

Splice variants as novel targets in pancreatic ductal adenocarcinoma

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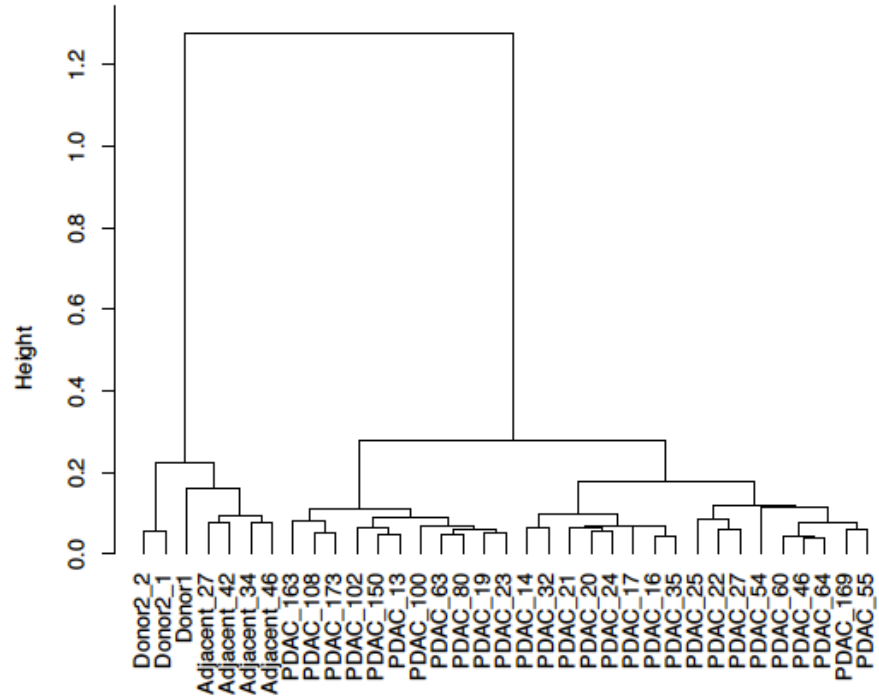
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A



B

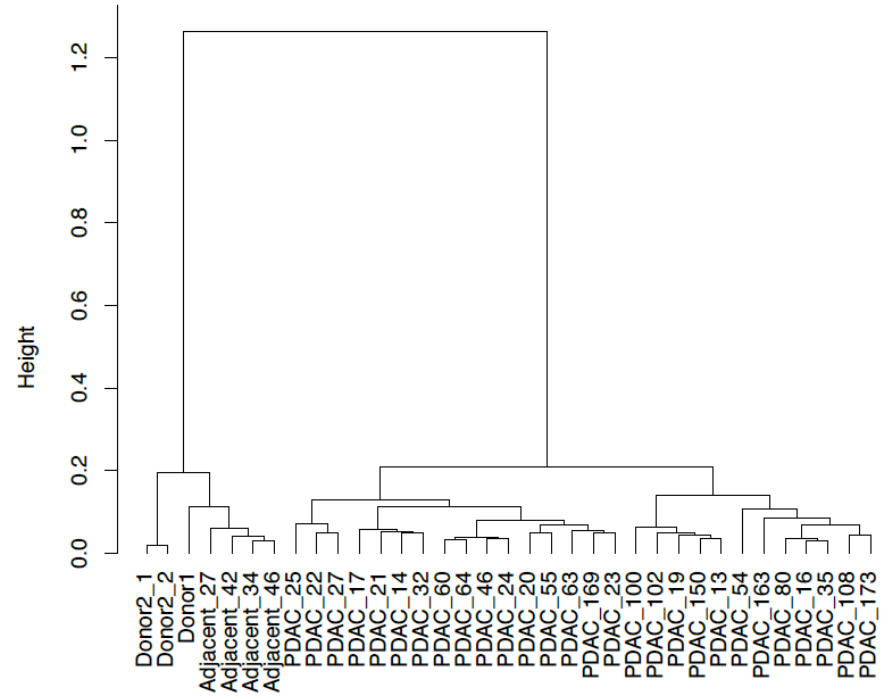


Figure S1. Unsupervised hierarchical clustering based on probeset (A) and transcript (B) expression level

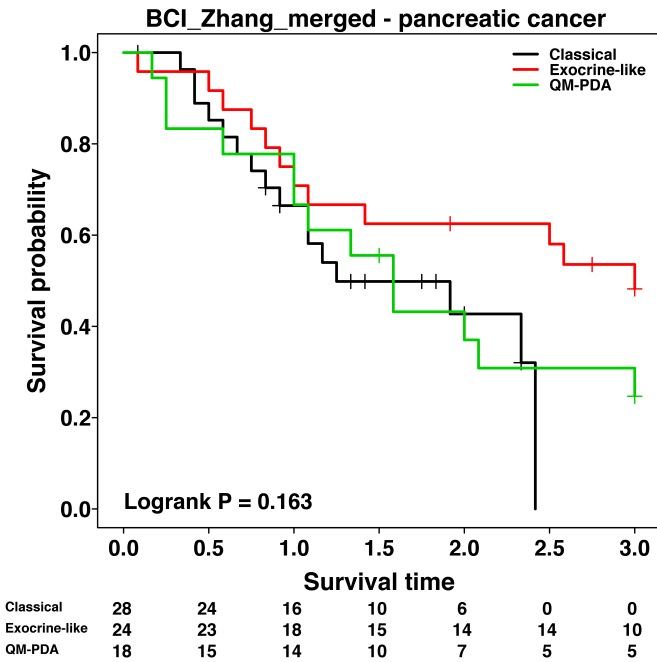
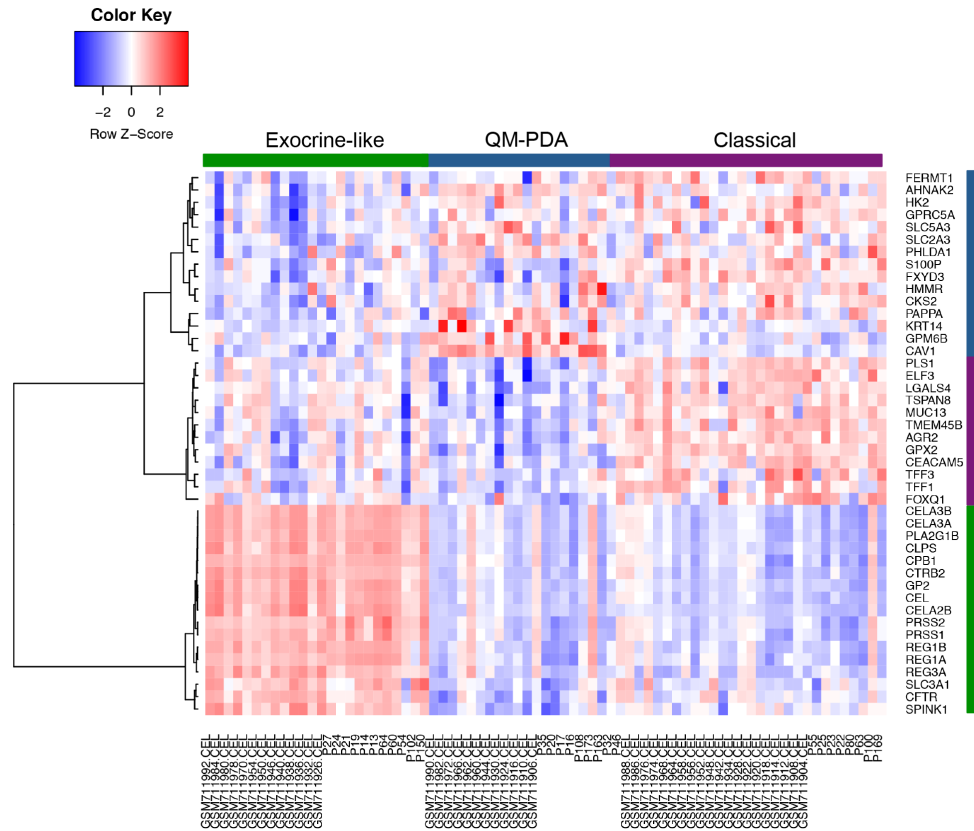


Figure S2. Gene expression and sample clustering of Collisson signature (62 genes) in BCI and Zhang merged dataset

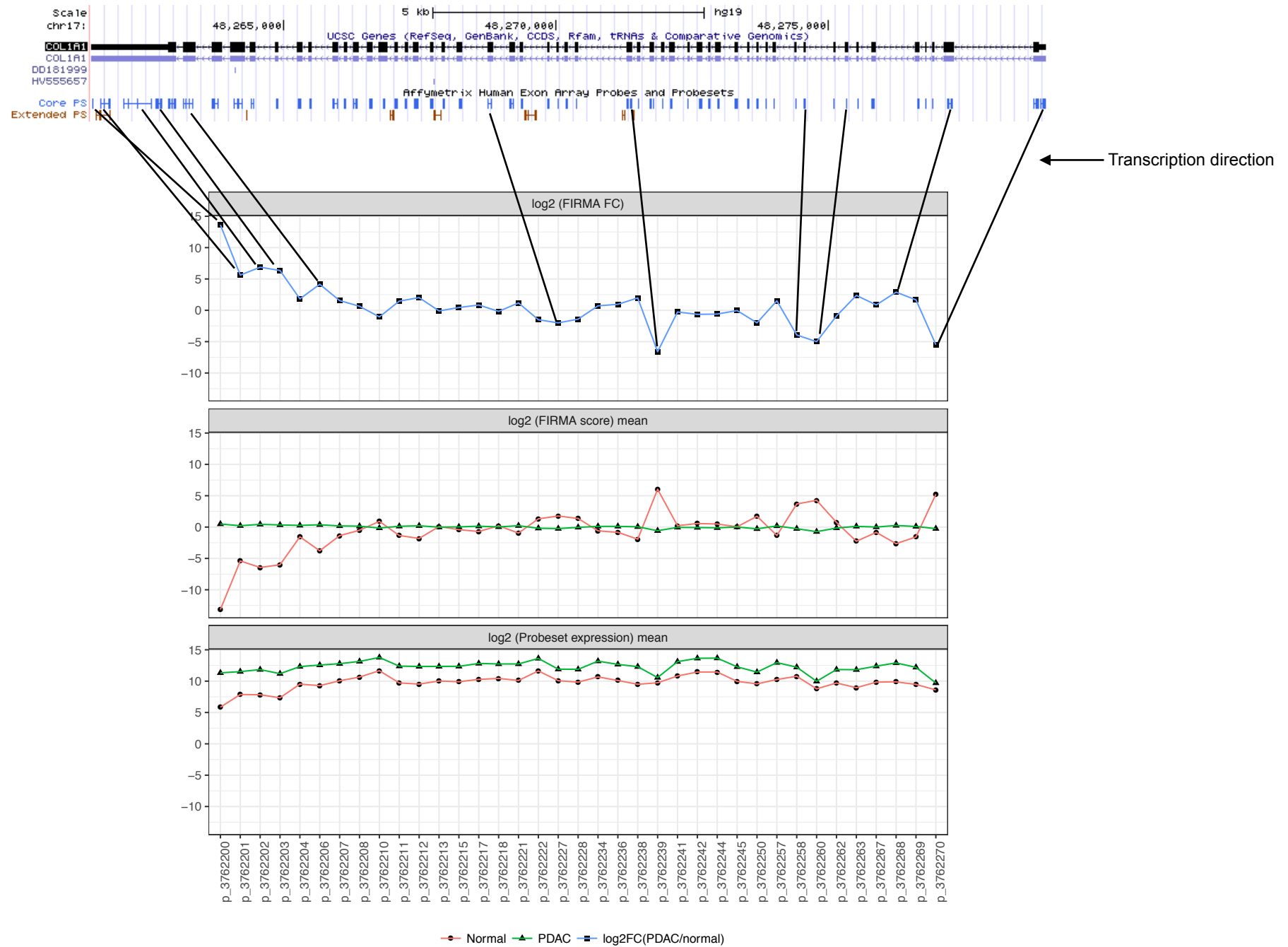


Figure S3A. alternative splicing in COL1A1

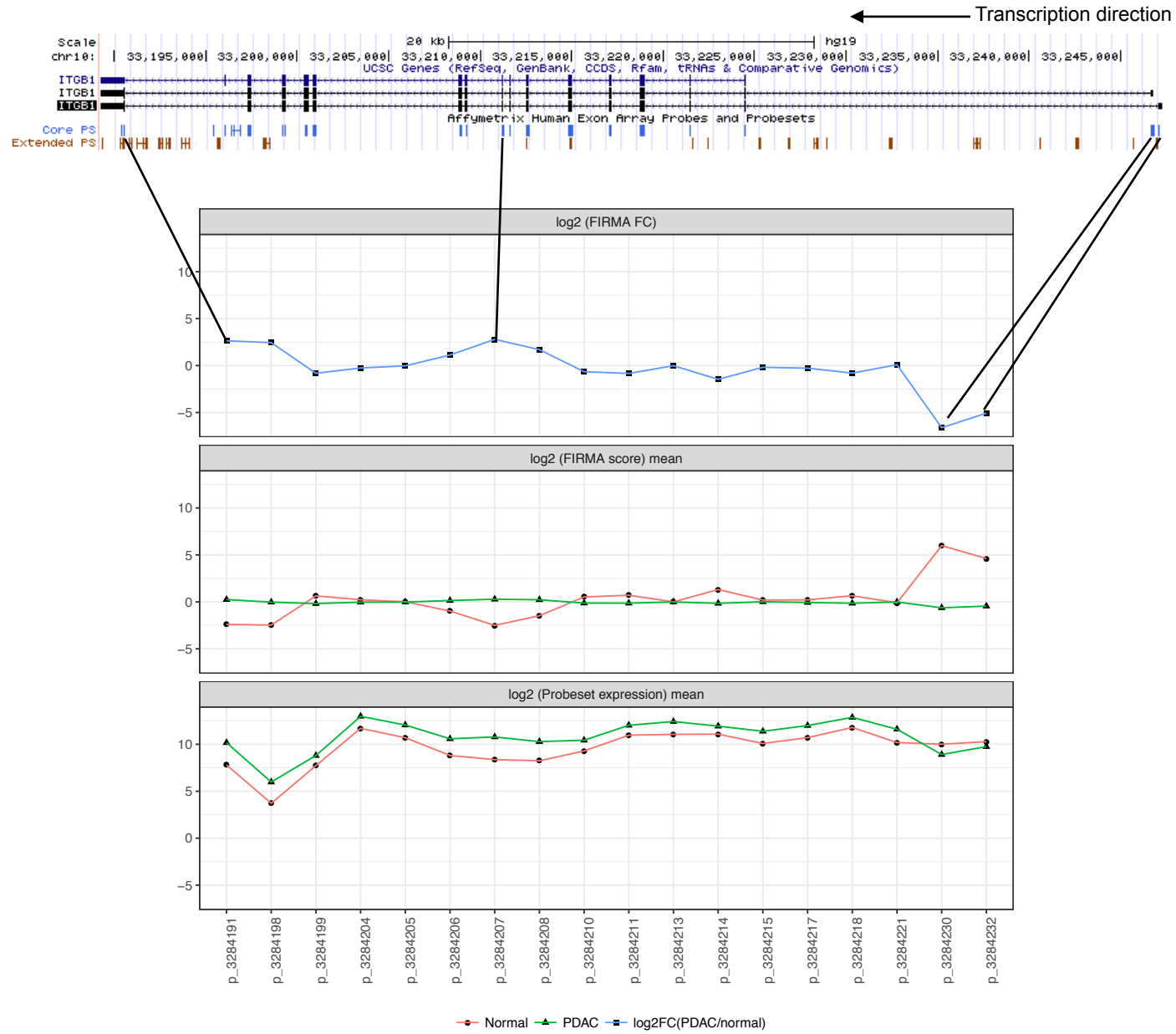
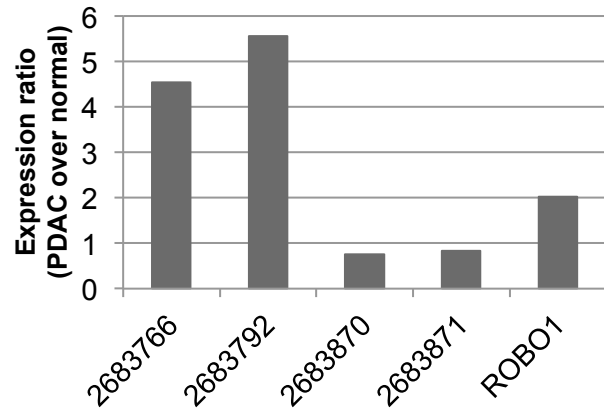


Figure S3B. alternative splicing in ITGB1

A



B

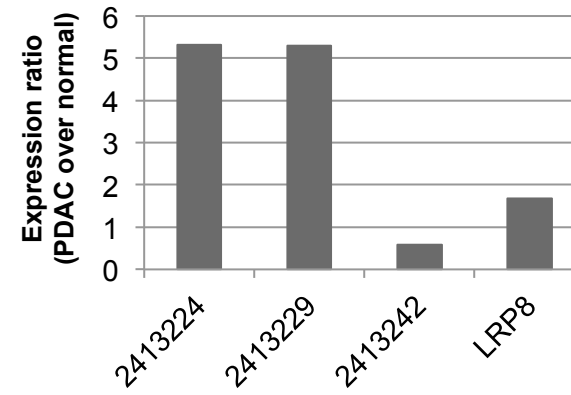
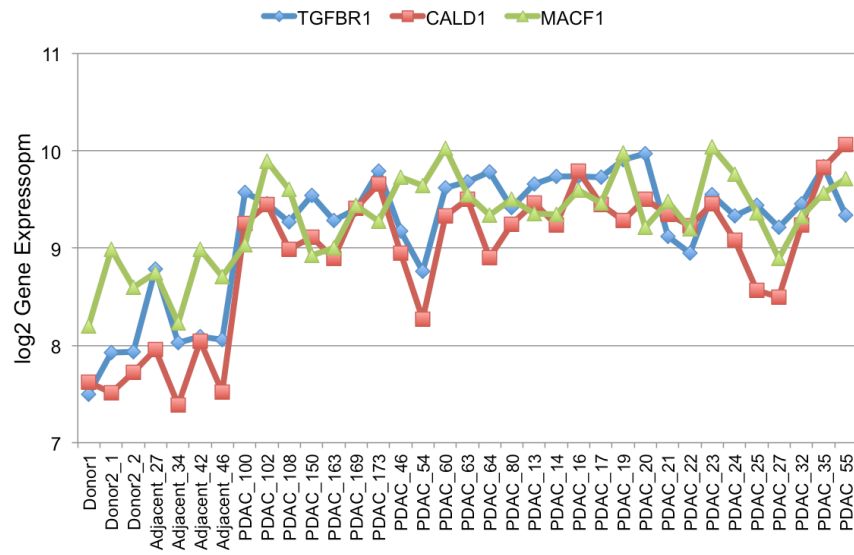


Figure S4. The expression ratio (PDAC over normal) of AS probesets and gene for ROBO1 and LRP8

A



B

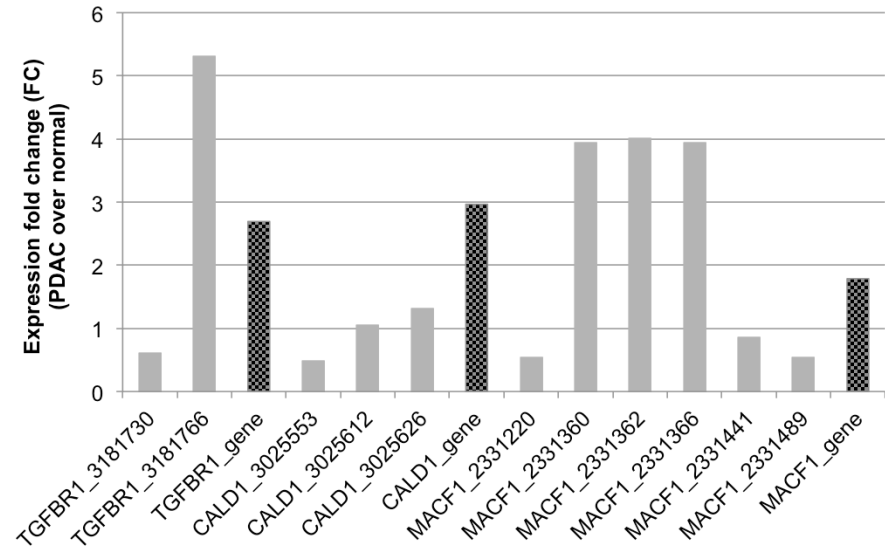


Figure S5A/B. Expression fold changes for TGFBR1, CALD1 and MACF1 in gene and probeset/exon levels

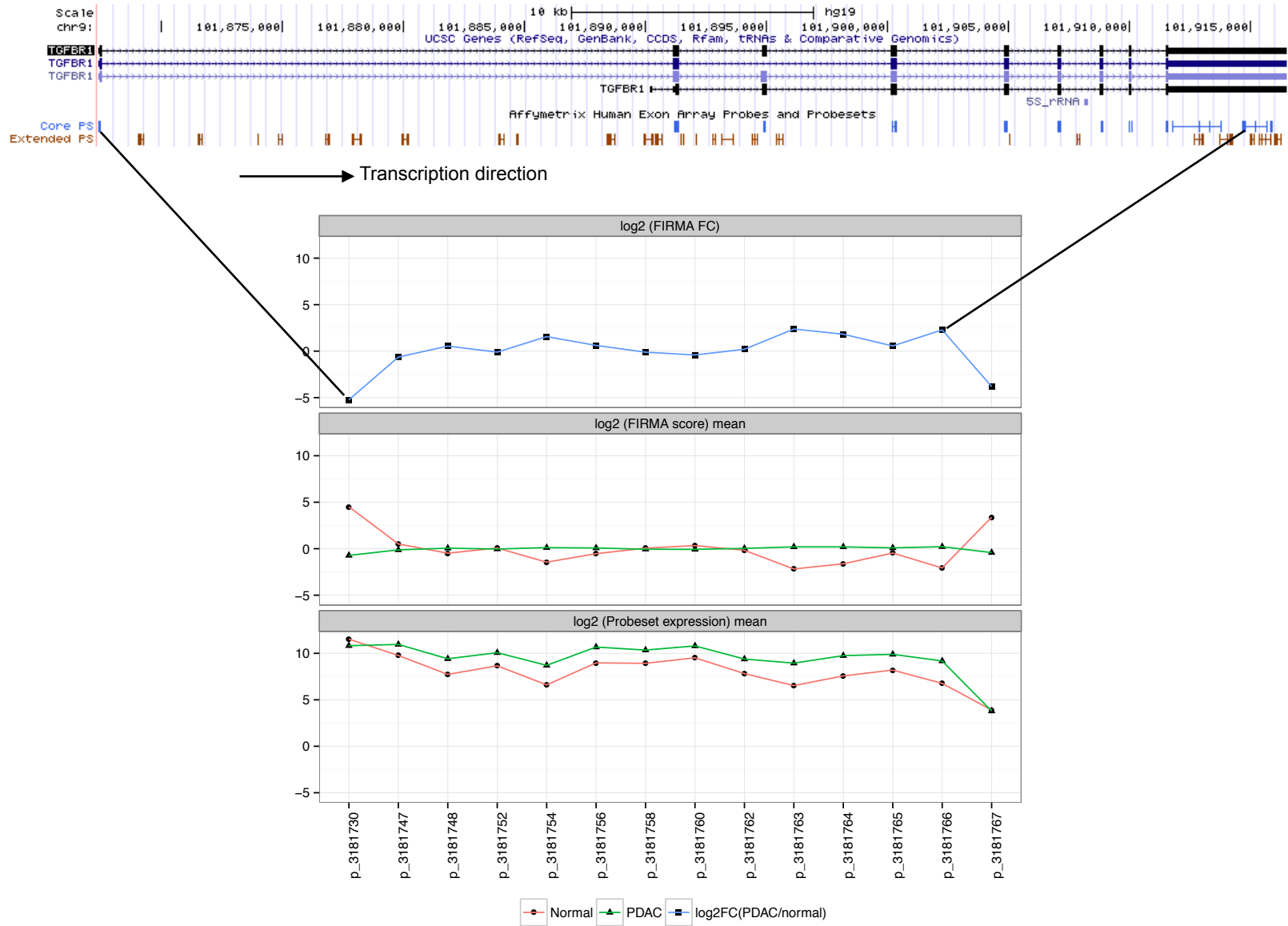


Figure S5C. Alternative splicing in TGFBR1

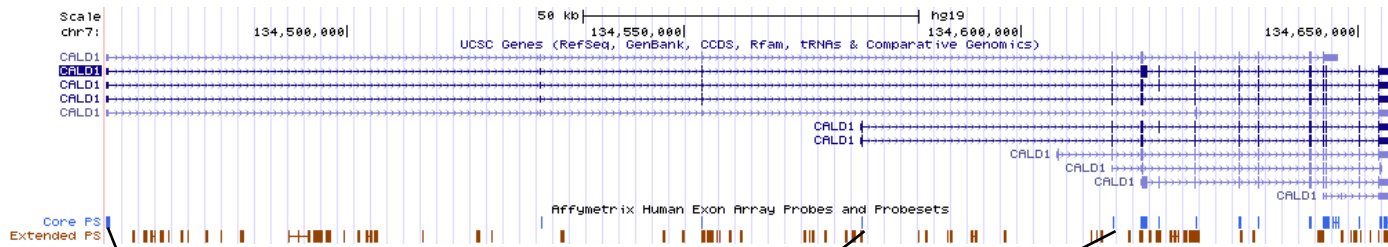


Figure S5D. Alternative splicing in CALD1

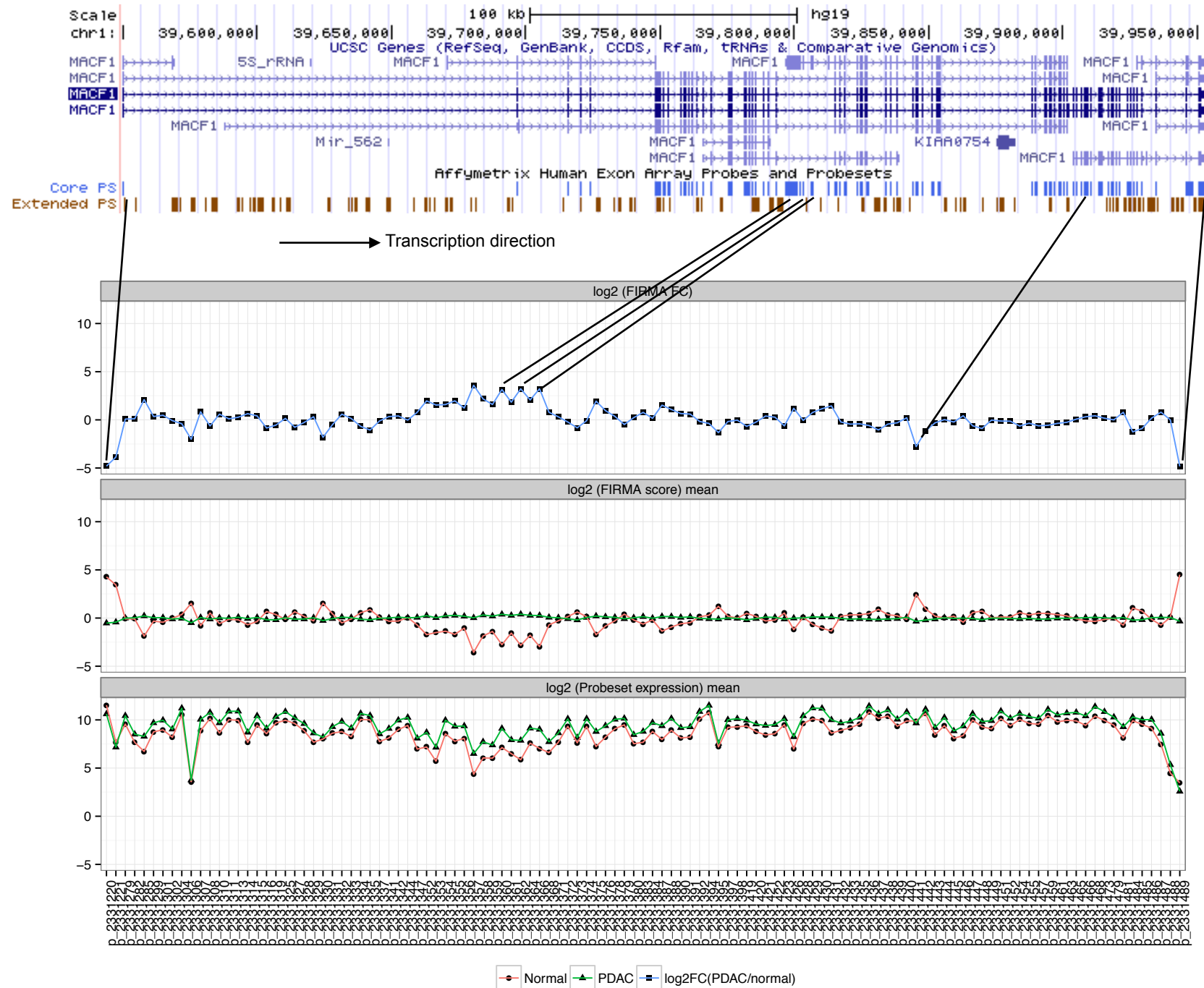


Figure S5E. Alternative splicing in MACF1

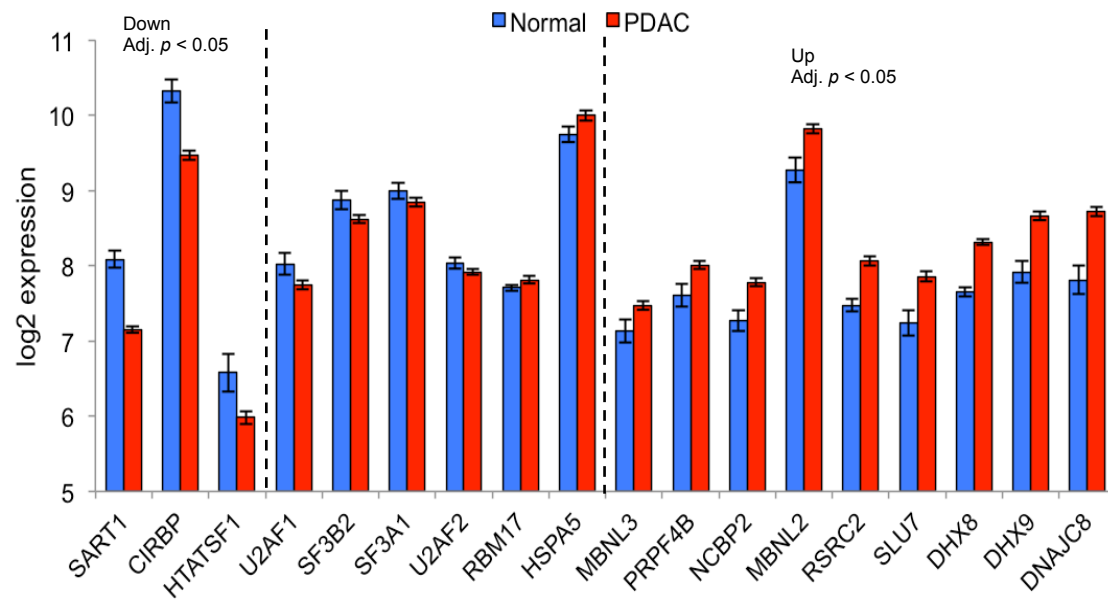


Figure S6. The DE signatures for previously reported spliceosomal genes