

Expanded View Figures

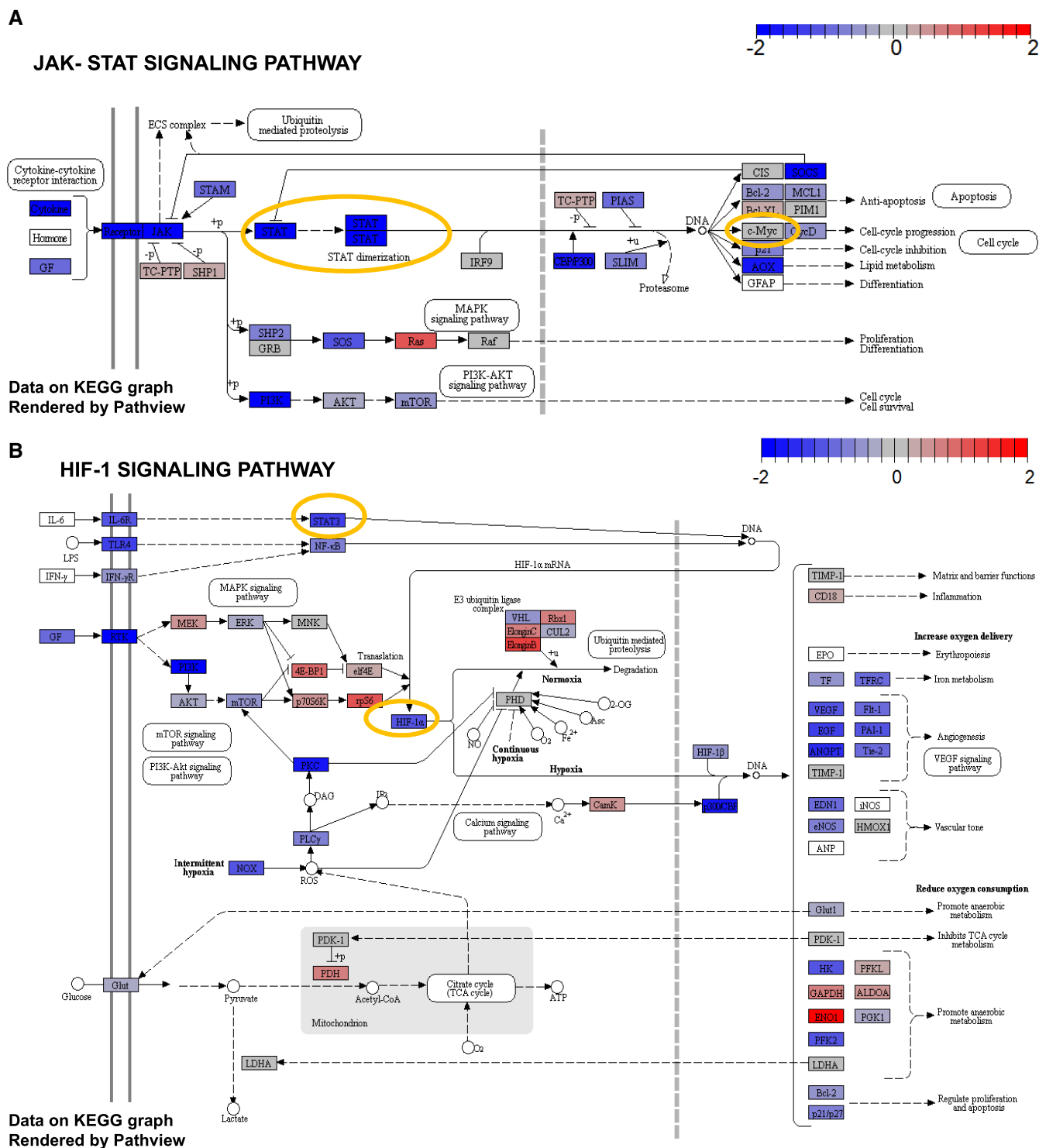


Figure EV1.

**Figure EV1. Scheme of down-regulated KEGG pathways in low STAT3 TCGA samples.**

- A KEGG representation of the JAK-STAT signaling pathway in low STAT3 versus high STAT3 TCGA samples after testing for signaling KEGG pathways. *STAT3* and *c-Myc* are encircled in yellow. Color bar indicates z-scored deregulation of genes. Blue, down-regulation; red, up-regulation.
- B KEGG representation of the HIF-1 signaling pathway in low STAT3 versus high STAT3 TCGA samples after testing for signaling KEGG pathways. *STAT3* and *HIF-1 α* are encircled in yellow. Color bar indicates z-scored deregulation of genes. Blue, down-regulation; red, up-regulation.

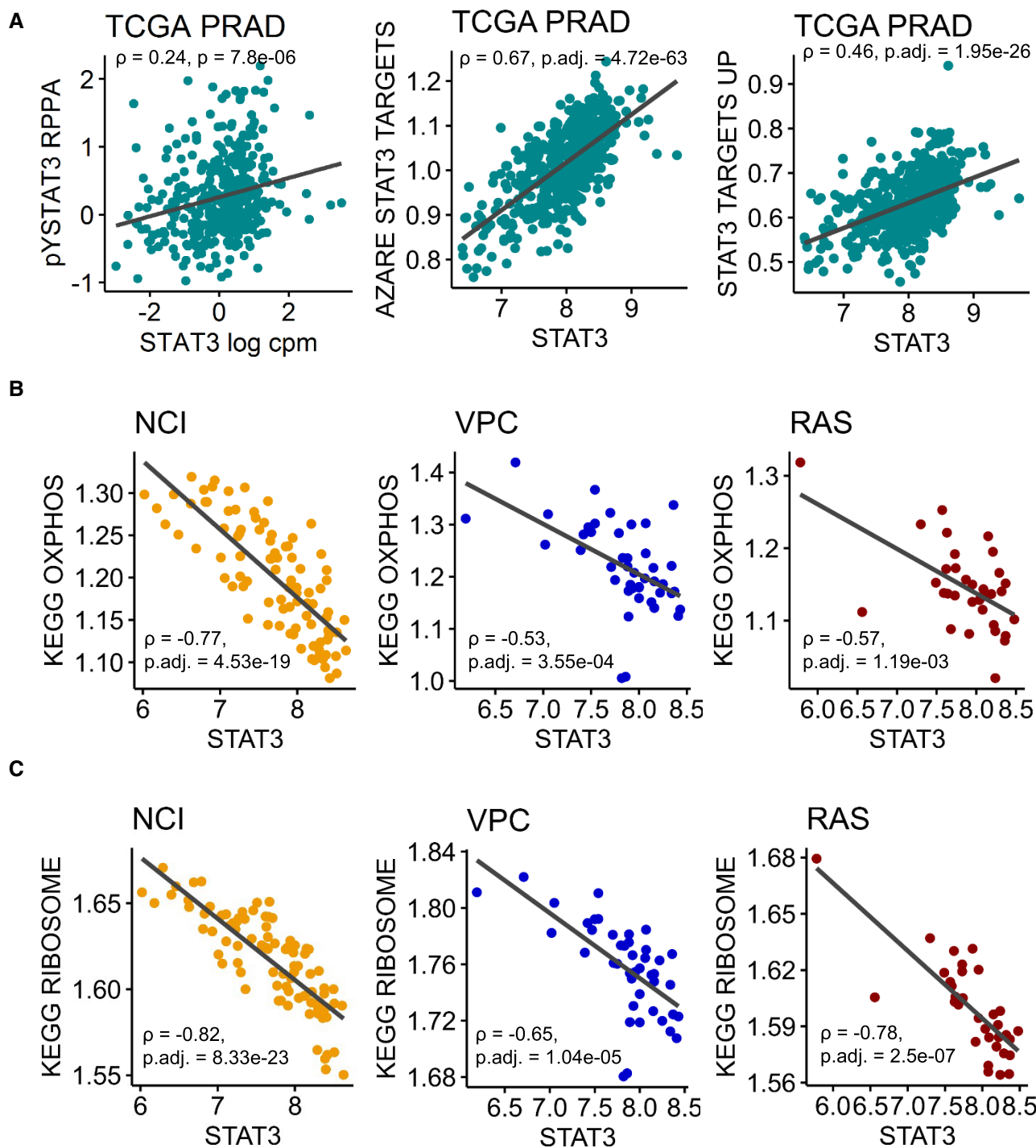


Figure EV3.

Figure EV3. Correlation of STAT3 with STAT3 target, ribosome, and OXPHOS signatures.

- A Pearson correlation of *STAT3* log counts per million (cpm) with tyrosine-phosphorylated (pY) *STAT3* Reverse Phase Protein Array (RPPA) protein levels (left, z-scored), "AZARE *STAT3* TARGETS" (middle), and "STAT3 TARGETS UP" gene signatures (right) in TCGA PRAD. Gene signatures were assessed with ssGSEA. *P*-values were adjusted with Benjamini–Hochberg method. *P*. adj., adjusted *P*-value.
- B Pearson correlation of *STAT3* log cpm with KEGG "OXPHOS" gene signature in three prostate cancer data sets. Gene signatures were assessed with ssGSEA. *P*-values were adjusted with Benjamini–Hochberg method. NCI, The Netherlands Cancer Institute; VPC, The Vancouver Prostate Center; RAS, The Russian Academy of Science.
- C Pearson correlation of *STAT3* log cpm with KEGG "Ribosome" gene signature in three prostate cancer data sets. Gene signatures were assessed with ssGSEA. *P*-values were adjusted with Benjamini–Hochberg method.

Source data are available online for this figure.

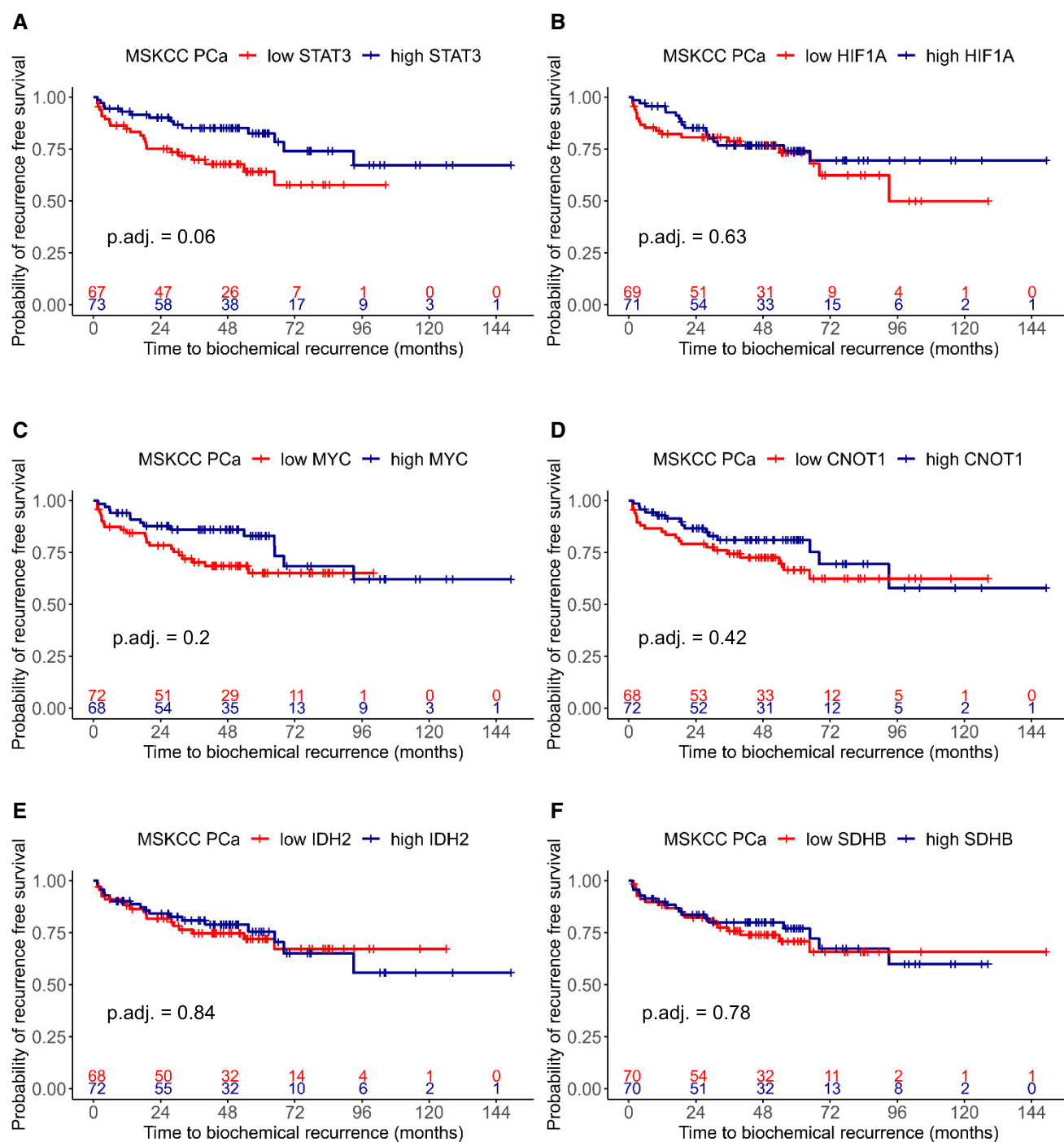


Figure EV4. Kaplan-Meier curves of additional candidate genes.

A-F Time to BCR in months for *STAT3* (A), *HIF-1 α* (B), *c-MYC* (C), *CNOT1* (D), *IDH2* (E), and *SDHB* (F) in the MSKCC PCa GSE21032 data set. Groups were generated by a median split. *P*-values were estimated by log-rank test and adjusted with Benjamini-Hochberg method. + = censored.

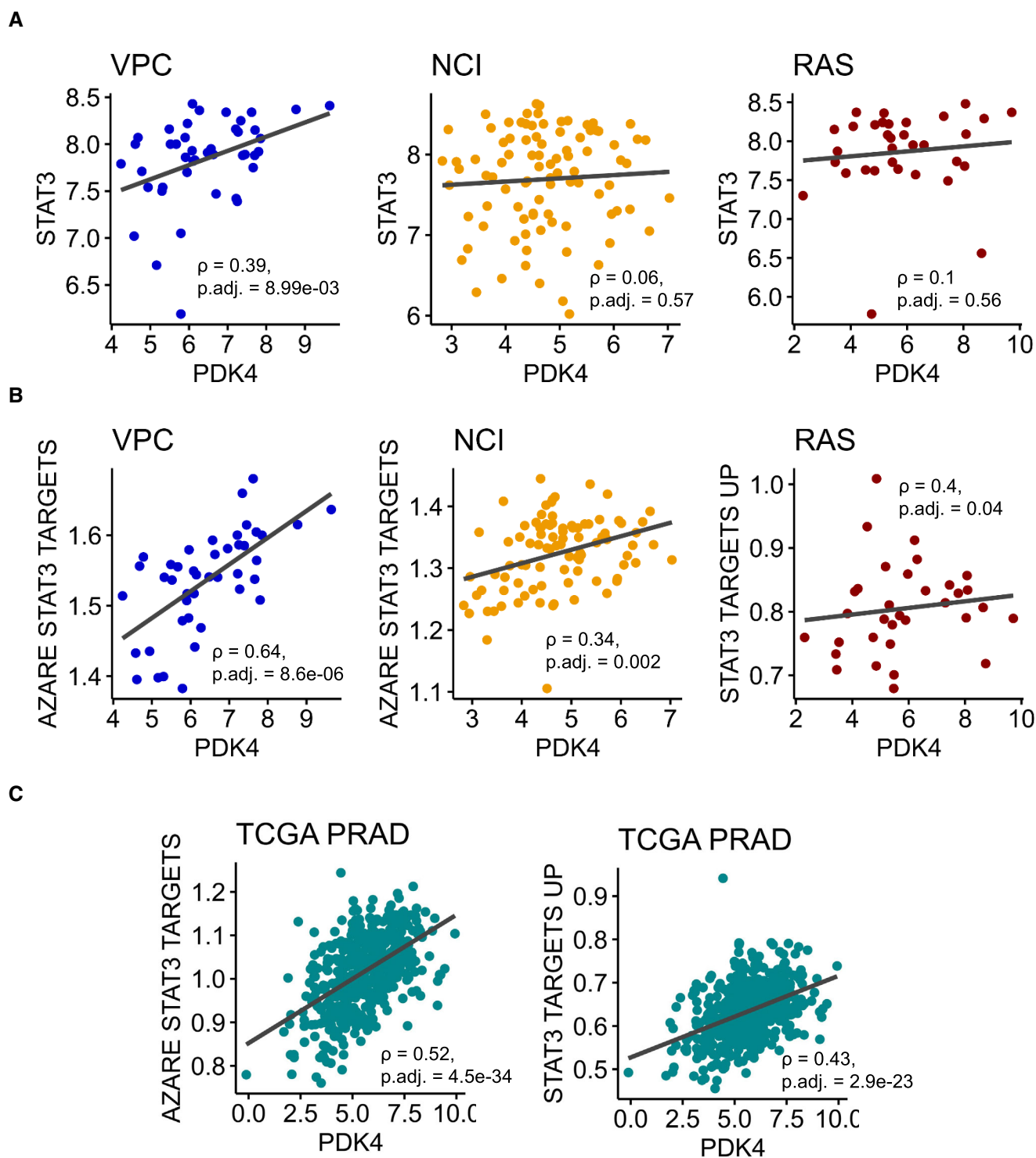


Figure EV5.

Figure EV5. Correlation of *PDK4* with *STAT3* and *STAT3* target signatures.

- A Pearson correlation of *PDK4* log counts per million (cpm) with *STAT3* log cpm in three prostate cancer data sets. *P*-values were adjusted with Benjamini–Hochberg method. *P*. adj., adjusted *P*-value. NCI, The Netherlands Cancer Institute; VPC, The Vancouver Prostate Center; RAS, The Russian Academy of Science.
- B Pearson correlation of *PDK4* log cpm with “AZARE *STAT3* TARGETS” gene signatures in three prostate cancer data sets. Gene signatures were assessed with ssGSEA. *P*-values were adjusted with Benjamini–Hochberg method.
- C Pearson correlation of *PDK4* log cpm with “AZARE *STAT3* TARGETS” (left) and “*STAT3* TARGETS UP” gene signatures (right) in TCGA PRAD. Gene signatures were assessed with ssGSEA. *P*-values were adjusted with Benjamini–Hochberg method. *P*. adj., adjusted *P*-value.

Source data are available online for this figure.