

Chr	AssemblyCoord	B6Allele	B10Allele	AmpliconId*	CoordAtAmp	PCRSize	PCR_F	PCR_R	Seq_F	Seq_R
1	4905893	C	A	B10SNP2G0001	229	568	TGTCCTGGCCGACAGATACAGTG	TCAGCCCCAGGTTTCAAAGCT	GTGAGACACCTGCTACTTCTGAG	CCTGATGCCTGGGACTACTAAAAAG
1	24618794	A	G	B10SNPS0003	214	557	AGCTTCAACATCGCCGCTTTGGTAGT	GCCTAACACTTCTATGACAAAACCAGCA	TTGGTAGTCATAGTGAACCTCC	TTAACAGCCTGATTACTGCCAC
1	43063842	T	A	B10SNPS0005	299	502	TTTTGCCCAAGGTCGAGGACAG	TGCTCAAGGCCACGTTTCCCTAAC	GTAAAGTGCCTACTGTGCAAAAC	GCCACGTTTCCCTAACCTGGAAG
1	61228463	C	C	B10SNPSG0001	152	494	ACTCTGGATTTGCCTATCATTGTGACTC	GCAAACCTGTGTAATGAGCCACCAAG	GACTCTAAAGTCAACCACCTTGG	CTGTGTAAATGAGGACCAAGATACC
1	75483331	G	A	B10SNP2G0002	305	496	CAACCTTGTAGTGTAGTCTCCCGC	GTTCGGTCTTAAAGCCGCTCCG	CATAGGTATAGCTGGCCACTG	ATTAAGGCGTGTCCGCC
1	95571814	T	C	B10SNP2G0015	207	983	TGAGTTTTCAACACGACAAACAAGGACG	GCCCAGCTTCTATACCAAAATGCC	CAGGGAAGGAGCCTGTG	TGCTATAGCAGCCTCAGATG
1	118565405	C	A	B10SNP2G0019	247	635	GCATAGTGGTGTCAATCTGGTCC	CAACATCATGTTCCCTGTAGTCC	ACACTGAAGTCTGTACTGGC	GAGCTCAACTTCGATTCTCTG
1	131470919	C	T	B10SNPS0014	186	650	TTTTAAGCATGAGGTAGTCAGGGCAC	ACAAGCACACCTGTCATCTGGTTC	CATTTAATGGAAGAGCAAGACTCC	TTGCAGGCTCAATGACAAGC
1	152988092	C	T	B10SNPSG0013	203	435	ACCATGACACCTGGGACTCTGAAC	TCCCTGTCAAGGCTGTCTGAAAAG	CCTGGGACTCTGAACCAAGATG	AGCTCAAAATTCAGCCCCC
1	17342737	T	A	B10SNPSG0020	241	412	TCCGAGGCGCATTATCCGCTAAAC	CCAGTGCCCAAGTGCATCATGTTC	GCGCATTTATCCGCTAAACTAAGG	CAAGTGCATCTGTCAAGGC
1	188081175	A	G	B10SNPS0019	189	668	AAGCCAGCATCTGTCACTTGGACC	TCTGTCTGGAAAGAAAGCCAGAG	TTGACCCCGTGGAAAGGTG	GGTGACAGCAAAATTCGACGTTT
2	3582646	A	G	B10SNPS0021	154	437	ACCGATTACTGTGACTGACTGCAC	GGGCTTTCTAAATGGCACAGACC	TGACTGCACAGGTGCTCAAG	AAGCTAACCCTTTCAGCTGG
2	25034194	C	G	B10SNPS0024	156	446	AGCCGGGAATCCTGTAACCATCAC	AGCAGAGCCTTACTTTCATCAAGCC	CATCACCTAAGAAGTCTGTGGGTAG	TCTGAGATGCTTCCCAGAAC
2	50942492	C	T	B10SNPS0026	232	491	ATGTGCTTCTCTGATGTGACCCCTG	TGCAGTCTAGCTTCTCCCTAGTGG	TGATGTACCCTGTCTCTTTG	TTTCTGAGGCTCAGCACAG
2	67362739	G	A	B10SNPS0028	213	534	CTCAGAGGTCATGGTGTGCACAG	TGGTGGGTAAAGATCCCAAG	CATGTGTGGCACAGTTTTGG	GCCTCCGCTGGGAAATAAATC
2	84313007	A	G	B10SNPS0030	313	759	AAACACACATGGCTCTGGCTC	GAAGTTGTGGTCAGATGTCCCTC	GGTTCATCATCTTCTGAGAGACTG	TCCCAGGTGCTGGGATTAAC
2	103735349	C	A	B10SNPS0032	403	589	TGTTCACTGAACGCCATAGCCC	CCAACTTTGCACAGGTTCAACG	GTTATCACCATGCTCTAGATGAGG	ACAGGTTACGCGCTGATCC
2	122094116	T	G	B10SNPSG0021	491	651	GCTCTACATAAGGCCGGAAGCGAG	GCATCCTGAAGAAGCCACAGC	GAGAGTGGTTCTAGTACATTTCTTC	CTGAGGCCCTGGATGACAAG
2	146096051	C	T	B10SNPS0036	325	539	ACTGATGCCATGAACCTCAAGAAGG	GGAAACATGTCCATCCCCGTTACAC	AAAAGGCAGGTGTTACATCTTGG	CCGTTACACAGGTGCAGAATG
2	164025160	A	G	B10SNPS0037	304	559	AGGAGAAGCTGAGCTGTGCCATCTG	CCTGGACAACCTTGTACTGAAAGT	AGCTGTGCCATCTGTCAAGG	ACTGTAGCTGAGTGGCCC
3	4365615	T	C	B10SNPS0041	208	546	TCTCACGGTGAAGATAGGACAGG	TGCATAGTGTCCACCTTCAACAG	TGAAGATAGGACAGGTTGATCCTAC	TGTCACCTTCAACAGAAGGC
3	25440271	C	G	B10SNPS0044	227	750	CCATTGTGCCCTTAGTACTGTGTG	GGGCGGCCATGACTTAATGTAATGC	GCTCATTGAACCTCCAGAAAAAATC	CCCATGCTTCCAGAAGGTTATG
3	51646346	T	C	B10SNPS0046	193	435	TTATCCACTGCCAAGTCTGTCTGG	TCAGCCAGTTCACACAACAAAGGTT	GCTGCGTGCATATTTGAAC	GTTCCACACAACAAAGTCTAGATGG
3	67807084	G	A	B10SNPSG0029	157	702	TGTCCTGAAAGGACTTGAGGCAG	AGCCGTAGCACTCCCTCAATAGTAG	TTGAGCATGTCAACCCGACT	GAGGAACAAGTGTCTCTCTCAG
3	84907155	T	C	B10SNPS0050	157	452	ATCAGGAGACAGCCAGCCATTTTC	TGTCAAAAGAGCCCAAGTAGG	GCCAGCCCATTTCTAGAAAC	CCCAGCCATTTCTAGAAAC
3	107273295	A	G	B10SNPS0051	376	558	TGATCTCCCTTGAAGCCTAAGCAC	TGAAATGAATCCACAGCCAGCTCG	AAAGGTTCCCAAGGTGTCTC	CAGCTCTGGAGCCTTTAAATG
3	122116882	C	T	B10SNPSG0034	238	407	ATGAGGACAAGTCTGAAGCGACC	CCGGAGAAGCCCTGAAGTTAATG	ACAGACCAGGTTCAAATAC	GATCAATAATCAGTGTCCAGGC
3	146593495	C	T	B10SNPS0056	227	686	CCCAGCCTGGTGTGAACCTTTAAC	TCTGCTAAACCTCATGTGGCAATG	AGTTCAAAGTGCATGACCTAGC	CTCATGTGGCAATGTGACGC
4	7149610	C	T	B10SNPSG0036	213	643	GCTCCAGAAGTACCATCAGCGG	GTGGCTGAGACAGCCCTCAAGTAAAC	GTACCTAGACACATCCAGAATATC	CAAGTAACTGAGATGTGCTGCC
4	28249560	T	C	B10SNPS0060	380	693	TTCTTACTAGAGAACCAGTGAGAGC	GGGCTGTCATTTAGTATCCCATGAC	TGGGATGTGAAGGCTCTAGC	CCCATGACTGGATGGAATCTAAC
4	45462131	T	G	B10SNPS0062	188	488	CTGGCCGACACTGTAACCTCTACTG	TGGAATAGATGTCTCCCTCCCTGC	ACTGAATGAATGATAGGCTCTGG	GCCTACAGTGGGAATCTTACG
4	66040938	A	G	B10SNPS0064	224	575	CCTTCAGGGAAGTGAAGTTGGGAAC	AGTGCCCAACCAGGACATGTAATC	TTGGGAACAGGCACAGC	TGCTACTGAGGAACACAGTGG
4	87804727	C	A	B10SNPS0065	370	549	AGGACCCGGAAGGTTTACCAGAG	GCCAGGAAGTCAAGAAAGGATGCTC	TGTCGGCCATCAACTGGAAG	TTCAAGGAAGTACTGCTGAAGG
4	112653568	G	T	B10SNPS0067	340	564	GCACATGAGAGACCAATGAGTCCATC	TGCGACTTTGGAGAGTGACACAATG	ACTGACTTGAGATTTGATGCTC	TTGAGAGTGACACAAGTAAATTC
4	126253529	G	C	B10SNPS0069	208	401	TGCCACATTGCTAAATAGAGTGGC	TGGCTCTGAGTGTCTTCCAAAC	TTGCTAAATAGAGTGCCTCCAG	GTGTCATCTTCCAAACAGAAGTGG
4	142217407	T	C	B10SNP2G0026	183	650	TCAAGCCTAGAGCCAGAAGGACTC	TGCCCAACAATGCTTGAAGTAAAG	GAGGGACTCATTAACTCACTTAC	TGACTGAATGCAAGTCCAG
5	23345000	A	G	B10SNPSG0050	444	692	CAGTGGGACTCAAGCAAGATTC	CTGGGACTAATAGTAGGTTCAAGCG	TAGCCAGATATGGTGGTACTAGC	GAAACAAAATATGTTGTGTGCTTG
5	44059873	A	G	B10SNPS0077	299	530	GTTCTAGCTCTCTGCTCAATGGAAAG	ACCTGGCCACTGTCTGATGTGCG	GACAGAAATGGTCTTTGTCATTC	AGTTACTCGGAGCATTGTTTTTTG
5	67382789	A	G	B10SNPS0079	328	479	TTGAAGTTCAGATCCATCCCGAAC	CTGTTGGAATGGACAAAGGACGCC	ATAAGCTCCGAGTTCGAGTTG	AGCCAACAAAGGACTGTG
5	88988451	G	A	B10SNPS0081	262	719	TGCCAAGTATGTTAGGCCAAAAGCAA	TCTCCATGCCTACACACTGTTACAGA	GAGGGTTAAATCACACATACAC	GCTGGCCTTGAATTAACGC
5	109001097	C	A	B10SNP2G0043	153	459	GTAAGACCTTAGCTGTGACAGGCG	TCTGTGAGGCAGAGTCCACACAAG	TGGGAGATTTGCCTGC	CCTGGACCATTCAAGCAGATG
5	129799057	T	C	B10SNPS0086	380	741	ACCTTGTGAAACCCGCTCC	GCACCAAGTACCAAGTGTCTACTCT	AGGGGAACCATTTCTGCGAC	TGACAGATGTCACTCATTGCTG
5	148405352	C	T	B10SNPS0087	248	576	TGTCATGGAGCAAGCACTACGAG	ATGATGTTGTCAAGCCCAACCC	CTACGAGAGTTGGACACCTC	TCTAGTACTAGACTACTAGGTGGAG
6	4944845	C	A	B10SNPS0089	220	749	AGCTGAGGTCTACTACAGTAATGAGC	CTTTCACGCAGCTAGGCAAAAGC	CTCGGAGAACAGGACAGC	CCTTCTGGATGAAACTCAGTGC
6	23322761	T	A	B10SNPS0091	291	444	TGATTACCCAGTCCATGCTAATCAAG	TGGAATGAATCCTGCCAGCCTC	CTCAGGATAAGCTTTTTAAGGGTG	TGCCAGCACTCATCTTTG
6	42395982	C	T	B10SNPSG0054	210	427	AGCTGGGCTATGTCTTGGGCAAC	AGGCAGTCCCAGCACTTTGAAAATG	ATGTCTTGGGCAACATGAC	CCAGCACTTTGAAAATGTAGAGC
6	67742189	C	A	B10SNPSG0061	211	405	TGCAGGCGAGGAGCAATTTGAGTC	AGACAGTCTTCCAGAATGGGGAGC	GAGGCAATTTGAGTCTTATCTCC	TCCAGAATGGGGAGCCAGAG
6	84280591	C	T	B10SNPS0097	241	703	CAGATAGGTGTGGATGGATCATGGC	TCCCATGTTGAGGATGGAGGAAGG	GATGGATCATGGCTTAAGATCCC	TTTCAGAGCCAGGAATGTGAC
6	104875242	A	C	B10SNPS0099	315	656	GCACTTTTGAAGCAGAGCATTTAC	TGAATCCATCAACAGGAAAGGCC	TTTAAAGCCTGTGACGACCAAAAG	GGCATGACCCTACTTATGCTAC
6	125060262	A	G	B10SNPSG0065	236	400	AGGAAGCCCCTAAGATGCCATATGG	CAAATGACTGCTGGAGAAAAGACAC	ATGATGGCAGTGCCTTAATC	CTGGAAAAGAGACACTTCTCTTAC
6	147720182	A	G	B10SNPS0104	230	493	TTCTCTCAGTCAAAGTGCAGAGCC	CCCGAGATGTTTTCTGACTCCAG	AGAGCCACTGGTGCAAC	GTGATACTCTGAGGCTTAACTTACG
7	7014667	T	C	B10SNPS0105	469	691	GGAAGCTGTCTCATGGAATCCACG	TGCATTTCTGGCTGCTGAGGAG	TGAAACCTGCTGTGCTCAGGG	CTGGCTCCAGAAAGTTCATATTC
7	28467081	T	A	B10SNP2G0049	228	748	TGTAAGCAGCCAGACCTGCAT	TGAGCTTCTCACAGTCCACCCA	CAGACCTGCATCTCAGG	CCAAGGGTACTTTGAACTTC
7	38216957	A	C	B10SNP2G0052	162	496	GTGTCACTTGAAGCAGCCAGAGAG	TTGCCAGAAAGATATGCTCCGCC	GCAGCCAGAGAGTTTCTTTTATTACG	ATCCAGAGAGACTTTGTGCC
7	54410823	C	T	B10SNP2G0058	280	674	CGTGTGTAAGTCTAGTATGAGCC	TGACTTAGTGAACCTGCAAAATACACCC	AAGGCCCTACTCTCATGTA	TACTTCTGAAAGGCTGAAGACACTG
7	71519895	G	T	B10SNP2G0060	347	644	GCACATAAAGAGCCTGGTATAGCAA	AAATACGCCAACATTTCCCTTTGTGTC	CTAACACCTTAAAGTGTGGGGAG	ATTTGCTCCGGCCAAAAG
7	87465557	G	A	B10SNPS0113	424	709	ATCCAAGAGAGCCTCTCTGTGAGC	CAGCCACCATTCAGTGTACAGTCTG	TCTGGGGTACATAGGCAC	CATCCGAGTATGATATTTGCC
7	104565567	A	G	B10SNPS0115	239	410	TTCTGTCTCTGTAGGAGGTCACG	TGAGAACGAGCCTGCTGAAAGC	TTCTCAACTGGGTGAGAAGGC	CTGTGAAACGGAGGAGG
7	130492865	A	G	B10SNPS0118	175	690	TTATGCTGGAGCCACTTTCAGC	CTCCTGGAGATGACCTTTTGGTTCAC	GCCACCAACAAGACCTGAG	GCGTTTTCTGCAAGTCAAGC
7	141188625	A	G	B10SNP2G0065	253	599	ACGAACATTGGCTCTGTACACC	CTGGGGAGAACGAGACACACTTAC	TGTGTCAAGATGCATCGCC	CGATGGAATCCCATTTGAGCTTC
8	4235918	C	T	B10SNPS0122	163	541	TCAACAAGCTGGAGACTCTGCC	TGCTGAGCTGCACAAAACCAGC	TGGAGACTTGCCCAACC	GCAGCTCCTATAAAGGTTG
8	24145986	C	T	B10SNPS0123	496	651	TTTGTAGGACAGCAGGTTCCCG	CCTCAGGTGAGCAGCAAGAAATTC	AGCCTAAGGCTGTCACTAC	TGTAGCAGCAGAAATGAAAATCTAC
8	48705306	G	A	B10SNPS0126	607	778	TGAATTCATGACAACTACCTCCCG	ACTTCCCTCCCTGAGTGTGAAAGC	GCGAAATGCCTCCATGAGATCC	CCTGACTGTGAAACGAGAAATAAC
8	64124535	G	A	B10SNPS0127	213	470	TGAAAACATCTCTTACACAGCCGCT	GCTAAGGTAACTGACCTTCTCTC	TCCACTGTAAAGTACCTAAGAGG	AGCTCAGTCTCTGTGAAAGC
8	86611947	C	T	B10SNPS0130	382	573	CAAGGTGGTACCATTGCTTCTCG	TGGCTGAGCAACACCTAAGGCCAAC	GCAAGCACCAGCTACTATGAG	TAAGGCAACACCAGATGAG
8	106217064	C	A	B10SNPS0132	216	520	TGTAACCAACATGGCTGCGTTCTC	TATGTGAAAGCCAACCAGGCCAG	TGCGTTCTGTGAAGCAC	GTGTTTATCACAGAAGGCTCAAG

8	126154896	A	G	B10SNPS0133	173	590	TGGTAAACCATCCCAAGCGG	AGTCGGGGCACATTCACAACATC	CGGCAGAGCTGTAAGTCTGG	AACAGGCAGTGTCTCTGAC
9	8307298	T	C	B10SNP2G0067	178	531	GATCATTTTACCAAGGTCCTGCTGAG	TCAGGCAGTATAAGGCTCCCATTTCTC	CAAGGTCCGTCAGGGATAATC	TCCTTCCCAAGGTTGTTGATG
9	25697557	A	G	B10SNPSG0092	379	595	AGGAGAACCCTGCCTGTTCAAACCC	TCAGACCTGGCTCTAAGACCCCTG	CCCATACAAAGTCATTTCTGGACTG	TGAAATAGCCCTGGTATCCCG
9	44891469	G	A	B10SNPS0139	301	540	CAAGCGGTTAGAGTTGGGGTCCAC	CCTCCGGCTGAATTGAATTCAC	TATGGCAGTAGTCTGACCC	GGAAATGCACCTTGAACATGC
9	65069297	A	T	B10SNPS0141	191	720	CTGTCTCCAGCTCACAAGCTCTCAG	GAACGCACATGGCCACCCATTTTC	AGTCACAAGCTCTCAGCTCTG	TGGGCTATGCAGTAAACTCC
9	87513872	T	G	B10SNPS0144	244	493	TGGCTGTGACGCTGTAGGTAACAG	TAGACTTTGGAGGGCAACCACCTC	AAAGACTACGGCTTTTCAGCTTG	GGCAAAACCCTCTCTCTTTGTTG
9	106375830	A	C	B10SNPS0145	192	554	TGGCATACGCTTGACCTGGAAAC	AGCAAAGGTCCAGTGGCCGTTATC	CCGTGAAACTGGTCAAGGTTG	TCCGAGTACAAGGTGCAACTCTG
9	122496139	A	T	B10SNPS0147	229	632	GCCTGCACAGGGATTATATCTGCC	GTACCCCAAAGGCTTACGCTCG	GCTCAATTAGATGTTCCAGAAGC	TTGACAGGTTATTTCCAGCAG
10	25103948	A	T	B10SNPS0152	159	517	CATAATTTGTCTTCCCAGGCCACTGA	AGGACATGGATAAACCAAGCCACATTT	CCACTGATTCAGTTTGGAGCC	CTGTCTACCCAGAGGTGTAGAAAC
10	43717117	C	T	B10SNPS0153	148	403	TTCAAGAAATACCTCCACGCCATCG	GGCTAGAAAACAGCAGCCTTTTCTC	CATCGCTTCTTCAGTTTGG	TCTGCCACAAGCAAAGCTTTTTC
10	62547650	C	T	B10SNPSG0099	450	619	TGTTTAGGCCACCTCAATGGCTC	GGCTGATGAAATTCACAACTGCC	AGCTCTATAAGCAGTCTGGC	TGCCCTGTACCTTAAATAAAC
10	83411614	C	T	B10SNPS0157	183	443	TGCCGTCTAAGAGTCTCCAGCTATC	TGTCATGCCACAGCATTAACCTCCC	AAGAGTGGCCAGCTATCATCTTC	CATGCAGCTAAGGTAGGTACTC
10	104474937	A	C	B10SNPS0159	227	766	GTGAAGTCAAATATTGCCAACAGACC	TCACATGGGTCCAAATCAGAAATCTGC	ATCATGTACCACACTTTCAGTTTGG	CAGACTGTGTATAATGGACTCTC
10	126774961	C	A	B10SNPS0162	459	689	TGATGAAAGCCACCAGGGAGC	GCCAACTTATGTGAGGGTCCCG	GCCGTCTCTCAAAGAATCTGAG	TCCCAAGGTTATGGAGCCAG
11	5927550	A	G	B10SNPS0163	367	553	ACCCCTGTGGGAAGACAAGCAGC	GCAATCTCTGAACCTGATGGGGAC	ATATGAACTGTCTCACACTGG	ACCTGATGGGGACCTTCAAG
11	24352635	T	C	B10SNPS0165	339	562	GGAATTTGGCTCGGAAATCTGCAATG	TGGCTTCTAGTACTAGACGGCAAG	AAACTGCAATGGGCTTGTCTC	CCTCTGAACCTCGATTTATAGGGC
11	46027800	G	T	B10SNPS0168	175	447	GGAACAGGCCAGAAATCAGGGCTTC	TTCACCCCGAGGTTGTCAAAG	AGAAATCAGGCTTCCCAC	ACATTTGCTTGTAGGCCAGC
11	65237281	A	G	B10SNPS0170	178	634	TCAAGTCCCATAAATCTCAATGAGCTG	TGGAGCCAGATCCACACTATTAGG	GAACTTCAATGAGCTGTAGAAAG	CAACACTTCTCAGCTAGGTATG
11	83361835	C	T	B10SNPS0171	297	452	AAAGGTCAGACCCCTATCCAGAG	AAAGCTTGCAGCCAGAGCTAC	ACACACGCTTAAAGTCTGTGC	GCCCAAGTCTACTGCAAAAAG
11	105208941	A	C	B10SNPS0173	273	487	TGTGTGAGAGCCGAATCCGAG	GAAAGACTAGCCCAGACTCTTCC	AACACCAGTGTGGATCCG	TCTCCAGAACCCACTGC
12	4035991	C	T	B10SNPS0175	391	622	GTAATCTGTGACCTTTGGGAGCC	GCTGCCTTTGTCTGATAGGAGACC	CCCTTGGGAGCCATTTAAGAAC	TCTTCTCGGAGGCCACAG
12	256226291	A	G	B10SNPS0178	153	465	AGACTGGAACCTTCTCAGTGTCCCC	TGTCTCAGAGGCCAGGCAAGT	CTCAGTGTCCCCAGGTT	GATCCCTGGACCCAAATGATG
12	33783681	T	G	B10SNPS0179	541	729	GCCATCCAGTACGCTTGTCTAATTTTC	TGGCAGAGAATCACAAGACTTCCAG	GAACTTGTCTCAATGGCTCAG	AAGACTTCCAGGCCGCC
12	55293511	C	G	B10SNPSG0101	196	690	CAAAGGCTCGACCCAGATGTTAG	CCATTACAATCAGGGACGTGTGCAG	GCAAGTGTGTCTCTAAAACC	TGAGGCACTCAGGTGGAAGT
12	69022193	T	C	B10SNP2G0069	480	666	TGAGACACACGAGATCCCACAG	ACGTGGTAATGGGCTCTTGTAGCC	CCTTGACCAAGGTATCATTGAGAAG	ATGGGCTCTTATGCCATTTAAC
12	85893620	T	C	B10SNPS0184	222	434	CTTACCACATAGCTTATGGCACCC	GTACCTATTTCCCAAGCCAGGAG	ATTGGCACCCACCCTGG	GCTGTGGAAATTTAAGAAAGAGTCC
12	106196191	G	C	B10SNPS0185	181	499	GCCCTCGAGAACAAAGTGTGATGCC	TGCTCAGTGCCATCAAGTTCCC	GAAACAAGTGTATGCTCTCTCG	TGTCATACACACTTGTGGTATG
13	23458896	T	A	B10SNPS0190	231	607	GACATGCACAACTGCTCTCAGTAGCC	CCAGATGCACATTTGGAGCCCAAG	CTGCTCTCAGTAGCCAAAGAAATATG	TTACGTCTGAGACTTACTGCTAC
13	44605368	G	A	B10SNPS0192	242	482	GGTCAGCACTTTCAAGGTAGGAAGC	GACTCTAGTGAAGTGGGCTTGTAGC	AGCTCAGAAAGCAGTGTCC	AGCTCTGGGTATGCTGAGAC
13	60294898	T	C	B10SNP2G0077	196	444	AAGCTGGCAGCCAACTTCTGAC	ACATGCCACGAGAGACTAGGTAG	CAACTCTGACAGGGGC	GAAAGACGTGCCGAGTTTATG
13	83826961	T	G	B10SNPSG0116	201	467	ACCCAAAGTGAGGCAATGCTGG	ACTCCGCTACATATGAGGAGCAGG	CAATGCTGGAGATAGAAAACCTTG	GTTGACTTGACTGACTCATATTCG
13	107699046	G	A	B10SNPS0198	190	409	TGGAAAAGGCTGCTTCCAGACCAC	ATTGACAGCCTGAGCCATCCAG	GCTGCTCAGACCACATGTTAAG	ATCCAAACTTTTTCAGGGATGGC
14	13021464	C	T	B10SNPS0200	325	657	GGAATCCCATATGCTACTGCTTCTCG	TGCCTGACATAAGCCATGCAACCG	TGGAGACTGCTCTCACACTG	GAAAAGGCTTATTACTTGGC
14	30518255	C	T	B10SNPS0202	155	504	ACTGCAATCAGGTGTGAATGCTGAC	AGTGCCGTTGAAGTAGCCACTCTC	TGTGAATGCTGACACTGCC	TCTTCCCAAATAGGTTGCAGG
14	55673056	T	G	B10SNPSG0125	199	535	TACCGTCACTCGTGTGCTGTG	AGCAGAGTAACTCCTCTCTCTCC	GCTGTGTCTTGCCACC	AGTTGTAGTCCCAACAGCTG
14	77195309	C	T	B10SNPSG0131	196	416	ATGCAACTCTGCCCTGATTACTCG	GAAAGCGGCGTCAAATGTTCTCTC	CCCTGATTACTGCTGTGCTTG	GCGTCAAATGTTCTCTGTTATG
14	96734196	C	A	B10SNP2G0083	303	518	GACCCTACCCATGTAACCATTAAGTGCAG	CACCCCTCAAGCCCATTTGTCAATAT	TTAATCCCGACCTTGGGAG	TTGTCAATCTTCCAAAATTTGTGTC
14	116124073	A	G	B10SNPSG0139	694	851	GACCCAGTGGCAGCTTTACATGATT	TTCAATCTTCAATGCAAGAGGGAC	ATTGAATCTCTCAGGCTCAAGG	GGACTTCGGACATAGACATTTCTC
15	7117980	A	G	B10SNPS0212	318	493	TGAAAAGGTCATTCGGGCTCCAG	TCTTCAGCAAAAGTGGGGAAGC	GAATGTCCCTCGGGAATCAC	GGGAAGCCCTCCACACTC
15	25941148	C	T	B10SNPS0214	161	826	AATGGCTTTACCCCTTTTGGCTTATGGAT	GCGGAAACCTTCTCTGTGTGAC	TATTCAGCAGTACCTCTAAGTAC	AGTAAGCCTTACAGATGGGTCTC
15	42051029	A	G	B10SNPSG0142	150	966	AAAGGCTTGTCTACGTCGCCCTG	CCCAAGGCTGCACAATAATGAGA	CCTGCTGCTTCCAGGTTAG	TTGTCCCAAGAGCTGTAACG
15	63931032	G	A	B10SNPS0218	165	797	TAGCAGCGTGTCTCTGAGAAGGG	AGTAGTCTCCATCTGGACGAACTAC	GGGTCAATTTCTCAAGGAACTACAG	CTACATAGTGAATCCAGGCCAG
15	83618701	G	A	B10SNPS0219	234	440	CAAGACTTAAGCCAGTCCCAAGTG	GTTTTCAGACAGTAGCTGCCCTCC	TAGGCCCAGAACTGTCAAACCTG	TGCCTCCAGAACTGCAAGCTTAG
15	100309099	G	A	B10SNP2G0093	174	457	CAAAGAACAGTGCAGCTTACTCTGG	TGGCTTAGTGAACACTGGGAGG	GCCGACTGGTTTTCTTATGCCC	CCCATGATAGTGCAGGAGAGAA
16	4972820	A	G	B10SNPSG0155	302	538	TGCAAGCACATCTGAGCTGAAAGG	GCTGGCACAGCACTGCTCATTAG	AGCAAAGTACAGGGCCTATTC	GTCTTCAACAGGATTTGCAAGCG
16	29856457	A	G	B10SNPS0225	466	651	AGCAACCACAGCGTGAGTTTCC	CACCTTGAGTTTTCAAGACCACC	CATGAGAGCCATTGCATGGTG	GAGTTTTCAAGACCACCTTCAAC
16	44261352	A	G	B10SNPS0227	183	414	AGATGCTTCCCTGCTGTAAGGTCC	ATGTCACGGTAAGATGCAGTGTCC	TGTAAGTCTCCAGGAC	TAAGCAGCCTGACCTTTACAG
16	54901204	G	A	B10SNP2G0097	727	950	GCAATGCCCTTAATTCAGTTCAACCACA	ACTCAGAGATTTACTTGCTCTGTCTC	TGTGAGACTAGAGTAGCAGCCTC	CTCTGTCTCGACTGACATAAAGG
16	87736505	C	T	B10SNPS0232	315	479	GCTTGCCATTTAGCCAGACACAAC	TCCCTGGCCCTTAGAGAATGCC	ACCATAGGTAGTAGATTTCTGCG	GCCTTAGAGAATGCCGTTTTGATAC
17	3690688	G	A	B10SNPS0234	207	544	TTATCACAGGCAAGCAAGCAGG	TGTGGTTTTCCAGGCCCAAAAG	GCAAAGAAAGGGCTCTCTG	GGTGGAAAGGAACTCTTTACTCTG
17	24310623	T	A	B10SNPS0236	306	472	ACAGAACTGTCTGTCTGCTGCTGG	GGGCACACATCCCTTTACTAGCAAAC	GGCTCTCGATAAGTTGAATATCAC	ATCTAGCAAACCCATTTCTGCG
17	47451200	G	A	B10SNPS0237	387	587	GGCTCTGCTGATGACCTGTTCAA	CGCTGGCCTGGGAATAGTGTATG	TGTGGCTGAACACTATAAGC	AAGTGTATTGGTAGCCATCAGC
17	66263080	G	A	B10SNPS0239	484	693	ACAGACTACAGACTTCTGCTTGGC	CCTGTCCAAGTGTACCACATGG	ATTGCCAGGCTCTGTAGCAAG	GTGAGAACTAGCTTGTAGAGAG
17	84624403	A	G	B10SNPSG0168	254	478	AGTTACGCAAGTACCCTGTGCTC	ACATGGCTCACTAGGCCCTTTCTG	GTGCTCTCATCTCCAAGG	TACTGCCTCATCATCTGCTG
18	15408257	C	T	B10SNPSG0174	385	638	GTTCAGACACAGAGAGCTTGGCTTG	GTCTCAAATAGACATGCTGACAC	ACCCTAATTTATCAGGGGTGTC	TGCCTGACACAGTCTGCTG
18	35366160	A	T	B10SNPSG0180	241	722	CTGGGAAGATCAAGGCCAAGTACTG	AGGTTACCAAAGCTCCAGTGTGCTC	CAAGGCCAAGTACTGTTCTATTG	GTGGCCTTAATCTCAGTACTCAGG
18	46803584	T	C	B10SNPS0247	196	483	CTCCAGGATCTCAGTTGATCTGTTGC	GGATGCTCGGTGAAGTCTGACTTAC	GATCTGTTGCATGGCTCAC	GGGCATATAGTCCCAGTATACAC
18	65425288	C	T	B10SNPS0249	155	440	GCACTGATTTCCAAATGGGACATGAC	GAATGGCATGCTTCCAGCT	GACTATGAAGGCATACGCACCTTAC	TCTCCAGACTAGCTTGTAGAGAG
18	8349271	G	A	B10SNPS0251	176	426	GGCAAGTTCCGAGGAAATCTGCTG	TGATGGTGCCTTTGTACCAAGT	CAAATTCGAGAAAGTGGCAGG	AGGACATCTTGTCCGACTACTG
19	23378788	T	G	B10SNPS0255	358	615	ACACAAGTGTGTTACCAAGGGAGC	TTGCCACATCTGTTAGGCTATGTC	ACCAGGGACAGCTTTTGTAG	ACATCTCTTAGGCTATGCCCTTTGG
19	46875560	A	G	B10SNPS0258	402	563	GATTTGTACCCCTGTGGATGGAAGCC	TGCTGTGCTCACTGTGGAAGAGC	TGAGCACACAGTTGGTGGTC	GAGCTTTTGTCTTTGAACTCCAG
X	55120804	A	G	B10SNP2G0120	169	621	GCTTTTGTCTGGCCTTCCAGCAGAC	AACCTCGGCAGTGAAGCATTTG	TTGGCTTCCAGCAGCAAAAAG	CTTACCAGGAACCCGCTGTGATG
X	147904667	A	G	B10SNP2G0150	151	502	TGTACCTACTGAAGTCCAGTAGGGC	CCAGAGAGTGAAGTCAACATAGC	CAGAGAGTGAAGTGTGAC	GGAAAAATCCAGCTTCTTTCG
X	158414344	G	T	B10SNPSG0223	180	692	ACTGCACTTCTGAAATCCCAACTG	TGGACAACAGGCATCTGGAGAC	TCCCAACTGAATTTATGATCTTAC	ACACACTCTCTCTGGAAATGG

* Please click here to see DNA sequencing traces for all markers.