Supplementary Material. The role of migration in the evolution of phenotypic switching

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Supplementary Material

Supplementary Material 1. Robustness of the results to different parameters ranges.

We conducted extensive analyses over all dimensions of the parameter space to test the robustness of the results presented in the main text to changes in the parameter range. This work is presented in the **Supplementary Figures 1-5**.

Supplementary Material 2. Extending the model to include recombination.

Here we detail an extended version of the model that incorporates recombination. We aim to understand how recombination between the phenotypic locus and the modifier locus affects the evolutionarily stable switching rate.

Model.

Consider an infinite, haploid population divided spatially into two demes, E_x and E_y. Each individual in the population is defined by two biallelic loci: a major locus A/a which controls the phenotype and thus the fitness of the individual, and a modifier locus M/m which controls the switching rate between phenotypes A and a. Switching occurs only at the phenotypic locus, at a rate that is assumed to be the same in both directions. Selection acts only on the phenotypes A and a. The modifier locus M/m is assumed to be selectively neutral.

Within each deme, the environment varies temporally between two states, T_1 and T_2. At each time-step, individuals first experience selection, followed by switching, recombination, and finally migration. The recursions representing the change in frequency at each generation are presented below.

Equations describing the change in frequency at every generation.

Denote by x_1, x_2, x_3, x_4 the frequencies of MA, Ma, mA, and ma in deme E_x and let y_1, y_2, y_3, and y_4 be the analogous frequencies in deme E_y.

The fitness of phenotype i in temporal state j within deme l is denoted by $w_{i,jl}$ (i in $\{A, a\}$, j in $\{1, 2\}$, l in $\{x, y\}$). The mean fitness in deme l is denoted by $\bar{w}_l$, $l \in \{x, y\}$. After selection, there is a process of switching between phenotypic states. There are two possible switching rates: μ_M, associated with allele M and μ_m associated with allele m. After selection and switching, the equations for the frequencies of the four genotypes in the two demes are

$$
\begin{aligned}
\tilde{x}_1 &= (1-\mu_M)\frac{w_{A,jx}}{\bar{w}_x}x_1 + \mu_M\frac{w_{a,jx}}{\bar{w}_x}x_2 \\
\tilde{x}_2 &= \mu_M\frac{w_{A,jx}}{\bar{w}_x}x_1 + (1-\mu_M)\frac{w_{a,jx}}{\bar{w}_x}x_2 \\
\tilde{x}_3 &= (1-\mu_m)\frac{w_{A,jx}}{\bar{w}_x}x_3 + \mu_m\frac{w_{a,jx}}{\bar{w}_x}x_4 \\
\tilde{x}_4 &= \mu_m\frac{w_{A,jx}}{\bar{w}_x}x_3 + (1-\mu_m)\frac{w_{a,jx}}{\bar{w}_x}x_4 \\
\tilde{y}_1 &= (1-\mu_M)\frac{w_{A,ky}}{\bar{w}_y}y_1 + \mu_M\frac{w_{a,ky}}{\bar{w}_y}y_2 \\
\tilde{y}_2 &= \mu_M\frac{w_{A,ky}}{\bar{w}_y}y_1 + (1-\mu_M)\frac{w_{a,ky}}{\bar{w}_y}y_2 \\
\tilde{y}_3 &= (1-\mu_m)\frac{w_{A,ky}}{\bar{w}_y}y_3 + \mu_m\frac{w_{a,ky}}{\bar{w}_y}y_4 \\
\tilde{y}_4 &= \mu_m\frac{w_{A,ky}}{\bar{w}_y}y_3 + (1-\mu_m)\frac{w_{a,ky}}{\bar{w}_y}y_4,
\end{aligned}
\tag{1}
$$

where the $\bar{w}_x$ and $\bar{w}_y$ are the mean fitnesses in demes E_x and E_y, respectively. (For example, $\bar{w}_x = w_{A,jx}x_1 + w_{a,jx}x_2 + w_{A,jx}x_3 + w_{a,jx}x_4$.) The indices j and k denote the current temporal state within each deme ($j, k \in \{1, 2\}$). The index j refers to deme E_x, while the index k refers to deme E_y.

After recombination at rate r and migration at rate ν, the frequencies x_i' and y_i' ($i \in \{1, 2, 3, 4\}$) at

the start of the next generation can be written in terms of the post-switching frequencies $\tilde{x}_i$ and $\tilde{y}_i$ as

$$\begin{aligned}
x_1' &= (1-\nu)(\tilde{x}_1 - rD_{\tilde{x}}) + \nu(\tilde{y}_1 - rD_{\tilde{y}}) \\
x_2' &= (1-\nu)(\tilde{x}_2 + rD_{\tilde{x}}) + \nu(\tilde{y}_2 + rD_{\tilde{y}}) \\
x_3' &= (1-\nu)(\tilde{x}_3 + rD_{\tilde{x}}) + \nu(\tilde{y}_3 + rD_{\tilde{y}}) \\
x_4' &= (1-\nu)(\tilde{x}_4 - rD_{\tilde{x}}) + \nu(\tilde{y}_4 - rD_{\tilde{y}}) \\
y_1' &= \nu(\tilde{x}_1 - rD_{\tilde{x}}) + (1-\nu)(\tilde{y}_1 - rD_{\tilde{y}}) \\
y_2' &= \nu(\tilde{x}_2 + rD_{\tilde{x}}) + (1-\nu)(\tilde{y}_2 + rD_{\tilde{y}}) \\
y_3' &= \nu(\tilde{x}_3 + rD_{\tilde{x}}) + (1-\nu)(\tilde{y}_3 + rD_{\tilde{y}}) \\
y_4' &= \nu(\tilde{x}_4 - rD_{\tilde{x}}) + (1-\nu)(\tilde{y}_4 - rD_{\tilde{y}}),
\end{aligned} \tag{2}$$

where $D_{\tilde{x}}$ and $D_{\tilde{y}}$ are the linkage disequilibria in deme E_x and E_y, respectively ($D_{\tilde{x}} = \tilde{x}_1\tilde{x}_4 - \tilde{x}_2\tilde{x}_3$ and $D_{\tilde{y}} = \tilde{y}_1\tilde{y}_4 - \tilde{y}_2\tilde{y}_3$).

Recombination decreases the stable switching rate.

The evolutionarily stable switching rate declines linearly with increasing recombination rate r for all of the different selection regimes presented above. **Supplementary Figure S6** presents a case in which there is symmetric selection (selection coefficients are all 0.1), the environments switch after an expected time of 5 generations in both demes and the migration rate ν is 0.05. The stable switching rate decreases linearly with increasing recombination rate. This result suggests that recombination, by mixing genotypes, can amplify the effect of switching. From the perspective of a modifier allele, a recombination event can simulate the act of switching, as that allele may end up on a background with a different phenotype.

Supplementary Figure Legends

Figure S1. Invasion trials showing the convergence on the stable switching rate for different runs of the simulation. We show 50 runs of the simulation for a fixed set of parameters starting from different initial resident mutation rates. The repeated invasion trials, as the simulation progresses, are presented on the *x-axis* and the resident mutations are presented on the *y-axis*. We show that for all these different initial conditions of the starting switching rate, the different runs of the simulation, as presented by the different lines, converge on the same final stable switching rate. The selection coefficients are all 0.1. Migration rate is 0.1. The expected time before an environmental change in both demes is 10 generations, and the environmental variability ψ is 0.1.

Figure S2. Robustness of the result to different symmetric selection pressures. All selection coefficients are equal and presented in the legend. The expected time before an environmental change in both demes is 10 generations, and the environmental variability ψ (the variance of the gamma distribution divided by the square of its mean) is 0.1. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines

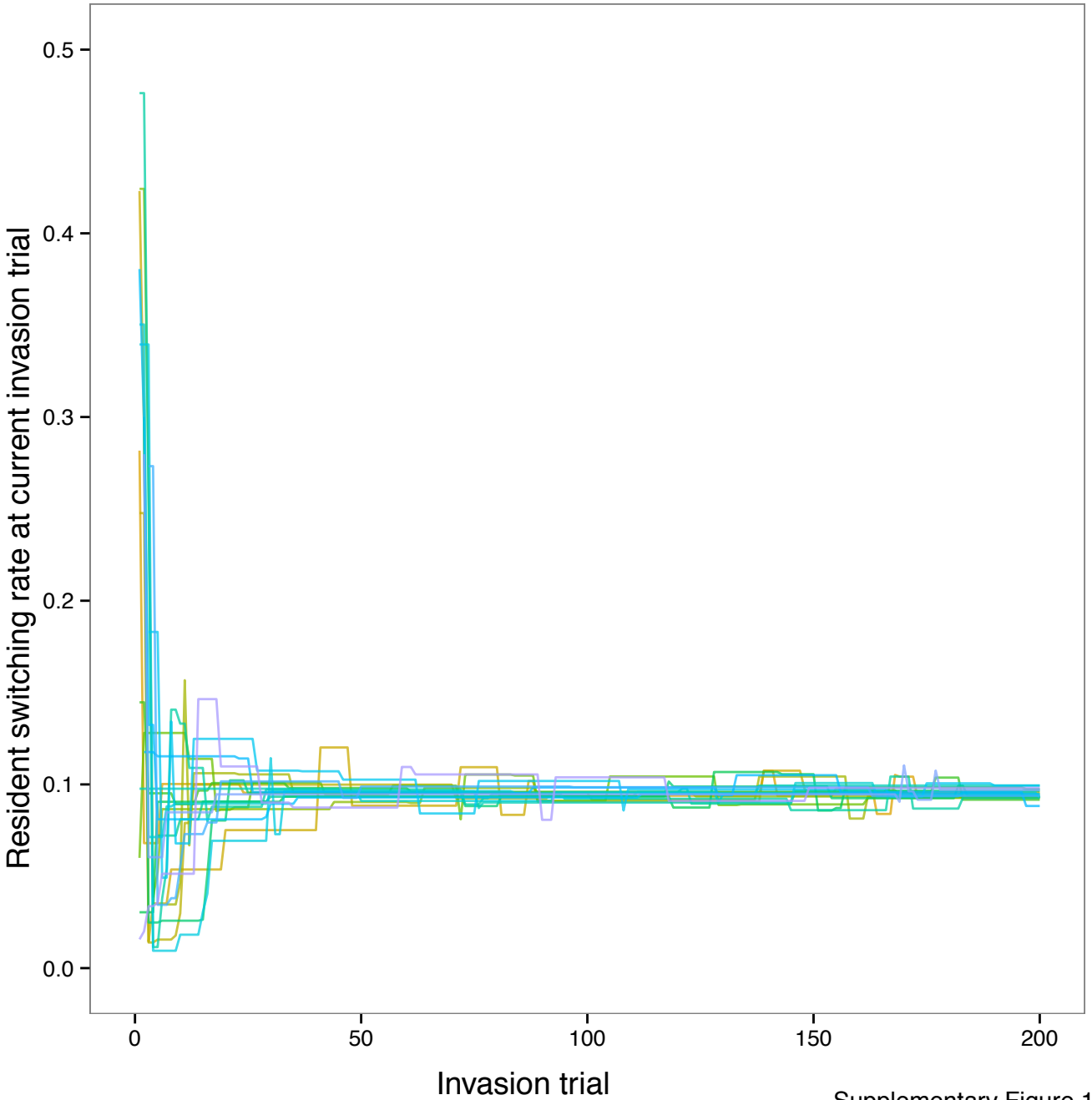
Figure S3. Robustness of the symmetric selection results to different environmental mean waiting times. The selection coefficients are all 0.1. The environmental variability ψ is 0.1. **Panel A**: The expected time before an environmental change is the same in both demes and presented in the legend. **Panel B**: The expected time before an environmental change is 10 generations in deme E_x. The expected time before an environmental change in deme E_x is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.

Figure S4. The stable switching rate as a function of migration when selection strengths differ between demes. The selection coefficients are $s_1 = s_2 = 0.4$ and $s_3 = s_4 = 0.1$. The expected time before and environmental change in both demes is 10, and the environmental variability ψ in both demes is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.

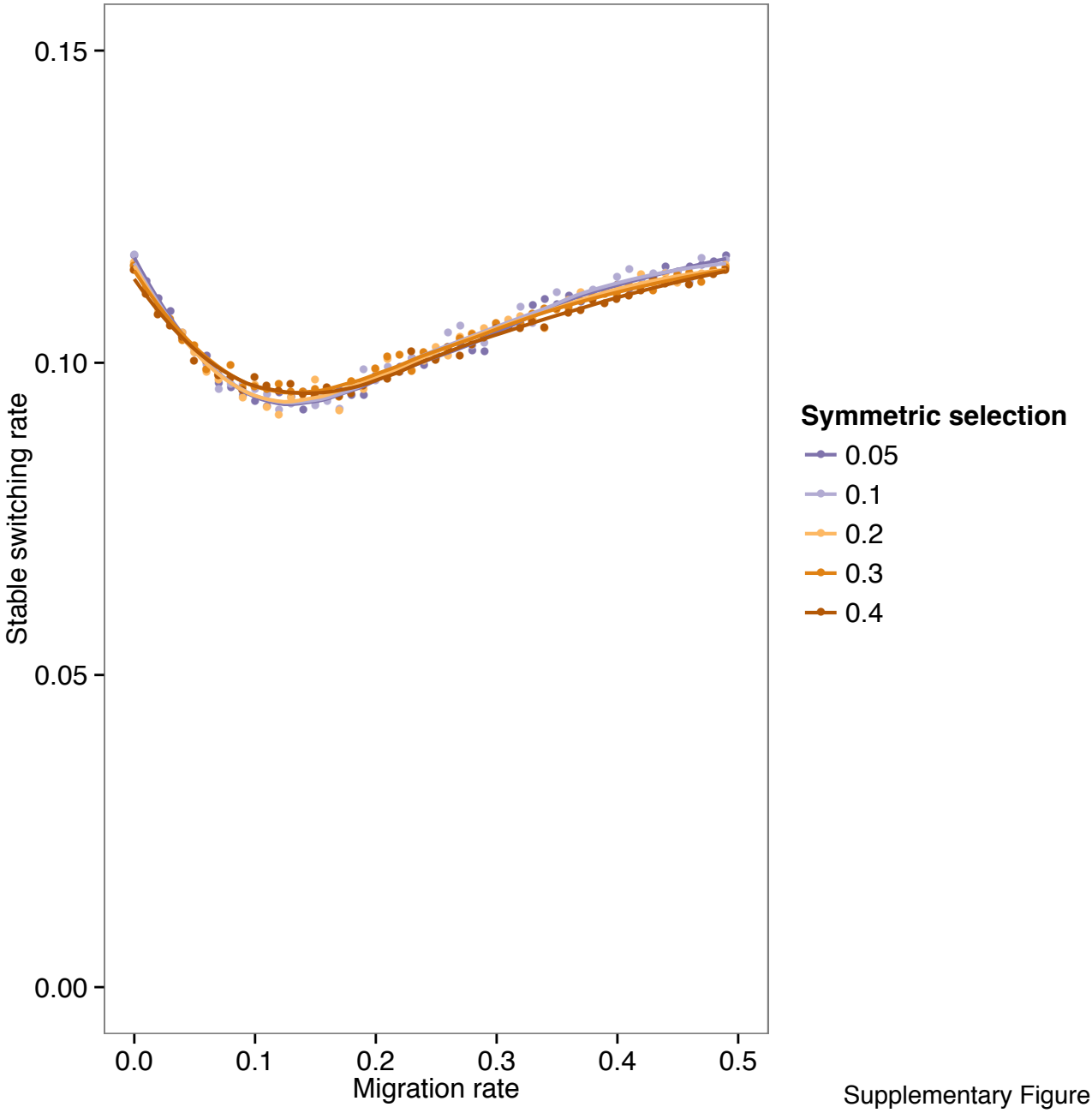
Figure S5. Robustness of the asymmetric selection results to different environmental mean waiting times. The selection coefficients are $s_1 = s_3 = 0.4$ and $s_2 = s_4 = 0.1$. The environmental variability ψ is 0.1. **Panel A**: The expected time before an environmental change is the same in both demes and presented in the legend. **Panel B**: The expected time before an environmental change is 10

generations in deme E_x. The expected time before an environmental change in deme E_y is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.

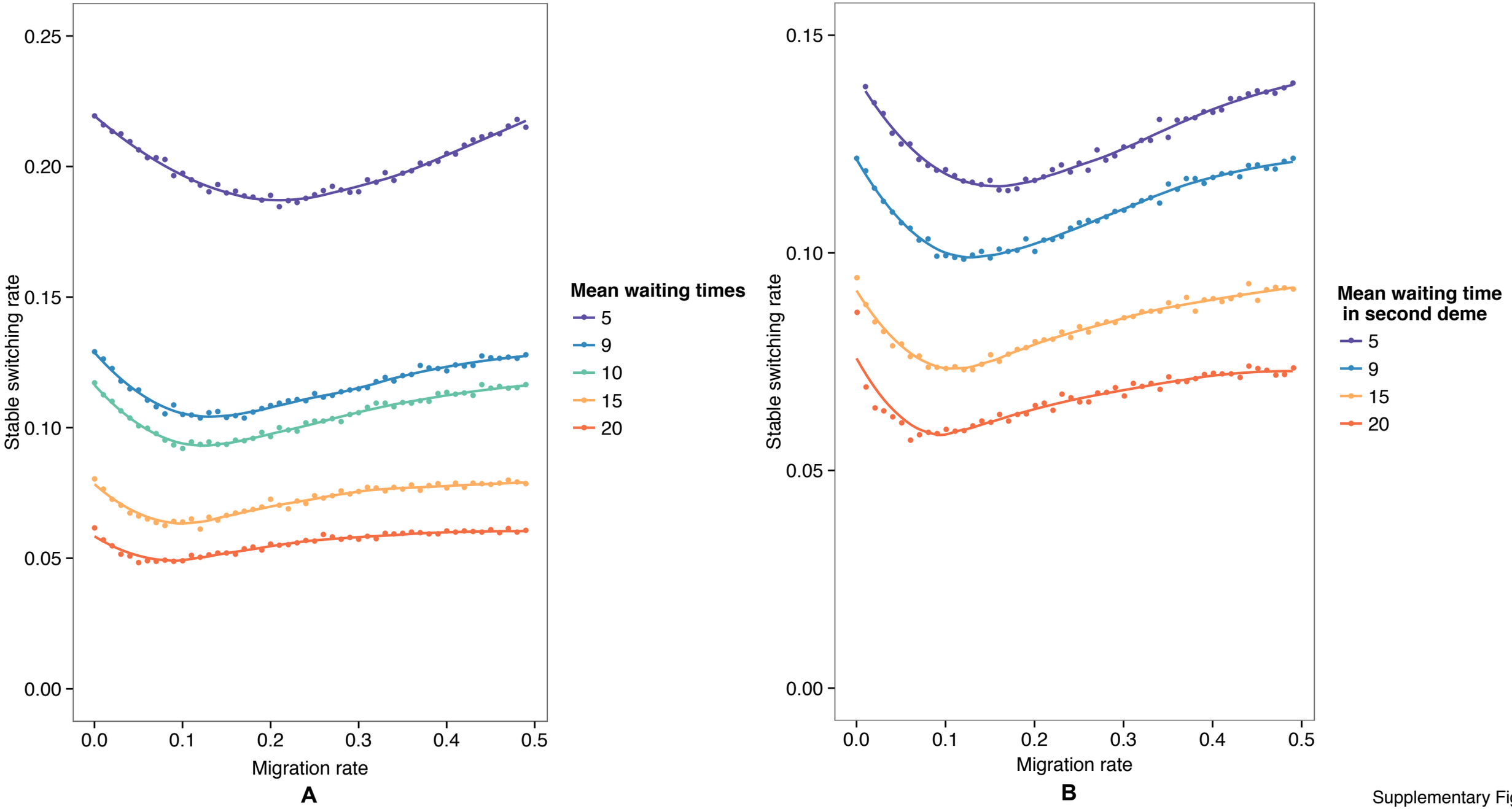
Figure S6. Recombination and the stable switching rate. The selection coefficients are all 0.1 and the environments switch after an expected time of 5 generations. The migration rate $\nu = 0.05$, and the environmental variability ψ is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.



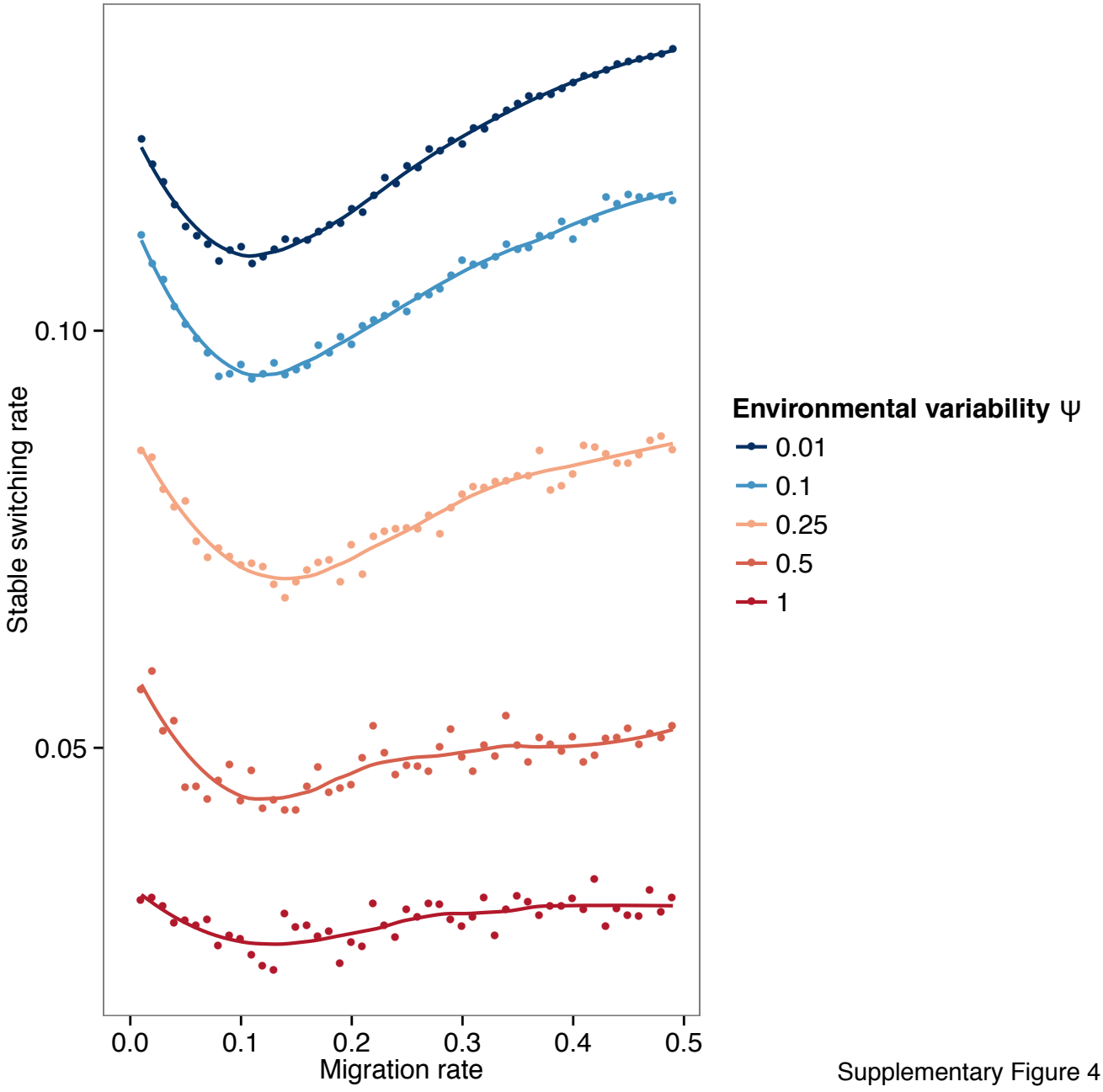
Supplementary Figure 1



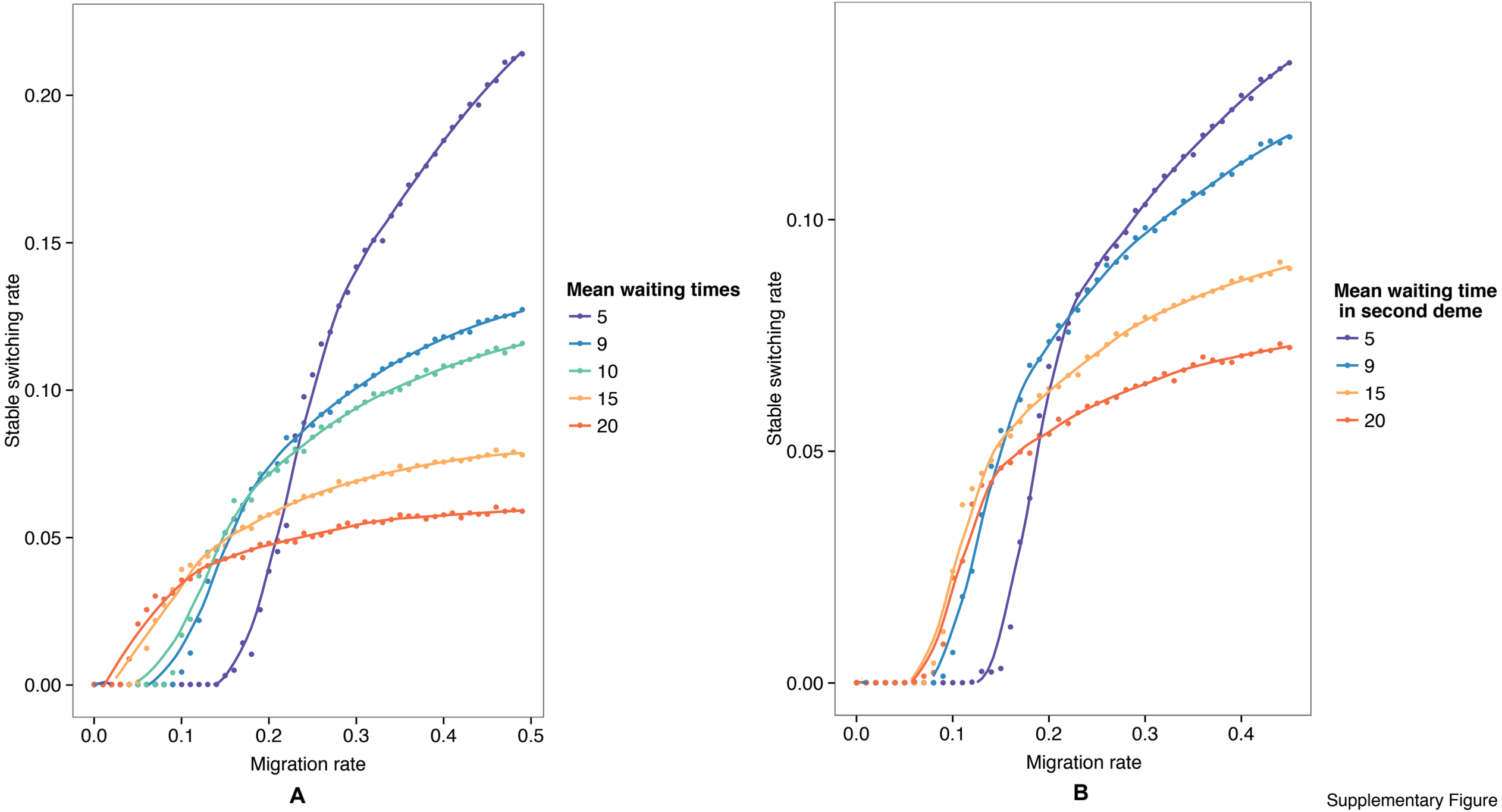
Supplementary Figure 2



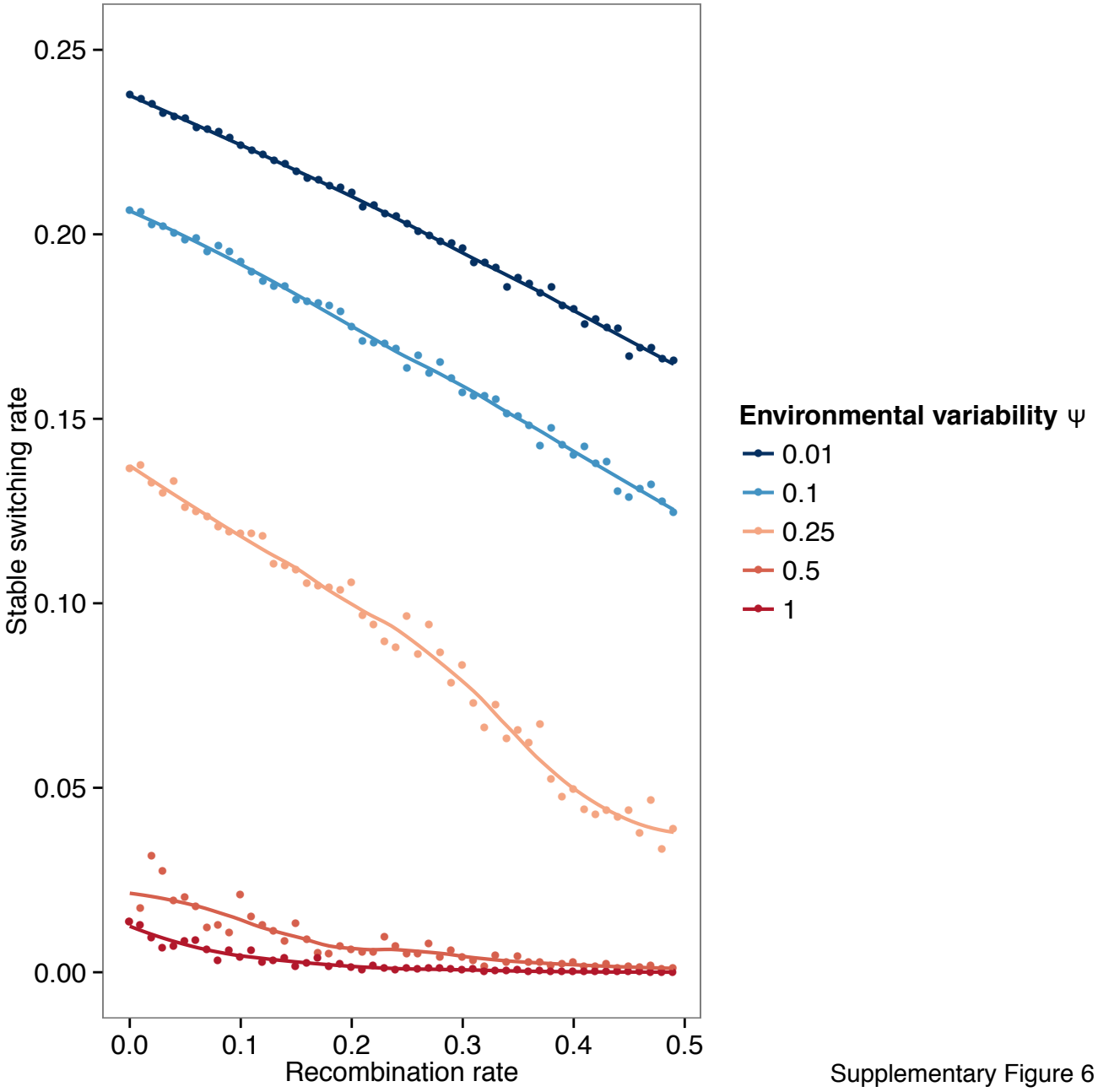
Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5



Supplementary Figure 6