Supplemental Figure 1:

A) Oncoprint of mTOR alterations within MSK IMPACT dataset. Top panel indicates each sample within the dataset, with color coded alteration of mTOR shown in 3% of samples. Middle panel shows samples with mTOR alterations at higher magnification. Bottom panel shows only putative driver mTOR alterations. PD = putative driver, US = unknown significance. **B)** Gene alteration frequency of different oncogenes within the MSK IMPACT dataset. RTKs include EGFR, ERBB2, ERBB3, ERBB4, MET, ALK, RET, ROS1, FGFR1, FGFR2, FGFR3, KDR, FLT1, FLT2, FLT3, FLT4, and PDGFRA. Akt includes Akt1, Akt2, and Akt3. TSC includes TSC1 and TSC2. **C)** Gene alteration frequency of oncogenes within the Breast TCGA cancer study. Akt includes Akt1, Akt2, Akt3. TSC includes TSC1 and TSC2. **D)** MutSigCV analysis of mTOR (red), PTEN (gray), and PIK3CA (dark blue) from the Pan-Cancer Analysis of Whole Genomes (PCAWG) cancer studies, showing p-values to indicate the significance of the mutational frequency of each gene within each cancer study. **E)** MutSigCV analysis of Titin (light blue), TP53 (dark blue), Kras (green), BRCA1 (orange), and BRCA2 (yellow) from the TCGA pan-cancer studies, shown as p-values for the significance of the mutational frequency of each gene within each cancer study. **F)** Enrichment of putative driver mTOR mutations by cancer type within the TCGA cancer studies. **G)** Venn diagram of mTOR, PTEN, and PIK3CA mutational co-occurrence in renal clear cell carcinoma and endometrial carcinoma from the TCGA cancer studies, as retrieved from cBioPortal.