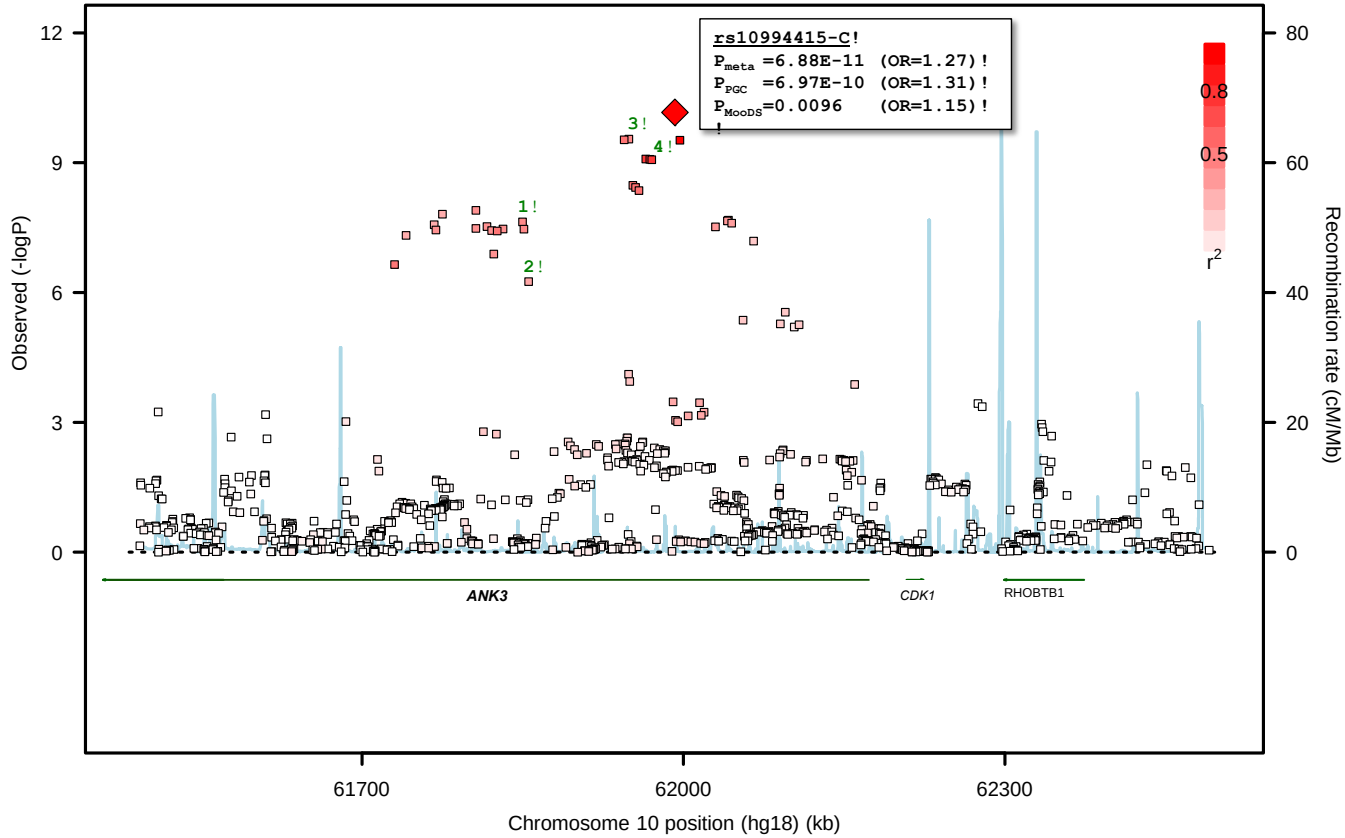
Supplementary Figures

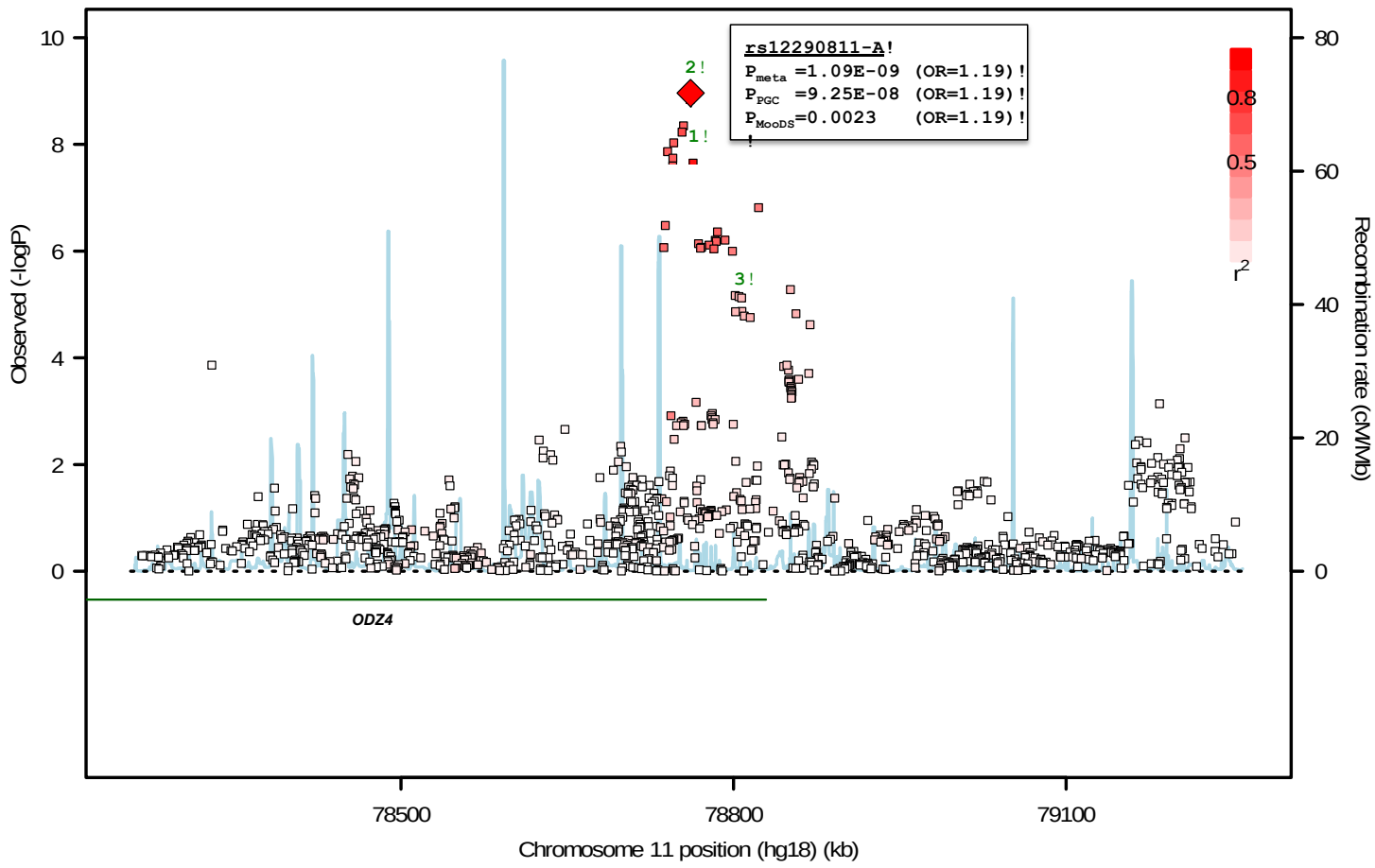
a

1: rs10994336-T: P_{Meta}=2.34E-08 (OR=1.27); P_{PGC}=4.01E-09 (OR=1.35); P_{MooDS}=0.171 (OR=1.11); Ferreira et al. (2008)[1!]
2: rs4948418-T: P_{Meta}=5.60E-07 (OR=1.23); P_{PGC}=7.02E-08 (OR=1.32); P_{MooDS}=0.281 (OR=1.08); Chen et al. (2011)[2!]
3: rs10994397-T: P_{Meta}=2.86E-10 (OR=1.29); P_{PGC}=5.54E-10 (OR=1.35); P_{MooDS}=0.032 (OR=1.17); PGC-BD (2011)[3!]
4: rs1938526-G: P_{Meta}=8.55E-10 (OR=1.27); P_{PGC}=1.85E-09 (OR=1.32); P_{MooDS}=0.034 (OR=1.16); Ferreira et al. (2008)[1!]



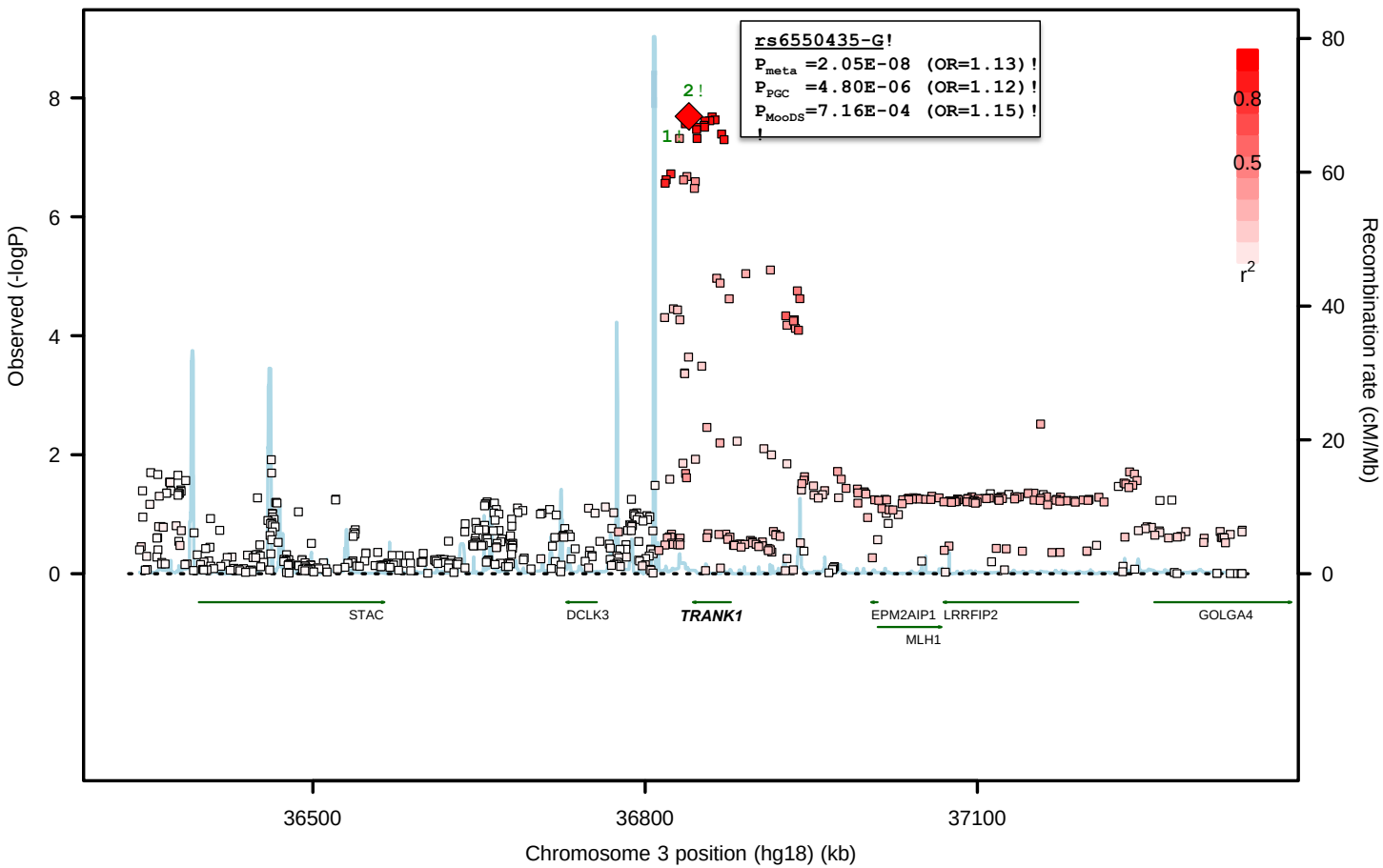
b

1: rs12576775-G: P_{meta}=4.46E-09 (OR=1.17); P_{PGC}=2.66E-08 (OR=1.18); P_{MooDS}=0.0294 (OR=1.13); PGC-BD (2011)[3]; PGC-CD (2013)[4!]
2: rs12290811-A: P_{meta}=1.09E-09 (OR=1.19); P_{PGC}=9.25E-08 (OR=1.19); P_{MooDS}=0.0023 (OR=1.19); Ferreira et al. (2008)[1!]
3: rs2175420-T: P_{meta}=6.77E-06 (OR=1.13); P_{PGC}=7.45E-06 (OR=1.15); P_{MooDS}=0.175 (OR=1.07); PGC-BD (2011)[3!]
!



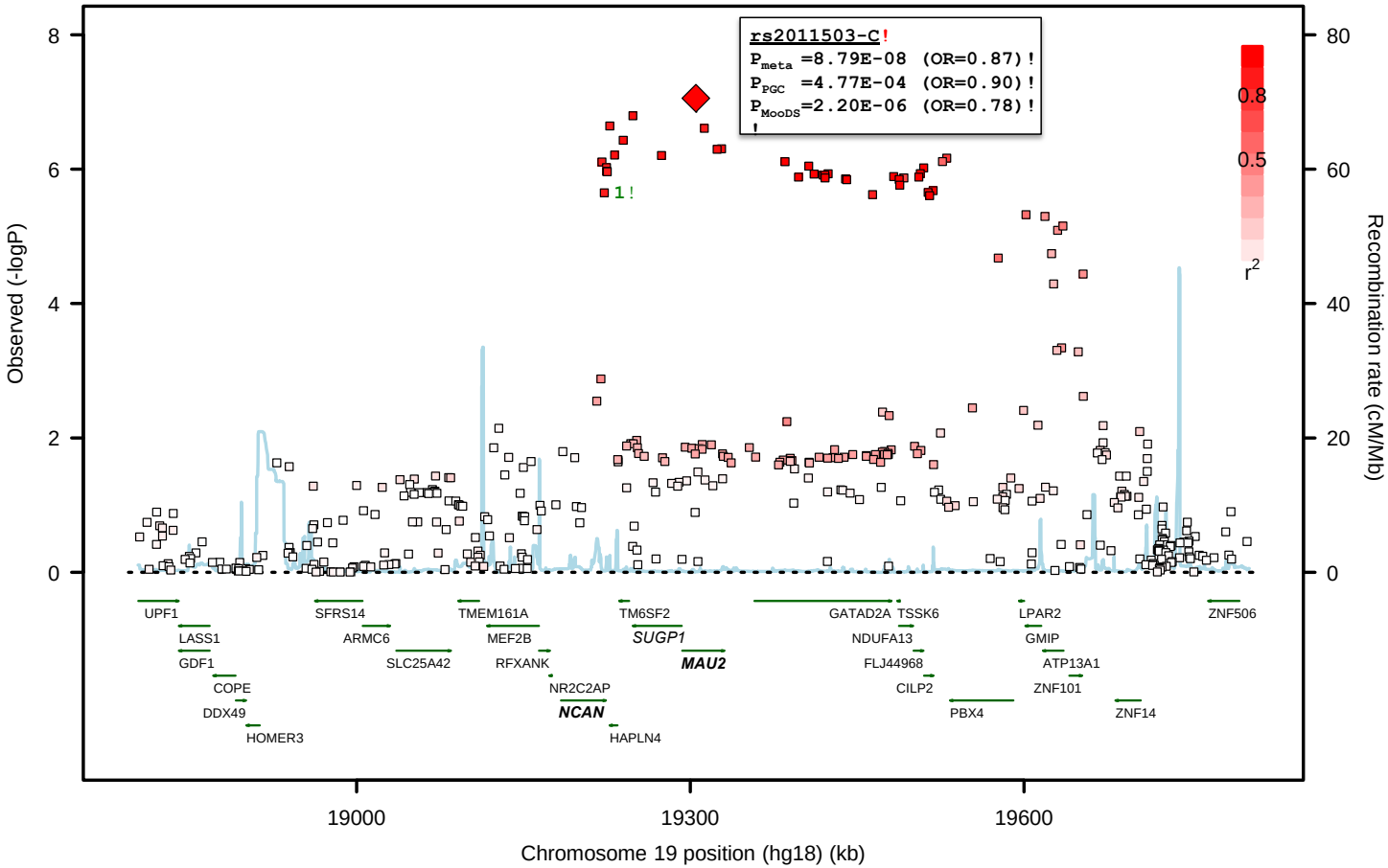
c

1: rs9834970-C: P_{Meta}=4.81E-08 (OR=1.12); P_{PGC}=6.19E-06 (OR=1.11); P_{MooDS}=0.0014 (OR=1.15); Chen et al. (2011)[2]; Goes et al. (2012)[5!]
2: rs6550435-G: P_{Meta}=2.05E-08 (OR=1.13); P_{PGC}=4.80E-06 (OR=1.12); P_{MooDS}=7.16E-04 (OR=1.15); PGC-BD (2011)[3]; Green et al. (2012)[6!]



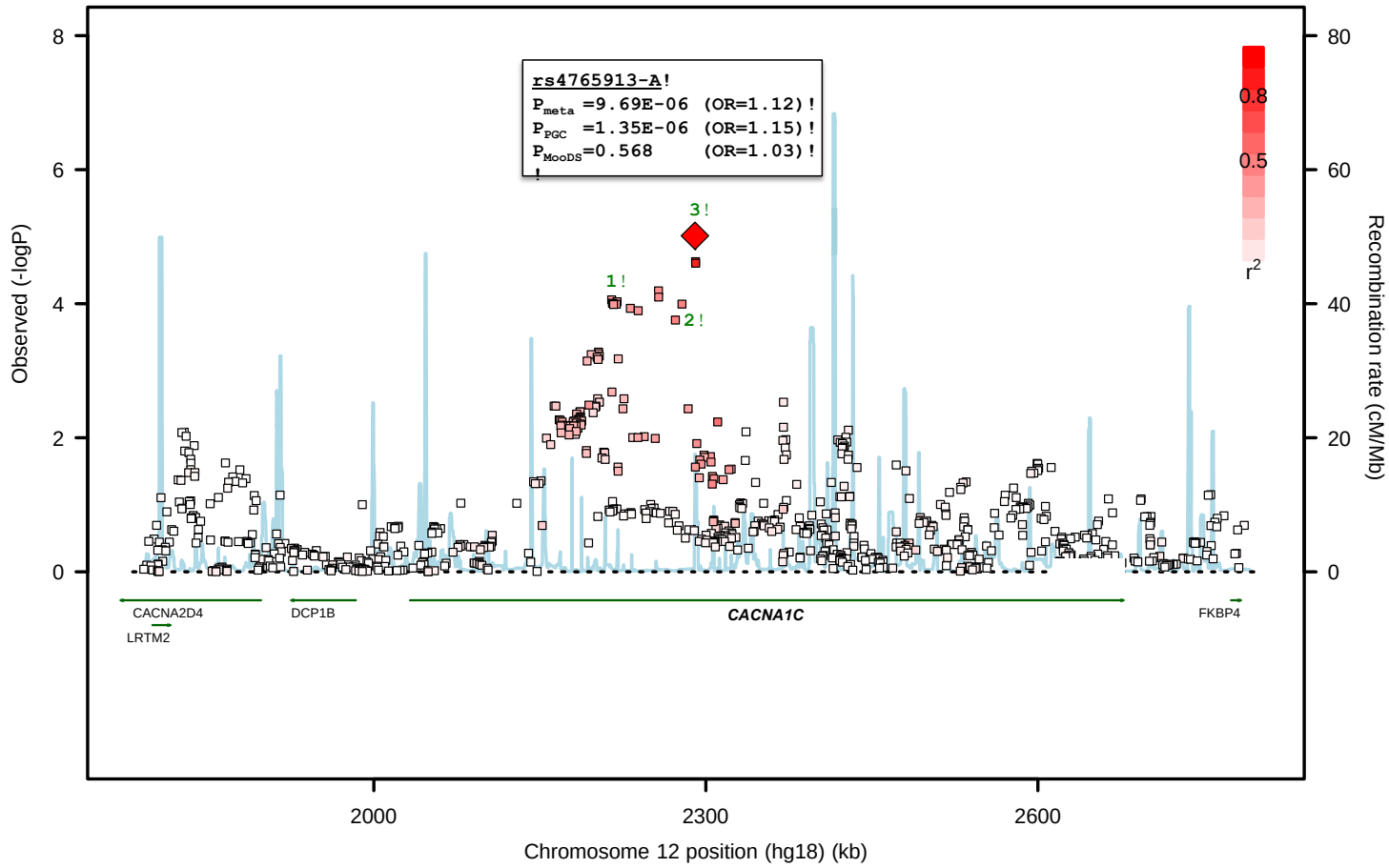
d

1: rs1064395-A: P_{Meta}=2.25E-06 (OR=1.14); P_{PGC}=0.00216 (OR=1.10); P_{MooDS}=2.76E-05 (OR=1.25); Cichon et al. (2011)[7]!



e

1: rs1006737-A: P_{Meta}=9.80E-05 (OR=1.09); P_{PGC}=1.73E-05 (OR=1.11); P_{MooDS}=0.643 (OR=1.02); Ferreira et al. (2008)[1!]
2: rs1024582-A: P_{Meta}=1.76E-04 (OR=1.08); P_{PGC}=4.41E-05 (OR=1.11); P_{MooDS}=0.614 (OR=1.02); Ferreira et al. (2008)[1!]
3: rs4765913-A: P_{Meta}=9.69E-06 (OR=1.12); P_{PGC}=1.35E-06 (OR=1.15); P_{MooDS}=0.568 (OR=1.03); PGC-BD (2011)[3!]



Supplementary Figure 1 | Association results for previously reported risk loci for BD displayed in the order of their significance level in the present study. (**a**) *ANK3* (10q21.2), (**b**) *ODZ4* (11q14.1), (**c**) *TRANK1* (3p22.2). (**d**) *NCAN* (19p13.11), and (**e**) *CACNA1C* (12p13.33). Regional association plots for SNPs were generated using SNAP[8] and data for LD (red) and recombination frequency (blue line) from the 1000 Genomes Project. SNP identifiers and original references of the known risk variants as well as their association results in the present study are shown on top of the plot. The chromosomal positions of the known variants are marked by numbers that refer to the numbers on top of the plot. The indicated alleles are the effect alleles (A1) from the present study. For SNPs in *ANK3*, *ODZ4*, and *TRANK1*, further details are provided by Supplementary Tables 1, 2, and 5.
The following abbreviations are used: P_{meta}, genomic control *P*-value (P_{GC}) of the fixed-effects meta-analysis using the MooDS-PGC samples (Methods); P_{PGC}: *P*-value of the fixed-effects meta-analysis using the published PGC-BD data[7] only; P_{MooDS}: *P*-value of the fixed-effects meta-analysis using the MooDS data only.

Supplementary Figure 2 | Multi-dimensional scaling analysis (MDS) during the second QC. To identify potential population stratification, we used the first two MDS dimensions. Population outliers were visually determined and excluded before the third QC (Methods and Supplementary Table 9). The plot shows the population structures when all seven MooDS samples are analyzed in parallel. In addition, we performed a MDS analysis between patients and controls within each MooDS sample. The significant MDS dimensions were used as covariates in the sample-specific association analyses (Methods).

Supplementary Tables

Supplementary Table 1 | 35 SNPs (P_{GC}<5x10^{-5}) in the *ANK3* region (10q21.3) showing evidence for association with BD in the combined analysis (MooDS-PGC).

SNP Data		Association Data					Gene Data	
Marker	Position	A1	A2	Directions	P_{GC}	OR	Nearest Gene or Transcript	Evidence by Previous BD GWAS
rs10994415	chr10:62,322,034	C	T	++-+++++	**6.88E-11**	1.27	*ANK3*, intron	
rs10994397[a,b]	chr10:62,279,124	T	C	+++++-++	**2.86E-10**	1.29	*ANK3*, intron	PGC-BD (2011)[3]
rs9633553	chr10:62,274,737	G	T	+++++-++	**2.96E-10**	1.29	*ANK3*, intron	
rs2154393	chr10:62,326,687	T	C	++-+-+++	**3.03E-10**	1.26	*ANK3*, intron	
rs1938540	chr10:62,294,814	T	C	++++-+++	**8.22E-10**	1.27	*ANK3*, intron	
rs10821792	chr10:62,298,616	T	C	++++++++	**8.34E-10**	1.27	*ANK3*, intron	
rs1938526[b]	chr10:62,300,383	G	A	++++++++	**8.55E-10**	1.27	*ANK3*, intron	Ferreira *et al.* (2008)[1]
rs12412135	chr10:62,282,834	T	C	++++++++	**3.33E-09**	1.24	*ANK3*, intron	
rs10821789	chr10:62,285,338	A	G	++++++++	**3.72E-09**	1.24	*ANK3*, intron	
rs10994404	chr10:62,288,445	C	T	++++++++	**4.41E-09**	1.24	*ANK3*, intron	
rs10821745	chr10:62,136,206	G	T	++-+++++	**1.26E-08**	1.27	*ANK3*, intron	PGC-BD (2011)[3]
rs10821736	chr10:62,105,053	T	C	++-++-++	**1.55E-08**	1.28	*ANK3*, intron	PGC-BD (2011)[3]
rs10994430	chr10:62,371,953	T	G	++++++++	**2.14E-08**	1.18	*ANK3*, intron	
rs10994429	chr10:62,371,079	T	C	++++++++	**2.22E-08**	1.18	*ANK3*, intron	
rs10994336[b]	chr10:62,179,812	T	C	+++++-++	**2.34E-08**	1.27	*ANK3*, intron	Ferreira *et al.* (2008)[1]
rs16915231	chr10:62,375,046	A	G	++++++++	**2.49E-08**	1.18	*ANK3*, intron	
rs1380459	chr10:62,097,331	T	C	++-++-++	**2.71E-08**	1.27	*ANK3*, intron	
rs4948412	chr10:62,146,576	C	T	++-++-++	**2.99E-08**	1.27	*ANK3*, intron	
rs16915196	chr10:62,359,859	G	A	++++++++	**3.04E-08**	1.18	*ANK3*, intron	
rs10994322	chr10:62,136,279	T	C	++-+++++	**3.30E-08**	1.27	*ANK3*, intron	
rs4948417	chr10:62,161,618	G	A	++-+++++	**3.40E-08**	1.27	*ANK3*, intron	
rs10994338	chr10:62,181,128	A	G	+++++-++	**3.44E-08**	1.26	*ANK3*, intron	
rs10994308	chr10:62,098,952	A	G	++-++-++	**3.60E-08**	1.27	*ANK3*, intron	
rs3808943	chr10:62,151,015	T	C	++-+-+++	**3.71E-08**	1.27	*ANK3*, intron	
rs12416380	chr10:62,156,154	G	A	++-+++++	**3.78E-08**	1.27	*ANK3*, intron	
rs10509129	chr10:62,071,041	T	G	-+-++-++	**4.77E-08**	1.29	*ANK3*, intron	
rs10994443	chr10:62,395,518	A	G	++++++++	6.51E-08	1.23	*ANK3*, intron	
rs10821748	chr10:62,152,938	C	G	++-+++++	1.29E-07	1.25	*ANK3*, intron	
rs10761473	chr10:62,060,382	G	C	-+---+++	2.26E-07	1.26	*ANK3*, intron	
rs4948418[b]	chr10:62,185,494	T	C	-+++--++	5.60E-07	1.23	*ANK3*, intron	Chen *et al.* (2011)[2]
rs10509136	chr10:62,425,124	T	C	+++-++++	2.85E-06	1.16	*ANK3*, intron	
rs10994435	chr10:62,385,605	T	C	++++++++	4.36E-06	1.16	*ANK3*, intron	
rs10994465	chr10:62,420,405	A	G	+++-++++	5.32E-06	1.15	*ANK3*, intron	
rs10509138	chr10:62,437,910	C	A	+++-++++	5.56E-06	1.15	*ANK3*, intron	
rs12218617	chr10:62,433,440	T	A	+++-++++	6.28E-06	1.15	*ANK3*, intron	

[a]This SNP showed the best-fit for BD using a multinomial logistic model by Bayesian information criteria in the PGC-CD GWAS (2013)[4].
[b]In the PGC-BD meta-analysis[3], the effect alleles (A1) for rs10994397, rs1938526, rs10994336, and rs4948418 were considered to be C, A, C, and C. In the present meta-analysis, T, G, T, and T, all being the minor alleles in populations with European ancestry, were considered as effect alleles. Due to this formal reason, the four SNPs show allelic effect sizes with ORs>1.
SNPs are sorted according to their genomic control *P*-values (P_{GC}) from the fixed-effects meta-analysis using the MooDS-PGC samples (Methods). Genome-wide significance is defined by the formal threshold of $P_{GC}<5x10^{-8}$ (bold). Allele directions refer to the effect allele (A1) in each sample (in the order Germany II, Poland, Australia, Canada, Germany III, Spain, Russia, PGC). SNP names and chromosomal positions refer to dbSNP build 137 and the genome build GRCh37 (hg19).
The following abbreviations are used: A1, the effect allele to which the odds ratio (OR) is predicted; MooDS, Systematic Investigation of the Molecular Causes of Major Mood Disorders and Schizophrenia; PGC-BD, Psychiatric GWAS Consortium Bipolar Disorder Working Group; PGC-CD, Psychiatric GWAS Consortium Cross-disorder Working Group.

Supplementary Table 2 | 34 SNPs (P_{GC}<5x10^{-5}) in the *ODZ4* region (11q14.1) showing evidence for association with BD in the combined analysis (MooDS-PGC).

SNP Data		Association Data					Gene Data	
Marker	Position	A1	A2	Directions	P_{GC}	OR	Nearest Gene or Transcript	Evidence by Previous BD GWAS
rs12290811	chr11:79,083,620	A	T	+++-++++	**1.09E-09**	1.19	*ODZ4*, intron	Ferreira et al. (2008)[1]
rs1944449	chr11:79,083,249	T	C	+++--+++	**1.43E-09**	1.19	*ODZ4*, intron	
rs12576775[a,b]	chr11:79,077,193	G	A	+++--+++	**4.46E-09**	1.17	*ODZ4*, intron	PGC-BD (2011)[3]
rs17138230	chr11:79,075,852	T	A	+++--+++	**5.88E-09**	1.17	*ODZ4*, intron	
rs7932890	chr11:79,068,394	G	A	+++--+++	**9.35E-09**	1.17	*ODZ4*, intron	
rs17138171	chr11:79,062,930	C	T	+++--+++	**1.37E-08**	1.16	*ODZ4*, intron	
rs12279388	chr11:79,067,674	G	A	+++--+++	**1.81E-08**	1.16	*ODZ4*, intron	
rs10501439	chr11:79,085,846	G	A	+++--+++	**2.24E-08**	1.17	*ODZ4*, intron	
rs11237799	chr11:79,067,472	C	A	+++--+++	**2.53E-08**	1.16	*ODZ4*, intron	
rs11237805	chr11:79,078,669	G	A	+++--+++	**2.96E-08**	1.16	*ODZ4*, intron	
rs12577093	chr11:79,057,097	T	C	+++--+++	1.04E-07	1.15	*ODZ4*, intron	
rs7127580	chr11:79,144,856	G	C	++++++-+	1.53E-07	1.19	*ODZ4*, intron	
rs954129	chr11:79,060,796	A	T	+++--+++	3.31E-07	1.14	*ODZ4*, intron	
rs7108878	chr11:79,107,807	G	T	+++--+-+	4.35E-07	1.17	*ODZ4*, intron	
rs1511237	chr11:79,114,684	T	C	+++--+-+	6.22E-07	1.17	*ODZ4*, intron	
rs12275195	chr11:79,105,799	C	A	+++--+-+	6.25E-07	1.17	*ODZ4*, intron	
rs11237821	chr11:79,106,804	T	C	+++--+-+	6.59E-07	1.17	*ODZ4*, intron	
rs11237815	chr11:79,090,800	G	A	+++--+++	7.24E-07	1.18	*ODZ4*, intron	
rs12277834	chr11:79,100,156	T	C	+++-++-+	7.71E-07	1.17	*ODZ4*, intron	
rs12577328	chr11:79,093,474	G	C	+++-++++	8.49E-07	1.17	*ODZ4*, intron	
rs11237796	chr11:79,059,444	G	A	+++--+++	8.60E-07	1.13	*ODZ4*, intron	
rs12289486	chr11:79,092,527	T	C	+++-++++	8.78E-07	1.17	*ODZ4*, intron	
rs11237820	chr11:79,104,665	A	G	+++--+-+	9.09E-07	1.17	*ODZ4*, intron	
rs12286448	chr11:79,121,342	G	T	++++-+-+	1.01E-06	1.17	*ODZ4*, intron	
rs4529900	chr11:79,173,703	T	C	++--+-++	5.26E-06	1.13	*ODZ4*, intron	
rs2175420[b]	chr11:79,123,883	T	C	+++-+--+	6.77E-06	1.13	*ODZ4*, intron	PGC-BD (2011)[3]
rs12275848	chr11:79,127,329	C	G	+++-+--+	7.11E-06	1.12	*ODZ4*, intron	
rs12273727	chr11:79,129,616	G	A	+++-+--+	7.54E-06	1.12	*ODZ4*, intron	
rs12279943	chr11:79,129,926	C	G	+++-+--+	1.35E-05	1.12	*ODZ4*, intron	
rs1567540	chr11:79,124,084	G	A	+++-+--+	1.37E-05	1.12	*ODZ4*, intron	
rs1943849	chr11:79,178,631	G	C	++--+--+	1.49E-05	1.13	*ODZ4*, intron	
rs17138318	chr11:79,132,083	T	G	+++-+--+	1.65E-05	1.12	*ODZ4*, intron	
rs10501444	chr11:79,137,378	G	C	+++-+--+	1.75E-05	1.12	*ODZ4*, intron	
rs2512637	chr11:79,191,457	G	A	+++-+--+	2.39E-05	1.13	*ODZ4*, intron	

[a]This SNP showed the best-fit for BD using a multinomial logistic model by Bayesian information criteria in the PGC-CD GWAS (2013)[4].
[b]In the PGC-BD meta-analysis[3], the effect alleles (A1) for rs12576775 and rs2175420 were considered to be A and C. In the present meta-analysis, G and T, both being the minor alleles in

populations with European ancestry, were considered as effect alleles. Due to this formal reason, the two SNPs show allelic effect sizes with ORs>1.

SNPs are sorted according to their genomic control P-values (P_{GC}) from the fixed-effects meta-analysis using the MooDS-PGC samples (Methods). Genome-wide significance is defined by the formal threshold of $P_{GC}<5x10^{-8}$ (bold). Allele directions refer to the effect allele A1 in each sample (in the order Germany II, Poland, Australia, Canada, Germany III, Spain, Russia, PGC). SNP names and chromosomal positions refer to dbSNP build 137 and the genome build GRCh37 (hg19).

The following abbreviations are used: A1, the effect allele to which the odds ratio (OR) is predicted; PGC-CD, Cross-Disorder Group of the Psychiatric Genomics Consortium; MooDS, Systematic Investigation of the Molecular Causes of Major Mood Disorders and Schizophrenia; PGC-BD, Psychiatric GWAS Consortium Bipolar Disorder Working Group.

Supplementary Table 3 | 14 SNPs (P_{GC}<5x10^{-5}) in the *ADCY2* region (5p15.31) showing evidence for association with BD in the combined analysis (MooDS-PGC).

SNP Data		Association Data					Gene Data	
Marker	Position	A1	A2	Directions	P_{GC}	OR	Nearest Gene or Transcript	Evidence by Previous GWAS of BD
rs17826816	chr5:7,519,298	G	A	++++++++	**9.89E-09**	1.14	*ADCY2*, intron	
rs13166360	chr5:7,520,881	T	G	++++++++	**1.81E-08**	1.14	*ADCY2*, missense	
rs17231202	chr5:7,546,287	G	A	++-+++++	9.09E-08	1.14	*ADCY2*, intron	
rs17826395	chr5:7,503,056	C	A	++++++++	1.96E-07	1.14	*ADCY2*, intron	
rs11948030	chr5:7,493,177	C	T	++++++++	2.08E-07	1.14	*ADCY2*, intron	
rs10512928	chr5:7,546,411	T	C	++-+++++	2.92E-07	1.14	*ADCY2*, intron	
rs884964	chr5:7,548,854	C	T	++-+++++	3.68E-07	1.14	*ADCY2*, intron	
rs4530734	chr5:7,565,152	T	G	++++++++	4.23E-07	1.16	*ADCY2*, intron	
rs12519539	chr5:7,583,156	G	A	++++++++	5.54E-07	1.13	*ADCY2*, intron	
rs12522444	chr5:7,553,501	A	G	++++++++	7.06E-07	1.13	*ADCY2*, intron	
rs17826588	chr5:7,516,555	T	C	+++-+-++	8.78E-06	1.1	*ADCY2*, intron	
rs13166852	chr5:7,595,762	C	T	+++-+-++	2.07E-05	1.1	*ADCY2*, intron	
rs13180878	chr5:7,536,194	C	G	++++++++	4.04E-05	1.09	*ADCY2*, intron	
rs10061240	chr5:7,535,800	A	G	++++++++	4.37E-05	1.09	*ADCY2*, intron	

SNPs are sorted according to their genomic control *P*-values (P_{GC}) from the fixed-effects meta-analysis using the MooDS-PGC samples (Methods). Genome-wide significance is defined by the formal threshold of P_{GC}<5x10^{-8} (bold). Allele directions refer to the effect allele A1 in each sample (in the order Germany II, Poland, Australia, Canada, Germany III, Spain, Russia, PGC). SNP names and chromosomal positions refer to dbSNP build 137 and the genome build GRCh37 (hg19).
The following abbreviations are used: A1, the effect allele to which the odds ratio (OR) is predicted; MooDS, Systematic Investigation of the Molecular Causes of Major Mood Disorders and Schizophrenia; PGC-BD, Psychiatric GWAS Consortium Bipolar Disorder Working Group.

Supplementary Table 4 | 51 SNPs (P_{GC}<5x10^{-5}) in the *MIR2113-POU3F2* region (6q16.1) showing evidence for association with BD in the combined analysis (MooDS-PGC).

SNP Data		Association Data					Gene Data	
Marker	Position	A1	A2	Directions	P_{GC}	OR	Nearest Gene or Transcript	Evidence by Previous GWAS of BD
rs12202969	chr6:98,576,223	A	G	++++++++	**1.08E-08**	1.12	*MIR2113; POU3F2*	
rs12206087	chr6:98,582,900	A	G	++++++++	**1.64E-08**	1.12	*MIR2113; POU3F2*	
rs1906252	chr6:98,550,289	A	C	++++++++	**3.39E-08**	1.12	*MIR2113; POU3F2*	
rs1487441	chr6:98,553,894	A	G	++++++++	**3.57E-08**	1.12	*MIR2113; POU3F2*	
rs1872841	chr6:98,576,688	A	C	++++++++	4.61E-07	1.11	*MIR2113; POU3F2*	
rs9388171	chr6:98,575,726	G	C	++++++++	4.66E-07	1.11	*MIR2113; POU3F2*	
rs10457441	chr6:98,572,120	C	T	++++++++	4.99E-07	1.11	*MIR2113; POU3F2*	
rs9401634	chr6:98,578,511	C	T	++++++++	5.11E-07	1.11	*MIR2113; POU3F2*	
rs12204181	chr6:98,579,481	C	T	++++++++	5.53E-07	1.11	*MIR2113; POU3F2*	
rs9375225	chr6:98,588,754	T	G	++++++++	6.83E-07	1.11	*MIR2113; POU3F2*	
rs9385269	chr6:98,547,979	T	C	++++++++	8.74E-07	1.10	*MIR2113; POU3F2*	
rs9375195	chr6:98,562,720	A	G	++++++++	1.46E-06	1.1	*MIR2113; POU3F2*	
rs9385308	chr6:98,632,010	T	G	++++++++	5.17E-06	1.11	*MIR2113; POU3F2*	
rs9375371	chr6:98,751,680	A	G	++++++++	5.33E-06	1.11	*MIR2113; POU3F2*	
rs1376503	chr6:98,704,423	A	G	--------	5.41E-06	0.9	*MIR2113; POU3F2*	
rs12203171	chr6:98,613,792	A	T	++++++++	5.51E-06	1.11	*MIR2113; POU3F2*	
rs1487439	chr6:98,611,300	G	A	++++++++	5.56E-06	1.11	*MIR2113; POU3F2*	
rs9385344	chr6:98,748,500	T	C	++++++++	5.58E-06	1.11	*MIR2113; POU3F2*	
rs6939461	chr6:98,750,517	A	G	++++++++	5.98E-06	1.11	*MIR2113; POU3F2*	
rs9320942	chr6:98,628,831	G	A	++++++++	5.98E-06	1.11	*MIR2113; POU3F2*	
rs4565311	chr6:98,714,495	T	C	++++++++	6.13E-06	1.11	*MIR2113; POU3F2*	
rs7754741	chr6:98,749,329	C	T	++++++++	6.23E-06	1.11	*MIR2113; POU3F2*	
rs9401757	chr6:98,733,864	C	T	++++++++	6.32E-06	1.11	*MIR2113; POU3F2*	
rs1487447	chr6:98,632,082	G	A	++++++++	6.51E-06	1.1	*MIR2113; POU3F2*	
rs6911443	chr6:98,722,903	A	G	--------	6.56E-06	0.9	*MIR2113; POU3F2*	
rs9388268	chr6:98,633,802	G	A	++++++++	6.56E-06	1.1	*MIR2113; POU3F2*	
rs9388349	chr6:98,734,648	G	T	++++++++	6.59E-06	1.11	*MIR2113; POU3F2*	
rs12215368	chr6:98,617,582	A	G	++++++++	6.64E-06	1.11	*MIR2113; POU3F2*	
rs12195240	chr6:98,636,905	A	G	++++++++	6.65E-06	1.11	*MIR2113; POU3F2*	
rs9320996	chr6:98,726,528	C	G	++++++++	6.76E-06	1.11	*MIR2113; POU3F2*	
rs10499017	chr6:98,724,638	C	G	++++++++	6.83E-06	1.11	*MIR2113; POU3F2*	
rs1562865	chr6:98,747,312	C	T	++++++++	6.84E-06	1.11	*MIR2113; POU3F2*	
rs9388352	chr6:98,739,949	A	T	++++++++	6.92E-06	1.11	*MIR2113; POU3F2*	
rs1451346	chr6:98,729,160	A	G	++++++++	7.16E-06	1.11	*MIR2113; POU3F2*	
rs1868885	chr6:98,719,233	T	C	++++++++	7.23E-06	1.11	*MIR2113; POU3F2*	
rs9375351	chr6:98,739,867	G	A	++++++++	7.30E-06	1.11	*MIR2113; POU3F2*	
rs9320990	chr6:98,713,523	G	T	++++++++	7.49E-06	1.11	*MIR2113; POU3F2*	
SNP Data		Association Data					Gene Data	

Marker	Position	A1	A2	Directions	P_{GC}	OR	Nearest Gene or Transcript	Evidence by Previous GWAS of BD
rs9375350	chr6:98,739,311	A	G	++++++++	7.49E-06	1.11	*MIR2113; POU3F2*	
rs9375352	chr6:98,739,938	A	T	++++++++	7.63E-06	1.11	*MIR2113; POU3F2*	
rs12205529	chr6:98,713,048	T	G	++++++++	8.01E-06	1.11	*MIR2113; POU3F2*	
rs717296	chr6:98,741,067	A	C	++++++++	8.26E-06	1.11	*MIR2113; POU3F2*	
rs6569382	chr6:98,709,685	T	C	--------	8.28E-06	0.9	*MIR2113; POU3F2*	
rs12216178	chr6:98,637,119	G	A	++++++++	8.34E-06	1.1	*MIR2113; POU3F2*	
rs6927284	chr6:98,741,419	A	G	++++++++	8.38E-06	1.11	*MIR2113; POU3F2*	
rs12203165	chr6:98,613,744	A	T	++++++++	8.50E-06	1.11	*MIR2113; POU3F2*	
rs2063144	chr6:98,713,238	A	C	--------	8.50E-06	0.91	*MIR2113; POU3F2*	
rs2892512	chr6:98,744,946	C	T	++++++++	9.00E-06	1.1	*MIR2113; POU3F2*	
rs9388303	chr6:98,687,387	G	A	++++++++	9.69E-06	1.1	*MIR2113; POU3F2*	
rs9375321	chr6:98,706,822	C	A	++++++++	9.89E-06	1.1	*MIR2113; POU3F2*	
rs12192372	chr6:98,673,904	G	A	++++++++	1.05E-05	1.1	*MIR2113; POU3F2*	
rs9388292	chr6:98,669,276	C	A	++++++++	1.05E-05	1.1	*MIR2113; POU3F2*	

SNPs are sorted according to their genomic control *P*-values (P_{GC}) from the fixed-effects meta-analysis using the MooDS-PGC samples (MooDS). Genome-wide significance is defined by the formal threshold of $P_{GC}<5x10^{-8}$ (bold). Allele directions refer to the effect allele A1 in each sample (in the order Germany II, Poland, Australia, Canada, Germany III, Spain, Russia, PGC). SNP names and chromosomal positions refer to dbSNP build 137 and the genome build GRCh37 (hg19).
The following abbreviations are used: A1, the effect allele to which the odds ratio (OR) is predicted; MooDS, Systematic Investigation of the Molecular Causes of Major Mood Disorders and Schizophrenia; PGC-BD, Psychiatric GWAS Consortium Bipolar Disorder Working Group.

Supplementary Table 5 | 33 SNPs (P_{GC}<5x10^{-5}) in the *TRANK1* region (3p22.2) showing evidence for association with BD in the combined analysis (MooDS-PGC).

SNP Data		Association Data					Gene Data	
Marker	Position	A1	A2	Directions	P_{GC}	OR	Nearest Gene or Transcript	Evidence by Previous GWAS of BD
rs6550435	chr3:36,864,489	G	T	-+++++-+	**2.05E-08**	1.13	TRANK1, downstr.	PGC-BD (2011)[3]; Green et al. (2012)[6]
rs9882911	chr3:36,885,392	C	T	-+++++++	**2.09E-08**	1.13	*TRANK1*, intron	
rs4678910	chr3:36,887,973	G	C	-+++++++	**2.35E-08**	1.13	*TRANK1*, intron	
rs9821223	chr3:36,883,369	C	T	-+++++++	**2.43E-08**	1.13	*TRANK1*, intron	
rs4234258	chr3:36,878,970	G	A	-+++++++	**2.45E-08**	1.13	*TRANK1*, intron	
rs4624519	chr3:36,862,980	T	C	-+++++++	**2.61E-08**	1.13	*TRANK1*, downstr.	
rs1532965	chr3:36,861,196	G	T	-+++++++	**2.73E-08**	1.12	*TRANK1*, downstr.	
rs9811916	chr3:36,878,086	G	A	-+++++++	**2.88E-08**	1.12	*TRANK1*, intron	
rs3732386	chr3:36,871,993	T	C	-+++++++	**3.12E-08**	1.12	*TRANK1*, intron	
rs4678909	chr3:36,878,563	G	A	-+++++++	**3.12E-08**	1.12	*TRANK1*, intron	
rs7652637	chr3:36,871,507	C	T	-+++++++	**3.41E-08**	1.12	*TRANK1*, intron	
rs17807744	chr3:36,894,048	T	C	-+++++++	**4.07E-08**	1.12	*TRANK1*, intron	
rs12637912	chr3:36,871,894	A	C	-+++++++	**4.81E-08**	1.12	*TRANK1*, intron	
rs9834970	chr3:36,856,030	C	T	-+++++++	**4.81E-08**	1.12	*TRANK1*, downstr.	Chen *et al.* (2011)[2]; Goes *et al.* (2012)[5]
rs11706780	chr3:36,896,235	T	C	-+++++++	5.04E-08	1.12	*TRANK1*, intron	
rs9876421	chr3:36,848,316	T	C	-+++++-+	1.89E-07	1.12	*TRANK1*, downstr.	
rs4072458	chr3:36,862,680	C	T	-+++++++	2.10E-07	1.11	*TRANK1*, downstr.	
rs9882879	chr3:36,844,071	T	C	-+++++-+	2.38E-07	1.12	*TRANK1*, downstr.	
rs1553656	chr3:36,859,705	C	T	-+++++++	2.40E-07	1.11	*TRANK1*, downstr.	
rs11129735	chr3:36,870,230	G	A	-+++++++	2.56E-07	1.11	*TRANK1, intron*	
rs931913	chr3:36,843,149	A	G	-+++++-+	2.74E-07	1.12	*TRANK1, downstr.*	
rs4789	chr3:36,869,439	C	T	-+++++++	3,33E-07	1,11	*TRANK1, 3'UTR*	
rs4328757	chr3:36,938,180	T	C	-+++++++	7,84E-06	1.10	*TRANK1, intron*	
rs4296548	chr3:36,915,814	G	T	-+++++++	9,04E-06	1.10	*TRANK1, intron*	
rs9985296	chr3:36,889,621	C	T	-+++++++	1,08E-05	1.11	*TRANK1, intron*	
rs4441609	chr3:36,892,717	C	T	-+++++++	1,30E-05	1.10	*TRANK1, intron*	
rs13314421	chr3:36,962,388	G	A	-+++++-+	1,75E-05	1.09	*TRANK1, intron*	
rs4678915	chr3:36,964,583	A	G	++++++-+	2,38E-05	1.09	*TRANK1, intron*	
rs4642070	chr3:36,900,944	T	C	-+++++++	2,39E-05	1.09	*TRANK1, intron*	
rs11707149	chr3:36,850,490	T	C	+-------	3,52E-05	0.92	*TRANK1, downstr.*	
rs925135	chr3:36,854,253	A	G	+-------	3,69E-05	0.92	*TRANK1, downstr.*	
rs4425211	chr3:36,951,898	G	A	++++++-+	4,62E-05	1.09	*TRANK1, intron*	
rs13072940	chr3:36,842,623	A	T	+-------	4,95E-05	0.92	*TRANK1, intron*	

SNPs are sorted according to their genomic control *P*-values (P_{GC}) from the fixed-effects meta-analysis using the MooDS-PGC samples (Methods). Genome-wide significance is defined by the formal threshold of P_{GC}<5x10^{-8} (bold). Allele directions refer to the effect allele A1 in each sample (in the order Germany II, Poland, Australia, Canada, Germany III, Spain, Russia, PGC). SNP names

and chromosomal positions refer to dbSNP build 137 and the genome build GRCh37 (hg19).
The following abbreviations are used: A1, the effect allele to which the odds ratio (OR) is predicted; downstr., downstream; MooDS, Systematic Investigation of the Molecular Causes of Major Mood Disorders and Schizophrenia; PGC-BD, Psychiatric GWAS Consortium Bipolar Working Group; 3'UTR, 3' untranslated region.

Supplementary Table 6 | SNP-Proxy relationships in the *ADCY2* region that were used for the *in silico* follow-up analysis.

SNP	Tagged by N Proxies	Best Proxy	LD [r^2]	Distance [bp]
rs17826816	7	rs13166360 *	0.95	1,583
rs13166360	7	rs71604175	1.00	10,831
rs17231202	9	rs10512928 *	1.00	124
rs17826395	7	rs77557833	1.00	3,408
rs11948030	7	rs17826395 *	0.95	9,879
rs10512928	9	rs17231202 *	1.00	124
rs884964	9	rs10512928 *	1.00	2,443
rs4530734	9	rs34818287	1.00	3,444
rs12519539	9	rs34818287	1.00	14,560
rs12522444	9	rs55882341	1.00	2,322
rs17826588	0	NA	NA	NA
rs13166852	5	rs7726187	0.90	45,483
rs13180878	8	rs11134237	1.00	2,702
rs10061240	8	rs13180878 *	0.97	394
Proxy	**Tags N SNPs**	**Best tagged SNP**	**LD [r^2]**	**Distance [bp]**
rs71604175	4	rs13166360	1.00	10,831
rs78308718	4	rs13166360	1.00	13,104
rs28565152	4	rs13166360	0.95	22,030
rs77557833	4	rs17826395	1.00	3,408
rs34774166	6	rs4530734	1.00	5,300
rs34818287	6	rs4530734	1.00	3,444
rs35775745	6	rs12519539	0.90	7,946
rs55882341	6	rs12522444	1.00	2,322
rs17232317	1	rs13166852	0.87	31,610
rs7726187	1	rs13166852	0.90	45,483
rs2892634	1	rs13166852	0.90	46,201
rs2388912	1	rs13166852	0.90	55,916
rs75053571	1	rs13166852	0.87	64,686
rs12514129	2	rs13180878	0.97	4,806
rs4701786	2	rs13180878	1.00	3,739
rs13179602	2	rs13180878	0.90	791
rs11134237	2	rs13180878	1.00	2,702
rs4702476	2	rs13180878	0.97	3,055
rs2221182	2	rs13180878	1.00	3,102

*The best proxy is a SNP in the marker set of the present study (GWAS SNP).
The first column in the upper part of the table contains the 14 GWAS SNPs at the 5p15.31 locus that show strong to moderate association with BD as described in Supplementary Table 3. The numbers of proxies that tag a particular GWAS SNP (column 1) with a r^2-value of at least 0.8 are provided in column 2. The best proxy that shows the strongest pairwise LD-value (column 4) and the smallest distance to a particular GWAS SNP (column 5) is shown in column 3.
The first column in the lower part of the table contains the 20 proxies that were used to broaden the search range in data from prior studies or databases that did not contain the GWAS SNP from our study. The numbers of GWAS SNPs that are tagged by particular proxy (column 1) with a r^2-value of at least 0.8 are provided in column 2. The best tagged GWAS SNPs, their LD- and distance-values are given in columns 3, 4, and 5. Proxies were selected using SNAP[8] based on HapMap-CEU LD data from the 1000 Genomes Project (pilot 1).
The following abbreviations are used: bp, base pairs; LD, linkage disequilibrium; N, number of markers; NA, proxy not available.

Supplementary Table 7 | SNP-Proxy relationships in the *MIR2113-POU3F2* region region that were used for the *in silico* follow-up analysis.

SNP	Tagged by N Proxies	Best Proxy	LD [r^2]	Distance [bp]
rs12202969	20	rs12206087 *	1.00	6,677
rs12206087	20	rs12202969 *	1.00	6,677
rs1906252	20	rs9401593	1.00	488
rs1487441	20	rs1906252 *	1.00	3,605
rs1872841	20	rs9401634 *	1.00	1,823
rs9388171	20	rs10457441 *	1.00	3,606
rs10457441	20	rs9388171 *	1.00	3,606
rs9401634	20	rs1872841 *	1.00	1,823
rs12204181	20	rs9401634 *	0.97	970
rs9375225	20	rs9401634 *	0.97	10,243
rs9385269	19	rs9375195 *	0.97	14,741
rs9375195	20	rs1487446	1.00	2,492
rs9385308	86	rs1487447 *	1.00	72
rs9375371	85	rs1828075	1.00	946
rs1376503	85	rs12195792	1.00	872
rs12203171	86	rs12203165 *	1.00	48
rs1487439	86	rs12203165 *	1.00	2,444
rs9385344	85	rs9401770	1.00	492
rs6939461	85	rs1828075	1.00	217
rs9320942	84	rs9385308 *	0.96	3,179
rs4565311	85	rs9320990 *	1.00	972
rs7754741	85	rs7750492	1.00	93
rs9401757	85	rs9375344	1.00	137
rs1487447	86	rs9385308 *	1.00	72
rs6911443	85	rs6569386	1.00	492
rs9388268	86	rs72934581	1.00	784
rs9388349	85	rs9375344	1.00	647
rs12215368	85	rs12196119	1.00	12,768
rs12195240	77	rs12216178 *	0.92	214
rs9320996	85	rs9320995	1.00	147
rs10499017	85	rs12175163	1.00	524
rs1562865	85	rs9401770	1.00	696
rs9388352	85	rs9375352 *	1.00	11
rs1451346	85	rs4839946	1.00	1,156
rs1868885	85	rs12191679	1.00	329
rs9375351	85	rs9375352 *	0.96	71
rs9320990	85	rs9320989	1.00	49
rs9375350	85	rs2063146	1.00	189
rs9375352	85	rs9388352 *	1.00	11
rs12205529	83	rs9320989	0.92	426
rs717296	85	rs6927284 *	1.00	352
rs6569382	83	rs9375328	0.92	1,536
rs12216178	86	rs9388268 *	1.00	3,317
rs6927284	85	rs717296 *	1.00	352
rs12203165	86	rs12203171 *	1.00	48
rs2063144	68	rs9320989	0.85	236
rs2892512	85	rs1562865 *	1.00	2,366
rs9388303	85	rs12192372 *	1.00	13,483
rs9375321	85	rs12195792	1.00	1,527
rs12192372	85	rs72936319	1.00	1,386
rs9388292	85	rs72936319	1.00	3,242
Proxy	**Tags N SNPs**	**Best tagged SNP**	**LD [r^2]**	**Distance [bp]**
rs9372734	12	rs12202969	0.97	1,466
rs968050	12	rs12202969	0.97	1,663
rs1487445	12	rs12202969	0.97	11,012
rs2388334	12	rs12206087	1.00	8,722
rs62422665	12	rs12206087	0.97	1,742
rs9320913	11	rs12206087	0.91	1,833
rs9401593	12	rs1906252	1.00	488
rs13208578	12	rs1872841	1.00	3,712

Proxy	Tags N SNPs	Best tagged SNP	LD [r^2]	Distance [bp]
rs1487446	12	rs9375195	1.00	2,492
rs12190064	39	rs9385308	1.00	7,868
rs12195792	39	rs1376503	1.00	872
rs4839945	39	rs1376503	0.96	57
rs55711239	39	rs1376503	0.96	5,922
rs6927085	39	rs12203171	1.00	2,489
rs12190650	36	rs12203171	0.92	5,254
rs9388203	39	rs1487439	1.00	12,873
rs9385288	39	rs1487439	1.00	13,170
rs1487440	38	rs1487439	0.96	24
rs9401770	39	rs9385344	1.00	492
rs1828075	39	rs6939461	1.00	217
rs9388334	37	rs4565311	0.92	2,312
rs1979969	37	rs4565311	0.88	52
rs7750492	39	rs7754741	1.00	93
rs9375344	39	rs9401757	1.00	137
rs72938320	39	rs9401757	1.00	1,047
rs6569386	39	rs6911443	1.00	492
rs12210016	39	rs6911443	1.00	841
rs72934581	39	rs9388268	1.00	784
rs1376505	39	rs9388349	1.00	963
rs12196119	38	rs12215368	1.00	12,768
rs9398724	38	rs12215368	1.00	15,996
rs72934530	38	rs12215368	0.96	13,871
rs1823601	39	rs12215368	0.96	62,913
rs9398720	8	rs12215368	0.85	22,873
rs9320995	39	rs9320996	1.00	147
rs9375338	39	rs9320996	1.00	770
rs72938314	37	rs9320996	0.92	891
rs12175163	39	rs10499017	1.00	524
rs4839946	39	rs1451346	1.00	1,156
rs12191679	39	rs1868885	1.00	329
rs12191745	39	rs1868885	1.00	410
rs12665591	39	rs1868885	1.00	778
rs12202066	39	rs1868885	1.00	939
rs6569384	39	rs1868885	1.00	1,334
rs11154238	39	rs1868885	1.00	1,507
rs1451345	37	rs1868885	0.88	455
rs72936319	39	rs12192372	1.00	1,386
rs9388206	36	rs12205529	0.92	112,213
rs12661492	2	rs12205529	0.87	17,151
rs9375282	38	rs12216178	0.96	9,793
rs6933464	39	rs6927284	0.96	317
rs9320989	39	rs9320990	1.00	49
rs9388329	39	rs9320990	1.00	2,165
rs9375328	39	rs9320990	1.00	2,302
rs2063146	39	rs9375350	1.00	189
rs9375292	39	rs9388292	1.00	8,071
rs11154193	39	rs9388292	1.00	9,902
rs1451343	37	rs9388292	0.92	11,433

*The best proxy is a SNP in the marker set of the present study (GWAS SNP).
The first column in the upper part of the table contains the 51 GWAS SNPs at the 6q16.1 locus that show strong to moderate association with BD as described in Supplementary Table 4. The numbers of proxies that tag a particular GWAS SNP (column 1) with a r^2-value of at least 0.8 are provided in column 2. The best proxy that shows the strongest pairwise LD-value (column 4) and the smallest distance to a particular GWAS SNP (column 5) is shown in column 3.
The first column in the lower part of the table contains the 58 proxies that were used to broaden the search range in data from prior studies or databases that did not contain the GWAS SNP from our study. The numbers of GWAS SNPs that are tagged by particular proxy (column 1) with a r^2-value of at least 0.8 are provided in column 2. The best tagged GWAS SNPs, their LD- and distance-values are given in columns 3, 4, and 5. Proxies were selected using SNAP[8] based on HapMap-CEU LD data from the 1000 Genomes Project (pilot 1). The following abbreviations are used: bp, base pairs; LD, linkage disequilibrium; N, number of markers; NA, proxy not available.

Supplementary Table 8 | Genome-wide genotyping and quality control for the seven new MooDS samples of BD.

	Chip type		
Sample	Patients (N)	Controls (N)	Generated for study (Patients / Controls)
Australia	I610Q (330)	I610Q (1,811)	Cichon, Mühleisen *et al.* (2011)[7], PGC-BD (2011)[3] / Medland *et al.* (2009)[9], Cichon, Mühleisen *et al.* (2011)[7], PGC-BD (2011)[3]
Germany III	I610Q, I660Q (490)	I550 (880)	Cichon, Mühleisen *et al.* (2011)[7], PGC-BD (2011)[3] / Muglia *et al.* (2010)[10]
Poland	I660Q (411)	I300 (689)	Mühleisen, Leber, Schultze *et al.* / McKay *et al.* (2011)[11]
Canada	IO1Q (285)	I610Q (341)	Mühleisen, Leber, Schultze *et al.* / Moffat *et al.* (2010)[12]
Russia	IO1Q (316)	I610Q (486)	Mühleisen, Leber, Schultze *et al.* / Moffat *et al.* (2010)[12]
Germany II	IO1Q (181)	IO1Q (527)	Cichon, Mühleisen *et al.* (2011)[8], PGC-BD (2011)[3] / Mühleisen, Leber, Schultze *et al.*
Spain	IO1Q (253)	I610Q (294)	Mühleisen, Leber, Schultze *et al.*, Moffat *et al.* (2010)[12]

MooDS samples are sorted according to decreasing sample size (N) following QC. None of these samples has been used in a genome-wide discovery step for BD before.
The following abbreviations are used: I300, Illumina HumanHap300; I550, Illumina HumanHap550; I610Q, Illumina Human610-Quad; I660Q, Illumina Human660W-Quad; IO1Q, Illumina HumanOmni1-Quad; N, sample size after QC; PGC-BD, Psychiatric GWAS Consortium Bipolar Working Group.

Supplementary References

1. Ferreira, M.A.R. et al. Collaborative genome-wide association analysis supports a role for ANK3 and CACNA1C in bipolar disorder. Nature Genetics 40, 1056–8 (2008).
2. Chen, D. T. et al. Genome-wide association study meta-analysis of European and Asian-ancestry samples identifies three novel loci associated with bipolar disorder. Molecular Psychiatry 18, 195-205 (2013).
3. Psychiatric GWAS Consortium Bipolar Disorder Working Group. Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nature Genetics 43, 977–83 (2011).
4. Cross-disorder Group of the Psychiatric Genomics Consortium. Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. Lancet 381, 1371–9 (2013).
5. Goes, F. S. et al. Genome-wide association of mood-incongruent psychotic bipolar disorder. Translational Psychiatry 2, e180 (2012).
6. Green, E. K. et al. Replication of bipolar disorder susceptibility alleles and identification of two novel genome-wide significant associations in a new bipolar disorder case-control sample. Molecular Psychiatry epub ahed of print, 16 October, 1–6 (2012).
7. Cichon, S. et al. Genome-wide association study identifies genetic variation in neurocan as a susceptibility factor for bipolar disorder. American Journal of Human Genetics 88, 372-81 (2011).
8. Johnson, A. D., Handsaker, R. E., Pulit, S., Nizzari, M. M., O'Donnell, C. J., de Bakker, P. I. W. SNAP: A web-based tool for identification and annotation of proxy SNPs using HapMap Bioinformatics 24, 2938-2939 (2008).

9. Medland, S. E. et al. Common variants in the trichohyalin gene are associated with straight hair in Europeans. American Journal of Human Genetics 85, 750–5 (2009).
10. Muglia, P. et al. Genome-wide association study of recurrent major depressive disorder in two European case-control cohorts. Molecular Psychiatry 15, 589–601 (2010).
11. McKay, J. D. et al. A genome-wide association study of upper aerodigestive tract cancers conducted within the INHANCE consortium. PLoS Genetics 7, e1001333 (2011).
12. Moffatt, M. F. et al. A large-scale, consortium-based genomewide association study of asthma. The New England Journal of Medicine 363, 1211–21 (2010).

Supplementary Data 1. Quality control procedure for the genotype and the imputed MooDS data.

			Australia [a]				Germany III [b]				Poland				Canada				Russia				Germany II [c]				Spain			
	Step	**Exclusion criteria**	**Patients**	**SNPs**	**Controls**	**SNPs**	**Patients**	**SNPs**	**Controls**	**SNPs**	**Patients**	**SNPs**	**Controls**	**SNPs**	**Patients**	**SNPs**	**Controls**	**SNPs**	**Patients**	**SNPs**	**Controls**	**SNPs**	**Patients**	**SNPs**	**Controls**	**SNPs**	**Patients**	**SNPs**	**Controls**	**SNPs**
1	Number of subjects and SNPs before QC										427	657,366	763	317,139	332	1,020,068	398	582,892	358	1,018,415	640	582,892					270	1,138,747	360	582,892
2	SNP genotyping	Call rate < 95%									(+/-) 0	(-) 99,844	(+/-) 0	(-) 7,748	(+/-) 0	(-) 246,378	(+/-) 0	(-) 4739	(+/-) 0	(-) 5,188	(+/-) 0	(-) 4,920					(+/-) 0	(-) 126,225	(+/-) 0	(-) 4,226
3	Sex	Ambigous coding									(+/-) 0	(+/-) 0	(+/-) 0	(+/-) 0	(-) 4	(+/-) 0	(+/-) 0	(+/-) 0	(+/-) 0	(+/-) 0	(+/-) 0	(+/-) 0					(+/-) 0	(+/-) 0	(+/-) 0	(+/-) 0
4	Subject genotyping	Call rate < 98%									(-) 4	(+/-) 0	(-) 13	(+/-) 0	(-) 26	(+/-) 0	(-) 5	(+/-) 0	(-) 4	(+/-) 0	(-) 24	(+/-) 0					(-) 1	(+/-) 0	(-) 18	(+/-) 0
5	Deviation from Hardy-Weinberg-Equilibrium	P ≤ 1E-06									(+/-) 0	(-)258	(+/-) 0	(-) 181	(+/-) 0	(-) 115	(+/-) 0	(-) 725	(+/-) 0	(-) 590	(+/-) 0	(-) 509					(+/-) 0	(-) 508	(+/-) 0	(-) 243
6	Cryptic relatedness	IBS > 1.98 or SD > 6									(-) 9	(+/-) 0	(-) 7	(+/-) 0	(-) 6	(+/-) 0	(-) 42	(+/-) 0	(-) 9	(+/-) 0	(-) 14	(+/-) 0					(-) 7	(+/-) 0	(-) 5	(+/-) 0
7	Number of subjects and SNPs following **first QC**										414	557,264	743	309,210	296	773,575	351	577,428	345	1,012,632	602	577,463					262	1,012,014	337	578,423
8	Merging of patient and control data		**Patients and controls**				**Patients and controls**				**Patients and controls**				**Patients and controls**				**Patients and controls**				**Patients and controls**				**Patients and controls**			
9			**Subjects**		**SNPs**		**Subjects**		**SNPs**		**Subjects**		**SNPs**		**Subjects**		**SNPs**		**Subjects**		**SNPs**		**Subjects**		**SNPs**		**Subjects**		**SNPs**	
10	Number of subjects and SNPs after merging										1,157		300,058		647		264,377		947		335,817						599		341,021	
11	Coding conflicts for SNPs	A/T and C/G SNPs [d]											(+/-) 0				(-) 9759				(-) 1,115								(-) 5,898	
12	Population stratification	MDS (visual identification of outlier)									(+/-) 0		(+/-) 0		(-) 10		(+/-) 0		(-) 144		(+/-) 0						(-) 38		(+/-) 0	
13	Excess of heterzygosity	Inbreeding coefficient > 4 SD									(-) 11		(+/-) 0		(-) 8		(+/-) 0		(-) 1		(+/-) 0						(-) 9		(+/-) 0	
14	Cryptic relatedness	IBS > 1.98 or SD > 6									(-) 4		(+/-) 0		(-) 3		(+/-) 0		(+/-) 0		(+/-) 0						(-) 5		(+/-) 0	
15	Monomorphic SNPs	MAF < 0.01%									(+/-) 0		(-) 5,601		(+/-) 0		(-) 4,103		(+/-) 0		(-) 5,267						(+/-) 0		(-) 1,770	
16	Number of SNPs following **second QC**				506,837				449,874				294,457				250,515				329,435				789,613				333,353	
17	Imputation by IMPUTE				(+) 36,782,916				(+) 36,553,495		(+/-) 0		(+) 37,114,958		(+/-) 0		(+) 41,788,149		(+/-) 0		(+) 38,955,869				(+) 41,296,947		(+/-) 0		(+) 38,950,856	
18	Sample-specific association analysis by SNPTEST	MAF < 0.03 or IMPUTE info score < 0.4			(-) 30,547,262				(-) 30,319,981		(+/-) 0		(-) 30,770,296		(+/-) 0		(-) 34,477,246		(+/-) 0		(-) 32070,895				(-) 34,525,162		(+/-) 0		(-) 32,085,318	
19	Number of subjects and SNPs following **third QC**		**2141**		6,742,491		**1370**		6,683,388		**1100**		6,639,119		**626**		7,561,398		**802**		7,214,409		**708**		7,561,398		**547**		7,198,891	
20	Alignment of MooDS and PGC SNP sets	SNP is absent in three or more SNP sets and/or SNP is absent for PGC			(-) 4,474,549				(-) 4,415,446				(-) 4,371,177				(-) 5,293,456				(-) 4,946,467				(-) 5,293,456				(-) 4,930,949	
	Final number of SNPs for meta-analysis																**2,267,487**													

[a-c]Genome-wide genotyping and quality control for the samples Australia, Germany II and III have been performed in previous studies (for further details see Methods and Table 1 in the manuscript as well as Supplementary Table 8).

[d]The rationale for this filter is exolained in Methods in the manuscriot.

MooDS samples are sorted from left to right according to their sample size.

The following abrevialions are used: A, adenine; C, cytosine; IBS, identity-by-state; G, guanine, MAF, minor allele frequency; MDS, mult-dimensional scaling; SD, standard deviation, SNP, single-nucleotide polymorphism; T, thymine.