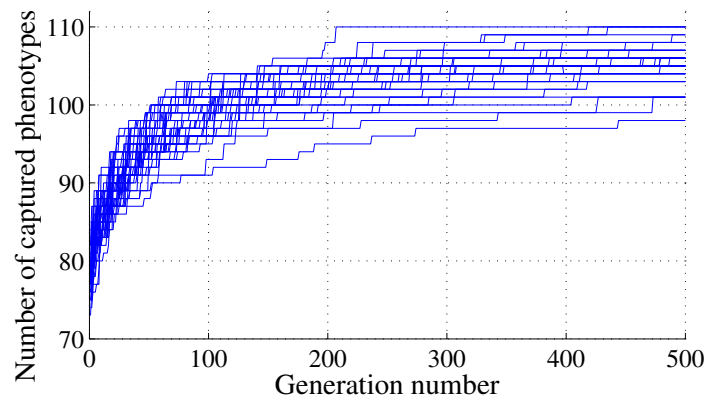# Supplementary Figures

Figure S1. Evolution of the number of mutants captured with 50 independent DE runs. Each run starts with a different initial population of 19 LH samples (independently generated populations with $\pm 40\%$ LH sampling, wild type viability not enforced). The number of phenotypes captured after 500 generations has a 105.42 mean and 2.48 standard deviation (Table S6).
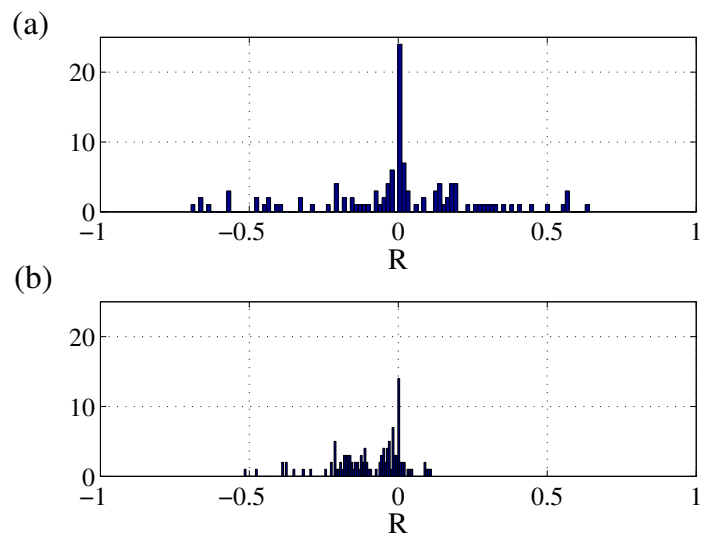

Figure S2. Distribution of the pairwise correlations (R values) of Phenotype 12 with the remaining 118 phenotypes in (a) 100 LH samples and (b) 19,000 DE samples (trial parameter vectors).