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1. Supplemental figures

Figure S1. QQ plot of the primary (A) and restricted (B) cross-disorder meta-analyses.

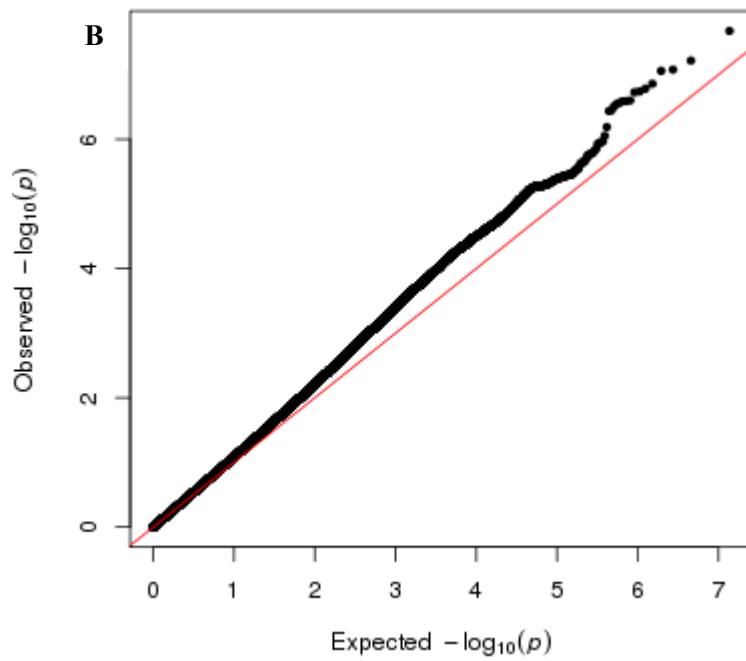
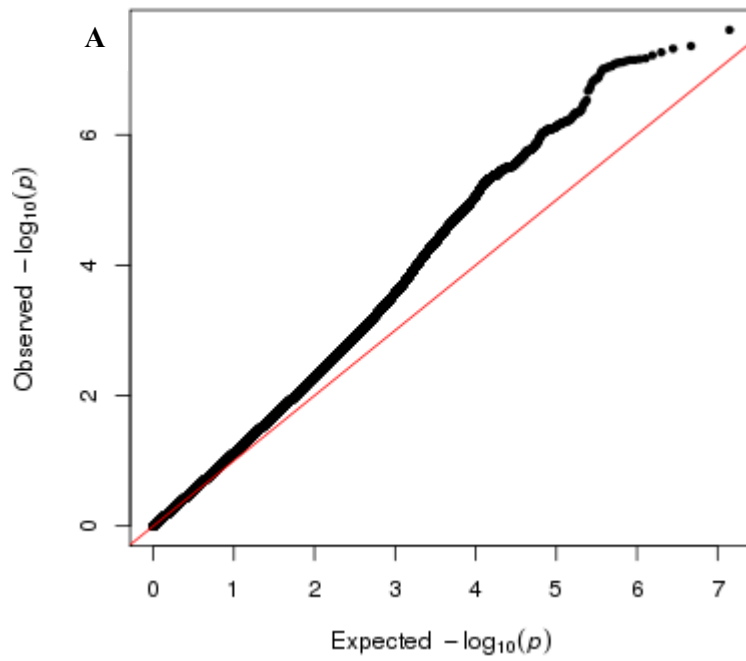


Figure S2. Manhattan plot of the primary (A) and restricted (B) BPD meta-analyses. Only SNPs with p values ≤ 0.05 are shown; Horizontal lines show threshold for genome-wide significance ($p < 5 \times 10^{-8}$ in red) and suggestive association ($p < 1 \times 10^{-6}$ in blue).

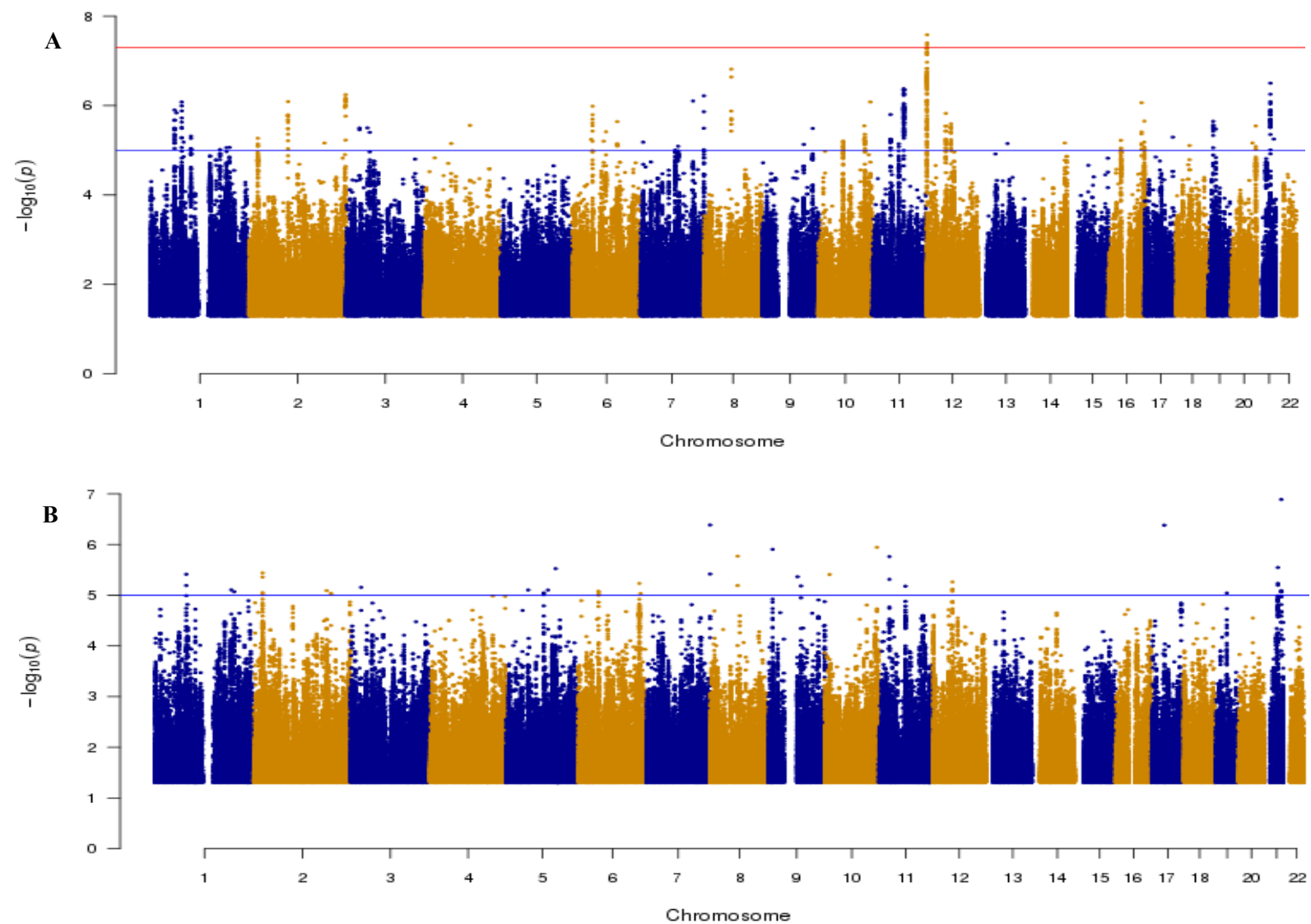
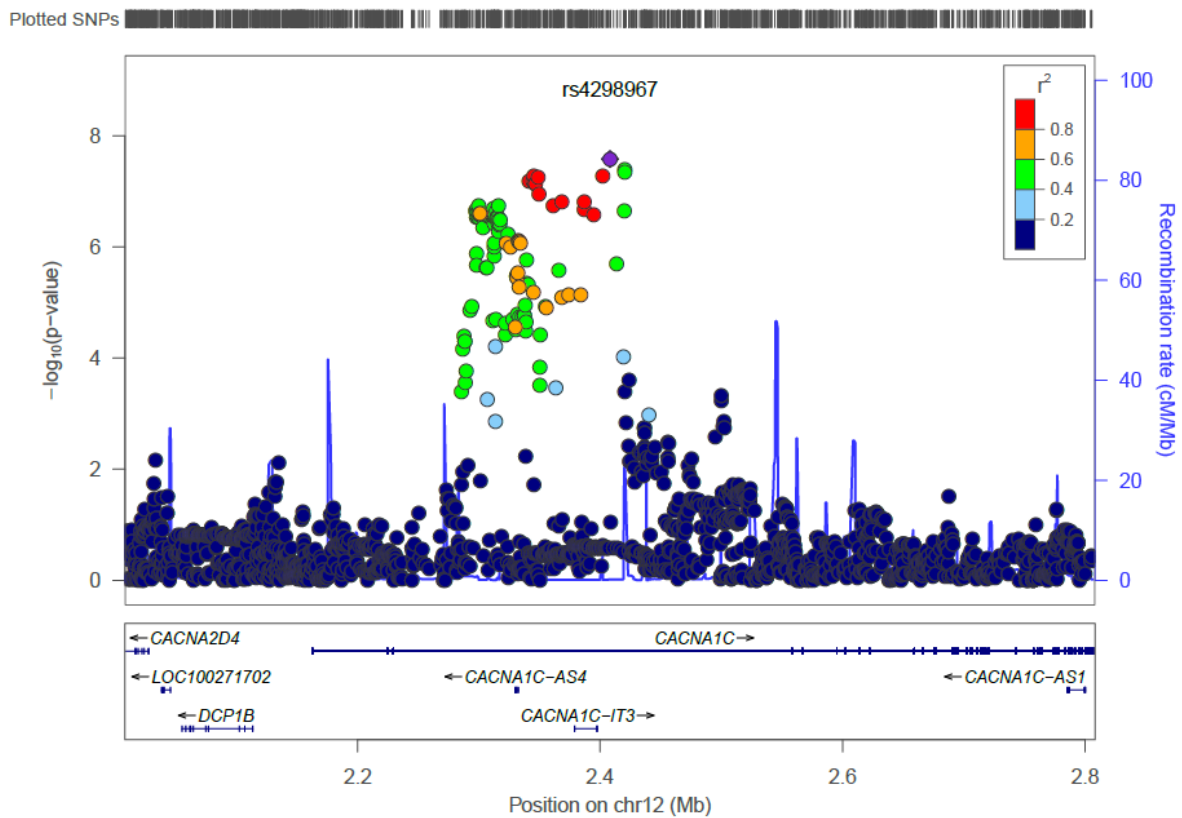


Figure S3. Regional plot for genome-wide significant locus on chromosome 12 for the primary BPD meta-analysis.



Results are shown as $-\log(p\text{-value})$ for genotyped and imputed SNPs. The SNP showing strongest association is shown in the purple circle. The color of the remaining markers reflects r^2 of the strongest associated SNP. The recombination rate is plotted in blue.

Figure S4. Manhattan plot of ADHD meta-analysis. Horizontal line shows threshold for suggestive association ($p < 1 \times 10^{-6}$).

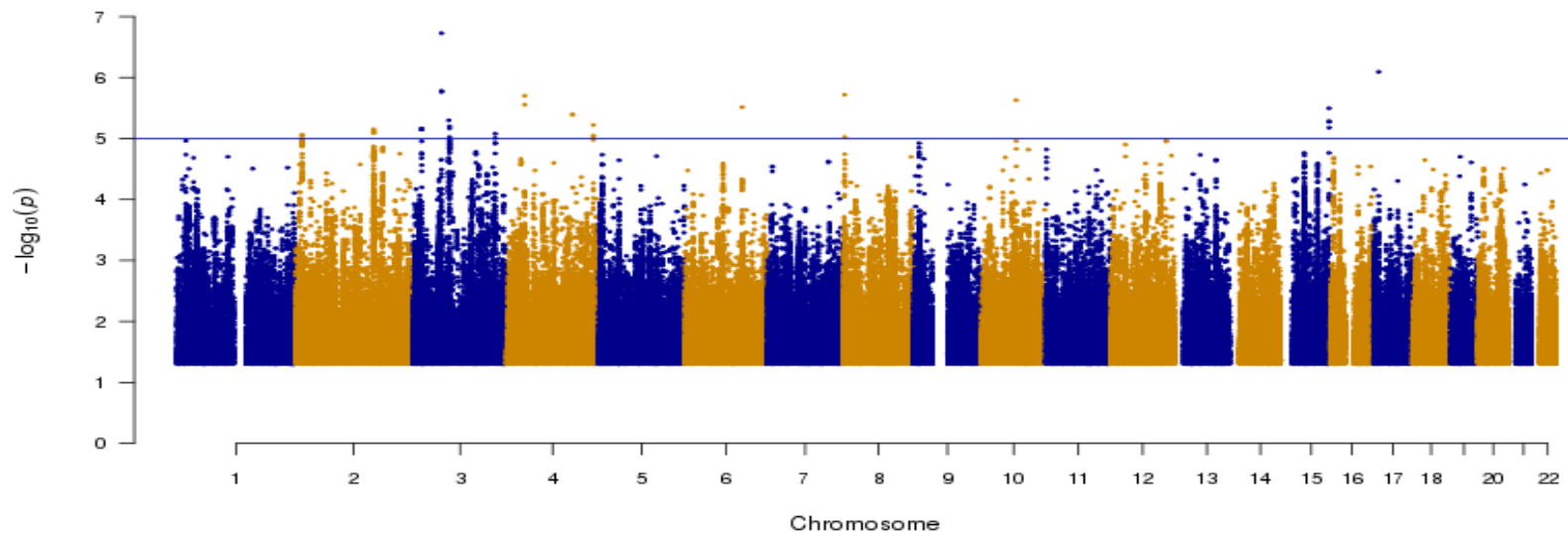


Figure S5. Forest plots of markers reaching genome-wide significance in cross-disorder analyses; the contribution of results from individual GWAS to disorder-specific meta-analyses is shown.

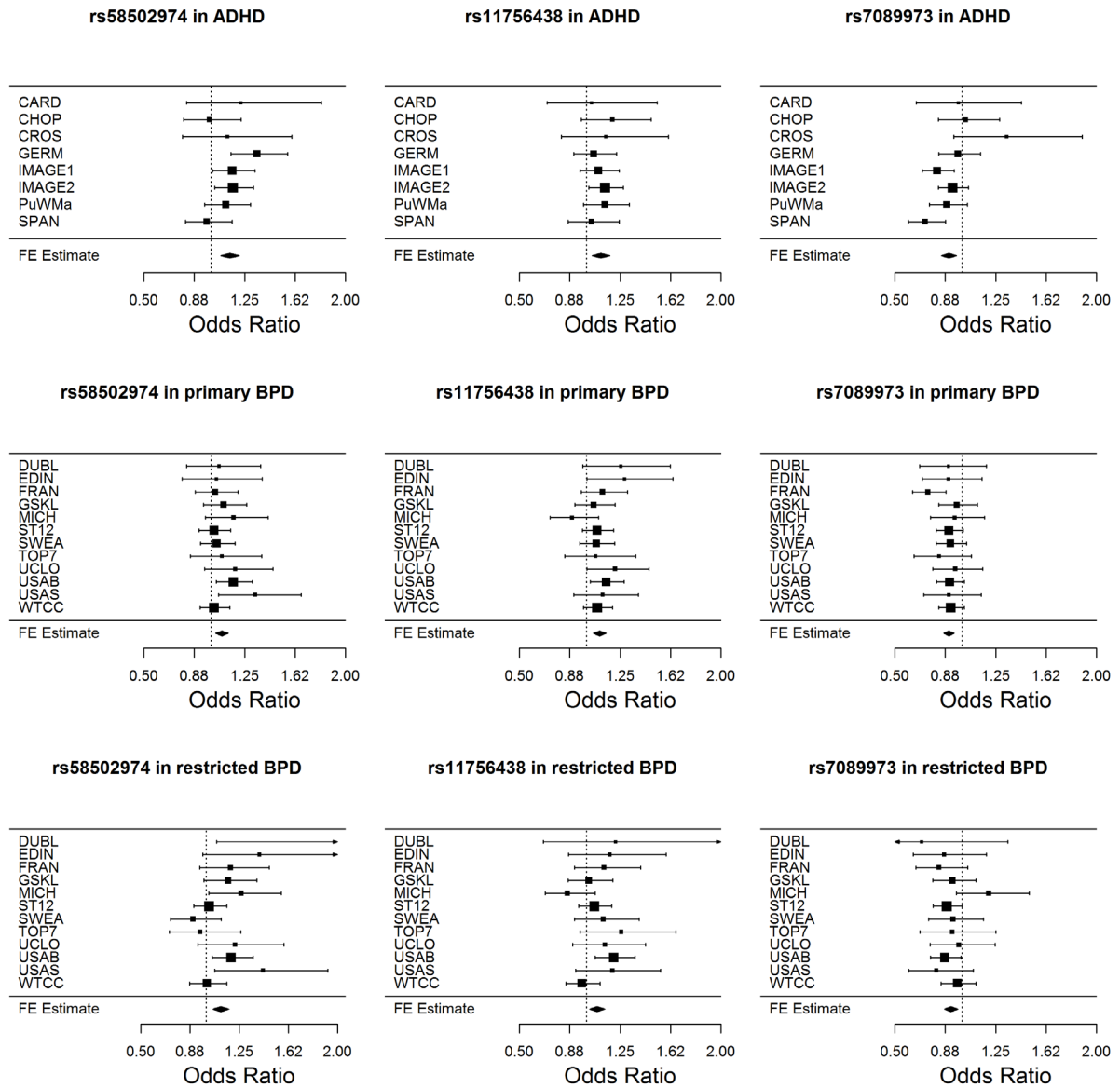


Table S1a. Description of individual study sample data contributions and genotyping platforms for studies included in the ADHD meta-analysis.

Study name		Study design	Ancestry	Cases (N)	Controls (N)	Genotyping platform	Reference^a
Short	Full sample name						
CARD	Cardiff University	Case/control	Caucasian	641	1,752	Illumina Human660W-Quad BeadChip (ADHD cases) and Illumina Human 1.2M BeadChip (controls)	[1]
GERM	ADHD patient sample consisted of children and adolescents Aachen, Cologne, Essen, Marburg, Regensburg, and Würzburg	Case/control	Caucasian	494	1,297	Illumina Human660W-Quadv1(ADHD cases) and Illumina HumanHap550v3 (controls)	[2]
IMAGE2	Phase II of IMAGE	Case/control	Predominantly European origin	787	2,942	Affymetrix 5.0 array (ADHD cases) and Affymetrix 6.0 array (controls)	[3]
SPAN	Hospital Universitari Vall d'Hebron, Barcelona	Case/control	Caucasian	591	432	Illumina HumanOmni1-Quad BeadChip platform	[4]
CHOP	Children's Hospital of Philadelphia	Trio	European descent	358		Illumina Infinium II HumanHap550 BeadChip	[5]
CROS	Canadian sample (SickKids)	Trio	Mainly Caucasian	170		Affymetrix 6.0 array	[6]
IMAGE1	Phase I of the International Multisite ADHD Genetics Project	Trio	Western European origin	866		Perlegen Sciences 600 K	[7]
PuWMa	Pfizer funded study from the University of California, Los Angeles, Washington University and the Massachusetts General Hospital	Trio	Mainly Caucasian	702		Illumina Human1M or Human1M-Duo BeadChip platform	[8]
TOTAL				4,609	8,519^b		

^a Primary publication reporting individual study sample. ^b Including 2,096 pseudocontrols.

Table S1b. Description of individual study sample data contributions and genotyping platforms for studies included in the BPD meta-analysis.

Short	Study name		Ancestry	Cases (N) (Cases in restricted sample between brackets)	Controls (N)	Genotyping platform	Reference ^a
	Full sample name	Study design					
DUBL	Trinity College Dublin	Case/control	Irish	150 (26)	796	Affymetrix 500K, 5.0 and 6.0	[9]
EDIN	University of Edinburgh	Case/control	Scottish	282 (141)	275	Affymetrix 500K Illumina	[10] [11]
FRAN	French	Case/control	French	451 (198)	1631	HumanHap300, HumanHap550, Human610-Quad Illumina	[12]
GSKL	GlaxoSmithKline	Case/control	British/Canadian/Scottish	745 (510)	903	HumanHap550 Illumina	[10]
MICH	NIMH/Pritzker	Case/control	European/American	723 (471)	533	HumanHap550 Illumina	[10]
ST12	Systemic Treatment Enhancement Program for Bipolar Disorder (STEP1 and STEP2)	Case/control	European-American	1574 (1150)	1416	Affymetrix 500K	[10]
SWEA	Stockholm	Case/control	Swedish	789 (201)	2041	Affymetrix 5.0 and 6.0	[13]
TOP7	Thematically Organized Psychosis	Case/control	Norwegian	407 (213)	221	Affymetrix 6.0	[14]
UCLO	University College London	Case/control	British	465 (227)	494	Affymetrix 500K	[10]
USAB	Intermittent WAVE2 sample B	Case/control	European/American	1922 (1059)	1100	Affymetrix 6.0	--
USAS	Intermittent WAVE2 sample S	Case/control	European/American	435 (209)	500	Affymetrix 6.0	--
WTCC	Welcome Trust Case-Control Consortium	Case/control	British	1712 (762)	2934	Affymetrix 500K	[15]
TOTAL				9,650 (5,167)	12,844		

Table S2. Results and sample sizes of previous LDSR analyses.

Trait 1	Trait 2	Heritability (trait 2)	SE_{h2}	RG	SE_{rg}	Z	P-value
ADHD	BPD*	0.431	0.039	0.404	0.151	26.792	0.007
BPD full sample	ADHD [†]	0.278	0.112	0.262	0.140	18.695	0.061
BPD age restricted	ADHD [†]	0.260	0.110	0.271	0.195	13.902	0.164

Trait1: Input information from the ADHD and BPD samples used in this paper; **Trait 2:** Input information from: *Bipolar Disease sample from PGC BIP working group 2011, N=16,731; [†]ADHD sample from Neale 2010[3], N=5,422; **heritability (trait 2):** Observed SNP-based heritability of trait 2 (univariate); **SE_{h2}:** Standard error of the observed SNP-based heritability of trait 2; **RG:**genetic correlation between trait 1 and trait 2; **SE_{rg}:**Standard error of the estimated genetic correlation between trait 1 and trait 2; **Z:**Z-score of genetic correlation between trait 1 and trait 2; **P-value:** P-value estimated for genetic correlation between trait 1 and trait 2.

Table S3. Association p-values $<10^{-6}$ of the Primary Cross disorder meta-analysis and the corresponding p-values for the Restricted Cross disorder MA, Primary BDP MA, Restricted BDP MA and the ADHD MA.

SNP	CHR	BP	P		P		P		Gene
			Primary cross MA	Restricted cross MA	Primary BDP MA	Restricted BDP MA	ADHD MA		
rs7089973	10	116569565	2,47E-08	1,12E-05	2,14E-03	4,39E-06	1,56E-03	TAF9BP2	
rs11756438	6	118993632	4,36E-08	1,31E-05	5,29E-03	1,85E-05	6,14E-04	CEP85L	
rs11756440	6	118993642	4,79E-08	1,43E-05	5,29E-03	1,85E-05	6,81E-04	CEP85L	
rs17794346	10	116643095	5,45E-08	2,35E-05	4,77E-03	1,10E-05	1,38E-03	TAF9BP2	
rs1334489	6	118639387	6,06E-08	7,25E-06	1,72E-02	1,77E-04	4,65E-05	CEP85L	
rs55711292	10	116604870	6,75E-08	4,05E-05	3,54E-03	5,13E-06	3,73E-03	TAF9BP2	
rs2093369	6	118649044	6,94E-08	9,69E-06	2,05E-02	1,88E-04	5,08E-05	CEP85L	
rs36089581	10	116623059	7,13E-08	3,46E-05	3,42E-03	6,26E-06	3,26E-03	TAF9BP2	
rs7772845	6	118646016	7,14E-08	1,01E-05	2,09E-02	1,90E-04	5,20E-05	CEP85L	
rs749649	10	116641999	7,36E-08	3,20E-05	3,57E-03	7,50E-06	2,82E-03	TAF9BP2	
rs6911339	6	118653621	7,72E-08	1,01E-05	2,08E-02	2,02E-04	5,26E-05	CEP85L	
chr6_118642268_D	6	118642268	7,84E-08	9,16E-06	1,63E-02	1,68E-04	7,10E-05	CEP85L	
rs17721283	10	116644141	7,95E-08	3,28E-05	3,17E-03	6,87E-06	3,33E-03	TAF9BP2	
rs6906332	6	118653336	8,27E-08	1,15E-05	2,24E-02	2,08E-04	5,53E-05	CEP85L	
rs12775180	10	116639754	8,92E-08	3,78E-05	4,21E-03	9,16E-06	2,81E-03	TAF9BP2	
rs6911035	6	118653705	8,98E-08	1,29E-05	2,33E-02	2,11E-04	6,00E-05	CEP85L	
rs12771956	10	116576228	9,37E-08	4,66E-05	5,52E-03	1,04E-05	2,59E-03	TAF9BP2	
rs68085797	10	116632130	9,70E-08	4,31E-05	3,28E-03	6,39E-06	4,35E-03	TAF9BP2	
rs61867966	10	116584362	9,76E-08	5,27E-05	4,30E-03	6,97E-06	4,02E-03	TAF9BP2	
rs12772800	10	116630962	1,05E-07	5,23E-05	3,68E-03	6,32E-06	4,75E-03	TAF9BP2	
rs34096808	3	173540106	1,22E-07	7,82E-05	1,91E-02	3,31E-05	1,01E-03	NLGN1	
rs35157674	3	173494503	1,37E-07	4,94E-05	6,10E-03	1,58E-05	2,52E-03	NLGN1	
rs58502974	5	7755900	1,39E-07	2,11E-08	2,34E-04	6,74E-04	1,85E-05	ADCY2	
rs11750832	5	7756170	1,42E-07	6,07E-08	4,64E-04	5,57E-04	2,65E-05	ADCY2	
rs10489744	1	165380623	1,52E-07	7,25E-06	2,46E-03	4,84E-05	8,36E-04	RXRG	
rs2134095	1	165377552	1,60E-07	6,91E-06	2,59E-03	5,63E-05	7,42E-04	RXRG	
chr2_188776397_I	2	188776397	1,87E-07	4,80E-05	2,03E-03	6,88E-06	8,09E-03	ds LINC01090	
rs7706982	5	7758622	2,06E-07	8,39E-08	6,26E-04	7,60E-04	2,63E-05	ADCY2	
rs4380617	5	7758961	2,14E-07	8,75E-08	6,29E-04	7,68E-04	2,73E-05	ADCY2	
rs34187191	10	116644972	2,93E-07	7,75E-05	8,05E-03	2,96E-05	2,93E-03	TAF9BP2	
rs968847	10	116758079	3,11E-07	4,12E-06	3,82E-04	2,77E-05	3,35E-03	TAF9BP2	
chr10_116769011_D	10	116769011	3,29E-07	4,32E-06	4,68E-04	3,38E-05	2,88E-03	TAF9BP2	
rs3767339	1	165378064	3,45E-07	9,46E-06	4,03E-03	1,37E-04	6,19E-04	RXRG	
rs7711377	5	7772199	3,82E-07	2,87E-07	4,82E-04	4,16E-04	1,47E-04	ADCY2	
rs7700884	5	7779142	4,25E-07	3,12E-07	6,20E-04	5,24E-04	1,19E-04	ADCY2	
rs11162556	1	79261383	4,27E-07	1,62E-06	3,86E-06	1,90E-06	4,29E-02	us ADGRL4	
chr6_118801236_D	6	118801236	4,51E-07	4,15E-06	4,66E-02	4,29E-03	3,06E-06	CEP85L	
rs11153768	6	118988152	4,54E-07	2,55E-05	7,02E-03	1,23E-04	9,39E-04	CEP85L	
rs2078383	6	118706643	4,62E-07	1,17E-05	6,25E-03	2,32E-04	4,25E-04	CEP85L	
rs10872167	6	118988362	4,62E-07	2,53E-05	7,22E-03	1,30E-04	9,03E-04	CEP85L	
rs7703532	5	7756316	4,69E-07	1,65E-07	4,79E-04	7,67E-04	8,17E-05	ADCY2	
rs12661338	6	118794690	4,71E-07	1,86E-05	9,87E-03	2,51E-04	3,90E-04	CEP85L	
rs72836518	10	116763984	5,24E-07	7,79E-06	6,06E-04	3,88E-05	4,09E-03	TAF9BP2	
rs4235588	5	7756917	5,44E-07	1,88E-07	5,19E-04	8,43E-04	8,59E-05	ADCY2	
chr10_116764076_D	10	116764076	5,45E-07	7,92E-06	6,02E-04	3,95E-05	4,19E-03	TAF9BP2	
rs12774597	10	116755682	5,72E-07	8,80E-06	6,98E-04	4,29E-05	4,04E-03	TAF9BP2	
rs4072341	5	7757705	5,97E-07	1,38E-07	6,86E-04	1,40E-03	4,22E-05	ADCY2	
rs9608816	22	30216900	5,97E-07	2,01E-05	1,27E-03	3,47E-05	5,25E-03	ASCC2	
rs17427116	6	118986198	5,98E-07	3,08E-05	8,54E-03	1,65E-04	9,12E-04	CEP85L	
chr10_116760754_D	10	116760754	6,17E-07	2,65E-06	2,16E-04	5,06E-05	3,68E-03	TAF9BP2	
rs11153730	6	118667522	6,20E-07	9,15E-05	4,99E-02	4,70E-04	2,33E-04	CEP85L	
rs34453431	10	116759683	6,28E-07	9,64E-06	6,65E-04	4,12E-05	4,65E-03	TAF9BP2	
rs72958930	6	118983681	6,39E-07	3,33E-05	8,70E-03	1,67E-04	9,75E-04	CEP85L	
rs35029749	6	118892120	6,44E-07	2,25E-05	9,32E-03	2,63E-04	5,43E-04	CEP85L	
rs72952795	6	118894271	6,53E-07	2,29E-05	9,29E-03	2,61E-04	5,59E-04	CEP85L	
rs12761122	10	116753548	6,59E-07	3,52E-06	2,58E-04	4,85E-05	4,13E-03	TAF9BP2	
rs11968176	6	118900940	6,60E-07	2,22E-05	9,27E-03	2,71E-04	5,38E-04	CEP85L	
rs4945623	6	118980556	6,70E-07	3,36E-05	8,74E-03	1,73E-04	9,82E-04	CEP85L	
rs17795212	10	116753297	6,71E-07	9,54E-06	7,47E-04	4,97E-05	4,10E-03	TAF9BP2	
rs7097580	10	116754502	6,73E-07	5,60E-06	7,27E-04	8,12E-05	2,42E-03	TAF9BP2	
chr6_118978895_D	6	118978895	6,93E-07	3,47E-05	9,05E-03	1,80E-04	9,75E-04	CEP85L	
rs3935156	5	7757812	6,98E-07	2,52E-07	7,39E-04	1,11E-03	7,74E-05	ADCY2	
rs72967533	6	118655020	7,09E-07	6,20E-05	3,98E-02	5,81E-04	2,05E-04	CEP85L	
rs11752928	6	118977768	7,16E-07	3,47E-05	9,06E-03	1,86E-04	9,74E-04	CEP85L	
rs2356497	6	118876539	7,25E-07	2,07E-05	9,25E-03	3,15E-04	4,91E-04	CEP85L	
rs4072339	5	7758039	7,26E-07	2,59E-07	7,46E-04	1,14E-03	7,91E-05	ADCY2	
rs4072340	5	7757867	7,40E-07	2,73E-07	7,46E-04	1,11E-03	8,40E-05	ADCY2	
rs4479814	5	7757715	7,48E-07	1,83E-07	6,03E-04	1,26E-03	6,88E-05	ADCY2	
rs11758454	6	118848799	7,70E-07	1,63E-05	5,36E-03	2,35E-04	7,80E-04	CEP85L	
rs13061878	3	61620234	7,77E-07	8,79E-05	4,08E-02	4,83E-04	2,60E-04	PTPRG	
chr6_118933064_D	6	118933064	7,81E-07	2,94E-05	1,04E-02	2,76E-04	6,49E-04	CEP85L	
rs78757409	6	118789259	7,88E-07	2,68E-05	1,25E-02	3,68E-04	4,39E-04	CEP85L	
rs16998572	20	52551884	7,90E-07	8,27E-06	4,57E-03	3,72E-04	4,14E-04	ds BCAS1	
rs11967858	6	118835543	7,98E-07	2,58E-05	1,10E-02	3,35E-04	5,09E-04	CEP85L	

rs117344633	6	118837268	8,00E-07	2,67E-05	1,10E-02	3,26E-04	5,30E-04	CEP85L
rs6569024	6	118953374	8,08E-07	3,12E-05	1,15E-02	2,97E-04	6,11E-04	CEP85L
chr6_119001874_D	6	119001874	8,08E-07	8,35E-06	5,29E-04	4,95E-05	5,01E-03	CEP85L
rs34955242	3	173561266	8,19E-07	1,18E-04	7,74E-03	4,78E-05	5,23E-03	NLGN1
rs55892056	6	118995297	8,26E-07	6,09E-05	7,65E-03	1,01E-04	2,39E-03	CEP85L
rs11970286	6	118680374	8,28E-07	4,38E-05	1,76E-02	3,55E-04	4,97E-04	CEP85L
rs6906287	6	118962740	8,28E-07	3,37E-05	1,24E-02	3,09E-04	6,00E-04	CEP85L
rs114951787	6	118839081	8,28E-07	2,89E-05	1,18E-02	3,37E-04	5,29E-04	CEP85L
rs11965985	6	118789834	8,30E-07	2,60E-05	1,19E-02	3,76E-04	4,55E-04	CEP85L
rs151118422	6	118839487	8,30E-07	2,80E-05	1,17E-02	3,47E-04	5,11E-04	CEP85L
rs12135723	1	79196848	8,31E-07	3,54E-05	2,46E-04	5,21E-06	3,61E-02	us ADGRL4
rs11752626	6	118788652	8,34E-07	2,61E-05	1,19E-02	3,78E-04	4,55E-04	CEP85L
rs71420669	2	195851665	8,57E-07	1,56E-05	6,72E-03	3,43E-04	5,65E-04	intergenic
rs36030485	9	2411646	8,71E-07	1,94E-05	4,43E-04	1,91E-05	1,31E-02	LOC105375956
rs56037433	2	162575985	8,73E-07	1,75E-04	2,77E-02	1,59E-04	1,51E-03	SLC4A10
rs4307206	6	118813320	8,77E-07	2,91E-05	1,14E-02	3,40E-04	5,62E-04	CEP85L
rs17825652	6	118788986	8,77E-07	2,71E-05	1,21E-02	3,88E-04	4,68E-04	CEP85L
rs17226667	6	118721628	8,89E-07	2,30E-05	1,13E-02	4,26E-04	4,20E-04	CEP85L
rs17825393	6	118772583	9,10E-07	2,75E-05	1,23E-02	4,03E-04	4,65E-04	CEP85L
rs12246008	10	116761769	9,16E-07	1,27E-05	8,12E-04	5,58E-05	5,07E-03	TAF9BP2
rs17227124	6	118741382	9,17E-07	2,51E-05	1,17E-02	4,20E-04	4,45E-04	CEP85L
chr10_116760251_D	10	116760251	9,18E-07	1,60E-05	1,15E-03	6,19E-05	4,55E-03	TAF9BP2
rs11967375	6	118823975	9,39E-07	3,33E-05	1,25E-02	3,54E-04	5,77E-04	CEP85L
rs968849	10	116757731	9,59E-07	1,20E-05	8,00E-04	6,09E-05	4,85E-03	TAF9BP2
rs11197023	10	116756226	9,67E-07	1,28E-05	8,29E-04	5,97E-05	4,99E-03	TAF9BP2
chr2_195851664_D	2	195851664	9,83E-07	1,16E-05	7,51E-03	5,67E-04	3,35E-04	intergenic

Highlighted lines show genome-wide significant associations ($p < 5 \times 10^{-8}$); ds=downstream; us=upstream.

Table S4. Number of associated eQTLs per gene filtered for $p < 1 \times 10^{-4}$ in primary or restricted CD-GWASMA.

Gene	CD-GWASMA complete	CD-GWASMA restricted
	$p < 1 \times 10^{-4}$	$p < 1 \times 10^{-4}$
<i>ABHD8</i>	0	1
<i>CACNB3</i>	2	0
<i>CASKIN2</i>	0	1
<i>DNPH1</i>	2	2
<i>ENSG00000249624</i>	28	1
<i>FAM26F</i>	0	2
<i>FRK</i>	0	17
<i>IL10RB</i>	9	1
<i>IL10RB-AS1</i>	28	1
<i>LRFN4</i>	40	25
<i>NT5DC1</i>	0	17
<i>NT5DC2</i>	73	16
<i>PRKAR1B</i>	1	1
<i>RPL8</i>	0	1
<i>SLC27A3</i>	0	22
<i>TRIM65</i>	3	0

Table S5. Polymorphisms with allele-specific binding of transcription factors or miRNAs. Neuro-relevant transcription factors are highlighted in bold.

CD-GWASMA	rank	CHR:BP	SNP_ID	Alleles			Nearby Gene	Strand of gene location upstream downstream	SNP Location upstream downstream	Binding Site	
				A	B	p				Allele A	Allele B
restricted	17	1:160044520	rs115077140	T	C	6,47E-07	KCNJ10 KCNJ9	- +	promoter promoter	EVII	VBP
restricted	21	21:43062771	rs4919921	T	C	1,14E-06	LINC001111 LOC105372813	+ +	intergenic promoter	CEBPB	-
restricted	30	10:104605760	rs146504787	A	T	1,98E-06	CYP17A1 PFN1P11 C10orf32	- + +	promoter promoter promoter	ZNF410	-
restricted	71	6:118801236	chr6_118801236_D	AC	Del	4,15E-06	LOC105377968 CEP85L LOC105377971	- + +	promoter intron intron	GMEB2	-
primary	1	10:116569565	rs7089973	A	C	2,47E-08	ABLIM1 FAM160B1	- +	intron promoter	ETS2 , NFAT	-
primary	8	10:116623059	rs36089581	C	G	7,13E-08	FAM160B1 RPL15P13	+ +	UTR-3 promoter	IRX5 , hsa-miR-3668, hsa-miR-4666a-5p	BCL6, hsa-miR-6508-5p, hsa-miR-8067
primary	15	10:116639754	rs12775180	T	C	8,92E-08	FAM160B1 RPL15P17	+ +	intron promoter	SMARCA3	-
primary	19	10:116584362	rs61867966	T	C	9,76E-08	ABLIM1 FAM160B1	- +	promoter intron	GKLF	-
primary	37	6:118801236	chr6_118801236_D	AC	Del	4,51E-07	LOC105377968 CEP85L LOC105377971	- + +	promoter intron intron	GMEB2	-
primary	56	6:118983681	rs72958930	C	G	6,39E-07	CEP85L LOC105377969	+ +	intron promoter	CEBPE_ATF4	-
primary	61	6:118980556	rs4945623	C	G	6,70E-07	CEP85L LOC105377969	+ +	intron promoter	PAX6_HD	PAX4
primary	67	6:118977768	rs11752928	C	G	7,16E-07	CEP85L LOC105377969	+ +	intron promoter	-	HRE , XBPI
primary	75	6:118789259	rs78757409	T	C	7,88E-07	LOC105377968 CEP85L LOC105377971	- + +	promoter intron intron	TCF7	-
primary	78	6:118837268	rs117344633	T	C	8,00E-07	CEP85L LOC105377970 PLN	- + + '	intron intron promoter	-	TEAD4
primary	88	6:118789834	rs11965985	T	C	8,30E-07	LOC105377968 CEP85L LOC105377971	- + +	promoter intron intron	PRE	GRE
primary	91	6:118788652	rs11752626	T	G	8,34E-07	LOC105377968 CEP85L LOC105377971	- + +	promoter intron UTR-5	FOXP1_ES	CAAT , GRHL2
primary	99	6:118772583	rs17825393	T	C	9,10E-07	LOC105377968 CEP85L	- -	promoter intergenic	BLIMP1 , E2F	ZNF217

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