

Description of Additional Supplementary Files:

Supplementary Data 1: Library sequences. Library designs consist of three sequence categories: model-designed GB1 sequences, calibration sequences to compare our experimental measurements with previously published work, and 3 wildtype sequences with synonymous codon sequences for binding controls. These categories are noted under the Model column by model architecture, 'Calibration', or 'WT'. For each sequence, we include the amino acid sequence starting with methionine (Amino Acid Sequence column) and the codon optimized DNA sequence (DNA Sequence column) used for the expression experiments in yeast.