

Supplementary Information

Table S1. Genetic model of single nucleotide polymorphisms and analysis of their association with acute mountain sickness (AMS).

SNP Number	Model	Genotype	AMS ⁺ [n (%)]	AMS ⁻ [n (%)]	OR (95% CI)	<i>p</i> Value	AIC	BIC
rs1054399	Codominant	CC	156 (82.5%)	158 (83.2%)	1.00	—	—	—
		CT	30 (15.9%)	28 (14.7%)	0.91 (0.52–1.60)	—	—	—
		TT	3 (1.6%)	4 (2.1%)	0.96 (0.19–4.86)	0.95	537.8	569.3
	Dominant	CC	156 (82.5%)	158 (83.2%)	1.00	—	—	—
		CT + TT	33 (17.5%)	32 (16.8%)	1.79 (1.13–2.84)	0.75	535.8	563.3
	Recessive	CC + CT	186 (98.4%)	186 (97.9%)	1.00	—	—	—
		TT	3 (1.6%)	4 (2.1%)	0.98 (0.52–1.60)	0.98	535.9	563.4
	Overdominant	CC + TT	159 (84.1%)	162 (85.3%)	1.00	—	—	—
		CT	30 (15.9%)	28 (14.7%)	0.91 (0.52–1.60)	0.75	535.8	563.3
	Logadditive	—	—	—	0.93 (0.58–1.50)	0.78	535.8	563.3
rs11190613	Codominant	TT	156 (82.1%)	158 (83.7%)	1.00	—	—	—
		CT	31 (16.3%)	28 (14.7%)	0.88 (0.50–1.54)	—	—	—
		CC	3 (1.6%)	3 (1.6%)	0.96 (0.19–4.87)	0.91	514.4	545.6
	Dominant	TT	156 (82.1%)	159 (83.7%)	1.00	—	—	—
		CT + CC	34 (17.9%)	31 (16.3%)	0.89 (0.52–1.52)	0.67	512.7	540
	Recessive	TT + CT	187 (98.4%)	187 (98.4%)	1.00	—	—	—
		CC	3 (1.6%)	3 (1.6%)	0.98 (0.20–4.95)	0.98	518.2	545.6
	Overdominant	TT + CC	159 (83.7%)	162 (85.3%)	1.00	—	—	—
		CT	31 (16.3%)	28 (14.7%)	0.88 (0.57–1.46)	0.66	518.8	546.1
	Logadditive	—	—	—	0.91 (0.57–1.46)	0.7	513.6	540.9
rs11816840	Codominant	GG	156 (82.1%)	159 (83.7%)	1.00	—	—	—
		CG	31 (16.3%)	28 (14.7%)	0.88 (0.50–1.54)	—	—	—
		CC	3 (1.6%)	3 (1.6%)	0.96 (0.19–4.87)	0.82	537.3	568.8
	Dominant	GG	156 (82.1%)	159 (83.7%)	1.00	—	—	—
		CG + CC	34 (17.9%)	31 (16.3%)	0.89 (0.52–1.52)	0.76	535.6	563.1
	Recessive	GG + CG	187 (98.9%)	187 (98.4%)	1.00	—	—	—
		CC	2 (1.1%)	3 (1.6%)	0.98 (0.20–4.95)	0.65	535.4	563
	Overdominant	GG + CC	159 (83.7%)	162 (85.3%)	1.00	—	—	—
		CG	31 (16.3%)	28 (14.7%)	0.88 (0.57–1.46)	0.64	535.4	563
	Logadditive	—	—	—	0.96 (0.50–1.53)	0.88	535.6	563.2

Table S1. *Cont.*

SNP Number	Model	Genotype	AMS ⁺ [n (%)]	AMS ⁻ [n (%)]	OR (95% CI)	<i>p</i> Value	AIC	BIC
rs3750633	Codominant	GG	156 (82.5%)	159 (83.6%)	1.00	—	—	—
		AG	30 (15.9%)	28 (14.8%)	0.91 (0.52–1.60)	—	—	—
		AA	3 (1.6%)	3 (1.6%)	0.96 (0.19–4.86)	0.95	535.8	563.3
	Dominant	GG	156 (82.5%)	159 (83.6%)	1.00	—	—	—
		AG + AA	33 (17.5%)	31 (16.3%)	0.92 (0.53–1.57)	0.75	533.8	557.4
	Recessive	GG + AG	186 (98.4%)	186 (98.4%)	1.00	—	—	—
		AA	3 (1.6%)	3 (1.6%)	0.98 (0.19–4.92)	0.98	533.9	557.5
	Overdominant	GG + AA	159 (84.1%)	161 (85.3%)	1.00	—	—	—
		AG	30 (15.9%)	28 (14.8%)	0.91 (0.52–1.60)	0.75	533.8	557.4
	Logadditive	—	—	—	0.93 (0.58–1.50)	0.78	553.8	557.4
rs11292	Codominant	TT	156 (82.1%)	159 (83.6%)	1.00	—	—	—
		CT	30 (16.3%)	28 (14.8%)	0.88 (0.50–1.54)	—	—	—
		CC	3 (1.6%)	3 (1.6%)	0.96 (0.19–4.86)	0.91	537	564.6
	Dominant	TT	156 (82.1%)	158 (83.6%)	1.00	—	—	—
		CT + CC	33 (17.9%)	31 (16.4%)	0.89 (0.52–1.52)	0.67	535	558.7
	Recessive	TT + CT	187 (98.4%)	186 (98.4%)	1.00	—	—	—
		CC	3 (1.6%)	3 (1.6%)	0.98 (0.20–4.95)	0.98	535.2	558.8
	Overdominant	TT + CC	159 (83.7%)	161 (85.2%)	1.00	—	—	—
		CT	31 (16.3%)	28 (14.8%)	0.88 (0.50–1.54)	0.66	535	558.6
	Logadditive	—	—	—	0.91 (0.57–1.46)	0.7	553.1	558.7
rs2009873	Codominant	AA	72 (38.3%)	60 (31.8%)	1.00	—	—	—
		AG	85 (45.2%)	87 (46%)	1.23 (0.78–1.95)	—	—	—
		GG	31 (16.5%)	42 (22.2%)	1.61 (0.91–2.87)	0.26	532.5	564
	Dominant	AA	72 (38.3%)	60 (31.8%)	1.00	—	—	—
		AG + GG	116 (61.7%)	129 (68.2%)	1.34 (0.87–2.04)	0.18	531.4	559
	Recessive	AA + AG	157 (83.5%)	147 (77.8%)	1.00	—	—	—
		GG	31 (16.5%)	42 (22.2%)	1.43 (0.86–2.40)	0.17	531.3	558.8
	Overdominant	AA + GG	103 (54.8%)	102 (54%)	1.00	—	—	—
		AG	85 (45.2%)	87 (46%)	1.04 (0.69–1.56)	0.85	533.2	560.7
	Logadditive	—	—	—	1.26 (0.95–1.68)	0.1	530.5	558.1

Table S1. *Cont.*

SNP Number	Model	Genotype	AMS ⁺ [n (%)]	AMS ⁻ [n (%)]	OR (95% CI)	<i>p</i> Value	AIC	BIC
rs2486729	Codominant	AA	73 (38.4%)	61 (32.5%)	1.00	–	–	–
		AG	84 (44.2%)	84 (44.7%)	1.23 (0.78–1.95)	–	–	–
		GG	33 (17.4%)	43 (22.9%)	1.57 (0.89–2.78)	0.29	534	565.5
	Dominant	AA	73 (38.4%)	61 (32.5%)	–	–	–	–
		AG + GG	117 (61.6%)	127 (67.5%)	1.33 (0.87–2.03)	0.19	532.8	560.4
	Recessive	AA + AG	157 (82.6%)	145 (77.1%)	–	–	–	–
		GG	33 (17.4%)	43 (22.9%)	1.40 (0.84–2.33)	0.19	532.8	560.4
	Overdominant	AA + GG	106 (55.8%)	104 (55.3%)	–	–	–	–
		AG	84 (44.2%)	84 (44.7%)	1.05 (0.70–1.57)	0.83	534.5	562
	Logadditive	–	–	–	1.25 (0.95–1.65)	0.11	532	559.6
rs2739513	Codominant	AA	71 (38.4%)	62 (33.7%)	1.00	–	–	–
		AG	84 (45.4%)	80 (43.5%)	1.10 (0.70–1.75)	–	–	–
		GG	30 (16.2%)	42 (22.8%)	1.59 (0.89–2.84)	0.28	521	548.3
	Dominant	AA	71 (38.4%)	62 (33.7%)	1.00	–	–	–
		AG + GG	114 (61.6%)	122 (66.3%)	1.23 (0.81–1.89)	0.33	520.6	544.1
	Recessive	AA + AG	155 (83.8%)	142 (77.2%)	1.00	–	–	–
		GG	30 (16.2%)	42 (22.8%)	1.51 (0.89–2.54)	0.12	519.1	542.6
	Overdominant	AA + GG	101 (54.6%)	104 (56.5%)	1.00	–	–	–
		AG	84 (45.4%)	80 (43.5%)	0.94 (0.62–1.42)	0.77	521.5	544.9
	Logadditive	–	–	–	1.24 (0.93–1.64)	0.14	519.3	542.8

Numbers and frequencies of AMS⁺ or AMS⁻ in each genotype were shown; SNP: Single nucleotide polymorphism; AMS: Acute mountain sickness; AIC: Akaike's information criterion; and BIC: Bayesian information criterion.