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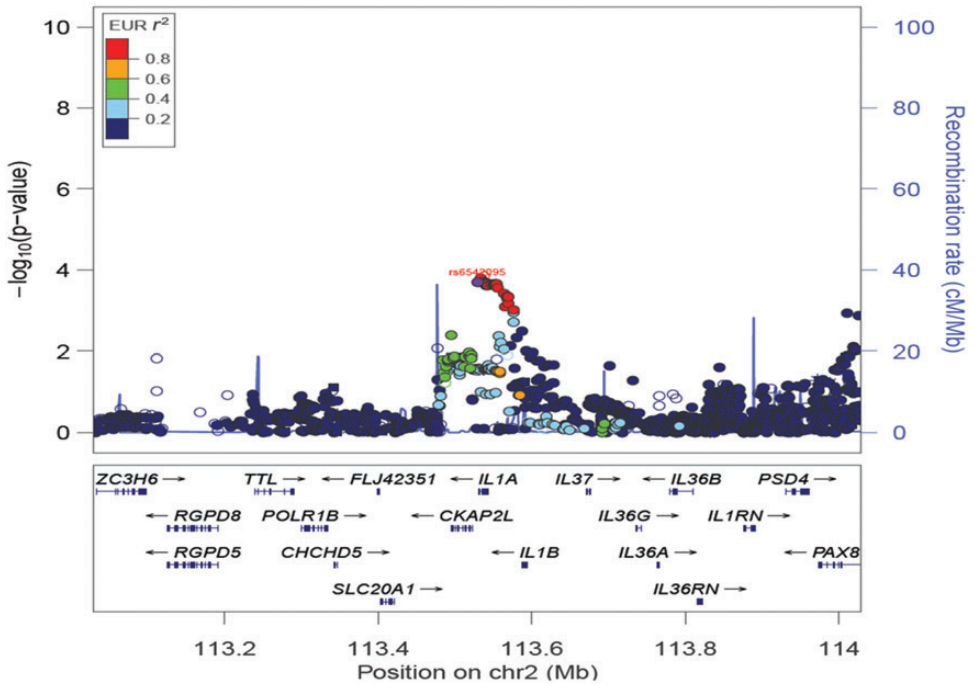
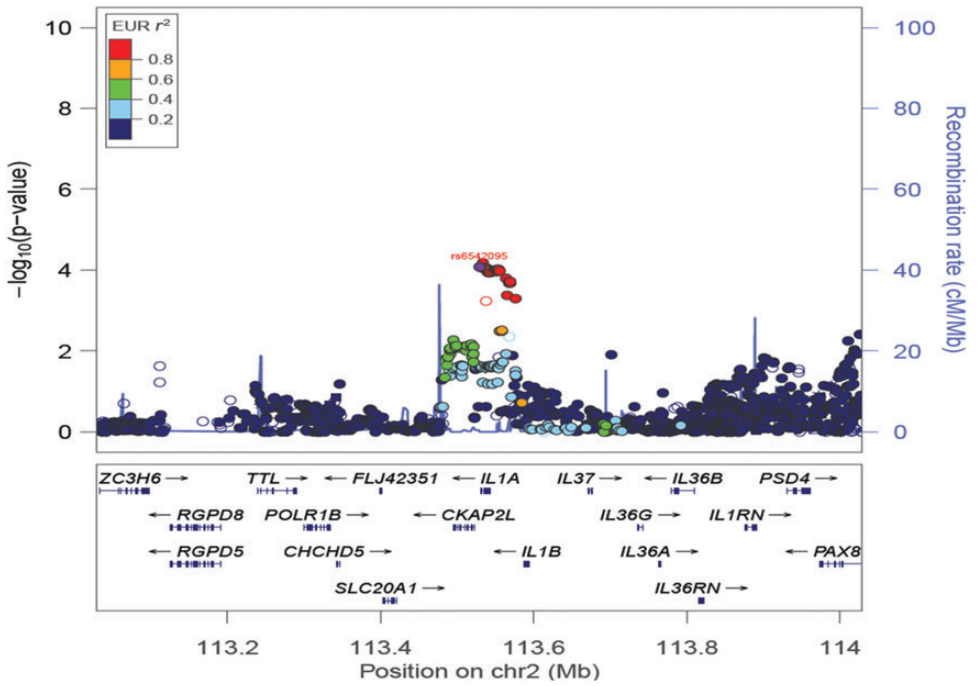
SUPPLEMENTARY DATA



Supplementary Figure S1 Evidence of association in 'All' endometriosis from the fixed-effect meta-analysis of variants in the *IL1A* region, using imputed data from QIMRHCS, OX and BBJ. Circles in the plot represent SNPs with no functional annotations. Squares represent SNPs located in either coding or untranslated regions. The index SNP (rs6542095) is represented by a purple circle. All other SNPs are colour coded according to the strength of LD with the best SNP (as measured by r^2 in the European 1000 Genomes data).



Supplementary Figure S2 Evidence of association in 'Grade_B' endometriosis from the fixed-effect meta-analysis of variants in the *IL1A* region, using imputed data from QIMRHCS, OX and BBJ. Circles in the plot represent SNPs with no functional annotations. Squares represent SNPs located in either coding or untranslated regions. The index SNP (rs6542095) is represented by a purple circle. All other SNPs are colour coded according to the strength of LD with the best SNP (as measured by r^2 in the European 1000 Genomes data).

Supplementary Table SI **Top SNPs in meta-analysis of all variants in the *IL1A* regions, using individual QIMRHCS, OX and BBJ imputed data.**

Chr	SNP	Position (bp)	RA	OA	QIMRHCS + OX + BBJ ('All')					QIMRHCS + OX + BBJ ('Grade_B')				
					OR (95% CI)	*P*	*Q* statistic *P*	I^2	Direction	OR (95% CI)	*P*	*Q* statistic *P*	I^2	Direction
2	rs1969294	113 538 490	G	A	0.89 (0.84–0.95)	1.35E−04	5.93E−01	0.00	–	0.88 (0.82–0.95)	5.77E−04	2.06E−01	0.37	–
2	rs13000462	113 534 024	C	T	0.89 (0.84–0.95)	1.56E−04	1.91E−01	0.40	–	0.86 (0.80–0.93)	6.42E−05	6.29E−02	0.64	–
2	rs3783543	113 536 651	G	A	0.90 (0.84–0.95)	1.90E−04	2.41E−01	0.30	–	0.87 (0.81–0.93)	8.57E−05	7.26E−02	0.62	–
2	rs2071376	113 535 395	T	G	0.90 (0.84–0.95)	1.94E−04	2.40E−01	0.30	–	0.87 (0.80–0.93)	8.52E−05	7.26E−02	0.62	–
2	rs3783550	113 532 885	T	G	0.90 (0.84–0.95)	1.94E−04	2.40E−01	0.30	–	0.87 (0.80–0.93)	8.47E−05	7.33E−02	0.62	–
2	rs3783546	113 534 830	C	G	0.90 (0.84–0.95)	1.95E−04	2.39E−01	0.30	–	0.87 (0.80–0.93)	8.52E−05	7.26E−02	0.62	–
2	rs3783533	113 538 779	A	G	0.90 (0.84–0.95)	1.97E−04	2.43E−01	0.29	–	0.87 (0.81–0.93)	8.86E−05	7.26E−02	0.62	–
2	rs6542095	113 529 183	T	C	0.90 (0.84–0.95)	1.98E−04	2.34E−01	0.31	–	0.86 (0.80–0.93)	8.03E−05	7.40E−02	0.62	–
2	rs1533463	113 538 782	A	G	0.90 (0.85–0.95)	2.04E−04	2.36E−01	0.31	–	0.87 (0.81–0.93)	8.93E−05	7.15E−02	0.62	–
2	rs3783539	113 537 579	C	T	0.90 (0.85–0.95)	2.10E−04	2.25E−01	0.33	–	0.87 (0.81–0.93)	9.64E−05	6.63E−02	0.63	–
2	rs3783525	113 541 819	A	T	0.90 (0.85–0.95)	2.13E−04	2.52E−01	0.27	–	0.87 (0.81–0.93)	9.87E−05	7.34E−02	0.62	–

Chr, chromosome; Position, chromosomal position (bp) based on Human Build 37 (GRCh37/hg19); RA, risk allele; OA, other allele; OR, odds ratio; CI, confidence interval; *Q* statistic *P*, Cochran's *Q* between-study heterogeneity test *P*-value; I^2, percentage of variance attributable to between-study heterogeneity.

Supplementary Table II **Association of the *IL1A* variants in the European imputed data, conditioned on rs6542095.**

Chr	SNP	Pos (bp)	RA	OA	QIMRHCS + OX ('All Endo')		QIMRHCS + OX ('Grade_B')	
					OR (95% CI)	*P*		*P*
2	rs11677416	113 529 240	T	C	1.05 (0.97–1.13)	2.05E−01	1.08 (0.97–1.2)	1.55E−01
2	rs2856836	113 532 083	A	G	1.05 (0.97–1.13)	2.04E−01	1.08 (0.97–1.2)	1.55E−01
2	rs1304037	113 532 236	T	C	1.05 (0.97–1.13)	2.04E−01	1.08 (0.97–1.2)	1.48E−01
2	rs17561	113 537 223	C	A	1.05 (0.97–1.13)	2.02E−01	1.08 (0.97–1.2)	1.55E−01

Chr, chromosome; Position, chromosomal position (bp) based on Human Build 37 (GRCh37/hg19); RA, risk allele; OA, other allele; OR, odds ratio; CI, confidence interval.