Table S3. Expression of glycolytic enzymes detected by LC-MS/MS analyses of MCF7 and MDA-MB-231 protein lysates.

| Gene Name | Protein Name                                | MW (Da) | MCF7 (Heavy) | MDA-MB-231 (Light) | MCF7/MDA-MB-231 Ratio |
|-----------|---------------------------------------------|---------|--------------|--------------------|-----------------------|
| ALDOA     | Fructose-bisphosphate aldolase A            | 39,420  | 46           | 121                | 0.38                  |
| ENO1      | Alpha-enolase                               | 47,168  | 69           | 216                | 0.32                  |
| GAPDH     | Glyceraldehyde-3-phosphate dehydrogenase    | 36,053  | 314          | 406                | 0.77                  |
| G6PI      | Glucose-6-phosphate isomerase               | 63,146  | 62           | 36                 | 1.72                  |
| PKM       | Pyruvate kinase                             | 57,936  | 120          | 389                | 0.31                  |
| LDHA      | L-Lactate dehydrogenase A                   | 36,688  | 13           | 80                 | 0.16                  |
| LDHB      | L-Lactate dehydrogenase B                   | 36,638  | 1            | 44                 | 0.02                  |
| PFKM      | ATP-dependent 6-phosphofructokinase         | 85,595  | 23           | 25                 | 0.92                  |
| PGAM1     | Phosphoglycerate mutase 1                   | 28,804  | 14           | 49                 | 0.29                  |
| PGK1      | Phosphoglycerate kinase 1                   | 44,796  | 13           | 29                 | 0.45                  |
| PGM1      | Phosphoglucomutase-1                        | 61,448  | 3            | 18                 | 0.17                  |
| TPIS      | Triosephosphate isomerase                   | 30,791  | 31           | 49                 | 0.63                  |

Mass-spectrometry (MS)-based identification of glycolytic enzymes in MCF7 and MDA-MB-231 cell lines using stable isotope labeling of amino acids in cell culture (SILAC) in combination with LC-MS/MS analysis using protocols provided by the manufacturer (Thermo Fisher Scientific, Inc.). In this approach, MCF7 cell lines were grown in DMEM media containing stable isotope labeled (heavy) amino acids $^{13}$C$_6$-Lys (K6) and $^{13}$C$_6$-Arg (R6) while the MDA-MB-231 cells were grown in media containing regular (light) amino acids ($^{12}$C$_6$-Lys (K0) and $^{12}$C$_6$-Arg (R0)). Equal amounts of cell lysates obtained from heavy- and light-labeled, MCF7 and MDA-MB 231, respectively, were combined and separated on a 14% SDS-PAGE. The protein lanes containing MCF7 and MDA-MB-231 were divided into ~1 mm pieces and subjected to trypsin digestion. The tryptic digests were analyzed by LC-MS/MS, which consisted of a Surveyor auto sampler and HPLC and an LTQ linear ion trap mass spectrometer (Thermo Fisher Scientific, Inc.). Protein identification was performed by Mascot Distiller (Matrix Science). The number of heavy- and light-labeled peptides of glycolytic enzymes detected by LC-MS/MS is directly proportional to protein expression in these cell lines.