	Dominant			Additive			Recessive		
Marker	P	Slope	Slope SE	P	Slope	Slope SE	P	Slope	Slope SE
COMT rs4680	0.26	-1.41	1.24	0.03	-1.57	0.73	0.03	-2.59	1.15
DRD2 rs2283265	0.59	0.60	1.10	0.47	0.71	0.97	0.41	2.64	3.17
HTR2A rs6311	0.38	-0.95	1.08	0.62	-0.35	0.70	0.91	0.14	1.22
HTR2A rs6314	0.14	1.94	1.30	0.05	2.29	1.17	0.02	10.22	4.40
MAOA pVNTR	0.48	0.75	1.05	0.37	0.71	0.80	0.46	1.22	1.67
MAOA rs1801291	0.13	1.54	1.00	0.05	1.46	0.74	0.08	2.76	1.57
SLC6A3 In8 VNTR	0.86	0.19	1.04	0.95	0.06	0.89	0.79	-0.70	2.62
SLC6A3 rs6347	0.38	0.90	1.01	0.67	0.34	0.78	0.57	-1.00	1.76
SLC6A3 rs27072	0.24	1.35	1.14	0.46	0.70	0.95	0.51	-1.74	2.62
SERTLPR	0.97	-0.04	1.06	1.00	-0.003	0.73	0.97	0.05	1.35
TPH2 rs7305115	0.92	-0.10	1.06	0.78	-0.21	0.75	0.68	-0.58	1.42

Table S4: Genetic association summary of functional polymorphisms in the additional seven candidate genes with EPDS score.