

Media recipes

All the following media recipes are for the scale of one liter.

L (Luria): 10 g tryptone, 5 g yeast extract, 5 g NaCl, 1 g glucose, pH7.0. For solid medium, 10 g agar was included.

LB: 10 g tryptone, 5 g yeast extract, 10 g NaCl, pH 7.0. For solid medium, 10g agar was included.

King's B: 20 g Peptone, 1.5g Heptahydrated Magnesium Sulfate, 1.5g Potassium Hydrogen Phosphate, 10mL glycerol, pH7.0. For solid medium, 10 g agar was included.

GM: 4.3 g MS salts, 0.59 g MES, 0.1 g myo-inositol, 1 ml of 1000x GM vitamin stock, 8 g Bacto agar, pH was adjusted to 5.7 with KOH. (100 ml of 1000x GM vitamins contains 0.1 g thiamine, 0.05 g pyridoxine, 0.05 g nicotinic acid)

PDB: 200g potato (or 4g potato infusion), 20g dextrose

Antibiotics

For bacteria selection in liquid or solid media, final concentrations of 50 µg/mL, 25 µg/mL, 100 µg/mL, 100 µg/mL and 50 µg/mL were used for kanamycin, gentamycin, carbenicillin, rifampicin and spectinomycin, respectively.

For the selection of Arabidopsis transgenic lines, 50 µg/mL of kanamycin was used.

All antibiotic solutions were filter sterilized using 22 µm micro-filters.

Stainings

Trypan blue staining solution: Dissolve 10mg Trypan blue in 30mL Lactophenol (NBS Biological Limited). Store at room temperature. Dilute with 1 vol 100% EtOH before use.

Chloral hydrate solution: Add 200mL dH₂O to a 500g bottle of chloral hydrate and stir overnight in the fume hood.

List of primers used in this thesis work

Chapter 3	KS-349	Col/Ws RPP13 F	CGGCATGAGTCCAAACTCT		
	KS-351	Col/Ws RPP13 R	GGTACCTCAAGTGGATCAG		
	SP-57	<i>rpp13</i> -Ws-F	ATGGTAGATGCGATCACGGAG		
	SP-58	<i>rpp13</i> -Ws-R	TCAGCAGTAGATTTGACCAAACG		
	SP-59	<i>rpp13</i> -Ws-R1	AGCCTCTATACCATAAGTCTCCC		
	SP-60	<i>rpp13</i> -Ws-R2	ACTCCAGCTTTCTTCAACGTC		
	SP-61	<i>rpp13</i> -Ws-F1	TGTTTGAAACAAAGAGCATTCAAG		
	SP-62	<i>rpp13</i> -Ws-F2	AAACATGAGTTGCTCATAAATCTTCG		
	SP-63	<i>rpp13</i> -Ws-R3	CTGTCAGAGGAGATAGACCTCAAGG		
	SP-64	RB4	TCACGGTTGGGGTTTCTACAGGAC		
	SP-65	LB4	CGTGTGCCAGGTGCCACGGAATAGT		
Chapter 4	SP-161	G4539-F	GGACGTAGAATCTGAGAGCTC		
	SP-162	G4539-R	GGTCATCCGTTCCAGGTAAAG		
	SP-7	CA72-F	CCCACTCTAACCAAGCACAC		
	SP-8	CA72-R	AATCCAGTAACCAACACACA		
	SP-9	CIW7-F	AATTTGGAGATTAGCTGGAAT		
	SP-10	CIW7-R	CCATGTTGATGATAAGCACAA		
	SP-11	ALS-F	GGCAACACATGTTCTTGGTG		
	SP-12	ALS-R	ATCACAGGACAAAGTCCCTCG		
	SP-13	RGA-F	TTCGATTCAAGTTCGGTTAG		
	SP-14	RGA-R	GTTTAAGCAAGCGAGATATGC		
	SP-15	1055234-F	GCCTAAGCCAGAACGAGAAA		
Chapter 5	SP-16	1055234-R	CTTCTTTGTGAGCCTCCCC		
	SP-23	24191155-F	TCTACAGGTTCCCAATCAGC		
	SP-24	24191155-R	GGAAGAGAGGGAGCTAGATGC		
	SP-27	26278640-F	GACATTAGGCTCGTAAACAG		
	SP-28	26278640-R	AACCTGAAATTGGAAAAGACTTCAG		
	SP-29	CIW12-F	AGGTTTTATTGCTTTTCA		
	SP-30	CIW12-R	CTTTCAAAAGCACATCAC		
	SP-31	JV28/29-F	CACCTGTTCTGAAACGAAATTGA		
	SP-32	JV28/29-R	GCTTCTCATTCGACTCCTTTG		
	SP-33	ER-F	GAGTTTATTCTGTGCCAAGTCCCTG		
	SP-34	ER-R	CTAATGTAGTGATCTGCGAGGTAATC		
Chapter 6	SP-35	JV65/66-F	TTTCTTTACCGGTTCTAACTTTT		
	SP-36	JV65/66-R	TCATCTCCCTTTAATCTGATGA		
	SP-37	M59-F	GTGCATGATTTGATGTACGC		
	SP-38	M59-R	GAATGACATGAACACTTACACC		
	SP-39	JV18/19-F	TGTCGTATATCAATCGAAAAAGAGAT		
	SP-40	JV18/19-R	AATTTCAGTATCGAGATACCCCTCT		
	2-33	LID-39F	GTTACGGGACAAAGAGCCTGAAAT		
	2-34	LID-39R	AAGCAGTCAATATTGACGGAAGGG		
	2-3	Ch1-5653F	GAAGAACTTGGTCGGTTGTT		
	2-4	Ch1-5653R	AACTGAGAACAGATTGATTTCTGC		
	2-1	Ch1-11016F	TCAATGGGATCGAAACTGGT		
Chapter 7	2-2	Ch1-11016R	ACTGAAAAGCGAGCCAAAAG		
	2-5	CIW1F	ACATTTTCTCAATCCTTACTC		
	2-6	CIW1R	GAGAGCTCTTTATTGTGAT		
		NGA280-F	GGCTCCATAAAAAAGTGACC		
		NGA280-R	CTGATCTCACGGACAATAGTGC		
	2-7	NGA111F	TGTTTTTTAGGACAAATGGCG		
	2-8	NGA111R	CTCCAGTTGGAAGCTAAAGGG		
	2-15	Ch3-3514F	GGATTAGATGGGATTCTGG		
	2-16	Ch3-3514R	TTGCTCGTATCAACACACAGg		
	2-17	CIW11F	CCCCGAGTTGAGGTATT		
	2-18	CIW11R	GAAGAAATTCCTAAAGCATTC		
Chapter 8	2-25	Ch4-6422F	GCCAAACCCAAAATTGTAAAAAC		
	2-26	Ch4-6422R	TAGAGGGAACAATCGGATGC		
	2-29	CIW9F	CAGACGTATCAAAATGACAAATG		
	2-30	CIW9R	GACTACTGCTCAAACTATTCGG		
	2-31	MBK-5F	GAGCATTTACAGAGACG		
	2-32	MBK-5R	ATCACTGTTGTTTACCATTA		
	2-13	NGA168F	TCGCTACTGCACTGCCG		
	2-14	NGA168R	GAGGACATGTATAGGAGCTCG		
	SP-111	NGA6F	ATGGAGAAGCTTACACTGATC		
	SP-112	NGA6R	TGGATTTCTTCTCTCTTTCAC		
	SP-107	NGA172F	CATCCGAATGCCATTGTTT		
Chapter 9	SP-108	NGA172R	AGCTGCTTCTTATAGCGTCC		
	SP-115	NGA8F	TGGCTTTCTGTTTATAAACATCC		
	SP-116	NGA8R	GAGGGCAAACTTTTATTTCTGG		
	SP-97	CIW6F	CTCGTAGTGCACCTTTCATCA		
	SP-98	CIW6R	CACATGGTTAGGGAACAATA		
	SP-99	CAT2F	GACCAGTAAGAGATCCAGATACTGCG		
	SP-100	CAT2R	CACAGTCATGCGACTCAAGACTTG		
	SP-101	NGA1107F	CGACGAATCGACAGAATTAGG		
	SP-102	NGA1107R	GCGAAAAACAAAAAATCCA		
	SP-95	CTR1.2F	CCACTTGTCTCTCTCTCTAG		
	SP-96	CTR1.2R	TATCAACAGAAACGCACGAG		
Chapter 10	SP-109	NGA151F	CAGTCTAAAAGCGAGAGTATGATG		
	SP-110	NGA151R	GTTTTGGGAAGTTTTGCTGG		
	SP-117	NGA76F	AGGCATGGGAGACATTTACG		
	SP-118	NGA76R	GGAGAAAATGTCACCTCTCCACC		
Chapter 11		HaRxL65-F	CACCATGGCTCCTATGGATCACTCATCC		
		HaRxL65-R	TCAATTCCTTATTCAAAAACCACTTTCC		
		HaRxL79-F	CACCATGCTGCCAGCTCGCGTAGCCG		
		HaRxL79-R1	TGCGTAAATCGCCGGATTGATGC		
		HaRxL79-R2	TGCTTAAATCGCCGGATTGATGC		
	SP310	RACE-125-F1 (GSP1)	ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCC		
	SP311	RACE-125-F2 (GSP2)	AAAGAAAGACACGAAGGGTGCGGCTGATGAAGAAAG		
		GeneRacer oligodT	GCTGTCAACGATACGCTACGTAACGGCATGACAGTG(T) ₂₄		
		GeneRacer 3'	GCTGTCAACGATACGCTACGTAACG		
		GeneRacer 3' nested	CGCTACGTAACGGCATGACAGTG		
	SP348	line18(klc)-LP	GTTCTTGAGTTCGGTTTTAGG		
Chapter 12	SP349	line18(klc)-RP	GTCCAGGGCGAGTTTTATTTC		
	LBb1.3	genotyping	ATTTTGCCGATTTCGGAAC		
	SP298	KLC-F	CACCATGGACGTAGGAGAGCAATGAGAGG		
	SP300	KLC-R1	TCAATAAACCGGTCTCTGTCCATTTC		
	SP301	KLC-R2	ATAAACCGGTCTCTGTCCATTTC		
	SP239	NAP1;2-F1	CACCATGAGCAACGATAAGGACAGTT		
	SP241	NAP1;2-R1	TTACTGTTGTTTGATTCAGGAGGC		
	SP243	NAP1;1-F1	CACCATGAGCAACGACAAGGATAGC		
	SP245	NAP1;1-R1	TTACTGTTGCTTGATTCGGGTG		
	SP247	NAP1;3-F1	CACCATGAGCAACGACAAGGACAG		
	SP249	NAP1;3-R1	TCATCTGCTGTTACATTCCGGTGG		
Chapter 13	SP399	PR1-F-Qpcr	GGCACGAGGAGCGGTAGGCG		
	SP400	PR1-R-Qpcr	CACGGCGGAGACGCCAGACA		
	SP403	PAD4-F-Qpcr	GGCGGTATCGATGATTTCAGT		
	SP404	PAD4-R-Qpcr	CGGTTATCACCAACGAGTTT		
	SP405	PDF1.2-F-Qpcr	CACCCCTTATCTTCGCTGCTC		
	SP406	PDF1.2-R-Qpcr	GTTGCATGATCCATGTTTGG		
	SP407	EF1a-F-Qpcr	CAGGCTGATTGTGCTGTTCTTA		
	SP408	EF1a-R-Qpcr	GTTGTATCCGACCTTCTTCAGG		
		HaRxL67-F	CACCATGGAACCATCTGCACCTGTGC		
		HaRxL67-R	ATTGATGGCCAAAGCAATATTGTTGG		
	M13-F	sequencing	GTTGTAACACGACGCCAGT		
Chapter 14	M13-R	sequencing	CACAGGAAACAGCTATGACC		

MAFFT alignment of *Hpa HaRxL79* paralogs nucleotide sequences

CLUSTAL format alignment by MAFFT G-INS-i (v6.850b)

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HaRxL30      ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
HaRxL79      ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
HaRxLL73     ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
HaRxL39      ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
HaRxL47      ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
HaRxL40      ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
HaRxL41      ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
HaRxL42      ATGACCAAGTGCTCCCTACTTCTCGTGCCCTTCCTCGTCGCAATTGCTGTCAGTGACGCT
*****

HaRxL30      CTGCCAGCTCGCGCAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
HaRxL79      CTGCCAGCTCGCGTAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
HaRxLL73     CTGCCAGCTCGCGCAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
HaRxL39      CTGCCAGCTCGCGCAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
HaRxL47      CTGCCAGCTCGCGCAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
HaRxL40      CTGCCAGCTCGCGCAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
HaRxL41      CTGCCAGCTCGCGCAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
HaRxL42      CTGCCAGCTCGCGCAGCCGGCACGCTGCCACAAAGCGCAACATCGGTCCAAGACAAGGCT
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HaRxL30      ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
HaRxL79      ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
HaRxLL73     ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
HaRxL39      ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
HaRxL47      ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
HaRxL40      ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
HaRxL41      ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
HaRxL42      ACTGAGTCGACCGTGAGCGGCAAAACGAGCGCTTCAATCAAAGGAAGACACGAAGGGTGCG
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HaRxL30      GCTGATGAAGAAAGAGCGCTAATTAGTCCT---TCGAGACTGGAGCCGTTGAGCACC AAG
HaRxL79      GCTGATGAAGAAAGAGCGCTACTTAGTCCT---TCGATACTGGAGCCGTTGAGCACC AAG
HaRxLL73     GCTGATGAAGAAAGAGCGCTAAATTGGCTTCAGTCGGTACCGGAGTGGTTGAGCACC ATG
HaRxL39      GCTGATGAAGAAAGAGCGCCAAATTGGCTTCAGTCGGTACCGGAGTGGTTGAGCACC ATG
HaRxL47      GCTGATGAAGAAAGAGCGCTAAATCGGCTTCAGTCGGTACCGGAGTGGTTGAGCACC ATG
HaRxL40      GCTGATGAAGAAAGAGCGCTAAATTGGCTTCAGTCGGTACCGGAAAGGTTGAGCACC ATG
HaRxL41      GCTGATGAAGAAAGAGCGCTAAAGTGGCTTCAGTCGGTACCGAGTGGTTGAGCACC ATG
HaRxL42      GCTGATGAAGAAAGAGCGCTAAATCGGCTTCAGTCGGTACCGGAGTGGTTGAGCACC ATG
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HaRxL30      ATGAAGAGCAGCACTGACTGGATGGCTCAGACGAGGAAAGGAGCTTCTTTTGGCGTGTCG
HaRxL79      ATGAAGAGCAGCACTGACTGGATGGCTCAGACGAGGAAAGGAGCTTCTTTTAGCGTGTCG
HaRxLL73     ATGAAGAGACCACTGACTGGATGGCTCGGACGTGGAAAGGAGCTTCTTTTAGCGTGTCG
HaRxL39      ATGAAGAGACCACTAACTGGACGGCTCGCACGTGGAAAGGAACTGCTTTTAGCATGTCC
HaRxL47      ACAAAGAGCATCACTAACTGGACGGCTCGCACGTGG-----
HaRxL40      ATAAAGAGCATCACTAACTGGACGGCTCGCACGTGG-----
HaRxL41      ATAAAGAGCATCACTAACTGGACGACTCGCACGTGG-----
HaRxL42      ACAAAGAGCATCACTAACTGGACGGCTCGCACGTGG-----
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HaRxL30      AGGATGCGGCAGAAAGA-----
HaRxL79      GGGGTGTCGCAGAAAGA-----
HaRxLL73     GGGGTGTCGCAGAAAGAAGCTTCTTTAGCGCGTCGGGGGTGTGCGCAGAAAGAAGCTTCT
HaRxL39      AGGGTGCCGCCGAAAGA-----
HaRxL47      -----
HaRxL40      -----
HaRxL41      -----
HaRxL42      -----

HaRxL30      -----GCTG
HaRxL79      -----GCTG
HaRxLL73     GTTAGCGCGTCGGGGGTGTGCGCAGAAAGAGCTTCTGTTAGCGCGTCGGGGGTGTGCGCAG
HaRxL39      -----CATG
HaRxL47      -----
HaRxL40      -----
HaRxL41      -----
HaRxL42      -----
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HaRxL30 GTGGAGTCGAAGGATGCCGTGGTGAGATTGGAGAACTCTACAGCGCAACTTCCAGAAGAGT
 HaRxL79 GGGGAGTCGAAGGATGTCTGGTGAGATTGGAGAACTCTACAGCGCGACTTCCAGAAGAGT
 HaRxLL73 GAAGACCTGGAGGATGCCGAAGGCTGTCTGGTTAATCTACAGAGCAAGCTCGAGAAGGCT
 HaRxL39 GTGGAGGCGAAGGCTGTCTTGACGGAAATGGAGATTGTACGTACCATCGTTCGATGGGG
 HaRxL47 -----
 HaRxL40 -----
 HaRxL41 -----
 HaRxL42 -----

HaRxL30 ACGGAACGCATGATAATTGAGATGGCGAGGGATCTGACGTTTTCGGGGG-----
 HaRxL79 ACGGAACAAATGACAAATTGATATGGCGAGGGATCTGACGTTTTCGGGGG-----
 HaRxLL73 AACGAACGCTT---AACTACGGCGACGAGGGATCGACAGTATTGGAAGGAAAATGACCAA
 HaRxL39 TACCGATTCTTTTTATTCTGAAGGCGGCTTGGGAGGCGGCTTGGGAGG-----
 HaRxL47 -----
 HaRxL40 -----
 HaRxL41 -----TCGAAGG-----
 HaRxL42 -----TCGAAGG-----

HaRxL30 ----CAACTCGGAAGGTGGG--AAGACGGGAAATTACTTGGCTCCCGTT-----
 HaRxL79 ----CAACTCGGAAGGTGG--GACGGGGAATTACTTGGCTCCCGTT-----
 HaRxLL73 AATATGAATTGGGAAGGCGGC--AGGATGGGGAATTATCGGCTCCACT-----
 HaRxL39 ----CGGCTTGGGAAGGCGGCTTCCGAAGGCGAGTGAATTGACTAGCGTGCTGCGGAGACGT
 HaRxL47 -----TCGAAGGCGGCTTCCGAAGGCGAGTGAATTGACTAGGGTGCTGCTGAGACAC
 HaRxL40 -----TCGAAGGCGGCTTTAAAAAATAAATTTTATAGCGGCGCTGCGGACACCT
 HaRxL41 ----CGGCTTCCGAAGGCGGCTTTAAAAAATAAATTTTATAGGCGCTGTATAAACCT
 HaRxL42 ----CGGCTTCCGAAGGTGGCTTTAATAAAAAAATCTTTTATGGAGCTGGA-----
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HaRxL30 -----GAATCGTGTTTGCAGAACAGAAAGGATCGTGAA
 HaRxL79 -----GAATCGTGTTTGCAGGACAGAAAAATATCGTGAA
 HaRxLL73 -----GCAACTGAAGTGGCGACTAATGCAGAAAGAAATGTATCGTGAA
 HaRxL39 CAGTCGCA-----TAGACCTAACTTGCGAAAGCTGCACGAGGAAATCTATCAGATC
 HaRxL47 CAGTCGCA-----GAGACGTCACTTGCGAAAGATGCGCGAGGAATTCGATCAGGCC
 HaRxL40 ACTCCTAAGGCACGGCGGAAAGATAAGATGCAAAAGCTGCACGAGAGAAAAGTTGAGGAC
 HaRxL41 GATCCTGA-----TAGAGAGGAGATGCGAATGTGGTTCAAGAAAAAGTTGAGGCC
 HaRxL42 -----GAGACGTGAGGAACGAAAGCTGGACAAGAGAAATTTGAGGAC
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HaRxL30 TTGCTGGAGACCATGAGCAAAAGGGATGCCACGCTGCTAAGCTGGAAGAGTTGATCGCC
 HaRxL79 TGGCTGGAGACCATGAGCAAGAGGGATGCCACGCTGCTAAGCTGGAAGAGTTGATCGCC
 HaRxLL73 CTGCGGAAGGACATGCGCGAGGCGAAGGCCACCGCTGCTAAGCTGGCAAGGCCGATCGCC
 HaRxL39 TGGCTGG---CCGCATTGAGAGTGCAATTACAGTGAAAGAGCTGAAAAAGGAGGTCGAT
 HaRxL47 TGGCCGGTGCTCACATTGAGACTAGTGTCGAATTGAAAGTGCTGAAAAAGTTCGATCGGC
 HaRxL40 CA-----CCGTAAACGAGAGGAAAGT-----GAGCTGGCAAGTTGGTCGCC
 HaRxL41 CAC--GA---CCGTAAACAGAGGAAAGT-----GAGCTGGTAAAGTTGGTCGCC
 HaRxL42 TACCTGG---CCGTAAACGGGAAAGAACT-----
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HaRxL30 GCGGCGAAAAAAGGTAGACGACATCACTGCGGCGATT-----
 HaRxL79 GCGGCGAAAAAAGGGTAGACGGCATCAATCCGGCGATT-----
 HaRxLL73 GAGGCGAAAAAAGGTAGACGACATCAATGCGGCGATTCAAGCAAGAAAGGAATACC---
 HaRxL39 AAGTTACATAAAAAAGGTAAATGGACTTCAGTGCGGCGATCGAGGCTAAGAAAAGTGGCCCCCT
 HaRxL47 GAGATAAATGAAAAAGCTAAATGGACCTCATTGCGGTGATTGAGGCTAAGAAAAGTGGCCCCCT
 HaRxL40 GAGGTGGAAAAAAGG-----
 HaRxL41 GAGGTGGAAAAAAGG-----
 HaRxL42 -----CAA-----
 * *** *

HaRxL30 -----TAA
 HaRxL79 -----TAA
 HaRxLL73 -----CTGTCGATATAG
 HaRxL39 AGCGATTTCGTTAGACCGTCAGAGTGA
 HaRxL47 CGCGATTTCGTTAGACCGTCAGAGTGA
 HaRxL40 -----TAA
 HaRxL41 -----TAA
 HaRxL42 -----TGA
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Details on Illumina sequence reads used for the comparative genomics section in Chapter 4.

Flow Cell	Run ID	Lane	Sample	Paired End?	Insert size (calculated by MAQ)	Race	Type	Concentration	Length	# Reads	bp	# Mapped	%	# Mapped as pair	%	Map Params
30H8TAAXX	ID62	1	Hpa Waco9	PE	334.305772 +/- 45.584579	waco9	dna	6pM	36	16685148	600665328	15095272	90.50%	13986920	92.70%	n3e100a500
30H8TAAXX	ID62	2	Hpa Hind2	PE	352.198133 +/- 43.512337	hind2	dna	6pM	36	18790428	676455408	18057108	96.10%	16795632	93.00%	n3e100a500
30H8TAAXX	ID62	3	Hpa Emco5	PE	359.373364 +/- 48.609409	emco5	dna	6pM	36	18497806	665921016	16666120	90.10%	15510497	93.10%	n3e100a500
30DFYAAXX	ID64	1	Hpa Hind2	PE	348.531576 +/- 46.663678	hind2	dna	6pM	36	13339720	480229920	12843674	96.30%	11945476	93.00%	n3e100a500
30DFYAAXX	ID64	2	Hpa Hind2	PE	348.368804 +/- 47.207299	hind2	dna	6pM	36	11995426	431835336	11531996	96.10%	10716573	92.90%	n3e100a500
30DFYAAXX	ID64	3	Hpa Hind2	PE	348.436872 +/- 47.151158	hind2	dna	6pM	36	14346168	516462048	13800882	96.20%	12842010	93.10%	n3e100a500
30DFYAAXX	ID64	5	Hpa Emco5	PE	355.161022 +/- 53.034060	emco5	dna	6pM	36	13642658	491135688	12293546	90.10%	11434248	93.00%	n3e100a500
30DFYAAXX	ID64	6	Hpa Emco5	PE	355.096081 +/- 53.164785	emco5	dna	6pM	36	13705996	493415856	12355664	90.10%	11492812	93.00%	n3e100a500
30DFYAAXX	ID64	7	Hpa Emco5	PE	355.052176 +/- 53.120832	emco5	dna	6pM	36	13377394	481586184	12055990	90.10%	11211957	93.00%	n3e100a500
30DFYAAXX	ID64	8	Hpa Emoy2	PE	339.052529 +/- 43.744176	emoy2	dna	6pM	36	11039680	397428480	10371172	93.90%	9606994	92.60%	n3e100a500
30DYGAAXX	ID66	3	Hpa Emoy2	PE	338.813991 +/- 43.742254	emoy2	dna	6pM	36	12317750	443439000	11577286	94.00%	10789809	93.20%	n3e100a500
30DW9AAXX	ID69	1	Hpa Emoy2	PE	338.685350 +/- 43.706918	emoy2	dna	6pM	36	12727044	458173584	11983134	94.20%	11164556	93.20%	n3e100a500
30DW9AAXX	ID69	2	Hpa Emoy2	PE	338.568591 +/- 44.134278	emoy2	dna	6pM	36	11085642	399083112	10421860	94.00%	9697772	93.10%	n3e100a500
30DW9AAXX	ID69	3	Hpa Emoy2	PE	338.675867 +/- 43.822840	emoy2	dna	6pM	36	9794370	352597320	9208542	94.00%	8539768	92.70%	n3e100a500
30DW9AAXX	ID69	5	Hpa Emoy2	PE	338.877557 +/- 43.778193	emoy2	dna	6pM	36	13776136	495940896	12969038	94.10%	12094156	93.30%	n3e100a500
30DW9AAXX	ID69	6	Hpa Cala2	PE	327.371724 +/- 46.945084	cala2	dna	6pM	36	14797458	532708488	6289980	42.50%	5853788	93.10%	n3e100a500
30DW9AAXX	ID69	7	Hpa Cala2	PE	327.443553 +/- 46.651466	cala2	dna	6pM	36	14879458	535660488	6348260	42.70%	5907826	93.10%	n3e100a500
30DW9AAXX	ID69	8	Hpa Cala2	PE	327.378922 +/- 46.903094	cala2	dna	6pM	36	12956184	466422624	5559592	42.90%	5168738	93.00%	n3e100a500
30DHHAAXX	ID71	1	Hpa Cala2	PE	327.043908 +/- 46.746053	cala2	dna	6pM	36	12591470	453292920	5492170	43.60%	5106118	93.00%	n3e100a500
30DHHAAXX	ID71	2	Hpa Maks9	PE	333.627462 +/- 39.240630	maks9	dna	6pM	36	11398246	410336856	8873846	77.90%	8182076	92.20%	n3e100a500
30DHHAAXX	ID71	3	Hpa Maks9	PE	333.914869 +/- 38.790438	maks9	dna	6pM	36	12808634	461110824	9970848	77.80%	9209107	92.40%	n3e100a500
30DHHAAXX	ID71	5	Hpa Maks9	PE	334.095602 +/- 38.827157	maks9	dna	6pM	36	12943886	465979896	10033954	77.50%	9269401	92.40%	n3e100a500
30E09AAXX	ID74	1	Hpa Noco2	PE	336.995617 +/- 34.091977	noco2	dna	6pM	36	12692042	456913512	11798836	93.00%	11017641	93.40%	n3e100a500
30E09AAXX	ID74	2	Hpa Noco2	PE	337.123654 +/- 34.208484	noco2	dna	6pM	36	13959594	502545384	12977324	93.00%	12129499	93.50%	n3e100a500
30E09AAXX	ID74	3	Hpa Noco2	PE	337.087019 +/- 34.268842	noco2	dna	6pM	36	14078192	506814912	13075734	92.90%	12218574	93.40%	n3e100a500

30E09AAXX	ID74	5	Hpa Noco2	PE	337.310454 +/- 34.094262	noco2	dna	6pM	36	14282786	514180296	13252360	92.80%	12388198	93.50%	n3e100a500
30E09AAXX	ID74	8	Hpa Maks9	PE	334.466367 +/- 37.941812	maks9	dna	6pM	36	13410342	482772312	10453976	78.00%	9647107	92.30%	n3e100a500
30DWEAAXX	ID75	1	Hpa Waco9	PE	330.821535 +/- 50.870072	waco9	dna	6pM	36	13330010	479880360	12103674	90.80%	11212096	92.60%	n3e100a500
30DWEAAXX	ID75	2	Hpa Waco9	PE	330.629955 +/- 51.417488	waco9	dna	6pM	36	14006684	504240624	12716900	90.80%	11788424	92.70%	n3e100a500
30DWEAAXX	ID75	3	Hpa Waco9	PE	329.992848 +/- 52.163552	waco9	dna	6pM	36	9837618	354154248	8924588	90.70%	8238468	92.30%	n3e100a500
30DWEAAXX	ID75	5	Hpa Waco9	PE	331.021138 +/- 50.880626	waco9	dna	6pM	36	13552462	487888632	12268596	90.50%	11369725	92.70%	n3e100a500
30DWEAAXX	ID75	6	Hpa Waco9	PE	331.167094 +/- 51.013012	waco9	dna	6pM	36	14329742	515870712	12972372	90.50%	12026029	92.70%	n3e100a500
30Y4AAAXX	ID79	2	Hpa Emoy2	PE	339.291135 +/- 42.760396	emoy2	dna	6pM	36	13849592	498585312	13013004	94.00%	12074329	92.80%	n3e100a500
30Y4AAAXX	ID79	3	Hpa Emoy2	PE	339.348849 +/- 42.578734	emoy2	dna	6pM	36	14059650	506147400	13126898	93.40%	12115612	92.30%	n3e100a500
30Y7LAAXX	ID80	1	Hpa Noco2	PE	337.236591 +/- 33.780184	noco2	dna	6pM	36	16274756	585891216	15058918	92.50%	13986140	92.90%	n3e100a500
30Y7LAAXX	ID80	2	Hpa Noco2	PE	337.119928 +/- 33.892590	noco2	dna	6pM	36	14117014	508212504	13060484	92.50%	12071628	92.40%	n3e100a500
30Y7LAAXX	ID80	3	Hpa Cala2	PE	327.009732 +/- 46.690504	cala2	dna	6pM	36	9715162	349745832	4184672	43.10%	3726379	89.00%	n3e100a500
30UGJAAXX	ID87	3	Hpa Waco9	PE	332.110200 +/- 50.398237	waco9	dna	8pM	36	14153536	509527296	12731634	90.00%	11472012	90.10%	n3e100a500
30UGJAAXX	ID87	4	Hpa Waco9	PE	331.922077 +/- 50.975731	waco9	dna	8pM	36	13976824	503165664	12592714	90.10%	11481291	91.20%	n3e100a500
30UGJAAXX	ID87	5	Hpa Hind2	PE	349.398150 +/- 46.992682	hind2	dna	8pM	36	13518100	486651600	12959370	95.90%	12019154	92.70%	n3e100a500
30UGJAAXX	ID87	6	Hpa Hind2	PE	349.466094 +/- 46.938720	hind2	dna	8pM	36	13838710	498193560	13271042	95.90%	12309314	92.80%	n3e100a500
30UGJAAXX	ID87	7	Hpa Hind2	PE	349.527070 +/- 46.807906	hind2	dna	8pM	36	14034950	505258200	13458644	95.90%	12484770	92.80%	n3e100a500
313UMAAXX	ID88	1	Hpa Emco5	PE	355.199558 +/- 53.455711	emco5	dna	9pM	36	16440814	591869304	14760388	89.80%	13712630	92.90%	n3e100a500
313UMAAXX	ID88	2	Hpa Emco5	PE	355.669794 +/- 52.755553	emco5	dna	9pM	36	16900940	608433840	15174842	89.80%	14091510	92.90%	n3e100a500
313UMAAXX	ID88	3	Hpa Emco5	PE	355.876003 +/- 52.436018	emco5	dna	9pM	36	16038510	577386360	14401108	89.80%	13363382	92.80%	n3e100a500
313UMAAXX	ID88	4	Hpa Emco5	PE	355.857802 +/- 52.516396	emco5	dna	9pM	36	15969604	574905744	14334176	89.80%	13242956	92.40%	n3e100a500
313UMAAXX	ID88	5	Hpa Hind2	PE	349.195154 +/- 46.825088	hind2	dna	9pM	36	16978272	611217792	16243064	95.70%	14906746	91.80%	n3e100a500
42UBDAAXX	ID106	4	Hpa Emco5	PE	356.988865 +/- 48.284072	emco5	dna	12pM	76	29750734	2261055784	25989400	87.40%	23624272	90.90%	n3e100a500
42UBDAAXX	ID106	5	Hpa Cala2	PE	328.725489 +/- 43.721368	cala2	dna	12pM	76	36247384	2754801184	14491106	40.00%	13256142	91.50%	n3e100a500
313VEAAXX	ID108	2	Hpa Noco2	PE	338.662604 +/- 32.772048	noco2	dna	12pM	76	30669042	2330847192	28020922	91.40%	26045020	92.90%	n3e100a500
313VEAAXX	ID108	3	Hpa Maks9	PE	335.986928 +/- 36.052768	maks9	dna	12pM	76	29857228	2269149328	22421842	75.10%	20333987	90.70%	n3e100a500