Table S4. Logistic regression analysis between SNPs and controls and "solo and depressed" groups.						
SNP	Model	Genotype	**CONTROL** (N)	**SOLO AND DEPRESSED** (N)	OR (95% CI)	P-value
rs182549	Log-additive	CC	38	14	0,51 (0,27-0,96)	0,03
		CT	59	16		
		TT	23	1		
rs2154110	Recessive	TT/GT	119	27	1	
		GG	1	4	17,63 (1,89-164,09)	0,0035
rs4902100	Recessive	AA/AG	119	27	1	
		GG	1	4	17,63 (1,89-164,09)	0,0035
rs6265	Log-additive	CC	81	14	2,94 (1,42-6,11)	0,0034
		CT	39	14		
		TT	0	3		

Table 8b. Logistic regression analysis between SNPs and controls and depressed groups.						
SNP	Model	Genotype	**CONTROLS** (N)	**DEPRESSED** (N)	OR (95% CI)	P-value
rs10904887	Dominant	TT	33	4	1	0.017
		CT/CC	87	1	0.09 (0.01-0.88)	
rs10904896	Dominant	GG	33	4	1	
		AG/AA	87	1	0.09(0.01-0.88)	0.017
rs12335203	Log-additive	TT	25	4	0.09(0.01-0.74)	
		CT	67	1		
		CC	28	0		0,0041
rs2154110	Log-additive	TT	64	1	6.88 (1.03-46.13)	0.031
		GT	55	3		
		GG	1	1		
rs391300	Log-additive	CC	27	4	0.09(0.01-0.80)	0.0056
		CT	66	1		
		TT	27	0		
		GG	1	1		

Table 8C. Logistic regression analysis between SNPs and controls and solo groups.						
SNP	Model	Genotype	**CONTROLS** (N)	**SOLO** (N)	OR (95% CI)	P-value

rs10509637	Dominant	AA AG/GG	79 41	118 35	1 0.57 (0.33-0.99)	0.039
rs12335203	Dominant	CC CT/TT	28 92	53 100	1 0.57(0.34-0.98)	0.041
rs2154110	Codominant	TT GT GG	64 55 1	91 48 14	1 9.85(1.26-76.78)	0.0007
rs391300	Dominant	CC CT/TT	27 93	60 92	1 0.45(0.26-0.76)	0.0026
rs4902100	Codominant	AA AG GG	67 52 1	92 47 14	1 10.20(1.31-79.44)	0.001
rs7675998	Dominant	GG AG/AA	56 64	95 58	1 0.53(0.33-0.87)	0.011
rs7412	Log-additive	CC TC TT	98 19 3	138 14 1	0.51(0.27-0.96)	0.032