

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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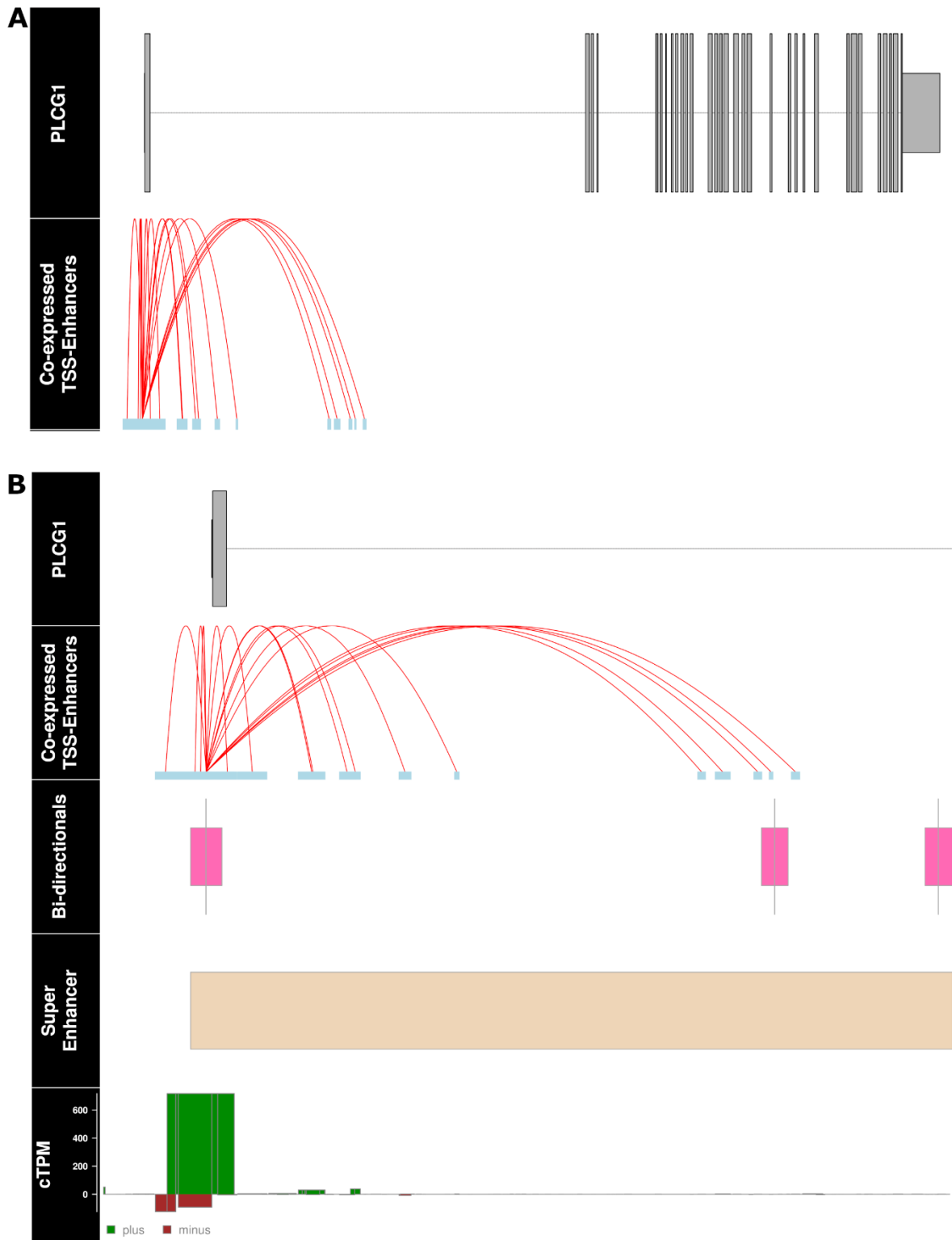
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Supplementary Figure 2 – Significantly co-expressed TSS and Enhancer profiles for the *PLCG1* gene. A) full length gene model and B) 5'UTR zoomed version of the gene models is shown using a genomic track layout. The correlation estimate between the co-expressed pairs is shown in red lines in the “Co-expressed TSS-Enhancers” tracks. The expression level of clusters is shown in normalised cTPM values in the “cTPM” tracks.