Scripts in this folder are for analyzing and plotting Fig. S7, S14, S16-27. “util.py” is the package code for python scripts.

1. **Relationship between the read count and the standard deviation of fitness of each genotype**

Implement:  
“FigS7A\_analysis.py”  
“FigS7A\_plot.R”

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

Output:  
Fig. S7A

1. **Relationship between fitness and its coefficient of variation of each genotype**

Implement:  
“FigS7B \_analysis.py”  
“FigS7B\_plot.R”

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

Output:  
Fig. S7B

1. **Correlation between the fitness of 3 genotypes characterized by three replicate experiments**

Implement:  
“FigS7C\_LibraryCorrelation3D.py”

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

Output:  
Fig. S7C

1. **Relationship between the nucleotide content and the fitness of genotypes**

Implement:  
“FigS14.py”

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

Output:  
Fig. S14

1. **Fitness effects of mutations**

Implement:  
“FigS16-27\_MutationEffectTotal.R”

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

Output:  
Fig. S16-27