

Table S1 Default parameters in the SMR analyses

Parameter	Meaning	Default value
Maf	Removes SNPs based on a minor allele frequency (MAF) threshold in the reference sample	0.01
Diff-freq	Excludes SNPs with allele frequency differences between any pairwise data sets larger than the specified threshold	0.2
Diff-freq-prop	Stops the analysis if the proportion of SNPs being excluded by --diff-freq is larger than the specified value	0.05
Peqtl-smr	P value threshold to select the top associated eQTL for the SMR test	5.00E-08
Peqtl-heidi	Threshold of eQTL P value to select eQTLs for the HEIDI test	1.57E-03
Ld-upper-limit	Upper LD r-squared threshold used to prune SNPs (eQTLs) in the HEIDI test	0.9
Ld-lower-limit	Lower LD r-squared threshold used to prune SNPs (eQTLs) in the HEIDI test	0.05
Heidi-min-m	Minimum requirement of the number of cis-SNPs used in the HEIDI test	3
Heidi-max-m	Maximum number of eQTLs used in the HEIDI test	20
Cis-wind	Defines a window centred around the probe to select cis-eQTLs (passing a P value threshold) for the SMR analysis	2,000 kb

eQTL, expression quantitative trait loci; HEIDI, heterogeneity in dependent instruments; MAF, minor allele frequency; LD, linkage disequilibrium; SNP, single-nucleotide polymorphism; SMR, summary data-based Mendelian randomization; FDR, false discovery rate; GWAS, genome-wide association studies.

Table S2 Genes showing potential pleiotropic association with EC using CAGE eQTL data

probeID	ProbeChr	Gene	Probe_bp	topSNP	topSNP_chr	topSNP_bp	A1	A2	Freq	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI	nsnp_HEIDI	p_SMR_FDR
ILMN_1751400	17	SKAP1	46210873	rs2938483	17	46318004	C	T	0.347561	-0.0886	0.015646	1.49E-08	0.479392	0.027469	3.32E-68	-0.185	0.034	7.19E-08	1.25E-05	20	0.000613
ILMN_2369018	17	EVI2A	29644832	rs7505	17	29644852	G	A	0.359756	0.074118	0.015541	1.85E-06	0.723888	0.027623	#####	0.102	0.022	2.70E-06	0.379	20	0.012
ILMN_1809347	15	SRP14	40328444	rs17722526	15	40320267	G	A	0.378049	0.08769	0.015726	2.46E-08	-0.21392	0.028925	1.41E-13	-0.410	0.092	8.49E-06	0.225	20	0.023
ILMN_1733579	17	EVI2A	29645189	rs2525570	17	29681245	A	G	0.371951	0.07104	0.015533	4.80E-06	-0.4421	0.027497	3.63E-58	-0.161	0.037	1.09E-05	0.425	20	0.023
ILMN_1683950	17	SNX11	46200008	rs62064953	17	46193967	C	T	0.189024	-0.08302	0.018841	1.05E-05	-0.59093	0.031734	2.15E-77	0.140	0.033	1.80E-05	0.000	20	0.031
ILMN_1696051	17	SNX11	46188096	rs12949879	17	46158050	C	T	0.189024	-0.08257	0.018836	1.17E-05	-0.46116	0.031266	3.09E-49	0.179	0.043	2.65E-05	0.000	20	0.038

The GWAS summarized data can be downloaded at <https://www.ebi.ac.uk/gwas/studies/GCST006464>. The CAGE eQTL data can be downloaded at <https://cnsgenomics.com/data/SMR/#eQTLsummarydata>. PeQTL is the P-value of the top associated cis-eQTL in the eQTL analysis, and PGWAS is the P-value for the top associated cis-eQTL in the GWAS analysis. Beta is the estimated effect size in SMR analysis, SE is the corresponding standard error, PSMR is the P value for SMR analysis and PHEIDI is the P value for the HEIDI test. CAGE, Consortium for the Architecture of Gene Expression; CHR, chromosome; EC, endometrial cancer; eQTL, expression quantitative trait loci; HEIDI, heterogeneity in dependent instruments; SNP, single-nucleotide polymorphism; SMR, summary data-based Mendelian randomization; FDR, false discovery rate; GWAS, genome-wide association studies.

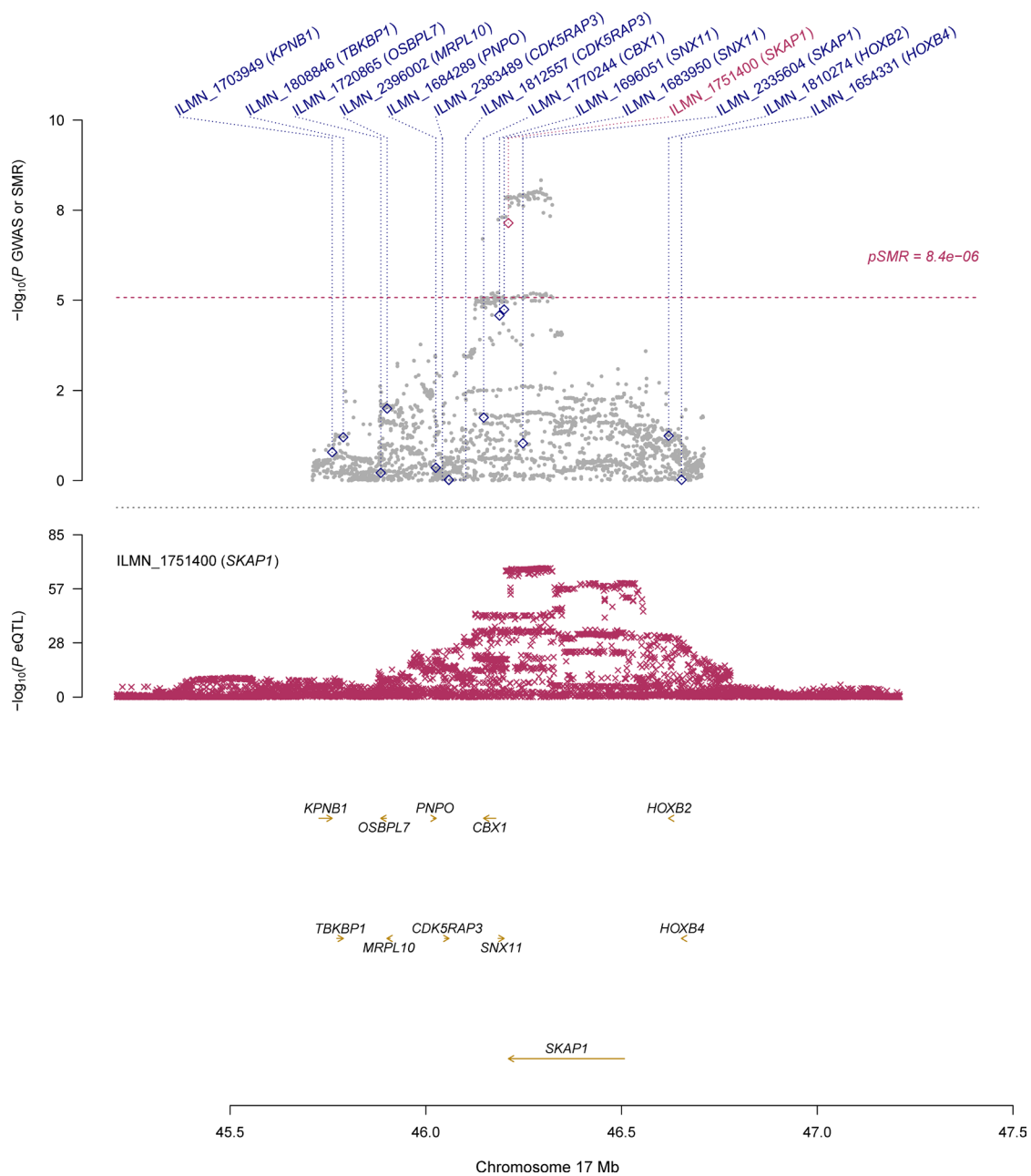


Figure S1 Pleiotropic association of *SKAP1* and *SNX11* with EC. Top plot, grey dots represent the $-\log(P)$ values for SNPs from the GWAS of EC, with hollow rhombuses indicating that the probes do not pass the HEIDI test. Middle plot, eQTL results. Bottom plot, location of genes tagged by the probes. EC, endometrial cancer; eQTL, expression quantitative trait loci; GWAS, genome-wide association study; HEIDI, heterogeneity in dependent instruments; SMR, Summary-based Mendelian Randomization; SNP, single nucleotide polymorphism.

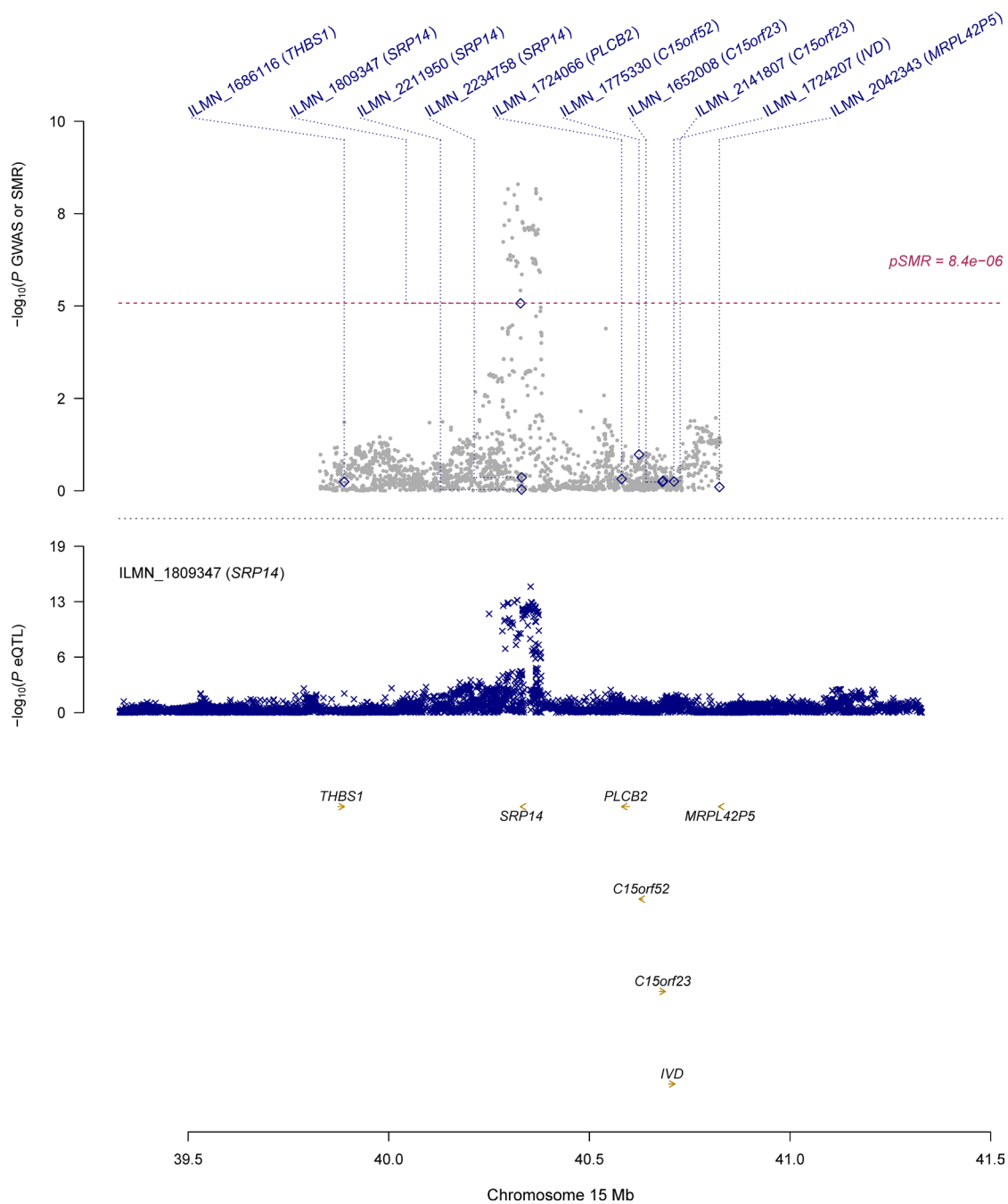


Figure S2 Pleiotropic association of *SRP14* with EC. Top plot, grey dots represent the $-\log(P \text{ values})$ for SNPs from the GWAS of EC, with hollow rhombuses indicating that the probes do not pass the HEIDI test. Middle plot, eQTL results. Bottom plot, location of genes tagged by the probes. EC, endometrial cancer; eQTL, expression quantitative trait loci; GWAS, genome-wide association study; HEIDI, heterogeneity in dependent instruments; SMR, Summary-based Mendelian Randomization; SNP, single nucleotide polymorphism.

Table S3 Significant genes identified by transcriptome-wide association analysis in 22 tissues

Gene	CHR	P0	P1	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P	tissue	FDR
<i>HECTD4</i>	12	112,597,992	112,819,896	0.0617	rs11066188	-5.21	rs7294902	0.004402	-3.92	2.1589	323	15	enet	0.019	0.01	-5.8429	5.13E-09	Adipose_Subcutaneous	1.79E-05
<i>EIF3CL</i>	16	28,390,900	28,415,200	0.1102	rs28472312	-4.78	rs7189927	0.078487	6.2	3.18832	247	9	enet	0.14	7.70E-12	4.74853	2.05E-06	Adipose_Subcutaneous	0.002392
<i>ATF7IP2</i>	16	10,420,291	10,577,495	0.2442	rs12597514	4.36	rs11645096	0.13105	-7.12	4.05767	659	4	lasso	0.17	5.70E-14	-4.74734	2.06E-06	Adipose_Subcutaneous	0.002392
<i>SNX11</i>	17	46,180,719	46,200,436	0.1422	rs8072282	-5.73	rs2051821	0.105497	-6.9	-4.38272	451	9	lasso	0.12	2.60E-10	4.64529	3.40E-06	Adipose_Subcutaneous	0.002961
<i>LINC00674</i>	17	66,098,049	66,111,659	0.1164	rs6504548	4.68	rs6504574	0.126682	6.32	3.992899	311	6	enet	0.14	9.80E-12	4.18625	2.84E-05	Adipose_Subcutaneous	0.019783
<i>EIF3C</i>	16	28,699,879	28,747,051	0.1219	rs28472312	-4.78	rs28472312	0.041134	-5.22	-4.78103	197	12	enet	0.073	1.40E-06	4.08701	4.37E-05	Adipose_Subcutaneous	0.025368
<i>SH3GL1P3</i>	17	66,130,816	66,131,745	0.0773	rs6504548	4.68	rs6504574	0.059905	4.52	3.99733	309	1	top1	0.06	1.20E-05	3.99733	6.41E-05	Adipose_Subcutaneous	0.031894
<i>C17orf67</i>	17	54,869,274	54,916,134	0.1509	rs7209070	3.86	rs7209070	0.057799	-4.93	3.863544	476	5	lasso	0.059	1.30E-05	-3.8969	9.74E-05	Adipose_Subcutaneous	0.041796
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.3819	rs937213	5.85	rs17722526	0.084883	7.29	5.57613	472	18	enet	0.23	4.70E-19	3.8725	0.000108	Adipose_Subcutaneous	0.041796
<i>S100B</i>	21	48,018,875	48,025,121	0.2013	rs2070429	4.06	rs2239574	0.16764	-8.46	3.6126	297	6	enet	0.19	1.30E-15	-3.8363	0.000125	Adipose_Subcutaneous	0.043538
<i>TEFM</i>	17	29,224,354	29,231,547	0.1178	rs8065496	5.04	rs11651802	0.019455	-3.18	2.38646	272	14	lasso	0.052	0.00	-5.22526	1.74E-07	Adipose_Visceral_Omentum	0.000353
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.2304	rs937213	5.85	rs3736290	0.0806	4.8	4.9687	472	7	lasso	0.15	2.70E-08	4.86223	1.16E-06	Adipose_Visceral_Omentum	0.001177
<i>SNX11</i>	17	46,180,719	46,200,436	0.2685	rs8072282	-5.73	rs11079808	0.26913	-7.12	-4.42744	451	1	top1	0.27	2.80E-14	4.427437	9.54E-06	Adipose_Visceral_Omentum	0.006455
<i>SNX11</i>	17	46,180,719	46,200,436	0.1157	rs8072282	-5.73	rs11079806	0.12	-4.99	-4.32706	451	1	top1	0.12	3.90E-07	4.327061	1.51E-05	Artery_Aorta	0.025394
<i>NUPR1</i>	16	28,548,606	28,550,495	0.0896	rs28472312	-4.78	rs4788076	0.007311	-4.19	3.3712	198	5	lasso	0.041	0.00	-4.2993	1.71E-05	Artery_Aorta	0.025394
<i>HECTD4</i>	12	112,597,992	112,819,896	0.051	rs11066188	-5.21	rs11066320	0.019542	3.84	-4.80838	323	1	top1	0.02	0.01	-4.8084	1.52E-06	Artery_Tibial	0.005711
<i>NFE2L1</i>	17	46,125,691	46,138,849	0.1279	rs8072282	-5.73	rs8067470	0.003582	3.73	-4.44	411	1	top1	0.0036	0.16	-4.44	9.12E-06	Artery_Tibial	0.017094
<i>CBX1</i>	17	46,147,414	46,178,883	0.0533	rs8072282	-5.73	rs11079806	0.056956	-4.46	-4.33	437	1	top1	0.057	2.90E-05	4.33	1.51E-05	Artery_Tibial	0.017094
<i>SNX11</i>	17	46,180,719	46,200,436	0.1058	rs8072282	-5.73	rs1468270	0.081904	-5.31	-4.16	451	8	lasso	0.082	5.10E-07	4.29	1.82E-05	Artery_Tibial	0.017094
<i>EIF3CL</i>	16	28,390,900	28,415,200	0.0515	rs28472312	-4.78	rs149299	0.034286	4.6	2.9778	247	2	lasso	0.035	0.00	4.214	2.51E-05	Artery_Tibial	0.01886
<i>SIVA1</i>	14	105,219,437	105,234,831	0.1532	rs2498804	4.21	rs7142772	0.138778	-6.69	3.5669	355	10	enet	0.15	6.90E-12	-4.0856	4.40E-05	Artery_Tibial	0.025387
<i>TIPARP</i>	3	156,391,024	156,424,559	0.1309	rs414683	4.13	rs343992	0.019177	4.43	2.88177	426	17	enet	0.05	8.20E-05	4.06842	4.73E-05	Artery_Tibial	0.025387
<i>PVT1</i>	8	128,806,779	129,113,499	0.1438	rs7813501	5.93	rs687279	0.003503	3.58	1.6739	753	3	lasso	0.0065	0.09	3.9196	8.87E-05	Artery_Tibial	0.041656
<i>COPZ2</i>	17	46,103,533	46,115,392	0.1253	rs8072282	-5.73	rs17618704	0.00884	-3.75	-3.87	407	1	top1	0.0088	0.06	3.87	0.000107	Artery_Tibial	0.042078
<i>C17orf67</i>	17	54,869,274	54,916,134	0.1145	rs7209070	3.86	rs7209070	0.02909	-4.52	3.86	476	1	top1	0.029	0.00	-3.86	0.000112	Artery_Tibial	0.042078
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.2391	rs937213	5.85	rs3736290	0.104	5.05	4.9687	472	1	top1	0.1	5.30E-06	4.9687	6.74E-07	Breast_Mammary_Tissue	0.001331
<i>SNX11</i>	17	46,180,719	46,200,436	0.1434	rs8072282	-5.73	rs2051821	0.108	-5.45	-4.38272	451	1	top1	0.11	3.40E-06	4.38272	1.17E-05	Breast_Mammary_Tissue	0.008624
<i>ATF7IP2</i>	16	10,420,291	10,577,495	0.2624	rs12597514	4.36	rs12597514	0.147065	-5.63	4.3592	659	1	top1	0.15	5.50E-08	-4.3592	1.31E-05	Breast_Mammary_Tissue	0.008624
<i>RQCD1</i>	2	219,433,303	219,461,803	0.1925	rs10208728	-4	rs10208728	0.0147	3.59	-4.00042	365	5	lasso	0.025	0.02	-3.87861	0.000105	Breast_Mammary_Tissue	0.04582
<i>AC074289.1</i>	2	64,370,373	64,479,993	0.1672	rs6750096	3.68	rs2251764	0.128	-5.31	3.40334	421	16	enet	0.15	3.80E-08	-3.85355	0.000116	Breast_Mammary_Tissue	0.04582
<i>RP5-890E16.2</i>	17	46,122,503	46,125,435	0.1359	rs8072282	-5.73	rs1860862	0.03217	-3.89	-5.67228	410	1	top1	0.032	0.01	5.67228	1.41E-08	Colon_Transverse	2.54E-05
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.3972	rs937213	5.85	rs17722526	0.162509	5.7	5.5761	472	1	top1	0.16	3.60E-08	5.5761	2.46E-08	Colon_Transverse	2.54E-05
<i>SNX11</i>	17	46,180,719	46,200,436	0.1876	rs8072282	-5.73	rs2109984	0.17196	-5.56	-4.51318	451	1	top1	0.17	1.40E-08	4.51318	6.39E-06	Colon_Transverse	0.004392
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.3021	rs937213	5.85	rs17722526	0.10926	6.13	5.57613	472	6	lasso	0.14	9.40E-10	5.56726	2.59E-08	Esophagus_Mucosa	8.57E-05
<i>EEFSEC</i>	3	127,965,679	128,127,485	0.0737	rs10934853	-4.86	rs2687729	0.079724	-4.65	-4.80734	417	1	top1	0.08	1.40E-05	4.80733	1.53E-06	Esophagus_Muscularis	0.002842

Table S3 (continued)

Table S3 (continued)

Gene	CHR	P0	P1	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P	tissue	FDR
<i>RP5-890E16.2</i>	17	46,122,503	46,125,435	0.0694	rs8072282	-5.73	rs8067470	0.011161	-3.88	-4.43704	410	8	lasso	0.013	0.05	4.7786	1.76E-06	Esophagus_Muscularis	0.002842
<i>LRRC37A16P</i>	17	66,121,918	66,148,609	0.1159	rs6504548	4.68	rs4791212	0.030822	3.71	4.5439	323	1	top1	0.031	0.01	4.5439	5.52E-06	Esophagus_Muscularis	0.005941
<i>SH2B1</i>	16	28,857,921	28,885,526	0.0642	rs28472312	-4.78	rs2008514	0.029065	-4.4	3.5494	172	21	enet	0.059	0.00	-4.0134	5.98E-05	Esophagus_Muscularis	0.048274
<i>ADAM1A</i>	12	112,337,067	112,340,042	0.1963	rs653178	-6.27	rs3741993	0.072441	-4.24	-0.0154	180	22	enet	0.1	4.30E-06	4.0591	4.93E-05	Heart_Left_Ventricle	0.038124
<i>FAM46C</i>	1	118,148,556	118,170,994	0.2517	rs731017	-4.17	rs7549770	0.137532	-6.02	-4.0936	406	4	lasso	0.17	1.90E-09	4.0562	4.99E-05	Heart_Left_Ventricle	0.038124
<i>EIF3C</i>	16	28,699,879	28,747,051	0.0352	rs28472312	-4.78	rs7189927	0.015046	3.89	3.18832	197	4	lasso	0.02	0.01	4.6097	4.03E-06	Lung	0.008013
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.1414	rs937213	5.85	rs17722526	0.116805	5.83	5.57613	472	10	enet	0.12	2.00E-09	4.5414	5.59E-06	Lung	0.008013
<i>SNX11</i>	17	46,180,719	46,200,436	0.2001	rs8072282	-5.73	rs1468270	0.121	-6.2	-4.1609	451	1	top1	0.12	1.70E-09	4.1609	3.17E-05	Lung	0.030295
<i>EEFSEC</i>	3	127,965,679	128,127,485	0.05	rs10934853	-4.86	rs2248668	0.01193	-4.4	-4.6629	417	5	lasso	0.02	0.00	4.9759	6.49E-07	Muscle_Skeletal	0.001875
<i>RP5-890E16.2</i>	17	46,122,503	46,125,435	0.0891	rs8072282	-5.73	rs16953461	0.039407	4.8	3.010733	410	3	lasso	0.068	3.10E-07	4.585159	4.54E-06	Muscle_Skeletal	0.006558
<i>UQCCL1</i>	20	33,890,369	33,999,944	0.0963	rs224333	4.03	rs6088832	0.04434	-5.24	3.58551	354	19	enet	0.049	1.20E-05	-4.0668	4.77E-05	Muscle_Skeletal	0.045935
<i>EEFSEC</i>	3	127,965,679	128,127,485	0.0739	rs10934853	-4.86	rs6439119	0.05753	-5.31	-4.83856	417	2	lasso	0.06	4.50E-05	4.77717	1.78E-06	Nerve_Tibial	0.007183
<i>SNX11</i>	17	46,180,719	46,200,436	0.2389	rs8072282	-5.73	rs1468270	0.182191	-6.92	-4.16091	451	7	lasso	0.21	5.30E-15	4.649355	3.33E-06	Nerve_Tibial	0.007183
<i>EIF3C</i>	16	28,699,879	28,747,051	0.1451	rs28472312	-4.78	rs8045689	0.0534	4.53	2.35097	197	6	lasso	0.083	1.80E-06	4.466735	7.94E-06	Nerve_Tibial	0.009836
<i>RP5-890E16.2</i>	17	46,122,503	46,125,435	0.1642	rs8072282	-5.73	rs8067470	0.085057	-5.58	-4.43704	410	1	top1	0.085	1.30E-06	4.437039	9.12E-06	Nerve_Tibial	0.009836
<i>ABCC5</i>	3	183,637,722	183,735,803	0.2401	rs9818518	-3.65	rs3792583	0.11342	5.76	-3.49753	526	40	enet	0.12	4.80E-09	-4.16385	3.13E-05	Nerve_Tibial	0.027006
<i>LRRC37A16P</i>	17	66,121,918	66,148,609	0.0854	rs6504548	4.68	rs7211282	0.075572	4.59	4.005139	323	1	top1	0.076	5.00E-06	4.005139	6.20E-05	Nerve_Tibial	0.044578
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.3958	rs937213	5.85	rs3736290	0.28556	6.63	4.9687	472	5	lasso	0.29	7.60E-13	5.68123	1.34E-08	Pancreas	2.18E-05
<i>SNX11</i>	17	46,180,719	46,200,436	0.2802	rs8072282	-5.73	rs9905800	0.108999	-6.01	-4.44303	451	13	lasso	0.14	3.10E-08	5.52429	3.31E-08	Skin_Not_Sun_Exposed_Suprapubic	8.13E-05
<i>ATF7IP2</i>	16	10,420,291	10,577,495	0.3615	rs12597514	4.36	rs12165003	0.16592	-6.47	4.24847	659	1	top1	0.17	2.10E-09	-4.24847	2.15E-05	Skin_Not_Sun_Exposed_Suprapubic	0.026413
<i>ADSSL1</i>	14	105,190,523	105,213,647	0.316	rs2498804	4.21	rs2498804	0.154735	-6.65	4.21182	353	24	enet	0.2	1.80E-11	-4.10471	4.05E-05	Skin_Not_Sun_Exposed_Suprapubic	0.03317
<i>EIF3C</i>	16	28,699,879	28,747,051	0.073	rs28472312	-4.78	rs10499	0.0132	3.73	3.20978	197	14	enet	0.048	0.00	4.02012	5.82E-05	Skin_Not_Sun_Exposed_Suprapubic	0.035749
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.336	rs937213	5.85	rs3736290	0.154	7.51	4.9687	472	1	top1	0.15	8.90E-13	4.9687	6.74E-07	Skin_Sun_Exposed_Lower_leg	0.002446
<i>RP5-890E16.2</i>	17	46,122,503	46,125,435	0.0844	rs8072282	-5.73	rs2109984	0.0501	-4.26	-4.51318	410	1	top1	0.05	5.30E-05	4.513181	6.39E-06	Skin_Sun_Exposed_Lower_leg	0.010524
<i>SNX11</i>	17	46,180,719	46,200,436	0.2241	rs8072282	-5.73	rs9899461	0.288	-9.54	-4.4374	451	1	top1	0.29	4.30E-24	4.437401	9.11E-06	Skin_Sun_Exposed_Lower_leg	0.010524
<i>BPTF</i>	17	65,821,640	65,980,494	0.1041	rs6504548	4.68	rs6504573	0.00973	-3.82	3.406292	384	14	enet	0.026	0.00	-4.38458	1.16E-05	Skin_Sun_Exposed_Lower_leg	0.010524
<i>ATF7IP2</i>	16	10,420,291	10,577,495	0.2595	rs12597514	4.36	rs12165003	0.175169	-7.87	4.24847	659	16	enet	0.19	2.10E-15	-4.22098	2.43E-05	Skin_Sun_Exposed_Lower_leg	0.017637
<i>HINT3</i>	6	126,277,927	126,301,387	0.0803	rs984040	-6.06	rs6900105	0.013817	3.97	-3.30416	270	4	lasso	0.028	0.00	-4.00298	6.25E-05	Skin_Sun_Exposed_Lower_leg	0.03504
<i>EIF3C</i>	16	28,699,879	28,747,051	0.0739	rs28472312	-4.78	rs10499	0.05707	5.54	3.20978	197	4	lasso	0.066	4.10E-06	3.92755	8.58E-05	Skin_Sun_Exposed_Lower_leg	0.03504
<i>ADSSL1</i>	14	105,190,523	105,213,647	0.2345	rs2498804	4.21	rs12590163	0.21736	-8.16	3.9246	353	1	top1	0.22	7.20E-18	-3.9246	8.69E-05	Skin_Sun_Exposed_Lower_leg	0.03504
<i>SIVA1</i>	14	105,219,437	105,234,831	0.083	rs2498804	4.21	rs12590163	0.0312	-4.61	3.9246	355	1	top1	0.031	0.00	-3.9246	8.69E-05	Skin_Sun_Exposed_Lower_leg	0.03504
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.2093	rs937213	5.85	rs17722526	0.131	4.84	5.5761	472	1	top1	0.13	7.90E-07	5.5761	2.46E-08	Stomach	3.58E-05
<i>SNX11</i>	17	46,180,719	46,200,436	0.1965	rs8072282	-5.73	rs11079808	0.08901	-5.01	-4.42744	451	6	lasso	0.11	1.00E-05	4.48164	7.41E-06	Stomach	0.005391
<i>RP5-890E16.2</i>	17	46,122,503	46,125,435	0.2898	rs8072282	-5.73	rs9905800	0.121284	-6.41	-4.44303	410	36	enet	0.23	2.00E-10	5.17967	2.22E-07	Testis	0.0007

Table S3 (continued)

Table S3 (continued)

Gene	CHR	P0	P1	HSQ	BEST.GWAS.ID	BEST.GWAS.Z	EQTL.ID	EQTL.R2	EQTL.Z	EQTL.GWAS.Z	NSNP	NWGT	MODEL	MODEL.CV.R2	MODEL.CV.PV	TWAS.Z	TWAS.P	tissue	FDR
<i>EIF3C</i>	16	28,699,879	28,747,051	0.0918	rs28472312	-4.78	rs28472312	0.0514	-4.38	-4.78103	197	4	lasso	0.079	0.00	4.7621	1.92E-06	Testis	0.003025
<i>NUPR1</i>	16	28,548,606	28,550,495	0.0623	rs28472312	-4.78	rs12448482	0.0139	3.66	-3.49454	198	19	enet	0.025	0.03	-4.6016	4.19E-06	Testis	0.003324
<i>COPZ2</i>	17	46,103,533	46,115,392	0.3384	rs8072282	-5.73	rs16953461	0.134379	6.7	3.01073	407	22	enet	0.32	8.90E-15	4.60039	4.22E-06	Testis	0.003324
<i>SNX11</i>	17	46,180,719	46,200,436	0.2151	rs8072282	-5.73	rs11079808	0.124638	-4.75	-4.42744	451	1	top1	0.12	3.70E-06	4.42744	9.54E-06	Testis	0.006012
<i>NAV3</i>	12	78,224,685	78,606,790	0.2452	rs1272489	5.05	rs1920428	0.25696	6.43	4.07487	700	1	top1	0.26	8.80E-12	4.07487	4.60E-05	Testis	0.024158
<i>ADSSL1</i>	14	105,190,523	105,213,647	0.5106	rs2498804	4.21	rs7142772	0.557414	9.34	3.56695	353	9	enet	0.59	3.50E-32	4.03167	5.54E-05	Testis	0.024938
<i>EIF2AK4</i>	15	40,226,347	40,327,797	0.3093	rs937213	5.85	rs17722526	0.182	7.67	5.57613	472	15	enet	0.23	3.00E-17	4.59471	4.33E-06	Thyroid	0.016247
<i>RP5-890E16.2</i>	17	46,122,503	46,125,435	0.0852	rs8072282	-5.73	rs7224155	0.01513	-4.46	-4.45894	410	1	top1	0.015	0.02	4.45894	8.24E-06	Thyroid	0.016247
<i>SNX11</i>	17	46,180,719	46,200,436	0.0812	rs8072282	-5.73	rs11079806	0.087504	-5.48	-4.32706	451	1	top1	0.088	3.20E-07	4.32706	1.51E-05	Thyroid	0.016247
<i>SEC61A1</i>	3	127,770,484	127,790,526	0.139	rs10934853	-4.86	rs1030655	0.0749	5.19	-4.31005	389	1	top1	0.075	2.30E-06	-4.31	1.63E-05	Thyroid	0.016247
<i>SRP14-AS1</i>	15	40,331,512	40,359,491	0.1712	rs937213	5.85	rs2291620	0.0509	4.4	-3.96291	446	1	top1	0.051	9.00E-05	-3.96291	7.40E-05	Thyroid	0.049173
<i>AKT1</i>	14	105,235,686	105,262,088	0.4006	rs2498804	4.21	rs12590163	0.34144	9.77	3.92458	358	8	lasso	0.34	4.30E-27	3.93437	8.34E-05	Thyroid	0.049173
<i>ZBTB42</i>	14	105,266,933	105,271,049	0.1645	rs2498804	4.21	rs4983543	0.11376	6.01	3.90051	348	1	top1	0.11	5.10E-09	3.90051	9.60E-05	Thyroid	0.049173
<i>RP11-982M15.2</i>	14	105,235,686	105,236,608	0.3751	rs2498804	4.21	rs12590163	0.25111	8.97	3.92458	349	40	enet	0.27	7.00E-21	3.86665	0.00011	Thyroid	0.049173
<i>PDLIM1</i>	10	96,997,329	97,050,781	0.0797	rs7921420	3.83	rs501603	0.0038	3.79	3.19622	533	4	lasso	0.006	0.10	3.86616	0.000111	Thyroid	0.049173
<i>EVI2A</i>	17	29,647,391	29,648,902	0.0655	rs8065496	5.04	rs12940802	0.038824	-4.61	4.73147	359	1	top1	0.039	0.00	-4.73147	2.23E-06	Whole_Blood	0.004444
<i>SNX11</i>	17	46,180,719	46,200,436	0.1202	rs8072282	-5.73	rs9899461	0.104701	-6.31	-4.4374	451	18	enet	0.11	2.90E-10	4.40843	1.04E-05	Whole_Blood	0.010364

HSQ, heritability of the gene; BEST.GWAS.ID, rsID of the most significant GWAS SNP in locus; BEST.GWAS.Z, Z-score of the most significant GWAS SNP in locus; EQTL.ID, rsID of the best eQTL in the locus; EQTL.R2, cross-validation R2 of the best eQTL in the locus; EQTL.Z, Z-score of the best eQTL in the locus; EQTL.GWAS.Z, GWAS Z-score for this eQTL; NSNP, number of SNPs in the locus; NWGT, Number of SNPs with non-zero weights in the model; MODEL, best performing model; MODEL.CV.R2, cross-validation R2 of the best performing model; MODEL.CV.PV, cross-validation P value of the best performing model; TWAS.Z, TWAS Z-score (our primary statistic of interest); TWAS.P, TWAS P value; FDR, false-discovery-rate adjusted P value.