Virus Yellows: the consequences of strain variation on future sugar beet varieties

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In memory of my grandmother, Nancy Mattey, who delighted in

looking after 'the special yellow sugar beets'

during the 2020 lockdown.

Thesis Abstract

Virus yellows disease is a major threat to the UK sugar beet industry, reducing yields in sugar beet crops by up to 47%. Reductions in available chemical control options, and a shift to reduce the environmental impact of farming practices, means virus yellows-resistant varieties are now seen as the most sustainable and long-term solution. Progress is being made by European sugar beet breeders in the development of such sugar beet varieties, however our understanding of the diversity of strains which may challenge these varieties in the field remains limited. A three-year survey, utilising next generation sequencing of small RNAs and conducted across sugar, fodder, and sea beet plants, identified Beet chlorosis virus (BChV) as more prevalent than Beet mild yellowing virus (BMYV) in symptomatic plants – a finding which goes against previous research but supports more recent studies conducted in France. Further analysis of this sequencing data showed genetic variation within the yellowing virus species. The resilience of resistant varieties to infection with differing virus isolates was then determined. Various plant growth facilities were trialled to establish their suitability for phenotyping the performance of sugar beet varieties under virus infection. The results of these trials indicated that varieties developed against BMYV also performed well under BChV infection, however sugar yield could not be determined under controlled environment conditions. Novel field trials, challenging susceptible and resistant sugar beet varieties with six differing virus isolates were conducted in 2022 and 2023. The results of these trials indicated that despite differences in pathogenicity between virus isolates, the resistant varieties tested proved to have a robust resistance mechanism.

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Abbreviations

ABBREVIATION	FULL FORM
°C	Degrees Celsius
µl	Microlitre
AGO	Argonaute (protein)
BBRO	British Beet Research Organisation
BChV	Beet chlorosis virus
BMYV	Beet mild yellowing virus
BtMV	Beet mosaic virus
BWYV	Beet western yellows virus
BYV	Beet yellows virus
CABYV	Cucurbit aphid-borne yellows virus
DAS-ELISA	Double antibody sandwich enzyme-linked immunosorbent assay
DCL	Dicer-like protein
DEPC	Diethyl pyrocarbonate
DNA	Deoxyribonucleic acid
dsRNA	Double-stranded ribonucleic acid
ELISA	Enzyme-linked immunosorbent assay
HD	High definition
ICTV	International Committee on Taxonomy of Viruses
IGV	Integrative Genomics Viewer
Kb	Kilobases
LSD	Least significant difference
mg	milligram
ml	millilitre
NCBI	National Center for Biotechnology Information
nm	nanometre
nt	Nucleotide
PBST	Phosphate buffered saline with 0.05% Tween
PCR	Polymerase chain reaction
PLRV	Potato leafroll virus
qPCR	Quantitative real-time polymerase chain reaction
rcf	Relative centrifugal force
RdRp	Ribonucleic acid-dependent ribonucleic acid polymerase
RISC	Ribonucleic acid-induced silencing complex
RNA	Ribonucleic acid
RNAi	Ribonucleic acid interference
RT	Reverse transcription
RT-qPCR	Reverse transcription quantitative real-time polymerase chain reaction

sRNA	Small RNA
ssRNA	Single-stranded ribonucleic acid
TAS-ELISA	Triple antibody sandwich enzyme-linked immunosorbent assay
TBE	Tris-Borate-EDTA Buffer
TuYV	Turnip yellows virus
UK	United Kingdom
USA	United States of America
V	volts
VPg	Viral genome-linked protein
w/v	Weight per volume
w/w	Weight by weight
YWP	Yellow water pan trap

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Chapter 1: General Introduction

1.1 Plant viruses

Plant viruses cause severe yield losses to agricultural crops worldwide. Whilst some viruses reduce the quality and appearance of produce reducing their commercial value, other viruses can cause entire crops to fail. When such crop failures occur in staple food crops, such as potato or rice, food security is threatened with potentially devastating consequences. The need to feed a rapidly growing human population, particularly under the increasing pressures of climate change, makes protecting crops from these viral diseases increasingly important.

1.1.1 Virus classification

As of July 2022 there were 11273 recognised virus species (Zerbini et al., 2023). The variation between these species is large, with virus species parasitising all known living organisms including animals, plants, fungi, and bacteria (Cann, 2012b). Given this huge diversity a classification system is vital for the organisation of research and inference of characteristics. The International Committee on Taxonomy of Viruses (ICTV) is responsible for the classification of all viruses. Established in 1966, and renamed to its current title in 1977, the ICTV determines the criteria for assigning viruses to the recognised taxonomic groups: order, family, subfamily, genus, and species (Lefkowitz et al., 2018a). The high mutation rate of viruses, particularly RNA viruses, can make the assigning these taxa difficult and, occasionally, changes to taxonomic classifications are necessary (Yuan et al., 2022). Such taxonomic changes are made annually after being ratified by ICTV members (Walker et al., 2021). One notable change occurred in March 2021, when a binomial nomenclature format was adopted (Zerbini et al., 2022). As such viral binomial names are used where relevant and helpful in this thesis.

In 1991 the ICTV defined a virus species as:

> *"A viral species is a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche"*

(Francki, Knudson and Brown, 1991)

Virus species are not entirely uniform. As with animals or plant species, a virus species is comprised of a genetic population expressing variation (Hull, 2009a). This variation can make distinguishing what constitutes a different species difficult. Differences in mutation rates between virus families and genera can further compound this problem. To overcome this, species demarcation criteria are outlined for each genus by the ICTV subcommittee study groups (Lefkowitz et al., 2018a). For example, the criteria considered when defining species in the *Polerovirus* genus compared to the *Closterovirus* genus are shown in Table 1.1.

Table 1.1: Factors considered by the ICTV when defining new polerovirus and Closterovirus species. Adapted from Fuchs et al., 2020 *and* Sõmera et al., 2021.

Polerovirus	Closterovirus
Host range	Host range
Occurrence of cross-protection	Particle size
Serological specificity with discriminatory antibodies	Serological specificity with discriminatory antibodies
Gene products differing in amino acid sequence by more than 10%	More than a 25% difference in amino acid sequence of the: • Coat protein • RNA dependent RNA polymerase • 70-kDa heat shock protein homologue (HSP70h)
	Coat protein size
	Vector species
	Cytopathological features

The terms 'strain' and 'isolate' are frequently used by virologists and worthy of defining here. The key difference between these terms is that a virus strain exhibits some unique and recognisable phenotypic characteristics. For example, there are multiple strains of the species *Potyvirus potato virus Y* which exhibit different symptoms in different host plants (Hull, 2009b). Whereas a virus isolate is simply the name given to a specific virus culture that is being studied and is not associated with any taxonomic level (Van Regenmortel, 2007).

1.1.2 Virus transmission

Viruses are obligate intracellular parasites which rely on host cells to replicate. Unlike other organisms, viruses do not grow and then divide but instead produce components which assemble (Cann, 2012b). To produce these components all viruses are at least somewhat dependent on accessing the cellular machinery contained within the host cell (Cann, 2012c). Therefore the ability to move between hosts and infect new cells is a fundamental feature of any virus. Plant viruses have many different transmission pathways. Some plant viruses are directly transferred from one host to another via mechanical transmission, where the tissue of an infected plant rubs against an uninfected plant. Others infect or contaminate seeds or are transferred via contaminated soil or water. Examples of the different transmission mechanisms used by plant viruses are given in Table 1.2.

Table 1.2: different transmission mechanisms used by plants viruses and examples of agriculturally important viruses which utilise each mechanism.

Transmission mechanism	Example of agriculturally important virus	Key crop affected	
Mechanical	Potato virus X	*Solanum tuberosum* L. (Potato)	(Roberts, 1946)
Seed-borne	Barley stripe mosaic virus	*Hordeum vulgare* L. (Barley)	(Slack, 1975)
Pollen-borne	Tobacco streak virus	*Gossypium hirsutum* (Cotton)	(Sdoodee and Teakle, 1993)
Fungal vector	Mirafiori lettuce virus	*Lactuca sativa* (Lettuce)	(Lot et al., 2002)
Nematode vector	Tobacco rattle virus	*Solanum tuberosum* L. (Potato)	(Ploeg et al., 1992)
Insect vector	Beet yellows virus	*Beta vulgaris* ssp. *Vulgaris* (Sugar beet)	(Watson, 1946)
Arachnid vector	Wheat streak mosaic virus	*Triticum aestivum* L.	(Tatineni and Hein, 2018)

1.1.3 Insects as virus vectors

Vector transmission is one of the most common ways plant viruses use to move between hosts (Stevens and Lacomme, 2017). Fungi, bacteria, nematodes, insects, and arachnids are all known to spread viruses (Cann, 2012c). But of all these organisms, aphids are particularly important, utilised by an estimated 50% of insect-vectored viruses (James and Perry, 2004; Nault, 1997). Aphids make ideal plant virus vectors thanks to their feeding behaviour. All aphids use needle-like stylets to pierce into plant tissues and access the food source of phloem contained within the plant. Through the stylet phloem assimilates are taken up and virus particles may be transmitted in either direction. Species such as *Myzus persicae* (Figure 1.1) make particularly good virus vectors because of their polyphagous nature. By feeding on multiple plant species, aphids such as *M. persicae* enable virus infection of multiple plant species from a single vector species.

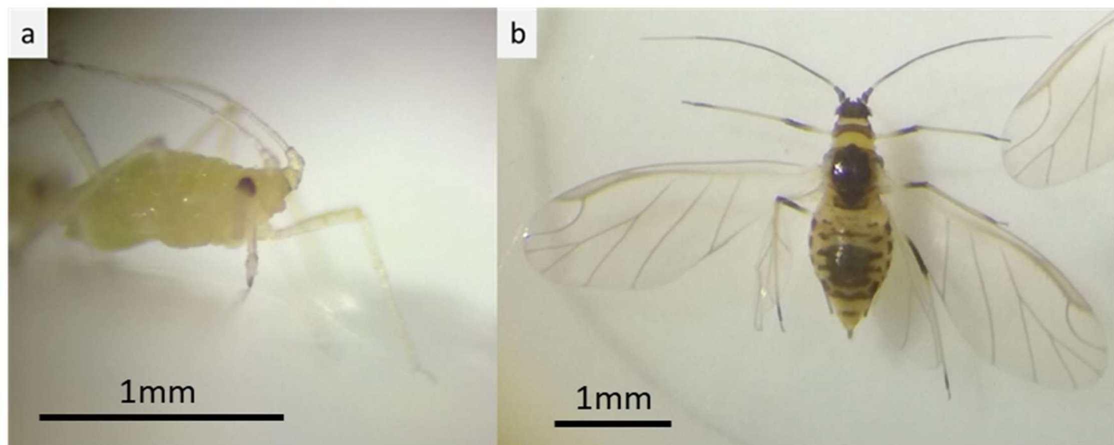


Figure 1.1: images of Myzus persicae *taken through a dissecting microscope (photos by Suzannah Harder). Scale of each image shown in millimetres by horizontal line. a) apterous (wingless) form of* M. persicae, *b) alate (winged) form of* M. persicae.

1.1.3.1 Types of aphid transmission

The transmission of viruses by aphids can be categorised as circulative or noncirculative. Non-circulative viruses remain in the mouthparts and foregut of their aphid vector and do not enter the haemocoel (James and Perry, 2004). Non-circulative viruses can be further defined as either non-persistently or semi-persistently transmitted. Non-circulative, non-persistent virus transmission is the most common form of transmission for aphid vectored viruses (Stevens and Lacomme, 2017). The time it takes for an aphid to take up virus particles is termed 'acquisition time'. Non-persistent viruses have a very short acquisition time of less than one minute. However, the virus is not retained within the aphid for very long and can be 'lost' within minutes of the aphid feeding on an uninfected

plant (James and Perry, 2004). Semi-persistent viruses have longer acquisition times, normally requiring at least 15 minutes of aphid feeding, but can then be transmitted by the aphid for days (Stevens and Lacomme, 2017). Notably, both nonpersistent and semipersistent viruses are lost during aphid moulting (James and Perry, 2004), with previously viruliferous aphids returning to a non-viruliferous state.

Circulative viruses, in comparison, travel much further through their aphid hosts crossing multiple membrane barriers (Figure 1.2). After being taken up by an aphid through its stylet, circulative virus particles pass through the food canal, foregut, midgut and hindgut before entering the haemocoel. Once in the haemocoel, the virus travels to the accessory salivary gland and then leaves the aphid through the salivary canal into the plant (James and Perry, 2004). Due to the longer routes circulatively transmitted viruses take within the aphid, and because they are normally phloem limited (restricted to the phloem cells of host plants), the acquisition period is much longer than for noncirculative viruses (taking hours or days). The persistency of these viruses within the aphid, and the fact they are retained even during aphid moulting, has led to them being termed 'persistent' even though not all are maintained throughout the aphid's life.

Some viruses can replicate within their aphid vectors and are called 'propagative'. These viruses belong to the *Reoviridae* and *Rhabdoviridae,* families and are transovarial meaning the virus is passed from the aphid to its progeny. 'Non-propagative' circulative viruses, do not replicate within the aphid vector and do not exhibit transovarian transmission (Hull, 2009c).

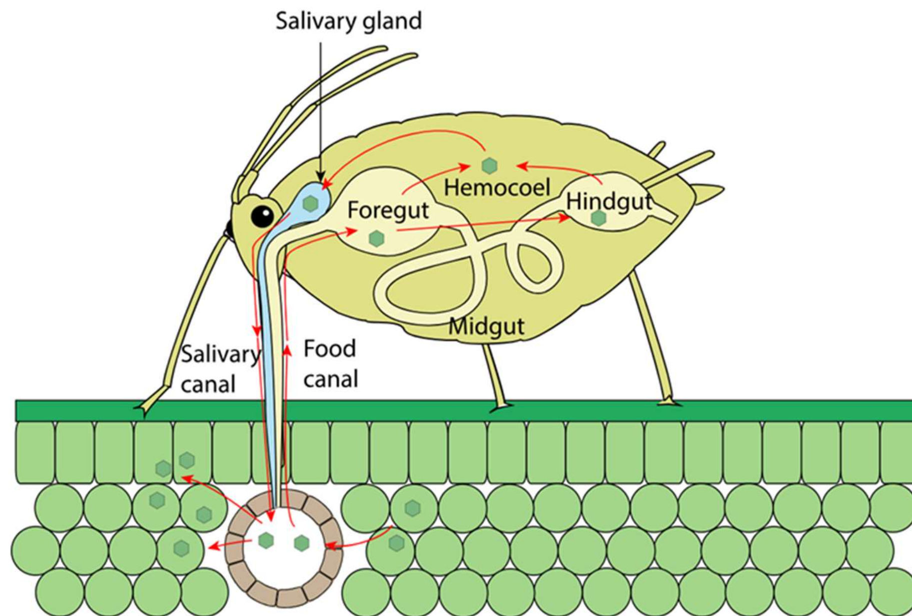


Figure 1.2: cartoon depicting the route of circulative viruses within aphids. Virus particles (shown as dark green hexagons) are taken up by the aphid through the food canal within the stylet, particles then cross multiple membrane barriers through the foregut, midgut and hindgut entering the hemocoel and into the salivary gland. From the salivary gland virus particles then travel through the salivary canal contained within the stylet into the plant. Reproduced from (Hulo et al., 2011).

1.1.4 Spread of viruses

Insect vectors facilitate the spread of viruses across large geographical areas. This is especially true for windborne vectors such as aphids and leafhoppers carrying persistent or semi-persistent viruses. Although often not strong fliers, aphids and leafhoppers can be taken up by wind currents and transported hundreds of miles (Irwin and Thresh, 1988). This can have a major effect on disease epidemiology. One recent example of this is the rice stripe mosaic virus outbreak, which spread from the Jiangsu province of eastern China to Japan and Korea due to a slow-moving cold vortex system transporting the planthopper vector species (Otuka, 2013).

Given the impact of vector distribution on disease occurrence many attempts to control plant viruses target the vector. Detailed monitoring and forecasting systems, enable control strategies to be optimised both in terms of their timing and location of use (Harrington and Hullé, 2017). For example, the Rothamsted Insect Survey aphid forecast predicts the first flight and abundance of different aphid species, including *M. persicae,* based on winter temperatures (Greenslade and Bell, 2023). This information is then used by the sugar beet industry to inform when close monitoring of crops for aphids should begin (Stevens and Bowen, 2023a).

1.2 Sugar beet

There are two major crops grown as a source of sugar throughout the world: sugar beet (*Beta vulgaris* ssp. *vulgaris*) and sugar cane (*Saccharum* officinarum). Sugar beet dominates sugar production in temperate countries, whilst sugar cane is cultivated in tropical and sub-tropical regions (Draycott, 2006). The UK is the tenth largest producer of sugar beet globally, growing 7,420,000 tonnes in 2021 (FAOSTAT, 2023). All UK sugar beet is grown under contract to British Sugar and is focused around their four processing factories in East Anglia and the East Midlands.

Sugar beet is a biennial plant, with a vegetative growth stage followed by a reproductive phase (Milford, 2006). During the vegetative stage, a storage root is produced with a sucrose concentration of around 20% (Draycott, 2006). The production of a flowering shoot and seeds is termed 'bolting' and is triggered by a period of cold vernalisation (Francis, 2006). Bolting reduces sugar yield, therefore commercial crops are planted in the spring and harvested in the autumn or winter before the reproductive stage is initiated (Milford, 2006). During harvesting the leaves of sugar beet plants are removed and the roots lifted and transported to a processing factory where the sugar is extracted and purified (British Sugar, 2023a).

1.2.1 Factors which affect sugar beet yield

Weeds, pests, diseases and adverse weather conditions can all impact sugar beet yields (Draycott, 2006). The distribution and relative importance of these factors has changed over time, affected by changes to agricultural practices and climate change. For example, historically, UK summers were not warm or humid enough to permit the development of the foliar fungal disease cercospora leaf spot (Dunning and Byford, 1982). However now it is considered a major threat to the UK sugar beet crop with multiple fungicide applications used to control the disease in outbreak years. Other examples include insect pests such as tortoise beetle (*Cassida nebulosa*), which are being observed more frequently in UK sugar beet crops (Dunning and Byford, 1982; Stevens and Bowen, 2023b), and beet moth (*Scrobipalpa ocellatella*) which for the first time caused significant damage to sugar beet crops in 2022 likely due to the exceptionally hot and dry summer (Dunning and Byford, 1982; Stevens et al., 2023).

1.2.2 Viruses of sugar beet

Some of the most damaging sugar beet diseases are caused by plant viruses. In western USA the sugar beet industry came close to ruin in the 1920s because of curly top disease (Harveson, Hanson

and Hein, 2009). Caused by three viruses from the *Curtovirus* genus of *Geminiviridae,* and spread by the beet leafhopper (*Circulifer tenellus*), curly top disease can completely destroy infected plants in the arid regions where it is found (Dunning and Byford, 1982). In Europe, Rhizomania ("root maddess") caused by beet necrotic yellow vein virus (BNYVV) and transmitted by *Polymyxa betae*, was first reported in Italy in 1959 (Harveson et al., 2009). By the 1980s the virus was identified in the UK where it caused yield losses of up to 72% and left some fields unviable for sugar beet production (Henry, 1966). Both curly top disease and rhizomania have been brought under control by the development of partially resistant sugar beet varieties. However resistant varieties have not been developed for all sugar beet viruses.

1.2.3 Virus yellows complex

Virus yellows is a disease of sugar beet caused by a complex of aphid-transmitted viruses (Table 1.3). The disease can significantly reduce sugar yields, as evidenced during the 2020 virus yellows outbreak which saw UK yields drop by 25% causing a £67 million loss to the UK sugar industry (Department for Environment, 2023). Historically, however, yield loss during virus yellows epidemic years has been even greater, with the most severe losses to date occurring in 1974 when an estimated 40% of sugar yield was lost to the disease (Werker, Dewar and Harrington, 1998).

Table 1.3: viruses which cause virus yellows disease in sugar beet.

Virus name	Abbreviation
Beet mild yellowing virus	BMYV
Beet yellows virus	BYV
Beet chlorosis virus	BChV
Beet western yellows virus	BWYV

1.2.3.1 History of discovery

Many pathogens and nutrient deficiencies cause yellowing in sugar beet leaves (Figure 1.3). Capsid beetles can bite into main leaf veins, causing yellowing and necrosis above the puncture point. Magnesium deficiency can cause interveinal leaf yellowing. Downy mildew (*Peronospora farinosa*) can cause yellowing to older leaves (Dunning and Byford, 1982). This ubiquity of leaf yellowing as a symptom of disease and deficiency made early identification and characterisation of sugar beet viruses difficult (Russell, 1958).

Figure 1.3: images of yellowing symptoms on sugar beet caused by a) magnesium deficiency, b) downy mildew infection, c) virus yellows infection, d) manganese deficiency, e) herbicide damage due to suspected sprayer contamination. (Photos a,b,d,e provided by Simon Bowen; photo c by Suzannah Harder).

The virus we now know as Beet yellows virus (BYV) was first identified in 1940 by Watson whilst investigating yellowing sugar beet plants in England (Watson, 1940). However, suggestions of a viral cause for these symptoms had been persisting since the 1930s (Quanjer, 1934; Roland, 1936). Naming the virus Beet yellows virus, Watson went on to show it was transmitted by aphid species including *Aphis fabae* and *M. persicae,* which was deemed the principal vector (Watson et al., 1951).

The discovery and classification of Beet mild yellowing virus (BMYV) was less straightforward. In 1948 a virus thought to be a strain of BYV was reported in Ireland and named “Irish mild yellows” (Clinch and Loughane, 1948). In 1954 a similar virus was found in sugar beet in England (Hull and Blencowe, 1954). The presence of this second yellowing virus was confirmed by Russell who, when studying the distribution of yellowing virus strains in East Anglia in 1955 to 1957, identified a virus which did not react with BYV antisera (Russell, 1958). Crucially, when viewed under an electron microscope, the infected sap also did not contain the long filamentous particles known to be BYV. Naming the virus “sugar beet mild yellowing virus” Russell recorded it decreased root yield and caused leaf yellowing but to a lesser extent than sugar beet yellows virus (BYV).

Meanwhile in the USA, Duffus also identified a second sugar beet yellowing virus which he initially named "radish yellows" before re-naming it Beet western yellows virus (BWYV) (Duffus, 1960). These joint discoveries have been marked as the start of confusion surrounding the poleroviruses which cause virus yellows (Stevens et al., 2005a).

Duffus and Russell undertook many studies to elucidate the relationship between their respective viruses (Duffus and Russell, 1970, 1972, 1975). Sugar beet mild yellowing virus, or Beet mild yellowing virus (BMYV) as it became known, had a narrower host range to BWYV and was unable to infect *Brassica* sp. (Duffus and Russell, 1970). BWYV isolates were found in Europe which had a broad host range like American BWYV but could not infect sugar beet. Ultimately these non-sugar beet infecting European strains of BWYV were categorised as a separate species; Turnip yellows virus (TuYV), (Graichen and Rabenstein, 1996).

A similar situation of co-discovery occurred in the late 1980s early 1990s with the virus now named Beet chlorosis virus. In 1991 (Duffus and Liu, 1991) identified a virus causing mild yellowing symptoms which were serologically distinct from BYV yet failed to infect the BMYV indicator species *Capsella bursa-pastoris.* In 1994, Stevens, Smith and Hallsworth (1994a) reported what they referred to as a distinct strain of BMYV which failed to react with the BMYV diagnostic antibody BYDV-PAV-IL-1 and did not infect *C. bursa-pastoris.* Owing to the chlorosis symptoms seen in sugar beet infected with this 'new' virus the name Beet chlorosis virus (BChV) was proposed and approved in 2002 (Mayo, 2002).

1.2.4 Beet poleroviruses

1.2.4.1 Taxonomy

The term beet polerovirus is used to define viruses belonging to the Genus *Polerovirus* which infect *Beta vulgaris* and cause yellowing symptoms (Stevens et al., 2005a). The three viruses belonging to this group are *Polerovirus Beet mild yellowing virus*, *Polerovirus Beet chlorosis virus,* and *Polerovirus Beet western yellows virus* (Walker et al., 2021). The genus *Polerovirus* was moved from the family *Luteoviridae* to the family *Solemoviridae* following a proposal to abolish the *Luteoviridae* classification in 2020, placing a greater emphasis on RNA dependent RNA polymerase phylogeny (Scheets, Miller and Somera, 2020; Walker et al., 2021).

The *Solemoviridae* family contains many economically important plant pathogens. Viruses within the family have icosahedral shaped particles which are non-enveloped and between 20 to 34nm in

diameter. They have a non-segmented positive-sense RNA genome with a genome-linked protein (VPg) at the 5’ terminus but no polyadenylated tail (Sõmera et al., 2021).

1.2.4.2 Genome organisation

Within the *Solemoviridae* family there are four genera, each with slightly differing genomic organisation. Polerovirus genomes are between 5 to 6kb in size and organised into overlapping open reading frames (ORFs), which increase the amount of genetic information that can be encoded (Figure 1.4), (Pagán and Holmes, 2010). The beet poleroviruses have 6 ORFs, compared to the 8 ORFs identified in Potato leafroll virus (PLRV) and Cucurbit aphid-borne yellows virus (CABYV) (Ashoub, Rohde and Prüfer, 1998; Hwang et al., 2013; Stevens et al., 2005a). Polerovirus genomes also contain three non-coding regions which permit the recombination events frequently seen in the polerovirus family (Moonan et al., 2000; Pagán and Holmes, 2010; Stevens et al., 2005a).

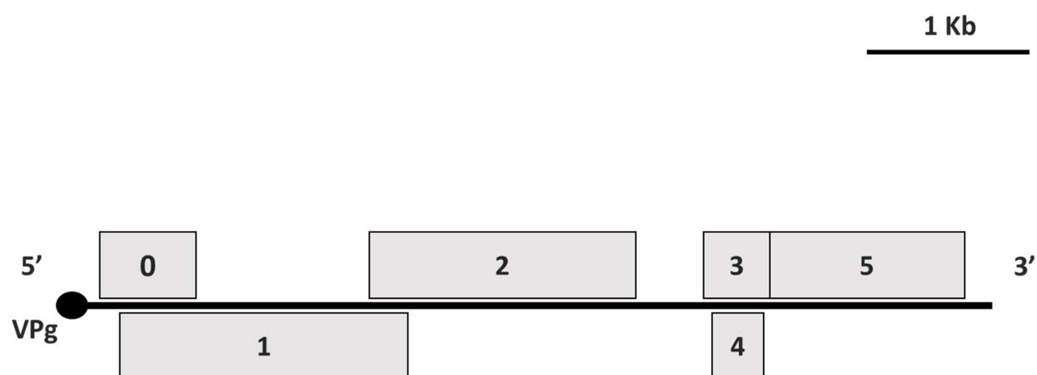


Figure 1.4: schematic diagram showing the shared genomic organisation of Beet mild yellowing virus and Beet chlorosis virus. The 5.5kb single stranded RNA genome (shown as horizontal black line) contains five overlapping open reading frames (ORFs), indicated by grey boxes. These ORFs are named ORF0 through to ORF5 as shown by the number within the grey box. A genome-linked protein (VPg) is associated with the 5’ end of the genome and is shown as a black circle. Based on Stevens et al. (2005a).

1.2.4.3 Transmission

Poleroviruses are circulative, non-propagative aphid vectored viruses (Gray and Gildow, 2003; Stevens et al., 2005a). *M. persicae* and *Macrosiphum euphorbiae* are the most efficient vectors and as such the focal point for epidemiological studies and disease control (BBRO, 2023a; Kozłowska-Makulska et al., 2009). Notably, unlike BYV, BMYV and BChV are not transmitted by *A. fabae* (Bjorling and Nilsson, 1966; Kozłowska-Makulska et al., 2009; Russell, 1963). Poleroviruses are phloem limited and as such have long acquisition times (Stevens and Lacomme, 2017). In the case

of BMYV, aphids need to feed on an infected host plant for at least 24 hours to acquire the virus and then feed on a healthy plant for at least eight hours to transfer it (Russell, 1962).

1.2.4.4 Symptoms and consequences

BMYV

Initial infection with BMYV is associated with chlorotic areas on fully expanded leaves. As the infection develops, older leaf tissue turns “golden yellow” (Stevens et al., 2004) between the leaf veins and becomes thick and brittle (Harveson et al., 2009). Both root weight and sugar yield are reduced in infected plants, whilst root impurities (which have a detrimental effect on sugar extraction) are increased (Stevens et al., 2004). BMYV infection also increases plant susceptibility to *Alternaria* spp. particularly later in the growing season, further compounding yield losses (Smith et al., 1995). Yield losses to BMYV can be up to 29% when plants are infected early in the season. Later infection has a reduced impact, with field trials inoculated with BMYV in July showing no significant loss of yield (Smith and Hallsworth, 1990). Although virus-infected sugar beet plants have been shown to have reduced rates of net photosynthesis (Hall and Loomis, 1972), the exact way virus infection results in these yield losses has not been conclusively established (Peters, 1988).

BChV

BChV infection causes paler interveinal leaf yellowing than the golden yellow seen with BMYV (Stevens et al., 2004), and the green leaf veins are more pronounced (Harveson et al., 2009). However, the same thicken brittle older leaves are observed and distinguishing between these viruses in the field is difficult. Overall, BChV has a smaller impact on yield than BMYV (up to 24%) but later infections result in higher yield losses than BMYV (Stevens et al., 2004).

1.2.5 Beet yellows virus

1.2.5.1 Taxonomy

BYV is a *Closterovirus* in the *Closteroviridae* family and has the species name *Closterovirus Beet yellows virus*. Members of the *Closteroviridae* family are characterised by very long filamentous particles of between 650 to 2200nm and large positive-sense single-stranded RNA genomes (between 13 and 19.3kb). The family is comprised of four genera that are classified based on the

phylogenetic relationship of key proteins, their genome organisation, particle length, and vector species (Fuchs et al., 2020).

BYV particles have a complex molecular structure which has been described as having a 'rattlesnake' like appearance (Agranovsky et al., 1995). The 'body' of the virion encapsidates 96% of the BYV genome and is formed of the major coat protein. The 5' end of the genome is surrounded by the 'tail' which is comprised of at least four proteins including the minor coat protein (Peremyslov et al., 2004). This tail region has a vital role in cell-to-cell movement of the particle, with experimental mutations to the tail proteins inhibiting movement (Napuli et al., 2003).

1.2.5.2 Genomic organisation

The BYV genome is significantly larger than that of the beet poleroviruses. Although some other genera in the *Closteroviridae* family have segmented genomes (where the viral genome is split across two or more RNA molecules), *Closteroviruses* have a monopartite genome of between 14.5 and 19.3kb (Fuchs et al., 2020). Across its 15.5kb genome BYV has nine ORFs, two of which are directly translated from the genomic RNA and the remaining seven in a set of subgenomic messenger RNAs (mRNA) (Agranovsky et al., 1994; Dolja, 2003; He, Rao and Creamer, 1997).

1.2.5.3 Transmission

BYV is transmitted semi-persistently by its aphid vectors. The virus has a wider vector range than the beet poleroviruses with 23 different aphid species known to acquire and transmit the virus (Fuchs et al., 2020; Harveson et al., 2009; Kirk et al., 1991; Summers et al., 1990). Of these *M. persicae* and *A. fabae* are seen as the most important vectors due to their efficiency of transmission and tendency to colonise sugar beet (Heathcote, 1966; Limburg et al., 1997). Acquisition of the virus can occur within five minutes of feeding, and transmission within one hour (Watson, 1946). BYV virus is not as strictly phloem limited as the beet poleroviruses, spreading into mesophyll and epidermis cells during the later stages of infection (Esau et al., 1967; Peters, 1988).

1.2.5.4 Symptoms and consequences

Later symptoms of BYV are very similar to those caused by BMYV or BChV infection. However, initial symptoms are distinctive with BYV causing vein clearing, particularly on younger leaves (Wintermantel, 2005). As the infection proceeds, BYV causes leaf yellowing with older leaves

becoming thick and brittle. In advanced infections, necrotic brown/red spots can appear on older leaves (Harveson et al., 2009). As with BMYV, the impact of BYV on yield decreases with later infection. 47% losses in sugar yield have been reported for infection occurring in early or mid-season inoculated trials, compared to no significant losses in trials inoculated after the end of July (Smith and Hallsworth, 1990).

1.3 Plant virus diagnostics in relation to virus yellows

Currently when a plant becomes infected with virus there is no feasible cure. Yet this does not make knowing exactly which virus is causing disease in a crop a purely academic exercise (Rubio et al., 2020). As previously discussed, different viruses have different transmission mechanisms and therefore different disease control methods may need to be deployed, especially in crops. Likewise, knowing which viruses were present in a previous crop may impact growers' choices of future varieties, particularly if resistant ones are available. Therefore, when working with plant viruses in either a research or agricultural setting, accurate and reliable plant diagnostics are fundamental. Much effort has been given to the development of plant diagnostics, the methodology of some are covered below.

1.3.1 Microscopy

In some cases, the size and shape of a virus particle can be sufficient to identify it. Given virus particles are not visible with the naked eye, the use of microscopy is vital in this approach. The first virus to be seen through an electron microscope was the tobacco mosaic virus (TMV) in 1939 (Kausche et al., 1939). Since then, the electron microscope has been used to identify many plant viruses including BYV. Prepared leaf sap from symptomatic plants consistently showed the characteristic long filamentous particles of BYV, enabling the disease to be diagnosed (Horne et al., 1959). However, this technique does not permit the differentiation of viruses which have similar sized and shaped particles. For example, the beet poleroviruses share the same small icosahedral particle shape making distinguishing them via microscopy alone impossible (Hull, 2009d; Sõmera et al., 2021).

Using electron microscopy to identify plant viruses can also be challenging when a single plant is infected with multiple viruses. This was shown during the discovery of BYV, during which spherical particles were also observed in sap preparations containing the filamentous BYV particles (Horne et al., 1959; Nixon and Watson, 1951). These particles could be evidence of a mixed infection with

one or more other viruses. However these particles were also recorded as present in healthy plants, highlighting the difficulty of differentiating virus particles from normal cellular components (Hull, 2009d).

1.3.2 Host range techniques

Some plants display characteristic symptoms when infected with a particular virus. These plants are known as indicator hosts and were one of the earliest plant diagnostic techniques. Other plants can be immune to infection by a specific virus, and hence allow identification by their lack of infection (Hull, 2009d).

Unlike electron microscopy, indicator hosts can be used to differentiate BMYV and BChV. The host range of BChV is reported as narrower than BMYV (Hauser et al., 2002; Stevens et al., 1994a). This characteristic has been utilised to distinguish between these closely related species. BChV causes interveinal reddening on *Chenopodium capitatum* but does not infect *Capsella bursa-pastoris.* Conversely, BMYV causes reddening of *C. bursa-pastoris* but does not infect *C. capitatum* (Harveson et al., 2009; Stevens et al., 2005a). *C. capitatum* has also been used as an indicator host for BYV because it produces severe symptoms faster than in sugar beet (Russell, 1960). However the symptoms of BYV in *C. capitatum* are so severe that they often cause premature death and hence *Tetragonia expansa* is favoured for use in laboratory studies (Polák, 1971).

Host range is rarely now used in isolation to identify plant viruses, because there are many draw backs to the approach. Host range techniques are more time-consuming than serological or molecular approaches, with indicator plants often taking days/weeks to produce any characteristic symptoms. It is also vital to 'back inoculate' from an immune to an indicator host to ensure virus infection was not merely asymptomatic, which further lengthens the diagnostic process. There is also the problem of infection itself, with specific vectors the only way to achieve inoculation of some viruses. Plus there is the containment issues which arise when potentially multiplying plant pathogens and the risk this could cause to nearby crops (Hull, 2009d).

1.3.3 Serological based approaches

Serological diagnostics exploit the interaction between protein (antigen) and antibody. Most serological diagnostics are based on antibodies specifically binding the viral coat proteins, though some antibodies instead target protein subunits from disrupted plant viruses or viral proteins expressed during infection. Whichever antigen is targeted, the antibodies used in these diagnostics

are either monoclonal or polyclonal. Monoclonal antibodies target one specific region of protein (called an epitope). Polyclonal antibodies contain a mixture of different antibodies that bind to the different epitopes available on the antigen. Monoclonal antibodies are therefore more specific than polyclonal antibodies. However high specificity may not always be an advantage. For example, a polyclonal antibody may be beneficial when detecting a virus with many strains or variant.

One of the most used serological approaches in plant diagnostics is the enzyme-linked immunosorbent assay (ELISA). ELISA works by using antibodies to specifically bind the virus proteins and then using an enzyme linked antibody to visualise the reaction. There are many variations of the basic ELISA methodology, varying in the number and type of antibodies used. The double-antibody sandwich method (DAS-ELISA) and triple-antibody sandwich method (TAS-ELISA) both used in the detection of virus yellows are outlined in figure 1.4 (D'Arcy et al., 1989; DSMZ, 2023; Polák et al., 1980).

ELISA diagnostics are widely used to identify viral diseases in plants because they are economical in reagent use, adaptable for use with large sample numbers and allow some degree of quantification (Hull, 2009d). However they are also often time consuming, taking up to two days to produce results. ELISA also relies on the successful production of specific antibodies, a process which can be costly and sometimes not possible. This is particularly true for closely related viruses which have largely homologous coat proteins such as the case for the beet poleroviruses. Although an ELISA diagnostic is commercially available for BYV (such as from (DSMZ, 2023)), no specific ELISA diagnostic is currently available to differentiate BMYV and BChV. Attempts have been made to produce such a test, which were successful in the 1990s (Stevens et al., 1994a). However this antibody was subsequently lost and due to high similarity of the two viruses efforts to replace it have been unsuccessful (BBRO, personal communication).

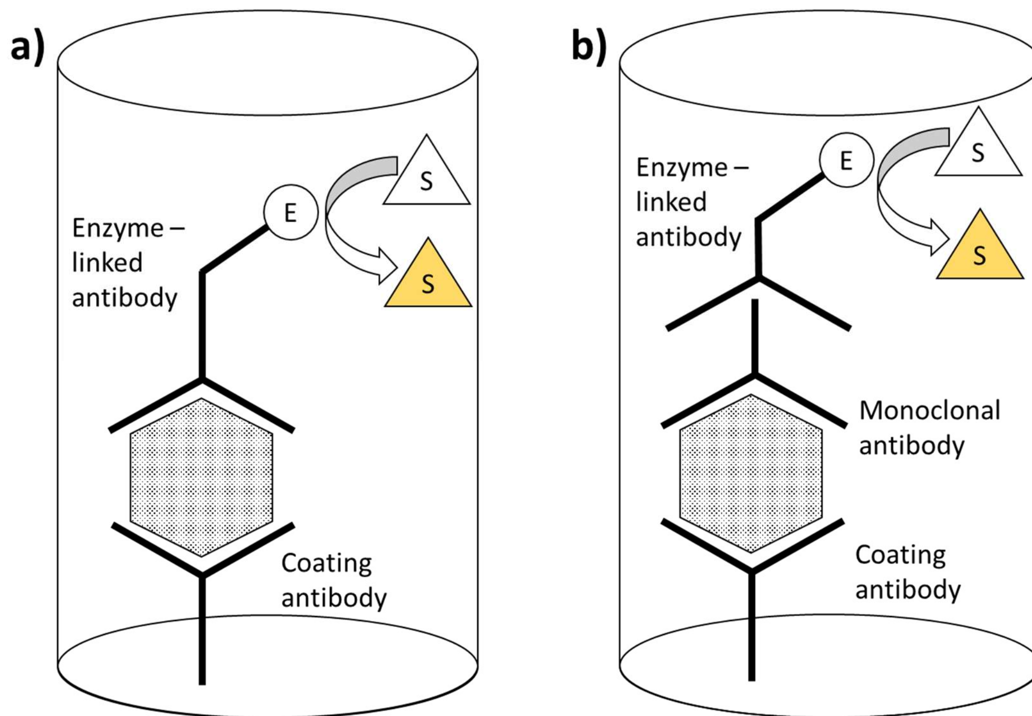


Figure 1.5: schematic diagram showing principle of double antibody sandwich (DAS) and triple antibody sandwich (TAS) enzyme-linked immunosorbent assays (ELISA). In both approaches, polyclonal coating antibody is bound to the microplate well, virus particles (shown as hexagons) then bind to the antibody, before being bound in turn by a monoclonal antibody. In DAS-ELISA (a) this second antibody is conjugated to an enzyme (circle, marked 'E') such as alkaline phosphatase, in TAS-ELISA (b) the monoclonal antibody binds to the virus particle but does is not enzyme-linked. Instead, a third antibody with a conjugated enzyme is added which binds to the monoclonal antibody. When a colourless substrate (such as p-nitrophenyl phosphate) is added (shown as triangle, marked 'S') in the presence of the bound target virus, the substrate is cleaved by the enzyme and converted into a yellow compound which can be quantified (D'Arcy et al., 1989; DSMZ, 2023).

1.3.4 Molecular approaches

A polymerase chain reaction (PCR) is used to amplify specific fragments of DNA. This technique is now ubiquitous in modern laboratories, however is not directly applicable to most plant viruses because of their RNA genomes. Therefore most plant virus diagnostics, utilising PCR, first require a complementary-DNA (cDNA) template to be made via a suitable primer and reverse transcriptase enzyme. Following reverse-transcription PCR (RT-PCR), traditionally, the amplified DNA is visualised using gel-electrophoresis with a DNA 'band' of the expected size indicative of a positive sample.

Such an approach can be highly specific and sensitive, enabling detection of very low virus titres and reliably discriminating between closely related viruses based on their genome sequences.

However, one major disadvantage of conventional RT-PCR diagnostics is the high risk of false positives. The high sensitivity of the technique means that even small amounts of amplified DNA can be detected and every time a test tube containing amplified DNA is opened the risk of such contamination increases (Boonham et al., 2014). Real-time or quantitative PCR (qPCR) goes some way to overcome this issue. qPCR or RT-qPCR involves the association of amplified DNA with a fluorescent signal. This signal can be detected within a 'closed tube' either during the reaction or at the end, therefore greatly reducing the contamination risk. A published RT-qPCR methodology for the detection of BYV is available (Stevens et al., 1997), however to date, no qPCR-based assay able to differentiate between BMYV and BChV has been published.

1.3.5 Sequencing

The financial and time burden of genome sequencing previously prohibited its adoption as a diagnostic tool in most practical settings. Now, with the continual advance of next generation sequencing technology, sequencing based approaches to plant virus diagnostics are increasing in popularity (Boonham et al., 2014). The ability of these approaches to detect viruses is largely dependent on the type of nucleic acid sequenced. For example, rolling circle amplification can be used to clone circular DNA plant viruses enabling them to be sequenced and identified (Inoue-Nagata et al., 2004; Schubert et al., 2007). Other approaches, such as total messenger RNA (mRNA) sequencing is not limited to one singular virus type and has been successfully used to identify known and previously unknown viruses (Al Rwahnih et al., 2009). However, because of the relative concentrations of host plant mRNA to viral RNA, much of the sequencing data generated by total mRNA sequencing is plant mRNA and not useful in a diagnostic sense (Boonham et al., 2014).

Techniques to improve the ratio of host to virus sequences are therefore often deployed. One such technique is small RNA (sRNA) sequencing, which targets short RNA fragments (Kreuze et al., 2009). These sRNAs are the result of plants naturally occurring RNA interference (RNAi) pathway which combats pathogens by targeting double stranded RNA (dsRNA).

Although the RNAi pathway is not specific to virus infection it is particularly important because of the dsRNA produced by plant viruses during their replication (Muhammad et al., 2019). This dsRNA is recognised by dicer-like (DCL) proteins (specifically DCL2 and DCL4) which cleave the RNA into

short 22 and 21 nucleotide (nt) fragments through their RNase III endoribonuclease activity (Carmell and Hannon, 2004). These sRNAs can be selected for sequencing, however in the natural plant response they are loaded into argonaute (AGO) proteins 1 and 2 (Wang et al., 2011) where they form an RNA-induced silencing complex (RISC) (Hammond et al., 2001). RNA-dependent RNA polymerase (RDR) proteins amplify this silencing function by recognising single-stranded RNAs and synthesising dsRNA which are in turn recognised by DCL proteins, continuing the RNA silencing process (Muhammad et al., 2019).

Sequencing the sRNA produced by the plant RNAi pathway reduces the amount of host RNA sequenced, compared to total mRNA sequencing and permits the detection of both known and novel viruses (Kreuze et al., 2009). For example, Zhang et al. (2017) used sRNA sequencing to identify a previously unknown polerovirus which was causing yellowing symptoms in wheat in China.

1.4 Control strategies for virus yellows

Given the impact of virus yellows on sugar beet yield there is a clear need to control the disease to ensure crop profitability. Methods of controlling virus yellows have changed and developed since its discovery in the 1930s (Roland, 1936). Many of these methods, both historically and currently, have centred around the application of a chemical insecticide to kill the aphid vector. However, growing concern over the environmental impacts of these chemicals is placing increasing focus on more sustainable control strategies.

1.4.1 Chemical control

Chemicals which target the aphid vector of virus yellows have proved very successful at reducing virus yellows disease incidence. Over time different chemical classes have been introduced and then withdrawn from use in sugar beet either due to safety concerns (e.g. organophosphates such as Schradan (Broadbent, 1957)) or the emergence of aphid resistance (e.g. carbamates such as Aphox, Syngenta (Stevens, 2013)).

One insecticide class of particular importance in the story of virus yellows control in the UK is the neonicotinoids. These chemicals are neurotoxins which act on the nicotinic acetylcholine receptors of insects, causing paralysis and death (Goulson, 2013). Unlike previous insecticides which had to be sprayed onto the crop or applied as granules, neonicotinoids were applied to sugar beet seed.

The chemical was then taken up systemically by the plant as it germinated, providing protection from biting, or sucking insects for up to 14 weeks after planting (BBRO, 2016).

The first neonicotinoid sugar beet seed treatment used in the UK was Gaucho introduced by Bayer CropScience in 1994. Containing imidacloprid, Gaucho was widely adopted by growers with 70% of the crop being Gaucho treated seed by 2006. (Foster and Dewar, 2013). Other neonicotinoid-based seed treatments followed (Cruiser SB containing thiamethoxam and Poncho Beta containing clothianidin by Bayer Crop Science, and Poncho Beta). The treatments provided very effective control against virus yellows, evidenced by the low disease incidence observed during their use (Dewar and Qi, 2021). They were also recommended for protection against other major sugar beet pests such as leaf miner (BBRO, 2016). However following concerns regarding the impact of neonicotinoids on pollinators and other non-target organisms, their use on sugar beet was banned by the European Union in 2018 (The European Commission, 2018a, 2018b). Since 2018, neonicotinoid seed treatments have still been used on the UK sugar beet crop in 2022 and 2023 due to emergency authorisations from the UK government.

Aside from concerns regarding their environmental impacts, chemical control options are also vulnerable to the development of resistance. This is particularly true in the case of combating *M. persicae* which has a remarkable ability to evolve mechanisms through which it can overcome chemical modes of action (Foster et al., 2017). The first chemical resistance reported in *M. persicae* was to organophosphates in 1955 (Anthon, 1955). Since then, resistance mechanisms have been identified against at least seven different chemical classes, including neonicotinoids (reviewed in Bass et al., 2014). Therefore reliance on chemical control strategies is not considered a long term solution to the issue of virus yellows.

1.4.2 Integrated pest management

The use of integrated pest management (IPM), whereby sustainable approaches are prioritised, and chemical applications only used as a last resort, is now seen as the future of agriculture (EASAC, 2023). IPM integrates alternative plant protection methods with an aim of reducing reliance on chemical inputs. In the case of sugar beet, this currently involves removing sources of virus infection, monitoring aphid populations, encouraging natural aphid predators, and ensuring optimum plant populations are achieved.

If these strategies fail to control aphid numbers, applications of foliar insecticides may be required but their use is determined by an economic threshold. This is currently set at one green wingless

aphid per four plants up to the 12-leaf stage, rising to one green wingless aphid per plant between the 12-16 leaves (BBRO, 2023a). This changing threshold reflects the development of mature plant resistance (MPR). Around the 10-leaf stage, sugar beet plants develop a natural resistance to aphids associated with the development of black deposits in the aphid gut, reduced fecundity, and increased mortality (Schop et al., 2022). Agronomic practices which increase the rate of plant development, and the onset of MPR, consequently reduce the risk of virus yellows. Measures such as waiting for optimum weather conditions before planting seed, ensuring optimal fertiliser applications are used, and avoiding herbicide damage are all recommended as part of a sugar beet IPM strategy (BBRO, 2023a).

1.4.3 Monitoring and forecasting

Forecasting and monitoring crop pests is also a crucial part of the IPM system (EASAC, 2023). Accurate predictions of disease risk enable control strategies to be implemented in a timely manner. Sugar beet benefits from a virus yellows forecasting model which estimates the proportion of crop predicted to become infected with virus yellows in the absence of any control strategies (Werker et al., 1998). Forecasting also provides predictions on the first *M. persicae* flight, giving advanced warning on when active crop monitoring should commence.

Since their ban in 2018, emergency authorisations have been granted by the UK government for the use of neonicotinoid seed treatments in 2021, 2022 and 2023. These authorisations were dependent on the virus yellows forecasting model predicting disease incidences above a defined threshold. This threshold was met in 2022 and in 2023, resulting in 70% and 60% of the UK sugar beet crop being treated with neonicotinoids in 2022 and 2023 respectively (BBRO, personal communication).

1.4.4 Virus sources

In isolation, aphids rarely pose a threat to the sugar beet crop. It is only as vectors of viruses that they become economically devastating pests. Therefore, one way to reduce the threat they pose is to reduce the sources of virus in the area surrounding the crop, thereby reducing the chance of an aphid acquiring viruses. This approach has been used ever since the discovery of the viral cause of virus yellows in the 1940s (Watson et al., 1946). Since then our understanding of what species and situations present the biggest viral sources has developed.

Plants which host both aphids and yellowing viruses present the greatest risk as virus sources. Many agricultural weed species are known hosts of virus yellows. A study in 1991 found 3% of weeds collected contained BMYV, equating to 2000 infected weeds per hectare (Stevens et al., 1994b). Hence effective weed control programmes can reduce the risk of virus infection. Clamps (the heaps in which roots are stored after harvest) can also act as sources of virus infection. These are particularly problematic because they bridge the gap between the previous years harvest and the subsequent season, providing a site for both aphids and virus to 'overwinter'. One study identified 17% of aphids found feeding on a clamp were carrying BMYV, while 10% carried BYV (Heathcote and Byford, 1975). Therefore, it is recommended to destroy or remove clamps (and other overwintering hosts such as cover crops) before sowing any nearby crops the next year (BBRO, 2023a).

1.4.5 Varietal resistance

Although cultural practices, and applications of insecticide when needed, can control the spread of virus yellows it is rarely enough to prevent any yield losses, particularly in epidemic years. The development of varieties which can overcome virus infection is therefore often heralded as the ultimate solution to virus yellows.

There are many different types of virus resistance exhibited by plants. Examples include resistance to virus replication and accumulation, resistance to virus movement between cells, and resistance to virus inoculation. Alternatively, plants may have resistance to the effects of virus infection an ability often termed 'tolerance' (Lecoq et al., 2004). To avoid confusion, precise and consistent terminology is crucial when describing a plants' susceptibility to a pathogen (Oliver and Fuchs, 2011). For consistency the terms susceptible, tolerance and resistance are defined in relation to virus infection below. These definitions are maintained throughout this thesis.

Susceptible

Susceptible plants become infected by the virus and the virus replicates uninhibited within them. The symptoms of infection are fully expressed, and resultant yield loss is suffered.

Tolerant

Tolerant plants become infected by the virus and do not inhibit virus replication or accumulation. However, the plant may not express symptoms of the infection as strongly as a susceptible plant, and the resultant yield loss is decreased or negligible.

Resistant

Resistant plants inhibit virus replication or accumulation, and therefore resulting symptoms and yield loss are decreased.

The development of tolerant and resistant varieties has already proved successful in combating some sugar beet diseases. As discussed previously, rhizomania posed a major threat to the UK sugar beet industry in the 1980s. The discovery of the 'Holly' resistance and subsequent resistance genes, now means rhizomania rarely causes yield losses in the UK (Stevens, 2015). All varieties on the 2024 recommended list contain at least the *Rz1* gene, with specialist varieties also containing resistance to the resistance breaking AYPR strain of rhizomania.

Aside from viruses, yield loss from beet cyst nematode (BCN) can now also be combated by using partially resistant sugar beet varieties. Four varieties are included on the 2024 recommended list claiming tolerance to BCN, some of which outperform non-BCN tolerant varieties under BCN free conditions (BBRO, 2023b). This demonstrates that the yield drag, the drop in yield associated with the introduction of specialist traits into a varieties, can be overcome.

Previous studies have identified potential resistance sources from other species within the *Beta* genus. In 2008 Grimmer et al. successfully transferred BMYV resistance from garden, fodder and leaf beet into sugar beet cultivars through traditional breeding approaches. For BYV resistance, quantitative trait loci (QTLs) have been identified (Grimmer et al., 2008b). However, for a virus yellows variety to be completely effective it must be able to overcome BMYV, BYV and BChV both in isolation and as mixed infections.

The most recent advance in the production of virus yellows-resistant sugar beet varieties is gene editing technology. The gene editing bill, passed by the UK government in 2023, permits the use of genetically-edited crops in the UK market. Gene editing differs from genetic modification in that no genetic material from an unrelated species is incorporated into the target species (UK Government, 2023). This technique has been highlighted as one way of achieving virus yellows-resistant sugar beet varieties, but the timeline for their development and deployment is uncertain and expected to take at least five years (British Sugar, 2023b; Seccombe, 2023).

The development of a virus yellows resistant variety would be environmentally and commercially beneficial. However, currently only one variety, Maruscha KWS has been listed on the UK recommended variety list with recognised tolerance to virus yellows (BBRO, 2021, 2023b). Crucially this variety also only claims tolerance against one of the yellowing viruses, BMYV (KWS, 2021), and

suffers a yield penalty compared to other listed varieties when grown in the absence of BMYV (BBRO, 2023b).

Currently the BBRO undertakes a large-scale screening programme of both current and future sugar beet varieties to determine their performance under virus infection (Wright and Stevens, 2023). At the start of this PhD project, in 2020, the BBRO routinely tested varieties against BYV and BMYV. During this project a UK BChV culture was established and subsequently the BBRO's variety screening has been broadened to include BChV. This screening is conducted via field trials, hand inoculated using viruliferous *M. persicae* aphids reared on the BBRO in-house virus cultures.

The BBRO in-house virus cultures have, however, never been sequenced and little is known about how they compare to 'wild' virus found in the UK crop. Equally, to date, no studies have explored the level of genetic variation seen within BMYV, BChV or BYV in the UK, or indeed the impact this variation may have on future varieties. Therefore, determining this variation and its consequences on the durability of future resistant sugar beet varieties is crucial.

1.5 Project Aims

This project aimed to categorise the molecular and biological variability of virus yellows disease complex. Through identification of the virus species responsible, and assessment of the intra-species genetic variation, the diversity of virus yellows disease complex in the UK was determined. The effect of this diversity on the durability of future resistant/tolerant sugar beet varieties was then evaluated. Controlled environments were trialled to determine their suitability as a replacement for field trials for the assessment of variety performance under virus infection. However, as no reliable alternative was identified, ultimately a novel field trial was conducted assessing the performance of varieties under multiple virus populations.

Chapter 2: General materials and methods

2.1 Aphid and virus cultures

All virus cultures were maintained within separate Versatile Environment Test Chambers (Panasonic, MLR-352) at the BBRO laboratories. Plants were grown under a 16-hour photoperiod, with light provided by 15 fluorescent tube lights (FL4055 ENW/37, Panasonic). Temperatures were set at 22°C during the light period, and 18°C during the dark period.

Unless otherwise stated, cultures of BMYV were maintained on the indicator host *Capsella bursa-pastoris* to ensure they did not become contaminated with any other beet virus (Harveson et al., 2009). Cultures of BChV and BYV were maintained on the sugar beet variety Lightning (SESVanderHave). All plants were grown in commercially available compost such as Premium All Purpose (Miracle-Gro), in 9cm pots (0.36l capacity).

Virus-free *Myzus persicae* aphid cultures were maintained on *Brassica rapa* subspecies *chinensis.* To produce viruliferous aphids, colonies of these aphids were moved onto virus containing plants and allowed to feed. Viruliferous aphids were then transferred to either inoculate experimental plants, or onto fresh plants for culture maintenance. Aphids were removed from cultures using an insecticide (0.1g/L InSyst containing 20% w/w acetamiprid, CertisBelchim). Whenever possible, cultures were kept free of aphids to minimise the risk of contamination.

Whenever aphids were present on the virus cultures, strict contamination control measures were put in place. These included housing the different viruses in separate laboratories whenever possible and avoiding watering different virus cultures on the same day (to prevent aphid transfer from one culture to another).

2.2 Production of total RNA

2.2.1 Total RNA extraction

Total RNA extraction was completed using Tri Reagent Solution (Invitrogen^{TM}, AM9738) following the manufacturers protocol with some adaptations. Plant material was snap frozen in liquid nitrogen and then stored at -80°C prior to extraction.

In a liquid nitrogen environment, 0.4g of sugar beet leaf tissue was ground using a pestle and mortar. The resulting powder was transferred to a 50ml centrifuge tube (Corning, 4558), 4ml Tri Reagent Solution (Invitrogen^{TM}, AM9738) added then the solution mixed thoroughly by shaking. The solution was then aliquoted into four microcentrifuge tubes with leak proof lids (Eppendorf, 0030120221), before being vortexed briefly and incubated at room temperature for five minutes. After this, 200µl chloroform (Fisher Scientific) was added to each tube, then mixed gently by inverting. The aliquots were then incubated at room temperature for eight minutes before being centrifuged for 15 minutes at 14000rcf in a 4°C room. The clear top phase (containing the RNA) was then transferred to a clean microcentrifuge tube and 1000µl of 100% ethanol (approximately double the sample volume) added. The microcentrifuge tubes were then incubated at -80°C for two hours.

The supernatant was then removed, and the precipitate washed by adding 980µl of 80% ethanol and centrifuging for three minutes at 7500rcf. This step was repeated, then the pellet dried for five minutes in a 70°C heat block. The pellet was then resuspended in 10µl deionised water, and the sample aliquots recombined.

2.2.2 Quantification of total RNA

The concentration of the total RNA produced was determined using a Nanodrop 8000 spectrophotometer (Thermo Fisher Scientific).

The quality of the total RNA was checked by visualising on a 1.5% (w/v) agarose gel in 0.5 X Tris-Borate-EDTA buffer (TBE) with 10mg/ml ethidium bromide (Fisher Scientific). 5µl of Loading Buffer II (Invitrogen^{TM}, AM8546G) was added to 1µg of sample RNA and the volume made up to 10µl with deionised water. Gels were run at 110V for 45minutes, then imaged using a Typhoon FLA 9500 (GE Healthcare Life Sciences).

2.2.3 Total RNA clean-up

Total RNA samples were cleaned using the mirVana isolation kit (Ambion, AM1560) following the manufacturers protocol with some modifications. In a microcentrifuge tube, 20µg of total RNA was made up to 50µl with deionised water. Samples which did not yield 20µg of total RNA were still cleaned if at least 5µg of total RNA was available. Then 250µl of Lysis/Binding Buffer was added to the mixture and mixed thoroughly by pipetting, 30µl of miRNA Homogenate Additive was then added, the mixture mixed thoroughly and then kept on ice for 10 minutes. After this, 412.5µl of 100% ethanol was added and mixed thoroughly. The mixture was then passed through a mirVana Filter Cartridge in a Collection Tube by centrifuging for 30 seconds at 10,000rcf. The flow-through was discarded, then 700µl of miRNA Wash Solution 1 was passed through the filter by centrifuging as before. The filter was then washed by adding 500µl of Wash Solution 2/3 and centrifuging for 30 seconds at 10,000rfc. This wash step was repeated, then the empty filter/collection tube assembly centrifuged for one minute at 7500rcf to remove any residual wash solution. The filter was then transferred to a clean collection tube and 50µl of Elution Solution pre-heated to 95°C added. The filter/Elution Solution was left for two minutes (for the Elution Solution to bind to the RNA within the filter) before being centrifuged for 30 seconds at maximum speed. This step was repeated to yield a final volume of 100µl, then 10µl NAOAc (Sigma-Aldrich, S2889) and 100µl 100% ethanol were added to the RNA elute. The mixture was then left to precipitate overnight at -80°C.

The following morning the mixture was centrifuged for 30 minutes at maximum speed in a 4°C room. The supernatant was discarded and 700µl of 80% ethanol was then added directly onto the pellet to wash it. The mixture was then centrifuged for three minutes at 7500rcf and the supernatant removed. The pellet was then centrifuged again for one minute at 7500rcf and as much of the remaining supernatant as possible removed. The pellet was then dried on a 37°C heat block for five minutes, and then resuspended in 16µl nuclease free water.

2.2.4 Quantification of cleaned total RNA

The resulting cleaned total RNA was then quantified, and quality checked as for the total RNA (Section 2.2.2).

2.3 sRNA library construction and sequencing

2.3.1 3' Adapter Adenylation

sRNA libraries were prepared following the protocol published by Xu et al (Xu et al., 2015). This protocol utilises High Definition (HD) adapters which contain four random nucleotides at their ligating ends. The 3' HD adapter was purchased phosphorylated but requires adenylation prior to use. This was achieved using the 5' DNA Adenylation Kit (New England BioLabs, E2610L) following the manufacturers protocol. The reaction was then cleaned up using an Oligo Clean and Concentrator Kit (Zymo Research, D4060) following the manufacturers protocol. The concentration of the resulting 3' adenylated HD adapter was determined using a Nanodrop 8000 spectrophotometer (Thermo Fisher Scientific). The concentration was then made up to 10µM using nuclease free water.

To confirm that the adenylation was successful a 16% urea polyacrylamide gel was run using both the newly adenylated 3' HD adapter and a non-adenylated 3' HD adapter control. If adenylation had been successful, the 3' HD adapter would be heavier than the non-adenylated control and be seen as a higher band on the gel.

For one gel 2.1g of urea (Fisher Scientific, U/0500/63), 1.4ml of deionised water and 0.5ml 5 X TBE were mixed in a 50ml centrifuge tube (Corning, 4558) and heated for 20 seconds in a microwave until the urea had dissolved. The solution was then left to cool before 2ml of 40% acrylamide/bis solution 19:1 (Bio-Rad, 1610144), 2.5µl of Tetramethylethylenediamine (Bio-Rad, 161-0800) and 50µl 10% Ammonium Persulfate solution (Sigma-Aldrich, A3678) was added. The mixture was poured between two 1mm glass plates (Bio-Rad, 1653311 and 1651824) and a 1mm comb added (Bio-Rad, 1653359). The gel was allowed to set, then transferred to a Mini-Protean Tetra Vertical Electrophoresis Cell (Bio-Rad) and 0.5 X TBE added as running buffer.

To 1µl of 3' HD adapter, 2µl of Novex™ Hi-Density TBE Sample Buffer (Invitrogen™, LC6678) was added and the volume made up to 10µl with deionised water. The gel was run at 120V for around 45 minutes or until the Bromophenol blue tracking dye reached the bottom of the gel. The gel was then removed and stained using SYBR™ Gold Nucleic Acid Gel Stain (Invitrogen™, S11494) before being imaged using a Typhoon FLA 9500 (GE Healthcare Life Sciences).

2.3.2 Adapter ligation and cDNA synthesis

To 1.5µl of adenylated 3' HD adapter, 2µg of mirVana cleaned sample total RNA was added and the volume made up to 7.5µl with deionised water. The sRNA library was then constructed following

the protocol set out in Xu et al (Xu et al., 2015). Firstly, the adenylated 3' HD adapter was ligated to the sample RNA using a T4 RNA ligase 2 (New England BioLabs, K227Q). An RNA Clean and Concentrator -5 kit (Zymo Research, R1015) was used to clean up the reaction, before de-adenylation using a 5' deadenylase (New England BioLabs, M0331S). The excess 3' adapter was removed using a RecJ exonuclease (New England BioLabs, M0264S), before the 5' HD adapter was ligated to the sample RNA using a T4 RNA Ligase 1 (New England BioLabs, M0204L). The di-tagged RNA was purified again using the RNA Clean and Concentrator -5 kit then cDNA was produced via reverse transcription using High Performance MMLV Reverse Transcriptase (Biosearch technologies, RT80125K).

2.3.3 sRNA library PCR and size selection

The resulting cDNA was amplified via PCR as described in Xu et al (Xu et al., 2015), using 10, 12 and 14 cycles of amplification and Phusion™ High-Fidelity DNA polymerase (Thermo Scientific™, F-530).

The PCR products were then separated on an 8% polyacrylamide gel. For one gel, 5ml deionised water, 1.5ml 40% acrylamide/bis solution 19:1 (Bio-Rad, 1610144), and 0.75ml 5 X TBE were mixed together in a 50ml centrifuge tube (Corning, 4558). 75µl 10% Ammonium Persulfate solution (Sigma, A3678-100G) and 3.75µl Tetramethylethylenediamine (Bio-Rad, 161-0800) were then added, and the gel poured between two 1mm glass plates (Bio-Rad, 1653311 and 1651824). A 1mm comb was added (Bio-Rad, 1653359) and the gels left to set. Once set, the gel was transferred to a Mini-Protean Tetra Vertical Electrophoresis Cell (Bio-Rad) and 0.5 X TBE buffer added.

The PCR products were combined with 5µl Novex™ Hi-Density TBE Sample Buffer, 5X (Invitrogen™, LC6678) and loaded into the gel along with 10µl 20 bp DNA ladder (Jenna Bioscience). The gel was run at 120V until the Xylene Cyanol dye had reached the very bottom of the gel. The gel was then stained and the bands of 145-150bp removed as described in Xu et al (Xu et al., 2015).

2.3.4 sRNA library sequencing

The constructed sRNA libraries were sent for sequencing where they were first quantified and pooled then sequenced using Illumina NextSeq 550 at a depth of approximately 33million reads by the Quadram Institute (Norwich).

Sequencing was completed in three batches; 2019, 2020 and 2021 samples. In each batch, control libraries from the BBRO cultures (BBRO BMYV, BBRO BChV and BBRO BYV) along with non-virus infected sugar beet were also prepared and sequenced.

2.3.5 Visualising sequencing data

Raw sequencing data was received and processed by Rocky Payet (UEA). After being trimmed of adapter sequences and mapped to all known virus reference genomes, the resulting data was provided as BAM and BAI files.

The software package Integrative Genomics Viewer (IGV) version 2.3.75 (Thorvaldsdóttir, Robinson and Mesirov, 2013) was used to visualise reads mapping to the reference genomes of viruses of interest. The reference genomes used are outlined in Table 2.1.

Table 2.1: details of the reference genomes of Beet yellows virus, Beet mild yellowing virus, Beet chlorosis virus, Beet western virus and Turnip yellows virus to which generated sequence data was mapped to.

Virus	Definition as listed on GenBank	NCBI reference sequence number	Publication reference
Beet yellows virus (BYV)	Beet yellows virus, complete genome	NC_001598.1	(Agranovsky et al., 1994)
Beet mild yellowing virus (BMYV)	Beet mild yellowing virus, complete genome	NC_003491.1	(Guilley, Richards and Jonard, 1995)
Beet chlorosis virus (BChV)	Beet chlorosis virus, complete genome	NC_002766.1	(Hauser et al., 2002)
Beet western yellows virus (BWYV)	Beet western yellow virus, complete genome	NC_004756.1	(Beuve and Lemaire, 2002)
Turnip yellows virus (TuYV)	Turnip yellows virus, complete genome	NC_003743.1	(Veidt et al., 1988)

2.3.6 Producing consensus sequences

Consensus sequences were produced by firstly setting the relevant reference genome in IGV. The sample data set was then loaded to show any reads from the sample mapping to the specified reference genome. The IGV copy consensus sequence command was then used to create the consensus sequence for the entire virus genome. The method behind this consensus sequence calculation is taken from (Cavener, 1987), and is based on the frequency of a nucleotide at each position. Briefly, a nucleotide is assigned if it is present at a frequency greater than 50% and more than twice that of the second most frequent nucleotide. A co-consensus nucleotide is assigned when two nucleotides have a combined frequency greater than 75% but neither meet the criteria

of a single nucleotide. When neither of these two criteria are met, or no mapping reads were present at that location, an 'N' is assigned.

2.4 Enzyme-linked immunosorbent assay

2.4.1 Antibody test kits

Enzyme-linked immunosorbent assay (ELISA) antibody sets were purchased from The Leibniz Institute DSMZ. Details of the specific test kits used, and their specificity are outlined in Table 2.2.

Table 2.2: details of ELISA antibody test kits used to detect Beet chlorosis virus, Beet mild yellowing virus, Beet western yellows virus, Beet yellows virus and Turnip yellows virus in plant leaf samples.

Antiserum test name	DSMZ number	Test format	Detects
Beet western yellows virus	RT-0049-0049/1	TAS-ELISA	BWYV, TuYV, BMYV, BChV
Beet yellows virus	RT-0185	DAS-ELISA	BYV

2.4.2 TAS-ELISA

2.4.2.1 Coating and blocking

96-well flat-bottomed microplates (Thermo Scientific, 3455 or Star lab, E2996-1600) were coated with 100µl polyclonal immunoglobulin G antibody, diluted 1:1000 in carbonate-bicarbonate with sodium azide coating buffer (Bioreba, 110110). Plates were covered with clingfilm and incubated at 37°C for two hours. Plates were washed with phosphate buffered saline with 0.05% Tween® (Sigma Aldrich, P3563) using an automated plate washer (Wellwash, Thermo Scientific), programmed to wash each well three times with 200µl PBST and then aspirate. To each well, 100µl of 2% dried skimmed milk (less than 1% fat) in PBST blocking buffer was added. The plates were then recovered and incubated at 37°C for 30 minutes. The blocking buffer was then removed and the plates blotted dry.

Plates were either stored at 4°C for use on the same day or stored at -20°C for use within five days.

2.4.2.2 Antigen binding

Two 2.5cm diameter leaf discs were taken from each leaf being tested. Wherever possible these discs were taken from leaf blade, avoiding the midrib. Extraction buffer was prepared by dissolving 2% polyvinylpyrrolidone (Fisher BioReagents, BP431-500) in PBST. The two leaf discs were placed

in a standard extraction bag (Bioreba) with 1ml of prepared extraction buffer and crushed using a Homex 6 semi-automated homogeniser. Of the resulting leaf extract, 100µl was added to the relevant well on the coated plate. Each plate was also loaded with at least two negative and two positive controls. Wherever possible healthy sugar beet leaf tissue was used as a negative control. When it was not possible to guarantee sugar beet had not been contaminated with virus, prepared extraction buffer was used as a negative control. Freeze-dried positive controls were purchased from DSMZ (Table 2.3) and prepared following the manufacturers protocols.

Table 2.3: details of positive controls used for ELISA tests, purchased from DSMZ.

Positive control name	DSMZ catalogue number	ELISA test providing positive result
Beet mild yellowing virus	PV-1210	Beet western yellows virus
Beet chlorosis virus	PV-1211	Beet western yellows virus
Beet yellows virus	PC-0981	Beet yellows virus

Plates were covered with clingfilm and incubated at 4°C overnight. Leaf extract was removed from the plate and washed once by hand using PBST. Plates were then washed using the automated plate washer (Wellwash, Thermo Scientific) using the same wash/aspirate programme as described previously (Section 2.4.2.1).

2.4.2.3 Monoclonal antibody

The monoclonal antibody was diluted 1:1000 in conjugate buffer (Bioreba, 110140), and 100µl added to each well. The plate was then covered with clingfilm and incubated at 37°C for 2 hours. The plate was then emptied and washed using the automated plate washer (Wellwash, Thermo Scientific) using the same wash/aspirate programme as described previously (Section 2.4.2.1).

2.4.2.4 Enzyme-linked rabbit anti-mouse antibody

To each well, 100µl of rabbit anti-mouse alkaline phosphatase conjugate antibody, diluted 1:1000 in conjugate buffer (Bioreba, 110140) was then added. The plate was covered with clingfilm and incubated at 37°C for two hours. The plate was then emptied and washed using the automated plate washer (Wellwash, Thermo Scientific) using the same wash/aspirate programme as described previously (Section 2.4.2.1).

2.4.2.5 Substrate addition and absorbance measurement

Substrate was freshly prepared by dissolving one 5mg p-nitrophenyl phosphate tablet (Thermo Scientific, 34047) in 5ml substrate buffer (Bioreba, 110130). Of this prepared substrate, 100µl was added to each well of the plate. The plate was then covered with clingfilm and kept under dark conditions at room temperature. An absorbance microplate reader (Spectrostar Nano, BMG Labtech) was used to measure the absorbance of each well at 405nm. Results were viewed and exported using MARs data analysis software 3.3 (BMG Labtech).

2.4.3 DAS-ELISA

Coating was completed for DAS-ELISA as for TAS-ELISA, with the omission of the blocking step. Leaf extract and antigen binding protocol was also the same as for TAS-ELISA.

Immunoglobulin G alkaline phosphatase conjugate antibody, diluted 1:1000 in conjugate buffer (Bioreba, 110140), was added to each well. The plate was then covered with clingfilm and incubated at 37°C for two hours. The plate was then emptied and washed using the automated plate washer (Wellwash, Thermo Scientific) as per the TAS-ELISA protocol. Substrate was added and plates measured as described in TAS-ELISA protocol above.

2.5 Detection of beet poleroviruses by single step RT-qPCR

A single step RT-qPCR diagnostic was developed by Wulf Menzel (DSMZ, personal communication) to identify BMYV and BChV infection in plant material. The probe and primer sequences used in this assay are detailed in Table 2.4.

Firstly, total RNA was extracted from the sample leaf tissue as described in section 2.2. Then in a 96-well PCR plate (Star lab, E1403-8200), 1µl of sample RNA was added to 12.5µl TaqMan™ Fast Advanced Master Mix (Applied Biosystems™, 4444556), 0.75µl of forward and reverse primers (10µM), 0.75µl of each probe (10µM), 0.1µl RevertAID RT (Thermo Scientific, 10612191) and 6.9µl of nuclease free water (Invitrogen™, AM9932). The plate was sealed with a MicroAmp optical adhesive film (Applied Biosystems, 4311971) and centrifuged for one minute at 2500rcf. The reaction was carried out in a QuantStudio™ 3 Real-Time PCR System (Applied Biosystems™, A28567) with cycling conditions of; 52°C for 10 minutes, 95°C for 10 minutes for cDNA synthesis, followed by 40 cycles of 95°C for 15 seconds and 60°C for one minute. Results were viewed using QuantStudio Design and Analysis software v1.5.2.

Table 2.4: Primer and probe sequences used in the single step RT-qPCR diagnostic developed by Wulf Menzel (DSMZ, personal communication) for the detection of Beet mild yellowing virus and Beet chlorosis virus in plant tissue.

Type	Shorthand name	Sequence 5’-3’	Target gene
BMYV forward primer	BMYV_F	GAGTGACGTACACATCTGAGAA	P1
BMYV reverse primer	BMYV_R	TCACCATCCGACAGAGCAA	P1
BMYV probe	BMYV_probe	VIC-CCAAACTGGGAAGGAGTTCTTGC	P1
BChV forward primer	BChV_F	AGTCATGACGACGGTTCACA	P1
BChV reverse primer	BChV_R	TTGCCAGTGACGGTTGAGA	P1
BChV probe	BChV_probe	FAM-TGATAACCTGCTCGCATGCTCC	P1

2.6 Detection of beet poleroviruses in aphids by RT-qPCR

To identify the presence of Turnip yellows virus (TuYV) and BMYV and/or BChV an unpublished two-step RT-qPCR protocol developed at Rothamsted Research (Martin Williamson, personal communication) was used. The probe and primer sequences used in this assay are detailed in Table 2.5. Importantly, this assay was designed to detect both BMYV and BChV using the same probe and therefore cannot be used to differentiate between the two viruses.

Table 2.5: primer and probe sequences used in the two-step RT-qPCR protocol for detection of Turnip yellows virus (TuYV) and Beet mild yellowing virus (BMYV)/Beet chlorosis virus (BChV) in aphids. Developed by Martin Williamson (Rothamsted Research, personal communication).

Type	Shorthand name	Sequence 5’-3’	Target gene
Reverse transcription primer	VR2	GAACCATTGCCTTTGTAGRGG	P3/4
qPCR forward primer	Pol_F	CGTTTACAGCGTCTTACATCAACG	P3/4
qPCR reverse primer	Pol_R	CCATTGCCTTTGTAGAGGATCCT	P3/4
TuYV qPCR probe	Tu_probe	FAM-TGGTCCTCGGCAAC	P3/4
BMYV/BChV qPCR probe	Pol_probe	VIC- TGGTCCTTGGCAACG	P3/4

2.6.1 Sample preparation

To each well of a lidded 96-well plate (CytoOne, CC7682-7596), 50µl of phosphate buffered saline (Fisher BioReagents, 12821680) was added, then one aphid was added to each well using a paintbrush. Aphids were homogenised using a 96-well plate multiple homogenizer (Burkard Scientific, BAMH-96), then plates sealed using a clear polypropylene seal (Starlabs, E2796-0793), and plate lids secured. Plates were then incubated in a water bath (Edulab) at 96°C for nine minutes, before centrifuging for two minutes at 2500rcf.

2.6.2 cDNA synthesis

To each well of a 96-well PCR plate (Star lab, E1403-8200), 1ul 10µM VR2 reverse transcription primer, 0.5µl 10mMol dNTP and 3.75µl diethyl pyrocarbonate treated water were added. Then 2µl of prepared sample was added, the plate re-sealed and centrifuged for 15 seconds at 2500rcf. The plate was then heated to 70°C for three minutes in a thermocycler (SimpliAmp, Applied biosystems) to anneal the primer to the RNA template. The plate was then placed on ice.

Following this, 0.15µl RevertAID reverse transcriptase (200U/µl) and 2µl RT buffer (provided as set from Thermo Scientific, 10612191), 0.30µl RNaseOUT recombinant ribonuclease inhibitor (10777019) and 0.30µl DEPC treated water was added to each well. The plate was then sealed with a fresh clear polypropylene seal and centrifuged for one minute at 2500rcf. DNA polymerisation and enzyme deactivation was carried out in the thermocycler; 42°C for 45 minutes, 50°C for 15 minutes, 70°C for 10 minutes. The plate was then placed on ice.

2.6.3 qPCR

To each well of a new 96-well PCR plate, 5µl TaqMan™ Fast Advanced Master Mix (Applied Biosystems™, 4444556), 0.2µl 10µM TuYV-2 probe, 0.2µl 10µM BMYV-2 probe, 0.08µl 100µM polero-forward-primer-2, 0.08µl 100µM polero-reverse-primer-2 and 2.44µl DEPC treated water was added. After this, 2µl of synthesised cDNA was added to each well and the reaction mixed by pipetting. The plate was then sealed using a MicroAmp optical adhesive film (Applied Biosystems, 4311971), and centrifuged for one minute at 2500rcf. The reaction was completed in a QuantStudio™ 3 Real-Time PCR System (Applied Biosystems™, A28567), cycling conditions were a pre-read hold at 60°C for 30 seconds, UNG incubation hold at 50°C for two minutes, polymerase activation hold at 95°C for 20 seconds. Then 40 cycles of 95°C for one second and 60°C for 20 seconds, followed by a post-read hold at 60°C for 30 seconds. Results were viewed and exported in Microsoft Excel using QuantStudio Design and Analysis software v1.5.2.

Chapter 3: Occurrence and prevalence of yellowing viruses in the UK 2019-22

3.1 Chapter Contributions

Leaf samples were collected by a combination of the BBRO network, British Sugar and Belchim Crop Protection. I conducted the molecular work myself. Rocky Payet processed the raw sequencing data, completed the initial bioinformatic analysis (preparing the data into BAM and BAI files, as outlined in section 2.3.5) and conducted the sequencing alignment (to determine the sample total read number and the number of sample reads mapping to each virus). Subsequent sequencing data analysis using Integrative Genomics Viewer, I completed myself.

3.2 Introduction

Virus yellows is a global issue, affecting sugar beet crops worldwide (Hossain et al., 2021; Kaya and Yilmaz, 2016; Kyriakou et al., 1983; Yoshida and Tamada, 2019). The prevalence of the viruses which cause the disease, however, varies between countries (Hossain et al., 2021; Stevens et al., 2005b). In the UK, virus yellows is caused by three viruses: BMYV, BYV and BChV (Stevens et al., 2005b). Previous studies, undertaken prior to the widespread use of neonicotinoid seed treatments, identified BMYV as the predominant cause of virus yellows in the UK sugar beet crop. BChV in comparison, was found to only account for around 10% of diseased plants in 1990 (Stevens et al., 2005b).

However, such studies become significantly rarer following the widespread adoption of neonicotinoid seed treatments. One UK survey from 2003, referenced in Stevens et al. (2005b), confirmed BMYV was still the dominant beet polerovirus in the UK finding only 25% of polerovirus infected sugar beet leaves had BChV. However, as the methodology of this study is unpublished and the sample size unknown this result must be interpreted with caution. Nevertheless, the prevailing opinion of the UK sugar beet industry for the last thirty years has been that the lower

incidence of BChV, compared to BMYV, and its smaller yield penalty (Stevens et al., 2004) make BChV of lesser importance to UK sugar beet growers (BBRO, 2017; Bowen, 2020). This is evidenced by the first virus yellows tolerant variety to appear on the UK recommended list only having recognised tolerance to BMYV (BBRO, 2021; KWS, 2021).

The European ban on neonicotinoid seed treatments in 2019 increased the need for virus yellows surveillance (The European Commission, 2018a, 2018b). In 2021 Hossain et al. published a large-scale study of 10 European countries, including the UK, assessing virus yellows between 2017 and 2019. From symptomatic leaves sampled in the UK, between 3.6% and 25.8% were found to be infected with polerovirus. A subset of these polerovirus positive leaves were further analysed via qPCR to identify the specific polerovirus present. This analysis identified BChV present in between 33% to 100% of polerovirus positive leaves, suggesting an increasing occurrence of BChV in the UK (Hossain et al., 2021). However, the samples size was small with only one polerovirus positive sample being tested via qPCR in 2018. It is also important to note that in two of the three years this study was conducted over (2017 and 2018) the UK sugar beet crop was grown with neonicotinoid seed treatments which may have influenced virus epidemiology.

BYV incidence is much more variable than the beet poleroviruses (Hossain et al., 2021; Stevens et al., 2005b). The most recently published survey found 56.8% of symptomatic sugar beet leaves sampled from the UK were infected with BYV in 2017, compared to only 4.8% in 2018 (Hossain et al., 2021). This varying occurrence is perhaps one reason why resistance breeding efforts have prioritised BMYV over BYV in the UK, despite BYV having a larger impact on yield. Alternatively, it may be due to difficulties in identifying BYV resistance sources.

BYV, BChV and BMYV are not the only viruses known to cause yellowing symptoms in beet. BWYV, though present in America and Asia, has not yet been isolated in the UK or Europe (Beuve et al., 2008; Stevens et al., 2005a; Xiang et al., 2008). There is also continued confusion around Turnip yellows virus (TuYV). In 2002 the International Committee on Taxonomy of Viruses (ICTV) reclassified European isolates of Beet western yellows virus (BWYV) which do not infect sugar beet to a new species in the Polerovirus genus named TuYV (Mayo, 2002). Despite this, some isolates of TuYV have been found to infect sugar beet and recent studies claim to have identified TuYV from surveyed symptomatic sugar beet plants (Newbert, 2016; Puthanveed et al., 2023). Newbert (2016) inoculated sugar beet plants with three separate isolates of TuYV, identifying one isolate (Cau74-R) which infected sugar beet plants. Meanwhile survey work in Sweden conducted by (Puthanveed et al., (2023) found two field grown sugar beet plants infected with a mixed polerovirus infection of BMYV, BChV and TuYV. In both studies, the identification of TuYV in sugar beet was confirmed

through sequencing however to date no evidence of naturally occurring TuYV infection in UK sugar beet has been found.

The availability of reliable and accurate diagnostics has also played an important role in our understanding of the distribution of yellowing viruses in the UK. Early studies on the distribution of yellowing viruses relied on basic serological methods which could not discriminate between closely related viruses (Duffus and Russell, 1970; Russell, 1963). Advances in molecular techniques have improved the reliability of virus detection and discrimination firstly via enzyme-linked immunosorbent assay (ELISA) and now increasingly by quantitative real-time polymerase chain reaction (qPCR) (D'Arcy, Torrance and Martin, 1989; Lemaire et al., 1995; Stevens et al., 2005a). Although an improvement in diagnostic specificity compared to ELISA, one downside of qPCR diagnostics is that it requires the generation of specific primers for each virus of interest (Stevens et al., 2005a). One novel technique which overcomes this need is the production and sequencing of small RNA (sRNA) libraries (Pooggin, 2018). An important benefit of this technique is that, theoretically, any virus can be identified from a single sample data set removing the need for multiple separate diagnostic assays (Kreuze et al., 2009). The sequencing data can also be stored and used in the future to determine if currently unknown viruses were present in these now historical samples.

In this chapter I aim to update our knowledge on the prevalence of yellowing viruses, establishing if BMYV remains the most prevalent and important of the virus yellows complex in the UK. Across three years (2019 to 2021) I have determined the frequency of each yellowing virus, sampling symptomatic fodder and sea beet as well as sugar beet. Using novel sRNA library techniques and sequencing for virus detection, as well as utilising established ELISA and qPCR diagnostics. I also searched for evidence of poleroviruses which are yet to be found in sugar beet in the UK, namely BWYV and TuYV.

3.3 Materials and methods

3.3.1 Sample collection

Symptomatic sugar, fodder and sea beet were collected between August and October 2019 to 2021. Fully expanded leaves showing virus symptoms were selected by British Sugar contract managers, agronomists and other industry professionals and sent to the BBRO laboratory.

3.3.2 Virus diagnostics – 2019

In 2019, leaf samples were stored at 4°C prior to testing via ELISA with the BWYV and BYV antibody sets to confirm infection with either a beet polerovirus or BYV as outlined in Chapter 2 (section 2.4). Leaves were then freeze dried and stored at -80°C prior to the project start date. Unfortunately, due to Covid-19 laboratory closures, work on these samples was delayed and they remained in storage until June 2020. In June 2020 clean total RNA was extracted from ELISA positive leaves (as per Chapter 2, section 2.2). sRNA libraries were then produced and sequenced as outlined in Chapter 2 (section 2.3). In total sRNA libraries were produced via 15 leaves from 11 locations from samples collected in 2019 (Figure 3.1).

3.3.3 Virus diagnostics – 2020

As in 2019, in 2020 sampled leaves were initially stored at 4°C prior to determining their polerovirus and BYV infectivity via ELISA. Samples of leaf tissue from ELISA positive leaves were snap frozen in liquid nitrogen and stored at -80°C. Cleaned total RNA was extracted from this tissue and used to produce sRNA libraries. In total sRNA libraries were made from 14 leaves from the 12 locations in 2020 (Figure 3.1).

3.3.4 Virus diagnostics – 2021

In 2021, 338 leaves were received from 96 locations (Figure 3.1). These leaf samples were also used to create new virus cultures as detailed in Chapter 5 and as such, samples needed to be maintained as fresh as possible to permit aphid feeding. To achieve this, the leaf petioles were trimmed, and the remaining leaf placed upright in a beaker of deionised water at room temperature out of direct sunlight.

As in 2019 and 2020, all 2021 sampled leaves were first tested via ELISA. Polerovirus positive leaves were then randomly sub-sampled for further testing to determine if either BMYV or BChV was present. To do this RNA was extracted from sampled leaves via total RNA extraction (Chapter 2 section 2.2), then the single-step qPCR BMYV and BChV assay developed by Wulf Menzel (DSMZ, personal communication) was used (Chapter 2, section 2.5).

From the leaves determined polerovirus positive by ELISA, an additional sub-sample of 16 leaves was taken from which sRNA libraries were made. An additional sRNA library was also produced from one leaf collected from Fochabers, Scotland which exhibited yellowing symptoms but tested negative via ELISA and qPCR diagnostics. These libraries were produced predominantly for the

genetic variation investigation detailed in Chapter 5; data are included here for determining the presence of viruses other than BMYV, BChV and BYV. The controls sequenced with the 2021 library set are included to assist with determining positive thresholds. An aliquot of the extracted RNA that was used for creating these sRNA libraries was then tested using the single-step qPCR BMYV and BChV assay.

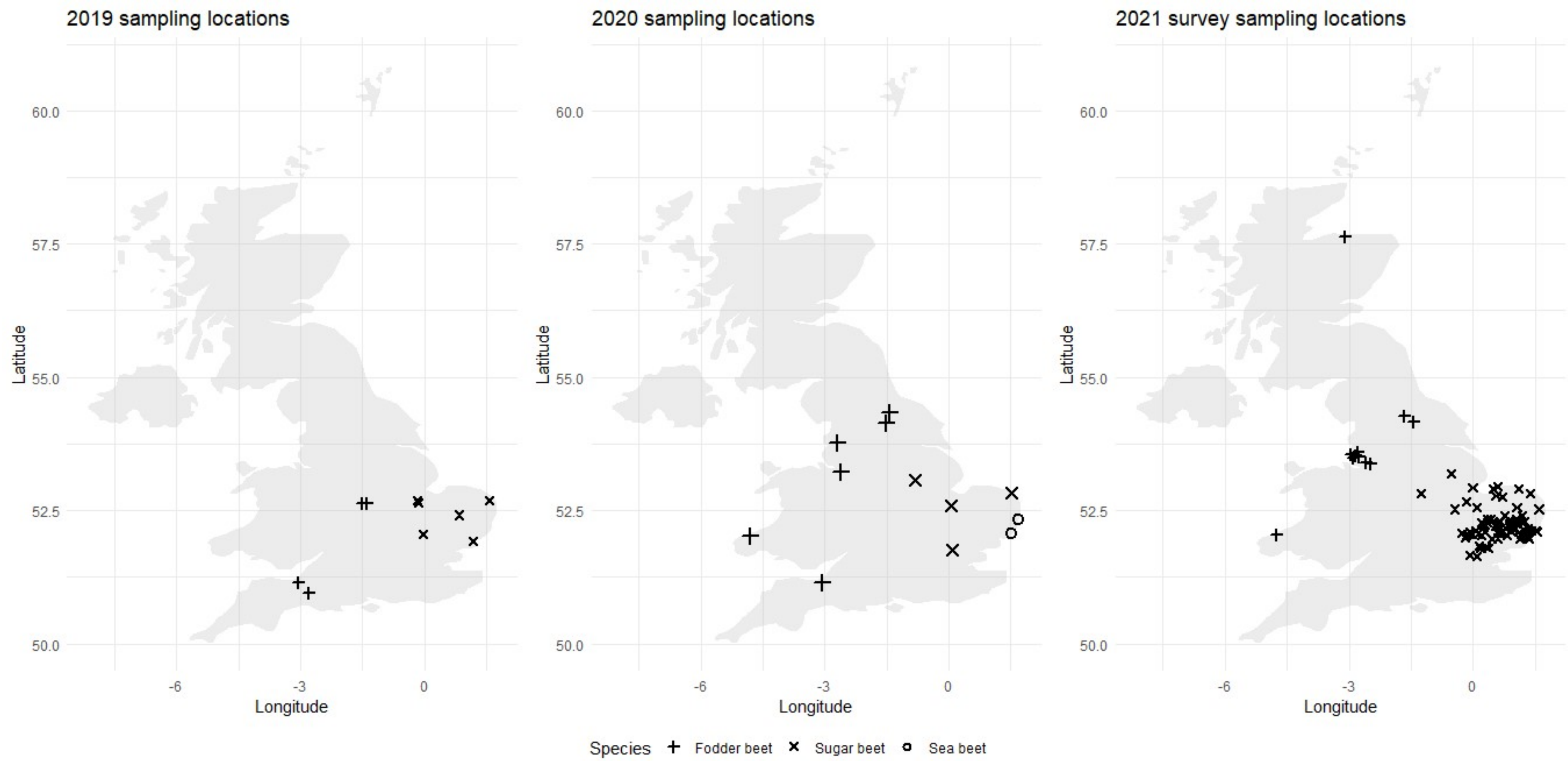


Figure 3.1: map showing sugar beet, fodder beet and sea beet sampling locations in the United Kingdom in 2019, 2020 and the larger scale survey sites in 2021.

3.3.5 Determining virus infection using sRNA library sequencing data

3.3.5.1 Calculating the number of reads mapping to viruses of interest

The total reads for each sRNA library and the number of reads mapping to each virus were provided by Rocky Payet (UEA). To normalise these data, and enable comparisons between libraries with different total read numbers, the number of reads mapping to each virus of interest was divided by the total read number for that sample. To aid interpretation this value was then converted into a percentage.

3.3.5.2 Calculating the percentage of a virus genome present in sample library

Firstly, Integrative Genomics Viewer (IGV) was used to produce a consensus sequence for the virus of interest (Chapter 2 section 2.3.6). This sequence was exported into Notepad++ (v8.4.9) and the number of 'N' nucleotides counted using the find/count function. To determine if an 'N' had been assigned due to high read variation at a location, or because no reads mapped at that location, the mapped reads were checked manually using IGV. Genome locations where reads differed from the consensus sequence are highlighted to enable quick identification. All instances where an 'N' had been assigned in the consensus sequence were due to no reads mapping at that location.

The percentage of the virus genome mapped by at least one read in the sample data set was then determined using the formula:

$$\left(\frac{100}{Total\ nucleotides\ in\ reference\ genome}\right) \times \left(\begin{matrix} Total\ nucleotides \\ in\ reference\ genome \end{matrix} - \begin{matrix} Number\ of\ Ns\ in \\ consensus\ sequence \end{matrix}\right)$$

3.3.5.3 Defining ORF0, 1 and 2 genome regions

To permit comparisons between genome regions of different poleroviruses, standardised genome regions were defined spanning open reading frames (ORF) 0, 1 and 2 based on the ORF locations as detailed by Hauser et al (2002). ORF0 region refers to nucleotides (nt) 30-750, ORF1 region to 160-2130nt and ORF2 region to 1540-3400nt.

3.3.5.4 Filtering sequencing reads to ORF0 genome region

IGV was used to determine the percentage of the ORF0 region of a virus genome present in sample libraries. After loading the reference sequence as detailed in Chapter 2 section 2.3.5, the region 30-

750nt was specified and a consensus sequence produced for this specific region. The percentage of the region present in the sample was then determined as above.

3.3.5.5 Percentage identity

Similarity of poleroviruses was determined by percentage identity calculated using the multiple sequence alignment tool Clustal Omega 2.1 (Sievers et al., 2011).

3.4 Results

3.4.1 BMYV and BChV

3.4.1.1 Normalised read data

Very few reads from any sample sRNA library mapped to BChV, with the percentage of mapping reads ranging from 0-1.6% (Figure 3.2). Low mapping read numbers were also seen in the positive controls, with both having less than 1.25% BChV mapping reads. Although the negative controls had fewer BChV mapping reads than the positive controls, the difference between the closest negative and positive controls was small (0.2%). Overall, no obvious grouping of samples or controls was present.

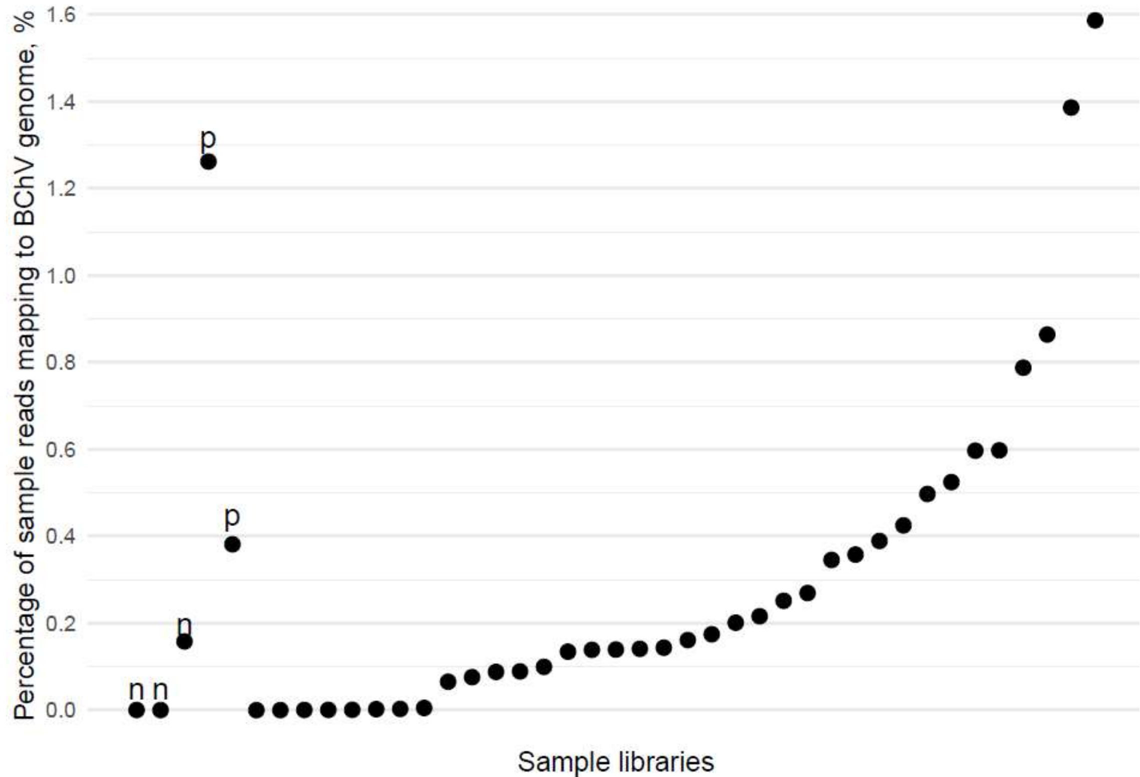


Figure 3.2: scatter plot showing the percentage of total small RNA (sRNA) reads mapping to the Beet chlorosis virus (BChV) reference genome for each of the 2019 and 2020 sample sRNA libraries, alongside the negative control libraries (indicated by 'n') and BChV positive control libraries (indicated by 'p').

mapping to BMYV (Figure 3.3). Again, the overall abundance of mapped reads was low with a maximum of 2.8% of reads mapping to BMYV. The BMYV positive controls grouped more closely than the BChV controls, ranging from 0.5-0.8%. However, the negative controls showed a greater variation of between 0-0.97%. Two outlying samples were identified which had more than twice the number of reads mapping to BMYV compared to the mean of the positive controls. One of these samples (with 2.77% BMYV mapping reads) was from a plant known to contain both BMYV and BYV. The other sample (with 2.57% BMYV mapping reads) was a BYV positive control. Given these relatively small percentages and large variation amongst the controls, an alternative way to interpret this data was needed.

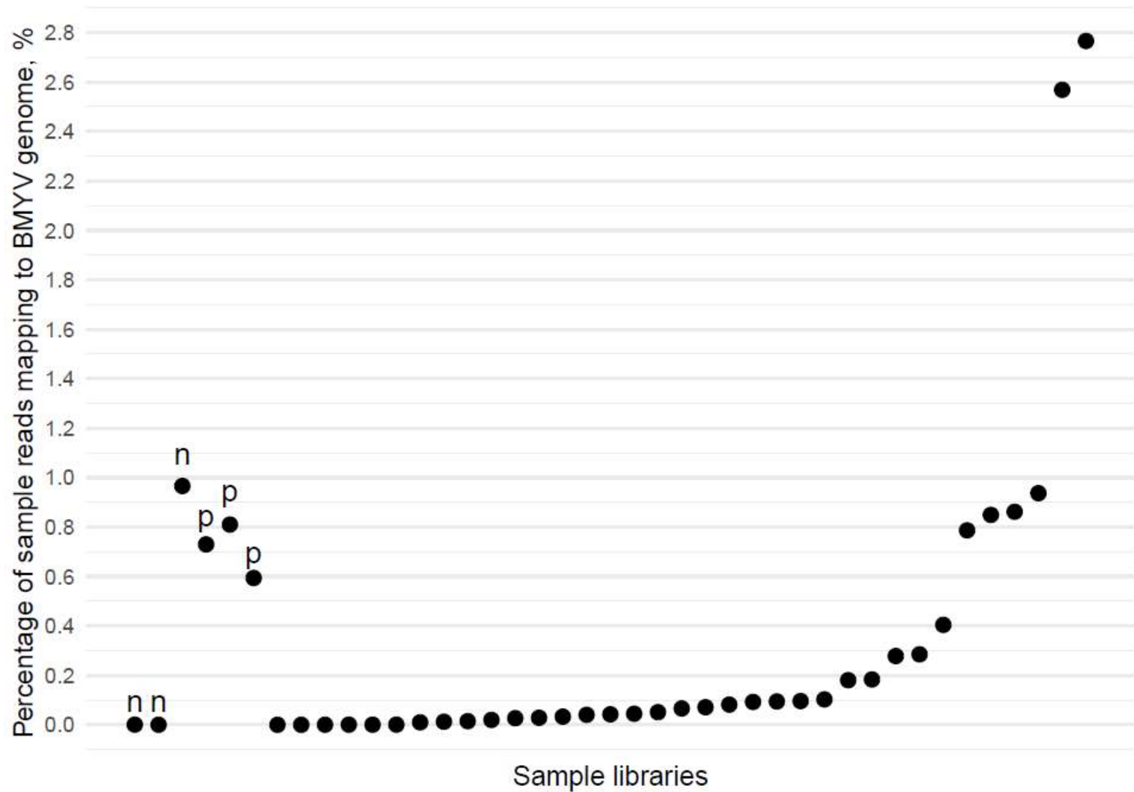


Figure 3.3: scatter plot showing the percentage of total small RNA (sRNA) library reads mapping to the Beet mild yellowing virus (BMYV) reference genome for each of the 2019 and 2020 sample sRNA libraries, alongside the negative control libraries (indicated by 'n') and BMYV positive control libraries (indicated by 'p').

3.3.1.2 Refined read data

Polerovirus reference genomes were compared to ascertain an infection threshold which could be applied to the survey data (Table 3.1). The highest percentage identity was found between BMYV and BWYV, at 73.99% and therefore a value of 74% was set as a threshold above which samples were deemed positive here.

Table 3.1: whole Beet chlorosis virus (BChV), Beet mild yellowing virus (BMYV), Beet western yellows virus (BWYV) and Turnip yellows virus (TuYV) genome percentage identity matrix produced using Clustal Omega 2.1 multiple sequence alignment.

	BChV	BMYV	BWYV	TuYV
BChV	100.00			
BMYV	67.03	100.00		
BWYV	66.89	73.99	100.00	
TuYV	66.50	68.26	68.55	100.00

sRNA library reads were filtered to only include reads mapping to the virus of interest. The percentage of the BMYV genome present in the sRNA library of each sample is shown in Figure 3.4. This approach produced a clear difference between positive and negative controls, with the three BMYV positive controls ranging from 88.12-88.68% and negative controls between 9.4-26.69%. Survey samples fell into two loose groups: below 45% and above 60%. Using the 74% threshold, 7 samples were classed as positive for BMYV. Two of the BYV controls and one control known to be infected with both BMYV and BYV also passed this threshold.

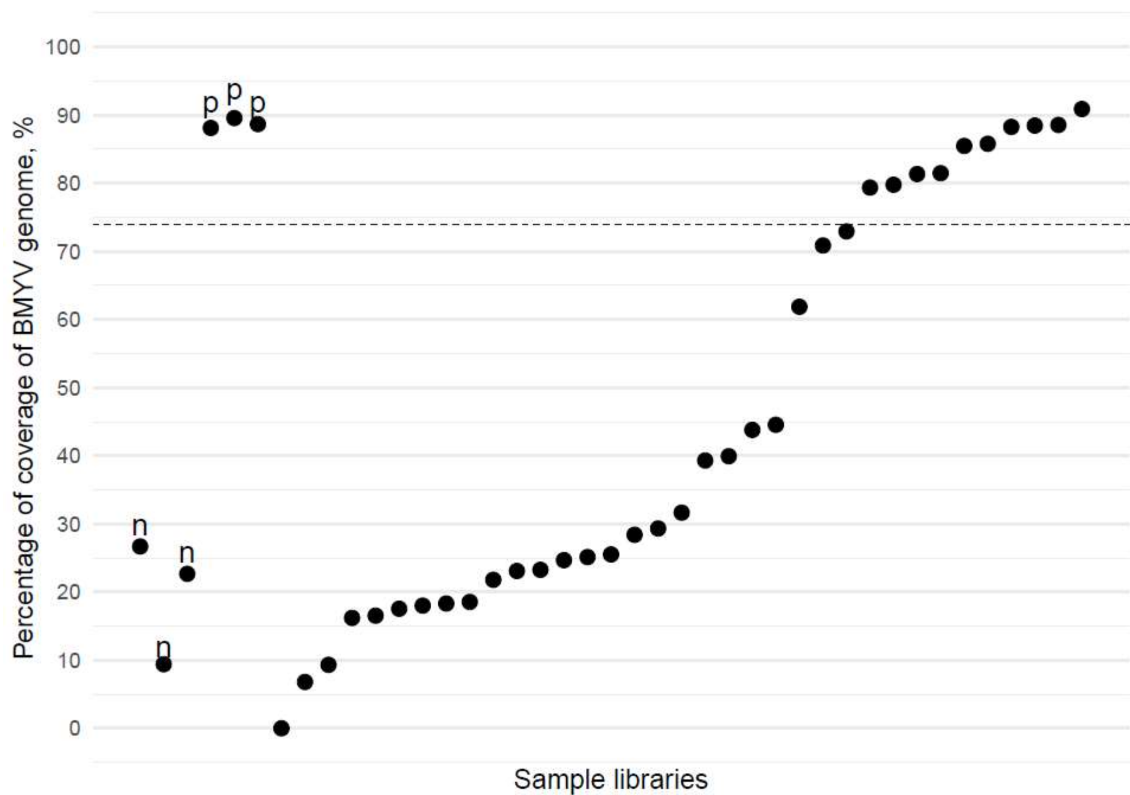


Figure 3.4: scatter plot showing the percentage coverage of the Beet mild yellowing virus (BMYV) genome of each of the 2019 and 2020 sample small RNA libraries. p indicates BMYV positive control libraries. n indicates negative control libraries. The dotted line marks threshold value of 74%.

The same clear difference between positive and negative controls was also seen when focusing on reads mapping to BChV. Both BChV positive controls had more than 90% of the BChV genome present, compared to the negative controls which all had less than 40%. None of the BMYV or BYV positive controls reached the 74% threshold. However, unlike BMYV, no grouping of survey samples was observed as shown in Figure 3.5. Using the 74% threshold, 17 samples were classed as positive for BChV.

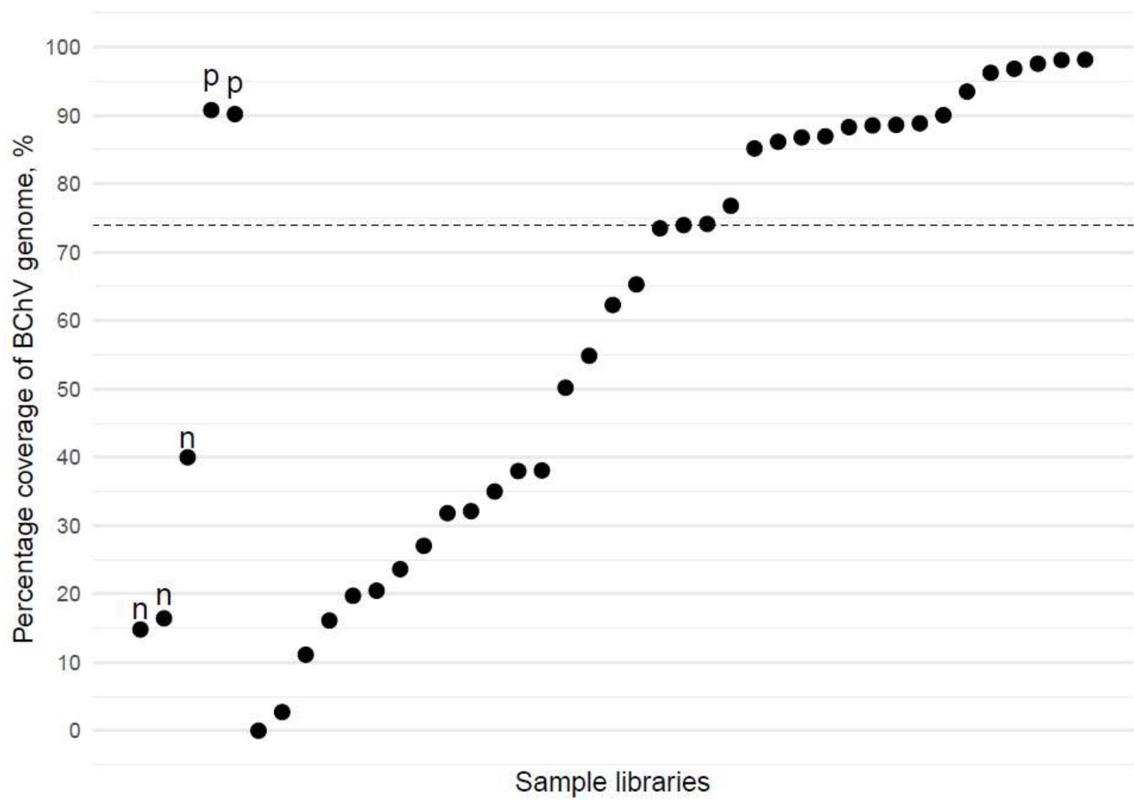


Figure 3.5: scatter plot showing the percentage coverage of the Beet chlorosis virus (BChV) genome of each of the 2019 and 2020 sample small RNA libraries. p indicates BChV positive control libraries. n indicates negative control libraries. The dotted line marks threshold value of 74%.

3.3.1.3 Read data mapping to the ORF0 region

Analysis of the 5’ reading frames of BMYV, BChV, TuYV and BWYV identified the genome region spanning ORF0 as the least homologous, with lower percentage identities across all virus pairings compared to ORF1 and ORF2 (Table 3.2, 3.3 and 3.4).

Table 3.2: percentage identity matrix of 30-750nt region (open reading frame 0) of Beet chlorosis virus (BChV), Beet mild yellowing virus (BMYV), Beet western yellows virus (BWYV) and Turnip yellows virus (TuYV) produced by Clustal Omega 2.1 multiple sequence alignment. Overall mean percentage identity = 46.045%

	BChV	BMYV	BWYV	TuYV
BChV	100.00			
BMYV	43.34	100.00		
BWYV	42.20	56.50	100.00	
TuYV	43.71	43.65	46.77	100.00

Table 3.3: percentage identity matrix of 16-2130nt region (open reading frame 1) of Beet chlorosis virus (BChV), Beet mild yellowing virus (BMYV), Beet western yellows virus (BWYV) and Turnip yellows virus (TuYV) produced by Clustal Omega 2.1 multiple sequence alignment. Overall mean percentage identity = 50.945%

	BChV	BMYV	BWYV	TuYV
BChV	100.00			
BMYV	47.24	100.00		
BWYV	47.60	61.31	100.00	
TuYV	46.99	49.97	52.56	100.00

Table 3.4: percentage identity matrix of 1540-3400nt region (open reading frame 2) Beet chlorosis virus (BChV), Beet mild yellowing virus (BMYV), Beet western yellows virus (BWYV) and Turnip yellows virus (TuYV) produced by Clustal Omega 2.1 multiple sequence alignment. Overall mean percentage identity = 63.178%

	BChV	BMYV	BWYV	TuYV
BChV	100.00			
BMYV	59.79	100.00		
BWYV	61.42	70.82	100.00	
TuYV	60.32	62.98	63.74	100.00

The percentage of sample reads mapping to the ORF0 region of BMYV is shown in Figure 3.6. The percentage of this genome region found in both the positive and negative controls was slightly lower than the percentage of the whole genome. Despite this, both sets of controls still grouped together and were clearly separated from each other with the negative controls ranging 6.0-24.3% and the positives 82.5-85.9%. The survey samples fell into at least two, possibly three, discrete

groups: less than 31% (classed as negative), above 80% (classed as positive) and between 31-80% which were likely to contain a polerovirus but could not be reliably called as BMYV infected.

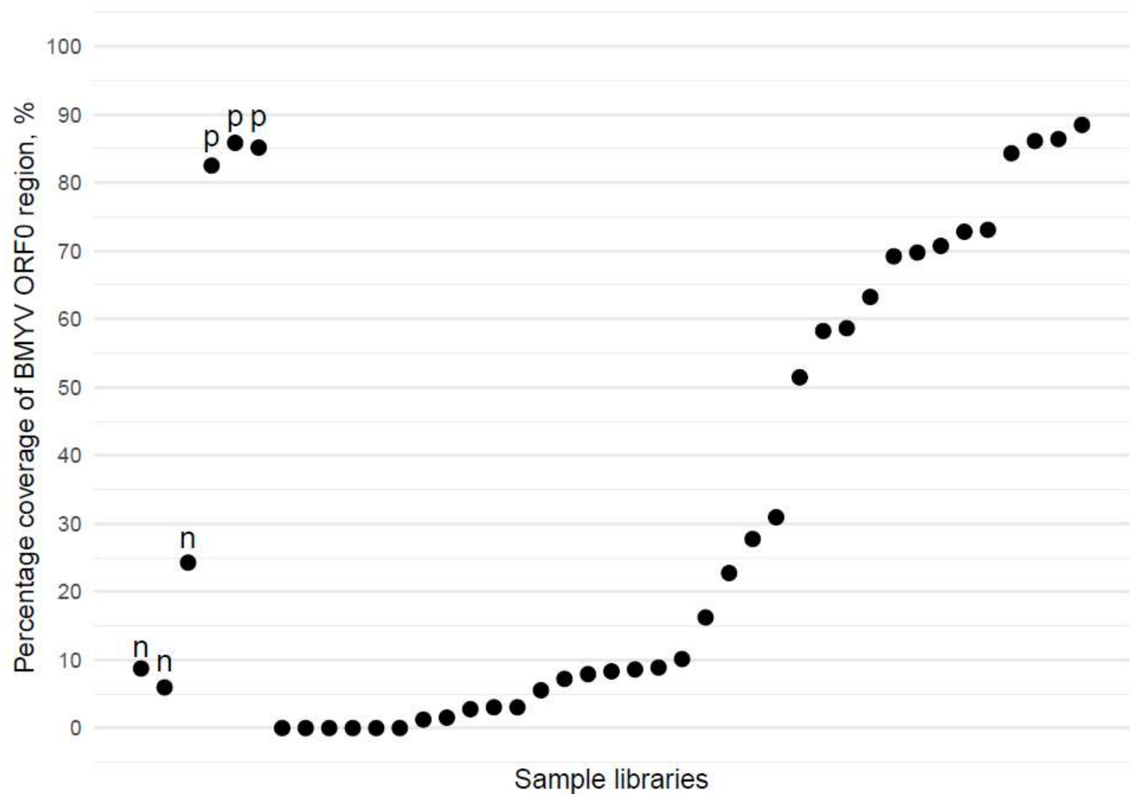


Figure 3.6: scatter plot showing the percentage coverage of the Beet mild yellowing virus (BMYV) open reading frame (ORF) 0 genome region of each of the 2019 and 2020 sample small RNA libraries. p indicates BMYV positive control libraries. n indicates negative control libraries.

The grouping of samples was less obvious when assessing the percentage of sample reads mapping to the ORF0 region of BChV (Figure 3.7). As with BMYV, positive and negative controls were clearly distinguishable with ranges of 99.6-97.8% and 0-31.8% respectively. Of the 29 survey samples, 18 contained more than 80% of the ORF0 BChV genome region and were determined to be BChV positive. Samples with less than 32% of the genome region present were considered negative based on the grouping seen with the BMYV data and the BChV negative controls. The three BMYV controls contained 11.65, 15.12 and 55.2% of the BChV ORF0 region, compared to 0-8.6% of the BMYV ORF0 found in the BChV positive controls. As such, samples with between 32-80% of the BChV ORF0 region were classed as polerovirus positive but not specifically BChV positive.

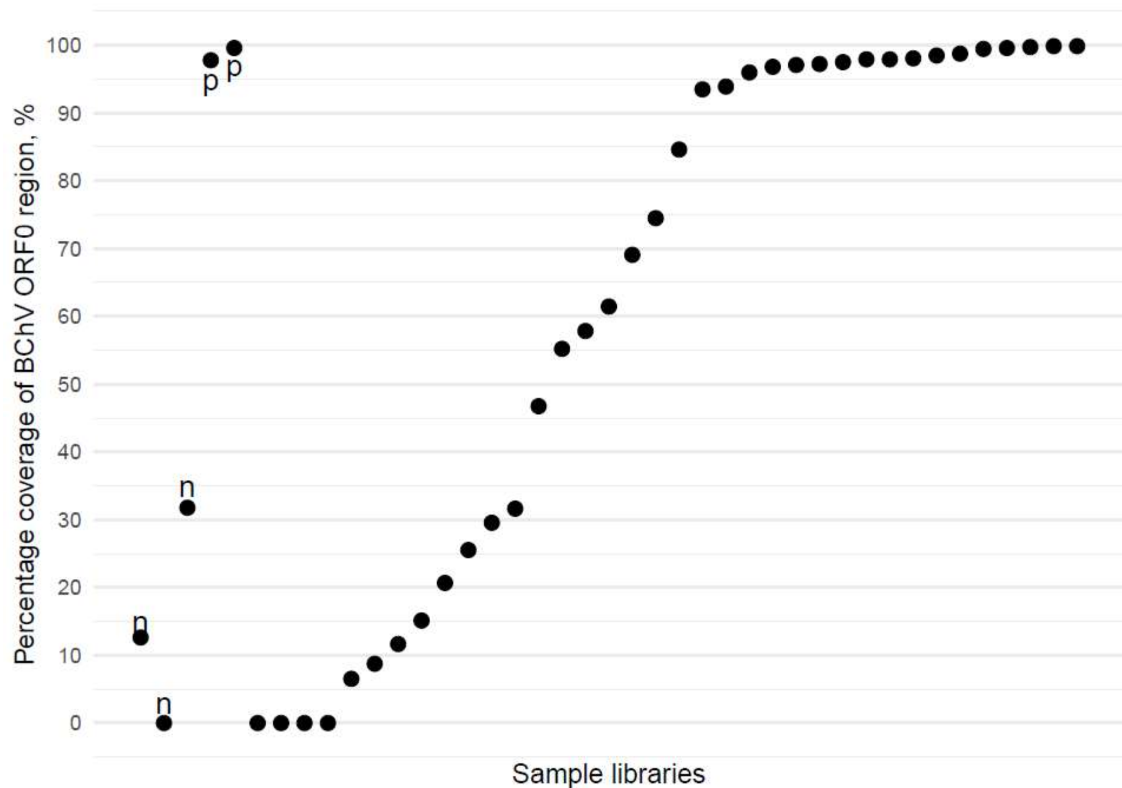


Figure 3.7: scatter plot showing the percentage coverage of the Beet chlorosis virus (BChV) open reading frame (ORF) 0 genome region of each of the 2019 and 2020 sample small RNA libraries. p indicates BChV positive control libraries. n indicates negative control libraries.

3.4.2 TuYV and BWYV

As with BMYV and BChV the percentage of sRNA library reads mapping to TuYV was low, between 0-0.46% (Figure 3.8). The negative controls contained between 0-0.15% of reads mapping to TuYV, however as no TuYV positive controls were used it was not possible to compare these results to a known positive. Two outliers were observed in the data set having 0.46% and 0.43% of reads mapping to TuYV and could be considered positive for TuYV as they had more than twice the number of mapping reads compared to the mean of the negative controls. These two samples were the same samples identified as outliers when investigating the percentage of reads mapping to BMYV.

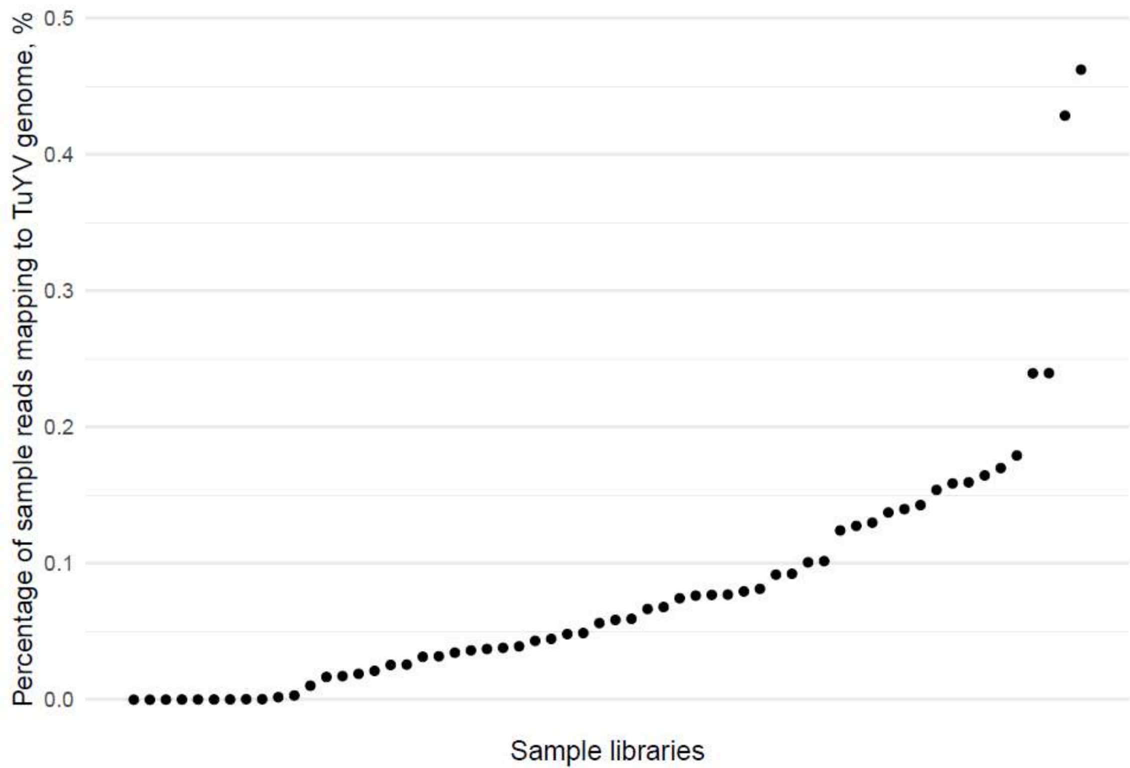


Figure 3.8: scatter plot showing the percentage of total small RNA (sRNA) library reads mapping to the Turnip yellows virus (TuYV) reference genome for each of the 2019, 2020 and 2021 sample sRNA libraries.

When refining the read data to measure the percentage of the TuYV genome found within the sRNA libraries, two distinct groups of samples emerged: those with less than 30% of the TuYV genome present and those with more than 40% (Figure 3.9). Two of the negative controls were in the <30% group, but one negative control had 44.7% of the TuYV present. Overall, the percentage of TuYV genome present was lower than that seen for both BMYV and BChV genomes with no samples containing more than 55% of the TuYV genome.

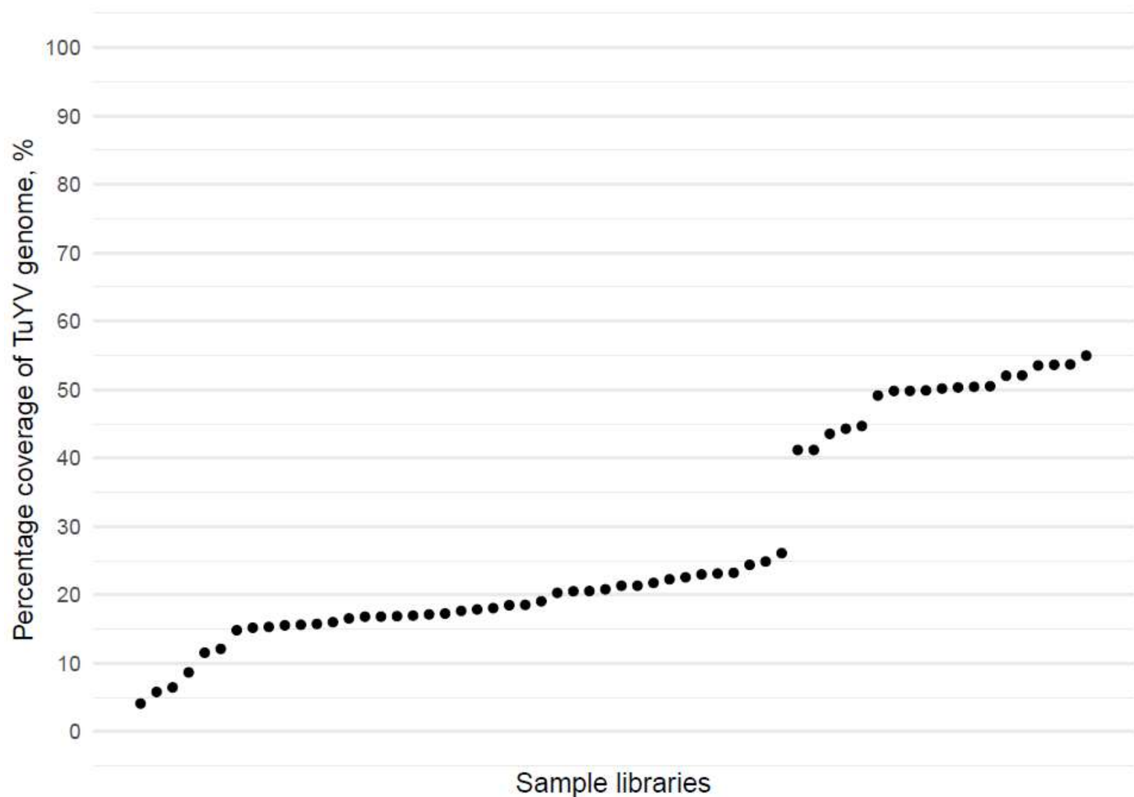


Figure 3.9: scatter plot showing the percentage coverage of the Turnip yellows virus (TuYV) reference genome of each of the 2019, 2020 and 2021 sample small RNA libraries.

By focusing on the ORF0 region of the TuYV genome it became clear than none of the survey samples were infected with TuYV (Figure 3.10). None of the samples had more than one read mapping to this region, including the two outlying samples from the first analysis approach. The results of reads mapping to BWYV was very similar to that of TuYV, with up to 57% of the BWYV genome present in some sample sRNA libraries. However, as no reads were found in any sample to map to the ORF0 region of BWYV all samples were determined negative for BWYV.

Figure 3.10: scatter plot showing the percentage coverage of the Turnip yellows virus (TuYV) open reading frame (ORF) 0 genome region of each of the 2019, 2020 and 2021 sample small RNA libraries.

3.4.3 BYV

A much larger proportion of sample sRNA library reads mapped to BYV than to the poleroviruses (Figure 3.11). There was also a much greater distribution of samples with survey libraries ranging from 0 -71.8% reads mapping to BYV. There was a clear discrimination between positive and negative controls with BYV positive controls having between 5.3-31.9% of BYV mapping reads, whilst all three negative controls contained 0.0%. Given the clear negative results, any survey sample containing more reads mapping to BYV than the lowest positive control (5.3%) was considered infected with BYV.

Figure 3.11: scatter plot showing the percentage of total small RNA (sRNA) reads mapping to the Beet yellows virus (BYV) reference genome for each of the 2019 and 2020 sample sRNA libraries, alongside the negative control libraries (indicated by 'n') and BYV positive control libraries (indicated by 'p').

3.4.4 2021 survey

Of the 338 leaves received in the 2021 autumn virus survey, 117 were determined to be positive for BYV (34.6%) by ELISA. 156 of the 338 leaves were determined positive for polerovirus, of which 75 were followed up with qPCR analysis to determine if they carried BMYV and/or BChV. Of these 75 leaves 45 were positive for BChV, 14 were positive for BMYV and 20 were negative for both viruses. 4 of the 75 leaves were found to be infected with both BMYV and BChV. This higher incidence of BChV compared to BMYV supports the findings of the 2019 and 2020 surveys conducted by the sRNA library sequencing approach.

The results from the comparison between qPCR and sRNA library diagnostic approaches, in identifying BMYV and BChV infection, are shown in Table 3.5. Only three samples were identified as BChV negative via qPCR. This result was supported by the ORF0 analysis, with the sRNA libraries of these samples both containing less than 80% of the ORF0 region. For BMYV, no samples passed the 80% ORF0 region threshold. However, 3 samples were determined BMYV positive by qPCR,

these samples contained the three highest percentages of the ORF0 region in the data set, ranging from 67.1 to 71.4%.

Table 3.5: comparison of qPCR call and percentage coverage of open reading frame (ORF) 0 region of Beet mild yellowing virus (BMYV) and Beet chlorosis virus (BChV) present in each sample.

Sample number	BChV qPCR call	BMYV qPCR call	Percentage coverage of BChV ORF0 region	Percentage coverage of BMYV ORF0 region
21-071	Positive	Negative	98.34	26.21
21-039	Positive	Negative	97.92	20.11
21-278	Positive	Negative	96.39	12.07
21-303	Negative	Negative	69.07	10.68
21-187	Positive	Negative	98.47	10.54
21-196	Positive	Negative	96.26	9.15
21-111	Positive	Negative	98.47	8.88
21-024	Positive	Negative	99.58	5.41
21-020	Positive	Negative	97.78	0.00
21-294	Positive	Positive	99.72	67.13
21-254	Negative	Positive	19.83	69.07
21-056	Positive	Positive	98.06	71.43
21-179	Positive	Negative	96.95	2.77
21-121	Positive	Negative	99.03	13.31
21-097	Negative	Negative	35.51	65.19
21-290	Positive	Negative	99.31	0.00
21-256	Positive	Negative	95.84	53.81

3.5 Discussion

3.5.1 Prevalence of BYV

Using sRNA library sequencing to identify viruses is a novel approach to plant diagnostics and has not been exploited previously for studying the virus yellows complex in sugar beet. In this study, initially the percentage of total sRNA library reads, mapping to the virus of interest, was calculated. This methodology proved successful in determining BYV positive samples using the lowest value of the BYV positive controls as a threshold above which survey samples were deemed BYV positive.

However, one sample from 2020 narrowly missed the threshold value, having 4.5% of reads mapping to BYV, compared to the threshold value of 5.3%. This result may be a false negative, perhaps due to a low BYV titre in the sample leaf. Alternatively, it may be a true negative with mapping reads caused by contamination during the sRNA library preparation, particularly as some of the other samples had such a high level of BYV present. However even when treating this sample as negative there were a higher number of BYV positive samples in 2020 compared to 2019.

In 2019, 26.6% of samples were found to be positive for BYV compared to 57.1% in 2020. In 2019 the leaf samples used were freeze dried and stored for much longer than those from 2020. As the lower incidence of BYV was detected in the 2019 samples the impact of longer storage cannot be ruled out; degrading the viral RNA and therefore reducing the abundance of BYV RNA present in the sRNA library. Nevertheless, this variation in prevalence between years fits with findings of previous studies (Hossain et al., 2021; Stevens et al., 2005b). The 2021 larger scale survey also showed variation in BYV prevalence between years, with 34.6% of samples testing positive for BYV via ELISA. This is a decrease of 22.5% compared to the 2020 BYV prevalence (Figure 3.12).

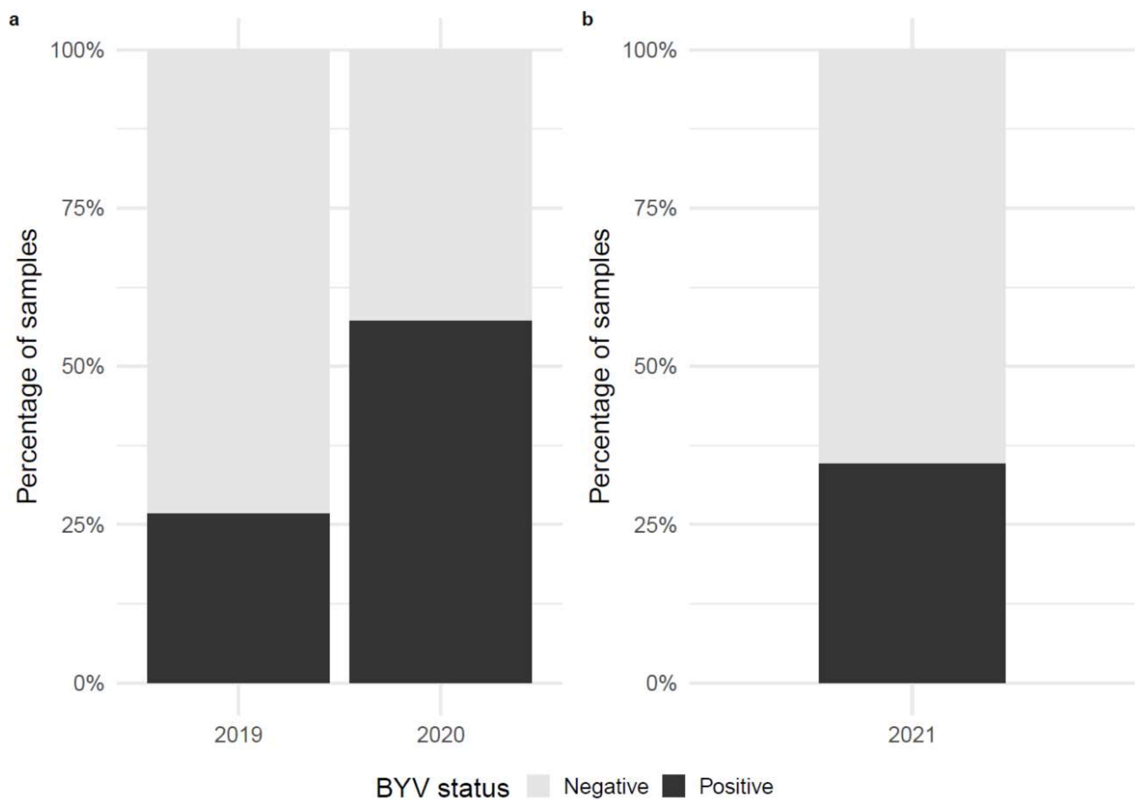


Figure 3. 12: bar plots showing prevalence of Beet yellows virus (BYV) in 2019, 2020 and 2021. a – percentage of samples determined to be positive for BYV in 2019 and 2020 based on the percentage of total small RNA library reads mapping to the BYV reference genome, based on a threshold value of 5.3%. b – percentage of 2021 survey samples containing BYV determined by enzyme-linked immunosorbent assay (ELISA) result.

The reasons for the variation in BYV prevalence between years has not yet been ascertained. One possible explanation is the impact of winter weather conditions on the survival of virus host species and therefore the abundance of virus sources. BYV is reported to have a narrower host range than BMYV and BChV and does not survive harsh winter conditions in many plant species other than *Beta* species (Hani, 1988; Stevens et al., 2005b). Therefore, harsh winters are more likely to reduce sources of BYV than the beet poleroviruses, leading to lower relative prevalence of BYV in the subsequent sugar beet crop. The mild winter of 2019/20 followed by the higher BYV prevalence in 2020 would support this hypothesis. However, it is still not clear what, if any, legacy effect the use of neonicotinoid seed treatments may be having on virus epidemiology.

Although the interpretation of sRNA library sequencing data was straightforward in determining the presence of BYV, the approach still took much longer than the established BYV ELISA method and did not provide any major benefits. The DSMZ BYV antibody set has no known cross-reactivity

with other plant viruses, making it as reliable, yet cheaper and faster than the sRNA sequencing approach (DSMZ, 2023). Therefore, when solely diagnosing a suspected BYV infection sRNA library sequencing is not the best diagnostic to use.

3.5.2 Prevalence of BMYV and BChV

Compared to BYV, only a very small proportion (<2.8%) of sample sRNA library reads mapped to either the BMYV or BChV genomes. There was also no clear differentiation between the positive or negative controls, hence this approach did not appear to be a suitable method to determine virus infection. One explanation for this is that unlike BYV, both BMYV and BChV are phloem limited (Peter et al., 2009) and are unlikely to be found at high titres within the leaf blade used for RNA extraction and subsequent sRNA library production. Some isolates of BMYV have also been shown to have RNA silencing suppression activity which would further reduce the abundance of BMYV viral sRNA within the sample sRNA library (Kozlowska-Makulska et al., 2010).

Given the low read numbers mapping to the beet poleroviruses the methodology was refined to focus on the percentage of the BMYV and BChV genomes present within the sample libraries. This approach provided clearer differentiation between positive and negative controls and enabled partial grouping of samples. Using a threshold value of 74%, 13.3% of samples in 2019 and 35.7% of samples from 2020 were deemed positive for BMYV compared to 46.7% and 71.4% for BChV in 2019 and 2020. However, this approach has a high risk of yielding false negative results because it is possible sampled leaves were infected with one of these viruses but by chance the sRNA library produced did not include more than 74% of the virus genome. Conversely, reducing this threshold increases the risk of false positives due to the short read length and high sequence homology between poleroviruses. This makes it likely for reads originating from one virus to cross map to other viruses.

To further improve the methodology the less homogenous 5’ end of the polerovirus genomes was targeted. Focusing specifically on the 30-750nt region surrounding ORF0, which had the lowest percentage identity of the 5’ ORFs, reduced the likelihood of reads cross-mapping between poleroviruses. This approach identified more samples in both 2019 and 2020 as positive for BChV than BMYV. Using the conservative 80% threshold, 62.1% of samples had BChV compared to only 3.4% with BMYV (Figure 3.13 a). This trend was still seen if the lower 31% BMYV, and 32% BChV threshold was used with 79.3% of samples determined BChV positive and 34% BMYV positive (Figure 3.13 b).

The qPCR assay run in 2021 for BMYV and BChV was run using the same extracted RNA that the sRNA libraries were made from, enabling a direct comparison between the two diagnostic approaches (Table 3.5). The results of the BChV qPCR assay supported the use of the 80% ORF0 threshold as used to interpret the sRNA sequencing data. Results were more contradictory for BMYV. The 80% ORF0 threshold was not supported by the qPCR results, with the three BMYV-positive qPCR samples not surpassing the 80% threshold. The BMYV qPCR assay has been tested against BChV, BWYV, TuYV, Beet leaf yellowing virus (BLYV), Brassica yellowing virus (BrYV), Potato leafroll virus (PLRV) and Cucurbit aphid-borne yellows virus (CABYV) along with healthy plant tissue including beta vulgaris (Wulf Menzel personal communication). Therefore, the results are unlikely to be false positives caused by cross-reactivity with the plant tissue or other polerovirus.

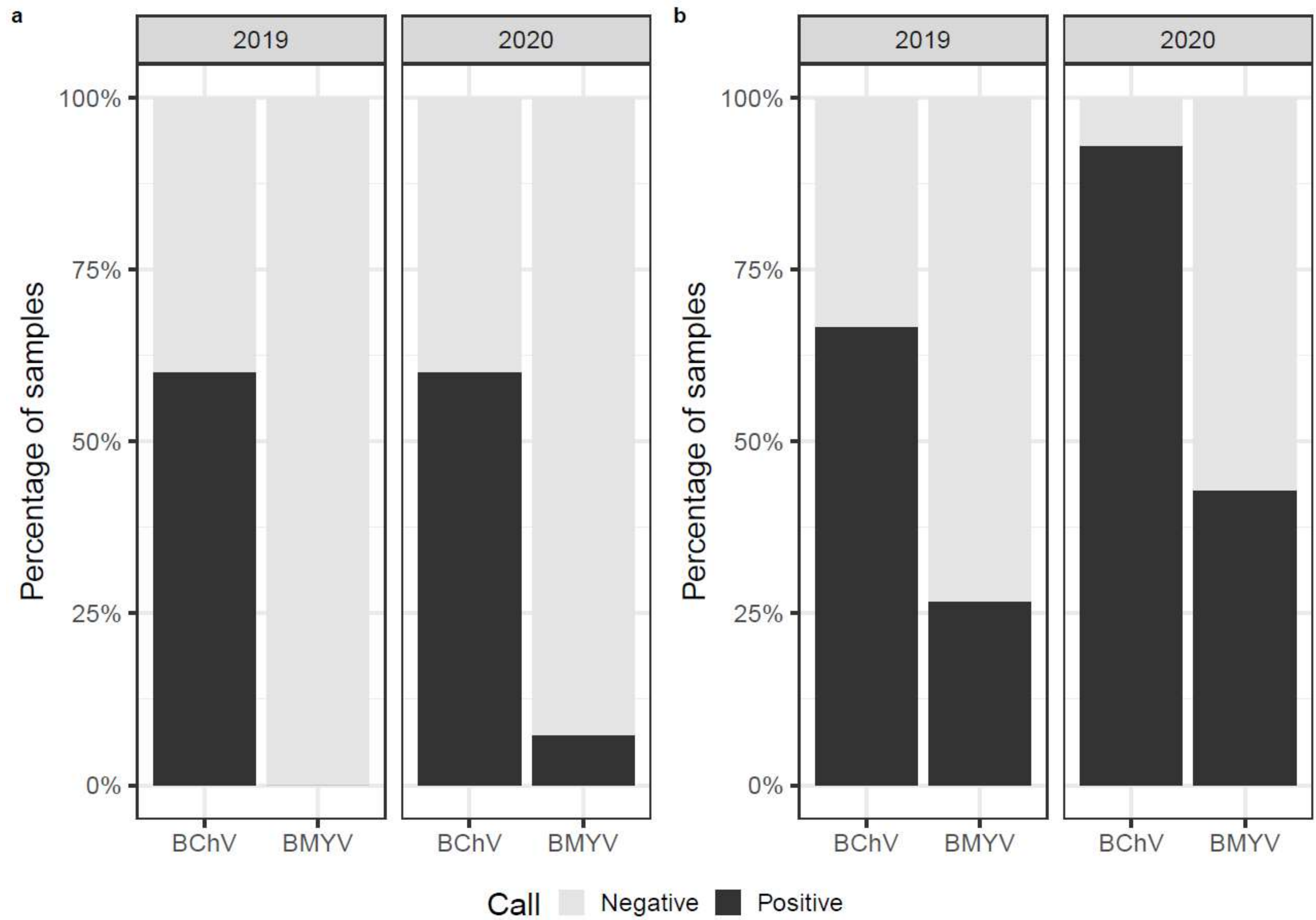


Figure 3. 13: Prevalence of Beet mild yellowing virus (BMYV) and Beet chlorosis virus (BChV) in 2019 and 2020 determined by percentage of open reading frame (ORF) 0 region present in small RNA library. a - using conservative threshold of 80% above which samples were considered positive, b - using lower threshold of 31% for BMYV and 32% for BChV above which samples were considered positive.

The higher prevalence of BChV compared to BMYV was also observed in the larger survey conducted in 2021. 46.2% of the 338 sampled leaves were determined polerovirus positive by ELISA (Figure 3.14 a). Of the subset of these positive leaves which were tested via qPCR, 60.0% were found BChV positive, compared to 18.6% BMYV positive (Figure 3.14 b). Only a randomly stratified sample of leaves which were polerovirus positive (as determined by ELISA) were analysed via qPCR. It is possible that the polerovirus positive leaves which were not qPCR tested were all BMYV positive, however this is unlikely especially given the supporting results from 2019 and 2020.

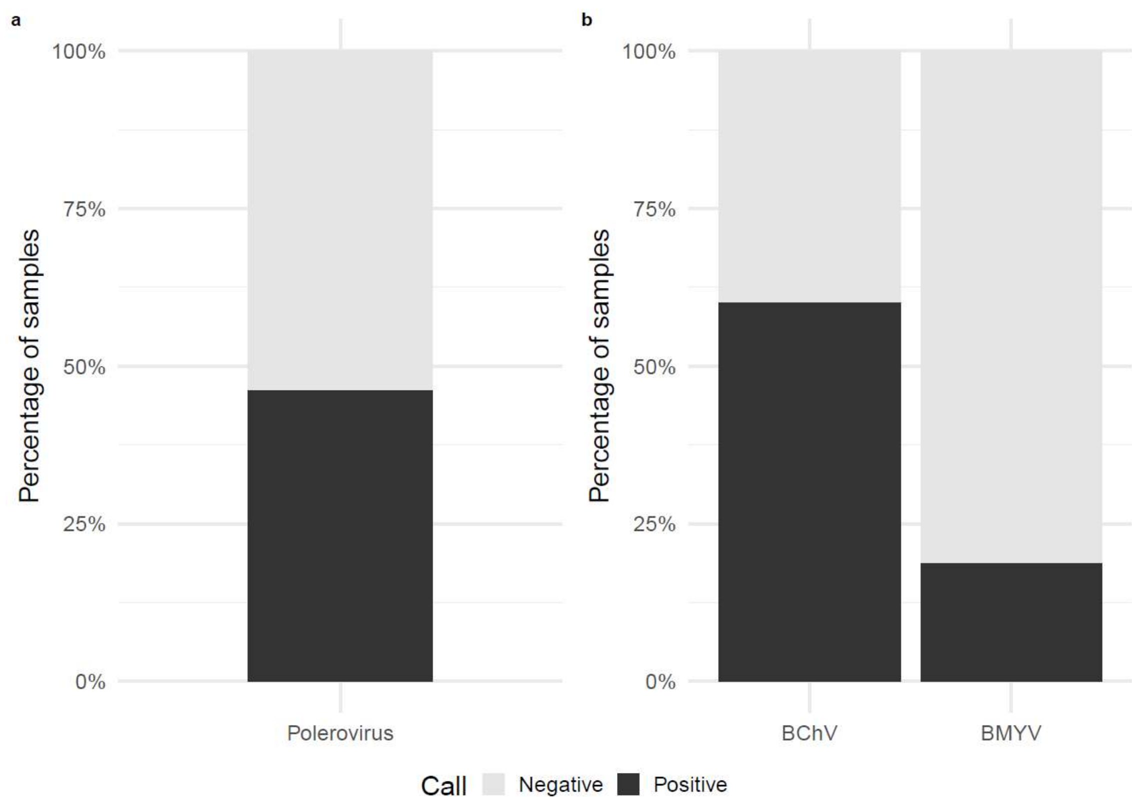


Figure 3.14: bar charts showing prevalence of Beet chlorosis virus (BChV) and Beet mild yellowing virus (BMYV) amongst samples collected during the 2021 larger scale survey. a - percentage of samples with polerovirus based on enzyme-linked immunosorbent (ELISA) assay result. b - percentage of samples with BChV and BMYV as determined by qPCR.

sRNA library sequencing is an improvement on the currently available ELISA diagnostics in its greater ability to discriminate between BMYV and BChV. However, because of the low read numbers, and high homogeneity between poleroviruses it was still not always possible to determine a sample as BMYV or BChV positive, or indeed a mixed BMYV and BChV infection. In 2020 at the start of this project, no qPCR assay for reliable BChV and BMYV detection was available. Although this project could have aimed to design such an assay it was decided that trialling the

sRNA sequencing approach would yield more information on potential other poleroviruses present; consequently this was the approach taken.

In December 2020 Wulf Menzel shared a yet unpublished qPCR assay developed to differentiate between BMYV and BChV. This diagnostic produced clearer results than the sRNA library approach and was also more cost and time efficient. qPCR assays rely on the specificity of primers, and the homogeneity of those primer target sequences across the targeted virus species. There is a chance that some virus positive samples were determined negative via qPCR owing to sequence variation in the primer target site. Twenty samples which had tested positive for polerovirus via ELISA, were negative with the qPCR assay. There are a number of possible explanations for these results. Firstly, the samples could be ELISA false positives, made more likely given the high throughput approach. Alternatively, they may be infected with isolates of BMYV and/or BChV which do not contain the primer target sequence. Or they may contain a polerovirus which is not BMYV or BChV, such as BWYV or TuYV, though this is not supported by the sRNA library sequencing data.

The higher incidence of BChV compared to BMYV goes against the findings of previous UK virus yellows surveys. Historical surveys identified BMYV as the most prevalent polerovirus in the UK (Stevens et al., 2005b). Nevertheless, the results presented here do align with the findings of (Hossain et al., 2021) for France, where BChV was also identified as more prevalent than BMYV. It is not apparent whether these findings indicate a stable shift towards BChV or if they are a snapshot in a longer-term cycle of alternating polerovirus abundance. To understand this interaction, further studies should be undertaken, ideally annually, so that long-term prevalence data can be collected and changes in virus epidemiology reliably identified. These results do, however, highlight the importance of developing sugar beet varieties which are resistant to BChV not only BMYV.

3.5.3 Occurrence of TuYV and BWYV in UK beet

This survey did not identify TuYV or BWYV in *Beta vulgaris* sp. in the UK in 2019, 2020 or 2021. Although 14.6% sRNA libraries contained more than 50% of the TuYV genome, all these libraries each also contained more than 70% of either the BMYV or BChV genome. The same situation was seen with BWYV, with the 14.6% of sRNA libraries containing more than 50% of the BWYV each also containing more than 80% of either the BMYV or BChV genome. These results could be interpreted as showing mixed infections of TuYV or BWYV with BMYV or BChV. Yet given only one read from one sample mapped to the 30-750nt region of TuYV or BWYV, it is more likely the mapping reads originated from either BMYV and/or BChV and were cross-mapping to TuYV and BWYV.

Some studies have identified isolates of TuYV which infect sugar beet, suggesting a broadening of the TuYV host range and potential risk to the sugar beet crop (Newbert, 2016; Puthanveed et al., 2023). However to date, no TuYV has been isolated from commercially grown sugar or fodder beet in the UK. This is despite a known high incidence of TuYV in *Myzus persicae* and *Macrosiphum euphorbiae* aphids entering UK sugar beet crops. The yellow water pan network run by the BBRO, catches *M. persicae* and *M. euphorbiae* aphids entering UK sugar beet crops between April and July each year. The aphids caught in these traps are tested via qPCR for BMYV/BChV and TuYV. Over the last seven years (2017 to 2023), on average 81.3% of tested aphids have been carrying TuYV (BBRO personal communication). Given this high pressure, if TuYV was entering UK sugar beet plants it seems likely we would have identified at least one infected plant during this survey, or indeed see a much higher incidence of symptomatic sugar beet plants.

Reliable differentiation between these closely related poleroviruses is challenging. Sequencing approaches, such as the sRNA library sequencing used here, theoretically permit this differentiation. However in practice, when working with short read lengths and potentially mixed infections, reliably identifying each and every polerovirus present within a sample is still difficult. The main focus of this survey was to understand the prevalence of BMYV, BChV and BYV in the UK and as such no TuYV or BWYV positive control sRNA library was produced or sequenced. Future efforts to identify if these two viruses are present in the UK sugar beet crop must include such positive controls if a reliable and accurate methodology is to be devised. Were these viruses to be isolated from sugar beet, host range and transmission studies would be needed to better understand the risk posed to the UK sugar beet crop. For example, if TuYV were to be transmissible from one sugar beet plant to another the potential consequences would be much more severe than if sugar beet were to be a ‘dead-end’ host to the virus.

3.5.4 Sea and fodder beet implications

This survey also included symptomatic sea beet and fodder beet leaves. Identifying sources of virus infection is important in predicting virus risk to the sugar beet crop. The British Beet Research Organisation (BBRO) monitors virus yellows in the UK sugar beet crop however fodder beet falls outside of its remit. As such levels of virus yellows in fodder beet crops are largely unknown, despite fodder beet often being grown in close proximity to sugar beet and being a potential source of virus yellows. BMYV, BChV and BYV were all identified in fodder beet samples, confirming their risk as virus sources.

Only two symptomatic sea beet leaves were found and tested, one of which was positive for BMYV. Future virus studies on sea beet should include samples not exhibiting virus infection. *Beta maritima* has been used as a source of disease resistance and bred into commercial sugar beet lines (Asher et al., 2001). Therefore, it is possible that some virus-infected *B. maritima* plants do not express symptoms. Expanding sampling to include non-symptomatic plants would provide a more thorough dataset on the prevalence of virus in *B. maritima* plants.

Although only a limited number of sea beet leaves were tested, the results illustrate the potential risk posed by non-agricultural plant species to the UK sugar beet industry by providing sources of virus infection. In this study only *Beta* species were tested, however all three viruses within the virus yellows complex are known to infect other plant species (Hani, 1988; Hauser et al., 2002; Stevens et al., 1994b). These plants can act as a 'green bridge' maintaining virus from one sugar beet growing season to the next. The relative abundance of non-sugar beet hosts may also impact virus yellows epidemiology from year to year. For example, if winter weather conditions favoured the survival of BYV host species over BMYV host species this may result in higher BYV prevalence in the sugar beet crop. Expanding virus prevalence surveys, such as this one, to include known non-beet hosts would improve out understanding of the risks posed by such species to the sugar beet crop and potentially allow for targeted control of those species in field margins, for example.

3.5.5 Diagnostic technique development

Three different diagnostic techniques were used to determine virus infection during this survey. ELISA is a long-established method for virus detection and continues to be used in agricultural diagnostics thanks to it being high through put and relatively low cost. However, there is currently no antibody which can differentiate BMYV and BChV. qPCR overcomes this issue, discriminating between BMYV and BChV infection but the current protocol is not as high throughput as ELISA. In 2021, testing all 338 sampled leaves by total RNA extraction followed by RT-qPCR would have taken a considerable amount of time and was not financially viable.

Neither qPCR or ELISA provides sequencing data and can only be used to detect the virus for which the specific diagnostic was used. The sRNA libraries produced in this study could be used to identify any virus, including those yet to be identified. This provides a powerful tool for future epidemiological research. sRNA library sequencing is, however, more expensive and time consuming compared to qPCR, and therefore unlikely to be widely adopted.

Chapter 4: Phenotyping varietal virus responses under controlled conditions

4.1 Chapter Contributions

All work presented in this chapter was completed by me.

4.2 Introduction

Phenotyping is a crucial tool in sugar beet variety development through which advantageous traits can be identified and increased (Bosemark, 2006). When assessing a variety's performance under pest or disease pressure, variety trials are either left to become naturally infected or are purposely inoculated. In the case of developing varieties to combat virus yellows disease, future varieties ideally need to overcome all three of the major UK yellowing viruses: BMYV, BChV and BYV. Therefore sugar beet breeding lines need to be assessed for their performance under each virus.

Assessment of sugar beet varieties response to virus infection, is currently largely based on field trial performance. Such trials can be conducted on a large scale, with multiple replicates, and provide reliable data on how varieties will perform when affected with virus in a field environment. However, these types of trials have several disadvantages. Fundamentally, being located outdoors, variety field trials are at the mercy of the weather. This can have direct consequences for plant health, for example late frosts killing off vulnerable seedlings, but also makes comparisons of data across multiple years and trial locations difficult. The same is true for naturally arising pests and diseases, such as foliar fungal infections or beet leaf miner which may be present in a trial one year but absent the next.

When assessing variety performance under virus infection specifically, there is also the difficulty of successfully inoculating test plants with virus whilst minimising the risk of contaminating the wider environment. Where multiple viruses are being introduced into the same field, this issue of containment is exacerbated with contamination risks not only to the wider environment but also between virus treatments. In an outdoor field trial setting, all these challenges are combined with the need to prevent 'wild' aphids entering the trial and introducing other viruses or transferring

virus from one treatment to another. These problems can be mitigated (as discussed in Chapter 6), however, it raises many practical challenges and ultimately increases the cost of such research.

Even when all the above factors are considered, and controlled as much as they can be, field trials can still only be conducted once a year with seedlings being sown in the spring and harvested in the autumn/winter. This creates a significant delay in the generation of data on which seed breeders base their variety development upon, increasing the time it takes for resistant or tolerant varieties to come to market. There is, therefore, a clear need for an alternative to field trials for phenotyping variety virus responses.

Controlled environment facilities could provide a solution to many of these challenges. Hence, the research presented in this chapter aimed to develop a method of simultaneously phenotyping multiple viruses and varieties under controlled environment conditions. In this chapter I trialled three different controlled environment facilities to identify which, if any, could provide a viable alternative to variety field trials. A summary of the rationale behind choosing these three facilities is given below.

4.2.1 MLR growth chamber

The Versatile Environment Test Chambers (Panasonic, MLR-352) is a plant growth chamber used frequently in laboratory studies. Regarding sugar beet research specifically, the MLR-352 chambers have been used to rear virus yellows cultures at the BBRO since 2014. BMYV, BChV and BYV can all be maintained in MLR-352 chambers, as confirmed via ELISA and qPCR diagnostic testing (BBRO, personal communication). Anecdotally, although yellowing symptoms are observed in sugar beet plants in the BBRO BYV culture, rarely are symptoms of either beet polerovirus seen. Nevertheless, no published trials quantifying phenotypic response to virus yellows have been conducted in MLR-352 growth chambers, and therefore the lack of symptom expression needs to be confirmed.

4.2.2 Glasshouse

One benefit of glasshouse facilities over most reach-in controlled environment chambers is that they are generally larger providing greater growing space. This enables trials to be conducted with a larger sample size and therefore yield more reliable results. Glasshouse facilities have been used successfully to identify Turnip yellows virus (TuYV) resistance in oilseed rape varieties (Ibrahim et al., 2023), as well as sources of resistance genes in sugar beet (Asher et al., 2001). However, both these studies used viral titre (determined via qPCR (Ibrahim et al., 2023) and ELISA (Asher et al.,

2001)) to determine resistance and did not provide information on crop yield or visual symptom expression. As defined in Chapter 1 section 1.4.5, true tolerant sugar beet varieties become infected by the virus but do not express symptoms of infection and suffer no resultant yield loss. Consequently, tolerant varieties cannot be distinguished from susceptible varieties based on viral titre data alone and other phenotypic characteristics need to be assessed. A standard protocol for phenotyping sugar beet leaf yellowing to virus infection, under glasshouse conditions, has not been published to date.

One disadvantage of using glasshouse facilities for phenotyping work is that the environmental conditions are more variable than controlled environment chambers. The glasshouse facility available for this project to use at UEA, for example, is made of polycarbonate which is partially whitewashed. Although supplementary lighting and temperature control fans are present, the external weather conditions can have a large influence on both the available light and temperature inside the glasshouse. Nevertheless, the higher sample size permitted by glasshouse facilities could outweigh this reduced environmental control.

4.2.3 Conviron growth chamber fitted with LED lights

In June 2021 the UK government announced a ban on fluorescent light bulbs effective from September 2023 (Department for Business Energy and Industrial Strategy, 2021). This has triggered a move away from fluorescent light bulbs in controlled environment chambers, and the increased use of LED bulbs. LED bulbs have a lower power usage than fluorescent bulbs resulting in lower running costs, whilst still permitting full control of light levels. The GEN1000 reach-in growth chamber (Conviron) is one controlled environment chamber which utilises LED light (Conviron, 2020a). Positioned above the plant growth shelves, these LED bulbs provide broad-spectrum white light with a maximum intensity of 700 $\mu mol/m^2/sec$. Importantly the GEN1000 chambers can be programmed to ramp up and down light intensity, mimicking natural diurnal light fluctuation (Conviron, 2020b).

Given the increased plant growth area (compared to the MLR chambers) and the more advanced environmental controls (compared to both the MLR chamber and glasshouse facility), the GEN1000 controlled environment has strong potential for virus/variety phenotyping studies.

4.3 Materials and methods

4.3.1 Clip cage virus inoculation

Clip cages (BDC1540-12, BugDorm) can be used to contain viruliferous aphids on plants such as described by (Davis et al., 2005; Gray, 1991). Crucial to their successful use is achieving a sufficiently tight seal between the foam of the cage and the leaf, ensuring that aphids placed within the cage do not escape. Based on the BugDorm manufacturer's instructions, staples are used to secure the cage to the leaf. However previous testing had found this method did not produce a sufficient seal on sugar beet leaves (personal communication, BBRO). As such an adapted fixing method was developed using fine brass pins (such as Hemline Brass Craft Pins 450 Pack, Hobbycraft).

Plants were inoculated approximately two weeks after transplantation, at the two-true leaf stage. One half of the aphid cage was secured to a flat bamboo skewer (such as 123912940, Sainsbury's), and the skewer then positioned in the plant pot. This adaption meant that the weight of the cage was supported by the skewer rather than the young seedling. 10 wingless aphids were then gently transferred using a paintbrush into the second half of the aphid cage. This cage was then placed on the underside of a true-leaf and secured in place using the brass pins (Figure 4.1). Aphids were allowed to feed for 48 hours, before the cages were carefully removed and all aphids finger crushed. After the cages were removed, and to ensure all aphids were destroyed, an insecticide spray was applied to all plants aphicide (0.1g/L InSyst containing 20% w/w acetamiprid, CertisBelchim). Experiments were concluded after four weeks (pilot study in Panasonic MLR-352) or eight weeks (glasshouse and LED study).

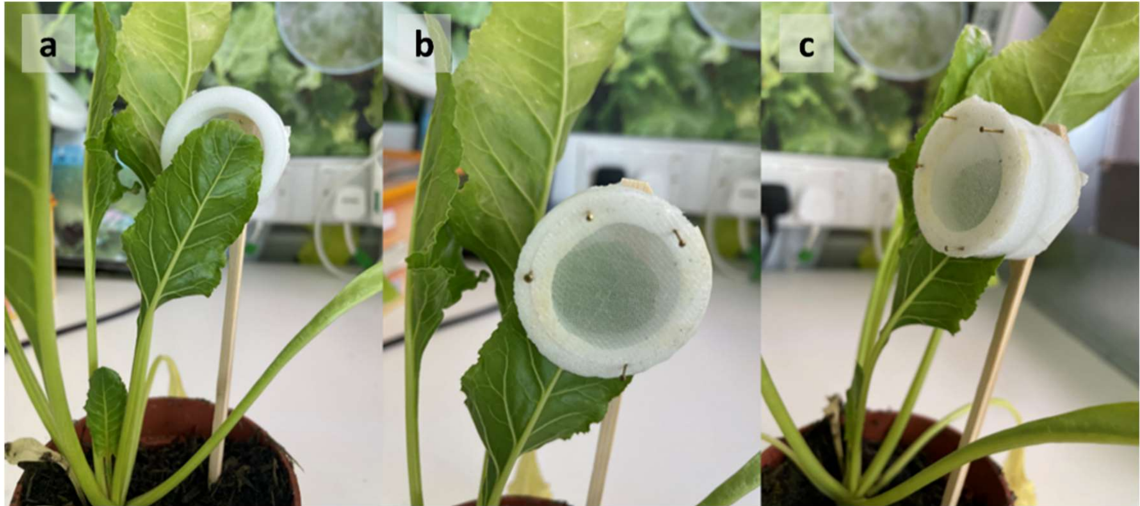


Figure 4.1: images showing the set-up of the adapted aphid cages. Image a shows the clip cage connected to the support positioned alongside the adaxial surface of a first true leaf. Images b and c show the second half of the clip cage, containing the 10 wingless aphids positioned on the abaxial surface of the leaf and attached to the support cage via fine pins.

4.3.2 Phenotype measurements

4.3.2.1 Canopy area and symptom expression

To quantify the size of plant canopy, plants were photographed from above using a PowerShot G7X camera (Canon) positioned on a tripod against a black background with a measuring tape. Images were imported into the image analysis software, ImageJ (version 1.53t) and the scale set using the known distance of the measuring tape. The 'colour threshold' tool was then applied to select the leaf area by adjusting the hue, saturation, and brightness filters (Figure 4.2). Once optimum filter settings had been determined (selecting only non-sensing canopy), based on three randomly selected plants, the canopy area was calculated using a batch process macro that measured the area of the filtered image (Wright et al., 2018).

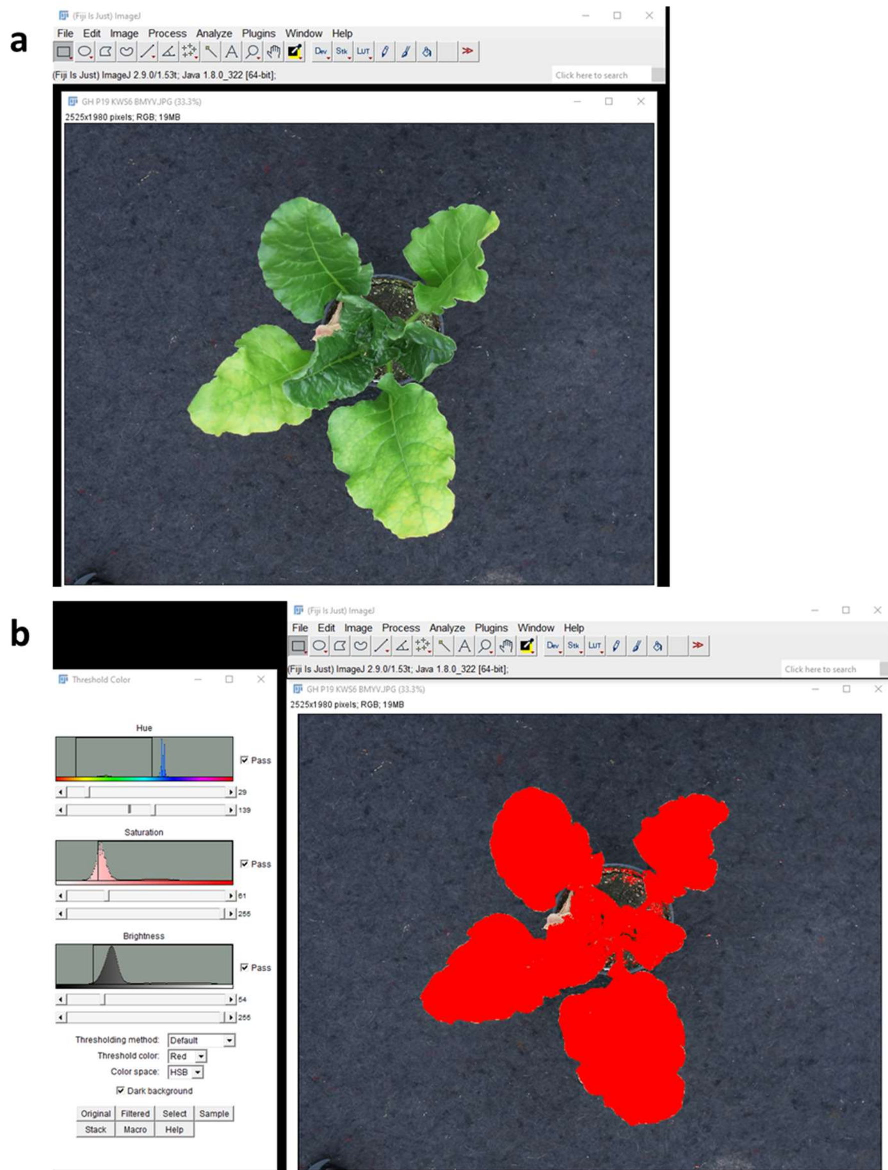


Figure 4.2: ImageJ screen shots showing user interface whilst conducting the canopy area selection process. Image a shows an example experimental image loaded into the ImageJ software. Image b shows the hue, saturation and brightness filters adjusted to select all non-senescing leaf tissue, whilst discounting the image background.

The same images were used for visual assessment of symptom expression. Symptom expression was compared to those observed in field-grown sugar beet, namely interveinal leaf yellowing and leaf thickening such as described by (Harveson et al., 2009).

4.3.2.2 Leaf weight and ELISA sampling

After photographing, all leaves were removed from the plant at the point where the leaf petiole joined the root crown. Leaves were weighed ('entire fresh weight') and then leaf disc samples

removed for ELISA testing. The remaining leaf was then reweighed ('fresh weight of sample'), and placed in a paper bag (PAP7B, polybags.co.uk). Leaves were dried at 80°C in an oven (MK53 climate chamber, Binder) until their weight no longer decreased. All samples were then reweighed in the paper bag ('dry weight including bag'). Three new, unused empty paper bags were also dried for the same time as the leaf samples to establish the weight of the dried paper bag.

To determine the total dry leaf weight the following calculation was used:

$$Weight\ of\ dried\ sample\ =\ Dry\ weight\ including\ bag\ -\ mean\ dry\ bag\ weight$$

$$Total\ dry\ leaf\ weight\ =\ \frac{Weight\ of\ dried\ sample}{Fresh\ weight\ of\ sample} \times Entire\ fresh\ weight$$

ELISA testing was conducted using the beet western yellows virus antibody sets (DSMZ) as described in Chapter 2 section 2.4.2.

4.3.2.3 Root weight

Roots were removed from the pots and carefully washed to detach any soil or compost. During the pilot study it became clear that removing all the compost from the root hairs was not a viable method. As such it was decided to remove the root hairs, leaving the tap root which could be cleaned of compost more consistently. This method was used for all subsequent experiments.

After washing the roots were blotted dry on paper towel and then weighed and placed into gusseted paper bags (PAPBG2, polybags.co.uk). Any larger roots were cut into smaller pieces to quicken the drying process. Roots were dried under the same conditions as the leaves, 80°C until their weight no longer decreased alongside three new empty paper bags. After drying was completed the roots were reweighed in their bags, and the mean empty dry bag weight removed to determine the dry root weight for each sample.

4.3.3 Pilot study

The pilot study was conducted using two varieties, KWS-1 and KWS-5 (further variety details included in Appendix A). Variety KWS-5 was understood to be susceptible at the time the trial was conducted, however was later described by the seed breeder as having medium resistance to

BMYV. KWS-1 had high resistance to BMYV infection. The study comprised of two treatments, inoculation with BMYV infective aphids, and inoculation with non-viruliferous aphids (total of 16 plants, four plants per variety/treatment). Seed from each variety was germinated in compost (Premium All Purpose, Miracle-Gro), 10 days after sowing (when most seedlings had expanded cotyledons) individual seedlings were transplanted into separate 9cm diameter pots (0.36l capacity) filled with compost. The trial was split across two Versatile Environment Test Chambers (Panasonic, MLR-352), arranged in a randomised block design comprising of four blocks. The compost contained a pre-mixed granular fertiliser, and therefore no additional fertiliser was applied.

The plants were grown under a 16-hour photoperiod, with the chamber set to 'full light' provided by 15 fluorescent tubes (FL4055 ENW/37, Panasonic), arranged to provide light from three sides. During this phase, the temperature was set to 22°C. An 8-hour dark period followed during which the temperature was set to 18°C.

Plants were inoculated with aphids, as described above, using BMYV infective aphids reared in the BBRO BMYV virus culture on *Capsella bursa-pastoris* and non-viruliferous aphids reared in the BBRO 'healthy' aphid culture on *Brassica rapa* subsp*. pekinensis* (Chapter 2, section 2.1).

The trial was concluded four weeks after inoculation. Using the methodologies described above, ELISA testing was conducted on the oldest non-senescing leaf and measurements were taken to assess canopy coverage, leaf dry weight and root dry weight.

4.3.4 Glasshouse study

The glasshouse study contained varieties KWS-1, KWS-2, KWS-3, KWS-4, KWS-6, and KWS-7 (see Appendix A for further variety details), which were trialled under non-inoculated, BChV inoculated, BMYV inoculated and combined BChV and BMYV inoculation. Seed from each variety was germinated in compost (Premium All Purpose, Miracle-Gro), in a climate-controlled glasshouse. Ten days after sowing, individual seedlings were transplanted into separate 1L (11cm diameter) pots filled with a sand-soil mix (Baileys of Norfolk). Approximately three days after transplanting 50ml ammonium sulphate fertiliser (2.9g/l) equating to 0.03g nitrogen was applied directly to the soil of each plant. A second application of fertiliser was given at the same rate one week later. Plants were arranged across four trays in a randomised block design with each tray containing one replicate of each treatment.

Plants were grown in a glasshouse at 18-22°C with additional supplementary lighting to provide a 16-hour photoperiod. Plants were inoculated with aphids, as described in section 4.3.1. The BChV

treatment was inoculated with ten viruliferous BChV infective aphids reared in the BBRO BChV virus culture on *Chenopodium capitatum.* The BMYV treatment was inoculated with ten viruliferous BMYV infective aphids reared in the BBRO BMYV virus culture on *C.bursa-pastoris.* For the mixed infection, plants were inoculated with ten BMYV and ten BChV viruliferous aphids. No aphids or clip cages were applied to the uninoculated plants.

The glasshouse study was concluded 8 weeks after inoculation. Using the methodologies described previously, measurements were taken of canopy coverage, leaf dry weight and root dry weight. As in the pilot study ELISA testing was conducted, however in this study leaf five and leaf ten from each plant was tested rather than the oldest non-senescing leaf.

4.3.5 LED light study

The LED light study contained varieties KWS-1, KWS-2, KWS-3, KWS-4, KWS-6, and KWS-7, under three test treatments; BMYV inoculated, BChV inoculated and uninoculated. Seed from each variety was germinated in compost (Premium All Purpose, Miracle-Gro) before being transplanted into 1L pots of soil-sand mix (Baileys of Norfolk). As with the glasshouse study, two doses of ammonium sulphate fertiliser (2.9g/l) were applied to the soil of each plant; the first dose approximately three days after transplanting and the second one week later. The trial was arranged across two Gen1000 reach-in chambers (Conviron), in a randomised block trial design comprised of four blocks each containing one replicate of each treatment.

Plants were inoculated as described in section 4.3.1. Each week following inoculation plants were removed from the reach-in chamber and photographed as described in section 4.3.2.1 so that canopy growth could be measured. The trial was concluded 8 weeks after inoculation, with measurements being taken as per the glasshouse study of ELISA absorbance for leaves five and ten, root and leaf dry weight, and final canopy coverage.

The plants were grown under a 16-hour photoperiod, with the chamber set to 400µmol light at canopy level provided by broad spectrum/white light LED (12 watt T5 LED fixture) arranged above the plants. During this phase, the temperature was set to 22°C. An 8-hour dark period followed during which the temperature was set to 18°C.

4.3.6 Statistical analysis

Data from all experiments were analysed using GenSTAT 22nd edition (VSN International). All graphs were produced using RStudio version 2022.02.1+461 "Prairie Trillium" released for Windows (RStudio Team 2022).

4.3.6.1 Pilot and Glasshouse study

In the pilot study two-way analysis of variance (ANOVA) in randomised blocks were conducted using the GenSTAT 'General Analysis of Variance' statistical test. The experiment design was set to "General analysis of variance', and the Y-variate to the relevant dependent variable (ELISA result, leaf area, leaf dry weight or root dry weight). The treatment structure was defined using the fixed factors 'Variety x Treatment' and the block structure to the randomised block plants had been assigned to. The least significant difference (LSD) at 5% significance calculation was included in the ANOVA.

4.3.6.2 LED study

In the LED study, two-way ANOVA in randomised blocks were conducted as detailed in section 4.3.6.1 for the ELISA, leaf area, leaf dry weight and root dry weight results. In addition, leaf area data were analysed using the GenSTAT 'repeated measures ANOVA' to assess how the treatment effects developed. The Y-variate was set as the leaf area data sets at successive time points, and the treatment structure defined using the fixed factors 'Variety x Treatment'. The block structure was set to the randomised block plants had been assigned to.

4.4 Results

4.4.1 Pilot study

4.4.1.1 ELISA results

ELISA results from the oldest non-senescing leaf showed significant differences between the plants inoculated with BMYV viruliferous aphids and those inoculated with non-viruliferous aphids, (Figure 4.3, ANOVA p = 0.008). The absorbance of the ELISA negative controls ranged from 0.204 to 0.492, resulting in a threshold of 0.793 above which a sample would be called positive. The mean absorbance for the non-viruliferous treatment was 0.27. None of the non-viruliferous treatment plants had ELISA results above the positive threshold indicating no contamination occurred between the treatments.

Although the mean absorbance for the BMYV inoculated plants was 0.93, and therefore above the positive threshold, the range of ELISA results for this treatment varied widely from 0.148 to 1.948. There was no significant difference in ELISA results between the varieties and no significant difference in the way the varieties responded to the treatments.

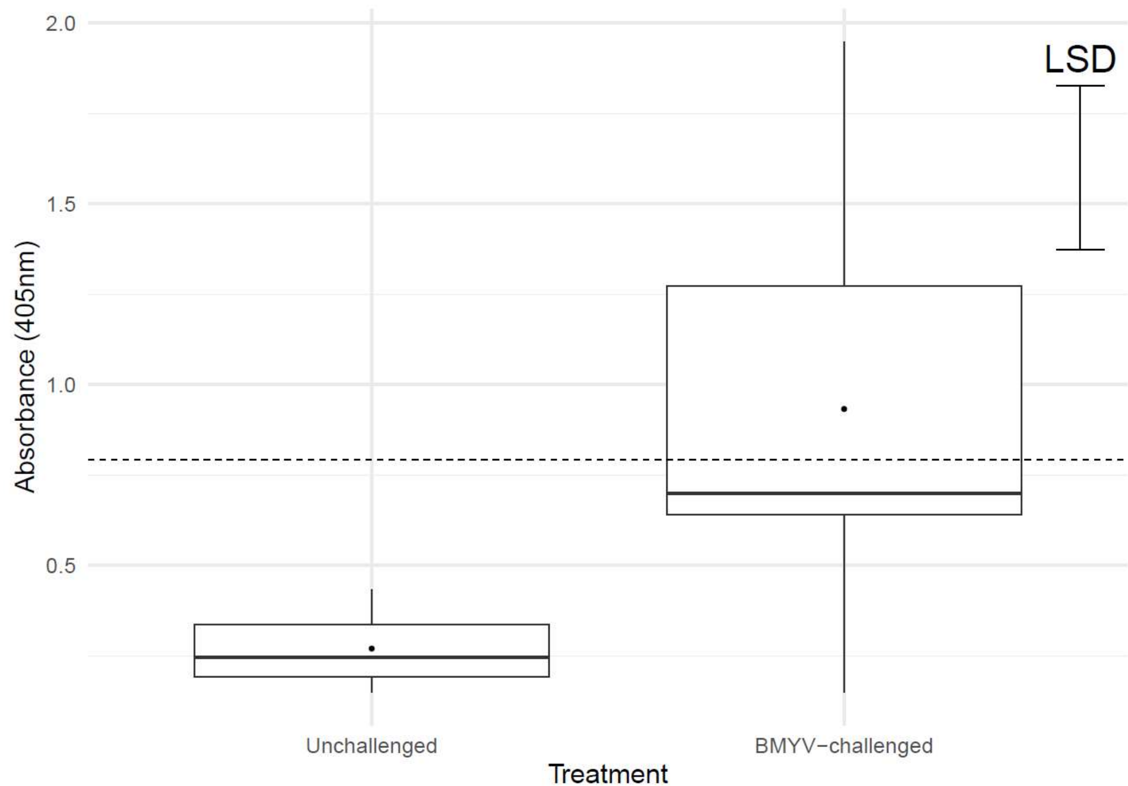


Figure 4.3: boxplot showing the combined enzyme-linked immunosorbent assay (ELISA) absorbances of varieties KWS-1 and KWS-5 of the Beet mild yellowing virus (BMYV)-challenged (inoculated with BMYV viruliferous Myzus persicae *aphids) and unchallenged (inoculated with non-viruliferous* M. persicae *aphids) treatments. The mean absorbance is indicated for each treatment by the black circular point. The dashed horizontal line indicates the ELISA absorbance value above which a sample is deemed positive (calculated by the mean of the negative controls plus three times the standard deviation), set at 0.793. Error bar shows least significant difference (LSD) at 5% significance between treatments (analysis of variance (ANOVA), p = 0.008, n = 16).*

4.4.1.2 Symptom expression

Despite significant differences in ELISA absorbance between the virus challenged and unchallenged treatments, no typical yellowing symptoms were observed in either variety (Figure 4.4). There were also no other visual phenotypic differences between the BMYV-challenged and unchallenged treatments for either variety.

Figure 4.4: photos taken from above of every plant in the pilot study at the end of the trial (4 weeks after inoculation) for both the Beet mild yellowing virus (BMYV)-challenged ((inoculated with BMYV viruliferous Myzus persicae *aphids) and unchallenged (inoculated with non-viruliferous* M. persicae *aphids) treatments. a = variety KWS-5 unchallenged, b = variety KWS- 5 BMYV-challenged, c = variety KWS-1 unchallenged, d = variety KWS-1 BMYV-challenged.*

4.4.1.3 Leaf area and dry weight

As quantitatively observed, the canopy area at the end of the study (4 weeks after inoculation) did not differ significantly between treatment (ANOVA, p = 0.705) or variety (ANOVA, p = 0.915). The mean canopy area of KWS-5 was slightly larger in the infected treatment than the uninfected (48.0cm^2 compared to 45.0cm^2 respectively). The opposite was seen with KWS-1 which had a larger canopy when uninfected compared to infected (mean of 50.9cm^2 compared to 43.4cm^2 respectively). None of these results were statistically significant.

The dry weight of the uninfected plants was higher, on average than the infected (0.671g compared to 0.570g respectively), however this difference was not statistically significant (ANOVA, p = 0.411). Neither was there any significant difference between varieties (ANOVA, p = 0.203), or in how the varieties responded to the treatments (ANOVA, p = 0.358).

4.4.1.4 Root weight

As shown in Figure 4.5, KWS-5 had a lower mean dry root weight when inoculated with BMYV than in the uninoculated treatment. Conversely, KWS-1 had a higher mean dry root weight when inoculated with BMYV. However, none of these differences were significant (ANOVA, p = 0.131), and the spread of these data were large.

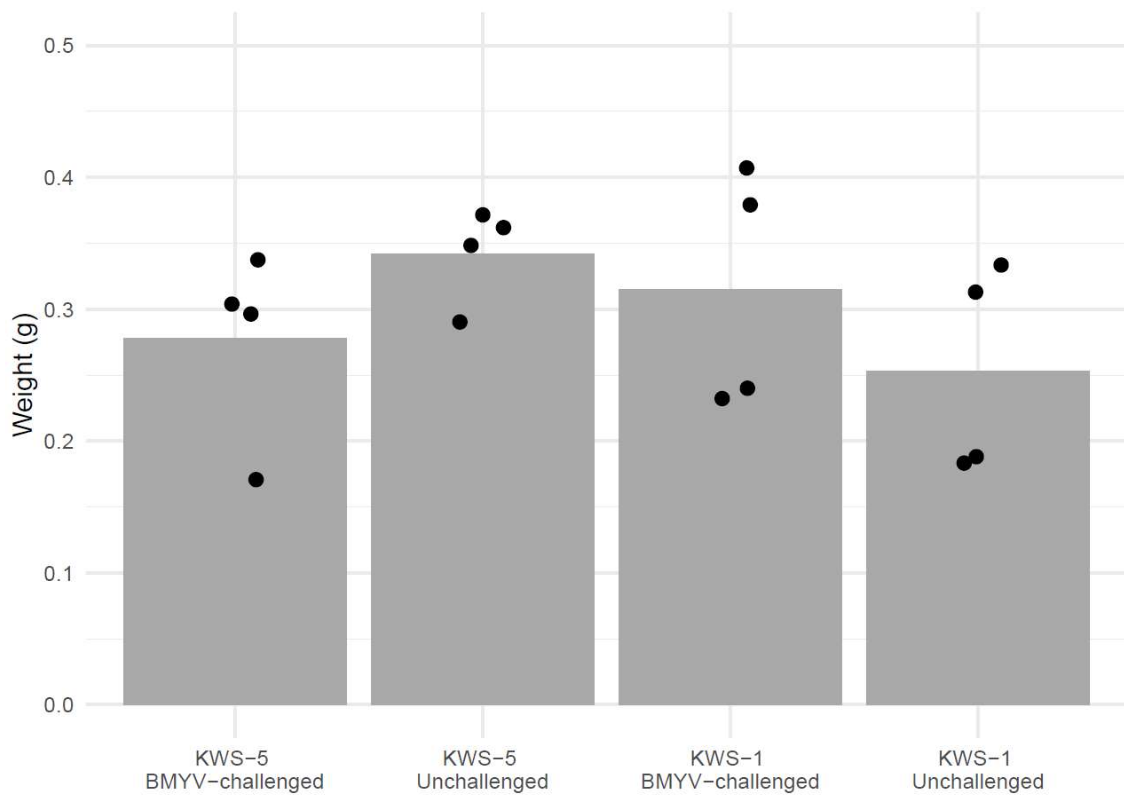


Figure 4.5: bar chart showing the mean dry root weight of each variety under Beet mild yellowing virus (BMYV) challenged (plants inoculated with BMYV viruliferous Myzus persicae *aphids) and unchallenged (plants inoculated with non-viruliferous* M. persicae *aphids) conditions. Scatter points overlayed show individual data point and the variation seen. No significant differences in dry root weight were found between the different varieties or between the virus treatments (analysis of variance (ANOVA), p = 0.131, n = 16).*

4.4.2 Glasshouse study

4.4.2.1 ELISA results

Both leaf 5 and leaf 10 were sampled for ELISA testing in the glasshouse study. ELISA results from both leaves found that the mean ELISA absorbance of the virus inoculated plants was above the threshold set by the negative controls and significantly higher than the mean absorbance of the uninoculated plants (Figure 4.6). The mean ELISA results for inoculated plants were higher in leaf 5 than leaf 10, with an average absorbance of 2.32 from leaf 5 compared to 0.99 for leaf 10.

Based on the ELISA results of leaf 5, only one virus-inoculated plant failed to pass the positive threshold (0.457). The plant was KWS-7, BMYV-inoculated, and had a leaf 5 ELISA absorbance of 0.109 compared to the other KWS-7 BMYV-inoculated plants which had leaf 5 ELISA results of 1.405, 1.868 and 2.773. This plant also had a low leaf 10 ELISA result of 0.173, which was also below the positive threshold (0.321). As such the results from this plant were removed from subsequent analysis. Other virus inoculated plants were below the positive threshold for leaf 10, however none failed to pass the threshold for leaf 5 and so all other plants were kept in the data analysis.

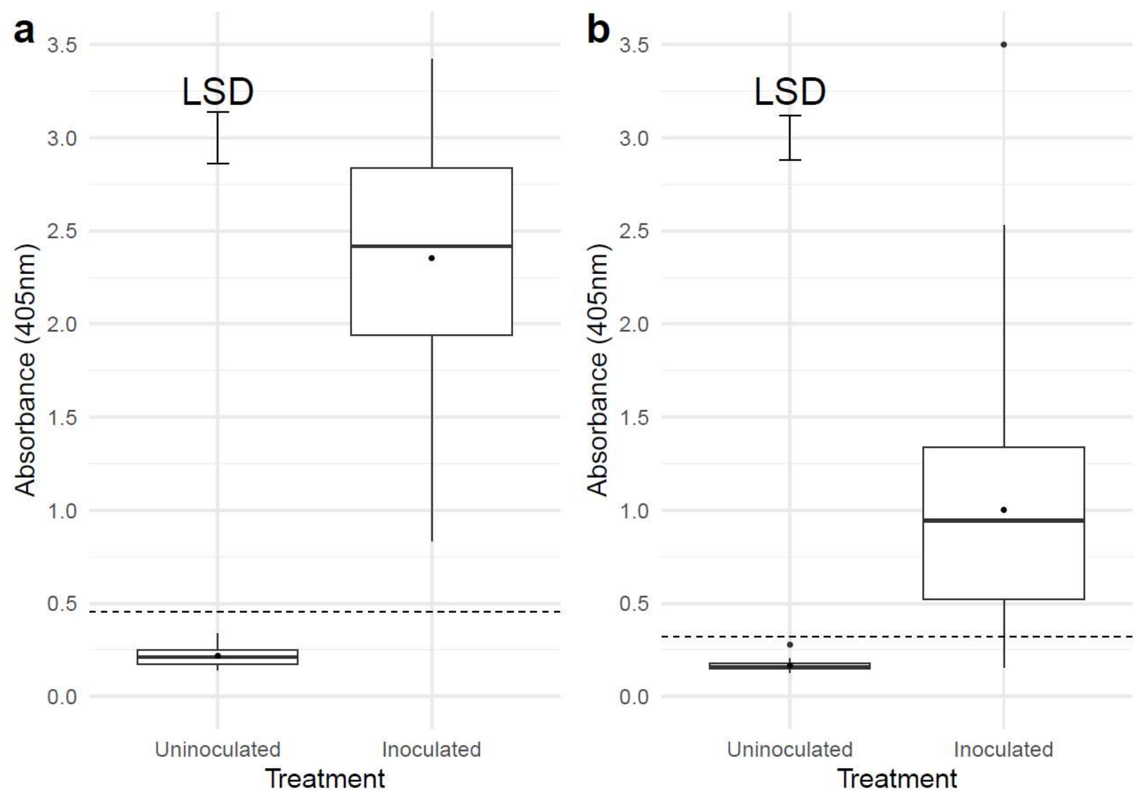


Figure 4.6: boxplots showing enzyme-linked immunosorbent assay (ELISA) absorbances of the uninoculated treatment and inoculated with viruliferous aphid treatments (Beet mild yellowing virus (BMYV), Beet chlorosis virus (BChV) and combined BMYV and BChV treatments) across all varieties. a = Leaf 5 ELISA results, b = Leaf 10 ELISA results. The mean absorbance is indicated for each treatment by the black circular point. The dashed horizontal line indicates the ELISA absorbance value above which a sample is deemed positive (calculated by the mean of the negative controls plus three times the standard deviation), set at 0.457 for leaf 5 and 0.321 for leaf 10. Error bars show least significant difference (LSD) at 5% significance between treatments (analysis of variance (ANOVA), p<0.001 for leaf 5, p=0.001 for leaf 10, n = 95).

The ELISA results of leaf 5 were broadly similar between all virus inoculated treatments (data not shown), with no statistically significant differences identified (ANOVA excluding uninoculated, p = 0.162). Significant differences were seen between the virus inoculated treatments in the ELISA results of leaf 10. The combined BMYV and BChV treatment had a significantly higher mean ELISA absorbance of 1.276 compared to either BMYV (0.765) and BChV (0.951) treatments (ANOVA excluding uninoculated, p = 0.008.

Focusing on the virus inoculated treatments, varieties differed significantly in their leaf 5 ELISA absorbances (Figure 4.7). Combining the data from the virus inoculated treatments (BMYV, BChV

and combined BMYV and BChV treatment), the “high resistance” varieties KWS-1 and KWS-2, and the “low resistance” variety KWS-6, had significantly lower mean ELISA values (ANOVA excluding uninoculated, p = 0.002) than “medium resistance” varieties KWS-3 and KWS-4. No significant difference was found between KWS-1 and KWS-2 and the “low resistance” varieties KWS-6 and KWS-7. These differences were not seen in the leaf 10 ELISA results; analysis identified no significant differences between varieties under virus inoculation (ANOVA excluding uninoculated, p = 0.874).

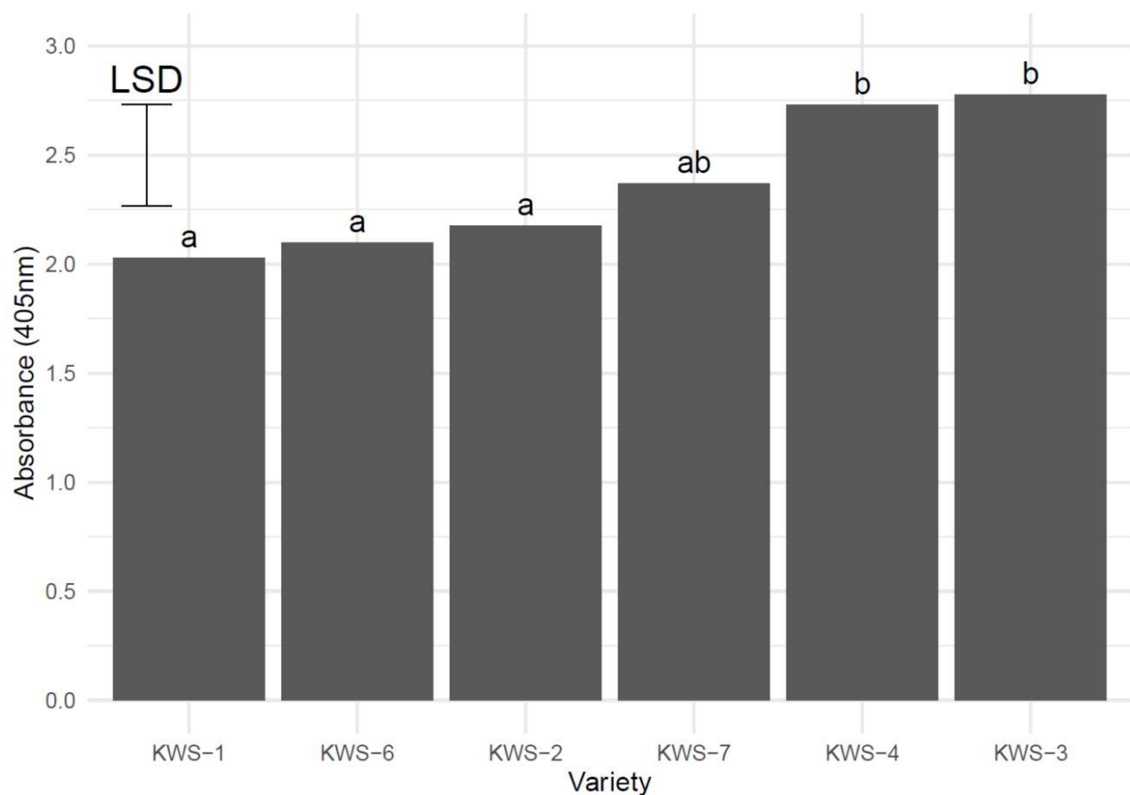


Figure 4.7: mean enzyme-linked immunosorbent assay (ELISA) absorbance of leaf 5 across all virus-inoculated treatments (Beet mild yellowing virus (BMYV), Beet chlorosis virus (BChV) and combined BMYV and BChV inoculated treatments) for each variety. Error bar shows least significant difference (LSD) at 5% significance between varieties (analysis of variance (ANOVA), excluding uninoculated p = 0.002, n = 71). Varieties KWS-1, KWS-2 and KWS-6 differed significantly from KWS-3 and KWS-4, shown by the differing letters above each bar in the graph.

4.4.2.2 Symptom expression

Unlike in the pilot study conducted in the MLR-352 growth cabinets, some virus infected plants in the glasshouse study did exhibit yellowing symptoms. The strongest symptoms were observed in variety KWS-7, and for this variety it was possible to distinguish the uninoculated and virus inoculated treatments based on visual symptoms (Figure 4.13). However, for all other varieties

symptoms expression was not consistent, and no clear differences could be identified between treatments or varieties (Figures 4.8 to 4.12). Some leaf paling/yellowing was also visible in the uninoculated controls, despite these plants testing negative for virus via ELISA. Plants across all varieties and treatments also exhibited a more elongated growth habit compared to field grown sugar beet. This was particularly noticeable in the length of leaf petioles.

Figure 4.8: photos taken from above of each test plant of variety KWS-1 in the glasshouse study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV)-inoculated, d = combined BMYV and BChV-inoculated.

Figure 4.9: photos taken from above of each test plant of variety KWS-2 in the glasshouse study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV) -inoculated, c = Beet chlorosis virus (BChV) -inoculated, d = combined BMYV and BChV-inoculated.

Figure 4.10: photos taken from above of each test plant of variety KWS-3 in the glasshouse study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV) - inoculated, d = combined BMYV and BChV-inoculated.

Figure 4.11: photos taken from above of each test plant of variety KWS-4 in the glasshouse study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV) -inoculated, c = Beet chlorosis virus (BChV)-inoculated, d = combined BMYV and BChV-inoculated.

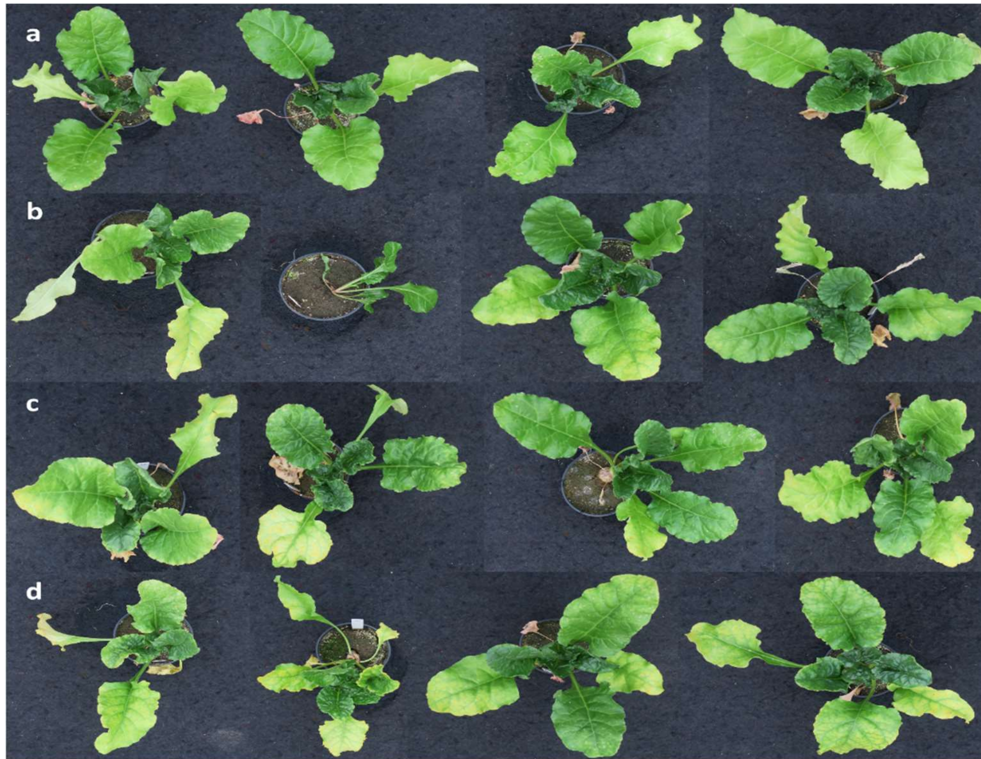


Figure 4.12: photos taken from above of each test plant of variety KWS-6 in the glasshouse study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV) -inoculated, c = Beet chlorosis virus (BChV)-inoculated, d = combined BMYV and BChV-inoculated.

Figure 4.13: photos taken from above of each test plant of variety KWS-7 in the glasshouse study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV)-inoculated, d = combined BMYV and BChV-inoculated.

4.4.2.3 Leaf area and weight

Virus treatment did not have a significant impact on leaf dry weight (ANOVA, p= 0.870). All treatments showed a large range, for example the uninoculated plants had leaf dry weights ranging from 1.8 to 5.5g compared to 2.6 to 5.3g for the mixed BMYV and BChV infection. Variety did have a significant impact on leaf dry weight (ANOVA, p <0.001), with the greatest leaf dry weight found in KWS-4 and the lowest in KWS-6 (Figure 4.14). However, no differences were identified in how the varieties responded to virus inoculation was found (ANOVA, treatment variety interaction, p = 0.370). Canopy area was also not affected by virus treatment (ANOVA, p = 0.428), or variety (ANOVA, p = 0.109).

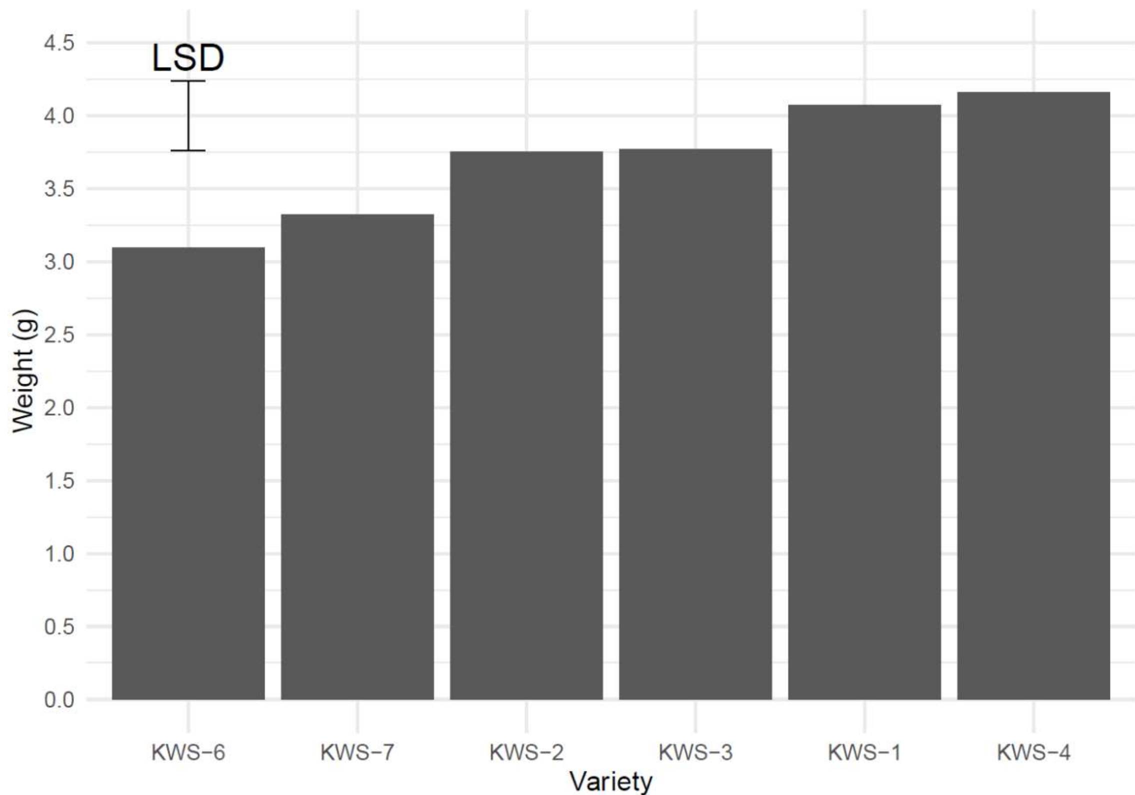


Figure 4.14: bar chart showing mean dry leaf weight of each variety across all treatments (uninoculated, Beet mild yellowing virus (BMYV)-inoculated, Beet chlorosis virus (BChV)-inoculated and combined BMYV- and BChV-inoculated). Error bar shows least significant difference (LSD) at 5% significance between varieties (analysis of variance (ANOVA), p <0.001, n = 95).

4.4.2.4 Root yield

The uninoculated treatment produced a significantly larger mean dry root weight than the virus inoculated treatments (ANOVA, p = 0.013). Although there was no significant difference between the different virus treatments, the mixed BMYV and BChV inoculation gave the lowest mean dry root weight (2.79g) and the BChV treatment the highest (3.28g), (Figure 4.15). Focusing on the virus inoculated treatments, significant differences were found between the varieties (ANOVA without uninoculated, p = 0.005), (Figure 4.16). KWS-7 produced the smallest mean dry root weight, significantly lower than all other varieties apart from KWS-2. All varieties showed a high level of variation in root weight with variety KWS-6 being the most variable ranging from 0.16 to 4.87g.

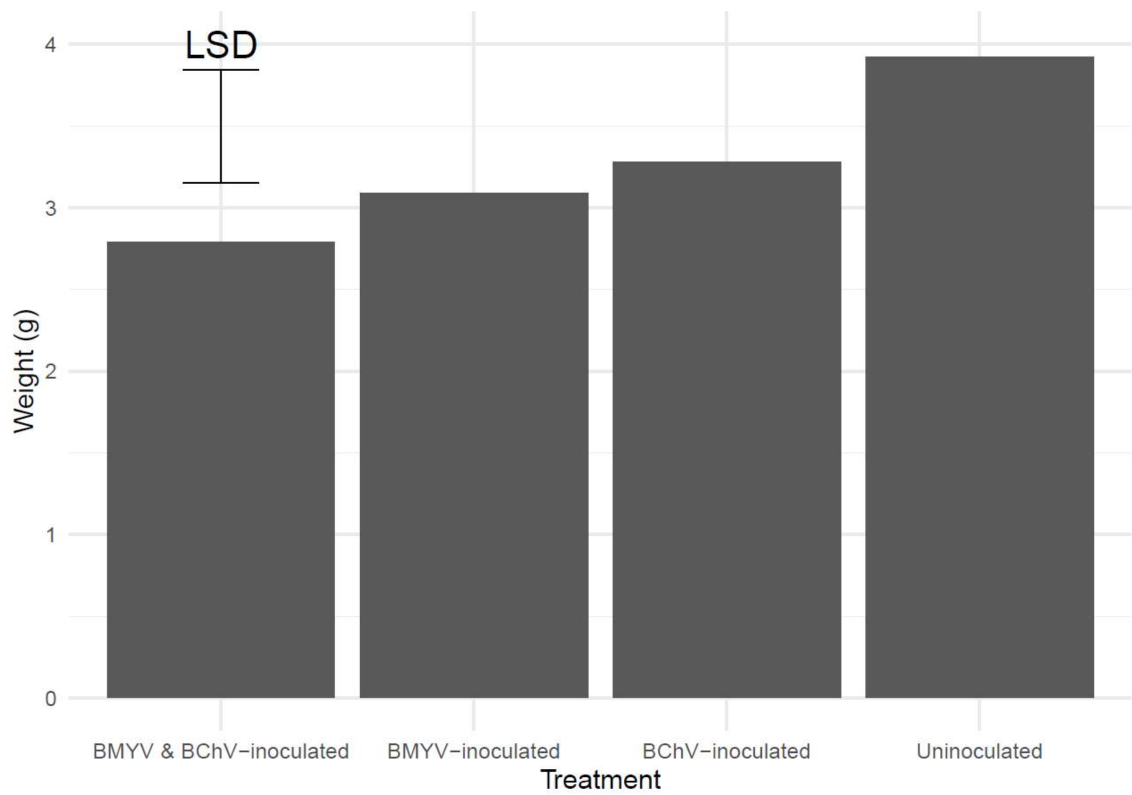


Figure 4.15: bar chart showing effect of virus inoculation on mean root dry weight across all varieties (KWS-1, KWS-2, KWS-3, KWS-4, KWS-6, KWS-7). Error bar shows least significant difference (LSD) at 5% significance between treatments (analysis of variance (ANOVA), p=0.013, n = 95).

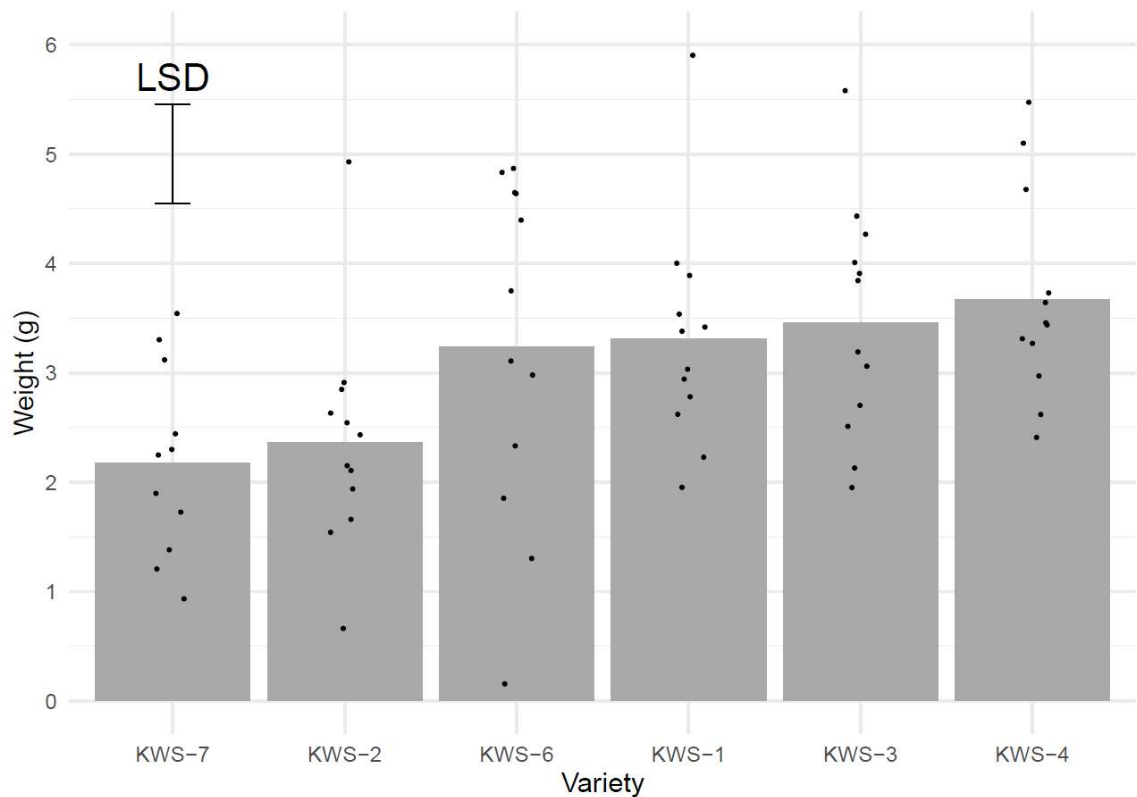


Figure 4.16: bar chart showing the mean dry root weight of each variety under the virus inoculated treatments (Beet mild yellowing virus (BMYV)-inoculated, Beet chlorosis virus (BChV)-inoculated and combined BMYV and BChV-inoculated). Overlayed points are the individual data point showing the large range in results. Error bar shows least significant difference (LSD) at 5% significance (analysis of variance (ANOVA), p<0.001 for leaf 5, p=0.001 for leaf 10, n = 71).

4.4.3 LED study

4.4.3.1 Symptoms

The plants in this study, grown under LED light, had an overall shorter canopy architecture and more typical petiole length compared to the plants grown in the glasshouse study. Nevertheless, the plants still had a different growth habit to field grown sugar beet, with the leaves twisting in towards the crown rather than opening out. Many plants, including from the uninoculated treatment, exhibited leaf yellowing making assessment of virus symptoms difficult (Figure 4.17 to 4.22). No obvious differences were present between the uninoculated and virus treatments for any variety.

Figure 4.17: photos taken from above of each test plant of variety KWS-1 in the LED study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV) -inoculated.

Figure 4.18: photos taken from above of each test plant of variety KWS-2 in the LED study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV) -inoculated.

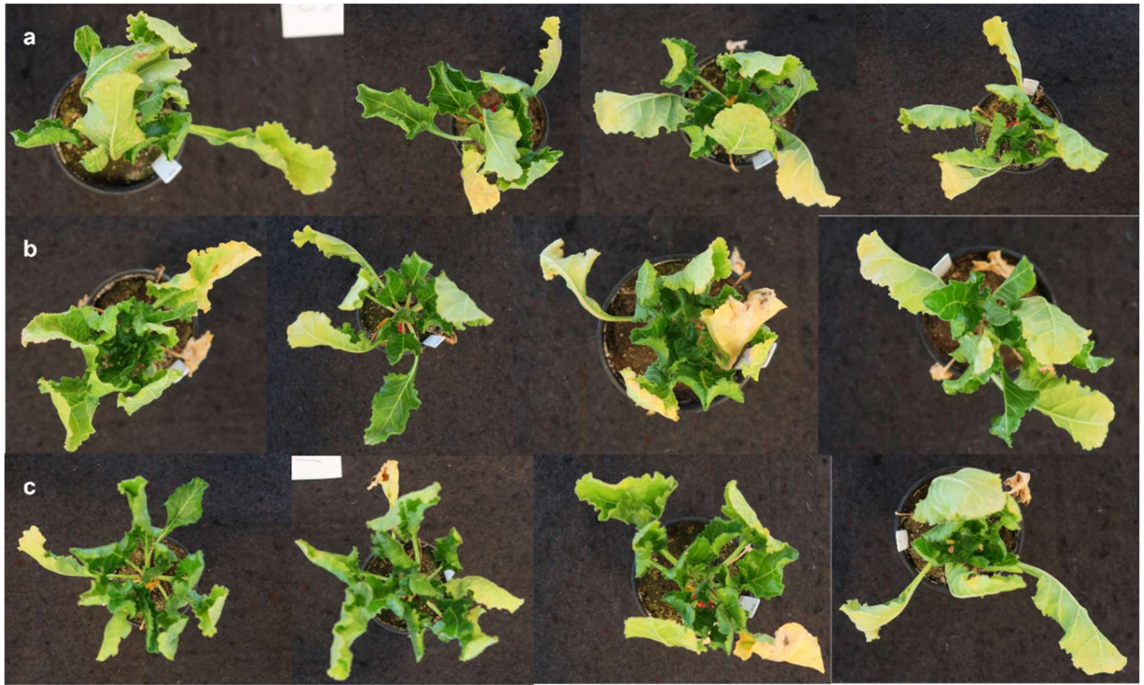


Figure 4.19: photos taken from above of each test plant of variety KWS-3 in the LED study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV) -inoculated.

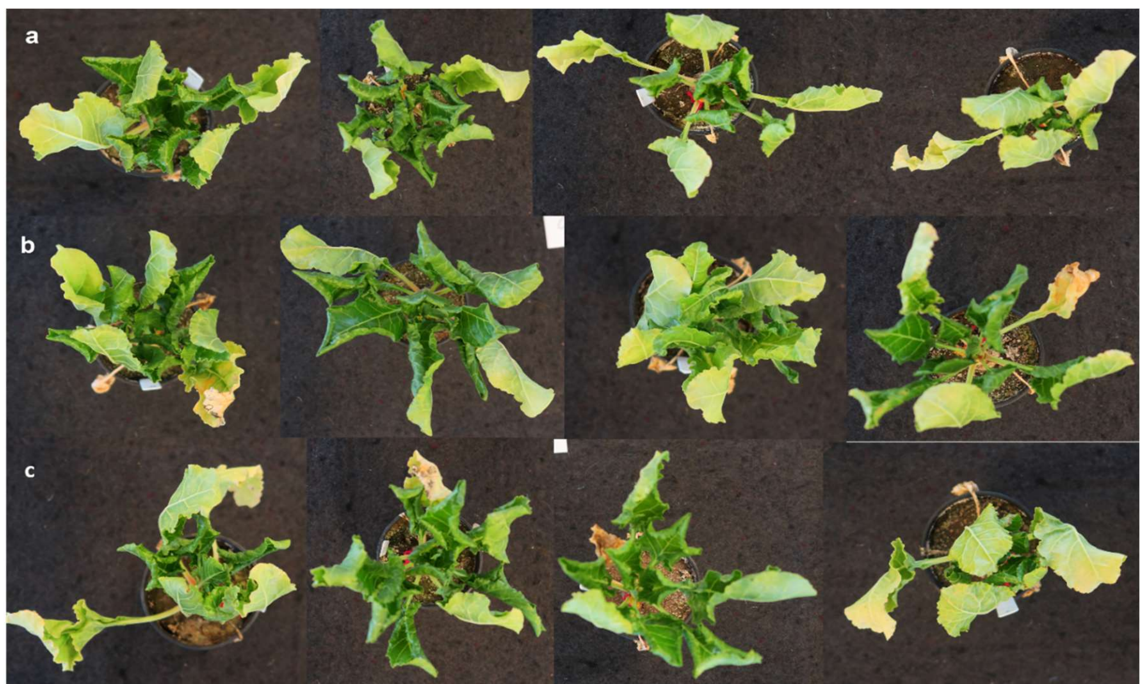


Figure 4.20: photos taken from above of each test plant of variety KWS-4 in the LED study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV) -inoculated.

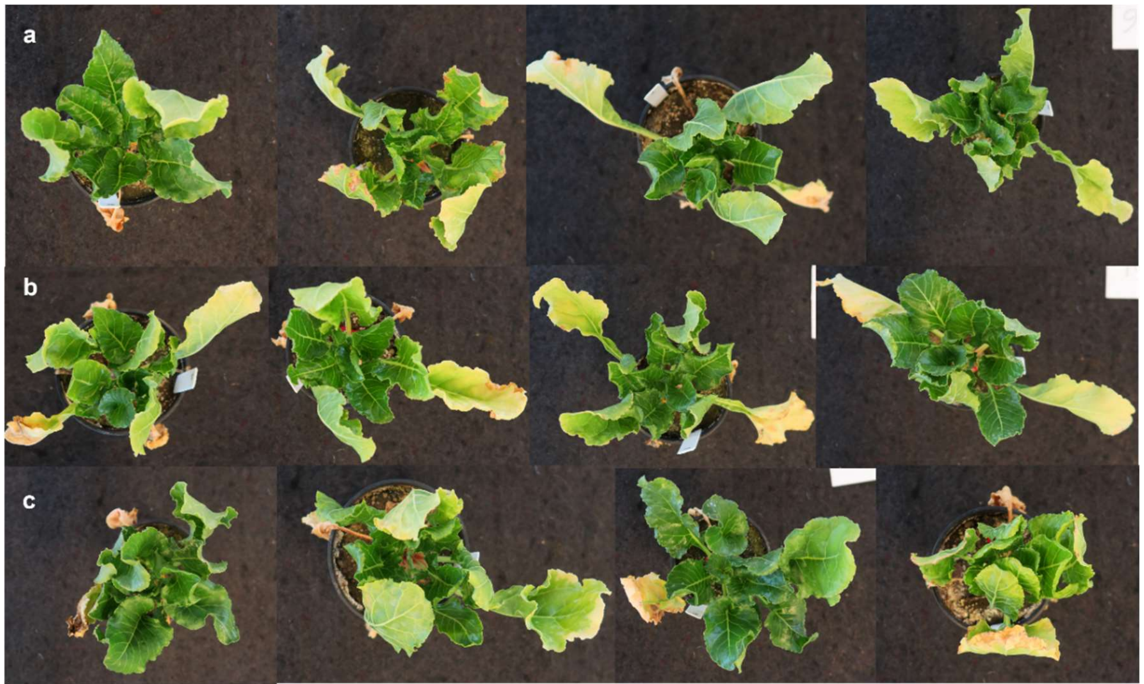


Figure 4.21: photos taken from above of each test plant of variety KWS-6 in the LED study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV) -inoculated.

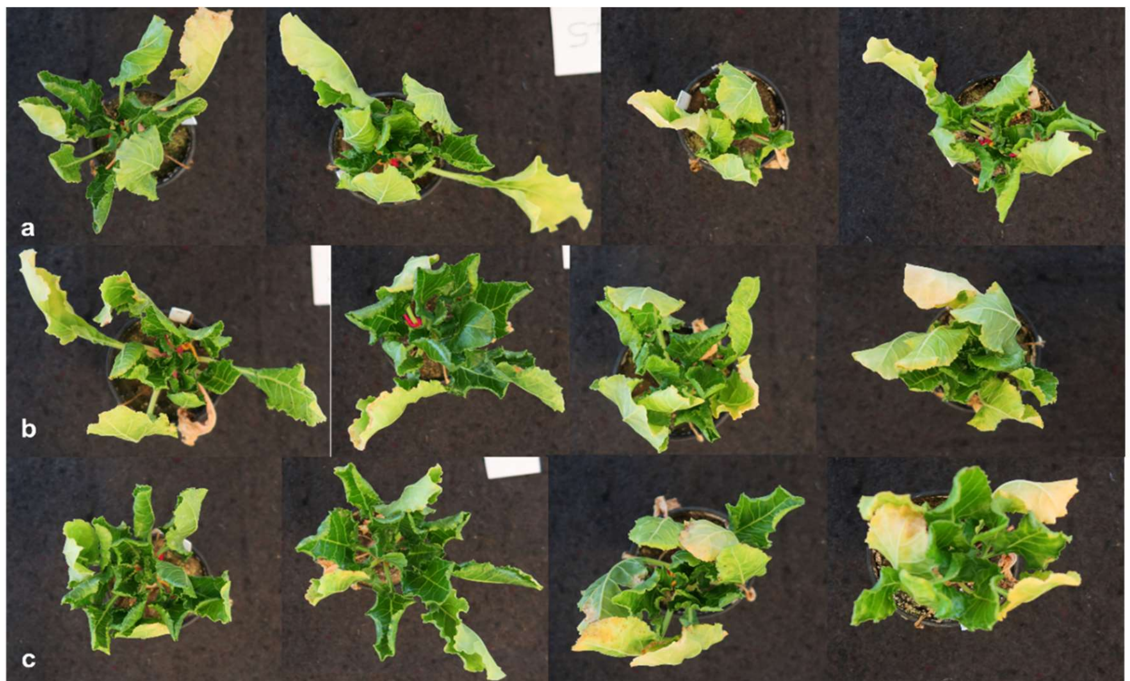


Figure 4.22: photos taken from above of each test plant of variety KWS-7 in the LED study, 8 weeks after inoculation. a = uninoculated, b = Beet mild yellowing virus (BMYV)-inoculated, c = Beet chlorosis virus (BChV) -inoculated.

4.4.3.2 ELISA results

The ELISA results from leaf 5 were much more variable across all varieties than leaf 10 (Figure 4.23). The threshold, as determined by the negative controls, above which a sample was classed as positive was 0.533. Leaf 5 results did not indicate a successful inoculation, with 68.8% of virus inoculated plants failing to pass this threshold. ELISA results from leaf 10 were much more consistent, with clear differences between inoculated and uninoculated plants. Based on the leaf 10 ELISA results, only 17% of inoculated plants did not pass the positive threshold, whilst none of the uninfected plants were deemed positive. The overall mean ELISA result for leaf 10 of the uninoculated plants was 0.224, this was significantly lower than the mean for the inoculated plants of 1.215, (ANOVA $p < 0.001$). No significant difference in the ELISA results of leaf 10 was found between the BMYV and BChV treatments (ANOVA, $p = 0.417$).

As in the glasshouse experiment, when focusing on the virus-inoculated treatments KWS-1 had the lowest mean ELISA result at 0.858 followed by KWS-6 at 0.911. KWS-7 had the highest mean ELISA result at 1.781, however none of these differences were statistically significant (ANOVA, $p = 0.051$). No differences were found in how the varieties responded to the different virus treatments (ANOVA, $p = 0.388$).

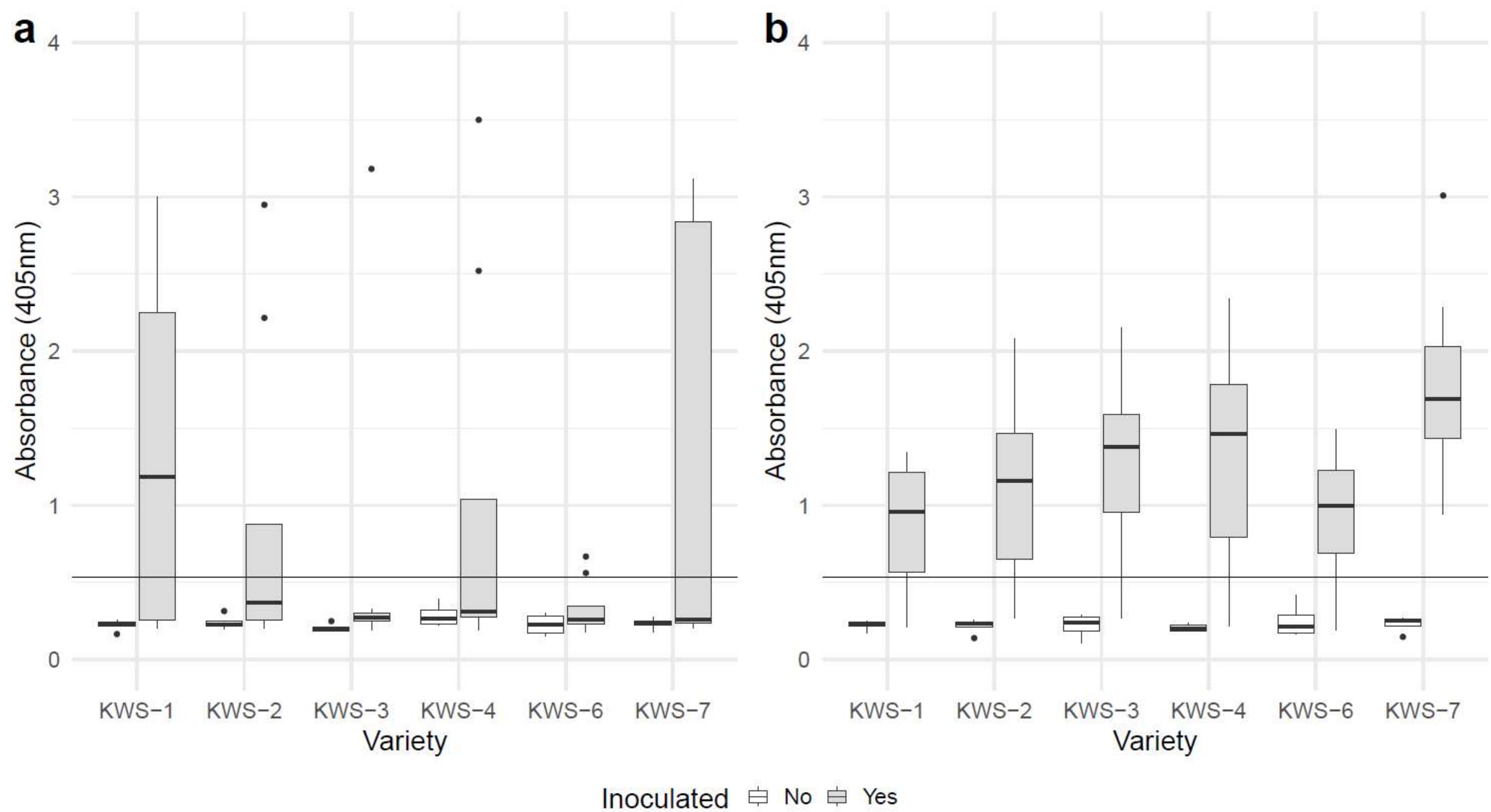


Figure 4.23: box and whisker plots showing enzyme-linked immunosorbent assay (ELISA) results for each variety in the LED study when uninoculated and inoculated with viruliferous aphids (Beet mild yellowing virus (BMYV)-inoculated and Beet chlorosis virus (BChV)-inoculated treatments). a – ELISA results of leaf 5, b – ELISA results of leaf 10.

4.4.3.3 Leaf weight and canopy area

Although time had a significant impact on canopy cover (repeated measures ANOVA, $p < 0.001$), canopy cover did not increase linearly (Figure 4.24). All varieties and treatments decreased canopy area six weeks after inoculation, before increasing again. The one exception to this was variety KWS-2 under BMYV infection which also reduced in canopy area between seven and eight weeks after inoculation.

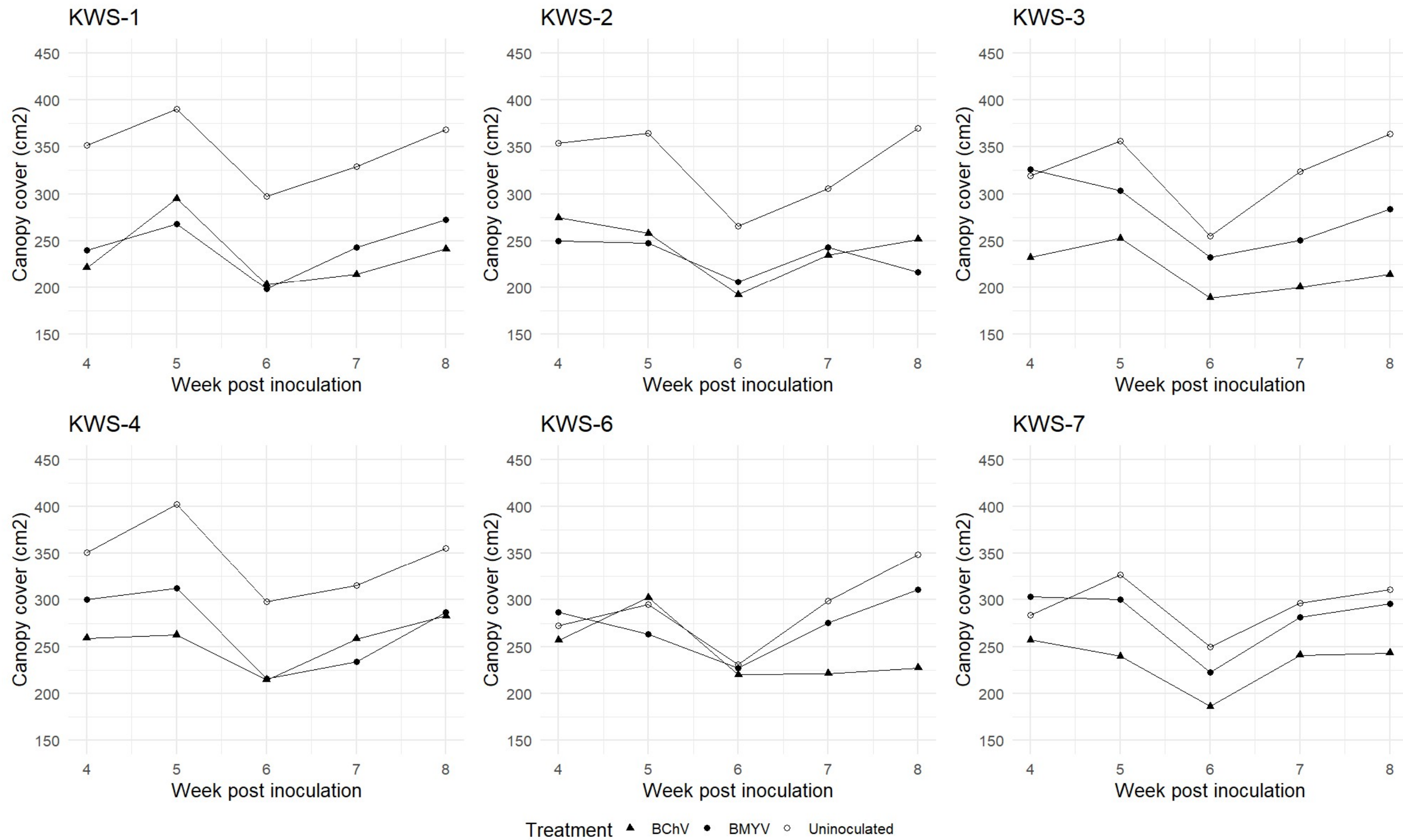


Figure 4.24: line charts showing change in canopy area in each variety in the LED study, under different virus treatments (Beet mild yellowing virus (BMYV)-inoculated, Beet chlorosis virus (BChV)-inoculated and uninoculated), between four weeks after inoculation and harvest at eight weeks after inoculation.

Despite these changes in canopy cover over time, virus infection was found to have a significant impact on canopy area (repeated measures ANOVA, p = 0.003), with the BMYV and BChV-inoculated plants having a significantly smaller canopy area than the uninoculated (Figure 4.25). Between the BMYV and BChV treatments no significant differences in canopy area were found. There were also no significant differences between varieties or in how the varieties interacted with virus treatments identified at any time point.

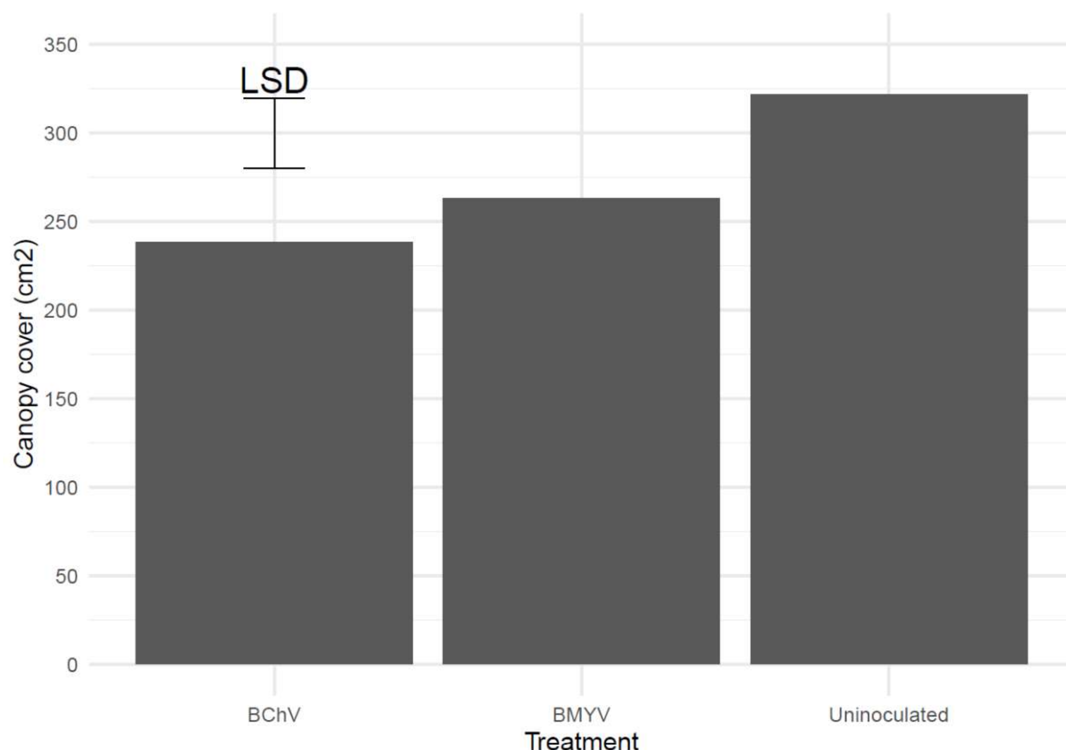


Figure 4.25: bar chart showing effect of virus treatment (Beet chlorosis virus (BChV) inoculated, Beet mild yellowing virus (BMYV)-inoculated and uninoculated) on mean canopy cover across all varieties (KWS-1, KWS-2, KWS-3, KWS-4, KWS-6 and KWS-7) in the LED study. Error bar shows least significant difference (LSD) at 5% significance between treatments (repeated measures analysis of variance, p=0.003, n = 72).

Consistent with the uninoculated treatment having the largest canopy area, the uninoculated plants also had the highest mean leaf dry weight at 3.327g compared to 3.249g for BMYV-inoculated plants and 3.247g for BChV. However there was no statistical difference between any of the treatments (ANOVA, p=0.667). Leaf dry weight did differ significantly between the varieties (Figure 4.26, ANOVA, p <0.001) but the response of the varieties to virus infection was equal (ANOVA, p = 0.165 variety treatment interaction).

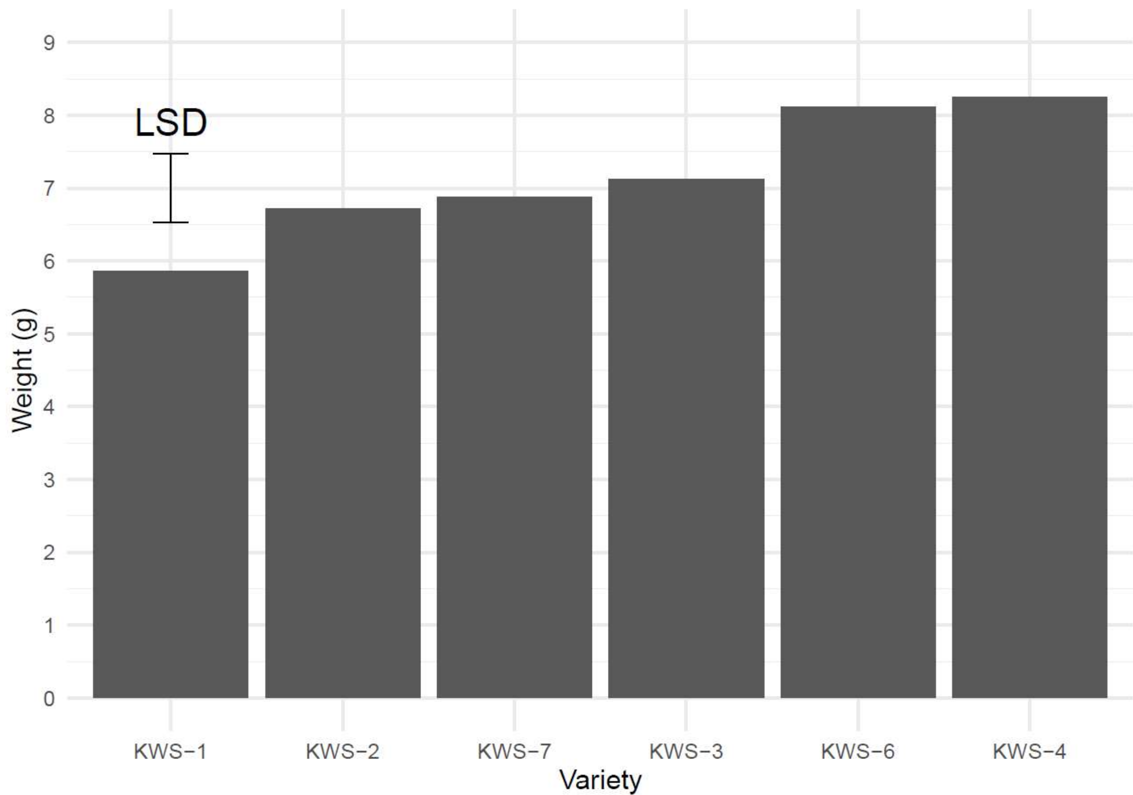


Figure 4.26: bar chart showing effect of variety on mean leaf dry weight across all treatments (uninoculated, Beet mild yellowing virus (BMYV)-inoculated and Beet chlorosis virus (BChV)-inoculated) in the LED study. Error bar shows least significant difference (LSD) at 5% significance between varieties (analysis of variance (ANOVA), p<0.001, n = 72).

4.4.3.4 Root dry weight

Inoculation with either BMYV or BChV had no significant impact on root dry weight. The mean root dry weight for the uninoculated plants was 6.81g compared to 6.96g for BChV and 7.35g for BMYV. Significant differences were found between varieties (ANOVA, p <0.001), with variety KWS-1 producing the smallest roots (Figure 4.27) and KWS-4 the largest. No significant differences in how the varieties responded to virus infection was identified (ANOVA, p = 0.327).

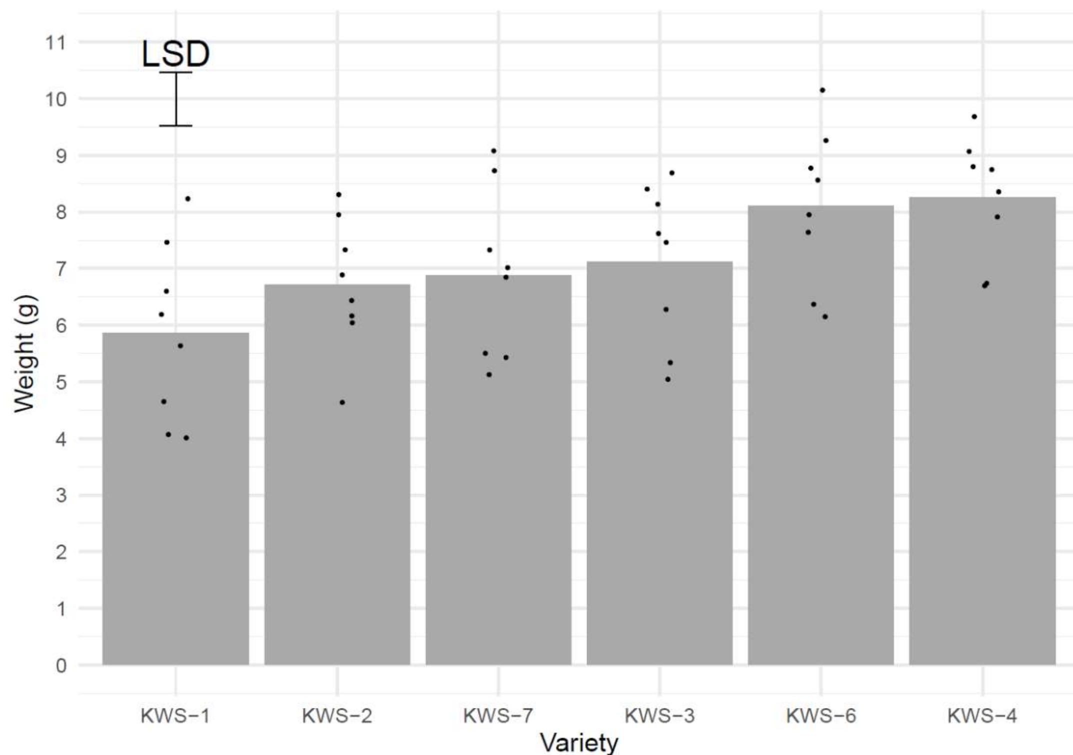


Figure 4.27: bar chart showing the effect of variety on mean dry root weight when inoculated with virus (Beet mild yellowing virus (BMYV)-inoculated and Beet chlorosis virus (BChV)-inoculated treatments) in the LED study. Scatter points overlayed show individual data points. Error bar shows least significant difference (LSD) at 5% significance between varieties (analysis of variance (ANOVA), p<0.001, n =54).

4.5 Discussion

4.5.1 ELISA results

The adapted clip cage method using fine pins to secure the cages provided excellent aphid containment. ELISA results of the uninoculated treatments in all studies indicated no contamination with viruliferous aphids, with the ELISA results of the uninoculated plants falling below the positive threshold. Although the mean ELISA results for the inoculated treatments were above the positive threshold in all studies, some individual plants did not pass this threshold. When the pilot study was conducted variety KWS-5 was understood to be susceptible to virus infection, however following discussions with the seed breeder KWS, it was identified as having medium resistance to BMYV and therefore was not the most suitable susceptible control variety to use. Nevertheless, KWS-5 is not fully resistant to BMYV infection and therefore variety resistance was unlikely to be the only cause of these ELISA results. One explanation of these results is that the interval of only four weeks between inoculation and ELISA testing was not adequate time for virus infection to establish and any differences in titre be identified.

This hypothesis is supported by the ELISA results of both the glasshouse and LED studies, in which there was an eight-week interval between inoculation and ELISA testing. In both experiments significant differences were seen in the ELISA results of leaf ten between the inoculated and uninoculated plants, indicating the clip cage method of inoculation was successful. Notably, for the ELISA results of leaf five, although significant differences were found between inoculated and uninoculated plants in the glasshouse study, no differences were found in the LED study.

When sampling leaf five for ELISA testing, a higher level of leaf senesce was observed in the LED study compared to the glasshouse study. Senescing leaves are known to have lower virus titres (Peters, 1988) and is therefore likely to have caused the large variation seen in leaf five ELISA results in the LED study and the lower mean virus titres. In the glasshouse study, where lower levels of leaf senescence were observed, higher virus titres were found in leaf five than in leaf ten for the inoculated treatments. This could indicate differences in virus localisation within infected plants, consistent with the findings of Peters (1988), with a source-sink relationship arising between older and younger leaves. Virus is transported from older leaves with higher virus concentrations to younger leaves in a similar way to the translocation of photosynthates. However, as all the leaf five and all of the leaf ten samples were grouped together on the ELISA plates, these differences could be a consequence of variation between plates. In subsequent studies, randomising the samples across the ELISA plates would permit more reliable comparisons of results.

Focussing on the ELISA results of leaf five, the glasshouse study identified varieties KWS-3 and KWS-4 as having significantly higher ELISA results for the inoculated treatments than KWS-1 and KWS-2. Interestingly no significant differences were identified between KWS-1 and KWS-2, and KWS-6 and KWS-7 despite KWS-6 and KWS-7 being described as susceptible by the seed breeder. Only in the glasshouse study were significant differences in ELISA result found between varieties, indicating the glasshouse environment may be the better growth environment for ELISA based phenotyping. Nevertheless, both the glasshouse and the LED study identified KWS-1 as the variety with the lowest ELISA absorbance when inoculated. This indicates KWS-1 may have some resistance to beet polerovirus infection.

In all three experiments some inoculated plants did not pass the virus-positive ELISA threshold. This may be evidence for varietal resistance to virus infection, but equally could indicate that infection was not achieved via the clip cage method. Certainly, in the case of the susceptible varieties, namely KWS-6 and KWS-7, the latter explanation is more likely given no varietal resistance is described by the seed breeder (KWS).

One alternative to a clip cage method of inoculation would have been to move the plants into separate virus cultures to be infected, before returning them to the trialled growth conditions after the aphids had been removed. This methodology would have avoided any stress to the aphids resulting from transferring them into, and containing them within, the clip cage. Instead, the viruliferous aphids would have been able to feed on the test plants, and transmit the virus, unimpeded by the clip cage. This method would have significantly less time consuming, and more suited to large scale studies. However, the clip cage method utilised in this study has other advantages, such as allowing control over exactly how many viruliferous aphids are permitted to feed on each plant. Importantly, the clip cage approach also allows multiple virus treatments to be tested within the same controlled environment chamber, reducing the number of chambers required and the associated costs. Given the facilities available, conducting the trials described in this chapter would not have been possible if separate chambers were needed for each virus treatment. There is also no need to move plants between environments, minimising the stress incurred by the plants and reducing the risk of contamination.

As previously discussed, the use of fine pins to secure the aphid cages proved a successful method of containing aphids on sugar beet plants and had other practical advantages. Nevertheless, this approach was skilled and very time consuming (taking three to four minutes to affix one cage). Cages were positioned on one of the first true leaves, however on some plants it was not possible to situate the cage such that the pins did not go through the leaf tissue. This left holes in the leaves, which though very small would have placed additional stress on affected plants. Inoculating the first true leaves was reflective of the field situation, where aphids are attracted to younger sugar beet plants (Watson et al., 1946). However, the shape of the cotyledon leaves may be more conducive for clip cage attachment, avoiding the need to pin through the leaf tissue.

One change that was made between the pilot study and the subsequent glasshouse and LED studies regarding the clip cage methodology was the decision to not inoculate the non-virus treatments with non-viruliferous aphids in the latter experiments. With the increase in replicates from the 16 plants tested in the pilot study to the 72 and 96 plants tested in the second LED and glasshouse study respectively, it became impossible to clip cage every plant in a sustainable time frame. This may have affected the reliability of the results, with the inoculated plants suffering additional stress not only via virus inoculation but also the physical impacts of the clip cages. Best scientific practice would have been to continue to use non-viruliferous aphids contained within clip cages as the non-infected control treatment, and future studies should do this. One way around this problem would be to have more than one person affixing the cages, ensuring all plants were inoculated within a reasonable time frame.

4.5.2 Root weight

Dry root weight was used as a proxy of harvest yield across all three experiments. In the pilot study, the "high" BMYV resistant variety KWS-1 tended to yield higher than the "medium" BMYV resistant variety KWS-5, however these results were not significant. As previously discussed, KWS-5 although understood to be susceptible to BMYV was later confirmed by the breeder to have medium resistance to BMYV and therefore was not the best control to compare the high resistance variety KWS-1 phenotype to. However, a number of other factors may well have contributed to the lack of statistically significant differences in this pilot study.

Sugar beet plants produce a long tap root, known to reach depths of more than one metre under field conditions (Jaggard and Qi, 2006). The small 9cm diameter, 9cm tall pots used in the pilot study, would not have allowed for normal sugar beet root development and may have prevented differences in varietal phenotypes being observed. There is therefore a trade-off between the convenience and practicality of smaller pot sizes and the closer to 'normal' root development permitted by larger pots. The decision to switch to 11cm diameter, 13.5cm tall pots in the subsequent studies described here, reflects this trade-off.

Another factor which is likely to have prevented phenotypic differences between virus treatments and varieties being identified in the pilot study is time between inoculation and harvest. During the pilot study, the plants were harvested four weeks after inoculation. This is enough time for symptom expression to develop under field conditions (Hossain et al., 2019), but when combined with the small pot size may not have been long enough for any yield differences to be distinguished under controlled conditions. Despite this, growing plants for long periods after inoculation was not practical in terms of resource use and negates the potential time benefits of controlled environment phenotyping. As a result of this trade off, in subsequent studies, test plants were grown for eight weeks after inoculation.

Following the pilot study, as well as altering the pot size and experiment length, it was also decided to change growing medium. In the pilot study, standard compost was used. Compost is a very convenient medium for growing plants under controlled conditions. It is lightweight, easy to use (requiring no mixing of multiple component mediums), and normally consistent in composition and readily available. Compost is also known to be a suitable medium for growing sugar beet under controlled conditions, being used by the BBRO to grow sugar beet plants to maintain their virus yellows cultures (BBRO, private communication).

However, during the first two years of this project the quality and availability of compost was reduced. This was caused in part by supply issues arising from the Covid19 pandemic and due to

manufacturers altering their compost recipes in response to the upcoming UK ban on horticultural peat use (Department for Environment, Natural England and The Rt Hon Lord Benyon, 2022). One example of these quality issues was demonstrated when growing sugar beet plants to maintain the virus cultures described in Chapter 2 section 2.1. As shown in Figure 4.28 multiple fungi and their fruiting bodies emerged from the compost (Premium All Purpose, Miracle-Gro), and as a result the seedlings showed reduced vigour.

Figure 4.28: images of fungal fruiting bodies which emerged from commercial compost (Premium All Purpose, Miracle-Gro) used to maintain virus cultures. Mushrooms shown here were kindly identified by Dr Tony Leech (the Norfolk county fungi recorder) in consultation with Kew Gardens as Leucocoprinus straminellus, this is the first recording of this species in East Anglia.

Aside from the issues described above, the other key issue with using compost as a growing medium is it is difficult to accurately control the available nutrients. Commercial compost such as that used in the pilot study described here, often has nutrients added (Evergreen garden care, 2023).

However, it is not possible to quantify the nutrients available to each test plant. Soil, or a soil-sand mix, is available without pre-mixed nutrients and therefore enables greater control of nutrients within the experimental design. It was owing to these issues, that the decision to switch to a 50:50 soil-sand growing medium was made following the pilot study.

Using a soil-sand mix avoided many of the problems associated with the compost growing medium, however it was not a perfect solution. The soil-sand medium lacked body, with little if any structure. Future studies may benefit from adding a courser sand or some organic matter to the soil-sand mix to improve the overall soil structure and drainage.

Following these changes in methodology, promising results were obtained with the uninoculated treatments producing significantly higher root yields than the inoculated treatments in the glasshouse study. Although not significant, the trend seen between the different virus treatments in the glasshouse trial was also consistent with the literature; BChV infection causing a smaller yield loss than BMYV infection (Stevens et al., 2004). When assessing the performance of each variety under virus infection, of the two high resistance varieties KWS-1 which was identified as having a lower virus titre in both the glasshouse and LED studies compared to KWS-2, yielded higher. However, overall, there was a high level of variation in root yields across the glasshouse trial.

Lower variation was seen in root yield results from the LED study, and overall larger root weights were achieved. As in the glasshouse study no significant differences in how the varieties responded to the different virus treatments was identified. This suggests that the high resistant varieties are able to overcome the effects of both BMYV and BChV infection. Under virus infection the lowest mean root yields were seen in KWS-1 and KWS-2, despite these varieties having high resistance. Although initially these results seem contrary to expectation (resistant varieties suffer lower yield losses than susceptible), it may be explained by the yield drag seen between novel resistant varieties and susceptible varieties which may be elite yielding varieties. As such, although the susceptible varieties suffer a greater yield loss, they may still outperform the lower yielding resistant varieties. This is analysed further in Chapter 6.

4.5.3 Symptom development

None of the growth environments trialled here produced the typical yellowing symptoms of beet polerovirus infection consistently. The glasshouse proved the most promising controlled environment for phenotyping based on foliar symptoms, however as all treatments including the uninoculated showed some degree of pale leaf yellowing it was not possible to quantify these results. This pale yellowing could have many causes, including too low nutrient levels, watering regime or a possible stress response due to fluctuating temperatures within the glasshouse.

The LED environment provided much more consistent temperatures and permits experiments to be repeated under identical growth conditions. However, in the LED study plants across all varieties and treatments showed an unusual growth habit with canopy cover decreasing sharply six weeks after inoculation, explained by the onset of severe leaf rolling. This issue would need addressing if the controlled environment was to become a viable alternative to field trials. One explanation for the leaf rolling could be light stress. The light levels recorded during this experiment averaged 539µmol $m^{-2}s^{-1}$ s, significantly higher than that of the MLR chamber (258 µmol $m^{-2}s^{-1}$ s).

Despite the unusual phenotype, only in the LED study was the canopy stunting effect of BMYV and BChV infection observed, with the inoculated treatments exhibiting smaller canopies (both in terms of area and dry weight) compared to the uninoculated. Although differences between the high resistance and susceptible varieties were not detected, adjusting the light intensity and achieving a closer to field-like growth habit may allow for such differences to be found.

Chapter 5: Characterising genetic variation between virus yellows isolates

5.1 Chapter Contributions

The sequence data further analysed here, were produced from the leaf samples collected as part of the work described in Chapter 3 by a combination of the BBRO network, British Sugar and Belchim Crop Protection. The consensus sequences were produced by Rocky Payet. All other data analysis (including sequence alignment and identification of changes to encoded amino acids) I completed myself.

5.2 Introduction

Recombination has been identified as a key driver behind polerovirus evolution (LaTourrette et al., 2021; Pagán and Holmes, 2010). This process, whereby the genetic material of two separate virus genomes is exchanged and combined giving rise to a new distinct virus (Cann, 2012a), has occurred frequently in the evolution of the polerovirus family (Pagán and Holmes, 2010). Genetic variation also arises thanks to the error prone nature of the RNA-dependent RNA-polymerase (RdRp). These mutations can be in the form of insertions, deletions or substitutions and, as with all genetic changes, selection pressure will then act determining if the mutation is maintained or removed (LaTourrette et al., 2021).

In the more extreme cases, the genetic variation arising from these events can give rise to viruses which meet the International Committee on Taxonomy of Viruses classification for a new polerovirus species (see Chapter 1 section 1.4.5). Examples of this include *Pepo aphid-borne yellows virus* (Ibaba et al., 2017) and *Pepper yellow leaf curl virus* (Dombrovsky et al., 2013). However, even when the genetic changes are not great enough to result in a new virus species, they can still affect viral properties particularly because of the overlapping nature of polerovirus genomes. This means that a single nucleotide mutation could result in alterations to the encoded amino acid in multiple proteins (LaTourrette et al., 2021), with possible consequences in virus pathogenicity.

As discussed in the previous chapter, assessment of sugar beet varieties' response to virus infection is predominantly undertaken via inoculated trials. The BBRO BMYV culture has been widely used by sugar beet seed breeders, such as KWS, to develop BMYV-resistant varieties. This virus isolate was brought into culture in 2013 and has been maintained in continuous culture, predominantly

within controlled glasshouse conditions or MLR-352 (Panasonic) growth chambers, ever since. In May 2020 a BChV culture was established at the BBRO and maintained within a Panasonic-MLR chamber. This culture has been used to challenge novel virus yellows resistant varieties.

Crucially, neither the BMYV nor BChV culture have been sequenced and their current similarity to 'wild' virus isolates is unknown. As both cultures are now being used to test sugar beet varieties, ensuring that they are representative of the virus isolates likely to infect commercial sugar beet crops in the field is vital. If the BBRO cultures were to exhibit genetic differences there is a risk that varieties developed to overcome the BBRO BMYV isolate, for example, may not stand up against 'wild' BMYV infection. The rate of genetic change within the BMYV or BChV cultures is also unknown. This has potential consequences when comparing trial data conducted across multiple years, particularly if the pathogenicity of the virus is changing.

More generally, since the introduction of neonicotinoid seed treatments in the 1990s limited, if any, research has been conducted into the genetic variation within beet polerovirus species. It is therefore not known whether the virus populations are largely homogeneous, or if differing, dominant genotypes are present. This could have important effects on virus-resistant varieties, particularly if isolates are present with resistance-breaking characteristics. Intra-species variation also has consequences on the reliability of current diagnostics, especially those deploying molecular techniques. If the target regions of primer-based assays are variable within virus populations, infection may be going undetected with symptoms instead being attributed to another cause of sugar beet leaf yellowing (see Chapter 1 section 1.2.3.1).

In the research presented here, I have further interrogated the sequencing data generated in Chapter 3 to elucidate the genetic variation within BMYV and BChV populations within this study. As part of the virus prevalence study outlined in Chapter 3, the BBRO BMYV and BChV cultures were sequenced across multiple years to act as positive control small RNA (sRNA) libraries. This also allows us to compare the changes in these data between years and gain an understanding of the impact of continuous culture on these virus isolates.

5.3 Materials and Methods

5.3.1 Sample collection and sequencing

The sequencing data, generated from the symptomatic sugar, fodder and sea beet leaves collected in the virus prevalence survey (reported in Chapter 3), were analysed further to identify genetic

variation between isolates. The locations of sequenced samples are shown in Figure 5.1, whilst additional sampling details are listed in appendix B.

The percentage of target genome present in a sRNA library sample was calculated using the software Integrative Genomics Viewer (IGV) as described in Chapter 3 section 3.3.5.2. Samples were then filtered to include only those containing more than 80% of the target virus genome.

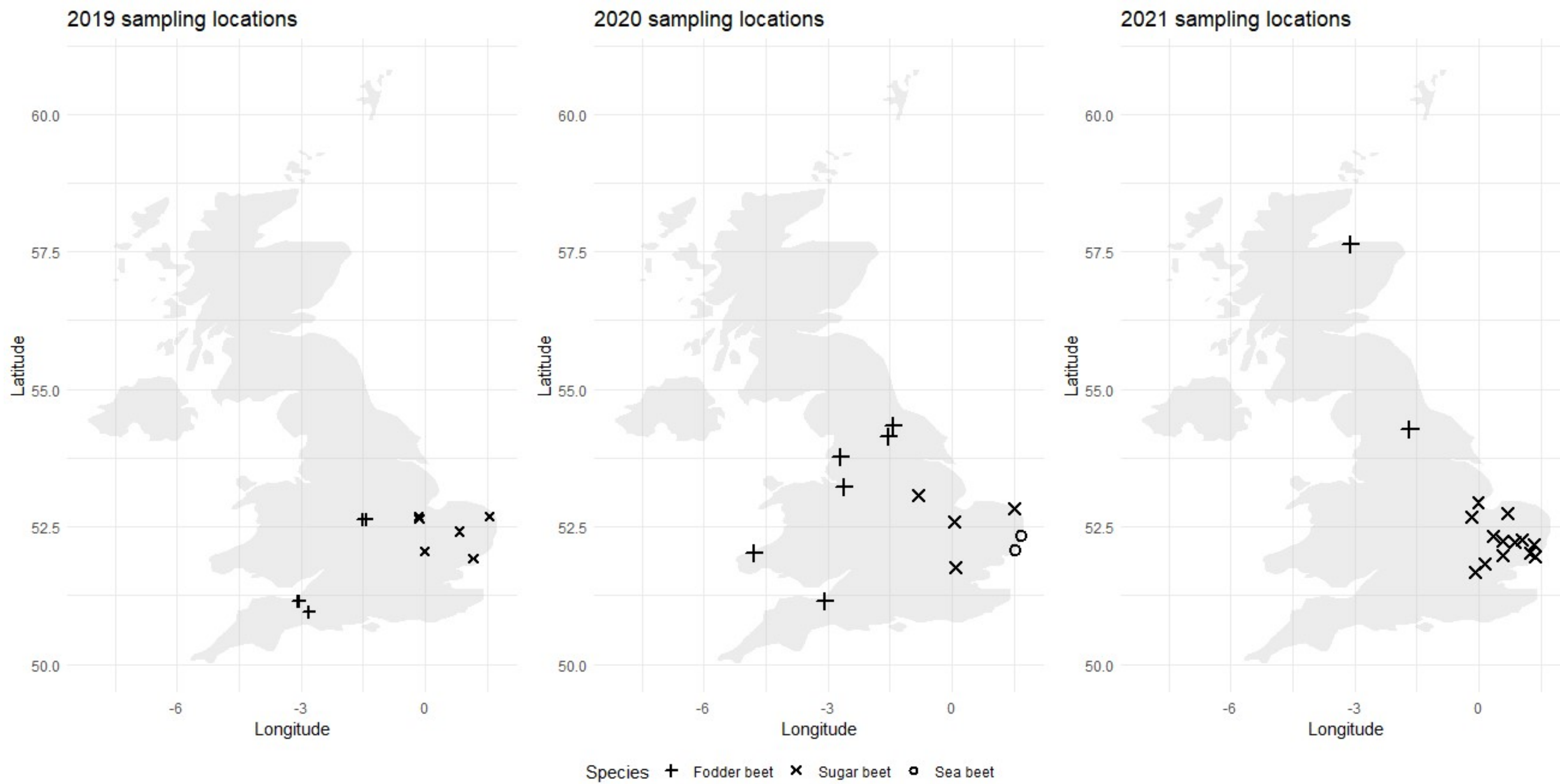


Figure 5.1: sampling locations of virus yellows symptomatic sugar, fodder and sea beet leaves collected between August and October 2019 – 2021, from which small RNA libraries were produced and next generation sequencing data analysed.

5.3.2 BCFtools consensus sequences

Consensus sequences for each sample were produced by Rocky Payet (UEA), using the variant-calling tool BCFtools (Li, 2011). The sample consensus sequences produced via BCFtools are based on a reference genome which is adjusted according to the input sequence data. When no mapping data is available the reference genome is defaulted to. Hence, using only samples known to contain more than 80% of the target genome reduced the risk of sample homogeneity arising because of the bioinformatic analysis methodology.

The NCBI reference sequences for each virus were used as the reference genomes in this analysis as detailed in Table 5.1.

Table 5.1: National Center for Biotechnology Information (NCBI) reference genomes for Beet chlorosis virus, Beet mild yellowing virus and Beet yellows virus from which variation was called by BCFtools to the sample consensus sequences.

Virus	**GenBank accession number**	**Origin location**	**Reference**
Beet chlorosis virus	NC_002766.1	East Anglia, England	Hauser et al., 2002
Beet mild yellowing virus	NC_003491.1	France	Guilley et al., 1995
Beet yellows virus	NC_001598.1	Ukraine	Agranovsky et al., 1994

5.3.3 Sequence alignment and percentage identity

The resultant sample consensus sequences were aligned, and the percentage identity determined, using ClustalOmega multiple sequence alignment tool (Sievers et al., 2011). When only two samples were compared, pairwise identity was determined using EMBOSS Needle (Needleman and Wunsch, 1970).

5.3.4 Locations of nucleotide differences and predictions of amino acid changes

Additional analysis to identify the open reading frames (ORFs) affected by the nucleotide variation was conducted on the samples which were brought into culture and included in the field trials described in Chapter 6. These samples were: BMYV isolate 21-254, BChV isolates 21-024, 21-278 and 21-290, and the BBRO cultures of BMYV and BChV as sequenced in 2021.

ORF locations were determined based on genome annotations of (Hauser et al., 2002) for BChV and (Guilley et al., 1995) for BMYV. The effect of the nucleotide variation on the amino acid encoded, by the affected triplet codon, was then predicted for each ORF.

5.3.5 Sequence alignment to current diagnostics

Any genetic variability occurring in the target sites of the qPCR diagnostic assays used within this thesis was also determined, namely the DSMZ qPCR assay used on leaf tissue (detailed in Chapter 2, section 2.5) and the Rothamsted Research assay used to detect viruliferous aphids (detailed in Chapter 2, section 2.6). Nucleotide variation in the primer/probe binding sites was determined via alignment of all generated sample consensus sequences with the ClustalOmega multiple sequence tool (Sievers et al., 2011).

5.4 Results

5.4.1 BMYV

Overall genetic diversity between sequenced BMYV genomes within this study was low. The nucleic acid pairwise identity between isolates ranged from 99.49 to 99.91% (Figure 5.2). The highest divergence was seen in the BBRO BMYV isolate sequenced in 2021 (BBRO-BMYV21), which had a pairwise identity of 99.49 to 99.60% when compared to the other BMYV isolates. Notably this high divergence was not observed in the BBRO BMYV isolate sequenced in 2019 or 2020, indicating the isolate may have become more distinct from the collected isolates over time. Isolate 21-254 also had a relatively high level of divergence, with pairwise identity ranging from 99.56 and 99.76%. The closest related isolates, based on nucleic acid sequence, were 20-009, 20-014 and 21-056 all sharing 99.91% sequence identity.

Geographic location and host plant had limited effect on genetic similarity. Comparing isolates collected in the same year, 20-009 and 20-010 originated from fodder beet fields approximately 22km apart and shared 99.79% nucleic acid identity. In comparison, isolates 21-056 (from sugar beet) and 21-294 (from fodder beet) were separated by approximately 317km yet shared 99.88% identity.

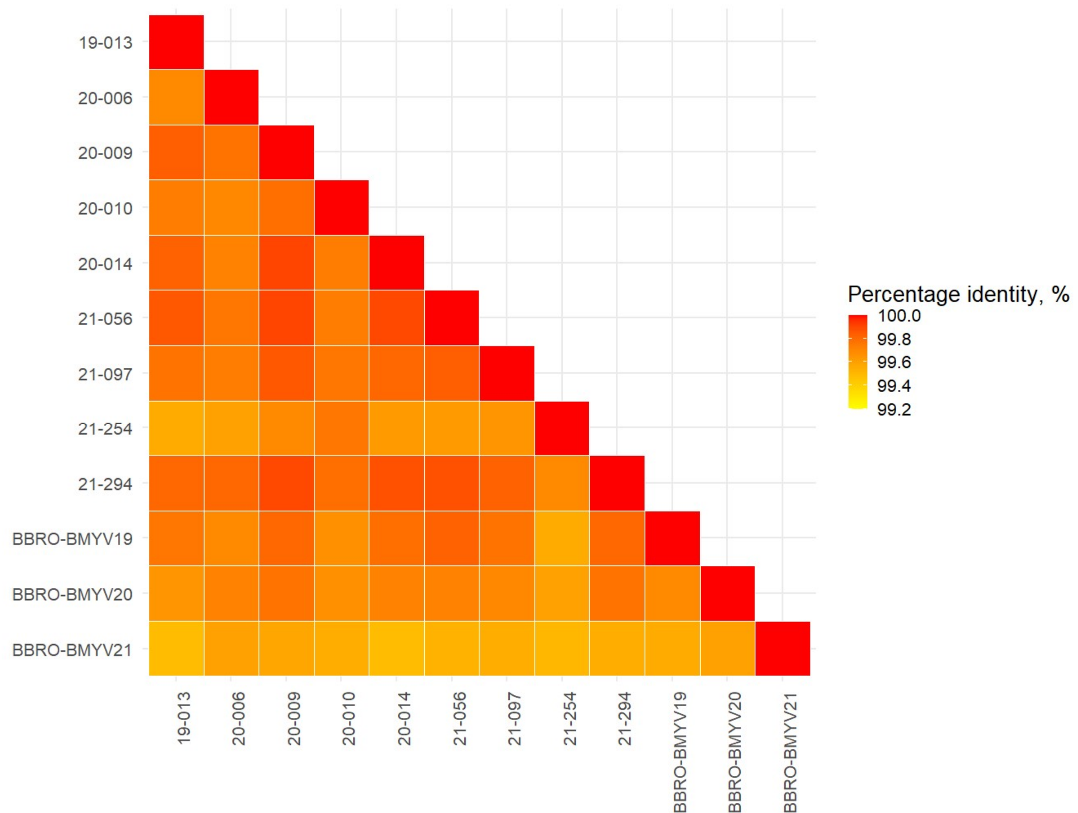
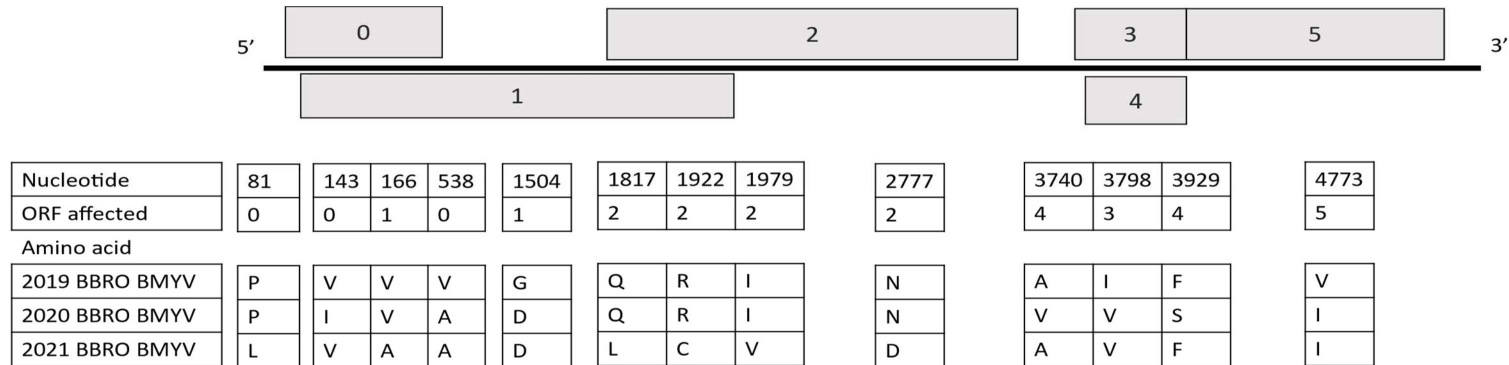


Figure 5.2: pairwise identity matrix depicting the whole genome nucleotide identity between Beet mild yellowing virus (BMYV) isolates. Full descriptions of the isolate collection details are given in appendix B. The 2019, 2020 and 2021 sequences of the BBRO BMYV isolate are included in the matrix (BBRO-BMYV19, BBRO-BMYV20 and BBRO-BMYV21 respectively).

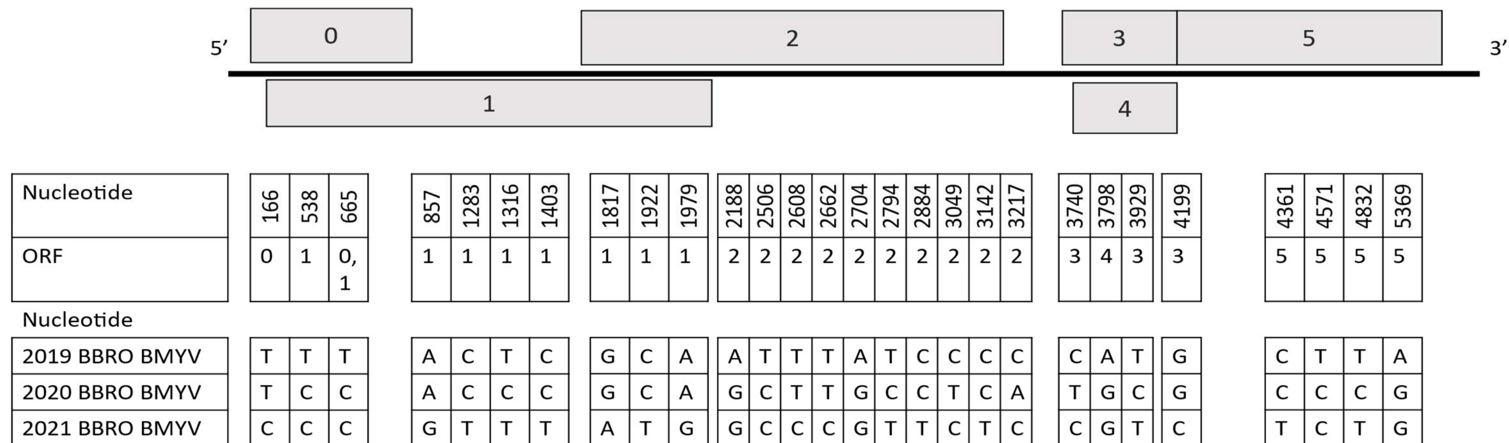
As previously discussed, comparison of the BBRO BMYV isolate sequences produced in 2019, 2020 and 2021 showed genetic variation over time. Between the 2019 and 2020 sequencing, eighteen nucleotide changes were identified. Seven of these changes were predicted to alter the encoded amino acid in at least one ORF (Figure 5.3). ORF0 and ORF4 each had two predicted amino acid changes, whilst ORF1, 3 and 5 each had one amino acid change. Greater variation was found between 2020 and 2021, with a total of 23 differing nucleotides identified. Nine of these nucleotide changes were predicted to alter the encoded amino acid; four changes to ORF2, two changes in ORF0 and ORF4 and one change in ORF1.

The majority of nucleotide changes which were predicted to be synonymous were identified in ORF1 and 2 (Figure 5.4). No nucleotide changes were identified in the intergenic region between ORF2 and 3.



Nucleotide	81	143	166	538	1504	1817	1922	1979	2777	3740	3798	3929	4773
ORF affected	0	0	1	0	1	2	2	2	2	4	3	4	5
Amino acid													
2019 BBRO BMYV	P	V	V	V	G	Q	R	I	N	A	I	F	V
2020 BBRO BMYV	P	I	V	A	D	Q	R	I	N	V	V	S	I
2021 BBRO BMYV	L	V	A	A	D	L	C	V	D	A	V	F	I

Figure 5.3: schematic diagram showing the organisation of the Beet mild yellowing virus (BMYV) open reading frames (ORFs) and the predicted effect of nucleotide changes in the BBRO BMYV isolate between 2019 and 2021 on the encoded amino acid.



Nucleotide	166	538	665	857	1283	1316	1403	1817	1922	1979	2188	2506	2608	2662	2704	2794	2884	3049	3142	3217	3740	3798	3929	4199	4361	4571	4832	5369
ORF	0	1	0, 1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	3	4	3	3	5	5	5	5
Nucleotide																												
2019 BBRO BMYV	T	T	T	A	C	T	C	G	C	A	A	T	T	T	A	T	C	C	C	C	C	A	T	G	C	T	T	A
2020 BBRO BMYV	T	C	C	A	C	C	C	G	C	A	G	C	T	T	G	C	C	T	C	A	T	G	C	G	C	C	C	G
2021 BBRO BMYV	C	C	C	G	T	T	T	A	T	G	G	C	C	C	G	T	T	C	T	C	C	G	T	C	T	C	T	G

Figure 5.4: schematic diagram showing the organisation of the Beet mild yellowing virus (BMYV) open reading frames (ORFs) and the nucleotide changes in the BBRO BMYV isolate between 2019 and 2021 predicted to not alter the encoded amino acid.

5.4.2 BMYV included in field trial

The two cultured BMYV isolates (BBRO BMYV and 21-254), included in the field trial described in Chapter 6, differed at 28 nucleotide (nt) positions, with a pairwise identity of 99.51%. Further analysis of these nucleotide differences identified nine potential amino acid changes (Figure 5.5). Most of these changes affected the 5' coding region, with four amino acids differing in ORF 2. Three of these changes in ORF2 (nt1817, 1979 and 2777) along with the ORF0 change (nt81) were only seen in the BBRO BMYV isolate and none of the other sequenced BMYV isolates (data shown in appendix C). At the 3' end of the genome, only two amino acid differences were predicted between BBRO BMYV and isolate 21-254; one change within ORF3 and one within ORF5. No amino acid changes were predicted within ORF4.

Nucleotide changes between isolate 21-254 and the BBRO BMYV which were predicted not to result in an amino acid change (synonymous) were also identified (Figure 5.6). Again, these changes were more prevalent in the 5' coding region than the 3'. ORF1 contained the majority of these changes, with twelve differing nucleotides. Six synonymous changes were identified in ORF2, four in ORF3 and one change in each of ORF0, ORF3 and ORF4. No nucleotide changes were identified in the intergenic region between ORF2 and 3.

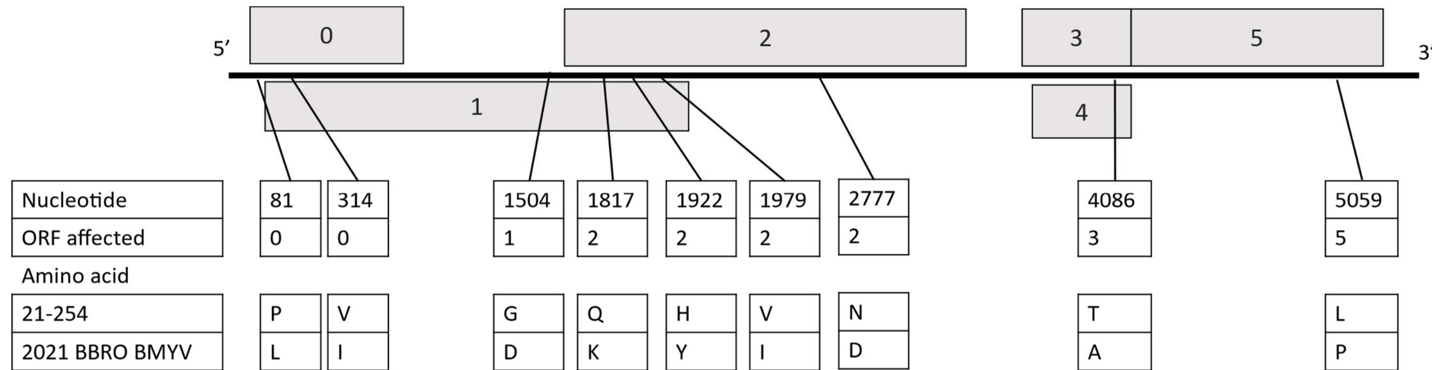


Figure 5.5: schematic diagram showing the organisation of the Beet mild yellowing virus (BMYV) open reading frames (ORFs) and the predicted effect of nucleotide differences on the encoded amino acid, between the two BMYV isolates included in the field trial discussed in Chapter 6 (isolate 21-254 and the BBRO BMYV isolate as sequenced in 2021).

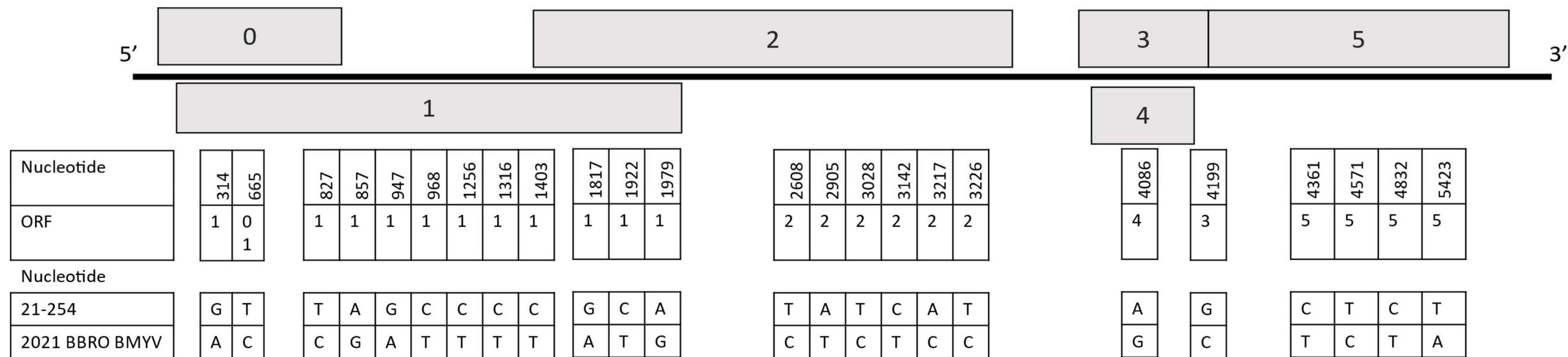


Figure 5.6: schematic diagram showing the organisation of the Beet mild yellowing virus (BMYV) open reading frames (ORFs) and the nucleotide differences, predicted to not affect the encoded amino acid, between the two BMYV isolates included in the field trial discussed in Chapter 6 (isolate 21-254 and the BBRO BMYV isolate as sequenced in 2021).

5.4.3 BChV

Comparison of the BChV isolates showed a larger range of genetic diversity than seen between the BMYV isolates, with the nucleic acid pairwise identity between isolates ranging from 99.27% to 100% (Figure 5.7). The highest divergence was seen in isolate 19-016 originating from fodder beet in Somerset, sharing only 99.53% identity with the most closely related isolate, BBRO BChV. Isolates 19-010, 20-017 and 20-018-1 shared identical nucleic acid sequences, however these sequences were also identical to the reference genome used by the variant-calling tool BCFtools.

Overall, based on the sequencing data from 2021, the BBRO BChV had a greater similarity to the collected BChV isolates than the BBRO BMYV had to the BMYV isolates, sharing between 99.53 and 99.84% sequence identity with the collected samples. Alignment of the 2020 and 2021 BBRO BChV sequences was broadly similar with no clear divergence of the BBRO BChV isolate away from the collected isolates.

As with the BMYV sequences, geographic location and host plant had limited effect on genetic similarity. Isolate 19-016 shared only 99.48% identity with 19-015 despite both samples originating from neighbouring fodder beet fields. In comparison, despite being separated by approximately 265km and originating from different hosts, isolates 20-012 and 20-021 shared 99.84% identity. Unlike the BMYV isolates, the BChV isolates did group loosely according to the year they were collected. However, this trend was not strong and was largely confined to the 2019 and 2020 isolates with the 2021 isolates showing more variation.

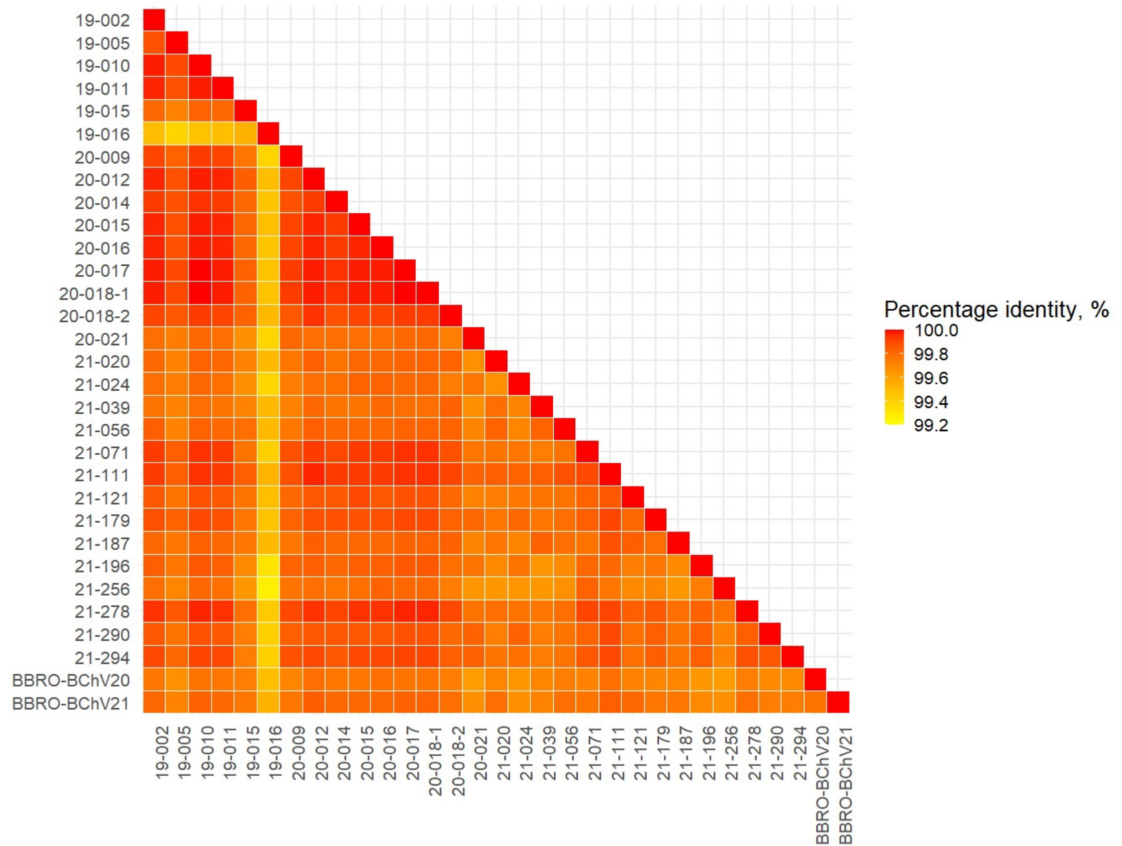


Figure 5.7: pairwise identity matrix depicting the whole genome nucleotide identity between Beet chlorosis virus (BChV) isolates. Full descriptions of the isolate collection details are given in appendix D. Both the 2020 and 2021 sequences of the BBRO BChV isolate are included in the matrix (BBRO-BChV20 and BBRO-BChV21 respectively).

The BBRO BChV isolate was sequenced in 2020 and 2021. Comparison of the 2020 and 2021 sequences showed 13 nucleotide changes, equating to a pairwise identity of 99.77%. All these nucleotides were located in the 5' proximal ORFs, with no changes detected in ORF3, 4, 5 or in the intergenic regions. Five nucleotide changes were predicted to alter the encoded amino acid in at least one ORF. Three of these changes occurred in ORF0, whilst two occurred in ORF2 (Figure 5.8). Six nucleotide changes which were predicted to be synonymous were identified in ORF1 and five in ORF2 (Figure 5.9).

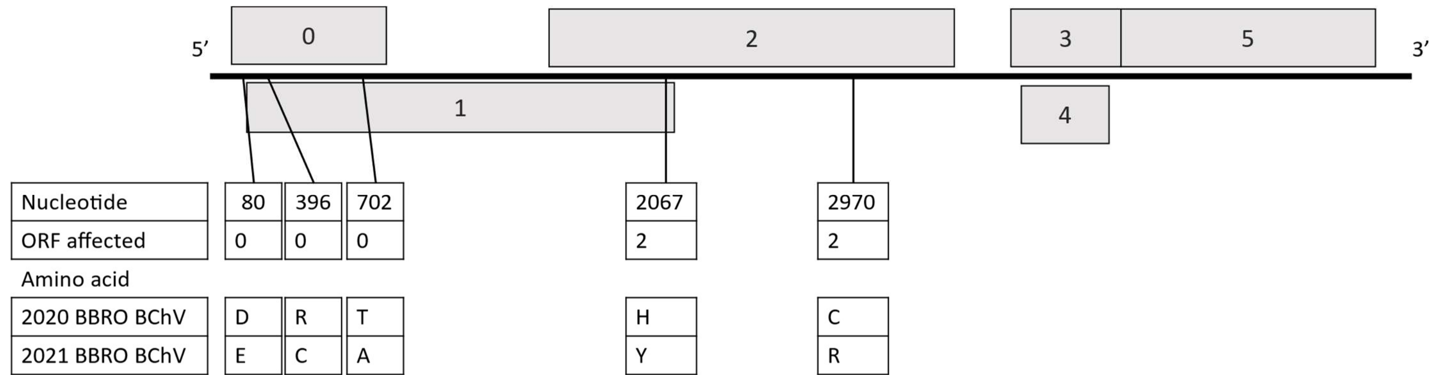


Figure 5.8: schematic diagram showing the organisation of the Beet chlorosis virus (BChV) open reading frames (ORFs) and the predicted effect of nucleotide changes in the BBRO BChV isolate between 2020 and 2021 on the encoded amino acid.

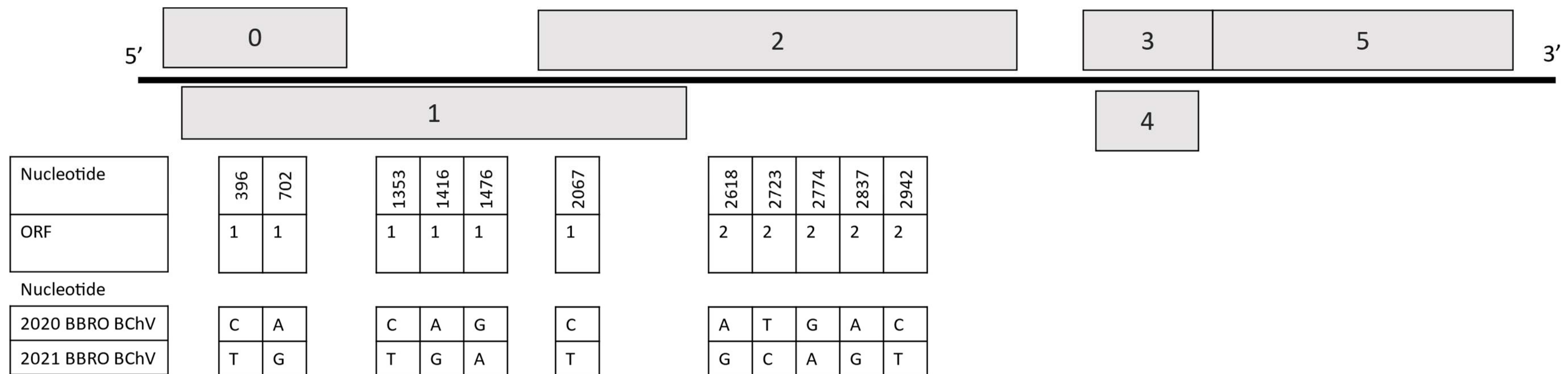


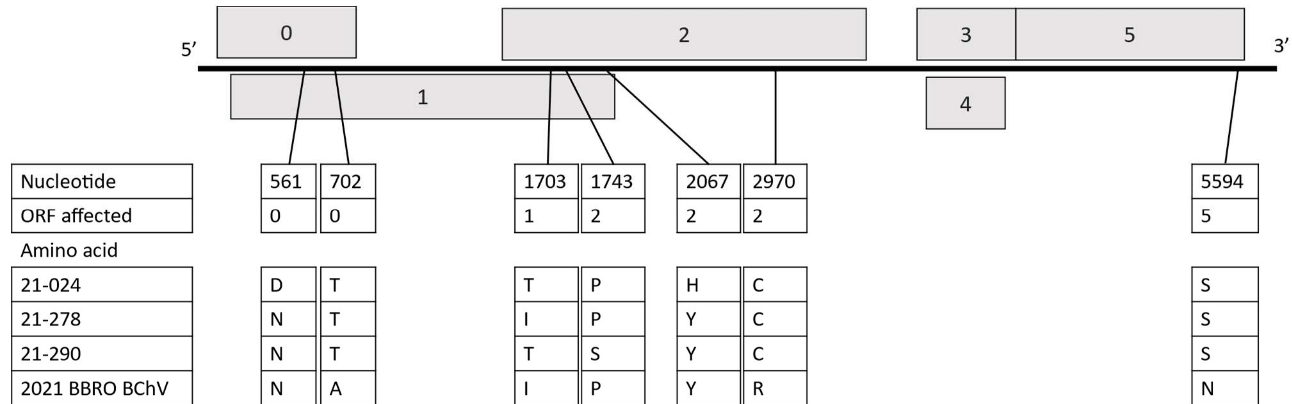
Figure 5.9: schematic diagram showing the organisation of the Beet chlorosis virus (BChV) open reading frames (ORFs) and the nucleotide changes in the BBRO BChV isolate between 2020 and 2021 predicted to not alter the encoded amino acid.

5.4.4 BChV included in field trial

Of the three BChV isolates brought into culture, for the field trial described in Chapter 6, 21-278 was the most similar to BBRO BChV, with 99.79% pairwise identity. The other two BChV isolates, 21-024 and 21-290 each shared 99.67% and 99.74% identity with BBRO BChV respectively. Further analysis of these nucleotide differences identified potential amino acid differences between isolates (Figure 5.10). Three of these predicted changes were conserved across all three of the new BChV cultures but differed in BBRO BChV, suggesting a change in the BBRO BChV genome. These amino acid changes were located in ORF0, ORF2 and ORF5. These were the only amino acid changes predicted between isolate 21-278 and BBRO BChV, however additional amino acid changes were predicted between the other two new BChV cultures and BBRO BChV. Isolate 21-024 had the most potentially differing amino acids compared to BBRO BChV, with three additional changes affected ORF0, ORF1 and ORF2. Two additional amino acid changes were predicted between isolate 21-290 and BBRO BChV affecting ORF1 and ORF2.

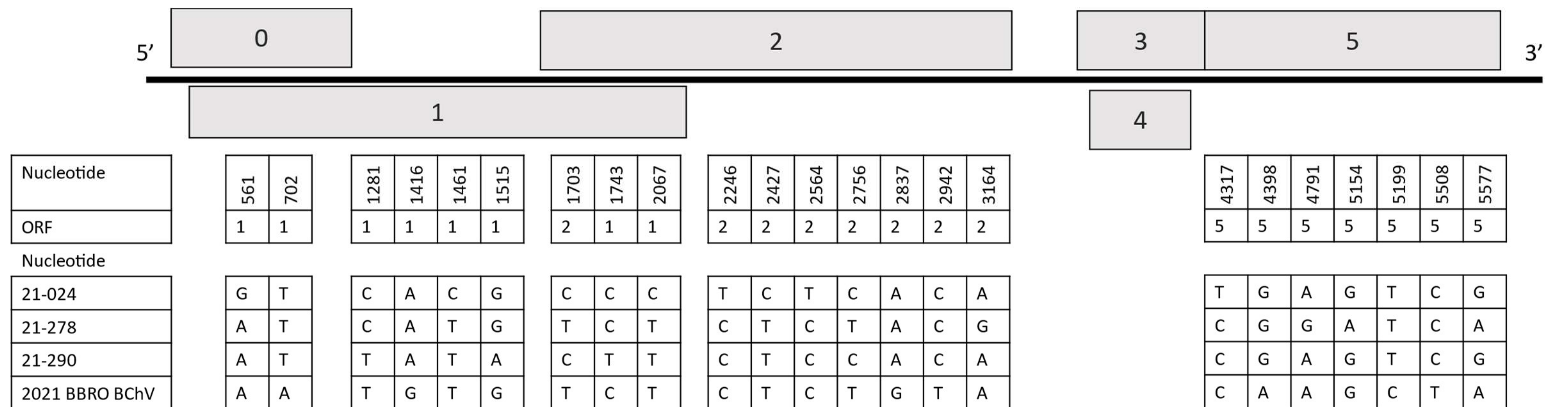
Nucleotide changes between BBRO BChV and the newly cultured isolates which were predicted to be synonymous were also identified (Figure 5.11). Eight nucleotides were conserved across all three newly cultured BChV isolates but differed in BBRO BChV. Two of these changes were in ORF1, two in ORF2 and four in ORF5. In addition to these eight nucleotide changes, isolate 21-024 differed to BBRO BChV by a further nine nucleotides, isolate 21-290 by five nucleotides and isolate 21-278 by three nucleotides.

Like the BMYV cultures, most nucleotide changes were found in the ORFs located at the 5’ end of the genome. Genetic variation was also present in ORF5, but unlike the BMYV cultures no nucleotide changes were identified in ORF3 or ORF4.



Nucleotide	561	702	1703	1743	2067	2970	5594
ORF affected	0	0	1	2	2	2	5
Amino acid							
21-024	D	T	T	P	H	C	S
21-278	N	T	I	P	Y	C	S
21-290	N	T	T	S	Y	C	S
2021 BBRO BChV	N	A	I	P	Y	R	N

Figure 5.10: schematic diagram showing the organisation of the Beet chlorosis virus (BChV) open reading frames (ORFs) and the predicted effect of nucleotide differences on the encoded amino acid, between the four BChV isolates included in the field trial discussed in Chapter 6.



Nucleotide	561	702	1281	1416	1461	1515	1703	1743	2067
ORF	1	1	1	1	1	1	2	1	1
Nucleotide									
21-024	G	T	C	A	C	G	C	C	C
21-278	A	T	C	A	T	G	T	C	T
21-290	A	T	T	A	T	A	C	T	T
2021 BBRO BChV	A	A	T	G	T	G	T	C	T

Nucleotide	2246	2427	2564	2756	2837	2942	3164	4317	4398	4791	5154	5199	5508	5577
ORF	2	2	2	2	2	2	2	5	5	5	5	5	5	5
Nucleotide														
21-024	T	C	T	C	A	C	A	T	G	A	G	T	C	G
21-278	C	T	C	T	A	C	G	C	G	G	A	T	C	A
21-290	C	T	C	C	A	C	A	C	G	A	G	T	C	G
2021 BBRO BChV	C	T	C	T	G	T	A	C	A	A	G	C	T	A

Figure 5.11: schematic diagram showing the organisation of the Beet chlorosis virus (BChV) open reading frames (ORFs) and the nucleotide differences (not predicted to alter the encoded amino acid) between the four BChV isolates included in the field trial discussed in Chapter 6.

5.4.5 Influence of genetic diversity on reliability of current diagnostics

Sequence alignment of all the BMYV isolates showed no nucleotide variation in the primer binding sites for the DSMZ BMYV RT-qPCR assay (Figure 5.12). At the probe binding site, isolate 20-006 differed by one nucleotide whilst all other isolates showed 100% complementarity. The risk of cross-reactivity with the DSMZ BChV RT-qPCR assay was very low. Only mis-matching alignment of the primer sequences were identified and at sites too distant to produce a viable amplicon (forward primer at site 827-841nt, reverse primer at 5618-5636nt).

```
a
BMYV_F        ---GAGTGACGTACACATCTGAGAA---
19-013        TCAGAGTGACGTACACATCTGAGAAAAG 1021
20-006        TCAGAGTGACGTACACATCTGAGAAAAG 1021
20-009        TCAGAGTGACGTACACATCTGAGAAAAG 1021
20-010        TCAGAGTGACGTACACATCTGAGAAAAG 1021
20-014        TCAGAGTGACGTACACATCTGAGAAAAG 1021
21-056        TCAGAGTGACGTACACATCTGAGAAAAG 1021
21-097        TCAGAGTGACGTACACATCTGAGAAAAG 1021
21-254        TCAGAGTGACGTACACATCTGAGAAAAG 1021
21-294        TCAGAGTGACGTACACATCTGAGAAAAG 1021
BBRO-BMYV21   TCAGAGTGACGTACACATCTGAGAAAAG 1021
              ****************************

b
BMYV_R        ---TTGCTCTGTCGGATGGTGA---
19-013        TCTTTGCTCTGTCGGATGGTGAATG 1150
20-006        TCTTTGCTCTGTCGGATGGTGAATG 1150
20-009        TCTTTGCTCTGTCGGATGGTGAATG 1150
20-010        TCTTTGCTCTGTCGGATGGTGAATG 1150
20-014        TCTTTGCTCTGTCGGATGGTGAATG 1150
21-056        TCTTTGCTCTGTCGGATGGTGAATG 1150
21-097        TCTTTGCTCTGTCGGATGGTGAATG 1150
21-254        TCTTTGCTCTGTCGGATGGTGAATG 1150
21-294        TCTTTGCTCTGTCGGATGGTGAATG 1150
BBRO-BMYV21   TCTTTGCTCTGTCGGATGGTGAATG 1150
              *************************

c
BMYV_probe    ---CCAAACTGGGAAGGAGTTCTTGC---
19-013        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
20-006        CCCCCAAATTGGGAAGGAGTTCTTGCCTG 1072
20-009        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
20-010        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
20-014        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
21-056        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
21-097        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
21-254        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
21-294        CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
BBRO-BMYV21   CCCCCAAACTGGGAAGGAGTTCTTGCCTG 1072
              ******** ********************
```

Figure 5.12: DSMZ Beet mild yellowing virus (BMYV) reverse transcription-qPCR assay alignment with the produced BMYV isolate sequences. a – BMYV forward primer, b – BMYV reverse primer (shown in reverse compliment), c – BMYV probe.

Similarly, no nucleotide variation was seen amongst the BChV isolate sequences at the DSMZ BChV primer binding site locations (Figure 5.13). All isolates showed exact complementarity to the BChV probe, except for isolate 19-016 which varied by one nucleotide. No viable binding sites for the DSMZ BMYV primers or probe were identified in the BChV sequences.

a

```
BChV_F        ---AGTCATGACGACGGTTCACA---
19_005        ATAAGTCATGACGACGGTTCACACGC 881
19_010        ATAAGTCATGACGACGGTTCACACGC 881
19_011        ATAAGTCATGACGACGGTTCACACGC 881
19_015        ATAAGTCATGACGACGGTTCACACGC 881
19_016        ATAAGTCATGACGACGGTTCACACGC 881
19-002        ATAAGTCATGACGACGGTTCACACGC 881
20-009        ATAAGTCATGACGACGGTTCACACGC 881
20-012        ATAAGTCATGACGACGGTTCACACGC 881
20-014        ATAAGTCATGACGACGGTTCACACGC 881
20-015        ATAAGTCATGACGACGGTTCACACGC 881
20-016        ATAAGTCATGACGACGGTTCACACGC 881
20-017        ATAAGTCATGACGACGGTTCACACGC 881
20-018-1      ATAAGTCATGACGACGGTTCACACGC 881
20-018-2      ATAAGTCATGACGACGGTTCACACGC 881
20-021        ATAAGTCATGACGACGGTTCACACGC 881
21_024        ATAAGTCATGACGACGGTTCACACGC 881
21_278        ATAAGTCATGACGACGGTTCACACGC 881
21_290        ATAAGTCATGACGACGGTTCACACGC 881
21-020        ATAAGTCATGACGACGGTTCACACGC 881
21-039        ATAAGTCATGACGACGGTTCACACGC 881
21-056        ATAAGTCATGACGACGGTTCACACGC 881
21-071        ATAAGTCATGACGACGGTTCACACGC 881
21-111        ATAAGTCATGACGACGGTTCACACGC 881
21-121        ATAAGTCATGACGACGGTTCACACGC 881
21-179        ATAAGTCATGACGACGGTTCACACGC 881
21-187        ATAAGTCATGACGACGGTTCACACGC 881
21-196        ATAAGTCATGACGACGGTTCACACGC 881
21-256        ATAAGTCATGACGACGGTTCACACGC 881
21-294        ATAAGTCATGACGACGGTTCACACGC 881
BBRO-BChV21   ATAAGTCATGACGACGGTTCACACGC 881
              **************************
```

b

```
BChV_probe    ---TGATAACCTGCTCGCATGCTCC---
19_005        GTTTGATAACCTGCTCGCATGCTCCCAT 959
19_010        GTTTGATAACCTGCTCGCATGCTCCCAT 959
19_011        GTTTGATAACCTGCTCGCATGCTCCCAT 959
19_015        GTTTGATAACCTGCTCGCATGCTCCCAT 959
19_016        GTTTGATAACCTGCTCGCATGCCCCCAT 959
19-002        GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-009        GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-012        GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-014        GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-015        GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-016        GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-017        GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-018-1      GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-018-2      GTTTGATAACCTGCTCGCATGCTCCCAT 959
20-021        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21_024        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21_278        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21_290        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-020        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-039        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-056        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-071        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-111        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-121        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-179        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-187        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-196        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-256        GTTTGATAACCTGCTCGCATGCTCCCAT 959
21-294        GTTTGATAACCTGCTCGCATGCTCCCAT 959
BBRO-BChV21   GTTTGATAACCTGCTCGCATGCTCCCAT 959
              ********************** *****
```

c

```
BChV_R        ---TCTCAACCGTCACTGGCAA--- 1015
19_005        TTTTCTCAACCGTCACTGGCAATAA 1015
19_010        TTTTCTCAACCGTCACTGGCAATAA 1015
19_011        TTTTCTCAACCGTCACTGGCAATAA 1015
19_015        TTTTCTCAACCGTCACTGGCAATAA 1015
19_016        TTTTCTCAACCGTCACTGGCAATAA 1015
19-002        TTTTCTCAACCGTCACTGGCAATAA 1015
20-009        TTTTCTCAACCGTCACTGGCAATAA 1015
20-012        TTTTCTCAACCGTCACTGGCAATAA 1015
20-014        TTTTCTCAACCGTCACTGGCAATAA 1015
20-015        TTTTCTCAACCGTCACTGGCAATAA 1015
20-016        TTTTCTCAACCGTCACTGGCAATAA 1015
20-017        TTTTCTCAACCGTCACTGGCAATAA 1015
20-018-1      TTTTCTCAACCGTCACTGGCAATAA 1015
20-018-2      TTTTCTCAACCGTCACTGGCAATAA 1015
20-021        TTTTCTCAACCGTCACTGGCAATAA 1015
21_024        TTTTCTCAACCGTCACTGGCAATAA 1015
21_278        TTTTCTCAACCGTCACTGGCAATAA 1015
21_290        TTTTCTCAACCGTCACTGGCAATAA 1015
21-020        TTTTCTCAACCGTCACTGGCAATAA 1015
21-039        TTTTCTCAACCGTCACTGGCAATAA 1015
21-056        TTTTCTCAACCGTCACTGGCAATAA 1015
21-071        TTTTCTCAACCGTCACTGGCAATAA 1015
21-111        TTTTCTCAACCGTCACTGGCAATAA 1015
21-121        TTTTCTCAACCGTCACTGGCAATAA 1015
21-179        TTTTCTCAACCGTCACTGGCAATAA 1015
21-187        TTTTCTCAACCGTCACTGGCAATAA 1015
21-196        TTTTCTCAACCGTCACTGGCAATAA 1015
21-256        TTTTCTCAACCGTCACTGGCAATAA 1015
21-294        TTTTCTCAACCGTCACTGGCAATAA 1015
BBRO-BChV21   TTTTCTCAACCGTCACTGGCAATAA 1015
              **************************
```

Figure 5.13:DSMZ Beet chlorosis virus (BChV) reverse transcription-qPCR assay alignment with the produced BChV isolate sequences. a – BChV forward primer, b – BChV probe, c – BChV reverse primer (shown in reverse compliment).

Aligning the BMYV isolate sequences with the Rothamsted Research aphid RT-qPCR primers, identified one nucleotide mismatch in the reverse transcription primer and two nucleotide mismatches in the qPCR forward primer, (Figure 5.14). All three of these sites were conserved amongst the BMYV sequences. The qPCR reverse primer and qPCR probe had exact complementarity to all BMYV sequences with no sequence variation identified at these genome regions.

Alignment to the BChV sequences showed no variation in the qPCR primer or probe binding sites, with the primers and probes binding with exact complementarity. The same nucleotide mismatch that was identified in the reverse transcription primer binding site to the BMYV sequences was also present in the BChV sequences (Figure 5.15).

a

```
VR2           ---CCrCTACAAAGGCAATGGTTC---
19-013        GATCCTCTACAAAGGCAATGGTTCTTC 4086
20-006        GATCCTCTACAAAGGCAATGGTTCTTC 4086
20-009        GATCCTCTACAAAGGCAATGGTTCTTC 4086
20-010        GATCCTCTACAAAGGCAATGGTTCTTC 4086
20-014        GATCCTCTACAAAGGCAATGGTTCTTC 4086
21-056        GATCCTCTACAAAGGCAATGGTTCTTC 4086
21-097        GATCCTCTACAAAGGCAATGGTTCTTC 4086
21-254        GATCCTCTACAAAGGCAATGGTTCTTC 4086
21-294        GATCCTCTACAAAGGCAATGGTTCTTC 4086
BBRO-BMYV21   GATCCTCTACAAAGGCAATGGTTCTTC 4086
              ***************************
```

b

```
Pol_F         ---CGTTTACAGCGTCTTACATCAACG---
19-013        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
20-006        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
20-009        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
20-010        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
20-014        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
21-056        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
21-097        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
21-254        GGGCATTTGCAGCGTCTTACATCAACGGGA 4086
21-294        GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
BBRO-BMYV21   GGGCATTTGCAGCGTCTTACATCAACGGGG 4086
              **** *** ********************
```

c

```
Pol_R         ---AGGATCCTCTACAAAGGCAATGG---
19-013        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
20-006        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
20-009        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
20-010        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
20-014        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
21-056        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
21-097        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
21-254        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
21-294        TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
BBRO-BMYV21   TTCAGGATCCTCTACAAAGGCAATGGTTC 4144
              *****************************
```

d

```
Pol_probe     ---CGTTGCCaAGGACCA---
19-013        TGACGTTGCCAAGGACCAATT 4017
20-006        TGACGTTGCCAAGGACCAATT 4017
20-009        TGACGTTGCCAAGGACCAATT 4017
20-010        TGACGTTGCCAAGGACCAATT 4017
20-014        TGACGTTGCCAAGGACCAATT 4017
21-056        TGACGTTGCCAAGGACCAATT 4017
21-097        TGACGTTGCCAAGGACCAATT 4017
21-254        TGACGTTGCCAAGGACCAATT 4017
21-294        TGACGTTGCCAAGGACCAATT 4017
BBRO-BMYV21   TGACGTTGCCAAGGACCAATT 4017
              *********************
```

Figure 5.14:Rothamsted Research aphid reverse transcription-qPCR assay (which detects both Beet mild yellowing virus (BMYV) and Beet chlorosis virus (BChV) aligned with the produced BMYV isolate sequences. Bold letters indicate mismatching sites in the primer/probe where the sequence is conserved amongst the sequenced isolates. a – reverse transcription primer, VR2 (shown in reverse compliment), b – qPCR forward primer, Pol_F, c - qPCR reverse primer, Pol_r (shown in reverse compliment), d – qPCR probe, Pol_probe (shown in reverse compliment)

a

```
VR2            ---CCrCTACAAAGGCAATGGTTC---
19_005         GATCCTCTACAAAGGCAATGGTTCTTC 4157
19_010         GATCCTCTACAAAGGCAATGGTTCTTC 4157
19_011         GATCCTCTACAAAGGCAATGGTTCTTC 4157
19_015         GATCCTCTACAAAGGCAATGGTTCTTC 4157
19_016         GATCCTCTACAAAGGCAATGGTTCTTC 4157
19-002         GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-009         GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-012         GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-014         GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-015         GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-016         GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-017         GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-018-1       GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-018-2       GATCCTCTACAAAGGCAATGGTTCTTC 4157
20-021         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21_024         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21_278         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21_290         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-020         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-039         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-056         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-071         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-111         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-121         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-179         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-187         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-196         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-256         GATCCTCTACAAAGGCAATGGTTCTTC 4157
21-294         GATCCTCTACAAAGGCAATGGTTCTTC 4157
BBRO-BChV21    GATCCTCTACAAAGGCAATGGTTCTTC 4157
               ***************************
```

b

```
Pol_F          ---CGTTTACAGCGTCTTACATCAACG---
19_005         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
19_010         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
19_011         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
19_015         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
19_016         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
19-002         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-009         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-012         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-014         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-015         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-016         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-017         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-018-1       GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-018-2       GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
20-021         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21_024         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21_278         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21_290         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-020         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-039         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-056         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-071         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-111         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-121         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-179         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-187         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-196         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-256         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
21-294         GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
BBRO-BChV21    GGGCGTTTACAGCGTCTTACATCAACGGGA 4096
               ******************************
```

c

```
Pol_R          ---AGGATCCTCTACAAAGGCAATGG---
19_005         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
19_010         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
19_011         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
19_015         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
19_016         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
19-002         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-009         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-012         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-014         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-015         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-016         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-017         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-018-1       TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-018-2       TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
20-021         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21_024         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21_278         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21_290         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-020         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-039         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-056         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-071         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-111         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-121         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-179         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-187         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-196         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-256         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
21-294         TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
BBRO-BChV21    TTCAGGATCCTCTACAAAGGCAATGGTTC 4154
               *****************************
```

d

```
Pol_probe      ---CGTTGCCaAGGACCA--- 4127
19_005         TGACGTTGCCAAGGACCAATT 4127
19_010         TGACGTTGCCAAGGACCAATT 4127
19_011         TGACGTTGCCAAGGACCAATT 4127
19_015         TGACGTTGCCAAGGACCAATT 4127
19_016         TGACGTTGCCAAGGACCAATT 4127
19-002         TGACGTTGCCAAGGACCAATT 4127
20-009         TGACGTTGCCAAGGACCAATT 4127
20-012         TGACGTTGCCAAGGACCAATT 4127
20-014         TGACGTTGCCAAGGACCAATT 4127
20-015         TGACGTTGCCAAGGACCAATT 4127
20-016         TGACGTTGCCAAGGACCAATT 4127
20-017         TGACGTTGCCAAGGACCAATT 4127
20-018-1       TGACGTTGCCAAGGACCAATT 4127
20-018-2       TGACGTTGCCAAGGACCAATT 4127
20-021         TGACGTTGCCAAGGACCAATT 4127
21_024         TGACGTTGCCAAGGACCAATT 4127
21_278         TGACGTTGCCAAGGACCAATT 4127
21_290         TGACGTTGCCAAGGACCAATT 4127
21-020         TGACGTTGCCAAGGACCAATT 4127
21-039         TGACGTTGCCAAGGACCAATT 4127
21-056         TGACGTTGCCAAGGACCAATT 4127
21-071         TGACGTTGCCAAGGACCAATT 4127
21-111         TGACGTTGCCAAGGACCAATT 4127
21-121         TGACGTTGCCAAGGACCAATT 4127
21-179         TGACGTTGCCAAGGACCAATT 4127
21-187         TGACGTTGCCAAGGACCAATT 4127
21-196         TGACGTTGCCAAGGACCAATT 4127
21-256         TGACGTTGCCAAGGACCAATT 4127
21-294         TGACGTTGCCAAGGACCAATT 4127
BBRO-BChV21    TGACGTTGCCAAGGACCAATT 4127
               *********************
```

Figure 5.15: Rothamsted Research aphid reverse transcription-qPCR assay (which detects both Beet mild yellowing virus (BMYV) and Beet chlorosis virus (BChV) aligned with the produced BChV isolate sequences. Bold letters indicate mismatches in the primer/probe where the sequence is conserved amongst the sequenced isolates. a – reverse transcription primer, VR2 (shown in reverse compliment), b – qPCR forward primer, Pol_F, c - qPCR reverse primer, Pol_r (shown in reverse compliment), d – qPCR probe, Pol_probe (shown in reverse compliment)

5.5 Discussion

Overall levels of intra-species genetic variation were similar for both BMYV and BChV. No isolates showed greater than 10% difference in amino acid sequence identity for any gene product and therefore would be not classed as a separate species under the International Committee on Taxonomy of Viruses guidelines (Sõmera et al., 2021). One fundamental limitation of using this approach, to understanding the genetic diversity within BMYV and BChV isolates, is that it cannot be used to detect recombination. Recombination events result in the swapping of genetic material between genetically distinct viruses. The approach taken here was to map the aligned short reads to a reference genome and then 'correct' that reference to give a consensus sequence of the sample. Were recombination to have occurred giving rise to a virus which differed significantly from the reference sequence, the reads would not have aligned and therefore would not contribute to the consensus sequence. Consequently, the results discussed here reflect the smaller genetic changes most likely arising from errors in replication caused by the viral RdRp.

Importantly, from a diagnostic perspective, very little genetic variation was identified in the regions targeted by the DSMZ BMYV or BChV assays. Both the primers and probes showed a high level of complementarity to the sequenced isolates indicating the assays are reliable at detecting multiple virus isolates. High sequence conservation was also seen in the genome region targeted by the Rothamsted Research diagnostics, however based on the sequence data generated here, there is the potential for slight adjustments to the reverse transcription primer and forward qPCR primer which may improve primer binding and diagnostic sensitivity.

When drawing conclusions from this data set it is important to remember the origins of the sequencing data. Each sequenced sRNA library was derived from RNA extracted from virus-infected leaves collected from the field. Crucially this means leaves may have been initially infected with a population of genetically differing virus particles, rather than one single virion. As such, the consensus sequences of the isolates may not represent a single virus genome but rather give the consensus of the most prevalent nucleotides at each genome position across the viral population contained within the isolate.

As previously discussed, BCFtools is a variant calling software which has been used here to create the sample consensus sequences from which viral genetic variation has been investigated. The stringency parameters of the tool mean that nucleotide variants occurring at a low rate within the sample sequencing data will be discounted. This reduces the risk of nucleotide variation arising from sequencing errors being mistakenly attributed to true genetic variation, however it increases the risk of low frequency mutations going undetected. This may explain why three of BChV isolates

(19-010, 21-017 and 20-018-1) all shared 100% identity with the BChV reference genome; with any genetic variation present not being consistent enough within each isolate to appear within the generated consensus sequence. Despite this potential draw back, the stringency parameters used in the analysis do provide assurance that where nucleotide differences are seen they are true reflections of differences observed within that virus population.

Alternative approaches of analysing this data set, such as *de novo* assembly of the viral sRNAs may permit the identification of low frequency mutations (Singh et al., 2020). However, adopting such a methodology is problematic when samples may be infected with multiple closely related viruses (such as both BMYV and BChV). Such mixed infections could result in erroneous contigs, formed from reads originating from two separate viruses, giving the illusion of greater genetic diversity (Boonham et al., 2014).

It was hypothesised that greater genetic variation would be seen between virus isolates with further geographic separation, however the results presented here do not support this. This suggests that other factors have a larger influence on virus genetic diversity than geographic location. One such factor may be the host plant from which the virus was acquired by the aphid prior to infecting the beet plant, particularly the overwinter host. Isolates which originated from the same weed species, for example, may share similar mutations which proved advantageous to replication within that host. This would be consistent with the differences seen in the BBRO BMYV culture which is maintained predominantly in *Capsella bursa-pastoris* rather than sugar beet to help prevent contamination.

Alternatively, the species of aphid which transmitted the virus to the beet plant may contribute to the genetic variation, with certain viral mutations favouring aphid transmission by *Macrosiphum euphorbiae,* for example, over *Myzus persicae.* Again, this could have contributed to the differences seen in the BBRO BMYV culture which is only transmitted to new plants using the BBRO *M. persicae* culture and never *M. euphorbiae.*

The intra-species genetic variation which was identified was predominantly in the ORFs located at the 5' end of the viral genome. Variation within ORF0 and ORF1 is consistent with plant host and aphid vector adaptation. P0, encoded by ORF0, is a silencing suppression protein acting against the host plant gene silencing system. It has also been linked to viral pathogenicity and host symptom development, as well as affecting plant-aphid interactions through the control of phytohormones. ORF1, aside from its role in viral replication, encoding the viral genome-binding protein, also has a phytohormone regulation activity. Therefore, alterations to these proteins could affect both virus-host and virus-vector interactions, potentially providing resistance-breaking properties.

Nevertheless, the ORF most affected by nucleotide changes predicted to alter the encoded amino acid was ORF2. Translation of ORF2 arises through a ribosomal frame shift from ORF1 resulting in the P1P2 fusion protein. Previous studies have identified the ORF2 region as encoding the viral RdRp and therefore this region has a fundamental role in viral replication. Hence, it is surprising that the highest number of predicted amino acid changes were identified within this protein, a finding which goes against research conducted into variation seen between poleroviruses species (Huang et al., 2005; LaTourrette et al., 2021). This may be a consequence of the sRNA sequencing methodology and using a variant-calling tool to identify nucleotide differences between isolates. The shorter reads lengths of sRNA library sequencing may have permitted sample reads originating from other parts of the virus genome, or indeed different viruses present within the sample, to mis-align to the P2 region of the reference sequence. This would cause an artificially increased nucleotide diversity within the region. Future studies, utilising longer-read methodology, would help clarify if this is the case or if the result is true; indicating a greater intra-species variation in this genome region than previously understood.

In both the BMYV and BChV isolates, synonymous nucleotide differences were also identified between isolates. As these differences were not predicted to alter the encoded amino acid, they are less likely to significantly alter the physical properties of the virus. Nevertheless, previous studies have shown that synonymous mutations in RNA viruses can affect RNA secondary structure and alter the codon use bias, in turn affecting the physical properties of the virus. As with the amino acid altering nucleotides, the synonymous changes in both the BMYV and BChV isolates were most prevalent in the 5' proximal ORFs and so may further contribute to changes within these proteins.

The BChV isolate 19-016, originating from a fodder beet field in Somerset, had the lowest similarity of any of the virus isolates. The reasons for this are not clear, particularly as the same differences were not seen in isolate 19-015 despite it also originating from a fodder beet plant in a neighbouring field. Although these results may be a true reflection of a viral population, we cannot rule out a methodology cause; possibly contamination during the sRNA library preparation. Storage of the sample and resulting RNA degradation may also have contributed to these results, particularly given that the 2019 sample had to be freeze-dried and stored for longer than planned due to the laboratory lockdowns during the Covid-19 pandemic. However why only this isolate may have been affected is unclear.

Focusing on the virus isolates maintained in culture at the BBRO, both the BMYV and BChV cultures showed genetic changes over time, becoming more genetically distinct from the 'wild' virus isolates. These findings have important consequences in both fundamental virus yellows research

and virus resistant variety development. Fundamental research conducted using BMYV or BChV viruses maintained in continuous culture may result in findings which would not be consistent with other BMYV or BChV isolates. From a breeding perspective, the genetic differences identified here may result in differences in pathogenicity and therefore varieties developed to overcome the BBRO BMYV or BChV isolate may not respond as expected when infected with other virus isolates. In the future, to ensure the reliability and relevance of the BBRO virus cultures, the cultures should be 'refreshed' periodically with a mixture of field collected virus isolates. Routine sequencing would also be valuable providing data on how closely the culture genetically reflects 'wild' isolates.

Chapter 6: The effect of different virus populations on susceptible and resistant sugar beet varieties under field conditions

6.1 Chapter Contributions

The agronomic work described in this chapter was conducted by the BBRO trials team. Inoculation of the trial (see section 6.3.2.3) in 2022 was conducted by me and Stuart Harder alongside Mark Stevens, Simon Bowen, Alistair Wright, Kate Orman, Georgina Barratt all from the BBRO. In 2023 the trial was inoculated by me alongside Simon Bowen, Eleanor Towler, Hannah Carthy, Alistair Wright and Stephen Aldis from the BBRO. The BBRO trials team harvested the trial. Subsequent root weight, sugar content and impurity analysis were completed by operatives of the British Sugar BBRO tarehouse, with the results being verified by the independent National Farmers Union tarehouse representatives. Drone flights were completed by Alistair Wright. Leaf samples for ELISA testing were collected by me with support from Eleanor Towler and Ollie Hammond. All other work including aphid monitoring and aphid species identification I completed myself.

6.2 Introduction

The results of the previous chapter (Chapter 5) show that genetic variation is present within the BChV and BMYV species analysed as part of this study. However, as outlined in Chapter 1, for a virus isolate to be termed a ‘strain’ it must exhibit unique and recognisable phenotypic characteristics. Based on genetic data alone we cannot definitively say any of the virus isolates collected and cultured here are distinct enough to be called a “strain”. As discussed in Chapter 5, we can begin to make predictions about the effects of genetic differences, based on the genomic locations of nucleotide differences, but to fully appreciate the consequences of these differences, assessing the effect of the virus isolates on sugar beet plants is necessary.

No recent studies (since this identification of BChV) have characterised the effect on sugar beet of differing isolates from the same beet polerovirus species. Were the genetic differences identified between isolates (Chapter 5) to result in different disease severities this could have important consequences for resistance breeding. Predominantly in the UK, resistant sugar beet varieties have been developed through challenging them with the BBRO BMYV isolate. The results detailed in Chapter 5 show the BBRO BMYV isolate genome has diverged from the 'wild' BMYV isolates. It is therefore possible that the resistant sugar beet varieties that have been developed may be specific to this isolate and less effective against other BMYV isolates.

Currently only one variety is included on the UK recommended list, and available for sugar beet growers, with virus yellows resistance. This variety is Maruscha KWS, with claimed partial tolerance against BMYV. Given the findings outlined in Chapter 3, where BChV was identified as the most prevalent cause of virus yellows disease in the UK, it is important to determine whether resistant varieties which have been developed to overcome BMYV infection can also combat BChV. As with BMYV, confirming any resistance mechanism is functional against all isolates of BChV is also important for the effective deployment of these varieties in the field.

As demonstrated in Chapter 4 it is difficult to simulate the yield impact of virus infection under controlled conditions. Randomised field trials enable experimental plants to be treated more akin to a commercial crop, whilst maintaining scientific rigour. Previous studies have utilised field trials to assess the impact of different virus yellows species on sugar beet yield (Hossain et al., 2021; Stevens et al., 2004), as well as for identifying resistant varieties (Wintermantel, 2005). Although some trials are conducted exploiting natural aphid/virus infection alone (Dunning and Winder, 1965), trials aiming to assess variety performance typically involve inoculating experimental plants with viruliferous aphids. This latter method ensures uniform virus pressure across the trial and has proven a successful method of identifying resistant sugar beet varieties (Wright and Stevens, 2023).

To determine the effect of the collected virus isolates on resistant and susceptible sugar beet varieties I conducted virus inoculated field trials. Replicated across two years, these experiments helped clarify the consequences of the genetic variation identified within BMYV and BChV isolates. I have also improved our understanding on the resilience and durability of resistant varieties, assessing their performance under mixed virus infection.

6.3 Materials and Methods

6.3.1 Creation of virus cultures

To establish varietal response under differing virus isolates, cultures of virus populations were established. This was achieved using the virus-infected beet leaves received in the 2021 larger scale virus survey described in Chapter 3. Based on the qPCR assay results of this survey, one BMYV infected and three BChV infected leaves were selected. These specific leaves were chosen based on their origin location, high virus titre as determined via ELISA, (Chapter 2, section 2.4) and their suitability to support aphid feeding (i.e. how fresh the leaves had arrived in the lab).

Virus cultures were established prior to the sRNA sequencing, due to time constraints and the need to collect leaves before commercial fields were harvested. Genetic variation was presumed to exist between virus isolates, and hypothesised to be greater between isolates which were more geographically distinct. As discussed in Chapter 5, geographic location did not correlate to genetic variation, however genetic differences were seen between the isolates brought into culture.

To keep the leaf samples turgid and viable for aphid feeding, approximately 2cm was trimmed from the basal end of the leaf petiole and the leaf placed in a beaker of deionised water. Five virus-free *Myzus persicae* were transferred onto the leaf blade using a paintbrush. The leaf and beaker were then sealed within an aphid proof bag. After three days the aphids, including any progeny, were carefully transferred from the leaf to a healthy sugar beet seedling with two to four true leaves. A plastic cup was placed over the plant to contain the aphids. Aphids were allowed to feed and transfer the virus for one week, before being sprayed with insecticide (0.1g/L InSyst containing 20% w/w acetamiprid, CertisBelchim).

Subsequent ELISA and qPCR testing (using the assay detailed in Chapter 2 section 2.4-2.5), confirmed the presence of BMYV in the 21-254 culture and BChV in cultures 21-278 and 21-024. The other BChV culture (21-290) was found to also contain BYV (Table 6.1). Unfortunately, no plant host suitable to filter out the BYV from the culture was available, however, the culture was still included in the field trial to assess the impact of combined BChV and BYV infection on the varieties. Whilst the cultures were being maintained between inoculation of the 2022 field trial and the 2023 field trial, the 21-024 BChV culture became contaminated with BYV. As such in the 2023 field trial, plots inoculated with this culture became infected with both BChV and BYV.

Following this protocol, a total of four virus cultures were established (Table 6.1). These were used alongside the BBRO BMYV and BChV reference cultures. Once established, cultures were maintained as per the virus culture protocol detailed in Chapter 2 section 2.1.

Table 6.1: origin details of virus cultures established in 2021 and used to inoculate field trials in 2022 and 2023.

Sample ID	Original leaf location	Original crop	Virus
21-254	Crowland, Lincolnshire	Sugar beet	Beet mild yellowing virus
21-278	Rougham, Norfolk	Sugar beet	Beet chlorosis virus
21-290	Thirn, North Yorkshire	Fodder beet	Beet chlorosis virus and Beet yellows virus
21-024	Letheringham, Suffolk	Sugar beet	Beet chlorosis virus (Beet yellows virus present in culture in 2023)

6.3.2 Field Experiment

6.3.2.1 Layout

A field experiment was designed to assess the performance of sugar beet varieties under the different virus isolates. Four varieties were included in the trial, two with resistance to polerovirus infection (KWS-1, KWS-10) and two susceptible varieties (KWS-6, KWS-9). These varieties were challenged with six different virus isolates: the four established cultures (Table 6.1), and the BBRO cultures of BMYV and BChV. In addition, a control treatment, which was not inoculated with aphids, since this would pose an even greater risk of contamination, was also included to assess variety performance when uninoculated with virus.

The experiment was arranged in a split-split-split plot design with four replicates of virus inoculated treatments and eight replicates of the uninoculated control treatment, split across two main blocks and four blocks (Figures 6.1 and 6.2). The uninoculated treatment was fixed at each end of the trial blocks to reduce the risk of contamination from the virus inoculated plots. These replicates are described as “Uninoculated 1” and “Uninoculated 2” for clarity. Each individual plot measured 1.5 by 4.5m and consisted of three rows of the allocated sugar beet variety.

Virus treatments were randomly assigned within in Block 1 and 3, then the same randomisation applied to Block 2 and 4 to minimise virus contamination between treatments. To reduce the risk of secondary spread of virus outside of the inoculated plots, KWS-1, a sugar beet variety with breeder-claimed resistance to BMYV, was used as a ‘buffer’ to surround each treatment. Spring rye (*Secale cereale)* was sown around the experimental area, and between the two main blocks to act as a wind break, in line with standard BBRO protocol for virus experiments. This reduced the risk of viruliferous aphids released into the treated plots being blown between the main blocks and helped

to shield the plots from naturally occurring aphids. In 2023 a strip of oil radish (*Raphinus sativus*) was sown along the field margin of the experimental area to act as a trap crop for aphids migrating into the field and other invertebrate pests such as flea beetle.

6.3.2.2 Agronomy

In both 2022 and 2023 the field experiments were hosted within commercial sugar beet fields at Morley Farms Ltd. In 2022 the field was located at (52.56 N, 1.029 E) and in 2023 at (52.57 N, 1.021 E) on a loam soil. In 2022 the field trial was sown on the 14th April by the BBRO field trials team using a John Deere 6130R (RTK Guidance) with a Wintersteiger automated plot drill (6 row x 50cm). In 2023 the experiment was sown on the 25th April. Plots were double sown at a 9cm seed-spacing, then gapped (excess plants removed) prior to inoculation to provide a uniform plant stand with a target intra-row plant spacing of 18cm. All seed was treated with proprietary priming and pelleting technology (EPD 2.0) by KWS, along with the plant protection products tefluthrin (Force ST, Syngenta) and hymexazol (Tachigaren).

A standard commercial sugar beet herbicide, fertiliser and fungicide programme was conducted by the BBRO field trials team to keep the plots in good agronomic condition and free from weeds. Aphid numbers were monitored within the experiment from seedling emergence until the 16-leaf stage, after which the risk posed from virus infection is negligible (BBRO, 2023a; Schop et al., 2022). In 2022, aphid numbers were high and an insecticide (0.1g/L InSyst containing 20% w/w acetamiprid, CertisBelchim) was applied on 9th May to control numbers. No aphicide was required in 2023.

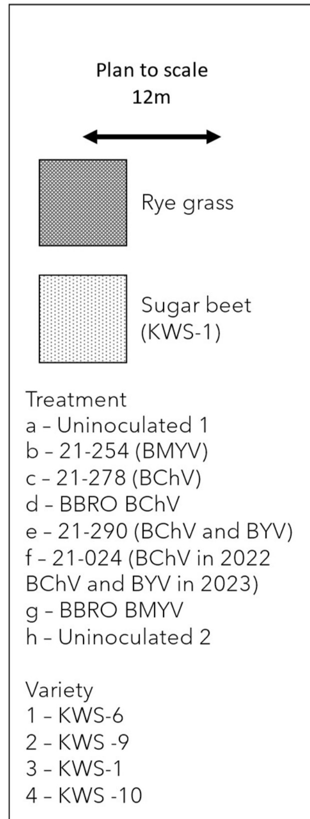


Figure 6.1: Experimental plan showing layout of sugar beet varieties and Beet mild yellowing virus (BMYV) and Beet chlorosis virus (BChV) virus treatments. Each plot (shown as white box) contained three rows of the specified sugar beet varieties, KWS-1 and KWS-10 had resistance to BMYV infection and KWS-6 and KWS-9 were susceptible. Plots were grouped together in treatments blocks, each receiving the same virus treatment. A buffer area of sugar beet was planted around each treatment block, then rye grass surrounding each main block.

Figure 6. 2: drone image of 2023 field trial, showing main blocks surrounded by rye taken on 23rd September 2023 taken by Alistair Wright (BBRO).

6.3.2.3 Virus inoculation

Viruliferous aphids of each virus culture were reared in MLR-352 (Panasonic) reach-in growth chambers as described in Chapter 2 section 2.1. BMYV-viruliferous aphids were reared on *Capsella bursa-pastoris* to minimise the risk of contamination with BChV cultures. BChV-viruliferous aphids were reared on sugar beet as no reliable, discriminative host suitable for aphid rearing was available.

Inoculation of plots with viruliferous aphids was conducted on the 26th May in 2022 and 25th May in 2023 when plants were at the 2-4 true leave stage. Migration of *M. persicae* into sugar beet fields typically peaks around the end of May beginning of June, hence inoculation was timed to mimic the likely timing of natural infection. Inoculation was achieved by placing a small piece of leaf tissue containing approximately 10 viruliferous aphids into the centre of every-other sugar beet plant within each plot.

Controlling the release of viruliferous aphids into the trial was vital to prevent contamination between treatments and minimise the risk to any neighbouring sugar beet crops. As such, multiple steps were taken to mitigate these risks. Inoculation was conducted by six different people, each responsible for one virus culture. Working entirely independently, each person prepared the inoculum containing the viruliferous aphids at the BBRO laboratory then travelled to the field trial site in separate vehicles. Once at the trial, 'inoculators' followed a pre-arranged specific route

walking through the rye to the plots they were to inoculate, avoiding walking near any other treatment plots or inoculator. Any viruliferous aphids which may have been present on clothing were brushed off into the plot before moving between blocks. After each inoculator had finished infecting every plot of their corresponding virus treatment, they exited the trial following the pre-arranged route, again walking through the rye and avoiding any other sugar beet plots.

In 2022 aphids were left to feed, and transfer the virus for 7 days, before being killed with an aphicide. In 2023 aphid numbers were low, with generally fewer than 10 viruliferous aphids per inoculated plant and aphid predator numbers were high. Consequently, 7 days after inoculation aphid numbers had not reached the agronomic threshold required to apply an aphicide (one green wingless aphid per four plants up to the twelve-leaf stage). Aphid numbers were continually closely monitored, however they did not reach the spray threshold as beneficial insects remained high throughout.

6.3.2.4 Harvest

Plots were harvested into large bags by the BBRO trial team on the 31st October 2022 and the 4th October 2023 using a John Deere 6135R with modified Garford Victor sugar beet plot harvester (Figure 6.3). Bags were then transported to the BBRO plot facility tarehouse at the Wissington Beet Sugar factory (Norfolk, UK), where each plot was weighed dirty then washed and reweighed by the British Sugar BBRO tarehouse operatives. Samples from each plot were taken for sugar content and impurity analysis (ICUMSA, 2007) by the British Sugar BBRO tarehouse operatives and then verified by the independent National Farmers Union tarehouse representatives. Sucrose yield was calculated by multiplying the plot clean weight by the percentage sugar.

Figure 6.3: the BBRO trials team harvesting the 2023 field trial on the 4th October 2023, a) sugar beet plot harvester lifting roots from trial plots into large bags. b) harvested roots from one trial plot ready to be delivered to the BBRO tarehouse (photos by Suzannah Harder).

6.3.3 ELISA testing

ELISA testing of leaf samples was conducted to measure virus titre across the varieties and virus treatments. In 2022, ELISA testing was conducted four, eight, twelve and nineteen weeks after inoculation. The nineteen-week time point was not planned but added in response to the exceptionally high temperatures and dry conditions experienced at the trial site. Due to these conditions, at the twelve-week time point, all plants were severely droughted. By the nineteen-week time point plants were no longer showing symptoms of drought stress.

To avoid repeat sampling of the same plant, prior to any symptom development, five plants per experimental plot were randomly selected and marked using a cane. At the first sampling point, the plant nearest the cane was used. At the second sampling point, the plant one away from the cane was used and so on. At each time point, the largest leaf was taken from the selected plant as shown in Figure 6.4. In 2022, due to a beet moth (*Scrobipalpa ocellatella*) infestation, by the nineteen-week time point, only a very limited number of plants had an intact canopy (Figure 6.5), however the same protocol of sampling the largest leaf from the selected plant was followed. In 2023 ELISA testing was conducted at a single timepoint, fourteen weeks after inoculation. As in 2022, five plants were selected at random from each plot and the largest leaf sampled. In 2023 no beet moth damage was recorded.

Figure 6. 4: taking leaf samples from field trial plots for ELISA testing. a) sugar beet plant in trial plot marked with a cane prior to any symptom development, b) at first sampling time point, plant closest to the cane was selected. The largest leaf was identified by grouping the canopy together and determining the tallest leaf (photos by Suzannah Harder).

Figure 6.5: photos taken from field trial plots in 2022 showing damage caused by beet moth infestation (photos by Suzannah Harder).

All sampled leaves were placed in plastic sample bags and transported back to the laboratory where two 2.5cm diameter leaf discs were taken from each leaf. ELISA testing was conducted following the methodology described in Chapter 2 section 2.4. At every time point all leaves were tested using the Beet western yellows virus (BWYV) antibody set (RT-0049-0049/1, DSMZ). At the nineteen-

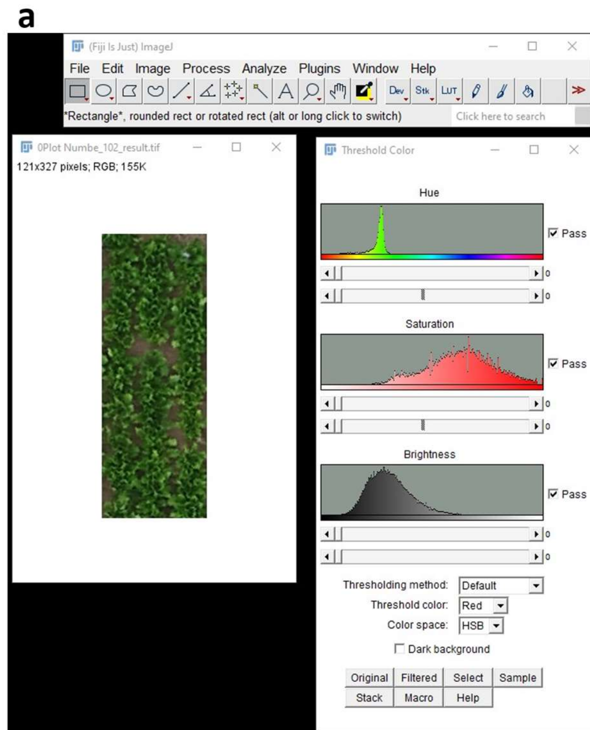
week post inoculation time points in 2022 and in 2023 the leaves were also tested using the BYV antibody set (RT-0185, DSMZ).

6.3.4 Canopy cover and canopy chlorophyll estimation

Canopy cover and canopy chlorophyll estimation were determined based on aerial images captured by drone. Drone flights and subsequent image processing and analysis was undertaken by Alistair Wright (BBRO) following the methodology detailed by Wright et al. (2022). Drone flights were conducted on 22nd July and 15th September in 2022 and 9th July and 23rd September in 2023. Data was received in the form of RGB images, and the spectral reflectance index mNDblue (used to estimate canopy chlorophyll, (Jay et al., 2017)) of each experimental plot.

The percentage canopy cover per plot was calculated using a similar methodology to that described in Chapter 4 section 4.2.2.1. Plot images were loaded into the image analysis software ImageJ (version 1.53t). Then the 'colour threshold' tool used to remove any exposed ground by adjusting the hue settings to 40-145 (Figure 6.6) and a batch process macro run to calculate the percentage of image area selected.

a



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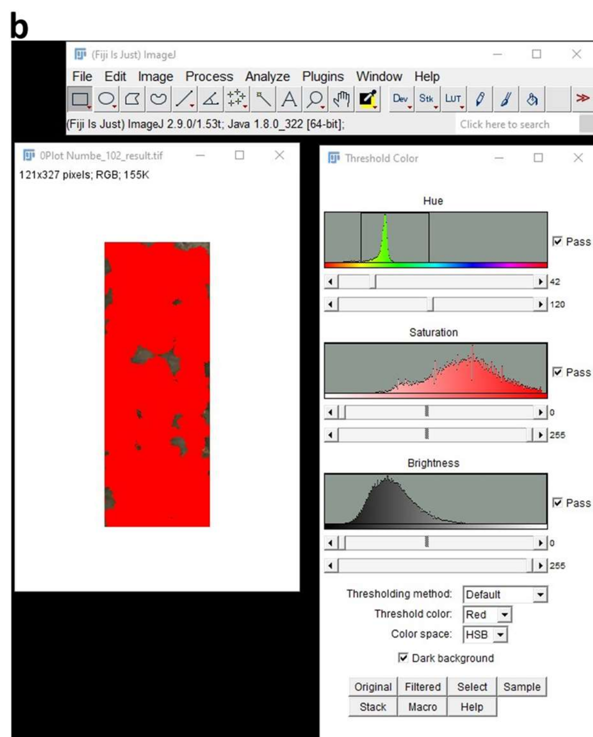

Figure 6.6: screen shots of user interface of ImageJ (version 1.53t) used to determine canopy cover, a) experimental plant image loaded into ImageJ, b) hue filter applied to select green/yellow image area.

6.3.5 Weather data

Air temperature and precipitation data was retrieved from the Morley Farm Weather Station (iMetos 3.3) via the Field Climate website (Pessl Instruments) and downloaded as an .xls file.

6.3.6 Monitoring natural aphid populations

Yellow water pan traps (YWP) were used to monitor the occurrence and abundance of naturally occurring *M. persicae* and *Macrosiphum euphorbiae* at the field trial site. Monitoring took place during the spring aphid migration from 25th April to 4th July (standard week 17 to 27) (Taylor, 2013). Three YWPs were installed as per the manufacturer's instructions (MN59930, Ringot France) in the discard sugar beet in the field experiment. YWPs were placed approximately 15m apart and the pans adjusted to be at sugar beet canopy height, as shown in Figure 6.7.

YWPs were filled with water containing approximately three drops of domestic washing up liquid. The detergent breaks the surface tension of the water to ensure any insects which landed in the pan were captured. The pans were emptied twice a week by pouring the contents into a funnel lined with a fine net cloth. The cloth and insects where then carefully transferred to a storage pot and taken for analysis in the lab.

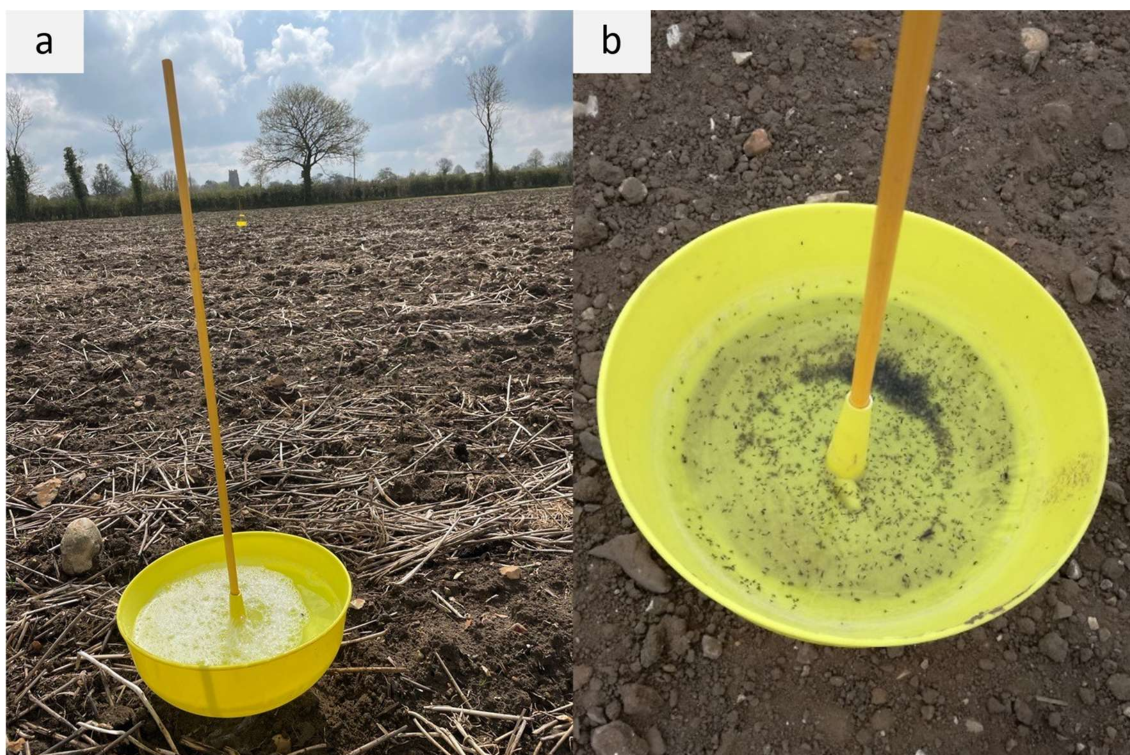

Figure 6.7: a) freshly filled yellow water pan (YWP) in discard beet of 2023 field trial, b) YWP on day of sample collection in 2022, (photos by Suzannah Harder).

In the laboratory, all insects were washed from the cloth into a white larval tray (such as A115, Watkins & Doncaster). Aphids of all species were identified and separated from the rest of the insect catch. A dissecting microscope (HN-3, Microtec) was used to identify the *M. persicae* and *M. euphorbiae* from all other aphid species (Figure 6.8). *M. persicae* and *M. euphorbiae* were identified based on their morphologically distinguishing features as described by Blackman (2010), and the total number of each species recorded. The total number of *Coccinellinae* sp (ladybirds) was also recorded, as an indication of natural aphid predator levels within the field.

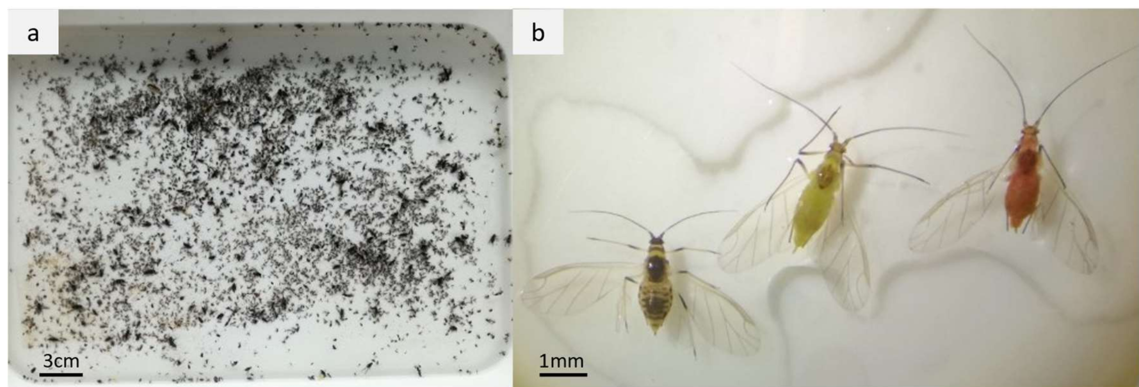

Figure 6.8: processing of yellow water pan (YWP) samples. a) contents of YWP sample emptied into white larval tray ready for aphid species to be separated, b) from left to right M. persicae, *green form of* M. euphorbiae, *red form of* M. euphorbiae, *identified from YWP sample (photos by Suzannah Harder).*

6.3.6.1 Identification of polerovirus in YWP aphids

M. persicae and *M. euphorbiae* aphids caught in the YWPs were tested via two-step RT-qPCR to determine if they were carrying BMYV and/or BChV using an unpublished protocol developed at Rothamsted Research (Martin Williamson, personal communication), as outlined in Chapter 2 section 2.6. The aphids were also tested for TuYV. TuYV is known to be carried by around 80% of the *M. persicae* population in the sugar beet growing region (BBRO, personal communication) and therefore acts as an inline positive control to confirm that poleroviruses were not lost through the capture process.

6.3.7 Statistical analysis

Results were analysed using GenSTAT 22nd edition (VSN International). All graphs were produced using RStudio version 2022.02.1+461 "Prairie Trillium" released for Windows (RStudio Team 2022).

6.3.7.1 Analysis of canopy cover, canopy chlorophyll, sucrose yield and ELISA data

To analyse the canopy cover, canopy chlorophyll (estimated by mNDblue values) and sucrose yield data two-way analysis of variance (ANOVA) in randomised blocks were conducted using the GenSTAT 'General Analysis of Variance' statistical test. The experiment design was set to 'General analysis of variance', and the Y-variate to the relevant dependent variable (canopy cover, mNDblue value, sucrose yield). The treatment structure was defined using the fixed factors 'Variety x Treatment'. The block structure was set to 'Main block / Block / Treatment / Variety' where '/' indicates the nested blocking structure of the split-split-split plot trial design. The least significant difference (LSD) at 5% significance calculation was included in the ANOVA.

For analysis of ELISA data, prior to conducting the two-way ANOVAs as described above, the data were first summarised to prevent pseudo-replication. Data were loaded into GenSTAT and the 'Summary Statistics' function used to calculate the mean ELISA result of the five individual plants tested for each plot.

6.3.7.1 Linear regression

Regression analysis was conducted on the percentage of the uninoculated sucrose yield achieved and the change in mNDblue value from the uninoculated using the GenSTAT 'Linear regression' statistical test. The regression type was set to 'simple linear regression' using the response variate (Y) 'percentage of uninoculated sucrose yield achieved' for the specified year (2022 or 2023). The explanatory variate (X) was set to 'change in mNDblue value from the uninoculated' for the relevant time point (July 2022, September 2022, July 2023 or September 2023).

Any improvement in the statistical significance of the model by the incorporation of the factors 'variety' and 'virus treament' were explored using the GenSTAT 'Linear regression with groups' statistical test. This was conducted using the response variate and explanatory variate set as described above, with the addition of the 'Groups' structure set to 'Variety, Treatment'.

6.4 Results

6.4.1 Weather data

Weather conditions varied considerably between the two years the field experiments were conducted (Figure 6.9). In 2022, the field trial site experienced exceptionally hot and dry conditions resulting in plants being placed under considerable drought stress (Figure 6.10). In comparison, the 2023 experimental site experienced significantly more rainfall with 244.2mm recorded between the beginning of June and end of August compared to 39.6mm across the same period in 2022.

Air temperatures were also higher in 2022, with a total of 25 days having a mean air temperature above 20°C, compared to only 14 days in 2023. Exceptionally high maximum air temperatures were also recorded in 2022, with a maximum air temperature of 38.05°C being recorded (on the 19th July) compared to a maximum of 32.23°C in 2023 (on the 10th September).

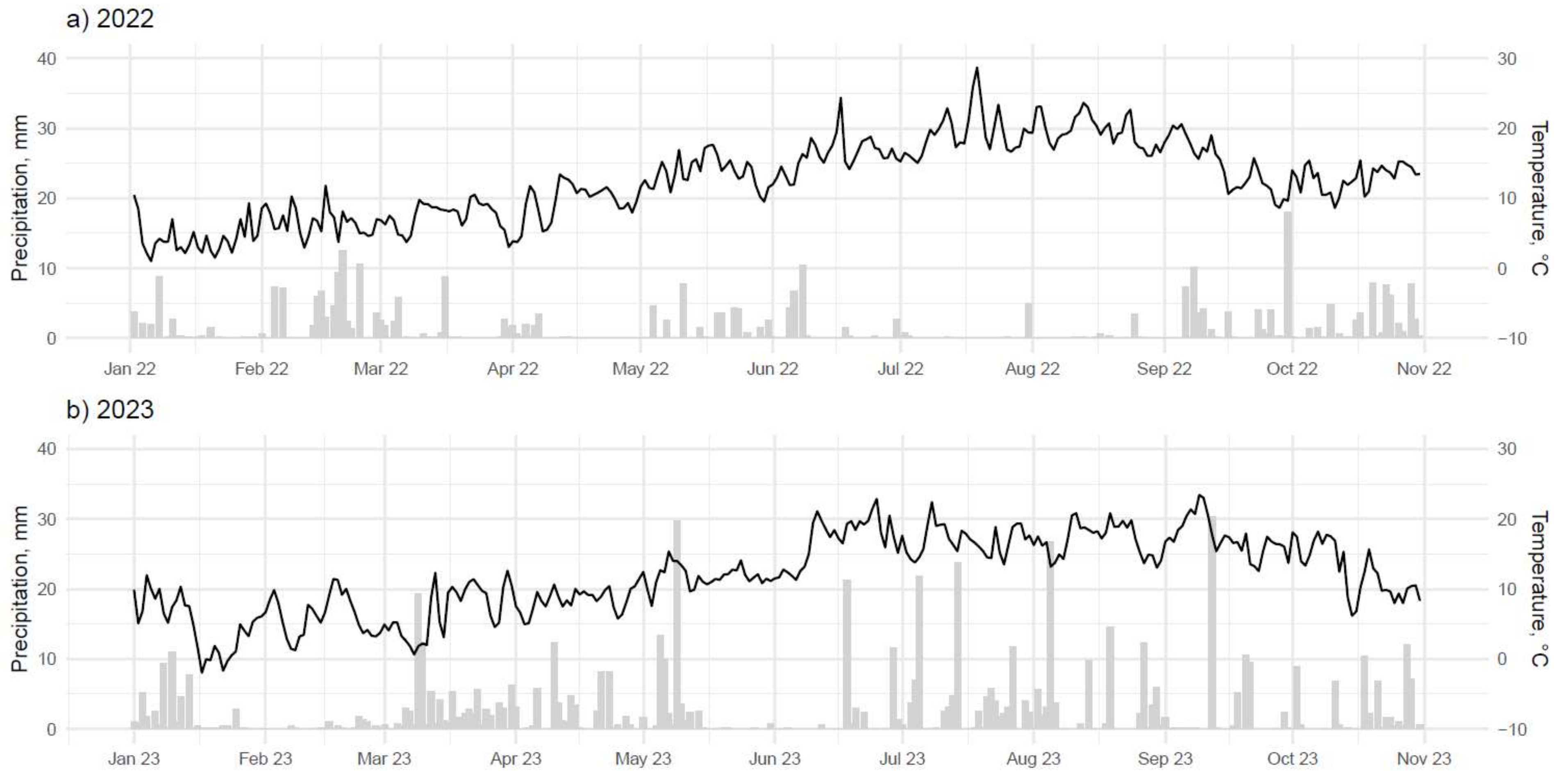

Figure 6.9: mean air temperature (shown as line) and daily total precipitation (shown as bar) recorded at the Morley weather station between 1st January and 31st October in a) 2022 b) 2023.

Figure 6.10: photo taken on 8th August 2022 of sugar beet plants in trial plot showing symptoms of severe drought stress (photo by Suzannah Harder).

6.4.2 Aphid pressure – YWP22 and YWP23

Natural aphid pressure was significantly lower at the trial site location in 2023 than it was in 2022 (Figure 6.11). In 2022, 1002 *M. persicae* and 87 *M. euphorbiae* were captured and identified from the trial site YWPs, compared to only 128 *M. persicae* and 34 *M. euphorbiae* in 2023. Ladybird numbers were broadly similar between years, with a total of 59 and 46 ladybirds identified in the YWP catches in 2022 and 2023 respectively.

In 2022, seven *M. persicae* aphids captured in the YWPs were found to be positive for either BMYV and/or BChV. No BMYV and/or BChV positive aphids were identified from the 2023 YWP catches.

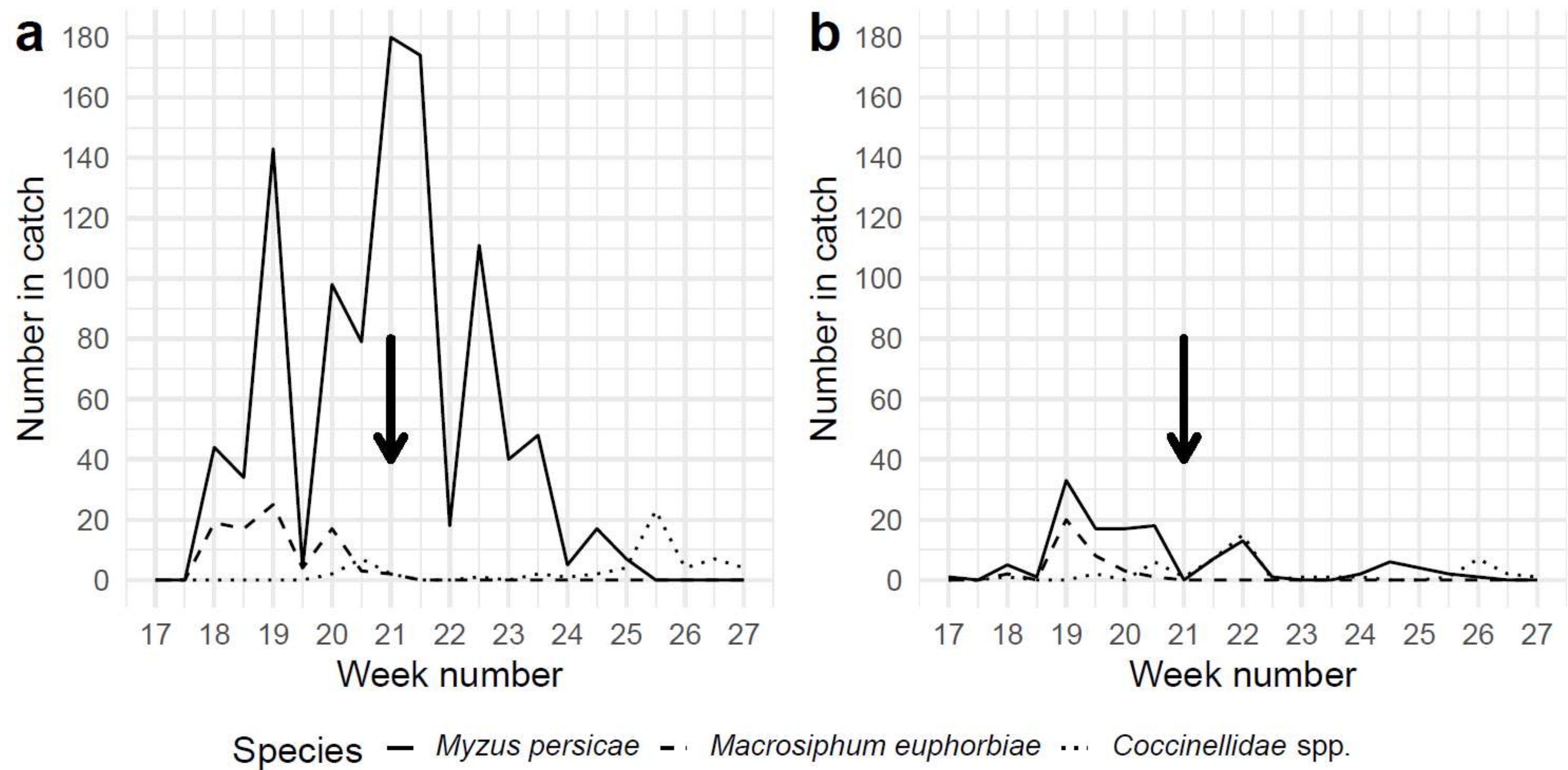

Figure 6.11: number of Myzus persicae, Macrosiphum euphorbiae *and* Coccinellidae *species identified in the trial site yellow water pans (YWPs) in a) 2022, b) 2023. Arrow indicates when trial inoculation with* M. persicae *took place.*

6.4.3 ELISA results

6.4.3.1 BYV

ELISA results from both 2022 and 2023 show BYV was present within the field trials (Figure 6.12). In 2022, the threshold above which a sample was deemed positive (as determined by the ELISA plate negative controls) was 0.159. The mean BYV ELISA result of every treatment exceeded this threshold, including both uninoculated treatments. However, the only treatment in which the ELISA result of every plot exceeded this threshold was 21-290 (known to contain both BChV and BYV) with individual plots ranging from 0.187 to 0.643. In 2022, Uninoculated 2 had a slightly higher mean BYV ELISA result than Uninoculated 1 at 0.2104 compared to 0.1725.

In 2023, only the two treatments known to contain BYV exceeded the negative control threshold determined to be 0.298. These were 21-290 which had a mean BYV ELISA result of 1.146, and 21-024 which had a mean ELISA result of 0.888. Both the uninoculated treatments fell below the positive threshold with mean ELISA results of 0.198 and 0.200 for Uninoculated 1 and 2 respectively.

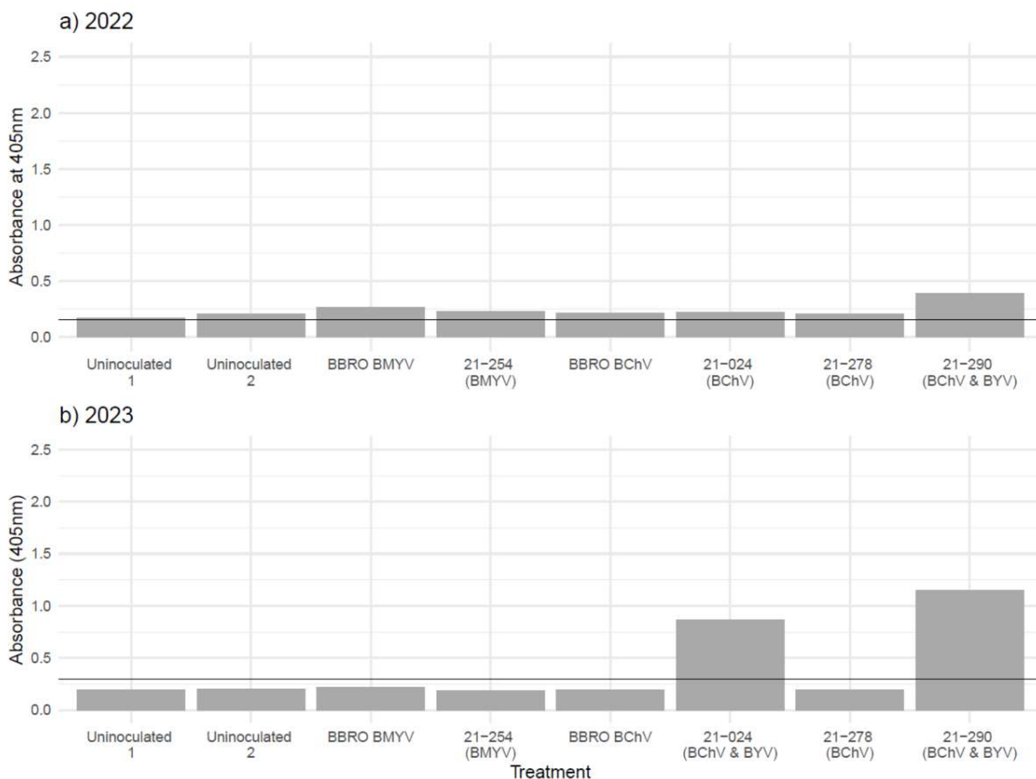

*Figure 6.12: mean Beet yellows virus (BYV) ELISA results across all varieties (*Polerovirus *resistant varieties KWS-1 and KWS-10 and susceptible varieties KWS-6 and KWS-9) for each treatment included in the field trial in a) 2022, b) 2023. Solid horizontal line indicates threshold set by negative controls above which a sample is deemed positive. BMYV – Beet mild yellowing virus, BChV – Beet chlorosis virus.*

6.4.3.2 Beet polerovirus - 2022

In 2022, significant differences in ELISA absorbance were identified between the different treatments at every sampling time point (Figure 6.13). Combining the ELISA results of all varieties, four weeks after inoculation, the BChV treatment 21-024 had the highest mean ELISA result at 2.41. This was significantly higher than both the BMYV treatments (BBRO BMYV and 21-254) which had ELISA results of 0.892 and 1.114 respectively (ANOVA, $p < 0.001$). There was no significant difference between 21-024 and the BBRO BChV treatment, but 21-024 did have a significantly higher ELISA result than the other BChV cultures 21-278 and 21-290.

The lowest mean ELISA results for all virus inoculated treatments were seen eight weeks post inoculation when the site was under significant drought stress. As at the four-week time point, treatment 21-024 had the highest mean ELISA absorbance at 0.781, significantly higher than all other treatments (ANOVA, $p < 0.001$). Of the virus inoculated treatments, 21-290 had the lowest ELISA absorbance with a mean of 0.292. Notably, the mean ELISA results of both treatments 21-290 and the BBRO BMYV did not reach the threshold set by the negative controls above which a sample was determined positive (0.513).

ELISA absorbances recovered somewhat at the twelve-week post inoculation time point, but none of the virus inoculated treatments reached the ELISA absorbances seen four weeks after inoculation. Again 21-024 had the highest mean ELISA result, significantly higher than all other treatments at 1.732 (ANOVA, $p < 0.001$). No significant difference was found in ELISA results of treatments 21-254, 21-278, BBRO BMYV or BBRO BChV, however all these treatments did have significantly higher ELISA results than treatment 21-290.

Unlike at all other time points, where 21-290 had the lowest ELISA result, nineteen-weeks after inoculation BBRO BMYV had the lowest ELISA result, significantly lower than all other inoculated treatments (ANOVA, $p < 0.001$). No difference was seen between treatments 21-254, 21-278, 21-290 and BBRO BChV, however 21-024 again had a significantly higher mean ELISA absorbance than all other treatments.

The uninoculated treatments fell below the positive threshold as determined by the negative controls at both four- and eight-weeks post inoculation. However, at 12- and 19- weeks post inoculation, Uninoculated 2 had a mean ELISA result which exceeded this threshold and therefore was classed as positive for either BMYV and/or BChV.

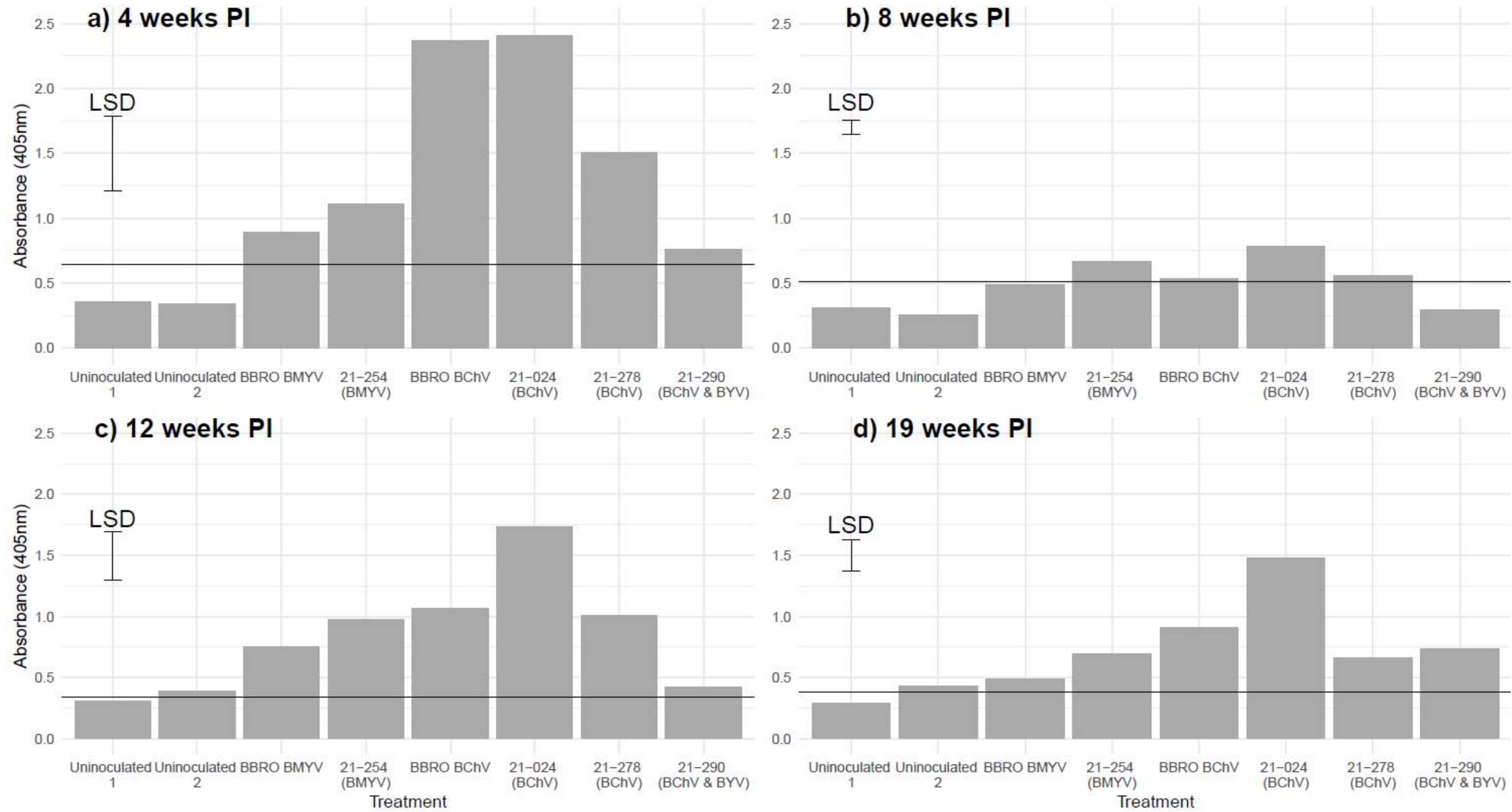

Figure 6.13: mean ELISA result of each treatment in the 2022 field trial across four time points. a) Four-weeks post inoculation (ANOVA p<0.001), b) eight-weeks post inoculation (ANOVA p<0.001) c) twelve-weeks post inoculation (ANOVA p<0.001), d) nineteen-weeks post inoculation (ANOVA p<0.001). Error bar shows least significant difference (LSD) at 5% significance. Solid horizontal line indicates threshold set by negative controls above which a sample is deemed positive. BMYV – Beet mild yellowing virus, BChV – Beet chlorosis virus, BYV – Beet yellows virus.

Focusing on the polerovirus treatments (removing the uninoculated and 21-290 BYV contaminated treatment from the analysis), significant differences were seen in mean ELISA result between the different varieties (Figure 6.14). Four weeks after inoculation, the resistant variety KWS-1 had the lowest mean ELISA result at 1.480, significantly lower than both susceptible varieties KWS-6 and KWS-9 (ANOVA, $p<0.001$). Although the other resistant variety, KWS-10, had a lower mean ELISA than both susceptible varieties, it was only significantly lower than KWS-6.

In comparison, at both the eight- and twelve-week time point, KWS-9 had a significantly higher mean ELISA result than any of the other varieties (eight-weeks; ANOVA, $p = 0.005$. twelve-weeks; ANOVA, $p = 0.001$). Although no significant differences were identified between varieties at the nineteen-week time point, KWS-9 still had the highest mean ELISA result at 1.017. No significant differences between varieties KWS-1, KWS-10 and KWS-6 were identified at either eight- or twelve-weeks post inoculation.

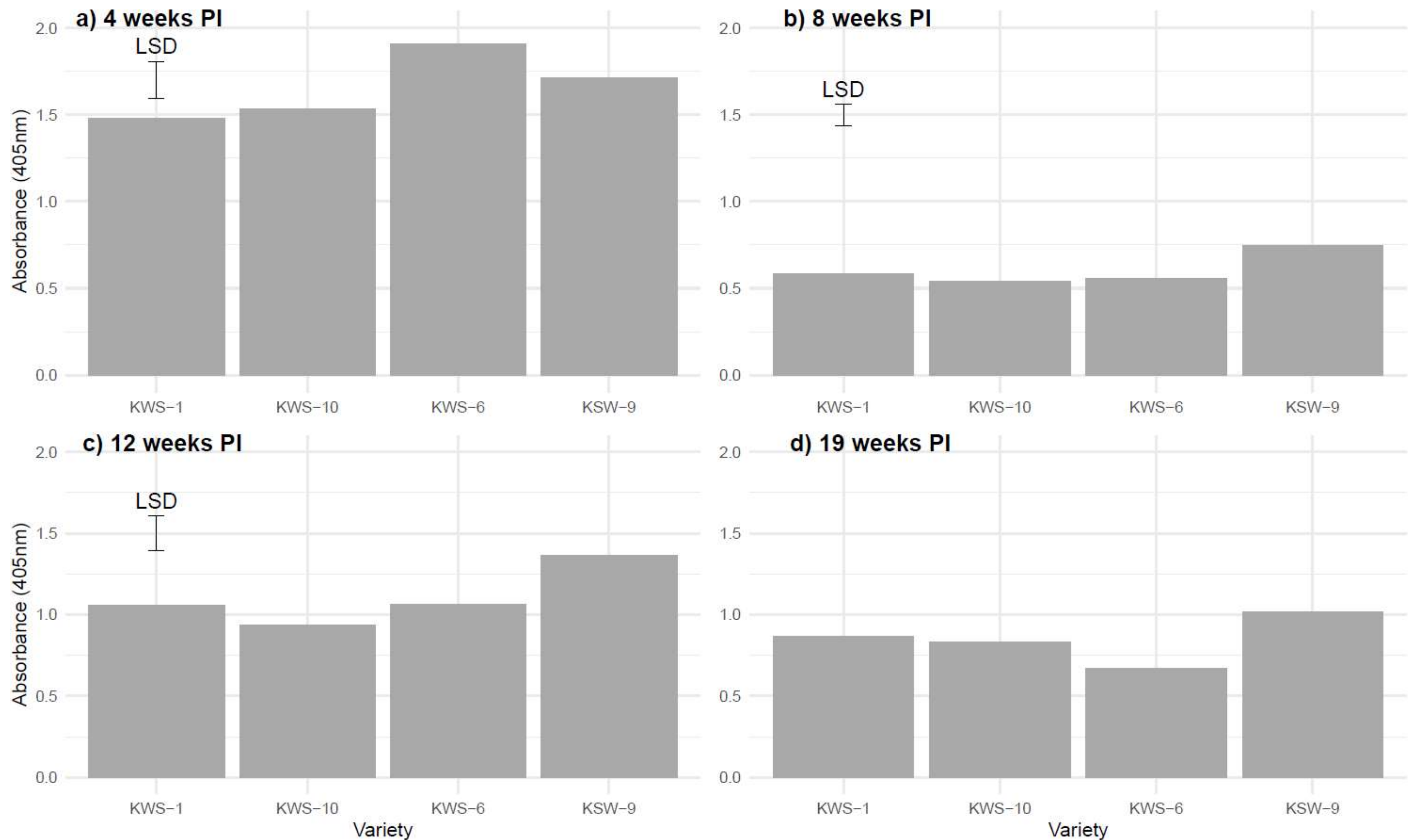

Figure 6.14: ELISA results from 2022 of varieties under Polerovirus *infection (uninoculated and BYV inoculated treatments removed). KWS-1 and KWS-10 had resistance to* Polerovirus *infection and KWS-6 and KWS-9 were susceptible. a) 4 weeks post inoculation, ANOVA p <0.001, b) 8 weeks post inoculation, ANOVA p = 0.005, c) 12 weeks post inoculation p = 0.001, d) 19 weeks post inoculation. Error bar shows least significant difference (LSD) at 5% significance.*

At the twelve-week point a significant difference in varietal response to polerovirus treatment was detected (ANOVA treatment x variety, p = 0.019). Under both the 21-254 and 21-278 virus treatments, KWS-9 had significantly higher mean ELISA results than the other varieties (Figure 6.15). In comparison, no differences were seen between the varieties when inoculated with 21-024, BBRO BMYV or BBRO BChV.

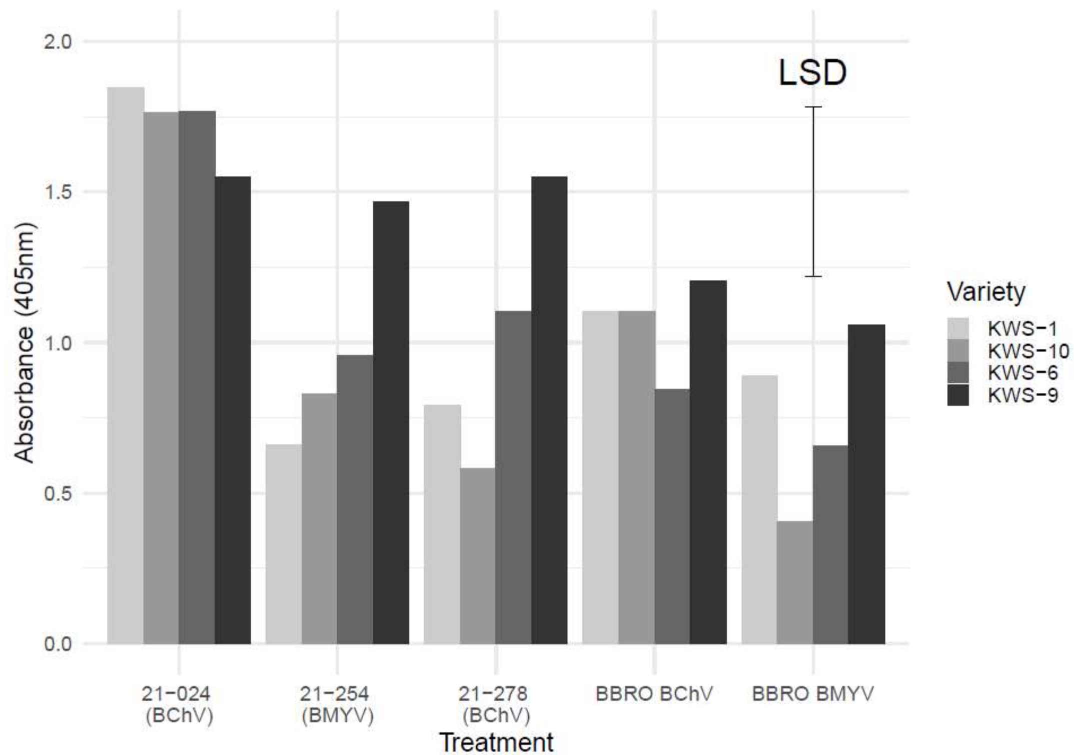

*Figure 6.15: mean ELISA results of Beet mild yellowing virus (BMYV) and Beet chlorosis virus (BChV) inoculated treatments from 2022, 12 weeks post inoculation for each variety (*Polerovirus *resistant varieties KWS-1 and KWS-10 and susceptible varieties KWS-6 and KWS-9). ANOVA (variety x treatment) p = 0.019, least significant difference (LSD) at 5% significance shown as error bar in figure. When comparing different varieties under the same treatment the LSD = 0.466.*

6.4.3.3 Beet polerovirus – 2023

In 2023 no significant difference in mean ELISA result was found between the virus inoculated treatments 14 weeks post inoculation (Figure 6.16). The mean ELISA result of both uninoculated treatments fell below the negative control threshold of 0.480 with ELISA results of 0.313 and 0.290 for Uninoculated 1 and Uninoculated 2 respectively. Both uninoculated treatments were also significantly lower than any of the virus treatments (ANOVA, p < 0.001).

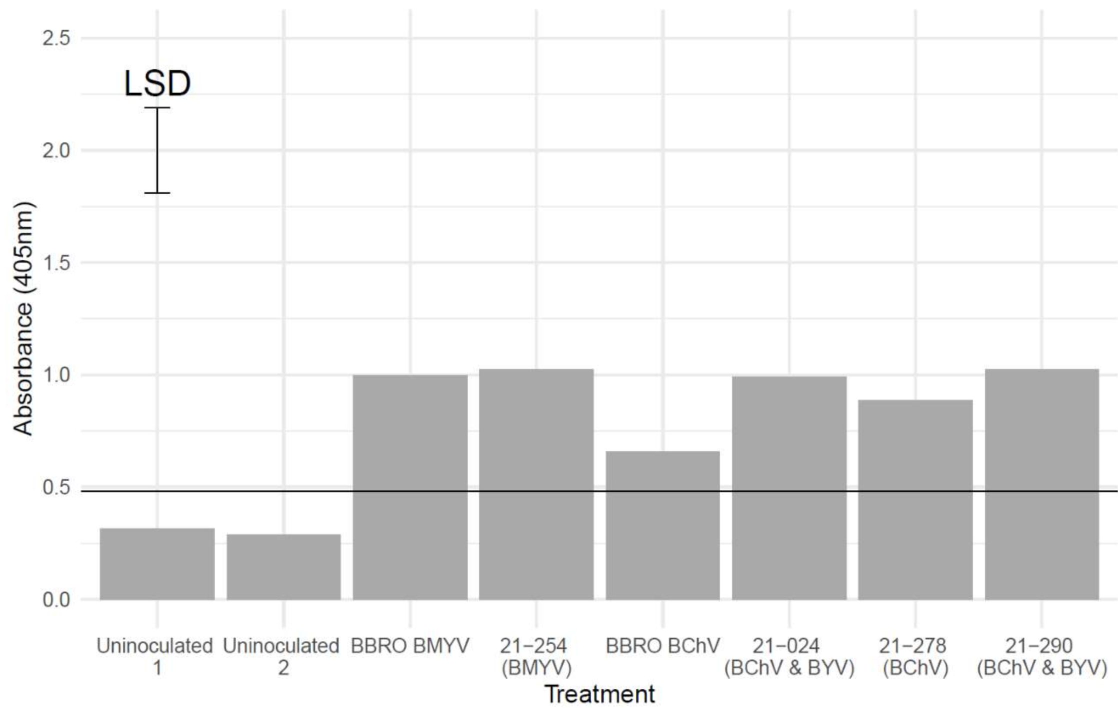

Figure 6.16: mean ELISA result for each treatment from 2023 field trial, 14 weeks post inoculation. Solid line indicates threshold set by negative controls above which an ELISA result is considered positive. ANOVA p < 0.001. Error bar shows least significant difference (LSD) at 5% significance. BMYV – Beet mild yellowing virus, BChV – Beet chlorosis virus, BYV – Beet yellows virus.

Under polerovirus inoculation (excluding uninoculated and BYV contaminated treatments), KWS-9 had significantly higher mean ELISA result compared to the other three varieties (Figure 6.17, ANOVA p = 0.001). The resistant variety KWS-10 had the lowest mean ELISA result, however it was not significantly lower than either the susceptible variety KWS-6 or the other resistant variety KWS-1.

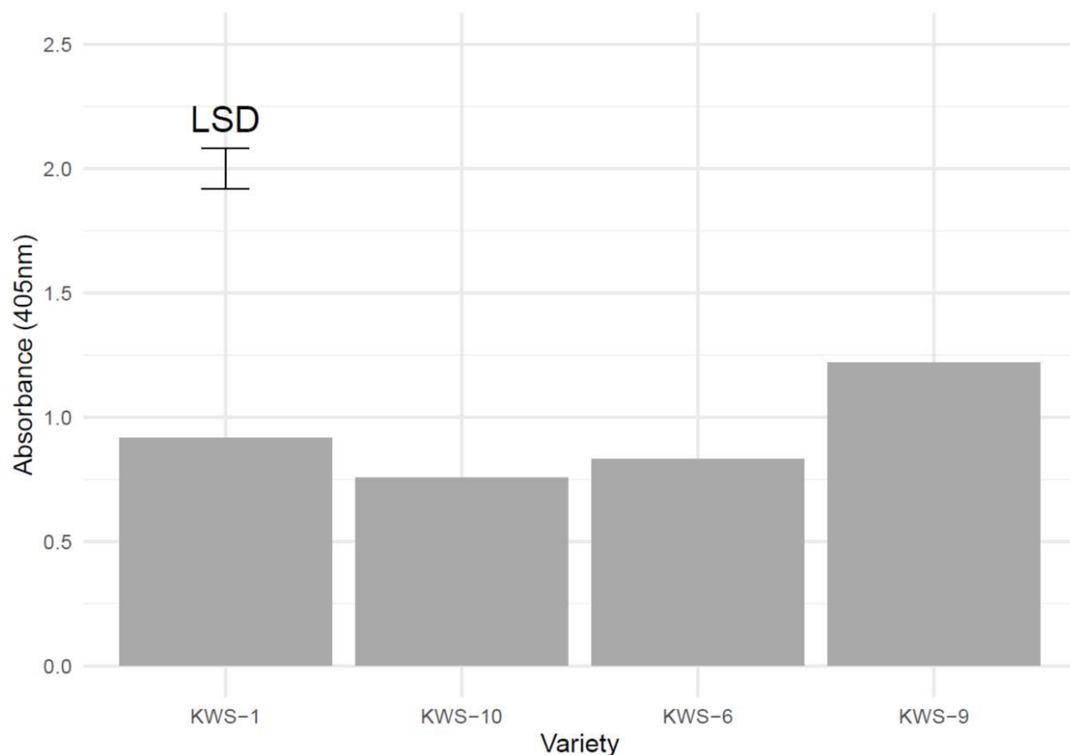

*Figure 6. 17: mean ELISA result for each variety (*Polerovirus *resistant varieties KWS-1 and KWS-10 and susceptible varieties KWS-6 and KWS-9) under* Polerovirus *infection (excluding uninoculated and BYV infected treatments 21-290 and 21-024). Error bar shows least significant difference (LSD) at 5% significance. ANOVA p = 0.001.*

6.4.4 Canopy cover

In 2022, under virus inoculation, the resistant varieties KWS-1 and KWS-10 had significantly larger canopy cover than the susceptible varieties KWS-6 and KWS-9 (Figure 6.18, ANOVA, p<0.001 at both time points). There was no significant difference in canopy area between the two resistant varieties, however KWS-6 did have a significantly larger canopy area than KWS-9 in both July and September. Notably, the mean canopy areas of all varieties decreased between July and September most likely as result of the beet moth infestation (see Figure 6.5).

The mean canopy area of Uninoculated 1 was 74.21% in July 2022 and 69.47% in September 2022. This was higher than the mean canopy area of Uninoculated 2 which was 55.63% and 57.09% respectively. This corresponds to the ELISA data which identified a higher level of beet polerovirus and BYV in Uninoculated 2 plots compared to Uninoculated 1.

In July 2023, of the virus inoculated treatments, those infected only with a beet polerovirus (treatments BBRO BMYV, BBRO BChV, 211-254 and 21-278) had significantly larger canopy areas than those treatments which also contained BYV (21-024 and 21-290), (Figure 6.19a, ANOVA, p = 0.024). Although significant differences were seen in canopy area between the varieties under virus

infection, they did not support the findings of 2022. In 2023, KWS-6 had the smallest mean canopy area under virus infection (Figure 6.19b), with no significant difference between the other three varieties. No significant differences in canopy area were identified in September 2023, with all but two plots (both in Uninoculated 2 treatments) having greater than 90% canopy cover.

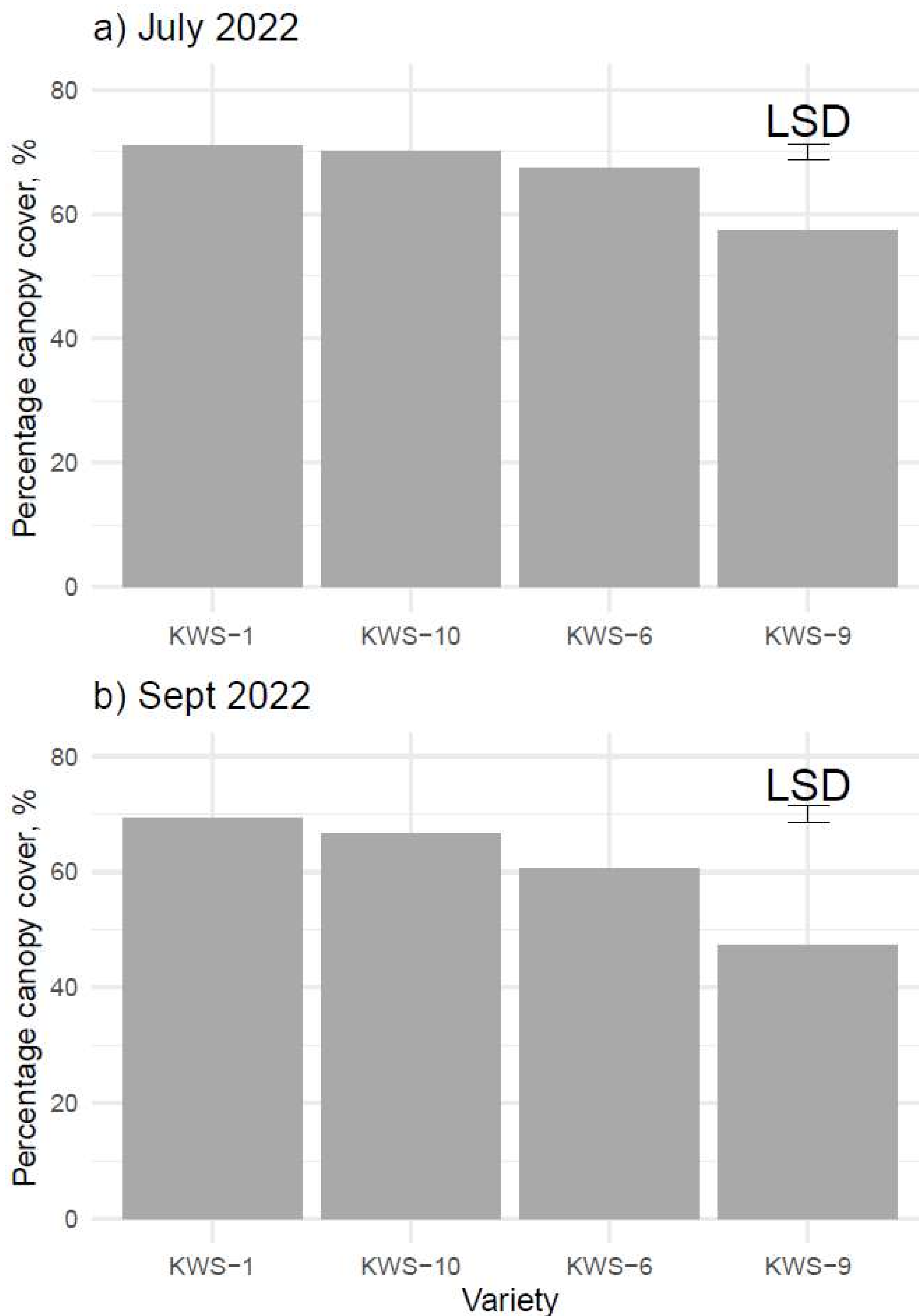

Figure 6.18: mean canopy cover (as a percentage of plot area) of each variety (KWS-1 and KWS-10 polerovirus resistant, KWS-6 and KWS-9 susceptible) in the 2022 field trial under virus inoculation (excluding both uninoculated treatments). a) on 22th July 2022, ANOVA p <0.001, b) on 15th September 2022, ANOVA p<0.001. Error bar shows least significant difference (LSD) at 5% significance.

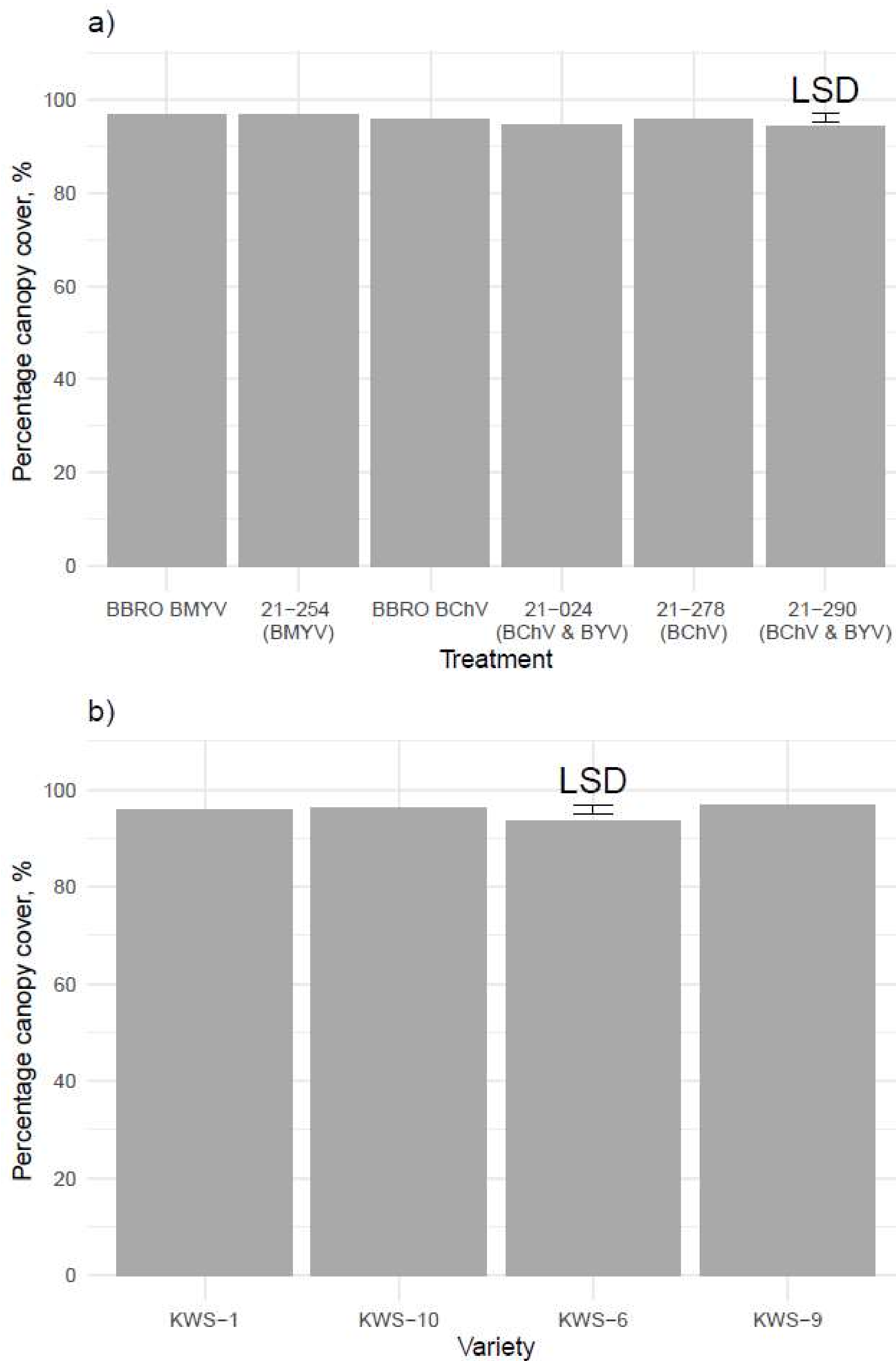

Figure 6.19: mean canopy cover (as percentage of plot area) for 2023 field trial a) mean of Beet mild yellowing virus (BMYV), Beet chlorosis virus (BChV) and Beet yellows virus (BYV) inoculated treatments, ANOVA p = 0.024. b) mean of each variety (KWS-1 and KWS-10 polerovirus resistant, KWS-6 and KWS-9 susceptible) under virus infection, ANOVA p<0.001. Error bars show least significant difference (LSD) at 5% significance.

6.4.5 Canopy chlorophyll

In September 2022 canopy chlorophyll levels (as estimated by mNDblue value) were significantly higher in the resistant varieties than the susceptible varieties across all treatments (Figure 6.20, ANOVA, $p<0.001$). Under all virus treatments, KWS-10 had the highest mNDblue value though it was only significantly higher than KWS-1 under BBRO BChV, 21-278 and 21-290. Of the susceptible varieties, KWS-9 had higher canopy chlorophyll levels under virus infection than KWS-6. All varieties exhibited the lowest canopy chlorophyll levels under the 21-290 treatment (which contained both BChV and BYV). mNDblue results from July 2022 showed no significant differences, however the same trend of the susceptible varieties having lower values than the resistant varieties was observed.

Results from both July and September 2023 confirmed the findings of 2022, with higher canopy chlorophyll levels in the resistant varieties when under virus infection. However, of the two susceptible varieties, only KWS-6 had significantly lower mNDvalues than the resistant varieties across all virus treatments (ANOVA, July 2023 $p=0.001$, September 2023 $p<0.001$). As in 2022, the lowest mNDblue values for all varieties were identified under the virus treatments that contained BYV (21-290 and 21-024 in 2023).

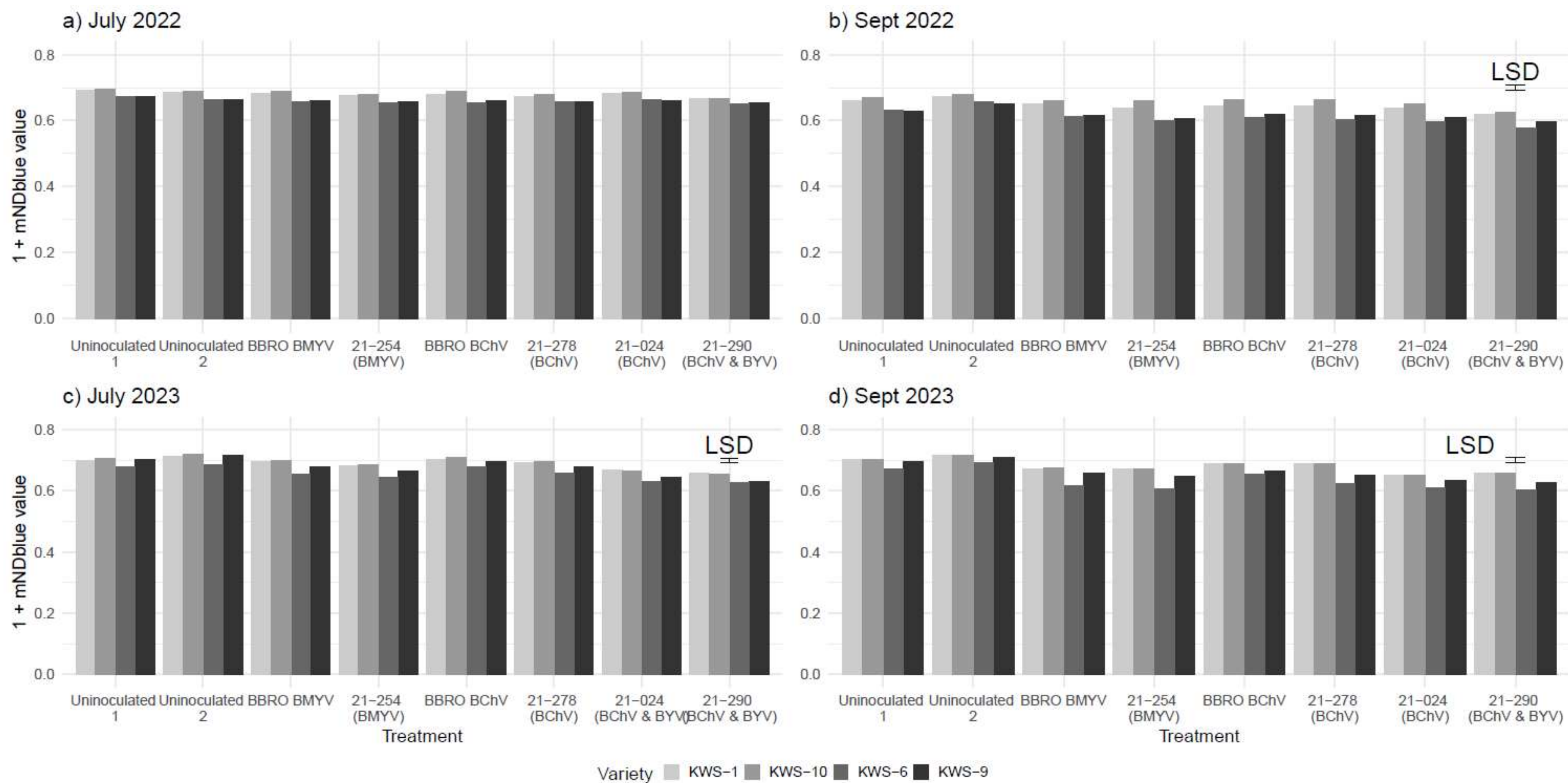

Figure 6.20: mean mNDblue value of varieties (KWS-1 and KWS-10 Polerovirus *resistant, KWS-6 and KWS-9 susceptible) under different virus treatments. Results shown as 1 + mNDblue value to give a positive number and aid result interpretation, higher mNDblue values indicated plots with greater chlorophyll content, as measured on a) 22nd July 2022, b) 15th September 2022, ANOVA (variety x treatment) $p < 0.001$, c) 9th July 2023, ANOVA (variety x treatment) $p = 0.001$, d) 23rd September 2023, ANOVA (variety x treatment) $p < 0.001$. Error bars show least significant difference (LSD) at 5% significance. BMYV – Beet mild yellowing virus, BChV – Beet chlorosis virus, BYV – Beet yellows virus.*

6.4.6 Sucrose yield

In both 2022 and 2023 the Uninoculated 2 treatment was removed from the harvest data analysis. In 2022 this was due to higher polerovirus ELISA result in the Uninoculated 2 treatment compared to the Uninoculated 1, indicating a higher level of virus contamination. In 2023 Uninoculated 2 was removed due to higher variation in the sucrose yield compared to Uninoculated 1. No other plots were removed from the analysis in 2023, however in 2022 three plots were removed due to low clean sample weights (each outside the range of the mean clean sample weight plus two times the standard deviation).

Overall, yields were higher in 2023 than in 2022 (Figure 6.21). In 2023, the mean sucrose yield across all varieties for the uninoculated treatment was 15.07 $tonnes.ha^{-1}$ compared to just 8.82 $tonnes.ha^{-1}$ in 2022. In both years, significant differences in sucrose yield were identified between treatments, however these differences were not consistent. In 2022 no significant difference was found between the sucrose yield of the uninoculated and the BBRO BMYV treatments, although all other virus inoculated treatments did yield significantly lower than the uninoculated (ANOVA, $p = 0.001$). Whereas in 2023, all virus treatments yielded significantly lower than the uninoculated including the BBRO BMYV treatment (ANOVA, $p<0.001$). The treatments containing BYV yielded the lowest in both 2022 and 2023. In 2023 the two BYV containing treatments (21-290 and 21-024) had sucrose yields significantly lower than any other treatment (ANOVA, $p<0.001$).

*Figure 6. 21: mean sucrose yield across all varieties (*Polerovirus *resistant varieties KWS-1 and KWS-10 and susceptible varieties KWS-6 and KWS-9) from a) 2022 field trial, ANOVA p = 0.001, b) 2023 field trial, ANOVA p<0.001. Error bars show least significant difference (LSD) at 5% significance. BMYV – Beet mild yellowing virus, BChV – Beet chlorosis virus, BYV - Beet yellows virus.*

Under virus infection, in 2022 the resistant varieties had higher mean sucrose yields than the susceptible varieties (Figure 6.22). However the only significant difference was between the resistant variety KWS-10, which had the highest yield at 7.60 tonnes.ha^{-1}, and the susceptible variety KWS-9, which had the lowest yield at 6.63 tonnes.ha^{-1} (ANOVA, p = 0.043). These differences were not found in 2023, when KWS-1 (resistant variety) yielded significantly higher than any other variety at 11.58 tonnes.ha^{-1} (ANOVA, p=0.004).

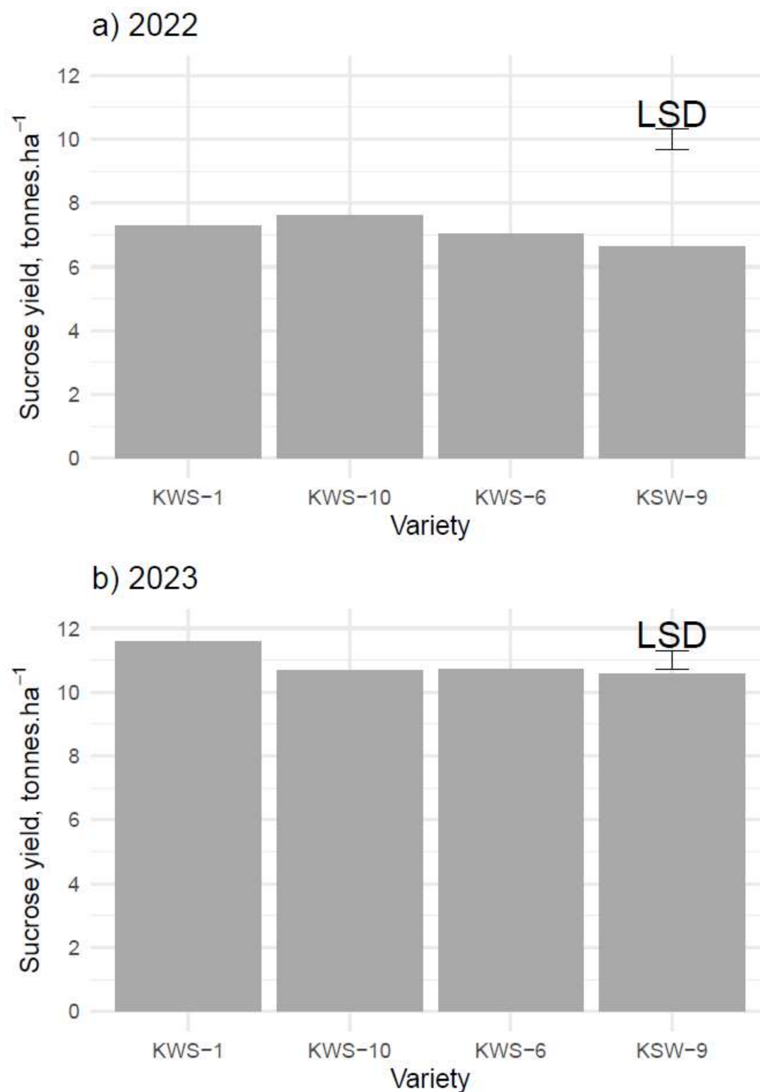

*Figure 6.22: mean sucrose yield of each variety (*Polerovirus *resistant varieties KWS-1 and KWS-10 and susceptible varieties KWS-6 and KWS-9) when under virus infection (uninoculated treatments removed), a) from 2022 field trial, ANOVA p = 0.043. b) from 2023 field trial, ANOVA p=0.004. Error bars show least significant difference (LSD) at 5% significance.*

Assessing the sucrose yield lost by each variety under virus infection (when compared to the uninoculated) in 2023 a clear trend was observed (Figure 6.23). Under all virus treatments, the resistant varieties (KWS-1 and KWS-10) maintained more of their uninoculated yield than the susceptible varieties. This trend was not seen in 2022, when the susceptible varieties had a lower yield loss under the 21-290 virus treatment than the resistant varieties.

Linear regression showed a significant relationship between mNDblue and sucrose yield achieved, in both 2022 and 2023 (Figure 6.24). This relationship shows that as plot mNDblue values deviate away from the controls the percentage yield achieved decreases. Overall, this relationship was more significant in 2023 than 2022, and in both years the July mNDblue data had higher R^2 values

than the September data; Linear regression, July 2022 $p < 0.001$ $R^2 = 0.51$, September 2022 $p = 0.009$ $R^2 = 0.27$, July 2023 $p < 0.001$ $R^2 = 0.87$, September 2023 $p < 0.001$ $R^2 = 0.84$.

In both years, the lowest percentage of uninoculated yield achieved and the greatest change in mNDblue was seen in the BYV containing treatments. The BBRO BChV had the smallest mNDblue change however the model was not significantly improved by incorporating virus treatment or variety.

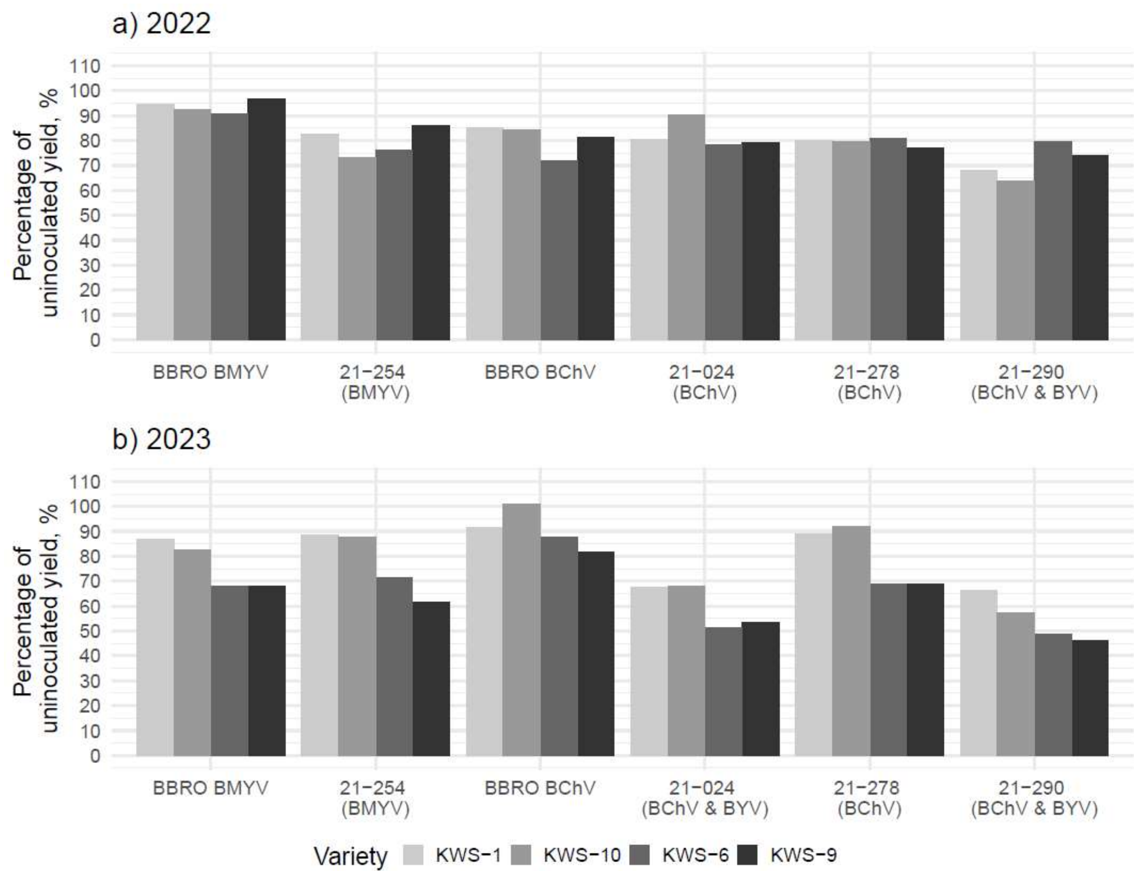

Figure 6.23: percentage of uninoculated yield achieved under virus infection (calculated as percentage of mean sucrose yield of the Uninoculated 1 treatment for each variety) a) from 2022 field trial b) from 2023 field trial. KWS-1 and KWS-10 had resistance to Polerovirus *and KWS-6 and KWS-9 were susceptible. BMYV-Beet mild yellowing virus, BChV – Beet chlorosis virus, BYV – Beet yellows virus.*

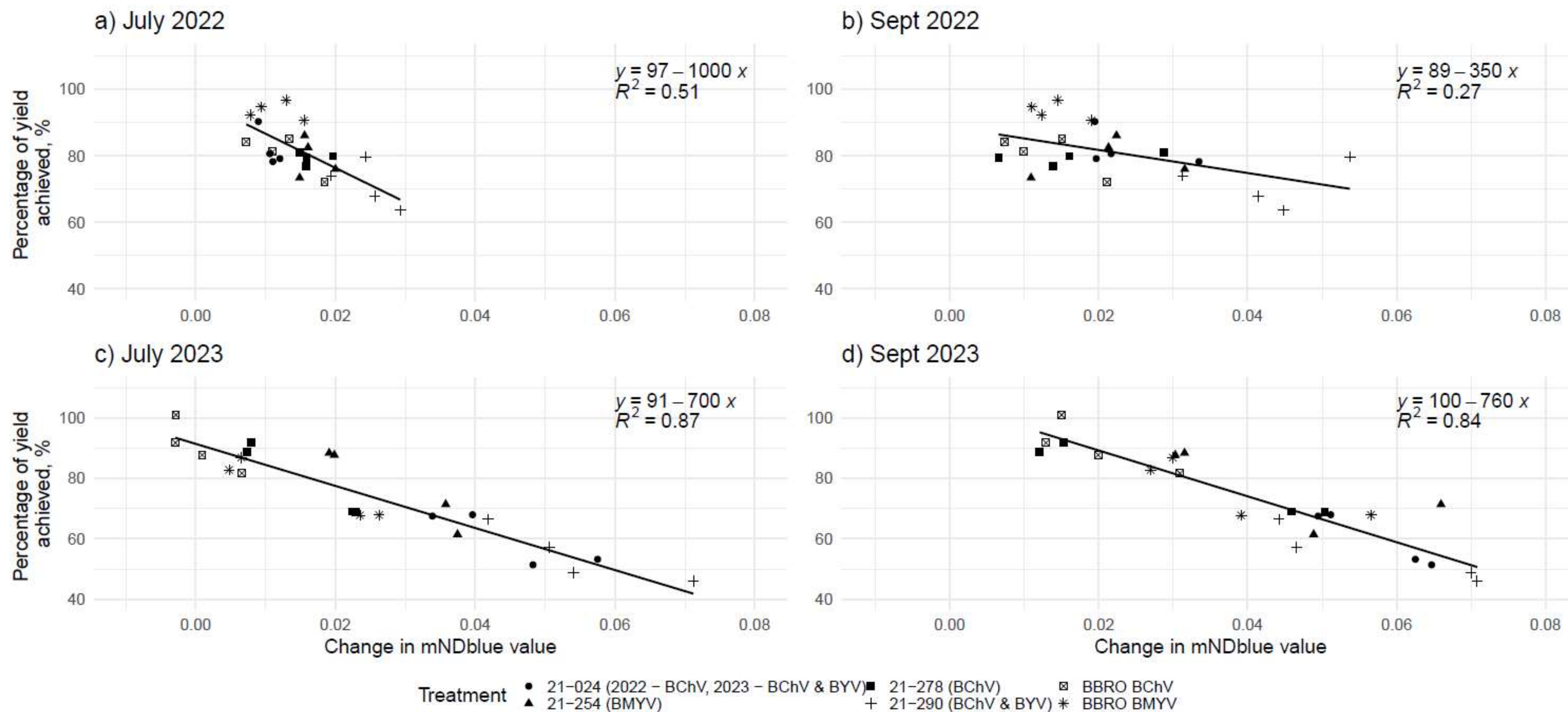

*Figure 6.24: linear regression of percentage of uninoculated yield achieved and change in mNDblue value from the uninoculated across all varieties (*Polerovirus *resistant varieties KWS-1 and KWS-10 and susceptible varieties KWS-6 and KWS-9) under different virus treatments a) 2022 field trial using mNDblue value from 22nd July 2022, b) 2022 field trial using mNDblue value from 15th September 2022 c) 2023 field trial using mNDblue value from 9th July 2023, d) 2023 field trial using mNDblue value from 23rd September 2023. BMYV – Beet mild yellowing virus, BChV – Beet chlorosis virus, BYV – Beet yellows virus.*

6.5 Discussion

6.5.1 Methodology

Ensuring the field experiments were kept free from natural aphid infection posed a significant challenge, particularly under the naturally high aphid pressure experienced in 2022. ELISA results from the uninoculated plots in 2022 showed that, unfortunately, contamination with naturally occurring viruliferous aphids had occurred. Some of this impact was mitigated by incorporating twice the number of uninoculated control plots into the experimental design, allowing for the less contaminated uninoculated controls to be used in the data analysis. However, it is likely that the virus treated plots were also contaminated with naturally occurring aphids and yellowing viruses. The lower natural aphid pressure in 2023 helped ensure a 'cleaner' experiment, with the uninoculated plots remaining free from natural virus infection and, presumably, therefore also the virus-treated plots.

Nevertheless, in both 2022 and 2023 the inoculation methodology was successful with susceptible varieties in all treatments becoming infected with virus. Importantly, good control of virus spread was also achieved, particularly in 2023 where BYV was only detected in those plots inoculated with a BYV containing virus culture. This was also evidenced by visual assessment of the trial showing a clear demarcation between trial plots and the non-inoculated discard sugar beet (Figure 6.25).

In 2022 visual assessment of yellowing symptoms also showed that, although only a 50% inoculation rate was used (infecting every other plant with viruliferous aphids), close to 100% infection was achieved. In 2023 aphid numbers in the laboratory virus cultures were lower than in 2022, particularly in the BBRO BChV culture. This meant that fewer aphids were released into the trial plots, and consequently yellowing symptoms were not visible in a small number of the susceptible variety plants. This may have contributed to the lower mean ELISA result and higher sucrose yield for this treatment compared to the other BChV treatment. Due to the scale of these field trials, counting an exact number of aphids on to each plant was not feasible, however future studies could do more to ensure aphid numbers were consistent between virus treatments. Nevertheless, the yield loss caused by the BBRO BChV treatment of around 20% for susceptible variety KWS-9 was consistent with published findings (Hossain et al., 2021; Stevens et al., 2004), and the overall effect of the few uninfected plants is likely to be minimal.

Figure 6. 25: Image of inoculated trial plots on 30th June 2022, showing inoculated sugar beet within plots with yellowing symptoms whilst plants outside of treatment area remaining green (photo by Suzannah Harder).

6.5.2 ELISA

Although the resistant varieties tended to have lower ELISA absorbances than the susceptible varieties (particularly KWS-9), their ELISA results still indicated virus infection under all virus treatments. This suggests these varieties have only partial, rather than complete, resistance to BMYV and BChV infection. Interestingly, KWS-6, although being described by the seed breeder as susceptible, tended to align more closely to the resistant varieties than the other susceptible variety. This indicates it may have a low level of virus resistance, for example due to the involvement of a minor resistance gene not declared by the seed breeder. In 2022 the ELISA results from twelve-weeks after inoculation suggested than the resistant varieties resisted infection from some virus cultures better than others. However, this finding was not supported in 2023, or at any other time point in 2022 and is therefore more likely to be a consequence of the challenging growing conditions experienced in 2022.

Generally, ELISA results were not a good predictor of yield loss. In 2022 the 21-024 BChV treatment gave the highest mean ELISA results at every time point, however this treatment did not cause the

greatest yield loss. Virus titre also differed throughout the season, with the challenging growing conditions of 2022, namely the high air temperatures and drought conditions, clearly affecting virus titre within the inoculated plants. Reliably assessing variety performance under virus infection by ELISA is therefore difficult as weather conditions and time after inoculation has a large influence on results. From a diagnostic perspective, the ELISA results from 2022 show that virus testing via ELISA should not be conducted whilst test plants are under drought stress as false negative results are likely.

ELISA testing, as a tool for assessing variety performance, has the joint disadvantage of being time consuming whilst only considering a small number of plants per plot. The ELISA testing conducted here, assessed only five plants per plot yet took five days to complete at each time point. The methodology followed in 2023, where a single ELISA test was conducted shortly before harvest, would be more practical to adopt in future trials, in combination with remote sensing using multispectral and RGB imaging to monitor symptom development. This approach enables the resistance of test varieties to be established whilst minimising the time commitment and, in most years, avoiding the need to sample when the crop is under drought stress.

6.5.3 Canopy cover and chlorophyll estimation

The most severe foliar symptoms were observed under the combined BChV and BYV virus treatments. This result was expected and consistent with previous studies which identify BYV as the most damaging virus in the virus yellows complex (Smith and Hallsworth, 1990) and the findings of Hossain et al (Hossain et al., 2021) who found combined BYV and BChV infection caused more significant yield losses than either virus individually.

Unlike ELISA, drone assessments of canopy cover and chlorophyll levels considered whole trial plots, rather than a subset of plants from each plot. This made the measurements more reliable, with less chance of outliers skewing the data set. Drone analysis is also less time consuming, taking approximately one day to complete (including image analysis). This makes it an attractive phenotyping tool for this type of large-scale experiment. One drawback of these measurements, however, is that canopy health is affected by multiple factors not just virus infection. Nutrient deficiency, fungal infection and pest damage can all cause yellowing symptoms easily confused with virus infection (Stevens, 2019). Any measurement of yellowing symptoms, such as mNDblue measurements, are therefore not virus specific and should be used in conjunction with a diagnostic tool (such as ELISA) to ensure symptoms are due to virus infection.

Canopy cover measurements can also be affected by external factors. For example, in 2022 canopy cover was much smaller than in 2023 across all varieties due to the drought conditions experienced. Although differences between the varieties were identified in 2022, with the resistant varieties showing larger canopy areas than the susceptible, it is possible these differences were due to the varieties ability to tolerate the other stresses affecting the 2022 crop, particularly as these differences were not identified in the 2023 trial.

mNDblue measurements were used to estimate canopy chlorophyll levels, enabling quantification of the visible yellowing symptoms. As previously discussed, visual assessment of yellowing showed clear demarcation between inoculated and uninoculated plants. However, it was also possible to identify the susceptible and resistant varieties based on yellowing symptoms in both years (Figure 6.26). mNDblue measurements supported these observations, with the resistant varieties having higher mNDblue values than the susceptible under virus inoculation. Previously, yellowing symptoms have been scored through visual assessment (Hossain et al., 2021; Smith and Hallsworth, 1990), but this approach risks assessor bias, as well as inconsistency between assessors. Utilising drone based mNDblue measurements, which are captured within a short time period (approximately ten minute flight time to cover these experiments) and calibrated using a reflectance panel to correct the imagery, overcomes these risks whilst allowing significant differences in varietal performance under virus infection to be identified.

Figure 6. 26: Image taken of 2022 field trial, showing clear differences in yellowing symptoms between BBRO Beet chlorosis virus inoculated plots. Plot on left is resistant variety KWS-10, plot on right is susceptible variety KWS-9. Image taken on 31st October 2022 (the same day the trial was harvested).

6.5.4 Yields

The confounding factors of drought and beet moth infestation clearly affected yields in 2022, with all treatments yielding lower than in 2023, including the uninoculated controls. Work by Clover et al (1999) showed no interaction between BYV infection and drought stress, with their effects on yield being additive. To date no studies have investigated the combined effect of BMYV or BChV and drought, but they are assumed to exhibit the same additive relationship as BYV. Confirming this relationship will become more pertinent should drought conditions become more commonplace with future climate volatility.

Although beet moth is native to the UK, 2022 was the first year it caused significant damage to the UK sugar beet crop (Collier, 2023). It was unfortunate that beet moth occurred in the trial in 2022, but the infestation was at least consistent with visual assessment of the trial at the end of September confirming all plants within the trial field were infested. No differences in infestation

levels were observed between varieties or treatments and therefore the effect was presumed to be equal across the entire trial.

It was hypothesised that although the resistant varieties may not have higher sucrose yields than the susceptible varieties (due to yield drag (BBRO, 2023b)), they would achieve more of their potential yield when under virus infection. Given the challenges of the 2022 sugar beet growing season it is unsurprising that yield results were closer to this expectation in 2023 than they were in 2022. Nevertheless, the results of the 2022 experiment should not be assumed purely as consequence of the unusual growing season. One key finding from 2022, was the significantly lower yield loss caused by BBRO BMYV inoculation compared to inoculation with the BMYV culture 21-254. This result does fit with observations from BBRO virus trials, where the BBRO BMYV culture appears to be having a lesser impact on yield year on year (personal communication, BBRO) and with the genetic divergence of the BBRO BMYV isolate as outlined in Chapter 5.

The 2023 field trial results did not confirm the BBRO BMYV culture as being 'weaker' than 21-254. There are many possible reasons for this. Firstly, although it is assumed that BMYV will respond similarly to BYV when in combination with drought stress this may not be the case. The pathogenicity of the BBRO BMYV culture may have been weakened by the drought conditions, whilst the 21-254 isolate was not. Alternatively, either isolate may have evolved between 2022 and 2023 with consequences on pathogenicity. Unfortunately, as the isolates were not re-sequenced ahead of the 2023 field trial it is not possible to confirm this. Future trials working with multiple virus strains should sequence all cultures at the point of trial inoculation to allow identification of genetic changes between years.

Conversely to the BMYV results, although in 2022 no significant differences in yield loss were seen between the BChV cultures, differences were found in 2023 with the BBRO BChV causing lower yield loss than the 21-278 isolate. Importantly from a breeding perspective, however, under all virus treatments in 2023 the resistant varieties achieved more of their potential yield than the susceptible varieties. Therefore, although there do appear to be differences in pathogenicity between the BMYV and BChV isolates tested here, none are considered "resistance breaking" strains.

In 2022 and 2023 the most severe yield losses were seen in the plots inoculated with BChV and BYV. As previously discussed, this is consistent with the findings of previous studies (Hossain et al., 2021; Smith and Hallsworth, 1990). Notably, although neither KWS-1 or KWS-10 have BYV resistance according to the seed breeder, both varieties achieved more of their potential yield under the combined BChV and BYV treatments in 2023 than the susceptible varieties. Nevertheless, these

varieties still suffered the greatest yield loss under these treatments and these results do not indicate the varieties have resistance to BYV. However, it does suggest that the resistance mechanism of both KWS-1 and KWS-10 to beet poleroviruses still holds whilst under BYV infection. Mixed infections are known to occur within the UK, a finding confirmed by the data outlined in Chapter 3. Therefore, to be of optimum benefit, resistant varieties will need to withstand combined infections and ideally also have BYV resistance.

6.5.5 Predicting yield loss

One major drawback of field trials for assessment of variety performance is their significant time cost. Consequently, any way in which variety yield performance can be reliably predicted earlier in the growing season, rather than waiting for harvest in autumn/winter, is advantageous. The significant relationship identified here between mNDblue value and yield, enables such predictions and therefore has potentially large benefits to the sugar beet industry. The simplicity of the model is encouraging, accounting for all virus treatments and varieties tested here. The ability of the model to estimate yield even in challenging seasons like 2022, where confounding factors such as drought and beet moth infestation also affected the trial, is particularly promising. The model will, however, need further validation, for example, across different soil types and varieties from other seed houses.

Chapter 7: General Discussion

7.1 Context of the project

It is ninety years since yellowing symptoms observed in sugar beet plants were suggested to arise from a viral infection (Quanjer, 1934). Since that time huge progress has been made in characterising the different viruses now known to cause virus yellows disease. From a disease control point of view, arguably the greatest breakthrough has been the use of neonicotinoid treated sugar beet seed since its introduction in 1994 until it was banned by the European Union in 2018. Although emergency authorisations, from the UK government, have resulted in the use of neonicotinoid treated sugar beet seed twice since 2018 (2022 and 2023), concerns over environmental safety and the need to adopt more sustainable farming practices mean neonicotinoid seed treatments are not a long-term solution (EASAC, 2023). Instead, the development of virus-resistant sugar beet varieties is now seen as the best solution to the problem of virus yellows disease, both in the UK and in Europe integrated alongside other aphid/virus management strategies.

Although progress was, and is, being made to develop novel tolerant and resistant sugar beet varieties, the need to renew our understanding of the profile of the disease and the likely durability of these varieties is vital. Through the survey work, genetic analysis, phenotyping assessments and field trials described in this thesis I have initiated an update to our knowledge base on this subject. Below the key findings of this thesis are discussed and areas of future work suggested.

7.2 Consequences of virus yellows species variation

To better understand the distribution and prevalence of the yellowing viruses in the UK a survey was undertaken between 2019 and 2022. The results of this survey (detailed in Chapter 2) indicated that BChV is now more prevalent in the UK than previous studies have found (Stevens et al., 2005b). This finding is important when considering the use of virus resistant or tolerant sugar beet varieties. Obviously, the ideal situation for growers and industry alike, would be to have sugar beet varieties with resistance to all three yellowing viruses. However, currently such a variety is not available.

The results of the survey conducted here indicate BMYV is now the least likely cause of virus yellows disease in the UK, with BYV the most prevalent in epidemic years and BChV more common than

BMYV. Therefore, there is a potentially high risk that if a variety such as Maruscha KWS (with partial tolerance against BMYV) is used by a grower and becomes infected with BChV it may suffer significant yield loss. Fortunately, from an industry perspective, the results of the controlled environment phenotyping trials (Chapter 4) and the field trials (Chapter 6) conducted here, indicate resistance mechanisms may be shared against both BMYV and BChV. However, all the sugar beet varieties tested as part of this research were from the same seed house, and it is plausible that different seed houses may not have this shared cross-protection.

Following the results of this survey, an in-house BChV culture was established by the BBRO and incorporated into their virus yellows variety trials. This means the BBRO now assess sugar beet variety performance under all three yellowing viruses, providing growers with more information on which to base their variety choice. Nevertheless, whilst work towards a variety with resistance to all three yellowing viruses is ongoing, it may be beneficial for growers to better understand their localised virus risk and utilise varieties with resistance to the virus most frequently detected in their fields.

To achieve this level of detailed epidemiological knowledge, reliable diagnostic methods are needed. Detecting and differentiating between the yellowing viruses, and particularly between the closely related beet poleroviruses, has proved challenging. Although the sRNA library sequencing technique used in Chapter 2, did permit this differentiation it does not present a realistic diagnostic approach for routine use owing to the time and economic cost involved. Previously, at the BBRO, routine virus testing has been conducted by ELISA however this approach does not differentiate BMYV from BChV. Adopting a qPCR approach would allow BMYV and/or BChV infections to be identified and provide growers with a better understanding of the viruses most prevalent in their area.

As has been previously found, BYV prevalence continues to vary significantly between years (Hossain et al., 2021). As discussed in Chapter 2 the reasons for this variation are not yet clear and warrant further investigation. One potential influencing factor is the availability and survival of overwinter host species. Increasingly, beet crops are being grown in the UK which are not destined for sugar production but instead for animal feed (fodder beet) or energy production via anaerobic digestion plants (energy beet). The survey conducted in this project (Chapter 2) included samples from fodder beet plants across the UK, finding virus yellows in regions across England and Wales. Future surveys would benefit from also including energy beet samples, as these crops are often not harvested until the spring and therefore provide an ideal source and green bridge of disease from which the next years sugar beet crop may become infected.

Late harvested sugar beet crops, and any root remnants which are left in the field after harvest and able to re-sprout in the spring, also provide potential sources of infection. With the impacts of climate change, and wetter winters favouring the survival of such material, the risk of virus infection arising from these sources is increasing. Therefore, sampling in the spring of such material would be beneficial.

It is also worth noting that the use of neonicotinoid seed treatments may still be having a legacy impact on the relative prevalence of the yellowing viruses. The use of neonicotinoid seed treatments does not prevent a sugar beet plant becoming infected with virus, because the aphid needs to feed on the plant to acquire the insecticide, but instead prevents the secondary spread of virus and hence controls the disease within a crop. During this feeding time, prior to aphid death, any virus present in the aphid may be transferred to the plant. The shorter transmission time of BYV compared to the beet poleroviruses (detailed in Chapter 1 section 1.2.4.3 and 1.2.5.3) means that it may be more likely to be transferred into a neonicotinoid treated plant than BMYV or BChV. This in turn may alter the abundance of virus overwintering in beet crops and hence the risk posed in subsequent years.

If the reasons for the variation in BYV prevalence can be ascertained, the occurrence of the virus may be able to be better predicted, and more effective control measures put in place. Future work, sampling potential BYV overwinter hosts and mapping BYV presence to overwinter weather conditions, for example, would help to clarify the hypothesised impact of winter weather conditions on BYV prevalence. Such studies are particularly important given the results of the field trial (Chapter 6) which found the highest yield losses, of both resistant and susceptible varieties, occurred under combined BChV and BYV infection. This highlights the threat posed by BYV, and the importance of developing sugar beet varieties able to overcome infection to all yellowing viruses.

7.3 Consequences of beet polerovirus strain variation

Given the progress in the development of varieties able to overcome BMYV infection, a more detailed investigation was undertaken to establish the genetic diversity of BMYV and BChV isolates. Perhaps of most note, from the genetic analysis detailed in Chapter 5, was the divergence of the BBRO BMYV isolate, which had been kept in continuous culture since 2013, from the ‘wild’ BMYV isolates collected between 2019 and 2022. This finding is of particular importance because it is this BMYV isolate which has been widely supplied to and used by sugar beet seed breeders to develop and trial resistant varieties. The consequences of this variation have not been completely

elucidated, with differing results between the 2022 and 2023 field trials (discussed in Chapter 6). Nonetheless, based on the genetic differences and potential changes in pathogenicity identified through this project, in 2023 the BBRO took the decision to replace their original BMYV culture with isolate 21-254. It was also decided that the culture should be more frequently 'refreshed' with wild BMYV isolates to help prevent any divergence arising through continued culture.

The field trials were conducted using both susceptible and "high resistance" varieties, as described by the seed breeder. Using the definitions outlined in Chapter 1 section 1.4.5, however, neither of these high resistance varieties were truly resistant to either BMYV or BChV, as both tested positive for virus via ELISA. Based on the field trial results from 2023, and the findings from the controlled environment studies (Chapter 4), these varieties do, however, exhibit partial resistance having a lower virus titre than susceptible varieties. Crucially this partial resistance appears, based on the virus isolates tested here, to be robust with resistant varieties consistently suffering lower yield losses than susceptible varieties.

Based on these results, and the definition of a virus strain being an isolate which displays a unique and recognisable phenotypic characteristic, none of the virus isolates studied here should be described as distinct strains. Nevertheless, given the risk posed by 'resistance-breaking' virus strains, and the very limited number of isolates tested here, research in this area should continue. To date, the adoption of the BMYV tolerant variety Maruscha KWS in commercial crops has been limited, likely due to its lower yield potential, and as such the effect of the use of tolerant varieties on the evolution of virus strains is not yet clear. In the future, it is feasible that partially resistant varieties may have a large impact on the development of resistance-breaking strains. Such varieties could act as a filter with only the more pathogenic virus strains able to infect. These infected plants may then act as a virus source from which other plants become infected. Therefore, specifically targeting partially resistant varieties would be beneficial when searching for resistance-breaking virus strains.

7.4 Assessment of variety performance under virus yellows infection

Characterising how a variety performs when infected with virus is vital in the development of resistant sugar beet. Predominantly such assessments are conducted via virus inoculated field trials. As discussed in Chapter 4, these trials have many drawbacks including their large time and resource cost. It was therefore hoped that a methodology for phenotyping variety performance under virus yellows inoculation could be developed utilising controlled environment facilities. Unfortunately no

viable alternative was identified, out of the three controlled environments tested here, which provided notable benefits over a field trial approach. Despite this, future efforts to identify such an environment should continue, particularly as technological advances in lighting and the control of other variables such as humidity and air circulation are made; an area both breeders and BBRO are investigating further.

As no controlled environment was found to be as good as the field (Chapter 4), the consequences of the genetic variation identified between polerovirus isolates (Chapter 5) was elucidated through a field trial (Chapter 6). In what is believed to be the first field trial of its kind, sugar beet varieties were assessed under inoculation with six differing virus isolates in a commercial field setting. Undertaking these trials was extremely challenging and the methodology developed, as well as the results achieved, are of significant benefit to the sugar beet industry. The most demanding aspect of these field trials was rearing enough inoculum, of the six differing virus isolates, to inoculate the field trials, whilst preventing any contamination between cultures. This was made more difficult as the cultures needed to be reared at the same time as the BBRO were rearing thousands of plants for their own field trials, and hence there was the added risk of contamination from neighbouring glasshouse facilities. Unfortunately, as shown in the results of Chapter 6, some contamination with BYV did occur. Paradoxically, this contamination event did give unintended but fascinating insights into the impact of 'mixed' infections on variety performance used in this study. Nevertheless, given the considerable pressures, maintaining these six cultures was a significant achievement.

The benefits of conducting research in controlled environment facilities was made clear during the 2022 field trial. The drought and beet moth issues experienced highlight the challenges and risks of conducting experimental trials outdoors where they are fundamentally at the mercy of the weather and pest challenges of that year. These conditions clearly affected both the final yield of the trial plots, as well as the in-season measurements such as canopy cover. The relationship between virus and plant also appears to have been affected, with lower virus titre (as determined via ELISA) when plants were under severe drought stress. It is important to note that, in the field trial study, ELISA testing was conducted on the largest non-senescing leaf. In the controlled environment studies (Chapter 4), differences were observed in virus titre between leaves of different ages, a finding which indicated a source-sink relationship of virus movement through the infected plant. It therefore suggests that drought stress may alter this relationship, even to the point where the older leaves of plants known to be infected with virus give a negative ELISA result.

This finding has potential consequences both for variety assessment and diagnostic testing of sugar beet more generally. To permit reliable comparisons to be made between variety-virus studies, the

industry would benefit from agreeing a standard virus titre assessment protocol with defined sampling times. A single sampling point shortly prior to harvest (such as that undertaken in the 2023 field trial) would likely provide a balance between the need to gather the necessary information on variety resistance and the significant time and resource cost of such testing. From a more general perspective, avoiding any assessment of virus titres whilst plants are under severe drought stress would help prevent false negative results as clearly highlighted by the differences shown between my 2022 and 2023 trials.

In spite of the difficulties experienced during these field trials, a significant relationship between canopy chlorophyll levels and subsequent yield loss was identified. If this model is upheld, following the necessary validation across different soil types and sugar beet varieties from other seed houses, it would provide a useful tool to both researchers and growers alike. For researchers and breeders, when used on inoculated field trials, it could provide a time benefit enabling high yielding varieties to be identified ahead of harvest. For growers, it may be possible to estimate yield losses on a field scale, better informing subsequent agronomic decisions such as when to harvest particular fields. However, as previously discussed (Chapter 1 section 1.2.3.1), multiple pathogens and deficiencies can give rise to sugar beet leaf yellowing and could interfere with this model. Future validation studies must, therefore, assess the impact of these factors on the model prior to any widespread adoption.

As well as achieving resistance to each virus individually, ultimately varieties will also need to overcome mixed infections. These mixed infections may include differing virus species (such as those identified in the survey in Chapter 3), and differing isolates or strains. Preliminary investigations into the effect of mixed infections on sugar beet varieties were conducted under glasshouse conditions (with BMYV and BChV, Chapter 4) and field conditions (with BYV and BChV, Chapter 6). In both environments, these mixed infections resulted in the most severe symptoms. However further work is needed to validate these findings, and study in more detail the effect of these virus-virus interactions on resistance mechanisms.

7.5 Final conclusion

At the time this project was created, in 2019, there was growing concern in the sugar beet industry of the threat posed by virus yellows disease. The loss of neonicotinoid seed treatments, and the lack of alternative control strategies, raised fears of widespread virus yellows outbreaks, the like of which had not been seen since the mid-1970s. These fears were realised, in part, in 2020 when the

industry lost an estimated £67 million to the disease. Understandably, this increased threat led to a rapid acceleration in the development of a virus yellows strategy and research funding, which this PhD project forms part of (British Sugar, NFU Sugar and BBRO, 2023).

Arguably the most important finding of this project, for the sugar beet industry, is that the resistant varieties trialled here proved to be durable against differing isolates of both BMYV and BChV. Given the genetic diversity amongst these isolates, this result is encouraging and possibly indicates a reliable and robust resistance mechanism that should be exploited by the industry. However, my findings also highlight the complexity of the virus yellows issue. Changing virus species dynamics, future strain variation and the ultimate need for varietal resistance to all three yellowing viruses must all be appreciated by the UK sugar beet industry to provide long term durability for disease management. The battle with virus yellows continues…

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A.J., Łobocka, M., Oksanen, H.M., Robertson, D.L., Rubino, L., Sabanadzovic, S., Simmonds, P., Suzuki, N., Van Doorslaer, K., Vandamme, A.M. and Varsani, A. 2022. Differentiating between viruses and virus species by writing their names correctly. *Archives of Virology*, **167(4)**:1231–1234.

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Appendix A – variety table

Additional information on the sugar beet varieties used in this project as provided by the seed breeder KWS.

Level of resistance	Description	Code	Decoding
High	res. source A	KWS-1	Maruscha KWS
High	res. source B	KWS-2	
Medium		KWS-3	
Medium		KWS-4	
Medium		KWS-5	
Low		KWS-6	
Low		KWS-7	
Low		KWS-9	
High	res. source A	KWS-10	

Appendix B – sRNA library sample collection details

Collection details of samples used for sRNA library sequencing.

Sample code	Collection year	Sample type	Collection location
19-002	2019	Fodder beet	Field A, Market Bosworth, Leicestershire
19-003	2019	Fodder beet	Field B, Market Bosworth, Leicestershire
19-004	2019	Sugar beet	Field A, Brettenham, Norfolk
19-005	2019	Sugar beet	Field B, Brettenham, Norfolk
19-006	2019	Sugar beet	Field A, Crowland, Lincolnshire
19-007	2019	Sugar beet	Field B, Crowland, Lincolnshire
19-008	2019	Sugar beet	Wrabness, Suffolk
19-009	2019	Fodder beet	Charlinch, Somerset
19-010	2019	Fodder beet	Twycross, Leicestershire
19-011	2019	Fodder beet	Ashdown, Somerset
19-012	2019	Sugar beet	Field A, Royston, Hertfordshire
19-013	2019	Sugar beet	Field B, Royston, Hertfordshire
19-014	2019	Sugar beet	Thurne, Norfolk
19-015	2019	Fodder beet	Field A, South Petherton, Somerset
19-016	2019	Fodder beet	Field B, South Petherton, Somerset
20-006	2020	Sea beet	Southwold, Suffolk
20-008	2020	Sea beet	Havergate Island, Suffolk
20-009	2020	Fodder beet	Northallerton, North Yorkshire
20-010	2020	Fodder beet	Ripon, North Yorkshire
20-011	2020	Fodder beet	Field A, Cannington, Somerset
20-012	2020	Fodder beet	Field B, Cannington, Somerset
20-014	2020	Fodder beet	Field A, Cheshire
20-015	2020	Fodder beet	Field B, Lancashire
20-016	2020	Fodder beet	Nevern, Pembrokeshire
20-017	2020	Sugar beet	Walcott, Norfolk
20-018-1	2020	Sugar beet	Field A, Harlow, Essex
20-018-2	2020	Sugar beet	Field B, Harlow, Essex
20-020	2020	Sugar beet	Guyhirn, Cambridgeshire
20-021	2020	Sugar beet	Newark-on-Trent, Nottinghamshire
21-020	2021	Sugar beet	Barrow, Suffolk
21-024	2021	Sugar beet	Letheringham, Suffolk
21-039	2021	Sugar beet	Drinkstone, Suffolk
21-056	2021	Sugar beet	Nacton, Suffolk
21-071	2021	Sugar beet	Felixstowe, Suffolk
21-097	2021	Sugar beet	Spellbrook, Hertfordshire
21-111	2021	Sugar beet	Frampton, Lincolnshire
21-121	2021	Sugar beet	Cotton, Suffolk
21-179	2021	Sugar beet	Clay Hill, London
21-187	2021	Sugar beet	Soham, Cambridgeshire
21-196	2021	Sugar beet	Sible Hedingham, Essex
21-254	2021	Sugar beet	Field C, Crowland, Lincolnshire
21-256	2021	Sugar beet	Field D, Crowland, Lincolnshire
21-278	2021	Sugar beet	Rougham, Norfolk

21-290	2021	Fodder beet	Field A, Thirn, North Yorkshire
21-294	2021	Fodder beet	Field B, Thirn, North Yorkshire
21-303	2021	Fodder beet	Fochabers, Moray, Scotland
BBRO-BMYV19	2019	Sugar beet	BBRO BMYV culture
BBRO-BMYV20	2020	Sugar beet	BBRO BMYV culture
BBRO-BMYV21	2021	Sugar beet	BBRO BMYV culture
BBRO-BChV20	2020	Sugar beet	BBRO BChV culture
BBRO-BChV21	2021	Sugar beet	BBRO BChV culture

Appendix C – BMYV consensus sequence alignment

BMYV consensus sequences produced using BCFtools (see Chapter 5 section 5.3.2), and aligned using ClustalOmega.

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CLUSTAL O(1.2.4) multiple sequence alignment


21-BMYV      ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
21-254       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
20-BMYV      ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
20-010       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
20-006       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
19-BMYV      ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
21-097       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
19-013       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
21-294       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
21-056       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
20-009       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
20-014       ACAAAAGAAACCAGCGAGGATCTAGCAGTCTATGCAATTTCAGCTTAAAACAAACAGTTT   60
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20-BMYV      CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
20-010       CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
20-006       CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
19-BMYV      CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
21-097       CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
19-013       CACTTGTTCATTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
21-294       CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
21-056       CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
20-009       CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
20-014       CACTTGTTCGTTGAACCGACCGCTAACAGCTACAGAGCGAGTTTTAAACACCGCGTATTT   120
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20-006       TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
19-BMYV      TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
21-097       TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
19-013       TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
21-294       TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
21-056       TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
20-009       TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
20-014       TCTTACGAATCATTTACCGCTCGTAACTTTTGAGAATGAAAACTGTATTCGTTCTCTTCT   180
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20-BMYV      CGCTGCTCTGCCTTTGCTGCTCAGTAAGCAGCTCGACCCCGGAGCTTCATTTACACTCC   240
20-010       CGCTGCTCTGCCTTTGCTGCTCAGTAAGCAGCTCGACCCCGGAGCTTCATTTACACTCC   240
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19-BMYV      CGCTGCTCTGCCTTTGCTGCTCAGTAAGCAGCTCGACCCCGGAGCTTCATTTACACTCC   240
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21-056       CGCTGCTCTGCCTTTGCTGCTCAGTAAGCAGCTCGACCCCGGAGCTTCATTTACACTCC   240
20-009       CGCTGCTCTGCCTTTGCTGCTCAGTAAGCAGCTCGACCCCGGAGCTTCATTTACACTCC   240
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20-010       CGGGAAACGCCAGTCTTTACGACTGGCCAGGTTCTACAATTACTGCGGAGCCGTGTTACC   300
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20-006       CAGCACTCGCAACATTGACTTACGAGTGCCCCCCAGAAAAGACGTTAAAAGATTTTACCT   360
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21-097       CAGCACTCGCAACATTGACTTACGAGTGCCCCCCAGAAAAGACGTTAAAAGATTTTACCT   360
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21-294       CAGCACTCGCAACATTGACTTACGAGTGCCCCCCAGAAAAGACGTTAAAAGATTTTACCT   360
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20-009       CAGCACTCGCAACATTGACTTACGAGTGCCCCCCAGAAAAGACGTTAAAAGATTTTACCT   360
20-014       CAGCACTCGCAACATTGACTTACGAGTGCCCCCCAGAAAAGACGTTAAAAGATTTTACCT   360
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20-010       TGCCCGAAATTCAGGCAGAAATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
20-006       TGCCCGAAATTCAGGCAGAGATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
19-BMYV      TGCCCGAAATTCAGGCAGAGATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
21-097       TGCCCGAAATTCAGGCAGAGATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
19-013       TGCCCGAAATTCAGGCAGAAATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
21-294       TGCCCGAAATTCAGGCAGAGATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
21-056       TGCCCGAAATTCAGGCAGAGATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
20-009       TGCCCGAAATTCAGGCAGAGATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
20-014       TGCCCGAAATTCAGGCAGAGATCTGGGGGAGAGGCTACAACGCCGCAGAGAAATTTTCTC   420
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19-BMYV      TCGCGGTGAAGCAGAGTTTAAAAAGTTCCTTTCAGTATGGTGTGCTGAAAGCGAGAGAAA   480
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20-010       TATGGGCACTCTCTTGCACCGTCTGGTACTTGTTGAAGAACTATACCATAGAAATACTTA   600
20-006       TATGGGCACTCTCTTGCACCGTCTGGTACTTGTTGAAGAACTATACCATAGAAATACTTA   600
19-BMYV      TATGGGCACTCTCTTGCACCGTCTGGTACTTGTTGAAGAACTATACCATAGAAATACTTA   600
21-097       TATGGGCACTCTCTTGCACCGTCTGGTACTTGTTGAAGAACTATACCATAGAAATACTTA   600
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21-294       TATGGGCACTCTCTTGCACCGTCTGGTACTTGTTGAAGAACTATACCATAGAAATACTTA   600
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20-009       TATGGGCACTCTCTTGCACCGTCTGGTACTTGTTGAAGAACTATACCATAGAAATACTTA   600
20-014       TATGGGCACTCTCTTGCACCGTCTGGTACTTGTTGAAGAACTATACCATAGAAATACTTA   600
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21-254       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
20-BMYV      TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
20-010       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
20-006       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
19-BMYV      TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
21-097       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
19-013       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
21-294       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
21-056       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
20-009       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
20-014       TGCTGAGCTCGCTTTTTGCGTTCACCACCTTTTTGGTGAAGCTCGTGGTATGGATTTTTG   660
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20-BMYV      GCGGCTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
20-010       GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
20-006       GCGGCTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
19-BMYV      GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
21-097       GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
19-013       GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
21-294       GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
21-056       GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
20-009       GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
20-014       GCGGTTGGCTAACTTCCCTGGTAAATGGTTTATTTGCTCTCACGAAATGTATTTTGAAAA   720
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20-BMYV      CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
20-010       CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
20-006       CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
19-BMYV      CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
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19-013       CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
21-294       CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
21-056       CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
20-009       CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
20-014       CTCTTTCATCCAGAAAGAGCTACGTTTGTGAGCGATCTGTAAAAGGTTTTCTCACCTTTA   780
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21-254       CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACATGCAGACGGTTCCC   840
20-BMYV      CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
20-010       CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACATGCAGACGGTTCCC   840
20-006       CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACATGCAGACGGTTCCC   840
19-BMYV      CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
21-097       CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
19-013       CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
21-294       CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
21-056       CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
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20-009      CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
20-014      CCATCAAACAAAGCCCGCCGCGTAATTGCATTCTTCAAATACAACACGCAGACGGTTCCC   840
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21-254      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
20-BMYV     ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
20-010      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
20-006      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
19-BMYV     ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
21-097      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
19-013      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
21-294      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
21-056      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
20-009      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
20-014      ATGCCGGTTATGCAACATGCGTAACCTTATTCGACGGGACAAACGGATTGTTGACTGCGC   900
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21-BMYV     AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
21-254      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTGAAAGTCGTCTCCA   960
20-BMYV     AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
20-010      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
20-006      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
19-BMYV     AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
21-097      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
19-013      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
21-294      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
21-056      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
20-009      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
20-014      AACATGTAGTTGACGATTTTTACGAAGGAGACCCGAGAAAGACTCTAAAAGTCGTCTCCA   960
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21-BMYV     CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
21-254      CCCGCAACGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
20-BMYV     CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
20-010      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
20-006      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
19-BMYV     CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
21-097      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
19-013      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
21-294      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
21-056      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
20-009      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
20-014      CCCGCAATGGAAACAAAATCCCCCTTGATGAATTCAGAGTGACGTACACATCTGAGAAAA   1020
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21-BMYV     GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
21-254      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
20-BMYV     GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
20-010      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
20-006      GGGATCAGTTGTTGATGCATGGGCCCCCAAATTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
19-BMYV     GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
21-097      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
19-013      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
21-294      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
21-056      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
20-009      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
20-014      GGGATCAGTTGTTGATGCATGGGCCCCCAAACTGGGAAGGAGTTCTTGCCTGCAAGGCAG   1080
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21-BMYV     TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
21-254      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
20-BMYV     TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
20-010      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
20-006      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
19-BMYV     TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
21-097      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
19-013      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
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21-294      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
21-056      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
20-009      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
20-014      TTCACATGATTCCGGCATCGAGTGTTGCAAAATCGAAAGCAACTTTCTTTGCTCTGTCGG   1140
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21-BMYV     ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
21-254      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
20-BMYV     ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
20-010      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
20-006      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
19-BMYV     ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
21-097      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
19-013      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
21-294      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
21-056      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
20-009      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
20-014      ATGGTGAATGGCATTCCTCTAATGCCGAGCTCGTTGGCACATCCAAGTGCGGAAAATTCA   1200
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21-BMYV     TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
21-254      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGCAAGA   1260
20-BMYV     TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
20-010      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
20-006      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
19-BMYV     TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
21-097      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
19-013      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCAGGCACTCCCTATTTCAATGGTAAGA   1260
21-294      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
21-056      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
20-009      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
20-014      TTTCTGTACTCAGTGACACAAAGAGTGGTCATTCGGGCACTCCCTATTTCAATGGTAAGA   1260
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21-BMYV     GTGTTCTTGGAGTTCACATAGGTTCTCCGAAAGAATTTGAGTCGGAAAATGTTAATTACA   1320
21-254      GTGTTCTTGGAGTTCACATAGGTTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
20-BMYV     GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
20-010      GTGTTCTTGGAGTTCACATAGGTTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
20-006      GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
19-BMYV     GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAATTACA   1320
21-097      GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
19-013      GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
21-294      GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
21-056      GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
20-009      GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
20-014      GTGTTCTTGGAGTTCACATAGGCTCTCCGAAAGAATTTGAGTCGGAAAATGTTAACTACA   1320
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21-BMYV     TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
21-254      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
20-BMYV     TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
20-010      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
20-006      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
19-BMYV     TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
21-097      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
19-013      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
21-294      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
21-056      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
20-009      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
20-014      TGTCTCCTATACCACGTTTTCCTGGATTAACCAGCCCGAACTACATATTTGAAACCACAG   1380
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21-BMYV     CCCTTGCTGGAAAATTTTTCAGTCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
21-254      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
20-BMYV     CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
20-010      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
20-006      CCCTTGCTGGAAAATTTTTCAGTCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
19-BMYV     CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
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21-097      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
19-013      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
21-294      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGATTTCTCTC   1440
21-056      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
20-009      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
20-014      CCCTTGCTGGAAAATTTTTCAGCCAAGAGGAAGTCGAAGAGCTAATGGAAGACTTCTCTC   1440
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21-BMYV     TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
21-254      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
20-BMYV     TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
20-010      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
20-006      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
19-BMYV     TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
21-097      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
19-013      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
21-294      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
21-056      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
20-009      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
20-014      TCCAAGAGATTTATTCTATAGCGACGGCACGTGGGAAGTACATAAAATATGAGGCTTGTC   1500
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21-BMYV     CAGATGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
21-254      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
20-BMYV     CAGATGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
20-010      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
20-006      CAGATGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
19-BMYV     CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
21-097      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
19-013      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
21-294      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
21-056      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
20-009      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
20-014      CAGGTGAAGAGACATTCCATGATGTGCTAACAGAGTCCTCCCCGATGCAGGGGGAAGGAA   1560
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21-BMYV     GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
21-254      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
20-BMYV     GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
20-010      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
20-006      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
19-BMYV     GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
21-097      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
19-013      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
21-294      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
21-056      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
20-009      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
20-014      GGGCGGCTCCGACCGCCGGAACAACCGGAAACGCAAGCACCCACGAGAGATCCGCAGGAA   1620
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21-BMYV     ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
21-254      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
20-BMYV     ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
20-010      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
20-006      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
19-BMYV     ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
21-097      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
19-013      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
21-294      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
21-056      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
20-009      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
20-014      ATGGAAAAAGCCCTCGTGCTGCTCCTTCTACACCGCGGGAACCCTTGGTGAAAACTGCAC   1680
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21-BMYV     CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
21-254      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
20-BMYV     CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
20-010      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
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20-006      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
19-BMYV     CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
21-097      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
19-013      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
21-294      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
21-056      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
20-009      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
20-014      CGCAAGCCACGTACATTGTACCTCAAAAGAGGAATATGACGAATGGCCGAGATGCTGGTG   1740
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21-BMYV     CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
21-254      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
20-BMYV     CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
20-010      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
20-006      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
19-BMYV     CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
21-097      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
19-013      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
21-294      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
21-056      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
20-009      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
20-014      CCAAATTGCAGGCCACGACTGCCACTACCGATCAAATCTCAGAGATAAAGAAGGCTCTGA   1800
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21-BMYV     TAGACAAAATGGATTTAAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
21-254      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
20-BMYV     TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
20-010      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
20-006      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
19-BMYV     TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
21-097      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
19-013      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
21-294      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
21-056      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
20-009      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
20-014      TAGACAAAATGGATTTGAAATCGATCGAGAGACAAGTGGTAGAGACACTATCGTCGATGG   1860
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21-BMYV     CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
21-254      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
20-BMYV     CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
20-010      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
20-006      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
19-BMYV     CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
21-097      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
19-013      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
21-294      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
21-056      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
20-009      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
20-014      CCATGAAGAAGCCCCGCTCAAGAGGGCGGAGAAGATCCAAGAACAAGCAAAACAATTTGG   1920
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21-BMYV     ATGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCGT   1980
21-254      ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
20-BMYV     ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
20-010      ATGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
20-006      ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
19-BMYV     ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
21-097      ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
19-013      ATGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
21-294      ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
21-056      ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
20-009      ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
20-014      ACGCTTCTTCAAAACCCAGTACCACTGGGAAAGAGCCGCAGAGGTCTGCCCCGGTTTCAT   1980
            * ******************************************************** *

21-BMYV     CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
21-254      CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
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20-BMYV      CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
20-010       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
20-006       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
19-BMYV      CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
21-097       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
19-013       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
21-294       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
21-056       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
20-009       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
20-014       CAAAGTCGGTGAGCTCCCCAAGTTTTACTTCTCTAAACAAAAAGGATGCTCGGATTGGGG   2040
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21-BMYV      CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
21-254       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
20-BMYV      CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
20-010       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
20-006       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
19-BMYV      CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
21-097       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
19-013       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
21-294       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
21-056       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
20-009       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
20-014       CACGAAGCTCACCAGCCTCCACCCAGAATTGGAGGAGAAAACCCGAGGCTTCGGGTGGCC   2100
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21-BMYV      CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
21-254       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
20-BMYV      CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
20-010       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
20-006       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
19-BMYV      CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
21-097       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
19-013       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
21-294       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
21-056       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
20-009       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
20-014       CAAGTTCGGGCCAGCGGCGGAACTGAAATCCTTGCGGCTACAAGCCGCAAGATGGCTCGA   2160
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21-BMYV      ACGCGCCGAGCAAGTTAAAATCCCTTCGACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
21-254       ACGCGCCGAGCAAGTTAAAATCCCTTCGACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
20-BMYV      ACGCGCCGAGCAAGTTAAAATCCCTTCGACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
20-010       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
20-006       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
19-BMYV      ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
21-097       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
19-013       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
21-294       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
21-056       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
20-009       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
20-014       ACGCGCCGAGCAAGTTAAAATCCCTTCAACTGAGGAAAGGGAGCGCGTCGTGAGGAAATG   2220
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21-BMYV      TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
21-254       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
20-BMYV      TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
20-010       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
20-006       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
19-BMYV      TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
21-097       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
19-013       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
21-294       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
21-056       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
20-009       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
20-014       TGTGGAAGCATTCTCGCCCACTCAAACACGAGGTCCCATGGCCACGAGAGGAAACAAACT   2280
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21-BMYV      GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
21-254       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
20-BMYV      GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
20-010       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
20-006       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
19-BMYV      GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
21-097       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
19-013       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
21-294       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
21-056       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
20-009       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
20-014       GTCTTGGAACAATTTCCTTGAAGATTTTAAAACGGCAGTTTTCTCTCTCGAGCTCGAAGC   2340
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21-BMYV      CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
21-254       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
20-BMYV      CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
20-010       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
20-006       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
19-BMYV      CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
21-097       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
19-013       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
21-294       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
21-056       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
20-009       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
20-014       CGGCGTAGGCGTCCCGTATGTTGCTTACGGTCGACGCACGCACAGAGGCTGGATTGAAGA   2400
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21-BMYV      TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
21-254       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
20-BMYV      TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
20-010       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
20-006       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
19-BMYV      TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
21-097       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
19-013       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
21-294       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
21-056       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
20-009       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
20-014       TCCAGATCTGTTGCCGGTTTTAGCTCGTTTCACCTTCGATCGATTACAGAAGTTATCGGA   2460
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21-BMYV      GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGCCTGTGTGACCCAAT   2520
21-254       GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGCCTGTGTGACCCAAT   2520
20-BMYV      GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGCCTGTGTGACCCAAT   2520
20-010       GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGCCTGTGTGACCCAAT   2520
20-006       GGCGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGCCTGTGTGACCCAAT   2520
19-BMYV      GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGTCTGTGTGACCCAAT   2520
21-097       GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGCCTGTGTGACCCAAT   2520
19-013       GGTGAAATTTGAGCACATGAGCCCTGAACAATTGGTTCAGGAAGGTCTGTGTGACCCAAT   2520
21-294       GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGTCTGTGTGACCCAAT   2520
21-056       GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGTCTGTGTGACCCAAT   2520
20-009       GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGTCTGTGTGACCCAAT   2520
20-014       GGTGAAATTTGAGCATATGAGCCCTGAACAATTGGTTCAGGAAGGTCTGTGTGACCCAAT   2520
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21-BMYV      ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
21-254       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
20-BMYV      ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
20-010       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
20-006       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
19-BMYV      ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
21-097       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
19-013       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
21-294       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
21-056       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
20-009       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
20-014       ACGGTTATTCGTAAAAGGCGAGCCACACAAACAATCCAAACTTGATGAAGGACGCTACCG   2580
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21-BMYV     CCTCATCATGAGTGTCTCATTGGTTGACCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
21-254      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
20-BMYV     CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
20-010      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
20-006      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
19-BMYV     CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
21-097      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
19-013      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
21-294      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
21-056      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
20-009      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
20-014      CCTCATCATGAGTGTCTCATTGGTTGATCAACTGGTAGCCCGGGTTCTGTTTCAAAATCA    2640
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21-BMYV     GAACAAGCGCGAGATCGCGCTCTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
21-254      GAACAAGCGCGAGATCGCGCTCTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
20-BMYV     GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
20-010      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
20-006      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
19-BMYV     GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
21-097      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
19-013      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
21-294      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
21-056      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
20-009      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
20-014      GAACAAGCGCGAGATCGCGCTTTGGAGGGCGATTCCCTCAAAACCCGGATTCGGATTGTC    2700
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21-BMYV     CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
21-254      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
20-BMYV     CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
20-010      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
20-006      CACAGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
19-BMYV     CACAGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
21-097      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
19-013      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
21-294      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
21-056      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
20-009      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
20-014      CACGGACGGACAAGTCGTCGATTTCATGCAAGCATTATCGGCGCAGGTGGGAGTGAACAC    2760
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21-BMYV     TGCTGAATTACTCCAAGATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
21-254      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
20-BMYV     TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATCCCTACAGATTGCTCTGGTTTTGA    2820
20-010      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
20-006      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
19-BMYV     TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
21-097      TGCTGAATTACTCCAAAATTGGAAATCCCACCTCATTCCTACAGATTGCTCTGGTTTTGA    2820
19-013      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
21-294      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
21-056      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
20-009      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
20-014      TGCTGAATTACTCCAAAATTGGAAATCCCACCTTATTCCTACAGATTGCTCTGGTTTTGA    2820
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21-BMYV     CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
21-254      CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
20-BMYV     CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
20-010      CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
20-006      CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
19-BMYV     CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
21-097      CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
19-013      CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
21-294      CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
21-056      CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT    2880
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20-009     CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT   2880
20-014     CTGGAGCGTTTCGGACTGGCTTCTAGAGGATGAAATGGAAGTCCGGAACAGGCTCACGTT   2880
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21-BMYV    GGATATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
21-254     GGATATAAATGATCTAACCAGGCGACTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
20-BMYV    GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
20-010     GGACATAAATGATCTAACCAGGCGACTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
20-006     GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
19-BMYV    GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
21-097     GGACATAAATGATCTAACCAGGCGACTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
19-013     GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
21-294     GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
21-056     GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
20-009     GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
20-014     GGACATAAATGATCTAACCAGGCGTCTGCGAGCTGGATGGCTTAAATGCCTCGCAAATAG   2940
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21-BMYV    TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
21-254     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
20-BMYV    TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
20-010     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
20-006     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
19-BMYV    TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
21-097     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
19-013     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
21-294     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
21-056     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
20-009     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
20-014     TGTTCTCTGTCTATCAGATGGAACATTGCTCTCGCAGCAAGTGCCTGGTGTACAAAAGAG   3000
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21-BMYV    TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
21-254     TGGCAGCTACAACACCTCCTCGTCTAATTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
20-BMYV    TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCTGCTTACCACTC   3060
20-010     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
20-006     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
19-BMYV    TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
21-097     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
19-013     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
21-294     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
21-056     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
20-009     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
20-014     TGGCAGCTACAACACCTCCTCGTCTAACTCTAGAATTCGAGTGATGGCCGCTTACCACTC   3060
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21-BMYV    CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
21-254     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
20-BMYV    CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
20-010     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
20-006     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
19-BMYV    CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
21-097     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
19-013     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
21-294     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
21-056     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
20-009     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
20-014     CGGAGCCTCCTGGGCCATCGCCATGGGTGATGATGCCCTTGAATCTGTAGATGCAGACCT   3120
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21-BMYV    AAGTCGATACTCATCCTTAGGTTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
21-254     AAGTCGATACTCATCCTTAGGCTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
20-BMYV    AAGTCGATACTCATCCTTAGGCTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
20-010     AAGTCGATACTCATCCTTAGGCTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
20-006     AAGTCGATACTCATCCTTAGGTTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
19-BMYV    AAGTCGATACTCATCCTTAGGCTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
21-097     AAGTCGATACTCATCCTTAGGTTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
19-013     AAGTCGATACTCATCCTTAGGTTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
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21-294      AAGTCGATACTCATCCTTAGGCTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
21-056      AAGTCGATACTCATCCTTAGGTTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
20-009      AAGTCGATACTCATCCTTAGGTTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
20-014      AAGTCGATACTCATCCTTAGGCTTCAAAGTCGAGGTTTCTTCACAACTGGAATTCTGCTC   3180
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21-BMYV     TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTCAACAAAGCTAAAATGCTTTATAA   3240
21-254      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCCAAAATGCTTTATAA   3240
20-BMYV     TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
20-010      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
20-006      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
19-BMYV     TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTCAACAAAGCTAAAATGCTTTATAA   3240
21-097      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTCAACAAAGCTAAAATGCTTTATAA   3240
19-013      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
21-294      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
21-056      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
20-009      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
20-014      TCACATTTTTGAGGAGGAGAACCTCGCCGTTCCGGTAAACAAAGCTAAAATGCTTTATAA   3240
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21-BMYV     ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
21-254      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
20-BMYV     ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
20-010      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
20-006      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
19-BMYV     ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
21-097      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
19-013      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
21-294      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
21-056      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
20-009      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
20-014      ATTGATACATGGTTATGAACCGGAATGTGGCAACCTTGAAGTTCTGACGAACTATCTTGC   3300
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21-BMYV     AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
21-254      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
20-BMYV     AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
20-010      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
20-006      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
19-BMYV     AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
21-097      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
19-013      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
21-294      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
21-056      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
20-009      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
20-014      AGCTTGTTTCTCAATTTTAAACGAGCTGAGATCCGATCAAGAACTCGTTGCCTCCCTCTA   3360
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21-BMYV     TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
21-254      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
20-BMYV     TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
20-010      CCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
20-006      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
19-BMYV     TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
21-097      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
19-013      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
21-294      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
21-056      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
20-009      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
20-014      TCAGTGGCTGGTCCTTCCAGTGCAGCCACAAAAGATATAACGAGGGACAATATAAACAGC   3420
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21-BMYV     CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
21-254      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
20-BMYV     CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
20-010      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
20-006      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
19-BMYV     CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
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21-097      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
19-013      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
21-294      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
21-056      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
20-009      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
20-014      CGGGTAAACATCAGTTGCAAACGCCGGAAGTTTAAAGTCTGATTACATAACAAGCCAAAA   3480
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21-BMYV     TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
21-254      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
20-BMYV     TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
20-010      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
20-006      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
19-BMYV     TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
21-097      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
19-013      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
21-294      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
21-056      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
20-009      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTAACGGT   3540
20-014      TAGATTTCAAGTTTTTAGCAGGATTTTCAAGTGGTCTATGTCAGCAATACCTGTGACGGT   3540
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21-BMYV     AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
21-254      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
20-BMYV     AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
20-010      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
20-006      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
19-BMYV     AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
21-097      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
19-013      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
21-294      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
21-056      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
20-009      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
20-014      AGTTGGCTTGTATTTCGTCTACCTTAAGATTTCTCACCACGTCAGATCAATTGTTAATGA   3600
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21-BMYV     ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
21-254      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
20-BMYV     ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
20-010      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
20-006      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
19-BMYV     ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
21-097      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
19-013      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
21-294      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
21-056      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
20-009      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
20-014      ATACGGTCGTGGGTAGGAGAACGATCAATGGAAGAAGACGACCACGTAGGCAAACACGAC   3660
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21-BMYV     GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
21-254      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
20-BMYV     GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
20-010      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
20-006      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
19-BMYV     GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
21-097      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
19-013      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
21-294      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
21-056      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
20-009      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
20-014      GCGCTCAGCGCTCTCAGCCAGTGGTTGTGGTCCAAGCCTCTCGGACAACACAACGCCGAC   3720
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21-BMYV     CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
21-254      CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
20-BMYV     CTAGACGACGACGAAGAGGTAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
20-010      CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
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20-006        CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
19-BMYV       CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
21-097        CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
19-013        CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
21-294        CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
21-056        CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
20-009        CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
20-014        CTAGACGACGACGAAGAGGCAACAACCGGACAAGAAGAACTGTTTCTACCAGAGGAACAG   3780
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21-BMYV       GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
21-254        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
20-BMYV       GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
20-010        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
20-006        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
19-BMYV       GTTCGAGCGAGACATTCATTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
21-097        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
19-013        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
21-294        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
21-056        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
20-009        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
20-014        GTTCGAGCGAGACATTCGTTTTCTCAAAAGACAATCTCGCGGGAAGTTCCAGCGGAGCAA   3840
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21-BMYV       TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
21-254        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
20-BMYV       TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
20-010        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
20-006        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
19-BMYV       TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
21-097        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
19-013        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
21-294        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
21-056        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
20-009        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
20-014        TCACGTTCGGGCCGAGTCTATCAGACTGCCCGGCATTCGCTGATGGAATGCTCAAGGCCT   3900
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21-BMYV       ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
21-254        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
20-BMYV       ACCATGAGTATAAAATCTCAATGGTCATCTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
20-010        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
20-006        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
19-BMYV       ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
21-097        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
19-013        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
21-294        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
21-056        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
20-009        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
20-014        ACCATGAGTATAAAATCTCAATGGTCATTTTGGAGTTCGTCTCCGAGGCCTCTTCCCAAA   3960
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21-BMYV       ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
21-254        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
20-BMYV       ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
20-010        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
20-006        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
19-BMYV       ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
21-097        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
19-013        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
21-294        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
21-056        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
20-009        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
20-014        ATTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAGTGCCCTTTCATCAA   4020
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21-BMYV       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
21-254        CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
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20-BMYV      CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
20-010       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
20-006       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
19-BMYV      CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
21-097       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
19-013       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
21-294       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
21-056       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
20-009       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
20-014       CCATTAACAAGTTCGGGATCACAAAACCCGGCAGGAGGGCATTTGCAGCGTCTTACATCA   4080
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21-BMYV      ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
21-254       ACGGGACGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
20-BMYV      ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
20-010       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
20-006       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
19-BMYV      ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
21-097       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
19-013       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
21-294       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
21-056       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
20-009       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
20-014       ACGGGGCGGACTGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTACAAAGGCAATG   4140
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21-BMYV      GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCCA   4200
21-254       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
20-BMYV      GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
20-010       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
20-006       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCCA   4200
19-BMYV      GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
21-097       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
19-013       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
21-294       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
21-056       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
20-009       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
20-014       GTTCTTCATCGATAGCTGGTTCTTTTAGAATCACCATGAAGTGCCAGTTCCACAATCCGA   4200
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21-BMYV      AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
21-254       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
20-BMYV      AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
20-010       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
20-006       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
19-BMYV      AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
21-097       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
19-013       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
21-294       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
21-056       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
20-009       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
20-014       AATAGGTAGACAAGGAACCCGGCCCTAGCCCAGGGCCTTCTCCCTCTCCACAACCCACAC   4260
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21-BMYV      CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
21-254       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
20-BMYV      CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
20-010       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
20-006       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
19-BMYV      CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
21-097       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
19-013       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
21-294       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
21-056       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
20-009       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
20-014       CCTCAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGTATAATGGCCC   4320
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21-BMYV     AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCTCAACGGTTTCGCTACATAG   4380
21-254      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
20-BMYV     AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
20-010      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
20-006      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
19-BMYV     AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
21-097      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
19-013      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
21-294      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
21-056      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTCCGCTACATAG   4380
20-009      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTTCGCTACATAG   4380
20-014      AATCCACTGATGACGCCATCTCTCTGTACGACATGCCTTCCCAACGGTTCCGCTACATAG   4380
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21-BMYV     AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
21-254      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
20-BMYV     AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
20-010      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
20-006      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
19-BMYV     AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
21-097      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
19-013      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
21-294      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
21-056      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
20-009      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
20-014      AAGACGAGAATATGAACTGGACAAACCTCGATTCTCGATGGTATTCCCAGAATTCTTTGA   4440
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21-BMYV     AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
21-254      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
20-BMYV     AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
20-010      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
20-006      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
19-BMYV     AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
21-097      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
19-013      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
21-294      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
21-056      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
20-009      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
20-014      AAGCCATCCCAATGATAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTGGAAATTTCGA   4500
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21-BMYV     TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
21-254      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
20-BMYV     TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
20-010      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
20-006      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
19-BMYV     TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
21-097      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
19-013      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
21-294      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
21-056      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
20-009      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
20-014      TGGAGGGGTATCAACCAACCTCAAGCACCACAGATCCTAATAAGGACAAACAAGATGGTC   4560
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21-BMYV     TTATTGCATACAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
21-254      TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
20-BMYV     TTATTGCATACAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
20-010      TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
20-006      TTATTGCATACAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
19-BMYV     TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
21-097      TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
19-013      TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
21-294      TTATTGCATACAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
21-056      TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
20-009      TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
20-014      TTATTGCATATAATGATGACCTCAAGGAGGGTTGGAATGTAGGGGTTTATAACAATGTGG   4620
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21-BMYV            AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
21-254             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
20-BMYV            AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
20-010             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
20-006             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
19-BMYV            AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
21-097             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
19-013             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
21-294             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
21-056             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
20-009             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
20-014             AGATAACCAACAATAAGGCTGATAACACTTTGAAGTACGGCCATCCAGACATGGAGCTCA   4680
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21-BMYV            ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
21-254             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
20-BMYV            ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
20-010             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
20-006             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
19-BMYV            ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
21-097             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
19-013             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
21-294             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
21-056             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGTCACG   4740
20-009             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGCCACG   4740
20-014             ATAGTTGTCATTTTAATCAAGGACAATGTTTGGAAAGAGATGGAGATTTGACTTGCCACG   4740
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21-BMYV            TTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
21-254             TTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
20-BMYV            TTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
20-010             TTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
20-006             TTAAAACAACTGGTGACAATGCCTCCTTCTTTGTTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
19-BMYV            TTAAAACAACTGGTGACAATGCCTCCTTCTTTGTTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
21-097             TTAAAACAACTGGTGACAATGCCTCCTTCTTTGTTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
19-013             TTAAAACAACTGGTGACAATGCCTCCTTCTTTGTTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
21-294             TTAAAACAACTGGTGACAATGCCTCCTTCTTTGTTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
21-056             TTAAAACAACTGGTGACAATGCCTCCTTCTTTGTTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
20-009             TTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
20-014             TTAAAACAACTGGTGACAATGCCTCCTTCTTTGTTGTTGGTCCCGCTGTCCAGAAGCAAT   4800
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21-BMYV            CCAAATACAATTATGCCGTTTCATACGGAGCTTGGACAGATCGGATGATGGAGATAGGGA   4860
21-254             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
20-BMYV            CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
20-010             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
20-006             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
19-BMYV            CCAAATACAATTATGCCGTTTCATACGGAGCTTGGACAGATCGGATGATGGAGATAGGGA   4860
21-097             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
19-013             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
21-294             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
21-056             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
20-009             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
20-014             CCAAATACAATTATGCCGTTTCATACGGAGCCTGGACAGATCGGATGATGGAGATAGGGA   4860
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21-BMYV            TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
21-254             TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
20-BMYV            TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
20-010             TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
20-006             TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
19-BMYV            TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
21-097             TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
19-013             TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
21-294             TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
21-056             TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
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20-009      TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
20-014      TGATAGCCATAGCACTTGATGAACAAGGCTCATCCGGTTCCGCAAAGATAGAAAGACCAA   4920
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21-BMYV     AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
21-254      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
20-BMYV     AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
20-010      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
20-006      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
19-BMYV     AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
21-097      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
19-013      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
21-294      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
21-056      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
20-009      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
20-014      AGAGAGTCGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTACCGGAGAAGG   4980
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21-BMYV     AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
21-254      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
20-BMYV     AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
20-010      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
20-006      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
19-BMYV     AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
21-097      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
19-013      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
21-294      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
21-056      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
20-009      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
20-014      AAAACTCCGGTGAATTCAAAACCGATCAAAGACAAGATCTCAAAACTCCTCCCACATCTG   5040
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21-BMYV     GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
21-254      GTGGGAGTTCCGATATGCTGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
20-BMYV     GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
20-010      GTGGGAGTTCCGATATGCTGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
20-006      GTGGGAGTTCCGATATGCTGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
19-BMYV     GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
21-097      GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
19-013      GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
21-294      GTGGGAGTTCCGATATGCTGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
21-056      GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
20-009      GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
20-014      GTGGGAGTTCCGATATGCCGGATATCGTTCAAGGAGGCTTACCCCTTCCCATTGAAGAAG   5100
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21-BMYV     ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
21-254      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
20-BMYV     ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
20-010      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
20-006      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
19-BMYV     ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
21-097      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
19-013      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
21-294      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
21-056      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
20-009      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
20-014      ACATTCCTGATTTCATCAGGGATGACCCTTGGTCCAACATACCGGCCAAGACTTCGCGGG   5160
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21-BMYV     AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
21-254      AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
20-BMYV     AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
20-010      AAGACGAGGCTGTGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
20-006      AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
19-BMYV     AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
21-097      AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
19-013      AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC   5220
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21-294       AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC    5220
21-056       AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC    5220
20-009       AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC    5220
20-014       AAGACGAGGCTGCGTCATCAAAGAGTGGTTTTAAACCCCAATTGAAGCCTCCTGGCTTGC    5220
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21-BMYV      CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
21-254       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
20-BMYV      CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
20-010       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
20-006       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
19-BMYV      CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
21-097       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
19-013       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
21-294       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
21-056       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
20-009       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
20-014       CAAAGCCACAACCGGTCAGAACGATCCGAAACTTCGATCCAGAACCTGACTTGGTTGAGG    5280
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21-BMYV      CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
21-254       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
20-BMYV      CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
20-010       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
20-006       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
19-BMYV      CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
21-097       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
19-013       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
21-294       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
21-056       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
20-009       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
20-014       CATGGCGACCTGACGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCGGCCACTGTTA    5340
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21-BMYV      TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
21-254       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
20-BMYV      TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
20-010       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
20-006       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
19-BMYV      TGTACGGGGGTTCCGTTAATGAAGGCCGATCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
21-097       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGAGATAAAGCTGTGT    5400
19-013       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
21-294       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
21-056       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
20-009       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
20-014       TGTACGGGGGTTCCGTTAATGAAGGCCGGTCTATGATTGACAAGCGTGATAAAGCTGTGT    5400
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21-BMYV      TAGACGGCCGCAAGAGTTGGGGATCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
21-254       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
20-BMYV      TAGACGGCCGCAAGAGTTGGGGATCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
20-010       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
20-006       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
19-BMYV      TAGACGGCCGCAAGAGTTGGGGATCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
21-097       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
19-013       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
21-294       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
21-056       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
20-009       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
20-014       TAGACGGCCGCAAGAGTTGGGGTTCTTCCTTGGCGTCCTCCTTGACGGGAGGCACGCTTA    5460
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21-BMYV      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
21-254       AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
20-BMYV      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
20-010       AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
20-006       AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
19-BMYV      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
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21-097      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
19-013      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
21-294      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
21-056      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
20-009      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
20-014      AGGCCTCTGCAAAGTCAGAGAAGCTTGCCAAACTCACTTCGAGTGAAAGGGCGCAGTTCA    5520
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21-BMYV     AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
21-254      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
20-BMYV     AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
20-010      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
20-006      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
19-BMYV     AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
21-097      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
19-013      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTCTTAGAACAACTTCTGG    5580
21-294      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
21-056      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
20-009      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTTTTAGAACAACTTCTGG    5580
20-014      AACGAATTAAGCGCCAGCAAGGTGCCACACGAGCTTCAGAATTCTTAGAACAACTTCTGG    5580
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21-BMYV     CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
21-254      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
20-BMYV     CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
20-010      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
20-006      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
19-BMYV     CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
21-097      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
19-013      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
21-294      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
21-056      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
20-009      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
20-014      CTGGCACAAACCCTGACCCAAGGTCCTGATGAACCTTTCCCAATCATCACAGTCAAGCCC    5640
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21-BMYV     GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
21-254      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
20-BMYV     GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
20-010      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
20-006      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
19-BMYV     GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
21-097      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
19-013      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
21-294      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
21-056      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
20-009      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
20-014      GTGACTTTAAACGCGGAACGACTCCGAAAGGATAGGCAACGAGTGTTTTACGCTGGGATA    5700
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21-BMYV     ACTCCCTACGGCACTTCGGTGT        5722
21-254      ACTCCCTACGGCACTTCGGTGT        5722
20-BMYV     ACTCCCTACGGCACTTCGGTGT        5722
20-010      ACTCCCTACGGCACTTCGGTGT        5722
20-006      ACTCCCTACGGCACTTCGGTGT        5722
19-BMYV     ACTCCCTACGGCACTTCGGTGT        5722
21-097      ACTCCCTACGGCACTTCGGTGT        5722
19-013      ACTCCCTACGGCACTTCGGTGT        5722
21-294      ACTCCCTACGGCACTTCGGTGT        5722
21-056      ACTCCCTACGGCACTTCGGTGT        5722
20-009      ACTCCCTACGGCACTTCGGTGT        5722
20-014      ACTCCCTACGGCACTTCGGTGT        5722
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Appendix D – BChV consensus sequence alignment

BChV consensus sequences produced using BCFtools (see Chapter 5 section 5.3.2), and aligned using ClustalOmega.

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CLUSTAL O(1.2.4) multiple sequence alignment


19_016          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-256          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21_024          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-021          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
BBRO21-BChV     ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-039          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-020          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
19_015          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-196          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-187          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-056          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21_290          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-121          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
19_005          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-294          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-179          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-009          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-071          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-018-2        ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-014          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21_278          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
21-111          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-016          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-015          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-012          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
19_011          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
19-002          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
19_010          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-017          ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
20-018-1        ACAAAAGAATAGCAGGAGGACAGTGAATGAACTTTGAGATTTGCTTCAAAACGAACAGCG    60
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19_016          AACTACTAGTGACGAGCGACAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-256          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21_024          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-021          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
BBRO21-BChV     AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-039          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-020          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATTGGAA    120
19_015          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-196          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-187          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-056          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21_290          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-121          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
19_005          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-294          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-179          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-009          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-071          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-018-2        AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-014          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21_278          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
21-111          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-016          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-015          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-012          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
19_011          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
19-002          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
19_010          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-017          AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
20-018-1        AACTACTAGTGACGAGCGAAAGACACTTGCCACTAAAAGAGAGATCATTCATAATCGGAA    120
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19_016          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
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21-256          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21_024          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-021          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
BBRO21-BChV     GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-039          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-020          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
19_015          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-196          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-187          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-056          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21_290          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-121          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
19_005          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-294          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-179          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-009          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-071          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-018-2        GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-014          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21_278          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
21-111          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-016          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-015          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-012          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
19_011          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
19-002          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
19_010          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-017          GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
20-018-1        GATTTCTCACGCAAATCCCTCAACTTTTGCACCATTTCAAATATGGACACCAAGTTGAAC    180
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19_016          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-256          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21_024          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-021          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
BBRO21-BChV     AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-039          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-020          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
19_015          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-196          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-187          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-056          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21_290          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-121          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
19_005          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-294          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-179          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-009          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-071          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-018-2        AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-014          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21_278          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
21-111          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-016          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-015          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-012          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
19_011          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
19-002          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
19_010          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-017          AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
20-018-1        AGTTCTTACGCTCTATTCTTTTTCAGCTCCCTAATCTTATTTGGAGCTCTTGGGACCATG    240
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19_016          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21-256          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21_024          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
20-021          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
BBRO21-BChV     GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21-039          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21-020          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
19_015          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21-196          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21-187          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21-056          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21_290          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
21-121          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
19_005          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC    300
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21-294          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
21-179          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-009          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
21-071          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-018-2        GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-014          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
21_278          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
21-111          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-016          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-015          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-012          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
19_011          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
19-002          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
19_010          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-017          GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
20-018-1        GCACCATCTTATATGGTGACAGGCCCTTTACACGCGCCGAAGATCTCCTCAGATTTTCCC     300
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19_016          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-256          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21_024          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-021          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
BBRO21-BChV     TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-039          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-020          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
19_015          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-196          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-187          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-056          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21_290          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-121          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
19_005          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-294          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-179          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-009          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-071          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-018-2        TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-014          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21_278          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
21-111          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-016          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-015          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-012          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
19_011          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
19-002          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
19_010          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-017          TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
20-018-1        TTACCACCGGATATTACCCAACTCCTACTAACACAGGACTCCGTGTGGGACTGCCCTCTT     360
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19_016          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-256          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21_024          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
20-021          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
BBRO21-BChV     CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-039          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-020          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
19_015          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-196          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-187          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-056          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21_290          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-121          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
19_005          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-294          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-179          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
20-009          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-071          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
20-018-2        CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
20-014          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21_278          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
21-111          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
20-016          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
20-015          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
20-012          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
19_011          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
19-002          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC     420
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19_010          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC    420
20-017          CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC    420
20-018-1        CAGAAAAAGCTGTCAGATTACAGCTACAAAGAACTTGTAATACACGTCTTGCAAAGAGGC    420
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19_016          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-256          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21_024          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-021          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
BBRO21-BChV     TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-039          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-020          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
19_015          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-196          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-187          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-056          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21_290          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-121          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
19_005          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-294          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-179          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-009          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-071          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-018-2        TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-014          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21_278          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
21-111          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-016          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-015          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-012          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
19_011          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
19-002          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
19_010          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-017          TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
20-018-1        TACAACGACACCCAGAAATACTTGCCACAACTAGCATCAATGGATTTCGGAAAGCACTGG    480
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19_016          GATACCATCTCAGGGCAATTCACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-256          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21_024          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-021          GATACCATCTCAGGGCAATTCACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
BBRO21-BChV     GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-039          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-020          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
19_015          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-196          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-187          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-056          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21_290          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-121          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
19_005          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-294          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-179          GATACCATCTCAGGGCAATTCACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-009          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-071          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-018-2        GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-014          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21_278          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
21-111          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-016          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-015          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-012          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
19_011          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
19-002          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
19_010          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-017          GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
20-018-1        GATACCATCTCAGGGCAATTAACAGGATTGAATATCCTGGAAAGATTGATGTGGGGCCTC    540
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19_016          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
21-256          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
21_024          ATACGGTTATGGGGTTATGTGATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
20-021          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
BBRO21-BChV     ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
21-039          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
21-020          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
19_015          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG    600
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21-196          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21-187          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21-056          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21_290          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21-121          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
19_005          ATACGGTTATGGGGTTATGTGATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21-294          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21-179          ATACGGTTATGGGGTTATGTGATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-009          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21-071          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-018-2        ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-014          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21_278          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
21-111          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-016          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-015          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-012          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
19_011          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
19-002          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
19_010          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-017          ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
20-018-1        ATACGGTTATGGGGTTATGTAATCTGGGTTGTCAGCTCATCCACGATGAGCTTCTTGATG     600
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19_016          AACAACTTGAGCCTAGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-256          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21_024          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-021          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
BBRO21-BChV     AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-039          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-020          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
19_015          AACAACTTGAGCCTAGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-196          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-187          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-056          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21_290          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-121          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
19_005          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-294          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-179          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-009          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-071          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-018-2        AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-014          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21_278          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
21-111          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-016          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-015          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-012          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
19_011          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
19-002          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
19_010          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-017          AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
20-018-1        AACAACTTGAGCCTGGCTATAATAGTGGCCTCATTGATGGCCTTAAGCGTGCTTATGGCA     660
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19_016          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTGCCTGTGTTGGCGGCAAGG     720
21-256          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21_024          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
20-021          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
BBRO21-BChV     CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTGCCTGTGTTGGCGGCAAGG     720
21-039          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-020          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
19_015          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-196          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-187          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-056          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21_290          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-121          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
19_005          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-294          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-179          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
20-009          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21-071          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
20-018-2        CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
20-014          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
21_278          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG     720
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21-111          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
20-016          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
20-015          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
20-012          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
19_011          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
19-002          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
19_010          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
20-017          CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
20-018-1        CGGGCAGCTCAATTATTCTTCAAAATATTACAACTATGCCTACCTGTGTTGGCGGCAAGG    720
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19_016          ATGGTGGTGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-256          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21_024          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-021          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
BBRO21-BChV     ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-039          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-020          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
19_015          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-196          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-187          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-056          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21_290          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-121          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
19_005          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-294          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-179          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-009          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-071          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-018-2        ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-014          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21_278          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
21-111          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-016          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-015          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-012          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
19_011          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
19-002          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
19_010          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-017          ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
20-018-1        ATGGTGATGAGCGCGTTCACCACGATGAAGAGAGTTTGCATAGAGAGACCTAAATCCTAT    780
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19_016          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-256          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21_024          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-021          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
BBRO21-BChV     GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-039          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-020          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
19_015          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-196          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-187          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-056          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21_290          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-121          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
19_005          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-294          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-179          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-009          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-071          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-018-2        GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-014          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21_278          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
21-111          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-016          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-015          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-012          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
19_011          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
19-002          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
19_010          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-017          GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
20-018-1        GTAAAAGAGTGTGCAGTCCGGGGGTTCACTACATGGGCTGTACCAATGAAACCCCCAAAG    840
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19_016          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG    900
21-256          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG    900
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21_024          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-021          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
BBRO21-BChV     AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-039          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-020          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
19_015          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-196          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-187          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-056          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21_290          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-121          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
19_005          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-294          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-179          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-009          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-071          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-018-2        AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-014          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21_278          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
21-111          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-016          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-015          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-012          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
19_011          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
19-002          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
19_010          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-017          AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
20-018-1        AATTCGATTTTGCTCATAAGTCATGACGACGGTTCACACGCAGGTTATGCAACTTGCGTG      900
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19_016          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCCCCCATC      960
21-256          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21_024          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-021          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
BBRO21-BChV     ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-039          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-020          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
19_015          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-196          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-187          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-056          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21_290          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-121          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
19_005          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-294          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-179          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-009          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-071          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-018-2        ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-014          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21_278          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
21-111          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-016          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-015          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-012          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
19_011          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
19-002          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
19_010          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-017          ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
20-018-1        ACTTTACACGACAGACAATCAACCACCATTGGTTTGATAACCTGCTCGCATGCTCCCATC      960
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19_016          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-256          AATGGAAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21_024          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
20-021          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
BBRO21-BChV     AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-039          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-020          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
19_015          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-196          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-187          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-056          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21_290          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-121          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
19_005          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
21-294          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT      1020
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21-179          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-009          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
21-071          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-018-2        AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-014          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
21_278          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
21-111          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-016          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-015          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-012          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
19_011          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
19-002          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
19_010          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-017          AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
20-018-1        AATGGGAGTGTTTTCTCAACCGTCACTGGCAATAAGATCAAAATGGAGAGTTTTAAAACT     1020
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19_016          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-256          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21_024          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-021          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
BBRO21-BChV     CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-039          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-020          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
19_015          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-196          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCAAATTGGGAAAGC     1080
21-187          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-056          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21_290          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-121          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
19_005          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-294          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCAAATTGGGAAAGC     1080
21-179          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-009          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-071          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-018-2        CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-014          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21_278          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
21-111          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-016          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-015          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-012          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
19_011          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
19-002          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
19_010          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-017          CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
20-018-1        CTCTATGATGACGCTGAAACAGATGTAAAGATCTTATTTGGCCCACCCAATTGGGAAAGC     1080
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19_016          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-256          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21_024          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-021          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
BBRO21-BChV     GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-039          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-020          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCT     1140
19_015          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-196          GTCATGGGATGCAAAGCCTTAAAACTCGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-187          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-056          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21_290          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-121          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
19_005          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-294          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-179          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-009          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-071          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-018-2        GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-014          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21_278          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
21-111          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-016          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-015          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-012          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
19_011          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
19-002          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
19_010          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
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20-017          GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
20-018-1        GTCATGGGATGCAAAGCCTTAAAACTTGTCACTAGAGACAGCTTGGCGAAGGGGCCAGCC     1140
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19_016          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATCAGTGGCGCA     1200
21-256          ACTATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21_024          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-021          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
BBRO21-BChV     ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-039          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-020          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
19_015          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-196          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-187          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-056          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21_290          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-121          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
19_005          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-294          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-179          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-009          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-071          ACTATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-018-2        ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-014          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21_278          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
21-111          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-016          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-015          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-012          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
19_011          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
19-002          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
19_010          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-017          ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
20-018-1        ACCATTTACACTTTTGGTGATAATGGATGGACTCTTTCACAAGCCTCGATTAGTGGCGCA     1200
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19_016          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
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21_024          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-021          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
BBRO21-BChV     TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-039          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-020          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
19_015          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-196          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-187          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-056          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21_290          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-121          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
19_005          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-294          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-179          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-009          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-071          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-018-2        TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-014          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21_278          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
21-111          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-016          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-015          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-012          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
19_011          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
19-002          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
19_010          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-017          TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
20-018-1        TACGATAAAAATAAAGCATCCGTACTGAGCATAACCGATAAAGGGCATAGTGGAGCCCCG     1260
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19_016          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-256          TACATTAGTGGCAAAAACGTTATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21_024          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-021          TACATTAGTGGCAAAAACGTTATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
BBRO21-BChV     TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-039          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-020          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
19_015          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-196          TACATTAGTGGCAAAAACGTTATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
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21-187          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-056          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21_290          TACATTAGTGGCAAAAACGTTATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-121          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
19_005          TACATCAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-294          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-179          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-009          TACATTAGTGGCAAAAACGTTATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-071          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-018-2        TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-014          TACATCAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21_278          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
21-111          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-016          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-015          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-012          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
19_011          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
19-002          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
19_010          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-017          TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
20-018-1        TACATTAGTGGCAAAAACGTCATAGGAATCCACTCAGGAGGAGACGTCGTAGACAATGTG     1320
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19_016          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-256          AATGTTTGTTCCACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTTTTCGAG     1380
21_024          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-021          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
BBRO21-BChV     AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-039          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-020          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
19_015          AATGTTTGTTCTACGATTCCAAAGATTGTAAACCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-196          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-187          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-056          AATGTTTGTTCTACGATTCCAAAGATTGTAAACCTTACAACCCCTCAACTAGTCTTCGAG     1380
21_290          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-121          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
19_005          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-294          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-179          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-009          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-071          AATGTTTGTTCCACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-018-2        AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-014          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21_278          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
21-111          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-016          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-015          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-012          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
19_011          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
19-002          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
19_010          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-017          AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
20-018-1        AATGTTTGTTCTACGATTCCAAAGATTGTAAATCTTACAACCCCTCAACTAGTCTTCGAG     1380
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19_016          ACTACAGCCCCGCAAGGGAGATTATTTCTCGAGAAGGAAATGGATGACCTGCTCGAATAC     1440
21-256          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21_024          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
20-021          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
BBRO21-BChV     ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAGGAAATGGATGACCTGCTCGAATAC     1440
21-039          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-020          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAGGAAATGGATGACCTGCTCGAATAC     1440
19_015          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-196          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-187          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-056          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21_290          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-121          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
19_005          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-294          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-179          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
20-009          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-071          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
20-018-2        ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
20-014          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21_278          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
21-111          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC     1440
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20-016          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
20-015          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
20-012          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
19_011          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
19-002          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
19_010          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
20-017          ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
20-018-1        ACCACAGCCCCGCAAGGGAGATTATTTCTCGAGAAAGAAATGGATGACCTGCTCGAATAC    1440
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19_016          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-256          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21_024          GATTGGTCAGGCCAAGAGGCCCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
20-021          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
BBRO21-BChV     GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-039          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAC    1500
21-020          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
19_015          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-196          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-187          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-056          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21_290          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-121          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
19_005          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-294          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-179          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
20-009          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-071          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
20-018-2        GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
20-014          GATTGGTCAGGCCAAGAGGCTCGCGCCATTATCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21_278          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
21-111          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
20-016          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
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20-012          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
19_011          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
19-002          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
19_010          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
20-017          GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
20-018-1        GATTGGTCAGGCCAAGAGGCTCGCGCCATTGTCAAAGAAAGATTTGAGCGCGGGTTATAT    1500
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19_016          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-256          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAATGTCTCCTATCCT    1560
21_024          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
20-021          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
BBRO21-BChV     GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-039          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-020          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
19_015          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-196          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAATGTCTCCTATCCT    1560
21-187          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-056          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21_290          GAGGGCAAAGGAGTAAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-121          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
19_005          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-294          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-179          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
20-009          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-071          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
20-018-2        GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
20-014          GAGGGCAAAGGAGTAAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21_278          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
21-111          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
20-016          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
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19_011          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
19-002          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
19_010          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
20-017          GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
20-018-1        GAGGGCAAAGGAGTGAAGTCTTACGACTTTGAAACTACCAGTGATAACGTCTCCTATCCT    1560
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19_016          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC    1620
21-256          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC    1620
21_024          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC    1620
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20-021          ATTGTCCCCCCGCATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
BBRO21-BChV     ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-039          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-020          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
19_015          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-196          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-187          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-056          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21_290          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-121          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
19_005          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-294          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-179          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-009          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-071          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-018-2        ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-014          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21_278          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
21-111          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-016          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-015          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-012          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
19_011          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
19-002          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
19_010          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-017          ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
20-018-1        ATTGTCCCCCCACATCTGCCGGGAAATGGACTGAGCGGCGCCGACCGCCAAACAACCGGC     1620
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19_016          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCGCGATCTT     1680
21-256          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21_024          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-021          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
BBRO21-BChV     ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-039          ACCTTCGAAAGCATCCAAAGTCAAATGCTCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-020          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
19_015          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCGCGATCTT     1680
21-196          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-187          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-056          ACCTTCGAAAGCATCCAAAGTCAAATGCTCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21_290          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-121          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
19_005          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-294          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-179          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-009          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAAGCACGATCTT     1680
21-071          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-018-2        ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-014          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21_278          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
21-111          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-016          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-015          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-012          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
19_011          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
19-002          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
19_010          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-017          ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
20-018-1        ACCTTCGAAAGCATCCAAAGTCAAATGCCCGCTTGTGGAGATTCCTCAAGGCACGATCTT     1680
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19_016          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-256          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21_024          GCTGCGACTCAGCCAAATTTCACACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-021          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
BBRO21-BChV     GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-039          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-020          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
19_015          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-196          GCTGCGACTCAGCCAAATTTCACACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-187          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-056          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21_290          GCTGCGACTCAGCCAAATTTCACACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-121          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
19_005          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-294          GCTGCGACTCAGCCAAATTTCACACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-179          GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
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20-009         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-071         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-018-2       GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-014         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21_278         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
21-111         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-016         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-015         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-012         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
19_011         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
19-002         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
19_010         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-017         GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
20-018-1       GCTGCGACTCAGCCAAATTTCATACCCACAACGCAAGTGGCTGGAACACAGATGACACCC     1740
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19_016         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-256         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21_024         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-021         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
BBRO21-BChV    GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-039         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-020         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
19_015         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-196         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-187         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-056         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21_290         GTTCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-121         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
19_005         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-294         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-179         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-009         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-071         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-018-2       GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-014         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21_278         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
21-111         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-016         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-015         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-012         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
19_011         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
19-002         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
19_010         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-017         GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
20-018-1       GTCCAAGGTGTTTCTGTGATGACCCAAGCCATACCGAGTGCACCTTCGGTTCCAAACACC     1800
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19_016         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-256         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21_024         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
20-021         GAAGTGGAATTGATGGGTCTTCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
BBRO21-BChV    GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-039         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-020         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
19_015         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-196         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-187         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-056         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21_290         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-121         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
19_005         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-294         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-179         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
20-009         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-071         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
20-018-2       GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
20-014         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21_278         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
21-111         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
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19_011         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
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19_010         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
20-017         GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA     1860
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20-018-1        GAAGTGGAATTGATGGGTCTCCTATTGAACCGAATAAATCTCGGGAATATAGAAGAGAAA    1860
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19_016          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-256          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21_024          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
20-021          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
BBRO21-BChV     GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-039          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-020          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
19_015          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-196          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-187          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-056          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21_290          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-121          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
19_005          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-294          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-179          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
20-009          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-071          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
20-018-2        GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
20-014          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21_278          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
21-111          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
20-016          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
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19_011          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
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19_010          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
20-017          GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
20-018-1        GTGGCTGGACTGATAGCGAAAAACGTCGAGAAGCTATCAAGACCCAGGCGAAGGATTTCG    1920
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19_016          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-256          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21_024          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
20-021          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
BBRO21-BChV     AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-039          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-020          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
19_015          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-196          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-187          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-056          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21_290          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-121          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
19_005          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-294          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-179          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
20-009          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-071          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
20-018-2        AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
20-014          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21_278          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
21-111          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
20-016          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
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19_011          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
19-002          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
19_010          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
20-017          AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
20-018-1        AAAAATTTTTCGAAGGTCAATACCGGTGGGGCATGGGTCCCACCACACAGGAGGTCTGTG    1980
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19_016          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
21-256          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
21_024          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
20-021          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
BBRO21-BChV     GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
21-039          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
21-020          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
19_015          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
21-196          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
21-187          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG    2040
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21-056          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
21_290          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
21-121          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
19_005          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
21-294          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
21-179          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-009          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
21-071          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-018-2        GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-014          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
21_278          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
21-111          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-016          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-015          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-012          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
19_011          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
19-002          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
19_010          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-017          GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
20-018-1        GATTCGAAGAAGTCGGATCCCTCCCCAAGTTCTACCACTCTAAACAAAGGCTCAACTCAG        2040
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19_016          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-256          AATACGGGGTTAGAGTGGCGGAAGAGCACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21_024          AATACGGGGTTAGAGTGGCGGAAGAGCACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-021          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
BBRO21-BChV     AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-039          AATACGGGGTTAGAGTGGCGGAAGAGCACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-020          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
19_015          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-196          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-187          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-056          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21_290          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-121          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
19_005          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-294          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-179          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-009          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-071          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-018-2        AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-014          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21_278          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
21-111          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-016          AATACGGGGTTAGAGTGGCGGAAGAGCACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-015          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
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19_011          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
19-002          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
19_010          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-017          AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
20-018-1        AATACGGGGTTAGAGTGGCGGAAGAGTACAGTGAGCTCAAAGAGCTCACAGCGGGATTTG        2100
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19_016          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-256          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAGGCTGACAGGT        2160
21_024          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
20-021          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
BBRO21-BChV     GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-039          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-020          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
19_015          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-196          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-187          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-056          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21_290          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-121          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
19_005          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-294          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-179          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
20-009          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-071          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
20-018-2        GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
20-014          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21_278          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
21-111          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
20-016          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT        2160
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20-015          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT    2160
20-012          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT    2160
19_011          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT    2160
19-002          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT    2160
19_010          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT    2160
20-017          GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT    2160
20-018-1        GGTGGCCCAAGTTCGGCGCCCAAGCCGAATTAACTTCCCTGCGACTGCAAGCTGACAGGT    2160
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19_016          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-256          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21_024          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-021          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
BBRO21-BChV     GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-039          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTCATAA    2220
21-020          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
19_015          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-196          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-187          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-056          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21_290          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-121          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
19_005          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-294          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-179          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-009          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-071          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-018-2        GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-014          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21_278          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
21-111          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-016          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-015          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
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19_011          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
19-002          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
19_010          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-017          GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
20-018-1        GGCTCCAACGGATGGAGTCCGCACAAATACCCTCGACAGAAGGCGAGGAATCCGTGATAA    2220
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19_016          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-256          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21_024          ACAGGCTAGTTGAAGCCTATAGTTGTGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-021          ACAGGCTAGTTGAAGCCTATAGTTGTGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
BBRO21-BChV     ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-039          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-020          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
19_015          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-196          ACAGGCTAGTTGAAGCCTATAGTTGTGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-187          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-056          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21_290          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-121          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
19_005          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-294          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-179          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-009          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-071          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-018-2        ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-014          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21_278          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
21-111          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-016          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-015          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-012          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
19_011          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
19-002          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
19_010          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-017          ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
20-018-1        ACAGGCTAGTTGAAGCCTATAGTTGCGCGCGCACTAACGCACCAACATCAACCGCCGGCA    2280
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19_016          ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT    2340
21-256          ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT    2340
21_024          ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT    2340
20-021          ATTCCCTAACGTGGGAAGGTTTTATTGAAGATATCAAGGAAGCTGTAAGCTCCTTAGAAT    2340
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BBRO21-BChV       ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
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21-020            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
19_015            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-196            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-187            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-056            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21_290            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-121            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
19_005            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-294            ATTCCCTAACGTGGGAAGGTTTTATTGAAGATATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-179            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
20-009            ATTCCCTAACGTGGGAAGGTTTTATTGAAGATATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-071            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
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20-014            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21_278            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
21-111            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
20-016            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
20-015            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
20-012            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
19_011            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
19-002            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
19_010            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
20-017            ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
20-018-1          ATTCCCTAACGTGGGAAGGTTTTATTGAAGACATCAAGGAAGCTGTAAGCTCCTTAGAAT          2340
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19_016            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
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21_024            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-021            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
BBRO21-BChV       TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-039            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-020            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
19_015            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-196            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-187            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-056            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21_290            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-121            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
19_005            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-294            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
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21-071            TAGACGCCGGTGTTGGGGTTCCGTACATTGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-018-2          TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-014            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21_278            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
21-111            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-016            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-015            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-012            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
19_011            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
19-002            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
19_010            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-017            TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
20-018-1          TAGACGCCGGTGTTGGGGTTCCGTACATCGCCTACGGGACTCGTACCCACAGAGACTGGG          2400
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19_016            TGTTCAACCAAGAGTTGCTACCCGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
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21_024            TGTTCAACCAAGAGTTGCTACCTGTGCTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
20-021            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
BBRO21-BChV       TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-039            TGTTCAACCAAGAGTTGCTACCCGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-020            TGTTCAACCAAGAGTTGCTACCCGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
19_015            TGTTCAACCAAGAGTTGCTACCCGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-196            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-187            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-056            TGTTCAACCAAGAGTTGCTACCCGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21_290            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-121            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
19_005            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-294            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
21-179            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
20-009            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA          2460
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21-071            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
20-018-2          TGTTCAACCAAGAGTTGCTACCCGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
20-014            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
21_278            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
21-111            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
20-016            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
20-015            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
20-012            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
19_011            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
19-002            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
19_010            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
20-017            TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
20-018-1          TGTTCAACCAAGAGTTGCTACCTGTGTTGACTCGACTGACTTTCAACCGCCTACAGAAGA      2460
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19_016            TGTTGGAAGTCAACTCGGACGACCTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-256            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21_024            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-021            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
BBRO21-BChV       TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-039            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-020            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
19_015            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-196            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-187            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-056            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21_290            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-121            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
19_005            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-294            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-179            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-009            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-071            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-018-2          TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-014            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21_278            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
21-111            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-016            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-015            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-012            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
19_011            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
19-002            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
19_010            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-017            TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
20-018-1          TGTTGGAAGTCAACTCGGACGACTTGAATGCGGAACAACTGGTTCAACACGGACTTTGCG      2520
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19_016            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCTAAGCTGGAAGAAGGTC      2580
21-256            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21_024            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCTAAGCTGGAAGAAGGTC      2580
20-021            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
BBRO21-BChV       ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-039            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-020            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
19_015            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-196            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-187            ACCCAATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-056            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21_290            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-121            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCTAAGCTGGAAGAAGGTC      2580
19_005            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-294            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-179            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
20-009            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-071            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
20-018-2          ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
20-014            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21_278            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
21-111            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
20-016            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
20-015            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCTAAGCTGGAAGAAGGTC      2580
20-012            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
19_011            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
19-002            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
19_010            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
20-017            ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
20-018-1          ACCCGATAAGGGTATTTGTTAAGGGAGAACCCCACAAAGTCTCCAAGCTGGAAGAAGGTC      2580
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19_016          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAATTGGTAGCCAGAGTTCTGTTCC     2640
21-256          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21_024          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-021          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
BBRO21-BChV     GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-039          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAATTGGTAGCCAGAGTTCTGTTCC     2640
21-020          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
19_015          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-196          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-187          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAATTGGTAGCCAGAGTTCTGTTCC     2640
21-056          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21_290          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-121          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAATTGGTAGCCAGAGTTCTGTTCC     2640
19_005          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-294          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-179          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-009          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-071          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-018-2        GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-014          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21_278          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
21-111          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-016          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-015          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-012          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
19_011          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
19-002          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
19_010          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-017          GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
20-018-1        GCTACCGCCTTATAATGAGTGTATCCCTAGTGGATCAGTTGGTAGCCAGAGTTCTGTTCC     2640
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19_016          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCTGTGCCCTCGAAGCCGGGATTTG     2700
21-256          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21_024          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-021          AAAATCAGAACAAACGAGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
BBRO21-BChV     AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-039          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-020          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
19_015          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-196          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-187          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-056          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21_290          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-121          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
19_005          AAAATCAGAACAAACGAGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-294          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-179          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-009          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-071          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-018-2        AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-014          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21_278          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
21-111          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-016          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-015          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-012          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
19_011          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
19-002          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
19_010          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-017          AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
20-018-1        AAAATCAGAACAAACGGGAAATAGAACTCTGGAGGGCAGTGCCCTCGAAGCCGGGATTTG     2700
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19_016          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
21-256          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
21_024          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTCGGTG     2760
20-021          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTCGGTG     2760
BBRO21-BChV     GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
21-039          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
21-020          GTTTATCAACCGATGACCAGATTGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
19_015          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
21-196          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTCGGTG     2760
21-187          GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
21-056          GTTTATCAACCGATGACCAGATTGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG     2760
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21_290        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTCGGTG    2760
21-121        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
19_005        GTTTATCGACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
21-294        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
21-179        GTTTATCAACTGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-009        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
21-071        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-018-2      GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-014        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
21_278        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
21-111        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-016        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-015        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-012        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
19_011        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
19-002        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
19_010        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-017        GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
20-018-1      GTTTATCAACCGATGACCAGATCGAAGACTTTGTTAAAGTCTTGGCTTCACAACTTGGTG    2760
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19_016        AGGAACCACAAGAGGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-256        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21_024        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-021        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
BBRO21-BChV   AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-039        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-020        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
19_015        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-196        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-187        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-056        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21_290        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-121        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
19_005        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-294        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-179        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-009        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-071        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-018-2      AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-014        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21_278        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
21-111        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-016        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-015        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-012        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
19_011        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
19-002        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
19_010        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-017        AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
20-018-1      AGGAACCACAAGAAGTTTTCAATAACTGGTCCACCAAGTTGATACCAACAGATTGCTCTG    2820
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19_016        GTTTTGACTGGAGTGTGGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-256        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21_024        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-021        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
BBRO21-BChV   GTTTTGACTGGAGTGTGGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-039        GTTTTGACTGGAGTGTGGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-020        GTTTTGACTGGAGTGTGGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
19_015        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-196        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-187        GTTTTGACTGGAGTGTGGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-056        GTTTTGACTGGAGTGTGGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21_290        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-121        GTTTTGACTGGAGTGTGGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
19_005        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-294        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-179        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-009        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-071        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-018-2      GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-014        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21_278        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
21-111        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-016        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-015        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
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20-012          GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
19_011          GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
19-002          GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
19_010          GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-017          GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
20-018-1        GTTTTGACTGGAGTGTAGCGGACTGGATGCTCGAAGATGACATGGAAGTCCGCAATCGCT    2880
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19_016          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-256          TGACCAGAAACAATAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21_024          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-021          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
BBRO21-BChV     TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-039          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-020          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
19_015          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-196          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-187          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-056          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21_290          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-121          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
19_005          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-294          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-179          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-009          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-071          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-018-2        TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-014          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21_278          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
21-111          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-016          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-015          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-012          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
19_011          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
19-002          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
19_010          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-017          TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
20-018-1        TGACCAGAAACAACAACCACACAACAAAACGATTACGATCAGTGTGGTTAAAATGCATAA    2940
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19_016          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-256          GCAATTCAGTCTTATGCCTTTCTGATGGGCGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21_024          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-021          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
BBRO21-BChV     GTAATTCAGTCTTATGCCTTTCTGATGGGCGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-039          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-020          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
19_015          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-196          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-187          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-056          GCAATTCAGTCTTATGCCTTTCTGATGGGCGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21_290          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-121          GTAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
19_005          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-294          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-179          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-009          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-071          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-018-2        GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-014          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21_278          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
21-111          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-016          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-015          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-012          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
19_011          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
19-002          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
19_010          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-017          GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
20-018-1        GCAATTCAGTCTTATGCCTTTCTGATGGGTGCCTTCTTTCACAGAGAGTGCCTGGAGTTC    3000
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19_016          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-256          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21_024          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-021          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
BBRO21-BChV     AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
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21-039          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-020          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
19_015          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-196          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-187          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-056          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21_290          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-121          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
19_005          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-294          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-179          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-009          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-071          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-018-2        AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-014          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21_278          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
21-111          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-016          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-015          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-012          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
19_011          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
19-002          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
19_010          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-017          AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
20-018-1        AGAAAAGTGGAAGTTACAATACTTCTTCTTCAAACTCCCGTATCAGAGTTATGGCTGCAT    3060
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19_016          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-256          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21_024          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-021          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
BBRO21-BChV     ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-039          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-020          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
19_015          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-196          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-187          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-056          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21_290          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-121          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
19_005          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-294          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-179          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-009          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-071          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-018-2        ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-014          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21_278          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
21-111          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-016          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-015          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-012          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
19_011          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
19-002          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
19_010          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-017          ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
20-018-1        ATCATTGCGGCGCTTCCTGGGCTATGGCGATGGGCGATGACGCCCTAGAATCTGTTGACT    3120
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19_016          CTAACCTAACAGAGTATAAAAAGTTAGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-256          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21_024          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-021          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
BBRO21-BChV     CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-039          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-020          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
19_015          CTAACCTAACAGAGTATAAAAAGTTAGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-196          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-187          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-056          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21_290          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-121          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
19_005          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-294          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-179          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-009          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21-071          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
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20-018-2        CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-014          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
21_278          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTGGCCAAACAACTGGAAT    3180
21-111          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-016          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-015          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-012          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
19_011          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
19-002          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
19_010          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-017          CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
20-018-1        CTAACCTAACAGAGTATAAAAAGTTGGGTTTCAAAGTCGAGGTAGCCAAACAACTGGAAT    3180
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19_016          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-256          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21_024          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-021          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
BBRO21-BChV     TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-039          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-020          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
19_015          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-196          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-187          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-056          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21_290          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-121          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
19_005          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-294          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-179          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-009          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-071          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-018-2        TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-014          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21_278          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
21-111          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-016          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-015          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-012          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
19_011          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
19-002          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
19_010          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-017          TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
20-018-1        TTTGCTCACATATCTTTAAGAATGAGCGCCTCGCATTACCGCTGAATGTAAAGAAGATGC    3240
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19_016          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-256          TTTACAAACTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21_024          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-021          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
BBRO21-BChV     TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-039          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-020          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
19_015          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-196          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-187          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAATTTGGAAGCGATCAAGAATT    3300
21-056          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21_290          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-121          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
19_005          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-294          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-179          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-009          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-071          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-018-2        TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-014          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21_278          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
21-111          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-016          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-015          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-012          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
19_011          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
19-002          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
19_010          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-017          TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
20-018-1        TTTACAAGCTAATTTACGGGTACAATCCTGATAGCGGTAACTTGGAAGCGATCAAGAATT    3300
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19_016          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAAAGCTTGGTCCAGA     3360
21-256          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21_024          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-021          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
BBRO21-BChV     ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-039          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-020          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
19_015          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-196          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-187          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-056          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21_290          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-121          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
19_005          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-294          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-179          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-009          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-071          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-018-2        ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTTCAGA     3360
20-014          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21_278          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
21-111          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-016          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-015          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-012          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
19_011          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAAAGCTTGGTCCAGA     3360
19-002          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
19_010          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-017          ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
20-018-1        ACCTTGACGCTTGCCACTCGATCGTGAATGAAATTCGTCACGACGAGAGCTTGGTCCAGA     3360
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19_016          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-256          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21_024          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-021          AAATAATATCGTGGTTGGTTATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
BBRO21-BChV     AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-039          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-020          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
19_015          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-196          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-187          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-056          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21_290          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-121          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
19_005          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-294          AAATAATATCGTGGTTGGTTATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-179          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-009          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-071          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-018-2        AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-014          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21_278          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
21-111          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-016          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-015          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-012          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
19_011          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
19-002          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
19_010          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-017          AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
20-018-1        AAATAATATCGTGGTTGGTCATTCCAGTCCAACCACAAAACTAATTCAGGAGGATCAAGC     3420
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19_016          ATATAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21-256          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21_024          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
20-021          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
BBRO21-BChV     ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21-039          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21-020          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
19_015          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21-196          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21-187          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21-056          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
21_290          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA     3480
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21-121          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
19_005          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
21-294          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
21-179          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-009          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
21-071          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-018-2        ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-014          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
21_278          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
21-111          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-016          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-015          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-012          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
19_011          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
19-002          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
19_010          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-017          ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
20-018-1        ATACAAACAGCCGGGTAAACATCAGTTGCAAACACCGGAAGTTTTAGTCTGATTACACAA      3480
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19_016          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-256          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21_024          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-021          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
BBRO21-BChV     CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-039          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-020          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
19_015          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-196          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-187          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-056          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21_290          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-121          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
19_005          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-294          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-179          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-009          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-071          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-018-2        CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-014          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21_278          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
21-111          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-016          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-015          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-012          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
19_011          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
19-002          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
19_010          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-017          CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
20-018-1        CAAGCCAAAATAGACTTCAAATTTTTAGCAGGATTTTCAAGCGGTCTATGTCAGCAATAC      3540
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21-256          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21_024          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
20-021          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
BBRO21-BChV     CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-039          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-020          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
19_015          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-196          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-187          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-056          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21_290          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-121          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
19_005          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-294          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-179          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
20-009          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-071          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
20-018-2        CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
20-014          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21_278          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
21-111          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
20-016          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
20-015          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
20-012          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA      3600
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19_011          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA    3600
19_002          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA    3600
19_010          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA    3600
20_017          CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA    3600
20-018-1        CCGTAACGGTAATTGGCTTGTATTTTGTCTACCTGAAAATCTCCCAACACGTAAGATCAA    3600
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19_016          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_256          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_024          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20_021          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
BBRO21-BChV     TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21-039          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21-020          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
19_015          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_196          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21-187          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21-056          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_290          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_121          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
19_005          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_294          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21-179          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20-009          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21-071          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20-018-2        TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20-014          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_278          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
21_111          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20-016          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20-015          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20-012          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
19_011          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
19_002          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
19_010          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20_017          TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
20-018-1        TCGTTAATGAATACGGTCGTGGGTAGGAGAACAATCAATGGAAGAAGACGACCACGAAGG    3660
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19_016          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_256          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_024          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20_021          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
BBRO21-BChV     CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21-039          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21-020          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
19_015          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_196          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21-187          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21-056          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_290          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_121          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
19_005          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_294          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21-179          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20-009          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21-071          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20-018-2        CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20-014          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_278          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
21_111          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20-016          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20-015          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20-012          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
19_011          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
19_002          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
19_010          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20_017          CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
20-018-1        CAAACACGACGCGCTCAGCGCAATCAGCCAGTGGTTGTGGTCCAAACCTCTCGGAGAACA    3720
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19_016          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC    3780
21_256          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC    3780
21_024          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC    3780
20_021          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC    3780
BBRO21-BChV     CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC    3780
21-039          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC    3780
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21-020          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
19_015          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-196          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-187          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-056          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21_290          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-121          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
19_005          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-294          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-179          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-009          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-071          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-018-2        CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-014          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21_278          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
21-111          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-016          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-015          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-012          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
19_011          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
19-002          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
19_010          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-017          CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
20-018-1        CAACGCCGACCTAGACGACGACGAAGAGGTAATAACCGGGCAGGAAGAACTGTTTCTACC        3780
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19_016          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATATCGCGGGAAGTTCC        3840
21-256          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21_024          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-021          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
BBRO21-BChV     AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21-039          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATATCGCGGGAAGTTCC        3840
21-020          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
19_015          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21-196          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21-187          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATATCGCGGGAAGTTCC        3840
21-056          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21_290          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21-121          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
19_005          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATATCGCGGGAAGTTCC        3840
21-294          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21-179          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-009          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21-071          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-018-2        AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATATCGCGGGAAGTTCC        3840
20-014          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21_278          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
21-111          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-016          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-015          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-012          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
19_011          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
19-002          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
19_010          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-017          AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
20-018-1        AGAGGAACAGGTCAAAGCGAGACATTTGTTTTCTCGGAAGACAATCTCGCGGGAAGTTCC        3840
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19_016          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-256          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21_024          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
20-021          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
BBRO21-BChV     AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-039          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-020          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
19_015          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-196          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-187          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-056          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21_290          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-121          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
19_005          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-294          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-179          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
20-009          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
21-071          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
20-018-2        AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG        3900
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20-014          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
21_278          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
21_111          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
20-016          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
20-015          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
20-012          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
19_011          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
19_002          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
19_010          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
20_017          AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
20-018-1        AGCGGAGCAATCACGTTCGGGCCGAGTCTATCAGACTGCCCAGCATTCTCTAATGGAATG    3900
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19_016          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_256          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_024          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20_021          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
BBRO21-BChV     CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21-039          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21-020          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
19_015          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_196          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21-187          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21-056          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_290          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_121          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
19_005          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_294          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21-179          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20-009          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21-071          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20-018-2        CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20-014          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_278          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
21_111          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20-016          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20-015          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20-012          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
19_011          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
19_002          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
19_010          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20_017          CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
20-018-1        CTCAAGGCCTACCATGAGTACAAAATCTCGATGGTCATTTTGGAGTTCGTCTCCGAAGCC    3960
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19_016          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_256          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_024          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20_021          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
BBRO21-BChV     TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21-039          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21-020          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
19_015          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_196          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21-187          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21-056          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_290          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_121          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
19_005          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_294          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21-179          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20-009          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21-071          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20-018-2        TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20-014          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_278          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
21_111          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20-016          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20-015          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20-012          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
19_011          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
19_002          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
19_010          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20_017          TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
20-018-1        TCTTCCCAAAGTTCCGGTTCCATCGCTTACGAGCTGGACCCACACTGTAAACTCAACTCC    4020
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19_016          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-256          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21_024          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-021          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
BBRO21-BChV     CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-039          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-020          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
19_015          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-196          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-187          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-056          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21_290          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-121          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
19_005          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-294          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-179          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-009          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-071          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-018-2        CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-014          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21_278          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
21-111          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-016          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-015          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-012          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
19_011          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
19-002          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
19_010          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-017          CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
20-018-1        CTTTCCTCAACTATCAATAAGTTCGGGATCACGAAGCCCGGGAGGAGGGCGTTTACAGCG    4080
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19_016          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-256          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21_024          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-021          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
BBRO21-BChV     TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-039          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-020          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
19_015          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-196          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-187          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-056          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21_290          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-121          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
19_005          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-294          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-179          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-009          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-071          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-018-2        TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-014          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21_278          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
21-111          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-016          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-015          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-012          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
19_011          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
19-002          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
19_010          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-017          TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
20-018-1        TCTTACATCAACGGGACGGAATGGCATGACGTTGCCAAGGACCAATTCAGGATCCTCTAC    4140
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19_016          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-256          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21_024          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-021          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
BBRO21-BChV     AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-039          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-020          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
19_015          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-196          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-187          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-056          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21_290          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-121          AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
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19_005         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21_294         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-179         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-009         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21-071         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-018-2       AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-014         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21_278         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
21_111         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-016         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-015         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-012         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
19_011         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
19_002         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
19_010         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20_017         AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
20-018-1       AAAGGCAATGGTTCTTCATCGATAGCTGGTTCTTTCAGGATCACTATAAAGTGTCACTTC    4200
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19_016         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_256         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_024         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20_021         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
BBRO21-BChV    CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21-039         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21-020         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
19_015         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_196         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21-187         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21-056         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_290         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_121         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
19_005         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_294         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21-179         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20-009         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21-071         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20-018-2       CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20-014         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_278         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
21_111         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20-016         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20-015         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20-012         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
19_011         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
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19_010         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20_017         CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
20-018-1       CATAACCCCAAATAGGTAGACGAGGAACCCGGCCCTGGCCCAGGGCCTTCTCCTTCTCCA    4260
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19_016         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
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20_021         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
BBRO21-BChV    CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21-039         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21-020         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
19_015         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21_196         CAACCCGTACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21-187         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21-056         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21_290         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21_121         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
19_005         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21_294         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
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21-071         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
20-018-2       CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
20-014         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21_278         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
21_111         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
20-016         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
20-015         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
20-012         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
19_011         CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT    4320
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20-018-1        CAACCCGCACCCCAAAAGAAATATCGTTTTATCGTCTATACTGGTGTCCCTGTGACCCGT      4320
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21_024          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
20-021          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
BBRO21-BChV     ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-039          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-020          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
19_015          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-196          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-187          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-056          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21_290          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-121          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
19_005          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-294          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-179          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
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21-071          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
20-018-2        ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
20-014          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21_278          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
21-111          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
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19_010          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
20-017          ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
20-018-1        ATAATGGCCCAATCTACAGATGATGCCATCTCCTTGTACGACATGCCTTCTCAAAGGTTT      4380
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21_024          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-021          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
BBRO21-BChV     CGTTACATAGAGGACGAAAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-039          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-020          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
19_015          CGTTACATAGAGGACGAAAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-196          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-187          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-056          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21_290          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-121          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
19_005          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-294          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-179          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-009          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-071          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-018-2        CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-014          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21_278          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
21-111          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-016          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-015          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-012          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
19_011          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
19-002          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
19_010          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-017          CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
20-018-1        CGTTACATAGAGGACGAGAATATGAACTGGACGAACCTCGACTCTCGATGGTATTCCCAG      4440
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19_016          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG      4500
21-256          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG      4500
21_024          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG      4500
20-021          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG      4500
BBRO21-BChV     AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG      4500
21-039          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGCGAGTGGACTGTG      4500
21-020          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGCGAGTGGACTGTG      4500
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19_015          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21_196          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21-187          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21-056          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21_290          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21_121          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
19_005          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21_294          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
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20-009          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21-071          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
20-018-2        AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
20-014          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21_278          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
21_111          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
20-016          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
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20_017          AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
20-018-1        AATTCTTTAAAAGCCATCCCCATGGTAATAGTACCAGTCCCTCAAGGTGAGTGGACTGTG       4500
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19_016          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_256          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_024          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
20_021          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
BBRO21-BChV     GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21-039          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21-020          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
19_015          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_196          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21-187          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21-056          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_290          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_121          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
19_005          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_294          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
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21-071          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
20-018-2        GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
20-014          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_278          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
21_111          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
20-016          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
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20_017          GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
20-018-1        GAAATCTCAATGGAGGGGTATCAACCAACCTCAAGTACCACGGATCCTAATAAGGACAAA       4560
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19_016          CAAGACGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21_256          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21_024          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
20_021          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
BBRO21-BChV     CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21-039          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21-020          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
19_015          CAAGATGGTCTCATTGCATACAATGATGACCTTAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21_196          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21-187          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21-056          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21_290          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21_121          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
19_005          CAAGATGGTCTCATTGCATACAACGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21_294          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21-179          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
20-009          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
21-071          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
20-018-2        CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
20-014          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC       4620
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21_278          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
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20-016          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
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20-012          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
19_011          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
19-002          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
19_010          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
20-017          CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
20-018-1        CAAGATGGTCTCATTGCATACAATGATGACCTCAAGGAAGGTTGGAACGTGGGGGTTTAC     4620
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19_016          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-256          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21_024          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
20-021          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
BBRO21-BChV     AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-039          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-020          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
19_015          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-196          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-187          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-056          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21_290          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-121          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
19_005          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-294          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-179          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
20-009          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-071          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
20-018-2        AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
20-014          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21_278          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
21-111          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
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19-002          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
19_010          AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
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20-018-1        AACAATGTGGAGATAACCAACAATAAGGCCGATAATACTTTAAAGTATGGACACCCGGAC     4680
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21_024          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
20-021          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
BBRO21-BChV     ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21-039          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21-020          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
19_015          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21-196          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21-187          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21-056          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21_290          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21-121          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
19_005          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
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20-018-2        ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
20-014          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21_278          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
21-111          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
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19_010          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
20-017          ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
20-018-1        ATGGAACTTAATAGTTGTCATTTCAATCAACAACAATGTCTGGAAAGAGATGGAGACTTG     4740
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BBRO21-BChV     ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
21-039          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
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21-187          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
21-056          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
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19_005          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
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21-071          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
20-018-2        ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
20-014          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
21_278          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGGCCTGCTGTC      4800
21-111          ACTTGTCACATTAAAACAACTGGTGACAATGCCTCCTTCTTTATTGTTGGACCTGCTGTC      4800
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21-256          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21_024          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
20-021          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
BBRO21-BChV     CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21-039          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21-020          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
19_015          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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21-187          CAAAAGCAATCCAAATATAATTATGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21-056          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21_290          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21-121          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
19_005          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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21-179          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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21-071          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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20-014          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21_278          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
21-111          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
20-016          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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19_011          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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19_010          CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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20-018-1        CAAAAGCAATCCAAATATAATTACGCCGTTTCATACGGAGCTTGGACAGATCGAATGGTG      4860
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21_024          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
20-021          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
BBRO21-BChV     GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
21-039          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
21-020          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
19_015          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
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21-187          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
21-056          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
21_290          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
21-121          GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA      4920
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20-009        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
21-071        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
20-018-2      GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
20-014        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
21_278        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
21-111        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
20-016        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
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19_011        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
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19_010        GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
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20-018-1      GAGATAGGGATGATAGCCATAGCACTAGATGAACAAGGCTCATCCGGTTCCGCAAGGACA    4920
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21_024        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
20-021        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
BBRO21-BChV   GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-039        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-020        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
19_015        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-196        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-187        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-056        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21_290        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-121        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
19_005        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-294        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-179        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
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20-014        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21_278        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
21-111        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
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19_010        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
20-017        GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
20-018-1      GAAAGACCAAAGAGAGTTGGGCACTCCATGGCAGTCTCAACCTGGGAGACTATAAACTTA    4980
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21_024        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
20-021        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
BBRO21-BChV   CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
21-039        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
21-020        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
19_015        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
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20-018-2      CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
20-014        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
21_278        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
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19_011        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
19-002        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
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19_010          CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
20_017          CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
20-018-1        CCGGAGAAGGAAGACTCCGAGAAACTCAAAACCGGTCAAAGACAAGACCTTAAAACTCCT    5040
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19_016          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
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21_024          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
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21-039          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
21-020          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
19_015          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
21_196          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
21-187          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
21-056          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
21_290          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
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21-071          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
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20-014          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
21_278          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
21_111          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
20-016          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
20-015          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
20-012          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
19_011          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
19_002          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
19_010          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
20_017          TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
20-018-1        TTCACGATTAGTGGAAGCTCCGATGTGAAGGGCATCGAGAAGAGAGACTTGCCCCTTCCT    5100
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19_016          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21_256          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
21_024          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
20_021          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
BBRO21-BChV     GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21-039          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21-020          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
19_015          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21_196          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
21-187          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21-056          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21_290          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21_121          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
19_005          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
21_294          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
21-179          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
20-009          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
21-071          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
20-018-2        GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
20-014          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
21_278          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
21_111          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCGATCAGG    5160
20-016          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
20-015          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
20-012          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
19_011          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
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19_010          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
20_017          GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
20-018-1        GCTGATGAGGACATTCCTGATTTTATCGGGAATGATCCTTGGTCTAATGTATCAATCAGG    5160
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21_256          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGCCTTAGACCCCAGTTGAAACCT    5220
21_024          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT    5220
20_021          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT    5220
BBRO21-BChV     AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGCCTTAGACCCCAGTTGAAACCT    5220
21-039          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT    5220
21-020          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGCCTTAGACCCCAGTTGAAACCT    5220
19_015          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT    5220
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21-196          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21-187          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21-056          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21_290          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21-121          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
19_005          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21-294          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21-179          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-009          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21-071          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-018-2        AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-014          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21_278          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
21-111          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-016          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-015          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-012          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
19_011          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
19-002          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
19_010          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-017          AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
20-018-1        AAGTTGCAAGAAGAAGAGGCTATGACGTCTAAGAGTGGTCTTAGACCCCAGTTGAAACCT      5220
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19_016          CCCGGTCTCCCAAAACCACAACCGGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-256          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21_024          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-021          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
BBRO21-BChV     CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-039          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-020          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
19_015          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-196          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-187          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-056          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21_290          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-121          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTCAATCCAACGCCGGAA      5280
19_005          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-294          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-179          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-009          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-071          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-018-2        CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-014          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21_278          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
21-111          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-016          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-015          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
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19_011          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
19-002          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
19_010          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-017          CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
20-018-1        CCCGGTCTCCCAAAACCACAACCAGTTAGAACGATTGGAAATTTTAATCCAACGCCGGAA      5280
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19_016          TTGGTTGAATCGTGGAGACCCGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-256          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21_024          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
20-021          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
BBRO21-BChV     TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-039          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-020          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
19_015          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-196          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-187          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-056          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21_290          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-121          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
19_005          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-294          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-179          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
20-009          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21-071          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
20-018-2        TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
20-014          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
21_278          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC      5340
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21-111          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
20-016          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
20-015          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
20-012          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
19_011          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
19-002          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
19_010          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
20-017          TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
20-018-1        TTGGTTGAATCGTGGAGACCTGATGTGAACCCCGGATATTCCAAGGAAGACGTGGCAGCC    5340
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19_016          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-256          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21_024          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
20-021          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
BBRO21-BChV     GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-039          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-020          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
19_015          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-196          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-187          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-056          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21_290          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-121          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
19_005          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-294          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-179          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
20-009          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-071          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
20-018-2        GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
20-014          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21_278          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
21-111          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
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20-012          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
19_011          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
19-002          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
19_010          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
20-017          GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
20-018-1        GCCACTATTCTTTATGGAGGTTCTATCAAAGACGGCCGGTCTATGATCGATAAACGCGAT    5400
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19_016          AAAGCTGTGTTAGACGGCCGCAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-256          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21_024          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
20-021          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
BBRO21-BChV     AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-039          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-020          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
19_015          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-196          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-187          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-056          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21_290          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-121          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
19_005          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
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21-179          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
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21-071          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
20-018-2        AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
20-014          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21_278          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
21-111          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
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20-012          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
19_011          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
19-002          AAAGCTGTGTTAGACGGCCGCAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
19_010          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
20-017          AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
20-018-1        AAAGCTGTGTTAGACGGCCGTAAGCATTGGGGTTCTTCCTTAGCTTCCTCCTTAACAGGA    5460
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19_016          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG    5520
21-256          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG    5520
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21_024          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
20-021          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
BBRO21-BChV     GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
21-039          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
21-020          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
19_015          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
21-196          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
21-187          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
21-056          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
21_290          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
21-121          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
19_005          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
21-294          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
21-179          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
20-009          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
21-071          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
20-018-2        GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
20-014          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
21_278          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
21-111          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
20-016          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
20-015          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
20-012          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACTTCGCGTGAGAGG        5520
19_011          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
19-002          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
19_010          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
20-017          GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
20-018-1        GGAACGCTTAAGGCCTCTGCAAAGTCGGAGAAGCTTGCTAAACTCACCTCGCGTGAGAGG        5520
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19_016          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
21-256          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
21_024          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
20-021          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
BBRO21-BChV     GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
21-039          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
21-020          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
19_015          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACTACACAAGCTTCAGAATACTTAGAA        5580
21-196          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
21-187          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACTACACAAGCTTCAGAATACTTGGAA        5580
21-056          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
21_290          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
21-121          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACTACACAAGCTTCAGAATACTTAGAA        5580
19_005          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
21-294          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
21-179          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
20-009          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
21-071          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
20-018-2        GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
20-014          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
21_278          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
21-111          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTGGAA        5580
20-016          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
20-015          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
20-012          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
19_011          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
19-002          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
19_010          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
20-017          GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
20-018-1        GCGGAATTCGAACGAATTAAACGCCAGCAAGGCACCACACAAGCTTCAGAATACTTAGAA        5580
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19_016          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-256          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21_024          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
20-021          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
BBRO21-BChV     TTTATTCTGAAGAACATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-039          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-020          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
19_015          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-196          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-187          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-056          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21_290          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-121          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
19_005          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
21-294          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT        5640
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21-179          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-009          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
21-071          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-018-2        TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-014          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
21_278          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
21-111          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-016          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-015          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-012          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
19_011          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
19-002          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
19_010          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-017          TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
20-018-1        TTTATTCTGAAGAGCATGAACCCCGACTAATGGTTTTGAAGGGATATAGCCTAACCCTTT      5640
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19_016          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-256          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21_024          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-021          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
BBRO21-BChV     CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-039          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-020          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
19_015          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-196          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-187          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-056          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21_290          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-121          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
19_005          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-294          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-179          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-009          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-071          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-018-2        CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-014          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21_278          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
21-111          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-016          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-015          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-012          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
19_011          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
19-002          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
19_010          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-017          CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
20-018-1        CTGGTCCTGATGAACCTGTCTAAATCATCACCGTCAAGCCCGTGACGTTAAACTAGGAAC      5700
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19_016          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTGAAGGGTTATACAGTAGGATCC      5760
21-256          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21_024          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
20-021          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
BBRO21-BChV     GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-039          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-020          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
19_015          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-196          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-187          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-056          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21_290          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-121          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
19_005          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-294          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-179          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
20-009          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-071          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
20-018-2        GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
20-014          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21_278          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
21-111          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
20-016          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
20-015          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
20-012          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
19_011          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
19-002          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
19_010          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC      5760
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20-017          GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC         5760
20-018-1        GACTCCCGAAAGGATAGGCACGAATGTTCCCCTTATTTAAAGGGTTATACAGTAGGATCC         5760
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19_016          TACGGCACTTCGGTGT     5776
21_256          TACGGCACTTCGGTGT     5776
21_024          TACGGCACTTCGGTGT     5776
20_021          TACGGCACTTCGGTGT     5776
BBRO21-BChV     TACGGCACTTCGGTGT     5776
21-039          TACGGCACTTCGGTGT     5776
21-020          TACGGCACTTCGGTGT     5776
19_015          TACGGCACTTCGGTGT     5776
21_196          TACGGCACTTCGGTGT     5776
21-187          TACGGCACTTCGGTGT     5776
21-056          TACGGCACTTCGGTGT     5776
21_290          TACGGCACTTCGGTGT     5776
21_121          TACGGCACTTCGGTGT     5776
19_005          TACGGCACTTCGGTGT     5776
21_294          TACGGCACTTCGGTGT     5776
21-179          TACGGCACTTCGGTGT     5776
20-009          TACGGCACTTCGGTGT     5776
21-071          TACGGCACTTCGGTGT     5776
20-018-2        TACGGCACTTCGGTGT     5776
20-014          TACGGCACTTCGGTGT     5776
21_278          TACGGCACTTCGGTGT     5776
21_111          TACGGCACTTCGGTGT     5776
20-016          TACGGCACTTCGGTGT     5776
20-015          TACGGCACTTCGGTGT     5776
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19_011          TACGGCACTTCGGTGT     5776
19_002          TACGGCACTTCGGTGT     5776
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20_017          TACGGCACTTCGGTGT     5776
20-018-1        TACGGCACTTCGGTGT     5776
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