

Genotype distributions of the significant SNPs in TF pathway genes in cases and controls. ORs, 95% CI and *P*-values determined with respect to the risk allele (**bold**) using logistic regression (additive model). Alleles for the positive DNA strand (UCSC annotated) are shown.

SNP	Cases (n)	Controls (n)	OR	95% CI	<i>P</i> -value (unadj)
rs12120605 (F5)					
GG	262	244			
TG	88	59	1.49	1.05-2.11	0.024
TT	6	1			
rs6427202 (F5)					
TT	99	103			
CT	191	165	1.32	1.04-1.66	0.021
CC	66	38			
rs9332542 (F5)					
GG	185	124			
AG	140	155	1.32	1.04-1.68	0.022
AA	32	28			
rs6427199 (F5)					
GG	146	97			
AG	156	161	1.27	1.02-1.59	0.036
AA	50	48			
rs3093261 (F10)					
CC	106	118			
TC	175	137	1.31	1.06-1.63	0.013
TT	77	51			
rs2069948 (EPCR)					
TT	103	118			
TC	173	125	1.25	1.01-1.54	0.037
CC	80	62			