

**Supplementary Table 3. 20 strongest associations with change on positive subscale of BPRS in genome-wide analysis.**

Rank	Chromosome	rsID	Gene	Region	$-\log_{10}$ p-value
1	8	rs1561296	<i>CSMD1</i>	Intron	6.79
2	18	rs8091220	intergenic	-	6.60
3	18	rs4939668	intergenic	-	5.96
4	8	rs10504371	intergenic	-	5.77
5	8	rs6981424	intergenic	-	5.63
6	18	rs9957078	intergenic	-	5.48
7	2	rs1561296	<i>SPATS2L</i>	Intron	5.37
8	13	rs1330968	intergenic	-	5.11
9	4	rs2071680	<i>ZFYVE28</i>	Exon	5.09
10	1	rs10802563	<i>ACTN2</i>	Downstream	5.02
11	3	rs2367607	intergenic	-	4.97
12	5	rs4398676	<i>LPCAT1</i>	Intron	4.96
13	8	rs2624095	<i>CSMD1</i>	Intron	4.82
14	20	rs6046528	<i>RIN2</i>	Downstream	4.79
15	9	rs773146	<i>NMRK1</i>	Downstream	4.77
16	20	rs6017147	<i>MYBL2</i>	Intron	4.58
17	1	rs2076590	<i>FAM212B</i>	Downstream	4.56
18	14	rs1956243	intergenic	-	4.50
19	18	rs12954691	<i>MRO</i>	Upstream	4.50
20	5	rs1191746	intergenic	-	4.46