



Fig. S1



Fig. S2. Effects of WBP2 on growth ability in ER positive cells. (A) Cell viabilities of WBP2 overexpressed/silenced MCF-7 cells. **(B)** Cell viabilities of WBP2 overexpressed/silenced BT474 cells.

Fig. S2



Fig. S3. Body weight of four group breast cancer bearing mice. WBP2+Dox: WBP2 overexpressed MCF-7 cells treated with doxorubicin. WBP2: WBP2 overexpressed MCF-7 cells. EGFP+Dox: Control MCF-7 cells treated with doxorubicin. EGFP: Control MCF-7 cells.

Fig. S3



Fig. S4. Correlation analysis among WBP2, MDR1, and ESR1 using online available dataset. (A) The correlation analysis between MDR1 and WBP2 using TCGA dataset. **(B)** The correlation analysis between WBP2 expression and progression and poor clinical outcomes of ER positive tumors utilizing GOBO Gene Set Analysis. N indicates samples number. –[-2.512,-0.189), –[-0.1890.373), –[0.3732.073) indicate Log2 median-centered intensity of *WBP2* mRNA in all these samples. **(C)** The correlation analysis between WBP2 and ER (ESR1) in ER positive breast cancer patients by using Breast Cancer Gene-Expression Miner v4.1. R indicates Pearson's coefficient.



Fig. S5. Results of genome wide mRNA screen assay in MCF-7 cells. (A) Heat map of differentially expressed genes between EGFP and EGFP-WBP2 cells. **(B)** Scatter plot of differentially expressed genes between EGFP and EGFP-WBP2 cells. EGFP-WBP2: WBP2 overexpressed MCF-7 cells. EGFP: Control MCF-7 cells.