

Transcriptional analysis of metastatic uveal melanoma survival nominates NRP1 as a therapeutic target

Running Title: Correlates of survival in uveal melanoma

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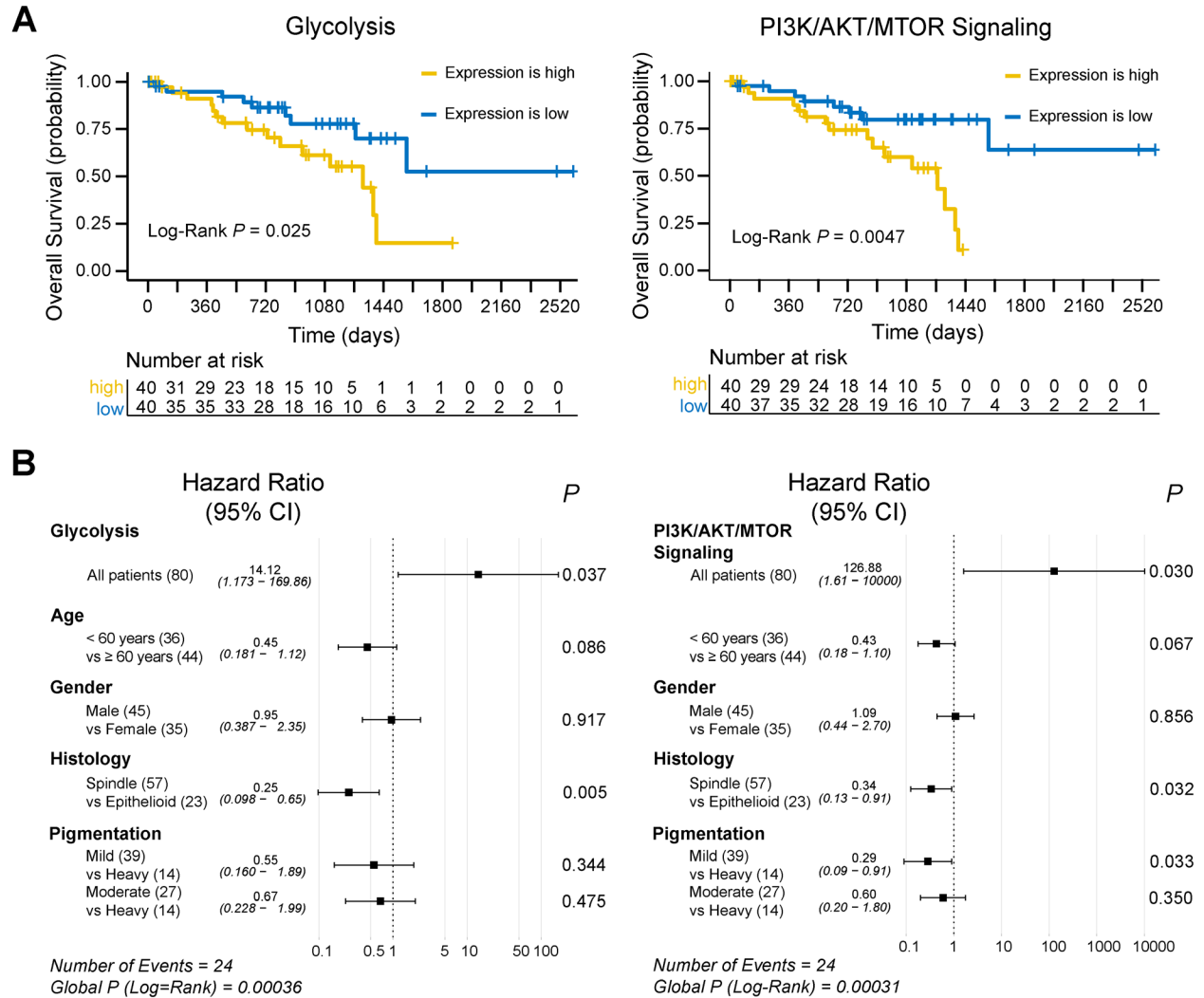
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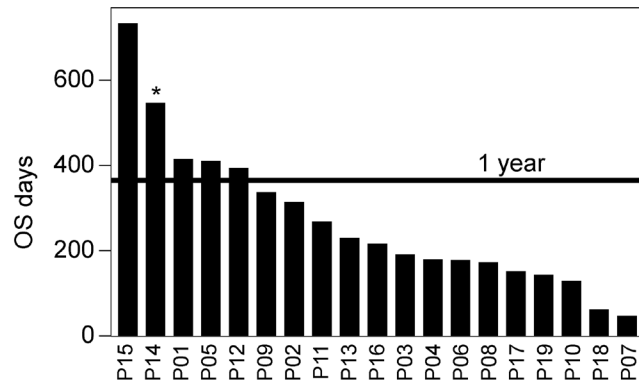
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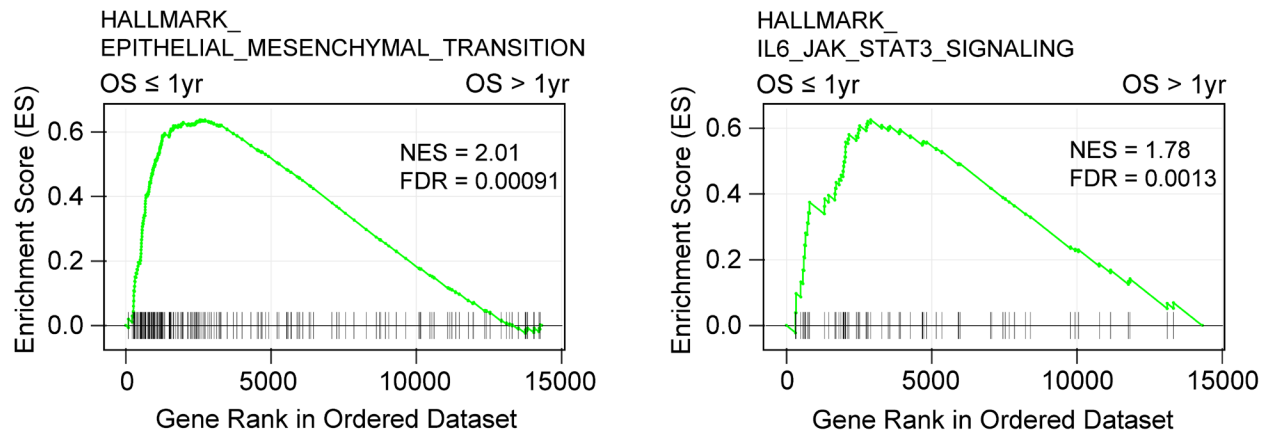
Supplementary Figures



Supplementary Figure 1. Association of glycolysis, PI3K/AKT/MTOR signaling and overall survival in pUM from TCGA. (A) Kaplan-Meier survival curves of glycolysis and PI3K/AKT/MTOR signaling gene expression in primary uveal melanoma (UM), split by median expression of each signature (high vs low). Survival risk table is shown below the Kaplan-Meier plot in each panel. **(B)** Forest plots showing the odds ratio and p-values in cox proportional hazards (PH) multivariate model of the signaling pathways with demographic and clinical covariates. $n = 80$ patients in the TCGA primary UM cohort for **A** and **B**. Log-Rank test was used in **A**, and Cox PH multivariate model was used in **B**.



Supplementary Figure 2. Distribution of overall survival in 19 patients with metastatic uveal melanoma. Asterisks labels patient alive upon the last follow up. Horizontal lines label the position of one year (365 days).



Supplementary Figure 3. Gene Set Enrichment Analysis (GSEA) of epithelial mesenchymal transition genes (left panel) and IL6/JAK/STAT3 signaling genes (right panel) from Hallmark (H) gene sets of MSigDB database using the full list of 14,307 genes from differential gene expression analysis. Numbers shown in each panel represent NES (normalized enrichment score) and FDR-corrected p-values. The enrichment score (ES) is shown on the y-axis. Gene rank is shown on the x-axis, where genes were sorted by the \log_2FC metrics in GSEA.