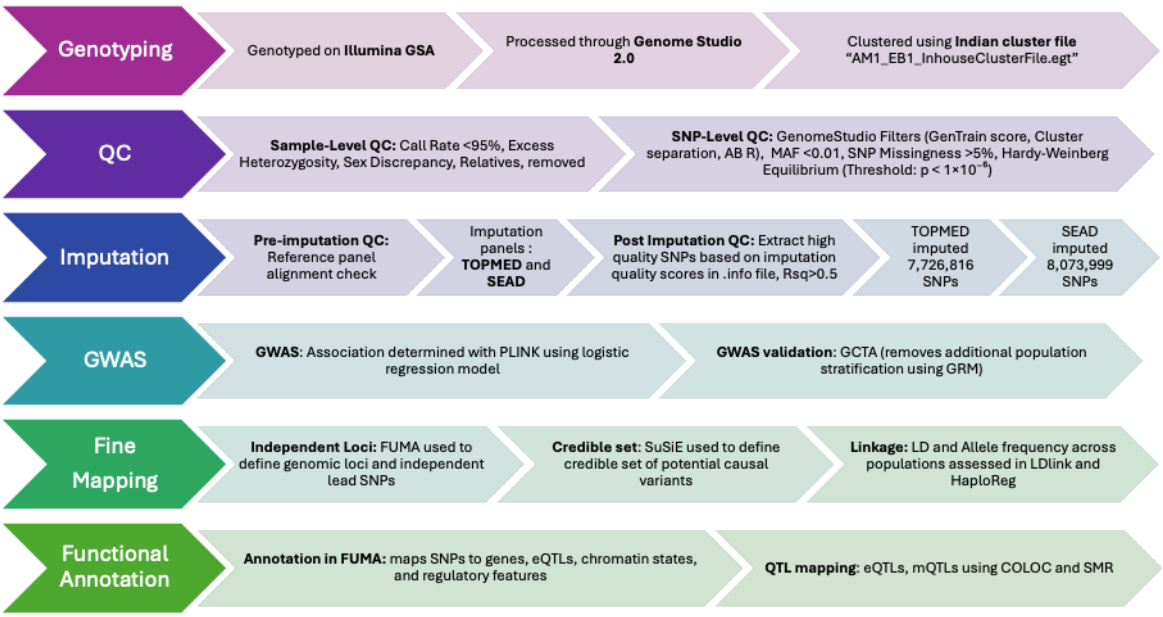
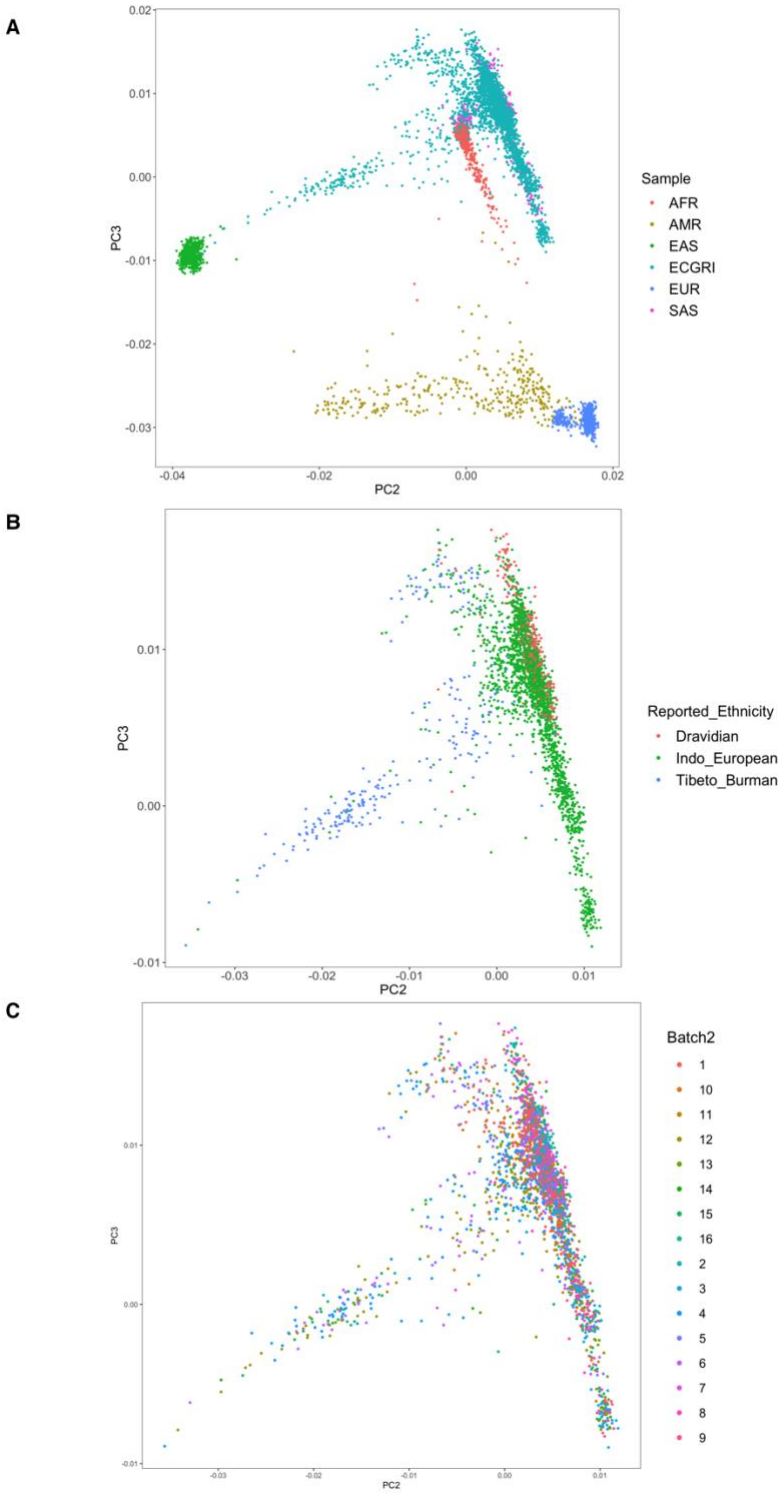
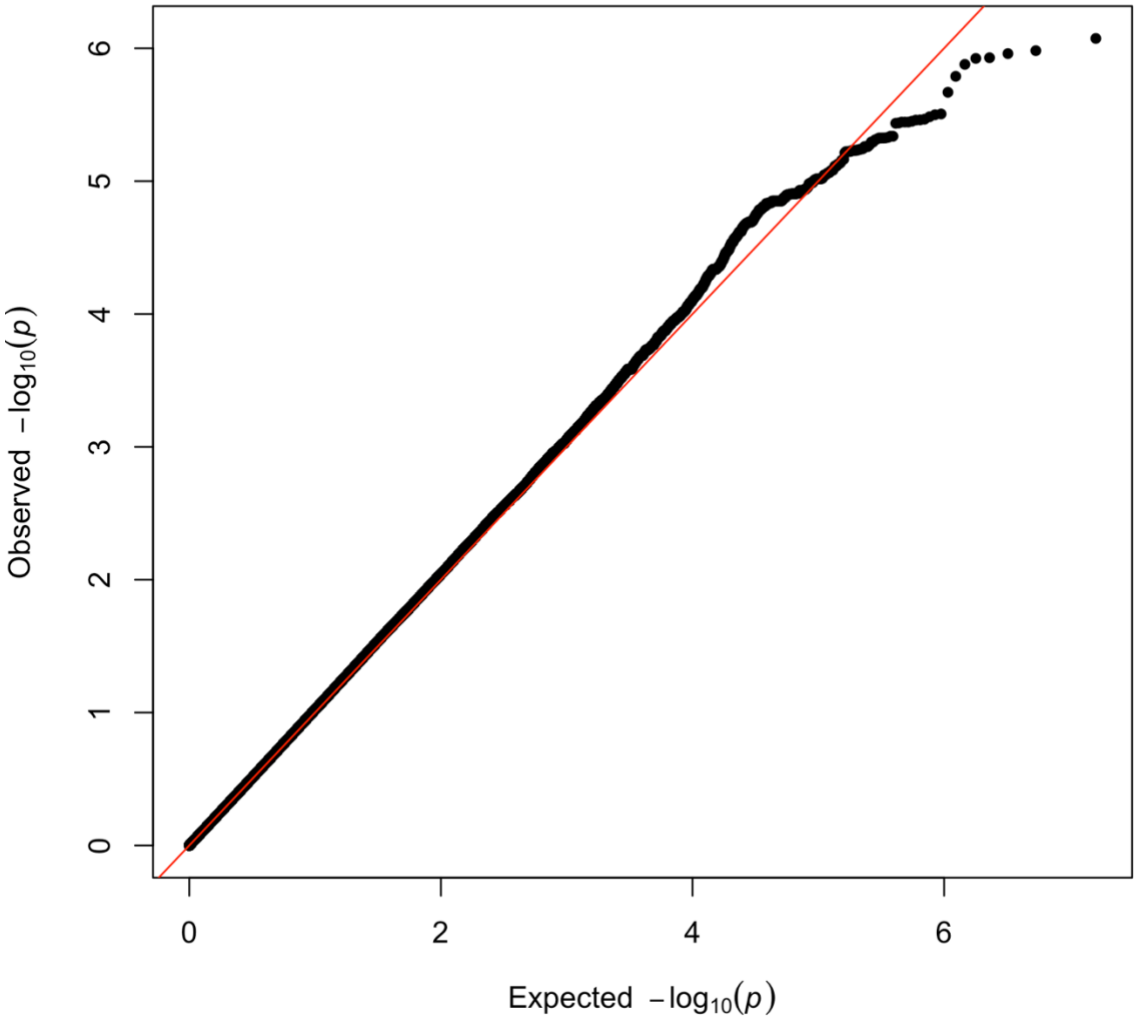
Supplementary Figures:



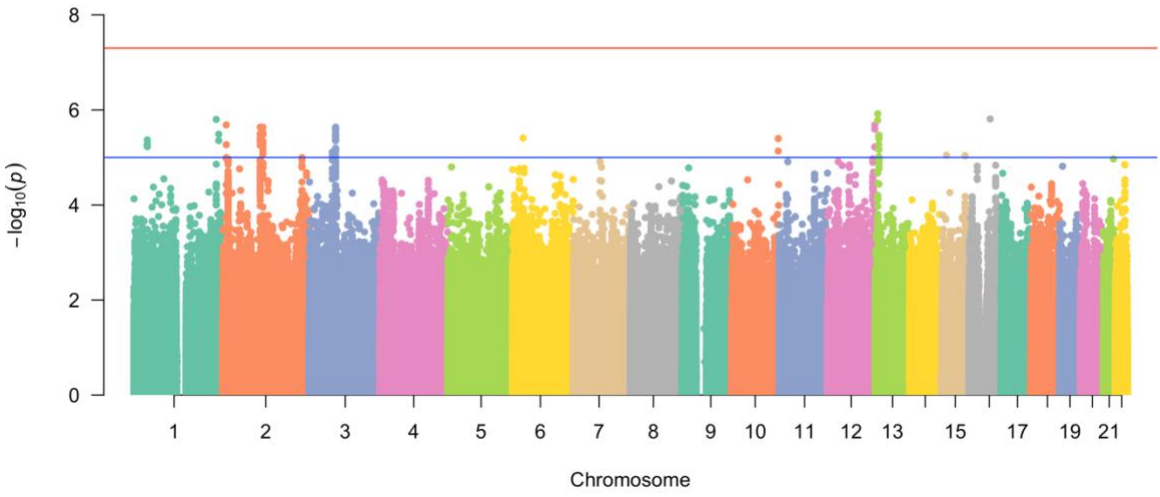
Supplementary Figure S1: GWAS analysis pipeline
The figure describes the various steps and methods used in the present study for GWAS and further downstream analysis.



Supplementary Figure S2: Principal Component Analysis plots for ancestry, ethnicity and batch effect (A) PCA plot showing the ECGRI data combined with the data from 1000 Genomes. Each population is represented by a different colour. (B) ECGRI population clustered by ethnicity. Each ethnicity is represented by a different colour. (C) PCA of the study population clustered by genotyping batch. Each batch is represented by a different colour.

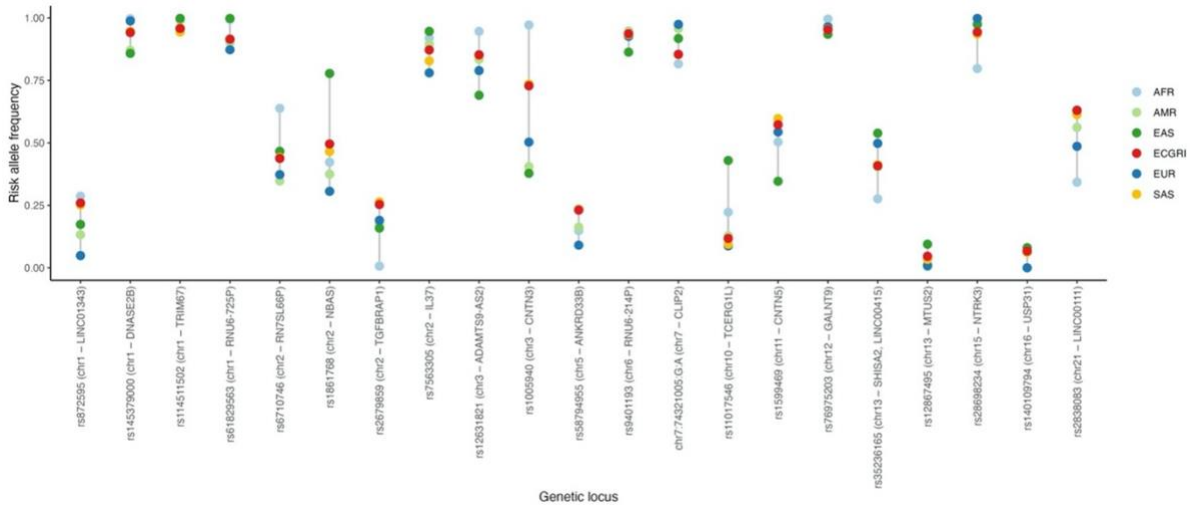


Supplementary Figure S3: Q-Q plot for Indian GWAS
Q-Q plot for genome-wide association study in Indian population ($\lambda = 1{\cdot}028$).

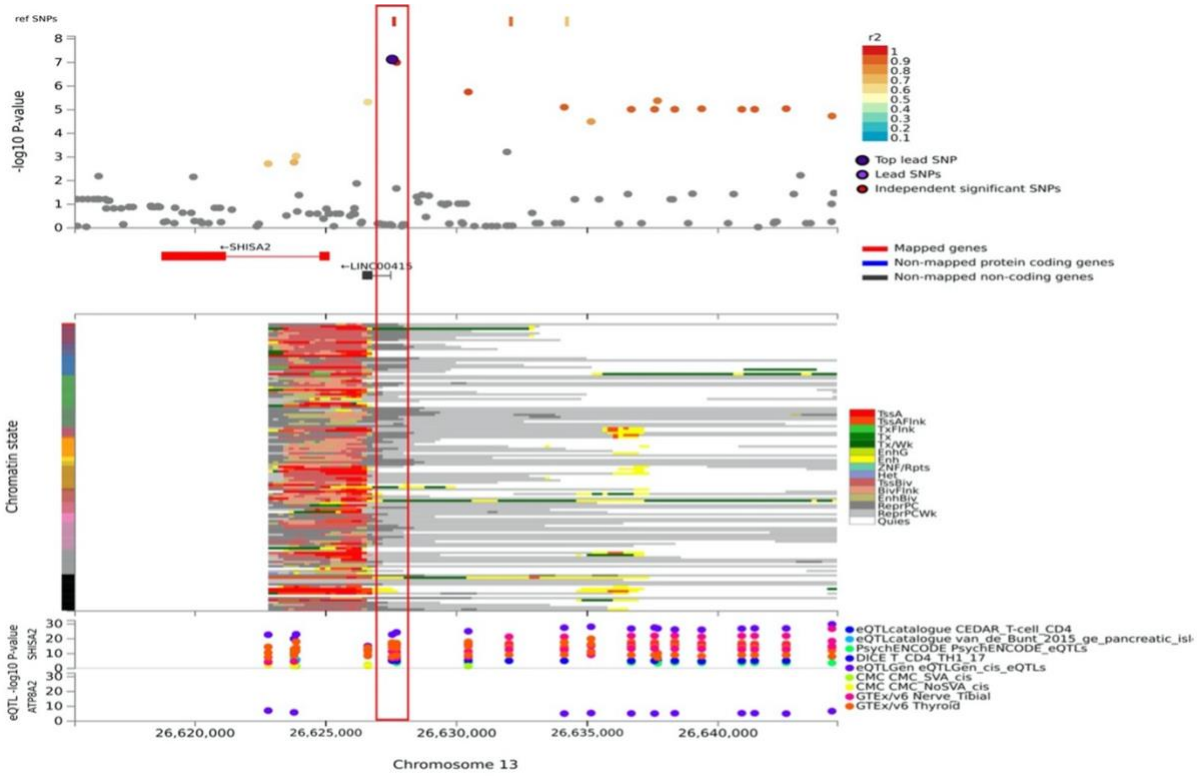


Supplementary Figure S4: Manhattan plot for genome-wide associations for endometriosis in the Indian population with linear mixed model in GCTA

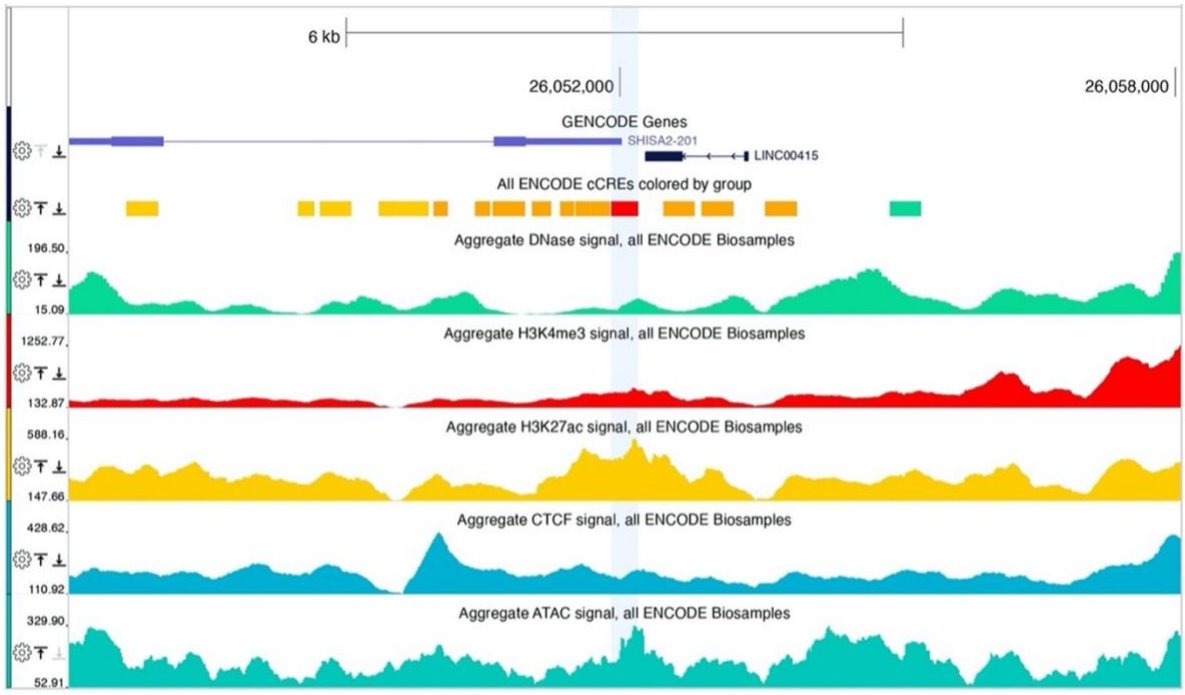
Manhattan plot shows the genome-wide association results for endometriosis in 1288 cases and 1235 controls in Indian population using GCTA. The x-axis shows the chromosomal position and y axis shows the -log10Pvalue. The red horizontal line represents the genome-wide significant threshold ($p < 5x10^{-8}$) and the blue horizontal line represents the suggestive genome-wide significance ($p < 1x10^{-5}$). The lead variant was rs35236165 on chromosome 13 ($p = 1{\cdot}21x10^{-6}$).



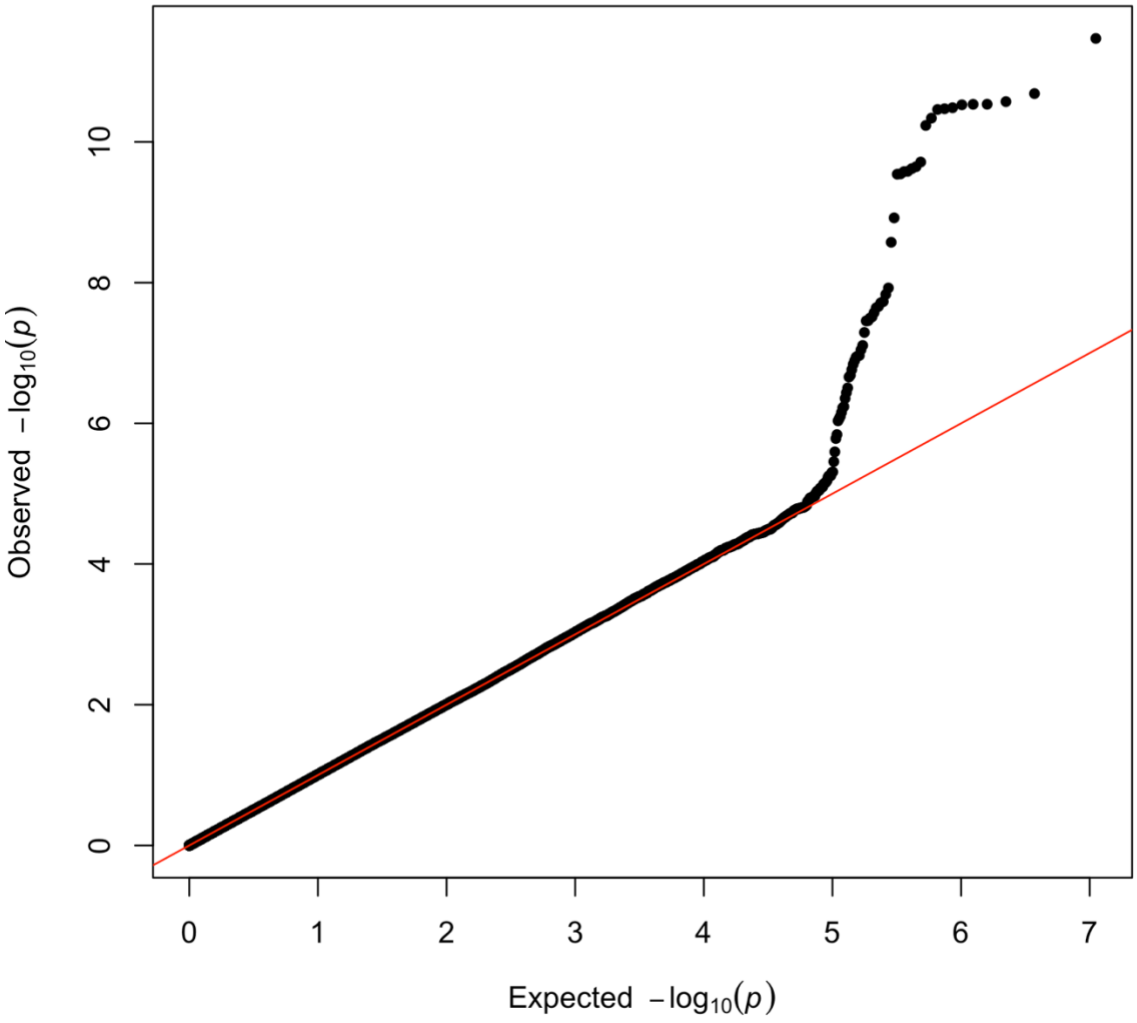
Supplementary Figure S5: Allele frequencies of the 21 genomic risk loci across different populations
The graph shows the risk allele frequencies of the lead variants at the 21 genomic risk loci, across African, American, East Asian, European, South Asian populations and the Indian population (ECGRI). The x-axis shows the lead variants annotated with chromosome and the closest gene, and the y-axis shows the risk allele frequency. Each population is plotted as a different colored dot. Dots joined by a grey line represent allele frequencies of the same variant.



Supplementary Figure S6: FUMA regional plot of the Chr 13 risk locus
Regional plot of locus surrounding lead variant rs35236165 on chromosome 13. The top plot shows the lead SNP in purple and variants in high linkage disequilibrium in red and orange. Each dot representing a variant plotted according to chromosomal position of the x-axis and -log10 p-value for the association with endometriosis on the y-axis. Genes in the region are plotted under the x-axis. The middle plot shows the chromatin states across several tissue types, each state denoted by a different colour. The bottom plot displays variants associated with SHISA2 expression across multiple tissues, with colours representing tissue types. The lead SNP lies within an exon of LINC00415 and is in strong LD with variants in an enhancer variant upstream of SHISA2. eQTLs for SHISA2 were observed in thyroid, nerve, and blood.



Supplementary Figure S7: Mapping of credible SNP on Chr 13 to regulatory marks
Genomic browser view of *chr13:26,046,044–26,058,057* showing GENCODE gene models, ENCODE candidate cis-regulatory elements (cCREs), and aggregate epigenomic signals across ENCODE biosamples, including H3K4me3, H3K4me1, H3K27ac, CTCF, and ATAC-seq profiles represented by different colours. The shaded region corresponds to cCRE EH38E3056662 a regulatory region containing credible variant rs3088377 and promoter associated histone marks for *SHISA2*.



Supplementary Figure S8: Q-Q plot for Asian GWAS Meta-analysis
Q-Q plot for Asian genome-wide association meta-analysis (λ=1·007).

Supplementary Tables:

Supplementary Table S1: Demographic details of the study participants

		Participants Recruited			Participants in GWAS analysis		
Ancestry	**Region**	**Cases**	**Controls**	**Total**	**Cases**	**Controls**	**Total**
Indo-European	Central	383	378	761	357	335	692
	North	335	354	689	316	320	636
	East/North-East	152	154	306	134	130	264
	South	18	7	25	18	7	25
	West	184	187	371	170	165	335
Dravidian	Central	7	13	20	6	10	16
	North	2	0	2	2	0	2
	East/North-East	0	1	1	0	1	1
	South	120	131	251	115	119	234
	West	36	31	67	35	30	65
Tibeto-Burman	Central	1	0	1	1	0	1
	North	0	0	0	0	0	0
	East/North-East	145	132	277	134	118	252
	South	0	0	0	0	0	0
	West	0	0	0	0	0	0
				2771			**2523**

Supplementary Table S2: List of variants associated with endometriosis at suggestive p-value threshold of $p < 1x10^{-5}$

ID	CHR	POS	A1	A2	A1_FREQ	OR	LOG(OR)_SE	P
rs10829835	10	130886033	T	C	0·118	1·560	0·094	2·14E-06
rs11017546	10	130888190	T	A	0·117	1·579	0·094	1·19E-06
rs4558133	11	98912199	T	C	0·427	0·767	0·060	9·60E-06
rs1599468	11	98912283	T	A	0·427	0·767	0·060	9·60E-06
rs1599469	11	98912309	G	A	0·427	0·767	0·060	9·60E-06
rs1599470	11	98912544	T	C	0·427	0·767	0·060	9·60E-06
rs1599472	11	98912776	C	A	0·427	0·767	0·060	9·60E-06
rs11217546	11	98912833	G	T	0·427	0·767	0·060	9·60E-06
rs1948092	11	98913353	A	C	0·427	0·767	0·060	9·60E-06
rs76975203	12	132277711	T	C	0·047	0·519	0·141	3·12E-06
rs28564301	12	132281083	G	C	0·047	0·517	0·142	3·28E-06
rs75739121	12	132283304	A	G	0·045	0·527	0·144	8·60E-06
rs35236165	13	26053425	A	T	0·408	1·341	0·060	8·43E-07
rs9512061	13	26053591	C	A	0·408	1·336	0·059	1·10E-06
rs35687292	13	29267577	G	A	0·046	1·930	0·148	8·32E-06
rs12867495	13	29268386	T	C	0·046	1·955	0·147	5·50E-06
rs34076296	13	29270237	T	A	0·046	1·955	0·147	5·50E-06
rs12877613	13	29270464	T	C	0·046	1·955	0·147	5·50E-06
rs12870203	13	29272734	G	A	0·049	1·913	0·143	5·97E-06
rs35903443	13	29272875	G	A	0·049	1·913	0·143	5·97E-06
rs77404082	13	29286098	A	G	0·030	2·274	0·184	8·42E-06
rs28375533	15	87724733	T	C	0·056	0·556	0·130	5·87E-06
rs28520525	15	87724996	A	C	0·056	0·556	0·130	5·87E-06
rs28698234	15	87724997	C	T	0·056	0·556	0·130	5·87E-06
rs28533879	15	87725040	C	T	0·056	0·556	0·130	5·87E-06
rs140109794	16	23156928	A	C	0·067	1·715	0·120	7·37E-06
chr16:59317869:C:G	16	59317869	G	C	0·050	0·536	0·134	3·47E-06
rs114511502	1	231190846	T	C	0·042	0·470	0·155	1·18E-06
rs112337089	1	231228172	C	T	0·043	0·509	0·153	9·29E-06
rs35300422	1	238101137	G	A	0·066	0·577	0·120	4·82E-06
rs61829563	1	238237586	G	A	0·085	0·600	0·107	1·63E-06
rs1755302	1	38238517	G	A	0·260	1·369	0·068	3·67E-06
rs872595	1	38240243	C	T	0·260	1·371	0·068	3·46E-06
rs2637880	1	38245336	C	T	0·457	1·307	0·060	7·98E-06
rs2637881	1	38245701	G	C	0·456	1·313	0·060	5·69E-06
rs913862	1	38246795	G	A	0·462	1·310	0·060	6·97E-06
rs145379000	1	84446195	A	C	0·058	0·570	0·126	8·67E-06
rs2838083	21	41642884	G	A	0·370	0·766	0·060	7·46E-06

rs11688814	2	10271707	G	A	0·387	1·315	0·060	5·08E-06
rs10929649	2	10272345	T	C	0·389	1·316	0·060	4·74E-06
rs4618024	2	10274155	T	G	0·437	1·314	0·059	3·42E-06
rs6710746	2	10274597	G	A	0·438	1·330	0·059	1·32E-06
rs893249	2	105308854	C	T	0·255	1·342	0·066	9·50E-06
rs2679859	2	105311154	C	A	0·253	1·351	0·066	5·85E-06
rs1010029	2	105327112	G	C	0·255	1·347	0·066	7·42E-06
rs2576760	2	105332898	C	T	0·255	1·346	0·066	7·69E-06
rs1469938	2	105333650	T	A	0·255	1·346	0·066	7·69E-06
rs1133218	2	105334049	G	A	0·255	1·346	0·066	7·69E-06
rs2679865	2	105370193	A	G	0·416	0·767	0·059	6·89E-06
chr2:112894946:G:T	2	112894946	T	G	0·111	0·655	0·095	8·28E-06
rs7563305	2	112915893	T	C	0·128	0·672	0·089	8·74E-06
rs1861768	2	15485062	C	A	0·495	1·294	0·058	9·86E-06
rs36043123	3	65045903	A	G	0·147	0·696	0·081	8·28E-06
rs10866071	3	65047092	T	G	0·147	0·694	0·081	6·84E-06
rs12631821	3	65047978	T	C	0·148	0·693	0·081	5·99E-06
rs10866072	3	65049572	A	T	0·148	0·693	0·081	5·99E-06
rs11130999	3	65049657	G	T	0·148	0·693	0·081	5·99E-06
rs62253916	3	65050902	T	C	0·147	0·695	0·081	7·26E-06
rs1005940	3	74172342	G	A	0·272	0·731	0·067	3·16E-06
rs34992948	3	74174794	A	G	0·271	0·737	0·067	5·80E-06
rs11712141	3	74178025	A	C	0·271	0·738	0·067	6·11E-06
rs11128379	3	74180509	T	C	0·270	0·743	0·067	9·57E-06
rs7651186	3	74182665	T	C	0·267	0·743	0·067	9·92E-06
rs1440623	3	74186288	A	C	0·271	0·741	0·067	8·66E-06
rs1078070	3	74186927	G	A	0·272	0·733	0·067	3·59E-06
rs2019007	3	74187038	C	T	0·272	0·733	0·067	3·59E-06
rs750807	3	74187820	T	G	0·271	0·735	0·067	4·74E-06
rs2323733	3	74188122	A	T	0·271	0·735	0·067	4·74E-06
rs10865680	3	74189063	C	T	0·272	0·733	0·067	3·59E-06
rs6783776	3	74190875	C	T	0·272	0·733	0·067	3·54E-06
rs935040	3	74192930	A	T	0·272	0·736	0·067	4·89E-06
rs4677378	3	74193317	C	G	0·272	0·736	0·067	5·08E-06
rs13094651	3	74193593	C	A	0·272	0·733	0·067	3·65E-06
rs34614059	3	74194175	T	C	0·270	0·742	0·067	8·99E-06
rs35153582	3	74194469	T	C	0·270	0·742	0·067	8·99E-06
rs6549585	3	74195053	T	C	0·271	0·737	0·067	5·73E-06
rs148151835	3	74196715	C	T	0·272	0·735	0·067	4·59E-06
rs141892440	3	74196719	A	T	0·272	0·735	0·067	4·59E-06
rs13059749	3	74197090	T	C	0·272	0·737	0·067	5·33E-06
rs4277644	3	74197302	G	A	0·272	0·736	0·067	4·73E-06

rs1470554	3	74199064	G	C	0·270	0·742	0·067	9·73E-06
rs12631211	3	74199350	T	C	0·270	0·742	0·067	9·73E-06
rs10511035	3	74200796	C	G	0·272	0·738	0·067	5·76E-06
rs58794955	5	10571781	T	C	0·231	1·376	0·070	4·69E-06
rs9401193	6	119963843	C	A	0·063	0·581	0·123	9·65E-06
rs76573413	6	29670697	C	T	0·037	0·455	0·161	1·04E-06
rs67922716	7	74308247	A	G	0·142	0·682	0·086	9·00E-06
chr7:74321005:G:A	7	74321005	A	G	0·146	0·685	0·085	8·87E-06

A1, effect allele; A2, other allele; OR, Odds Ratio estimated for effect allele; A1_FREQ, Frequency of A1 allele.

Supplementary Table S3: Allele frequency variation of the 21 genomic risk loci across ethnic groups in the Indian GWAS dataset

SNP	Genotype	Dravidian	Tibeto_Burman	Indo_European
chr1:38240243:T:C	Prop_Hom_A1	0·104	0·051	0·063
	Prop_Het	0·412	0·399	0·380
	Prop_Hom_A2	0·484	0·549	0·557
chr1:84446195:C:A	Prop_Hom_A1	0·006	0·016	0·003
	Prop_Het	0·113	0·146	0·102
	Prop_Hom_A2	0·881	0·838	0·895
chr1:231190846:C:T	Prop_Hom_A1	0·000	0·000	0·002
	Prop_Het	0·079	0·103	0·079
	Prop_Hom_A2	0·921	0·897	0·920
chr1:238237586:A:G	Prop_Hom_A1	0·006	0·000	0·009
	Prop_Het	0·145	0·083	0·165
	Prop_Hom_A2	0·849	0·917	0·826
chr2:10274597:G:A	Prop_Hom_A1	0·182	0·221	0·195
	Prop_Het	0·472	0·490	0·485
	Prop_Hom_A2	0·346	0·289	0·321
chr2:15485062:C:A	Prop_Hom_A1	0·204	0·202	0·280
	Prop_Het	0·450	0·474	0·490
	Prop_Hom_A2	0·346	0·324	0·230
chr2:105311154:A:C	Prop_Hom_A1	0·066	0·071	0·073
	Prop_Het	0·349	0·360	0·365
	Prop_Hom_A2	0·585	0·569	0·562
chr2:112915893:C:T	Prop_Hom_A1	0·028	0·012	0·014
	Prop_Het	0·204	0·217	0·230
	Prop_Hom_A2	0·767	0·771	0·756
chr3:65047978:C:T	Prop_Hom_A1	0·038	0·032	0·027
	Prop_Het	0·270	0·257	0·231
	Prop_Hom_A2	0·692	0·711	0·743
chr3:74172342:A:G	Prop_Hom_A1	0·035	0·099	0·076
	Prop_Het	0·352	0·482	0·393
	Prop_Hom_A2	0·613	0·419	0·531
chr5:10571781:C:T	Prop_Hom_A1	0·063	0·036	0·057
	Prop_Het	0·321	0·391	0·350
	Prop_Hom_A2	0·616	0·573	0·593
chr6:119963843:A:C	Prop_Hom_A1	0·003	0·008	0·004
	Prop_Het	0·126	0·126	0·116
	Prop_Hom_A2	0·871	0·866	0·881
chr7:74321005:G:A	Prop_Hom_A1	0·038	0·024	0·017
	Prop_Het	0·283	0·213	0·249

	Prop_Hom_A2	0·679	0·763	0·733
chr10:130888190:A:T	Prop_Hom_A1	0·009	0·051	0·013
	Prop_Het	0·230	0·360	0·176
	Prop_Hom_A2	0·761	0·589	0·810
chr11:98912309:G:A	Prop_Hom_A1	0·179	0·202	0·176
	Prop_Het	0·478	0·538	0·495
	Prop_Hom_A2	0·343	0·261	0·329
chr12:132277711:C:T	Prop_Hom_A1	0·003	0·004	0·003
	Prop_Het	0·113	0·087	0·085
	Prop_Hom_A2	0·884	0·909	0·912
chr13:26053425:T:A	Prop_Hom_A1	0·208	0·221	0·159
	Prop_Het	0·472	0·482	0·472
	Prop_Hom_A2	0·321	0·296	0·368
chr13:29268386:C:T	Prop_Hom_A1	0·003	0·004	0·001
	Prop_Het	0·075	0·111	0·089
	Prop_Hom_A2	0·921	0·885	0·910
chr15:87724997:T:C	Prop_Hom_A1	0·006	0·008	0·004
	Prop_Het	0·113	0·103	0·101
	Prop_Hom_A2	0·881	0·889	0·894
chr16:23156928:C:A	Prop_Hom_A1	0·006	0·008	0·004
	Prop_Het	0·179	0·166	0·110
	Prop_Hom_A2	0·814	0·826	0·886
chr21:41642884:A:G	Prop_Hom_A1	0·167	0·150	0·143
	Prop_Het	0·459	0·419	0·448
	Prop_Hom_A2	0·374	0·431	0·409

Prop_Hom_A1, proportion of individuals homozygous for allele 1; Prop_Het, proportion of heterozygous individuals; Prop_Hom_A2, proportion of individuals homozygous for allele 2.

Supplementary Table S4: Allele frequency variation of the 21 genomic risk loci across major global ethnic groups

rsID	CHR	NEAREST GENE	RAF_ ECGRI	RAF_ AFR	RAF_ AMR	RAF_ EAS	RAF_ EUR	RAF_ SAS	AF_ min_ global	AF_ max_ global	AF_ range_ global
rs872595	1	LINC01343	0·260	0·287	0·133	0·174	0·049	0·252	0·049	0·287	0·238
rs145379000	1	DNASE2B	0·942	0·997	0·870	0·858	0·988	0·947	0·858	0·997	0·139
rs114511502	1	TRIM67	0·958	0·999	0·990	0·998	0·955	0·944	0·944	0·999	0·055
rs61829563	1	RNU6-725P	0·915	0·994	0·902	0·998	0·873	0·915	0·873	0·998	0·125
rs6710746	2	RN7SL66P	0·438	0·638	0·347	0·466	0·373	0·442	0·347	0·638	0·291
rs1861768	2	NBAS	0·495	0·423	0·375	0·778	0·306	0·465	0·306	0·778	0·472
rs2679859	2	TGFBRAP1	0·253	0·007	0·173	0·159	0·190	0·264	0·007	0·264	0·257
rs7563305	2	IL37	0·872	0·920	0·895	0·946	0·780	0·828	0·780	0·946	0·166
rs12631821	3	ADAMTS9-AS2	0·852	0·946	0·834	0·691	0·789	0·850	0·691	0·946	0·256
rs1005940	3	CNTN3	0·728	0·972	0·405	0·378	0·503	0·735	0·378	0·972	0·594
rs58794955	5	ANKRD33B	0·231	0·148	0·163	0·234	0·091	0·233	0·091	0·234	0·144
rs9401193	6	RNU6-214P	0·937	0·934	0·948	0·863	0·926	0·934	0·863	0·948	0·085
chr7:74321005:G:A	7	CLIP2	0·854	0·816	0·957	0·918	0·974	0·853	0·816	0·974	0·158
rs11017546	10	TCERG1L	0·117	0·222	0·128	0·430	0·088	0·094	0·088	0·430	0·342
rs1599469	11	CNTN5	0·573	0·504	0·592	0·346	0·544	0·597	0·346	0·597	0·251
rs76975203	12	GALNT9	0·953	0·996	0·967	0·935	0·964	0·954	0·935	0·996	0·061
rs35236165	13	SHISA2, LINC00415	0·408	0·276	0·404	0·539	0·498	0·412	0·276	0·539	0·263
rs12867495	13	MTUS2	0·046	0·012	0·004	0·094	0·009	0·034	0·004	0·094	0·090
rs28698234	15	NTRK3	0·944	0·797	0·978	0·974	0·998	0·936	0·797	0·998	0·201
rs140109794	16	USP31	0·067	0·000	0·000	0·080	0·000	0·061	0·000	0·080	0·080
rs2838083	21	LINC00111	0·630	0·343	0·562	0·631	0·486	0·614	0·343	0·631	0·288

RAF_ECGRI, Risk allele frequency in the ECGRI dataset
RAF_AFR, Risk allele frequency in the African population
RAF_AMR, Risk allele frequency in the American population
RAF_EAS, Risk allele frequency in the East Asian population
RAF_EUR, Risk allele frequency in the European population
RAF_SAS, Risk allele frequency in the South Asian population
AF_min_global, the minimum allele frequency observed across all populations
AF_max_global, the maximum allele frequency observed across all populations
AF_range_global, difference between the maximum and minimum allele frequencies

Supplementary Table S5: Replication of previously identified endometriosis genetic risk variants.

GWAS	SNP	Locus	CHR:POS	RA	OR – ECGRI	OR – Original GWAS	p_ECGRI	p_Original GWAS
European	rs7907732	RNLS/10q23·31	chr10:88423007	T	1·12	1·05	$4.74x10^{-2}$	$2.19x10^{-10}$
European	rs12320196	VEZT/12q22	chr12:95251609	G	1·13	1·05	$3.86x10^{-2}$	$6.74x10^{-14}$
European	rs2421985	DNM3/1q24·3	chr1:172129996	C	1·17	1·05	$6.6x10^{-3}$	$6.73x10^{-14}$
European	rs10917151	WNT4/1p36·12	chr1:22096228	A	1·29	1·14	$2.0x10^{-4}$	$5.08x10^{-44}$
European	rs1903068	KDR/4q12	chr4:55142310	A	1·21	1·08	$4.0x10^{-3}$	$1.55x10^{-24}$
European	rs1451383	7p15·2/7p15·2	chr7:25852189	G	1·19	1·06	$2.7x10^{-3}$	$8.66x10^{-12}$
European	rs10122243	CDKN2B-AS1/9p21·3	chr9:22158925	T	1·22	1·06	$1.2x10^{-3}$	$1.49x10^{-17}$
Taiwanese	rs12037376	WNT4/1p36·12	chr1: 22135618	A	1·28	NA	$5.0x10^{-4}$	2.96×10^{-9}
Multiancestry	rs2779747	CDKN2B-AS1/DMRTA1	chr9:22171485	T	0.808402	0.932	5.56×10^{-4}	1.45×10^{-22}
Multiancestry	rs61768001	WNT4	chr1:22139327	C	1.24679	1.125	1.41×10^{-3}	2.56×10^{-40}
Multiancestry	rs1903068	KDR	chr4:55142310	G	0.823419	0.919	4.03×10^{-3}	2.77×10^{-25}
Multiancestry	rs7759516	CCDC170	chr6:151517110	C	1.16961	1.100	1.08×10^{-2}	3.92×10^{-28}
Multiancestry	rs6538622	VEZT	chr12:95233461	G	1.12085	1.072	4.84×10^{-2}	2.96×10^{-23}

RA, Risk allele

Supplementary Table S6: Differences in the allele frequencies of the known endometriosis risk loci between the European and Indian population

RSID	CHR	Nearest_gene	RA_2023	RAF_EUR	AF_ECGRI	AF_diff_EUR_ECGRI
rs10828249	10	MLLT10	A	0·35	0·24	0·11
rs7907732	10	RNLS	T	0·39	0·50	0·11
rs3858429	11	FSHB	C	0·84	0·92	0·08
rs7924571	11	WT1	C	0·76	0·63	0·13
rs11111267	12	IGF1	A	0·82	0·82	0·00
rs10860864	12	IGF1	C	0·82	0·82	0·00
rs56090796	12	PTPRO	A	0·33	0·25	0·08
rs3803042	12	HOXC10	A	0·42	0·27	0·15
rs12320196	12	VEZT	G	0·47	0·48	0·01
rs7334326	13	DLEU1	C	0·16	0·24	0·08
rs57281976	14	RIN3	G	0·77	0·73	0·04
rs12441483	15	SRP14-AS1	C	0·47	0·60	0·13
rs66683298	17	SKAP1	C	0·6	0·78	0·18
rs2967684	19	ACTL9	A	0·16	0·10	0·06
rs12030576	1	NGF	G	0·65	0·45	0·20
rs2421985	1	DNM3	C	0·49	0·56	0·07
rs10917151	1	WNT4	A	0·17	0·24	0·07
rs7580473	2	GREB1	T	0·14	0·06	0·08
rs11674184	2	GREB1	T	0·61	0·62	0·01
rs6435157	2	BMPR2	T	0·77	0·91	0·14
rs1430787	2	ETAA1	A	0·31	0·17	0·14
rs1352889	3	BSN	T	0·17	0·05	0·12
rs1903068	4	KDR	A	0·68	0·76	0·08
rs2946160	5	EBF1	A	0·74	0·66	0·08
rs2226158	6	HEY2	G	0·46	0·47	0·01
rs851980	6	SYNE1	T	0·74	0·84	0·10
rs71575922	6	SYNE1	G	0·15	0·03	0·12
rs74636305	6	SYNE1	A	0·07	0·06	0·01
rs11756073	6	FAM120B	A	0·17	0·27	0·10
rs6456259	6	ID4	G	0·16	0·08	0·08
rs4540228	6	CD109	C	0·66	0·71	0·05
rs1451383	7	7p15·2	G	0·74	0·49	0·25
rs55909142	7	7p12·3	C	0·59	0·82	0·23
rs17053711	8	KCTD9	G	0·73	0·88	0·15
rs10090060	8	GDAP1	A	0·57	0·55	0·02
rs10983311	9	ASTN2	T	0·77	0·52	0·25

rs10757278	9	CDKN2B-AS1	A	0·52	0·50	0·02
rs10122243	9	CDKN2B-AS1	T	0·41	0·67	0·26
rs3133150	4	PDLIM5	A	0·31265	0·16	0·15
rs3779456	7	HOXA10	T	0·562685	0·64	0·07
rs3110398	8	VPS13B	C	0·2174	0·15	0·07
rs635634	9	9q34·2	T	0·1905	0·16	0·03
rs11652557	17	CEP112	G	0·92816	0·99	0·06
rs7775980	6	CCDC170	A	0·8	0·67	0·13
rs73625140	6	SYNE1	T	0·04	0·03	0·01

RA_2023, Risk allele as reported in reference (11)
RAF_EUR, Risk allele frequency in the European population
AF_ECGRI, the allele frequency of the same allele in the ECGRI dataset
AF_diff_EUR_ECGRI, the difference in allele frequency between the European and ECGRI dataset

Supplementary Table S7: Credible set identified within 1Mb region surrounding the lead variant rs35236165

snp_id	chr	pos	a1	a2	PIP
chr13:26053425:T:A	13	26053425	A	T	0·386
chr13:26053591:A:C	13	26053591	C	A	0·306
chr13:26052491:T:C	13	26052491	C	T	0·033
chr13:26056334:C:T	13	26056334	T	C	0·032
chr13:26063570:A:T	13	26063570	T	A	0·020
chr13:26060006:T:C	13	26060006	C	T	0·011
chr13:26073836:A:G	13	26073836	G	A	0·010
chr13:26068491:C:T	13	26068491	T	C	0·010
chr13:26065258:A:G	13	26065258	G	A	0·010
chr13:26062566:C:T	13	26062566	T	C	0·009
chr13:26063458:C:T	13	26063458	T	C	0·009
chr13:26064230:C:A	13	26064230	A	C	0·009
chr13:26066793:T:A	13	26066793	A	T	0·009
chr13:26067286:C:G	13	26067286	G	C	0·009
chr13:26072834:G:T	13	26072834	T	G	0·007
chr13:26073675:T:C	13	26073675	C	T	0·004
chr13:26070243:T:C	13	26070243	C	T	0·004
chr13:26061029:A:G	13	26061029	G	A	0·004
chr13:26080704:A:G	13	26080704	G	A	0·003
chr13:26082752:T:A	13	26082752	A	T	0·003
chr13:26082757:G:A	13	26082757	A	G	0·003
chr13:26082838:G:A	13	26082838	A	G	0·003
chr13:26082410:G:A	13	26082410	A	G	0·002
chr13:26090329:G:C	13	26090329	C	G	0·002
chr13:26090459:T:A	13	26090459	A	T	0·002
chr13:26090694:T:C	13	26090694	C	T	0·002
chr13:26090994:T:C	13	26090994	C	T	0·002
chr13:26080947:T:C	13	26080947	C	T	0·002
chr13:26081034:C:T	13	26081034	T	C	0·002
chr13:26088117:T:C	13	26088117	C	T	0·002
chr13:26089160:T:C	13	26089160	C	T	0·002
chr13:26089469:T:C	13	26089469	C	T	0·002
chr13:26093645:G:A	13	26093645	A	G	0·002
chr13:26094003:G:A	13	26094003	A	G	0·002
chr13:26094625:G:A	13	26094625	A	G	0·002
chr13:26095852:A:C	13	26095852	C	A	0·002
chr13:26095932:A:G	13	26095932	G	A	0·002
chr13:26092276:G:C	13	26092276	C	G	0·002
chr13:26078915:A:G	13	26078915	G	A	0·002

chr13:26083296:T:C	13	26083296	C	T	0·002
chr13:26078754:G:A	13	26078754	A	G	0·002
chr13:26079372:G:T	13	26079372	T	G	0·002
chr13:26079999:G:A	13	26079999	A	G	0·002
chr13:26080426:G:A	13	26080426	A	G	0·002
chr13:26099594:G:A	13	26099594	A	G	0·001
chr13:26100518:T:C	13	26100518	C	T	0·001
chr13:26100742:T:C	13	26100742	C	T	0·001
chr13:26102228:G:A	13	26102228	A	G	0·001
chr13:26079806:A:G	13	26079806	G	A	0·001
chr13:26096389:A:G	13	26096389	G	A	0·001
chr13:26103904:C:G	13	26103904	G	C	0·001
chr13:26109089:A:G	13	26109089	G	A	0·001
chr13:26112408:G:A	13	26112408	A	G	0·001
chr13:26104660:A:G	13	26104660	G	A	0·001
chr13:26104888:C:T	13	26104888	T	C	0·001
chr13:26107467:G:A	13	26107467	A	G	0·001
chr13:26108383:T:A	13	26108383	A	T	0·000
chr13:26210802:T:C	13	26210802	C	T	0·000
chr13:26057814:C:G	13	26057814	G	C	0·000
chr13:26207391:G:A	13	26207391	A	G	0·000
chr13:26216037:C:A	13	26216037	A	C	0·000
chr13:26202118:G:A	13	26202118	A	G	0·000
chr13:26224755:T:C	13	26224755	C	T	0·000
chr13:26244765:C:T	13	26244765	T	C	0·000
chr13:26331754:G:A	13	26331754	A	G	0·000

a1, effect allele; a2, other allele; PIP, posterior inclusion probability

Supplementary Table S8: SMR analysis using ECGRI GWAS summary statistics and expression quantitative trait loci (eQTL) and methylation quantitative trait loci (mQTL) datasets

QTL Dataset	Gene	nsnps	PP·H0·abf	PP·H1·abf	PP·H2·abf	PP·H3·abf	PP·H4·abf	topSNP	A1	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI
Blood_eQTL	RNF6	1366	2·08E-07	5·97E-07	0·254	0·730	0·016	rs1175716	A	-0·101	0·059	9·01E-02	0·057	0·008	1·85E-12	-1·768	1·073	9·94E-02	5·64E-02
Blood_eQTL	SHISA2	1366	4·32E-64	1·24E-63	0·255	0·735	0·010	rs9578952	A	-0·042	0·069	5·43E-01	0·142	0·008	2·59E-70	-0·295	0·486	5·43E-01	1·46E-01
Thyroid_eQTL	SHISA2	1284	8·57E-16	2·45E-15	0·093	0·264	0·644	rs2419807	G	0·228	0·059	1·19E-04	-0·261	0·028	1·78E-20	-0·873	0·246	3·78E-04	6·82E-02
Blood_mQTL	cg07984168	634	5·92E-119	1·64E-118	0·016	0·044	0·939	rs4770916	T	0·242	0·060	4·90E-05	-0·553	0·023	8·42E-126	-0·438	0·109	6·26E-05	2·15E-01
Blood_mQTL	cg27012920	565	5·50E-153	8·33E-154	0·277	0·041	0·682	rs9319282	A	-0·228	0·074	1·92E-03	-0·720	0·026	2·11E-163	0·317	0·103	2·05E-03	1·41E-01
Endometrium_mQTL	cg01600817	161	3·37E-07	1·75E-08	0·372	0·019	0·609	rs34584161	G	-0·221	0·074	2·92E-03	-0·109	0·015	2·48E-13	2·037	0·739	5·83E-03	2·25E-01
Endometrium_mQTL	cg05581851	212	5·51E-15	2·08E-15	0·325	0·122	0·553	rs9319282	A	-0·228	0·074	1·92E-03	-0·231	0·024	2·80E-22	0·989	0·335	3·13E-03	1·08E-01
Endometrium_mQTL	cg07984168	369	8·99E-58	2·45E-57	0·025	0·068	0·907	rs7321426	T	0·243	0·060	4·64E-05	-0·454	0·026	1·01E-68	-0·534	0·135	7·27E-05	5·81E-02
Endometrium_mQTL	cg15020125	395	5·10E-51	1·40E-50	0·037	0·100	0·863	rs1028769	G	0·223	0·059	1·73E-04	-0·208	0·013	2·42E-61	-1·070	0·292	2·51E-04	2·12E-01
Endometrium_mQTL	cg19014360	360	1·07E-19	2·95E-19	0·022	0·059	0·920	rs7321426	T	0·243	0·060	4·64E-05	-0·177	0·017	3·47E-25	-1·373	0·362	1·50E-04	1·24E-01
Endometrium_mQTL	cg27012920	256	5·56E-19	3·50E-20	0·369	0·023	0·608	rs3759469	G	-0·221	0·075	3·16E-03	-0·263	0·024	1·38E-27	0·839	0·295	4·39E-03	2·72E-01

nsnps - number of SNPs in region used in analysis
PP.H0.abf - posterior probability of hypothesis 0: neither trait has a genetic association in the region.
PP.H1.abf - posterior probability of hypothesis 1: only trait 1 has a genetic association in the region.
PP.H2.abf - posterior probability of hypothesis 2: only trait 2 has a genetic association in the region.
PP.H3.abf - posterior probability of hypothesis 3: both traits are associated, but with different causal variants.
PP.H4.abf - posterior probability of hypothesis 4: both traits are associated and share a single causal variant.
topSNP, the most significant SNP associated with the gene/probe in the QTL dataset; A1, effect allele; b_GWAS, effect size of the SNP in the GWAS dataset; se_GWAS, standard error of the SNP in the GWAS dataset; p_GWAS, p value of the SNP in the GWAS dataset; b_eQTL, effect size of the SNP in the QTL dataset; se_eQTL, standard error of the SNP in the QTL dataset; p_eQTL, p value of the SNP in the QTL dataset; b_SMR, effect estimate from the SMR test; se_SMR, standard error from the SMR test, p_SMR, p value from the SMR test; p_HEIDI, p value from the HEIDI test

Supplementary Table S9: Genome wide significant variants (p<1x10-8) identified from Meta-analyses

MarkerName	chr	pos	Allele1	Allele2	Effect	StdErr	P-value	Direction	HetISq	HetChiSq	HetDf	HetPVal
chr1:22468215:C:T	1	22468215	t	c	0·210	0·032	2·97E-11	++	0	0·449	1	0·503
chr1:22422721:G:A	1	22422721	a	g	0·207	0·031	2·92E-11	++	0	0·674	1	0·412
chr1:22436446:G:C	1	22436446	c	g	0·220	0·032	3·38E-12	++	0	0·373	1	0·541
chr1:22465820:T:C	1	22465820	t	c	-0·209	0·031	2·91E-11	--	0	0·034	1	0·855
chr1:22367073:T:G	1	22367073	t	g	-0·184	0·031	2·67E-09	--	0	0·046	1	0·831
chr9:22164309:A:G	9	22164309	a	g	0·176	0·031	1·94E-08	++	0	0·390	1	0·533
chr1:22414785:G:T	1	22414785	t	g	0·207	0·031	2·06E-11	++	0	0·517	1	0·472
chr9:22169700:C:T	9	22169700	t	c	-0·173	0·031	3·50E-08	--	0	0·339	1	0·560
chr9:22172259:A:T	9	22172259	a	t	0·177	0·032	1·86E-08	++	0	0·646	1	0·421
chr9:22171484:G:T	9	22171484	t	g	-0·176	0·032	2·68E-08	--	0	0·474	1	0·491
chr1:22470451:G:C	1	22470451	c	g	0·200	0·032	2·87E-10	++	0	0·003	1	0·956
chr1:22378280:T:A	1	22378280	a	t	0·196	0·031	2·64E-10	++	0	0·002	1	0·964
chr1:22374808:T:C	1	22374808	t	c	-0·197	0·031	2·25E-10	--	0	0·015	1	0·903
chr1:22388872:C:T	1	22388872	t	c	0·206	0·031	3·27E-11	++	0	0·303	1	0·582
chr9:22158924:T:C	9	22158924	t	c	0·177	0·031	1·47E-08	++	0	0·198	1	0·656
chr9:22161212:T:C	9	22161212	t	c	0·174	0·031	2·28E-08	++	0	0·269	1	0·604
chr1:22371065:T:G	1	22371065	t	g	-0·188	0·031	1·20E-09	--	0	0·038	1	0·846
chr1:22462131:G:T	1	22462131	t	g	0·195	0·031	2·40E-10	++	0	0·229	1	0·633
chr9:22162794:C:A	9	22162794	a	c	-0·177	0·031	1·19E-08	--	0	0·474	1	0·491
chr1:22420852:G:A	1	22420852	a	g	0·204	0·031	3·46E-11	++	0	0·218	1	0·640
chr9:22172893:C:T	9	22172893	t	c	-0·173	0·031	3·07E-08	--	0	0·690	1	0·406
chr1:22415410:A:T	1	22415410	a	t	-0·204	0·031	3·38E-11	--	0	0·179	1	0·672
chr1:22396998:T:C	1	22396998	t	c	-0·202	0·031	5·83E-11	--	0	0·102	1	0·750
chr9:22173075:A:T	9	22173075	a	t	0·173	0·031	3·19E-08	++	0	0·694	1	0·405

chr1:22450487:C:T	1	22450487	t	c	0·198	0·031	1·93E-10	++	0	0·098	1	0·755
chr1:22470407:C:T	1	22470407	t	c	0·200	0·032	2·85E-10	++	0	0·003	1	0·957
chr1:22462111:G:A	1	22462111	a	g	0·210	0·032	2·68E-11	++	0	0·300	1	0·584
chr9:22173676:A:G	9	22173676	a	g	-0·174	0·032	3·48E-08	--	0	0·562	1	0·453
chr1:22403357:G:A	1	22403357	a	g	0·203	0·031	4·59E-11	++	0	0·156	1	0·693
chr9:22173407:C:T	9	22173407	t	c	-0·176	0·032	2·18E-08	--	0	0·572	1	0·449
chr1:22378880:C:A	1	22378880	a	c	0·196	0·031	2·62E-10	++	0	0·002	1	0·963

Effect, estimated effect size of Allele1; StdErr, standard error; P-value, significance of association; Direction, direction of effect of Allele1; HetISq, percentage of total variation across studies attributable to heterogeneity; HetChiSq, Cochran's Q statistic for heterogeneity; HetDf, degrees of freedom; HetPVal, p-value assessing heterogeneity across studies.

Supplementary Table S10: Colocalization analysis using Meta-analysed data and expression quantitative trait loci (eQTL) and methylation quantitative trait loci (mQTL) datasets

QTL Dataset	Chr	Gene/CpG	nsnps	PP·H0·abf	PP·H1·abf	PP·H2·abf	PP·H3·abf	PP·H4·abf	Closest Gene
Blood_eQTL	1	CDC42	1037	2·05500620741398e-311	6·71E-306	6·86E-07	0·223	0·777	NA
Blood_eQTL	1	HSPG2	1020	2·75E-120	8·98E-115	3·06E-06	1·000	0·000	NA
Blood_eQTL	1	LINC00339	1034	0·00E+00	0·00E+00	3·06E-06	1·000	0·000	NA
Blood_eQTL	1	CDC42-IT1	876	1·07E-08	3·16E-03	3·36E-06	0·997	0·000	NA
Thyroid_eQTL	1	CDC42	1012	1·01E-06	3·29E-01	1·85E-07	0·060	0·611	NA
Thyroid_eQTL	1	CDC42-IT1	1012	7·95E-08	2·59E-02	2·98E-06	0·972	0·002	NA
Thyroid_eQTL	1	LINC00339	1012	2·89E-81	9·43E-76	3·06E-06	1·000	0·000	NA
Thyroid_eQTL	1	WNT4	1012	2·09E-21	6·82E-16	3·06E-06	1·000	0·000	NA
Ovary_eQTL	1	LINC00339	1007	7·67E-27	2·50E-21	3·06E-06	1·000	0·000	NA
Pituitary_eQTL	1	LINC00339	1007	7·24E-31	2·36E-25	3·06E-06	1·000	0·000	NA
Uterus_eQTL	1	LINC00339	1011	4·60E-25	1·50E-19	3·06E-06	1·000	0·000	NA
Endometrium_eQTL	1	CDC42	720	2·69E-07	7·40E-02	3·34E-06	0·919	0·007	NA
Endometrium_eQTL	1	WNT4	720	1·98E-08	5·45E-03	3·62E-06	0·994	0·001	NA
Endometrium_eQTL	1	LINC00339	720	5·45E-08	1·50E-02	3·58E-06	0·984	0·002	NA
Endometrium_eQTL	1	CDC42	720	9·48E-08	2·60E-02	3·54E-06	0·971	0·003	NA
Blood_eQTL	9	CDKN2B	738	0·00E+00	0·00E+00	1·48E-03	0·998	0·000	NA
Blood_eQTL	9	CDKN2A	739	1·79E-16	1·21E-13	1·42E-03	0·961	0·037	NA
Pituitary_eQTL	9	CDKN2B-AS1	706	6·57E-05	4·44E-02	1·41E-03	0·952	0·003	NA
Endometrium_mQTL	1	cg03519931	301	2·56E-19	7·62E-14	2·55E-08	0·007	0·993	Wnt4
Endometrium_mQTL	1	cg00356045	246	5·41E-13	1·61E-07	3·68E-08	0·010	0·990	Wnt4
Endometrium_mQTL	1	cg13692526	385	2·32E-16	6·88E-11	5·30E-08	0·015	0·985	Wnt4
Endometrium_mQTL	1	cg25011003	399	4·00E-29	1·19E-23	1·10E-07	0·032	0·968	Wnt4

Endometrium_mQTL	1	cg15582954	333	2·61E-27	7·76E-22	1·65E-07	0·048	0·952	Wnt4
Endometrium_mQTL	1	cg22488750	114	1·05E-06	2·98E-07	6·92E-02	0·019	0·912	NA
Endometrium_mQTL	1	cg18628801	122	2·16E-11	4·19E-10	1·59E-02	0·308	0·676	CDC42
Blood_mQTL	1	cg00356045	351	2·39E-14	7·91E-09	4·12E-08	0·013	0·987	Wnt4
Blood_mQTL	1	cg01781529	329	1·25E-12	4·15E-07	4·82E-08	0·015	0·985	Wnt4
Blood_mQTL	1	cg15582954	433	1·28E-26	4·23E-21	2·09E-07	0·068	0·932	Wnt4
Blood_mQTL	1	cg25011003	506	1·55E-38	5·14E-33	2·10E-07	0·069	0·931	Wnt4
Blood_mQTL	1	cg18768612	204	1·65E-07	5·46E-02	7·34E-08	0·023	0·922	CDC42
Blood_mQTL	1	cg07180649	179	1·30E-07	4·32E-02	1·38E-07	0·045	0·912	Wnt4
Blood_mQTL	1	cg09938164	361	1·05E-17	2·60E-16	1·12E-02	0·276	0·713	Wnt4
Blood_mQTL	1	cg21772489	117	1·73E-08	1·97E-07	3·69E-02	0·418	0·545	CDC42
Blood_mQTL	1	cg13962372	164	1·44E-06	4·70E-01	7·74E-08	0·025	0·506	CDC42
Blood_mQTL	1	cg15086279	186	1·08E-15	2·52E-14	2·04E-02	0·477	0·502	LINC00339
Endometrium_mQTL	9	cg16606671	111	3·03E-14	1·01E-14	3·76E-03	0·000	0·996	CDKN2A
Endometrium_mQTL	9	cg26269171	79	9·56E-28	3·20E-28	3·69E-03	0·000	0·996	CDKN2A

nsnps - number of SNPs in region used in analysis
PP.H0.abf - posterior probability of hypothesis 0: neither trait has a genetic association in the region.
PP.H1.abf - posterior probability of hypothesis 1: only trait 1 has a genetic association in the region.
PP.H2.abf - posterior probability of hypothesis 2: only trait 2 has a genetic association in the region.
PP.H3.abf - posterior probability of hypothesis 3: both traits are associated, but with different causal variants.
PP.H4.abf - posterior probability of hypothesis 4: both traits are associated and share a single causal variant.

Supplementary Table S11: SMR analysis using Meta-analysed data and expression quantitative trait loci (eQTL) and methylation quantitative trait loci (mQTL) datasets

QTL Dataset	probeID	Gene/CpG	topSNP	topSNP_chr	topSNP_bp	A1	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI
Blood_eQTL	ENSG00000070831	CDC42	rs2473290	1	22358457	T	0·159	0·031	2·19E-07	0·344	0·009	0·00E+00	0·463	0·090	2·78E-07	5·00E-02
Edometrium_mQTL	cg25011003	cg25011003	rs55938609	1	22470451	C	0·200	0·032	2·87E-10	0·219	0·018	1·99E-33	0·911	0·163	2·24E-08	8·23E-02
Edometrium_mQTL	cg15582954	cg15582954	rs55938609	1	22470451	C	0·200	0·032	2·87E-10	0·437	0·037	1·80E-31	0·456	0·082	2·81E-08	6·12E-02
Edometrium_mQTL	cg03519931	cg03519931	rs12037376	1	22462111	A	0·210	0·032	2·68E-11	-0·266	0·029	3·14E-20	-0·790	0·146	6·50E-08	3·59E-01
Edometrium_mQTL	cg13692526	cg13692526	rs55938609	1	22470451	C	0·200	0·032	2·87E-10	0·148	0·018	6·73E-17	1·350	0·268	4·75E-07	1·37E-01
Blood_mQTL	cg25011003	cg25011003	rs55938609	1	22470451	C	0·200	0·032	2·87E-10	0·424	0·032	2·26E-39	0·471	0·083	1·27E-08	2·63E-02
Blood_mQTL	cg15582954	cg15582954	rs55938609	1	22470451	C	0·200	0·032	2·87E-10	0·348	0·032	7·80E-27	0·574	0·105	5·31E-08	5·64E-02

A1, effect allele; b_GWAS, effect size of the SNP in the GWAS dataset; se_GWAS, standard error of the SNP in the GWAS dataset; p_GWAS, p value of the SNP in the GWAS dataset; b_eQTL, effect size of the SNP in the QTL dataset; se_eQTL, standard error of the SNP in the QTL dataset; p_eQTL, p value of the SNP in the QTL dataset; b_SMR, effect estimate from the SMR test; se_SMR, standard error from the SMR test, p_SMR, p value from the SMR test; p_HEIDI, p value from the HEIDI test