A

Rate of polymorphism (θ) vs Rate of deleterious mutation (4*Nu*)

B

Ratio of deleterious to neutral polymorphism vs Rate of deleterious mutation (4*Nu*)

C

Rate of polymorphism (θ) vs Strength of negative selection (4*Ns*)

D

Ratio of deleterious to neutral polymorphism vs Strength of negative selection (4*Ns*)

E

Rate of polymorphism (θ) vs Rate of adaptive mutation (4*Nu*)

F

Ratio of deleterious to neutral polymorphism vs Rate of adaptive mutation (4*Nu*)

G

Rate of polymorphism (θ) vs Strength of positive selection (4*Ns*)

H

Ratio of deleterious to neutral polymorphism vs Strength of positive selection (4*Ns*)

Legend (panels A, C, E, G)

Multiple hitchhiking events

Without	With
θ_W	θ_W
θ_π	θ_π
θ_H	θ_H
θ_π (neutral)	θ_π (neutral)

Legend (panels B, D, F, H)

- Without hitchhiking
- With hitchhiking

Figure S1

Figure S1. The effect of hitchhiking on neutral and deleterious polymorphism as a function of the rate and strength of advantageous and deleterious mutations. The rate of low, intermediate and high frequency deleterious polymorphism measured by θ_W, θ_π and θ_H, respectively, in the presence (squares) and absence (crosses) of multiple hitchhiking events (A, C, E, G). Average heterozygosity (θ_π) of neutral polymorphism is shown in gray. The ratio of deleterious to neutral polymorphism, measured by θ_W, in the absence (black) and presence (red) of multiple hitchhiking events (B, D, F, H). Unless shown on the x-axis, all panels show the mean of 500 simulations for which $4Nu_n$ = 70, $4Nu_d$ = 70, $4Ns_d$ = -10, $4Nu_a$ = 0.5, $4Ns_a$ = 100 and $4Nr$ = 100, where N is the population size, u is the mutation rate, s is the selection coefficient, and subscripts n, a and d refer to neutral, advantageous and deleterious mutations.