

Table S1: Pearson's correlation tests for the association between the coefficient of background selection (B) and H_s . P -values and r are computed on the simulations with BGS only.

<i>Treatment</i>	<i>Generation after split</i>	<i>r</i>	<i>P</i>	<i>Bonferroni correction</i>
<i>Default</i>	1	0.063	4.0×10^{-5}	**
	5	0.061	0	***
	158	0.060	0	***
	1581	0.065	0	***
	10000	0.063	4.0×10^{-5}	**
<i>High Migration</i>	1	0.061	4.0×10^{-5}	**
	5	0.060	0	***
	158	0.060	4.0×10^{-5}	**
	1581	0.057	4.0×10^{-5}	**
	10000	0.074	0	***
<i>Large N</i>	10	0.076	4.0×10^{-4}	.
	50	0.075	0.001	
	1580	0.073	1.3×10^{-3}	
	15810	0.070	1.8×10^{-3}	
	100000	0.085	2.0×10^{-4}	*
<i>Human genetic map</i>	1	-0.005	0.729	
	5	-0.007	0.617	
	158	-0.013	0.424	
	1581	-0.029	0.080	
	10000	-0.007	0.659	
<i>Low selection pressure</i>	1	0.142	0	***
	5	0.151	0	***
	158	0.156	0	***
	1581	0.206	0	***
	10000	0.217	0	***
<i>Constant μ</i>	1	0.399	0	***
	5	0.406	0	***
	158	0.411	0	***
	1581	0.521	0	***
	10000	0.535	0	***
<i>No Migration</i>	1	0.066	0	***
	5	0.065	4.0×10^{-5}	**
	158	0.068	0	***
	1581	0.069	0	***
	10000	0.067	0	***
<i>No Recombination</i>	1	0.160	0	***
	5	0.163	0	***
	158	0.165	0	***
	1581	0.193	0	***
	10000	0.215	0	***

Table S2: Pearson's correlation tests for the association between the coefficient of background selection (B) and F_{ST} . P -values and r are computed on the simulations with BGS only.

<i>Treatment</i>	<i>Generation after split</i>	<i>r</i>	<i>P</i>	<i>Bonferroni correction</i>
<i>Default</i>	1	-0.011	0.458	
	5	0.007	0.653	
	158	-0.032	0.053	
	1581	-0.030	0.062	
	10000	-0.019	0.243	
<i>High Migration</i>	1	-0.016	0.313	
	5	0.026	0.094	
	158	0.033	0.029	
	1581	-0.004	0.779	
	10000	-0.010	0.522	
<i>Large N</i>	10	0.021	0.348	
	50	-0.022	0.332	
	1580	-0.038	0.086	
	15810	-0.097	0	***
	100000	-0.040	0.072	
<i>Human genetic map</i>	1	-0.017	0.286	
	5	0.004	0.836	
	158	-0.013	0.398	
	1581	0.013	0.434	
	10000	0.025	0.116	
<i>Low selection pressure</i>	1	-0.013	0.577	
	5	-0.017	0.432	
	158	0.023	0.304	
	1581	-0.026	0.258	
	10000	-0.038	0.092	
<i>Constant μ</i>	1	-0.025	0.256	
	5	-0.030	0.185	
	158	-0.052	0.021	
	1581	-0.039	0.081	
	10000	-0.058	0.010	
<i>No Migration</i>	1	0.008	0.646	
	5	0.009	0.585	
	158	-0.061	2.8×10^{-4}	.
	1581	-0.087	0	***
	10000	-0.102	0	***
<i>No Recombination</i>	1	-0.008	0.612	
	5	-0.037	0.021	
	158	-0.006	0.706	
	1581	-0.022	0.168	
	10000	-0.007	0.658	

Table S3: Pearson's correlation tests for the association between the coefficient of background selection (B) and F_{ST} (average of ratios). P -values and r are computed on the simulations with BGS only.

<i>Treatment</i>	<i>Generation after split</i>	<i>r</i>	<i>P</i>	<i>Bonferroni correction</i>
<i>Default</i>	1	0.016	0.307	
	5	0.060	4.0×10^{-5}	**
	158	0.030	0.053	
	1581	0.022	0.162	
	10000	0.031	0.041	
<i>High Migration</i>	1	-0.007	0.649	
	5	0.042	5.9×10^{-3}	
	158	0.048	1.7×10^{-3}	
	1581	0.011	0.480	
	10000	0.025	0.112	
<i>Large N</i>	10	0.093	4.0×10^{-5}	**
	50	0.067	2.8×10^{-3}	
	1580	0.033	0.143	
	15810	-0.011	0.618	
	100000	0.050	0.024	
<i>Human genetic map</i>	1	-0.011	0.491	
	5	0.039	9.2×10^{-3}	
	158	0.024	0.128	
	1581	0.023	0.139	
	10000	0.038	0.012	
<i>Low selection pressure</i>	1	0.012	0.579	
	5	0.021	0.357	
	158	0.071	1.4×10^{-3}	
	1581	0.012	0.583	
	10000	0.004	0.856	
<i>Constant μ</i>	1	0.030	0.180	
	5	0.084	2.8×10^{-4}	.
	158	0.064	4.0×10^{-3}	
	1581	0.080	4.8×10^{-4}	.
	10000	0.055	0.015	
<i>No Migration</i>	1	0.018	0.251	
	5	0.058	8.0×10^{-5}	*
	158	0.026	0.078	
	1581	0.034	0.030	
	10000	-0.003	0.851	
<i>No Recombination</i>	1	0.019	0.245	
	5	0.067	0	***
	158	0.103	0	***
	1581	0.102	0	***
	10000	0.129	0	***

Table S4: Pearson's correlation tests for the association between the coefficient of background selection (B) and d_{XY} . P -values and r are computed on the simulations with BGS only.

<i>Treatment</i>	<i>Generation after split</i>	<i>r</i>	<i>P</i>	<i>Bonferroni correction</i>
<i>Default</i>	1	0.063	0	***
	5	0.061	0	***
	158	0.060	4.0×10^{-5}	**
	1581	0.065	0	***
	10000	0.062	4.0×10^{-5}	**
<i>High Migration</i>	1	0.061	8.0×10^{-5}	*
	5	0.060	0	***
	158	0.060	0	***
	1581	0.057	8.0×10^{-5}	*
	10000	0.074	0	***
<i>Large N</i>	10	0.076	5.2×10^{-4}	
	50	0.075	6.4×10^{-4}	
	1580	0.073	1.2×10^{-3}	
	15810	0.070	1.6×10^{-3}	
	100000	0.085	8.0×10^{-5}	*
<i>Human genetic map</i>	1	-0.005	0.725	
	5	-0.007	0.647	
	158	-0.012	0.425	
	1581	-0.029	0.081	
	10000	-0.006	0.668	
<i>Low selection pressure</i>	1	0.142	0	***
	5	0.150	0	***
	158	0.157	0	***
	1581	0.204	0	***
	10000	0.215	0	***
<i>Constant μ</i>	1	0.399	0	***
	5	0.404	0	***
	158	0.409	0	***
	1581	0.520	0	***
	10000	0.533	0	***
<i>No Migration</i>	1	0.066	0	***
	5	0.066	0	***
	158	0.063	4.0×10^{-5}	**
	1581	0.043	3.5×10^{-3}	
	10000	0.024	0.117	
<i>No Recombination</i>	1	0.160	0	***
	5	0.162	0	***
	158	0.166	0	***
	1581	0.192	0	***
	10000	0.215	0	***

Table S5: Pearson's correlation tests for the association between the coefficient of background selection (B) and d_{XY-SNP} . P -values and r are computed on the simulations with BGS only.

<i>Treatment</i>	<i>Generation after split</i>	<i>r</i>	<i>P</i>	<i>Bonferroni correction</i>
<i>Default</i>	1	0.127	0	***
	5	0.116	0	***
	158	0.117	0	***
	1581	0.127	0	***
	10000	0.127	0	***
<i>High Migration</i>	1	0.089	0	***
	5	0.098	0	***
	158	0.098	0	***
	1581	0.092	0	***
	10000	0.150	0	***
<i>Large N</i>	10	0.250	0	***
	50	0.247	0	***
	1580	0.231	0	***
	15810	0.242	0	***
	100000	0.258	0	***
<i>Human genetic map</i>	1	0.070	0	***
	5	0.071	0	***
	158	0.055	4.4×10^{-4}	.
	1581	0.022	0.167	
	10000	0.063	0	***
<i>Low selection pressure</i>	1	0.092	8.0×10^{-5}	*
	5	0.118	0	***
	158	0.101	0	***
	1581	0.118	0	***
	10000	0.121	0	***
<i>Constant μ</i>	1	0.256	0	***
	5	0.256	0	***
	158	0.235	0	***
	1581	0.299	0	***
	10000	0.305	0	***
<i>No Migration</i>	1	0.117	0	***
	5	0.121	0	***
	158	0.108	0	***
	1581	0.042	6.5×10^{-3}	
	10000	-0.003	0.841	
<i>No Recombination</i>	1	0.249	0	***
	5	0.244	0	***
	158	0.265	0	***
	1581	0.318	0	***
	10000	0.353	0	***