

# miR-489 confines uncontrolled estrogen signaling through a negative feedback mechanism and regulates tamoxifen resistance in breast cancer

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## Research article

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## Abstract

**Background** Approximately 75% of diagnosed breast cancer tumors are Estrogen receptor (ER) positive tumors and are associated with better prognosis due to their response to hormonal therapies. However, around 40% of patients relapse after hormonal therapies. In the current study, we aimed to evaluate miR-489 as a novel molecular target to combat tamoxifen resistance.

**Methods** Genomic analysis of gene expression profiles in primary breast cancers and tamoxifen resistant cell lines unveiled the potential role of miR-489 in regulation of estrogen signaling and development of tamoxifen resistance. We manipulated miR-489 expression in breast cancer cell lines by transient transfection of miR-489 mimic or establishment of knockout cell lines using the CRISPR/Cas9 system to study the reciprocal regulation of miR-489 and estrogen/ER signaling pathways. Cell proliferation, tumor sphere formation assay and flow cytometry analysis were conducted to investigate the role of miR-489 on estrogen-induced cell proliferation, cancer stem cells expansion and development of tamoxifen resistance.

**Results** miR-489 expression was significantly downregulated in tamoxifen-resistant cell lines. Low levels of miR-489 were associated with poor clinical outcomes in patients with hormone treatment. *In vitro* analysis showed that loss of miR-489 expression promoted tamoxifen resistance while overexpression of miR-489 in tamoxifen-resistant cells restored tamoxifen sensitivity. Mechanistically, we found that miR-489 is an estrogen regulated miRNA that negatively regulated estrogen receptor signaling by using at least the following two mechanisms: i) modulation of ER phosphorylation status by inhibiting MAPK and AKT kinase activities; ii) regulation of nucleus to cytosol translocation of estrogen receptor  $\alpha$  (ER $\alpha$ ) by decreasing p38 expression and consequently ER phosphorylation. In addition, miR-489 could break the positive feed-forward loop between estrogen-ER $\alpha$  axis and p38 MAPK in breast cancer cells which was necessary for its function as transcription factor.

**Conclusion** Our study unveiled the underlying molecular mechanism by which miR-489 regulates estrogen signaling pathway through a negative feedback loop and uncovered its role in the development of and overcoming tamoxifen resistance in breast cancers.

## Introduction

Oncogenic activation of the estrogen receptor (ER) signaling pathway occurs in over 70% of breast cancers(1). Although, this subtype of breast cancer has best prognosis due to targeted endocrine therapies, most patients with advanced disease eventually develop resistance to these endocrine therapies, and even for patients treated in the adjuvant setting, a considerable risk of relapse persists indefinitely(2). Furthermore, approximate 50% of patients with locally advanced or metastatic ER + breast cancer do not respond to first-line endocrine treatment(3). Besides, most patients who initially respond to the therapy eventually develop acquired resistance(4). Despite significant research efforts and discoveries made in recent years, the exact reasons for endocrine therapy failure in patients with ER +

breast cancer remain largely unknown. Published studies have implicated the mutations in the ESR1 gene; epigenetic silencing of ESR1, activated growth factor receptor signaling, including EGFR/HER2 pathway, PI3K-AKT pathway and MAPK pathway and overexpression of co-activators such as NCOA3 and FOXA1, as important mechanisms of *de novo* or acquired resistance (5, 6). However, the only mechanisms of antiestrogen resistance that are supported in the clinic are HER2 amplification, mutations in the ligand-binding domain (LBD) of ESR and dysregulation of the CDK4/6 pathway(7–9). Discovery of novel agents that simultaneously modulates these pathways may help development of improved targeted combination strategies to combat endocrine resistance.

Dysregulation of miRNAs has been increasingly recognized as a critical contributor to cancer development, progression and therapy resistance. Many miRNAs have been reported to contribute to endocrine resistance. Downregulation of miR-489 has been observed in tamoxifen-resistant breast cancer but its functional involvement remains unexplored(10, 11). In this study, we systematically investigated the functional roles of miR-489 in ER<sup>+</sup> breast cancer. We demonstrated that downregulated miR-489 expression significantly stimulates estrogen dependent and independent growth and also promoted tamoxifen resistance through hyper activation of E2-ER $\alpha$ , HER2-PI3K-AKT and ERK signaling pathways. Thus, patients with ER + breast cancer together with low miR-489 expression may be intrinsically resistant to endocrine therapies.

## Materials And Methods

The detailed procedures of cell culture, antibody and immunoblot, flow cytometry, qRT-PCR, luciferase reporter assay, microarray, tumorsphere formation assay, colony formation assay, CRISPR/Cas9-mediated genomic editing, and immunochemical staining, are described in Supplemental Experimental Procedures (Additional file 1).

### Cell Lines And Culture

MCF7, T47D and HCC1954 were purchased from ATCC in 2013. MDA-MB231, MDA-MB-468, MDA-MB361, Hs578T, ZR-75-1 and BT474 cells were obtained from Dr. Saraswati Sukuma (Johns Hopkins University), in 2008. MCF7 vector and MCF7 HER2 cell lines were kindly provided by Dr. Rachel Schiff (Baylor College of Medicine). MCF7-WT and tamoxifen resistant MCF7-TAMR cells were established as previously reported (12). Cells were grown under standard conditions(13–15).

### Tamoxifen-sensitization Assays

Tamoxifen resistant cell lines were treated with control siRNA or miR-489 mimic with or without tamoxifen at indicated concentrations for 72 hours. Similarly, tamoxifen sensitive cell lines were treated with control siRNA or miR-489 inhibitor with or without tamoxifen at indicated concentrations for 72 hours. MTT based cell viability assay and colony formation assay were carried out to examine tamoxifen sensitization.

## **Generation Of Knock Out Cells**

CRISPR/Cas9 gene editing method was used to generate miR-489 knock out cell line as shown in our previous publication(15). Two guide RNAs flanking pre-miR-489 were designed using guide RNA designing tool ([crispr.mit.edu](http://crispr.mit.edu)). G-block guide RNAs were purchased from IDT technologies; Cas9-GFP plasmid was obtained from Dr. Philip Buckhaults. Gblock guide RNA and Cas9-GFP were co-transfected in T47D cells using T47D avalanche transfection reagent (ez biosystem). 72 hours post transfection, GFP positive cells were sorted using the Fluorescent activated cell sorter. Sorted cells were then diluted to single cell and seeded in 96-well plate. Rest of the cells were seeded on 10-cm dish. Colonies grown from individual clones were then expanded and screened for miR-489 deletion using genotyping.

## **Statistical Analyses**

Statistical analyses were conducted with R and GraphPad software packages. A Student t test or ANOVA test was used for comparison of quantitative data. Gene expression profiles of miR-489, its host gene calcitonin receptor, estrogen receptor alpha and progesterone receptor were evaluated using a published data set containing 1302 breast cancer patients (38, 39) that were stratified by the mean value of miR-489 expression levels. The linear correlations between miR-489 and CALCR, ER- $\alpha$  and PGR genes expression in primary breast cancer tissues were evaluated with Pearson correlation coefficient analysis. Values of  $p < 0.05$  were considered statistically significant.

miR-489 signature was generated by using the most up or downregulated genes (-2 < FC < 2, n = 304) upon miR-489 overexpression. Expression of the signature genes in patients was converted into z-scores. To calculate a miR-489 signature score for each patient, sum of z-scores of downregulated genes was subtracted from sum of z-scores of up regulated genes (1). PI3K\_ERBB2, p38/MAPK and estradiol responsive gene signatures (<https://reactome.org>) in patients were generated by summing up the z-scores of the signature genes for each patient (1). Significance for the survival analysis was calculated following a Log-Rank test.

## **Results**

### **miR-489 expression is lost in tamoxifen resistance, predicts breast cancer aggressiveness and is regulated by estrogen/ER $\alpha$ axis**

To specifically identify miRNAs that are clinically relevant in endocrine resistance, we analyzed miRNA screening datasets of endocrine resistant models previously published by three independent laboratories including our own (Fig. 1A)(11, 12, 16). Since, all three models are derived through completely different processes, they represent independent tamoxifen resistant models with different resistant mechanisms. MCF7-HER2 cell line represents *de novo* resistance while MCF7-TAM and MCF7:2A represent acquired resistance. miRNAs that are dysregulated in all three cell lines suggest their potential roles in regulation of multiple mechanisms involved in tamoxifen resistance, which therefore may be more clinically relevant with promising therapeutic promise to address tamoxifen resistance. Although, many miRNAs were

dysregulated in these cell lines we only found few miRNAs that were aberrantly expressed in all three cell lines (Fig. 1B). Out of these miRNAs, miR-135b, miR-33b and miR-505 showed opposite expression pattern among these cell lines. miR-378a-3p and miR-218 were significantly upregulated in all three cell lines while miR-342-5p and miR-489 were significantly downregulated. Intriguingly, miR-489 was one of the top downregulated miRNAs in all three datasets, suggesting its role in tamoxifen resistance. We validated these results using qRT-PCR and indeed found significant downregulation of miR-489 in both resistant cell lines (Fig. 1C). To determine whether the expression of miR-489 was associated with endocrine resistance in patient cohorts, we examined miR-489 expression in hormone-therapy treated ER<sup>+</sup> breast cancer patients. We observed a statistically significant association between lower miR-489 expression and poorer overall survival in these patients. In fact, miR-489 expression remained as an independent prognostic factor in hormone-therapy treated breast cancer patients obtained from two independent datasets GSE19783 and METBRIC (Fig. 1D). These results suggest that loss of miR-489 may promote tamoxifen resistance.

Previously we have observed that average expression of miR-489 was notably higher in luminal cells compared to basal cells (13, 16). Furthermore, analysis of miR-489 expression on 13 different breast cancer cell lines also demonstrated that it was expressed at a higher level in hormone positive luminal breast cancer cell lines (Fig. 1E) compared to the cells lines from other subtypes. Similarly, analysis of primary breast tumors revealed that miR-489 along with its host gene CALCR was positively correlated with expression of estrogen receptor and its responsive genes such as PGR and TFF1 (Fig. 1F), suggesting miR-489 and its host gene CALCR expression may be regulated by estrogen signaling. To examine this hypothesis, we stimulated three ER<sup>+</sup> breast cancer cell lines (T47D, MCF7 and BT474) with estrogen or ethanol for indicated time periods and measured the expression of miR-489 and its host gene CALCR. We found significant upregulation of miR-489 and CALCR in all three cell lines treated with estrogen (Fig. 1G). Estrogen regulation of miR-489 was further investigated in complete media or estrogen deprived media. As expected, depletion of estrogen drastically reduced the expression of miR-489 and CALCR like other classical ER target genes such as trefoil factor 1 (TFF1), progesterone receptor (PGR), and C-X-C motif chemokine ligand 12 (CXCL12) (Fig. 1H). In summary, these data strongly suggest that miR-489 is an estrogen regulated miRNA in breast cancer and may play a regulatory role in tamoxifen resistance.

### **miR-489 restoration overcomes acquired and *de novo* tamoxifen resistance.**

Since miR-489 was lost in tamoxifen resistant tumors and cell lines, we hypothesized that restoration of miR-489 would sensitize the resistant cell lines. Our previous studies have shown that overexpression of miR-489 inhibited breast cancer cells proliferation(13, 16). We first tested whether Tamoxifen-resistant cells were still sensitive to miR-489 mimics. Notably, we observed that both acquired and de novo resistant cell lines were equally sensitive to miR-489 mimics as their sensitive counterpart as opposed to their different sensitivities to tamoxifen (Fig. 2A, 2B). These results further bolstered a possibility that miR-489 might target pathways involved in resistance and could potentially sensitize these resistant cell lines to tamoxifen. Indeed, forced expression of miR-489 significantly sensitized both resistant cell lines

to tamoxifen. Tamoxifen failed to cause any significant death in both resistant cell lines at 5 µM while combination with miR-489 led to around 40% death in MCF7-TAM (Fig. 2C) and 30% death in MCF7-HER2 cells (Fig. 2D). To directly assess the role of miR-489 in tamoxifen resistance, we inhibited endogenous miR-489 in tamoxifen sensitive cells MCF7-Vec and MCF7-WT cells. As expected, inhibition of miR-489 significantly increased tamoxifen resistance in both sensitive cell lines. At the highest concentration tested, inhibition of miR-489 increased the survival by 25% and 40% in sensitive counterpart of MCF7-Vec and MCF7-WT, respectively (Fig. 2E, 2F). Similarly, colony formation assays also revealed that forced expression of miR-489 significantly reduced the survival and colony forming ability in resistant cell lines while inhibition of endogenous miR-489 enhanced the survival of sensitive counterpart and promoted tamoxifen resistance. (Fig. 2G, 2H).

### **miR-489 acts as an endogenous negative feedback regulator to balance estrogen signaling**

To elucidate the underlying pathways targeted by miR-489 to induced tamoxifen sensitization, we re-examined the gene expression profiles of T47D cells transfected with miR-489 mimics and scrambled RNA(13). Interestingly, gene expression analysis revealed enrichment of multiple pathways involved in estrogen signaling and tamoxifen resistance (Fig. 3A, 3B). We observed enrichment of ErBB signaling pathway and several stress associated pathways including endoplasmic reticulum (ER)-stress and lysosomal pathways. All of these pathways have been previously reported to be involved in tamoxifen resistance (9, 17–21) (4). Meanwhile, these results are also in accordance with our previous studies showing role of miR-489 in HER2 singling and metabolic stress and autophagy regulation (13, 14, 16). Interestingly, we noticed significant enrichment of estrogen dependent gene expression and ESR-mediated signaling. Upon further analysis, we found substantial downregulation of estrogen responsive genes (Fig. 3C). This data suggested that estrogen regulated miR-489 might function as a negative regulator of estrogen signaling. To determine the clinical significance of these data, we applied miR-489 gene expression signature to a gene expression profiling obtained from patient datasets. Consistent with our microarray results, we found strong inverse correlation between estrogen responsive gene signature and miR-489 signature ( $p$  value < 0.0001) (Fig. 3D) and between PI3K-ERBB2 signature and miR-489 signature ( $p$  value < 0.0001) (Fig. 3E). In addition, we also noticed that low miR-489 expression in ER + breast cancer was indicative of worse overall survival (Fig. 3F), further supporting essential tumor suppressive role of miR-489 in ER + breast cancer.

To examine how miR-489 negatively regulated estrogen signaling, we measured transcriptional activity of estrogen receptor by performing Luciferase reporter assay in T47D-ERE-Luc reporter cell line. We observed the inhibition of estrogen receptor transcriptional activity upon miR-489 overexpression and increased activity upon inhibition of endogenous miR-489 (Fig. 3G). We then validated the microarray results by performing qRT-PCR analysis on ER + and ER- cell lines. As expected, miR-489 caused down regulation of estrogen responsive genes only in ER + cell lines including T47D, MCF7 and BT474 cells but did not affect or in some instances increased the expression of these genes in ER- cell lines such as AU565 and HCT116 cells (Fig. 3H-I). These results suggest that miR-489 regulates the expression of these ERα-downstream genes by inhibiting estrogen signaling.

## **miR-489 inhibits ER-induced cell proliferation and cancer stem cells expansion**

Our previous studies have shown that miR-489 inhibits proliferation of all breast cancer cell lines including ER $\alpha$  + cell lines (13, 16). However, it remains unknown whether miR489-mediated growth inhibition in ER + breast cancer cells is due to its effects on ER signaling. To this end, we examined the effects of miR-489 on estrogen-induced cell proliferation in MCF7 and T47D cells. Both cell lines showed poor proliferation when treated with vehicle (Ethanol) while estrogen treatment enhanced proliferation by more than 2-fold and 4-fold in MCF7 and T47D cell lines respectively. Restoration of miR-489 completely abolished estrogen induced proliferation in both cell lines while inhibition of endogenous miR-489 further increased estrogen induced proliferation by more than 2 fold in MCF7 and more than 3 fold in T47D cell lines (Fig. 4A-B). Estrogen treatment has been previously shown to enhance population of stem-like in ER $\alpha$  cell lines(22). These so-called cancer stem cells have been thought to be the responsible population for tumor relapse(23). We hypothesized that miR-489 may inhibit estrogen induced population of cancer stem like cells by its effect on estrogen signaling. Therefore, we studied the effect of miR-489 on estrogen induced cancer stem cell population using colony formation assay, mammosphere assay and flow cytometry. Consistent with previous results, estrogen treatment significantly increased colony formation ability of both MCF7 and T47D cells. Forced expression of miR-489 almost completely inhibited estrogen induced colony formation of both cells. Interestingly, inhibition of endogenous miR-489 drastically enhanced estrogen mediated colony formation (Fig. 4C). We then examined the effect of miR-489 on cancer stem like cells by measuring CD44 $^{+}$ CD24 $^{-}$  population using flow cytometry and by measuring mammosphere forming efficiency (MFE) analysis. Consistent with previous results, estrogen increased cancer stem like cell population (CD44 $^{+}$ CD24 $^{-}$ ) by 3-fold in MCF7 cells and 10-fold in T47D cells (Fig. 4D). As observed in clonogenic assay, inhibition of endogenous miR-489 increased cancer stem like cell population by more than 3-fold in MCF7 cells and by more than 11-fold in T47D cells (Fig. 4D). Similarly, we also observed increased MFE upon estrogen treatment and miR-489 inhibition not only increased MFE but also increased the mammosphere size. As observed in colony formation assay, forced expression of miR-489 almost completely prevented mammosphere formation (Fig. 4E). Together, these results suggest that estrogen regulated miR-489 as a feedback regulator to confine estrogen induced tumor cell growth and inhibit population of cancer stem like cells.

## **miR-489 inhibits estrogen induced signaling by inhibiting p38 MAPK, PI3K-AKT and MAPK-ERK pathways**

We further seek to elucidate the molecular mechanism responsible for miR-489 mediated inhibition of estrogen-ER $\alpha$  axis. Multiple mechanisms have been identified for regulation of estrogen-ER $\alpha$  mediated gene expression(24, 25). Direct inhibition of ER $\alpha$  or its co-factors, inhibition of kinases that activates ER $\alpha$ , and inhibition of estrogen induced nuclear localization of ER $\alpha$  have been previously reported to regulate estrogen induced gene transcription (26). We first examined if miR-489 exerted its effects by affecting localization of estrogen receptor. Interestingly, forced expression of miR-489 strongly promoted translocalization of estrogen receptor from nucleus to cytoplasm in MCF7 and T47D cell lines (Fig. 5A-B). In contrast, inhibition of endogenous miR-489 resulted in increased nuclear localization (Fig. 5A-B). Searching through factors which have been reported to regulate localization of estrogen receptor, we

found that one of these factors, p38 MAPK, is a potential miR-489 target (26) (Fig. 5C). Interestingly, forced expression of miR-489 significantly downregulated total p38 MAPK (Fig. 5D). We then performed 3'UTR assay to examine if p38 MAPK is a direct target of miR-489. Forced expression of miR-489 significantly reduced luciferase activity of wild type construct while it did not affect luciferase activity of construct with mutant miR-489 binding site (Fig. 5E). This result confirms that p38 MAPK is a direct target of miR-489. Next, we examined the effect of p38 MAPK inhibitor SB203580 can phenocopy the effect of miR-489 on estrogen receptor localization. We transfected control siRNA or miR-489 mimic for 72hrs or treated with DMSO or 10 µM SB203580 for 24hrs in hormone starved cells followed by treatment with estrogen to examine estrogen induced nuclear localization of estrogen receptor. Indeed, cells treated with p38 MAPK inhibitor phenocopied the effect of miR-489 on ER localization in both cell line (Fig. 5F). These results indicate miR-489 affects nuclear translocation of ER $\alpha$  by at least partially by downregulating p38 MAPK. Considering that phosphorylation of ER $\alpha$  protein is also a critical step for its transcription activity, we investigated changes in their expression upon modulation of miR-489 expression. Western blot analysis of total ER $\alpha$  protein and its phosphorylated forms suggest that forced expression of miR-489 reduced the phosphorylation of ER $\alpha$  at both S118 and S167 sites (Fig. 5G). This data suggests that miR-489 may further regulate ligand dependent activation of ER $\alpha$  through inhibition of kinases that phosphorylates ER $\alpha$  at residues S118 and S167 residue. MAPK and AKT have been known to regulate ER $\alpha$  phosphorylation at S118 and S167 respectively. Indeed, miR-489 restoration significantly reduced the activated form of these kinases while its inhibition enhanced their activation (Fig. 5G).

All three kinase pathways have been shown to prompt the tamoxifen resistance. We examined the effect of miR-489 modulation in MCF7-HER2 and its isogenic cell line MCF7-Vec on estrogen-independent growth. We found that miR-489 inhibition alone was sufficient to promote estrogen-independent growth while miR-489 restoration prevented estrogen independent growth in MCF7-HER2 cell line (Fig. S1A, additional file 2). Western blot analysis confirmed the upregulation of HER2, pAKT and pERK in MCF7-HER2 cell line compared to MCF7-Vec. Consistent with previous results, MCF7-HER2 cell line showed increased estrogen independent phosphorylation of ER $\alpha$  at S118 and S167 residue and restoration of miR-489 abolished this hyperactivation and ER $\alpha$  phosphorylation (Fig. S2B, additional file 2). In summary, these results suggest that miR-489 regulates tamoxifen resistance by targeting multiple kinase signaling pathways and therefore could potentially be used as a therapeutic sensitizer to treat resistant patients.

### **p38 MAPK, PI3K-Akt and MAPK inhibitors phenocopy the effect of miR-489 in ER+ breast cancer cell lines**

Next, we examined whether inhibition of all three responsible kinase signaling pathways phenocopies the effect of miR-489. We inspected estrogen induced transcription and proliferation after inhibition of all three kinases. To a variable extent, we observed significant inhibition of transcriptional activity of ER $\alpha$  using ERE-reporter cell line (Fig. 6A). qRT-PCR analysis also showed downregulation of estrogen responsive genes (Fig. 6B). Consistently, these data were also supported by diminished estrogen induced proliferation upon inhibition of all three kinases (Fig. 6C, 6D). However, downregulation of endogenous miR-489 was partially able to rescue cells from the growth inhibitory effect of kinase inhibitors (Fig. 6E).

This data suggests that miR-489 may exert its inhibitory effect on estrogen signaling partially, if not completely, by simultaneously inhibiting p38 MAPK, AKT and ERK signaling pathways.

Intriguingly, we observed that p38 MAPK inhibition had significant inhibitory effect only in the presence of estrogen and did not affect estrogen independent growth (Fig. 6F) indicating p38 MAPK activation may be estrogen dependent. Therefore, we tested if estrogen activates p38 MAPK and then mediates nuclear translocation. Since estrogen induced ER $\alpha$  nuclear translocation occurs within 5–30 minutes(27), we performed time course of estrogen treatment on MCF7 and T47D cell lines. We observed a sharp increase in phospho-p38 MAPK and its downstream target phospho-ATF2 upon estrogen treatment in both cell lines (Fig. 6G). These results are consistent with previous studies that showed estrogen mediated activation of p38 MAPK in various tissues(26) (28). This provided an evidence of positive feedback loop between E2-ER $\alpha$  axis and p38 MAPK in mammary cells. Binding of E2 leads to activation of p38 MAPK and activation of p38 MAPK leads to nuclear translocation of ER $\alpha$  which is necessary for its function as transcription factor (Fig. 6H). This data together with ER $\alpha$  nuclear localization data, demonstrated that estrogen may cause p38 MAPK activation upon binding to ER $\alpha$  and this activated p38 MAPK in turn increases nuclear localization of ER $\alpha$ . Indeed, we observed that increased p38 MAPK phosphorylation starting as early as 5 min of estrogen treatment (Fig. 6G). This mutual activation of E2-ER $\alpha$  and p38 MAPK was previously demonstrated in endometrial cell lines (26). As p38 MAPK activation was estrogen dependent, we therefore suspected p38 MAPK inhibition might have a pronounced effect in pre-menopausal women as compared to post-menopausal women. Indeed, we observed higher p38 MAPK gene signature score in pre-menopausal luminal patients compared to post-menopausal luminal patients (Fig. 6I). Furthermore, luminal pre-menopausal patients with higher tumor grade also showed higher p38 MAPK gene signature (Fig. 6J). Additionally, high p38 MAPK expression in pre-menopausal patients predicted poor survival more significantly compared to post-menopausal patients. Our correlation analysis of miR-489 and p38 MAPK signature showed statistically significant inverse correlation in pre-menopausal patients. However, this correlation was reduced in post-menopausal patients (Fig. 6K). In summary, these results suggest that miR-489 regulates tamoxifen resistance by targeting multiple kinase signaling pathways and therefore could potentially be used as a therapeutic sensitizer to treat resistance patients.

### **miR-489 knock out cells possess increased sensitivity to estrogen induced signaling and proliferation**

To systematically investigate whether loss of miR-489 potentiated the estrogen signaling and estrogen-dependent growth of ER+ breast cancer cells, we utilized CRISPR/ Cas9 gene editing to create a miR-489 knock out cell line (Additional file 2, Fig. S2). We validated these knock out cells using genotyping and sequencing to ensure deletion of miR-489. We characterized these cells using western blot analysis of previously established miR-489 targets. We then carried out functional assays to examine the effect of miR-489 knock out on these cells. As expected, we noticed that these cells exhibited increased growth rate (Fig. 7A, 7B). Consistent with above results, loss of miR-489 showed increased sensitivity to estrogen stimulated growth and colony forming ability (Fig. 7C). We also noticed more than 6-fold increase in estrogen induced cancer stem cell expansion (Fig. 7D, 7E). To confirm loss of miR-489 enhanced estrogen

signaling, we examined gene expression level of estrogen responsive genes and found increased upregulation of these genes upon estrogen stimulation in knock out cells compared to wild type cells (Fig. 7F). Our western blot analysis also showed increased phosphorylation of ER $\alpha$  at Ser 167 and Ser 118 along with increased activity of respective kinases AKT and ERK (Fig. 7G). We also noticed significant increase in total p38 MAPK and observed dramatic increase in nuclear localized estrogen receptor (Fig. 7H). Hyperactivity of all three kinases have been reported to increase estrogen dependent proliferation. To test their contribution in increased estrogen dependent proliferation of knock out cells, we stimulated WT and KO cells with E2 in presence of their inhibitors. Knock out cells demonstrated resistance towards these inhibitors to different extent with almost complete resistance to p38 MAPK and AKT inhibitors (Fig. 7I-J). These knockout cells also showed significant resistance to tamoxifen evidenced by MTT based cell viability assay and colony formation assay (Fig. 7K, 7L). These results provide direct evidence of miR-489 as an auto-regulatory loop of estrogen signaling and in tamoxifen resistance.

## Discussion

Defining the role of the differentially regulated miRNAs in breast cancer and drug-resistant cells could lead to the development of new diagnostic tools and therapeutic approaches. In the present study, we provide new evidence for the role of miR-489 in breast cancer and development of tamoxifen resistance. We demonstrate that expression of miR-miR-489 is induced by estrogen and strongly correlates with cellular ER $\alpha$  status. The induction of miR-489 seems to mainly occur at the transcriptional level because the mRNA levels of its host gene CALCR are increased in several ER + breast cancer cells upon estrogen treatment and correlate with miR-489 expression levels in breast cancers. However, the induction of CALCR gene expression appears more robust than induction of miR-489 in two ER + breast cancer cell lines MCF7 and T47D, indicating additional regulatory mechanism may be involved. Apart from regulating the expression of miRNAs at the transcriptional level, there are evidences to suggest that ER $\alpha$  may be able to regulate microRNA processing and maturation. For example, ER $\alpha$  regulates the processing of the primary transcripts of the two miRNA clusters mir-17–92 and mir-106a-363, and therefore, miRNAs that are processed from the same precursor transcript accumulate to different levels(29). Further studies are warranted to find out the detailed mechanisms of estrogen-regulated miR-489 expression in breast cancer cells.

Our previous studies have demonstrated that miR-489 functions as tumor suppressor microRNA in breast cancer(13, 16). Estrogen exposure is generally associated with increased risk for breast cancer. To better understand the apparent paradox, we further studied the signaling interplay between miR-489 and estrogen. Microarray analysis of the gene expression profiles of miR-489 overexpressing T47D cells indicated enriched ER-regulated signaling pathways. Consistently, *in silico* data analysis of gene expression in large cohorts of breast cancer samples confirmed the inverse correlation between miR-489 signature and estrogen responsive genes. Molecular experiments validated that overexpression of miR-489 suppressed ER $\alpha$  signaling pathways. These results led us to hypothesize that induction of miR-489 by estrogen may serve as a fail-safe mechanism to prevent over activation of ER $\alpha$  downstream signaling

pathways in response to high levels of estrogen. The corollary of this hypothesis is that loss of miR-489 will promote estrogen-induced tumorigenesis or aggressiveness of cancer cells. Indeed, we observed that inhibition of endogenous miR-489 robustly enhanced estrogen-induced cell proliferation and expansion of cancer stem-like cell populations, in contrast to the relatively mild effects of overexpression of miR-489 in breast cancer cells.

Previous studies have described a negative feedback loop between ER $\alpha$  and several miRNAs that are induced upon estrogenic stimulation and that downregulate ER $\alpha$  (29, 30). For example, estrogen induced expression of miR-1792 family of microRNAs which can restrict estrogen actions in a feedback through different ways. While several microRNAs like miR-18a, miR-19b, and miR-20b can directly downregulate ER $\alpha$  expression and other microRNAs such as miR-20a, miR-17–5p, miR-106a, and miR-20b downregulate expression of ER $\alpha$  transcriptional co-factor AIB1(29). ER $\alpha$  is not a predicted target of miR-489. We did not observe any changes in its expression levels after manipulations of miR489 as expected. However, we found that overexpression of miR-489 drastically suppressed ER $\alpha$  phosphorylation at ser118 and Ser167. Given that AKT and ERK kinases are known to phosphorylate ER $\alpha$  at Ser118 and Ser167 respectively and enhances its transcriptional activity (9, 31–35), one mechanism of miR-489 mediated restriction of estrogen activities is through inhibition of MAPK and AKT activities. In addition, previous studies have demonstrated that p38 kinase can phosphorylate ER $\alpha$  and affect its cellular localization(18, 28, 36). p38 is one of the predicted target genes of miR-489 which is validated by transient transfection of p38 promoter reporter assay. Consistently, overexpression of miR-489 resulted in translocation of ER $\alpha$  from nuclear to cytoplasm, adding another mechanism of miR-489 restriction of estrogen action.

Interestingly, we also observed a positive feedback loop between E2-ER $\alpha$  signaling and p38 MAPK. Estrogen activates p38 MAPK within few minutes upon binding to its receptor ER $\alpha$ . This activated p38 MAPK leads to nuclear translocation of ER $\alpha$  which is essential for its transcriptional activity. Similar observations have also been reported for ERK and AKT in regard to estrogen signaling (37, 38). Like p38 MAPK, estrogen also activates AKT and ERK(39). Activated ERK and AKT then activate ER $\alpha$  by phosphorylating ER $\alpha$  at Ser1018 and Ser167, respectively (40). miR-489 regulates this positive feedback loop by inhibiting p38 MAPK, AKT and ERK activity.

We posit that the physical function of the negative feedback loop between ER $\alpha$  and the miR-489 would be to create a fail-safe mechanism to avoid high ER $\alpha$  activity. High ER $\alpha$  activity is potentially dangerous for the cell and is a major risk factor for breast cancer. In addition, miR-489 could serve as a potential prognostic marker in ER + breast cancer where ER + patients with low miR-489 may possess hyper activation of E2-ER $\alpha$  signaling and may potentially represent aggressive cancers. Indeed, clinical analysis of ER + breast cancer patients suggest that patients with low miR-489 expression have worse survival and are more likely to develop drug resistance. Despite a strong correlation between expression of ER $\alpha$  and a favorable response to endocrine therapy, 40–50% of patients with ER $\alpha$  + breast cancer develop resistance or exhibit de novo resistance, and patients with luminal B and ER $\alpha$ +/PGR – breast cancer exhibit a poor response to tamoxifen(41). The underlying mechanism appears to be deregulation in estrogen receptor signaling pathways due to crosstalk of growth factor signaling pathways such as PI3K/AKT/mTOR and

epidermal growth factor receptor (EGFR) crosstalk with ER $\alpha$  signaling to enhance pro-proliferative ER $\alpha$  regulated gene expression and suppression of PGR gene expression(9, 18, 42–44). Our observations here indicate that miR-489 could potentially serve as a useful therapy sensitizer to treat tamoxifen resistance tumors. First, our study along with other reports showed miR-489 is significantly downregulated in tamoxifen resistant cell lines. Intriguingly, it is lost in both acquired and de novo resistant. Second, miR-489 directly inhibits AKT and MAPK pathways which are well established mechanism that promote estrogen independent growth and tamoxifen resistance. Third, miR-489 directly targets HER2 and its downstream molecules including SHP2 and AKT(16). Fourth, p38 MAPK can potentiate the ER in part through increased phosphorylation of ER at Thr311 (26), and enhance ER signaling through coactivator regulation(36). Increased p38 activity has been associated with breast cancer drug resistance and invasion. Our results suggest that miR-489 directly targets p38 to break the positive feedback loop between ER and p38. Furthermore, autophagy and EMT has been reported to promote tamoxifen resistance. MCF7-TAM cells have been reported to undergo EMT and possesses higher basal autophagy(10, 45). Inhibition of both processes have been previously shown to reverse the tamoxifen resistance. Interestingly, miR-489 has previously been reported reverse EMT through inhibition of Smad3 expression which leads to sensitization of doxorubicin(46). Previously, we have reported its role in autophagy and chemo-resistance(13). These data support a general role of miR-489 in modulation of drug resistance.

## Conclusions

In summary, this study revealed a new negative feedback loop between miR-489 and estrogen and demonstrated the potential role of miR-489 in development of ER+ breast cancer and tamoxifen resistance. miR-489 based therapy may be an useful adjuvant therapy not only in tamoxifen resistant patients but also in treatment naïve patients since apart from inhibiting estrogen signaling, it also blocks HER2-PI3K-AKT and MAPK pathways and may potentially reduce emergence of resistance to tamoxifen. These results contribute to the understanding of the complex regulatory pathways regulating ER $\alpha$  activity and are therefore may provide insights to develop novel ER+ breast cancer therapy.

## Abbreviations

**miR-489:** microRNA 489

**miRNA:** microRNA

**ER+:** Estrogen receptor positive

**ER $\alpha$ :** Estrogen receptor  $\alpha$

**ESR1:** Estrogen Receptor 1

**EGFR:** Epidermal growth factor receptor

**HER2:** Human epidermal growth factor receptor 2

**LBD:** Ligand-binding domain

**qRT-PCR:** Quantitative reverse transcription polymerase chain reaction

**siRNA:** Small interfering RNA

**GFP:** Green fluorescent protein

**CALCR:** Calcitonin Receptor

**PGR:** Progesterone Receptor

**ERBB:** Epidermal growth factor

**TFF1:** Trefoil factor 1

**CXCL12:** C-X-C motif chemokine ligand 12

**TAM:** Tamoxifen

**MFE:** Mammosphere forming efficiency

**E2:** Estradiol

**KO:** Knockout

**CRISPR:** Clustered regularly interspaced short palindromic repeats

**Cas9:** CRISPR-associated protein 9

**PBS:** Phosphate-buffered saline

**MAPK:** Mitogen-activated protein kinase

**AKT:** Protein kinase B

**PI3K:** Phosphoinositide 3-kinase

**SHP2:** Protein tyrosine phosphatase

**mTOR:** Mammalian target of rapamycin

**ERK:** Extracellular signal-regulated kinase

## Declarations

## **Ethical Approval and Consent to participate**

Not applicable

## **Consent for publication**

Not applicable

## **Availability of supporting data**

The microarray data in this manuscript is available on the GEO database (GSE99728)..

## **CONFLICT OF INTEREST**

The authors declare no conflict of interest.

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### **Authors' contributions**

### **Contributions**

M.S. designed experiments, conducted experiments, analyzed data, and drafted the manuscript. M.S., O.S., Y.P. and M.K. conducted experiments and analyzed data. X.L., P.X., H.W., D.F. and O.S. interpreted data and edited manuscript. H.C. and M.S. designed experiments, analyzed data, and wrote the manuscript. The authors read and approved the final manuscript.

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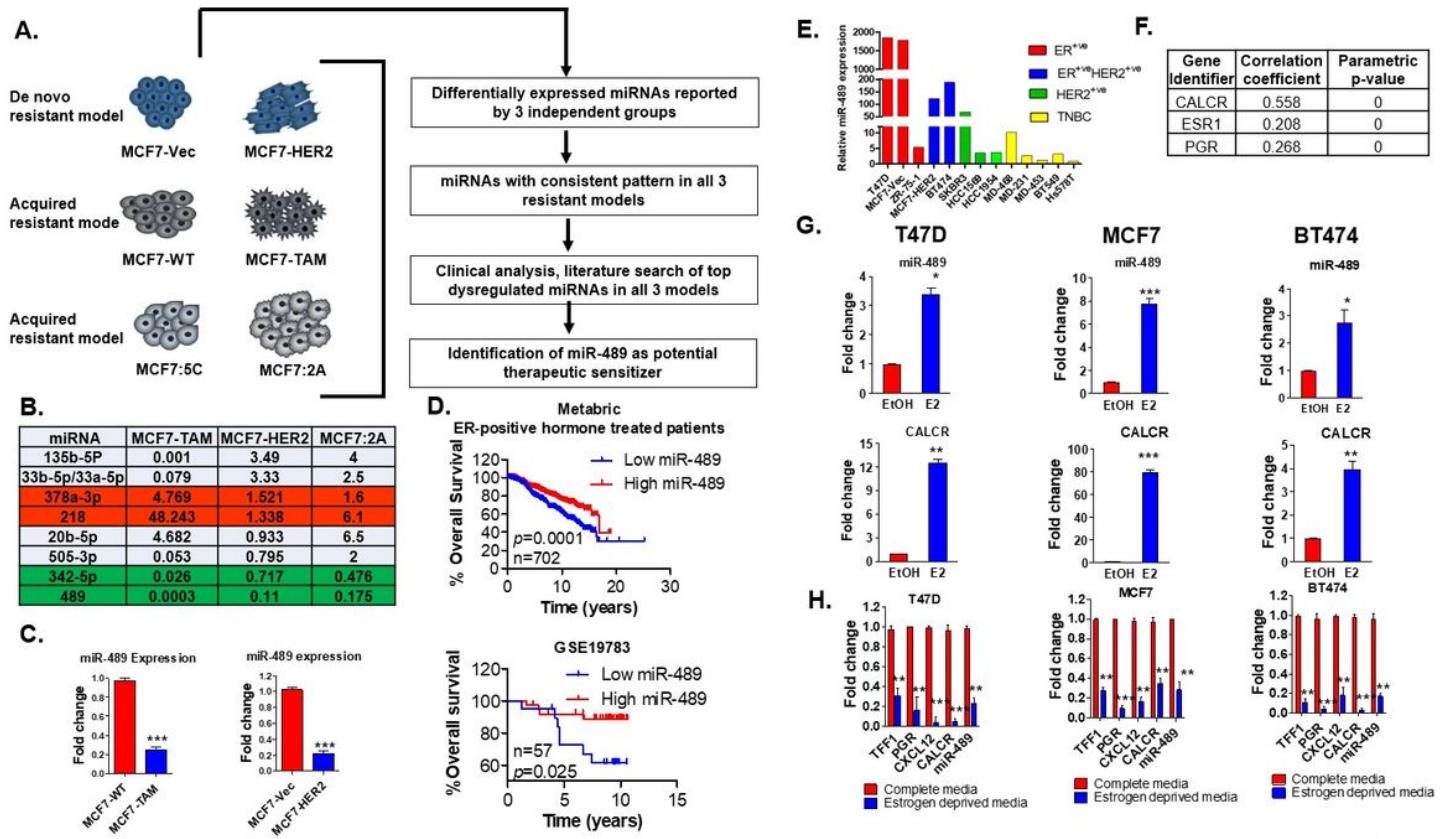
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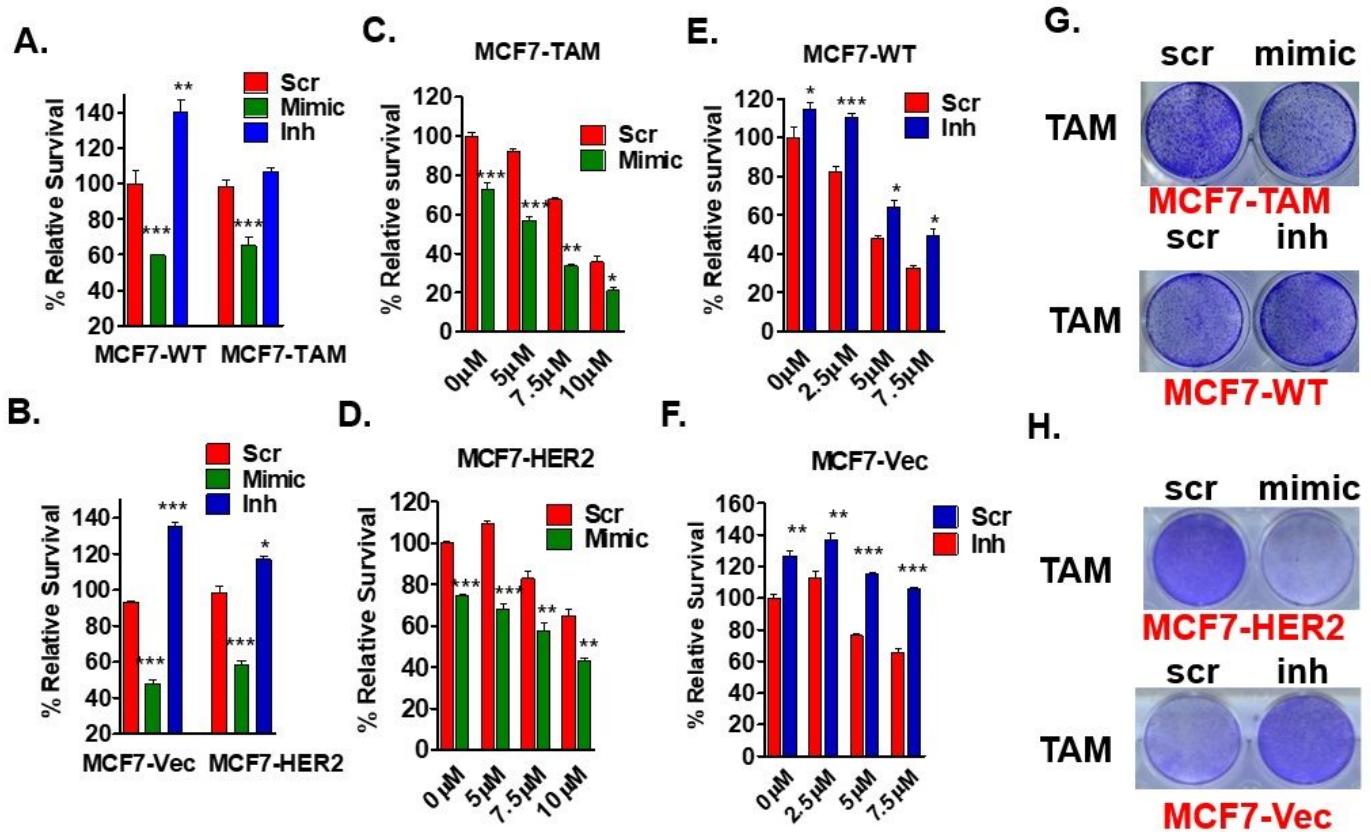
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## Figures



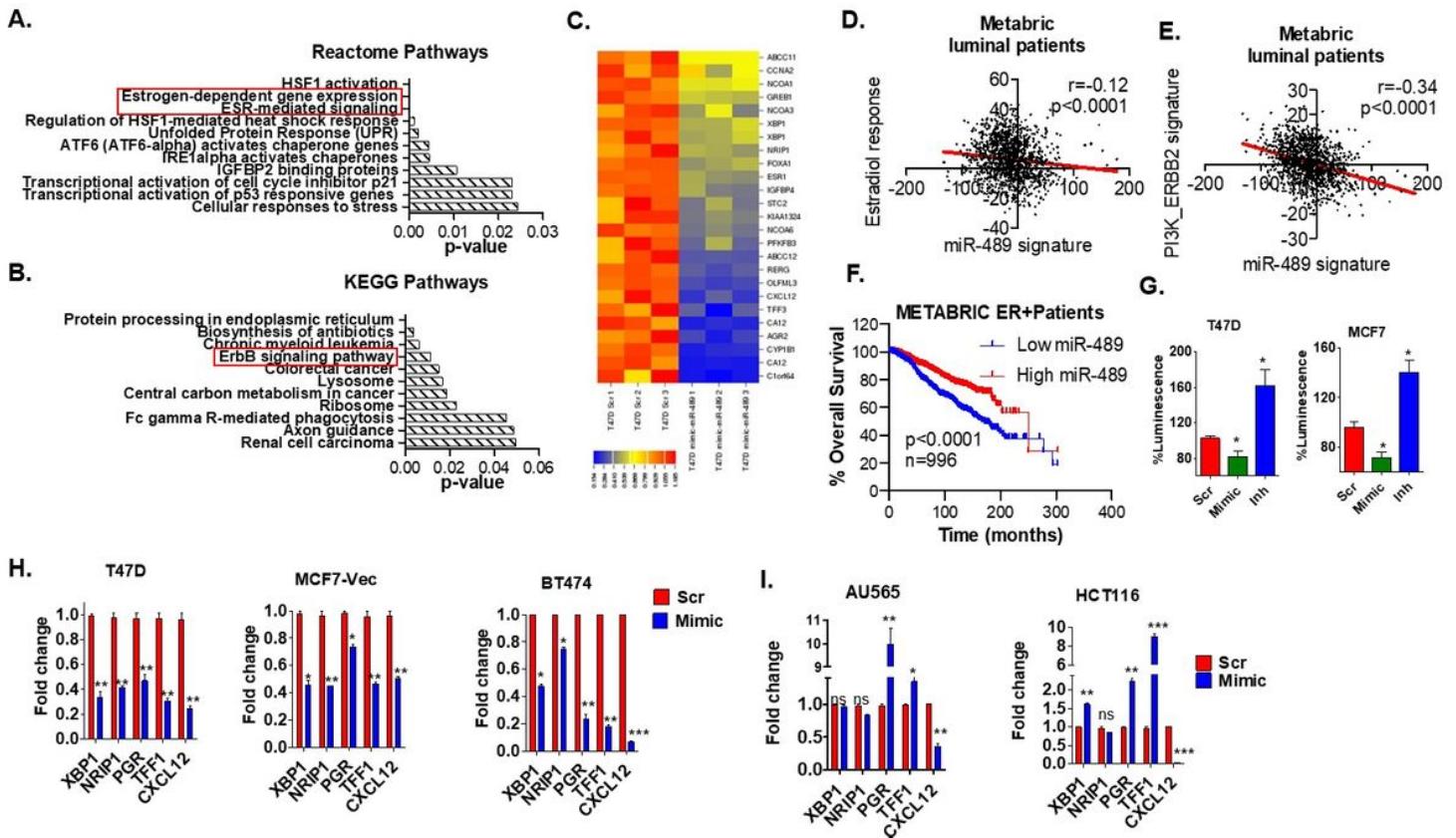
**Figure 1**

miR-489 expression is lost in tamoxifen resistance, predicts breast cancer aggressiveness and is regulated by estrogen/ERα axis. A. Schematic diagram for the identification and validation of miRNAs involved in tamoxifen resistance. miRNA analysis from three independent studies using three independent tamoxifen resistant model systems. B. List of top dysregulated miRNAs in all three Tamoxifen resistant cell lines. C. qRT-PCR validation of miR-489 in MCF7-TAM and MCF7-HER2 cell line. D. Clinical analysis of two datasets (Metabric and GSE19783) analyzing miR-489 expression in ER-positive breast cancer patients receiving hormone therapy. E. miR-489 expression in breast cancer cell lines. F. Correlation of miR-489 expression with expression of ERα and PGR. G. qRT-PCR analysis of miR-489 expression upon estrogen stimulation in three ER+ breast cancer cell lines. H. qRT-PCR analysis of miR-489 expression upon estrogen deprivation in three ER+ breast cancer cell lines. \*\*, p < 0.01; \*\*\*, p < 0.001. Data are representative of three independent experiments.



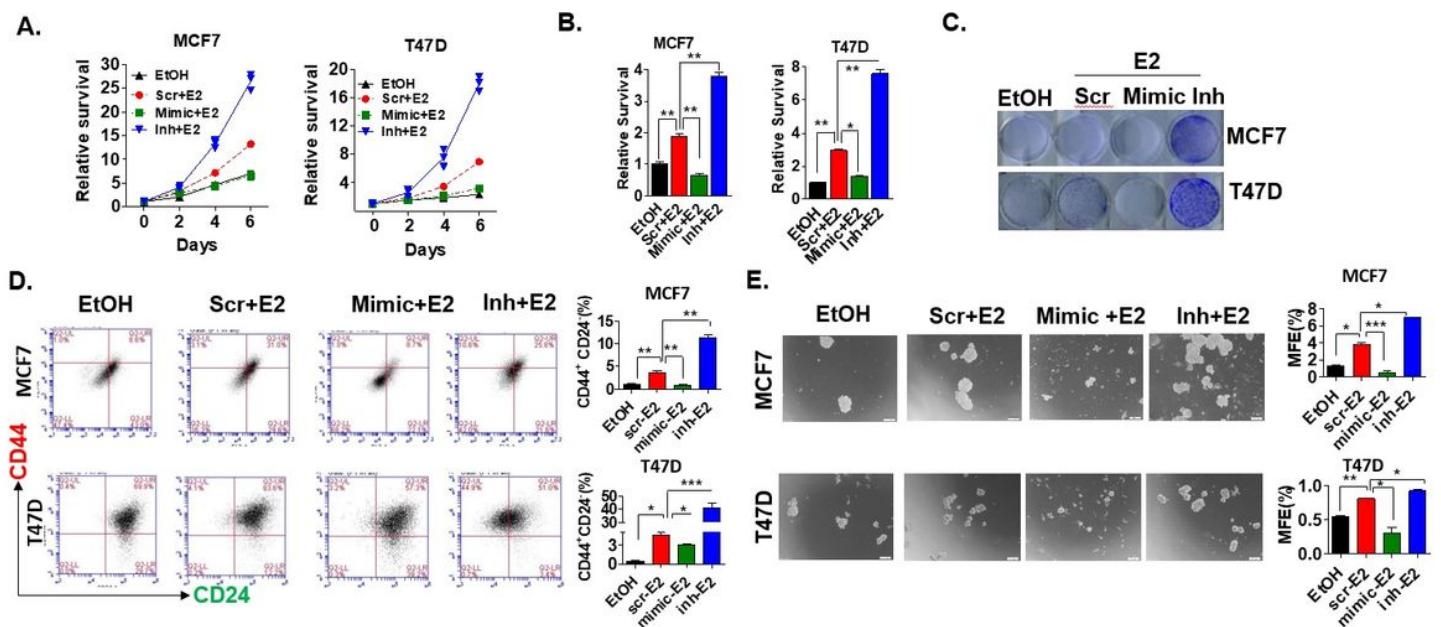
**Figure 2**

miR-489 restoration overcomes acquired and de novo tamoxifen resistance. A-B. Effect of miR-489 modulation on proliferation of two Tamoxifen resistant cell lines. 28nM of Scramble siRNA, miR-489 mimic and miR-489 inhibitor was transfected for 72hours followed by MTT based viability assay. C-D. miR-489 restoration sensitizes MCF7-TAM and MCF7-HER2 cell lines to tamoxifen. Scramble siRNA or miR-489 mimic was transfected with or without Tamoxifen for 72hours followed by MTT based viability assay. E-F Depletion of miR-489 promotes tamoxifen resistance in tamoxifen sensitive cell line MCF7-TAM and MCF7-HER2 cell lines to tamoxifen. Scramble siRNA or miR-489 inhibitor was transfected with or without Tamoxifen for 72hours followed by MTT based viability assay. G-H. Colony formation assay showing miR-489 modulates tamoxifen resistance. Cells were treated with indicated microRNA mimics or inhibitors with or without Tamoxifen for 72 hours followed by colony formation assay for 7-10 days. \*\*, p < 0.01; \*\*\*, p < 0.001. Data are representative of three independent experiments.



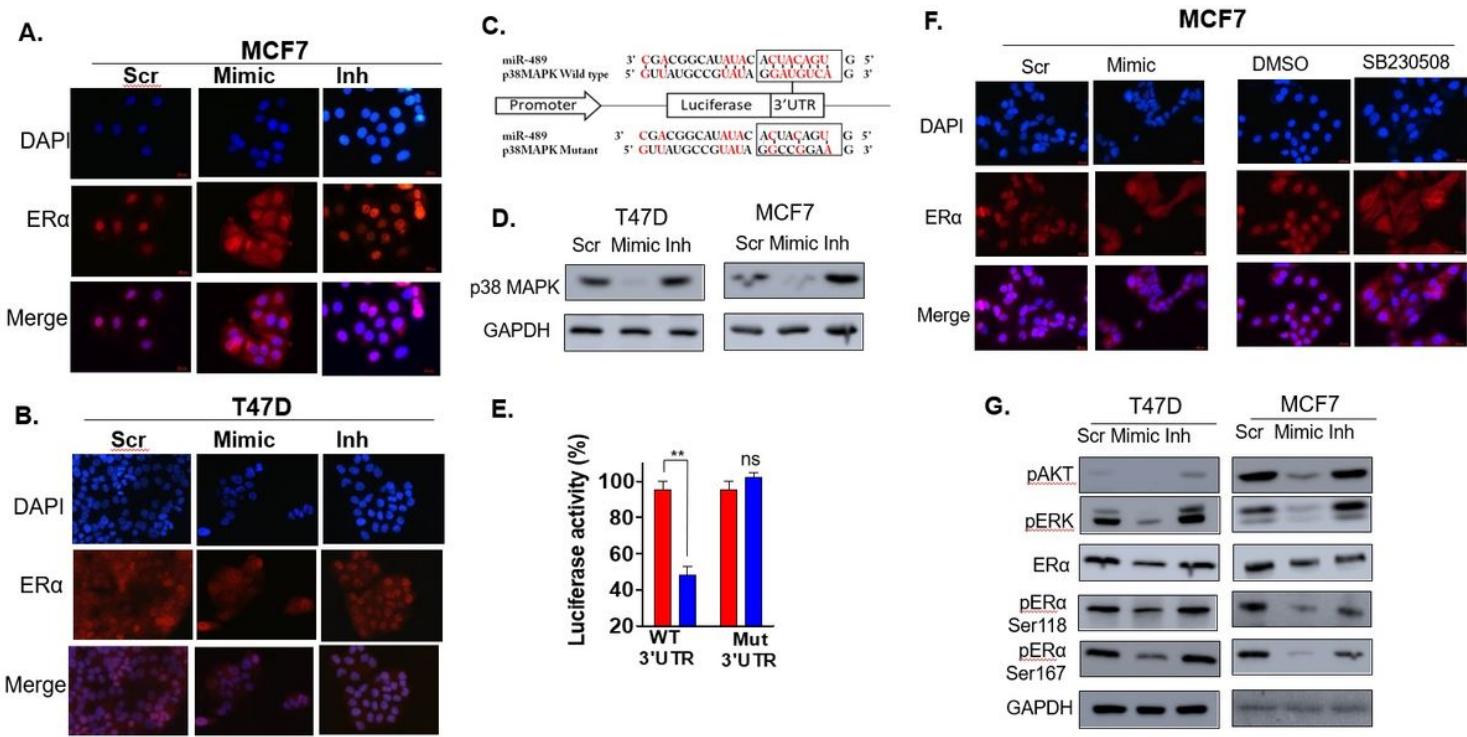
**Figure 3**

Gene Expression Analysis revealed enrichment of multiple pathways involved in estrogen signaling and tamoxifen resistance A-B. Whole transcriptome analysis of miR-489 transfected and control T47D cells followed by pathway enrichment analysis revealed multiple pathways involved in tamoxifen resistance including ESR-mediated signaling and ErBB2 pathways. C. Heatmap demonstrating downregulation of multiple estrogen responsive genes in miR-489 transfected T47D cells. D-E. Expression analysis of patient datasets showed inverse correlation between miR-489 signature and estradiol signature and miR-489 signature and PI3K-ErBB2 signature. F. Loss of miR-489 expression predicts poor survival in ER+ breast cancer patients. G. miR-489 negatively regulates estrogen induced transcription by transient transfection of cells with ERE-reporter system. H-I. qRT-PCR analysis of estrogen responsive genes upon miR-489 restoration shows downregulation of estrogen responsive genes only in ER+ breast cancer cell lines.



**Figure 4**

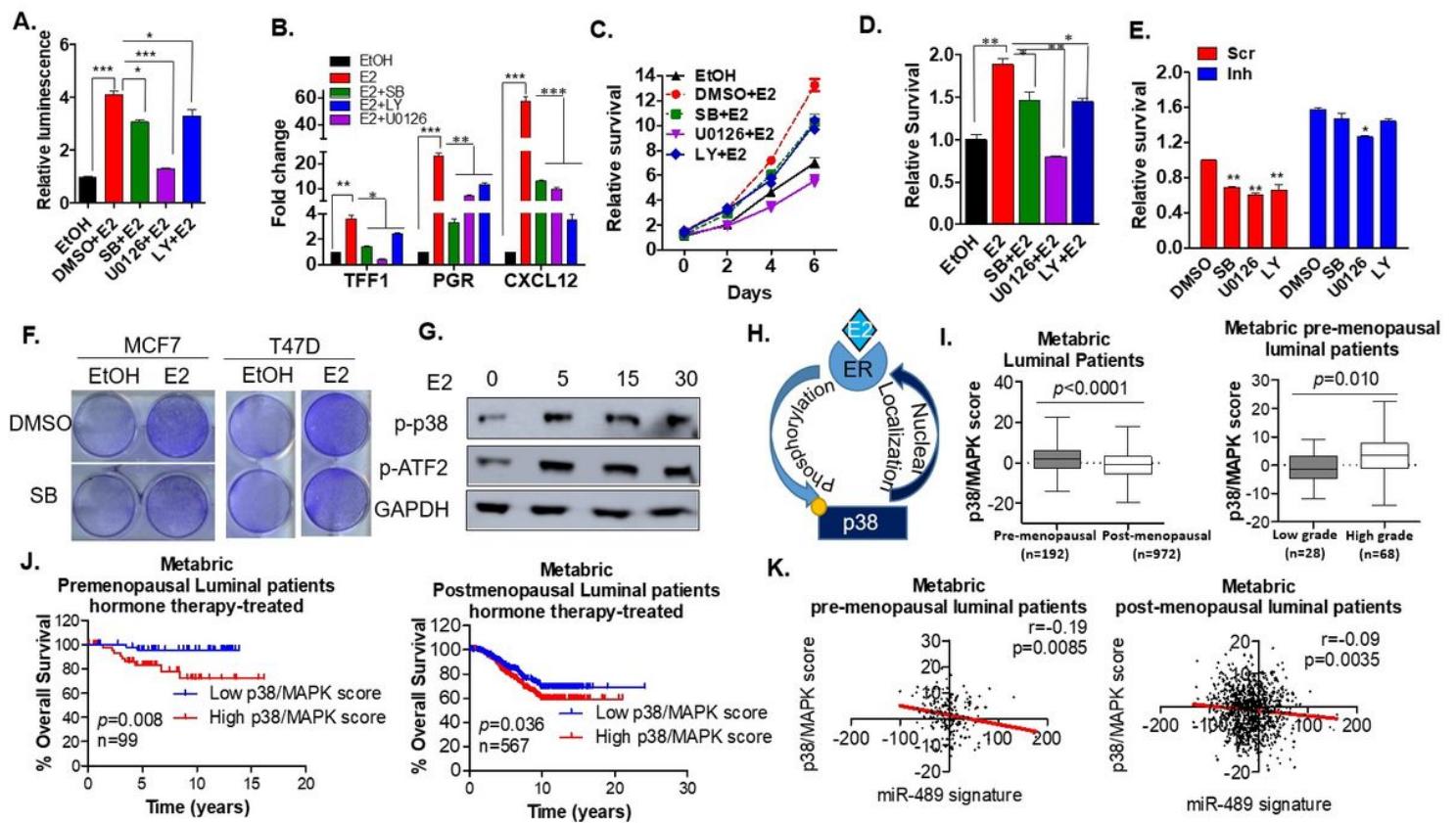
miR-489 acts as an endogenous negative feedback loop to balance estrogen signaling. A. miR-489 restoration inhibits proliferation of ER+ breast cancer cell line while inhibition of endogenous miR-489 dramatically enhances proliferation of MCF7 and T47D. Scramble siRNA, miR-489 mimic or miR-489 inhibitor was transfected in presence or absence of estrogen for 72hours followed by MTT based viability assay. B. Quantification of viable cells on day 6 post treatment of MCF7 and T47D. C. Inhibition of endogenous miR-489 dramatically enhances estrogen induced colony formation. MCF7 and T47D cells were transfected with scramble siRNA, miR-489 mimic and miR-489 inhibitor in presence or absence of estrogen for followed by colony formation assay. D. Breast cancer cell lines were transfected with scr, mimic or inhibitor in presence of estrogen for 72hrs followed by flow cytometry to examine CD24 and CD44 surface markers. E. Breast cell lines were transfected with scr, mimic or inhibitor in presence of estrogen for 72hrs followed by mammosphere assay. Scr. Scramble control; Inh. Inhibitor of miR-489. \*\*, p < 0.01; \*\*\*, p < 0.001. Data are representative of three independent experiments.



**Figure 5**

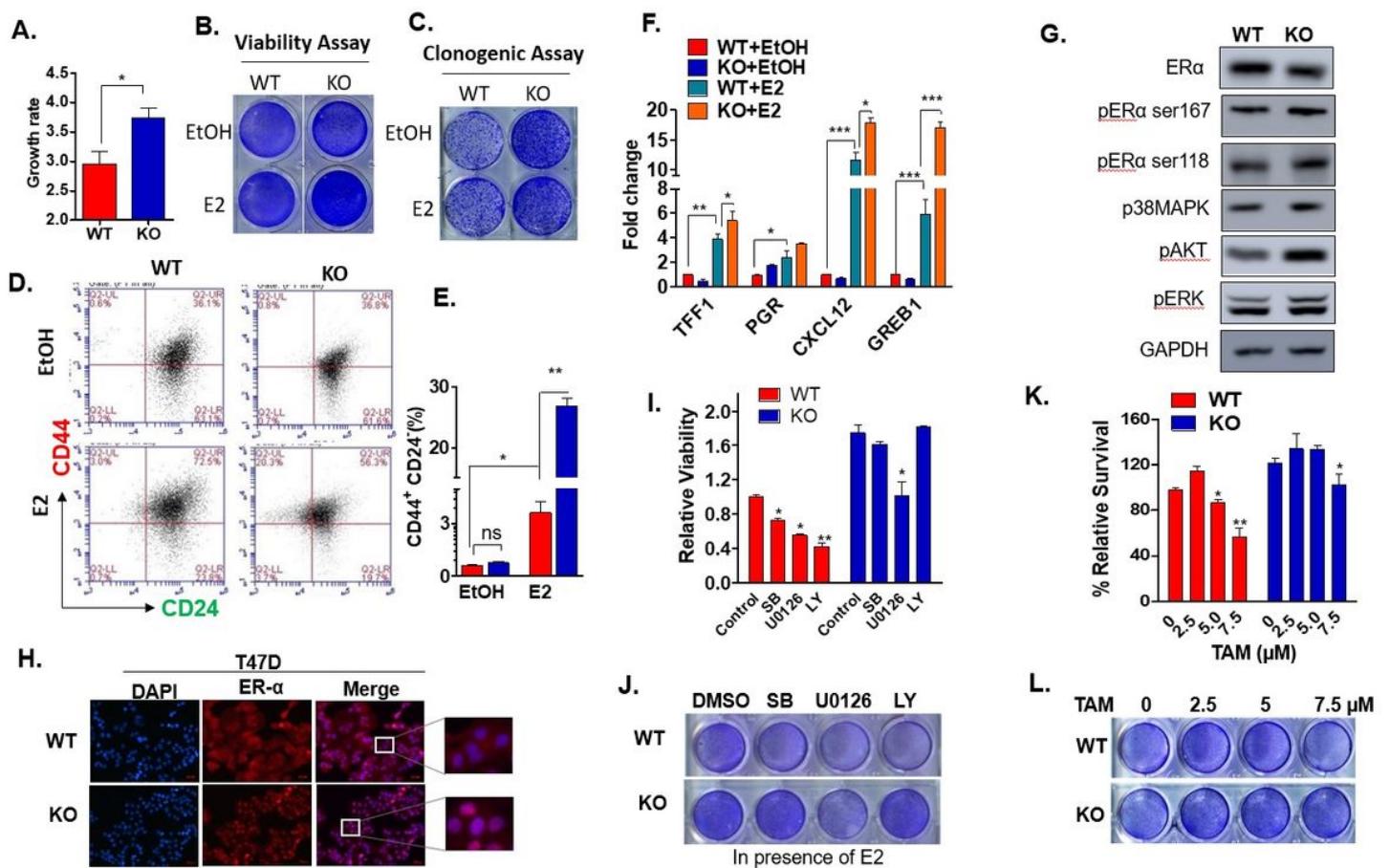
miR-489 inhibits estrogen induced signaling by inhibiting p38 MAPK, PI3K-AKT and MAPK-ERK pathways

A-B. MCF7 and T47D cells were transfected with scramble, mimic or inhibitor for 72hrs in estrogen deprived media followed by estrogen stimulation for 15 minutes. Data represents localization of estrogen receptor using immunofluorescence. C. miR-489 binding site in p38 MAPK 3' UTR. D. scramble, mimic or inhibitor was transfected, and western blot analysis was performed to examine total p38 MAPK protein. E. 3' UTR transfection assay showing miR-489 directly binds to 3'UTR of p38 MAPK. Data are means of three replicates + SEM. F. MCF7 cells were transfected with scramble or mimic or treated with DMSO or p38 MAPK inhibitor SB23508 and ER $\alpha$  localization was examined using immunofluorescence. G. T47D and MCF7 cells were transfected with scramble, mimic or inhibitor for 72 hours and ER $\alpha$  phosphorylation and responsible kinases were examined using western blot analysis.



**Figure 6**

p38 MAPK, PI3K-Akt and MAPK inhibitors phenocopies effect of miR-489 in ER+ breast cancer cell line. A. MCF7 cells were treated with inhibitors of p38 MAPK, ERK and PI3k\_AKT pathways and their role on estrogen induced transcription was examined using luciferase reporter assay. B. MCF7 cells were treated with inhibitors for 24 hours and expression of estrogen responsive genes were examined using qRT-PCR. C-D. MCF7 cells were treated with inhibitors and effect on estrogen induced proliferation was examined using MTT assay. E. MCF7 cells were transfected with scramble or inhibitors and treated with inhibitors for 72 hours in presence of estrogen and effect on proliferation was examined using MTT assay. F. MCF7 cells were treated with DMSO or p38 MAPK inhibitor in presence or absence of estrogen and colony formation assay was performed. G. MCF7 cells were treated with estrogen for indicated time and activation of p38 MAPK signaling was examined using western blot. H. Schematic diagram suggesting positive feedback loop between estrogen signaling and MAPK signaling. I. Analysis of patient dataset showing higher p38 MAPK score in pre-menopausal patients compared to post-menopausal patients. J. p38 MAPK signature predicting survival analysis of patients receiving hormone-therapy in pre- and post-menopausal patients. K. Correlation of p38 MAPK signature and estradiol signature in pre- and post-menopausal patients. \*, p < 0.05; \*\*, p < 0.01; \*\*\*, p < 0.001. Data are means of three replicates + SEM.



**Figure 7**

miR-489 knockout cells possess increased sensitivity to estrogen induced signaling and proliferation. A. WT and KO cells were seeded in 96 well plate for 96hrs. MTT based viability assay was performed to determine growth rate. B. Hormone starved WT and KO cells were seeded in 12-well plate and treated with ethanol or E2 for 6-days and cell viability was measured by crystal violet staining. C. Cell were seeded in media with/without estrogen for colony formation assay. D. Hormone starved WT and KO cells were treated with ethanol or E2 for 6 days and cancer stem cell population were analyzed using flow cytometry. E. Quantification of cancer stem cells after estrogen treatment. F. miR-489 WT and miR-489 knock out cells were treated with ethanol or estrogen for 6 hours and expression of estrogen responsive genes was examined using qRT-PCR. G. Western blot analysis of WT and KO cells. H. Immunofluorescence analysis of ER $\alpha$  in WT and KO cells. I-J. WT and KO cells were treated with inhibitors in presence of estrogen and cell viability was examined using MTT assay (I) and and colony formation assay (J). K-L. WT and KO cells were treated with indicated concentration of tamoxifen and viability was examined using MTT assay (K) and colony formation assay (L). \*, p < 0.05; \*\*, p < 0.01; \*\*\*, p < 0.001.

## Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- Additionalfile1.pdf
- Additionalfile2.pdf