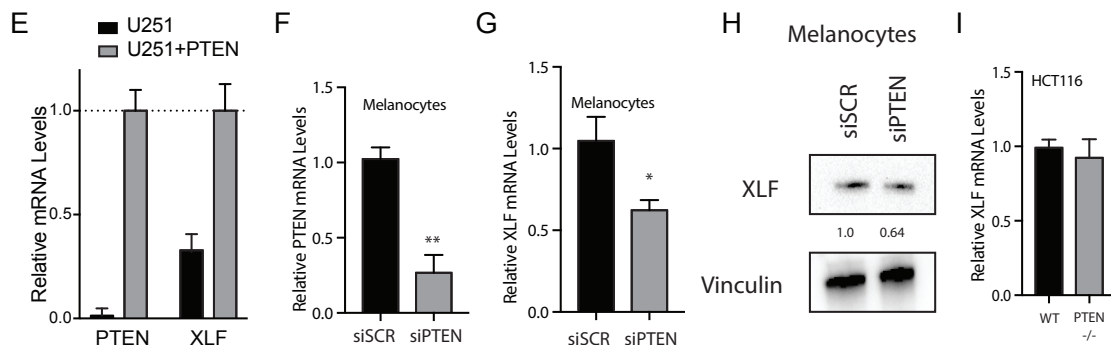
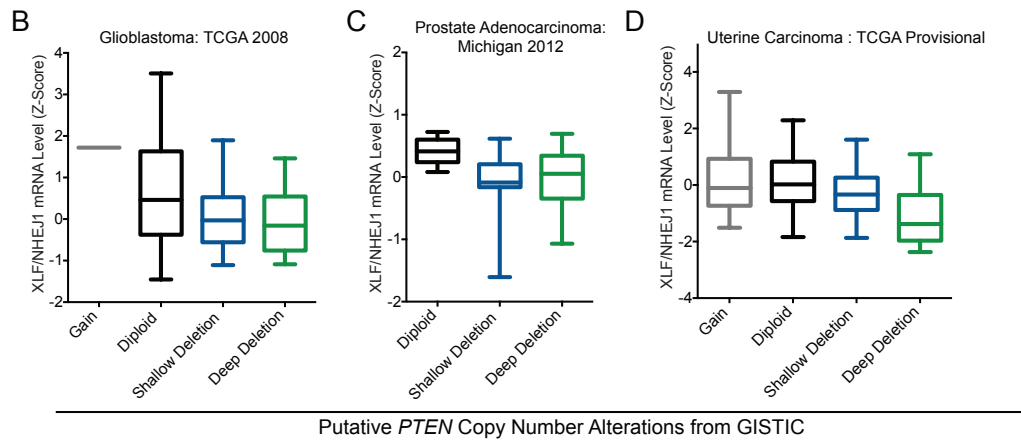
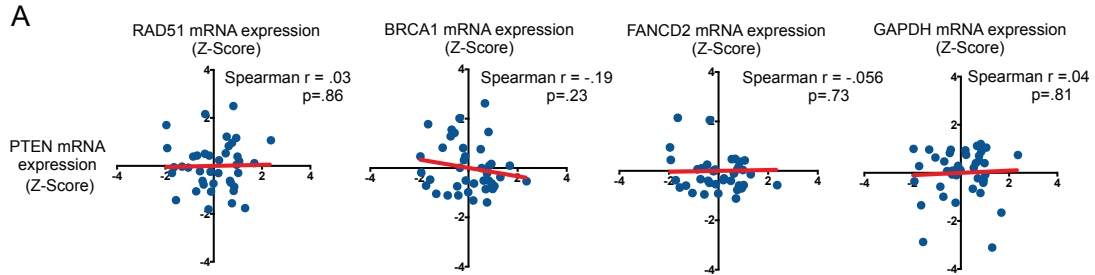


Supplementary Figure S3



Supplementary Figure S3

(A) Scatter plot of Z-score expression values for PTEN and RAD51, BRCA1, and GAPDH (n=40). Statistical analysis was by Spearman's rank correlation and correlation regression analysis two-tailed t- test. (B-D) Box plot (5-95% interval) of XLF mRNA expression Z-scores from publically available (B) microarray expression data from glioblastomas (n=91) (Network 2008), (C) RNA-seq data from metastatic prostate adenocarcinomas (n=61) (Grasso et al. 2012), and (D) RNA-seq data from uterine adenocarcinomas (n=232) (Network 2013). (E) Quantification of PTEN and XLF mRNA levels in the U251 cells with or without doxycycline induction of PTEN expression. mRNA levels are normalized to GAPDH and then to the U251 + PTEN sample. (F) PTEN and (G) XLF mRNA quantification by RT-qPCR 96 h after transfection of human melanocytes with siRNA targeting PTEN or scrambled control. (H) XLF protein quantification 96 h after transfection of human melanocytes with siRNA targeting PTEN or scrambled control. (I) XLF mRNA quantification by RT-qPCR in PTEN $-/-$ and parental HCT116 cells.