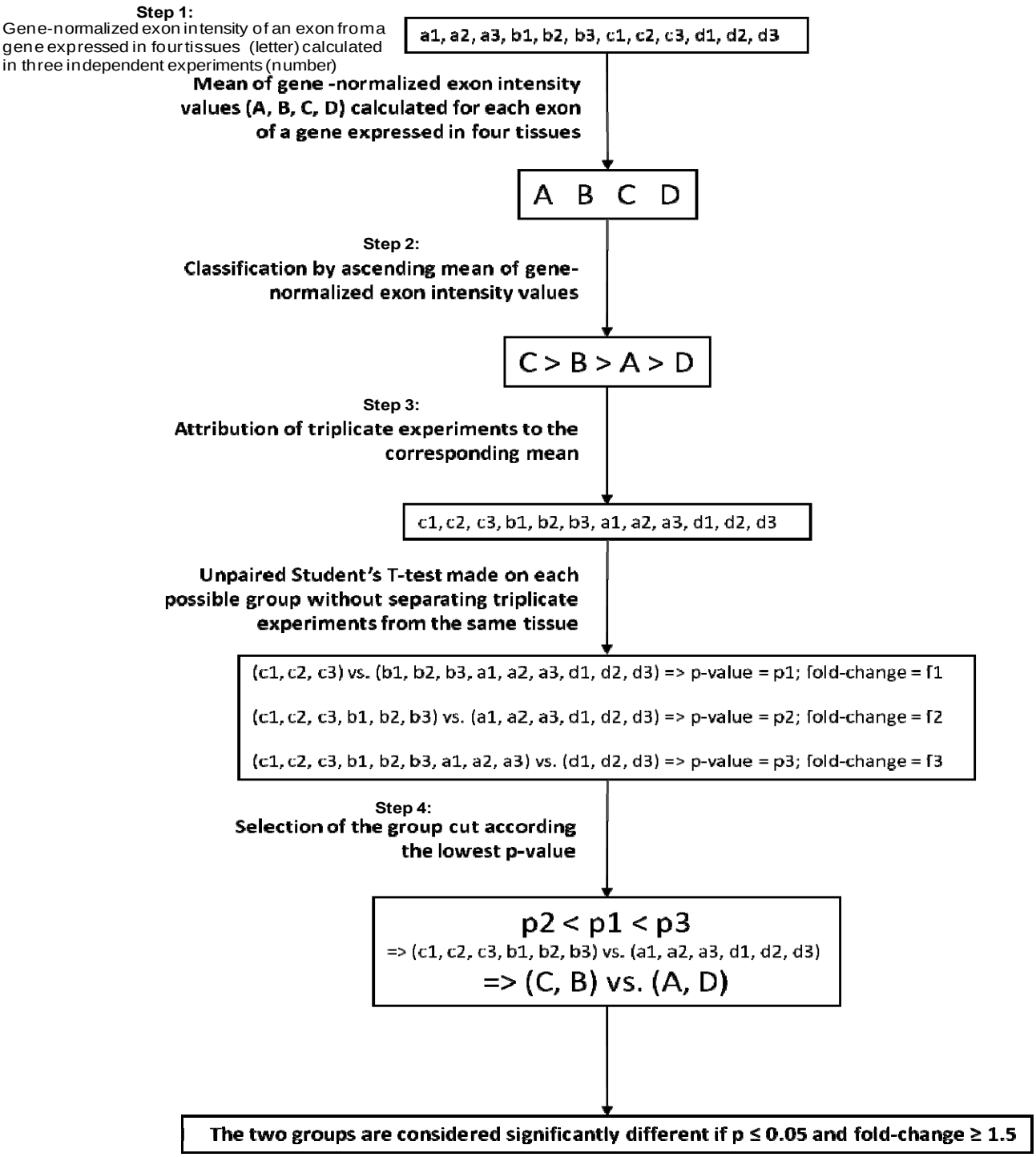
Supplementary Figure 1



Supplementary Figure 1: Strategy to identify differentially expressed exons of transcripts by considering all the tissues where the transcripts are expressed.

Step1: "Gene-normalized exon intensity" values (a1, a2, …) in each experiment were calculated by considering only tissues expressing the gene (four tissues in this example); a1, a2, and a3 corresponded to the gene-normalized exon intensity values in experiment 1, 2 and 3, respectively, in tissue "a".

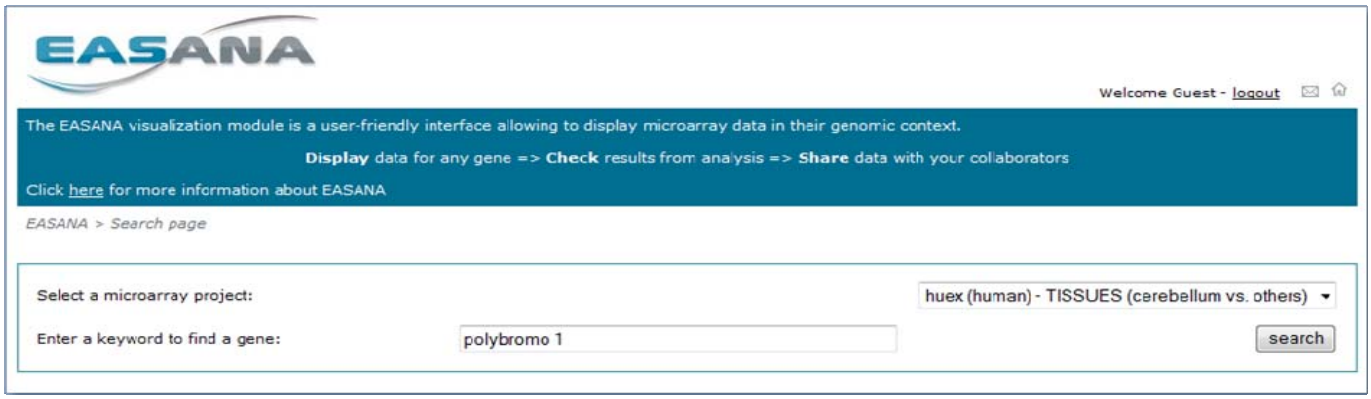
Step2: Average (A, B, C, D) of the "gene-normalized exon intensity" values classified by ascending order.

Step3: The averages of the gene-normalized exon intensity values were then replaced by the corresponding values obtained in the three experiments. An unpaired Student's t-test was performed by comparing "gene-normalized exon intensity" values for each possible group of tissues, that is, one tissue (or group of tissues) compared to all the other tissues.

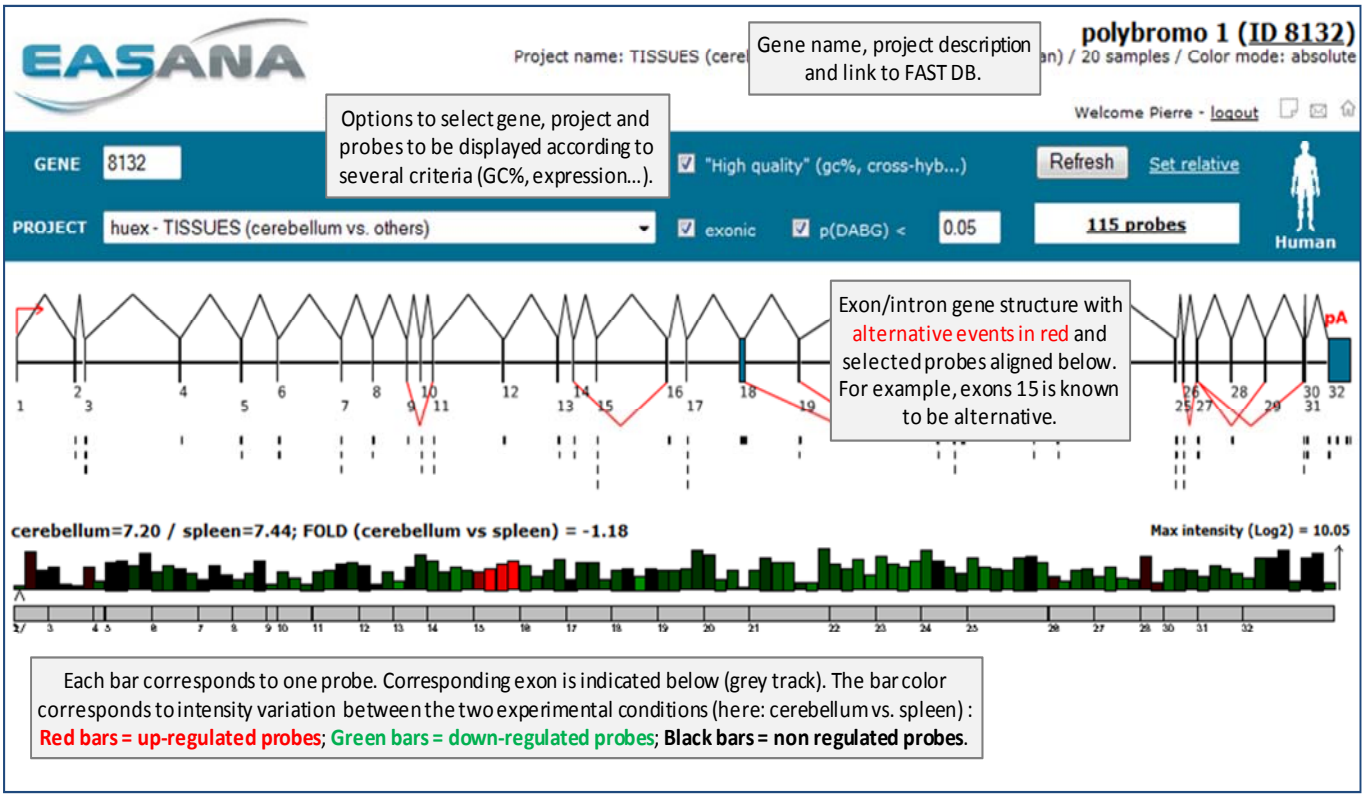
Step4: The cut point defining two groups, which means a group of values statistically higher than another group of values, was chosen according to the lowest associated p-value of each possible comparison. Exons were considered as differentially regulated between the two defined group if the p-value (e.g., p2) was $\leq$ 0.05 and if the fold-change (e.g., f2) comparing the gene-normalized exon intensity values was $\geq$ 1.5.

Supplementary Figure 2

A

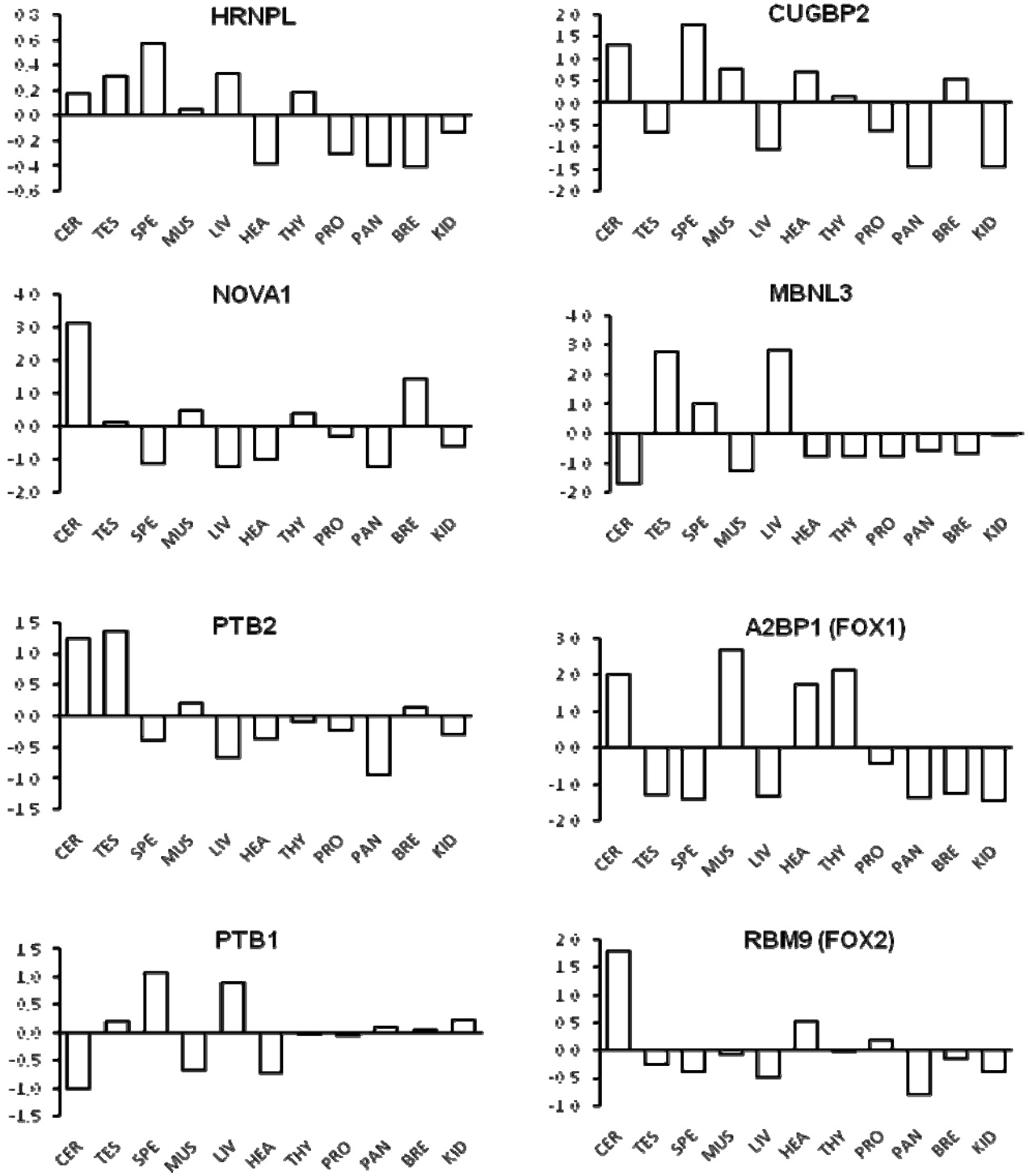


B

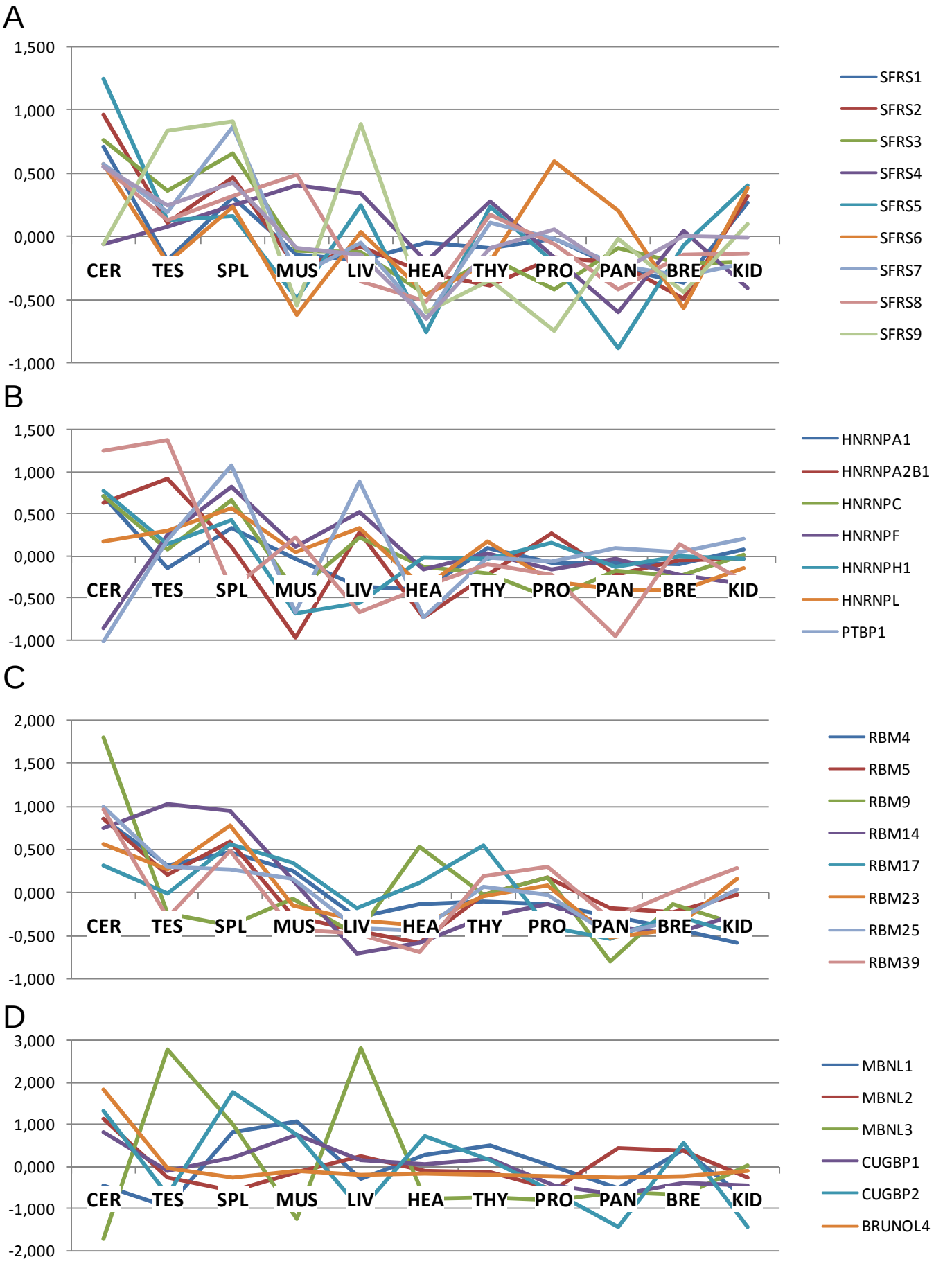


Supplementary Figure 2: **A.** After the user's registration, any name or gene symbol can be entered to retrieve the information of alternative splicing on the gene of interest, as described in panel B. **B.** Screenshot of the polybromo 1 gene expression in the cerebellum versus spleen comparison. Most of the bars representing exonic probes are green or dark and indicate that the polybromo 1 gene is slightly less expressed in the cerebellum than in the spleen. The bars corresponding to exon 15 are red and indicate that exon 15 may be preferentially included in the cerebellum when compared to the spleen. RT-PCR validation is shown on Figure 3C.

Supplementary Figure 3

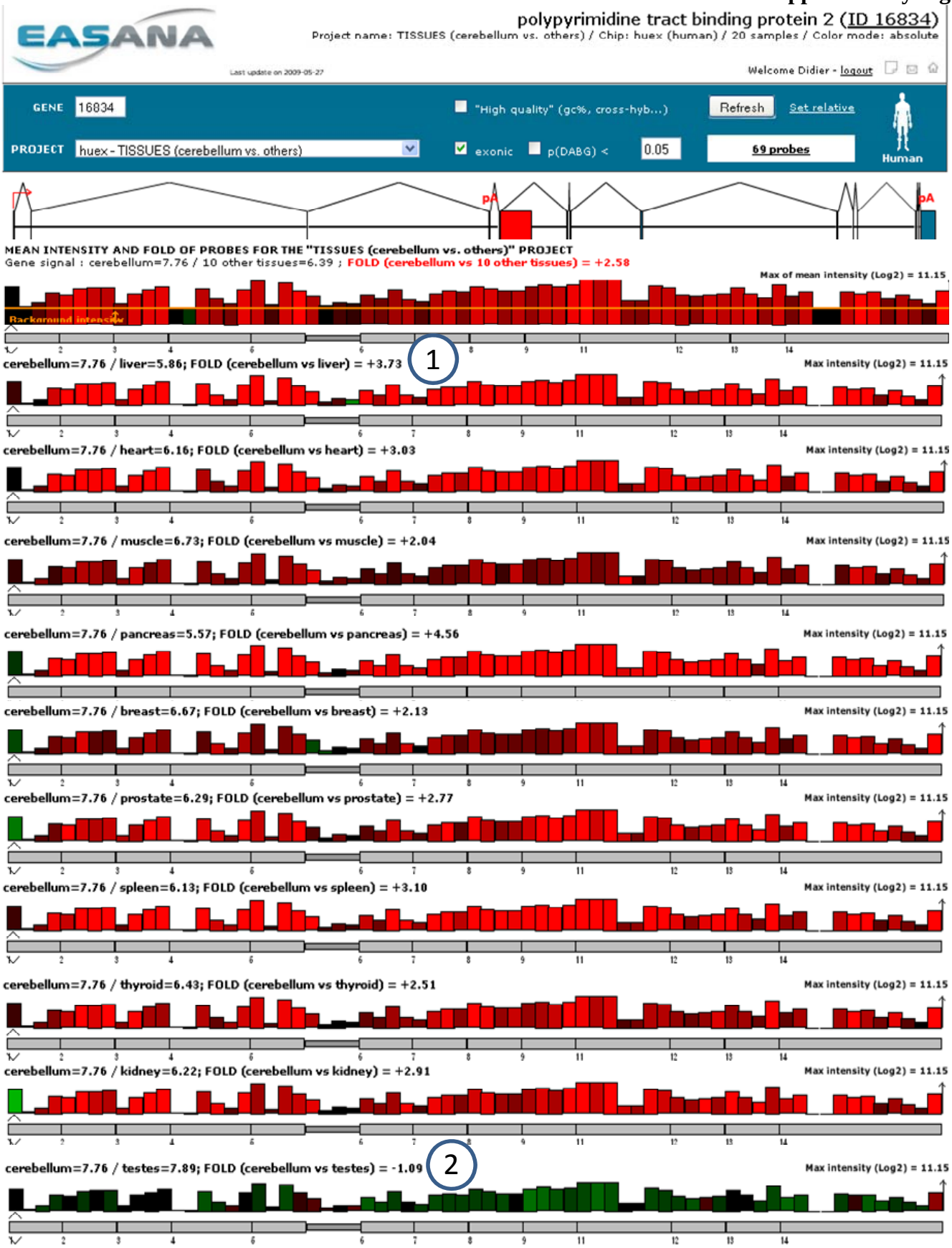


Supplementary Figure 3: Expression profile of selected splicing factors across normal human tissues based on the distance (ordinate) between the gene signal in a given tissue and the corresponding mean in the 11 tissues.



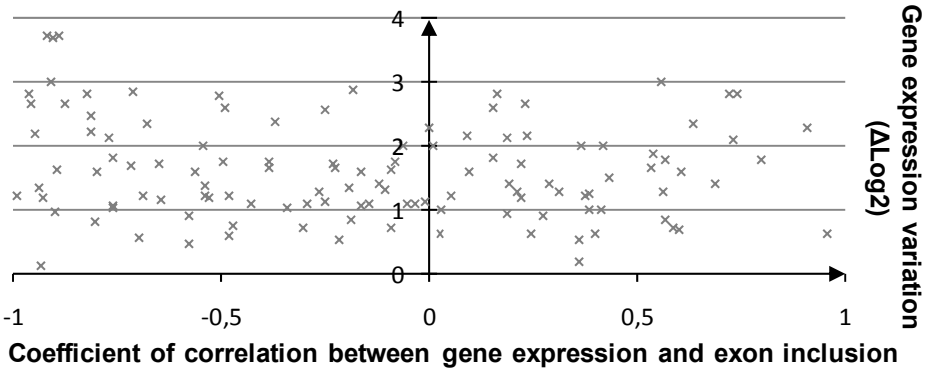
Supplementary Figure 4: Expression profile of splicing factors from the SR **(A)**, hnRNP **(B)**, RBM **(C)**, MBNL, and CUGBP **(D)** protein families across normal human tissues based on the distance (ordinate) between the gene signal in a given tissue and the corresponding mean in the 11 tissues.

Supplementary Figure 5



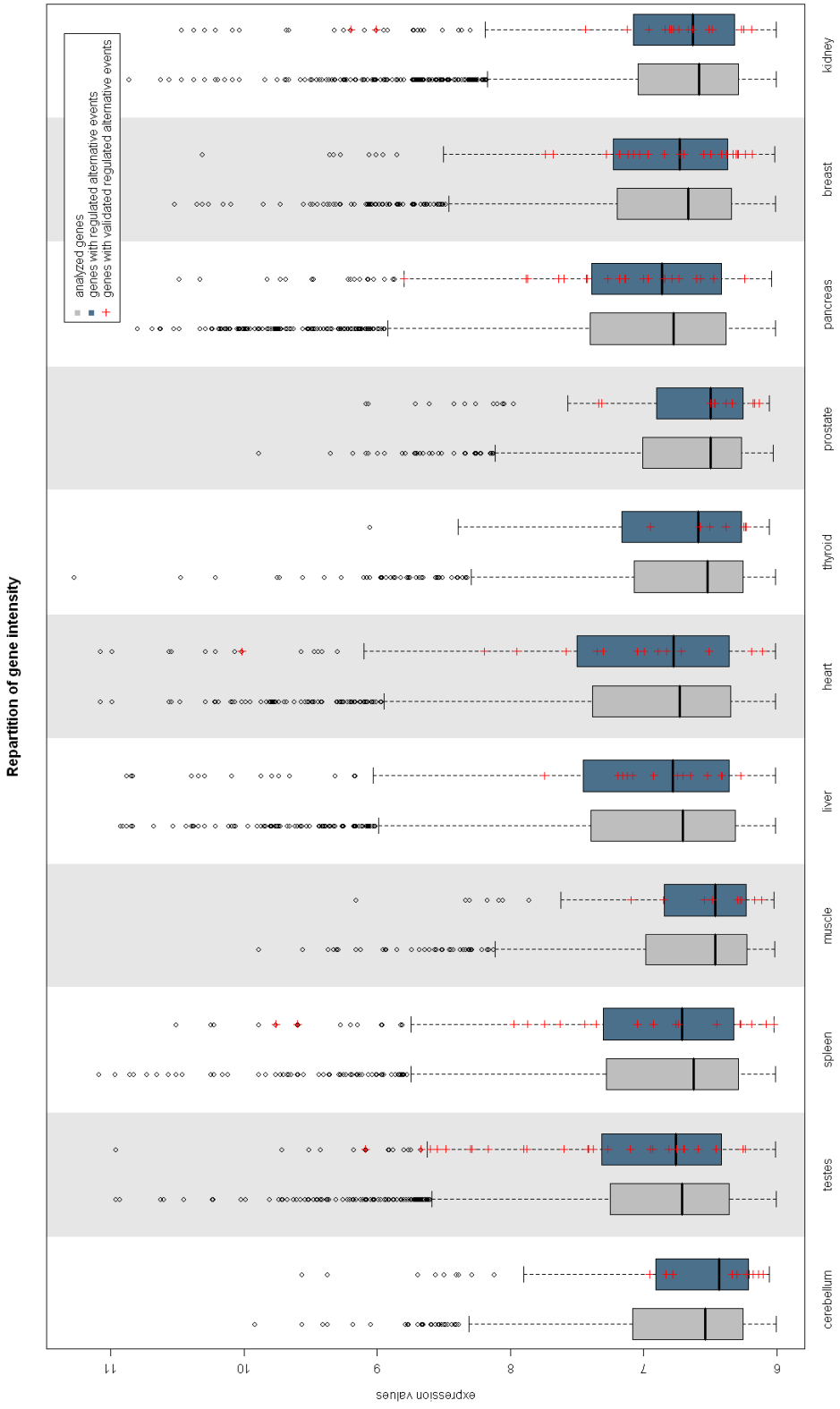
Supplementary Figure 5: The expression of any gene, like genes coding for splicing factor, can be analyzed in tissue paired comparison thanks to the EASANA web interface by using the query page described on Supplementary Figure 2. For example, nPTB is more expressed in the cerebellum when compared to most of the tissues, as indicated by the red color bar and by the fold change of gene expression level (e.g., item 1), but not when compared to testis (item 2).

Supplementary Figure 6



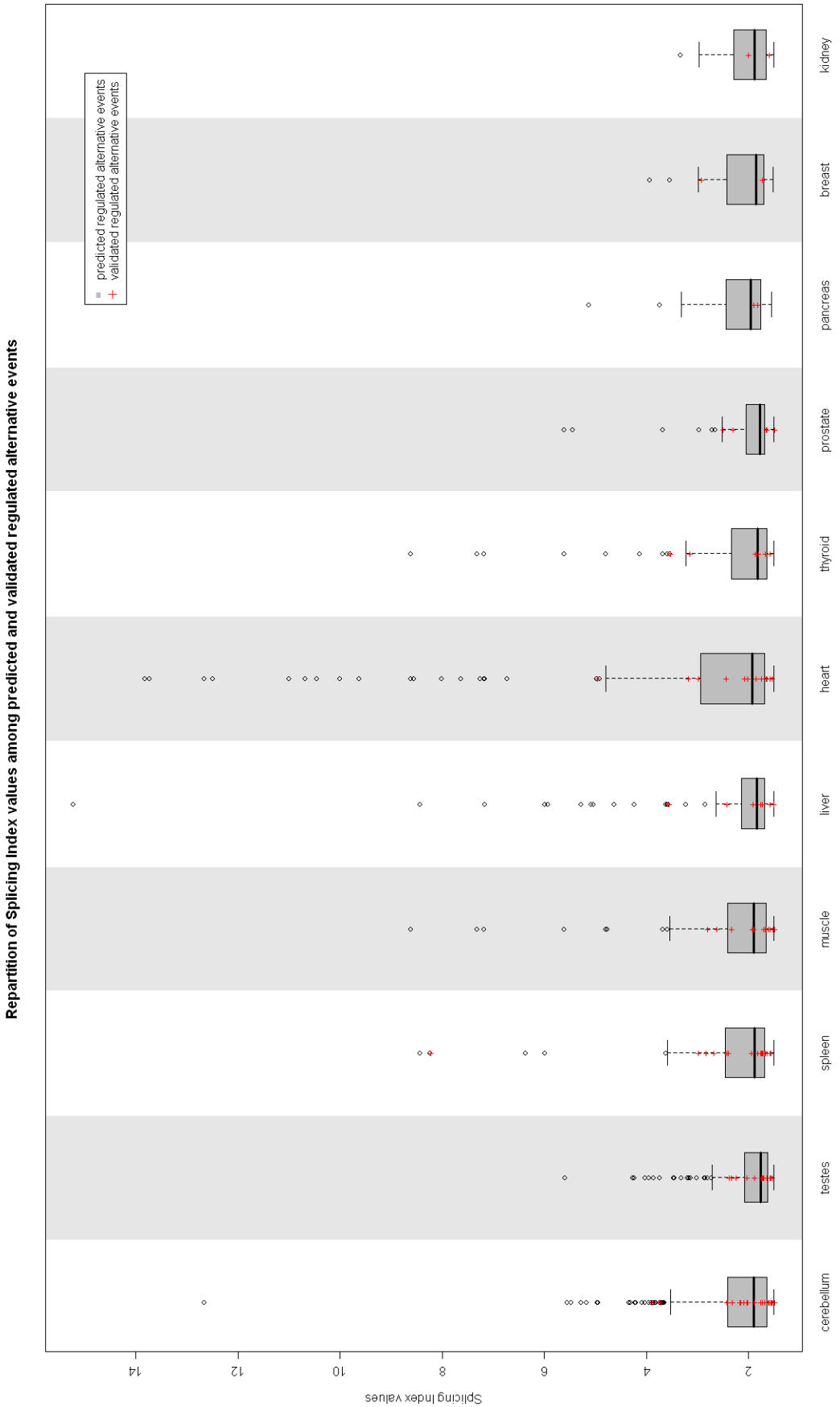
Supplementary Figure 6: No correlation between gene expression regulation and exon inclusion. The Pearson correlation coefficient was calculated between the gene signal and the gene-normalized exon intensity value matrixes corresponding to 135 genes expressed in at least five tissues and bearing differentially expressed alternatively spliced exons. Correlation coefficients were plotted with the corresponding gene expression variation value among the gene signal matrix. As tissues with the largest number of differentially expressed exons had the largest number of genes being over-expressed, we tested whether there was a correlation between splicing (exon inclusion) and gene expression level. Indeed, highly expressed genes may have a different splicing pattern. We calculated a correlation coefficient between gene expression and inclusion of differentially expressed exons. The result showed that there was no correlation between alternative exon and gene expression level.

Supplementary Figure 7



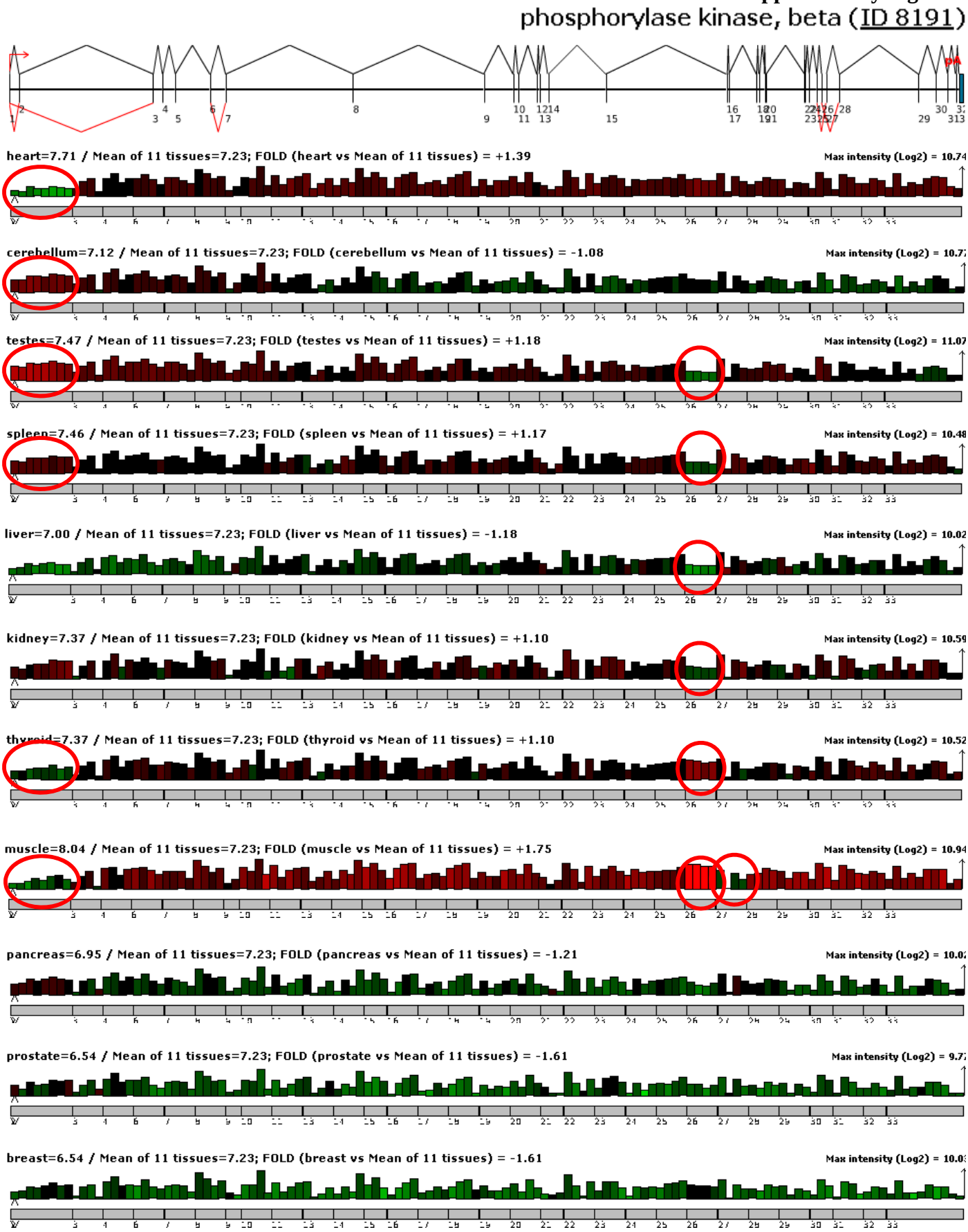
Supplementary Figure 7: No correlation between gene expression level and alternative splicing. For each tissue, this figure displays the intensity of analyzed genes (grey boxplot); the intensity of genes with a predicted regulated event (blue boxplot); and the intensity of genes with predicted regulated events that were validated by RT-PCR (red cross).

Supplementary Figure 8



Supplementary Figure 8: No correlation between Splicing Index fold-change of predicted events and RT-PCR validation. For each tissue, this figure displays the splicing index fold-change of the predicted regulated events (grey boxplot); and the splicing index fold-change of the predicted regulated events that were validated by RT-PCR (red cross).

Supplementary Figure 9



Supplementary Figure 9: The beta phosphorylase kinase gene is expressed in 11 tissues and contains several alternative exons (exons 2, 26, and 27) that are differentially expressed across human tissues, as it is shown by using the "11 NORMAL HUMAN TISSUES" track in the EASANA web interface.