binomial linear model on genomic features glm **Estimate** z.value Intercept HNRNPC eCLIP ALKBH5 PARCLIP GGACT FTO eCLIP FTO CLIP METTL14 TRE YTHDF2 TRE long exon YTHDF1 TREW YTHDC1 TREW METTL3 AGACT HK genes FC 1bp Stop codons pos exons Start codons miR targeted genes TSS pos cds last exon 400bp TargetScan length UTR5 dist sj 5 p2000 PC 1bp length cds GC cont genes length gene ex exon num isoform num Verified miRtargets PC 101bp FC 101bp struct loop AAACT last exon sc400 length UTR3 GC cont 101bp abs length gene full dist nearest p200 WTAP TREW **AGACA** GC cont 101bp pos UTR5 dist sj 3 p2000 struct hybridize **IncRNA** dist nearest p2000 internal exon GAACA last exon TSS A pos UTR3 constitutive exon alternative exon exon stop -1010 -1010 -5 value