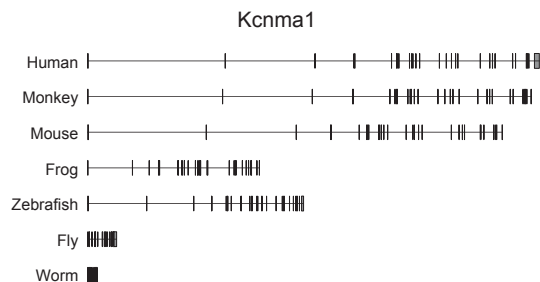
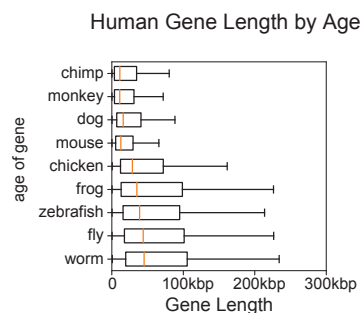


A

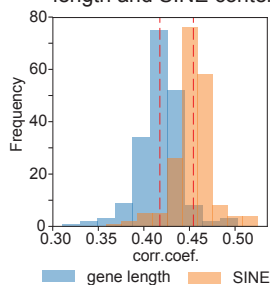


B



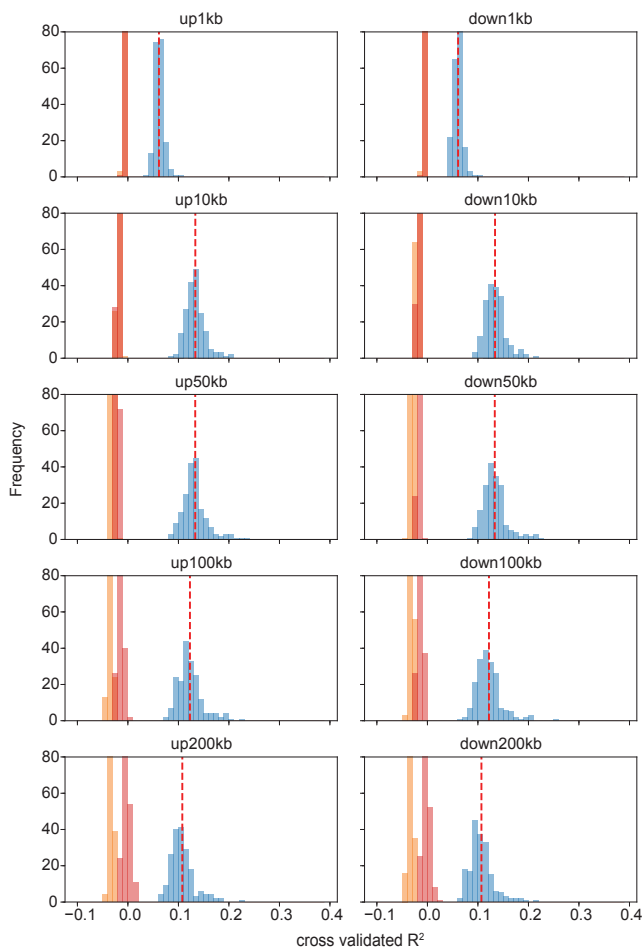
C

Expression rank is correlated with length and SINE content



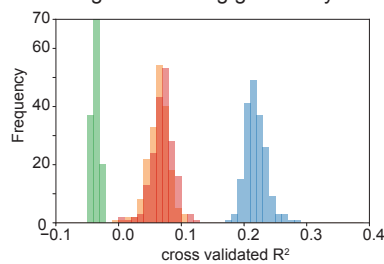
D

Regression using different surrounding intervals

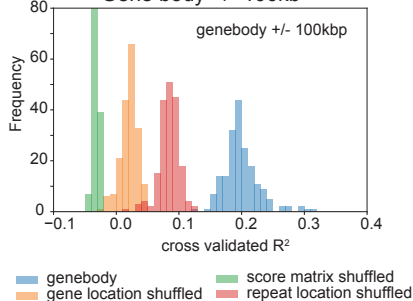


E

Regression using gene body

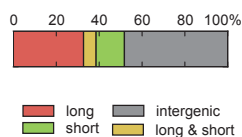


Gene body +/- 100kb



F

Percentage of genome covered by long and short genes and intergenic regions



G

Percentage of genes with TE insertions

