binomial linear model on genomic features hg19 miCLIP z.value **Estimate** METTL14 TREW METTL3 TREW ...GGACT HK genes long exon FC 1bp GAACT YTHDF1 YTHDF2 TREW miR targeted genes GGACA Stop codons PC 1bp YTHDC1 TREW FTO eCLIP FTO ČLIP ALKBH5 PARCLIP length cds GC cont genes pos exons dist sj 5 p2000 Start codons last exon 400bp pos cds TargetScan length UTR5 length gene ex Intercept HNRNPC eCLIP Verified miRtargets exon stop exon num pos UTR5 AAACT isoform num struct loop last exon sc400 lncRNA TSS A PC 101bp FC 101bp struct hybridize AGACA length UTR3 WTAP TREW last exon internal exon GC cont 101bp abs length gene full GAACA pos UTR3 dist nearest p200 dist sj 3 p2000 alternative exon constitutive exon AGACC GC cont 101bp AAACC dist nearest p2000 10 15 -10 10 5 value