Table 1: Allele frequencies

		All affecteds*					SCZ + SA				
SNP ID (dbSNP No)	Alleles (major/ minor) *	MAF Controls	MAF Cases	p-value	Trend p-value	OR (95%CI)	MAF Controls	MAF Cases	p-value	Trend p-value	OR (95%CI)
		n = 467	n = 394				n = 467	n = 258			
rs2097063 (287A/G)	**A**/G	0.414	0.346	*0.004*	*0.006*	1.34 (1.10, 1.64)	0.414	0.347	*0.015*	*0.019*	1.33 (1.06, 1.67)
rs737865	T/C	0.309	0.332	0.315	0.321	1.11 (0.90, 1.37)	0.309	0.329	0.438	0.448	1.10 (0.87, 1.39)
rs4680 (Val/Met)	A/**G**	0.475	0.524	*0.050*	*0.048*	1.21 (1.00, 1.47)	0.475	0.504	0.304	0.299	1.12 (0.90, 1.40)
rs165599	A/**G**	0.326	0.376	*0.035*	*0.040*	1.25 (1.02, 1.53)	0.326	0.364	0.160	0.175	1.18 (0.94, 1.49)

		SCZ					Affective disorder*				
SNP ID (dbSNP No)	Alleles (major/ minor) *	MAF Controls	MAF Cases	p-value	Trend p-value	OR (95%CI)	MAF Controls	MAF Cases	p-value	Trend p-value	OR (95%CI)
		n = 467	n = 196				n = 467	n = 112			
rs2097063 (287A/G)	**A**/G	0.414	0.338	*0.011*	*0.014*	1.39 (1.08, 1.79)	0.414	0.346	*0.062*	*0.067*	1.34 (0.98, 1.82)
rs737865	T/C	0.309	0.327	0.511	0.518	1.09 (0.84, 1.41)	0.309	0.329	0.560	0.556	1.10 (0.80, 1.50)
rs4680 (Val/Met)	A/**G**	0.475	0.500	0.419	0.414	1.10 (0.87, 1.41)	0.475	0.565	*0.018*	*0.015*	1.43 (1.06, 1.93)
rs165599	A/**G**	0.326	0.362	0.221	0.240	1.17 (0.91, 1.51)	0.326	0.400	*0.039*	*0.043*	1.38 (1.02, 1.87)

		Major depressive disorder					BP				
SNP ID (dbSNP No)	Alleles (major/ minor) *	MAF Controls	MAF Cases	p-value	Trend p-value	OR (95%CI)	MAF Controls	MAF Cases	p-value	Trend p-value	OR (95%CI)
		n = 467	n = 30				n = 467	n = 82			
rs2097063 (287A/G)	**A**/G	0.414	0.283	*0.046*	*0.049*	1.79 (1.01, 3.18)	0.414	0.369	0.280	0.290	1.21 (0.86, 1.71)
rs737865	T/C	0.309	0.333	0.688	0.689	1.12 (0.64, 1.95)	0.309	0.327	0.638	0.634	1.09 (0.76, 1.56)
rs4680 (Val/Met)	A/**G**	0.475	0.586	0.101	0.093	1.56 (0.91, 2.68)	0.475	0.557	*0.058*	*0.050*	1.39 (0.99, 1.95)
rs165599	A/**G**	0.326	0.414	0.169	0.184	1.46 (0.85, 2.51)	0.326	0.395	0.088	0.095	1.35 (0.96, 1.91)

* All Affecteds: SCZ (schizophrenia), SA (schizoaffective disorder), BP (bipolar disorder), Major depressive disorder, psychotic disorder NOS, depressive disorder NOS
* Affective Disorder: Bipolar disorder and major depressive disorder

remained significant (p = 0.015; OR = 1.33). This SNP also remained significant when only patients with schizophrenia were included (n = 196; p = 0.011, OR = 1.39). None of the SNPs yielded significant p-values in the group of patients with schizoaffective disorder (n = 62; data not shown). In the set of patients who were diagnosed with an affective disorder (n = 112; 82 bipolar disorder, 30 major depressive disorder), significant p-values were obtained for the G (Val) allele of the Val/Met polymorphism (p = 0.018; OR = 1.43) and the G allele of rs165599 (p = 0.039; OR = 1.38). The A allele of SNP -278A/G showed a trend for significance in this group (p = 0.062; OR = 1.34). When broken down into subcategories, -278A/G was marginally associated in the major depressive group (n = 30; p = 0.046; OR = 1.79) and Val158Met showed a trend towards association in the group of bipolar patients (n =

82; p = 0.058, OR = 1.39). Overall evidence for association was most robust for the promoter polymorphism -278 A/G.

Marker-to-Marker Linkage Disequilibrium
Linkage disequilibrium (LD) between the four SNPs was assessed in cases and controls via Lewontin's D' statistic (Table 2). The markers span 28.5 kb on genomic DNA. In general, LD was higher between markers located in the 5' region of the gene. SNP -287 A/G is located only 2 kb from SNP rs737865 and is in complete LD with it. LD was also high for marker pair rs737865 – Val/Met. SNP rs165599 showed modest LD with the Val/Met polymorphism. This pattern is consistent with previous reports [40,45]. In contrast, a recent study by Chen *et al.* found only modest LD between rs737865 and the Val/Met polymorphism [22].