



**Fig. S4.4: Probability of evolutionary rescue as a function of recombination for various population sizes  $N_0$  with  $N_0 s_{AB} = 2000$  kept constant (Panel A), recombination  $r$  for various values of  $s$  (Panel B), and the strength of selection against single mutants in the old environment  $\sigma$  (Panel C).** The figure varies parameters from Fig. 3A. For all Panels:  $u = 2 \cdot 10^{-6}$ ,  $\sigma_{AB} = -0.1$ ,  $s_{ab} = -1$ . Panel A:  $N_0 s_{AB} = 2000$ ,  $\sigma = -0.01$ ,  $s = -0.01$ ; Panel B:  $s_{AB} = 0.002$ ,  $\sigma = -0.01$ ,  $N_0 = 10^6$ ; Panel C:  $s_{AB} = 0.002$ ,  $r = 0.5$ ,  $N_0 = 10^8$ . Symbols denote simulation results. Each simulation point is the average of  $5 \cdot 10^4$  replicates.

## File S4: Limits of the approximations

Our approximations assume that wildtype individuals and single mutants are sufficiently frequent to describe their dynamics deterministically. This requires a sufficiently large population size and a sufficiently high fitness of single mutants prior to the change in the environment. Fig. S4.4 takes Fig. 3A as a starting point and varies several parameters in order to probe the limits of the approximations. Panel A shows  $P_{\text{rescue}}$  for various initial population sizes  $N_0$  with the product  $N_0 s_{AB}$  kept constant such that the theoretical predictions virtually coincide. However, as the population size gets smaller, simulation results greatly deviate from this prediction. Note that the number of single mutants for  $N_0 = 10^5$  is as low as  $\bar{n}_{Ab} = \bar{n}_{aB} = 20$ . While in Panel A the number of single mutants in the standing genetic variation differs for different population sizes, it is – on average – the same at the right edge of Panel B ( $N_0 = 10^6$ ,  $\sigma = -0.01$ ) and the left edge of Panel C ( $N_0 = 10^8$ ,  $\sigma = -1$ ) but stochasticity is higher in Panel B, leading to larger deviations between the analytical prediction and simulation results.

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