Table S2 Estimates of genetic parameters (standard errors in parenthesis) and goodness-of-fit measures using Vitezica *et al.* (2013) parameterization.

	P_A	M_A	P_AD	M_AD	P_A#A	M_A#A	P_D#D	M_D#D	P_A#D	M_A#D
h^2	0.32	0.347	0.235	0.239	0.233	0.10	0.228	0.162	0.231	0.149
SE(h^2)	(0.017)	(0.018)	(0.047)	(0.027)	(0.047)	(0.041)	(0.046)	(0.03)	(0.047)	(0.032)
d^2			0.056	0.076	0.055	0.000	0.058	0.006	0.056	0.000
SE(d^2)	na	na	(0.033)	(0.02)	(0.033)	(0.000)	(0.032)	(0.023)	(0.043)	(0.000)
i^2					0.000	0.164	0.000	0.112	0.000	0.124
SE(i^2)	na	na	na	na	(0.000)	(0.032)	(0.000)	(0.031)	(0.000)	(0.024)
H^2	0.32	0.347	0.29	0.315	0.288	0.265	0.286	0.280	0.288	0.273
SE(H^2)	(0.017)	(0.018)	(0.021)	(0.018)	(0.021)	(0.019)	(0.021)	(0.018)	(0.021)	(0.018)
LogL	-1299.40	-1323.73	-1295.37	-1306.69	-1294.83	-1293.75	-1293.90	-1294.81	-1294.38	-1293.55
AIC	2606.80	2655.46	2602.74	2625.38	2605.66	2603.50	2603.80	2605.62	2604.76	2603.10

*Each column represents a different model. See Table 1 for model description