

Supplementary Table 10. SNPs in, or in close proximity to, NF- κ B binding sites within the MHC region that play a role in susceptibility to Schizophrenia, and expression of their neighboring genes.

SNP	Position	LD block ^{*1}	Disease association (reference)	P value	Distance (bp) ^{*2}	Matching Score ^{*3}	Putative NF- κ B binding sequence ^{*4}	Neighbouring genes ^{*5}	Expressions in post-mortem brains of SCZ and/or BD patients ^{*6}	Expressions in PFC of Shn-2 KO mice ^{*7}
rs3734534	26240649	Block 1	SCZ(4)	3.33E-02	41	0.819	AAGGGAGCGCCAA	HIST1H3E, HIST1H2APS3, HIST1H1D, HIST1H4F, HIST1H4G, HIST1H3F	HIST1H1D: \uparrow (7) HIST1H3F: \downarrow (7)	
rs2072803	26392515		SCZ(3)	8.19E-07	5	0.944	GGGGTTCCC	BTN2A2, BTN3A2, BTN3A1		
rs13219354	27185664		SCZ(3)	1.12E-07	-7	0.907	GGTAATGCC	RPL10P2, TRNAV28, TRNAS7, TRNAR17, TRNAL10, TRNAV12, TRNAI17		
rs6917419	27243480	Block 3	SCZ(4)	1.42E-02	18	0.908	GGATATCCC	PRSS16, LOC442172, TRNAI28P, TRNAS32P, TRNAI1, TRNAI11, TRNAV27, TRNAV31, TRANAQ27, TRNAS5		
rs3800316	27256102		SCZ(1)	3.80E-08	17	0.911	AGGATATCCCG			
rs7746199	27261324	Block 4	SCZ(3)	3.81E-08	37	0.826	GGAGTTTCC	LOC442172, TRNAI28P, TRNAS32P, TRNAI1, TRNAI11, TRNAV27, TRNAV31, TRANAQ27, TRNAS5		
rs3800318	27263641		SCZ(1)	5.00E-08	-32	0.911	TGGGAATATCCT	TRNAS5P, TRNAI1, TRNAI11, TRNAV27, TRNAI28P, TRNAV31, TRNAS32P, TRANAQ27, TRNAS5, POM121L2		
rs12182446	27745738		SCZ(3)	4.77E-07	15	0.885	AGGACTTACC	TRNAI1, TRNAI11, TRNAV27, TRNAI28P, TRNAV31, TRNAS32P, TRANAQ27, TRNAS5, POM121L2		
rs17693963	27710165	Block 5	SCZ(3)	2.81E-07	41	0.894	AGGAATTACC	TRNAV7, LOC100131289, TRNAM2, RSL24D1P1, TRANAQ27, TRNAQ10, HISTH4PS1, HIST1HNB, HIST1H2AI		
rs200991	27815494		SCZ(4)	1.37E-02	39	0.842	GGGTTTTTC	TRNAT18, TRNAV15, GPR89P, TRNAV7, LOC100131289		
rs184215243	27925555	Block 6	SCZ(4)	1.72E-02	-9	0.820	GGAACTGCT	LOC100996513, HIST1H2AK, HIST1H4K, HIST1H2BN, HIST1H1B, HIST1H2BPS2, HIST1H2AL	HIST1H2BN: \uparrow (7) HIST1H4K: \uparrow (8) HIST1H1B: \uparrow (8)	
rs1150683	28155314		SCZ(4)	2.85E-02	11	0.877	GNGAAGTCCC	OR2W6P, OR2B6, RPLP2P1, OR2W4P		
rs2299030	28198755		SCZ(4)	2.85E-02	3	0.831	TGGTTCTCC	ZNF192P2, ZNF603P		
rs114108814	28251663	Block 6	SCZ(4)	2.85E-02	3	0.805	GTGCATTCCC	ZNF193, TRNAS13, TOB2P1, ZKSCAN4		
rs13211507	28257377		SCZ(2)	8.30E-11	0	0.867	AGGAAGATCCCN	ZNF187, PGBD1		
rs6918631	28312456		SCZ(4)	1.06E-04	-10	0.853	GTGAAGCCC	PGDB1, ZNF187		
rs13213152	28349698	Block 6	SCZ(4)	1.06E-04	18	0.920	GGGAATTCCA	ZNF323, ZKSCAN3		
rs6927023	28454221		SCZ(5)	8.43E-06	0	0.805	[A/G]GGAGGTCCC	ZSCAN12, ZKSCAN3		
rs2269554	28994989		SCZ(4)	2.93E-05	-19	0.876	GGAAGAACCC	TRNAL12, TRNAL47P, TRMEP1, TRNAT5, GPX6		
rs2394514	29023214	Block 6	SCZ(4)	2.96E-02	42	0.847	TGGTCTTGCC	ZNF211, DR2AD1P, LOC100129636		
rs11961013	29471934		SCZ(4)	1.16E-05	-14	0.838	CAGAATTTCC	LOC100129636		
rs112248026	29542215		SCZ(4)	3.11E-02	-29	0.825	CCTGAATATCCCCC	MAS1L, RPS17P1		
rs3129090	29664131	Block 6	SCZ(4)	3.11E-02	0	0.734	GTGAGTNC	UBD, OR2H5P, TMEM183AP1, RPL13AP, OR2H2		
rs3871467	29677249		SCZ(4)	3.24E-02	34	0.894	GGGAACCCCA	ZFP57, ZDHC20P1		
rs1611388	29680789		SCZ(4)	7.27E-03	-8	0.857	GGCCACTCCC	ZDHC20P1, HLA-F, HCG4P11, RPL23AP1, HLA-F-AS1		
rs2072898	29692729	Block 6	SCZ(4)	7.27E-03	-8	0.857	GGCCACTCCC	ZDHC20P1, HLA-F, HCG4P11, RPL23AP1, HLA-F-AS1		
rs1736913	29704400		SCZ(4)	4.24E-02	28	0.841	AGGGGACTTGCTTC	ZDHC20P1, HLA-F, HCG4P11, RPL23AP1, HLA-F-AS1		
rs9258215	29707307		SCZ(4)	5.14E-04	-26	0.960	GGAAACCCCA	HCG4P11, HLA-F, RPL23AP1, HLA-F-AS1, MICE		
rs1737055	29733742	Block 6	SCZ(4)	4.60E-05	1	0.930	TGGTGTTTCC	HCG4P11, HLA-F, RPL23AP1, HLA-F-AS1, MICE, HCG9P5, IFITM4P		
rs1737030	29737563		SCZ(4)	1.50E-02	22	0.828	GAGAGATCCC	HCG4P11, HLA-F, RPL23AP1, HLA-F-AS1, MICE, HCG9P5, IFITM4P		
rs2734990	29812505		SCZ(4)	1.50E-02	22	0.828	GAGAGATCCC	HCG4P11, HLA-F, RPL23AP1, HLA-F-AS1, MICE, HCG9P5, IFITM4P		
rs1611627	29926741	Block 6	SCZ(4)	3.50E-02	10	0.991	GGAACTCCC	3.8-1.5, HLA-F-AS1, IFITM4P, MICE, HCG9P5		
rs1737030	29737563		SCZ(4)	3.50E-02	26	0.847	AGGGGAACCTCAGA	3.8-1.5, HLA-F-AS1, IFITM4P, MICE, HCG9P5		
rs2734990	29812505		SCZ(4)	3.70E-02	-11	0.858	GGGAATTGTC	3.8-1.5, HLA-F-AS1, IFITM4P, MICE, HCG9P5		
rs1611627	29926741	Block 6	SCZ(4)	2.14E-02	4	0.820	ATGAGTTTCC	HCG4P8, HLA-G, HCGVIII-2, MICE	HLA-G: \uparrow (9)	
rs1611627	29926741		SCZ(4)	2.22E-02	-10	0.863	TGGCTTTCCC	3.8-1.5		

rs1011037	29650741	SCZ(4)	4.44E-02	19	0.814 CAAGTATTTCCCCT	3.0E-14		
rs9259843	29896001			0	0.810 ATGGAANCTTCCAG	MCCD1P1, 3.8-1.3, HCG4B, HLA-K, HLA-U, HCG4P5, HLA-A		
rs2524005	29899677	SCZ(5)	3.81E-07	10	0.824 GTCAAGCCCC	HCG4B, HLA-K, HLA-U, HCG4P5, HLA-A	HLA-A: ↑ (10)	
rs6925061	29992286	SCZ, BD(5)	4.95E-07	12	0.838 GGAAATTC	HLA-J, HCG8, ZNRD1-AS1, ETF1P1, HCG4P3	HLA-J: ↑ (8)	
rs11965452	30011802	SCZ(4)	1.17E-02	28	0.835 GGAATCACCT	ZNRD1-AS1, ETF1P1, ZNRD1		
rs145478650	30128479	SCZ(4)	3.98E-02	0	0.801 GGGGACTNCTCC	TRIM40, TRIM10, TRIM15	TRIM15: ↑ (7, 9)	
rs12663184	30301600	SCZ(4)	2.80E-02	-42	0.972 CAGGAACTTCCCCA	HCG18, HCG17, TRIM39, TRIM39-RPP21, HLA-N	HCG18: ↑ (7)	
rs4713325	30383442	SCZ(4)	2.14E-02	-40	0.921 AGGCGTTTCC	MICC		
rs4713328	30383876	SCZ(4)	7.51E-03	-13	0.829 CTGACTTTCC	MICC		
rs4713328	30383876	SCZ(4)	7.51E-03	-15	0.814 GGGGCTTGGC	MICC		
rs2157605	30454076	SCZ(4)	4.12E-03	14	0.808 GGGTGTTC	TMPOP1, SUCLA2P1, RANP1, HLA-E	HLA-E: ↓	
rs188502980	30530949			0	0.721 TGTGACTTCCNA	GNL1, PRR3, ABCF1	GNL1: ↓ (7, 12)	
rs148600920	30670918			0	0.916 TGGGGATTCCCN	PPP1R18, NRM, RPL7P4, MDC1, TUBB		
rs150040417	30680130			0	0.729 GCNGGACTTCCTTC	RPL7P4, MDC1, TUBB	TUBB: ↓ (7), ↑ (9)	
rs142435078	30864590			0	0.748 AGTGGATTTCCNTC	DDR1, GTF2H4, VARS2	DDR1: ↑ (7, 9) GTF2H4: ↑ (7)	
rs2530709	30940569	SCZ(4)	3.80E-02	-25	0.830 AGTGGATGTACCCA	DPCR1, LOC100422429, LOC100420530, MUC21,		
rs12528087	30980603	SCZ(4)	4.98E-02	-5	0.847 GGGGCTTTGC	MUC22		
rs9263715	31095801	SCZ(4)	5.48E-04	-40	0.852 GGCAGGGCCC	C6orf15, CDSN, PSORS1C1, PSORS1C2, POLR2LP, CCHCR1		
rs3134762	31210866	SCZ(4)	1.24E-02	30	0.881 AGGATATTCC			
rs1050437	31239585							
rs72558135	31239586							
rs1050438	31239592							
rs41542719				0	0.870 GGAGAGCCCCN	HLA-C, USP8P1, RPL3P2, WASF5P		
rs3177890	31239593							
rs41542719								
rs45574634	31239594							
rs16899205	31266361	SCZ(4)	4.47E-02	-42	0.815 ATGGGAGTTCTCA	USP8P1, RPL3P2, WASF5P		
rs2524089	31266522	SCZ(4)	1.46E-02	28	0.840 GGGACAGACC	USP8P1, RPL3P2, WASF5P		
rs2844569	31336604	SCZ(4)	3.85E-02	36	0.825 AAGGACAATCCACA	HLA-B, DHFRP2, FGFR3P1, ZDHHC20P2, HLA-S	HLA-B: ↓ (9)	
rs2524094	31240041	Block 7		0	0.819 NGGATTCTCC	HLA-C, USP8P1, RPL3P2, WASF5P		
rs2442749	31352040	SCZ(4)	6.65E-04	43	0.923 GGGGACTTCC	DHFRP2, FGFR3P1, ZDHHC20P2, HLA-S, MICA		
rs78961316	31325125			0	0.900 TGGNGAATCCCC	HLA-B, DHFRP2	HLA-B: ↓ (9)	
rs75369119								
rs191718782	31528188			0	0.884 NGGGGTTCCC	ATP6V1G2-DDX39B, DDX39B, ATP6V1G2, NFKBIL1, LOC100287329, LTA, TNF	ATP6V1G2: ↓ (7)	
rs147118182	31550289			0	0.706 GGAATTTCCN	LOC100287329, LTA, TNF, LTB, LST1, LST1	LST1: ↓ (11)	
rs2857597	31585000	SCZ(4)	2.57E-02	42	0.914 GGAATCCCCC	UQCRHP1, AIF1, SNORA38, PRRC2A	AIF1: ↓ (11), ↑ (12)	AIF1: ↑
rs151200532	31601179			0	0.885 CNGGGGCTTCCCCT	AIF1, SNORA38, PRRC2A, BAG6, APOM	AIF1: ↓ (11), ↑ (12)	AIF1: ↑
rs113819636	31601185			0	0.900 GGGGANGCCC	AIF1, SNORA38, PRRC2A, BAG6, APOM	AIF1: ↓ (11), ↑ (12)	AIF1: ↑
rs2272593	31601344			0	0.810 GGGAGCAGCC	AIF1, SNORA38, PRRC2A, BAG6, APOM	AIF1: ↓ (11), ↑ (12)	AIF1: ↑
rs1046089	31602967	SCZ(4)	1.19E-02	-38	0.821 GGAATCACA	PRRC2A, BAG6, APOM, C6orf47, GPANK1, CSNK2B, LY6G5B		
rs805301	31618121	SCZ(4)	4.55E-03	45	0.821 GGAATCACA	PRRC2A, BAG6, APOM, C6orf47, GPANK1, CSNK2B, LY6G5B		
rs147925659	31615449			0	0.772 GGGGCANGCTCCTC	PRRC2A, BAG6, APOM, C6orf47, GPANK1, CSNK2B		
rs142009508	31627341			0	0.803 GGACACCCCN	BAG6, APOM, C6orf47, GPANK1, CSNK2B, LY6G5B, LY6G5C		

rs11549123	31702008			0	0.778	TTGGGAACTGNCCA	LY6G6D, LY6G6C, C6orf25, CLIC1, MSH5-SAPCD1, MSH5	CLIC1: ↑ (12)	
rs707928	31742590	SCZ(4)	2.34E-03	-10	0.811	TGTGTTTTCC	MSH5, MSH5-SAPCD1, SAPCD1, VMA7, VARS	VMA7: ↓ (9)	
rs140366323	31749648			0	0.819	AGNGGACACTCCGA	MSC5, MSH5-SAPCD1, SAPCD1, VMA7, VARS, LSM2	VMA7: ↓ (9)	
rs145442830	31749658			0	0.891	GGGGACNGTCCAG	C4A [*] , C4B, CYP21A2, TNXB	C4A: ↑ (12)	C4A: ↑ C4B: ↑
rs41258944	32017242			0	0.855	CNGGGACCATCCAG	C4A [*] , C4B, CYP21A2, TNXB	C4A: ↑ (12)	C4A: ↑ C4B: ↑
rs61745920	32017243			0	0.758	CGGNGACTGTCCAG	TNXB		
rs61746537	32021355			0	0.806	NGGAACTGTCCA	TNXB		
rs61740712	32021358			0	0.806	GGGNCTCGCC	TNXB		
rs141752970	32032790			0	0.797	AGAAAGNCCC	PRRT1, LOC100507547, PPT2, PPT2-EGFL8, EGFL8, AGPAT1	PRRT1: ↑ (7)	
rs142409885	32036357			0	0.868	TTGGAACITTCNA	PPT2-EGFL8, EGFL8, AGPAT1, RNF5, AGER, PBX2, GPSM3, NOTCH4	AGER: ↑ (9) PBX2: ↑ (8) GPSM3: ↑ (8)	
rs3749962	32036363			0	0.894	GTGAATTCCC	AGER, PBX2, GPSM3, NOTCH4	AGER: ↑ (9) PBX2: ↑ (8) GPSM3: ↑ (8)	
rs61744966	32036363			0	0.709	AGGTNCCCC	GPSM3, NOTCH4		
rs112581362	32057142			0	0.834	NGTGGACCCTCTG	NOTCH4		
rs117182156	32057148			0	0.864	TNGGAAGGTCCATT	HCG23, BTNL2		
rs186990718	32121861			0	0.894	GGNACTCCCC	HLA-DRB5	HLA-DRB5: ↑ (7, 12)	
rs1661134	32155121			0	0.847	CTGGAAGTCCCT	C6orf10, HCG23, BTNL2		C6orf10: ↑
rs146965329	32155125	SCZ(2)	2.30E-10	37	0.977	AGGAATTTCC	HLA-DQA1	HLA-DQA1: ↑ (13)	HLA-DQA1: ↑
rs3131296	32172993			0	0.901	GGGATTNCCC	HLA-DQA1	HLA-DQA1: ↑ (13)	HLA-DQA1: ↑
rs143622513	32181942			0	0.894	GGGATTCCN	HLA-DQB1	HLA-DQB1: ↑ (7, 12, 13)	
rs146606566	32181945			0	0.885	GGCAACTCCT	HLA-DQA2		
rs138205668	32188865			0	0.843	TGGAAANTACCT	HLA-DOB, TAP2, PSMB8, LOC100507463, TAP1	TAP2: ↑ (9) TAP1: ↑ (12)	
rs141236527	32188869			0	0.798	NGTGACTCCCCA	HLA-DMA, BRD2	HLA-DMA: ↑ (12)	
rs146677249	32364137			0	0.901	NGGAGTTCCC	BRD2		
rs115417906	32489822			0	0.754	GGNGACTTTGCC	COL11A2, RXRB, RNY4P10, SLC39A7, MIR219-1, HSD17B8, RING1, ZNF70P1	RXRB: ↓ (7), ↑ (9)	
rs148834340	32489825			0	0.732	GGCNCCTTCC	COL11A2, RXRB, RNY4P10, SLC39A7, MIR219-1, HSD17B8, RING1, ZNF70P1	RXRB: ↓ (7), ↑ (9)	
rs3117099	32358270	SCZ(5)	4.12E-06	6					
		SCZ, BD(5)	2.70E-06						
rs9272219	32602269	SCZ(1)	6.90E-08	-2					
		SCZ(3)	6.88E-08						
rs115222936	32605039			0					
rs9274652	32636235	Block 8		0					
rs9276227	32700684	SCZ(4)	1.06E-02	-15					
rs17220178	32794947			0					
rs147219068	32940687			0					
rs140566548	32940694			0					
rs142520217	32940695			0					
rs34652619	32942636			0					
rs1048780	33170841			0					
rs150581613	33173227			0					

Abbreviations: SNP, single-nucleotide polymorphism; LD, linkage disequilibrium; SCZ, schizophrenia; BD, bipolar disorder

- *1: LD blocks reported in a previous study (3) (Blocks 6–8; estimated based on Figure S10 in (3))
- *2: distance (bp) between the predicted NF- κ B binding region and the most proximal (0–40bp) SNP site (plus, 5'→3'; minus, 3'→5'; 0, SNP on NF- κ B binding region)
- *3: matching score between a matrix of NF- κ B binding sites and an arbitrary section of the input sequence (calculated using Match (<http://www.gene-regulation.com/cgi-bin/pub/programs/match/bin/match.cgi>) using a library of mononucleotide weight matrices fromTRANSFAC)
- *4: NF- κ B binding site sequence predicted by TRANSFAC (N: position of the SNPs)
- *5: genes in the flanking regions (approximately 20-kb) of the SNPs (identified using the 1000 Genomes Browser (<http://www.ncbi.nlm.nih.gov/variation/tools/1000genomes/>))
- *6: genes up- (↑) or down-regulated (↓) in the post-mortem brains of SCZ and/or BD patients (identified by curated studies in NextBio (<http://www.nextbio.com>))
- *7: genes up- or down-regulated in the PFC of Shn-2 KO mice (identified using NextBio)
- *8: 26.8kbp apart from rs61745920

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