Additional File 4: A representation of the relationship between common genes in both the breast cancer cell lines, MCF-7 and ZR75-1. Depiction of some pathways operating in individual cell lines.

Figure 1. A regression plot of fold change of 77 common genes in MCF7 and ZR75-1 cells. Here, we have used regression, a statistical analysis which depicts the relationship between two variables, which in this case were the fold change of common (77) genes between NBr/MCF7 or MCF7/NBr and NBr/ZR75-1 or ZR75/NBr. A plot of fold change was computed using the BioMedCAChe (Bio Medical Computer Aided Chemistry, V 6.2, 2003, Oxford Molecular Limited Fujitsu Limited). The equation as depicted on the plot, gave a value of 0.55 for the regression coefficient r².

Figure 2. A plot of fold change of 77 common genes in MCF7 and ZR75-1 cells. The X axis represents fold change of genes and the Y axis consists of gene number.

Figure 3. (a) The tight junction pathway operating in MCF7 cells. (b) The table at the bottom depicts the fold change of the respective genes. Claudin4 was highly down-regulated and Rab13, a member of the Ras family of oncogenes was highly down-regulated. The heavy polypeptide 9 is not shown in the GenMAPP pathway.

Figure 4. The TGF beta signaling pathway operating in MCF7 cells. The transcription factors STAT3 and Jun are down-regulated, while STAT1 was up-regulated. The gene encoding for the cadherin-associated protein, beta-catenin, which was up-regulated (7.6 fold) is common between the tight junction the TGF beta and the Wnt signaling pathways respectively.

Figure 5. The Wnt signaling pathway in MCF7 cells. Besides catenin B1, the transcription factor Jun is common between the Wnt and TGF beta signaling pathways. GenMAPP and DAVID have predicted this pathway for MCF7 cells.

Figure 6. The Down-regulated of MTA3 in ER(-)ve breast tumors pathway was selected by BIOCARTA pathway (a component of DAVID) for ZR75-1 cells. The up-regulated genes are denoted in red.
Figure 3
Figure 5

MCF-7

Frizzled Ligands

WNT1  WNT3A  WNT6
WNT7  WNT4  WNT7A
WNT2B  WNT5A  WNT7B
WNT3  WNT1B  WNT11

LDLR

Cytoskeleton

DVL1  DVL2  DVL3

ARHIA  RAC1  MAPK9

MAPK10

Apoptosis

PRKCA  PRKCB1  PRKCG  PRKCD  PRKCE  PRKCI
PRKCH  PRKCM  PRKCO  PRKCY  PRKCI

CSNK1E

AXIN1

PPP2R5E  PPP2R5C

GSK3B  APC

CTNNB1

Phosphorylated β-Catenin

Recruitment to Unknown Ubiquitin Conjugating Enzyme

FBXW2  PAFAH1B1

Ubiquitin Tagged β-Catenin

26S Proteasome Degradation

Transcriptional Activation

MYC  CCND1  CCND2  CCND3  FOSL1  JUN  PLA2

Nucleus

TCF-1/LEF

Figure 5