

Supplementary Table 1: Replication results in the UK Biobank for all three-depression outcomes (broad depression, probable MDD and ICD-coded MDD)¹ for the 22 genome-wide significant SNPs from bivariate discovery meta-analyses.

gSNP	A1	A2	Chr	Position/ Ch37/hg19	EAF	Imputation accuracy	Broad depression			Probable MDD			ICD-coded MDD		
							Beta	SE	P-value (2-sided)	Beta	SE	P-value (2-sided)	Beta	SE	P-value (2-sided)
rs12407717	T	C	1	30426014	0.13	0.998	-0.0016	0.0018	3.64x10 ⁻¹	-0.0022	0.0019	2.47x10 ⁻¹	-7.29 x10 ⁻⁴	8.71 x10 ⁻⁴	4.03x10 ⁻¹
rs12128108	T	C	1	50293421	0.23	1.000	0.0021	0.0014	1.33x10 ⁻¹	0.0010	0.0015	5.07x10 ⁻¹	5.37 x10 ⁻⁴	6.91 x10 ⁻⁴	4.37x10 ⁻¹
rs2422320	T	C	1	73293332	0.43	0.997	-0.0048	0.0012	7.32x10⁻⁵	-0.0028	0.0013	3.11x10⁻²	-0.0010	5.92 x10 ⁻⁴	8.81x10 ⁻²
rs2318763	A	G	1	150115974	0.17	0.999	0.0015	0.0016	3.37x10 ⁻¹	0.0027	0.0017	1.10x10 ⁻¹	0.0010	7.77 x10 ⁻⁴	1.91x10 ⁻¹
rs16836940	A	G	1	150416913	0.22	1.000	7.64x10 ⁻⁴	0.0014	5.91x10 ⁻¹	4.66x10 ⁻⁴	0.0016	7.64x10 ⁻¹	1.22 x10 ⁻⁴	7.01 x10 ⁻⁴	8.62x10 ⁻¹
rs7597593	T	C	2	185533580	0.62	0.998	0.0025	0.0012	4.28x10⁻²	0.0024	0.0013	7.05x10 ⁻²	0.0013	6.00 x10 ⁻⁴	2.58x10⁻²
rs2535629	A	G	3	52833219	0.33	1.000	-0.0031	0.0013	1.32x10⁻²	-0.0008	0.0014	5.79x10 ⁻¹	-7.23 x10 ⁻⁴	6.18 x10 ⁻⁴	2.43x10 ⁻¹
rs1966136	A	C	3	61153578	0.41	1.000	-0.0039	0.0012	1.29x10⁻³	-0.0004	0.0013	7.87x10 ⁻¹	-4.47 x10 ⁻⁴	5.91 x10 ⁻⁴	4.49x10 ⁻¹
rs7714851	T	C	5	164475774	0.52	1.000	-0.0057	0.0012	1.07x10⁻⁶	-0.0021	0.0013	1.03x10 ⁻¹	-0.0014	5.82 x10 ⁻⁴	1.31x10⁻²
rs911186	A	G	6	27150599	0.23	1.000	0.0040	0.0014	3.99x10⁻³	0.0019	0.0015	2.18x10 ⁻¹	7.56 x10 ⁻⁴	6.92 x10 ⁻⁴	2.75x10 ⁻¹
rs2894052 ^A	C	G	6	30938128	0.14	0.999	0.0044	0.0017	9.50x10⁻³	0.0029	0.0019	1.18x10 ⁻¹	0.0019	0.0008	2.48x10⁻²
rs1265099	A	G	6	31105413	0.41	1.000	0.0030	0.0012	1.38x10⁻²	8.06x10 ⁻⁴	0.0013	5.40x10 ⁻¹	5.21 x10 ⁻⁴	5.93 x10 ⁻⁴	3.79x10 ⁻¹
rs389883	T	G	6	31947460	0.68	1.000	0.0051	0.0013	4.73x10⁻⁵	0.0026	0.0014	5.91x10 ⁻²	0.0016	6.23 x10 ⁻⁴	1.00x10⁻²
rs4976976	A	G	8	143311653	0.40	0.999	-0.0016	0.0012	1.85x10 ⁻¹	-0.0016	0.0013	2.31x10 ⁻¹	-6.31 x10 ⁻⁴	5.94 x10 ⁻⁴	2.88x10 ⁻¹
rs2026194	T	C	9	85082899	0.24	1.000	0.0037	0.0014	7.24x10⁻³	0.0029	0.0015	5.46x10 ⁻²	1.89 x10 ⁻⁴	6.76 x10 ⁻⁴	7.80x10 ⁻¹
rs4765914	T	C	12	2420377	0.79	0.997	0.0025	0.0014	8.48x10 ⁻²	0.0012	0.0016	4.35x10 ⁻¹	-2.94 x10 ⁻⁴	7.16 x10 ⁻⁴	6.82x10 ⁻¹
rs10774037	A	G	12	2420526	0.79	0.997	-0.0025	0.0015	8.95x10 ⁻²	-0.0014	0.0016	3.91x10 ⁻¹	2.80 x10 ⁻⁴	7.17 x10 ⁻⁴	6.96x10 ⁻¹
rs2182139	T	C	14	60149233	0.75	1.000	0.0040	0.0014	3.71x10⁻³	0.0010	0.0015	4.94x10 ⁻¹	4.88 x10 ⁻⁴	6.74 x10 ⁻⁴	4.70x10 ⁻¹
rs9323497	T	C	14	67873128	0.05	0.998	5.96x10 ⁻⁴	0.0027	8.24x10 ⁻¹	-0.0014	0.0029	6.30x10 ⁻¹	-0.0016	0.0013	2.21x10 ⁻¹
rs4906335	A	C	14	104021141	0.28	0.998	0.0042	0.0013	1.45x10⁻³	0.0033	0.0014	2.18x10⁻²	-5.96 x10 ⁻⁵	6.51 x10 ⁻⁴	9.27x10 ⁻¹
rs4843613	T	C	16	87489698	0.83	0.999	0.0026	0.0016	8.96x10 ⁻²	-0.0011	0.0017	5.25x10 ⁻¹	-4.91 x10 ⁻⁴	7.68 x10 ⁻⁴	5.22x10 ⁻¹
rs9951150	A	G	18	52821124	0.46	0.999	-0.0031	0.0012	9.27x10⁻³	-5.46x10 ⁻⁴	0.0013	6.74x10 ⁻¹	-3.77 x10 ⁻⁴	5.85 x10 ⁻⁴	5.19x10 ⁻¹

Abbreviations: A1, effect allele; A2, other allele; EAF, effect allele frequency

Replication p-values < 0.05 are **bolded**. Beta effect sizes and standard errors are reported on the 0-1 scale

^A Proxy for rs9368649 with r²=1