

Supplementary materials

Article

Molecular Subtyping and Survival Analysis of Osteosarcoma Reveals Prognostic Biomarkers and Key Canonical Pathways

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Supplementary materials

Supplementary Figures



Figure S1: (A) Oncoplot of the top 15 most frequently mutated genes 123 OS patients. Colored squares show mutated genes, while grey squares show non mutated genes. Each color represents a different type of mutations. Each color represents different type of mutations as labelled in figure. **(B)** Oncoplot of the frequency of mutation in MUC family genes in 123 OS patients. Colored squares show mutated genes, while grey squares show non mutated genes. Each color represents a different type of mutations. Each color represents different type of mutations as labelled in figure.

Supplementary materials

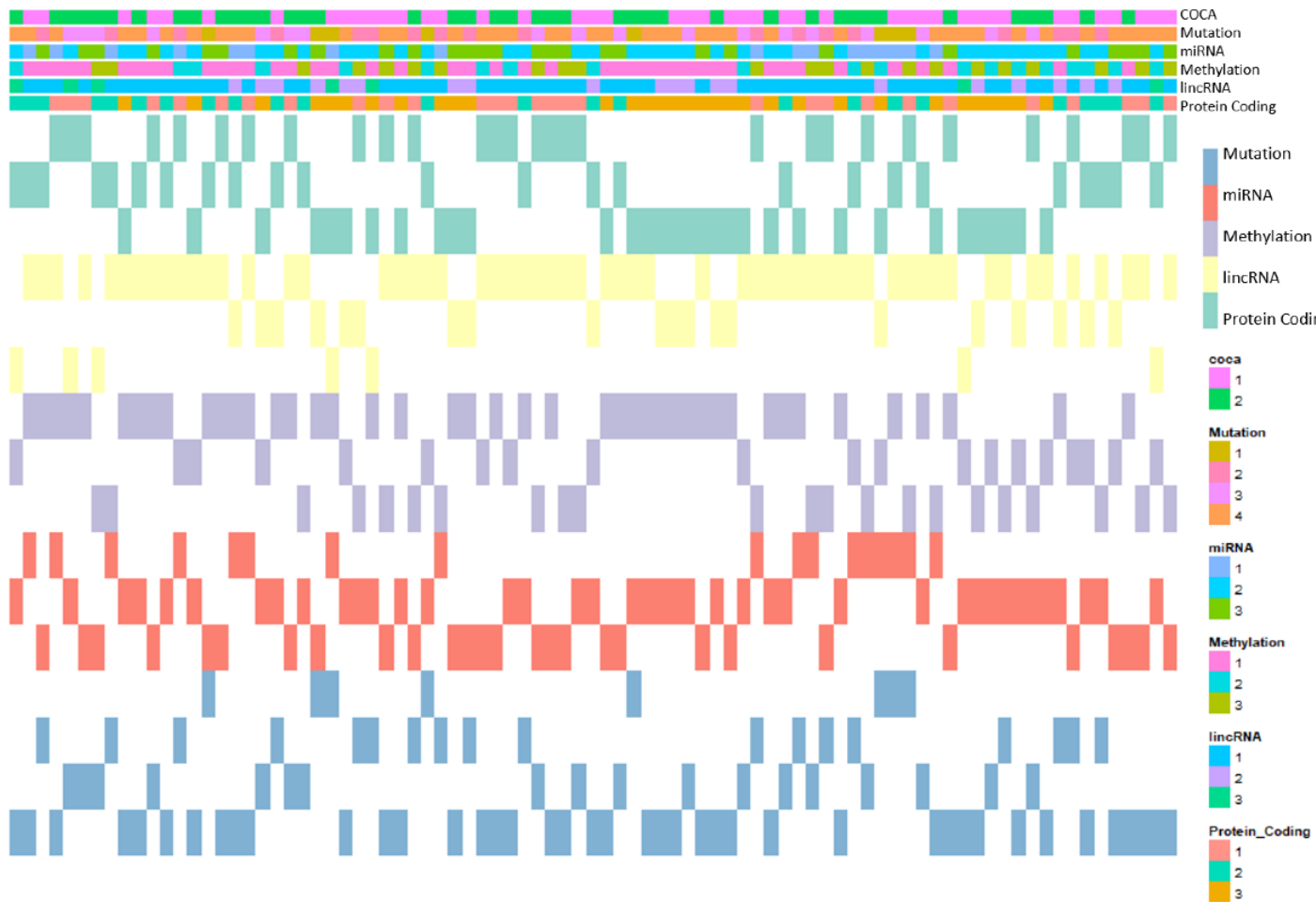


Figure S2: Clustering of 85 OS patients into two molecular subtypes based on multi-omics data using cluster-of-cluster analysis. The final multi-omics based molecular subtypes consisted of 44 and 41 samples respectively. The vertical sidebar shows the annotation of cluster labels obtained using individual of 'omics' data and the final multiomics-based clustering for each sample.

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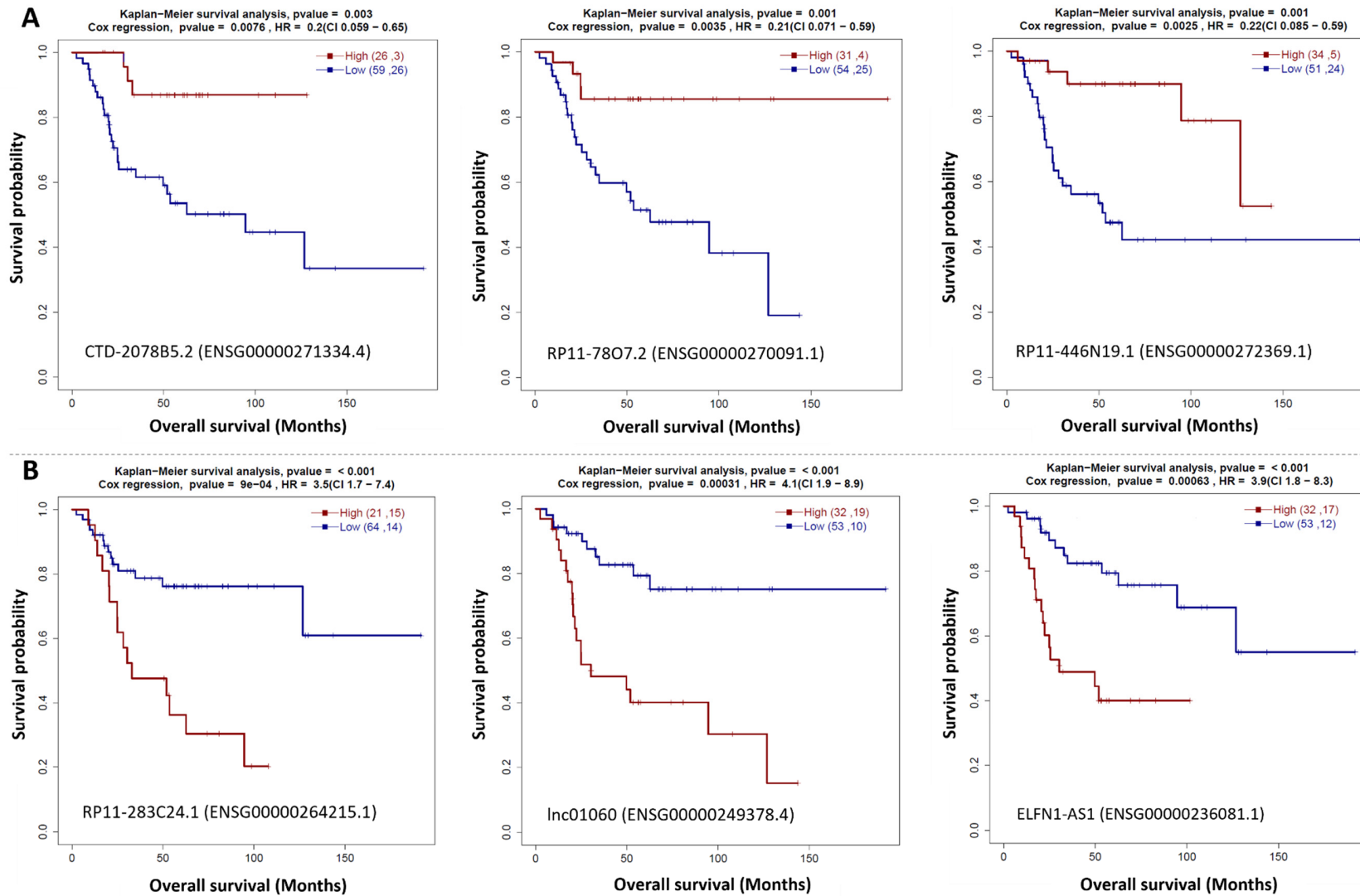


Figure S3: Kaplan-Meier plot for high versus low expression group in TARGET OS data with p-value from log-rank test and Cox regression model for lncRNAs *CTD-2078B5.2*, *RP11-78O7.2*, and *RP11-446N19.1* (HR < 1) (A), and *ELFN1-AS1*, *RP11-283C24.1* and *lnc01060* (HR > 1) (B)

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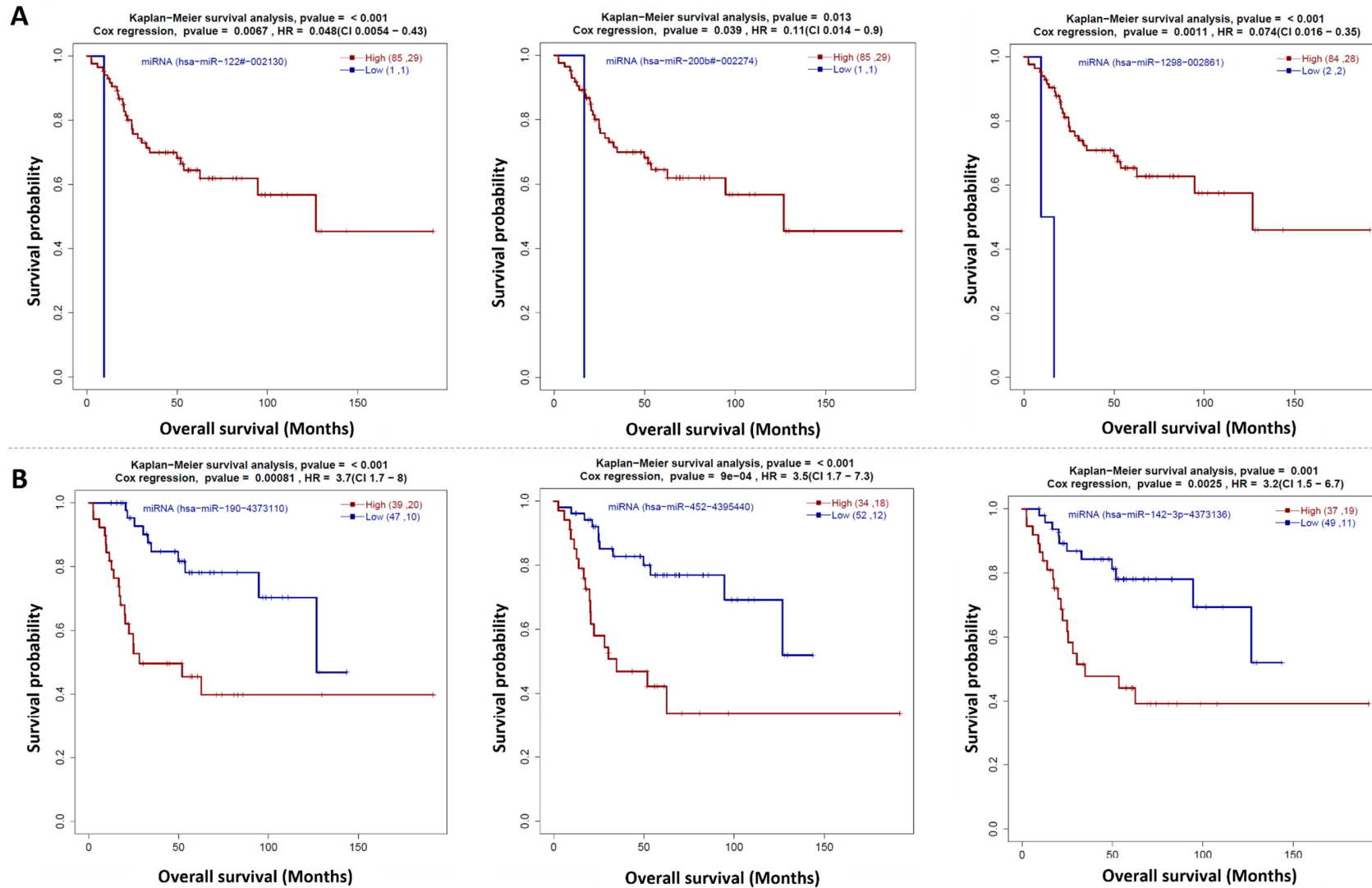


Figure S4: Kaplan-Meier plot for high vs low expression group in TARGET OS data with p-value from log-rank test and Cox regression model for miRNAs miR-122, miR-200b, miR-1298 (HR < 1) (A), and miR-190, miR-452, and miR-488 (HR > 1) (B)

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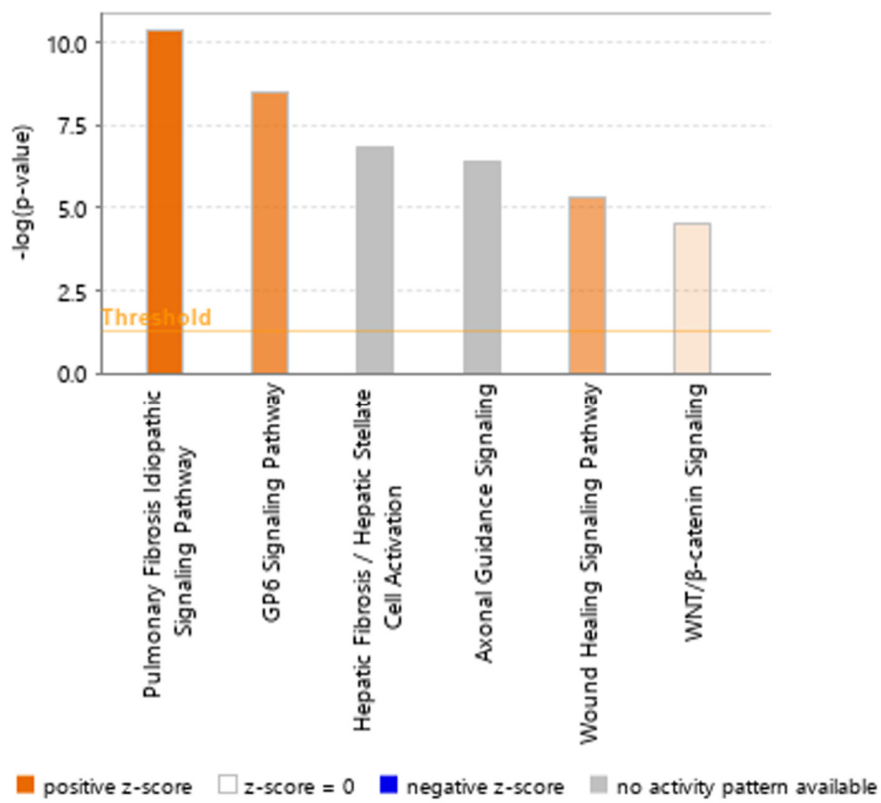


Figure S5: Top canonical pathway enriched between OS subtype 1 and subtype 2. (Analysis performed by IPA)