

Table 1. Top *cis* - and *trans* -eQTL effects of depression- and Alzheimer's-associated SNPs.

The 10 most significant SNP–gene interactions extracted from MetaBrain[32] are shown.

	HGNCName	PValue	SNPName	ProbeName	SNP Type	Allele Assessed	Overall ZScore	Chr.	BasePosition	FDR	Found InProx
<i>AD cis-eQTL</i>											
	CR1	6.14x10 ⁻¹³⁹	rs3818361	ENSG00000203710.11	G/A	A	25.0917515	1	207611623	0	Y
	CR1	2.35x10 ⁻¹³⁷	rs6656401	ENSG00000203710.11	G/A	A	24.9462086	1	207518704	0	Y
	ZNF284	2.79x10 ⁻²⁵	rs2061333	ENSG00000186026.7	T/C	C	-10.3884106	19	44110055	0	N
	CR2	8.13x10 ⁻²³	rs3818361	ENSG00000117322.17	G/A	A	9.8329847	1	207611623	0	Y
	IL17RC	1.03x10 ⁻²¹	rs1552244	ENSG00000163702.20	A/G	G	-9.5738314	3	10093893	0	N
	MRPL39	6.39x10 ⁻²¹	rs2298369	ENSG00000154719.13	C/G	C	-9.383293	21	25583969	0	Y
	CR2	1.06x10 ⁻¹⁹	rs6656401	ENSG00000117322.17	G/A	A	9.082746	1	207518704	0	Y
	MUC6	4.68x10 ⁻¹⁶	rs10794342	ENSG00000184956.16	C/T	C	8.1197985	11	924904	0	N
	CEACAM19	2.52x10 ⁻¹⁵	rs8103315	ENSG00000186567.13	C/A	A	7.912609	19	44750911	0	Y
	SRA1	6.67x10 ⁻¹⁵	rs11168036	ENSG00000213523.10	T/G	T	-7.7904846	5	140327854	0	N
<i>Dep cis-eQTL</i>											
	GSDME	6.07x10 ⁻¹²³	rs2721811	ENSG00000105928.16	A/G	G	23.5809379	7	24709810	0	Y
	PCDHA8	7.23x10 ⁻⁸⁸	rs3806843	ENSG00000204962.6	T/C	T	19.8713492	5	140832953	0	N
	PCDHA13	1.45x10 ⁻⁷¹	rs3806843	ENSG00000239389.8	T/C	T	-17.888582	5	140832953	0	N
	PCDHA10	8.73x10 ⁻⁶¹	rs3806843	ENSG00000250120.8	T/C	T	16.4477652	5	140832953	0	N
	ZSCAN31	4.47x10 ⁻⁵⁸	rs853679	ENSG00000235109.7	C/A	A	16.0652087	6	28329086	0	Y
	GMPPB	4.76x10 ⁻⁵⁴	rs13084037	ENSG00000173540.12	A/G	G	15.4796759	3	49176633	0	N
	AMT	1.48x10 ⁻⁵²	rs13084037	ENSG00000145020.15	A/G	G	-15.2568199	3	49176633	0	Y
	PCDHA7	2.18x10 ⁻⁴⁶	rs3806843	ENSG00000204963.6	T/C	T	14.3005182	5	140832953	0	N
	AREL1	5.42x10 ⁻⁴⁶	rs1045430	ENSG00000119682.17	T/G	T	14.2368404	14	74663532	0	Y
	SPPL3	4.62x10 ⁻⁴³	rs3213572	ENSG00000157837.16	G/A	A	-13.7568749	12	120767275	0	Y
<i>AD trans-eQTL</i>											
	AFF3	3.25x10 ⁻⁰⁷	rs6857	ENSG00000144218.19	C/T	T	-5.108585	19	44888997	0	N
<i>Dep trans-eQTL</i>											
	NPR3	6.24x10 ⁻¹⁵	rs3823612	ENSG00000113389.16	G/C	C	7.7991773	7	12219129	0	N
	NPR3	1.26x10 ⁻¹⁴	rs2043539	ENSG00000113389.16	G/A	A	7.7098298	7	12214254	0	N
	NPR3	5.05x10 ⁻¹²	rs10950398	ENSG00000113389.16	G/A	A	6.9043607	7	12225245	0	N
	SMAD4	5.73x10 ⁻¹¹	rs10950398	ENSG00000141646.13	G/A	A	6.5507623	7	12225245	0	N
	DSTYK	1.27x10 ⁻¹⁰	rs10950398	ENSG00000133059.17	G/A	A	6.4302364	7	12225245	0	N
	NR4A2	1.69x10 ⁻¹⁰	rs10950398	ENSG00000153234.14	G/A	A	-6.3868337	7	12225245	0	Y
	KCND3	3.56x10 ⁻¹⁰	rs2043539	ENSG00000171385.9	G/A	A	6.2725143	7	12214254	0	N
	KCND3	5.65x10 ⁻¹⁰	rs3823612	ENSG00000171385.9	G/C	C	6.1999724	7	12219129	0	N
	CHRNA2	9.22x10 ⁻¹⁰	rs10950398	ENSG00000120903.13	G/A	A	6.1224055	7	12225245	0	N
	KCND3	3.33x10 ⁻⁰⁹	rs10950398	ENSG00000171385.9	G/A	A	5.9146398	7	12225245	0	N

FoundInProx refers to the identification of the gene through classical GWAS and proximity analysis.

Note that genes annotated No (N) in this column might have previously been implicated in either disease but through other means.