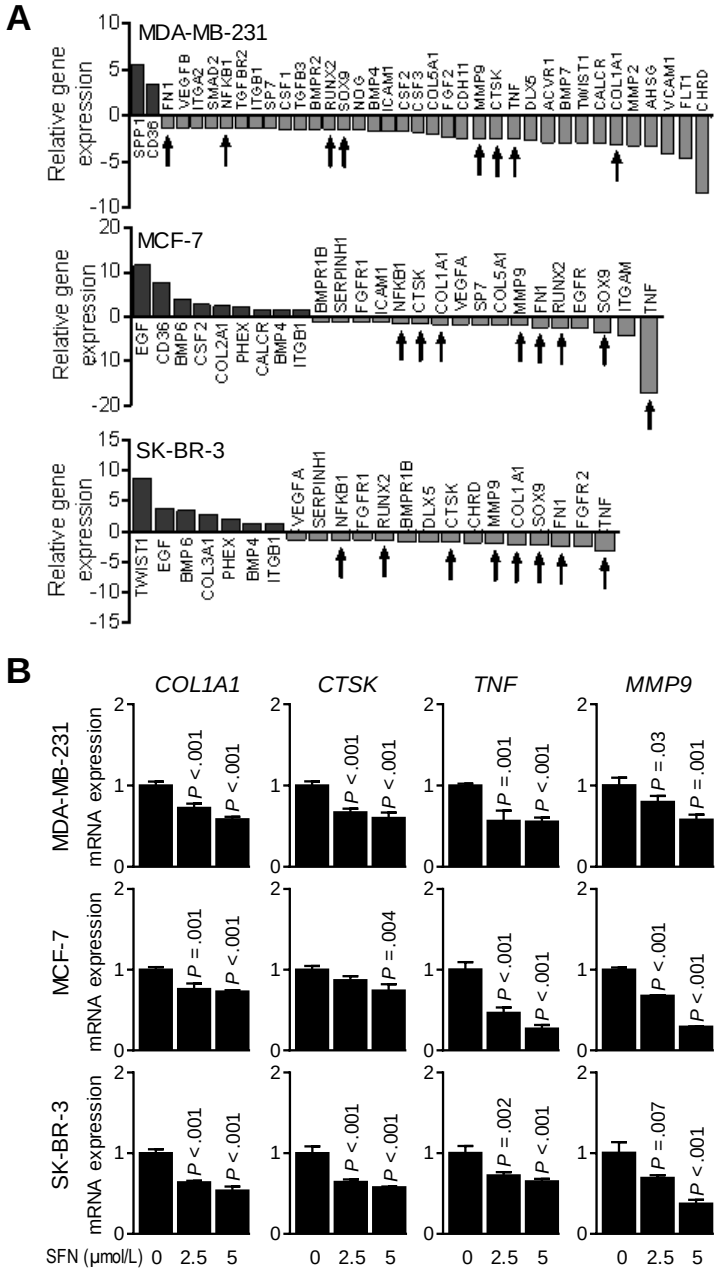
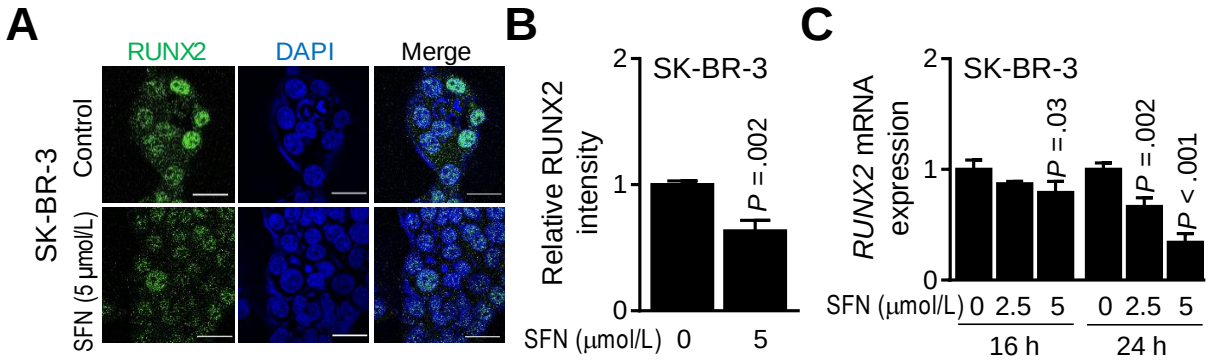
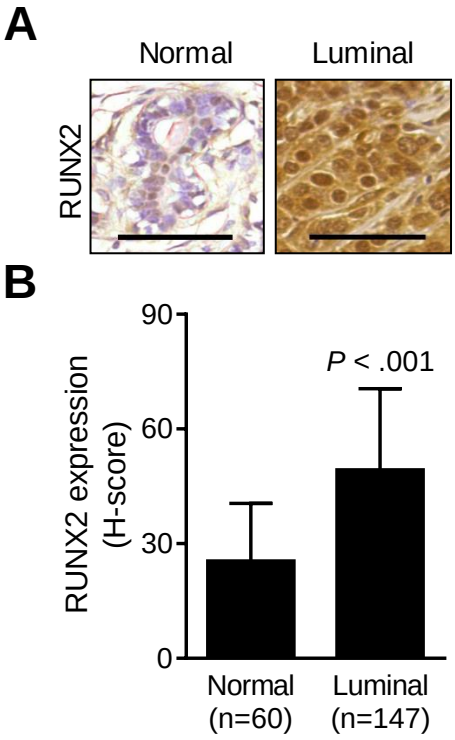
Supplementary Figure S1: Summary of gene expression changes following sulforaphane (SFN) treatment in breast cancer cells. **A,** Relative gene expression in SFN-treated cells in comparison with control. Arrows indicate common down-regulated genes in all three cell lines. **B,** Quantitative reverse transcription-polymerase chain reaction (qRT-PCR) for *collagen, type I, alpha 1* (*COL1A1*), *cathepsin K* (*CTSK*), *tumor necrosis factor* (*TNF*), and *matrix metalloproteinase* (*MMP9*) gene expression in control and SFN-treated cells (24-hour treatment). Results shown are mean ± SD (n=3). Statistical significance of difference was analyzed by ANOVA followed by Dunnett's test. Consistent results were obtained from two independent experiments.



Supplementary Figure S2: Sulforaphane (SFN) treatment downregulated expression of Runt-related transcription factor 2 (RUNX2) in SK-BR-3 cell line. **A,** Representative confocal microscopic images (×60 objective magnification in oil) of RUNX2 protein (green) in SK-BR-3 cells after 24 hours of treatment with dimethyl sulfoxide (DMSO) or 5 µmol/L SFN. Nuclei were stained with 4′,6-diamidino-2-phenylindole (blue). **B,** Quantitation of RUNX2 protein level intensity in SK-BR-3 cells. Results shown are mean RUNX2 intensity ± SD (n=3). Statistical significance of difference was analyzed by two-sided Student's t-test. **C,** Quantitative real-time PCR analysis of *RUNX2* mRNA expression in SK-BR-3 cells treated with DMSO or the indicated doses of SFN for specified time points. Results shown are mean ± SD (n=3). Statistical significance of difference was analyzed by one-way analysis of variance (ANOVA) followed by Dunnett's test. Consistent results were obtained from repeated experiments.

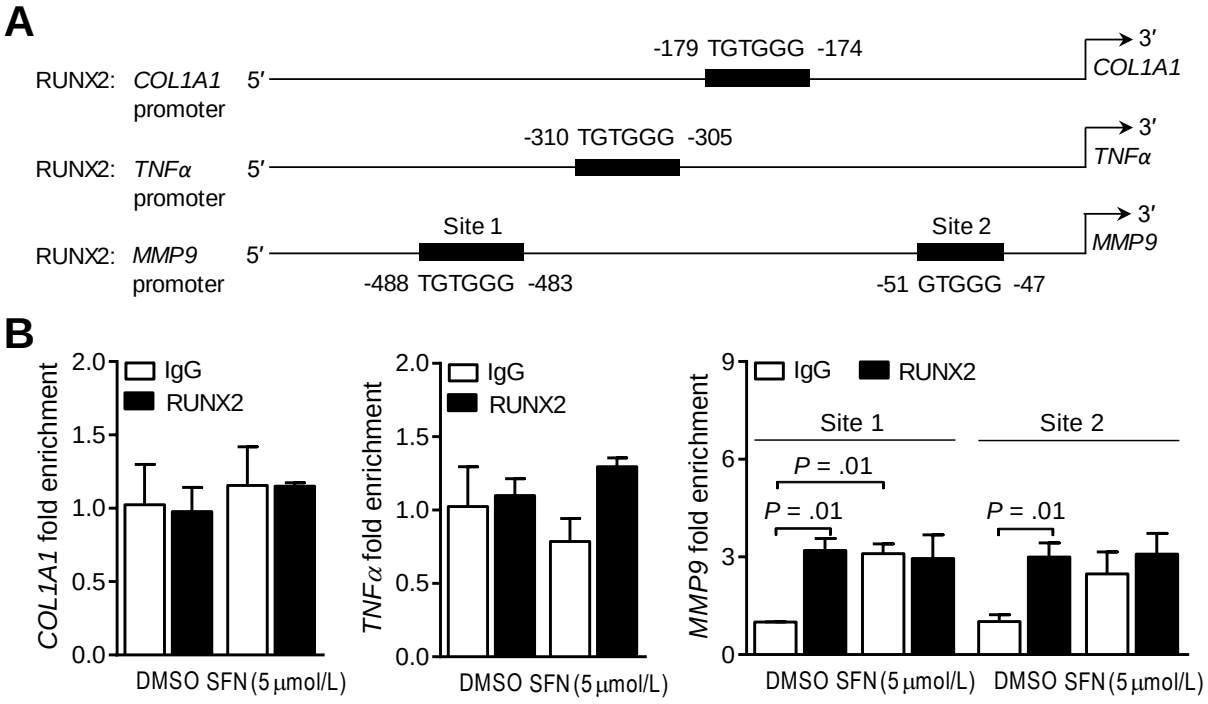


Supplementary Figure S3: Expression of runt-related transcription factor 2 (RUNX2) protein was higher in luminal-type breast cancers than in normal mammary tissues. **A,** Immunohistochemical images for RUNX2 protein (scale bar = 100 μm; 20× objective magnification) in a representative normal marry tissue and in a luminal-type breast cancer tissue. **B,** Quantitation (H-score) of RUNX2 protein level in normal mammary tissues (n = 60) and luminal-type breast cancer tissues (n = 147). Results shown are mean ± SD. Statistical significance was determined by two-sided Student's t-test.



Supplementary Figure S4: Runt-related transcription factor 2 (RUNX2) was recruited at the promoter of *matrix metallopeptidase 9* (*MMP9*) **A**, Putative RUNX2 binding sequence sites in the promoter region of *collagen, type I, alpha 1* (*COL1A1*), *tumor necrosis factor α* (*TNFα*), and *matrix metallopeptidase (MMP9*). The primers were as follows: *COL1A1*- Forward 5'-ATTGGAGGTCCCAGGAAGAG-3'
Reverse 5'- TTGGGAGTTGGAATGGAGAG; *MMP9*- Primer for: -488 TGTGGG -483 Forward 5'-AGGCTGCTACTGTCCCCTTT-3' Reverse 5'-TCTGAAAGCCTCCAGTGGTC-3'; Primer for -51 GTGGG -47 Forward 5'-GAGTCAGCACTTGCCTGTCA-3'Reverse 5'-AAGAGCACAAGGGTGGACTG-3'; and *TNFα*- Forward 5'-GACAGATGTGGGGTGTGAGA-3' Reverse 5'-ACCTTCCAGGCATTCAACAG-3'. **B,** Chromatin immunoprecipitation assay using MDA-MB-231 cells showing the binding of RUNX2 transcription factor to the *MMP9*. Results shown are the mean ± SD (n = 2-3). Statistical significance of difference was analyzed by Bonferroni's multiple comparisons test.

Supplementary Figure S4



Supplementary Table S1

Correlation between genes altered by SFN treatment (TCGA BrCa dataset, n = 1097). The ns signifies not significant.

Gene	**Gene**	**Pearson r**	***P***
RUNX2	*NFKB1*	.22	<.001
RUNX2	*SOX9*	.059	.05
RUNX2	*CTSK*	.69	<.001
RUNX2	*COL1A1*	.68	<.001
RUNX2	*TNF*	.11	.004
RUNX2	*MMP9*	.24	<.001
NFKB1	*SOX9*	.08	.01
NFKB1	*CTSK*	.18	<.001
NFKB1	*COL1A1*	.11	<.001
NFKB1	*TNF*	.16	<.001
NFKB1	*MMP9*	.03	ns

Supplementary Table S2

Consensus binding sequences for transcription factors

Transcription factor	Target gene	No. of sites	Position
RUNX2	*NFKB1*	3	-1161 *TGTGGG* -1152; -901 *TGTGGG* -896; -793 *GTGGG* -789
RUNX2	*RELA*	4	-988 *AGTGGG* -983; -712 *TGTGGG* -707; -640 *GTGGG* -635; -322 *GTGGG* -318
RUNX2	*COL1A1*	1	-179 *TGTGGG* -174
RUNX2	*MMP9*	2	-488 *TGTGGG* -483; -51 *GTGGG* -47
RUNX2	*TNF*	1	-310 *TGTGGG* -305
RUNX2	*SOX9, CTSK*	0	No match
NFKB1	*RELA*	5	-1054 *TCCCC* -1050; -798 *GGGGAT* -793; -780 *GGGGGTxxxxxxxCCCC* -764; -729 *GGGGGA* -724; -350 *ATTCCCC* -344
NFKB1	*COL1A1*	5	-902 *GGGGGAT* -896; -886 *GGGGAT* -881; -848 *GAATCCCC* -841; -588 *GTTCCCC* -582; -416 *GGAGGACCCCC* -406
NFKB1	*MMP9*	2	-619 *GGGGGTTGCCCC* -608; -332 *GGGGGATCCC* -323
NFKB1	*RUNX2, SOX9, CTSK, TNF*	0	No match

Consensus binding sequences according to JASPAR (http://jaspar.genereg.net/) browser:

RUNX2: TGTGGTTT; NF-κB1: GGGGATTCCCC