**SUPPLEMENTARY FIGURE LEGEND**

**Supplementary File – Tissue Sample IDs.** Excel spreadsheet containing the specific tissue samples used in these analyses.

**Supplementary Table 1.** Patient and tumor characteristics. Tissue samples used for this study were obtained from the Lester and Sue Smith Breast Cancer Tumor bank at Baylor College of Medicine. We studied 102 breast tumors from this bank that were collected from sites in the US and Europe. Study demographics define the majority of the population to be postmenopausal women, 97% Caucasian, and the median subject age to be 53 years. In this cohort, 95% of the tumors were invasive ductal carcinomas, 47% presented no lymph node involvement, all were without metastasis, and 76% of study participants had tumors ≥2cm3 at the time of diagnosis. The ER and PR status of each tissue sample was determined through immunohistochemistry (IHC) analysis, and HER2 status by fluorescent in-situ hybridization (FISH). This identified 49 ER-positive tumors and 53 triple-negative tumors. Of the ER-positive breast cancers, 12 tumors were also HER2-positive (24%), and 42 PR positive (86%).

**Supplementary Table 2.** Cox proportional hazard ratio analysis of the Curtis Data set.

**Supplementary Table 3.** Excel spreadsheet containing the gene list used to identify phosphatases and phosphatase-interacting proteins.

**Supplementary Figure 1*.*** *Differentially expressed phosphatase genes in human breast cancer*. Hierarchical clustering analysis of phosphatase expression (shown on the vertical axis) in 102 human breast cancers (shown on horizontal axis) demonstrates differential expression that distinguishes triple-negative from ER-positive human breast tumors. Gene expression analysis of 102 human breast tumors reveals 276 probe sets representing phosphatases and phosphatase-associated genes that are differentially expressed between triple-negative and ER-positive human breast tumors (FDR = 0.05).

**Supplementary Figure 2.** Analysis of RPPA results from breast cancers in the TCGA data set. Cleaved caspase 7 is selective increased in basal-like breast cancers with low PTP4A3 expression

**Supplementary Figure 3.** *Inhibition of PTP4A3 reduces tumor growth of MDA MB231 cells in mice.* **A-B)** Average tumor growth of MDA MB231 shPTP4A3 and control tumors treated with doxycycline or vehicle. **C)** mRNA expression of MDA MB231 control tumors and PTP4A3 tumors treated with doxycycline or vehicle. **D)** Average tumor growth of MDA MB468 control tumors and PTP4A3 tumors treated with doxycycline or vehicle. **D)** Tumor growth rate is not reduced in tumors from the ER-positive breast cancer cell lines.**E)**. Tumor growth slopes of MCF-7 control tumors and PTP4A3 tumors treated with doxycycline or vehicle.

**Supplementary Figure 4.** **A)** Curtis data set analyzed for expression levels of PTP4A3 in normal breast tissue compared to invasive ductal carcinoma (IDC). **B)** Curtis data set analyzed for expression levels of PTP4A3 in non-TNBCs versus TNBCs. **C)** Kaplan-Meier curves of overall survival of all breast cancer patients (Kao Dataset) stratified by *PTP4A3* expression and ER. **D)** Kaplan-Meier curves of disease-specific survival of all breast cancer patients (Curtis Dataset) stratified by *PTP4A3* expression.

**Supplementary Figure 5.** **A)** PTP4A3 and Myc amplification status in Luminal A/B and Basal-like breast cancers from TCGA data set. **B)** PTP4A3 and Myc amplification status in ovarian cancer from TCGA data set. **C)** Map detailing the location of the genes analyzed for gene amplification. **D)** Comparative analysis of PTP4A3 gene copy number and expression levels.