

Fis1p tail anchor sequence

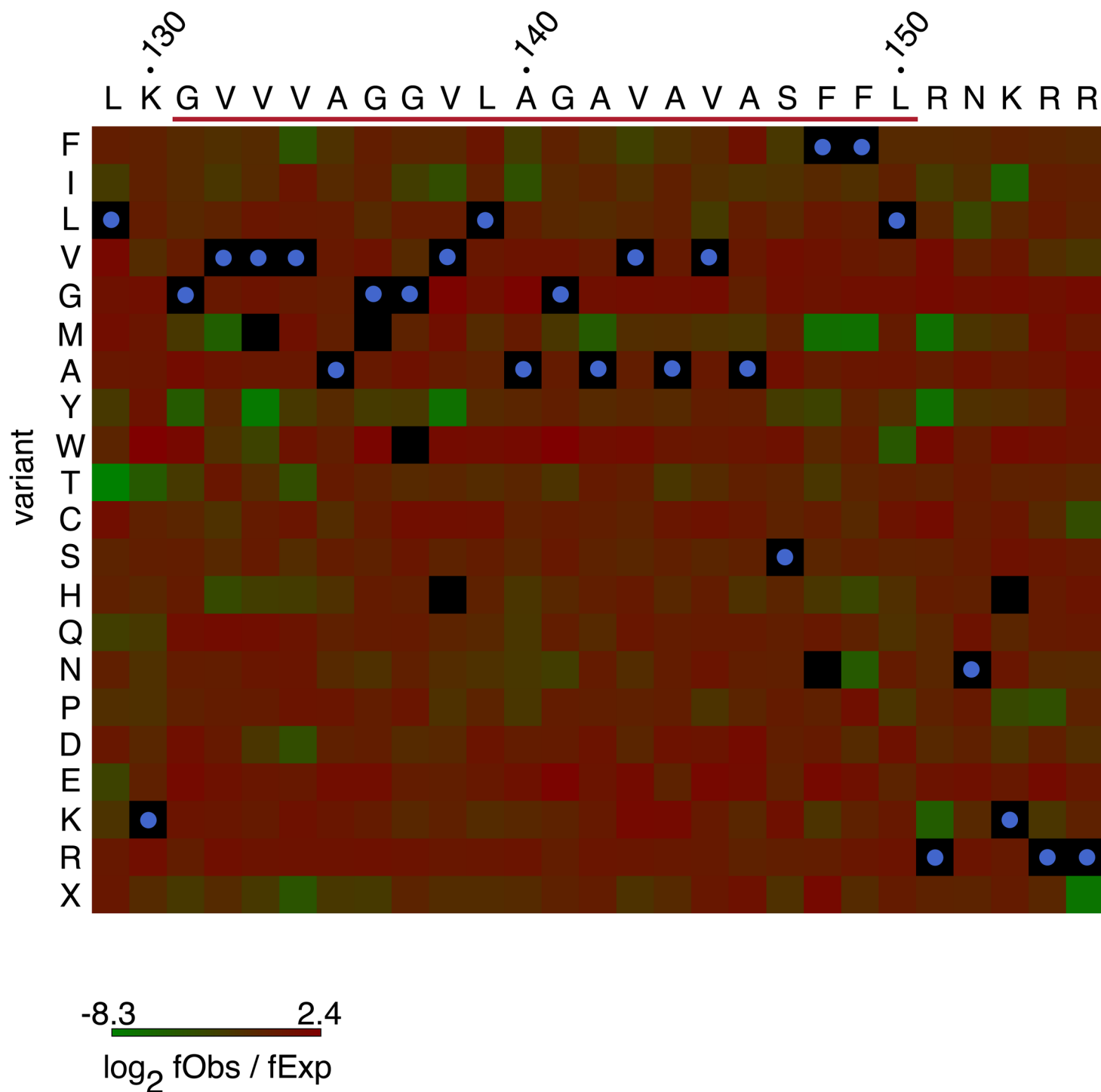


Figure S2. Amino acid replacement representation within the Gal4-sfGFP-Fis1p TA library. The fraction of counts representing each amino acid replacement in the starting SC-Trp library (f_{Obs}) was compared to the fraction that would be expected based on randomized codon recovery (f_{Exp}). Native amino acids are represented by a black square with a blue dot. Amino acid replacements with no representation in the library are represented by empty black squares. The predicted MAD is indicated by a red line.