Mutational Scanning Library Completeness. Panel (a) is a heat map of log(sequencing counts) for each DHFR mutation in the three TYMS backgrounds. White pixels indicate variants with no counts (absent or very low frequency in the library). Panels (b-d) depict histograms of the log(counts) for each DHFR mutation in the three TYMS backgrounds. Together, these data show that the library is near-complete and well distributed across variants.