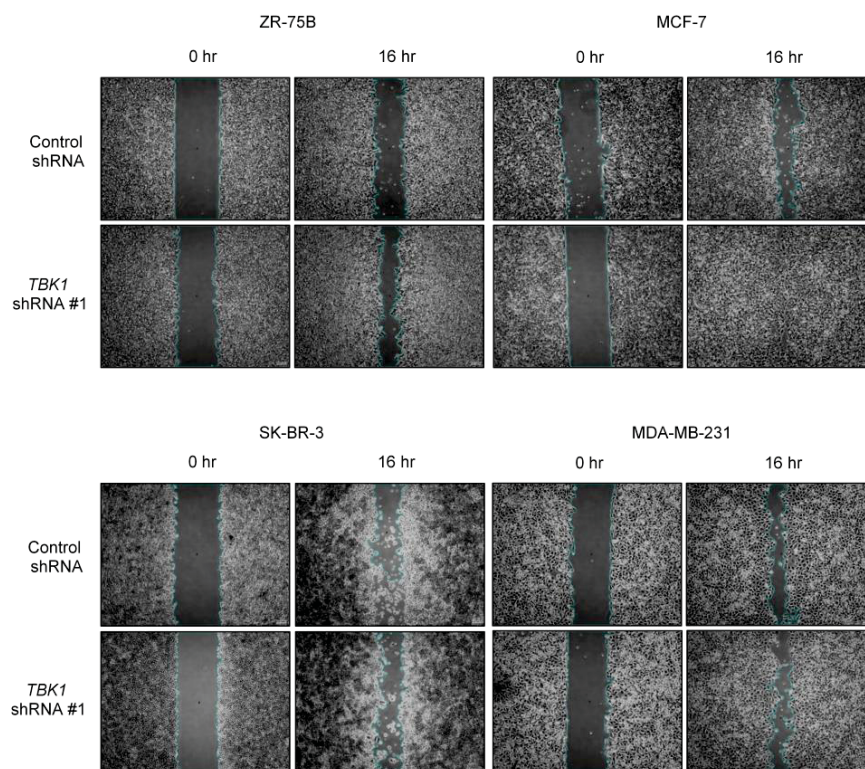


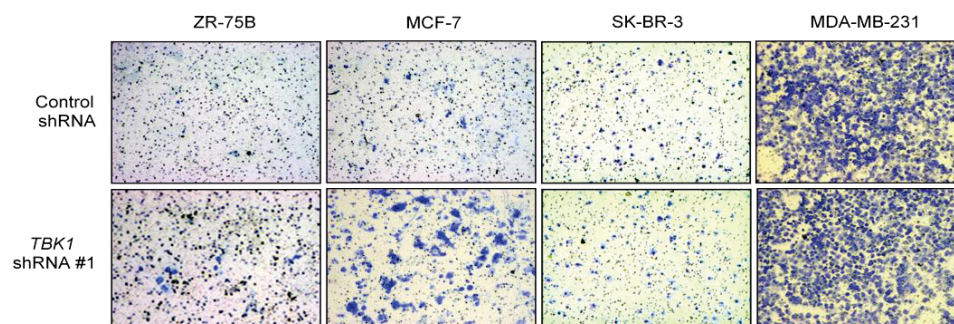
SUPPLEMENTAL FIGURES S1-S4

Supplementary Fig. S1.



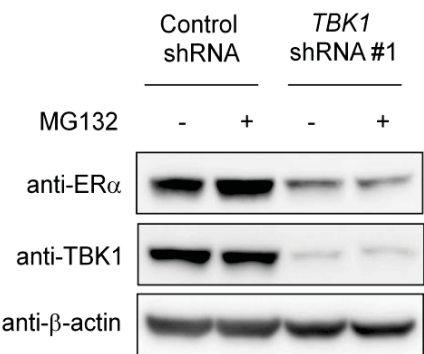
Supplementary Fig. S1. TBK1 knockdown increases cell migration. Phase-contrast microscopy image of an *in vitro* wound healing assay at 0 and 16 hr after wounding in TBK1-knockdown breast cancer cells. Original magnification, 100 $\times$.

Supplementary Fig. S2.



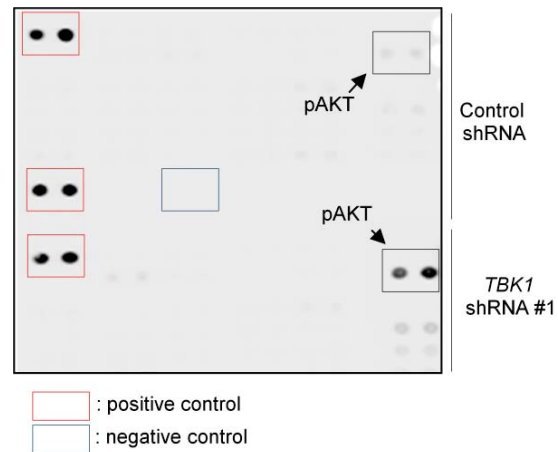
Supplementary Fig. S2. TBK1 knockdown increases cell invasion. Transwell invasion assays of TBK1-knockdowned breast cancer cells. Cell invasion was assayed in transwell coated with Matrigel. After 24 hr, cells crossed the Matrigel-coated filter were fixed, stained with toluidine blue and counted. Representative pictures of the bottom surface are shown. Original magnification, 100 $\times$.

Supplementary Fig. S3.



Supplementary Fig. S3. *TBK1* knockdown did not inhibit the expression of ER α proteins via the proteasomal degradation pathway. Immunoblot analysis of ER α and TBK1 in MCF-7 breast cancer cells expressing *TBK1*-specific shRNA after treatment with the proteasome inhibitor MG132. Cells were treated with or without 10 μ M MG132 for 4 hr.

Supplementary Fig. S4.



Supplementary Fig. S4. TBK1 knockdown induces phosphorylation of AKT in ER α -positive breast cancer cells. Analysis of proteome profiler in 46 human phosphor-protein kinase array assessed in lysates from ZR-75B breast cancer cell lines expressing *TBK1*-specific shRNA.

SUPPLEMENTAL TABLE 1 and TABLE 2**Supplementary Table 1. ER α promoter-specific primer pairs.**

Regions	primer sequence
-3,219/-2,951	Forward: 5'-AGCTGAGAGCATGGCAATTT-3' Reverse: 5'-ATCTGCCACCCCAGATGATA-3'
-2,208/-1,907	Forward: 5'-GCACGTGTGTTCCCATAGTG-3' Reverse: 5'-TCCAACCAGAGGTTGATTGA-3'
-1,834/-1,534	Forward: 5'-TGCCAGTACTGAACATGACTTTG-3' Reverse: 5'-TTGATATTCGTTTGCATTCCA-3'
-1,258/-1,032	Forward: 5'-TTTCGCTTTCAAAACACTTGA-3' Reverse: 5'-TCCAGAATACATAGAGCAGGACA-3'
-624/-251	Forward: 5'-TGATTTTACAGCCCCTTTGC-3' Reverse: 5'-GACAGGCATGTGGAGTTGG-3'
-350/-111	Forward: 5'-CTTGCCCCTGCTTTTAGTTT-3' Reverse: 5'-CCAGGCCCGAATCTAACTTT-3'

Supplementary Table 2. Sequence of putative FOXO3A binding site in the 4-kb ER α promoter.

Regions	Putative FOXO3A binding sequence		
-3,219/-2,951	-3,197CTTAGAAC ^{-3,190}	-3,152CAGGTAAG ^{-3,145}	
-2,208/-1,907	-2,074CTTAATCT ^{-2,067}	-2,020CTTACCTC ^{-2,013}	-1,992CTTAAACT ^{-1,985}
-1,834/-1,534	-1,746ATTATAAG ^{-1,739}	-1,631ATACTAAG ^{-1,624}	
-1,258/-1,032	-1,170CTTACAGA ^{-1,163}	-1,127TGTGTAAG ^{-1,120}	
-624/-251	-587CTTAGTGT ⁻⁵⁸⁰	-552CTTAAAAA ⁻⁵⁴⁵	-391TGAGTAAG ⁻³⁸⁴
-350/-111	-149CTTAATGG ⁻¹⁴²	-139GTGCTAAG ⁻¹³²	