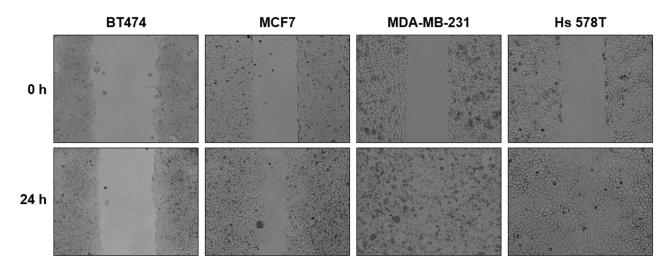
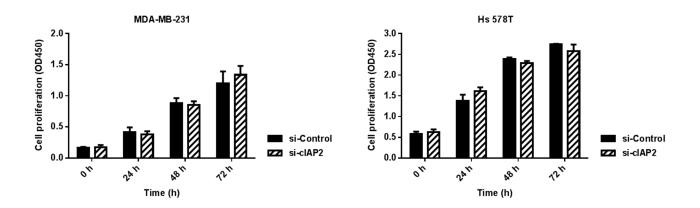
Cellular inhibitor of apoptosis protein 2 promotes the epithelialmesenchymal transition in triple-negative breast cancer cells through activation of the AKT signaling pathway

## SUPPLEMENTARY MATERIALS



Supplementary Figure 1: Cell motility in various breast cancer cell lines (BT474, MCF7, MDA-MB-231, Hs 578T). Cell migration capacity was examined by wound healing assays. Images were taken at 0 and 24 h. The wound width was 500  $\mu$ m (10× magnification).



Supplementary Figure 2: Effect of cIAP2 silencing on cell proliferation in two TNBC cell lines (MDA-MB-231 and Hs 578T). Cell proliferation rates of the indicated cell lines were measured using a Cell Counting Kit-8 (CCK-8). Values are represented as means ± standard deviations.

Cell line	ER	PR	HER2	Classification
MCF7	+	+	-	Luminal <sup>[18-20]</sup>
T-47D	+	+	-	Luminal <sup>[18-20]</sup>
BT474	+	+	+	Luminal <sup>[18-20]</sup>
SK-BR-3	-	-	+	HER2-positive <sup>[18-20]</sup>
MDA-MB-231	-	-	-	Triple-negative [18-20]
Hs 578T	-	-	-	Triple-negative [18-20]

Supplementary	Table 1:	Characteristics of	f the breast cancer c	ell lines used in this study
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Statuses of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2)/neu as well as breast cancer subtypes are indicated based on previously published data.

% Staining score	% Nuclei staining	
0	0%	
1	1-4%	
2	5-9%	
3	10–19%	
4	> 20%	
5	> 50%	
Intensity score	Staining intensity	
0	No staining	
1	Weak staining	
2	Moderate staining	
3	Strong staining	

Quick score = % Staining score + Intensity score Giving a range from 0 to 8 www.impactjournals.com/oncotarget/

Gene product	Sense	Antisense
<i>CDH1</i> (E-cadherin)	GTCAGTTCAGACTCCAGCCC	AAATTCACTCTGCCCAGGACG
EPCAM (EpCAM)	CTCCAGAACAATGATGGGCT	CCAGTAGGTTCTCACTCGCTC
CDH2 (N-cadherin)	GGTGGAGGAGAAGAAGACCAG	GGCATCAGGCTCCACAGT
Vim (vimentin)	GTTTCCAAGCCTGACCTCAC	GCTTCAACGGCAAAGTTCTC
ACTA2 (a-SMA)	GTGAAGAAGAGGACAGCACTG	CACATACATGGCTGGGACATTG
SNAI2 (Slug)	CAAGGACACATTAGAACTCAC	GTGCAGGAGAGACATTCTGGA
SNAI1 (Snail)	ACTTCAGTCTCTTCCTTGGAG	TGACATCTGAGTGGGTCTGG
BIRC1 (NAIP)	CGTCCCATTTGTTGCCAGT	GATCAGTTTGGCCACTCG
BIRC2 (cIAP1)	GTGGTGGGAAGCTCAGTAAC	CATCATCATTGCGACCCACA
BIRC3 (cIAP2)	AATGCTTTTGCTGTGATGGTG	GCTTGAACTTGACGGATGAAC
BIRC4 (XIAP)	GGGGTTCAGTTTCAAGGACAT	CCACAAGGAACAAAAACGATAG
BIRC5 (survivin)	GACGACCCCATAGAGGAACAT	GCCAGAGGCCTCAATCCAT
BIRC6 (BRUCE)	ATGTGCTTCCAACCCTTCCT	GGCTCAGTTTGATTCACGC
BIRC7 (livin)	CTGGGACCCGTGGGAAGAAC	TCCTGGGCACTTTCAGACTG
BIRC8 (ILP2)	GAGACGGTGGACAAGTCCTA	TTGCCACCTGTCTACCGCTT
GAPDH	GATGGCATGGACTGTGGTCA	GCAATGCCTCCTGCACCACC

Supplementary Table 3: Sequences of the primers used in this study