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)	*LNX1, 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)	*RAP2C*
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

[b]Loci previously associated with endometriosis

[c]Loci previously associated with UL

which replaces the previous incorrect version:

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Locus	Lead SNP	RA	OA	RAF_{EUR}	P_{Meta}	OR (95% CI)	Gene(s) of interest[a]
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This has been corrected in both the PDF and HTML versions of the Article.