Table S1 Ordinary correlation coefficients between initial population genetic diversity variables and response to selection for a structured population

		$Nm < 0.5$			$Nm > 0.5$		
		R_{10}	$R_{10\text{-}100}$	R_T	R_{10}	$R_{10\text{-}100}$	R_T
	V_W	0.786	0.269	0.450	0.839	–0.515	0.084
QT	V_B	–0.011	0.270	0.228	–0.715	0.543	0.052
	V_T	0.050	0.293	0.264	–0.455	0.468	0.178
	Q_{ST}	–0.774	–0.251	–0.431	–0.833	0.536	–0.055
QTL	H_S^*	0.738	0.487	0.623	0.726	–0.387	0.143
	D_G^*	–0.678	–0.417	–0.547	–0.930	0.581	–0.082
	H_T^*	–0.458	–0.268	–0.357	0.009	0.082	0.105
	G_{ST}^*	–0.830	–0.500	–0.659	–0.904	0.544	–0.104
	A_S^*	0.690	0.634	0.734	0.414	0.033	0.382
	D_A^*	–0.433	0.079	–0.054	–0.519	0.615	0.299
	A_T^*	0.443	0.598	0.635	0.249	0.175	0.414
	K_T^*	–0.385	0.009	–0.100	–0.097	0.428	0.427
	A_{ST}^*	–0.805	–0.672	–0.800	–0.749	0.613	0.107
	D^*	–0.621	–0.369	–0.490	–0.889	0.561	–0.072
Markers	H_S	0.660	0.690	0.774	0.248	0.165	0.401
	D_G	–0.779	–0.550	–0.689	–0.882	0.562	–0.065
	H_T	–0.483	–0.116	–0.234	–0.225	0.454	0.353
	G_{ST}	–0.782	–0.650	–0.774	–0.875	0.473	–0.165
	A_S	0.531	0.694	0.742	0.385	0.090	0.426
	D_A	–0.091	0.425	0.337	–0.368	0.561	0.360
	A_T	0.344	0.646	0.648	0.248	0.198	0.441
	K_T	–0.137	0.373	0.280	–0.150	0.458	0.419
	A_{ST}	–0.748	–0.710	–0.816	–0.895	0.601	–0.029
	D	–0.774	–0.521	–0.662	–0.881	0.568	–0.057

The scenario refers to a subdivided population with $n = 10$ subpopulations, Nm migrants per generation and subpopulation, mutation rate $u = 0.00001$ and strength of stabilising selection given by $\omega^2 = 25$. The variables included in the model are for quantitative trait (QT) and QTLs: V_W, V_B, V_T, Q_{ST}, H_S^*, D_G^*, H_T^*, G_{ST}^*, A_S^*, D_A^*, A_T^*, A_{ST}^*, D^* and K_T^*; and for neutral markers: H_S, D_G, H_T, G_{ST}, A_S, D_A, A_T, A_{ST}, D and K_T (see main text for definitions). R_{10}: response to selection until generation 10; $R_{10\text{-}100}$: response from generations 10 to 100; R_T: total response until generation 100. Average values (and its standard deviation) of K_T^* across runs was 3.6 (0.9) and that of K_T was 3.0 (0.8). The results are based on 5 sets of 2000 simulation runs varying the subpopulation size (N) randomly between 100 and 1000, and the migration rate (m) between 0.0001 and 0.1.