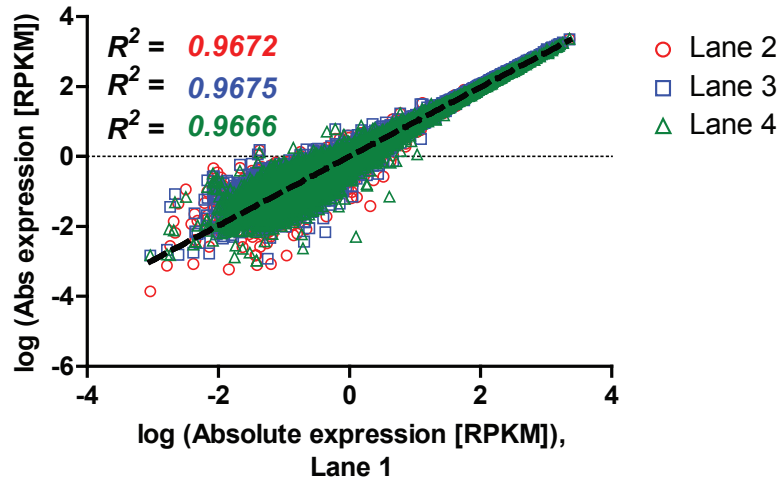
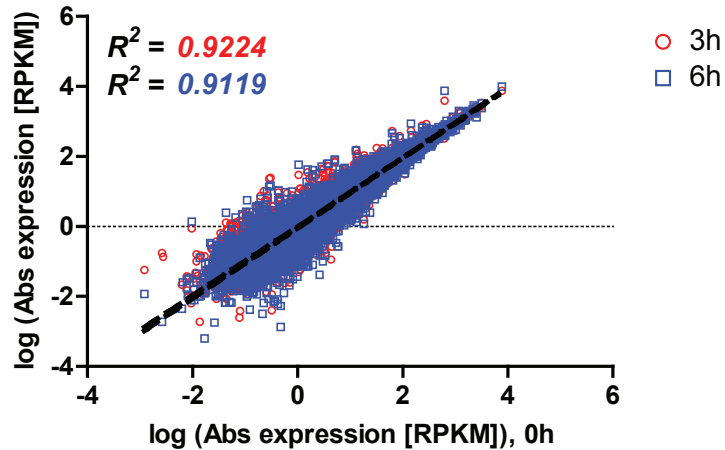
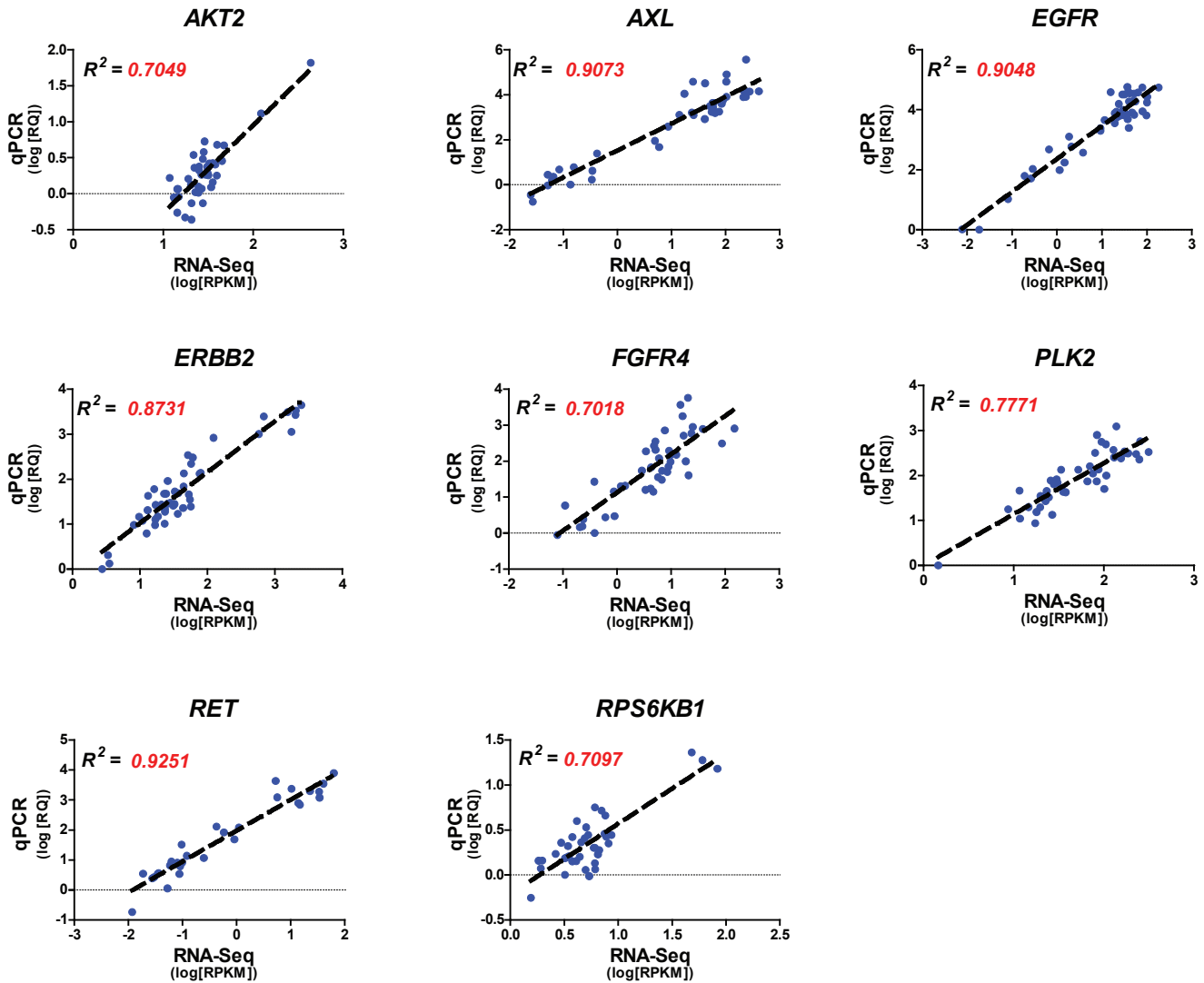
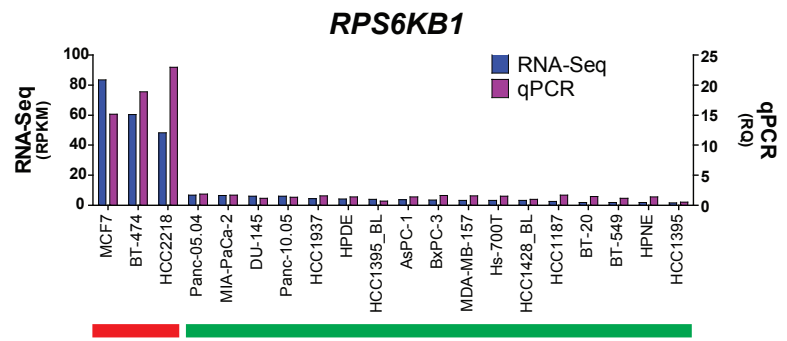
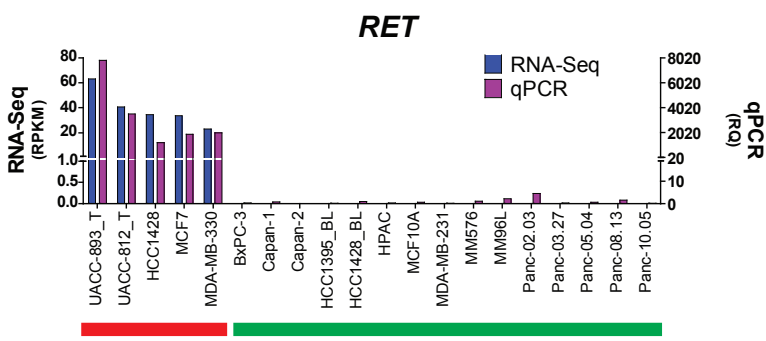
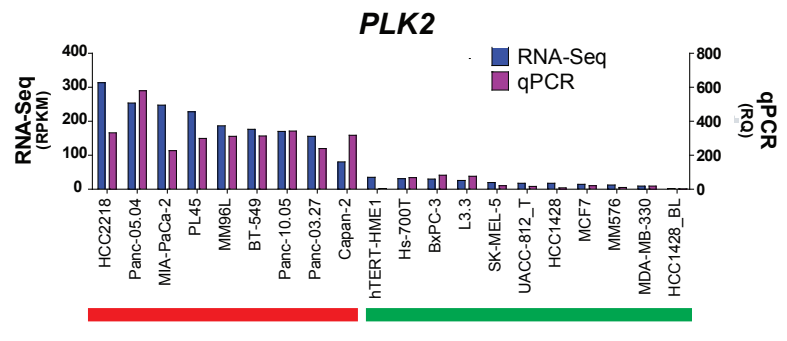
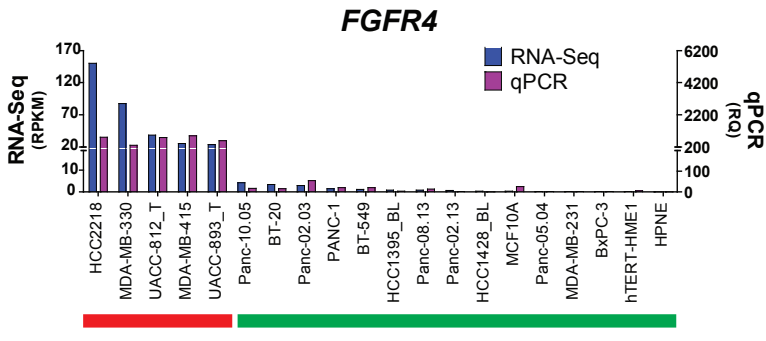
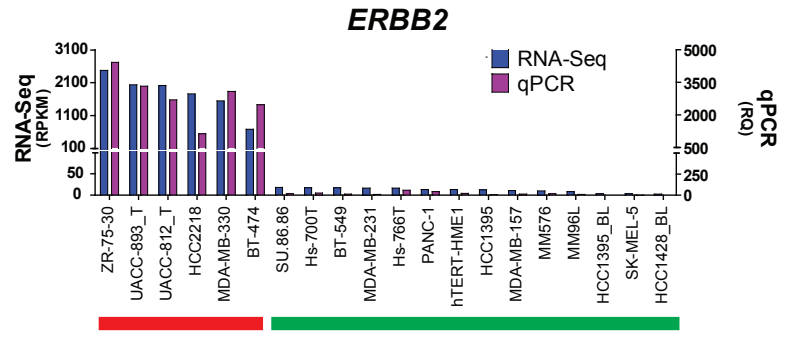
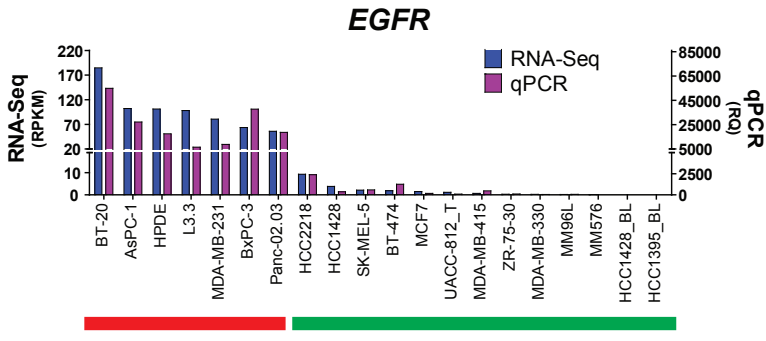
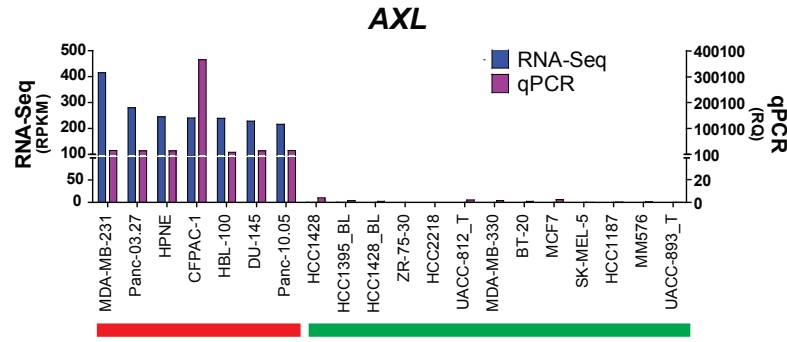
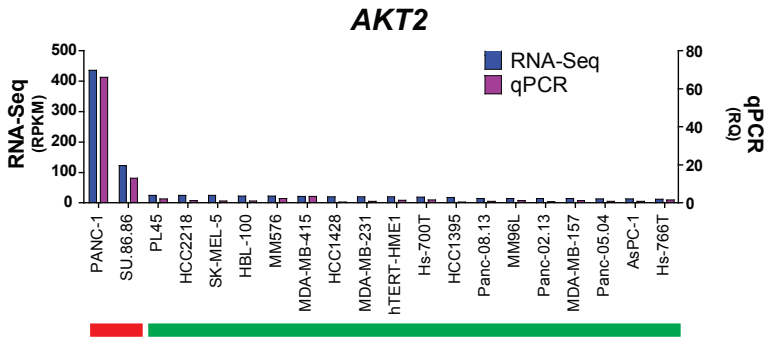


A**DU145****B****MCF-7**

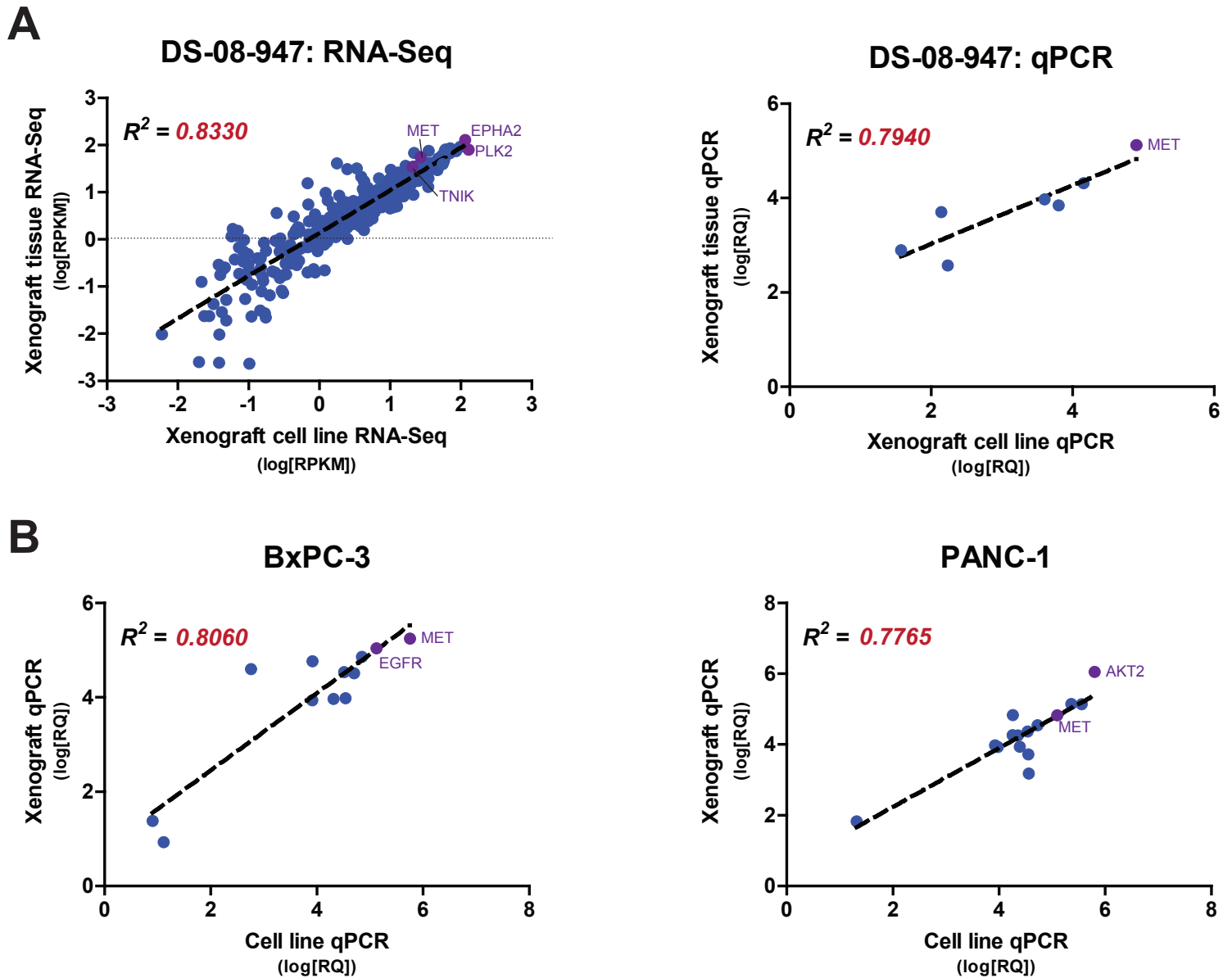
Supplementary Figure S1. RNA-Seq reads are concordant over multiple runs. Scatter plots show log-transformed, entire transcriptome RNA-Seq reads for prostate cancer cell line DU145 (A) across 4 technical replicates (Lanes 1 - 4) and for breast cancer cell line MCF-7 (B) across 3 biological replicates during early estrogen time-course experiment (0 - 6 hours). Dashed black lines are linear regressions. R^2 , correlation coefficients.



Supplementary Figure S2. RNA-Seq reads correlate with gene expression. Log-transformed RNA-Seq expression for 8 different kinases, measured as RPKM, are plotted against log-transformed gene expression, measured as relative quantity (RQ) by qPCR. Each point represents a unique sample. Dashed black lines are linear regressions. R^2 , correlation coefficients.



Supplementary Figure S3. Validation of outlier expression predicted by RNA-Seq. RNA-Seq reads (blue) and qPCR gene expression (purple) of 8 kinases are plotted for 20 different samples. Samples with predicted outlier expression of the respective kinase by RNA-Seq are highlighted by the red bars. Samples with predicted non-outlier expression are highlighted by the green bars.



Supplementary Figure S4. Gene expression is concordant for matched cell lines and xenografts.

(A, left) Log-transformed RNA-Seq expression of all 468 kinases for primary pancreatic adenocarcinoma tissue xenograft DS-08-947 are plotted against log-transformed RNA-Seq expression for its derived cell line. Kinases highlighted in purple have outlier expression in both xenograft tissue and matched cell line. (A, right) Log-transformed expression levels of random genes for DS-08-947 are plotted against log-transformed expression levels for its derived cell line by qPCR. (B) Log-transformed expression levels of random genes for commercial pancreatic adenocarcinoma cell lines, BxPC-3 and PANC-1, are plotted against log-transformed expression levels for the corresponding xenografts by qPCR. Genes with outlier expression nominated by RNA-Seq are highlighted in purple. Dashed black lines are linear regressions. R^2 , correlation coefficients.