Scripts in this folder are for analyzing and plotting Fig. 3A, B, C. “util.py” is the package code for python scripts.

1. **Relationship between fitness and nucleotide composition**

Implement:  
“Fig3A\_NucleotideComposition.py”

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

Output:  
Fig. 3A

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

Implement:  
“Fig3B\_NucleotideContent.R”

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

Output:  
Fig. 3B

1. **Influence of sequence motifs on fitness**

Implement:  
“Fig3C\_ConsensusMotif.py”

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

Output:  
Fig. 3C