Online material

Supplemental data (online only)

Table A. Results of genotypic association test for the SNP significantly associated with CVL for the extended case-control cohort assuming different genetic models: [1]general, [2]recessive, [3]codominant, and [4]dominant. * p-value < 0.05; ** p-value < 0.01. [5]Risk genotype corresponds to the genotype positively associated with cases. We have applied a Fisher exact test for the analysis of the SNP of the promoter (A180G and G318A). $^{+}$ Haldane correction applied.

SNP	Risk genotype[5]	Odds ratio	95% CI	p-value
A180G	GG[1]	–	–	0.082
	GG[2]	3.70^{+}	0.15–92.31^{+}	0.451
	AG[3]	8.90	0.45–175.60	0.089
	AG + GG[4]	11.63^{+}	0.61–220.22^{+}	0.039*
G318A	AA	–	–	0.082
	AA	6.26^{+}	0.30–132.75^{+}	0.202
	AG	6.26^{+}	0.30–132.75^{+}	0.202
	AA + AG	11.63^{+}	0.61–220.22^{+}	0.039*
A4549G	GG	–	–	0.140
	GG	1.83	1.02–3.30	0.042*
	AA + GG	1.03	0.44–2.40	0.944
	AG + GG	1.57	0.76–3.26	0.262
C4859T	TT	–	–	0.006**
C4859T	TT	–	–	0.006**
	TT	14.45^{+}	0.76–273.68^{+}	0.013*
	CT	2.18	0.93–5.08	0.067
	CT + TT	3.04	1.34–6.91	0.006**