

Scotland's Rural College

## Improving the annotation of the cattle genome by annotating transcription start sites in a diverse set of tissues and populations using Cap Analysis Gene Expression sequencing

BovReg consortium

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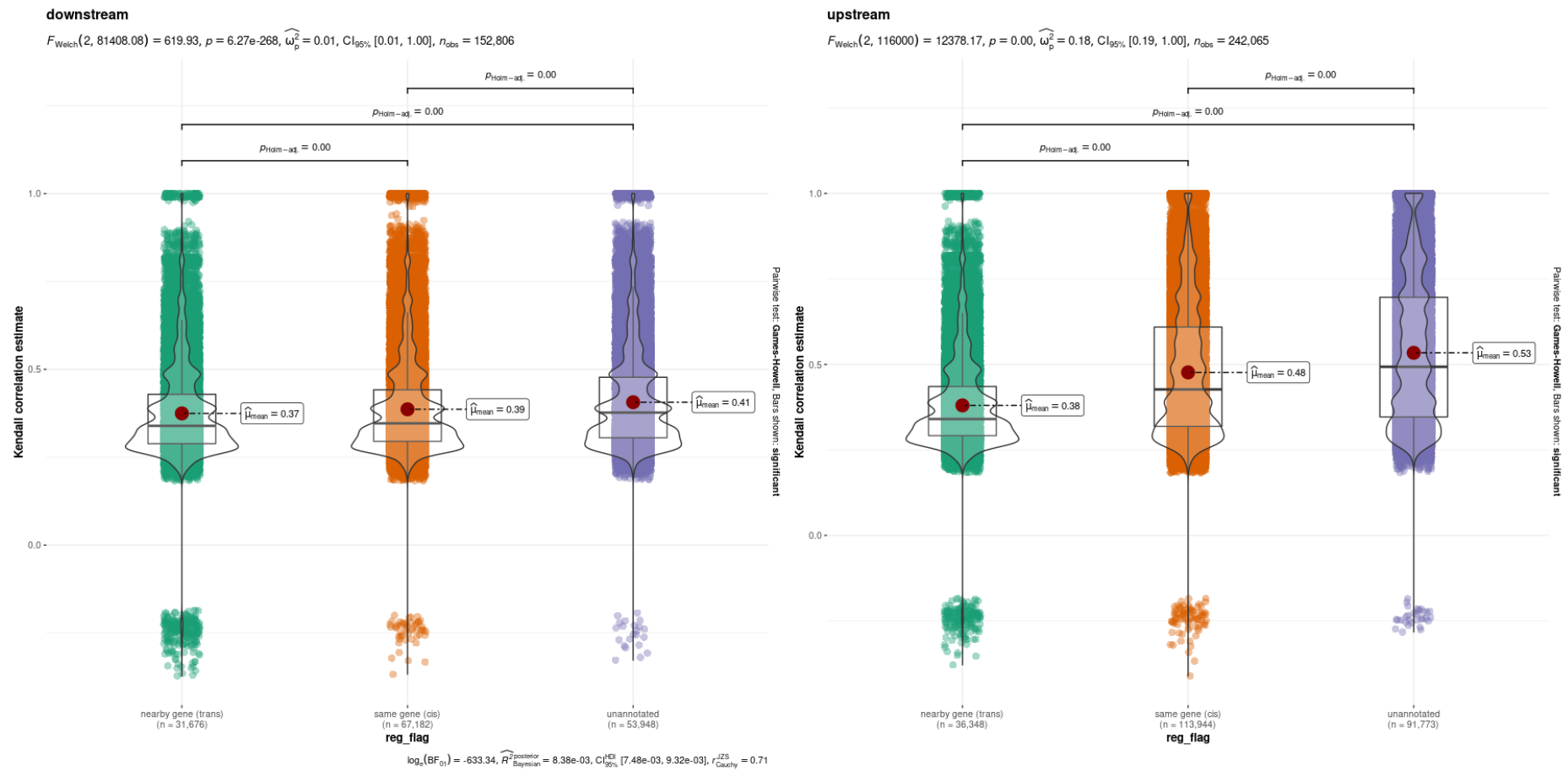
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Supplementary Figure 1 – The comparison of correlation estimates between 3 categories of the link between TSS and Enhancer regions in the cattle CAGE dataset. A grouped Welch test was carried out between nearby gene, same gene and unannotated groups of TSS-Enhancer links. Significant level  $p < 0.01$ .