

A

Comparison		Gene Expression	FC>2 # of Genes	FDR<5% # of Genes	FC>2 & FDR<5% # of Genes
MCF7 cells in tumor (n=3)	vs. MCF7 cells <i>in vitro</i> (n=2)	Upregulated	2142	1	1
		Downregulated	1564	0	0
MDA-MB-231 cells in tumor (n=4)	vs. MDA-MB-231 cells <i>in vitro</i> (n=2)	Upregulated	1456	1770	1112
		Downregulated	897	1189	717
MDA-MB-231 cells <i>in vitro</i> (n=2)	vs. MCF7 cells <i>in vitro</i> (n=2)	Upregulated	2935	1	1
		Downregulated	3459	0	0
MDA-MB-231 cells in tumor (n=4)	vs. MCF7 cells in tumor (n=3)	Upregulated	3562	4635	3388
		Downregulated	3709	4609	3479

B

Comparison		Gene Expression	FC>2 # of Genes	FDR<5% # of Genes	FC>2 & FDR<5% # of Genes
MCF7 tumor stroma (n=3)	vs. Mammary Gland (n=1)	Upregulated	7123	1	1
		Downregulated	959	0	0
MDA-MB-231 tumor stroma (n=4)	vs. Mammary Gland (n=1)	Upregulated	4090	1	1
		Downregulated	2171	0	0
MCF7 tumor stroma (n=3)	vs. MDA-MB-231 tumor stroma (n=4)	Upregulated	4394	3598	3113
		Downregulated	743	736	609

Table S5: Fold change and false discovery rate for analysis of gene expression in tumor and stroma.

A comparison of the number of genes up- or downregulated, using noted cutoffs, in cells (A) and stroma (B).

As false discovery rate (FDR) is influenced by the number of samples in a comparison group, and as the sample group size (n) differs between comparison groups, gene expression with a fold-change (FC) greater than 2 was used for analyses in this study.

For the algorithm which generated these FDR values, both comparison groups cannot have n=1, but one group with n=1 can be compared with another group with n>1. For these latter comparisons, the FDR variations come from the n>1 group rather than the n=1 group.