



Author Correction: Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis

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The original version of this Article contained an error in Table 1, in which the odds ratios were incorrectly calculated. The correct version of Table 1 is:

Table 1 | Overview of lead SNPs with significant associations at 29 independent loci in UL GWAS meta-analysis

Locus	Lead SNP	RA	OA	RAF _{EUR}	P _{Meta}	OR (95% CI)	Gene(s) of interest ^a
1p36.12 ^{b,c}	rs7412010	C	G	0.15	2.4 × 10 ⁻²⁹	1.13 (1.11–1.16)	WNT4, CDC42
2p23.2	rs55819434	A	G	0.91	5.6 × 10 ⁻⁰⁹	0.92 (0.90–0.95)	BABAM2
2p25.1 ^{b,c}	rs35417544	T	C	0.69	2.3 × 10 ⁻¹⁹	1.09 (1.07–1.10)	GREB1
3q26.2 ^c	rs35446936	A	G	0.24	1.0 × 10 ⁻⁰⁸	0.95 (0.93–0.96)	TERC
4q12 ^c	rs62323682	T	C	0.94	4.9 × 10 ⁻¹⁸	0.87 (0.84–0.90)	LNK1, PDGFRA
4q13.3 ^c	rs12640488	A	G	0.52	4.0 × 10 ⁻¹⁴	0.94 (0.92–0.96)	SULT1B1
4q22.3	rs4699299	T	C	0.69	4.7 × 10 ⁻⁰⁸	0.95 (0.94–0.97)	PDLIM5
5p15.33 ^c	rs72709458	T	C	0.23	4.7 × 10 ⁻²¹	1.10 (1.08–1.13)	TERT
5q35.2 ^c	rs2456181	C	G	0.49	1.1 × 10 ⁻¹¹	0.94 (0.93–0.96)	ZNF346, UIMC1
6p21.31	rs116251328	A	T	0.02	3.0 × 10 ⁻⁰⁸	1.15 (1.09–1.21)	GRM4, HMGA1
6q25.2 ^{b,c}	rs58415480	C	G	0.84	1.9 × 10 ⁻⁵⁴	0.84 (0.82–0.86)	SYNE1, ESR1
7q31.2	rs2270206	A	C	0.16	4.6 × 10 ⁻⁰⁸	1.06 (1.04–1.09)	WNT2
9p24.3 ^c	rs10976689	A	G	0.60	2.4 × 10 ⁻¹³	0.94 (0.93–0.96)	ANKRD15
10q24.3 ^c	rs9419958	T	C	0.13	1.1 × 10 ⁻¹⁶	1.10 (1.08–1.13)	OBFC1, SLK
10p11.22	rs10508765	A	G	0.80	1.5 × 10 ⁻¹⁰	1.07 (1.05–1.09)	ZEB1, ARHGAP12
11p15.5 ^c	rs547025	T	C	0.92	1.5 × 10 ⁻¹⁴	1.13 (1.09–1.16)	RIC8A, BET1L
11p14.1 ^b	rs11031006	A	G	0.14	5.7 × 10 ⁻¹⁵	0.91 (0.89–0.93)	FSHB
11p13 ^c	rs61889186	C	G	0.86	1.4 × 10 ⁻²⁵	0.89 (0.87–0.91)	WT1
11p13 ^c	rs2785202	C	G	0.55	6.9 × 10 ⁻¹⁴	1.06 (1.05–1.08)	PDHX, CD44
11q22.3 ^c	rs149934734	T	C	0.03	1.1 × 10 ⁻²⁷	1.33 (1.26–1.40)	C11orf65, KDELC2
12q13.11 ^c	rs2131371	A	C	0.28	1.6 × 10 ⁻¹⁸	0.93 (0.91–0.94)	SLC38A2
12q15	rs11178393	T	C	0.89	3.3 × 10 ⁻⁰⁸	1.08 (1.05–1.10)	PTPRR
12q24.31	rs28583837	A	G	0.22	2.3 × 10 ⁻⁰⁸	0.94 (0.92–0.96)	PITPNM2
13q14.11 ^c	rs117245733	A	G	0.02	5.7 × 10 ⁻¹⁴	1.31 (1.21–1.39)	FOXO1
17p13.1 ^c	rs78378222	T	G	0.99	7.1 × 10 ⁻³¹	0.65 (0.60–0.70)	SHBG, TP53
20p12.3 ^c	rs16991615	A	G	0.07	8.8 × 10 ⁻¹⁰	1.11 (1.07–1.14)	MCM8, TRMT6
22q13.1 ^c	rs4821939	A	T	0.20	7.8 × 10 ⁻¹⁶	1.08 (1.06–1.10)	TNRC6B
Xp26.2 ^c	rs12392108	A	T	0.31	5.9 × 10 ⁻⁴⁶	1.13 (1.11–1.15)	RAF2C
Xq13.1 ^c	rs4360450	A	G	0.37	2.1 × 10 ⁻¹⁸	1.08 (1.06–1.10)	MED12

SNP single-nucleotide polymorphism, RA risk allele, OA other allele, RAF_{EUR} average risk allele frequency in European samples, OR odds ratio

^a≤300 kb distant from association signal

^bLoci previously associated with endometriosis

^cLoci previously associated with UL

Corrections & amendments

which replaces the previous incorrect version:

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This has been corrected in both the PDF and HTML versions of the Article.

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