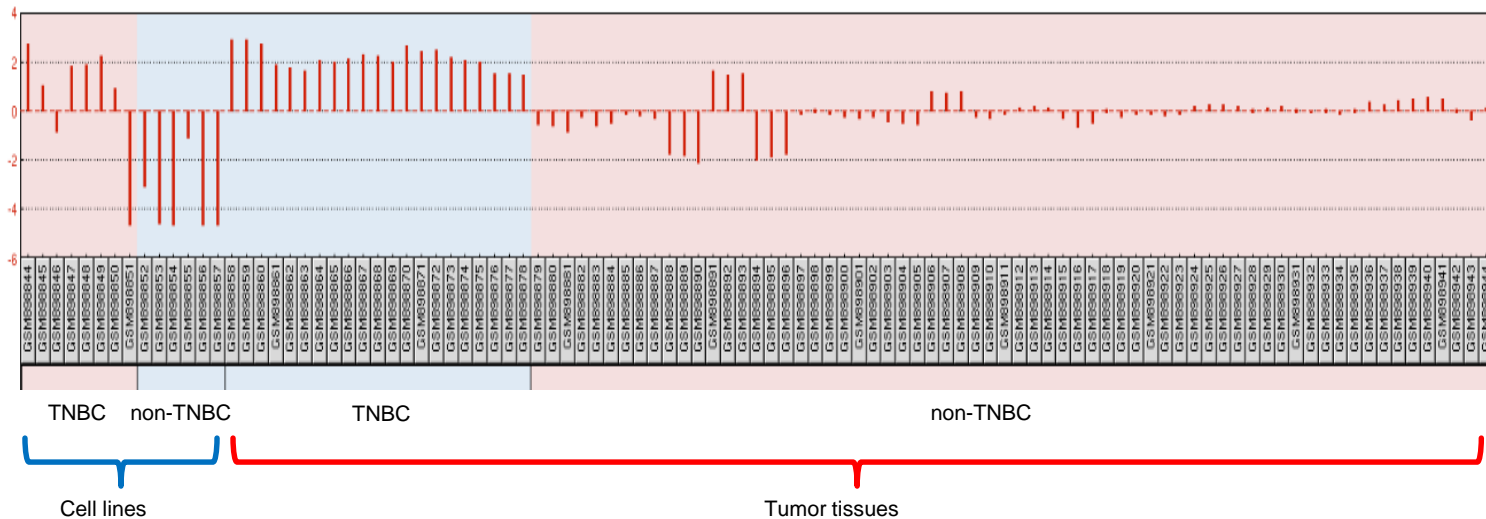
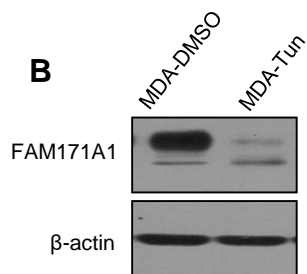
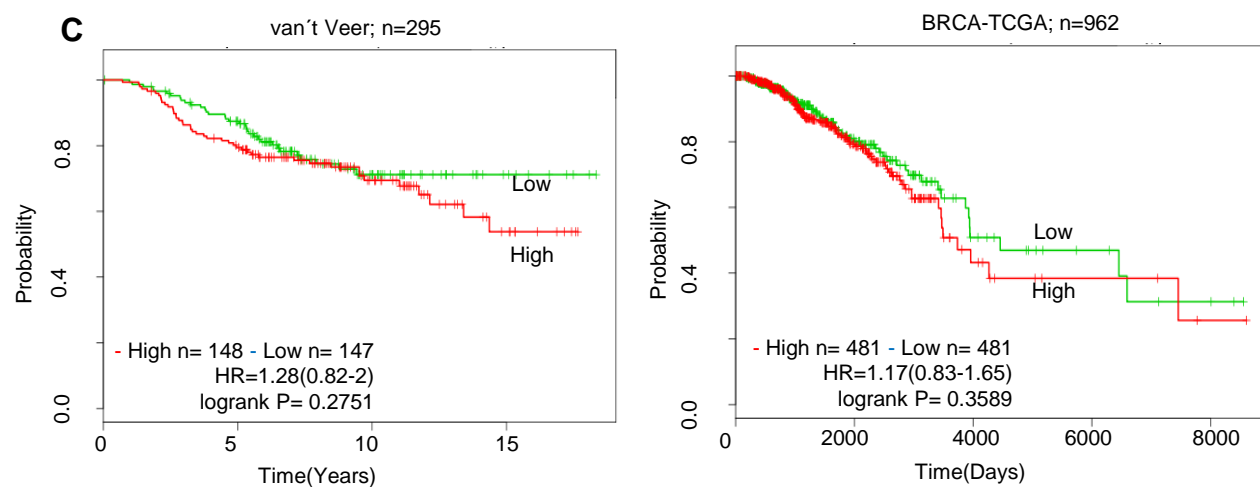
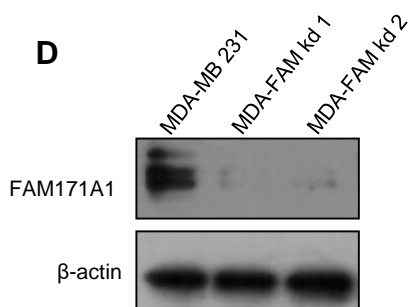
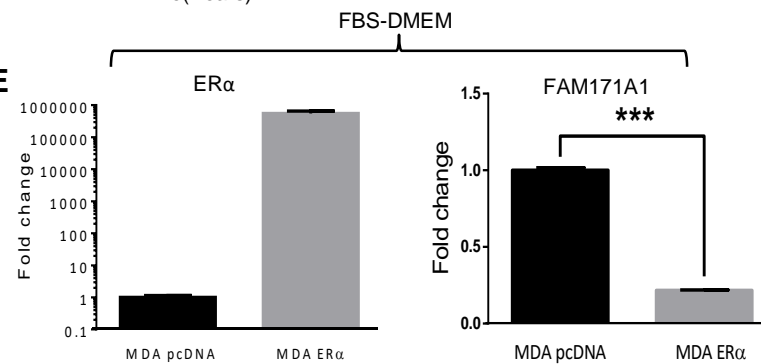
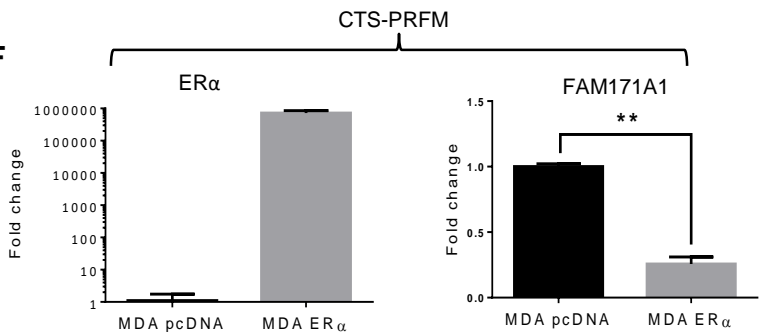


**A**

GSE36693/ILMN\_1749868/FAM171A1

**B****C****D****E****F**

Supplementary Figure 1

**A**

NCI-60 Cell lines(NCI, Cancer Res. 2012): n= 60/ 3genes

PGR: 3%

ESR1: 3%

FAM171A1: 1.7%

Cancer Cell Line Encyclopaedia (Novartis/Broad. Nature 2012): n=1020/3 genes

PGR: 3%

ESR1: 3%

FAM171A1: 0%

**B**

Breast Invasive Carcinoma, TCGA Provisional; n=1105/ 3 genes

PGR: 4%

ESR1: 4%

FAM171A1: 13%

Thyroid Carcinoma (TCGA, Provisional): n=516/3 genes

PGR: 0.4%

ESR1: 4%

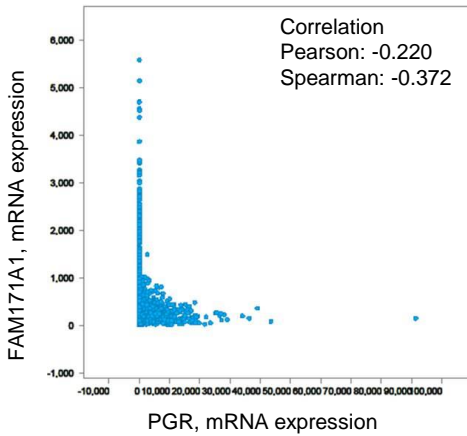
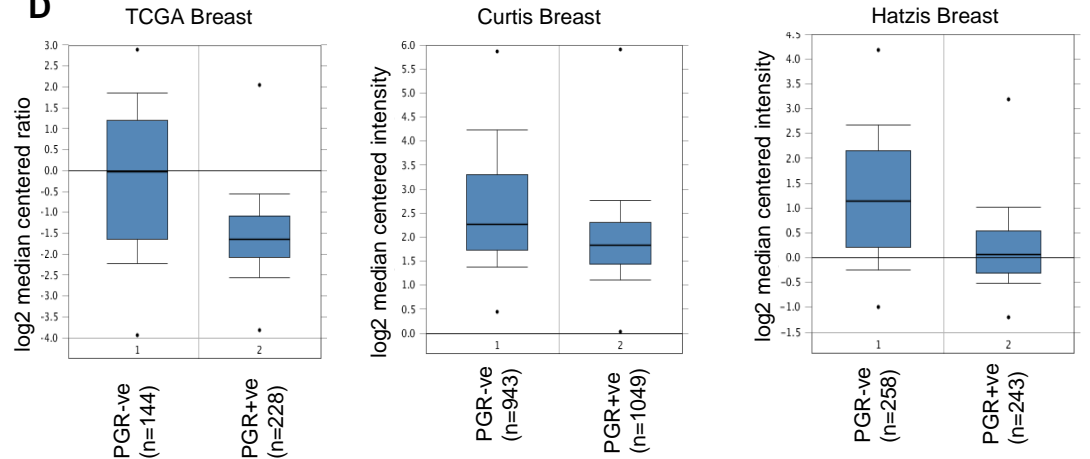
FAM171A1: 3%

Pancreatic Adenocarcinoma (TCGA Provisional) ; n=186/ 3genes

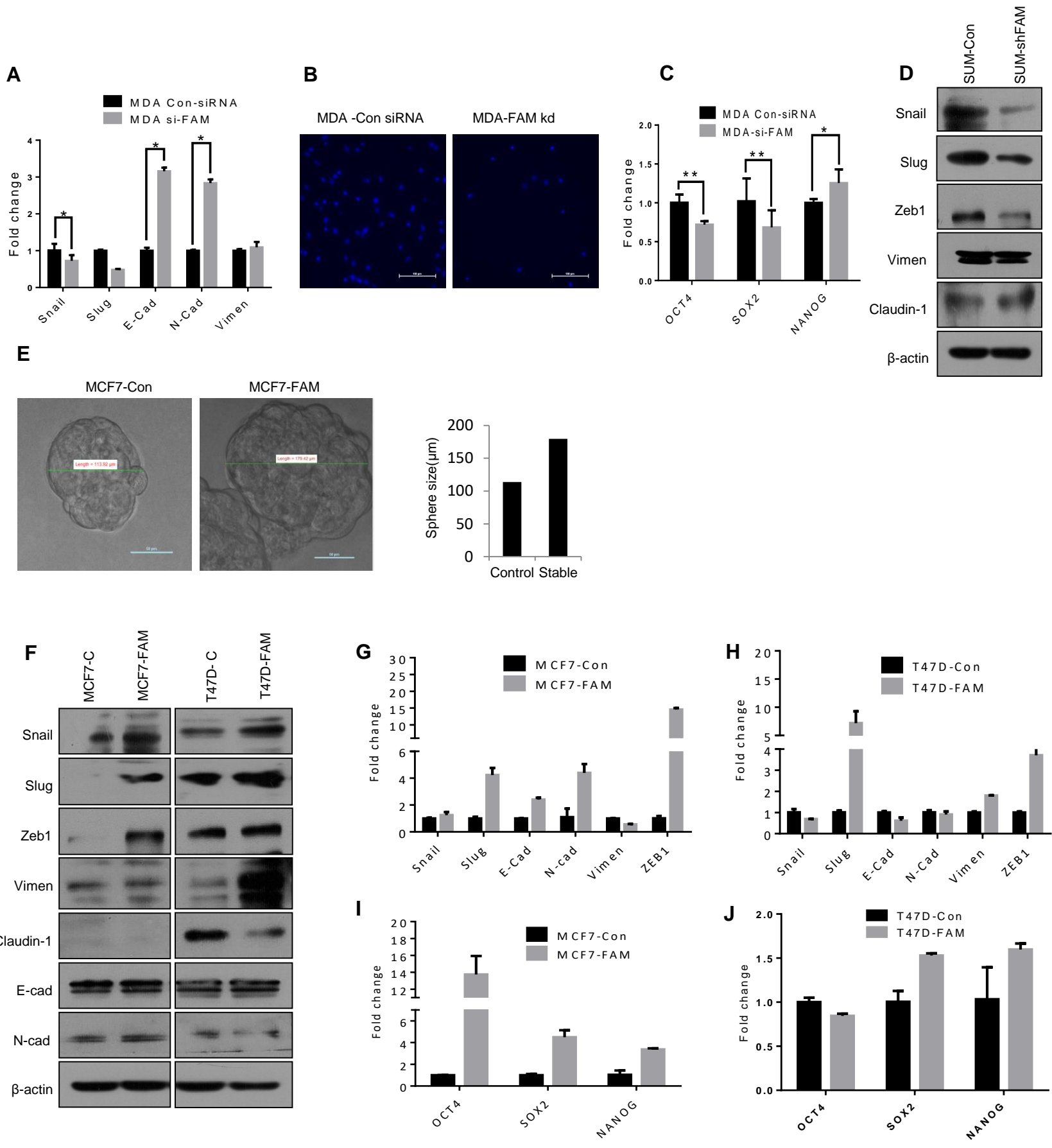
PGR: 4%

ESR1: 2.8%

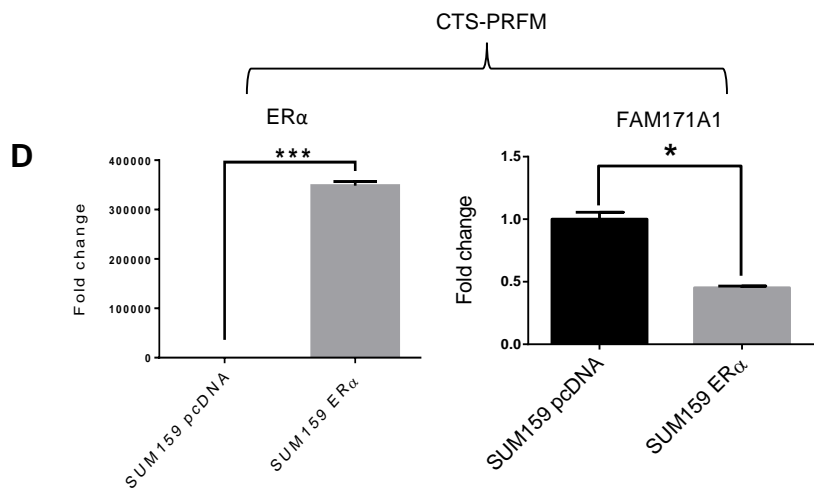
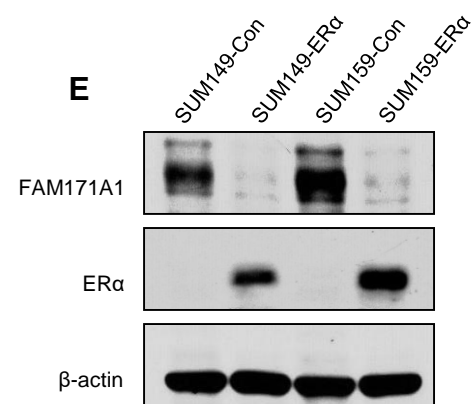
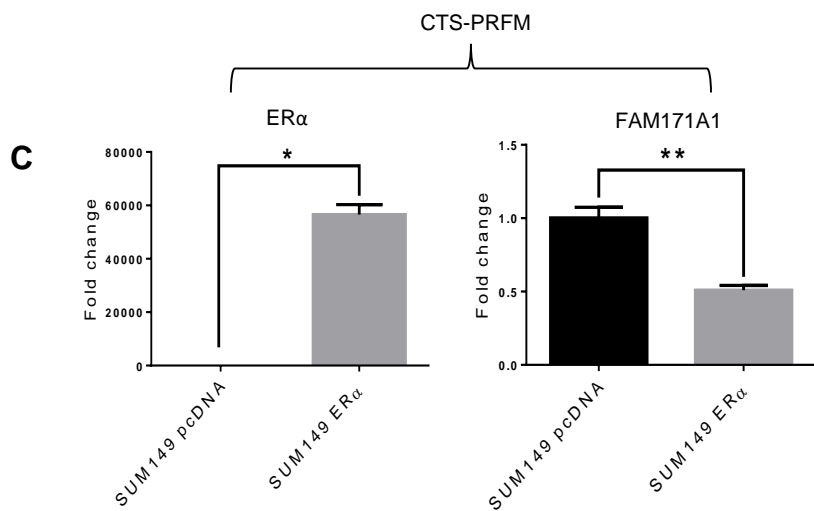
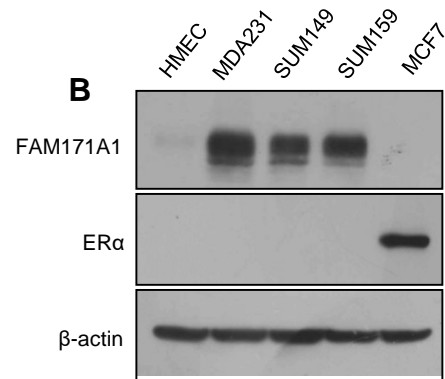
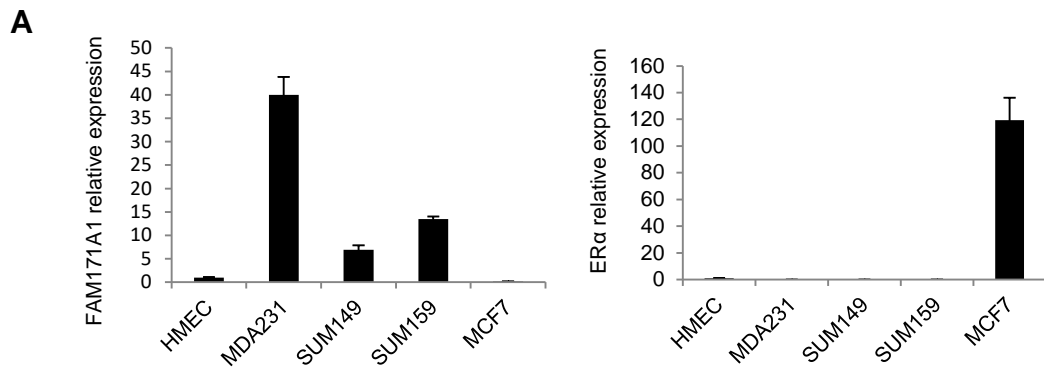
FAM171A1: 4%

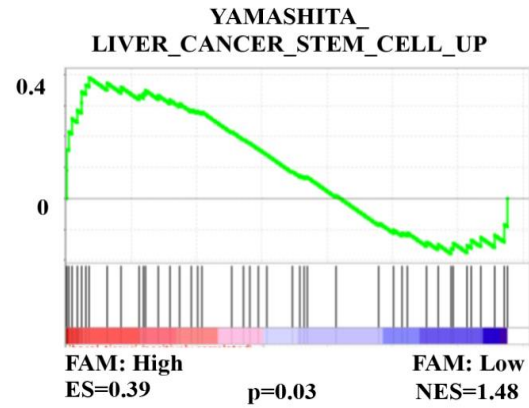
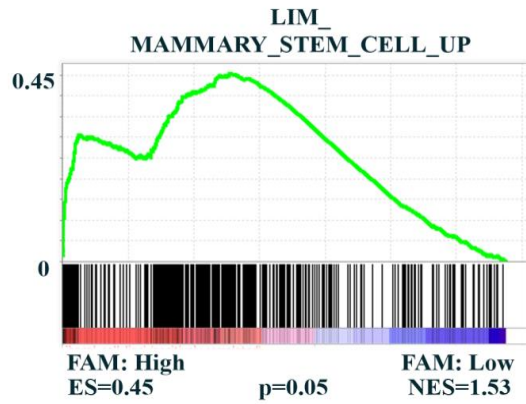
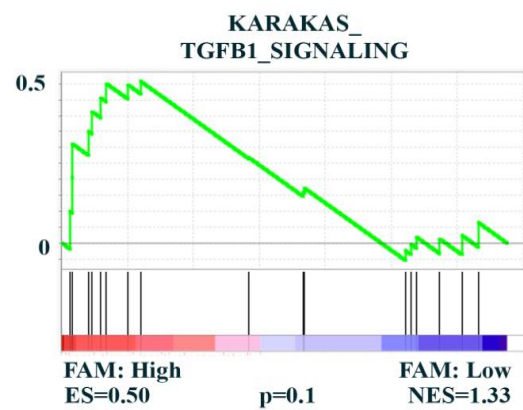
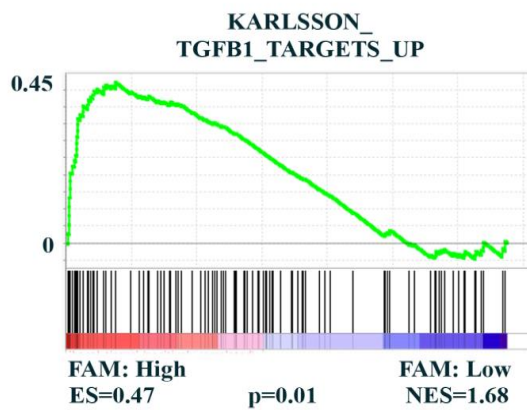
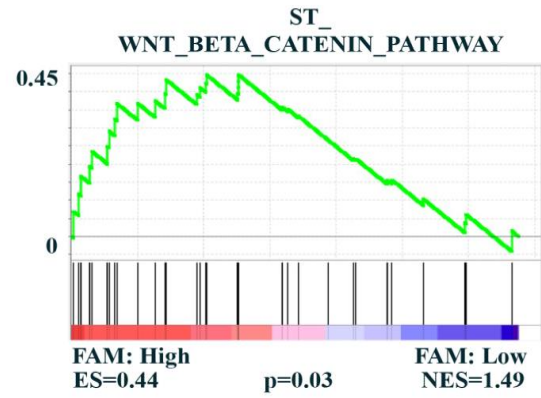
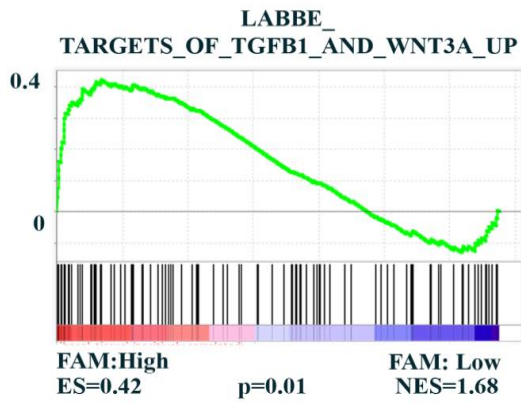
**C**Breast Invasive Carcinoma, TCGA  
Pan Atlas; n=1084**D**

Supplementary Figure 2



Supplementary Figure 3



**A****B**

## SUPPLEMENTARY INFORMATION

**Figure S1:** (A) Expression of FAM171A1 mRNA in TNBC and non-TNBC cell lines and tumors from GSE36693 dataset. (B) Effect of tunicamycin, a glycosylase inhibitor, on the electrophoretic mobility of FAM171A1. (C) Kaplan-Meier survival curve analyses of FAM171A1 expression in breast cancer patients in van't Veer (n=295) and BRCA-TCGA (n=962) datasets; data was stratified based on high (red) and low (green) FAM171A1 expression; log-rank test. (D) Immunoblot result showing silencing of FAM171A1 to see the effect on ER $\alpha$  in MDA-MB-231 cells. (E, F) qRT-PCR analysis of the effect of overexpression of ER $\alpha$  on FAM171A1 in MDA-MB-231 cells cultured in DMEM containing FBS (FBS-DMEM) as well as in phenol red free DMEM containing CTS (CTS-PRFM).

**Figure S2:** (A) Expression heat map of FAM171A1, ESR1 and PGR in NCI-60 Cell lines (NCI, Cancer Res. 2012) (n=60) and Cancer Cell Line Encyclopedia (Novartis/Broad, Nature 2012) (n=1020). (B) Heat map of FAM171A1, ESR1 and PGR in TCGA ; Breast Invasive Carcinoma TCGA Provisional (n=1105); Thyroid Carcinoma TCGA, Provisional (n=516); and Pancreatic Adenocarcinoma TCGA Provisional (n=186). (C) Scatter plot analysis of PGR and FAM171A1 mRNA expression in Breast Invasive Carcinoma dataset, TCGA Pan Atlas (n=1084) from cBioPortal; Pearson Correlation: -0.220; Spearman Correlation: -0.372. (D) Boxplots showing the mRNA expression of FAM171A1 in three Oncomine datasets stratified based on PGR-positive and negative status, TCGA (n=593), Curtis (n=2136), and Hatzis (n=508).

**Figure S3:** (A) qRT-PCR analysis of the MET markers in MDA-MB-231 cells upon FAM171A1 silencing. (B) Immunofluorescence of Hoest dye stained nuclei in MDA-MB-231 cells upon FAM171A1 silencing. Scale bar: 100 $\mu$ m. (C). qRT-PCR analysis of the stem cell markers in MDA-MB-231 cells upon FAM171A1 silencing. (D) Western blot analysis of EMT markers in SUM149C and SUM149 sh-FAM171A1 stable clone. (E) Representative image of a

single sphere generated from MCF-7 cells stable clones expressing FAM171A1 as compared to MCF-7 vector control. Control MCF-7/pcDNA Sphere size=113.92 $\mu$ m; MCF-7/FAM171A1 stable clone Sphere size=179.42 $\mu$ m. Scale bar: 50 $\mu$ m, quantitation on the right side. **(F)** Western blot analysis of EMT markers in MCF-7/FAM171A1 and T47D/FAM171A1 stable clones and their respective controls, stable clones no. 2 were used each for MCF7 and T47D. **(G, H)** qRT-PCR analysis of EMT markers in MCF-7/FAM171A1 and T47D/FAM171A1 and respective control cells. **(I, J)** qRT-PCR analysis of the stem cell markers in MCF-7 cells and T47D cells upon FAM171A1 overexpression.

**Figure S4:** **(A)** qRT-PCR analysis of the FAM171A1 and ER $\alpha$  in normal human mammary epithelial (HMEC) cells when compared to MDA-MB-231, SUM149 and SUM159 (positive controls for FAM171A1 whereas negative controls for ER $\alpha$ ) and MCF-7 (positive control for ER $\alpha$  whereas negative control for FAM171A1). **(B)** Western blot analysis showing the expression of FAM171A1 and ER $\alpha$  in HMEC cell line compared to TNBC and non-TNBC cell lines. **(C, D)** qRT-PCR analysis of the effect of overexpression of ER $\alpha$  on FAM171A1 in SUM149 and SUM159 cells cultured in CTS containing phenol-red free DMEM (CTS-PRFM). **(E)** Western blot analysis showing the effect of ectopic overexpression of ER $\alpha$  on FAM171A1 in SUM149 and SUM159 cells cultured in CTS containing phenol-red free DMEM (CTS-PRFM).

**Figure S5:** High expression of FAM171A1 is associated with activated Cancer Stem Cell (CSCs) gene signatures and associated TGF- $\beta$ /Smad and Wnt/ $\beta$ -catenin signalling genes. **(A)** Gene set enrichment analysis (GSEA) showing positive correlation between high FAM171A1 expression and stem cell gene signatures (LIM\_MAMMARY\_STEM\_CELL\_UP; YAMASHITA\_LIVER\_CANCER\_STEM\_CELL\_UP) in published breast cancer dataset GSE36693. **(B)** Gene set enrichment analysis (GSEA) plot showing the positive correlations between high expression of FAM171A1 and CSCs associated pathways- Wnt/ $\beta$ -catenin and TGF- $\beta$ /Smad pathway gene signatures (KARAKAS\_TGFB1\_SIGNALING; KARLSSON\_TGFB1\_TARGETS\_UP; LABBE\_TARGETS\_OF\_TGFB1\_AND\_WNT3A\_UP; ST\_WNT\_BETA\_CATENIN\_PATHWAY) in published GSE36693 data set.

### **Supplementary experimental procedures**

**Tunicamycin assay:** MDA-MB-231 cells were seeded in 6-well plates and grown until about 70% confluency in culture medium containing 10% FBS. Cells were treated with 10 nM tunicamycin for 2 hrs, and cell lysates were resolved onto an 8% SDS-PAGE gels.