Figure S14 Mean absorption time of A_1 as a function of the migration rate. Two approximations derived under the assumption of quasi-linkage eqilibrium (QLE) are compared. Solid curves show $\bar{t}_{\mathrm{QLE}}$ (Eq. 8) and thick dashed curves $\bar{t}_{\mathrm{QLE},\rho\gg0}$ (Eq. 114 in File S1). The effective population size N_e increases from light to dark grey, taking values of 100, 250, 500, and 1000. The vertical dotted lines denote the critical values of m below which A_1 can invade in the deterministic one-locus (orange) and two-locus (black) model. Dots and whiskers show the mean and 95% empirical interquantile range across 1000 runs of the mean absorption time in 1000 replicates per run. Where points and whiskers are missing, simulations could not be completed within the time limit of 72 hours per replicate on the computer cluster. Data points labelled by 1) are from parameter combinations for which fewer than 1000 replicates per run could be realised, because some took longer than the limit of 72 hours. (A) Monomorphic continent: $q_c = 0$. (B)–(D) Polymorphic continent with continental frequency of B_1 equal to $q_c = 0.2$, $q_c = 0.5$, and $q_c = 0.8$, respectively. Other parameters are $a = 0.02$, $b = 0.04$, $r = 0.1$, and $p_0 = 1/(2N)$ (we assumed $N_e = N$). Time is in multiples of $2N_e$ generations and plotted on the log scale.