

# Manuscript Title

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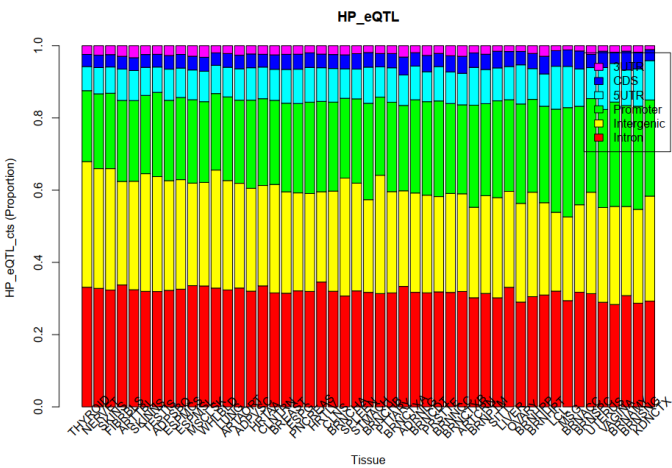
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# Abstract

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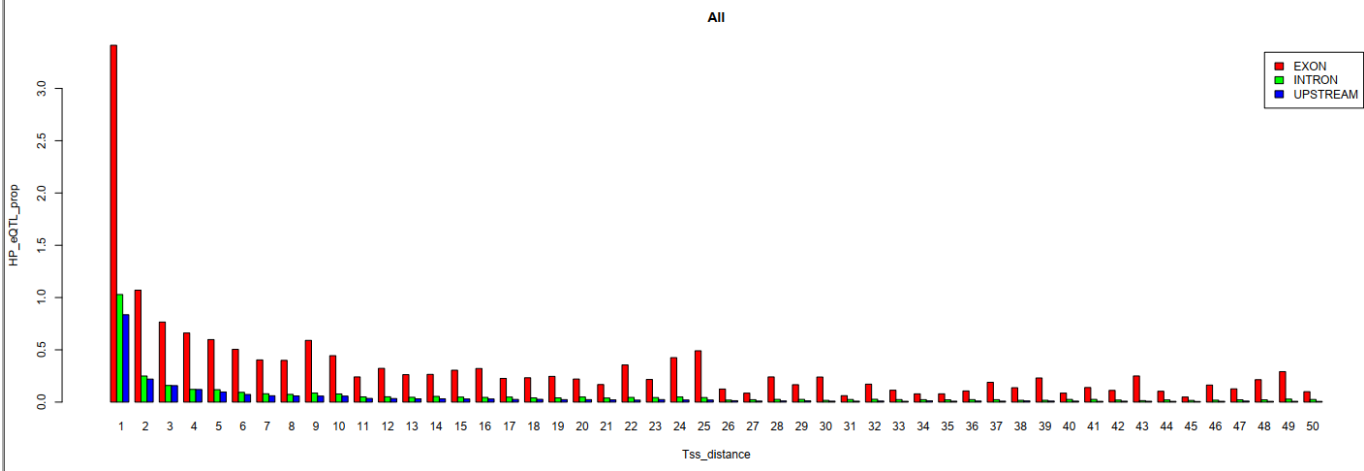
#Figure legends

##Section 1: genome wide distribution of genic eQTLs ###Figure 1a

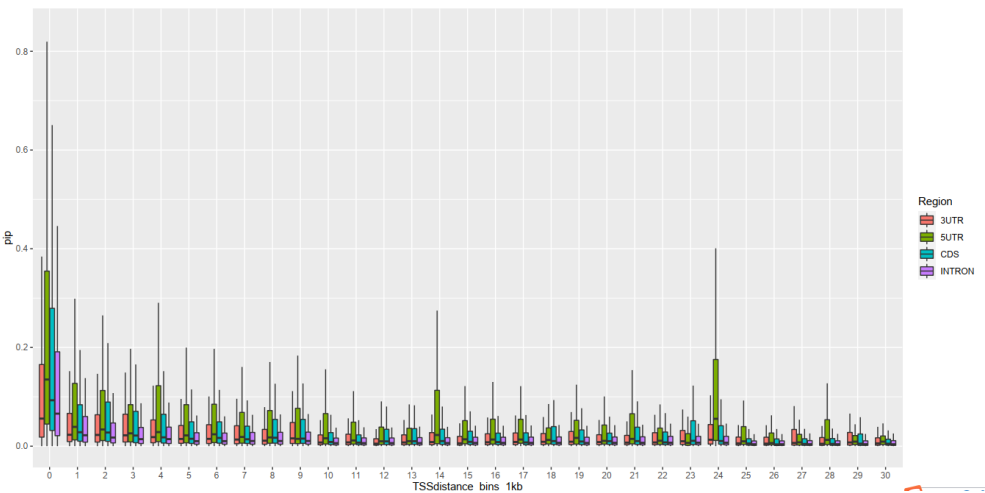


HP eQTL (PIP  $\geq 0.5$ ) in each of 49 tissues was annotated related to their associated genes based on the Gencode human gene annotations (v29) and split into 7 genome regions, the counts and proportion was obtained. Up1k means 1kbp upstream of gene TSS, other genome regions as name indicated.

###Figure 1b



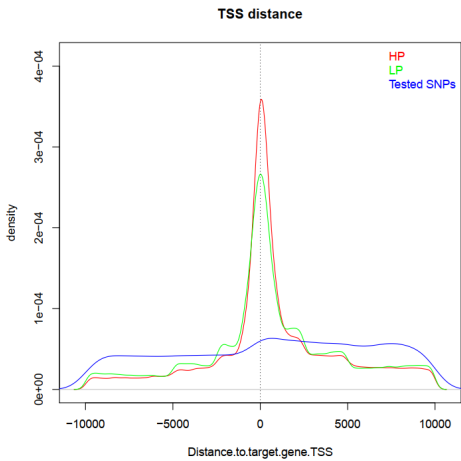
proportion of HP eQTL among all tested SNPs in Exons (including 5'UTR, CDS and 3'UTR), Introns and intergenic regions upstream of TSS within 1-kbp genome regions with different distance to TSS was shown.



Comparison of PIP score distributions for eQTLs between exon and intron in each 1 kbp genomic regions ordered by distance to TSS within 30kbp

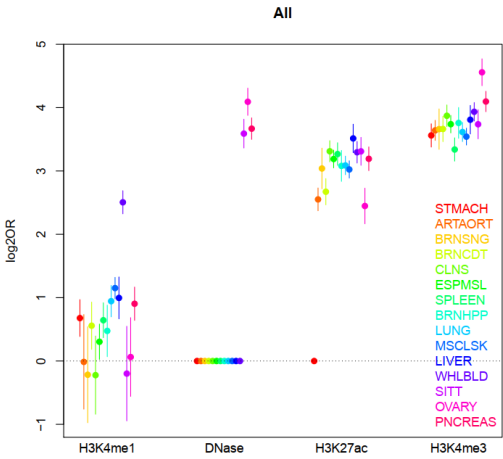
considering most gene length <30kbp. Boxplot to show PIP score variations with outliers removed and PIP score for eQTL from 49 tissues pooled together

###Figure 1c ###Figure 1d

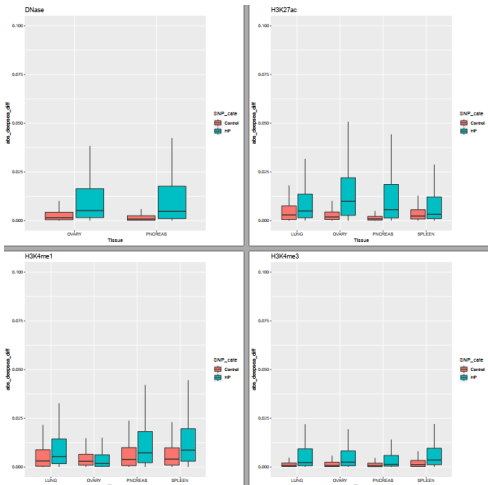


###Figure S1

##Section 2: enrichment of genic eQTLs within transcription regulation related features ###Figure 2a



HP eQTL enrichment within trnascription related epigenetic mark peaks obtained from ENCODE project for 15 matched tissues. The different colors represent tissues matched between Gtex eQTL dataset and ENCODE dataset: Brain\_Female. The enrichment odds ratio was obtained by comparison with MAF matched control SNPs randomly picked from all tested SNPs in Gtex dataset, error bar represent 95% confidence interval for log2 Odds ratio.



###Figure 2b ###Figure 2c Here, 4 different epigenetic features in 4 matched tissues between Gtex and deepsea features presented, comparison between Control SNPs and HP eQTLs shown.

###Figure 2d

###Figure S2

##Section 3: enrichment of genic eQTLs within post-transcription regulation related features ###Figure 3a ###Figure 3b  
###Figure 3c ###Figure 3d

###Figure S3

##Section 4: important post-transcription processes related to gene expression regulation ###Figure 4a ###Figure 4b  
###Figure 4c ###Figure 4d

###Figure S4

# References

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