Capture of Supplementary Figures, Table and Data.

Supplementary Figure S1. Survival analysis using regularized Cox regression identifies potential biomarkers linked to patient outcomes.

Supplementary Figure S2. *LMO1* correlation with the TCGA's annotated PAM50 subtypes.

Supplementary Figure S3. *PRAME* correlation with the TCGA's annotated PAM50 subtypes.

Supplementary Figure S4. *RSPO2* correlation with the TCGA's annotated PAM50 subtypes.

Supplementary Figure S5. PAM50 annotations per Cluster.

Supplementary Figure S6. *LMO1, PRAME*, and *RSPO2* relative expression analysis. Validation of the expression data of *LMO1, PRAME,* and *RSPO2* using RT-qPCR, in MCF-7, MCF-7pR and in BT549.

Supplementary Table S1. Significant Biomarkers in Breast Cancer.

Supplementary Data S1. Identification of 32 significant genes with regularized Cox regression analysis.

Supplementary Data S2. Expression of *LMO1*, *PRAME* and *RSPO2* in metastatic patients.