

Supplementary Table 2: Distribution of *VEGF* gene variations in all *del22q11S* cases and healthy controls

Genotypes Alleles	All <i>del22q11S</i> cases	Healthy controls		
	Number (Frequency) (N = 91)	Number (frequency) (N = 316)	P-value	Crude Odds Ratio (95% CI)
-2578C→A				
CC	26 (0.29)	97 (0.31)	0.38 ^a	1.4 (0.8-2.7)
CA	41 (0.45)	157 (0.50)		
AA	24 (0.26)	62 (0.20)		
C	93 (0.51)	351 (0.56)	0.29 ^b	1.2 (0.9-1.7)
A	89 (0.49)	281 (0.44)		
-1154G→A				
GG	35 (0.38)	152 (0.48)	0.18 ^a	1.9 (0.9-3.9)
AG	42 (0.46)	132 (0.42)		
AA	14 (0.15)	32 (0.10)		
G	112 (0.62)	436 (0.69)	0.06 ^b	1.4 (0.99- 2.0)
A	70 (0.38)	196 (0.31)		
-634G→C				
GG	39 (0.43)	147 (0.47)	0.74 ^a	1.0 (0.4-2.3)
GC	43 (0.47)	135 (0.43)		
CC	9 (0.10)	34 (0.11)		
G	121 (0.66)	429 (0.68)	0.72 ^b	0.9 (0.7-1.3)
C	61 (0.34)	203 (0.32)		

Distribution of genotypes and alleles (frequencies in brackets) for the indicated single nucleotide polymorphisms in all *del22q11S* cases and in healthy controls. *P*-values were calculated by comparing *del22q11S* cases to healthy controls using the χ^2 contingency test with 2 df ^a or 1df ^b.

Odds ratios (95% confidence intervals between brackets) were calculated

relative to the -2578CC, -1154GG or -634CC genotypes or to the -2578C, -1154G or -634C allele.