

Manuscript Title

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Figure legends

Section 1: genome wide distribution of genic eQTLs

Figure 1a

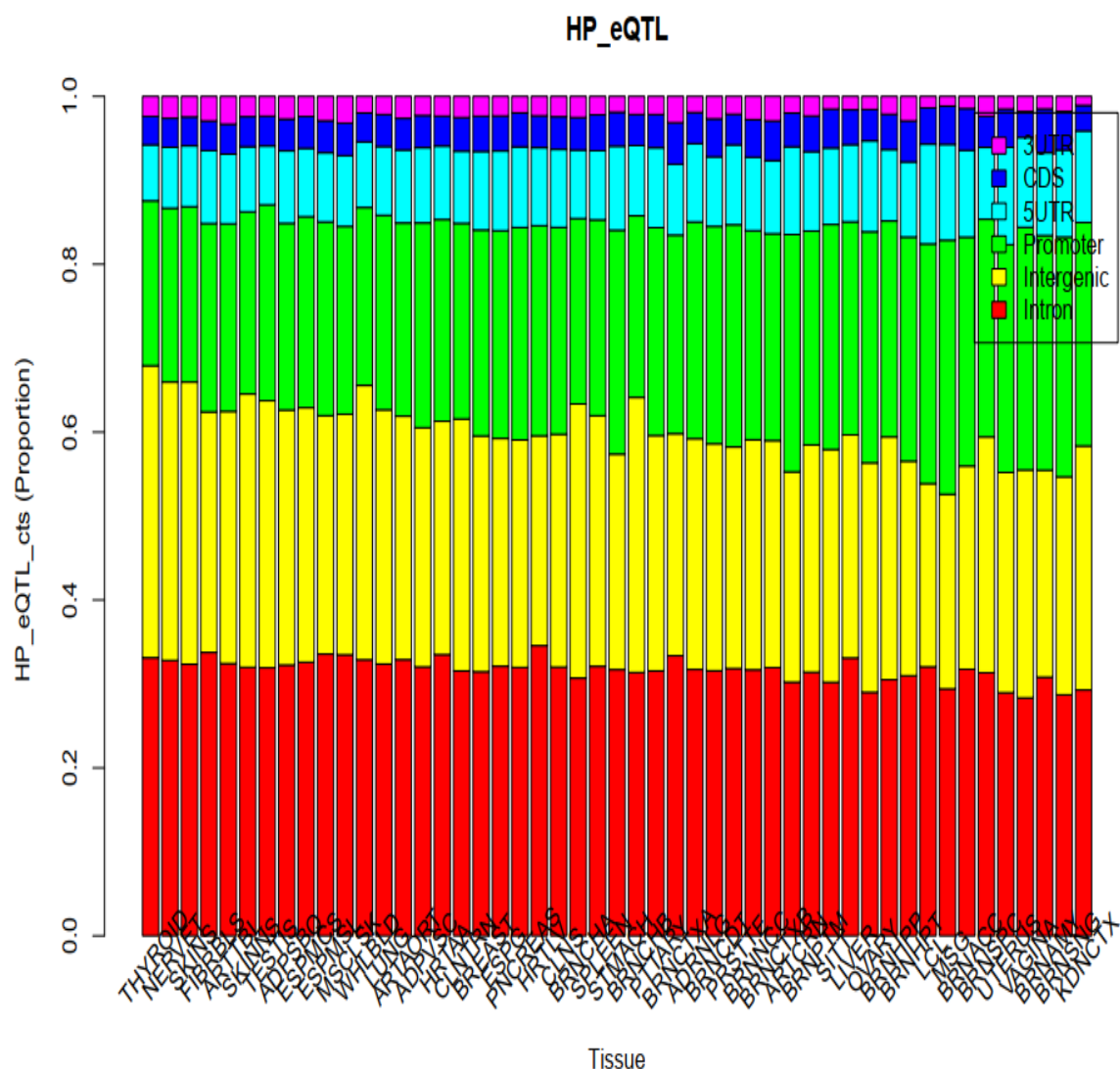
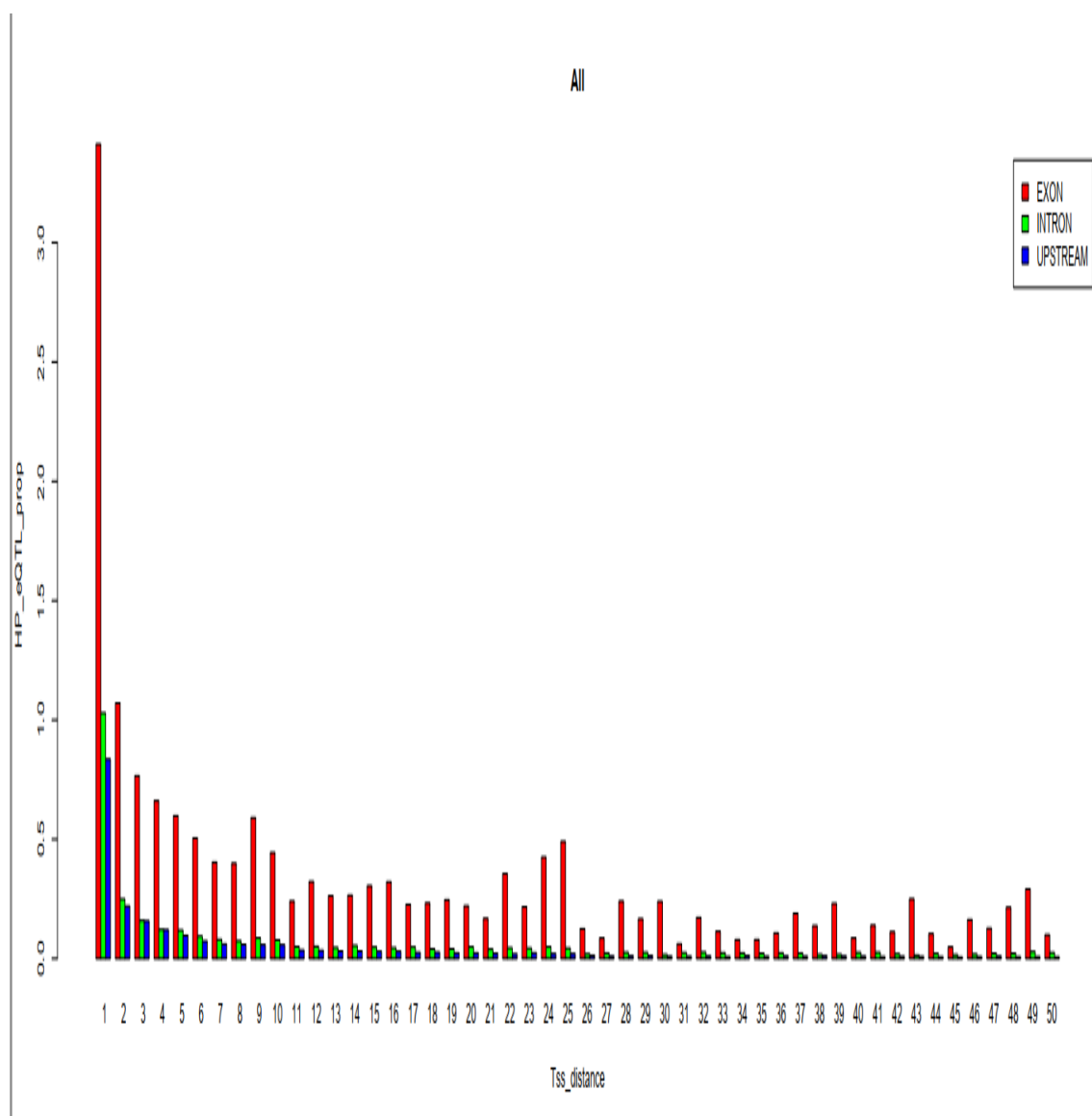


Figure 1: Counts and proportion of HP eQTL in different genome regions

HP eQTL (PIP ≥ 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.

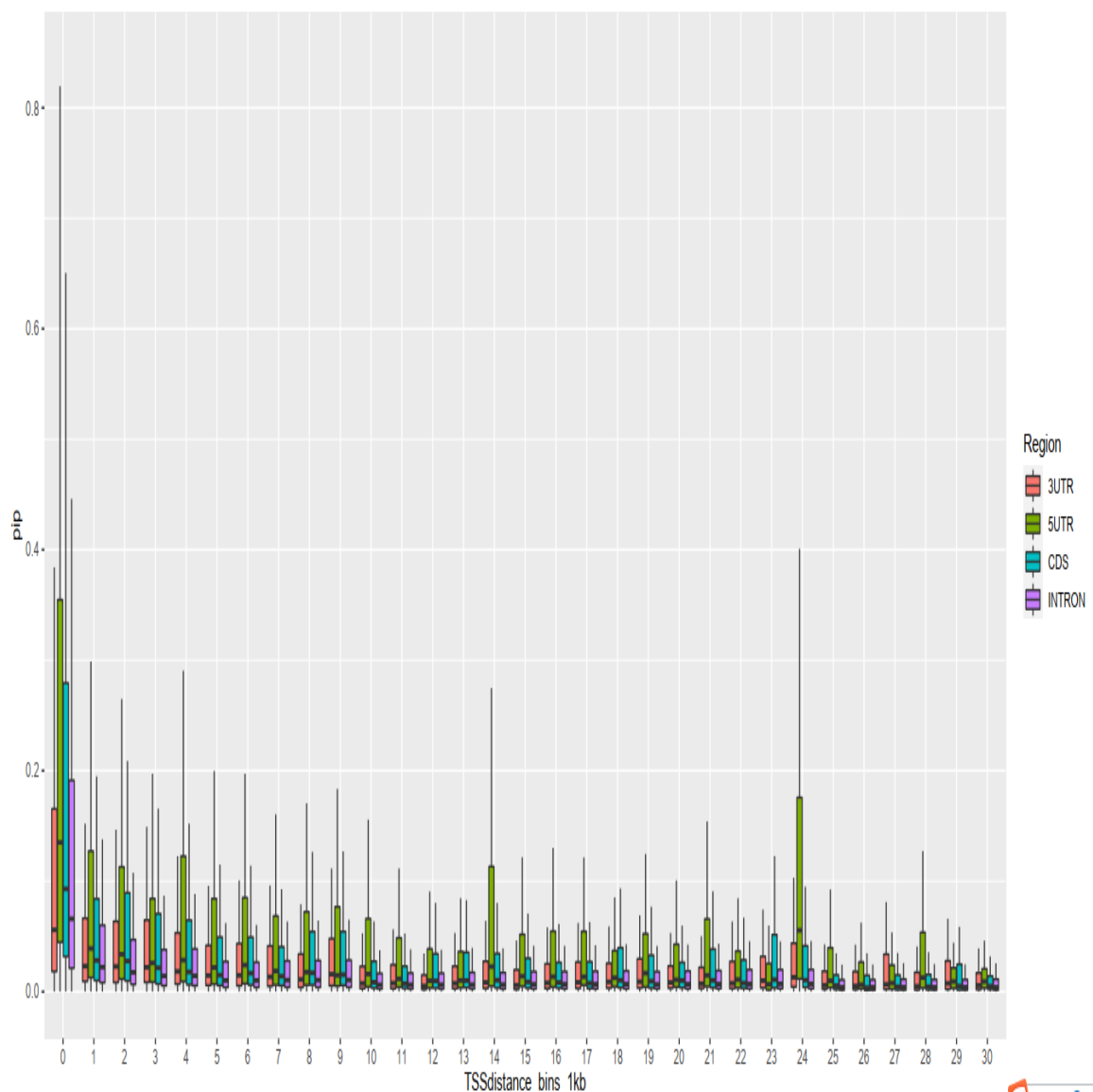


Figure 2: PIP score distributions for eQTLs for exon and intron in each 1 kbp genomic regions

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

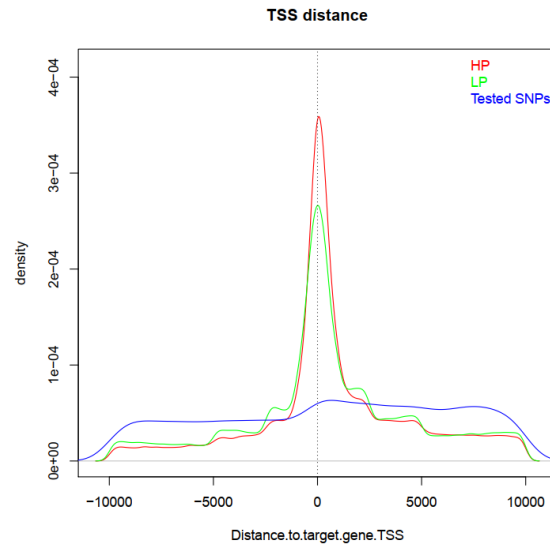


Figure 3: Density distribution of HP eQTL, LP eQTL (those not HP eQTL) and all tested SNPs around gene TSS

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

Figure 2a

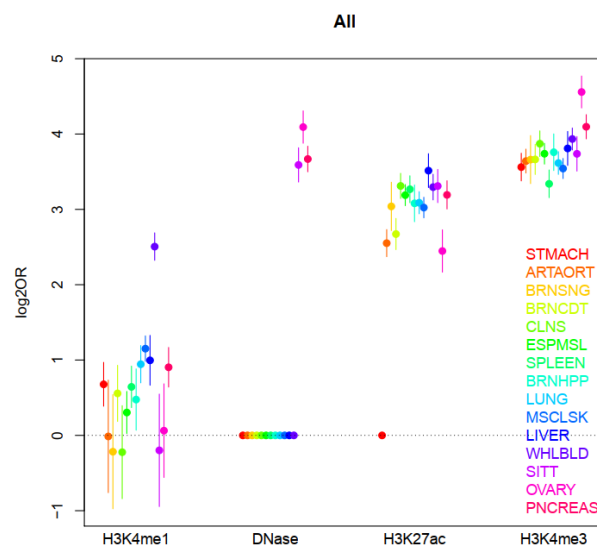


Figure 4: enrichment of HP eQTL within transcription features in different tissues

HP eQTL enrichment within transcription 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

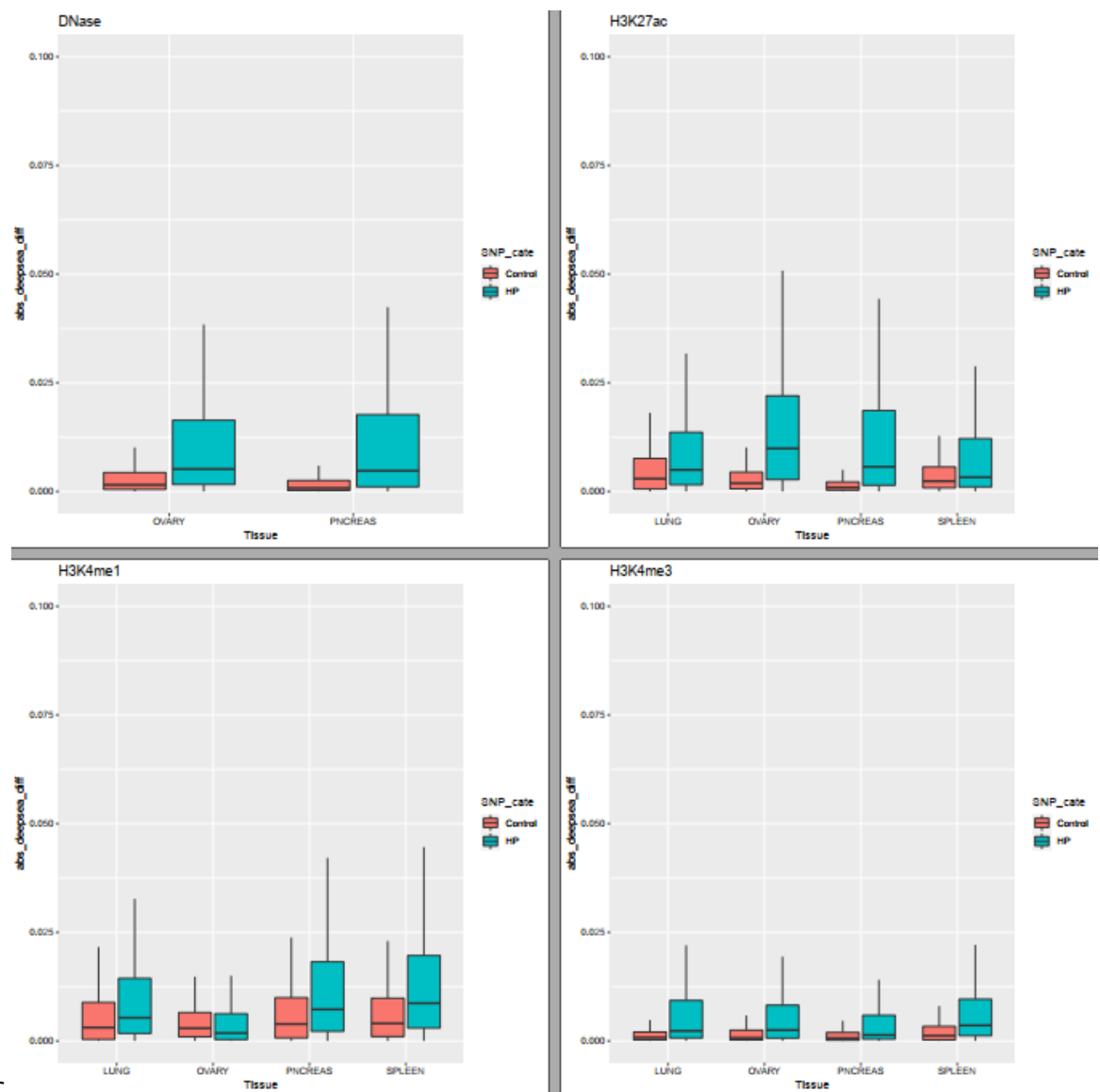


Figure 2c

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 5:

Figure S2

Figure 6:

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
