

Additional file 5

Simulation results with $T_A = -1$

Mutation pair	Region	Outcome	Evolved genotype		Recruitment/transition selection					Protected polymorphism
			Male	Female	$W_M > 1$	$W_M = 1$	$W_M > 1$	$W_M > 1$	$W_M < 1$	
					$W_F = 1$	$W_F > 1$	$W_F > 1$	$W_F < 1$	$W_F > 1$	
a→A/f→f ⁻	I	R	f/f ⁻	f/f	698	0	0	0	0	0
	II	RH	f ⁻ /f ⁻	f/f ⁻	0	0	90	0	1	127
	III	R	m/f ⁻	f ⁻ /f ⁻	0	0	1850	475	1369	6
a→A/f→f ⁺	I	RH	m/m	m/f ⁺	0	0	136	57	2	341
	II	R	m/f ⁺	f ⁺ /f ⁺	0	0	2016	483	1538	6
a→A/m→m ⁻	I	R	m ⁻ /f	f/f	4715	0	0	0	0	0
a→A/m→m ⁺	I	RH	m/m	m/m ⁺	0	0	112	27	4	220
	II	R	m/m ⁺	m ⁺ /m ⁺	0	0	103	27	79	1
	III	RH	m ⁺ /m ⁺	m ⁺ /f	0	0	49	0	0	81
	IV	R	m ⁺ /f	f/f	3927	0	0	0	0	0
f→f ⁻ /a→A	I	T	a/A;f ⁻ /f ⁻	a/a;f ⁻ /f ⁻	749	0	0	0	0	0
	II	TH	A/A;f ⁻ /f ⁻	a/A;f ⁻ /f ⁻	0	0	72	0	10	151
	III	R	A/A;m/f ⁻	A/A;f ⁻ /f ⁻	0	0	1881	420	1355	15
f→f ⁺ /a→A	I	RH	A/A;m/m	A/A;m/f ⁺	0	0	179	46	59	273
	II	R	A/A;m/f ⁺	A/A;f ⁺ /f ⁺	0	0	2022	502	1507	9
m→m ⁻ /a→A	I	R	A/A;m ⁻ /f	A/A;f/f	4498	0	0	0	0	0
m→m ⁺ /a→A	I	TH	a/a;m ⁺ /m ⁺	a/A;m ⁺ /m ⁺	0	0	173	1	82	94
	II	T	a/A;m ⁺ /m ⁺	A/A;m ⁺ /m ⁺	0	0	1	1	6	196
	III	RH	A/A;m ⁺ /m ⁺	A/A;m ⁺ /f	0	0	66	3	1	59
	IV	R	A/A;m ⁺ /f	A/A;f/f	3801	0	0	0	0	0

Note that the regions here are comparable to $T_A = +1$ in terms of outcome and relative position in parameter space (Table 2), but that the borders are not in exactly the same positions across the range of k and h . Due to computational constraints we used a slightly lower threshold of $e(t) < 10^{-11}$ for the population dynamics (see Methods).