Scripts in this folder are for analyzing and plotting Fig. 2A, B. “util.py” is the package code for python scripts.

1. **Correlations between the fitness of a genotype and the individual fitness or the mean fitness of its 27 single-mutation neighbors**

Implement:  
“Fig2A\_analysis.py”  
“Fig2A\_ plot.py”

Input:  
Read count tables (Supplemental File S2, S3, S4)

Output:  
Fig. 2A

1. **Relationship between the fitness of a genotype and the amount of beneficial, neutral, and deleterious mutations in this genetic background**

Implement:  
“Fig2B\_analysis.py”  
“Fig2B\_plot.R”

Input:  
Read count tables (Supplemental File S2, S3, S4)

Output:  
Fig. 2B