LEGENDS OF SUPPLEMENTAL DATA

Supplemental Table S1. Proteins significantly increased and decreased in the brain metastatic 231-BR cells, and corresponding changes in mRNA levels. Increases in protein and mRNA levels in 231-BR cells, as compared to MDA-MB-231 cells, are indicated by (+) and decreases by (-). For each regulated protein, the following information is presented: gene name, name of protein, Uniprot accession number, locality, function, best peptide E-value, number of unique peptides, % sequence coverage, fold protein changes and mRNA fold changes are indicated. nsc, non-significant changes in mRNA level. p-values for mRNA changes: *<0.05, **<0.01, ***<0.001.

Supplemental Table S2. Transitions obtained in Parallel Reaction Monitoring (PRM). For each protein analyzed in PRM (MMP1, EFN1, STOM1, MYCT1, TGM2, LCP1, S100A4, UAP1, and HSPD1), the following information is provided: gene symbol, protein accession number, sequence of analyzed peptides, target precursor ions, charge state, chromatography retention time of analyzed peptide, quantification (average area) in 231-BR vs. MDA-MB-231, p-value.

Supplemental Figure S3. Parallel Reaction Monitoring (PRM) mass spectrometry validation of SILAC quantification. The expression of significantly regulated proteins revealed by reciprocal SILAC labeling of the brain metastatic cell line 231-BR vs. MDA-MB-231 were validated using a label-free quantification PRM experiment. A total of 14 peptides from the most significantly regulated proteins were monitored in triplicate experiments (42 peptides including controls) using a minimum of 3 transitions per peptide. The quantification for 2 peptides per protein in 231-BR vs. MDA-MB-231 is presented for MMP1, EFN1, STOM1, MYCT1, TGM2, LCP1, S100A4 and UAP1. HSPD1 has been used as a control unregulated protein.
**Supplemental Table S4. mRNA differentially expressed in the brain metastatic 231-BR cells.** Fold change in expression of mRNAs found to be significantly different in 231-BR cells, as compared to MDA-MB-231 cells (>2-fold difference, p<0.05 and a false discovery rate (FDR) = 5.0%). For each regulated mRNA, the following information is presented: gene assignment, gene name, RefSeq number, p-value, fold change in 231-BR versus MDA-MB-231, probeset ID, chromosomal localization, start, stop, strand, p-value.

**Supplemental Table S5. microRNA (miRNA) differentially expressed in the brain metastatic 231-BR cells.** Fold change in expression of 45 miRNAs found to be significantly different in 231-BR cells as compared to MDA-MB-231 cells (>2-fold difference, p<0.05 and a false discovery rate (FDR) = 5.0%). For each regulated miRNA, the following information is presented: probe set ID, fold change in 231-BR vs. MDA-MB-231, p-value, corrected p-value. Note: hp refers to hairpin and these are pre-miRNAs.

**Supplemental Table S6. Potential correspondence between miRNA regulated in 231-BR cells and regulated proteins.** The potential targets of miRNAs regulated in 231-BR have been searched using sRNA Target Base, which integrates data from 21 Ago or TNRC6 CLIP-Seq sequence data sets with the target prediction programs Target Scan, Pictar and miRanda. miRNA that were validated by all 3 target-prediction algorithms have been selected. For each regulated miRNA potentially corresponding to a regulated target gene/protein, the following information is presented: miRNA name, miRNA fold change, gene/protein target name, mRNA fold change, protein fold change. Changes in green are increases and in red are decreases.
Access to raw data. The raw data (for proteins, mRNAs and miRMAs analyses) have been uploaded to the MassIVE public repository: ftp://MSV000078911@massive.ucsd.edu.

Annotated spectra can be viewed using MS-Viewer (http://prospector2.ucsf.edu/prospector/cgi-bin/msform.cgi?form=msviewer) using the following search keys: Biological Repeat 1 - p2iuesahfg; Biological Repeat 2 (reciprocal labeling) - lzcne57i8x.