

S2 Table

SLE associated *cis*-eQTL associations deemed to be causal as defined by the JLIM pipeline (this is the output from JLIM).

Level	Target	Name	idxRS	chrom	idxBP	idxP	idx2BP	idx2P	minP2	STAT	p	FDR
Exon	ENSG00000154319.10 11278972 11282145	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	5.10E-46	46.71504784	0	0
Trans	ENST00000284486.4	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	4.43E-45	48.80642864	0	0
Gene	ENSG00000154319.10	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	2.31E-40	42.24461359	0	0
Exon	ENSG00000154319.10 11301540 11302395	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	4.63E-33	26.5489187	0	0
Exon	ENSG00000136573.6 11417842 11418961	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.41E-31	14.15188659	0	0
Exon	ENSG00000136573.6 11407668 11407771	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	4.41E-30	15.35338136	0	0
Exon	ENSG00000136573.6 11412252 11412398	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	5.59E-30	8.78106877	0	0
Exon	ENSG00000136573.6 11414167 11414346	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.14E-29	10.05135904	0	0
Exon	ENSG00000136573.6 11420488 11420619	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.02E-29	9.697875438	0	0
Exon	ENSG00000136573.6 11415471 11415547	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.03E-29	10.58889714	0	0
Junction	8 11418961 11420488	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	7.60E-28	10.480584	0	0
Junction	8 11407771 11412252	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.65E-27	13.92766832	0	0
Junction	8 11412993 11414167	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.43E-27	3.659807232	0	0
Junction	8 11406631 11407668	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.47E-27	14.9105389	0	0
Gene	ENSG00000136573.6	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	3.29E-26	9.266974735	0	0
Exon	ENSG00000136573.6 11403561 11403612	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.39E-26	10.33062052	0	0
Exon	ENSG00000136573.6 11412841 11412993	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.42E-25	0.935131085	4.00E-04	0.04872
Exon	ENSG00000136573.6 11405541 11405634	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	3.68E-25	7.036497058	0	0
Junction	8 11400856 11403561	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	5.18E-25	7.581413942	0	0
Junction	8 11403612 11405541	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.35E-25	7.970289938	0	0
Exon	ENSG00000136573.6 11406533 11406631	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	7.44E-25	9.678824947	0	0
Junction	8 11414346 11415471	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	9.84E-25	8.137591462	0	0
Junction	8 11415547 11418811	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.25E-24	8.259710303	0	0
Junction	8 11405634 11406533	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.83E-24	4.015497492	0	0
Exon	ENSG00000136573.6 11400733 11400856	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	3.04E-24	7.703840438	0	0
Intron	8 11415547 11417842	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	3.14E-24	15.8312491	0	0
Intron	8 11418961 11420488	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.13E-24	11.91425144	0	0
Junction	8 11412398 11412841	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	3.08E-23	0.893095144	2.00E-04	0.035825
Junction	8 11282145 11301540	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.59E-22	16.81180857	0	0
Junction	8 11352100 11400733	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.33E-21	7.531245764	0	0
Exon	ENSG00000136573.6 11351510 11352100	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.64E-21	10.02643884	0	0
Trans	ENST00000526097.1	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.01E-19	5.784627111	0	0
Junction	8 11420619 11421412	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	5.06E-19	4.399510844	0	0
Intron	8 11414346 11415471	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.48E-19	5.986960326	0	0
Exon	ENSG00000154319.10 11324135 11324276	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.06E-16	13.07603944	0	0
Junction	8 11302317 11324135	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.06E-15	9.786471892	0	0
Intron	8 11367400 11400733	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	2.23E-15	4.423513021	0	0
Intron	8 11304130 11324135	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	7.42E-15	8.121289646	0	0
Exon	ENSG00000185651.10 21975804 21978323	<i>UBE2L3</i>	rs7444	22	21976934	2.64E-13	21929566	9.72E-14	9.94E-15	5.887594907	0	0
Trans	ENST00000458578.2	<i>UBE2L3</i>	rs7444	22	21976934	2.64E-13	21929566	9.72E-14	5.92E-14	9.106307634	0	0
Intron	8 11407771 11412252	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.06E-13	5.513216363	0	0
Intron	8 11420619 11421412	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.21E-12	3.125500681	0	0
Intron	8 11282145 11301129	<i>FAM167A</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	6.58E-12	1.880658068	0	0

Intron	8	11352100	11366659	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	7.31E-12	4.169880095	0	0
Trans		ENST00000533828.1		<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.52E-11	5.657495318	0	0
Trans		ENST00000526778.1		<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	5.85E-11	3.144335221	1.00E-04	0.0181
Intron	19	10473333	10475290	<i>TYK2</i>	rs2304256	19	10475652	1.54E-12	10466123	6.91E-13	2.24E-09	1.9265087	2.00E-04	0.0232
Exon		ENSG00000105397.7	10475527	<i>TYK2</i>	rs2304256	19	10475652	1.54E-12	10466123	6.91E-13	2.58E-09	3.196078064	0	0
Exon		ENSG00000185651.10	21965146	<i>UBE2L3</i>	rs7444	22	21976934	2.64E-13	21929566	9.72E-14	3.04E-09	2.82372309	0	0
Trans		ENST00000525206.1		<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	1.12E-08	4.971535832	0	0
Intron	8	11412993	11414166	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	3.41E-08	3.739940315	0	0
Trans		ENST00000292779.3		<i>CCDC116</i>	rs7444	22	21976934	2.64E-13	21929566	9.72E-14	1.45E-06	1.532076909	3.00E-04	0.048266667
Intron	2	213881768	213886189	<i>IKZF2</i>	rs3768792	2	21387170	3.78E-08	21389023	2.04E-08	1.15E-05	0.952921334	2.00E-04	0.0232
Exon		ENSG00000153064.7	102750965	<i>BANK1</i>	rs10028805	4	10273725	4.51E-10	10275609	8.16E-11	1.85E-05	0.57870071	4.00E-04	0.04872
Junction	8	11352100	11366659	<i>BLK</i>	rs2736340	8	11343973	2.14E-16	11339965	1.35E-18	2.08E-05	1.70950024	0	0
Gene		ENSG00000161180.5		<i>CCDC116</i>	rs7444	22	21976934	2.64E-13	21929566	9.72E-14	2.50E-05	1.159090612	5.00E-04	0.0439
Exon		ENSG00000029725.11	5241314	<i>RABEP1</i>	rs2286672	17	4712617	0.00033644	4697255	2.45E-05	7.41E-05	1.537192432	4.00E-04	0.04872
Exon		ENSG00000186517.8	161019214	<i>ARHGAP30</i>	rs1801274	1	16147974	5.56E-11	16147881	3.59E-12	0.000114	1.019783352	2.00E-04	0.029
Intron	1	114292211	114300321	<i>PHTF1</i>	rs2476601	1	11437756	8.38E-13	11437756	8.38E-13	0.000144	3.897248985	1.00E-04	0.012373333
Exon		ENSG00000030419.11	213886368	<i>IKZF2</i>	rs3768792	2	21387170	3.78E-08	21389023	2.04E-08	1.96E-04	1.16986173	3.00E-04	0.039717391
Junction	4	102993557	102994841	<i>BANK1</i>	rs10028805	4	10273725	4.51E-10	10275609	8.16E-11	0.000253	0.516404878	2.00E-04	0.035825
Exon		ENSG00000153064.7	102993502	<i>BANK1</i>	rs10028805	4	10273725	4.51E-10	10275609	8.16E-11	0.000348	0.57083328	4.00E-04	0.04872
Junction	19	10657929	10659580	<i>ATG4D</i>	rs2304256	19	10475652	1.54E-12	10466123	6.91E-13	0.000385	0.788939164	2.00E-04	0.035825
Exon		ENSG00000161180.5	21990721	<i>CCDC116</i>	rs7444	22	21976934	2.64E-13	21929566	9.72E-14	0.000495	0.590162924	4.00E-04	0.04872
Junction	1	235915471	235916344	<i>LYST</i>	rs9782955	1	23603987	0.00079168	23603427	0.00050178	0.001296	1.058660842	2.00E-04	0.035825

The lead SNPs from the *Bentham and Morris et al 2015* GWAS in persons of European descent were functionally annotated by *cis*-eQTL analysis in the Geuvadis RNA-Seq cohort in lymphoblastoid cell lines using RNA-Seq quantification profiled at five resolutions (gene, transcript, exon, junction, and intron). Only SNPs reaching genome-wide significance, not conditional peaks, outside of the major histocompatibility complex loci, and with minor allele frequency > 5% were included leaving 38 SLE lead SNPs in total. All SLE loci were densely imputed to the 1000 Genomes Phase 3 Imputation Panel as described in methods.

All 38 loci (+/-100kb of each lead SNP) comprised a nominally significant *cis*-eQTL ($P < 0.01$) for at least one gene within +/-500kb of the lead SNP at each resolution of RNA-Seq. Evidence of a single shared causal variant at each locus was assessed using the Joint Likelihood Mapping (JLIM) algorithm as described in methods.

Causal *cis*-eQTLs are defined where the disease association is consistent with a single shared effect for at least one *cis*-eQTL ($P < 0.01$ and JLIM FDR adjusted $P < 0.05$).

Level: RNA-Seq quantification type, Target: The expression target – defined by chromosome and genomic coordinate (hg19). IndexRs: the rs ID of the SLE GWAS SNP, idxP: The P -value of SLE association derived from the GWAS, idx2bp: the SLE association P -value of the most associated SNP within +/-100kb of the lead SNP (may be different due to the reporting of the most likely causal SNP from the original GWAS, idx2P: the P -value of the most associated SNP, minP2: The *cis*-eQTL P -value of the most associated SNP with the expression target, STAT: The JLIM statistic, p: The JLIM P -value, FDR: The false discovery rate adjusted P -value.