**Supplementary M&M**

*TCGA Analysis*

We used the data from the Breast Invasive Carcinoma (TCGA, Provisional and TCGA Nature 2012), available at <http://www.cbioportal.org/> ([Gao et al](http://www.ncbi.nlm.nih.gov/pubmed/23550210), 2013; [Cerami et al](http://cancerdiscovery.aacrjournals.org/content/2/5/401.abstract), 2012), with 1105 and 825 patients samples respectively.

The analysis was performed using R language. Attached below.



Briefly:

**mRNA expression data**: mRNA expression values (RNASeq V2 RSEM) of BRCA1 and PLK1 from TCGA provisional database, selecting only sample from primary tumors (n: 1093). A base-2 logarithm logarithmic transformation was performed.

**Markers:** data related to ER, PR and HER2 receptors were acquired from the TCGA provisional and TCGA Nature 2012 databases. Only samples tagged as positive or negative for each receptor were considered for the analysis to avoid conflicts with mislabeled samples. mRNA expression data and Makers data were fused in a final table for each patient.

Statistical analysis is shown in the following table:



Cerami, E., Gao, J., Dogrusoz, U., Gross, B. E., Sumer, S. O., Aksoy, B. A., Schultz, N. (2012). The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. *Cancer Discovery*, *2*(5), 401–404. <http://doi.org/10.1158/2159-8290.CD-12-0095>

Gao, J., Aksoy, B. A., Dogrusoz, U., Dresdner, G., Gross, B., Sumer, S. O., Schultz, N. (2013). Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. *Science Signaling*, *6*(269), pl1. <http://doi.org/10.1126/scisignal.2004088>

*Automated analysis of Flow cytometry data*

We developed a script using R to automatically import and analyze all the data from the screenings. Script attached below.

