

CORRECTION

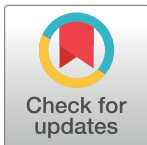
Correction: Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria

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In the Data Availability Statement, the URL does not fully match the data described. The URL should be: <https://doi.org/10.17863/CAM.36024>. The correct Data Availability Statement is: Summary statistic GWAS meta-analysis results for the combined dataset excluding 23andMe are available at <https://doi.org/10.17863/CAM.36024>. The most significant 10,000 SNPs for the meta-analysis including 23andMe are available at <https://doi.org/10.17863/CAM.36024>.

There is an error in [Table 2](#). The square brackets that indicate the effect allele are shown in error. Please see the correct [Table 2](#) here.

[S2 Table](#) is a duplicate of S6 Table. Please view the correct [S2 Table](#) below.



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Citation: Day F, Karaderi T, Jones MR, Meun C, He C, Drong A, et al. (2019) Correction: Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. *PLoS Genet* 15(12): e1008517. <https://doi.org/10.1371/journal.pgen.1008517>

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Table 2. The 14 genome-wide significant variants associated with PCOS in the meta-analysis.

Chr. Position ¹	rsID	EA ²	OA ³	EAF ⁴	Beta	OR ⁵	95% CI ⁶	Std. Error	Nearest Gene	P-value	Effective N ⁷	Ref ⁸
2:43561780	rs7563201	A	G	0.451	-0.108	0.90	(0.86±0.92)	0.0172	THADA	3.68e-10	17192	
2:213391766	rs2178575	A	G	0.151	0.166	1.18	(1.13±1.23)	0.0219	ERBB4	3.34e-14	17192	17
5:131813204	rs13164856	T	C	0.729	0.124	1.13	(1.08±1.17)	0.0193	IRF1/ RAD50	1.45e-10	17192	17
8:11623889	rs804279	A	T	0.262	0.128	1.14	(1.09±1.17)	0.0184	GATA4/ NEIL2	3.76e-12	16895	16
9:5440589	rs10739076	A	C	0.308	0.110	1.12	(1.07±1.15)	0.0197	PLGRKT	2.51e-08	17192	
9:97723266	rs7864171	A	G	0.428	-0.093	0.91	(0.88±0.94)	0.0168	FANCC	2.95e-08	17192	16
9:126619233	rs9696009	A	G	0.068	0.202	1.22	(1.15±1.30)	0.0311	DENND1A	7.96e-11	17192	
11:30226356	rs11031005	T	C	0.854	-0.159	0.85	(0.81±0.89)	0.0223	ARL14EP/ FSHB	8.66e-13	17192	16,17
11:102043240	rs11225154	A	G	0.094	0.179	1.20	(1.13±1.26)	0.0272	YAPI	5.44e-11	17192	17
11:113949232	rs1784692	T	C	0.824	0.144	1.15	(1.10±1.20)	0.0226	ZBTB16	1.88e-10	17192	
12:56477694	rs2271194	A	T	0.416	0.097	1.10	(1.06±1.13)	0.0166	ERBB3/ RAB5B	4.57e-09	17192	17
12:75941042	rs1795379	T	C	0.240	-0.117	0.89	(0.85±0.92)	0.0195	KRR1	1.81e-09	17192	17
16:52375777	rs8043701	A	T	0.815	-0.127	0.88	(0.84±0.91)	0.0208	TOX3	9.61e-10	17192	
20:31420757	rs853854	A	T	0.499	-0.098	0.91	(0.87±0.93)	0.0163	MAPRE1	2.36E-09	17192	

1. Chromosome and position in hg19.
2. EA—Effect allele.
3. OA—Other allele.
4. EAF—Effect allele frequency.
5. OR—Odds Ratio.
6. 95% CI— 95 percent confidence interval.
7. Effective N—effective sample size.
8. Ref.—reference.

<https://doi.org/10.1371/journal.pgen.1008517.t001>

Supporting information

S2 Table. All PCOS meta-analysis, PCOS meta-analysis without self-report, NIH, non-NIH Rotterdam and self-report meta-analysis results.
(XLSX)

Reference

1. Day F, Karaderi T, Jones MR, Meun C, He C, Drong A, et al. (2018) Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. *PLoS Genet* 14(12): e1007813. <https://doi.org/10.1371/journal.pgen.1007813> PMID: 30566500