A bioinformatics-based exploration on the promoter occupancy and alternative splicing pattern in the human genome

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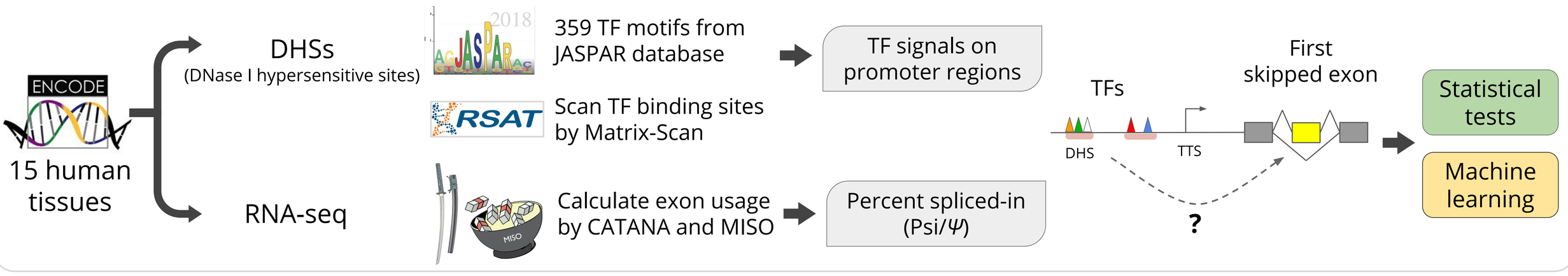
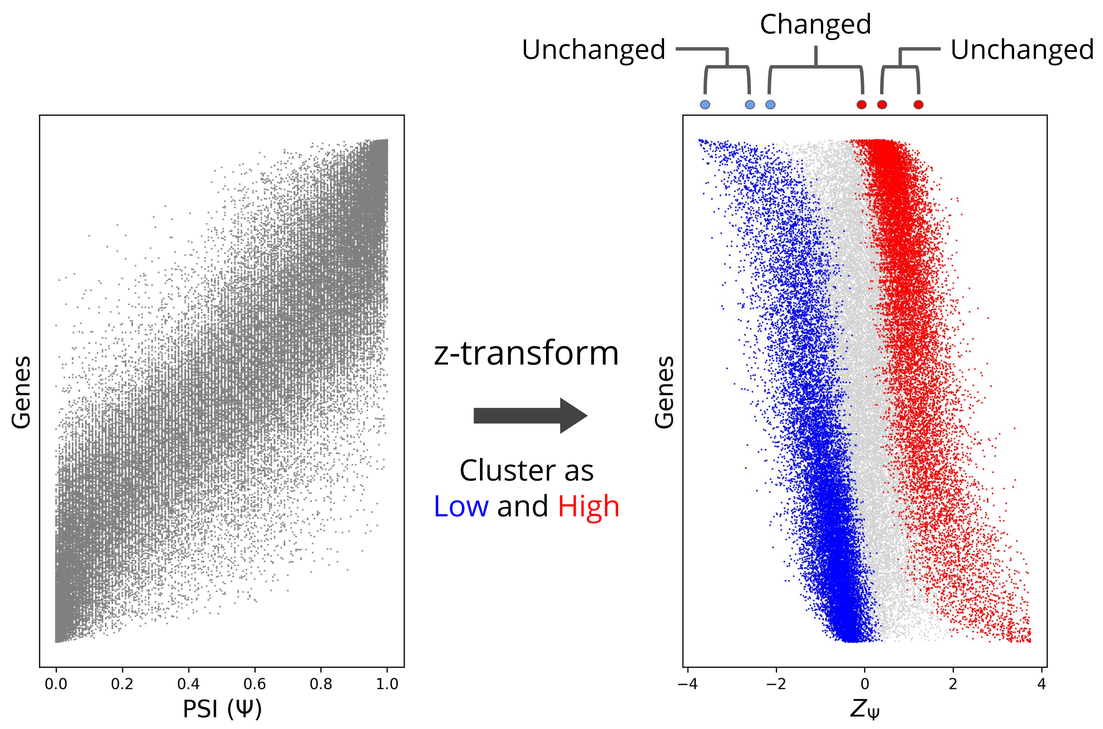
Introduction

Alternative splicing (AS), the selective removal of exons and reconnection of exons by multiple processes, shapes how genetic information controls important cellular functions in different tissues of higher metazoans. In the present study, we used publicly available open chromatin data and RNA-seq data of 15 human tissues to investigate the relationship between promoter and exon skipping. According to the statistical analysis, two-third of 345 TFs were significantly associated with splicing pattern change while most of those TFs (75%) were tissue-specifically expressed. Moreover, we identified several important TFs such as KLF14 and CEBPE that regulate splicing patterns genome-widely by importance analysis approaches. In summary, we have established a genome-wide association between AS and chromatin accessibility of promoter bound by different TFs.

Workflow

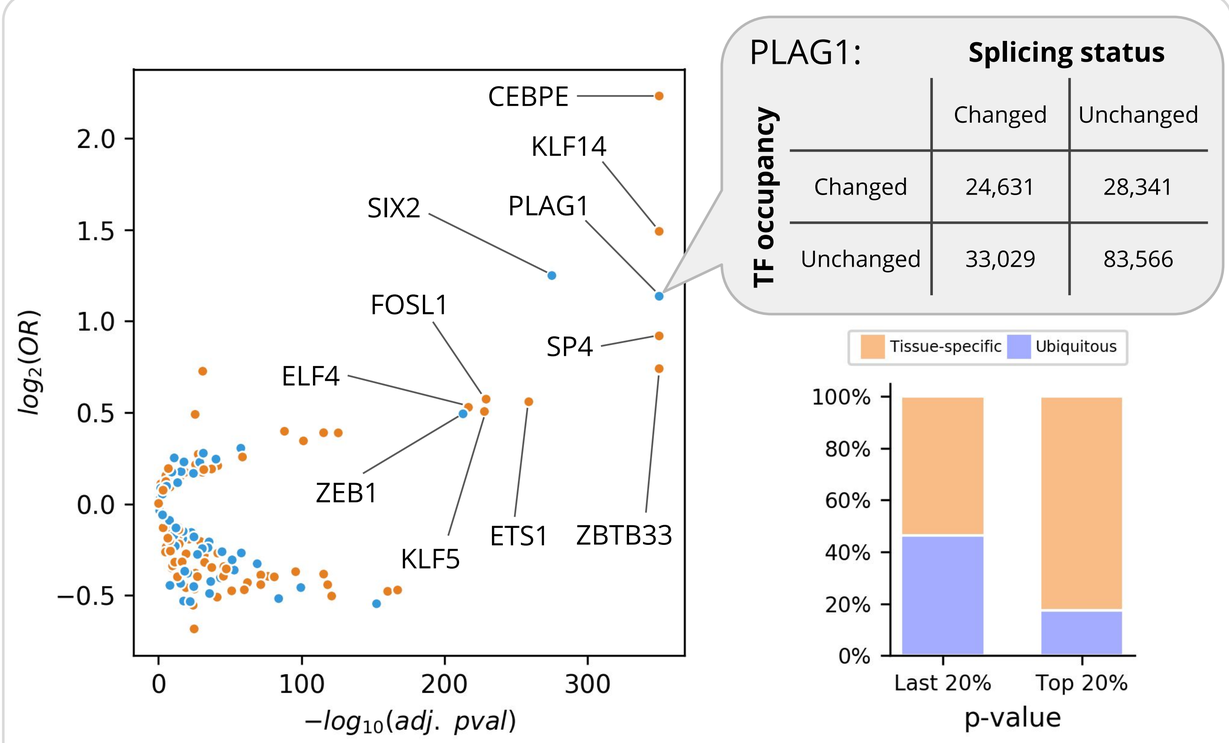


Distribution of raw PSI and z-transformed PSI of genes

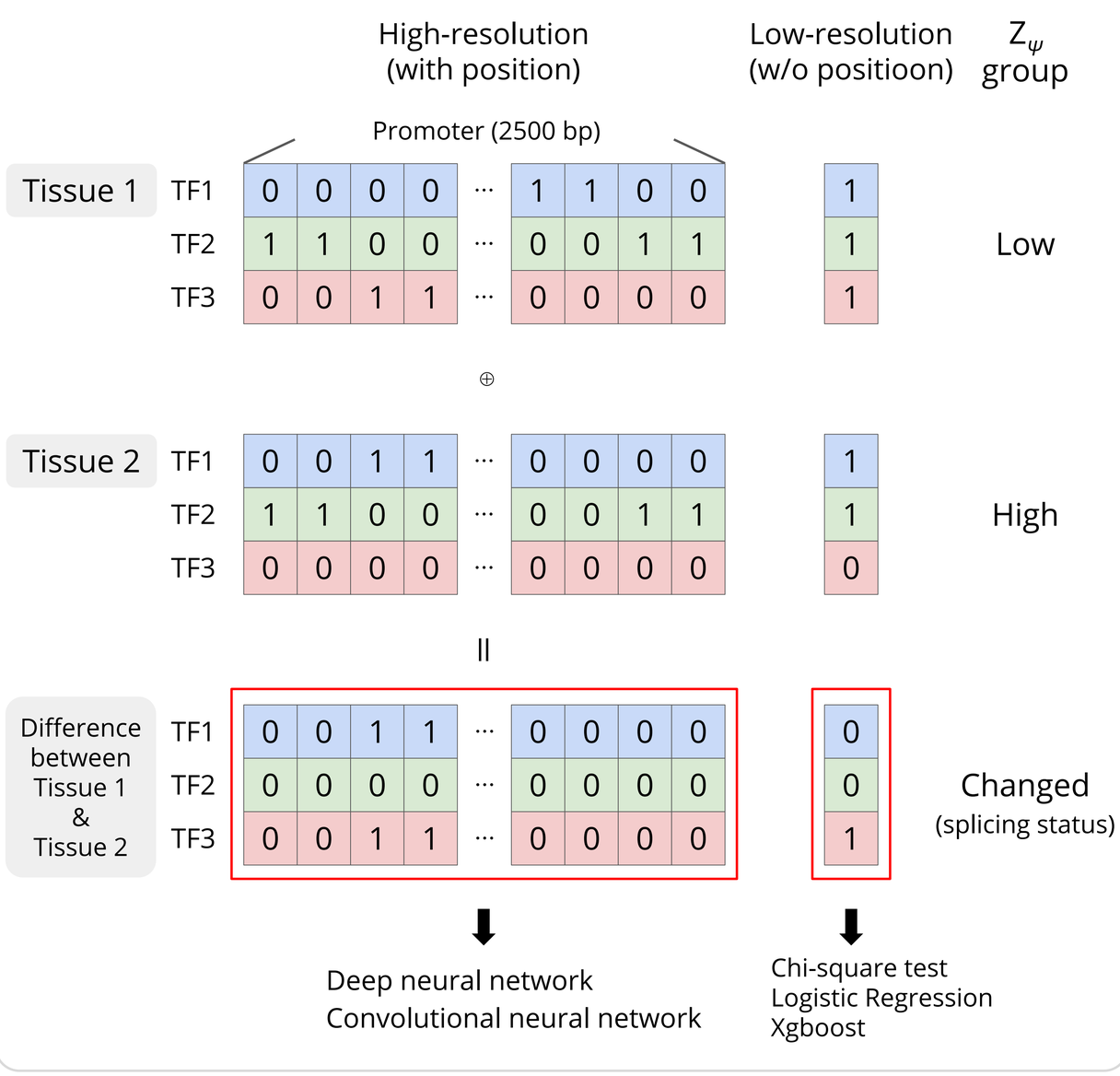


➢ The distribution of PSI scores of genes suggested that the exon usage status of many genes was distinct in certain tissues than others.

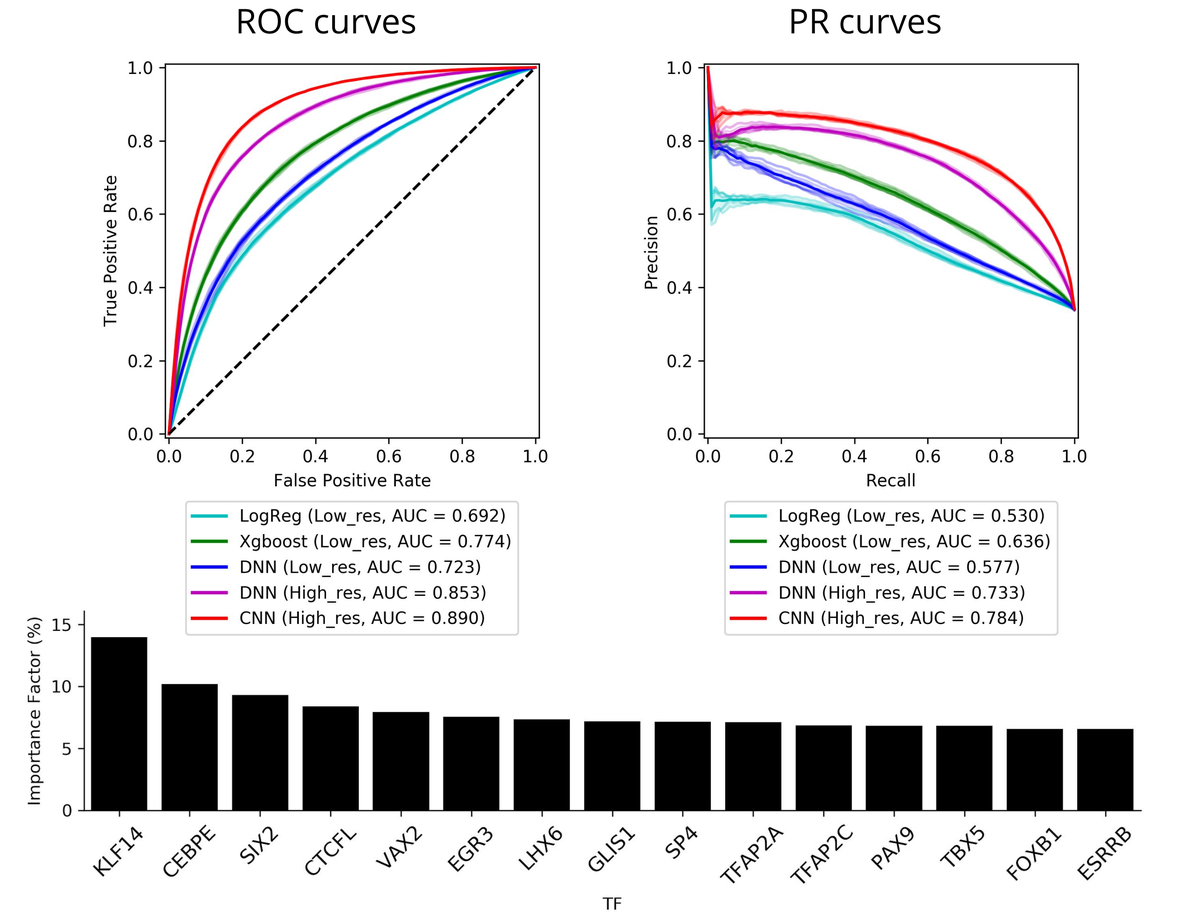
Most TFs having significantly associations with splicing changes are tissue-specifically expressed



Representation for the changes of TF occupancy and splicing



Identification of the TFs potentially harnessing changes of splicing



Conclusion

➢ We further identified the TFs that would influence splicing status.

➢ Majorities of those candidate TFs were tissue-specifically expressed.

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