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.