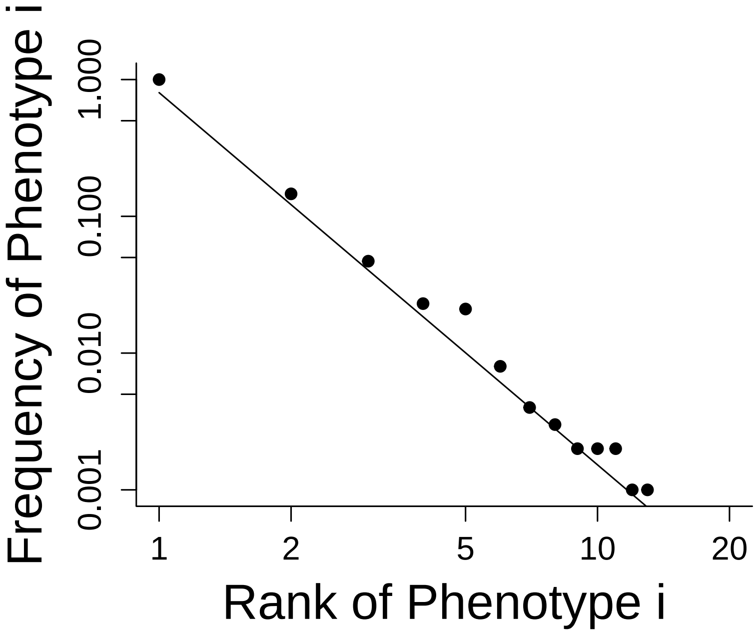

Figure S1: **Genotypes with different phenotypes occupy different fractions of genotype space.** The double-logarithm plot shows the rank of phenotype i (x-axis) versus a measure of its frequency $f(i)$ (y-axis), in genotype space. Data are shown for the 13 most frequent phenotypes, and were obtained by computing the phenotypes of the 2500 × 1000 1-mutant neighbors of 1000 genotypes uniformly sampled from genotype space. The frequency shown is the number of 1-mutant neighborhoods in which phenotype i appeared at least once. The rank distribution follows a power law.