

Supplemental Data

Allele-Specific Chromatin Remodeling
in the *ZBPB2/GSDMB/ORMDL3* Locus Associated
with the Risk of Asthma and Autoimmune Disease

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Figure S1. Mendelian transmission of AE observed for *ZBPB2*, *ZBPB2-GSDMB* intergenic region and *ORMDL3* in the LCLs from CEPH family 1420. Relative underexpression (-) or overexpression (+) is shown below the family member when data was available. The estimated fold differences between alleles, measured with the Illumina 1M BeadChip AE analysis, are shown in the bar graph for each family member. The red color represents the haplotype associated with underexpression of *GSDMB* (rs12936231>G) while the blue color represents the overexpressed-associated haplotype (rs12936231>C).

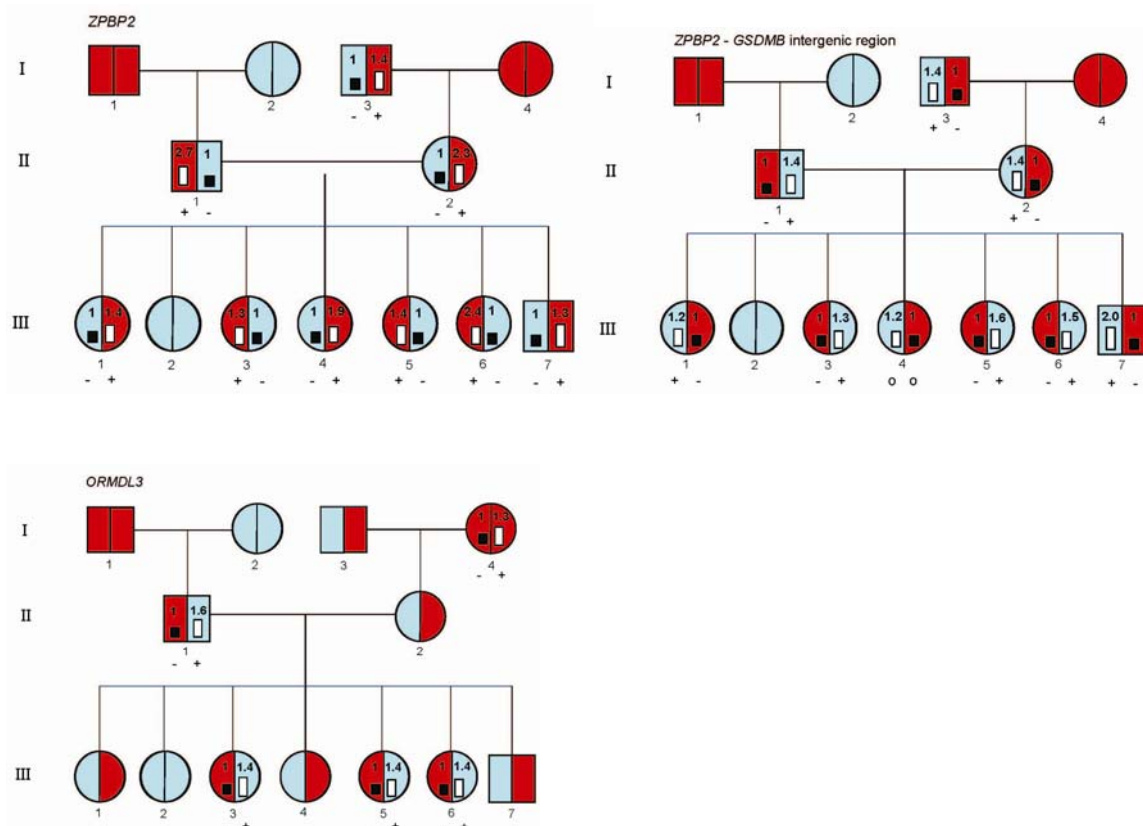


Figure S2. Analysis of chromatin states in LCLs. Number of LCLs analyzed in each experiment is given in parentheses. **A.** N-ChIP qPCR assay shows association of the rs12936231 C-allele with active and inactive chromatin marks. (n=5). **B.** As controls for N-ChIP assays, active and inactive histone modifications were evaluated by quantitative real-time PCR for the *NES* (active), *SNRPN* (imprinted) and *RPLP1* (inactive) genes (n=5). **C.** As controls for detection of allele-specific histone modifications in N-ChIP assays, enrichment of H3Ac and H3K9me3 at the imprinted *SNRPN* region were analyzed by PCR and sequencing. Allele-specific histone modifications are detected. **D.** Controls for X-ChIP assays. Active and inactive histone modifications were evaluated by quantitative real-time PCR at the *NES* and *SNRPN* genes (n=8). **E.** As controls for CTCF-specific X-ChIP assays, the *H19* (positive) and *SNRPN* (negative) regions were analyzed using quantitative real-time PCR at (n=8). As expected the *H19* region is CTCF-enriched, whereas the *SNRPN* region is not. The error bars represent standard deviation.

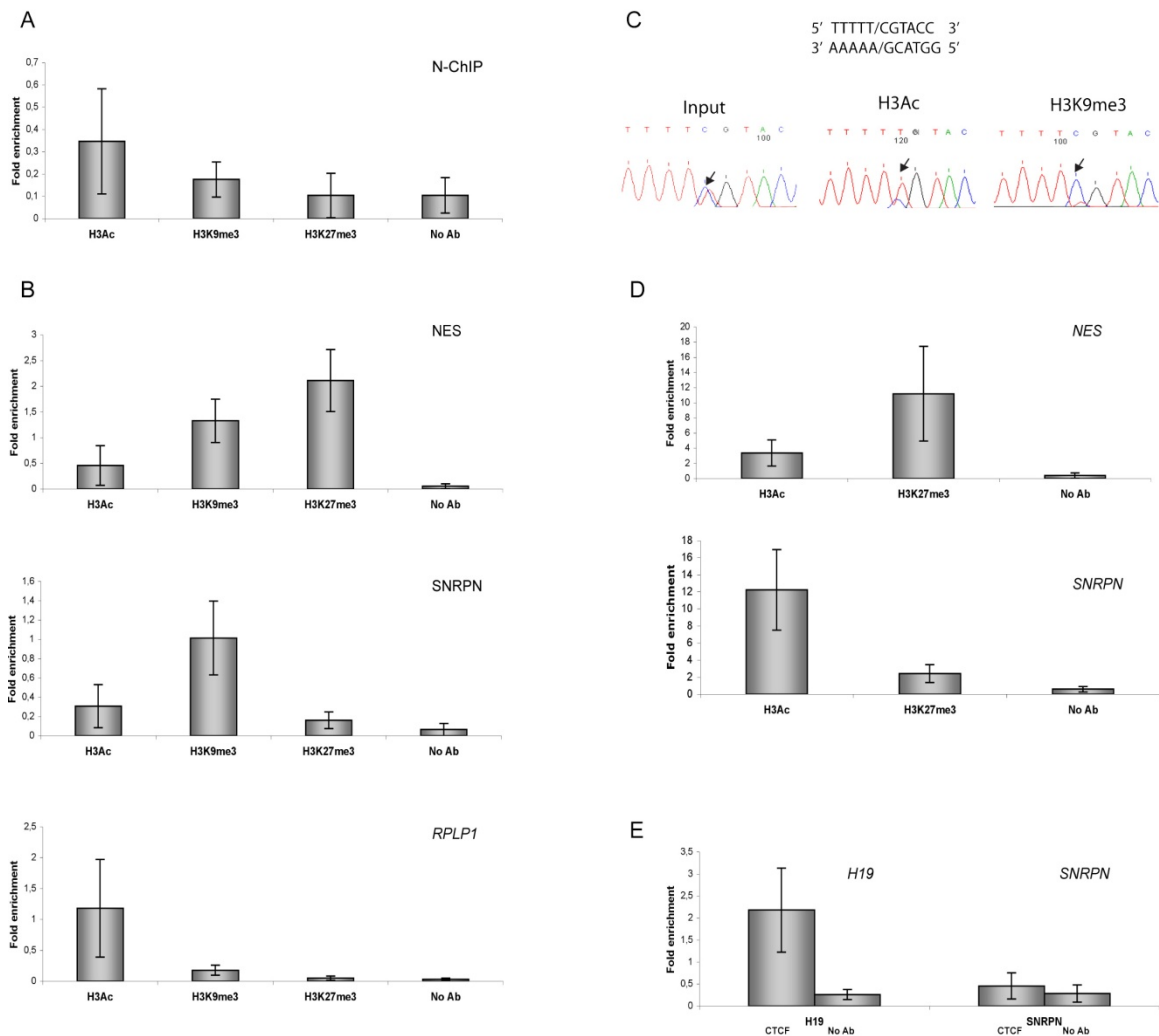


Figure S3. Overlapping polymorphic binding sites for CTCF and p300 in the rs12936231 region.

A) Comparison of the rs12936231 sequence (negative strand) to the consensus CTCF binding motif derived on the basis of genome-wide analysis of conserved sites (PMID: 17442748). The SNP is shown in red. Matching nucleotides are shown in gray boxes. The G-allele is closer to the consensus sequence the C-allele, however, none of them is a perfect match.

B) Comparison of the rs12936231 sequence (negative strand) to the consensus p300 binding motif. The SNP is shown in red. Matching nucleotides are shown in gray boxes.



Figure S4 ENCODE ChIP-seq showing LCL-specific CTCF-ChIP-seq. peak centered on the rs12936231 SNP, **A.** chromosomal location, **B.** RefSeq genes. ENCODE CTCF-ChIP-seq for: **C.** lymphoblastoid cell lines (LCL, GM12878, heterozygous at the rs12936231), **D.** Human Umbilical Vein Endothelial Cells (HUVEC), **E.** Human Myelogenous Leukaemia cells (K562) and **F.** Keratinocytes (Kera), **G.** Single Nucleotide Polymorphism (dbSNP build 129)

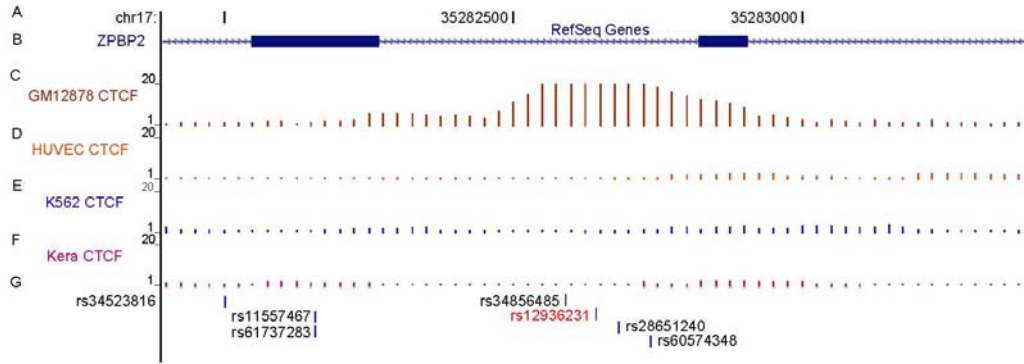


Figure S5 Lack of genotype effect on FAIRE enrichment at the *ORMDL3* promoter. FAIRE enrichment was compared in samples from homozygous (n=3 for the G-allele, n=3 for the C-allele) and heterozygous (n=6) FAIRE-treated LCLs using real-time qPCR. An unlinked region was used for normalization. The error bars represent standard deviation.

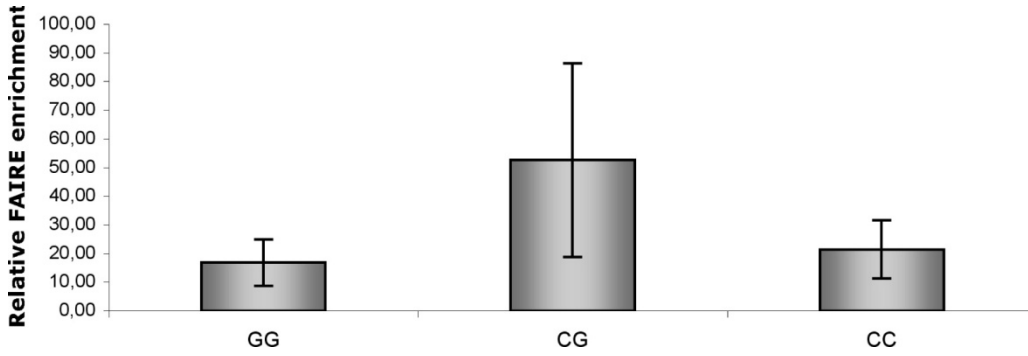


Figure S6. EMSA analyses showing allelic DNA-protein interactions for SNP (A) rs12936231, (B) rs7216389, (C) rs9303277 and (D) rs8067378 in HeLa, HEPG2, JEG-3, MG-63 and LCL. The unlabeled probes used to compete the DNA-protein interactions are indicated (+) at the top of each lane. Specific competitors corresponding to the unlabeled allele-specific probes were used in lanes 3, 4, 8 and 9 and a non-specific competitor was used in lanes 5 and 10.

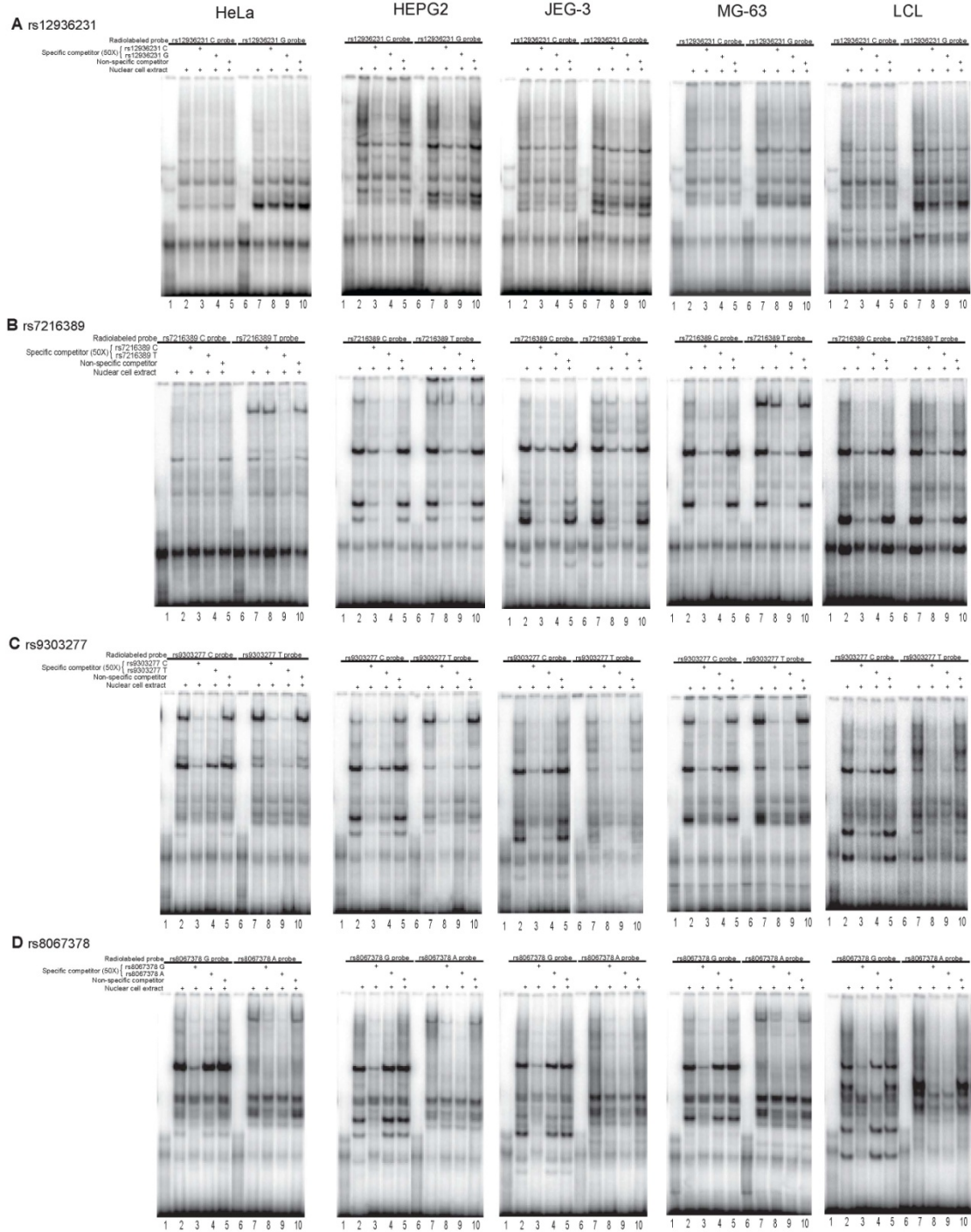


Figure S7. Linear regression analysis of rs2290400 genotypes (AA, AG, GG) and normalized expression scores (Illumina HumanRef8) for the *GSDMB* gene (probe ID: ILMN_19619) in 95 human primary bone samples collected from orthopedic surgery. Age and sex of donor were included as covariates in the model, giving an overall P-value of 0.14. Expression scores for each individual are averaged from two biological replicates and shown in red and regression line is indicated with blue dashes.

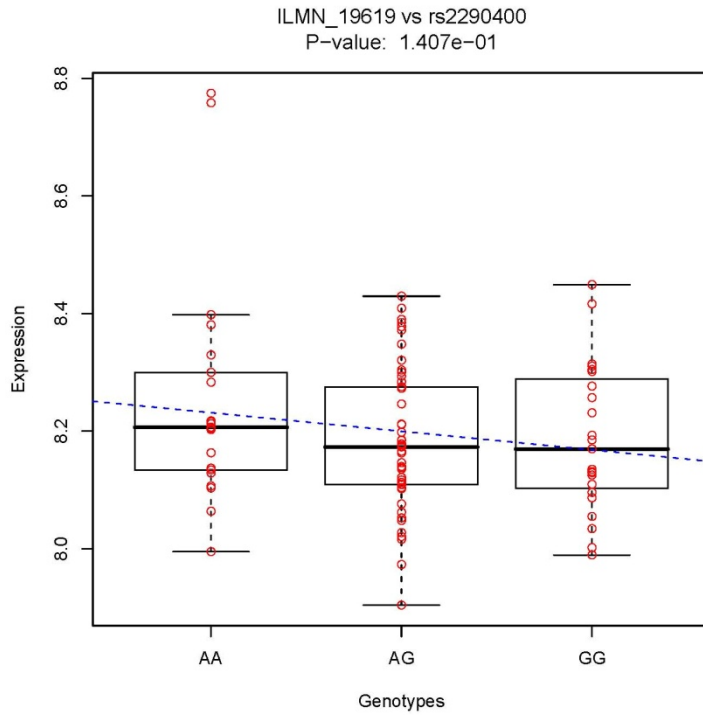


Table S1. List of primers used in functional assays

List of primers used in functional assays.

<i>Genic Location</i>	<i>SNP</i>	<i>Chr</i>	<i>Position</i>	<i>Forward primer 5'-3'</i>	<i>Reverse primer 5'-3'</i>	<i>Assay</i>
<i>IKZF3</i>	rs907091	17	35175268	TTCTCTTTGTGGATTTGCAT	TGTTTTCCCATCAGGGACTT	FAIRE
<i>IKZF3</i>	rs9303277	17	35229995	CAAGAAGGCTGGAAGGAGAG	GCTTTTCCTGACAATTCAGTCA	FAIRE
<i>IKZF3</i>	rs2060941	17	35236409	TGCAATGGAACTTGGCATA	CTCACCTCAAACACGCACAC	FAIRE
<i>IKZF3</i>	rs3816470	17	35239327	CAAAACCGCTGCACTTTCTA	CATCCCTTTTGGGTATGTGTG	FAIRE
Intergenic	rs4795397	17	35277271	GCCAAGAAGGAACCATCAAA	CCCAGTGCAAACGTATCTA	FAIRE
<i>ZBP2</i>	rs12150079	17	35278943	CCCAACCAAATTGTAGGAC	GACAGAACGATGGTATGCTT	FAIRE
<i>ZBP2</i>	rs11557467	17	35282160	TTTTAAAGCCTATCGGGAACC	GAGGCCATGTTCTGGAATTT	FAIRE
<i>ZBP2</i>	rs12936231	17	35282646	CTTACATTAGCCCCAGATG	TGCAGGCACATGTTTAGTCC	FAIRE/N-ChIP/X-ChIP
Intergenic	rs9901146	17	35296869	CCCTTCCATCTTTGTTTCCA	GCAGCAAGATCCTGTCTCAA	FAIRE
Intergenic	rs12950743	17	35302759	GGCTATGAGGGAGACAGCAC	CCACTCCCCATCACCTAGAA	FAIRE
Intergenic	rs7359623	17	35303115	AGCATTATGAGCAGGGAAGG	TCAAAATGAGATGTGCTATTATGGA	FAIRE
Intergenic	rs8067378	17	35304874	TCCCTCAGAAAGAAGAGCACA	TCCACTCTAGGCCACTGACA	FAIRE
<i>GSDMB</i>	rs2290400	17	35319766	CAGCTTCCTGGAGAGAGTGG	GGTGTGTGTTTCCTTGGTTT	FAIRE
<i>GSDMB</i>	rs1008723	17	35319793	CAGCTTCCTGGAGAGAGTGG	GGTGTGTGTTTCCTTGGTTT	FAIRE
<i>GSDMB</i>	rs1011082	17	35322040	GCTCATGAAAAGCAGGGA	TGGCTACCCTTGAAAAACAGG	FAIRE
<i>GSDMB</i>	rs7216389	17	35323475	AGGCAACCCTGGAAAGTCA	CTGGGAGGTTGGAGACAAAG	FAIRE
<i>GSDMB</i>	rs7216558	17	35323597	AGGTTCGTGGAGGATGTGTG	CCACCAGTTCCAAAATGGAT	FAIRE
<i>GSDMB</i>	rs9303281	17	35327572	TGATAATGCCACCACCCTT	TAAGGCAGGCAAATCATTCC	FAIRE
<i>GSDMB</i>	rs7219923	17	35328044	TCCCTTGGCTCTGATTCTTG	GGTAGGATGGGGAAGTGGAT	FAIRE
Intergenic	rs7224129	17	35328952	GAGTGTGGGCCAGACAATG	GCTGGTTCTGCTGGGTTATG	FAIRE
ORMDL3	rs4378650	17	35334391	CAGAGAAGTCAAGGCCCATC	CCTCACTTCCTTCCCTCCT	FAIRE
ORMDL3	rs1260333	17	35336333	CACCAGAGACCCCTGAAAAA	CGGCTCAACTCCTGTAGACC	FAIRE
ORMDL3 promoter	-	-	-	GTTACGCACAAAATTCTATCATCC	TTTTTCCTGGGCTCCGTTT	FAIRE (unlinked region)
Intergenic	-	-	-	TTGCTATTCTGCTGGCTTCA	GAAAGCTTTGGTCTGGGAAA	FAIRE (unlinked region)
<i>SNRPN</i>	rs200230	15	22750861	GGGTAGAAAAATCGCACCAA	CCTCACCCCTCAGGTCTTCC	N-ChIP/X-ChIP
<i>NES</i>	-	1	-	TCAGAAAGCCACCACCATCA	GCTGGAGAGTGGAACCAAAGAA	N-ChIP/X-ChIP
<i>RPLP1</i>	-	15	-	CTAACCAGGAGATTACGAACAATGTC	GGTCCATGAGTTGCTTGACTTG	N-ChIP/X-ChIP
<i>H19</i>	-	11	-	AGACCTGGGACGTTTCTGTG	AGAATCGGCTGTACGTGTGG	X-ChIP
<i>IKZF3</i>	-	17	-	TGAAAAATGTGGACAGTGGA	CATTTCCCATGGGTTCTGAC	qRT-PCR
<i>ZBP2</i>	-	17	-	CTGGACAGCTGATGGTGA	CCCGATAGGCAAAGACCATA	qRT-PCR
<i>GSDMB</i>	-	17	-	ACATGGAGGACCCAGACAAG	CACAGAGAATTCGTGCCTCA	qRT-PCR

<i>ORMDL3</i>	-	17	-	GTGGCATCTGGCTCTCCTAC	TCACCGTGTGCAGGAAGATA	qRT-PCR
<i>RPS18</i>	-	6	-	TGTGGTGTGAGGAAAGCAG	GGACCTGGCTGTATTTTCCA	qRT-PCR
<i>ORMDL3</i>	rs12603332	17	35336333	GGCCCGGATATTGTATGTG	CCCTACCCTAGATGGGGAGA	AE
<i>ORMDL3</i>	rs8076131	17	35334438	GGTTTGGGGAGATCCAGAAT	CAGAGAAGTCAAGGCCCATC	AE
<i>GSDMB</i>	rs1008723	17	35319793	TTTGTACCCACCCCTACCT	AAGGATCTCAGGGCCTTACC	AE
<i>GSDMB</i>	rs7216389	17	35323475	CTGCCTCCAAAACCTAGCAG	GCAGTTCTGTCGCTGTTGTT	AE
<i>GSDMB</i>	rs7219923	17	35328044	AGGAACCAGGGAGGAATGAC	AGGAGGAAGCAGTGAGTGGA	AE
<i>Genic Location</i>	<i>SNP</i>	<i>Chr</i>	<i>Position</i>	<i>EMSA PROBES</i>		<i>Assay</i>
<i>IKZF3</i>	rs9303277	17		GTCATGCGATGAATTA AAAA(C/T)AGGGCTGTGTTAAAAT		EMSA
<i>ZBP2</i>	rs12936231	17		CATTAGCCCCCAGATG(C/G)AGTGAAACCATCAAGTA		EMSA
Intergenic	rs8067378	17		TATTTGTAACGTTATAAAAT(A/G)GGGAAAAACGTTTATAT		EMSA
<i>GSDMB</i>	rs7216389	17		TGGAAAGTCACAAAACA(C/T)GCATGGACTCGGCCCTGA		EMSA
Intergenic	rs4795397	17		TCCATCCCTACAGAAAAGGCCA(A/G)TCGGGCTCCATCC		EMSA
	Non-specific DNA probe			GATCGAACTGACCGCTTGC GGCCCGT		EMSA

0.09939	rs3744806	35605152	G C G C C G C G C C C C C G C C C C C C C C C C C G C C C C G C G C G G C C C C C C C G C G G G G C C C C C G G	CCGCG
0.42577	rs9907683	35612427	A A A A A A A C A C A C A A A A A A A A A C C A A A A A A A A A	AAAAC
0.09939	rs8073925	35613046	C G C G G C G C G G G G G G G G G G G G G G G G G G C G G G G C G C G C C G G G G G G G G C C G C C C G G G G G C C	GGCGC
1	rs11867995	35627657	G G G G G G G G G G G G T G	GGGGG
1	rs11871303	35628133	T T T T T T T T T T T T G T	TTTTT
0.67187	rs9901109	35633374	T T T T T T T G T	TTTTG
0.70785	rs6503539	35636451	C C T C C C C T C	CCCCT
0.70785	rs9908034	35640001	T T C T T T T C T	TTTTC
0.67187	rs16965687	35641044	T T T T T T T C T	TTTTC
1	rs9916782	35641566	A A A A A A A G A G A A A A A A A A A A A A A A A A A	AAAAG
0.67187	rs8066144	35641717	T T T T T T T C T	TTTTC
0.70785	rs9904021	35652756	G G T G G G G T G G G G G G G T G G G G G G G G G G G G G G G T G G G T G G G G G G G G G G T T G G G G G G G G G	GGGGT
0.67187	rs9893520	35654671	C C C C C C C T C C C C C C C T C T T C C C C C C C C C C C C	CCCCT
0.67187	rs11078940	35663590	C C C C C C C T C C C C C C C T C T T C C C C C C C C C C C C	CCCCT
1	rs17679361	35666068	T T C T	TTTTT
0.47412	rs4566234	35667875	G G T G G G G T G G G G G G T G G G G G G G G G G G G G G G G G G G T G G G T G G G G G T G G G T G T G G G G G G	GGGGT
0.70785	rs4077125	35677005	G G A G G G G A G G G G G A G G G G G G G G G G G G G G G G A G G G A G G G G G G G G G A G A G G G G G G G G	GGGGA
0.67187	rs9916460	35681591	T T T T T T T C T T T T T C T	TTTTC
0.67187	rs9908257	35681648	G G G G G G G A G G G G G A G A G G G G G G G G G A G A G G G G G G G	GGGGA
1	rs9892946	35685801	T T T T T T T C T T T T T C C T	TTTTC
1	rs4134998	35698971	T T C T	TTTTT
0.49206	rs4134999	35699133	T T	TGTTT
0.70785	rs2077464	35700090	A A G A A A A G A A A A A A G A G A A A G A A A A A A A A A A A A A A	AAAAG
1	rs4135001	35700228	A A	AAAAA
1	rs4135010	35703285	A A	AAAAA
1	rs4135012	35703774	G G A G	GGGGG
1	rs4135018	35705761	T T T T T T T T T T T T T T T T C T	TTTTT
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1	rs4135021	35706860	G G A G	GGGGG
1	rs4135027	35709206	C C A C	CCCCC
0.67187	rs13706	35710677	G G G G G G G A G G G G G A G A G G G G G G G G G G G G	GGGGA
1	rs4135029	35710869	G T G G G G G G G G	GGGGG
1	rs4135030	35711074	A A G A G A A A A A A A A A A A A A A A A A	AAAAA
1	rs2120200	35713901	A A A A A A A G A A A A A G A G A A A A A A A A A A A A A A A A	AAAAG
1	rs2957325	35715569	C C C C C C C C C C C C C C C C T T C	CCCCC
0.47412	rs7217852	35723547	A A G A A A A G A A A A A G A G A A A G A A A A A G A A A G A G A A A A	AAAAG

Table S5. *ORMDL3* allelic expression data for YRI LCLs

Table includes Fisher's Exact test P-values for each SNP. The haplotype associated with overexpression of *ORMDL3* can be found in green

P value	snp	YRI LCLs # AE phenotype location	NA18502.c2	NA18504.c2	NA18517.c2	NA18856.c2	NA18858.c2	NA18871.c2	NA18912.c1	NA19159.c2	NA19207.c1	NA19239.c2	NA18502.c1	NA18504.c1	NA18517.c1	NA18856.c1	NA18858.c1	NA18871.c1	NA18912.c2	NA19159.c1	NA19207.c2	NA19239.c1
			-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+
0.474	rs11658678	34933622	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	T	
0.211	rs8065963	34934858	C	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	T	C	T
0.628	rs4404103	34936183	A	G	G	A	G	G	A	A	A	A	A	A	A	A	A	G	A	A	A	A
0.303	rs7226073	34938026	A	T	T	A	T	T	A	A	A	A	A	A	A	A	T	A	A	A	A	A
1.000	rs8069074	34938927	A	G	G	G	G	G	G	G	A	G	G	G	G	A	A	G	A	G	G	G
0.211	rs12450559	34948235	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	A	G	A	A
0.656	rs4239222	34949761	G	G	G	T	G	G	T	T	G	T	T	T	G	G	G	G	T	T	T	
0.211	rs7503069	34950654	C	C	C	C	C	C	C	C	C	C	C	C	G	C	C	C	C	G	C	G
1.000	rs11657058	34952904	T	G	G	G	G	G	G	T	G	G	G	G	T	T	G	T	G	G	G	
1.000	rs11657153	34953255	A	G	A	G	G	G	G	A	G	G	G	G	A	A	G	A	G	G	G	
0.211	rs11654018	34957266	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T	T	C	T	C	
0.474	rs2303316	34957743	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G	A	G
1.000	rs12947506	34961118	T	C	C	C	C	C	C	T	C	C	C	C	T	T	C	T	C	C	C	
1.000	rs7503377	34962367	T	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	C	C	
0.474	rs7216086	34962948	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	A	
0.303	rs9972899	34965091	C	T	T	C	T	T	C	C	C	C	C	C	C	C	T	C	C	C	C	
0.211	rs11078915	34968952	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T	T	C	T	C	
1.000	rs6503521	34969077	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	
0.211	rs12938115	34969252	C	C	C	T	C	C	T	T	C	C	C	C	C	C	C	C	C	C	C	
0.656	rs4795384	34970297	C	C	C	G	C	C	G	C	G	G	G	G	C	C	C	C	G	G	G	
1.000	rs4488484	34970903	T	A	A	A	A	A	A	T	A	A	A	A	T	T	A	T	A	A	A	
1.000	rs12944298	34973799	C	C	C	T	C	C	T	T	C	T	T	C	C	C	C	C	C	T	C	
1.000	rs7503195	34976041	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	
1.000	rs8081144	34976817	G	G	G	A	G	G	A	A	G	A	A	A	G	G	G	G	G	A	G	
1.000	rs903507	34979949	T	C	C	C	C	C	C	T	C	C	C	C	T	T	C	T	C	C	C	
0.656	rs8075737	34980842	T	T	T	C	T	T	C	C	T	C	C	C	T	T	T	T	C	C	C	
1.000	rs7224759	34981719	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
1.000	rs1874226	34982557	T	C	C	C	C	C	C	T	C	C	C	C	T	T	C	T	C	C	C	
1.000	rs4795385	34986674	G	A	A	A	A	A	A	G	A	A	A	A	G	G	A	G	A	A	A	
1.000	rs11657812	34987853	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
0.211	rs1619021	34992800	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	A	G	A	
1.000	rs1877030	34993687	T	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	C	C	
1.000	rs12453198	34995405	T	T	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	T	C	
1.000	rs11654954	34999505	A	A	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	A	G	
1.000	rs998480	35009251	T	T	A	T	A	A	T	T	A	T	T	T	T	A	A	A	T	T	T	
0.474	rs9916503	35011091	T	T	T	T	T	T	T	T	T	T	T	T	A	T	T	T	T	A	T	
0.628	rs9889354	35011493	A	A	G	G	G	G	G	G	G	G	G	G	A	G	G	G	A	A	A	
1.000	rs12453682	35023531	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	T	
1.000	rs12946926	35023628	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	
1.000	rs9915323	35024007	A	A	T	A	A	A	T	T	A	A	A	A	A	A	A	A	T	A	T	
0.628	rs1877032	35024590	T	T	T	C	C	C	T	T	T	C	C	C	T	T	T	T	T	T	T	
1.000	rs1874228	35028800	A	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G	A	G
0.370	rs879606	35035375	A	A	G	G	G	G	G	A	G	G	G	A	A	A	A	A	A	A	G	
1.000	rs2271309	35038516	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	A	
1.000	rs907094	35043897	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	A	
1.000	rs3764352	35044465	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	T	
0.474	rs9532	35046139	G	A	G	G	G	G	G	G	A	G	G	G	G	G	G	G	G	G	G	
0.170	rs1874224	35049186	T	T	T	G	G	G	G	T	G	G	G	T	T	T	T	T	T	T	T	
1.000	rs9913626	35051252	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
0.628	rs12937003	35054941	T	T	T	C	C	C	T	T	T	C	C	C	T	T	T	T	T	T	T	
0.170	rs9892427	35058384	T	T	T	C	C	C	C	T	C	C	C	T	T	T	T	T	T	T	T	
0.370	rs9972882	35061224	A	A	C	C	C	C	C	A	C	C	C	A	A	A	A	A	C	A	C	
1.000	rs881844	35063744	C	C	G	C	C	C	C	C	C	C	C	C	C	C	C	C	G	C	G	
1.000	rs11869286	35067382	G	G	C	G	G	G	G	G	G	G	G	G	G	G	G	G	C	G	C	

1.000	rs1877031	35067606	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	A	G	A		
0.370	rs2271308	35071008	T	T	C	C	C	C	C	T	C	C	C	T	T	T	T	C	T	C		
1.000	rs931992	35074961	G	G	T	G	G	G	G	G	G	G	G	G	G	G	G	T	G	T		
0.370	rs1053651	35075837	A	A	C	C	C	C	C	A	C	C	C	A	A	A	A	C	A	C		
0.370	rs876493	35078071	G	G	A	A	A	A	A	A	G	G	G	A	G	G	G	A	G	A		
1.000	rs14050	35081598	C	C	T	T	T	T	C	C	C	C	C	T	C	C	C	T	C	T		
0.370	rs2952151	35082022	T	T	C	C	C	C	C	T	T	T	C	T	T	T	T	C	T	C		
0.370	rs2941503	35082271	A	A	G	G	G	G	G	A	A	A	G	A	A	A	A	A	G	A	G	
1.000	rs907087	35082313	G	G	A	A	A	A	A	G	A	A	A	A	G	A	G	G	A	G	A	
1.000	rs903502	35083130	C	C	T	C	C	C	C	C	T	T	C	C	C	C	C	T	C	T		
0.370	rs2941504	35084426	A	A	G	G	G	G	G	A	G	G	G	A	A	A	A	A	G	A	G	
1.000	rs1565922	35084561	A	A	G	G	G	G	A	A	G	G	G	A	A	A	A	A	G	A	G	
1.000	rs2934953	35085841	T	T	A	A	A	A	T	T	T	A	A	A	T	T	T	T	A	T	A	
1.000	rs2934952	35085892	G	G	A	A	A	A	G	G	G	A	A	A	G	G	G	G	A	G	A	
1.000	rs2941505	35086230	A	A	G	G	G	G	A	A	A	G	G	G	A	A	A	A	G	A	G	
1.000	rs2941506	35086561	A	A	G	G	G	G	A	A	A	G	G	G	A	A	A	A	A	G	A	G
1.000	rs907089	35087126	G	G	A	A	A	A	G	G	G	A	A	A	G	G	G	G	A	G	A	
1.000	rs2313171	35087368	T	T	C	C	C	C	T	T	T	C	C	C	T	T	T	T	C	T	C	
1.000	rs12150298	35088067	T	T	C	C	C	C	T	T	T	C	C	C	T	T	T	T	C	T	C	
1.000	rs8078228	35088524	C	C	T	T	T	T	C	C	C	T	T	T	C	C	C	C	T	C	T	
1.000	rs11078919	35089281	T	T	C	C	C	C	T	T	T	C	C	C	T	T	T	T	C	T	C	
1.000	rs1476278	35089769	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	T	
1.000	rs9303274	35089879	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	C	T	C	
1.000	rs2517957	35092242	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	A	
1.000	rs2517958	35092277	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	A	
0.370	rs903501	35093019	T	T	C	C	C	C	C	T	C	C	C	T	T	T	T	T	C	T	C	
1.000	rs9892376	35094965	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
0.370	rs2517954	35097076	T	T	C	C	C	C	C	T	C	C	C	T	T	T	T	T	C	T	C	
1.000	rs2517955	35097207	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	T	
0.370	rs2517956	35097385	G	G	A	A	A	A	A	A	A	A	A	G	G	G	G	G	A	G	A	
1.000	rs4252600	35110508	G	G	G	G	G	G	G	G	C	C	G	G	G	G	G	G	G	G	G	
0.650	rs2952155	35115244	T	T	C	C	C	C	C	T	C	C	C	C	T	T	T	T	C	T	C	
1.000	rs4252612	35117234	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
0.650	rs1810132	35119531	C	C	T	T	T	T	T	C	T	T	T	T	C	C	C	C	T	C	T	
1.000	rs4252632	35125531	G	G	G	G	G	G	G	G	T	T	G	G	G	G	G	G	G	G	G	
1.000	rs4252643	35130293	A	A	A	A	A	A	A	A	G	G	A	A	A	A	A	A	A	A	A	
1.000	rs2952156	35130361	A	A	A	G	G	G	G	A	G	G	G	G	A	A	A	A	G	A	G	
1.000	rs4252658	35137889	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
1.000	rs4252664	35138827	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
1.000	rs2941518	35145896	C	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	C	C	
0.170	rs9896218	35147989	A	A	A	C	C	C	C	A	C	C	C	A	A	A	A	A	A	A	A	
1.000	rs9901670	35149058	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	
1.000	rs9896940	35149501	A	A	A	A	A	A	A	A	G	G	A	A	A	A	A	A	A	A	A	
1.000	rs8192704	35152248	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	
0.179	rs9891131	35165047	A	G	A	G	G	G	G	A	G	G	G	G	A	A	A	A	A	A	A	
0.628	rs907091	35175268	T	C	C	C	C	C	C	T	C	C	C	C	T	C	C	T	T	T	C	
1.000	rs907092	35175785	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	
1.000	rs16965328	35176217	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	
1.000	rs16965330	35176899	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	G	G	G	
1.000	rs9893628	35178039	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	
1.000	rs9893933	35179419	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	
0.170	rs9894370	35179530	G	C	G	G	C	C	C	G	C	C	C	G	G	G	G	G	G	G	G	
0.582	rs9652840	35182954	A	A	A	A	T	A	A	T	A	T	A	A	A	A	A	A	A	A	A	
1.000	rs2313429	35184185	A	A	A	A	G	A	A	G	A	G	A	G	A	A	A	A	A	A	A	
1.000	rs7503018	35184746	A	A	A	A	G	A	A	G	A	G	A	G	A	A	A	A	A	A	A	
1.000	rs9901483	35186300	T	T	T	T	A	T	T	A	T	A	A	T	A	T	T	T	T	T	T	
1.000	rs10445308	35191573	C	C	T	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	T	
1.000	rs12945567	35194121	A	A	A	A	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
1.000	rs1510475	35194906	A	A	A	A	C	A	A	A	A	C	C	A	A	A	A	A	A	A	A	
1.000	rs9911634	35197257	C	C	C	C	A	C	C	A	C	A	A	C	A	C	C	C	C	C	C	
1.000	rs9911669	35197293	C	C	C	C	G	C	C	C	C	G	G	C	C	C	C	C	C	C	C	
1.000	rs9911688	35197327	C	C	C	C	T	C	C	C	C	T	T	C	C	C	C	C	C	C	C	
1.000	rs9914516	35199651	C	C	C	C	T	C	C	C	C	T	T	C	C	C	C	C	C	C	C	
1.000	rs9913044	35199754	G	G	G	G	A	G	G	A	G	A	A	G	A	G	G	G	G	G	G	
1.000	rs12936634	35202163	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	

0.211	rs3803795	35202400	C	T	C	C	T	T	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs13313561	35207977	G	G	G	G	C	G	G	C	G	C	C	G	C	G	G	G	G	G
1.000	rs9899345	35208284	G	G	G	G	A	G	G	A	G	A	A	G	A	G	G	G	G	G
1.000	rs13313564	35209081	G	G	G	G	A	G	G	G	G	A	A	G	G	G	G	G	G	G
1.000	rs13313573	35209344	G	G	G	G	T	G	G	G	G	T	T	G	G	G	G	G	G	G
1.000	rs12937330	35210843	C	C	C	C	A	C	C	A	C	A	A	C	A	C	C	C	C	C
1.000	rs9941360	35213124	C	C	C	C	T	C	C	C	C	T	T	C	C	C	C	C	C	C
1.000	rs9941391	35215346	G	G	G	G	T	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	RS4795395	35216513	T	T	A	T	T	T	T	T	T	T	T	T	T	T	A	T	T	A
1.000	rs4337325	35217962	C	C	C	C	T	C	C	T	C	T	T	C	T	C	C	C	C	C
1.000	rs9909593	35223675	A	A	G	A	A	A	A	A	A	A	A	A	A	A	G	A	A	A
1.000	rs9898031	35226174	C	C	C	C	G	C	C	C	C	G	G	C	C	C	C	C	C	C
1.000	rs9913957	35228025	A	A	A	A	G	A	A	A	A	G	G	A	A	A	A	A	A	A
0.141	rs9303277	35229995	T	T	T	T	T	T	T	T	C	T	T	T	T	C	C	T	C	T
1.000	rs9904834	35230027	A	A	A	A	G	A	A	A	A	G	G	A	A	A	A	A	A	A
1.000	rs9911069	35230128	T	T	T	T	C	T	T	T	T	C	C	T	T	T	T	T	T	T
1.000	rs9908983	35230453	G	G	G	G	A	G	G	G	G	A	A	G	G	G	G	G	G	G
1.000	rs8076347	35231067	G	G	G	G	T	G	G	T	G	T	T	G	T	G	G	G	G	G
1.000	rs12942660	35235564	C	C	C	C	T	C	C	T	C	T	T	C	T	C	C	C	C	C
0.582	rs12946188	35237956	C	C	C	A	A	C	C	C	C	A	A	C	C	C	C	C	C	C
1.000	rs16965360	35238958	T	T	T	T	T	T	T	C	T	T	T	T	T	T	T	T	T	T
0.141	rs3816470	35239327	G	G	G	G	G	G	G	G	A	G	G	G	G	A	A	G	A	A
0.582	rs9913769	35239863	A	A	A	G	G	A	A	A	A	G	G	A	A	A	A	A	A	A
0.582	rs12945253	35244854	C	C	C	G	G	C	C	C	C	G	G	C	C	C	C	C	C	C
1.000	rs7215617	35245590	A	A	A	A	A	A	A	T	A	A	A	A	T	A	A	A	A	A
1.000	rs12948164	35247066	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
0.582	rs9900019	35248151	T	T	T	C	C	T	T	T	T	C	C	T	T	T	T	T	T	T
0.628	rs9908694	35251298	C	C	C	T	T	C	C	T	C	T	T	C	T	C	C	C	C	C
1.000	rs13341681	35256183	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
0.582	rs12939306	35262034	C	C	C	T	T	C	C	C	C	T	T	C	C	C	C	C	C	C
1.000	rs8069531	35262870	A	A	A	A	A	A	A	T	A	A	A	A	T	A	A	A	A	A
0.582	rs12950066	35262967	A	A	A	G	G	A	A	A	A	G	G	A	A	A	A	A	A	A
0.582	rs12947480	35263202	G	G	G	A	A	G	G	G	G	A	A	G	G	G	G	G	G	G
0.582	rs8079075	35264341	A	A	A	G	G	A	A	A	A	G	G	A	A	A	A	A	A	A
0.582	rs9900538	35265235	T	T	T	C	C	T	T	T	T	C	C	T	T	T	T	T	T	T
1.000	rs7212976	35265438	T	T	T	T	T	T	T	G	T	T	T	T	G	T	T	T	T	T
0.582	rs12943472	35265563	A	A	A	G	G	A	A	A	A	G	G	A	A	A	A	A	A	A
0.628	rs16965367	35267842	T	T	T	C	C	T	T	C	T	C	C	T	C	T	T	T	T	T
0.582	rs9915509	35268231	G	G	G	A	A	G	G	G	G	A	A	G	G	G	G	G	G	G
0.582	rs9916259	35268586	G	G	G	T	T	G	G	G	G	T	T	G	G	G	G	G	G	G
1.000	rs7220943	35269696	C	C	C	C	C	C	C	T	C	C	C	C	T	C	C	C	C	C
0.628	rs9899336	35271306	C	C	C	T	T	C	C	T	C	T	T	C	T	C	C	C	C	C
0.582	rs9907096	35272300	C	C	C	T	T	C	C	C	C	T	T	C	C	C	C	C	C	C
0.582	rs9907966	35272329	A	A	A	C	C	A	A	A	A	C	C	A	A	A	A	A	A	A
1.000	rs9635726	35273667	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
0.582	rs1453558	35275178	G	A	G	G	G	A	A	G	G	G	G	A	G	G	G	G	G	G
0.628	rs1453560	35276967	T	T	T	G	G	T	T	G	T	G	G	T	G	T	T	T	T	T
1.000	rs4795397	35277271	A	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G
1.000	rs11557466	35278152	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T
1.000	rs11078925	35278734	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C
1.000	rs12150079	35278943	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
0.582	rs9916369	35281792	T	T	T	C	C	T	T	T	T	C	C	T	T	T	T	T	T	T
1.000	rs11557467	35282160	G	G	T	T	T	G	G	G	G	T	T	G	T	G	G	G	G	T
0.057	rs12936231	35282646	G	G	G	G	G	G	G	C	G	G	G	G	C	C	C	C	C	G
0.628	rs11870965	35283731	T	T	A	A	A	T	T	T	T	A	A	T	T	T	T	T	T	A
0.628	rs10852936	35285240	C	C	T	T	T	C	C	C	C	T	T	C	T	C	C	C	C	T
0.628	rs1054609	35286803	A	A	C	C	C	A	A	A	A	A	C	C	A	A	A	A	A	C
1.000	rs8073948	35287322	T	T	T	T	A	T	T	T	T	A	A	T	T	T	T	T	T	T
0.628	rs9907088	35288642	G	G	A	A	A	G	G	G	G	A	A	G	G	G	G	G	G	A
1.000	rs12232497	35293645	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C
0.628	rs2872507	35294289	G	G	A	A	A	G	G	G	G	A	A	G	G	G	G	G	G	A
0.650	rs9901146	35296869	G	G	A	A	A	G	G	A	G	A	A	G	A	G	G	G	G	A
0.650	rs12950743	35302759	T	T	C	C	C	T	T	C	T	C	C	T	C	T	T	T	T	C
0.650	rs7359623	35303115	C	C	T	T	T	C	C	T	C	T	T	C	T	C	C	C	C	T
0.582	rs12943012	35303757	T	T	T	C	C	T	T	T	C	C	T	T	T	T	T	T	T	T

0.141	rs8067378	35304874	G	G	G	G	G	G	G	A	G	G	G	G	A	A	A	A	A	G	G
1.000	rs8069176	35310723	G	G	A	A	A	G	G	A	G	A	A	G	A	G	G	G	G	A	A
0.582	rs16965388	35315665	G	A	G	G	G	A	A	G	G	G	G	A	G	G	G	G	G	G	G
1.000	rs2305480	35315722	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A
1.000	rs2305479	35315743	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T
1.000	rs11078926	35316502	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A
1.000	rs11078927	35317931	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T
0.170	rs2290400	35319766	C	C	C	C	C	C	T	T	C	C	C	T	T	C	T	T	T	T	C
0.628	rs1008723	35319793	G	G	T	T	T	G	G	G	G	T	T	G	G	G	G	G	G	G	T
1.000	rs4795400	35320546	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T
1.000	rs869402	35321569	C	C	T	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	T
0.170	RS1011082	35322040	G	G	A	A	A	A	A	A	A	A	A	G	C	G	G	G	G	G	A
0.303	rs7216389	35323475	C	T	C	T	T	C	C	T	T	T	T	T	T	T	T	T	T	T	C
0.370	RS7216558	35323597	C	C	C	C	T	C	C	T	T	C	C	T	T	C	T	T	T	T	C
0.303	RS8065777	35325928	C	T	C	T	T	C	C	T	T	T	T	T	T	T	T	T	T	T	C
0.350	rs9303280	35327557	T	C	C	T	C	T	T	C	C	T	T	C	C	C	C	C	C	C	T
0.170	rs9303281	35327572	G	G	G	G	A	G	G	G	A	G	G	G	A	A	G	A	A	A	G
0.370	rs7219923	35328044	C	C	C	C	T	C	C	T	T	C	C	C	T	T	C	T	T	T	C
0.370	rs7224129	35328952	G	G	G	G	A	G	G	A	A	G	G	G	A	A	G	A	A	A	G
0.628	rs8076131	35334438	G	A	G	A	A	G	G	A	A	A	A	G	A	A	A	A	A	A	G
0.211	rs9910635	35334690	G	G	G	G	G	G	G	G	G	G	G	G	A	G	G	A	G	G	A
1.000	rs12603332	35336333	T	T	C	T	C	T	T	T	C	T	T	T	T	C	T	T	C	C	T
1.000	rs17608925	35336357	T	T	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	C
1.000	rs9900885	35336577	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
0.370	rs3744246	35337876	C	C	C	T	C	T	C	C	C	T	T	C	T	C	T	T	C	C	T
0.087	rs9894164	35338324	T	T	T	T	T	T	T	T	T	T	T	C	T	C	C	T	T	C	T
1.000	rs4795402	35338911	C	A	C	A	C	A	C	A	C	A	A	C	A	C	A	A	C	C	A
1.000	rs4795403	35339248	C	C	C	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	T
0.370	rs4795404	35339317	C	C	C	A	C	A	C	C	C	A	A	C	A	C	A	C	C	A	A
0.370	rs4795405	35341943	C	C	C	T	C	T	C	C	C	T	T	C	T	C	T	C	C	T	T
0.370	rs4794820	35342870	A	A	G	A	G	A	A	A	G	A	A	A	G	G	A	G	G	G	A
1.000	rs8065244	35344754	C	C	C	C	C	C	C	G	C	G	G	C	C	C	G	C	C	C	C
1.000	rs7207600	35345186	G	A	A	A	A	A	G	A	A	A	A	G	A	A	A	A	A	A	A
1.000	rs8079416	35346239	T	T	C	C	C	C	T	T	C	T	T	T	T	C	T	C	C	C	C
1.000	rs6503525	35348700	G	G	C	C	C	C	G	G	C	G	G	G	G	C	G	C	C	C	C
1.000	rs8065126	35352561	T	C	C	C	C	C	T	C	C	C	C	T	C	C	C	C	C	C	C
1.000	rs4065985	35355458	G	C	C	C	C	C	G	C	C	C	C	G	C	C	C	C	C	C	C
1.000	rs9905525	35358931	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs16965456	35360621	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
1.000	rs4795408	35361153	G	G	A	G	A	A	G	G	A	G	G	G	A	G	A	A	A	G	A
0.211	rs9895948	35361889	T	T	C	C	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C
0.211	rs17609240	35364215	T	T	G	G	G	G	T	G	G	G	G	G	G	G	G	G	G	G	G
0.211	rs8076474	35364760	G	G	C	C	C	C	G	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs1007654	35364880	A	G	G	G	G	A	G	G	G	G	A	G	G	G	G	G	G	G	G
1.000	rs1007655	35364945	G	A	A	A	A	A	G	A	A	A	A	G	A	A	A	A	A	A	A
1.000	rs2313640	35365371	C	T	T	T	T	T	C	T	T	T	T	C	T	T	T	T	T	T	T
1.000	rs7218742	35367887	A	G	G	G	G	A	G	G	G	G	A	G	G	G	G	G	G	G	G
0.582	rs7218321	35367995	C	C	T	T	T	T	C	T	T	T	T	C	T	T	T	T	T	T	T
0.582	rs7219080	35368042	A	A	C	C	C	C	A	C	C	C	C	A	C	C	C	C	C	C	C
1.000	rs6503526	35368124	C	C	T	C	T	T	C	C	T	C	C	C	C	T	C	C	T	T	C
0.303	rs3902025	35372780	G	G	T	G	T	T	G	T	T	T	T	G	T	T	T	T	T	T	T
1.000	rs3894194	35375519	G	G	A	G	A	A	G	G	A	G	G	G	A	G	G	G	A	G	A
1.000	rs16965465	35375643	G	G	G	A	G	G	G	A	G	A	A	G	A	G	A	G	G	A	G
1.000	rs7212938	35376206	T	T	G	T	T	G	T	T	G	T	T	T	T	T	T	T	G	T	G
1.000	rs3859192	35382174	C	C	T	C	T	T	C	C	T	C	C	C	T	C	T	T	T	C	T
1.000	rs8077456	35382291	C	G	G	G	G	G	C	G	G	G	G	C	G	G	G	G	G	G	G
1.000	rs921651	35387448	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs8075668	35391149	T	T	C	C	C	C	T	T	C	T	T	T	C	T	C	T	C	T	C
0.474	rs2305481	35392150	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	G	A	G
1.000	rs11655264	35392521	C	C	G	G	G	G	C	C	G	C	C	C	C	G	C	G	C	G	C
1.000	rs11655584	35392550	C	T	C	C	C	C	T	T	C	T	T	T	C	C	T	C	C	C	C
1.000	rs2305482	35394453	C	C	A	A	A	A	C	C	A	C	C	C	A	C	A	C	A	C	A
1.000	rs9912981	35395162	T	C	C	C	C	C	T	T	C	T	T	T	C	T	C	T	C	C	C
1.000	rs11078930	35395481	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs8068498	35395647	T	T	T	T	T	G	T	T	T	T	G	T	T	T	T	T	T	T	T

1.000	rs3859188	35396504	C	C	C	C	C	C	T	T	C	T	T	T	C	C	T	C	C	C	C
1.000	rs4795411	35396908	A	A	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs4065321	35397074	T	T	C	C	C	C	T	T	C	T	T	T	T	C	T	C	T	C	T
1.000	rs9913561	35398593	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs9915252	35398614	G	G	C	C	C	C	G	G	C	G	G	G	G	C	G	C	G	C	G
1.000	rs9916279	35399680	T	T	T	T	T	T	C	C	T	C	C	C	T	T	C	T	T	T	T
1.000	rs8066582	35400455	C	C	T	T	T	T	C	C	T	C	C	C	C	T	C	T	C	T	C
1.000	rs8080546	35400492	C	C	C	C	C	C	C	C	C	A	A	C	C	C	A	C	C	C	C
1.000	rs11652139	35402559	A	A	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs11658328	35402762	C	C	T	T	T	T	C	C	T	C	C	C	C	T	C	T	C	T	C
1.000	rs8073254	35402876	G	G	C	C	C	C	G	G	C	G	G	G	G	C	G	C	G	C	G
1.000	rs3826330	35403762	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
1.000	rs2241245	35404540	T	T	C	C	C	C	T	T	C	T	T	T	T	T	C	T	C	T	C
1.000	rs9899302	35405612	G	G	G	G	G	G	G	C	G	G	G	G	G	G	G	G	G	G	G
1.000	rs12453334	35406999	C	C	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs2012	35407610	G	G	G	G	G	G	C	C	G	C	C	C	G	G	C	G	G	G	G
0.656	rs4794822	35410238	C	C	T	C	T	T	C	C	T	C	C	C	T	T	C	T	C	T	T
1.000	rs8068076	35411096	G	G	G	G	G	G	A	A	G	A	A	A	G	G	A	G	G	G	G
1.000	rs9748108	35412757	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs8070454	35414280	C	C	T	C	T	T	C	C	T	C	C	C	C	T	C	T	C	T	C
1.000	rs11652972	35415443	G	G	G	G	G	G	T	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs6503531	35416009	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
1.000	rs7211771	35419310	C	C	C	C	C	C	T	C	C	C	C	T	C	C	C	C	C	C	C
1.000	rs8078723	35420405	T	T	C	T	C	C	T	T	C	T	T	T	T	C	T	C	T	C	T
1.000	rs7224260	35422139	C	C	C	C	C	C	C	C	C	T	T	C	C	C	T	C	C	C	C
1.000	rs11655821	35423220	C	C	C	C	C	C	T	C	C	C	C	T	C	C	C	C	C	C	C
1.000	rs2227319	35424371	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2227320	35424790	G	T	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2227321	35424820	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2227322	35425194	C	C	G	C	G	G	C	C	G	C	C	C	C	G	C	G	C	G	C
1.000	rs2071369	35425831	C	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs2227327	35425939	G	C	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2227328	35425968	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2071370	35425978	C	C	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs5820317	35426499	G	G	G	C	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2227329	35426583	C	C	C	C	C	C	A	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs2227330	35426634	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs25645	35426669	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2827	35427263	C	C	C	C	C	C	T	T	C	T	T	T	C	C	T	C	C	C	C
1.000	rs1042657	35427318	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
1.000	rs1042658	35427428	C	C	T	C	T	T	C	C	T	C	C	C	C	T	C	T	C	T	C
1.000	rs2227334	35427735	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs1045929	35428952	C	C	T	C	T	T	C	C	T	C	C	C	C	T	C	T	C	T	C
1.000	rs12309	35428988	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs709592	35429079	C	C	T	C	T	T	C	C	T	C	C	C	C	T	C	T	C	T	C
1.000	rs709591	35429087	T	T	A	T	A	A	T	T	A	T	T	T	T	A	T	A	T	A	T
1.000	rs16965540	35429557	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
1.000	rs2270401	35429782	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs9913632	35430958	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs2302776	35431675	A	G	A	G	A	A	G	G	A	A	A	A	G	A	A	A	G	A	G
1.000	rs3213762	35432153	A	A	G	A	G	G	A	A	G	A	A	A	A	G	A	G	A	G	A
1.000	rs9891598	35432319	G	G	G	G	G	G	G	A	G	G	G	G	G	G	G	G	G	G	G
1.000	rs12451897	35432801	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2302777	35433018	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs9915684	35435550	G	G	G	G	G	G	A	G	A	G	G	G	G	G	G	G	G	G	G
1.000	rs7503939	35435607	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs9916158	35435755	G	G	G	G	G	G	G	T	G	G	G	G	G	G	G	G	G	G	G
1.000	rs2302775	35436370	C	C	T	C	T	T	C	C	T	C	C	C	C	T	C	T	C	T	C
1.000	rs2302774	35436616	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs7501734	35441453	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs7502514	35442370	G	G	A	A	A	A	G	G	A	G	G	G	A	A	G	A	G	A	A
0.650	rs3935280	35442581	G	G	A	A	A	A	G	G	A	G	G	G	A	A	G	A	A	A	A
0.650	rs6503534	35445450	G	G	A	A	A	A	G	G	A	G	G	G	A	A	G	A	A	A	A
1.000	rs3934886	35449021	A	G	A	A	A	A	A	A	A	G	G	A	A	A	G	A	A	A	A
1.000	rs9895610	35449561	T	T	T	A	T	T	A	A	T	T	T	A	A	T	T	T	T	A	T

1.000	rs11078936	35451440	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
1.000	rs9907437	35454826	T	T	T	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T
1.000	rs11078937	35462079	G	G	G	G	G	A	A	G	G	G	A	G	G	G	G	G	G	G
1.000	rs8082130	35462417	G	G	G	G	G	A	A	G	G	G	A	G	G	G	G	G	G	G
0.656	rs8065443	35462466	G	G	A	G	A	A	G	G	A	G	G	A	A	G	A	G	A	A
0.656	rs868150	35466885	G	G	A	G	A	A	G	G	A	G	G	A	A	G	A	G	A	A
0.370	rs7502966	35470048	C	T	T	T	T	C	C	T	T	T	T	C	T	T	C	C	C	C
1.000	rs1568400	35474634	T	C	C	C	T	C	C	C	T	C	C	C	T	C	C	C	T	C
1.000	rs8078399	35478024	G	T	G	T	G	G	G	G	G	G	G	T	G	G	G	G	G	T
1.000	rs9893741	35478938	G	C	C	G	G	C	G	C	G	G	G	C	C	G	G	C	G	G
1.000	rs1879265	35484902	G	A	G	G	A	G	A	A	A	G	G	G	A	A	G	G	A	A
1.000	rs939348	35485379	C	C	C	T	T	C	C	C	C	C	C	C	T	C	C	C	T	C
1.000	rs2230701	35493742	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs8075021	35494287	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs12939700	35499317	C	C	C	C	C	A	C	A	C	C	C	C	C	C	A	C	C	C
0.628	rs3744805	35501880	C	C	C	T	C	C	C	C	C	T	T	C	C	T	C	C	T	C
0.628	rs2314339	35506738	C	C	C	T	C	C	C	C	C	T	T	C	C	T	C	C	T	C
1.000	rs9905506	35506995	G	G	G	G	G	G	A	G	G	G	G	G	G	G	G	G	G	A
1.000	rs2071427	35508018	T	T	C	C	T	T	T	T	T	T	T	C	T	T	C	T	T	T
1.000	rs2269457	35508215	C	C	T	T	T	T	C	C	C	T	C	T	C	T	T	C	C	C
1.000	rs9894283	35508575	C	C	C	C	C	C	C	T	C	C	C	C	C	C	C	C	C	T
0.650	rs12941497	35509120	A	A	G	A	G	A	A	G	A	A	A	G	A	G	A	A	A	G
0.350	rs939347	35510219	A	G	G	A	G	A	G	G	A	A	G	G	G	G	A	A	G	G
0.303	rs2071570	35510616	A	C	C	A	C	A	C	C	C	A	C	C	C	C	A	C	C	C
0.350	rs16965644	35517723	G	G	G	A	A	A	G	A	A	G	G	A	G	A	A	A	A	A
1.000	rs9898129	35519475	A	T	A	A	A	A	T	A	A	T	T	A	T	A	A	A	A	A
1.000	rs9890574	35525853	A	T	A	A	T	A	T	T	T	T	T	A	T	A	T	T	A	T
1.000	rs9897340	35526403	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs9903261	35530994	A	C	A	A	A	A	C	A	A	A	C	A	C	A	A	A	A	A
1.000	rs9906274	35535107	C	C	C	C	C	C	G	C	C	C	G	C	C	C	C	C	C	C
1.000	rs2030380	35535232	T	T	T	T	T	T	T	T	C	T	T	T	T	T	T	T	T	T
1.000	rs2030379	35535660	T	T	T	T	T	T	T	T	C	T	T	T	T	T	T	T	T	T
1.000	rs9900154	35536725	T	C	T	T	T	T	C	T	T	T	C	T	C	T	T	T	C	T
0.628	rs7211770	35542529	A	G	A	A	G	A	G	G	G	G	G	A	G	G	G	G	A	G
1.000	rs10512482	35542587	A	T	A	A	A	A	T	A	A	A	T	A	T	A	A	A	T	A
1.000	rs16965660	35545347	C	T	C	C	C	C	T	C	C	C	T	C	T	C	C	C	C	C
1.000	rs7212098	35551463	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs9910546	35555665	T	T	T	T	T	T	G	T	T	T	G	T	T	T	T	T	T	T
1.000	rs16965669	35557882	C	A	C	C	C	C	A	C	C	C	A	C	A	C	C	C	A	C
1.000	rs9898500	35558907	G	A	G	G	G	G	A	G	G	G	A	G	A	G	G	G	G	G
1.000	rs7206995	35559891	G	G	G	G	G	G	A	G	G	G	A	G	A	G	G	G	G	G
1.000	rs9910373	35561768	A	G	A	A	A	A	G	A	A	A	G	A	G	A	A	A	G	A
1.000	rs9909777	35561869	C	T	C	C	C	C	T	C	C	C	T	C	T	C	C	C	T	C
1.000	rs3923166	35570302	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
1.000	rs9896339	35576112	A	A	A	A	A	A	T	A	A	A	T	A	T	A	A	A	A	A
1.000	rs9909548	35579348	G	G	G	G	G	G	C	G	G	G	C	G	C	G	G	G	G	G
1.000	rs9909811	35579469	G	C	G	G	G	G	C	G	G	G	C	G	C	G	G	G	G	G
1.000	rs9894807	35583704	T	G	T	T	T	T	G	T	T	T	G	T	G	T	T	T	G	T
1.000	rs9911936	35586558	A	A	A	A	A	A	G	A	A	A	G	A	G	A	A	A	A	A
1.000	rs2280400	35602653	G	G	G	G	G	G	A	G	G	G	A	G	A	G	G	G	G	G
1.000	rs4254375	35604085	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
0.650	rs3744806	35605152	G	C	C	C	G	C	G	G	G	C	G	C	G	C	G	G	C	G
1.000	rs9907683	35612427	A	A	A	A	A	A	C	A	A	A	C	A	C	A	A	A	A	A
0.650	rs8073925	35613046	C	G	G	G	C	G	C	C	C	G	C	G	C	G	C	C	G	C
1.000	rs9901109	35633374	T	T	T	T	T	T	G	T	T	T	G	T	G	T	T	T	T	T
1.000	rs6503539	35636451	T	T	C	C	T	C	T	T	T	C	T	C	T	C	T	T	T	T
1.000	rs9908034	35640001	T	T	T	T	T	T	C	T	T	T	C	T	C	T	T	T	T	T
1.000	rs16965687	35641044	T	T	T	T	T	T	C	T	T	T	C	T	C	T	T	T	T	T
1.000	rs9916782	35641566	A	A	A	A	A	A	G	A	A	A	G	A	G	A	A	A	A	A
0.650	rs8066144	35641717	C	T	T	T	C	T	C	C	C	T	C	T	C	T	C	C	T	C
1.000	rs8076915	35645052	A	G	G	G	A	G	G	A	A	G	G	G	G	A	A	A	G	A
1.000	rs9904021	35652756	G	G	G	G	G	T	G	G	G	T	G	T	G	G	G	G	G	G
1.000	rs8072718	35653135	A	G	G	G	A	G	G	A	A	G	G	G	G	A	A	A	G	A
1.000	rs12936565	35658563	C	T	T	T	C	T	T	C	C	T	T	T	T	C	C	C	T	C
1.000	rs16965691	35663449	C	C	C	C	C	C	C	C	C	G	C	C	C	C	C	C	C	C

1.000	rs11078940	35663590	C	C	C	C	C	C	T	C	C	C	T	C	T	C	C	C	C	C	C
1.000	rs4566234	35667875	G	G	G	G	G	G	T	G	G	G	T	G	T	G	G	G	G	G	G
1.000	rs4077125	35677005	G	G	G	G	G	G	A	G	G	G	A	G	A	G	G	G	G	G	G
1.000	rs9916460	35681591	T	T	T	T	T	T	C	T	T	C	T	C	T	T	T	T	T	T	T
1.000	rs9908257	35681648	G	G	G	G	G	G	A	G	G	G	A	G	A	G	G	G	G	G	G
1.000	rs9899406	35699959	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
0.650	rs2077464	35700090	G	A	A	A	G	A	G	G	G	A	G	A	G	A	G	G	A	G	G
1.000	rs1130199	35701095	C	T	T	T	C	T	T	C	C	T	T	T	T	T	C	C	C	T	C
1.000	rs4135011	35703425	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs4135013	35703787	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
1.000	rs4135014	35704314	T	T	T	T	A	T	T	T	T	T	T	T	T	T	T	T	T	A	T
1.000	rs4135025	35708682	G	T	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
0.650	rs13706	35710677	A	G	G	G	A	G	A	A	A	G	A	G	A	G	A	A	A	G	A
1.000	rs9895942	35713623	G	G	G	G	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G
0.650	rs2120200	35713901	G	A	A	A	G	A	G	G	G	A	G	A	G	A	G	G	A	G	G
1.000	rs9892367	35716914	A	G	G	G	A	G	G	A	A	G	G	G	G	A	A	A	G	A	A
1.000	rs7222102	35718876	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
1.000	rs7217852	35723547	G	G	A	A	G	A	G	G	G	A	G	A	G	A	G	G	A	G	G
1.000	rs9904270	35733357	C	C	C	C	C	C	T	C	C	C	T	C	T	C	C	C	C	C	C
0.650	rs12946680	35734183	G	C	C	C	G	C	G	G	G	C	G	C	G	C	G	G	C	G	G
1.000	rs8065665	35735789	C	A	A	A	C	A	A	C	C	A	A	A	A	A	C	C	C	A	C

Table S6. Top 100 genes (known) associated with the rs12936231 SNP, from publically available datasets from Sanger et al. (Population genomics of human gene expression, *Nature Genetics* 39, 1217-1224, 2007) and from Kwan et al. (Genome-wide analysis of transcript isoform variation in humans, *Nature Genetics* 40, 225-231, 2008).

Top 100 genes associated with rs12936231

Sanger CEU	Sanger YRI	Kwan CEU
ORMDL3	ORMDL3	GSDML
LOC338949	PEX26	RHOD
LOC283010	KCNAB1	OR2L2
CECR1	LOC400964	ORMDL3
LOC401109	LOC377094	DKFZP564O0823
LOC375118	ETV6	P4HA2
RFXAP	ELAVL3	ACADVL
AP1G2	SUPT3H	SHF
FLJ32844	CASPR3	C22orf37
KCNJ1	ALS2CR7	CLIP2
ATM	STK38L	RBPJ
SLC11A1	GPR52	RAB27B
FLJ14082	RGPR	C8orf46
LOC403313	LOC401945	IL12RB2
ACY-3	LOC257407	PYCARD
CIZ1	CLCN5	ASCL4
STXBP2	LMO7	KRTAP4-2
KIAA1836	KIAA1596	ASTL
PDC	SEMA5B	TFCP2L1
LOC388832	PROSC	F9
LOC339065	LOC387736	PTTG3
ARTN	F8	ALS2CR13
MGC17791	LOC345525	SCG5
BTG4	LOC375819	KCNMB4
DNAJC6	MGC1136	ABCC4
C11ORF4	DECR2	LOC200383
GALNT8	DEFB125	CXCL14
DAB2IP	LOC399904	KIAA1505
LOC151242	LOC342619	C21orf62
KRTAP3-3	ANKRD2	MRPS26
GJE1	HGFAC	FAM26C
SPTBN1	KIAA0828	MGC4294
GNAI2	FLJ14297	KRTAP1-1
FLJ23306	THAP11	TFEC
DCTN1	LOC388957	RRAS2
LOC400154	RANBP2L1	TCEAL6
HIST1H2BK	LOC402630	PLEKHA7
BAT1	C14orf143	TMEM24
FLJ23360	LOC129870	LYZ

SIAT7E	FGA	SH3PXD2A
LOC390325	PPP1R13B	CCDC23
CNGA1	DDX31	ROBO1
CD8A	CCNDBP1	SMAD2
SLC22A1	NOTCH2	RASAL1
LOC400852	LOC286333	ARL11
LOC375521	LOC387833	GRM5
CBFA2T3	MGC3207	GPA33
PRO0659	TOB3	FBXO36
KIAA1985	QSCN6	NUMBL
DPP8	KRT18	GRASP
LOC389015	SOX12	PTHLH
SMARCD1	MYADM	PTTG1IP
LOC387836	LSM8	POU6F2
LOC346399	LOC388334	CAMK2G
RGS14	ZSWIM2	TNFSF14
LOC401627	PAMCI	SERPINB11
KCNJ3	ZNF319	CKM
HYPC	PNLIPRP2	TMEM185B
NR2E3	HSPD1	PRM3
FLJ23614	WNT2B	CTNNA1
SCRG1	HSPA12B	RAB27A
MDS1	DUSP15	TIGD6
TM6SF1	AMPD2	SHC4
LOC284938	FCRH3	C8orf77
LOC389334	LOC285401	PHLDB3
LOC387904	HOXD1	ENPP5
EZH1	CLASP2	CMYA5
LOC375092	SMAP1	GRLF1
FLJ40542	ABCC11	ACY3
LOC63920	ALDH3A2	TJP3
CACH-1	CCR8	NCOA6
C17orf31	LOC374833	LOC645261
LOC400958	RPH3AL	KATNB1
H2BFS	LOC285118	ARHGAP24
FLJ22390	LOC377625	TNNT3
LOC402577	LOC219954	PHACS
FLJ45778	SCNN1A	ARHGEF4
SLC29A4	DT1P1A10	TAF1
MFRP	EAF1	ZNF77
HHL	NIP30	KIRREL2
UPP2	RBL2	RDH5
MS4A2	LOC283385	ATP8B2
GPR6	NALP6	SERPINB10
DYRK2	PCDHGB7	EYA1
LOC375672	LOC339738	HAS3

LOC377839	SLC25A20	TMEM134
DPP6	LOC376401	P2RX7
LOC345970	TMPRSS6	MGC40574
OPCML	LOC342132	FAM5C
AKNA	CX3CR1	DPYD
LOC375509	DKFZP564D172	FLJ46020
LOC402592	LZIC	FLJ45530
HIST1H2AK	C10orf26	NR4A1
TGM1	GGN	SMARCA4
FOX11	LOC256280	ZNF33A
GPRC5D	ANK3	C17orf58
SLC22A1	A1BG	HLA-DRA
GP2	VPS41	C8orf16
ANKRD1	MT4	FLJ32214
LOC152485	SEPHS2	DUSP5P

Table S7. Information for SNPs that were heterozygous in at least two resequenced samples. r^2 value for each SNP with rs12936231 is given.

SNP	chr	location	Genic location	CEU				YRI				Genomic context of failed assay
				NA07056	NA07345	r^2	AE P value (GSDMB)	NA18858	NA18871	r^2	AE P value (GSDMB)	
RS2952144	17	35213543	IKZF3	htz	htz	£		htz		*		SINE repeat
RS4795395	17	35216513	IKZF3	htz	htz	0.800	3.01E-12		htz	0.036	1.000	
RS56380902	17	35319898	GSDMB	htz	htz	£			htz	0.321	0.003	
RS1011082	17	35322040	GSDMB	htz	htz	1.000	1.09E-18		htz	0.237	0.004	
RS921650	17	35322602	GSDMB	htz		£			htz	0.121	0.071	
RS921649	17	35322800	GSDMB	htz	htz	£			htz	*		SINE repeat
RS7216558	17	35323597	GSDMB	htz	htz	1.000	1.09E-18	htz	htz	0.402	7.96E-05	
RS7221605	17	35324315	GSDMB	htz		£			htz	*		SINE repeat
RS1031458	17	35325699	GSDMB	htz	htz	£			htz	0.132	0.243	
RS8065777	17	35325928	GSDMB	htz	htz	0.895	3.60E-17		htz	0.142	0.243	
RS9303279	17	35327494	GSDMB	htz	htz	0.800	3.01E-12		htz	£		
RS3902920	17	35328542	intergenic	htz	htz	£		htz	htz	0.102	0.120	
RS8074437	17	35329663	intergenic	htz	htz	£		htz	htz	0.294	2.75E-04	

£ Sequenom assay failed for these SNPs

* Sequenom genotyping and Sanger sequencing failed for these SNPs

htz: resequenced individual predicted to be heterozygous for that SNP