

Data supplement to Wu et al. Loci with genome-wide associations with schizophrenia in the Han Chinese population. Br J Psychiatry doi:
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Table DS1 Frequency information for the 9 PGC or PGC+CLOZUK indentified genome-wide significance SNPs in HAPMAP CEU and CHB populations.

SNP	CHR	Position	Nearby gene (locus)	P value in PGC or PGC+CLOZUK	Allele	CEU	CHB	P value in BIOX	SNPs tested in replication (r ² /D')
rs1625579	1	98275522	MIR137 (1p21.3)	1.59×10 ⁻¹¹	T	0.833	0.940	/	rs1198588 (1.00/1.00)
rs6703335	1	241675590	SDCCAG8	4.22×10 ⁻⁸	G	0.577	0.720	0.234	rs12045585 (0.02/0.19)
rs17662626	2	193692866	PCGEM1 (2q32.3)	4.65×10 ⁻⁸	A	0.879	1.000	Non-polymorphic in CHB	-
rs2239547	3	52830269	ITIH3/4	3.62×10 ⁻¹⁰	T	0.768	0.584	/	rs2239547
rs10503253	8	4168252	CSMD1 (8p23.2)	4.14×10 ⁻⁸	C	0.812	0.675	/	rs2740870 (0.03/0.31); rs17070157 (0.02/1.00)
rs7004633	8	89829427	MMP16 (8q21.3)	2.75×10 ⁻⁸	A	0.830	0.756	/	rs11780452 (0.07/0.75)
rs7914558	10	104765898	CNNM2 (10q24.32)	1.82×10 ⁻⁹	G	0.621	0.405	/	rs12246739 (0.70/1.00)
rs11191580	10	104896201	NT5C2 (10q24.33)	1.11×10 ⁻⁸	T	0.924	0.699	9.23×10 ⁻³	rs732998 (1.00/1.00)
rs4765905	12	2219845	CACNA1C	1.23×10 ⁻⁸	G	0.647	0.940	1.87×10 ⁻²	rs1558321(0.03/1.00); rs2887780(0.02/0.27)

Table DS2 Quality control metrics for the 18 SNPs

CHR	SNP	BP	Callrate	P_{HWE} in Control
1	rs1198588	98325420	98.9%	0.54
1	rs12045585	241739722	99.4%	0.74
3	rs2239547	52855229	98.8%	0.29
7	rs10277807	71151317	99.8%	0.54
7	rs2944829	71424657	99.9%	0.64
7	rs2192017	122054147	97.2%	0.35
8	rs11785476	3327152	98.4%	0.21
8	rs2740870	3916137	99.0%	0.35
8	rs17070157	4253682	97.9%	0.68
8	rs11780452	89912877	99.1%	0.08
10	rs12246739	104777009	99.9%	0.87
10	rs732998	104887891	98.4%	0.07
10	rs7069733	105287760	99.5%	0.80
10	rs10748844	105315160	99.4%	0.88
12	rs1558321	2100581	99.9%	0.29
12	rs2887780	2369887	99.7%	0.72
12	rs7965296	2442797	99.0%	0.56
14	rs2239259	71804589	99.9%	0.29

Table DS3 Association results of 18 SNPs in the BIOX GWAS, Follow up and the combined samples.

CHR	SNP	Position	A1	BIOX GWAS		Replication		Meta-analysis		Gene
				P	OR [95% CI]	P	OR [95% CI]	P	OR [95% CI]	
1	rs1198588	98325420	T	6.91×10 ⁻⁰²	0.87 [0.75-1.01]	0.801	0.99 [0.88-1.11]	0.192	0.94 [0.86-1.03]	MIR137
1	rs12045585	241739722	T	3.98×10 ⁻⁰²	0.91 [0.83-1.00]	0.481	1.03 [0.96-1.10]	0.491	0.98 [0.93-1.04]	SDCCAG8
3	rs2239547	52855229	G	/	/	1.17×10 ⁻¹⁰	0.81 [0.76-0.87]	/	/	ITIH3/4
7	rs10277807	71151317	T	6.01×10 ⁻⁰³	0.89 [0.82-0.97]	0.982	1.00 [0.94-1.07]	9.52×10 ⁻⁰²	0.96 [0.91-1.01]	CALN1
7	rs2944829	71424657	A	8.34×10 ⁻⁰⁴	0.86 [0.79-0.94]	3.17×10 ⁻⁰⁶	0.85 [0.80-0.91]	9.97×10 ⁻⁰⁹	0.85 [0.81-0.90]	CALN1
7	rs2192017	122054147	A	1.20×10 ⁻⁰³	1.13 [1.05-1.22]	2.78×10 ⁻⁰²	1.08 [1.01-1.15]	1.61×10 ⁻⁰⁴	1.10 [1.05-1.15]	CADPS2
8	rs11785476	3327152	G	8.33×10 ⁻⁰³	0.87 [0.78-0.96]	5.24×10 ⁻⁰²	0.92 [0.85-1.00]	1.62×10 ⁻⁰³	0.90 [0.85-0.96]	CSMD1
8	rs2740870	3916137	G	4.60×10 ⁻⁰⁴	0.86 [0.79-0.94]	0.116	1.05 [0.99-1.12]	0.422	0.98 [0.93-1.03]	CSMD1
8	rs17070157	4253682	G	1.46×10 ⁻⁰³	1.17 [1.06-1.29]	0.319	1.04 [0.96-1.12]	6.81×10 ⁻⁰³	1.08 [1.02-1.15]	CSMD1
8	rs11780452	89912877	A	3.28×10 ⁻⁰³	1.13 [1.04-1.23]	0.924	1.00 [0.93-1.09]	3.51×10 ⁻⁰²	1.06 [1.00-1.13]	MMP16
10	rs12246739	104777009	A	9.26×10 ⁻⁰³	1.15 [1.04-1.28]	7.05×10 ⁻⁰²	1.08 [0.99-1.17]	2.48×10 ⁻⁰³	1.11 [1.04-1.18]	CNNM2
10	rs732998	104887891	C	9.15×10 ⁻⁰³	0.89 [0.82-0.97]	0.991	1.00 [0.93-1.07]	0.111	0.96 [0.91-1.01]	NT5C2
10	rs7069733	105287760	C	6.10×10 ⁻⁰³	0.85 [0.76-0.96]	1.92×10 ⁻⁰²	1.11 [1.02-1.22]	0.902	1.00 [0.94-1.08]	NEURL
10	rs10748844	105315160	T	3.94×10 ⁻⁰³	1.12 [1.04-1.22]	1.92×10 ⁻⁰²	1.08 [1.01-1.15]	2.96×10 ⁻⁰⁴	1.09 [1.04-1.15]	NEURL
12	rs1558321	2100581	T	2.77×10 ⁻⁰³	0.85 [0.77-0.95]	0.907	1.00 [0.92-1.07]	6.53×10 ⁻⁰²	0.94 [0.89-1.00]	CACNA1C
12	rs2887780	2369887	C	6.11×10 ⁻⁰³	0.90 [0.83-0.97]	1.21×10 ⁻⁰³	0.90 [0.85-0.96]	2.25×10 ⁻⁰⁵	0.90 [0.86-0.95]	CACNA1C
12	rs7965296	2442797	A	4.69×10 ⁻⁰³	1.20 [1.06-1.37]	0.792	1.01 [0.92-1.11]	6.20×10 ⁻⁰²	1.07 [1.00-1.16]	CACNA1C

14	rs2239259	71804589	C	1.16×10^{-03}	1.19 [1.07-1.32]	0.647	1.02 [0.94-1.10]	1.95×10^{-02}	1.08 [1.01-1.15]	RGS6
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The position is based on the NCBI Genome browser build 36.1. A1, minor allele name (based on the whole sample); P, p-value; OR, odds ratio for A1; CI, confidence interval. rs2239547 was not available in our GWAS sample.