#### **Supplementary Information**

#### **Supplementary Figure Legends**

**Figure S1. TAZ is highly expressed in TNBC. A**, mRNA expression levels of TAZ in TNBC and non-TNBC were analyzed with Breast Cancer Integrative Platform database (<u>www.omicsnet.org/bcancer/database</u>). **B**, mRNA expression levels of TAZ in different breast cancer cell lines are examined with Cancer Cell Line Encyclopedia database (<u>https://portals.broadinstitute.org/ccle</u>). The red columns represent the TNBC cells, the blue ones represent the HER2<sup>+</sup> Breast Cancer cells, the green ones represent the luminal breast cancer. **C**, Copy number variation (CNV) analysis was performed by using the Breast Cancer Integrative Platform database (<u>http://www.omicsnet.org/bcancer/database</u>).

Figure S2. Early passages of TAZ-depleted cells show shortened telomeres but no changes of hTERT expression. A and B, Western blot analyses of TAZ in the indicated MDA-MB-231 and BT549 cells. Quantification of Western blots is shown in Fig. S5 O and P. C and D, qPCR analyses to determine hTERT mRNA levels in the indicated MDA-MB-231 and BT549 cells. E and F, Western blot analyses of hTERT in the indicated MDA-MB-231 and BT549 cells. E and F, Western blots is shown in Fig. S5Q. G and H, Telomere-specific qPCR analyses in the indicated MDA-MB-231 and BT549 cells. Quantification of MDA-MB-231 and BT549 cells to determine the relative telomere length. I and J, Southern analysis of TRFs in the indicated MDA-MB-231 and BT549 cells to determine the relative telomere length. For A-J, cells were lyzed after 48 h of transfection, representing the short-term knockdown of TAZ expression. K, TAZ-depleted MDA-MB-231 cells were prepared with shRNA and cultured for different passages as indicated. Telomere-specific qPCR analyses were performed. A progressively shortening of telomeres during passage elongation in TAZ-depleted cells was observed. L, The mRNA levels of TAZ and hTERT were examined by qPCR in BT549 cells transfected with TAZ-specific shRNA for 48 h. Data are presented as mean±SEM. At least three repeats were carried out for each test. The p values were determined by one-way ANOVA followed by Tukey's multiple-comparisons. NS, not significant, \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.

**Figure S3. Early passages of TAZ-depleted TNBC cells show no changes of shelterin proteins.** Western blot analysis of shelterin proteins in short-term TAZ knockdown (transfected with siRNA for 48 h) MDA-MB-231 cells (left panel) and BT549 cells (right panel). Quantification of MDA-MB-231 Western blots is shown in Fig. S5R.

Figure S4. Knockdown of TAZ activates TERRAs transcription and p53 nuclear translocation. A-D, qPCR analyses showing the changes of the expression of distinct TERRA transcripts from different chromosomes (chr-

2q, chr-9p, chr-10q, chr-13q, chr-17p and chr-xqyq) in MDA-MB-231 and BT549 cells with short-term TAZ knockdown (transfected with siRNA for 48 h) or long-term TAZ knockdown (infected with shRNA and cultured >6 passages). Data are presented as mean $\pm$ SEM. At least three repeats were carried out for each test. The p values were determined by one-way ANOVA followed by Tukey's multiple-comparisons. NS, not significant, \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.

**Figure S5. Quantification of western blotting. A**, Quantification of the data obtained in Fig1A. **B**, Quantification of the data obtained in Fig2D. **C**, Quantification of the data obtained in Fig2D. **E**, Quantification of the data obtained in Fig2G. **F**, Quantification of the data obtained in Fig3C. **G**, Quantification of the data obtained in Fig4D. **J**, Quantification of the data obtained in Fig5C. **L**, Quantification of the data obtained in Fig5E. **M**, Quantification of the data obtained in Fig5A. **N**, Quantification of the data obtained in Fig5E. **L**, Quantification of the data obtained in Fig6B. **O**, Quantification of the data obtained in FigS2A. **P**, Quantification of the data obtained in FigS2B. **Q**, Quantification of the data obtained in FigS2E. **R**, Quantification of the data obtained in FigS3. Data are presented as mean±SEM. At least three repeats were carried out for each test. Statistical analyses were performed with unpaired Student's t-test between two groups and one -way ANOVA followed by Tukey's multiple-comparisons for multiple groups. NS, not significant, \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.

si-Cont.	UUCUCCGAACGUGUCACGUTT
si-TAZ#1	GCUCAUGAGUAUGCCCAAUTT
si-TAZ#2	GGUACUUCCUCAAUCACAUTT
sh-Cont.	TTCTCCGAACGTGTCACG
sh-TAZ#1	GATGAATCAGCCTCTGAAT
sh-TAZ#2	CCTTTCTAACCTGGCTGTA
si-CTNNB1#1	GGAUGUGGAUACCUCCCAATT
si-CTNNB1#2	CCCACUAAUGUCCAGCGUUTT
si-p53	CCACUGGAUGGAGAAUAUUTT
si-RAD51C#1	CCAAAGAAGGAGCUAAUAATT
si-RAD51C#2	CCUUGCUACUGCCUGCAUUTT

### Supplementary Tables

#### Supplementary Table S1

## Supplementary Table S2

TAZ-F	GCUCAUGAGUAUGCCCAAUTT
TAZ-R	GGUACUUCCUCAAUCACAUTT
IL-1a-F	GATCAGTACCTCACGGCTGC
IL-1a-R	GCATCTCCTTCAGCAGCACT
IL-1b-F	CCAGCTACGAATCTCCGACC
IL-1b-R	GGGAAAGAAGGTGCTCAGGT
IL6-F	CCAGAGCTGTGCAGATGAGT
IL6-R	GCATTTGTGGTTGGGTCAGG
IL8-F	СТССАААССТТТССАССССА
IL8-R	TTCTCCACAACCCTCTGCAC
Tel-F	GGTTTTTGAGGGTGAGGGTGAGGGTGAGGGTGAGGGT
Tel-R	TCCCGACTATCCCTATCCCTATCCCTATCCCTA
HBG-F	GCTTCTGACACAACTGTGTTCACTAGC
HBG-R	CACCAACTTCATCCACGTTCACC
hTERT-F	GCCTTCAAGAGCCACGTC
hTERT-R	CCACGAACTGTCGCATGT
Terc-F	GTGGTGGCCATTTTTGTCTAAC
Terc-R	TGCTCTAGAATGAACGGTGGAA
Rad51C-F	GAAAAACACAAGGGAGAGGAAC
Rad51C-R	GTAACTCTGTGTAGTCACGACA
TERRA-chr-2q-F	GCCTTGCCTTGGGAGAATCT
TERRA-chr-2q-R	AAAGCGGGAAACGAAAAGC
TERRA-chr-9p-F	GAGATTCTCCCAAGGCAAGG
TERRA-chr-9p-R	ACATGAGGAATGTGGGTGTTAT
TERRA-chr-10q-F	AAAGCGGGAAACGAAAAGC
TERRA-chr-10q-R	GCCTTGCCTTGGGAGAATCT
TERRA-chr-13q-F	CCTGCGCACCGAGATTCT
TERRA-chr-13q-R	GCACTTGAACCCTGCAATACAG

TERRA-chr-17p-F	CTTATCCACTTCTGTCCCAAGG
TERRA-chr-17p-R	CCCAAAGTACACAAAGCAATCC
TERRA-chr-XqYq-F	CCCCTTGCCTTGGGAGAA
TERRA-chr-XqYq-R	GAAAGCAAAAGCCCCTCTGA
GAPDH-F	AGAAGGCTGGGGCTCATTTG
GAPDH-R	AGGGGCCATCCACAGTCTTC

Figure S1









