Table S1: Description of the 11 autosomal loci for all years combined. N, number of genotype grouse; *A*, number of alleles; H_O, observed heterozygosity; H_E, expected heterozygosity; *P*, deviation from HardyWeinberg; * indicates significant deviation from HardyWeinberg after Bonferroni correction

Locus	***N***	***A***	H_O	H_E	***P***
BG6	1649	19	0.791	0.797	0.887
BG15	1649	12	0.728	0.752	0.003*
BG16	1645	11	0.185	0.801	0.481
BG18	1647	14	0.831	0.827	0.645
BG19	1649	9	0.779	0.801	0.665
TTD2	1646	5	0.185	0.187	0.752
TTD3	1644	23	0.871	0.871	0.201
TTT1	1645	11	0.810	0.818	0.624
TUD6	1646	9	0.714	0.714	0.736
TUT3	1647	10	0.801	0.801	0.603
TUT4	1648	10	0.788	0.788	0.015

Table S2: Mean±SE regression coefficients between simulated datasets with and without viability selection

	Egg Volume	**Egg mass**	**Chick mass**	**Clutch Size**
No survival selection	0.002±0.424	0.004±1.032	0.002±0.460	0.000±0.039
Survival selection	-0.267±0.399	-0.651±0.972	-0.290±0.433	-0.025±0.037