Supplemental Figure 1. Top 10 significant biofunctions observed across proteins which were increased in abundance in each breast cancer cell line that directly correlated across all breast cancer cell lines. Figure reports average, significant p-values observed and mean number of proteins observed which clustered with a given biofunction.

Supplemental Figure 2. Top 10 significant biofunctions observed across proteins which were decreased in abundance in each breast cancer cell line that directly correlated across all breast cancer cell lines. Figure reports average, significant p-values observed and mean number of proteins observed which clustered with a given biofunction.

Supplemental Figure 3. Bright-field microscopy images of the breast cell lines analyzed in culture.

Supplemental Table 1. Raw peptide identifications for each cell line condition. M* designate oxidized methionine and C# designate carboxyamidomethylated cysteine.

Supplemental Table 2. A. Raw protein identifications for each cell line condition. Proteins highlighted in yellow did not map to Ingenuity Pathway Analysis (IPA) databases. Spectral counts designate combined spectral count peptides identified for a given protein. Log2 (Fold-Change) values are designated for those proteins which were observed as significantly, differentially abundant in a given breast cancer cell line versus MCF10A comparison by statistical analysis. **B.** Cellular localization and functional types of proteins identified across all breast cell lines analyzed.

Supplemental Table 3. A. Comparison of significantly, differentially abundant proteins relative to total proteins identified in each and across all breast cancer cell lines. Fold-change ratios and p-values highlighted in yellow designate significant fold-changes. **B.** Comparison of global, significantly, differentially abundant proteins relative to proteins with were mutually, differentially abundant across all breast cancer cell lines. Fold-change ratios and p-values highlighted in yellow designate significant fold-changes.

Supplemental Table 4. A. Significant biofunctions derived from "Core Analysis" of proteins which were increased in abundance in each breast cancer cell line which directly correlated across all breast cancer cell lines.**B.** Significant biofunctions derived from "Core Analysis" of proteins which were decreased in abundance in each breast cancer cell line which directly correlated across all breast cancer cell lines. The top 10 biofunctions displayed in supplemental figure 2 are highlighted. **C.** Significant biofunctions derived from "Core Analysis" of proteins which were mutually, differentially abundant across breast cancer cell lines.