

Table S3. Specifics of the IS elements IS407 A, ISBma 1, and ISBma 2 in the *B. mallei* strains.

IS element	Role	Strain	Strain	position	homologous IS type										
Chromosome 1															
IS 407 A															
						5'-ext	5'-IR	orfA	intergenic region	orfB	3'-IR	3'-ext	5'-DR	3'-DR	± duplication
						TGACCTGCCCCCT			AGGGGGCAGGTCA						
2*Chr1_89_IS407A_A	N	fmh	2	1003118-1004353	Chr1 IS407A	GCCCC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GCGCGGA	CCAG	GCGC	N	
7*Chr1_76_IS407A_7*Chr1_84b_IS407A_A	D-R	NCTC_10247	7	1003311-1004546	Chr1 IS407A	CGGGA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGGGC	GCCG	GTCG	N	
2*Chr1_91_IS407A_B	N	fmh	2	1006858-1008093	Chr1 IS407A	GACGC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGACC	TGTC	TGTC	Y	
5*Chr1_96_IS407A_5*Chr1_97_IS407A_A	D	ATCC_10399	5	1008495-1009730	Chr1 IS407A	GGCAC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	ACCGCCC	CCCC	ACCG	N	
3*Chr1_89_IS407A_A	N	JHU	3	1011927-1013162	Chr1 IS407A	GCCCC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GCGCGGA	CCAG	GCGC	N	
3*Chr1_91_IS407A_B	N	JHU	3	1015667-1016902	Chr1 IS407A	GACGC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGACC	TGTC	TGTC	Y	
6*Chr1_126a_IS407A_A	R	NCTC_10229	6	1024057-1025292	Chr1 IS407A	TGCCG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	CCTGCGA	AAAA	CCTG	N	
8*Chr1_78_IS407A_A	N	2002721280	8	1024801-1026036	Chr1 IS407A	CAGCA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTAGCTG	GTAG	GTAG	Y	
6*Chr1_43b_IS407A_A	D-R	NCTC_10229	6	1026593-1027828	Chr1 IS407A	AAAAA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	CGGGCG	AAGC	GCGG	N	
10*Chr1_89_IS407A_A	N	PRL20	10	1031797-1033032	Chr1 IS407A	GAGCC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	CTGGATG	CGCA	CTGG	N	
10*Chr1_92_IS407A_C	N	PRL20	10	1037784-1039019	Chr1 IS407A	CGCGC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	TTCTGGC	TTGC	TTGC	Y	
2*Chr1_77_IS407A_2*Chr1_94a_IS407A_A	D-R	fmh	2	1040287-1041522	Chr1 IS407A	ATGAT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	AACCGAT	AGGT	AACC	N	
7*Chr1_71_IS407A_7*Chr1_87a_IS407A_A	D-R	NCTC_10247	7	1044544-1045779	Chr1 IS407A	GAGCG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	TCGCTTCT	GAGC	TCGC	N	
3*Chr1_77_IS407A_3*Chr1_94a_IS407A_A	D-R	JHU	3	1049331-1050566	Chr1 IS407A	ATGAT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	AACCGAT	AGGT	AACC	N	
5*Chr1_95_IS407A_A	N	ATCC_10399	5	1051433-1052668	Chr1 IS407A	GCGCG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GCCCGCC	GATG	GCCC	N	
6*Chr1_42b_IS407A_6*Chr1_43a_IS407A_6*Chr1_45b_IS407A_A	D-R	NCTC_10229	6	1053882-1055117	Chr1 IS407A	GGCCT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GCGGTGC	TGCG	GCGG	N	
6*Chr1_136_IS407A_6*Chr1_45a_IS407A_A	D-R	NCTC_10229	6	1067579-1068814	Chr1 IS407A	GATCG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GATGCTC	GAAC	GATG	N	
10*Chr1_77_IS407A_10*Chr1_94a_IS407A_A	D-R	PRL20	10	1068513-1069748	Chr1 IS407A	TCAGA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	ACCTGTCA	GGTT	ACCT	N	
4*Chr1_74_IS407A_4*Chr1_75_IS407A_A	D	gb8_horse_4	4	1073497-1074418	Chr1 IS407A	#ISBma	~~~~~	~~~~~	GCCCATGCCACGCAGCA	CGAGATG	AGGGACTTTGCTAGAA	GTCATGC	#	GGTC	N.D.
4*Chr1_76_IS407A_4*Chr1_87b_IS407A_A	D-R	gb8_horse_4	4	1078636-1079871	Chr1 IS407A	CGGGA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	CGAGCGC	GCCG	CGAG	N	
1*Chr1_74_IS407A_1*Chr1_75_IS407A_A	D	ATCC_23344	1	1080184-1081105	Chr1 IS407A	#ISBma	~~~~~	~~~~~	GCCCATGCCACGCAGCA	CGAGATG	AGGGACTTTGCTAGAA	GTCATGC	#	GGTC	N.D.
1*Chr1_76_IS407A_1*Chr1_87b_IS407A_A	D-R	ATCC_23344	1	1085323-1086558	Chr1 IS407A	CGGGA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	CGAGCGC	GCCG	CGAG	N	
5*Chr1_69_IS407A_5*Chr1_94b_IS407A_A	D-R	ATCC_10399	5	1109938-1111173	Chr1 IS407A	GGCGA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	TGACGTTG	CTGG	TGAG	N	
4*Chr1_89_IS407A_A	N	gb8_horse_4	4	1116480-1117715	Chr1 IS407A	GCCCC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GCGCGGA	CCAG	GCGC	N	
4*Chr1_91_IS407A_B	N	gb8_horse_4	4	1120220-1121455	Chr1 IS407A	GACGC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGACC	TGTC	TGTC	Y	
1*Chr1_89_IS407A_A	N	ATCC_23344	1	1123337-1124572	Chr1 IS407A	GCCCC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGACC	CCAG	GCGC	N	
1*Chr1_91_IS407A_B	N	ATCC_23344	1	1127077-1128312	Chr1 IS407A	GACGC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGACC	TGTC	TGTC	Y	
8*Chr1_77_IS407A_8*Chr1_94a_IS407A_A	D-R	2002721280	8	1132308-1133543	Chr1 IS407A	ATGAT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	AACCGAT	AGGT	AACC	N	
2*Chr1_78_IS407A_2*Chr1_80_IS407A_A	D	fmh	2	1150542-1151777	Chr1 IS407A	GGGAC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTAGCTG	GTCA	GTAG	N	
6*Chr1_71_IS407A_6*Chr1_87a_IS407A_A	D-R	NCTC_10229	6	115281-116516	Chr1 IS407A	GAGCG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	TCGCTTCT	GAGC	TCGC	N	
4*Chr1_77_IS407A_4*Chr1_94a_IS407A_A	D-R	gb8_horse_4	4	1153315-1154550	Chr1 IS407A	ATGAT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	AACCGAT	AGGT	AACC	N	
1*Chr1_77_IS407A_1*Chr1_94a_IS407A_A	D-R	ATCC_23344	1	1160172-1161407	Chr1 IS407A	GCAAG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	AACCGAT	AGGT	AACC	N	
2*Chr1_81_IS407A_B	N	fmh	2	1160942-1162177	Chr1 IS407A	GCAAG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GGGCCAT	GGGC	GGGC	Y	
3*Chr1_78_IS407A_3*Chr1_80_IS407A_A	D	JHU	3	1161038-1162273	Chr1 IS407A	GGGAC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTAGCTG	GTCA	GTAG	N	
7*Chr1_68_IS407A_7*Chr1_69_IS407A_A	D	NCTC_10247	7	1163594-1164829	Chr1 IS407A	CCTAA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	CAGTTTGT	ACGT	CAGT	N	
8*Chr1_89_IS407A_A	N	2002721280	8	1167906-1169141	Chr1 IS407A	GCGAA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	CTGGATG	CCCG	CTGG	N	
3*Chr1_81_IS407A_B	N	JHU	3	1171909-1173144	Chr1 IS407A	GCAAG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GGGCCAT	GGGC	GGGC	Y	
10*Chr1_78_IS407A_10*Chr1_80_IS407A_A	D	PRL20	10	1172927-1174162	Chr1 IS407A	CAGCA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTAGCTG	GTAG	GTAG	Y	
2*Chr1_83_IS407A_A	N	fmh	2	1174009-1175244	Chr1 IS407A	CAAGT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	ATCAGGC	GGAT	ATCA	N	
9*Chr1_64a_IS407A_A	N	SAVP1	9	1180766-1182001	Chr1 IS407A	CCAGA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	TCGCTTCT	CTTG	TCGC	N	
5*Chr1_20_IS407A_5*Chr1_21_IS407A_A	D	ATCC_10399	5	118297-119532	Chr1 IS407A	ATGTC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCACGI	CCGG	GTCC	N	
3*Chr1_83_IS407A_A	N	JHU	3	1185197-1186432	Chr1 IS407A	CAAGT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	ATCAGGC	GGAT	ATCA	N	
2*Chr1_84a_IS407A_A	N	fmh	2	1189127-1190362	Chr1 IS407A	GTCGC	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGGGC	AAAG	GTCG	N	
10*Chr1_83_IS407A_A	N	PRL20	10	1192001-1193236	Chr1 IS407A	TTACG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	ATCCACCC	TGAT	ATCC	N	
3*Chr1_84a_IS407A_A	N	JHU	3	1200315-1201550	Chr1 IS407A	GTGCG	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGGGC	AAAG	GTCG	N	
8*Chr1_75_IS407A_A	D-R	2002721280	8	1205181-1206102	Chr1 IS407A	#ISBma	~~~~~	~~~~~	GCCCATGCCACGCAGCA	CGAGATG	AGGGACTTTGCTAGAA	CCATGGC	#	CCAT	N.D.
10*Chr1_84a_IS407A_A	N	PRL20	10	1209165-1210140	Chr1 IS407A	CGCGT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	#	#contig_br	CGAC	#con	N	
8*Chr1_76_IS407A_8*Chr1_84b_IS407A_8*Chr1_87b_IS407A_A	D-R	2002721280	8	1210321-1211556	Chr1 IS407A	CGGGA	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GTCGGGC	GCCG	GTCG	N	
5*Chr1_71_IS407A_5*Chr1_87a_IS407A_A	D-R	ATCC_10399	5	1229015-1230250	Chr1 IS407A	TTGAT	TGACCTGCCCCCTACA	ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG	TGTTGGCC	AGGGACTTTGCTAGAA	GCTCGAC	GCGA	GCTC	N	

7*Chr1_99_IS407A	7*Chr1_67_IS407A_A	D-R	NCTC_10247	7	1230358-1231593	Chr1	IS407A	TTCATATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATCGAGI	GTGG	GATC	N
2*Chr1_71_IS407A	2*Chr1_87a_IS407A_A	D-R	fmh	2	1233629-1234864	Chr1	IS407A	TTCGATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTCGAC	GCGA	GCTC	N
4*Chr1_21_IS407A	4*Chr1_8_IS407A_A	D-R	gb8_horse_4	4	123374-124609	Chr1	IS407A	GGCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCACG1	GACG	GTCC	N
1*Chr1_21_IS407A	1*Chr1_8_IS407A_A	D-R	ATCC_23344	1	123747-124982	Chr1	IS407A	GGGCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCACG1	GACG	GTCC	N
3*Chr1_71_IS407A	3*Chr1_87a_IS407A_A	D-R	JHU	3	1241561-1242796	Chr1	IS407A	TTCGATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCAGC	GCGA	GCTC	N
9*Chr1_65a_IS407A_A		N	SAVP1	9	1242873-1244108	Chr1	IS407A	GCGACTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGGGGGCA	GAAT	GGGG	N
10*Chr1_71_IS407A	10*Chr1_87a_IS407A_A	D-R	PRL20	10	1249788-1251023	Chr1	IS407A	TTCGATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTCGAC	GCGA	GCTC	N
8*Chr1_71_IS407A	8*Chr1_87a_IS407A_A	D-R	2002721280	8	1250846-1252081	Chr1	IS407A	GAGCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCGTTCT	GAGC	TCGN	N
4*Chr1_78_IS407A	4*Chr1_80_IS407A_A	D	gb8_horse_4	4	1259592-1260734	Chr1	IS407A	GGGACTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTAGCTG	GTCA	GTAG	N
6*Chr1_143a_IS407A_B		N	NCTC_10229	6	1262978-1264213	Chr1	IS407A	TTCGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCAAGC1	ATCA	ATCA	Y
1*Chr1_78_IS407A	1*Chr1_80_IS407A_A	D	ATCC_23344	1	1267713-1268948	Chr1	IS407A	GGGACTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTAGCTG	GTCA	GTAG	N
4*Chr1_81_IS407A_B		N	gb8_horse_4	4	1269471-1270706	Chr1	IS407A	GCAAGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGGGCCAT	GGGC	GGGC	Y
5*Chr1_84a_IS407A_A		N	ATCC_10399	5	1270273-1271508	Chr1	IS407A	GTGCCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCGGC1	AAAG	GTCC	N
1*Chr1_81_IS407A_B		N	ATCC_23344	1	1277696-1278931	Chr1	IS407A	GCAAGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGGGCCAT	GGGC	GGGC	Y
4*Chr1_83_IS407A_A		N	gb8_horse_4	4	1282759-1283994	Chr1	IS407A	CAAGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCAAGC1	GGAT	ATCA	N
5*Chr1_83_IS407A_A		N	ATCC_10399	5	1285391-1286626	Chr1	IS407A	CAAGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCAAGC1	GGAT	ATCA	N
1*Chr1_83_IS407A_A		N	ATCC_23344	1	1290984-1292219	Chr1	IS407A	CAAGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCAAGC1	GGAT	ATCA	N
9*Chr1_98_IS407A	9*Chr1_66_IS407A_A	D-R	SAVP1	9	1293994-1295229	Chr1	IS407A	CTCGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTAGGCA	CCCG	GTAG	N
4*Chr1_84a_IS407A_A		N	gb8_horse_4	4	1297816-1299051	Chr1	IS407A	GTGCCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCGGC1	AAAG	GTCC	N
5*Chr1_81_IS407A_B		N	ATCC_10399	5	1298670-1299905	Chr1	IS407A	GCAAGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGGGCCAT	GGGC	GGGC	Y
1*Chr1_84a_IS407A_A		N	ATCC_23344	1	1306102-1307337	Chr1	IS407A	GTGCCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCGGC1	AAAG	GTCC	N
5*Chr1_79_IS407A	5*Chr1_80_IS407A_A	D	ATCC_10399	5	1308729-1309964	Chr1	IS407A	GGGACTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCAAGCAG1	GTCA	CAAG	N
6*Chr1_145_IS407A_A		N	NCTC_10229	6	1331417-1332652	Chr1	IS407A	AAGCCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGGCTTCG1	ATAG	GGCT	N
4*Chr1_71_IS407A	4*Chr1_87a_IS407A_A	D-R	gb8_horse_4	4	1338734-1339969	Chr1	IS407A	TTCGATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTCGAC	GCGA	GCTC	N
7*Chr1_43b_IS407A_A		R	NCTC_10247	7	134379-135614	Chr1	IS407A	AAAAATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTGGCGG	AAGC	CGGG	N
1*Chr1_71_IS407A	1*Chr1_87a_IS407A_A	D-R	ATCC_23344	1	1347348-1348583	Chr1	IS407A	TTCGATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCAGC1	GCGA	GCTC	N
5*Chr1_78_IS407A_A		N	ATCC_10399	5	1351723-1352958	Chr1	IS407A	CAGCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTAGCTG	GTAG	GTAG	Y
9*Chr1_96_IS407A	9*Chr1_97_IS407A_A	D	SAVP1	9	1352573-1353808	Chr1	IS407A	GGCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTGGCC1	CCCC	CCCC	N
2*Chr1_68_IS407A	2*Chr1_69_IS407A_A	D	fmh	2	1353867-1355102	Chr1	IS407A	CCTAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCAGTTT1	ACGT	CCAG	N
3*Chr1_68_IS407A	3*Chr1_69_IS407A_A	D	JHU	3	1363269-1364504	Chr1	IS407A	CCTAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCAGTTT1	ACGT	CCAG	N
7*Chr1_126a_IS407A_A		R	NCTC_10247	7	136915-138150	Chr1	IS407A	TGCGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTGGCA1	AAAA	CCTG	N
8*Chr1_68_IS407A	8*Chr1_69_IS407A_A	D	2002721280	8	1369943-1371178	Chr1	IS407A	CCTAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCAGTTT1	ACGT	CCAG	N
9*Chr1_95_IS407A_A		N	SAVP1	9	1395694-1396929	Chr1	IS407A	GGCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCCGCC1	GATG	GCCC	N
4*Chr1_10_IS407A_A		N	gb8_horse_4	4	140426-141661	Chr1	IS407A	TCCGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCATATG1	ACAT	CCCT	N
10*Chr1_68_IS407A	10*Chr1_72_IS407A_A	D-R	PRL20	10	1412924-1414159	Chr1	IS407A	CCAGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTGTGCT	CGCG	ACGT	N
1*Chr1_10_IS407A_A		N	ATCC_23344	1	141323-142558	Chr1	IS407A	TCCGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCATATG1	ACAT	CCCT	N
3*Chr1_10_IS407A_A		N	JHU	3	14148-15383	Chr1	IS407A	TCCGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCATATG1	ACAT	CCCT	N
2*Chr1_99_IS407A	2*Chr1_67_IS407A_A	D-R	fmh	2	1420660-1421895	Chr1	IS407A	TTCATATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGATCGAGI	GTGG	GATC	N
3*Chr1_99_IS407A	3*Chr1_67_IS407A_A	D-R	JHU	3	1430062-1431297	Chr1	IS407A	TTCATATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGATCGAGI	GTGG	GATC	N
8*Chr1_99_IS407A	8*Chr1_67_IS407A_A	D-R	2002721280	8	1436504-1437739	Chr1	IS407A	TTCATATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCTGATT1	GTGG	ACCT	N
8*Chr1_10_IS407A_A		N	2002721280	8	14396-15631	Chr1	IS407A	CGCCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCATATG1	CCCT	CCCT	Y
9*Chr1_75_IS407A	9*Chr1_94b_IS407A_A	D-R	SAVP1	9	1454166-1455087	Chr1	IS407A	#ISBma~~~~~ GCCCATGCCACGAGCA(CGAGATG)AGGGACTTTGCTAGAAAGCTGTGCT #	ACGT	N.D.	
4*Chr1_68_IS407A	4*Chr1_69_IS407A_A	D	gb8_horse_4	4	1456856-1458091	Chr1	IS407A	CCTAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCAGTTT1	ACGT	CCAG	N
2*Chr1_10_IS407A_A		N	fmh	2	14571-15806	Chr1	IS407A	TCCGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCATATG1	ACAT	CCCT	N
5*Chr1_77_IS407A	5*Chr1_94a_IS407A_A	D-R	ATCC_10399	5	1459172-1460407	Chr1	IS407A	ATGATGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCAGT1	AGGT	AACC	N
9*Chr1_76_IS407A	9*Chr1_87b_IS407A_A	D-R	SAVP1	9	1459306-1460541	Chr1	IS407A	AATGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCGACG1	CTCG	CGGC	N
9*Chr1_158_IS407A_A		D-R	SAVP1	9	14627-15862	Chr1	IS407A	AGCGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTCCAC1	TGTT	AATC	N
1*Chr1_68_IS407A	1*Chr1_69_IS407A_A	D	ATCC_23344	1	1466275-1467510	Chr1	IS407A	CCTAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCAGTTT1	ACGT	CCAG	N
5*Chr1_10_IS407A_A		N	ATCC_10399	5	14735-15970	Chr1	IS407A	CGCCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCATATG1	CCCT	CCCT	Y
10*Chr1_99_IS407A	10*Chr1_67_IS407A_A	D-R	PRL20	10	1479698-1480933	Chr1	IS407A	TTCATATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGATCGAGI	GTGG	GATC	N
5*Chr1_91_IS407A_B		N	ATCC_10399	5	1492267-1493502	Chr1	IS407A	GAGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTGTGACC1	TGTC	TATC	Y
5*Chr1_91_IS407A_A		N	ATCC_10399	5	1496007-1497242	Chr1	IS407A	GCCCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGGCGCGG1	CCAG	GGGC	N
9*Chr1_89_IS407A_A		N	SAVP1	9	1497321-1498556	Chr1	IS407A	GAGCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTGGATG1	GCGA	CTGG	N
9*Chr1_93_IS407A_C		N	SAVP1	9	1503308-1504543	Chr1	IS407A	CGCGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGTTCGTGCC1	TTCG	TTCG	Y
4*Chr1_99_IS407A	4*Chr1_67_IS407A_A	D-R	gb8_horse_4	4	1523634-1524869	Chr1	IS407A	TTCATATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGATCGAGI	GTGG	GATC	N
1*Chr1_99_IS407A	1*Chr1_67_IS407A_A	D-R	ATCC_23344	1	1533068-1534303	Chr1	IS407A	TTCATATGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGATCGAGI	GTGG	GATC	N
5*Chr1_76_IS407A	5*Chr1_87b_IS407A_A	D-R	ATCC_10399	5	1534024-1535259	Chr1	IS407A	CGGGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCGAGCG1	GCCC	CGAG	N
9*Chr1_77_IS407A	9*Chr1_94a_IS407A_A	D-R	SAVP1	9	1534145-1535380	Chr1	IS407A	ATGATGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAAGCCAGT1	AGGT	AACC	N

10*Chr1_54_IS407;10*Chr1_58b_IS407A_A	D-R	PRL20	10	1994927-1996162	Chr1	IS407A	CGTCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGAACAG; GTGA CGAA N
5*Chr1_111_IS407;5*Chr1_64a_IS407A_A	D-R	ATCC_10399	5	2000844-2002079	Chr1	IS407A	CTTGTTTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTGCTGCC TCGC CTGC N
10*Chr1_53b_IS40 10*Chr1_56_IS407A_A	D-R	PRL20	10	2000800-2009315	Chr1	IS407A	TGGAA/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACGGCGA; GCGG ACGG N
6*Chr1_154b_IS407A_A	R	NCTC_10229	6	2019764-2020999	Chr1	IS407A	CGCGC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AACCTCC GCTT AAC N
8*Chr1_115a_IS407;8*Chr1_132b_IS407A_A	R	2002721280	8	2021618-2022853	Chr1	IS407A	TTCCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGACGGG GATG GGAC N
10*Chr1_48_IS407;10*Chr1_55_IS407A_A	D-R	PRL20	10	2021618-2022853	Chr1	IS407A	ATCAC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(TTCCGGCC GCGG TTCC N
5*Chr1_62_IS407A_C	N	ATCC_10399	5	2032228-2033345	Chr1	IS407A	#contig ~~~~~~ ACTTAATTAATTAAGTGTGTCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTTGTGNF # #contig_break N.D.
7*Chr1_132a_IS407;7*Chr1_58a_IS407A_A	R	NCTC_10247	7	2032685-2033920	Chr1	IS407A	ACGCT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTTCCGTC GGAC GTTC N
4*Chr1_48_IS407A 4*Chr1_58b_IS407A_A	D-R	gb8_horse_4	4	2039586-2040821	Chr1	IS407A	CGTCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GAAGTGG GTGA GAAG N
10*Chr1_132b_IS40 10*Chr1_47b_IS407A_A	R	PRL20	10	2040335-2041570	Chr1	IS407A	TGAGG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGACGGG CTTT GGAC N
1*Chr1_48_IS407A 1*Chr1_58b_IS407A_A	D-R	ATCC_23344	1	2051541-2052776	Chr1	IS407A	CGTCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GAAGTGG GTGA GAAG N
6*Chr1_20_IS407A 6*Chr1_21_IS407A_A	D	NCTC_10229	6	2052526-2053761	Chr1	IS407A	ATGTC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTCCACG1 CCGG GTCC N
4*Chr1_132b_IS40 4*Chr1_47b_IS407A_A	R	gb8_horse_4	4	2058486-2059721	Chr1	IS407A	TGAGG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGACGGG CTTT GGAC N
7*Chr1_47a_IS407;7*Chr1_57_IS407A_A	D-R	NCTC_10247	7	2060132-2061367	Chr1	IS407A	TCCGC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGAC AAGG CGTG N
1*Chr1_132b_IS40 1*Chr1_47b_IS407A_A	R	ATCC_23344	1	2070441-2071676	Chr1	IS407A	TGAGG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGACGGG CTTT GGAC N
2*Chr1_126b_IS40 2*Chr1_135_IS407A_A	D-R	fmh	2	2072203-2073438	Chr1	IS407A	TGGAC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAATCAG1 TCGC CAAT N
5*Chr1_61_IS407A_B	N	ATCC_10399	5	2078643-2079878	Chr1	IS407A	TTTGCT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCCCAC1 CCCC CCCC Y
7*Chr1_43a_IS407;7*Chr1_45b_IS407A_A	R	NCTC_10247	7	2084226-2085461	Chr1	IS407A	TTCTG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATTTGCC CCGC CATT N
3*Chr1_126b_IS40 3*Chr1_135_IS407A_A	D-R	JHU	3	2087663-2088898	Chr1	IS407A	TGGAC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAATCAG1 TCGC CAAT N
6*Chr1_18a_IS407A_A	N	NCTC_10229	6	2097220-2098455	Chr1	IS407A	CGTCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CACCGG1 CACC CACC Y
8*Chr1_134_IS407A_B	N	2002721280	8	2098656-2099891	Chr1	IS407A	CTTAT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCACGGG GCAC GCAC Y
7*Chr1_42b_IS407A_A	N	NCTC_10247	7	2105147-2106382	Chr1	IS407A	GCGCT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCCCAC1 TGCG CCCC N
7*Chr1_136_IS407;7*Chr1_45a_IS407A_A	D-R	NCTC_10247	7	2118845-2120080	Chr1	IS407A	GATCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGTC1 GAAC GATG N
8*Chr1_126b_IS40 8*Chr1_135_IS407A_A	D-R	2002721280	8	2132568-2133803	Chr1	IS407A	CTGGA/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGGAAG ATCG CCGG N
2*Chr1_37_IS407A_A	N	fmh	2	214482-215717	Chr1	IS407A	CGTCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GACCCGG CCAG GACC N
8*Chr1_37_IS407A_A	N	2002721280	8	214855-216090	Chr1	IS407A	CGCGA/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGTGCG1 CCGG GGTC N
10*Chr1_126b_IS40 10*Chr1_135_IS407A_A	D-R	PRL20	10	2149515-2150750	Chr1	IS407A	GCTCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGATGTG1 GATT CGAT N
3*Chr1_37_IS407A_A	N	JHU	3	215326-216561	Chr1	IS407A	CGTCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GACCCGG CCGA GACC N
10*Chr1_7_IS407A 10*Chr1_8_IS407A_A	D	PRL20	10	21550-22785	Chr1	IS407A	GGCGC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(TTTCCAGT GACG TTTC N
4*Chr1_126b_IS40 4*Chr1_135_IS407A_A	D-R	gb8_horse_4	4	2167514-2168749	Chr1	IS407A	TGGAC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAATCAG1 TCGC CAAT N
2*Chr1_132a_IS407;2*Chr1_57_IS407A_A	D-R	fmh	2	2174629-2175864	Chr1	IS407A	ACGCC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGAC1 GGAC CGTG N
1*Chr1_126b_IS40 1*Chr1_135_IS407A_A	D-R	ATCC_23344	1	2179445-2180680	Chr1	IS407A	TGGAC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAATCAG1 TCGC CAAT N
3*Chr1_132a_IS40 3*Chr1_57_IS407A_A	D-R	JHU	3	2190089-2191324	Chr1	IS407A	ACGCC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGAC1 GGAC CGTG N
5*Chr1_48_IS407A 5*Chr1_58b_IS407A_A	D-R	ATCC_10399	5	2200925-2202160	Chr1	IS407A	CGGCA/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GAAGTGG CCCC GAAG N
2*Chr1_47a_IS407;2*Chr1_58a_IS407A_A	R	fmh	2	2201933-2203168	Chr1	IS407A	GAGTT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCTTGGCC AACG CCTT N
3*Chr1_47a_IS407;3*Chr1_58a_IS407A_A	R	JHU	3	2217393-2218628	Chr1	IS407A	GAGTT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCTTGGCC AACG CCTT N
5*Chr1_132b_IS40 5*Chr1_47b_IS407A_A	R	ATCC_10399	5	22219825-2221060	Chr1	IS407A	TGAGG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGACGGG CTTT GGAC N
5*Chr1_133_IS407A_C	N	ATCC_10399	5	2224765-2226000	Chr1	IS407A	CCCGA/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGGCA GCGG GCGG Y
2*Chr1_43a_IS407;2*Chr1_45b_IS407A_A	R	fmh	2	2226033-2227268	Chr1	IS407A	GGTTG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGTGC CCGG GCGG Y
7*Chr1_20_IS407A 7*Chr1_21_IS407A_A	D	NCTC_10247	7	2231283-2232518	Chr1	IS407A	ATGTC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTCCACG1 CCGG GTCC N
8*Chr1_132a_IS40 8*Chr1_58a_IS407A_A	R	2002721280	8	2238334-2239569	Chr1	IS407A	ACGCC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTTCCGTC GGAC GTTC N
3*Chr1_43a_IS407;3*Chr1_45b_IS407A_A	R	JHU	3	2241493-2242728	Chr1	IS407A	GGTTG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGTGC CCGG GCGG Y
2*Chr1_42b_IS407A_A	N	fmh	2	2246967-2248202	Chr1	IS407A	GCGCT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCCCAC1 TGCG CCCC N
6*Chr1_31_IS407A_C	N	NCTC_10229	6	2252754-2253989	Chr1	IS407A	GCTAT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGATGAC1 CGAT CGAT Y
10*Chr1_132a_IS40 10*Chr1_58a_IS407A_A	R	PRL20	10	2255102-2256337	Chr1	IS407A	GACCT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTTTCGCT GGAC GTTT N
2*Chr1_136_IS407;2*Chr1_45a_IS407A_A	D-R	fmh	2	2260664-2261899	Chr1	IS407A	GATCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGTC1 GAAC GATG N
6*Chr1_30_IS407A 6*Chr1_6_IS407A_A	D-R	NCTC_10229	6	2261519-2262754	Chr1	IS407A	TTGAG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCCCAC1 TCGG CCCC N
3*Chr1_42b_IS407A_A	N	JHU	3	2262324-2263559	Chr1	IS407A	GCGCT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTTCCGTC TGCC CCCC N
7*Chr1_8_IS407A_A	D-R	NCTC_10247	7	2264036-2265271	Chr1	IS407A	GGCGC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AACCTCC GACC AAC N
9*Chr1_111_IS407;9*Chr1_53a_IS407A_B	D-R	SAVP1	9	2265201-2266436	Chr1	IS407A	GAAGG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTGTGCC ACGG CTGC N
8*Chr1_47a_IS407;8*Chr1_57_IS407A_A	D-R	2002721280	8	2265797-2267032	Chr1	IS407A	TCCGC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGAC AAGG CGTG N
4*Chr1_132a_IS40 4*Chr1_57_IS407A_A	D-R	gb8_horse_4	4	2269939-2271174	Chr1	IS407A	ACGCC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGAC1 GGAC CGTG N
6*Chr1_7_IS407A 6*Chr1_8_IS407A_A	D	NCTC_10229	6	2274369-2275604	Chr1	IS407A	GGCGC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(TGAGAGC1 GACC TGAG N
3*Chr1_136_IS407;3*Chr1_45a_IS407A_A	D-R	JHU	3	2276021-2277256	Chr1	IS407A	GATCG/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGTC1 GAAC GATG N
1*Chr1_132a_IS40 1*Chr1_57_IS407A_A	D-R	ATCC_23344	1	2281870-2283105	Chr1	IS407A	ACGCC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGAC1 GGAC CGTG N
10*Chr1_43b_IS40 10*Chr1_57_IS407A_A	D-R	PRL20	10	2282474-2283709	Chr1	IS407A	CCCGT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGAC1 CCCC CGTG N
7*Chr1_10_IS407A_A	N	NCTC_10247	7	2282563-2283798	Chr1	IS407A	GGCGC/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCTATGCC GACC CCTA N
8*Chr1_43a_IS407;8*Chr1_45b_IS407A_A	R	2002721280	8	2289894-2291129	Chr1	IS407A	GGCTT/TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGTGC GTGC CCGG N

6*Chr1_10_IS407A_A	N	NCTC_10229	6	2291924-2293159	Chr1	IS407A	CGCCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCTATGCC	CCCT	CCTA	N
4*Chr1_47a_IS407/4*Chr1_58a_IS407A_A	R	gb8_horse_4	4	2297269-2298504	Chr1	IS407A	GAGTTTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCTTGGCC	AACG	CCTT	N
7*Chr1_11_IS407A_C	N	NCTC_10247	7	2300118-2301353	Chr1	IS407A	CGCCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCTATGCC	CCCT	CCTA	N
1*Chr1_47a_IS407/1*Chr1_58a_IS407A_A	R	ATCC_23344	1	2309174-2310409	Chr1	IS407A	GAGTTTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCTTGGCC	AACG	CCTT	N
8*Chr1_42b_IS407A_A	N	2002721280	8	2310485-2311720	Chr1	IS407A	GCGCT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCTTGGCC	TGCC	CCCA	N
10*Chr1_38_IS407A_C	N	PRL20	10	2311172-2312193	Chr1	IS407A	#contig ~~~~~ ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CGTGAAAC	#	CGTG	N.D.
10*Chr1_40b_IS407A_C	R	PRL20	10	2312315-2313344	Chr1	IS407A	#contig ~~~~~ ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCC ~~~~~ #contig_br	#	#con	N.D.
10*Chr1_42a_IS40/10*Chr1_43a_IS407A_A	R	PRL20	10	2316739-2317974	Chr1	IS407A	GCGCT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCGGACG	TGCC	CCCG	N
4*Chr1_43a_IS407/4*Chr1_45b_IS407A_A	R	gb8_horse_4	4	2321369-2322604	Chr1	IS407A	GTTTG; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GCGGTGC	GCGG	GCGG	Y
8*Chr1_136_IS407/8*Chr1_45a_IS407A_A	D-R	2002721280	8	2323299-2324534	Chr1	IS407A	GATCG; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGCTC/	GAAC	GATG	N
5*Chr1_126b_IS40/5*Chr1_135_IS407A_A	D-R	ATCC_10399	5	2330125-2331360	Chr1	IS407A	TGGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCGTGACC	TCGC	CCTC	N
1*Chr1_43a_IS407/1*Chr1_45b_IS407A_A	R	ATCC_23344	1	2333274-2334509	Chr1	IS407A	GTTTG; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GCGGTGC	GCGG	GCGG	Y
10*Chr1_33_IS407/10*Chr1_40a_IS4/10*Chr1_42b_	D-R	PRL20	10	2337504-2338663	Chr1	IS407A	CCGCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCC CACACCGCT #can not f	CAAT	#can	N.D.
4*Chr1_42b_IS407A_A	N	gb8_horse_4	4	2342200-2343435	Chr1	IS407A	GCGCT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCCCAC	TGCC	CCCA	N
6*Chr1_77_IS407A/6*Chr1_94a_IS407A_A	D-R	NCTC_10229	6	234555-235790	Chr1	IS407A	ATGAT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA AACCGATC	AGGT	AACC	N
10*Chr1_35b_IS40/10*Chr1_45a_IS407A_A	R	PRL20	10	2350565-2351800	Chr1	IS407A	GTGAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGCTC/	GATT	GATG	N
1*Chr1_42b_IS407A_A	N	ATCC_23344	1	2354105-2355340	Chr1	IS407A	GCGCT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCCCAC	TGCC	CCCA	N
4*Chr1_136_IS407/4*Chr1_45a_IS407A_A	D-R	gb8_horse_4	4	2355846-2357081	Chr1	IS407A	GATCG; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGCTC/	GAAC	GATG	N
9*Chr1_112_IS407/9*Chr1_49_IS407A_A	D-R	SAVP1	9	2356417-2357652	Chr1	IS407A	TCATC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGGCTGA	TCAA	GGGC	N
1*Chr1_136_IS407/1*Chr1_45a_IS407A_A	D-R	ATCC_23344	1	2367803-2369038	Chr1	IS407A	GATCG; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGCTC/	GAAC	GATG	N
10*Chr1_126a_IS407A_A	R	PRL20	10	2373356-2374591	Chr1	IS407A	AAAAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA TTTTTCAT	AAGC	TTTT	N
10*Chr1_47a_IS407A_A	R	PRL20	10	2375892-2377127	Chr1	IS407A	TCCGC; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCTGCCA	AAGG	CCTG	N
10*Chr1_34_IS407/10*Chr1_45b_IS407A_A	D-R	PRL20	10	2399992-2401227	Chr1	IS407A	TTCTG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGGGGAT	CCGC	GGGG	N
7*Chr1_34_IS407A/7*Chr1_35b_IS407A_A	D-R	NCTC_10247	7	24007-25242	Chr1	IS407A	GTGAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGGGGAT	GATT	GGGG	N
5*Chr1_131_IS407A_C	N	ATCC_10399	5	2411631-2412866	Chr1	IS407A	CGCGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GAGGAAG	GAGG	GAGG	Y
10*Chr1_136_IS40/10*Chr1_35a_IS407A_A	D-R	PRL20	10	2417756-2418991	Chr1	IS407A	GATCG; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCGGAAC	GAAC	CCGG	N
9*Chr1_113_IS407/9*Chr1_114_IS407A_A	D	SAVP1	9	2426311-2427456	Chr1	IS407A	CGAGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATCCGGC	AGAT	GATC	N
5*Chr1_132a_IS40/5*Chr1_58a_IS407A_A	R	ATCC_10399	5	2431373-2432608	Chr1	IS407A	ACGCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CGTTCCGT	GGAC	ACGC	N
6*Chr1_33_IS407A/6*Chr1_35a_IS407A_A	D-R	NCTC_10229	6	2435363-2436598	Chr1	IS407A	CCGCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGGGCAG	CAAT	GGGG	N
7*Chr1_30_IS407A/7*Chr1_33_IS407A_A	D-R	NCTC_10247	7	2443334-2444659	Chr1	IS407A	CCGCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CGCCGCA	CAAT	GGCC	N
6*Chr1_34_IS407A/6*Chr1_35b_IS407A_A	D-R	NCTC_10229	6	2453363-2454598	Chr1	IS407A	GTGAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGGGGAT	GATT	GGGG	N
5*Chr1_47a_IS407/5*Chr1_57_IS407A_A	D-R	ATCC_10399	5	2458648-2459883	Chr1	IS407A	TCCGC; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CGTGGAC	AAGG	CGTG	N
5*Chr1_43a_IS407/5*Chr1_45b_IS407A_A	R	ATCC_10399	5	2482748-2483983	Chr1	IS407A	TTCTG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA AAGGGGG	CCGC	AAGG	N
6*Chr1_37_IS407A_A	N	NCTC_10229	6	2492041-2493276	Chr1	IS407A	CGCGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGTGCC	CGCC	GGTC	N
9*Chr1_115a_IS407A_A	N	SAVP1	9	2497406-2498641	Chr1	IS407A	TTCCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGACAI	GATG	GATG	Y
5*Chr1_42b_IS407A_A	N	ATCC_10399	5	2503596-2504831	Chr1	IS407A	GCGCT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCCCAC	TGCC	CCCA	N
8*Chr1_152b_IS40/8*Chr1_157_IS407A_A	D-R	2002721280	8	2512937-2514172	Chr1	IS407A	GAAAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGCCTI	GGTC	GATG	N
5*Chr1_136_IS407/5*Chr1_45a_IS407A_A	D-R	ATCC_10399	5	2517611-2517946	Chr1	IS407A	GATCG; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGCTC/	GAAC	GATG	N
2*Chr1_145_IS407A_A	N	fhm	2	2523638-2524540	Chr1	IS407A	#IS407/ ~~~~~ ACCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGCTTCG	#	GGCT	N.D.
7*Chr1_115b_IS40/7*Chr1_47b_IS407A_A	R	NCTC_10247	7	2523711-2523606	Chr1	IS407A	GAGCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GATGACAI	GAGC	GATG	N
2*Chr1_146_IS407A_B	N	fhm	2	2524541-2525776	Chr1	IS407A	AAGCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCGCAAI	ATAG	CCCG	N
5*Chr1_137_IS407A_C	N	ATCC_10399	5	2538164-2539399	Chr1	IS407A	CGGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA ATACGGT	ATAC	ATAC	Y
3*Chr1_145_IS407A_A	N	JHU	3	2540286-2541188	Chr1	IS407A	#IS407/ ~~~~~ ACCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGCTTCG	#	GGCT	N.D.
3*Chr1_146_IS407A_B	N	JHU	3	2541189-2542424	Chr1	IS407A	AAGCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCGCAAI	ATAG	CCCG	N
8*Chr1_152a_IS40/8*Chr1_154a_IS407A_A	R	2002721280	8	2560366-2561601	Chr1	IS407A	GACGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGGGAGC	CCCC	GGGA	N
6*Chr1_47a_IS407/6*Chr1_57_IS407A_A	D-R	NCTC_10229	6	2560595-2561830	Chr1	IS407A	TCCGC; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CGTGGAC	AAGG	CGTG	N
2*Chr1_154b_IS407A_A	R	fhm	2	2564570-2565805	Chr1	IS407A	GCGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA AACCTCC	GCTT	AACC	N
9*Chr1_122_IS407A_A	N	SAVP1	9	2567392-2568627	Chr1	IS407A	TAATG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CTTCTGCG	GCAC	CTTC	N
8*Chr1_160a_IS407A_A	R	2002721280	8	2576706-2577325	Chr1	IS407A	#contig ~~~~~ AGGGACTTTGCTAGAA GTCCGGG	#	GTCC	N.D.
8*Chr1_161_IS407A_A	D-R	2002721280	8	2577952-2578666	Chr1	IS407A	TACGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GTCCGGG	TTTT	GTCC	N
3*Chr1_154b_IS407A_A	R	JHU	3	2581218-2582453	Chr1	IS407A	CGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA AACCTCC	GCCT	AACC	N
6*Chr1_132a_IS40/6*Chr1_58a_IS407A_A	R	NCTC_10229	6	2588026-2589261	Chr1	IS407A	ACGCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GTTCGCTC	GGAC	GTTC	N
2*Chr1_152b_IS40/2*Chr1_157_IS407A_A	D-R	fhm	2	2598865-2600100	Chr1	IS407A	GAAAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GCCTGATC	GGTC	GCCT	N
9*Chr1_126a_IS407A_A	R	SAVP1	9	2614152-2615387	Chr1	IS407A	AAAAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA TTTTTCAT	AAGC	TTTT	N
7*Chr1_143a_IS40/7*Chr1_18b_IS407A_A	R	NCTC_10247	7	2614655-2615890	Chr1	IS407A	CGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA ATCAAGC	CACC	ATCA	N
3*Chr1_152b_IS40/3*Chr1_157_IS407A_A	D-R	JHU	3	2615744-2616979	Chr1	IS407A	GAAAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GCCTGATC	GGTC	GCCT	N
9*Chr1_47a_IS407A_A	R	SAVP1	9	2616688-2617923	Chr1	IS407A	TCCGC; TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA CCTGCCA	AAGG	CCTG	N
4*Chr1_145_IS407A_A	N	gb8_horse_4	4	2618181-2619083	Chr1	IS407A	#IS407/ ~~~~~ ACCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA GGCTTCG	#	GGCT	N.D.

4*Chr1_115a_JS407A_A	N	gb8_horse_4	4	526629-527864	Chr1	IS407A	TTCCGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCTGCGA1	GATG	CCTG	N
1*Chr1_115a_JS407A_A	N	ATCC_23344	1	528284-529519	Chr1	IS407A	TTCCGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCTGCGA1	GATG	CCTG	N
7*Chr1_65a_JS407A_A	N	NCTC_10247	7	533693-534928	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGGCA	GAAT	GGGG	N
5*Chr1_126a_JS407A_A	R	ATCC_10399	5	548676-549911	Chr1	IS407A	AAAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(TTTTCAT	AAGC	TTTT	N
5*Chr1_43b_JS407A_A	R	ATCC_10399	5	551212-552447	Chr1	IS407A	CCCGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCTGCGA1	CCCG	CCTG	N
9*Chr1_136_JS407A;9*Chr1_43a_JS407A_A	D-R	SAVP1	9	554720-555955	Chr1	IS407A	GATCG.TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGGAGC	GAAC	CCGG	N
2*Chr1_112_JS407A;2*Chr1_49_JS407A_A	D-R	fmh	2	560092-561327	Chr1	IS407A	TCATC(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGTGA	TCAA	GGGC	N
3*Chr1_112_JS407A;3*Chr1_49_JS407A_A	D-R	JHU	3	563350-564585	Chr1	IS407A	TCATC(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGTGA	TCAA	GGGC	N
5*Chr1_115a_JS407A_A	N	ATCC_10399	5	565315-566550	Chr1	IS407A	TTCCGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGACA	GATG	GATG	Y
4*Chr1_30_JS407A;4*Chr1_6_JS407A_A	D-R	gb8_horse_4	4	5679-6914	Chr1	IS407A	TTGAG(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCGCA	TCGG	CGCC	N
10*Chr1_114_JS407A_A	N	PRL20	10	570173-571408	Chr1	IS407A	ACGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATCCGG	GCAC	GATC	N
6*Chr1_98_JS407A;6*Chr1_66_JS407A_A	D-R	NCTC_10229	6	575108-576343	Chr1	IS407A	CTCGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA	CCCC	GTAG	N
9*Chr1_42b_JS407A_A	N	SAVP1	9	575340-576499	Chr1	IS407A	GCGCT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA	TGCG	#can not f	N.D.
10*Chr1_113_JS407A_A	N	PRL20	10	582185-583420	Chr1	IS407A	TGATT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ATCTACT	GAAG	ATCT	N
7*Chr1_98_JS407A;7*Chr1_66_JS407A_A	D-R	NCTC_10247	7	584779-586014	Chr1	IS407A	CTCGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA	CCCG	GTAG	N
9*Chr1_35b_JS407A;9*Chr1_45b_JS407A_A	R	SAVP1	9	588962-590197	Chr1	IS407A	GTGAA(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGCTC	GATT	GATG	N
4*Chr1_114_JS407A_A	N	gb8_horse_4	4	594406-595641	Chr1	IS407A	TGATT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATCCGG	GAAG	GATC	N
9*Chr1_149_JS407A;9*Chr1_29_JS407A_A	D-R	SAVP1	9	59560-60795	Chr1	IS407A	ATTTAT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCTCAG	CATT	CCTC	N
8*Chr1_64a_JS407A_A	N	2002721280	8	597797-599032	Chr1	IS407A	CTTGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(TCGTTCT	TCGC	TCGC	Y
1*Chr1_114_JS407A_A	N	ATCC_23344	1	599462-600697	Chr1	IS407A	TGATT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATCCGG	GAAG	GATC	N
1*Chr1_30_JS407A;1*Chr1_6_JS407A_A	D-R	ATCC_23344	1	6007-7242	Chr1	IS407A	TTGAG(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCGCA	TCGG	GATC	N
7*Chr1_35a_JS407A;7*Chr1_6_JS407A_A	R	NCTC_10247	7	6007-7242	Chr1	IS407A	TTGAG(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGCA	TCGG	GGGG	N
4*Chr1_113_JS407A_A	N	gb8_horse_4	4	608048-609283	Chr1	IS407A	TTTGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGGCG	CCTC	CAAC	N
1*Chr1_113_JS407A_A	N	ATCC_23344	1	613104-614339	Chr1	IS407A	TTTGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGGCG	CCTC	CAAC	N
2*Chr1_51_JS407A_B	N	fmh	2	625205-626440	Chr1	IS407A	ATGGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGCCG	GATG	GATG	Y
6*Chr1_65a_JS407A_A	N	NCTC_10229	6	626265-627500	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGGCA	GAAT	GGGG	N
7*Chr1_37_JS407A_A	N	NCTC_10247	7	62646-63881	Chr1	IS407A	GCGCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGTGCC	CGCG	GGTC	N
9*Chr1_37_JS407A_A	N	SAVP1	9	627670-628905	Chr1	IS407A	TGGGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GACCCGG	GACC	CACCC	Y
3*Chr1_51_JS407A_B	N	JHU	3	628699-629934	Chr1	IS407A	AGGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGCCG	GATG	GATG	Y
5*Chr1_114_JS407A_A	N	ATCC_10399	5	635855-637090	Chr1	IS407A	TGATT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATCCGG	GAAG	GATC	N
7*Chr1_112_JS407A;7*Chr1_97_JS407A_A	D	NCTC_10247	7	643362-644597	Chr1	IS407A	GGCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACCGCC	CCCC	ACCC	N
5*Chr1_113_JS407A_A	N	ATCC_10399	5	649478-650713	Chr1	IS407A	TTTGCTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ATCTACT	CCTC	ATCT	N
10*Chr1_112_JS40;10*Chr1_49_JS407A_A	D-R	PRL20	10	652265-653500	Chr1	IS407A	TCATC(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGTGA	TCAA	GGGC	N
8*Chr1_65a_JS407A_A	N	2002721280	8	659479-660714	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGGCA	GAAT	GGGG	N
2*Chr1_54_JS407A;2*Chr1_65b_JS407A_A	D-R	fmh	2	665167-666402	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGGT	GAAT	CCTG	N
3*Chr1_54_JS407A;3*Chr1_65b_JS407A_A	D-R	JHU	3	669375-670610	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGGT	GAAT	CGGG	N
4*Chr1_112_JS407A;4*Chr1_49_JS407A_A	D-R	gb8_horse_4	4	678191-679426	Chr1	IS407A	TCATC(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGTGA	TCAA	GGGC	N
1*Chr1_112_JS407A;1*Chr1_49_JS407A_A	D-R	ATCC_23344	1	683232-684467	Chr1	IS407A	TCATC(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGTGA	TCAA	GGGC	N
7*Chr1_95_JS407A_A	N	NCTC_10247	7	686514-687749	Chr1	IS407A	GGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCCGC	GATG	GCCC	N
6*Chr1_64a_JS407A_A	N	NCTC_10229	6	688082-689317	Chr1	IS407A	CTTGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(TCGTCT	TCGC	TCGC	Y
9*Chr1_43b_JS407A;9*Chr1_57_JS407A_A	D-R	SAVP1	9	699385-700620	Chr1	IS407A	CCCGTGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGGCA	CCCG	CGTG	N
8*Chr1_98_JS407A;8*Chr1_66_JS407A_A	D-R	2002721280	8	710666-711901	Chr1	IS407A	CTCGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA	CCCC	GTAG	N
2*Chr1_98_JS407A;2*Chr1_66_JS407A_A	D-R	fmh	2	717113-718348	Chr1	IS407A	CTCGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA	CCCC	GTAG	N
5*Chr1_112_JS407A;5*Chr1_49_JS407A_A	D-R	ATCC_10399	5	719456-720691	Chr1	IS407A	TCATC(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGTGA	TCAA	GGGC	N
3*Chr1_98_JS407A;3*Chr1_66_JS407A_A	D-R	JHU	3	722507-723742	Chr1	IS407A	CTCGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA	CCCG	GTAG	N
9*Chr1_132a_JS40;9*Chr1_58a_JS407A_A	R	SAVP1	9	726736-727971	Chr1	IS407A	ACGCC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTTCG	GGAC	CGTT	N
10*Chr1_65a_JS407A_A	N	PRL20	10	740650-741885	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGGCA	GAAT	GGGG	N
4*Chr1_51_JS407A_B	N	gb8_horse_4	4	743068-744303	Chr1	IS407A	AGGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGCCG	GATG	GATG	Y
7*Chr1_84a_JS407A;7*Chr1_94b_JS407A_A	R	NCTC_10247	7	745418-746653	Chr1	IS407A	GTGCC(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAAAG	AAAG	GTAA	N
1*Chr1_51_JS407A_B	N	ATCC_23344	1	748097-749332	Chr1	IS407A	AGGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGCCG	GATG	GATG	Y
7*Chr1_83_JS407A_A	N	NCTC_10247	7	760536-761771	Chr1	IS407A	TTACGTGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ATCCAC	TGAT	GATC	N
8*Chr1_96_JS407A;8*Chr1_97_JS407A_A	D	2002721280	8	769257-770492	Chr1	IS407A	GGCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACCGCC	CCCC	ACCC	N
2*Chr1_96_JS407A;2*Chr1_97_JS407A_A	D	fmh	2	776030-777265	Chr1	IS407A	GGCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACCGCC	CCCC	ACCC	N
3*Chr1_96_JS407A;3*Chr1_97_JS407A_A	D	JHU	3	782172-783407	Chr1	IS407A	GGCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACCGCC	CCCC	ACCC	N
7*Chr1_79_JS407A;7*Chr1_80_JS407A_A	D	NCTC_10247	7	782570-783805	Chr1	IS407A	GGGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCAG	GTCA	CAAG	N
4*Chr1_54_JS407A;4*Chr1_65b_JS407A_A	D-R	gb8_horse_4	4	783009-784244	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGGT	GAAT	CGGG	N
1*Chr1_54_JS407A;1*Chr1_65b_JS407A_A	D-R	ATCC_23344	1	788024-789259	Chr1	IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGGT	GAAT	CGGG	N
10*Chr1_98_JS407A;10*Chr1_66_JS407A_A	D-R	PRL20	10	791849-793084	Chr1	IS407A	CTCGT(TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA	CCCC	GTAG	N

8*Chr1_95_IS407A_A	N	2002721280	8	812487-813722	Chr1 IS407A	GGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCCGCC	GATG	GCCC	N
7*Chr1_78_IS407A_A	N	NCTC_10247	7	817833-819068	Chr1 IS407A	CAGCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGCTG	GTAG	GTAG	Y
2*Chr1_95_IS407A_A	N	fmh	2	819682-820917	Chr1 IS407A	GGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCCGCC	GATG	GCCC	N
5*Chr1_54_IS407A_5*Chr1_56_IS407A_A	D-R	ATCC_10399	5	823076-824311	Chr1 IS407A	TGGAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGGGTC	GCGG	GCGG	Y
9*Chr1_126b_IS407A_9*Chr1_135_IS407A_A	D-R	SAVP1	9	826175-827410	Chr1 IS407A	GCTCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGATGTG/	GATT	CGAT	N
3*Chr1_95_IS407A_A	N	JHU	3	826570-827805	Chr1 IS407A	GGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCCGCC	GATG	GCCC	N
4*Chr1_98_IS407A_4*Chr1_66_IS407A_A	D-R	gb8_horse_4	4	833765-835000	Chr1 IS407A	CTCGT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA/	CCCG	GTAG	N
5*Chr1_55_IS407A_5*Chr1_64b_IS407A_A	D-R	ATCC_10399	5	836600-837835	Chr1 IS407A	ATCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCGCTTC	GCGG	ACGC	N
1*Chr1_98_IS407A_1*Chr1_66_IS407A_A	D-R	ATCC_23344	1	839215-840450	Chr1 IS407A	CTCGT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA/	CCCG	GTAG	N
10*Chr1_96_IS407A_10*Chr1_97_IS407A_A	D	PRL20	10	850107-851342	Chr1 IS407A	GGCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACCGCCC	CCCG	ACCG	N
8*Chr1_72_IS407A_8*Chr1_94b_IS407A_A	D-R	2002721280	8	871391-872626	Chr1 IS407A	CCAGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAAAGC	GCGG	GTAA	N
2*Chr1_72_IS407A_2*Chr1_94b_IS407A_A	D-R	fmh	2	878580-879815	Chr1 IS407A	CCAGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GACGTT/	GCGG	TGAC	N
3*Chr1_72_IS407A_3*Chr1_94b_IS407A_A	D-R	JHU	3	885069-886304	Chr1 IS407A	CCAGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GACGTT/	GCGG	TGAC	N
6*Chr1_48_IS407A_6*Chr1_58b_IS407A_A	D-R	NCTC_10229	6	889050-890285	Chr1 IS407A	CGTCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GAAGTGG/	GTGA	GAAG	N
4*Chr1_96_IS407A_4*Chr1_97_IS407A_A	D	gb8_horse_4	4	891953-893188	Chr1 IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACCGCCC	CCCG	ACCG	N
10*Chr1_95_IS407A_A	N	PRL20	10	892871-894106	Chr1 IS407A	GGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCCGCC	GATG	GCCC	N
1*Chr1_96_IS407A_1*Chr1_97_IS407A_A	D	ATCC_23344	1	897797-899032	Chr1 IS407A	GGCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACCGCCC	CCCG	ACCG	N
5*Chr1_65a_IS407A_A	N	ATCC_10399	5	898663-899898	Chr1 IS407A	GCGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGGGCA	GAAT	GGGG	N
6*Chr1_115b_IS407A_6*Chr1_47b_IS407A_A	R	NCTC_10229	6	907313-908548	Chr1 IS407A	GAAGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGACA/	GAGC	GATG	N
7*Chr1_77_IS407A_7*Chr1_94a_IS407A_A	D-R	NCTC_10247	7	925312-926547	Chr1 IS407A	ATGAT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AACCGAT	AGT	AACC	N
4*Chr1_95_IS407A_A	N	gb8_horse_4	4	934492-935458	Chr1 IS407A	GGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCCGCC	GATG	GCCC	N
9*Chr1_132b_IS407A_9*Chr1_47b_IS407A_A	R	SAVP1	9	935361-936596	Chr1 IS407A	TGAGG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGACGGG	CCTT	GGAC	N
1*Chr1_95_IS407A_A	N	ATCC_23344	1	940960-942195	Chr1 IS407A	GGCGC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCCGCC	GATG	GCCC	N
6*Chr1_119_IS407A_C	N	NCTC_10229	6	942572-943807	Chr1 IS407A	GGATA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATGCGC/	GATG	GATG	Y
5*Chr1_98_IS407A_5*Chr1_66_IS407A_A	D-R	ATCC_10399	5	949835-951070	Chr1 IS407A	CTCGT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGGCA/	CCCG	GTAG	N
8*Chr1_74_IS407A_8*Chr1_84a_IS407A_A	D-R	2002721280	8	952291-953526	Chr1 IS407A	GTGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTGATG/	AAAG	GGTC	N
10*Chr1_69_IS407A_10*Chr1_94b_IS407A_A	D-R	PRL20	10	952619-953854	Chr1 IS407A	TGGCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGGGCC	CCTG	AAGG	N
9*Chr1_48_IS407A_9*Chr1_55_IS407A_9*Chr1_58b_I	D-R	SAVP1	9	954515-955386	Chr1 IS407A	ATCAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ITCCGGC	GCGG	ATCC	N
2*Chr1_74_IS407A_2*Chr1_75_IS407A_A	D	fmh	2	960048-960969	Chr1 IS407A	#ISBma ~~~~~ GCCCATGCCACGCGAC(CGAGATG/AGGGACTTTGCTAGAA(GGTCATG	#	GGTC	N.D.
7*Chr1_89_IS407A_A	N	NCTC_10247	7	960917-962152	Chr1 IS407A	GCGAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTGGATG	CCCG	CTGG	N
2*Chr1_76_IS407A_2*Chr1_87b_IS407A_A	D-R	fmh	2	965187-966422	Chr1 IS407A	GCGGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGAGCGC	GCGG	CGAG	N
8*Chr1_83_IS407A_A	N	2002721280	8	967415-968650	Chr1 IS407A	TTACG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ATCCACCC	TGAT	ATCC	N
3*Chr1_74_IS407A_3*Chr1_75_IS407A_A	D	JHU	3	967622-968543	Chr1 IS407A	#ISBma ~~~~~ GCCCATGCCACGCGAC(CGAGATG/AGGGACTTTGCTAGAA(GGTCATG	#	GGTC	N.D.
9*Chr1_53b_IS407A_9*Chr1_56_IS407A_A	D-R	SAVP1	9	967733-968968	Chr1 IS407A	TGGAA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACGGCGA	GCGG	ACGG	N
3*Chr1_76_IS407A_3*Chr1_87b_IS407A_A	D-R	JHU	3	972761-973996	Chr1 IS407A	GCGGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGAGCGC	GCGG	CGAG	N
6*Chr1_122_IS407A_A	N	NCTC_10229	6	978581-979816	Chr1 IS407A	GCGCA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTGCTGC	GAAG	GTGC	N
9*Chr1_54_IS407A_A	D-R	SAVP1	9	980886-982121	Chr1 IS407A	CGTCG TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGGAACG	GTGA	CGAA	N
10*Chr1_74_IS407A_10*Chr1_75_IS407A_A	D	PRL20	10	988786-989707	Chr1 IS407A	#ISBma ~~~~~ GCCCATGCCACGCGAC(CGAGATG/AGGGACTTTGCTAGAA(GGTCATG	#	GGTC	N.D.
8*Chr1_79_IS407A_8*Chr1_80_IS407A_A	D	2002721280	8	989538-990773	Chr1 IS407A	GGGAC TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCAG	GTCA	CAAG	N
4*Chr1_72_IS407A_4*Chr1_94b_IS407A_A	D-R	gb8_horse_4	4	992740-993975	Chr1 IS407A	CCAGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTAGCTTC	GCGG	TGAC	N
10*Chr1_76_IS407A_10*Chr1_87b_IS407A_A	D-R	PRL20	10	993925-995160	Chr1 IS407A	AATGT TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGACGAC	CTCG	GCGG	N
7*Chr1_75_IS407A_7*Chr1_87b_IS407A_A	D-R	NCTC_10247	7	998173-999094	Chr1 IS407A	#ISBma ~~~~~ GCCCATGCCACGCGAC(CGAGATG/AGGGACTTTGCTAGAA(CCATGGC	#	CCAT	N.D.
1*Chr1_72_IS407A_1*Chr1_94b_IS407A_A	D-R	ATCC_23344	1	999459-1000694	Chr1 IS407A	CCAGA TGACCTGCCCCCTACA ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTACGTT/	GCGG	TGAC	N

IS Bma 1

					5'-ext	5'-IR	ORF	3'-IR	3'-ext	5'-DR	3'-DR	rget duplicates
							GTTTCATCGC					
2*Chr1_88_ISBma1_B	N	fmh	2	1002861-1003118	Chr1 ISBma1	#IS407A ~~~~~ ACC			ATTTTTTTT#IS407A		ATTTTTTTT	N.D.
3*Chr1_88_ISBma1_B	N	JHU	3	1011670-1011927	Chr1 ISBma1	#IS407A ~~~~~ ACC			ATTTTTTTT#IS407A		ATTTTTTTT	N.D.
6*Chr1_125_ISBma1_A	N	NCTC_10229	6	1013610-1014914	Chr1 ISBma1	AGGCA GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC			AATTTTTT(AATTTTTT		AATTTTTTT	Y
10*Chr1_88_ISBma1_B	N	PRL20	10	1031539-1031835	Chr1 ISBma1	#IS407A ~~~~~ ACC			ATTTTTTTT#IS407A		ATTTTTTTT	N.D.
4*Chr1_73_ISBma1_A	N	gb8_horse_4	4	1059010-1060314	Chr1 ISBma1	GAGAG GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC			AAAAAAA/AAAAAAT		AAAAAAA/	Y
1*Chr1_73_ISBma1_A	N	ATCC_23344	1	1065697-1067001	Chr1 ISBma1	GAGAG GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC			AAAAAAA/AAAAAAT		AAAAAAA/	Y
9*Chr1_60_ISBma1_A	N	SAVP1	9	1081029-1082333	Chr1 ISBma1	CGGTA GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC			AAAAAAT/AAAAAATA		AAAAAAT/	Y
4*Chr1_88_ISBma1_B	N	gb8_horse_4	4	1116223-1116480	Chr1 ISBma1	#IS407A ~~~~~ ACC			ATTTTTTTT#IS407A		ATTTTTTTT	N.D.
1*Chr1_88_ISBma1_B	N	ATCC_23344	1	1123080-1123337	Chr1 ISBma1	#IS407A ~~~~~ ACC			ATTTTTTTT#IS407A		ATTTTTTTT	N.D.
2*Chr1_82_ISBma1_A	N	fmh	2	1173163-1174201	Chr1 ISBma1	CGAAA GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#			#IS407A TTTCTTTT		#IS407A	N
2*Chr1_82-1_ISBma1_A	N	fmh	2	1175227-1175705	Chr1 ISBma1	#IS407A ~~~~~ ACC			TTTCTTTT#IS407A		TTTCTTTT	N.D.

3*Chr1_82_ISBma1_A	N	JHU	3	1184351-1185389	Chr1	ISBma1	CGAAA GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A	TTTCITTT	#IS407A	N
3*Chr1_82-1_ISBma1_A	N	JHU	3	1186415-1186893	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTCITTT	#IS407A	TTTCITTT	N.D.
10*Chr1_82_ISBma1_A	N	PRL20	10	1191155-1192031	Chr1	ISBma1	CGAAA GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A	TTTCITTT	#IS407A	N
10*Chr1_82-1_ISBma1_A	N	PRL20	10	1193171-1193697	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTCITTT	#IS407A	TTTCITTT	N.D.
7*Chr1_103_ISBma1_A	N	NCTC_10247	7	1266623-1267927	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
4*Chr1_82_ISBma1_A	N	gb8_horse_4	4	1281913-1282951	Chr1	ISBma1	CGAAA GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A	TTTCITTT	#IS407A	N
4*Chr1_82-1_ISBma1_A	N	gb8_horse_4	4	1283977-1284455	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTCITTT	#IS407A	TTTCITTT	N.D.
5*Chr1_82-1_ISBma1_A	N	ATCC_10399	5	1284930-1285408	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTCITTT	#IS407A	TTTCITTT	N.D.
5*Chr1_82_ISBma1_A	N	ATCC_10399	5	1286434-1287472	Chr1	ISBma1	CGAAA GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A	TTTCITTT	#IS407A	N
1*Chr1_82_ISBma1_A	N	ATCC_23344	1	1290138-1291176	Chr1	ISBma1	CGAAA GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A	TTTCITTT	#IS407A	N
1*Chr1_82-1_ISBma1_A	N	ATCC_23344	1	1292202-1292680	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTCITTT	#IS407A	TTTCITTT	N.D.
4*Chr1_12_ISBma1_A	N	gb8_horse_4	4	141771-143075	Chr1	ISBma1	GAATT(GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTT	TTTTTCTT	TTTTTCTT	Y
10*Chr1_12_ISBma1_A	N	PRL20	10	1423-2727	Chr1	ISBma1	GAATT(GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTT	TTTTTCTT	TTTTTCTT	Y
1*Chr1_12_ISBma1_A	N	ATCC_23344	1	142668-143972	Chr1	ISBma1	GAATT(GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTT	TTTTTCTT	TTTTTCTT	Y
2*Chr1_103_ISBma1_A	N	fmh	2	1458477-1459781	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
6*Chr1_26_ISBma1_A	N	NCTC_10229	6	1463413-1464719	Chr1	ISBma1	GCGTG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA		ATAAAAA/	Y
3*Chr1_103_ISBma1_A	N	JHU	3	1467796-1469100	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
8*Chr1_103_ISBma1_A	N	2002721280	8	1472738-1474042	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
7*Chr1_125_ISBma1_A	N	NCTC_10247	7	147293-148597	Chr1	ISBma1	AGGCA GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTT(AATTTTTT		AATTTTTT	Y
9*Chr1_88_ISBma1_B	N	SAVP1	9	1497063-1497359	Chr1	ISBma1	#IS407/ ~~~~~ ACC	ATTTTTTC#IS407A		ATTTTTTT	N.D.
5*Chr1_88_ISBma1_B	N	ATCC_10399	5	1497242-1497500	Chr1	ISBma1	#IS407/ ~~~~~ ACC	ATTTTTTC#IS407A		ATTTTTTT	N.D.
10*Chr1_103_ISBma1_A	N	PRL20	10	1515896-1517200	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
3*Chr1_12_ISBma1_A	N	JHU	3	15493-16797	Chr1	ISBma1	GAATT(GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTT	TTTTTCTT	TTTTTCTT	Y
5*Chr1_73_ISBma1_A	N	ATCC_10399	5	1553580-1554884	Chr1	ISBma1	GAGAG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA`AAAAAAT		AAAAAAA`	Y
4*Chr1_103_ISBma1_A	N	gb8_horse_4	4	1561382-1562686	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
1*Chr1_103_ISBma1_A	N	ATCC_23344	1	1570802-1572106	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
2*Chr1_12_ISBma1_A	N	fmh	2	15916-17220	Chr1	ISBma1	GAATT(GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTT	TTTTTCTT	TTTTTCTT	Y
9*Chr1_26_ISBma1_A	N	SAVP1	9	160477-161783	Chr1	ISBma1	GCGTG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA		ATAAAAA/	Y
8*Chr1_12_ISBma1_A	N	2002721280	8	16877-18181	Chr1	ISBma1	GAATT(GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTT	TTTTTCTT	TTTTTCTT	Y
9*Chr1_82_ISBma1_A	N	SAVP1	9	1706788-1707664	Chr1	ISBma1	CGAAA GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A	TTTCITTT	#IS407A	N.D.
9*Chr1_82-1_ISBma1_A	N	SAVP1	9	1708804-1709330	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTCITTT	#IS407A	TTTCITTT	N.D.
5*Chr1_12_ISBma1_A	N	ATCC_10399	5	17216-18520	Chr1	ISBma1	GAATT(GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTT	TTTTTCTT	TTTTTCTT	Y
5*Chr1_103_ISBma1_A	N	ATCC_10399	5	1724494-1725798	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
2*Chr1_60_ISBma1_A	N	fmh	2	1842154-1843458	Chr1	ISBma1	CGGTA`GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAT/AAAAAATA		AAAAAAT/	Y
3*Chr1_60_ISBma1_A	N	JHU	3	1856886-1858190	Chr1	ISBma1	CGGTA`GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAT/AAAAAATA		AAAAAAT/	Y
10*Chr1_60_ISBma1_A	N	PRL20	10	1895357-1896661	Chr1	ISBma1	CGGTA`GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAT/AAAAAATA		AAAAAAT/	Y
2*Chr1_59_ISBma1_A	N	fmh	2	1925292-1925696	Chr1	ISBma1	CACCG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA`AAAAAAT		AAAAAAA`	Y
7*Chr1_103_ISBma1_A	N	NCTC_10247	7	1928819-1930125	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA/AAAAAATA		AAAAAAA/	Y
7*Chr1_129_ISBma1_A	N	NCTC_10247	7	1931826-1933130	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTA/TTTTTTTA		TTTTTTA	Y
4*Chr1_60_ISBma1_A	N	gb8_horse_4	4	1939412-1940716	Chr1	ISBma1	CGGTA`GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAT/AAAAAATA		AAAAAAT/	Y
3*Chr1_59_ISBma1_A	N	JHU	3	1940744-1942048	Chr1	ISBma1	CACCG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA`AAAAAAT		AAAAAAA`	Y
1*Chr1_60_ISBma1_A	N	ATCC_23344	1	1951374-1952678	Chr1	ISBma1	CGGTA`GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAT/AAAAAATA		AAAAAAT/	Y
6*Chr1_153_ISBma1_A	N	NCTC_10229	6	1952299-1953603	Chr1	ISBma1	CCGAT`GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTA/TTTTTTTA		TTTTTTA	Y
10*Chr1_59_ISBma1_A	N	PRL20	10	1975920-1977224	Chr1	ISBma1	CACCG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA`AAAAAAT		AAAAAAA`	Y
6*Chr1_156_ISBma1_A	N	NCTC_10229	6	1985332-1986531	Chr1	ISBma1	CCGCG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A	AAAAAATA	#IS407A	N.D.
9*Chr1_103_ISBma1_A	N	SAVP1	9	1987012-1988316	Chr1	ISBma1	AGTCG.GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTT		CTTTTTTT	Y
4*Chr1_59_ISBma1_A	N	gb8_horse_4	4	2020579-2021883	Chr1	ISBma1	CACCG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA`AAAAAAT		AAAAAAA`	Y
1*Chr1_59_ISBma1_A	N	ATCC_23344	1	2032534-2033838	Chr1	ISBma1	CACCG GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA`AAAAAAT		AAAAAAA`	Y
2*Chr1_127_ISBma1_A	N	fmh	2	2073439-2073769	Chr1	ISBma1	#IS407/ ~~~~~ ACC	AAAAAAA`#IS407A		AAAAAAA`	N.D.
2*Chr1_129_ISBma1_A	N	fmh	2	2075470-2076774	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTA/TTTTTTTA		TTTTTTA	Y
3*Chr1_127_ISBma1_A	N	JHU	3	2088899-2089229	Chr1	ISBma1	#IS407/ ~~~~~ ACC	AAAAAAA`#IS407A		AAAAAAA`	N.D.
3*Chr1_129_ISBma1_A	N	JHU	3	2090930-2092234	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTA/TTTTTTTA		TTTTTTA	Y
5*Chr1_60_ISBma1_A	N	ATCC_10399	5	2100644-2101948	Chr1	ISBma1	CGGTA`GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAT/AAAAAATA		AAAAAAT/	Y
2*Chr1_36_ISBma1_A	N	fmh	2	212072-213376	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTT	TTTTTCTT	TTTTTCTT	Y
8*Chr1_36_ISBma1_A	N	2002721280	8	212567-213871	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTT	TTTTTCTT	TTTTTCTT	Y
3*Chr1_36_ISBma1_A	N	JHU	3	212916-214220	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTT	TTTTTCTT	TTTTTCTT	Y
8*Chr1_127_ISBma1_A	N	2002721280	8	2134387-2135693	Chr1	ISBma1	GCCGC GGGTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA/AAAAAATA		AAAAAAA/	Y
8*Chr1_129_ISBma1_A	N	2002721280	8	2137833-2138804	Chr1	ISBma1	~~~~~ ACC	TTTTTTA/TTTTTTTA		TTTTTTA	N.D.

10*Chr1_127_ISBma1_A	N	PRL20	10	2150683-2151080	Chr1	ISBma1	#IS407/~~~~~ ACC	AAAAAA#IS407A	AAAAAA/	N.D.
10*Chr1_129_ISBma1_A	N	PRL20	10	2155991-2157225	Chr1	ISBma1	#IS407/~~~~~CATCGAATCGTTCAACGGCACC	TTTTTTTAT#IS407A	TTTTTTTA	N.D.
4*Chr1_127_ISBma1_A	N	gb8_horse_4	4	2168750-2169080	Chr1	ISBma1	#IS407/~~~~~ ACC	AAAAAAA#IS407A	AAAAAAA/	N.D.
4*Chr1_129_ISBma1_A	N	gb8_horse_4	4	2170781-2172085	Chr1	ISBma1	CGCGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
1*Chr1_127_ISBma1_A	N	ATCC_23344	1	2180681-2181011	Chr1	ISBma1	#IS407/~~~~~ ACC	AAAAAAA#IS407A	AAAAAAA/	N.D.
5*Chr1_129_ISBma1_A	N	ATCC_10399	5	2181906-2183210	Chr1	ISBma1	CACCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
1*Chr1_129_ISBma1_A	N	ATCC_23344	1	2182712-2184016	Chr1	ISBma1	CGCGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
6*Chr1_14_ISBma1_A	N	NCTC_10229	6	2204564-2205868	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTCC(TTTTTTCC	TTTTTTCC	Y
6*Chr1_12_ISBma1_A	N	NCTC_10229	6	2294405-2295709	Chr1	ISBma1	GAATT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTT TTTTTCTT	TTTTTCTT	Y
7*Chr1_12_ISBma1_A	N	NCTC_10247	7	2302599-2303903	Chr1	ISBma1	GAATT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTT TTTTTCTT	TTTTTCTT	Y
5*Chr1_127_ISBma5*Chr1_129_ISBma1_A	N	ATCC_10399	5	2331091-2332356	Chr1	ISBma1	#IS407/CGTCACGCTGAAGTTG ATGCCTTAACGAGCACTGGACC	TTTTTTTAT#IS407A	TTTTTTTA	N.D.
10*Chr1_125_ISBma1_A	N	PRL20	10	2362908-2364212	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTTT(AATTTTTT	AATTTTTT	Y
2*Chr1_142_ISBma1_B	N	fhh	2	2431313-2432619	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
3*Chr1_142_ISBma1_B	N	JHU	3	2447452-2448758	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
6*Chr1_36_ISBma1_A	N	NCTC_10229	6	2489753-2491057	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTT TTTTTTCT	TTTTTCTT	Y
8*Chr1_156_ISBma1_A	N	2002721280	8	2511737-2512936	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAAA	#IS407A	N.D.
4*Chr1_142_ISBma1_B	N	gb8_horse_4	4	2526053-2527359	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
1*Chr1_142_ISBma1_B	N	ATCC_23344	1	2538026-2539332	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
8*Chr1_153_ISBma1_A	N	2002721280	8	2544560-2545864	Chr1	ISBma1	CCGAT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
9*Chr1_124_ISBma1_B	N	SAVP1	9	2568741-2570045	Chr1	ISBma1	TCAGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTT TTTTTTCT	TTTTTCTT	Y
10*Chr1_142_ISBma1_B	N	PRL20	10	2584163-2585469	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
2*Chr1_156_ISBma1_A	N	fhh	2	2598014-2598869	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAAA	#IS407A	N.D.
9*Chr1_125_ISBma1_A	N	SAVP1	9	2603704-2605008	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTTT(AATTTTTT	AATTTTTT	Y
3*Chr1_153_ISBma3*Chr1_156_ISBma1_A	N	JHU	3	2614893-2615748	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS406A AAAAAAAA	#IS406A	N.D.
2*Chr1_153_ISBma1_A	N	fhh	2	2631429-2632733	Chr1	ISBma1	CCGAT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
5*Chr1_142_ISBma1_B	N	ATCC_10399	5	2688082-2689388	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
6*Chr1_127_ISBma6*Chr1_129_ISBma1_A	N	NCTC_10229	6	2688853-2690159	Chr1	ISBma1	GCCGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATAAAAAAA	TTTTTTTA	N
4*Chr1_156_ISBma1_A	N	gb8_horse_4	4	2692085-2692940	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAAA	#IS407A	N.D.
1*Chr1_156_ISBma1_A	N	ATCC_23344	1	2704469-2705324	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAAA	#IS407A	N.D.
4*Chr1_153_ISBma1_A	N	gb8_horse_4	4	2723665-2724969	Chr1	ISBma1	CCGAT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
1*Chr1_153_ISBma1_A	N	ATCC_23344	1	2737048-2738352	Chr1	ISBma1	CCGAT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
10*Chr1_156_ISBma1_A	N	PRL20	10	2755093-2756292	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAAA	#IS407A	N.D.
10*Chr1_153_ISBma1_A	N	PRL20	10	2787753-2789057	Chr1	ISBma1	CCGAT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
9*Chr1_12_ISBma1_A	N	SAVP1	9	2799403-2800707	Chr1	ISBma1	GAATT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTT TTTTTTCT	TTTTTCTT	Y
7*Chr1_26_ISBma1_A	N	NCTC_10247	7	2816595-2817901	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
5*Chr1_156_ISBma1_A	N	ATCC_10399	5	2854277-2855132	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAAA	#IS407A	N.D.
5*Chr1_153_ISBma1_A	N	ATCC_10399	5	2886389-2887693	Chr1	ISBma1	CCGAT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
9*Chr1_14_ISBma1_A	N	SAVP1	9	2887865-2888804	Chr1	ISBma1	#IS407/~~~~~ ACC	TTTTTTTCC#IS407A	TTTTTTCC	N.D.
9*Chr1_14-1_ISBma1_A	N	SAVP1	9	2889266-2890409	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A TTTTTTCC	#IS407A	N.D.
7*Chr1_59_ISBma1_A	N	NCTC_10247	7	2895712-290876	Chr1	ISBma1	CACCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAAA'AAAAAAAT	AAAAAAA'	Y
8*Chr1_26_ISBma1_A	N	2002721280	8	3035091-3036397	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
9*Chr1_156_ISBma1_A	N	SAVP1	9	3108437-3109636	Chr1	ISBma1	CCGCG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAAA	#IS407A	N.D.
9*Chr1_153_ISBma1_A	N	SAVP1	9	3141365-3142669	Chr1	ISBma1	CCGAT(GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
2*Chr1_26_ISBma1_A	N	fhh	2	3186645-3187951	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
3*Chr1_26_ISBma1_A	N	JHU	3	3203538-3204844	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
8*Chr1_14_ISBma1_A	N	2002721280	8	3221823-3223127	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTCC(TTTTTTCC	TTTTTTCC	Y
2*Chr1_14_ISBma1_A	N	fhh	2	3250236-3251540	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTCC(TTTTTTCC	TTTTTTCC	Y
3*Chr1_14_ISBma1_A	N	JHU	3	3268498-3269802	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTCC(TTTTTTCC	TTTTTTCC	Y
4*Chr1_26_ISBma1_A	N	gb8_horse_4	4	3273197-3274503	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
1*Chr1_26_ISBma1_A	N	ATCC_23344	1	3286945-3288251	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
10*Chr1_26_ISBma1_A	N	PRL20	10	3322621-3323927	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
4*Chr1_14_ISBma1_A	N	gb8_horse_4	4	3336103-3337407	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTCC(TTTTTTCC	TTTTTTCC	Y
1*Chr1_14_ISBma1_A	N	ATCC_23344	1	3349816-3351120	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTCC(TTTTTTCC	TTTTTTCC	Y
6*Chr1_103_ISBma1_A	N	NCTC_10229	6	3350430-3351734	Chr1	ISBma1	AGTCG.GGTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCTTTTTTTT	CTTTTTTT	Y
4*Chr1_36_ISBma1_A	N	gb8_horse_4	4	335870-337174	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTT TTTTTTCT	TTTTTCTT	Y
5*Chr1_26_ISBma1_A	N	ATCC_10399	5	3360914-3362220	Chr1	ISBma1	GCGTG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	ATAAAAA/ATAAAAA	ATAAAAA/	Y
1*Chr1_36_ISBma1_A	N	ATCC_23344	1	337256-338560	Chr1	ISBma1	GCGGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTT TTTTTTCT	TTTTTCTT	Y
7*Chr1_14_ISBma1_A	N	NCTC_10247	7	3397369-3398673	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTCC(TTTTTTCC	TTTTTTCC	Y

7*Chr1_153_ISBma1_A	N	NCTC_10247	7	3421451-3422755	Chr1	ISBma1	CCGATGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTTTATTTTTTTA	TTTTTTTA	Y
2*Chr1_124_ISBma1_B	N	fhm	2	342363-343435	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTTCTTT#IS407A	TTTTCTT	N.D.
5*Chr1_14_ISBma1_A	N	ATCC_10399	5	3424621-3425925	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCC(TTTTTTCC	TTTTTCC	Y
3*Chr1_124_ISBma1_B	N	JHU	3	343967-345039	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTTCTTT#IS407A	TTTTCTT	N
7*Chr1_156_ISBma1_A	N	NCTC_10247	7	3454484-3455683	Chr1	ISBma1	CCGCG GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A AAAAAAA	#IS407A	N.D.
9*Chr1_142_ISBma1_B	N	SAVP1	9	348750-350056	Chr1	ISBma1	GCGGC GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA'AAAAAAT	AAAAAA'	Y
10*Chr1_36_ISBma1_A	N	PRL20	10	350249-351553	Chr1	ISBma1	GCGGC GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTTTTTCT	TTTTTCT	Y
7*Chr1_60_ISBma1_A	N	NCTC_10247	7	370819-372123	Chr1	ISBma1	CGGTA' GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA/AAAAAATA	AAAAAA/	Y
5*Chr1_36_ISBma1_A	N	ATCC_10399	5	374206-375510	Chr1	ISBma1	GCGGC GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTTTTTCT	TTTTTCT	Y
8*Chr1_125_ISBma1_A	N	2002721280	8	377508-378812	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTT(AATTTTTT	AATTTTT	Y
2*Chr1_125_ISBma1_A	N	fhm	2	377515-378819	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTT(AATTTTTT	AATTTTT	Y
3*Chr1_125_ISBma1_A	N	JHU	3	378674-379978	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTT(AATTTTTT	AATTTTT	Y
6*Chr1_82_ISBma1_A	N	NCTC_10229	6	398477-399353	Chr1	ISBma1	CGAAA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A TTCTTTT	#IS407A	N.D.
6*Chr1_82-1_ISBma1_A	N	NCTC_10229	6	399914-401019	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTCTTTTT#IS407A	TTCTTTT	N.D.
8*Chr1_59_ISBma1_A	N	2002721280	8	422225-423530	Chr1	ISBma1	CACCG GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA'AAAAAAT	AAAAAA'	Y
10*Chr1_124_ISBma1_B	N	PRL20	10	455910-457214	Chr1	ISBma1	TCAGC GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTCTTTTTTTCTT	TTTTCTT	Y
4*Chr1_124_ISBma1_B	N	gb8_horse_4	4	464802-465874	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTTCTTT#IS407A	TTTTCTT	N.D.
1*Chr1_124_ISBma1_B	N	ATCC_23344	1	466488-467560	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTTCTTT#IS407A	TTTTCTT	N.D.
4*Chr1_125_ISBma1_A	N	gb8_horse_4	4	499540-500844	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTT(AATTTTTT	AATTTTT	Y
1*Chr1_125_ISBma1_A	N	ATCC_23344	1	501195-502499	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTT(AATTTTTT	AATTTTT	Y
8*Chr1_60_ISBma1_A	N	2002721280	8	502009-502817	Chr1	ISBma1	CGGTA' GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#contig_br AAAAAATA	#contig_	N.D.
5*Chr1_124_ISBma1_B	N	ATCC_10399	5	503499-504571	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTTCTTT#IS407A	TTTTCTT	N.D.
5*Chr1_125_ISBma1_A	N	ATCC_10399	5	538228-539532	Chr1	ISBma1	AGGCA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AATTTTT(AATTTTTT	AATTTTT	Y
7*Chr1_36_ISBma1_A	N	NCTC_10247	7	60358-61662	Chr1	ISBma1	GCGGC GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTTTTTCT	TTTTTCT	Y
9*Chr1_36_ISBma1_A	N	SAVP1	9	625260-626564	Chr1	ISBma1	GCGGC GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCTTTTTTCT	TTTTTCT	Y
7*Chr1_82-1_ISBma1_A	N	NCTC_10247	7	760075-761180	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTCTTTTT#IS407A	TTCTTTT	N.D.
7*Chr1_82_ISBma1_A	N	NCTC_10247	7	761741-762617	Chr1	ISBma1	CGAAA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A TTCTTTT	#IS407A	N.D.
6*Chr1_60_ISBma1_A	N	NCTC_10229	6	788886-790190	Chr1	ISBma1	CGGTA' GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA/AAAAAATA	AAAAAA/	Y
9*Chr1_127_ISBma1	N	SAVP1	9	825845-826242	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTTTTTAT#IS407A	TTTTTTA	N.D.
6*Chr1_59_ISBma1_A	N	NCTC_10229	6	870043-871347	Chr1	ISBma1	CACCG GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA'AAAAAAT	AAAAAA'	Y
10*Chr1_14_ISBma1_A	N	PRL20	10	89941-91245	Chr1	ISBma1	AAACA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	TTTTTCC(TTTTTTCC	TTTTTCC	Y
2*Chr1_73_ISBma1_A	N	fhm	2	945561-946865	Chr1	ISBma1	GAGAG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA'AAAAAAT	AAAAAA'	Y
3*Chr1_73_ISBma1_A	N	JHU	3	953135-954439	Chr1	ISBma1	GAGAG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA'AAAAAAT	AAAAAA'	Y
8*Chr1_82-1_ISBma1_A	N	2002721280	8	966954-968059	Chr1	ISBma1	#IS407/ ~~~~~ ACC	TTCTTTTT#IS407A	TTCTTTT	N.D.
8*Chr1_82_ISBma1	N	2002721280	8	968620-969496	Chr1	ISBma1	CGAAA GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC#	#IS407A TTCTTTT	#IS407A	N.D.
10*Chr1_73_ISBma1_A	N	PRL20	10	974551-975855	Chr1	ISBma1	GAGAG GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA'AAAAAAT	AAAAAA'	Y
9*Chr1_59_ISBma1_A	N	SAVP1	9	999824-1001128	Chr1	ISBma1	CACCG GTTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	AAAAAA'AAAAAAT	AAAAAA'	Y

IS Bma 2

						5'-ext	5'-IR	ORF	3'-IR	3'-ext	5'-DR	3'-DR	rget duplicates
								CAGATTGCTGACAAACC	GGGTCGTCAGCAGCTG				
2*Chr1_90_ISBma2_A	N	fhm	2	1003833-1005047	Chr1	ISBma2	#IS407/ ~~~~~	TCCCAGAAAGACAAAACCC	AAAGCCC(#IS407A			AAAGCCC	N.D.
3*Chr1_90_ISBma2_A	N	JHU	3	1012642-1013856	Chr1	ISBma2	#IS407/ ~~~~~	TCCCAGAAAGACAAAACCC	AAAGCCC(#IS407A			AAAGCCC	N.D.
7*Chr1_85_ISBma2_A	N	NCTC_10247	7	1012716-1014290	Chr1	ISBma2	GCCTC/CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AGCCAGC' AGCCAGCTTGGCTGGI/AGCCAGC'						N
6*Chr1_44a_ISBma2	R	NCTC_10229	6	1031963-1033543	Chr1	ISBma2	ACGGC CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AAAAGCGI/AACCCGGCTGGAGACC AAAAGCGI						N
10*Chr1_90_ISBma2_A	N	PRL20	10	1032539-1033726	Chr1	ISBma2	#IS407/ ~~~~~	TCCCAGAAAGACAAAACCC	AAAGCCC(#IS407A			AAAGCCC	N.D.
6*Chr1_41_ISBma2_A	N	NCTC_10229	6	1055116-1056005	Chr1	ISBma2	AATCA(CAGATTGCTGACAAC ATGCTGAAGACGCCATG#	#IS407A	CCCTCCACTGGAGGGC' #IS407A				N.D.
6*Chr1_39b_ISBma2	R	NCTC_10229	6	1061840-1063411	Chr1	ISBma2	GCAGG CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AAAAACC/CCGCCGCTCGGGGGC AAAAACC/						N
9*Chr1_25b_ISBma2	R	SAVP1	9	109336-110910	Chr1	ISBma2	CGCCG CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AGGCCG/CTGTCGACGACGGCC AGGCCG/						N
4*Chr1_90_ISBma2_A	N	gb8_horse_4	4	1117195-1118409	Chr1	ISBma2	#IS407/ ~~~~~	TCCCAGAAAGACAAAACCC	AAAGCCC(#IS407A			AAAGCCC	N.D.
1*Chr1_90_ISBma2_A	N	ATCC_23344	1	1124052-1125266	Chr1	ISBma2	#IS407/ ~~~~~	TCCCAGAAAGACAAAACCC	AAAGCCC(#IS407A			AAAGCCC	N.D.
6*Chr1_139a_ISBma2	R	NCTC_10229	6	1142674-1144265	Chr1	ISBma2	GCCCT(CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AGCCCGA/CCGGCGCATGGCCGCC AGCCCGA/						N
8*Chr1_90_ISBma2_A	N	2002721280	8	1167212-1168399	Chr1	ISBma2	#IS407/ ~~~~~	TCCCAGAAAGACAAAACCC	AAAGCCC(#IS407A			AAAGCCC	N.D.
2*Chr1_85_ISBma2_A	N	fhm	2	1198532-1200104	Chr1	ISBma2	GCCTC/CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AGCCAGC' AGCCAGCTTGGCTGGI/AGCCAGC'						Y
10*Chr1_23a_ISBma2_A	N	PRL20	10	120201-121772	Chr1	ISBma2	CGCCG CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC ACCCGAGI/ACCGCAGCAAGGCTG ACCCGAGI						Y
3*Chr1_85_ISBma2_A	N	JHU	3	1209720-1211292	Chr1	ISBma2	GCCTC/CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AGCCAGC' AGCCAGCTTGGCTGGI/AGCCAGC'						Y
10*Chr1_85_ISBma2_A	N	PRL20	10	1218305-1219877	Chr1	ISBma2	GCCTC/CAGATTGCTGACAAC ATGCTGAAGACGCCATG(TCCCAGAAAGACAAAACCC AGCCAGC' AGCCAGCTTGGCTGGI/AGCCAGC'						Y

8*Chr1_85_ISBma2_A	N	2002721280	8	1219726-1221298	Chr1	ISBma2	GCCTCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
6*Chr1_139b_ISBrr 6*Chr1_141b_ISBma2_A	R	NCTC_10229	6	1224724-1226315	Chr1	ISBma2	CCTCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
7*Chr1_101_ISBma7*Chr1_102_ISBma2_A	D	NCTC_10247	7	1257256-1258828	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGGCCAGT AGGCCCGCCGGAAGCGGGGCGT	N
5*Chr1_85_ISBma2_A	N	ATCC_10399	5	1260531-1262103	Chr1	ISBma2	GCCTCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
7*Chr1_39a_ISBma7*Chr1_44a_ISBma2_A	R	NCTC_10247	7	128672-130244	Chr1	ISBma2	ACCTCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
4*Chr1_85_ISBma2_A	N	gb8_horse_4	4	1307221-1308793	Chr1	ISBma2	GCCTCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
1*Chr1_85_ISBma2_A	N	ATCC_23344	1	1315507-1317079	Chr1	ISBma2	GCCTCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
6*Chr1_144_ISBma2_B	N	NCTC_10229	6	1324314-1325889	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
7*Chr1_104_ISBma2_A	N	NCTC_10247	7	1345232-1346804	Chr1	ISBma2	TACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
6*Chr1_22b_ISBma6*Chr1_147_ISBma2_A	D-R	NCTC_10229	6	1369886-1371461	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
6*Chr1_23a_ISBma2_A	N	NCTC_10229	6	1403305-1404881	Chr1	ISBma2	CGCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
6*Chr1_24_ISBma2_A	N	NCTC_10229	6	1432886-1432917	Chr1	ISBma2	GGCAAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
10*Chr1_22a_ISBma2_A	R	PRL20	10	1439664-144800	Chr1	ISBma2	#contig ~~~~~ TCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N.D.
2*Chr1_100_ISBma2_B	N	fmh	2	1446086-1447658	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
2*Chr1_101_ISBma2*Chr1_102_ISBma2_A	D	fmh	2	1449099-1450671	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGGCCAGT AGGCCCGCCGGAAGCGGGCCGT	N
3*Chr1_100_ISBma2_B	N	JHU	3	1455405-1456977	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
3*Chr1_101_ISBma3*Chr1_102_ISBma2_A	D	JHU	3	1458418-1459990	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGGCCAGT AGGCCCGCCGGAAGCGGGCCGT	N
6*Chr1_25a_ISBma6*Chr1_28a_ISBma2_A	R	NCTC_10229	6	1461808-1463379	Chr1	ISBma2	TCGAAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
8*Chr1_101_ISBma8*Chr1_102_ISBma2_A	D	2002721280	8	1463360-1464932	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGGCCAGT AGGCCCGCCGGAAGCGGGCCGT	N
6*Chr1_85_ISBma2_A	N	NCTC_10229	6	146802-148374	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
7*Chr1_105a_ISBm7*Chr1_107a_ISBma2_A	R	NCTC_10247	7	1482665-1484237	Chr1	ISBma2	TCGGGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
7*Chr1_105b_ISBrr 7*Chr1_107b_ISBma2_A	R	NCTC_10247	7	1486716-1488288	Chr1	ISBma2	AACGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
5*Chr1_90_ISBma2_A	N	ATCC_10399	5	1495313-1496527	Chr1	ISBma2	#IS407 ~~~~~ TCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N.D.
9*Chr1_90_ISBma2_A	N	SAVP1	9	1498063-1499250	Chr1	ISBma2	#IS407 ~~~~~ TCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N.D.
10*Chr1_101_ISBm10*Chr1_102_ISBma2_A	D	PRL20	10	1506540-1508112	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
6*Chr1_25b_ISBma6*Chr1_28b_ISBma2_A	R	NCTC_10229	6	1514301-1515875	Chr1	ISBma2	CGCCGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
7*Chr1_108_ISBma2_A	N	NCTC_10247	7	1518121-1519693	Chr1	ISBma2	CGTGGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
2*Chr1_104_ISBma2_A	N	fmh	2	1537752-1539324	Chr1	ISBma2	TACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
7*Chr1_110_ISBma2_A	N	NCTC_10247	7	1541726-1543298	Chr1	ISBma2	TCCCGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
3*Chr1_104_ISBma2_A	N	JHU	3	1548943-1550515	Chr1	ISBma2	TACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
4*Chr1_100_ISBma2_B	N	gb8_horse_4	4	1548991-1550563	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
8*Chr1_104_ISBma2_A	N	2002721280	8	1551398-1552969	Chr1	ISBma2	TACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
4*Chr1_101_ISBma4*Chr1_102_ISBma2_A	D	gb8_horse_4	4	1552004-1553576	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGGCCAGT AGGCCCGCCGGAAGCGGGCCGT	N
5*Chr1_19a_ISBma2_A	N	ATCC_10399	5	155357-156927	Chr1	ISBma2	CACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
1*Chr1_100_ISBma2_B	N	ATCC_23344	1	1558411-1559983	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
1*Chr1_101_ISBma1*Chr1_102_ISBma2_A	D	ATCC_23344	1	1561424-1562996	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGGCCAGT AGGCCCGCCGGAAGCGGGCCGT	N
7*Chr1_52_ISBma2_A	N	NCTC_10247	7	1590531-1592103	Chr1	ISBma2	CCGGAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
6*Chr1_163_ISBma2_A	N	NCTC_10229	6	1592743-1594343	Chr1	ISBma2	CCTTTAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
10*Chr1_104_ISBma2_A	N	PRL20	10	1594486-1596058	Chr1	ISBma2	TACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
6*Chr1_164_ISBma2_B	N	NCTC_10229	6	1625978-1627550	Chr1	ISBma2	ATGCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
9*Chr1_25a_ISBma9*Chr1_28a_ISBma2_A	R	SAVP1	9	163290-164556	Chr1	ISBma2	TCGAAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N.D.
4*Chr1_104_ISBma2_A	N	gb8_horse_4	4	1639670-1641242	Chr1	ISBma2	TACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
7*Chr1_50_ISBma2_A	N	NCTC_10247	7	1645048-1646622	Chr1	ISBma2	GCCGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
1*Chr1_104_ISBma2_A	N	ATCC_23344	1	1649393-1650965	Chr1	ISBma2	TACCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
6*Chr1_1a_ISBma26*Chr1_159b_ISBma2_A	R	NCTC_10229	6	1674101-1675677	Chr1	ISBma2	AGCTCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
2*Chr1_105a_ISBm2*Chr1_107a_ISBma2_A	R	fmh	2	1677003-1678575	Chr1	ISBma2	TCGGGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
2*Chr1_105b_ISBrr 2*Chr1_107b_ISBma2_A	R	fmh	2	1681054-1682626	Chr1	ISBma2	AACGAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
3*Chr1_105a_ISBm3*Chr1_107a_ISBma2_A	R	JHU	3	1688841-1690413	Chr1	ISBma2	TCGGGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
8*Chr1_105a_ISBm8*Chr1_107a_ISBma2_A	R	2002721280	8	1688922-1690494	Chr1	ISBma2	TCGGGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
3*Chr1_105b_ISBrr 3*Chr1_107b_ISBma2_A	R	JHU	3	1692892-1694464	Chr1	ISBma2	AACGAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
8*Chr1_105b_ISBrr 8*Chr1_107b_ISBma2_A	R	2002721280	8	1692973-1694545	Chr1	ISBma2	AACGAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	N
5*Chr1_100_ISBma2_B	N	ATCC_10399	5	1712081-1713653	Chr1	ISBma2	GCCGCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
2*Chr1_108_ISBma2_A	N	fmh	2	1713107-1714679	Chr1	ISBma2	GCGTGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
5*Chr1_101_ISBma5*Chr1_102_ISBma2_A	D	ATCC_10399	5	1715094-1716666	Chr1	ISBma2	GCATCCAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGGCCAGT AGGCCCGCCGGAAGCGGGCCGT	N
2*Chr1_109_ISBma2_B	N	fmh	2	1717544-1719116	Chr1	ISBma2	AGGCAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
8*Chr1_108_ISBma2_A	N	2002721280	8	1724386-1725958	Chr1	ISBma2	CGTGGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
3*Chr1_108_ISBma2_A	N	JHU	3	1725497-1727069	Chr1	ISBma2	GCGTGAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y
3*Chr1_109_ISBma2_B	N	JHU	3	1729934-1731506	Chr1	ISBma2	AGGCAAGATTTGCTGACAAACATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCGCCAGCAGCCAGCTTGGCTGGAGCCAGC	Y

9*Chr1_108_ISBma2_A	N	SAVP1	9	2238551-2240122	Chr1	ISBma2	CGTGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCGGGGCGCTTCGGCGCCGGGGCGC	Y
9*Chr1_109_ISBma2_B	N	SAVP1	9	2242987-2244559	Chr1	ISBma2	AGGCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGACGGC GGACGGCGGGACGCCGGACGGC	Y
2*Chr1_41_ISBma2_A	N	fmh	2	2248201-2249090	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(#IS407A CCCTCCACTGGAGGGC #IS407A	N.D.
2*Chr1_39b_ISBma2_2*Chr1_44b_ISBma2_A	R	fmh	2	2254925-2256496	Chr1	ISBma2	GCAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCTTCGGCGCCGGGGCG	N
7*Chr1_22a_ISBma2_A	R	NCTC_10247	7	2262477-2264039	Chr1	ISBma2	~~~~~AGGGGGCAGGTCAAAT ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCATTGGCCCTATAGCCCGC	N
3*Chr1_41_ISBma2_A	N	JHU	3	2263558-2264447	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(#IS407A CCCTCCACTGGAGGGC #IS407A	N.D.
9*Chr1_110_ISBma2_A	N	SAVP1	9	2263757-2265208	Chr1	ISBma2	#IS407A~~~~~TCCAGAAAGACAAAACCGGGCGCAGCCCT(#IS407A AAGCCCTC	N
8*Chr1_46a_ISBma2_A	N	2002721280	8	2267980-2269552	Chr1	ISBma2	GGAAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
3*Chr1_39b_ISBma2_3*Chr1_44b_ISBma2_A	R	JHU	3	2270282-2271853	Chr1	ISBma2	GCAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
9*Chr1_52_ISBma2_A	N	SAVP1	9	2285906-2287478	Chr1	ISBma2	CCGGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
10*Chr1_39a_ISBma2_10*Chr1_44a_ISBma2_A	R	PRL20	10	2287844-2289166	Chr1	ISBma2	ACGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
4*Chr1_46a_ISBma2_A	N	gb8_horse_4	4	2299455-2301027	Chr1	ISBma2	AATAC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
1*Chr1_46a_ISBma2_A	N	ATCC_23344	1	2311360-2312932	Chr1	ISBma2	AATAC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
8*Chr1_41_ISBma2_A	N	2002721280	8	2311719-2312608	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(#IS407A CCCTCCACTGGAGGGC #IS407A	N.D.
10*Chr1_41_ISBma2_A	N	PRL20	10	2315851-2316740	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(#IS407A CCCTCCACTGGAGGGC #IS407A	N.D.
8*Chr1_39b_ISBma2_8*Chr1_44b_ISBma2_A	R	2002721280	8	2318443-2320015	Chr1	ISBma2	GCAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
6*Chr1_13a_ISBma2_6*Chr1_32b_ISBma2_A	R	NCTC_10229	6	2330494-2332086	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
2*Chr1_139a_ISBma2_2*Chr1_141a_ISBma2_A	R	fmh	2	2335759-2337331	Chr1	ISBma2	CGCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
7*Chr1_13a_ISBma2_7*Chr1_32b_ISBma2_A	R	NCTC_10247	7	2338546-2340123	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
9*Chr1_50_ISBma2_A	N	SAVP1	9	2340294-2341866	Chr1	ISBma2	AGGCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
4*Chr1_41_ISBma2_A	N	gb8_horse_4	4	2343434-2344323	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(#IS407A CCCTCCACTGGAGGGC #IS407A	N.D.
10*Chr1_39b_ISBma2_10*Chr1_44b_ISBma2_A	R	PRL20	10	2344825-2346397	Chr1	ISBma2	GCAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
7*Chr1_118_ISBma2_A	N	NCTC_10247	7	2345666-2361338	Chr1	ISBma2	CGATC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
4*Chr1_39b_ISBma2_4*Chr1_44b_ISBma2_A	R	gb8_horse_4	4	2350107-2351678	Chr1	ISBma2	GCAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
3*Chr1_139a_ISBma2_3*Chr1_141a_ISBma2_A	R	JHU	3	2351116-2352688	Chr1	ISBma2	CGCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
1*Chr1_41_ISBma2_A	N	ATCC_23344	1	2355339-2356228	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(#IS407A CCCTCCACTGGAGGGC #IS407A	N.D.
2*Chr1_140_ISBma2_B	N	fmh	2	2357628-2359200	Chr1	ISBma2	GCGCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
1*Chr1_39b_ISBma2_1*Chr1_44b_ISBma2_A	R	ATCC_23344	1	2362064-2363635	Chr1	ISBma2	GCAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
3*Chr1_140_ISBma2_B	N	JHU	3	2372985-2374557	Chr1	ISBma2	GCGCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
10*Chr1_46a_ISBma2_A	N	PRL20	10	2378078-2379650	Chr1	ISBma2	AATAC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
8*Chr1_139a_ISBma2_8*Chr1_141a_ISBma2_A	R	2002721280	8	2398395-2399967	Chr1	ISBma2	CGCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
2*Chr1_139b_ISBma2_2*Chr1_141b_ISBma2_A	R	fmh	2	2418316-2419888	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
4*Chr1_139a_ISBma2_4*Chr1_141a_ISBma2_A	R	gb8_horse_4	4	2430897-2432469	Chr1	ISBma2	GCCCT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
3*Chr1_139b_ISBma2_3*Chr1_141b_ISBma2_A	R	JHU	3	2434455-2436027	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
7*Chr1_117a_ISBma2_A	N	NCTC_10247	7	243623-245215	Chr1	ISBma2	TCGAC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
1*Chr1_139a_ISBma2_1*Chr1_141a_ISBma2_A	R	ATCC_23344	1	2442898-2444470	Chr1	ISBma2	GCCCT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
4*Chr1_140_ISBma2_B	N	gb8_horse_4	4	2452766-2454338	Chr1	ISBma2	GCGCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
5*Chr1_46a_ISBma2_A	N	ATCC_10399	5	2460834-2462406	Chr1	ISBma2	AATAC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
1*Chr1_140_ISBma2_B	N	ATCC_23344	1	2464767-2466339	Chr1	ISBma2	GCGCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
8*Chr1_139b_ISBma2_8*Chr1_141b_ISBma2_A	R	2002721280	8	2478896-2480470	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
10*Chr1_22b_ISBma2_10*Chr1_141a_ISBma2_A	R	PRL20	10	2490911-2492483	Chr1	ISBma2	CGCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
8*Chr1_155_ISBma2_B	N	2002721280	8	2494952-2496499	Chr1	ISBma2	~CTTC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
7*Chr1_32a_ISBma2_7*Chr1_141a_ISBma2_A	R	NCTC_10247	7	2496018-2497590	Chr1	ISBma2	TGTGT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
5*Chr1_41_ISBma2_A	N	ATCC_10399	5	2504830-2505719	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(#IS407A CCCTCCACTGGAGGGC #IS407A	N.D.
9*Chr1_117a_ISBma2_A	N	SAVP1	9	2505752-2507325	Chr1	ISBma2	TTTTG(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
5*Chr1_39b_ISBma2_5*Chr1_44b_ISBma2_A	R	ATCC_10399	5	2511431-2513003	Chr1	ISBma2	GCAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
4*Chr1_139b_ISBma2_4*Chr1_141b_ISBma2_A	R	gb8_horse_4	4	2513056-2514628	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
9*Chr1_118_ISBma2_A	N	SAVP1	9	2514844-2516416	Chr1	ISBma2	CGATC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
1*Chr1_139b_ISBma2_1*Chr1_141b_ISBma2_A	R	ATCC_23344	1	2525029-2526601	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
9*Chr1_22b_ISBma2_9*Chr1_141a_ISBma2_A	R	SAVP1	9	254941-256513	Chr1	ISBma2	GCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
9*Chr1_120_ISBma2_A	N	SAVP1	9	2551397-2552969	Chr1	ISBma2	AGGCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	Y
6*Chr1_39a_ISBma2_6*Chr1_46b_ISBma2_A	R	NCTC_10229	6	2558075-2559647	Chr1	ISBma2	GGAAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
2*Chr1_147_ISBma2_A	D-R	fmh	2	2563010-2564573	Chr1	ISBma2	~~~~~AGGGGGCAGGTCAAAT ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
8*Chr1_151b_ISBma2_8*Chr1_159b_ISBma2_A	R	2002721280	8	2565718-2567265	Chr1	ISBma2	~~~~~NNNNNNNNNNNNNNI ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N.D.
9*Chr1_121_ISBma2_A	N	SAVP1	9	2567125-2567395	Chr1	ISBma2	#IS407A~~~~~TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N.D.
10*Chr1_139b_ISBma2_10*Chr1_141b_ISBma2_A	R	PRL20	10	2571166-2572738	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
7*Chr1_139b_ISBma2_7*Chr1_141b_ISBma2_A	R	NCTC_10247	7	2576418-2577992	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N
3*Chr1_147_ISBma2_A	D-R	JHU	3	2579658-2581221	Chr1	ISBma2	~~~~~AGGGGGCAGGTCAAAT ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCGCAGCCCTAGG AAAAGCG	N

5*Chr1_139a_ISBm5*Chr1_141a_ISBma2_A	R	ATCC_10399	5	2593046-2594618	Chr1	ISBma2	GCCCT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGCCG)CCGGCGATGGCCGCGAGCCCGA	N
5*Chr1_140_ISBma2_B	N	ATCC_10399	5	2614915-2616487	Chr1	ISBma2	GCGCA CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGCCCGACGCGCCGCGGGGACGCCCC	Y
9*Chr1_46a_ISBma2_A	N	SAVP1	9	2618874-2620446	Chr1	ISBma2	AATAC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAAAGCG)AAAAGCGCCCTAGG AAAAGCG	Y
7*Chr1_1b_ISBma2*7*Chr1_19a_ISBma2_A	R	NCTC_10247	7	2622004-2623575	Chr1	ISBma2	GCACG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)GAGGGCGTCGCCCTCC AACCCG	N
6*Chr1_130_ISBma2_B	N	NCTC_10229	6	2622284-2623857	Chr1	ISBma2	GTC(CA CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCGAT)AGCCGATGCGCGCAGCAGCGGAT	Y
8*Chr1_148_ISBma8*Chr1_159a_ISBma2_A	D-R	2002721280	8	2648477-2650049	Chr1	ISBma2	GGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AGGGCCGATGAAGCAGGCCCC	N
4*Chr1_147_ISBma2_A	D-R	gb8_horse_4	4	2657553-2659116	Chr1	ISBma2	~~~~~AGGGGGCAGGTCAA(ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCCCATTTGCCCTA)AGGCGCC	N
1*Chr1_147_ISBma2_A	D-R	ATCC_23344	1	2669533-2671096	Chr1	ISBma2	~~~~~AGGGGGCAGGTCAA(ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCCCATTTGCCCTA)AGGCGCC	N
5*Chr1_139b_ISBr5*Chr1_141b_ISBma2_A	R	ATCC_10399	5	2675065-2676637	Chr1	ISBma2	CCTCC(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)CCGAACCGGGTTC)AGCCCGG	N
10*Chr1_139a_ISB10*Chr1_147_ISBma2_A	D-R	PRL20	10	2714631-2716203	Chr1	ISBma2	GCCCT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)CCGGCGATGGCCGCGAGCCG	N
10*Chr1_138_ISBma2_C	N	PRL20	10	2727692-2728537	Chr1	ISBma2	~~~~~AGGGGGCAGGTCAA(ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCCCATTTGCCCTA)AGGCGCC	N.D.
2*Chr1_151a_ISBma2_A	N	fmh	2	2742888-2744460	Chr1	ISBma2	AGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCGCCCTTTCGGCC(AGCCCGC	N
8*Chr1_151a_ISBma2_A	R	2002721280	8	2747570-2749142	Chr1	ISBma2	ATTTCC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)GCCCGCTTCGGCGGG AACCCGC	N
7*Chr1_23b_ISBma7*Chr1_151a_ISBma2_A	R	NCTC_10247	7	2756502-2758099	Chr1	ISBma2	CGCGC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)ACCGCAGCGAAGGCTG AACCCGC	N
3*Chr1_151a_ISBma2_A	N	JHU	3	2758991-2760563	Chr1	ISBma2	AGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCCGCTTTCGGCC(AGCCCGC	N
9*Chr1_13a_ISBma9*Chr1_32b_ISBma2_A	R	SAVP1	9	2763087-2764659	Chr1	ISBma2	GCGAC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCG)GACCCGCTGGGCGGTGAGCGGC	N
2*Chr1_1b_ISBma2_A	R	fmh	2	2776259-2777831	Chr1	ISBma2	ATTTCC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)GCCCGCTTCGGCGGG AACCCGC	Y
7*Chr1_24_ISBma2_A	N	NCTC_10247	7	2784533-2786105	Chr1	ISBma2	GGCAA CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)AACCCGCTCGGAGGC AACCCGC	N
2*Chr1_148_ISBma2*Chr1_159a_ISBma2_A	D-R	fmh	2	2784984-2786556	Chr1	ISBma2	GGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AGGGCCGATGAAGCGAGGCCCG	N
8*Chr1_3_ISBma2_C	N	2002721280	8	2785321-2786893	Chr1	ISBma2	AAAGC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AGCCCGCATGAGCCGAGCCCG	Y
3*Chr1_1b_ISBma2_A	R	JHU	3	2791386-2792958	Chr1	ISBma2	ATTTCC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)GCCCGCTTCGGCGGG AACCCGC	N
2*Chr1_39a_ISBma2*Chr1_117b_ISBma2_A	R	fmh	2	279549-281121	Chr1	ISBma2	TTTCG(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAGCCCT(AACCCGGTGGAGCC AAGCCCT	N
3*Chr1_148_ISBma3*Chr1_159a_ISBma2_A	D-R	JHU	3	2800111-2801683	Chr1	ISBma2	GGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AGGGCCGATGAAGCGAGGCCCG	N
3*Chr1_39a_ISBma3*Chr1_117b_ISBma2_A	R	JHU	3	280544-282116	Chr1	ISBma2	TTTCG(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAGCCCT(AACCCGGTGGAGCC AAGCCCT	N
8*Chr1_39a_ISBma8*Chr1_117b_ISBma2_A	R	2002721280	8	280947-282519	Chr1	ISBma2	TTGAA(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCT)AACCCGCTTTCAGCGCAAGCCCTC	N
7*Chr1_25a_ISBma7*Chr1_28a_ISBma2_A	R	NCTC_10247	7	2814990-2816561	Chr1	ISBma2	TCAA(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)CCGCGCGTTCGGCGGGAGCCCGC	N
5*Chr1_147_ISBma2_A	D-R	ATCC_10399	5	2818680-2820243	Chr1	ISBma2	~~~~~AGGGGGCAGGTCAA(ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCCCATTTGCCCTA)AGGCGCC	N
8*Chr1_1a_ISBma2_A	N	2002721280	8	2824135-2825706	Chr1	ISBma2	AGCTG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)CCGCTGGTTTCAGCGC AACCCGC	N
4*Chr1_151a_ISBma2_A	N	gb8_horse_4	4	2834020-2835592	Chr1	ISBma2	AGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCGCCCTTTCGGCC(AGCCCGC	N
1*Chr1_151a_ISBma2_A	N	ATCC_23344	1	2847519-2849091	Chr1	ISBma2	AGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCCGCTTTCGGCC(AGCCCGC	N
4*Chr1_1b_ISBma2_A	R	gb8_horse_4	4	2866443-2868015	Chr1	ISBma2	ATTTCC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)GCCCGCTTCGGCGGG AACCCGC	N
7*Chr1_25b_ISBma7*Chr1_28b_ISBma2_A	R	NCTC_10247	7	2867420-2868994	Chr1	ISBma2	CGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)CTGTCGAGGACGGCG AGGCCCG	N
8*Chr1_164_ISBma2_B	N	2002721280	8	2872259-2873831	Chr1	ISBma2	ATGCC(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCAG)AGGAGCCGAGGGGAGGAGG	Y
4*Chr1_148_ISBma4*Chr1_159a_ISBma2_A	D-R	gb8_horse_4	4	2875168-2876717	Chr1	ISBma2	GGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AGGGCCGATGAAGCGAGGCCCG	N
1*Chr1_1b_ISBma2_A	R	ATCC_23344	1	2879914-2881486	Chr1	ISBma2	ATTTCC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)CCGCTGGTTTCAGCGC AACCCGC	N
9*Chr1_13b_ISBma9*Chr1_32a_ISBma2_A	R	SAVP1	9	2884897-2886468	Chr1	ISBma2	TGTGT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAGGCA)AGAGCGGCCCGAAGGCAACGGAC	N
2*Chr1_118_ISBma2_A	N	fmh	2	288595-290167	Chr1	ISBma2	CGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAGCG)AAGCGCCCGGGCAAC AAGCGCG	Y
1*Chr1_148_ISBma1*Chr1_159a_ISBma2_A	D-R	ATCC_23344	1	2888639-2890211	Chr1	ISBma2	GGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AGGGCCGATGAAGCGAGGCCCG	N
10*Chr1_151a_ISBma2_A	N	PRL20	10	2889009-2890581	Chr1	ISBma2	AGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAACCCG)AAGCGCCCTTTCGGCC(AACCCGC	N
10*Chr1_1b_ISBma2_A	R	PRL20	10	2896600-2898131	Chr1	ISBma2	#IS407)~~~~~GCTGAGAAGCGCCATG(TCCAGAAAGACAAAACCGAACCCG)AAGCCCGCTTTCAGCGC AACCCGC	N.D.
2*Chr1_1a_ISBma2*Chr1_159b_ISBma2_A	R	fmh	2	2900149-2901721	Chr1	ISBma2	AGCTG(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCCG)CCGCTGGTTTCAGCGC GGGCCG	N
8*Chr1_118_ISBma2_A	N	2002721280	8	290022-291594	Chr1	ISBma2	CGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAGCG)AAGCGCCCGGGCAAC AAGCGCG	Y
3*Chr1_118_ISBma2_A	N	JHU	3	290199-291771	Chr1	ISBma2	CGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAGCG)AAGCGCCCGGGCAAC AAGCGCG	Y
10*Chr1_148_ISBr10*Chr1_159a_ISBma2_A	D-R	PRL20	10	2904760-2906332	Chr1	ISBma2	GGATT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AGGGCCGATGAAGCGAGGCCCG	N
8*Chr1_163_ISBma2_A	N	2002721280	8	2905615-2907162	Chr1	ISBma2	~~~~~CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGTCTCGCGAAGGGCGAG TGCTCGC	Y
5*Chr1_151a_ISBma2_A	N	ATCC_10399	5	2907488-2909060	Chr1	ISBma2	AGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)AAGCGCCCTTTCGGCC(AGCCCGC	N
3*Chr1_1a_ISBma2*3*Chr1_159b_ISBma2_A	R	JHU	3	2915891-2917463	Chr1	ISBma2	AGCTG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCCG)CCGCTGGTTTCAGCGC GGGCCG	N
7*Chr1_1a_ISBma2*7*Chr1_159b_ISBma2_A	R	NCTC_10247	7	2928340-2929912	Chr1	ISBma2	AGCTG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCCG)CCGCTGGTTTCAGCGC GGGCCG	N
9*Chr1_17_ISBma2_C	N	SAVP1	9	2957135-2958707	Chr1	ISBma2	TGAG(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAAGCG)AAGCGCCCTGGGCGC AAGCGCC	Y
6*Chr1_50_ISBma2_A	N	NCTC_10229	6	2971768-2973340	Chr1	ISBma2	GCGAC CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCG)GGGGCGGAGCTACT GGGCCG	Y
7*Chr1_164_ISBma2_B	N	NCTC_10247	7	2974663-2978010	Chr1	ISBma2	~~~~~CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCAG)AGGAGCCCGAGGGAGC	Y
2*Chr1_163_ISBma2_A	N	fmh	2	2979940-2981512	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGTCTCGC)TGCTCGGAAGGGCGAG TGCTCGC	Y
8*Chr1_25b_ISBma8*Chr1_28b_ISBma2_A	R	2002721280	8	2983988-2985560	Chr1	ISBma2	CGCCG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCCCG)CTGTCGAGGACGGCG AGGCCCG	N
4*Chr1_1a_ISBma2*4*Chr1_159b_ISBma2_A	R	gb8_horse_4	4	2988475-2990047	Chr1	ISBma2	AGCTG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCCG)CCGCTGGTTTCAGCGC GGGCCG	N
3*Chr1_163_ISBma2_A	N	JHU	3	2996311-2997883	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGTCTCGC)TGCTCGGAAGGGCGAG TGCTCGC	Y
1*Chr1_1a_ISBma2*1*Chr1_159b_ISBma2_A	R	ATCC_23344	1	3002230-3003802	Chr1	ISBma2	AGCTG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGGGCCG)CCGCTGGTTTCAGCGC GGGCCG	N
9*Chr1_19a_ISBma2_A	N	SAVP1	9	3005415-3006987	Chr1	ISBma2	GACG CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGAGCG)AGCGGAGGCGTGCC AGCGGAG	Y
7*Chr1_163_ISBma2_A	N	NCTC_10247	7	3009753-3011300	Chr1	ISBma2	~~~~~CAGATTGCTGACAAACATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCGTCTCGC)TGCTCGGAAGGGCGAG TGCTCGC	Y

6*Chr1_52_ISBma2_A	N	NCTC_10229	6	3026236-3027808	Chr1	ISBma2	CCGGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC ACGGCCG)ACGGCCGCTCACGC ACGGCCG	Y
5*Chr1_1b_ISBma2_A	R	ATCC_10399	5	3029164-3030736	Chr1	ISBma2	ATTTC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACCCCG)GCCCCGCTCGCCGG AACCCGC	N
8*Chr1_25a_ISBma8*Chr1_28a_ISBma2_A	R	2002721280	8	3036431-3038003	Chr1	ISBma2	TCGAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG) CCGCGCGTCGCGCGG AGCCCGC	N
5*Chr1_148_ISBma5*Chr1_159a_ISBma2_A	D-R	ATCC_10399	5	3037889-3039461	Chr1	ISBma2	GGATT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)ACGGCCGATGAAGCGAGCCCGC	N
10*Chr1_1a_ISBma10*Chr1_159b_ISBma2_A	R	PRL20	10	3039719-3041290	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)CCCGCTGTTTCAGCG GGGCCGC	N
8*Chr1_23a_ISBma8*Chr1_24_ISBma2_A	D	2002721280	8	3066888-3068460	Chr1	ISBma2	GGCAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC ACCCGAG)ACCCGCTCGGAGGCG ACCGCAG	N
4*Chr1_163_ISBma2_A	N	gb8_horse_4	4	3068266-3069838	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC TGCTCGCT)TGCTCGGAAGGCGAG TGCTCGCC	Y
9*Chr1_108_ISBma2_A	R	SAVP1	9	3073996-3075559	Chr1	ISBma2	~~~~~AGGGGGCAGTCAAA ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG)ACCCATATGGCCCTATC AGCCCGC	N
6*Chr1_110_ISBma2_A	N	NCTC_10229	6	3075066-3076638	Chr1	ISBma2	TCCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AAGCCCT)GCCCTGCGATGCGAG AAGCCCT	N
1*Chr1_163_ISBma2_A	N	ATCC_23344	1	3082021-3083593	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC TGCTCGCT)TGCTCGGAAGGCGAG TGCTCGCC	Y
6*Chr1_108_ISBma2_A	N	NCTC_10229	6	3098671-3100243	Chr1	ISBma2	CGTGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCGC)GGGGCGCTTCGGCCGC GGGCCGC	Y
8*Chr1_22b_ISBma8*Chr1_147_ISBma2_A	D-R	2002721280	8	3100401-3101948	Chr1	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)AGCCCGCAGACGCGG AGGCCGC	N
10*Chr1_163_ISBma2_A	N	PRL20	10	3119525-3121095	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC TGCTCGCT)TGCTCGGAAGGCGAG TGCTCGCC	Y
6*Chr1_105b_ISBrr6*Chr1_107b_ISBma2_A	R	NCTC_10229	6	3130076-3131648	Chr1	ISBma2	AACGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AAGCCCG)CCCGCTGTTTCAGCG AAGCCCG	N
6*Chr1_105a_ISBrr6*Chr1_107a_ISBma2_A	R	NCTC_10229	6	3134127-3135699	Chr1	ISBma2	TCCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AAGCCCG)CCCGCTGTTTCAGCG AAGCCCG	N
2*Chr1_25b_ISBma2*Chr1_28b_ISBma2_A	R	fmh	2	3135195-3136770	Chr1	ISBma2	CGCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)CTGTCGAGGACGGG AGGCCCG	N
7*Chr1_148_ISBma7*Chr1_159a_ISBma2_A	D-R	NCTC_10247	7	3140775-3142376	Chr1	ISBma2	~~~~~CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)AGGGCCGATGAAGCG AGGCCCG	N
8*Chr1_144_ISBma2_B	N	2002721280	8	3145687-3147259	Chr1	ISBma2	CGCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)AGCCCGCAGTGCAGG AGGCCCG	N
7*Chr1_23a_ISBma2_A	R	NCTC_10247	7	3149499-3151071	Chr1	ISBma2	ATTTC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC ACCCGAG)GCCCGCTTCGGCGG ACCGCAG	N
3*Chr1_25b_ISBma3*Chr1_28b_ISBma2_A	R	JHU	3	3152397-3153972	Chr1	ISBma2	CGCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)CTGTCGAGGACGGG AGGCCCG	N
9*Chr1_125a_ISBma2_A	N	SAVP1	9	3162470-3164042	Chr1	ISBma2	AGCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACCCGC)AACCAGGCTTCGGCC ATCCCGC	N
5*Chr1_163_ISBma2_A	N	ATCC_10399	5	3169120-3170692	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC TGCTCGCT)TGCTCGGAAGGCGAG TGCTCGCC	Y
7*Chr1_22b_ISBma7*Chr1_147_ISBma2_A	D-R	NCTC_10247	7	3182889-3184461	Chr1	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)AGCCCGCAGACGCGG AGGCCCG	N
2*Chr1_25a_ISBma2*Chr1_28a_ISBma2_A	R	fmh	2	3187985-3189557	Chr1	ISBma2	TCGAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG) CCGCGCGTCGCGCGG AGCCCGC	N
3*Chr1_25a_ISBma3*Chr1_28a_ISBma2_A	R	JHU	3	3204878-3206450	Chr1	ISBma2	TCCGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG)CCCGCTCGCGCGG AGCCCGC	N
8*Chr1_13b_ISBma8*Chr1_32a_ISBma2_A	R	2002721280	8	3218859-3220433	Chr1	ISBma2	TGTGT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACGGAG)AGAGGGGGCCGAAGGCAACGGAG	N
2*Chr1_24_ISBma2_A	N	fmh	2	3218895-3220466	Chr1	ISBma2	GGCAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACCCCG)AACCCGCTCGGAGG ACCCCGC	Y
4*Chr1_25b_ISBma4*Chr1_28b_ISBma2_A	R	gb8_horse_4	4	3222056-3223631	Chr1	ISBma2	CGCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)ATGTCGAGGACGGG AGCCCGC	N
7*Chr1_144_ISBma2_B	N	NCTC_10247	7	3228362-3229936	Chr1	ISBma2	GCGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG)AGCCCGCAGTGCAGG AGCCCGC	Y
1*Chr1_25b_ISBma1*Chr1_28b_ISBma2_A	R	ATCC_23344	1	3235804-3237379	Chr1	ISBma2	CGCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)CTGTCGAGGACGGG AGCCCGC	Y
3*Chr1_24_ISBma2_A	N	JHU	3	3236786-3238357	Chr1	ISBma2	GGCAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACCCCG)AACCCGCTCGGAGG ACCCCGC	Y
2*Chr1_13b_ISBma2*Chr1_23b_ISBma2_A	R	fmh	2	3247169-3248741	Chr1	ISBma2	GCGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACGGAG)ACCCAGCGAAGGCTG AACGGAG	N
5*Chr1_1a_ISBma25*Chr1_159b_ISBma2_A	R	ATCC_10399	5	3248886-3250457	Chr1	ISBma2	AGCTG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCGC)CCCGCTGTTTCAGCG GGGCCGC	N
2*Chr1_120_ISBma2_A	N	fmh	2	325136-326708	Chr1	ISBma2	AGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCCG)GGCCCGCGAAGGGG GGGCCCG	Y
3*Chr1_13b_ISBma3*Chr1_23b_ISBma2_A	R	JHU	3	3265431-3267003	Chr1	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACGGAG)ACCCAGCGAAGGCTG AACGGAG	N
8*Chr1_120_ISBma2_A	N	2002721280	8	326581-328153	Chr1	ISBma2	AGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCCG)GGCCCGCGAAGGGG GGGCCCG	Y
3*Chr1_120_ISBma2_A	N	JHU	3	326740-328312	Chr1	ISBma2	AGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCCG)GGCCCGCGAAGGGG GGGCCCG	Y
6*Chr1_104_ISBma2_A	N	NCTC_10229	6	3271547-3273119	Chr1	ISBma2	TCCCC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC ACCGGCG)ACCCGCGATTTCGCGG AGCCCGC	Y
10*Chr1_25b_ISBrr10*Chr1_28b_ISBma2_A	R	PRL20	10	3271661-3273235	Chr1	ISBma2	CGCCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)CTGTCGAGGACGGG AGGCCCG	N
4*Chr1_25a_ISBma4*Chr1_28a_ISBma2_A	R	gb8_horse_4	4	3274537-3276109	Chr1	ISBma2	TCGAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG) CCGCGCGTCGCGCGG AGCCCGC	N
9*Chr1_163_ISBma2_A	N	SAVP1	9	3283458-3285029	Chr1	ISBma2	CGCTT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC TGCTCGCT)TGCTCGGAAGGCGAG TGCTCGCC	Y
1*Chr1_25a_ISBma1*Chr1_28a_ISBma2_A	R	ATCC_23344	1	3288285-3289857	Chr1	ISBma2	TCGAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG) CCGCGCGTCGCGCGG AGCCCGC	N
2*Chr1_16_ISBma2_B	N	fmh	2	3304741-3306313	Chr1	ISBma2	CAAGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC ACCGGAG)ACCCGAGCGGAGGCT ACCGGAG	Y
4*Chr1_24_ISBma2_A	N	gb8_horse_4	4	3305019-3306590	Chr1	ISBma2	GGCAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACCCCG)AACCCGCTCGGAGG ACCCCGC	Y
5*Chr1_25b_ISBma5*Chr1_28b_ISBma2_A	R	ATCC_10399	5	3309804-3311376	Chr1	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGGCCCG)CTGTCGAGGACGGG AGCCCGC	N
1*Chr1_24_ISBma2_A	N	ATCC_23344	1	3318742-3320313	Chr1	ISBma2	GGCAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACCCCG)AACCCGCTCGGAGG ACCCCGC	Y
3*Chr1_16_ISBma2_B	N	JHU	3	3322942-3324514	Chr1	ISBma2	CAAGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC ACCGGAG)ACCCGAGCGGAGGCT ACCGGAG	Y
10*Chr1_25a_ISBrr10*Chr1_28a_ISBma2_A	R	PRL20	10	3325434-3326700	Chr1	ISBma2	TCGAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACCCCG)AACCCGCTCGGAGG ACCCCGC	N.D.
4*Chr1_13b_ISBma4*Chr1_23b_ISBma2_A	R	gb8_horse_4	4	3333036-3334608	Chr1	ISBma2	GCGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACGGAG)ACCCAGCGAAGGCTG AACGGAG	N
8*Chr1_19a_ISBma2_A	N	2002721280	8	3336593-3338164	Chr1	ISBma2	GCAGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC ACCGGAG)AGCCGAGGGCGCTCGC ACCGGAG	N
1*Chr1_13b_ISBma1*Chr1_23b_ISBma2_A	R	ATCC_23344	1	3346749-3348321	Chr1	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AACGGAG)ACCCAGCGAAGGCTG AACGGAG	N
10*Chr1_24_ISBma2_A	N	PRL20	10	3356063-3357634	Chr1	ISBma2	GGCAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG)AACCCGCTCGGAGG AGCCCGC	N
9*Chr1_139b_ISBrr9*Chr1_141b_ISBma2_A	R	SAVP1	9	335753-337325	Chr1	ISBma2	CCTC1 CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCCG)CCGAACAGCGGTTG GGGCCCG	N
6*Chr1_101_ISBma6*Chr1_102_ISBma2_A	D	NCTC_10229	6	3359529-3361101	Chr1	ISBma2	CGATC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCCG)AGCCCGCGAAGCGG GGGCCGT	N
5*Chr1_25a_ISBma5*Chr1_28a_ISBma2_A	R	ATCC_10399	5	3362254-3363825	Chr1	ISBma2	TCGAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCCG) CCGCGCGTCGCGCGG AGCCCGC	N
9*Chr1_1a_ISBma29*Chr1_159b_ISBma2_A	R	SAVP1	9	3363178-3364749	Chr1	ISBma2	AGCTG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC GGGCCGC)CCCGCTGTTTCAGCG GGGCCGC	N
2*Chr1_19a_ISBma2_A	N	fmh	2	3368613-3370185	Chr1	ISBma2	CACGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCGAG)AGCCGAGGGCGCTCGC AGCCGAG	N
3*Chr1_19a_ISBma2_A	N	JHU	3	3387044-3388616	Chr1	ISBma2	GCAGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATG(TCCAGAAAGACAAAACCC AGCCGAG)AGCCGAGGGCGCTCGC AGCCGAG	Y

4*Chr1_16_ISBma2_B	N	gb8_horse_4	4	3388601-3390173	Chr1	ISBma2	CAAGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGGAGI ACCGGAGCGGAGGCT ACCGGAG	Y	
5*Chr1_24_ISBma2_A	N	ATCC_10399	5	3392781-3394352	Chr1	ISBma2	GGCAA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AACCCGCCTGGAGGC AACCCGC	Y	
7*Chr1_13b_ISBma2_7*Chr1_151b_ISBma2_A	R	NCTC_10247	7	3400063-3401662	Chr1	ISBma2	~~~~~ CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACGGAC(AAGCCGCCTTTCGGCC(AACGGAC	N	
1*Chr1_16_ISBma2_B	N	ATCC_23344	1	3402607-3404179	Chr1	ISBma2	CAAGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGGAGI ACCGGAGCGGAGGCT ACCGGAG	Y	
8*Chr1_3054-3404616	R	2002721280	8	3403054-3404616	Chr1	ISBma2	~~~~~ AGGGGGCAGTCAAAT ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AAGCCATTTGCCCTATC AACCCGC	N	
2*Chr1_121_ISBma2_A	N	fmh	2	340994-341134	Chr1	ISBma2	#IS407/~~~~~ TCCAGAAAGACAAAACCC AAGCCCTT#IS407A	AAGCCCTI	N.D.
5*Chr1_13b_ISBma2_5*Chr1_23b_ISBma2_A	R	ATCC_10399	5	3421617-3423189	Chr1	ISBma2	CGCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACGGAC(AACCCGCAGGAAGGCTG AACGGAC	N	
8*Chr1_121_ISBma2_A	N	2002721280	8	342439-342579	Chr1	ISBma2	#IS407/~~~~~ TCCAGAAAGACAAAACCC AAGCCCTT#IS407A	AAGCCCTI	N.D.
3*Chr1_121_ISBma2_A	N	JHU	3	342598-342738	Chr1	ISBma2	#IS407/~~~~~ TCCAGAAAGACAAAACCC AAGCCCTT#IS407A	AAGCCCTI	N.D.
4*Chr1_19a_ISBma2_A	N	gb8_horse_4	4	3452144-3453716	Chr1	ISBma2	GCACG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCGGAG AGCGGAGGGCGTCGCC AGCGGAG	Y	
1*Chr1_19a_ISBma2_A	N	ATCC_23344	1	3466142-3467714	Chr1	ISBma2	GCACG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCGGAG AGCGGAGGGCGTCGCC AGCGGAG	Y	
10*Chr1_19a_ISBma2_A	N	PRL20	10	3468840-3470412	Chr1	ISBma2	GCACG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCGGAG AGCGGAGGGCGTCGCC AGCGGAG	Y	
7*Chr1_155_ISBma2_B	N	NCTC_10247	7	3470928-3472505	Chr1	ISBma2	CCTTC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GGCTGGA GGCTGGAATCCGGGA GGCTGGA	Y	
2*Chr1_23a_ISBma2_2*Chr1_32a_ISBma2_A	R	fmh	2	3472335-3473907	Chr1	ISBma2	TGTGT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGCAGI AGAGCGGCCCGAAGGC ACCGCAGI	N	
5*Chr1_16_ISBma2_B	N	ATCC_10399	5	3477498-3479070	Chr1	ISBma2	CAAGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGGAGI ACCGGAGCGGAGGCT ACCGGAG	N	
9*Chr1_1b_ISBma2_A	R	SAVP1	9	3479600-3481131	Chr1	ISBma2	#IS407/~~~~~ GGTGAGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC#IS407A	AACCCGC	N.D.
3*Chr1_23a_ISBma2_3*Chr1_32a_ISBma2_A	R	JHU	3	3492452-3494024	Chr1	ISBma2	TGTGT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGCAGI AGAGCGGCCCGAAGGC ACCGCAGI	N	
2*Chr1_22a_ISBma2_A	N	fmh	2	3507025-3508597	Chr1	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCCCGC(AAGCCGCGAGACGCCG AGCCCGC	Y	
3*Chr1_22a_ISBma2_A	N	JHU	3	3527903-3529475	Chr1	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCCCGC(AAGCCGCGAGACGCCG AGCCCGC	Y	
2*Chr1_44a_ISBma2_2*Chr1_117a_ISBma2_A	R	fmh	2	393333-394905	Chr1	ISBma2	ACGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AACCCGGCTGGAAGCC AACCCGC	N	
3*Chr1_44a_ISBma2_3*Chr1_117a_ISBma2_A	R	JHU	3	394492-396064	Chr1	ISBma2	ACGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AACCCGGCTGGAAGCC AACCCGC	N	
8*Chr1_44a_ISBma2_8*Chr1_117a_ISBma2_A	R	2002721280	8	396339-397912	Chr1	ISBma2	ACGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AACCCGGCTGGAAGCC AACCCGC	N	
10*Chr1_118_ISBma2_A	N	PRL20	10	400418-401990	Chr1	ISBma2	CGATC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAGCGC(AAGCGCCCGGGCAAC AAGCGCC	Y	
4*Chr1_39a_ISBma2_4*Chr1_117b_ISBma2_A	R	gb8_horse_4	4	401987-403559	Chr1	ISBma2	TTTTCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAGCCCT(AACCCGGCTGGAAGCC AAGCCCT	N	
1*Chr1_39a_ISBma2_1*Chr1_117b_ISBma2_A	R	ATCC_23344	1	403674-405246	Chr1	ISBma2	TTTTCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAGCCCT(AACCCGGCTGGAAGCC AAGCCCT	N	
4*Chr1_118_ISBma2_A	N	gb8_horse_4	4	411034-412606	Chr1	ISBma2	CGATC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAGCGC(AAGCGCCCGGGCAAC AAGCGCC	Y	
1*Chr1_118_ISBma2_A	N	ATCC_23344	1	412720-414292	Chr1	ISBma2	CGATC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAGCGC(AAGCGCCCGGGCAAC AAGCGCC	Y	
10*Chr1_120_ISBma2_A	N	PRL20	10	436971-438543	Chr1	ISBma2	AGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GGCGCC(GGGCCCGCAAGGGCG GGGCCCG	Y	
5*Chr1_39a_ISBma2_5*Chr1_117b_ISBma2_A	R	ATCC_10399	5	440655-442227	Chr1	ISBma2	TTTTCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAGCCCT(AACCCGGCTGGAAGCC AAGCCCT	N	
4*Chr1_120_ISBma2_A	N	gb8_horse_4	4	447575-449147	Chr1	ISBma2	AGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GGCGCC(GGGCCCGCAAGGGCG GGGCCCG	Y	
1*Chr1_120_ISBma2_A	N	ATCC_23344	1	449261-450833	Chr1	ISBma2	AGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GGCGCC(GGGCCCGCAAGGGCG GGGCCCG	Y	
5*Chr1_118_ISBma2_A	N	ATCC_10399	5	449701-451273	Chr1	ISBma2	CGATC(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAGCGC(AAGCGCCCGGGCAAC AAGCGCC	Y	
10*Chr1_121_ISBma2_A	N	PRL20	10	452829-452969	Chr1	ISBma2	#IS407/~~~~~ TCCAGAAAGACAAAACCC AAGCCCTT#IS407A	AAGCCCTI	N.D.
10*Chr1_123_ISBma2_C	N	PRL20	10	454308-455880	Chr1	ISBma2	TGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCCCGC(AAGCCGCTGGAAGG AGCCCGC	Y	
4*Chr1_121_ISBma2_A	N	gb8_horse_4	4	463433-463573	Chr1	ISBma2	#IS407/~~~~~ TCCAGAAAGACAAAACCC AAGCCCTT#IS407A	AAGCCCTI	N.D.
1*Chr1_121_ISBma2_A	N	ATCC_23344	1	465119-465259	Chr1	ISBma2	#IS407/~~~~~ TCCAGAAAGACAAAACCC AAGCCCTT#IS407A	AAGCCCTI	N.D.
9*Chr1_139a_ISBma2_9*Chr1_147_ISBma2_A	D-R	SAVP1	9	479288-480860	Chr1	ISBma2	GCCCT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCGCC(CCGCGCATGGCGCC AGGGCC	N	
5*Chr1_120_ISBma2_A	N	ATCC_10399	5	486272-487844	Chr1	ISBma2	AGCCA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GGCGCC(GGGCCCGCAAGGGCG GGGCCCG	Y	
10*Chr1_117a_ISBma2_A	N	PRL20	10	489817-491390	Chr1	ISBma2	TTTTCG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AACCCGGCTGGAAGCC AACCCGC	N	
5*Chr1_121_ISBma2_A	N	ATCC_10399	5	502130-502270	Chr1	ISBma2	#IS407/~~~~~ TCCAGAAAGACAAAACCC AAGCCCTT#IS407A	AAGCCCTI	N.D.
4*Chr1_44a_ISBma2_4*Chr1_117a_ISBma2_A	R	gb8_horse_4	4	515358-516930	Chr1	ISBma2	ACGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AACCCGGCTGGAAGCC AACCCGC	N	
3*Chr1_13a_ISBma2_3*Chr1_32b_ISBma2_A	R	JHU	3	51562-53134	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GAGCGGC GACCCGCTGGGCGGT GAGCGGC	N	
1*Chr1_44a_ISBma2_1*Chr1_117a_ISBma2_A	R	ATCC_23344	1	517013-518585	Chr1	ISBma2	ACGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AACCCGGCTGGAAGCC AACCCGC	N	
2*Chr1_13a_ISBma2_2*Chr1_32b_ISBma2_A	R	fmh	2	51985-53557	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GAGCGGC GACCCGCTGGGCGGT GAGCGGC	N	
8*Chr1_13a_ISBma2_8*Chr1_32b_ISBma2_A	R	2002721280	8	52889-54461	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GAGCGGC GACCCGCTGGGCGGT GAGCGGC	N	
5*Chr1_13a_ISBma2_5*Chr1_23a_ISBma2_A	R	ATCC_10399	5	53180-54752	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGCAGI GACCCGCTGGGCGGT ACCGCAGI	N	
5*Chr1_44a_ISBma2_5*Chr1_117a_ISBma2_A	R	ATCC_10399	5	556580-558152	Chr1	ISBma2	GCACG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AACCCGC(AAAACCCGGCTGGAAG AACCCGC	N	
2*Chr1_50_ISBma2_A	N	fmh	2	575878-577450	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GGGCGC(GGGCGCGACTACT GGGCGCG	Y	
9*Chr1_41_ISBma2_A	N	SAVP1	9	576498-577387	Chr1	ISBma2	AATCA(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCT# #IS407A CCCTCCACTGGAGGGC #IS407A	N.D.	
3*Chr1_50_ISBma2_A	N	JHU	3	579136-580708	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC GGGCGC(GGGCGCGACTACT GGGCGC	Y	
9*Chr1_39b_ISBma2_9*Chr1_44b_ISBma2_A	R	SAVP1	9	583222-584794	Chr1	ISBma2	GCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AAAAAACCC(CGGCCCTCCGGGGC AAAAAAC	N	
4*Chr1_23a_ISBma2_4*Chr1_32a_ISBma2_A	R	gb8_horse_4	4	58363-59935	Chr1	ISBma2	TGTGT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGCAGI AGAGCGGCCCGAAGGC ACCGCAGI	N	
1*Chr1_23a_ISBma2_1*Chr1_32a_ISBma2_A	R	ATCC_23344	1	58691-60263	Chr1	ISBma2	TGTGT(CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACCGCAGI AGAGCGGCCCGAAGGC ACCGCAGI	N	
2*Chr1_52_ISBma2_A	N	fmh	2	631884-633456	Chr1	ISBma2	CCGGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACGCGC(AAGCCGCGCTCACGC ACGCGCG	Y	
3*Chr1_52_ISBma2_A	N	JHU	3	635378-636950	Chr1	ISBma2	CCGGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC ACGCGC(AAGCCGCGCTCACGC ACGCGCG	Y	
10*Chr1_50_ISBma2_A	N	PRL20	10	668438-670010	Chr1	ISBma2	AGCGA CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC #contig_br GGGGGCGGACTACT #contig_br	N	
9*Chr1_39a_ISBma2_9*Chr1_44a_ISBma2_A	R	SAVP1	9	693678-695250	Chr1	ISBma2	ACGGC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC AGCCCTC(AACCCGGCTGGAAGCC AGCCCTC	N	
4*Chr1_50_ISBma2_A	N	gb8_horse_4	4	693979-695542	Chr1	ISBma2	GCGAC CAGATTGCTGACAAAC ATGCTGAAGACGCCATGCTCCAGAAAGACAAAACCC #contig_br GGGGGCGGACTACT #contig_br	N.D.	

3*Chr2_72_IS407A_A	N	Bm_JHU	3	113583-114818	Chr2	IS407A	CACATGTACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
3*Chr2_44b_IS407;3*Chr2_48_IS407A_A	D-R	Bm_JHU	3	1143190-1144425	Chr2	IS407A	GACAG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_44a_IS407A_A	N	Bm_NCTC_102	7	1145841-1147076	Chr2	IS407A	GACAG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_33_IS407A	D-R	Bm_ATCC_103	5	1160971-1162206	Chr2	IS407A	GTTCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
3*Chr2_45_IS407A_B	N	Bm_JHU	3	1178167-1179402	Chr2	IS407A	GCCCG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
9*Chr2_44a_IS407A_A	R	Bm_SAVP1	9	117856-119091	Chr2	IS407A	CGATG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
8*Chr2_6_IS407A_A	N	Bm_200272128	8	1188221-1189456	Chr2	IS407A	GCGCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
8*Chr2_13b_IS407;8*Chr2_57b_IS407A_A	R	Bm_200272128	8	1194967-1196202	Chr2	IS407A	CAAGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_31b_IS407A_A	R	Bm_ATCC_103	5	1198234-1199469	Chr2	IS407A	GAACG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_13a_IS407A_A	R	Bm_ATCC_103	5	1200293-1201483	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_10a_IS407A_A	N	Bm_ATCC_103	5	1214324-1215557	Chr2	IS407A	CGCGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
4*Chr2_27_IS407A	D-R	Bm_gb8_horse	4	1219713-1220948	Chr2	IS407A	CTGGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
1*Chr2_27_IS407A	D-R	Bm_ATCC_233	1	1225576-1226811	Chr2	IS407A	CTGGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
1*Chr2_27_IS407A	D-R	Bm_ATCC_233	1	1225576-1226811	Chr2	IS407A	CTGGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_9b_IS407A	R	Bm_ATCC_103	5	1236549-1237784	Chr2	IS407A	CATGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
10*Chr2_42_IS407A_A	N	Bm_PRL20	10	1242592-1243827	Chr2	IS407A	ATCGAT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
9*Chr2_2_IS407A	D-R	Bm_SAVP1	9	1244526-1245761	Chr2	IS407A	CGCTG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
2*Chr2_27_IS407A	D-R	Bm_fmh	2	1246300-1247535	Chr2	IS407A	CTGGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_70_IS407A_A	N	Bm_ATCC_103	5	125421-126656	Chr2	IS407A	CAACA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_48_IS407A_A	N	Bm_NCTC_102	7	1257060-1258295	Chr2	IS407A	CATTC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
9*Chr2_72_IS407A_A	N	Bm_SAVP1	9	1267326-1268561	Chr2	IS407A	CACAT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_49_IS407A_A	N	Bm_NCTC_102	7	1284838-1286073	Chr2	IS407A	CAGAC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_26_IS407A	D	Bm_ATCC_103	5	1298656-1299890	Chr2	IS407A	CTGGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_51_IS407A_A	N	Bm_NCTC_102	7	1306894-1308129	Chr2	IS407A	CGGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
6*Chr2_3_IS407A	D-R	Bm_NCTC_102	6	1307203-1308438	Chr2	IS407A	GGGCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
3*Chr2_27_IS407A_A	D-R	Bm_JHU	3	1310457-1311650	Chr2	IS407A	CTGGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
3*Chr2_42_IS407A_A	D-R	Bm_JHU	3	1311687-1312631	Chr2	IS407A	#contig~~~~~ GCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
4*Chr2_42_IS407A_A	N	Bm_gb8_horse	4	1318264-1319499	Chr2	IS407A	ATCGAT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
10*Chr2_70_IS407A	D-R	Bm_PRL20	10	132158-133393	Chr2	IS407A	CAACA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
1*Chr2_42_IS407A_A	N	Bm_ATCC_233	1	1324421-1325656	Chr2	IS407A	ATCGAT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
10*Chr2_40_IS407A	D	Bm_PRL20	10	1330658-1331893	Chr2	IS407A	GAAGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
9*Chr2_70_IS407A_A	N	Bm_SAVP1	9	1334773-1336008	Chr2	IS407A	CAACA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
8*Chr2_58_IS407A_A	N	Bm_200272128	8	1343603-1344838	Chr2	IS407A	CGCGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
8*Chr2_34_IS407A	D-R	Bm_200272128	8	134525-135760	Chr2	IS407A	CGCGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
2*Chr2_42_IS407A_A	N	Bm_fmh	2	1349579-1350814	Chr2	IS407A	ATCGAT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_52_IS407A_A	N	Bm_NCTC_102	7	1386349-1387584	Chr2	IS407A	GAAAT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_51_IS407A_A	N	Bm_ATCC_103	5	1390265-1391500	Chr2	IS407A	CGGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
3*Chr2_40_IS407A	D	Bm_JHU	3	1401133-1402368	Chr2	IS407A	GAAGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
4*Chr2_20_IS407A	D	Bm_gb8_horse	4	1406420-1407655	Chr2	IS407A	GAAGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_49_IS407A_A	N	Bm_ATCC_103	5	1410524-1411759	Chr2	IS407A	CCCAA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_33_IS407A	D-R	Bm_NCTC_102	7	1411874-1413109	Chr2	IS407A	GTGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
1*Chr2_40_IS407A	D	Bm_ATCC_233	1	1412717-1413952	Chr2	IS407A	GAAAG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
6*Chr2_33_IS407A	D-R	Bm_NCTC_102	6	142183-143418	Chr2	IS407A	GTGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
9*Chr2_67_IS407A	N	Bm_SAVP1	9	1432613-1433848	Chr2	IS407A	CAGCG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_24_IS407A	D-R	Bm_ATCC_103	5	1438414-1439649	Chr2	IS407A	CGGGA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
2*Chr2_40_IS407A	D	Bm_fmh	2	1439497-1440732	Chr2	IS407A	GAAGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_28_IS407A	D	Bm_NCTC_102	7	1449126-1450361	Chr2	IS407A	GAAAG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
8*Chr2_59_IS407A_A	N	Bm_200272128	8	1453446-1454681	Chr2	IS407A	CGCGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_52_IS407A_A	N	Bm_ATCC_103	5	1465100-1466335	Chr2	IS407A	GAAAT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
3*Chr2_33_IS407A	D-R	Bm_JHU	3	1468774-1470009	Chr2	IS407A	GTCCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
4*Chr2_33_IS407A	D-R	Bm_gb8_horse	4	1474062-1475297	Chr2	IS407A	GTCCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
8*Chr2_60_IS407A	D	Bm_200272128	8	1474566-1475801	Chr2	IS407A	CGCCG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
1*Chr2_33_IS407A	D-R	Bm_ATCC_233	1	1480359-1481594	Chr2	IS407A	GTCCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
5*Chr2_9a_IS407A	D-R	Bm_ATCC_103	5	1489755-1490990	Chr2	IS407A	GCGCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
9*Chr2_62b_IS407	D-R	Bm_SAVP1	9	1496137-1497372	Chr2	IS407A	CTAGA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
7*Chr2_26_IS407A	D	Bm_NCTC_102	7	1497556-1498791	Chr2	IS407A	GGATT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
8*Chr2_62a_IS407	D-R	Bm_200272128	8	1498717-1499952	Chr2	IS407A	CCATC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
10*Chr2_6_IS407A_A	N	Bm_PRL20	10	1504574-1505809	Chr2	IS407A	GCGCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y
3*Chr2_9a_IS407A	D-R	Bm_JHU	3	1506899-1508134	Chr2	IS407A	GAAAG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAAATGATGGAT/GATG	GATG	Y

6*Chr2_10a_IS407;6*Chr2_13a_IS407_A	R	Bm_NCTC_102;	6	6183-7418	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT)CTCG	AAGC	N
10*Chr2_37_IS407;10*Chr2_57a_IS407A_A	D-R	Bm_PRL20	10	622831-624066	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCCG)ACCT	CGCC	N
8*Chr2_49_IS407A_A	N	Bm_200272128	8	630594-631829	Chr2	IS407A	CCGAC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AGCGACG)AGCG	AGCG	Y
3*Chr2_34_IS407A_3*Chr2_54_IS407A_A	D-R	Bm_JHU	3	631977-633212	Chr2	IS407A	CGCGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGATAGA)GAGG	GGAT	N
5*Chr2_83_IS407A_C	N	Bm_ATCC_103f	5	6354-7589	Chr2	IS407A	ACGGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGGCAG)CGGG	CGGG	Y
9*Chr2_57a_IS407A_A	D-R	Bm_SAVP1	9	639673-640908	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAGAGAC)ACCT	CAGA	N
4*Chr2_35_IS407A_A	N	Bm_gb8_horse	4	655266-656501	Chr2	IS407A	CGATC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCAGC)CATC	CATC	Y
1*Chr2_35_IS407A_A	N	Bm_ATCC_233f	1	656707-657942	Chr2	IS407A	CGATC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCAGC)CATC	CATC	Y
8*Chr2_48_IS407A_A	N	Bm_200272128	8	658424-659659	Chr2	IS407A	CATT(CGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GCCGCT)CCGG	GCCG	Y
2*Chr2_35_IS407A_A	N	Bm_fmh	2	668220-669455	Chr2	IS407A	CGATC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCAGC)CATC	CATC	Y
6*Chr2_38_IS407A_6*Chr2_56_IS407A_A	D-R	Bm_NCTC_102;	6	675587-676822	Chr2	IS407A	GTC(CATGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCGAG)GAAC	CATC	N
9*Chr2_23_IS407A_A	D-R	Bm_SAVP1	9	686954-688189	Chr2	IS407A	AATGG(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ATCGGCC)CCAT	ATCG	N
5*Chr2_37_IS407A_5*Chr2_57a_IS407A_A	D-R	Bm_ATCC_103f	5	689319-690554	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCCG)ACCT	CGCC	N
3*Chr2_35_IS407A_A	N	Bm_JHU	3	696599-697834	Chr2	IS407A	CGATC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCAGC)CATC	CATC	Y
7*Chr2_13b_IS407A_7*Chr2_57b_IS407A_A	R	Bm_NCTC_102;	7	714504-715739	Chr2	IS407A	CAAGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ATCTTCCC)GGTT	ATCT	N
7*Chr2_6_IS407A_A	N	Bm_NCTC_102;	7	721251-722486	Chr2	IS407A	GCGCA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGTGAAC)CGTG	CGTG	Y
10*Chr2_31b_IS407_10*Chr2_56_IS407A_A	D-R	Bm_PRL20	10	726908-728143	Chr2	IS407A	GAACG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCGGC)GATC	CATC	N
4*Chr2_37_IS407A_4*Chr2_57a_IS407A_A	D-R	Bm_gb8_horse	4	732439-733674	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCCG)ACCT	CGCC	N
1*Chr2_37_IS407A_1*Chr2_57a_IS407A_A	D-R	Bm_ATCC_233f	1	733880-735115	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCCG)ACCT	CGCC	N
2*Chr2_37_IS407A_2*Chr2_57a_IS407A_A	D-R	Bm_fmh	2	746706-747941	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCCG)ACCT	CGCC	N
10*Chr2_9a_IS407;10*Chr2_24_IS407_10*Chr2_32a	D-R	Bm_PRL20	10	749164-750399	Chr2	IS407A	CGGGA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCG)CCAC	CAAG	N
9*Chr2_19_IS407A_B	N	Bm_SAVP1	9	764597-765832	Chr2	IS407A	TTATG(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGGTATT)GGGT	GGGT	Y
8*Chr2_44a_IS407A_A	N	Bm_200272128	8	769677-770912	Chr2	IS407A	GACAG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AGGGGTA)CGCC	AGGG	N
3*Chr2_37_IS407A_3*Chr2_57a_IS407A_A	D-R	Bm_JHU	3	773773-775008	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCCG)ACCT	CGCC	N
10*Chr2_25_IS407A_C	N	Bm_PRL20	10	778318-779553	Chr2	IS407A	GGTTA(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ATCAGCG)ATCG	ATCG	Y
6*Chr2_37_IS407A_6*Chr2_57a_IS407A_A	D-R	Bm_NCTC_102;	6	780241-781476	Chr2	IS407A	CCCTT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGCCCG)ACCT	CGCC	N
10*Chr2_26_IS407;10*Chr2_27_IS407A_A	D	Bm_PRL20	10	783043-784278	Chr2	IS407A	GGCGT TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTCGGG)GAAA	CTCG	N
5*Chr2_44b_IS407_5*Chr2_56_IS407A_A	D-R	Bm_ATCC_103f	5	793863-795098	Chr2	IS407A	GACAG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCGGC)CGCC	CATC	N
9*Chr2_15a_IS407;9*Chr2_18_IS407A_A	D-R	Bm_SAVP1	9	799543-800778	Chr2	IS407A	AGACC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGATCAG)AGAT	GGAT	N
4*Chr2_2_IS407A_4*Chr2_73_IS407A_A	D-R	Bm_gb8_horse	4	80307-81542	Chr2	IS407A	CGCTG(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCG)GTGT	CAAC	N
1*Chr2_2_IS407A_1*Chr2_73_IS407A_A	D-R	Bm_ATCC_233f	1	80328-81563	Chr2	IS407A	CGCTG(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCG)GTGT	CAAC	N
7*Chr2_2_IS407A_7*Chr2_73_IS407A_A	D-R	Bm_NCTC_102;	7	81697-82932	Chr2	IS407A	CGCTG(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCG)GTGT	CAAC	N
5*Chr2_45_IS407A_B	N	Bm_ATCC_103f	5	828859-830094	Chr2	IS407A	GCCGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GAAAGG)GGGC	GAAA	N
4*Chr2_24_IS407A_4*Chr2_56_IS407A_A	D-R	Bm_gb8_horse	4	836729-837964	Chr2	IS407A	CGGGA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCGGC)CCAC	CATC	N
1*Chr2_24_IS407A_1*Chr2_56_IS407A_A	D-R	Bm_ATCC_233f	1	838658-839893	Chr2	IS407A	CGGGA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCGGC)CCAC	CATC	N
7*Chr2_9a_IS407A_A	N	Bm_NCTC_102;	7	840090-841325	Chr2	IS407A	CATGC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCG)CAAG	CAAG	Y
10*Chr2_9b_IS407;10*Chr2_31a_IS407A_A	R	Bm_PRL20	10	845139-846374	Chr2	IS407A	CATGC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GATCGAG)CAAG	GATC	N
2*Chr2_24_IS407A_2*Chr2_56_IS407A_A	D-R	Bm_JHU	2	852556-853791	Chr2	IS407A	CGGGA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCGGC)CCAC	CATC	N
6*Chr2_35_IS407A_A	N	Bm_NCTC_102;	6	859532-860767	Chr2	IS407A	CGATC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCAGC)CATC	CATC	Y
7*Chr2_10a_IS407;7*Chr2_13a_IS407A_A	R	Bm_NCTC_102;	7	862482-863717	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT)CTCG	AAGC	N
4*Chr2_9b_IS407A_4*Chr2_26_IS407A_A	D-R	Bm_gb8_horse	4	865037-866272	Chr2	IS407A	CATGC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTGGATA)CAAG	CTGG	N
10*Chr2_10a_IS407;10*Chr2_13a_IS407A_A	D-R	Bm_PRL20	10	867383-868618	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT)CTCG	AAGC	N
1*Chr2_9b_IS407A_1*Chr2_26_IS407A_A	D-R	Bm_ATCC_233f	1	869730-870965	Chr2	IS407A	CATGC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTGGATA)CAAG	CTGG	N
8*Chr2_42_IS407A_A	N	Bm_200272128	8	875084-876319	Chr2	IS407A	ATCGA(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTCGGC)CTCG	CTCG	Y
7*Chr2_10b_IS407A_A	R	Bm_NCTC_102;	7	876441-877676	Chr2	IS407A	GCCCT(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGGGC)CGGG	CCGG	N
10*Chr2_32b_IS407A_C	R	Bm_PRL20	10	878187-878956	Chr2	IS407A	GTTAA(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCC# #contig_br AGTG #con N.D.		N.D.
7*Chr2_38_IS407A_A	D-R	Bm_NCTC_102;	7	878410-879645	Chr2	IS407A	GTC(CATGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGAGTT)GAA	GGAG	N
3*Chr2_24_IS407A_3*Chr2_56_IS407A_A	D-R	Bm_JHU	3	881257-882492	Chr2	IS407A	CGGGA TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CATCGGC)CCAC	CATC	N
2*Chr2_9b_IS407A_2*Chr2_26_IS407A_A	D-R	Bm_fmh	2	883719-884954	Chr2	IS407A	CATGC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTGGATA)CAAG	CTGG	N
4*Chr2_10a_IS407A_A	N	Bm_gb8_horse	4	887110-888345	Chr2	IS407A	GTTAA(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT)AGTG	AAGC	N
1*Chr2_10a_IS407A_A	N	Bm_ATCC_233f	1	891974-893209	Chr2	IS407A	GTTAA(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT)AGTG	AAGC	N
10*Chr2_33_IS407;10*Chr2_53_IS407A_A	D-R	Bm_PRL20	10	894908-896143	Chr2	IS407A	GCGAC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTCCAG)CCTG	GTCC	N
2*Chr2_2_IS407A_2*Chr2_73_IS407A_A	D-R	Bm_fmh	2	89553-90788	Chr2	IS407A	CGCTG(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCG)GTGT	CAAC	N
4*Chr2_13a_IS407A_A	R	Bm_gb8_horse	4	903023-904258	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGGGC)CTCG	CCGG	N
4*Chr2_53_IS407A_A	D-R	Bm_gb8_horse	4	904992-906227	Chr2	IS407A	GCGAC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGAGTT)CCTG	GGAG	N
2*Chr2_10a_IS407A_A	N	Bm_fmh	2	905698-906933	Chr2	IS407A	GTTAA(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT)AGTG	AAGC	N
5*Chr2_44a_IS407A_A	R	Bm_ATCC_103f	5	906115-907350	Chr2	IS407A	CGATC(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AGGGGTA)GCGG	AGGG	N
3*Chr2_2_IS407A_3*Chr2_73_IS407A_A	D-R	Bm_JHU	3	90720-91955	Chr2	IS407A	CGCTG(TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CAAGCG)GTGT	CAAC	N

1*Chr2_13a_IS407A_A	R	Bm_ATCC_2334	1 907887-909122	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGGGCCG CTGG	CCGG	N
1*Chr2_53_IS407A_A	D-R	Bm_ATCC_2334	1 909856-911091	Chr2	IS407A	GCGAC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGAGTTC1CTG	GGAG	N
10*Chr2_21_IS407A_10*Chr2_52_IS407A_A	N	Bm_PRL20	10 920084-921319	Chr2	IS407A	GAATT1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGTACC GGAT	CCGT	N
2*Chr2_13a_IS407A_A	R	Bm_fmh	2 922047-923283	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGGGCCG CTGG	CCGG	N
2*Chr2_53_IS407A_A	D-R	Bm_fmh	2 924017-925252	Chr2	IS407A	GCGAC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGAGTTC1CTG	GGAG	N
6*Chr2_34_IS407A_6*Chr2_54_IS407A_A	D-R	Bm_NCTC_1024	6 924390-925625	Chr2	IS407A	CGCGG TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGATAGAI GAGG	GGAT	N
8*Chr2_13a_IS407A_A	R	Bm_200272128	8 92450-93685	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT1CTG	AAGC	N
4*Chr2_40_IS407A_A	N	Bm_gb8_horse	4 930168-931403	Chr2	IS407A	GAATT1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGTACC GGAT	CCGT	N
1*Chr2_52_IS407A_A	N	Bm_ATCC_2334	1 935032-936267	Chr2	IS407A	GAATT1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGTACC GGAT	CCGT	N
3*Chr2_9b_IS407A_3*Chr2_26_IS407A_A	D-R	Bm_JHU	3 944285-945520	Chr2	IS407A	CATGC1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CTGGATAI CAAG	CTGG	N
7*Chr2_40_IS407A_A	N	Bm_NCTC_1024	7 946055-947290	Chr2	IS407A	CGCGT1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGAACTGI CAGG	CGAA	N
2*Chr2_52_IS407A_A	N	Bm_fmh	2 949193-950428	Chr2	IS407A	GAATT1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGTACC GGAT	CCGT	N
6*Chr2_17_IS407A_6*Chr2_55_IS407A_A	D-R	Bm_NCTC_1024	6 950458-951693	Chr2	IS407A	AGCGT1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GTGCGT1GCC	GTGC	N
6*Chr2_15b_IS407A_A	R	Bm_NCTC_1024	6 966292-967527	Chr2	IS407A	CGCGC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(ACAGT1TT GCTT	ACAG	N
3*Chr2_10a_IS407A_A	N	Bm_JHU	3 967328-968563	Chr2	IS407A	GTTAA1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(AAGCCGT1 AGTG	AAGC	N
8*Chr2_40_IS407A_A	N	Bm_200272128	8 968920-970155	Chr2	IS407A	CGCGT1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CGAACTGI CAGG	CGAA	N
9*Chr2_3_IS407A_9*Chr2_76_IS407A_A	D-R	Bm_SAVP1	9 977425-978660	Chr2	IS407A	AGTCG1TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(TCTTCTT1GGT	TCTT	N
3*Chr2_13a_IS407A_A	R	Bm_JHU	3 983241-984476	Chr2	IS407A	GAGCC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(CCGGGCCG CTGG	CCGG	N
3*Chr2_53_IS407A_A	D-R	Bm_JHU	3 986093-987328	Chr2	IS407A	GCGAC TGACCTGCCCC~TAC ATGAAGAAGCGCTTTACGCGCCCGCAAGCCAAACGCG; TGTTGGCCAGGGACTTTGCTAGAA(GGAGTTC1CTG	GGAG	N

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					5'-ext	5'-IR	ORF	3'-IR	3'-ext	5'-DR	3'-DR	rget duplicates	
						GTTTCATCGC	GCGATGA ACC						
7*Chr2_43_ISBma1_A	N	Bm_NCTC_1024	7 1053553-1054857	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CAAGGAA, CAAGGAAA		CAAGGAA,	Y	
9*Chr2_79_ISBma1_A	N	Bm_SAVP1	9 1107451-1108755	Chr2	ISBma1	GTTT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CTTTTTTC, CTTTTTTC		CTTTTTTC	Y	
4*Chr2_29_ISBma1_B	N	Bm_gb8_horse	4 1169546-1170852	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			AAATTTTT, AAATTTTT		AAATTTTT	Y	
1*Chr2_29_ISBma1_B	N	Bm_ATCC_2334	1 1175066-1176372	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			AAATTTTT, AAATTTTT		AAATTTTT	Y	
2*Chr2_29_ISBma1_B	N	Bm_fmh	2 1194495-1195801	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			AAATTTTT, AAATTTTT		AAATTTTT	Y	
10*Chr2_43_ISBma1_A	N	Bm_PRL20	10 1229130-1230350	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CAAGGAA, CAAGGAAA		CAAGGAA,	Y	
5*Chr2_69-1_ISBma1_A	N	Bm_ATCC_1034	5 125354-125421	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	N.D.	
3*Chr2_29_ISBma1_B	N	Bm_JHU	3 1258947-1260253	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			AAATTTTT, AAATTTTT		AAATTTTT	Y	
5*Chr2_69_ISBma1_A	N	Bm_ATCC_1034	5 126655-127898	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
6*Chr2_4_ISBma1_B	N	Bm_NCTC_1024	6 1284442-1285746	Chr2	ISBma1	TCCGT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			TTTTTAA1TTTTTAA		TTTTTAA	Y	
4*Chr2_43_ISBma1_A	N	Bm_gb8_horse	4 1304618-1305922	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CAAGGAA, CAAGGAAA		CAAGGAA,	Y	
1*Chr2_43_ISBma1_A	N	Bm_ATCC_2334	1 1310749-1312053	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CAAGGAA, CAAGGAAA		CAAGGAA,	Y	
10*Chr2_69_ISBma1_A	N	Bm_PRL20	10 133392-134635	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
9*Chr2_69-1_ISBma1_A	N	Bm_SAVP1	9 1334706-1334773	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	Y	
2*Chr2_43_ISBma1_A	N	Bm_fmh	2 1335542-1336846	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CAAGGAA, CAAGGAAA		CAAGGAA,	Y	
9*Chr2_69_ISBma1_A	N	Bm_SAVP1	9 1336007-1337250	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
6*Chr2_79_ISBma1_A	N	Bm_NCTC_1024	6 1436997-1448301	Chr2	ISBma1	GTTT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CTTTTTTC, CTTTTTTC		CTTTTTTC	Y	
6*Chr2_69_ISBma1_A	N	Bm_NCTC_1024	6 1600893-1602136	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
8*Chr2_69-1_ISBma1_A	N	Bm_200272128	8 1609838-1609906	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	N.D.	
4*Chr2_69-1_ISBma1_A	N	Bm_gb8_horse	4 170220-170747	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	N.D.	
1*Chr2_69-1_ISBma1_A	N	Bm_ATCC_2334	1 170527-170594	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	N.D.	
4*Chr2_69_ISBma1_A	N	Bm_gb8_horse	4 171521-172764	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
7*Chr2_69-1_ISBma1_A	N	Bm_NCTC_1024	7 171689-171756	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	N.D.	
1*Chr2_69_ISBma1_A	N	Bm_ATCC_2334	1 171828-173071	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
7*Chr2_69_ISBma1_A	N	Bm_NCTC_1024	7 172990-174233	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
2*Chr2_69-1_ISBma1_A	N	Bm_fmh	2 180027-180094	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	N.D.	
2*Chr2_69_ISBma1_A	N	Bm_fmh	2 181328-182571	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
8*Chr2_4_ISBma1_B	N	Bm_200272128	8 2007904-2009208	Chr2	ISBma1	TCCGT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			TTTTTAA1TTTTTAA		TTTTTAA	Y	
3*Chr2_69-1_ISBma1_A	N	Bm_JHU	3 207599-207666	Chr2	ISBma1	#IS4071 ~~~~~ ACC			TAAAAAA, #IS407A		TAAAAAA,	N.D.	
3*Chr2_69_ISBma1_A	N	Bm_JHU	3 208900-210143	Chr2	ISBma1	CAGGC1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC #			#IS407A TAAAAAAA		#IS407A	N.D.	
9*Chr2_43_ISBma1_A	N	Bm_SAVP1	9 209882-211186	Chr2	ISBma1	GCGCT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CAAGGAA, CAAGGAAA		CAAGGAA,	Y	
10*Chr2_79_ISBma1_A	N	Bm_PRL20	10 2104725-2106029	Chr2	ISBma1	GTTT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CTTTTTTC, CTTTTTTC		CTTTTTTC	Y	
7*Chr2_4_ISBma1_B	N	Bm_NCTC_1024	7 2142029-2143333	Chr2	ISBma1	TCCGT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			TTTTTAA1TTTTTAA		TTTTTAA	Y	
5*Chr2_79_ISBma1_A	N	Bm_ATCC_1034	5 2227856-2229160	Chr2	ISBma1	GTTT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CTTTTTTC, CTTTTTTC		CTTTTTTC	Y	
4*Chr2_79_ISBma1_A	N	Bm_gb8_horse	4 2257635-2258939	Chr2	ISBma1	GTTT1GGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCAC ACC			CTTTTTTC, CTTTTTTC		CTTTTTTC	Y	

1*Chr2_79_ISBma1_A	N	Bm_ATCC_2334	1 2265680-2266984	Chr2	ISBma1	GTTTGTGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTTC	CTTTTTTC	Y
3*Chr2_79_ISBma1_A	N	Bm_JHU	3 2280857-2282161	Chr2	ISBma1	GTTTGTGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTTC	CTTTTTTC	Y
7*Chr2_79_ISBma1_A	N	Bm_NCTC_1024	7 2294384-2295688	Chr2	ISBma1	GTTTGTGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTTC	CTTTTTTC	Y
2*Chr2_79_ISBma1_A	N	Bm_fmh	2 2306093-2307397	Chr2	ISBma1	GTTTGTGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CTTTTTTCCTTTTTTC	CTTTTTTC	Y
6*Chr2_43_ISBma1_A	N	Bm_NCTC_1024	6 5003674-5016668	Chr2	ISBma1	GCGCTGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CAAGGAA,CAAGGAAA	CAAGGAA,	Y
8*Chr2_43_ISBma1_A	N	Bm_200272128	8 861441-862745	Chr2	ISBma1	GCGCTGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CAAGGAA,CAAGGAAA	CAAGGAA,	Y
5*Chr2_43_ISBma1_A	N	Bm_ATCC_1034	5 991262-992566	Chr2	ISBma1	GCGCTGGTTCATCGCAGAAAA TTGCTCGATCGCAAGGCACACC	CAAGGAA,CAAGGAAA	CAAGGAA,	Y

IS Bma 2

			5'-ext	5'-IR	ORF	3'-IR	3'-ext	5'-DR	3'-DR	rget	duplicates
			CAGATTGCTGACAAACC			GGGTTGCTCAGCAGTCTG					
8*Chr2_12_ISBma2_A	N	Bm_200272128	8 101363-102937	Chr2	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GCGCTCC/GCGCTCCATTGCGAGC/GCGCTCC/					Y
9*Chr2_80a_ISBma2_A	N	Bm_SAVP1	9 1108780-1110352	Chr2	ISBma2	:GCCCT CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG CGAAAAAAGGGCCGCAAGGGCCG					N
10*Chr2_47_ISBma2_A	N	Bm_PRL20	10 1133963-1135535	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGCGCAC/GCGGATGCGAGCGCACAGCGCAC/					N
6*Chr2_5a_ISBma26*Chr2_14b_ISBma2_A	R	Bm_NCTC_1024	6 1142945-1144517	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N
9*Chr2_47_ISBma2_A	D-R	Bm_SAVP1	9 116165-117737	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGCGCAC/GCGGATGCGAGCGCACAGCGCAC/					N
4*Chr2_30_ISBma24*Chr2_47_ISBma2_A	D-R	Bm_gb8_horse	4 1166671-1168243	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AACAGCC/GCGGATGCGAGCGCACAGAACGCC/					N
1*Chr2_30_ISBma21*Chr2_47_ISBma2_A	D-R	Bm_ATCC_2334	1 1172191-1173763	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AACAGCC/GCGGATGCGAGCGCACAGAACGCC/					N
8*Chr2_5b_ISBma28*Chr2_14a_ISBma2_A	R	Bm_200272128	8 1189961-1191534	Chr2	ISBma2	8189961-1191534					N
2*Chr2_30_ISBma22*Chr2_47_ISBma2_A	D-R	Bm_fmh	2 1191620-1193192	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AACAGCC/GCGGATGCGAGCGCACAGAACGCC/					N
5*Chr2_12_ISBma2_A	N	Bm_ATCC_1034	5 1209160-1210732	Chr2	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GCGCTCC/GCGCTCCATTGCGAGC/GCGCTCC/					Y
5*Chr2_11_ISBma2_B	N	Bm_ATCC_1034	5 1214269-1214325	Chr2	ISBma2	TCAGC CAGATTGCTGACAAAC ATGACTGCCCTTCGATG#	#IS407A	ACAAAGCCCCGTCAT/	#IS407A		N.D.
5*Chr2_71a_ISBma5*Chr2_80b_ISBma2_A	R	Bm_ATCC_1034	5 121539-123111	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					N
5*Chr2_30_ISBma2_A	N	Bm_ATCC_1034	5 1246578-1248150	Chr2	ISBma2	ACAGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AACAGCC/AAACAGCGCCGCCG AACAGCC/					N
7*Chr2_47_ISBma2_A	N	Bm_NCTC_1024	7 1255366-1256940	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGCGCAC/GCGGATGCGAGCGCACAGCGCAC/					N
3*Chr2_30_ISBma23*Chr2_47_ISBma2_A	D-R	Bm_JHU	3 1256072-1257644	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AACAGCC/GCGGATGCGAGCGCACAGCGCAC/					N
6*Chr2_77_ISBma26*Chr2_78_ISBma2_A	D	Bm_NCTC_1024	6 1328449-1330024	Chr2	ISBma2	TGACC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCTT/GCGGGAAGCGCCGCG/AGGGCTT/					N
9*Chr2_71b_ISBma2_A	N	Bm_SAVP1	9 1330891-1332463	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					Y
6*Chr2_80a_ISBma2_A	N	Bm_NCTC_1024	6 1438326-1439898	Chr2	ISBma2	:GCCCT CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG CGAAAAAAGGGCCGCAAGGGCCG					N
9*Chr2_65_ISBma2_B	N	Bm_SAVP1	9 1478060-1479632	Chr2	ISBma2	CCTTA/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGAGCGG AGCGGGCTGCAGCCG AGACGGG					Y
6*Chr2_82_ISBma2_B	N	Bm_NCTC_1024	6 1490409-1491981	Chr2	ISBma2	TGGCA/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC CTGGGCC/GAAACGGGGCCCGCTGCTGGGCC/					N
9*Chr2_63_ISBma2_B	N	Bm_SAVP1	9 1493768-1495340	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AAGCCGG/AAAAAGCCGGCGTGCA AAGCCGG					N
10*Chr2_5b_ISBma10*Chr2_14a_ISBma2_A	R	Bm_PRL20	10 1506314-1507887	Chr2	ISBma2	TGTGC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					N
6*Chr2_12_ISBma2_A	N	Bm_NCTC_1024	6 15095-16668	Chr2	ISBma2	GCCGC CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GCGCTCC/GCGCTCCATTGCGAGC/GCGCTCC/					Y
8*Chr2_65_ISBma2_B	N	Bm_200272128	8 1592660-1594232	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GACGGGC GACGGGCTGACGCCG GACGGGC					Y
5*Chr2_7_ISBma2_5*Chr2_14a_ISBma2_A	D-R	Bm_ATCC_1034	5 1600353-1601926	Chr2	ISBma2	TGTGC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					N
8*Chr2_71b_ISBma2_A	N	Bm_200272128	8 1612147-1613720	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					Y
4*Chr2_5b_ISBma24*Chr2_14a_ISBma2_A	R	Bm_gb8_horse	4 1631568-1633144	Chr2	ISBma2	TGTGC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					N
3*Chr2_5b_ISBma23*Chr2_14a_ISBma2_A	R	Bm_JHU	3 1632858-1634434	Chr2	ISBma2	TGTGC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					N
1*Chr2_5b_ISBma21*Chr2_14a_ISBma2_A	R	Bm_ATCC_2334	1 1638049-1639625	Chr2	ISBma2	TGTGC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					N
7*Chr2_36_ISBma2_B	N	Bm_NCTC_1024	7 1655136-1656709	Chr2	ISBma2	ACGCC CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AAGCCGG/CAAGCGCTCGGCAAC AAGCGCC					N
4*Chr2_71b_ISBma2_A	N	Bm_gb8_horse	4 166405-167977	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					Y
1*Chr2_71b_ISBma2_A	N	Bm_ATCC_2334	1 166712-168284	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					Y
2*Chr2_5b_ISBma22*Chr2_14a_ISBma2_A	R	Bm_fmh	2 1668531-1670107	Chr2	ISBma2	TGTGC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					N
7*Chr2_71b_ISBma2_A	N	Bm_NCTC_1024	7 167874-169446	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					Y
9*Chr2_12_ISBma2_A	D-R	Bm_SAVP1	9 1707496-1709043	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AAGCCGG/CAAGCGCTCGGCAAC AAGCGCC					N
6*Chr2_65_ISBma2_B	N	Bm_NCTC_1024	6 1744134-1745709	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GACGGGC GACGGGCTGACGCCG GACGGGC					Y
2*Chr2_71b_ISBma2_A	N	Bm_fmh	2 176212-177784	Chr2	ISBma2	CGCGG CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCCG AGGGCCGCTGCTAGCG AGGGCCG					Y
8*Chr2_82_ISBma2_B	N	Bm_200272128	8 1784937-1785906	Chr2	ISBma2	#contig ~~~~~ TCCAGAAAGACAAAACCC CTGGGCC(#contig_break					N.D.
10*Chr2_5a_ISBma10*Chr2_14b_ISBma2_A	R	Bm_PRL20	10 1809463-1811035	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N
8*Chr2_5a_ISBma28*Chr2_14b_ISBma2_A	R	Bm_200272128	8 1866602-1868174	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N
5*Chr2_5a_ISBma25*Chr2_14b_ISBma2_A	D-R	Bm_ATCC_1034	5 1933847-1935419	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N
4*Chr2_5a_ISBma24*Chr2_14b_ISBma2_A	R	Bm_gb8_horse	4 1964034-1965606	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N
1*Chr2_5a_ISBma21*Chr2_14b_ISBma2_A	R	Bm_ATCC_2334	1 1971717-1973289	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N
3*Chr2_5a_ISBma23*Chr2_14b_ISBma2_A	R	Bm_JHU	3 1979924-1981496	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N
10*Chr2_77_ISBma10*Chr2_78_ISBma2_A	D	Bm_PRL20	10 1995877-1997449	Chr2	ISBma2	TGACC/CAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC AGGGCTT/GCGGGAAGCGCCGCG/AGGGCTT/					N
7*Chr2_5a_ISBma27*Chr2_14b_ISBma2_A	R	Bm_NCTC_1024	7 2000703-2002275	Chr2	ISBma2	TAAAACAGATTGCTGACAAAC ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCC GGCCTTC/AAACGCCCCGACGAA GGCCTTC/					N

2*Chr2_5a_ISBma22*Chr2_14b_ISBma2_A	R	Bm_fmh	2	2007940-2009512	Chr2	ISBma2	TAAAA(CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGCCCTTCAAACGCCCGCCACGAA	GGCCTTC/	N				
3*Chr2_71b_ISBma2_A	N	Bm_JHU	3	203784-205356	Chr2	ISBma2	CGCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AGGGCCGCTCGTAGCG	AGGGCCG	Y		
8*Chr2_77_ISBma28*Chr2_80a_ISBma2_A	D-R	Bm_200272128	8	2051909-2053481	Chr2	ISBma2	TGCCG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAAAAGCGCGCTTCGCG	AGGGCCG	N		
10*Chr2_80a_ISBma2_A	N	Bm_PRL20	10	2106054-2107626	Chr2	ISBma2	:GCCCT	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	CGAAAAAGGGCCGCA	AGGGCCG	N		
5*Chr2_77_ISBma25*Chr2_78_ISBma2_A	D	Bm_ATCC_103f	5	2119130-2120702	Chr2	ISBma2	TGACCC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AGGGCGCG	AGGGCGTTC	N		
6*Chr2_5b_ISBma26*Chr2_14a_ISBma2_A	R	Bm_NCTC_102i	6	2146943-2148516	Chr2	ISBma2	TGTGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AGGGCGTTCATCTGGCG	AGGGCCG	N		
4*Chr2_77_ISBma24*Chr2_78_ISBma2_A	D	Bm_gb8_horse	4	2149249-2150821	Chr2	ISBma2	TGACC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGTTC	GCGGGAAGCGCCGCG	AGGGCGTTC	N		
1*Chr2_77_ISBma21*Chr2_78_ISBma2_A	D	Bm_ATCC_233z	1	2157201-2158773	Chr2	ISBma2	TGACC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGTTC	GCGGGAAGCGCCGCG	AGGGCGTTC	N		
3*Chr2_77_ISBma23*Chr2_78_ISBma2_A	D	Bm_JHU	3	2168372-2169944	Chr2	ISBma2	TGACC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGTTC	GCGGGAAGCGCCGCG	AGGGCGTTC	N		
7*Chr2_77_ISBma27*Chr2_78_ISBma2_A	D	Bm_NCTC_102i	7	2186019-2187594	Chr2	ISBma2	TGACC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGTTC	GCGGGAAGCGCCGCG	AGGGCGTTC	N		
2*Chr2_77_ISBma22*Chr2_78_ISBma2_A	D	Bm_fmh	2	2194588-2196160	Chr2	ISBma2	TGACC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGTTC	GCGGGAAGCGCCGCG	AGGGCGTTC	N		
5*Chr2_71b_ISBma25*Chr2_80a_ISBma2_A	R	Bm_ATCC_103f	5	2229185-2230757	Chr2	ISBma2	TTTTCT	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AGGGCGCAAGCGCC	AGGGCCG	N		
4*Chr2_80a_ISBma2_A	N	Bm_gb8_horse	4	2258964-2259023	Chr2	ISBma2	:GCCCT	CAGATTGCTGACAAAC	~TGACCTGCCCTTCGAT.#	#IS407A	AGGGCGCAAGCGCC	#IS407A	N.D.	
4*Chr2_80a-1_ISBma2_A	N	Bm_gb8_horse	4	2260253-2261776	Chr2	ISBma2	#IS407i	~~~~~	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	#IS407A	AGGGCGCG	AGGGCGCG	N.D.	
1*Chr2_80a_ISBma2_A	N	Bm_ATCC_233z	1	2267009-2267068	Chr2	ISBma2	:GCCCT	CAGATTGCTGACAAAC	~TGACCTGCCCTTCGAT.#	#IS407A	AGGGCGCAAGCGCC	#IS407A	N.D.	
1*Chr2_80a-1_ISBma2_A	N	Bm_ATCC_233z	1	2268298-2269821	Chr2	ISBma2	#IS407i	~~~~~	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	#IS407A	AGGGCGCG	AGGGCGCG	N.D.	
3*Chr2_80a_ISBma2_A	N	Bm_JHU	3	2282186-2282245	Chr2	ISBma2	:GCCCT	CAGATTGCTGACAAAC	~TGACCTGCCCTTCGAT.#	#IS407A	AGGGCGCAAGCGCC	#IS407A	N.D.	
3*Chr2_80a-1_ISBma2_A	N	Bm_JHU	3	2283475-2284998	Chr2	ISBma2	#IS407i	~~~~~	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	#IS407A	AGGGCGCG	AGGGCGCG	N.D.	
7*Chr2_80a_ISBma2_A	N	Bm_NCTC_102i	7	2295713-2297285	Chr2	ISBma2	:GCCCT	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	CGAAAAAGGGCCGCA	AGGGCGCG	N		
2*Chr2_80a_ISBma2_A	N	Bm_fmh	2	2307422-2307481	Chr2	ISBma2	:GCCCT	CAGATTGCTGACAAAC	~TGACCTGCCCTTCGAT.#	#IS407A	AGGGCGCAAGCGCC	#IS407A	N.D.	
2*Chr2_80a-1_ISBma2_A	N	Bm_fmh	2	2308711-2310234	Chr2	ISBma2	#IS407i	~~~~~	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	#IS407A	AGGGCGCG	AGGGCGCG	N.D.	
4*Chr2_82_ISBma2_B	N	Bm_gb8_horse	4	2310538-2312110	Chr2	ISBma2	CGCAC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAACGGG	AAACGGGGCCCGCTGG	AAACGGG	Y	
1*Chr2_82_ISBma2_B	N	Bm_ATCC_233z	1	2320471-2322043	Chr2	ISBma2	CGCAC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAACGGG	AAACGGGGCCCGCTGG	AAACGGG	Y	
7*Chr2_82_ISBma2_B	N	Bm_NCTC_102i	7	2347787-2349359	Chr2	ISBma2	TCCGA	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	CTGGCCCTGGCCCGCT	CTGGCCCG	Y		
8*Chr2_36_ISBma2_B	N	Bm_200272128	8	260811-262383	Chr2	ISBma2	ACGGCC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	CAAGCGCTCGGCAAC	AAGGGCG	N		
10*Chr2_65_ISBma2_B	N	Bm_PRL20	10	274212-275784	Chr2	ISBma2	CTCTA	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AGACGGG	AGACGGGCTGCAGCC	AGACGGG	Y	
5*Chr2_64_ISBma2_B	N	Bm_ATCC_103f	5	274296-275868	Chr2	ISBma2	CCACG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGT	AGGCGGTT	AGGCGGTTTCGATT	CGA/	AGGCGGT	Y
10*Chr2_63_ISBma2_B	N	Bm_PRL20	10	289920-291492	Chr2	ISBma2	CCGGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAAAAGCGCGCTGCA	AAGCCCG	N		
6*Chr2_47_ISBma2_A	N	Bm_NCTC_102i	6	298358-299930	Chr2	ISBma2	CGCGG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AGGCGCAC	GCGGATGACGCGCACG	AGGCGCAC	N	
7*Chr2_65_ISBma2_B	N	Bm_NCTC_102i	7	316219-317791	Chr2	ISBma2	CGCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	GACGGG	GACGGGCTGACGGC	GACGGG	Y	
4*Chr2_47_ISBma2_B	N	Bm_gb8_horse	4	318688-320260	Chr2	ISBma2	CCACG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGT	AGGCGGTT	AGGCGGTTTCGATT	CGA/	AGGCGGT	Y
1*Chr2_64_ISBma2_B	N	Bm_ATCC_233z	1	319482-321054	Chr2	ISBma2	CCACG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGT	AGGCGGTT	AGGCGGTTTCGATT	CGA/	AGGCGGT	Y
2*Chr2_64_ISBma2_B	N	Bm_fmh	2	328979-330551	Chr2	ISBma2	CCACG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGT	AGGCGGTT	AGGCGGTTTCGATT	CGA/	AGGCGGT	Y
3*Chr2_64_ISBma2_B	N	Bm_JHU	3	357598-359170	Chr2	ISBma2	CCACG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGT	AGGCGGTT	AGGCGGTTTCGATT	CGA/	AGGCGGT	Y
3*Chr2_82_ISBma2_B	N	Bm_JHU	3	3773-5345	Chr2	ISBma2	CGCAC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAACGGG	AAACGGGGCCCGCTGG	AAACGGG	Y	
2*Chr2_82_ISBma2_B	N	Bm_fmh	2	4374-5946	Chr2	ISBma2	CGCAC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAACGGG	AAACGGGGCCCGCTGG	AAACGGG	Y	
8*Chr2_47_ISBma2_A	N	Bm_200272128	8	659779-661351	Chr2	ISBma2	CGCGG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCAC	GCGGATGACGCGCACG	AGGCGCAC	N		
7*Chr2_5b_ISBma27*Chr2_14a_ISBma2_A	R	Bm_NCTC_102i	7	719172-720746	Chr2	ISBma2	TGTGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AGGGCGTTCATCTGGCG	AGGGCCG	N		
6*Chr2_36_ISBma2_B	N	Bm_NCTC_102i	6	797475-799047	Chr2	ISBma2	ACGCC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	CAAGCGCTCGGCAAC	AAGGGCG	N		
9*Chr2_5a_ISBma29*Chr2_14b_ISBma2_A	D-R	Bm_SAVP1	9	813639-815211	Chr2	ISBma2	TAAAA	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGCCCTTCAAACGCCCGCCACGAA	GGCCTTC/	AAAAAGCGCGCCG	CGAA	GGCCTTC/	N
10*Chr2_30_ISBma2_A	N	Bm_PRL20	10	834777-836349	Chr2	ISBma2	ACAGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAAAAGCGCGCCG	AAAAAGCGCGCCG	AAAAAGCGCG	N	
7*Chr2_12_ISBma2_A	N	Bm_NCTC_102i	7	871394-872967	Chr2	ISBma2	GCCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	CGCTCC/	GCGTCCATT	CGGAGC	GCGTCC/	Y
10*Chr2_12_ISBma2_A	D-R	Bm_PRL20	10	876295-877868	Chr2	ISBma2	GCCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAGCCCG	GCGTCCATT	CGGAGC	AAGCCCG	N
4*Chr2_11_ISBma2_B	N	Bm_gb8_horse	4	888664-890236	Chr2	ISBma2	TCAGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAGCCCG	ACAAAAGCCCGTCAAT	AAGCCCG	N	
1*Chr2_11_ISBma2_B	N	Bm_ATCC_233z	1	893528-895100	Chr2	ISBma2	TCAGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAGCCCG	ACAAAAGCCCGTCAAT	AAGCCCG	N	
4*Chr2_12_ISBma2_A	N	Bm_gb8_horse	4	893773-895346	Chr2	ISBma2	GCCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	GCGTCC/	GCGTCCATT	CGGAGC	GCGTCC/	Y
1*Chr2_12_ISBma2_A	N	Bm_ATCC_233z	1	898637-900210	Chr2	ISBma2	GCCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	GCGTCC/	GCGTCCATT	CGGAGC	GCGTCC/	Y
5*Chr2_47_ISBma2_A	N	Bm_ATCC_103f	5	904424-905996	Chr2	ISBma2	CGCGG	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCAC	AGGCGCAC	GCGGATGACGCGCAC	AGGCGCAC	N	
2*Chr2_11_ISBma2_B	N	Bm_fmh	2	907252-909260	Chr2	ISBma2	TCAGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAGCCCG	ACAAAAGCCCGTCAAT	AAGCCCG	N	
2*Chr2_12_ISBma2_A	N	Bm_fmh	2	912797-914370	Chr2	ISBma2	GCCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	GCGTCC/	GCGTCCATT	CGGAGC	GCGTCC/	Y
3*Chr2_11_ISBma2_B	N	Bm_JHU	3	968882-970454	Chr2	ISBma2	TCAGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	AAGCCCG	ACAAAAGCCCGTCAAT	AAGCCCG	N	
3*Chr2_12_ISBma2_A	N	Bm_JHU	3	973991-975564	Chr2	ISBma2	GCCGC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGCG	GCGTCC/	GCGTCCATT	CGGAGC	GCGTCC/	Y
9*Chr2_77_ISBma29*Chr2_78_ISBma2_A	D	Bm_SAVP1	9	998682-1000254	Chr2	ISBma2	TGACC	CAGATTGCTGACAAAC	ATGCTGAAGACGCCCATG(TCCAGAAAGACAAAACCGAGGCGTTC	GCGGGAAGCGCCGCG	AGGGCGTTC	N		