

Molecular Characterization of Cancer Associated Fibroblasts in Prostate Cancer

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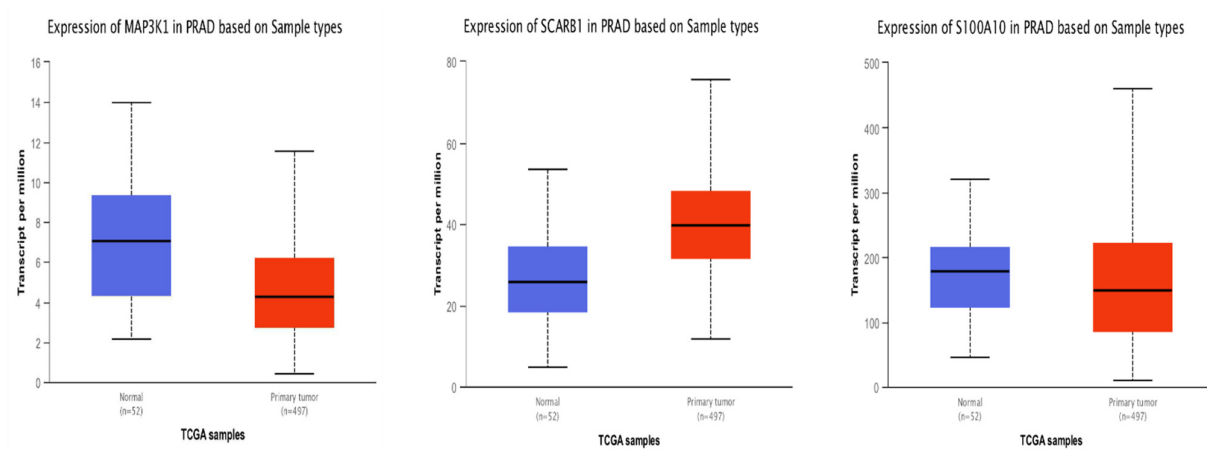
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A

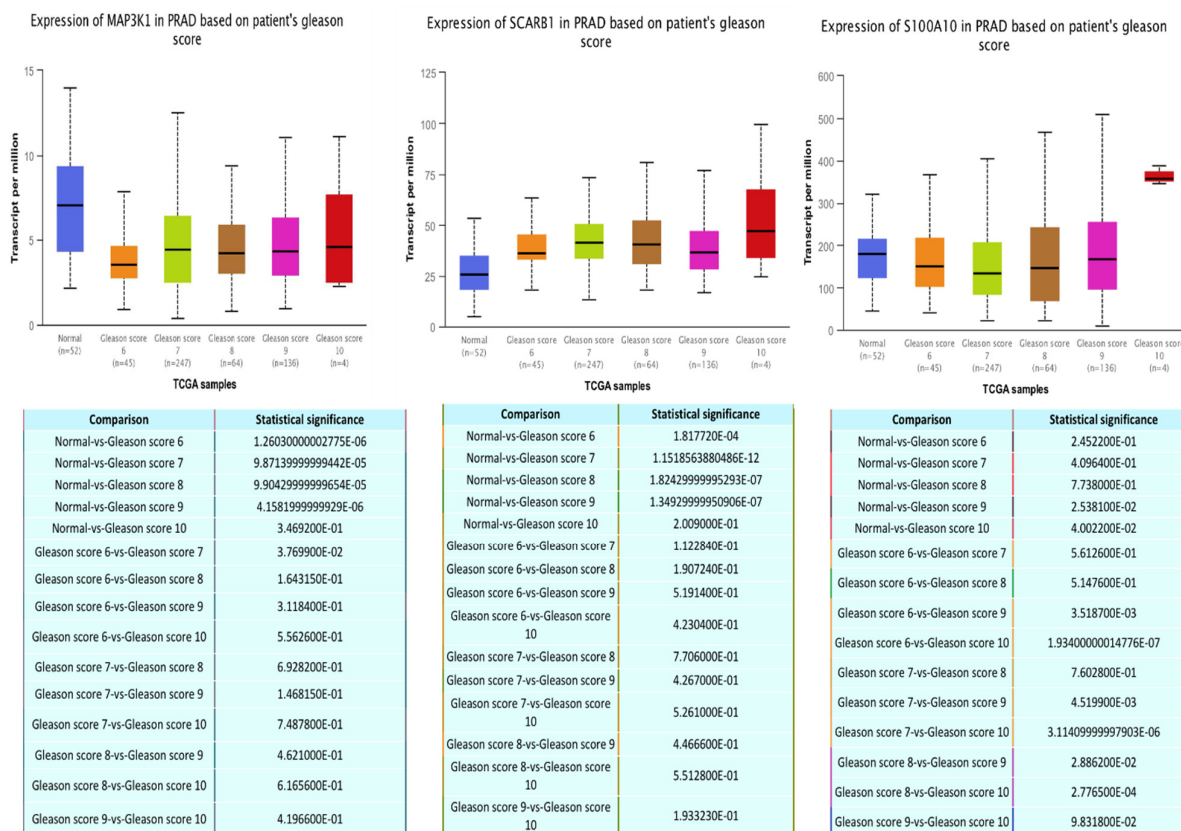


Comparison	Statistical significance
Normal-vs-Primary	2.08489999999895E-05

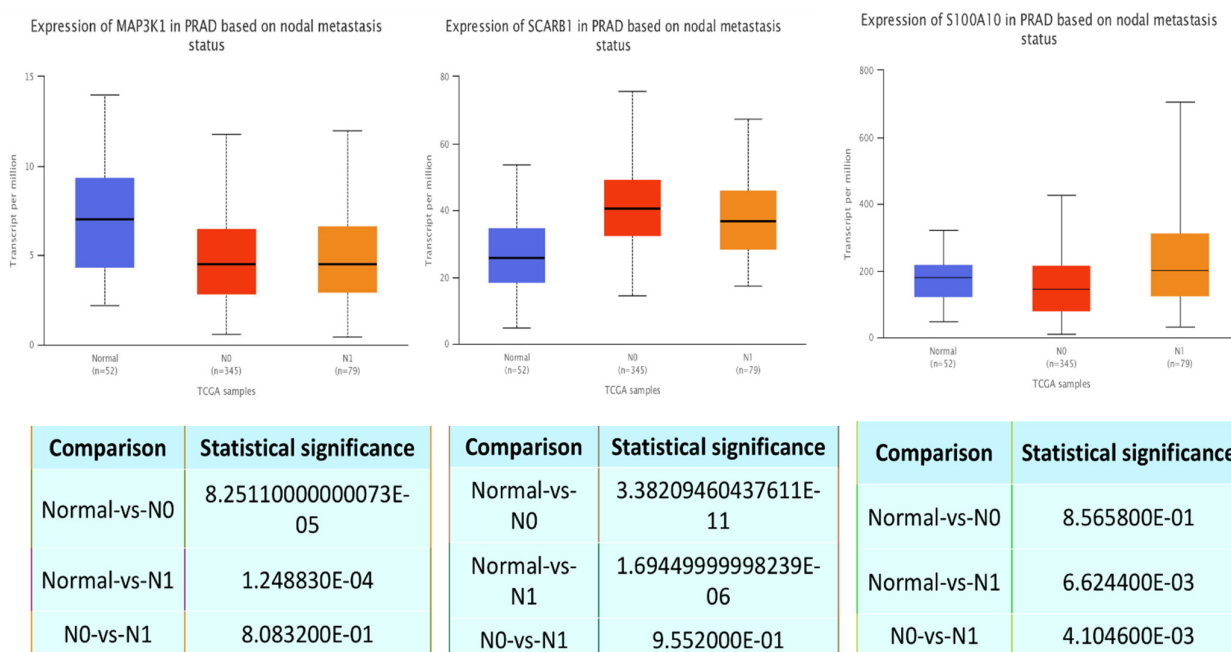
Comparison	Statistical significance
Normal-vs-Primary	4.98880048382944E-10

Comparison	Statistical significance
Normal-vs-Primary	4.833600E-01

B



C



D

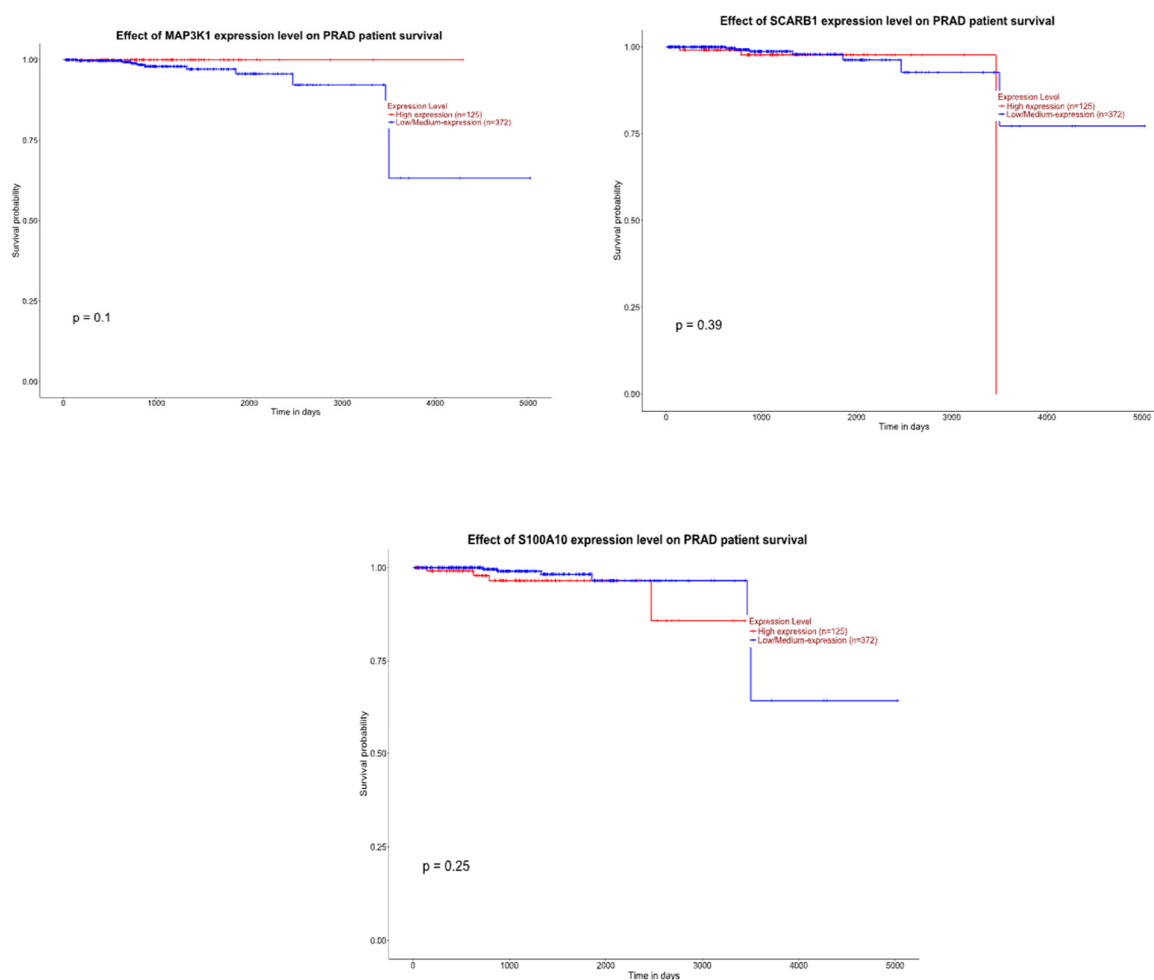


Figure S1 legend

Figure S1. Correlation analysis between MAPK3K1, SCARB1 and S100A10 expressions and clinical pathological characteristics or patient outcomes. (A) TCGA-based UALCAN database screening and analysis showing a significant difference in the MAPK3K1, SCARB1 and S100A10 expressions between normal tissue and PCa tissue (B) UALCAN database analysis showing that the transcriptional level of MAPK3K1, SCARB1 and S100A10 significantly correlated with increasing Gleason score. (C) UALCAN database analysis showing that the transcriptional level of MAPK3K1, SCARB1 and S100A10 significantly correlated with nodal metastasis status. (D) Cox regression analysis showing that patients in the low SCARB1 groups and in the high MAPK3K1 and S100A10 groups had a significant better overall survival (OS).

Bioinformatic Analysis

Gene Expression Profiling Interacting Analysis (GEPIA2; <http://gepia2.cancer-pku.cn/>) was used to analyze the RNA sequencing expression data derived from TCGA and GTEx datasets. In details, we analyzed the differential expression of SCARB1, MAPK3K1, and S100A10 between tumor and normal tissues by using the “PRAD” dataset. We used UALCAN software and selected the prostate cancer dataset from TCGA to analyze the correlation between Gleason scores and the three selected gene expressions as well as other clinico-pathological characteristics. The P value cutoff value was 0.05. Student’s t-test was performed to calculate a P value for expression analysis. The “Survival Analysis” module supplied a Kaplan-Meier curve that represents the relationship between the three genes and survival prognosis.