

Angiogenesis signaling associated with worse survival in gastric cancer

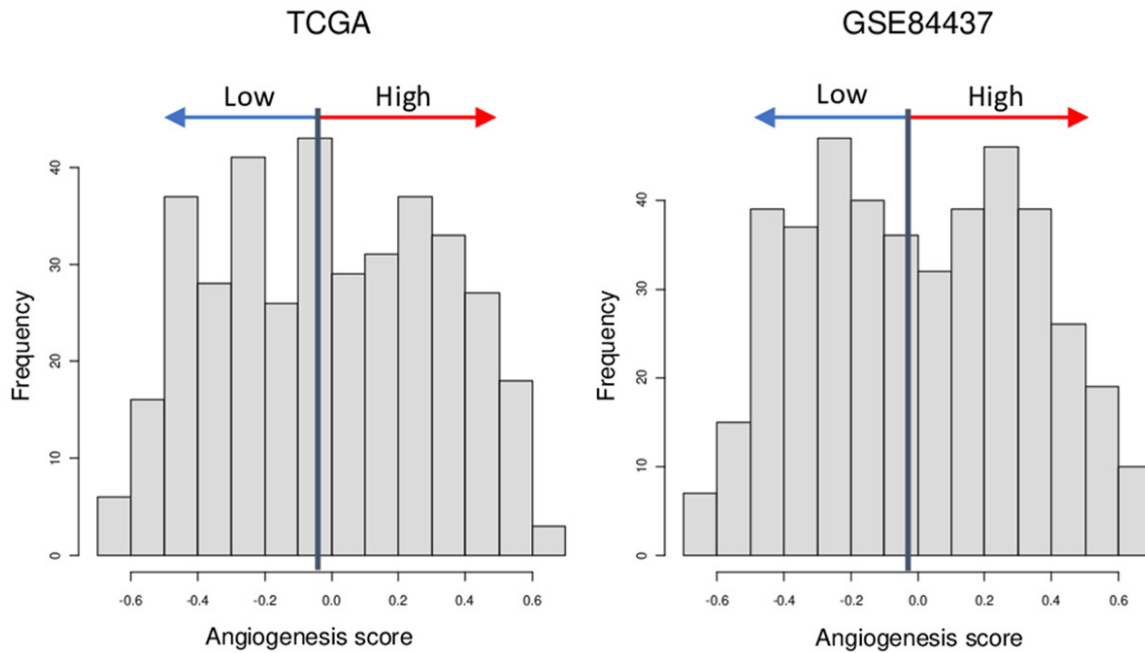


Figure S1. Histogram of the angiogenesis score in the TCGA and GSE84437 cohorts.

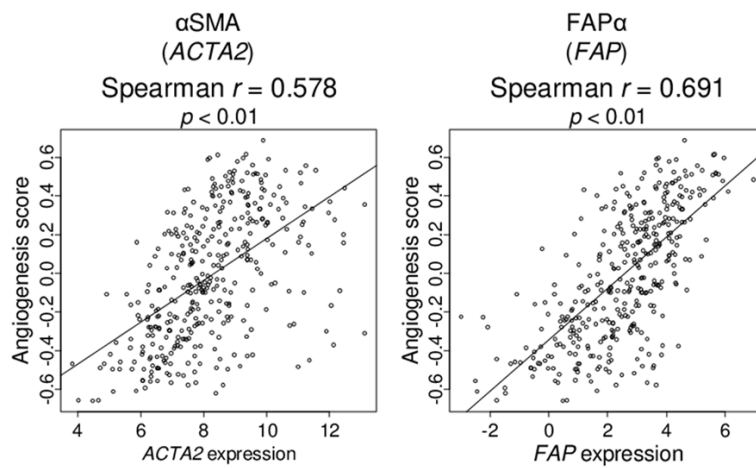


Figure S2. Correlation of the angiogenesis score with fibroblast-related genes in the TCGA cohort. Correlation plots of the angiogenesis score with *ACTA2* and *FAP* gene expression. Spearman rank correlation was used to the analysis.

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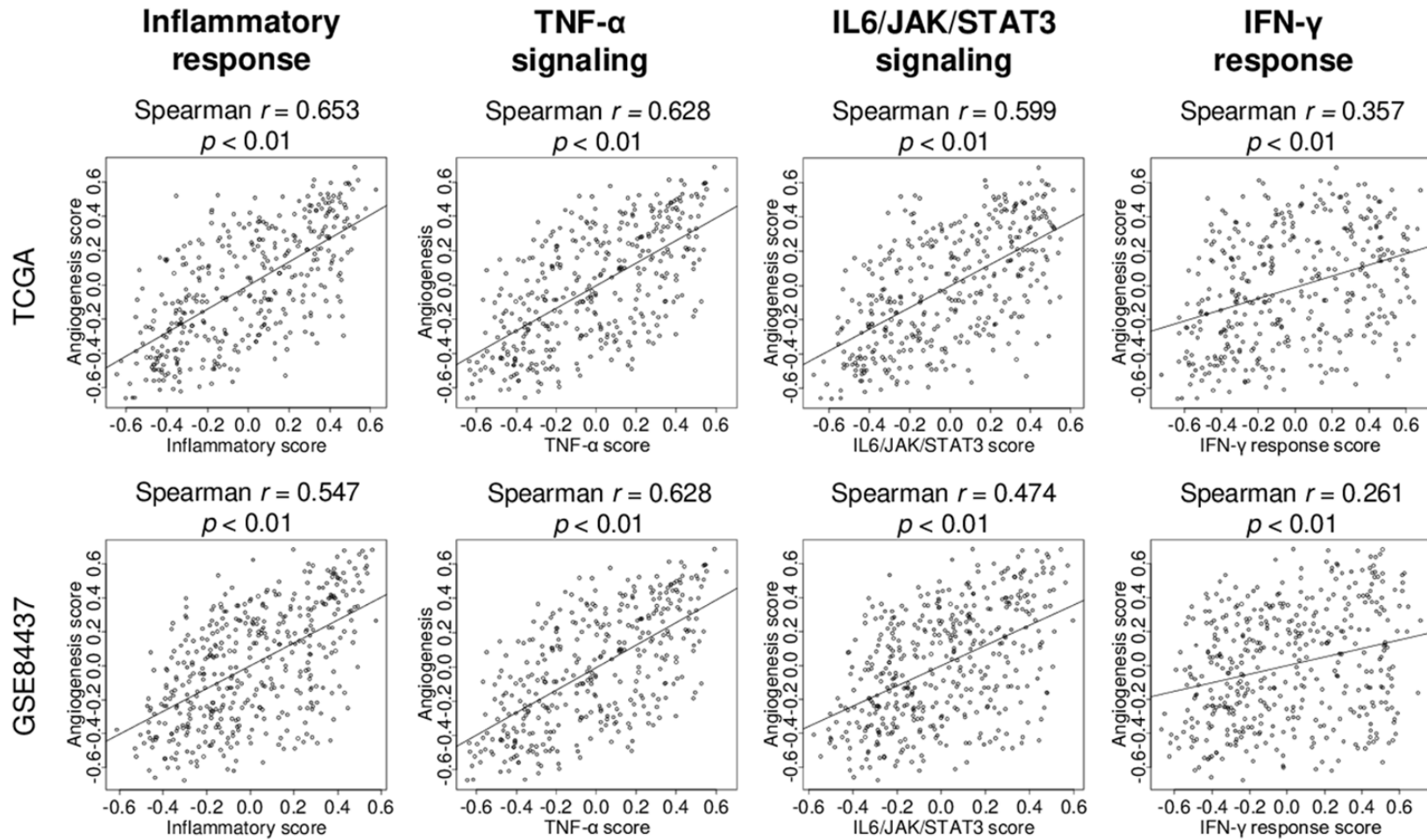


Figure S3. Correlation of the angiogenesis score with inflammation-related and immune response-related pathway scores in the TCGA and GSE84437 cohorts. Correlation curves of the angiogenesis score with inflammation-related pathway scores; inflammatory response, TNF- α signaling, IL6/JAK/STAT3 signaling, and immune response-related pathway score; Interferon (IFN)- γ response score in both cohorts. Spearman rank correlation was used to the analysis.

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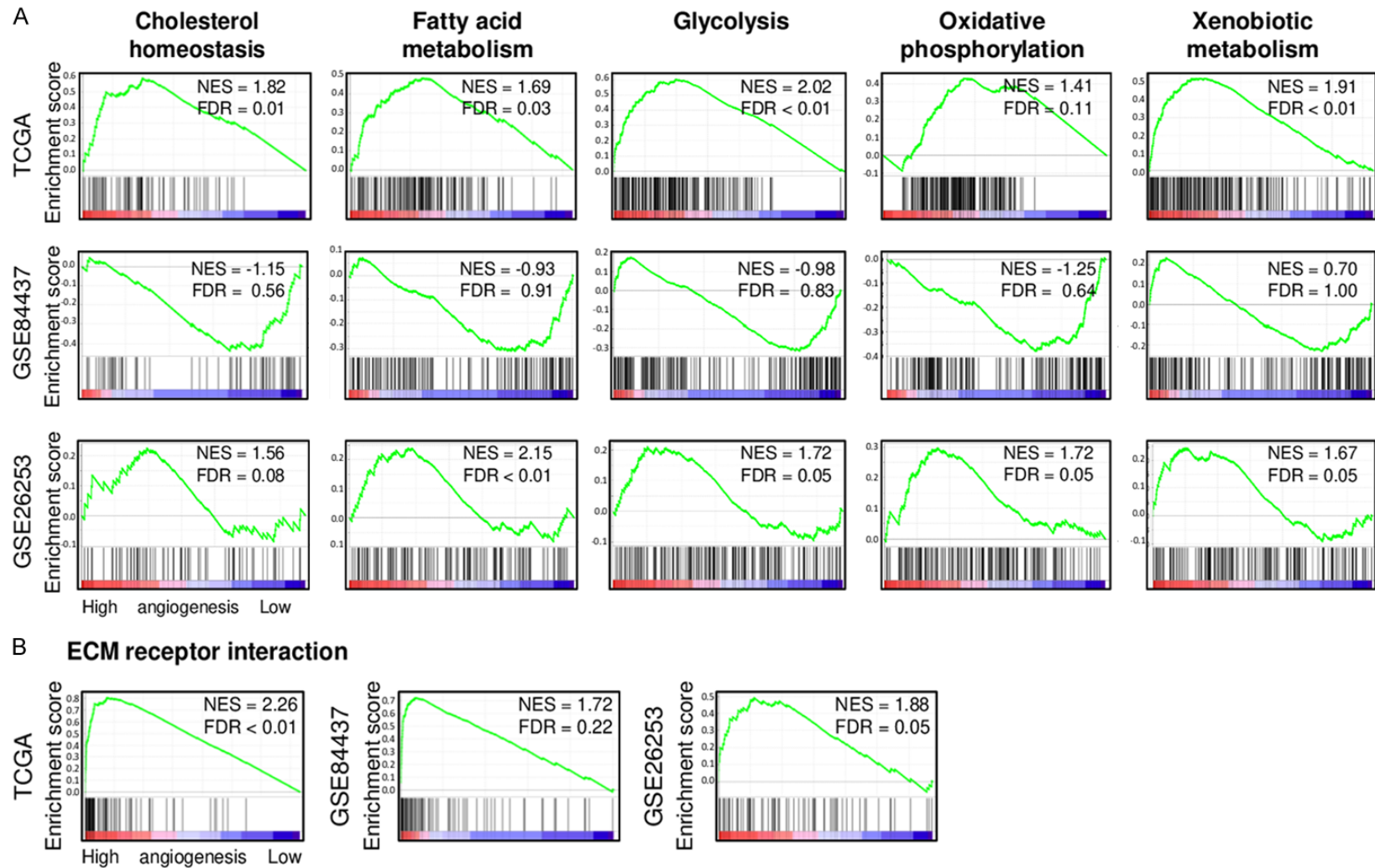


Figure S4. Gene Set Enrichment Analysis comparing high and low angiogenesis score tumors with metabolism-related Hallmark gene sets and KEGG extracellular matrix (ECM) receptor interaction gene set in the TCGA, GSE84437, and GSE26253 cohorts. Correlation curve of (A). cholesterol homeostasis, fatty acid metabolism, glycolysis, oxidative phosphorylation, and xenobiotic metabolism hallmark gene sets. (B) ECM receptor interaction KEGG gene set. FDR; false discovery rate, NES; normalized enrichment score.