









Supplementary Figure 1. Analysis of gene expression of TG2-lncRNA, TG2 and TGH transcripts in MCF-7 and MDA-MB-231 BrCa cells. Two µg of total RNA of the samples were reverse transcribed. Levels of mRNA indicated were obtained using $2^{-\Delta CT}$ method to compare the levels of the amplified target genes by RT-q-PCR, and HPRT1 as reference. Error bars represent standard deviation of three independent replicates and the labels represent significantly different expression ($p < 0.05$, two-tailed Unpaired t test).

Supplementary Figure 2. Apoptotic rate after TG2-lncRNA silencing. Early, late and total apoptotic cells/ml were analyzed using Annexin V assay. The measurements were performed after 48 (upper) and 72 h (lower) of treatment with 50 nM siRNA against TG2-lncRNA (Black) and negative control siRNA (White). The data represent means of 3 evaluations from 2 independent experiments ($p < 0.05$ compared to negative control, two-tailed Unpaired t test).

Supplementary Figure 3. Validation of genes modulated in PDGF signaling pathway. Levels of the target genes (TG2-lncRNA, TG2, STAT1, STAT2, STAT5A, AKT1 and B-actin) were evaluated by RT-qPCR using as control one among the samples treated with siRNA neg. Primers and amplification conditions are reported in Supplementary Table 1. Fold Change was calculated with $2^{-\Delta\Delta CT}$ formula and HPRT1 as reference gene. In Black, are depicted samples treated with siRNA neg, while in Grey, samples treated with siRNA against TG2-lncRNA. Error bars represent standard deviation ($n=3$ independent experiments) and significant differences labeled (*), ($p < 0.05$, Paired t test using parametric test).

Supplementary Figure 4. Location of TG2-lncRNA within the intron 1 of *TGM2* gene. The Black blocks represent the exons of *TGM2* gene, whereas the Grey ones depict the 5' and 3' untranslated regions. The Red blocks are the two untranslated exons that constitute TG2-lncRNA (LOC107987281). Thus, TG2-lncRNA transcript (XR_001754586.1) is obtained by the splicing and junction of these two genomic elements. The sequence recognized by the siRNA is also shown.