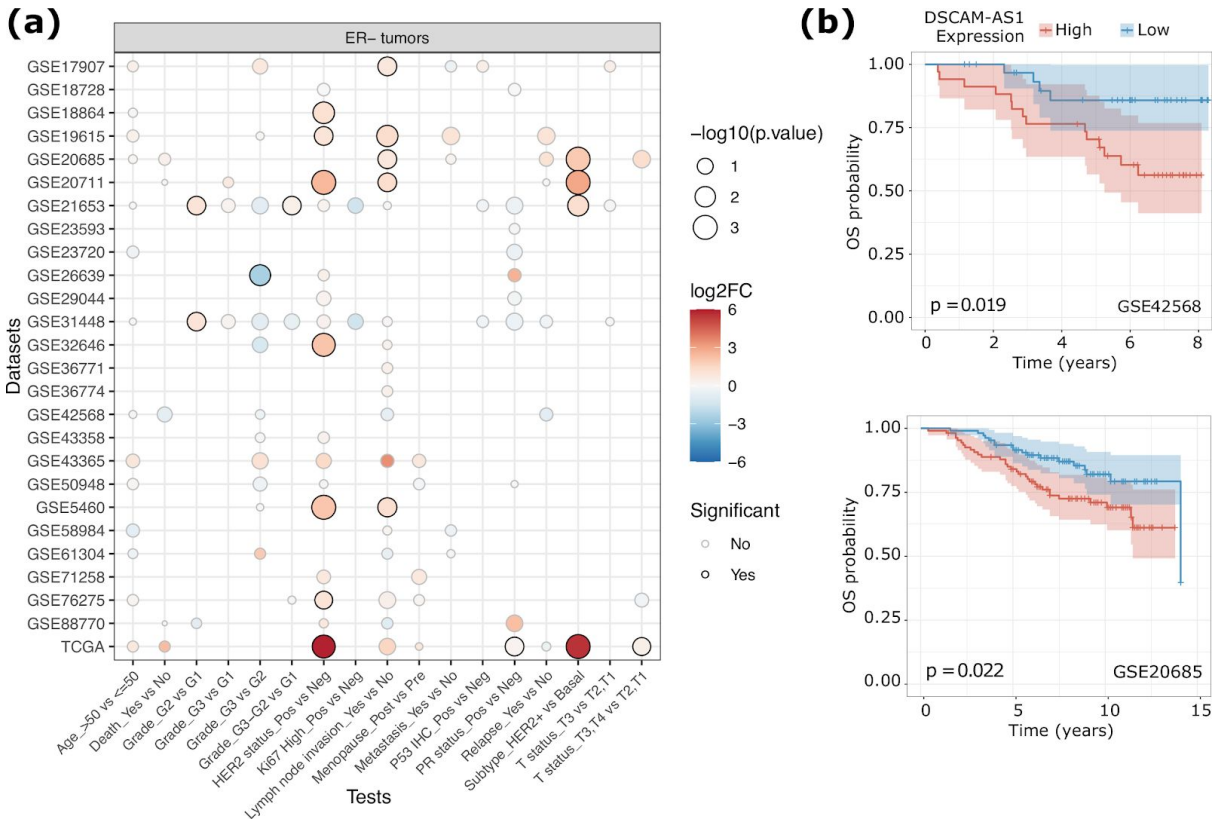
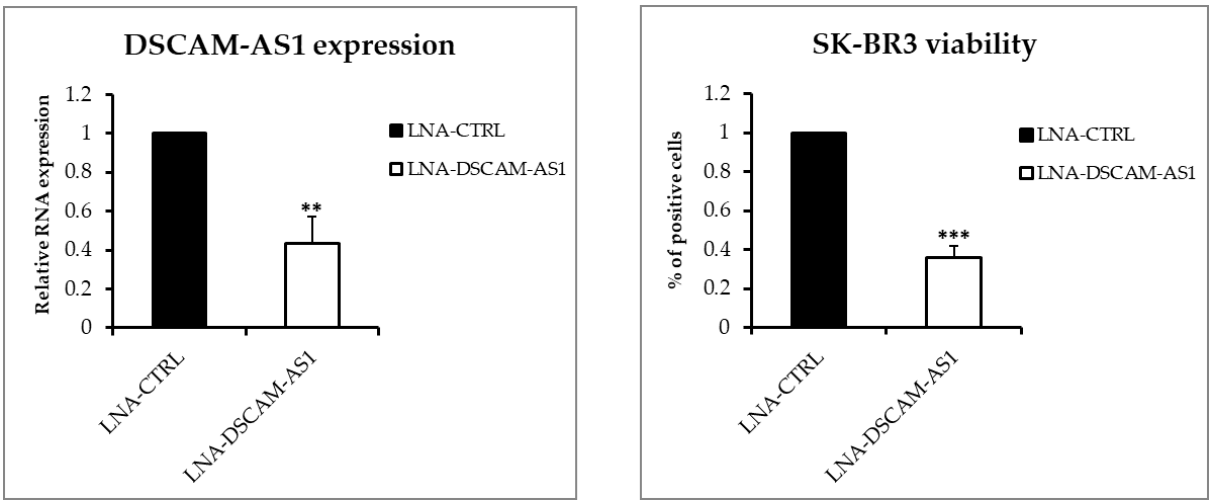
Supplementary Figures

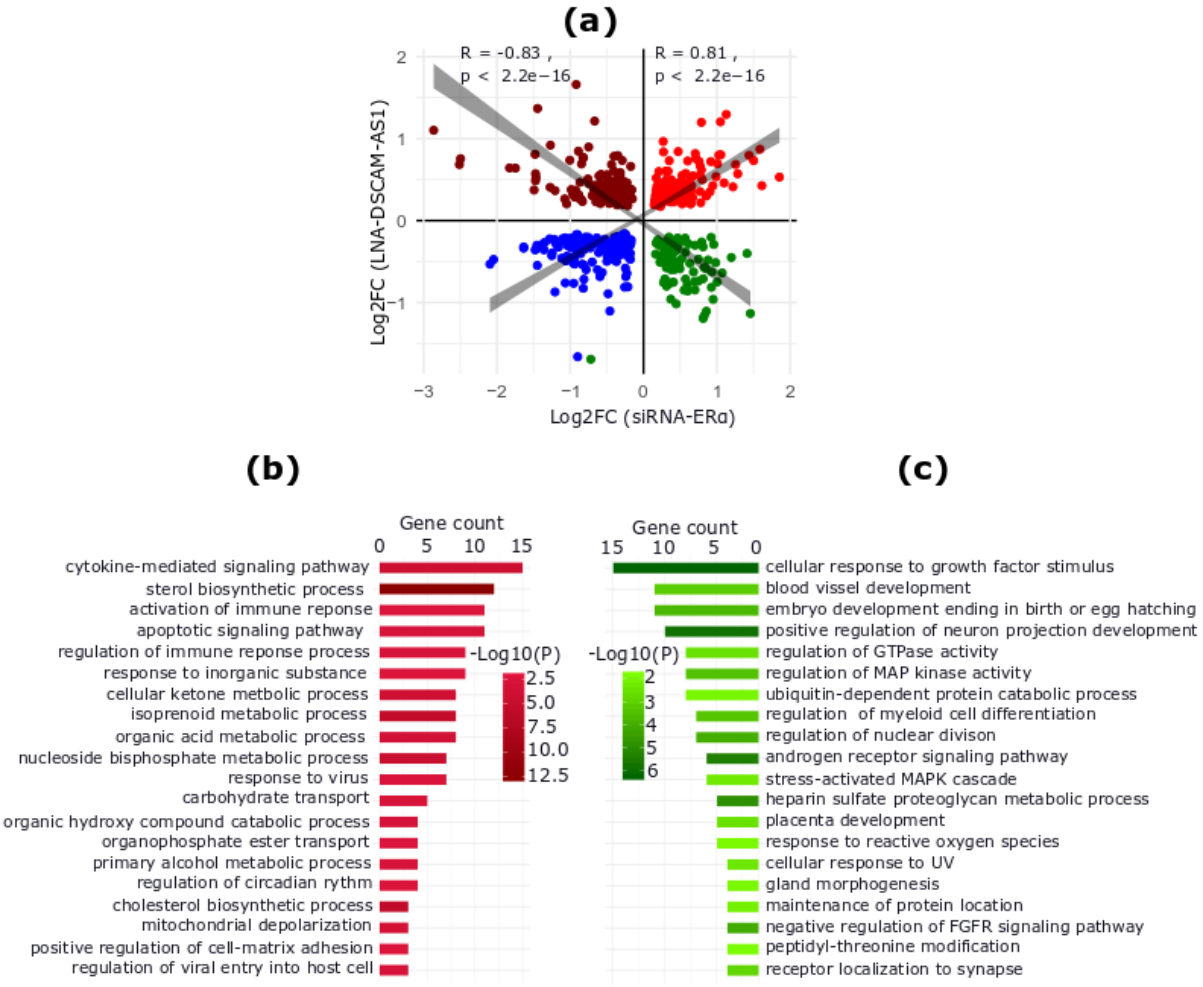


Supplementary Figure 1. (a) Dot plot reporting the level of statistical significance of the differential *DSCAM-AS1* expression analyses between groups of ER-negative BC patients separated with respect to specific clinical data. The size of the dot is proportional to the significance of the results while the color code represents the log2FC of expression. ER, Estrogen Receptor; Pos, positive; Neg, negative; PR, Progesterone Receptor. (**b**) Kaplan-Meier curves representing the Overall Survival (OS) of BC patients based on the median level of DSCAM-AS1 expression. P-value by log-rank test.

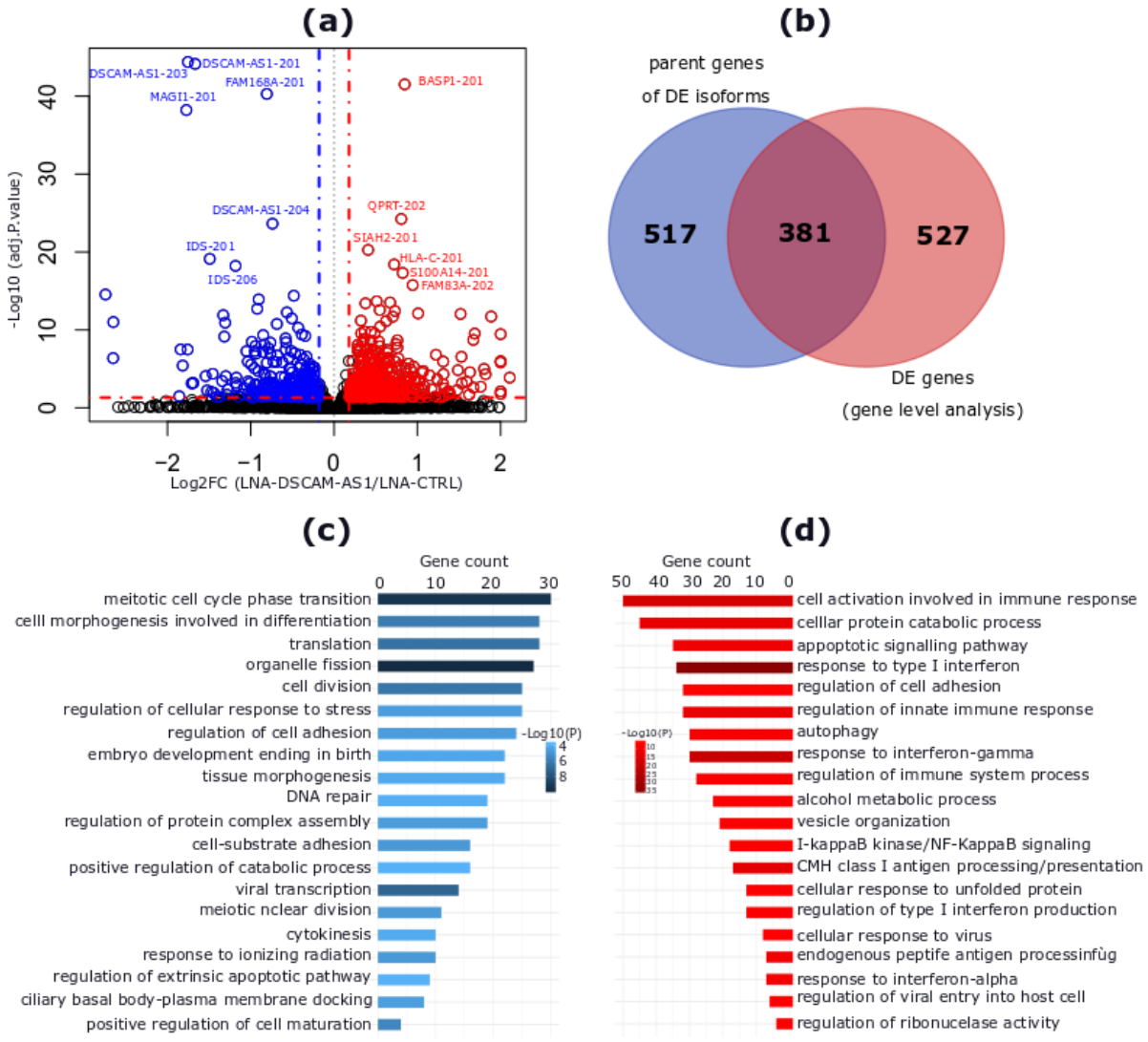
(a) **(b)**



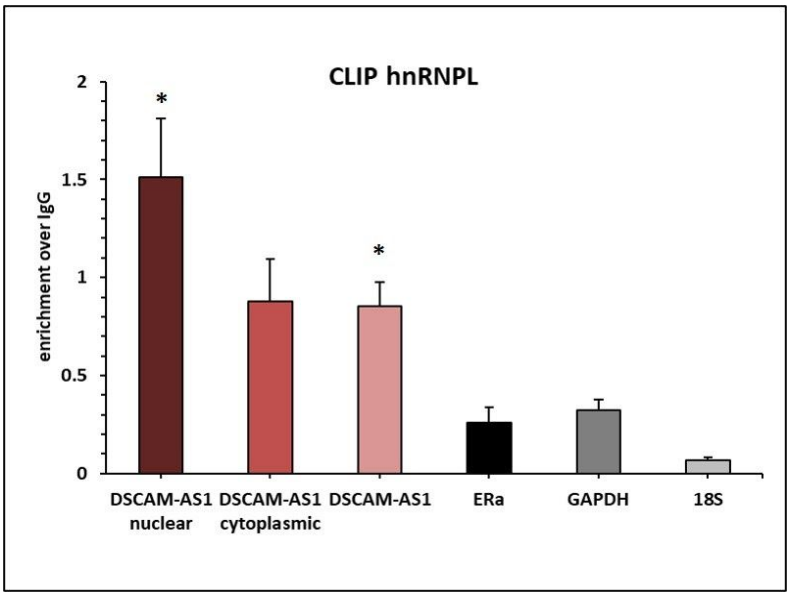
Supplementary Figure 2. **(a)** Expression levels of *DSCAM-AS1* and **(b)** viability measure by Crystal Violet Assay in SK-BR-3 cells upon transection of *DSCAM-AS1*-targeting or control LNA. Error bars represent the standard deviation of three biological replicates. Significance from T-test: **, p-value < 0.01; ***, p-value < 0.001.



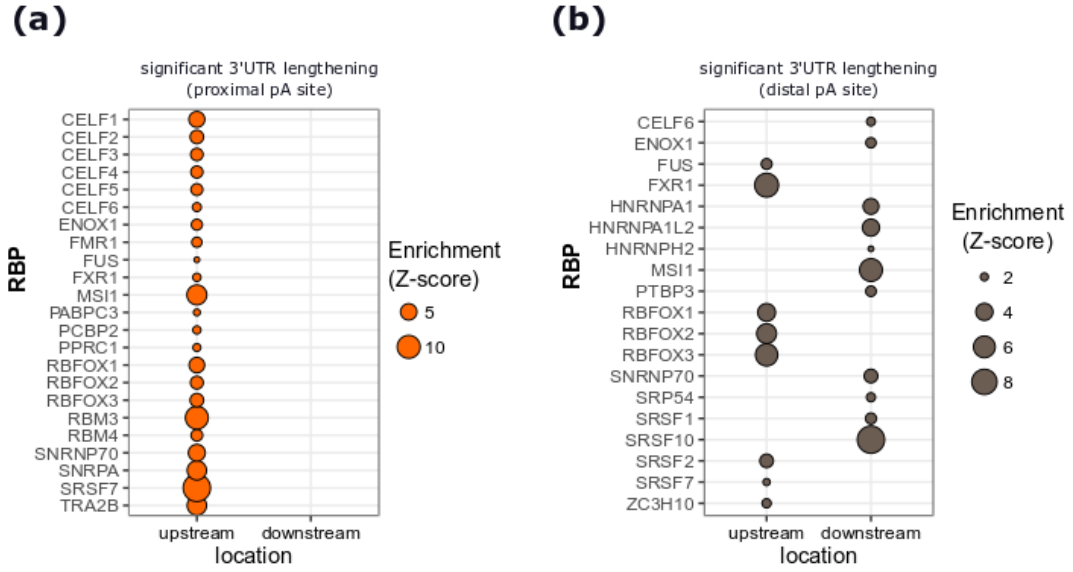
Supplementary Figure 3. **(a)** The scatter plot shows the log2 fold change of DE genes between this study and those obtained upon ERα silencing (siERα) [1]. Dark red and green dots represent genes upregulated in this study while downregulated in the siER experiment, and those downregulated in this study and upregulated in the siERα experiment, respectively. Blue and red dots represent those genes downregulated or upregulated in both studies, respectively. **(b)** GO terms enriched for genes upregulated in this study and downregulated in the siERα experiment. **(c)** GO terms enriched for genes downregulated in this study while upregulated in the siERα experiment.



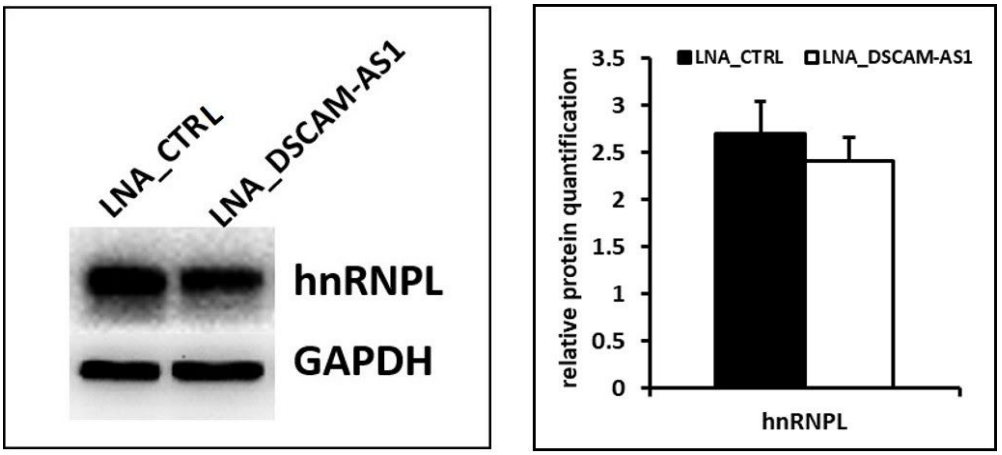
Supplementary Figure 4. (a) Volcano plot showing the log2FC of gene expression and the statistical significance of the differential expression (DE) analysis at isoform level performed between MCF-7 cells transfected with control or *DSCAM-AS1*-targeting LNA GapmeRs. In red are reported the up-regulated isoforms while in blue the down-regulated ones. **(b)** Venn diagram showing the overlap between DE genes and parent genes of DE isoforms. **(c-d)** Enriched GO biological processes related to parent genes of downregulated and upregulated isoforms, respectively.



Supplementary Figure 5. Cross-linking ImmunoPrecipitation (CLIP) of hnRNPL in MCF-7 cells shows evidence for physical interaction with *DSCAM-AS1* transcripts, considering separately the nuclear and the cytoplasmic isoforms. ERα, GAPDH and 18S were used as the negative control. Error bars represent the standard error of three biological replicates. Significance from T-test (*DSCAM-AS1* versus 18S enrichment): *, p-value < 0.05.



Supplementary Figure 6: The list of RBPs predicted to have an enrichment of their binding motifs in the 3'UTR lengthening events upon *DSCAM-AS1* silencing. The enrichment is shown for a selected region upstream and downstream of proximal **(a)** and distal **(b)** APA sites, respectively. Significance: z-score > 1.96.



Supplementary Figure 7. Left. Representative image of Western blot analysis of hnRNPL protein, GAPDH: loading control. **Right.** The histogram shows the protein level of hnRNPL in MCF-7 cells transfected with *DSCAM-AS1* or control LNA. hnRNPL values are relative to GAPDH. Error bars represent the standard error of three biological replicates.

References

1. Miano, V.; Ferrero, G.; Rosti, V.; Manitta, E.; Elhasnaoui, J.; Basile, G.; De Bortoli, M. Luminal lncRNAs Regulation by ERα-Controlled Enhancers in a Ligand-Independent Manner in Breast Cancer Cells. *Int. J. Mol. Sci.* **2018**, *19*.