All supplementary plots and tables show results for the following 7 sets of parameter values:

A) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 2 dimensions. This is identical to the figures in the main text

B) $\mu = 10^{-4}$, $\theta = 1$, $\lambda = 1/2$ and 2 dimensions

C) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 2$ and 2 dimensions

D) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/4$ and 2 dimensions

E) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 3 dimensions

F) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 4 dimensions

G) $\mu = 10^{-6}$, $\theta = 0.01$, $\lambda = 1/2$ and 7 dimensions

Figure S1. Phenotypic distribution of homozygous alleles as in Figure 1 for all sets of parameter values. For simulations containing more than two dimensions (plots E-G), only the first two dimensions are shown.

Figure S2. Epistasis as a function of overdominance as in Figure 3 for all sets of parameter values.

Figure S3. Maximum pairwise distance statistic as in Figure 4 for all sets of parameter values.

Figure S4. Maximum distance from optimal trajectory statistic as in Figure 5 for all sets of parameter values.

Figure S5. Effective number of paths statistic as in Figure 6 for all sets of parameter values.

Figure S6. Mean path divergence statistic as in Lobkovsky et. al. (2011) for all sets of parameter values.

Table S1. Pairwise Epistasis (n=5,000)

Table S2. Conditional Mutations

Table S3. Backwards Predictability Counts

Table S4. Backwards Predictability Summary

Table S5. Epistasis and Predictability P values