

CORRECTION

Correction: Literature-Informed Analysis of a Genome-Wide Association Study of Gestational Age in Norwegian Women and Children Suggests Involvement of Inflammatory Pathways

The *PLOS ONE* Staff

The captions for Tables 1 and 4 were incorrectly incorporated in the manuscript text. The authors have provided the correct tables and captions here. The publisher apologizes for this error.



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Citation: The *PLOS ONE* Staff (2016) Correction: Literature-Informed Analysis of a Genome-Wide Association Study of Gestational Age in Norwegian Women and Children Suggests Involvement of Inflammatory Pathways. *PLoS ONE* 11(10): e0165328. doi:10.1371/journal.pone.0165328

Published: October 19, 2016

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Table 1. Top 20 independent loci from maternal GWAS of gestational age in labor-initiated deliveries.

Chr	BP	SNP	P	E/R	Mod	nEE	nER	nRR	mEE	mER	mRR	Genes
6	164389165	rs593254	3.32e-6	A/G	ADD	76	480	851	260	264	268	
2	134837980	rs13410504	5.64e-6	G/A	REC	7	237	1163	221	265	267	
1	226209989	rs17515010	1.00e-5	G/A	REC	4	141	1261	205	264	266	<i>SDE2, PYCR2, LEFTY2, H3F3A, H3F3AP4</i>
1	81391541	rs17105699	1.03e-5	G/A	DOM	6	165	1232	273	259	267	
20	7618077	rs6086132	1.06e-5	A/G	DOM	162	649	596	269	268	263	
5	10501076	rs2589658	1.15e-5	C/A	REC	330	684	393	262	267	267	<i>ROPN1L, ROPN1L-AS1, MARCH6, ANKRD33B</i>
4	103537442	rs1609798	1.48e-5	A/G	REC	128	601	677	259	266	268	<i>NFKB1, MANBA</i>
9	130417033	rs10117075	1.55e-5	A/G	REC	12	190	1205	237	268	266	<i>TTC16, TOR2A, STXBP1, SH2D3C, PTRH1, FAM129B</i>
14	91352234	rs6575165	1.56e-5	A/G	ADD	87	478	842	260	264	268	<i>TTC7B, RPS6KA5</i>
10	88336279	rs2588278	1.58e-5	A/G	ADD	260	680	467	270	266	264	<i>WAPAL, OPN4, LDB3</i>
1	36879232	rs3007217	1.81e-5	G/A	ADD	150	593	664	270	268	264	<i>STK40, SH3D21, OSCP1, MRPS15, LSM10, EVA1B, CSF3R</i>
16	18067234	rs151699	1.86e-5	C/A	REC	1	133	1272	161	266	266	
16	3344618	rs220381	2.12e-5	G/A	DOM	159	559	689	270	268	264	<i>ZSCAN32, TIGD7, OR2C1, OR1F2P, OR1F1, MTRNR2L4, MEFV</i>
10	87762136	rs11201867	2.33e-5	A/G	ADD	22	304	1081	275	270	265	<i>GRID1</i>
1	22345093	rs3117048	2.49e-5	A/G	REC	146	633	628	273	266	265	<i>WNT4, HSPG2, CELA3B, CELA3A, CDC42</i>
4	112524778	rs10015214	2.60e-5	A/G	DOM	312	675	420	266	268	263	
6	41164005	rs6915083	2.64e-5	G/A	REC	197	648	561	261	268	266	<i>TREM*, TREML*, NFYA, ADCY10P1</i>
16	85941774	rs305080	2.67e-5	A/G	REC	143	586	678	273	266	265	<i>IRF8</i>
1	88453303	rs3008465	2.67e-5	C/A	ADD	71	532	802	272	268	264	
6	123749752	rs1343962	2.80e-5	A/G	ADD	303	713	390	263	266	269	<i>TRDN</i>

Table 1 was pruned to show only independent loci. *BP*—physical position on the chromosome in hg19 coordinates, *P*—the most extreme empirical p-value from three genetic models, *E/R*—the effect allele and the reference allele, *Mod*—the most significant genetic model for that SNP, *nXX*—number of individuals in each genotypic group, *mXX*—mean gestational age in each genotypic group. Interpretation of mean gestational age values should take into account the bimodal phenotype distribution of genotyped individuals (S1 Fig). *Genes* were assigned to SNPs based on a 100 kb offset rule. Asterisk (*) indicates a gene family with multiple genes in that locus. No multiple-test correction is applied. Bolded genes are described in the literature-informed analyses. Genes with unknown function (*LINC*, *LOC* etc.) are not listed.

doi:10.1371/journal.pone.0165328.t001

Table 4. Loci of biological relevance from maternal GWAS of gestational age in labor-initiated deliveries.

Rank	SNP	Chr	BP	P	E/R	Mod	nEE	nER	nRR	mEE	mER	mRR	Genes
5	rs17515010	1	226209989	1.00e-5	G/A	REC	4	141	1261	205	264	266	LEFTY2
10	rs1609798	4	103537442	1.48e-5	A/G	REC	128	601	677	259	266	268	NFKB1
11	rs10117075	9	130417033	1.55e-5	A/G	REC	12	190	1205	237	268	266	ENG
13	rs2287116	9	130420813	1.55e-5	A/C	REC	12	210	1185	237	267	266	TOR2A
19	rs220381	16	3344618	2.12e-5	G/A	DOM	159	559	689	270	268	264	MEFV
22	rs3117048	1	22345093	2.49e-5	A/G	REC	146	633	628	273	266	265	WNT4
24	rs6915083	6	41164005	2.64e-5	G/A	REC	197	648	561	261	268	266	TREM1, TREML2, TREML4
25	rs305080	16	85941774	2.67e-5	A/G	REC	143	586	678	273	266	265	IRF8
41	rs4312673	3	48401307	3.67e-5	A/G	DOM	1	72	1332	282	256	267	CAMP
65	rs634335	1	36335862	5.63e-5	C/A	DOM	23	310	1074	266	262	267	AGO3
66	rs6718188	2	174761611	5.73e-5	A/C	ADD	157	611	638	269	268	264	SP3
75	rs12336969	9	107679500	6.10e-5	A/C	REC	7	201	1199	229	267	266	ABCA1
88	rs2177539	7	16652523	7.24e-5	G/A	REC	109	566	728	259	267	267	ANKMY2
98	rs3913369	3	55481075	8.22e-5	A/C	ADD	69	498	840	262	264	268	WNT5A
100	rs12138039	1	156918137	8.29e-5	A/G	DOM	6	185	1214	259	261	267	ARHGEF11
101	rs4075688	3	195848264	8.30e-5	G/A	REC	177	668	559	261	266	268	TFRC
106	rs4789863	17	76897347	8.52e-5	A/G	DOM	1	122	1281	251	259	267	TIMP2
109	rs11866271	16	24881152	8.74e-5	C/A	DOM	107	582	713	266	264	268	TNRC6A
117	rs3021274	22	40395084	9.22e-5	A/G	DOM	230	653	524	269	267	264	TNRC6B
138	rs12202611	6	154237443	1.08e-4	G/A	REC	7	295	1105	230	266	266	OPRM1
146	rs395643	14	56541638	1.12e-4	G/A	REC	14	310	1083	242	266	266	PELI2
157	rs2301137	12	7018949	1.22e-4	A/G	DOM	86	536	784	267	263	268	GNB3, SPSB2
173	rs12435366	14	35838389	1.41e-4	A/G	REC	97	550	745	259	267	266	NFKBIA
197	rs7045953	9	120485795	1.56e-4	G/A	ADD	37	379	991	272	269	265	TLR4
266	rs3746512	20	44592636	2.18e-4	A/G	REC	34	394	979	253	266	267	MMP9
284	rs4849122	2	113560921	2.34e-4	G/A	REC	7	158	1242	233	266	266	IL1A, IL1B
293	rs1457776	8	133360660	2.39e-4	A/G	REC	52	433	922	256	266	267	KCNQ3
299	rs942364	13	28896097	2.44e-4	A/G	DOM	20	307	1080	270	262	267	PAN3

The SNPs were selected from the top 300 GWAS results, based on their proximity and/or functional relationship with genes biologically relevant to gestational age. *Rank*—the rank of that SNP among all GWAS results, based on the most significant empirical p-value (*P*) from three genetic models, *BP*—physical position on the chromosome (*Chr*) in hg19 coordinates, *E/R*—the effect allele and the reference allele, *Mod*—the most significant genetic model for that SNP, *nXX*—number of individuals in each genotypic group, *mXX*—mean of gestational age in each genotypic group. Interpretation of mean gestational age values should take into account the bimodal phenotype distribution of genotyped individuals (**S1 Fig**). No multiple-test correction is applied.

doi:10.1371/journal.pone.0165328.t002

Reference

1. Bacelis J, Juodakis J, Sengpiel V, Zhang G, Myhre R, Muglia LJ, et al. (2016) Literature-Informed Analysis of a Genome-Wide Association Study of Gestational Age in Norwegian Women and Children Suggests Involvement of Inflammatory Pathways. *PLoS ONE* 11(8): e0160335. doi: [10.1371/journal.pone.0160335](https://doi.org/10.1371/journal.pone.0160335) PMID: [27490719](https://pubmed.ncbi.nlm.nih.gov/27490719/)