

Toll-like Receptor 1 Polymorphisms Affect Innate Immune Responses and Outcomes in Sepsis

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ONLINE DATA SUPPLEMENT

Supplemental Table 1. TagSNPs genotyped in Normal Volunteers.

SNP location as denoted by IIPGA (http://innateimmunity.net/IIPGA2/index_html) or Seattle SNPs (<http://pga.gs.washington.edu/>). SNPs denoted in flanking sequence by square brackets.

Gene	SNP		Alleles	Chr	Strand	Flanking Sequence
	Location	dbSNP				
CD14	4775	rs2569192	G/C	5	forward	TTTGTCATGTCTGTGTCCCAGGGCTTTCTA[G/C]CAACCCTAGTACTCGGTAGACAAATGRT
CD14	5074	rs5744448	A/C	5	forward	TTTTACAGAAGGGAGGCCCAAGTCTCATAA[A/C]CTCAGTCGTAAAGCTGGGATTCCAAGAC
CD14	6675	rs5744455	T/C	5	forward	AAAAAAGGAAGGGGAATTTTCTTTAGAC[C/T]AACTTCCTTTTCTTGAACCTAATTCTAC
CHUK	1866	rs12770784	A/G	10	reverse	GTGGTTCCGTTCCAGCCCTCCCGGAAAATAC[A/G]TAGGGGACTTAAAGAGCGGACSGAGTAC
CHUK	11962	rs11595324	G/A	10	reverse	AAATAAAAATTAATAGCCACCTGTATTCA[A/G]TTTTTACCATGTACCAAGCACTGTGTTA
CHUK	12184	rs17886121	T/C	10	reverse	AGCCCAAGGTCCTCACCCTACCCTGTCTA[C/T]AGCCTCGTAAGGATATTGTTGTCTTTCC
CHUK	14883	rs11591741	G/C	10	reverse	GTGTACCCAGAAACAACCTCTCATCAATAGT[G/C]TTTACATTTGTATTGATTGTTGTAGTA
CHUK	15958	rs17112745	C/T	10	reverse	AGTTACTGAAATATTTCCCTTTTGAAAAA[C/T]AGCTTAGCAAGTCTGATTGTATGCATAT
CHUK	27073	rs17880383	T/C	10	reverse	GAAAGCTAAATTGGAGTTTTTTCACAAAAG[C/T]ATTCAGCTTGACTTGGAGAGATACAGCG
CHUK	28086	rs7923726	C/A	10	reverse	CTAAAAACATATACTTGTCTGAGCAAACCT[A/C]TGTGTATCTCAGAGTAAACAATCAATAG
CHUK	30214	rs17885986	T/C	10	reverse	CCTGGGACTGTCCAGTTTATACTTAATGT[C/T]TTGCCATAATTATCAGTAGTAGTCCCTT
CHUK	36383	rs7358099	A/T	10	reverse	TGCATTTAGGCTTAATTATTGTCCAAAGAA[A/T]ATACCAGCATGATGCATAAGCAACTTTC
CSF3	1158	rs2227319	A/G	17	forward	GTGTCCACTTCAAGGTGAATGACCAGGGAA[A/G]TCACGTGTCCCAATCCCGCAGTTCCAAA
CSF3	2504	rs2227324	G/A	17	forward	ACTGCAGGGCCAACATCCTCTGGAAGGGAC[A/G]TGGGAGAATATTAGGAGCAGTGGAGCTG
CSF3	4050	rs2827	T/C	17	forward	CTGGGGTCCACGAATTTGCTGGGGAATCT[C/T]GTTTTTCTTCTTAAGACTTTTGGGACAT
CSF3	4215	rs1042658	T/C	17	forward	GGCAGGTGCCTGGACATTTGCCTTGCTGGA[C/T]GGGGACTGGGGATGTGGGAGGGAGCAGA
FOS	1058	rs2239615	T/A	14	forward	CTCGTACTCCAACCGCATCTGCAGCGAGCA[A/T]CTGAGAAGCCAAGACTGAGCCGGCGGCC
FOS	1651	rs4645854	T/C	14	forward	CACAACTCGCTAACTAGAGCCTGGCTTCT[C/T]CGGGGAGGTGGCAGAAAAGCGCAATCCC
FOS	2376	rs4645855	A/G	14	forward	ACTCTAGCGTACTTCTCTGGGAATGTGGG[A/G]GCTGGGTGGGAAGCAGCCCCGGAGATGC
FOS	2765	rs4645856	C/T	14	forward	TACTGAATGTCCGGTCTTTTTTTGTGATTAT[C/T]CTAGTTATCTCCAGAAGAAGAAGAGAAA
FOS	5382	rs4645869	A/G	14	forward	GCCCTATCCCTTATTAATAAATGCATTGTG[A/G]TTTCTGGTTTCTCTAATACCATATGCC
FOS	5506	rs4645870	T/C	14	forward	AAACAGCACAAATAATGGCTGATCGTTCTG[C/T]AAACAAAAAGTTACATAATAGCTCAAGA
IKBKB	2581	rs3747811	A/T	8	forward	AAAAAACCAGTTGTATTTTTCTTCTCTCCC[A/T]TCAAGAGCAGTGGTATCTCTTGYCTTC
IKBKB	8758	rs17875741	A/G	8	forward	TAGTAGAAGTCAGCTTGACAGAGAAGGKGG[A/G]AGGAGAGTTCCAGGCCAAGGGAGAGGCT
IKBKB	13627	rs5029748	T/G	8	forward	TCTATGCCAGTATTTTCAAGACTTGTTC[A/G/T]GTTCACATTGCTGAGTTCAGTCTTTTT

IKBKB	18383	rs17875672	G/A	8	forward	TAAATGGCACAGTTGGAATTTGAACCAGCC[A/G]GTGTTTCATCTGCTATATTATGCCATAT
IKBKB	36666	rs10105951	C/G	8	forward	CAAGTCTGGGTTTAGCTGTCTTGAGGGGTG[G/C]TGCCCTGTTCTGTTCAATCAGCTTCCCTC
IKBKB	46756	rs17875746	T/G	8	forward	CTGTGTGTATACTGGGAGACGCACACTGT[A/G/T]CCCAACATTGGCTGGAAGTGTCTCCTCA
IKBKB	59283	rs10958715	A/G	8	forward	TTATAGAAAAGAGAGAGATCAGATTAGATG[A/G]AACCAATCCCAGAATTGATTTTCAAC
IKBKB	60792	rs6474389	G/A	8	forward	GTGAGTGCTGTGAGCCACAGTGGTACTGAC[A/G]TCGACTTTCTAATCCCACAGTCACAGA

SNP

Gene	Location	dbSNP	Alleles	Chr	Strand	Flanking Sequence
IL10	213	rs1800894	A/G	1	reverse	CAGTAGGGTGAGGAAACCAAATTCAGTT[A/G]GCACTGGTGTACCCTTGACAGGTGATG
IL10	1927	rs3021094	C/A	1	reverse	CCAGATTTTTTAAATAAATTGACTCTGAGG[A/C]GGAGGACCTGATTTAAGTGATGGTCCCA
IL10	2911	rs3024493	T/G	1	reverse	TAACTACTCCCTCTCTCTTCATAAAAGGA[G/T]CCAGAGCTTCAGTCAGGCTCCACTGC
IL10	5351	rs3024498	G/A	1	reverse	TGTCTCTGGGCTTGGGGCTTCTAACTGCT[A/G]CAAATACTTTAGGAAGAGAAACCAGGG
IL1B	3298	rs3917356	A/G	2	reverse	CAGCCTAGCTAGGTCAAGTTGTGCAGGTTGG[A/G]AGGCAGCCACTTTTCTCTGGCTTTATTT
IL1B	4392	rs3136558	C/T	2	reverse	AGCCACCACGCCTGGCCAGAGAGGGATGA[C/T]CTTTAGAAGCTCGGGATTCTTTCAAGCC
IL1B	5277	rs1143634	T/C	2	reverse	TGTGCTCCACATTTCAGAACCTATCTTCTT[C/T]GACACATGGGATAACGAGGCTTATGTGC
IL1B	7114	rs1143642	T/C	2	reverse	AAATAGATGACTTAAAGGGTCCCATTATCA[C/T]GTCCACTCCACTCCAAAAATYACCACCA
IL1B	12885	rs3917368	A/G	2	reverse	TGCAATGCGTAGTCTGTAGGGACAGGCTGT[A/G]GCTTATCCTATAGGCTTGGGCTGGAGTC
IL1RN	1018	rs4251961	C/T	2	forward	AGCCCTAAGTCTAAGATAGGGCAGATAGCA[C/T]CAGGTCCATTTTGAGCTGTCAAATGA
IL1RN	2765	rs315919	T/G	2	forward	ACAATAAAGCAAGCAGATAAAATATTTAA[A/G/T]TATAAGCTGCCAGTTTGAACCTCCGGT
IL1RN	5848	rs3213448	A/G	2	forward	TGATCCCCTTCATCATCCAGGAGAGCAGAG[A/G]TGGTCACCCTGATAGCAGCAAGCCTGGG
IL1RN	10257	rs315934	C/T	2	forward	AGCCATCRTTTTGAAACACGTTTGAGAAA[C/T]AGTGTCTTCCTTTGAGGGCCAAGGAGAC
IL1RN	13888	rs2232354	G/T	2	forward	GCAGCATGGCCTGCCTGCACAAACCCTAGG[G/T]GCMATGTCCTAATMCTTGTGGGTCTTT
IL1RN	15132	rs432014	C/T	2	forward	AAATACCCRGGGTCTTTCATTATTGCTGC[C/T]TCCTCTTCTATTAACCTGACCCTCCCT
IL1RN	15453	rs380092	T/A	2	forward	CACTTTGGAAGCTGCATTCAGCAGAGTGCC[A/T]GGCTTGCCTGGGCAATCCAAGGTGGTCC
IL1RN	17163	rs4252041	T/C	2	forward	TCACAASAACCTGGTCACAGGACTCTGCCT[C/T]CTCTTCAACTGACCAGCCTCCATGCTGC
IL6	95	rs2069824	C/T	7	forward	ATGCAGGAAAGAGAACTTGGTTCAGGAGTG[C/T]CTACGTTGCTTAAGACAGGAGAGCACTA
IL6	321	rs2069827	T/G	7	forward	TAAATGCCAACAGAGGTCACTGTTTTATC[G/T]ATCTTGAAGAGATCTTCTTAGCAAAG
IL6	3114	rs2066992	T/G	7	forward	YTTTCTGGCTGTGGTTGAACAATGAAAAG[G/T]CCCTCTAGTGGTGTGTTTTAGGGACA
IL6	3437	rs2069840	G/C	7	forward	AATGTTATGTAATTTTCATGAGGAGGCCAA[G/C]TTCAAGCTTTTTTAAAGGCAGTTTATTC
IL6	5014	rs2069845	A/G	7	forward	AAGGTGTTTCCCAGTCTCTTTACACCACC[A/G]GATCAGTGGTCTTTCAACAGATCCTAAA
IL6	6021	rs2069849	T/C	7	forward	TCATCTCATTCTGCGCAGCTTTAAGGAGTT[C/T]CTGCAGTCCAGCCTGAGGGCTCTCGGC
IL8	2968	rs2227532	C/T	4	forward	ATTCTGCTCTTATGCCTCCACTGGAATTA[C/T]GTCTTAGTACCACCTGTCTATTCTGCTA
IL8	3470	rs4073	A/T	4	forward	TAAAGTTATCTAGAAATAAAAAAGCATACA[A/T]TTGATAATTCACCAAATGTGGAGCTTC
IRAK1	6151	rs1059702	T/C	X	forward	CAGTGTCCCTCCTGCAGGGAGCCCRCCCCT[C/T]TCCGTTTTGCTGGCCCCCTCWGTGAGATT
IRAK2	5352	rs11465853	C/G	3	forward	GCCGCCRCTGCGCTCTGAGTCCAGAGAACG[G/C]TGGGTACGGGGCCCTCCTGTCAGCGCT
IRAK2	17525	rs11465861	G/T	3	forward	TTCTGGGGAAGTAACAGTGAACCAACAGG[G/T]AGAGCTCCCTGCCTACAGGACCTTCCA
IRAK2	18096	rs1681663	A/G	3	forward	TGAACTGTGAGTAACTCAGGGCCCTCCTT[G/A/G]GTGGGGCCCATCACGCTCCTGAGCAGTT

IRAK2	29090	rs155266	A/T	3	forward	ATGAAAACACAGCCAAGGTCTCAGGCCTCA[A/T]GGAGCTTACAGTCCASTGGGAGATGAAT
IRAK2	40262	rs263409	G/A	3	forward	GTCTACYGCATTTTACAGATGGGGAGGCCG[A/G]GGCCAGAAAGGGAAAGACCCTCCCGCCC
IRAK2	40350	rs263410	A/C	3	forward	GAATTAGAACCCAGGTCTSTGACTTCCAGA[A/C]CCAGTCTCTCAATGGCTACCCCACTTCA
IRAK2	45753	rs11465883	C/T	3	forward	GTACACAGAACCTGGGTGTTAGCACAAATA[C/T]AGATCATGTGTAGAAGAACTAGGGACTT
IRAK2	49325	rs1169674	T/A	3	forward	GAGATAGTGCAGGGCCTAGAAGTCAAACAG[A/T]TTCCGTCTGAATTCGGCTCTACCATC

SNP

Gene	Location	dbSNP	Alleles	Chr	Strand	Flanking Sequence
IRAK2	49704	rs464286	G/C	3	forward	CCAGCCTCCTGAAGAAGATGCCCTCATT[G/C]TTGAGAAGCGACCTCCCCACTTCGTCTG
IRAK2	53160	rs11465897	A/C	3	forward	TACAGTTTCCATTGGATAAGTTGATCCCCT[A/C]CATCCCTCCATCTCTGGTGTCCAAGGT
IRAK2	57504	rs6780464	A/G	3	forward	YRTCATGGTTCTGGAGGTGTTAGCCAAATGC[A/G]GTAGGACAAGAAAAAGAATTAAGAGGTA
IRAK2	62841	rs3844283	C/G	3	forward	CTGCCAGAGGATTTTATCCGGGTGGGGMAG[G/C]TGACAAAGCGAGTGGACATCTTCAGCTG
IRAK2	73835	rs776514	T/C	3	forward	AAAAGACTATTGAATGTTCCGTGTCAGATR[C/T]CACTCTCTGTGCTTTAGGTGCACTGTTT
IRAK3	3600	rs1732887	G/A	12	forward	YAGATACATTTTTATGAAGATTTTCGCTG[A/G]CAAACCAATTCAGGTAGGGGCATGAAAT
IRAK3	5719	rs11465939	G/T	12	forward	ATTTTCTTAATTAATCTTATTTACCCAAT[G/T]TCGTTGAATGAAGGTTTATGCTAAAGRG
IRAK3	26988	rs2293657	T/A	12	forward	GCTGATCTCTTTGAGAGGAGGTAAAAATC[A/T]CAATGCTGCTGTCCGAAGAAACCCTTTG
IRAK3	27210	rs1152888	A/G	12	forward	TTATCTCCCCCTACTTTCCTTCCCTAAGGA[A/G]TACTGCTTAAATCTTCCATCAGCTTTCA
IRAK3	55668	rs11176095	C/T	12	forward	GKTTTTTCTGTCTCTCCATTGTCTTAAAA[C/T]GTCTGGAAAATACGTTTGCCCAGAACTT
IRAK3	55891	rs1152912	A/G	12	forward	AATGGACATAGGATGGACAATGGCCAGCCT[A/G]TATCCTTTAAAGCATACTTGTAGCCCTC
IRAK3	64458	rs11465990	C/G	12	forward	CCCTCTTGTTTTTGGTTAATCCCTGACTA[G/C]CCTGCTTGTCTGAAAATGAGCCAGGTTT
IRAK4	3536	rs4251429	C/G	12	forward	CCATGTCCTTGCTGTTGCCAGTGGGCCCA[G/C]TTCCAACCTTGCATTTACATTTGTTTT
IRAK4	11902	rs4251460	C/A	12	forward	TCAGCATTAATCTGGGAAAGAACCTAAAAG[A/C]CTTGGCTCCCTTGCAGGAAATTTTCT
IRAK4	13823	rs1461567	A/G	12	forward	GAGCTTTGCCCTTATGAGTGGATTAATGTC[A/G]TCATGGCAGGAGTGGGTTAGTTATCTAG
IRAK4	23338	rs4251513	C/G	12	forward	GGAAGGATCCAGATTTAAAGGGAGAGGATA[G/C]TATGGAAGAGAGAAATGAGATGATGTGT
IRAK4	24472	rs4251520	C/T	12	forward	CCTGGAGTGCCTTTCTTCCCTCATATAAC[C/T]ATTAACCTCTAATAATCCTTCAACTA
JAK3	290	rs2110586	A/G	19	reverse	TGATTTTATTTCTATAAAGGGCAAACCTAG[A/G]CATCAATCTCTCTGTGGGAGAGATGGGG
JAK3	575	rs3212701	A/G	19	reverse	TGACACTTTAGGCCTGGATTGCGCTCAGCA[A/G]ACCACCTCAATGAGGATGCTGGGGAGTC
JAK3	6427	rs3212741	T/C	19	reverse	TCTCTCTGTCTTCTTCTATCTCTGACTCCT[C/T]CCCATTCCCTCTCACCTTCCCCACAGT
JAK3	8873	rs3212752	G/A	19	reverse	CAAGCACAAGAAGTGCATGGAGGTGAGAGC[A/G]ATGTGGACCAGACTTTTGGAGTCGGGGC
JAK3	10196	rs3212762	C/T	19	reverse	AGAGGGGTGTTCTAGGCAGAGGACACMGAA[C/T]ATGCAAAGGGTTAGAAGTGAATACAGA
JAK3	11552	rs2072496	T/C	19	reverse	CAAACAGACTCTTCATTCATCAAACCTCC[C/T]GGGCATTTTCTGTGTCTGGCCCCCTTA
JAK3	11910	rs3213409	A/G	19	reverse	GGCGCCACGGTCTGGGAAGTGTGTTAGTGGC[A/G]TCACCATGCCATCAGTGCCTGGATCC
JAK3	16765	rs3212780	T/C	19	reverse	GGCCGGGTCTCGGGCAAGCCAGCTGGCGC[C/T]TGAGTCTCTGTACTGAGAAGAAAGGSTA
JAK3	19853	rs3212798	A/G	19	reverse	ACRCTGAATGGGAGTTGTGCTCTTTGGACT[A/G]CTCAGGCACGACCCCAATTATCTGTCCCC
JAK3	20182	rs3008	C/T	19	reverse	TGAGGGTCTCTACTTCAGGAACACCCCCA[C/T]GACATTGCATTTGSGGGGCTCCCGTGG
JUN	535	rs2760501	C/A	1	reverse	TTCCGTGATTTGCTTGCTTACACTGTGGT[A/C]GCCTGGCCACGAAAGAACCAGGATCCC
JUN	3641	rs11688	A/G	1	reverse	GCCCCTGTCCCCATCGACATGGAGTCCCA[A/G]GAGCGGATCAAGGCGGAGAGGAAGCGCA

LBP	548	rs1780616	T/C	20	forward	TGCTCAATAAATATCAGTTTCTTTCCAATT[C/T]CTGCTGGGTGCTGCAAGGATCTCAGGAA
LBP	1605	rs5741812	T/A	20	forward	TACCCCCACAACCAGAGACAATGCCTCATG[A/T]CTCCTTGCTAAATATTTCCAGATTGTT
LBP	1763	rs1780617	G/A	20	forward	ACCTTTAWTTCTGCAGCCTCACTTTAAGGG[A/G]CATGTCATAATTCATTTAACCAATGCC
LBP	1900	rs2232573	C/T	20	forward	GATTTACTGGCACACTGACTCAATTATGTA[C/T]TTAAGGGCAAGTCCCTGAAATTGAATTC
LBP	2321	rs2232578	G/A	20	forward	TAGGAGTCAGGCTTCTCATCCACTGATCT[A/G]GGCAGTGAAAAGTGGCTTCTAAGTATGA

SNP

Gene	Location	dbSNP	Alleles	Chr	Strand	Flanking Sequence
LBP	10548	rs5744204	A/G	20	forward	CCTCCAGCTGCAGCAGTGACNATCGCTGAC[A/G]TGGAGGTGGACATGTCCGGGAGACTTGGG
LBP	17119	rs1780623	T/C	20	forward	ATATTTGTAAATCAGTGATCACTGAGCAC[A/C/T]GTGTGGAATAATGTGACTGCAGTGATCA
LBP	20377	rs2232599	C/G	20	forward	GTTAACTCANTCCAAGGGAATCCATGTAGT[G/C]TCTTTCTTGAAGAAGCAATCTTTGCCCT
LBP	21126	rs2232606	G/A	20	forward	CTSCCCACGATAGGCTTTGAAAAGNTCCA[A/G]TTGGACCCTATTTCCCTCTCCAGGGTGA
LBP	23297	rs1739639	T/C	20	forward	GGAGAAGCGACAGTCTTGACATCCCCCTG[C/T]CTCCCAATCTCTTTAGACCTTCAGCT
LBP	27937	rs2232616	T/C	20	forward	GCATTGCTTAAACTTGATAAAGCCACAC[C/T]YTTTNAATCTTCTCTGATTACATTACAGG
LTA	2619	rs2229094	C/T	6	forward	CCACCTGAACGTCTTCTCCTCCCAAGGGT[G/C/T]GTGGCACCACCCTACACCTCCTCCTTCT
LTA	2847	rs1041981	A/C	6	forward	AGCMCCCAAGATGCATCTTGCCACAGCA[A/C]CCTCAAACCTGCTGCTCACCTCATTGGT
LTA	4545	rs1799724	T/C	6	forward	TGGAAGTCGAGTATGGGGACCCCMCTTAA[C/T]GAAGACAGGGCCATGTAGAGGGCCCCAG
LTB	2222	rs3093553	C/A	6	reverse	GAGCAGACTGTCTCTCCTTCCCCGCTTCA[G/A/C]CCCTCAGGGGCTCCAGCTCCCTGCTGC
LY96	440	rs1812615	T/A	8	reverse	GAGACTTTATCTCTAAAAAATGAAAAA[A/T]TCACACTTCTGTTGTAATAATTTTTACC
LY96	874	rs11465996	G/C	8	forward	ACTGTTTACTTCAGATCTATAGGTGCAGCT[C/G]TCTGGCCATGATAATTTGATTTGTTGT
LY96	40185	rs11466004	T/C	8	forward	TTTTGCTTGGAGTTTGTATCCTACACCAA[C/T]CTAATTCAAATTAGAATAAATTGAGTAT
MD1	2422	rs977785	A/C	6	forward	CTAAAATTTGAGAAGTGAAACTGAACATCC[A/C]ACTGCCTTGGTGAGGGGAGAGGAAGAAA
MD1	2889	rs3765286	C/T	6	forward	RCAAAGAGTACAAGAAAGAGAAATTGAATC[C/T]AAATATAGCCATTTACTAACACCACAGA
MD1	63232	rs5743650	T/G	6	forward	CCGACCAATATTTGTGGCATGAATGAATAA[G/T]TGAATGAATGGTAGGTGTAGATCAGGAA
NFKB1	37516	rs230525	G/A	4	forward	AAGATTACGGGAAAAGTGATTCTTGTTTAC[A/G]GAGCCCTCTTTCACAGTTTCATGTTTTT
NFKB1	39746	rs4648004	G/A	4	forward	AAAACAAGGGAGAGAGAGGGCTCACTGGTCA[A/G]TGGGTACTCAGGTATTGGGGAAGCCAGG
NFKB1	40198	rs4648006	T/C	4	forward	CAGTCACAAAATAATTTACAAATGAAACAA[C/T]TAGTGGGCATTAGATGTTCTGTAGAA
NFKB1	40458	rs4648009	T/G	4	forward	AAGCTGTCATTGTTCCCTTAGCTTGTGATT[G/T]TCACTGAAAATTGAAATGTTCTGCTG
NFKB1	94202	rs4648057	T/C	4	forward	TTRCTACGTCAGAGGGCATGACATCTAATG[C/T]CATCTGTTTTCCCAAAGATTSTACCAS
NFKB1	98030	rs4648075	A/G	4	forward	AACATTCCAAACACCATGCCTTCCATTCTT[A/G]CTATTACTGAGATTGATTTGCAAAGCC
NFKB1	105701	rs4648090	A/G	4	forward	AGCATAGAATCATGGCACTTTTGTAAATTG[A/G]TTTCTATTGACTTTATTTAAATTTT
NFKB1	114547	rs4648127	T/C	4	forward	CCTTCARCTTCAGACCGTCTCCATTCTGG[C/T]TCCCTCCACAGCACACTCCCCGGCTGGC
NFKB1	114680	rs4648130	T/C	4	forward	AAGCCCAATACTGGCTRCATCTGTCAGWAG[C/T]GCTGCCATCTTCCAGGAGATTAAGACAA
NFKB1	114903	rs230547	T/C	4	forward	CTCCCTTCAGTCCATTCTCTGCCAAACAGA[C/T]GGTATGATTCTTCTAAAAAATCAGTGAC
NFKB1	115543	rs4648141	A/G	4	forward	AACAAATCAGTCAATACCAAATGATAGTY[A/G]TGCCACTGGCATTAAAGTCTTAATTTT
NFKBIA	1665	rs2233409	T/C	14	reverse	TCGATCGTGGGAAACCCAGGGAAAGAAGG[C/T]TCACTTGACAGGGGACAGGATTACAGGG
NFKBIA	4754	rs8904	T/C	14	reverse	TGTTTGGAGGCCAGCGTCTGACGTTATGAG[C/T]GCAAAGGGGCTGAAASAACATGGACTTG

NFKBIA	5519	rs3138055	G/A	14	reverse	GCTGTTTGGCCTGTGGTTGGAGACCTCTCC[A/G]TTGTCATTCTGTCATCCCGTTGATTTAA
NFKBIB	1198	rs17884442	T/A	19	forward	CGGGGCAACTTATGTTCTTTGCAGCGAGGG[A/T]CCTTAGCAACCAAGGTGCGAGAAACACG
NFKBIB	2243	rs2053071	G/C	19	forward	TTCCTCATTAACTCTGATCCCTGAGGCTT[G/C]CTAACCTCATACTCCTAAATCTGACTTC
NFKBIB	3130	rs12979755	T/C	19	forward	TGTATGCCAGTGATGCAAGCAGGGCCTGA[C/T]CCAGGAGGCACTGAATATTGATCTCAAC
RAF1	46239	rs4684867	C/T	3	reverse	CAGGGCACTGACACCAGCCACTTAGTTCTG[C/T]GTAGTTTATTTTTTCAGTGCCAGTGACA

SNP

Gene	Location	dbSNP	Alleles	Chr	Strand	Flanking Sequence
RAF1	51933	rs5746195	C/T	3	reverse	GAAGGATATTTTCCCCAATTAATATATCA[C/T]GGACTCCTCTCCATCCAGGTCATTATAA
RAF1	59734	rs2648367	G/A	3	reverse	ACTCTCCTTTTCATTGAATCCCAATACAT[A/G]TATTATTTCCGTGTTCCAAATTTTGATG
RAF1	64217	rs2246390	T/C	3	reverse	AATAMATTCAATGAAGGAGATTATAAATGT[C/T]ACTGTCTATTTTGGCACACTTGCATCAG
RAF1	64310	rs5746223	G/A	3	reverse	CTCAAAGACAAAAATTGGAAGTATGGTTA[A/G]TATGTTTATCTTTAAAAGATATGGAAAC
RAF1	79220	rs3729931	T/C	3	reverse	GTTAGGACTTGTATTATCTGTTGTTTATT[C/T]ACCCCCATTAGCTCAGCTGTTTTCTTT
RAF1	79989	rs1051208	T/C	3	reverse	CCATGCTCAAGGCCAGCCTTCTGTAGATG[C/T]GCAAGTGGATGTTGATGGTAGTACAAAA
RELA	8813	rs11227247	G/T	11	reverse	TCACCTCTAAATTAGCAAGATGTGTGTGCC[G/T]GTGCGAGGCTCAAAAAGTACAAAGCTCT
RELA	10549	rs1049728	G/C	11	reverse	AGTTTTTACTGAACAATCAAAGCACTTGGG[A/G]TCTTGCTCTTTCTACTCTGAACTAATAA
RELA	10906	rs10896027	C/G	11	reverse	CAGCTGAGAGTGGATGTCAAAGAGGGACTA[G/C]CCAGCGTCAGAGGTAAGAGAAACGATGT
STAT1	4377	rs10195683	A/G	2	forward	TCCATCTAGAAGGAAAAGTGAAGCTGTGGGT[A/G]AGGTCATCACAGCACAGCGTTTAGGAGA
STAT1	4798	rs36234022	C/T	2	forward	AGCACGTCCTTCTGATCGTTCTCTAAGATA[C/T]GTAACAGAACGCCAGTCCAGCGTGG
STAT1	5450		G/A	2	forward	AAGAGGACTTGTGAAATATAATTTTCTCT[A/G]GAAGGCACTGCACCTCCCATTTACCGT
STAT1	8902	rs36077929	A/G	2	forward	TGAAGAAAAATAAACCAGGGAAAAGAGAGA[A/G]CATGTTTCCAGGGTGGGAGGTGGTTGCA
STAT1	9270		C/T	2	forward	CTAAAATTCCTGGAGCAGGTTCCACCAGCT[C/T]TATGATGACAGTTTTCCCATGGAATCA
STAT1	28422	rs7562024	A/G	2	forward	GATGGATTTATAGCTTTTATCAGTTTCTCA[A/G]AGCAGTCCGTGATATAAATATCTGTGGA
STAT1	33177	rs2280232	G/T	2	forward	GCTCAGAGATTGACGTCCACTTGAGGGCAG[G/T]TGGACCTGGAGTCACTGGGCCAGCCTG
STAT1	33377	rs2280233	G/A	2	forward	CAGACTGGTGTCCGCACCATGAGGCCACTG[A/G]GGAAACGTGCTTCTGCTCATGGACCCTG
STAT1	37953	rs3755312	C/G	2	forward	AAGTCAAGTATCAGTTACATTGAAGATCTA[G/C]GGGTGATCTTGGGCACCTAGGTTGAACT
STAT1	40500	rs13010343	T/C	2	forward	CAGATCTTATACTTACCCCAATGAGCCCC[C/T]GATAGGATTTAATAAACCACCACAAATG
STAT1	43236	rs17749316	C/G	2	forward	CCTTAAAGTTTTAGGAGGCTAAGCTGTCTA[G/C]AAACACAGTAGAACTTAATCCCCCGA
STAT1	48027	rs7575823	A/G	2	forward	AGGCAGCTGGGCAGAAGGCACTGGTGGGA[A/G]GGTGAAGGGTTCTTAGTAATTCTGCTT
STAT2	11773	rs4759016	G/T	12	reverse	GGCACAACAAGGAAGAGGGGATTTGGGA[G/T]ATGGACAAAGGAGATGGCGAGATCTGA
STAT2	15182	rs2066807	C/G	12	reverse	CCAGGAGCGCCGGCTGCTGAAGAAGACCAT[G/C]TCTGGCACCTTTCTACTGCGTTCAGTG
STAT3	47616	rs8069645	C/T	17	reverse	GAAGATCATGTTCAAAGACAGAAACAGAAA[C/T]GTGTATTCTTGGGAGAAGGTAGAAAGT
STAT3	50838	rs2306580	C/G	17	reverse	TTTGAATTTTTTGACATACTTGCCCATGAG[G/C]TTTTTGAAGGCATAGACCATGTCTTAGC
STAT3	60990	rs2293152	C/G	17	reverse	AGCTCCCCTTACAAAAGGGCCTCTGGCTGC[G/C]GGAGAGGGCTAGGGAGAGCCTCACAGGA
STAT3	65854	rs17881940	C/G	17	reverse	ACCCGCCAGAAAAGGGATCCGGCCCATAG[G/C]GCTGTTTATTGGGCCATGTCTACTGAG
STAT3	67661	rs8064496	C/T	17	reverse	GCAAAACACATTTGSGTGACTTCTAAATCC[C/T]TCCAGCTGAAGGATTGTTTGTCTTTGTT
STAT3	74526	rs17882369	A/C	17	reverse	GTTAAGGTGGGAATGAGAAAGGACCCTTCC[A/C]GAGGCAGGGTCTCCAGGGAGGAGGGTA

STAT4	13429	rs3024847	A/T	2	reverse	CTTTAGGAATAACATTTTAAAAAGAGAAGG[A/T]ACTTTGACAATAATTCAGTTCATTCAAC
STAT4	14441	rs932169	G/C	2	reverse	TCACATGCAAGATATCAATCGTAAAAGACT[G/C]GAATAAAATTTTGAAACCAGCAATATACT
STAT4	14897	rs3024851	A/T	2	reverse	TAATACAAGCTGGCATTCCCAGTCTATGTA[A/T]GCACACATGCAATGAAATGTAGATACTA
STAT4	19113	rs3024861	A/T	2	reverse	GGTATAAAAAGGAAGGTGGAGAGGAAAAAC[A/T]TCTGGCCTGATTTTATGTGACTATGCC
STAT4	38829	rs3024877	A/G	2	reverse	TGACTATGYGCTCCTTGAAGGCAGGACACC[A/G]TGAATSAATCAGTGCATGAATGAACAAA

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STAT4	39162	rs3024879	T/C	2	reverse	ATAAAGTAGAAAACCACAGAACCAAGAGTA[C/T]TAAATTGAGTTAGTTCTGTAACAATAGC
STAT4	46178	rs925847	A/G	2	reverse	ATCTAAGGGCATGTGGAGGTCAAAGCCTTA[A/G]AAATGAAGTGGTATGTCAGCAGTTCCTG
STAT4	48516	rs3024904	T/A	2	reverse	TGCATTTCTAGAACCCGGAGCCTCATCAAT[A/T]ATATATGAATAACAGTCAATGGCATAAT
STAT4	50631	rs3024912	G/T	2	reverse	CCTGCCCAAGGCCAGTTCCTTTACTCCTT[G/T]GTGAGCGCCTAAATGCTTTTAGGGTGGGA
STAT4	52147	rs3024919	A/C	2	reverse	TTGCAGCAGCAGCCCCAATCCCATGGCTCC[A/C]CTAGGCATTACCCAGAGAGGACACTCT
TIRAP	3846	rs8177349	A/G	11	forward	GCGGCTCCCCTTTCGCTTGCCTCGCTGGAA[A/G]AGCCTGGCGCTCAGTGCCTTGTGGATAT
TIRAP	4346	rs8177352	G/A	11	forward	CATTTCTGATTCAGAGCAATCAATAAAAC[A/G]TGACTACATCCCTGGCTTCTAACGCCAT
TIRAP	7482	rs595022	T/C	11	forward	CCCCATCACAAGGTTCTTAATCACAGCTGC[C/T]GAATCCCCTTTTGCCACGGAAGGTAACA
TIRAP	9537	rs646005	C/T	11	forward	GTCTTCTCTGGTTCCTGTACCCATTCCAAC[C/T]CTTTGCTCTGCCTCCTTTGCTGCTATGG
TIRAP	13365	rs7932766	T/C	11	forward	CCCCCTGCTGTGCGCCCTCAGCAGAGCTGC[C/T]TACCCACCTGAGCTCCGATTCATGACT
TIRAP	14194	rs611953	A/G	11	forward	AAATGTGACAAGAGGTATAGGGAGTGAGTY[A/G]CAGCGCTTTGCTCGTGACCCTGGGATCA
TIRAP	15935	rs4937116	T/C	11	forward	CTTTGTGCCCTGAATTGCAGTCTCCCCTT[C/T]CCCACCAGAAATAACCAGCATTTTGAAT
TIRAP	16971	rs8177382	A/C	11	forward	TCAATAATACCCTACTCATATCTCTCACTC[A/C]CCACAAGATCATTTGAAGCAAACCTCAG
TLR1	1260	rs5743551	G/A	4	forward	TGGGGAAAAACAGGAATTCAGAGTGTGAG[A/G]AGCTTCCCTTACTGCCCTGCCCACTTCC
TLR1	1725	rs5743553	A/T	4	forward	AGGCAGTCAGCTGGAATCCCATAGCTTTAT[A/T]TGCCCATTTATTGTGTTGTTATTTTGT
TLR1	3076	rs5743567	T/C	4	forward	AGGCCACTAACACTGTTCTGGGGAGCTAGA[C/T]GTGAGGTAGAATTGCAGGTTTTGAAAAT
TLR1	6165	rs5743594	T/C	4	forward	AGGATTTCAACATAAGAATTTACAGGGCA[C/T]AAACATTCAAGCTATAACATCCATTGAA
TLR1	6752	rs5743599	T/C	4	forward	CATCCCAACACAGCTCCCTCTGTTCTCATA[C/T]GCCACTGGAATGCTGACCACAAAATGGT
TLR1	11040	rs4624663	G/A	4	forward	TAACCTTGATTTAAACAGTTCTGACACATA[A/G]GGGATCCACTTGTCTTTGCTATAACT
TLR2	7884	rs2083287	G/A	4	forward	ATATAAAAACCTTGTCAGATGCACCTAAACT[A/G]TTGCTTAAAGGAAACTTACAACTTAAG
TLR2	21502		A/C	4	forward	AATATAGTGTGTTGCTGGTATAGGGATAGA[A/C]AAATGAACATTGGATCAGAATAGCACTG
TLR2	24212	rs3804099	C/T	4	forward	TGAGCCAAAAAGTTTGAAGTCAATTCAGAA[C/T]GTAAGTCATCTGATCCTTCATATGAAGC
TLR2	24965	rs3804100	C/T	4	forward	TTTGAACTTATCCAGCACACGAATACACAG[C/T]GTAACAGGCTGCATTCCCAAGACTGG
TLR4	851	rs2770150	G/A	9	forward	TTGACACATGGTCTGCCTTCTGGAAGAGCA[A/G]CATAGAACCTAGATGTCTTTGATTAAGG
TLR4	7260	rs7864330	G/T	9	forward	AGCAGACATACGAATGAAGATCTGCATGTT[G/T]GAACTCTGACTTTGCGCATATTACTTCA
TLR4	7764	rs1927911	A/G	9	forward	ATCACTTTGCTCAAGGGTCAATGAGCCAAG[A/G]AAAAGAATGCAGTTKCAAAATCTGGGC
TLR4	9263	rs11536878	A/C	9	forward	GGTGATAAATTATGTTTAAACTAAAGGTAA[A/C]TAATTGTATTTTTCAGAAGAGGGCCTT
TLR4	10478	rs1927907	T/C	9	forward	TTTTTTTTTCAAACAAGAAGTAGTTTTTCA[C/T]YAAACAATGTCTCTTATGTAATTCATCT
TLR4	15745	rs7869402	T/C	9	forward	CACAGATGGCTGGGATCCCTCCCCTGTACC[C/T]TTCTCACTGCCAGGAGAACTACGTGTGA

TLR4	15844	rs11536889	C/G	9	forward	GGGCAATGCTCCTTGACCACATTTTGGGAA[G/C]AGTGGATGTTATCATTGAGAAAAAATG
TLR4	17723	rs11536897	A/G	9	forward	TTCTGCATAAGTGTGTTTTATTCAAGCAAAT[A/G]TACAAGGCTCTGAGAAGGAAGATCAACA
TLR4	17828	rs1927906	C/T	9	forward	GCCTCCTTCCATCAGTTCCTCTCCCAGA[C/T]GGAAATCTAGAAATGGCAGGTGAGGTG
TLR4	17923	rs11536898	A/C	9	forward	AGGAGAAGAAAGAGTAAAGTCAGGCCTCAG[A/C]CAGCCTCTTTTTAGCTCTTTAATCCTC
TLR5	3048	rs5744105	G/C	1	forward	CAGCAGGGCCATGGAAATCCCAGAAAGTCA[G/C]TGAGCTGCTCAACAAAAGGCCCTAAACA

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TLR5	3645	rs5744109	C/T	1	forward	CCNATGTGGTTTCATCAATTTTCTCCTGCA[T/C]TTACCCAGCCCCCTCCGAATTCTGAGAAG
TLR5	34054	rs5744168	A/G	1	reverse	TTCCTGGAAAAATTACAGACCTTGGATCTC[C/T]GAGACAATGCTCTTACAACCATTCAATT
TLR5	34655	rs2072493	G/A	1	forward	TTTGTGAATGTGAACCTTAGCACTTTTATCA[A/G]TTGGCTTAATCACACCANTGTCACTATA
TLR5	35403	rs1053954	G/A	1	forward	ACTCTCTCAACAGATACTAAAGAAAGAAAA[A/G]GAAAAAGAAAGNCAATAACATTCCGT
TLR6	1166	rs5743795	A/G	4	forward	TGCAAGGTTTGTGTTATTTTCAGGGCAAAC[A/G]TAGAGCAAGTCCACTGGCAAATCTGGGG
TLR6	2157	rs1039560	G/A	4	forward	AGCCCTTGCTCAGGTGGCTGCAGCTAGTAT[A/G]TTTGCCTTAATTGTTTACAGCAAACAC
TLR6	3829	rs3775073	G/A	4	forward	CTGGAATTCTTTGGAATCTGGTAGACATAA[A/G]GAAAAGTGCCTTGGGYYTGGAGTATAG
TLR7	5307	rs1634323	G/A	X	forward	TGTTAAATGAAAAAGCAAGCTAGAAATGG[A/G]TAAGTACCGTGTATTCCCTCATGTTTTTA
TLR7	6893	rs5743733	G/C	X	forward	CCCGCCATCACAGAAAGCCCTCGCTCACA[G/C]GTCTTGGCTCAAGCAACTCTTTGTCTTA
TLR7	7212	rs1634322	A/T	X	forward	CATCTCAAGATAAATTTCTTTTGCCTAAGA[A/T]TGCTGCTGAAAAAATCCATTGTAGCCA
TLR7	7335	rs179018	C/T	X	forward	AAGGTGAGGGTTTCATTTGCTGGGGTGTAG[C/T]GGGTGGGAGAATTCCTTATTGCAATCAC
TLR7	9149	rs5743740	G/A	X	forward	TCCCTTTATTTTTGTAACCTTAGTAGTAG[A/G]TCATGCATAGCTTTTTATGTGCATACCC
TLR7	11629	rs179016	C/G	X	forward	AACAAACCAATTTCTCTATGCCCAAAC[C/G]CTAAGTAGCACAAAATAGAAACATTAGA
TLR7	20091	rs179010	T/C	X	forward	GTTATACGGTTCCTCTGATTATGTATCACC[C/T]AGGCAGTGCCCTGACTCTACTACTATCT
TLR7	20241	rs1634319	C/T	X	forward	CAAAAACAATCCAAGACAAGAGCCAGATTA[C/T]GGAATGTCAGTGCCAGAATGGCAGGAAT
TLR7	23236	rs864058	A/G	X	forward	TGTGTGGTTTGTCTGGTGGGTTAACCATAC[A/G]GAGGTGACTATTCCTTACCTGGCCACAG
TNF	282	rs1800629	A/G	6	forward	AAATGGAGGCAATAGGTTTTGAGGGGCATG[A/G]GGACGGGGTTCAGCCTCCAGGGTCTAC
TNF	1078	rs1800610	A/G	6	forward	GCTGATAGGGAGGGATGGAGAGAAAAAAC[A/G]TGGAGAAAGACGGGGATGCAGAAAGAGA
TNF	1440	rs3093662	G/A	6	forward	AGCTGTTGAATGCCTGGAAGGTGAATACAC[A/G]GATGAATGGAGAGAGAAAACCAGACACC
TOLLIP	645	rs5743851	C/T	11	forward	AAGGCGTCCACCTGGGTACGCTTGTATA[C/T]GTAAGATAAAAGCCAAAAACATCACGG
TOLLIP	1211	rs5743854	C/G	11	forward	CCTCCGGCAGGCAGCTGAGGGAAAGATCGC[G/C]CTGCAGGGGATGTCGGGCCTGTCACTGC
TOLLIP	2662	rs5743856	G/A	11	forward	TCTCCTGAGAGTTGCCTGGCAGTTTCTTCT[A/G]TAGCATTAAATTTGCAGGAGAGCTGGTG
TOLLIP	2930	rs5743857	T/C	11	forward	AGGCCAAGTGGGAGCTTACACGTCACATGG[C/T]GAAAGCAGCAAGAGAGTTGGGGGTGGGG
TOLLIP	5754	rs5743881	T/C	11	forward	GGTGTGCGCTGGCTGTCTGAAACACAATT[C/T]GTGAAAGAAAGGCAAGTGAGATGCTTTT
TOLLIP	6671	rs5743890	G/A	11	forward	GCTGCCCGGCTAAAGAATAAATAAAGAAGA[A/G]GTTAATCATTGTCTGTGCCACCTCCGGA
TOLLIP	8937	rs5743899	G/A	11	forward	AGGCTGGCACTTCACTCTGAAACCTCGC[A/G]CACTGAGGGGTGAGTCACTGGGCAGAG
TOLLIP	10552	rs5743911	G/A	11	forward	GGACTGCATGTGTTCAAGACTCCACGTCCT[A/G]GGCTGAGCTGGGCTCTTCCGGGGCTCTG
TOLLIP	10905	rs5743915	T/C	11	forward	GAGACCTCTTTTCTTTCTGTGGAAAGGTA[C/T]GCTGCAGTGGTTAGAGCTCTGGCGTCA
TOLLIP	31878	rs3829223	A/G	11	forward	GAGGGCCAGTCGGCGCCACATCCCCTCATT[A/G]TCAGCAGAGCAGGTTTCTCGGGACACCC

TOLLIP	36047	rs5744034	C/T	11	forward	AAATSACATTTTGAAGGCCTTTAATTA AAA[C/T]AAGATTCTTCTTTCCTTCATTTTATGCT
TOLLIP	36848	rs5744038	G/A	11	forward	TCCCAGATTGAATTAGAGGAGGGAAGTCCC[A/G]GGTGCTCCTCCCTCAACAGTGGCAGTGG
TRAF2	138	rs10781520	G/A	9	forward	TCACTGAGCCTGCAGGTGCGGACTTGGGAC[A/G]TTCCATGGCTGCTTGCAGCAA ACTCAG
TRAF2	26041	rs17250841	T/C	9	forward	GGGCTGGGGGACGGGACAGGGCTGTCTCCT[C/T]ACCTCTTCCACTTGTCTGTTAAATGTC
TRAF2	35927	rs17244180	A/G	9	forward	CCCTTCATTTCTGAGTCCTGTCTCATCTAAGG[A/G]ACCCAAACCCTGGAAGGTCCTAGAGGCC

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TRAF2	37779	rs10283820	A/G	9	forward	AAGCAATGCTGGTGAACACAGCTTGTGTGC[A/G]GCACGCGTGCAGGCTGAGGACAGGCAGA
TRAF2	41191	rs7852970	G/A	9	forward	GGCACAGCCGGCTCACGGAGGGGCCACCAC[A/G]CTGGGCCAGGGTCTCACTGTACAAGTGG
TRAF6	973	rs5030409	T/C	11	reverse	TGCAGGTGGATTGACTTTCCAAGGCAACTG[C/T]CCTTCATACATCAACTGAGTGATACATC
TRAF6	1105	rs5030411	C/T	11	reverse	CTTTGACCTAGGAATGATATGCATCCTTCT[C/T]GTCATAGCTCACAGGCCAGA ACTAGWCA
TRAF6	2288	rs331449	G/A	11	reverse	TAAGTATTTTACCTGAATCACACATTTATT[A/G]TAGGAAAACCGGATTGGAACCAAGCAT
TRAF6	4115	rs5030419	G/C	11	reverse	CTCTGAGAGCAGATTACTATTACTGAATGT[G/C]TTGTTACACAGGTTCCATGTAGAAACGA
TRIF	4839	rs4807000	T/C	19	forward	GCTCACACTTGCTGAACGTGACCGCAAGGG[C/T]TGGGAAGAGAGCGCATGGGTGCGGGGGCG
TRIF	5497	rs10404543	T/C	19	forward	TTCTACCTCACACCCCATATTTCTCTCAA[C/T]GCCCTGRATTTCTCCCTGACACCCAAGG
TRIF	18230	rs10415014	T/G	19	forward	CAGCTCCTGCAGAACCTGGAACAGTGAATS[G/T]GTAGGGGACACTGGGCGTGCAGAAGGCC
TRIF	20001	rs2292151	T/C	19	forward	AGCCCTGCGGGAACAGAGCCAACACCTGGA[C/T]GGTGAGCGGATGCAGGCGGCGGCACTGA
TTRAP	1319	rs3181227	T/C	6	reverse	AAGTCCCTCCCAGCCTTGGAACTGTCTCCA[C/T]GAGTCATAACCATACTTATCTATGTTTA
TTRAP	1456	rs3181228	A/G	6	reverse	ACAGGCGTACTAGAACACAACCTAACAGA[A/G]ATAATTATTCAAAGCTCACAAACGGCACC
TTRAP	3004	rs6456628	T/G	6	reverse	TGAAACTTCGTAAGATCTTTATTACCTGT[G/T]CCTGGAATTTTTTCTTTCCCTTCCTT
TTRAP	3114	rs1061925	C/A	6	reverse	GCTTTTCTGATGTCTTAAGTCTGGGTAAG[A/C]GTCCCTTTTAGGTA CTCTTATAGCATC
TTRAP	3418	rs17249862	C/T	6	reverse	TTGGTCTTTTCAGCTACACTGGCTTACAGA[C/T]GTGATAAGATATTTCTTTAGGTTCTT
TTRAP	10740	rs3212229	G/T	6	reverse	TGAAAGAAACATTGAAAGCATCTCTTAGTG[G/T]GTAGGACCATTGAAGTCTCTCAATATGG
TTRAP	11170	rs3212231	C/A	6	reverse	TCAGTGAAAGAGATAAATCAAAGTTGGTCT[A/C]TTGGGACATAGAGAGGAAAAAGCACAAA
TTRAP	14691	rs3181238	G/A	6	reverse	TTTAAATGCAGATAGAATTCTCAGTCTATT[A/G]TTTTCTTAAAGAATATTTGAGTTTGCTGA
TTRAP	17823	rs3181245	C/G	6	reverse	GTTAGTGGGCAAAAGGCTATGTGTATCTTA[G/C]JAGAGTATTCTTCTTCTTTTTCAGTTTACC
TTRAP	18382	rs3087943	C/T	6	reverse	AAAGCCTGTCTCAGAGTTTCAACGGTGCTTA[C/T]JAGCTGCCAGCTGGATTCCAAACAGGTAC
TTRAP	18472	rs707887	G/A	6	reverse	TCCATTGAGGACCCGAAATAGTTAATTTT[A/G]AAATAAGTCTTCAAAGAAAAACATAAGA