XBPI promotes triple-negative breast cancer by controlling the HIF1α pathway

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Cancer cells induce a set of adaptive response pathways to survive in the face of stressors due to inadequate vascularization. One such adaptive pathway is the unfolded protein (UPR) or endoplasmic reticulum (ER) stress response mediated in part by the ER-localized transmembrane sensor IRE1 (ref. 2) and its substrate XBP1 (ref. 3). Previous studies report UPR activation in various human tumours, but the role of XBPI in cancer progression in mammary epithelial cells is largely unknown. Triple-negative breast cancer (TNBC)—a form of breast cancer in which tumour cells do not express the genes for oestrogen receptor, progesterone receptor and HER2 (also called ERBB2 or NEU)—is a highly aggressive malignancy with limited treatment options. Here we report that XBPI is activated in TNBC and has a pivotal role in the tumorigenesis and progression of this human breast cancer subtype. In breast cancer cell line models, depletion of XBPI inhibited tumour growth and tumour relapse and reduced the CD44highCD24low population. Hypoxia-inducing factor 1α (HIF1α) is known to be hyperactivated in TNBCs. Genome-wide mapping of the XBPI transcriptional regulatory network revealed that XBPI drives TNBC tumorigenesis by assembling a transcriptional complex with HIF1α that regulates the expression of HIF1α targets via the recruitment of RNA polymerase II. Analysis of independent cohorts of patients with TNBC revealed a specific XBPI gene expression signature that was highly correlated with HIF1α and hypoxia-driven signatures and that strongly associated with poor prognosis. Our findings reveal a key function for the XBPI branch of the UPR in TNBC and indicate that targeting this pathway may offer alternative treatment strategies for this aggressive subtype of breast cancer.

We determined UPR activation status in several breast cancer cell lines. XBPI expression was readily detected in both luminal and basal-like breast cancer cell lines, but the level of its spliced form was higher in the latter which consist primarily of TNBC cells; XBPI activation was also higher in primary TNBC patient samples (Fig. 1a, b). PERK but not ATF6 was also activated (Extended Data Fig. 1a), and transmission electron microscopy revealed more abundant and dilated ER in multiple TNBC cell lines (Extended Data Fig. 1b). These data reveal a state of basal ER stress in TNBC cells.

XBPI silencing impaired soft agar colony-forming ability and invasiveness (Extended Data Fig. 1c) of multiple TNBC cell lines, indicating that XBPI regulates TNBC anchorage-independent growth and invasiveness. We next used an orthotopic xenograft mouse model with inducible expression of two XBPI short hairpin RNAs (shRNAs) in MDA-MB-231 cells. Tumour growth and metastasis to lung were significantly inhibited by XBPI shRNAs (Fig. 1c–e and Extended Data Fig. 1d–g). This was not due to altered apoptosis (caspase 3), cell proliferation (Ki67) or hyperactivation of IRE1 and other UPR branches (Fig. 1e and Extended Data Fig. 1h, i). Instead, XBPI depletion impaired angiogenesis as demonstrated by the presence of fewer intratumoral blood vessels (CD31 staining) (Fig. 1e). Subcutaneous xenograft experiments using two other TNBC cell lines confirmed our findings (Extended Data Fig. 1j, k). Notably, XBPI silencing in a patient-derived TNBC xenograft model (BCM-2147) significantly decreased tumour incidence (Fig. 1f and Extended Data Fig. 1l, m).

TNBC patients have the highest rate of relapse within 1–3 years despite adjuvant chemotherapy. To examine XBPI’s effect on tumour relapse after chemotherapy treatment, we treated MDA-MB-231 xenograft-bearing mice with doxorubicin and XBPI shRNA. Notably, combination treatment not only blocked tumour growth but also inhibited or delayed tumour relapse (Fig. 2a).

Tumour cells expressing CD44highCD24low have been shown to mediate tumour relapse in some instances. To test whether XBPI targeted the CD44highCD24low population, we examined the mammosphere-forming ability of cells derived from treated tumours (day 20). Mammosphere formation was increased in doxorubicin-treated tumour cells, whereas tumours treated with doxorubicin plus XBPI shRNA displayed substantially reduced mammosphere formation (Fig. 2b), a finding confirmed using another chemotherapeutic agent, paclitaxel (Extended Data Fig. 2a, b). Hypoxia activates the UPR, and XBPI knockdown also markedly reduced mammosphere formation in hypoxic conditions (Extended Data Fig. 2b). Furthermore, CD44 expression was reduced in XBPI-depleted tumours (Extended Data Fig. 2c).

To interrogate XBPI’s effect on CD44highCD24low cell function further, we used mammary epithelial cells (MCF10A) carrying an inducible Src oncogene (ER-Src), where v-Src is fused with the oestrogen receptor ligand-binding domain. Tamoxifen treatment results in neoplastic transformation and gain of a CD44highCD24low population that has been previously associated with tumour-initiating properties. In transformed MCF10A-ER-Src cells, XBPI splicing was increased in the CD44highCD24low population (Fig. 2c), whereas XBPI silencing reduced the CD44highCD24low fraction (Extended Data Fig. 2d, e) and markedly suppressed mammosphere formation (Extended Data Fig. 2f, g).

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LETTER

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Tumour formation by MDA-MB-231 cells as in Extended Data Fig. 1d. Bioluminescent images were obtained 5 days after transplantation and serially after mice were begun on chow containing doxycycline (day 19) for 8 weeks. Knowing this, we began these transplants on day 19. Patients were treated with tamoxifen (TX) until day 64. Mice were sacrificed, and tumours were stained with H&E, Ki67, cleaved caspase 3 or CD31 immunostaining of tumours or lungs 8 weeks after mice were fed chow containing doxycycline. Black arrows indicate metastatic nodules. Tumour incidence in mice transplanted with BCM-2147 tumour cells (10 weeks after transplantation). Statistical significance was determined by Barnard’s test. 

Figure 1 | \( XBP1 \) silencing blocks TNBC cell growth and invasiveness. a, RT–PCR analysis of \( XBP1 \) splicing in luminal and basal-like cell lines (a) or primary tissues from 6 TNBC patients and 5 oestrogen/progesterone-positive (ER/PR+) patients (b). \( XBP1u \), unspliced \( XBP1 \); \( XBP1s \), spliced \( XBP1 \). \( \beta \)-actin was used as loading control. c, Representative bioluminescent images of orthotopic tumours formed by MDA-MB-231 cells as in Extended Data Fig. 1d. Bioluminescent images were obtained 5 days after transplantation and serially after mice were begun on chow containing doxycycline (day 19) for 8 weeks. Figures show the day 19 image (before dox) and day 64 image (after dox). d, Quantification of imaging studies as in c. Data are shown as mean + s.d. of biological replicates (\( n = 8 \)). * \( P < 0.05 \), ** \( P < 0.01 \). e, Haematoxylin and eosin (H&E), Ki67, cleaved caspase 3 or CD31 immunostaining of tumours or lungs 8 weeks after mice were fed chow containing doxycycline. Black arrows indicate metastatic nodules. f, Tumour incidence in mice transplanted with BCM-2147 tumour cells (10 weeks after transplantation). Statistical significance was determined by Barnard’s test.

Figure 2 | \( XBP1 \) is required for tumour relapse and CD44\textsuperscript{high}CD24\textsuperscript{low} cells. Figure 2 | \( XBP1 \) is required for tumour relapse and CD44\textsuperscript{high}CD24\textsuperscript{low} cells. a, Tumour growth of MDA-MB-231 cells untreated or treated with doxorubicin (dox), or doxorubicin plus control shRNA (shCtrl), or doxorubicin plus \( XBP1 \) shRNA (sh\( XBP1 \)) in athymic nude mice. Data are shown as mean ± s.d. of biological replicates (\( n = 5 \)). TX indicates treatment. b, Number of mammospheres per 1,000 cells generated from day 20 xenograft tumours under different treatments as indicated. Data are shown as mean ± s.d. of biological replicates (\( n = 3 \)). c, RT–PCR analysis of \( XBP1 \) splicing in tamoxifen-treated CD44\textsuperscript{low}CD24\textsuperscript{high} and CD44\textsuperscript{high}CD24\textsuperscript{low} cells purified from a TNBC patient. f, Number of mammospheres per 1,000 cells generated from primary tissue samples from five patients with TNBC (br ca 1–5) that were untreated or infected with lentiviruses encoding control shRNA or \( XBP1 \) shRNA. Data are shown as mean ± s.d. of technical triplicates.
Co-immunoprecipitation experiments revealed a physical interaction of HIF1α, but not HIF2α, with XBP1 in 293T cells co-expressing HIF1α and XBP1s, consistent with the Notch1 interaction. Expression of HIF1α in XBP1s knockdown MDA-MB-231 cells (treated with 0.1% O2 for 24 h) was monitored by western blot analysis. HIF1α and XBP1s were co-immunoprecipitated with anti-HIF1α antibodies, indicating a physical interaction between the two proteins.

**Figure 3** | **HIF1α is a co-regulator of XBP1.** a, Motif enrichment analysis in the XBP1 binding sites in untreated (Un) or stressed (0.1% O2 and glucose deprivation; HG) MDA-MB-231 or Hs578T cells. The 1-kilobase (kb) region surrounding the summit of the XBP1 peak is equally divided into 50 bins. The average HIF1α motif occurrence over top 1,000 XBP1 peaks in each bin is plotted. The sequence logo for HIF1α motifs is shown as an inset. The corresponding P values of each condition are: M231_Un, 7.78 × 10−20; M231_HG, < 1.08 × 10−33; Hs578T_HG, < 1.08 × 10−30. b, Nuclear extracts from MDA-MB-231 cells (treated with 0.1% O2 for 10 h and then with 1 μg ml−1 tunicamycin for another 6 h in 0.1% O2) were subjected to ChIP using anti-HIF1α antibodies or rabbit IgG. IB, immunoblot. c, Schematic of the luciferase reporter constructs. 3 × HRE reporter was co-transfected with doxycycline (dox)-inducible constructs encoding control or two XBP1 shRNAs into MDA-MB-231 cells. Cells were treated with 0.1% O2 for 24 h and luciferase activity assayed. Experiments were performed in triplicate and data are shown as mean ± s.d. d, Gene expression microarray heat map showing that genes involved in the HIF1α-mediated hypoxia response were differentially expressed after XBP1 knockdown. e, RT–PCR analysis of HIF1α target gene expression after knockdown of XBP1 in MDA-MB-231-derived xenograft tumours in NOD/SCID/Il2rg−/− mice. Results are presented relative to β-actin expression. n = 5. f, Plot showing the genome-wide association between the strength of XBP1 binding and the occurrence of the HIF1α motif. The signal of XBP1 ChIP-seq peaks is shown as a heat map using red (the strongest signal) and white (the weakest signal) colour scheme. Each row shows ± 300 bp centred on the XBP1 ChIP-seq peak sums. Rows are ranked by XBP1 occupancy. The horizontal blue lines denote the presence of the HIF1α motif. g, h, Chromatin extracts from control, XBP1 knockdown (g) or HIF1α knockdown (h) MDA-MB-231 cells (treated with 0.1% O2 for 24 h) were subjected to ChIP using anti-HIF1α (g) or anti-XBP1 antibodies (h). Data are shown as mean ± s.d. of technical triplicates. Results show a representative of two independent experiments. i, Growth curve of tumours formed by MDA-MB-231 cells infected with inducible control shRNA (shCtrl), XBP1 shRNA (shXBP1) or XBP1 shRNA plus constitutively activated HIF1α (shXBP1 + HIF1α dPA). Mice were fed with doxycycline chow from day 7. Data are shown as mean ± s.d. of biological replicates (n = 5). *P < 0.05, **P < 0.01.

We next established that XBP1 and HIF1α co-occupied several well-known HIF1α targets using ChIP-qPCR (Extended Data Fig. 5a–c). ChIP-re-ChIP assays using anti-XBP1s followed by anti-HIF1α antibodies confirmed that XBP1s and HIF1α simultaneously co-occupy these common targets (Extended Data Fig. 5d). DNA pull-down assays with a HIF1α (ref. 18) specific probe precipitated XBP1s in MDA-MB-231 nuclear extracts under hypoxia, indicating their presence in the same complex (Extended Data Fig. 5e, f). XBP1 depletion by two independent shRNA constructs markedly reduced hypoxia response element (HRE) luciferase activity under hypoxia (Fig. 3c). Conversely, XBP1s expression dose-dependently transactivated the HRE reporter (Extended Data Fig. 5g, h), confirming that XBP1 augments HIF1α activity.

When we profiled the differential transcriptome induced by XBP1 silencing in MDA-MB-231 cells, gene-set enrichment analysis identified significant enrichment of HIF1α-mediated hypoxia response pathway genes (Fig. 3d and Extended Data Fig. 6a). XBP1 depletion downregulated
HIF1α targets VEGFA, PDK1, GLUT1 (also called SLC2A1) and DDIT4 expression in both normoxic and hypoxic conditions (Extended Data Fig. 6b), and these results were validated in breast cancer xenografts (Fig. 3e) and Hs578T cells (Extended Data Fig. 6c). However, XBP1 depletion in luminal tumours did not affect these targets (Extended Data Fig. 6d).

To explore the consequences of this cooperation further, we examined how XBP1 or HIF1α loss affected the transcription of common target genes. We found that high XBP1 occupancy at its binding sites was associated with increased occurrence of the HIF1α motif across the genome in TNBC (Fig. 3f). Whereas XBP1 depletion had no immediate effect on HIF1α expression, it substantially attenuated concurrent HIF1α and RNA polymerase II occupancy (Extended Data Fig. 6e–g).

Integrated analysis of XBP1 ChIP-seq data and gene expression profiles identified 96 genes directly bound and upregulated by XBP1. This gene set was defined as the XBP1 signature (Fig. 4a and Supplementary Table 1). Its expression was highly correlated with hypoxia-driven signatures in TNBC (Pearson’s correlation coefficient = 0.61; \( P = 2.28 \times 10^{-50} \)) but not in ER+ breast cancer patients (coefficient = 0.03; \( P = 0.64 \)) (Extended Data Fig. 9a, b). Survival analysis using an aggregate breast cancer dataset for 193 TNBC patient samples demonstrated that tumours with an elevated XBP1 signature displayed shorter relapse-free survival (log-rank test, \( P = 0.00677 \)) (Fig. 4b). Cox regression analysis showed that association of the signature with relapse-free survival remained significant after controlling for tumour size, grade and chemotherapy treatment (\( P = 0.00453 \), Supplementary Table 2). These findings were validated in a separate cohort of 190 TNBC patients (Fig. 4c). Importantly, the XBP1 signature did not correlate with clinical outcome of ER+ breast cancer patients (\( P = 0.553 \)) (Extended Data Fig. 9c), indicating its specific prognostic value for TNBC. Expression of the XBP1-regulated HIF1α program was also associated with decreased relapse-free survival only in TNBC (\( P = 0.00911 \)) (Fig. 4d and Extended Data Fig. 9d). Although XBP1 silencing also affects luminal breast cancer growth, it does so via a mechanism not involving HIF1α (Extended Data Figs 4g, 6d and 10).

In conclusion, we have uncovered a key function of XBP1 in the tumorigenicity, progression and recurrence of TNBC, and have identified XBP1’s control of the HIF1α transcriptional program as the major mechanism. XBP1 pathway activation correlates with poor patient survival in TNBC patients, indicating that UPR inhibitors in combination with standard chemotherapy may improve the effectiveness of anti-tumour therapies.

**METHODS SUMMARY**

**Orthoptopic tumour growth assays.** Female NOD/SCID/Il2rg−/− or nude mice (Taconic) were injected orthotypically with \( 1.5 \times 10^6 \) viable tumour cells re-suspended in 40 μl Matrigel (BD Biosciences) into mammary glands and fed chow containing 6% doxycycline per kg (Bioserv). For bioluminescent detection, mice were given a single intraperitoneal injection of luciferin, ketamine and xylazine and imaged with an IVIS imaging camera (Xenogen). Imaging intensity was normalized to the luminescence signal of individual mice before doxycycline Chow treatment. The average luminescence ratio of treatment groups (lacZ or XBP1 shRNA) was plotted over the course of doxycycline chow treatment and results presented as mean ± s.d. Mammosphere formation assay. Mammospheres were generated from cells in suspension (1,000 cells ml−1) in serum-free DMEM/F12 media, supplemented with B27 (1:50, Invitrogen), 0.4% BSA, 20 ng ml−1 EGF and 4 μg ml−1 insulin. After 6 days mammospheres were typically >75 μm in size with ~97% CD44high/CD24−low. For serial passage, 6-day-old mammospheres were collected, dissociated to single cells with trypsin and re-grown in suspension for 6 days.
METHODS

Cell culture and treatments. The non-transformed breast cell line MCF10A contains an integrated fusion of the v-Src oncoprotein with the ligand-binding domain of the oestrogen receptor (ER-Src). These cells were grown in DMEM/F12 medium supplemented with 5% donor horse serum (Invitrogen), 20 ng/ml epidermal growth factor (EGF) (R&D systems), 10 μg/ml insulin (Sigma), 100 μg/ml hydrocortisone (Sigma), 100 ng/ml 1-cholaer toxin (Sigma), 50 units/ml penicillin/streptomycin (Gibco), with the addition of puromycin (Sigma). Src induction and cellular transdifferentiation was achieved by treatment with 1 μM 4-OH tamoxifen, typically for 36 h, as described previously. All breast cancer cells were from ATCC cultured according to ref. 2. After retroviral or lentiviral infection, cells were maintained in the presence of puromycin (2 μg/ml) (Sigma). For all hypoxia experiments, cells were maintained in an anaerobic chamber (Coy laboratory) with 0.1% O2. For glucose deprivation experiments, cells were maintained in DMEM without glucose medium (Gibco) with 10% FBS (Gibco) and 50 units/ml of penicillin/streptomycin.

ChIP and ChIP-seq. ChIP was performed with XPB1 antibody (Biologend, 619502); HIF1α antibody (Abcam, ab2188), RNA polymerase II (Millipore, 05-623) or GST antibody (Santa Cruz, sc-33613) as described. See list of primers used in Fig. 3 (Supplementary Table J). ChIP-seq libraries were prepared using the ChIP-seq DNA Sample Prep kit (Illumina). XBP1 ChIP-seq peaks were first identified using MACS package with a P value cutoff of 1 × 10−7 on individual replicates. Correlations of the ChIP-seq signal in the union peak regions between two biological replicates are: MDA-MB-231_untreated, 0.97 (P < 2.2 × 10−16); MDA-MB-231_HG, 0.96 (<2.2 × 10−16); Hs578T_HG, 0.98 (<2.2 × 10−16); T47D_HG, 0.99 (<2.2 × 10−16). The correlations were calculated by cor.test() function in R (http://www.r-project.org/). The highly common peaks between replicates were further identified using an irreproducible discovery rate (IDR) cutoff of 20%. IDR is a statistical measure that assesses the consistency of the rank orders of the common ChIP-seq peaks between two replicates. The methodology and details of the implementation of IDR can be found in ref. 26.

Tumour initiation assay using patient-derived tumours. Tumour graft line BCM-2147 was derived by transplantation of a fresh patient breast tumour biopsy (ER ‘PR' HER2') into the cleared mammary gland fat pad of immune-compromised SCID/Beige mice and retained the patient biomarker status and morphology across multiple transplant generations in mice. To overcome the challenge of limited cell viability by dissociation of solid tumours, 10 mg tumour pieces containing 1.3 × 105 cells were transplanted with basal membrane extract (Trevigen). The cell number was calculated as average cell yield 1.3 × 106 cells per gram × 0.01 g × 1.3 × 106 cells. For sustained sRNA release in the first 2 weeks after transplantation, porous silicon particles loaded with sRNA (scrambled control or XPB1 sRNA) packaged in nanoliposomes were injected into the tumour tissue with basal membrane extract at the time of transplantation. Scrambled sequence, 5'-GGAGAGUGUGUGUGUGUGUGUGUGTdT-3'; XPB1 sRNA sequence 5'-CACCCUGAUUAUCAGUGCUCdT T-3'. Two weeks after transplantation, nanoliposomes containing sRNA (15 mg per mouse) were injected intravenously twice weekly for 8 weeks. Mice were monitored thrice weekly for tumour development, and tumours were calibrated and recorded using LABCAT Tumour Analysis and Tracking System version 6.4 (Innovative Programming Associates, Inc.). Tumour incidence is reported at 10 weeks after transplantation. The human patient samples were procured and used according to approved IRB protocols for research in human subjects.

Invasion assay. We performed invasion assays according to ref. 14. Invasion of the matrigel was conducted by using standardized conditions with BD BioCoat growth-factor-reduced matrigel invasion chambers (PharMingen). Assays were conducted according to manufacturer’s protocol, by using 5% horse serum (Gibco) and 20 ng/ml EGF (R&D Systems) as chemo-attractants.

Colony formation assay. 1 × 104 breast cancer cells were mixed 4:1 (v/v) with 2.0% agarose in growth medium for a final concentration of 0.4% agarose. The cell mixture was plated on top of a solidified layer of 0.8% agarose in growth medium. Cells were fed every 6–7 days with growth medium containing 0.4% agarose. The number of colonies was counted after 20 days. The experiment was repeated three times and the statistical significance was calculated using a Student’s t-test.

Subcutaneous xenograft experiments. MCF10A ER-Src tamoxifen-treated (36 h) cells or MDA-MB-436 or HBL-100 breast cancer cells were injected subcutaneously in the right flank of athymic nude mice (Charles River Laboratories). Tumour growth was monitored every 5 days and tumour volumes were calculated by the equation V (mm3) = a2b/2, where a is the largest diameter and b is the perpendicular diameter. When the tumours reached a size of ~100 mm3 (15 days) mice were randomly divided into 3 groups (5 mice per group). The first group was used as control (non-treated), the second group was intratumorally treated with shCtrl and the third group was intratumorally treated with shXPB1. For each injection 10 μg of shRNA was mixed with 2 μl of vivo-jetPEI (polyethylenimine) reagent (catalogue no. 201-50G, PolyPlus Transfection SA) in a final volume of 100 μl. These treatments were repeated every 5 days for 4 cycles (days 15, 20, 25 and 30). In addition, in vivo dilution xenotransplantation assays were performed in NOD/SCID/IL2γ−/− mice. Mice were evaluated on a weekly basis for tumour formation. All mice were maintained in accordance with Dana-Farber Cancer Institute Animal Care and Use Committee procedures and guidelines.

Purification of CD44highCD24low and CD44lowCD24high cells from patients with TNBC. Five human invasive triple-negative ductal carcinoma tissues (stage III) were used in our experiments. Immunomagnetic purification of CD44highCD24low and CD44lowCD24high cells was performed according to ref. 27. Briefly, the breast tissues were minced into small pieces (1 mm) using a sterile razor blade. The tissues were digested with 2 mg/ml collagenase I (C10310, Sigma) and 2 mg/ml hyalurondase (H3506, Sigma) in 37°C for 3 h. Cells were filtered, washed with PBS and followed by Percoll gradient centrifugation. The first purification step was to remove the immune cells by immunomagnetic purification using an equal mix of CD45 (leukocytes), CD15 (granulocytes), CD14 (monocytes) and CD19 (B cells) Dynabeads (Invitrogen). The second purification step was to isolate fibroblasts from the cell population by using CD10 beads for magnetic purification. The third step was to isolate the endothelial cells by using an ‘endothelial cocktail’ of beads (CD31 BD Pharmingen catalogue no. 555444, CD44 P1H12 MCAM BD Pharmingen catalogue no. 550314, CD105 Abcam catalogue no. Ab2525, cadherin 5 Immunotech catalogue no. 1597, and CD34 BD Pharmingen catalogue no. 558520). In the final step the CD44high cells were purified from the remaining cell population using CD44 beads. These cells were sorted for CD44highCD24low cells, CD24highCD44low cells were also purified using CD24 beads. These cells were sorted for CD44lowCD24low cells. These cell populations were sorted again with CD44 antibody (FTTC-conjugated) (555478, BD Biosciences) and CD24 antibody (PE-conjugated) (555428, BD Biosciences) to increase their purity (>99.2% in all cases).

Gene expression microarray analysis. MDA-MB-231 cells infected with control or XPB1 shRNA lentivirus were grown in supplemented medium were treated in 0.1% O2 in a hypoxia chamber for 24 h. Total RNA was extracted by using RNeasy mini kit with on column DNase digestion (Qiagen). Biotin-labelled cRNA was prepared from 1 μg of total RNA, fragmented, and hybridized to Affymetrix human U133 plus 2.0 expression array. All gene expression microarray data were normalized and summarized using RNA. The differentially expressed genes were identified using Limma (p < 0.1%).

Motif analysis. Flanking sequences around the summits (±300 bp) of the top 1,000 XPB1 binding sites were extracted and the repetitive regions in these flanking sequences were masked. The consensus sequence motifs were derived using Segpos.

XPB1 signature generation. The XPB1 signature was generated by integrative analysis of ChIP-seq and differential expression data using the method as previously described. Briefly, we first calculated the regulatory potential for a given gene, Seqp, as the sum of the nearby binding sites weighted by the distance from each site to the transcription start site (TSS) of the gene Seqp = Σi j=1 x e−0.5×|δi|, where k is the number of binding sites within 100 kb of gene g and δ is the distance between site i and the TSS of gene g normalized to 100 kb for (example, 0.5 for a 50-kb distance). We then applied the Breitling’s rank product method to combine regulatory potentials with differential expression t-values to rank all genes based on the probability that they were XPB1 targets. Only genes with at least one binding site within 100 kb from its TSS and a differential expression t-value above the 75th percentile were considered. The FDR of XPB1 target prediction was estimated by permutation. At a FDR cutoff of 20% and differential expression fold-change cutoff of 1.5, we obtained 96 upregulated genes (HUGO gene symbol) as direct targets of XPB1.

Survival analysis. We performed survival analysis using an aggregated compendium of gene expression profiles of 383 TNBC samples from 21 breast cancer data sets. Of the 96 XPB1 signature genes, 70 genes had corresponding probes in this data set. To avoid potential confounding factors such as heterogeneity among the samples, we randomly split all 383 TNBC samples into two data sets with similar size (193 and 190 cases) and evaluated the correlation of the XPB1 gene signature with relapse-free survival using these two data sets, respectively. We separated patients into two subgroups: one with higher and the other with lower expression of the XPB1 signature. The subgroup classification was performed as described previously. Patients were considered to have a higher XPB1 signature if they had average expression values of all the genes in the XPB1 signature above the 58th percentile. Kaplan–Meier survival analysis was performed and log-rank test was used to assess the statistical significance of survival difference between these two subgroups. We also performed multivariate Cox regression analysis to evaluate the significance of the association between XPB1 signature and relapse-free survival in the presence of other clinical variables including tumour stage, tumour grade and the treatment with chemotherapy. A similar analysis was performed for the HIF pathway signature (VEGFA, PDK1, DDIT4, SLC2A1, KDM3A, NDRG1, PFKFB3,...
PK3CA, RORB, CREBBP, PIK3CB, HK2 and EGLN1). Similar to the analysis for TNBC, the survival analysis was performed for ER+ breast cancer using gene expression profiles and clinical annotations of 209 ER+ breast cancer patients26.

**Virus production and infection.** The Phoenix packaging cell line was used for the generation of ecotropic retroviruses and the 293T packaging cell line was used for lentiviral amplification. In brief, viruses were collected 48 and 72 h after transfection, filtered, and used for infecting cells in the presence of 8 μg ml−1 polybrene before drug selection with puromycin (2 μg ml−1). ssRNA constructs were generated by The Broad Instrumet Targeting the BFP mRNA with ssRNA served as a control. Optimal targeting sequences identified for human XBP1 were 5'-GACCCAGTCTGTCCTCAAA-3' and 5'-GAACACAGAAGGGTAGATTTA-3', respectively. Knockdown efficiency was assessed by real-time PCR for XBP1.

**Luciferase assay.** For Extended Data Fig. 5g, MDA-MB-231 cells were co-transfected with 3×HRE luciferase (3×HRE-Luc) plasmid and XBP1s overexpression construct or control vector by using Lipofectamine 2000 (Invitrogen). A Renilla luciferase plasmid (pRL-CMV from Promega) was co-transfected as an internal control. Cells were collected 36 h after transfection, and the luciferase activities of the cell lysates were measured by using the Dual-luciferase Reporter Assay System (Promega). For Fig. 3c, MDA-MB-231 cells were co-transfected with 3×HRE-Luc and two inducible XBP1 ssRNA constructs (in pLKO.Tet-On vector) or control ssRNA construct by using Lipofectamine 2000 (Invitrogen). Cells were treated with doxycycline for 48 h and hypoxia for 24 h before the luciferase activities of the cell lysates were measured.

**Statistical analysis.** The significance of differences between treatment groups was measured with a Student’s t-test. P values of less than 0.05 were considered statistically significant.

**Co-immunoprecipitation.** Transfected cells were lysed in cell lysis buffer (50 mM Tris HCl, pH 8.0, 150 mM NaCl, 1 mM EDTA, 1% Nonidet P-40, and 10% glycerol for 4°C overnight). The beads were washed with cell lysis buffer four times. Finally, the beads were boiled in 2× sample buffer for 10 min. The eluates were analysed by western blot. Nuclear extracts were used to perform the endogenous co-immunoprecipitation. Briefly, 5 mg of nuclear extracts were incubated with 5μg of anti-HIF1α antibody (Novus Biologicals, NB100-479) at 4°C overnight. The protein complexes were precipitated by addition of protein A agarose beads (Roche) with incubation for 4 h at 4°C. The beads were washed four times and boiled for 5 min in 2× sample buffer.

**Real-time PCR analysis.** 1 μg of RNA sample was reverse-transcribed to form cDNA, which was subjected to SYBR-green-based real-time PCR analysis. Primers used for β-actin forward 5' CCCTAGCCCAAACACAGTGCG-3' and reverse 5'-ATATCTCTGCTTGTGATCC-3'; for VEGFA forward 5'-CACACAGGATGGTGGGGAAG-3' and reverse 5'-AGGGCAAGATCATACAGAGG-3'; for PDK1 forward 5'-GGAGGCTCCAAACAGGATCG-3' and reverse 5'-GTCTGATCGCAGCTTGAATTA-3'; for GLUT1 forward 5'-TGAGGACCATGCTTTGTTGTA-3' and reverse 5'-ATGGAGCAGCAGACCAAA-3'; for JMJD1A forward 5'-TCAGGAGCTGGTTCACCC-3' and reverse 5'-CCGGAGCTTACCAAAGAGG-3'; for DDDT forward 5'-CATTGGTGTTGACAAGGAATG-3' and reverse 5'-CCTGGAAGCTGGCAGCTG-3'; for MCT4 forward 5'-TACATGTAGACGTGGG-3'; for CD31 (1:50, Abcam, ab28364), cleaved caspase 3 (1:200, Cell Signaling, 9664), CD44 (1:100, Novocarsta), Ki67 (1:50, Dako, Clone MIB-1), and carbonic anhydrase IX (1:40, Novus Biologicals). Subsequently, we incubated the slides with biotinylated secondary antibody and ABC-HRP (both from Vector Lab). EnVision + system (Dako) was used to amplify caspase 3 and carbonic anhydrase IX. Mouse on Mouse ImmunPRESS Polymer kit (Vector Lab) was applied to increase CD44 signal-to-noise ratio. For all slides, final detectable signal was visualized by DAB as the location of antigens. After counterstaining with haematoxylin, slides were mounted.

**Immunoblot analysis.** Total cell extracts or nuclear extracts were separated by SDS–PAGE and transferred to PVDF membranes. IR1ε phosphorylation was monitored by Phos-tag SDS–PAGE. PERK phosphorylation was monitored by 5% SDS–PAGE. The following antibodies were used for immunoblot analysis: anti-XBP1s (Biolegend, 619502); anti-Perk (Cell Signaling, 5683); anti-IRE1α (Cell Signaling, 3294); anti-ATF6 (Cosmo bio, BM-73-500-EX); anti-ATF4 (Santa Cruz, sc-200); anti-Hsp90 (Santa Cruz, sc-9747); anti-TBP (Abcam, 51841); and anti-EIF2z (Santa Cruz, sc-11386); anti-phospho-EIF2z (Cell Signaling, 9721).

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Extended Data Figure 1 | Effect of XBP1 silencing on TNBC cells and UPR.

a, Activation of UPR in different breast cancer cells. Immunoblot of PERK phosphorylation, IRE1α activation (phos-tag SDS–PAGE) and EIF2α phosphorylation in whole-cell lysates, and ATF6α processing (pATF6α) in nuclear extract of basal-like breast cancer cells (1, HCC1937; 2, MDA-MB-231; 3, SUM159; 4, MDA-MB-157; 5, HCC70) and luminal breast cancer cells (6, ZR-75-1; 7, T47D; 8, MCF7). TM, positive control (whole-cell lysates or nuclear extracts from MDA-MB-231 cells treated with 5 µg ml⁻¹ tunicamycin for 6 h). HSP90 was used as loading control for whole-cell lysates, TBP was used as loading control for nuclear extract.

b, Transmission electron microscopic analysis of ER in basal-like and luminal breast cancer cell lines. Black arrows indicate the endoplasmic reticulum. All images are at original magnification of 30,000x. Scale bar, 1 µM.

c, Quantification of soft agar colony formation and number of invasive cells in untreated and control shRNA or XBP1 shRNA infected breast cancer cells. Experiments were performed in triplicate and data are shown as mean ± s.d. **P < 0.01.

d, Quantitative RT–PCR analysis of XBP1 expression in MDA-MB-231 cells infected with lentiviruses encoding doxycycline (dox) inducible shRNAs against XBP1 or scrambled LacZ control, in the presence or absence of doxycycline for 48 h. Data are presented relative to β-actin and shown as mean ± s.d. of technical triplicates.

e, Knockdown efficiency of total XBP1 (e) and XBP1s (f) in MDA-MB-231-derived xenograft tumour (as in Fig. 1d). Data are presented relative to β-actin. n = 5.

f, Bioluminescent images of orthotopic tumours formed by luciferase-expressing MDA-MB-231 cells infected with different lentiviruses. A total of 1.5 × 10⁶ cells were injected into the fourth mammary glands of nude mice. Bioluminescent images were obtained 1 week later and serially after mice were begun on chow containing doxycycline (dox) (day 10). Pictures shown are the day 10 images (before dox) and day 45 images (after dox).

g, Effect of XBP1 knockdown on ER stress marker BIP expression in MDA-MB-231-derived xenograft tumours. Quantitative RT–PCR analysis of BIP expression in shCtrl or shXBP1 xenograft tumour. Data are presented relative to β-actin. n = 5.

h, Immunoblot of IRE1α activation (phos-tag SDS–PAGE) and PERK phosphorylation in whole-cell lysates; ATF6α processing and ATF4 expression in nuclear extracts of two shCtrl or shXBP1 xenograft tumours. HSP90 was used as loading control for whole-cell lysates; TBP was used as loading control for nuclear extract.

i, Tumour growth of untreated or control shRNA, or XBP1 shRNA treated MDA-MB-436 (i) or HBL-100 cells (k) in nude mice. Data are shown as mean ± s.e.m. of biological replicates (n = 3). **P < 0.01. Tx: treatment with shRNA.

j, Kaplan–Meier tumour-free survival curve of mice from Fig. 1f.

k, Tumour growth (mean ± s.e.m.) of BCM-2147 tumours as in Fig. 1f (Scr siRNA, n = 7; XBP1 siRNA, n = 2).
Extended Data Figure 2 | Effect of XBP1 on tumour relapse and CD44^high/CD24^low cells. a, Tumour growth of MDA-MB-231 cells untreated or treated with paclitaxel (20 mg kg^-1), or paclitaxel + XBP1 shRNA, or paclitaxel + control shRNA, or paclitaxel + XBP1 shRNA in nude mice. TX, treatment with paclitaxel or paclitaxel + shRNA. Data are shown as mean ± s.d. of biological replicates (n = 5). b, Number of mammospheres per 1,000 cells generated from day 20 xenograft tumours under different treatments as indicated under normoxic or hypoxic condition (0.1% O2). Data are shown as mean ± s.d. of biological replicates (n = 3). Asterisk denotes significantly different from paclitaxel shCtrl control in each treatment; *P < 0.05, **P < 0.01. c, Effect of XBP1 knockdown on cell death in hypoxic regions (assessed by CA9 and cleaved caspase 3 staining) or accumulation of CD44^high/CD24^low cells (assessed by CD44 staining). Immunohistochemical staining of CA9 and cleaved caspase 3 (consecutive sections) showed that cell death was not induced in hypoxic region in XBP1 knockdown tumours. Immunohistochemical staining of CD44 showed significant reduction of CD44 expression in XBP1 knockdown tumours. All tumour sections are from MDA-MB-231-derived xenograft with different treatment as indicated. d, Knockdown efficiency of XBP1 in MCF10A-ER-Src cells. Data are shown as mean ± s.d. of technical triplicates. e, Left panel: flow cytometry analysis of CD44 and CD24 expression of tamoxifen-treated (36 h) MCF10A ER-Src cells infected with control shRNA or XBP1 shRNA encoding lentivirus. Right panel: percentage of CD44^high/CD24^low cells in tamoxifen (4-OH-tamoxifen)-treated MCF10A-ER-Src cells infected with control shRNA or XBP1 shRNA encoding lentivirus. Experiments were performed in triplicate and data are shown as mean ± s.d. *P < 0.05. f, Number of mammospheres per 1,000 cells generated by tamoxifen-treated MCF10A ER-Src cells uninfected, or infected with control shRNA or XBP1 shRNA encoding lentivirus. Experiments were performed in triplicate and data are shown as mean ± s.d. g, Cell viability assay (Cell-titer Glo) on CD44^high/CD24^low or CD44^low/CD24^high cells isolated from tamoxifen-treated MCF10A-ER-Src cells infected with control shRNA or XBP1 shRNA encoding lentivirus (72 h after infection). Data were normalized to the control (cell infected with shCtrl). Experiments were performed in triplicate and data are shown as mean ± s.d. h, Cleaved caspase 3 ELISA assays on CD44^high/CD24^low or CD44^low/CD24^high cells isolated from tamoxifen-treated MCF10A-ER-Src cells infected with control shRNA or XBP1 shRNA encoding lentivirus (72 h after infection). Experiments were performed in triplicate and data are shown as mean ± s.d.
Extended Data Figure 3 | Effect of XBP1 on CD44\textsuperscript{high}CD24\textsuperscript{low} cells. a, UPR markers are upregulated in CD44\textsuperscript{high}CD24\textsuperscript{low} cells. Quantitative RT–PCR analysis of UPR markers BIP, CHOP, ERDJ4, HERP and MBTPS1 in CD44\textsuperscript{low}CD24\textsuperscript{high} cells and CD44\textsuperscript{high}CD24\textsuperscript{low} cells sorted from two TNBC patients. Data are shown as mean ± s.d. of technical triplicates. *P < 0.05, **P < 0.01. b, XBP1s overexpression in CD44\textsuperscript{low}CD24\textsuperscript{high} cells generates mammosphere-forming ability. Number of mammospheres per 1,000 cells generated by sorted CD44\textsuperscript{low}CD24\textsuperscript{high} cells transduced with empty vector or XBP1s expressing retrovirus. Experiments were performed in triplicate and data are shown as mean ± s.d. c, CD44\textsuperscript{low}CD24\textsuperscript{high} cells overexpressing XBP1s are more resistant to chemotherapy. MTT (3-[4,5-dimethylthiazol-2-yl]-2,5-diphenyl tetrazolium bromide) assay was performed to measure the dose–response curves of CD44\textsuperscript{low}CD24\textsuperscript{high} cells or CD44\textsuperscript{low}CD24\textsuperscript{high} cells expressing XBP1s treated with doxorubicin. Experiments were performed in triplicate and data are shown as mean ± s.d. *P < 0.05, **P < 0.01. d, 1,000 or 100 CD44\textsuperscript{low}CD24\textsuperscript{high} cells sorted from transformed MCF10A ER-Src cells or CD44\textsuperscript{low}CD24\textsuperscript{high} cells overexpressing XBP1s were injected into NOD/SCID/IL2R\gamma\textsuperscript{−/−} mice and the incidence of tumours was monitored. e, Ten CD44\textsuperscript{low}CD24\textsuperscript{high} cells sorted from two human patients with TNBC or CD44\textsuperscript{low}CD24\textsuperscript{high} cells overexpressing XBP1s were injected into NOD/SCID/IL2R\gamma\textsuperscript{−/−} mice and the incidence of tumours was monitored.
Extended Data Figure 4 | HIF1α is a co-regulator of XBP1.  

a, Identification of XBP1 motif in MDA-MB-231 ChIP-seq data set. Matrices predicted by the de novo motif-discovery algorithm Seqpos. 

b, Induction of XBPI splicing by hypoxia. RT–PCR analysis of the ratio of XBPIs to total XBPI in MDA-MB-231 cells cultured under normoxic condition or hypoxic condition (0.1% O2) for 24 h. Data are shown as mean ± s.d. of technical triplicates. 

c, Induction of XBPI splicing by glucose deprivation. RT–PCR analysis of the ratio of XBPIs to total XBPI in MDA-MB-231 cells cultured in normal medium or glucose-free medium for 24 h or 48 h. Data are shown as mean ± s.d. of technical triplicates. 

d, Induction of XBPI splicing by oxidative stress. RT–PCR analysis of the ratio of XBPIs to total XBPI in MDA-MB-231 cells untreated or treated with different doses of H2O2 for 1 h, 4 h or 24 h. Data are shown as mean ± s.d. of technical triplicates. 

e, Western blotting analysis of XBPIs expression in nuclear extract of MDA-MB-231 cells cultured under normoxia or hypoxia (0.1% O2) and glucose-free condition for 16 h. Lamin B was used as loading control. 
f, Venn diagram showing the overlap between XBPI targets in MDA-MB-231 breast cancer cells cultured under normoxic conditions (untreated) or hypoxia and glucose deprivation conditions (treated). 
g, Motif enrichment analysis in the XBPI binding sites in untreated or stressed (0.1% O2 and glucose deprivation: HG) MDA-MB-231, Hs578T or T47D cells. The 1-kb region surrounding the summit of the XBPI peak is equally divided into 50 bins. The average HIF1α motif occurrence over top 1,000 XBPI peaks in each bin is plotted. The corresponding P values of each condition are listed as follows: M231_Un, 7.78 × 10⁻²⁰; M231_HG, <1.08 × 10⁻³⁰; Hs578T_HG, <1.08 × 10⁻³⁰; T47D_HG, 6.14 × 10⁻²⁸.  
h, Flag-tagged HIF1α and XBPIs were co-expressed in 293T cells, and the cells were treated in 0.1% O2 for 16 h. Co-immunoprecipitation was performed with M2 anti-Flag antibody. Western blot was carried out with anti-XBP1s antibody, anti-Flag antibody or anti-HIF1α antibody. Empty vector was used as control. 
i, Nuclear extracts from Hs578T cells treated with tunicamycin (1 μg ml⁻¹, 6 h) in 0.1% O2 (16 h) were subjected to co-immunoprecipitation with anti-HIF1α antibody or rabbit IgG. Western blot was carried out with anti-XBP1s antibody or anti-HIF1α antibody. Empty vector was used as control. 
j, HA-tagged HIF2α and XBPIs were co-expressed in 293T cells, and the cells were treated in 0.1% O2 for 16 h. Co-immunoprecipitation was performed with anti-HA antibody. Western blot was carried out with anti-XBP1s antibody or anti-HA antibody. Empty vector was used as control. 
k, Localization of XBPIs and HIF1α in MDA-MB-231 cells. Western blotting analysis of XBPIs and HIF1α expression in cytosolic extracts and nuclear extracts of MDA-MB-231 cells cultured under 0.1% O2 condition for 24 h. HSP90 and TBP were used as control. 
l, XBP1u is not expressed in MDA-MB-231 cells. Western blotting analysis of XBP1u in MDA-MB-231 cells untreated or treated with 1 μM or 10 μM MG132 for 4 h. HSP90 was used as loading control. 
m, Schematic diagram of full-length and truncated forms of XBPIs protein. 

n, A GST pull-down assay was performed using GST-tagged XBPIs proteins and 293T cell lysates overexpressing HA-tagged HIF1α. Western blotting was performed with an anti-HA antibody. Lower panel: Coomassie blue staining of GST-tagged different truncated forms of XBPIs proteins. 

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Extended Data Figure 5 | XBP1 and HIF1α co-occupy HIF1α targets.

a, Track view of XBP1 ChIP-seq density profile (two biological replicates) on HIF1α target genes. b, XBP1 and HIF1α co-bind to DDT4, VEGFA and PDK1 promoters under hypoxic conditions. A ChIP assay was performed using anti-XBP1 or anti-HIF1α antibody to detect enriched fragments. GST antibody was used as mock ChIP control. c, XBP1 and HIF1α co-bind to JMJD1A and JMJD2C promoters under hypoxic conditions. Upper panel: schematic diagram of the primer locations across the JMJD2C or JMJD1A promoter. Grey boxes indicate exon. A ChIP assay was performed using anti-XBP1 polyclonal antibody or anti-HIF1α polyclonal antibody to detect enriched fragments. Fold enrichment is the relative abundance of DNA fragments at the amplified region over a control amplified region. GST antibody was used as mock ChIP control. d, XBP1s and HIF1α co-occupy JMJD1A, DDT4, NDRG1, PDK1 and VEGFA promoters. A ChIP-re-ChIP assay was performed using the anti-XBP1s antibody first (X). The eluants were then subjected to a second ChIP assay using an anti-HIF1α antibody (XH) or a control IgG antibody (XC). All ChIP data (b–d) are shown as mean ± s.d. of technical triplicates. Results show a representative of two independent experiments. *P < 0.05; **P < 0.01.

e, HIF1α, but not XBP1s, binds to a probe in Twist promoter in 293T cells. DNA pull-down assay was used to analyse the binding of XBP1s or HIF1α on a probe in Twist promoter. f, XBP1s binds to Twist promoter in MDA-MB-231 cells under 0.1% O2. The nuclear extract of MDA-MB-231 cells cultured under 0.1% O2 for 24 h was incubated with the wild-type or mutant probe (HIF1α consensus sequence was mutated) and immunoblot analysis was performed with anti-XBP1s or anti-HIF1α antibody. g, 3XHRE reporter was co-transfected with XBP1s expression plasmid or empty vector into MDA-MB-231 cells and luciferase activity measured. Experiments were performed in triplicate and data are shown as mean ± s.d. **P < 0.01. h, RT–PCR analysis of XBP1 expression as in g. Data are shown as mean ± s.d. of technical triplicates.
**Extended Data Figure 6 | XBP1 regulates HIF1α targets.** a, Plot from GSEA showing enrichment of the HIF1α-mediated hypoxia response pathway in XBP1-upregulated genes. b, Quantitative RT–PCR analysis of VEGFA, PDK1, GLUT1 and DDIT4 expression after knockdown of XBP1 in MDA-MB-231 under both normoxic or hypoxic conditions. c, Quantitative RT–PCR analysis of VEGFA, PDK1, GLUT1, MCT4, JMJD1A and XBP1 expression after knockdown of XBP1 in Hs578T cells treated with 0.1% O2 for 24 h. Results are presented relative to β-actin expression. Experiments were performed in triplicate and data are shown as mean ± s.d. *P < 0.05, **P < 0.01. d, Plot from GSEA showing no enrichment of the HIF1α-mediated hypoxia response pathway in XBP1-regulated genes in T47D cells (P = 0.1684). e–k, Cooperative binding of XBP1 and HIF1α on common targets. e, Immunoblotting analysis of control MDA-MB-231 cell lysates and XBP1 knockdown lysates (treated with 0.1% O2 for 24 h) were performed using anti-HIF1α or anti-HSP90 antibody. f, g, Chromatin extracts from control MDA-MB-231 cells or XBP1 knockdown MDA-MB-231 cells (treated with 0.1% O2 for 24 h) were subjected to ChIP using anti-XBP1s antibody (f), or anti-RNA polymerase II antibody (g). The primers used to detect ChIP-enriched DNA were the peak pair of primers in JMJD1A, DDIT4, NDRG1, PDK1 and VEGFA promoters (Supplementary Table 3). Primers in the β-actin region were used as control. h, i, Chromatin extracts from control MDA-MB-231 cells or HIF1α knockdown MDA-MB-231 cells (treated with 0.1% O2 for 24 h) were subjected to ChIP using anti-HIF1α antibody (h), or anti-RNA polymerase II antibody (i). j, k, Chromatin extracts from control MDA-MB-231 cells or XBP1 knockdown MDA-MB-231 cells (treated with 1% O2 for 24 h) were subjected to ChIP using anti-HIF1α antibody (j), and anti-XBP1s antibody (k). All ChIP data (f–k) are shown as mean ± s.d. of technical triplicates. Results show a representative of two independent experiments. *P < 0.05, **P < 0.01. l, Quantitative RT–PCR analysis of VEGFA, PDK1, GLUT1 and JMJD1A after knockdown of XBP1 in MDA-MB-231 cells treated with 1% O2 for 24 h. Results are presented relative to β-actin expression. Data are shown as mean ± s.d. of technical triplicates. *P < 0.05, **P < 0.01.
Extended Data Figure 7 | Overexpression of constitutively activated HIF1α rescues XBP1 knockdown phenotype. a, Immunoblotting analysis of cell lysates of MDA-MB-231 cells infected with retrovirus encoding control vector or HA–HIF1α dPA was performed using anti-HA or anti-actin antibody. b, XBP1 splicing is not affected by HIF1α or HIF2α activation. RT–PCR analysis of the ratio of XBP1s to total XBP1 in MDA-MB-231 cells expressing control vector, HA–HIF1α or HA–HIF2α dPA. Expression of HA–HIF1α dPA is shown in a and expression of HIF2α is shown in the right panel. c, XBP1 splicing is not affected by HIF1α or HIF2α depletion. RT–PCR analysis of the ratio of XBP1s to total XBP1 in MDA-MB-231 cells infected with control, shHIF1α or shHIF2α lentivirus. Knockdown efficiency of HIF1α or HIF2α is shown in the middle and right panels. d, e, Expression of constitutively activated HIF1α doesn’t affect XBP1 expression (d), but restores HIF1α targets expression (e). RT–PCR analysis of XBP1 total (d). XBP1s (d) and VEGFA, PDK1, DDIT4 (e) in control shRNA (shCtrl), XBP1 shRNA (shXBP1), or XBP1 shRNA plus constitutively activated HIF1α (shXBP1 + HIF1α dPA) infected MDA-MB-231 cells. Data (b–e) are shown as mean ± s.d. of technical triplicates. *P < 0.05, **P < 0.01. f, Quantification of soft agar colony formation in control shRNA (shCtrl), XBP1 shRNA (shXBP1), or XBP1 shRNA plus constitutively activated HIF1α (shXBP1 + HIF1α dPA) infected MDA-MB-231, MDA-MB-468, or MDA-MB-157 cells. Experiments were performed in triplicate and data are shown as mean ± s.d. **P < 0.01. g, Quantification of mammosphere formation in control shRNA (shCtrl), XBP1 shRNA (shXBP1), or XBP1 shRNA plus constitutively activated HIF1α (shXBP1 + HIF1α dPA) infected MDA-MB-231 cells. Experiments were performed in triplicate and data are shown as mean ± s.d. **P < 0.01. h, CD31 immunostaining of tumours formed by MDA-MB-231 cells infected with control shRNA (shCtrl), XBP1 shRNA (shXBP1) or XBP1 shRNA plus constitutively activated HIF1α (shXBP1 + HIF1α dPA). i, Silencing of HIF1α inhibits the XBP1s-sustained mammosphere-forming ability. Quantification of mammosphere formation in MCF10A cells expressing control vector, XBP1s, XBP1s plus control shRNA or XBP1s plus HIF1α shRNA. Experiments were performed in triplicate and data are shown as mean ± s.d. **P < 0.01.
Extended Data Figure 8 | Schema depicting the interaction of XBP1 and HIF1α in TNBC. XBP1 and HIF1α cooperatively regulate HIF1α targets in TNBC. In the setting of a tumour microenvironment, hypoxia further induces XBP1 activation; active XBP1s in turn interacts with HIF1α to stimulate and augment the transactivation of HIF1 target genes that promote cancer progression.
Extended Data Figure 9 | Correlation of XBP1 with HIF1α in patients with TNBC. 

**a, b.** Expression of XBP1 signature is highly correlated with two publicly available hypoxia-driven signatures in TNBC patients (a), but not in ER− breast cancer patients (b). The scatter plots of XBP1 and two publicly available HIF1α signatures (left panel, HIF1α pathway; right panel, hypoxia via HIF1α pathway) across different tumours were drawn for TNBC (a) and ER− breast cancer patients (b), respectively. The corresponding Pearson’s correlation coefficient (r) between XBP1 and HIF1α signature is shown.

**c, d.** Kaplan–Meier graphs demonstrating no significant association of the expression of the XBP1 signature (red line) (c) or HIF signature (d) with relapse-free survival in oestrogen-receptor-positive breast cancer patients. The log-rank test P values are shown.
Extended Data Figure 10 | Role of XBP1 in luminal breast cancer. 

**a** | XBP1 splicing is induced by hypoxia and glucose deprivation in luminal cancer cells. RT–PCR of XBP1 splicing in T47D and SKBR3 cells under different treatments for 24 h. XBP1u, unspliced XBP1; XBP1s, spliced XBP1. Hypoxia: 0.1% O2.

**b** | Left panel: quantification of soft agar colony formation in untreated and control shRNA or XBP1 shRNA infected breast cancer cells. Experiments were performed in triplicate and data are shown as mean ± s.d. **P** < 0.01. Right panel: effect of XBP1 depletion on soft agar colony formation in luminal versus basal cell lines. Percentages of soft agar colonies formed from cells infected with XBP1 shRNA lentivirus relative to the same cell line infected with shCtrl lentivirus (set as 100%) are presented. 5 cell lines in each group (as in left panel) and data are shown as mean ± s.d.

**c** | Tumour growth (mean ± s.d.) of ZR-75-1 cells treated with control shRNA (n = 4), paclitaxel (20 mg kg⁻¹) + control shRNA (n = 4), XBP1 shRNA (n = 4) or paclitaxel + XBP1 shRNA (n = 3) in nude mice. TX, treatment with shRNA or paclitaxel + shRNA. Asterisk denotes shXBP1-treated tumours significantly different from shCtrl-treated tumours; *P* < 0.05.

**d** | Number of mammospheres per 1,000 cells generated by control shRNA or XBP1 shRNA-encoding lentivirus infected T47D or SKBR3 breast cancer cell lines cultured under normoxia and glucose deprivation conditions (treated). Experiments were performed in triplicate and data are shown as mean ± s.d. e, Venn diagram showing the overlap between XBP1 targets in MDA-MB-231, Hs578T cells and T47D cells cultured under hypoxia and glucose deprivation conditions. f, XBP1s overexpression is not capable of converting a luminal phenotype to basal phenotype. RT–PCR analysis of luminal marker (CK8, CK18, CK19 and E-cadherin) and basal marker (CK5, CK14, p63, fibronectin and vimentin) expression in luminal breast cancer cells (MCF7 or T47D) infected with lentivirus encoding empty vector or XBP1s. Data are shown as mean ± s.d. of technical triplicates.