

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-USMARC-PARENT-AY761135-RS29003723	Verification	rs29003723	ss38341018	A/T	A/T	1	127426647	UMD3.1	ARS-USMARC-Parent-AY761135-rs29003723-0_B_R_1511686386	TTCTTTATTACGCTCCTCTGAAGAAGGAAAAACGATTTCTCTTATTCATGAGAAGGTAAAG[A/T]GTCTTTGGGTCCCCTGAACCTCCTAGCTCCA CTGCAATGATTCTCAAACCTTAATTGCAAG
ARS-USMARC-PARENT-AY776154-NORS	Verification	rs41257512	ss117966901	A/G	A/G	2	26997623	UMD3.1	ARS-USMARC-Parent-AY776154-no-rs-0_T_F_1544362783	TAAGTACATAAGTACATATCTACTGGCCTTTGATCTGACTAGTTCCCCAGTCTCAGGTCT[A/G]TTTTGCTGTTAATCACCAGTGAGAGAAGGTCCTACCCTATCTTAAGTGGTTCTCATRTCTC
ARS-USMARC-PARENT-AY842472-RS29001941	Verification	rs29001941	ss38339339	C/G	C/G	3	40399136	UMD3.1	ARS-USMARC-Parent-AY842472-rs29001941-0_T_F_1511686337	TCTATTAATTAATAATTGTA TATCTTGCTGCTCAGATGCTAGAGCACCTGTTCCATAT[C/G]GTGAAAACYGAGTTGGGAGCTGAGACTGTGACTGAGGAGGGAAGGCAGRAGACTATTGCT
ARS-USMARC-PARENT-AY842473-RS29001956	Verification	rs29001956	ss38339354	A/G	A/G	3	49703647	UMD3.1	ARS-USMARC-Parent-AY842473-rs29001956-0_B_R_1511686054	CACTGAGTTTCAGAGAGGGCCAGAACTCTTCTGTCCA CAAGGTCTGGCTCCATCC TGGTG[A/G]GGTGGGCAGAGAACCATGAGTTCTTGAGTAGCTCCAAGACCTATGGCATCAAGTGGCATG
ARS-USMARC-PARENT-AY842474-RS29003226	Verification	rs29003226	ss38340448	G/C	C/G	3	51976646	UMD3.1	ARS-USMARC-Parent-AY842474-rs29003226-0_T_R_1511685807	TGCATTTACACCTGCTGCAGCTTACCACCTGCACATGGATATTGTCTCTCCCTCCTCTAAA[C/G]TTCTCATCATGTGCCAATTGTACCTTGACC TAAATTGAAGGCAAAAGACTATCTTGTTT
ARS-USMARC-PARENT-AY842475-RS29002127	Verification	rs29002127	ss38339556	A/G	A/G	4	20181749	UMD3.1	ARS-USMARC-Parent-AY842475-rs29002127-0_T_F_1511685857	AAGGTATTATGAGTTGTGTGGGTTTTTAAAAGCTTGCA TCTCTAAGCTGTATGTGTGAGC[A/G]GTGTGWGTTAGATTTAATAACATCTCTGATAAAGCTCAGATTAGGTAAGAGGATGTATCAG
ARS-USMARC-PARENT-AY844963-RS17871338	Verification	rs17871338	ss28451679	A/G	A/G	5	98102349	UMD3.1	ARS-USMARC-Parent-AY844963-rs17871338-0_T_F_1511685889	ACAGACTCTTTGTATGTTT TAAATCTTGTTTTCTTCTGTAGATGTTAACTGGTAACCA[A/G]GTGACAAAAGGGTGGATCTCACCTTCAGGATATCTGAAATTTACAGTTTATTGTCCGTT
ARS-USMARC-PARENT-AY849381-RS29003287	Verification	rs29003287	ss38340521	A/G	A/G	6	23562312	UMD3.1	ARS-USMARC-Parent-AY849381-rs29003287-0_T_F_1544362791	TGGGAAACCCTATGAGCCAGAGTTTACGTCTGATGATTTGTCTGGCACAAGGTGAGCTGTG[A/G]GAGAACCAGGTGCCCTGAGCCAGTGTCACCTCCATCCTGACCCTGA AAGGGGCTGAGGGA
ARS-USMARC-PARENT-AY850194-NORS	Verification	rs41255750	ss117969490	T/C	A/G	8	59996431	UMD3.1	ARS-USMARC-Parent-AY850194-no-rs-0_B_F_1511686156	GACAAAACCAACCACAAA CAGAAAARGCCAAGTGAGGTGATACTACTGGTTCAGACGAG[A/G]GTGTAGGAAT TCTTATCTTCTCTATGATTGACACAATGAGTGTGATGAGTTTGGGCCAG
ARS-USMARC-PARENT-AY851162-NORS	Verification	rs41255717	ss117970419	A/G	A/G	11	46411100	UMD3.1	ARS-USMARC-Parent-AY851162-no-rs-0_B_R_1544362778	GAAACCCCTCTCCCTAAA GAAAGCCATACCCAGGGA GTCCACKTGGGCTGAATAACCCC[A/G]AGGACTGGCA GAAAGGAAGGGAAGAATGTAGCTGCAGCCTGAACTTCACTGTTGTCTKAT
ARS-USMARC-PARENT-AY851163-RS17871661	Verification	rs17871661	ss28452002	T/C	A/G	11	103047474	UMD3.1	ARS-USMARC-Parent-AY851163-rs17871661-0_T_R_1511686095	CATTCAACGACATTTACTGAGCTCCTCCTGATTCCA GACTTGGAGAGCGGCTACTTCC[A/G]GATGGGATGTTCTCTGCCCTCCCCCTCTCA CGGGGCAGGGAGGCCAGCGGGTGCGGCCTCGG
ARS-USMARC-PARENT-AY853302-NORS	Verification	rs41257524	ss117970873	A/G	A/G	13	47397987	UMD3.1	ARS-USMARC-Parent-AY853302-no-rs-v2-1_T_F_1924250844	CTTTCTATGTGGCTTCCTGTATTCCCTTTGTGCTAA TGTCAGAAACTATAACTATCTA[A/G]TTCACACTAGGTTCTCTATAAATTTATTGCTG AACAAAATATTTCTCTTTT GAAAATAA

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ARS-USMARC-PARENT-AY853303-NORS	Verification	rs41257490	ss117970875	T/C	A/G	13	75383374	UMD3.1	ARS-USMARC-Parent-AY853303-no-rs-0_B_F_1511686244	TGACTGTGAAATKGGTATG ATTGCCCTTTTGTACAGA TGGAGAAACTGAGGCTCA GAAA[A/G]GCTAAGGGATT GCCCACAGGTCCACAGTT CCCAGGCTTCCCAATCC ACTCTCCACTCCC
ARS-USMARC-PARENT-AY856094-RS17871190	Verification	rs17871190	ss28451531	A/G	A/G	29	9160939	UMD3.1	ARS-USMARC-Parent-AY856094-rs17871190-0_B_R_1544362770	AGCTAATTCTCTTGACTTG CAGGCGGAGACTGAGGCT CAACAAGGGGCTTCAGC AACCC[A/G]TGGAGATGCA GCTCTTCCCCTCACATCC AATTCAGTGCCTTTATTGA GTTATTGACTTT
ARS-USMARC-PARENT-AY858890-RS29002256	Verification	rs29002256	ss38339696	C/G	C/G	17	29936157	UMD3.1	ARS-USMARC-Parent-AY858890-rs29002256-0_B_R_1511686322	TATATCCCAATTAACATA CTCTAGAATGGTTGTAAG TTTACCCTTTTACTAATAG CAT[C/G]TGCTTTTCTACGT CCTTACCAACTGTTTAT TATAAATCTTTTCTTGATA GATTGAGA
ARS-USMARC-PARENT-AY860426-NORS	Verification	rs41255724	ss117972311	T/G	A/C	17	56512519	UMD3.1	ARS-USMARC-Parent-AY860426-no-rs-0_T_R_1511686089	GTGCCACTGAAATAGGCA ATGTTGGCAAAACAATGTC TGTTACAATAAATACATT AGAC[A/C]TTTAAATAAATA ACCTTAAAACTATGTGAG GGGACATGAACCCAGTCG ATTGAATCTGG
ARS-USMARC-PARENT-AY863214-RS17871744	Verification	rs17871744	ss28452085	T/C	A/G	18	46647177	UMD3.1	ARS-USMARC-Parent-AY863214-rs17871744-0_T_R_1511686253	AGAAATTGAGGTCCCAGT CTCCTCCTTCAGCAAGACT CAGGCCCTTCTCTCTTG GGACC[A/G]AAGAATCGGC GTCCCCTGCCACTTCATC CTCTGGACCCAAGAACCC AGGCCCCAGACCC
ARS-USMARC-PARENT-AY914316-RS17871403	Verification	rs17871403	ss28451744	T/G	A/C	18	48812014	UMD3.1	ARS-USMARC-Parent-AY914316-rs17871403-0_T_R_1511686395	AAAAGCCGCATCAAGCAT GCTCTCCTTGTCTGGGAA GAGCCGGCTGAGATGAA AGGAAT[A/C]GGAAATCAG GCAATCTGAGAAGAGCTC TCCTCTCCTCCCATGGAT GAAGAAGTGACYAA
ARS-USMARC-PARENT-AY916666-NORS	Verification	rs41257460	ss117972636	A/G	A/G	19	44799390	UMD3.1	ARS-USMARC-Parent-AY916666-no-rs-0_B_R_1511686100	CCTGAGTCCCTGCCAGC CGGGACTGCCTGGATCTG AGAGGTGGGACAAGGAGG TGCTT[A/G]GCCCGCAGGT CACCCGGCTCGAAGTCTG AGTCTCTGGGAAAGGCAA GTGTCCCGTTGAMTK
ARS-USMARC-PARENT-AY919868-RS29002211	Verification	rs29002211	ss38339648	A/G	A/G	20	46066109	UMD3.1	ARS-USMARC-Parent-AY919868-rs29002211-0_B_R_1544362786	TGCAAGATCTGAAGGAATT GAAAATGTCTACCATTAT ATGAAAAATATTGTTTAAA ATG[A/G]AAGGATACATTTT TTAACCTGAAAAGCTTTCA GACAGTTAATCGCTAATTG TAGAAGTTC
ARS-USMARC-PARENT-AY929334-NORS	Verification	rs41255852	ss117973373	T/C	A/G	23	7219975	UMD3.1	ARS-USMARC-Parent-AY929334-no-rs-0_T_R_1511686227	GAAGAGGCTGTTGAAGGA ATCTGAGGAGATCTAGAA CCTCTGGGAAAGAAAAG GGTTGA[A/G]TACAAGTCT CAGATTTTGAAGTGGGG CCAGGGAGCCAACAGAGG CCTGAGGGGTGGGGC
ARS-USMARC-PARENT-AY937242-RS17872223	Verification	rs17872223	ss28452564	A/G	A/G	23	27306795	UMD3.1	ARS-USMARC-Parent-AY937242-rs17872223-1_B_R_2022483098	TTCTAGGTTCTGTGAATAC AGTTRTGAACAAAACAGAG CAAAAATCCTTGCCCTTCAT GGG[A/G]TAGGGAATGGG GAGACAGACAATATACATA ATAAATAACTAAATGTATTT TTTGTGTTAA
ARS-USMARC-PARENT-AY939849-RS17870274	Verification	rs17870274	ss28450615	A/G	A/G	24	56415794	UMD3.1	ARS-USMARC-Parent-AY939849-rs17870274-0_T_F_1511686403	TTTTATGTCTAGCCCTCAC TCCCAGTGTAACCTGTTG TGTTCCCTGTATTTTCCCT GCA[A/G]TGTGTGCACAGA GGAAGTGGGGTAGTGTAG TTCTGCCTTGATCACGCTK TCTCTRCTTA
ARS-USMARC-PARENT-AY941204-RS17872131	Verification	rs17872131	ss28452472	T/C	A/G	25	14683151	UMD3.1	ARS-USMARC-Parent-AY941204-rs17872131-0_B_F_1511686056	CTCAACGTCCTCAAAGGAT CACAAAACAATGCCCTTTAT GGGCRGCTTCTGACCC TGAA[A/G]TATACTACGTGA AACTGCTTAGCTTGCCA TGAGAAAACCTTCAAATA CATACAAGTG

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ARS-USMARC-PARENT-AY943841-RS17871566	Verification	rs17871566	ss28451907	A/G	A/G	1	138583183	UMD3.1	ARS-USMARC-Parent-AY943841-rs17871566-0_B_R_1544362784	TCAGATGATCAGGACAGC CAAGGAAACTCTAGAGGG CCTAAACTCCAATCTTCT GTCCC[A/G]AGTCAAGTGT CTTTGTGAGAAGCAGGCC ACAAGGAACAATATGTTTT ATTCTAGAGTCTT
ARS-USMARC-PARENT-DQ381152-RS29002408	Verification	rs29002408	ss38339879	T/A	A/T	17	17616950	UMD3.1	ARS-USMARC-Parent-DQ381152-rs29002408-0_T_R_1511686131	CATCATATCTGAGGAAAG GGCAGGTTTAAAGAATTT TAAAGCATTTCAGTCTATGT GAAA[A/T]GAAAACCAAG AATATATGCGTGTGTATGT ATATACATAAATATACATG TGTGCTTTGAG
ARS-USMARC-PARENT-DQ381153-RS29012842	Verification	rs29012842	ss38323940	T/G	A/C	1	3249057	UMD3.1	ARS-USMARC-Parent-DQ381153-rs29012842-0_B_F_1511686340	AAATGTTAAAGTAGCGYYTG TCCTTTGTCTGTCAGAAATG GATGGGACCTGGCCAGGC ATTA[A/C]TATTACGTAGAG AGATGCCCTGGGAGCTT GGAGAGCGGTGCAGCAA TGAACACTCAGA
ARS-USMARC-PARENT-DQ404149-NORS	Verification	rs42939801	ss117966457	T/C	A/G	1	99314925	UMD3.1	ARS-USMARC-Parent-DQ404149-no-rs-0_B_F_1511686220	TGTCCTGGGAGGGCCAGA GATGGGGCATAGAACTCC TTGAAAATGGGATGGAGT AATCTC[A/G]AAGAAATGCT GAAATTCTGAGAGAAGCA AAAGCTTTATCTTATGAGC CCCTTTAAGAATC
ARS-USMARC-PARENT-DQ404150-RS29012530	Verification	rs29012530	ss38323621	T/G	A/C	1	59409838	UMD3.1	ARS-USMARC-Parent-DQ404150-rs29012530-0_B_F_1511686232	GAGCTCTTCTAAAACAAGT AAAGCCACTTTCACTCAAA GGCATAGGACCAATTAG GAAG[A/C]ATTTTTTTCTTG CATTTATCTTTTTGAAAAC AATTGTTGATTGGTTTAGA ACTTTAAGC
ARS-USMARC-PARENT-DQ404151-RS29019282	Verification	rs29019282	ss38327170	T/C	A/G	1	151349514	UMD3.1	ARS-USMARC-Parent-DQ404151-rs29019282-0_B_F_1511686396	AAGAACCCTCACACATAAA GGACCCGGAGGAACAATC GCCCAACATTGTAGGGGG YGGGG[A/G]GTGCGTATCA TGGGAGCAGTAATTCAGC AGTATCATGGAGAAAAGG AAAGATGAGAGAAA
ARS-USMARC-PARENT-DQ404152-RS29022245	Verification	rs29022245	ss38330740	A/G	A/G	2	5306838	UMD3.1	ARS-USMARC-Parent-DQ404152-rs29022245-0_B_R_1511686398	TTTGAAGCMAAGAGCAG CTGGTTTCTATACCTGTG CCATYGGGCCCYCTCTTC CCCTC[A/G]CCCCCTCTCC TAGGGTCATAGGGCACAT CCTGGGCTGTCTGCATAT CTTCTCCCTACAT
ARS-USMARC-PARENT-DQ404153-NORS	Verification	rs110843280	ss117974529	T/C	A/G	29	44756502	UMD3.1	ARS-USMARC-Parent-DQ404153-no-rs-0_B_F_1544362792	AGAAGACCTGCAAACAAG GAGCCCCATTAAGAGGAC CATGTGGCCAAGCAGTCA GGGCTC[A/G]GTGAGCCA GACAGGAGAGAACTGCAG GAAAACCTGGCCAAACACT ACCTCCCTATACCCA
ARS-USMARC-PARENT-DQ435443-RS29010802	Verification	rs29010802	ss38325087	A/C	A/C	3	58040470	UMD3.1	ARS-USMARC-Parent-DQ435443-rs29010802-0_B_R_1511686400	TTTTAAAAGTGCTATCATG TGCTTTGAAGGTTGTAGC AGAAGCGGAATAATTCAT AATT[A/C]TTTTAGCTAGGT TGGTGACCACTAGATAGTA GGCTGCTTTAAAGTCTGTG TTTTATTTAC
ARS-USMARC-PARENT-DQ451555-RS29010795	Verification	rs29010795	ss38325080	A/G	A/G	1	29524658	UMD3.1	ARS-USMARC-Parent-DQ451555-rs29010795-0_B_R_1511686404	TTTTATTATGCTTCATATTT GAATGATAAGAYACCTGTA ATTTTAAATTCAGGACTATT T[A/G]TTGGATAACCAAGAC TAAATTCTTCCATTGAGTG TTTCTCAATTATGAAGGCA CAGACTAA
ARS-USMARC-PARENT-DQ468384-RS29003967	Verification	rs17871378	ss28451719	T/G	A/C	5	113137320	UMD3.1	ARS-USMARC-Parent-DQ468384-rs29003967-0_T_R_1511686215	TCCTTCCCTCTCAGGGGTT ACCTGGAGAATTCAGGGG CCCTTCTAGCTAGAACAAA GGCT[A/C]ACRGAAGGAGG TACAGGTGGGGCAGGGTG TAGGAGGGCAACCCCTCCC CTCCCTCCCCTC
ARS-USMARC-PARENT-DQ470475-NORS	Verification	rs43710106	ss117967919	T/A	A/T	5	7651053	UMD3.1	ARS-USMARC-Parent-DQ470475-no-rs-0_B_F_1511686348	AGAGTGAACACAGGAATG AAAGCAAGCCAGTTGCTTT TCCTGAGACTCTCTCCCCT GTCT[A/T]CTTCTATGCTTCC CGCTTATGTTTTCCACAGAG AAATGGAAGCACTACTATG AATGCTATCA

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ARS-USMARC-PARENT-DQ489377-RS29026932	Verification	rs29026932	ss38329318	T/C	A/G	3	98188384	UMD3.1	ARS-USMARC-Parent-DQ489377-rs29026932-v2-1_B_F_1924250892	GCTGGGTGGCYGACCTCACTGCCCTGTGCCGACCTC ACGTGGCCRTGATGACCT GCATCA[A/G]ACAAACCAC AACTAAAGGTTCATATTG CTATTTCTCCTGCTGTACA GAGCCAGGCACRC
ARS-USMARC-PARENT-DQ500958-NORS	Verification	rs43708500	ss117967922	A/G	A/G	5	27825118	UMD3.1	ARS-USMARC-Parent-DQ500958-no-rs-0_T_F_1511686177	ARS-USMARC-Parent-DQ500958-no-rs-0_T_F_1511686177 AAACAGGGATGCTAAAAT CTGAAA[A/G]CATTAGCAG AGTGGGGAGGGATGCTGA AAAAGCATTGACCTTTGTC TGGGTGGGCAAGGG CCTCCTATACTTACCCATG
ARS-USMARC-PARENT-DQ647186-RS29014143	Verification	rs29014143	ss38323045	A/G	A/G	4	17200594	UMD3.1	ARS-USMARC-Parent-DQ647186-rs29014143-0_T_F_1511686097	ARS-USMARC-Parent-DQ647186-rs29014143-0_T_F_1511686097 TATGTGTAGCTGGCTAGG GATCTGACTGCTTCTCACC AGCT[A/G]TGCTTTTCTCA TAAACTTCCCTTCTCCCT GTCTTCTCAGTGCTCTAY RGAGAACTGC
ARS-USMARC-PARENT-DQ647187-RS29010510	Verification	rs29010510	ss38325021	A/G	A/G	3	21146877	UMD3.1	ARS-USMARC-Parent-DQ647187-rs29010510-0_T_F_1511686203	ARS-USMARC-Parent-DQ647187-rs29010510-0_T_F_1511686203 GACTTTTCACATGTGAGGC AAACGTGATAACCACTACA CCACGGAAAGGCGACAGT CGCT[A/G]CCACTGAGCCC TGTATCCAGGAAAACCCAA GGTTCAGCCGCCACTATC CAAGCCACCAAC
ARS-USMARC-PARENT-DQ647189-RS29012226	Verification	rs29012226	ss38323313	T/C	A/G	5	63273386	UMD3.1	ARS-USMARC-Parent-DQ647189-rs29012226-0_B_F_1511686076	ARS-USMARC-Parent-DQ647189-rs29012226-0_B_F_1511686076 TGTAACCGAGCAGGACTC ACTGCTGATGTAACCGAG TGAGCCCTTTTCAGGACA GACCCC[A/G]CTCCACAT GCTCTCAGAAGTACCCAG ATAAATAGTAGCTCATGCCT GAGTTTTTCAGATG GTGATTCTGTTTCAGTGATT
ARS-USMARC-PARENT-DQ647190-RS29013632	Verification	rs29013632	ss38322528	A/G	A/G	6	13897068	UMD3.1	ARS-USMARC-Parent-DQ647190-rs29013632-0_B_R_1511686282	ARS-USMARC-Parent-DQ647190-rs29013632-0_B_R_1511686282 CTGCAATTGGTCCAGGGA CACCAGTCTATGGGCTCC ATGT[C/A/G]TTGGAACATC ACTAACCCTTTTCGTACTTG GGTCTTCATATGTTCTCA ACTGTTTATAGC
ARS-USMARC-PARENT-DQ650635-RS29012174	Verification	rs29012174	ss38323259	T/C	A/G	7	55116289	UMD3.1	ARS-USMARC-Parent-DQ650635-rs29012174-0_B_F_1511686366	ARS-USMARC-Parent-DQ650635-rs29012174-0_B_F_1511686366 CCTCTTCTCCCCGCTTGTA ACAGTTCYCATACTGACAA CTTGAGCTTCCCACTCAA CTG[A/G]GTGTTTCTGAAC CCTGAAATTCTTTGTGTA TTAGCCCTCTGATTGCTAAA GATTATCCCA
ARS-USMARC-PARENT-DQ650636-RS29024525	Verification	rs29024525	ss38334625	T/C	A/G	8	28799249	UMD3.1	ARS-USMARC-Parent-DQ650636-rs29024525-0_B_F_1511686124	ARS-USMARC-Parent-DQ650636-rs29024525-0_B_F_1511686124 AAAGGAGGCAAAATAAATT AATKCTCTGCTATTAATA TCAGATAGCAGTCASTTA TGT[A/G]GAAGACTTTGATA ATTTTCCATTCCATGACCC AGGTGCTGTTATAAGTCA TACACATAG
ARS-USMARC-PARENT-DQ674265-RS29011266	Verification	rs29011266	ss38325554	T/C	A/G	8	106174871	UMD3.1	ARS-USMARC-Parent-DQ674265-rs29011266-0_T_R_1511686025	ARS-USMARC-Parent-DQ674265-rs29011266-0_T_R_1511686025 CATACTAGTTTATTCTGA ATCTTTAAAGCTACTGAGC TGTTCCACAAGTAGTCTAAC TT[C/A/G]GGCATGTGSCAC CGTGCATGTTAAAGCTTTT GTCCGTGARGACATAGTT AYGGGAAGAAT
ARS-USMARC-PARENT-DQ786757-RS29019900	Verification	rs29019900	ss38327796	A/G	A/G	2	111155237	UMD3.1	ARS-USMARC-Parent-DQ786757-rs29019900-0_T_F_1511685817	ARS-USMARC-Parent-DQ786757-rs29019900-0_T_F_1511685817 AAACGAAATAAAAACCTTGC TGCCAGGGAAGGTTCTGA TGTTGTGTGATATTGCATA GGCA[A/G]TTATAAACAAC GTGTCTGATAGYAGTTATC CACTGATATGTCCTCGT GCCCTACTTCC
ARS-USMARC-PARENT-DQ786758-RS29024430	Verification	rs29024430	ss38334530	T/G	A/C	7	18454636	UMD3.1	ARS-USMARC-Parent-DQ786758-rs29024430-0_T_R_1511686389	ARS-USMARC-Parent-DQ786758-rs29024430-0_T_R_1511686389 TATGCCTCCATGCTTTTTTC AAACATGGCCAAGAGCAC AGAATAAAGACTAACTTC AAAC[A/C]ATAACATTAGAG GAGAAAAACTGCATTCCCA ACTCAAGAAACCCTAGTA GTTTCTCTCAA
ARS-USMARC-PARENT-DQ786759-RS29026696	Verification	rs29026696	ss38329081	A/G	A/G	7	94259472	UMD3.1	ARS-USMARC-Parent-DQ786759-rs29026696-0_B_R_1511686192	ARS-USMARC-Parent-DQ786759-rs29026696-0_B_R_1511686192 GACACACATACYACTGCA CAATCACATAAACACACG CTCAGGAGTGAACCGTGC CAAAG[A/G]AGGAGGAAGA CAGATTTAAGCAAGATAA CAAGAATAAATGAACATTG CATGTGGTATTG

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ARS-USMARC-PARENT-DQ786761-RS29012840	Verification	rs29012840	ss38323938	T/C	A/G	10	44103665	UMD3.1	ARS-USMARC-Parent-DQ786761-rs29012840-0_B_F_1511685832	ATTATTAGAAATACTAGACCCTTTTCAAGTTTCTTTTGTTCCTTARGTGCTTTTATAAG[A/G]TTTAACTTCATATTCAGTAAGCTAAGGGAAAAATACTATGGTATATGTATTCTTAATTT
ARS-USMARC-PARENT-DQ786762-RS29010772	Verification	rs29010772	ss38325057	T/G	A/C	10	81572252	UMD3.1	ARS-USMARC-Parent-DQ786762-rs29010772-0_T_R_1511685887	ACGACTCGGCATAGATGATTTGTATGTAATGAGTAAGCACTGGCTGAATGGGTGATCTT[A/C]TGTTAGAAAAAGCGCATCACCATGAAGCCCAGGTAACAGGTCACCTTGCACGTGCTTCTGT
ARS-USMARC-PARENT-DQ786763-RS29020472	Verification	rs29020472	ss38328160	A/T	A/T	12	11824653	UMD3.1	ARS-USMARC-Parent-DQ786763-rs29020472-0_B_R_1511686292	GTTATCAATTATTTGCAGATGCCACRGTCATAGAAGCCTTGGCCAGAGACTCAATGT[A/T]GTTTGTCTAAAAAGCTAAATAATGTGGGGACTCAGGAAAAGACAAGTCTATCRTTTGAC
ARS-USMARC-PARENT-DQ786764-NO-RS	Verification	rs109943112	ss117970659	T/G	A/C	12	25668974	UMD3.1	ARS-USMARC-Parent-DQ786764-no-rs-0_T_R_1511686313	TACGTATTACCAAACACTACTTTTCGGAAGAGTTCCATCAGGTTAATCTTGAACCGAGTCAT[A/C]TGAGATGACTGGTTTCTCCTAAGCTTGCCAACCCTGCATATTATTATTTATTATTATA
ARS-USMARC-PARENT-DQ786766-RS29012070	Verification	rs29012070	ss38323155	A/G	A/G	10	3530271	UMD3.1	ARS-USMARC-Parent-DQ786766-rs29012070-0_B_R_1511686058	CACTTTCTAGGTCCATCCATGTTGCTGCAAATTGCTCATCATGGATCCTGTGATCTA[TC/A/G]TTCATTCTAGGTATATCCTATAGGCAAAGTCACAGGTGAAGGTGTTC TTGCCAGTA
ARS-USMARC-PARENT-DQ789028-RS29017713	Verification	rs29017713	ss38334020	T/C	A/G	6	46936182	UMD3.1	ARS-USMARC-Parent-DQ789028-rs29017713-0_B_F_1511686254	AATTAACCTCTCAAATCTGAGTGAAGTGRAAAGGCA GTGAAAAATTTCAGGAAAGGCC[A/G]AGCAGGTTGGTGAGTGATGACCAGATGTG TTGCTTTGAAAAGGCAAATCCACATGGCACC
ARS-USMARC-PARENT-DQ837643-RS29018818	Verification	rs29018818	ss38335912	A/G	A/G	11	66341589	UMD3.1	ARS-USMARC-Parent-DQ837643-rs29018818-0_T_F_1511685855	AAGGGATATTATGTTTTTAA TGCACTGCTGTATAATTCA TCAGCCCTCACCCCTCCCAGTC[A/G]AAATTAAGTATG GAAATAAGCAAACACCCC AAATTTGCTATTTCCCTTTCCCAATGCCAA
ARS-USMARC-PARENT-DQ837644-RS29010468	Verification	rs29010468	ss38324977	A/C	A/C	8	88974063	UMD3.1	ARS-USMARC-Parent-DQ837644-rs29010468-0_B_R_1511686264	GTACAAGATAGGCYGCCA AAGGCTKCTCTCTTTCAGGCCAAAACTCTCAAGGCAATTRC[A/C]AAGCCTTGATATCTGCTAGAAAATATGGAGCAGATACTTGAGGAAAATAG AATAGATATTT
ARS-USMARC-PARENT-DQ837645-RS29015870	Verification	rs29015870	ss38332364	T/C	A/G	11	24553007	UMD3.1	ARS-USMARC-Parent-DQ837645-rs29015870-0_B_F_1511685930	CCTGCTGGTCAGGACCCCCTCTTCCCAAATGCTAGGAGGCTCCCGCTATCTCC CCCRC[A/G]GCCGACTGCTGCCGAGCTGCCACCTGTTGTCTGTCCACACCCCTTGCCACTGCGTTCT
ARS-USMARC-PARENT-DQ839235-RS29012691	Verification	rs29012691	ss38323789	A/C	A/C	3	116448759	UMD3.1	ARS-USMARC-Parent-DQ839235-rs29012691-0_B_R_1511686108	CCTTGCCAAGGACTCGTTTCGTGTGGAGGCTTTGAAA GGCTGTCAATCACAAACAAACCK[A/C]GATCATTATCTA GTTTTTAACTCTCATTTTCTTAGCACTGAAAATGCTTTAAAGCCCT
ARS-USMARC-PARENT-DQ846688-RS29023691	Verification	rs29023691	ss38336986	T/C	A/G	5	119261609	UMD3.1	ARS-USMARC-Parent-DQ846688-rs29023691-0_T_R_1511686201	GTAACACTGGGTGCTGAGTGTGGAGCTGAGTGACTGAGCAGAAAATCGGCATCCG GCCTCC[A/G]GTGACCTCGGATCCTGGTGTAGCCCCCGCCTAGGCAGGCTGCCTGTATTCTTCGAGGTC
ARS-USMARC-PARENT-DQ846690-NO-RS	Verification	rs43710049	ss117971671	T/C	A/G	14	10171919	UMD3.1	ARS-USMARC-Parent-DQ846690-no-rs-0_B_F_1511686328	AGGCTCTGCCGTACAGGGTCAAGTGTGACGGGCTGCAGGCCAGCTGCAAGGTGGCATG[A/G]GGTATAGATCACAGTGGAACTAAGCTGTTTTAAAGTTCTAACTAGACATTTCTCTCTGA

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-USMARC-PARENT-DQ846691-RS29019814	Verification	rs29019814	ss38327708	T/C	A/G	14	48380429	UMD3.1	ARS-USMARC-Parent-DQ846691-rs29019814-0_B_F_1511686062	AGGTTAAAGGGAAGAGAGAGAACCCCAAGAACATGCGGATATAGWGATGTTTAAAYTAA[A/G]TGAAGCTCAGTTCACAAACTAGCATACAACCTTGAAATTCATCTCTTTTTT TTAGATCTCTG
ARS-USMARC-PARENT-DQ846692-RS29010281	Verification	rs29010281	ss38324786	A/G	A/G	14	80082923	UMD3.1	ARS-USMARC-Parent-DQ846692-rs29010281-0_T_F_1511685981	AGTGCCTAAGGGTAATGATGTCCCATAGTCAGCACTTTGTAAGCACCCTAACTTGCA[A/G]CCAAAATGAACATTTATCTGTTGGAATTCA TAGTTTATAGAATATTAGA GATACTTTTTA
ARS-USMARC-PARENT-DQ846693-RS29017621	Verification	rs29017621	ss38333927	A/G	A/G	16	9855276	UMD3.1	ARS-USMARC-Parent-DQ846693-rs29017621-0_T_F_1511685979	AGTCCAGTGAGTAAAAGACCAGGGTTTTACAGCTTTATGTCTGTACAGCATTTGCC TATG[A/G]TTGCCTGTTTGC AGARCTGCCCAGAAGCCA AGAAGCTGGTCTATYAATT TGGGGGAATT
ARS-USMARC-PARENT-DQ866817-NO-RS	Verification	rs43706884	ss117971908	A/G	A/G	15	38078775	UMD3.1	ARS-USMARC-Parent-DQ866817-no-rs-0_T_F_1511686325	TATTCAGATTGATGGTCCAGCATCTTTAACCCTGACTA AATAGGTTTGGGACAATCT ACT[A/G]AAATTCCTGTGGT GGACATATTTCTGAAAGC CTCTTTGAGATCACCCTC CTAGAGGCT
ARS-USMARC-PARENT-DQ866818-RS29011701	Verification	rs29011701	ss38325997	A/C	A/C	15	79187295	UMD3.1	ARS-USMARC-Parent-DQ866818-rs29011701-0_T_F_1511686199	GACATCTTTGCTTTCTGTG ATTTACAGGTGTCAGCTCCT GAGCTTTAGAACATGGCT GCTA[A/C]AAGCAATGTGA CTGAAATCATTTTCTTGGG ATTCTCCAGAACCAGGG TGCCAGAAGGT
ARS-USMARC-PARENT-DQ888309-RS29013741	Verification	rs29013741	ss38322638	T/G	A/C	7	8272794	UMD3.1	ARS-USMARC-Parent-DQ888309-rs29013741-0_B_F_1511686294	CAGGGACGGTGATTCAG TAAATAACTTCAATTTAATG AGATTTCAATGTGCCTTTA TAA[A/C]TAACAATTTTT TGAGTGATTTTTTTAAAG GCATTTTCAAGTTTAACT GCAGTGAAC
ARS-USMARC-PARENT-DQ888310-RS29012422	Verification	rs29012422	ss38323509	A/C	A/C	17	991486	UMD3.1	ARS-USMARC-Parent-DQ888310-rs29012422-0_T_F_1511686239	GGCAGGGACTTAGAATGG ACTCCATAGCTGATACGG CCATTGGTTGGGAGCTAA ATCAG[A/C]AATGCTTCCA GCTGAGCTCTGTGGCCAG ACAAGGTCAACAGTTTGG CTCTGCAGATAGCC
ARS-USMARC-PARENT-DQ888311-RS29017313	Verification	rs29017313	ss38333605	A/C	A/C	19	8505317	UMD3.1	ARS-USMARC-Parent-DQ888311-rs29017313-0_T_F_1544362775	CTGTGGCAGCAGCCCGAT TCTAACAGAGCAGCTTGT CTTTAGGATGGCCAGCTC TCCAG[A/C]GGAGCCCCCT GGCCTTCAGCAGTGGGGT GAGCACCCTCCTCTTA ACCTCTCTTAGCTC
ARS-USMARC-PARENT-DQ888313-NO-RS	Verification	rs43708490	ss117972867	T/C	A/G	20	17837675	UMD3.1	ARS-USMARC-Parent-DQ888313-no-rs-0_B_F_1544362772	GGGAGAAAAAAAYGGAA CCCAACTTTTTAATCTGCT TCTGGAGCTCACCCACCA TTTAC[A/G]TGGCATGGTG ACTAAACCCGAACCTCTGC CAGGAGCCAGTTTAAACGA TGCAGTTAAATGAG
ARS-USMARC-PARENT-DQ916057-RS29009979	Verification	rs29009979	ss38324475	T/A	A/T	7	81591587	UMD3.1	ARS-USMARC-Parent-DQ916057-rs29009979-0_B_F_1511685798	TTTGTTTTAGTTTGACAGA ACATAGTTTTCTCCACAG TCAACCCAACTGTGAGGA AMAT[A/T]TCAGAAATAAA CTAGACTAAGTTAAACTAA ATTAATGGAATGCCTCTAC TGAGTTTTTT
ARS-USMARC-PARENT-DQ916058-RS29016146	Verification	rs29016146	ss38332645	A/G	A/G	8	1554706	UMD3.1	ARS-USMARC-Parent-DQ916058-rs29016146-0_T_F_1511686287	GTGGATGCGCACAGTCCC AACCCTGGAGCACCAGG GCATTACCTATCAGGAT TTTTAA[A/G]GGAACCGGAC AGCCCGCGGCTTGAGAAT CTATTAAGAGCGCAAGT CTAACCACTGACGT
ARS-USMARC-PARENT-DQ916059-RS29009907	Verification	rs29009907	ss38324402	T/C	A/G	18	23426214	UMD3.1	ARS-USMARC-Parent-DQ916059-rs29009907-0_B_F_1511685808	AGGTGCCCCACATATGATT GTTAATGAATAGATGAAAC AAAGCAAAACAAAGGCTCT AAC[A/G]GTGGACTGCTTT GTGGCCAGGAAGCAACA TGTATGTGGAGGAATGTC ATATTGGTGT

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-USMARC-PARENT-DQ984825-RS29012457	Verification	rs29012457	ss38323545	T/C	A/G	10	98230479	UMD3.1	ARS-USMARC-Parent-DQ984825-rs29012457-0_T_R_1511686053	TATAATAACTCGGGTTCGG CAAGATTCAAGTGTTCCTC TCTGAATGGCTTTTAAAGG CTC[A/G]GTCTCTCTTAGTT CGAAATGGAGATGGGGAA GGAAGGAGTCGGTTGGGG ACGTCTGAGTG
ARS-USMARC-PARENT-DQ984826-RS29027559	Verification	rs29027559	ss38329949	T/A	A/T	14	27751888	UMD3.1	ARS-USMARC-Parent-DQ984826-rs29027559-0_B_F_1511686362	GASCCTGATGACACCCAG TCACATTGAGAGCTKGTAG GTAGCCTTTTGGTTCACCTT AGCA[A/T]TGGGGCTGGAG CAGTATTTCCAACCTTAGA ATCTGCTGCTACTACAACC CACAGAGGCCA
ARS-USMARC-PARENT-DQ984827-RS29012019	Verification	rs29012019	ss38323104	T/C	A/G	10	55611885	UMD3.1	ARS-USMARC-Parent-DQ984827-rs29012019-0_T_R_1511686393	CCATTATTCATAGGTACC CTGTATTCTTTCAAATGAG TATGTTCACTGCCTTTACT TAA[A/G]GTACTGATAAGTA GTGTTTTTGTAYRATTTCA GTCCCTGCATTTGTATTTT AGTATGCAA
ARS-USMARC-PARENT-DQ990832-RS29015065	Verification	rs29015065	ss38326759	A/G	A/G	22	11038205	UMD3.1	ARS-USMARC-Parent-DQ990832-rs29015065-0_B_R_1511686084	CCAAGAACCACTGTGATA GGAGTAGCCCAACACTGG GGATTGAGGAGAGCTCCA GATTCC[A/G]CTCTCTGGC CAGGAGCAAGTCTTGTTC CCTCTTTTCTTAAAAAATT ATTTATTTTTTAAT
ARS-USMARC-PARENT-DQ990833-RS29010147	Verification	rs29010147	ss38324647	A/G	A/G	24	15447771	UMD3.1	ARS-USMARC-Parent-DQ990833-rs29010147-0_T_F_1511685823	AAAGGTGACCTCCTCTGG CAACCCTGTATAAGGCCA CTATTCTTAATCACTCTCT DQ990833-rs29010147-0_T_F_1511685823 ACAGCCTTTAAATGACAAA AAGTATACAGGTTTTCCAC AGCTATGTCAG
ARS-USMARC-PARENT-DQ990834-RS29013727	Verification	rs29013727	ss38322624	A/G	A/G	26	8221270	UMD3.1	ARS-USMARC-Parent-DQ990834-rs29013727-0_B_R_1511686280	GTGAGTGTGTTTCGAGAC AGGGTTCATAAGAATGTAA TTAAGTTTAAACGGGGTTG TGAA[A/G]GTGGGGCTCTG ATGTGATAGAATTTGTGTC CTTGTGGAAGAGATGCA AGAAACTCTCT
ARS-USMARC-PARENT-DQ995976-NO-RS	Verification	rs43706859	ss117973059	T/C	A/G	21	3088886	UMD3.1	ARS-USMARC-Parent-DQ995976-no-rs-0_B_F_1511686372	GCAAAAGGGCAATAAAAC TGTTGCTGGATTTAATTAA AAACAACAAATCATTGGT CAGT[A/G]GTAATGGATGC TACAACAACCCATCAGGT GCATGGCTATTTAAGGAG CCAATATTTTTAA
ARS-USMARC-PARENT-DQ995977-RS29020834	Verification	rs29020834	ss38328525	T/C	A/G	24	1854953	UMD3.1	ARS-USMARC-Parent-DQ995977-rs29020834-0_T_R_1511686267	ATTCGTTTCATGAAAAGGT AGCCAGGTGTGCCTGCC CTGAGGCCAGTACCTTC CTCCC[A/G]ACCCCGTGGC ACCAGAGTCTCAGCCCT CGCCGTGACACCTGGCAG CCTCRCCTTGTAC
ARS-USMARC-PARENT-EF026084-RS29025380	Verification	rs29025380	ss38331266	T/C	A/G	19	15345312	UMD3.1	ARS-USMARC-Parent-EF026084-rs29025380-0_T_R_1511686165	TCATCTTTTGTCTTTTGT CTAGCACCAGTCCAGTT CTAGCCTGTCAGGGCAAA TTCA[A/G]TAATAAATTAATA GCTGTTGATGAGCCAGTT GTTCTAGAATCCATTTTTT TTTTAATAAG
ARS-USMARC-PARENT-EF026086-RS29013660	Verification	rs29013660	ss38322556	T/C	A/G	28	35331560	UMD3.1	ARS-USMARC-Parent-EF026086-rs29013660-0_B_F_1511686344	AACGACAAGGARTTTGC AGATGTGATCAAGGCTAC AAACCCTRASATGGGGAA CATACT[A/G]TAGATTATCC AGCGGGCCTATGAGTCC TTTCTAGCTATGGTAAGG ATGAAAAGAAAAGA
ARS-USMARC-PARENT-EF026087-RS29011643	Verification	rs29011643	ss38325939	T/C	A/G	13	1982209	UMD3.1	ARS-USMARC-Parent-EF026087-rs29011643-0_T_R_1511686381	CTCTCCAAAGCAAACAAGT TAGTGCTGGCTTTGGGGA CTGTGCATCCACGGGCTT CAACC[A/G]CAGYGRGCCA AAATTAAGGTTCTGTCCAGA GCAGGTGGGTGGAAGGCA AAACCAAAGGAA
ARS-USMARC-PARENT-EF028073-RS29014953	Verification	rs29014953	ss38326646	T/C	A/G	18	1839733	UMD3.1	ARS-USMARC-Parent-EF028073-rs29014953-0_T_R_1511686033	TTGATGCCCAATACCAG GTCCTGCCTGTCAATAATC AAGTTGCCTCGCATAATT AGT[A/G]TCTACCCTGCCY CTGTCAATGTCTTATCAGA CAACCTTAAATACAATCCT TATCATCTTG

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence	
ARS-USMARC-PARENT-EF034080-RS29024749	Verification	rs29024749	ss38334851	A/G	A/G	29	28647816	UMD3.1	ARS-USMARC-Parent-EF034080-rs29024749-0_T_F_1511685993	ATATCACACAACCTCCTAGAAGCCAACACCACGGTCACATGATCCTGGTGGCCAATATGGC[A/G]GTGCTTCTACACTATAGAATGGAATACGCTTTAATAGCTYTTACATTATTGGCTTCATTT	
ARS-USMARC-PARENT-EF034081-RS29009668	Verification	rs29009668	ss38324161	A/T	A/T	13	25606469	UMD3.1	ARS-USMARC-Parent-EF034081-rs29009668-F2BT-1_T_F_1923529952	GCTAGGACTGAGGACTTCTCCTCCTTATGTAAGCATCAATCAGAAAATGCTGGGTTGACA[A/T]GCACTACTATCTATAAAAATAGATGGCTGGTGAAAGCTGCTGTATAGCACAGGGAGCTCACGAGCTATCATAGTATGTTCTTTTCCCTTATAAACAACTTTGTGGTGGTATATTTTAC[A/G]KATCCTGAGATTTATTTATTGCAGGAATRTACTTCAGTGATTTTTAGTAAATTTACATAG	
ARS-USMARC-PARENT-EF034082-RS29013532	Verification	rs29013532	ss38322427	A/G	A/G	22	56526462	UMD3.1	ARS-USMARC-Parent-EF034082-rs29013532-0_T_F_1511686117	CAGCCACACCCTGACAAC TGCCAAGCTGGCCAGCACCTCCATTCTATAGTCAATCTTCA[A/C]GCAAAAATGTGCCAAGTTCTATGGGGAGAAACAAGACTCCAAACCTCGCCTGGTCTGTCTTTCTTTCATGAGAAATCAGCCACATATCATGCAATTCACACTCACATATATCAGTTGAA[C/G]GASTGTGAGAAATCAGAAATCATATWATTTACAGTGTTTAAATACATTACACAGCAGGTA	
ARS-USMARC-PARENT-EF034083-RS29018286	Verification	rs29018286	ss38335376	T/G	A/C	25	3126438	UMD3.1	ARS-USMARC-Parent-EF034083-rs29018286-0_B_F_1511686194	AATCTTAGAAAACAGCCTSCCAGGCAGATGGTTTTAACAACCGGTGCAGAATGTAGACTCA[A/G]TAATGCCAGAA TAGCCACGTGATTCATATAAAACCCAGCACTACAGTCTATATTATCTTTAGATCTTCCCCAACAGTAC TTATTACCACATAATAAAAACCCATCACAAGCTTCAGCTTC[A/G]TGGTACTCTGAGAGTAAATAAGAGATTATTGCAAATTCAAATGTGCTGAACAGGTTGG	
ARS-USMARC-PARENT-EF034084-RS29016185	Verification	rs29016185	ss38332685	C/G	C/G	27	21480570	UMD3.1	ARS-USMARC-Parent-EF034084-rs29016185-0_T_F_1511686171	ARS-USMARC-Parent-EF034084-rs29016185-0_T_F_1511686171	ARS-USMARC-Parent-EF034084-rs29016185-0_T_F_1511686171
ARS-USMARC-PARENT-EF034085-RS29025677	Verification	rs29025677	ss38331569	A/G	A/G	28	5913226	UMD3.1	ARS-USMARC-Parent-EF034085-rs29025677-0_B_R_1511685872	ARS-USMARC-Parent-EF034085-rs29025677-0_B_R_1511685872	ARS-USMARC-Parent-EF034085-rs29025677-0_B_R_1511685872
ARS-USMARC-PARENT-EF034086-NORS	Verification	rs43708440	ss117974174	T/C	A/G	26	38233337	UMD3.1	ARS-USMARC-Parent-EF034086-no-rs-0_T_R_1511686083	ARS-USMARC-Parent-EF034086-no-rs-0_T_R_1511686083	ARS-USMARC-Parent-EF034086-no-rs-0_T_R_1511686083
ARS-USMARC-PARENT-EF034087-NORS	Verification	rs110665639	ss117974397	T/C	A/G	28	16097749	UMD3.1	ARS-USMARC-Parent-EF034087-no-rs-0_B_F_1511686140	ARS-USMARC-Parent-EF034087-no-rs-0_B_F_1511686140	ARS-USMARC-Parent-EF034087-no-rs-0_B_F_1511686140
ARS-USMARC-PARENT-EF042090-NORS	Verification	rs43708441	ss117971911	A/G	A/G	15	21207529	UMD3.1	ARS-USMARC-Parent-EF042090-no-rs-0_T_F_1511686079	ARS-USMARC-Parent-EF042090-no-rs-0_T_F_1511686079	ARS-USMARC-Parent-EF042090-no-rs-0_T_F_1511686079
ARS-USMARC-PARENT-EF042091-RS29014974	Verification	rs29014974	ss38326667	A/G	A/G	28	44261945	UMD3.1	ARS-USMARC-Parent-EF042091-rs29014974-0_B_R_1511686334	ARS-USMARC-Parent-EF042091-rs29014974-0_B_R_1511686334	ARS-USMARC-Parent-EF042091-rs29014974-0_B_R_1511686334
ARS-USMARC-PARENT-EF093509-RS29015170	Verification	rs29015170	ss38326868	T/A	A/T	22	22573121	UMD3.1	ARS-USMARC-Parent-EF093509-rs29015170-0_B_F_1511686160	ARS-USMARC-Parent-EF093509-rs29015170-0_B_F_1511686160	ARS-USMARC-Parent-EF093509-rs29015170-0_B_F_1511686160
ARS-USMARC-PARENT-EF093511-RS29012316	Verification	rs29012316	ss38323403	T/G	A/C	21	26620013	UMD3.1	ARS-USMARC-Parent-EF093511-rs29012316-0_B_F_1511686206	ARS-USMARC-Parent-EF093511-rs29012316-0_B_F_1511686206	ARS-USMARC-Parent-EF093511-rs29012316-0_B_F_1511686206



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-USMARC-PARENT-EF093512-RS29013546	Verification	rs29013546	ss38322441	G/C	C/G	27	15141319	UMD3.1	ARS-USMARC-Parent-EF093512-rs29013546-0_B_F_1511686298	AAATTCATGATCCTGGGACTGGGTTGTTTTATTAAC AACCTTGATCTTTTTACAA CAA[C/G]CTTGATCTAATCT TTGCCAAAGTTGCAACATC CAGCTATAAGCAAAGAAAC ACAAGAAAC
ARS-USMARC-PARENT-EF141102-RS29015783	Verification	rs29015783	ss38332274	A/G	A/G	27	37513923	UMD3.1	ARS-USMARC-Parent-EF141102-rs29015783-0_B_R_1511686234	GGAATAGCTTGCAATTTAT TTTTTGTCCTTTTTTCATTT TGTAAAATTTCCAGCTCAG AA[A/G]TCCCTCAGTGTTTT GATTATTCTCCTCTGGATA TGTACCAGTTTGATAGTCT TTTTAAAA
ARS-USMARC-PARENT-EF150946-RS29023666	Verification	rs29023666	ss38336959	A/G	A/G	26	13229219	UMD3.1	ARS-USMARC-Parent-EF150946-rs29023666-0_B_R_1511686350	TGATGGCAGACCCAGCC RTATGGCCACSCACACTTC TCTCTGCTTTCCACCA CCGC[A/G]TGGTTATTGCC ACTTCCTGCCTTTTTTCTT GGTGCCCTTCTGGAACAC CGTCTCTATTCC
ARS-USMARC-PARENT-EF164803-RS29011141	Verification	rs29011141	ss38325429	A/G	A/G	19	55174260	UMD3.1	ARS-USMARC-Parent-EF164803-rs29011141-0_T_F_1511686247	GGGCAGGGAGGGGGCCC TTGGACGCTTTCTCATGTT ATTCCGTGGGGTTATCTCT GAGAC[A/G]GTGTGAATGA GAGCACGGTCACAGTGCC CTGACCCCGACCCTGGGC CACGGCCCTTCCCTG
ARS-BFGL-BAC-19454	Verification	rs109516152	ss105246072	A/G	A/G	16	13695211	UMD3.1	ARS-BFGL-BAC-19454-0_B_R_1544342906	AAAAGATGGCACTTCAAAG TGAAGACTCTCATAAAT TGAGACCTGAAATAAATTT TCC[A/G]CAGTGCCATGAC TGGCCAGATGAGCCATA TGGAGTCAAAATCTCCCC CACCTGACATAT
ARS-BFGL-BAC-27364	Verification	rs110487850	ss105254853	A/C	A/C	1	8437530	UMD3.1	ARS-BFGL-BAC-27364-0_T_F_1511663145	AAAATCTTAGAATCTGACA TTGATGCCTTTATGATCAT CTAAGGAAAATTCATGCC AGC[A/C]GTAAGATGCTTC TTCATTAGGAATTCAGAAT ATATTTTCTTATGGAATTT TTTATTTCT
ARS-BFGL-BAC-35552	Verification	rs41256483	ss105263926	A/G	A/G	2	12823369	UMD3.1	ARS-BFGL-BAC-35552-0_T_F_1511664229	CAATATGAACATTAAGTAA CTTTGTATAGTTTCTTTTC TCCCATCCCTGCAATCTC TAC[A/G]CTAATCAGTAGA GTCTCAGTATCTCATATCA AGAGTAGCTCTGTCTCCC ATTCTCAGCTC
ARS-BFGL-NGS-10035	Verification	rs110008575	ss86293049	T/C	A/G	26	39952154	UMD3.1	ARS-BFGL-NGS-10035-0_T_R_1511669153	TGTTGGACGTTAGGAGAC TCTTCTCATCGGCAGAAAC ATATTTGAGACCCTGGCCA TCGT[A/G]AAGCACAGGGT GGTCCCCAGGGGGATTGT CCTGCCTGCCCTTGGGTC TGGATTAGCTGG
ARS-BFGL-NGS-101456	Verification	rs43526009	ss86330195	T/C	A/G	7	82825197	UMD3.1	ARS-BFGL-NGS-101456-0_T_R_1511669761	GCTGTTTTGGTATGGATG GCTGCCACCTTTAGTGT GGGCCAGCTGTTAATCCC CTTGAC[A/G]GGAGGTGTG ACTGTGTTGTGGTGAGCA GACCCTGCCCTGGTTGTG GAGCGGGGCCCTTCTC
ARS-BFGL-NGS-102169	Verification	rs110612889	ss86332885	A/C	A/C	27	12930436	UMD3.1	ARS-BFGL-NGS-102169-0_B_R_1511667660	AACCACACGGGCATTTTC CCACCTCCCTGGACCTCT CGGCAGCCTTTGGTGTGG CCGCCCC[A/C]TTGCTACTT CTGGAAACACTGTTCCGC GTGCTCCCTAACGTCATA GTCTTCCCTGCAGC
ARS-BFGL-NGS-106015	Verification	rs109496638	ss86287153	A/G	A/G	6	61199572	UMD3.1	ARS-BFGL-NGS-106015-0_T_F_1511678403	ATGCTTAGGACTCAGTTA GTCCACAATCTTACCTGT GCCTCCCTGCTCTTGC CCA[A/G]CAGGGGGCA ACACCTGGCCCTTTAAGT CCTTCAGCATGCCAGCT TCCTCCAGCCTTA
ARS-BFGL-NGS-111053	Verification	rs110813850	ss86339707	T/C	A/G	5	72264603	UMD3.1	ARS-BFGL-NGS-111053-0_B_F_1511637622	CTCTTTCCAAAACCCTCTG CTTTGGCCAGAGTTAGC AAGTGGGCTAAGGAGAGG GCCTG[A/G]GGAACCTTAT GATGCAAAGTTGTGACAC CTTCACATGATTGGGAG ATACTGACTTCTT



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-BFGL-NGS-14740	Verification	rs10954 8782	ss86311 604	A/G	A/G	9	14436985	UMD3.1	ARS-BFGL-NGS-14740-0_T_F_1544344933	AAGCAGCAAGAGGAGAAC CAGTTTTTATGTTTCATGAG CGGCCAAAGAATGAACCA TCAGT[A/G]TGTTAAAGGAT TCAGACTCAAAGGAAGGA AAAGTATCCTCTTACATAT CAAAAAGAAGGGA GCCTGGCATGCTGCGAGTC CATGGGGTTGTGAAGAGC CAGACATGACTGAGCAAC TGAAC[T/A]GAACTGAATC CAAAAAGTGGCCTTTTCTC CATCACCTCTCTCTCTCTT ATCCAGAGAAATT TGCAAGACTGAGCCAGCT GCCCTCTGCGATTTTCATT GGTATCACATCCTTGCTG GGCTT[A/G]CTTCTTTCTG GCCCTGCACTCCCAACCT TCTATTTGCTTTCTGAGC AAATTTCTAAT TCAACAAAGCCAAGAACC ATTCTTAGAATCATTTCGAC CTACTCAGTAGAATCAAGG CCTG[A/G]TTTTCTAGATCC TAAGGATATAGGCAGAGA GACAAGGGCACAAGGGCA GAGCACAAAGTA AAGGCTTACTACTTCTTCT CCCTGGTGAAGAGCTGTT TCCATTCTGGTTACCAGAA AAC[A/G]TGGTGTATTTTT CACTGATTGGCCTGCATTT TTAAAGCTGACAATTTTGC TTAATATCAT AGAGAAAGAAATGACAGGA AAATGAGAGATAGAGAAA GAGAGTTAGTTAGTTAGTT TTAGA[A/G]GTGGGAAAAC AGAGAAGCAATGGGCCAG AGACTATATATGAACCA TAGCTGAAGTTCC AGCAGATGACTAGGACAC AGCTTGGAAAGTGAGTTTTC ATGGCCGCAAGGTTACAA ATTGC[A/G]AACTCAATGTC CTAATGTCAACACATTACC AGTGTATGGGCTAGGACA AGCAGATCTAGA AGTCTTGGCAGTGAAAGC CCAGAATCCTAACCACCA GGCCGCCTGGGGGACTCT TAATTA[A/G]ATTGTGGCAT ATAGTCAAATTTATTTCCAT GGTCTGGCTCTTACTATA ATAGTTTTTATA GCTGCCCGTGGTGACTCT CTGACATTCTGTTCCGCAATG TCCTTTCTCTTTTGT CTA[A/G]ACTATGGGCTCT TTGAGGCCAGAGATTGATG CCTAAACTGGTGAGAGTTA GTGTCTCTCC ATCACACTTGTGAACAAT TCAGTATTAATTTTAACCC CTCTCTAGGCCACAGTCT CCTT[A/G]TCTCTACCTCAT GGGGCTGCATCAGAATA GAGAAGTGGGAGTAGGGG TAGCACTTGGCC GCTCTGCTCAGTGCTCCC TGCGGACCTCAATGGGAG GCAAAATCCAAAACAGAGG GCCTGC[A/G]TGTAACGCT ACACGCATGCATACGCTG ACTCACCGCCGAGAGCA GCGACAAGCACAGCC AAGGTTGCAGCAGCCCT GTGAAAACAAGTGACACT CTAGAGAGTAGTTCTGG AAAGGC[A/G]GGTAGCCCT CACCCAGGCTGTAGATG TTCTAAAGCTGACAAAGGC AGCAGAGCAGAGAA
ARS-BFGL-NGS-15506	Verification	rs10944 8272	ss86285 779	T/C	A/G	5	88334676	UMD3.1	ARS-BFGL-NGS-15506-0_B_F_1511639440	
ARS-BFGL-NGS-15731	Verification	rs11022 0596	ss86301 690	T/C	A/G	7	96936145	UMD3.1	ARS-BFGL-NGS-15731-0_B_F_1511640156	
ARS-BFGL-NGS-24419	Verification	rs42002 380	ss86317 653	T/C	A/G	22	11756783	UMD3.1	ARS-BFGL-NGS-24419-0_B_F_1511661234	
ARS-BFGL-NGS-26517	Verification	rs10965 1210	ss86291 238	A/G	A/G	21	52139183	UMD3.1	ARS-BFGL-NGS-26517-0_B_R_1544345992	
ARS-BFGL-NGS-27577	Verification	rs11073 5554	ss86284 992	A/G	A/G	7	26066004	UMD3.1	ARS-BFGL-NGS-27577-0_B_R_1511658878	
ARS-BFGL-NGS-31640	Verification	rs10896 1088	ss86289 247	A/G	A/G	9	52430564	UMD3.1	ARS-BFGL-NGS-31640-0_T_F_1544347209	
ARS-BFGL-NGS-31807	Verification	rs43638 065	ss86311 676	A/G	A/G	10	61684704	UMD3.1	ARS-BFGL-NGS-31807-153_B_R_2084992678	
ARS-BFGL-NGS-36513	Verification	rs11080 3034	ss86327 338	A/G	A/G	19	17236707	UMD3.1	ARS-BFGL-NGS-36513-0_T_F_1544349663	
ARS-BFGL-NGS-38423	Verification	rs11064 3545	ss86285 582	A/G	A/G	3	12709854	UMD3.1	ARS-BFGL-NGS-38423-0_T_F_1511681877	
ARS-BFGL-NGS-38620	Verification	rs41902 634	ss86313 444	A/G	A/G	18	64382705	UMD3.1	ARS-BFGL-NGS-38620-0_B_R_1511682206	
ARS-BFGL-NGS-39978	Verification	rs11042 5983	ss86287 493	A/G	A/G	2	5757355	UMD3.1	ARS-BFGL-NGS-39978-0_T_F_1544349913	

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-BFGL-NGS-42283	Verification	rs109007372	ss86295624	T/C	A/G	11	95543411	UMD3.1	ARS-BFGL-NGS-42283-0_T_R_1511687559	TATGAATGAGAATCTGCATGCCCTCAGGACTGGGCTGTGGTCCCTGAGACCTTCTAGACT[A/G]TGAGGCCTGGTGGAAACTCCAGGAGGAGATGCAGGAACTGGGCGTCTGGGCAGTGCTGGATTTCAGTGCTTCTCTGATGCCTGTGAAATGATTTCCTATTATGCCTGTGACACCCA
ARS-BFGL-NGS-42505	Verification	rs109614825	ss86323142	A/G	A/G	14	62478242	UMD3.1	ARS-BFGL-NGS-42505-0_T_F_1511684693	GGCC[A/G]CTGGTGAGCTTGGGCTTCTGCTGAAAGGATGCTGGACTTGTTGAATTGGGATAAAGGGCTTTGGCTGTGTGATCTAGGTCAAGTAGCTTAATTTCTATGGCCCTGTTTCTCATT
ARS-BFGL-NGS-55943	Verification	rs110196141	ss86285855	T/C	A/G	15	64628706	UMD3.1	ARS-BFGL-NGS-55943-0_T_R_1511646111	TGT[A/G]AAGTAGTGATGTGTGTATGTGTGTGTATGTGTGTGTGTGGTCAGTCACTCAGTTGTTCCTACAGCCCCCTCCCC
ARS-BFGL-NGS-57711	Verification	rs110925558	ss86288575	A/G	A/G	19	40692429	UMD3.1	ARS-BFGL-NGS-57711-0_T_F_1511647417	TCAAGCGTGGGGTGACCCACCAATTCTGCCATATTTAGCTGA[A/G]ATGCAGGGCCGTGCCAGAAAGTGAGCATTTGGTGGGGACACCAACGGCCGGGCCCTCAA
ARS-BFGL-NGS-58613	Verification	rs42254761	ss86288950	A/G	A/G	4	78609385	UMD3.1	ARS-BFGL-NGS-58613-0_B_R_1511646378	AGGAAAAATGACATATGAGAGGATGGTGAGGTCTCGAGTGAGTCCCTGGGACGGCCACAC[A/G]CGTGAGAGTCTTTGGCTTTGGGCAGGAAAGAATTCAAGAGTGAAACATAGTAAAGTGAA
ARS-BFGL-NGS-67146	Verification	rs109136926	ss86297381	T/C	A/G	2	118773633	UMD3.1	ARS-BFGL-NGS-67146-0_B_F_1544351966	GTCAGCGTGGGAAGGAGGGAAAGAAAAGACTCAGCCAAAGTGTCCCGAGGAGAGCCGGCC[A/G]GGGAGGGGAGAAAGGGGAGGATTTCTTTTCCAGGGTAGGGTTTAATTACGGGAGATTTTGT
ARS-BFGL-NGS-70946	Verification	rs109933901	ss86300858	A/C	A/C	10	14574453	UMD3.1	ARS-BFGL-NGS-70946-0_T_F_1511672045	GAGTAAAACAGAAAAGAGATAGTAGGACAAAATTTCAAGAATCTCAAGGTGTTGGCCACA[A/C]TAGTGAATTTGAGGTACCTGTGCTGTGATTAGTAGATTAACCAGACAAGTTAAGCGCAAACCTTTATGACCCTAAG
ARS-BFGL-NGS-72471	Verification	rs109989231	ss86302621	A/C	A/C	7	103375625	UMD3.1	ARS-BFGL-NGS-72471-0_T_F_1511661821	CAAACATGATCCAAAGGCCCTTCACTGATTTTAAACAAGGTC[A/C]ACTCATTATTCCACCTTTAAGATCACTACAGATGGTGACGGCAGCCATGAAATAAAAAG
ARS-BFGL-NGS-76191	Verification	rs110846944	ss86306783	A/G	A/G	11	62732451	UMD3.1	ARS-BFGL-NGS-76191-0_T_F_1511671491	AGTCACACATCTCTCACTTTAAATCAAAAAGGTACGAATGATTGAGCAGAGAGGAGAC[A/G]TGTCAAAAGTTGAGATAGGCCAAAATCTAGGCTCTTGACCAAACA
ARS-BFGL-NGS-76330	Verification	rs109978585	ss86306259	A/G	A/G	28	33449126	UMD3.1	ARS-BFGL-NGS-76330-0_B_R_1544351882	GATAGCCAGGTTGAACGTCTCCAGACTGGCTTTCACCTGGAACACTCTTTGTAAGTCCAGTGCCAGGCCCG[A/G]TAAGGCACTC
ARS-BFGL-NGS-86662	Verification	rs110949105	ss86316540	T/G	A/C	1	40206017	UMD3.1	ARS-BFGL-NGS-86662-0_T_R_1511691827	AAAAGATGCTTGTAAAGTGTAGTCACTGAATGTCCATTTCCAACATGGGGA
ARS-BFGL-NGS-93119	Verification	rs109133051	ss86323810	T/C	A/G	9	28149131	UMD3.1	ARS-BFGL-NGS-93119-0_T_R_1511691943	GCCTCATAAGAAAAGTTTGC

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-BFGL-NGS-96125	Verification	rs42640153	ss86326564	A/G	A/G	20	58449212	UMD3.1	ARS-BFGL-NGS-96125-0_B_R_1511694234	GCAAGGAGAAGCGGGGA GGGCTCTGGGTGGGGCTT TGAGTGTATGGAGCAGAG TCTGCTC[A/G]GGGCTCAC AGAGAAGAGGCTGGGCCT GGGGATGGAGGGATGA GAGGTCTGGGTGAGGTCA TAATCCTAGGCTCCCATAG AACAAAAGTGCCTAATGGC CTGATACTGGCCTGTGGC CTGG[A/G]AGTTGGGGATC CCAGCGTTAAACGCGAGC ATTCTCATCTGAGGTTGAG CTGGGGAAGACT AAGATTGCAGAAAGGCAC CAGGACAGCCACCTAGA TTAATCAGAAAGGCTGTCA ATACC[A/G]TTTCTCTAAG ATGCGACCAGTACAGAGG TGGCTGAGATCAGCTTGT CCTCTGCTCAGAC CCTAAACAAAAATGAGAAA TATTGACTACAGCCCTCA CAGTTGATTAATGATAGCA GAA[A/C]AACAMACCTGAA TTCCATGAACCATCTTTGG AAGGCAAGCCTTATTACTT TATTTTCTTA
ARS-BFGL-NGS-99210	Verification	rs110578763	ss86329428	T/C	A/G	17	52740918	UMD3.1	ARS-BFGL-NGS-99210-0_T_R_1511693633	AAGGCAAGACCTATGGTC GAACTGCGGGACACTGGG CCTCCGTA AAAAAGCTGGG GGATCG[A/C]GGCTAACCA GCTCACCAGCACATACCC CAAAGGGTCCAGGAAAGG 686274 ARS- USMARC- Parent- EF026085- rs29021607- 0_B_R_1511 685904 ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
ARS-USMARC-569	Verification	rs109650557	ss117962557	A/G	A/G	17	30360942	UMD3.1	ARS-USMARC-569-0_T_F_1544362799	ARS- USMARC- Parent- AY841151- rs29003466- 0_T_R_1544 362781
ARS-USMARC-PARENT-AY841151-RS29003466	Verification	rs29003466	ss38340727	T/G	A/C	2	45832887	UMD3.1	ARS-USMARC-Parent-AY841151-rs29003466-0_T_R_1544362781	AAGGCAAGCCTTATTACTT TATTTTCTTA
ARS-USMARC-PARENT-DQ786765-RS29009858	Verification	rs29009858	ss38324353	T/G	A/C	9	98483346	UMD3.1	ARS-USMARC-Parent-DQ786765-rs29009858-0_B_F_1511686274	ARS- USMARC- Parent- EF026085- rs29021607- 0_B_R_1511 685904 ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
ARS-USMARC-PARENT-EF026085-RS29021607	Verification	rs29021607	ss38330092	A/C	A/C	21	65198296	UMD3.1	ARS-USMARC-Parent-EF026085-rs29021607-0_B_R_1511685904	ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
ARS-USMARC-PARENT-EF089234-RS29020870	Verification	rs29020870	ss38328561	A/T	A/T	23	50884052	UMD3.1	ARS-USMARC-Parent-EF089234-rs29020870-0_T_F_1511686061	ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
BTA-100621-NORS	Verification	rs41611675	ss61512369	A/G	A/G	22	25598780	UMD3.1	BTA-100621-no-rs-0_T_F_1511593240	ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
BTA-11701-RS29017459	Verification	rs29017459	ss38333753	T/C	A/G	11	61989432	UMD3.1	BTA-11701-rs29017459-0_B_F_1511622709	ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
BTA-30857-NORS	Verification	rs41579524	ss61479561	A/G	A/G	12	80058952	UMD3.1	BTA-30857-no-rs-0_T_F_1511625792	ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
BTA-37062-NORS	Verification	rs41632769	ss61536141	T/G	A/C	15	51528617	UMD3.1	BTA-37062-no-rs-0_B_F_1511533983	ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061
BTA-73768-NORS	Verification	rs41647805	ss61555892	T/C	A/G	5	67031023	UMD3.1	BTA-73768-no-rs-0_T_R_1511550568	ARS- USMARC- Parent- EF089234- rs29020870- 0_T_F_15116 86061

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
BTA-92021-NORS	Verification	rs41663009	ss61565762	A/T	A/T	11	9385008	UMD3.1	BTA-92021-no-rs-0_B_R_1511548279	AATGCTCCAATCAAAGAC ATAGAATGGCTGAATGGG TAAAACACAAGATCATA ACAC[A/T]CTGCCTCCAAG AGATTCACTTGAGACCTAA AGATACACAGAGACTGGA AGTGAAGGTCTG
BTB-00188171	Verification	rs43396375	ss65312019	A/G	A/G	4	57787437	UMD3.1	BTB-00188171-v2-1_T_F_1924252375	AAAAATGAGATTGTGAAGG GCAATGCCAAGGAAAGTG ACTCCTAATCTCACTGCCA GAAT[A/G]TGGGAGGCTTC AGGGCATCTGCTATACAA GCTCATTCCAAGAGGTTT CTCATAACTGCAG ATTTGCTCCCTTGTGTTAGG TTGCAGTTCTGAGCTCTTT
BTB-00394801	Verification	rs43599414	ss65518069	A/C	A/C	9	59383405	UMD3.1	BTB-00394801-0_T_F_1511574086	AGTTGCTATGGTGACAGTA ATA[A/C]TAAAGGCTGATTG GAAGAAGACATCTTATCTG GGATTTTTGTTGTTGAGAG AGGAGACCA CTACATTATAATCCCTTGT TCAGACACTCAGCGGCTA TGCCCCAACCAAGTTTCT TAAA[A/C]MTGAACCAACC AAGCACACCAACAGCTC GGGATTCTGTTTTGTGTC ACCTCTACATTC GTGGCAATTTATTCTGAT TCTTTTTTCAGAAGTAAGA TAAAATTTGTAATAA ACC[A/G]GAAGTCTGCTAG TTGAACTTACCCATTGAC AAATAACATACGTGCCTCC ATTGTCAAAA TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-00420215	Verification	rs43625528	ss65543436	A/C	A/C	10	44920804	UMD3.1	BTB-00420215-0_T_F_1511581596	GTGGCAATTTATTCTGAT TCTTTTTTCAGAAGTAAGA TAAAATTTGTAATAA ACC[A/G]GAAGTCTGCTAG TTGAACTTACCCATTGAC AAATAACATACGTGCCTCC ATTGTCAAAA TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-00818821	Verification	rs41981646	ss62736870	A/G	A/G	21	40408803	UMD3.1	BTB-00818821-0_B_R_1544355596	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-01057979	Verification	rs42223561	ss63390705	T/C	A/G	1	114085424	UMD3.1	BTB-01057979-0_T_R_1511598216	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-01285245	Verification	rs42411615	ss63968561	T/C	A/G	1	63277846	UMD3.1	BTB-01285245-0_B_F_1511617607	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-01371672	Verification	rs42492955	ss64140877	T/C	A/G	15	50566485	UMD3.1	BTB-01371672-0_T_R_1544358117	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-01416427	Verification	rs42537334	ss64230252	T/C	A/G	19	52911677	UMD3.1	BTB-01416427-0_T_R_1511613730	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-01478115	Verification	rs42595691	ss64353011	A/G	A/G	4	42103377	UMD3.1	BTB-01478115-0_T_F_1511627148	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-01902778	Verification	rs43014084	ss64919224	A/G	A/G	6	114165533	UMD3.1	BTB-01902778-0_B_R_1511543811	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC
BTB-01980499	Verification	rs43084864	ss64996227	T/C	A/G	12	61345454	UMD3.1	BTB-01980499-0_T_R_1511562008	TCATACTAAACTCCTTT CAGTTGAATGTTGGCTACA GGCTTCTATATCTGATC ATC[A/G]TGATATTTGTAT TGGGATACTAGAACTTCTG AGTTATTTTTCTATTGGAT ATGTTCTA TGTGTTAATTTTATGTTATC CCTTTATCTTTAGGATTAA AATGGAACTTTCTAATTA GT[A/G]TCATATAATCAGTT ATGGTCATTATTCTTTGA TGACCAAATTGAACAGTTG TGTGTGTA TACAGGAAATTGTGAAGGT ATTTGCATATGCACACATG TATCACTTATCCAAATTTT AA[A/G]AATGAAGTTTTAAT AAAAATTTGTTGGAGTAC AGCTCTGAATCTATGAAA TTATCATC TTGCATTTATACATTAAGA GGATAAACCCAGTTGCATCT AAACTCTTTGGGACTTGT GAT[A/G]GCTTTAATTAGTT TACAACCTTCTGGTTTATTT CCTCTAATTTTTCTATCTC CCTAATCT TAATGGGCTCCAAATGTT TGCTTGTATAGCATACAA TGCTTGAGAGGAAAGGGT TTAA[A/G]CTGATGTTTGT TATTCATATGGTAAGGGAA AGCCTGTTTTTATTAGCAC TTTTCCCCCA AGCATCCTGGTGACTTCA GGGGTAGATGTGTATATT GAGCTCACATCAGAACAA CTGCAG[A/G]AAAAAAGA AGAAAAGGAAAGCCAGACA AGGAAAGTGAGATGGGGT GAATATCCCTGCTGG TGTGAGCAACAGTACAAA GTACACATGCTTTCTAAT CCAAGATCTAGACTCCATT ATTT[A/G]ACTGAACAGGGG CCTCTGAGGCCCATCAGC TGTCTAGAAGGCCCATG TCAGGTATTTC

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
HAPMAP24215-BTA-163266	Verification	rs109704141	ss117974193	T/G	A/C	27	10764825	UMD3.1	Hapmap24215-BTA-163266-0_B_F_1510715935	ACTGTACACATAGGAATTT TAATAATAGTTGTACAGAA GTATAATGAAAAATAATGG TCC[A/C]GCTGAATCCTTAA CCATCCCCAGTGTACTTTC CCAGAGGCCAAACACTTTTA ACTATTTTTT
HAPMAP31098-BTA-136127	Verification	rs109479519	ss117972951	T/C	A/G	21	62028408	UMD3.1	Hapmap31098-BTA-136127-0_T_R_1510715012	GCTTTCCAGGGAGACCCT TTGTCTCTGCAGTGATTAT CAGCCGAAAATCACCCTTC TTTGC[A/G]CCCTTTCAATA CTTCCATGGTTAACCCAC GGCTGGAGGGCTGCCTAA CGACATTTTTAT
HAPMAP34424-BES10_CONTIG566_926	Verification	rs43708462	ss66538092	A/G	A/G	24	6408329	UMD3.1	Hapmap34424-BES10_Contig566_926-0_T_F_1510715130	CAGAAGGTTTTAATTTGC TTTGATCAGATCCATCAGT AGAATAACCATTATGACC GCA[A/G]TAACCTTACAAAA TATAATTCTCAAAAGTAAA AATTACTCCTTTGATCCAT GGGCTGCAG
HAPMAP35535-SCAFFOLD86180_8791	Verification	rs29023461	ss117973345	T/C	A/G	23	41700829	UMD3.1	Hapmap35535-SCAFFOLD86180_8791-0_B_F_1511627625	ATGAAGAAGGCTAAAGGG AGAGGAGGGGTCTCAGT TACTCTGCCGCAAGGCA CTGCTC[A/G]AGAAAGGAT CTTACTGTCTATACCGTAA TGTGAACTCGCAAGACAG CAAGCTATGAACTT
HAPMAP36588-SCAFFOLD90561_9460	Verification	rs29023669	ss117972848	A/G	A/G	20	2289049	UMD3.1	Hapmap36588-SCAFFOLD90561_9460-0_B_R_1511629069	GTCTGTCTCCCAAGTCC CGGATCTAAGCCCCCTAC TGTGAAACGTGGAAAGGAG TCAGCG[A/G]TACAGGAAA CCTTAGTTCCAGTAGTTAC CAGTAAACATATACAAGGT GCTGCTTCTTAGA
HAPMAP39425-BTA-70290	Verification	rs41586923	ss61489805	T/G	A/C	4	10737673	UMD3.1	Hapmap39425-BTA-70290-0_T_R_1509317762	GATATGATTCTGGAGCTTC GGTCACAAAAATGCCACA CTCCAACAAGCGTCAGTC TACTC[A/C]ACACCCACT CTTGTAAAGGGGACATCCA AATTGGATTGACACCAAAA TTTGATTACAATA
HAPMAP39461-BTA-109898	Verification	rs41611358	ss61517053	T/G	A/C	21	27927781	UMD3.1	Hapmap39461-BTA-109898-0_B_F_1509322909	AGTGTGGTATGACAAGAAT TACAAAAGCTAACCCAAGA AAGAATCCAGACCTGATCA TTA[A/C]GGTTCTCTGCCTT TTCAGTCTGGCAGCAATTG AAAATCACAACTCGGAAAC ACGTACCAT
HAPMAP40148-BTA-92999	Verification	rs41592395	ss61495728	T/G	A/C	11	36713471	UMD3.1	Hapmap40148-BTA-92999-0_T_R_1509312964	GGAAGTAAAAATAAATG GCAAGTTAGAATTCTACTC ACAGCAAAGATATTTTTCA AGA[A/C]TGAAAGTAAAAT AAAAAACATGGAGACAAA AAAAATCTAAAACAGTTTT GAATCACCAG
HAPMAP40729-BTA-40319	Verification	rs41635414	ss61537824	T/C	A/G	16	19882683	UMD3.1	Hapmap40729-BTA-40319-0_B_F_1509322497	AATTCAATCTAGAGTTTGA AGAAACCAAAAAATGAGCA TATAGGTAAGAGCACCC CAAG[A/G]AAGAGAAAGGA GGGCCATGTTAGTATTCAT CCTGTGCTAGAGAACTAG GCTTGCTGGCCT
HAPMAP41591-BTA-59790	Verification	rs41649671	ss117973994	T/C	A/G	25	27912102	UMD3.1	Hapmap41591-BTA-59790-0_B_F_1509322371	AAGACCCACATGTGGCC TGGAAATGCCGGAAAAAAA AAATGCTCCCCTTTAACAA CCAGG[A/G]AAGGAAGAAT GAGTCTTACCTTGCAGT ACTCTACACATAGAATGTC TATAACAGTGTC
HAPMAP42648-BTA-71195	Verification	rs41653000	ss61554558	T/C	A/G	4	71061224	UMD3.1	Hapmap42648-BTA-71195-0_T_R_1511567042	TCAACCCCTCATGTCCTTG AGAAGGTAACAGAGACCT CAGAAAGGATGTGTGTTG TCCAC[A/G]TGTTCAGT AATACGATGACAGAGTCAT CACAGAGTCAGGCACTGG CCCAGGGCCCTGC
HAPMAP43057-BTA-80741	Verification	rs41588251	ss61492499	T/C	A/G	7	13279972	UMD3.1	Hapmap43057-BTA-80741-0_B_F_1511566361	GCAAAAGAGTCAGACATG ACTTTGTGACTAAACAACA ATGACAATAACAAGAGTCT TTAC[A/G]CATCTTTCAGAG ATGTCAGCAGCAACAGAG GATGGAGTAGGGATCTGT GTGAAACCATGT

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
HAPMAP43142-BTA-107561	Verification	rs41567696	ss61472156	A/G	A/G	6	29556343	UMD3.1	Hapmap43142-BTA-107561-0_B_R_1511566213	AAGAGAGCTAGATTACTGATGGATGATAGCTTTTACTTTAATTTTCTCTATTTTTCAC TG[A/G]TGCTTTCAAGCTTGTGATTCTTTACTAAATTTCTTGATGGCCAAGTGAATGAGTACAT
HAPMAP43792-BTA-122725	Verification	rs41620645	ss61524403	T/C	A/G	13	83437845	UMD3.1	Hapmap43792-BTA-122725-0_T_R_1511566454	TTCATAATTACTTTTCTCAA TGCTGTACCAAGTTTTTTG CATGTAGTAGGGGAATCAATAA[A/G]TATCTGTTCACATTCTAAAAGGAAGAATGCAGGTAGTCAGTGAGTATTTGATGAATTGCT
HAPMAP43953-BTA-83292	Verification	rs41656801	ss61561086	A/G	A/G	22	54103673	UMD3.1	Hapmap43953-BTA-83292-0_B_R_1509287143	ATTTTAAAGCAGATTTAGT TTGTTCTATTAAGAATAC AGGAAAGATTATTGATATTTTAA[A/G]TAGGGACTTAAAC TTCTGGCTTTTTAAGAGTT GTTAAATTCTGCTTGGTAAACAAAACGT
HAPMAP46550-BTA-103548	Verification	rs41615770	ss61513810	A/T	A/T	20	30928803	UMD3.1	Hapmap46550-BTA-103548-0_B_R_1509274573	TGTATTGGAAAAAGATTTTG AGCATTACATAAAGCCTATTAAGGGTGTCTAATACATAGA[A/T]GCAAAAATAAAAAGTGAAAATATATGGCTGAAGTAAAAGGAGGGAGTGCCAGTTTGTTC
HAPMAP46653-BTA-47447	Verification	rs41573026	ss61467906	T/A	A/T	2	41938704	UMD3.1	Hapmap46653-BTA-47447-0_T_R_1509284426	ACACTAAGACCCTGATAAATAGGCAAAAAGGAGAGATTACAAAAGAGGAAATATAAC TATT[A/T]AAAAACATAAAGCAAAAATTTCAAATTTTTATTAATCAAAGGATATAAACTAAAATATTG
HAPMAP47281-BTA-40051	Verification	rs41582312	ss61481907	A/G	A/G	16	72931875	UMD3.1	Hapmap47281-BTA-40051-0_B_R_1511577277	GCAATCTCGCCTGAGCA GTACCAGAACCGGGGAGC CTTTGGAGTGAGTGGCCTGAGAGG[A/G]AGAGAATACCTTAGCCACAGCTTGGCATTG CAGGTATCAGTCAGAGGGAAGAAAGTTGGGCGTTGGACACAACCTGAGCACTAACAGTTTCATTTTCA
HAPMAP49452-BTA-112834	Verification	rs41569794	ss61473375	A/G	A/G	4	72987997	UMD3.1	Hapmap49452-BTA-112834-0_B_R_1509305577	TAATTAACAAAGTGCCTTCCAT[A/G]AATTAGATCATTATGCCTCACAGGAAGCC TGTAATAAAGAATTACAG AAGTTCCTCTG AAGTCATTATTAATATAAC CCTCTTTTACTTTCAAAAATGCATATGTTTGGACAATGAA TC[A/G]TATGATCCTTAG TTAATCAGGATGAAACTCTAGGTTATATTGCATTTATTTTA
HAPMAP50598-BTA-122724	Verification	rs41575075	ss61475502	A/G	A/G	19	4670556	UMD3.1	Hapmap50598-BTA-122724-0_B_R_1511601629	CATTGCAGGTGGATTCTCTACCAACTGAGCTATGAGGGAAGTCCATATAAACCATGTACT[A/G]TTTTATTCTATCTGTTAAAAAGGACACTACAAGAATATTGTAAGTCTATGTTCTGAACT
HAPMAP51227-BTA-41809	Verification	rs41634345	ss61538562	A/G	A/G	17	67216420	UMD3.1	Hapmap51227-BTA-41809-0_T_F_1511602462	GTTTTCTTCTTGGGATTTTATGGAAAAATAATACAGACTAAAGTAAATATGAATCAT[A/G]TATTGCACAAACC AATAATTTTGTGTTTGCCTACCATCCATGTTTACATATTTTGTAT
HAPMAP51527-BTA-97415	Verification	rs41665299	ss61568611	A/G	A/G	6	44461834	UMD3.1	Hapmap51527-BTA-97415-0_B_R_1509318683	TGGGGCAGATAGGGGTGA GAAATATTGAACAAATGAA GCAAAAGATAATGAATAAATGTAC[A/G]TACATGATTTGT TTTTATTGTTGTTTTCAGTAACTAAGTCCTGCTGACTCTGCAACCC
HAPMAP51908-BTA-63031	Verification	rs41648007	ss61550226	T/C	A/G	27	41049981	UMD3.1	Hapmap51908-BTA-63031-0_T_R_1509319646	TGAGAATTAGGACTGCAACATATGAATTTGAGGAGAACATAACTCAGACCCTGCTCTAAA[A/C]CACTGGTAGTCTTAGAACCAATGTAACAAAATCCACCATCTCCACAAAA TAAAATTTCAAAT
HAPMAP52240-RS29013844	Verification	rs29013844	ss38322744	T/G	A/C	28	20453054	UMD3.1	Hapmap52240-RS29013844-0_T_R_1511602284	



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
HAPMAP54020-RS29023153	Verification	rs29023153	ss38336442	A/G	A/G	18	6776532	UMD3.1	Hapmap54020-rs29023153-0_T_F_1509313606	AAGAGAAGATGAACTTATT TACCTCCTCTGGAGGAG TTCATAAGATCCCCTCAGT GAGA[A/G]JTTCCTCTCTCT CTCCTTTCCATGGCCTCCC CTGACTGTGTGTTTGAGTC CAGGACAATC TCTCAGCACTCATTCCCAT GGGTAGCTTTGAAATGG
HAPMAP54313-RS29012632	Verification	rs29012632	ss38323727	T/C	A/G	9	83320792	UMD3.1	Hapmap54313-rs29012632-0_T_R_1511548090	ATTAACCTTCTGCTAGAGT GGTA[A/G]JAATCCAGTGCA TATATAAAAAGCGCATTAT TTAAGAGCTTGAAGCTGAA AGGGGATTTGA AAGCAGCAGCAGCTAAGG GGAAACGTGATCTCGAAT
HAPMAP54547-RS29012198	Verification	rs29012198	ss38323285	T/C	A/G	4	110776624	UMD3.1	Hapmap54547-rs29012198-0_T_R_1509327754	AACACAAAAAATATGCAAC CTTCC[A/G]TTTACAATCAA ATGCTAGGTGTCATCCTCA TGACTGATGGAGTGAGGA GGTAAGGCGTGA TATATGTATCAGTCATCTT GAACTTAAGAATCATTITTC
HAPMAP55441-RS29010990	Verification	rs29010990	ss38325276	A/G	A/G	8	103137122	UMD3.1	Hapmap55441-rs29010990-0_B_R_1509329479	TCAAGTTCAAAAAAATAAT AAA[A/G]CCAGGGGAATTT ATACAACCTCTGGAAATGA TAGGGATATATTATAAAAT GTCCTTTCTC TGTCAATATCAAAAAAAGA AAAAGAAAAACAGAAAAT
HAPMAP59876-RS29018046	Verification	rs29018046	ss38335133	A/G	A/G	2	13853729	UMD3.1	Hapmap59876-rs29018046-0_B_R_1509290295	ACAGGTAGTTTGTCTTATA TTA[A/G]JAATCTTTTTTGT GGGTGGGTTCTCTAGAGA CCTGTCTGATATCCCAGTA TTTGTTCAG GATGATAGTTTGACAATTA GAACAGTTATTCTGTTCCA
HAPMAP60017-RS29023471	Verification	rs29023471	ss38336762	A/G	A/G	7	81668727	UMD3.1	Hapmap60017-rs29023471-0_T_F_1511552944	TTTGAATGTTACCTAATAT CCT[A/G]GCTTTTTTAAAAA AAAGTATGGCTAGCATTTT CACAATATTCAAAATACTT TAGAAGCCC TGCCATTCTTATGATTTA TTCAAATACTCATTACAGT
UA-IFASA-5034	Verification	rs29024763	ss117965805	T/C	A/G	29	29052623	UMD3.1	UA-IFASA-5034-0_B_F_1511686988	CAATCTATTTTTACACAGA GGT[A/G]JAAGATGTGCGCT GATAACGGTTAATCATTTA TAATTCCATGGACTGGTTG GGAGCCAATG GGATAGACTCTTTCTCGCC TCGCCCTTCCTTTGATCCT GTCTGTGCCCCTTGCTCT
UA-IFASA-6532	Verification	rs41640891	ss117965542	T/C	A/G	22	21770149	UMD3.1	UA-IFASA-6532-0_B_F_1511687122	CGC[A/G]JTCAGATCCTGGA AGCCGTCACGATGCAGCA CATCTTCATGAACAACCTT CAACTGTGCAG GACACAGACTATCTAAATA AATTAAGTGATAAGTATTT ATAAATGGAATCTTTTTCTT
BTA-108007-no-rs	Discovery	rs41664832	ss61570066	T/G	A/C	1	116419981	UMD3.1	BTA-108007-no-rs-0_B_F_1511607063	GG[A/C]JAACCTTTGATTTCA TGAGAATTTCTCTATGTAT ATTAATACAGTCATTGCT CTGACATG AATTCTAACAAAGTCAGCA ACTCCCAAGAGTCTTCA
Hapmap49586-BTA-36632	Discovery	rs41582641	ss61481018	A/G	A/G	1	79700956	UMD3.1	Hapmap49586-BTA-36632-0_T_F_1509284406	AAAATAGATTGTCTGTGTA GAC[A/G]JAGAAAGCTAGCA GTCCAAGGAGAGAAGGAA AAATACCTTCTTTAAGTAA AAGAAATCATA ATTGTGCCTTCAGTTTACT TCCTCCACCTGAAGCAC TGTGGAACCATCAGTCATC
ARS-BFGL-NGS-103086	Discovery	rs109595377	ss86330023	A/G	A/G	2	2858436	UMD3.1	ARS-BFGL-NGS-103086-0_T_F_1511673189	TCTT[A/G]GGATTAGGGCC CACCAGAGAACAGACTTG GATACTGGAAGCAAGAAA CCCCACACAAGTC ATTTTCTAATCTAGAGCAT TTTTTTTTGTCTTTATGACT
BTB-01294230	Discovery	rs42418154	ss63986515	A/G	A/G	2	55038193	UMD3.1	BTB-01294230-0_B_R_1544352864	CAGCTGGTATTGAAATGA AA[A/G]JTGATACCGACTT TGTCCTTAGTAAGATAACA GGCAGCAAAAAGGAAGTA GGTGGACTAG



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
BTA-09064-rs29025231	Discovery	rs29025231	ss38331116	A/C	A/C	7	112265796	UMD3.1	BTA-09064-rs29025231-0_B_R_1511596353	ACAATGTACATGATTTTGAA AAAAAAAAAAAAAAGTATTG ATTGTTTTTTTTCATCAAG[ A/C]CATTACACAAGTTTCAA AACGTATGTGCCTACACAC GCATTACAGAGTGTCTGCC ACGTGAG
ARS-BFGL-NGS-28141	Discovery	rs109555469	ss86325310	T/C	A/G	8	97241486	UMD3.1	ARS-BFGL-NGS-28141-0_B_F_1544346378	GAAGTTTAAAAAGTTAAAC AAGCCAGCCATCCTACAG ACTTTTTTTTTTTTTTATC TCT[A/G]TTGTGGCCACTC CTCCAACCTCCATGATGTG TTCTCCATACTGTTGACT TTGGGAGGTG
UA-IFASA-2534	Discovery	rs29009895	ss117963993	T/C	A/G	8	45804905	UMD3.1	UA-IFASA-2534-0_T_R_1511685815	AAATAGGAAATAAACAGCA TCAGAGCTAACAGACCAA CCTGGGAGATGAACCTTTC CAGGC[A/G]AGGATACCAC AGTGAAGAAACACGTGGA CACTTGGCTGAGGGGGGG ACTGACCGGGGTTT
ARS-USMARC-Parent-DQ837646-rs29012894	Discovery	rs29012894	ss38323993	A/C	A/C	11	1703612	UMD3.1	ARS-USMARC-Parent-DQ837646-rs29012894-0_T_F_1511686081	CCAAAYGGTCTACTGGGG TCCCTCTGGCCACCCTC CAATCCATCTCCAGTGGG TAGCCA[A/C]AAATCACCC TCAGATGTACATCTAAGTC ATGTYACTCTCTCCAACG GCTTTCCTGTTTT
BTA-88608-no-rs	Discovery	rs41597697	ss61494512	A/G	A/G	11	24317047	UMD3.1	BTA-88608-no-rs-0_T_F_1511561294	CATTTGAAAGACTTGCCAT TGATGGTCAGATTACTCTC TGTTCTGTTTTTCATCTG TAA[A/G]GGAGACTAAACA ATAGCACCTACTTAATGAA ACTGGATTAATTGAGATAA TACTGGTAAA
Hapmap41140-BTA-107332	Discovery	rs41616688	ss61515739	T/C	A/G	11	78545016	UMD3.1	Hapmap41140-BTA-107332-0_T_R_1511629008	TGAAGGAGAGGCCAACTG AATATTAAGGAGAGGCCA GAGGCATATCCCTGAATAT AAAC[A/G]TGCTGGATAG GGTGGGGTTCTCCAGCT TTTTATGGTTTTTCAGAGG GAAATCCTGGCC
BTA-92697-no-rs	Discovery	rs41661000	ss61566157	T/C	A/G	13	50910557	UMD3.1	BTA-92697-no-rs-0_T_R_1511561324	TCTGAGCTAATATGAGGG CTTATTGGAAAACCTTGAAA CAACCAATAGAGACCATG AAAA[A/G]TTAGTATCAGA AATACATAGAATAAAAAATT TTGTTAAGACCAGCTATGA ATTTAAAAATGG
Hapmap39398-BTA-31996	Discovery	rs41632359	ss61533405	A/C	A/C	13	26708860	UMD3.1	Hapmap39398-BTA-31996-0_T_F_1509317720	GATCTCCATCTAAAACAAG AACCAGTTAACACCCAAAT GTGCACAGACAGAATCTC AGGC[A/C]TCTCCTGTCCC TGTTCTATTGCCTTCTATT GGCAAAGTCTCAGCTAATA CTAATCACTTC
Hapmap48136-BTA-96744	Discovery	rs41663038	ss61568240	T/C	A/G	13	719908	UMD3.1	Hapmap48136-BTA-96744-0_T_R_1509285590	GAAAAAGGACATTGCCTG TATAAGGTAACCTGCTCTCT TCAGTTTGACCCAGTTTTTC TGGT[A/G]TGGGAAGACTG AGTCAGCATAATTTCTTTT ATTCAGTACAGAAAACAG ATAAGAATTAT
ARS-USMARC-Parent-DQ888312-rs29015945	Discovery	rs29015945	ss38332442	A/G	A/G	19	36437188	UMD3.1	ARS-USMARC-Parent-DQ888312-rs29015945-0_B_R_1511685970	AGGTTTAAAGGGAATTTTG CACCTGTCTCTGGATCACA GAAGAGGCTGAGGGGTGTG TGCC[A/G]TAGAGAATTGG CCGTGAGGCCTTTCTCAG AATCCCTGTACAGTTATT CAAATACTCCTT
Hapmap39390-BTA-22146	Discovery	rs41630136	ss61528095	T/G	A/C	19	4509536	UMD3.1	Hapmap39390-BTA-22146-0_T_R_1511627958	GAAGGATTCAGAGAGAG TTTTTAAAGGCAAAATTTGT AGGGAGTGTACAGAGTG TGTC[A/C]TCTCTCTAGT TTGTCGGTCCCGGGGTAA CAGGGTGGTGTCTCCAGGA ATCTCAGTCATCT
ARS-BFGL-NGS-19437	Discovery	rs110023442	ss86302854	T/C	A/G	21	47400719	UMD3.1	ARS-BFGL-NGS-19437-0_T_R_1511645885	TTTGGATGCACAAACTGAA TGGTGACATGGCACATCT AACCTTTCAGAAGATGATG GCAA[A/G]GGCCAGAGCA GAGCCCCAGAAATGAGAT GAAAGGGAAGGAACAT CTCTGTGGCTGTAA

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence	
Hapmap35472-SCAFFOLD35342_21388	Discovery	rs29017723	ss117973024	T/C	A/G	21	66107076	UMD3.1	Hapmap35472-SCAFFOLD35342_21388-0_B_F_1511627671	TGGGTGGGGTTTTGCTGT TGTTGCCGTTGGGGTTGC GTGCTTCCTGCTTTTGCTC TGCGC[A/G]CTGACTCTGC CTGGGACTGATGCTGGCA GACAGTCTGATGTGAGAA TTCAGTGCCTCATT	
ARS-BFGL-NGS-35219	Discovery	rs108960855	ss86324609	T/C	A/G	4	106885171	UMD3.1	ARS-BFGL-NGS-35219-0_T_R_1511675805	TGCCATGGAGAAGAGCAC TACAGAACGTGAGTTTAG GCAATGTAAGGCCACTAG AAATG[A/G]CJCAAGTCATT CTAACAGGGGACAGAGGC TCTTACTCTCTACCTGAG CAGATGGTGGCC	
ARS-USMARC-Parent-DQ485413-no-rs	Discovery	rs41590225	ss140469302	T/C	A/G	4	94176209	UMD3.1	ARS-USMARC-Parent-DQ485413-no-rs-0_B_F_1511686038	GCTAAGGGACAAGCTTGC CAAAGGYGAGAGAGAGAC AAACCTCCAGACRAGACT ACAAGT[A/G]GGAACCTG GAGGTTTCCCTAGCACAG CCCAGGTTTCTCAGGTTCT GGCTCACTGGTGTG GTCTGGAACAAAATAAATA AGGACATTCATTTCTCCTA ATTTATATTGATGTGGATG TTCT[A/G]TTAATTTGAAATG ATTTGTTAATTACCAAAG CTCTTAAACCCCTTTACTA AAAAAATCA	
BTA-82216-no-rs	Discovery	rs41590598	ss61492850	A/G	A/G	4	52308430	UMD3.1	BTA-82216-no-rs-0_T_F_1511543206	CATTTTCATTCTCCAAAAGA AGCAACCAGGCAGAGAGT CGATGATGCATACAAGCA GCTCA[A/G]ATTTAATCCTC AGGGGATCTCAGTTATTT TAGCTGATACTTCACCTTC TTTTGTCAGTG	
BTB-01902057	Discovery	rs43013883	ss64918503	T/C	A/G	4	6604523	UMD3.1	BTB-01902057-0_T_R_1511552598	CAATGAAACTTCAAACAA ATCTACTTCAAGTGCCTCAT GTAAGTGTGGGTCTGGT GTAG[A/G]GTTGTCAGATA AAATACAGGATGTCCAGTT ATATTTGAATTTAAGTAAA ACAATGAATA GTTAAAATGATCATATGAT TTATCATCAATATTGAGAT ACCTTTGAGAGTAAAATGG GGC[A/G]CTATTAATACTTA AGCCAAAGTAACAAGTATAA TTGGGGTGAAGTGGGAAA ACTGGGACCT	
ARS-USMARC-Parent-AY849380-no-rs	Discovery	rs41255758	ss49846084	A/G	A/G	6	90562665	UMD3.1	ARS-USMARC-Parent-AY849380-no-rs-0_T_F_1511686037	TATTCACACATGAAGCAAA GAAGACTGGGATCTGAGA TCTGAACAAAATGCCCTCT GGCC[A/G]JTAAGCTTCAC CTTTTATGAGCTGGAAGG AAAAATGACTTTTCAACCT TTACAAATTGA AACTCAAGCCCAGAGAGT CCAGAAGCTTTCATAGTTAG AAAAATCTCTGTAGATG AGAA[A/G]JGGCCACCATTT GCCATAGTTGTGCCAGAT CTATTTCTGAAATTAACCT TTGTTTTCTAG	
Hapmap50460-BTA-75791	Discovery	rs41595940	ss61491244	T/C	A/G	6	8478503	UMD3.1	Hapmap50460-BTA-75791-0_B_F_1509303979	GTTAATCAACTATATKTGT ACATATATAGAGAGGCTC CCTCKGAGAGCTCCCTTM CACC[A/G]JCGCTCCCTATT CTTTTGTTTTTAAGTGAATA ATAAGGCTCTGTCTCTACT TTAGAAACTT ACTAATTTCAACTGTTG TGTCTCAAGGAACAGGGA GGCCTCAGGCAAAGGGCT GGTTG[A/G]JTAAGCAGTC AGAACATACACATATTTAT CAATTGAGTTTGTCTGTCTT ACTTCTCTAAG	
ARS-BFGL-NGS-26056	Discovery	rs110616633	ss86285011	A/G	A/G	9	3651455	UMD3.1	ARS-BFGL-NGS-26056-0_T_F_1544346887	TAAAAGGAAGTTGGCATAA ATTTGGTTGAGCCTGTCTG CTGTACCTGCTACAGAATG CCC[A/G]JTTGGCTACTTAA CATCCATACCTTGCCCTTCT TTCCATTCTTAAACCTCCA GACCAGGAC	
ARS-BFGL-NGS-3465	Discovery	rs109170761	ss86314662	A/G	A/G	9	87606681	UMD3.1	ARS-BFGL-NGS-3465-0_B_R_1511665702	ARS-USMARC-Parent-DQ846689-rs29011985-0_B_R_1511686290	TTAGAAACTT ACTAATTTCAACTGTTG TGTCTCAAGGAACAGGGA GGCCTCAGGCAAAGGGCT GGTTG[A/G]JTAAGCAGTC AGAACATACACATATTTAT CAATTGAGTTTGTCTGTCTT ACTTCTCTAAG
ARS-USMARC-Parent-DQ846689-rs29011985	Discovery	rs29011985	ss38323070	A/G	A/G	9	45729853	UMD3.1	ARS-USMARC-Parent-DQ846689-rs29011985-0_B_R_1511686290	TTAGAAACTT ACTAATTTCAACTGTTG TGTCTCAAGGAACAGGGA GGCCTCAGGCAAAGGGCT GGTTG[A/G]JTAAGCAGTC AGAACATACACATATTTAT CAATTGAGTTTGTCTGTCTT ACTTCTCTAAG	
ARS-BFGL-NGS-35455	Discovery	rs110493467	ss86298634	A/G	A/G	10	10795992	UMD3.1	ARS-BFGL-NGS-35455-0_B_R_1511674364	TTAGAAACTT ACTAATTTCAACTGTTG TGTCTCAAGGAACAGGGA GGCCTCAGGCAAAGGGCT GGTTG[A/G]JTAAGCAGTC AGAACATACACATATTTAT CAATTGAGTTTGTCTGTCTT ACTTCTCTAAG	
Hapmap25493-BTA-109827	Discovery	rs43711263	ss61498362	T/C	A/G	10	4383927	UMD3.1	Hapmap25493-BTA-109827-0_B_F_1511587427	TTAGAAACTT ACTAATTTCAACTGTTG TGTCTCAAGGAACAGGGA GGCCTCAGGCAAAGGGCT GGTTG[A/G]JTAAGCAGTC AGAACATACACATATTTAT CAATTGAGTTTGTCTGTCTT ACTTCTCTAAG	

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-USMARC-Parent-DQ832700-rs29012872	Discovery	rs29012872	ss38323971	A/C	A/C	12	80629629	UMD3.1	ARS-USMARC-Parent-DQ832700-rs29012872-0_B_R_1511686106	CCTTCAAAGTCCGTTTTYCCACAGCCCTCCAGGCCAACCCACCCAYTTGATKGCT[A/C]TTTCTGTAGCTTCTAATCCCTTAAGCACCTTACAGATGGACTCGCTTGCACTTTTAAT
BTA-23867-no-rs	Discovery	rs41630989	ss61528978	A/G	A/G	12	50865733	UMD3.1	BTA-23867-no-rs-0_T_F_1511622594	AGGACTGTGCTATGTGTCTAAGAAGTGTGACAGTTGACCCAGGGCCTAAGGGGTTTTATGTT[A/G]TAATTGGACGAGAAAAGACACAAAGGAAAAACATTAATAATTAAGACAGCGAATAGTATAATTAAGAGTTTAAAAAATCTGGACAAGATTTA
Hapmap48641-BTA-119400	Discovery	rs41617704	ss61522219	T/C	A/G	12	10996119	UMD3.1	Hapmap48641-BTA-119400-0_T_R_1511577776	CTGTACCAAAAGAACCTTCC[A/G]AATGCACTCTCACAATCTCTTGATTGATTCTTGAGATAAAACATTACC
ARS-BFGL-NGS-103346	Discovery	rs110365259	ss86334026	A/G	A/G	14	68578968	UMD3.1	ARS-BFGL-NGS-103346-0_B_R_1511670578	ACACAGGCAGGGTATGACTAGAAAAATGGCGGTATACCGTGTGTGTATGTGTGTGTTTGA[A/G]GGCCATCGCTCTCACAATCATCCTGTACATGATAGAATCACAGGAGTTAGTAGTGAAGTGGAGGAGGCAGGGCAGGGTATGTGGTGCCTTAGATGGAGAAAGGCTGCTA
ARS-BFGL-NGS-12610	Discovery	rs108991969	ss86325725	T/C	A/G	15	27822630	UMD3.1	ARS-BFGL-NGS-12610-0_B_F_1544345676	AAGGGCC[A/G]TTTTACCTCTGGTAGGTAGTGGGGAGCAGGTAGTAAGAACTCTGTGAGAGGACTTCCCTCCTTATACATAAAGTTCAATTTTTTTATATGGTATAAAA
BTB-01912619	Discovery	rs43020250	ss64929001	A/G	A/G	15	20712027	UMD3.1	BTB-01912619-0_B_R_1511552693	TGCCCTTAAAGATCTGGCTCA[A/G]TGCTTCTTATCAA
Hapmap32097-BTA-150519	Discovery	rs109737932	ss117971819	A/G	A/G	15	56302387	UMD3.1	Hapmap32097-BTA-150519-0_B_R_1509306355	CCTCATTTTTTCACTTCCCA
ARS-USMARC-Parent-DQ846695-no-rs	Discovery	rs41825023	ss117972104	T/C	A/G	16	80747557	UMD3.1	ARS-USMARC-Parent-DQ846695-no-rs-0_B_F_1544362788	AGAAACAGGTGAGCAGAAACACTATCTAGAGATTTAA
BTB-00689316	Discovery	rs41853796	ss62371709	T/C	A/G	17	71925055	UMD3.1	BTB-00689316-0_B_F_1544349116	CCATGAAGTGATACGACCTTAC[A/G]TAAATCCACTA
BTB-01715543	Discovery	rs42825187	ss64733230	A/G	A/G	17	45185286	UMD3.1	BTB-01715543-0_T_F_1511528916	ATGACATATCCATTAGGAACTGATAGTCTTTGAAAATCAGTTTTCTGGTCAGCRCTGTG[A/G]TAGCACATAGCAGAAAGCCCATGGGTCTGTTTGATTTGGATTACTAAGAACAAGCA
ARS-BFGL-NGS-37708	Discovery	rs41885368	ss86298769	A/G	A/G	18	49928003	UMD3.1	ARS-BFGL-NGS-37708-0_T_F_1511681943	CGCCACCGCCACCTCTTCCTGCCCCTGGCGCGTGTCTGGCTCTCATACTCTGGGACGG[A/G]GGCTTCATCAACCGCACATCGTCGCTGCCTTCTCCACCCTAGGGAGAACCCAGTGTGTTGACTGGTCCCTGGGGACAA
Hapmap47949-BTA-43407	Discovery	rs41581677	ss61482794	A/G	A/G	18	44524702	UMD3.1	Hapmap47949-BTA-43407-1_T_F_2022483083	GATAAAAAGGACACACAAA

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-USMARC-Parent-DQ990835-rs29012811	Discovery	rs29012811	ss38323909	G/C	C/G	20	36570529	UMD3.1	ARS-USMARC-Parent-DQ990835-rs29012811-0_B_F_1511686376	AAGCASRCCAATGACTCCTTGCCCCATCACATAAAGTCATTCTTCCCAGTGCCAGGCT[C/G]CTTCTGAAAGAGCTAGAGCCCTGCCAGTTACAGTAGCTGGTATAAAAAGCTAATCTTATAA
BTB-00041743	Discovery	rs43252624	ss65165964	A/G	A/G	20	46735404	UMD3.1	BTB-00041743-0_T_F_1511575806	CATTGTTTCAAATATTATGTGGGTATGTTGGGATCTTGTGGGATGTTGGGATCTCAGTAGATT[A/G]AAATAATAGCCC
BTB-01565998	Discovery	rs42680109	ss64530672	A/G	A/G	20	37915840	UMD3.1	BTB-01565998-0_T_F_1511532864	TAGAACATTGTCAGGATGATGAAAAAGTCTTTTTTTTTTTTAAACACA
Hapmap32669-BTA-50759	Discovery	rs41606327	ss61502418	A/G	A/G	20	50999239	UMD3.1	Hapmap32669-BTA-50759-0_T_F_1544361425	CTTGGCACAGAGTTAGAGCTCATGACATGTCAATTGTGGGAAATGAGACAGGGAAGGAC[A/G]AGAGGGACTGGAACAGTCTCCTCAAAGGATGGTCTGGGCTGGAGCGTTGTCCTCCAAAC
Hapmap40826-BTA-87264	Discovery	rs41594336	ss61494128	A/G	A/G	20	496304	UMD3.1	Hapmap40826-BTA-87264-v2-1_B_R_1924255188	TTAGTATTATATTGTAAACCTATCAGAACTTCTATAGAACACTCAGAACTCCACAA
ARS-BFGL-NGS-119059	Discovery	rs110019581	ss86338680	A/G	A/G	22	58748602	UMD3.1	ARS-BFGL-NGS-119059-0_B_R_1511662796	TGT[A/G]CATTAGAGACTTAGTAACATTATGAATTAATACATCATCTCTCTCCAATCCTGCATGAA
ARS-BFGL-NGS-31568	Discovery	rs109579577	ss86316172	A/G	A/G	23	51795496	UMD3.1	ARS-BFGL-NGS-31568-0_T_F_1511665627	CCACTGTATATCATAGAAAATCATTATAATAATAAATAAAATAGTCTCCCACCTTGTA
Hapmap23842-BTA-56935	Discovery	rs41600226	ss61502810	T/G	A/C	23	47219946	UMD3.1	Hapmap23842-BTA-56935-0_B_F_1511565757	AA[A/G]AGTCCCAGTTGCTCCCCAGGGGAGTAACTAAACGCCTTTGATTGAAGGGACCGTTGA
ARS-BFGL-NGS-2592	Discovery	rs109874767	ss86335484	T/C	A/G	24	12775555	UMD3.1	ARS-BFGL-NGS-2592-0_B_F_1511660374	GCACGGGCCAGGCCCTGCGCCAGGAGCCTTGAGTGGCCTGTCTCGCAGGACTTACTAA[A/G]TCAAGCCCTGCCTTAACCCAAAGTAAACCAAGACCCAGAGGTGACTTGCTTGAGCCAC
ARS-BFGL-NGS-85334	Discovery	rs109014300	ss86315535	A/G	A/G	24	54964769	UMD3.1	ARS-BFGL-NGS-85334-0_T_F_1511692375	AAAGTTTACCTATTCCTTCCAAACCTCAGCACCTTCATTACCCCTGACGCGTG
ARS-BFGL-NGS-16739	Discovery	rs109106222	ss86304574	T/C	A/G	25	20723432	UMD3.1	ARS-BFGL-NGS-16739-0_T_R_1511640115	GGAC[A/G]TGCCCCGTGCTGGCCTGGCGACGGTCTGTCCC[G]GAGGAGTCTGTCCCAGAGTTTGGAGTGAAGCTGGGACCCCAAGAGTTCTAAGCAGTGAG
ARS-USMARC-Parent-AY942198-rs29003010	Discovery	rs29003010	ss38340199	T/C	A/G	25	40851475	UMD3.1	ARS-USMARC-Parent-AY942198-rs29003010-0_B_F_1511686256	TCAATCCTTTTGCCAAAAATGCCTCCTCATGTCACTTTCTTTCCAGACAAATACCGA[A/G]GAGGGGTGAAGGGCCCTGTTCTGTGCGT



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-BFGL-NGS-19741	Discovery	rs109629400	ss86316456	A/G	A/G	1	80548510	UMD3.1	ARS-BFGL-NGS-19741-v2-1_B_R_1924247358	AAACAAGAAAACCCCCTG CCCAACGTGGAGGAGGAG TTGATGATGGAAGTTCCGAT GTCT[A/G]TTCCAAAATGA GGAAGAAGTAGGCCTTTC CCCCTCTCCACTTTTCCTT TGATTATAAAAC
ARS-BFGL-NGS-32083	Discovery	rs42356323	ss86307480	T/C	A/G	1	109099488	UMD3.1	ARS-BFGL-NGS-32083-0_T_R_1511666321	TGAAGTAGACCAGAATTCC AGGCAAATGGACGGAGCA GTTAGGACCAGCATGAAA GAGAA[A/G]CTTGCCCCGC AGGCCTGTGTGTTTTGAG AGAAGACTCTGAATCCCAT CCCTCGAATTCCCT CATACCTGAAAAGGGATT AGGGATTATTCCTGGTTTG CTGAAGGCCACAGAGATG
ARS-BFGL-NGS-40229	Discovery	rs109327270	ss86288046	A/G	A/G	1	62184184	UMD3.1	ARS-BFGL-NGS-40229-0_T_F_1511685113	TTCC[A/G]TGATACACTCAT ACATTTGCATTTGGAAAAT AACATGATTATGACCGAG GTCCTTGACACA TGTTCTGAATTTTGAAGACA TCAGACACAGCTTTCTCCT TGAGGATGAGGGCCAGAG CTGC[A/G]TGACATAAAAA CTCCTTGGCTGTGTCTTTC CGGTCGGGCAACAGTTCT TTGCGGTGTTGA CAGTACAACACTAGAGCATG AGACTCAAGAGGAGGAAG GCAGGAGACACAGAGATC CAGTGA[A/G]CGGGCCCTC TGTGATGAGTGGCTGCAG AATTTTTTCTGGCATGGAA ATCCATTTGGGCCT TTAAAAGTTAGATAAAAA GGATCAGGAATGTGAGTC ATAGATTTAGGCTGGTTC ACCA[A/G]TTCACTGCTTG GTTTGAGTCAATTTTCACAT AATTAACTTTTTGGAAAAA TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
ARS-BFGL-NGS-4047	Discovery	rs110710269	ss86289851	T/C	A/G	1	84614199	UMD3.1	ARS-BFGL-NGS-4047-0_B_F_1511689272	CGGTCGGGCAACAGTTCT TTGCGGTGTTGA CAGTACAACACTAGAGCATG AGACTCAAGAGGAGGAAG GCAGGAGACACAGAGATC CAGTGA[A/G]CGGGCCCTC TGTGATGAGTGGCTGCAG AATTTTTTCTGGCATGGAA ATCCATTTGGGCCT TTAAAAGTTAGATAAAAA GGATCAGGAATGTGAGTC ATAGATTTAGGCTGGTTC ACCA[A/G]TTCACTGCTTG GTTTGAGTCAATTTTCACAT AATTAACTTTTTGGAAAAA TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
ARS-BFGL-NGS-67754	Discovery	rs41583110	ss86297683	T/C	A/G	1	148816004	UMD3.1	ARS-BFGL-NGS-67754-0_B_F_1511656742	TTAAAAGTTAGATAAAAA GGATCAGGAATGTGAGTC ATAGATTTAGGCTGGTTC ACCA[A/G]TTCACTGCTTG GTTTGAGTCAATTTTCACAT AATTAACTTTTTGGAAAAA TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
ARS-BFGL-NGS-76111	Discovery	rs110775913	ss86306448	A/G	A/G	1	103219606	UMD3.1	ARS-BFGL-NGS-76111-0_T_F_1511672473	TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
BTA-122684-NORS	Discovery	rs41619822	ss61524374	A/G	A/G	1	139231307	UMD3.1	BTA-122684-no-rs-0_T_F_1511617076	TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
BTA-23353-NORS	Discovery	rs41628641	ss61528709	A/C	A/C	1	60787763	UMD3.1	BTA-23353-no-rs-0_B_R_1511616787	TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
BTA-35637-NORS	Discovery	rs41580510	ss61480774	T/C	A/G	1	5610335	UMD3.1	BTA-35637-no-rs-0_T_R_1511540926	TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
BTA-46150-NORS	Discovery	rs41639071	ss61540930	T/C	A/G	1	102792723	UMD3.1	BTA-46150-no-rs-0_B_F_1511533155	TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
BTA-49375-NORS	Discovery	rs41578204	ss61484351	T/C	A/G	1	121363361	UMD3.1	BTA-49375-no-rs-0_B_F_1511540531	TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA
BTB-00012128	Discovery	rs43223035	ss65136409	A/C	A/C	1	28599381	UMD3.1	BTB-00012128-0_T_F_1544347969	TAAGCTGGGAA GCTGAGTTCAGCTGAGAA AGGATACCAAGCAGCATC TTCTCTCTCTGATCTCCA TGAGA[A/G]AAGGGCCAC GCAGATGCCATCTGGTTC ATTAAGGTCACCACTGCTT CTTTCCCTCCCCC ATTATAGGCCTTTTCCATT GCTTTTGAAAAAAAAGT CTCTCTTTTTTTTTATGTTT TA[A/C]JAATAAAAATGCCTGT TTACAATTTAAAACAAAAA ATTGGGGGGAGCAATAAG ACTGGAACA GAGGAAGCTATCTCAAAG GGAGACCTGAAGCTTGAA TGCTACATTTCTCTTTG CAAAT[A/G]TTTCAGTTTCAG TTCAGTTTCAGTTGTGCCA ACTCTTTGGGACCCCATG GACTGCAGCACT TTTTAAAATATCAATAAAATA TCTAGTCATCAATAAAATA TGAAAGGCATAGAAAATTT CA[A/G]AGTGACATCAGTA AAATAATGGAATAGGAGGT TCTAGTCTCAACTCTCCA CAAAAATAC ATATTCTTAGAATACAAT AATGAATTAATAATATGAT AGAATTTACATGCATTTTTTA AAA[A/G]TCCCATTATTCATA TGACATAGAAAATGATCACA ATTAAGTTATTAAGTGGG AAATCCTGT CTTCAAAAAAAAATGATAA TAGATTGATTTATGCCACA CATTAATATCAGGAGTGCC ACA[A/C]JAAATTTGCACAAA GTTCTCATTTATAAAACTG GAGTTCTTTGTACTGCTTT ACATTA AAAA





SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
HAPMAP39712-BTA-109811	Discovery	rs110858680	ss61517016	T/G	A/C	1	101583260	UMD3.1	Hapmap39712-BTA-109811-0_B_F_1511627845	TAAATTAGGATACAATGTG AATAGCTTTATCTGTTT GCTACAGGGTTGTGACAG TTYA[A/C]GTTGTTACAAG ATCACTGGTGGGAAATGA TTCAGCATGGAATCCATG GCCAGACTCAGT
HAPMAP43297-BTA-57357	Discovery	rs41583126	ss117966440	T/C	A/G	1	152189521	UMD3.1	Hapmap43297-BTA-57357-0_T_R_1509273582	ACATGGCAACATCATTGAT TTCATGATTGTGACTGGTT ACTTGAGTATATTTGAGCA CCC[A/G]TTTTCTTTGAAT GGGAATCATAACTCTTATA GAGTTACGACTGAGGACA GGAGGAGAAG
HAPMAP44395-BTA-64864	Discovery	rs41648924	ss61551244	A/G	A/G	1	153919758	UMD3.1	Hapmap44395-BTA-64864-0_B_R_1509275729	TTCATTGGTGCAAACTTT GGGAGACTTTAAAAATGAA GATTAATGTTAAAAATGGTA AGA[A/G]GAAAGGAAGAAG AAAACCTTAAAGACTGAAT GAACAAACAAGCTTAGTAG AAATAGAAA
HAPMAP48717-BTA-31633	Discovery	rs41630790	ss61533227	A/G	A/G	1	59971879	UMD3.1	Hapmap48717-BTA-31633-0_T_F_1511577672	ATATGGAGGATATCTGTAA AGACCAGAAATGAGAGTG AGGT[A/G]GTGTGCTGAAAG TATGAAAAGAAGTTCAGTA TGATTGGAGCATGGGCTT CCCTTGTGGCTC
HAPMAP49061-BTA-122268	Discovery	rs41624979	ss61524032	A/G	A/G	1	63742577	UMD3.1	Hapmap49061-BTA-122268-0_B_R_1511601511	AACCCAGGAGCCAGCAGG CTGAGCACCAACAGTGGA TCTGGAATCACTGGGTTTG GAGAC[A/G]TCTTGGTAAA CAGTGTATTCTGTGACTTT TTTAATACAGACCAGCTAC AGCATGTGGTAA
HAPMAP50048-BTA-59263	Discovery	rs41586446	ss61486868	A/G	A/G	1	27465349	UMD3.1	Hapmap50048-BTA-59263-0_T_F_1509284828	TAAATCTTTGATAATAAAA GAACAAACCATCAAAAATGA CAGGGATGTTTCTGCATTA AAA[A/G]ATGTGATATCCCT TAGTGGTTCAGACAGTAAA GAATCTGCATGCAATGCG GCAGACCCAG
HAPMAP52559-RS29015773	Discovery	rs29015773	ss38332264	T/G	A/C	1	8998063	UMD3.1	Hapmap52559-RS29015773-0_T_R_1511617980	TTCTCACTTGAAAAGAATT TTGTGAGTCTCATTGAGAA AGTCACGTTCCAAAAGCAA ATG[A/C]GAATGCAGATTTT ATCTTAAATTTGGTTAAG TAGGAATGAAAGTTAGAAA CAGGAGTTA
HAPMAP57299-SS46527085	Discovery	rs41255628	ss46527085	T/C	A/G	1	145059132	UMD3.1	Hapmap57299-SS46527085-0_B_F_1511542773	GTCCGTCCTGGGACTTCC CCAACCCCTATCGTTTCCC CTGCATCTCGGGGCCAG TGTGC[A/G]GTCTGACTG ACCCACACCAAATAGCATT GAGCTGTAACCTTTTTTT ATTATTGGATTT
ARS-BFGL-BAC-29664	Discovery	rs110341860	ss105257401	T/C	A/G	2	30635269	UMD3.1	ARS-BFGL-BAC-29664-0_B_F_1544343794	TTTGTGTAGTTATTCTTAA CTCTTTGTAGCATGCTTTA ACTCAAGTTGTAAGCAAGT TTC[A/G]TATACCAATTAGG CTTTGTGCCAGCTAAGTTC AACTGAAACCAGACCTTGA ATCCCTAAA
ARS-BFGL-BAC-30348	Discovery	rs110419748	ss105258160	A/G	A/G	2	22151093	UMD3.1	ARS-BFGL-BAC-30348-0_T_F_1511663383	AATAATCCAGGGTTTCCCA GTTACGAGAACCTTGCTTA TAAAAATGCCTTAGGACCT CAT[A/G]GTGGGCAACAA TCTGAGTTAACAACTACTT CTAAGTGCCTGAGAATTCA TGAGACTCAA
ARS-BFGL-BAC-32404	Discovery	rs109320395	ss105260440	T/C	A/G	2	13343685	UMD3.1	ARS-BFGL-BAC-32404-0_B_F_1511663544	TGCAGGTGCTTGGCAATA ACCCTCAGGACTAAAATTC CCTTTAACAGAGATCAATA CTTT[A/G]GTAAGTTGACAGA ATCCTGAACCTTGATTTTAT GCCACTGGCTTCTCCTTAC CCAGCACTGT
ARS-BFGL-NGS-116761	Discovery	rs110011842	ss86339699	T/C	A/G	2	136483623	UMD3.1	ARS-BFGL-NGS-116761-0_T_R_1511655013	GAAGCGGAGGACGTCTGC CTCCAGCCGCTGCTCCAG GTCCTGCAGGAACCTGAA AGGGCA[A/G]CCAGGGGT CAGGGCTGGGGCCAGGA GGAGATCCAGAGCCGG GAGCCAGCCAGCTGCAG

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-BFGL-NGS-118138	Discovery	rs42457132	ss86336697	A/G	A/G	2	67292723	UMD3.1	ARS-BFGL-NGS-118138-0_T_F_1511653365	ACTGAGCTTCGGTCTAACA CCATGTAGAAAATGGGAG ATTGACTCTATTGCTCAAT TCCA[A/G]ATTTTCATGGTAA AACAAATGAGCCCCAGTCT GAGCCCACTCATTCTTATT GATTGCAGAAAG GAGCCTGAGGGATGGTAC TCTGTGAGGATGATGTTAT CGTTCTCGCAGTAGCCCA GCAGC[A/G]TGATCACGTG CTTGTTCTTCGGGGCCTG CAGCATTGCGAGCCTGTG CAGGAAGTCGTCTC GGGCAGGTAGGTGCTGCC CCACCTGGATGGATGCCT CTTTTTGAGAGTCATTGTG GGGTC[A/G]GTAAGGCCT TCTGAAAAGCACATAATAT CAGAGCTTGGCATTITCCC TCTTCAGATTGA AGGGATCGCAGCATTAGG GAAGAAAAGCAACATTA CCTCCTTTGGCCAGGGG GCTTGG[A/G]GATCCTTCT GTGCCAGGGGTGCAGGAA GAGCTGGATACAAAACG GAACTCTGTTTCCAA ATTCAATGAAGACTTTAAA AATGGTCAGCAAAATGGT CAGCATCAAAAAAATCTT AAAA[A/G]ATAGTATCTCTT CCTGAAGGCCTTTTCTTAG CTCCCAGGATGGGGCTTC TCGGTGCCCCA CAGGAACCTAAGTATTTTT CTAAGAGTGATTAACATAG AGCAGAGGGCCGCTGTTTC ATCG[A/C]ATCAGTTCAGTT GCTCAGTTATGTCGACTC TTTGGGACCCCAAAACC ACAATATGCCA TCCCACCTCCCACCGCAA CCTGACTCCAGATGAAA ACCCATGCTTTGAACCTAG GCAGG[A/G]JAGCCCAAGC CAGGCCTGGTCATTACACA AGATGCCTGGAGTCACAG CTGTATGCTTTTTTCA AAGCCAGATGCATGGAAA GCAGGTTACGGAAGACA GTGATTCAAAACCTCACACA GACAC[A/G]TCTCCAAAGT CCTGAGGCCAGCTCCCTG GAGGAAATCCGGCAGCCT CTGCCATCGAAAGA TGACTGATGGCTGACTGA AAGACAAGGATTCCATCCA AGGAGCAGTGAGCTCAGG CCAGA[A/G]JTCACCAACCA CATACGGTCATGTGAATGT AATTTTAATGTAAAAATAAA TAAAAATAATT AGCTCTTGCTCTTCTCTCC TTCCCCAGCCTTTTCATT CCGGCCTTATCTCTTGCC CAAG[A/G]JCTCTCTCTT CCGGCAGCCTTCTCTTG GCTGGCTTTTGTCTGCCA GGTTCGGCTTCCC TCAGTTTATAACATTTGTG AAGACATATCAAGTAGGG CAGTTTCTGGCTGAATGT ACTC[A/G]JAGGCCCATAG TCTCAGCTGACCTTTGGTA GTTAATATTCAGTTGTAGA TTATCAGGGTC TGCTAGCTCATCCTGGG CTGGGACCCAGGCATCT GGAAGGCCAGACTCTAGA CTCAGA[A/C]JAGAGCATCC CGCCTGGGTGCTGTGGG GATTTGACTGGGAAACA CTAGCCCTCTCTGT
ARS-BFGL-NGS-118876	Discovery	rs109264826	ss86339741	T/C	A/G	2	66585600	UMD3.1	ARS-BFGL-NGS-118876-0_T_R_1511655277	
ARS-BFGL-NGS-15250	Discovery	rs109386162	ss86326904	A/G	A/G	2	89845085	UMD3.1	ARS-BFGL-NGS-15250-0_B_R_1511641324	
ARS-BFGL-NGS-15508	Discovery	rs110868968	ss86328344	A/G	A/G	2	119595498	UMD3.1	ARS-BFGL-NGS-15508-0_B_R_1511639918	
ARS-BFGL-NGS-33709	Discovery	rs109419732	ss86315136	A/G	A/G	2	130187033	UMD3.1	ARS-BFGL-NGS-33709-0_B_R_1511674856	
ARS-BFGL-NGS-35963	Discovery	rs110551793	ss86303585	A/C	A/C	2	105193025	UMD3.1	ARS-BFGL-NGS-35963-0_T_F_1511681193	
ARS-BFGL-NGS-40189	Discovery	rs109189655	ss86321720	A/G	A/G	2	89008935	UMD3.1	ARS-BFGL-NGS-40189-0_T_F_1511689293	
ARS-BFGL-NGS-57870	Discovery	rs110568121	ss86288122	A/G	A/G	2	37813654	UMD3.1	ARS-BFGL-NGS-57870-0_T_F_1544350841	
ARS-BFGL-NGS-60640	Discovery	rs109370370	ss86291691	T/C	A/G	2	3242217	UMD3.1	ARS-BFGL-NGS-60640-0_T_R_1511650779	
ARS-BFGL-NGS-67260	Discovery	rs109453608	ss86297852	A/G	A/G	2	135190642	UMD3.1	ARS-BFGL-NGS-67260-1_T_F_2128295783	
ARS-BFGL-NGS-72192	Discovery	rs109205936	ss86301441	T/C	A/G	2	65044427	UMD3.1	ARS-BFGL-NGS-72192-0_T_R_1511672013	
ARS-BFGL-NGS-89098	Discovery	rs109154008	ss86318772	T/G	A/C	2	13901492	UMD3.1	ARS-BFGL-NGS-89098-0_B_F_1511689922	

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
BTA-114831-NO-RS	Discovery	rs41574370	ss61473860	T/C	A/G	2	39709004	UMD3.1	BTA-114831-no-rs-0_T_R_1544353375	TTTCCCCAAATAAAAATC ACAGAGGGCCCCCTAAAC CAGATGCTGAAATATGTTT ACCT[A/G]TTGAAGCTCAG AATTGCTTTAGCAGGATC TGAAAACATCCACATGTC CCTTTACCTAT
BTA-19852-NO-RS	Discovery	rs41628437	ss61526969	A/G	A/G	2	42986890	UMD3.1	BTA-19852-no-rs-0_B_R_1511616743	ATATTATTGTCCTGAACTT CAAAACAACACATAGTTTT CCTAGATGAGGAAGACAA GACA[A/G]TTTTACCTCTTCT TTATGCAGAGGTCCCGCT AGCAAGGGAATGTTTAGTA AAGGGTTAAAT ATATCTTGATCATTCTTTG GGCCCCCTATAACATACTA GACATAATAGGTGGCAAC AAAT[A/G]TGCCCACTTA GAATAACGCTTTCGAAATA TTGAAAGTGTAGATTCTGA ACTCATATAC TAATTCTTGCTTTGTTTATA ATTTTATTCTCATCTAGAAT GTCCTTCTTCTTCTCTAT T[A/C]CTTTCCAACCCCTG CCCATTTTTAAAGTTTTCTG TTTAAACCTTTCATCTTGA AAAGTTCT
BTB-00079213	Discovery	rs43288464	ss65203384	A/G	A/G	2	8476975	UMD3.1	BTB-00079213-0_T_F_1511575540	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
BTB-00082871	Discovery	rs43293394	ss65207039	T/G	A/C	2	20699862	UMD3.1	BTB-00082871-0_B_F_1544353914	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
BTB-00089384	Discovery	rs43300334	ss65213533	T/C	A/G	2	35264900	UMD3.1	BTB-00089384-0_T_R_1511575544	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
BTB-00098773	Discovery	rs43304762	ss65222905	A/G	A/G	2	52497009	UMD3.1	BTB-00098773-0_T_F_1544354015	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
BTB-01753605	Discovery	rs42862169	ss64771163	T/C	A/G	2	55729126	UMD3.1	BTB-01753605-0_T_R_1511529124	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
HAPMAP33049-BTA-153946	Discovery	rs109475468	ss117966789	A/G	A/G	2	79320427	UMD3.1	Hapmap33049-BTA-153946-0_B_R_1544355884	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
HAPMAP35220-BES9_CONTIG365_495	Discovery	rs43710074	ss66538228	T/C	A/G	2	70895063	UMD3.1	Hapmap35220-BES9_Contig365_495-0_B_F_1509283901	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
HAPMAP35744-SCAFFOLD60587_8279	Discovery	rs29018369	ss117966872	A/C	A/C	2	111361143	UMD3.1	Hapmap35744-SCAFFOLD60587_8279-0_T_F_1509222362	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
HAPMAP42104-BTA-121232	Discovery	rs41619967	ss61523297	T/C	A/G	2	81159639	UMD3.1	Hapmap42104-BTA-121232-0_T_R_1509308138	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT
HAPMAP43869-BTA-49512	Discovery	rs41636478	ss61542755	T/C	A/G	2	120301651	UMD3.1	Hapmap43869-BTA-49512-0_B_F_1511566101	TTGTCGTTCATATAACAAA TATAGTTCTCAGTGAGGCA TAGTTATAAGCCAAGTTTT GAT[A/G]TTTTAAATATTACC TGGGGGAAGAACTTTTTG GTATAGCCTTTTTTTGTGC TCAAGAATAT ATTAACACTTGCCATCTT CATATAACATTGGGTCTTG TTGGTACAGTAGCAGTCAA GTA[A/G]GAATACTACTGTT ACGCCTGACCCCTCCTCC CCTCCCTGTCTTTGATCTG GGTGGGCTCA TTTCAGATTTTATAGAGTA TATTTTATGATAAGTTAGG TTATGATAGGCTCATTTCA CAG[A/G]GGGAAAAATTAC ATTCAGAAAAGTAAATTA CTTAACAACTGTCAAAGT TTGTCTTAGG AAATTGATAAAACAATAAT AATAATGTCTTGTGAGCTT AGAAACATAGTACAACGTA AAT[A/G]ATGGACATCAAC ACCACATTTATAAAGGAGA GCTAAAATTAATAATTCTT GGGTTTTGT GCACCCCTCCCTGGCTGC AGGGCGACACCACACTTC CATCAGGGATGCCTGGGT CCTGGA[A/G]AAAGATTCT TTGCAAGTTGAAGAGCAG AGCCTTTTAATTGCCATGT CCCCAGTGACATAA AACTAAGATACATTTTCCA AAAAGCAATTTGGCAGTTC GTGTGAAGAGTTCTGAAAT AAG[A/C]TTTTCTCCAGTT CTCCGGAAACAATTAATA TTTAACTCCAGTTGAAGT ACAAAGATA CAAGAAAGCAGCATCTGT CTCACACTCAAGCTGT GTGTTCTTCCCTCCCAAT CTTTG[A/G]ATGTTATTGTC AACTCCAGCTCCCAAGA CTCCTCCTCTAAGTAGTAT CACACCTGCTGC TTATTTTTAAACTTTTTAAA CTGAATAAATTTATCGTGT TCATAATTTTTGAAGATAG GT[A/G]TTAATACTTTGAAAT TGACGCCAGTGACATAGA TTTGTACAGAAAAGCCTTA TACTAGTTT

SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence	
HAPMAP44545-BTA-47658	Discovery	rs41637159	ss61541725	T/C	A/G	2	52339443	UMD3.1	Hapmap44545-BTA-47658-0_B_F_1509288953	TACAATTTATATTTTTTTAG AAAGGCTTTCCTGGAGGG AATTAACCTTTTACTCTTAT AA[A/G]TTTAATAGAAATGA TATATCACCTCTCTGTTAG ATTGATAATTTGTACAACA GTAGTTAA	
HAPMAP49925-BTA-24427	Discovery	rs41633771	ss61529263	A/G	A/G	2	86704498	UMD3.1	Hapmap49925-BTA-24427-0_T_F_1511602514	CCCTGAGTAACCTGGACAT CTGAAGGCTATCAGTGAA CCACACATTTTGTAGCTGG AAAGT[A/G]AGTCCCTTTATT GAAGAAGAACTCTGAGTGT GGCATCTCTGTTTGACATC TAACTTACACAC TAACAATAAATAAGAACAA CACTTTTTTCCACGTCTC	
HAPMAP51412-BTA-16926	Discovery	rs41621063	ss61525448	A/G	A/G	2	59690093	UMD3.1	Hapmap51412-BTA-16926-0_T_F_1511602922	AGGAGAAGAACACTTAAT GGAT[A/G]ACAGAGAAAGA TACATAATAAATAAATGC TTTGAAGTGGCAGTACTA AAAGTGAAGAA TAGTTCCTCCTTCTTTTC TCCTGCTAAACTACTATTAT AAGAAGTTTTAAATTTTGT TT[A/G]CATTGAAAAATCAC AGGCCTAAAAGAGACA CACATTTATATCAGACCAA AAATCTTTG	
HAPMAP51598-BTA-47943	Discovery	rs41638281	ss61541849	T/C	A/G	2	65700940	UMD3.1	Hapmap51598-BTA-47943-0_B_F_1509318833	TAATCCAATATCATCTCT ATATTTCCATGATGTTCTTT GCAATTTTTTGTGTTTCATT T[A/C]TGATTTTTATTAGTTG AGCTCTTTTTTTTTTTTTTT TTCTTATGAGGCTTGCCA AAGTTT AAGTGGCACTGTTTGTTAA CCGACTGACTGACCTGAG GGGCTTTGCAAGTTGATA GAACT[A/G]CATGTCTAAG CATCATTTATCCTGCTGCT ACTGCTGCTAAGTCACCTC AGTCGTGTCCGA AAAACAACCTGAGTCATGTC TTGACAATAAATGAGTGAG TGAATGAATGAGTAACAAA AAA[A/G]CACATACTCACT GTGTGAACTGTTCTTAAG CTTTTCGAGGGTTAAGTG GCTTTTGTGAA	
HAPMAP52627-RS29014567	Discovery	rs29014567	ss38326256	T/G	A/C	2	100273809	UMD3.1	Hapmap52627-RS29014567-0_T_R_1511601434	TGGTATATATACAATGGAA TATTACTCAGCCATTAATA AGAATGAGATAATACCATC TG[C/A/G]GCAACATGGTTA GACCTGGAGGTTATTCTTC TAAGGGAGGTAATTAGA GAAGGACCAAT TTAGGCCAAAACCCCAAC CCTATTAACACAGATGACCA TTGGTTGCAAGGTATCCCA ACT[A/G]GAGCCTTCTGCC TAGGGGAGAGCTGAAAGC CATGGATAGGGAGGCACA GGGCATACTGCA TCTACCTTCAGACCCAACC TGCACTGGAGTTTCTTGA TGAGGTTTCATGCAGTTAT CCC[A/G]TTTTGGTAATAAT AGAGGCAAATTTTAATA AAAGTAGAGGGAAAATATA GGCTTGCTT TAAAAAAGGGGGGGGTG CATCTTGAATACATTTTAA GGGAAGAGCAGGCCCTCAC TTGCC[A/C]CTTGCACTTT TTCCCATGCAAAAAGAG CTGCTACTTTCCTGATACC CCAGATGGTGCC GAAGCCCCCTGCACATTA GCAAAGTTCTGCCACCA AGCCTGAGGGGAAACAA GACTCA[A/G]GTGAGTCCA GCACTTCTACCTATGACCC AGTTCTTATTTAGTTTTT GTAATCAGGCCTC	
HAPMAP54320-RS29012920	Discovery	rs29012920	ss38324019	T/C	A/G	2	5037866	UMD3.1	Hapmap54320-RS29012920-0_T_R_1509313654	AGTGGTGTCCGA AAAACAACCTGAGTCATGTC TTGACAATAAATGAGTGAG TGAATGAATGAGTAACAAA AAA[A/G]CACATACTCACT GTGTGAACTGTTCTTAAG CTTTTCGAGGGTTAAGTG GCTTTTGTGAA	
HAPMAP54766-RS29012658	Discovery	rs29012658	ss38323754	T/C	A/G	2	14451633	UMD3.1	Hapmap54766-RS29012658-0_B_F_1509320651	TGGTATATATACAATGGAA TATTACTCAGCCATTAATA AGAATGAGATAATACCATC TG[C/A/G]GCAACATGGTTA GACCTGGAGGTTATTCTTC TAAGGGAGGTAATTAGA GAAGGACCAAT TTAGGCCAAAACCCCAAC CCTATTAACACAGATGACCA TTGGTTGCAAGGTATCCCA ACT[A/G]GAGCCTTCTGCC TAGGGGAGAGCTGAAAGC CATGGATAGGGAGGCACA GGGCATACTGCA TCTACCTTCAGACCCAACC TGCACTGGAGTTTCTTGA TGAGGTTTCATGCAGTTAT CCC[A/G]TTTTGGTAATAAT AGAGGCAAATTTTAATA AAAGTAGAGGGAAAATATA GGCTTGCTT TAAAAAAGGGGGGGGTG CATCTTGAATACATTTTAA GGGAAGAGCAGGCCCTCAC TTGCC[A/C]CTTGCACTTT TTCCCATGCAAAAAGAG CTGCTACTTTCCTGATACC CCAGATGGTGCC GAAGCCCCCTGCACATTA GCAAAGTTCTGCCACCA AGCCTGAGGGGAAACAA GACTCA[A/G]GTGAGTCCA GCACTTCTACCTATGACCC AGTTCTTATTTAGTTTTT GTAATCAGGCCTC	
HAPMAP58509-RS29024139	Discovery	rs29024139	ss38334232	T/C	A/G	2	37635484	UMD3.1	Hapmap58509-RS29024139-0_B_F_1509331449	TTAGGCCAAAACCCCAAC CCTATTAACACAGATGACCA TTGGTTGCAAGGTATCCCA ACT[A/G]GAGCCTTCTGCC TAGGGGAGAGCTGAAAGC CATGGATAGGGAGGCACA GGGCATACTGCA TCTACCTTCAGACCCAACC TGCACTGGAGTTTCTTGA TGAGGTTTCATGCAGTTAT CCC[A/G]TTTTGGTAATAAT AGAGGCAAATTTTAATA AAAGTAGAGGGAAAATATA GGCTTGCTT TAAAAAAGGGGGGGGTG CATCTTGAATACATTTTAA GGGAAGAGCAGGCCCTCAC TTGCC[A/C]CTTGCACTTT TTCCCATGCAAAAAGAG CTGCTACTTTCCTGATACC CCAGATGGTGCC GAAGCCCCCTGCACATTA GCAAAGTTCTGCCACCA AGCCTGAGGGGAAACAA GACTCA[A/G]GTGAGTCCA GCACTTCTACCTATGACCC AGTTCTTATTTAGTTTTT GTAATCAGGCCTC	
UA-IFASA-4619	Discovery	rs29014393	ss117963586	T/C	A/G	2	76309053	UMD3.1	UA-IFASA-4619-0_T_R_1511687463	UA-IFASA-4619-0_T_R_1511687463	UA-IFASA-4619-0_T_R_1511687463
UA-IFASA-8833	Discovery	rs41643750	ss117963637	T/C	A/G	2	116087072	UMD3.1	UA-IFASA-8833-0_T_R_1511694635	UA-IFASA-8833-0_T_R_1511694635	UA-IFASA-8833-0_T_R_1511694635
ARS-BFGL-NGS-103524	Discovery	rs110713161	ss86332467	T/G	A/C	3	85253155	UMD3.1	ARS-BFGL-NGS-103524-0_B_F_1511673760	ARS-BFGL-NGS-103524-0_B_F_1511673760	ARS-BFGL-NGS-103524-0_B_F_1511673760
ARS-BFGL-NGS-105811	Discovery	rs110161964	ss86306287	A/G	A/G	3	22706379	UMD3.1	ARS-BFGL-NGS-105811-0_B_R_1511679734	ARS-BFGL-NGS-105811-0_B_R_1511679734	ARS-BFGL-NGS-105811-0_B_R_1511679734





SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
INRA-638	Discovery	rs110438768	ss117962838	A/G	A/G	3	62004226	UMD3.1	INRA-638-0_B_R_1511657600	AAGACTTTCTCCTTGCATG TTAGCACTGGGGCACTCT TTCTGAAGGATATGGTTAC AGAA[A/G]CCTGAACCTGCT CCAGCCATTTTGTCTATCAT GAAAGAAGTGATCTGCA GATGCAGCTGGC
ARS-BFGL-NGS-103280	Discovery	rs109268659	ss86332959	T/C	A/G	5	84523411	UMD3.1	ARS-BFGL-NGS-103280-0_T_R_1511673681	GTCCATGGAGTTGTAAAG AGTTAAGTATTCAGTCTAG AGTAGTGGCCAGAGGAC TGACT[A/G]TGATGTTGGG AAAGCTGACTGACAGTGG AGGGGAGGAGCAGAATAA GAAATGGAGTGTC
ARS-BFGL-NGS-107085	Discovery	rs109223185	ss86289994	T/C	A/G	5	28660813	UMD3.1	ARS-BFGL-NGS-107085-0_B_F_1511677970	ATCATCTGAACGGAGGAT CACTGCACGGGTCTGCAG GCCTGGCCCGTTGGATA CCCTTG[A/G]CGTGGGCTG TCCGTCCAGTCCCACACT CCAAACGTTGGGAGTGTC AGTCTCCAAGAGGCT CCCAAGAACAACTGTGTGTC
ARS-BFGL-NGS-14632	Discovery	rs110117542	ss86329869	A/G	A/G	5	118501191	UMD3.1	ARS-BFGL-NGS-14632-0_T_F_1511640527	TTCCAGGAGCTGGACTTG TACCATCAGGTCCGGGGC TGCAA[A/G]AGGCCAGGG GGGCAGGGACACAACCTGC AGAAAGAGGTGCACCTGG AGACCAGGGAGAAAAG TGGGGCAGGAGCGGTT AGGAGATCTGTGAGTCAG AAGTATCTCACTTAGAATG
ARS-BFGL-NGS-21717	Discovery	rs109513912	ss86313314	T/C	A/G	5	117102295	UMD3.1	ARS-BFGL-NGS-21717-0_T_R_1511649969	TACGGA[A/G]GGCCCCCTG CCCATGACACCCAAACGGA TTGATGGATCCTGCCTCTT ACACCCAGTGATGG GGCAGGGAGGGCCATTTT CCTGTCTCAGCCTACAAG
ARS-BFGL-NGS-23432	Discovery	rs109724164	ss86277105	G/C	C/G	5	40112322	UMD3.1	ARS-BFGL-NGS-23432-0_T_R_1511658967	GACTGATGAGATGAATC TTTAGT[C/G]TGCTCTGTG GCAAAATTTCTTGGCCAAA GTGGAAAGCAAAGGCAAT TATCCAAGAATCT AGAGGGGAGAGCAGACCT CCTGGAGTGTCTGGAGAC
ARS-BFGL-NGS-23961	Discovery	rs110038808	ss86311819	A/G	A/G	5	25995476	UMD3.1	ARS-BFGL-NGS-23961-v2-1_B_R_1924247630	TCAGAAAAAGGGTACTGT GGCCCC[A/G]CAGCCCTTG ACATTGCTCGAGGACTCC TTGCTGATGACTTTGAGGA AAGGTCTAGCGTCC AGTCCAGCCCTTTAGCTG CCTGCTACCCGGACCCAC GTGTCTTCTCCGTGAAAAG
ARS-BFGL-NGS-25107	Discovery	rs109607671	ss86319576	A/G	A/G	5	119408760	UMD3.1	ARS-BFGL-NGS-25107-0_B_R_1544346228	GGCC[A/G]CCTTTCCATA ACAGAGTCCCTCCCGGAT GTCTCCTGGAGACATTCC CTGCAGCTCCCCTA CAGAATTGGCTCTGGGCG GAAGTTAAAAAAGAAGTCT
ARS-BFGL-NGS-30677	Discovery	rs110873570	ss86294546	A/G	A/G	5	43565856	UMD3.1	ARS-BFGL-NGS-30677-0_T_F_1511666719	CTCCACAAAATGTTGGCCA TTAT[A/G]CTATCTTCACAA GGGTCTGGAGTCTAAATC TTCTGTAGTTGAGGGTTGA GATTTAAGTGG GATGTCAAGCATTTGGAAT ATAATAGAACCAAATGGAG
ARS-BFGL-NGS-33745	Discovery	rs110258843	ss86297916	A/G	A/G	5	51064864	UMD3.1	ARS-BFGL-NGS-33745-0_T_F_1511675641	CAGGCCCCCTCCTGACA CTTA[A/G]GTCTGGAGGA GGCTCTCCACGTCTGGT TAGACATTTGTTGGCTCCT CCCCACAGGCCA CAGGAGGCCGTTTCAGAC CCTGAAAATAGGATCAGG GCCATTTGGCAGGGAAT
ARS-BFGL-NGS-39913	Discovery	rs109168591	ss86320410	A/C	A/C	5	85535871	UMD3.1	ARS-BFGL-NGS-39913-0_B_R_1511685024	CCCTAG[A/C]ACTGAGTAT TTGGAGTCTGTCTAGAAAA GGTCCAGTCAACTGCTT GCTCCAAGGAGGTC GGTGGCTTCGCCCTCACT CAGCTCCCTTTGCTGGATT
ARS-BFGL-NGS-44153	Discovery	rs109783698	ss86307990	T/C	A/G	5	97430973	UMD3.1	ARS-BFGL-NGS-44153-0_T_R_1511688905	GACAGGCCACAACTCAG AAGAA[A/G]AGAAAAGAGT GGAGGAGGACTCCCCTGG TGTCGGTCCAGTGTTA AGACTCCGAGCTC





SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
HAPMAP40581-BTA-73771	Discovery	rs109701457	ss61555894	A/G	A/G	5	67153683	UMD3.1	Hapmap40581-BTA-73771-0_T_F_1511629002	GGATTGCTGACTGAGACTGCAGCTAGGATTAACGGGAGAGAGTGCGGTGGTTGATTAAG[A/G]WTGTCTGCGTCAGTTGCTGGAAAGGAGAGTGGTGGTTGTACTTTTGTACATATTTTGCAA
HAPMAP44400-BTA-72792	Discovery	rs41587982	ss61490476	A/G	A/G	5	15696963	UMD3.1	Hapmap44400-BTA-72792-0_T_F_1509273674	ACTTGATCACTCATTTCATTAGTAACCATTTTCAGCACTGTAAAACTATCAAGAGTAGACA[A/G]JTTTTACTTTGAAATATTTAAGGTTGTATTTTTAGCATCTACCAACATATTTTGTGTTGAG
HAPMAP47185-BTA-114173	Discovery	rs41573130	ss61473714	T/C	A/G	5	99044605	UMD3.1	Hapmap47185-BTA-114173-0_B_F_1511577057	TTGCCCATAAATCAAGTTTTCACAGGCCATGGTGAATAATAATTTGCCAGAGAGCTCTC[A/G]JAAGTGAAGAAGCAACAAGGTGGCATAATTCATCAAGAAAGGAAAAAACTTGTTTATG
HAPMAP50837-BTA-98392	Discovery	rs41593990	ss61497060	T/C	A/G	5	46995137	UMD3.1	Hapmap50837-BTA-98392-0_B_F_1509318315	AAGTACAGAAAGGCAATATGATGAGCAACGGGAGAGAACGTTATTACTTTTGTATTC[A/G]TAACTACTTGTTCAGGGAGGATCCAGTGTCTCCAAATGCAGATCTTCTCAAAGGGCTT
HAPMAP51304-BTA-74559	Discovery	rs41591921	ss61490918	A/G	A/G	5	93718582	UMD3.1	Hapmap51304-BTA-74559-0_T_F_1511602314	CAAATATGCCATAAGGAGACTTGGACAATAGCTTACATTTTAAATTTGTAGTAAITGTG[A/G]GTGCTACTAACCTGACAATCTCAAATATATTTATAAACTACACACAAAAATGAAATGA
HAPMAP59828-RS29027014	Discovery	rs29027014	ss38329400	T/C	A/G	5	66830677	UMD3.1	Hapmap59828-rs29027014-0_T_R_1509289834	ATAGAAGTTAAGTAAATAATGTTTTACACTCAACCCACTCCTATATTCTGTGGCTAGTAT[A/G]GTTTTAACTTTGATTTGGGAATCTCTATAAGATCTAGTTGTCTACCAGAACTACTCTCT
HAPMAP60420-RS29010136	Discovery	rs29010136	ss38324636	A/C	A/C	5	112045991	UMD3.1	Hapmap60420-rs29010136-0_B_R_1511547925	CTTTGATGTATAACTCATTTTATTTGCTCCTGAATTACAGAGTTTTGGTGTGCCATAAGG[A/C]TGGGCTCTGCA
ARS-BFGL-NGS-102603	Discovery	rs110351681	ss86331087	T/G	A/C	7	67495781	UMD3.1	ARS-BFGL-NGS-102603-0_B_F_1544343612	GGAACCTTAGATCCAAAATGGCAGCTGAGCTTCTGAAACTCACCAGAGCCGGCTGGAGTGGGTGAGGAGATGGAGCCGACAAAGTGGCCAGGGGATCCTGTTCCTCCAG[A/C]JTTCATCC
ARS-BFGL-NGS-109750	Discovery	rs110303958	ss86336681	A/G	A/G	7	45412030	UMD3.1	ARS-BFGL-NGS-109750-0_B_R_1511644208	AATGGTCAATCTAAGTCTGACTCTTGACTCAACCATTGGCATGCACTCCATACTTGTGTTTTATTTTATTTGGCGGCGGAGGGACTGGAGGGCACACGGTGGCC[A/G]JCGTTACCGCCGTGCTGCTCCCGGAGGATTA
ARS-BFGL-NGS-110438	Discovery	rs109370616	ss86335506	T/C	A/G	7	27258897	UMD3.1	ARS-BFGL-NGS-110438-0_B_F_1511653326	TAACCTTTCTCCTCCCATGTCAGTATGCTTGGAGTATTTCCCTCCTCCAAATAATCATCCGCTCTGGAA[A/G]JGGGCCACAAGAGCCATGTGCTGAGAGTTGAATAAGCTGTGAGATGTGTACAGTCAACGT
ARS-BFGL-NGS-117421	Discovery	rs43494965	ss86341439	A/G	A/G	7	4286714	UMD3.1	ARS-BFGL-NGS-117421-0_B_R_1511653258	ACCCCTCGCACTCCTGCGCCTGCTTGGAGCGGAGGAGGGAGAGCTGTCCCTGGCAGG[A/G]JTGCCCGGGAAAGGTTGTGGCCAGAGCACATTCTGGTTTGGACAAAGTCTGGCTTTA
ARS-BFGL-NGS-11889	Discovery	rs111029549	ss86320413	A/C	A/C	7	43292715	UMD3.1	ARS-BFGL-NGS-11889-0_T_F_1511678427	ATGGTGGTGGGAATGTATTGGAGCTGCCATGTTCAATATATGCGGCCCTGTGCTGAC[A/C]GATCCCCTACCAGGACAAGATGGTATCAGCCTTACACCATCTCACTCCATGCTGA



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
BTB-01920914	Discovery	rs43026255	ss64937240	A/G	A/G	7	86936090	UMD3.1	BTB-01920914-0_B_R_1544360918	ATGTTTGAIAAAAAAAAAATTGCC TTCTACTCTACAAAGATA TGCTGTGTATCTGATATT CTT[A/G]TTTGAGATGTTCA TTTGGACTTAGGCACTGA GGACTCTGGATGAAATAAT ATTTGAAATA
HAPMAP30362-BTA-79378	Discovery	rs41605127	ss61504352	A/G	A/G	7	59353807	UMD3.1	Hapmap30362-BTA-79378-0_B_R_1544359594	TAGAGAAAGTTCTCCCAGA GCCTCCAGCCTGTGCA GTCATCCAGACTGGTTGC TTACT[A/G]TAGGCATGCA CGAATGTCATCTGGGATG TTCTCCACTGTACTTAG GATTTCCCTTAGTT
HAPMAP33032-BTA-148803	Discovery	rs42277425	ss117969067	A/G	A/G	7	68830299	UMD3.1	Hapmap33032-BTA-148803-0_T_F_1511592802	ATTTATTCTGCTACAGATA GTAACTATAAACTCTGGAC AAAATGTAAAAACACAACCTG CTT[A/G]AAGAATCTAATAA ACAAAAGCAGGAGAAATCC AGAGAGTGATAGAAATTTG GGAAATGGGA GCTCAGCTGCAGTTTACCT CTATAGCCTCCTTGAGCC CCACTTTTGAIAAATGATTTC CTGT[A/G]ATGCAAGCCTT TTATTCTGTGCTCAGTTT TCCTTACTAATGCTCGTCA TGATTTGTAGT
HAPMAP50109-BTA-79983	Discovery	rs41656547	ss61559313	T/C	A/G	7	81964652	UMD3.1	Hapmap50109-BTA-79983-0_T_R_1511601812	GCAGAATTGAATAATCTGC AAGGCAGCAAGAATGAGA GATGGTGTTTCAITTCACAA CACC[A/G]JAGAAAGTACTG AAATGAGGAAAAATGTCTGA GAAGTGAGAAACTAGGAT TAGCCAACGAG
HAPMAP50113-BTA-80661	Discovery	rs41597420	ss61492473	A/G	A/G	7	8860921	UMD3.1	Hapmap50113-BTA-80661-0_B_R_1509285709	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC
UA-IFASA-4904	Discovery	rs29015019	ss117963926	T/C	A/G	7	35153271	UMD3.1	UA-IFASA-4904-0_T_R_1511687421	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC
ARS-BFGL-NGS-106379	Discovery	rs42390350	ss86307964	T/C	A/G	8	113159018	UMD3.1	ARS-BFGL-NGS-106379-0_B_F_1511679852	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC
ARS-BFGL-NGS-108099	Discovery	rs109279813	ss86317401	T/C	A/G	8	23116314	UMD3.1	ARS-BFGL-NGS-108099-0_T_R_1511672675	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC
ARS-BFGL-NGS-108549	Discovery	rs110503484	ss86306174	T/C	A/G	8	82311830	UMD3.1	ARS-BFGL-NGS-108549-0_T_R_1544343919	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC
ARS-BFGL-NGS-110811	Discovery	rs110481266	ss86339546	T/C	A/G	8	69343704	UMD3.1	ARS-BFGL-NGS-110811-0_T_R_1511637675	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC
ARS-BFGL-NGS-111788	Discovery	rs43578821	ss86340085	G/C	C/G	8	101231366	UMD3.1	ARS-BFGL-NGS-111788-0_B_F_1511638894	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC
ARS-BFGL-NGS-117122	Discovery	rs109443931	ss86340374	A/G	A/G	8	20608192	UMD3.1	ARS-BFGL-NGS-117122-0_T_F_1511654401	TTTGTTAAACTAACCAAAA CTATCACCTTGTCACTGAC AAACAAATTGCCAGTGAG GAGC[A/G]TGGGCAAGTCT TCATTAAGGATTACACGAA AGGGAAGCAGGTGATACC ACATGGTAGCTA GGCGTCACTTTAGGCACG AGGCAGCCAAGCCCCGA GGGGAGGTCCTGGCTGG GCCAGAC[A/G]GCGTCAAGC GGCAAGTCTGTGTGAGAA TTCGGATTGCCTTCTTCCC ACCCCGGGGCTCCTC CCCCAAGAAGAACCAGGA TTCTGGTGGGATATTGG CCAGTCTGTGGAGGAAA ATAGGT[A/G]TCCAGATG AAAATGGTGGAAAGAAAG GGCGATGTCTGTAATAGT CCTGACTTGATGGTT CAGTAAGTAAAAATCCCAGA GAAAGATTCTGACTGCTCC AGCCTGGGTCATGCTCTG TCCC[A/G]GTGCTTCAAAT GATTGGCCTGGCCCCGGG AACCCTGGGACAGTTTTG GGAAAGGAGCATT CACATAGAAACATCATCCC AATCTCTGCCTTCATTTTC ACATGGAGCTCTCCCTATA TGT[A/G]TGGCCCTGTGTC CAAATGTCCCTTTGGTTAG GACTCATCCTAATGACCCC ATTTCAACTT TTGTCAATGCTCTGCTCTC TCTCTGTATGTCTTTGGG GGTAGATCTTCTCGGCC TCTC[C/G]CGGCTTCTGGT ACCCAGGTCTTTCTTGGT TTGTAGCTGCATCACTCTA GCCTCTGTCTC CATCTGGCCTCATTCTGTT GTGTACAAGCTCTGTGTC CTCTCTAGTTTCAAGTCAT GTGA[A/G]TACCAAGCGTT GCCACATGGCCGAGGCTA AGGAGATGCTACCTATTAG TACTAGTATTTTC



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
BTB-01276763	Discovery	rs42400277	ss63951620	A/C	A/C	8	3798414	UMD3.1	BTB-01276763-0_T_F_1511617542	CACTCCCAGTATATGTTTT GCAAGATAAGATAGTGAAT GGTCATGCAAGAAGGCTG GTTT[A/C]GACAGGGACAG AGCAAAGGACAAAGTAAG TGATCAAACAGGTAATCCC ACTCTGGGACTG
BTB-01944037	Discovery	rs43053569	ss64960232	A/G	A/G	8	108772548	UMD3.1	BTB-01944037-0_B_R_1511543993	CACAGAGCCAGGAGCTGG GATATTCATGGTCCCGAGT GCCAGAGCCACCACAAGG CCCTC[A/G]GAGTTAGTCA ATGAAAGGCTGGAAGCTA ATACTAATTGCTGGCTTAT GCATCTCTTCTGC TAACTTCCAACTTATATTA TGAGGCTAGCATCACCTT GTTACCAAAAAAGAGAAG GACA[A/C]GAGAAGAAAA ATACAAACCAGTATCACTG ATAAACATAGAAGTAAAC TTCTCAACAAG AAAGCTATCATCATAGTGC ATACAATTTTATATCCTGC TTTTTTCACCTAACACTGA AAC[A/C]GCAGTAATTTTAG CCAGCTACATGGACGTCA GTAATTGTGTTTTATTGGC TCCATGGTTG GCTACATAACTCTTCATCA TTATGTCCTCCAGATTTT AACATCTGTCTTATTCTT CTT[C/G]GATATAGCGTTT GAGATCTGGCATTTTCAGT GCTTCACGTAAGAGTCTTC TGTGGGCTTTT CAGGAGACAGGATAGCAG GTGGGAAAAGTAGGTTCT ATGCCGAGTGACCTTGAG AGATTT[A/G]GTAACCGAA CTATATCCCAACAGGAACA CAACAAGTGCTTCAAGCAA ACACAGCTGGTAT ATTGATTTACCTCCACATA GTCTCCCAATACACTCCA ACTCTACCCTTAACCGAAG TTTT[A/G]GGAGAAGGAAAA AAATGAGGACAGTGGCTT TTGGGAGTTCTCATATCTC TGGGAACCCTA TCTGAACAGATCCACTCTG TTAAGCCTGTGTCTGTGGA TGAAGCATAAACAGAGGT CCCC[A/G]TGCTGGTACAC AAGCCTCACTGCCTAAGA AGCGACATATTCAAATGTC CGCGTTAACTAT ATTTAACTTGGCAACCAC AGGTCTATTCTTCAGATTG TGAACCAATATTCAATA GCT[A/G]ATGAAGTGGATT CCCCATCGAATGACACAG GTTGCATTGAAGATGCCG ACCACAGATTTG GTCACTTAGTTTCATGATT TTAAAAATTACTTTTCCCTAAC TTAAAAAGCTTTTCCGAGA CT[A/G]ACAGTTGCTTAGTT TTTCACTTATACACTACC CGGGAGGGGGCCGTAGG CACTTTGAAA TCCTCAATTTTGATTCCAT TCCCAGCAGGTTCTTCTTG GGGTGGGGGACTCTCTGA GAAC[A/G]TCATCATAGAG GGTGAGTCTCAAAAGTTCA TAGAAGCAAGAATGCTCC AGTTCTTCTAGT ATGCCTCAGGCTGGAGGT TGGGAGCTCTGCGTGTTA GACCATCTGGTCTCAGTT CTGCC[A/G]TGCTCCTCAGG CAAGTTATTCATCTGGTTT CTGTTTGGATGTTGGCCTT GACTTAGGAATG
HAPMAP24224-BTA-93350	Discovery	rs41606159	ss61505413	A/C	A/C	8	65960156	UMD3.1	Hapmap24224-BTA-93350-0_T_F_1510717348	
HAPMAP39690-BTA-82650	Discovery	rs41590921	ss61492973	A/C	A/C	8	104829510	UMD3.1	Hapmap39690-BTA-82650-0_B_R_1511627385	
HAPMAP45337-BTA-109277	Discovery	rs41618019	ss61516718	G/C	C/G	8	4955143	UMD3.1	Hapmap45337-BTA-109277-0_B_F_1509286771	
HAPMAP49049-BTA-119736	Discovery	rs41571461	ss61475068	T/C	A/G	8	55892688	UMD3.1	Hapmap49049-BTA-119736-0_T_R_1511602078	
HAPMAP49333-BTA-82773	Discovery	rs41609510	ss61510981	A/G	A/G	8	109321402	UMD3.1	Hapmap49333-BTA-82773-0_T_F_1509295000	
HAPMAP57430-RS29016504	Discovery	rs29016504	ss38333008	A/G	A/G	8	1154683	UMD3.1	Hapmap57430-RS29016504-0_B_R_1509324941	
HAPMAP58894-RS29013940	Discovery	rs29013940	ss38322841	T/C	A/G	8	99957737	UMD3.1	Hapmap58894-RS29013940-0_B_F_1509290019	
HAPMAP58990-RS29020862	Discovery	rs29020862	ss38328553	T/C	A/G	8	9962339	UMD3.1	Hapmap58990-RS29020862-0_B_F_1509309093	
UA-IFASA-6154	Discovery	rs41590851	ss117964020	T/C	A/G	8	104158107	UMD3.1	UA-IFASA-6154-0_B_F_1511686662	
ARS-BFGL-BAC-14220	Discovery	rs109677705	ss105240266	A/G	A/G	11	13914771	UMD3.1	ARS-BFGL-BAC-14220-0_B_R_1511664100	



SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-BFGL-NGS-68030	Discovery	rs43659115	ss86298860	T/C	A/G	11	1901787	UMD3.1	ARS-BFGL-NGS-68030-0_T_R_1511657421	TGCCTGAACTCATTTTGAA AACACCCAAAATGGACAGG CCTAAGTTAGATTAAAGTT GATT[A/G]AGGTTTTTGGG GAAGTAAAAAGCAGTCAG CCTTAGGACTTCCCTGGT GGGCCAGTGGTTA CACACAAGACCAGAGCTG GGACAACATCCTTCTGCC ATATTTTGTGGCCAAAAGC AGTTA[A/G]CAAACCAGCT GAGATTCAGAGGTTGAGA GACAGCCTTCCCTGACAG AGGCAGGGCAATGT TTTATTAGTTAGTTATCAAT TAAGTACAGAATAAAAAAA ATCATATATAAATACAATG TG[A/G]AACACACACATA CATGCATTAACACACACAG AACCATGAAGGAAATAAAG GATAAATCA ATAAATGATAAATAATAAC CAAGAAAAGTTTGAAAGAA AATAACAAAAGAAATATTTA ATT[A/C]AGGAGATTAAAA ACCTGGAGTTATATTTAAA ATGCTGAGATACTGGTGC AGAAATTGGC CATTGACTTTTAGATAAGT CAGTTAATGTGCTTGGGAT TAGGTTTCTGTTTTGAAG AAT[A/G]AAGACTTTGAAAT CAGGAAATTTCTGAAGGG TCTCTTAAAGCCCAATTT TTATGCTTGT CACTTTGGGCATGACTTG GATTTGCATAACAGAAGTT CCTTTGGTTAAGCCTAGTT CTCT[A/G]TATTAGTAGAA CTCAGAGAAATGCCTTATG ACTAGACAGGATCGATGG TATTGCCTGTG TGTCCTGTGTTAGAATGA TCAATAATCACTCATGCTT TCAGTTATGATTTACCTC AAG[A/G]JAGCAGAAATGAT CTTTAGCCTAGTGTCAAAT ATTAAGATGTAGGCCCATG ACCTTTTCCA TATGGCCTGCAGTGTACAT GTTTGATGAACAAGTAGTG AGTCAATGTGTGAATGACC AAG[A/C]JGTGTGGATAAGT GAGGGAGTGAATGAATGA TCCGTCTTCCCTGGCTGTCA TGGTGTCTCTC GAAAATACACCATTTGTGC AACATGATAGAGTAAGAGT TTGTTCTTTTTCCTTGTT AAA[A/G]AAGTTTGATTTAA TTTCTCATAAGTTGGTCTA TTTTGGGCTGCAGTCATGA AATTTTTGT TTCCATCAAGATGAATAGT AAATTGTTTTTATTGTAGT AAGTAAAAACTAGTCAGTG AAC[A/G]JTACTGATCATC TCTAGTAACAGCAATTCT GAGTTTAGGTATAGCCAG GCTATTTTTT ATTCCAAAAATGGGCTATT GCAGAGACCAGAGTGATG TGAGTGAGGCACCTAGGG GGCAA[A/G]ATTTAAGATT GCATTACACTAGGGGGC TGAACCACACTTGTACTG CCCTTATGAGAAC AAACTAGCCTTATTGAGGT GAATTCCTCCTGTACCAAG TTTAATACATGTACGAAA GAT[A/G]JGGATGTGTTGGT GATTATGGAAAGGTAGGG GGGATGTGGAATTATATCT TCTGATGTGAG
ARS-BFGL-NGS-68850	Discovery	rs42274427	ss86298915	T/C	A/G	11	5252617	UMD3.1	ARS-BFGL-NGS-68850-0_T_R_1511656561	
BTA-99659-NORS	Discovery	rs41596833	ss61497406	T/C	A/G	11	30945111	UMD3.1	BTA-99659-no-rs-0_B_F_1511576291	
BTB-00458773	Discovery	rs43663587	ss65581933	A/C	A/C	11	10753131	UMD3.1	BTB-00458773-0_B_R_1511574455	
BTB-00474688	Discovery	rs43680229	ss65597810	T/C	A/G	11	50431031	UMD3.1	BTB-00474688-0_B_F_1511574523	
BTB-01397485	Discovery	rs42520028	ss64192391	T/C	A/G	11	33236456	UMD3.1	BTB-01397485-0_T_R_1511613640	
BTB-01426876	Discovery	rs42552262	ss64251080	T/C	A/G	11	34482175	UMD3.1	BTB-01426876-0_B_F_1544360628	
HAPMAP22963-BTA-91941	Discovery	rs41604980	ss61505330	T/G	A/C	11	1806374	UMD3.1	Hapmap22963-BTA-91941-0_T_R_1544359493	
HAPMAP33373-BTA-148341	Discovery	rs110590483	ss117970339	A/G	A/G	11	39437937	UMD3.1	Hapmap33373-BTA-148341-0_T_F_1544359173	
HAPMAP43815-BTA-23051	Discovery	rs41626586	ss61528544	T/C	A/G	11	44583035	UMD3.1	Hapmap43815-BTA-23051-0_B_F_1511566041	
HAPMAP48543-BTA-98093	Discovery	rs41668260	ss61568981	A/G	A/G	11	59319163	UMD3.1	Hapmap48543-BTA-98093-0_B_R_1511577685	
ARS-BFGL-BAC-11276	Discovery	rs110053849	ss105237002	A/G	A/G	13	2153905	UMD3.1	ARS-BFGL-BAC-11276-0_B_R_1511657522	





SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
ARS-BFGL-NGS-81428	Discovery	rs110541329	ss86311680	A/G	A/G	13	20735468	UMD3.1	ARS-BFGL-NGS-81428-0_B_R_1511676410	AGCTTCTGCATTGGAACT TGGCATCGTAACCACTGG ATGGCCAGGAAAGTCCAG TAAAT[A/G]CACTTGGAAAT GTCACCCTCTGCTTCATT AGGTAAAGAAGCATTTGG AAAGCAATTACG
ARS-BFGL-NGS-84327	Discovery	rs41681601	ss86314715	T/C	A/G	13	5774000	UMD3.1	ARS-BFGL-NGS-84327-0_B_F_1511690432	TGGTACATACTTGAGAA GGGTGGTCCGGCAGTGG GGGATCACCTGGGGGCTT GTGAGCA[A/G]CGTAGAAC CCCGGGCCCCAGTCAGAC TCACAGACTCACAGTCTCT GCAGGATTGAAGCCT TGACAGAAGGGGTTAGGA GCAGCCACAGAGGGAATT GAAGAATGTGGACTCAGT CGTCGT[A/G]GGGTGTAG GCTGAGGCCCGCTTACC CCTGCAGCTCAGTTGACT GCAGTGCATCACAG ATTCTGAGCCTCTGTCT TTGTCCCTGTGCTCCACTG CCTAAATCTTCAATTACAG ATG[A/C]TTTTTTAGAGTAA ATTATAGTATATCCACAA AAGGAACATTGTACAGTTA TAAAAAGTA CTTAAAGCTTTGAGTAGAT AATAGGAATTGTGATGACT TAGCATTTATACATATGTA TGC[A/G]TGACTTAGTGTT CGGATGTATATTTAGGATC AGTGGAAAGATCAAATAGA GAGGTGAGTC TTGTAATAACAATGTAAAG AAGGAGAATTTAAGATTGA AAGTGCTAACAGGATAAAA GGAA[A/C]ATTATGCACAA GAAAAGGTACAATTACTGA TGAAGATAACAAGTTATAG ACTAATGAATA CTTCTTGTGGACTAGCCTT AGCTATAAAGTTGCTTGGC AGGTTTGGGTTCCCAAGA GTGT[A/G]AGATTAAGCT ACAGACAAAAGTTAGACAA AGAAGTGTAGTACTCACAC ATAGGGGGAAAT AAAGCAAGGGCGCATGCC AGGGAAATATGCAGTAAC ACCTTTTGCACAGAATTA CGGGG[A/G]JAAAAAAGGCA AGGAGGCGGAGAGAACCT GCTGGACCACCTTCTTATT AACACCGGAGGC GTTTAAATCACGTAGGATTT TACATGTGTCAAGCGTTCA ATATAACATTTCTTGGGC TTA[A/C]TGCTTCCAAAGG CCTGGAGGAGACTTCTAC AAAGGGACAACTGGGAG AAGGGAGCCAGA CTGAGTCTGTGAACTGCAT ATCTTCCCTTTCTCTGT GTTCTGTCAACTCAAAAAT GTG[A/G]JTAAATAGCC TTCTCCAGCCTCTTGAG ATTTTCTGTGTAGATTGAT GATAATAAAA TAGAATTATGTTTTATAAAA TGATGGGGAAGTCACTCT CATTGCCTTTGGTAAAATC AAC[A/G]GATTGATTATCTT CTTGGCAATGAGCCAGCT AATTATCATCTACAGCAAA TGTGGGGCAA TTTTAAGATAAAAAGATATTA TGGAGTACATGCTGATGG AATAATCCTCTAGAGCAGA TGG[A/G]TTTTACTTTTCATT GTTGCTACTAAGGCCAAAA GCTATGATAATGTATAAAT AGCAGTTCA
ARS-BFGL-NGS-92946	Discovery	rs41679621	ss86323130	T/C	A/G	13	16399441	UMD3.1	ARS-BFGL-NGS-92946-0_T_R_1511691623	TGACAGAAGGGGTTAGGA GCAGCCACAGAGGGAATT GAAGAATGTGGACTCAGT CGTCGT[A/G]GGGTGTAG GCTGAGGCCCGCTTACC CCTGCAGCTCAGTTGACT GCAGTGCATCACAG ATTCTGAGCCTCTGTCT TTGTCCCTGTGCTCCACTG CCTAAATCTTCAATTACAG ATG[A/C]TTTTTTAGAGTAA ATTATAGTATATCCACAA AAGGAACATTGTACAGTTA TAAAAAGTA CTTAAAGCTTTGAGTAGAT AATAGGAATTGTGATGACT TAGCATTTATACATATGTA TGC[A/G]TGACTTAGTGTT CGGATGTATATTTAGGATC AGTGGAAAGATCAAATAGA GAGGTGAGTC TTGTAATAACAATGTAAAG AAGGAGAATTTAAGATTGA AAGTGCTAACAGGATAAAA GGAA[A/C]ATTATGCACAA GAAAAGGTACAATTACTGA TGAAGATAACAAGTTATAG ACTAATGAATA CTTCTTGTGGACTAGCCTT AGCTATAAAGTTGCTTGGC AGGTTTGGGTTCCCAAGA GTGT[A/G]AGATTAAGCT ACAGACAAAAGTTAGACAA AGAAGTGTAGTACTCACAC ATAGGGGGAAAT AAAGCAAGGGCGCATGCC AGGGAAATATGCAGTAAC ACCTTTTGCACAGAATTA CGGGG[A/G]JAAAAAAGGCA AGGAGGCGGAGAGAACCT GCTGGACCACCTTCTTATT AACACCGGAGGC GTTTAAATCACGTAGGATTT TACATGTGTCAAGCGTTCA ATATAACATTTCTTGGGC TTA[A/C]TGCTTCCAAAGG CCTGGAGGAGACTTCTAC AAAGGGACAACTGGGAG AAGGGAGCCAGA CTGAGTCTGTGAACTGCAT ATCTTCCCTTTCTCTGT GTTCTGTCAACTCAAAAAT GTG[A/G]JTAAATAGCC TTCTCCAGCCTCTTGAG ATTTTCTGTGTAGATTGAT GATAATAAAA TAGAATTATGTTTTATAAAA TGATGGGGAAGTCACTCT CATTGCCTTTGGTAAAATC AAC[A/G]GATTGATTATCTT CTTGGCAATGAGCCAGCT AATTATCATCTACAGCAAA TGTGGGGCAA TTTTAAGATAAAAAGATATTA TGGAGTACATGCTGATGG AATAATCCTCTAGAGCAGA TGG[A/G]TTTTACTTTTCATT GTTGCTACTAAGGCCAAAA GCTATGATAATGTATAAAT AGCAGTTCA
BTA-102818-NORS	Discovery	rs41612098	ss61513418	A/C	A/C	13	83632355	UMD3.1	BTA-102818-no-rs-0_T_F_1511596590	AGCTTCTGCATTGGAACT TGGCATCGTAACCACTGG ATGGCCAGGAAAGTCCAG TAAAT[A/G]CACTTGGAAAT GTCACCCTCTGCTTCATT AGGTAAAGAAGCATTTGG AAAGCAATTACG
BTB-01124378	Discovery	rs42283006	ss63589116	A/G	A/G	13	6600008	UMD3.1	BTB-01124378-0_B_R_1511612899	TGACAGAAGGGGTTAGGA GCAGCCACAGAGGGAATT GAAGAATGTGGACTCAGT CGTCGT[A/G]GGGTGTAG GCTGAGGCCCGCTTACC CCTGCAGCTCAGTTGACT GCAGTGCATCACAG ATTCTGAGCCTCTGTCT TTGTCCCTGTGCTCCACTG CCTAAATCTTCAATTACAG ATG[A/C]TTTTTTAGAGTAA ATTATAGTATATCCACAA AAGGAACATTGTACAGTTA TAAAAAGTA CTTAAAGCTTTGAGTAGAT AATAGGAATTGTGATGACT TAGCATTTATACATATGTA TGC[A/G]TGACTTAGTGTT CGGATGTATATTTAGGATC AGTGGAAAGATCAAATAGA GAGGTGAGTC TTGTAATAACAATGTAAAG AAGGAGAATTTAAGATTGA AAGTGCTAACAGGATAAAA GGAA[A/C]ATTATGCACAA GAAAAGGTACAATTACTGA TGAAGATAACAAGTTATAG ACTAATGAATA CTTCTTGTGGACTAGCCTT AGCTATAAAGTTGCTTGGC AGGTTTGGGTTCCCAAGA GTGT[A/G]AGATTAAGCT ACAGACAAAAGTTAGACAA AGAAGTGTAGTACTCACAC ATAGGGGGAAAT AAAGCAAGGGCGCATGCC AGGGAAATATGCAGTAAC ACCTTTTGCACAGAATTA CGGGG[A/G]JAAAAAAGGCA AGGAGGCGGAGAGAACCT GCTGGACCACCTTCTTATT AACACCGGAGGC GTTTAAATCACGTAGGATTT TACATGTGTCAAGCGTTCA ATATAACATTTCTTGGGC TTA[A/C]TGCTTCCAAAGG CCTGGAGGAGACTTCTAC AAAGGGACAACTGGGAG AAGGGAGCCAGA CTGAGTCTGTGAACTGCAT ATCTTCCCTTTCTCTGT GTTCTGTCAACTCAAAAAT GTG[A/G]JTAAATAGCC TTCTCCAGCCTCTTGAG ATTTTCTGTGTAGATTGAT GATAATAAAA TAGAATTATGTTTTATAAAA TGATGGGGAAGTCACTCT CATTGCCTTTGGTAAAATC AAC[A/G]GATTGATTATCTT CTTGGCAATGAGCCAGCT AATTATCATCTACAGCAAA TGTGGGGCAA TTTTAAGATAAAAAGATATTA TGGAGTACATGCTGATGG AATAATCCTCTAGAGCAGA TGG[A/G]TTTTACTTTTCATT GTTGCTACTAAGGCCAAAA GCTATGATAATGTATAAAT AGCAGTTCA
BTB-01141508	Discovery	rs42300745	ss63640372	T/G	A/C	13	679009	UMD3.1	BTB-01141508-0_T_R_1544355623	AGCTTCTGCATTGGAACT TGGCATCGTAACCACTGG ATGGCCAGGAAAGTCCAG TAAAT[A/G]CACTTGGAAAT GTCACCCTCTGCTTCATT AGGTAAAGAAGCATTTGG AAAGCAATTACG
BTB-01141770	Discovery	rs42303607	ss63641158	T/C	A/G	13	777430	UMD3.1	BTB-01141770-0_T_R_1544349343	TGACAGAAGGGGTTAGGA GCAGCCACAGAGGGAATT GAAGAATGTGGACTCAGT CGTCGT[A/G]GGGTGTAG GCTGAGGCCCGCTTACC CCTGCAGCTCAGTTGACT GCAGTGCATCACAG ATTCTGAGCCTCTGTCT TTGTCCCTGTGCTCCACTG CCTAAATCTTCAATTACAG ATG[A/C]TTTTTTAGAGTAA ATTATAGTATATCCACAA AAGGAACATTGTACAGTTA TAAAAAGTA CTTAAAGCTTTGAGTAGAT AATAGGAATTGTGATGACT TAGCATTTATACATATGTA TGC[A/G]TGACTTAGTGTT CGGATGTATATTTAGGATC AGTGGAAAGATCAAATAGA GAGGTGAGTC TTGTAATAACAATGTAAAG AAGGAGAATTTAAGATTGA AAGTGCTAACAGGATAAAA GGAA[A/C]ATTATGCACAA GAAAAGGTACAATTACTGA TGAAGATAACAAGTTATAG ACTAATGAATA CTTCTTGTGGACTAGCCTT AGCTATAAAGTTGCTTGGC AGGTTTGGGTTCCCAAGA GTGT[A/G]AGATTAAGCT ACAGACAAAAGTTAGACAA AGAAGTGTAGTACTCACAC ATAGGGGGAAAT AAAGCAAGGGCGCATGCC AGGGAAATATGCAGTAAC ACCTTTTGCACAGAATTA CGGGG[A/G]JAAAAAAGGCA AGGAGGCGGAGAGAACCT GCTGGACCACCTTCTTATT AACACCGGAGGC GTTTAAATCACGTAGGATTT TACATGTGTCAAGCGTTCA ATATAACATTTCTTGGGC TTA[A/C]TGCTTCCAAAGG CCTGGAGGAGACTTCTAC AAAGGGACAACTGGGAG AAGGGAGCCAGA CTGAGTCTGTGAACTGCAT ATCTTCCCTTTCTCTGT GTTCTGTCAACTCAAAAAT GTG[A/G]JTAAATAGCC TTCTCCAGCCTCTTGAG ATTTTCTGTGTAGATTGAT GATAATAAAA TAGAATTATGTTTTATAAAA TGATGGGGAAGTCACTCT CATTGCCTTTGGTAAAATC AAC[A/G]GATTGATTATCTT CTTGGCAATGAGCCAGCT AATTATCATCTACAGCAAA TGTGGGGCAA TTTTAAGATAAAAAGATATTA TGGAGTACATGCTGATGG AATAATCCTCTAGAGCAGA TGG[A/G]TTTTACTTTTCATT GTTGCTACTAAGGCCAAAA GCTATGATAATGTATAAAT AGCAGTTCA
BTB-01656080	Discovery	rs42771121	ss64674033	A/G	A/G	13	51621880	UMD3.1	BTB-01656080-0_B_R_1544359918	AGCTTCTGCATTGGAACT TGGCATCGTAACCACTGG ATGGCCAGGAAAGTCCAG TAAAT[A/G]CACTTGGAAAT GTCACCCTCTGCTTCATT AGGTAAAGAAGCATTTGG AAAGCAATTACG
HAPMAP23870-BTA-128381	Discovery	rs41690422	ss117970697	T/G	A/C	13	43427963	UMD3.1	Hapmap23870-BTA-128381-0_B_F_1509277687	TGACAGAAGGGGTTAGGA GCAGCCACAGAGGGAATT GAAGAATGTGGACTCAGT CGTCGT[A/G]GGGTGTAG GCTGAGGCCCGCTTACC CCTGCAGCTCAGTTGACT GCAGTGCATCACAG ATTCTGAGCCTCTGTCT TTGTCCCTGTGCTCCACTG CCTAAATCTTCAATTACAG ATG[A/C]TTTTTTAGAGTAA ATTATAGTATATCCACAA AAGGAACATTGTACAGTTA TAAAAAGTA CTTAAAGCTTTGAGTAGAT AATAGGAATTGTGATGACT TAGCATTTATACATATGTA TGC[A/G]TGACTTAGTGTT CGGATGTATATTTAGGATC AGTGGAAAGATCAAATAGA GAGGTGAGTC TTGTAATAACAATGTAAAG AAGGAGAATTTAAGATTGA AAGTGCTAACAGGATAAAA GGAA[A/C]ATTATGCACAA GAAAAGGTACAATTACTGA TGAAGATAACAAGTTATAG ACTAATGAATA CTTCTTGTGGACTAGCCTT AGCTATAAAGTTGCTTGGC AGGTTTGGGTTCCCAAGA GTGT[A/G]AGATTAAGCT ACAGACAAAAGTTAGACAA AGAAGTGTAGTACTCACAC ATAGGGGGAAAT AAAGCAAGGGCGCATGCC AGGGAAATATGCAGTAAC ACCTTTTGCACAGAATTA CGGGG[A/G]JAAAAAAGGCA AGGAGGCGGAGAGAACCT GCTGGACCACCTTCTTATT AACACCGGAGGC GTTTAAATCACGTAGGATTT TACATGTGTCAAGCGTTCA ATATAACATTTCTTGGGC TTA[A/C]TGCTTCCAAAGG CCTGGAGGAGACTTCTAC AAAGGGACAACTGGGAG AAGGGAGCCAGA CTGAGTCTGTGAACTGCAT ATCTTCCCTTTCTCTGT GTTCTGTCAACTCAAAAAT GTG[A/G]JTAAATAGCC TTCTCCAGCCTCTTGAG ATTTTCTGTGTAGATTGAT GATAATAAAA TAGAATTATGTTTTATAAAA TGATGGGGAAGTCACTCT CATTGCCTTTGGTAAAATC AAC[A/G]GATTGATTATCTT CTTGGCAATGAGCCAGCT AATTATCATCTACAGCAAA TGTGGGGCAA TTTTAAGATAAAAAGATATTA TGGAGTACATGCTGATGG AATAATCCTCTAGAGCAGA TGG[A/G]TTTTACTTTTCATT GTTGCTACTAAGGCCAAAA GCTATGATAATGTATAAAT AGCAGTTCA
HAPMAP26649-BTA-128159	Discovery	rs41679704	ss117970743	T/C	A/G	13	19734286	UMD3.1	Hapmap26649-BTA-128159-0_T_R_1509296202	AGCTTCTGCATTGGAACT TGGCATCGTAACCACTGG ATGGCCAGGAAAGTCCAG TAAAT[A/G]CACTTGGAAAT GTCACCCTCTGCTTCATT AGGTAAAGAAGCATTTGG AAAGCAATTACG
HAPMAP50266-BTA-13664	Discovery	rs29018622	ss38335716	A/G	A/G	13	18536707	UMD3.1	Hapmap50266-BTA-13664-0_B_R_1511602957	TGACAGAAGGGGTTAGGA GCAGCCACAGAGGGAATT GAAGAATGTGGACTCAGT CGTCGT[A/G]GGGTGTAG GCTGAGGCCCGCTTACC CCTGCAGCTCAGTTGACT GCAGTGCATCACAG ATTCTGAGCCTCTGTCT TTGTCCCTGTGCTCCACTG CCTAAATCTTCAATTACAG ATG[A/C]TTTTTTAGAGTAA ATTATAGTATATCCACAA AAGGAACATTGTACAGTTA TAAAAAGTA CTTAAAGCTTTGAGTAGAT AATAGGAATTGTGATGACT TAGCATTTATACATATGTA TGC[A/G]TGACTTAGTGTT CGGATGTATATTTAGGATC AGTGGAAAGATCAAATAGA GAGGTGAGTC TTGTAATAACAATGTAAAG AAGGAGAATTTAAGATTGA AAGTGCTAACAGGATAAAA GGAA[A/C]ATTATGCACAA GAAAAGGTACAATTACTGA TGAAGATAACAAGTTATAG ACTAATGAATA CTTCTTGTGGACTAGCCTT AGCTATAAAGTTGCTTGGC AGGTTTGGGTTCCCAAGA GTGT[A/G]AGATTAAGCT ACAGACAAAAGTTAGACAA AGAAGTGTAGTACTCACAC ATAGGGGGAAAT AAAGCAAGGGCGCATGCC AGGGAAATATGCAGTAAC ACCTTTTGCACAGAATTA CGGGG[A/G]JAAAAAAGGCA AGGAGGCGGAGAGAACCT GCTGGACCACCTTCTTATT AACACCGGAGGC GTTTAAATCACGTAGGATTT TACATGTGTCAAGCGTTCA ATATAACATTTCTTGGGC TTA[A/C]TGCTTCCAAAGG CCTGGAGGAGACTTCTAC AAAGGGACAACTGGGAG AAGGGAGCCAGA CTGAGTCTGTGAACTGCAT ATCTTCCCTTTCTCTGT GTTCTGTCAACTCAAAAAT GTG[A/G]JTAAATAGCC TTCTCCAGCCTCTTGAG ATTTTCTGTGTAGATTGAT GATAATAAAA TAGAATTATGTTTTATAAAA TGATGGGGAAGTCACTCT CATTGCCTTTGGTAAAATC AAC[A/G]GATTGATTATCTT CTTGGCAATGAGCCAGCT AATTATCATCTACAGCAAA TGTGGGGCAA TTTTAAGATAAAAAGATATTA TGGAGTACATGCTGATGG AATAATCCTCTAGAGCAGA TGG[A/G]TTTTACTTTTCATT GTTGCTACTAAGGCCAAAA GCTATGATAATGTATAAAT AGCAGTTCA
HAPMAP54459-RS29016219	Discovery	rs29016219	ss38332719	A/G	A/G	13	12436043	UMD3.1	Hapmap54459-rs29016219-0_T_F_1509330608	AGCTTCTGCATTGGAACT TGGCATCGTAACCACTGG ATGGCCAGGAAAGTCCAG TAAAT[A/G]CACTTGGAAAT GTCACCCTCTGCTTCATT AGGTAAAGAAGCATTTGG AAAGCAATTACG









SNP name	Group	rs	ss	Forward A/B alleles	Top A/B alleles	Chromosome	Position	Assembly	Illumina Probe ID	Genomic flanking sequence
HAPMAP53212-RS29015272	Discovery	rs29015272	ss38326971	T/C	A/G	21	25704052	UMD3.1	Hapmap53212-rs29015272-0_B_F_1511601897	AGTGGCTTACAGAAAAGT CCAGAACTGGTACTCCC TCACAGGGCCAGGACAAG GGTGAA[A/G]GAAGTGAGA CATACACCCAGATGCAA AATTTAGGATGTGCATGCT CAGTCATTAAGTCT
HAPMAP57137-RS29011525	Discovery	rs29011525	ss38325820	T/C	A/G	21	18454966	UMD3.1	Hapmap57137-rs29011525-0_T_R_1509328136	GGAAAATATTAATTGAAAT GAACTAATCCACTCAGTAC TGAGTGCCAGAACAACTT GGGC[A/G]TCAAGCTGGAG AAGGAAGTTCCACTCCCT GTTTGCCTCTCAGATCCAG GTAACCAAGTCT