***‘The therapeutic response of ER-positive breast cancers differs according to the molecular Basal- or Luminal-type’***

Supplemental methods

Here are described the classifiers used in the study of Bertucci et al., NPJ Breast Cancer 2019 (*submitted*) and related to custom code included in the R script file ‘Breast\_cancer\_classifications.r’ and the R object ‘Breast\_cancer\_classifications.Rda’. R functions were built in respect of methodology and tools of each original source.

**Custom code, R ‘*functions*’** :

`*BluePrint*`1, A nearest-centroid classification model built utilizing the 80-gene profile defined by authors for ‘Basal’, ‘HER2’ and ‘Luminal’ molecular subtypes.

`*PAM50*`2, A nearest-centroid classification model built utilizing the 50-gene profile defined by authors for ‘Basal-like’, ‘ERBB2-enriched’, ‘LuminalA’, ‘LuminalB’ and ‘Normal-like’ molecular subtypes.

`*Mammaprint*`3, A Pearson correlation score utilizing the prognostic 70-gene profile defined by authors to classify samples in ‘low/good-risk’ and ‘high/poor-risk’ groups.

`*EndoPredict*`4, A prognostic score built utilizing 8 genes of interest and 3 references genes associated with clinical risk factors based on a ER+/HER2- breast cancer population to classify samples in ‘low-risk’ and ‘high-risk’ groups.

`*breastHierarch*`5, A metagene score model built utilizing subpopulations gene expression signatures of the breast epithelial cell hierarchy defined by authors.

`*CD44CD24*`6, A Pearson correlation score utilizing the gene profile of 493 probes defined by authors in mammospheres (MS) forming cells to classify samples in ‘CD44+/CD24- MS-like ’ and ‘noCD44+/CD24- MS-like’ groups.

`*DLDA30*`7, A multigene predictor model of pathological complete response (pCR) built utilizing the 30-gene profile defined authors and their associated data with a Diagonal Linear Discriminant Analysis (DLDA, R package *sfsmisc* v1.1) to classify samples in ‘pCR-like’ and ‘RD-like’ groups.

`*E2F4*`8, A metagene Z-score built utilizing 24 gene-profile of E2F4 target activation defined by authors.

`*ICR*`9, An unsupervised classification model built utilizing the 20-gene profile of immune phenotypes defined by authors performed with consensus clustering (R package *ConsensusClusterPlus* v1.46) to classify samples in 4 ICR groups.

`*Immunome*`10, A metagene score model built utilizing gene expression signatures of 28 different immune cell types of infiltrating tumors defined by authors.

*`RBsig`*11, A Z-score metagene model built utilizing the 87-gene profile to be correlated with E2F1 and E2F2 expression defined by authors.

*`E2Fregulon`*12, A Z-score metagene built utilizing the profile of 200 genes defined in the ‘E2F targets’ gene set from Molecular Signatures Database (Hallmark base, version 6.2, <http://software.broadinstitute.org/gsea/msigdb/>)

**Additional molecular variables used not using custom code** :

`Gatza`13, A prediction model based on Bayesian Factor Regression Modeling to define activation probability of multiple molecular pathway using the web-tool SIGNATURE14.

*`PDL1 , mRNA expression (log2)`* of PD-L1 (*CD274*) exported from each used data sets as previously described15. Briefly, prior to extraction of PD-L1 in each data set, data were standardized using the ‘Luminal A’ population as reference to make PD-L1 comparable across all sets.

*`PIK3CA mut`* & `*TP53 mut*`, mutational status of *PIK3CA* and *TP53* were retrieved from TCGA BRCA data16 using National Cancer Institute (NCI) Genomic Data Commons (GDC) web-tool were silent mutations were excluded.

*`HRD score`*, Homozygous Recombination Deficience (HRD) score was retrieved from TCGA BRCA data16 using NCI GDC web-tool.

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