 0.418 0.263	SPO1154 SPO1155 SPO1156	0.65 0.97 0.95	0.665 SPO1155 0.924 SPO1156 0.324 SPO1157	0.84 0.95 0.99	0.642 0.299 0.788	SPO1153 SPO1154	0.74 0.90 0.86	0.250 0.819 0.812	SPO1152 SPO1153 SPO1154	0.78 0.93 0.95	0.134 0.940 0.375	SPO1152 SPO1153 SPO1154	0.97 1.00 0.94	0.998	SPO1152 SPO1153 SPO1154	1.01 0.99 0.94	0.696 0.978 0.774
SPO1157 SPO1158	0.83 1.38 0.84	0.03 0.495 0.323	SPO1156 SPO1157 SPO1158	1.3 1.03 1.43	0.444 0.723 0.535	SPO1157 SPO1158 SPO1159	0.93 0.93 0.92	0.041 SPO1158 0.89 SPO1159 0.179 SPO1160	0.82 0.68 0.93	0.988 0.428 0.107	SPO1155 SPO1156	0.78 0.89 0.81	0.453 0.726 0.251	SPO1155 SPO1156 SPO1157	0.80 0.79 0.76	0.260 0.637 0.456	SPO1155 SPO1156 SPO1157	0.93 0.91 1.37	0.837 0.280 0.409	SPO1155 SPO1156 SPO1157	0.92 0.84 1.31	0.629 0.285 0.693
SPO1159 SPO1160 SPO1161	0.75 1.09	0.273	SPO1159 SPO1160	0.78 0.79	0.242 0.466	SPO1160 SPO1161	0.92 0.93 0.91	0.664 SPO1161 0.194 SPO1162	1 0.96	0.204 0.651	SPO1158 SPO1159	1.22 1.61	0.500 0.053	SPO1158 SPO1159	1.27 1.82	0.459 0.015	SPO1158 SPO1159	1.10 0.80	0.817 0.154	SPO1158 SPO1159	1.04 0.85	0.908 0.237
SPO1162 SPO1163 SPO1164	1.26 1.1	0.352 0.651 0.97	SPO1161 SPO1162 SPO1163	1.1 1.32 1.08	0.199 0.104 0.554	SPO1162 SPO1163 SPO1164	0.96 0.86	0.529 SPO1163 0.995 SPO1164 0.815 SPO1165	0.96 0.8 1.02	0.931 0.66 0.838	SPO1160 SPO1161 SPO1162	1.16 0.94 1.91	0.150 0.878 0.029	SPO1160 SPO1161 SPO1162	1.17 0.95 1.97	0.549 0.991 0.003	SPO1160 SPO1161 SPO1162	1.03 0.93 0.93	0.985 0.658 0.511	SPO1160 SPO1161 SPO1162	1.18 0.93 1.03	0.469 0.408 0.761
SPO1165 SPO1166 SPO1168	0.68 0.94 0.84	0.549 0.867 0.338	SPO1164 SPO1165 SPO1166	0.92 0.78 0.85	0.809 0.22 0.86	SPO1165 SPO1166	0.95 0.92	0.584 SPO1166 0.705 SPO1168 0.977 SPO1171	0.72 0.89 0.84	0.718 0.251 0.62	SPO1163 SPO1164 SPO1165	1.97 0.80 0.82	0.030 0.406 0.791	SPO1163 SPO1164 SPO1165	2.01 0.81 0.65	0.015 0.234 0.334	SPO1163 SPO1164 SPO1165	1.08 0.96 0.93	0.687 0.894 0.894	SPO1163 SPO1164 SPO1165	1.04 0.88 0.95	0.712 0.578 0.926
SPO1168 SPO1171 SPO1172	1.16 0.88	0.235 0.254	SPO1168 SPO1171	0.83 0.99	0.501 0.929	SPO1168 SPO1171 SPO1172	0.77 0.8 0.75	0.977 SPO1171 0.771 SPO1172 0.233 SPO1173	0.84 0.81 0.9	0.62 0.431 0.949	SPO1166 SPO1168	0.82 0.60 0.56	0.791	SPO1165 SPO1166 SPO1168	0.65 0.61 0.52	0.334	SPO1166 SPO1168	1.05 1.05	0.894 0.646 0.883	SPO1166	1.06 1.00	0.925 0.946
SPO1173 SPO1174 SPO1175	0.83 0.73 1.5	0.126 0.178	SPO1172 SPO1173 SPO1174	0.98 1.01 0.77	0.95 0 0.122	SPO1173 SPO1174 SPO1175	0.37 0.35 0.79	0 SPO1174 0.314 SPO1175 0.03 SPO1176	0.94 0.95 0.65	0.437 0.601 0.264	SPO1171 SPO1172 SPO1173	1.24 1.44 0.54	0.126 0.004 0.687	SPO1171 SPO1172 SPO1173	1.33 1.46 0.53	0.061 0.041 0.644	SPO1171 SPO1172 SPO1173	1.09 0.99	0.349 0.898	SPO1171 SPO1172 SPO1173	1.08 0.93 0.58	0.354 0.798 0.746
SPO1176 SPO1177	0.93 1.07	0.938 0.857	SPO1175 SPO1176	1.34 0.88	0.011	SPO1176 SPO1177	0.96 0.96	0.739 SPO1177 0.146 SPO1178	0.62 0.9	0.218 0.412	SPO1174 SPO1175	1.26 0.74	0.191 0.191	SPO1174 SPO1175	1.24 0.85	0.118 0.213	SPO1174 SPO1175	1.29		SPO1174 SPO1175	1.18 1.10	0.545 0.660
SPO1178 SPO1179 SPO1180	1.03 1.16 1.01	0.811 0.706 0.863	SPO1177 SPO1178 SPO1179	0.95 1.1 1.07	0.916 0.722 0.706	SPO1178 SPO1179 SPO1180	0.7 0.93 0.79	0.288 SPO1179 0.064 SPO1180 0.053 SPO1181	0.91 0.87 0.51	0.097 0.039 0.033	SPO1176 SPO1177 SPO1178	0.87 0.10 2.05	0.718 0.017 0.044	SPO1176 SPO1177 SPO1178	1.38 0.10 2.00	0.686 0.017 0.066	SPO1176 SPO1177 SPO1178	1.25 0.77 0.81		SPO1176 SPO1177 SPO1178	1.06 0.67 0.78	0.391 0.597 0.501
SPO1181 SPO1182 SPO1183	1.03 1.14 0.89	0.495 0.247 0.284	SPO1180 SPO1181 SPO1182	0.98 0.93 1.14	0.948 0.885 0.268	SPO1181 SPO1182 SPO1183	0.89 0.83 0.88	0.01 SPO1182 0.065 SPO1183 0.054 SPO1184	0.96 0.8 0.94	0.027 0.034 0.782	SPO1179 SPO1180 SPO1181	1.85 1.95	0.032 0.023 0.016	SPO1179 SPO1180 SPO1181	1.84 1.95	0.035 0.014 0.008	SPO1179 SPO1180 SPO1181	0.95 0.96 1.10	0.860	SPO1179 SPO1180 SPO1181	0.88 0.97 1.02	0.577 0.928 0.418
SPO1184 SPO1185	1.09 0.66	0.793	SPO1183 SPO1184	1.02 0.97	0.617 0.972	SPO1184 SPO1185	0.98 0.79	0.284 SPO1185 0.062 SPO1186	0.96 0.72	0.403 0.215	SPO1181 SPO1182 SPO1183	2.40	0.011 0.020	SPO1182 SPO1183	2.80	0.002	SPO1182 SPO1183	1.05 0.98	0.719 0.973	SPO1182 SPO1183	1.00 0.94	0.772 0.410
SPO1186 SPO1187 SPO1188	0.8 1.31 1.27	0.187 0.332 0.452	SPO1185 SPO1186 SPO1187	0.76 0.87 1.1	0.204 0.26 0.287	SPO1186 SPO1187 SPO1188	0.89 0.95 0.98	0.163 SPO1187 0.684 SPO1188 0.768 SPO1189	0.91 0.89 0.91	0.781 0.322 0.963	SPO1185 SPO1186	1.21 0.88 0.85	0.368 0.110 0.566	SPO1184 SPO1185 SPO1186	1.06 0.81 0.85	0.408 0.277 0.394	SPO1184 SPO1185 SPO1186	0.81 0.87 0.91	0.809 0.120 0.711	SPO1184 SPO1185 SPO1186	0.84 0.88 0.90	0.279 0.395 0.642
SPO1189 SPO1190 SPO1191	0.7 1.57 0.61	0.317 0.365 0.014	SPO1188 SPO1189 SPO1190	1.17 0.85 1.09	0.178 0.357 0.498	SPO1189 SPO1190 SPO1191	0.92 0.76 0.86	0.68 SPO1190 0.32 SPO1191 0.213 SPO1192	0.88 0.62 0.92	0.432 0.146 0.498	SPO1187 SPO1188 SPO1189	0.70 1.52 0.74	0.121 0.329 0.162	SPO1187 SPO1188 SPO1189	0.72 1.56 0.75	0.171 0.035 0.317	SPO1187 SPO1188 SPO1189	1.06 1.18 1.09	0.905 0.748 0.896	SPO1187 SPO1188 SPO1189	0.97 1.16 0.95	0.915 0.510 0.786
SPO1192 SPO1193	0.74 0.85	0.126 0.602	SPO1191 SPO1192	0.6 0.79	0.012 0.104	SPO1192 SPO1193	0.84	0.776 SPO1193 0.622 SPO1194	0.77 0.89	0.508 0.031	SPO1190 SPO1191	0.61 1.57	0.450 0.010	SPO1190 SPO1191	0.62 1.58	0.311	SPO1190 SPO1191	0.87 1.21	0.770	SPO1190 SPO1191	0.51 1.32	0.294 0.026
SPO1194 SPO1195 SPO1196	1.42 0.87 1.12	0.067 0.165 0.649	SPO1193 SPO1194 SPO1195	0.79 1.34 0.88	0.137 0.083 0.271	SPO1194 SPO1195 SPO1196	0.86 0.67 0.89	0.1 SPO1195 0.005 SPO1196 0.23 SPO1197	0.86 0.97 0.87	0.02 0.247 0.967	SPO1192 SPO1193 SPO1194	1.60 1.33 2.07	0.096 0.185 0.009	SPO1192 SPO1193 SPO1194	1.58 1.60 1.93	0.031 0.022 0.005	SPO1192 SPO1193 SPO1194	1.16 1.04 0.96	0.282 0.957 0.986	SPO1192 SPO1193 SPO1194	1.22 1.04 0.86	0.079 0.975 0.179
SPO1197 SPO1198 SPO1199	1.29 1.8 1.25	0.801 0.066 0.103	SPO1196 SPO1197 SPO1198	1.09 1.06 1.46	0.719 0.939 0.192	SPO1197 SPO1198 SPO1199	1.01 0.76 0.84	0.991 SPO1198 0.861 SPO1199 0.146 SPO1200	0.97 0.92 0.99	0.855 0.372 0.273	SPO1195 SPO1196	3.77 2.76 0.96	0.005 0.016 0.962	SPO1195 SPO1196	3.41 2.50 1.00	0.010 0.021 0.912	SPO1195 SPO1196 SPO1197	1.18 1.14 0.92	0.063	SPO1195 SPO1196 SPO1197	1.08 1.03 0.93	0.309 0.573 0.959
SPO1200 SPO1201	0.89 0.81	0.799	SPO1199 SPO1200	1.12 0.88	0.276 0.315	SPO1200 SPO1201	0.99 0.91	0.202 SPO1201 0.013 SPO1202	0.88 1.01	0.025 0.013	SPO1198 SPO1199	0.78 1.22	0.268 0.185	SPO1197 SPO1198 SPO1199	0.78 1.25		SPO1198 SPO1199	0.96 1.00	0.710 0.948	SPO1198 SPO1199	1.00 0.96	0.908 0.893
SPO1202 SPO1203 SPO1204	1.18 1.08 0.74	0.037 0.479 0.031	SPO1201 SPO1202 SPO1203	0.78 1.04	0.043 0.091 0.712	SPO1202 SPO1203 SPO1204	0.96 0.92 0.52	0.001 SPO1203 0.023 SPO1204 0.6 SPO1205	0.8 0.73 0.78	0.086 0.04 0.083	SPO1200 SPO1201 SPO1202	1.43 2.63 2.45	0.236 0.003 0.007	SPO1200 SPO1201 SPO1202	1.74 2.62 2.61	0.018 0.003 0.001	SPO1200 SPO1201 SPO1202	1.13 1.01 0.97	0.246	SPO1200 SPO1201 SPO1202	1.07 1.03 0.94	0.591 0.352 0.533
SPO1205 SPO1206 SPO1207	1.53 1.28 1.24	0.008 0.057 0.279	SPO1204 SPO1205 SPO1206	0.76 1.44 1.34	0.054 0.031 0.014	SPO1205 SPO1206 SPO1207	0.94 0.95 0.93	0.062 SPO1206 0.095 SPO1207 0.906 SPO1208	0.35 0.33 0.79	0.184 0.978 0.011	SPO1203 SPO1204	1.75 1.30 0.79	0.003 0.022 0.513	SPO1203 SPO1204	1.82 1.36 0.79	0.012 0.005 0.670	SPO1203 SPO1204 SPO1205	0.89 0.89 1.34	0.487 0.499 0.067	SPO1203 SPO1204 SPO1205	0.85 0.92 1.24	0.117 0.266 0.053
SPO1208 SPO1209	1 0.63	0.311	SPO1207 SPO1208	1.12 1.33	0.687 0.061	SPO1208 SPO1209	0.93 0.96	0.006 SPO1209 0.816 SPO1210	0.95 0.91	0.655 0.325	SPO1206 SPO1207	0.79 0.74	0.150 0.667	SPO1206 SPO1207	0.76 0.75	0.104 0.700	SPO1206 SPO1207	0.80 1.09	0.247 0.819	SPO1206 SPO1207	0.84 1.00	0.334 0.952
SPO1210 SPO1211 SPO1212	0.97 0.6	0.791 0.053 0.993	SPO1209 SPO1210 SPO1211	0.66 0.94 0.65	0.188 0.797 0.081	SPO1210 SPO1211 SPO1212	0.99 0.85 0.78	0.395 SPO1211 0.256 SPO1212 0.975 SPO1213	0.91 0.75 0.92	0.009 0.975 0.081	SPO1208 SPO1209 SPO1210	0.46 0.83 1.37	0.006 0.643 0.066	SPO1208 SPO1209 SPO1210	0.50 0.85 1.30	0.002 0.569 0.168	SPO1208 SPO1209 SPO1210	0.58 0.94 0.92	0.056 0.875 0.205	SPO1208 SPO1209 SPO1210	0.72 1.07 0.92	0.080 0.692 0.435
SPO1213 SPO1214 SPO1215	0.7 0.54 0.76	0.045 0.032 0.34	SPO1212 SPO1213 SPO1214	0.91 0.76 0.57	0.911	SPO1213 SPO1214 SPO1215	0.92 1 0.64	0.189 SPO1214 0.128 SPO1215 0.231 SPO1216	0.89 0.8 0.89	0.104 0.172 0.001	SPO1211 SPO1212	2.20 0.97 1.61	0.026 0.914	SPO1211 SPO1212	2.04 1.00 1.57	0.002	SPO1211 SPO1212 SPO1213	1.13 0.97 1.08	0.386 0.983 0.445	SPO1211 SPO1212 SPO1213	1.23 0.96 1.11	0.236 0.975 0.233
SPO1216 SPO1217	0.1 3.07	0.002	SPO1215 SPO1216	0.76 0.1	0.387	SPO1216 SPO1217	0.89 0.89	0.001 SPO1217 0.109 SPO1218	0.96 0.88	0.014 0.895	SPO1214 SPO1215	1.79	0.003 0.732	SPO1214 SPO1215	1.74	0.001	SPO1214 SPO1215	0.95 0.95	0.593 0.949	SPO1214 SPO1215	1.06	0.233 0.315 0.901
SPO1218 SPO1219 SPO1220	0.93 0.83 0.96	0.99 0.481 0.863	SPO1217 SPO1218 SPO1219	1.02 0.81	0.013 0.438 0.493	SPO1218 SPO1219 SPO1220	0.75 0.97 0.89	0.83 SPO1219 0.241 SPO1220 0.741 SPO1221	0.88 0.93 0.83	0.334 0.786 0.957	SPO1216 SPO1217 SPO1218	0.56 0.86	0.003 0.002 0.476	SPO1216 SPO1217 SPO1218	7.05 0.50 1.07	0.002 0.007 0.757	SPO1216 SPO1217 SPO1218	0.64 1.38	0.003 0.117 0.435	SPO1216 SPO1217 SPO1218	0.61 1.23	0.005 0.083 0.084
SPO1221 SPO1222 SPO1223	0.64 0.75	0.213 0.681 0.387	SPO1220 SPO1221 SPO1222	0.97 0.63 0.7	0.092	SPO1221 SPO1222 SPO1223	0.86 0.81 0.87	0.797 SPO1222 0.926 SPO1223 0.825 SPO1225	0.95 0.79 0.76	0.942 0.72 0.969	SPO1219 SPO1220 SPO1221	0.92 0.55 0.92	0.675 0.028 0.854	SPO1219 SPO1220 SPO1221	0.95 0.53 0.85	0.782 0.033	SPO1219 SPO1220 SPO1221	1.08 1.30 1.05	0.209	SPO1219 SPO1220 SPO1221	1.09 1.28 1.11	0.712 0.074 0.647
SPO1225 SPO1226	0.89 0.44	0.953	SPO1223 SPO1225	1.05 0.95	0.774 0.983	SPO1224 SPO1225	0.93 0.79	0 SPO1226 0.906 SPO1227	1.02 0.85	0.341 0.28	SPO1222 SPO1223	1.48 0.96	0.452 0.540	SPO1222 SPO1223	1.42 0.97	0.299 0.553	SPO1222 SPO1223	1.37 0.72	0.631 0.358	SPO1222 SPO1223	1.09 0.96	0.922 0.829
SPO1227 SPO1228 SPO1229	0.74 0.85 0.91	0.018 0.731 0.844	SPO1226 SPO1227 SPO1228	0.49 0.82 0.83	0.035 0.397 0.703	SPO1226 SPO1227 SPO1228	0.77 0.88 0.96	0.25 SPO1228 0.063 SPO1229 0.715 SPO1230	0.92 0.66 0.88	0.185 0.353 0.793	SPO1225 SPO1226 SPO1227	0.79 0.94 1.75	0.753 0.955 0.058	SPO1225 SPO1226 SPO1227	0.88 0.87 1.76		SPO1225 SPO1226 SPO1227	0.72 1.12 1.36	0.575 0.021	SPO1224 SPO1225 SPO1226	0.86 0.68 1.21	0.188 0.746 0.483
SPO1230 SPO1231 SPO1232	0.49 0.94 0.66	0.378 0.887 0.411	SPO1229 SPO1230 SPO1231	0.89 0.68 0.96	0.623 0.497 0.961	SPO1229 SPO1230 SPO1231	0.96 0.68 0.71	0.602 SPO1231 0.49 SPO1232 0.817 SPO1233	0.94 0.91 0.72	0.806 0.304 0.729	SPO1228 SPO1229 SPO1230	1.50 1.08 1.34	0.274 0.674 0.520	SPO1228 SPO1229 SPO1230	1.44 1.17 1.20	0.241	SPO1228 SPO1229 SPO1230	1.18 1.40 1.20		SPO1227 SPO1228 SPO1229	1.25 1.24 1.30	0.007 0.510 0.082
SPO1233 SPO1234 SPO1235	0.64 0.77 0.68	0.705 0.307 0.41	SPO1232 SPO1233 SPO1234	0.76 0.74 0.81	0.442 0.826 0.218	SPO1232 SPO1233 SPO1234	0.96 0.98 0.93	0.436 SPO1234 0.651 SPO1235 0.948 SPO1236	0.95 0.85 0.96	0.882 0.911 0.058	SPO1231 SPO1232 SPO1233	0.99 1.10 0.54	0.773 0.425 0.495	SPO1231 SPO1232 SPO1233	1.06 1.14 0.54	0.974 0.087 0.522	SPO1231 SPO1232 SPO1233	1.02 1.01 0.91	0.936	SPO1230 SPO1231 SPO1232	1.33 0.93 1.02	0.735 0.848 0.950
SPO1236 SPO1237	0.62 0.63	0.049	SPO1234 SPO1235	0.73 0.66	0.282	SPO1235 SPO1236	0.88 0.93	0.743 SPO1237 0.121 SPO1239	0.96 0.91 0.94	0.023 0.747	SPO1234 SPO1235	1.51 1.55	0.038 0.049	SPO1234 SPO1235	1.32	0.522 0.102 0.041	SPO1233 SPO1234 SPO1235	0.93			0.91 0.93	0.921 0.762
SPO1239 SPO1240 SPO1241	1.16 0.9 0.97	0.129 0.347 0.682	SPO1237 SPO1239 SPO1240	0.68 1.18 0.87	0.023 0.19 0.005	SPO1237 SPO1239 SPO1240	0.93 0.87 0.93	0.435 SPO1240 0.444 SPO1241 0.623 SPO1242	0.4 0.93 0.9	0.798 0.842 0.124	SPO1236 SPO1237 SPO1239	3.09 2.82 0.85	0.003 0.008 0.989	SPO1236 SPO1237 SPO1239	3.00 2.39 0.84		SPO1236 SPO1237 SPO1239	1.34 1.33 0.93	0.116	SPO1235 SPO1236 SPO1237	1.01 1.51 1.41	0.876 0.017 0.024
SPO1242 SPO1243 SPO1244	1.57 0.86 1.08	0.009 0.062 0.433	SPO1241 SPO1242 SPO1243	0.98 1.43 0.88	0.987 0.026 0.287	SPO1241 SPO1242 SPO1243	0.83 0.83 0.99	0.482 SPO1243 0.042 SPO1244 0.135 SPO1245	0.98 0.88 0.96	0.164 0.88 0.972	SPO1240 SPO1241 SPO1242	0.88 0.88 0.76	0.815 0.934 0.143	SPO1240 SPO1241 SPO1242	0.86 0.85 0.71	0.844	SPO1240 SPO1241 SPO1242	0.99 0.96	0.875 0.995	SPO1239 SPO1240 SPO1241	0.96 1.08 0.92	0.953 0.225 0.709
SPO1245 SPO1246	0.77 0.96	0.229 0.953	SPO1244 SPO1245	1.24 0.81	0.074 0.654	SPO1244 SPO1245	0.69 0.93	0.261 SPO1246 0.86 SPO1247	0.94 0.85	0.225 0.873	SPO1243 SPO1244	0.65 0.81	0.135 0.066	SPO1243 SPO1244	0.60 0.76	0.019 0.411	SPO1243 SPO1244	0.95 1.10	0.931 0.541	SPO1242 SPO1243	1.00 0.85	0.960 0.255
SPO1247 SPO1249 SPO1250	1.14 1.1 1.03	0.888 0.427 0.72	SPO1246 SPO1247 SPO1249	0.95 1.09 1.1	0.893 0.914 0.158	SPO1246 SPO1247 SPO1249	0.88 0.99 0.88	0.516 SPO1249 0.891 SPO1250 0.399 SPO1251	0.79 0.75 0.92	0.841 0.873 0.935	SPO1245 SPO1246 SPO1247	1.16 0.91 1.01	0.156 0.628 0.967	SPO1245 SPO1246 SPO1247	1.13 0.99 0.91	0.387 0.595 0.987	SPO1245 SPO1246 SPO1247	0.99 0.99 0.93	0.949	SPO1244 SPO1245 SPO1246	1.10 1.01 1.02	0.609 0.984 0.813
SPO1251 SPO1252 SPO1253	1.11 0.67	0.943 0.128	SPO1250 SPO1251 SPO1252	1.01	0.984	SPO1250 SPO1251	0.75 0.96	0.957 SPO1252 0.907 SPO1253	0.7	0.815 0.047	SPO1249 SPO1250 SPO1251	1.01 0.85	0.979 0.638	SPO1249 SPO1250 SPO1251	0.93 0.76	0.217	SPO1249 SPO1250	1.22	0.964	SPO1247 SPO1249 SPO1250	0.99	0.997 0.160
SPO1254 SPO1255	0.95 0.81 0.91	0.186 0.324 0.594	SPO1253 SPO1254	0.71 0.93 0.97	0.573 0.976	SPO1252 SPO1253 SPO1254	0.65 0.96 0.95	0.489 SPO1254 0.163 SPO1255 0.585 SPO1256	0.73 0.99 0.89	0.476 0.8 0.502	SPO1252 SPO1253	0.75 1.23 1.41	0.912 0.422 0.006	SPO1252 SPO1253	0.78 1.09 1.36	0.314	SPO1251 SPO1252 SPO1253	0.86 1.05 1.28	0.877 0.042	SPO1251 SPO1252	0.95 0.83 1.06	0.919 0.910 0.713
SPO1256 SPO1257 SPO1258	0.68 1.02 0.53	0.538 0.619 0.052	SPO1255 SPO1256 SPO1257	0.84 0.71 1.02	0.419 0.582 0.436	SPO1255 SPO1256 SPO1257	0.99 0.97 0.79	0.924 SPO1257 0.526 SPO1258 0.687 SPO1259	0.93 0.98 0.83	0.379 0.422 0.567	SPO1254 SPO1255 SPO1256	0.65 0.79 2.81	0.143 0.468 0.191	SPO1254 SPO1255 SPO1256	0.59 0.88 3.01		SPO1254 SPO1255 SPO1256	1.17 0.98 1.14	0.995	SPO1253 SPO1254 SPO1255	1.18 1.21 0.98	0.033 0.235 0.981
SPO1259 SPO1260	0.67 1.66 1.33	0.042 0.251 0.385	SPO1258 SPO1259	0.63 0.78 1.46	0.076 0.017 0.264	SPO1258 SPO1259	0.96 0.94 0.52	0.367 SPO1260 0.778 SPO1261	0.82 0.78 0.74	0.592 0.541 0.773	SPO1257 SPO1258 SPO1259	0.60 1.01 0.88	0.076 0.819 0.512	SPO1257 SPO1258 SPO1259	0.58 1.00 0.80	0.033 0.717	SPO1257 SPO1258	0.88 0.94 0.96		SPO1256 SPO1257	1.25 0.86 1.02	0.752 0.234 0.906
SPO1261 SPO1262 SPO1263	1.08 1.45	0.82	SPO1260 SPO1261 SPO1262	1.25 0.92	0.42 0.942	SPO1260 SPO1261 SPO1262	0.82 0.81	0.606 SPO1262 0.785 SPO1263 0.864 SPO1264	0.85 0.97	0.349 0.318	SPO1259 SPO1260 SPO1261	0.76 0.35	0.514 0.043	SPO1259 SPO1260 SPO1261	0.75 0.34	0.338	SPO1259 SPO1260 SPO1261	1.04 1.05	0.887 0.751	SPO1258 SPO1259 SPO1260	0.91 1.01	0.431 0.975
SPO1264 SPO1265 SPO1266	1.11 0.98 0.76	0.156 0.985 0.191	SPO1263 SPO1264 SPO1265	1.32 1.12 1.03	0.062 0.085 0.942	SPO1263 SPO1264 SPO1265	0.7 0.85 0.95	0.554 SPO1265 0.874 SPO1266 0.907 SPO1267	0.62 0.75 0.93	0.925 0.041 0.652	SPO1262 SPO1263 SPO1264	0.60 0.75 0.84	0.432 0.143 0.273	SPO1262 SPO1263 SPO1264	0.51 0.72 0.85		SPO1262 SPO1263 SPO1264	0.75 1.10 1.00		SPO1261 SPO1262 SPO1263	1.15 0.83 1.04	0.474 0.686 0.678
SPO1267 SPO1268	1.59 1.01	0.01 0.3 0.522	SPO1266 SPO1267	0.79 1.39	0.251 0.12	SPO1266 SPO1267	0.89 0.94	0.079 SPO1268 0.325 SPO1269	0.92 0.86	0.364 0.525	SPO1265 SPO1266 SPO1267	0.99	0.893 0.067 0.023	SPO1265 SPO1266 SPO1267	0.94 1.28		SPO1265 SPO1266	0.98 1.20	0.998 0.719	SPO1264 SPO1265	1.01 0.97	0.414 0.990
SPO1269 SPO1270 SPO1271	0.85 0.6 0.91	0.002	SPO1268 SPO1269 SPO1270	1.03 0.9 0.64	0.014	SPO1270	0.83 0.98 0.99	0.133 SPO1271 0.434 SPO1272	0.96 0.94 0.87	0.68 0.637 0.042	SPO1268 SPO1269	0.82 1.14	0.210 0.334	SPO1268 SPO1269	0.83 1.02	0.127 0.182	SPO1267 SPO1268 SPO1269	1.02 1.17	0.718	SPO1266 SPO1267 SPO1268	1.21 1.42 0.98	0.416 0.517 0.760
SPO1272 SPO1273 SPO1274	0.64 0.99 1.07	0.043 0.957 0.655	SPO1271 SPO1272 SPO1273	0.9 0.7 0.95	0.689 0.083 0.903	SPO1271 SPO1272 SPO1273	0.98 0.81	0.54 SPO1273 0.117 SPO1274 0.571 SPO1275	0.89 0.82 0.86	0.945 0.616 0.908	SPO1270 SPO1271 SPO1272	0.86 3.29 1.55	0.120 0.034 0.038	SPO1270 SPO1271 SPO1272	0.83 3.42 1.48	0.171 0.023 0.038	SPO1270 SPO1271 SPO1272	0.84 1.14 1.02	0.475	SPO1269 SPO1270 SPO1271	1.12 0.86 1.05	0.606 0.121 0.884
SPO1275 SPO1276	0.48	0.006 0.256	SPO1274 SPO1275	1.14 0.53	0.639 0.015	SPO1274 SPO1275	0.85 0.75	0.618 SPO1276 0.013 SPO1277	0.97 0.66	0.793 0.351	SPO1273 SPO1274 SPO1276	1.75 0.58	0.073 0.242	SPO1273 SPO1274	1.49 0.60	0.108	SPO1273 SPO1274	1.15 0.90	0.578 0.816	SPO1272 SPO1273	1.03 1.08	0.463 0.767
SPO1277 SPO1278	1.33 0.9	0.235 0.875	SPO1276 SPO1277	0.97 1.31		SPO1276 SPO1277	0.82 0.71	0.563 SPO1278 0.546 SPO1279	0.84 0.71	0.164 0.181	SPO1275 SPO1276	0.95 1.45	0.091	SPO1275 SPO1276	0.97 1.52	0.040	SPO1275 SPO1276	0.99 1.05		SPO1274 SPO1275	0.90 1.00	0.711 0.610

SPO1279 SPO1280	0.47	0.003	SPO1278 SPO1279	0.85		SPO1278 SPO1279	0.87 0.93	0.467 SPO1280 0.053 SPO1281	0.65 1.01	0.06 SPO127	7 0.6	3 0.098	SPO1277 SPO1278	0.59		SPO1277 SPO1278	1.07	0.555 SPO127 0.873 SPO127		0.395 0.832
SPO1281 SPO1282	0.77 1.32	0.513 0.14	SPO1280 SPO1281	0.63 0.7	0.379 0.274	SPO1280 SPO1281	0.83 0.76	0.007 SPO1282 0.808 SPO1283	0.89 0.96	0.732 SPO127 0.85 SPO128	0.7	0.005	SPO1279 SPO1280	0.76 5.48	0.183 0.016	SPO1279 SPO1280	1.09 0.93	0.346 SPO127 0.437 SPO127	8 0.90 9 1.09	0.437 0.397
SPO1283 SPO1284 SPO1285	0.86 0.54 0.85	0.054	SPO1282 SPO1283 SPO1284	0.88 0.63	0.343	SPO1282 SPO1283 SPO1284	0.77 0.85 0.82	0.967 SPO1284 0.363 SPO1285 0.19 SPO1286	0.97 0.98 0.78	0.023 SPO128 0.684 SPO128 0.615 SPO128	2 0.9			0.29 0.86 1.00	0.221	SPO1281 SPO1282 SPO1283	1.06 1.11 0.99	0.834 SPO128 0.782 SPO128 0.979 SPO128	1 0.88	0.648 0.757 0.554
SPO1286 SPO1287 SPO1288	0.99 0.84 0.61	0.283	SPO1285 SPO1286 SPO1287	0.91 0.93 0.83	0.944	SPO1285 SPO1286 SPO1287	0.57 0.83 0.95	0.53 SPO1287 0.695 SPO1288 0.308 SPO1289	0.93 0.93 0.67	0.403 SPO128 0.541 SPO128 0.748 SPO128	0.7	7 0.713	SPO1284 SPO1285 SPO1286	1.76 0.71 0.78	0.372	SPO1284 SPO1285 SPO1286	1.07 0.94 0.87	0.551 SPO128 0.930 SPO128 0.650 SPO128	4 1.11	0.946 0.316 0.987
SPO1289 SPO1290	1.41 0.95	0.618 0.947	SPO1288 SPO1289	0.68 1.23	0.058 0.728	SPO1288 SPO1289	0.93 0.64	0.61 SPO1290 0.756 SPO1291	0.83 0.8	0.664 SPO128 0.28 SPO128	7 0.8 3 1.3	3 0.336 2 0.337		0.81 1.35	0.140 0.125	SPO1287 SPO1288	0.93 1.10	0.485 SPO128 0.366 SPO128	6 0.89 7 0.92	0.614 0.626
SPO1291 SPO1292 SPO1293	0.8 0.63 0.5	0.046	SPO1290 SPO1291 SPO1292	0.75 0.65	0.067	SPO1290 SPO1291 SPO1292	0.86 0.95 0.74	0.76 SPO1292 0.067 SPO1293 0.252 SPO1294	0.76 0.92 0.93	0.125 SPO128 0.004 SPO129 0.219 SPO129		0.967	SPO1289 SPO1290 SPO1291	0.64 0.90 0.59	0.991	SPO1289 SPO1290 SPO1291	0.99 0.81 0.91	0.985 SPO128 0.755 SPO128 0.427 SPO129	9 0.87	0.909 0.849 0.574
SPO1294 SPO1295 SPO1298	0.98 0.96 0.65	0.95	SPO1293 SPO1294 SPO1295	0.62 1.04	0.109	SPO1293 SPO1294 SPO1295	0.81 0.74 0.96	0.002 SPO1295 0.235 SPO1298 0.971 SPO1299	0.9 0.93 0.85	0.973 SPO129 0.514 SPO129 0.654 SPO129	3 1.4	1 0.023	SPO1293	2.02 1.25 0.87	0.032	SPO1292 SPO1293 SPO1294	1.02 0.92 1.06	0.805 SPO129 0.637 SPO129 0.749 SPO129	2 1.07	0.580 0.342 0.428
SPO1299 SPO1300	0.93 1.07	0.871	SPO1298 SPO1299	0.93 0.97	0.941 0.63	SPO1298 SPO1299	0.8 0.86	0.559 SPO1300 0.213 SPO1301	0.93 0.87	0.508 SPO129 0.04 SPO129	5 0.i	3 0.640 8 0.620	SPO1295	0.68 0.99	0.469 0.725	SPO1295 SPO1298	1.04 0.99	0.927 SPO129 0.912 SPO129	4 0.95 5 1.14	0.874 0.804
SPO1301 SPO1302 SPO1303	0.54 0.64 1.15		SPO1300 SPO1301 SPO1302	1.05 0.58 0.7	0.003	SPO1300 SPO1301 SPO1302	0.95 0.91 0.86	0.516 SPO1302 0.106 SPO1303 0.045 SPO1304	0.93 0.83 0.7	0.008 SPO129 0.614 SPO130 0.12 SPO130		6 0.428	SPO1299 SPO1300 SPO1301	2.13 1.04 1.65	0.640	SPO1299 SPO1300 SPO1301	1.26 1.11 1.29	0.276 SPO129 0.612 SPO129 0.133 SPO130	9 1.25	0.920 0.354 0.685
SPO1304 SPO1305	0.9 1.15	0.514 0.182	SPO1303 SPO1304	1.11 0.93	0.027 0.743	SPO1303 SPO1304	1 0.85	0.93 SPO1305 0.627 SPO1306	0.77 0.69	0.887 SPO130 0.207 SPO130	2 2.0	0.002 0.069	SPO1302 SPO1303	2.05 1.49	0.011	SPO1302 SPO1303	1.14 1.19	0.123 SPO130 0.298 SPO130	1 1.36 2 1.24	0.073 0.059
SPO1306 SPO1307 SPO1308	0.51 1.03 0.97	0.736	SPO1305 SPO1306 SPO1307	1.09 0.55 1.01	0.101	SPO1305 SPO1306 SPO1307	0.97 0.69 0.93	0.969 SPO1307 0.423 SPO1308 0.78 SPO1309	0.91 0.82 0.93	0.895 SPO130 0.791 SPO130 0.978 SPO130	5 1.4	9 0.080		1.36 1.36 1.13	0.042	SPO1304 SPO1305 SPO1306	1.00 0.98 1.05	0.886 SPO130 0.981 SPO130 0.747 SPO130	4 1.12	0.439 0.423 0.764
SPO1309 SPO1310 SPO1311	1.21 1.09		SPO1308 SPO1309 SPO1310	0.99 1.11 1.03	0.827	SPO1308 SPO1309 SPO1310	0.97 0.93 0.95	0.969 SPO1310 0.981 SPO1311 0.18 SPO1312	0.9 0.79 0.82	0.109 SPO130 0.293 SPO130 0.597 SPO130		3 0.510	SPO1307 SPO1308 SPO1309	1.22 1.23 1.03		SPO1307 SPO1308 SPO1309	0.88 1.09 0.96	0.664 SPO130 0.882 SPO130 0.974 SPO130	7 0.93	0.039 0.762 0.814
SPO1312 SPO1313	1.25 1.59	0.232	SPO1311 SPO1312	1.02 1.33	0.8 0.151	SPO1311 SPO1312	0.93 0.84	0.208 SPO1313 0.783 SPO1314	0.95 0.87	0.19 SPO131 0.96 SPO131	0.8	2 0.707 3 0.005	SPO1310 SPO1311	0.85 0.57	0.956 0.011	SPO1310 SPO1311	1.03 0.88	0.729 SPO130 0.185 SPO131	9 0.97 0 0.99	0.991 0.886
SPO1314 SPO1315 SPO1316	0.9 1.06 1.17	0.74	SPO1313 SPO1314 SPO1315	1.66 1.03 1.02	0.856	SPO1313 SPO1314 SPO1315	0.7 0.42 0.97	0.192 SPO1315 0.928 SPO1316 0.836 SPO1317	0.85 0.65 0.85	0.916 SPO131 0.896 SPO131 0.509 SPO131	3 0.7	2 0.233	SPO1312 SPO1313 SPO1314	1.18 0.68 0.46	0.282	SPO1312 SPO1313 SPO1314	1.17 0.97 0.92	0.271 SPO131 0.940 SPO131 0.852 SPO131	2 1.04	0.196 0.751 0.401
SPO1317 SPO1318 SPO1319	2.61 1.36 1.29	0.217	SPO1316 SPO1317 SPO1318	1.13 2.09 1.46	0.025	SPO1316 SPO1317 SPO1318	0.95 0.81 0.93	0.561 SPO1318 0.63 SPO1319 0.767 SPO1320	0.9 0.59 0.83	0.164 SPO131 0.03 SPO131 0.671 SPO131	0.7		SPO1315 SPO1316 SPO1317	0.34 0.77 0.75	0.142	SPO1315 SPO1316 SPO1317	0.91 1.04 1.14	0.121 SPO131 0.267 SPO131 0.799 SPO131	5 0.93	0.633 0.710 0.965
SPO1320 SPO1321	0.93 1.13	0.751 0.092	SPO1319 SPO1320	1.27 0.92	0.006 0.586	SPO1319 SPO1320	0.56 0.68	0.832 SPO1321 0.408 SPO1322	0.94 0.92	0.555 SPO131 0.938 SPO131	3 0.9	8 0.279 2 0.012	0. 0.0	0.81 1.23	0.258	SPO1318 SPO1319	0.99 1.01	0.966 SPO131 0.549 SPO131	7 1.12 8 0.96	0.792 0.898
SPO1322 SPO1323 SPO1324	0.9 1.32 1.07	0.043	SPO1321 SPO1322 SPO1323	1.17 0.91 1.37	0.847	SPO1321 SPO1322 SPO1323	0.98 0.31 0.98	0.916 SPO1323 0.92 SPO1324 0.045 SPO1325	0.84 0.98 0.73	0.132 SPO132 0.942 SPO132 0.577 SPO132		4 0.808		0.82 1.06 1.04	0.719	SPO1320 SPO1321 SPO1322	0.85 1.09 0.97	0.196 SPO131 0.449 SPO132 0.984 SPO132	0.84	0.084 0.271 0.627
SPO1325 SPO1326 SPO1327	0.97 0.95 0.93	0.949	SPO1324 SPO1325 SPO1326	1.12 0.94 1.05	0.954	SPO1324 SPO1325 SPO1326	0.89 1 0.86	0.967 SPO1326 0.865 SPO1327 0.033 SPO1328	0.86 0.84 1.01	0.518 SPO132 0.742 SPO132 0.819 SPO132	0.7	8 0.834	SPO1323 SPO1324 SPO1325	1.09 0.85 0.82	0.896	SPO1323 SPO1324 SPO1325	1.26 1.08 0.88	0.431 SPO132 0.921 SPO132 0.501 SPO132	2 1.09 3 1.19	0.856 0.395 0.878
SPO1328 SPO1329	0.81 1.03	0.429	SPO1327 SPO1328	0.92 0.88	0.453 0.146	SPO1327 SPO1328	0.36 0.66	0.88 SPO1329 0.578 SPO1330	0.78 0.85	0.987 SPO132 0.003 SPO132	5 1.5 7 1.0	0.023 7 0.309	SPO1326 SPO1327	1.71	0.038	SPO1326 SPO1327	0.93 1.10	0.480 SPO132 0.132 SPO132	5 0.87 6 1.02	0.365 0.886
SPO1330 SPO1331 SPO1332	2.69 0.85 1.04		SPO1329 SPO1330 SPO1331	1 1.77 0.83	0.081	SPO1329 SPO1330 SPO1331	0.85 0.94 0.97	0.428 SPO1331 0.396 SPO1332 0.322 SPO1333	0.99 0.97 0.79	0.024 SPO132 0.191 SPO132 0.156 SPO133			SPO1328 SPO1329 SPO1330	0.68 0.62 0.39	0.104	SPO1328 SPO1329 SPO1330	1.11 1.24 1.30	0.520 SPO132 0.171 SPO132 0.342 SPO132	8 1.14	0.391 0.047 0.092
SPO1333 SPO1334	0.96 0.71	0.332	SPO1332 SPO1333	0.99 0.99	0.288 0.984	SPO1332 SPO1333	0.95 0.94	0.659 SPO1334 0.213 SPO1335	0.85 1.01	0.295 SPO133 0.92 SPO133	1 1.0	8 0.197 2 0.354		1.16 1.05	0.009	SPO1331 SPO1332	1.17 1.08	0.100 SPO133 0.579 SPO133	0 1.33 1 1.15	0.012 0.039 0.335
SPO1335 SPO1336 SPO1337	1.31 1.07 1.05	0.817	SPO1334 SPO1335 SPO1336	0.83 1.17 1.16	0.846 0.557	SPO1334 SPO1335 SPO1336	0.81 0.95 0.86	0.094 SPO1336 0.867 SPO1337 0.756 SPO1339	0.83 0.99 0.6	0.609 SPO133 0.601 SPO133	1.1	5 0.274 5 0.665	SPO1334 SPO1335	0.61 1.18 0.83	0.089	SPO1333 SPO1334 SPO1335	0.91 1.12 0.90	0.345 SPO133 0.278 SPO133 0.880 SPO133	3 0.94 4 1.22	0.551 0.115
SPO1339 SPO1340 SPO1341	0.88 0.89 1.19		SPO1337 SPO1339 SPO1340	1.1 0.86 0.94	0.57	SPO1337 SPO1339 SPO1340	0.83 0.93 0.9	0.974 SPO1340 0.846 SPO1341 0.949 SPO1342	0.93 0.93 0.95	0.951 SPO133 0.638 SPO133 0.797 SPO133	7 1.2	3 0.461	SPO1336 SPO1337 SPO1339	0.92 1.13 0.93		SPO1336 SPO1337 SPO1339	0.97 1.05 1.08	0.988 SPO133 0.910 SPO133 0.518 SPO133	6 0.93	0.928 0.879 0.407
SP01342 SP01343	1.16 0.81	0.074	SPO1341 SPO1342	1.16 0.97	0.938	SPO1341 SPO1342	0.92 0.85	0.45 SPO1343 0.663 SPO1344	0.9	0.092 SPO134 0.91 SPO134	0.8	3 0.943 1 0.860	0. 0.0.0	0.87 1.01	0.849	SPO1340 SPO1341	0.97 1.08	0.987 SPO133 0.752 SPO134	0.93	0.456 0.967
SPO1344 SPO1345 SPO1346	0.94 1.73 1.32	0.002	SPO1343 SPO1344 SPO1345	0.88 0.93 1.41	0.975	SPO1344 SPO1345	0.95 0.51 0.9	0.445 SPO1345 0.955 SPO1346 0.143 SPO1347	0.71 0.43 0.98	0.036 SPO134 0.697 SPO134 0.701 SPO134	1 0.9	2 0.025 3 0.985		0.79 1.15 0.96	0.341	SPO1342 SPO1343 SPO1344	1.05 0.95 0.93	0.951 SPO134 0.538 SPO134 0.944 SPO134	2 1.03 3 1.05	0.796 0.922 0.416
SPO1347 SPO1348 SPO1349	1.53 1.35 1.33	0.319	SPO1346 SPO1347 SPO1348	1.09 1.18 1.36	0.742	SPO1346 SPO1347 SPO1348	0.85 0.92 0.79	0.956 SPO1348 0.86 SPO1349 0.086 SPO1351	0.89 0.83 0.96	0.638 SPO134 0.57 SPO134 0.065 SPO134	3.0	7 0.902	SPO1346	1.51 0.88 0.70	0.876	SPO1345 SPO1346 SPO1347	1.16 0.85 1.19	0.215 SPO134 0.340 SPO134 0.881 SPO134	5 1.17	0.925 0.148 0.295
SPO1350 SPO1351	1.15 0.57	0.291	SPO1349 SPO1351	1.15 0.64	0.527 0.03	SPO1349 SPO1351	0.97 0.89	0.555 SPO1352 0.015 SPO1353	0.95 0.9	0.648 SPO134 0.175 SPO134	3 1.0	5 0.161 5 0.388	SPO1348 SPO1349	1.03 0.77	0.285	SPO1348 SPO1349	0.94 1.00	0.900 SPO134 0.983 SPO134	7 1.01 8 0.97	0.967 0.999
SPO1352 SPO1353 SPO1354	1.17 1.55 1.09	0.278	SPO1352 SPO1353 SPO1354	1.09 1.58 1.03	0.052	SPO1352 SPO1353 SPO1354	0.89 0.9 0.88	0.984 SPO1354 0.144 SPO1355 0.948 SPO1356	0.54 0.53 0.98	0.898 SPO135 0.758 SPO135 0.234 SPO135			SPO1350 SPO1351 SPO1352	1.48 0.12 0.68		SPO1350 SPO1351 SPO1352	0.95 1.49 1.03	0.600 SPO134 0.040 SPO135 0.673 SPO135	0 0.95 1 1.58	0.971 0.606 0.101
SPO1355 SPO1356 SPO1357	1.21 0.65 0.82	0.139	SPO1355 SPO1356 SPO1357	1.32 0.71 0.93	0.102	SPO1355 SPO1356 SPO1357	0.89 0.78 0.88	0.205 SPO1357 0.462 SPO1358 0.039 SPO1359	0.92 0.29 0.89	0.027 SPO135 0.962 SPO135 0.818 SPO135	5 0.9	8 0.644	SPO1353 SPO1354 SPO1355	0.76 1.08 1.00	0.265	SPO1353 SPO1354 SPO1355	0.95 1.06 1.04	0.841 SPO135 0.465 SPO135 0.721 SPO135	3 0.83	0.486 0.354 0.602
SPO1358 SPO1359	1.39 0.89	0.073	SPO1358 SPO1359	1.33 0.81	0.172 0.824	SPO1358 SPO1359	0.93 0.95	0.742 SPO1360 0.908 SPO1361	0.97 0.93	0.143 SPO135 0.237 SPO135	7 2.1	0.005 8 0.461	SPO1356	1.44 1.98	0.038	SPO1356 SPO1357	0.99 1.14	0.965 SPO135 0.164 SPO135	5 1.01 6 1.12	0.930 0.306
SPO1360 SPO1361 SPO1362	0.98 0.97 1.61		SPO1360 SPO1361 SPO1362	1.08 0.98 1.42	0.827	SPO1360 SPO1361 SPO1362	0.96 0.89 0.79	0.055 SPO1362 0.293 SPO1363 0.813 SPO1364	0.7 0.35 0.66	0.702 SPO135 0.863 SPO136 0.801 SPO136		0.010	SPO1358 SPO1359 SPO1360	0.76 0.83 0.53	0.901	SPO1358 SPO1359 SPO1360	1.04 0.88 0.97	0.748 SPO135 0.819 SPO135 0.908 SPO135	8 1.00	0.238 0.981 0.910
SPO1363 SPO1364 SPO1365	1.14 1.34	0.807 0.026	SPO1363 SPO1364 SPO1365	1.09 1.31	0.81 0.035 0.468	SPO1363 SPO1364 SPO1365	0.88 0.76	0.688 SPO1365 0.929 SPO1366 0.664 SPO1367	0.99 0.98	0.133 SPO136 0.493 SPO136 0.859 SPO136	2 0.6 3 0.8		SPO1361 SPO1362 SPO1363	1.03 0.69		SPO1361 SPO1362 SPO1363	1.04 0.99	0.813 SPO136 0.978 SPO136 0.382 SPO136		0.812 0.749
SPO1366 SPO1367	1.11	0.867	SPO1366 SPO1367	1.11	0.838	SPO1366 SPO1367	0.98	0.147 SPO1368 0.963 SPO1369	0.99	0.949 SPO136 0.013 SPO136	5.6	0.008	SPO1365	0.85 1.02	0.814	SPO1364 SPO1365	0.90	0.299 SPO136 0.583 SPO136	4 0.83	0.632 0.162
SPO1368 SPO1369 SPO1370	0.78 1.07 1.45	0.634	SPO1368 SPO1369 SPO1370	0.75 1.11 1.21	0.234	SPO1368 SPO1369 SPO1370	0.78 0.77 0.86	0.892 SPO1370 0.021 SPO1371 0.585 SPO1372	0.85 0.78 0.97	0.517 SPO136 0.656 SPO136 0.65 SPO136	3 0.9		SPO1367	2.38 1.01	0.286	SPO1366 SPO1367 SPO1368	1.11 0.99 0.87	0.676 SPO136 0.968 SPO136 0.888 SPO136	6 1.04	0.550 0.883 0.952
SPO1371 SPO1372 SPO1373	1.4 1.14 1.17	0.257	SPO1371 SPO1372 SPO1373	1.42 1.17 1.06	0.166	SPO1371 SPO1372 SPO1373	0.87 0.89 0.97	0.903 SPO1373 0.43 SPO1374 0.692 SPO1375	0.93 0.99 0.95	0.251 SPO137 0.404 SPO137 0.51 SPO137	1 0.6			0.79 0.93 0.61	0.857	SPO1369 SPO1370 SPO1371	1.12 1.12 1.24	0.555 SPO136 0.219 SPO136 0.386 SPO137	9 1.12	0.853 0.321 0.401
SPO1374 SPO1375	1.39 0.91	0.054	SPO1374 SPO1375	1.32 0.98	0.133 0.949	SPO1374 SPO1375	0.82 0.75	0.098 SPO1376 0.52 SPO1377	1 0.9	0.991 SPO137 0.947 SPO137	3 0.8	6 0.606 4 0.428	SPO1372 SPO1373	0.41 1.01	0.010	SPO1372 SPO1373	1.51 1.50	0.202 SPO137 0.368 SPO137	1 1.18 2 1.46	0.487 0.044
SPO1376 SPO1377 SPO1378	1.23 1.51 1.19	0.053	SPO1376 SPO1377 SPO1378	1.54 1.36 1.04	0.11	SPO1376 SPO1377 SPO1378	0.95 0.88 0.9	0.838 SPO1378 0.665 SPO1379 0.447 SPO1380	0.71 0.53 0.96	0.375 SPO137 0.981 SPO137 0.972 SPO137	6 0.1	0.006	SPO1374 SPO1375 SPO1376	0.81 1.42 0.23	0.019	SPO1374 SPO1375 SPO1376	1.02 1.01 0.75	0.727 SPO137 0.428 SPO137 0.207 SPO137	4 1.02	0.063 0.691 0.700
SPO1379 SPO1380 SPO1381	0.82 0.81 0.75	0.399	SPO1379 SPO1380 SPO1381	1.01 0.85 0.79	0.472	SPO1379 SPO1380 SPO1381	0.92 0.88 0.92	0.98 SPO1381 0.952 SPO1382 0.649 SPO1383	0.79 0.89 0.78	0.314 SPO137 0.997 SPO137 0.117 SPO138			SPO1378	1.21 0.49 0.68	0.152	SPO1377 SPO1378 SPO1379	1.40 0.93 0.72	0.118 SPO137 0.926 SPO137 0.771 SPO137	7 1.21	0.415 0.138 0.792
SPO1382 SPO1383	0.65 0.74	0.318	SPO1382 SPO1383	0.7 0.79	0.413 0.06	SPO1382 SPO1383	0.97 0.92	0.924 SPO1384 0.628 SPO1385	0.93 0.96	0.742 SPO138 0.951 SPO138	1 1.5 2 1.6	6 0.014 0 0.387	SPO1380 SPO1381	1.34 1.96	0.258	SPO1380 SPO1381	0.96 1.06	0.876 SPO137 0.512 SPO138	9 0.83 0 1.06	0.771 0.727
SPO1384 SPO1385 SPO1386	0.83 0.92	0.879	SPO1384 SPO1385 SPO1386	1.22 1.03 0.94	0.954	SPO1384 SPO1385 SPO1386	0.88 0.55 0.79	0.607 SPO1386 0.993 SPO1387 0.537 SPO1388	0.88 0.84 0.94	0.279 SPO138 0.733 SPO138 0.728 SPO138	1.1	8 0.107	SPO1383	1.48 0.81 1.20	0.801	SPO1382 SPO1383 SPO1384	0.91 0.93 1.15	0.868 SPO138 0.781 SPO138 0.332 SPO138	2 1.00	0.289 0.941 0.336
SPO1387 SPO1388 SPO1389	1.26 0.88 1.31	0.873	SPO1387 SPO1388 SPO1389	1.17 0.91 1.38	0.924	SPO1387 SPO1388 SPO1389	0.9 0.83 0.79	0.733 SPO1389 0.636 SPO1390 0.651 SPO1392	0.85 0.83 0.76	0.943 SPO138 0.13 SPO138 0.589 SPO138	7 0.1	0.018		0.84	0.015	SPO1385 SPO1386 SPO1387	1.15 1.02 0.98	0.896 SPO138 0.255 SPO138 0.942 SPO138	5 1.03	0.470 0.977 0.423
SPO1390 SPO1392	1.05 0.68	0.628	SPO1390 SPO1392	1.03 0.78	0.109 0.292	SPO1390 SPO1392	0.88 0.92	0.07 SPO1393 0.885 SPO1394	0.92 0.93	0.132 SPO138 0.749 SPO139	0 0.7	4 0.429 9 0.388	SPO1388 SPO1389	1.08	0.683	SPO1388 SPO1389	1.15 1.45	0.675 SPO138 0.485 SPO138	7 0.94 8 1.15	0.888 0.775
SPO1393 SPO1394 SPO1395	1.1 1.28 1.21	0.122	SPO1393 SPO1394 SPO1395	1.04 1.21 1.29	0.171	SPO1393 SPO1394 SPO1395	0.93 0.85 0.72	0.635 SPO1395 0.372 SPO1396 0.185 SPO1397	0.95 0.97 0.96	0.442 SPO139 0.857 SPO139 0.808 SPO139	3 0.1	0.010 0.017 1 0.132	SPO1392 SPO1393	0.75 0.26 0.26	0.014	SPO1390 SPO1392 SPO1393	1.03 0.98 1.06	0.877 SPO138 0.887 SPO139 0.950 SPO139	0 1.04	0.352 0.812 0.932
SPO1396 SPO1397 SPO1398	0.93 0.79 0.65	0.28	SPO1396 SPO1397 SPO1398	0.91 0.77 0.67	0.192	SPO1396 SPO1397 SPO1398	0.71 0.68 0.71	0.91 SPO1398 0.714 SPO1399 0.101 SPO1400	0.97 0.76 0.86	0.313 SPO139 0.733 SPO139 0.078 SPO139	5 0.5 5 1.9	2 0.049 7 0.289	SPO1395	0.88 0.51 1.92	0.037	SPO1394 SPO1395 SPO1396	1.08 0.93 1.03	0.669 SPO139 0.543 SPO139 0.963 SPO139	3 1.13 4 1.08	0.429 0.834 0.837
SPO1399 SPO1400	0.76	0.141 0.858	SPO1399 SPO1400	0.71 0.95	0.392 0.955	SPO1399 SPO1400	0.49 0.89	0.505 SPO1401 0.511 SPO1402	0.71 0.99	0.883 SPO139 0.204 SPO139	9 0.6	7 0.003 8 0.436	SPO1397 SPO1398	1.92 1.96 5.39	0.155	SPO1397 SPO1398	0.96 0.93	0.786 SPO139 0.616 SPO139	6 0.95 7 0.95	0.945 0.917
SPO1401 SPO1402 SPO1403	1.08 0.89 1.16	0.62	SPO1401 SPO1402 SPO1403	1.03 0.96 1.21	0.925	SPO1401 SPO1402 SPO1403	0.96 0.8 0.69	0.717 SPO1403 0.101 SPO1404 0.766 SPO1405	0.96 0.84 0.76	0.666 SPO140 0.829 SPO140 0.243 SPO140	1 0.6	9 0.005	SPO1399 SPO1400 SPO1401	0.47 0.85 0.69	0.086	SPO1399 SPO1400 SPO1401	0.72 0.97 0.79	0.065 SPO139 0.812 SPO139 0.490 SPO140	9 0.72	0.580 0.179 0.999
SPO1404 SPO1405	0.78 0.66 0.87	0.438 0.459	SPO1404 SPO1405	0.8 0.68 0.86	0.446 0.419	SPO1404 SPO1405	0.64 0.88	0.777 SPO1406 0.213 SPO1407	0.87 0.77 0.95	0.625 SPO140 0.29 SPO140	3 1.0 4 0.6	0 0.230 3 0.383	SPO1402 SPO1403	0.51 1.01 0.59	0.107	SPO1402 SPO1403	0.94 0.96	0.936 SPO140 0.717 SPO140	1 0.92 2 0.92	0.618 0.868
SPO1406 SPO1407 SPO1408	0.99	0.86	SPO1406 SPO1407 SPO1408	1.03	0.595 0.611	SPO1406 SPO1407 SPO1408	0.69 0.93 0.88	0.489 SPO1409 0.657 SPO1410	0.91 0.78	0.015 SPO140 0.74 SPO140	6 1.0 7 1.1	8 0.945 7 0.088	SPO1405 SPO1406	0.78	0.611	SPO1404 SPO1405 SPO1406	1.63 1.35	0.804 SPO140 0.186 SPO140 0.545 SPO140	4 0.93 5 1.60	0.919 0.900 0.211
SPO1409 SPO1410 SPO1411	1.29 1.31 1.08	0.734	SPO1409 SPO1410 SPO1411	1.24 1.28 0.93	0.011 0.783	SPO1409 SPO1410 SPO1411	0.85 0.98 0.8	0.002 SPO1411 0.637 SPO1412 0.489 SPO1413	0.83 0.97 0.96	0.084 SPO140 0.464 SPO140 0.753 SPO141	9 0.1	0.001	SPO1408	1.18 1.20 0.19	0.041	SPO1407 SPO1408 SPO1409	1.09 1.26 0.93	0.334 SPO140 0.745 SPO140 0.705 SPO140	6 1.33 7 1.08	0.655 0.537 0.744
SPO1412 SPO1413	1.13	0.365	SPO1412 SPO1413	1.43 1.13	0.125 0.557	SPO1412 SPO1413	0.87 0.78	0.321 SPO1414 0.881 SPO1415	0.91 0.86	0.337 SPO141 0.069 SPO141	1 0.7	9 0.457 7 0.030	SPO1410 SPO1411	0.58 0.82	0.548 0.158	SPO1410 SPO1411	0.82 0.88	0.766 SPO140 0.632 SPO141	9 0.89 0 0.81	0.331 0.810
SPO1414 SPO1415 SPO1416	1.02 1.44 0.85	0.083	SPO1414 SPO1415 SPO1416	1.02 1.08 0.86	0.185 0.178	SPO1414 SPO1415 SPO1416	0.89 0.74 0.87	0.608 SPO1416 0.119 SPO1417 0.081 SPO1418	0.85 0.94 0.95	0.279 SPO141 0.061 SPO141 0.994 SPO141	1.4	5 0.082 5 0.920	SPO1413 SPO1414	0.60 0.74 1.35	0.580	SPO1412 SPO1413 SPO1414	1.59 1.04 0.82	0.171 SPO141 0.795 SPO141 0.205 SPO141	2 1.42 3 1.01	0.898
SPO1417 SPO1418 SPO1419	0.81 1.27 2.04		SPO1417 SPO1418 SPO1419	0.92 1.28 1.9	0.736	SPO1417 SPO1418 SPO1419	0.9 0.94 0.9	0.167 SPO1419 0.97 SPO1420 0.036 SPO1421	0.88 1 0.87	0.014 SPO141 0.064 SPO141 0.874 SPO141	7 1.3	1 0.046	SPO1416	0.85 1.07 1.29	0.234	SPO1415 SPO1416 SPO1417	0.75 1.02 1.09	0.012 SPO141 0.758 SPO141 0.139 SPO141	5 0.72	0.099 0.047 0.642
SPO1420 SPO1421	0.77 1.04		SPO1420 SPO1421	0.87 1.03		SPO1420 SPO1421	0.86 0.95	0.237 SPO1422 0.155 SPO1423	0.74 0.83	0.961 SPO141 0.844 SPO142		0.008 6 0.565	SPO1418 SPO1419	1.09 0.25		SPO1418 SPO1419	1.02 1.03	0.963 SPO141 0.807 SPO141	7 1.10	0.171 0.977

SPONGE 158 0.19 SPONGE 150 0.00 SPONGE 0.00 0.00 SPONGE 150 0.00 SPONGE 0.00 0.00	0.967 0.159 0.080 0.3111 0.812 0.586 0.460 0.648 0.149 0.855 0.131 0.820 0.794 0.122 0.999 0.064 0.832 0.999 0.065 0.808 0.175 0.323 0.795 0.323 0.795 0.323 0.793 0.808 0.079
SPOILED 111 102	0.311 0.812 0.586 0.460 0.648 0.149 0.855 0.131 0.820 0.794 0.122 0.999 0.064 0.979 0.065 0.808 0.175 0.323 0.988 0.175 0.323 0.988 0.793 0.988 0.793 0.988
POPULATE 1.16	0.460 0.648 0.149 0.855 0.794 0.122 0.999 0.064 0.832 0.015 0.979 0.086 0.808 0.175 0.323 0.988 0.017 0.933 0.938 0.938 0.440 0.808 0.479 0.888
SPOILAGE Color C	0.855 0.131 0.820 0.794 0.122 0.999 0.064 0.832 0.015 0.979 0.085 0.808 0.175 0.323 0.988 0.4793 0.933 0.933 0.938 0.799 0.808 0.410 0.569
SPOILAGE 122 0.15 SPOILAGE 1.16 0.22 SPOILAGE 0.96 0.75 SPOILAGE 0.07 SPOILAGE	0.820 0.794 0.122 0.999 0.064 0.832 0.979 0.085 0.175 0.323 0.988 0.031 0.793 0.933 0.938 0.799 0.808
SPOILABS	0.999 0.064 0.832 0.015 0.979 0.085 0.808 0.175 0.323 0.988 0.031 0.793 0.933 0.358 0.799 0.808 0.410 0.569
SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.59 0.005 SPOINT 0.505 SP	0.015 0.979 0.085 0.808 0.175 0.323 0.988 0.031 0.793 0.933 0.358 0.799 0.808 0.410
SPO1444 0.09	0.808 0.175 0.323 0.988 0.031 0.793 0.933 0.358 0.799 0.808 0.410 0.569
SPO1446 0.98 D0445 0.98 SPO1446 0.97 0.97 D0472 SPO1448 0.30 0.397 SPO1445 1.34 0.040 SPO1444 1.15 0.340 SPO1445 1.15 0.340 SPO14	0.323 0.988 0.031 0.793 0.933 0.358 0.799 0.808 0.410 0.569
SPO1449	0.793 0.933 0.358 0.799 0.808 0.410 0.569
SPO1452 0.85 0.509 SPO1452 0.94 0.953 SPO1452 0.92 0.958 SPO1456 0.77 0.63 SPO1451 1.28 0.657 SPO1450 1.17 0.552 SPO1450 1.03 0.901 SPO1451 1.18 SPO1451 0.94 SPO1451 0.94 SPO1451 0.94 SPO1451 0.94 SPO1451 0.95 0.655 SPO1456 0.95 0.955 SPO1456 0.95 0.955 SPO1456 0.95 0.955 SPO1456 0.95 SPO145	0.799 0.808 0.410 0.569
SPO1454 0.34 0.73 SPO1454 0.91 0.85 SPO1454 0.95 0.566 SPO1456 0.96 0.865 SPO1454 0.70 0.22 SPO1435 1.02 0.25 SPO1452 0.87 0.400 SPO1455 1.13 0.76 SPO1456 0.96 0.96 0.96 SPO1456 0	0.569
SP01467	
SPO1460	0.527 0.710
SPO1463 0.97 0.887 SPO1463 1.07 0.126 SPO1463 0.06 0.056 SPO1465 0.98 0.564 SPO1462 0.06 0.280 SPO1464 1.0 0.666 SPO1461 0.95 0.722 SPO1464 0.75 0.77	0.431 0.258 0.930
SP01466	0.745 0.750 0.709
SP01468 0.33 0.972 SP01468 0.84 0.309 SP01468 0.96 0.041 SP01470 0.76 0.16 SP01467 0.51 0.055 SP01466 0.54 0.007 SP01466 0.83 0.447 SP01466 0.55 SP01470 0.76 0.16 SP01470 0.76 0.16 SP01476 0.7	0.203 0.391 0.230
SP01471 0.82 0.055 SP01471 0.83 0.358 SP01471 1 0.625 SP01473 0.78 0.044 SP01472 1.54 0.063 SP01489 1.26 0.190 SP01489 1.06 0.394 SP01489 1.25 0.914 SP01472 0.70 0.045 SP01473 0.79 0.046 SP01473 0.78 0.646 SP01471 1.58 0.063 SP01471 1.58 0.063 SP01473 0.79	0.636 0.512
SPO1474 0.84 0.58 SPO1474 0.89 0.146 SPO1474 0.97 0.513 SPO1476 0.97 0.674 SPO1474 1.45 0.072 SPO1472 1.73 0.016 SPO1472 1.03 0.823 SPO1471 1.15 SPO1476 1.10 0.885 SPO1475 1.12 0.305 SPO1474 0.97 0.872 SPO1474 1.22 0.305 SPO1474 1.26 0.305 SPO1474 0.305 SPO1	0.062 0.208 0.940
SP01476 1 0.912 SP01476 1.03 0.883 SP01478 0.79 0.309 SP01478 0.30 0.568 SP01474 1.22 0.217 SP01474 1.30 0.136 SP01474 1.00 0.742 SP01473 1.15 SP01479 0.82 0.825 SP01479 0.82 0.825 SP01476 1.22 0.217 SP01474 1.30 0.136 SP01474 1.00 0.742 SP01473 1.15 SP01479 0.82 0.825 SP01479 0.82 0.825 SP01476 1.22 0.213 SP01475 1.32 0.131 SP01475 0.93 0.868 SP01479 0.82 0.825 SP01476 1.25 0.825 SP01477 0.825 SP0147	0.942 0.757 0.436
SPO1479 1.18 0.345 SPO1479 0.99 0.517 SPO1479 0.89 0.048 SPO1481 1.01 0.526 SPO1478 0.41 0.201 SPO1477 0.99 0.938 SPO1476 1.16 SPO1480 1.11 0.75 SPO1480 1.18 0.526 SPO1481 0.94 0.952 SPO1479 0.87 0.699 0.970478 0.43 0.185 SPO1478 0.43 0.185 SPO1478 0.47 SPO1481 0.07 SPO1481 0.9 0.551 SPO1482 0.91 0.955 SPO1482 0.81 0.955 SPO1480 0.81 0.907 SPO1479 0.33 0.831 SPO1478 0.43 0.85 SPO1478 0.48 0.07 SPO1478 0.43 0.85 SPO1478 0.43 0.85 </td <td>0.850 0.554 0.779</td>	0.850 0.554 0.779
SPO1482 0.91 0.965 SPO1482 0.93 0.991 SPO1482 1 0.988 SPO1484 1 0.696 SPO1481 1.02 0.831 SPO1480 0.78 0.354 SPO1480 0.78 0.526 SPO1479 1.0	0.984 0.909
SPO1483 1.37 0.459 SPO1483 1.14 0.376 SPO1483 0.88 0.55 SPO1485 0.85 0.7 SPO1482 0.89 0.739 SPO1481 1.20 0.442 SPO1481 0.80 0.469 SPO1480 0.6	0.130 0.945 0.361
SPO1484 1.29 0.301 SPO1484 0.96 0.908 SPO1484 0.98 0.476 SPO1486 0.91 0.706 SPO1483 1.09 0.709 SPO1482 0.87 0.770 SPO1482 0.99 0.945 SPO1481 0.10 SPO1485 0.83 0.721 SPO1485 0.83 0.721 SPO1485 0.85 0.853 0.722 SPO1485 0.99 0.945 SPO1484 0.99	0.227 0.967 0.744
SP01487 1.14 0.399 SP01487 1.02 0.73 SP01487 0.93 0.618 SP01489 0.88 0.95 SP01485 1.16 0.528 SP01485 1.08 0.881 SP01485 1.64 0.294 SP01484 1.15 SP01488 0.78 0.791 SP01488 0.84 0.822 SP01488 0.9 0.973 SP01490 0.93 0.313 SP01487 0.83 0.133 SP01486 1.06 0.941 SP01486 1.15 0.847 SP01485 1.2	0.769 0.656
SPO1490 1.28 0.119 SPO1490 0.97 0.813 SPO1490 0.83 0.68 SPO1492 0.91 0.817 SPO1488 1.03 SPO1488 0.94 0.947 SPO1488 1.01 0.99 SPO1491 0.99 0.629 SPO1491 0.89 0.288 SPO1491 0.49 0.926 SPO1493 0.94 0.729 SPO1490 1.32 0.530 SPO1489 0.92 0.416 SPO1489 0.50 0.122 SPO1488 0.94	0.298 0.664 0.940
\$\begin{array}{cccccccccccccccccccccccccccccccccccc	0.653 0.887 0.446
\$PO1495	0.926 0.897 0.548
SP01498 1.8 0.005 SP01498 1.47 0.054 SP01499 0.82 0.47 SP01499 0.83 0.067 SP01499 0.87 0.255 SP01497 0.42 0.354 SP01496 0.85 0.720 SP01496 1.09 0.81 SP01499 0.83 SP01499 0.82 0.474 SP01499 0.83 0.361 SP01499 0.68 0.386 SP01501 0.57 0.85 SP01498 1.12 0.122 SP01497 0.43 0.481 SP01497 0.77 0.707 SP01496 1.1	0.678 0.898
SPO1500 0.33 0.019 SPO1500 0.44 0.227 SPO1500 0.76 0.832 SPO1502 0.81 0.651 SPO1499 0.91 0.499 SPO1498 1.23 0.199 SPO1498 1.07 0.702 SPO1497 0.8	0.861 0.871 0.952
SPO1503 0.33 0.034 SPO1503 0.32 0.025 SPO1503 0.82 SPO1503 0.82 SPO1505 0.95 0.535 SPO1502 5.13 0.003 SPO1501 0.83 0.861 SPO1501 0.81 0.732 SPO1500 1.1	0.837 0.783 0.640
SPO1506	0.867 0.010 0.977
SP01509 0.79 0.757 SP01509 0.76 0.807 SP01509 0.62 0.51 SP01511 0.97 0.573 SP01508 1.98 0.108 SP01507 2.83 0.023 SP01507 0.93 0.775 SP01506 1.1 SP01510 0.64 0.008 SP01510 0.63 0.047 SP01512 0.98 0.681 SP01509 0.81 0.803 SP01508 5.20 0.078 SP01508 0.93 0.934 SP01507 0.1 SP01511 0.82 0.12 SP01510 0.65 0.677 SP01511 0.88 0.118 SP01510 0.81 0.803 SP01508 5.20 0.078 SP01508 0.93 0.934 SP01507 0.1 SP01512 0.82 0.12 SP01510 0.65 0.675 SP01501 0.88 0.118 SP01510 1.85 0.108 SP01508 0.33 0.905 SP01509 0.93 0.984 SP01508 0.108 0.108 SP01509 <td>0.563 0.492 0.856</td>	0.563 0.492 0.856
SP01512 0.5 0.03 SP01512 0.48 0.015 SP01512 0.91 0.91 0.93 SP01514 0.67 0.548 SP01511 1.71 0.269 SP01510 2.12 0.018 SP01510 1.26 0.043 SP01509 0.71 SP01513 0.46 0.021 SP01513 0.5 0.051 SP01513 0.91 0.096 SP01515 0.71 0.798 SP01512 1.83 0.030 SP01511 1.70 0.324 SP01511 1.26 0.490 SP01510 1.4	0.662 0.712
SPO1514 0.30 0.002 SPO1514 0.48 0.01 SPO1516 0.92 0.746 SPO1515 0.776 0.959 SPO1515 1.88 0.026 SPO1512 2.12 0.010 SPO1512 1.06 0.883 SPO1515 1.2	0.331 0.800 0.353
SPO1517 0.14 0.003 SPO1517 0.17 0.003 SPO1517 0.19 0.003 SPO1517 0.19 0.003 SPO1517 0.19 0.003 SPO1518 0.10 0.003 SPO1518 0.003	0.974 0.581 0.530
SP01520 0.48 0.024 SP01520 0.5 0.445 SP01520 0.89 0.347 SP01522 0.99 0.757 SP01519 1.39 0.045 SP01518 1.99 0.080 SP01518 0.91 0.586 SP01517 0.5 SP01521 0.09 0.018 SP01521 0.09 0.018 SP01521 0.09 0.018 SP01521 0.09 0.018 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.014 SP01521 0.005 SP01520 1.80 0.005	0.998 0.799 0.042
SPO1522 1.15 0.601 0.185 SPO1522 0.62 0.555 SPO1522 0.99 0.565 SPO1525 0.29 0.79 0.160 SPO1522 0.80 0.174 SPO1521 2.75 0.000 SPO1521 1.30 0.522 SPO15139 0.18 SPO1523 0.61 0.185 SPO1525 0.01 0.01 0.185 SPO1525 0.01 0.01 0.185 SPO1525 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.0	0.694 0.505 0.710
SPO1526 1.17 0.518 SPO1526 1.07 0.942 SPO1528 0.74 0.815 SPO1528 0.96 0.165 SPO1525 0.96 0.985 SPO1524 2.12 0.019 SPO1524 0.93 0.421 SPO1523 1.0 SPO1527 0.85 0.935 SPO1527 0.84 0.91 SPO1527 0.93 0.81 SPO1529 0.84 0.997 SPO1526 0.62 0.439 SPO1525 1.07 0.958 SPO1525 0.94 0.994 SPO1524 0.62	0.975 0.446
SPO1528 0.87 0.71 SPO1528 1.03 0.564 SPO1528 0.87 0.669 SPO1520 0.44 0.728 SPO1527 0.55 0.487 SPO1526 0.71 0.805 SPO1526 1.02 0.964 SPO1525 1.15 SPO1529 1.14 0.676 SPO1529 1.13 0.741 SPO1529 1.13 0.742 SPO1529 0.76 0.772 SPO1529 0.76 0.772 SPO1529 0.774 SPO1520 0.774	0.989 0.899 0.824
SP01531 1.02 0.847 SP01531 1.04 0.612 SP01531 0.93 0.66 SP01533 0.76 0.048 SP01530 0.81 0.671 SP01529 0.88 0.286 SP01529 1.10 0.788 SP01528 1.1	0.641 0.669 0.912
SPO1534 1.48 0.022 SPO1534 1.22 0.069 SPO1534 0.98 0.424 SPO1536 0.68 0.657 SPO1533 2.48 0.030 SPO1532 0.88 0.565 SPO1532 0.98 0.899 SPO1531 1.2 SPO1535 1.17 0.749 SPO1535 0.97 0.971 SPO1535 0.76 0.559 SPO1534 0.66 0.065 SPO1533 2.28 0.018 SPO1533 1.25 0.215 SPO1535 0.98 0.99 0.985 SPO1534 0.66 0.99 0.985 SPO1535 0.99 0.985 SPO1535 0.99 0.985 SPO1535 0.99 0.985 SPO1535 0.99 0.985 SPO1535 0.99 0.985 SPO1535 0.99 0.99 SPO1535 0.99 0.985 SPO1535 0.99 0.985 SPO1535 0.99 0.985 SPO1535 0.99 0.99 SPO1535 0.99 0.985 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 0.99 SPO1535 0.99 SPO1535 0.99 0.99 SPO1535 0.99	0.533 0.787 0.277
SP01537 1.1 0.574 SP01537 1.14 0.20s SP01537 0.617 SP01539 0.78 0.647 SP01535 0.90 0.947 SP01535 0.78 0.576 SP01535 0.95 0.883 SP01534 1.1 SP01538 1.15 0.581 SP01538 1.05 0.783 SP01538 0.87 0.899 SP01540 0.69 0.718 SP01537 0.90 0.436 SP01536 0.85 0.375 SP01536 1.06 0.932 SP01535 0.93	0.955 0.954
SPO1559 1.25 0.018 SPO1539 1.19 0.199 SPO1539 0.85 0.85 SPO1541 0.88 0.987 SPO1536 0.76 0.482 SPO1537 1.13 0.548 SPO1537 1.77 0.829 SPO1536 1.15 SPO1540 1.18 0.13 SPO1540 1.18 0.13 SPO1540 0.86 0.788 SPO1542 0.99 0.947 SPO1549 0.81 0.268 SPO1538 0.81 0.557 SPO1538 0.85 SPO1538 0.85 SPO1538 0.85 SPO1538 0.85 SPO1538 0.85 SPO1538 0.85 SPO1542 0.99 SPO1541 0.91 SPO1540 0.78 SPO1540 0.78 SPO1540 0.78 SPO1549 0.78 SPO15	0.897 0.911 0.666
\$P01542 0.59 0.431 \$P01542 0.67 0.578 \$P01542 0.97 0.912 \$P01544 0.93 0.69 \$P01541 1.94 0.085 \$P01540 0.78 0.287 \$P01540 0.93 0.597 \$P01589 1.4 \$P01543 0.81 0.69 \$P01543 0.81 0.89 \$P01543 0.81 0.223 \$P01545 0.9 0.819 \$P01542 1.27 0.654 \$P01541 1.83 0.131 \$P01541 1.13 0.195 \$P01541 1.13 0.195 \$P01540 1.1 \$P01540 0.85 0.87 \$P01540 0.85	0.833 0.998 0.272
SP01545 1.09 0.861 SP01545 0.96 0.998 SP01545 0.93 0.766 SP01547 0.88 0.915 SP01544 1.40 0.433 SP01543 1.72 0.046 SP01543 0.77 0.308 SP01542 0.84 SP01546 1.04 0.647 SP01546 0.95 0.979 SP01546 0.98 0.765 SP01548 0.83 0.027 SP01545 0.91 0.953 SP01544 1.22 0.507 SP01544 0.79 0.574 SP01543 0.1	0.832 0.141 0.679
SP01548 0.52 0.13 SP01548 0.52 0.012 SP01549 0.89 0.754 SP01547 1.47 0.083 SP01546 1.68 0.048 SP01546 0.78 0.255 SP01549 0.81 0.11 SP01549 0.86 0.587 SP01549 0.97 0.226 SP01551 1 0.923 SP01548 3.80 0.003 SP01547 1.44 0.042 SP01547 0.87 0.495 SP01546 0.88	0.679
SPO1550 1.1 0.447 SPO1550 1.04 0.843 SPO1550 0.74 0.829 SPO1552 0.86 0.947 SPO1549 1.55 0.199 SPO1548 3.30 0.002 SPO1548 1.11 0.137 SPO1547 0.85 SPO1551 0.77 0.576 SPO1551 0.77 0.578 SPO1551 0.78 SPO1552 0.79 SPO1552 0.79 SPO1553 1.57 0.379 SPO1554 1.10 0.081 SPO1549 1.11 0.378 SPO1554 1.11 0.378 SPO1549 1.11 0.378 SPO1552 0.388 SPO1549 1.11 0.378 SPO1552 0.378 SPO1550 1.12	0.461
SP01553 0.85 0.802 SP01553 0.84 0.804 SP01553 0.97 0.759 SP01555 0.91 0.054 SP01552 1.06 0.851 SP01551 1.24 0.379 SP01551 1.0 SP01554 1 0.61 SP01554 0.88 0.65 SP01555 0.99 0.90	0.461 0.467 0.375 0.642
SP01556 0.22 0.003 SP01556 0.32 0.002 SP01556 0.91 0.11 SP01558 0.9 0.65 SP01556 0.52 0.004 SP01554 1.53 0.098 SP01555 0.39 0.92 SP01557 1.41 0.186 SP01557 1.44 0.022 SP01557 0.96 0.025 SP01559 0.96 0.172 SP01556 0.59 0.004 SP01555 0.23 0.003 SP01556 0.39 0.932 SP01554 1.15 0.186 SP01553 0.10 SP01556 0.59 0.004 SP01557 0.39 0.932 SP01554 1.15 0.186 SP01553 0.10 SP01556 0.59 0.99 0.172 SP01556 0.59 0.004 SP01556 0.59 0.004 SP01556 0.39 0.937 SP01556 0.59 0.997 SP01556 0.597 SP01556 0.59 0.997 SP01556 0.597	0.461 0.467 0.375
SPO1550 1.58 0.166 SPO1560 1.5 0.016 SPO1560 0.93 0.192 SPO1562 0.99 0.423 SPO1559 0.53 0.041 SPO1558 0.7 0.410 SPO1558 0.7 0.410 SPO1559 0.93 0.678 SPO1557 0.53 0.041 SPO1559 0.93 0.678 SPO1559 0.93 0.93 0.678 SPO1559 0.93 0.93 0.93 0.93 0.	0.461 0.467 0.375 0.642 0.953 0.605

SPO1561 SPO1562	1.07	0.148	SPO1561 SPO1562	1.04	0.722 SPO1561 0.057 SPO1562	0.82	0.619 SPO1563 0.74 SPO1564	0.97	0.176 SPO1560 0.268 SPO1561	1.25	0.025	SPO1559 SPO1560	0.48 1.16		SPO1559 SPO1560	1.09		SPO1558 SPO1559	0.97	0.944
SPO1563 SPO1564	0.83	0.19 0.081	SPO1563 SPO1564	0.99	0.767 SPO1563 0.024 SPO1564	0.93 0.78	0.905 SPO1565 0.021 SPO1566	0.69 1	0.365 SPO1562 0.813 SPO1563	0.87	0.016 0.503	SPO1561 SPO1562	0.97 0.93	0.709 0.322	SPO1561 SPO1562	1.12 0.99	0.711 0.858	SPO1560 SPO1561	1.04 1.09	0.638 0.715
SPO1565 SPO1566 SPO1567	0.83 0.42		SPO1565 SPO1566 SPO1567	0.85 0.51	0.006 SPO1565 0.666 SPO1566 0.028 SPO1567	0.91 0.73 0.85	0.015 SPO1567 0.986 SPO1568 0.604 SPO1569	0.78 0.96 0.78	0.532 SPO1564 0.209 SPO1565 0.123 SPO1566	4.37 1.12	0.093 0.003 0.675	SPO1563 SPO1564 SPO1565	0.94 2.59 3.88	0.339 0.146 0.006	SPO1563 SPO1564 SPO1565	1.15 1.35 1.56		SPO1562 SPO1563 SPO1564	0.93 1.22 1.32	0.599 0.055 0.363
SPO1568 SPO1569 SPO1570	0.42 0.31 0.44	0.022 0.023 0.028	SPO1568 SPO1569 SPO1570	0.44 0.32 0.53	0.004 SPO1568 0.021 SPO1569 0.012 SPO1570	0.81 0.75 0.92	0.668 SPO1570 0.231 SPO1571 0.172 SPO1572	0.98 0.66 0.98	0.048 SPO1567 0.793 SPO1568 0.1 SPO1569	1.19 1.70	0.292 0.064 0.035	SPO1566 SPO1567 SPO1568	0.93 1.14 1.80	0.719 0.575 0.013	SPO1566 SPO1567 SPO1568	0.92 1.04 1.22		SPO1565 SPO1566 SPO1567	1.54 0.90 1.18	0.093 0.630 0.213
SPO1571 SPO1572	0.96 0.93	0.756 0.822	SPO1571 SPO1572	0.83 0.93	0.075 SPO1571 0.845 SPO1572	0.95 0.88	0.04 SPO1573 0.222 SPO1574	0.95 0.99	0.053 SPO1570 0.042 SPO1571	1.27	0.000	SPO1569 SPO1570	2.14 2.80	0.020	SPO1569 SPO1570	1.31 1.20	0.172 0.451	SPO1568 SPO1569	1.34 1.37	0.102 0.099
SPO1573 SPO1574 SPO1575	0.65 0.53	0.615 0.033 0.259	SPO1573 SPO1574 SPO1575	0.71 0.57	0.02 SPO1573 0.086 SPO1574 0.038 SPO1575	0.91 0.88 0.95	0.16 SPO1575 0.031 SPO1576 0.018 SPO1577	0.78 0.84 0.82	0.032 SPO1572 0.892 SPO1573 0.997 SPO1574	0.74 1.81 1.16	0.154 0.006 0.165	SPO1571 SPO1572 SPO1573	1.47 0.70 1.80	0.049 0.059 0.005	SPO1571 SPO1572 SPO1573	1.14 1.36 1.25	0.069	SPO1570 SPO1571 SPO1572	1.38 1.16 1.26	0.038 0.090 0.176
SPO1576 SPO1577 SPO1578	0.67 0.93	0.774 0.313	SPO1576 SPO1577 SPO1578	0.73 0.85 1.04	0.863 SPO1576 0.44 SPO1577 0.734 SPO1578	0.95 0.88 0.83	0.814 SPO1578 0.698 SPO1579 0.937 SPO1580	0.88 0.95 0.89	0.949 SPO1575 0.382 SPO1576 0.717 SPO1577	1.85 1.24 1.30	0.046 0.859 0.069	SPO1574 SPO1575 SPO1576	1.10 1.84 1.29	0.075 0.031 0.745	SPO1574 SPO1575 SPO1576	0.93 1.07 0.98	0.740	SPO1573 SPO1574 SPO1575	1.08 1.01 1.16	0.670 0.953 0.218
SPO1579 SPO1580	0.52 0.61	0.149	SPO1579 SPO1580	0.55 0.68	0.178 SPO1579 0.037 SPO1580	0.77 0.71	0.442 SPO1581 0.499 SPO1582	0.96 0.96	0.324 SPO1578 0.964 SPO1579	1.04 1.32	0.917 0.265	SPO1577 SPO1578	1.63 1.03	0.068 0.832	SPO1577 SPO1578	1.28 1.07	0.258	SPO1576 SPO1577	1.01 1.15	0.989 0.626
SPO1581 SPO1582 SPO1583	0.47 0.79 1.47		SPO1581 SPO1582 SPO1583	0.75 0.84 1.41	0.044 SPO1581 0.718 SPO1582 0.274 SPO1583	0.79 0.85 0.93	0.688 SPO1583 0.861 SPO1584 0.675 SPO1585	0.99 0.88 0.98	0.819 SPO1580 0.904 SPO1581 0.986 SPO1582	1.12 1.26 0.88	0.130 0.248 0.805	SPO1579 SPO1580 SPO1581	1.29 1.05 1.44		SPO1579 SPO1580 SPO1581	0.94 0.99 1.03	0.910	SPO1578 SPO1579 SPO1580	0.89 0.98 0.98	0.584 0.937 0.775
SPO1584 SPO1585 SPO1586	0.79 1.14 0.9	0.889 0.908 0.62	SPO1584 SPO1585 SPO1586	0.84 1.06 0.89	0.936 SPO1584 0.924 SPO1585 0.83 SPO1586	0.79 0.89 0.92	0.925 SPO1586 0.986 SPO1587 0.676 SPO1588	0.99 0.97 0.96	0.554 SPO1583 0.428 SPO1584 0.177 SPO1585	0.98 1.26 0.86	0.929 0.844 0.935	SPO1582 SPO1583 SPO1584	0.86 0.92 1.66	0.608 0.910 0.716	SPO1582 SPO1583 SPO1584	0.97 1.03 0.91	0.951	SPO1581 SPO1582 SPO1583	1.00 0.90 0.95	0.828 0.741 0.929
SPO1587 SPO1588	0.93 1.14	0.984	SPO1587 SPO1588	0.9 1.21	0.905 SPO1587 0.062 SPO1588	0.83 0.75	0.623 SPO1589 0.245 SPO1590	0.99 0.67	0.489 SPO1586 0.836 SPO1587	1.02 0.37	0.835 0.087	SPO1585 SPO1586	0.85 1.13	0.939 0.631	SPO1585 SPO1586	0.88 0.96	0.921 0.274	SPO1584 SPO1585	0.92 0.87	0.969 0.943
SPO1589 SPO1590 SPO1591	0.75 1.11 0.92	0.183 0.487 0.323	SPO1589 SPO1590 SPO1591	0.78 1.06 0.94	0.162 SPO1589 0.316 SPO1590 0.917 SPO1591	0.69 0.92 0.88	0.198 SPO1591 0.948 SPO1592 0.067 SPO1593	0.79 1 0.89	0.455 SPO1588 0.545 SPO1589 0.18 SPO1590	1.41 1.10 1.23	0.421 0.360 0.474	SPO1588 SPO1589	1.84 1.12	0.113 0.257 0.190	SPO1587 SPO1588 SPO1589	1.06 1.18 0.95	0.710	SPO1586 SPO1587 SPO1588	1.00 0.98 1.13	0.902 0.965 0.325
SPO1592 SPO1593 SPO1594	0.88 0.53 1.19	0.919 0.159 0.711	SPO1592 SPO1593 SPO1594	0.89 0.57 1.14	0.79 SPO1592 0.245 SPO1593 0.812 SPO1594	0.94 0.96 0.9	0.781 SPO1594 0.057 SPO1595 0.939 SPO1596	0.92 0.94 0.97	0.957 SPO1591 0.352 SPO1592 0.727 SPO1593	1.36 1.00	0.216 0.903 0.028	SPO1590 SPO1591 SPO1592	1.18 1.23 0.94	0.042	SPO1590 SPO1591 SPO1592	0.89 1.01 0.89	0.943	SPO1589 SPO1590 SPO1591	0.93 0.89 1.05	0.745 0.534 0.734
SPO1595 SPO1596	0.69 0.75	0.438 0.528	SPO1595 SPO1596	0.64 0.71	0.475 SPO1595 0.584 SPO1596	0.93 0.83	0.14 SPO1597 0.662 SPO1598	0.77 0.96	0.406 SPO1594 0.518 SPO1595	1.14	0.907 0.322	SPO1593 SPO1594	5.49 1.21	0.085	SPO1593 SPO1594 SPO1595	1.18 0.83	0.807 0.809	SPO1592 SPO1593	0.92 1.14	0.690 0.874
SPO1597 SPO1598 SPO1599	0.94 1.03 0.69	0.795	SPO1597 SPO1598 SPO1599	0.87 1 0.99	0.187 SPO1597 0.804 SPO1598 0.969 SPO1599	0.81 0.86 0.71	0.731 SPO1599 0.916 SPO1600 0.778 SPO1601	0.78 0.89 0.93	0.991 SPO1596 0.875 SPO1597 0.256 SPO1598	1.94 0.78 0.93	0.026 0.184 0.830	SPO1595 SPO1596 SPO1597	1.39 1.57 0.84	0.319	SPO1595 SPO1596 SPO1597	1.32 1.11 0.89	0.402	SPO1594 SPO1595 SPO1596	0.95 1.17 0.99	0.935 0.837 0.984
SPO1600 SPO1601 SPO1602	1.14 1.12 0.9	0.431 0.688 0.203	SPO1600 SPO1601 SPO1602	1.05 1.04 0.96	0.39 SPO1600 0.499 SPO1601 0.907 SPO1602	0.67 0.59 0.96	0.855 SPO1602 0.604 SPO1603 0.797 SPO1604	0.95 0.55 0.75	0.995 SPO1599 0.481 SPO1600 0.81 SPO1601	0.73 0.86 0.83	0.739 0.306 0.184	SPO1598 SPO1599 SPO1600	0.99 0.57 0.96		SPO1598 SPO1599 SPO1600	1.01 0.89 1.11	0.417	SPO1597 SPO1598 SPO1599	0.94 0.96 0.91	0.360 0.833 0.765
SPO1603 SPO1604	0.73 1.03	0.455 0.924	SPO1603 SPO1604	0.79 0.99	0.083 SPO1603 0.959 SPO1604	0.88 0.86 0.88	0.828 SPO1605 0.99 SPO1606	0.92 0.99	0.035 SPO1602 0.387 SPO1603	0.96 0.99	0.798 0.778	SPO1601 SPO1602	0.67 0.97	0.063 0.517	SPO1601 SPO1602 SPO1603	1.03 0.95	0.963 0.744	SPO1600 SPO1601	1.07 1.02 0.99	0.904 0.998
SPO1605 SPO1606 SPO1607	0.68 0.68 0.5	0.051 0.161 0.09	SPO1605 SPO1606 SPO1607	0.74 0.74 0.52	0.038 SPO1605 0.275 SPO1606 0.039 SPO1607	0.9 0.78	0.05 SPO1607 0.731 SPO1608 0.185 SPO1609	0.69 0.8 0.84	0.245 SPO1604 0.927 SPO1605 0.901 SPO1606	1.46 1.09	0.286 0.033 0.189	SPO1603 SPO1604 SPO1605	0.99 0.44 1.49	0.347	SPO1604 SPO1605	0.90 0.85 1.30	0.859	SPO1602 SPO1603 SPO1604	1.10 0.91	0.911 0.525 0.907
SPO1608 SPO1609 SPO1610	1.09 0.62 1.16	0.824 0.615 0.069	SPO1608 SPO1609 SPO1610	0.94 0.64 1.11	0.998 SPO1608 0.706 SPO1609 0.128 SPO1610	0.95 0.91 0.96	0.955 SPO1610 0.993 SPO1611 0.586 SPO1612	0.7 1 0.97	0.105 SPO1607 0.961 SPO1608 0.653 SPO1609	1.91 1.02 1.48	0.092 0.968 0.426	SPO1606 SPO1607 SPO1608	0.98 1.90 0.93	0.702 0.077 0.746	SPO1606 SPO1607 SPO1608	0.99 1.19 0.98		SPO1605 SPO1606 SPO1607	1.23 1.00 1.14	0.092 0.572 0.327
SPO1611 SPO1612	0.98 0.95 1.26	0.992 0.825 0.135	SPO1611 SPO1612	0.98 1.06 1.1	0.992 SPO1611 0.679 SPO1612 0.643 SPO1613	0.81 0.66 0.89	0.938 SPO1613 0.955 SPO1614 0.747 SPO1615	0.86 0.92 0.85	0.89 SPO1610 0.978 SPO1611 0.605 SPO1612	1.19 0.91 1.09	0.296 0.989 0.994	SPO1609 SPO1610 SPO1611	1.77 1.50	0.461	SPO1609 SPO1610 SPO1611	0.90 1.10 0.85	0.793	SPO1608 SPO1609 SPO1610	1.01 0.95 1.07	0.994 0.954 0.653
SPO1613 SPO1614 SPO1615	1.02 1.18	0.979		0.93 1.12	0.977 SPO1614 0.391 SPO1615	0.91 0.85	0.983 SPO1616 0.816 SPO1617	0.91 0.88	0.37 SPO1613 0.673 SPO1614	0.97 0.89	0.546 0.972	SPO1612 SPO1613	1.04	0.735	SPO1612 SPO1613	1.07 0.97	0.968 0.882	SPO1611 SPO1612	0.86 1.14	0.945 0.858
SPO1616 SPO1617 SPO1618	1.28 0.88 0.9	0.136 0.878 0.854		1.36 0.98 0.85	0.179 SPO1616 0.939 SPO1617 0.807 SPO1618	0.94 0.83 0.83	0.213 SPO1618 0.673 SPO1619 0.043 SPO1620	0.83 0.79 0.81	0.997 SPO1615 0.783 SPO1616 0.438 SPO1617	1.40 0.85 0.96	0.040 0.567 0.291	SPO1614 SPO1615 SPO1616	1.06 1.42 0.86	0.894 0.050 0.166	SPO1614 SPO1615 SPO1616	0.89 1.36 0.81		SPO1613 SPO1614 SPO1615	0.94 0.93 1.23	0.597 0.938 0.324
SPO1620 SPO1621 SPO1622	0.82 0.86 0.74	0.346 0.494 0.207	SPO1619 SPO1620 SPO1621	0.84 0.92	0.848 SPO1619 0.649 SPO1620 0.462 SPO1621	0.85 0.91 0.93	0 SPO1621 0.403 SPO1622 0.823 SPO1623	0.64 0.81 0.87	0.831 SPO1618 0.224 SPO1619 0.684 SPO1620	1.03 0.82 1.41	0.948 0.468 0.051	SPO1617 SPO1618 SPO1619	0.76 1.29 1.04	0.373	SPO1617 SPO1618 SPO1620	0.62 1.06 1.13		SPO1616 SPO1617 SPO1618	0.86 0.77 1.02	0.591 0.417 0.966
SPO1623 SPO1624	1.17	0.099 0.187	SPO1622 SPO1623	0.79 1.21	0.111 SPO1622 0.358 SPO1623	0.96 0.9	0.122 SPO1624 0.432 SPO1625	0.94 0.76	0.53 SPO1621 0.893 SPO1622	0.90 1.28	0.682 0.215	SPO1620 SPO1621	1.55 0.93	0.098	SPO1621 SPO1622	1.03 1.11	0.799 0.589	SPO1619 SPO1620	0.83 1.08	0.701
SPO1625 SPO1626 SPO1627	1.14 1.24 0.91	0.67 0.054 0.81	SPO1624 SPO1625 SPO1626	1.29 1.1 1.23	0.027 SPO1624 0.79 SPO1625 0.036 SPO1626	0.99 0.92 0.93	0.785 SPO1626 0.861 SPO1627 0.108 SPO1628	0.91 0.94 0.98	0.103 SPO1623 0.995 SPO1624 0.545 SPO1625	0.71 0.88 0.53	0.219 0.541 0.298	SPO1622 SPO1623 SPO1624	1.35 0.62 1.02	0.027	SPO1623 SPO1624 SPO1625	0.99 1.10 0.85	0.814	SPO1621 SPO1622 SPO1623	0.97 1.09 0.85	0.955 0.390 0.186
SPO1628 SPO1629 SPO1630	0.57 1.07 1.55	0.076 0.419 0.036	SPO1627 SPO1628 SPO1629	0.94 0.58 1.08	0.94 SPO1627 0.041 SPO1628 0.572 SPO1629	0.93 0.9 0.81	0.432 SPO1629 0.659 SPO1630 0.649 SPO1631	0.78 0.75 0.75	0.838 SPO1626 0.535 SPO1627 0.51 SPO1628	0.78 0.91 0.70	0.089 0.484 0.161	SPO1625 SPO1626 SPO1627	0.52 0.80 1.01		SPO1626 SPO1627 SPO1628	1.22 0.99 0.94	0.974	SPO1624 SPO1625 SPO1626	1.02 0.85 1.23	0.915 0.806 0.201
SPO1631 SPO1632 SPO1633	1.09 0.95	0.563 0.898	SPO1630	1.4 1.16	0.063 SPO1630 0.077 SPO1631	0.87 0.43	0.647 SPO1632 0.213 SPO1633	0.97 0.99	0.841 SPO1629 0.998 SPO1630 0.866 SPO1631	0.88 0.76 0.87	0.451	SPO1628 SPO1629 SPO1630	0.71 0.76	0.120 0.298	SPO1629 SPO1630 SPO1631	1.00 1.04	0.958 0.852	SPO1627 SPO1628 SPO1629	0.86 0.98 1.01	0.800 0.581
SPO1634 SPO1635	0.99 1.27 1.2	0.091 0.157	SPO1633 SPO1634	1.01 1.76 1.37	0.888 SPO1632 0.069 SPO1633 0.021 SPO1634	0.83 0.97 0.98	0.845 SPO1634 0.307 SPO1635 0.875 SPO1636	0.88 0.95 0.94	0.777 SPO1632 0.932 SPO1633	1.67 0.53	0.621 0.026 0.059	SPO1631 SPO1632	0.73 0.85 1.60	0.049 0.561 0.101	SPO1632 SPO1633	0.83 1.79	0.169 0.319	SPO1630 SPO1631	1.05 0.93	0.987 0.774 0.734
SPO1636 SPO1637 SPO1638	0.67 1.31	0.98 0.031 0.152	SPO1635 SPO1636 SPO1637	1.09 1.01 0.83	0.382 SPO1635 0.922 SPO1636 0.295 SPO1637	0.91 0.83 0.94	0.592 SPO1637 0.848 SPO1638 0.397 SPO1639	0.93 0.83 0.95	0.231 SPO1634 0.757 SPO1635 0.695 SPO1636	1.19 0.76 1.03	0.300 0.661 0.766	SPO1633 SPO1634 SPO1635	0.78 1.13 0.68	0.092 0.049 0.473	SPO1634 SPO1635 SPO1636	1.17 0.92 0.94		SPO1632 SPO1633 SPO1634	0.88 1.31 1.03	0.742 0.504 0.481
SPO1639 SPO1640 SPO1641	1.55 1.04 0.76		SPO1638 SPO1639	1.33 1.32 1.05	0.1 SPO1638 0.127 SPO1639 0.14 SPO1640	0.76 0.85	0.431 SPO1640 0.819 SPO1641 0.858 SPO1642	0.75 0.68 0.54	0.908 SPO1637 0.54 SPO1638 0.806 SPO1639	1.26 1.05 1.30	0.065 0.497 0.058	SPO1636 SPO1637 SPO1638	0.96 1.18 1.10	0.901 0.066	SPO1637 SPO1638 SPO1639	1.06 0.93 1.10	0.439 0.784	SPO1635	0.88 0.93	0.780 0.921 0.376
SPO1642 SPO1643	0.98 0.68	0.967 0.35	SPO1641 SPO1642	0.83 0.86	0.125 SPO1641 0.653 SPO1642	0.94 0.87	0.084 SPO1643 0.101 SPO1644	0.93 0.83	0.237 SPO1640 0.903 SPO1641	1.30 1.22	0.337	SPO1639 SPO1640	1.25 1.44	0.106	SPO1640 SPO1641	1.24 1.04	0.695 0.853	SPO1638 SPO1639	0.83 1.02	0.689 0.923
SPO1644 SPO1645 SPO1646	0.87 1.01 0.93	0.933 0.6 0.966	SPO1644 SPO1645	0.75 0.93 1.12	0.257 SPO1643 0.99 SPO1644 0.387 SPO1645	0.92 0.93 0.92	0.454 SPO1645 0.893 SPO1646 0.546 SPO1647	0.83 0.96 0.81	0.783 SPO1642 0.984 SPO1643 0.911 SPO1644	1.24 1.17 1.02	0.440 0.146 0.972	SPO1641 SPO1642 SPO1643	1.16 1.10 1.16	0.157 0.527 0.111	SPO1642 SPO1643 SPO1644	1.25 1.21 0.89	0.287	SPO1640 SPO1641 SPO1642	1.14 1.18 1.02	0.567 0.450 0.958
SPO1647 SPO1648 SPO1649	0.93 1.07 1.26		SPO1646 SPO1647 SPO1648	0.93 0.96 1.04	1 SPO1646 0.905 SPO1647 0.746 SPO1648	0.93 0.96 0.9	0.93 SPO1648 0.949 SPO1649 0.72 SPO1650	0.83 0.79 0.61	0.634 SPO1645 0.422 SPO1646 0.637 SPO1647	0.94 0.88 1.12	0.701 0.770 0.735	SPO1644 SPO1645 SPO1646	0.89 1.08 0.93	0.867	SPO1645 SPO1646 SPO1647	1.10 0.87 1.09	0.727	SPO1643 SPO1644 SPO1645	1.33 0.90 1.03	0.295 0.913 0.987
SPO1650 SPO1651	0.92 1.03	0.766	SPO1649 SPO1650	1.32 1.13	0.139 SPO1649 0.274 SPO1650	0.91 0.86	0.827 SPO1651 0.96 SPO1652 0.823 SPO1655	0.93 0.92	0.359 SPO1648 0.326 SPO1649	1.04 0.91	0.893 0.057	SPO1647 SPO1648	1.14 1.07	0.499 0.916	SPO1648 SPO1649	1.01 1.27	0.856 0.150	SPO1646 SPO1647 SPO1648	0.86 1.04 0.97	0.787 0.937
SPO1652 SPO1655 SPO1656	0.83 1.11 0.85	0.781	SPO1651 SPO1652 SPO1655	1.02 0.78 1.14	0.513 SPO1651 0.271 SPO1652 0.799 SPO1655	0.72 0.9 0.94	0.823 SPO1655 0.434 SPO1656 0.989 SPO1657	0.89 0.92 0.83	0.599 SPO1650 0.908 SPO1651 0.394 SPO1652	0.58 0.73 1.32	0.009 0.281 0.467	SPO1650 SPO1651	1.21 0.59 0.79	0.130	SPO1652	0.69 0.79 1.12	0.397	SPO1649 SPO1650	1.05 0.79	0.820 0.921 0.191
SPO1657 SPO1658 SPO1659	1.11 0.75 0.45		SPO1656 SPO1657 SPO1658	0.81 0.96 0.74	0.307 SPO1656 0.865 SPO1657 0.344 SPO1658	0.88 0.85 0.83	0.838 SPO1658 0.061 SPO1659 0.728 SPO1660	0.8 0.86 0.94	0.717 SPO1655 0.93 SPO1656 0.937 SPO1657	0.92 1.42 1.06	0.825 0.033 0.157	SPO1652 SPO1655 SPO1656	1.42 0.90 1.40		SPO1655 SPO1656 SPO1657	0.84 0.89 0.85	0.484	SPO1651 SPO1652 SPO1655	0.84 1.44 0.94	0.483 0.065 0.866
SPO1660 SPO1661	1.21 1.29 0.78	0.626	SPO1659 SPO1660 SPO1661	0.65 1.22 1.32	0.036 SPO1659 0.585 SPO1660 0.728 SPO1661	0.78 0.85 0.81	0.691 SPO1661 0.892 SPO1662 0.91 SPO1663	0.9 0.84 0.86	0.873 SPO1658 0.431 SPO1659 0.594 SPO1660	2.15 1.15 0.97	0.108 0.021 0.931	SPO1657 SPO1658 SPO1659	1.06 2.04 0.99	0.126	SPO1658 SPO1659 SPO1660	0.96 1.21 1.04	0.951 0.024	SPO1656 SPO1657 SPO1658	0.94 0.88 0.96	0.642 0.394 0.932
SPO1662 SPO1663 SPO1664	1.09 0.99	0.698 0.785	SPO1662 SPO1663	0.77 1.04	0.619 SPO1662 0.815 SPO1663	0.88 0.91	0.534 SPO1664 0.687 SPO1665	0.97 0.89	0.914 SPO1661 0.563 SPO1662	0.86 0.67	0.898 0.215	SPO1660 SPO1661	1.11 0.84	0.947 0.875	SPO1661 SPO1662	0.93 0.97	0.912 0.988	SPO1659 SPO1660	1.29 0.96	0.018 0.946
SPO1665 SPO1666 SPO1667	1.66 1.5 0.83	0.025	SPO1664 SPO1665 SPO1666	1.1 1.49 1.28	0.285 SPO1664 0.045 SPO1665 0.194 SPO1666	0.79 0.73 0.76	0.842 SPO1666 0.483 SPO1667 0.113 SPO1668	0.95 0.98 0.82	0.364 SPO1663 0.383 SPO1664 0.987 SPO1665	1.06 0.95 0.92	0.676 0.162 0.515	SPO1663 SPO1664	0.65 1.12 0.87	0.556 0.722	SPO1663 SPO1664 SPO1665	1.07 1.01 1.00	0.642 0.500	SPO1661 SPO1662 SPO1663	0.99 0.93 1.03	0.987 0.860 0.879
SPO1668 SPO1669 SPO1670	1.6 1.78	0.567 0.031 0.013	SPO1667 SPO1668 SPO1669	0.93 1.23 1.37	0.736 SPO1667 0.823 SPO1668 0.018 SPO1669	0.97 0.83 0.63	0.348 SPO1669 0.973 SPO1670 0.872 SPO1671	0.88 0.43 0.83	0.619 SPO1666 0.179 SPO1667 0.078 SPO1668	0.81 2.08 0.78	0.090 0.007 0.916	SPO1665 SPO1666 SPO1667	0.98 0.81		SPO1666 SPO1667 SPO1668	0.85 1.01 1.10	0.307	SPO1664 SPO1665 SPO1666	0.99 0.97 0.92	0.774 0.956 0.292
SPO1671 SPO1672 SPO1673	1.28 0.89 1.72	0.048	SPO1670 SPO1671 SPO1672	1.26 1.23 0.79	0.143 SPO1670 0.052 SPO1671 0.123 SPO1672	0.98 0.96 0.93	0.027 SPO1672 0.058 SPO1673 0.263 SPO1674	0.95 0.94 0.92	0.453 SPO1669 0.192 SPO1670 0.871 SPO1671	0.69 0.77 0.84	0.428 0.079 0.284	SPO1668 SPO1669 SPO1670	0.70 0.68 0.85	0.826	SPO1669 SPO1670 SPO1671	0.86 0.95 1.02	0.761	SPO1667 SPO1668 SPO1669	1.03 1.04 0.70	0.346 0.940 0.195
SPO1674 SPO1675	1.74 1.3	0.317 0.308	SPO1673 SPO1674	1.48 1.55	0.003 SPO1673 0.533 SPO1674	0.71 1	0.214 SPO1675 0.952 SPO1676	0.78 0.93	0.447 SPO1672 0.505 SPO1673	0.88 0.76	0.852 0.063	SPO1671 SPO1672	0.85 1.06	0.544 0.462	SPO1672 SPO1673	1.04 1.13	0.714	SPO1670 SPO1671	0.98 0.94	0.926 0.562
SPO1676 SPO1677 SPO1678	1.22 1.06 0.62	0.875	SPO1675 SPO1676 SPO1677	1.29 1.16 1.14	0.023 SPO1675 0.064 SPO1676 0.418 SPO1677	0.88 0.83	0.139 SPO1677 0.631 SPO1678 0.253 SPO1679	0.94 0.65 0.88	0.171 SPO1674 0.156 SPO1675 0.508 SPO1676	0.63 1.51 1.03	0.619 0.013 0.640		0.78 0.60 1.49	0.577	SPO1674 SPO1675 SPO1676	0.90 1.13 1.06	0.777	SPO1672 SPO1673 SPO1674	1.05 1.04 0.86	0.843 0.322 0.827
SPO1679 SPO1680 SPO1681	0.63 1.01 1.07		SPO1678 SPO1679 SPO1680	0.65 0.68 1.03	0.012 SPO1678 0.496 SPO1679 0.709 SPO1680	0.96 0.83 0.79	0.602 SPO1680 0.564 SPO1681 0.823 SPO1682	0.83 0.98 0.93	0.866 SPO1677 0.87 SPO1678 0.009 SPO1679	0.87 0.90	0.983 0.307 0.016	SPO1676 SPO1677 SPO1678	1.09 0.85 0.89	0.268	SPO1677 SPO1678 SPO1679	0.98 1.24 0.84	0.998	SPO1675 SPO1676 SPO1677	1.11 1.04 0.95	0.682 0.857 0.944
SPO1682 SPO1683	0.44 1.24	0.007	SPO1681 SPO1682	1.15 0.43	0.596 SPO1681 0.011 SPO1682	0.93 0.96	0.737 SPO1683 0.065 SPO1684	0.91 0.95	0.674 SPO1680 0.11 SPO1681	0.95 0.95	0.835 0.599	SPO1679 SPO1680	0.36 0.88	0.207 0.951	SPO1680 SPO1681	0.84 0.92 1.17	0.822 0.598	SPO1678 SPO1679	1.25 0.96	0.247 0.959
SPO1684 SPO1685 SPO1686	1.59 1.23 1.33		SPO1683 SPO1684 SPO1685	1.1 1.38 1.29	0.778 SPO1683 0.056 SPO1684 0.008 SPO1685	0.98 0.81 0.97	0.688 SPO1685 0.642 SPO1686 0.933 SPO1687	0.98 0.95 0.81	0.5 SPO1682 0.64 SPO1683 0.296 SPO1684	1.92 0.63 0.55	0.014 0.398 0.084	SPO1681 SPO1682 SPO1683	1.12 1.99 0.68	0.012	SPO1682 SPO1683 SPO1684	2.59 1.03 0.86		SPO1680 SPO1681 SPO1682	0.93 1.04 2.55	0.849 0.954 0.009
SPO1687 SPO1688 SPO1689	0.67 1.33 0.98	0.059 0.012		1.31 0.77 1.2	0.46 SPO1686 0.031 SPO1687 0.013 SPO1688	0.92 0.93 0.88	0.823 SPO1688 0.351 SPO1689 0.295 SPO1690	0.88 0.74 0.96	0.073 SPO1685 0.021 SPO1686 0.664 SPO1687	1.10 1.32 1.29	0.539 0.498 0.093	SPO1684 SPO1685 SPO1686	0.53 0.99 1.39	0.001	SPO1685 SPO1686 SPO1687	1.22 1.18 1.03	0.205 0.729	SPO1683 SPO1684 SPO1685	0.99 0.87 1.17	0.992 0.314 0.139
SPO1690 SPO1691	1.17 0.91	0.507 0.323	SPO1689 SPO1690	0.93 1.04	0.612 SPO1689 0.657 SPO1690	0.95 0.72	0.574 SPO1691 0.494 SPO1692	0.93 0.81	0.342 SPO1688 0.547 SPO1689	0.79	0.078	SPO1687 SPO1688	1.39 1.28 0.84	0.014 0.036	SPO1688 SPO1689	1.02 1.16	0.797 0.195	SPO1686 SPO1687	1.12 1.07	0.756 0.332
SPO1692 SPO1693 SPO1694	0.6 0.61	0.013	SPO1691 SPO1692 SPO1693	1.14 2.01 0.6	0.471 SPO1691 0.166 SPO1692 0.066 SPO1693	0.85 0.83 0.88	0.207 SPO1693 0.591 SPO1694 0.66 SPO1695	0.88 0.82 0.78	0.925 SPO1690 0.168 SPO1691 0.738 SPO1692	0.45 2.13 1.01	0.068 0.004 0.618	SPO1689 SPO1690 SPO1691	0.08 0.47 1.93	0.002 0.024 0.001	SPO1690 SPO1691 SPO1692	1.16 1.26 1.31	0.474	SPO1688 SPO1689 SPO1690	0.96 1.14 1.11	0.513 0.061 0.453
SPO1695 SPO1696 SPO1697	0.71 0.97 0.75		SPO1694	0.59 0.83 0.9	0.035 SPO1694 0.484 SPO1695 0.194 SPO1696	0.99 0.65 0.9	0.612 SPO1696 0.883 SPO1697 0.026 SPO1698	0.92 0.81 0.88	0.015 SPO1693 0.243 SPO1694 0.662 SPO1695	1.01 1.54 1.59	0.428 0.044 0.070	SPO1692 SPO1693 SPO1694	1.09 1.01 1.54		SPO1693 SPO1694 SPO1695	0.87 1.10 1.24	0.316	SPO1691 SPO1692 SPO1693	1.20 1.09 0.84	0.267 0.762 0.338
SPO1698 SPO1699	0.85 0.58	0.611	SPO1697 SPO1698	0.77 0.9	0.295 SPO1697 0.563 SPO1698	0.94 0.92	0.05 SPO1699 0.722 SPO1700	0.88 0.79	0.095 SPO1696 0.171 SPO1697	1.15	0.048	SPO1695 SPO1696	1.67 1.12	0.110	SPO1696 SPO1697	1.10 1.08	0.442	SPO1694 SPO1695	1.16 1.29	0.128 0.369
SPO1700 SPO1701 SPO1702	0.58 0.63 0.89	0.162	SPO1699 SPO1700 SPO1701	0.64 0.65 0.73	0.035 SPO1699 0.036 SPO1700 0.331 SPO1701	0.96 0.76 0.95	0.089 SPO1701 0.075 SPO1702 0.75 SPO1703	0.75 0.7 0.94	0.481 SPO1698 0.383 SPO1699 0.661 SPO1700	0.99 1.31 1.20	0.964 0.022 0.294	SPO1697 SPO1698 SPO1699	1.20 0.98 1.32	0.911	SPO1698 SPO1699 SPO1700	1.13 1.05 1.11	0.117	SPO1696 SPO1697 SPO1698	1.12 1.02 1.15	0.155 0.948 0.510
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SPO1703 SPO1704	0.77	0.715 SPO1703 0.868 SPO1703			SPO1702 SPO1703	0.85	0.138 SPO1704 0.899 SPO1705	0.99	0.957	SPO1701 SPO1702	1.21	0.229	SPO1700 SPO1701	1.19		SPO1701 SPO1702	1.06	0.757	SPO1699 SPO1700	1.15	0.284
SPO1705 SPO1707	0.59 0.95	0.529 SPO170 0.992 SPO170	0.62	0.904	SPO1704 SPO1705	0.93 0.85	0.776 SPO1707 0.759 SPO1708	0.92 0.95	0.934 0.089	SPO1703 SPO1704 SPO1705	1.41 1.18	0.591 0.806	SPO1702 SPO1703	1.06 1.31	0.940 0.655	SPO1703 SPO1704	0.99 1.04	0.962 0.973	SPO1701 SPO1702	1.03 1.04	0.857 0.725
SPO1708 SPO1709 SPO1711	0.69 0.92 1.03	0.325 SPO170 0.977 SPO170 0 SPO170	0.52	0.028	SPO1707 SPO1708 SPO1709	0.9 0.94 0.98	0.908 SPO1709 0.426 SPO1711 0.951 SPO1712	0.94 0.68 0.99	0.997 0.43 0.569	SPO1705 SPO1707 SPO1708	1.35 0.80 1.54	0.641 0.509 0.189	SPO1704 SPO1705 SPO1707	1.06 1.19 0.74	0.995 0.808 0.345	SPO1705 SPO1707 SPO1708	1.11 0.86 1.17	0.881 0.645 0.634	SPO1703 SPO1704 SPO1705	1.19 0.94 1.13	0.855 0.910 0.891
SPO1712 SPO1713 SPO1714	0.83 0.74 0.77	0.094 SPO171 0.609 SPO171 0.547 SPO171	0.96	0.907	SPO1711 SPO1712 SPO1713	0.93 0.97 0.92	0.65 SPO1713 0.617 SPO1714 0.671 SPO1715	0.98 0.66 0.69	0.262 0.934 0.808	SPO1709 SPO1711 SPO1712	0.67 0.57 0.88	0.861 0.243 0.183	SPO1708 SPO1709 SPO1710	1.47 0.77 1.07	0.060 0.851	SPO1709 SPO1710 SPO1711	0.52 2.30 0.86	0.702	SPO1707 SPO1708 SPO1709	0.84 1.23 0.78	0.515 0.501 0.792
SPO1715 SPO1716	0.85 0.63	0.94 SPO171- 0.235 SPO171:	0.93	0.985 0.979	SPO1714 SPO1715	0.95 0.99	0.892 SPO1716 0.979 SPO1717	0.89 0.96	0.033 0.195	SPO1713 SPO1714	0.66 0.97	0.548 0.828	SPO1711 SPO1712	0.65 0.94	0.185 0.446	SPO1712 SPO1713	1.15 0.99	0.616 0.976	SPO1710 SPO1711	1.28 0.79	0.430 0.689
SPO1717 SPO1718 SPO1719	1.01 0.71 1.15	0.652 SPO171 0.102 SPO171 0.666 SPO171	0.97	0.334	SPO1716 SPO1717 SPO1718	0.98 1.01 0.74	0.042 SPO1718 0.398 SPO1719 0.039 SPO1720	0.82 0.78 0.92	0.128 0.953 0.965	SPO1715 SPO1716 SPO1717	0.83 1.72 0.95	0.712 0.191 0.676	SPO1713 SPO1714 SPO1715	0.63 0.81 0.76	0.325 0.704 0.415	SPO1714 SPO1715 SPO1716	1.13 0.99 1.24	0.904	SPO1712 SPO1713 SPO1714	1.08 1.05 1.03	0.627 0.841 0.993
SPO1720 SPO1721 SPO1722	1.13 0.83 0.83	0.849 SPO171 0.65 SPO172 0.496 SPO172	1.07	0.899	SPO1719 SPO1720 SPO1721	0.93 0.73 0.88	0.621 SPO1721 0.981 SPO1722 0.453 SPO1723	0.89 0.92 0.83	0.401 0.224 0.298	SPO1718 SPO1719 SPO1720	3.35 1.08 0.96	0.010 0.970 1.000	SPO1716 SPO1717 SPO1718	1.47	0.079 0.832 0.022	SPO1717 SPO1718 SPO1719	1.05 2.00	0.010	SPO1715 SPO1716 SPO1717	1.03 1.22 1.15	0.992 0.601 0.459
SPO1723 SPO1724	0.94 1.11	0.818 SPO172: 0.871 SPO172:	0.86	0.42 0.832	SPO1722 SPO1723	0.99 0.97	0.195 SPO1724 0.129 SPO1725	0.96 0.98	0.98 0.83	SPO1721 SPO1722	1.80	0.173 0.003	SPO1719 SPO1720	1.19 0.93	0.826 0.978	SPO1720 SPO1721	0.88 1.01	0.890 0.970	SPO1718 SPO1719	1.74 1.24	0.044 0.785
SPO1725 SPO1727 SPO1728	0.86 0.93 1.2	0.522 SPO172 0.643 SPO172 0.142 SPO172	0.91		SPO1724 SPO1725 SPO1727	0.88 0.63 0.91	0.935 SPO1727 0.98 SPO1728 0.997 SPO1729	0.99 0.64 0.85	0.95 0.742 0.184	SPO1723 SPO1724 SPO1725	0.79 1.04	0.015 0.873 0.267	SPO1721 SPO1722 SPO1723	1.68 2.48 2.04	0.212 0.013 0.124	SPO1722 SPO1723 SPO1724	1.24 1.02 0.89		SPO1720 SPO1721 SPO1722	0.98 1.00 1.16	0.978 0.978 0.551
SPO1729 SPO1732	0.75 1.42 1.66	0.028 SPO172 0.022 SPO172 0.064 SPO173	0.81	0.202	SPO1728 SPO1729 SPO1732	0.94 0.87 0.87	0.774 SP01732 0.282 SP01733 0.25 SP01734	0.98 0.96 0.77	0.43 0.652 0.62	SPO1727 SPO1728	0.98 1.05	0.618 0.368 0.169	SPO1724 SPO1725 SPO1727	0.67 0.99 0.96	0.569 0.627 0.438	SPO1725 SPO1727 SPO1728	1.00 1.03 1.09	0.955 0.608 0.081	SPO1723 SPO1724 SPO1725	0.98 0.84 0.96	0.979 0.518 0.939
SPO1733 SPO1734 SPO1735	1.37 0.78	0.112 SPO173 0.27 SPO173	1.35	0.116 0.056	SPO1733 SPO1734	0.72 0.86	0.046 SPO1735 0.52 SPO1736	0.79 0.85	0.441 0.089	SPO1732 SPO1733	1.14 0.95 0.65	0.866 0.012	SPO1728 SPO1729	1.02 1.16	0.481	SPO1729 SPO1732	1.04 1.14	0.842 0.702	SPO1727 SPO1728	1.07 1.05	0.491 0.738
SPO1736 SPO1737 SPO1738	1.14 1.05 0.93	0.724 SPO173 0.532 SPO173 0.957 SPO173	1.19		SPO1735 SPO1736 SPO1737	0.96 0.79 0.76	0.817 SPO1737 0.541 SPO1738 0.885 SPO1739	0.89 0.97 0.6	0.465 0.867 0.018	SPO1734 SPO1735 SPO1736	1.07 1.01 1.23	0.494 0.558 0.298	SPO1732 SPO1733 SPO1734	0.95 0.68 1.06	0.752 0.101 0.238	SPO1733 SPO1734 SPO1735	1.17 1.10 1.03	0.532 0.719 0.879	SPO1729 SPO1732 SPO1733	1.09 1.09 1.14	0.520 0.761 0.277
SPO1739 SPO1740	0.8 1.14	0.037 SPO173 0.366 SPO173	0.83	0.129	SPO1738 SPO1739	0.81	0.932 SPO1740 0.02 SPO1741	0.89	0.418	SPO1737 SPO1738 SPO1739	1.03	0.579	SPO1735 SPO1736 SPO1737	0.95 1.18	0.468 0.132 0.838	SPO1736 SPO1737	0.81 1.00	0.045	SPO1734 SPO1735	1.07	0.726 0.327
SPO1741 SPO1742 SPO1743	0.89 0.66 0.93	0.724 SPO174 0.056 SPO174 0.368 SPO174	0.94	0.925	SPO1740 SPO1741 SPO1742	0.67 0.69 0.91	0.847 SPO1743 0.32 SPO1744	0.88 0.74 0.78	0.361 0.526 0.95	SPO1740 SPO1741	1.04 0.79 0.70	0.165 0.194 0.425	SPO1737 SPO1738 SPO1739	0.99 1.11 0.93	0.838 0.780 0.267	SPO1738 SPO1739 SPO1740	1.08 1.40 1.04	0.865 0.004 0.607	SPO1736 SPO1737 SPO1738	1.02 1.21	0.435 0.620 0.662
SPO1744 SPO1745 SPO1746	0.79 1.04 0.89	0.757 SPO174: 0.921 SPO174: 0.674 SPO174:	0.82	0.885	SPO1743 SPO1744 SPO1745	0.87 0.96 0.98	0.512 SPO1745 0.989 SPO1746 0.851 SPO1747	0.94 0.84	0.887 0.935 0.768	SPO1742 SPO1743 SPO1744	0.91 0.57 0.74	0.996 0.067 0.837	SPO1740 SPO1741 SPO1742	0.85 0.65 0.95	0.538 0.438 0.339	SPO1741 SPO1742 SPO1743	0.84 0.98 0.97	0.997	SPO1739 SPO1740 SPO1741	1.36 0.94 0.87	0.059 0.785 0.747
SPO1747 SPO1748	1.14 1.1	0.403 SPO174 0.156 SPO174	0.93	0.668 0.595	SPO1746 SPO1747	0.97 0.95	0.95 SPO1748 0.553 SPO1749	0.98 0.95	0.718	SPO1745 SPO1746	0.67 0.76	0.492 0.135	SPO1743 SPO1744	0.55 0.75	0.108 0.862	SPO1744 SPO1745	0.80 0.95	0.735 0.945	SPO1742 SPO1743	0.94 0.88	0.390 0.435
SPO1749 SPO1750 SPO1751	0.7 0.73 1.01	0.034 SPO174 0.026 SPO174 0.939 SPO175	0.76	0.206	SPO1748 SPO1749 SPO1750	0.95 0.83 0.96	0.896 SPO1750 0.564 SPO1751 0.088 SPO1752	0.99 0.96 0.97	0.012 0.403 0.667	SPO1748 SPO1749	0.63 0.93 1.47	0.068 0.705 0.051	SPO1745 SPO1746 SPO1747	0.66 0.76 0.63	0.580 0.015 0.278	SPO1746 SPO1747 SPO1748	0.91 0.99 0.88		SPO1744 SPO1745 SPO1746	0.88 0.96 0.93	0.870 0.964 0.566
SPO1752 SPO1753 SPO1754	0.87 0.97	0.581 SPO175 0.875 SPO175 0.521 SPO175	0.99	0.442	SPO1751 SPO1752 SPO1753	0.85 0.83 0.96	0.475 SPO1753 0.929 SPO1754 0.174 SPO1755	0.96 0.93 0.96	0.198 0.837 0.341	SPO1750 SPO1751 SPO1752	1.35 0.53 0.69	0.022 0.140 0.147	SPO1748 SPO1749 SPO1750	0.90 1.59	0.633 0.006 0.010	SPO1749 SPO1750 SPO1751	1.15 1.12 1.11		SPO1747 SPO1748 SPO1749	1.00 0.83 1.34	0.996 0.084 0.080
SPO1755 SPO1756	0.96 0.79	0.974 SPO175 0.054 SPO175	1.25	0.759 0.858	SPO1754 SPO1755	0.96 0.89	0.865 SPO1756 0.692 SPO1757	0.83 0.98	0.538 0.016	SPO1753 SPO1754	1.01	0.098 0.958	SPO1751 SPO1752	0.52 0.64	0.060 0.028	SPO1752 SPO1753	1.07 0.87	0.802 0.206	SPO1750 SPO1751	1.26 1.04	0.186 0.383
SPO1757 SPO1758 SPO1759	1.08 0.93 1.2	0.375 SPO175 0.949 SPO175 0.303 SPO175	1.01	0.568	SPO1756 SPO1757 SPO1758	0.9 0.97 0.74	0.228 SPO1758 0.163 SPO1759 0.885 SPO1760	0.7 0.93 0.75	0.538 0.959 0.957	SPO1755 SPO1756 SPO1757	2.58 1.37 1.41	0.090 0.019 0.144	SPO1753 SPO1754 SPO1755	0.94 0.88 2.73	0.322 0.968 0.001	SPO1754 SPO1755 SPO1756	0.97 1.21 0.77	0.985 0.500 0.166	SPO1752 SPO1753 SPO1754	1.02 0.91 0.92	0.837 0.625 0.934
SPO1760 SPO1761 SPO1762	1.23 0.91 0.93	0.365 SPO175 0.79 SPO176 0.586 SPO176	1.35	0.017	SPO1759 SPO1760 SPO1761	0.78 0.9 0.83	0.825 SPO1761 0.911 SPO1762 0.682 SPO1763	0.85 0.93 0.93	0.653 0.032 0.495	SPO1758 SPO1759 SPO1760	0.81 0.83 1.00	0.144 0.535 0.601	SPO1756 SPO1757 SPO1758	1.39 1.66 0.92	0.001 0.187 0.093	SPO1757 SPO1758 SPO1759	1.02 1.06 1.01	0.997 0.893 0.900	SPO1755 SPO1756 SPO1757	1.22 0.82 1.06	0.406 0.063 0.616
SPO1763 SPO1764	1.53 0.93	0.004 SPO176: 0.514 SPO176:	0.95	0.946	SPO1762 SPO1763	0.75 0.9	0.298 SPO1764 0.137 SPO1765	0.85 0.69	0.973 0.565	SPO1761 SPO1762	0.89 0.94	0.960 0.768	SPO1759 SPO1760	0.82 0.85	0.619 0.243	SPO1760 SPO1761	1.03 0.97	0.859 0.988	SPO1758 SPO1759	0.91 0.99	0.713 0.974
SPO1765 SPO1766 SPO1767	1.02 0.75 0.68	0.861 SPO176 0.13 SPO176 0.063 SPO176	1.11	0.089	SPO1764 SPO1765 SPO1766	0.92 0.98 0.84	0.656 SPO1766 0.371 SPO1767 0.173 SPO1769	0.92 0.96 0.88	0.174 0.237 0.207	SPO1763 SPO1764 SPO1765	0.72 0.96 0.45	0.283 0.568 0.037	SPO1761 SPO1762 SPO1763	0.87 0.95 0.71	0.948 0.690 0.326	SPO1762 SPO1763 SPO1764	1.09 0.97 1.12	0.380 0.937 0.429	SPO1760 SPO1761 SPO1762	0.93 0.97 1.18	0.781 0.986 0.223
SPO1769 SPO1770 SPO1771	0.69 0.94 0.98	0.274 SPO176 0.739 SPO176 0.961 SPO177	0.72	0.092	SPO1767 SPO1769 SPO1770	0.88 0.95 0.73	0.577 SP01770 0.107 SP01771 0.331 SP01772	0.86 0.75 0.85	0.074 0.844 0.198	SPO1766 SPO1767	1.21 0.92	0.174	SPO1764 SPO1765	1.04 0.46 1.17	0.620 0.040 0.157	SPO1765 SPO1766 SPO1767	0.85 1.42 0.97		SPO1763 SPO1764 SPO1765	0.93 1.08 0.85	0.817 0.661 0.761
SPO1772 SPO1773	0.83 0.51	0.391 SPO177 0.046 SPO177	0.95	0.999 0.101		0.97 0.78	0.947 SPO1773 0.7 SPO1774	0.83 0.77	0.369	SPO1770 SPO1771	1.12 0.88	0.196 0.518	SPO1766 SPO1769	0.82 2.05	0.561 0.036	SPO1769 SPO1770	0.98 1.32	0.964	SPO1766 SPO1767	1.38 0.92	0.053 0.508
SPO1774 SPO1775 SPO1776	0.38 1.04 0.53	0.006 SPO177: 0.752 SPO177: 0.015 SPO177:	0.54	0.004	SPO1773 SPO1774 SPO1775	0.62 0.64 0.71	0.869 SPO1775 0.003 SPO1776 0.156 SPO1777	0.81 0.69 0.61	0.351 0.318 0.719	SPO1772 SPO1773 SPO1774	1.29 1.28 1.49	0.218 0.191 0.108	SPO1770 SPO1771 SPO1772	1.11 0.89 1.59	0.280 0.645 0.054	SPO1771 SPO1772 SPO1773	1.01 0.95 1.01	0.939	SPO1769 SPO1770 SPO1771	0.98 1.37 1.00	0.976 0.142 0.978
SPO1777 SPO1779 SPO1780	0.51 1.45 1.86	0.11 SPO1770 0.008 SPO1770 0.024 SPO1779	0.52		SP01776 SP01777 SP01779	0.88	0.326 SPO1779 0.973 SPO1780 0.809 SPO1781	0.64 0.88 0.98	0.899 0.038 0.09	SPO1775 SPO1776	1.04 1.06 0.65	0.685 0.104 0.242	SPO1773 SPO1774	1.28 1.26 1.15	0.052 0.149 0.360	SPO1774 SPO1775 SPO1776	1.21 1.01 0.97		SP01772 SP01773 SP01774	1.00 1.07 1.42	0.902
SPO1781 SPO1782	0.68	0.04 SPO178 0.18 SPO178	0.66	0.049	SPO1780 SPO1781	1.01	0.473 SPO1782 0.023 SPO1783	0.91 0.99	0.822 0.813	SPO1779 SPO1780	0.67	0.096 0.009	SPO1776 SPO1777	0.99 0.63	0.210 0.147	SPO1777 SPO1778	1.01 1.18	0.977 0.840	SPO1775 SPO1776	0.94 1.05	0.792
SPO1783 SPO1784 SPO1785	0.49 0.54 1.01	0.069 SPO1783 0.029 SPO1783 0.727 SPO1784	0.59	0.332 0.134 0.072	SPO1782 SPO1783 SPO1784	0.88 0.98 0.85	0.55 SPO1784 0.808 SPO1785 0.584 SPO1786	0.91 1 0.97	0.931 0.215 0.24	SPO1781 SPO1782 SPO1783	0.39 0.52 0.62	0.003 0.073 0.008	SPO1779 SPO1780 SPO1781	0.68 0.31 0.41	0.278 0.001 0.001	SPO1779 SPO1780 SPO1781	1.00 1.07 0.93	0.951 0.802 0.220	SP01777 SP01778 SP01779	1.11 0.87 0.99	0.650 0.380 0.989
SPO1786 SPO1787 SPO1788	1.02 0.6 0.78	0.791 SPO178 0.089 SPO178 0.104 SPO178	0.91	0.54	SPO1785 SPO1786 SPO1787	0.85 0.77 0.97	0.908 SPO1787 0.503 SPO1788 0.492 SPO1789	1.02 0.96 1.01	0.324 0.667 0.003	SPO1784 SPO1785	0.75 0.57 0.57	0.091 0.042 0.080	SPO1782 SPO1783	0.54 0.62 0.72	0.139 0.041 0.089	SPO1782 SPO1783 SPO1784	0.93 0.98 1.05	0.701 0.926 0.802	SPO1780 SPO1781 SPO1782	1.00 0.92 0.99	0.869 0.358 0.987
SPO1789 SPO1790	0.05 0.08	0.012 SPO178 0.02 SPO178	0.76	0.179	SPO1788 SPO1789	0.93 0.84	0.738 SPO1790 0.006 SPO1791	0.85 0.78	0.097 0.029	SPO1788 SPO1788	1.11	0.244 0.058	SPO1785 SPO1786	0.57 0.60	0.005	SPO1785 SPO1786	1.22 0.77	0.027 0.272	SPO1783 SPO1784	1.02 1.05	0.809 0.730
SPO1791 SPO1792 SPO1793	0.09 1.24 0.69	0.019 SPO179 0.252 SPO179 0.097 SPO179	0.13 0.17 2 1.17	0.107 0.003 0.425	SPO1790 SPO1791 SPO1792	0.93 0.75 0.93	0.101 SPO1792 0.016 SPO1793 0.547 SPO1794	0.79 0.97 0.89	0.367 0.528 0.208	SPO1789 SPO1790 SPO1791	2.81 3.54 3.43	0.005 0.105 0.020	SPO1787 SPO1788 SPO1789	1.24 1.32 2.87	0.306 0.040 0.005	SPO1787 SPO1788 SPO1789	1.01 1.22 0.79	0.883 0.444 0.058	SPO1785 SPO1786 SPO1787	1.07 0.85 1.04	0.177 0.484 0.708
SPO1794 SPO1795 SPO1796	1.04 1.25 0.9	0.735 SPO179 0.264 SPO179 0.135 SPO179	0.96	0.959	SPO1793 SPO1794 SPO1795	0.89 0.93 0.82	0.301 SPO1795 0.532 SPO1796 0.016 SPO1797	0.92 0.89 0.96	0.003 0.01 0.082	SPO1792 SPO1793 SPO1794	0.88 2.95	0.555 0.013 0.087	SPO1790 SPO1791 SPO1792	3.42 3.01 0.88	0.089 0.041	SPO1790 SPO1791 SPO1792	0.91 0.92 0.93	0.810	SPO1788 SPO1789 SPO1790	1.22 0.82 0.88	0.181 0.115 0.844
SPO1797 SPO1798	0.71 0.47	0.26 SPO179 0.041 SPO179	0.97	7 0.965 I 0.158	SPO1796 SPO1797	0.96 0.86	0.015 SPO1798 0.024 SPO1799	0.93 0.79	0.59 0.825	SPO1795 SPO1796	12.30 31.30	0.003 0.001	SPO1793 SPO1794	2.44 4.50	0.027	SPO1793 SPO1794	0.98 0.85	0.757 0.595	SPO1791 SPO1792	0.98 0.90	0.917 0.565
SPO1799 SPO1800 SPO1801	0.53 0.44 0.8	0.035 SPO179 0.079 SPO179 0.626 SPO180	0.62		SPO1798 SPO1799 SPO1800	0.78 0.93 0.79	0.382 SPO1800 0.55 SPO1801 0.935 SPO1802	0.89 0.85 0.88	0.816 0.927 0.76	SPO1797 SPO1798 SPO1799	1.34 2.87 2.88	0.013 0.015 0.001	SPO1795 SPO1796 SPO1797	12.60 24.80 1.42	0.000 0.001 0.063	SPO1795 SPO1796 SPO1797	0.79 0.93 0.85	0.698	SPO1793 SPO1794 SPO1795	0.98 0.87 0.86	0.714 0.393 0.011
SPO1802 SPO1803 SPO1804	0.87 1.06 1.1	0.135 SPO180 0.737 SPO180 0.13 SPO180	0.91	0.432	SPO1801 SPO1802 SPO1803	0.91 0.94	0.95 SPO1803 0.305 SPO1804 0.804 SPO1805	0.85 0.89 0.92	0.651 0.266 0.816	SPO1800 SPO1801 SPO1802	1.19 0.95 0.79	0.629 0.942 0.307	SPO1798 SPO1799 SPO1800	2.72 3.01 0.99	0.012	SPO1798 SPO1799 SPO1800	0.93 0.88 0.87	0.304	SPO1796 SPO1797 SPO1798	1.00 0.85 0.90	0.853 0.600 0.622
SPO1805 SPO1806	1.36 1.44	0.548 SPO180 0.269 SPO180	1.03	0.806 0.568	SPO1804 SPO1805	0.96	0.455 SPO1806 0.839 SPO1807	0.82	0.996 0.192	SPO1803 SPO1804	0.68 0.99	0.175 0.409	SPO1801 SPO1802	0.99 0.88	0.470 0.625	SPO1801 SPO1802	1.00 1.04	0.934 0.455	SPO1799 SPO1800	0.91 0.84	0.469 0.269
SPO1807 SPO1808 SPO1809	0.87 0.94 1.16	0.283 SPO180 0.963 SPO180 0.471 SPO180	0.85		SPO1806 SPO1807 SPO1808	0.96 0.93 0.81	0.97 SPO1808 0.813 SPO1809 0.392 SPO1810	0.76 0.95 0.84	0.007 0.35 0.923	SPO1805 SPO1806 SPO1807	0.75 1.10 1.36	0.641 0.564 0.446	SPO1803 SPO1804 SPO1805	0.58 1.04 0.77	0.029 0.178 0.750	SPO1803 SPO1804 SPO1805	0.94 0.95		SPO1801 SPO1802 SPO1803	1.10 1.04 0.92	0.549 0.361 0.748
SPO1810 SPO1811 SPO1812	1.02 0.61 1.13	0.956 SPO180 0.321 SPO181 0.783 SPO181	0.99	0.958	SPO1809 SPO1810 SPO1811	0.96 0.84 0.85	0.982 SPO1811 0.919 SPO1812 0.372 SPO1813	0.54 0.67 0.72	0.403 0.813 0.048	SPO1808 SPO1809 SPO1810	1.22 0.69 0.79	0.006 0.035 0.756	SPO1806 SPO1807 SPO1808	0.96 1.25 1.08	0.213	SPO1806 SPO1807 SPO1808	0.93 1.22 1.07	0.785 0.295	SPO1804 SPO1805 SPO1806	0.93 0.92 0.98	0.668 0.932 0.939
SPO1813 SPO1814	0.81	0.062 SPO181: 0.316 SPO181:	1.04	0.918	SPO1812 SPO1813	0.84 0.8	0.856 SPO1814 0.205 SPO1815	0.91 0.97	0.556 0.549	SPO1811 SPO1812	1.20 0.61	0.403 0.413	SPO1809 SPO1810	0.78	0.064 0.778	SPO1809 SPO1810	1.16 1.14	0.270 0.864	SPO1807 SPO1808	1.29 1.06	0.374 0.792
SPO1815 SPO1816 SPO1817	1.33 1.41 1.48	0.358 SPO181 0.068 SPO181 0.022 SPO181	1.19	0.198		0.67 0.96 0.87	0.548 SPO1816 0.643 SPO1817 0.514 SPO1818	0.48 0.9	0.538 0.018 0.251	SPO1813 SPO1814 SPO1815	0.65 0.82 1.62	0.032 0.588 0.119	SPO1811 SPO1812 SPO1813	1.29 0.57 0.65	0.331 0.423 0.018	SPO1811 SPO1812 SPO1813	1.20 0.85 1.06	0.780	SPO1809 SPO1810 SPO1811	1.11 1.18 1.25	0.291 0.815 0.410
SPO1818 SPO1819 SPO1820	1 0.92 0.74	0.982 SPO181 0.976 SPO181 0.457 SPO181	0.99	0.929	SPO1817 SPO1818 SPO1819	0.85 0.99	0.323 SPO1819 0.542 SPO1820 0.983 SPO1821	1.02 0.93 0.84	0.958 0.753 0.415	SPO1816 SPO1817 SPO1818	1.74 0.65 0.87	0.008 0.390 0.995	SPO1814 SPO1815 SPO1816	0.75 1.53 1.55	0.146 0.045 0.045	SPO1814 SPO1815 SPO1816	0.72 0.82 1.03	0.595	SPO1812 SPO1813 SPO1814	0.88 1.09 0.83	0.804 0.517 0.523
SPO1821 SPO1822	1.06 0.86	0.669 SPO182 0.896 SPO182	0.83	0.58 0.586	SPO1820 SPO1821	0.97 0.96	0.76 SPO1822 0.956 SPO1823	0.77 0.75	0.824 0.054	SPO1819 SPO1820	0.93 1.04	0.962 0.980	SPO1817 SPO1818	0.61 0.96	0.225 0.637	SPO1817 SPO1818	0.71 0.98	0.301 0.977	SPO1815 SPO1816	0.87 1.04	0.441 0.493
SPO1823 SPO1824 SPO1825	0.75 0.82 0.72	0.62 SPO182 0.643 SPO182 0.549 SPO182	0.71	0.432	SPO1822 SPO1823 SPO1824	0.85 0.98	0.726 SPO1824 0.125 SPO1825 0.281 SPO1826	0.77 0.92 0.83	0.852 0.938 0.271		0.75 1.00 2.58	0.079 0.986 0.207	SPO1819 SPO1820 SPO1821	0.85 1.21 0.76	0.422	SPO1819 SPO1820 SPO1821	0.90 1.22 0.56	0.632	SPO1817 SPO1818 SPO1819	0.76 0.98 0.88	0.035 0.981 0.887
SPO1826 SPO1828 SPO1829	0.92 1.1 0.72	0.727 SPO1829 0.587 SPO1829 0.069 SPO182	1.03	0.506	SPO1825 SPO1826 SPO1828	0.97 0.78 0.86	0.604 SPO1828 0.755 SPO1829 0.393 SPO1830	0.95 0.83 0.94	0.59 0.642 0.228	SPO1824 SPO1825 SPO1826	0.92 0.94 1.37	0.983 0.987 0.249	SPO1822 SPO1823 SPO1824	0.76 1.97 0.88		SPO1822 SPO1823 SPO1824	0.82 1.09 0.93	0.929	SPO1820 SPO1821 SPO1822	1.19 0.74 0.91	0.377 0.025 0.888
SPO1830 SPO1831	0.78 1.12	0.174 SPO182 0.614 SPO182	0.75	0.065	SPO1829 SPO1830	0.69 0.82	0.894 SPO1831 0.472 SPO1832	0.85 0.83	0.378 0.819	SPO1827 SPO1828	0.98 0.87	0.361	SPO1825 SPO1826	0.70 1.37	0.715	SPO1825 SPO1826	0.91 0.99	0.803	SPO1823 SPO1824	1.16 1.02	0.856 0.958
SPO1832 SPO1833 SPO1834	1.04 0.74 0.91	0.695 SPO183 0.416 SPO183 0.635 SPO183	1.15	0.433	SPO1831 SPO1832 SPO1833	0.95 0.93 0.86	0.594 SPO1833 0.913 SPO1834 0.697 SPO1835	0.96 0.79 0.98	0.246 0.569 0.135	SPO1829 SPO1830 SPO1831	1.11 1.61 1.01	0.128 0.024 0.944	SPO1827 SPO1828 SPO1829	0.86 1.10 1.08		SPO1827 SPO1828 SPO1829	1.13 1.15 0.93		SPO1825 SPO1826 SPO1827	1.01 0.94 0.99	0.972 0.586 0.740
SPO1835 SPO1836 SPO1837	0.9 0.72 0.93	0.692 SPO183 0.143 SPO183 0.831 SPO183	0.76	0.033	SPO1834 SPO1835 SPO1836	0.74 0.97 0.95	0.695 SPO1836 0.575 SPO1837 0.951 SPO1838	0.93 0.97 0.85	0.648 0.682 0.948		0.68 1.13 0.87	0.122 0.536 0.565	SPO1830 SPO1831 SPO1832	1.70 0.97 0.75	0.002 0.783	SPO1830 SPO1831 SPO1832	0.98 0.93 0.70	0.877 0.524	SPO1828 SPO1829 SPO1830	1.04 0.94 1.02	0.902 0.813 0.728
SPO1838 SPO1839	0.83 0.69	0.266 SPO183 0.149 SPO183	0.75	0.147	SPO1837 SPO1838	0.94 1.01	0.496 SPO1839 0.509 SPO1840	0.93 0.88	0.788 0.112	SPO1835 SPO1836	1.17 1.78	0.556 0.030	SPO1833 SPO1834	1.14 0.95	0.081 0.743	SPO1833 SPO1834	1.04 1.10	0.950 0.801	SPO1831 SPO1832	0.89 0.70	0.411 0.146
SPO1840 SPO1841 SPO1842	0.35 1.05 0.71	0.014 SPO183 0.294 SPO183 0.36 SPO184	0.68		SPO1839 SPO1840 SPO1841	0.96 0.9 0.94	0.684 SPO1841 0.135 SPO1842 0.275 SPO1843	0.7 0.97 0.99	0.318 0.441 0.658	SPO1837 SPO1838 SPO1839	1.42 1.58 1.32	0.125 0.062 0.053	SPO1835 SPO1836 SPO1837	1.21 1.83 1.22	0.126 0.021 0.035	SPO1835 SPO1836 SPO1837	0.95 0.93 0.92	0.453	SPO1833 SPO1834 SPO1835	1.07 1.00 0.81	0.686 0.973 0.542
SPO1843 SPO1844 SPO1845	0.93 1.25 0.76	0.864 SPO184 0.699 SPO184 0.588 SPO184	1.04	0.269	SPO1842 SPO1843 SPO1844	0.99 0.93 0.91	0.054 SPO1844 0.485 SPO1845 0.825 SPO1846	0.97 0.99 0.83	0.79 0.587 0.466	SPO1841	2.68 1.27 1.32	0.013 0.022 0.071	SPO1838 SPO1839 SPO1840	1.57 1.32	0.018 0.059	SPO1838 SPO1839 SPO1840	0.76 0.88 0.86	0.121 0.370	SPO1836 SPO1837 SPO1838	1.03 0.85 0.82	0.776 0.154 0.104
SPO1846 SPO1847	0.85 0.41	0.436 SPO184 0.035 SPO184	1.28	0.78 0.668	SPO1845 SPO1846	0.84 0.94	0.649 SPO1847 0.311 SPO1848	0.55 0.94	0.019 0.055	SPO1843 SPO1844	1.58 0.71	0.093 0.821	SPO1841 SPO1842	1.36	0.012	SPO1841 SPO1842	0.93 1.01	0.602 0.982	SPO1839 SPO1840	0.95 0.99	0.894 0.955
SPO1848 SPO1849	0.64	0.022 SPO184 0.889 SPO184			SPO1847 SPO1848	0.97 0.6	0.076 SPO1849 0.071 SPO1850	0.96	0.647 0.761	SPO1845 SPO1846	2.02	0.113	SPO1843 SPO1844	1.68 0.63	0.006	SPO1843 SPO1844	1.05 0.81		SPO1841 SPO1842	0.99 0.95	0.837 0.729

SPO1850 SPO1851 SPO1852	0.69 0.93 0.61		SPO1848 SPO1849 SPO1850	0.68 0.79 0.68	0.682 SPO1850 0.582 SPO1851	0.94 0.98 0.9	0.646 SPO1851 0.524 SPO1852 0.026 SPO1853	0.73 0.96 0.91	0.201 SPO1847 0.18 SPO1848 0.73 SPO1849	5.16 4.12 3.10	0.012 0.016 0.183	SPO1845 SPO1846 SPO1847	2.07 2.04 5.24		SPO1845 SPO1846 SPO1847	0.94 0.97 1.03	0.990	SPO1843 SPO1844 SPO1845	0.94 0.81 0.91	0.797 0.774 0.798
SPO1853 SPO1854 SPO1855	0.51 1.07 1.35	0.05 0.835	SPO1851 SPO1852 SPO1853	0.94 0.68 0.57	0.691 SPO1852 0.068 SPO1853 0.138 SPO1854	0.74 0.89 1.01	0.541 SPO1854 0.772 SPO1855 0.648 SPO1856	0.85 0.81 0.82	0.786 SPO1850 0.137 SPO1851 0.12 SPO1852	2.37 3.21 1.54	0.346 0.000 0.035	SPO1848 SPO1849 SPO1850	4.44 3.16 2.20		SPO1848	1.01 1.09 1.02	0.859 0.910		0.99 1.11 1.06	0.886 0.306 0.553
SPO1856 SPO1858 SPO1859	1 1.5 1.31	0.97 0.266	SPO1854 SPO1855 SPO1856	0.96 1.25 0.95	0.997 SPO1855 0.01 SPO1856	0.88 0.97 0.85	0.037 SPO1858 0.308 SPO1859 0.801 SPO1860	0.9 0.66 0.88	0.633 SPO1853 0.841 SPO1854 0.573 SPO1855	1.57 0.55	0.144 0.160	SPO1851 SPO1852 SPO1853	2.79 1.40 1.63	0.007	SPO1851 SPO1852 SPO1853	1.03 0.95	0.535 0.924	SPO1849 SPO1850 SPO1851	1.05 1.07 0.98	0.915 0.839 0.850
SPO1860 SPO1861	0.88 0.38	0.695	SPO1858 SPO1859	1.4 1.19	0.179 SPO1859 0.679 SPO1860	0.97 0.98	0.84 SPO1861 0.957 SPO1862	0.85 0.94	0.01 SPO1856 0.013 SPO1858	0.53 0.94	0.239 0.850	SPO1854 SPO1855	0.61 1.25	0.284	SPO1854 SPO1855	0.99 1.12	0.962 0.013	SPO1852 SPO1853	0.89 0.99	0.566 0.997
SPO1862 SPO1863 SPO1864	0.45 1.45	0.013 0.05	SPO1860 SPO1861 SPO1862	0.85 0.39 0.37	0.461 SPO1861 0.01 SPO1862 0.002 SPO1863	0.93 0.93 0.99	0.003 SPO1863 0.073 SPO1864 0.026 SPO1865	0.98 0.95 0.79	0.06 SPO1859 0.162 SPO1860 0.884 SPO1861	0.64 3.33 3.06	0.496 0.031 0.004	SPO1856 SPO1858 SPO1859	0.50 0.94 0.65	0.558 0.909 0.335	SPO1856 SPO1858 SPO1859	0.70 1.12 0.95	0.077 0.880	SPO1854 SPO1855 SPO1856	0.99 1.01 0.76	0.981 0.369 0.513
SPO1865 SPO1866 SPO1867	1.56 0.85 0.98	0.299 0.483		1.42 1.48	0.026 SPO1864 0.047 SPO1865 0.418 SPO1866	0.98 0.56 0.9	0.94 SPO1866 0.833 SPO1867 0.621 SPO1868	0.92 0.94 0.95	0.293 SPO1862 0.527 SPO1863 0.483 SPO1864	3.17 2.30 1.27	0.002 0.018 0.040	SPO1860 SPO1861 SPO1862	3.92 3.11 3.09	0.004 0.001 0.004	SPO1860 SPO1861 SPO1862	1.03 1.51 1.29	0.042	SPO1858 SPO1859 SPO1860	0.98 0.92 1.09	0.939 0.807 0.565
SPO1868 SPO1869 SPO1870	1.01 0.9 0.93	0.993 0.067 0.783	SPO1866 SPO1867 SPO1868	0.87 1.08 1.05	0.259 SPO1867 0.793 SPO1868 0.35 SPO1869	0.86 1 0.88	0.928 SPO1869 0.623 SPO1870 0.343 SPO1871	0.97 0.92 0.77	0.213 SPO1865 0.188 SPO1866 0.285 SPO1867	0.99 0.81 0.61	0.835 0.607 0.027	SPO1863 SPO1864 SPO1865	2.14 1.30 0.97	0.015 0.011 0.860	SPO1863 SPO1864 SPO1865	1.56 1.12 1.02	0.033 0.261 0.944	SPO1861 SPO1862 SPO1863	1.58 1.42 1.54	0.003 0.086 0.068
SPO1871 SPO1872 SPO1873	0.66 1.25 1.23	0.067 0.684 0.335	SPO1869 SPO1870 SPO1871	0.85 1.09 0.76	0.171 SPO1870 0.298 SPO1871 0.192 SPO1872	0.83 0.95 0.99	0.583 SPO1872 0.609 SPO1873 0.901 SPO1874	0.84 0.74 0.9	0.72 SPO1868 0.377 SPO1869 0.967 SPO1870	0.64 1.02 1.57	0.155 0.216 0.010	SPO1866 SPO1867 SPO1868	0.77 0.56 0.65	0.212 0.243 0.077	SPO1866 SPO1867 SPO1868	0.90 0.83 1.02	0.337	SPO1864 SPO1865 SPO1866	1.10 1.01 0.92	0.225 0.967 0.838
SPO1874 SPO1875 SPO1876	1.4	0.141 0.059 0.972	SPO1872 SPO1873 SPO1874	1.24 1.13 1.25	0.525 SPO1873 0.249 SPO1874 0.296 SPO1875	0.86 1 0.88	0.402 SPO1875 0.908 SPO1876 0.625 SPO1877	0.82 0.97 0.95	0.251 SPO1871 0.185 SPO1872 0.798 SPO1873	0.99 1.34	0.511 0.448 0.026	SPO1869 SPO1870 SPO1871	1.07 1.56	0.024 0.011 0.110	SPO1869 SPO1870 SPO1871	1.05 1.01 1.06		SPO1867 SPO1868 SPO1869	0.84 0.99 1.10	0.431 0.757 0.203
SPO1877 SPO1878 SPO1879	1 2.88 1.03	0.963 0.025 0.94	SPO1875 SPO1876 SPO1877	1.51 1.04 0.96	0.065 SPO1876 0.384 SPO1877 0.836 SPO1878	0.96 0.96 0.83	0.069 SPO1878 0.886 SPO1879 1 SPO1880	0.92 0.76 0.76	0.977 SPO1874 0.934 SPO1875 0.654 SPO1876	1.58 1.14 0.66	0.150 0.147 0.029	SPO1872 SPO1873 SPO1874	1.29 0.42 1.78	0.224 0.034 0.046	SPO1872 SPO1873 SPO1874	0.95 1.09 1.13	0.902 0.649	SPO1870 SPO1871 SPO1872	1.05 1.06 0.93	0.516 0.018 0.727
SPO1880 SPO1881 SPO1882	1.48 1.21 1.01	0.088		2.62 1.05	0.027 SPO1879 0.914 SPO1880	0.96 0.87 0.92	0.871 SPO1881 0.759 SPO1882	0.97 0.91 0.99	0.693 SPO1877 0.777 SPO1878	0.71 0.50 0.76	0.183 0.076 0.691	SPO1875 SPO1876	1.20 0.67 0.71		SPO1875 SPO1876	1.08 0.89	0.622	SPO1873 SPO1874 SPO1875	1.01 1.08 1.02	0.958 0.346 0.699
SPO1883 SPO1884	1.4 0.75	0.017 0.079	SPO1881 SPO1882	1.21 0.88	0.154 SPO1882 0.482 SPO1883	0.94 0.88	0.215 SPO1883 0.736 SPO1884 0.296 SPO1886	0.94 0.92	0.071 SPO1879 0.829 SPO1880 0.853 SPO1881	0.64 0.90	0.126	SPO1877 SPO1878 SPO1879	0.63 0.75	0.066 0.656	SPO1877 SPO1878 SPO1879	1.05 0.74	0.992 0.728	SPO1876 SPO1877	0.93 1.11	0.630 0.150
SPO1886 SPO1887 SPO1888	1.07 1.04 2.22	0.637 0.001	SPO1883 SPO1884 SPO1886	1.43 0.76 0.98	0.031 SPO1884 0.089 SPO1886 0.954 SPO1887	0.98 0.91 0.69	0.714 SPO1887 0.991 SPO1888 0.337 SPO1889	0.92 0.97 0.99	0.221 SPO1882 0.441 SPO1883 0.221 SPO1884	0.91 0.68 1.66	0.913 0.060 0.025	SPO1880 SPO1881 SPO1882	0.68 0.95 0.90	0.185 0.807 0.942	SPO1880 SPO1881 SPO1882	1.03 1.13 1.02	0.048 0.906	SPO1878 SPO1879 SPO1880	1.08 0.75 0.95	0.855 0.744 0.901
SPO1889 SPO1890 SPO1891	1.39 0.86 0.74	0.041 0.12 0.127	SPO1887 SPO1888 SPO1889	1.1 1.91 1.48	0.545 SPO1888 0.009 SPO1889 0.017 SPO1890	0.8 0.88 0.63	0.051 SPO1890 0.013 SPO1891 0.29 SPO1892	0.88 0.95 0.87	0.609 SPO1885 0.657 SPO1886 0.306 SPO1887	0.54 0.50 1.27	0.237 0.012 0.016	SPO1883 SPO1884 SPO1885	0.76 1.89 0.51	0.028 0.007 0.005	SPO1883 SPO1884 SPO1885	1.07 1.20 0.92		SPO1881 SPO1882 SPO1883	1.10 1.00 1.02	0.577 0.975 0.943
SPO1892 SPO1893 SPO1895	1.09 0.96 1.37	0.142 0.651 0.1	SPO1890 SPO1891 SPO1892	0.94 0.78 1.1	0.743 SPO1891 0.23 SPO1892 0.16 SPO1893	0.69 0.95 0.68	0.881 SPO1893 0.23 SPO1895 0.775 SPO1896	0.93 0.98 0.98	0.529 SPO1888 0.46 SPO1889 0.434 SPO1890	0.94 1.67 1.40	0.514 0.005 0.007	SPO1886 SPO1887 SPO1888	0.53 1.15 0.87	0.005 0.128 0.403	SPO1886 SPO1887 SPO1888	1.09 1.08 1.25		SPO1884 SPO1885 SPO1886	1.17 0.84 1.05	0.068 0.788 0.072
SPO1896 SPO1897 SPO1898	1.02 0.83 1.06	0.898 0.247 0.438	SPO1893 SPO1895 SPO1896	1.01 1.12	0.423 SPO1895 0.058 SPO1896 0.978 SPO1897	0.97 0.94 0.74	1 SPO1897 0.777 SPO1898 0.331 SPO1899	0.74 0.88 0.94	0.578 SPO1891 0.445 SPO1892 0.92 SPO1893	0.79 0.98 1.78	0.585 0.118 0.000	SPO1889 SPO1890 SPO1891	1.61 1.46 0.79	0.022 0.173 0.640	SPO1889 SPO1890 SPO1891	1.17 1.03 0.95	0.552	SPO1887 SPO1888 SPO1889	1.14 1.15 1.15	0.123 0.447 0.413
SPO1899 SPO1900 SPO1901	1.11 1.32 0.88	0.232 0.163 0.162	SPO1897 SPO1898 SPO1899	0.81 0.97 0.95	0.304 SPO1898 0.902 SPO1899 0.791 SPO1900	0.81 0.89 0.92	0.071 SPO1900 0.511 SPO1901 0.348 SPO1902	0.93 0.76 0.91	0.511 SPO1895 0.522 SPO1896 0.533 SPO1897	1.07 0.60 0.98	0.766 0.077 0.966	SPO1892 SPO1893 SPO1895	0.97 1.78	0.053 0.001 0.221	SPO1892 SPO1893 SPO1895	0.85 0.99 1.25	0.125	SPO1890 SPO1891 SPO1892	1.12 1.01 0.88	0.675 0.826 0.207
SPO1902 SPO1903 SPO1904	0.73 0.7 0.81	0.321 0.147	SPO1900 SPO1901 SPO1902	1.18 0.92 0.83	0.086 SPO1901 0.319 SPO1902 0.605 SPO1903	0.79 0.98 0.97	0.206 SPO1903 0.751 SPO1904 0.39 SPO1905	0.97 0.79 1.01	0.354 SPO1898 0.751 SPO1899 0.127 SPO1900	1.07 1.70 1.34	0.605 0.009 0.222	SPO1896 SPO1897 SPO1898	0.66 1.05 1.08	0.316	SPO1896 SPO1897 SPO1898	0.90 0.93 0.97	0.894 0.730	SPO1893 SPO1895 SPO1896	1.06 1.22 0.95	0.071 0.108 0.944
SPO1905 SPO1906	0.56 1.16	0.014 0.343	SPO1903 SPO1904	0.77 0.8	0.276 SPO1904 0.816 SPO1905	0.99 0.88	0.695 SPO1906 0.157 SPO1907	0.97 0.96	0.652 SPO1901 0.534 SPO1902	1.16 1.48	0.110 0.249	SPO1899 SPO1900	1.64 1.35	0.022	SPO1899 SPO1900	1.12 0.94	0.083 0.640	SPO1897 SPO1898	0.97 1.03	0.856 0.873
SPO1907 SPO1908 SPO1909	0.63 0.99 0.95	0.873 0.993	SPO1905 SPO1906 SPO1907	0.64 1.12 0.74	0.063 SPO1906 0.482 SPO1907 0.13 SPO1908	0.98 1 0.32	0.97 SPO1908 0.2 SPO1909 0.288 SPO1911	0.88 0.93 0.87	0.6 SPO1903 0.971 SPO1904 0.99 SPO1905	1.15 1.11 1.12	0.366 0.558 0.249	SPO1901 SPO1902 SPO1903	1.31 1.50 1.15	0.064 0.476		1.04 1.02 1.06	0.955 0.704	SPO1899 SPO1900 SPO1901	1.02 0.95 1.11	0.723 0.719 0.677
SPO1911 SPO1912 SPO1913	1.12 0.85 0.81	0.482 0.401	SPO1908 SPO1909 SPO1911	0.98 1.09 0.94	0.768 SPO1909 0.786 SPO1911 0.996 SPO1912	0.94 0.85 0.96	0.946 SPO1912 0.987 SPO1913 0.353 SPO1914	0.94 0.99 0.9	0.888 SPO1906 0.092 SPO1907 0.079 SPO1908	0.58 1.08 1.02	0.020 0.158 0.863	SPO1904 SPO1905 SPO1906	1.44 1.08 0.66		SPO1906	1.42 1.07 1.11	0.443 0.528	SPO1902 SPO1903 SPO1904	1.10 1.14 1.61	0.671 0.541 0.141
SPO1914 SPO1915 SPO1916	0.68 1.05	0.84 0.042 0.61	SPO1912 SPO1913 SPO1914	0.99 0.77 1.05	0.833 SPO1913 0.075 SPO1914 0.839 SPO1915	0.92 0.99 0.96	0.359 SPO1915 0.075 SPO1916 0.025 SPO1917	0.98 0.98 0.92	0.055 SPO1909 0.253 SPO1911 0.712 SPO1912	0.12 0.39 1.03	0.019 0.036 0.987	SPO1907 SPO1908 SPO1909	0.83 0.99 0.12	0.972 0.843 0.009	SPO1907 SPO1908 SPO1909	1.02 1.05 1.01	0.726	SPO1905 SPO1906 SPO1907	1.14 0.98 0.99	0.311 0.940 0.922
SPO1917 SPO1918 SPO1919	0.9 0.81 0.83	0.922 0.531 0.767	SPO1915 SPO1916 SPO1917	0.68 0.98 0.83	0.034 SPO1916 0.894 SPO1917 0.843 SPO1918	0.79 0.89	0.244 SPO1918 0.767 SPO1919 0.515 SPO1920	0.42 0.82 0.97	0.451 SPO1913 0.485 SPO1914 0.391 SPO1915	1.27 1.17 1.45	0.194 0.003 0.271	SPO1911 SPO1912 SPO1913	1.01 1.30	0.031 0.908 0.028	SPO1911 SPO1912 SPO1913	0.98 1.03 1.12	0.979	SPO1908 SPO1909 SPO1911	1.02 1.04 0.88	0.916 0.877 0.658
SPO1920 SPO1921 SPO1922	0.99 1.16 1.09	0.995 0.047 0.531	SPO1918 SPO1919 SPO1920	0.89 0.84 0.99	0.732 SPO1919 0.756 SPO1920 0.935 SPO1921	0.98 0.84 0.85	0.858 SPO1921 0.439 SPO1922 0.043 SPO1923	0.83 0.92 0.88	0.21 SPO1916 0.964 SPO1917 0.418 SPO1918	0.71 0.93 0.96	0.418 0.897 0.836	SPO1914 SPO1915 SPO1916	1.16 1.48 0.88		SPO1914 SPO1915 SPO1916	1.23 1.46 1.05	0.030 0.198	SPO1912 SPO1913 SPO1914	1.09 1.18 1.18	0.626 0.466 0.151
SPO1923 SPO1925 SPO1926	0.9 0.64 0.6	0.361 0.148 0.259	SPO1921 SPO1922 SPO1923	1.04 1.1 1.01	0.541 SPO1922 0.398 SPO1923 0.843 SPO1925	0.65 0.85 0.74	0.935 SPO1925 0.748 SPO1926 0.702 SPO1927	0.98 0.95 0.84	0.623 SPO1919 0.863 SPO1920 0.08 SPO1921	0.76 1.89 0.81	0.886 0.114 0.358	SPO1917 SPO1918 SPO1919	0.96 0.92 0.66	0.912 0.959 0.570	SPO1917 SPO1918 SPO1919	0.93 0.76 0.97	0.826 0.319	SPO1915 SPO1916 SPO1917	1.40 1.08 0.91	0.271 0.073 0.829
SPO1927 SPO1928	1.01	0.786 0.043	SPO1925 SPO1926	0.72 0.63	0.395 SPO1926 0.356 SPO1927	0.93 0.93	0.937 SPO1928 0.057 SPO1929	0.98 0.99	0.134 SPO1922 0.009 SPO1923	1.16 1.09	0.315 0.426	SPO1920 SPO1921 SPO1922	1.78 0.81	0.171 0.627	SPO1920 SPO1921	1.41 1.05	0.231 0.631	SPO1918 SPO1919	0.75 0.93	0.251 0.933
SPO1929 SPO1930 SPO1931	0.76 1.48	0.057 0.013	SPO1927 SPO1928 SPO1929	1.01 1.13 0.47	0.688 SPO1928 0.182 SPO1929 0.055 SPO1930	0.99 0.91 0.92	0.193 SPO1930 0.027 SPO1931 0.719 SPO1932	0.9 0.95 0.95	0.64 SPO1926 0.867 SPO1927	1.26 1.38 0.83	0.042 0.254 0.398	SPO1923 SPO1925	1.15 1.01 1.27	0.075	SPO1922 SPO1923 SPO1925	1.14 1.16 1.00	0.722 0.942	SPO1920 SPO1921 SPO1922	1.34 0.98 1.07	0.374 0.973 0.309
SPO1932 SPO1933 SPO1934	1.64 1.53 0.74		SPO1930 SPO1931 SPO1932	0.88 1.68 1.62	0.516 SPO1931 0.004 SPO1932 0.018 SPO1933	0.99 0.84 0.95	0.167 SPO1933 0.927 SPO1934 0.144 SPO1935	0.97 0.86 0.88	0.214 SPO1928 0.009 SPO1929 0.222 SPO1930	0.84 1.43 1.13	0.726 0.005 0.283	SPO1926 SPO1927 SPO1928	1.33 0.87 0.79	0.313 0.055	SPO1926 SPO1927 SPO1928	1.03 0.85 0.82	0.237	SPO1923 SPO1925 SPO1926	1.17 1.00 0.99	0.514 0.830 0.993
SPO1935 SPO1936 SPO1937	1.64 1.2 1.12	0.473 0.475	SPO1933 SPO1934 SPO1935	1.26 0.79 1.53	0.028 SPO1934 0.089 SPO1935 0.018 SPO1936	0.96 0.87 0.63	0.248 SPO1936 0.343 SPO1937 0.84 SPO1938	0.86 0.86 0.99	0.669 SPO1931 0.864 SPO1932 0.612 SPO1933	1.05 1.18 0.72	0.158 0.611 0.021	SPO1929 SPO1930 SPO1931	1.22 0.93 1.02	0.929	SPO1929 SPO1930 SPO1931	1.12 1.05 0.98	0.788 1.000	SPO1927 SPO1928 SPO1929	1.01 0.85 1.17	0.870 0.005 0.160
SPO1938 SPO1939 SPO1940	0.64 0.81	0.046	SPO1936 SPO1937 SPO1938	1.07 1.15 1.14	0.596 SPO1937 0.388 SPO1938 0.222 SPO1939	0.63 0.6 0.64	0.91 SPO1939 0.912 SPO1940 0.209 SPO1941	1.02 0.75	0.095 SPO1934 0.827 SPO1935 0.013 SPO1936	1.40 1.59 2.42	0.006 0.095 0.078	SPO1932 SPO1933 SPO1934	1.26 0.72 1.36	0.032	SPO1932 SPO1933 SPO1934	1.22 1.19 1.03	0.031	SPO1930 SPO1931 SPO1932	1.11 0.89 1.14	0.667 0.490 0.619
SPO1941 SPO1942 SPO1943	0.8 0.95 1.24		SPO1939 SPO1940 SPO1941	0.54 0.79 0.88	0.034 SPO1940 0.599 SPO1941 0.378 SPO1942	0.98 0.96	0.823 SPO1942 0.479 SPO1943 0.864 SPO1944	0.73 0.75 0.88	0.474 SPO1937 0.862 SPO1938 0.597 SPO1939	2.55 3.90 1.50	0.047 0.009 0.057	SPO1935 SPO1936 SPO1937	1.71 2.49 2.10		SPO1935 SPO1936 SPO1937	0.91 1.00 1.07	0.967	SPO1933 SPO1934 SPO1935	1.06 1.09 0.96	0.194 0.053 0.799
SPO1944 SPO1945 SPO1946	0.81 0.69 0.82	0.243 0.038	SPO1942 SPO1943 SPO1944	1.07 1.26 0.88	0.166 SPO1943 0.315 SPO1944 0.769 SPO1945	0.41 0.95 0.9	0.786 SPO1945 0.687 SPO1946 0.026 SPO1947	0.98 0.74 0.96	0.11 SPO1940 0.475 SPO1941 0.796 SPO1942	0.72 0.86 0.62	0.067 0.334 0.027	SPO1938 SPO1939 SPO1940	3.90 1.58 0.74	0.001	SPO1938 SPO1939 SPO1940	1.04 1.18 0.83	0.488 0.228	SPO1936 SPO1937 SPO1938	1.01 1.14 1.03	0.925 0.276 0.639
SPO1947 SPO1948 SPO1949	1.09 1.5 0.87	0.192 0.084 0.459		0.72 0.9 1.06	0.006 SPO1946 0.753 SPO1947 0.362 SPO1948	0.67 0.92 0.89	0.655 SPO1948 0.683 SPO1949 0.326 SPO1950	0.76 0.94 0.91	0.179 SPO1943 0.835 SPO1944 0.808 SPO1945	0.36 1.08 1.30	0.022 0.636 0.090	SPO1941 SPO1942 SPO1943	0.91 0.60		SPO1941 SPO1942 SPO1943	0.97 1.02 0.68	0.919 0.361	SPO1939 SPO1940 SPO1941	1.16 0.79 0.97	0.185 0.575 0.837
SPO1950 SPO1951 SPO1952	1.03 0.78 1.27	0.924 0.302 0.126	SPO1948 SPO1949 SPO1950	1.38 0.93 0.97	0.142 SPO1949 0.891 SPO1950 0.968 SPO1951	0.56 0.95 0.93	0.569 SPO1951 0.707 SPO1952 0.827 SPO1953	0.89 0.78 0.97	0.953 SPO1946 0.986 SPO1947 0.12 SPO1948	0.71 1.17 0.60	0.168 0.092 0.067	SPO1944 SPO1945 SPO1946	1.11 1.31 0.72	0.669 0.043	SPO1944 SPO1945 SPO1946	0.97 1.10 0.92	0.871 0.502	SPO1942 SPO1943 SPO1944	1.02 0.71 1.06	0.418 0.092 0.660
SPO1953 SPO1954 SPO1955	1.45 0.87 1.01	0.036 0.172	SPO1951 SPO1952 SPO1953	0.89 1.25 1.44	0.688 SPO1952 0.173 SPO1953 0.009 SPO1954	0.83 0.78 0.68	0.841 SPO1954 0.174 SPO1955 0.193 SPO1956	0.95 0.93 0.99	0.457 SPO1949 0.741 SPO1950 0.826 SPO1951	1.03 0.93 0.71	0.496 0.844 0.278	SPO1947 SPO1948	1.03 0.61	0.050	SPO1947 SPO1948 SPO1949	1.15 1.01 1.10	0.571 0.893	SPO1945 SPO1946 SPO1947	1.09 1.03	0.176 0.620 0.740
SPO1956 SPO1957	1.15 0.63	0.36 0.006	SPO1954 SPO1955	1.01 1.04	0.199 SPO1955 0.788 SPO1956	0.68 0.81	0.661 SPO1957 0.935 SPO1958	0.88	0.915 SPO1952 0.659 SPO1953	0.83 0.75	0.448	SPO1950 SPO1951	0.96 0.68	0.878 0.130	SPO1950 SPO1951 SPO1952	1.25 0.91	0.723 0.618	SPO1948 SPO1949 SPO1950	1.09 1.19	0.532 0.708
SPO1958 SPO1959 SPO1960	1.56 1.18 0.65	0.284	SPO1956 SPO1957 SPO1958 SPO1959	1.01 0.58 1.48	0.816 SPO1957 0.173 SPO1958 0.079 SPO1959	0.67 1 0.94	0.813 SPO1959 0.828 SPO1960 0.673 SPO1961	0.85 0.92	0.92 SPO1954 0.615 SPO1955 0.676 SPO1956	1.81 1.10 0.76	0.006 0.611 0.352	SPO1952 SPO1953 SPO1954	0.88 0.78 1.67	0.009	SPO1953 SPO1954	1.20 1.18 1.03	0.163 0.665	SPO1951 SPO1952	1.17 0.99 1.14	0.128 0.943 0.578
SPO1961 SPO1962 SPO1963	1.06 0.96 0.7	0.96	SPO1960 SPO1961	1.12 0.69 0.99	0.284 SPO1960 0.013 SPO1961 0.8 SPO1962	0.98 1 0.74	0.641 SPO1962 0.631 SPO1963 0.66 SPO1964	0.99 1.01 0.95	0.851 SPO1957 0.017 SPO1958 0.264 SPO1959	1.14 0.84 1.01	0.259 0.476 0.607	SPO1955 SPO1956 SPO1957	1.15 0.81 1.11	0.242	SPO1955 SPO1956 SPO1957	0.79 0.89 15.90	0.572	SPO1953 SPO1954 SPO1955	1.19 1.05 0.73	0.050 0.291 0.185
SPO1964 SPO1965 SPO1966	1.04 0.76 0.83	0.129 0.61	SPO1962 SPO1963 SPO1964	0.93 0.74 0.94	0.777 SPO1963 0.359 SPO1964 0.941 SPO1965	0.96 0.83 0.96	0.068 SPO1965 0.706 SPO1966 0.249 SPO1967	0.78 0.9 0.93	0.052 SPO1960 0.31 SPO1961 0.149 SPO1962	1.24 1.48 1.13	0.229 0.253 0.500	SPO1958 SPO1959 SPO1960	0.90 0.97 1.25	0.884		0.99 0.94 0.96	0.635 0.855	SPO1956 SPO1957 SPO1958	0.94 15.70 1.00	0.734 0.002 0.938
SPO1967 SPO1968 SPO1969	0.66 0.9 0.88		SPO1965 SPO1966 SPO1967	0.79 0.88 0.71	0.145 SPO1966 0.479 SPO1967 0.043 SPO1968	0.81 0.68 0.99	0.229 SPO1968 0.268 SPO1969 0.383 SPO1970	0.93 0.95 0.95	0.146 SPO1963 0.958 SPO1964 0.849 SPO1965	2.78 1.59 1.72	0.002 0.239 0.068	SPO1961 SPO1962 SPO1963	1.65 1.09 2.55	0.289	SPO1961 SPO1962 SPO1963	0.98 0.91 1.05	0.560	SPO1959 SPO1960 SPO1961	0.96 1.00 0.97	0.831 0.993 0.925
SPO1970 SPO1971 SPO1972	0.93 0.76 0.71	0.865 0.539 0.303	SPO1969	0.88 0.91 0.88	0.044 SPO1969 0.804 SPO1970 0.857 SPO1971	0.67 0.93 0.9	0.576 SPO1971 0.95 SPO1972 0.645 SPO1973	0.83 0.68 0.83	0.685 SPO1966 0.384 SPO1967 0.238 SPO1968	1.77 2.23 1.69	0.193 0.026 0.043	SPO1964 SPO1965	1.64 1.76 1.70		SPO1964 SPO1965 SPO1966	1.01 0.94 0.94	0.510	SPO1962 SPO1963 SPO1964	0.88 1.08 0.93	0.550 0.368 0.684
SPO1973 SPO1974 SPO1975	0.7 0.64 2.69	0.311 0.284	SPO1971 SPO1972 SPO1973	0.84 0.75 0.7	0.686 SPO1972 0.046 SPO1973 0.187 SPO1974	0.87 0.75 0.92	0.512 SPO1974 0.322 SPO1975 0.527 SPO1976	0.79 0.86 0.89	0.369 SPO1969 0.022 SPO1970 0.907 SPO1971	1.35 0.72 3.58	0.126 0.719 0.082	SPO1967 SPO1968 SPO1969	2.23 1.83 1.28	0.036	SPO1967 SPO1968 SPO1969	0.88 0.84 0.88	0.299 0.053	SPO1965 SPO1966 SPO1967	1.02 0.96 0.85	0.863 0.910 0.068
SPO1976 SPO1977 SPO1978	1.35 0.5 0.62	0.321 0.016	SPO1974 SPO1975 SPO1976	0.71 2.38	0.27 SPO1975 0.015 SPO1976 0.452 SPO1977	0.91 0.95 0.86	0.034 SPO1977 0.958 SPO1978 0.002 SPO1979	0.98 0.94 0.98	0.007 SPO1972 0.01 SPO1973 0.253 SPO1974	2.22	0.049 0.061 0.004	SPO1970 SPO1971 SPO1972	0.65 2.93	0.427 0.062	SPO1970 SPO1971 SPO1972	0.83 1.01 0.87	0.667 0.996	SPO1968 SPO1969 SPO1970	0.85 0.93 0.90	0.250 0.801 0.791
SPO1979 SPO1980	1.36 1.7	0.445 0.197	SPO1977 SPO1978	0.52 0.66	0.027 SPO1978 0.016 SPO1979	0.97 0.81	0.022 SPO1980 0.718 SPO1981	0.98 0.93 0.79	0.986 SPO1975 0.99 SPO1976	0.78 1.06	0.440 0.291	SPO1973 SPO1974	2.08 2.12 1.96	0.040 0.005	SPO1973 SPO1974	1.62 1.40	0.235	SPO1971 SPO1972	0.95 0.91	0.870 0.795
SPO1981 SPO1982 SPO1983	1.03 0.85 0.96	0.506 0.946	SPO1979 SPO1980 SPO1981	1.18 1.61 1.09	0.374 SPO1980 0.026 SPO1981 0.378 SPO1982	0.95 1.01 1	0.789 SPO1982 0.874 SPO1983 0.654 SPO1984	0.96 0.84	0.392 SPO1977 0.642 SPO1978 0.548 SPO1979	1.61 1.36 0.69	0.026 0.058 0.154	SPO1975 SPO1976 SPO1977	0.69 0.93 1.93	0.669	SPO1975 SPO1976 SPO1977	0.92 1.01 2.19	0.862	SPO1973 SPO1974 SPO1975	1.66 1.44 0.76	0.148 0.027 0.202
SPO1984 SPO1985 SPO1986	1.2 1.15 1.29	0.135 0.341	SPO1982 SPO1983 SPO1984	1.05 1.12 1.17	0.451 SPO1983 0.233 SPO1984 0.086 SPO1985	0.91 0.95 0.99	0.535 SPO1985 0.86 SPO1986 0.2 SPO1987	0.65 0.67 0.61	0.093 SPO1980 0.777 SPO1981 0.653 SPO1982	1.16 0.97 0.73	0.371 0.896 0.220	SPO1978 SPO1979 SPO1980	1.51 0.65 1.14	0.200 0.578	SPO1978 SPO1979 SPO1980	1.77 0.72 1.12	0.055 0.839	SPO1976 SPO1977 SPO1978	1.04 2.15 1.77	0.667 0.018 0.009
SPO1987 SPO1988 SPO1989	0.88 0.83 1.6	0.043	SPO1986 SPO1987	1.18 1.35 0.86	0.071 SPO1986 0.023 SPO1987 0.263 SPO1988	0.88 0.92 0.98	0.943 SPO1988 0.282 SPO1989 0.864 SPO1990	0.58 0.91 0.99	0.811 SPO1983 0.058 SPO1984 0.259 SPO1985	0.26 0.91 1.44	0.003 0.806 0.030	SPO1981 SPO1982 SPO1983	0.93 0.69 0.23	0.070	SPO1981 SPO1982 SPO1983	0.90 1.05 0.83	0.799 0.278	SPO1979 SPO1980 SPO1981	0.77 0.98 0.88	0.362 0.793 0.569
SPO1990 SPO1991 SPO1992	1.37 1.01 1.03	0.86 0.529	SPO1990	0.83 1.73 1.21	0.504 SPO1989 0.064 SPO1990 0.087 SPO1991	0.57 0.54 0.9	0.138 SPO1991 0.171 SPO1992 0.402 SPO1994	0.4 0.93 0.69	0.827 SPO1986 0.7 SPO1987 0.901 SPO1988	1.09 0.88 0.99	0.156 0.931 0.659	SPO1984 SPO1985 SPO1986	0.94 1.41 1.13	0.008	SPO1984 SPO1985 SPO1986	1.11 1.14 1.36	0.167 0.062	SPO1982 SPO1983 SPO1984	1.05 0.85 1.10	0.709 0.507 0.279
SPO1994	0.93		SPO1991	0.97	0.916 SPO1992	0.98	0.898 SPO1995	0.91	0.304 SPO1989	0.92	0.539	SPO1987	0.93		SPO1987	1.06		SPO1985	1.15	0.061

SPO1995 SPO1996	0.82	0.021	SPO1992 SPO1994	0.96 0.96	0.833 SPO1994 0.993 SPO1995	0.78	0.929 SPO1996 0.25 SPO1997	0.91	0.048 SPO199 0.874 SPO199	1.29	0.031 0.256	SPO1988 SPO1989	1.01		SPO1988 SPO1989	1.11		SPO1986 SPO1987	1.27	0.292 0.172
SPO1997 SPO1998	0.66 0.68	0.156 0.112	SPO1995 SPO1996	0.74 0.58	0.201 SPO1996 0.002 SPO1997	0.88 0.89	0.016 SPO1998 0.72 SPO1999	0.86 0.94	0.082 SPO199 0.391 SPO199	0.83	0.167 0.560	SPO1990 SPO1991	1.30 1.26	0.066 0.122	SPO1990 SPO1991	0.98 1.13	0.873	SPO1988 SPO1989	1.12 1.15	0.566 0.243
SPO1999 SPO2000 SPO2001	0.83 1.22 0.63	0.609 0.512 0.294		0.66 0.74 0.8	0.217 SPO1998 0.075 SPO1999 0.628 SPO2000	0.93 0.95 0.86	0.17 SPO2000 0.134 SPO2001 0.765 SPO2002	0.85 0.8 0.67	0.832 SPO199 0.268 SPO199 0.998 SPO199		0.583 0.032 0.525	SPO1992 SPO1994 SPO1995	0.88 0.80 1.10	0.185	SPO1992 SPO1994 SPO1995	0.87 1.31 1.36	0.175	SPO1990 SPO1991 SPO1992	1.04 1.01 0.83	0.211 0.940 0.212
SPO2002 SPO2003 SPO2004	0.96 0.83 1.06	0.98 0.694 0.283	SPO2000 SPO2001 SPO2002	1.04 0.61 0.95	0.855 SPO2001 0.026 SPO2002 0.993 SPO2003	0.73 0.66 0.78	0.653 SPO2003 0.937 SPO2004 0.267 SPO2005	0.59 0.74 0.6	0.553 SPO199 0.657 SPO199 0.11 SPO200		0.131 0.371 0.560	SPO1996 SPO1997 SPO1998	1.08 0.76 1.56	0.107 0.597 0.059	SPO1996 SPO1997 SPO1998	1.26 0.95 1.20		SPO1994 SPO1995 SPO1996	1.17 1.43 1.35	0.300 0.421 0.043
SPO2005 SPO2006	1.04 0.79	0.212	SPO2003 SPO2004	0.88 1.05	0.715 SPO2004 0.572 SPO2005	0.95 0.99	0.468 SPO2006 0.043 SPO2007	0.99	0.884 SPO200 0.697 SPO200	1 1.44	0.262	SPO1999 SPO2000 SPO2001	1.60 0.81	0.834	SPO1999 SPO2000	2.29 0.97	0.981	SPO1997 SPO1998	1.00	0.910 0.283
SPO2007 SPO2008 SPO2009	0.6 1.09 1.19		SPO2005 SPO2006 SPO2007	1.11 0.85 0.68	0.328 SPO2006 0.854 SPO2007 0.118 SPO2008	0.93 1.1 1.04	0.852 SPO2008 0.395 SPO2009 0.836 SPO2010	0.91 0.93 0.87	0.613 SPO200 0.069 SPO200 0.113 SPO200	0.95	0.919 0.846 0.652		1.20 0.89 1.30	0.414	SPO2001 SPO2002 SPO2003	0.85 0.72 0.99	0.287 0.924	SPO2000 SPO2001	1.81 0.95 0.89	0.097 0.936 0.817
SPO2010 SPO2013 SPO2014	0.55 0.99 1.28	0.001 0.888 0.064	SPO2008 SPO2009 SPO2010	0.95 1.04 0.6	0.878 SPO2009 0.548 SPO2010 0.136 SPO2013	1.16 1.23 1.03	0.296 SPO2013 0.023 SPO2014 0.839 SPO2015	0.99 0.74 0.91	0.985 SPO200 0.174 SPO200 0.115 SPO200	7 1.23	0.498 0.470 0.788	SPO2004 SPO2005 SPO2006	1.24 0.81 1.31	0.192	SPO2004 SPO2005 SPO2006	0.97 0.97 0.97	0.556	SPO2002 SPO2003 SPO2004	0.82 0.82 0.84	0.796 0.645 0.302
SPO2015 SPO2016 SPO2017	1.32 1.51 1.23		SPO2013 SPO2014 SPO2015	1.12 1.15 1.41	0.347 SPO2014 0.168 SPO2015 0.042 SPO2016	1.14 1.06 1.1	0.118 SPO2016 0.245 SPO2017 0.035 SPO2018	0.9 1.01 0.78	0.019 SPO200 0.057 SPO201 0.009 SPO201		0.968 0.008 0.279	SPO2007 SPO2008 SPO2009	1.22 0.95 0.95		SPO2007 SPO2008 SPO2009	0.83 1.02 0.84	0.960	SPO2005 SPO2006 SPO2007	0.87 0.88 0.86	0.276 0.741 0.553
SPO2018 SPO2019	0.9	0.16 0.34	SPO2016 SPO2017	1.63 1.25	0.039 SPO2017 0.387 SPO2018	1.1 1.17	0.348 SPO2019 0.007 SPO2020	0.7 0.91	0.759 SPO201 0.221 SPO201	0.64	0.074 0.569	SPO2010 SPO2013	2.19 0.85	0.008	SPO2010 SPO2013	1.23 0.98	0.216 0.747	SPO2008 SPO2009	0.97 0.93	0.552 0.531
SPO2020 SPO2021 SPO2022	1.55 1.31 1.49	0.434 0.106 0.044	SPO2018 SPO2019 SPO2020	0.92 0.73 1.44	0.316 SPO2019 0.127 SPO2020 0.165 SPO2021	1.07 1.02 1.19	0.548 SPO2021 0.087 SPO2022 0.243 SPO2023	0.62 0.86 0.85	0.178 SPO201 0.029 SPO201 0.108 SPO201	0.63 7 0.56 8 0.53	0.020 0.257 0.008	SPO2014 SPO2015 SPO2016	0.63 0.82 0.61	0.062 0.466 0.054	SPO2014 SPO2015 SPO2016	0.65 0.62 0.53	0.027	SPO2010 SPO2013 SPO2014	1.27 1.00 0.64	0.136 0.989 0.112
SPO2023 SPO2025 SPO2026	1.32 1.47 0.99	0.175 0.06 0.907	SPO2021	1.26 1.45 1.26	0.097 SPO2022 0.027 SPO2023 0.241 SPO2025	1.33 1.17 1.21	0.028 SPO2025 0.157 SPO2026 0.087 SPO2027	0.83 0.73 0.94	0.114 SPO201 0.852 SPO202 0.733 SPO202	0.42	0.309 0.039 0.009	SPO2017 SPO2018 SPO2019	0.50 0.53 1.09	0.042 0.004 0.115	SPO2017 SPO2018 SPO2019	0.41 0.43 0.63	0.006	SPO2015 SPO2016 SPO2017	0.62 0.52	0.058 0.004
SPO2027 SPO2028	1.36 1.35	0.083	SPO2025 SPO2026	1.23 1.01	0.02 SPO2026 0.728 SPO2027	1.08 1.01	0.992 SPO2028 0.872 SPO2029	0.79 0.93	0.946 SPO202 0.609 SPO202	2 0.33	0.005 0.008	SPO2020 SPO2021	0.41	0.070 0.010	SPO2020 SPO2021	0.53 0.42	0.073 0.003	SPO2018 SPO2019	0.47 0.71 0.58	0.002
SPO2029 SPO2030 SPO2031	0.82 0.88 1.08	0.689 0.597 0.64	SPO2027 SPO2028 SPO2029	1.36 1.26 0.77	0.024 SPO2028 0.341 SPO2029 0.563 SPO2030	1.2 1.06 1.19	0.898 SPO2030 0.662 SPO2031 0.662 SPO2032	0.97 0.92 1	0.583 SPO202 0.013 SPO202 0.766 SPO202	0.73 7 0.83	0.216 0.277 0.564	SPO2022 SPO2023 SPO2025	0.34 0.24 1.48		SPO2022 SPO2023 SPO2025	0.42 0.43 0.38	0.024	SPO2020 SPO2021 SPO2022	0.58 0.44 0.45	0.290 0.004 0.006
SPO2032 SPO2033 SPO2034	1.17 1 0.84	0.268 0.854 0.575	SPO2030 SPO2031 SPO2032	0.95 1.2	0.957 SPO2031 0.041 SPO2032 0.42 SPO2033	1.03 1.04 1.04	0.053 SPO2033 0.845 SPO2034 0.886 SPO2035	0.75 0.95 0.98	0.769 SPO202 0.558 SPO202 0.711 SPO203	1.75	0.783 0.248 0.557	SPO2026 SPO2027 SPO2028	0.72 0.80 1.17	0.0.0	SPO2026 SPO2027 SPO2028	0.97 1.07	0.448	SPO2023 SPO2025 SPO2026	0.43 0.40 0.96	0.034 0.017 0.957
SPO2035 SPO2036	0.85 1.15	0.826 0.591 0.042	SPO2033 SPO2034	1.18 0.83	0.218 SPO2034 0.541 SPO2035	1.16	0.318 SPO2036 0.802 SPO2037	0.95	0.903 SPO203 0.126 SPO203		0.006 0.425	SPO2029	1.78	0.0.0	SPO2029 SPO2030	1.05 0.96	0.909	SPO2027 SPO2028	1.07	0.272 0.894
SPO2037 SPO2038 SPO2039	1.16 1.46 1.52	0.561 0.005	SPO2035 SPO2036 SPO2037	0.84 1.09 1.32	0.801 SPO2036 0.714 SPO2037 0.006 SPO2038	1.12 1.01 1.32	0.98 SPO2038 0.416 SPO2039 0.828 SPO2040	0.93 0.95 0.95	0.878 SPO203 0.235 SPO203 0.412 SPO203	0.55	0.040 0.180 0.615	SPO2032 SPO2033	1.66 0.98 1.08	0.571 0.020	SPO2031 SPO2032 SPO2033	1.16 1.03 0.96	0.741 0.979		1.03 0.98 1.07	0.912 0.932 0.790
SPO2040 SPO2041 SPO2042	0.75 1.12 0.79	0.198	SPO2038 SPO2039 SPO2040	1.42 1.45 0.78	0.465 SPO2039 0.157 SPO2040 0.319 SPO2041	1.16 1.06 1.04	0.913 SPO2041 0.236 SPO2042 0.752 SPO2044	0.9 0.96 0.95	0.298 SPO203 0.212 SPO203 0.813 SPO203	7 1.46	0.138 0.070 0.813	SPO2034 SPO2035 SPO2036	0.56 1.30 0.63	0.533	SPO2034 SPO2035 SPO2036	1.62 1.20 0.88	0.745	SPO2032 SPO2033 SPO2034	1.02 1.00 1.37	0.854 0.486 0.542
SPO2044 SPO2045 SPO2046	0.79 1.07	0.778	SPO2041 SPO2042 SPO2044	1.02 0.76 0.99	0.135 SPO2042 0.083 SPO2044 0.888 SPO2045	1.06 1.08 0.98	0.687 SPO2045 0.957 SPO2046 0.594 SPO2047	0.6 0.63 0.92	0.898 SPO203 0.623 SPO204 0.744 SPO204		0.133 0.277 0.221	SPO2037 SPO2038 SPO2039	1.54 1.04 0.82		SPO2037 SPO2038 SPO2039	1.22 1.16 1.05	0.698	SPO2035 SPO2036 SPO2037	1.22 0.83 1.23	0.710 0.158 0.244
SPO2047 SPO2048	1.54	0.067 0.007	SPO2045 SPO2046	0.97 1.85	0.996 SPO2046 0.07 SPO2047	1.08	0.334 SPO2048 0.484 SPO2049	0.96 0.77	0.952 SPO204 0.153 SPO204	1.11	0.270 0.215	SPO2040 SPO2041	1.45 1.01	0.062 0.327	SPO2040 SPO2041	0.97 1.04	0.848 0.506	SPO2038 SPO2039	1.16 1.00	0.697 0.865
SPO2049 SPO2050 SPO2051	0.83 0.98 1.44	0.529 0.842 0.07	SPO2047 SPO2048 SPO2049	1.51 2.07 0.79	0.079 SPO2048 0.018 SPO2049 0.206 SPO2050	1.16 1.11 0.99	0.876 SPO2050 0.358 SPO2051 0.069 SPO2052	0.87 0.92 0.77	0.254 SPO204 0.867 SPO204 0.727 SPO204	0.40	0.997 0.018 0.070	SPO2042 SPO2044 SPO2045	1.16 0.63 0.90	0.226	SPO2042 SPO2044 SPO2045	0.99 0.99 0.96	0.978	SPO2040 SPO2041 SPO2042	1.01 1.08 1.06	0.999 0.176 0.326
SPO2052 SPO2053 SPO2054	1.01 1.5 1.32	0.633 0.126 0.165		1.1 1.31 1.06	0.51 SPO2051 0.087 SPO2052 0.606 SPO2053	1.02 1.28 1.1	0.507 SPO2053 0.809 SPO2054 0.801 SPO2055	0.91 0.98 0.88	0.665 SPO204 0.883 SPO204 0.095 SPO205	0.00	0.028 0.910 0.058	SPO2046 SPO2047 SPO2048	0.37 0.52	0.007	SPO2046 SPO2047 SPO2048	0.93 0.95 1.05	0.854	SPO2044 SPO2045 SPO2046	1.01 0.99 0.90	0.776 0.988 0.517
SPO2055 SPO2056	1.37 1.49	0.294	SPO2053 SPO2054	1.23 1.16	0.374 SPO2054 0.329 SPO2055	1.27 1.06	0.628 SPO2056 0.834 SPO2057	0.74 0.66	0.681 SPO205 0.046 SPO205	1 1.03	0.197 0.047	SPO2049 SPO2050 SPO2051	0.97 0.70	0.172	SPO2049 SPO2050	1.23 0.93	0.626 0.199	SPO2047 SPO2048	0.98 1.03	0.967 0.797
SPO2057 SPO2058 SPO2059	1.5 0.85 0.55	0.089 0.244 0.026	SPO2055 SPO2056 SPO2057	1.36 1.32 1.1	0.007 SPO2056 0.622 SPO2057 0.039 SPO2058	1.33 1.12 1.17	0.664 SPO2058 0.047 SPO2059 0.821 SPO2060	0.77 0.97 0.94	0.789 SPO205 0.15 SPO205 0.173 SPO205		0.656 0.542 0.121	SPO2051 SPO2052 SPO2053	1.03 0.68 1.05		SPO2051 SPO2052 SPO2053	1.14 1.08 1.09	0.663	SPO2049 SPO2050 SPO2051	1.13 0.89 1.09	0.253 0.724 0.840
SPO2060 SPO2061 SPO2062	0.98 1.16 0.92	0.992 0.36 0.708	SPO2058 SPO2059 SPO2060	0.92 0.57 1.02	0.804 SPO2059 0.103 SPO2060 0.535 SPO2061	1 1.21 0.99	0.156 SPO2061 0.223 SPO2062 0.162 SPO2063	0.99 1.02	0.442 SPO205 0.941 SPO205 0.213 SPO205	7 0.55	0.909 0.032 0.632	SPO2055	0.77 1.21 1.00	0.057	SPO2054 SPO2055 SPO2056	1.05 1.21 1.02	0.201	SPO2052 SPO2053 SPO2054	1.04 1.06 1.00	0.587 0.698 0.893
SPO2063 SPO2064 SPO2065	1.65 0.99 0.78	0.092 0.978 0.1	SPO2061 SPO2062 SPO2063	1.2 0.94 1.38	0.253 SPO2062 0.888 SPO2063 0.061 SPO2064	1.05 1.1 1.08	0.553 SPO2064 0.084 SPO2065 0.357 SPO2066	1.1 1.23 1.09	0.452 SPO205 0.278 SPO206 0.132 SPO206	1.50	0.022 0.018 0.205	SPO2057 SPO2058 SPO2059	0.55 0.84 1.70	0.018 0.750 0.082	SPO2057 SPO2058 SPO2059	0.92 0.89 1.25		SPO2055 SPO2056 SPO2057	1.28 0.98 0.83	0.033 0.996 0.237
SPO2066 SPO2067	0.92 0.94	0.684 0.974	SPO2064 SPO2065	0.98 0.83	0.983 SPO2065 0.134 SPO2066	1.17 1.2	0.297 SPO2067 0.309 SPO2068	1.1 1.04	0.009 SPO206 0.477 SPO206	2 0.85	0.720 0.297	SPO2060 SPO2061	1.46 1.44	0.040	SPO2060 SPO2061	1.22 1.21	0.279 0.387	SPO2058 SPO2059	0.95 1.39	0.649 0.118
SPO2068 SPO2069 SPO2070	1.99 0.88 0.76	0.278	SPO2066 SPO2067 SPO2068	0.88 1.01 1.88	0.479 SPO2067 0.488 SPO2068 0.017 SPO2069	1.04 1.03 1.19	0.092 SPO2069 0.607 SPO2070 0.735 SPO2071	1.07 1.09 1.12	0.545 SPO206 0.885 SPO206 0.012 SPO206	0.66	0.795 0.054 0.028	SPO2062 SPO2063 SPO2064	0.94 0.93 0.95	0.756 0.737 0.844	SPO2062 SPO2063 SPO2064	1.09 1.36 0.95	0.235 0.888	SPO2060 SPO2061 SPO2062	1.28 1.17 1.12	0.137 0.526 0.371
SPO2071 SPO2072 SPO2073	1.53 0.81 1.2	0.016 0.197 0.104	SPO2069 SPO2070 SPO2071	0.96 0.88 1.38	0.999 SPO2070 0.769 SPO2071 0.001 SPO2072	1.19 1.09 1.16	0.882 SPO2072 0.06 SPO2073 0.483 SPO2074	1.23 1.07 1.19	0.504 SPO206 0.705 SPO206 0.815 SPO206		0.063 0.566 0.346	SPO2066	0.65 2.38 0.61	0.164 0.020 0.003	SPO2065 SPO2066 SPO2067	0.94 0.92 0.98		SPO2063 SPO2064 SPO2065	1.19 0.93 0.91	0.301 0.653 0.439
SPO2074 SPO2075	1.31 1.2 0.9	0.073 0.471 0.567	SPO2072 SPO2073	0.85 1.13 1.33	0.203 SPO2073 0.209 SPO2074	1.29 1 1.22	0.597 SPO2075 0.703 SPO2076 0.59 SPO2077	1.35 1.19 1.14	0.782 SPO207 0.528 SPO207 0.052 SPO207	0.88	0.883 0.129 0.034	SPO2068 SPO2069 SPO2070	0.83 1.09 0.89	0.385 0.470 0.964	SPO2068 SPO2069	1.27 1.09 1.04	0.342	SPO2066 SPO2067 SPO2068	0.97 0.90 1.10	0.821 0.488 0.666
SPO2076 SPO2077 SPO2078	1	0.383 0.981	SPO2074 SPO2075 SPO2076	1.23 0.93	0.283 SPO2076 0.694 SPO2077	1.15 1.15	0.812 SPO2078 0.011 SPO2079	1.1 1.04	0.178 SPO207 0.422 SPO207	0.87 1.75	0.119 0.019	SPO2071 SPO2072	1.72 0.72	0.007	SPO2070 SPO2071 SPO2072	1.19 1.11	0.202 0.540	SPO2069 SPO2070	1.05 1.04	0.535 0.921
SPO2079 SPO2080 SPO2081	1.79 1 0.53	0.005 0.879 0.023	SPO2077 SPO2078 SPO2079	1.05 0.93 1.66	0.719 SPO2078 0.676 SPO2079 0.008 SPO2080	1.2 1.08 1.06	0.324 SPO2080 0.638 SPO2081 0.116 SPO2082	1.19 1.13 1.06	0.153 SPO207 0.504 SPO207 0.407 SPO207		0.521 0.588 0.027	SPO2073 SPO2074 SPO2075	0.86 1.95 1.13	0.312 0.009 0.386	SPO2073 SPO2074 SPO2075	1.04 1.08 1.05	0.629	SPO2071 SPO2072 SPO2073	1.15 1.13 1.03	0.052 0.119 0.550
SPO2082 SPO2083 SPO2084	1.23 1.33 1.35		SPO2080 SPO2081 SPO2082	1.08 0.65 0.95	0.055 SPO2081 0.03 SPO2082 0.956 SPO2083	1.28 1.38 1.01	0.828 SPO2083 0.874 SPO2084 0.418 SPO2085	1.23 1.07 1.18	0.03 SPO207 0.332 SPO207 0.136 SPO208	1.29 1.28 2 2.68	0.016 0.030 0.009		0.93 1.26 1.38	0.854 0.040 0.022	SPO2076 SPO2077 SPO2078	0.88 0.87 0.81		SPO2074 SPO2075 SPO2076	1.10 1.01 0.93	0.417 0.883 0.545
SPO2085 SPO2086 SPO2087	0.89 0.82 0.98	0.177	SPO2083 SPO2084 SPO2085	1.33 1.38 0.89	0.008 SPO2084 0.154 SPO2085 0.33 SPO2086	1.12 1.12 1.05	0.307 SPO2086 0.287 SPO2087 0.257 SPO2088	1.02 1.17 1.22	0.193 SPO208 0.384 SPO208 0.118 SPO208	2 1.01	0.587 0.585 0.661	SPO2080	1.43 2.43 0.77	0.003	SPO2079 SPO2080 SPO2081	1.08 1.25 0.90	0.300	SPO2077 SPO2078 SPO2079	0.88 0.84 1.06	0.315 0.113 0.666
SPO2088 SPO2089	1.19 1.44	0.254 0.425	SPO2086 SPO2087	0.82 0.82	0.333 SPO2087 0.071 SPO2088	1.04 1.06	0.342 SPO2089 0.214 SPO2090	1.12 1.05	0.718 SPO208 0.228 SPO208	0.54 5 1.23	0.052 0.127	SPO2082 SPO2083	1.03 0.92	0.499	SPO2082 SPO2083	0.93 0.99	0.567 0.940	SPO2080 SPO2081	1.14 0.91	0.355 0.207
SPO2090 SPO2091 SPO2092	1.15 1.04 1.22		SPO2088 SPO2089 SPO2090	1.1 1.22 1.11	0.074 SPO2089 0.651 SPO2090 0.07 SPO2091	0.99 1.11 1.05	0.761 SPO2091 0.633 SPO2092 0.835 SPO2093	1.24 1.13 1.08	0.847 SPO208 0.579 SPO208 0.181 SPO208	7 0.83	0.004 0.458 0.139		0.65 1.32 1.65	0.012	SPO2084 SPO2085 SPO2086	1.29 1.02 1.02	0.835	SPO2082 SPO2083 SPO2084	0.95 0.96 1.17	0.720 0.831 0.510
SPO2093 SPO2094 SPO2095	0.74 1.38 1.13	0.07	SPO2091 SPO2092 SPO2093	1.07 1.11 0.65	0.864 SPO2092 0.212 SPO2093 0.403 SPO2094	1.07 1.05	0.512 SPO2094 0.19 SPO2095 0.145 SPO2096	1.03 1.05 1.02	0.157 SPO208 0.547 SPO209 0.885 SPO209	0.92	0.509 0.677 0.775	SPO2087 SPO2088 SPO2089	0.85 0.87 0.63	0.042	SPO2087 SPO2088 SPO2089	0.81 0.94 1.02	0.180	SPO2085 SPO2086 SPO2087	0.96 1.00 0.83	0.850 0.945 0.291
SPO2096 SPO2097 SPO2098	1.75 1.42 1.19		SPO2094 SPO2095 SPO2096	1.19 1.09 1.53	0.045 SPO2095 0.273 SPO2096 0.071 SPO2097	1.07 1.03 1.04	0.46 SPO2097 0.824 SPO2098 0.92 SPO2099	1.04 1.04 1.17	0.071 SPO209 0.989 SPO209 0.651 SPO209	2.76	0.936 0.200 0.082	SPO2090 SPO2091	1.03 1.08 1.16	0.773	SPO2090 SPO2091 SPO2092	1.20 1.06 1.19	0.799	SPO2088 SPO2089 SPO2090	1.14 0.82 1.13	0.389 0.654 0.266
SPO2099 SPO2100	0.93 0.64	0.899	SPO2097 SPO2098	1.43	0.008 SPO2098 0.878 SPO2099	1.11 1.21	0.974 SPO2100 0.613 SPO2101	1.14 1.02	0.843 SPO209 0.858 SPO209	0.92 1.18	0.513 0.104		1.79 0.75	0.361 0.066	SPO2093 SPO2094	1.14 1.05	0.882 0.846	SPO2091 SPO2092	1.07 1.12	0.802 0.429
SPO2101 SPO2102 SPO2103	1.5 1.03 1.33	0.055 0.516 0.29		0.84 0.71 1.37	0.737 SPO2100 0.072 SPO2101 0.361 SPO2102	1.07 1.02 1.21	0.909 SPO2102 0.908 SPO2103 0.093 SPO2104	1.18 1.08 1.39	0.582 SPO209 0.836 SPO209 0.521 SPO209	0.78	0.663 0.781 0.575	SPO2095 SPO2096 SPO2097	0.96 1.12 0.99	0.271	SPO2095 SPO2096 SPO2097	1.13 0.98 0.95	0.878	SPO2093 SPO2094 SPO2095	1.32 0.88 0.99	0.593 0.389 0.960
SPO2104 SPO2105 SPO2106	0.77 0.86 1.24	0.287 0.468 0.444	SP02102 SP02103 SP02104	1.05 1.32 0.85	0.23 SPO2103 0.209 SPO2104 0.306 SPO2105	0.99 1.3 1.13	0.626 SPO2105 0.767 SPO2106 0.322 SPO2107	1.02 1.31 1.13	0.801 SPO210 0.726 SPO210 0.269 SPO210	1 0.38	0.032 0.068 0.005	SPO2098 SPO2099 SPO2100	0.83 1.34 1.74	0.837 0.388 0.028	SPO2098 SPO2099 SPO2100	0.89 1.15 0.94	0.803	SPO2096 SPO2097 SPO2098	1.00 0.88 0.93	0.955 0.059 0.943
SPO2107 SPO2108 SPO2109	2.55 1.1 0.97	0.054 0.228 0.84	SPO2105 SPO2106 SPO2107	0.93 1.41	0.312 SPO2106 0.464 SPO2107 0.06 SPO2108	1.25	0.436 SPO2108 0 SPO2109 0.352 SPO2110	1.2 1.2	0.06 SPO210 0.032 SPO210 0.923 SPO210	1.25	0.440 0.127 0.279	SPO2101 SPO2102 SPO2103	0.40 0.21 0.82	0.002	SPO2101 SPO2102 SPO2103	1.00 0.98 1.03	0.987	SPO2099 SPO2100 SPO2101	0.99 0.91 0.99	0.995 0.537 0.951
SPO2110 SPO2111	0.85	0.855	SPO2108 SPO2109	1 0.99	0.134 SPO2109 0.806 SPO2110	1.02	0.036 SPO2111 0.91 SPO2112	1.13	0.733 SPO210 0.946 SPO210	0.23 0.39	0.032 0.028	SPO2104 SPO2105	1.11	0.382 0.457	SPO2104 SPO2105	1.06	0.848 0.925	SP02102 SP02103	0.99	0.829
SPO2112 SPO2113 SPO2116	1.02 0.88 1.17	0.479	SP02110 SP02111 SP02112	0.88 1.08 1.07	0.928 SPO2111 0.584 SPO2112 0.899 SPO2113	1.62 1.19 1.11	0.882 SPO2113 0.799 SPO2116 0.069 SPO2117	1.03 1.04 1.21	0.246 SPO210 0.732 SPO210 0.696 SPO211	2.39	0.388 0.018 0.653	SPO2107	0.23 0.37 0.85	0.011	SPO2106 SPO2107 SPO2108	0.76 0.85 0.68	0.404	SPO2104 SPO2105 SPO2106	1.09 1.09 0.81	0.603 0.776 0.384
SPO2117 SPO2118 SPO2119	1.22 1.06 0.95		SPO2113 SPO2116 SPO2117	0.84 1.12 0.91	0.012 SPO2116 0.66 SPO2117 0.732 SPO2118	1.06 1.06 1.21	0.875 SPO2118 0.303 SPO2119 0.875 SPO2120	1.32 1.02 1.12	0.932 SPO211 0.166 SPO211 0.75 SPO211	0.63	0.335 0.109 0.632		2.31 1.48 0.74		SPO2109 SPO2110 SPO2111	1.08 1.05 0.72	0.946	SP02107 SP02108 SP02109	1.05 0.71 1.13	0.915 0.024 0.289
SPO2120 SPO2121 SPO2122	0.8 1.21 1.13	0.827 0.224	SPO2118 SPO2119 SPO2120	1.06 1.05	0.931 SPO2119 0 SPO2120 0.618 SPO2121	1.14 1.13 1.18	0.674 SPO2121 0.395 SPO2122 0.356 SPO2123	1.17 1.13	0.033 SPO211 0.104 SPO211 0.949 SPO211	7 0.46	0.571 0.216 0.740	SPO2112 SPO2113 SPO2116	0.85 1.03 1.02	0.975 0.232	SPO2112 SPO2113 SPO2116	0.91 0.86 0.86	0.865 0.384	SPO2110 SPO2111 SPO2112	1.08 0.80	0.920 0.474 0.992
SPO2123 SPO2124	1.13 0.83 1.27	0.593	SPO2121 SPO2122	1.15 1.18	0.265 SPO2122 0.01 SPO2123	1.12 1.18	0.117 SPO2124 0.971 SPO2125	1.19 1.33	0.638 SPO211 0.623 SPO212	0.83	0.854 0.272	SPO2117 SPO2118	0.45 0.72	0.054 0.785	SPO2117 SPO2118	0.68 0.91	0.647 0.904	SPO2113 SPO2116	0.97 0.92	0.871 0.645
SPO2125 SPO2126 SPO2127	2.1 1.63 1.04		SPO2123 SPO2124 SPO2125	0.83 1.26 1.7	0.693 SPO2124 0.162 SPO2125 0.082 SPO2126	1.09 1.02 1.1	0.517 SPO2126 0.534 SPO2127 0.778 SPO2128	1.26 1.03 1.22	0.408 SPO212 0.272 SPO212 0.6 SPO212		0.068 0.078 0.351	SPO2120	1.09 0.86 0.57		SPO2119 SPO2120 SPO2121	1.66 1.10 1.10	0.677	SP02117 SP02118 SP02119	0.68 0.90 1.18	0.555 0.931 0.373
SPO2128 SPO2129 SPO2130	1.01 1.7 1.79		SPO2126	1.52 1.04 0.99	0.009 SPO2127 0.725 SPO2128 0.984 SPO2129	1.1 1.14 1.24	0.517 SPO2129 0.401 SPO2130 0.695 SPO2131	1.15 1.05 1.25	0.883 SPO212 0.788 SPO212 0.059 SPO212	1.74	0.036 0.197 0.306	SPO2122 SPO2123 SPO2124	1.34 0.58 1.74		SPO2122 SPO2123 SPO2124	1.15 0.99 1.14	0.496 0.991	SPO2120 SPO2121 SPO2122	1.03 1.07 1.01	0.943 0.719 0.964
SPO2131 SPO2132	0.95 1.63	0.705 0.13	SPO2129 SPO2130	1.71 1.72	0.619 SPO2130 0.074 SPO2131	1.22 0.99	0.635 SPO2132 0.071 SPO2133	1.35 1.17	0.5 SPO212 0.509 SPO212	7 0.72 3 0.93	0.310 0.475	SPO2125 SPO2126	1.31 0.79	0.134 0.106	SPO2125 SPO2126	1.16 1.07	0.238 0.217	SPO2123 SPO2124	0.94 1.10	0.891 0.553
SPO2133 SPO2134 SPO2135	1.42 0.54 1.32	0.19 0.079	SPO2131 SPO2132 SPO2133	1.04 1.55 1.28	0.558 SPO2132 0.128 SPO2133 0.106 SPO2134	1.19 1.38 1.33	0.18 SPO2134 0.39 SPO2135 0.322 SPO2136	1.08 1.06 1.06	0.107 SPO212 0.207 SPO213 0.073 SPO213	0.15		SPO2127 SPO2128 SPO2129	0.65 0.97 0.41	0.320 0.085	SPO2127 SPO2128 SPO2129	0.78 0.79 1.20	0.153 0.723	SP02125 SP02126 SP02127	1.23 0.99 0.83	0.403 0.937 0.487
SPO2136 SPO2137 SPO2139	1.01 0.95 0.93	0.902	SPO2134 SPO2135 SPO2136	0.54 1.09 1.01	0.09 SPO2135 0.631 SPO2136 0.568 SPO2137	1.24 1.15 1.13	0.023 SPO2137 0.012 SPO2139 0.422 SPO2140	1.1 0.99 1.1	0.082 SPO213 0.428 SPO213 0.323 SPO213	2.76	0.680 0.001 0.174	SPO2131	0.15 0.12 1.05	0.001	SPO2130 SPO2131 SPO2132	1.07 1.13 1.09	0.224	SPO2128 SPO2129 SPO2130	0.93 1.13 0.95	0.912 0.810 0.885
SPO2140	1.25		SP02137	0.97	0.947 SPO2139	1.08	0.01 SPO2141	1.19	0.118 SPO213			SPO2133	2.66		SPO2133	1.02		SP02131	1.10	0.111

SPO2141 SPO2142	1.1		SP02139 SP02140	0.98	0.839	SPO2140 SPO2141	1.13		SPO2142 SPO2143	1.03	0.349	SPO2136 SPO2137	2.46 0.86	0.008 0.717	SPO2134 SPO2135	1.97	0.012	SPO2134 SPO2135	1.57	0.365 SPO2132 0.117 SPO2133		0.453
SPO2143 SPO2144	1.01 1.38	0.026	SPO2141 SPO2142	0.97 0.97	0.957	SPO2142 SPO2143	1.09 1.04	0.568 0.874	SPO2144 SPO2145	1.12 1.02	0.042 0.552	SPO2139 SPO2140	1.42 1.17	0.214 0.385	SPO2136 SPO2137	2.30 0.85	0.004 0.285	SPO2136 SPO2137	0.96 0.88	0.981 SPO2134 0.747 SPO2135	1.32 0.83	0.118
SPO2145 SPO2146 SPO2147	0.98 1.11 1.32		SPO2143 SPO2144 SPO2145	1.05 1.29 1.03	0.067	SPO2144 SPO2145 SPO2146	1.02 1.01 1.29	0.04	SPO2146 SPO2147 SPO2148	1.04 1.04 1.24	0.296 0.409 0.914	SPO2141 SPO2142 SPO2143	0.62 1.10 1.07	0.156 0.260 0.546	SPO2140 SPO2141	1.42 1.20 0.65		SPO2139 SPO2140 SPO2141	0.96 1.06 0.83	0.911 SPO2136 0.847 SPO2137 0.493 SPO2139	0.92	0.463 0.612 0.827
SPO2148 SPO2149	1.04 0.97		SPO2146 SPO2147	1.13 1.33	0.199	SPO2147 SPO2148	1.03 1.02	0.102 0.906	SPO2149 SPO2150	1.05	0.394 0.554	SPO2144 SPO2145	1.12 0.92	0.042 0.782	SPO2142 SPO2143	1.10 1.12	0.353 0.409	SPO2142 SPO2143	1.11 1.06	0.488 SPO2140 0.731 SPO2141	1.03 0.87	0.853
SPO2150 SPO2151 SPO2152	0.6 1.14	0.007	SPO2148 SPO2149 SPO2150	1.02 1.01		SPO2149 SPO2150 SPO2151	1.11 0.99 1.02		SPO2151 SPO2152 SPO2153	1.16 1.11 0.98	0.049 0.053 0.545	SPO2146 SPO2147 SPO2148	1.37 1.71 1.00	0.196 0.054 0.319	SPO2144 SPO2145 SPO2146	1.14 0.89 1.38	0.011 0.442 0.019	SPO2144 SPO2145 SPO2146	1.13 1.04 1.15	0.190 SPO2142 0.676 SPO2143 0.459 SPO2144	1.14	0.339 0.559 0.011
SPO2153 SPO2154	1.15 0.43	0.196	SPO2151 SPO2152	0.68 1.02		SPO2152 SPO2153	1.11	0.964	SPO2154 SPO2155	1.48	0.348	SPO2149 SPO2150 SPO2151	0.78 0.85	0.307	SPO2147 SPO2148 SPO2149	1.59 0.94		SPO2147 SPO2148	1.11 0.94	0.402 SPO2145 0.380 SPO2146	1.14	0.437
SPO2155 SPO2156 SPO2157	0.95 1.55 1.65	0.558 0.027	SPO2153 SPO2154 SPO2155	0.41 0.99		SPO2154 SPO2155 SPO2156	1.07 1.11 1.04		SPO2156 SPO2157 SPO2158	1.22 1.76 3.83	0.933 0.466 0.046	SPO2152 SPO2153	1.54 1.08 1.32	0.008 0.115 0.309	SPO2150 SPO2151	0.76 0.91 1.52	0.057 0.981 0.018	SPO2149 SPO2150 SPO2151	0.93 0.89 1.06	0.645 SPO2147 0.577 SPO2148 0.447 SPO2149	0.95	0.195 0.245 0.664
SPO2158 SPO2159 SPO2160	1.47 0.6 0.52	0.127	SPO2156 SPO2157 SPO2158	1.43 1.54 1.32	0.037	SPO2157 SPO2158 SPO2159	1.13 1.08 1.12	0.092	SPO2159 SPO2160 SPO2161	2.69 1.59 1.17	0.08 0.254 0.269	SPO2154 SPO2155 SPO2156	2.45 0.83 0.63	0.158 0.466 0.674	SPO2152 SPO2153 SPO2154	1.06 1.47	0.037	SPO2152 SPO2153 SPO2154	1.05	0.570 SPO2150 0.696 SPO2151 0.197 SPO2152	1.11	0.428 0.093 0.528
SPO2161 SPO2162	0.79 0.73	0.106 0.142	SPO2159 SPO2160	0.56 0.5	0.025	SPO2160 SPO2161	1.32 1.01	0.274	SPO2162 SPO2163	1.05 1.09	0.651 0.566	SPO2157 SPO2158	0.42 0.48	0.028 0.021	SPO2155 SPO2156	0.78 0.66	0.492 0.765	SPO2155 SPO2156	0.93 0.97	0.809 SPO2153 0.992 SPO2154	1.04 1.82	0.681 0.266
SPO2163 SPO2164 SPO2165	0.76 1.17 1.22	0.35 0.338 0.474	SPO2161 SPO2162 SPO2163	0.83 0.81 0.99	0.279		1.1 1.02 1.32		SPO2164 SPO2165 SPO2166	1.05 1.04 1.29	0.387 0.143 0.163	SPO2159 SPO2160 SPO2161	2.26 2.71 1.84	0.051 0.046 0.032	SPO2157 SPO2158 SPO2159	0.40 0.49	0.039 0.028 0.025	SPO2157 SPO2158 SPO2159	0.96 1.00 1.92	0.986 SPO2155 0.956 SPO2156 0.088 SPO2157	0.95	0.867 0.965 0.982
SPO2166 SPO2167	1.53 0.92	0.024 0.575	SPO2164 SPO2165	1.25 1.18	0.282 0.432	SPO2165 SPO2166	1.03 1.08	0.357 0.334	SPO2167 SPO2168	1.11 1.05	0.142 0.543	SPO2162 SPO2163	0.68 0.62	0.026 0.103	SPO2160 SPO2161	2.63 1.94	0.048	SPO2160 SPO2161	1.50 0.86	0.221 SPO2158 0.540 SPO2159	0.94 1.87	0.698 0.041
SPO2168 SPO2169 SPO2170	1.72 1.62 0.46	0.005	SPO2166 SPO2167 SPO2168	1.39 0.89 1.7		SPO2167 SPO2168 SPO2169	1.09 1.18 1.22	0.528	SPO2169 SPO2170 SPO2171	1.2 1.03 1.19	0.032 0.326 0.612	SPO2164 SPO2165 SPO2166	0.97 0.68 0.63	0.676 0.084 0.004	SPO2162 SPO2163 SPO2164	0.65 0.60 1.16	0.021 0.071 0.607	SPO2162 SPO2163 SPO2164	0.83 0.62 1.05	0.437 SPO2160 0.144 SPO2161 0.977 SPO2162	0.95	0.405 0.762 0.198
SPO2171 SPO2173 SPO2174	0.85 1.02 1.08		SPO2169 SPO2170 SPO2171	1.51 0.51 0.81	0.012	SPO2170 SPO2171	1.07 1.47 1.06	0.588 0.771	SP02173 SP02174 SP02176	1.04 1.03 1.03	0.973 0.814 0.643	SPO2167 SPO2168	1.56 1.47 1.03	0.006 0.118 0.581	SPO2165 SPO2166	0.65 0.64 1.63	0.037 0.039 0.012	SPO2165 SPO2166 SPO2167	0.97 0.97 1.01	0.897 SPO2163 0.772 SPO2164 0.794 SPO2165		0.018 0.932 0.287
SP02176 SP02177	0.96 1.15	0.958	SPO2171 SPO2174	0.93	0.826	SPO2174 SPO2176	1.24	0.641	SPO2176 SPO2177 SPO2178	1.12	0.976	SPO2170 SPO2171	2.04 1.88	0.142	SPO2168 SPO2169	1.39	0.107	SPO2168 SPO2169	1.19	0.671 SPO2166 0.491 SPO2167	0.84	0.185 0.326
SPO2178 SPO2179 SPO2180	1.15 1.04 0.73	0.712	SPO2176 SPO2177 SPO2178	0.88 1.08 1.09	0.949	SPO2177 SPO2178 SPO2179	1.1 1.06 1.07	0.76	SPO2179 SPO2180 SPO2181	1.08 1.29 1.27	0.137 0.47 0.164	SPO2174 SPO2176	0.83 1.35 0.82	0.471 0.162 0.208	SPO2170 SPO2171 SPO2173	1.82 1.89 0.91	0.250 0.006 0.402	SPO2170 SPO2171 SPO2173	1.23 1.26 1.05	0.360 SPO2168 0.759 SPO2169 0.550 SPO2170		0.410
SPO2181 SPO2182	1.18 1.03	0.087 0.589	SPO2179 SPO2180	1 0.73	0.77	SPO2180 SPO2181	1.07 0.99	0.66 0.861	SPO2182 SPO2183	1.05 1.16	0.544 0.84	SPO2178 SPO2178	0.91 0.94	0.970 0.863	SPO2174 SPO2176	1.26 0.97	0.289 0.778	SPO2174 SPO2176	1.08 1.02	0.781 SPO2171 0.792 SPO2173	1.12 1.01	0.317
SPO2183 SPO2184 SPO2185	1.04 0.71 0.82	0.154	SPO2181 SPO2182 SPO2183	1.07 1.05 0.98	0.603	SPO2182 SPO2183 SPO2184	0.99 1.25 1.03	0.889	SPO2184 SPO2185 SPO2186	1.34 0.99 1.33	0.004 0.757 0.649	SPO2179 SPO2180 SPO2181	0.63 0.72 0.81	0.089 0.263 0.277	SPO2177 SPO2178 SPO2179	0.88 0.96 0.58	0.964 0.821 0.077	SPO2177 SPO2178 SPO2179	0.92 0.95 0.95	0.959 SPO2174 0.879 SPO2176 0.892 SPO2177	1.05	0.547 0.554 0.962
SPO2186 SPO2187	0.79 0.78	0.303 0.035	SPO2184 SPO2185	0.65 0.82	0.065 0.106	SPO2185 SPO2186	1.1 1.27	0.876 0.825	SPO2187 SPO2188	1.26 1.19	0.033	SPO2182 SPO2183	0.82 0.78	0.309 0.759	SPO2180 SPO2181	0.73 0.85	0.339 0.534	SPO2180 SPO2181	1.57 0.92	0.091 SPO2178 0.571 SPO2179	0.93 0.93	0.851 0.713
SPO2188 SPO2189 SPO2190	1.26 1.27 0.91	0.006 0.643	SPO2186 SPO2187 SPO2188	0.73 0.71 1.25	0.603	SPO2187 SPO2188 SPO2189	1.04 1.19 1.03	0.979 0.393	SPO2189 SPO2190 SPO2191	1.08 1.03 1.06	0.137 0.902 0.842	SPO2184 SPO2185 SPO2186	1.70 1.74 1.87	0.010 0.036 0.017	SPO2182 SPO2183 SPO2184	0.79 0.80 2.01	0.001	SPO2182 SPO2183 SPO2184	1.00 0.84 1.51	0.888 SPO2180 0.813 SPO2181 0.054 SPO2182	0.99 1.01	0.079 0.948 0.990
SPO2191 SPO2192 SPO2193	0.88 0.82 0.87	0.892 0.792	SPO2189 SPO2190 SPO2191	1.29 1.04 0.93	0.049 0.646	SPO2190	1.1 1.17 1.03	0.957 0.824	SPO2192 SPO2193 SPO2194	1.18 1.11 1.05	0.861 0.913 0.378	SPO2187 SPO2188 SPO2189	1.13 1.17 1.12	0.063 0.759 0.340	SPO2185 SPO2186 SPO2187	1.85 1.98 1.18	0.014 0.002 0.005	SPO2185 SPO2186 SPO2187	1.12 0.97 1.07	0.586 SPO2183 0.995 SPO2184 0.181 SPO2185	0.83 1.45	0.838 0.028 0.067
SPO2194 SPO2195	1.07 0.91	0.636 0.89	SPO2192 SPO2193	0.85 0.81	0.71 0.219	SPO2193 SPO2194	1.08 1.19	0.998 0.897	SPO2195 SPO2196	1.28 1.1	0.481 0.823	SPO2190 SPO2191	1.07 0.97	0.384 0.924	SPO2188 SPO2189	1.14 1.16	0.800 0.035	SPO2188 SPO2189	1.10 1.00	0.904 SPO2186 0.970 SPO2187	1.07 1.07	0.579
SPO2196 SPO2197 SPO2198	1.12 1.24 0.58		SPO2194 SPO2195 SPO2196	1.03 1.04 1.12		SPO2195 SPO2196 SPO2197	1.05 1.41	0.852	SPO2197 SPO2198 SPO2199	1.03 1.19 1.14	0.598 0.035 0.097	SPO2192 SPO2193 SPO2194	1.16 1.04 1.68	0.540 0.661 0.051	SPO2190 SPO2191 SPO2192	0.99 0.83 1.06	0.932 0.785 0.801	SPO2190 SPO2191 SPO2192	0.96 0.89 0.99	0.808 SPO2188 0.604 SPO2189 0.970 SPO2190	1.12	0.914 0.326 0.990
SPO2199 SPO2200	1.88 1.27	0.037 0.557	SPO2197 SPO2198	1.11 0.54	0.564 0.042	SPO2198 SPO2199	1.13	0.068 0.211	SPO2200 SPO2201	1.07 1.06	0.585 0.447	SPO2195 SPO2196	0.60 0.59	0.017 0.257	SPO2193 SPO2194	0.98 1.76	0.976 0.058	SPO2193 SPO2194	0.93 1.16	0.567 SPO2191 0.638 SPO2192	0.91 0.93	0.787 0.693
SPO2201 SPO2202 SPO2203	0.79 1.14 0.91	0.681	SPO2199 SPO2200 SPO2201	1.56 1.12 0.87	0.723	SPO2200 SPO2201 SPO2202	1.1 1.02 1.16	0.321	SPO2202 SPO2203 SPO2204	1.03 1.14 1.13	0.771 0.81 0.073	SPO2197 SPO2198 SPO2199	0.58 2.14 0.65	0.222 0.068 0.165	SPO2195 SPO2196 SPO2197	0.62 0.61 0.54	0.038 0.333 0.059	SPO2195 SPO2196 SPO2197	0.90 0.94 0.89	0.504 SPO2193 0.882 SPO2194 0.702 SPO2195	1.10	0.803 0.676 0.088
SPO2204 SPO2205 SPO2206	0.68 0.79	0.344	SPO2202 SPO2203 SPO2204	1.07 0.91 0.76	0.895	SPO2203 SPO2204 SPO2205	1.16 1.04 1.17	0.103	SPO2205 SPO2206 SPO2207	1.16 1.3 1.18	0.723	SPO2200 SPO2201 SPO2202	0.82	0.819 0.015 0.890	SPO2198 SPO2199 SPO2200	2.24 0.64 0.87	0.102	SPO2198 SPO2199 SPO2200	0.93 0.81 0.89	0.795 SPO2196 0.314 SPO2197 0.832 SPO2198	0.95	0.888 0.885 0.347
SP02206 SP02207 SP02208	0.55 1.33	0.092	SPO2204 SPO2205 SPO2206	0.76 0.81 0.85	0.144	SPO2205 SPO2206 SPO2207	1.17 1.12 1.56	0.464	SPO2208 SPO2209	0.99 1.35	0.188 0.992 0.146	SPO2203 SPO2204	0.92 0.89 1.55	0.890 0.975 0.140	SPO2201 SPO2202	0.87 0.47 0.96	0.026	SPO2201 SPO2202	0.90 0.92	0.499 SPO2199 0.814 SPO2200	0.80	0.362
SPO2209 SPO2210 SPO2211	0.63 0.84 1.02	0.094	SPO2207 SPO2208 SPO2209	0.55 1.26 0.69		SPO2208 SPO2209 SPO2210	1.33 1.2 1.08	0.493	SPO2210 SPO2211 SPO2212	1.09 1.04 1.04	0.045 0.642 0.934	SPO2205 SPO2206 SPO2207	0.83 0.95	0.550 0.975 0.071	SPO2203 SPO2204 SPO2205	0.91 1.35 0.79	0.926 0.261 0.206	SPO2203 SPO2204 SPO2205	0.88 1.16 1.00	0.777 SPO2201 0.401 SPO2202 0.976 SPO2203	0.89	0.236 0.763 0.513
SPO2212 SPO2213	1.23 1.2	0.764 0.17	SPO2210 SPO2211	0.71 0.96	0.036	SPO2211 SPO2212	0.98	0.869 0.957	SPO2213 SPO2214	1.1 1.17	0.659 0.895	SPO2208 SPO2209	1.06	0.816 0.567	SPO2206 SPO2207	1.11 2.02	0.746	SPO2206 SPO2207	1.20 1.02	0.223 SPO2204 0.875 SPO2205	1.19 0.96	0.236 0.797
SP02214 SP02215 SP02216	0.89 0.89 0.8	0.87 0.659 0.492	SPO2212 SPO2213 SPO2214	1.27 0.96 0.83	0.699 0.934 0.691	SP02214	1.21 1.08	0.708	SPO2215 SPO2216 SPO2217	1.12 1.24 1.17	0.677 0.962 0.951	SPO2210 SPO2211 SPO2212	0.45 1.16 1.47	0.004 0.698 0.669	SPO2208 SPO2209 SPO2210	1.05 0.63 0.43		SPO2208 SPO2209 SPO2210	1.11 0.90 0.98	0.472 SPO2206 0.725 SPO2207 0.860 SPO2208	0.97	0.906 0.986 0.832
SP02217 SP02218	0.93 0.91 0.85		SPO2215 SPO2216	0.91 0.94 0.96	0.704 0.953 0.983	SP02217	1.01 1.15 0.99		SPO2218 SPO2219 SPO2220	1.45 1.15 1.04	0.891 0.732 0.954	SPO2213 SPO2214 SPO2215	1.47 0.77 1.25	0.098 0.363 0.256	SPO2211 SPO2212 SPO2213	1.25 1.75 1.45		SPO2211 SPO2212 SPO2213	0.99 1.07 1.19	0.961 SPO2209 0.964 SPO2210	0.95	0.528 0.862 0.921
SPO2219 SPO2220 SPO2221	0.85 0.85		SPO2217 SPO2218 SPO2219	0.96 0.92 0.89		SPO2219	1.08 1.02	0.764	SPO2221 SPO2222	1.04 1.16 1.15	0.954 0.202 0.519	SPO2216 SPO2217	1.25 1.00 0.98	0.256 0.937 0.977	SPO2214 SPO2215	0.76 1.24		SPO2214 SPO2215	1.04	0.466 SPO2211 0.965 SPO2212 0.500 SPO2213	1.05	0.974
SPO2222 SPO2223 SPO2224	0.97 1.01 0.97	0.858	SPO2220 SPO2221 SPO2222	0.88 0.84 0.93	0.182	SPO2221 SPO2222 SPO2223	1.37 1.01 1.18	0.45	SPO2223 SPO2224 SPO2225	1.05 1.12 1.05	0.24 0.651 0.749	SPO2218 SPO2219 SPO2220	0.87 1.66 0.72	0.920 0.640 0.276	SPO2216 SPO2217 SPO2218	0.84 0.99 0.85	0.673 0.975 0.940	SPO2216 SPO2217 SPO2218	0.96 1.11 1.12	0.848 SPO2214 0.854 SPO2215 0.498 SPO2216	1.01	0.970 0.974 0.819
SPO2225 SPO2226	1.09	0.698 0.447	SPO2223 SPO2224	1.04 0.95	0.134 0.576	SPO2224 SPO2225	1.25 1.08	0.836 0.982	SPO2226 SPO2227	1.06	0.944 0.805	SPO2221 SPO2222	0.96 0.16	0.717 0.017	SPO2219 SPO2220	1.61 0.71	0.608	SPO2219 SPO2220	0.84 1.01	0.878 SPO2217 0.994 SPO2218	0.99 1.05	0.964 0.757
SPO2227 SPO2228 SPO2229	1.11 0.62 0.79	0.094	SPO2225 SPO2226 SPO2227	1.04 2.12 1.02	0.24	SPO2226 SPO2227 SPO2228	1.06 1.14 1.3	0.774	SPO2228 SPO2229 SPO2230	1.38 1.01 1.17	0.278 0.2 0.136	SPO2223 SPO2224 SPO2225	0.66 0.68 1.02	0.035 0.096 0.824	SPO2222	1.02 0.18 0.65	0.926 0.006 0.010	SPO2221 SPO2222 SPO2223	1.37 1.00 1.11	0.202 SPO2219 0.950 SPO2220 0.331 SPO2221	1.00	0.995 0.964 0.089
SPO2230 SPO2231 SPO2232	0.58 0.88 0.93	0.187	SPO2228 SPO2229 SPO2230	0.74 0.76 0.67	0.322	SPO2229 SPO2230 SPO2231	1.08 1.34 1.36	0.221	SP02231 SP02232 SP02233	1.33 1 1.14	0.357 0.465 0.358	SPO2226 SPO2227 SPO2228	1.42 1.53 1.18	0.705 0.255 0.148		0.65 1.05 1.21	0.846	SPO2224 SPO2225 SPO2226	1.05 0.85 1.19	0.764 SPO2222 0.576 SPO2223 0.829 SPO2224	1.08	0.892 0.164 0.698
SPO2233 SPO2234	1.63 0.64	0.003 0.071	SPO2231 SPO2232	1.01 0.99	0.922	SPO2232 SPO2233	1.18 1.12	0.541 0.398	SPO2234 SPO2235	1.09 1.1	0.215 0.741	SPO2229 SPO2230	1.76 1.23	0.131 0.072	SPO2227 SPO2228	1.70 1.12	0.137 0.357	SPO2227 SPO2228	0.91 1.10	0.703 SPO2225 0.627 SPO2226	0.93 1.00	0.753 0.983
SPO2235 SPO2236 SPO2237	1.19 1 0.92	0	SPO2233 SPO2234 SPO2235	1.29 0.7 1.02		SPO2234 SPO2235 SPO2236	1.27 1.29	0.988	SPO2236 SPO2237 SPO2238	1.04 1.06 1.2	0.391 0.399	SPO2231 SPO2232 SPO2233	0.86 0.53 0.56	0.744 0.027 0.035	SPO2229 SPO2230 SPO2231	1.85 1.20 0.85	0.035	SPO2229 SPO2230 SPO2231	1.05 0.95 0.97	0.857 SPO2227 0.989 SPO2228 0.604 SPO2229	1.14	0.970 0.549 0.479
SPO2238 SPO2239	1.09	0.533 0.575	SPO2236 SPO2237	1.05 0.9	0.668	SPO2237 SPO2238	1.34 1.16	0.334 0.808	SPO2239 SPO2240	1 1.56	0.345 0.568	SPO2234 SPO2235	1.09 0.48	0.071 0.264	SPO2232 SPO2233	0.62 0.57	0.008	SPO2232 SPO2233	1.03 0.87	0.967 SPO2230 0.005 SPO2231	0.99 0.95	0.705 0.872
SPO2241 SPO2242	0.48 0.67 0.79	0.044 0.135	SPO2238 SPO2239 SPO2240	1.07 0.99 0.54	0.842 0.139		1.24 1.08 1.05	0.765 0.522	SP02241 SP02242 SP02243	1.1 1.1 1.14	0.175 0.309 0.074	SPO2236 SPO2237 SPO2238	1.60 0.93 1.07	0.347 0.472 0.725	SPO2234 SPO2235 SPO2236	0.95 0.39 2.15	0.182	SPO2234 SPO2235 SPO2236	1.15 0.79 2.01	0.076 SPO2232 0.687 SPO2233 SPO2234	0.87 1.07	0.432 0.056 0.534
SP02243 SP02244 SP02245	0.87 0.76 0.57	0.249 0.503	SP02241 SP02242 SP02243	0.69 0.79 0.8		SPO2242 SPO2243	1.09 1.26 1.17	0.139 0.08	SPO2244 SPO2245 SPO2246	1.34 1.33 1.2	0.823 0.515 0.174	SPO2239 SPO2240 SPO2241	1.41 0.23 0.24	0.244 0.035 0.003	SPO2237 SPO2238 SPO2239	0.88 0.96 1.32	0.566	SPO2237 SPO2238 SPO2239	1.46 1.16 1.07	0.116 SPO2235 0.064 SPO2236 0.827 SPO2237	0.79 1.65	0.365
SPO2246 SPO2247	1.25 0.84	0.222 0.077	SPO2244 SPO2245	0.77 0.63	0.298	SPO2245 SPO2246	1.09 1.02	0.793 0.314	SPO2247 SPO2248	0.98 1.09	0.043 0.507	SPO2242 SPO2243	0.28 1.69	0.019 0.026	SPO2240 SPO2241	0.24 0.21	0.006	SPO2240 SPO2241	1.29 1.03	0.694 SPO2238 0.675 SPO2239	1.22 1.07	0.399 0.538
SPO2248 SPO2249 SPO2250	0.88 1.84 0.99	0.08	SPO2246 SPO2247 SPO2248	1.36 0.88 0.93		SPO2247 SPO2248 SPO2249	1.23 1.01 1.02		SPO2249 SPO2250 SPO2251	1.59 1.22 1.3	0.846 0.564 0.857	SPO2244 SPO2245 SPO2246	0.98 0.72 0.12	0.811 0.212 0.001	SPO2242 SPO2243 SPO2244	0.31 1.73 1.23	0.006 0.012 0.461	SPO2242 SPO2243 SPO2244	1.22 1.35 1.04	0.453 SPO2240 0.074 SPO2241 0.980 SPO2242		0.399 0.315 0.032
SPO2251 SPO2252 SPO2253	2.11 5.5	0.091 0.018	SPO2249 SPO2250 SPO2251	1.58 0.88 1.98	0.06	SPO2250 SPO2251 SPO2252	1.04 1.15	0.582 0.67	SPO2252 SPO2253 SPO2255	1.08 0.99	0.449 0.165 0.801	SPO2247 SPO2248 SPO2249	0.27 0.86 0.85	0.001 0.447 0.470	SPO2245 SPO2246 SPO2247	0.68 0.10	0.176 0.005 0.001	SPO2245 SPO2246 SPO2247	1.07 0.93	0.800 SPO2243 0.865 SPO2244 0.700 SPO2245	1.30 0.94	0.056 0.639 0.869
SPO2255 SPO2256	2.5 2.82 1.45	0.108	SPO2252 SPO2253	4.02 2.06	0.009	SPO2253 SPO2255	1.2 1.17	0.933 0.644	SPO2256 SPO2257	1.02 1.21	0.751 0.267	SPO2250 SPO2251	0.93 0.42	0.840	SPO2248 SPO2249	0.96 0.94	0.593 0.480	SPO2248 SPO2249	1.14 1.23	0.684 SPO2246 0.612 SPO2247	0.99	0.894 0.346
SPO2257 SPO2258 SPO2259	4.47 1.79 2.03	0.714	SPO2255 SPO2256 SPO2257	2.18 1.14 4.82	0.605	SPO2256 SPO2257 SPO2258	1.04 1.16 1.17	0.726	SPO2258 SPO2259 SPO2260	1.03 1.03 1.08	0.955 0.922 0.858	SPO2252 SPO2253 SPO2255	0.38 0.51 0.51	0.026 0.248 0.184		0.97 0.49 0.50		SPO2250 SPO2251 SPO2252	1.12 0.65 0.91	0.706 SPO2248 0.451 SPO2249 0.540 SPO2250	1.01	0.981 0.925 0.574
SPO2260 SPO2261	1.96 9.77	0.111 0.004	SPO2258 SPO2259	1.39	0.857 0.601	SPO2259 SPO2260	1.14 1.15	0.959 0.832	SPO2261 SPO2262	1.13	0.068 0.719	SPO2256 SPO2257	0.58 0.29	0.285 0.022	SPO2253 SPO2255	0.57 0.56	0.017 0.091	SPO2253 SPO2255	1.04 0.99	0.994 SPO2251 0.937 SPO2252	0.80 0.81	0.706
SPO2262 SPO2263 SPO2264	6.77 4.95	0.018 0.117 0.018	SPO2260 SPO2261 SPO2262	7.11 7.69	0.214 0.002 0.002	SPO2261 SPO2262 SPO2263	1.06 1.36 1.08	0.905	SPO2263 SPO2264 SPO2266	0.99 1.06 1.32	0.805 0.266 0.255	SPO2258 SPO2259 SPO2260	0.47 0.48 0.49	0.649 0.369 0.519	SPO2256 SPO2257 SPO2258	0.64 0.29 0.51	0.001	SPO2256 SPO2257 SPO2258	0.81 0.71 0.96	0.555 SPO2253 0.205 SPO2255 0.972 SPO2256	1.02	0.779 0.920 0.269
SPO2266 SPO2267	1.37	0.46 0	SPO2263 SPO2264	3.07 11.4	0.192 0.003	SPO2264 SPO2266	1.1 1.04	0.9 0.853	SPO2267 SPO2268	1.01 1.17	0.163 0.377	SPO2261 SPO2262	0.08 0.12	0.000 0.006	SPO2259 SPO2260	0.53 0.51	0.497 0.232	SPO2259 SPO2260	0.72 0.94	0.557 SPO2257 0.922 SPO2258	0.80 0.95	0.242
SPO2268 SPO2269 SPO2270	1.04 1.22 1.38	0.068	SP02266 SP02267 SP02268	0.94 0.92 1.02	0.42	SPO2267 SPO2268 SPO2269	1.1 1.16 1.39	0.798 0.635	SPO2269 SPO2270 SPO2271	1.3 1.12 1.08	0.448 0.239 0.158	SPO2263 SPO2264 SPO2266	0.34 0.11 0.69	0.006 0.003 0.271	SPO2261 SPO2262 SPO2263	0.09 0.13 0.35	0.005 0.002	SPO2261 SPO2262 SPO2263	0.81 0.87 0.91	0.241 SPO2259 0.234 SPO2260 0.649 SPO2261	1.02 0.87	0.766 0.991 0.569
SP02271 SP02272 SP02273	1.32 1.18 1.27	0.309	SP02269 SP02270 SP02271	1.3 1.45 1.18	0.079	SPO2270 SPO2271	1.04 1.23 1.04	0.187 0.736	SP02272 SP02273 SP02274	1.12 1.3 1.18	0.922 0.018 0.932	SPO2267 SPO2268 SPO2269	1.12 0.93 0.68	0.969 0.588 0.094	SPO2264 SPO2266 SPO2267	0.12 0.66 0.98		SPO2264 SPO2266 SPO2267	0.50 0.92 1.17	0.180 SPO2262 0.861 SPO2263 SPO2264	0.91	0.418 0.850 0.004
SPO2274 SPO2275	1.33	0.025 0.872	SPO2272 SPO2273	1.11 1.17	0.094 0.014	SPO2273 SPO2274	1.3 1.39	0.108 0.35	SPO2275 SPO2276	1.36 1.31	0.007	SPO2270 SPO2271	1.51 1.09	0.016 0.035	SPO2268 SPO2269	1.06 0.76	0.485 0.025	SPO2268 SPO2269	1.06 0.90	0.701 SPO2266 0.438 SPO2267	1.04 1.02	0.927 0.948
SPO2276 SPO2277 SPO2278	0.88 0.71 0.49	0.161	SPO2274 SPO2275 SPO2276	1.16 0.99 0.93	0.823	SPO2275 SPO2276 SPO2277	1.45 1.08 1.27	0.066	SPO2277 SPO2278 SPO2279	1.21 1.12 1.12	0.565 0.471 0.294	SPO2272 SPO2273 SPO2274	0.48 0.98 0.92		SPO2270 SPO2271 SPO2272	1.43 1.09 0.46	0.007 0.125 0.013	SPO2270 SPO2271 SPO2272	0.95 1.05 0.98	0.869 SPO2268 0.277 SPO2269 0.774 SPO2270	0.88	0.851 0.434 0.981
SPO2279 SPO2280	0.52 0.87	0.059 0.173	SPO2277 SPO2278	0.8 0.53	0.464 0.094	SPO2278 SPO2279	1.15 1.21	0.614 0.418	SPO2280 SPO2281	1.3 1.33	0.388 0.037	SPO2275 SPO2276	1.24 1.85	0.021 0.037	SPO2273 SPO2274	1.00	0.061 0.073	SPO2273 SPO2274	0.81 1.11	0.005 SPO2271 0.183 SPO2272	1.05 1.01	0.531 0.949
SPO2281 SPO2282 SPO2283	0.93 1.08 2.23	0.133	SPO2279 SPO2280 SPO2281	0.49 0.88 1.08		SPO2280 SPO2281 SPO2282	1.03 1.09 1.07	0.423	SPO2282 SPO2283 SPO2284	1.32 1.07 1.11	0.036 0.345 0.732	SPO2277 SPO2278 SPO2279	1.50 1.38 1.80	0.008 0.264 0.027	SPO2275 SPO2276 SPO2277	1.26 1.74 1.35	0.012 0.000 0.281	SPO2275 SPO2276 SPO2277	1.19 1.15 1.13	0.245 SPO2273 0.387 SPO2274 0.704 SPO2275	1.01	0.016 0.609 0.046

SPO2284 SPO2285	1.37 0.81	0.061 SPO2282 0.034 SPO2283	1.32 1.95	0.102	SP02283 SP02284	1.01	0.219 SPO2285 0.476 SPO2286	1.23	0.044 SPO2280 0.732 SPO2281	0.81 1.69	0.335 SF 0.006 SF	PO2278 PO2279	1.31	0.051	SPO2278 SPO2279	1.31	0.422	SPO2276 SPO2277	1.20	0.033
SPO2286 SPO2287 SPO2288	0.79 0.59 2.03	0.716 SPO2284 0.016 SPO2285 0.063 SPO2286	0.83 0.83	0.062 S	SPO2285 SPO2286 SPO2287	1.1 1.16 1.28	0.063 SPO2287 0.791 SPO2288 0.669 SPO2289	1.11 1.18 1.22	0.607 SPO2282 0.252 SPO2283 0.791 SPO2284	1.98 0.81 1.35	0.002 SF 0.840 SF 0.133 SF	PO2280 PO2281 PO2282	0.76 1.51 1.69	0.019 0.019	SPO2280 SPO2281 SPO2282	0.85 1.04 1.02	0.420 5	SPO2278 SPO2279 SPO2280	1.30 1.17 0.83	0.250 0.098 0.327
SPO2289 SPO2290 SPO2292	0.31 0.58 0.96	0.168 SPO2287 0.03 SPO2288 0.841 SPO2289	0.74 1.91 0.38	0.066 0.245	SPO2288 SPO2289 SPO2290	1.01 1.08 1.11	0.384 SPO2290 0.676 SPO2292 0.193 SPO2293	0.99 1.19 1.04	0.167 SPO2285 0.472 SPO2286 0.887 SPO2287	0.52 0.75 0.42	0.010 SF 0.764 SF 0.012 SF	PO2283 PO2284 PO2285	0.70 1.37 0.51	0.001	SPO2283 SPO2284 SPO2285	1.01 0.85 0.94	0.460 0.715	SPO2281 SPO2282 SPO2283	1.12 1.07 0.84	0.237 0.536 0.743
SPO2293 SPO2294 SPO2295	0.91 0.75 1.66	0.426 SPO2290 0.028 SPO2292 0.252 SPO2293	0.79 0.94 0.98	0.71 S	SPO2292 SPO2293 SPO2294	1.05 1.11 1.01	0.324 SPO2294 0.861 SPO2295 0.811 SPO2296	1.29 1.08 1.05	0.606 SPO2288 0.245 SPO2289 0.008 SPO2290	0.88 4.11 0.75	0.957 SF 0.085 SF 0.038 SF	PO2286 PO2287 PO2288	0.65 0.35 0.85	0.029	SPO2286 SPO2287 SPO2288	0.93 0.98 1.00	0.408 5	SPO2284 SPO2285 SPO2286	0.83 0.93 1.00	0.421 0.330 0.975
SPO2296 SPO2297 SPO2298	0.51 0.9 1.04	0.03 SPO2294 0.289 SPO2295 0.894 SPO2296	0.84 1.46 0.54	0.215	SPO2295 SPO2296 SPO2297	1.05 1.17 1.19	0.52 SPO2297 0.124 SPO2298 0.24 SPO2299	1.06 1 1.14	0.043 SPO2292 0.141 SPO2293 0.571 SPO2294	1.87 1.01 0.54	0.066 SF 0.854 SF 0.006 SF	PO2289 PO2290 PO2292	0.80 1.91		SPO2289 SPO2290 SPO2292	1.39 1.06 0.90	0.892	SPO2287 SPO2288 SPO2289	0.83 0.90 1.48	0.363 0.684 0.535
SPO2299 SPO2300 SPO2301	0.63 0.89 0.67	0.474 SPO2297 0.907 SPO2298 0.055 SPO2299	1.04 0.88 0.72		SPO2298 SPO2299 SPO2300	1.08 1.43 1.08	0.218 SPO2300 0.768 SPO2301 0.956 SPO2302	1.01 1.13 1.29	0.922 SPO2295 0.813 SPO2296 0.485 SPO2297	0.24 1.32 0.61	0.048 SF 0.126 SF 0.030 SF	PO2293 PO2294 PO2295	0.97 0.51		SPO2293 SPO2294 SPO2295	1.05 1.03 1.04	0.155	SPO2290 SPO2292 SPO2293	1.22 1.04 1.01	0.161 0.722 0.913
SPO2302 SPO2303 SPO2304	0.88 1.07	0.499 SPO2300 0.577 SPO2301 0.515 SPO2302	0.97 0.81 0.95	0.905 0.111	SPO2301 SPO2302 SPO2303	1.2 1.09 1.01	0.892 SPO2303 0.265 SPO2304	1.17 1.02 1.18	0.82 SPO2298 0.331 SPO2299	1.56 0.77	0.125 SF 0.241 SF 0.162 SF	PO2296 PO2297 PO2298	1.34 0.56	0.121	SPO2296 SPO2297 SPO2298	1.04 0.78 1.02	0.798 0.071	SPO2294 SPO2295 SPO2296	1.07 0.98 1.09	0.327 1.000 0.441
SPO2305 SPO2306	1.17 0.73	0.141 SPO2303 0.14 SPO2304	1.05 1.05	0.694 0.163	SPO2304 SPO2305	1.04 1.18	0.114 SPO2306 0.371 SPO2307	1.18 1.17	0.602 SPO2301 0.667 SPO2302	0.61 0.53 0.93	0.026 SF 0.284 SF	PO2298 PO2299 PO2300	0.80 0.58	0.139 0.024	SPO2299 SPO2300	0.77 0.96	0.552 0.353	SPO2297 SPO2298	0.82 1.03	0.051 0.757
SPO2307 SPO2308 SPO2309	1.01 1 1.26	0.636 SPO2305 0.691 SPO2306 0.524 SPO2307	1.23 0.86	0.597	SPO2306 SPO2307 SPO2308	1.22 1.22 1.17	0.285 SPO2308 0.79 SPO2309 0.154 SPO2310	1.23 1.11 1.47	0.217 SPO2303 0.876 SPO2304 0.339 SPO2305	1.24 1.05 1.24	0.015 SF 0.643 SF 0.099 SF	PO2301 PO2302 PO2303	0.49 0.98 1.43	0.070 0.097	SPO2301 SPO2302 SPO2303	1.04 1.11 1.09	0.470 0.320	SPO2299 SPO2300 SPO2301	1.05 1.11 1.02	0.921 0.585 0.813
SPO2310 SPO2311 SPO2312	1.26 1.07 1.49	0.299 SPO2308 0.22 SPO2309 0.046 SPO2310	1 1.28 1.24	0.789	SPO2309 SPO2310 SPO2311	1.02 1.14 1.03	0.65 SPO2311 0.377 SPO2312 0.331 SPO2313	1.11 1.11 1.13	0.697 SPO2306 0.128 SPO2307 0.461 SPO2308	0.59 0.76 0.74	0.115 SF 0.020 SF 0.141 SF	PO2304 PO2305 PO2306	1.04 1.28 0.61	0.452 0.063 0.144	SPO2304 SPO2305 SPO2306	0.89 1.16 0.75	0.134	SPO2302 SPO2303 SPO2304	1.12 1.03 0.93	0.032 0.873 0.811
SPO2313 SPO2314 SPO2315	1.22 1.31 1.52	0.417 SPO2311 0.414 SPO2312 0.071 SPO2313	1.1 1.44 1.33		SPO2312 SPO2313 SPO2314	1.11 1.14 1.15	0.09 SPO2314 0.416 SPO2315 0.813 SPO2316	1.18 1.17 1.35	0.892 SPO2309 0.953 SPO2310 0.862 SPO2311	0.92 0.74 0.57	0.751 SF 0.081 SF 0.157 SF	PO2307 PO2308 PO2309	0.75 0.93 0.79	0.036 0.085 0.755	SPO2307 SPO2308 SPO2309	0.91 1.07 0.88	0.830	SPO2305 SPO2306 SPO2307	1.16 0.77 0.86	0.220 0.137 0.054
SPO2316 SPO2317 SPO2318	1.19 1.38 1.43	0.781 SPO2314 0.389 SPO2315 0.142 SPO2316	1.26 1.38 1.11	0.057	SPO2315 SPO2316 SPO2317	1.12 1.07 1.14	0.547 SPO2317 0.94 SPO2318 0.707 SPO2319	1.16 1.22 1.38	0.52 SPO2312 0.943 SPO2313 0.739 SPO2314	0.74 0.59 1.01	0.263 SF 0.022 SF 0.625 SF	PO2310 PO2311 PO2312	0.74 0.61 0.75		SPO2310 SPO2311 SPO2312	0.83 1.24 1.13	0.194 0.361	SPO2308 SPO2309 SPO2310	1.16 0.90 0.81	0.586 0.864 0.281
SPO2319 SPO2320 SPO2321	1.31 1.87 1.12	0.57 SPO2317 0.052 SPO2318 0.131 SPO2319	1.28 1.37 1.07	0.274 0.162	SPO2318 SPO2319 SPO2320	1.11 1.22 1.1	0.889 SPO2320 0.809 SPO2321 0.375 SPO2322	1.49 1.07	0.544 SPO2315 0.568 SPO2316 0.328 SPO2317	0.93 1.02 0.71	0.881 SF 0.925 SF 0.214 SF	PO2313 PO2314 PO2315	0.57 1.09 0.92	0.226 0.570	SPO2313 SPO2314 SPO2315	0.95 1.09	0.738 0.719	SPO2311 SPO2312 SPO2313	1.30 1.03 0.94	0.293 0.743 0.772
SPO2322 SPO2323	0.89	0.148 SPO2320 0.618 SPO2321	1.66 1.29	0.014 0.038	SPO2321 SPO2322	1.11 1.1	0.891 SPO2323 0.16 SPO2324	1.11 1.21	0.883 SPO2318 0.365 SPO2319	1.04 0.76	0.908 SF 0.739 SF	PO2316 PO2317	1.00 0.69	0.940 0.256	SPO2316 SPO2317	0.96 0.79	0.948 0.259	SPO2314 SPO2315	1.06 1.07	0.879 0.344
SPO2324 SPO2325 SPO2326	0.91 1 0.66	0.721 SPO2322 0.995 SPO2323 0.063 SPO2324	0.96 0.79 1.06	0.73 S	SPO2323 SPO2324 SPO2325	1.22 1.17 1.13	0.898 SPO2325 0.103 SPO2326 0.449 SPO2327	1.16 1.03 1.01	0.514 SPO2320 0.248 SPO2321 0.033 SPO2322	0.66 1.52 1.25		PO2318 PO2319 PO2320	0.89 0.69 0.71	0.217	SPO2318 SPO2319 SPO2320	1.11 0.88 0.96	0.814 0.907	SPO2316 SPO2317 SPO2318	0.98 0.84 1.05	0.988 0.383 0.908
SPO2327 SPO2328 SPO2329	0.95 0.99 1.49	0.655 SPO2325 0.935 SPO2326 0.159 SPO2327	0.91 0.7 1.06	0.096	SPO2326 SPO2327 SPO2328	1.19 1.39 1.21	0.234 SPO2328 0.018 SPO2329 0.892 SPO2330	1.09 1.01 1.25	0.582 SPO2323 0.414 SPO2324 0.816 SPO2325	0.89 0.33 1.09	0.905 SF 0.042 SF 0.501 SF	PO2321 PO2322 PO2323	1.52 1.19 0.83	0.005	SPO2321 SPO2322 SPO2323	1.04 0.94 0.83	0.887	SPO2319 SPO2320 SPO2321	0.98 0.95 1.08	0.987 0.909 0.224
SPO2330 SPO2331 SPO2332	1.28 2.14 1.52	0.402 SPO2328 0.027 SPO2329 0.043 SPO2330	0.94 1.37 1.29	0.213	SPO2329 SPO2330 SPO2331	1.09 1.17 1.07	0.42 SPO2331 0.755 SPO2332 0.008 SPO2333	1.11 1.36 1.34	0.016 SPO2326 0.04 SPO2327 0.373 SPO2328	1.22 0.51 1.47	0.120 SF 0.027 SF 0.024 SF	PO2324 PO2325 PO2326	1.05 1.31		SPO2324 SPO2325 SPO2326	0.91 0.93 1.34	0.862	SPO2322 SPO2323 SPO2324	0.96 0.81 0.81	0.960 0.744 0.487
SPO2333 SPO2334 SPO2335	1.38 1.11 1.42	0.179 SPO2331 0.909 SPO2332 0.04 SPO2333	2.06 1.7 1.42	0.064	SPO2332 SPO2333 SPO2334	1.08 1.23 1.03	0.008 SPO2334 0.193 SPO2335 0.95 SPO2336	1.01 1.07 1.08	0.947 SPO2329 0.644 SPO2330 0.734 SPO2331	0.70 0.92	0.276 SF 0.929 SF 0.009 SF	PO2327 PO2328 PO2329	0.46 1.42 0.70	0.004	SPO2327 SPO2328 SPO2329	1.01 1.18 1.10	0.117	SPO2325 SPO2326 SPO2327	0.97 1.26 0.97	0.966 0.208 0.957
SPO2336 SPO2337 SPO2338	0.99 1.1	0.971 SPO2334 0.05 SPO2335 0.243 SPO2336	1.04 1.44 1.04	0.957 0.288	SPO2335 SPO2336 SPO2337	1.04 1.11 1.06	0.467 SPO2337 0.652 SPO2338 0.816 SPO2339	1.1 1.11	0.957 SPO2332 0.764 SPO2333 0.719 SPO2334	0.51 0.99 0.89	0.041 SF 0.860 SF 0.961 SF	PO2330 PO2331	0.89 0.35 0.53	0.961 0.015	SPO2330 SPO2331 SPO2332	1.02 0.92 1.00	0.910 0.763	SPO2328 SPO2329 SPO2330	1.27 0.99 0.99	0.062 0.942 0.969
SPO2339 SPO2340 SPO2341	1.34 1.65 1.36	0.493 SPO2337 0.056 SPO2338 0.07 SPO2339	1.17 1.39 1.22	0.188 0.494	SPO2338 SPO2339	1.04 1.31	0.784 SPO2340 0.697 SPO2341	1.08 1.18 1.14	0.545 SPO2335 0.493 SPO2336 0.073 SPO2337	4.09 0.99	0.007 SF 0.645 SF 0.404 SF	PO2333 PO2334	1.09	0.506 0.931	SPO2333 SPO2334 SPO2335	0.91 0.88 1.20	0.789 0.921	SPO2331 SPO2332	0.80 0.99 0.94	0.339 0.816 0.797
SPO2342 SPO2343	0.59 0.55	0.001 SPO2340 0.025 SPO2341	1.37 1.32	0.285 0.201	SPO2340 SPO2341 SPO2342	1.15 1.04 1.14	0.68 SPO2343 0.004 SPO2344	1.06 0.97	0.215 SPO2338 0.116 SPO2339	1.10 0.85 0.61	0.776 SF 0.483 SF	PO2336 PO2337	0.95	0.776 0.279	SPO2336 SPO2337	1.05 0.99	0.720 S	SPO2333 SPO2334 SPO2335	1.00 1.12	0.997 0.316
SPO2344 SPO2345 SPO2346	0.57 0.62 0.85	0.08 SPO2342 0.033 SPO2343 0.478 SPO2344	0.74 0.63 0.63	0.038	SPO2343 SPO2344 SPO2345	1.15 1.03 1.1	0.346 SPO2345 0.138 SPO2346 0.014 SPO2347	1.42 1.06 1.12	0.045 SPO2340 0.429 SPO2341 0.571 SPO2342	0.50 0.94 1.10	0.209 SF 0.912 SF 0.006 SF	PO2338 PO2339 PO2340	0.88 0.63 0.51	0.873 0.502 0.132	SPO2338 SPO2339 SPO2340	1.02 0.97 1.18	0.989	SPO2336 SPO2337 SPO2338	1.01 1.07 0.99	0.849 0.588 0.976
SPO2347 SPO2348 SPO2349	0.85 0.89 1.21	0.402 SPO2345 0.31 SPO2346 0.37 SPO2347	0.64 0.86 0.88		SPO2346 SPO2347 SPO2348	1.1 1.06 1.11	0.157 SPO2348 0.687 SPO2349 0.05 SPO2350	1.07 0.98 1.09	0.374 SPO2343 0.009 SPO2344 0.09 SPO2345	1.08 0.51 0.56	0.273 SF 0.086 SF 0.044 SF	PO2341 PO2342 PO2343	0.99 0.91 1.04		SPO2341 SPO2342 SPO2343	1.12 0.85 0.87	0.184	SPO2339 SPO2340 SPO2341	0.97 1.14 1.13	0.986 0.631 0.350
SPO2350 SPO2351 SPO2352	1.21 1.25 1.39	0.029 SPO2348 0.023 SPO2349 0.253 SPO2350	0.81 0.88 1.13	0.343	SPO2349 SPO2350 SPO2351	1.06 1.46 1.06	0.079 SPO2351 0.19 SPO2352 0.633 SPO2353	1.05 1.22 1.03	0.904 SPO2346 0.967 SPO2347 0.123 SPO2348	0.34 0.47 0.36	0.014 SF	PO2344 PO2345 PO2346	0.54 0.58 0.32	0.037	SPO2344 SPO2345 SPO2346	1.03 1.10 1.02	0.488	SPO2342 SPO2343 SPO2344	0.83 0.90 1.25	0.100 0.617 0.222
SPO2353 SPO2354 SPO2355	1.01 1.61 1.37	0.569 SPO2351 0.02 SPO2352 0.083 SPO2353	1.16 1.31 1.08	0.211	SPO2352 SPO2353 SPO2354	1.33 1.07 1.16	0.884 SPO2354 0.656 SPO2355 0.859 SPO2356	1.22 1.18 1.15	0.72 SPO2349 0.576 SPO2350 0.543 SPO2351	0.83 0.88	0.024 SF 0.444 SF 0.619 SF	PO2347 PO2348 PO2349	0.44 0.37 1.73	0.013	SPO2347 SPO2348 SPO2349	1.07 1.05 0.93	0.731	SPO2345 SPO2346 SPO2347	1.14 1.01 1.05	0.298 0.913 0.777
SPO2356 SPO2357 SPO2358	1.23 1.01 0.85	0.258 SPO2354 0.846 SPO2355 0.924 SPO2356	1.41 1.29	0.006	SPO2355 SPO2356 SPO2357	1.07 1.08 1.15	0.783 SPO2357 0.258 SPO2358 0.899 SPO2359	0.99 1.24 1.02	0.809 SPO2352 0.851 SPO2353 0.783 SPO2354	0.93 1.11 0.72	0.682 SF 0.656 SF 0.054 SF	PO2350 PO2351 PO2352	0.84 0.92 1.00	0.753 0.424 0.591	SPO2350 SPO2351 SPO2352	0.76 1.15 1.08	0.005 0.398	SPO2348 SPO2349 SPO2350	1.05 1.05 0.77	0.729
SPO2359 SPO2361	1.08 0.93	0.759 SPO2357 0.938 SPO2358	1.09 0.8	0.221 0.913	SPO2358 SPO2359	1.01 1.2	0.859 SPO2361 0.983 SPO2362	1.15 1.23	0.511 SPO2355 0.765 SPO2356	1.00 0.96	0.755 SF 0.898 SF	PO2353 PO2354	1.16 0.79	0.361 0.153	SPO2353 SPO2354	1.11	0.799 0.730	SPO2351 SPO2352	1.12 1.15	0.009
SPO2362 SPO2363 SPO2364	0.93 0.83	0.317 SPO2359 0.967 SPO2361 0 SPO2362	1.17 0.83 0.91	0.162 0.281	SPO2361 SPO2362 SPO2363	1.01 1.04 1.01	0.719 SPO2363 0.573 SPO2365 0.928 SPO2366	1.16 1.04 1.07	0.217 SPO2357 0.506 SPO2358 0 SPO2359	1.03 1.48 1.04	0.944 SF 0.814 SF 0.936 SF	PO2355 PO2356 PO2357	1.07 0.93 0.89	0.331 0.773 0.391	SPO2355 SPO2356 SPO2357	1.16 1.04 0.90	0.953 0.715	SPO2353 SPO2354 SPO2355	0.95 0.94 1.09	0.783 0.502 0.091
SPO2365 SPO2366 SPO2367	0.97 0.82 0.92	0 SPO2363 0.726 SPO2364 0.983 SPO2365	0.95 0.98 0.93	0.983	SPO2364 SPO2365 SPO2366	1.05 1 1.16	0 SPO2367 0.276 SPO2369 0.914 SPO2370	1.15 1.03 1.2	0.959 SPO2361 0.417 SPO2362 0.563 SPO2363	1.21 1.05 0.79	0.352 SF 0.695 SF 0.755 SF	PO2358 PO2359 PO2361	1.33 0.90 1.37	0.853 0.748 0.006	SPO2358 SPO2359 SPO2361	0.93 0.95 1.05	0.779 0.827	SPO2356 SPO2357 SPO2358	0.98 0.88 0.94	0.954 0.656 0.975
SPO2369 SPO2370 SPO2371	1.13 1.3 0.38	0.689 SPO2366 0.254 SPO2367 0.001 SPO2369	0.8 1 1.11	0.976	SPO2367 SPO2369 SPO2370	1.32 1.41 1.1	0.984 SPO2371 0.875 SPO2372 0.4 SPO2373	1.13 1 1.09	0.048 SPO2364 0.773 SPO2365 0.901 SPO2366	1.22 0.84 1.02	0.849 SF 0.147 SF SF	PO2362 PO2363 PO2364	1.14 0.73 0.77		SPO2362 SPO2363 SPO2365	1.07 0.74 1.05	0.436	SPO2359 SPO2361 SPO2362	0.84 1.06 1.08	0.695 0.900 0.480
SPO2372 SPO2373 SPO2374	1.04 1.15 1.48	0.618 SPO2370 0.189 SPO2371 0.01 SPO2372	0.98 0.43 1.09	0.013	SPO2371 SPO2372 SPO2373	1.1 1.01 1.29	0.048 SPO2374 0.817 SPO2376 0.851 SPO2377	1.11 1.14 1.03	0.077 SPO2367 0.646 SPO2368 0.087 SPO2369	1.90 1.04 1.17	0.722 SF 1.000 SF 0.433 SF	PO2365 PO2366 PO2367	0.69 0.75 1.41	0.063	SPO2366 SPO2367 SPO2369	0.77 1.15 1.14	0.939	SPO2363 SPO2365 SPO2366	0.85 0.79 0.88	0.392 0.575 0.656
SPO2376 SPO2377 SPO2378	0.87 0.84 0.75	0.709 SPO2373 0.531 SPO2374 0.148 SPO2376	1.13 1.56 0.95	0.103 0.084	SPO2374 SPO2376 SPO2377	1.16 1 0.99	0.359 SPO2378 0.77 SPO2380 0.793 SPO2381	1.25 1.15 1.23	0.734 SPO2370 0.7 SPO2371 0.979 SPO2372	0.29 0.27 1.72		PO2369 PO2370	1.21 0.25 0.26	0.031	SPO2370 SPO2371 SPO2372	0.92 1.38 0.97	0.599 0.034	SPO2367 SPO2368 SPO2369	0.98 0.97 1.17	0.985
SPO2380 SPO2381 SPO2382	0.97 0.81 0.71	0.936 SPO2377 0.82 SPO2378 0.362 SPO2380	0.85 0.88 0.97	0.393 0.586	SPO2378 SPO2380 SPO2381	1.12 1.04 1.02	0.511 SPO2382 0.514 SPO2383 0.955 SPO2384	1.52 1.22 1.07	0.601 SPO2373 0.171 SPO2374 0.147 SPO2376	1.33 0.82 1.50	0.022 SF		1.55 1.28 0.85	0.044	SPO2373 SPO2374 SPO2376	1.14 0.88 0.98	0.036 0.035	SPO2370 SPO2371 SPO2372	0.86 1.48 0.93	0.508 0.054 0.583
SPO2383 SPO2384 SPO2385	1.43 1.03 0.83	0.203 SPO2381 0.85 SPO2382 0.521 SPO2383	0.82 0.72 1.26	0.916 0.22	SPO2382 SPO2383	1.02 1.02 1.02	0.585 SPO2385 0.562 SPO2386 0.618 SPO2387	1.21 1.04 1.19	0.914 SPO2377 0.615 SPO2378 0.93 SPO2380	1.39 1.57 1.59	0.207 SF 0.085 SF 0.287 SF	PO2376 PO2377 PO2378	1.46 1.82	0.198 0.021	SPO2377 SPO2378 SPO2380	0.84 1.04	0.574 0.824	SPO2373 SPO2374 SPO2376	1.11 0.87 0.93	0.160 0.183 0.482
SPO2386 SPO2387	0.83 0.91	0.301 SPO2384 0.963 SPO2385	0.96 0.83	0.811 S 0.268 S	SPO2384 SPO2385 SPO2386	1.07 1.2	0.958 SPO2388 0.952 SPO2389	1.05 1.05	0.925 SPO2381 0.359 SPO2382	1.34 1.66	0.734 SF 0.172 SF	PO2380 PO2381	1.35	0.390	SPO2381 SPO2382	0.97 0.95	0.944 0.847	SPO2377 SPO2378	1.08	0.704
SPO2388 SPO2389 SPO2390	0.77 1.28	0.73 SPO2386 0.392 SPO2387 0.158 SPO2388	0.85 1.1 0.89	0.83 0.755	SPO2387 SPO2388 SPO2389	1.03 1.15 1.09	0.852 SPO2390 0.595 SPO2393 0.722 SPO2394	1.04 1.15 1.35	0.029 SPO2383 0.836 SPO2384 0.819 SPO2385	1.02 1.11 1.14	0.927 SF 0.930 SF 0.625 SF	PO2382 PO2383 PO2384	1.66 1.03 0.82	0.803 0.190	SPO2383 SPO2384 SPO2385	0.99 1.35 0.99	0.502 0.856	SPO2380 SPO2381 SPO2382	1.00 1.04 1.03	0.974 0.971 0.930
SPO2393 SPO2394 SPO2395	0.58 0.54 0.57	0.379 SPO2389 0.171 SPO2390 0.042 SPO2393	0.85 1.02 0.72	0.772	SPO2390 SPO2393 SPO2394	1.03 1.13 1.13	0.407 SPO2395 0.801 SPO2396 0.395 SPO2397	1.16 1.04 1.07	0.254 SPO2386 0.071 SPO2387 0.441 SPO2388	1.44 1.20 1.13	0.412 SF 0.861 SF 0.887 SF	PO2385 PO2386 PO2387	1.22 1.45 0.93	0.065	SPO2386 SPO2387 SPO2388	1.13 0.85 0.93	0.333	SPO2383 SPO2384 SPO2385	0.96 1.24 1.01	0.744 0.350 0.953
SPO2396 SPO2397 SPO2398	0.32 0.29 0.05	0.019 SPO2394 0.082 SPO2395 0 SPO2396	0.63 0.55 0.33	0.166	SPO2395 SPO2396 SPO2397	1.22 1.1 1.09	0.079 SPO2398 0.182 SPO2399 0.461 SPO2400	1.18 1.01 1.05	0.001 SPO2389 0.013 SPO2390 0.656 SPO2393	0.66 0.57 0.88	0.135 SF 0.024 SF 0.932 SF	PO2388 PO2389 PO2390	1.07 0.61 0.41	0.774 0.037 0.069	SPO2389 SPO2390 SPO2393	0.89 0.58 0.87	0.363	SPO2386 SPO2387 SPO2388	1.06 1.05 0.88	0.686 0.931 0.241
SPO2399 SPO2400 SPO2401	0.06 1 1.02	0.002 SPO2397 0.932 SPO2398 0.815 SPO2399	0.34 0.07 0.07	0.063 0.001	SPO2398 SPO2399 SPO2400	1 1.25 1.04	0.004 SPO2401 0.043 SPO2406 0.355 SPO2408	1.13 1.22 1.07	0.179 SPO2394 0.627 SPO2395 0.955 SPO2396	1.61 1.41 1.90	0.092 SF 0.222 SF 0.013 SF	PO2393 PO2394 PO2395	0.84 1.38 1.24	0.871 0.239	SPO2394 SPO2395 SPO2396	1.15 1.23 1.77	0.523 0.111	SPO2389 SPO2390 SPO2393	0.86 0.57	0.293 0.048 0.986
SPO2406 SPO2408 SPO2409	0.95 0.93 1.19	0.819 SPO2399 0.952 SPO2400 0.998 SPO2401 0.443 SPO2406	1.01 0.96 0.99	0.888 0.865	SPO2400 SPO2401 SPO2406 SPO2408	1.04 1.02 1.45 1.06	0.11 SPO2409 0.645 SPO2410 0.983 SPO2411	1.45 1.43 1.09	0.935 SP02398 0.217 SP02398 0.881 SP02398 0.277 SP02399	2.16	0.013 SF 0.131 SF 0.007 SF 0.002 SF		2.02	0.075 0.087	SPO2396 SPO2397 SPO2398 SPO2399	1.77 1.77 3.29	0.246 0.013	SPO2394 SPO2395 SPO2396	1.13 1.18 1.84	0.868 0.569 0.103
SPO2410 SPO2411	1.06 0.94	0.64 SPO2408 0.89 SPO2409	0.97 1.17	0.984 0.137	SPO2409 SPO2410	1.04 1.07	0.844 SPO2412 0.669 SPO2413	1.11 1.08	0.755 SPO2400 0.305 SPO2401	0.81 1.61	0.619 SF 0.144 SF	PO2399 PO2400	8.18 0.84	0.009 0.713	SPO2400 SPO2401	0.84	0.704 0.270	SPO2397 SPO2398	1.80	0.161
SPO2412 SPO2413 SPO2414	1.41 1.17 0.95	0.037 SPO2410 0.226 SPO2411 0.985 SPO2412	1.01 1.03 1.29	0.517 0.042	SPO2411 SPO2412 SPO2413	1.56 1.08 1.01	0.012 SPO2414 0.449 SPO2415 0.646 SPO2416	1.02 1.25 1.04	0.504 SPO2406 0.926 SPO2407 0.314 SPO2408	0.78 0.85	0.051 SF 0.886 SF	PO2401 PO2406 PO2408	1.43 1.41 0.84	0.006 0.860	SPO2406 SPO2408 SPO2409	1.32 0.78 1.09	0.850 0.892	SPO2399 SPO2400 SPO2401	0.87 1.20	0.063 0.774 0.409
SPO2415 SPO2416 SPO2417	1.07 0.87 0.81	0.655 SPO2413 0.657 SPO2414 0.888 SPO2415	1.22 1.01 0.97	0.231 S 0.942 S	SPO2414 SPO2415 SPO2416	1.07 1.04 1.1	0.923 SPO2417 0.761 SPO2418 0.346 SPO2419	1.17 1.05 1.04	0.945 SPO2409 0.309 SPO2410 0.947 SPO2411	0.58 0.50 0.95	0.037 SF 0.028 SF 0.436 SF	PO2409 PO2410 PO2411	0.61 0.56 0.95	0.019 0.659	SPO2410 SPO2411 SPO2412	0.80 1.01 1.03	0.937 0.946	SPO2406 SPO2407 SPO2408	1.19 1.55 0.95	0.172 0.957
SPO2418 SPO2419 SPO2420	1.1 0.93 0.85	0.176 SPO2416 0.957 SPO2417 0.867 SPO2418	0.99 1.18 1.07	0.71 S	SPO2417 SPO2418 SPO2419	1.21 1.16 1.15	0.893 SPO2420 0.568 SPO2421 0.992 SPO2422	1.13 1.33 1.38	0.622 SPO2412 0.069 SPO2413 0.851 SPO2414	0.86 1.05 0.79	0.181 SF 0.917 SF 0.275 SF	PO2412 PO2413 PO2414	0.85 0.96 0.85	0.336 0.175 0.442	SPO2413 SPO2414 SPO2415	1.01 0.81 1.04	0.893 0.205	SPO2410 SPO2411	1.03 0.87 1.09	0.873 0.361 0.825
SPO2421 SPO2422 SPO2423	0.93 1.11 0.91	0.995 SPO2419 0.411 SPO2420 0.918 SPO2421	0.95 0.89 0.93	0.948 0.751	SPO2420 SPO2421 SPO2422	1.08 1.07 1.02	0.919 SPO2423 0.064 SPO2424 0.357 SPO2425	1.06 1.19 1.16	0.42 SPO2415 0.58 SPO2416 0.25 SPO2417	0.78 0.71 0.62	0.194 SF 0.118 SF 0.720 SF	PO2415 PO2416 PO2417	0.81 0.90 0.59	0.329 0.186	SPO2416 SPO2417 SPO2418	0.88 0.90 0.85	0.514 0.939	SPO2412 SPO2413 SPO2414	1.02 0.95 0.85	0.944 0.755 0.178
SPO2424 SPO2425 SPO2426	1.17 1.42 1.17	0.542 SPO2422 0.204 SPO2423 0.283 SPO2424	1.2 1.02	0.511 S	SPO2423 SPO2424 SPO2425	1.18 1.16	0.671 SPO2426 0.611 SPO2427 0.915 SPO2428	1.3 1.1 1.03	0.914 SPO2418 0.213 SPO2419 0.574 SPO2420	0.76 0.67 0.79	0.031 SF 0.440 SF 0.526 SF	PO2418 PO2419 PO2420	0.73 0.67 0.83	0.052	SPO2419 SPO2420 SPO2421	0.82 0.79 0.92	0.582 0.500	SPO2415 SPO2416 SPO2417	1.03 0.95 0.88	0.974 0.477 0.915
SPO2427 SPO2428	0.9 1.03	0.759 SPO2425 0.797 SPO2426	1.51 1.1	0.021 0.586	SPO2426 SPO2427	1.04 1.08	0.653 SPO2429 0.089 SPO2430	1.07 1.05	0.792 SPO2421 0.588 SPO2422	0.67 0.60	0.088 SF 0.141 SF	PO2421 PO2422	0.65	0.021	SPO2422 SPO2423	0.85 1.13	0.270 0.744	SPO2418 SPO2419	0.85 0.92	0.336 0.778
SPO2429 SPO2430 SPO2431	1.12 1.05 1.2	0.67 SPO2427 0.565 SPO2428 0.125 SPO2429	0.91 0.96 1.35	0.971 S	SPO2428 SPO2429 SPO2430	1.14 1.03 1.1	0.629 SPO2431 0.717 SPO2432 0.815 SPO2433	1.06 1.06 1.02	0.401 SPO2423 0.364 SPO2424 0.723 SPO2425	0.99 0.88 0.68	0.715 SF 0.846 SF 0.093 SF	PO2423 PO2424 PO2425	1.08 0.80 0.73	0.172 0.042	SPO2424 SPO2425 SPO2426	0.85 1.01 0.96	0.921 0.848	SPO2420 SPO2421 SPO2422	0.79 0.94 0.91	0.217 0.149 0.760
SPO2432 SPO2433 SPO2434	1.31 0.85 0.6	0.334 SPO2430 0.678 SPO2431 0.024 SPO2432	0.98 1.11 1.36	0.443	SPO2431 SPO2432 SPO2433	1.11 1.12 1.03	0.694 SPO2434 0.321 SPO2435 0.556 SPO2436	1.07 1.05 1.35	0.059 SPO2426 0.158 SPO2427 0.952 SPO2428	1.27 1.11 1.10		PO2426 PO2427 PO2428	1.09 1.14 1.18	0.448	SPO2427 SPO2428 SPO2429	0.95 1.06 0.91	0.842	SPO2423 SPO2424 SPO2425	1.12 0.90 0.94	0.683 0.695 0.364

SPO2435 SPO2436	0.85		O2433 O2434	0.85		SP02434 SP02435	1.14	0.015 SPO2437 0.243 SPO2438	1.2	0.915	SPO2429 SPO2430	1.01	0.602 0.573	SPO2429 SPO2430	0.97		SPO2430 SPO2431	1.11	0.809	SPO2426 SPO2427	0.95	0.615 0.789
SPO2437 SPO2438	0.96 0.7	0.963 SP0 0.284 SP0	O2435 O2436	0.93	0.561 0.888	SPO2436 SPO2437	1.02 1.15	0.891 SPO2439 0.975 SPO2440	1.12 1.14	0.713 0.685	SPO2431 SPO2432	0.83 1.25	0.264	SPO2431 SPO2432	0.72 1.32	0.065 0.501	SPO2432 SPO2433	0.97 1.09	0.760 0.919	SPO2428 SPO2429	0.99 0.75	0.961 0.349
SPO2439 SPO2440 SPO2441	0.89 0.86 0.88	0.7 SP0	O2437 O2438 O2439	0.72 0.89	0.876 0.405 0.66	SPO2438 SPO2439 SPO2440	1.03 1.09 1.07	0.151 SPO2441 0.779 SPO2442 0.941 SPO2443	1.32 1 1.03	0.68 0.785 0.293	SPO2434 SPO2435	1.09 1.75 0.94	0.027 0.340	SPO2434 SPO2435	1.38 1.71 0.97	0.018	SPO2434 SPO2435 SPO2436	1.01 0.96 0.95	0.934 0.766 0.849	SPO2430 SPO2431 SPO2432	1.00 0.98 0.97	0.932 0.813 0.829
SPO2442 SPO2443 SPO2444	0.88 0.85 1.32	0.759 SP0	O2440 O2441 O2442	0.86 1.02 1.01	0.198 0.383 0.645	SPO2441 SPO2442 SPO2443	1.09 1.02 1.15	0.419 SPO2444 0.858 SPO2445 0.197 SPO2446	1.33 1.08 1.05	0.545 0.937 0.349	SPO2436 SPO2437 SPO2438	0.90 1.50 1.69	0.932 0.306 0.068	SPO2436 SPO2437 SPO2438	1.06 1.75 1.57	0.989 0.515 0.133	SPO2437 SPO2438 SPO2439	1.05 1.14 1.13	0.980 0.783 0.585	SPO2433 SPO2434 SPO2435	1.08 1.11 0.97	0.789 0.383 0.946
SPO2445 SPO2446	1.23 1.26	0.093 SP0	O2443 O2444	0.78 1.51	0.014	SPO2444 SPO2445	1.07	0.644 SPO2447 1 SPO2448	1.54	0.987	SPO2439 SPO2440	1.56 1.24	0.204	SPO2449 SPO2440 SPO2441	1.28	0.187	SPO2440 SPO2441	1.02 0.89	0.767	SPO2436 SPO2437	0.93 1.20	0.904 0.770
SPO2447 SPO2448 SPO2449	1.05 1.25 1.09	0.736 SP0 0.423 SP0	O2445 O2446 O2447	0.92 1.36 1.22	0.028 0.464	SPO2446 SPO2447 SPO2448	1.06 1 1.12	0.247 SPO2449 0.878 SPO2450 0.956 SPO2451	1.02 1.08 1.48	0.619 0.058 0.84	SPO2441 SPO2442 SPO2443	1.53 0.96 2.54	0.043 0.952 0.048	SPO2442 SPO2443	1.41 0.72 2.31	0.014	SPO2442 SPO2443 SPO2444	0.86 1.14 1.07	0.393 0.550	SPO2438 SPO2439 SPO2440	1.17 1.08 1.02	0.578 0.566 0.922
SPO2450 SPO2451 SPO2452	0.96 1.03 1.38	0.976 SP0	O2448 O2449 O2450	1.24 1.06 0.7	0.676	SPO2449 SPO2450 SPO2451	1.18 1.18 1.15	0.109 SPO2452 0.287 SPO2453 0.96 SPO2454	1.09 1.07	0.842 0.181 0.183	SPO2444 SPO2445 SPO2446	0.73 0.93 1.40	0.163 0.735 0.068	SPO2444 SPO2445 SPO2446	0.70 0.85 1.47	0.458	SPO2445 SPO2446 SPO2447	0.97 1.19 0.93	0.055	SPO2441 SPO2442 SPO2443	0.93 0.95 1.01	0.796 0.460 0.932
SPO2453 SPO2454	0.93 1.33	0.425 SP0 0.038 SP0	O2451 O2452	0.97 1.26	0.916 0.649	SPO2452 SPO2453	1.27 1.1	0.994 SPO2455 0.35 SPO2456	1.21 1.16	0.828 0.131	SPO2447 SPO2448	1.20	0.482	SPO2448 SPO2449	1.18 1.07		SPO2448 SPO2449	0.90 1.05	0.693	SPO2444 SPO2445	1.01 1.00	0.844 0.984
SPO2455 SPO2456 SPO2457	0.79 1.15 1.1	0.223 SP0 0.326 SP0	O2453 O2454 O2455	0.93 1.3 0.83	0.484	SPO2454 SPO2455 SPO2456	1.08 1.03 1.08	0.205 SPO2457 0.61 SPO2458 0.186 SPO2459	1.15 1.06 1.09	0.48 0.982 0.027	SPO2450 SPO2451	2.88 0.78	0.022 0.095 0.924	SPO2450 SPO2451	0.57 4.49 0.63	0.021 0.010 0.421	SPO2450 SPO2451 SPO2452	1.05 1.15 0.98	0.894 0.988	SPO2446 SPO2447 SPO2448	1.09 1.06 0.97	0.144 0.830 0.991
SPO2458 SPO2459 SPO2460	1.37 0.67	0.009 SP0	O2456 O2457 O2458	1.15 1.1 1.26	0.293 0.228 0.783	SPO2457 SPO2458 SPO2459	1.38 1 1.14	0.163 SPO2460 0.976 SPO2461 0.601 SPO2462	1.07 1.1 1.01	0.467 0.907 0.792	SPO2452 SPO2453 SPO2454	0.88 1.47 0.92	0.953 0.009 0.937	SPO2452 SPO2453 SPO2454	0.76 1.45 0.91	0.820 0.004 0.841	SPO2453 SPO2454 SPO2455	0.99 1.07 1.00	0.863 0.511 0.915	SPO2449 SPO2450 SPO2451	1.07 1.18 1.05	0.561 0.349 0.896
SPO2461 SPO2462 SPO2463	1.64 1.03 1.2	0.005 SP0 0.652 SP0	O2459 O2460 O2461	0.71 1.77 1.55	0.016 0.01 0.052	SPO2460 SPO2461 SPO2462	1.01 1.17 1.05	0.815 SPO2463 0.995 SPO2464 0.667 SPO2465	1.09	0.926 0.669 0.726	SPO2455 SPO2456	1.00 0.70 1.10	0.657 0.249 0.513	SPO2455 SPO2456	1.02 0.65 1.08	0.487 0.035 0.024	SPO2456 SPO2457 SPO2458	0.85 0.93 0.99	0.479 0.723 0.989	SPO2452 SPO2453 SPO2454	0.91 1.00 0.98	0.876 0.451 0.948
SPO2464 SPO2465	1.08 1.38	0.668 SP0 0.118 SP0	O2462 O2463	0.95 1.21	0.957 0.587	SPO2463 SPO2464	1.12 1.11	0.752 SPO2466 0.832 SPO2467	1.08	0.245 0.928	SPO2458 SPO2459	0.76 2.56	0.830 0.015	SPO2457 SPO2458 SPO2459	0.74 2.70	0.808	SPO2459 SPO2460	1.00 1.32	0.819 0.243	SPO2455 SPO2456	0.99 0.78	0.935 0.050
SPO2466 SPO2467 SPO2468	0.59 0.87 0.73	0.794 SP0	O2464 O2465 O2466	1.01 1.16 0.63	0.808 0.7 0.029	SPO2465 SPO2466 SPO2467	1.23 1.21 1.29	0.643 SPO2468 0.176 SPO2469 0.763 SPO2470	1.05 1.13 1.1	0.541 0.433 0.589	SPO2460 SPO2461 SPO2462	0.99 1.21 0.71	0.924 0.132 0.215	SPO2460 SPO2461 SPO2462	0.99 1.23 0.69	0.790 0.153 0.206	SPO2461 SPO2462 SPO2463	1.32 0.86 1.01	0.098 0.451 0.931	SPO2457 SPO2458 SPO2459	0.96 0.94 1.15	0.883 0.947 0.661
SPO2469 SPO2470 SPO2471	0.97 0.78 0.85	0.39 SPC	O2467 O2468 O2469	1.02 0.82 0.97	0.173	SPO2468 SPO2469 SPO2470	1.72 1.42 1.44	0.685 SPO2471 0.666 SPO2472 0.476 SPO2473	1.16 1.22 1.06	0.353 0.195 0.283	SPO2463 SPO2464 SPO2465	1.23 0.97 0.71	0.291 0.867 0.360	SPO2463 SPO2464 SPO2465	1.37 1.04 0.83	0.492 0.713 0.515	SPO2464 SPO2465 SPO2466	0.96 1.02 1.05	0.860	SPO2460 SPO2461 SPO2462	1.10 1.19 0.90	0.226 0.053 0.573
SPO2472 SPO2473	1.15 1.97	0.357 SP0 0.005 SP0	O2470 O2471	0.83 0.84	0.654 0.419	SPO2471 SPO2472	1.46 1.25	0.007 SPO2474 0.719 SPO2475	1.13 1.06	0.122 0.203	SPO2466 SPO2467	0.61 1.01	0.017 0.842	SPO2466 SPO2467	0.66 1.06	0.021 0.777	SPO2467 SPO2468	0.83 0.93	0.710 0.734	SPO2463 SPO2464	1.10 0.98	0.839 0.966
SPO2474 SPO2475 SPO2476	1.87 1.3 0.77	0.019 SP0	O2472 O2473 O2474	0.98 1.62 1.66		SP02473 SP02474 SP02475	1.11 1.01 1.16	0.843 SPO2476 0.289 SPO2477 0.936 SPO2479	1.03 1.2 1.07	0.521 0.01 0.611	SPO2469 SPO2470	1.12 0.70 0.99	0.019 0.011 0.743	SPO2468 SPO2469 SPO2470	1.19 0.72 0.93	0.087 0.009 0.939	SPO2469 SPO2470 SPO2471	0.98 1.03 1.15		SPO2465 SPO2466 SPO2467	0.95 1.16 0.85	0.884 0.331 0.761
SPO2477 SPO2479 SPO2480	1.12 1.29 0.82	0.474 SP0	O2475 O2476 O2477	1.29 0.79 1.1	0.327	SPO2476 SPO2477 SPO2479	1.2 1.09 1.15	0.092 SPO2480 0.021 SPO2481 0.862 SPO2482	1.19 1.09 1.19	0.413 0.998 0.053	SPO2471 SPO2472 SPO2473	1.07 1.32 0.75	0.456 0.628 0.007	SPO2471 SPO2472 SPO2473	1.10 1.42 0.80	0.097	SPO2472 SPO2473 SPO2474	1.31 1.07 1.09	0.174	SPO2468 SPO2469 SPO2470	0.99 0.98 1.09	0.880 0.901 0.851
SPO2481 SPO2482	1.02 1.01	0.927 SP0 0.671 SP0	O2479 O2480	1.18 0.82	0.783 0.22	SPO2480 SPO2481	1.28 1.15	0.489 SPO2483 0.981 SPO2484	1.1 1.06	0.914 0.689	SPO2474 SPO2475	0.61 0.60	0.043 0.009	SPO2474 SPO2475 SPO2476	0.57 0.62	0.007 0.005	SPO2475 SPO2476	1.38 0.91	0.143 0.230	SPO2471 SPO2472	1.10 1.18	0.718 0.592
SPO2483 SPO2484 SPO2485	1.17 1.19 0.88	0.575 SP0	O2481 O2482 O2483	0.88 0.98 1.1	0.918 0.355	SPO2482 SPO2483 SPO2484	1.22 1.06 1.19	0.887 SPO2486 0.602 SPO2487	1.05 1.09 1.13	0.614 0.734 0.963	SPO2476 SPO2477 SPO2479	1.15 0.95 0.71	0.297 0.694 0.133	SPO2477 SPO2479	1.19 0.94 0.77	0.160 0.466 0.519	SPO2477 SPO2479 SPO2480	1.03 1.40 1.12	0.350 0.125	SPO2473 SPO2474 SPO2475	1.04 1.04 1.34	0.722 0.486 0.099
SPO2486 SPO2487 SPO2488	1.22 1.53 1.01	0.317 SP0	O2484 O2485 O2486	1.16 0.86 1.13	0.593 0.874 0.875	SPO2485 SPO2486 SPO2487	1.16 1.32 1.03	0.273 SPO2488 0.392 SPO2489 0.965 SPO2490	1.03 1.15 1.26	0.537 0.544 0.866	SPO2480 SPO2481 SPO2482	1.12 0.92 1.43	0.169 0.948 0.058	SPO2480 SPO2481 SPO2482	1.19 0.82 1.24	0.350 0.870 0.131	SPO2481 SPO2482 SPO2483	0.79 0.97 0.88	0.549 0.915 0.687	SPO2476 SPO2477 SPO2479	0.94 1.06 1.13	0.728 0.045 0.697
SPO2489 SPO2490 SPO2491	1.05 0.97 0.83	0.887 SP0 0.819 SP0	O2487 O2488 O2489	1.38 1.04 1.12	0.431 0.78 0.8	SPO2488 SPO2489 SPO2490	1.17 1.05 1.03	0.486 SPO2491 0.52 SPO2492 0.479 SPO2493	1.15 1.3 1.16	0.209 0.518 0.77	SPO2483 SPO2484 SPO2485	0.83 0.88 0.83	0.377 0.947 0.915	SPO2483 SPO2484 SPO2485	0.80 0.86 0.81	0.227 0.946 0.892	SPO2484 SPO2485 SPO2486	1.02 0.85	0.885 0.762 0.382	SPO2480 SPO2481 SPO2482	1.15 0.88 1.07	0.368 0.883 0.421
SPO2492 SPO2493	1.02 1.35	0.944 SP0 0.276 SP0	O2490 O2491	1.01 0.93	0.674 0.761	SPO2491 SPO2492	1.04 1.12	0.578 SPO2494 0.532 SPO2495	1.11	0.954 0.124	SPO2486 SPO2487	0.38 1.26	0.148 0.394	SPO2486 SPO2487	0.30 1.34	0.152 0.403	SPO2487 SPO2488	0.99 1.38	0.970 0.233	SPO2483 SPO2484	1.05 0.98	0.777 0.988
SPO2494 SPO2495 SPO2496	1.38 1.11 0.9	0.488 SP0	O2492 O2493 O2494	1.09 1.52 1.32	0.268 0.14 0.095	SPO2493 SPO2494 SPO2495	1.19 1.01 1.09	0.939 SPO2496 0.859 SPO2498 0.029 SPO2499	1.09 1.43 1.05	0.359 0.908 0.793	SPO2488 SPO2489 SPO2490	1.98 0.36 0.93	0.059 0.181 0.560	SPO2488 SPO2489 SPO2490	1.98 0.35 0.91	0.088 0.179 0.507	SPO2489 SPO2490 SPO2491	0.87 0.97 1.24	0.850 0.967 0.791	SPO2485 SPO2486 SPO2487	0.84 0.31 0.98	0.610 0.417 0.967
SPO2498 SPO2499 SPO2500	1.31 0.67 0.81	0.004 SP0	O2495 O2496 O2498	1.06 0.92 1.32	0.578 0.589 0.061	SPO2496 SPO2498 SPO2499	1.09 1.01 1.02	0.35 SPO2500 0.445 SPO2501 0.216 SPO2502	1.05 1 1.09	0.238 0.06 0.432	SPO2491 SPO2492 SPO2493	1.95 1.24 1.73	0.207 0.019 0.076	SPO2491 SPO2492 SPO2493	2.05 1.23 1.74	0.015 0.041 0.098	SPO2492 SPO2493 SPO2494	0.98 0.95 1.06	0.938	SPO2488 SPO2489 SPO2490	1.23 0.89 0.95	0.523 0.881 0.856
SPO2501 SPO2502	0.71 1.05	0.017 SP0 0.668 SP0	O2499 O2500	0.8 0.83		SPO2500 SPO2501	1.22 1.29	0.734 SPO2503 0.019 SPO2504	1.04 1.05	0.547 0.879	SPO2494 SPO2495	1.35 0.56	0.056 0.034	SPO2494 SPO2495	1.36 0.63	0.020	SPO2495 SPO2496	0.82 0.94	0.393 0.959	SPO2491 SPO2492	1.13 0.98	0.667 0.842
SPO2503 SPO2504 SPO2505	0.83 1.29 0.96	0.114 SP0	O2501 O2502 O2503	0.72 1.06 1.06		SPO2502 SPO2503 SPO2504	1.01 1.27 1.15	0.118 SPO2505 0.377 SPO2506 0.838 SPO2507	1.14 1.03 1.17	0.497 0.237 0.032	SPO2496 SPO2498 SPO2499	0.89 1.02 0.98	0.918 0.692 0.216	SPO2496 SPO2498 SPO2499	0.85 1.20 0.93	0.959 0.101 0.113	SPO2498 SPO2499 SPO2500	1.39 0.84 0.99	0.980	SPO2493 SPO2494 SPO2495	0.93 1.03 0.81	0.854 0.741 0.192
SPO2506 SPO2507 SPO2508	1.57 0.71 0.62	0.068 SP0	O2504 O2505 O2506	1.32 1.09 1.29	0.207 0.5 0.097	SPO2505 SPO2506 SPO2507	1.1 1.07	0.32 SPO2508 0.177 SPO2509 0.063 SPO2510	1.1 1.01 1.21	0.208 0.963 0.901	SPO2500 SPO2501 SPO2502	2.08 2.88 2.19	0.289 0.017 0.017	SPO2500 SPO2501 SPO2502	2.28 2.99 2.09	0.048 0.011 0.059	SPO2501 SPO2502 SPO2503	1.02 1.02 0.89	0.885 0.774 0.479	SPO2496 SPO2498 SPO2499	0.95 1.21 0.90	0.959 0.192 0.354
SPO2509 SPO2510	1.02	0.923 SP0 0.892 SP0	O2507 O2508	0.74	0.008 0.049 0.951	SPO2508 SPO2509	1.13	0.029 SPO2511 0.947 SPO2512 0.952 SPO2513	1.19	0.532	SPO2503 SPO2504	1.68 0.94	0.022 0.890 0.698	SPO2503 SPO2504	1.35 0.93 0.86	0.041 0.901 0.752	SPO2504 SPO2505	1.01 0.94 0.93	0.903 0.899 0.794	SPO2500 SPO2501	1.01 1.00 0.97	0.889 0.751
SPO2511 SPO2512 SPO2513	1.29 0.82 0.82	0.389 SP0 0.007 SP0	O2509 O2510 O2511	0.99 1.52 1.37	0.712 0.032	SPO2510 SPO2511 SPO2512	1.07 1.26 1.3	0.587 SPO2514 0.761 SPO2515	1.73 1.37 1.4	0.101 0.935 0.887	SPO2506 SPO2507	0.93 0.43 0.44	0.025 0.010	SPO2505 SPO2507	0.86 0.38 0.43	0.013	SPO2506 SPO2507 SPO2508	1.04 0.78	0.528 0.311	SPO2502 SPO2503 SPO2504	0.77 0.97	0.972 0.194 0.977
SPO2514 SPO2515 SPO2516	1.27 1.3 0.93	0.129 SP0	O2512 O2513 O2514	0.83 0.85	0.316 0.037 0.116	SPO2513 SPO2514 SPO2515	1.25 1.39 1.19	0.178 SPO2516 0.833 SPO2517 0.064 SPO2518	1.55 1.25 1.12	0.399 0.469 0.112	SPO2508 SPO2509 SPO2510	0.10 0.67 0.85	0.001 0.441 0.910	SPO2508 SPO2509 SPO2510	0.10 0.66 0.99	0.001 0.411 0.995	SPO2509 SPO2510 SPO2511	0.95 1.08 0.99	0.877 0.947 0.730	SPO2505 SPO2506 SPO2507	0.95 0.92 1.20	0.904 0.769 0.389
SPO2517 SPO2518 SPO2519	0.96 0.97 1.57	0.947 SP0	O2515 O2516 O2517	1.27 0.89 0.99	0.2 0.442 0.898	SPO2516 SPO2517 SPO2518	1.18 1.29 1.13	0.786 SPO2519 0.499 SPO2520 0.256 SPO2521	1.01 1.16 1.14	0.849 0.063 0.746	SPO2511 SPO2512 SPO2513	1.21 0.88 1.07	0.020 0.849 0.137	SPO2511 SPO2512 SPO2513	1.07 0.83 1.12	0.035 0.506 0.025	SPO2512 SPO2513 SPO2514	1.05 1.09 1.03	0.793 0.454 0.853	SPO2508 SPO2509 SPO2510	0.87 0.97 0.99	0.328 0.952 0.986
SPO2520 SPO2521 SPO2522	1.91 0.81 0.88	0.066 SP0 0.161 SP0	O2518 O2519 O2520	0.98 1.66	0.617 0.023	SPO2519 SPO2520 SPO2521	1.41 1.03	0.7 SPO2522 0.63 SPO2523 0.851 SPO2524	1.12 1.08 1.26	0.356 0.415 0.438	SPO2514 SPO2515	1.07	0.600 0.626	SPO2514 SPO2515 SPO2516	0.90	0.922 0.320 0.007	SPO2515 SPO2516 SPO2517	1.11 0.75	0.569 0.562	SPO2511 SPO2512 SPO2513	0.92 1.05	0.474 0.648 0.044
SPO2523 SPO2524	1.18 0.83	0.497 SP0 0.248 SP0	O2521 O2522	0.79 0.96	0.215 0.984	SPO2522 SPO2523	1.24 1.35	0.443 SPO2525 0.826 SPO2526	1.21 1.18	0.694	SPO2516 SPO2517 SPO2518	0.62 1.18	0.190 0.040	SPO2517 SPO2518	0.65 1.30	0.299	SPO2518 SPO2519	1.25	0.258 0.258	SPO2514 SPO2515	1.04	0.794 0.500
SPO2525 SPO2526 SPO2527	1.09 1.08 1.07	0.499 SP0	O2523 O2524 O2525	1.05 1.02 1.03	0.933	SPO2524 SPO2525 SPO2526	1.73 1.12 1.12	0.646 SPO2527 0.967 SPO2528 0.894 SPO2529	1.05 1.17 1.22	0.882 0.257 0.024	SPO2519 SPO2520 SPO2521	1.78 1.07 0.83	0.084 0.511 0.753	SPO2519 SPO2520 SPO2521	1.90 1.02 0.81	0.505	SPO2520 SPO2521 SPO2522	1.11 0.83 1.01	0.399	SPO2516 SPO2517 SPO2518	0.68 1.05 1.18	0.030 0.839 0.151
SPO2528 SPO2529 SPO2530	0.69 0.88 1.04	0.507 SP0	O2526 O2527 O2528	1.07 1.07 0.79		SPO2527 SPO2528 SPO2529	1.19 1.23 1.06	0.665 SPO2530 0.513 SPO2531 0.458 SPO2532	1.22 1.03	0.857 0.914 0.742	SPO2522 SPO2523 SPO2524	1.13 0.97 0.60	0.558 0.995 0.447	SPO2522 SPO2523 SPO2524	1.04 1.11 0.51		SPO2523 SPO2524 SPO2525	1.19 0.94 0.85	0.891	SPO2519 SPO2520 SPO2521	1.05 1.08 0.79	0.754 0.227 0.198
SPO2531 SPO2532 SPO2533	1.08 0.99	0 SP0 0.398 SP0	O2529 O2530 O2531	0.91 1.07	0.909 0.858	SPO2530 SPO2531	1.01 2.15	0.997 SPO2534 0.148 SPO2535	1.11 1.24	0.28 0.635	SPO2525 SPO2526 SPO2527	0.48 0.91	0.424 0.466	SPO2525 SPO2526 SPO2527	0.52 0.86	0.042	SPO2526 SPO2527 SPO2528	0.78 0.94	0.668	SPO2522 SPO2523 SPO2524	1.02 1.22	0.937 0.580 0.862
SPO2534 SPO2535	1.24 0.71 0.83	0.112 SP0 0.614 SP0	O2532 O2534	0.99 1.13 0.71	0.522	SPO2532 SPO2534 SPO2535	1.49 2.02 1.26	0.267 SPO2536 0.208 SPO2537 0.362 SPO2538	1.03 1.11 1.13	0.418 0.802 0.84	SPO2528 SPO2529	0.96 1.41 1.32	0.756 0.278 0.467	SPO2528 SPO2529	0.96 1.15 1.43	0.861	SPO2529 SPO2530	0.96 1.11 0.92	0.672 0.856	SPO2525 SPO2526	0.93 0.81 0.91	0.350 0.709
SPO2536 SPO2537 SPO2538	1.08 0.78 1.01	0.17 SP0	O2535 O2536 O2537	0.74 0.98 0.99	0.394 0.855 0.825	SPO2536 SPO2537 SPO2538	1.18 1.02	0.615 SPO2539 0.932 SPO2540 0.996 SPO2541	1.03 1.2 1.18	0.671 0.806 0.411	SPO2530 SPO2531 SPO2532	1.02 0.88 1.12	0.993 0.384 0.923	SPO2530 SPO2531 SPO2532	0.85 0.97 1.12	0.196	SPO2531 SPO2532 SPO2533	0.36 1.00 0.95	0.374 0.859 0.725	SPO2527 SPO2528 SPO2529	0.92 1.00 1.07	0.648 0.929 0.810
SPO2539 SPO2540 SPO2541	1.03 0.71 0.81	0.586 SP0 0.417 SP0	O2538 O2539 O2540	1.13 0.98 1.03	0.292	SPO2539 SPO2540 SPO2541	1.03 1.24 1.41	0.414 SPO2542 0.724 SPO2543 0.432 SPO2544	1.02 1.22 1.12	0.75 0.191 0.918	SPO2534 SPO2535 SPO2536	2.53 1.09 1.62	0.079 0.911 0.303	SPO2534 SPO2535 SPO2536	2.19 0.97 1.53	0.071 0.537	SPO2534 SPO2535 SPO2536	1.14 0.83 1.62	0.344 0.675	SPO2530 SPO2531 SPO2532	0.91 1.00 1.09	0.839 0.822 0.709
SPO2542 SPO2543	0.69 1.09	0.128 SP0 0.386 SP0	O2541 O2542	0.8 0.87	0.154 0.56	SPO2542 SPO2543	1.19 1.17	0.82 SPO2545 0.068 SPO2546	1.09 1.05	0.809 0.58	SPO2537 SPO2538	1.19 1.00	0.760 0.848	SPO2537 SPO2538	1.39 0.99	0.331	SPO2537 SPO2538	0.94 0.84	0.834	SPO2533 SPO2534	1.00 1.18	0.683 0.169
SPO2544 SPO2545 SPO2546	1.04 0.79 0.89	0.81 SP0	O2543 O2544 O2545	1.09 1.27 0.81	0.813 0.904	SPO2544 SPO2545 SPO2546	1.24 1.15 1.02	0.89 SPO2547 0.813 SPO2548 0.919 SPO2549	1.08 1.02 1.24	0.879 0.327 0.941	SPO2540 SPO2541	0.92 0.81 1.03	0.761 0.666 0.948	SPO2540 SPO2541	0.84 0.74 0.94	0.685 0.182	SPO2539 SPO2540 SPO2541	0.81 0.87 0.99	0.741 0.748	SPO2535 SPO2536 SPO2537	0.90 1.25 0.93	0.499 0.597 0.507
SPO2547 SPO2548 SPO2549	1.06 0.79 1.07	0.279 SP0	O2546 O2547 O2548	0.91 1.1 0.65		SPO2547 SPO2548 SPO2549	1.11 1.1 1.08	0.868 SPO2550 0.159 SPO2551 0.951 SPO2552	1.31 1.04 1.28	0.268 0.949 0.256	SPO2542 SPO2543 SPO2544	1.59 0.79 0.85	0.183 0.166 0.863	SPO2542 SPO2543 SPO2544	1.48 0.84 0.71	0.044 0.496 0.836	SPO2542 SPO2543 SPO2544	0.92 0.93 0.98	0.631	SPO2538 SPO2539 SPO2540	0.83 0.99 0.85	0.590 0.741 0.802
SPO2550 SPO2551 SPO2552	0.98 1 1.16	0.819 SP0 0.976 SP0	O2549 O2550 O2551	1.11 1.04 1.03	0.645	SPO2550 SPO2551 SPO2552	1.24 1.05 1.04	0.506 SPO2553 0.954 SPO2554 0.236 SPO2555	1.28 1.21 1.37	0.974 0.968	SPO2545 SPO2546 SPO2547	2.18 1.08 0.76	0.462 0.955 0.522	SPO2545 SPO2546 SPO2547	2.40 0.90 0.68	0.443 0.205	SPO2545 SPO2546 SPO2547	1.12 1.01 0.75	0.879 0.793	SPO2541 SPO2542 SPO2543	0.96 0.98 0.85	0.826 0.802 0.489
SPO2553 SPO2554	1.08 0.96	0.93 SP0 0.995 SP0	O2552 O2553	1.03 1.1 0.99	0.195 0.984	SPO2553 SPO2554	1.04 1.12 1.12	0.966 SPO2556 1 SPO2559	1.13 1.25	0.938 0.419 0.955	SPO2548 SPO2549	1.64 0.87	0.016 0.710	SPO2548 SPO2549	1.84 0.96	0.079 0.772	SPO2548 SPO2549	1.22 0.85	0.446 0.767	SPO2544 SPO2545	0.92 1.04	0.901 0.948
SPO2555 SPO2556 SPO2559	1.01 0.87 1.04	0.698 SP0	O2554 O2555 O2556	1 1.06 0.93		SPO2555 SPO2556 SPO2559	1 1.06 1.24	0.382 SPO2560 0.7 SPO2561 0.924 SPO2562	1.3 1.16 1.38	0.826 0.867 0.125	SPO2550 SPO2551 SPO2552	1.56 1.00 0.70	0.056 0.994 0.132	SPO2550 SPO2551 SPO2552	1.48 0.97 0.85		SPO2550 SPO2551 SPO2552	1.01 0.82 0.66		SPO2546 SPO2547 SPO2548	0.83 0.60 1.18	0.285 0.709 0.625
SPO2560 SPO2561 SPO2562	0.65 0.75 0.76	0.014 SP0 0.064 SP0	O2559 O2560 O2561	0.91 0.69 0.76	0.865 0.021	SPO2560 SPO2561 SPO2562	1.05 1.41 1.03	0.762 SPO2563 0.872 SPO2564 0.232 SPO2565	1.08 1.09 1.21	0.295 0.674 0.939	SPO2553 SPO2554 SPO2555	0.71 1.20 1.11	0.825 0.879 0.949	SPO2553 SPO2554 SPO2555	0.71 1.07	0.826 0.949	SPO2553 SPO2554 SPO2555	0.93 0.84	0.952 0.864 0.782	SPO2549 SPO2550 SPO2551	0.93 0.99 0.93	0.889 0.925 0.949
SPO2563 SPO2564	0.66 1.06	0.029 SP0 0.747 SP0	O2562 O2563	0.72 0.68	0.134 0.049	SPO2563 SPO2564	0.99 1.25	0.119 SPO2566 0.913 SPO2567	1.25 1.77	0.45 0.041	SPO2556 SPO2559	0.78 0.81	0.615 0.653	SPO2556 SPO2559	0.78 0.83	0.207	SPO2556 SPO2559	0.46	0.622	SPO2552 SPO2553	0.75 0.88	0.057 0.932
SPO2565 SPO2566 SPO2567	1.03 1.33 0.85	0.013 SP0	O2564 O2565 O2566	1.1 0.99 1.24		SPO2565 SPO2566 SPO2567	1.16 1.24 1.03	0.954 SPO2568 0.342 SPO2569 0.021 SPO2570	1.09 1.15 1.11	0.008 0.672 0.117	SPO2560 SPO2561 SPO2562	0.97 1.23 1.14	0.934 0.164 0.139	SPO2560 SPO2561 SPO2562	1.11 1.31 1.09	0.016	SPO2560 SPO2561 SPO2562	0.97 1.02 1.13		SPO2554 SPO2555 SPO2556	0.90 0.98 0.76	0.913 0.880 0.671
SPO2568 SPO2569 SPO2570	1.62 1.05 1.3	0.037 SP0 0.815 SP0	O2567 O2568 O2569	0.84 1.49 0.98	0.058	SPO2568 SPO2569 SPO2570	1.08 1.05 1.04	0.005 SPO2571 0.418 SPO2572 0.183 SPO2573	1.37 1 2.33	0.88 0.602 0.094	SPO2563 SPO2564 SPO2565	0.93 0.75 1.28	0.871 0.495 0.660	SPO2563 SPO2564 SPO2565	0.92 0.65 1.15	0.630 0.083 0.871	SPO2563 SPO2564 SPO2565	0.84 0.84 1.34	0.141	SPO2559 SPO2560 SPO2561	0.95 0.93 0.98	0.927 0.669 0.855
SPO2571 SPO2572	0.83	0.106 SP0 0.173 SP0	O2570 O2571	1.21 0.95	0.135 0.644	SPO2571 SPO2572	1.12 1.35	0.906 SPO2574 0.534 SPO2575	1.71 2.14	0.254 0.798	SPO2566 SPO2567	0.99	0.844 0.012 0.002	SPO2566 SPO2567	0.98	0.531	SPO2566 SPO2567	1.49 0.93	0.050 0.893	SPO2562 SPO2563	1.18 0.79	0.230 0.255
SPO2573 SPO2574 SPO2575	0.49 0.78 0.93	0.131 SP0 0.947 SP0	O2572 O2573 O2574	0.67 0.58 0.76	0.049 0.042	SPO2573 SPO2574 SPO2575	1.06 1.13 1.28	0.007 SPO2576 0.056 SPO2577 0.845 SPO2578	1.34 1.07 1.19	0.057 0.015 0.228	SPO2568 SPO2569 SPO2570	0.28 0.86 1.04	0.820 0.239	SPO2568 SPO2569 SPO2570	0.26 0.93 1.05	0.933 0.226	SPO2568 SPO2569 SPO2570	1.22 1.18 1.03	0.586 0.851	SPO2564 SPO2565 SPO2566	0.87 1.28 1.19	0.782 0.735 0.198
SPO2576 SPO2577	0.45 0.52		O2575 O2576	0.87 0.45		SPO2576 SPO2577	1.21	0.094 SPO2579 0.015 SPO2580	1.05 0.98	0.027 0.093	SPO2571 SPO2572	0.65 0.79	0.392 0.627	SPO2571 SPO2572	0.61 0.76	0.019 0.818	SPO2571 SPO2572	1.04		SPO2567 SPO2568	1.08	0.436 0.824

SPO2578 SPO2579	1.11	0.557 SPO25 0.367 SPO25		0.46	0.064	SPO2578 SPO2579	1.28	0.054 SPO2581 0.222 SPO2582	1.14	0.616	SPO2573 SPO2574	1.38	0.002	SPO2573	1.02		SP02573 SP02574	1.53	0.069	SPO2569 SPO2570	1.06	0.842
SPO2580 SPO2581	1.51 1.15	0.093 SPO25 0.071 SPO25	79 80	1.43 1.36	0.129	SPO2580 SPO2581	1.03 1.01	0.15 SPO2583 0.553 SPO2584	1.24 0.98	0.267 0.735	SPO2575 SPO2576	0.88 1.78	0.936 0.093	SPO2575 SPO2576	1.26 1.66	0.741	SPO2575 SPO2576	1.17	0.872	SPO2571 SPO2572	1.02 1.22	0.702 0.117
SPO2582 SPO2583 SPO2584	1.11 0.92 1.08	0.507 SPO25 0.389 SPO25 0.838 SPO25	82	1.09 1.04 0.91	0.344 0.52 0.26	SPO2582 SPO2583 SPO2584	1.07 1.04 1.01	0.448 SPO2585 0.993 SPO2586 0.641 SPO2587	1.28 1.03 1.22	0.871 0.667 0.339	SPO2577 SPO2578 SPO2579	1.59 1.12 0.83	0.018 0.286 0.432	SPO2577 SPO2578 SPO2579	1.54 1.13 0.87	0.059 0.174 0.447	SPO2577 SPO2578 SPO2579	1.01 1.03	0.021 0.866 0.546	SP02573 SP02574 SP02575	1.55 1.10 1.14	0.013 0.660 0.883
SPO2585 SPO2586 SPO2587	1.42 1.45 1.58	0.169 SPO25 0.15 SPO25 0.028 SPO25	85	0.99 1.39 1.34	0.935 0.122 0.101	SPO2585 SPO2586 SPO2587	1.02 1.17 1.07	0.656 SPO2588 0.197 SPO2589 0.376 SPO2590	1.21 1.12 1.21	0.871 0.768 0.646	SPO2580 SPO2581 SPO2582	0.25 1.49 0.76	0.004 0.087 0.130	SPO2580 SPO2581 SPO2582	0.24 1.50 0.74	0.003 0.167 0.206	SPO2580 SPO2581 SPO2582	0.72 0.82 0.92	0.044 0.613 0.572	SPO2576 SPO2577 SPO2578	1.91 2.39 1.00	0.082 0.005 0.918
SPO2588 SPO2589	1.22 1.07	0.237 SPO25 0.35 SPO25	87 88	1.41 1.18	0.053 0.284	SPO2588 SPO2589	1.06 1.09	0.721 SPO2591 0.184 SPO2592	1.02 1.4	0.326 0.898	SPO2583 SPO2584	0.83 0.85	0.386 0.790	SPO2583 SPO2584	0.75 0.95	0.024 0.931	SPO2583 SPO2584	1.08 0.85	0.574 0.748	SPO2579 SPO2580	0.90 0.68	0.346 0.082
SPO2590 SPO2591 SPO2592	0.69 0.85 1.43	0.014 SPO25 0.008 SPO25 0.518 SPO25	90	1.17 0.78 0.88	0.335 0.331 0.732	SPO2590 SPO2591 SPO2592	1.17 1.42 1.17	0.395 SPO2593 0.102 SPO2594 0.904 SPO2595	1.09 1.11 1.05	0.704 0.578 0.8		1.07 1.14 0.72	0.205 0.096 0.296	SPO2585 SPO2586 SPO2587	1.11 1.23 0.68	0.015 0.018 0.250	SPO2585 SPO2586 SPO2587	0.93 0.93 0.98	0.683	SPO2581 SPO2582 SPO2583	0.81 0.90 1.00	0.504 0.550 0.951
SPO2593 SPO2594 SPO2595	1.04 1.34 1.39	0.742 SPO25 0.132 SPO25 0.759 SPO25	93	1.33 0.99	0.584 0.774 0.041	SPO2593 SPO2594 SPO2595	1.38 1.03	0.549 SPO2596 0.262 SPO2597 0.992 SPO2598	1.03 1.19	0.1 0.049 0.958	SPO2589	1.12 1.21 1.16	0.202 0.137 0.035	SPO2588 SPO2589 SPO2590	1.19 1.26 0.97	0.284 0.419 0.532	SPO2588 SPO2589 SPO2590	1.05 1.06 0.96	0.782	SPO2584 SPO2585 SPO2586	0.89 0.98 0.92	0.842 0.951 0.515
SPO2596 SPO2597	1.5	0.043 SPO25 0.518 SPO25	95 96	1.96 1.41	0.471 0.018	SPO2596 SPO2597	1.14	0.726 SPO2601 0.304 SPO2602	1.05 1.46	0.73 0.353		0.88	0.962	SPO2591 SPO2592	0.77 0.96	0.434	SPO2591 SPO2592	1.00 0.96	0.943 0.920	SPO2587 SPO2588	0.93 0.98	0.711 0.945
SPO2598 SPO2601 SPO2602	1.24 0.91 1.12	0.196 SPO25 0.894 SPO25 0.59 SPO26	98 01	0.99 1.26 0.96	0.897	SPO2598 SPO2601 SPO2602	1.06 1.14 1.02	0.882 SPO2603 0.988 SPO2604 0.639 SPO2605	1.07 1.19 1.16	0.512 0.571 0.586	SPO2594 SPO2595	0.43 0.65 0.41	0.051 0.028 0.299	SPO2594 SPO2595	0.72 0.68 0.48	0.484 0.024 0.452	SPO2593 SPO2594 SPO2595	1.49 0.80 1.96	0.172 0.672	SPO2589 SPO2590 SPO2591	1.05 1.10 1.02	0.919 0.722 0.793
SPO2603 SPO2604 SPO2605	0.9 0.93 0.76	0.948 SPO26 0.868 SPO26 0.499 SPO26	03	1.1 1.09	0.327 0.216 0.756	SPO2603 SPO2604 SPO2605	1.18 1.23 1.06	0.898 SPO2606 0.12 SPO2607 0.656 SPO2608	1.11 1.03 1.11	0.017 0.143 0.025	SPO2596 SPO2597 SPO2598	0.61 0.84 1.11	0.012 0.211 0.429	SPO2596 SPO2597 SPO2598	0.59 0.86 1.14	0.023 0.576 0.540	SPO2596 SPO2597 SPO2598	1.04 0.94 1.07	0.535 0.734 0.367	SPO2592 SPO2593 SPO2594	1.00 1.47 0.92	0.989 0.426 0.521
SPO2606 SPO2607 SPO2608	0.69 0.62 0.62	0.189 SPO26 0.006 SPO26 0.019 SPO26	05 06	0.8 0.65 0.66	0.601 0.054 0.074	SPO2606 SPO2607 SPO2608	1.08 1.12 1.05	0.019 SPO2609 0.272 SPO2610 0.045 SPO2612	1.26 1.38 1.06	0.691 0.136 0.759	SPO2601 SPO2602	1.29 1.09 1.52	0.100	SPO2601 SPO2602	1.39 1.32 1.37		SPO2601 SPO2602 SPO2603	0.96 1.09 1.20	0.809 0.858 0.572	SPO2595 SPO2596 SPO2597	1.21 0.99 0.93	0.949 0.929 0.561
SPO2609 SPO2610	0.69 0.68	0.086 SPO26 0.025 SPO26	08 09	0.71 0.77	0.047	SPO2609 SPO2610	1.04 1.02	0.517 SPO2613 0.127 SPO2614	1.08 1.27	0.704 0.222	SPO2604 SPO2605	1.31	0.227	SPO2604 SPO2605	1.07	0.770 0.485	SPO2604 SPO2605	1.05 1.06	0.855 0.848	SPO2598 SPO2601	1.05 1.07	0.846 0.398
SPO2612 SPO2613 SPO2614	0.69 1.13 1.1	0.022 SPO26 0.465 SPO26 0.061 SPO26	12	0.77 0.75 1.13	0.168 0.021 0.631	SPO2612 SPO2613 SPO2614	1.03 1.04 1.22	0.868 SPO2615 0.857 SPO2616 0.905 SPO2617	1.21 1.31 1.29	0.6 0.222 0.249	SPO2606 SPO2607 SPO2608	2.53 1.45 1.39	0.004 0.106 0.146	SPO2606 SPO2607 SPO2608	2.63 1.49 1.21	0.000 0.081 0.065	SPO2606 SPO2607 SPO2608	1.18 1.06 1.08	0.149 0.323 0.770	SPO2602 SPO2603 SPO2604	1.07 0.95 0.99	0.565 0.888 0.749
SPO2615 SPO2616 SPO2617	1.18 2.36 0.81	0.523 SPO26 0.013 SPO26 0.274 SPO26	15	1.11 1.12 1.86	0.34 0.452 0.018	SPO2615 SPO2616 SPO2617	1.17 1.22 1.06	0.359 SPO2618 0.223 SPO2619 0.111 SPO2620	1.42 1.14 1.02	0.033 0.938 0.429	0. 0.0.0	0.88 1.87	0.799 0.003 0.013	SPO2609 SPO2610 SPO2612	0.79 1.96 1.49	0.571 0.002 0.032	SPO2609 SPO2610 SPO2612	0.93 1.02 0.93		SPO2605 SPO2606 SPO2607	0.99 1.21 1.08	0.954 0.035 0.417
SPO2618 SPO2619	0.79 1.15	0.418 SPO26 0.663 SPO26	17 18	0.87 0.92	0.322	SPO2618 SPO2619	1.15 1.03	0.219 SPO2621 0.672 SPO2622	1.03 1.04	0.829 0.151	SPO2613 SPO2614	0.76 0.06	0.518 0.001	SPO2613 SPO2614	0.68 0.06	0.443 0.001	SPO2613 SPO2614	1.11 1.28	0.623 0.063	SPO2608 SPO2609	1.18 0.95	0.209 0.747
SPO2620 SPO2621 SPO2622	0.81 1.5 0.93	0.45 SPO26 0.523 SPO26 0.883 SPO26	20 21	1.27 0.85 1.27	0.135 0.095 0.535	SPO2620 SPO2621 SPO2622	1.2 1.01 1.21	0.863 SPO2623 0.879 SPO2624 0.48 SPO2625	1.09 1.22 1.04	0.788 0.543 0.671	SPO2615 SPO2616 SPO2617	0.06 0.84 0.42	0.002 0.052 0.059	SPO2615 SPO2616 SPO2617	0.05 0.98 0.38	0.003 0.517 0.040	SPO2615 SPO2616 SPO2617	1.35 1.18 1.28	0.326 0.511	SPO2610 SPO2612 SPO2613	1.05 0.94 1.00	0.132 0.668 0.952
SPO2623 SPO2624 SPO2625	0.85 1.28 1.16	0.875 SPO26 0.203 SPO26 0.89 SPO26	23	0.88 0.72 1.26		SPO2623 SPO2624 SPO2625	1.07 1.11 1.1	0.752 SPO2626 0.625 SPO2627 0.725 SPO2628	1.13 1.21 1.18	0.022 0.894 0.003	SPO2618 SPO2619 SPO2620	0.50 0.24 0.52	0.007 0.017 0.179	SPO2618 SPO2619 SPO2620	0.42 0.23 0.52	0.012 0.015 0.006	SPO2618 SPO2619 SPO2620	1.36 1.29 1.12	0.587	SPO2614 SPO2615 SPO2616	1.42 1.36 1.06	0.106 0.282 0.780
SPO2626 SPO2627 SPO2628	1.07 0.46	0.53 SPO26 0.002 SPO26 0.001 SPO26	26	1.14 1 0.53	0.888 0.854 0.056	SPO2626 SPO2627 SPO2628	1.16 1.13 1.05	0.013 SPO2629 0.196 SPO2630 0.002 SPO2631	1.42 1.24 1.35	0.198 0.408 0.295	SPO2621 SPO2622	0.69 1.69 1.03	0.584 0.073 0.972	SPO2621 SPO2622 SPO2623	0.56 1.51 0.90	0.513 0.020 0.612	SPO2621 SPO2622 SPO2623	0.98 1.11 0.74	0.979 0.706 0.432	SPO2617 SPO2618 SPO2619	1.43 1.47 1.32	0.261 0.034 0.144
SPO2629 SPO2630	1.79 1.81	0.014 SPO26 0.083 SPO26	28 29	0.26 1.65	0.001	SPO2629 SPO2630	1.11 1.08	0.263 SPO2632 0.301 SPO2633	1.13	0.102 0.335	SPO2624 SPO2625	1.01 0.81	0.998 0.871	SPO2624 SPO2625	1.02 0.85	0.989 0.879	SPO2624 SPO2625	0.96 0.96	0.649 0.960	SPO2620 SPO2621	1.13 0.96	0.037 0.939
SPO2631 SPO2632 SPO2633	1.59 1.93 1.68	0.095 SPO26 0.004 SPO26 0.029 SPO26	31	1.63 1.55 1.92	0.165 0.037 0.055	SPO2631 SPO2632 SPO2633	1.03 1.24 1.15	0.18 SPO2634 0.11 SPO2635 0.365 SPO2636	1.11 1.11 1.1	0.377 0.106 0.913		1.51 3.03 3.77	0.003 0.001 0.000	SPO2626 SPO2627 SPO2628	1.56 2.89 3.47	0.006 0.004 0.000	SPO2626 SPO2627 SPO2628	0.80 0.90 1.24	0.140 0.735 0.278	SPO2622 SPO2623 SPO2624	1.17 0.77 0.88	0.468 0.651 0.575
SPO2634 SPO2635 SPO2636	2.43 1.27 2.23	0.011 SPO26 0.075 SPO26 0.322 SPO26	34	1.67 2.43 1.37	0.021 0.013 0.096	SPO2634 SPO2635 SPO2636	1.09 1.02 1.07	0.046 SPO2637 0.317 SPO2638 0.941 SPO2639	1.05 1.26 1.2	0.73 0.1 0.827	SPO2629 SPO2630 SPO2631	0.48 0.42 0.24	0.037 0.025 0.015	SPO2629 SPO2630 SPO2631	0.50 0.45	0.031 0.036 0.017	SPO2629 SPO2630 SPO2631	0.85 0.83 0.94	0.253 0.402 0.639	SPO2625 SPO2626 SPO2627	0.88 0.78 0.94	0.863 0.041 0.919
SPO2637 SPO2638 SPO2639	1.54 1.46	0.006 SPO26 0.029 SPO26	36 37	2.22 1.59	0.371 0.044 0.097	SPO2637 SPO2638	1.12	0.179 SPO2640 0.162 SPO2641	1.02 1.02	0.8 0.786 0.592		0.12 0.12 0.10	0.000 0.001	SPO2632 SPO2633	0.11	0.005 0.001 0.002	SPO2632 SPO2633 SPO2634	0.92 0.95	0.693 0.910 0.517	SPO2628 SPO2629	1.15 0.87	0.035 0.195
SPO2640 SPO2641	1.01 0.76 1.2	0.212 SPO26 0.465 SPO26	39	0.93 0.78	0.097	SPO2640 SPO2641	1.13	0.629 SPO2642 0.807 SPO2643 0.862 SPO2644	1.03 1.01 1.05	0.592 0.29 0.382	SPO2635 SPO2636	0.10 0.24 0.13	0.001 0.005 0.060	SPO2635 SPO2636	0.09 0.21 0.12	0.002 0.006 0.077	SPO2635 SPO2636	1.05	0.517 0.513 0.872	SPO2630 SPO2631 SPO2632	0.86 0.89 0.93	0.656 0.662 0.618
SPO2642 SPO2643 SPO2644	1.02 0.67 0.61	0.978 SPO26 0.602 SPO26 0.031 SPO26	42	0.95 1.02 0.93	0.801	SPO2642 SPO2643 SPO2644	1.2 1.16 1.27	0.326 SPO2645 0.21 SPO2646 0.692 SPO2647	0.98 1.04 1.24	0.004 0.247 0.945	SPO2637 SPO2638 SPO2639	0.18 0.54 0.89	0.002 0.099 0.765	SPO2637 SPO2638 SPO2639	0.18 0.52 0.86	0.001 0.074 0.822	SPO2637 SPO2638 SPO2639	1.00 1.09 0.93	0.395	SPO2633 SPO2634 SPO2635	0.94 1.01 0.97	0.855 0.542 0.972
SPO2645 SPO2646 SPO2647	0.5 0.75 0.84	0.012 SPO26 0.09 SPO26 0.733 SPO26	45	0.57 0.57 0.76	0.033 0.001 0.399	SPO2645 SPO2646 SPO2647	1 1.01 1.33	0.078 SPO2648 0.427 SPO2649 0.958 SPO2650	1.1 1.1 1.13	0.507 0.272 0.854	SPO2640 SPO2641	0.93 0.87 0.78	0.978 0.479 0.429	SPO2640 SPO2641	0.92 0.92 0.76	0.999 0.621 0.648	SPO2640 SPO2641 SPO2642	1.14 0.67 0.74		SPO2636 SPO2637 SPO2638	1.05 0.98 0.95	0.921 0.796 0.839
SPO2648 SPO2649	0.79 0.84	0.171 SPO26 0.273 SPO26	47 48	0.88 0.87	0.809 0.295	SPO2648 SPO2649	1.07 1.15	0.895 SPO2651 0.983 SPO2652	1.14 1.02	0.682 0.943	SPO2644	1.20 2.30	0.392 0.043	SPO2643 SPO2644	1.24 2.31	0.330	SPO2643 SPO2644	0.96 1.08	0.745	SPO2639 SPO2640	0.97 1.03	0.855 0.719
SPO2650 SPO2651 SPO2652	1.37 0.95 0.79	0.504 SPO26 0.94 SPO26 0.806 SPO26	50 51	0.84 1.16 0.92	0.186 0.289 0.908	SPO2650 SPO2651 SPO2652	1.01 1.02 1.04	0.952 SPO2653 0.888 SPO2654 0.922 SPO2655	1.16 1.09 1.24	0.119 0.226 0.257	SPO2645 SPO2646 SPO2647	1.14 1.13 1.78	0.430 0.030 0.175	SPO2645 SPO2646 SPO2647	1.05 1.20 1.66	0.194 0.139 0.229	SPO2645 SPO2646 SPO2647	1.87 1.17 0.93	0.078 0.273 0.903	SPO2641 SPO2642 SPO2643	0.83 0.75 0.90	0.654 0.069 0.541
SPO2653 SPO2654 SPO2655	0.88 1.51 1.07	0.532 SPO26 0.245 SPO26 0.313 SPO26	53	0.93 0.83 1.38	0.906 0.055 0.017	SPO2653 SPO2654 SPO2655	1.06 1.15	0.047 SPO2656 0.435 SPO2657 0.491 SPO2658	1.14 1.06 1.08	0.325 0.959 0.129	SPO2648 SPO2649 SPO2650	1.71 1.62	0.028 0.034 0.372	SPO2648 SPO2649 SPO2650	1.66 1.67 1.20	0.020 0.049 0.198	SPO2648 SPO2649 SPO2650	1.01 0.91 1.01	0.903 0.355 0.947	SPO2644 SPO2645 SPO2646	1.09 1.74 1.15	0.484 0.034 0.284
SPO2656 SPO2657 SPO2658	1.01 0.58 0.65	0.769 SPO26 0.461 SPO26 0.192 SPO26	55 56	1.02 0.86 0.71	0.487 0.487 0.424	SPO2656 SPO2657 SPO2658	1.22 1.17 1.11	0.185 SPO2659 0.964 SPO2660 0.437 SPO2661	1.02 1.24 1.14	0.591 0.962 0.957	SPO2651 SPO2652	1.24 1.18 1.25	0.366 0.646 0.090	SPO2651 SPO2652 SPO2653	1.35 1.12 1.35	0.403 0.725 0.024	SPO2651 SPO2652 SPO2653	1.06 0.84 1.11	0.757 0.776 0.228	SPO2647 SPO2648 SPO2649	0.88 1.04 0.94	0.770 0.616 0.303
SPO2659 SPO2660	0.88	0.686 SPO26 0.772 SPO26	58 59	0.69 0.87	0.208	SPO2659 SPO2660	1.01	0.344 SPO2662 0.772 SPO2663	1.12 1.13	0.618 0.745	SPO2654 SPO2655	0.99 1.40	0.828 0.093	SPO2654 SPO2655	1.05 1.45	0.653	SPO2654 SPO2655	1.26 1.05	0.629 0.572	SPO2650 SPO2651	0.93	0.829 0.883
SPO2661 SPO2662 SPO2663	1.15 0.97 0.85	0.367 SPO26 0.798 SPO26 0.74 SPO26	61	0.95 1.02 0.95	0.939 0.585 0.736	SPO2661 SPO2662 SPO2663	1.16 1.16	0.771 SPO2664 0.791 SPO2665 0.75 SPO2666	1.11 1.08 1.03	0.977 0.051 0.842	SPO2656 SPO2657 SPO2658	1.47 1.33 1.68	0.133 0.785 0.071	SPO2656 SPO2657 SPO2658	1.21 1.13 1.62	0.066 0.897 0.037	SPO2656 SPO2657 SPO2658	1.04 0.89 1.16	0.809 0.788 0.248	SPO2652 SPO2653 SPO2654	0.89 1.18 1.14	0.868 0.169 0.635
SPO2664 SPO2665 SPO2666	0.83 1.09 0.83	0.812 SPO26 0.37 SPO26 0.887 SPO26		0.8 0.93 1.18		SPO2664 SPO2665 SPO2666	1.11 1.95 1.1	0.989 SPO2667 0.271 SPO2668 0.918 SPO2669	1.27 1.03 1.13	0.455 0.934 0.214		1.51 1.15 0.90	0.049 0.790 0.028	SPO2659 SPO2660 SPO2661	1.27 1.19 1.01	0.425 0.694 0.492	SPO2659 SPO2660 SPO2661	1.12 1.18 0.96		SPO2655 SPO2656 SPO2657	0.97 1.13 0.89	0.819 0.565 0.745
SPO2667 SPO2668 SPO2669	1.01 1.18 0.57	0.772 SPO26 0.275 SPO26 0.065 SPO26	67	0.93 0.82 1.15	0.507	SPO2667 SPO2668 SPO2669	1.13 1.03 1.06	0.411 SPO2670 0.962 SPO2671 0.174 SPO2672	1.09 1.03 1.15	0.798 0.997 0.871	SPO2663	1.28 0.83 0.99	0.550 0.436 0.963	SPO2662 SPO2663 SPO2664	1.32 0.86 0.99	0.528	SPO2662 SPO2663 SPO2664	1.10 0.58 0.91	0.117	SPO2658 SPO2659 SPO2660	1.22 1.26 1.11	0.148 0.396 0.796
SPO2670 SPO2671	1.01 1.52	0.822 SPO26 0.1 SPO26	69 70	0.61 1.06	0.299 0.396	SPO2670 SPO2671	1.38	0.885 SPO2673 0.759 SPO2674	1.16 1.53	0.698 0.371	SPO2665 SPO2666	0.81 0.80	0.153 0.680	SPO2665 SPO2666	0.65 0.63	0.161 0.523	SPO2665 SPO2666	1.00 0.74	0.842	SPO2661 SPO2662	0.86 1.09	0.355 0.917
SPO2672 SPO2673 SPO2674	0.92 0.86 0.97	0.868 SPO26 0.232 SPO26 0.939 SPO26	72 73	1.31 1.06 1.01	0.459	SPO2672 SPO2673 SPO2674	1.05 1.2	0.887 SPO2675 0.831 SPO2676 0.714 SPO2677	1.11 1.24 1.03	0.959 0.578 0.877	SPO2669	1.23 0.58 2.17	0.668 0.073 0.064	SPO2668 SPO2669	1.46 0.62 1.89	0.178	SPO2667 SPO2668 SPO2669	0.88 1.19 1.11	0.478 0.706	SPO2663 SPO2664 SPO2665	0.71 0.94 0.72	0.565 0.902 0.301
SPO2675 SPO2676 SPO2677	1.01 1.23 1.24	0.968 SPO26 0.709 SPO26 0.634 SPO26	75	1.01 1.16 1.16	0.212 0.09 0.792	SPO2675 SPO2676 SPO2677	1.6 1.05 1.15	0.13 SPO2678 0.552 SPO2679 0.974 SPO2680	1.23 1.13 1.16	0.54 0.413 0.921	SPO2670 SPO2671 SPO2672	1.20 1.01 1.66	0.174 0.418 0.256	SPO2670 SPO2671 SPO2672	1.15 1.13 1.52	0.403	SPO2670 SPO2671 SPO2672	0.96 0.98 1.09	0.964	SPO2666 SPO2667 SPO2668	0.91 1.04 0.97	0.869 0.807 0.820
SPO2678 SPO2679 SPO2680	1.45 1.66 1.14	0.445 SPO26 0.122 SPO26 0.436 SPO26	78	1.22 1.49 1.8	0.083 0.398 0.243	SPO2678 SPO2679 SPO2680	0.99 1.77 1.04	0.602 SPO2681 0.647 SPO2682 0.345 SPO2683	1.08 1.04 1.19	0.348 0.113 0.82	SPO2674	1.06 0.95 0.80	0.516 0.809 0.192	SPO2673 SPO2674 SPO2675	1.06 0.83 0.79	0.472	SPO2673 SPO2674 SPO2675	0.98 0.89 0.92		SPO2669 SPO2670 SPO2671	1.13 0.95 1.03	0.596 0.748 0.851
SPO2681 SPO2682 SPO2683	1.38 0.76 1.05	0.085 SPO26 0.078 SPO26 0.802 SPO26	80 81	1.03 1.29 1.02	0.462 0.167	SPO2681 SPO2682 SPO2683	1.36 1.03	0.687 SPO2684 0.036 SPO2685 0.551 SPO2686	1.11 1.21 1.04	0.581 0.793 0.002	SPO2676 SPO2677	0.53 0.76 1.45	0.363 0.666 0.014	SPO2676 SPO2677	0.79 0.79	0.451 0.513	SPO2676 SPO2677 SPO2678	0.97 1.06 0.82	0.934	SPO2672 SPO2673 SPO2674	1.00 1.06 0.93	0.973 0.704 0.531
SPO2684 SPO2685	0.79 0.94	0.05 SPO26 0.975 SPO26	83 84	1.11 0.75	0.508	SPO2684 SPO2685	1.05 1.01	0.516 SPO2687 0.681 SPO2688	1.09 1.02	0.183 0.507	SPO2680	0.99 0.97	0.180 0.715	SPO2678 SPO2679 SPO2680	0.89	0.526 0.402	SPO2679 SPO2680	1.16 1.12	0.043 0.335	SPO2675 SPO2676	0.96 0.89	0.902 0.858
SPO2686 SPO2687 SPO2688	0.7 0.68 1.12	0.012 SPO26 0.005 SPO26 0.312 SPO26	86	0.98 0.63 0.78		SPO2686 SPO2687 SPO2688	1.08 1.04 1.1	0.003 SPO2689 0.376 SPO2690 0.176 SPO2691	1.07 1.17	0.352 0.695 0.925	SPO2682	1.40 1.54 1.12	0.035 0.013 0.062	SPO2681 SPO2682 SPO2683	1.44 1.40 1.14	0.035 0.008 0.022	SPO2681 SPO2682 SPO2683	1.19 1.11 0.88	0.244	SPO2677 SPO2678 SPO2679	1.08 0.85 1.13	0.599 0.120 0.241
SPO2689 SPO2690 SPO2691	1.9 1.53 1.16	0.03 SPO26 0.039 SPO26 0.246 SPO26	89	1.03 1.74 1.4		SPO2689 SPO2690 SPO2691	1.29 1.6 1.01	0.071 SPO2692 0.18 SPO2693 0.828 SPO2694	1.15 1.13 1.11	0.77 0.36 0.24		0.58 1.73 5.87	0.051 0.602 0.001	SPO2684 SPO2685 SPO2686	0.56 1.54 5.84	0.011 0.748 0.001	SPO2684 SPO2685 SPO2686	1.11 1.06 1.17	0.962	SPO2680 SPO2681 SPO2682	1.10 1.19 1.16	0.080 0.188 0.122
SPO2692 SPO2693 SPO2694	0.85 1.03 0.65	0.126 SPO26 0.763 SPO26 0.05 SPO26	91 92	1.13 0.88 1.09	0.695 0.452	SPO2692 SPO2693 SPO2694	1.04 1.08 1.05	0.544 SPO2695 0.131 SPO2696 0.755 SPO2697	1.02 1.07 1.15	0.069 0.954 0.965	SPO2687 SPO2688	1.16 1.16 0.57	0.049 0.152 0.113	SPO2687 SPO2688 SPO2689	1.04 1.23 0.56	0.041 0.061 0.002	SPO2687 SPO2688 SPO2689	1.04 0.97	0.809 0.947	SPO2683 SPO2684 SPO2685	0.98 1.16 1.20	0.881 0.306 0.896
SPO2695 SPO2696	1.33 0.99	0.017 SPO26 0.726 SPO26	94 95	0.68 1.36	0.143	SPO2695 SPO2696	1.07 1.36	0.053 SPO2698 0.746 SPO2699	1.16 1.09	0.497 0.686	SPO2690 SPO2691	0.66 0.88	0.027 0.421	SPO2690 SPO2691	0.69 0.93	0.056 0.827	SPO2690 SPO2691	1.11 0.99	0.304 0.979	SPO2686 SPO2687	1.22 0.95	0.074 0.881
SPO2697 SPO2698 SPO2699	0.9 1.1 1	0.917 SPO26 0.377 SPO26 0.945 SPO26	97	0.87 0.91	0.946 0.873	SPO2697 SPO2698 SPO2699	1.14 1.13 1.2	0.947 SPO2700 0.095 SPO2701 0.243 SPO2702	1.02 2.02 1.09	0.947 0.674 0.064	SPO2693	0.83 0.81 0.82	0.322 0.491 0.432	SPO2692 SPO2693 SPO2694	0.85 0.80 0.83		SPO2692 SPO2693 SPO2694	0.99 0.91 1.04	0.735	SPO2688 SPO2689 SPO2690	0.93 1.12 1.11	0.636 0.647 0.180
SPO2700 SPO2701 SPO2702	1.15 1 0.72	0.899 SPO26 0.815 SPO27 0.078 SPO27	99 00	1.12 1.12 1.04	0.795 0.931 0.661	SPO2700 SPO2701 SPO2702	1.01 1.25	0.874 SPO2703 0.886 SPO2704 0.155 SPO2705	1.18 1.05 1.01	0.482 0.954 0.732	SPO2696	1.66 0.98 1.06	0.024 0.670 0.959	SPO2695 SPO2696 SPO2697	1.77 0.75 1.00	0.016	SPO2695 SPO2696 SPO2697	1.14 0.85 0.94	0.311 0.662 0.942	SPO2691 SPO2692 SPO2693	0.99 0.99 0.85	0.950 0.981 0.679
SPO2703 SPO2704	0.96 1.23	0.928 SPO27 0.104 SPO27	02 03	0.78 0.77	0.434	SPO2703 SPO2704	1.05	0.438 SPO2706 0.056 SPO2707	1.5 1.07	0.003 0.938	SPO2698 SPO2699	1.05 0.61	0.845 0.473	SPO2698 SPO2699	1.26 0.51	0.412	SPO2698 SPO2699	1.06 0.68	0.955 0.601 0.944	SPO2694 SPO2695	1.11 1.09	0.387 0.233
SPO2705 SPO2706 SPO2707	0.92 0.51 0.79	0.146 SPO27 0.446 SPO27	05 06	1.17 1.01 0.58	0.334 0.771 0.061	SPO2705 SPO2706 SPO2707	1.19 1.06 1.03	0.049 SPO2709 0.962 SPO2710	0.98 1.04 1.19	0.58 0.943 0.911	SPO2701 SPO2702	0.74 1.56 3.22	0.840 0.148 0.027	SPO2700 SPO2701 SPO2702	0.76 1.40 2.21	0.327 0.051	SPO2700 SPO2701 SPO2702	0.93 1.09 1.33	0.764 0.400	SPO2696 SPO2697 SPO2698	0.83 0.97 1.00	0.568 0.961 0.896
SPO2708 SPO2709 SPO2710	0.63 1.1 0.81	0.214 SPO27 0.89 SPO27 0.393 SPO27	08	0.92 0.7 0.98	0.881 0.292 0.98	SPO2708 SPO2709 SPO2710	1.09 1.01 1.03	0.519 SPO2711 0.933 SPO2712 0.924 SPO2713	1 1.56 1.2	0.424 0.691 0.902	SPO2704	2.05 1.24 1.21	0.235 0.045 0.176	SPO2703 SPO2704 SPO2705	0.90 1.26 1.54	0.630 0.151 0.060	SPO2703 SPO2704 SPO2705	0.63 1.18 1.01	0.586 0.071 0.932	SPO2699 SPO2700 SPO2701	0.66 0.82 1.01	0.564 0.883 0.966
SPO2711 SPO2712 SPO2713	0.88 0.61 1.01	0.825 SPO27 0.232 SPO27 0.749 SPO27	11	0.88 0.89 0.74		SP02711 SP02712 SP02713	0.99 1.23 1.14	0.57 SPO2714 0.997 SPO2715 0.237 SPO2716	1 1.98 1.27	0.823 0.792 0.13	SPO2707	0.90 1.12	0.002 0.650 0.497	SPO2706 SPO2707 SPO2708	0.76 1.22	0.000 0.388 0.460	SPO2706 SPO2707 SPO2708	0.99 1.00 0.88	0.934	SP02702 SP02703 SP02704	1.25 1.06 1.05	0.529 0.940 0.743
SPO2714 SPO2715	0.85 1.06	0.497 SPO27 0.861 SPO27	13 14	0.99	0.689 0.491	SPO2714 SPO2715	1.04 1.12	0.743 SPO2717 0.865 SPO2718	1.01 1.07	0.201 0.555	SPO2709 SPO2710	0.91 0.99	0.906 0.680	SPO2709 SPO2710	0.98 1.15	0.955 0.403	SPO2709 SPO2710	0.93 0.98	0.918 0.788	SPO2705 SPO2706	1.04 1.18	0.964 0.105
SPO2716 SPO2717 SPO2718	1.39 1.1 1.65	0.048 SPO27 0.851 SPO27 0.477 SPO27	16 17	1.06 1.2 1.04	0.052	SPO2716 SPO2717 SPO2718	1.19 1.1 1.01	0.68 SPO2719 0.118 SPO2720 0.607 SPO2721	1.09 1.11 1.26	0.095 0.939 0.005	SPO2712 SPO2713	0.95 1.23 1.83	0.692 0.561 0.181	SP02711 SP02712 SP02713	0.93 1.24 1.79	0.040	SPO2711 SPO2712 SPO2713	1.12 0.97 1.10	0.799 0.837	SPO2707 SPO2708 SPO2709	0.99 0.93 0.98	0.947 0.643 0.965
SP02719	1.04	0.319 SPO27	18	1.5	0.464	SP02719	1.16	0.547 SPO2722	1.43	0.044	SPO2714	1.47	0.061	SPO2714	1.48	0.041	SPO2714	0.79	0.192	SP02710	0.88	0.061

SPO2720 SPO2721	0.74 0.76	0.766	SPO2719 SPO2720	0.98 0.73	0.669	SP02720 SP02721	1.17	0.857 SPO2723 0.039 SPO2724	0.99	0.622	SPO2715 SPO2716	1.14	0.650	SPO2715 SPO2716	1.05	0.840	SPO2715 SPO2716	0.91	0.850	SP02711 SP02712	0.88	0.746
SPO2722 SPO2723	0.98 0.65	0.954 0.161	SPO2721 SPO2722	0.88 0.94	0.614 0.887	SPO2722 SPO2723	1.23 1.21	0.022 SPO2725 0.445 SPO2726	1.11	0.278 0.907	SPO2717 SPO2718	1.37 1.05	0.551 0.925	SPO2717 SPO2718	1.32 1.02		SPO2717 SPO2718	1.10 0.93	0.874	SPO2713 SPO2714	1.01 0.81	0.972 0.224
SPO2724 SPO2725 SPO2726	0.74 1.05 0.71	0.118 0.634 0.52	SP02723 SP02724 SP02725	0.67 0.79 1.17	0.223 0.188 0.433	SPO2724 SPO2725 SPO2726	1.3 1.77 1.15	0.724 SPO2729 0.543 SPO2730 0.898 SPO2731	1.05 1.38 1.11	0.995 0.662 0.01	SPO2719 SPO2720 SPO2721	1.07 0.75 0.44	0.080 0.669 0.043	SPO2719 SPO2720 SPO2721	1.10 0.99 0.38	0.035 0.912 0.011	SPO2719 SPO2720 SPO2721	0.88 1.03 0.88	0.025 0.999 0.672	SP02715 SP02716 SP02717	0.85 0.88 1.06	0.739 0.389 0.923
SPO2729 SPO2730 SPO2731	0.79 0.91 1.17	0.761 S 0.7 S 0.424 S	SPO2726 SPO2729 SPO2730	0.98 0.8 0.93	0.947 0.913 0.991	SPO2729 SPO2730 SPO2731	0.99 1.15 1.01	0.983 SPO2733 0.874 SPO2734 0.035 SPO2735	1.01 1.07 1.2	0.757 0.836 0.902	SPO2722 SPO2723 SPO2724	0.59 1.11 1.41	0.090 0.492 0.035	SPO2722 SPO2723 SPO2724	0.53 1.08 1.35	0.113 0.495 0.122	SPO2722 SPO2723 SPO2724	0.85 0.91 0.91	0.671 0.771 0.571	SPO2718 SPO2719 SPO2720	0.86 0.85 1.06	0.804 0.084 0.977
SPO2733 SPO2734	1.22	0.111	SPO2731 SPO2733	1.4	0.017	SPO2733 SPO2734	0.99 1.03	0.939 SPO2736 0.834 SPO2738	1.04	0.791	SPO2725 SPO2726	0.44 0.83	0.087 0.886 0.882	SPO2725 SPO2726	0.52 0.69	0.046	SPO2725 SPO2726	0.83 0.76	0.871	SP02721 SP02722	0.90	0.261 0.591
SPO2735 SPO2736 SPO2738	1.08 1.67 0.69		SPO2734 SPO2735 SPO2736	1.04 1.03 1.44	0.686 0.649 0.018	SPO2738	1.11 1.29 1.26	0.54 SPO2739 0.466 SPO2740 0.015 SPO2741	1.02 1.11 1.06	0.541 0.564 0.711	SPO2729 SPO2730 SPO2731	1.28 0.86 0.52	0.519 0.112	SPO2729 SPO2730 SPO2731	1.19 0.92 0.38	0.004	SPO2729 SPO2730 SPO2731	0.41 0.85 0.69	0.483 0.290	SPO2723 SPO2724 SPO2725	0.92 0.99 0.72	0.839 0.914 0.112
SPO2739 SPO2740 SPO2741	1.08 1.11 0.84	0.399 0.14 0.634	SPO2738 SPO2739 SPO2740	0.73 1.07 1.04	0.039 0.827 0.93	SPO2739 SPO2740 SPO2741	1.2 1.07 1.02	0.7 SPO2742 0.345 SPO2743 0.769 SPO2744	1.23 1.17 1.18	0.96 0.365 0.702	SPO2733 SPO2734 SPO2735	0.95 1.07 1.07	0.912 0.519 0.463	SPO2733 SPO2734 SPO2735	0.93 1.10 1.10	0.965 0.454 0.359	SPO2733 SPO2734 SPO2735	1.02 1.06 0.92	0.909	SPO2726 SPO2729 SPO2730	0.87 0.92 0.83	0.900 0.958 0.447
SPO2742 SPO2743 SPO2744	1.13 1.35 1.34	0.629	SPO2741 SPO2742 SPO2743	0.95 1.26 1.31	0.961 0.31 0.211	SPO2742 SPO2743 SPO2744	1.01 1.03 1.15	0.848 SPO2745 0.21 SPO2746 0.906 SPO2747	1.14	0.933 0.166 0.992	SPO2736 SPO2738	1.34 1.43 0.86	0.062 0.040 0.979	SPO2736 SPO2738	1.39 1.35 0.76	0.116 0.013 0.505	SPO2736 SPO2738 SPO2739	1.21 1.00 0.83	0.622	SP02731 SP02733 SP02734	0.66 1.03 1.01	0.009 0.869 0.957
SPO2745 SPO2746	1.28 0.66	0.83	SPO2744 SPO2745	1.3 1.31	0.03 0.726	SPO2745 SPO2746	0.99 1.01	0.958 SPO2748 0.211 SPO2749	1.04	0.889 0.558	SPO2740 SPO2741	0.89 1.86	0.861 0.232	SPO2740 SPO2741	0.92 1.67	0.396 0.282	SPO2740 SPO2741	0.98 1.08	0.926 0.790	SPO2735 SPO2736	1.00 1.21	0.960 0.110
SPO2747 SPO2748 SPO2749	0.84 1.17 0.88	0.473 0.508 0.69	SPO2746 SPO2747 SPO2748	0.7 0.86 1.17	0.475 0.723 0.488	SPO2747 SPO2748 SPO2749	1.25 1.17 1.11	0.117 SP02750 0.618 SP02751 0.877 SP02752	1.03 0.99 1.16	0.275 0.957 0.971	SPO2742 SPO2743 SPO2744	0.93 1.46 1.45	0.907 0.153 0.021	SPO2742 SPO2743 SPO2744	0.91 1.33 1.43	0.890 0.235 0.008	SPO2742 SPO2743 SPO2744	0.96 1.16 0.99	0.972 0.625 0.810	SPO2738 SPO2739 SPO2740	1.06 0.82 0.95	0.595 0.221 0.693
SPO2750 SPO2751 SPO2752	0.66 1.13 1.08	0.178 0.849 0.442	SPO2749 SPO2750 SPO2751	0.96 0.66 1.09	0.995 0.071 0.911	SPO2750 SPO2751 SPO2752	1.13 1.13 1.13	0.526 SPO2753 0.996 SPO2754 0.604 SPO2755	1.18 1.14 1.15	0.713 0.744 0.478	SPO2745 SPO2746 SPO2747	0.76 0.85 0.76	0.646 0.929 0.394	SPO2745 SPO2746 SPO2747	0.66 0.88 0.76		SPO2745 SPO2746 SPO2747	1.08 1.23 0.97	0.952 0.074 0.914	SPO2741 SPO2742 SPO2743	1.12 0.96 1.15	0.774 0.956 0.609
SPO2753 SPO2754	1.24 1.25	0.298	SPO2752 SPO2753	1.15 1.11	0.235 0.27 0.386	SPO2753 SPO2754	1.07 1.05	0.561 SPO2756 0.737 SPO2757	1.16 1.09	0.952 0.014	SPO2748 SPO2749	0.47 1.10 0.56	0.108 0.272	SPO2748 SPO2749	0.51 1.16	0.086 0.069 0.071	SPO2748 SPO2749	1.04 0.89	0.893 0.113 0.191	SPO2744 SPO2745	0.97 0.99	0.701 0.989
SPO2755 SPO2756 SPO2757	0.79 0.99 0.52	0.939	SPO2754 SPO2755 SPO2756	1.25 0.73 1.08	0.548	SPO2755 SPO2756 SPO2757	1.01 1.16 1.2	0.913 SPO2759 0.002 SPO2760	1.26 1.29 1.21	0.368 0.744	SPO2750 SPO2751 SPO2752	0.85 0.85	0.057 0.954 0.102	SPO2750 SPO2751 SPO2752	0.60 0.80 1.49	0.071	SPO2750 SPO2751 SPO2752	0.81 0.95 1.05	0.975	SP02746 SP02747 SP02748	1.22 0.97 1.00	0.070 0.906 0.994
SPO2758 SPO2759 SPO2760	1.07 1.28 1.08	0.736 0.136 0.499	SPO2757 SPO2758 SPO2759	0.71 1.08 1.18	0.432 0.308 0.232	SPO2758 SPO2759 SPO2760	1.18 1.01 1.34	0.927 SPO2761 0.512 SPO2762 0.237 SPO2763	1.94 1.23 1.03	0.237 0.762 0.112	SPO2753 SPO2754 SPO2755	0.34 0.78 1.40	0.007 0.363 0.413	SPO2753 SPO2754 SPO2755	0.36 0.78 1.91	0.007 0.345 0.115	SPO2753 SPO2754 SPO2755	0.84 0.94 1.07	0.728	SPO2749 SPO2750 SPO2751	0.92 0.87 0.96	0.480 0.124 0.982
SPO2761 SPO2762	1.03 1.12	0.663	SPO2760 SPO2761	1.13 1.01		SPO2761 SPO2762	1.18	0.345 SPO2764 0.808 SPO2765 0.024 SPO2766	1.18	0.166	SPO2756 SPO2757 SPO2758	1.18 1.63	0.814	SPO2756 SPO2757	1.19 2.08 0.81		SPO2756 SPO2757	1.00	0.004	SP02752 SP02753	1.12 0.85	0.052 0.650
SPO2763 SPO2764 SPO2765	1.27 1.3 1.17	0.103 5 0.147 5 0.043 5	SPO2762 SPO2763 SPO2764	1.09 1.08 1.34	0.78 0.213 0.018	SPO2763 SPO2764 SPO2765	1.18 1.11 1.02	0.754 SPO2767 0.53 SPO2768	1.04 1.16	0.965 0.649 0.299	SPO2759 SPO2760	0.81 0.76 1.70	0.745 0.284 0.015	SPO2758 SPO2759 SPO2760	0.86 1.61	0.034	SPO2758 SPO2759 SPO2760	1.21 1.07 0.95	0.534 0.641	SPO2754 SPO2755 SPO2756	0.94 1.12 1.08	0.807 0.600 0.912
SPO2766 SPO2767 SPO2768	1.14 1.13 1.08	0.776 S 0.14 S 0.045 S	SPO2765 SPO2766 SPO2767	1.17 1.17 1.17	0.069 0.588 0.263		1.24 1.02 1.67	0.945 SP02769 0.015 SP02770 0.004 SP02771	1.26 1.32 1.02	0.004 0.036 0.569	SPO2761 SPO2762 SPO2763	1.90 2.19 1.31	0.046 0.087 0.056	SPO2761 SPO2762 SPO2763	1.99 2.21 1.39	0.036 0.128 0.022	SPO2761 SPO2762 SPO2763	1.16 1.05 1.18	0.876	SP02757 SP02758 SP02759	1.58 1.16 0.97	0.003 0.186 0.857
SPO2769 SPO2770 SPO2771	1.08 0.94 1.07	0.469 0.414	SPO2768 SPO2769 SPO2770	1.14 1.12 1.09	0.196 0.123 0.023	SPO2769 SPO2770 SPO2771	1.02 1.12 1.14	0.129 SP02772 0.127 SP02773 0.088 SP02774	1.04 1.03 1.14	0.412 0.827 0.014	SPO2764 SPO2765 SPO2766	1.16 1.67 1.42	0.060 0.004 0.302	SPO2764 SPO2765 SPO2766	1.10 1.52 1.34	0.116 0.006 0.363	SPO2764 SPO2765 SPO2766	1.04 1.02 0.88	0.178	SPO2760 SPO2761 SPO2762	0.94 1.12 1.11	0.809 0.425 0.778
SPO2772 SPO2773	1.2 0.94	0.637	SPO2771 SPO2772	1.16 1.18	0.322 0.182	SPO2772 SPO2773	1.06 1.33	0.336 SPO2775 0.9 SPO2776	1.17 1.07	0.264 0.264	SPO2767 SPO2768	1.29 1.36	0.074 0.015	SPO2767 SPO2768	1.28 1.50	0.019 0.025	SPO2767 SPO2768	0.86 0.90	0.488 0.564	SPO2763 SPO2764	1.16 1.03	0.190 0.707
SPO2774 SPO2775 SPO2776	0.98 1.24 1.22	0.793 5 0.059 5 0.112 5	SP02773 SP02774 SP02775	0.85 0.88 1.14	0.879 0.547 0.147	SPO2774 SPO2775 SPO2776	1.01 0.99 0.97	0.08 SPO2777 0.2 SPO2778 0.388 SPO2779	1.09 1.08 1.07	0.506 0.417 0.132	SPO2769 SPO2770 SPO2771	1.40 1.73 2.03	0.031 0.015 0.006	SPO2769 SPO2770 SPO2771	1.38 1.71 1.86	0.008 0.008	SPO2769 SPO2770 SPO2771	1.01 0.95 0.97	0.898 0.926 0.945	SP02765 SP02766 SP02767	1.00 0.94 0.88	0.727 0.957 0.277
SPO2777 SPO2778 SPO2779	0.94 0.88 1.02	0.474 0.068 0.886	SPO2776 SPO2777 SPO2778	1.12 0.95 0.98	0.104 0.757 0.984	SPO2777 SPO2778 SPO2779	1.1 1.01 1.13	0.687 SPO2780 0.789 SPO2781 0.502 SPO2782	0.99 1.03 1.24	0.666 0.222 0.88	SPO2772 SPO2773 SPO2774	1.97 0.86 1.99	0.024 0.993 0.000	SPO2772 SPO2773 SPO2774	1.88 0.91 2.12	0.096 0.928 0.042	SPO2772 SPO2773 SPO2774	0.98 0.85 1.04	0.990 0.899 0.328	SP02768 SP02769 SP02770	0.93 1.04 1.01	0.472 0.743 0.308
SPO2780 SPO2781 SPO2782	1.04 1 1.19	0.757 0.839 0.671	SPO2779 SPO2780 SPO2781	1.08 1.08	0.352 0.302 0.11	SPO2780 SPO2781 SPO2782	1.07 1.18 1.06	0.251 SPO2783 0.811 SPO2784 0.803 SPO2785	1.16 1.11 1.12	0.487 0.744 0.568	SPO2775 SPO2776	1.58 1.50 1.20	0.015 0.117 0.081	SPO2776 SPO2776	1.58 1.62	0.009 0.008 0.024	SPO2775 SPO2776 SPO2777	0.98 1.09 0.98	0.942 0.472 0.958		0.98 1.05 0.89	0.950 0.862 0.918
SPO2783 SPO2784	1.01 1.18	0.848	SPO2782 SPO2783	1.18	0.072 0.178	SPO2783 SPO2784	1.12 1.06	0.502 SPO2786 0.26 SPO2787	1.11 1.12	0.065	SPO2778 SPO2779	2.43 2.06	0.003	SPO2778 SPO2779	2.45 1.96	0.001	SPO2778 SPO2779	0.93 1.15	0.575	SPO2774 SPO2775	1.08 1.03	0.286 0.696
SPO2785 SPO2786 SPO2787	1.2 0.99 1.07	0.094 0.786 0.856	SPO2784 SPO2785 SPO2786	1.27 1.08 1.08	0.035 0.477 0.371	SPO2785 SPO2786 SPO2787	1.13 1.06 1.44	0.058 SPO2788 0.309 SPO2789 0.772 SPO2790	1.04 1.1 1.12	0.28 0.464 0.063	SPO2780 SPO2781 SPO2782	1.54 1.09 1.22	0.008 0.052 0.209	SPO2780 SPO2781 SPO2782	1.53 1.06 1.33	0.040 0.071 0.151	SPO2780 SPO2781 SPO2782	0.87 0.92 1.02	0.616	SP02776 SP02777 SP02778	1.11 1.02 0.99	0.250 0.640 0.304
SPO2788 SPO2789 SPO2790	0.67 0.88 0.85	0.01 5 0.431 5 0.508 5	SPO2787 SPO2788 SPO2789	0.89 0.65 0.92	0.619 0.058 0.691	SPO2788 SPO2789 SPO2790	1.44 1.39 1.22	0.058 SPO2791 0.579 SPO2792 0.315 SPO2793	1.11 1.21 1.06	0.882 0.991 0.931	SPO2783 SPO2784 SPO2785	2.52 2.02 1.42	0.011 0.075	SPO2783 SPO2784 SPO2785	2.94 1.92 1.39	0.083	SPO2783 SPO2784 SPO2785	1.02 1.06 0.96		SPO2779 SPO2780 SPO2781	1.02 0.95 0.99	0.901 0.885 0.415
SPO2791 SPO2792	0.9 1	0.927	SPO2790 SPO2791	0.81 0.85	0.312 0.621	SPO2791 SPO2792	1.06 1.06	0.797 SPO2794 0.991 SPO2795	1.42 1.04	0.487 0.856	SPO2786 SPO2787	1.61 1.14	0.007 0.801	SPO2786 SPO2787	1.56 1.05		SPO2786 SPO2787	0.93 1.30	0.527 0.689	SPO2782 SPO2783	1.07 1.04	0.514 0.269
SPO2793 SPO2794 SPO2795	0.86 0.63 1.05	0.78 5 0.341 5 0.794 5	SPO2792 SPO2793 SPO2794	1.07 0.88 0.65	0.882 0.883 0.437	SPO2793 SPO2794 SPO2795	1.22 1.12 1.41	0.886 SPO2796 0.482 SPO2797 0.848 SPO2798	1.02 1.22 1.23	0.964 0.091 0.299	SPO2788 SPO2789 SPO2790	0.70 0.97 1.59	0.116 0.997 0.045	SPO2788 SPO2789 SPO2790	0.75 1.04 1.71	0.669 0.012	SPO2788 SPO2789 SPO2790	1.20 1.02 1.40	0.420 0.731 0.375	SPO2784 SPO2785 SPO2786	1.10 0.95 1.01	0.508 0.777 0.114
SPO2796 SPO2797 SPO2798	1.55 0.91 1.3	0.199 5 0.863 5 0.016 5	SPO2795 SPO2796 SPO2797	0.97 1.27 0.95	0.972 0.629 0.773	SPO2796 SPO2797 SPO2798	1.19 1.03 1.12	0.474 SPO2799 0.466 SPO2800 0.03 SPO2801	1.11 1.08 1.05	0.954 0.107 0.848	SPO2791 SPO2792 SPO2793	1.23 1.13 0.68	0.199 0.933 0.514	SPO2791 SPO2792 SPO2793	1.43 1.05 0.71	0.323 0.984 0.564	SPO2791 SPO2792 SPO2793	0.88 0.90	0.353 0.900 0.985	SPO2787 SPO2788 SPO2789	1.08 1.25 1.14	0.459 0.292 0.439
SPO2799 SPO2800 SPO2801	0.87 0.85 1.31	0.449 0.491 0.211	SPO2798 SPO2799 SPO2800	1.31 0.89 0.91	0.022 0.6 0.71	SPO2799 SPO2800 SPO2801	1.23 1.05 1.01	0.689 SPO2802 0.435 SPO2803 0.479 SPO2804	1.34 1.13 1.71	0.951 0.64 0.509	SPO2794 SPO2795 SPO2796	0.84 0.81 0.75	0.700 0.745 0.406	SPO2794 SPO2795 SPO2796	1.00 0.81 0.75	0.989 0.781 0.652	SPO2794 SPO2795 SPO2796	0.74 0.96 0.99	0.577 0.902 0.972	SPO2790 SPO2791 SPO2792	1.35 0.99 1.04	0.189 0.931 0.981
SPO2802 SPO2803	0.52 0.76	0.027	SPO2801 SPO2802	1.27 0.51	0.103	SPO2802 SPO2803	1.11 0.99	0.119 SPO2805 0.855 SPO2806	1.11 1.11	0.767 0.755	SPO2797 SPO2798	1.53 1.07	0.272 0.222	SPO2797 SPO2798	1.46 1.08	0.029	SPO2797 SPO2798	1.20 1.16	0.570 0.046	SPO2793 SPO2794	0.96 0.79	0.937 0.349
SPO2804 SPO2805 SPO2806	0.88 0.91 0.85	0.325 5 0.805 5 0.714 5	SPO2803 SPO2804 SPO2805	0.76 0.97 0.95	0.362 0.812 0.978	SPO2804 SPO2805 SPO2806	1.05 1.21 1.02	0.43 SPO2807 0.69 SPO2808 0.777 SPO2809	1.19 1.35 1.02	0.335 0.469 0.091	SPO2799 SPO2800 SPO2801	0.82 1.74 0.57	0.584 0.028 0.226	SPO2799 SPO2800 SPO2801	0.81 1.79 0.60	0.634 0.013 0.257	SPO2799 SPO2800 SPO2801	1.03 1.23 1.06	0.929 0.302 0.739	SPO2795 SPO2796 SPO2797	0.94 1.01 1.21	0.804 0.981 0.005
SPO2807 SPO2808 SPO2809	1.25 0.98 0.64	0.203 5 0.448 5 0.119 5	SPO2806 SPO2807 SPO2808	0.84 1.61 0.81	0.637 0.229 0.131		1.22 1.01 1.16	0.701 SPO2810 0.553 SPO2811 0.114 SPO2812	1.02 1.08 1.14	0.255 0.74 0.71	SPO2802 SPO2803 SPO2804	0.31 0.44 0.30	0.004 0.009 0.010	SPO2802 SPO2803 SPO2804	0.32 0.44 0.33	0.002 0.017 0.012	SPO2802 SPO2803 SPO2804	1.01 0.93 1.04		SPO2798 SPO2799 SPO2800	1.21 0.98 1.26	0.317 0.997 0.062
SPO2810 SPO2811 SPO2812	0.58 0.68 0.77	0.134	SPO2809 SPO2810 SPO2811	0.7 0.65 0.75	0.012	SPO2810 SPO2811 SPO2812	1.03 1.1 1.08	0.014 SPO2813 0.689 SPO2814 0.809 SPO2815	1.01 1.21 1.09	0.361 0.006 0.182	SPO2805 SPO2806 SPO2807	0.42 0.44	0.003 0.041 0.008	SPO2805 SPO2806 SPO2807	0.41 0.45 0.57	0.028 0.053 0.041	SPO2805 SPO2806 SPO2807	0.77 0.96 1.47	0.895	SPO2801 SPO2802 SPO2803	1.00 1.05 0.99	0.966 0.271 0.982
SPO2813 SPO2814	0.7 0.56	0.071 0.012	SPO2812 SPO2813	0.78 0.71	0.197 0.04	SPO2813 SPO2814	1.31 1.3	0.075 SPO2816 0.174 SPO2817	1.21 1.11	0.565 0.072	SPO2808 SPO2809	0.93	0.293 0.293	SPO2808 SPO2809	1.06 1.16	0.026 0.149	SPO2808 SPO2809	1.05 0.98	0.100	SPO2804 SPO2805	1.01 0.76	0.986 0.455
SPO2815 SPO2816 SPO2817	0.65 1.48 1.44	0.161 S 0.069 S 0.04 S	SPO2814 SPO2815 SPO2816	0.63 0.65 1.19	0.065 0.106 0.213	SPO2815 SPO2816 SPO2817	1.27 1.26 1.04	0.624 SPO2818 0.168 SPO2819 0.035 SPO2820	1.22 1.01 1.4	0.134 0.535 0.532	SPO2810 SPO2811 SPO2812	1.56 1.46 1.20	0.154 0.088 0.024	SPO2810 SPO2811 SPO2812	1.44 1.47 1.23	0.092	SPO2810 SPO2811 SPO2812	1.11 0.93 0.89	0.654 0.543	SPO2806 SPO2807 SPO2808	0.93 1.31 1.02	0.884 0.326 0.383
SPO2818 SPO2819 SPO2820	1.23 1.95 1.33	0.069	SPO2817 SPO2818 SPO2819	1.7 1.14 1.67	0.036 0.303 0.058	SPO2818 SPO2819 SPO2820	1.06 1.09 1.18	0.171 SPO2821 0.459 SPO2822 0.391 SPO2823	1.04 1.42 1.38	0.562 0.471 0.348	SPO2813 SPO2814 SPO2815	1.16 1.39 1.10	0.095 0.008 0.344	SPO2813 SPO2814 SPO2815	1.13 1.33 1.01	0.001	SPO2813 SPO2814 SPO2815	1.14 0.99 0.96	0.066 0.292 0.986	SPO2809 SPO2810 SPO2811	1.06 1.04 0.88	0.623 0.850 0.632
SPO2821 SPO2822 SPO2823	1.63 0.88 0.53		SPO2820 SPO2821 SPO2822	1.22 1.54 0.95	0.026 0.005 0.97	SPO2821 SPO2822 SPO2823	1.18 1.24 1.14	0.903 SPO2824 0.321 SPO2825 0.421 SPO2826	1.27 1.11 1.05	0.911 0.04 0.297	SPO2816 SPO2817 SPO2818	0.57 0.23 0.36	0.068 0.007 0.061	SPO2816 SPO2817 SPO2818	0.54 0.22	0.250	SPO2816 SPO2817 SPO2818	0.88 0.98 1.68		SPO2812 SPO2813 SPO2814	0.91 1.07 1.02	0.262 0.387 0.193
SPO2824 SPO2825	1.46 1 0.85	0.451 0.859 0.71	SPO2823 SPO2824	0.61 1.37	0.053 0.468 0.71	SPO2824 SPO2825	1.1 1.16	0.913 SPO2827 0.052 SPO2828	1.2	0.03 0.479 0.989	SPO2819 SPO2820	0.85 0.74 1.01	0.580 0.235 0.509	SPO2819 SPO2820	0.88 0.80 0.98	0.408	SPO2819 SPO2820	1.20 0.85	0.420 0.287	SPO2815 SPO2816	1.03 0.78 0.96	0.743 0.626 0.895
SPO2826 SPO2827 SPO2828	1.13 1.12	0.22	SPO2825 SPO2826 SPO2827	0.84 0.98	0.618	SPO2826 SPO2827 SPO2828	1.23 1.02	0.061 SPO2830 0.343 SPO2831	1.53 1.32	0.576 0.59	SPO2821 SPO2822 SPO2823	0.85 0.94	0.566 0.814	SPO2821 SPO2822 SPO2823	0.83 0.83	0.084 0.411	SPO2821 SPO2822 SPO2823	0.85	0.682 0.921	SPO2817 SPO2818 SPO2819	1.38 1.05	0.451 0.799
SPO2829 SPO2830 SPO2831	0.81 0.95	0.647 0.618 0.912	SPO2828 SPO2829 SPO2830	1.09 0.96 0.85	0.727 0.94 0.738	SPO2829 SPO2830 SPO2831	1.06 1.15 1.22	0.215 SPO2832 0.605 SPO2833 0.355 SPO2834	1.02 1.02 1.15	0.938 0.244 0.42	SPO2824 SPO2825 SPO2826	0.90 0.90 1.91	0.868 0.359 0.168	SPO2824 SPO2825 SPO2826	0.88 0.90 1.88	0.818 0.744 0.157	SPO2824 SPO2825 SPO2826	0.94 0.79 0.69	0.909 0.062 0.457	SPO2820 SPO2821 SPO2822	0.90 1.08 0.91	0.587 0.243 0.338
SPO2832 SPO2833 SPO2834	0.85 1.12 1.22	0.798 0.178 0.383	SPO2831 SPO2832 SPO2833	0.99 0.81 1.22	0.89 0.825 0.106	SPO2832 SPO2833 SPO2834	1.09 1.2 1.17	0.914 SPO2835 0.04 SPO2836 0.921 SPO2837	1.38 1.07 1.13	0.589 0.047 0.423	SPO2827 SPO2828 SPO2829	2.40 1.27 0.94	0.020 0.598 0.695	SPO2827 SPO2828 SPO2829	2.32 1.15 0.89	0.020 0.708 0.669	SPO2827 SPO2828 SPO2829	0.71 0.97 1.03		SPO2823 SPO2824 SPO2825	0.97 0.93 0.79	0.903 0.915 0.049
SPO2835 SPO2836	1.12 1.43	0.746	SPO2834 SPO2835	0.75 0.99	0.42 0.845	SPO2835 SPO2836	1.26	0.726 SPO2838 0.18 SPO2839	1.31 1.01	0.851	SPO2830 SPO2831	0.66 0.73	0.294 0.331	SPO2830 SPO2831	0.59 0.77	0.194	SPO2830 SPO2831	0.76 0.82	0.144 0.543	SPO2826 SPO2827	0.79 0.83	0.709 0.289
SPO2837 SPO2838 SPO2839	0.81 1.37 1.61	0.123 0.668 0.071	SPO2836 SPO2837 SPO2838	1.34 0.83 1.54		SPO2837 SPO2838 SPO2839	1.05 1.08	0.212 SPO2840 0.916 SPO2841 0.005 SPO2842	1.04 1.11 1.31	0.391 0.925 0.869	SPO2832 SPO2833 SPO2834	1.27 0.89 1.05	0.729 0.607 1.000	SPO2832 SPO2833 SPO2834	1.19 0.75 1.27	0.100	SPO2832 SPO2833 SPO2834	0.81 0.98 0.68	0.651	SPO2828 SPO2829 SPO2830	0.96 1.05 0.81	0.925 0.705 0.186
SPO2840 SPO2841 SPO2842	0.83 0.98 1.01	0.58 0.957 0.803	SPO2839 SPO2840 SPO2841	1.67 0.78 0.93	0.048 0.566 0.834	SPO2840 SPO2841 SPO2842	1.29 1 1.17	0.52 SPO2843 0.95 SPO2844 0.993 SPO2845	1.22 1.01 1.14	0.329 0.825 0.408	SPO2835 SPO2836 SPO2837	1.43 1.04 0.96	0.463 0.854 0.533	SPO2835 SPO2836 SPO2837	1.66 1.19 1.01		SPO2835 SPO2836 SPO2837	1.10 1.01 0.88		SPO2831 SPO2832 SPO2833	0.87 0.93 0.87	0.233 0.894 0.477
SPO2843 SPO2844 SPO2845	0.67 0.81 1.07	0.151 0.711 0.842	SPO2842 SPO2843 SPO2844	1.01 0.84 0.75	0.868 0.059 0.769	SPO2843 SPO2844 SPO2845	1.1 1.09	0.742 SPO2846 0.662 SPO2847 0.576 SPO2848	1.08	0.396 0.848 0.242	SPO2838 SPO2839 SPO2840	0.50 0.20 0.95	0.580 0.010 0.436	SPO2838 SPO2839 SPO2840	0.50 0.20	0.514	SPO2838 SPO2839 SPO2840	0.95 1.14	0.968 0.242	SPO2834 SPO2835 SPO2836	0.93 1.03 0.93	0.642 0.972 0.207
SPO2846 SPO2847	0.79 1.81	0.168	SPO2845 SPO2846	1.02 0.76	0.744	SPO2846 SPO2847	1.1 1.01	0.303 SPO2849 0.995 SPO2850	1.01 1.43	0.928 0.233	SPO2841 SPO2842	0.47 0.92	0.264 0.787	SPO2841 SPO2842	0.40	0.043 0.237	SPO2841 SPO2842	0.91 0.96	0.847	SPO2837 SPO2838	0.95 0.99	0.860 0.996
SPO2848 SPO2849 SPO2850	0.79 1.04 0.84	0.198 0.732 0.108	SPO2847 SPO2848 SPO2849	1.56 0.85 1.16	0.325 0.133 0.775	SPO2848 SPO2849 SPO2850	1.05 1.12 1.1	0.174 SPO2851 0.984 SPO2852 0.042 SPO2853	1.32 1.28 1.39	0.817 0.889 0.325	SPO2844 SPO2845	0.83 0.97 1.05	0.257 0.833 0.727	SPO2843 SPO2844 SPO2845	0.64 0.93 1.04		SPO2843 SPO2844 SPO2845	0.67 0.91 1.02		SPO2839 SPO2840 SPO2841	1.07 1.08 0.93	0.761 0.502 0.780
SPO2851 SPO2852 SPO2853	1.1 0.83 1.17	0.873 0.546 0.552	SPO2850 SPO2851 SPO2852	0.99 1.11 0.93	0.782 0.841 0.989		1.07 1.08 1.09	0.962 SPO2854 0.22 SPO2855 0.345 SPO2856	1.17 1.04 1.13	0.446 0.825 0.862	SPO2846 SPO2847 SPO2848	0.25 0.68 1.64	0.002 0.536 0.007	SPO2846 SPO2847 SPO2848	0.27 0.71 1.73	0.009	SPO2846 SPO2847 SPO2848	1.20 1.00 0.96	0.500 0.957	SP02842 SP02843 SP02844	0.97 0.75 0.98	0.924 0.482 0.936
SPO2854 SPO2855	1.14 1.08	0.038 0.545	SPO2853 SPO2854	1.06 1.03	0.346 0.506	SPO2854 SPO2855	1.02	0.548 SPO2857 0.925 SPO2858	1.19 1.02	0.873 0.511	SPO2849 SPO2850	0.92 0.77	0.995 0.222	SPO2849 SPO2850	0.98 0.69	0.839 0.106	SPO2849 SPO2850	0.83 0.88	0.360 0.078	SPO2845 SPO2846	0.91 1.24	0.774 0.323
SPO2856 SPO2857 SPO2858	0.75 0.78 1.13	0.03 0.557 0.26	SPO2855 SPO2856 SPO2857	1.05 0.79 0.85		SPO2857 SPO2858	1.14 1.01 1.07	0.824 SPO2859 0.852 SPO2860 0.15 SPO2861	1.44 1.04 1.1	0.444 0.922 0.029		0.93 1.16 0.58	0.940 0.703 0.045	SPO2851 SPO2852 SPO2853	0.88 1.41 0.61	0.308 0.053	SPO2851 SPO2852 SPO2853	0.97 0.88 1.00	0.468 0.558	SPO2849	0.96 1.09 0.79	0.974 0.170 0.135
SPO2859 SPO2860 SPO2861	0.84 0.81 0.87	0.33 0.888 0.102 5	SPO2858 SPO2859 SPO2860	1.09 0.85 1.01	0.423	SPO2859 SPO2860 SPO2861	1.24 1.17 1.24	0.624 SPO2862 0.922 SPO2863 0.095 SPO2864	1.05 1.02 1.02	0.018 0.807 0.022	SPO2854 SPO2855 SPO2856	1.17 0.88 1.09	0.181 0.740 0.145	SPO2854 SPO2855 SPO2856	1.20 0.88 1.07	0.095	SPO2854 SPO2855 SPO2856	1.10 1.12 1.03	0.397	SPO2850 SPO2851 SPO2852	0.90 0.87 1.02	0.486 0.817 0.985
SPO2862	1.08		SPO2861	0.93		SPO2862	1.04	0.014 SPO2865	1.15	0.13		1.02	0.686	SPO2857	0.99		SPO2857	1.07		SPO2853	0.93	0.683

SPO2863 SPO2864	1.23	0.537 SPO2862 0.061 SPO2863	1.06	0.691 SPO2863 0.339 SPO2864	1.04	0.729 SPO2866 0.085 SPO2867	1.07	0.06 SPO2858 0.377 SPO2859	0.86	0.643 Si 0.139 Si	PO2858	0.88	0.896	SPO2858 SPO2859	1.02	0.838 SPO2854 0.921 SPO2855	1.19	0.500
SPO2865 SPO2866	0.85 1.23	0.261 SPO2864 0.506 SPO2865	0.92 0.86	0.125 SPO2865 0.293 SPO2866	1.26 1.19	0.077 SPO2868 0.137 SPO2869	1.04 1.23	0.605 SPO2860 0.975 SPO2861	1.06	0.932 SI	PO2860 PO2861	1.11		SPO2860 SPO2861	0.86 1.12	0.862 SPO2856 0.299 SPO2857	1.01 0.94	0.570 0.892
SPO2867 SPO2868 SPO2869	0.81 1 1.24	0.6 SPO2866 0.851 SPO2867 0.531 SPO2868	1.05 0.85 1.18	0.786 SPO2867 0.834 SPO2868 0.08 SPO2869	1.08 1.02 1.1	0.383 SPO2870 0.57 SPO2871 0.922 SPO2872	1.04 1.14 1.26	0.354 SPO2862 0.097 SPO2863 0.044 SPO2864	2.15 1.25	0.023 SI 0.548 SI 0.010 SI	PO2862 PO2863 PO2864	2.22 1.15 2.99	0.005 0.574 0.003	SPO2862 SPO2863 SPO2864	1.38 0.93 1.25	0.079 SPO2858 0.862 SPO2859 0.055 SPO2860	0.93 1.00 0.86	0.841 0.968 0.880
SPO2870 SPO2871	1.03	0.79 SPO2869 0.844 SPO2870	1.12 1.06	0.751 SPO2870 0.636 SPO2871	1.03	0.227 SPO2873 0.098 SPO2874	1.53 1.07	0.669 SPO2865 0.053 SPO2866	1.98 2.34	0.083 SI 0.007 SI	PO2865 PO2866	1.82 2.80	0.102 0.032	SPO2865 SPO2866	1.15 1.30	0.474 SPO2861 0.235 SPO2862	1.27 1.38	0.029 0.012
SPO2872 SPO2873 SPO2874	1.16 1.03 1.11	0.562 SPO2871 0.84 SPO2872 0.453 SPO2873	1.04 1.1 1.09	0.561 SPO2872 0.454 SPO2873 0.749 SPO2874	1.09 1.04	0.122 SPO2875 0.651 SPO2876 0.032 SPO2877	1.03 1.06 1.2	0.111 SPO2867 0.393 SPO2868 0.974 SPO2869	1.29 1.02	0.094 SI 0.086 SI 0.856 SI	PO2867 PO2868 PO2869	1.33 0.99	0.106 0.062 0.882	SPO2867 SPO2868 SPO2869	1.11 1.30 0.96	0.812 SPO2863 0.081 SPO2864 0.955 SPO2865	0.95 1.36 1.23	0.930 0.108 0.276
SPO2875 SPO2876	0.59 0.66	0.057 SPO2874 0.125 SPO2875	1.06	0.133 SPO2875 0.004 SPO2876	1.03 1.02	0.334 SPO2878 0.958 SPO2879	1.04 1.01	0.188 SPO2870 0.205 SPO2871	2.22 3.29		PO2870 PO2871	2.23 3.00	0.031 0.011	SPO2870 SPO2871	1.22	0.302 SPO2866 0.130 SPO2867	1.28 1.10	0.349
SPO2877 SPO2878 SPO2879	1.12 1.6	0.205 SPO2876 0.006 SPO2877 0.313 SPO2878	0.75 1.07 1.5	0.361 SPO2877 0.475 SPO2878 0.019 SPO2879	1.18 1.01 1.05	0.705 SPO2880 0.806 SPO2881 0.571 SPO2882	1.07 1.14 1.02	0.875 SPO2872 0.808 SPO2873 0.938 SPO2874	3.24 1.51 2.59		PO2872 PO2873 PO2874	3.12 1.19 2.67	0.007 0.623 0.011	SPO2872 SPO2873 SPO2874	1.21 1.08 1.27	0.741 SPO2868 0.816 SPO2869 0.100 SPO2870	1.26 0.98 1.22	0.112 0.999 0.417
SPO2880 SPO2881 SPO2882	1.06 0.78 0.78	0.878 SPO2879 0.43 SPO2880 0.813 SPO2881	1.19 0.93 0.83	0.152 SPO2880 0.993 SPO2881 0.54 SPO2882	1.02 1 1.04	0.851 SPO2883 0.798 SPO2884 0.876 SPO2885	1.17 1.1 1.12	0.843 SPO2875 0.528 SPO2876 0.395 SPO2877	2.06 4.55 1.98	0.000	PO2875 PO2876	2.05 3.88 1.82	0.001 0.018 0.163	SPO2875 SPO2876 SPO2877	1.13 1.40 1.10	0.179 SPO2871 0.127 SPO2872 0.193 SPO2873	1.31 1.27 1.06	0.218 0.219 0.593
SPO2883 SPO2884	1.01 0.42	0.696 SPO2882 0.199 SPO2883	0.76 0.93	0.801 SPO2883 0.61 SPO2884	1.03 1.02	0.876 SPO2885 0.618 SPO2886 0.559 SPO2887	1.12	0.395 SPO2877 0.688 SPO2878 0.052 SPO2879	0.75	0.058 SI	PO2877 PO2878 PO2879	0.73	0.059	SPO2878 SPO2879	1.16 0.96	0.157 SPO2874 0.819 SPO2875	1.32	0.028 0.239
SPO2885 SPO2886 SPO2887	0.82 0.91 0.88	0.256 SPO2884 0.501 SPO2885 0.008 SPO2886	0.53 0.8 0.97	0.148 SPO2885 0.04 SPO2886 0.98 SPO2887	1.26 1.18 1.12	0.89 SPO2888 0.856 SPO2889 0.081 SPO2890	1.13 1.02 1.15	0.208 SPO2880 0.051 SPO2881 0.272 SPO2882	0.81 0.99 0.93	0.789 SI 0.689 SI 0.899 SI	PO2880 PO2881	0.89 1.03 0.85	0.870 0.425 0.790	SPO2880 SPO2881 SPO2882	0.90 0.78 0.92	0.867 SPO2876 0.597 SPO2877 0.832 SPO2878	1.39 1.05 1.08	0.075 0.087 0.356
SPO2888 SPO2889	1.5 1.03	0.098 SPO2887 0.914 SPO2888	1.01 1.38	0.54 SPO2888 0.035 SPO2889	1.06 1.1	0.221 SPO2891 0.296 SPO2892	1.22 1.18	0.881 SPO2883 0.785 SPO2884	0.61 0.97	0.044 SI 0.929 SI	PO2883 PO2884	0.67 0.98	0.016 0.934	SPO2883 SPO2884	0.99 1.03	0.842 SPO2879 0.985 SPO2880	1.02	0.879 0.994
SPO2890 SPO2891 SPO2892	0.74 0.88 1.14	0.207 SPO2889 0.931 SPO2890 0.207 SPO2891	1.06 0.59 0.98	0.238 SPO2890 0.031 SPO2891 0.996 SPO2892	1.27 1.08 1.14	0.572 SPO2893 0.849 SPO2894 0.792 SPO2895	1.21 1.23 1.19	0.411 SPO2885 0.433 SPO2886 0.546 SPO2887	0.61 0.54	0.049 SI 0.015 SI 0.002 SI	PO2885 PO2886 PO2887	0.67 0.53	0.013 0.016 0.005	SPO2885 SPO2886 SPO2887	0.98 0.88 1.07	0.784 SPO2881 0.309 SPO2882 0.432 SPO2883	1.03 1.00 0.97	0.990 0.989 0.874
SPO2893 SPO2894	0.89 1.43	0.314 SPO2892 0.181 SPO2893	1.07 0.92	0.827 SPO2893 0.492 SPO2894	1.12 1.04	0.396 SPO2896 0.308 SPO2897	1.03 1.01	0.651 SPO2888 0.286 SPO2889	1.65 2.55	0.021 SI 0.043 SI	PO2888 PO2889	1.60 2.50	0.035	SPO2888 SPO2889	0.98 1.12	0.999 SPO2884 0.837 SPO2885	1.08 1.05	0.865 0.705
SPO2895 SPO2896 SPO2897	0.96 0.96 0.72	0.885 SPO2894 0.839 SPO2895 0.29 SPO2896	1.25 1.01 0.92	0.216 SPO2895 0.853 SPO2896 0.61 SPO2897	1.15 1.14 1.01	0.964 SPO2898 0.989 SPO2899 0.304 SPO2900	1.1 1.03 1.18	0.267 SPO2890 0.594 SPO2891 0.569 SPO2892	1.35 1.57 0.62	0.457 SI 0.728 SI 0.285 SI	PO2890 PO2891 PO2892	1.24 1.61 0.61	0.077 0.727 0.391	SPO2890 SPO2891 SPO2892	0.74 0.77 0.87	0.349 SPO2886 0.854 SPO2887 0.621 SPO2888	0.91 0.95 0.97	0.440 0.743 0.953
SPO2898 SPO2899	0.52 1.28	0.315 SPO2897 0.472 SPO2898	0.75 0.7	0.002 SPO2898 0.056 SPO2899	1.12	0.198 SPO2901 0.785 SPO2902	1.01	0.414 SPO2893 0.366 SPO2894	0.91	0.819 SI 0.450 SI	PO2893 PO2894	0.93	0.638	SPO2893 SPO2894	0.94 0.94	0.784 SPO2889 0.851 SPO2890	1.14 0.88	0.248 0.826
SPO2900 SPO2901 SPO2902	0.89 0.63	0.081 SPO2899 0.795 SPO2900 0.203 SPO2901	1.25 1.34 0.87	0.366 SPO2900 0.085 SPO2901 0.532 SPO2902	1.05 1.05	0.511 SPO2903 0.474 SPO2904 0.559 SPO2905	1.31 1.13 1.05	0.906 SPO2895 0.387 SPO2896 0.902 SPO2897	1.09 0.89 0.90	0.0.0	PO2895 PO2896 PO2897	1.03 0.99 0.90	0.479 0.427 0.863	SPO2895 SPO2896 SPO2897	1.01 0.99 0.93	0.831 SPO2891 0.938 SPO2892 0.681 SPO2893	0.87 0.92 0.96	0.937 0.862 0.804
SPO2903 SPO2904 SPO2905	1.34 0.88 1.12	0.709 SPO2902 0.325 SPO2903 0.433 SPO2904	0.71 1.22 0.84	0.074 SPO2903 0.776 SPO2904 0.207 SPO2905	1.08 1.03 1.11	0.888 SPO2906 0.215 SPO2907 0.882 SPO2908	1.04 1.18 1.29	0.524 SPO2898 0.146 SPO2899 0.967 SPO2900	1.26 0.78 1.30	0.411 SI	PO2898 PO2899 PO2900	1.30 0.83 1.39	0.042 0.573 0.044	SPO2898 SPO2899 SPO2900	0.96 0.98 1.16	0.888 SPO2894 0.938 SPO2895 0.222 SPO2896	1.00 0.99 1.02	0.966 0.949 0.786
SPO2906 SPO2907	1.33 1.5	0.025 SPO2905 0.073 SPO2906	1.06 1.36	0.64 SPO2906 0.018 SPO2907	1.08	0.934 SPO2909 0.445 SPO2910	1.07 1.04	0.829 SPO2901 0.064 SPO2902	0.88 0.93	0.694 SI 0.256 SI	PO2901 PO2902	0.95 0.90	0.936	SPO2901 SPO2902	1.06 1.11	0.392 SPO2897 0.375 SPO2898	0.99 1.04	0.941 0.667
SPO2908 SPO2909 SPO2910	1.4 1.73 0.88	0.577 SPO2907 0.358 SPO2908 0.264 SPO2909	1.26 1.47 1.57	0.146 SPO2908 0.61 SPO2909 0.361 SPO2910	1.02 1.09 1.06	0.936 SPO2911 0.901 SPO2912 0.071 SPO2913	1.05 1.14 1.07	0.908 SPO2903 0.584 SPO2904 0.825 SPO2905	0.67 0.98 1.02	0.624 Si 0.251 Si 0.634 Si	PO2903 PO2904 PO2905	0.70 1.02 0.98	0.716 0.295 0.770	SPO2903 SPO2904 SPO2905	1.34 0.90 1.00	0.826 SPO2899 0.388 SPO2900 0.900 SPO2901	0.93 1.17 1.03	0.843 0.237 0.795
SPO2911 SPO2912	1.03 0.79	0.749 SPO2910 0.015 SPO2911	0.93 1.05	0.69 SPO2911 0.496 SPO2912	1.03 1.33	0.718 SPO2914 0.428 SPO2915	1.1 1.31	0.97 SPO2906 0.32 SPO2907	1.23 1.21	0.120 SI 0.297 SI	PO2906 PO2907	1.20	0.089	SPO2906 SPO2907	1.01 1.17	0.855 SPO2902 0.395 SPO2903	1.17 1.08	0.271 0.959
SPO2913 SPO2914 SPO2915	1.06 0.68 0.68	0.915 SPO2912 0.536 SPO2913 0.119 SPO2914	0.79 0.97 0.68	0.007 SPO2913 0.961 SPO2914 0.408 SPO2915	1.32 1.06 1.06	0.689 SPO2916 0.815 SPO2917 0.117 SPO2918	1.02 1.06 1.13	0.288 SPO2908 0.324 SPO2909 0.73 SPO2910	0.81 0.70 1.22	0.898 SI 0.437 SI 0.167 SI	PO2908 PO2909 PO2910	0.85 0.78 1.24	0.617	SPO2908 SPO2909 SPO2910	0.96 1.01 1.14	0.977 SPO2904 1.000 SPO2905 0.164 SPO2906	0.90 1.02 0.96	0.548 0.567 0.933
SPO2916 SPO2917	0.86 0.66	0.272 SPO2915 0.072 SPO2916	0.74 0.96	0.091 SPO2916 0.951 SPO2917	1.16 1.22	0.089 SPO2919 0.107 SPO2920	1.11	0.878 SPO2911 0.325 SPO2912	0.74 0.72	0.155 SI 0.033 SI	PO2911 PO2912	0.78 0.79	0.081	SPO2911 SPO2912	0.95 0.99	0.434 SPO2907 0.704 SPO2908	1.14 0.96	0.465 0.963
SPO2918 SPO2919 SPO2920	0.95 0.69 0.92	0.879 SPO2917 0.011 SPO2918 0.829 SPO2919	0.7 0.86 0.71	0.029 SPO2918 0.479 SPO2919 0.139 SPO2920	1.03 1.08 1.54	0.83 SPO2921 0.643 SPO2922 0.317 SPO2923	1.12 1.01 1.13	0.013 SPO2913 0.217 SPO2914 0.168 SPO2915	0.57 0.77 0.52	0.188 SI 0.564 SI 0.039 SI	PO2913 PO2914 PO2915	0.53 0.78 0.53	0.234 0.613 0.010	SPO2913 SPO2914 SPO2915	0.99 0.88 0.88	0.986 SPO2909 0.742 SPO2910 0.638 SPO2911	1.00 1.17 0.96	0.990 0.191 0.784
SPO2921 SPO2922 SPO2923	1.39 1.25 1.15	0.189 SPO2920 0.469 SPO2921 0.518 SPO2922	0.93 1.38 1.15	0.862 SPO2921 0.047 SPO2922 0.163 SPO2923	1.17 1.26 1.08	0.022 SPO2924 0.199 SPO2925 0.664 SPO2926	1.03 1.15 1.1	0.172 SPO2916 0.929 SPO2917 0.559 SPO2918	0.58 0.92 0.79	0.134 Si 0.758 Si 0.369 Si	PO2916 PO2917 PO2918	0.54 0.85 0.79	0.114 0.105 0.243	SPO2916 SPO2917 SPO2918	0.75 0.84 0.85	0.182 SPO2912 0.022 SPO2913 0.557 SPO2914	0.98 0.96 0.91	0.857 0.961 0.893
SPO2924 SPO2925	0.99	0.973 SPO2923 0.55 SPO2924	0.95 1.14	0.987 SPO2924 0.025 SPO2925	1.03	0.371 SPO2927 0.965 SPO2928	1.14	0.429 SPO2919 0.461 SPO2920	1.31	0.054 SI 0.393 SI	PO2919 PO2920	1.30	0.006 0.279	SPO2919 SPO2920	0.79	0.461 SPO2915 0.190 SPO2916	0.91	0.181 0.199
SPO2926 SPO2927 SPO2928	0.85 0.71 0.91	0.312 SPO2925 0.325 SPO2926 0.76 SPO2927	1.33 0.8 0.72	0.083 SPO2926 0.094 SPO2927 0.14 SPO2928	1.15 1.03 1.13	0.9 SPO2929 0.575 SPO2930 1 SPO2931	1.03 1.12 1.02	0.083 SPO2921 0.262 SPO2922 0.138 SPO2923	0.40 0.68	0.012 SI	PO2921 PO2922 PO2923	0.39 0.69	0.012 0.018 0.207	SPO2921 SPO2922 SPO2923	0.99 0.93 1.60	0.914 SPO2917 0.499 SPO2918 0.460 SPO2919	0.96 0.95 0.88	0.487 0.771 0.429
SPO2929 SPO2930	1.11 1.13	0.635 SPO2928 0.674 SPO2929	0.88 1.14	0.704 SPO2929 0.098 SPO2930	1.03 1.09	0.791 SPO2932 0.197 SPO2933	1.03 1.19	0.428 SPO2924 0.581 SPO2925	1.23	0.012 SI 0.231 SI	PO2924 PO2925	1.15	0.042 0.061	SPO2924 SPO2925	0.89 1.91	0.328 SPO2920 0.156 SPO2921	0.78 0.90	0.357 0.214
SPO2931 SPO2932 SPO2933	0.64 1.07 0.76	0.046 SPO2930 0.381 SPO2931 0.056 SPO2932	1.05 0.65 1.1	0.194 SPO2931 0.018 SPO2932 0.251 SPO2933	1.05 1.25 1.02	0.258 SPO2934 0.05 SPO2935 0.461 SPO2936	1.04 1.12 1.03	0.012 SPO2926 0.019 SPO2927 0.449 SPO2928	0.36 0.54 0.51	0.007 SI 0.056 SI 0.032 SI	PO2926 PO2927 PO2928	0.40 0.60 0.53	0.000 0.044 0.009	SPO2926 SPO2927 SPO2928	0.93 1.07 1.01	0.323 SPO2922 0.720 SPO2923 0.964 SPO2924	0.93 1.06 0.84	0.404 0.736 0.041
SPO2934 SPO2935	0.99 0.44	0.916 SPO2933 0.023 SPO2934	0.8 1.01	0.222 SPO2934 0.085 SPO2935	1.1	0.092 SPO2937 0.39 SPO2938	1.11 1.27	0.978 SPO2929 0.618 SPO2930	0.36 0.24	0.089 SI 0.011 SI	PO2929 PO2930	0.38 0.28	0.050 0.010	SPO2929 SPO2930	0.94 1.13	0.938 SPO2925 0.703 SPO2926	1.36 0.97	0.194 0.915
SPO2936 SPO2937 SPO2938	0.95 0.81	0.976 SPO2935 0.935 SPO2936 0.166 SPO2937	0.51 1.03 0.86	0.205 SPO2936 0.945 SPO2937 0.763 SPO2938	1.01 1.05 1.12	0.583 SPO2939 0.974 SPO2941 0.416 SPO2942	1.29 1.15 1.07	0.816 SPO2931 0.095 SPO2932 0.982 SPO2933	1.05 0.24 0.99	0.481 SI 0.005 SI 0.643 SI	PO2931 PO2932 PO2933	1.03 0.26 0.92	0.070 0.002 0.873	SPO2931 SPO2932 SPO2933	1.01 0.93 0.93	0.488 SPO2927 0.779 SPO2928 0.770 SPO2929	1.09 0.96 0.99	0.564 0.842 0.997
SPO2939 SPO2941 SPO2942	1.26 1.59 0.98	0.051 SPO2938 0.068 SPO2939 0.974 SPO2941	0.85 1.2 1.42	0.598 SPO2939 0.045 SPO2941 0.134 SPO2942	1.13 1.13	0.043 SPO2943 0.605 SPO2944 0.99 SPO2945	1.17 0.99 1.22	0.159 SPO2934 0.071 SPO2935 0.709 SPO2936	0.99	0.053 SI 0.751 SI 0.405 SI	PO2934 PO2935	1.38	0.009 0.864 0.299	SPO2934 SPO2935 SPO2936	1.22 1.12 0.85	0.192 SPO2930 0.298 SPO2931 0.519 SPO2932	0.99 1.06 0.90	0.985 0.581 0.359
SPO2943 SPO2944	1.28 1.28	0.376 SPO2942 0.129 SPO2943	0.93	0.959 SPO2943 0.738 SPO2944	1.03	0.592 SPO2946 0.066 SPO2947	1.13 1.09	0.683 SPO2937 0.133 SPO2938	0.69 0.72	0.324 SI 0.222 SI	PO2937 PO2938	0.77 0.68	0.448 0.144	SPO2937 SPO2938	1.20 0.93	0.503 SPO2933 0.271 SPO2934	0.92 1.31	0.629 0.019
SPO2945 SPO2946 SPO2947	1.08 0.82 1.04	0.63 SPO2944 0.374 SPO2945 0.297 SPO2946	1.16 0.98 0.81	0.068 SPO2945 0.875 SPO2946 0.63 SPO2947	1.08	0.601 SPO2948 0.618 SPO2949 0.2 SPO2950	1.57 1.04	0.283 SPO2939 0.851 SPO2941 0.947 SPO2942	1.18 1.20 0.67	0.474 SI 0.246 SI 0.791 SI	PO2939 PO2941 PO2942	1.20 1.15 0.76	0.072 0.695 0.933	SPO2939 SPO2941 SPO2942	1.34 1.30 0.83	0.138 SPO2935 0.231 SPO2936 0.816 SPO2937	1.16 0.82 1.03	0.358 0.676 0.962
SPO2948 SPO2949	0.61 1.36	0.087 SPO2947 0.115 SPO2948	0.94 0.59	0.979 SPO2948 0.261 SPO2949	1.15	0.192 SPO2951 0.683 SPO2952	1.04	0.903 SPO2943 0.687 SPO2944	0.61	0.467 SI 0.015 SI	PO2943 PO2944	0.52 0.68		SPO2943 SPO2944	0.89	0.854 SPO2938 0.576 SPO2939	0.93 1.10	0.350
SPO2950 SPO2951 SPO2952	0.86 0.68	0.37 SPO2949 0.028 SPO2950 0.631 SPO2951	1.18 0.89 0.74	0.203 SPO2950 0.297 SPO2951 0.093 SPO2952	1.18 1.14 1.14	0.912 SPO2953 0.886 SPO2954 0.531 SPO2955	1.1 1.02 1.13	0.977 SPO2945 0.949 SPO2946 0.755 SPO2947	0.66 1.06 1.79	0.940 SI	PO2945 PO2946 PO2947	0.70 0.99 1.54	0.946	SPO2945 SPO2946 SPO2947	0.89 1.02 1.22	0.715 SPO2941 0.996 SPO2942 0.564 SPO2943	1.31 0.88 0.85	0.158 0.892 0.192
SPO2953 SPO2954 SPO2955	1.68 1.42 1.25	0.06 SPO2952 0.529 SPO2953 0.058 SPO2954	1.01 1.41 1.24	0.71 SPO2953 0.223 SPO2954 0.682 SPO2955	1.31 0.99 1.23	0.663 SPO2956 0.97 SPO2957 0.246 SPO2958	1.17 1.05 1.02	0.183 SPO2948 0.411 SPO2949 0.204 SPO2950	1.46 0.66 1.28		PO2948 PO2949 PO2950	1.77 0.69 1.34		SPO2948 SPO2949 SPO2950	1.13 0.99 1.04	0.454 SPO2944 0.970 SPO2945 0.866 SPO2946	0.89 0.83	0.289 0.282 0.652
SPO2956 SPO2957	1.11	0.043 SPO2955 0.327 SPO2956	1.15 1.14	0.157 SPO2956 0.12 SPO2957	1.09 1.12	0.87 SPO2959 0.096 SPO2960	1.26 1.09	0.01 SPO2951 0.804 SPO2952	0.60 0.98	0.040 SI 0.934 SI	PO2951 PO2952	0.56 0.97	0.007	SPO2951 SPO2952	0.99 0.90	0.954 SPO2947 0.824 SPO2948	1.20 1.11	0.197 0.708
SPO2958 SPO2959 SPO2960	1.07 0.76 0.87	0.573 SPO2957 0.149 SPO2958 0.451 SPO2959	1.08 1.06 0.66	0.628 SPO2958 0.666 SPO2959 0.047 SPO2960	1.01 0.98 1.11	0.354 SPO2961 0.11 SPO2962 0.762 SPO2963	1.13 1.1 1.09	0.505 SPO2953 0.835 SPO2954 0.058 SPO2955	0.88 0.81 0.78	0.866 SI 0.785 SI 0.052 SI	PO2953 PO2954 PO2955	0.96 0.79 0.76	0.739	SPO2953 SPO2954 SPO2955	1.18 1.08 1.01	0.587 SPO2949 0.915 SPO2950 0.871 SPO2951	1.07 0.96 1.02	0.696 0.871 0.632
SPO2961 SPO2962	0.89	0.047 SPO2960 0.01 SPO2961	0.94 0.93	0.931 SPO2961 0.765 SPO2962	1.04	0.722 SPO2964 0.471 SPO2965	1.13	0.225 SPO2956 0.185 SPO2957	1.18 0.87	0.233 SI 0.230 SI	PO2956 PO2957	1.10 0.98		SPO2956 SPO2957	1.07 0.97	0.741 SPO2952 0.303 SPO2953	0.92 1.06	0.794
SPO2963 SPO2964 SPO2965	1.06 0.99 2.31	0.849 SPO2962 0.783 SPO2963 0.004 SPO2964	0.54 1 0.94	0.027 SPO2963 0.974 SPO2964 0.558 SPO2965	1.18 1.22 1.14	0.142 SPO2967 0.11 SPO2968 0.053 SPO2969	1.19 1.2 1.21	0.676 SPO2958 0.866 SPO2959 0.035 SPO2960	0.75 0.70 1.28	0.218 SI 0.125 SI 0.104 SI	PO2958 PO2959 PO2960	0.74 0.70 1.25	0.153 0.038 0.376	SPO2958 SPO2959 SPO2960	0.94 1.02 0.93	0.917 SPO2954 0.230 SPO2955 0.861 SPO2956	1.04 1.02 1.05	0.941 0.881 0.777
SPO2967 SPO2968 SPO2969	1.23 0.92 1.08	0.207 SPO2965 0.523 SPO2967 0.011 SPO2968	1.84 1.2 1.04	0.007 SPO2967 0.188 SPO2968	1.06 1.16 1.14	0.992 SPO2970 0.851 SPO2971 0.212 SPO2972	1.06 1.22 1.1	0.645 SPO2961 0.987 SPO2962 0.565 SPO2963	0.58 0.10	0.080 SI 0.005 SI	PO2961 PO2962 PO2963	0.52	0.008	SPO2961 SPO2962 SPO2963	1.12 1.15 1.03	0.416 SPO2957 0.425 SPO2958 0.627 SPO2959	0.95 0.86 0.98	0.436 0.071 0.833
SPO2970 SPO2971	1.38	0.013 SPO2969 0.171 SPO2970	1.12 1.27	0.62 SPO2969 0.014 SPO2970 0.034 SPO2971	1.09	0.589 SPO2974 0.806 SPO2975	1.01 1.02	0.455 SPO2964 0.818 SPO2965	0.56 0.79	0.032 SI 0.242 SI	PO2964 PO2965	0.52 0.79	0.054	SPO2964 SPO2965	1.01 1.25	0.741 SPO2960 0.090 SPO2961	1.01	0.942 0.738
SPO2972 SPO2974 SPO2975	1.27 1.1 1.2	0.172 SPO2971 0.253 SPO2972 0.67 SPO2974	1.07 1.19 1.11	0.521 SPO2972 0.341 SPO2974 0.003 SPO2975	2.26 1.86 1.77	0.897 SPO2976 0.528 SPO2977 0.856 SPO2978	1.2 1.16 1.16	0.528 SPO2967 0.856 SPO2968 0.927 SPO2969	2.12 1.15 1.03	0.028 SI 0.057 SI 0.052 SI	PO2967 PO2968 PO2969	2.05 1.13 1.08	0.023 0.287 0.006	SPO2967 SPO2968 SPO2969	1.00 0.96 1.08	0.990 SPO2962 0.922 SPO2963 0.195 SPO2964	1.25 0.99 0.97	0.132 0.802 0.995
SPO2976 SPO2977	0.76 0.98	0.112 SPO2975 0.969 SPO2976	1.08 0.77	0.67 SPO2976 0.077 SPO2977	1.1 1.03	0.886 SPO2979 0.552 SPO2980	1.05 1.22	0.759 SPO2970 0.764 SPO2971	0.70 1.04	0.910 SI	PO2970 PO2971	0.71 0.99	0.887	SPO2970 SPO2971	0.94 0.93	0.793 SPO2965 0.756 SPO2967	0.94 0.96	0.699 0.839
SPO2978 SPO2979 SPO2980	0.9 0.86 1.08	0.892 SPO2977 0.477 SPO2978 0.716 SPO2979	0.9 0.88	0.857 SPO2978 0.907 SPO2979 0.599 SPO2980	1.02 1.07 0.99	0.88 SPO2981 0.214 SPO2982 0.685 SPO2983	1.17 1.07 1.05	0.136 SPO2972 0.786 SPO2974 0.986 SPO2975	1.03 0.70 1.18		PO2972 PO2974 PO2975	1.15 0.79 1.15		SPO2972 SPO2974 SPO2975	1.67 0.85 0.95	0.021 SPO2968 0.118 SPO2969 0.951 SPO2970	0.97 1.10 0.94	0.992 0.036 0.615
SPO2981 SPO2982 SPO2983	1.17 0.99	0.232 SPO2980 0.882 SPO2981 0.993 SPO2982	1.06 1.19 1.03	0.9 SPO2981 0.077 SPO2982	1.1 1 1.05	0.007 SPO2984 0.632 SPO2985 0.967 SPO2986	1.01 1.11	0.35 SPO2976 0.164 SPO2977 0.695 SPO2978	0.90 0.97 0.81		PO2976 PO2977 PO2978	0.94 1.00 0.81	0.753 0.946	SPO2976 SPO2977 SPO2978	1.02 1.00 0.84	0.718 SPO2971 0.995 SPO2972 0.538 SPO2974	0.93 1.07 0.87	0.827 0.790 0.070
SPO2984 SPO2985	0.93 0.73	0.849 SPO2983 0.359 SPO2984	0.96 1.03	0.998 SPO2984 0.755 SPO2985	1.09 1.38	0.981 SPO2987 0.591 SPO2988	1.16 1.11	0.024 SPO2979 0.315 SPO2980	1.36 0.65	0.033 SI 0.462 SI	PO2979 PO2980	1.38 0.65	0.124 0.532	SPO2979 SPO2980	1.19 0.75	0.286 SPO2975 0.348 SPO2976	0.90 0.93	0.667 0.634
SPO2986 SPO2987 SPO2988	0.71 0.66 0.99	0.255 SPO2985 0.013 SPO2986 0.993 SPO2987	0.8 0.74 0.71	0.29 SPO2986 0.342 SPO2987 0.116 SPO2988	1.12 1.1 1.08	0.681 SPO2989 0.023 SPO2990 0.395 SPO2991	1.25 2.13 1.95	0.308 SPO2981 0.214 SPO2982 0.071 SPO2983	0.76 0.99 0.83	0.046 SI 0.835 SI 0.958 SI	PO2981 PO2982 PO2983	0.79 1.03 0.83	0.021 0.768 0.967	SPO2981 SPO2982 SPO2983	0.85 0.87 0.83	0.262 SPO2977 0.545 SPO2978 0.932 SPO2979	0.93 0.90 1.17	0.896 0.746 0.374
SPO2989 SPO2990	0.95 0.96	0.495 SPO2988 0.911 SPO2989	1.03	0.871 SPO2989 0.093 SPO2990	1.07 1.01	0.162 SPO2992 0.218 SPO2993	1.7 1.07	0.65 SPO2984 0.958 SPO2985	1.81 1.13	0.034 SI 0.444 SI	PO2984 PO2985	1.73 1.15	0.009	SPO2984 SPO2985	1.08 0.94	0.704 SPO2980 0.840 SPO2981	0.81 0.79	0.127 0.135
SPO2991 SPO2992 SPO2993	0.75 0.95 1.21	0.23 SPO2990 0.701 SPO2991 0.812 SPO2992	0.88 0.77 0.95	0.386 SPO2991 0.233 SPO2992 0.908 SPO2993	1.07 1.06 1.09	0.417 SPO2994 0.475 SPO2995 0.954 SPO2996	1.08 1.08 1.16	0.075 SPO2986 0.895 SPO2987 0.875 SPO2988	1.15 1.79 0.91	0.349 Si 0.039 Si 0.988 Si	PO2986 PO2987 PO2988	1.15 1.86 0.88	0.003	SPO2986 SPO2987 SPO2988	1.00 1.18 1.01	0.922 SPO2982 0.354 SPO2983 0.913 SPO2984	0.93 0.85 1.17	0.744 0.938 0.272
SPO2994 SPO2995	0.43 0.63	0.017 SPO2993 0.345 SPO2994	1.03 0.49	0.945 SPO2994 0.424 SPO2995	1.21 1.05	0.073 SPO2997 0.716 SPO2998	1.1	0.955 SPO2989 0.675 SPO2990	1.04 1.51	0.189 SI 0.044 SI	PO2989 PO2990	1.02 1.72	0.133	SPO2989 SPO2990	0.93 1.21	0.581 SPO2985 0.087 SPO2986	0.94 1.06	0.324 0.806
SPO2996 SPO2997 SPO2998	0.79 0.82 1.23	0.606 SPO2995 0.22 SPO2996 0.075 SPO2997	0.66 0.85 0.83	0.159 SPO2996 0.759 SPO2997 0.499 SPO2998	1.16 1.4 1.02	0.884 SPO2999 0.823 SPO3000 0.498 SPO3001	1.06 1.16 0.98	0.322 SPO2991 0.984 SPO2992 0.982 SPO2993	1.31 1.35	0.025 SI	PO2991 PO2992 PO2993	1.27 1.46	0.037	SPO2991 SPO2992 SPO2993	0.95 1.09 0.87	0.808 SPO2987 0.405 SPO2988 0.774 SPO2989	1.24 0.98 0.93	0.181 0.969 0.222
SPO2999 SPO3000	1.16 0.67	0.576 SPO2998 0.262 SPO2999	1.13 1.11	0.564 SPO2999 0.569 SPO3000	1.12 1.02	0.353 SPO3002 0.58 SPO3003	1.51 1.06	0.969 SPO2994 0.795 SPO2995	1.47 1.64	0.064 SI 0.043 SI	PO2994 PO2995	1.41 1.52	0.127	SPO2994 SPO2995	0.86 0.85	0.123 SPO2990 0.676 SPO2991	1.23 0.98	0.241 0.921
SPO3001 SPO3002 SPO3003	0.98 1.22 0.69	0.997 SPO3000 0.552 SPO3001 0.492 SPO3002	0.75 0.86 1.02	0.323 SPO3001 0.93 SPO3002 0.637 SPO3003	1 1.07 1.03	0.929 SPO3004 0.791 SPO3005 0.791 SPO3008	1.18 1.04 1.19	0.104 SPO2996 0.873 SPO2997 0.707 SPO2998	1.74 1.54 1.37	0.216 SI 0.004 SI	PO2996 PO2997 PO2998	1.57 1.48 1.39	0.229	SPO2996 SPO2997 SPO2998	0.82 0.85 1.05	0.660 SPO2992 0.496 SPO2993 0.110 SPO2994	1.07 0.88 0.88	0.348 0.872 0.625
SPO3004	0.51	0.062 SPO3003	0.71	0.548 SPO3004		0.126 SPO3009	1.2	0.584 SPO2999	0.95	0.801 SI	PO2999	1.13		SPO2999	1.02	0.991 SPO2995	0.88	0.245

SPO3005 SPO3008	1.12	0.889 SPO3004 0.333 SPO3005	0.52	0.101	SPO3005 SPO3008	1.06	0.815 SPO3010 0.846 SPO3011	1.13	0.896	SPO3000 SPO3001	0.66	0.294	SPO3000 SPO3001	0.56 0.63	0.063	SPO3000 SPO3001	0.86	0.412	SPO2996 SPO2997	0.86	0.686 0.754
SPO3009 SPO3010	0.95 1.08	0.951 SPO3008 0.33 SPO3009	0.76 1.02	0.213 0.139	SPO3009 SPO3010	1.03 1.07	0.85 SPO3012 0.858 SPO3013	1.02 1.05	0.342 0.721	SPO3002 SPO3003 SPO3004	1.38	0.045 0.362	SPO3002 SPO3003 SPO3004	1.46	0.061 0.352	SPO3002 SPO3003	1.05 0.93	0.801 0.906	SPO2998 SPO2999	0.93 0.93	0.887 0.503
SPO3011 SPO3012 SPO3013	0.97 1.62 0.71	0.927 SPO3010 0.075 SPO3011 0.402 SPO3012	0.94 0.94 1.5	0.953 0.889 0.091	SPO3011 SPO3012 SPO3013	1.24 1.02 1.12	0.738 SPO3014 0.551 SPO3015 0.796 SPO3016	1.1 1.32 1.08	0.01 0.245 0.568	SPO3004 SPO3005 SPO3008	0.66 0.53	0.071 0.808 0.079	SPO3004 SPO3005 SPO3008	0.71 0.51	0.049 0.896 0.038	SPO3004 SPO3005 SPO3008	0.96 0.90 0.95	0.973 0.938 0.712	SPO3000 SPO3001 SPO3002	0.87 1.04 1.03	0.512 0.955 0.706
SPO3014 SPO3015 SPO3016	1.74 1.19 0.52	0.018 SPO3013 0.243 SPO3014 0.027 SPO3015	0.66 1.38 1.02	0.372 0.003 0.495	SPO3014 SPO3015 SPO3016	1.07 1.19 1.02	0.003 SPO3017 0.329 SPO3018 0.304 SPO3019	1.12 1.53 1.08	0.054 0.627 0.479	SPO3009 SPO3010 SPO3011	2.15 1.12 0.65	0.027 0.835 0.176	SPO3009 SPO3010 SPO3011	1.97 1.21 0.65	0.038 0.057 0.053	SPO3009 SPO3010 SPO3011	1.24 0.95 0.94	0.320 0.820 0.602	SPO3003 SPO3004 SPO3005	0.96 0.97 0.85	0.966 0.990 0.891
SPO3017 SPO3018	0.46	0.045 SPO3016 0.594 SPO3017	0.46 0.46	0.004	SPO3017 SPO3018	0.99 1.17	0.209 SPO3020 0.975 SPO3021	1.1	0 0.81	SPO3012 SPO3013	0.66 0.77	0.266 0.503	SPO3012 SPO3013	0.60 0.79	0.083 0.626	SPO3012 SPO3013	1.62	0.194 0.974	SPO3008 SPO3009	0.94 1.21	0.783 0.479
SPO3019 SPO3020 SPO3021	1.02 0.85 0.75	0.75 SPO3018 0 SPO3019 0.674 SPO3021	0.89 0.97 0.75	0.462 0.962 0.83	SPO3019 SPO3020 SPO3021	1.06 1.13 1.1	0.377 SPO3022 0.902 SPO3023 0.965 SPO3024	1.19 1.07	0.892 0.943 0.875	SPO3014 SPO3015 SPO3016	0.16 1.25 1.97	0.001 0.249 0.004	SPO3014 SPO3015 SPO3016	0.14 1.48 1.99	0.003 0.012 0.001	SPO3014 SPO3015 SPO3016	1.38 1.28		SPO3010 SPO3011 SPO3012	0.94 0.93 1.26	0.778 0.697 0.590
SPO3022 SPO3023 SPO3024	1.36 0.94 0.68	0.388 SPO3022 0.858 SPO3023 0.384 SPO3024	1.27 1.03 0.81	0.154	SPO3022 SPO3023 SPO3024	1.07 1.27 0.99	0.726 SPO3025 0.824 SPO3026 0.655 SPO3027	1.16 1.02 1.11	0.376 0.93	SPO3017 SPO3018 SPO3019	0.69 0.60	0.003 0.105 0.019	SPO3017 SPO3018 SPO3019	3.74 0.71 0.60	0.006 0.036 0.004	SPO3017 SPO3018 SPO3019	1.58 0.95 0.88	0.668	SPO3013 SPO3014 SPO3015	1.01 2.11 1.32	0.951 0.024 0.194
SPO3025 SPO3026	0.85 1.03	0.123 SPO3025 0.81 SPO3026	0.94 0.99	0.955 0.897	SPO3025 SPO3026	1.41 1.14	0.51 SPO3028 0.684 SPO3029	1.12 0.99	0.743 0.971	SPO3020 SPO3021	0.98 1.41	0.835 0.592	SPO3020 SPO3021	0.94 1.21	0.172 0.875	SPO3020 SPO3021	0.82 1.07	0.547 0.948	SPO3016 SPO3017	1.07 1.44	0.110 0.079
SPO3027 SPO3028 SPO3029	0.81 1.69 0.93	0.394 SPO3027 0.019 SPO3028 0.209 SPO3029	0.75 1.64 0.92	0.355 0.145 0.346	SPO3027 SPO3028 SPO3029	1.08 1.15 1.02	0.027 SPO3030 0.947 SPO3031 0.826 SPO3032	1.07 1.07 1.22	0.675 0.976 0.809	SPO3022 SPO3023 SPO3024	0.65 0.84 1.11	0.075 0.357 0.925	SPO3022 SPO3023 SPO3024	0.67 0.96 1.38	0.097 0.970 0.078	SPO3022 SPO3023 SPO3024	0.93 1.18 1.42	0.103	SPO3018 SPO3019 SPO3020	0.94 0.85 0.64	0.514 0.081 0.151
SPO3030 SPO3031	1.1 2.67 1.74	0.428 SPO3030 0.36 SPO3031 0.019 SPO3032	1.2 2.09 1.87	0.64 0.163	SPO3030 SPO3031 SPO3032	1.1 1.08 1.04	0.5 SPO3033 0.993 SPO3034 0.873 SPO3035	1 1.02 0.99	0.696 0.557 0.398	SPO3025 SPO3026	0.63 1.03	0.094	SPO3025 SPO3026 SPO3027	0.58 1.10	0.033	SPO3025 SPO3026 SPO3027	0.75 1.06 0.93	0.064 0.522 0.821	SPO3021 SPO3022 SPO3023	1.02 1.02 1.14	1.000 0.871 0.425
SPO3032 SPO3033 SPO3034	2.26 1.65	0.094 SPO3033 0.029 SPO3034	2.29 1.18	0.244 0.292	SPO3033 SPO3034	1.06 1.25	0.796 SPO3036 0.313 SPO3037	1.13 1.04	0.053 0.448	SPO3028 SPO3029	0.72 0.57	0.030	SPO3028 SPO3029	0.76 0.56	0.463 0.046	SPO3028 SPO3029	1.11 0.89	0.730 0.596	SPO3024 SPO3025	1.14 0.71	0.484
SPO3035 SPO3036 SPO3037	1.37 0.92 0.82	0.042 SPO3035 0.658 SPO3036 0.188 SPO3037	1.45 0.9 0.87	0.065 0.187 0.489	SPO3035 SPO3036 SPO3037	1.04 1.12 1.06	0.298 SPO3038 0.245 SPO3039 0.79 SPO3040	1.14 1.03 1.09	0.757 0.935 0.991	SPO3030 SPO3031 SPO3032	0.81 0.33 0.26	0.321 0.510 0.034	SPO3030 SPO3031 SPO3032	0.81 0.28 0.24	0.465 0.488 0.057	SPO3030 SPO3031 SPO3032	0.89 0.94 0.95	0.213 0.980 0.762	SPO3026 SPO3027 SPO3028	1.09 0.99 0.95	0.589 0.846 0.903
SPO3038 SPO3039 SPO3040	0.93 0.79 0.91	0.981 SPO3038 0.581 SPO3039 0.951 SPO3040	0.81 0.94	0.873 0.664 0.984	SPO3038 SPO3039	1.03 1.08 1.05	0.542 SPO3041 0.659 SPO3042 0.908 SPO3043	1.16 1.06 1.25	0.862 0.432 0.221	SPO3033 SPO3034 SPO3035	0.25 0.55 0.90	0.025 0.009 0.912	SPO3033 SPO3034 SPO3035	0.28 0.60 0.95	0.073 0.169 0.658	SPO3033 SPO3034 SPO3035	1.21 0.97	0.422 0.818 0.899	SPO3029 SPO3030 SPO3031	0.91 0.89 0.96	0.637 0.703 0.987
SPO3041 SPO3042	0.91 0.92	0.955 SPO3041 0.923 SPO3042	0.77 1.05	0.686	SPO3040 SPO3041 SPO3042	1.05	0.549 SPO3044 0.888 SPO3045	1.01	0.221 0.812 0.357	SPO3036 SPO3037	0.74 1.44	0.103 0.137	SPO3035 SPO3036 SPO3037	0.74 1.38	0.658 0.382 0.050	SPO3036 SPO3037	0.97	0.944	SPO3032 SPO3033	0.99	0.969 0.610
SPO3043 SPO3044 SPO3045	0.81 1.11 0.72	0.771 SPO3043 0.726 SPO3044 0.5 SPO3045	0.81 1.12 0.78	0.738 0.665 0.593	SPO3043 SPO3044 SPO3045	1.04 1.03 1.03	0.591 SPO3046 0.816 SPO3047 0.461 SPO3048	1.13 1.07 1.15	0.409 0.182 0.706	SPO3038 SPO3039 SPO3040	1.11 0.92 1.21	0.889 0.819 0.769	SPO3038 SPO3039 SPO3040	1.11 1.00 1.05	0.951	SPO3038 SPO3039 SPO3040	1.08 0.94 1.04	0.851	SPO3034 SPO3035 SPO3036	1.00 0.96 0.92	0.988 0.857 0.538
SPO3046 SPO3047	0.86 1.14	0.388 SPO3046 0.554 SPO3047	0.83 1.13	0.093 0.542	SPO3046 SPO3047	0.99 1	0.645 SPO3049 0.351 SPO3050	1.08	0.55 0.197	SPO3041 SPO3042	0.78 0.76	0.377 0.345	SPO3041 SPO3042	0.82 0.74	0.792 0.062	SPO3041 SPO3042	0.82 0.80	0.340 0.143	SPO3037 SPO3038	1.04 0.94	0.762 0.885
SPO3048 SPO3049 SPO3050	1.22 0.97 1.43	0.824 SPO3048 0.836 SPO3049 0.13 SPO3050	1.25 0.9 1.45	0.805 0.871 0.085	SPO3048 SPO3049 SPO3050	1.2 1.07 1.41	0.747 SPO3051 0.66 SPO3052 0.136 SPO3053	1.1 1.08 1.04	0.092 0.066 0.822	SPO3044 SPO3045	1.51 1.05 1.46	0.277 0.977 0.387	SPO3044 SPO3045	1.34 0.85 1.49	0.716 0.677 0.301	SPO3043 SPO3044 SPO3045	1.05 0.91 1.24		SPO3039 SPO3040 SPO3041	0.96 1.00 0.92	0.881 0.948 0.705
SPO3051 SPO3052 SPO3053	1.2 0.89 1.26	0.22 SPO3051 0.068 SPO3052 0.41 SPO3053	1.15 0.95 1.18	0.31 0.388 0.705	SPO3051 SPO3052 SPO3053	1.32 1.02 1.04	0.289 SPO3054 0.069 SPO3055 0.84 SPO3056	1.28 1.02 1.1	0.576 0.541 0.376	SPO3046 SPO3047 SPO3048	1.37 0.83 0.86	0.112 0.445 0.848	SPO3046 SPO3047 SPO3048	1.41 0.81 0.77	0.009 0.197 0.743	SPO3046 SPO3047 SPO3048	0.90 0.86 0.81	0.530	SPO3042 SPO3043 SPO3044	0.88 1.17 0.87	0.461 0.646 0.706
SPO3054 SPO3055	1.11	0.119 SPO3054 0.02 SPO3055	1.09 1.7	0.303 0.048	SPO3054 SPO3055	1.12 1.14	0.389 SPO3057 0.052 SPO3058	1.05	0.615 0.878	SPO3049 SPO3050	1.38 0.68	0.395 0.184	SPO3049 SPO3050	1.45 0.65	0.394 0.103	SPO3049 SPO3050	1.44 0.93	0.334 0.378	SPO3045 SPO3046	1.25 0.96	0.549 0.611
SPO3056 SPO3057 SPO3058	0.76 1.18 1.42	0.178 SPO3056 0.162 SPO3057 0.472 SPO3058	0.79 1.02 1.41	0.23 0.45 0.425	SPO3056 SPO3057 SPO3058	1.35 1.03 1.04	0.439 SPO3059 0.594 SPO3060 0.833 SPO3062	1.03 1.11	0.835 0.395 0.124	SPO3051 SPO3052 SPO3053	0.65 0.74 0.43	0.057 0.095 0.076	SPO3051 SPO3052 SPO3053	0.65 0.77 0.42	0.012 0.214 0.093	SPO3051 SPO3052 SPO3053	1.01 0.95 0.99	0.854 0.373 0.963	SPO3047 SPO3048 SPO3049	0.88 0.81 1.39	0.479 0.814 0.500
SPO3059 SPO3060 SPO3062	0.81 0.79 1.26	0.397 SPO3059 0.021 SPO3060 0.04 SPO3062	0.86 0.83 1.22	0.419 0.195 0.016	SPO3059 SPO3060 SPO3062	1.25 1.04 1.02	0.842 SPO3063 0.908 SPO3064 0.031 SPO3065	1 1.11 1.75	0.249 0.042 0.755	SPO3054 SPO3055 SPO3056	0.44 0.69 1.00	0.002 0.095 0.652	SPO3054 SPO3055 SPO3056	0.45 0.68 0.95	0.013 0.021 0.509	SPO3054 SPO3055 SPO3056	1.15 1.11 0.98	0.595 0.684 0.997	SPO3050 SPO3051 SPO3052	0.85 1.02 0.91	0.371 0.569 0.337
SPO3063 SPO3064	1.16 0.85	0.241 SPO3063 0.248 SPO3064	1.02 0.82	0.564 0.197	SPO3063 SPO3064	1.02 1.03	0.295 SPO3066 0.049 SPO3067	1.07	0.233 0.965	SPO3057 SPO3058	0.85 0.79	0.474 0.719	SPO3057 SPO3058	0.88 0.69	0.609 0.521	SPO3057 SPO3058	0.98 1.10	0.938	SPO3053 SPO3054	0.94 1.08	0.896 0.637
SPO3065 SPO3066 SPO3067	0.73 1.39 1.12	0.345 SPO3065 0.07 SPO3066 0.38 SPO3067	0.87 1.28 1.21	0.223 0.193 0.186	SPO3065 SPO3066 SPO3067	0.99 1.01	0.483 SPO3068 0.187 SPO3069 0.691 SPO3070	1.01 1.06	0.7 0.911 0.006	SPO3059 SPO3060 SPO3062	0.50 0.47 0.90	0.014 0.009 0.724	SPO3059 SPO3060 SPO3062	0.53 0.46 0.82	0.014 0.003 0.036	SPO3059 SPO3060 SPO3062	1.21 1.13 1.08	0.747 0.230 0.817	SPO3055 SPO3056 SPO3057	1.02 1.05 1.09	0.909 0.670 0.519
SPO3068 SPO3069 SPO3070	1.15 1.47 1.15	0.613 SPO3068 0.143 SPO3069 0.19 SPO3070	1.08 1.26 1.17	0.765 0.443 0.021	SPO3068 SPO3069 SPO3070	0.99 1.01 1.32	0.516 SPO3071 0.945 SPO3072 0.043 SPO3073	1.06 1.1 1.07	0.007 0.263 0.099	SPO3063 SPO3064 SPO3065	0.71 1.45 1.96	0.061 0.040 0.009	SPO3063 SPO3064 SPO3065	0.69 1.49 1.69	0.011 0.018 0.057	SPO3063 SPO3064 SPO3065	0.97 1.00 1.14	0.824 0.967 0.600	SPO3058 SPO3059 SPO3060	1.09 1.19 1.07	0.761 0.441 0.357
SPO3071 SPO3072	0.96 1.22	0.387 SPO3071 0.169 SPO3072	0.93 1.18	0.375 0.053	SPO3071 SPO3072	1.06 1.48	0.106 SPO3074 0.224 SPO3075	1.54 1.21	0.762 0.264	SPO3066 SPO3067	1.10 1.01	0.227 0.705	SPO3066 SPO3067	1.15 1.02	0.155 0.791	SPO3066 SPO3067	1.22 1.09	0.095 0.606	SPO3062 SPO3063	0.93 0.94	0.383 0.614
SPO3073 SPO3074 SPO3075	0.77 0.7 1.47	0.141 SPO3073 0.642 SPO3074 0.087 SPO3075	0.87 0.79 1.48	0.295 0.529 0.049	SPO3073 SPO3074 SPO3075	1.39 1.1 1.12	0.937 SPO3076 0.731 SPO3077 0.162 SPO3078	1.07 1.09 1.07	0.831 0.626 0.258	SPO3068 SPO3069 SPO3070	0.69 1.17 1.43	0.379 0.552 0.112	SPO3068 SPO3069 SPO3070	0.71 1.19 1.44	0.372 0.267 0.004	SPO3068 SPO3069 SPO3070	0.95 0.92 1.21	0.642	SPO3064 SPO3065 SPO3066	0.85 1.12 1.14	0.100 0.706 0.139
SPO3076 SPO3077 SPO3078	1.21 1.15 1.01	0.606 SPO3076 0.474 SPO3077 0.67 SPO3078	1.12 1.08 1.06	0.619 0.635 0.782	SPO3076 SPO3077 SPO3078	1.18 1.31 1.17	0.723 SPO3079 0.579 SPO3080 0.53 SPO3081	1.39 1.04 1.08	0.918 0.908 0.023	SPO3071 SPO3072 SPO3073	0.91 0.95 1.41	0.802 0.685	SPO3071 SPO3072 SPO3073	0.97 0.99 1.58	0.418 0.400 0.008	SPO3071 SPO3072 SPO3073	1.22 1.19 0.97	0.069 0.334 0.587	SPO3067 SPO3068 SPO3069	1.07 0.85 0.93	0.613 0.661 0.708
SPO3079 SPO3080 SPO3081	0.91 1.04 0.67	0.739 SPO3079 0.963 SPO3080 0.075 SPO3081	1.01 1.16	0.923 0.903	SPO3079 SPO3080	1.65 1.04 1.03	0.837 SPO3082 0.904 SPO3083	1.16 0.99 1.06	0.257 0.858 0.801	SPO3074 SPO3075	2.60 1.83 0.88	0.052 0.035	SPO3074 SPO3075 SPO3076	2.58 1.87 0.93	0.090 0.016	SPO3074 SPO3075 SPO3076	1.08 0.90 0.93	0.623 0.756	SPO3070 SPO3071 SPO3072	1.23 1.26 1.16	0.041 0.206
SPO3081 SPO3082 SPO3083	0.56 0.98	0.07 SPO3081 0.07 SPO3082 0.862 SPO3083	0.65 0.65 0.95	0.114 0.093 0.8	SPO3081 SPO3082 SPO3083	1.03 1.05 1.04	0.021 SPO3084 0.555 SPO3085 0.679 SPO3086	1.06	0.801 0.827 0.842	SPO3076 SPO3077 SPO3078	0.88 0.75 0.27	0.877 0.038 0.013	SPO3076 SPO3077 SPO3078	0.93 0.75 0.27	0.685 0.225 0.004	SPO3076 SPO3077 SPO3078	1.00	0.950 0.970 0.320	SP03072 SP03073 SP03074	1.16	0.153 0.050 0.687
SPO3084 SPO3085 SPO3086	0.93 0.71 0.93	0.62 SPO3084 0.06 SPO3085 0.552 SPO3086	0.83 0.75 0.96	0.184 0.113 0.936	SPO3084 SPO3085 SPO3086	1.14 1.07 1.05	0.811 SPO3087 0.351 SPO3088 0.871 SPO3089	1.08 1.05 1.01	0.506 0.038 0.93	SPO3079 SPO3080 SPO3081	2.04 1.97 4.39	0.151 0.624 0.007	SPO3079 SPO3080 SPO3081	1.88 1.95	0.284 0.615 0.009	SPO3079 SPO3080 SPO3081	1.06 0.81 1.16	0.828 0.898 0.531	SP03075 SP03076 SP03077	0.88 0.93 0.98	0.496 0.915 0.982
SPO3087 SPO3088 SPO3089	1.05 0.84 0.77	0.807 SPO3087 0.223 SPO3088 0.585 SPO3089	1.05 0.79 0.82	0.166 0.054 0.773	SPO3087 SPO3088 SPO3089	1.03 1.12 1.15	0.07 SPO3090 0.218 SPO3091 0.75 SPO3092	1.38 1.06	0.567 0.17 0.461	SPO3082 SPO3083 SPO3084	1.34 0.96	0.099 0.423 0.044	SPO3082 SPO3083 SPO3084	1.31 0.93 1.54	0.064 0.632 0.011	SPO3082 SPO3083 SPO3084	1.20 1.28 0.73	0.340 0.174 0.083	SPO3078 SPO3079 SPO3080	0.89 1.05 0.88	0.351 0.873 0.931
SPO3090 SPO3091	0.73	0.119 SPO3090 0.052 SPO3091	0.82	0.423	SPO3090 SPO3091	1.17	0.893 SPO3093 0.304 SPO3094	1.42	0.033 0.036	SPO3085 SPO3086	0.88 0.83	0.276 0.901	SPO3085 SPO3086	0.75	0.920	SPO3085 SPO3086	0.65	0.022	SPO3081 SPO3082	1.27	0.186 0.036
SPO3092 SPO3093 SPO3094	0.86 0.54 0.71	0.509 SPO3092 0.024 SPO3093 0.03 SPO3094	0.92 0.61 0.78	0.245	SPO3092 SPO3093 SPO3094	1.17 1.12 1.15	0.318 SPO3095 0.105 SPO3096 0.03 SPO3097	1.14 1.26	0.057 0.037 0.073	SPO3087 SPO3088 SPO3089	1.29 1.86 1.17	0.051 0.015 0.241	SPO3087 SPO3088 SPO3089	1.26 1.88 1.25	0.033 0.006 0.191	SPO3087 SPO3088 SPO3089	0.94 0.92 0.88	0.727	SPO3083 SPO3084 SPO3085	1.19 0.75 0.59	0.386 0.031 0.026
SPO3095 SPO3096 SPO3097	0.89 0.81 0.71	0.728 SPO3095 0.578 SPO3096 0.035 SPO3097	0.89 0.85 0.77	0.200	SPO3095 SPO3096 SPO3097	1.05 1.03 1.03	0.142 SPO3098 0.235 SPO3099 0.022 SPO3100	1.17 1.46 1.09	0.618 0.988 0.074	SPO3090 SPO3091 SPO3092	1.16 1.06 0.78	0.288 0.081 0.556	SPO3090 SPO3091 SPO3092	1.14 1.00 0.72		SPO3090 SPO3091 SPO3092	0.94 0.87 0.91	0.418	SPO3086 SPO3087 SPO3088	0.94 0.89 1.01	0.836 0.490 0.556
SPO3098 SPO3099 SPO3100	0.71 1.02	0.228 SPO3098 0.883 SPO3099	0.73 1.11	0.025 0.8	SPO3098 SPO3099	1.31 1.02	0.796 SPO3103 0.186 SPO3104	1.02 1.11	0.304 0.935	SPO3093 SPO3094 SPO3095	2.67	0.000 0.002 0.021	SPO3093 SPO3094 SPO3095	2.41	0.004	SPO3093 SPO3094	0.85 0.93	0.133 0.531	SPO3089 SPO3090 SPO3091	0.93 0.99	0.639 0.962
SPO3103 SPO3104	1.45 1.44 0.93	0.048 SPO3100 0.145 SPO3103 0.904 SPO3104	1.49 1.47 0.99	0.945	SPO3100 SPO3103 SPO3104	1.11 1.15 1.05	0.023 SPO3105 0.063 SPO3106 0.891 SPO3107	1.07 0.98 1.15	0.101 0.594 0.152	SPO3096 SPO3097	2.20 3.62	0.034 0.007	SPO3096 SPO3097	2.21 2.90	0.007	SPO3095 SPO3096 SPO3097	1.01 0.99 1.27	0.967	SPO3092 SPO3093	0.88 0.85 0.85	0.442 0.066 0.138
SPO3105 SPO3106 SPO3107	0.85 1.08 1.12	0.025 SPO3105 0.235 SPO3106 0.581 SPO3107	0.98 1.11 1.21	0.851 0.059 0.154	SPO3105 SPO3106 SPO3107	1.11 1.05 1.32	0.098 SPO3108 0.518 SPO3109 0.363 SPO3110	1.18 1.24 1.16	0.016 0.215 0.274	SPO3098 SPO3099 SPO3100	1.24 1.33 1.06	0.443 0.310 0.386	SPO3098 SPO3099 SPO3100	1.11 1.44 1.13		SPO3098 SPO3099 SPO3100	1.00 1.37 1.09	0.975 0.151 0.544	SPO3094 SPO3095 SPO3096	0.93 1.08 0.98	0.429 0.217 0.939
SPO3108 SPO3109 SPO3110	0.6 1.02 0.79	0.002 SPO3108 0.84 SPO3109 0.383 SPO3110	0.68 0.94 0.76	0.053 0.131 0.097	SPO3108 SPO3109 SPO3110	1.12 1.08 1.02	0.006 SP03111 0.113 SP03112 0.438 SP03113	1.11 1.23 1.14	0.329 0.371 0.226	SPO3103 SPO3104 SPO3105	0.33 0.83 0.56	0.031 0.857 0.017	SPO3103 SPO3104 SPO3105	0.30 0.82 0.57	0.021 0.774 0.002	SPO3103 SPO3104 SPO3105	1.03 1.09 1.06	0.790 0.875 0.188	SPO3097 SPO3098 SPO3099	1.21 1.09 1.37	0.252 0.704 0.417
SP03111 SP03112	1.32 1.59	0.075 SPO3111 0.049 SPO3112	1.26 1.44	0.199 0.044	SP03111 SP03112	1.03 1.17	0.111 SPO3114 0.305 SPO3115	1.08	0.911 0.96	SPO3106 SPO3107	1.46	0.018 0.062	SPO3106 SPO3107	1.62	0.017	SPO3106 SPO3107	1.21 0.97	0.315 0.984	SP03100 SP03103	1.09 0.96	0.589 0.873
SPO3113 SPO3114 SPO3115	1.29 1.3 1.03	0.126 SPO3113 0.6 SPO3114 0.843 SPO3115	1.21 1.16 0.93	0.149 0.714 0.859	SPO3113 SPO3114 SPO3115	1.12 1.42 1.18	0.179 SPO3116 0.782 SPO3117 0.598 SPO3118	1.02 1.26 1.06	0.983 0.547 0.06	SPO3108 SPO3109 SPO3110	2.58 1.93 2.31	0.003 0.002 0.062	SPO3108 SPO3109 SPO3110	2.65 2.04 2.64	0.003 0.001 0.014	SPO3108 SPO3109 SPO3110	1.03 0.91 0.89		SP03104 SP03105 SP03106	1.04 1.02 1.05	0.901 0.284 0.753
SPO3116 SPO3117 SPO3118	1.12 0.68 0.96	0.456 SPO3116 0.43 SPO3117 0.991 SPO3118	0.93 0.65 1.08	0.438 0.144 0.25	SP03116 SP03117 SP03118	1.44 0.99 1.05	0.977 SPO3119 0.442 SPO3120 0.177 SPO3121	1 1.07 1.08	0.176 0.917 0.596	SPO3111 SPO3112 SPO3113	1.66 1.38 0.88	0.066 0.022 0.716	SPO3111 SPO3112 SPO3113	1.57 1.32 0.93	0.036 0.016 0.890	SPO3111 SPO3112 SPO3113	0.90 0.85 0.90	0.760 0.264 0.587	SP03107 SP03108 SP03109	0.95 1.00 0.89	0.949 0.670 0.433
SPO3119 SPO3120	1.48 1.48	0.084 SPO3119 0.012 SPO3120	1.24 1.38	0.089	SPO3119 SPO3120	1.12 1.01	0.185 SPO3122 0.833 SPO3123	1.1	0.46 0.996	SPO3114 SPO3115	1.26 1.42	0.545 0.136	SPO3114 SPO3115	1.33 1.43	0.539 0.103	SPO3114 SPO3115	1.31 1.19	0.508	SP03110 SP03111	0.91 0.88	0.812 0.494
SPO3121 SPO3122 SPO3123	1.42 1.14 1.02	0.022 SPO3121 0.699 SPO3122 0.641 SPO3123	1.32 1.12 1.04	0.48	SPO3121 SPO3122 SPO3123	1.09 1.15 1.76	0.8 SPO3124 0.754 SPO3125 0.799 SPO3126	1.16 1.11	0.949 0.886 0.203	SPO3116 SPO3117 SPO3118	0.89 1.49 0.17	0.954 0.087 0.001	SPO3116 SPO3117 SPO3118	0.96 1.66 0.16	0.017	SPO3116 SPO3117 SPO3118	1.08 1.28 0.75	0.074	SP03112 SP03113 SP03114	0.74 0.85 1.39	0.122 0.359 0.653
SPO3124 SPO3125 SPO3126	1.07 0.81 1.11	0.174 SPO3124 0.835 SPO3125 0.033 SPO3126	1.21 0.93 1.07	0.177 0.972 0.425	SPO3124 SPO3125 SPO3126	0.99 1.05 1.16	0.526 SPO3127 0.815 SPO3128 0.27 SPO3129	1.12 1.03 1.1	0.366 0.453 0.997	SPO3119 SPO3120 SPO3121	0.56 0.88 1.03	0.018 0.364 0.967	SPO3119 SPO3120 SPO3121	0.63 0.88 1.04	0.043 0.220 0.937	SPO3119 SPO3120 SPO3121	1.06 1.14 1.17	0.288	SP03115 SP03116 SP03117	1.09 1.03 1.29	0.698 0.342 0.045
SP03127 SP03128	1.19 1.39	0.021 SPO3127 0.082 SPO3128	1.19 1.3	0.045 0.054	SPO3127 SPO3128	1.15 1.05	0.583 SPO3130 0.549 SPO3131	1.19	0.64 0.693	SPO3122 SPO3123	1.22 1.03	0.349 0.702	SPO3122 SPO3123	1.12 1.24	0.425 0.648	SPO3122 SPO3123	1.15 0.95	0.328 0.727	SP03118 SP03119	0.72 1.06	0.200 0.328
SPO3129 SPO3130 SPO3131	1.32 1.5 1.13	0.23 SPO3129 0.12 SPO3130 0.53 SPO3131	1.33 1.46 1.14	0.083 0.033 0.355	SPO3129 SPO3130 SPO3131	1.16 1.03 1.11	0.934 SPO3132 0.743 SPO3133 0.98 SPO3134	1.05 1.09 1.41	0.99 0.088 0.223	SPO3124 SPO3125 SPO3126	1.05 0.79 0.84	0.910 0.817 0.261	SPO3124 SPO3125 SPO3126	1.07 0.81 0.90	0.877	SPO3124 SPO3125 SPO3126	1.09 0.91 1.01	0.916 0.831	SP03120 SP03121 SP03122	1.03 1.11 1.14	0.498 0.630 0.417
SPO3132 SPO3133 SPO3134	1.06 0.99 0.74	0.802 SPO3132 0.926 SPO3133 0.04 SPO3134	1 1.03 0.78	0.949 0.414 0.029	SP03132 SP03133 SP03134	1.12 1.02 1.05	0.915 SPO3135 0.269 SPO3136 0.272 SPO3137	1.16 1.51 1.03	0.796 0.843 0.781	SPO3127 SPO3128 SPO3129	1.10 0.85 1.93	0.612 0.598 0.029	SPO3127 SPO3128 SPO3129	1.31 0.92 1.95	0.125	SPO3127 SPO3128 SPO3129	1.71 1.01 1.03		SPO3123 SPO3124	0.85 1.11 0.81	0.389 0.705 0.856
SPO3135 SPO3136	1.29 1.51	0.134 SPO3135 0.016 SPO3136	1.44 1.49	0.024	SPO3135 SPO3136	1.01 1.12	0.701 SPO3138 0.922 SPO3139	1.1	0.9 0.855	SPO3130 SPO3131	2.38 1.05	0.041 0.544	SPO3130 SPO3131	2.54 1.02	0.012 0.535	SPO3130 SPO3131	0.93 1.04	0.788 0.551	SP03126 SP03127	0.88 1.27	0.174 0.171
SP03137 SP03138 SP03139	0.96 1.17 0.69	0.804 SPO3137 0.854 SPO3138 0.408 SPO3139	1.02 1.39 0.83	0.727 0.842	SPO3137 SPO3138 SPO3139	1.03 1.04 1.06	0.924 SPO3140 0.996 SPO3141 0.826 SPO3142	1.08 1.16 1.74	0.28 0.333 0.228	SPO3132 SPO3133 SPO3134	1.03 0.71 1.12	0.938 0.205 0.280	SPO3132 SPO3133 SPO3134	1.09 0.70 1.08	0.197 0.154	SPO3132 SPO3133 SPO3134	1.08 1.02 0.93	0.682	SPO3128 SPO3129 SPO3130	1.02 1.04 0.90	0.486 0.771 0.501
SPO3140 SPO3141 SPO3142	1.29 1.2 1.21	0.028 SPO3140 0.094 SPO3141 0.149 SPO3142	1.27 1.15	0.121 0.508 0.062	SPO3140 SPO3141 SPO3142	1.01 1.81 1.3	0.249 SP03143 0.092 SP03144 0.284 SP03145	1.13 1.11 1.28	0.496 0.321 0.937	SPO3135 SPO3136 SPO3137	1.53 1.07 1.20	0.089 0.269 0.099	SPO3135 SPO3136 SPO3137	1.55 1.12 1.08	0.084 0.091 0.294	SPO3135 SPO3136 SPO3137	0.96 1.15 1.12	0.489	SP03131 SP03132 SP03133	1.12 1.17 0.91	0.487 0.712 0.150
SPO3143 SPO3144	1.3 0.9	0.428 SPO3143 0.507 SPO3144	1.33	0.15 0.595	SPO3143 SPO3144	1.12 1.1	0.815 SPO3146 0.393 SPO3147	1.04	0.807 0.424	SPO3138 SPO3139	0.64 0.30	0.694 0.073	SPO3138 SPO3139	0.69 0.30	0.731 0.176	SPO3138 SPO3139	0.96 0.89	0.970 0.864	SP03134 SP03135	0.97 1.04	0.802 0.925
SPO3145 SPO3146 SPO3147	0.92 1.06 1.41	0.625 SPO3145 0.044 SPO3146 0.07 SPO3147	1.04 1.47	0.056 0.016	SPO3147	1.04 1.11 1.03	0.951 SPO3148 0.969 SPO3149 0.402 SPO3150	1.06 1.17 1.09	0.845 0.808 0.922	SPO3140 SPO3141 SPO3142	0.69 0.81 0.93	0.140 0.111 0.798	SPO3140 SPO3141 SPO3142	0.64 0.83 0.89	0.822 0.557	SPO3140 SPO3141 SPO3142	1.20 1.05 1.02	0.777 0.634	SP03136 SP03137 SP03138	1.15 1.21 0.93	0.349 0.277 0.948
SP03148	1.13	0.527 SPO3148	1.06	0.514	SPO3148	1.02	0.495 SPO3151	1.05	0.048	SPO3143	1.59	0.198	SPO3143	1.66	0.089	SPO3143	1.15	0.775	SPO3139	0.98	0.988

SP03149 SP03150	0.69		SPO3149 SPO3150	0.65	0.519 SPO3149 0.9 SPO3150	1.03	0.611 SPO3152 0.936 SPO3153	1.13	0.5 SPO3144 0.963 SPO3145	0.62	0.008	SPO3144 SPO3145	0.70		SPO3144 SPO3145	0.87		SPO3140 SPO3141	1.07	0.806
SP03151 SP03152	0.87 0.93	0.21 0.796	SP03151 SP03152	0.96 0.98	0.957 SPO3151 0.954 SPO3152	1.22 1.02	0.125 SPO3154 0.195 SPO3155	0.98 0.99	0.691 SPO3146 0.213 SPO3147	1.63 0.93	0.064	SPO3146 SPO3147	1.72 0.85	0.005 0.542	SPO3146 SPO3147	1.20 1.15	0.166 0.354	SP03142 SP03143	0.97 1.23	0.848 0.201
SPO3153 SPO3154 SPO3155	0.81 1.29 0.95	0.807 0.368 0.823		0.85 1.3 0.95	0.867 SPO3153 0.152 SPO3154 0.962 SPO3155	0.99 1 1.08	0.867 SPO3156 0.901 SPO3157 0.268 SPO3158	1.14 1.06 1.1	0.336 SPO3148 0.451 SPO3149 0.913 SPO3150	0.86 0.97 0.76	0.554 0.906 0.882	SPO3148 SPO3149 SPO3150	0.93 1.03 0.76	0.961	SPO3148 SPO3149 SPO3150	0.92 1.06 0.92	0.933	SPO3144 SPO3145 SPO3146	0.88 1.04 1.09	0.132 0.700 0.692
SPO3156 SPO3157 SPO3158	1.42 0.9 0.85	0.063 0.554 0.357	SPO3156 SPO3157 SPO3158	1.38 1.02 0.87	0.189 SPO3156 0.633 SPO3157 0.677 SPO3158	0.99 1.08 1.07	0.941 SPO3159 0.91 SPO3160 0.953 SPO3161	1.05 1.72 1.39	0.513 SPO3151 0.228 SPO3152 0.035 SPO3153	1.34 1.47 0.93	0.015 0.084 0.675	SPO3151 SPO3152 SPO3153	1.30 1.39 0.63	0.007 0.191 0.437	SPO3151 SPO3152 SPO3153	1.13 0.90 0.79		SPO3147 SPO3148 SPO3149	1.10 0.90 1.08	0.508 0.373 0.890
SP03159 SP03160	1.34	0.299	SPO3159 SPO3160	1.28 1.36	0.491 SPO3159 0.043 SPO3160	1.01	0.519 SPO3162 0.067 SPO3163	1.2	0.727 SPO3154 0.606 SPO3155	1.16 1.40	0.380	SPO3154 SPO3155	1.13		SPO3154 SPO3155	1.17		SPO3150	0.90	0.943 0.093
SP03161 SP03162 SP03163	3.08 1.22 1.07	0.002 0.161 0.703	SP03161 SP03162 SP03163	2.23 1.12 1.08	0.002 SPO3161 0.195 SPO3162 0.71 SPO3163	1.3 1.18 1.15	0.006 SPO3164 0.808 SPO3165 0.619 SPO3166	1.07 1.08 1.07	0.638 SPO3156 0.044 SPO3157 0.514 SPO3158	0.61 0.89 0.68	0.009 0.878 0.267	SPO3156 SPO3157 SPO3158	0.62 0.81 0.68	0.078 0.206 0.447	SPO3156 SPO3157 SPO3158	0.97 0.93 0.92	0.679	SPO3152 SPO3153 SPO3154	1.00 0.93 1.08	0.966 0.896 0.628
SP03164 SP03165	1.13 0.86	0.188	SP03164 SP03165	1.01 0.92	0.791 SPO3164 0.529 SPO3165	1.27 1.15	0.138 SPO3167 0.015 SPO3168	1.01 1.22	0.042 SPO3159 0.804 SPO3160	1.17 1.06	0.547 0.473	SPO3159 SPO3160	1.10 1.03	0.695	SPO3159 SPO3160	1.09 0.92	0.747	SP03155 SP03156	1.05 0.91	0.691 0.233
SP03166 SP03167 SP03168	0.61 1.01 0.67	0.054 0.266 0.007	SPO3166 SPO3167 SPO3168	0.71 1.17 0.74	0.101 SPO3166 0.304 SPO3167 0.514 SPO3168	1.11 1.11 1.05	0.162 SPO3169 0.089 SPO3170 0.581 SPO3171	1.06 1.05 1.09	0.084 SPO3161 0.061 SPO3162 0.312 SPO3163	0.74 1.07 1.45	0.210 0.083 0.119	SPO3161 SPO3162 SPO3163	0.77 1.03 1.33	0.190	SPO3161 SPO3162 SPO3163	1.24 1.02 1.09	0.552	SP03157 SP03158 SP03159	0.88 0.92 1.05	0.504 0.835 0.827
SP03169 SP03170	0.99 1.28	0.078	SP03169 SP03170	0.91 1.26	0.55 SPO3169 0.232 SPO3170	1.04	0.044 SPO3172 0.084 SPO3173	0.97 1.08	0.256 SPO3164 0.967 SPO3165	1.30	0.006	SPO3164 SPO3165	1.30	0.002 0.008 0.805	SPO3164 SPO3165	1.08 1.27 0.78	0.254	SP03160 SP03161	1.01	0.951
SP03171 SP03172 SP03173	1.15 1.62 1.42	0.401 0.17 0.051	SP03171 SP03172 SP03173	1.03 1.4 1.23	0.701 SPO3171 0.059 SPO3172 0.782 SPO3173	1.04 1.13 1.2	0.074 SPO3174 0.346 SPO3175 0.141 SPO3176	1.18 1.09 1.02	0.695 SPO3166 0.895 SPO3167 0.015 SPO3168	0.80 0.77 0.79	0.614 0.426 0.074	SPO3166 SPO3167 SPO3168	0.79 0.78 0.85	0.805	SPO3166 SPO3167 SPO3168	1.01	0.996	SP03162 SP03163 SP03164	1.06 1.13 1.15	0.028 0.411 0.050
SP03174 SP03175 SP03176	0.81 0.97 0.95	0.075 0.99 0.634	SP03174 SP03175 SP03176	0.87 0.96 1.01	0.768 SPO3174 0.956 SPO3175 0.327 SPO3176	0.99 1.16 1.3	0.541 SPO3177 0.536 SPO3178 0.009 SPO3179	1.31 1.13 1.09	0.89 SPO3169 0.772 SPO3170 0.883 SPO3171	0.40 0.82 0.57	0.048 0.217 0.066	SPO3169 SPO3170 SPO3171	0.42 0.86 0.60	0.003	SPO3169 SPO3170 SPO3171	1.03 1.00 0.82	0.941	SPO3165 SPO3166 SPO3167	1.36 0.85 1.06	0.214 0.342 0.718
SP03177 SP03178	1.24 0.53	0.503 0.424	SP03177 SP03178	1.26 0.9	0.123 SPO3177 0.936 SPO3178	1.34 1.23	0.941 SPO3180 0.611 SPO3181	1.15 1.07	0.815 SPO3172 0.267 SPO3173	0.63 0.63	0.207	SPO3172 SPO3173	0.65 0.75	0.070	SPO3172 SPO3173	0.92 1.02	0.850 0.986	SPO3168 SPO3169	0.88 1.07	0.794 0.194
SP03179 SP03180 SP03181	0.93 1.18 1.66	0.825 0.221 0.094	SPO3179 SPO3180 SPO3181	1.13 1.3	0.107 SPO3179 0.031 SPO3180 0.063 SPO3181	0.99 1.3 1.05	0.462 SPO3182 0.602 SPO3183 0.148 SPO3184	1.15 1.09 1.09	0.05 SPO3174 0.472 SPO3175 0.997 SPO3176	0.52 1.09 1.60	0.275 0.418 0.026	SPO3174 SPO3175 SPO3176	0.55 1.00 1.64	0.423 0.782 0.039	SPO3174 SPO3175 SPO3176	0.77 0.99 1.35		SPO3170 SPO3171 SPO3172	0.88 0.82 0.88	0.330 0.356 0.383
SPO3182 SPO3183 SPO3184	1.5	0.028 0.807 0.92	SPO3182 SPO3183 SPO3184	1.34 1.05	0.049 SPO3182 0.584 SPO3183 0.828 SPO3184	1.01 1.32 1.32	0.098 SPO3185 0.501 SPO3186 0.991 SPO3187	1.13 1.24 1.33	0.544 SPO3177 0.467 SPO3178 0.989 SPO3179	0.98 0.79 1.01	0.830 0.537 0.938	SPO3177 SPO3178 SPO3179	0.93 0.74 0.99	0.901 0.604 0.654	SPO3177 SPO3178 SPO3179	0.99 0.80	0.610	SP03173 SP03174 SP03175	0.96 0.85 1.03	0.956 0.442 0.783
SPO3185 SPO3186	0.83	0.36 0.891		0.78	0.332 SPO3185 0.738 SPO3186	1.02	0.847 SPO3188 0.216 SPO3189	1.06 1.11	0.815 SPO3180 0.956 SPO3181	1.07	0.226 0.118	SPO3180 SPO3181	1.05	0.020	SPO3180 SPO3181	1.07	0.591	SP03176 SP03177	1.48	0.010 0.934
SP03187 SP03188 SP03189	0.88 0.79 0.92		SPO3187 SPO3188 SPO3189	0.88 0.92 1.01	0.801 SPO3187 0.963 SPO3188 0.917 SPO3189	1.02 1.14 1.25	0.952 SPO3190 0.78 SPO3191 0.739 SPO3192	1.23 1.05 1.19	0.272 SPO3182 0.552 SPO3183 0.664 SPO3184	1.22 0.80 1.04	0.032 0.171 0.994	SPO3182 SPO3183 SPO3184	1.19 0.85 1.02	0.292	SPO3182 SPO3183 SPO3184	0.92 0.85	0.329	SPO3178 SPO3179 SPO3180	1.00 1.02 1.02	0.965 0.947 0.818
SPO3190 SPO3191	0.61 0.6	0.14 0.21	SP03190 SP03191	0.72 0.68	0.131 SPO3190 0.236 SPO3191	1.02 1.29	0.503 SPO3193 0.369 SPO3194	1.45 0.98	0.018 SPO3185 0.651 SPO3186	1.14 0.93	0.301	SPO3185 SPO3186	0.91 0.89	0.991 0.773	SPO3185 SPO3186	0.89 0.79	0.661 0.172	SP03181 SP03182	0.89 0.96	0.634 0.914
SPO3192 SPO3193 SPO3194	1.34 1.12 1.21	0.076 0.689	SPO3192 SPO3193 SPO3194	1.12 1.05 1.01	0.198 SPO3192 0.206 SPO3193 0.905 SPO3194	1.16 1.02 1.19	0.646 SPO3195 0.017 SPO3196 0.641 SPO3197	1.27 1.24 1.14	0.709 SPO3187 0.724 SPO3188 0.599 SPO3189	1.25 1.68 1.10	0.571 0.586 0.884	SPO3187 SPO3188 SPO3189	1.43 1.63 1.04	0.252 0.632 0.995	SPO3187 SPO3188 SPO3189	1.06 0.88 0.85	0.914	SPO3183 SPO3184 SPO3185	0.86 1.07 0.93	0.658 0.937 0.714
SPO3195 SPO3196 SPO3197	0.89 0.78 1.64	0.756	SPO3195 SPO3196	0.85 0.96 1.29	0.681 SPO3195 0.949 SPO3196 0.504 SPO3197	1.08 1.07 1.09	0.723 SPO3198 0.437 SPO3199 0.74 SPO3200	1.42 0.98 1.35	0.226 SPO3190 0.298 SPO3191 0.146 SPO3192	1.48 1.36	0.091 0.243 0.655	SPO3190 SPO3191 SPO3192	1.60 1.89	0.028 0.388 0.617	SPO3190 SPO3191 SPO3192	0.99 0.93	0.864 0.745	SPO3186 SPO3187 SPO3188	0.78 1.09 0.91	0.097 0.884 0.935
SPO3198 SPO3199	1.91 1.18	0.018	SPO3198 SPO3199	1.7 1.22	0.029 SPO3198 0.027 SPO3199	1.01 1.13	0.87 SPO3201 0.573 SPO3202	1.39 1.01	0.262 SPO3193 0.306 SPO3194	0.72 0.88	0.070 0.931	SPO3193 SPO3194	0.71 0.94	0.040	SPO3193 SPO3194	0.83 1.07	0.231 0.837	SP03189 SP03190	0.92 1.00	0.868 0.915
SPO3200 SPO3201 SPO3202	0.87 0.95 0.91	0.098 0.506 0.43	SPO3200 SPO3201	0.92 1.08 0.98	0.236 SPO3200 0.201 SPO3201 0.924 SPO3202	1.12 1 0.98	0.441 SPO3203 0.6 SPO3204 0.595 SPO3205	1.22 1.17 1.13	0.367 SPO3195 0.112 SPO3196 0.721 SPO3197	0.62 0.75 0.65	0.370 0.154 0.538	SPO3195 SPO3196 SPO3197	0.61 0.52 0.60	0.339 0.153 0.464	SPO3195 SPO3196 SPO3197	0.88 0.77 0.96	0.651	SPO3191 SPO3192 SPO3193	1.01 1.17 0.83	0.988 0.374 0.076
SPO3203 SPO3204	1.06 0.87	0.154	SPO3203 SPO3204	1.05	0.193 SPO3203 0.967 SPO3204	1.08 1.31	0.039 SPO3206 0.008 SPO3207	1.05 1.15	0.892 SPO3198 0.977 SPO3199	1.37 1.62	0.059	SPO3198 SPO3199	1.53 1.55	0.167 0.018	SPO3198 SPO3199	1.07 0.99	0.461 0.866	SPO3194 SPO3195	1.11 0.95	0.695 0.885
SPO3205 SPO3206 SPO3207	0.76 0.66 1.31	0.413 0.072 0.339	SPO3205 SPO3206 SPO3207	0.8 0.69 1.2	0.225 SPO3205 0.167 SPO3206 0.107 SPO3207	1.23 1.2 1.1	0.556 SPO3208 0.796 SPO3209 0.781 SPO3210	1.11 1.13 1.06	0.964 SPO3200 0.294 SPO3201 0.891 SPO3202	1.03 0.72 1.93	0.081 0.003 0.021	SPO3200 SPO3201 SPO3202	0.97 0.65 1.79	0.041 0.070 0.026	SPO3200 SPO3201 SPO3202	0.95 0.97 1.01	0.757 0.799 0.881	SPO3196 SPO3197 SPO3198	0.82 0.98 1.05	0.165 0.985 0.392
SPO3208 SPO3209 SPO3210	1.68 0.78 0.94	0.318 0.245 0.746	SPO3208 SPO3209 SPO3210	1.46 0.76 0.95	0.013 SPO3208 0.139 SPO3209 0.915 SPO3210	2.04 1.81 1.2	0.553 SPO3211 0.838 SPO3212 0.655 SPO3213	1.01 1.14 1.02	0.898 SPO3203 0.725 SPO3204 0.817 SPO3205	1.24 0.82 1.52	0.012 0.851 0.120	SPO3203 SPO3204 SPO3205	1.21 0.72 1.57	0.050 0.375 0.025	SPO3203 SPO3204 SPO3205	0.91 0.86	0.127 0.048	SPO3199 SPO3200 SPO3201	0.96 1.12 0.93	0.956 0.090 0.107
SP03211 SP03212	0.93 1.34	0.458 0.087	SP03211 SP03212	0.98 1.24	0.932 SPO3211 0.156 SPO3212	1.09 1.04	0.796 SPO3214 0.705 SPO3215	1.16 1.1	0.806 SPO3206 0.485 SPO3207	1.57 0.59	0.019	SPO3206 SPO3207	1.41 0.62	0.061 0.067	SPO3206 SPO3207	1.01	0.756 0.739	SPO3202 SPO3203	0.98 0.95	0.993 0.836
SP03213 SP03214 SP03215	0.98 1.4 0.95	0.957 0.085 0.927	SPO3213 SPO3214 SPO3215	1.02 1.17 1.18	0.831 SPO3213 0.205 SPO3214 0.196 SPO3215	1.11 1.24 1.29	0.884 SPO3216 0.51 SPO3217 0.275 SPO3218	0.98 0.97	0.522 SPO3208 0.735 SPO3209 0.827 SPO3210	1.03 0.71 0.92	0.736 0.159 0.936	SPO3208 SPO3209 SPO3210	0.93 0.76 0.90	0.695 0.025 0.963	SPO3208 SPO3209 SPO3210	1.27 0.89 1.07	0.269	SPO3204 SPO3205 SPO3206	0.79 1.18 1.00	0.227 0.207 0.709
SP03216 SP03217 SP03218	1.5 1.22 1.2	0.035	SPO3216 SPO3217 SPO3218	1.42 1.24 1.23	0.002 SPO3216 0.134 SPO3217 0.115 SPO3218	1.05 1.13 1.18	0.207 SPO3219 0.639 SPO3220 0.766 SPO3221	1.43 1.24 1.22	0.73 SPO3211 0.496 SPO3212 0.544 SPO3213	1.32 1.11 0.62	0.016 0.224 0.496	SPO3211 SPO3212 SPO3213	1.29 1.24 0.51	0.065 0.039 0.026	SPO3211 SPO3212 SPO3213	1.07 1.06 0.84	0.490	SPO3207 SPO3208 SPO3209	1.10 1.29 1.07	0.175 0.139 0.466
SPO3219 SPO3220	1.32 0.65	0.192	SPO3219 SPO3220	1.29 0.67	0.137 SPO3219 0.044 SPO3220	1.12 1.02	0.907 SPO3222 0.85 SPO3223	1.07 2.24	0.991 SPO3214 0.344 SPO3215	0.67 0.77	0.127 0.535	SPO3214 SPO3215	0.62 0.72	0.140 0.296	SPO3214 SPO3215	0.79 1.00	0.482 0.965	SPO3210 SPO3211	1.06 1.02	0.830 0.763
SP03221 SP03222 SP03223	0.63 0.61 0.97	0.031 0.342 0.998	SPO3221 SPO3222 SPO3223	0.69 0.74 0.95	0.039 SPO3221 0.839 SPO3222 0.978 SPO3223	1.02 1.53	0.449 SPO3224 0.934 SPO3225 0.347 SPO3226	1.79 1.18 1.1	0.929 SPO3216 0.436 SPO3217 0.108 SPO3218	0.80 1.16 1.10	0.549 0.309 0.395	SPO3216 SPO3217 SPO3218	0.81 1.18 1.12	0.383 0.340 0.063	SPO3216 SPO3217 SPO3218	1.13 1.13 1.04		SPO3212 SPO3213 SPO3214	1.09 0.81 0.86	0.504 0.589 0.704
SP03224 SP03225	1.38 1.41	0.181	SPO3224 SPO3225	1.26	0.574 SPO3224 0.005 SPO3225	1.02	0.863 SPO3227 0.215 SPO3228	1.02	0.323 SPO3219 0.141 SPO3220	1.07 0.71	0.442	SPO3219 SPO3220	1.17 0.71	0.023	SPO3219 SPO3220	1.17	0.187	SPO3215 SPO3216	0.95 1.00	0.898 0.932
SP03226 SP03227 SP03228	0.68 1.11 1.4	0.112 0.728 0.174	SPO3227 SPO3228	0.67 1.01 1.2	0.124 SPO3226 0.833 SPO3227 0.25 SPO3228	1.2 1.05 1.17	0.128 SPO3229 0.243 SPO3230 0.141 SPO3231	1.23 1.21 1.13	0.753 SPO3221 0.972 SPO3222 0.994 SPO3223	0.89 1.19 0.51	0.474 0.504 0.080	SPO3221 SPO3222 SPO3223	0.87 0.97 0.56	0.982	SPO3221 SPO3222 SPO3223	0.90 0.94 0.87	0.773 0.526	SPO3219	1.15 1.08 1.17	0.256 0.118 0.110
SP03229 SP03230 SP03231	1.16 0.98 0.79	0.459 0.998 0.585	SPO3229 SPO3230 SPO3231	1.14 0.99 0.85	0.108 SPO3229 0.969 SPO3230 0.747 SPO3231	1.17 1.16 1.14	0.551 SPO3232 0.859 SPO3233 0.95 SPO3234	1.17 1.15 1.2	0.484 SPO3224 0.165 SPO3225 0.027 SPO3226	0.80 1.05	0.698 0.776 0.044	SPO3224 SPO3225 SPO3226	0.89 1.05	0.915	SPO3224 SPO3225 SPO3226	1.04 1.12 1.43		SPO3220 SPO3221 SPO3222	1.04 0.86 1.07	0.362 0.258 0.937
SP03232 SP03233	1.38	0.184 0.054	SPO3232 SPO3233	1.26 1.87	0.23 SPO3232 0.062 SPO3233	1.35 1.16	0.335 SPO3235 0.117 SPO3236	1 1.04	0.277 SPO3227 0.285 SPO3228	0.55 1.09	0.020 0.617	SPO3227 SPO3228	0.52 1.11		SPO3227 SPO3228	0.97 1.05	0.932 0.787	SPO3223 SPO3224	0.89 0.99	0.500 0.998
SPO3234 SPO3235 SPO3236	2.18 1.15	0.005 0.015 0.291	SPO3234 SPO3235 SPO3236	1.73 1.78 1.23	0.003 SPO3234 0.023 SPO3235 0.15 SPO3236	1.27 1.01 1.05	0.081 SPO3237 0.215 SPO3238 0.102 SPO3239	1.46 1.15 1.03	0.375 SPO3229 0.998 SPO3230 0.882 SPO3231	0.25 0.96	0.044 0.085 0.895	SPO3229 SPO3230 SPO3231	0.38 0.23 0.92	0.977		0.78 0.98 0.93	0.988	SPO3225 SPO3226 SPO3227	0.99 1.48 0.91	0.650 0.080 0.796
SPO3237 SPO3238 SPO3239	0.88 1.1 1.29	0.385	SPO3237 SPO3238 SPO3239	0.88 1.07 1.15	0.653 SPO3237 0.582 SPO3238 0.791 SPO3239	1.02 1.09 1.02	0.506 SPO3240 0.987 SPO3241 0.786 SPO3242	1.08 1.12 1.14	0.988 SPO3232 0.167 SPO3233 0.609 SPO3234	0.68 0.88 0.75	0.190 0.586 0.308	SPO3232 SPO3233 SPO3234	0.69 0.85 0.83	0.550	SPO3232 SPO3233 SPO3234	0.96 1.10 1.01	0.395	SPO3228 SPO3229 SPO3230	0.87 0.86 0.88	0.534 0.177 0.876
SPO3240 SPO3241	1.16 0.68	0.409	SPO3240 SPO3241	1.08 0.71	0.573 SPO3240 0.007 SPO3241	1.19	0.862 SPO3243 0.88 SPO3244	1.06 1.01	0.568 SPO3235 0.991 SPO3236	0.88 1.16	0.274	SPO3235 SPO3236	0.73 1.14	0.688	SPO3235 SPO3236	1.06 1.01	0.244	SPO3231 SPO3232	0.93 0.93	0.875 0.773
SP03242 SP03243 SP03244	1.2 1.06 0.87	0.875	SPO3242 SPO3243 SPO3244	1.19 1.15 0.97	0.298 SPO3242 0.397 SPO3243 0.994 SPO3244	2.81 1.16 1.01	0.513 SPO3245 0.704 SPO3246 0.884 SPO3247	1.25 1.23 1.42	0.721 SPO3237 0.555 SPO3238 0.057 SPO3239	0.88 1.07	0.066 0.735 0.803	SPO3237 SPO3238 SPO3239	0.80 1.05		SPO3237 SPO3238 SPO3239	1.04 1.12 0.96	0.660	SPO3233 SPO3234 SPO3235	1.04 1.00 1.03	0.480 0.415 0.067
SPO3245 SPO3246	1.08 1.05		SPO3245 SPO3246	1.14 1.19 1.55	0.559 SPO3245 0.111 SPO3246 0.066 SPO3247	1.01	0.831 SPO3248 0.399 SPO3249 0.439 SPO3250	1.03 1.57 1.22	0.904 SPO3240 0.204 SPO3241 0.629 SPO3242	1.23 0.79 1.01	0.230 0.443 0.634	SPO3240 SPO3241 SPO3242	1.17 0.87 1.04	0.680	SPO3240 SPO3241 SPO3242	1.12 0.84 0.96	0.290	SPO3236 SPO3237 SPO3238	0.96 1.22 1.21	0.956 0.439 0.540
SPO3247 SPO3248 SPO3249	1.38	0.441	SPO3247 SPO3248 SPO3249	1.53 1.66	0.272 SPO3248 0.002 SPO3249	1.11 1.06 1.19	0.799 SPO3251 0.161 SPO3252	1.19 1.03	0.677 SPO3243 0.023 SPO3244	1.66 1.48	0.063 0.695	SPO3243 SPO3244	1.54	0.059 0.791	SPO3243 SPO3244	1.19 1.04	0.421	SPO3239 SPO3240	0.99 1.01	0.988
SPO3250 SPO3251 SPO3252	1.81 1.29 0.98	0.151	SPO3250 SPO3251 SPO3252	1.74 1.17 1.01	0.108 SPO3250 0.068 SPO3251 0.599 SPO3252	1.01 1.3 1.15	0.82 SPO3253 0.873 SPO3254 0.019 SPO3255	1.09 1.02 1.08	0.281 SPO3245 0.692 SPO3246 0.744 SPO3247	0.96 0.85	0.038 0.660 0.322	SPO3245 SPO3246 SPO3247	0.88 0.88		SPO3245 SPO3246 SPO3247	1.31 1.02	0.774	SPO3241 SPO3242 SPO3243	0.98 0.93 1.14	0.971 0.840 0.439
SPO3253 SPO3254 SPO3255	1.3 1.85	0.014 0.014	SPO3253 SPO3254 SPO3255	1.37 1.47 1.49	0.033 SPO3253 0.015 SPO3254 0.226 SPO3255	1.19 1.13 1.03	0.161 SPO3256 0.949 SPO3257 0.801 SPO3258	1.16 1.1 1.07	0.026 SPO3248 0.357 SPO3249 0.144 SPO3250	1.50 1.20 1.00	0.430 0.085 0.934	SPO3248 SPO3249 SPO3250	1.47 1.28 1.12	0.394	SPO3248 SPO3249 SPO3250	1.00 1.04 1.04	0.991 0.777	SPO3244 SPO3245 SPO3246	1.03 1.32 1.00	0.961 0.248 0.895
SPO3256 SPO3257	2.13 0.9	0.002	SPO3256 SPO3257	1.8 0.96	0.013 SPO3256 0.436 SPO3257	0.98 1	0.022 SPO3259 0.045 SPO3260	3.42 1.02	0.73 SPO3251 0.112 SPO3252	1.19	0.160	SPO3251 SPO3252	1.11	0.142	SPO3251 SPO3252	1.03	0.820	SPO3247 SPO3248	1.21 1.01	0.175
SPO3258 SPO3259 SPO3260	1.15 1.2	0.164	SPO3258 SPO3259 SPO3260	1.07 1.21 1.02	0.53 SPO3258 0.353 SPO3259 0.543 SPO3260	1.05 1.05	0.244 SPO3261 0.753 SPO3262 0.361 SPO3263	1.03 1.04 1.13	0.004 SPO3253 0.742 SPO3254 0.607 SPO3255	1.11 1.41 1.10	0.055 0.087 0.680	SPO3253 SPO3254 SPO3255	1.09 1.34	0.044	SPO3253 SPO3254 SPO3255	0.89 1.12 1.05	0.312	SPO3249 SPO3250 SPO3251	1.05 0.98 1.12	0.224 0.881 0.304
SPO3261 SPO3262	1.13	0.165 0.138	SPO3261 SPO3262	1.08 0.88	0.187 SPO3261 0.554 SPO3262	1.09 1.12	0.025 SPO3270 0.274 SPO3271	1.01 1.11	0.588 SPO3256 0.683 SPO3257	0.63 1.50	0.008	SPO3256 SPO3257	0.70 1.51	0.081	SPO3256 SPO3257	1.01 1.06	0.688 0.217	SPO3252 SPO3253	1.15 0.90	0.037 0.269
SPO3263 SPO3270 SPO3271	1.35 1.35 1.08		SPO3263 SPO3270 SPO3271	1.3 1.31 0.96	0.218 SPO3263 0.144 SPO3270 0.973 SPO3271	1.02 1.05 1.26	0.064 SPO3272 0.371 SPO3273 0.805 SPO3274	1.11 1.17 1.32	0.461 SPO3258 0.56 SPO3259 0.93 SPO3260	1.60 0.67 1.06	0.061 0.488 0.246	SPO3258 SPO3259 SPO3260	1.78 0.61 1.08	0.018 0.350 0.148	SPO3258 SPO3259 SPO3260	1.37 0.85 1.04	0.490	SPO3254 SPO3255 SPO3256	1.09 1.06 0.81	0.270 0.860 0.136
SP03272 SP03273 SP03274	0.74 1.03 0.79		SPO3272 SPO3273 SPO3274	0.78 1.05 0.86	0.035 SPO3272 0.746 SPO3273 0.816 SPO3274	1.02 1.56 1.01	0.91 SPO3275 0.277 SPO3276 0.366 SPO3277	1.06 1.18 1.05	0.695 SPO3261 0.235 SPO3262 0.229 SPO3263	1.32 1.43 0.75	0.164 0.118 0.129	SPO3261 SPO3262 SPO3263	1.42 1.39 0.66		SPO3261 SPO3262 SPO3263	0.91 0.93 0.92	0.348	SPO3257 SPO3258 SPO3259	1.11 1.32 0.79	0.110 0.201 0.483
SP03275 SP03276	0.81 1.34	0.88	SPO3275 SPO3276	0.84 1.23	0.93 SPO3275 0.115 SPO3276	1.45 1.08	0.706 SPO3278 0.143 SPO3279	1.02 1.06	0.797 SPO3270 0.815 SPO3271	0.78 0.51	0.306 0.057	SPO3270 SPO3271	0.66 0.49	0.070 0.113	SPO3270 SPO3271	0.94 0.92	0.744 0.658	SPO3260 SPO3261	1.06 0.95	0.562 0.591
SPO3277 SPO3278 SPO3279	0.99 1.12 1.16	0.982 0.156 0.262	SPO3277 SPO3278 SPO3279	0.94 1.18 1.09	0.677 SPO3277 0.119 SPO3278 0.501 SPO3279	1.07 1.03	0.174 SPO3280 0.634 SPO3281 0.878 SPO3282	1.04 1.03 1.1	0.667 SPO3272 0.252 SPO3273 0.408 SPO3274	0.59 0.81 1.37	0.029 0.497 0.355	SPO3272 SPO3273 SPO3274	0.58 0.80 1.40	0.040 0.481 0.231	SPO3272 SPO3273 SPO3274	0.76 0.89 1.06	0.214	SPO3262 SPO3263 SPO3270	0.89 0.88 0.99	0.375 0.768 0.932
SPO3280 SPO3281 SPO3282	1.15 0.83 1.25	0.33 0.442	SPO3280	1.11 0.88 1.17	0.347 SPO3280 0.593 SPO3281 0.084 SPO3282	1.46 1.31 1.09	0.351 SPO3284 0.148 SPO3285 0.501 SPO3286	1.17 1.05 1.06	0.016 SPO3275 0.737 SPO3276 0.998 SPO3277	4.24 0.79 0.87	0.339 0.436 0.540	SPO3275 SPO3276 SPO3277	4.23 0.78 0.81	0.227	SPO3275 SPO3276 SPO3277	0.84 1.09 0.96	0.911 0.571	SPO3271 SPO3272 SPO3273	0.88 0.83 0.81	0.513 0.189 0.457
SPO3284 SPO3285	2.67 0.7	0.003	SPO3284 SPO3285	2.01 0.73	0.01 SPO3284 0.441 SPO3285	1.1 1.32	0.11 SPO3287 0.718 SPO3288	1.09 1.09	0.019 SPO3278 0.272 SPO3279	1.74	0.017 0.979	SPO3278 SPO3279	1.56 1.29	0.038 0.487	SPO3278 SPO3279	1.12 1.04	0.264	SPO3274 SPO3275	1.32 0.96	0.518 0.989
SPO3286 SPO3287 SPO3288	0.76 1.07 1.74		SPO3286 SPO3287 SPO3288	0.79 1.24 1.46	0.695 SPO3286 0.053 SPO3287 0.077 SPO3288	0.99 1.07 1.05	0.835 SPO3289 0.067 SPO3290 0.61 SPO3291	1.12 1.01 1.57	0.044 SPO3280 0.598 SPO3281 0.237 SPO3282	0.97 1.51 0.80	0.985 0.054 0.138	SPO3280 SPO3281 SPO3282	0.95 1.71 0.77	0.882 0.097 0.009	SPO3280 SPO3281 SPO3282	0.94 1.10 0.96	0.722	SPO3276 SPO3277 SPO3278	1.03 0.85 1.10	0.857 0.282 0.286
SPO3289 SPO3290 SPO3291	1.03 1.21 1.14	0.449	SPO3289 SPO3290 SPO3291	1.12 1.24 1.14	0.438 SPO3289 0.257 SPO3290 0.259 SPO3291	1.12 1.05 1.17	0.732 SPO3292 0.513 SPO3293 0.251 SPO3294	1.45 1.05 1.09	0.751 SPO3284 0.767 SPO3285 0.958 SPO3286	1.06 1.56 1.27	0.155 0.272 0.632	SPO3284 SPO3285	1.11 1.50 1.36	0.050 0.274	SPO3284 SPO3285 SPO3286	1.32 0.95 0.91	0.176 0.927	SPO3279 SPO3280 SPO3281	0.97 0.87 1.06	0.845 0.667 0.887
SP03292 SP03293	0.93 1.11	0.946 0.325	SPO3292 SPO3293	0.79 1.13	0.856 SPO3292 0.179 SPO3293	0.99 1.28	0.791 SPO3295 0.749 SPO3296	1.1 1.03	0.649 SPO3287 0.873 SPO3288	0.02 0.26	0.006	SPO3287 SPO3288	0.02 0.26	0.001	SPO3287 SPO3288	0.50 1.16	0.039 0.615	SPO3282 SPO3284	0.98 1.07	0.907 0.106
SPO3294	1.05	0.417	SPO3294	1.09	0.61 SPO3294	1	0.567 SPO3297	1.43	0.407 SPO3289	1.72	0.108	SPO3289	1.62	0.017	SPO3289	0.99	0.958	SPO3285	1.01	0.971

SPO3295 SPO3296	1.18 1.15	0.341	SPO3295 SPO3296	1.2	0.196	SPO3295 SPO3296	1.07	0.265 SPO3298 0.921 SPO3299	1.24	0.249	SPO3290 SPO3291	1.36 1.92	0.182	SPO3290 SPO3291	1.29		SPO3290 SPO3291	0.81	0.478	SPO3286 SPO3287	0.97	0.937
SPO3297 SPO3298	1 0.82	0.927	SPO3297 SPO3298	0.97 0.96	0.827 0.957	SPO3297 SPO3298	1.1 1.11	0.704 SPO3300 0.74 SPO3301	1.05	0.978 0.472	SPO3292 SPO3293 SPO3294	0.97 1.53	0.957 0.002	SPO3292 SPO3293 SPO3294	1.04 1.58	0.908	SPO3292 SPO3293	1.00 0.93	0.984 0.723	SPO3288 SPO3289	1.14 1.10	0.454 0.695
SPO3299 SPO3300 SPO3301	1.28 0.97 1.36	0.107 0.986 0.087	SPO3299 SPO3300 SPO3301	1.33 0.96 1.32	0.068 0.934 0.329	SPO3299 SPO3300 SPO3301	1.03 1.08 1.13	0.446 SPO3302 0.996 SPO3303 0.205 SPO3304	1.14 1.33	0.534 0.726 0.862	SPO3294 SPO3295 SPO3296	1.50 1.56 1.38	0.196 0.005 0.773	SPO3294 SPO3295 SPO3296	1.63 1.61 1.37	0.270 0.024 0.795	SPO3294 SPO3295 SPO3296	1.08 1.00 0.95	0.532 0.936 0.950	SPO3290 SPO3291 SPO3292	0.84 1.04 1.05	0.403 0.532 0.945
SPO3302 SPO3303 SPO3304	0.57 0.88 1.18	0.042 5 0.585 5 0.078 5	SPO3302 SPO3303 SPO3304	0.68 0.85 1.13	0.113 0.296 0.114	SPO3302 SPO3303 SPO3304	1.07 1.18 1.28	0.555 SPO3305 0.519 SPO3306 0.698 SPO3307	1.15 1.08 1.11	0.895 0.224 0.292	SPO3297 SPO3298 SPO3299	1.45 1.42	0.337 0.016 0.498	SPO3297 SPO3298 SPO3299	1.24 1.34 1.62	0.183 0.102 0.210	SPO3297 SPO3298 SPO3299	1.23 1.09 1.02	0.790 0.328 0.993	SPO3293 SPO3294 SPO3295	0.90 1.07 1.08	0.581 0.882 0.756
SPO3305 SPO3306	1.24 0.76	0.441 5	SPO3305 SPO3306	1.34 0.87	0.416 0.129	SPO3305 SPO3306	1.13 1.03	0.892 SPO3308 0.6 SPO3309	1 1.02	0.099 0.253	SPO3300 SPO3301	1.21 0.65	0.640 0.247	SPO3300 SPO3301	1.12 0.61	0.127 0.085	SPO3300 SPO3301	1.02 1.08	0.964 0.776	SPO3296 SPO3297	0.95 1.09	0.947 0.399
SPO3307 SPO3308 SPO3309	0.83 0.98 0.81	0.201 S 0.995 S 0.34 S	SPO3307 SPO3308 SPO3309	0.88 0.92 0.87	0.448 0.692 0.403	SPO3307 SPO3308 SPO3309	1.2 1.05 1.07	0.688 SPO3310 0.461 SPO3311 0.138 SPO3312	1.2 0.98 1.4	0.356 0.06 0.214	SPO3302 SPO3303 SPO3304	0.73 1.11 0.88	0.218 0.400 0.856	SPO3302 SPO3303 SPO3304	0.70 1.20 0.93	0.123 0.052 0.822	SPO3302 SPO3303 SPO3304	1.08 0.99 0.91	0.964	SPO3298 SPO3299 SPO3300	1.01 1.12 1.03	0.998 0.671 0.861
SP03310 SP03311 SP03312	0.78 0.53 0.72	0.417 0.5 0.154	SP03310 SP03311 SP03312	0.76 0.6 0.77	0.003 0.06 0.048	SPO3310 SPO3311 SPO3312	1.13 1.03 1.04	0.297 SPO3313 0.023 SPO3314 0.177 SPO3315	1.1 1.19 1.04	0.504 0.765 0.87	SPO3305 SPO3306 SPO3307	1.02 1.14 1.02	0.798 0.047 0.516	SPO3305 SPO3306 SPO3307	0.96 1.07 0.95	0.909 0.117 0.880	SPO3305 SPO3306 SPO3307	1.09 1.07 0.96	0.178	SP03301 SP03302 SP03303	1.16 1.09 1.02	0.652 0.626 0.387
SPO3313 SPO3314	0.78 1.51	0.365	SPO3313 SPO3314	0.88 1.38	0.683 0.381	SP03313 SP03314	1.13 1.04	0.19 SPO3316 0.76 SPO3317	1.1 1.03	0.688 0.163	SPO3308 SPO3309	1.05 1.25	0.581 0.139	SPO3308 SPO3309	0.98 0.98	0.199	SPO3308 SPO3309	0.95 1.09	0.918 0.449	SP03304 SP03305	0.88 1.05	0.493 0.826
SPO3315 SPO3316 SPO3317	1.1 1.47 1.17	0.507 S 0.377 S 0.427 S	SPO3315 SPO3316 SPO3317	0.99 1.37 1.24	0.961 0.707 0.012	SPO3315 SPO3316 SPO3317	1.09 1.91 2.11	0.617 SPO3318 0.679 SPO3319 0.131 SPO3320	1.08 1.1 1.06	0.706 0.68 0.052	SPO3310 SPO3311 SPO3312	2.59 1.81 1.18	0.140 0.011 0.024	SPO3310 SPO3311 SPO3312	1.90 1.37	0.023 0.019 0.050	SPO3310 SPO3311 SPO3312	1.34 1.14 1.14	0.139	SPO3306 SPO3307 SPO3308	1.10 1.00 1.01	0.290 0.853 0.869
SPO3318 SPO3319	0.8 0.91	0.466	SPO3318 SPO3319	0.81 0.92	0.104 0.932	SP03318 SP03319	1.17 1.32	0.317 SPO3321 0.737 SPO3322	1.04 1.11	0.197 0.454	SPO3313 SPO3314	0.57 0.36	0.160 0.031	SPO3313 SPO3314	0.44 0.37	0.097 0.078	SPO3313 SPO3314	0.72 1.24	0.322 0.772	SPO3309 SPO3310	1.18 1.36	0.272 0.268
SPO3320 SPO3321 SPO3322	1.29 0.67 0.98	0.077 5 0.011 5 0.93 5	SP03320 SP03321 SP03322	1.13 0.85 0.94	0.134 0.106 0.763	SPO3320 SPO3321 SPO3322	1.02 2.3 2.38	0.104 SPO3323 0.047 SPO3324 0.226 SPO3325	1.22 1.03 1.17	0.821 0.611 0.333	SPO3315 SPO3316 SPO3317	0.78 0.66 1.09	0.428 0.460 0.588	SPO3315 SPO3316 SPO3317	0.81 0.58 1.03		SPO3315 SPO3316 SPO3317	0.83 0.76 0.93	0.263 0.567 0.733	SP03311 SP03312 SP03313	1.24 1.16 0.81	0.147 0.549 0.518
SPO3323 SPO3324 SPO3325	0.86 1.06 0.84	0.552 5 0.559 5 0.226 5	SPO3323 SPO3324 SPO3325	0.86 0.93 0.87	0.494 0.693 0.212	SPO3323 SPO3324 SPO3325	1.46 1.77 1.08	0.464 SPO3326 0.981 SPO3327 0.152 SPO3328	1.09 1.09 1.19	0.127 0.814 0.894	SPO3318 SPO3319 SPO3320	1.22 2.13 0.68	0.030 0.338 0.103	SPO3318 SPO3319 SPO3320	1.27 2.12 0.68	0.108 0.341 0.069	SPO3318 SPO3319 SPO3320	1.06 0.96 0.93	0.599 0.971 0.836	SP03314 SP03315 SP03316	1.23 0.81 0.79	0.752 0.407 0.527
SPO3326 SPO3327	1.05 1.23	0.757	SPO3326 SPO3327	1.11 1.18	0.548 0.846	SPO3326 SPO3327	1.07	0.157 SPO3329 0.783 SPO3330	1.08 1.21	0.088 0.237	SPO3321 SPO3322	1.11 0.88	0.295 0.667	SPO3321 SPO3322	1.03 1.00	0.423 0.365	SPO3321 SPO3322	1.12 1.04	0.253 0.584	SP03317 SP03318	0.95 1.02	0.510 0.735
SPO3328 SPO3329 SPO3330	1.04 1.3 1.18	0.766 0.307 0.212	SPO3328 SPO3329 SPO3330	0.86 1.56 1.11	0.452 0.033 0.371	SPO3328 SPO3329 SPO3330	1.26 1.12 1.25	0.631 SPO3331 0.521 SPO3332 0.107 SPO3333	1.05 1.03 1.23	0.995 0.058 0.273	SPO3323 SPO3324 SPO3325	0.82 0.98 0.69	0.714 0.575 0.085	SPO3323 SPO3324 SPO3325	0.83 1.06 0.67	0.683 0.173 0.081	SPO3323 SPO3324 SPO3325	1.01 1.17 0.93	0.942 0.059 0.097	SP03319 SP03320 SP03321	0.98 0.93 1.14	0.996 0.719 0.260
SP03331 SP03332 SP03333	1 1.74 0.76	0.989 0.017 0.631	SP03331 SP03332 SP03333	0.95 1.52 0.81	0.994 0.044 0.576	SP03331 SP03332 SP03333	1.17 1.06 1.15	0.949 SPO3334 0.039 SPO3335 0.41 SPO3336	1.03 1.1 1.27	0.135 0.192 0.754	SPO3326 SPO3327 SPO3328	0.76 0.85 0.62	0.157 0.788 0.188	SPO3326 SPO3327 SPO3328	0.76 0.81 0.61	0.085 0.781 0.086	SPO3326 SPO3327 SPO3328	0.83 0.85 1.03	0.645	SP03322 SP03323 SP03324	1.02 1.09 1.25	0.793 0.596 0.128
SPO3334 SPO3335	0.76 1.99	0.15 0.031	SPO3334 SPO3335	0.79 1.93	0.396	SPO3334 SPO3335	1.14 1.1	0.157 SPO3337 0.223 SPO3338	1.09	0.186 0.95	SPO3329 SPO3330	0.29 1.37	0.003 0.165	SPO3329 SPO3330	0.31 1.41	0.001 0.184	SPO3329 SPO3330	1.13 1.01	0.550 0.966	SP03325 SP03326	1.03 0.86	0.620 0.605
SPO3336 SPO3337 SPO3338	1.5 1.5 1.15	0.28 5 0.069 5 0.792 5	SPO3336 SPO3337 SPO3338	1.44 1.44 1.18		SPO3336 SPO3337 SPO3338	1.09 1.04 1.07	0.529 SPO3339 0.394 SPO3340 0.863 SPO3341	2.27 1.15 1.33	0.613 0.271 0.792	SPO3331 SPO3332 SPO3333	0.62 0.63 3.16	0.820 0.158 0.034	SPO3331 SPO3332 SPO3333	0.63 0.68 2.87	0.827 0.041 0.037	SPO3331 SPO3332 SPO3333	0.88 1.01 0.97	0.935	SPO3327 SPO3328 SPO3329	0.83 1.03 1.08	0.675 0.721 0.646
SPO3339 SPO3340 SPO3341	1.11	0.359 0.015 0.596	SP03339 SP03340 SP03341	0.98 1.46	0.751 0.044	SPO3339 SPO3340 SPO3341	1.13	0.353 SPO3342 0.014 SPO3343 0.586 SPO3344	1.05 2.4	0.532	SPO3334 SPO3335 SPO3336	3.26 0.84	0.015	SPO3334 SPO3335 SPO3336	2.73 0.93	0.012	SPO3334 SPO3335 SPO3336	0.95	0.436	SP03330 SP03331 SP03332	0.98 0.87 0.94	0.950
SPO3342 SPO3343	1.1 1.37 0.67	0.155	SPO3342 SPO3343	0.97 1.27 0.69	0.548	SPO3342 SPO3343	1.05 1 1.08	0.787 SPO3345 0.905 SPO3346	1.42 1.82	0.948 0.547 0.389	SPO3336 SPO3337 SPO3338	0.48 0.58 0.71	0.206 0.043 0.699	SPO3336 SPO3337 SPO3338	0.42 0.63 0.71	0.400 0.098 0.666	SPO3337 SPO3338	0.66 0.86 0.99	0.106 0.961	SP03333 SP03334	0.99 0.94	0.453 0.982 0.828
SPO3344 SPO3345 SPO3346	1.24 1.38 1.19	0.327 S 0.111 S 0.223 S	SPO3344 SPO3345 SPO3346	1.14 1.17 1.2	0.261 0.122 0.1	SPO3344 SPO3345 SPO3346	1.07 1.6 1.53	0.658 SPO3347 0.373 SPO3348 0.522 SPO3349	1.13 1.1 1.09	0.918 0.517 0.251	SPO3339 SPO3340 SPO3341	0.81 0.96 0.76	0.315 0.832 0.717	SPO3339 SPO3340 SPO3341	0.79 0.98 0.78	0.495 0.705 0.104	SPO3339 SPO3340 SPO3341	1.03 1.07 0.93	0.929 0.766 0.853	SP03335 SP03336 SP03337	0.79 0.71 0.91	0.223 0.658 0.627
SPO3347 SPO3348	1.58 1.32	0.565	SPO3347 SPO3348	1.37 1.35	0.616	SP03347 SP03348	1.12 1.2 1.4	0.96 SPO3350 0.555 SPO3351 0.452 SPO3352	1.19 1.04 1.14	0.508	SPO3342 SPO3343 SPO3344	1.60 1.24	0.011	SPO3342 SPO3343 SPO3344	1.82	0.030 0.521 0.760	SPO3342 SPO3343	1.12 0.84 1.01	0.170 0.725 0.969	SP03338 SP03339	0.99 0.93 0.96	0.965 0.702 0.841
SPO3349 SPO3350 SPO3351	1.32 0.83	0.135 0.383 0.723	SPO3349 SPO3350 SPO3351	1.11 1.15 0.9	0.054 0.588 0.588	SPO3349 SPO3350 SPO3351	1.12	0.453 SPO3353 0.39 SPO3354	1.19 1.03	0.88 0.88 0.105	SPO3345 SPO3346	0.85 0.56 1.15	0.766 0.051 0.311	SPO3345 SPO3346	0.87 0.58 1.17	0.050	SPO3344 SPO3345 SPO3346	0.98 0.96	0.946	SP03342	0.88 1.17	0.211 0.065
SPO3352 SPO3353 SPO3354	0.77 1.33 1.12	0.362 5 0.523 5 0.332 5	SPO3352 SPO3353 SPO3354	0.84 1.36 1.21	0.686 0.447 0.041	SPO3352 SPO3353 SPO3354	1.16 1.16 1.07	0.766 SPO3355 0.589 SPO3356 0.008 SPO3357	1.1 1.32 1.15	0.815 0.113 0.25	SPO3347 SPO3348 SPO3349	0.80 0.85 1.43	0.905 0.908 0.031	SPO3348 SPO3349	0.74 0.87 1.60	0.840 0.435 0.012	SPO3347 SPO3348 SPO3349	0.89 0.96 1.18	0.923 0.979 0.282	SPO3343 SPO3344 SPO3345	0.85 1.08 0.98	0.738 0.741 0.971
SPO3355 SPO3356	1.02	0.284	SPO3355 SPO3356	1.86 0.72	0.358 0.016	SP03355 SP03356	1.08	0.49 SPO3358 0.029 SPO3359	1.17	0.526	SPO3350 SPO3351	0.59 1.04	0.253	SPO3350 SPO3351	0.60	0.234	SPO3350 SPO3351	1.10 0.95	0.844	SP03346 SP03347	1.02 0.85	0.849 0.823
SPO3357 SPO3358 SPO3359	1.08 0.98 0.75	0.48 5 0.924 5 0.099 5	SPO3357 SPO3358 SPO3359	1.06 1.09 0.79	0.43 0.165 0.036	SPO3357 SPO3358 SPO3359	1.17 1.03 1.04	0.492 SPO3360 0.555 SPO3361 0.135 SPO3362	1.1 1.06 1.17	0.034 0.387 0.368	SPO3353 SPO3354	1.21 0.61 0.28	0.627 0.336 0.007	SPO3352 SPO3353 SPO3354	1.08 0.57 0.27	0.817 0.319 0.001	SPO3352 SPO3353 SPO3354	0.97 1.04 1.09	0.948	SP03348 SP03349 SP03350	0.96 1.14 1.08	0.945 0.167 0.804
SPO3360 SPO3361 SPO3362	0.6 0.88 1.23	0.078 0.436 0.365	SPO3360 SPO3361 SPO3362	0.58 0.88	0.625	SPO3360 SPO3361 SPO3362	1.14 0.99	0.018 SPO3363 0.757 SPO3364 0.513 SPO3365	1.17 1.04 1.17	0.001 0.016 0.003	SPO3355 SPO3356 SPO3357	0.18 0.85 1.26	0.015 0.275 0.239	SPO3355 SPO3356 SPO3357	0.19 0.83 1.55	0.015 0.128 0.064	SPO3355 SPO3356 SPO3357	1.28 1.00 1.08	0.962	SPO3351 SPO3352 SPO3353	0.97 1.03 1.01	0.943 0.919 0.976
SPO3363 SPO3364	3.7 2.25	0.002	SPO3363 SPO3364	3.87 1.68	0.01 0.093	SPO3363 SPO3364	1.01	0 SP03366 0.014 SP03367	1.21 1.62	0.003	SPO3358 SPO3359	0.88	0.527 0.002	SPO3358 SPO3359 SPO3360	0.96	0.925 0.002	SPO3358 SPO3359	0.95 1.99	0.588 0.034	SPO3354 SPO3355	1.10 1.15	0.239 0.592
SPO3365 SPO3366 SPO3367	2.73 0.81	0.065	SPO3365 SPO3366 SPO3367	2.75 0.77		SP03365 SP03366 SP03367	1.03 1.09 1.01	0.003 SPO3368 0.003 SPO3369 0.221 SPO3370	1.47 1.05 1.2	0.103 0.649 0.019	SPO3360 SPO3361 SPO3362	1.75	0.003 0.060 0.076	SPO3361 SPO3362	1.70	0.001 0.008 0.101	SPO3360 SPO3361 SPO3362	1.95 1.16 1.04	0.088 0.536 0.830	SP03356 SP03357 SP03358	1.04 1.13 0.90	0.854 0.059 0.364
SPO3368 SPO3369 SPO3370	0.85 0.92 1.22	0.559 0.909 0.085	SPO3368 SPO3369 SPO3370	0.86 0.94 1.17	0.298 0.972 0.147	SPO3368 SPO3369 SPO3370	1.13 1.11 1.02	0.139 SPO3371 0.119 SPO3372 0.075 SPO3373	1.36 1.17 1.35	0.201 0.917 0.103	SPO3363 SPO3364 SPO3365	4.27 1.72 4.87	0.070 0.289	SPO3363 SPO3364 SPO3365	4.59 1.61	0.000	SPO3363 SPO3364 SPO3365	1.31 1.08 1.20	0.492 0.881 0.414	SPO3359 SPO3360 SPO3361	1.93 2.02 1.15	0.044 0.043 0.538
SP03371 SP03372 SP03373	1.11 1.08 1.43	0.731	SP03371 SP03372 SP03373	1.1 1.03 1.39	0.715 0.274 0.126	SP03371 SP03372 SP03373	1.08 1.03 1.12	0.53 SPO3374 0.214 SPO3375	1.2 1.25 1.12	0.906 0.114 0.248	SPO3366 SPO3367	3.66 0.66 0.60	0.006 0.037 0.064	SPO3366 SPO3367	3.85 0.68 0.60	0.002 0.175 0.036	SPO3366 SPO3367 SPO3368	1.13 0.98 0.91	0.386 0.906 0.258	SP03362 SP03363 SP03364	0.98 1.23 1.03	0.955 0.249 0.847
SPO3374 SPO3375	1.67 0.81	0.003	SPO3374 SPO3375	1.42 0.82	0.018 0.066	SPO3374 SPO3375	1.83 1.02	0.646 SPO3377 0.262 SPO3378	1.02 1.55	0.61 0.524	SPO3369 SPO3370	0.73 0.53	0.087 0.016	SPO3369 SPO3370	0.84 0.54	0.169 0.006	SPO3369 SPO3370	0.95 0.81	0.419 0.129	SPO3365 SPO3366	1.15 1.10	0.417 0.234
SPO3376 SPO3377 SPO3378	1.11 0.93 1.15	0.594 0.626 0.78	SPO3376 SPO3377 SPO3378	1.1 1.05 0.81	0.8 0.477 0.714	SPO3376 SPO3377 SPO3378	1.09 1.1 1.1	0.794 SPO3379 0.961 SPO3380 0.795 SPO3381	1.12 1.08 1.09	0.942 0.771 0.852	SPO3371 SPO3372 SPO3373	0.57 0.86 1.45	0.234 0.608 0.073	SPO3371 SPO3372 SPO3373	0.59 0.99 1.41	0.067 0.206 0.089	SPO3371 SPO3372 SPO3373	0.90 1.11 1.14	0.841 0.242 0.135	SPO3367 SPO3368 SPO3369	1.04 0.90 0.94	0.807 0.644 0.524
SPO3379 SPO3380 SPO3381	0.87 0.88	0.968 0.213 0.965	SPO3379 SPO3380 SPO3381	1.1 0.84 0.93	0.451	SPO3379 SPO3380 SPO3381	1.08 1.14 1.12	0.993 SPO3382 0.746 SPO3383 0.871 SPO3384	0.99 1.17 0.99	0.067 0.179 0.257	SPO3374 SPO3375 SPO3376	1.03 1.70 0.62	0.348 0.089 0.154	SPO3374 SPO3375 SPO3376	1.03 1.97 0.70	0.230 0.001	SPO3374 SPO3375 SPO3376	1.14 0.98 0.86	0.963	SP03370 SP03371 SP03372	0.84 0.95 1.03	0.218 0.919 0.104
SPO3382 SPO3383	1.05 1.03	0.684 0.875	SPO3382 SPO3383	1 0.97	0.734	SPO3382 SPO3383	1.07 1.06	0.263 SPO3385 0.744 SPO3386	1.07 1.08	0.267 0.553	SPO3377 SPO3378	1.45 0.89	0.012 0.961	SPO3377 SPO3378	1.43 0.99	0.046 0.813	SPO3377 SPO3378	1.08 0.82	0.335	SP03373 SP03374	1.07 1.01	0.477 0.856
SPO3384 SPO3385 SPO3386	1.58 1.27 1.02	0.115 0.074 0.73	SPO3384 SPO3385 SPO3386	1.38 1.19 1.05		SPO3384 SPO3385 SPO3386	1.3 1.11 1.15	0.39 SPO3387 0.123 SPO3388 0.18 SPO3389	1.35 1.23	0.874 0.881 0.863	SPO3379 SPO3380 SPO3381	0.83 1.17 3.80	0.868 0.478 0.545	SPO3379 SPO3380 SPO3381	0.74 1.18 3.98	0.812 0.616 0.561	SPO3379 SPO3380 SPO3381	0.78 0.96 0.86	0.477	SP03375 SP03376 SP03377	1.03 0.85 1.05	0.726 0.480 0.696
SPO3387 SPO3388 SPO3389	1.15 1.15 1.8	0.56 5 0.246 5 0.305 5	SPO3387 SPO3388 SPO3389	1.11 1.12 1.67		SP03387 SP03388 SP03389	1.47 1.22 1.04	0.571 SPO3390 0.305 SPO3391 0.778 SPO3392	1.01 1.02 1.89	0.326 0.362 0.251	SPO3382 SPO3383 SPO3384	0.61 1.05 0.66	0.078 0.175 0.199	SPO3382 SPO3383 SPO3384	0.68 1.01 0.65		SPO3382 SPO3383 SPO3384	0.88 1.11 0.97	0.330	SP03378 SP03379 SP03380	0.85 0.75 1.02	0.586 0.700 0.977
SPO3390 SPO3391	0.85 1.66	0.499 5	SPO3390 SPO3391	0.96 1.59	0.934	SPO3390 SPO3391	1.1 1.09	0.438 SP03393 0.223 SP03394	0.99 1.07	0.402 0.887	SPO3385 SPO3386	0.87 1.20	0.683 0.437	SPO3385 SPO3386	1.03	0.045 0.735	SPO3385 SPO3386	1.10 1.07	0.586 0.857	SP03381 SP03382	0.84 0.88	0.950 0.089
SPO3392 SPO3393 SPO3394	1.53 1 1.01		SPO3392 SPO3393 SPO3394	1.36 1 1.04	0.109 0.845 0.938	SPO3392 SPO3393 SPO3394	1.03 1.07 1.06	0.044 SPO3395 0.372 SPO3396 0.845 SPO3397	1.11 1 1.05	0.031 0.271 0.767	SPO3387 SPO3388 SPO3389	1.14 1.25 1.00	0.690 0.507 0.770	SPO3387 SPO3388 SPO3389	1.00 1.25 0.90	0.902 0.418 0.882	SPO3387 SPO3388 SPO3389	0.96 1.03 1.04	0.705 0.917 0.881	SPO3383 SPO3384 SPO3385	1.10 1.04 1.00	0.079 0.637 0.984
SPO3395 SPO3396 SPO3397	1.66 1.15 1.03	0.031 0.118 0.801	SPO3395 SPO3396 SPO3397	1.59 1.19 0.96	0.009 0.213 0.962	SPO3395 SPO3396 SPO3397	1.04 1.11 1.06	0.29 SPO3398 0.47 SPO3399 0.796 SPO3400	1.02 1.12 1.11	0.043 0.466 0.941	SPO3390 SPO3391 SPO3392	0.79 0.95 1.24	0.404 0.680 0.257	SPO3390 SPO3391 SPO3392	0.76 1.02 1.25	0.868	SPO3390 SPO3391 SPO3392	1.18 1.17 1.30		SP03386 SP03387 SP03388	1.16 1.06 1.00	0.635 0.868 0.943
SPO3398 SPO3399	1.3 1.05	0.239	SPO3398 SPO3399	1.22 1.05	0.029	SPO3398 SPO3399	2.42 1.99	0.115 SPO3401 0.597 SPO3402	1.11 1.04	0.351 0.78	SPO3393 SPO3394	0.65 0.89	0.157 0.920	SPO3393 SPO3394	0.65 0.97	0.120	SPO3393 SPO3394	0.85 0.82	0.216 0.824	SPO3389 SPO3390	1.06 1.07	0.835 0.795
SPO3400 SPO3401 SPO3402	1.17 0.76 1.11	0.713 0.387 0.638	SPO3400 SPO3401 SPO3402	1.13 0.78 1.16	0.873 0.258 0.63	SPO3400 SPO3401 SPO3402	1.21 1.05 1.31	0.926 SPO3403 0.451 SPO3404 0.738 SPO3405	1.02 1.26 1.35	0.074 0.245 0.908	SPO3395 SPO3396 SPO3397	0.63 0.83 0.97	0.051 0.126 0.875	SPO3395 SPO3396 SPO3397	0.72 0.88 0.91	0.013 0.237 0.712	SPO3395 SPO3396 SPO3397	1.15 1.11 0.89	0.568 0.598 0.705	SPO3391 SPO3392 SPO3393	1.01 1.03 0.86	0.887 0.780 0.567
SPO3403 SPO3404 SPO3405	1.1 2.14 1.47	0.112 5 0.039 5 0.102 5	SPO3403 SPO3404 SPO3405	1.05 1.9	0.221 0.022 0.626	SPO3403 SPO3404 SPO3405	1.06 1.8 1.1	0.003 SPO3406 0.096 SPO3407 0.888 SPO3408	1.12 1.1 1.01	0.848 0.829 0.793	SPO3398 SPO3399 SPO3400	0.93 0.52 1.06	0.250 0.475 0.916	SPO3398 SPO3399 SPO3400	1.08 0.45 1.13	0.711 0.380 0.869	SPO3398 SPO3399 SPO3400	0.93 0.81 0.95		SPO3394 SPO3395 SPO3396	0.82 0.93 1.10	0.836 0.389 0.623
SPO3406 SPO3407	1.13 1.03	0.409	SPO3406 SPO3407	1.14 1.15	0.377 0.177	SPO3406 SPO3407	1.06 1.06	0.872 SPO3409 0.771 SPO3410	1.07 1.05	0.289 0.35	SPO3401 SPO3402	1.38 0.71	0.065 0.651	SPO3401 SPO3402	1.08 0.75	0.648	SPO3401 SPO3402	1.10	0.798 0.636	SP03397 SP03398	0.95 0.89	0.851 0.362
SPO3408 SPO3409 SPO3410	1.54 1.29 1.26	0.054 5 0.208 5 0.117 5	SPO3408 SPO3409 SPO3410	1.36 1.45 1.16	0.027	SPO3408 SPO3409 SPO3410	1.06 1 1.04	0.901 SPO3411 0.027 SPO3412 0.747 SPO3413	1.02 1.02 1.12	0.813 0.005 0.115	SPO3404	1.20 0.83 0.70	0.527 0.145 0.580	SPO3403 SPO3404 SPO3405	0.91 0.75	0.661 0.379 0.550	SPO3403 SPO3404 SPO3405	1.04 1.15 1.13	0.701	SP03399 SP03400 SP03401	0.86 1.01 1.12	0.817 0.996 0.362
SPO3411 SPO3412 SPO3413	1.01 0.96 1.12	0.746 0.324 0.154	SP03411 SP03412 SP03413	1.01 0.96 1.15	0.687 0.798 0.329	SP03411 SP03412 SP03413	1.12 1.04 1.14	0.942 SPO3414 0.023 SPO3415 0.04 SPO3416	1.14 1.07 2.73	0.894 0.119 0.153	SPO3406 SPO3407 SPO3408	1.55 1.34 0.68	0.020 0.116 0.370	SPO3406 SPO3407 SPO3408	1.70 1.35 0.67	0.028 0.270 0.352	SPO3406 SPO3407 SPO3408	1.03 1.02 1.01		SP03402 SP03403 SP03404	0.75 1.06 1.11	0.660 0.822 0.798
SPO3414 SPO3415	1.01	0.943	SPO3414 SPO3415	1.08 1.02	0.521 0.299	SPO3414 SPO3415	1 1.08	0.952 SPO3417 0.086 SPO3418	2.21	0.517 0.81	SPO3409 SPO3410	0.16 0.25	0.002 0.008	SPO3409 SPO3410	0.19 0.25	0.003	SPO3409 SPO3410	1.04 1.01	0.981 0.876	SPO3405 SPO3406	1.09 1.01	0.864 0.971
SPO3416 SPO3417 SPO3418	0.85 0.75	0.994 5 0.419 5 0.012 5	SP03416 SP03417 SP03418	0.91 0.86 0.84	0.49 0.542 0.443	SPO3416 SPO3417 SPO3418	1.1 1.03 1.13	0.136 SPO3419 0.444 SPO3420 0.283 SPO3421	1.04 1.46 1.12	0.87 0.15 0.857	SPO3411 SPO3412 SPO3413	0.61 0.83 0.93	0.069 0.481 0.504	SP03411 SP03412 SP03413	0.60 0.86 0.97	0.006 0.833 0.636	SPO3411 SPO3412 SPO3413	0.92 0.98 1.05	0.886	SP03407 SP03408 SP03409	1.10 1.03 0.97	0.627 0.685 0.732
SPO3419 SPO3420 SPO3421	1.1 1.12 1.28	0.14 0.335 0.105	SPO3419 SPO3420 SPO3421	1.25 1.13 1.18	0.014 0.256 0.699	SPO3419 SPO3420 SPO3421	0.99 1.04 1.15	0.555 SPO3422 0.831 SPO3423 0.732 SPO3424	1.88 1.08 1.02	0.174 0.029 0.53		1.37 1.00	0.040 0.007 0.019	SPO3414 SPO3415 SPO3416	1.37 1.01	0.032 0.022 0.025	SPO3414 SPO3415 SPO3416	0.92 1.07	0.359 0.497	SP03410 SP03411 SP03412	0.94 0.92 0.99	0.709 0.505 0.732
SPO3422 SPO3423	0.87 1.25	0.346	SP03422 SP03423	0.94 1.18	0.702 0.005	SP03422 SP03423	1.19 1	0.307 SPO3425 0.059 SPO3426	1.11 0.99	0.217 0.871	SPO3417 SPO3418	1.64 0.99	0.094 0.573	SPO3417 SPO3418	1.72 0.94	0.092 0.802	SPO3417 SPO3418	0.93 1.10	0.847 0.835	SPO3413 SPO3414	1.08 0.94	0.275 0.920
SPO3424 SPO3425 SPO3426	0.91 0.87 0.57	0.818 5 0.351 5 0.069 5	SP03424 SP03425 SP03426	0.9 0.77 0.64	0.498 0.095 0.047	SPO3424 SPO3425 SPO3426	1.15 1.17 1.04	0.935 SPO3427 0.257 SPO3428 0.591 SPO3429	1.04 1.09 1.04	0.072 0.962 0.369	SPO3419 SPO3420 SPO3421	0.96 1.62 0.68	0.768 0.013 0.116	SPO3419 SPO3420 SPO3421	0.99 1.83 0.68	0.692 0.084 0.451	SPO3419 SPO3420 SPO3421	1.03 1.22 1.01		SP03415 SP03416 SP03417	1.02 0.96 0.91	0.269 0.904 0.741
SPO3427 SPO3428 SPO3429	1.13 1.22 1.1	0.151 0.28 0.732	SPO3427 SPO3428 SPO3429	1.13 1.02 1.09	0.153 0.929 0.702	SPO3427 SPO3428 SPO3429	1.06 1.07	0.3 SPO3430 0.972 SPO3431 0.647 SPO3432	1.03 1.14	0.265 0.384 0.58	SPO3422 SPO3423 SPO3424	1.32 0.61 0.94	0.101 0.059 0.616	SPO3422 SPO3423 SPO3424	1.24 0.64 0.87	0.023 0.017 0.304	SPO3422 SPO3423 SPO3424	1.06 1.07 0.96	0.480 0.358 0.830	SPO3418 SPO3419	1.07 0.99 1.24	0.791 0.983 0.038
SPO3430 SPO3431	1.47	0.313	SPO3430 SPO3431	1.15 1.2	0.664	SPO3430 SPO3431	1.08 1.06	0.696 SPO3433 0.225 SPO3434	1.02 1.02	0.784 0.665	SPO3425 SPO3426	1.21 0.43	0.045 0.016	SPO3425 SPO3426	1.22 0.44	0.002	SPO3425 SPO3426	0.99 1.03	0.916 0.640	SPO3421 SPO3422	0.93 1.13	0.900
SPO3432 SPO3433	1.35 1.37	0.307	SP03432 SP03433	1.29	0.335 0.587	SPO3432 SPO3433	1.08 1.06	0.726 SPO3435 0.772 SPO3436	1.17	0.584 0.148	SPO3427 SPO3428	0.88 0.98	0.135 0.984	SPO3427 SPO3428	0.96 0.97	0.896 0.982	SPO3427 SPO3428	0.99 1.20		SP03423 SP03424	1.03 0.91	0.394 0.563

SPO3434 SPO3435	1.11	0.575	SP03434 SP03435	1.13	0.551	SPO3434 SPO3435	1.07	0.513 SPO3437 0.561 SPO3438	1.1	0.875	SPO3429 SPO3430	0.64	0.445	SPO3429 SPO3430	0.60		SPO3429 SPO3430	0.85	0.650	SPO3425 SPO3426	1.04	0.733 0.191
SPO3436 SPO3437	1.61 1.3	0.106 0.23	SPO3436 SPO3437	1.36 1.25	0.154 0.305	SPO3436 SPO3437	1.11 1.31	0.629 SPO3439 0.651 SPO3440	0.99 1.18	0.795 0.168	SPO3431 SPO3432 SPO3433	0.90 1.00	0.771 0.712	SPO3431 SPO3432 SPO3433	0.91 1.09	0.706 0.013	SPO3431 SPO3432	0.92 1.14	0.577 0.562	SPO3427 SPO3428	0.95 1.15	0.598 0.789
SPO3438 SPO3439 SPO3440	0.83 1.48 1.09	0.904 0.234 0.246	SP03438 SP03439 SP03440	0.97 1.5 1.04	0.992 0.019 0.448	SPO3438 SPO3439 SPO3440	1.07 1.06	0.976 SPO3441 0.501 SPO3442 0.095 SPO3443	1.09 1.05 1.05	0.263 0.657 0.91	SPO3434 SPO3435	0.88 1.08 0.48	0.923 0.677 0.078	SPO3434 SPO3435	0.90 1.05 0.48	0.972 0.741 0.064	SPO3433 SPO3434 SPO3435	0.93 0.91 0.96	0.887 0.739 0.958	SP03429 SP03430 SP03431	0.84 0.76 0.93	0.452 0.454 0.736
SPO3441 SPO3442 SPO3443	0.68 1.39 1.12	0.102 0.41 0.745	SP03441 SP03442 SP03443	0.75 1.21 1.14	0.082 0.538 0.76	SPO3441 SPO3442 SPO3443	1.27 1.24 1.49	0.492 SPO3444 0.773 SPO3445 0.977 SPO3446	1.04 1.08 1.03	0.668 0.016 0.05	SPO3436 SPO3437 SPO3438	1.05 1.45 0.86	0.571 0.179 0.929	SPO3436 SPO3437 SPO3438	1.14 1.45 0.74	0.279 0.342 0.815	SPO3436 SPO3437 SPO3438	0.93 1.14 0.85	0.249 0.302 0.899	SP03432 SP03433 SP03434	1.13 0.91 0.89	0.518 0.872 0.682
SPO3444 SPO3445	1.13 0.75	0.756	SPO3444 SPO3445	1.13 0.85	0.441 0.126	SPO3444 SPO3445	1.11	0.761 SPO3447 0.011 SPO3448	1.08 1.03	0.168 0.788	SPO3439 SPO3440	1.51 1.33	0.046 0.013	SPO3439 SPO3440	1.52 1.37	0.071 0.052	SPO3439 SPO3440	1.22 1.13	0.162 0.170	SPO3435 SPO3436	0.95 1.11	0.900 0.651
SPO3446 SPO3447 SPO3448	1.34 0.52 0.81	0.04 0.195 0.295	SP03446 SP03447 SP03448	1.41 0.62 0.89	0.024 0.011 0.502	SPO3446 SPO3447 SPO3448	1.15 1.06	0.044 SPO3449 0.021 SPO3450 0.93 SPO3451	1.01 1.01 1.04	0.863 0.139 0.376	SPO3441 SPO3442 SPO3443	1.00 0.79 0.96	0.288 0.634 0.975	SPO3441 SPO3442 SPO3443	0.98 0.80 0.93	0.154 0.758 0.979	SPO3441 SPO3442 SPO3443	1.26 1.02 0.99		SPO3437 SPO3438 SPO3439	1.04 0.91 1.19	0.816 0.931 0.164
SPO3449 SPO3450 SPO3451	0.71 1.27 0.78	0.682 0.078 0.223	SPO3449 SPO3450 SPO3451	0.88 1.23 0.8	0.78 0.023 0.189	SPO3449 SPO3450 SPO3451	1.45 2.04 1.69	0.913 SPO3452 0.366 SPO3453 0.393 SPO3454	1.11 1.24 1.08	0.015 0.797 0.152	SPO3444 SPO3445 SPO3446	1.02 7.72 0.57	0.861 0.020 0.003	SPO3444 SPO3445 SPO3446	0.95 7.42 0.53	0.841 0.004 0.008	SPO3444 SPO3445 SPO3446	0.97 0.83 0.96	0.463	SP03440 SP03441 SP03442	1.10 1.32 0.99	0.216 0.139 0.958
SPO3452 SPO3453	0.74 0.88	0.154 0.113	SPO3452 SPO3453	0.85 0.88	0.389 0.803	SPO3452 SPO3453	1.4 1.16	0.423 SPO3455 0.574 SPO3456	1.26 1.22	0.676 0.855	SPO3447 SPO3448	1.16 1.26	0.151 0.242	SPO3447 SPO3448	1.27 1.27	0.040	SPO3447 SPO3448	1.08 1.10	0.666 0.551	SP03443 SP03444	0.97 1.05	0.959 0.845
SPO3454 SPO3455 SPO3456	1.12 0.95 1.17	0.031 0.902 0.717	SP03454 SP03455 SP03456	1.16 0.94 1.34		SPO3454 SPO3455 SPO3456	1.21 1.05 1.4	0.333 SPO3457 0.344 SPO3458 0.855 SPO3459	1.3 1.54 1.16	0.51 0.562 0.834	SPO3449 SPO3450 SPO3451	1.07 0.62 1.97	0.746 0.013 0.033	SPO3449 SPO3450 SPO3451	1.02 0.70 1.82	0.799 0.096 0.062	SPO3449 SPO3450 SPO3451	1.01 1.17 1.11	0.257	SPO3445 SPO3446 SPO3447	0.93 0.94 1.04	0.885 0.689 0.748
SPO3457 SPO3458 SPO3459	1.09 1.04 1.57	0.359 0.326 0.077	SP03457 SP03458 SP03459	1.02 1.19 1.34	0.78 0.19	SPO3457 SPO3458 SPO3459	1.29 1.1 1.05	0.494 SPO3460 0.709 SPO3461 0.969 SPO3462	1.1 1.06 1.44	0.042 0.859 0.142	SPO3452 SPO3453 SPO3454	1.82 0.81 0.92	0.033 0.226 0.185	SPO3452 SPO3453 SPO3454	1.94 0.81 0.92	0.016 0.638 0.389	SPO3452 SPO3453 SPO3454	1.26 0.92 0.94	0.299 0.767 0.500	SPO3448 SPO3449 SPO3450	1.12 1.03 1.09	0.597 0.923 0.417
SPO3460 SPO3461	0.78 0.74	0.232	SPO3460 SPO3461	0.79 0.81	0.154 0.72	SPO3460 SPO3461	1.17	0.265 SPO3463 0.789 SPO3464	1.81 1.7	0.979 0.665	SPO3455 SPO3456	0.37 0.37	0.019 0.189	SPO3455 SPO3456	0.38 0.45	0.024 0.409	SPO3455 SPO3456	1.00 0.93	0.918 0.871	SPO3451 SPO3452	1.07 1.16	0.572 0.171
SPO3462 SPO3463 SPO3464	0.78 1.04 0.92	0.236 0.849 0.735	SP03462 SP03463 SP03464	0.81 1.05 0.99	0.119 0.792 0.843	SPO3462 SPO3463 SPO3464	1.01 1 1.44	0.632 SPO3465 0.602 SPO3466 0.873 SPO3467	1.36 1.14 1.03	0.443 0.73 0.983	SPO3457 SPO3458 SPO3459	0.33 0.33 0.19	0.066 0.011 0.003	SPO3457 SPO3458 SPO3459	0.33 0.44 0.21	0.011 0.020 0.005	SPO3457 SPO3458 SPO3459	0.98 0.94 1.13	0.829 0.809 0.461	SPO3453 SPO3454 SPO3455	0.88 0.95 1.00	0.702 0.084 0.952
SPO3465 SPO3466 SPO3467	1.15 1.22 0.76	0.18 0.717	SP03465 SP03466 SP03467	1.02 1.11 0.82	0.509 0.828 0.211	SPO3465 SPO3466	1.02	0.861 SPO3468 0.761 SPO3469 0.617 SPO3470	1.47 1.41 1.11	0.847 0.483 0.507	SPO3460 SPO3461 SPO3462	0.25 0.20 0.75	0.002 0.028 0.107	SPO3460 SPO3461 SPO3462	0.26 0.24 0.75	0.000 0.016 0.171	SPO3460 SPO3461 SPO3462	1.05 0.98 1.01	0.912 0.901 0.967	SPO3456 SPO3457 SPO3458	1.00 0.95 1.04	0.982 0.858 0.945
SPO3468 SPO3469	0.69	0.505	SP03468 SP03469	0.82 0.7 0.59	0.148	SPO3467 SPO3468 SPO3469	1.14 1 1.03	0.617 SPO3470 0.938 SPO3471 0.515 SPO3472	1.11 1.05 1.06	0.507 0.746 0.561	SPO3463 SPO3464	0.75 0.56 1.37	0.107 0.081 0.114	SPO3463 SPO3464	0.54 1.44	0.171	SPO3463 SPO3464	0.95 1.11	0.896	SP03459 SP03460	1.11 1.13	0.724 0.489
SPO3470 SPO3471 SPO3472	0.85 0.81 0.61	0.57 0.64 0.034	SP03470 SP03471 SP03472	0.89 0.88 0.7	0.698 0.765 0.031	SPO3470 SPO3471 SPO3472	1.16 1.03 1.12	0.334 SPO3473 0.818 SPO3474 0.706 SPO3475	1.2 1.11 1.04	0.357 0.633 0.486	SPO3465 SPO3466 SPO3467	1.23 0.99 1.44	0.083 0.892 0.005	SPO3465 SPO3466 SPO3467	1.19 0.97 1.37	0.222 0.905 0.014	SPO3465 SPO3466 SPO3467	1.12 0.88 1.00	0.849	SP03461 SP03462 SP03463	0.94 0.96 0.93	0.731 0.711 0.831
SP03473 SP03474	0.83 0.83	0.391 0.36	SPO3473 SPO3474	0.83 0.88	0.648	SPO3473 SPO3474	1.16 1.03	0.922 SPO3476 0.385 SPO3477	1.41 1.18	0.54 0.802	SPO3468 SPO3469	1.53 1.58	0.071 0.073	SPO3468 SPO3469	1.65 1.50	0.042	SPO3468 SPO3469	0.95 1.03	0.899 0.827	SPO3464 SPO3465	1.05 0.99	0.874 0.926
SPO3475 SPO3476 SPO3477	0.95 0.89 1.04	0.25 0.695 0.646	SP03475 SP03476 SP03477	0.9 0.88 1.04		SPO3475 SPO3476 SPO3477	1.06 1.02 1.11	0.274 SPO3478 0.681 SPO3479 0.598 SPO3480	1.02 1.16 1.04	0.892 0.454 0.585	SPO3470 SPO3471 SPO3472	0.76 0.86 0.99	0.325 0.870 0.370	SPO3470 SPO3471 SPO3472	0.79 0.81 0.89	0.383 0.743 0.369	SPO3470 SPO3471 SPO3472	0.92 1.02 0.96		SP03466 SP03467 SP03468	0.88 0.99 0.98	0.817 0.997 0.966
SPO3478 SPO3479 SPO3480	1.15 1.18 1.24	0.845 0.264 0.143	SPO3478 SPO3479 SPO3480	1.05 1.17 1.27	0.897 0.176 0.067	SPO3478 SPO3479 SPO3480	1.13 1.04 1.03	0.942 SPO3481 0.447 SPO3482 0.381 SPO3483	1.17 1.13 1.1	0.11 0.054 0.153	SPO3473 SPO3474 SPO3475	2.05 0.93 0.81	0.091 0.741 0.589	SPO3473 SPO3474 SPO3475	1.58 0.85 0.85	0.020 0.673 0.700	SPO3473 SPO3474 SPO3475	1.16 0.90 0.78	0.136 0.895 0.066	SPO3469 SPO3470 SPO3471	1.02 0.99 1.01	0.763 0.983 0.950
SPO3481 SPO3482	1.24 1.33	0.378	SPO3481 SPO3482	1.17 1.36	0.052 0.204	SPO3481 SPO3482	1.03 1.08	0.116 SPO3484 0.04 SPO3485	1 1.25	0.664 0.219	SPO3476 SPO3477	0.62 0.84	0.040 0.299	SPO3476 SPO3477	0.63 0.82	0.024 0.191	SPO3476 SPO3477	0.99 1.05	0.891 0.705	SP03472 SP03473	1.00 1.16	0.860 0.429
SPO3483 SPO3484 SPO3485	1.37 1.29 1.2	0.043 0.675 0.228	SPO3483 SPO3484 SPO3485	1.26 1.09 1.08	0.091 0.86 0.37	SPO3483 SPO3484 SPO3485	1.12 1.3 1.02	0.012 SPO3486 0.683 SPO3487 0.418 SPO3488	1.03 1.08 1.15	0.073 0.893 0.907	SPO3478 SPO3479 SPO3480	0.82 0.75 0.71	0.757 0.159 0.025	SPO3478 SPO3479 SPO3480	0.77 0.78 0.74	0.699 0.296 0.211	SPO3478 SPO3479 SPO3480	0.85 0.73 0.64	0.802 0.269 0.109	SP03474 SP03475 SP03476	0.90 0.83 0.99	0.673 0.161 0.897
SPO3486 SPO3487 SPO3488	0.96 1.16 0.97	0.867 0.436 0.954	SP03486 SP03487 SP03488	1.02	0.601 0.678 0.53	SPO3486 SPO3487 SPO3488	1 1.09 1.15	0.661 SPO3489 0.919 SPO3490 0.634 SPO3491	1.12 1.09 1.03	0.199 0.245 0.252	SPO3481 SPO3482 SPO3483	0.81 0.68 1.00	0.044 0.115 0.961	SPO3481 SPO3482 SPO3483	0.85 0.55	0.172 0.084 0.523	SPO3481 SPO3482 SPO3483	0.93 0.83 1.30	0.426 0.377 0.175	SP03477 SP03478 SP03479	1.10 0.81 0.75	0.375
SPO3489 SPO3490	1.57	0.008	SPO3489 SPO3490	1.44 1.49	0.014	SPO3489 SPO3490	1.09 1.23	0.661 SPO3492 0.344 SPO3493	1.05 1.09	0.903 0.918	SPO3484 SPO3485	0.21 0.63	0.125 0.190	SPO3484 SPO3485	0.22	0.155 0.015	SPO3484 SPO3485	1.02 0.94	0.952 0.746	SPO3480 SPO3481	0.71 0.98	0.161 0.863
SPO3491 SPO3492 SPO3493	0.71 0.73 1.08	0.06 0.038 0.702	SPO3491 SPO3492 SPO3493	0.79 0.75 0.98	0.164 0.134 0.905	SPO3491 SPO3492 SPO3493	1.04 1 1.06	0.623 SPO3494 0.708 SPO3495 0.906 SPO3496	1.09 1.29 1.08	0.214 0.229 0.009	SPO3486 SPO3487 SPO3488	0.60 0.98 1.82	0.374 0.616 0.056	SPO3486 SPO3487 SPO3488	0.60 0.91 2.11	0.265 0.780 0.010	SPO3486 SPO3487 SPO3488	0.69 1.27 1.20	0.551 0.411 0.496	SP03482 SP03483 SP03484	0.83 1.11 1.07	0.316 0.186 0.882
SPO3494 SPO3495 SPO3496	0.68 0.92 0.87	0.089 0.102 0.798	SP03494 SP03495 SP03496	0.71 1.05 0.98	0.009 0.447 0.347	SPO3494 SPO3495 SPO3496	1.06 1.01 1.05	0.143 SPO3499 0.042 SPO3500 0.049 SPO3501	1.15 1.15 1.13	0.905 0.032 0.553	SPO3489 SPO3490	0.81 0.86 1.45	0.120 0.197 0.090	SPO3489 SPO3490	0.76 0.99 1.48	0.009 0.560 0.008	SPO3489 SPO3490 SPO3491	0.91 0.89 0.99		SPO3485 SPO3486 SPO3487	0.91 0.72 1.09	0.324 0.321 0.919
SPO3499 SPO3500	1.15 0.76	0.465	SPO3499 SPO3500	1.47 0.84	0.232	SPO3499 SPO3500	1.12 1.14	0.18 SPO3502 0.038 SPO3503	1.18 1.04	0.843 0.333	SPO3492 SPO3493	0.95 0.60	0.601 0.336	SPO3491 SPO3492 SPO3493	0.96 0.62	0.587 0.045	SPO3492 SPO3493	0.87 0.97	0.313 0.950	SPO3488 SPO3489	0.98 0.90	0.960 0.138
SPO3501 SPO3502 SPO3503	1.08 1.14 0.84	0.724 0.808 0.168	SPO3501 SPO3502 SPO3503	1.11 1.07 0.91	0.484 0.799 0.383	SPO3501 SPO3502 SPO3503	1.26 1.19 1.03	0.631 SPO3504 0.915 SPO3505 0.144 SPO3506	1.1 1.12 1.02	0.953 0.044 0.876	SPO3494 SPO3495 SPO3496	0.61 2.62 2.71	0.041 0.012 0.007	SPO3494 SPO3495 SPO3496	0.60 2.41 2.54	0.009 0.005 0.004	SPO3494 SPO3495 SPO3496	0.85 0.83 0.92	0.315	SPO3490 SPO3491 SPO3492	0.89 1.10 0.88	0.758 0.573 0.379
SPO3504 SPO3505 SPO3506	1.39 1.04 0.89	0.053 0.094 0.51	SPO3504 SPO3505 SPO3506	1.22 0.79 0.83	0.408 0.19 0.119	SPO3504 SPO3505 SPO3506	1.08 1.24 1.68	0.608 SPO3507 0.429 SPO3508 0.3 SPO3509	1.1 1.03	0.027 0.18 0.139	SPO3499 SPO3500	1.25 2.14 1.65	0.027 0.002 0.013	SPO3499 SPO3500 SPO3501	0.93 1.98 1.62	0.439 0.004 0.021	SPO3499 SPO3500 SPO3501	1.09 1.13 1.05	0.099 0.026 0.328	SPO3493 SPO3494 SPO3495	1.04 0.92 0.80	0.926 0.201 0.159
SPO3507 SPO3508	2.05 1.18	0.015	SPO3507 SPO3508	1.84	0.013 0.089	SPO3507 SPO3508	1.2 1.09	0.025 SPO3510 0.316 SPO3511	1.11 1.22	0.024 0.545		0.97 1.24	0.938 0.250	SPO3502 SPO3503	0.97 1.05	0.895 0.404	SPO3502 SPO3503	0.95 1.04	0.939 0.784	SPO3496 SPO3499	0.90 1.23	0.408 0.034
SPO3509 SPO3510 SPO3511	1.04 1.5	0.002 0.869 0.086	SPO3509 SPO3510 SPO3511	0.93 1.22	0.016 0.506 0.089	SPO3509 SPO3510 SPO3511	1.02 1 1.3	0.115 SPO3512 0.068 SPO3513 0.068 SPO3514	1.09 1.05 1.03	0.604 0.369 0.11	SPO3504 SPO3505 SPO3506	1.05 0.98 0.72	0.598 0.741 0.132	SPO3504 SPO3505 SPO3506	1.05 1.10 0.79	0.796 0.788 0.134	SPO3504 SPO3505 SPO3506	1.16 1.01 1.00	0.248 0.910 0.978	SPO3500 SPO3501 SPO3502	1.19 1.07 1.02	0.027 0.449 0.952
SPO3512 SPO3513 SPO3514	0.92 2.49 1.79	0.921	SP03512 SP03513 SP03514	0.92 2.09 1.58	0.527 0.051 0.005	SPO3512 SPO3513 SPO3514	1.14 1.17 1.12	0.533 SPO3515 0.507 SPO3516 0.124 SPO3517	1.36 1.8 1.14	0.294 0.227 0.042	SPO3507 SPO3508	0.65 1.56 0.88	0.031 0.052 0.835	SPO3507 SPO3508	0.68 1.45 0.89	0.108 0.018 0.632	SPO3507 SPO3508 SPO3509	0.88 1.08 0.97	0.084 0.665 0.906	SPO3503 SPO3504 SPO3505	0.97 1.02 1.06	0.912 0.964 0.580
SPO3515 SPO3516	1.26 1.67	0.744	SPO3515 SPO3516	1.69 1.54	0.356 0.018	SPO3515 SPO3516	1.29 1	0.689 SPO3518 0.268 SPO3519	1.14 1.04	0.474 0.721	SPO3510 SPO3511	2.38 0.76	0.004 0.170	SPO3510 SPO3511	2.30 0.79	0.002	SPO3510 SPO3511	1.41 0.93	0.357 0.781	SPO3506 SPO3507	0.96 0.91	0.758 0.405
SPO3517 SPO3518 SPO3519	1.56 0.93 0.87	0.005 0.574 0.465	SPO3517 SPO3518 SPO3519	0.92 0.91	0.03 0.479 0.578	SPO3517 SPO3518 SPO3519	1.06 1.03 1.2	0.038 SPO3520 0.223 SPO3521 0.873 SPO3522	1.41 1.21 1.11	0.091 0.629 0.28	SPO3512 SPO3513 SPO3514	1.01 0.82 0.93	0.363 0.753 0.197	SPO3512 SPO3513 SPO3514	0.93 0.80 1.00	0.695 0.740 0.102	SPO3512 SPO3513 SPO3514	0.86 1.08 0.98	0.438 0.699 0.651	SPO3508 SPO3509 SPO3510	1.12 0.96 1.32	0.563 0.951 0.009
SPO3520 SPO3521 SPO3522	0.74 0.74 0.54	0.491 0.173 0.058	SPO3520 SPO3521 SPO3522	0.79 0.8 0.6		SPO3520 SPO3521 SPO3522	1.2 1.04 1.07	0.027 SPO3523 0.359 SPO3524 0.072 SPO3525	1.08 1.48 1.07	0.147 0.049 0.114	SPO3515 SPO3516 SPO3517	0.40 0.88 0.68	0.123 0.935 0.017	SPO3515 SPO3516 SPO3517	0.42 0.99 0.69	0.254 0.571 0.046	SPO3515 SPO3516 SPO3517	0.82 1.10 1.09	0.775	SPO3511 SPO3512 SPO3513	0.92 0.93 0.99	0.811 0.409 0.947
SPO3523 SPO3524	0.85 0.77	0.128 0.089	SPO3523 SPO3524	0.85 0.77	0.168 0.171	SPO3523 SPO3524	1.02	0.224 SPO3526 0.176 SPO3527	1.01 1.01	0.04 0.147	SPO3518 SPO3519	0.99 0.93	0.575 0.962	SPO3518 SPO3519	1.04	0.580 0.936	SPO3518 SPO3519	1.06 0.88	0.167 0.662	SP03514 SP03515	0.95 0.99	0.815 0.952
SPO3525 SPO3526 SPO3527	0.71 0.85 0.5	0.069 0.235 0.027	SP03525 SP03526 SP03527	0.76 0.74 0.52		SPO3525 SPO3526 SPO3527	1.12 1.02 1.21	0.015 SPO3528 0.115 SPO3529 0.154 SPO3530	1.26 1.23 1.1	0.201 0.846 0.985	SPO3520 SPO3521 SPO3522	2.93 2.55 2.49	0.022 0.006 0.057	SPO3521 SPO3522	2.59 2.54	0.010 0.032	SPO3520 SPO3521 SPO3522	1.38 1.08 0.95	0.623	SP03516 SP03517 SP03518	1.02 1.01 1.07	0.804 0.565 0.221
SPO3528 SPO3529 SPO3530	0.91 0.85 1.06	0.108 0.487 0.814	SPO3528 SPO3529 SPO3530	0.85 0.88 0.92	0.487 0.565 0.923	SPO3528 SPO3529 SPO3530	1.12 1.08 1.47	0.661 SPO3531 0.801 SPO3532 0.323 SPO3533	1.06 1 1.02	0.119 0.124 0.047	SPO3523 SPO3524 SPO3525	6.21 7.48 8.39	0.002 0.001 0.001	SPO3523 SPO3524 SPO3525	5.68 6.68	0.001 0.001 0.000	SPO3523 SPO3524 SPO3525	1.15 1.06 1.17	0.573	SPO3519 SPO3520 SPO3521	0.86 1.36 0.99	0.366 0.058 0.971
SPO3531 SPO3532 SPO3533	1.44 0.69 0.97		SP03531 SP03532 SP03533	1.32 0.67 0.88	0.018 0.02 0.304	SPO3531 SPO3532 SPO3533	1.29	0.4 SPO3534 0.004 SPO3535 0.039 SPO3536	1.1 1.01 1.11	0.673 0.554 0.671	SPO3526 SPO3527 SPO3528	6.83 4.65 0.68	0.002 0.006 0.069	SPO3526 SPO3527 SPO3528	6.66 4.95 0.67	0.001 0.003 0.010	SPO3526 SPO3527 SPO3528	1.10 1.21 1.05	0.132 0.010 0.458	SPO3522 SPO3523 SPO3524	1.04 1.09 1.12	0.770 0.412 0.193
SPO3534 SPO3535	1.38	0.082	SP03534 SP03535	1.18	0.126 0.176	SPO3534 SPO3535	1 1.06	0.949 SPO3537 0.434 SPO3538	1.12	0.762 0.523	SPO3529 SPO3530	0.16 0.88	0.002 0.840	SPO3529 SPO3530	0.17 0.79	0.010 0.000 0.618	SPO3529 SPO3530	0.94		SP03525 SP03526	1.20	0.034 0.052
SPO3536 SPO3537 SPO3538	1.02 1 1.35	0.916 0.967 0.387	SPO3536 SPO3537 SPO3538	0.97 1.01 1.31	0.995 0.897 0.361	SPO3536 SPO3537 SPO3538	1.02 1.06 1.1	0.862 SPO3539 0.746 SPO3540 0.564 SPO3541	1.34 1.3 1.5	0.408 0.44 0.526	SPO3531 SPO3532 SPO3533	0.60 6.07 0.34	0.021 0.004 0.006	SPO3531 SPO3532 SPO3533	0.62 4.93 0.36	0.021 0.003 0.010	SPO3531 SPO3532 SPO3533	1.02 1.30 0.88	0.045	SPO3527 SPO3528 SPO3529	1.30 1.07 0.88	0.176 0.057 0.390
SPO3539 SPO3540 SPO3541	1.31 2.3 1.1	0.126 0.113 0.597	SPO3539 SPO3540 SPO3541	1.27 2.09 1.15	0.084 0.046 0.419	SPO3539 SPO3540 SPO3541	1.02 1.1 1.06	0.454 SPO3542 0.098 SPO3543 0.638 SPO3544	0.99 1.06 1.09	0.978 0.576 0.857	SPO3534 SPO3535 SPO3536	0.82 0.98 1.33	0.152 0.843 0.353	SPO3534 SPO3535 SPO3536	0.88 1.07 1.30	0.222 0.164 0.186	SPO3534 SPO3535 SPO3536	1.05 0.99 0.98	0.824	SPO3530 SPO3531 SPO3532	1.00 0.99 1.28	0.983 0.957 0.108
SPO3542 SPO3543	1.04 1.57	0.874 0.444	SPO3542 SPO3543	1.02 1.55	0.787 0.426	SPO3542 SPO3543	1.17 1.23	0.89 SPO3545 0.548 SPO3546	1.06 1.08	0.891 0.792	SPO3537 SPO3538	0.87 0.58	0.867 0.260	SPO3537 SPO3538	0.88 0.56	0.940	SPO3537 SPO3538	0.95 0.98	0.949 0.980	SPO3533 SPO3534	0.87 1.01	0.636 0.972
SPO3544 SPO3545 SPO3546	0.92 1.05 1.01	0.977 0.903 0.899	SPO3544 SPO3545 SPO3546	0.84 1.05 1.02	0.804 0.917 0.713	SPO3544 SPO3545 SPO3546	1.08 1.09 1.01	0.733 SPO3547 0.852 SPO3548 0.985 SPO3549	1.05 1.18 1.26	0.043 0.782 0.528	SPO3539 SPO3540 SPO3541	1.20 0.71 1.13	0.085 0.043 0.399	SPO3539 SPO3540 SPO3541	1.24 0.75 1.04	0.070 0.098 0.596	SPO3539 SPO3540 SPO3541	0.95 1.33 0.96	0.438	SPO3535 SPO3536 SPO3537	1.03 1.06 0.96	0.711 0.731 0.955
SPO3547 SPO3548 SPO3549	0.5 1.22 0.97	0.025 0.819 0.932	SPO3547 SPO3548 SPO3549	0.56 1.07 1.03	0.018	SPO3547 SPO3548 SPO3549	1.03 1.12 1.08	0.094 SPO3550 0.748 SPO3551 0.377 SPO3552	1.09 1.05 1.03	0.543 0.974 0.693	SPO3542 SPO3543 SPO3544	0.97 0.66 1.10	0.864 0.332 0.964	SPO3542 SPO3543 SPO3544	1.03 0.88 0.96	0.747	SPO3542 SPO3543 SPO3544	0.81 0.53 0.99	0.480	SPO3538 SPO3539 SPO3540	0.94 1.02 1.08	0.906 0.927 0.789
SPO3550 SPO3551	1.09 1.12	0.834 0.8	SPO3550 SPO3551	1.01 1.21	0.9 0.43	SPO3550 SPO3551	1.07 1.1	0.668 SPO3553 0.977 SPO3554	1.03 1.05	0.285 0.297	SPO3545 SPO3546	0.98 0.71	0.991 0.179	SPO3545 SPO3546	1.02 0.70	0.980 0.258	SPO3545 SPO3546	0.78 1.03	0.749 0.868	SPO3541 SPO3542	0.91 0.85	0.410 0.354
SPO3552 SPO3553 SPO3554	1.22 1.36 1.35	0.316 0.195 0.283	SPO3552 SPO3553 SPO3554	1.21 1.19 1.15	0.097 0.382 0.566	SPO3552 SPO3553 SPO3554	1.2 1.37 1.06	0.646 SPO3555 0.743 SPO3556 0.511 SPO3557	1.08 1.01 1.13	0.107 0.567 0.991	SPO3548 SPO3549	8.61 0.55 1.07	0.001 0.665 0.767	SPO3548 SPO3549	8.45 0.57 1.17		SPO3548 SPO3549	1.26 0.85 1.08		SPO3544 SPO3545	0.65 1.02 0.87	0.628 0.912 0.838
SPO3555 SPO3556 SPO3557	0.94 1.54 1.08	0.797 0.205 0.56	SPO3555 SPO3556 SPO3557	0.89 1.46 0.97	0.248 0.369 0.925	SPO3555 SPO3556 SPO3557	1 1.12 1.09	0.055 SPO3558 0.191 SPO3559 0.566 SPO3560	1.19 1.01 0.99	0.037 0.108 0.778	SPO3550 SPO3551 SPO3552	0.68 1.08 1.07	0.434 0.818 0.803	SPO3550 SPO3551 SPO3552	0.80 1.05 1.13	0.550 0.841	SPO3550 SPO3551 SPO3552	0.99 1.07 1.20	0.914	SPO3546 SPO3547 SPO3548	0.99 1.25 0.87	0.987 0.038 0.893
SPO3558 SPO3559	0.74 0.78	0.333 0.187	SPO3558 SPO3559	0.74 0.79	0.221 0.14	SPO3558 SPO3559	1.06 1.06	0.168 SPO3561 0.143 SPO3562	1.26	0.832 0.55	SPO3553 SPO3554	0.86 0.72	0.450 0.403	SPO3553 SPO3554	1.11 0.72	0.214	SPO3553 SPO3554	1.03 0.93	0.878 0.828	SPO3549 SPO3550	1.09 0.87	0.579 0.774
SPO3560 SPO3561 SPO3562	0.93 1.05 1.16	0.977 0.886 0.19	SPO3560 SPO3561 SPO3562	1.25 1.15 1.03	0.545 0.806 0.653	SPO3560 SPO3561 SPO3562	1.02 1.17 0.99	0.672 SPO3563 0.817 SPO3564 0.949 SPO3565	1.07 1.07 1.05	0.67 0.416 0.713	SPO3555 SPO3556 SPO3557	0.90 0.59 1.11	0.568 0.313 0.761	SPO3555 SPO3556 SPO3557	0.90 0.59 1.13		SPO3555 SPO3556 SPO3557	0.92 0.89 1.05		SPO3551 SPO3552 SPO3553	1.03 1.15 1.02	0.922 0.443 0.924
SPO3563 SPO3564	0.9 0.81	0.849 0.274	SPO3563 SPO3564	1.02 0.77 1.34	0.598 0.477	SPO3563 SPO3564	1.14 1.17	0.683 SPO3566 0.915 SPO3567	1.16 1.02 1.05	0.16 0.763	SPO3558 SPO3559 SPO3560	1.66 2.24 0.96	0.155 0.075	SPO3558 SPO3559 SPO3560	1.91 1.84	0.057 0.023	SPO3558 SPO3559	1.36 1.05 0.58	0.168 0.918	SPO3554 SPO3555	0.98 0.93	0.930 0.115
SPO3565 SPO3566 SPO3567	1.52 0.9 1.01	0.02 0.62 0.727	SPO3565 SPO3566 SPO3567	1.08 0.94	0.899	SPO3565 SPO3566 SPO3567	1.15 1.15 1.12	0.093 SPO3569 0.971 SPO3570	1.09 1.18	0.244 0.412 0.72	SPO3561 SPO3562	0.75 1.16	0.678 0.696 0.585	SPO3561 SPO3562	1.00 0.71 1.12	0.782	SPO3560 SPO3561 SPO3562	0.88 0.98	0.811 0.825	SPO3556 SPO3557 SPO3558	0.82 0.92 1.24	0.649 0.678 0.315
SPO3568 SPO3569 SPO3570	0.93 1.57 1.32	0.766 0.052 0.347	SPO3568 SPO3569 SPO3570	0.94 1.39 1.32	0.622 0.183 0.114	SPO3568 SPO3569 SPO3570	1.04 1.01 1.05	0.158 SPO3571 0.18 SPO3572 0.729 SPO3573	1.04 1.01 1.11	0.509 0.731 0.437	SPO3563 SPO3564 SPO3565	1.01 0.88 0.80	0.973 0.930 0.847	SPO3563 SPO3564 SPO3565	1.10 0.93 0.66	0.705 0.348 0.569	SPO3563 SPO3564 SPO3565	0.98 0.93 0.85	0.834	SPO3559 SPO3560 SPO3561	1.24 0.83 0.86	0.060 0.648 0.829
SPO3571 SPO3572	1.5 0.93	0.052 0.98	SPO3571 SPO3572	1.43 0.93	0.02 0.992	SPO3571 SPO3572	1.05 1.37	0.646 SPO3574 0.972 SPO3575	1.13 1.02	0.386 0.57	SPO3566 SPO3567	2.19 0.81	0.004 0.749	SPO3566 SPO3567 SPO3568	2.10 0.75	0.017 0.566	SPO3566 SPO3567	0.92 0.94	0.595 0.796	SPO3562 SPO3563	1.00 0.99	0.928 0.892
SPO3573 SPO3574	0.74	0.065	SP03573 SP03574	0.77 0.92	0.163 0.698	SPO3573 SPO3574	1.44	0.783 SPO3576 0.258 SPO3577	1.16	0.627 0.989	SPO3569	0.85 0.88	0.720 0.939	SPO3569	0.88	0.950 0.774	SPO3568 SPO3569	1.02 0.89		SPO3564 SPO3565	1.02 0.88	0.898 0.518

SPO3575 SPO3576	1.21	0.554	SP03575 SP03576	1.13	0.728	SPO3575 SPO3576	1.22	0.855 SPO3578 0.725 SPO3579	1.11	0.741	SPO3570 SPO3571	1.86	0.047	SPO3570 SPO3571	1.97	0.005	SPO3570 SPO3571	1.12	0.575	SP03566 SP03567	0.97	0.967 0.961
SPO3577 SPO3578	0.97 0.91	0.901 0.404	SPO3577 SPO3578	0.95 0.99	0.945 0.887	SPO3577 SPO3578	1.13 1.11	0.321 SPO3580 0.235 SPO3581	1.22 1.17	0.03 0.278	SPO3572 SPO3573	0.85 1.37	0.781 0.110	SPO3572 SPO3573	0.78 1.38	0.510 0.020	SPO3572 SPO3573	0.93 1.15	0.819 0.332	SPO3568 SPO3569	1.05 0.86	0.702 0.463
SPO3579 SPO3580 SPO3581	0.94 1.09 1.08	0.944 0.023 0.944	SPO3579 SPO3580 SPO3581	1.03 0.81 1.04	0.674 0.081 0.387	SPO3579 SPO3580 SPO3581	1.11 1.27 1.12	0.617 SPO3582 0.555 SPO3583 0.76 SPO3584	1.14 1.12 1.04	0.447 0.319 0.557	SPO3574 SPO3575 SPO3576	1.55 0.91 1.38	0.005 0.879 0.087	SPO3574 SPO3575 SPO3576	1.70 0.83 1.31	0.060 0.720 0.079	SPO3574 SPO3575 SPO3576	1.11 0.76 1.15	0.754 0.090 0.438	SP03570 SP03571 SP03572	1.14 1.20 0.95	0.195 0.457 0.808
SPO3582 SPO3583 SPO3584	1.39 1.02 1.45	0.036 0.692 0.063	SPO3582 SPO3583 SPO3584	1.37 1.08	0.021 0.269 0.087	SPO3582 SPO3583 SPO3584	1.15 1.13 1.12	0.937 SPO3585 0.2 SPO3586 0.364 SPO3587	1.36 1.47 1.56	0.805 0.361 0.036	SPO3577 SPO3578 SPO3579	1.00 0.68	0.938 0.041 0.115	SPO3577 SPO3578 SPO3579	0.99 0.68	0.725 0.014 0.072	SPO3577 SPO3578 SPO3579	0.99 0.89 1.04	0.865 0.334 0.868	SPO3573 SPO3574 SPO3575	1.20 0.97 0.80	0.108 0.916 0.155
SPO3585 SPO3586	0.97 0.75	0.936	SPO3585 SPO3586	0.98 0.85	0.94	SPO3585 SPO3586	1.02	0.78 SPO3588 0.552 SPO3589	1.19	0.591	SPO3580 SPO3581 SPO3582	1.13 1.43	0.611	SPO3580 SPO3581 SPO3582	1.99	0.025	SPO3580 SPO3581	1.14	0.766	SPO3576 SPO3577 SPO3578	1.09	0.424
SPO3587 SPO3588 SPO3589	0.89 1.12 1	0.232 0.525 0.697	SPO3588 SPO3589	0.86 0.83 1.19	0.284 0.664 0.093	SPO3588 SPO3589	1.02 1.31 1.13	0.245 SPO3590 0.477 SPO3591 0.787 SPO3592	1.14 1.12 1.12	0.147 0.114 0.118	SPO3583 SPO3584	1.00 0.96 0.88	0.369 0.873 0.580	SPO3583 SPO3584	0.96 1.13 1.00	0.563	SPO3582 SPO3583 SPO3584	1.00 1.00 1.00	0.930 0.805	SPO3579 SPO3580	0.90 1.00 1.26	0.796 0.790 0.277
SPO3590 SPO3591 SPO3592	0.58 1.36 0.88	0.019 0.06 0.252	SPO3590 SPO3591 SPO3592	0.67 1.17 0.93	0.016 0.036 0.662	SPO3590 SPO3591 SPO3592	1.04 1.15 0.98	0.103 SPO3593 0.155 SPO3594 0.138 SPO3595	1.37 1.14 1.17	0.591 0.942 0.179	SPO3585 SPO3586 SPO3587	1.07 1.03 1.07	0.552 0.707 0.030	SPO3585 SPO3586 SPO3587	1.02 0.96 1.13	0.564 0.811 0.023	SPO3585 SPO3586 SPO3587	0.91 1.00 1.16	0.931	SPO3581 SPO3582 SPO3583	1.07 1.08 1.05	0.430 0.634 0.796
SPO3593 SPO3594	0.69 1.46	0.474 0.526	SPO3593 SPO3594	0.75 1.38	0.133 0.422	SPO3593 SPO3594	1.07 1.19	0.885 SPO3596 0.958 SPO3597	1.15 1.15	0.059 0.037	SPO3588 SPO3589	0.83 0.67	0.408	SPO3588 SPO3589	0.95 0.71	0.516	SPO3588 SPO3589	0.92 0.53	0.642 0.091	SPO3584 SPO3585	1.02 0.95	0.990 0.855
SPO3595 SPO3596 SPO3597	1.04 0.71 1.36	0.432 0.492 0.379	SPO3595 SPO3596 SPO3597	1.11 0.76 1.18	0.385 0.616 0.427	SPO3595 SPO3596 SPO3597	1.2 1.57 1.06	0.087 SPO3598 0.03 SPO3599 0.053 SPO3600	1.12 0.99 1.21	0.351 0.089 0.141	SPO3591 SPO3592	0.76 0.57 0.95	0.185 0.068 0.568	SPO3590 SPO3591 SPO3592	0.68 0.58 1.00	0.030 0.001 0.279	SPO3590 SPO3591 SPO3592	1.06 0.93 1.17	0.560	SPO3586 SPO3587 SPO3588	1.04 1.29 1.09	0.749 0.018 0.878
SPO3598 SPO3599 SPO3600	1.25 0.99	0.358 0.939 0.035	SPO3598 SPO3599 SPO3600	1.39 1.28	0.003 0.238 0.048	SPO3598 SPO3599 SPO3600	1.17 1.12 1.11	0.123 SPO3601 0.601 SPO3602 0.133 SPO3603	1.09 1.13 1.1	0.906 0.432 0.94	SPO3593 SPO3594 SPO3595	0.83 0.92 0.97	0.467 0.976 0.763	SPO3593 SPO3594 SPO3595	0.79 0.92 1.03	0.324 0.958 0.828	SPO3593 SPO3594 SPO3595	0.90 0.98 0.88	0.490 0.987 0.267	SPO3589 SPO3590 SPO3591	0.63 1.08 0.97	0.400 0.605 0.835
SPO3601 SPO3602	1.01 0.79	0.927 0.286 0.766	SPO3601 SPO3602	1.03 0.85 0.98	0.655 0.501 0.998	SPO3601 SPO3602	1.26 1.02	0.653 SPO3604 0.68 SPO3605	1.06 1.08	0.328 0.11 0.849	SPO3596 SPO3597	0.62 0.56 0.88	0.551 0.168 0.628	SPO3596 SPO3597	0.61 0.60 0.89		SPO3596 SPO3597	0.86 0.93 0.87	0.822 0.581 0.755	SPO3592 SPO3593	1.19 0.92	0.348 0.216
SPO3603 SPO3604 SPO3605	0.89 1.29 1.01	0.141 0.58	SPO3603 SPO3604 SPO3605	1.11 1.05	0.358 0.165	SPO3603 SPO3604 SPO3605	1.63 1.3 1.03	0.711 SPO3607 0.018 SPO3608	1.08 1.14 1.02	0.837 0.357	SPO3599 SPO3600	1.02 0.26	0.180 0.034	SPO3599 SPO3600	0.82 0.25	0.967 0.027	SPO3598 SPO3599 SPO3600	0.88 1.42	0.408 0.069	SPO3594 SPO3595 SPO3596	1.02 1.01 0.87	0.942 0.992 0.729
SPO3606 SPO3607 SPO3608	1.22 0.56 0.88	0.129 0.642 0.541	SPO3606 SPO3607 SPO3608	1.21 0.68 0.85	0.438 0.789 0.283	SPO3606 SPO3607 SPO3608	1.05 1.24 1.19	0.683 SPO3609 0.874 SPO3610 0.263 SPO3611	1.14 1.54 1.05	0.867 0.948 0.229	SPO3601 SPO3602 SPO3603	1.25 1.63 0.90	0.376 0.028 0.993	SPO3601 SPO3602 SPO3603	1.12 1.52 0.85	0.442 0.010 0.982	SPO3601 SPO3602 SPO3603	0.98 1.02 0.99	0.909 0.861 0.989	SPO3597 SPO3598 SPO3599	0.88 0.86 0.95	0.488 0.350 0.884
SPO3609 SPO3610	1.78	0.025 0.859	SPO3609 SPO3610	1.4	0.042	SPO3609 SPO3610	1 1.06	0.656 SPO3612 0.95 SPO3613	1.11	0.394 0.059	SPO3604 SPO3605	0.29 0.42	0.014 0.006 0.005	SPO3604 SPO3605	0.31 0.38	0.014	SPO3604 SPO3605	1.15 1.25	0.187	SP03600 SP03601 SP03602	1.47 0.90	0.138 0.483
SPO3611 SPO3612 SPO3613	0.77 1.36 1.19	0.402 0.216 0.44	SPO3611 SPO3612 SPO3613	0.82 1.33 0.99	0.104 0.051 0.433	SPO3611 SPO3612 SPO3613	1.01 1.06 1.21	0.351 SPO3614 0.195 SPO3615 0.768 SPO3616	1.19 1.25 1	0.244 0.04 0.514	SPO3606 SPO3607 SPO3608	0.19 0.25 2.06	0.005 0.523 0.032	SPO3606 SPO3607 SPO3608	0.19 0.24 2.05	0.006 0.495 0.013	SPO3606 SPO3607 SPO3608	0.99 1.75 1.06	0.658	SP03602 SP03603 SP03604	1.05 1.06 1.12	0.563 0.894 0.318
SPO3614 SPO3615 SPO3616	1.02 0.87 1.62	0.597 0.591	SPO3614 SPO3615 SPO3616	1.02 0.89 1.52	0.425 0.765 0.026	SPO3614 SPO3615 SPO3616	1.02	0.288 SPO3617 0.062 SPO3618 0.468 SPO3619	1.02 1.72 1.35	0.227 0.996 0.991	SPO3609 SPO3610 SPO3611	1.67 0.61 1.46	0.059 0.742 0.296	SPO3610 SPO3611	1.69 0.67 1.47	0.008 0.811 0.042	SPO3609 SPO3610 SPO3611	1.25 0.95 1.01		SPO3605 SPO3606 SPO3607	1.25 0.99 1.65	0.110 0.974 0.664
SPO3617 SPO3618	1.11 1.41	0.174	SPO3617 SPO3618	1.04 1.2	0.318	SPO3617 SPO3618	1.2	0.406 SPO3620 0.74 SPO3621	1.07 1.18	0.659 0.445	SPO3612 SPO3613	2.00 0.15	0.048 0.006	SPO3612 SPO3613	2.10 0.18	0.004	SPO3612 SPO3613	0.82 1.05	0.301 0.974	SPO3608 SPO3609	1.10 1.20	0.485 0.132
SPO3619 SPO3620 SPO3621	1.34 0.99 0.8	0.01 0.963 0.015	SPO3619 SPO3620 SPO3621	1.12 1 0.94	0.152 0.846 0.426	SPO3619 SPO3620 SPO3621	1.34 1.17 1.1	0.755 SPO3622 0.525 SPO3623 0.526 SPO3625	1.09 1.02 1.07	0.192 0.32 0.053	SPO3614 SPO3615 SPO3616	1.05 0.93 0.69	0.966 0.879 0.073	SPO3614 SPO3615 SPO3616	1.01 0.90 0.69	0.771 0.759 0.031	SPO3614 SPO3615 SPO3616	1.01 1.01 1.04		SP03610 SP03611 SP03612	0.88 0.92 0.85	0.932 0.805 0.276
SPO3622 SPO3623 SPO3625	1.34 1.7 1.12	0.018 0.039 0.083	SPO3622 SPO3623 SPO3625	1.25 1.64 0.98	0.044 0.08 0.916	SPO3622 SPO3623 SPO3625	1.01 1.12 1.14	0.065 SPO3626 0.859 SPO3627 0.017 SPO3628	1.01 1.26 1.03	0.913 0.914 0.891	SPO3617 SPO3618	2.12 1.35 1.07	0.003 0.369 0.154	SPO3618 SPO3618	2.23 1.45 1.00	0.000 0.332 0.171	SPO3617 SPO3618 SPO3619	0.93 1.04 1.00	0.470 0.876 0.774	SP03613 SP03614 SP03615	0.98 1.03 0.92	0.676 0.986 0.609
SPO3626 SPO3627	1.12 1.23	0.748 0.597	SPO3626 SPO3627	0.98 1.29	0.997 0.815	SPO3626 SPO3627	1.19 1.03	0.822 SPO3629 0.926 SPO3630	1.15 1.19	0.599 0.47	SPO3620 SPO3621	0.97 1.48	0.544 0.040	SPO3620 SPO3621	0.97 1.51	0.427	SPO3620 SPO3621	0.97 1.02	0.974 0.852	SP03616 SP03617	0.99 0.87	0.847 0.094
SPO3628 SPO3629 SPO3630	1.32 1.23 1.11	0.047 0.227 0.293	SPO3628 SPO3629 SPO3630	1.25 1.11 1.18	0.132 0.078 0.178	SPO3628 SPO3629 SPO3630	1.03 1.02 1.02	0.282 SPO3631 0.329 SPO3632 0.464 SPO3633	1.19 1.34 1.15	0.672 0.337 0.662	SPO3622 SPO3623 SPO3625	1.06 1.18 1.24	0.173 0.031 0.064	SPO3622 SPO3623 SPO3625	1.20 1.19 1.14	0.138 0.076 0.052	SPO3622 SPO3623 SPO3625	1.08 1.31 1.17	0.496 0.035 0.296	SPO3618 SPO3619 SPO3620	1.06 0.99 0.91	0.895 0.872 0.646
SPO3631 SPO3632 SPO3633	0.96 1.32 1.57	0.831 0.037 0.253	SPO3631 SPO3632 SPO3633	1.12 1.25 1.38	0.32 0.049 0.042	SPO3631 SPO3632 SPO3633	1.26 1.32 1.4	0.251 SPO3634 0.037 SPO3635 0.928 SPO3636	1.18 1.01 1.03	0.434 0.418 0.928	SPO3626 SPO3627 SPO3628	0.85 0.70 1.00	0.865 0.460 0.723	SPO3626 SPO3627 SPO3628	0.92 0.57 1.02	0.908 0.708 0.435	SPO3626 SPO3627 SPO3628	1.01 0.97 1.32	0.913 0.948 0.093	SPO3621 SPO3622 SPO3623	0.96 1.05 1.15	0.835 0.735 0.077
SPO3634 SPO3635	1.53 1.27	0.235 0.067	SPO3634 SPO3635	1.41 1.3	0.141 0.063	SPO3634 SPO3635	1.07	0.727 SPO3637 0.525 SPO3638	1.2 1.18	0.973 0.292	SPO3629 SPO3630	1.15 0.93	0.052 0.837	SPO3629 SPO3630	1.22 0.89	0.025 0.632	SPO3629 SPO3630	1.14 0.99	0.375 0.979	SPO3625 SPO3626	1.07 1.05	0.625 0.852
SPO3636 SPO3637 SPO3638	0.86 0.98 1.29	0.614 0.995 0.351	SPO3636 SPO3637 SPO3638	0.85 1.04 1.28	0.49 0.47 0.399	SPO3636 SPO3637 SPO3638	1.24 1.49 1.11	0.926 SPO3639 0.959 SPO3640 0.35 SPO3641	1.09 1.14 1.11	0.086 0.553 0.818	SPO3631 SPO3632 SPO3633	1.17 0.86 1.05	0.062 0.442 0.876	SPO3631 SPO3632 SPO3633	1.01 0.96 1.00	0.507 0.141 0.982	SPO3631 SPO3632 SPO3633	0.81 0.93 1.20		SPO3627 SPO3628 SPO3629	0.99 1.22 1.21	0.996 0.300 0.287
SPO3639 SPO3640 SPO3641	1.51 1.45 1.14	0.119 0.431 0.343	SPO3639 SPO3640 SPO3641	1.33 1.39 1.1	0.04 0.388 0.606	SPO3639 SPO3640 SPO3641	1.46 1.49 1.25	0.103 SPO3642 0.053 SPO3643 0.447 SPO3644	1.05 1.3 1.28	0.938 0.308 0.395	SPO3634 SPO3635 SPO3636	0.66 1.11 1.08	0.467 0.111 0.656	SPO3634 SPO3635 SPO3636	0.67 1.06 1.15	0.335 0.187 0.328	SPO3634 SPO3635 SPO3636	0.89 1.02 0.92	0.813	SPO3630 SPO3631 SPO3632	1.02 0.76 0.88	0.875 0.286 0.284
SPO3642 SPO3643	0.84 1.49	0.457 0.385	SPO3642 SPO3643	0.92 1.32	0.733 0.094	SPO3642 SPO3643	1.27 1.1	0.76 SPO3645 0.915 SPO3646	1.5 0.98	0.447 0.372	SPO3637 SPO3638	1.07 1.04	0.624 0.721	SPO3637 SPO3638	1.11 0.99	0.251 0.825	SPO3637 SPO3638	1.17 1.04	0.238 0.821	SPO3633 SPO3634	1.02 0.93	0.885 0.848
SPO3644 SPO3645 SPO3646	0.97 1.1 0.88	0.769 0.409 0.377	SPO3644 SPO3645 SPO3646	1.1 1.11 0.96	0.379 0.105 0.837	SPO3644 SPO3645 SPO3646	1.11 1.14 1.07	0.106 SPO3647 0.212 SPO3648 0.529 SPO3649	0.98 1.13 1.59	0.878 0.757 0.798	SPO3639 SPO3640 SPO3641	1.05 1.09 0.65	0.112 0.592 0.201	SPO3639 SPO3640 SPO3641	1.10 1.16 0.69	0.073 0.572 0.168	SPO3639 SPO3640 SPO3641	1.02 1.14 0.91	0.814 0.550 0.630	SPO3635 SPO3636 SPO3637	0.95 0.86 1.07	0.768 0.466 0.705
SPO3647 SPO3648 SPO3649	0.68 1.22 1.32	0.257 0.377 0.07	SPO3648 SPO3649	0.78 1.28 1.2	0.137 0.204 0.131	SPO3647 SPO3648 SPO3649	1.07 1.33 1.35	0.305 SPO3650 0.805 SPO3651 0.727 SPO3652	1.1 1.4 1.54	0.504 0.177 0.863	SPO3642 SPO3643 SPO3644	0.86 0.85 1.05	0.667 0.620 0.980	SPO3642 SPO3643 SPO3644	0.93 0.81 0.87	0.983 0.232 0.217	SPO3642 SPO3643 SPO3644	0.96 1.08 0.89	0.883 0.769 0.483	SPO3638 SPO3639 SPO3640	0.98 0.97 1.09	0.948 0.888 0.883
SPO3650 SPO3651	0.81 0.77	0.543 0.246	SPO3650 SPO3651	0.91 0.8	0.61 0.729	SPO3650 SPO3651	1.15 1.15	0.373 SPO3653 0.838 SPO3654	1.19 1.25	0.467 0.794	SPO3645 SPO3646	1.02 0.61	0.512 0.022	SPO3645 SPO3646	1.23 0.60	0.173 0.053	SPO3645 SPO3646	0.92 0.90	0.512 0.550	SPO3641 SPO3642	0.93 0.94	0.711 0.875
SPO3652 SPO3653 SPO3654	1.16 1.52 1.19	0.322 0.073 0.247	SPO3652 SPO3653 SPO3654	1.07 1.22 1.28	0.268 0.172 0.117	SPO3652 SPO3653 SPO3654	1.29 1.04 1.53	0.282 SPO3655 0.769 SPO3656 0.878 SPO3657	1.05 1.18 1.05	0.571 0.135 0.44	SPO3648 SPO3649	0.97 0.85 1.15	0.885 0.672 0.276	SPO3648 SPO3649	0.82 0.85 1.17	0.191 0.704 0.195	SPO3647 SPO3648 SPO3649	1.05 1.08 1.15	0.870 0.709 0.595	SP03644 SP03645	0.99 0.81 0.96	0.940 0.276 0.842
SPO3655 SPO3656 SPO3657	1.23 1.17 1.12	0.456 0.164 0.451	SPO3655 SPO3656 SPO3657	1.16 1.18 1.03	0.799 0.066 0.785	SPO3655 SPO3656 SPO3657	1.21 1.11 1.08	0.783 SPO3658 0.316 SPO3659 0.554 SPO3660	1.15 1.03	0.611 0.741 0.084	SPO3650 SPO3651 SPO3652	0.71 0.50	0.243 0.001 0.141	SPO3650 SPO3651 SPO3652	0.65 0.52 0.64	0.007 0.005 0.215	SPO3650 SPO3651 SPO3652	0.78 1.02 1.06	0.297 0.975 0.675	SPO3646 SPO3647 SPO3648	0.91 1.02 1.09	0.587 0.942 0.750
SPO3658 SPO3659 SPO3660	0.92 1.41 1.02	0.62 0.016 0.523	SPO3658 SPO3659 SPO3660	0.89 1.17 1.02	0.7 0.098 0.246	SPO3658 SPO3659 SPO3660	1.04 1.06	0.829 SPO3661 0.817 SPO3662 0.745 SPO3663	1.25 1.33 1.15	0.966 0.382 0.997	SPO3653 SPO3654	0.68 0.81 0.87	0.185 0.888 0.777	SPO3653 SPO3654	0.71 0.84 0.86	0.188 0.820 0.817	SPO3653 SPO3654 SPO3655	1.02 1.01 0.93	0.901	SPO3649 SPO3650 SPO3651	1.09 0.84 0.97	0.582 0.088 0.806
SPO3661 SPO3662	1.22	0.166 0.139	SPO3661 SPO3662	1.22	0.019	SPO3661 SPO3662	1.23	0.462 SPO3664 0.412 SPO3665	1.13	0.966 0.942	SPO3656 SPO3657	0.94	0.949	SPO3656 SPO3657	0.89	0.237	SPO3656 SPO3657	0.98 0.96	0.932	SP03652 SP03653	1.03	0.875 0.848
SPO3663 SPO3664 SPO3665	1.31 1.13 0.85	0.555 0.079 0.093	SPO3663 SPO3664 SPO3665	1.24 1.24 0.95	0.734 0.096 0.819	SPO3663 SPO3664 SPO3665	1.07 1.07 1.09	0.977 SPO3666 0.923 SPO3667 0.995 SPO3668	1.07 1.53 1.12	0.578 0.085 0.612	SPO3658 SPO3659 SPO3660	1.63 1.02 1.43	0.062 0.503 0.069	SPO3658 SPO3659 SPO3660	1.80 1.00 1.50	0.015 0.929 0.016	SPO3658 SPO3659 SPO3660	0.84 1.18 1.13	0.360	SPO3654 SPO3655 SPO3656	1.00 0.88 1.01	0.952 0.656 0.908
SPO3666 SPO3667 SPO3668	1.54 0.82 1.17	0.011 0.427 0.628	SP03666 SP03667 SP03668	1.53 0.95 1.15	0.015 0.852 0.493	SPO3666 SPO3667 SPO3668	1.14 1.19 1.11	0.843 SPO3670 0.375 SPO3671 0.555 SPO3672	1.13 1.16 1.07	0.75 0.018 0.85	SPO3662	1.03 1.34 0.93	0.931 0.274 0.967	SPO3661 SPO3662 SPO3663	1.09 1.23 0.91	0.403	SPO3661 SPO3662 SPO3663	1.01 1.12 1.09	0.662	SPO3657 SPO3658 SPO3659	0.89 0.73 1.17	0.358 0.080 0.135
SPO3670 SPO3671	0.38	0.679	SPO3670 SPO3671	1.08 0.44	0.548	SPO3670 SPO3671	1.02 1.05	0.67 SPO3673 0.012 SPO3675	1.12 1.19	0.01 0.47	SPO3664 SPO3665	1.45 1.69	0.093 0.057	SPO3664 SPO3665	1.34 1.65	0.004 0.016	SPO3664 SPO3665	1.12 1.01	0.329 0.759	SPO3660 SPO3661	1.23 1.09	0.366 0.494
SP03672 SP03673 SP03675	0.72 0.92 1.02	0.555 0.082 0.71	SP03672 SP03673 SP03675	0.67 0.95 1.06	0.465 0.64 0.645	SPO3672 SPO3673 SPO3675	1.03 1.01 1.15	0.827 SPO3676 0.018 SPO3677 0.585 SPO3678	1.27 1.08	0.472 0.232 0.839	SPO3666 SPO3668	0.95 0.84 1.04	0.594 0.096 0.979	SPO3666 SPO3668	1.13 0.88 0.95	0.040	SPO3666 SPO3667 SPO3668	1.18 0.97 0.94	0.768	SP03662 SP03663 SP03664	1.20 1.13 1.09	0.042 0.776 0.175
SPO3676 SPO3677 SPO3678	1.3 0.82 0.96	0.281 0.345 0.995	SPO3676 SPO3677 SPO3678	1.04 0.83 0.98	0.24 0.12 0.948	SPO3676 SPO3677 SPO3678	1.23 1.08 1.04	0.112 SPO3679 0.43 SPO3680 0.83 SPO3681	1.07 1.15	0.641 0.425 0.686	SPO3670 SPO3671 SPO3672	0.73 1.31 1.03	0.208 0.070 0.733	SPO3670 SPO3671 SPO3672	0.86 1.26 0.93	0.032	SPO3670 SPO3671 SPO3672	1.58 1.12 1.07	0.280 0.067 0.865	SPO3665 SPO3666 SPO3667	1.05 1.14 0.86	0.612 0.467 0.292
SPO3679 SPO3680	0.7 0.96	0.144	SPO3679 SPO3680	0.79 0.93	0.281 0.885	SPO3679 SPO3680	1.21 1.36	0.905 SPO3682 0.474 SPO3684	1.07 1.19	0.853 0.054	SPO3673 SPO3675	1.70 0.48	0.009	SPO3673 SPO3675	1.70 0.45	0.024	SPO3673 SPO3675	1.06 1.04	0.213 0.911	SPO3668 SPO3670	0.97 1.21	0.937 0.716
SPO3681 SPO3682 SPO3684	0.62 0.83 1.06	0.169 0.35 0.635	SPO3681 SPO3682 SPO3684	0.69 0.81 1.15	0.132 0.344 0.136	SPO3681 SPO3682 SPO3684	1.17 1.15 1.27	0.817 SPO3685 0.763 SPO3686 0.397 SPO3687	1.17 1.02 1.17	0.088 0.181 0.632	SPO3676 SPO3677 SPO3678	1.07 2.22 0.93	0.996 0.031 0.921	SPO3676 SPO3677 SPO3678	1.19 1.67 1.02	0.047 0.951	SPO3676 SPO3677 SPO3678	1.24 1.18 1.00	0.000	SP03671 SP03672 SP03673	1.16 1.06 1.14	0.329 0.873 0.068
SPO3685 SPO3686 SPO3687	1.06 0.76 0.8	0.744 0.017 0.121	SPO3685 SPO3686 SPO3687	1.06 0.76 0.78	0.7 0.399 0.082	SPO3685 SPO3686 SPO3687	1.29 1.32 1.08	0.321 SPO3688 0.419 SPO3689 0.698 SPO3690	1.18 1.05 1.06	0.922 0.986 0.158	SPO3679 SPO3680 SPO3681	1.16 0.65 0.86	0.449 0.174 0.605	SPO3679 SPO3680 SPO3681	1.06 0.68 0.83	0.477 0.090 0.328	SPO3679 SPO3680 SPO3681	0.95 0.83 0.88	0.309 0.189 0.360	SPO3675 SPO3676 SPO3677	1.09 1.06 1.12	0.542 0.732 0.485
SPO3688 SPO3689 SPO3690	0.93 0.88	0.959 0.332	SPO3688 SPO3689	0.92 0.97	0.953 0.978	SPO3688 SPO3689	1.16	0.818 SPO3691 0.958 SPO3692	1.28 1.55 1.03	0.361 0.32	SPO3682 SPO3684	1.49 0.56	0.063 0.014	SPO3682 SPO3684	1.42 0.57	0.150 0.016	SPO3682 SPO3684	1.04 0.96	0.973	SPO3678 SPO3679	0.93 0.97	0.877 0.836 0.534
SP03690 SP03691 SP03692	0.56 0.92 0.76	0.04 0.677 0.175	SPO3690 SPO3691 SPO3692	0.63 0.87 0.82	0.018 0.265 0.179	SPO3690 SPO3691 SPO3692	1.13 1.08 1.09	0.562 SPO3693 0.86 SPO3694 0.119 SPO3695	1.03 1.04 1.01	0.089 0.229 0.963	SPO3685 SPO3686 SPO3687	1.10 1.05 1.03	0.502 0.141 0.736	SPO3685 SPO3686 SPO3687	1.10 1.07 1.16	0.150	SPO3685 SPO3686 SPO3687	1.60 0.98 1.07	0.960	SPO3680 SPO3681 SPO3682	0.87 0.89 1.08	0.534 0.508 0.834
SPO3693 SPO3694 SPO3695	0.6 1.01 1.06	0.014 0.771 0.892	SPO3693 SPO3694 SPO3695	0.67 0.97 1.04	0.024 0.993 0.866	SPO3693 SPO3694 SPO3695	1.17 1.13 1.15	0.002 SPO3696 0.236 SPO3697 0.917 SPO3698	1.17 1.4 1.25	0.65 0.127 0.247	SPO3688 SPO3689 SPO3690	1.13 1.19 1.62	0.768 0.218 0.011	SPO3688 SPO3689 SPO3690	1.16 1.06 1.60	0.758 0.097 0.002	SPO3688 SPO3689 SPO3690	1.01 1.10 0.97	0.635	SPO3684 SPO3685 SPO3686	0.92 1.63 1.06	0.226 0.105 0.598
SPO3696 SPO3697	0.6 0.72	0.207 0.153	SPO3696 SPO3697	0.72 0.78	0.322	SPO3696 SPO3697	1.09 1.04	0.206 SPO3699 0.171 SPO3700	1.24 1.16	0.025 0.015	SPO3691 SPO3692	1.22	0.043 0.037	SPO3691 SPO3692	1.19	0.081 0.029	SPO3691 SPO3692	1.06 1.03	0.115 0.790	SPO3687 SPO3688	1.08 0.94	0.523 0.902
SPO3698 SPO3699 SPO3700	0.85 0.65 0.57	0.245 0.046 0.066	SPO3698 SPO3699 SPO3700	0.86 0.67 0.65	0.335 0.013 0.043	SPO3698 SPO3699 SPO3700	1.09 1 1.08	0.273 SPO3701 0.126 SPO3702 0.032 SPO3703	1.13 1.01 1.12	0.317 0.686 0.939	SPO3693 SPO3694 SPO3695	2.33 1.83 1.10	0.004 0.013 0.751	SPO3693 SPO3694 SPO3695	1.79 1.05	0.026 0.779	SPO3693 SPO3694 SPO3695	0.96 0.93 0.86	0.575 0.814	SPO3689 SPO3690 SPO3691	1.00 0.97 1.04	0.953 0.837 0.447
SP03701 SP03702 SP03703	0.69 0.76 0.81	0.388 0.502 0.865	SP03701 SP03702 SP03703	0.69 0.89 0.97	0.374 0.745 0.981	SPO3701 SPO3702 SPO3703	1.52 0.98 1.1	0.138 SPO3704 0.47 SPO3705 0.898 SPO3706	1 1.08 1.18	0.296 0.054 0.948	SPO3696 SPO3697 SPO3698	1.74 2.39 1.61	0.137 0.014 0.170	SPO3696 SPO3697 SPO3698	1.64 2.27 1.66	0.157 0.005 0.152	SPO3696 SPO3697 SPO3698	0.95 0.96 0.97	0.808 0.800 0.908	SPO3692 SPO3693	1.04 0.91 0.93	0.783 0.714 0.547
SPO3704 SPO3705	1.1 0.56	0.552 0.018	SP03704 SP03705	1.1 0.62	0.44 0.091	SPO3704 SPO3705	1.33 1.07	0.286 SPO3707 0.497 SPO3708	1.05 1.14	0.798 0.755	SPO3699 SPO3700	2.53 4.33	0.020 0.009	SPO3699 SPO3700	2.26 4.09	0.004	SPO3699 SPO3700	1.10 0.91	0.463 0.529	SPO3695 SPO3696	0.88 0.96	0.772 0.887
SPO3706 SPO3707 SPO3708	1.04 0.67 1.07	0.474 0.561 0.658	SP03706 SP03707 SP03708	1.07 0.68 1.03	0.756 0.523 0.769	SPO3706 SPO3707 SPO3708	1.24 1.22 1.07	0.437 SPO3709 0.99 SPO3710 0.765 SPO3711	1.12 1.09 1.1	0.997 0.594 0.252	SPO3701 SPO3702 SPO3703	3.19 0.48 0.58	0.056 0.075 0.293	SPO3701 SPO3702 SPO3703	3.33 0.43 0.56	0.072 0.077 0.288	SPO3701 SPO3702 SPO3703	1.05 0.88 0.96	0.841 0.958	SPO3697 SPO3698 SPO3699	0.96 0.96 1.04	0.836 0.890 0.788
SPO3709 SPO3710 SPO3711	1.04 0.84 1.14	0.765 0.561 0.313	SP03709 SP03710 SP03711	0.97 1.01 1.17	0.991 0.5 0.023	SPO3709 SPO3710 SPO3711	1.01 1.21 1.31	0.981 SPO3712 0.436 SPO3713 0.647 SPO3714	1.57 0.98 1.16	0.413 0.184 0.819	SPO3704 SPO3705 SPO3706	0.80 1.13 1.73	0.395 0.458 0.068	SPO3704 SPO3705 SPO3706	0.83 1.05 1.71	0.103 0.369 0.023	SPO3704 SPO3705 SPO3706	0.91 0.92 0.97	0.687	SP03700 SP03701 SP03702	1.01 1.11 0.91	0.906 0.783 0.812
SP03712 SP03713	1.49 0.88	0.073 0.069	SP03712 SP03713	1.43 0.79	0.04 0.036	SP03712 SP03713	1.11 1.02	0.217 SPO3715 0.729 SPO3716	1.28 1.03	0.84 0.736	SPO3707 SPO3708	1.41 0.98	0.476 0.901	SPO3707 SPO3708	1.42 0.79	0.183 0.389	SPO3707 SPO3708	1.31 0.92	0.683 0.773	SP03703 SP03704	0.93 0.99	0.778 0.909
SP03714 SP03715 SP03716	1.64 1.22 0.87	0.003 0.194 0.851	SP03714 SP03715 SP03716	1.82 1.25 1.32		SPO3714 SPO3715 SPO3716	1.07 1.11 1.3	0.854 SPO3717 0.866 SPO3718 0.817 SPO3719	1.24 1.13 1.11	0.864 0.079 0.961	SPO3709 SPO3710 SPO3711	0.92 0.91 0.90	0.969 0.550 0.192	SPO3709 SPO3710 SPO3711	0.83 0.87 0.87	0.378	SPO3709 SPO3710 SPO3711	0.87 0.93 0.95	0.281	SP03705 SP03706 SP03707	0.93 0.94 1.23	0.449 0.719 0.729
SP03717	0.92	0.738		0.88		SPO3717	1.08	0.979 SPO3720	1.25	0.175	SPO3712	0.94	0.681	SPO3712	0.93		SPO3712	1.06		SP03708	0.92	0.789

SPO3718 SPO3719	1.18	0.293	SPO3718 SPO3719	1.19	0.057	SP03718 SP03719	1.1	0.249 SPO3721 0.948 SPO3722	1.34	0.202	SPO3713 SPO3714	1.58	0.005	SPO3713 SPO3714	1.57	0.005	SPO3713 SPO3714	1.06	0.127	SP03709 SP03710	0.88	0.934 0.952
SPO3720 SPO3721	1.38 1.43	0.055 S 0.111 S	SP03720 SP03721	1.48 1.49	0.015 0.147	SP03720 SP03721	1.09 1.09	0.173 SPO3723 0.565 SPO3724	0.99 1.04	0.416	SPO3715 SPO3716	0.88 1.06	0.988 0.906	SPO3715 SPO3716	0.83 1.08	0.883 0.991	SPO3715 SPO3716	1.08 1.21	0.737 0.293	SP03711 SP03712	0.96 1.01	0.771 0.782
SP03722 SP03723 SP03724	0.85 1.06 0.94	0.522 S 0.336 S 0.846 S	SPO3722 SPO3723 SPO3724	0.9 0.9 1.06	0.681 0.686 0.552	SP03722 SP03723 SP03724	1.1 1 1.22	0.766 SPO3725 0.342 SPO3726 0.751 SPO3727	1.1 1.11 1.32	0.768 0.997 0.064	SPO3717 SPO3718 SPO3719	0.88 0.57 0.96	0.586 0.087 0.517	SPO3717 SPO3718 SPO3719	0.87 0.53 0.94	0.599 0.004 0.264	SPO3717 SPO3718 SPO3719	0.97 0.74 1.00	0.846 0.015 0.747	SP03713 SP03714 SP03715	1.08 1.46 1.07	0.421 0.071 0.737
SP03725 SP03726 SP03727	0.98 1.07 0.86	0.969 S 0.714 S 0.333 S	SPO3725 SPO3726 SPO3727	0.98 1.09 0.94	0.952 0.71 0.813	SP03725 SP03726 SP03727	1.09 1.05 1.06	0.732 SPO3728 0.783 SPO3729 0.346 SPO3730	1.19 1.08 1.08	0.685 0.041 0.063	SPO3720 SPO3721 SPO3722	0.58 0.15 0.19	0.018 0.002 0.001	SPO3720 SPO3721 SPO3722	0.54 0.14	0.009 0.001 0.007	SPO3720 SPO3721 SPO3722	1.00 0.93 0.99	0.733 0.679 0.850	SP03716 SP03717 SP03718	1.07 1.04 0.74	0.779 0.817 0.113
SPO3728 SPO3729	0.99 1.05	0.951 S 0.704 S	SPO3728 SPO3729	0.97 0.96	0.838 0.918	SPO3728 SPO3729	1.25 1.05	0.811 SPO3731 0.252 SPO3732	1.17 1.12	0.728 0.757	SPO3723 SPO3724	0.44 0.45	0.026 0.007	SPO3723 SPO3724	0.41	0.021 0.016	SPO3723 SPO3724	0.97 1.00	0.660 0.826	SP03719 SP03720	1.04 1.01	0.790 0.783
SP03730 SP03731 SP03732	1.61 1.02 1.02	0.102 S 0.601 S 0.651 S	SPO3730 SPO3731 SPO3732	1.5 1.05 1.04	0.075 0.279 0.226	SPO3730 SPO3731 SPO3732	1.5 1.39 1.14	0.481 SP03733 0.278 SP03734 0.334 SP03736	1.01 1.24 1.06	0.4 0.019 0.941	SPO3725 SPO3726 SPO3727	1.04 0.94 1.65	0.566 0.694 0.050	SPO3725 SPO3726 SPO3727	1.07 0.95 1.55	0.460 0.460 0.013	SPO3725 SPO3726 SPO3727	0.88 1.06 1.05	0.734	SP03721 SP03722 SP03723	1.03 0.96 1.02	0.937 0.672 0.994
SPO3733 SPO3734 SPO3735	1.1 0.99 1.16	0.309 S 0.926 S 0.399 S	SPO3733 SPO3734 SPO3735	1.09 1.06 0.99	0.221	SP03733 SP03734 SP03735	1.14 1.18 1.02	0.038 SP03737 0.432 SP03738 0.058 SP03739	1.05 1.06 1.22	0.546 0.203 0.888	SPO3728 SPO3729 SPO3730	1.39 1.43 0.54	0.020 0.046 0.037	SPO3728 SPO3729 SPO3730	1.44 1.53 0.61	0.011 0.022 0.375	SPO3728 SPO3729 SPO3730	0.88 1.00 1.16	0.882	SP03724 SP03725 SP03726	1.15 0.91 1.09	0.734 0.707 0.626
SP03736 SP03737	0.99 1.26	0.93 0.224	SP03736 SP03737	1.05 1.25	0.665 0.037	SP03736 SP03737	1.22 1.34	0.936 SPO3740 0.2 SPO3741	1.05 1.33	0.28 0.235	SPO3731 SPO3732	2.05 1.05	0.046 0.328	SPO3731 SPO3732	1.95 1.04	0.012 0.349	SPO3731 SPO3732	0.95 0.99	0.160 0.902	SP03727 SP03728	1.16 0.92	0.063 0.560
SPO3738 SPO3739 SPO3740	1.32 0.79 0.79	0.069 S 0.263 S 0.127 S	SPO3738 SPO3739 SPO3740	1.35 0.85 0.75		SPO3738 SPO3739 SPO3740	1.31 1.15 1.13	0.514 SPO3742 0.663 SPO3743 0.307 SPO3744	1.39 1.23 1.13	0.771 0.47 0.81	SPO3733 SPO3734 SPO3735	0.73 1.11 0.88	0.070 0.718	SPO3733 SPO3734 SPO3735	0.73 1.08 0.73	0.166 0.654 0.086	SPO3733 SPO3734 SPO3735	1.15 0.96 1.20	0.912	SPO3729 SPO3730 SPO3731	1.04 1.09 0.98	0.527 0.249 0.932
SPO3741 SPO3742	0.59 0.74	0.092 S 0.13 S 0.219 S	SPO3741 SPO3742 SPO3743	0.6 0.81 1.18	0.033 0.274 0.119	SP03741 SP03742 SP03743	1.42 1.3 1.27	0.282 SPO3745 0.914 SPO3746 0.578 SPO3747	1.05 1.13 1.37	0.379 0.121 0.692	SPO3736 SPO3737 SPO3738	0.76 0.85 1.46	0.397	SPO3736 SPO3737 SPO3738	0.74 0.88 1.71	0.227 0.577 0.001	SPO3736 SPO3737 SPO3738	1.02 1.08 1.11	0.868 0.790 0.662	SP03732 SP03733 SP03734	1.07 1.11 0.94	0.463 0.434 0.670
SPO3743 SPO3744 SPO3745	1.21 0.94 0.97	0.853	SPO3744 SPO3745	0.96 1.01	0.95 0.723	SPO3744 SPO3745	1.23 1.15	0.721 SPO3748 0.123 SPO3749	1.34 1.22	0.791 0.786	SPO3739 SPO3740	0.72 0.46	0.128 0.395 0.005	SPO3739 SPO3740	0.66 0.44	0.499	SPO3739 SPO3740	0.97 0.97	0.952 0.984	SP03735 SP03736	0.85 1.02	0.483 0.816
SP03746 SP03747 SP03748	0.84 0.9 0.75	0.065 S 0.194 S 0.082 S	SPO3746 SPO3747 SPO3748	0.88 0.85 0.71	0.317 0.139 0.029	SPO3746 SPO3747 SPO3748	1.13 1.04 1.06	0.005 SPO3750 0.103 SPO3751 0.64 SPO3752	1.02 1.42 1.18	0.205 0.238 0.554	SPO3741 SPO3742 SPO3743	0.55 0.71 0.89	0.132 0.110 0.706	SPO3741 SPO3742 SPO3743	0.57 0.76 0.88	0.036 0.025 0.548	SPO3741 SPO3742 SPO3743	0.98 0.91 1.05	0.992 0.397 0.491	SP03737 SP03738 SP03739	1.05 1.15 0.97	0.337 0.029 0.943
SPO3749 SPO3750 SPO3751	0.75 0.56	0.426 S 0.082 S	SPO3749 SPO3750 SPO3751	0.68 0.68	0.641 0.149 0.025	SPO3749 SPO3750 SPO3751	1.09 1.05 1.07	0.671 SPO3753 0.568 SPO3754 0.558 SPO3755	1.33 1.22 1.03	0.358 0.301 0.179	SPO3744 SPO3745 SPO3746	0.77 2.67	0.845 0.003 0.015	SPO3744 SPO3745 SPO3746	0.82 1.73	0.998 0.020 0.023	SPO3744 SPO3745 SPO3746	0.86 1.09	0.829 0.453 0.872	SP03740 SP03741 SP03742	1.03 1.06 0.87	0.138 0.796 0.171
SP03752 SP03753	1.46	0.272 5	SP03752 SP03753	1.53	0.025 0.06 0.045	SP03752 SP03753	1.28 1.11	0.574 SPO3756 0.583 SPO3757	1.2 1.04	0.29 0.622	SPO3747 SPO3748	0.88	0.380 0.744	SPO3746 SPO3747 SPO3748	0.96 0.75	0.906	SPO3746 SPO3747 SPO3748	0.96	0.276 0.504	SP03743 SP03744	1.01 0.96	0.856 0.991
SPO3754 SPO3755 SPO3756	0.71 0.86	0.004 S 0.168 S 0.383 S	SPO3754 SPO3755 SPO3756	0.66 0.91 1.32	0.444	SPO3754 SPO3755 SPO3756	1.12 1.03 1.12	0.837 SPO3758 0.05 SPO3759 0.396 SPO3760	1.11 1.05 1.1	0.333 0.985 0.357	SPO3749 SPO3750 SPO3751	0.99 1.43 0.59	0.938 0.162 0.017	SPO3749 SPO3750 SPO3751	0.96 1.44 0.60	0.977 0.068 0.106	SPO3749 SPO3750 SPO3751	0.99 1.20 1.08	0.398	SPO3745 SPO3746 SPO3747	0.97 1.02 0.99	0.917 0.716 0.982
SP03757 SP03758	0.9	0.253	SP03757 SP03758	0.89 0.85	0.444	SP03757 SP03758	16.3 7.12	0.639 SPO3761 0.229 SPO3762	1.1	0.934	SP03752 SP03753	0.66 0.55	0.027	SPO3752 SPO3753	0.75 0.55	0.112	SPO3752 SPO3753	1.06	0.546	SP03748 SP03749 SP03750	0.78 1.00	0.206
SPO3759 SPO3760 SPO3761	1.61 0.97 1.14	0.128 S 0.98 S 0.335 S	SPO3759 SPO3760 SPO3761	1.55 1 1.08	0.378	SPO3759 SPO3760 SPO3761	9.92 1.33	0.271 SPO3763 0.308 SPO3764 0.872 SPO3765	1.25 1.1 1.13	0.968 0.807 0.556	SP03755 SP03756	0.90 1.29 1.03	0.366 0.121 0.701	SPO3755 SPO3756	1.00 1.28 1.08	0.038	SPO3754 SPO3755 SPO3756	1.09 1.08 1.07		SP03751 SP03752	1.24 1.21 1.06	0.244 0.559 0.811
SPO3762 SPO3763 SPO3764	1.65 1.51 1.25	0.087 S 0.031 S 0.135 S	SPO3762 SPO3763 SPO3764	1.53 1.56	0.028 0.033 0.083	SPO3762 SPO3763 SPO3764	1.34 1.02 1.01	0.708 SPO3766 0.904 SPO3767 0.541 SPO3768	1.07 1.18 14.7	0.652 0.024 0.021	SPO3757 SPO3758 SPO3759	0.91 1.29 1.00	0.763 0.074 0.549	SPO3757 SPO3758 SPO3759	0.93 1.22 0.98	0.136 0.027 0.484	SPO3757 SPO3758 SPO3759	0.91 0.95 1.11	0.953	SPO3753 SPO3754 SPO3755	1.07 1.04 1.07	0.674 0.556 0.533
SPO3765 SPO3766	0.75 1.21 0.65		SPO3765 SPO3766	0.75 1.21 0.65	0.311	SP03765 SP03766	1.03 1.28 1.17	0.381 SPO3769 0.614 SPO3770 0.01 SPO3771	6.08 16.4	0.733 0.514 0.865	SPO3760 SPO3761	1.48	0.322	SPO3760 SPO3761 SPO3762	1.42	0.302 0.014 0.024	SPO3760 SPO3761	1.18 1.05	0.543 0.498 0.160	SP03756 SP03757	1.07 0.91 0.99	0.336 0.351
SPO3767 SPO3768 SPO3769	2.29 1.27	0.615	SPO3767 SPO3768 SPO3769	1.97 1.28	0.017 0.002 0.694	SPO3767 SPO3768 SPO3769	1.21 1.1	0.019 SP03772 0.685 SP03774	1.25 1.34	0.252 0.394	SPO3763 SPO3764	1.27	0.016 0.047 0.351	SPO3763 SPO3764	1.32 1.10	0.106 0.208	SPO3762 SPO3763 SPO3764	1.27 0.96 0.93	0.804 0.709	SPO3758 SPO3759 SPO3760	1.07 1.20	0.863 0.456 0.519
SP03770 SP03771 SP03772	1.61 0.88 1.73	0.729	SPO3770 SPO3771 SPO3772	1.56 1.11 1.65	0.067 0.868 0.043	SP03770 SP03771 SP03772	1.11 1.07 1.17	0.549 SP03775 0.958 SP03776 0.404 SP03777	1.01 1 1.1	0.725 0.663 0.943	SPO3765 SPO3766 SPO3767	0.84 0.96 4.19	0.789 0.902 0.006	SPO3765 SPO3766 SPO3767	0.75 0.94 4.19	0.392 0.776 0.005	SPO3765 SPO3766 SPO3767	0.81 1.04 1.23	0.538 0.942 0.045	SP03761 SP03762 SP03763	1.07 1.26 0.88	0.360 0.097 0.386
SP03774 SP03775 SP03776	0.88 0.96 1.15	0.61	SP03774 SP03775 SP03776	0.88 0.93 1.03	0.505 0.899 0.846	SP03774 SP03775 SP03776	1.35 1.14 1.21	0.429 SPO3778 0.324 SPO3779 0.46 SPO3780	1.08 1.08 1.04	0.44 0.361 0.173	SPO3768 SPO3769 SPO3770	0.21 0.59	0.001	SPO3768 SPO3769	0.21 0.55	0.002 0.521 0.026	SPO3768 SPO3769 SPO3770	1.12 1.16 1.05	0.201 0.801 0.823	SP03764 SP03765 SP03766	0.94 0.85 1.03	0.428 0.354 0.872
SP03777 SP03778	0.89 0.85	0.79	SP03777 SP03778	0.97 0.98	0.886	SP03777 SP03778	1.18 1.19	0.854 SPO3781 0.374 SPO3782	1.35 1.17	0.298 0.823	SPO3771 SPO3772	1.16	0.505 0.403	SPO3771 SPO3772	1.22	0.352 0.267	SPO3771 SPO3772	1.02 1.04	0.881 0.687	SP03767 SP03768	1.26 1.05	0.122 0.676
SPO3779 SPO3780 SPO3781	1.68 1.56 0.63	0.099 S 0.09 S 0.616 S	SPO3779 SPO3780 SPO3781	1.57 1.44 0.67	0.32 0.076 0.626	SPO3779 SPO3780 SPO3781	1.08 1.08 1.24	0.87 SPO3783 0.123 SPO3784 0.416 SPO3785	1.14 1.21 1.04	0.449 0.949 0.029	SPO3774 SPO3775 SPO3776	1.93 1.11 0.83	0.064 0.546 0.673	SPO3774 SPO3775 SPO3776	1.96 1.13 0.79	0.037 0.451 0.592	SPO3774 SPO3775 SPO3776	0.55 0.78 0.73		SP03769 SP03770 SP03771	1.15 1.08 1.08	0.830 0.718 0.724
SPO3782 SPO3783 SPO3784	1.08 1.11 1.29	0.755 S 0.499 S 0.662 S	SPO3782 SPO3783 SPO3784	0.93 1.18 1.19	0.972	SPO3782 SPO3783 SPO3784	1.5 1.05 1.23	0.952 SPO3786 0.459 SPO3787 0.939 SPO3788	1.02 1.12 1.31	0.608 0.146 0.787	SPO3777 SPO3778 SPO3779	1.22 0.91 0.89	0.401 0.824 0.660	SPO3777 SPO3778 SPO3779	1.19 0.81 0.85	0.426 0.419 0.446	SPO3777 SPO3778 SPO3779	0.77 0.70 0.97	0.348 0.245	SP03772 SP03774 SP03775	1.08 0.55 0.83	0.394 0.045 0.074
SPO3785 SPO3786	1.14 1.09	0.255	SPO3785 SPO3786	1.11 1.01	0.138 0.776	SP03785 SP03786	1.21 1.2	0.101 SPO3789 0.928 SPO3790	1.14 1.3	0.48 0.929	SPO3780 SPO3781	0.64 4.86	0.163 0.216	SPO3780 SPO3781	0.61 4.46	0.121 0.191	SPO3780 SPO3781	0.93 1.05	0.830 0.955	SP03776 SP03777	0.77 0.85	0.503 0.306
SPO3787 SPO3788 SPO3789	1.69 1.18 1.21		SPO3787 SPO3788 SPO3789	1.63 1.12 1.18	0.169 0.548 0.576	SPO3787 SPO3788 SPO3789	1.11 1.05 0.99	0.164 SPO3791 0.219 SPO3792 0.83 SPO3794	1.18 1.22 1.15	0.275 0.824 0.686	SPO3782 SPO3783 SPO3784	1.28 1.17 1.05	0.615 0.831 0.990	SPO3782 SPO3783 SPO3784	1.26 1.46 1.26	0.594 0.162 0.824	SPO3782 SPO3783 SPO3784	1.14 1.13 1.10	0.759 0.698 0.911	SPO3778 SPO3779 SPO3780	0.79 0.96 0.92	0.310 0.747 0.754
SPO3790 SPO3791 SPO3792	1.26 1.04 1.02	0.714	SPO3790 SPO3791 SPO3792	1.18 1.02 1.08	0.712 0.467 0.308	SPO3790 SPO3791 SPO3792	1.19 1.03 1.02	0.819 SPO3795 0.294 SPO3802 0.988 SPO3803	1.15 1.21 1.62	0.726 0.705 0.419	SPO3785 SPO3786 SPO3787	1.00 1.08 0.67	0.580 0.816 0.222	SPO3785 SPO3786 SPO3787	0.91 1.01 0.73	0.146 0.823 0.051	SPO3785 SPO3786 SPO3787	0.94 1.08 0.97	0.752 0.771 0.731	SP03781 SP03782 SP03783	1.07 1.11 1.00	0.860 0.817 0.936
SPO3794 SPO3795	0.76 0.79	0.734 5	SPO3794 SPO3795	0.77 0.81	0.817 0.82	SP03793 SP03794	1.41 0.99	0 SPO3804 0.803 SPO3805	1.05 1.23	0.865 0.045	SPO3788 SPO3789	1.06 0.94	0.906 0.684	SPO3788 SPO3789	1.11	0.475 0.473	SPO3788 SPO3789	0.92 1.01	0.753 0.898	SP03784 SP03785	0.95 0.94	0.908 0.581
SPO3802 SPO3803 SPO3804	0.92 1.46 0.9	0.928 S 0.493 S 0.866 S	SPO3802 SPO3803 SPO3804	0.92 1.22 0.91	0.932 0.443 0.894	SPO3795 SPO3802 SPO3803	1.12 1.1 1.26	0.809 SPO3806 0.746 SPO3807 0.575 SPO3808	1.32 1.26 1.11	0.24 0.444 0.987	SPO3790 SPO3791 SPO3792	0.87 1.27 1.39	0.828 0.122 0.600	SPO3790 SPO3791 SPO3792	1.00 1.33 1.17	0.907 0.248 0.734	SPO3790 SPO3791 SPO3792	0.87 1.06 1.16	0.819 0.914 0.416	SP03786 SP03787 SP03788	1.09 1.12 0.96	0.807 0.632 0.843
SPO3805 SPO3806 SPO3807	0.73 1.22 1.01	0.081 S 0.428 S	SPO3805 SPO3806 SPO3807	0.85 1.2 0.89	0.122 0.335 0.668	SPO3804 SPO3805 SPO3806	1.04 1.11 1.01	0.847 SPO3809 0.057 SPO3810 0.384 SPO3811	1.07 1.07 1.09	0.921 0.368 0.621	SPO3793 SPO3794 SPO3795	1.07 0.82 1.72	0.851	SPO3793 SPO3794 SPO3795	0.93 0.65 1.82	0.710	SPO3794 SPO3795 SPO3802	0.65 0.88 1.04	0.623 0.825 0.969	SPO3789 SPO3790 SPO3791	1.07 0.93 1.10	0.569 0.904 0.569
SPO3808 SPO3809	0.92	0.881	SPO3808 SPO3809	0.95	0.979	SPO3807 SPO3808	1.22	0.253 SPO3812 0.942 SPO3813	1.12	0.63	SPO3802 SPO3803	0.71	0.400	SPO3802 SPO3803	0.81 0.64	0.565	SPO3803 SPO3804	0.76	0.515	SPO3792 SPO3793	1.22 1.00	0.421
SP03810 SP03811 SP03812	0.67 0.89 1.23	0.044 S 0.681 S 0.516 S	SPO3810 SPO3811 SPO3812	0.78 0.98 1.14	0.893	SPO3809 SPO3810 SPO3811	1.11 1.07 1.14	0.856 SPO3814 0.719 SPO3815 0.453 SPO3816	1.35 1.03 1.17	0.116 0.422 0.257	SPO3804 SPO3805 SPO3806	0.91 1.83 1.38	0.973 0.051 0.015	SPO3804 SPO3805 SPO3806	0.85 1.67 1.52	0.904 0.015 0.007	SPO3805 SPO3806 SPO3807	1.01 1.04 0.95	0.718	SPO3794 SPO3795 SPO3802	0.72 0.96 0.95	0.705 0.950 0.905
SPO3813 SPO3814 SPO3815	1.27 1.05 1.21	0.021 S 0.563 S 0.559 S	SPO3813 SPO3814 SPO3815	1.15 1.11 1.17		SPO3812 SPO3813 SPO3814	1.19 1.17 1.03	0.692 SPO3817 0.253 SPO3818 0.49 SPO3819	1.02 1.08 1.24	0.286 0.018 0.521	SPO3807 SPO3808 SPO3809	0.89 0.76 0.85	0.823 0.754 0.917	SPO3807 SPO3808 SPO3809	0.85 0.68 0.81		SPO3808 SPO3809 SPO3810	0.87 0.83 0.95	0.846	SPO3803 SPO3804 SPO3805	0.78 1.02 1.16	0.475 0.960 0.186
SPO3816 SPO3817	1.1 1.07	0.116	SPO3816 SPO3817	1.13 1.13	0.089 0.123	SPO3815 SPO3816	1.13 1.02	0.383 SPO3820 0.296 SPO3821	1.07 1	0.909 0.895	SPO3810 SPO3811	2.32 1.68	0.025 0.026	SPO3810 SPO3811	2.08 1.54	0.019 0.070	SPO3811 SPO3812	0.92 0.97	0.746 0.991	SPO3806 SPO3807	1.07 0.88	0.426 0.732
SPO3818 SPO3819 SPO3820	1.17 1.38 0.99	0.153	SPO3818 SPO3819 SPO3820	1.12 1.36 1.02	0.086 0.205 0.923	SPO3817 SPO3818 SPO3819	1.18 1.13	0.899 SPO3822 0.251 SPO3823 0.244 SPO3824	1.15 1.37 1.73	0.584 0.176 0.218	SPO3812 SPO3813 SPO3814	0.83 0.89 1.31	0.842 0.572 0.022	SPO3812 SPO3813 SPO3814	0.79 0.94 1.23		SPO3813 SPO3814 SPO3815	0.93 0.92 1.11		SPO3808 SPO3809 SPO3810	0.95 0.89 1.08	0.919 0.915 0.555
SPO3821 SPO3822 SPO3823	0.74 0.84		SPO3821 SPO3822 SPO3823	0.78 0.83 2.03	0.573 0.089 0.012	SPO3820 SPO3821 SPO3822	1.11 1.09 1.16	0.901 SPO3825 0.783 SPO3826 0.163 SPO3827	1.08 1.1 1.17	0.937 0.476 0.843	SPO3815 SPO3816 SPO3817	0.63 0.62	0.333 0.013 0.190	SPO3815 SPO3816 SPO3817	0.65 0.61 0.97	0.346 0.023 0.187	SPO3816 SPO3817 SPO3818	0.98 0.98 1.29		SP03811 SP03812 SP03813	0.95 0.86 0.95	0.877 0.738 0.788
SPO3824 SPO3825	1.74 1.16 1.16		SPO3824 SPO3825	1.6 1.37 1.27		SPO3823 SPO3824 SPO3825	1.15 1.05 1.06	0.105 SPO3828 0.158 SPO3829 0.828 SPO3830	1.15 1.16 1.18	0.393 0.793 0.884	SPO3818 SPO3819 SPO3820	1.73 1.29 0.64	0.070 0.190 0.420	SPO3818 SPO3819 SPO3820	1.88 1.35 0.65	0.003 0.117 0.390	SPO3819 SPO3820	0.96 0.94 1.11	0.785 0.918 0.726	SPO3814 SPO3815 SPO3816	0.90 1.04 1.08	0.069 0.864 0.662
SPO3826 SPO3827 SPO3828	1.34 0.98	0.505	SPO3826 SPO3827 SPO3828	1.4 1.01	0.746 0.621	SPO3826 SPO3827	1.02 1.17	0.749 SPO3831 0.914 SPO3832	1.16 1.06	0.374 0.677	SPO3821 SPO3822	0.87 0.80	0.868 0.407	SPO3821 SPO3822	0.85 0.85	0.839 0.486	SPO3821 SPO3822 SPO3823	1.05 1.50	0.607 0.030	SP03817 SP03818	1.04 1.34	0.237 0.051
SPO3829 SPO3830 SPO3831	0.84 0.86 0.83	0.331 S 0.326 S 0.466 S	SPO3829 SPO3830 SPO3831	0.94 0.91 0.86	0.871 0.131 0.201	SPO3828 SPO3829 SPO3830	1.06 1.02 1.27	0.974 SPO3833 0.943 SPO3834 0.991 SPO3835	1.11 1.29 1.18	0.302 0.039 0.567	SPO3823 SPO3824 SPO3825	1.30 1.31 1.71	0.059 0.002 0.044	SPO3823 SPO3824 SPO3825	1.42 1.27 1.50	0.035 0.001 0.039	SPO3824 SPO3825 SPO3826	1.11 1.08 1.01		SPO3819 SPO3820 SPO3821	1.07 1.01 1.12	0.520 0.982 0.794
SPO3832 SPO3833 SPO3834	1.07 1.18	0.439 5	SPO3832 SPO3833 SPO3834	1.13 1.29 1.69	0.116 0.052 0.021	SPO3831 SPO3832 SPO3833	0.99 1.01 1.14	0.386 SPO3836 0.712 SPO3837 0.756 SPO3838	1.1 1.12 1.1	0.228 0.239 0.48	SPO3826 SPO3827 SPO3828	1.67 0.80 1.10	0.003 0.871 0.587	SPO3826 SPO3827 SPO3828	1.72 0.75 1.10	0.004 0.830 0.425	SPO3827 SPO3828 SPO3829	0.88 1.14 1.03	0.907 0.585 0.832	SPO3822 SPO3823 SPO3824	1.11 1.49 0.98	0.060 0.109 0.260
SPO3835 SPO3836	1.38 1.36	0.032 5	SPO3835 SPO3836	1.33 1.39	0.015	SP03834 SP03835	1.15 1.07	0.305 SPO3839 0.148 SPO3840	1.2 1.15	0.043 0.809	SPO3829 SPO3830	1.01 0.79	0.311 0.327	SPO3829 SPO3830	0.96 0.79	0.260	SPO3830 SPO3831	0.93 0.97	0.861 0.874	SPO3825 SPO3826	1.17 1.09	0.050 0.101
SPO3837 SPO3838 SPO3839	1.55 1.26 1.06	0.17 S 0.225 S 0.357 S	SPO3837 SPO3838 SPO3839	1.6 1.35	0.036	SPO3836 SPO3837 SPO3838	1.05 1.04 1.18	0.258 SPO3841 0.552 SPO3842 0.69 SPO3843	1.06 1.07 1.19	0.045 0.077 0.38	SPO3831 SPO3832 SPO3833	1.07 0.99 1.35	0.375 0.774 0.258	SPO3831 SPO3832 SPO3833	1.39 0.93 1.46	0.537	SPO3832 SPO3833 SPO3834	1.13 1.11 0.85	0.673	SPO3827 SPO3828 SPO3829	0.88 1.15 1.06	0.883 0.512 0.721
SPO3840 SPO3841 SPO3842	2.07 1.11 1.36		SPO3840 SPO3841 SPO3842	1.88 1.15 1.19		SPO3839 SPO3840 SPO3841	1.07 1.41 1.27	0.151 SPO3844 0.714 SPO3845 0.075 SPO3846	1.01 0.99 1.14	0.922 0.123 0.22	SPO3834 SPO3835 SPO3836	0.72 0.77 0.91	0.158 0.046 0.710	SPO3834 SPO3835 SPO3836	0.75 0.77 0.88	0.060 0.140 0.494	SPO3835 SPO3836 SPO3837	1.08 1.01 1.12	0.851	SPO3830 SPO3831 SPO3832	0.91 1.06 1.02	0.787 0.446 0.897
SPO3843 SPO3844	1.59 1.32	0.099	SPO3843 SPO3844	1.43 1.26	0.043	SPO3842 SPO3843	1.4 1.16	0.308 SPO3847 0.075 SPO3848	0.97 1.2	0.524 0.607	SPO3837 SPO3838	1.15 1.27	0.062 0.025	SPO3837 SPO3838	0.88 1.17 1.29	0.150 0.035	SPO3838 SPO3839	1.07 0.73	0.532 0.179	SP03833 SP03834	1.15 0.88	0.357 0.161
SPO3845 SPO3846 SPO3847	1.95 1.25 1.34	0.121 S 0.139 S 0.432 S	SPO3845 SPO3846 SPO3847	1.71 1.19 1.05	0.087 0.082 0.038	SPO3844 SPO3845 SPO3846	1.18 1.04 1.22	0.998 SPO3849 0.218 SPO3850 0.047 SPO3851	1.07 1.1 1.06	0.84 0.993 0.724	SPO3839 SPO3840 SPO3841	0.53 0.79 0.73	0.067 0.798 0.035	SPO3839 SPO3840 SPO3841	0.49 0.82 0.72	0.028 0.950 0.031	SPO3840 SPO3841 SPO3842	0.85 0.88 0.07	0.434 0.264 0.001	SPO3835 SPO3836 SPO3837	1.10 0.98 1.04	0.298 0.857 0.861
SPO3848 SPO3849	0.68 0.94	0.246	SPO3848 SPO3849	0.71 1.04	0.191 0.695 0.883	SPO3847 SPO3848	1.07 1.04	0.921 SPO3852 0.552 SPO3853	1.09 1.09	0.375 0.744	SPO3842 SPO3843	1.55 0.74	0.088 0.365	SPO3842 SPO3843	1.65 0.65	0.052 0.079 0.617	SPO3843 SPO3844	0.53 1.01		SPO3838 SPO3839	1.10 0.88	0.353 0.312
SPO3850 SPO3851 SPO3852	0.91 0.99 1.14	0.962 0.058	SPO3850 SPO3851 SPO3852	0.91 0.93 1.13	0.467	SPO3849 SPO3850 SPO3851	1.15 1.1 0.98	0.932 SPO3855 0.606 SPO3856	1.16 1.51	0.419 0.823 0.825	SPO3845 SPO3846	0.80 0.50 0.45	0.638 0.102 0.017	SPO3845 SPO3846	0.79 0.48 0.47	0.054	SPO3845 SPO3846 SPO3847	1.00 0.90 0.99	0.216 0.996	SPO3840 SPO3841 SPO3842	0.83 0.84 0.08	0.447 0.068 0.002
SPO3853 SPO3854 SPO3855	0.93 1.63 0.84	0.821 S 0.017 S 0.847 S	SPO3853 SPO3854 SPO3855	0.92 1.48 0.88	0.809 0.408 0.223	SPO3852 SPO3853 SPO3854	1.06 1.07 1.42	0.974 SPO3857 0.726 SPO3858 0.341 SPO3859	1.21 1.32 1.17	0.115 0.215 0.237	SPO3847 SPO3848 SPO3849	1.09 0.88 0.90	0.147 0.582 0.078	SPO3847 SPO3848 SPO3849	1.16 0.87 0.85	0.013 0.416 0.126	SPO3848 SPO3849 SPO3850	0.95 1.00 1.00	0.800 0.916 0.957	SPO3843 SPO3844 SPO3845	0.51 0.92 0.99	0.118 0.756 0.948
SPO3856 SPO3857	0.93 1.7	0.2 S 0.145 S	SPO3856 SPO3857	1.01 1.42	0.945 0.063	SPO3855 SPO3856	1.38 1.15	0.263 SPO3860 0.374 SPO3861	1.2 1.07	0.065 0.594	SPO3850 SPO3851	0.67 0.89	0.614 0.903	SPO3850 SPO3851	0.60 0.91	0.521 0.312	SPO3851 SPO3852	0.91	0.510	SPO3846 SPO3847	0.84 0.96	0.160 0.530
SPO3858 SPO3859 SPO3860	1.1 1.2 0.7	0.45 S 0.199 S 0.391 S	SPO3858 SPO3859 SPO3860	1 1.02 0.78	0.772 0.554	SPO3857 SPO3858 SPO3859	1.09 1.15 1.15	0.239 SPO3862 0.247 SPO3863 0.109 SPO3864	1.28 1.03 1.04	0.915 0.927 0.27	SPO3852 SPO3853 SPO3854	0.81 1.35 0.90	0.467 0.146 0.512	SPO3852 SPO3853 SPO3854	0.79 1.44 0.91		SPO3853 SPO3854 SPO3855	1.11 1.05 0.89	0.940 0.783	SPO3848 SPO3849 SPO3850	0.97 1.02 0.88	0.858 0.996 0.854
SPO3861 SPO3862 SPO3863	1.49 0.74 1.42	0.277 S 0.847 S 0.318 S	SPO3861 SPO3862 SPO3863	1.43 0.63 1.31		SPO3860 SPO3861 SPO3862	1.08 1.23 1.19	0.282 SPO3865 0.506 SPO3866 0.873 SPO3867	1.14 1.08 1.06	0.155 0.339 0.37	SPO3855 SPO3856 SPO3857	1.41 0.89 0.70	0.052 0.963 0.309	SPO3855 SPO3856 SPO3857	1.47 0.88 0.67	0.008 0.945 0.044	SPO3856 SPO3857 SPO3858	0.81 1.00 0.83	0.970	SPO3851 SPO3852 SPO3853	0.85 0.95 1.13	0.209 0.882 0.675
SPO3864	1.06		SPO3864	1.06		SPO3863	1.08	0.752 SPO3868	1.09	0.198		1.06	0.106	SPO3858	1.06		SPO3859	0.95		SPO3854	0.93	0.842

SPO3865	0.88		O3865	0.93	0.087	SP03864 SP03865	1.12	0.001 SPO3869 0.135 SPO3870	1.01	0.903	SPO3859 SPO3860	1.53	0.086	SPO3859 SPO3860	1.36	0.071	SPO3860	0.89	0.688	SPO3855 SPO3856	0.88	0.375
SPO3866 SPO3867 SPO3868	1.2 1.07 0.67	0.725 SP	PO3866 PO3867 PO3868	1.11 0.72		SPO3866 SPO3867	1.04 1.08 1.47	0.39 SPO3871 0.291 SPO3872	1.03 1.38 1.43	0.856 0.945 0.787	SPO3861 SPO3862	0.79 0.72 0.91	0.483 0.395 0.998	SPO3861 SPO3862	0.75 0.68 0.85	0.058 0.330 0.978	SPO3861 SPO3862 SPO3863	0.93 0.79 1.03	0.878	SP03856 SP03857 SP03858	0.85 0.90 0.85	0.528 0.676 0.117
SPO3869 SPO3870 SPO3871	0.83 1.24 1.02	0.107 SP	PO3869 PO3870 PO3871	0.89 1.14 1.1	0.784 0.213 0.59	SPO3868 SPO3869 SPO3870	1.01 1.16 1.08	0.292 SPO3873 0.965 SPO3874 0.569 SPO3875	1.15 1.14 1.26	0.692 0.083 0.037	SPO3863 SPO3864 SPO3865	0.90 0.92 0.98	0.749 0.939 0.223	SPO3863 SPO3864 SPO3865	0.98 0.91 1.04	0.976 0.986 0.467	SPO3864 SPO3865 SPO3866	0.99 1.01 1.07	0.971 0.772 0.705	SPO3859 SPO3860 SPO3861	0.74 0.93 0.93	0.286 0.589 0.874
SPO3872 SPO3873	1.02 0.79	0.924 SP 0.052 SP	O3872 O3873	1.02 0.94	0.4	SPO3871 SPO3872	1.26 1.06	0.474 SPO3876 0.515 SPO3877	1.2	0.127 0.912	SPO3866 SPO3867	0.79 0.79	0.403 0.432	SPO3866 SPO3867	0.86 0.85	0.454	SPO3867 SPO3868	1.02 0.87	0.971 0.278	SPO3862 SPO3863	0.85 0.97	0.896 0.971
SPO3874 SPO3875 SPO3876	1.62 1.02 0.91	0.574 SP	PO3874 PO3875 PO3876	1.37 1.03 0.95	0.147 0.219 0.974	SPO3873 SPO3874 SPO3875	1.12 1.13 1.35	0.789 SPO3878 0.067 SPO3879 0.058 SPO3880	1.3 1.29 1.09	0.073 0.529 0.54	SPO3868 SPO3869 SPO3870	1.09 0.93	0.034 0.582 0.385	SPO3868 SPO3869 SPO3870	1.14 0.99	0.034 0.219 0.976	SPO3869 SPO3870 SPO3871	0.98 1.20 1.10	0.982 0.011 0.475	SPO3864 SPO3865 SPO3866	0.93 1.01 1.13	0.364 0.341 0.534
SP03877 SP03878	1.02 1.41	0.037 SP	PO3877 PO3878	1.04		SP03876 SP03877	1.14	0.035 SPO3881 0.975 SPO3882	1.09	0.839	SPO3871 SPO3872	1.16 1.18	0.291	SPO3871 SPO3872	1.23	0.267	SPO3872 SPO3873	0.93	0.331	SPO3867 SPO3868	0.93	0.543 0.506
SPO3879 SPO3880 SPO3881	0.79 1.36 0.92	0.493 SP	PO3879 PO3880 PO3881	0.93 1.34 0.87	0.486 0.348 0.573	SPO3878 SPO3879 SPO3880	1.42 1.22 1.24	0.193 SPO3883 0.594 SPO3884 0.532 SPO3885	1.13 1.44 1.09	0.318 0.394 0.975	SPO3873 SPO3874 SPO3875	0.99 0.49 1.03	0.929 0.013 0.571	SPO3873 SPO3874 SPO3875	0.88 0.49 1.16	0.570 0.067 0.098	SPO3874 SPO3875 SPO3876	0.85 0.91 0.95		SP03869 SP03870 SP03871	1.02 1.11 1.07	0.900 0.441 0.792
SPO3882 SPO3883 SPO3884	0.78 1.65 1.31	0.221 SP	O3882 PO3883 PO3884	0.87 1.68 1.27	0.177	SPO3881 SPO3882 SPO3883	1.05 1.16 1.21	0.358 SPO3886 0.004 SPO3887 0.494 SPO3888	1.08 1.1 1.27	0.076 0.012 0.124	SPO3876 SPO3877 SPO3878	1.20 1.39 1.14	0.370 0.314 0.431	SPO3876 SPO3877 SPO3878	1.22 1.16 1.14	0.293 0.089 0.549	SPO3877 SPO3878 SPO3879	1.13 1.00 0.78	0.938	SPO3872 SPO3873 SPO3874	0.88 0.97 0.74	0.263 0.754 0.327
SPO3885 SPO3886	1.28 1.13	0.559 SP 0.724 SP	O3885 O3886	1.15 1.15	0.514 0.568	SPO3884 SPO3885	1.22 1.29	0.335 SPO3889 0.993 SPO3890	1.07 1.15	0.34 0.978	SPO3879 SPO3880	0.57 0.68	0.003 0.350	SPO3879 SPO3880	0.60 0.70	0.198	SPO3880 SPO3881	1.10 0.99	0.713 0.920	SPO3875 SPO3876	0.92 0.97	0.065 0.726
SPO3887 SPO3888 SPO3889	1.29 0.71 1.14	0.006 SP	PO3887 PO3888 PO3889	1.1 0.88 1.15	0.084 0.113 0.429	SPO3886 SPO3887 SPO3888	1.09 1.12 1.08	0.437 SPO3891 0.01 SPO3892 0.293 SPO3893	1.01 1.47 1.13	0.564 0.159 0.082	SPO3881 SPO3882 SPO3883	0.64 4.49 0.73	0.121 0.004 0.373	SPO3881 SPO3882 SPO3883	0.73 3.93 0.69	0.042 0.001 0.239	SPO3882 SPO3883 SPO3884	0.76 1.11 1.11		SP03877 SP03878 SP03879	1.15 1.03 0.85	0.163 0.969 0.688
SPO3890 SPO3891	1.07 1.37	0.668 SP 0.137 SP	PO3890 PO3891	1.07	0.077	SPO3889 SPO3890	1.03 1.01 1.38	0.444 SPO3894 0.552 SPO3895	1.06 1.35	0.272 0.793 0.536	SPO3884 SPO3885 SPO3886	0.87 1.26 0.67	0.514 0.589	SPO3884 SPO3885 SPO3886	0.88 1.45 0.63	0.624 0.530 0.044	SPO3885 SPO3886	1.03 1.02 1.01	0.936 0.904 0.837	SPO3880 SPO3881	1.05 0.99 0.88	0.859 0.725
SPO3892 SPO3893 SPO3894	1.17 0.93 1.44	0.754 SP 0.042 SP	PO3892 PO3893 PO3894	1.23 0.79 1.29	0.042 0.096 0.084	SPO3891 SPO3892 SPO3893	1.08 1.05	0.594 SPO3896 0.182 SPO3897 0.206 SPO3898	1.1 1.22 1.01	0.68 0.167	SPO3887 SPO3888	1.05	0.451 0.012 0.011	SPO3887 SPO3888	0.48 1.03	0.005 0.005	SPO3887 SPO3888 SPO3889	1.00 0.99	0.122 0.814	SP03882 SP03883 SP03884	1.06 1.08	0.208 0.719 0.298
SPO3895 SPO3896 SPO3897	1.27 0.92 0.76	0.55 SP	O3895 O3896 O3897	1.28 0.88 0.78	0.132 0.513 0.554	SPO3894 SPO3895 SPO3896	1.03 1.04 1.03	0.415 SPO3899 0.908 SPO3900 0.79 SPO3901	1.14 1.2 1.22	0.419 0.27 0.969	SPO3889 SPO3890 SPO3891	0.79 1.27 0.74	0.081 0.176 0.034	SPO3889 SPO3890 SPO3891	0.74 1.36 0.71	0.087 0.102 0.077	SPO3890 SPO3891 SPO3892	1.07 1.16 0.84	0.821 0.198 0.346	SPO3885 SPO3886 SPO3887	1.04 1.00 1.03	0.914 0.827 0.320
SPO3898 SPO3899	0.9 0.68	0.896 SP 0.286 SP	PO3898 PO3899	1.08 0.83	0.324 0.715	SPO3897 SPO3898	1.3	0.559 SPO3902 0.062 SPO3903	1.33 1.12	0.224 0.676	SPO3892 SPO3893	0.79 1.36	0.290	SPO3892 SPO3893	0.76 1.42	0.294 0.024	SPO3893 SPO3894	1.03 0.86	0.929 0.260	SPO3888 SPO3889	1.01 0.87	0.205 0.433
SPO3900 SPO3901 SPO3902	0.98 1.11 0.69	0.925 SP	PO3900 PO3901 PO3902	0.93 1.16 0.78	0.915 0.897 0.139	SPO3899 SPO3900 SPO3901	1.11 1.07 1.16	0.257 SPOA0001 0.183 SPOA0002 0.994 SPOA0003	1.12 1.17 1.3	0.459 0.105 0.212	SPO3894 SPO3895 SPO3896	1.87 1.15 1.06	0.017 0.219 0.200	SPO3894 SPO3895 SPO3896	1.80 1.19 1.11	0.003 0.300 0.349	SPO3895 SPO3896 SPO3897	0.92 0.92 1.31	0.569	SPO3890 SPO3891 SPO3892	1.06 1.07 0.88	0.819 0.356 0.461
SPO3903 SPOA0001 SPOA0002	1.79 0.94 1.42	0.934 SP	PO3903 POA0001 POA0002	1.67 0.95 1.3		SPO3902 SPO3903 SPOA0001	1.25 1.03 1.25	0.242 SPOA0004 0.047 SPOA0005 0.555 SPOA0006	1.08 1.06 1.16	0.034 0.015 0.065	SPO3897 SPO3898 SPO3899	1.74 0.92 1.96	0.196 0.516 0.013	SPO3897 SPO3898 SPO3899	1.71	0.167 0.970 0.027	SPO3898 SPO3899 SPO3900	1.15 1.09 1.04	0.625	SPO3893 SPO3894 SPO3895	1.01 0.86 0.96	0.689 0.088 0.842
SPOA0003 SPOA0004	0.81 0.98	0.43 SP 0.846 SP	POA0003 POA0004	0.77 1.03	0.097 0.486	SPOA0002 SPOA0003	3.98 2.46	0.165 SPOA0007 0.341 SPOA0008	1.16 1.09	0.107 0.795	SPO3900 SPO3901	1.03 0.66	0.784 0.842	SPO3900 SPO3901	1.17	0.346 0.623	SPO3901 SPO3902	0.97 0.94	0.988 0.771	SPO3896 SPO3897	0.97 1.28	0.927 0.574
SPOA0005 SPOA0006 SPOA0007	1.11 0.99 1.51	0.917 SP	POA0005 POA0006 POA0007	1.14 0.94 1.47	0.042 0.868 0.003	SPOA0004 SPOA0005 SPOA0006	1.24 1.16 1.18	0.017 SPOA0009 0.01 SPOA0010 0.162 SPOA0011	1.22 1.15 1.16	0.219 0.698 0.018	SPO3902 SPO3903 SPOA0001	0.52 0.90	0.083 0.043 0.752	SPO3902 SPO3903 SPOA0001	1.02 0.56 0.92	0.378 0.008 0.417	SPO3903 SPOA0001 SPOA0002	1.10 0.92 1.10	0.670	SPO3898 SPO3899 SPO3900	1.06 1.15 1.14	0.797 0.570 0.317
SPOA0008 SPOA0009 SPOA0010	0.72 1.18	0.281 SP 0.014 SP	POA0008 POA0009 POA0010	0.8 1.2	0.322	SPOA0007 SPOA0008	1.11 1.22	0.099 SPOA0012 0.847 SPOA0013	1.25 1.17	0.102	SPOA0002 SPOA0003	0.69 0.53	0.219 0.070	SPOA0002 SPOA0003	0.75 0.53	0.042	SPOA0003 SPOA0004 SPOA0005	1.03 0.92	0.907 0.674	SPO3901 SPO3902	0.99 0.93 1.09	0.997 0.239 0.771
SPOA0010 SPOA0012	1.17 1.13 1.29	0.046 SP	POA0010 POA0011 POA0012	1.1 1.21 1.27	0.109 0.046 0.183	SPOA0009 SPOA0010 SPOA0011	1.25 1.14 1.46	0.162 SPOA0014 0.158 SPOA0015 0.032 SPOA0017	1.05 1.2 3.97	0.126 0.943 0.966	SPOA0004 SPOA0005 SPOA0006	0.37	0.009 0.002 0.125	SPOA0005 SPOA0006	0.37	0.008 0.001 0.142	SPOA0005 SPOA0007	1.21 1.04 0.93	0.076 0.723 0.503	SPO3903 SPOA0001 SPOA0002	0.91 0.95	0.771
SPOA0013 SPOA0014 SPOA0015	0.81 1.09 1.46	0.749 SP	POA0013 POA0014 POA0015	0.83 0.88 1.59	0.079	SPOA0012 SPOA0013 SPOA0014	2.05 1.06 1.1	0.369 SPOA0018 0.374 SPOA0019 0.28 SPOA0020	2.66 1.24 1.27	0.447 0.409 0.138	SPOA0008	0.80 1.95 0.84	0.171	SPOA0008 SPOA0008	0.75 1.91 0.81	0.080 0.071 0.045	SPOA0008 SPOA0009 SPOA0010	0.98 0.89 1.04	0.948 0.301 0.864	SPOA0003 SPOA0004 SPOA0005	0.97 0.97 1.04	0.813 0.976 0.391
SPOA0017 SPOA0018	1.64 0.93	0.045 SP 0.944 SP	POA0017 POA0018	1.41 0.94	0.083	SPOA0015 SPOA0017	1.03 1.11	0.759 SPOA0021 0.965 SPOA0022	1.02 1.07	0.319 0.413	SPOA0010 SPOA0011	1.13 0.37	0.373	SPOA0010 SPOA0011	1.20 0.38	0.091 0.000	SPOA0011 SPOA0012	0.79 0.94	0.051 0.522	SPOA0006 SPOA0007	0.95 0.85	0.834 0.409
SPOA0019 SPOA0020 SPOA0021	1.3 0.81	0.407 SP	POA0019 POA0020 POA0021	1.25 0.8 1.08	0.266 0.732 0.305	SPOA0018 SPOA0019 SPOA0020	1.04 1.18 1.05	0.602 SPOA0023 0.307 SPOA0024 0.576 SPOA0025	1.2 1.08 1.17	0.271 0.447 0.755	SPOA0012 SPOA0013 SPOA0014	0.71 0.78 1.69	0.043 0.029 0.146	SPOA0012 SPOA0013 SPOA0014	0.69 0.86 1.77	0.059 0.280 0.105	SPOA0013 SPOA0014 SPOA0015	0.93 0.91 1.07	0.270 0.861 0.565	SPOA0008 SPOA0009 SPOA0010	1.02 0.88 1.09	0.905 0.246 0.608
SPOA0022 SPOA0023 SPOA0024	0.78 0.99 0.76	0.714 SP	POA0022 POA0023 POA0024	0.77 0.96 0.76	0.192 0.819 0.44	SPOA0021 SPOA0022 SPOA0023	1.09 1.11 1.04	0.164 SPOA0026 0.558 SPOA0027 0.976 SPOA0028		0.429 0.983 0.891	SPOA0015 SPOA0017	0.71 0.90 0.96	0.202 0.960 0.771	SPOA0015 SPOA0017	0.67 0.88 0.98	0.031 0.867 0.842	SPOA0017 SPOA0018 SPOA0019	0.92 0.86 0.93	0.321	SPOA0011 SPOA0012 SPOA0013	0.81 0.89 0.94	0.007 0.354 0.770
SPOA0025 SPOA0026	0.76 0.7 0.84	0.089 SP	POA0024 POA0025 POA0026	0.76 0.76 0.79	0.083	SPOA0024 SPOA0025	1.04 1.11 1.23	0.571 SPOA0029 0.85 SPOA0030	2.05	0.891 0.774 0.073	SPOA0018 SPOA0019 SPOA0020	0.96 0.91 0.63	0.691 0.603	SPOA0018 SPOA0019 SPOA0020	0.98 0.81 0.58	0.842 0.244 0.677	SPOA0020 SPOA0021	0.93 0.60 0.86	0.423	SPOA0013 SPOA0014 SPOA0015	0.94 0.97 1.09	0.770 0.988 0.558
SPOA0027 SPOA0028 SPOA0029	0.74 1.34 1.4	0.595 SP	POA0027 POA0028 POA0029	0.85 1.17 1.28	0.097 0.643 0.147	SPOA0026 SPOA0027 SPOA0028	1.02 1.1 1.08	0.58 SPOA0031 0.899 SPOA0032 0.901 SPOA0033	1 1.02 1.09	0.457 0.636 0.739	SPOA0021 SPOA0022 SPOA0023	1.16 0.99 1.18	0.459 0.647 0.518	SPOA0021 SPOA0022 SPOA0023	1.02 0.94 1.21	0.992 0.689 0.354	SPOA0022 SPOA0023 SPOA0024	0.93 1.14 1.14		SPOA0017 SPOA0018 SPOA0019	0.93 0.87 0.87	0.847 0.620 0.645
SPOA0030 SPOA0031	1.05 1.21	0.296 SP 0.432 SP	POA0030 POA0031	1 1.19	0.674	SPOA0029 SPOA0030	1 1.25	0.869 SPOA0034 0.176 SPOA0035	1.04 1.19	0.052 0.591	SPOA0024 SPOA0025	1.51 1.45	0.113 0.048	SPOA0024 SPOA0025	1.57 1.39	0.121 0.045	SPOA0025 SPOA0026	1.16 0.93	0.036 0.617	SPOA0020 SPOA0021	0.71 0.88	0.108 0.122
SPOA0032 SPOA0033 SPOA0034	1.23 1.7 0.75	0.094 SP	POA0032 POA0033 POA0034	1.33 1.5 0.8	0.207 0.123 0.005	SPOA0031 SPOA0032 SPOA0033	1.29 1.23 1.11	0.34 SPOA0036 0.863 SPOA0037 0.967 SPOA0038	1.13 1.06 1.15	0.774 0.363 0.329	SPOA0026 SPOA0027 SPOA0028	0.94 1.30 1.33	0.985 0.175 0.420	SPOA0026 SPOA0027 SPOA0028	0.91 1.20 1.34	0.951 0.520 0.401	SPOA0027 SPOA0028 SPOA0029	1.05 1.10 1.05	0.953 0.814 0.418	SPOA0022 SPOA0023 SPOA0024	1.02 1.08 1.17	0.834 0.799 0.545
SPOA0035 SPOA0036 SPOA0037	1.24 1.17 1.67	0.345 SP	POA0035 POA0036 POA0037	1.13 1.33 1.28	0.034 0.273 0.065	SPOA0034 SPOA0035 SPOA0036	1.04 1.01 1.13	0.676 SPOA0039 0.28 SPOA0040 0.785 SPOA0041	1.06 1.13 1.16	0.037 0.347 0.307	SPOA0029 SPOA0030	1.05 1.27	0.178 0.001 0.187	SPOA0029 SPOA0030	1.07 1.36 1.18	0.256 0.054 0.161	SPOA0030 SPOA0031 SPOA0032	1.13 1.10 0.95	0.352 0.702 0.940	SPOA0025 SPOA0026 SPOA0027	1.10 0.92 1.03	0.601 0.629 0.979
SPOA0038 SPOA0039	1.21 0.51	0.52 SP 0.019 SP	POA0038 POA0039	1.18 0.55	0.583 0.023	SPOA0037 SPOA0038	1.2 1.06	0.154 SPOA0042 0.266 SPOA0043	1.07 1.14	0.929 0.365	SPOA0032 SPOA0033	0.87 0.83	0.966 0.635	SPOA0032 SPOA0033	0.84 0.83	0.852 0.666	SPOA0033 SPOA0034	1.22 1.15	0.519 0.453	SPOA0028 SPOA0029	1.14 1.00	0.787 0.892
SPOA0040 SPOA0041 SPOA0042	1.07 1.61 1.02	0.016 SP	POA0040 POA0041 POA0042	1.18 1.5 0.94	0.109 0.029 0.991	SPOA0039 SPOA0040 SPOA0041	1.04 1.26 1.04	0.055 SPOA0044 0.833 SPOA0045 0.158 SPOA0046	1.11 1.01 1.23	0.766 0.695 0.749	SPOA0034 SPOA0035 SPOA0036	0.93 1.89 0.92	0.624 0.018 0.872	SPOA0034 SPOA0035 SPOA0036	0.78 2.18 0.94	0.083 0.022 0.931	SPOA0035 SPOA0036 SPOA0037	1.15 0.97 0.88	0.359 0.909 0.713	SPOA0030 SPOA0031 SPOA0032	1.11 1.10 1.02	0.360 0.386 0.723
SPOA0043 SPOA0044 SPOA0045	0.5 0.58 0.74	0.055 SP	POA0043 POA0044 POA0045	0.55 0.62 0.79	0.031 0.175 0.67	SPOA0042 SPOA0043 SPOA0044	1.04 1.03 1.1	0.958 SPOA0047 0.351 SPOA0048 0.335 SPOA0049	1.32 1.33 1.05	0.13 0.324 0.3	SPOA0038 SPOA0038	0.34 0.52 0.91	0.023 0.108 0.748	SPOA0038 SPOA0038	0.33 0.57 0.90	0.025 0.201 0.593	SPOA0038 SPOA0039 SPOA0040	0.67 1.51	0.358 0.048 0.947	SPOA0033 SPOA0034 SPOA0035	1.15 1.06 1.30	0.491
SPOA0046 SPOA0047	0.83 1.52	0.323 SP 0.283 SP	POA0046 POA0047	0.78 1.48	0.134 0.141	SPOA0045 SPOA0046	1.1 1.07	0.69 SPOA0050 0.833 SPOA0051	0.99	0.949		0.71 1.06	0.060 0.916		0.70 1.19	0.038 0.410	SPOA0041 SPOA0042	1.24 0.85	0.381 0.876	SPOA0036 SPOA0037	0.95 0.90	0.809
SPOA0048 SPOA0049 SPOA0050	0.65 1.14 0.76	0.848 SP	POA0048 POA0049 POA0050	0.54 1.09 0.74	0.747	SPOA0047 SPOA0048 SPOA0049	0.98 1.03 1.06	0.401 SPOA0052 0.198 SPOA0053 0.636 SPOA0054		0.411 0.768 0.643	SPOA0042 SPOA0043 SPOA0044	0.69 1.37 1.15	0.695 0.223 0.571	SPOA0042 SPOA0043 SPOA0044	0.79 1.26 1.24	0.799 0.034 0.148	SPOA0043 SPOA0044 SPOA0045	0.95 0.86 0.88	0.363	SPOA0038 SPOA0039 SPOA0040	0.66 1.42 1.03	0.323 0.011 0.915
SPOA0051 SPOA0052 SPOA0053	0.86 0.92 1.68	0.801 SP 0.947 SP	POA0052 POA0053 POA0054	0.88 1.35 0.89	0.687	SPOA0050 SPOA0051 SPOA0052	1.13 1.02 1.01	0.906 SPOA0055 0 SPOA0056 0.47 SPOA0057	1.07 1.13	0.7 0.534	SPOA0046	1.02 1.22 1.19	0.965 0.191 0.584	SPOA0045 SPOA0046	0.98 1.41 1.11	0.984	SPOA0046 SPOA0047 SPOA0048	1.04 0.99 1.03	0.821	SPOA0041 SPOA0042 SPOA0043	1.08 0.89 0.94	0.832 0.914 0.847
SPOA0054 SPOA0055	1.04	0.348 SP 0.023 SP	POA0055 POA0056	0.89 0.71 0.85	0.082	SPOA0053 SPOA0054	1.01 1.12 1.22	0.551 SPOA0058 0.569 SPOA0059	1.11	0.522 0.018 0.341	SPOA0047 SPOA0048 SPOA0049	1.19 1.31 0.79	0.451 0.489	SPOA0048 SPOA0049	1.11	0.794	SPOA0049 SPOA0050	0.85 0.94	0.486	SPOA0044 SPOA0045	0.94 0.92 0.93	0.498 0.877
SPOA0056 SPOA0057 SPOA0058	0.71 1.43 1.05	0.243 SP	POA0057 POA0058 POA0059	1.51 1.17 1.55	0.262 0.076 0.029	SPOA0055 SPOA0056 SPOA0057	1.08 1.16 1.08	0.744 SPOA0060 0.407 SPOA0061 0.75 SPOA0062	1.11 1.09 1.03	0.959 0.086 0.887	SPOA0050 SPOA0051 SPOA0052	1.49 1.15 0.80	0.569	SPOA0050 SPOA0051 SPOA0052	1.51 0.83 0.80	0.707 0.242 0.009	SPOA0051 SPOA0052 SPOA0053	1.23 0.83 1.00	0.365	SPOA0046 SPOA0047 SPOA0048	1.00 0.88 1.00	0.874 0.099 0.882
SPOA0059 SPOA0060	1.7 1.84	0.017 SP 0.302 SP	POA0060 POA0061	1.61 0.57	0.5 0.013	SPOA0058 SPOA0059	1.21 1.06	0.124 SPOA0063 0.143 SPOA0064	1.11	0.339 0.936	SPOA0053 SPOA0054	0.48	0.009	SPOA0053 SPOA0054	0.57 0.92	0.021 0.112 0.217	SPOA0054 SPOA0055	0.58 1.38 1.09	0.074 0.198	SPOA0049 SPOA0050	0.88 1.05 0.94	0.909 0.980
SPOA0061 SPOA0062 SPOA0063	0.52 0.78 0.6	0.399 SP 0.391 SP	POA0062 POA0063 POA0064	0.83 0.7 1.03	0.219 0.058 0.593	SPOA0060 SPOA0061 SPOA0062	1.12 1.01 1.04	0.049 SPOA0066 0.824 SPOA0067	1.03	0.872 0.5 0.845	SPOA0055 SPOA0056 SPOA0057	1.19 0.35 0.23	0.420 0.007 0.022	SPOA0055 SPOA0056 SPOA0057	1.26 0.32 0.22	0.002	SPOA0056 SPOA0057 SPOA0058	0.93 0.92	0.664	SPOA0051 SPOA0052 SPOA0053	0.90	0.335 0.142 0.874
SPOA0064 SPOA0065 SPOA0066	1.11 0.93 1.06	0.297 SP	POA0065 POA0066 POA0067	0.93 1.09 0.88	0.882 0.374 0.859	SPOA0063 SPOA0064 SPOA0065	1.19 1.03 1.21	0.891 SPOA0068 0.792 SPOA0069 0.896 SPOA0070	1.06 1.16	0.198 0.399 0.975	SPOA0058 SPOA0059 SPOA0060	0.33 0.28 0.44	0.003 0.014 0.213	SPOA0058 SPOA0059 SPOA0060	0.36 0.31 0.45	0.001 0.001 0.227	SPOA0059 SPOA0060 SPOA0061	0.79 0.98 1.17	0.972	SPOA0054 SPOA0055 SPOA0056	0.99 1.46 1.01	0.818 0.026 0.958
SPOA0067 SPOA0068	0.78 0.63	0.658 SP 0.025 SP	POA0068 POA0069	0.69 0.86	0.023	SPOA0066 SPOA0067	1.02 1.08	0.633 SPOA0071 0.813 SPOA0072	1.1	0.939 0.816	SPOA0061 SPOA0062	0.17 0.86	0.000 0.156	SPOA0061 SPOA0062	0.45 0.16 0.85	0.002	SPOA0062 SPOA0063	0.93 1.25	0.728 0.384	SPOA0057 SPOA0058	0.88 1.09	0.493 0.182
SPOA0069 SPOA0070 SPOA0071	0.88 1.38 1.19	0.148 SP	POA0070 POA0071 POA0072	1.32 1 0.85	0.005 0.737 0.146	SPOA0068 SPOA0069 SPOA0070	1.09 1.09 1.15	0.291 SPOA0073 0.635 SPOA0074 0.715 SPOA0075		0.582 0.38 0.401	SPOA0063 SPOA0064 SPOA0065	1.19 0.73 1.20	0.674 0.017 0.701	SPOA0063 SPOA0064 SPOA0065	1.23 0.76 1.35	0.065 0.182 0.249	SPOA0064 SPOA0065 SPOA0066	0.81 1.09 0.95	0.910	SPOA0059 SPOA0060 SPOA0061	0.78 1.00 1.14	0.279 0.995 0.153
SPOA0072 SPOA0073 SPOA0074	0.85 0.75 0.93	0.097 SP 0.283 SP	POA0073 POA0074 POA0075	0.83 0.97 0.9	0.492	SPOA0071 SPOA0072 SPOA0073	0.99 1.01 1.12	0.968 SPOA0076 0.063 SPOA0077 0.717 SPOA0078	1.08 1.01	0.575 0.121 0.85	SPOA0066 SPOA0067 SPOA0068	0.79 0.59 1.83	0.225 0.535 0.066	SPOA0066 SPOA0067 SPOA0068	0.88 0.53 1.93		SPOA0067 SPOA0068 SPOA0069	0.95 1.06 1.05	0.841 0.794	SPOA0062 SPOA0063 SPOA0064	1.00 1.15 0.83	0.992 0.708 0.385
SPOA0075 SPOA0076	0.76 1.11	0.074 SP 0.193 SP	POA0076 POA0077	1.03	0.238	SPOA0074 SPOA0075	1 1.12	0.542 SPOA0079 0.017 SPOA0081	1.04 1.13	0.715 0.755	SPOA0069 SPOA0070	2.19 1.14	0.011	SPOA0069 SPOA0070	2.28 1.24	0.005 0.708	SPOA0070 SPOA0071	0.96 0.91	0.631 0.746	SPOA0065 SPOA0066	1.14 1.00	0.495 0.838
SPOA0077 SPOA0078 SPOA0079	1.37 1.03 1.24	0.59 SP	POA0078 POA0079 POA0081	1.16 1.32 0.85		SPOA0076 SPOA0077 SPOA0078	1.07 1.09 1.08	0.327 SPOA0082 0.04 SPOA0083 0.694 SPOA0084		0.813 0.805 0.358	SPOA0071 SPOA0072 SPOA0073	0.82 1.19 1.55	0.674 0.209 0.113	SPOA0071 SPOA0072 SPOA0073	0.83 1.24 1.54	0.678 0.017 0.045	SPOA0072 SPOA0073 SPOA0074	0.89 0.91 1.01	0.835	SPOA0067 SPOA0068 SPOA0069	0.97 1.12 1.05	0.959 0.606 0.601
SPOA0081 SPOA0082 SPOA0083	0.79 0.65 0.58	0.741 SP 0.082 SP	POA0082 POA0083 POA0084	0.67 0.67 0.69	0.017	SPOA0079 SPOA0081 SPOA0082	1.04 1.11 1.06	0.69 SPOA0085 0.799 SPOA0086 0.53 SPOA0087	1.08 1.18 1.14	0.057 0.245 0.398	SPOA0074 SPOA0075 SPOA0076	1.71 2.03 1.74	0.018 0.055 0.032	SPOA0074 SPOA0075 SPOA0076	1.52 2.12 1.90	0.002 0.011 0.021	SPOA0075 SPOA0076 SPOA0077	1.08 1.32 0.96	0.597	SPOA0070 SPOA0071 SPOA0072	1.10 0.98 0.99	0.758 0.967 0.940
SPOA0084 SPOA0085	0.74 1.21	0.469 SP 0.126 SP	POA0085 POA0086	1.15 1.01	0.019 0.471	SPOA0083 SPOA0084	1.16 1.14	0.716 SPOA0088 0.077 SPOA0089	1.21	0.359 0.818	SPOA0077 SPOA0078	1.22	0.054 0.004	SPOA0077 SPOA0078	1.17	0.034 0.009	SPOA0078 SPOA0079	1.14 1.14	0.350 0.643	SPOA0073 SPOA0074	0.92 1.01	0.705 0.704
SPOA0086 SPOA0087 SPOA0088	1.04 0.84 0.65	0.117 SP	POA0087 POA0088 POA0089	0.86 0.68 1.34	0.792 0.057 0	SPOA0085 SPOA0086 SPOA0087	1.15 1.02 1.1	0.19 SPOA0091 0.409 SPOA0093 0.335 SPOA0094	1.11 1.16 1.17	0.752 0.92 0.751	SPOA0079 SPOA0081 SPOA0082	1.85 1.13 1.38	0.140 0.745 0.107	SPOA0079 SPOA0081 SPOA0082	1.96 1.15 1.49	0.153 0.719 0.018	SPOA0081 SPOA0082 SPOA0083	1.03 0.94 0.87		SPOA0075 SPOA0076 SPOA0077	1.07 1.20 0.92	0.732 0.180 0.351
SPOA0089 SPOA0091	1.47 0.85 0.75	0 SP 0.805 SP	POA0091 POA0093	0.82 0.78 0.94		SPOA0088 SPOA0089	1.17 1.11 1.23	0.433 SPOA0095 0.854 SPOA0096	1.07 1.03 1.06	0.924 0.294 0.967	SPOA0084 SPOA0086	1.18 1.05 1.31	0.292 0.930 0.099	SPOA0083 SPOA0084 SPOA0085	1.12 1.00 1.28	0.328 0.930	SPOA0084 SPOA0085	1.14 1.05 0.96	0.366 0.921	SPOA0078 SPOA0079	1.10 1.16 0.93	0.487 0.605
SPOA0093 SPOA0094 SPOA0095	0.95 1.05	0.812 SP 0.927 SP	POA0094 POA0095 POA0096	0.99 0.88	0.965 0.898	SPOA0091 SPOA0093 SPOA0094	1.09 1.11	0.836 SPOA0097 0.888 SPOA0098 0.47 SPOA0099	1.48 1.03	0.967 0.947 0.675	SPOA0085 SPOA0086 SPOA0087	1.10 0.89	0.391 0.671	SPOA0086 SPOA0087	1.09 0.77	0.765 0.520	SPOA0086 SPOA0087 SPOA0088	0.89 1.05	0.583 0.578	SPOA0081 SPOA0082 SPOA0083	1.14 0.89	0.862 0.181 0.268
SPOA0096 SPOA0097 SPOA0098	0.83 1.04 1.1	0.96 SP	POA0097 POA0098 POA0099	0.93 1.07 0.97	0.941	SPOA0095 SPOA0096 SPOA0097	1.23 1.06 0.99	0.898 SPOA0100 0.136 SPOA0101 0.993 SPOA0102	1.23	0.079 0.873 0.58	SPOA0088 SPOA0089 SPOA0091	1.05 0.68 0.95	0.432 0.805 0.694	SPOA0088 SPOA0089 SPOA0091	0.95 0.37 1.13		SPOA0089 SPOA0091 SPOA0093	0.75 0.69 0.93	0.480	SPOA0084 SPOA0085 SPOA0086	1.12 0.97 0.96	0.372 0.638 0.754
SPOA0099 SPOA0100	0.88 1.06	0.719 SP 0.207 SP	POA0100 POA0101	0.97 0.93	0.786 0.987	SPOA0098 SPOA0099	1.02 1.1	0.956 SPOA0103 0.868 SPOA0104	1.09 1.08	0.488 0.753	SPOA0093 SPOA0094	0.97 0.74	0.901 0.209	SPOA0093 SPOA0094	0.85 0.76	0.720 0.235	SPOA0094 SPOA0095	1.03 1.07	0.736 0.944	SPOA0087 SPOA0088	0.92 0.95	0.534 0.770
SPOA0101 SPOA0102 SPOA0103	0.81 0.72 0.57	0.331 SP 0.213 SP	POA0102 POA0103 POA0104	0.81 0.63 1.1	0.124	SPOA0100 SPOA0101 SPOA0102	1.08 1.12 1.15	0.768 SPOA0105 0.584 SPOA0106 0.674 SPOA0107	1.15 1.04	0.567 0.924 0.977	SPOA0095 SPOA0096 SPOA0097	0.95 0.78 0.99	0.978 0.042 0.990	SPOA0095 SPOA0096 SPOA0097	0.95 0.82 0.89	0.299 0.946	SPOA0096 SPOA0097 SPOA0098	0.85 0.86 0.85	0.905 0.916	SPOA0089 SPOA0091 SPOA0093	0.64 0.78 0.94	0.779 0.601 0.800
SPOA0104	1.06	0.846 SP	POA0105	0.97	0.546	SPOA0103	1.12	0.512 SPOA0108	1.12	0.929	SPOA0098	0.79	0.885	SPOA0098	0.83	0.185	SPOA0099	0.65	0.225	SPOA0094	0.99	0.956

SPOA0105 SPOA0106	0.88	0.95		0.83	0.872	SPOA0104 SPOA0105	1.31	0.449 SPOA0109 0.567 SPOA0110	1.14	0.157 SI 0.967 SI	POA0099 POA0100	0.84	0.583 0.481	SPOA0099 SPOA0100	0.74	0.050	SPOA0100 SPOA0101	0.88	0.398 SPOA0095 0.476 SPOA0096		0.901
SPOA0107 SPOA0108 SPOA0109	1.05 1.07 0.6	0.85	SPOA0108 SPOA0109 SPOA0110	1.09 0.67	0.153 0.922	SPOA0106 SPOA0107 SPOA0108	1.21 1.07 1.43	0.862 SPOA0111 0.968 SPOA0112 0.897 SPOA0113	1.01 1.01 1	0.968 SI 0.774 SI 0.983 SI	POA0101 POA0102 POA0103	0.99 0.81 1.67	0.825 0.362 0.159	SPOA0101 SPOA0102 SPOA0103	1.02 0.83 1.63	0.206 0.195	SPOA0102 SPOA0103 SPOA0104	0.86 1.13 0.56	0.369 SPOA0097 0.866 SPOA0098 0.552 SPOA0099	0.98	0.927 0.981 0.413
SPOA0110 SPOA0111 SPOA0112	0.93 0.75 0.82	0.818	SPOA0112 SPOA0113	0.93 0.81 0.81	0.781	SPOA0109 SPOA0110 SPOA0111	1.01 1.17 1.07	0.366 SPOA0114 0.799 SPOA0115 0.811 SPOA0116	1.03 1.06 1.11	0.321 SI 0.506 SI 0.287 SI	POA0104 POA0105 POA0106	0.54 1.33 0.97	0.509 0.046 0.987	SPOA0104 SPOA0105 SPOA0106	1.07 1.33		SPOA0105 SPOA0106 SPOA0107	0.93 0.88 1.01	0.778 SPOA0100 0.846 SPOA0101 0.986 SPOA0102	0.90	0.454 0.235 0.419
SPOA0113 SPOA0114 SPOA0115	0.84 0.71 0.69	0.111	SPOA0114 SPOA0115 SPOA0116	0.76 0.8 0.76	0.172	SPOA0112 SPOA0113 SPOA0114	1.18 1.18 1.14	0.81 SPOA0117 0.983 SPOA0118 0.866 SPOA0119	1.18 1.06 1.19	0.524 SI 0.947 SI 0.985 SI	POA0107 POA0108 POA0109	1.80 0.81 2.09	0.426 0.751 0.051	SPOA0107 SPOA0108 SPOA0109	1.68 0.85 2.07	0.786	SPOA0108 SPOA0109 SPOA0110	0.79 1.12 0.81	0.765 SPOA0103 0.626 SPOA0104 0.744 SPOA0105		0.479 0.525 0.771
SPOA0116 SPOA0117 SPOA0118	0.67 0.93 0.9	0.912	SPOA0117 SPOA0118 SPOA0119	0.87 0.83 0.86	0.867	SPOA0115 SPOA0116 SPOA0117	1.03 1.18 1.16	0.91 SPOA0120 0.435 SPOA0121 0.295 SPOA0122	1.2 1.28 1.37		POA0110 POA0111 POA0112	0.89 0.90 1.24	0.775 0.411 0.544	SPOA0110 SPOA0111 SPOA0112	0.79 0.88 0.96	0.452	SPOA0111 SPOA0112 SPOA0113	0.90 0.93 0.97	0.360 SPOA0106 0.805 SPOA0107 0.851 SPOA0108	0.94	0.894 0.922 0.833
SPOA0119 SPOA0120	0.95 0.72	0.996 0.315	SPOA0120 SPOA0121	0.76 0.99 0.88	0.026 0.783	SPOA0118 SPOA0119	1.36 1.1 1.23	0.986 SPOA0123 0.691 SPOA0124	1.24 1.28 1.11	0.954 SI 0.868 SI	POA0113 POA0114	1.28 1.58 0.93	0.559 0.141 0.436	SPOA0113 SPOA0114	1.05 1.25 0.85	0.932 0.204	SPOA0114 SPOA0115	1.13 0.88 0.96	0.525 SPOA0109 0.645 SPOA0110	1.21 0.78	0.272 0.688
SPOA0121 SPOA0122 SPOA0123	0.96 0.71 0.9	0.464 0.927	SPOA0122 SPOA0123 SPOA0124	0.88 0.81	0.883 0.649	SPOA0120 SPOA0121 SPOA0122	1.22 1.18	0.433 SPOA0125 0.761 SPOA0126 0.339 SPOA0127	1.44 1.04	0.99 SI 0.667 SI	POA0115 POA0116 POA0117	1.45 0.88	0.029 0.533	SPOA0115 SPOA0116 SPOA0117	1.60 0.86	0.032	SPOA0116 SPOA0117 SPOA0118	0.96 0.97	0.653 SPOA0111 0.875 SPOA0112 0.960 SPOA0113	0.96	0.343 0.874 0.861
SPOA0124 SPOA0125 SPOA0126	0.74 0.64 0.82	0.451 0.919	SPOA0125 SPOA0126 SPOA0127	0.68 0.93 1.02	0.988 0.837	SPOA0123 SPOA0124 SPOA0125	1.13 1.16 1.21	0.988 SPOA0128 0.746 SPOA0129 0.942 SPOA0130	1.11 1.03 1.15	0.679 SI 0.964 SI	POA0118 POA0119 POA0120	0.99 1.30 2.70	0.985 0.349 0.047	SPOA0118 SPOA0119 SPOA0120	1.01 1.36 2.38	0.381	SPOA0119 SPOA0120 SPOA0121	1.01 1.04 0.96	0.949 SPOA0114 0.601 SPOA0115 0.866 SPOA0116	1.01	0.437 0.992 0.384
SPOA0127 SPOA0128 SPOA0129	1.01 0.58 0.74	0.677	SPOA0128 SPOA0129 SPOA0130			SPOA0126 SPOA0127 SPOA0128	1.1 1.24 1.13	0.992 SPOA0131 0.723 SPOA0132 0.713 SPOA0133	1.31 1.09 1.13	0.395 SI 0.722 SI 0.631 SI	POA0121 POA0122 POA0123	1.37 0.71 1.05	0.436 0.391 0.798	SPOA0121 SPOA0122 SPOA0123	1.31 0.53 1.08	0.164	SPOA0122 SPOA0123 SPOA0124	0.85 1.01 0.91	0.657 SPOA0117 0.954 SPOA0118 0.728 SPOA0119		0.163 0.960 0.780
SPOA0130 SPOA0131 SPOA0132	0.87 0.96 0.76	0.943	SPOA0131 SPOA0132 SPOA0133	0.88 0.81 0.81	0.271	SPOA0129 SPOA0130 SPOA0131	1.01 1.11 1.07	0.449 SPOA0134 0.772 SPOA0136 0.967 SPOA0137	1.27 1 1.13	0.022 SI 0.889 SI 0.95 SI	POA0124 POA0125 POA0126	1.15 1.27 0.75	0.366 0.457 0.893	SPOA0124 SPOA0125 SPOA0126	1.06 1.26 0.69	0.316	SPOA0125 SPOA0126 SPOA0127	0.94 0.84 1.00	0.904 SPOA0120 0.917 SPOA0121 0.947 SPOA0122	1.03	0.487 0.942 0.182
SPOA0133 SPOA0134 SPOA0136	0.75 1.43 0.81		SPOA0134 SPOA0136 SPOA0137	1.45 0.93 1.02	0.693	SPOA0132 SPOA0133 SPOA0134	1.07 1.1 1.02	0.608 SPOA0138 0.498 SPOA0139 0.038 SPOA0140	1.07 1.22 1.11	0.715 SI 0.942 SI 0.585 SI	POA0127 POA0128 POA0129	0.98 1.26 1.12	0.916 0.853 0.954	SPOA0127 SPOA0128 SPOA0129	1.01 1.42 1.04		SPOA0128 SPOA0129 SPOA0130	1.09 1.04 1.15	0.962 SPOA0123 0.955 SPOA0124 0.650 SPOA0125	0.93	0.985 0.724 0.960
SPOA0137 SPOA0138 SPOA0139	1.01 1.62 1.35	0.696 0.093	SPOA0138 SPOA0139 SPOA0140	1.35 1.3 1.3	0.124 0.779	SPOA0136 SPOA0137 SPOA0138	0.98 1.14	0.732 SPOA0141 0.891 SPOA0142 0.693 SPOA0143	1.1 1.21 1.19	0.017 SI 0.261 SI 0.356 SI	POA0130 POA0131 POA0132	1.61 1.33 1.11	0.134 0.492 0.567	SPOA0130 SPOA0131 SPOA0132	1.46 1.52 1.12	0.210 0.257	SPOA0131 SPOA0132 SPOA0133	1.06 0.78	0.987 SPOA0126 0.489 SPOA0127 0.555 SPOA0128	0.93	0.964 0.781 0.898
SPOA0140 SPOA0141	1.29	0.392 0.016	SPOA0141 SPOA0142	1.32	0.032 0.29	SPOA0139 SPOA0140	1.02	0.991 SPOA0144 0.907 SPOA0145	0.98 1.06	0.134 SI 0.179 SI	POA0133 POA0134	1.45 0.53	0.028	SPOA0133 SPOA0134	1.42 0.37	0.004	SPOA0134 SPOA0136	0.68	0.105 SPOA0129 0.224 SPOA0130	0.91	0.799 0.687
SPOA0142 SPOA0143 SPOA0144	1.12 1.33 0.88	0.352 0.705	SPOA0144 SPOA0145	0.95 0.71	0.902 0.108	SPOA0141 SPOA0142 SPOA0143	1.15 1.11 1.15	0.015 SPOA0146 0.102 SPOA0147 0.597 SPOA0148	1.06 0.99 1.12	0.967 SI 0.972 SI	POA0136 POA0137 POA0138	1.47 1.11 0.93	0.037 0.251 0.883	SPOA0136 SPOA0137 SPOA0138	1.43 0.83 0.98	0.875 0.466	SPOA0137 SPOA0138 SPOA0139	0.88 0.97 0.93	0.224 SPOA0131 0.925 SPOA0132 0.947 SPOA0133	0.85	0.892 0.527 0.827
SPOA0145 SPOA0146 SPOA0147	0.7 0.87 1.04	0.838	SPOA0146 SPOA0147 SPOA0148	0.93 0.97 0.89		SPOA0144 SPOA0145 SPOA0146	1.13 1.03 1.56	0.312 SPOA0149 0.604 SPOA0150 0.976 SPOA0151	1.03 0.98 1.24		POA0139 POA0140 POA0141	1.06 0.85 0.57	0.913 0.732 0.036	SPOA0139 SPOA0140 SPOA0141	1.06 0.78 0.54	0.375	SPOA0140 SPOA0141 SPOA0142	0.87 0.88 0.91	0.615 SPOA0136 0.398 SPOA0136 0.551 SPOA0137	0.85	0.026 0.701 0.573
SPOA0148 SPOA0149 SPOA0150	1.13 1.29 1.19	0.124	SPOA0149 SPOA0150 SPOA0151	1.34 1.21 1.19	0.11	SPOA0147 SPOA0148 SPOA0149	1.12 1.22 1.14	0.651 SPOA0152 0.331 SPOA0154 0.096 SPOA0155	1 0.99 1.05	0.878 SI	POA0142 POA0143 POA0144	1.26 1.07 0.56	0.241 0.846 0.050	SPOA0142 SPOA0143 SPOA0144	1.21 1.14 0.53	0.614	SPOA0143 SPOA0144 SPOA0145	1.07 0.81 0.93	0.831 SPOA0138 0.474 SPOA0139 0.668 SPOA0140	0.91	0.728 0.928 0.522
SPOA0151 SPOA0153 SPOA0154	1.23 0.83 0.91	0	SPOA0154 SPOA0155 SPOA0156	0.97 1.87 0.85	0.042	SPOA0150 SPOA0151 SPOA0152	1 1.38 1.25	0.869 SPOA0156 0.289 SPOA0157 0 SPOA0158	1.13 1.07 1.18	0.994 SI 0.952 SI 0.942 SI	POA0145 POA0146 POA0147	1.00 0.68 0.73	0.912 0.406 0.177	SPOA0145 SPOA0146 SPOA0147	0.92 0.70 0.76		SPOA0146 SPOA0147 SPOA0148	1.01 0.88 0.80	0.987 SPOA0141 0.540 SPOA0142 0.367 SPOA0143	0.83	0.149 0.352 0.961
SPOA0155 SPOA0156	2.02 0.85	0.026 0.857	SPOA0157 SPOA0158	0.99 0.77	0.979 0.183	SPOA0154 SPOA0155	1.01 1.14	0.935 SPOA0159 0.254 SPOA0160	1.11	0.695 SI 0.319 SI	POA0148 POA0149	0.59 0.89	0.130 0.676	SPOA0148 SPOA0149	0.55 0.92	0.348	SPOA0149 SPOA0150	0.90 0.97	0.426 SPOA0144 0.733 SPOA0145	0.77	0.189 0.931
SPOA0157 SPOA0158 SPOA0159	0.91 0.79 1.23	0.285	SPOA0159 SPOA0160 SPOA0161	1.12 1.21 1.02	0.393 0.941	SPOA0156 SPOA0157 SPOA0158	1.16 1.05 1.01	0.911 SPOA0161 0.977 SPOA0162 0.737 SPOA0163	1.1 1.32 1.16	0.909 SI 0.892 SI 0.925 SI	POA0150 POA0151 POA0152	0.99 0.93 0.64	0.859 0.467 0.048	SPOA0150 SPOA0151 SPOA0152	0.94 0.93 0.68	0.519	SPOA0152 SPOA0154	0.95 0.65 0.85	0.263 SPOA0146 0.423 SPOA0147 0.689 SPOA0148	0.91	0.930 0.800 0.864
SPOA0160 SPOA0161 SPOA0162	1.14 1.03 0.87		SPOA0162 SPOA0163 SPOA0164	0.83 1.04 1.15	0.578	SPOA0159 SPOA0160 SPOA0161	1.01 1.24 1.11	0.52 SPOA0164 0.681 SPOA0165 0.936 SPOA0166	1.03 1.39 1.3	0.748 SI 0.769 SI 0.969 SI	POA0154 POA0155 POA0156	0.91 1.16 1.96	0.843 0.173 0.111	SPOA0153 SPOA0154 SPOA0155	1.21 0.85 1.18	0.623 0.507	SPOA0155 SPOA0156 SPOA0157	1.51 1.08 0.79	0.124 SPOA0149 0.861 SPOA0150 0.892 SPOA0151	0.85	0.464 0.425 0.301
SPOA0163 SPOA0164 SPOA0165	0.95 1.22 1.15	0.676	SPOA0165 SPOA0166 SPOA0167	1.05 0.93 1.03	0.978	SPOA0162 SPOA0163 SPOA0164	1.25 1.18 1.19	0.65 SPOA0167 0.823 SPOA0168 0.555 SPOA0169	1.09 1.02	0.333 SI 0.005 SI 0.901 SI	POA0157 POA0158 POA0159	0.84 1.06 0.89	0.934 0.612 0.717	SPOA0156 SPOA0157 SPOA0158	1.91 0.69 1.03	0.829	SPOA0158 SPOA0159 SPOA0160	0.93 0.89 0.84	0.748 SPOA0152 0.658 SPOA0153 0.404 SPOA0154	1.27	0.210 0.165 0.681
SPOA0166 SPOA0167 SPOA0168	0.89 0.86 1.28	0.909	SPOA0168 SPOA0169 SPOA0170	1.06 0.81 0.93	0.667	SPOA0165 SPOA0166 SPOA0167	1.36 1.2 1.09	0.703 SPOA0170 0.954 SPOA0171 0.361 SPOA0172	1.04 1.12 1.18	0.62 SI	POA0160 POA0161 POA0162	0.96 0.82 0.92	0.549 0.873 0.644	SPOA0159 SPOA0160 SPOA0161	0.81 0.63 0.72	0.198	SPOA0161 SPOA0162 SPOA0163	0.79 0.70	0.875 SPOA0156 0.307 SPOA0156 0.483 SPOA0157	1.09	0.113 0.726 0.942
SPOA0169 SPOA0170 SPOA0171	0.74 0.93 1.07	0.559 0.701	SPOA0171 SPOA0172 SPOA0173	0.84 0.92 0.82	0.629	SPOA0168 SPOA0169 SPOA0170	1.19 1.14 1.18	0.105 SPOA0173 0.844 SPOA0174 0.989 SPOA0175	1.11 1.29 1.17	0.186 SI	POA0163 POA0164 POA0165	1.11 0.94 1.06	0.985 0.905 0.860	SPOA0162 SPOA0163 SPOA0164	0.85 1.04 0.93	0.628 0.862	SPOA0164 SPOA0165 SPOA0166	0.76 1.00 0.98	0.646 SPOA0158 0.983 SPOA0159 0.947 SPOA0160	0.97 0.96	0.927 0.852 0.720
SPOA0172 SPOA0173	0.69 0.83	0.388 0.596	SPOA0174 SPOA0175	0.89	0.671	SPOA0171 SPOA0172	1.01 1.05	0.549 SPOA0176 0.276 SPOA0177	1.36 1.25	0.351 SI 0 SI	POA0166 POA0167	1.02 0.87	0.939 0.700	SPOA0165 SPOA0166	0.99 1.12	0.965 0.927	SPOA0167 SPOA0168	0.88	0.674 SPOA0161 0.890 SPOA0162	0.79	0.838 0.377
SPOA0174 SPOA0175 SPOA0176	0.81 0.9 1.01	0.842 0.832	SPOA0176 SPOA0177 SPOA0180	0.92 0.88 1.15	0.857 0.242	SPOA0173 SPOA0174 SPOA0175	1.04 1.89 1.34	0.74 SPOA0180 0.524 SPOA0181 0.576 SPOA0182	1.14 1.16 1.09	0.772 SI 0.113 SI	POA0168 POA0169 POA0170	0.75 0.99 0.91	0.011 0.902 0.463	SPOA0167 SPOA0168 SPOA0169	0.81 0.73 0.85	0.056 0.800	SPOA0169 SPOA0170 SPOA0171	0.96 0.96 0.94	0.905 SPOA0163 0.616 SPOA0164 0.707 SPOA0165	0.81	0.331 0.769 0.860
SPOA0177 SPOA0180 SPOA0181	1.14 1.29 0.78		SPOA0181 SPOA0182 SPOA0183	0.92 0.67 0.85	0.199	SPOA0176 SPOA0177 SPOA0180	1.29 1.43 1.24	0.375 SPOA0183 0 SPOA0184 0.966 SPOA0185	1.15 1.04 1.03	0.681 Si 0.985 Si 0.25 Si	POA0171 POA0172 POA0173	0.91 0.49 1.16	0.751 0.054 0.566	SPOA0170 SPOA0171 SPOA0172	0.97 0.93 0.41		SPOA0172 SPOA0173 SPOA0174	0.74 0.96 1.02	0.693 SPOA0166 0.787 SPOA0167 0.930 SPOA0168	0.87	0.933 0.427 0.102
SPOA0182 SPOA0183 SPOA0184	0.76 0.98 1.13	0.946	SPOA0184 SPOA0185 SPOA0186	0.99 0.63 0.9	0.098	SPOA0181 SPOA0182 SPOA0183	1.04 1.27 1.1	0.847 SPOA0186 0.188 SPOA0187 0.641 SPOA0188	1.9 1.37 1.27	0.037 SI 0.702 SI 0.709 SI	POA0174 POA0175 POA0176	1.22 0.93 1.06	0.045 0.792 0.905	SPOA0173 SPOA0174 SPOA0175	1.17 1.15 0.93	0.269	SPOA0175 SPOA0176 SPOA0177	0.87 1.16 0.65	0.709 SPOA0169 0.262 SPOA0170 0.828 SPOA0171		0.968 0.253 0.352
SPOA0185 SPOA0186 SPOA0187	0.55 0.96 0.96	0.065 0.878	SPOA0187 SPOA0188 SPOA0189	0.99 0.69 0.9	0.621 0.184	SPOA0184 SPOA0185 SPOA0186	1 1.44 1.48	0.798 SPOA0189 0.053 SPOA0190 0.027 SPOA0191	1.47 1.29 1.03	0.885 SI 0.966 SI 0.093 SI	POA0177 POA0180 POA0181	0.69 0.68 0.80	0.088	SPOA0176 SPOA0177 SPOA0180	0.94 0.62 0.87	0.138 0.643 0.179	SPOA0180 SPOA0181 SPOA0182	1.28 1.12 0.84	0.240 SPOA0172 0.799 SPOA0173 0.659 SPOA0174	0.94	0.577 0.173 0.872
SPOA0188 SPOA0189 SPOA0190	0.73 0.98 1.05	0.332 0.948	SPOA0190 SPOA0191 SPOA0192	0.93 1.07 0.68	0.47	SPOA0187 SPOA0188 SPOA0189	1.24 1.05 1.22	0.822 SPOA0192 0.385 SPOA0193 0.965 SPOA0194	1.29 1.13 0.99	0.327 SI 0.892 SI 0.841 SI	POA0182 POA0183	0.87	0.357 0.171 0.081	SPOA0181 SPOA0182 SPOA0183	0.86 0.75	0.250 0.044	SPOA0183 SPOA0184 SPOA0185	0.63 0.90 0.92	0.204 SPOA0175 0.674 SPOA0176 0.751 SPOA0177	1.03	0.961 0.757 0.930
SPOA0191 SPOA0192	1.06 0.77	0.632 0.506	SPOA0193 SPOA0194	0.94	0.989 0.75	SPOA0190 SPOA0191	1.11 1.01	0.373 SPOA0195 0.232 SPOA0196	1.43 1.43	0.782 SI 0.68 SI	POA0185 POA0186	0.60	0.147 0.005	SPOA0184 SPOA0185	0.47	0.052	SPOA0186 SPOA0187	0.93 0.87	0.461 SPOA0180 0.542 SPOA0181	1.07	0.737 0.761
SPOA0193 SPOA0194 SPOA0195	0.94 0.93 0.97	0.953 0.951	SPOA0195 SPOA0196 SPOA0197		0.767 0.707	SPOA0192 SPOA0193 SPOA0194	1.32 1.01 1.15	0.077 SPOA0197 0.955 SPOA0198 0.555 SPOA0199	1.21 1.2 1.1	0.969 SI 0.775 SI	POA0187 POA0188 POA0189	0.62 0.72 0.91	0.540 0.946		0.68 0.62	0.069 0.172	SPOA0188 SPOA0189 SPOA0190	0.99 1.06 1.08	0.750 SPOA0182 0.962 SPOA0183 0.810 SPOA0184	0.70	0.910 0.072 0.607
SPOA0196 SPOA0197 SPOA0198	0.98 0.68 0.58	0.658 0	SPOA0198 SPOA0199 SPOA0200		0.698	SPOA0195 SPOA0196 SPOA0197	1.22 1.16 1.17	0.639 SPOA0200 0.947 SPOA0201 0.637 SPOA0202	1.29 1.07 1.19	0.769 SI 0.874 SI	POA0190 POA0191 POA0192	0.61 0.48 0.94	0.591	SPOA0189 SPOA0190 SPOA0191	0.93 0.70 0.46	0.042 0.015	SPOA0191 SPOA0192 SPOA0193	0.85 0.96 0.88	0.229 SPOA0185 0.880 SPOA0186 0.725 SPOA0187	0.98	0.725 0.507 0.386
SPOA0200 SPOA0201	0.99 1.11 1.06	0.658	SPOA0201 SPOA0202 SPOA0203	1.19 1.28 1.01	0.077	SPOA0198 SPOA0199 SPOA0200	1.78 1.38 1.38	0.926 SPOA0203 0.856 SPOA0204 0.688 SPOA0205	1.12 1.22 1.14	0.683 SI	POA0193 POA0194 POA0195	0.74 1.02 0.54	0.259 0.923 0.099	SPOA0192 SPOA0193 SPOA0194	0.83 0.68 0.95	0.313	SPOA0194 SPOA0195 SPOA0196	0.90 0.61 1.10	0.643 SPOA0188 0.539 SPOA0189 0.872 SPOA0190	1.02	0.891 0.991 0.989
SPOA0202 SPOA0203 SPOA0204	1.22 1.07 0.88	0.859	SPOA0204 SPOA0205 SPOA0206	0.98 0.84 1.21	0.593	SPOA0201 SPOA0202 SPOA0203	1.23 1.04 1.13	0.663 SPOA0206 0.183 SPOA0207 0.743 SPOA0208	1.64 1.5 1.44		POA0196 POA0197 POA0198	0.94 0.85 1.01	0.851 0.849 0.946	SPOA0195 SPOA0196 SPOA0197	0.48 0.75 0.81	0.166	SPOA0197 SPOA0198 SPOA0199	0.81 0.91 0.53	0.790 SPOA0191 0.951 SPOA0192 0.381 SPOA0193		0.022 0.770 0.865
SPOA0205 SPOA0206 SPOA0207	0.92 1.4 0.95	0.734 0.379	SPOA0207 SPOA0208 SPOA0209	0.95 0.65	0.935 0.009	SPOA0204 SPOA0205 SPOA0206	1.06 1.36 1.25	0.745 SPOA0209 0.275 SPOA0210 0.177 SPOA0211	1.34 1.05 1.14	0.924 SI 0.273 SI	POA0199 POA0200 POA0201	0.98 0.80 0.80	0.701 0.732 0.616	SPOA0198 SPOA0199 SPOA0200	0.81 1.17 0.76	0.799 0.855	SPOA0200 SPOA0201 SPOA0202	0.89 0.89 1.08	0.690 SPOA0194 0.763 SPOA0195 0.325 SPOA0196	0.90 0.78	0.788 0.744 0.622
SPOA0208 SPOA0209 SPOA0210	0.61 0.86 1.21	0.014 0.803	SPOA0210 SPOA0211 SPOA0212	1.27	0.075 0.399	SPOA0207 SPOA0208 SPOA0209	1.12 1.01 1.07	0.736 SPOA0212 0.489 SPOA0213 0.835 SPOA0214	1.05 1.27 1.29	0.969 SI	POA0202 POA0203	1.02 1.13 1.37	0.335 0.620 0.223	SPOA0201 SPOA0202	0.65 1.03 1.04	0.318	SPOA0203 SPOA0204 SPOA0205	1.17 1.16 1.36	0.772 SPOA0197 0.353 SPOA0198 0.290 SPOA0199	0.88	0.728 0.924 0.416
SPOA0211 SPOA0212	1.02 1.05	0.653 0.946	SPOA0213 SPOA0214	1.21 1.06	0.308 0.77	SPOA0210 SPOA0211	1.21 1.33	0.389 SPOA0215 0.135 SPOA0216	1.11 1.01	0.899 SI 0.758 SI	POA0204 POA0205 POA0206	1.02 0.87	0.573 0.238	SPOA0204 SPOA0205	1.37 1.10	0.245 0.339	SPOA0206 SPOA0207	0.98 1.26	0.847 SPOA0200 0.336 SPOA0201	0.81 0.79	0.685 0.633
SPOA0213 SPOA0214 SPOA0215	1.14 1.02	0.875 0.638	SPOA0215 SPOA0216 SPOA0217	0.95 0.69	0.886 0.226	SPOA0212 SPOA0213 SPOA0214	1.14 1.07 1.04	0.997 SPOA0217 0.152 SPOA0218 0.249 SPOA0219	1.01 1.07 1.22	0.088 SI 0.27 SI	POA0207 POA0208 POA0209	1.32 1.18 0.58	0.024 0.005 0.065	SPOA0206 SPOA0207 SPOA0208	0.86 1.30 1.19	0.033	SPOA0208 SPOA0209 SPOA0210	1.14 1.06 1.00	0.040 SPOA0202 0.948 SPOA0203 0.960 SPOA0204	1.04	0.662 0.919 0.506
SPOA0216 SPOA0217 SPOA0218	0.97 0.75 1.22	0.204	SPOA0218 SPOA0219 SPOA0220	1.17	0.12	SPOA0215 SPOA0216 SPOA0217	1.05 1.1	0.331 SPOA0220 0.576 SPOA0221 0.995 SPOA0222	1.37 1.09 1.15	0.251 SI	POA0210 POA0211 POA0212	0.93 1.25 0.79	0.792 0.089 0.867		0.57 0.88 1.21	0.237	SPOA0211 SPOA0212 SPOA0213	1.09 0.94 0.69	0.701 SPOA0205 0.957 SPOA0206 0.012 SPOA0207	0.95	0.165 0.862 0.128
SPOA0219 SPOA0220 SPOA0221	1.17 0.93 0.93	0.991	SPOA0221 SPOA0222 SPOA0223		0.997	SPOA0218 SPOA0219 SPOA0220	1.25 1.59 1.03	0.18 SPOA0223 0.782 SPOA0224 0.975 SPOA0225	1.11 1.06 1.14	0.183 SI	POA0213 POA0214 POA0215	0.60 0.93 1.02	0.115 0.777 0.936	SPOA0212 SPOA0213 SPOA0214	0.81 0.53 0.70	0.060	SPOA0214 SPOA0215 SPOA0216	0.71 1.05 0.71	0.214 SPOA0208 0.928 SPOA0209 0.212 SPOA0210	1.08	0.015 0.903 0.671
SPOA0222 SPOA0223 SPOA0224	0.94 1.03 0.68	0.999 0.873	SPOA0224 SPOA0225 SPOA0226	0.64	0.648 0.294	SPOA0221 SPOA0222 SPOA0223	1.21 1.04 1.09	0.426 SPOA0226 0.685 SPOA0227 0.596 SPOA0228	1.36 1.54 1.08	0.963 SI 0.822 SI	POA0216 POA0217 POA0218	0.79 0.88 0.50	0.077	SPOA0215 SPOA0216 SPOA0217	1.03 0.82 0.93	0.842 0.288	SPOA0217 SPOA0218 SPOA0219	0.88 0.78 0.97	0.580 SPOA0211 0.258 SPOA0212 0.594 SPOA0213	0.93	0.636 0.971 0.039
SPOA0224 SPOA0225 SPOA0226 SPOA0227	0.94 0.83 0.88	0.893 0.36	SPOA0228 SPOA0228 SPOA0229		0.963 0	SPOA0224 SPOA0225 SPOA0226	1.19 1.02 1.24	0.063 SPOA0229 0.107 SPOA0230 0.874 SPOA0231	1.19 1.09 1.03	0.944 SI		0.91 0.98 1.02		SPOA0218 SPOA0219 SPOA0220	0.51 0.78 1.10	0.029 0.084	SPOA0220 SPOA0221 SPOA0222	1.13 1.04 0.76	0.852 SPOA0215 0.877 SPOA0215 0.572 SPOA0216	0.65	0.175 0.757 0.223
SPOA0228 SPOA0229	1.24 1.06	0.151 0.828	SPOA0230 SPOA0231	0.93 0.71	0.954 0.111	SPOA0227 SPOA0228	1.34 1.13	0.79 SPOA0232 0 SPOA0233	1.21 1.02	0.944 SI 0.723 SI	POA0222 POA0223	0.83 0.95	0.588 0.617	SPOA0221 SPOA0222	0.89 0.76	0.231 0.619	SPOA0223 SPOA0224	1.10 1.20	0.874 SPOA0217 0.927 SPOA0218	0.88	0.595 0.248
SPOA0230 SPOA0231 SPOA0232	1.01 0.68 0.97	0.287 0.952	SPOA0232 SPOA0233 SPOA0234		0.885 0.878	SPOA0229 SPOA0230 SPOA0231	1.07 1.23 1.04	0.887 SPOA0234 0.595 SPOA0235 0.731 SPOA0236	1.42 1.18 1.07	0.936 SI 0.586 SI	POA0224 POA0225 POA0226	1.11 1.08	0.073	SPOA0223 SPOA0224 SPOA0225	0.89 0.41 0.85	0.247 0.466	SPOA0225 SPOA0226 SPOA0227	0.36 1.19 0.81	0.293 SPOA0219 0.679 SPOA0220 0.652 SPOA0221	1.18 0.77	0.701 0.873 0.287
SPOA0233 SPOA0234 SPOA0235	1.27 0.74 0.88	0.781	SPOA0235 SPOA0236 SPOA0237		0.148	SPOA0232 SPOA0233 SPOA0234	1.01 1.11 1.04	0.91 SPOA0237 0.255 SPOA0238 0.998 SPOA0239	1.03 1.08 1.05		POA0227 POA0228 POA0229	0.92 0.90 0.71	0.536 0.576	SPOA0226 SPOA0227 SPOA0228	1.06 0.91 0.74		SPOA0228 SPOA0229 SPOA0230	0.93 0.79 0.97	0.503 SPOA0223 0.814 SPOA0224	1.03	0.739 0.979 0.869
SPOA0236 SPOA0237 SPOA0238	1.21 1.14 0.95	0.239 0.196	SPOA0238 SPOA0239 SPOA0240	1.1	0.683 0.451	SPOA0235 SPOA0236 SPOA0237	1.11 1.03 1.15	0.798 SPOA0240 0.364 SPOA0241 0.797 SPOA0242	1.03 1.09 1.18	0.323 SI 0.773 SI	POA0230 POA0231 POA0232	1.38 1.37 1.04	0.364 0.274 0.995	SPOA0229 SPOA0230 SPOA0231	0.63 1.41 1.28	0.299	SPOA0231 SPOA0232 SPOA0233	1.16 1.13 0.98	0.691 SPOA0225 0.876 SPOA0226 0.906 SPOA0227	0.64	0.197 0.794 0.813
SPOA0239 SPOA0240 SPOA0241	1.35 1.42 0.97	0.078	SPOA0241 SPOA0242 SPOA0243	1.11	0.395 0.483	SPOA0238 SPOA0239 SPOA0240	1.37 1.09	0.38 SPOA0243 0.115 SPOA0244 0.312 SPOA0245	1.04 1.32 1.14	0.597 SI 0.437 SI	POA0233 POA0234 POA0235	1.06 1.00 1.10	0.995	SPOA0232 SPOA0233 SPOA0234	1.40 0.96 0.91	0.757 0.911	SPOA0234 SPOA0235 SPOA0236	0.85 0.94 1.06	0.843 SPOA0228 0.835 SPOA0229 0.854 SPOA0230	1.09	0.259
SPOA0242 SPOA0243	0.69 1.12	0.383 0.176	SPOA0244 SPOA0245	0.94 1.08	0.889 0.908	SPOA0241 SPOA0242	1.08 1.07	0.45 SPOA0246 0.998 SPOA0247	1.16 1.04	0.909 SI 0.246 SI	POA0236 POA0237	1.09 0.81	0.553 0.509	SPOA0235 SPOA0236	0.86 1.04	0.270 0.289	SPOA0237 SPOA0238	1.01 0.81	0.898 SPOA0231 0.309 SPOA0232	1.15	0.179 0.980
SPOA0244 SPOA0245 SPOA0246	0.97 1.2 0.81	0.478	SPOA0246 SPOA0247 SPOA0248		0.316 0.917	SPOA0244 SPOA0245	1.21 1.12 1.11	0.876 SPOA0248 0.987 SPOA0249 0.685 SPOA0250	1.36 1.15 1.2	0.234 SI	POA0238 POA0239 POA0240	0.87 1.64 1.77	0.011	SPOA0237 SPOA0238 SPOA0239	0.76 0.91 1.59	0.740 0.111	SPOA0239 SPOA0240 SPOA0241	1.04 1.15	0.283 SPOA0233 0.470 SPOA0234 0.474 SPOA0235	0.93	0.857 0.919 0.891
SPOA0247	0.79	0.432	SPOA0249	0.89	0.749	SPOA0246	1.13	0.235 SPOA0251	1.14	0.877 SI	POA0241	1.59	0.161	SPOA0240	1.65	0.034	SPOA0242	0.93	0.857 SPOA0236	1.02	0.936

SPOA0248 SPOA0249	0.77 0.84	0.502 SPOA0250 0.464 SPOA0251	0.57 0.89		SPOA0247 SPOA0248	1.31	0.629 SPOA0252 0.342 SPOA0253	1.47	0.189	SPOA0242 SPOA0243	1.32	0.585 0.708	SPOA0241 SPOA0242	1.45		SPOA0243 SPOA0244	1.09		SPOA0237 SPOA0238	1.07	0.918 0.276
SPOA0250 SPOA0251 SPOA0252	0.58 0.9 0.7	0.348 SPOA0252 0.689 SPOA0253 0.007 SPOA0254	0.75 1.09 1.07	0.882	SPOA0249 SPOA0250 SPOA0251	1.08 1.1 1.23	0.596 SPOA0254 0.559 SPOA0255 0.841 SPOA0256	1.06 1.08 1.15	0.995 0.907 0.985	SPOA0245	1.13 0.55 1.91	0.538 0.501 0.079	SPOA0244 SPOA0246	1.07 1.16 0.55	0.422	SPOA0245 SPOA0246 SPOA0247	0.60 1.21 1.19	0.274	SPOA0239 SPOA0240 SPOA0241	0.89 1.04 1.11	0.662 0.534 0.467
SPOA0253 SPOA0254	0.97 1.36	0.959 SPOA0255 0.576 SPOA0256	1.2 1.1	0.547 0.76	SPOA0252 SPOA0253	1.09 1.13	0.537 SPOA0257 0.949 SPOA0258	1.09 1.09	0.925 0.635	SPOA0247 SPOA0248	1.62 1.57	0.127 0.414	SPOA0246 SPOA0247	1.72 1.28	0.108 0.458	SPOA0248 SPOA0249	1.12	0.819 0.891	SPOA0242 SPOA0243	0.95 1.02	0.868 0.876
SPOA0255 SPOA0256 SPOA0257	0.98 1.2 0.84	0.799 SPOA0257 0.656 SPOA0258 0.812 SPOA0259	0.93 0.82 0.87		SPOA0254 SPOA0255 SPOA0256	1.17 1.12 1.71	0.99 SPOA0259 0.622 SPOA0260 0.837 SPOA0261	1.41 1.1 1.32	0.996 0.897 0.42	SPOA0249 SPOA0250 SPOA0251	1.95 1.56 1.35	0.357 0.593 0.510	SPOA0248 SPOA0249 SPOA0250	1.36 1.87		SPOA0250 SPOA0251 SPOA0252	1.07 1.06	0.749	SPOA0244 SPOA0245 SPOA0246	1.11 0.83 1.13	0.390 0.693 0.785
SPOA0258 SPOA0259	0.79 0.79	0.778 SPOA0260 0.571 SPOA0261	1.04 1.28	0.448 0.582	SPOA0257 SPOA0258	1.05 1.16	0.999 SPOA0262 0.803 SPOA0263	1.09 1.07	0.533 0.383	SPOA0252 SPOA0253	1.37 1.16	0.166 0.842	SPOA0251 SPOA0252	0.92 1.45	0.644 0.014	SPOA0253 SPOA0254	0.93 1.11	0.863 0.909	SPOA0247 SPOA0248	1.17 1.19	0.460 0.703
SPOA0260 SPOA0261 SPOA0262	0.92 1.34 1.15	0.829 SPOA0262 0.6 SPOA0263 0.079 SPOA0264	1.05 0.76 0.63	0.154	SPOA0259 SPOA0260 SPOA0261	1.01 1.09 1.15	0.649 SPOA0264 0.887 SPOA0265 0.408 SPOA0266	1.1 1.09 1.19	0.716 0.582 0.05	SPOA0254 SPOA0255 SPOA0256	1.02 2.12 1.53	0.951 0.239 0.355	SPOA0254 SPOA0255	1.15 0.92 1.87	0.746	SPOA0255 SPOA0256 SPOA0257	1.11 1.05 0.87	0.947	SPOA0249 SPOA0250 SPOA0251	1.02 1.16 0.99	0.984 0.625 0.790
SPOA0263 SPOA0264	0.85 0.64	0.263 SPOA0265 0.695 SPOA0266	0.56 0.55	0.514 0.052	SPOA0262 SPOA0263	1.05 1.07	0.664 SPOA0267 0.022 SPOA0268	1.06 1.02	0.242 0.827	SPOA0257 SPOA0258	1.34 1.17	0.737 0.686	SPOA0256 SPOA0257	1.64 1.25	0.380	SPOA0258 SPOA0259	0.93 0.96	0.910 0.857	SPOA0252 SPOA0253	1.12 1.06	0.399 0.951
SPOA0265 SPOA0266 SPOA0267	0.61 0.47 0.59	0.539 SPOA0267 0.032 SPOA0268 0.184 SPOA0269	0.74 0.85 0.9	0.791	SPOA0264 SPOA0265 SPOA0266	1.07 1.15	0.667 SPOA0269 0.653 SPOA0270 0.222 SPOA0271	1.15 1.96 1.04	0.985 0.771 0.192	SPOA0259 SPOA0260 SPOA0261	1.39 1.62 0.70	0.190 0.029 0.571	SPOA0258 SPOA0259 SPOA0260	1.07 1.29 1.62	0.209	SPOA0260 SPOA0261 SPOA0262	1.07 0.87 0.72	0.808	SPOA0254 SPOA0255 SPOA0256	0.94 1.07 0.98	0.916 0.809 0.944
SPOA0268 SPOA0269	0.74 0.85	0.531 SPOA0270 0.77 SPOA0271	1.01 0.98	0.869	SPOA0267 SPOA0268	1.12 1.14	0.293 SPOA0272 0.993 SPOA0273	1.08 1.09	0.976 0.004	SPOA0262 SPOA0263	0.85 1.64	0.292 0.148	SPOA0261 SPOA0262	0.65 1.02	0.525 0.325	SPOA0263 SPOA0264	1.14 0.95	0.149 0.957	SPOA0257 SPOA0258	0.93 1.05	0.886 0.957
SPOA0270 SPOA0271 SPOA0272	0.87 0.85 0.93	0.836 SPOA0272 0.795 SPOA0273 0.865 SPOA0274	0.9 0.84 1.02	0.875 0.026 0.817	SPOA0269 SPOA0270 SPOA0271	1.75 1 1.06	0.967 SPOA0274 0.92 SPOA0275 0.564 SPOA0276	1.56 1.26 1.19	0.864 0.856 0.405	SPOA0264 SPOA0265 SPOA0266	2.35 1.67 2.23	0.352 0.409 0.191	SPOA0263 SPOA0264 SPOA0265	1.24 1.75 1.70		SPOA0265 SPOA0266 SPOA0267	1.00 1.05 1.39	0.951	SPOA0259 SPOA0260 SPOA0261	0.94 0.96 0.85	0.767 0.834 0.803
SPOA0273 SPOA0274	0.66 0.86	0.009 SPOA0275 0.887 SPOA0276	0.88 1.02	0.822 0.763	SPOA0272 SPOA0273	1.01 1.45	0.916 SPOA0277 0.008 SPOA0278	1.4 1.02	0.856 0.814	SPOA0267 SPOA0268	2.08 0.78	0.078 0.442	SPOA0266 SPOA0267	1.51 1.99	0.104 0.146	SPOA0268 SPOA0269	0.85 0.98	0.667 0.959	SPOA0262 SPOA0263	0.97 1.05	0.771 0.637
SPOA0275 SPOA0276 SPOA0277	0.98 1 1.01	0.468 SPOA0277 0.788 SPOA0278 0.811 SPOA0279	1.07 1.2 0.54	0.653	SPOA0274 SPOA0275 SPOA0276	1.29 1.07 1.38	0.957 SPOA0279 0.733 SPOA0280 0.322 SPOA0281	1.01 1.3 1.34	0.07 0.744 0.199	SPOA0269 SPOA0270 SPOA0271	0.96 0.78 1.13	0.978 0.663 0.892	SPOA0268 SPOA0269 SPOA0270	0.74 0.91 0.63	0.867	SPOA0270 SPOA0271 SPOA0272	0.89 0.99 0.99	0.814	SPOA0264 SPOA0265 SPOA0266	1.04 1.02 1.27	0.982 0.976 0.213
SPOA0278 SPOA0279 SPOA0280	1.13 0.61 0.65	0.76 SPOA0280 0.192 SPOA0281 0.225 SPOA0282	0.66 1.38 1.23		SPOA0277 SPOA0278 SPOA0279	1.08 1.3 1.05	0.849 SPOA0282 0.723 SPOA0283 0.01 SPOA0284	1.11 1.72 1.09	0.309 0.118 0.613	SPOA0272 SPOA0273	0.70 9.13 1.11	0.645 0.000 0.866	SPOA0271 SPOA0272	0.96	0.205 0.629	SPOA0273 SPOA0274 SPOA0275	0.75 1.01 1.02	0.038 0.965	SPOA0267 SPOA0268 SPOA0269	1.21 0.93 0.93	0.570 0.784 0.868
SPOA0281 SPOA0282	1.48	0.047 SPOA0283 0.188 SPOA0284	1.14	0.307	SPOA0279 SPOA0280 SPOA0281	1.13 4.99	0.68 SPOA0285 0.232 SPOA0286	1.28	0.382	SPOA0275 SPOA0276	1.11	0.831 0.554	SPOA0274 SPOA0275	0.93 1.14		SPOA0275 SPOA0276 SPOA0277	0.77	0.123	SPOA0270 SPOA0271	0.91 0.95	0.209
SPOA0283 SPOA0284 SPOA0285	1 1.38 0.89	0.548 SPOA0285 0.332 SPOA0286 0.646 SPOA0288	0.92 0.61 0.9	0.019	SPOA0282 SPOA0283 SPOA0284	1.03 1.29 1.02	0.247 SPOA0288 0.007 SPOA0289 0.772 SPOA0290	1.16 1.44 1.13	0.96 0.206 0.92	SPOA0277 SPOA0278 SPOA0279	1.13 1.16 1.48	0.954 0.842 0.099	SPOA0276 SPOA0277	0.75 1.01 1.04	0.835	SPOA0278 SPOA0279 SPOA0280	0.97 0.84 1.05	0.670	SPOA0272 SPOA0273 SPOA0274	0.91 0.88 0.96	0.891 0.243 0.890
SPOA0286 SPOA0287	0.52 1.03	0.012 SPOA0289 0.686 SPOA0290	0.74 1.01	0.405 0.981	SPOA0285 SPOA0286	1.07	0.297 SPOA0291 0.141 SPOA0292	1.06	0.364 0.159	SPOA0280 SPOA0281	1.41	0.187	SPOA0279 SPOA0280	1.41 1.40	0.157 0.125	SPOA0281 SPOA0282	0.93	0.493 0.438	SPOA0275 SPOA0276	1.10	0.658 0.183
SPOA0288 SPOA0289 SPOA0290	0.86 0.77 1.15	0.934 SPOA0291 0.49 SPOA0292 0.856 SPOA0293	0.9 1.3 1.2	0.001	SPOA0287 SPOA0288 SPOA0289	1.09 1.03 1.17	0 SPOA0293 0.926 SPOA0294 0.222 SPOA0295	1.2 1.03 1.25	0.168 0.687 0.86	SPOA0282 SPOA0283 SPOA0284	0.60 0.73 0.76	0.127 0.017 0.557	SPOA0281 SPOA0282 SPOA0283	0.90 0.68 0.72	0.017	SPOA0283 SPOA0284 SPOA0285	0.65 0.90 0.88	0.779	SPOA0277 SPOA0278 SPOA0279	0.91 0.94 0.92	0.778 0.894 0.550
SPOA0291 SPOA0292	0.82 1.26	0.562 SPOA0294 0.023 SPOA0295	1.02 0.96	0.518 0.965	SPOA0290 SPOA0291	1.15 1.02	0.889 SPOA0296 0.698 SPOA0297	1.39 1.01	0.705 0.111	SPOA0285 SPOA0286	0.81 0.95	0.129 0.914	SPOA0284 SPOA0285	0.74 0.82	0.506	SPOA0286 SPOA0287	1.09 0.83	0.316 0.532	SPOA0280 SPOA0281	1.02 0.92	0.949 0.560
SPOA0293 SPOA0294 SPOA0295	1.16 0.99 0.88	0.055 SPOA0296 0.933 SPOA0297 0.931 SPOA0298	0.68 0.71 0.66		SPOA0292 SPOA0293 SPOA0294	1.29 1.39	0.184 SPOA0298 0.378 SPOA0299 0.482 SPOA0300	1.08 1.18 1.04	0.242 0.088 0.14	SPOA0288 SPOA0289 SPOA0290	0.78 3.99 0.67	0.835 0.176 0.832	SPOA0286 SPOA0287 SPOA0288	1.00 0.79 0.60		SPOA0288 SPOA0289 SPOA0290	0.85 1.04 0.95	0.979	SPOA0282 SPOA0283 SPOA0284	0.78 0.77 0.83	0.019 0.093 0.640
SPOA0296 SPOA0297	0.72 0.61	0.457 SPOA0299 0.268 SPOA0300	0.67 0.57	0.058 0.251	SPOA0295 SPOA0296	1.24	0.787 SPOA0301 0.538 SPOA0302	1.16	0.803 0.969	SPOA0291 SPOA0292	0.77 1.12	0.078 0.090	SPOA0289 SPOA0290	4.59 0.63	0.258 0.808	SPOA0291 SPOA0292	0.86	0.151 0.314	SPOA0285 SPOA0286	0.92 1.04	0.103
SPOA0298 SPOA0299 SPOA0300	0.59 0.6 0.58	0.254 SPOA0301 0.061 SPOA0302 0.256 SPOA0303	1.08 0.91 1.3	0.732	SPOA0297 SPOA0298 SPOA0299	1.06 1.2 1.06	0.076 SPOA0303 0.615 SPOA0304 0.322 SPOA0305	1.24 1.08 1.23	0.189 0.317 0.159	SPOA0293 SPOA0294 SPOA0295	1.40 1.33 1.15	0.009 0.054 0.881	SPOA0291 SPOA0292 SPOA0293	0.74 1.11 1.39	0.007	SPOA0293 SPOA0294 SPOA0295	1.01 1.05 1.01	0.540	SPOA0288 SPOA0289	0.73 0.83 1.09	0.126 0.862 0.925
SPOA0301 SPOA0302 SPOA0303	0.95 0.88 1.23	0.991 SPOA0304 0.426 SPOA0305 0.069 SPOA0306	0.83 1.05 1.34	0.345	SPOA0300 SPOA0301 SPOA0302	1.14 1.3 1.07	0.361 SPOA0306 0.773 SPOA0309 0.967 SPOA0310	1.08 1.03 1.21	0.266 0.61 0.581	SPOA0296 SPOA0297 SPOA0298	1.35 2.41 1.92	0.688 0.091 0.071	SPOA0294 SPOA0295	1.32 1.20 1.25		SPOA0296 SPOA0297 SPOA0298	0.97 1.06 1.27	0.902	SPOA0290 SPOA0291 SPOA0292	0.91 0.91 0.95	0.947 0.660 0.163
SPOA0304 SPOA0305	0.81 1.06	0.137 SPOA0309 0.764 SPOA0310	0.81	0.433	SPOA0303 SPOA0304	1.34	0.316 SPOA0311 0.156 SPOA0312	1.35	0.842	SPOA0299 SPOA0300	1.36	0.221	SPOA0297 SPOA0298	1.88	0.042	SPOA0298 SPOA0299 SPOA0300	1.06	0.911	SPOA0293	1.05	0.694
SPOA0306 SPOA0309 SPOA0310	1.43 0.72 0.65	0.09 SPOA0311 0.596 SPOA0312 0.08 SPOA0313	0.92 1.1 1.02		SPOA0305 SPOA0306 SPOA0309	1.09 1.32 1.1	0.44 SPOA0313 0.8 SPOA0314 0.995 SPOA0315	1.17 1.09 1.25	0.194 0.97 0.133	SPOA0301 SPOA0302 SPOA0303	1.18 1.29 0.81	0.167 0.439 0.083	SPOA0300 SPOA0301	1.48 2.02 1.17		SPOA0301 SPOA0302 SPOA0303	0.93 1.10 0.80	0.664	SPOA0295 SPOA0296 SPOA0297	1.20 1.02 1.01	0.788 0.973 0.961
SPOA0311 SPOA0312	0.9 1.08	0.944 SPOA0314 0.77 SPOA0315	1.04 1.89	0.748 0.029	SPOA0310 SPOA0311	1.18 1.1	0.818 SPOA0316 0.911 SPOA0317	1.18 1.06	0.377 0.886	SPOA0304 SPOA0305	1.55 1.52	0.040 0.040	SPOA0302 SPOA0303	1.16 0.87	0.771 0.426	SPOA0304 SPOA0305	0.86 1.10	0.460	SPOA0298 SPOA0299	1.17 0.96	0.640 0.856
SPOA0313 SPOA0314 SPOA0315	0.84 0.98	0.813 SPOA0316 0.68 SPOA0317 0.128 SPOA0318	0.6 0.88 0.85	0.849	SPOA0312 SPOA0313 SPOA0314	1.21 1.25 1.31	0.197 SPOA0318 0.444 SPOA0319 0.91 SPOA0320	1.49 1.34 1.09	0.946 0.953 0.485	SPOA0306 SPOA0309 SPOA0310	1.17 1.53	0.181 0.227 0.088	SPOA0304 SPOA0305 SPOA0306	1.75 1.52 1.27	0.023	SPOA0306 SPOA0309 SPOA0310	1.16 0.94 1.11	0.853	SPOA0300 SPOA0301 SPOA0302	1.01 0.90 1.06	0.985 0.540 0.801
SPOA0316 SPOA0317	0.56 0.82	0.102 SPOA0319 0.561 SPOA0320	1.01 0.95	0.927 0.923	SPOA0315 SPOA0316	1.26 1.13	0.322 SPOA0321 0.826 SPOA0322	1.22 1.17	0.099 0.353	SPOA0311 SPOA0312	1.16 0.74	0.812 0.340	SPOA0309 SPOA0310	1.53 1.54	0.046 0.047	SPOA0311 SPOA0312	0.80 0.81	0.377 0.690	SPOA0303 SPOA0304	0.70 0.91	0.231 0.115
SPOA0318 SPOA0319 SPOA0320	0.74 1.02 0.91	0.876 SPOA0321 0.926 SPOA0322 0.867 SPOA0323	0.99 1.88 0.96	0.657 0.011 0.992	SPOA0317 SPOA0318 SPOA0319	1.24 1.05 1.31	0.583 SPOA0323 0.901 SPOA0324 0.946 SPOA0325	1.4 1.11 1.39	0.736 0.915 0.584	SPOA0313 SPOA0314 SPOA0315	1.07 1.01 0.22	0.931 0.934 0.043	SPOA0311 SPOA0312 SPOA0313	1.16 0.66 0.87	0.207	SPOA0313 SPOA0314 SPOA0315	0.78 0.98 1.27	0.786	SPOA0305 SPOA0306 SPOA0309	1.02 1.12 1.00	0.815 0.659 0.941
SPOA0321 SPOA0322	0.92 2.29	0.902 SPOA0324 0.002 SPOA0325	1.06 0.78	0.315	SPOA0320 SPOA0321	1.27	0.856 SPOA0326 0.201 SPOA0327	1.26	0.156	SPOA0316 SPOA0317	0.65 1.19	0.148	SPOA0314 SPOA0315	0.99	0.686	SPOA0316 SPOA0317	0.91	0.719	SPOA0310 SPOA0311	1.22	0.188
SPOA0323 SPOA0324 SPOA0325	0.94 1.13 0.67	0.956 SPOA0326 0.475 SPOA0327 0.43 SPOA0328	1.14 1.01 1.04	0.145 0.954 0.551	SPOA0322 SPOA0323 SPOA0324	1.56 1.06 1.11	0.502 SPOA0328 0.804 SPOA0329 0.585 SPOA0330	1.14 1.01 1.14	0.865 0.858 0.131	SPOA0318 SPOA0319 SPOA0320	0.65 0.72 0.80	0.792 0.541 0.507	SPOA0316 SPOA0317 SPOA0318	0.68 1.09 0.60	0.032 5 0.755 5 0.766 5	SPOA0318 SPOA0319 SPOA0320	0.93 0.98 0.68	0.944	SPOA0312 SPOA0313 SPOA0314	0.85 0.92 1.08	0.664 0.545 0.663
SPOA0326 SPOA0327 SPOA0328	1.18 0.99 1.19	0.296 SPOA0329 0.99 SPOA0330 0.476 SPOA0331	0.98 0.65 0.88		SPOA0325 SPOA0326 SPOA0327	1.11 1.22 1.03	0.846 SPOA0331 0.23 SPOA0332 0.688 SPOA0333	1.6 1.06	0.792 0.802 0.971	SPOA0321 SPOA0322	0.13 0.93 1.53	0.005 0.668 0.544	SPOA0319 SPOA0320	0.74 0.76	0.569 S 0.005 S 0.001 S	SPOA0321 SPOA0322 SPOA0323	1.10 1.02 0.93	0.970	SPOA0315 SPOA0316 SPOA0317	1.22 0.97 0.97	0.605 0.906 0.906
SPOA0329 SPOA0330	0.91 0.73	0.884 SPOA0332 0.408 SPOA0333	1.02 0.87	0.425 0.966	SPOA0328 SPOA0329	1.05 1.05	0.947 SPOA0334 0.639 SPOA0335	1.03 1.26	0.826 0.121	SPOA0324 SPOA0325	0.92 0.83	0.886 0.130	SPOA0322 SPOA0323	1.00	0.982 0.547	SPOA0324 SPOA0325	0.89 0.85	0.666 0.208	SPOA0318 SPOA0319	0.93 1.06	0.963 0.908
SPOA0331 SPOA0332 SPOA0333	0.73 1.05 1.01	0.643 SPOA0334 0.611 SPOA0335 0.976 SPOA0336	1.13 0.97 0.67	0.462 0.945 0.453	SPOA0330 SPOA0331 SPOA0332	1.13 1.01 1.35	0.179 SPOA0336 0.775 SPOA0337 0.986 SPOA0338	1.02 1.51 1.07	0.76 0.149 0.531	SPOA0326 SPOA0327 SPOA0328	0.70 1.00 1.90	0.030 0.929 0.014	SPOA0324 SPOA0325 SPOA0326	1.03 0.87 0.71	0.526 5 0.718 5 0.024 5	SPOA0326 SPOA0327 SPOA0328	0.92 0.79 0.98		SPOA0320 SPOA0321 SPOA0322	0.88 0.81 0.98	0.621 0.252 0.642
SPOA0334 SPOA0335	1.1 0.99	0.53 SPOA0337 0.892 SPOA0338	0.44 0.52		SPOA0333 SPOA0334		0.98 SPOA0339 0.465 SPOA0340 0.205 SPOA0341	1.09 1.22	0.281 0.03	SPOA0329 SPOA0330	1.02 1.22	0.933 0.369	SPOA0327 SPOA0328	0.97 1.97	0.010	SPOA0329 SPOA0330	1.18	0.624	SPOA0323 SPOA0324	0.93 0.88	0.920
SPOA0336 SPOA0337 SPOA0338	0.64 0.43 0.44	0.355 SPOA0339 0.007 SPOA0340 0.229 SPOA0341	0.08 0.08 0.05		SPOA0335 SPOA0336 SPOA0337	1.05 1.09 1.18	0.205 SPOA0341 0.557 SPOA0342 0.735 SPOA0343	1.06 1.38	0.029 0.848 0.385	SPOA0331 SPOA0332 SPOA0333	1.06 0.74 0.48	0.981 0.307 0.712	SPOA0329 SPOA0330 SPOA0331	1.07 1.11 1.19	0.716	SPOA0331 SPOA0332 SPOA0333	0.92 1.12 0.94	0.825	SPOA0325 SPOA0326 SPOA0327	0.91 0.84 0.81	0.582 0.057 0.679
SPOA0339 SPOA0340 SPOA0341	0.09 0.1 0.05	0.004 SPOA0342 0.029 SPOA0343 0 SPOA0344	0.08 0.06 1.45		SPOA0338 SPOA0339 SPOA0340	1.35 1.04 1.18	0.733 SPOA0344 0.389 SPOA0345 0.058 SPOA0346	1.08 1.16 1.32	0.27 0.77 0.215	SPOA0334 SPOA0335 SPOA0336	0.49 0.91 1.63	0.071 0.559 0.343	SPOA0332 SPOA0333 SPOA0334	0.77 0.44 0.58	0.690	SPOA0334 SPOA0335 SPOA0336	1.10 1.09 0.87	0.768	SPOA0328 SPOA0329 SPOA0330	1.07 1.09 1.29	0.806 0.896 0.168
SPOA0342 SPOA0343	0.09	0.012 SPOA0345 0.002 SPOA0346	0.13 0.14	0.006	SPOA0341 SPOA0342	1.37 1.21	0.132 SPOA0347 0.638 SPOA0348	1.17 1.34	0.681 0.024	SPOA0337 SPOA0338	1.62 3.54	0.037 0.025	SPOA0335 SPOA0336	0.94 1.66	0.738	SPOA0337 SPOA0338	1.11 2.25	0.660 0.347	SPOA0331 SPOA0332	1.12 1.04	0.871 0.951
SPOA0344 SPOA0345 SPOA0346	0.15 0.16	0.065 SPOA0347 0.013 SPOA0348 0.005 SPOA0349	0.2 0.3 2.15	0.003 0.006 0.011	SPOA0343 SPOA0344 SPOA0345	1.36 1.13 1.1	0.704 SPOA0349 0.234 SPOA0350 0.905 SPOA0351	1.26 1.09 1.07	0.017 0.087 0.949	SPOA0339 SPOA0340 SPOA0341	202.00 142.00 129.00	0.001 0.001 0.001	SPOA0337 SPOA0338 SPOA0339	1.61 4.15	0.021	SPOA0339 SPOA0340 SPOA0341	0.94 0.86 0.96	0.275	SPOA0333 SPOA0334 SPOA0335	0.86 1.18 1.13	0.927 0.506 0.505
SPOA0347 SPOA0348	0.23	0.001 SPOA0350 0.01 SPOA0351	1.14 0.83	0.059 0.83	SPOA0346 SPOA0347	1.25 1.11	0.34 SPOA0352 0.493 SPOA0353	1.17 1.08	0.815 0.286	SPOA0342 SPOA0343	44.10 88.80	0.002	SPOA0340 SPOA0341	109.00 164.00	0.002 0.001	SPOA0342 SPOA0343	1.03 0.93	0.805 0.831	SPOA0336 SPOA0337	0.93 1.26	0.915 0.062
SPOA0349 SPOA0350 SPOA0351	0.99 0.77	0.172 SPOA0352 0.833 SPOA0353 0.231 SPOA0354	0.98 0.82 0.93	0.119 0.826	SPOA0348 SPOA0349 SPOA0350	1.21 1.06 1.07	0.018 SPOA0354 0.478 SPOA0355 0.035 SPOA0356	1.07 1.03 1.23	0.097 0.608 0.144	SPOA0344 SPOA0345 SPOA0346	74.80 89.70	0.094 0.000 0.001	SPOA0342 SPOA0343 SPOA0344	47.40 86.50 1.19	0.001	SPOA0344 SPOA0345 SPOA0346	1.00 0.97 0.87	0.892	SPOA0338 SPOA0339 SPOA0340	1.26 0.96 0.78	0.488 0.965 0.047
SPOA0352 SPOA0353 SPOA0354	0.89 0.72 0.88	0.704 SPOA0355 0.126 SPOA0356 0.561 SPOA0357	0.85 1.11 1.01	0.381 0.135	SPOA0351 SPOA0352 SPOA0353	1.02 1.11 1.2	0.819 SPOA0357 0.93 SPOA0358 0.585 SPOA0359	1.27 1.24 1.54	0.733 0.313 0.09	SPOA0347 SPOA0348 SPOA0349	23.10 10.90 0.63	0.009 0.001 0.285	SPOA0345 SPOA0346 SPOA0347	79.80 91.20	0.000 S	SPOA0347 SPOA0348 SPOA0349	1.10 0.91 1.67	0.690 0.517	SPOA0341 SPOA0342 SPOA0343	0.94 1.09 0.92	0.794 0.775 0.548
SPOA0355 SPOA0356	0.93 1.25	0.891 SPOA0358 0.109 SPOA0359	1.19 1.1	0.066	SPOA0354 SPOA0355	1.05 1.09	0.384 SPOA0360 0.21 SPOA0361	1.37	0.1 0.566	SPOA0350 SPOA0351	0.79 0.43	0.197 0.075	SPOA0348 SPOA0349	10.40	0.000	SPOA0350 SPOA0351	0.77	0.368	SPOA0344 SPOA0345	1.03 0.97	0.813 0.855
SPOA0357 SPOA0358 SPOA0359	0.95 1.04 1.02	0.882 SPOA0360 0.526 SPOA0361 0.304 SPOA0362	0.87 0.97 0.96	0.692	SPOA0356 SPOA0357 SPOA0358	1.27 1.27 1.01	0.597 SPOA0362 0.718 SPOA0363 0.267 SPOA0364	1.12 1.43 1.1	0.969 0.96 0.628	SPOA0352 SPOA0353 SPOA0354	0.67 1.49 0.69	0.184 0.180 0.085	SPOA0350 SPOA0351 SPOA0352	0.62 0.39 0.69	0.195	SPOA0352 SPOA0353 SPOA0354	0.91 0.86 0.95	0.466	SPOA0346 SPOA0347 SPOA0348	0.80 1.02 0.93	0.156 0.414 0.660
SPOA0360 SPOA0361	0.81 0.87	0.624 SPOA0363 0.616 SPOA0364	1.16 0.82	0.284 0.332	SPOA0359 SPOA0360	1.13 1.06	0.331 SPOA0365 0.826 SPOA0366	1.02	0.328 0.99	SPOA0355 SPOA0356	0.82 0.87	0.084 0.296	SPOA0353 SPOA0354	1.52 0.65	0.029 0.035	SPOA0355 SPOA0356	0.88 0.97	0.208 0.778	SPOA0349 SPOA0350	1.46	0.014 0.881
SPOA0362 SPOA0363 SPOA0364	0.9 1.21 0.75	0.932 SPOA0365 0.465 SPOA0366 0.053 SPOA0368	1.14 1.05 0.74	0.917	SPOA0361 SPOA0362 SPOA0363	1.3 1.05 1.14	0.542 SPOA0368 0.967 SPOA0369 0.486 SPOA0370	1.17 1.23 1.03	0.028 0.405 0.693	SPOA0357 SPOA0358 SPOA0359	0.61 1.02 0.33	0.142 0.998 0.005	SPOA0355 SPOA0356 SPOA0357	0.86 1.00 0.61	0.680	SPOA0357 SPOA0358 SPOA0359	0.92 1.03 1.06	0.954	SPOA0351 SPOA0352 SPOA0353	0.55 0.96 1.02	0.334 0.860 0.949
SPOA0365 SPOA0366 SPOA0367	1.1 1.06 1.11	0.445 SPOA0369 0.935 SPOA0370 0 SPOA0371	0.81 0.93 1.27	0.997	SPOA0364 SPOA0365 SPOA0366	1.03 1.19 1.29	0.906 SPOA0371 0.398 SPOA0372 0.936 SPOA0373	1.06 1.02 1.07	0.647 0.911 0.718	SPOA0360 SPOA0361 SPOA0362	0.55 0.52	0.148 0.002 0.482	SPOA0358 SPOA0359 SPOA0360	0.99 0.34 0.54	0.006	SPOA0360 SPOA0361 SPOA0362	0.88 1.11 0.99	0.710	SPOA0354 SPOA0355 SPOA0356	0.94 0.85 0.93	0.184 0.326 0.433
SPOA0368 SPOA0369	0.65 0.65	0.023 SPOA0372 0.119 SPOA0373	1.07 0.88	0.899	SPOA0367 SPOA0368	1.01	0.523 SPOA0374 0.02 SPOA0375	1.04 1.19	0.951	SPOA0362 SPOA0363 SPOA0364	0.44 0.79 0.64	0.278 0.021	SPOA0360 SPOA0361 SPOA0362	0.55 0.44	0.010	SPOA0363 SPOA0364	1.07	0.896 0.586	SPOA0357 SPOA0358	0.90 0.93	0.425 0.529
SPOA0370 SPOA0371 SPOA0372	0.85 1.42 0.88	0.865 SPOA0374 0.473 SPOA0375 0.961 SPOA0376	0.74 0.97 0.87	0.909	SPOA0369 SPOA0370 SPOA0371	1.1 1.05 1.15	0.918 SPOA0376 0.943 SPOA0377 0.571 SPOA0378	1.33 1.15 1.37	0.21 0.608 0.406	SPOA0365 SPOA0366 SPOA0367	0.57 1.01 1.01	0.245 0.974	SPOA0363 SPOA0364 SPOA0365	0.75 0.66		SPOA0365 SPOA0366 SPOA0368	0.64 0.84 1.08	0.864	SPOA0359 SPOA0360 SPOA0361	1.00 0.94 1.24	0.841 0.814 0.303
SPOA0373 SPOA0374	0.96 0.91	0.918 SPOA0377 0.864 SPOA0378	1.01 1.12	0.758 0.205	SPOA0372 SPOA0373	1.23 1.21	0.932 SPOA0379 0.65 SPOA0380	1.03 1.12	0.144 0.876	SPOA0368 SPOA0369	1.64 0.68	0.015 0.143	SPOA0366 SPOA0367	0.92 1.03	0.902	SPOA0369 SPOA0370	1.02 0.93	0.993 0.784	SPOA0362 SPOA0363	0.99 1.02	0.894 0.992
SPOA0375 SPOA0376 SPOA0377	1.07 0.9 1.05	0.803 SPOA0379 0.907 SPOA0380 0.769 SPOA0381	1.22 0.93 0.94	0.967	SPOA0374 SPOA0375 SPOA0376	1.11 1.13	0.883 SPOA0381 0.464 SPOA0382 0.979 SPOA0383	0.99 1.18 1.17	0.834 0.993 0.915	SPOA0370 SPOA0371 SPOA0372	0.71 0.55 0.68	0.476 0.277 0.763	SPOA0368 SPOA0369 SPOA0370	1.59 0.61 0.77	0.252	SPOA0371 SPOA0372 SPOA0373	0.91 0.85 0.80	0.906	SPOA0364 SPOA0365 SPOA0366	1.13 0.83 1.01	0.611 0.648 0.989
SPOA0378 SPOA0379	1.39 1.34 0.85	0.368 SPOA0382 0.049 SPOA0383 0.611 SPOA0384	1.15 0.98	0.83 0.976	SPOA0377 SPOA0378	0.99	0.637 SPOA0384 0.427 SPOA0385 0.131 SPOA0386	1.28 1.38	0.69 0.953		0.90 1.00	0.195 0.554	SPOA0371 SPOA0372 SPOA0373	0.53 0.57	0.266 0.715	SPOA0374 SPOA0375 SPOA0376	1.07 0.87	0.909 0.783	SPOA0368 SPOA0369 SPOA0370	1.13 1.12	0.260 0.130
SPOA0380 SPOA0381 SPOA0382	0.85 1.07 1.16	0.611 SPOA0384 0.573 SPOA0385 0.81 SPOA0386	1.01 0.91 0.99	0.978	SPOA0379 SPOA0380 SPOA0381	1.14 1.18 1.41	0.131 SPOA0386 0.794 SPOA0387 0.913 SPOA0388	1.03 1.04 1.06	0.875 0.71 0.659	SPOA0375 SPOA0376 SPOA0377	0.63 0.85 0.92	0.372 0.431 0.722	SPOA0373 SPOA0374 SPOA0375	0.78 1.31 0.60	0.466	SPOA0376 SPOA0377 SPOA0378	0.93 0.81 0.79	0.500	SPOA0370 SPOA0371 SPOA0372	0.86 0.92 0.90	0.750 0.880 0.933
SPOA0383 SPOA0384 SPOA0385	0.93 0.99 0.88	0.972 SPOA0387 0.982 SPOA0388 0.947 SPOA0389	1.07 1.01 1.14	0.956	SPOA0382 SPOA0383 SPOA0384	1.3 1 1.06	0.921 SPOA0389 0.948 SPOA0390 0.844 SPOA0391	1.1 1.17 1.13	0.084 0.764 0.75	SPOA0378 SPOA0379 SPOA0380	0.78 1.07 1.19	0.121 0.678 0.570	SPOA0376 SPOA0377 SPOA0378	0.87 0.92 0.68	0.721	SPOA0379 SPOA0380 SPOA0381	1.00 0.89 1.02	0.745	SPOA0373 SPOA0374 SPOA0375	0.78 0.83 0.87	0.369 0.557 0.777
SPOA0386 SPOA0387	1.13 1.03	0.786 SPOA0390 0.9 SPOA0391	0.88 0.99	0.7	SPOA0385 SPOA0386	1.26 1.08	0.961 SPOA0392 0.855 SPOA0393	1.21 1.26	0.002	SPOA0381 SPOA0382	1.85 0.83	0.077 0.785	SPOA0379 SPOA0380	0.68 0.99 1.05	0.683 0.844	SPOA0382 SPOA0383	0.88	0.818 0.885	SPOA0376 SPOA0377	0.86 0.82	0.801 0.630
SPOA0388	0.86	0.585 SPOA0392	6.43	0.009	SPOA0387	1.07	0.621 SPOA0394	1.03	0.059	SPOA0383	1.05	0.947	SPOA0381	2.01	0.046	SPOA0384	0.85	0.737	SPOA0378	0.90	0.586

SPOA0389	1.15		SPOA0393	4.83		SPOA0388	1.13		SPOA0395	1.52	0.006	SPOA0384	0.80	0.683	SPOA0382	0.76		SPOA0385	0.87	0.899 SPOA0379	0.87	0.488
SPOA0390 SPOA0391	0.85	0.224		2.32		SPOA0389 SPOA0390	1.21	0.122	SPOA0396 SPOA0397	1.25	0.004	SPOA0385 SPOA0386	1.10 0.93	0.952	SPOA0383 SPOA0384	0.98		SPOA0386 SPOA0387	0.91	0.847 SPOA0380 0.935 SPOA0381	0.98 1.05	0.949
SPOA0391 SPOA0392	7.47	0.932	SPOA0395 SPOA0396	3.5 5.76	0.036	SPOA0390	1.02	0.789	SPOA0397	1.25	0.08	SPOA0386	1.59	0.841	SPOA0384	1.09		SPOA0388	0.98	0.935 SPOA0381 0.165 SPOA0382	0.88	0.731
SPOA0393	6		SPOA0397	4.06		SPOA0392	1.11	0.703	SPOA0399	1.20	0.003	SPOA0388	0.62	0.379	SPOA0386	0.87		SPOA0389	0.99	0.948 SPOA0383	0.00	0.022
SPOA0394	1.87		SPOA0398	6.03	0.003	SPOA0393	1.07	0.042	SPOA0400	1.11	0.264	SPOA0389	0.58	0.018	SPOA0387	1.49	0.367	SPOA0390	0.92	0.745 SPOA0384	0.90	0.853
SPOA0395	3.53	0.077	SPOA0399	8.53		SPOA0394	1.28		SPOA0401	1.41	0.955	SPOA0390	1.05	0.626	SPOA0388	0.49		SPOA0391	0.78	0.718 SPOA0385	1.04	0.978
SPOA0396	5.69	0.001	SPOA0400	0.99		SPOA0395	1.02		SPOA0402	1.13	0.793		0.66	0.498	SPOA0389	0.64		SPOA0392	0.10	0.007 SPOA0386	0.92	0.877
SPOA0397	5.29		SPOA0401	0.85		SPOA0396	1.25	0.004	SPOA0403	1.21	0.954	0. 0	0.56	0.012	SPOA0390	0.99		SPOA0393	0.11	0.023 SPOA0387	1.03	0.968
SPOA0398 SPOA0399	6.09	0.007	SPOA0402 SPOA0403	0.85		SPOA0397 SPOA0398	1.08	0.062	SPOA0404 SPOA0405	1.15	0.53	SPOA0393 SPOA0394	0.49	0.172	SPOA0391 SPOA0392	0.69		SPOA0394 SPOA0395	0.81	0.266 SPOA0388 0.031 SPOA0389	0.62	0.471
SPOA0400	1.05		SPOA0404	0.55		SPOA0399	1.28	0.002	SPOA0406	1.23	0.552		0.69	0.347	SPOA0392	0.54		SPOA0396	0.12	0.000 SPOA0390	0.99	0.983
SPOA0401	0.79	0.068	SPOA0405	0.95	0.988	SPOA0400	1.21	0.47	SPOA0407	1	0.961	SPOA0396	0.63	0.221	SPOA0394	0.71	0.122	SPOA0397	0.15	0.057 SPOA0391	0.79	0.736
SPOA0402	0.83	0.661	SPOA0406	0.82	0.076	SPOA0401	1.13	0.921	SPOA0408	1.08	0.876	SPOA0397	0.83	0.236	SPOA0395	0.65	0.377	SPOA0398	0.08	0.001 SPOA0392	0.13	0.005
SPOA0403	0.88	0.926		0.97		SPOA0402	1.2	0.773	SPOA0409	1.18	0.712	SPOA0398	0.38	0.032	SPOA0396	0.78		SPOA0399	0.06	0.002 SPOA0393	0.15	0.007
SPOA0404	0.73	0.02	SPOA0408	1		SPOA0403	1.12	0.906	SPOA0410	1.07	0.033	SPOA0399	0.30	0.007	SPOA0397	1.51		SPOA0400	0.84	0.195 SPOA0394	0.85	0.262
SPOA0405 SPOA0406	1.01	0.979		1.02	0.838	SPOA0404 SPOA0405	1.01	0.96	SPOA0411 SPOA0412	1.05 1.19	0.058		0.97 1.17	0.982	SPOA0398 SPOA0399	0.42		SPOA0401 SPOA0402	1.00 0.90	0.970 SPOA0395 0.680 SPOA0396	0.12	0.014
SPOA0408	0.93	0.597	SPOA0410	0.48		SPOA0405	1.05	0.962	SPOA0412	1.41	0.876	SPOA0401	1.17	0.488	SPOA0400	1.07		SPOA0402 SPOA0403	0.83	0.797 SPOA0397	0.09	0.055
SPOA0408	1.02	0.597	SPOA0412	0.71	0.261	SPOA0407	1.04	0.7	SPOA0414	1.15	0.464	SPOA0403	1.02	0.982	SPOA0401	1.22		SPOA0404	0.85	0.140 SPOA0398	0.09	0.001
SPOA0409	1.01	0.816		0.67		SPOA0408	1.09	0.994	SPOA0415	1.08	0.987	SPOA0404	1.30	0.008	SPOA0402	1.18		SPOA0405	0.85	0.905 SPOA0399	0.07	0.000
SPOA0410	0.38	0.003	SPOA0414	1.08		SPOA0409	1.21	0.692	SPOA0416	7.41	0.199	SPOA0405	0.69	0.840	SPOA0403	0.96		SPOA0406	0.93	0.756 SPOA0400	0.87	0.242
SPOA0411	0.41	0.046	SPOA0415	1.08		SPOA0410	1.23	0.008	SPOA0417	5.97	0.269	SPOA0406 SPOA0407	1.30	0.502	SPOA0404 SPOA0405	1.11		SPOA0407	0.81	0.546 SPOA0401	0.99	0.971
SPOA0412 SPOA0413	0.77	0.151		1.09		SPOA0411 SPOA0412	1.13	0.024	SPOA0418 SPOA0419	2.34 6.70	0.325	SPOA0407 SPOA0408	0.88 1.04	0.479	SPOA0405 SPOA0406	0.75 1.31		SPOA0408 SPOA0409	0.80	0.680 SPOA0402 0.461 SPOA0403	0.91	0.768
SPOA0414	1.12	0.58		1.05		SPOA0413	1.09	0.958	SPOA0420	10.2	0.346	SPOA0409	0.90	0.764	SPOA0407	0.85		SPOA0410	0.07	0.624 SPOA0404	0.92	0.335
SPOA0415	1.27	0.374		0.78		SPOA0414	8	0.55	SPOA0421	4.08	0.871	SPOA0410	2.71	0.009	SPOA0408	1.20		SPOA0411	3.90	0.044 SPOA0405	0.84	0.862
SPOA0416	0.97	0.843	SPOA0420	0.86		SPOA0415	6.01	0.94	SPOA0422	11.3	0.245	SPOA0411	1.51	0.076	SPOA0409	0.83		SPOA0412	0.98	0.911 SPOA0406	0.93	0.796
SPOA0417	1.3	0.222	SPOA0421	0.74		SPOA0416	1.84	0.407	SPOA0423	15.8	0.401	SPOA0412	2.00	0.039	SPOA0410	2.35		SPOA0413	0.83	0.488 SPOA0407	0.91	0.703
SPOA0418 SPOA0419	1.07	0.643	SPOA0422 SPOA0423	0.69		SPOA0417 SPOA0418	4.44	0.095	SPOA0424 SPOA0425	1.13	0.618	SPOA0413 SPOA0414	1.45	0.414	SPOA0411 SPOA0412	1.32		SPOA0414 SPOA0415	0.88	0.703 SPOA0408 0.729 SPOA0409	1.06	0.922
SPOA0419 SPOA0420	0.68	0.102		0.88		SPOA0418	7.13 5.20	0.252	SPOA0425	1.03	0.876	SPOA0414	1.26	0.225	SPOA0412 SPOA0413	1.49		SPOA0416	0.91	0.729 SPOA0409 0.265 SPOA0410	1.10	0.703
SPOA0421	0.65	0.103		0.76		SPOA0420	11.5	0.033	SPOA0427	1.25	0.219		1.27	0.087	SPOA0414	1.17		SPOA0417	0.90	0.490 SPOA0411	3.12	0.051
SPOA0422	0.64	0.009	SPOA0426	1.37	0.011	SPOA0421	16.5	0.407	SPOA0428	1.02	0.95	SPOA0417	0.90	0.482	SPOA0415	1.56		SPOA0418	1.09	0.723 SPOA0412	1.08	0.463
SPOA0423	0.83	0.129		1.08		SPOA0422	1.06	0.413	SPOA0429	1.08	0.407	SPOA0418	1.45	0.220	SPOA0416	1.23		SPOA0419	1.14	0.285 SPOA0413	0.85	0.653
SPOA0424	0.74	0.347	0. 00.0	0.68		SPOA0423	1.01	0.158	SPOA0430	1.2	0.076		1.02	0.979	SPOA0417	0.94		SPOA0420	0.85	0.068 SPOA0414	0.84	0.443
SPOA0425 SPOA0426	0.96	0.907	SPOA0429 SPOA0430	1.17 0.76	0.292	SPOA0424 SPOA0425	1.02	0.683	SPOA0431 SPOA0432	1.12	0.005	SPOA0420 SPOA0421	0.64 1.20	0.039	SPOA0418 SPOA0419	1.49		SPOA0421 SPOA0422	0.81	0.422 SPOA0415 0.343 SPOA0416	0.97	0.963
SPOA0426	1.13	0.695		1.94		SPOA0426	1.04	0.091	SPOA0433	1.07	0.253	SPOA0421	1.30	0.606	SPOA0419	0.63		SPOA0422	0.81	0.124 SPOA0417	0.98	0.874
SPOA0428	0.63	0.099		1.38		SPOA0427	1.04	0.699	SPOA0434	1.2	0.458		0.75	0.065	SPOA0421	1.03		SPOA0424	1.10	0.830 SPOA0418	1.05	0.855
SPOA0429	1.53	0	SPOA0433	0.78		SPOA0428	1.21	0.673	SPOA0435	1.02	0.093	SPOA0424	0.93	0.373	SPOA0422	1.45		SPOA0425	0.70	0.143 SPOA0419	1.04	0.899
SPOA0430	0.71	0.062		1.09		SPOA0429	1.1	0	SPOA0436	1.16	0.918	0. 0. 10 100	0.65	0.191	SPOA0423	0.85		SPOA0426	1.02	0.992 SPOA0420	0.83	0.055
SPOA0431	1.39	0.018	SPOA0435 SPOA0436	0.9		SPOA0430 SPOA0431	1.13 1.19	0.894	SPOA0437 SPOA0438	1.13	0.889	SPOA0426 SPOA0427	1.07	0.727	SPOA0424 SPOA0425	1.05		SPOA0427 SPOA0428	1.00	0.653 SPOA0421 0.160 SPOA0422	1.00	0.706
SPOA0432	0.7	0.092	SPOA0436	0.83		SPOA0431	1.19	0.011	SPOA0438	1.09	0.400		1.04	0.171	SPOA0426	1.06		SPOA0428	0.88	0.038 SPOA0423	0.83	0.513
SPOA0434	1.1	0.437	SPOA0438	0.88	0.3	SPOA0433	1.18	0.605	SPOA0440	1.13	0.73	SPOA0429	1.01	0.440	SPOA0427	0.76		SPOA0431	0.77	0.007 SPOA0424	1.02	0.980
SPOA0435	0.92	0.851	SPOA0439	1.09	0.305	SPOA0434	1.1	0.518	SPOA0441	1.12	0.857	SPOA0430	0.90	0.557	SPOA0428	0.99	0.822	SPOA0432	1.08	0.077 SPOA0425	0.69	0.184
SPOA0436	0.68	0.16	SPOA0440	1.1	0.16	SPOA0435	1.1	0.482	SPOA0442	1.07	0.109	0. 0.10.10.	0.51	0.029	SPOA0429	0.99		SPOA0433	1.04	0.785 SPOA0426	1.00	0.965
SPOA0437 SPOA0438	0.79	0.136	SPOA0441	0.77	0.904	SPOA0436 SPOA0437	1.16	0.919	SPOA0443	0.99	0.018	SPOA0432 SPOA0433	0.91	0.902	SPOA0430 SPOA0431	0.93		SPOA0434 SPOA0435	1.00	0.707 SPOA0427 0.919 SPOA0428	0.98	0.983
SPOA0438	1.01	0.853	SPOA0442 SPOA0443	0.52 0.75	0.035	SPOA0437	1.11	0.881	SPOA0444	1.08	0.495	SPOA0433	0.94 0.61	0.783	SPOA0431	0.53		SPOA0435	1.03	0.919 SPOA0428 0.315 SPOA0429	0.88	0.474
SPOA0440	1.06	0.763	SPOA0444	1.14	0.209	SPOA0439	1.07	0.207	SPOA0446	1.06	0.682	SPOA0435	0.79	0.396	SPOA0432	0.90		SPOA0437	1.03	0.644 SPOA0430	0.78	0.069
SPOA0441	0.68	0.797	SPOA0445	1.17	0.249	SPOA0440	1.11	0.865	SPOA0447	1.52	0.97	SPOA0436	0.66	0.613	SPOA0434	0.57	0.117	SPOA0438	1.09	0.551 SPOA0431	0.81	0.072
SPOA0442	0.51	0.025	SPOA0446	1.03	0.707	SPOA0441	1.16	0.848	SPOA0448	1.16	0.914		0.93	0.909	SPOA0435	0.81		SPOA0439	0.96	0.956 SPOA0432	1.03	0.564
SPOA0444	0.73	0.058	SPOA0448	0.93	0.987	SPOA0442	0.99	0.049	SPOA0449 SPOA0450	1.06	0.203	SPOA0438	1.54	0.009	SPOA0436	0.55		SPOA0440	0.89	0.849 SPOA0433 0.968 SPOA0434	0.97	0.985
SPOA0444 SPOA0445	1.11	0.415	SPOA0448	0.93		SPOA0443 SPOA0444	1.03	0.095	SPOA0450 SPOA0451	1.15	0.663	0.07000	0.61	0.079	SPOA0437 SPOA0438	0.89 1.63		SPOA0441 SPOA0442	0.94 1.27	0.968 SPOA0434 0.204 SPOA0435	1.04	0.609
SPOA0446	0.98	0.922	SPOA0450	1.29		SPOA0445	1.07	0.083	SPOA0452	1.17	0.167		2.68	0.485	SPOA0439	0.62		SPOA0443	0.16	0.002 SPOA0436	0.92	0.813
SPOA0447	0.8	0.902	SPOA0451	0.79	0.078	SPOA0446	1	0.641				SPOA0442	1.08	0.541	SPOA0440	0.57	0.024	SPOA0444	0.60	0.075 SPOA0437	1.08	0.495
SPOA0448	0.91	0.845	SPOA0452	0.85	0.162	SPOA0447	1.49	0.999				SPOA0443	1.40	0.032	SPOA0441	1.95		SPOA0445	4.04	0.001 SPOA0438	1.05	0.556
SPOA0449	0.74	0.227				SPOA0448	1.16	0.571				SPOA0444	1.12	0.042	SPOA0442	1.05		SPOA0446	0.64	0.253 SPOA0439	0.93	0.774
SPOA0450 SPOA0451	1.37 0.81	0.179				SPOA0449 SPOA0450	1.02	0.798				SPOA0445 SPOA0446	3.56 1.22	0.001	SPOA0443 SPOA0444	1.40		SPOA0447 SPOA0448	0.85	0.898 SPOA0440 0.846 SPOA0441	0.89	0.788
SPOA0451	0.81	0.529				SPOA0450 SPOA0451	1.18	0.701				SPOA0446 SPOA0447	1.22	0.632	SPOA0444 SPOA0445	3.49		SPOA0448 SPOA0449	1.02	0.846 SPOA0441 0.944 SPOA0442	1.25	0.957
5. 0.10-102	5.78	0.004				SPOA0452		0.068285				SPOA0448	1.16	0.523	SPOA0446	1.21		SPOA0450	1.02	0.880 SPOA0443	0.17	0.001
												SPOA0449	0.97	0.563	SPOA0447	0.88	0.917	SPOA0451	0.91	0.222 SPOA0444	0.57	0.020
												SPOA0450	1.70	0.223	SPOA0448	1.35		SPOA0452	0.83	0.289 SPOA0445	3.68	0.003
												SPOA0451	1.62	0.019	SPOA0449	0.98	0.572			SPOA0446	0.61	0.216
												SPOA0452	1.18	0.164	SPOA0450 SPOA0451	1.71	0.225			SPOA0447	0.97	0.977
															SPOA0451	1.04	0.162			SPOA0449	0.93	0.198
																				SPOA0450	1.00	0.971
																				SPOA0451	0.85	0.169
																				SPOA0452	0.83	0.287

Chapter 10 - Bibliography

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