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Author Correction: Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations

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Correction to: *Nature Communications* <https://doi.org/10.1038/s41467-019-09480-8>, published online 2 April 2019.

In the original version of this Article, several numbers were given incorrectly in Tables 1 and 2 in columns 5 (EAF), 6 (*N*) and 7 (*Z*-score). The mistakes arose when one population was removed from the analyses but the numbers were not updated in the tables. These have now been corrected in both the HTML and PDF versions of the Article. The incorrect versions of these tables appear below as Tables 1 and 2 and the correct versions as Tables 3 and 4, respectively.

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Table 1 Genome-wide significant associations for AUDIT-C in the trans-population meta-analysis

rsID	Chr:pos ^a	A1/A2	Gene ^b	EAF	N	Z-score	P_EA	P_AA	P_LA	P_EAA	P_SAA	Effect	P _{meta}
rs1260326	2:27730940	C/T	GCKR ^c	0.652	270,226	8.22	1.74 × 10 ⁻¹⁶	0.110	0.067	0.987	0.739	+++++	2.04 × 10 ⁻¹⁶
rs2683616	2:58035555	A/G	VRK2 ^d	0.624	211,399	6.22	1.80 × 10 ⁻⁹	NA	0.060	0.487	NA	+?+?	4.95 × 10 ⁻¹⁰
rs12639940	4:39420981	A/G	KLBC ^c	0.613	194,761	5.93	3.45 × 10 ⁻⁹	NA	NA	0.626	NA	+++?	3.06 × 10 ⁻⁹
rs1229984	4:100239319	C/T	ADH1B ^c	0.970	272,358	24.56	4.83 × 10 ⁻¹⁰²	1.31 × 10 ⁻¹⁹	4.40 × 10 ⁻¹⁶	9.05 × 10 ⁻³	NA	+++++	3.62 × 10 ⁻¹³³
rs142783062	4:100270960	D/I	ADH1C ^c	0.345	271,444	9.82	2.04 × 10 ⁻¹⁴	4.75 × 10 ⁻⁷	4.90 × 10 ⁻⁴	0.019	0.779	+++++	9.50 × 10 ⁻²³
rs13107325	4:103188709	C/T	SLC39A8 ^c	0.937	270,248	11.45	1.43 × 10 ⁻²⁵	1.07 × 10 ⁻⁴	2.23 × 10 ⁻³	NA	NA	+++??	2.24 × 10 ⁻³⁰
rs4423856	4:150984857	T/C	DCLK2 ^d	0.796	212,444	5.66	3.60 × 10 ⁻⁸	NA	0.289	0.574	0.144	+?+++	1.48 × 10 ⁻⁸
rs2961816	5:50443691	A/C	ISL1 ^d	0.683	260,828	5.74	1.24 × 10 ⁻⁷	0.021	0.641	0.932	0.137	+++++	9.75 × 10 ⁻⁹
rs4841132	8:9183596	A/G	PPP1R3B ^d	0.101	276,763	5.46	2.75 × 10 ⁻⁶	6.59 × 10 ⁻³	0.226	NA	0.148	---?+	3.62 × 10 ⁻⁸
rs62033408	16:53827962	A/G	FTO ^c	0.678	270,067	9.08	2.20 × 10 ⁻¹⁵	4.78 × 10 ⁻⁵	0.229	0.177	0.027	+++++	1.11 × 10 ⁻¹⁹
rs9902512	17:47094274	C/G	IGF2BP1 ^c	0.664	207,229	-5.81	3.81 × 10 ⁻⁸	NA	0.055	0.782	NA	-?+?	6.24 × 10 ⁻⁹
rs142997686	17:79419159	D/I	BAHCC1 ^c	0.384	211,314	5.84	1.77 × 10 ⁻⁹	NA	0.944	0.434	0.840	+?+?	5.39 × 10 ⁻⁹
rs75723348	22:41420679	T/G	RBX1 ^d	0.736	275,328	5.55	2.97 × 10 ⁻⁷	0.063	0.072	0.536	0.579	+++++	1.11 × 10 ⁻⁸

The loci shown represent completely independent signals after conditioning analyses
A1 effect allele, A2 other allele, EAF effective allele frequency, EA European American, AA African American, LA Latino American, EAA East Asian American, SAA South Asian American
^aHuman Genome hg19 assembly
^bGene nearest to the lead SNP
^cProtein-coding gene contains the lead SNP
^dProtein-coding gene nearest to the lead SNP

Table 2 Genome-wide significant associations for AUD in the trans-population meta-analysis

rsID	Chr:pos ^a	A1/A2	Gene ^b	EAF	N	Z-score	P_EA	P_AA	P_LA	P_EAA	P_SAA	Effect	P _{meta}
rs1260326	2:27730940	C/T	GCKR ^c	0.651	271,763	7.33	1.44 × 10 ⁻¹⁶	0.679	0.778	0.830	0.820	+++++	2.27 × 10 ⁻¹³
rs540606	2:45138507	A/G	SIX3 ^d	0.409	213,336	-6.49	2.84 × 10 ⁻¹⁰	NA	0.175	0.411	NA	-?+?	8.58 × 10 ⁻¹¹
rs5860563	4:100047157	D/I	ADH4 ^c	0.722	277,270	-6.21	7.63 × 10 ⁻⁵	9.85 × 10 ⁻⁷	0.035	NA	0.412	---?+	1.12 × 10 ⁻⁹
rs1229984	4:100239319	C/T	ADH1B ^c	0.969	273,904	19.54	4.51 × 10 ⁻⁷⁴	4.18 × 10 ⁻⁵	5.81 × 10 ⁻¹⁷	0.032	NA	+++++	4.68 × 10 ⁻⁸⁵
rs1612735	4:100258007	T/C	ADH1C ^c	0.656	271,471	-8.86	1.75 × 10 ⁻¹⁴	6.42 × 10 ⁻⁵	0.022	0.938	0.054	-----	7.90 × 10 ⁻¹⁹
rs13107325	4:103188709	C/T	SLC39A8 ^c	0.937	271,784	7.60	2.73 × 10 ⁻¹⁴	0.064	0.363	NA	NA	+++++	2.97 × 10 ⁻¹⁴
rs7906104	10:110497101	T/C		0.271	275,977	-5.98	3.15 × 10 ⁻⁷	8.72 × 10 ⁻³	0.357	0.195	0.106	-----	3.17 × 10 ⁻⁹
rs61902812	11:113374420	A/C	DRD2 ^d	0.306	276,977	-5.59	4.99 × 10 ⁻⁶	0.025	0.015	0.220	0.931	-----	2.44 × 10 ⁻⁸
rs4936277 ^e	11:113431960	A/G	DRD2 ^d	0.599	274,128	7.44	2.85 × 10 ⁻¹¹	0.073	4.36 × 10 ⁻⁴	0.200	0.357	+++++	1.01 × 10 ⁻¹³
rs1421085	16:53800954	T/C	FTO ^c	0.670	274,340	6.69	3.26 × 10 ⁻¹⁰	0.024	0.525	0.332	0.018	+++++	2.17 × 10 ⁻¹¹

The loci shown represent completely independent signals after conditioning analyses
A1 effect allele, A2 other allele, EAF effective allele frequency, EA European American, AA African American, LA Latino American, EAA East Asian American, SAA South Asian Americans
^aHuman Genome hg19 assembly
^bGene nearest to the lead SNP
^cProtein-coding gene contains the lead SNP
^dProtein-coding gene nearest to the lead SNP
^eDifferent signal than rs61902812

Table 3 Genome-wide significant associations for AUDIT-C in the trans-population meta-analysis

rsID	Chr:pos ^a	A1/A2	Gene ^b	EAF	N	Z-score	P_EA	P_AA	P_LA	P_EAA	P_SAA	Effect	P _{meta}
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rs13107325	4:103188709	C/T	SLC39A8 ^c	0.937	270,248	11.45	1.43 × 10 ⁻²⁵	1.07 × 10 ⁻⁴	2.23 × 10 ⁻³	NA	NA	+++??	2.24 × 10 ⁻³⁰
rs4423856	4:150984857	T/C	DCLK2 ^d	0.796	212,444	5.66	3.60 × 10 ⁻⁸	NA	0.289	0.574	0.144	+?+++	1.48 × 10 ⁻⁸
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rs4841132	8:9183596	A/G	PPP1R3B ^d	0.101	271,192	-5.51	2.75 × 10 ⁻⁶	6.59 × 10 ⁻³	0.226	NA	0.148	---?+	3.62 × 10 ⁻⁸
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Table 4 Genome-wide significant associations for AUD in the trans-population meta-analysis

rsID	Chr:pos ^a	A1/A2	Gene ^b	EAF	N	Z-score	P_EA	P_AA	P_LA	P_EAA	P_SAA	Effect	P_meta
rs1260326	2:27730940	C/T	GCKR ^c	0.651	271,763	7.33	1.44 × 10 ⁻¹⁶	0.679	0.778	0.830	0.820	+++++	2.27 × 10 ⁻¹³
rs540606	2:45138507	A/G	SIX3 ^d	0.409	213,336	-6.49	2.84 × 10 ⁻¹⁰	NA	0.175	0.411	NA	-?--?	8.58 × 10 ⁻¹¹
rs5860563	4:100047157	D/I	ADH4 ^c	0.723	271,487	-6.09	7.63 × 10 ⁻⁵	9.85 × 10 ⁻⁷	0.035	NA	0.412	---?+	1.12 × 10 ⁻⁹
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rs13107325	4:103188709	C/T	SLC39A8 ^c	0.937	271,784	7.60	2.73 × 10 ⁻¹⁴	0.064	0.363	NA	NA	+++??	2.97 × 10 ⁻¹⁴
rs7906104	10:110497101	T/C		0.272	270,278	-5.92	3.15 × 10 ⁻⁷	8.72 × 10 ⁻³	0.357	0.195	0.106	-----	3.17 × 10 ⁻⁹
rs61902812	11:113374420	A/C	DRD2 ^d	0.304	271,218	-5.58	4.99 × 10 ⁻⁶	0.025	0.015	0.220	0.931	-----	2.44 × 10 ⁻⁸
rs4936277 ^e	11:113431960	A/G	DRD2 ^d	0.599	274,128	7.44	2.85 × 10 ⁻¹¹	0.073	4.36 × 10 ⁻⁴	0.200	0.357	++++++	1.01 × 10 ⁻¹³
rs1421085	16:53800954	T/C	FTO ^c	0.670	274,340	6.69	3.26 × 10 ⁻¹⁰	0.024	0.525	0.332	0.018	++++++	2.17 × 10 ⁻¹¹

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^cProtein-coding gene contains the lead SNP
^dProtein-coding gene nearest to the lead SNP
^eDifferent signal than rs61902812