



Figure S6. Prediction of ClinVar and mouse modeled missense variants. A) Distribution of missense variants in two datasets. The variant numbers are indicated. B) Distribution of prediction scores by 10 algorithms. The red dotted line represents the cutoff, and the pink rectangle highlights the deleteriousness scores. C) Percentage of variants predicted as deleterious by indicated algorithms from the indicated catalogs (in rows). TP = true positives; FP = false positives; Del and D = deleterious; B = benign; LB = likely benign; VUS = variants of uncertain significance; P = pathogenic; LP = likely pathogenic.