LEGENDS TO SUPPLEMENTARY TABLE AND FIGURES

Table S1. Previously reported 29 non-MHC autosomal SLE loci that were supported at the SNP or locus level [gene(s) of interest ± 50 kb] in our Stage 1 discovery sample.

Figure S1. Quantile–quantile plot of the observed p-values vs. the expected p-values under the null hypothesis. The black dots represent the p-values for all autosomal common SNPs in Stage 1 discovery sample while the blue ones represent the p-values after removing the SNPs from the xMHC region at 6p21 (the strongest susceptibility locus for SLE). Significant deviation from the null distribution at the tail of the observed distribution, even after the removal of the markers from the xMHC region, suggests the presence of other compelling susceptibility loci. The red line indicates the distribution under the null hypothesis.

Figure S2. Manhattan plot showing the distribution of genome-wide association p-values for SLE in Stage 1 discovery sample for the common markers across 22 autosomal chromosomes. The blue and red lines indicate $P=5x10^{-8}$ and $P=5x10^{-6}$, respectively.

Figure S3. The SNP-centric eQTL analysis (cis-eQTL - SNP) results for the SNPs of interest at the 12q12 locus. The Genevar database was utilized to visualize the eQTL association patterns within our region of interest (http://www.sanger.ac.uk/resources/software/genevar/). The results were derived from the data obtained from the Multiple Tissue Human Expression Resource (MuTHER) on genetic variation and gene expression profiling [tissues: adipose (A-red), lymphoblastoid cell lines (L-blue), and skin (S-green)]. Observed SNP-probe associations are shown in a 2-Mb region (within 1-Mb on either side of the interrogated SNP). Genes/probes evaluated for all 4 SNPs included *GXYLT1*, *YAF2* (3 probes), *ZCRB1*, *PPHLN1* (3 probes), *PRICKLE1*, *ADAMTS20* (3 probes), and *PUS7L*. The evaluation of two additional genes/probes (*IRAK4* and *PTK9*) was available for only rs1914490

due to their long distance (>1-Mb) from the remaining SNPs. The analysis was performed using an external algorithm (preloaded). Significant probes (genes) are labeled for each SNP. The dotted line represents the p-value threshold of 0.05.

Figure S4. The gene-centric eQTL analysis (cis-eQTL - Gene) results in adipose tissue for the genes of interest at the 12q12 locus. The Genevar database was used to visualize the eQTL association patterns (http://www.sanger.ac.uk/resources/software/genevar/). The results were derived from the data obtained from the Multiple Tissue Human Expression Resource (MuTHER) on genetic variation and gene expression profiling. The analysis was performed using an external algorithm (preloaded). Observed eQTL SNPs (eSNPs) are shown in a 2-Mb window around a given probe/gene. Whenever our region of interest (NCBI36/hg18; chr12: 41417152-41500751) overlapped with 'the most relevant cis-eQTL SNPs region' for the implicated genes, a rectangle was used to mark our region of interest. *PPHLN1* and *ADAMTS20* had two additional probes for which the results are not shown. The dotted line represents the p-value threshold of 0.05.

Figure S5. The gene-centric eQTL analysis (cis-eQTL - Gene) results in lymphoblastoid cell lines for the genes of interest at the 12q12 locus. The Genevar database was used to visualize the eQTL association patterns (http://www.sanger.ac.uk/resources/software/genevar/). The results were derived from the data obtained from the Multiple Tissue Human Expression Resource (MuTHER) on genetic variation and gene expression profiling. The analysis was performed using an external algorithm (preloaded). Observed eQTL SNPs (eSNPs) are shown in a 2-Mb window around a given probe/gene. Whenever our region of interest (NCBI36/hg18; chr12: 41417152-41500751) overlapped with 'the most relevant cis-eQTL SNPs region' for the implicated genes, a rectangle was used to mark our region of interest. *PPHLN1* and *ADAMTS20* had two additional probes for which the results are not shown. The dotted line represents the p-value threshold of 0.05.

Figure S6. The SNP-centric mQTL analysis results for the SNPs of interest at the 12q12 locus.

The Genevar database was utilized to visualize the mQTL association patterns within our region of interest (http://www.sanger.ac.uk/resources/software/genevar/). The results were derived from the data obtained from the Multiple Tissue Human Expression Resource (MuTHER) on genetic variation and DNA methylation profiling (tissue: adipose). The mQTL analysis included the association testing between methylation levels and common variants (MAF>0.05) located close to the probes (probe ± 100 kb). The analysis was performed using an external algorithm (preloaded). Significant probes are labeled for each SNP. The dotted line represents the p-value threshold of 0.05.

Figure S7. Expression profiles of *ZCRB1*, *PPHLN1,* and *IRAK4* in human cells/tissues. The expression profiles were obtained from BioGPS gene annotation portal (http://biogps.org/#goto=welcome).

Figure S8. Expression profiles of *PRICKLE1* and *ADAMTS20* in human cells/tissues. The expression profiles were obtained from BioGPS gene annotation portal (http://biogps.org/#goto=welcome).

Figure S9. The enhancer enrichment analysis results for the SNPs of interest and their proxies (with category 1 or 2 RegulomeDB scores) at the 12q12 locus. HaploReg v2 (http://www.broadinstitute.org/mammals/haploreg/haploreg.php) was used to perform enhancer enrichment analysis for 4 SNPs of interest (rs10506216, rs1356422, rs11181677, rs1914490) and 3 proxy SNPs (rs868765, rs2897590, rs870972) falling into RegulomeDB categories 1 or 2 (see Methods and Results sections).

Table S1. Previously reported 29 non-MHC autosomal SLE loci that were supported at the SNP or locus level [gene(s) of interest ± 50 kb] in our Stage 1 discovery sample

Locus / Gene(s)	Chr	Band	SNP*	Position in bp (hg19)	Allele	Freq Cases (n=661)	Freq Controls (n=487)	OR	P**	Nearest Gene***	Location in the Gene****	RegulomeDB score*****
FCGR locus	1	q23.3	rs12722986	161465420	G	0.139	0.163	0.721	0.0215	*FCGR2A*		6
	1	q23.3	rs12746613	161467042	A	0.133	0.155	0.735	0.0318	*FCGR2A*		6
	1	q23.3	rs867624	161467837	T	0.133	0.155	0.735	0.0318	*FCGR2A*		**1f**
	1	q23.3	rs7552317	161479438	T	0.126	0.154	0.652	4.66E-03	*FCGR2A*	intron	ND
TNFSF4	1	q25.1	rs844645	173210090	G	0.486	0.431	1.222	0.0388	*LOC100506023*	intron	ND
NCF2	1	q25.3	rs3768591	183501774	G	0.042	0.061	0.6	0.0261	*SMG7*	intron	6
	1	q25.3	rs3754517	183562517	C	0.392	0.449	0.805	0.0270	*NCF2*		**1f**
	1	q25.3	rs10797891	183563808	C	0.403	0.456	0.823	0.0438	*NCF2*		6
	1	q25.3	rs2333685	183565989	C	0.362	0.417	0.789	0.0184	*NCF2*		6
	1	q25.3	rs2333686	183566100	A	0.372	0.429	0.776	0.0129	*NCF2*		6
	1	q25.3	rs41439047	183566913	T	0.332	0.384	0.808	0.0372	*NCF2*		5
	1	q25.3	rs2761559	183580279	T	0.386	0.437	0.813	0.0332	*ARPC5*		**1f**
	1	q25.3	rs2761560	183580370	T	0.385	0.438	0.803	0.0238	*ARPC5*		**1f**
	1	q25.3	rs2761561	183580653	G	0.385	0.437	0.81	0.0295	*ARPC5*		6
	1	q25.3	rs2761565	183581402	A	0.390	0.438	0.823	0.0454	*ARPC5*		6
	1	q25.3	rs16861241	183589167	T	0.025	0.039	0.549	0.0371	*ARPC5*		4
	1	q25.3	rs16861243	183589382	A	0.025	0.038	0.562	0.0455	*ARPC5*		**3a**
	1	q25.3	rs10797896	183589800	G	0.025	0.038	0.564	0.0472	*ARPC5*		ND
	1	q25.3	rs16861259	183593328	A	0.025	0.038	0.564	0.0472	*ARPC5*		ND
	1	q25.3	rs12043560	183594102	T	0.025	0.038	0.564	0.0472	*ARPC5*		5
	1	q25.3	rs4652822	183598350	T	0.328	0.380	0.807	0.0395	*ARPC5*	intron	**1f**
	1	q25.3	rs17436125	183601331	T	0.329	0.388	0.773	0.0142	*ARPC5*	intron	**1f**
	1	q25.3	rs2254972	183602795	G	0.409	0.476	0.756	3.75E-03	*ARPC5*	intron	**1f**
	1	q25.3	rs6673809	183603060	A	0.025	0.038	0.566	0.0482	*ARPC5*	intron	4
IL10	1	q32.1	**rs3024505**	206939904	T	0.173	0.156	1.3	0.0414	*IL10*		**2b**
RASGRP3	2	p22.3	rs2034693	33623306	G	0.449	0.506	0.773	8.76E-03	*LTBP1*	intron	5
	2	p22.3	rs662050	33627842	G	0.239	0.302	0.676	3.70E-04	*LTBP1*		ND
	2	p22.3	rs1869452	33630276	C	0.377	0.413	0.81	0.0327	*LTBP1*		5
	2	p22.3	rs588252	33631442	T	0.238	0.283	0.75	9.34E-03	*LTBP1*		ND
	2	p22.3	rs11680631	33694912	G	0.389	0.425	0.801	0.0344	*RASGRP3*	intron	6
	2	p22.3	rs17648308	33703217	G	0.117	0.144	0.722	0.0264	*RASGRP3*	intron	4
	2	p22.3	rs11687036	33753366	T	0.451	0.412	1.236	0.0316	*RASGRP3*	intron	ND
	2	p22.3	rs13391166	33805314	C	0.505	0.469	1.22	0.0427	*FAM98A*		ND
	2	p22.3	rs11066	33809294	A	0.208	0.262	0.683	1.12E-03	*FAM98A*		5
	2	p22.3	rs6708570	33815384	A	0.210	0.260	0.705	2.94E-03	*FAM98A*		6
TET3	2	p13.1	rs4384817	74226141	A	0.072	0.042	1.835	5.26E-03	*TET3*	intron	ND
STAT4	2	q32.2	rs34997637	191858830	T	0.269	0.213	1.333	0.0126	*STAT1*	intron	4
	2	q32.2	rs10167514	191860529	T	0.270	0.213	1.345	0.0102	*STAT1*	intron	**1f**
	2	q32.2	rs2030171	191869163	A	0.386	0.303	1.301	9.76E-03	*STAT1*	intron	5
	2	q32.2	rs10199181	191873553	T	0.439	0.359	1.362	2.00E-03	*STAT1*	intron	5
	2	q32.2	rs13029532	191875901	G	0.069	0.082	0.617	0.0115	*STAT1*	intron	**3a**
	2	q32.2	rs16833177	191887632	C	0.246	0.180	1.345	0.0163	*STAT4*		4
	2	q32.2	rs3024912	191893087	C	0.271	0.202	1.342	0.0125	*STAT4*		6
	2	q32.2	rs3024903	191895607	T	0.095	0.110	0.715	0.0367	*STAT4*	intron	4
	2	q32.3	**rs3821236**	191902758	T	0.265	0.175	1.647	3.78E-05	*STAT4*	intron	5
	2	q32.3	rs11676659	191919354	C	0.047	0.061	0.557	0.0113	*STAT4*	intron	5
	2	q32.3	**rs11893432**	191921874	G	0.258	0.176	1.562	2.47E-04	*STAT4*	intron	5
	2	q32.3	rs3024861	191924606	T	0.322	0.243	1.316	0.0132	*STAT4*	intron	5
	2	q32.3	rs1517352	191931464	A	0.457	0.395	1.232	0.0422	*STAT4*	intron	5
	2	q32.3	rs7594501	191938600	T	0.053	0.080	0.518	1.72E-03	*STAT4*	intron	6
	2	q32.3	**rs7601754**	191940451	G	0.148	0.207	0.567	1.71E-05	*STAT4*	intron	5
	2	q32.3	**rs6434435**	191953864	A	0.135	0.195	0.575	5.93E-05	*STAT4*	intron	6
	2	q32.3	**rs10931480**	191954047	C	0.147	0.206	0.582	4.85E-05	*STAT4*	intron	ND
	2	q32.3	**rs4274624**	191958656	C	0.321	0.214	1.784	4.48E-07	*STAT4*	intron	5
	2	q32.3	**rs7582694**	191970120	C	0.327	0.216	1.811	3.59E-07	*STAT4*	intron	4
	2	q32.3	rs16833260	191971565	C	0.400	0.313	1.385	2.05E-03	*STAT4*	intron	ND
PXK	3	p14.3	rs11706920	58279672	T	0.092	0.065	1.451	0.0435	*ABHD6*	exon-3'UTR	**1f**
	3	p14.3	rs1045115	58305199	T	0.094	0.065	1.47	0.0362	*RPP14*	exon-3'UTR	6
	3	p14.3	rs7643185	58311158	A	0.095	0.065	1.478	0.0327	*RPP14*		**1f**
	3	p14.3	rs9864325	58336846	C	0.096	0.068	1.458	0.0373	*PXK*	intron	**1f**
	3	p14.3	rs9850717	58351875	T	0.096	0.065	1.532	0.0206	*PXK*	intron	6
	3	p14.3	rs9864824	58394835	A	0.092	0.065	1.464	0.0405	*PXK*	intron	**1f**
TMEM39A/CD80	3	q13.33	rs747001	119102496	G	0.041	0.028	1.719	0.0458	*ARHGAP31*	intron	ND
	3	q13.33	rs1000199	119113762	A	0.125	0.098	1.558	4.36E-03	*ARHGAP31*	intron	ND
	3	q13.33	rs12495749	119129528	G	0.190	0.166	1.329	0.0233	*ARHGAP31*	intron	6
	3	q13.33	rs16829838	119138675	A	0.190	0.166	1.329	0.0233	*ARHGAP31*		**1f**
	3	q13.33	rs7430156	119161982	G	0.416	0.447	0.814	0.0384	*TMEM39A*	intron	ND
	3	q13.33	rs16829853	119165650	T	0.190	0.166	1.334	0.0218	*TMEM39A*	intron	6
	3	q13.33	rs4688007	119198873	G	0.204	0.242	0.772	0.0307	*POGLUT1*	exon	6
	3	q13.33	rs1967621	119225082	G	0.202	0.233	0.781	0.0426	*TIMMDC1*	intron	6
AFF1	4	q21.3	rs17012341	87983116	A	0.024	0.012	2.648	8.96E-03	*AFF1*	intron	6
	4	q21.3	rs10021879	87987215	T	0.024	0.011	2.751	8.73E-03	*AFF1*	intron	ND

Locus / Gene(s)	Chr	Band	SNP*	Position in bp (hg19)	Allele	Freq Cases (n=661)	Freq Controls (n=487)	OR	P**	Nearest Gene***	Location in the Gene****	RegulomeDB score*****
	4	q22.1	rs236988	88013680	G	0.024	0.012	2.561	0.0116	*AFF1*	intron	**3a**
	4	q22.1	rs236990	88015386	C	0.026	0.012	2.702	7.25E-03	*AFF1*	intron	5
BANK1	4	q24	rs6833249	102726073	G	0.090	0.103	0.66	0.0189	*BANK1*	intron	6
	4	q24	rs4385063	102831285	A	0.102	0.120	0.69	0.0243	*BANK1*	intron	ND
	4	q24	rs4337734	102832228	C	0.104	0.122	0.696	0.0259	*BANK1*	intron	**3a**
	4	q24	rs1809578	102852575	C	0.107	0.126	0.706	0.0295	*BANK1*	intron	ND
	4	q24	rs918363	102852939	A	0.108	0.129	0.687	0.0190	*BANK1*	intron	4
	4	q24	rs2631271	102914396	A	0.108	0.129	0.696	0.0231	*BANK1*	intron	5
	4	q24	rs6853274	102941663	T	0.025	0.039	0.526	0.0313	*BANK1*	intron	ND
	4	q24	rs2631265	102945076	A	0.107	0.118	0.732	0.0442	*BANK1*	intron	6
TNIP1	5	q33.1	rs11747116	150427285	A	0.477	0.449	1.222	0.0444	*TNIP1*	intron	5
	5	q33.1	rs4958435	150438284	T	0.495	0.437	1.266	0.0174	*TNIP1*	intron	**1f**
	5	q33.1	rs2233287	150440097	A	0.098	0.072	1.521	0.0156	*TNIP1*	intron	**2b**
	5	q33.1	rs6869605	150452866	G	0.158	0.108	1.494	5.25E-03	*TNIP1*	intron	5
	5	q33.1	rs4958882	150454787	G	0.155	0.106	1.539	3.10E-03	*TNIP1*	intron	ND
	5	q33.1	rs3792784	150455672	C	0.126	0.091	1.565	4.11E-03	*TNIP1*	intron	4
	5	q33.1	rs3792783	150455732	G	0.195	0.139	1.474	3.27E-03	*TNIP1*	intron	4
	5	q33.1	rs13168551	150462638	C	0.454	0.383	1.248	0.0262	*TNIP1*	intron	4
SNRPC/UHRF1BP1	6	p21.31	rs6932930	34677103	C	0.254	0.216	1.349	0.0126	*C6orf106*		5
	6	p21.31	**rs2477508**	34703695	A	0.412	0.327	1.299	0.0130	*SNRPC*		ND
	6	p21.31	**rs2764211**	34704613	C	0.408	0.326	1.314	8.92E-03	*SNRPC*		5
	6	p21.31	rs2764199	34706982	G	0.261	0.222	1.336	0.0119	*SNRPC*		5
	6	p21.31	**rs2814971**	34714209	A	0.405	0.324	1.295	0.0131	*SNRPC*		4
	6	p21.31	**rs2764208**	34714322	G	0.410	0.326	1.324	7.34E-03	*SNRPC*		5
	6	p21.31	**rs1998702**	34741917	G	0.406	0.327	1.31	9.66E-03	*SNRPC*		5
	6	p21.31	**rs10947531**	34765118	A	0.405	0.326	1.309	9.91E-03	*UHRF1BP1*	intron	5
	6	p21.31	**rs9296129**	34774414	C	0.406	0.326	1.316	8.56E-03	*UHRF1BP1*	intron	**2b**
	6	p21.31	**rs7774697**	34791027	C	0.405	0.326	1.309	9.91E-03	*UHRF1BP1*	intron	6
	6	p21.31	**rs6906129**	34801160	G	0.413	0.330	1.349	4.84E-03	*UHRF1BP1*	intron	5
	6	p21.31	**rs9469914**	34827693	T	0.403	0.327	1.28	0.0187	*UHRF1BP1*	intron	5
	6	p21.31	rs4646949	34845449	C	0.349	0.268	1.313	0.0127	*UHRF1BP1*		6
	6	p21.31	rs13219624	34861799	A	0.194	0.151	1.395	0.0110	*ANKS1A*	intron	6
	6	p21.31	rs9296139	34874002	G	0.194	0.151	1.399	0.0103	*ANKS1A*	intron	**1f**
	6	p21.31	rs6941065	34879203	A	0.096	0.067	1.437	0.0460	*ANKS1A*	intron	5
	6	p21.31	rs7753949	34882394	T	0.349	0.269	1.322	0.0118	*ANKS1A*	intron	**1f**
	6	p21.31	rs9380470	34886436	G	0.068	0.039	1.774	0.0108	*ANKS1A*	intron	5
PRDM1/ATG5	6	q21	rs9386510	106521653	G	0.220	0.194	1.326	0.0166	*PRDM1*		ND
	6	q21	rs9372117	106529777	G	0.339	0.316	1.236	0.0400	*PRDM1*		5
	6	q21	rs17066908	106821193	G	0.043	0.026	1.808	0.0350	*ATG5*		4
	6	q21	rs17066910	106821393	A	0.043	0.026	1.817	0.0338	*ATG5*		5
	6	q21	rs17066916	106822546	G	0.043	0.026	1.804	0.0356	*ATG5*		ND
OLIG3 /TNFAIP3	6	q23.3	rs1360605	137800894	G	0.030	0.045	0.556	0.0324	*OLIG3*		ND
	6	q23.3	rs595985	137926327	A	0.226	0.245	0.764	0.0240	*OLIG3*		ND
	6	q23.3	rs494739	137927444	T	0.218	0.225	0.778	0.0495	*OLIG3*		6
	6	q23.3	**rs2327832**	137973068	G	0.205	0.167	1.346	0.0161	*OLIG3*		6
	6	q23.3	**rs6920220**	138006504	A	0.205	0.172	1.321	0.0225	*LOC100130476*		6
	6	q23.3	rs7746779	138154501	C	0.159	0.199	0.721	0.0117	*LOC100130476*	intron	6
	6	q23.3	rs11970361	138179136	A	0.041	0.051	0.614	0.0433	*LOC100130476*	intron	ND
	6	q23.3	rs5029938	138195633	T	0.042	0.054	0.609	0.0382	*TNFAIP3*	intron	**2b**
	6	q23.3	**rs7749323**	138230389	T	0.054	0.033	1.625	0.0483	*TNFAIP3*		4
JAZF1	7	p15.2	rs7791865	27959430	A	0.074	0.095	0.701	0.0441	*JAZF1*	intron	5
	7	p15.1	rs4722753	28106929	C	0.435	0.479	0.746	2.71E-03	*JAZF1*	intron	5
	7	p15.1	rs6965411	28114036	G	0.391	0.429	0.745	4.43E-03	*JAZF1*	intron	5
HIP1	7	q11.23	rs237238	75211414	G	0.058	0.089	0.654	0.0263	*HIP1*	exon-synonymous	5
IRF5/TNPO3	7	q32.1	**rs12531711**	128617466	G	0.169	0.122	1.525	3.93E-03	*TNPO3*	intron	6
	7	q32.1	rs1154330	128625788	G	0.124	0.147	0.693	0.0135	*TNPO3*	intron	6
	7	q32.1	rs17166957	128687487	G	0.019	0.011	2.496	0.0180	*TNPO3*	intron	6
	7	q32.1	**rs17424602**	128687940	G	0.168	0.122	1.517	4.42E-03	*TNPO3*	intron	5
XKR6/FAM167A/BLK	8	p23.1	rs1991651	10706411	G	0.442	0.384	1.32	4.57E-03	*PINX1*		6
	8	p23.1	rs877116	10712945	G	0.470	0.423	1.27	0.0136	*PINX1*		**1f**
	8	p23.1	rs17777835	10718061	T	0.313	0.361	0.775	0.0157	*PINX1*		ND
	8	p23.1	rs17721796	10729454	C	0.135	0.171	0.766	0.0477	*XKR6*		ND
	8	p23.1	rs17778223	10729692	A	0.177	0.223	0.728	0.0104	*XKR6*		ND
	8	p23.1	rs11989027	10731271	A	0.409	0.461	0.824	0.0499	*XKR6*		ND
	8	p23.1	rs2163379	10732050	T	0.424	0.376	1.283	0.0117	*XKR6*		6
	8	p23.1	**rs10090444**	10745469	G	0.520	0.444	1.391	6.71E-04	*XKR6*		6
	8	p23.1	rs2898249	10745586	T	0.316	0.269	1.267	0.0238	*XKR6*		ND
	8	p23.1	**rs6985109**	10761585	G	0.522	0.442	1.393	6.27E-04	*XKR6*	intron	**1f**
	8	p23.1	**rs4326350**	10763655	C	0.456	0.523	0.764	5.25E-03	*XKR6*	intron	**1f**
	8	p23.1	rs4310166	10763736	G	0.334	0.417	0.709	5.24E-04	*XKR6*	intron	6
	8	p23.1	rs6987083	10764045	C	0.150	0.196	0.752	0.0307	*XKR6*	intron	5
	8	p23.1	**rs4240671**	10767748	A	0.455	0.519	0.773	7.38E-03	*XKR6*	intron	**1f**
	8	p23.1	rs6601537	10775412	C	0.174	0.229	0.75	0.0188	*XKR6*	intron	**1f**
	8	p23.1	rs6601538	10775454	G	0.182	0.234	0.75	0.0216	*XKR6*	intron	5
	8	p23.1	**rs7016385**	10779472	G	0.495	0.440	1.253	0.0224	*XKR6*	intron	**1f**

Locus / Gene(s)	Chr	Band	SNP*	Position in bp (hg19)	Allele	Freq Cases (n=661)	Freq Controls (n=487)	OR	P**	Nearest Gene***	Location in the Gene****	RegulomeDB score*****
	8	p23.1	rs7821438	10783223	C	0.173	0.208	0.753	0.0264	XKR6	intron	5
	8	p23.1	**rs11250092**	10786543	G	0.501	0.444	1.255	0.0207	XKR6	intron	**1f**
	8	p23.1	**rs6984496**	10796093	G	0.513	0.445	1.335	3.53E-03	XKR6	intron	**1f**
	8	p23.1	**rs11250093**	10798828	T	0.490	0.428	1.313	5.92E-03	XKR6	intron	**1f**
	8	p23.1	rs7821914	10805015	G	0.393	0.461	0.727	1.31E-03	XKR6	intron	**1f**
	8	p23.1	**rs11250099**	10818657	T	0.515	0.449	1.327	3.58E-03	XKR6	intron	**1f**
	8	p23.1	rs7825690	10858257	T	0.376	0.427	0.803	0.0279	XKR6	intron	6
	8	p23.1	rs7846545	10876603	G	0.235	0.259	0.792	0.0444	XKR6	intron	5
	8	p23.1	rs11250110	10878357	G	0.160	0.194	0.762	0.0397	XKR6	intron	5
	8	p23.1	rs6601550	10888425	A	0.235	0.288	0.768	0.0168	XKR6	intron	6
	8	p23.1	rs11996027	10891395	G	0.239	0.284	0.79	0.0332	XKR6	intron	ND
	8	p23.1	rs2898254	10892530	T	0.231	0.285	0.772	0.0199	XKR6	intron	ND
	8	p23.1	rs17722940	10898459	G	0.232	0.285	0.749	9.13E-03	XKR6	intron	ND
	8	p23.1	rs4349949	10900621	A	0.235	0.282	0.785	0.0279	XKR6	intron	6
	8	p23.1	rs6983680	10901931	A	0.235	0.283	0.762	0.0161	XKR6	intron	5
	8	p23.1	rs4841486	10911489	A	0.306	0.363	0.777	0.0151	XKR6	intron	5
	8	p23.1	rs13248300	10926675	G	0.297	0.361	0.752	5.69E-03	XKR6	intron	6
	8	p23.1	rs6980856	10938260	G	0.529	0.439	1.415	3.60E-04	XKR6	intron	**1f**
	8	p23.1	rs11991118	10939273	A	0.439	0.525	0.712	4.46E-04	XKR6	intron	**1f**
	8	p23.1	rs2409690	10940039	G	0.042	0.032	1.632	0.0497	XKR6	intron	5
	8	p23.1	rs17779791	10940241	G	0.298	0.354	0.813	0.0449	XKR6	intron	5
	8	p23.1	rs17152841	10942929	C	0.251	0.317	0.753	7.80E-03	XKR6	intron	5
	8	p23.1	rs2409691	10943276	T	0.423	0.526	0.659	2.78E-05	XKR6	intron	**1f**
	8	p23.1	rs9657544	10944616	C	0.285	0.350	0.762	9.91E-03	XKR6	intron	ND
	8	p23.1	rs10087767	10952613	T	0.247	0.312	0.754	8.18E-03	XKR6	intron	ND
	8	p23.1	rs10108618	10953092	G	0.461	0.553	0.679	8.58E-05	XKR6	intron	**1f**
	8	p23.1	rs17724226	10968926	T	0.390	0.473	0.721	1.23E-03	XKR6	intron	6
	8	p23.1	rs7460507	10969075	T	0.402	0.483	0.729	1.43E-03	XKR6	intron	6
	8	p23.1	rs4841498	10985432	C	0.526	0.449	1.328	3.80E-03	XKR6	intron	6
	8	p23.1	rs2409712	10986837	C	0.392	0.454	0.781	0.0130	XKR6	intron	**1f**
	8	p23.1	rs10503416	10987553	C	0.380	0.451	0.745	3.69E-03	XKR6	intron	**1b**
	8	p23.1	rs3021495	10994743	G	0.333	0.401	0.791	0.0270	XKR6	intron	4
	8	p23.1	rs17725480	11009317	T	0.264	0.316	0.784	0.0255	XKR6	intron	ND
	8	p23.1	rs17725534	11009669	G	0.256	0.319	0.741	6.62E-03	XKR6	intron	5
	8	p23.1	rs2409714	11010118	G	0.409	0.472	0.762	6.05E-03	XKR6	intron	6
	8	p23.1	rs17782554	11022106	G	0.342	0.417	0.75	4.29E-03	XKR6	intron	6
	8	p23.1	rs17726209	11022185	C	0.342	0.419	0.739	2.85E-03	XKR6	intron	6
	8	p23.1	rs9329238	11033737	T	0.331	0.406	0.72	1.47E-03	XKR6	intron	6
	8	p23.1	rs7813802	11033976	T	0.528	0.452	1.345	3.62E-03	XKR6	intron	6
	8	p23.1	rs4451268	11034859	G	0.334	0.408	0.728	2.05E-03	XKR6	intron	**1d**
	8	p23.1	rs11777887	11036799	C	0.330	0.406	0.715	1.21E-03	XKR6	intron	ND
	8	p23.1	rs11777918	11036919	A	0.335	0.411	0.737	3.18E-03	XKR6	intron	5
	8	p23.1	rs11250119	11037034	T	0.428	0.518	0.72	6.62E-04	XKR6	intron	**1f**
	8	p23.1	rs2409720	11037903	C	0.330	0.413	0.715	9.08E-04	XKR6	intron	**1f**
	8	p23.1	rs7819412	11045161	G	0.525	0.442	1.393	7.40E-04	XKR6	intron	6
	8	p23.1	rs4841507	11046394	G	0.382	0.453	0.723	1.34E-03	XKR6	intron	6
	8	p23.1	rs11989369	11055385	A	0.326	0.404	0.716	1.23E-03	XKR6	intron	6
	8	p23.1	rs11783045	11056175	G	0.330	0.411	0.7	5.29E-04	XKR6	intron	**1f**
	8	p23.1	rs7010590	11062882	C	0.464	0.544	0.721	8.55E-04	XKR6		**1f**
	8	p23.1	rs4412337	11072020	C	0.325	0.407	0.706	6.75E-04	XKR6		6
	8	p23.1	rs6601569	11073578	C	0.483	0.424	1.306	6.05E-03	XKR6		6
	8	p23.1	rs2409745	11076635	T	0.518	0.435	1.423	3.75E-04	XKR6		6
	8	p23.1	rs2736313	11086942	C	0.463	0.536	0.74	1.89E-03	XKR6		**1f**
	8	p23.1	rs920047	11087475	T	0.445	0.520	0.744	2.32E-03	XKR6		6
	8	p23.1	rs10092549	11089079	C	0.433	0.390	1.268	0.0160	XKR6		6
	8	p23.1	rs2572406	11092252	G	0.525	0.461	1.33	3.57E-03	XKR6		6
	8	p23.1	rs6601572	11093337	C	0.463	0.407	1.376	1.16E-03	XKR6		6
	8	p23.1	rs6601575	11097804	C	0.509	0.447	1.379	1.24E-03	XKR6		6
	8	p23.1	rs2572437	11098441	T	0.301	0.385	0.704	6.44E-04	XKR6		6
	8	p23.1	rs2572433	11101041	C	0.317	0.392	0.726	1.72E-03	MTMR9		**1f**
	8	p23.1	rs2572432	11101723	G	0.304	0.385	0.708	7.45E-04	MTMR9		**1f**
	8	p23.1	rs6601577	11102682	G	0.461	0.399	1.395	9.56E-04	MTMR9		6
	8	p23.1	rs958648	11103895	A	0.486	0.406	1.459	1.56E-04	MTMR9		6
	8	p23.1	rs7824557	11104111	C	0.433	0.366	1.471	1.41E-04	MTMR9		6
	8	p23.1	rs2572431	11105077	C	0.475	0.399	1.452	1.77E-04	MTMR9		6
	8	p23.1	rs2572430	11105304	T	0.487	0.409	1.477	1.63E-04	MTMR9		6
	8	p23.1	rs2572417	11111462	A	0.502	0.420	1.425	3.10E-04	MTMR9		6
	8	p23.1	rs2736374	11113828	G	0.356	0.444	0.697	2.49E-04	MTMR9		6
	8	p23.1	rs10503418	11118983	C	0.453	0.397	1.394	7.89E-04	MTMR9		**1f**
	8	p23.1	rs2251301	11119037	A	0.146	0.182	0.766	0.0473	MTMR9		5
	8	p23.1	rs11997943	11119981	G	0.210	0.260	0.754	0.0136	MTMR9		5
	8	p23.1	rs2099456	11127001	C	0.452	0.397	1.388	9.16E-04	MTMR9		**1f**
	8	p23.1	rs2736381	11132766	A	0.442	0.382	1.428	1.67E-03	MTMR9		6
	8	p23.1	rs3808518	11143272	A	0.453	0.391	1.437	2.67E-04	MTMR9	intron	**1f**
	8	p23.1	rs2117616	11145911	G	0.409	0.473	0.781	0.0140	MTMR9	intron	**1f**

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	8	p23.1	rs4841519	11146228	A	0.402	0.476	0.748	2.75E-03	MTMR9	intron	1f
	8	p23.1	rs2572426	11147123	C	0.398	0.471	0.743	2.39E-03	MTMR9	intron	1d
	8	p23.1	rs3808515	11156041	C	0.401	0.474	0.754	3.31E-03	MTMR9	intron	6
	8	p23.1	rs4410870	11156120	G	0.354	0.436	0.742	2.09E-03	MTMR9	intron	6
	8	p23.1	rs3808513	11157460	G	0.452	0.390	1.432	3.36E-04	MTMR9	intron	6
	8	p23.1	rs1545073	11167700	C	0.402	0.474	0.756	3.99E-03	MTMR9	intron	6
	8	p23.1	rs6985146	11170721	C	0.449	0.387	1.44	2.92E-04	MTMR9	intron	6
	8	p23.1	rs11784572	11174484	G	0.359	0.407	0.733	2.29E-03	MTMR9	intron	6
	8	p23.1	rs6995404	11182148	G	0.519	0.470	1.379	1.16E-03	MTMR9	exon-3'UTR	1f
	8	p23.1	rs12681987	11189488	A	0.444	0.498	0.733	1.76E-03	SLC35G5	exon-synonymous	1f
	8	p23.1	rs10098322	11196295	G	0.519	0.470	1.352	2.31E-03	TDH		6
	8	p23.1	rs11250130	11214455	T	0.425	0.484	0.741	2.39E-03	TDH	intron	1f
	8	p23.1	rs11781637	11214972	T	0.424	0.484	0.74	2.29E-03	TDH	intron	1f
	8	p23.1	rs2249804	11215617	C	0.406	0.477	0.72	9.34E-04	TDH	intron	6
	8	p23.1	rs2572371	11223793	G	0.475	0.515	0.803	0.0238	TDH	intron	6
	8	p23.1	rs2736282	11225480	C	0.477	0.523	0.779	0.0102	TDH	intron	1f
	8	p23.1	rs2736283	11225910	G	0.475	0.521	0.78	0.0108	TDH	exon	1f
	8	p23.1	rs2736286	11227104	G	0.479	0.522	0.804	0.0263	C8orf12	intron	5
	8	p23.1	rs2572452	11228254	T	0.474	0.522	0.778	0.0105	C8orf12	intron	6
	8	p23.1	rs13260727	11232860	A	0.407	0.464	0.737	2.28E-03	C8orf12	intron	6
	8	p23.1	rs2736292	11234500	A	0.411	0.472	0.735	1.93E-03	C8orf12	intron	1f
	8	p23.1	rs2736295	11234780	C	0.399	0.461	0.742	3.96E-03	C8orf12	intron	6
	8	p23.1	rs2572449	11239137	A	0.396	0.457	0.739	2.46E-03	C8orf12	intron	1f
	8	p23.1	rs2736306	11239762	A	0.414	0.473	0.752	4.48E-03	C8orf12	intron	1f
	8	p23.1	rs2409756	11242025	C	0.390	0.454	0.74	2.79E-03	C8orf12	intron	6
	8	p23.1	rs4841525	11249261	A	0.325	0.383	0.738	3.25E-03	C8orf12	intron	5
	8	p23.1	rs11250131	11251175	T	0.464	0.503	0.805	0.0305	C8orf12	intron	6
	8	p23.1	rs2736311	11252170	C	0.495	0.467	1.235	0.0361	C8orf12	intron	1f
	8	p23.1	rs7003840	11266131	T	0.443	0.396	1.267	0.0191	C8orf12	intron	6
	8	p23.1	rs2409764	11281273	C	0.403	0.483	0.73	2.05E-03	C8orf12/FAM167A	intron/3'UTR	1f
	8	p23.1	rs17153220	11285025	C	0.035	0.021	1.869	0.0393	C8orf12/FAM167A	intron/intron	4
	8	p23.1	rs4841529	11285581	G	0.422	0.488	0.734	2.33E-03	C8orf12/FAM167A	intron/intron	3a
	8	p23.1	rs10503423	11287081	G	0.413	0.343	1.492	1.30E-04	C8orf12/FAM167A	intron/intron	1f
	8	p23.1	rs6998387	11293458	T	0.395	0.312	1.553	1.87E-05	C8orf12/FAM167A	intron/intron	1f
	8	p23.1	rs2001462	11294810	A	0.165	0.251	0.697	2.20E-03	C8orf12/FAM167A	intron/intron	ND
	8	p23.1	rs7001675	11296600	G	0.490	0.437	1.311	5.03E-03	FAM167A	intron	1f
	8	p23.1	rs11779875	11302445	C	0.398	0.320	1.534	2.68E-05	FAM167A	intron	1f
	8	p23.1	rs9792375	11302481	C	0.461	0.407	1.329	2.99E-03	FAM167A	intron	1f
	8	p23.1	rs2409772	11306516	T	0.481	0.418	1.325	3.64E-03	FAM167A	intron	1f
	8	p23.1	rs2409773	11306615	G	0.401	0.310	1.581	9.53E-06	FAM167A	intron	1b
	8	p23.1	rs2409775	11306805	G	0.486	0.418	1.374	9.24E-04	FAM167A	intron	1f
	8	p23.1	rs9792175	11307118	A	0.466	0.404	1.361	1.79E-03	FAM167A	intron	5
	8	p23.1	rs4841537	11307572	C	0.489	0.419	1.388	6.25E-04	FAM167A	intron	1f
	8	p23.1	rs13439415	11310012	T	0.362	0.430	0.764	6.04E-03	FAM167A	intron	1f
	8	p23.1	rs9644687	11323025	A	0.332	0.270	1.336	6.35E-03	FAM167A	intron	1d
	8	p23.1	rs11250138	11323312	C	0.340	0.272	1.339	5.60E-03	FAM167A	intron	1f
	8	p23.1	rs11250139	11331046	A	0.411	0.444	0.806	0.0289	FAM167A		5
	8	p23.1	rs12680762	11332026	A	0.322	0.243	1.536	6.69E-05	FAM167A		4
	8	p23.1	rs2254891	11341129	C	0.296	0.341	0.801	0.0427	BLK		1f
	8	p23.1	rs978803	11343475	T	0.524	0.455	1.316	4.09E-03	BLK		6
	8	p23.1	**rs2736340**	11343973	T	0.305	0.225	1.575	5.42E-05	BLK		1f
	8	p23.1	rs2736342	11347289	A	0.511	0.442	1.28	0.0107	BLK		1f
	8	p23.1	rs4840567	11347625	A	0.526	0.453	1.319	4.06E-03	BLK		1f
	8	p23.1	**rs2618476**	11352541	G	0.328	0.237	1.625	2.39E-05	BLK	intron	1d
	8	p23.1	**rs998683**	11353000	A	0.320	0.233	1.549	7.66E-05	BLK	intron	1f
	8	p23.1	rs1478890	11355602	C	0.530	0.451	1.356	1.93E-03	BLK	intron	1f
	8	p23.1	rs2618443	11384556	A	0.503	0.421	1.411	3.40E-04	BLK	intron	6
	8	p23.1	**rs9329246**	11392880	G	0.393	0.317	1.462	3.42E-04	BLK	intron	6
	8	p23.1	rs17153419	11394233	C	0.339	0.267	1.467	3.25E-04	BLK	intron	1f
	8	p23.1	**rs1478897**	11395232	T	0.424	0.337	1.56	8.14E-06	BLK	intron	1d
	8	p23.1	rs2409784	11396856	T	0.457	0.539	0.698	2.10E-04	BLK	intron	1d
	8	p23.1	rs4841554	11408935	C	0.320	0.361	0.811	0.0446	BLK	intron	5
	8	p23.1	rs7007439	11415794	A	0.447	0.365	1.44	1.49E-04	BLK	intron	1f
	8	p23.1	rs6983727	11415812	A	0.418	0.490	0.75	2.39E-03	BLK	intron	1f
	8	p23.1	rs7011778	11416171	A	0.444	0.362	1.434	1.68E-04	BLK	intron	1d
	8	p23.1	rs1382563	11426790	C	0.421	0.491	0.763	4.29E-03	BLK		1f
	8	p23.1	rs12547947	11427341	C	0.407	0.344	1.327	3.55E-03	BLK		1f
	8	p23.1	rs10107563	11427492	A	0.040	0.024	1.821	0.0391	BLK		5
	8	p23.1	rs7831039	11427637	T	0.420	0.489	0.766	4.90E-03	BLK		1f
	8	p23.1	rs12679960	11430990	T	0.368	0.293	1.456	3.91E-04	LINC00208		1d
	8	p23.1	rs2409800	11439013	G	0.363	0.305	1.293	0.0132	LINC00208		6
	8	p23.1	rs11250149	11439961	G	0.359	0.292	1.301	9.31E-03	LINC00208		6
	8	p23.1	rs12677146	11450737	C	0.390	0.321	1.342	3.14E-03	LINC00208		1f
	8	p23.1	rs11250152	11454200	A	0.434	0.345	1.414	5.31E-04	LINC00208		1f
	8	p23.1	rs17807624	11463015	A	0.384	0.297	1.454	1.89E-04	LINC00208		6

Locus / Gene(s)	Chr	Band	SNP*	Position in bp (hg19)	Allele	Freq Cases (n=661)	Freq Controls (n=487)	OR	P**	Nearest Gene***	Location in the Gene****	RegulomeDB score*****
	8	p23.1	rs4840573	11463230	A	0.339	0.408	0.775	9.99E-03	LINC00208		**1f**
	8	p23.1	rs13278965	11466745	A	0.389	0.457	0.799	0.0236	LINC00208		6
WDFY4	10	q11.23	rs4838639	49901961	T	0.040	0.020	2.325	5.07E-03	WDFY4	intron	5
	10	q11.23	rs12245739	49906091	T	0.040	0.019	2.136	0.0145	WDFY4	intron	5
	10	q11.23	rs11101436	49919567	T	0.039	0.018	2.132	0.0146	WDFY4	intron	6
	10	q11.23	rs12267792	49921749	T	0.040	0.018	2.132	0.0146	WDFY4	intron	5
	10	q11.23	rs4838646	49945594	G	0.473	0.521	0.821	0.0415	WDFY4	intron	6
	10	q11.23	rs12768835	49976969	A	0.409	0.453	0.811	0.0316	WDFY4	intron	5
	10	q11.23	**rs2663038**	50099468	G	0.436	0.486	0.786	0.0185	WDFY4	intron	**2b**
	10	q11.23	rs17836512	50100434	C	0.052	0.033	1.698	0.0358	WDFY4	intron	6
	10	q11.23	rs17011569	50178485	C	0.091	0.065	1.451	0.0388	WDFY4	intron	5
	10	q11.23	rs17009410	50179201	A	0.048	0.026	1.903	0.0149	WDFY4	intron	6
ARID5B	10	q21.2	rs1530439	63645959	T	0.285	0.322	0.792	0.0351	ARID5B		ND
	10	q21.2	rs9415636	63826186	A	0.072	0.095	0.681	0.0335	ARID5B	intron	5
	10	q21.2	rs1122157	63861600	A	0.305	0.267	1.275	0.0260	ARID5B		5
PDHX/CD44	11	p13	rs16926365	34915650	T	0.031	0.042	0.515	0.0183	APIP	intron	6
	11	p13	rs17362114	34951533	G	0.030	0.042	0.513	0.0180	PDHX	intron	**2a**
	11	p13	rs41512444	34959234	G	0.030	0.042	0.513	0.0180	PDHX	intron	ND
	11	p13	rs7115217	34985327	C	0.035	0.042	0.552	0.0331	PDHX	intron	ND
	11	p13	rs11032960	34998014	A	0.035	0.044	0.54	0.0234	PDHX	intron	ND
	11	p13	rs11032963	34999861	T	0.032	0.042	0.565	0.0378	PDHX	intron	5
	11	p13	rs17436343	35019789	A	0.031	0.049	0.459	5.38E-03	PDHX		4
	11	p13	rs16926673	35022765	T	0.033	0.042	0.534	0.0247	PDHX		5
	11	p13	rs353647	35191445	C	0.474	0.430	1.229	0.0318	CD44	intron	4
ETS1	11	q24.3	rs12805120	128365685	A	0.283	0.253	1.286	0.0212	ETS1	intron	5
	11	q24.3	rs7929911	128369597	T	0.280	0.251	1.277	0.0264	ETS1	intron	5
	11	q24.3	rs7941606	128372168	A	0.283	0.253	1.282	0.0228	ETS1	intron	4
CREBL2/CDKN1B	12	p13.2	rs1014448	12746585	G	0.072	0.081	0.649	0.0221	CREBL2		ND
	12	p13.2	rs10492241	12750509	C	0.425	0.456	0.821	0.0411	CREBL2		ND
	12	p13.2	rs10845586	12751662	G	0.431	0.459	0.817	0.0357	CREBL2		6
	12	p13.2	**rs12822507**	12773521	C	0.304	0.343	0.804	0.0360	CREBL2	intron	5
	12	p13.1	rs10845601	12820134	A	0.349	0.395	0.821	0.0496	GPR19		ND
	12	p13.1	rs2024385	12888438	A	0.397	0.436	0.812	0.0318	APOLD1	intron	5
SLC15A4	12	q24.33	rs10847705	129343928	A	0.151	0.104	1.411	0.0189	GLT1D1	intron	5
ELF1	13	q14.11	rs7799	41533052	A	0.309	0.347	0.791	0.0280	ELF1	exon-missense	4
	13	q14.11	rs9594471	41562786	G	0.154	0.208	0.767	0.0347	ELF1	intron	ND
	13	q14.11	rs9566655	41578109	A	0.155	0.209	0.771	0.0364	ELF1	intron	ND
	13	q14.11	rs11617732	41580259	C	0.433	0.390	1.216	0.0492	ELF1	intron	4
	13	q14.11	rs9566656	41581930	A	0.168	0.225	0.79	0.0491	ELF1	intron	5
	13	q14.11	rs2772181	41632244	C	0.159	0.212	0.78	0.0419	WBP4		ND
PRKCB	16	p12.1	rs2214437	24275388	A	0.446	0.480	0.8	0.0228	CACNG3	intron	6
ITGAM/ITGAX/ITGAD	16	p11.2	rs4889640	31264267	C	0.270	0.314	0.779	0.0186	ITGAM		**1f**
	16	p11.2	rs7193943	31271063	C	0.259	0.304	0.759	0.0137	ITGAM		**1f**
	16	p11.2	**rs9938063**	31302938	C	0.194	0.118	1.394	0.0138	ITGAM	intron	5
	16	p11.2	**rs9888879**	31310372	C	0.194	0.120	1.349	0.0270	ITGAM	intron	4
	16	p11.2	**rs1143683**	31336888	A	0.233	0.153	1.462	2.99E-03	ITGAM	exon-missense	4
	16	p11.2	rs4077810	31340909	T	0.268	0.313	0.777	0.0209	ITGAM	intron	**1f**
	16	p11.2	rs4075052	31348233	T	0.269	0.315	0.766	0.0145	ITGAM		6
IRF8	16	q24.1	rs4843861	85950976	A	0.319	0.266	1.309	0.0169	IRF8	intron	**3a**
	16	q24.1	rs13338943	85952951	T	0.132	0.109	1.356	0.0428	IRF8	intron	5
	16	q24.1	rs385344	85967604	C	0.306	0.273	1.276	0.0212	IRF8		6
	16	q24.1	rs2934498	85968282	C	0.306	0.275	1.258	0.0297	IRF8		5
	16	q24.1	**rs11648084**	85972598	T	0.283	0.320	0.797	0.0355	IRF8		5
	16	q24.1	**rs11644034**	85972612	T	0.181	0.232	0.726	9.18E-03	IRF8		5
	16	q24.1	**rs12711490**	85973028	G	0.181	0.229	0.735	0.0133	IRF8		ND
	16	q24.1	**rs12598434**	85973059	T	0.283	0.318	0.807	0.0469	IRF8		ND
	16	q24.1	rs305097	85977911	A	0.314	0.279	1.249	0.0327	IRF8		5
	16	q24.1	rs11642873	85991705	G	0.152	0.211	0.745	0.0229	IRF8		4
	16	q24.1	rs11642511	86003392	G	0.328	0.383	0.804	0.0307	IRF8		4
	16	q24.1	rs9308364	86003446	G	0.501	0.443	1.284	0.0122	IRF8		4
	16	q24.1	rs4843329	86004239	T	0.486	0.427	1.269	0.0150	IRF8		4

Previously identified SLE loci/genes examined in this study included: (a) 2q32/STAT4, 3p14/PXK, 5q33-35/PTTG1-MIR146A, 6q21/PRDM1-ATG5, 6q23/OLIG3-TNFAIP3, 7q32/IRF5-TNPO3, 8p23/XKR6- BLK, 8q12-13/LYN, 11p15/PHRF1-IRF7, and 16p11/ITGAM-ITGAD loci identified in 3 high-density GWAS of European-descent subjects (PMIDs: 19165918, 18204446, 18204098), (b) 4q24/BANK1 locus identified in a low-density GWAS of European-descent subjects (PMID: 18204447), (c) 1q25/TNFSF4, 2p22/RASGRP3, 2p13/TET3, 3q13/CD80, 4q21/AFF1, 5q33/TNIP1, 7p12/IKZF1, 7q11/HIP1, 10q11/WDFY4, 10q21/ARID5B, 11q23/ETS1, 12p13-12/CREBL2-CDKN1B, 12q23/DRAM1, 12q24/SLC15A4, 13q13/ELF1, 16p11/PRKCB, and 22q11/HIC2-UBE2L3 loci identified in Chinese or Japanese GWAS or post-GWAS follow-up studies (PMIDs: 19838193, 22291604, 21134959, 20169177, 21044949, 23273568), some of which also reported in individuals of European ancestry, and (d) 1p13/PTPN22, 1q23/FCGR2A, 1q25/NCF2, 1q31/IL10, 2q24/IFIH1, 3q13/TMEM39A (near CD80 already mentioned above), 6p21/SNRPC-UHRF1BP1, 7p15/JAZF1, 11p13/PDHX-CD44, 16q24/IRF8, and 19p13/TYK2 loci identified by post-GWAS follow-up and large studies that included subjects of European ancestry (PMIDs: 22046141, 19838195, 19493061, 22203994, 21194677, 22464253, 21379322).

*__Bold/Underlined__: Replicated genome-wide significant SNP (__index__ or **proxy** with $r^2 \geq 0.8$ according to http://www.broadinstitute.org/mpg/snap/).

**P-value for additive genetic model, adjusted for relevant covariates (please see the methods section).

***The nearest gene within ± 500 kb (http://www.genome.ucsc.edu/).

****For the SNPs located within the gene (http://www.ncbi.nlm.nih.gov/projects/SNP/).

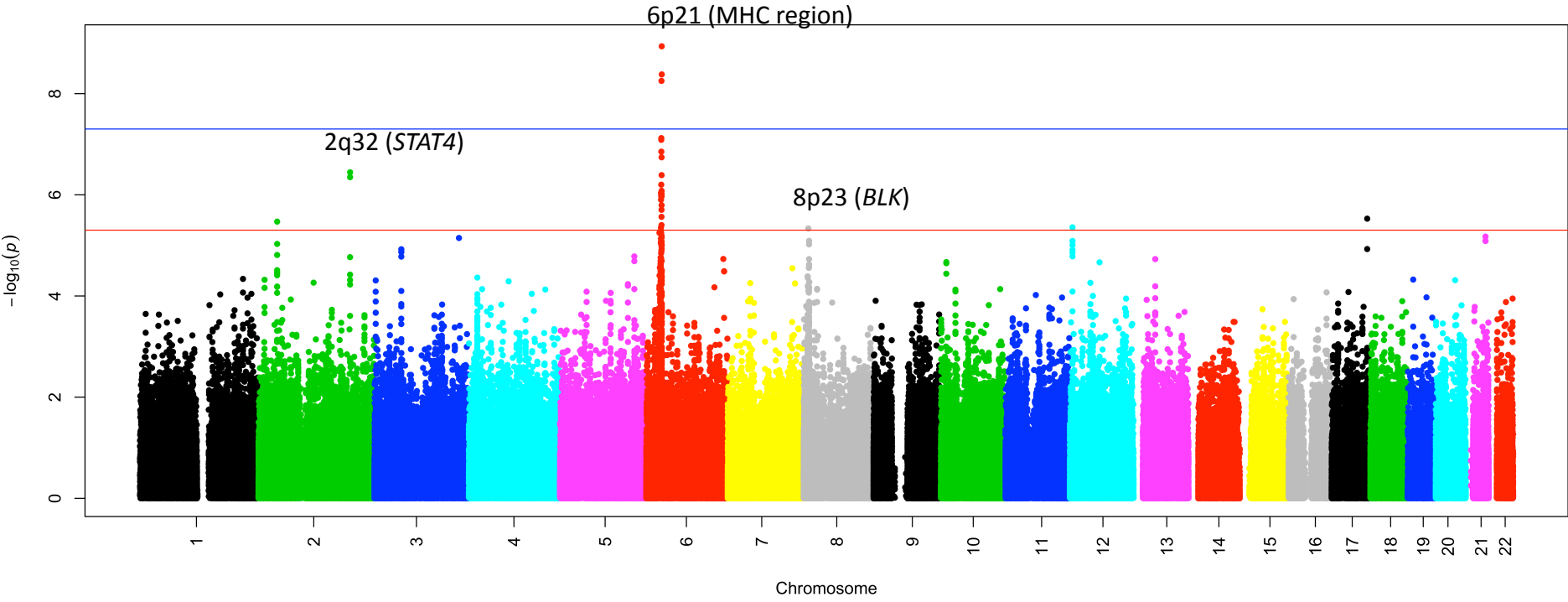*****Please see the methods section and http://www.regulomedb.org/help; ND: No Data.
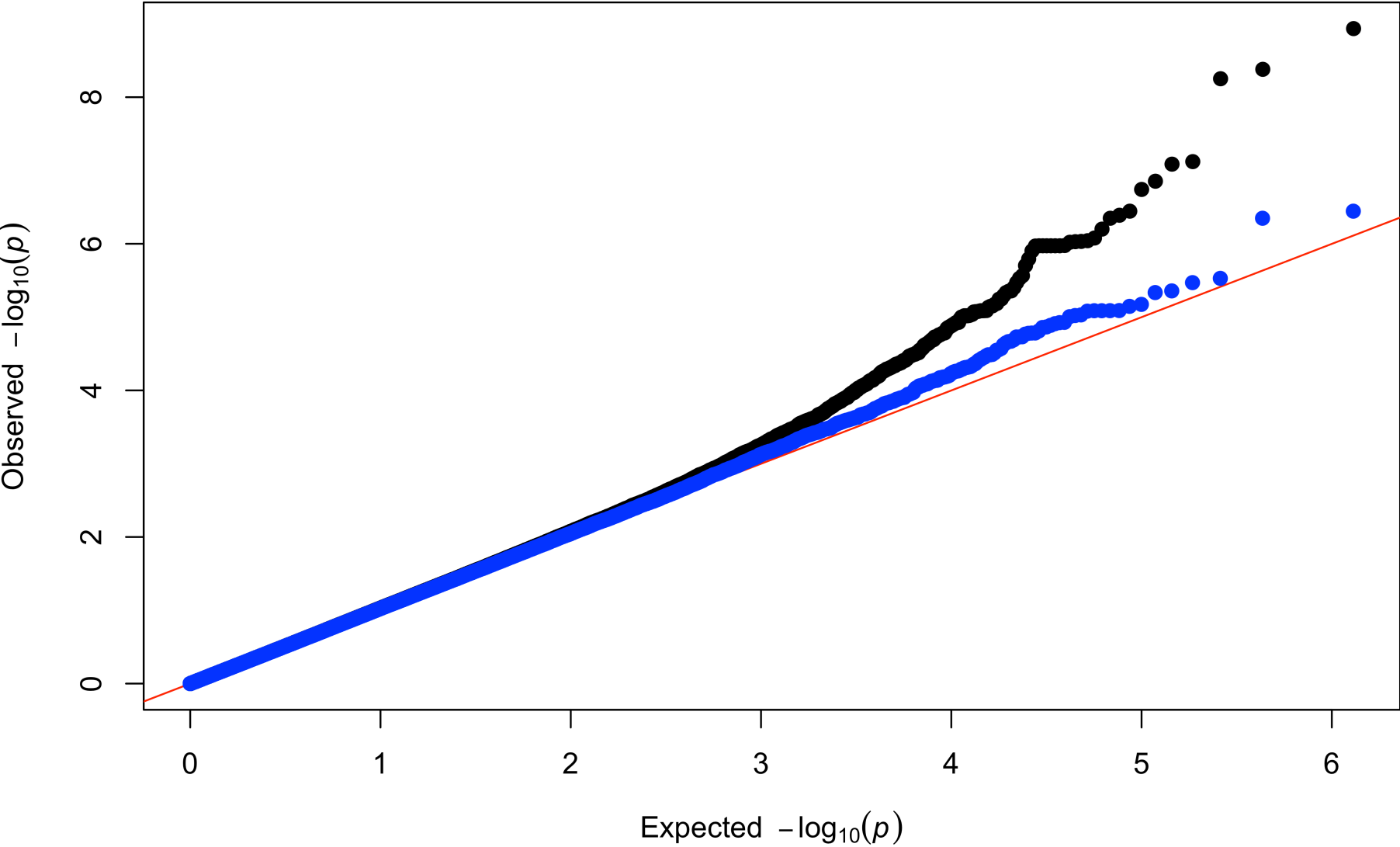
Figure S1

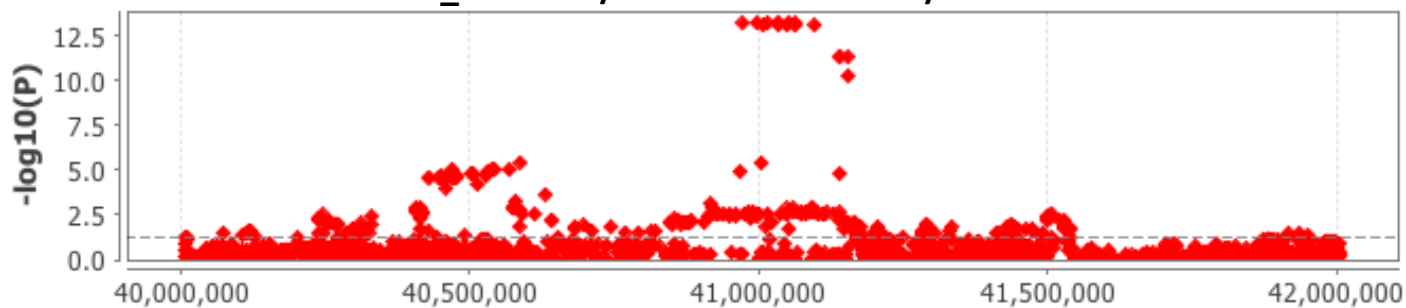**Figure S2**

Figure S3
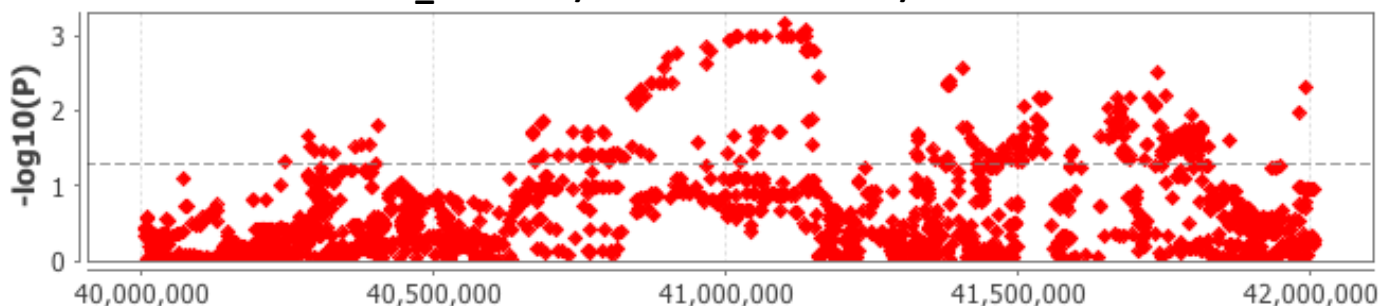
Figure S4

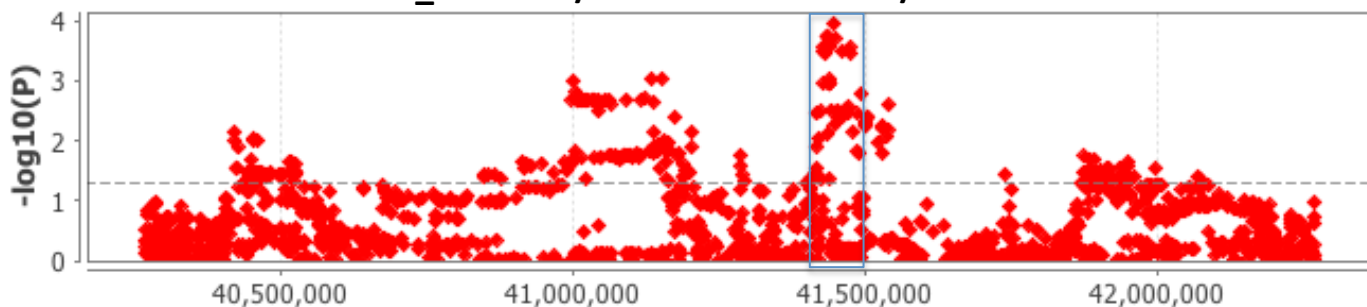TwinsUK-A

hg18
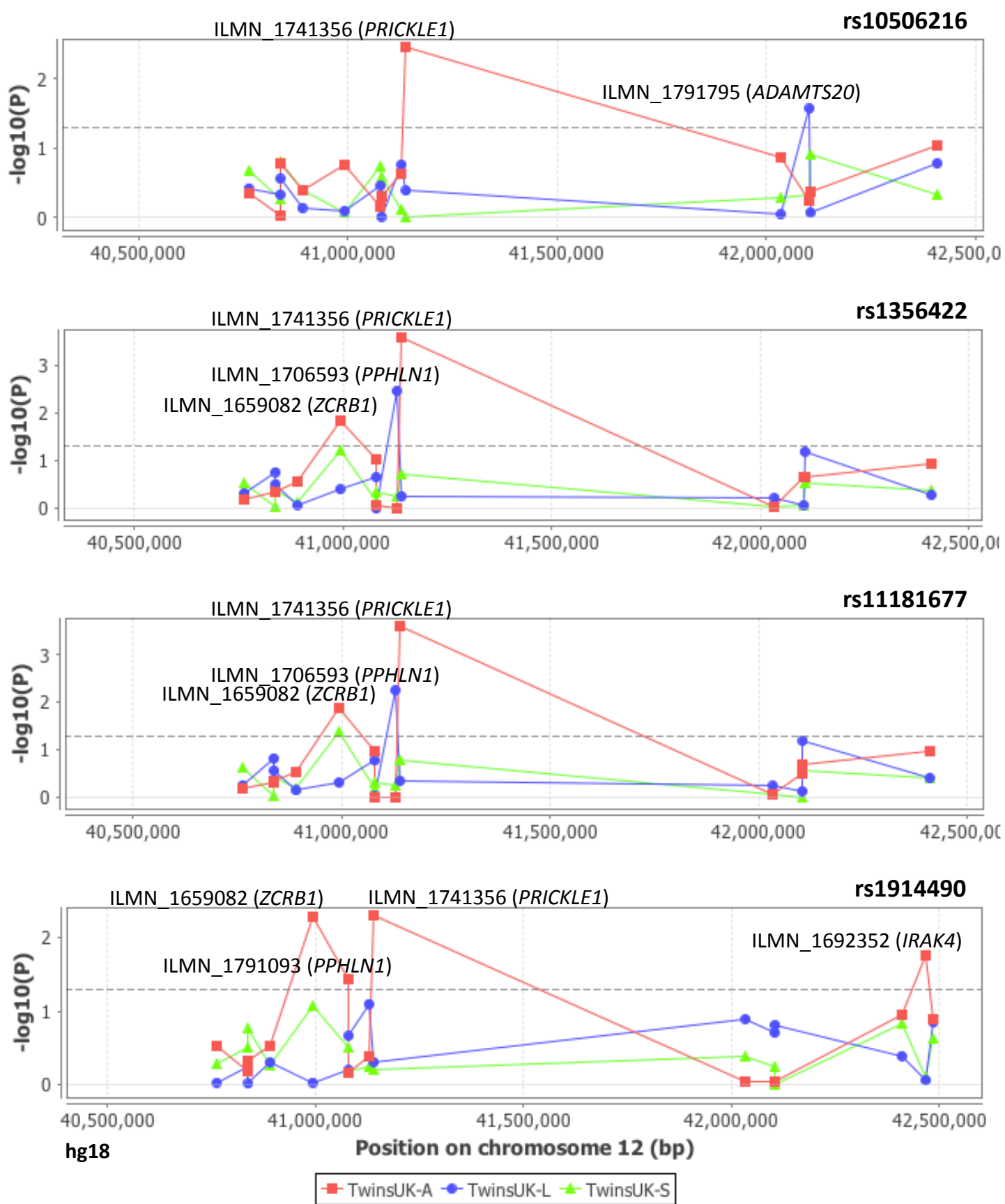
Position on chromosome 12 (bp)

Figure S5

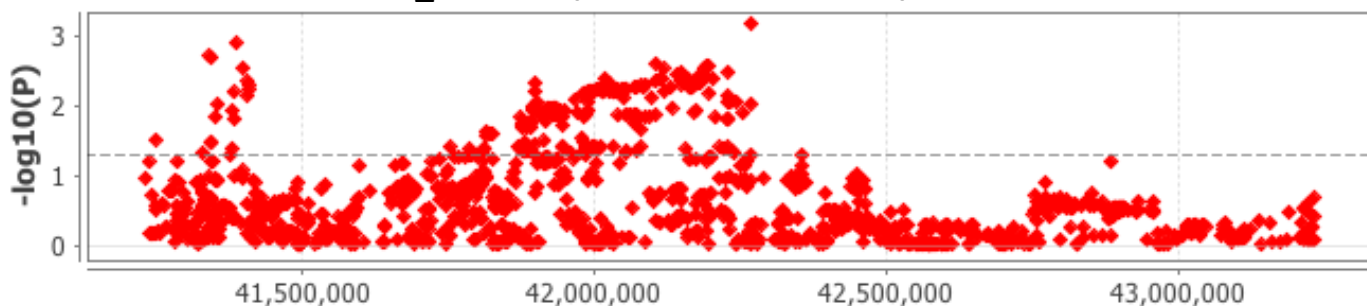ILMN_1659082 / ENSG00000139168 / ZCRB1
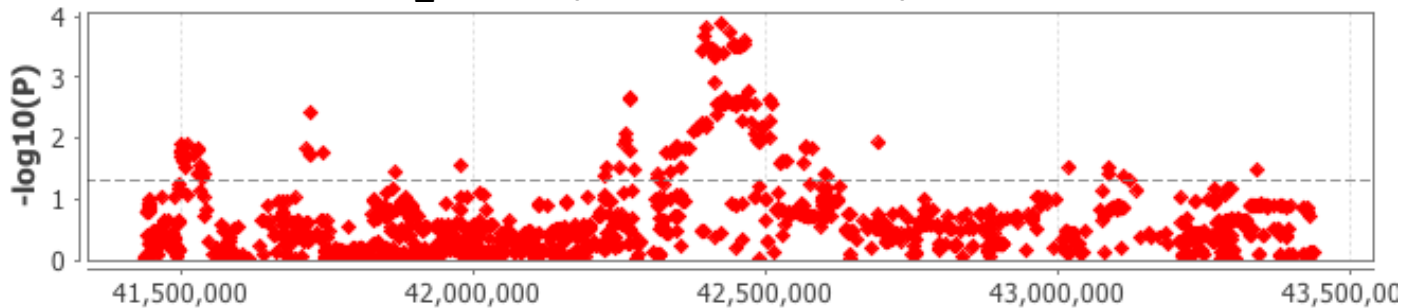
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ILMN_1791795 / ENSG00000173157 / ADAMTS20
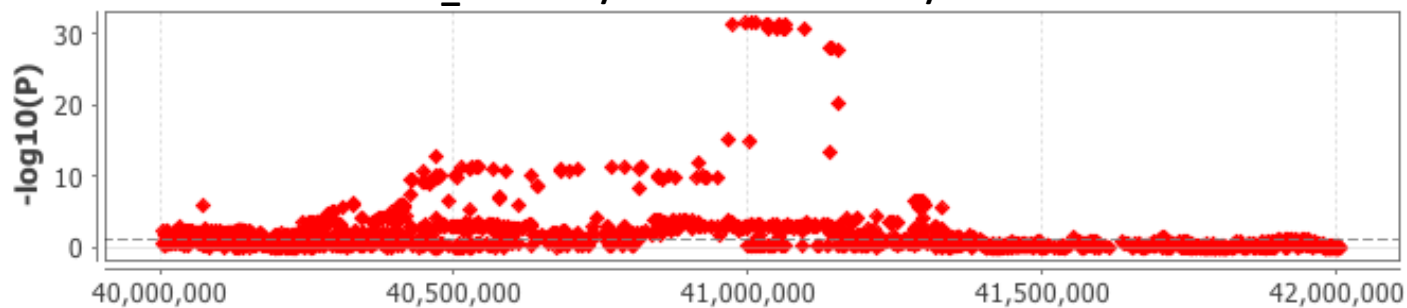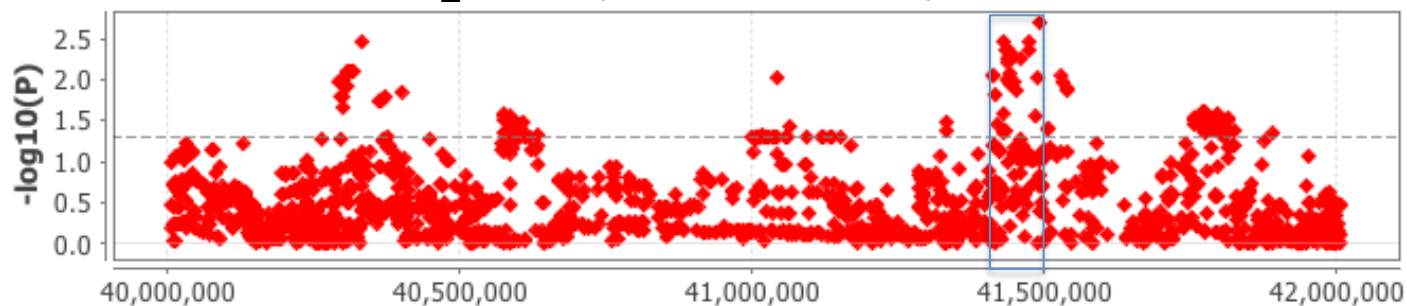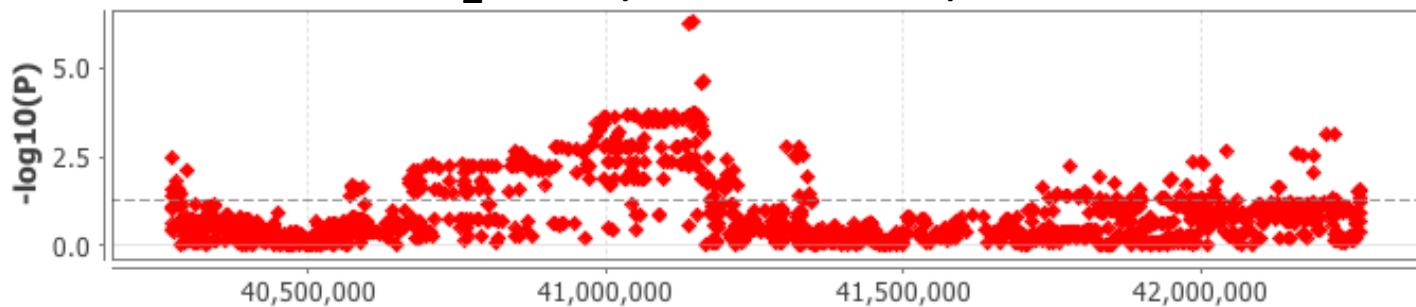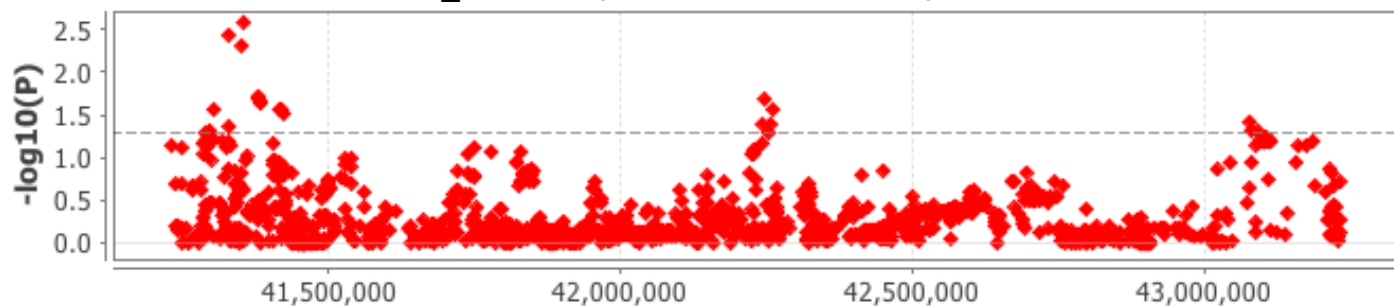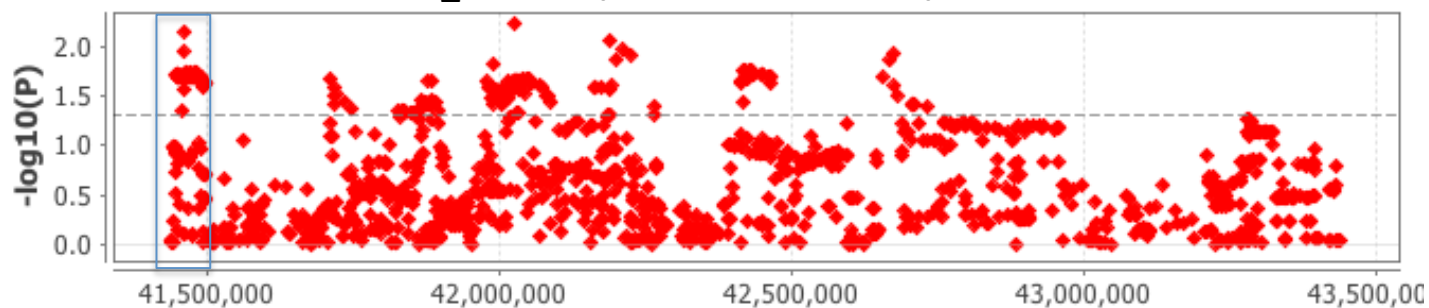
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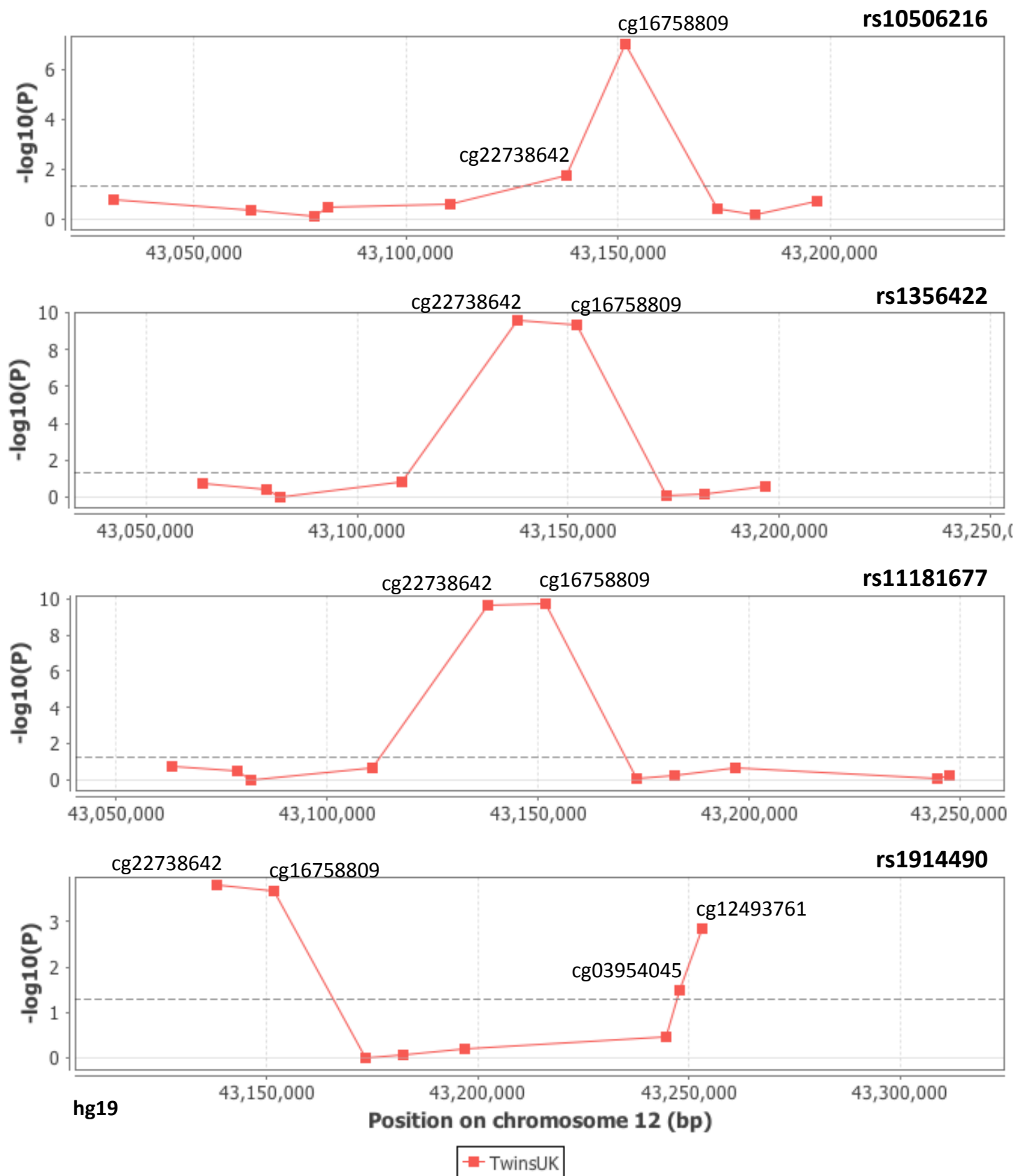
TwinsUK-L

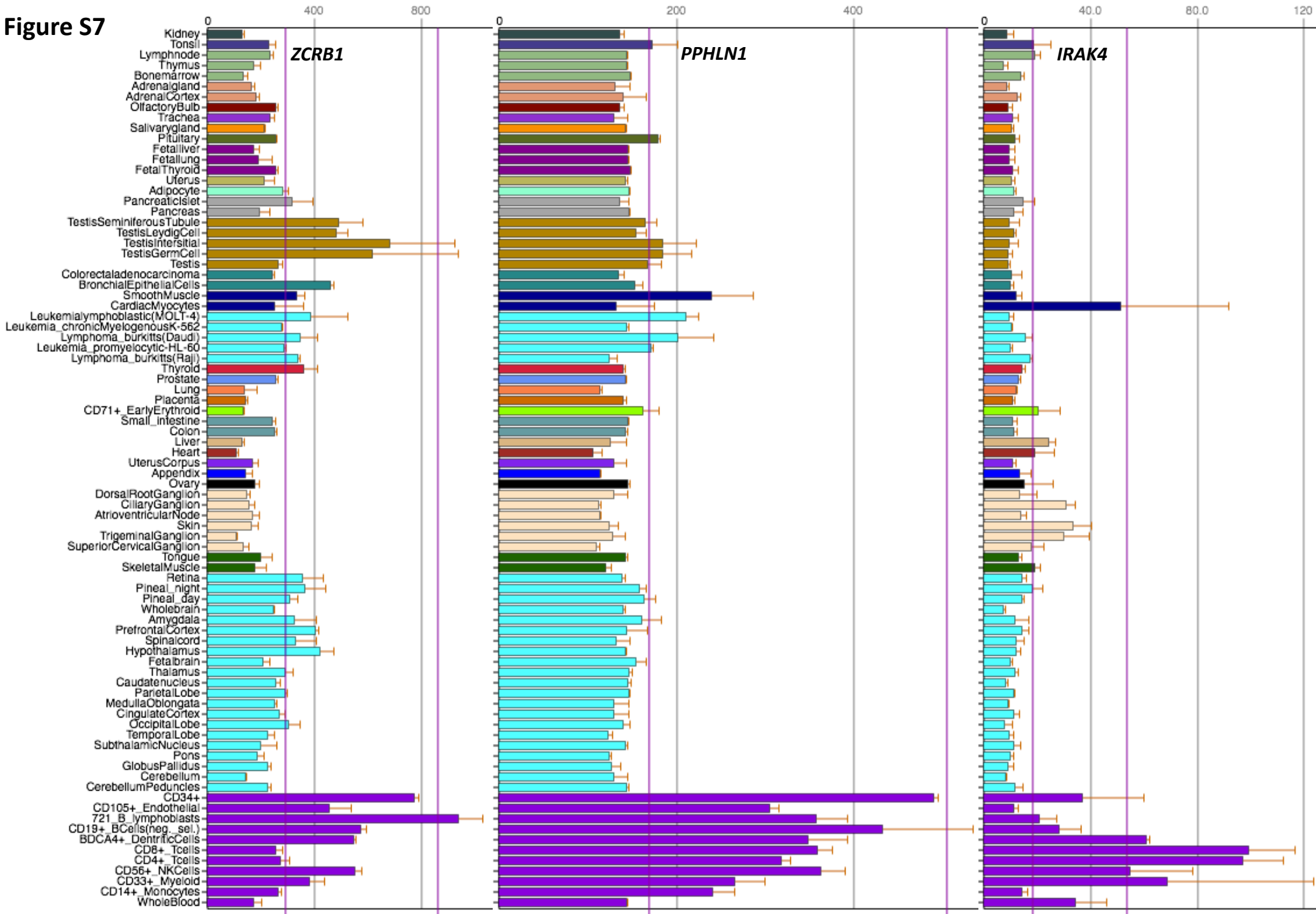Position on chromosome 12 (bp)

hg18

Figure S6

Figure S7

Figure S8

Figure S9
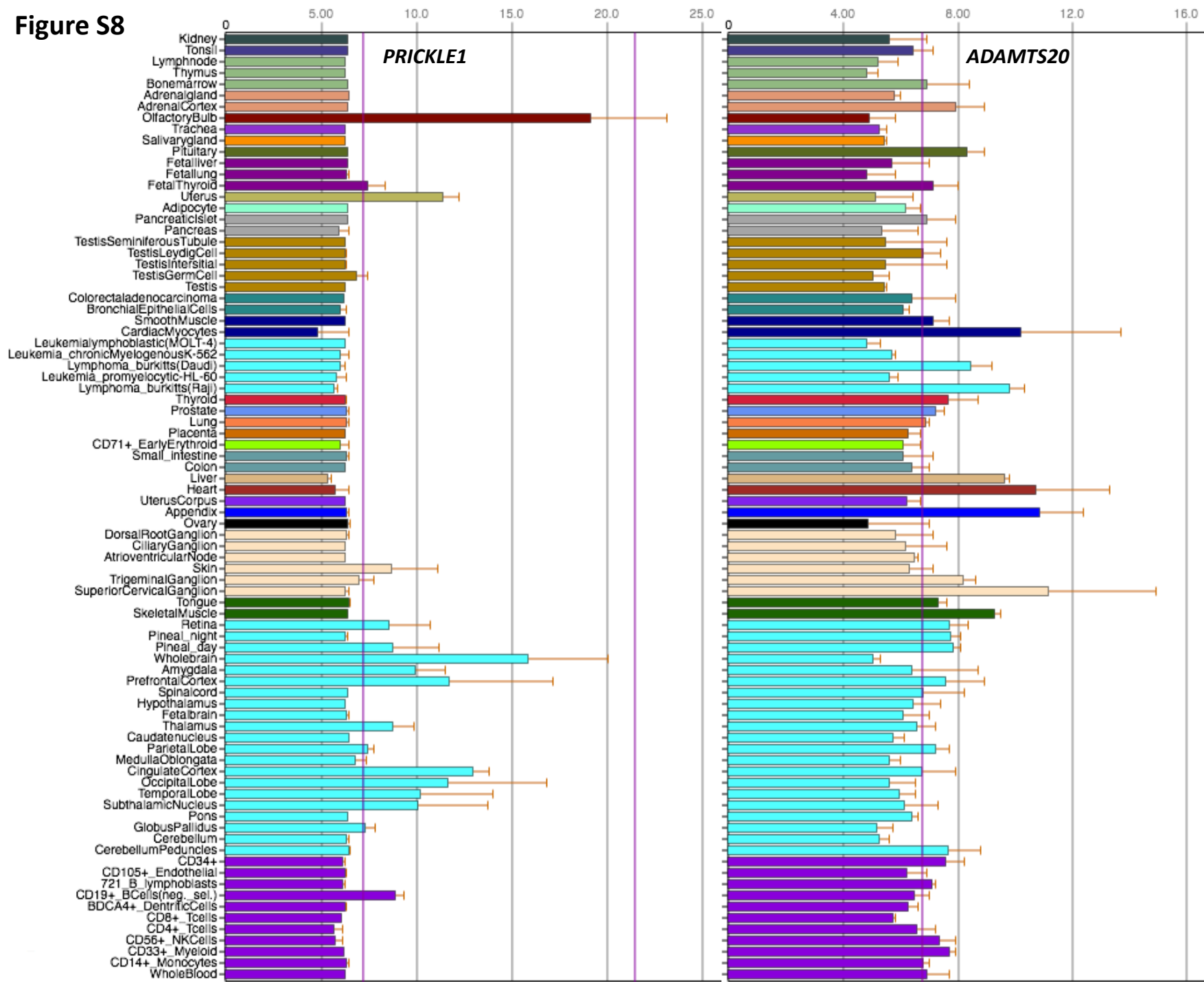
Build Query | Set Options | Documentation

LD threshold, r² (select NA to only show query variants): 0.8

1000G Phase 1 population for LD calculation: ○ AFR ○ AMR ○ ASN ● EUR

Source for epigenomes: ● ENCODE ○ Roadmap

Mammalian conservation algorithm: ○ GERP ● SiPhy-omega ○ both

Show position relative to: ● GENCODE genes ○ RefSeq genes ○ both

Condense lists in table longer than: 3

Condense indel oligos longer than: 6

Background set for enhancer enrichment analysis: All SNPs in 1KG CEU pilot

Output mode: ● HTML ○ Text

Submit Query

Enhancer enrichment analysis

Cell type		All enhancers				Strongest enhancers			
ID	Description	Obs	Exp	Fold	p	Obs	Exp	Fold	p
H1	H1 Cell Line	4	0.3	13.7	9.5E-5	3	0	123.1	1.0E-6
HSMM	skeletal muscle myoblasts	5	0.4	13.9	7.0E-6	2	0.2	12.8	0.009691
HMEC	mammary epithelial cells	4	0.4	9.6	0.000383	0	0.2	0	1
GM12878	B-lymphocyte, lymphoblastoid	3	0.3	9.1	0.003121	3	0.1	25.6	0.000157
NHEK	epidermal keratinocytes	4	0.4	11.1	0.00022	3	0.2	19	0.000373