Scripts in this folder are for analyzing and plotting Fig. 5A, C, E. “util.py” is the package code for python scripts.

1. **Mean effects of single nucleotides on fitness**

Implement:  
“Fig5A\_SingleNucleotide.R”

Input:  
“XXX\_SDR\_union\_count25\_e1.csv” (XXX indicates the library)

Output:  
Fig. 5A

1. **Mean effects of pairwise epistasis on fitness**

Implement:  
“Fig5C\_PairwiseEpistasis.R”

Input:  
“XXX\_SDR\_union\_count25\_e2.csv” (XXX indicates the library)

Output:  
Fig. 5C

1. **Explanatory power of the RBS context, single nucleotides, and pairwise epistasis on fitness**

Implement:  
“Fig5E\_LibraryCorrelation.py”

Input:  
“XXX\_SDR\_union\_count25\_o1.csv” (XXX indicates the library)  
“XXX\_SDR\_union\_count25\_o2.csv” (XXX indicates the library)  
Read count tables (Supplemental File S2, S3, S4)

Output:  
Fig. 5E