Functional annotation of ESR1 gene fusions in estrogen receptor-positive breast cancer

Jieya Shao  
*Washington University School of Medicine in St. Louis*

Jin Zhang  
*Washington University School of Medicine in St. Louis*

Michael Iglesia  
*Washington University School of Medicine in St. Louis*

Robert Crowder  
*Washington University School of Medicine in St. Louis*

Jeremy Hoog  
*Washington University School of Medicine in St. Louis*

*See next page for additional authors*

Follow this and additional works at: https://digitalcommons.wustl.edu/open_access_pubs

Please let us know how this document benefits you.

**Recommended Citation**

Shao, Jieya; Zhang, Jin; Iglesia, Michael; Crowder, Robert; Hoog, Jeremy; Phommaly, Chanpheng; Rogers, Anna; Davies, Sherri R.; Li, Shunqiang; Ma, Cynthia X.; Watson, Mark A.; Maher, Christopher A.; and et al, "Functional annotation of ESR1 gene fusions in estrogen receptor-positive breast cancer." Cell reports. 24, 6. 1434-1444.e7. (2018).  
https://digitalcommons.wustl.edu/open_access_pubs/7012

This Open Access Publication is brought to you for free and open access by Digital Commons@Becker. It has been accepted for inclusion in Open Access Publications by an authorized administrator of Digital Commons@Becker. For more information, please contact vanam@wustl.edu.
Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer

Highlights

- ESR1 fusions drive ligand-independent growth and endocrine therapy resistance
- ESR1 fusions reprogram the ER cistrome to drive EMT and metastasis
- CDK4/6 inhibition suppresses ESR1 fusion-induced growth

Authors

Jonathan T. Lei, Jieya Shao, Jin Zhang, ..., Charles M. Perou, Svasti Haricharan, Matthew J. Ellis

Correspondence

mjellis@bcm.edu

In Brief

Lei et al. show that transcriptionally active estrogen receptor gene (ESR1) fusions identified from late-stage, treatment-refractory estrogen receptor-positive (ER+) breast cancer drive pan-endocrine therapy resistance and metastatic progression. Growth of breast tumors driven by ESR1 fusions at primary and metastatic sites can be suppressed with a CDK4/6 inhibitor.
Functional Annotation of \textit{ESR1} Gene Fusions in Estrogen Receptor-Positive Breast Cancer


1Department of Medicine, Lester and Sue Smith Breast Center, Baylor College of Medicine, Houston, TX 77030, USA
2Interdepartmental Graduate Program in Translational Biology and Molecular Medicine, Baylor College of Medicine, Houston, TX 77030, USA
3Department of Medicine, Washington University in St. Louis, St. Louis, MO 63110, USA
4Siteman Cancer Center, Washington University in St. Louis, St. Louis, MO 63110, USA
5Cancer Biology Division, Department of Radiation Oncology, Washington University in St. Louis, St. Louis, MO 63110, USA
6Institute for Informatics (I^2), Washington University in St. Louis, St. Louis, MO 63110, USA
7Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX 77030, USA
8Department of Genetics, Lineberger Comprehensive Cancer Center, University of North Carolina, Chapel Hill, NC 27599, USA
9Department of Breast and Endocrine Surgery, Kitasato University School of Medicine, Sagamihara, Kanagawa 252-0375, Japan
10First Department of Surgery, Hamamatsu University School of Medicine, Hamamatsu, Shizuoka 431-3192, Japan
11Department of Obstetrics and Gynecology, University of São Paulo School of Medicine (FMUSP), Cerqueira César, São Paulo 01246-903, Brazil
12Department of Obstetrics and Gynecology, Faculty of Medical Science, State University of Campinas - UNICAMP, Campinas, São Paulo 13083-970, Brazil
13Queens’ College, University of Cambridge, Cambridge CB3 9ET, UK
14Division of Solid Tumor Oncology, Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, NY 10065, USA
15Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX 77030, USA
16University of Texas Southwestern Medical Center, Dallas, TX 75390, USA
17Alliance Statistical Center, Mayo Clinic, Rochester, MN 55905, USA
18Department of Breast Surgical Oncology, MD Anderson Cancer Center, Houston, TX 77030, USA
19Department of Pathology and Immunology, Washington University in St. Louis, St. Louis, MO 63110, USA
20Department of Cancer Biology, Mayo Clinic Comprehensive Cancer Center, Jacksonville, FL 32224, USA
21Department of Medicine, Baylor College of Medicine, Houston, TX 77030, USA
22The McDonnell Genome Institute, Washington University in St. Louis, St. Louis, MO 63108, USA
23Lead Contact
24These authors contributed equally
25Correspondence: mjellis@bcm.edu

SUMMARY

RNA sequencing (RNA-seq) detects estrogen receptor-alpha gene (\textit{ESR1}) fusion transcripts in estrogen receptor-positive (ER\textsuperscript{+}) breast cancer, but their role in disease pathogenesis remains unclear. We examined multiple \textit{ESR1} fusions and found that two, both identified in advanced endocrine treatment-resistant disease, encoded stable and functional fusion proteins. In both examples, \textit{ESR1-e6>YAP1} and \textit{ESR1-e6>PCDH11X}, \textit{ESR1} exons 1–6 were fused in frame to C-terminal sequences from the partner gene. Functional properties include estrogen-independent growth, constitutive expression of ER target genes, and anti-estrogen resistance. Both fusions activate a metastasis-associated transcriptional program, induce cellular motility, and promote the development of lung metastasis. \textit{ESR1-e6>YAP1} and \textit{ESR1-e6>PCDH11X}-induced growth remained sensitive to a CDK4/6 inhibitor, and a patient-derived xenograft (PDX) naturally expressing the \textit{ESR1-e6>YAP1} fusion was also responsive. Transcriptionally active \textit{ESR1} fusions therefore trigger both endocrine therapy resistance and metastatic progression, explaining the association with fatal disease progression, although CDK4/6 inhibitor treatment is predicted to be effective.

INTRODUCTION

The etiology of endocrine therapy resistance in estrogen receptor-positive (ER\textsuperscript{+}) breast cancer is complex (Ma et al., 2015) but
includes acquired somatic mutations within the ligand-binding domain (LBD) of the estrogen receptor gene (ESR1) causing ligand-independent activation (Pejerrey et al., 2018). RNA sequencing (RNA-seq) has also identified multiple ESR1 gene fusion events, but their role in endocrine therapy resistance and how they might be targeted therapeutically is unclear (Giltnane et al., 2017). The majority of ESR1 fusion transcripts have been identified in primary breast cancer, and in some of these instances patients have high-grade disease and/or resistance to endocrine therapy (Giltnane et al., 2017; Veeraraghavan et al., 2014), implying some functionality. In some cases, up to five ESR1 coding exons are included (exons 3–7), mostly fused out of frame but occasionally, and more interestingly, in frame. However, detailed characterization of the predicted chimeric proteins and a clear demonstration of a causal role for ESR1 fusions in endocrine therapy resistance have been largely lacking.

Several years ago, our group described an unequivocal stable and functional ESR1 fusion protein (Li et al., 2013). This was an in-frame fusion gene consisting of exons 1–6 of ESR1 fused to C-terminal sequences from the Hippo pathway coactivator YAP1 (ESR1-e6>YAP1), identified in a metastatic sample and matched patient-derived xenograft (PDX) from a patient with endocrine therapy-resistant disease. Limited functional characterization of ESR1-e6>YAP1 showed that the fusion protein drove resistance to endocrine therapy and estradiol-independent proliferation. Herein we build on our original report by contrasting the functional, transcriptional, and pharmacological properties of the ESR1-e6>YAP1 fusion with additional ESR1 gene fusion events identified by RNA-seq of both early-stage and metastatic ER+ breast cancers.

RESULTS

Identification and Verification of In-Frame ESR1 Gene Fusions

A systematic screen was conducted to identify ESR1 translocations in three datasets: 728 primary breast tumors from The Cancer Genome Atlas (TCGA) (Ciriello et al., 2015), 81 primary breast cancers from two neoadjuvant aromatase inhibitor (AI) clinical trials (Ellis et al., 2011; Olson et al., 2009), and 25 biopsy samples from patients with late-stage ER+ breast cancer (Figure 1A). From these analyses, 13 high-confidence ESR1 fusion transcripts were identified in 10 ER+ samples from the TCGA dataset (Table S1). Five of these fusion events were between ESR1 and CCDC170 and were recently reported (Veeraraghavan et al., 2014). Of these, only 1 CCDC170 out-of-frame fusion included exon 5 (e5) of ESR1 (ESR1-e5>CCDC170), thereby preserving sufficient ESR1 sequence to bind DNA. A single TCGA case displayed evidence for three ESR1 gene fusions: (1) a PCR-validated ESR1-e6 fused in frame to C-terminal sequences from AKAP12 (ESR1-e6>AKAP12) (Figure S1); (2) a PCR-validated in-frame ESR1-e7 fusion involving the entire coding sequence of POLH, a DNA polymerase in the xeroderma pigmentosum gene family (ESR1-e7>POLH), and (3) an out-of-frame ESR1-e4>CCDC170 fusion.

From an RNA-seq screen of 81 primary, treatment-naïve, ER+ breast cancers from two neoadjuvant AI clinical trials (Table S1, NeoAI Trials), two PCR-validated ESR1 fusions were identified. The first was an in-frame fusion retaining the first six exons of ESR1 (ESR1-e6) fused to C-terminal sequences of NOP2, a nucleolar protein (ESR1-e6>NOP2). The second fusion identified involved ESR1-e6 fused out of frame to AKR1D1, an aldo-keto reductase family member (ESR1-e6>AKR1D1). In the datasets of primary ER+ breast cancer examined, ESR1 fusion events are relatively rare, occurring at ~2% frequency. The majority of these fusions are out of frame, and 42% of these fusion events (8 of 19) include sufficient ESR1 exons to allow ESR1-specific nuclear binding.

To investigate ESR1 fusion events in late-stage ER+ disease, RNA-seq data from 25 biopsy samples obtained from patients with advanced endocrine therapy refractory disease were examined (Table S1, Late Stage, and Table S2). These samples included the ESR1-e6>YAP1 sample we originally described, as it was drawn from this series (Li et al., 2013), and of these 25 samples, 2 harbored in-frame ESR1 fusion events. The ESR1-e6>PCDH11X fusion was caused by ESR1-e6 fusion in frame with C-terminal sequences of protocadherin 11X. PCDH11X encodes for an atypical cell surface cadherin family member. The sample was a chest wall recurrence from a 49-year-old man who presented with locally advanced ER+ breast cancer and experienced progression on tamoxifen, letrozole/leuprolide, and fulvestrant before the sample was accrued.

Of the eight identified ESR1 fusions from all datasets that were PCR validated (Figure S1), only three in-frame fusions, ESR1-e6>YAP1 and ESR1-e6>PCDH11X from advanced disease and ESR1-e6>NOP2 from a primary tumor that showed subsequent resistance to endocrine therapy, produced stable proteins when expressed as cDNA, allowing further study (Figure 1B). Expression of all three fusion partner genes were highly expressed in patient tumors, as shown by expression rank plots for YAP1, PCDH11X, and NOP2 translation-bearing tumors relative to the expression of these genes among TCGA breast samples (Figure 1C). Relative RNA levels of transcripts were analyzed for each fusion partner, which showed increases in transcript levels beyond the fusion breakpoint for each gene examined, confirming that the fusion partner was disproportionally expressed versus the non-translocated allele (Figure 2A).

In-Frame ESR1 Fusions from Endocrine-Refractory Disease Confer Estrogen-Independent and Fulvestrant-Resistant Growth of ER+ Breast Cancer Cells

To test whether examples of ESR1 in-frame gene fusions were drivers of endocrine therapy resistance, each fusion was individually expressed in two ER+ breast cancer cell line models: T47D and MCF7. Expression of fusion ER proteins in T47D cells was similar or lower than that observed in the WHIM18 PDX bearing the ESR1-e6>YAP1 fusion, indicating that phenotypic conclusions are not based on excess expression (Figure 2B). In addition, several out-of-frame CCDC170 and an AKR1D1 fusion event identified in this study (Table S1) were also engineered into T47D cells. Growth of ESR1 fusion-expressing T47D was monitored in estradiol (E2)-deprived media and following addition of E2. Both in-frame fusions from advanced disease, ESR1-e6>YAP1 and ESR1-e6>PCDH11X, promoted estrogen-independent growth (Figure 2C, –E2), but the primary tumor...
fusion event, ESR1-e6>NOP2, had no growth-promoting properties. The out-of-frame events tested were also inactive (Figure S2A). E2 could stimulate growth in all conditions of fusion construct expression (Figure 2C, compare +E2 and −E2), suggesting that neither the ESR1 in-frame active fusions (ESR1-e6>YAP1 and ESR1-e6>PCDH11X) nor the ESR1-e6 truncation, and not even the in-frame but inactive ESR1-e6>NOP2 fusion, could function as a dominant-negative on endogenous ER. Cells were treated with fulvestrant to degrade endogenous ER, while retaining expression of intact ESR1 fusions that cannot bind drug or ligand, to test the specific contribution of the fusions to E2-independent growth. As expected, endogenous ER was degraded by fulvestrant, whereas levels of ESR1 fusion proteins, as well as an ESR1-e6 truncation construct, were unaffected (Figure S2B), and growth promoted by ESR1-e6>YAP1 and ESR1-e6>PCDH11X was resistant to fulvestrant treatment (Figure 2C, −E2, +Fulvestrant). There was lack of additional growth promotion by the fusions when E2 was added in the presence of fulvestrant (Figure 2C, compare +E2, +Fulvestrant and −E2, +Fulvestrant). However, under these same conditions (Figure 2C, +E2, +Fulvestrant), growth induced by the YAP1 and PCDH11X fusions remains significantly greater than controls (YFP and ESR1-WT [wild-type]). These results were confirmed in a second ER+ breast cancer cell line, MCF7 (Figures S2C–S2D). The NOP2 fusion was highly expressed in the MCF7 cell line, in contrast to NOP2 fusion-expressing T47D, but still lacked growth-promoting activity in hormone-deprived conditions, confirming that absence of functional effects was not due to inadequate expression of the NOP2 fusion.
The ability of the three ESR1-e6-containing in-frame fusions to induce estrogen-independent growth was further tested in vivo in a xenograft study with stable T47D cells without supplementary E2. As controls, T47D YFP cells were used with supplementary E2. Results showed that control YFP –E2 cells produced negligible tumor growth compared with YFP cells +E2 (Figure 2D). However, T47D cells expressing YAP1 and PCDH11X in-frame ESR1 fusions formed tumors significantly larger than YFP –E2, while the cells expressing the NOP2 fusion did not (Figure 2D).

**Active ESR1 Fusions Promote Estrogen-Independent Gene Expression**

To explore transcriptional properties associated with the ESR1 fusion proteins described above, genome-wide binding of HA-tagged ESR1 fusions was examined by HA chromatin immunoprecipitation followed by next-generation sequencing (ChIP-seq) in hormone-deprived stable T47D. ChIP-seq identified 445 binding regions shared by ESR1-WT, ESR1-e6>YAP1, and ESR1-e6>PCDH11X (Figure 3A). Very few sites were bound by ESR1-e6>NOP2 fusion despite high expression of HA-tagged NOP2 fusion (Figure S3E), supporting earlier observations of inactivity in functional studies (Figures 2C, 2D, and S2C). ChIP-qPCR confirmed recruitment of ER to regulatory regions of known estrogen-responsive genes in a ligand-dependent manner in cells expressing WT-ER (Figure 3B). Additionally, both YAP1 and PCDH11X fusions showed estrogen-independent enrichment at regulatory regions of established estrogen-responsive genes. For example, both fusions were enriched at the promoter of a canonical ER-regulated gene, GREB1, and the PCDH11X fusion was also enriched at enhancer estrogen response elements (EREs) of TFF1 and PGR (Figure 3B).

To investigate whether expression from genes bound by ESR1 fusions was modulated, RNA-seq was performed. Hierarchical
clustering was conducted on differentially expressed genes near 445 shared sites bound by ESR1-WT, YAP1, and PCDH11X fusions, as indicated by the ChIP-seq data (Figure 3C). Upon stimulation with E2, the expression pattern of YFP control cells clustered away from unstimulated YFP cells, with enrichment for differential expression of estrogen-responsive genes. The YAP1 and PCDH11X fusion-expressing cells had expression patterns that clustered together under estrogen-deprived and stimulated conditions and with E2-stimulated YFP cells. The transcriptionally active ESR1 fusions maintained expression of estrogen-regulated genes in low-estrogen conditions at levels observed in YFP control cells in the presence of E2, demonstrating strong estrogen-independent gene activation. mRNA-qPCR validation of GREB1, TFF1, and PGR expression confirmed estrogen-independent and fulvestrant-resistant gene regulation (Figures 3D and S3F), suggesting that the active ESR1 fusions drive endocrine resistance in a canonical manner through ERE-dependent activation. Moreover, the estrogen-independent activity of the YAP1 and PCDH11X fusions was also independent of endogenous WT-ER, as transcriptional activity was maintained after cells were treated with fulvestrant to degrade endogenous ER. Thus, functionally important heterodimer formation between ESR1 fusion protein and WT-ER is not likely. This conclusion was also supported by the lack of ESR1 fusion association with WT-ER in a co-immunoprecipitation assay (Figure S3D). In contrast, the ESR1-e6 truncation mutant and NOP2 fusion clustered together with YFP control cells displaying similar patterns of ligand-dependent ER gene expression, supporting our earlier observations that the NOP2 fusion lacks ability to bind a large repertoire of EREs but whose inactivity is not due to mislocalization outside the nucleus, as staining for HA-tagged ESR1 fusions constructs demonstrated nuclear localization (Figure S3A). These data were further supported by ERE-luciferase reporter experiments in HEK293T cells (Figure S3B); ESR1-WT drove estrogen-dependent expression of the ERE-luciferase reporter. In contrast, both ESR1-e6-YAP1 and ESR1-e6>PCDH11X as well as the ESR1-Y537S activating mutant drove estrogen-independent expression of the ERE-luciferase reporter. The level of activation by ESR1-e6-YAP1 was substantially higher than ESR1-e6>PCDH11X, which

Figure 3. Active ESR1 Fusions Promote Estrogen-Independent Expression of Target Genes
(A) Venn diagram depicting overlap of binding sites from hormone-deprived stable T47D cells expressing HA-tagged ESR1 constructs identified by HA-ChIP-seq. (B) HA-ChIP followed by qPCR for ER-binding regions of ER-responsive genes and negative ER-binding region. Bar graphs show average values from three experiments ± SEM. Asterisks denote significant differences as described in STAR Methods. (C) Heatmap showing differentially expressed genes near 445 sites bound by ESR1-e6-YAP1, ESR1-e6>PCDH11X, and ESR1-WT identified in (A). Known ER-responsive genes are indicated (CTSD, GREB1, PGR, TFF1, and PDZK1). Scale bar indicates row Z score. (D) Bar graphs depicting relative fold changes of estrogen-responsive genes whose ER-binding regions were examined in (B) from hormone-deprived stable T47D cells, normalized to YFP – E2 (dark blue bar), after E2 addition (+E2, red bar), or in combination with fulvestrant (light blue and pink bars). –E2 and +E2 for ESR1 fusion-expressing cells have been omitted for clarity; see Figure S3F for complete data. Data are shown as averages from two independent experiments ± SEM. See also Figure S3.
Figure 4. Active ESR1 Fusions Promote Metastasis by Upregulating an EMT-like Transcriptional Program
(A) Heatmap depicting genes upregulated by ESR1-e6>YAP1 and ESR1-e6>PCDH11X versus YFP and ESR1-e6>NOP2 (from bottom of Figure 3C). Scale bar indicates row Z score.
(B) GSEA using genes identified in (A).
(C) Bar graphs depicting expression of SNAI1 and VCAN, by mRNA-qPCR in hormone-deprived stable T47D cells (−E2). Values are normalized to YFP −E2 (dark blue bar), treated with E2 (+E2, red bar), and in combination with fulvestrant (light blue and pink bars). −E2 and +E2 conditions for all cell lines are shown in Figure S4 B. Data are averages of two independent experiments ± SEM.
(D) Immunoblotting for endogenous ER (ER) and ER fusion (asterisks) using an N-terminal ERα antibody, Snail, and E-cadherin in hormone-deprived stable T47D and MCF7 cells. Vertical line in E-cadherin blot indicates different exposures taken for T47D and MCF7.
(E) Scratch wound healing assay images of hormone-deprived stable T47D at 0 and 72 hr post-wounding. Dotted black line indicates leading edge of cells. Scale bar, 300 μm.

(legend continued on next page)
had activity intermediate to that achieved by the constitutively active ESR1-Y537S mutant and ESR1-e6>YAP1 (Li et al., 2013). In contrast to the ESR1-e6>YAP1 and ESR1-e6>PCDH11X fusions, neither the ESR1-e6 truncation mutation nor the ESR1-e6>NOP2 fusion drove expression of the ERE reporter. The transcriptional inactivity of the NOP2 fusion was not due to abrogation of ERE binding, as pull-down experiments with a biotinylated concatenated ERE probe with a mutant ERE as a control demonstrated sequence-specific binding for all in-frame fusions (Figure S3C). In summary, our observations suggest that the inactivity of the NOP2 fusion may be due to a failure to access chromatin in the nucleus of intact cells, rather than an inability to bind DNA per se.

**Active ESR1 Fusions Promote Metastasis by Upregulating an EMT-like Transcriptional Program**

A cluster of genes was identified that was selectively upregulated by the active YAP1 and PCDH11X fusions (Figures 3C and 4A). Gene set enrichment analysis (GSEA) was used to examine pathway enrichment in this cluster, which indicated significant enrichment of estrogen response pathways as well as an epithelial-to-mesenchymal transition (EMT)-like signature (Figure 4B). The EMT signature included TGM2, COL3A1, INHBA, and VCAN. One of the best-described EMT genes, SNAI1, was also selectively upregulated by both active fusions. Analysis of binding site distances to transcription start sites (TSSs) of genes in this cluster demonstrated that the majority of binding occurs at distances >50 kb from the TSS (Table S3). This suggests a propensity of the active YAP1 and PCDH11X fusions to bind in enhancer regions upstream and downstream of these genes, characteristic of the ER cistrome reported in the literature (Carroll et al., 2006). Motif analysis of these binding sites showed enrichment for the ERE motif (Figure S4A), suggesting that the direct regulation of EMT genes by the active YAP1 and PCDH11X fusions is mediated by enhancer and more distant range interactions. Upregulation of VCAN and SNAI1 transcripts (Figures 4C and S4B) and Snail protein (Figure 4D) was orthogonal validated. In MCF7 cells, whose basal levels of Snail were higher in YFP controls compared with T47D YFP, showed an induction of Snail by ESR1-e6>YAP1, but not by ESR1-e6>PCDH11X, suggesting a degree of cell context-dependent effects (Figure 4D). Upregulation of Snail protein was also confirmed in T47D xenograft tumors and in a PDX model naturally harboring the ESR1-e6>YAP1 fusion (WHIM18) (Figure 4G). Expression of SNAI1 was unaffected by fulvestrant treatment in T47D cells, consistent with the conclusion that upregulation of EMT genes by the active fusions is independent of endogenous WT-ER (Figures 4C and S4B).

ChIP-seq also identified 71 selectively bound sites by ESR1-e6>YAP1 and ESR1-e6>PCDH11X not bound by ESR1-WT nor ESR1-e6>NOP2 (Figure S4C). GSEA pathway analysis of differentially expressed genes near these sites showed enrichment for UV radiation response genes, as well as enrichment for EMT genes, with TGFB3 and GJA1 contributing to EMT pathway enrichment (Figure S4C). TGFB3 encodes for transforming growth factor-beta receptor III and has roles in migration and invasion (Gatza et al., 2010). GJA1 encodes for connexin-43, a gap junction protein whose expression in breast cancer cells has been implicated in pulmonary metastasis (Elzarrad et al., 2008), consistent with observed lung metastasis in both patients from which the ESR1-e6>YAP1 and ESR1-e6>PCDH11X fusions were identified.

A decrease in E-cadherin levels from YAP1 and PCDH11X fusion-expressing cells was observed relative to YFP control and NOP2 fusion-expressing cells (Figure 4D), and a decrease in cell surface E-cadherin was also observed, consistent with an EMT-like transition (Figures S4E and S4F). However, there was no detectable increase in vimentin levels, suggesting that the YAP1 and PCDH11X fusions drive a partial EMT gene expression pattern that nonetheless can be metastasis associated (Jolly et al., 2015). To examine the functional consequences of the active fusions with respect to the metastatic process, cell motility was examined. The YAP1 and PCDH11X fusions induced significantly greater wound recovery and motility than YFP controls and NOP2 fusion-expressing cells (Figure 4E, quantified in Figure S4D). To exclude the possibility that EMT-associated gene expression was due to phenotypic drift of cells under long-term selection, small interfering RNA (siRNA)-mediated knockdown of ESR1-e6>YAP1 fusion was examined to determine whether EMT-associated features could be reversed. Estrogen-deprived stable T47D YFP control or ESR1-e6>YAP1-expressing cells were pre-treated with fulvestrant to degrade endogenous WT-ER, before transfecting with negative control siRNA (siESR1-) or siESR1 against the N terminus of ESR1 (siESR1+). Forty-eight hours post-transfection, Snail protein levels were markedly reduced in ESR1-e6>YAP1 cells after siESR1 transfection with or without fulvestrant pre-treatment compared with siESR1- with or without fulvestrant (Figure 4F, compare lanes 5 and 7 with lanes 6 and 8). In addition, cells with decreased Snail as a result of ER-YAP1 fusion protein knockdown tended to have higher levels of E-cadherin, suggesting that knockdown of the ESR1-e6>YAP1 fusion transcript restores these aspects of a typical epithelial gene expression pattern. Similar effects were confirmed in stable MCF7 cells expressing ESR1-e6>YAP1 (Figure S4G, compare lanes 5 and 7 with lanes 6 and 8), although Snail levels were more affected by fulvestrant pre-treatment alone, showing that higher basal levels of Snail in MCF7 cells can also be driven by WT ESR1 (Figure S4G, compare lanes 1 and 3 for YFP-expressing cells and lanes 5 and 7 for ESR1-e6>YAP1-expressing cells). However,
Snail expression is resistant to fulvestrant suppression in the presence of the ESR1-e6->YAP1 fusion (Figure S4G, compare lanes 3 and 7). The metastatic potential of fusion-expressing cells in vivo was measured by ER immunohistochemistry from the lungs, liver, and bones of mice bearing T47D xenografts from Figure 2D. The number of micrometastatic ER+ cells in the lungs of YAP1 and PCDH11X fusion bearing mice was significantly greater than that in the lungs of mice bearing tumors generated from YFP control cells upon estrogen deprivation (Figure 4H). YFP control tumors grown with E2 supplementation were much larger (Figure 2D), but pulmonary micrometastasis was not significantly different from YFP controls – E2, demonstrating that differences in pulmonary metastasis potential associated with the active fusions were not due simply to differences in disease burden. Bone and hepatic micrometastases were not observed. Pulmonary metastasis in this model was not a feature of YFP control cells, even when disease burden was increased markedly with E2 supplementation. Taken together, these results suggest a role for active YAP1 and PCDH11X fusions in driving pulmonary metastasis in association with the expression of genes known to contribute to EMT biology and metastatic behavior.

**Growth Driven by ESR1 Fusions Can Be Suppressed with CDK4/6 Inhibitor Treatment**

The loss of the LBD renders the function of ESR1 fusion genes resistant to all endocrine treatments, and therefore alternative therapies will be necessary to treat patients who present with active ESR1 fusions. Palbociclib, a selective CDK4/6 inhibitor was chosen for study because of our recent report that this agent can antagonize the growth of tumors expressing ESR1 mutations as long as phospho-Rb (pRb) is present (Wardell et al., 2015). Because the target of activated CDK4/6 is Rb, pRb levels were examined by immunohistochemistry (IHC) in ESR1 fusion-expressing T47D xenograft tumor sections (Figure S5A). pRb levels in YAP1 and PCDH11X fusion xenograft tumors grown without E2 supplementation were comparable with YFP controls +E2 and were elevated relative to YFP –E2 and NOP2 fusion-containing tumors. T47D stable cells expressing YFP and the three in-frame ESR1 fusions were treated with palbociclib under hormone-deprived conditions and growth-inhibitory effects were assessed (Figure S5A). Palbociclib inhibited T47D cell growth driven by the YAP1 and PCDH11X fusions in a dose-dependent manner. A similar palbociclib effect was observed in ESR1 fusion-expressing MCF7 stable cells (Figure S5B). To test palbociclib sensitivity in vivo, a PDX model naturally harboring the ESR1-e6->YAP1 fusion (WHIM18) was exposed to palbociclib. Consistent with in vitro results, tumor growth in the PDX model was inhibited in mice treated with palbociclib compared with vehicle-treated mice (Figure 5B; tumor growth rates shown in Figure S5C). Palbociclib-treated WHIM18 tumors also showed significant reduction in pRb and marked decrease in Ki-67 levels, without altering levels of ER (Figure 5C) or progesterone receptor (PR) (Figure S5D). Areas containing micrometastatic ER+ cells observed in the lungs of vehicle-chow-treated WHIM18 mice were not seen in palbociclib-treated mice (Figure 5D), suggesting that pulmonary metastatic frequency could also be downregulated by CDK4/6 inhibition.

**DISCUSSION**

This study demonstrated that two in-frame ESR1 fusions in a small late-stage cohort of metastatic ER+ cases drive not only endocrine therapy resistance but also metastatic disease progression. The functional characterization of ESR1 fusions’ properties described herein should drive efforts to identify and further characterize additional ESR1 fusions in early- and late-stage ER+ breast cancer.

The ability to block active ESR1 fusion-induced growth with a CDK4/6 inhibitor has important implications for clinical practice. Patients with active ESR1 fusions may present with a clinical pattern of rapidly progressing disease despite adjuvant or metastatic endocrine therapy treatment and therefore be offered chemotherapy instead of a CDK4/6 inhibitor-containing regimen. Because therapeutically resistant disease is infrequently re-biopsied and even more rarely analyzed using RNA-seq, a prospective study of ESR1 in-frame fusion-expressing ER+ tumors will be required to establish an effective approach for these tumors.

Although ESR1 fusions are challenging to diagnose because of variable 3’ fusion partners, evidence for additional ESR1 fusions is emerging in the literature. For example, ESR1-e6->DAB2 and ESR1-e6->GYG1 were both identified in metastatic ER+ breast cancer (Hartmaier et al., 2018). Like the active ESR1 fusions we describe herein, ESR1-e6->DAB2 and ESR1-e6->GYG1 follow the same pattern (i.e., ESR1 exon 6 in-frame fusions with 3’ partners provided by inter-chromosomal translocation). Thus, this type of ESR1 fusion gene structure is most clearly linked to endocrine therapy resistance. Several precision medicine programs now include RNA-seq in their standard pipeline, and thus much more data on ESR1-e6 in-frame fusion prevalence should be available soon.

Because active ESR1 fusions induce pRb (Figure S5A), pRb might also be an appropriate marker to guide CDK4/6 inhibitor therapy and might provide strong pre-clinical rationale to potentially examine pRb levels in patients on AIs to define populations for CDK4/6 inhibition. This idea is supported by our previous report, in which the growth of endocrine-refractory PDX tumors remained sensitive to CDK4/6 inhibition, as long as those tumors express pRb under estrogen-deprived growth conditions (Wardell et al., 2015).

The inactivity of the ESR1-e6->NOP2 fusion is surprising, as the expressed recombinant protein is stable. This demonstrates that not every in-frame ESR1-e6 fusion is active with respect to endocrine therapy resistance. The NOP2 fusion may have other biological properties that we were unable to detect in our experimental model systems. The out-of-frame ESR1 fusions also had no growth-promoting properties but could also be active through novel mechanisms.

The role of active ESR1 fusions in promoting EMT-like gene expression changes follows a pattern associated with other members from a diverse family of cancer-associated gene fusion events. For example, the TMPRSS2-ERG fusion in prostate cancer has also been reported to directly regulate cell migration genes (Tian et al., 2014). Given the diverse structures of EMT-inducing ESR1 fusions revealed here with the study of just two, it is also possible that more EMT and motility-inducing
transcription factor gene fusions remain to be discovered, and the formation of these could be primary drivers of metastasis.

STAR METHODS

Detailed methods are provided in the online version of this paper and include the following:

- KEY RESOURCES TABLE
- CONTACT FOR REAGENT AND RESOURCE SHARING
- EXPERIMENTAL MODEL AND SUBJECT DETAILS
  - Cell Lines
  - In Vivo Animal Studies
  - Clinical Samples
- METHOD DETAILS
  - ESR1 Fusion Discovery Using ChimeraScan and INTEGRATE
  - Molecular Cloning to Generate ESR1 Fusion Constructs
  - Lentiviral Production and Stable Cell Line Generation
SUPPLEMENTAL INFORMATION

Supplemental Information includes five figures and four tables and can be found with this article online at https://doi.org/10.1016/j.celrep.2018.07.009.

AUTHOR CONTRIBUTIONS


DECLARATION OF INTERESTS

M.J.E. received ad hoc consulting fees from Pfizer, AstraZeneca, Celgene, NanoString, Puma, and Novartis. C.X.M. received research funding and ad hoc consulting fees from Pfizer and Novartis. C.M.P. and M.J.E. are equity stock holders, consultants, and Board of Directors members of BioClassifier, inventor on a patent for the Breast PAM50 assay. All other authors declare no competing of interests.

Received: November 20, 2017
Revised: May 8, 2018
Accepted: July 1, 2018
Published: August 7, 2018

REFERENCES


## STAR★METHODS

### KEY RESOURCES TABLE

<table>
<thead>
<tr>
<th>REAGENT or RESOURCE</th>
<th>SOURCE</th>
<th>IDENTIFIER</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Antibodies</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rabbit monoclonal HA (clone C29F4)</td>
<td>Cell Signaling Technology</td>
<td>Cat#3724; RRID:AB_1549585</td>
</tr>
<tr>
<td>Mouse monoclonal HA (clone 6E2)</td>
<td>Cell Signaling Technology</td>
<td>Cat#2367; RRID:AB_331789</td>
</tr>
<tr>
<td>Mouse monoclonal HA (clone F-7)</td>
<td>Santa Cruz Biotechnology</td>
<td>Cat#sc-7392; RRID:AB_627809</td>
</tr>
<tr>
<td>Rabbit monoclonal anti-ERα (clone 60C), N-terminal</td>
<td>Millipore</td>
<td>Cat#04-820; RRID:AB_1587018</td>
</tr>
<tr>
<td>Rabbit polyclonal anti-ERα, C-terminal</td>
<td>Santa Cruz Biotechnology</td>
<td>Cat#sc-543; RRID:AB_631471</td>
</tr>
<tr>
<td>Mouse monoclonal anti-ERα (clone 6F11)</td>
<td>Leica Microsystems</td>
<td>Cat#NCL-ER-6F11; RRID:AB_563706</td>
</tr>
<tr>
<td>Mouse monoclonal anti-β-Actin</td>
<td>Sigma-Aldrich</td>
<td>Cat#A5316; RRID:AB_147643</td>
</tr>
<tr>
<td>Mouse monoclonal anti-E-Cadherin (clone 4A2)</td>
<td>Cell Signaling Technology</td>
<td>Cat#14772; RRID:AB_1278770</td>
</tr>
<tr>
<td>Rabbit monoclonal anti-Vimentin (clone D21H3)</td>
<td>Cell Signaling Technology</td>
<td>Cat#5741; RRID:AB_10695459</td>
</tr>
<tr>
<td>Rabbit monoclonal anti-Snail (clone C15D3)</td>
<td>Cell Signaling Technology</td>
<td>Cat#3870; RRID:AB_2250511</td>
</tr>
<tr>
<td>Rabbit monoclonal anti-Phospho-Rb (Ser780) (clone D58957)</td>
<td>Cell Signaling Technology</td>
<td>Cat#B180; RRID:AB_1965072</td>
</tr>
<tr>
<td>Mouse monoclonal anti-Ki-67 (MIB-1) (clone Ki-67)</td>
<td>Beckman Coulter</td>
<td>Cat#IM1316; RRID:AB_131615</td>
</tr>
<tr>
<td>Mouse monoclonal anti-PR (clone PgR 1294)</td>
<td>Dako</td>
<td>Cat#M3568; RRID:AB_2252608</td>
</tr>
<tr>
<td><strong>Biological Samples</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WHIM18 patient-derived xenograft (PDX)</td>
<td>Li et al., 2013</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>Chemicals, Peptides, and Recombinant Proteins</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>β-Estradiol (E2)</td>
<td>Sigma-Aldrich</td>
<td>Cat#E4389</td>
</tr>
<tr>
<td>Fulvestrant</td>
<td>Selleckchem</td>
<td>Cat#S1191</td>
</tr>
<tr>
<td>Pablociclib</td>
<td>Pfizer and Selleckchem</td>
<td>N/A and Cat#1116</td>
</tr>
<tr>
<td><strong>Critical Commercial Assays</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dual-Luciferase Reporter Assay System</td>
<td>Promega</td>
<td>Cat#1910</td>
</tr>
<tr>
<td><strong>Deposited Data</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WGS and RNA-seq of WHIM18 PDX</td>
<td>Li et al., 2013</td>
<td>dbGaP: phs000611</td>
</tr>
<tr>
<td>RNA-seq of human primary breast tumors from two neoadjuvant aromatase inhibitor clinical trials (Z1031/POL)</td>
<td>Olson et al., 2009 and Ellis et al., 2011</td>
<td>dbGaP: phs000472</td>
</tr>
<tr>
<td>ChIP-seq and RNA-seq from T47D cell lines</td>
<td>This paper</td>
<td>GEO: GSE116170</td>
</tr>
<tr>
<td><strong>Experimental Models: Cell Lines</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Human: HEK293T</td>
<td>ATCC</td>
<td>CRL-3216</td>
</tr>
<tr>
<td>Human: T47D</td>
<td>ATCC</td>
<td>HTB-133</td>
</tr>
<tr>
<td>Human: MCF7</td>
<td>ATCC</td>
<td>HTB-22</td>
</tr>
<tr>
<td><strong>Experimental Models: Organisms/Strains</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NOD-SCID-IL2Rγc−/− mice</td>
<td>Jackson Laboratories</td>
<td>Cat#005557</td>
</tr>
<tr>
<td>Fox Chase SCID Beige mice</td>
<td>Charles River</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>Oligonucleotides</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>See Table S4 for sequences of mRNA-qPCR primers, ChIP-qPCR primers, and siRNA</td>
<td>N/A</td>
<td>N/A</td>
</tr>
</tbody>
</table>

(Continued on next page)
CONTACT FOR REAGENT AND RESOURCE SHARING

Further information and requests for resources and reagents should be directed and will be fulfilled by the Lead Contact Matthew J. Ellis (mjellis@bcm.edu).

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Cell Lines

All cell lines were purchased from ATCC and cultured at 37°C in 5% CO2. All cell lines were authenticated and tested for mycoplasma. HEK293T and MDA-MB-231 cells were cultured in DMEM with L-Glutamine and 4.5 g/L glucose (HyClone) supplemented with 10% FBS (cat# F0926, Sigma) and 1% penicillin-streptomycin (Invitrogen). T47D and MCF7 cells were cultured in RPMI1640 with L-Glutamine (Mediatech) supplemented with 10% FBS, glucose to 4.5 g/L (Sigma), 10 mM HEPES (GenDEPOT), 1 mM sodium pyruvate (GenDEPOT), and 50 μg/mL gentamycin (GenDEPOT). Estrogen/hormone deprivation was performed by plating cells in culturing media overnight followed by washing with PBS and replacing with hormone deprived media consisting of phenol red free media supplemented as described above but with 10% charcoal-stripped serum (CSS) (cat# F6765, Sigma), followed by changing with hormone-deprived media every 2-3 days for 5-7 days.

In Vivo Animal Studies

All animal experiments were carried out in strict accordance with the guidelines recommended for care and use of laboratory animals by the National Institutes of Health. The Animal Studies Committee at Washington University (St. Louis, MO, USA) approved all animal protocols used for T47D xenograft studies. Three-week old NOD/SCID gamma female mice were purchased from Jackson Laboratories. Stable T47D cells were trypsinized, counted, washed by PBS, and suspended in ice cold serum free RPMI medium at 10^6 cells per 100 μL. Matrigel was added to a final 33% by volume. 150 μL mix (10x10^6 cells) was injected subcutaneously into the mouse flanks bilaterally. Six mice were injected per group. Tumor volumes were measured by caliper weekly. For PDX studies, all animal procedures were approved by the Institutional Animal Care and Use Committee at Baylor College of Medicine (Houston, TX, USA) (protocol# AN-6934). 2-3 mm tumor pieces from a second generation growing WHIM18 tumor were engrafted into cleared mammary fat pads of 3-4 weeks old SCID/bg mice (Charles River) and allowed to grow without exogenous E2 supplementation until tumors reached 150-400 mm^3. Mice were then randomized to receive vehicle or palbociclib (Pfizer) containing chow (daily dose of 70mg/kg per day) for an additional 30 days (11 mice per group). Tumor volumes were measured by caliper every 3-4 days. For all animal experiments, tumor volumes were calculated by V = 4/3 × π × (length/2)^2 × (width/2). Animals were sacrificed when tumors reached 1500 mm^3 or at the study end time point. Tumors and organs were harvested and frozen in liquid nitrogen for storage or fixed in 4% formaldehyde overnight at RT, then held in 70% ethanol before paraffin embedding, sectioning (5 μm) and subsequent IHC processing.
Clinical Samples
The primary breast cancer samples for this study were either accrued from two neoadjuvant endocrine therapy trials (Ellis et al., 2011; Olson et al., 2009) or analyzed from TCGA breast samples (Ciriello et al., 2015). The methodologies for RNA extraction and expression profiling experiments have been previously published (Ellis et al., 2011). Frozen metastatic biopsy samples from patients with advanced breast cancer (Table S2) were accrued under a banking protocol approved by the Washington University School of Medicine Institutional Review Board (approval number 201102244).

METHOD DETAILS

ESR1 Fusion Discovery Using ChimeraScan and INTEGRATE
Fusion candidates were discovered using ChimeraScan (Iyer et al., 2011) and INTEGRATE (Zhang et al., 2016) when whole genome sequencing data were available from 38 cases previously reported (Ellis et al., 2012). The Illumina RNA-Seq paired-end reads in FASTQ format were provided to ChimeraScan version 0.4.5, which was run using default parameters. The alignments (BAM format by TopHat2) of the RNA-seq reads are provided to INTEGRATE version 0.1, which is run using default parameters in RNA only mode. All the analysis was based on hg19. ChimeraScan results (bedpe format) are filtered by removing records with types marked as read through, overlapping converging, overlapping diverging, adjacent converging, and adjacent diverging. These could be transcriptome only variations or chimeras reported because of certain annotation issues. The gene fusions with ESR1 gene as a fusion partner are picked out from all the fusion candidates discovered by the methods described above and from analysis done by TCGA.

Molecular Cloning to Generate ESR1 Fusion Constructs
cDNAs encoding ESR1-e6>NOP2, ESR1-e6>PCDH11X, and ESR1-e6>AKR1D1 were synthesized from patient RNAs via oligo-dT reverse transcription (RT) followed by polymerase chain reaction (PCR) using primers complementary to the 5’ and 3’ ends of the fusion genes. ESR1-e7>POLH and ESR1-e6>AKAP12 were generated from cDNAs encoding ESR1, POLH, and AKAP12 by overlapping PCR extension/amplification as previously described for ESR1-e6>YAP1 (Li et al., 2013). All other constructs were created by standard PCR using pre-existing cDNA templates. Amplified DNA fragments were inserted into the lentiviral vector pFLRu-FH as described previously (Li et al., 2013). ESR1-e6>AKAP12 was generated but due to its exceptionally large size, could not be cloned into the lentiviral vector and subsequently proved hard to express upon transfection and was not studied further. Carboxy-terminal HA-tagged ESR1 fusion constructs were generated by subcloning each construct from pFLRu-FH using primers for PCR that included BamHI and EcoRI restriction sites along with the HA sequence (STAR METHODS) into pCDH-CMV-MCS-ER1α-RFP-Puro vector (System Biosciences). All constructs in their final vectors were confirmed by Sanger sequencing.

Lentiviral Production and Stable Cell Line Generation
Lentiviral production was performed as described previously (Li et al., 2013). Briefly, ESR1 constructs cloned in pFLRu-FH and HA-tagged ESR1 constructs in pCDH-CMV-MCS-ER1α-RFP-Puro (System Biosciences) and pCDH-CMV-MCS-ER1α-Puro (System Biosciences) vector DNAs were co-transfected with the packaging plasmids into HEK293T cells using FuGene HD (Roche). Culture media containing viruses were harvested after 48 hr, filtered, and added to T47D and MCF7 cells in the presence of polybrene. Stably infected cells were selected by 2 μg/mL puromycin (Sigma) two days after infection. Three sets of T47D stable cell lines were generated, one set expressing non-HA-tagged ESR1 constructs (used in Figures 2, S2, 4G, 4H, 5A, and S5A), one set expressing HA-tagged ESR1 constructs in pCDH-CMV-MCS-ER1α-RFP-Puro (used in Figures 3, S3D–S3F, 4A–4F, and S4A–S4F) and one set expressing HA-tagged ESR1 constructs in pCDH-CMV-MCS-ER1α-Puro used in Figure S3A. Two sets of MCF7 cells were generated, one set expressing non-HA-tagged ESR1 constructs (used in Figures S2C, S2D, and S5B) and HA-tagged ESR1 constructs in pCDH-CMV-MCS-ER1α-Puro (used in Figures 4D and S4G).

In Vitro Growth Assays
Hormone independent cell growth was subsequently measured by low density triplicate plating of T47D or MCF7 cell lines in hormone-deprived media in 96-well plates (2000 cells/well) in the absence or presence of 10 nM E2 (Sigma) in combination without or with 10 nM fulvestrant (Selleckchem). Cell growth was quantified by Alamarblue assay at Day 1 and Day 12 post plating and relative growth was calculated as Day 12/Day 1 ratios. Remaining cells not used in the Alamarblue assay were plated in CSS containing media and grown further for 72h in the absence of 10 nM fulvestrant before harvesting and subsequent processing for immunoblot analysis. For palbociclib sensitivity assays, T47D and MCF7 cells were hormone deprived for seven days, then plated in 96-well plates as described above in the absence of presence of 3-fold dilutions of palbociclib (cat# S1116, Selleckchem) from 10 μM down to 0.0015 μM for 12 days, changing hormone-deprived media and palbociclib every 2-3 days. Cell growth was quantified similarly as above and relative growth was calculated by taking the palbociclib treated Day 12/Day 1 ratio divided by the vehicle treated Day 12/Day 1 ratio.

siRNA Knockdown
Stable T47D or MCF7 were hormone-deprived for 7-9 days before pre-treatment with DMSO vehicle or 1 μM fulvestrant for 24h prior to reverse transfection with RNAiMAX (Invitrogen) and 50 nM siRNA Universal Negative Control #1 (cat# SIC001, Sigma) or 50 nM
siESR1 targeting N-terminal sequences of ESR1 (Sigma). Fresh DMSO or 1 μM fulvestrant was added during the transfection. 48h post transfection, cells were collected by scraping and subjected to immunoblotting.

**Immunoprecipitation and Immunoblot Analysis**

For IP assays, hormone deprived stable T47D cells were left untreated or stimulated with 10 nM E2 for 15’ at 37°C. Cells were harvested then lysed in IP lysis buffer [0.5% NP-40, 10% glycerol, 280 mM NaCl, 50 mM Tris pH 8.0, 2 mM EGTA, 0.2 mM EDTA, 1 mM PMSE, 1 mM sodium orthovanadate, 1 mM DTT, 1 μg/mL pepstatin, phosSTOP phosphatase inhibitor tablet (Roche), and complete EDTA-free protease inhibitor tablet (Roche)] for 20 min. 0.5 mg of clarified lysates were immunoprecipitated with an Anti-HA antibody (cat# 3724, Cell Signaling, 1:50) overnight at 4°C with rotation. Protein A magnetic beads (cat# 1614013, Bio-Rad) were added and rotated for 1h at 4°C followed by extensive washing with IP lysis buffer. Immunoprecipitated samples along with 25 μg of whole cell lysates (inputs) were heated at 90°C before loading onto SDS-PAGE gels (Invitrogen) and electoblotted onto nitrocellulose membranes (Bio-Rad). Whole cell lysates for all other immunoblotting procedures were prepared in RIPA buffer and blotted as described previously (Li et al., 2013). Fresh frozen WHIM18 tumors were cryopulverized (Covaris CP02) then lysed in RIPA buffer. The following primary antibodies were used for blotting: N-terminal estrogen receptor α (cat# 04-820, Millipore, 1:1000), C-terminal estrogen receptor α (cat# sc-543, Santa Cruz, 1:1000), E-Cadherin (cat#14472, Cell Signaling, 1:1000), and Snail (cat #3879, Cell Signaling, 1:500). β-Actin (cat# A5316, Sigma, 1:5000) used as loading control for all immunoblotts.

**Dual Luciferase ERE Reporter Assay**

To test ER fusion effect on wild-type ERE activation ability, 60 ng of empty pCDH-CMV-MCS-ER1a (Hall and McDonnell, 1999) and 5 ng control Renilla luciferase vector (pGL4.70, Promega). Prior to transfection, HEK293T cells were cultured in hormone deprived media containing charcoal-stripped serum for seven days. One day after transfection, cells were either left unstimulated or stimulated with 2.5 nM E2 for 24h. On the following day, cells were quantified for the Dual Luciferase ERE Reporter Assay (Promega). Averages of Firefly/Renilla luminescence readings from each sample were calculated and expressed as fold change in activity relative to Vector transfected –E2.

**Biotinylated 3X ERE Pulldown**

All 5’ biotinylated DNA were synthesized by Integrated DNA Technologies. The sequence of the wild-type and mutant 3XERE were GTAGTCACCTGTGACCTAGACCGTCGTGACTGCACTGTGACCGT and GTAGATCCTGGAACCTAGCGCCAGGTCACTGTGACCGT, respectively. Each DNA and its complement were annealed by boiling at 95°C for 15 min and allowed to cool overnight at room temperature. Each biotinylated DNA was bound to streptavidin M-280 Dynabeads (Invitrogen) per manufacturer’s directions and washed with NETN buffer (20 mM Tris, pH 8.0, 150 mM NaCl, 0.2 mM EDTA, and 0.5% NP-40) before incubation with 200–1000 μg of HEK293T extracts (whole cell or nuclear extracts) transiently transfected with the indicated expression constructs. Protein/DNA extracts were rotated at 4°C for 1h then washed four times with NETN buffer and analyzed by immunoblotting.

**ChIP-seq**

**Chromatin preparation**

Stable T47D cells were hormone deprived for 7 days in charcoal-stripped containing media before fixing at 1% formaldehyde (cat# F8775, Sigma) while swirling for 10 min at RT. To quench, glycine was added to 0.2 M and incubated for another 5 min at RT. Cells were then washed and harvested in cold TBSE (20 mM Tris-HCl pH 7.5, 150 mM NaCl, 1 mM EDTA). After further washing in TBSE, cells were lysed in 0.1% SDS buffer (50 mM HEPES-KOH pH 7.5, 150 mM NaCl, 1 mM EDTA, 1% Triton X-100, 0.1% sodium deoxycholate, 0.1% SDS, complete EDTA-free protease inhibitor cocktail tablet) for 15 min at 4°C with rotation. Samples were centrifuged and washed 3X with 0.1% SDS buffer and resultant nuclear pellets were lysed with 1% SDS buffer for 15 min at 4°C with rotation.

**Chromatin immunoprecipitation**

Dynabeads Protein G (ThermoFisher) were equilibrated in 0.1% SDS buffer then a portion was added to chromatin extracts from above to pre-clear for 2h at 4°C with rotation. HA antibody (cat# sc-7392, Santa Cruz) was added to the remaining Protein G and allowed to bind to 2h at 4°C with rotation. Pre-cleared chromatin extracts were then added to antibody-bound beads and rotated overnight at 4°C followed by extensive 5 min washes 0.1% SDS buffer, then once in 0.1% SDS buffer containing 0.35 M NaCl, then once in ChIP wash buffer (10 mM Tris–HCl pH 8.0, 250 mM LiCl, 1 mM EDTA, 0.5% NP-40, 0.5% sodium deoxycholate), then once in TE buffer. Elution was performed by pelleting and resuspending in ChIP buffer and heating at 68°C for 1h with agitation. Samples were analyzed by immunoblotting.
were pelleted, reuspended in TE buffer and crosslinks were reversed with pronase and heating at 42°C for 2h followed by incubation at 67°C overnight. Chromatin isolation was then performed using phenol:chloroform extraction and used for ChIP-qPCR and subsequently processed for next generation sequencing as follows:

**Next generation sequencing**

The Biopolymers Facility (Harvard Medical School, Boston, MA, USA) conducted quality control testing on an Agilent BioAnalyzer followed by Wafergen PrepX DNA ChiP library preparation. Pooled libraries were loaded onto two lanes of HiSeq Rapid v2 flow cell with PhiX control adaptor-ligated library spiked-in at 5% by weight to ensure balanced diversity and to monitor clustering and sequencing performance. Single-end 100 bp reads were generated on a HiSeq 2500 Sequencing System.

**RNA-seq**

Stable T47D cells were hormone deprived for 5 days in charcoal-stripped containing media then grown for another 48h in the absence or presence of 10 nM E2. RNA was isolated using RNeasy Mini Kit (QIAGEN) according to manufacturer’s directions and subjected to column DNase (QIAGEN) digestion to remove genomic DNA before final elution in water. The Genomic and RNA Profiling Core (Baylor College of Medicine, Houston, TX, USA) conducted sample quality checks using the NanoDrop spectrophotometer and Agilent Bioanalyzer 2100 followed by subsequent Illumina TruSeq Stranded mRNA library preparation protocol (p/n 15031047, rev. E) as follows: A double-stranded DNA library was created using 180ng of total RNA (measured by picogreen), with the Illumina TruSeq Stranded mRNA-Seq Sample Prep Kit (cat# RS-122-2101). First, cDNA was created using the fragmented 3’ poly(A) selected portion of total RNA and random primers. During second strand synthesis, dTTP is replaced with dUTP which quenches the second strand during amplification, thereby achieving strand specificity. Libraries were created from the cDNA by first blunt ending the fragments, attaching an adenosine to the 3’ end and finally ligating unique adapters to the ends. The ligated products were then amplified using 15 cycles of PCR. The resulting libraries were quantified using a NanoDrop spectrophotometer and fragment size assessed on an Agilent Bioanalyzer. A qPCR quantification was performed on the libraries to determine the concentration of adaptor ligated fragments using Applied Biosystems Viia7 Real-Time PCR System and a KAPA Library Quant Kit (cat# KK4824).

Using the concentration from the Viia7 qPCR machine above, 27 pM of library was loaded onto two lanes of a high output v4 flow cell (Illumina p/n PE-401-4001) and amplified by bridge amplification using the Illumina cBot machine (cBot protocol: PE_HiSeq_Cluster_Kit_v4_cBot_recipe_v9.0). PhiX Control v3 adaptor-ligated library (Illumina p/n 15017666) is spiked-in at 2% by weight to ensure balanced diversity and to monitor clustering and sequencing performance. Paired-end 100 bp reads were generated on a HiSeq 2500 Sequencing System (Illumina p/n FC-401-4003).

**Quantitative PCR**

qPCR was performed using SsoAdvanced SYBR green Supermix (Bio-Rad) and 0.5 μM primers (Sigma) listed in Key Resources Table and run on a LightCycler 96 (Roche). All samples were run in triplicate and values shown are the average ± SEM of at least 2 independent experiments. For ChiP-qPCR, 1% inputs were run for each corresponding sample and primers against a region on Chr20 which ERα does not bind was used as a negative control. Chromatin captured from HA-ChiP in YFP-HA cells were used as control instead of IgG antibody alone. For mRNA-qPCR (Figures 3D, SSF, 4C, and S4B), RNA was extracted as described above from stable T47D cells grown in hormone deprived media for 5 days, before growing another 24h in the absence (−E2) or presence of 10 nM E2 and/or 1 μM fulvestrant as indicated. One step quantitative RT-PCR was performed using iScript reverse transcriptase (Bio-Rad) with 25 ng RNA. Expression was normalized to GAPDH and relative expression was calculated as fold change using the 2−ΔΔCt method with YFP −E2 set to 1.

**Immunohistochemistry**

IHC staining was performed with assistance from The Lester and Sue Smith Breast Center Pathology Core at Baylor College of Medicine (Houston, TX, USA). Tissue sections were incubated at 58°C overnight in a dry slide incubator and deparaffinized in xylene and graded alcohol washes. Antigen retrieval was performed in 0.1 M Tris-HCl pH 9.0 following by quenching in 3% H2O2. The following antibodies were used to stain for 1h at RT: ERα (clone 6F11, Novocasta, 1:200), pRb (Ser780) (clone D59B7, Cell Signaling, 1:25), Ki67 (clone MIB-1, Dako, 1:200), and PR (clone PgR 1294, Dako, 1:1600). After washing in TBS, EnVision labeled polymer-HRP anti-mouse or anti-rabbit antibodies (Dako) were added for 30 min. at RT. Slides were washed with TBS then developed with DAB+ solution (Dako) and DAB sparkle enhancer (Biocare). After washing in TBS, slides were counterstained with Hematoxylin, dehydrated, and cleared before coverslipping with Cytoseal (VWR). ER positive staining cells were quantified in lung sections from T47D xenograft bearing mice. Stained WHIM18 tumor and lung sections were quantified from 5 mice per treatment group.

**Scratch Wound Assay**

Stable T47D cells were hormone deprived for 7 days before seeding in hormone deprived media at 50,000 cell/well in a 96-well ImageLock plate (Essen BioScience). The following day, cells were treated 10 μg/mL mitomycin C (Sigma) for 2h before wounding with a WoundMaker (Essen BioScience). Cells were washed with hormone deprived media then fresh hormone deprived media containing mitomycin C was added. Images were acquired every 3h for 72h with an IncuCyte live-cell analysis system (Essen BioScience). Fresh hormone deprived media plus mitomycin C was changed every 24h. Cell motility assessed by the relative wound density (RWD) calculated by measuring density in the wound area relative to the density outside the wound area at 72h. The RWD is
0\% at 0h and 100\% when the density inside the wound is the same as the density outside the wound, therefore normalizing for changes in density due to proliferation outside the wound. Representative images are depicted and quantification from average of three independent experiments \( \pm \) SEM are shown. \( P \)-values based on ANOVA followed by Dunnett’s post hoc test for multiple comparisons correction.

**Immunofluorescence Microscopy**

Hormone deprived stable T47D cells were seeded onto poly-D-lysine coated coverslips (Fisher) and grown overnight. Cells were fixed with 4\% formaldehyde for 20 min. at RT followed by permeabilization with 0.2\% Triton X-100 for 10 min at RT and blocking with 10\% normal goat serum for 1h. Antibodies against E-cadherin (cat# 14472, Cell Signaling, 1:50), vimentin (cat# 5741, Cell Signaling, 1:100) or HA-tag (cat# 2367, Cell Signaling, 1:50) were incubated overnight at 4\°C then goat anti-mouse-488 (cat# A-11011, Invitrogen, 1:1000), goat anti-rabbit-488 (cat# A-11008, Invitrogen, 1:1000), or goat anti-mouse-648 (cat# A-11004, Invitrogen, 1:1000) was added for 30 min at RT. Coverslips were mounted onto slides with ProLong Gold Antifade Reagent (Invitrogen). Fluorescence images were acquired on a Nikon Eclipse Ti microscope equipped with a CoolSNAP EZ camera (Photometrics Scientific) using a Plan APO 40X/0.95 aperture objective and Nikon NIS elements software. Images were quantified with ImageJ by setting a threshold from E-cadherin fluorescence channel from ESR1-WT cells which gave cell surface appearance. The same threshold was applied to images acquired from all other cell lines and cells were considered E-cadherin\(^{\ast} \) when cell surface signal was present using the described threshold. 2-3 images per cell line were quantified and shown are averages from two independent experiments \( \pm \) SEM.

**QUANTIFICATION AND STATISTICAL ANALYSIS**

All statistical tests were performed with GraphPad Prism 7. \( P \)-values less than 0.05 were considered statistically significant (*\( p < 0.05 \), **\( p < 0.01 \), ***\( p < 0.001 \), ****\( p < 0.0001 \)). For box and whiskers plots, the box depicts interquartile range with median line and whiskers extending to minimum and maximum values for each group.

Immunofluorescence images were quantified with ImageJ by setting a threshold from E-cadherin fluorescence channel from ESR1-WT cells which gave cell surface appearance. The same threshold was applied to images acquired from all other cell lines and cells were considered E-cadherin\(^{\ast} \) when cell surface signal was present using the described threshold. 2-3 images per cell line were quantified and shown are averages from two independent experiments \( \pm \) SEM.

For cell proliferation assays, significance was determined based on one-way ANOVA followed by Tukey’s post hoc test for multiple comparisons correction for ESR1-e6>YFP1 or ESR1-e6>PCDH11x fusion-expressing cells compared to all other stable T47D cells within a treatment group (indicated by asterisks) or using two-way ANOVA followed by Bonferroni’s post hoc test for multiple comparisons correction for each construct after E2 stimulation, +E2 versus –E2 (####\( p < 0.0001 \)). Data are mean \( \pm \) SEM of three independent experiments. For palbociclib sensitivity assays in stable T47D and MCF7 cell lines, each point represents averages \( \pm \) SEM from 3-4 independent experiments of relative cell growth for indicated palbociclib dose, calculated by taking the palbociclib treated Day 12/Day 1 alamarBlue reading ratio divided by vehicle treated Day 12/Day 1 ratio. \( P \)-values describes significance between YFP +E2, ESR1-e6>YAP1, and ESR1-e6>PCDH11x slopes compared to YFP –E2 as measured by ANOVA with Tukey’s post hoc analysis for multiple comparisons.

For ChIP-qPCR assays, bar graphs depict enrichment of ER binding regions in hormone deprived stable T47D cells before and after stimulation with E2 (100 nm) for 45 min as determined by HA-ChIP followed by qPCR for ER binding regions of estrogen responsive genes as indicated and negative ER binding region. Average values from 3 experiments are shown \( \pm \) SEM. Asterisks denote significant differences in binding compared to WT-ER –E2 for each gene binding region as determined by ANOVA followed by Tukey’s post hoc test.

**In Vivo Analysis**

For T47D xenograft assays, significance of tumor volumes Day 146 post injection was determined based on Kruskal-Wallis test followed by Dunn’s post hoc analysis for multiple comparisons correction comparing YFP –E2 to all other groups with N = 6 mice per group. For ER\(^{\ast} \) cell counting in the lungs, ER\(^{\ast} \) cells from IHC images of 5 mice bearing xenografted tumors at Day 146 were manually counted. Statistical analysis was based on Kruskal-Wallis test with Dunn’s post hoc analysis for multiple comparisons correction comparing YFP versus fusion-bearing groups and YFP +E2.

For WHIM18 PDX assays, Figure 5B depicts averages of tumor volumes from 8-11 mice per group \( \pm \) SEM are shown. \( P \)-value determined by unpaired \( t \)-test describes significance of tumor growth rates (slopes) derived from tumor volumes at day of randomization/start of treatment (Day 61 post transplantation) to experiment end (Day 91 post transplantation) for vehicle and palbociclib treated mice. Figure 5Sc depicts tumor growth rates as described above for all tumors measured in each condition. Middle line represents mean tumor volume \( \pm \) SD. Day 0 post treatment is the same as treatment start/Day 61 post transplantation and represents the tumor growth rate from time tumors were palpable (Day 49 post transplantation) up to treatment start date. Day 30 is the same as Day 91 post transplantation and represents on-treatment tumor growth rates. \( P \)-values determined by one-way ANOVA with Tukey’s post hoc analysis for multiple comparisons. For IHC images, positive staining cells were quantified in tumor and lung sections from 5 mice per treatment group. Bar graphs represent mean \( \pm \) SD and \( P \)-values indicate significance as determined by Wilcoxon rank-sum tests.
**ChIP-seq Analysis**

Single-end 50 bp reads were aligned to hg19 (GRCh37) reference genome using BWA (Li and Durbin, 2010) and alignment files were converted to BED format using BEDTools (Quinlan and Hall, 2010). BED files were used for peak calling by MACS v1.4.2 (Zhang et al., 2008). MACS peaks (p < 1e−7 cutoff and associated FDRs) were annotated with GREAT (McLean et al., 2010) using default settings. Motif analysis was performed by taking ~100 bp sequences centered on the summit of peaks and submitted for enrichment analysis using MEME-ChIP in normal mode (Bailey and Elkan, 1994). P-values represent the probability that an equal or better site would be found in a random sequence of the same length conforming to the background letter frequencies (Bailey and Elkan, 1994).

**RNA-seq Analysis**

Paired-end 100 bp reads were aligned to hg19 (GRCh37) reference genome using RSEM v1.2.31 (Li and Dewey, 2011) and Bowtie 2 (Langmead and Salzberg, 2012). TPM (Transcripts Per Million) values calculated by RSEM were log2 transformed and row Z-scores were generated for the all heatmaps shown. Differential gene expression analysis was performed using EBseq (Leng et al., 2013) with FDR < 0.1 as a cutoff comparing 4 groups: (1) YFP +E2 versus YFP −E2, (2) ESR1-e6❯YAP1 −E2 versus YFP −E2, (3) ESR1-e6❯PCDH11X −E2 versus YFP −E2, and (4) ESR1-e6❯NOP2 −E2 versus YFP −E2. Hierarchical clustering was performed on differentially expressed genes for which a nearby binding site within 1 Mb was observed by ChIP-seq shared by ESR1-WT, ESR1-e6❯YAP1, ESR1-e6❯PCDH11X, and ESR1-e6❯NOP2 for Figure 3C. Clustering was also performed on differentially expressed genes for which a nearby site within 1 Mb was selectively bound by both ESR1-e6❯YAP1 and ESR1-e6❯PCDH11X but bound by ESR1-WT nor ESR1-e6❯NOP2 (Figure S4C).

**DATA SOFTWARE AND AVAILABILITY**

The accession number for the ChIP and RNA sequencing data from T47D reported in this paper is GEO: GSE116170. TCGA data for fusion gene discovery and for gene expression analysis can be downloaded from https://portal.gdc.cancer.gov/ and https://portal.gdc.cancer.gov/legacy-archive. RNA-seq of human primary breast tumors from two neoadjuvant aromatase inhibitor clinical trials can accessed through dbGaP phs000472.
Supplemental Information

Functional Annotation of *ESR1* Gene Fusions in Estrogen Receptor-Positive Breast Cancer

**Figure S1 related to Figure 1. PCR validation of ESR1 fusions.** cDNAs were synthesized from patient RNA or WHIM18 tumor RNA, followed by PCR amplification and sanger sequencing. Black line indicates fusion break point. Sequences contributed by ESR1 are to the left of the breakpoint and from fusion partner sequences to the right of the breakpoint.
Figure S2 related to Figure 2. Out-of-frame \( ESR1 \) fusions lack estrogen-independent growth promoting ability and in-frame \( ESR1 \) fusions from endocrine refractory disease promotes estrogen-independent and fulvestrant-resistant growth. (A) Bar graphs depicting growth of hormone deprived stable out-of-frame \( ESR1 \) fusion or \( ESR1 \) fragments expressing T47D cells in the absence (open bars) or presence of fulvestrant (black bars). Data are average of 3 independent experiments ±SEM. (B) Western blotting of \( ER\alpha \) in hormone deprived stable T47D cells treated in the absence of presence of fulvestrant. Asterisks denote \( ESR1 \) fusion or \( ESR1\)-e6. \( \beta\)-Actin used as loading control. (C) Similar to Figure 2C, except hormone deprived stable MCF7 cells expressing the indicated constructs were used. Significance was determined based on ANOVA followed by Tukey’s post-hoc test for multiple comparisons correction for \( ESR1\)-e6>YAP1 or \( ESR1\)-e6>PCDH11X fusion expressing cells compared to all other stable T47D cells within a treatment group (**** p < 0.0001, ** p < 0.01, * p < 0.05) or using two-way ANOVA followed by Bonferroni’s post-hoc test for multiple comparisons correction for each construct after E2 stimulation, –E2 vs +E2 (#### p < 0.0001). Data are mean ± SEM of three independent experiments. (D) Similar to (B) except hormone deprived stable MCF7 cells were used.
Figure S3 related to Figure 3. In-frame ESR1 fusions bind EREs but have differential abilities to drive transcription. (A) Immunofluorescence staining with Anti-HA antibody, pseudocolored in red, was performed on hormone-deprived stable T47D cells as indicated, showing nuclear localization of all HA-tagged ESR1-WT, ESR1 fusions, and ESR1-e6 truncation. Parental T47D cells lacking exogenous expression of any construct was used as a negative control. DAPI stained nuclei pseudocolored in blue. 10 µm scale bar. (B) Bar graphs depicting ERE-luciferase reporter activity in hormone-deprived HEK-293T cells ±2.5 nM E2 for 24h. Averages of Firefly/Renilla luminescence readings from each sample were calculated and expressed as fold change in activity relative to Vector transfected –E2. Shown are the averages of two independent experiments ±SEM. (C) Full-length ESR1(wt) or ESR1 fusions were transfected into HEK293T cells and subjected to pulldown with 3X ERE(wt) or ERE(mut) containing a DNA binding inactivating double zinc finger mutations as negative controls and analyzed by western blotting using a N-terminal ER antibody along with 10% input as positive controls. (D) Lysates from hormone deprived stable T47D cells stimulated with E2 (15 min) were immunoprecipitated with an HA antibody or rabbit IgG control then blotted with N-terminal ERα antibody demonstrating successful IP of fusion ER (asterisks) and WT-ER (top panel). Blotting with a C-terminal ERα antibody that recognizes only WT-ER detects strong co-IP with WT-ER but lack of WT-ER co-IP with ER fusions. (E) Whole cell lysates (inputs) analyzed by Western blot from (C) with N- and C-terminal ER antibodies along with β-Actin control. (F) Same as Figure 3D, except –E2 and +E2 conditions shown for all cell lines analyzed.
Motif enrichment analysis of binding sites for genes up-regulated by ESR1-YAP1 and ESR1-PCDH11X vs ESR1-WT and ESR1-NOP2:

<table>
<thead>
<tr>
<th>Name</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>ERE</td>
<td>7.5e-21</td>
</tr>
</tbody>
</table>

Figure S4 related to Figure 4. Active ESR1 fusions promote metastasis by up-regulating an EMT-like transcriptional program. (A) MEME-ChIP motif enrichment was performed using 100 bp sequences centered around each peak’s summit (derived from Table S3) for genes strongly upregulated by the active ESR1-e6>YAP1 and ESR1-e6>PCDH11X fusions (Figure 4A) demonstrating ERE motif enrichment with overall P-value of 7.5e-21. (B) Same as in Figure 4C, except ±E2 conditions shown for all T47D cell lines analyzed. Data are averages of two independent experiments ±SEM. (C) Hierarchical clustering was performed on differentially expressed genes within 1Mb of 71 selectively bound sites by ESR1-e6>YAP1 and ESR1-e6>PCDH11X (shaded gray overlap). GSEA hallmark pathway analysis for these genes demonstrates enrichment for UV response and EMT hallmark pathways. GJA1 and TGFBR3 (shown in red) contributed to EMT pathway enrichment. Scale bar indicates row Z-score. (D) Quantification of relative wound density 72h post wounding from Figure 4E. Data are averages from three independent experiments ±SEM. (E) Representative immunofluorescence images of two independent experiments from hormone deprived stable T47D cells expressing constructs as indicated and hormone deprived MDA-MB-231 stained with E-cadherin and vimentin antibodies pseudocolored in green and DAPI stained nuclei pseudocolored in blue. 50 μm scale bar. (F) Bar graphs depicting average number of cell surface E-cadherin positive (E-cadherin+) cells quantified from images in (E). Data are averages of two independent experiments ±SEM. (G) Same as in Figure 4F, except using stable MCF7 cell lines.
Figure S5 related to Figure 5. ESR1 fusions induce cell cycle activity through activation of Rb and ESR1 fusion driven growth can be suppressed with CDK4/6 inhibitor treatment. (A) IHC images of T47D xenograft tumor sections with indicated constructs grown in the absence or presence of E2 supplementation stained with a phospho-Rb (pRb) (Ser780) antibody. 100 µm scale bar. (B) Relative growth of hormone deprived stable MCF7 cells treated with increasing concentrations of a CDK4/6 inhibitor, palbociclib, and in the presence of E2 for YFP (+E2) normalized to vehicle treated cells for each condition. $P$-value describes significance between YFP +E2, ESR1-e6>YAP1, and ESR1-e6>PCDH11X slopes compared to YFP –E2 as measured by ANOVA with Tukey’s post-hoc analysis for multiple comparisons. Data shown are averages of three independent experiments ±SEM. (C) Day 0 post treatment WHIM18 tumor growth rates were calculated from slopes of tumor growth from Day 49 to Day 61 post tumor transplantation. Day 30 post treatment growth rate was calculated from Day 61 to Day 91 post tumor transplantation. Individual tumor growth rates from each mouse are plotted with middle line representing median value and extending from 25% to 75% percentile values. $P$-values determined by two way ANOVA with Tukey’s post-hoc analysis for multiple comparisons correction. (D) Progesterone receptor (PR) expression was examined by IHC in WHIM18 tumor sections from vehicle or palbociclib treated mice demonstrating that palbociclib does not alter PR levels. Quantification of IHC staining below with Wilcoxon rank-sum test used to calculate significance comparing treatment groups. Data are averages counts from 5 tumor sections from each treatment group with error bars representing SD. 100 µm scale bar.
Table S1. Related to Figure 1 and Table S2. Summary of ESR1 fusion transcripts from ER+ samples. The TCGA dataset includes 728 breast cancer patients (Ciriello et al., 2015). The NeoAI Trials dataset includes 41 aromatase inhibitor sensitive neoadjuvant primary samples, 40 aromatase inhibitor resistant neoadjuvant primary samples (Ellis et al., 2011; Olson et al., 2009). The Late Stage dataset includes 25 advanced ER+ endocrine therapy refractory, metastatic biopsy samples (Table S2) and includes WHIM18, a PDX derived from a metastatic biopsy from a patient with endocrine therapy resistant disease (Li et al., 2013). ChimeraScan (Iyer et al., 2011) and INTEGRATE (Zhang et al., 2016) were used to detect gene fusions in RNA-seq data and in some cases with whole genome data. ESR1 fusions are presented according to the number of 5' exons (top portion of table) or 3' exons (bottom portion of table) retained in each of the indicated ESR1 fusions with corresponding amino acids (aa). The first two 5' exons of ESR1 (e2) are non-coding exons. The -> indicates direction of fusion transcript from 5' to 3' direction. Also shown are mutational status of genes found to be significantly mutated in ER+ breast cancer representing common risk factors for hormone receptor positive breast cancer (Ellis et al., 2012) and platform used to determine mutational status (WES, whole-exome sequencing; WGS, whole-genome sequencing).
<table>
<thead>
<tr>
<th>Oligonucleotides</th>
<th>Reference</th>
<th>Identifier</th>
</tr>
</thead>
<tbody>
<tr>
<td>mRNA-qPCR primers:</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>GREB1</strong>: Forward, 5'-CAAAGAATAACCTGGCCCTGC-3'</td>
<td>This paper</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>GREB1</strong>: Reverse, 5'-GACATGCCCTGCCTCTCATACTTA-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TFF1</strong>: Forward, 5'-GTGGTACGCGGCTCCAGT-3'</td>
<td>This paper</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>TFF1</strong>: Reverse, 5'-GGACCCACAGAAGGATG-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>PGR</strong>: Forward, 5'-CTTAATCAACTAGCGAGAG-3'</td>
<td>This paper</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>PGR</strong>: Reverse, 5'-AAGCTCTACCCAGAATACT-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>SNAI1</strong>: Forward, 5'-TGGGAACCTACTACAGCGA-3'</td>
<td>This paper</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>SNAI1</strong>: Reverse, 5'-AGATGAGCATTGGGCACGGAG-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>VCAN</strong>: Forward, 5'-CCAGTGTGAACTTGATTG-3'</td>
<td>Sigma-Aldrich</td>
<td>FH1_VCAN</td>
</tr>
<tr>
<td><strong>VCAN</strong>: Reverse, 5'-CAACATAACTTGGAAGGAG-3'</td>
<td>Sigma-Aldrich</td>
<td>RH1_VCAN</td>
</tr>
<tr>
<td><strong>GAPDH</strong>: Forward, 5'-CTTTTGCCGCTGGCCAG-3'</td>
<td>Sigma-Aldrich</td>
<td>FH2_GAPDH</td>
</tr>
<tr>
<td><strong>GAPDH</strong>: Reverse, 5'-TGGATGCAACAAATCCAC-3'</td>
<td>Sigma-Aldrich</td>
<td>RH2_GAPDH</td>
</tr>
<tr>
<td>ChIP-qPCR primers:</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>GREB1 ERE</strong>: Forward, 5'-AGCAGTGATACCTGGGCAACG-3'</td>
<td>Lin et al., 2004</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>GREB1 ERE</strong>: Reverse, 5'-CGACCCACAGAATGAAAGCCAGCAAAC-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>TFF1 ERE</strong>: Forward, 5'-GTCGTTGCCAGCGTTTCCATG-3'</td>
<td>This paper</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>TFF1 ERE</strong>: Reverse, 3'-CTCTCCAGCCTGAAATT-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>PGR Enhancer</strong>: Forward, 5'-GATGACAGAAGGAGAACTTGAAG-3'</td>
<td>This paper</td>
<td>N/A</td>
</tr>
<tr>
<td><strong>PGR Enhancer</strong>: Reverse, 5'-ATATGGCATTGGAAGGAAG-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chr20 negative region: Forward, 5'-GAGGCTCTGCTGGAGTAG-3'</td>
<td>Carroll et al., 2006</td>
<td>N/A</td>
</tr>
<tr>
<td>Chr20 negative region: Reverse, 3'-CGTTCCCTGTGAAACAGTT-3'</td>
<td></td>
<td></td>
</tr>
<tr>
<td>siESR1: Sense, 5'-GAAAGAUUGGCAAGCUAC-3'</td>
<td>Sigma-Aldrich</td>
<td>Oligo#3020649250-000030</td>
</tr>
<tr>
<td>siESR1: Antisense, 5'-UGGUACUGGCAUCUUC-3'</td>
<td>Sigma-Aldrich</td>
<td>Oligo#3020649250-000040</td>
</tr>
</tbody>
</table>

Table S4. Sequences of mRNA-qPCR and ChIP-qPCR primers, and siRNA. Related to STAR Methods.