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### **Supplemental Information**

### circRNA\_0025202 Regulates Tamoxifen Sensitivity

#### and Tumor Progression via Regulating

#### the miR-182-5p/FOXO3a Axis in Breast Cancer

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Α

| IU                            | hsa_circ_0025202  |         |                                  |                                   |   |   |
|-------------------------------|---|---------|----------------------------------|-----------------------------------|---|---|
| Position                      | chr12:6646474-664   | 17162   |                                  |                                   |   |   |
| Strand                        | +   |         |                                  |                                   |   |   |
| Genomic<br>length             | 688   |         |                                  |                                   |   |   |
| Spliced<br>sequence<br>length | 495   |         |                                  |                                   |   |   |
| Annotation                    | ANNOTATED<br>CDS<br>coding<br>INTERNAL<br>OVCODE<br>OVERLAPTX<br>OVEXON |         |                                  |                                   |   |   |
| Repeats                       | NA  |         |                                  |                                   |   |   |
| Best<br>transcript            | NM_002046   |         |                                  |                                   |   |   |
| Gene<br>symbol                | GAPDH   |         |                                  |                                   |   |   |
|                               | circRNA study   | Sample  | total reads<br>circular junction | unique reads<br>circular junction | unique<br>reads<br>linear-5'<br>junctions | unique<br>reads<br>linear-3'<br>junctions |
| Scores                        | Salzman2013   | K562    |                                  |                                   |   |   |
|                               |   | Gm12878 |                                  |                                   |   |   |
|                               |   | Sknshra |                                  |                                   |   |   |
|                               |   | H1hesc  |                                  |                                   |   |   |
|                               |   | Nhek    |                                  |                                   |   |   |
|                               |   | Hepg2   |                                  |                                   |   |   |
|                               |   | A549    |                                  |                                   |   |   |









AnnexinV-FITC















#### Supplementary Figure Legends

**Figure S1:** Screening of differently expressed circRNAs between MCF7/P and MCF7/TR cell lines. **A.-H.** Verification of the expression level of other 9 candidates circRNAs in MCF7/P and MCF7/TR cell lines by qRT-PCR. **I.** Information of hsa\_circ\_0025202 in CircBase database. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001.

**Figure S2:** Features of MCF7/P and MCF7/TR cell lines. **A.** IC<sub>50</sub> and **B.** Cell viability assessed by MTT assay in MCF7/P and MCF7/TR treated with TAM or TAM at the indicated time points. **C.** Cell proliferation activity, **D.** colony formation capacity, **E.** cell migration, and **F.** cell apoptosis were measured respectively by MTT, cell colony formation, transwell assays and Annexin V-FITC assay in MCF7/P and MCF7/TR cell lines. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*\*p < 0.01, \*\*\*p < 0.001. Scale bar: 50 µm.

**Figure S3:** Hsa\_circ\_0025202 suppresses growth, metastasis and increases TAM sensitivity of HR-positive BC cells *in vitro*. **A.** Verification of the efficiency of hsa\_circ\_0025202 ove in MCF7 and T47D cells by qRT-PCR. **B.** Cell proliferation activity, **C.** colony formation capacity, **D.** cell migration potential and **G.** cell apoptosis were measured respectively by MTT, cell colony formation, transwell assay and Annexin V-FITC assay in MCF7 and T47D cells transfected with hsa\_circ\_0025202 ove. **E. and F.** cell cytotoxicity and IC<sub>50</sub> assays in MCF7 and T47D cells transfected with or without hsa\_circ\_0025202 ove. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*p < 0.05, \*\*, ##p < 0.01, \*\*\*, ###p < 0.001. Scale bar: 50 µm.

**Figure S4:** Knockdown of hsa\_circ\_0025202 promotes growth, metastasis and decreases TAM sensitivity of HR-positive BC cells *in vitro*. **A.** The expression of hsa\_circ\_0025202 and *GAPDH* were determined by qRT-PCR in MCF7/TR cells transfected with NC-si and si-circ\_0025202. **B.** MTT assay was conducted to evaluate cell proliferative ability. **C.** Colony formation in MCF7/TR cells. **D.** Transwell migration was conducted to evaluate cell migration ability (magnification,  $\times$  100). Scale bar: 50 µm. **E.** Cells were treated with TAM (25 nM) or ethanol (control) and subjected to Annexin V-FITC and propidium iodine staining to detect apoptotic rate. **F.** MTT assay demonstrates

cell viability of MCF7/TR treated together with TAM. **G.** IC<sub>50</sub> assay shows the variation in TAM sensitivity. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*p < 0.05, \*\*p < 0.01, \*\*\*, ###p < 0.001.

**Figure S5:** CCK8 assay was utilized for analyzing the cell viability. **A.** Cell viability of MCF7/TR cells transfected with PLCDH or circ\_0025202 ove. **B.** Cell viability of MCF7 and T47D cells transfected with NC-si or si-circ\_0025202. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*p < 0.05, \*\*p < 0.01.

**Figure S6:** Has\_circ\_0025202 sponges miR-182-5p to regulate the tumor progression and TAM sensitivity of BC cells. **A.** Verification of the efficiency of miR-182-5p mimics in MCF7 and T47D cells by qRT-PCR. **B.** Verification of the efficiency of miR-182-5p inhibitor in MCF7/TR cells by qRT-PCR. **C.** Cell proliferation activity, **D.** cell migration potential and **E.** cell apoptosis measured respectively by MTT assay, transwell assay and Annexin V-FITC assay in T47D cells after transfection of miR-182-5p mimics combined with or without hsa\_circ\_0025202 ove. **F. and G.** MTT analysis for cell cytotoxicity and IC<sub>50</sub> in T47D cells treated with TAM after transfection of miR-182-5p mimics combined with or without hsa\_circ\_0025202 ove. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*, \*p < 0.05, \*\*, \*\*p < 0.01, \*\*\*, \*\*\* p < 0.001. Scale bar: 50 µm.

**Figure S7:** FOXO3a downregulation decreases TAM sensitivity of MCF7/TR cells and protects cell form apoptosis. **A.** Verification of the efficiency of si-FOXO3a in MCF7/TR cells by qRT-PCR. **B.** MTT data for the proliferation of MCF7/TR cells treated with TAM after transfection of si-FOXO3a. **C.** MTT data for the cell cytotoxicity and IC<sub>50</sub> of MCF7/TR cells treated with TAM after transfection with si-FOXO3a. **D.** Annexin V-FITC assay was used to assess cell apoptosis in MCF7/TR cells transfected with si-FOXO3a. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*p < 0.05, \*\*p < 0.01, ###p < 0.001.

Figure S8: Verification of hsa\_circ\_0025202 level in the established stable M7/circ\_0025202 ove cells by qRT-PCR. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*\*\*p < 0.001.

**Figure S9:** Fold changes of tumor volume and weight in PBS group and TAM group between M7/PLCDH and M7/circ\_0025202 ove group. **A.** Fold changes of tumor volume in PBS group and TAM group between M7/PLCDH and M7/circ\_0025202 ove group. **B.** Fold changes of tumor weight in PBS group and TAM group between M7/PLCDH and M7/circ\_0025202 ove group. Data are presented as means  $\pm$  SEM of at least three independent experiments. \*\*p < 0.01, \*\*\*p < 0.001.

|                      | Table S1. Primers and oligoes used in this study |       |   |  |  |  |
|----------------------|--|-------|---|--|--|--|
| Name                 |  |       | Sequence  |  |  |  |
| Plasmid construction |  |       |   |  |  |  |
|                      | PLCDH-ciR  | F     | CGGAATTCTGAAATATGCTATCTTACAGCAATGCCTCCTGCACCACCAA |  |  |  |
|                      |  | R     | CGGGATCCTCAAGAAAAAATATATTCACCAGGAAATGAGCTTGACAAA  |  |  |  |
|                      | hsa circ 0025202 wt                              | F     | AGCTTTGTTTAAACCAATGCCTCCTGCACCACCAA               |  |  |  |
|                      |  | R     | CCGCTCGAGCAGGAAATGAGCTTGACAAAGTG                  |  |  |  |
|                      | hsa circ 0025202 mut                             | F     | CTAGAAAAACCTCGGTTTTATGATGACATCAAG                 |  |  |  |
|                      |  | R     | CTTGATGTCATCATAAAACCGAGGTTTTTCTAG                 |  |  |  |
|                      | FOXO3a 3'UTR wt1                                 | F     | CCGCTCGAGAGGATCACTGAGGAAGGGGAAGTG                 |  |  |  |
|                      |  | R     | GCTCTAGAGCTGTCCTCCACTGGCAGGCG                     |  |  |  |
|                      | FOXO3a 3'UTR wt2                                 | F     | CCGCTCGAGACCCGTCCAGGACAGAACCGT                    |  |  |  |
|                      |  | R     | GCTCTAGATGCCTCTCACTCATACACTTCTAGC                 |  |  |  |
|                      | FOXO3a 3'UTR mut1                                | F     | CTTGCTGAGAGCAGAGGGTTACCAGGGTTTTCTCTGTA            |  |  |  |
|                      |  | R     | TACAGAGAAAACCCTGGTAACCCTCTGCTCTCAGCAAG            |  |  |  |
|                      | FOXO3a 3'UTR mut2                                | F     | AACCCTTTAGTGACAGGGTTACCTGAGTGG AGAGCTGA           |  |  |  |
|                      |  | R     | TCAGCTCTCCACTCAGGTAACCCTGTCACTAAA                 |  |  |  |
| RT-PCR               |  |       |   |  |  |  |
|                      | hsa circ 0052375 (TRIM28)                        | div-F | CCAACCAGCGGAAATGTGAG                              |  |  |  |
|                      |  | div-R | TGCACACGCTTCTGTACGTC                              |  |  |  |
|                      | hsa_circ_0007556 (APP)                           | div-F | GGTGGGCGGTGTTGTCATA                               |  |  |  |
|                      |  | div-R | GGCATGAGAGCATCGTTTCC                              |  |  |  |
|                      | hsa_circ_0007647 (THAP4)                         | div-F | CTGTCGCCCAGCCGC                                   |  |  |  |
|                      |  | div-R | CGGTCAGGTGGAAGATGGATG                             |  |  |  |
|                      | hsa_circ_0014788 (HDGF)                          | div-F | TGCTGACTGTAGCTTTGGAAGT                            |  |  |  |
|                      |  | div-R | GGCTGTTGATTTCACGGCAG                              |  |  |  |
|                      | hsa_circ_0097922 (PGAM5)                         | div-F | ATGGCGTGGGGTTTAAGGTG                              |  |  |  |
|                      |  | div-R | ATCTTGTCGGGAGGCATGAA                              |  |  |  |
|                      | hsa_circ_0000837 (RBBP8)                         | div-F | TCCCAAGCAGCAGATGAAGAG                             |  |  |  |
|                      |  | div-R | TCTTGAACACCAAGTCCAAGTG                            |  |  |  |
|                      | hsa_circ_0001355 (RSRC1)                         | div-F | GTCGAAGTCGTTCAAGGGGT                              |  |  |  |
|                      |  | div-R | GCTCGAGGAGGACCGTCTA                               |  |  |  |
|                      | hsa_circ_0007761 (ATXN7)                         | div-F | AATCTGTGGGTTGAGGC                                 |  |  |  |
|                      |  | div-R | GCTCCGACATTCTTTCC                                 |  |  |  |
|                      | hsa_circ_0123878 (CDCP1)                         | div-F | TGTGACCAAGATGCCCAAAGT                             |  |  |  |
|                      |  | div-R | GGGTCCCCAGCTTTATGAGAA                             |  |  |  |
|                      | ACTIN  | F     | CACCATTGGCAATGAGCGGTTC                            |  |  |  |
|                      |  | R     | AGGTCTTTGCGGATGTCCACGT                            |  |  |  |
|                      | GAPDH  | F     | GTCTCCTCTGACTTCAACAGCG                            |  |  |  |
|                      |  | R     | ACCACCCTGTTGCTGTAGCCAA                            |  |  |  |
|                      | hsa_circ_0025202 (GAPDH)                         | div-F | TCATTTCCTGCAATGCCTCCT                             |  |  |  |
|                      |  | div-R | ATGATGTTCTGGAGAGCCCC                              |  |  |  |
|                      | ACTIN  | div-F | GATGTGGATCAGCAAGCAGG                              |  |  |  |
|                      |  | div-R | TACTTCAGGGTGAGGATGCC                              |  |  |  |
|                      | FOXO3a   | F     | TCTACGAGTGGATGGTGCGTTG                            |  |  |  |
|                      |  | R     | CTCTTGCCAGTTCCCTCATTCTG                           |  |  |  |
|                      | miR-182-5p                                       | F     | TTTGGCAATGGTAGAACTCACACT                          |  |  |  |
|                      | miR-34a-5p                                       | F     | TGGCAGTGTCTTAGCTGGTTGT                            |  |  |  |
|                      | miR-556-5p                                       | F     | GATGAGCTCATTGTAATATGAG                            |  |  |  |
|                      | miR-490-5p                                       | F     | CCATGGATCTCCAGGTGGGT                              |  |  |  |
|                      | miR-197-3p                                       | F     | TTCACCACCTTCTCCACCCAGC                            |  |  |  |
|                      | miR-516b-5n                                      | F     | ATCTGGAGGTAAGAAGCACTTT                            |  |  |  |
|                      | miR-885-3p                                       | F     | AGGCAGCGGGGTGTAGTGGATA                            |  |  |  |
|                      | miR-1271-5n                                      | F     | CTTGGCACCTAGCAAGCACTCA                            |  |  |  |
|                      | miR-382-5p                                       | F     | GAAGTTGTTCGTGGTGGATTCG                            |  |  |  |
|                      | miR-449a   | F     | TGGCAGTGTATTGTTAGCTGGT                            |  |  |  |
|                      | miR-183-5p                                       | F     | TATGGCACTGGTAGAATTCACT                            |  |  |  |

| miR-34c-5p           | F                | AGGCAGTGTAGTTAGCTGATTGC  |
|----------------------|------------------|--------------------------|
| miR-449b-5p          | F                | AGGCAGTGTATTGTTAGCTGGC   |
| miR-1225-3p          | F                | TGAGCCCCTGTGCCGCCCCAG    |
| miR-4306             | F                | TGGAGAGAAAGGCAGTA        |
| miR-185-5p           | F                | TGGAGAGAAAGGCAGTTCCTGA   |
| miR-940              | F                | AAGGCAGGGCCCCCGCTCCCC    |
| miR-1827             | F                | TGAGGCAGTAGATTGAAT       |
| miR-215-5p           | F                | ATGACCTATGAATTGACAGAC    |
| miR-491              | F                | AGTGGGGAACCCTTCCATGAGG   |
| miR-657              | F                | GGCAGGTTCTCACCCTCTCAGG   |
| miR-609              | F                | AGGGTGTTTCTCTCATCTCT     |
| miR-520h             | F                | ACAAAGTGCTTCCCTTTAGAGT   |
| miR-520g             | F                | ACAAAGTGCTTCCCTTTAGAGTGT |
| snRNA U6 F           | F                | GCGCGTCGTGAAGCGTTC       |
| snRNA U6 R           | R                | GTGCAGGGTCCGAGGT         |
| RNA oligos           |                  |                          |
| si-circ_0025202-1    | sense            | UCCUGCAAUGCCUCCUGCATT    |
|                      | ( <b>5'-3'</b> ) |                          |
|                      | antisense        | UGCAGGAGGCAUUGCAGGATT    |
|                      | (5'-3')          |                          |
| si-circ_0025202-2    | sense            | AAGCUCAUUUCCUGCAAUGTT    |
|                      | ( <b>5'-3'</b> ) |                          |
|                      | antisense        | CAUUGCAGGAAAUGAGCUUTT    |
|                      | (5'-3')          |                          |
| miR-182-5p mimics    | sense            | UUUGGCAAUGGUAGAACUCACACU |
|                      | ( <b>5'-3'</b> ) |                          |
|                      | antisense        | UGUGAGUUCGACCAUUGCCAAAUU |
|                      | (5'-3')          |                          |
| miR-182-5p inhibitor | sense            | AGUGUGAGUUCUACCAUUGCCAAA |
|                      | (5'-3')          |                          |
| si-FOXO3a            | sense            | CAACCUGUCACUGCAUAGU      |
|                      | ( <b>5'-3'</b> ) |                          |
|                      | antisense        | ACUAUGCAGUGACAGGUUG      |
|                      | (5'-3')          |                          |
| NC-si                | sense            | UUCUCCGAACGUGUCACGUTT    |
|                      | ( <b>5'-3'</b> ) |                          |
|                      | antisense        | ACGUGACACGUUCGGAGAATT    |
|                      | (5'-3')          |                          |
| NC                   | sense            | CAGUACUUUUGUGUAGUACAA    |
|                      | ( <b>5'-3'</b> ) |                          |