

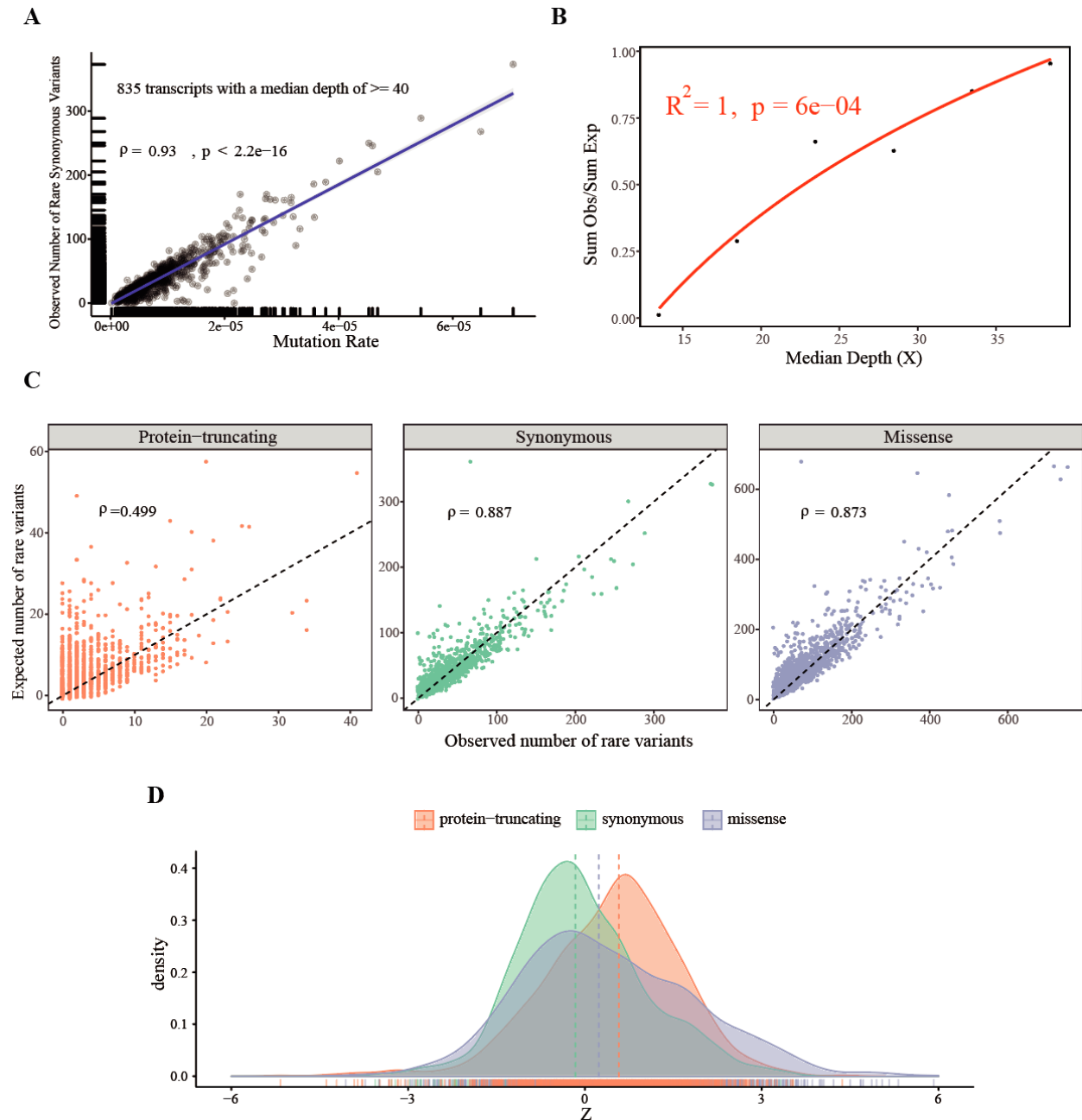


Figure S8. *pLI* calculation. (A) relation between mutation rates and observed number of synonymous variants; (B) depth correction of expected number of rare variants; (C) comparisons of the observed number of rare (MAF<0.1%) variants per gene to an expected number after depth correction; (D) corrected *Z* scores for each mutational class (synonymous, missense, and protein-truncating variants).