Scripts in this folder are for analyzing and plotting Fig. 1B, C, D. “util.py” is the package code for python scripts.

1. **Distribution of the fitness of genotypes**

Implement:  
“Fig1B\_LibraryDistribution.py”

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

Output:  
Fig. 1B (upper panels)

1. **Correlation with the SD:aSD base-pairing energy**

Implement:  
“Fig1B\_SDaSD\_analysis.py”  
“Fig1B\_SDaSD\_plot.R”

Input:  
“XXX\_RNAfold.csv” (XXX indicates the library)  
Read count tables (Supplemental File S2, S3, S4)

Output:  
Fig. 1B (middle panels)

1. **Correlation with the local mRNA folding energy**

Implement:  
“Fig1B\_Fold\_analysis.py”  
“Fig1B\_Fold\_plot.R”

Input:  
“RNAsubopt\_dG.csv”  
Read count tables (Supplemental File S2, S3, S4)

Output:  
Fig. 1B (lower panels)

1. **Phenotypic correlation of SD genotypes between fitness landscapes**

Implement:  
“Fig1C\_LibraryCorrelation.py”

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

Output:  
Fig. 1C