ACCSCIENCE PUBLISHING

Eurasian Journal of Medicine and Oncology

ORIGINAL RESEARCH ARTICLE

Exploring the therapeutic potential of gamma-glutamyl carboxylase in prostate cancer through integrated multi-omics analysis

Supplementary File

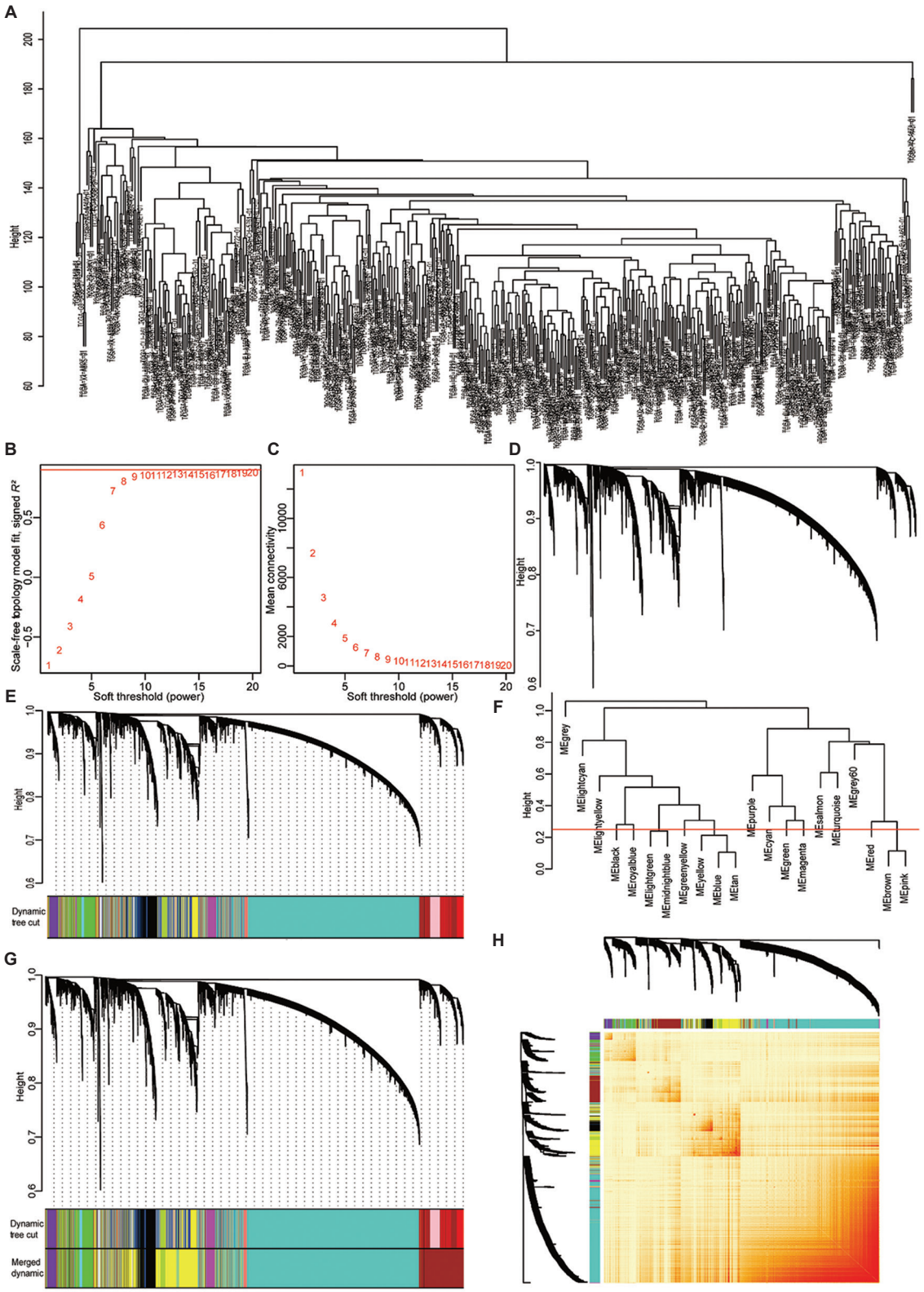


Figure S1. The weighted gene co-expression network analysis (WGCNA) identifies potential co-expression modules in PCa. (A) Sample to detect outliers. (B) Scale independence. (C) Mean connectivity. (D) Gene expression on topological overlap matrix-based dissimilarity. (E) Gene dendrogram and module colors. (F) Clustering of module eigengenes. (G) Gene dendrogram and module colors (expression). (H) Network heatmap plot for selected genes.

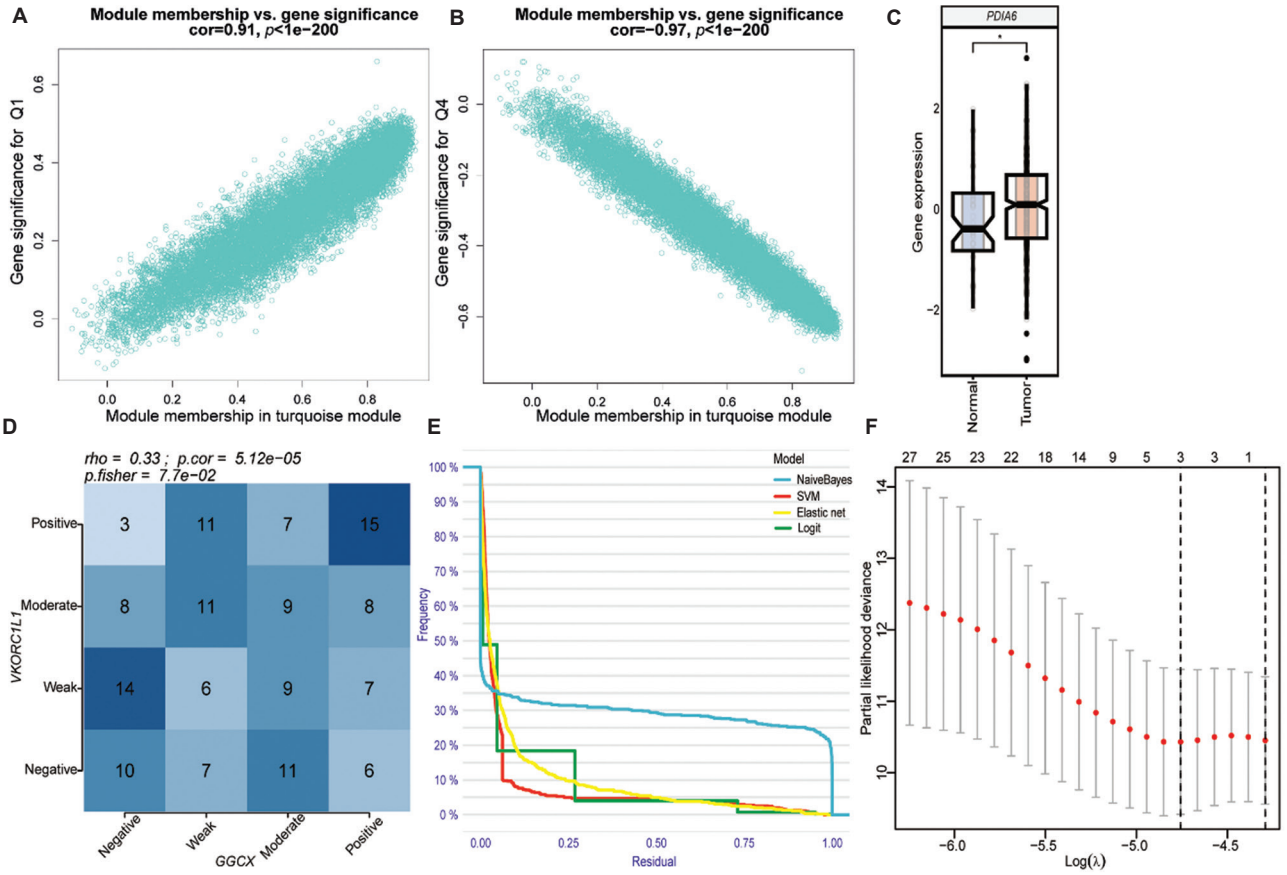


Figure S2. The supplementary data of this study. (A and B) Relationship of module membership with genes identified using weighted gene co-expression network analysis (WGCNA). (C) Gene expression of *PDIA6* in Pca. (D) Validation of the correlation between *GGCX* and *VKORC1L1* from the International Cancer Genome Consortium (ICGC). (E) Reverse cumulative distribution of residuals. The x-axis indicates residuals from the minimum to the maximum, while the y-axis represents the corresponding cumulative frequency, ranging from 100% (all samples) to 0% (no samples). The curve starts at the upper-left corner with the smallest residual (y = 100%) and decreases toward the lower-right corner with the largest residual (y = 0%). Clustering of most residuals near zero generally suggests minimal predictive error in the model. (F) Ten-fold cross-validation error plot. Two vertical dashed lines are shown: the first corresponds to the λ value that produces the minimal cross-validation error (the optimal λ), and the second marks the λ value at one standard error above the minimum error, a more conservative choice to reduce overfitting.

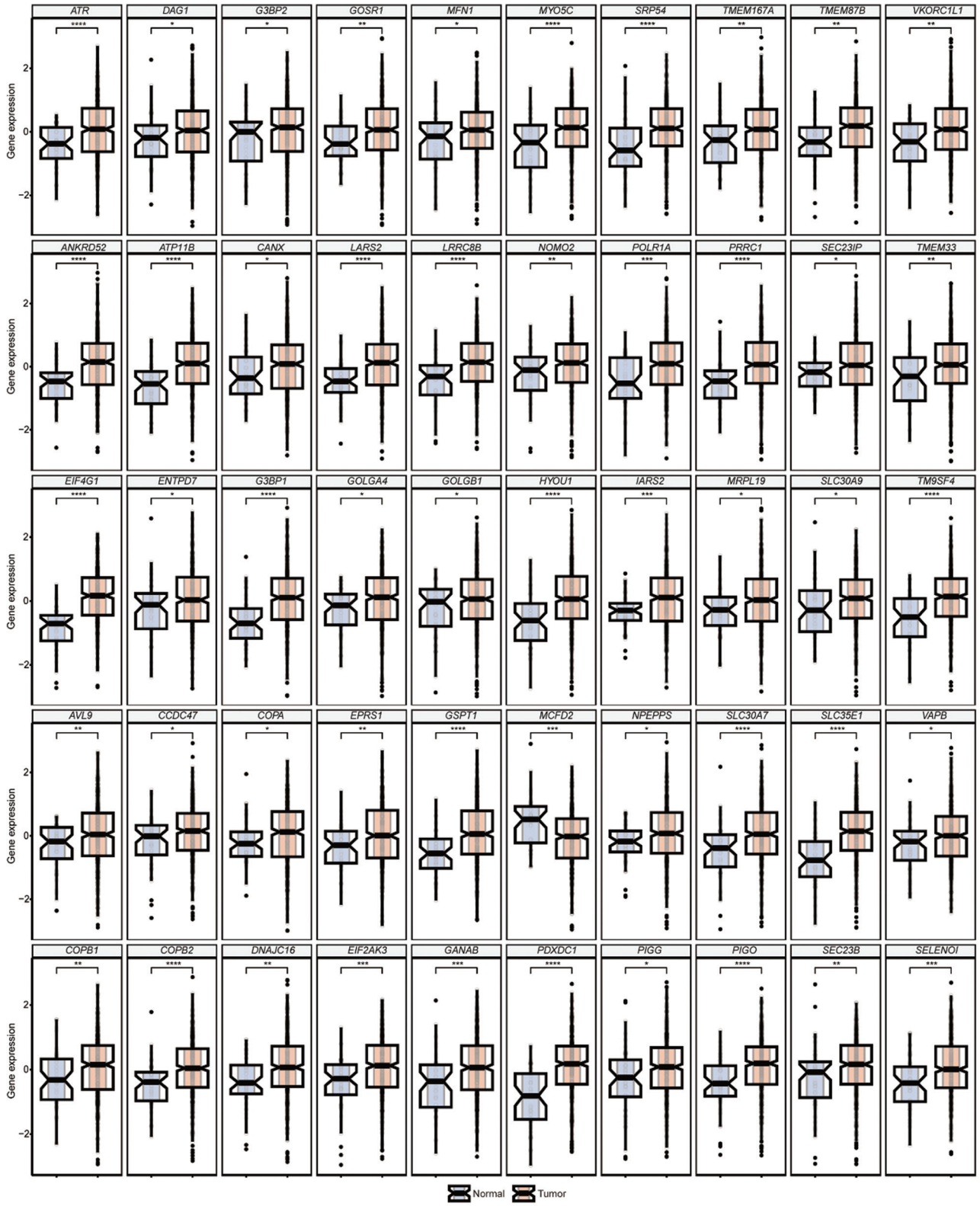


Figure S3. Differential expression analyses of gene sets in Pc.

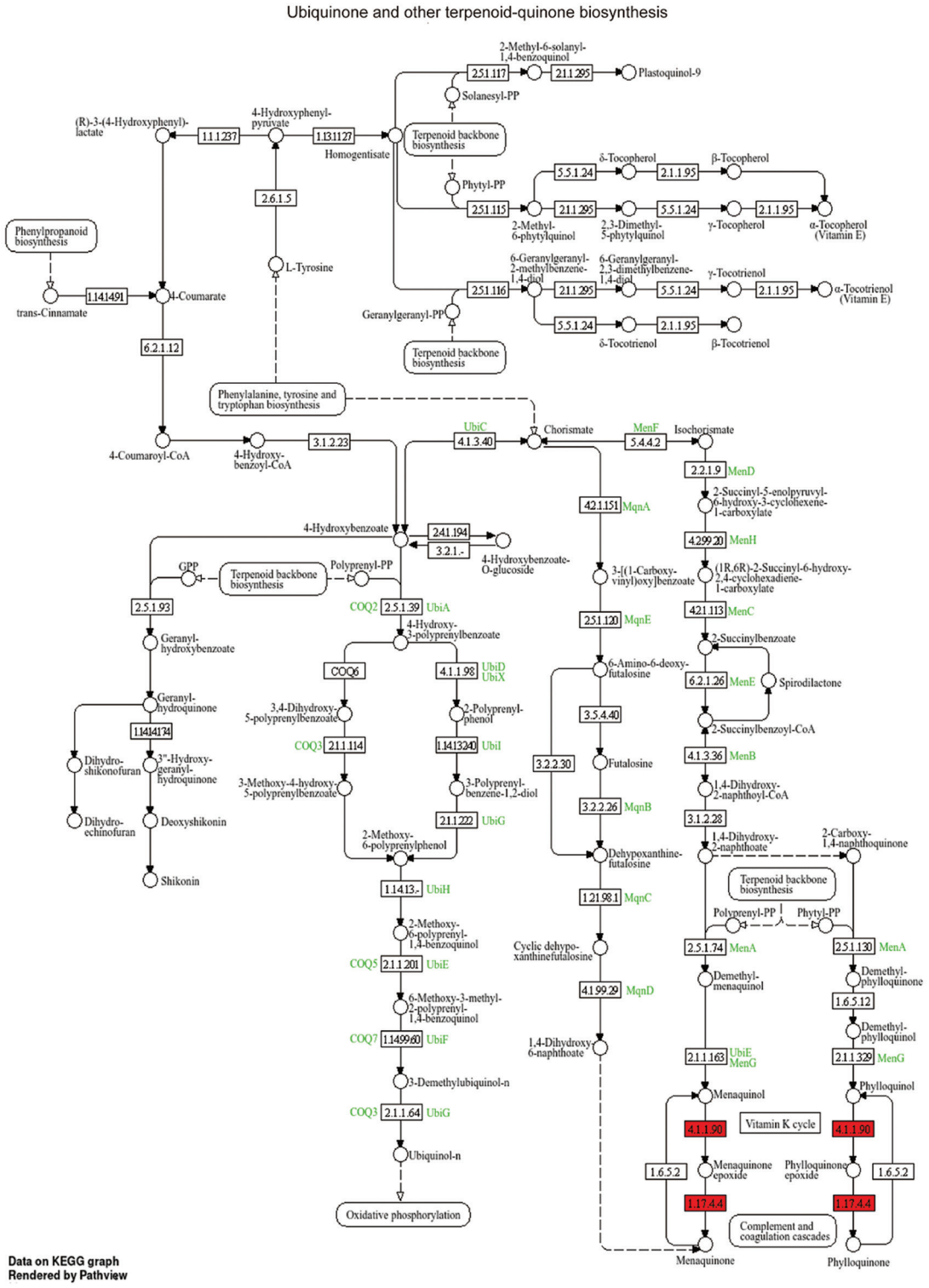


Figure S4. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of ubiquinone and terpenoid-quinone biosynthesis. The diagram illustrates key metabolic intermediates and enzymatic reactions with a particular emphasis on two crucial components highlighted in red boxes: the Vitamin K cycle and the complement/coagulation cascades (bottom right). Metabolic intermediates are represented as circles, while enzymatic reactions are shown as rectangles with their corresponding enzyme code numbers. Green labels indicate genes involved in specific reactions, while solid arrows represent direct metabolic conversions. Numbers in rectangles represent specific enzyme codes, as classified in the KEGG database.

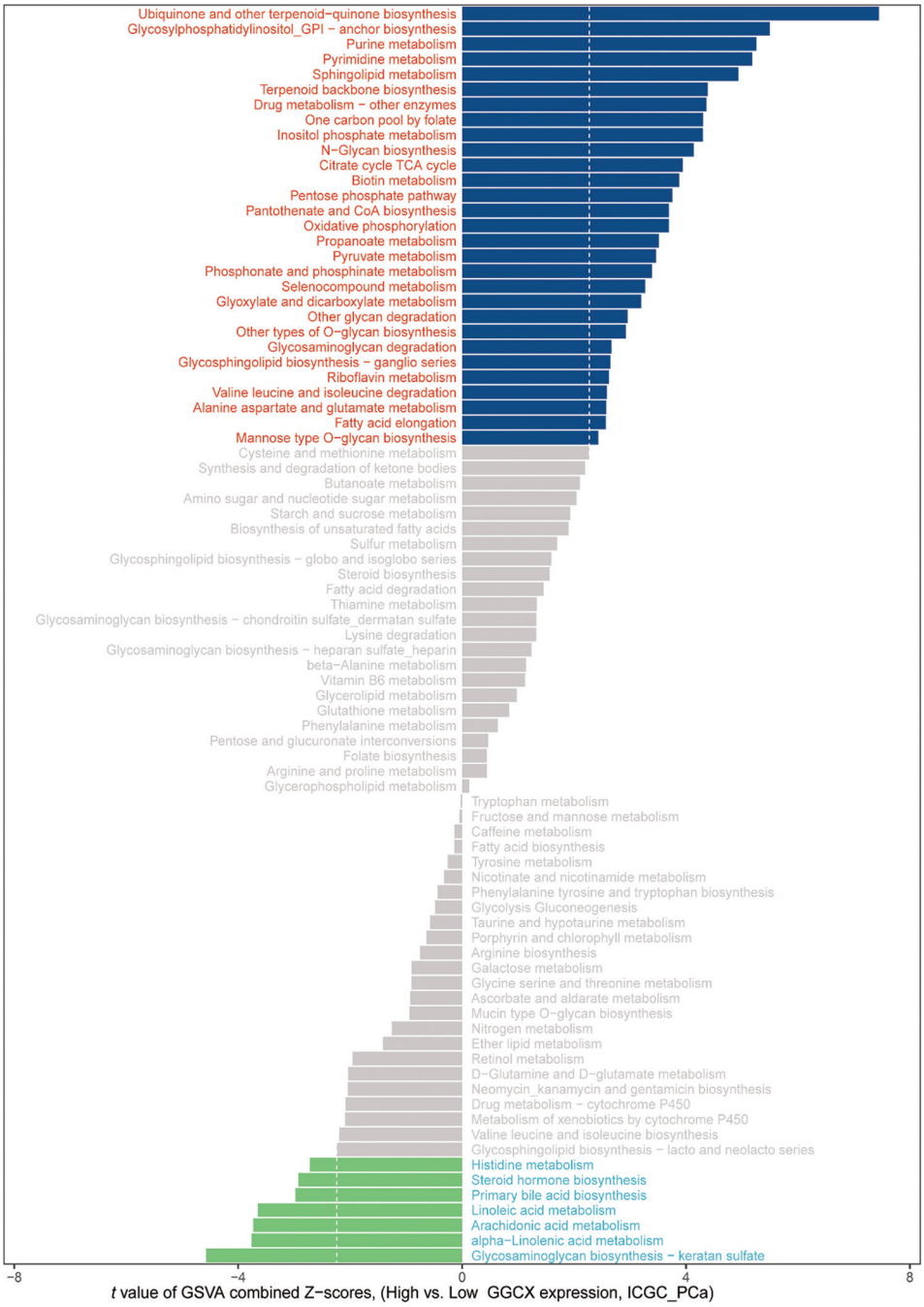


Figure S5. Differences in metabolic pathway Gene Set Variation Analysis (GSVA) scores between high and low-gene expression groups. The x-axis represents GSVA score *t*-values, and the y-axis represents metabolic gene sets. Gray bars indicate non-significant differences, blue bars with red labels denote higher scores in the high-expression group, and green bars with light blue labels denote lower scores in the high-expression group.
Abbreviations: ICGC: International Cancer Genome Consortium; PCa: Prostate cancer.