Supplemental Table 1. ***TCEAL7*** **Genotype Frequencies**

							All Cases			Controls		
SNP	**Chr X Position**	**Alleles**	**LD Bin**	**Location**	**MAF**	**HWE**	**AA**	**AB**	**BB**	**AA**	**AB**	**BB**
rs5987515	102,465,559	C>A	---	5′ upstream	0.40	0.80	364	427	136	377	476	179
rs5987724	102,465,772	G>T	---	5′ upstream	0.40	0.77	365	428	136	376	474	179
rs5945971	102,470,061	G>A	3	5′ upstream	0.40	0.96	365	421	138	376	478	177
rs17340307	102,470,522	A>C	---	5′ upstream	<0.01	1.00	918	8	0	1033	3	0
rs1045761	102,472,558	C>G	2	5′ UTR	0.49	0.83	275	448	204	286	488	260
rs5945680	102,478,489	C>T	1	3′ downstream	0.29	0.55	474	371	82	520	432	83

Position from genome build 36.3; dbSNP 129; Refseq Release 29 (May 4, 2008); call rate all participants; MAF, minor allele frequency, among controls; HWE p-value among Caucasian controls only; rs5945680 (LD bin 1) tags rs5945767 at $r^2 > 0.8$; AA, major allele homozygotes, AB heterozygotes, BB minor allele homozygotes.