

eTable. Coefficients obtained when fitting the model reported originally⁴ to the analysis set used in the present study. As in the original report, effect estimates are from models adjusted for age and sex.

Gene ¹ (rs ID), genotypic model ²	Original report		Present study	
	OR (95% CI)	P	OR (95% CI)	P
CDC42 (rs2056974), d	2.09 (1.24-3.52)	5.60E-03	2.10 (1.25-3.54)	5.1E-03
DCC ₁ (rs1160400), r ³	7.75 (1.06-57.01)	4.40E-02	6.63 (0.82-53.35)	7.5E-02
DCC ₂ (rs1466373), d	2.03 (1.14-3.64)	1.70E-02	2.05 (1.14-3.68)	1.6E-02
DCC ₃ (rs1502219), a	2.42 (1.55-3.79)	1.00E-04	2.43 (1.56-3.80)	9.4E-05
DCC ₄ (rs4334396), r	14.33 (3.92-52.34)	5.60E-05	14.38 (3.94-52.51)	5.5E-05
DCC ₅ (rs7506794), a	0.07 (0.03-0.19)	1.60E-07	0.07 (0.03-0.19)	1.6E-07
EFNA5 ₁ (rs152580), r	2.78 (1.49-5.19)	1.30E-03	2.77 (1.49-5.17)	1.3E-03
EFNA5 ₂ (rs252802), d	2.94 (1.58-5.47)	7.00E-04	2.96 (1.59-5.52)	6.5E-04
EFNA5 ₃ (rs6868410), r	0.67 (0.07-7.00)	7.40E-01	0.68 (0.07-7.12)	7.5E-01
EPHA4 (rs10498114), d	0.38 (0.21-0.68)	1.20E-03	0.38 (0.21-0.68)	1.2E-03
EPHB1 ₁ (rs11917038), a	0.93 (0.49-1.76)	8.20E-01	0.92 (0.49-1.75)	8.0E-01
EPHB1 ₂ (rs1404577), r	0.19 (0.06-0.66)	8.60E-03	0.19 (0.06-0.66)	8.6E-03
EPHB1 ₃ (rs6793828), r	0.48 (0.24-0.95)	3.50E-02	0.47 (0.23-0.94)	3.2E-02
EPHB1 ₄ (rs9865620), d	0.24 (0.13-0.45)	6.80E-06	0.24 (0.13-0.45)	7.0E-06
EPHB2 (rs11800828), d	1.89 (1.07-3.35)	3.00E-02	1.88 (1.06-3.33)	3.1E-02
FYN ₁ (rs11153311), a	0.36 (0.20-0.64)	5.50E-04	0.36 (0.20-0.64)	5.0E-04
FYN ₂ (rs809193), a	2.31 (1.48-3.62)	2.40E-04	2.31 (1.48-3.61)	2.5E-04
GSK3B (rs3108749), a	0.36 (0.20-0.66)	1.00E-03	0.36 (0.20-0.66)	9.0E-04
PAK7 ₁ (rs1033470), d	2.58 (1.51-4.43)	5.70E-04	2.58 (1.50-4.42)	5.8E-04
PAK7 ₂ (rs219861), d	0.53 (0.30-0.93)	2.60E-02	0.53 (0.30-0.93)	2.7E-02
PLXNA2 ₁ (rs2782934), r	0.19 (0.07-0.51)	1.00E-03	0.19 (0.07-0.51)	1.1E-03
PLXNA2 ₂ (rs6685511), d	2.26 (1.21-4.22)	1.10E-02	2.26 (1.21-4.22)	1.0E-02
PLXNC1 ₁ (rs10507033), r	0.02 (0.003-0.16)	1.70E-04	0.02 (0.003-0.16)	1.7E-04
PLXNC1 ₂ (rs865569), r	21.64 (2.41-194.15)	6.00E-03	21.53 (2.40-193.08)	6.1E-03
PPP3CA (rs2732504), d	0.48 (0.29-0.82)	6.30E-03	0.49 (0.29-0.82)	7.2E-03
RAC2 (rs9610680), a	1.95 (1.19-3.21)	8.20E-03	1.97 (1.20-3.24)	7.5E-03
RRAS2 (rs2970334), d	0.32 (0.17-0.60)	4.20E-04	0.33 (0.17-0.61)	5.3E-04
SEMA5A ₁ (rs1512508), d	2.38 (1.27-4.47)	6.70E-03	2.39 (1.28-4.48)	6.5E-03
SEMA5A ₂ (rs40701), r	0.98 (0.39-2.47)	9.60E-01	0.99 (0.39-2.51)	9.8E-01
SLIT3 ₁ (rs11746295), r	0.14 (0.03-0.58)	6.70E-03	0.14 (0.03-0.58)	7.0E-03
SLIT3 ₂ (rs1979923), r	0.2 (0.08-0.53)	1.20E-03	0.21 (0.08-0.54)	1.3E-03
SLIT3 ₃ (rs884787), d	3.48 (1.44-8.43)	5.80E-03	3.49 (1.44-8.46)	5.6E-03
UNC5C (rs6820369), d	2.22 (1.03-4.76)	4.10E-02	2.18 (1.01-4.70)	4.6E-02

Interactions

DCC ₅ * FYN ₁	17.01 (3.06-94.59)	1.20E-03	17.26 (3.11-95.80)	1.1E-03
EPHB1 ₁ * EPHB1 ₄	3.82 (1.39-10.48)	9.30E-03	3.85 (1.41-10.57)	8.7E-03
PLXNC1 ₁ * PLXNA2 ₂	29.53 (1.82-478.49)	1.70E-02	29.88 (1.83-486.68)	1.7E-02
RRAS2* SEMA5A ₂	4.85 (1.44-16.33)	1.10E-02	4.78 (1.42-16.14)	1.2E-02
SLIT3 ₃ * SEMA5A ₂	15.93 (2.00-127.05)	9.00E-03	15.77 (1.96-126.53)	9.4E-03
RRAS2* EFNA5 ₃	0.03 (0.001-0.67)	2.70E-02	0.03 (0.001-0.66)	2.6E-02

¹ Subscript is used to identify individual SNPs in interactions.

² a = log-additive, d = Mendelian dominant, r = Mendelian recessive.

³ The exceptional difference in OR between the two models must be seen in relation to the large confidence interval. Examination of models with this SNP only suggested no irregularities.