

: del. mut. resampled ?

Supplementary Tables

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.

Treatment	Generation after split	R	P	Bonferroni correction
Default	1	0.085	1.4×10^{-4}	**
	5	0.083	1.9×10^{-4}	**
	158	0.082	2.4×10^{-4}	**
	1581	0.096	1.8×10^{-5}	***
	10000	0.093	3.1×10^{-5}	**
High Migration	1	0.056	0.01	
	5	0.054	0.02	
	158	0.056	0.01	
	1581	0.062	5.3×10^{-3}	
	10000	0.079	4.4×10^{-4}	*
Human	1	-0.036	0.11	
	5	-0.039	0.09	
	158	-0.047	0.04	
	1581	-0.067	2.7×10^{-3}	.
	10000	-0.036	0.11	
Large N	10	0.097	2.2×10^{-3}	.
	50	0.096	2.3×10^{-3}	.
	1580	0.091	0.4×10^{-2}	
	15810	0.087	5.6×10^{-3}	
	100000	0.11	5.8×10^{-4}	*
No Migration	1	0.088	7.7×10^{-5}	**
	5	0.088	8.4×10^{-5}	**
	158	0.095	1.9×10^{-5}	***
	1581	0.089	6.2×10^{-5}	**
	10000	0.09	5.9×10^{-5}	**
No Recombination	1	0.086	1.3×10^{-4}	**
	5	0.086	1.3×10^{-4}	**
	158	0.088	9.1×10^{-5}	**
	1581	0.1	4.9×10^{-6}	***
	10000	0.16	1.9×10^{-12}	***

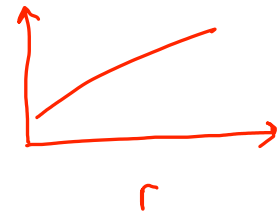
not defined

BGS + migr. : creates

sel. against migrants,

low \rightarrow expect

π



$$B = \frac{\pi_{BGS}}{\pi_0}$$

$$\pi_{BGS} = \pi_0 \exp\left(-\frac{u}{r}\right)$$

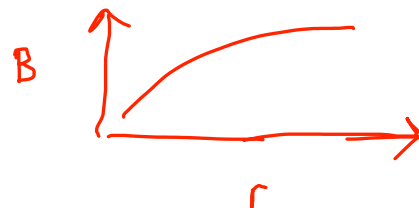
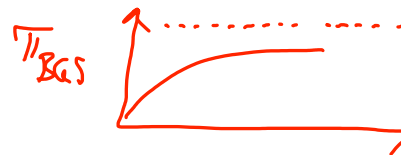
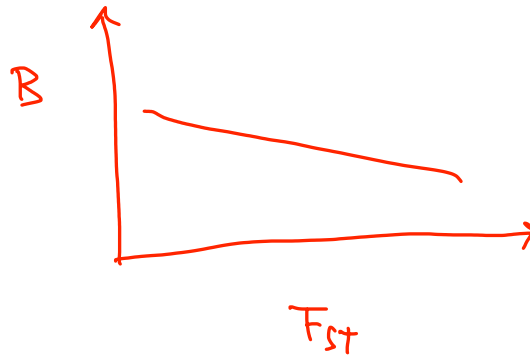


Table S2: Pearson's correlation tests for the association between the coefficient of background selection (B) and F_{ST} . P -values and R are computed on the simulations with BGS only.

Treatment	Generation after split	R	P	Bonferroni correction
Default	1	0.012	0.6	
	5	0.029	0.2	
	158	-0.015	0.49	
	1581	-0.021	0.35	
	10000	0.00014	0.99	
High Migration	1	-0.017	0.45	
	5	0.013	0.56	
	158	0.045	0.04	
	1581	-0.0023	0.92	
	10000	-0.0037	0.87	
Human	1	-0.012	0.6	
	5	0.033	0.14	
	158	-0.019	0.39	
	1581	0.028	0.22	
	10000	0.0077	0.73	
Large N	10	0.0084	0.79	
	50	-0.034	0.28	
	1580	-0.02	0.52	
	15810	-0.026	0.4	
	100000	-0.035	0.27	
No Migration	1	0.0061	0.78	
	5	0.028	0.21	
	158	-0.065	3.5×10^{-3}	
	1581	-0.053	0.02	
	10000	-0.11	6.3×10^{-7}	***
No Recombination	1	0.0058	0.8	
	5	-0.039	0.08	
	158	-0.0011	0.96	
	1581	-0.0048	0.83	
	10000	-0.0055	0.81	



$$B = \frac{\pi_s}{\pi_0}$$

$$F_{ST} = \frac{\pi_T - \pi_s}{\pi_T}$$

$$= 1 - \frac{\pi_s}{\pi_T}$$

$$\approx 1 - \frac{B \cdot \pi_0}{\pi_T}$$

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	0.032	0.15	
	5	0.065	3.6×10^{-2}	
	158	0.04	0.07	
	1581	0.028	0.20	
	10000	0.051	0.02	
<i>High</i>	1	-0.013	0.57	
	5	0.023	0.31	
	158	0.058	9.4×10^{-3}	
	1581	0.012	0.6	
	10000	0.041	0.07	
<i>Human</i>	1	-0.011	0.62	
	5	0.064	4.5×10^{-3}	
	158	0.022	0.32	
	1581	0.036	0.11	
	10000	0.031	0.17	
<i>Large N</i>	10	0.048	0.13	
	50	0.038	0.23	
	1580	0.038	0.23	
	15810	0.027	0.4	
	100000	0.04	0.2	
<i>No Migration</i>	1	0.014	0.54	
	5	0.073	1.1×10^{-3}	*
	158	0.022	0.32	
	1581	0.038	0.09	
	10000	-0.0012	0.96	
<i>No Recombination</i>	1	0.016	0.48	
	5	0.035	0.12	
	158	0.092	4.3×10^{-4}	**
	1581	0.097	1.5×10^{-5}	***
	10000	0.11	5.0×10^{-7}	***

} why qualitatively
different from

Table S2?

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.

Treatment	Generation after split	R	P	Bonferroni correction
Default	1	0.085	1.35×10^{-4}	**
	5	0.084	1.35×10^{-4}	**
	158	0.082	2.46×10^{-4}	**
	1581	0.095	2.12×10^{-5}	***
	10000	0.093	3.28×10^{-5}	**
High Migration	1	0.056	0.01	
	5	0.054	0.02	
	158	0.056	0.01	
	1581	0.062	5.26×10^{-3}	
	10000	0.079	4.36×10^{-4}	*
Human	1	-0.036	0.11	
	5	-0.037	0.10	
	158	-0.047	0.03	
	1581	-0.067	3.0×10^{-3}	
	10000	-0.036	0.11	
Large N	10	0.097	2.2×10^{-3}	.
	50	0.096	2.3×10^{-3}	.
	1580	0.091	4.0×10^{-3}	.
	15810	0.087	5.7×10^{-3}	.
	100000	0.11	5.8×10^{-4}	*
No Migration	1	0.088	7.6×10^{-5}	**
	5	0.089	6.7×10^{-5}	**
	158	0.086	1.2×10^{-4}	**
	1581	0.052	0.02	
	10000	0.029	0.20	
No Recombination	1	0.086	1.3×10^{-4}	**
	5	0.085	1.6×10^{-4}	**
	158	0.088	8.8×10^{-5}	**
	1581	0.1	4.9×10^{-5}	***
	10000	0.16	2.3×10^{-12}	***

$$\mu = 2.5 \cdot 10^{-8} / \text{bp}$$

$$\mu = \mu \cdot n$$

⚡

nr. of exonic sites

$$\text{estim: } \sim 1.25 \times 10^{-3}$$

$$\langle d_{XY} \rangle \approx \left(\frac{1}{2m} + 2\mu_e \right) 2\mu$$

$$= \pi_s + \frac{2\mu}{2m}$$

$$B = \frac{\pi_s}{\pi_0}$$

$$d_{XY} \approx B\pi_0 + \frac{\mu}{m}$$

$$m \in \{0.0, 0.005, 0.05\}$$

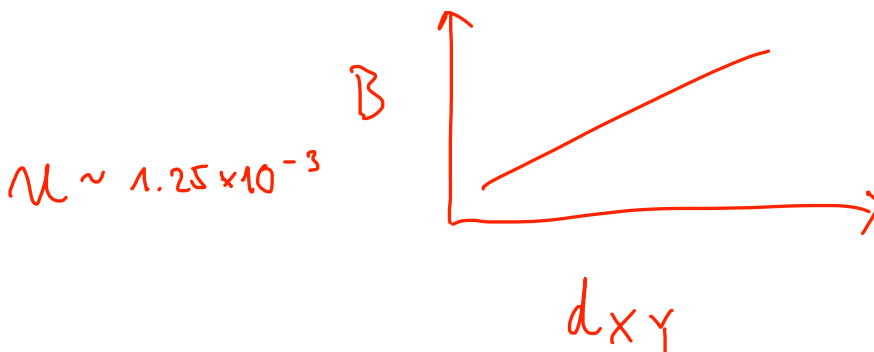


Table S5: Pearson's correlation tests for the association between the coefficient of background selection (B) and d_{XY-SNP} . P -values and R are computed on the simulations with BGS only.

<i>Treatment</i>	<i>Generation after split</i>	<i>R</i>	<i>P</i>	<i>Bonferroni correction</i>
<i>Default</i>	1	0.15	3.1×10^{-11}	***
	5	0.12	8.9×10^{-8}	***
	158	0.14	5.3×10^{-10}	***
	1581	0.16	2.8×10^{-13}	***
	10000	0.15	5.8×10^{-12}	***
<i>High Migration</i>	1	0.075	8.1×10^{-4}	*
	5	0.088	7.5×10^{-5}	**
	158	0.09	5.5×10^{-5}	**
	1581	0.12	5.7×10^{-8}	***
	10000	0.17	5.4×10^{-14}	***
<i>Human</i>	1	0.071	1.6×10^{-3}	.
	5	0.062	5.6×10^{-3}	.
	158	0.053	0.02	.
	1581	0.023	0.3	.
	10000	0.067	2.7×10^{-3}	.
<i>Large N</i>	10	0.22	6.4×10^{-12}	***
	50	0.21	1.2×10^{-11}	***
	1580	0.2	6.6×10^{-11}	***
	15810	0.19	2.2×10^{-9}	***
	100000	0.25	2.7×10^{-15}	***
<i>No Migration</i>	1	0.15	2.3×10^{-11}	***
	5	0.16	1.5×10^{-12}	***
	158	0.14	1.2×10^{-10}	***
	1581	0.048	0.03	.
	10000	-0.0014	0.95	.
<i>No Recombination</i>	1	0.18	6.3×10^{-16}	***
	5	0.16	4.0×10^{-13}	***
	158	0.18	2.7×10^{-15}	***
	1581	0.22	3.6×10^{-23}	***
	10000	0.3	6.6×10^{-42}	***