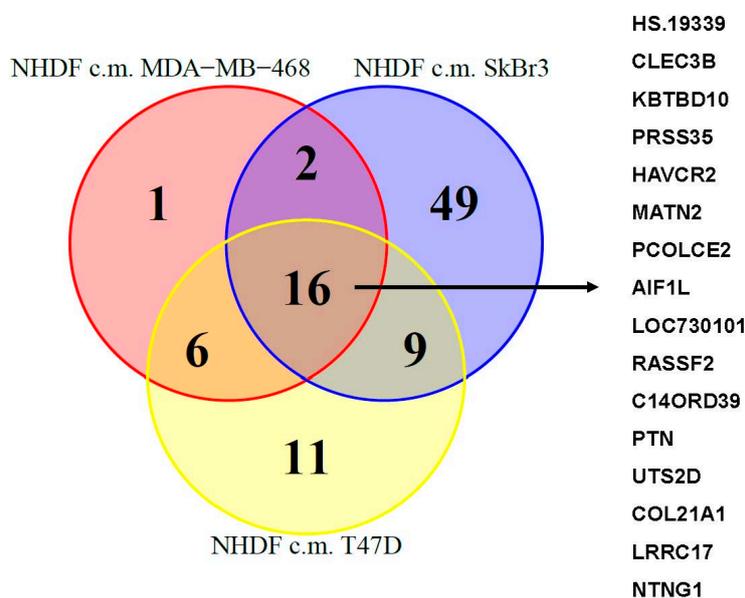
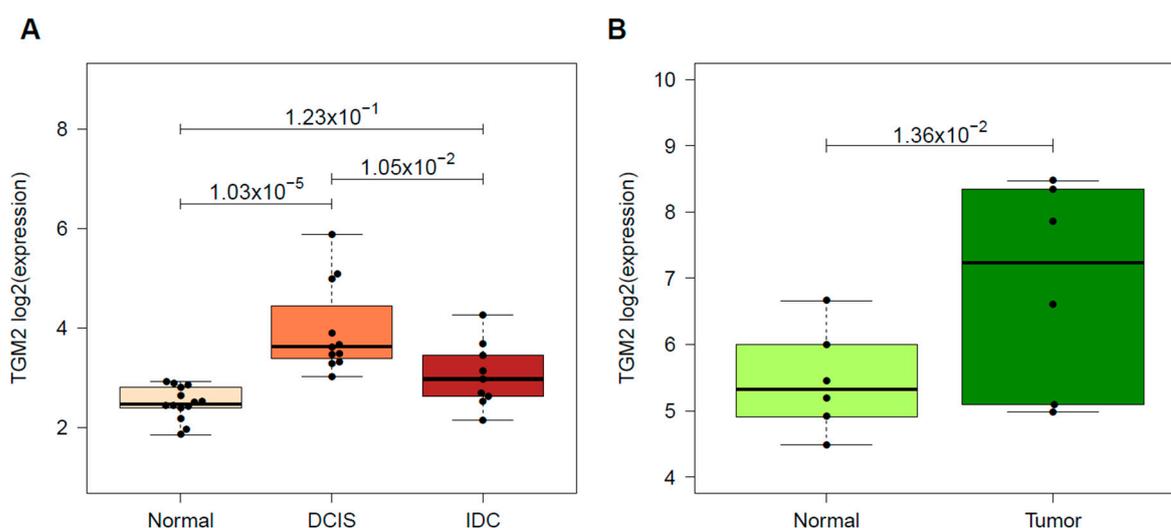


# Supplementary Materials: Stromal Activation by Tumor Cells: An *in Vitro* Study in Breast Cancer

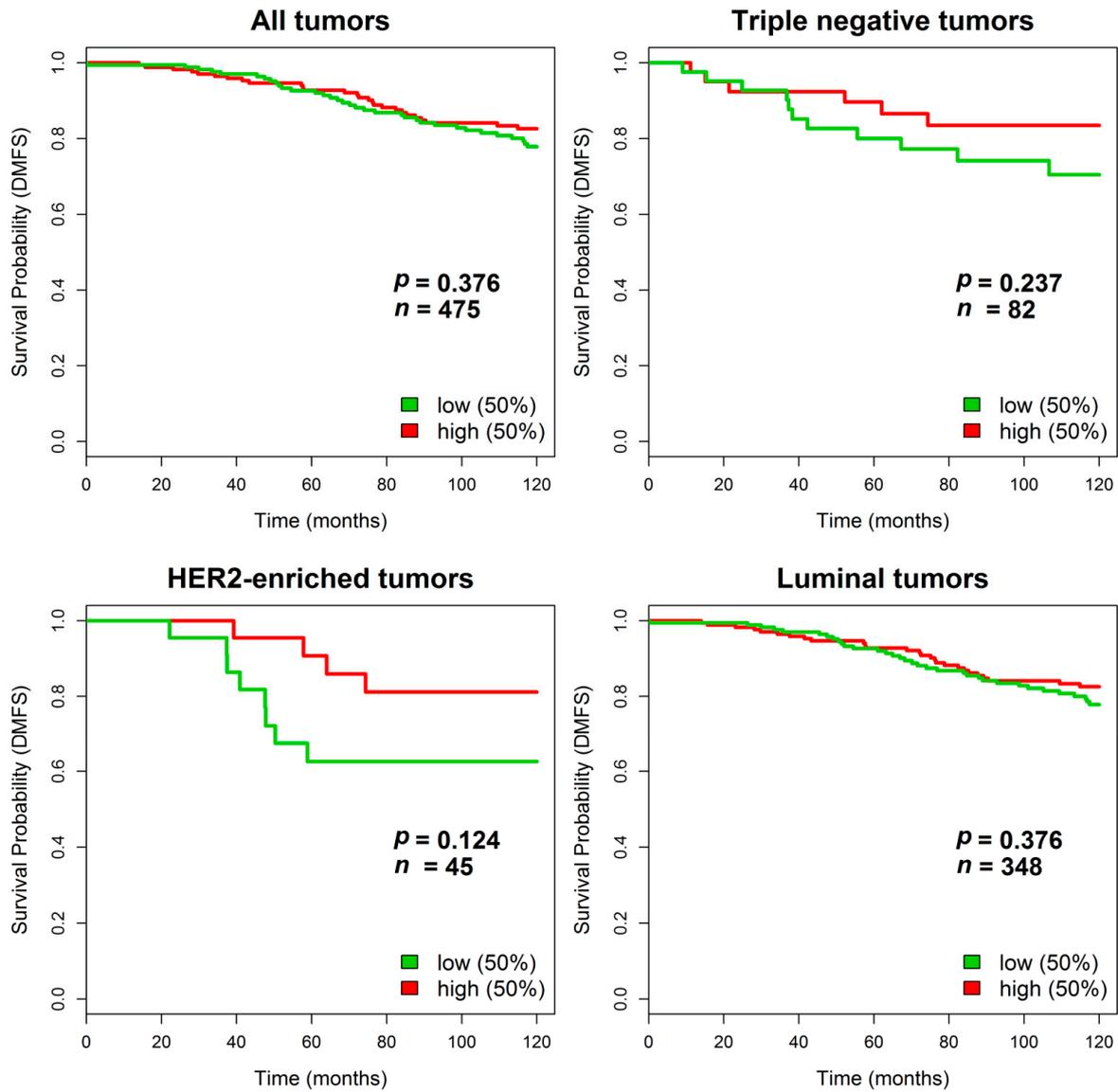
Giuseppe Merlino <sup>1</sup>, Patrizia Miodini <sup>1</sup>, Biagio Paolini <sup>2</sup>, Maria Luisa Carcangiu <sup>2</sup>, Massimiliano Gennaro <sup>3</sup>, Matteo Dugo <sup>4</sup>, Maria Grazia Daidone <sup>1</sup> and Vera Cappelletti <sup>1,\*</sup>



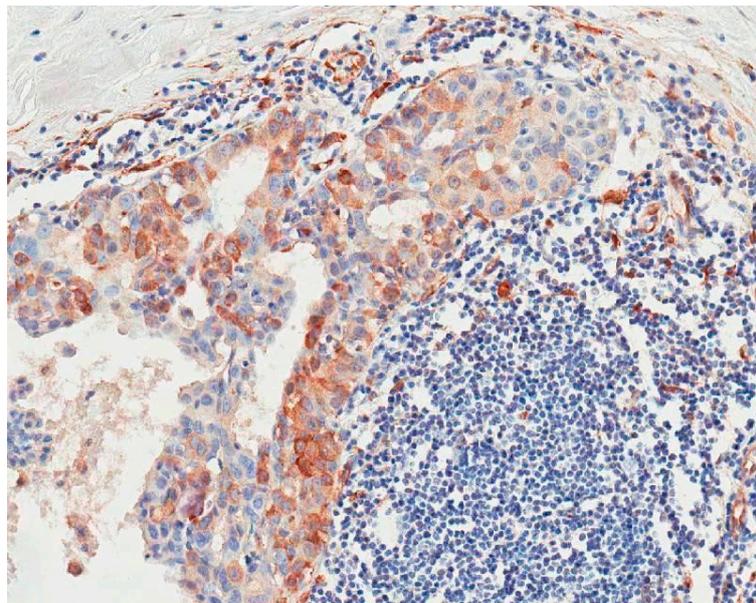
**Figure S1.** Venn diagram reporting common and private down-regulated genes in the class comparisons. Eulero-Venn diagram highlighting the numbers of differentially expressed (FDR < 0.0001) common and exclusive genes detected as down-regulated in samples derived from NHDF cells treated with serum-free medium conditioned by MDA-MB-468, by SkBr3 and by T47D breast cancer cell lines compared to their controls. The complete list of common down-regulated genes is also reported.



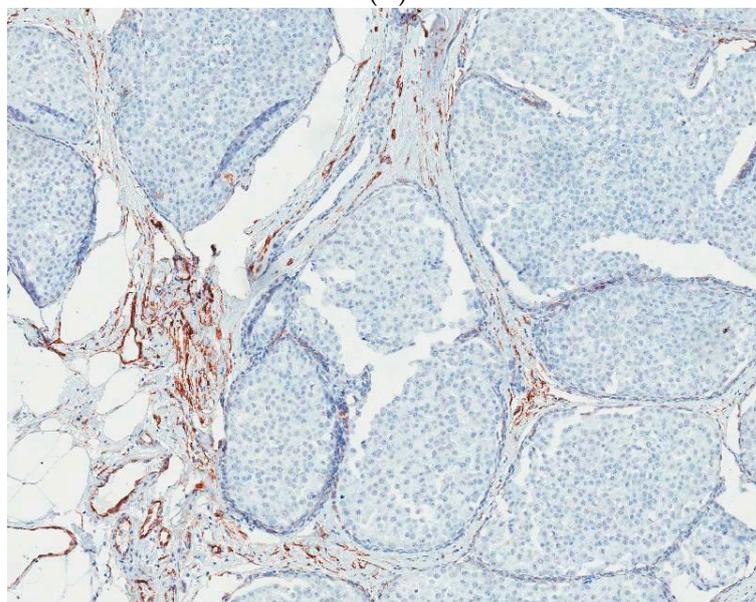
**Figure S2.** Expression of stromal TGM2 in literature datasets. **(A)** Boxplots of expression pattern of TGM2 as derived from microarray data (Ma *et al.*, ref [26]) in stromal cells adjacent to normal mammary cells, to DCIS and to invasive (IDC) lesions. Statistical significance was tested by ANOVA followed by Tukey's post-hoc test; **(B)** Boxplots of expression pattern of TGM2 as derived from microarray data (Planche *et al.*, ref [27]) in stromal cells adjacent to normal mammary cells and to tumor lesions. Statistical significance was assessed by two-tailed paired Student's *t*-test.



**Figure S3.** Kaplan-Meier analysis for the association of TGM2 expression stratified by median value in tumors from patients from the METABRIC dataset with disease-specific overall survival (DSS). Survival differences were evaluated by log-rank test.



(A)



(B)

**Figure S4.** TG2 staining in clinical sections from patients with DCIS. (A) Strong staining in tumor cells; (B) Positive staining for TG2 in stromal cells. Magnification 20 $\times$ .