Supplemental Table 1 Allelic Frequencies of SNPs identified in the coding region of *RAI1*.

Ref SNP	*RAI1* exon	Alleles (ancestral/variation)	A/A	A/B	B/B
rs61999281	3	G/A	0.896		0.103
rs3803763	3	G/C	0.137	0.655	0.206
rs35068024	3	GC/DEL	0.586		0.413
rs34083643	3	G/del	0.172	0.482	0.344
rs71944489	3	GCA/DEL	0.551		0.448
rs11649804	3	C/A	0.310	0.551	0.137
rs8067439	3	G/A	0.206	0.482	0.275
rs4925112	3	T/C	0.689	0.275	0.034
rs32686634	3	C/T	0.758		0.241
rs3818717	4	T/C	0.482	0.413	0.103
c.1143 C>T	3	C/T	0.986		0.013

(A – ancestral / B – variation)

Supplemental Table 2 *In silico* predictions of pathogenicity for variants described in this study.

Database	**c.3650G→A (R1217Q)**	**c.4166A→G (Q1389R)**
Panther	Probably damaging	Probably damaging
PolyPhen	Predicted to be benign	Probably damaging
Pmut	Pathological	Pathological
SIFT	Affect Protein Function	Affect Protein Function