Supplementary Data legends

Suppl. Data, Table 1: q-PCR primer and probe sequences.

*A SYBR green assay was used for genes lacking probes.

Suppl. Data, Table 2: SAFB1/SAFB2-binding sites identified by ChIP-on-chip.

To identify SAFB1/SAFB2 endogenous target genes in MCF-7 breast cancer cells, we performed a chromatin immunoprecipitation (ChIP)-on-chip. We utilized custom chips containing 1.5 kb upstream regulatory region of 24,275 genes. By using a stringent analysis, in which only overlapping peak enrichment in all three replicates was considered positive, we identified 818 binding sites for SAFB1/SAFB2, 541 of those sites map to promoters of known genes **(A)**, whereas 277 are upstream of unknown genes, containing high protein probability-coding sequences **(B)**.

Suppl. Data, Table 3: SAFB1/SAFB2 target genes

To identify SAFB1/SAFB2 endogenous target genes in MCF-7 breast cancer cells, we performed a gene expression array analysis, which was set up in a two-by-four design, with vehicle and estrogen treatment, and control, SAFB1, SAFB2, and SAFB1/SAFB2 siRNA as variables. 716 genes were significantly regulated by SAFB1, SAFB2, or the combination of SAFB1/SAFB2 siRNA in the presence of vehicle. Fold change is indicated for the three treatment group (SAFB1siRNA vs control, SAFB2siRNA vs control, SAFB1/SAFB2siRNA vs control), and 1 indicated significant change, and 0 non-significant. The cut-off for significance for this analysis was based on a BH adjusted p=0.1.

Suppl. Data, Table 4 A-C: Individual gene lists for SAFB1, SAFB2 and SAFB1/SAFB2

Out of 716 SAFB1/SAFB2-regulated genes, 680 genes were significantly regulated by SAFB1 **(A)**, 64 genes by SAFB2 **(B)**, and 483 genes by the combined knock-down of SAFB1 and SAFB2 **(C)**. The cut-off for this analysis was based on a BH adjusted p=0.1.

Suppl. Data, Table 5: Genes uniquely regulated by SAFB1

Out of the 716 SAFB1/SAFB2-regulated genes 163 target genes were significantly regulated by SAFB1 and not affected by SAFB2 siRNA. The cut-off for this analysis was based on a BH adjusted p=0.1.

Suppl. Data, Table 6: Estrogen-regulated genes

A subset analysis was performed by using the data from the 2x2 experimental design with control and SAFB1 siRNA, in the presence of vehicle and estrogen treatment. We identified a total of 585 genes which were significantly altered by estrogen (using adjusted p-value=0.1). Fold change E2 vs vehicle is indicated.

Suppl. Data, Table 7: Estrogen-regulated genes effected by SAFB1 siRNA

Out of 585 estrogen regulated genes, 68 genes were dependent on SAFB1 ($p < 0.1$, Fold change 20%).

Suppl. Data, Figure 1: ERα-regulated genes.

MCF-7 cells were transfected with ns or ERα siRNA, treated with E2, RNA was isolated, and q-PCR was performed for SAFB1 target genes, as indicated. The data are an average of three replicates $\pm$ SEM, and shown as relative expression compared to ns siRNA transfected cells.