Supplementary Figure Legends

Figure S1: SILAC-based proteomics of breast cancer. A. MCF7 cells were labeled with Lys8 and Arg10 and served as a spike-in standard for quantification of the experimental cells. B. Heavy and light cell lysates were mixed and digested with trypsin in three biological replicates. Peptides were separated by OffGel and each fraction was analyzed by LC-MS/MS in the LTQ-Orbitrap. C. Typical high resolution MS spectrum from the Orbitrap with a zoom-in on a single SILAC-pair in the inset.

Figure S2: Changes in gene-ontology biological processes. Hierarchical clustering of cell adhesion (A), cell cycle (B), mRNA splicing (C) and Golgi apparatus (D).