Supplementary methods

Immunoprecipitation (IP) and immunoblotting (IB)

For immunoprecipitation assays, whole cellular extracts were incubated with appropriate primary antibodies or normal rabbit/mouse immunoglobin G (IgG) on a rotator at 4℃ overnight, followed by addition of protein A/G Sepharose CL-4B beads for 2 h at 4℃. Beads were then washed with lysis buffer (50 mM Tris-Cl [pH 7.4], 150 mM NaCl, 1 mM EDTA, 0.5% NP-40, 0.25% sodium deoxycholate and protease inhibitor mixture). The immune complexes were subjected to SDS-PAGE followed by immunoblotting with appropriate secondary antibodies.

Glutathione S-transferase (GST) pull-down experiments

GST fusion constructs were expressed in BL21 *Escherichia coli* cells, and crude bacterial lysates were prepared by sonication in TEDGN (50 mM Tris-HCl [pH 7.4], 1.5 mM EDTA, 1 mM dithiothreitol, 10% (v/v) glycerol, 0.4 M NaCl) in the presence of the protease inhibitor mixture. The *in vitro* transcription and translation experiments were done with rabbit reticulocyte lysates (TNT Systems; Promega) according to the manufacturer's recommendation. In GST pull-down assays, about 5 μg of the appropriate GST fusion proteins were mixed with 15 μl of the *in vitro* transcribed/translated products and incubated in binding buffer (75 mM NaCl, 50 mM HEPES [pH 7.9]) at 4℃ for 30 min in the presence of the protease inhibitor mixture. The binding reaction was then added to 50 μl of glutathione-sepharose beads and mixed at 4 ℃ for 2 h. The beads were washed five times with washing buffer, resuspended in 30 μl of 2 × SDS-PAGE loading buffer, and analyzed by Western blotting with specific antibodies.

Quantitative real-time PCR (qPCR)

Total cellular RNAs were isolated with the TRIzol reagent (Invitrogen) and used for first strand cDNA synthesis with the Reverse Transcription System (Promega, A3500). Quantitation of all gene transcripts was done by qPCR using Power SYBR Green PCR Master Mix and an ABI PRISM 7300 sequence detection system (Applied Biosystems, Foster City, CA) with *GAPDH* expression as an internal control. The primer pairs used were as follows: *GAPDH* primers: 5'-TCCTCCTGTTTCATCCAAGC-3' (forward) and 5'-TAGTAGCCGGGCCCTACTTT-3' (reverse); *TWIST* primers: 5'-GGAGTCCGCAGTCTTACGAG-3' (forward) and 5'-TCTGGAGGACCTGGTAGAGG-3' (reverse); *E-cadherin* primers: 5'-CATTTCTTGGTCTACGCCTG-3' (forward) and 5'-GAGAGGAGTTGGGAAATGTG-3' (reverse); *N-cadherin* primers: 5'-CACTGCTCAGGACCCAGAT-3' (forward) and 5'-TAAGCCGAGTGATGGTCC-3' (reverse); *SET8* primers: 5'-ACTTACGGATTTCTACCCTGTC-3' (forward) and 5'-CGATGAGGTCAATCTTCATTCC-3' (reverse).

Construction of SET8 and TWIST mammalian expression vectors

For cloning of p3xFLAG-SET8 vector, the full-length SET8 coding DNA sequence (1059 nucleotides) was obtained from the MCF-7 cDNA first strand using the following PCR primer pair: 5'-AGTTGAATTCAATGGCTAGAGGCAGGAAG-3' (forward) and 5'-AATTGGATCCTTAATGCTTCAGCCACGG-3' (reverse). The resultant PCR products were doubly digested by enzymes and ligated into the EcoR I-BamH I sites of p3xFLAG-CMV (Sigma) to generate p3xFLAG-SET8 mammalian expression construct. For subcloning of p3xFLAG-TWIST vector, the TWIST sequence was subclonned into p3xFLAG-CMV vector using primers as follows:

5’-AAATTTGAATTCAATGATGCAGGACGTGTCCAGCTCGC-3’(forward) and 5’-AAATCTGGATCCCTAGTGGGACGCGGACATGGACCAG-3’(reverse).

Fluorescence confocal microscopy

Stably transfected MCF-7 cells were washed with PBS, fixed in 4% paraformaldehyde, permeablized with 0.1% Triton X-100, blocked in 3% BSA, and incubated with primary antibodies followed by addition of FITC-conjugated secondary antibodies. Cells were washed three times and a final concentration of 0.1 μg/ml 4,6-diamidino-2-phenylindole dihydrochloride (DAPI) (Sigma) was included in the final wash to stain nuclei. Images were visualized and recorded with Leica TCS SP5 confocal microscope.