Figure S1. Oncomine database analysis. The original data for the microarray analysis of UNC5C from different published reports was extracted from the Oncomine database. The box plot shows the 25th and 75th percentiles as the bottom and top boundaries of the box, respectively. The line within the box represents the median, and the whiskers above and below the box indicate the 90th and 10th percentiles. No significant difference between normal tissues and ductal breast carcinoma was detected. Significant differences were determined by unpaired Student's t-test. Normal, normal breast tissue; DBC, ductal breast carcinoma.

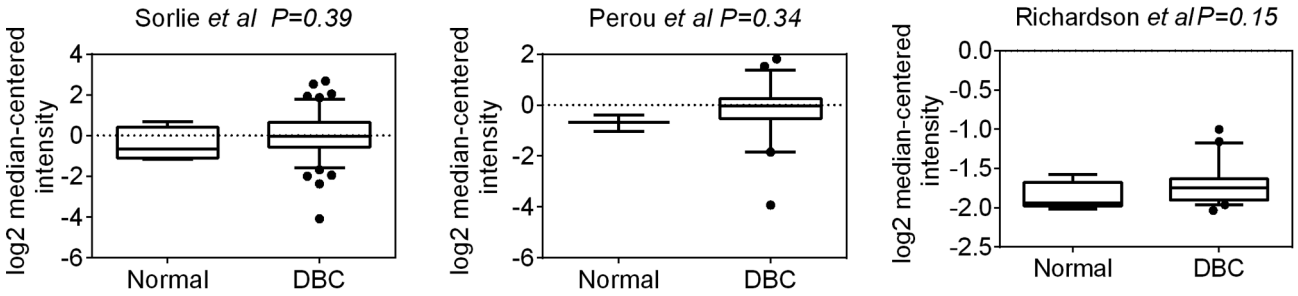

Figure S2. Effects of UNC5C knockdown and overexpression on NTN1 concentration in the culture medium of breast cancer cells as analyzed by ELISA. *P<0.05. NS, not significant; UNC5C, Unc-5 Netrin Receptor C; sh, short hairpin; Ctrl, control.

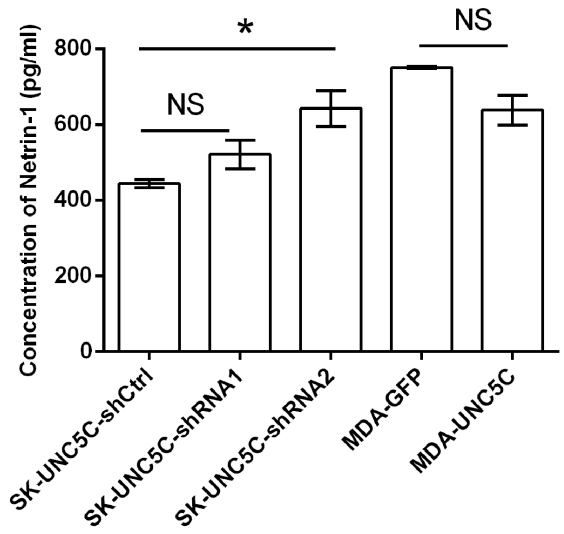

Figure S3. MMP expression in SK-BR-3 cells. Detection of the relative expression of MMP in SK-BR-3 cells by reverse transcription-quantitative PCR analysis. Data were first normalized to GAPDH and then normalized to the value of MMP3. **P<0.01. NS, not significant; MMP, matrix metalloproteinase.

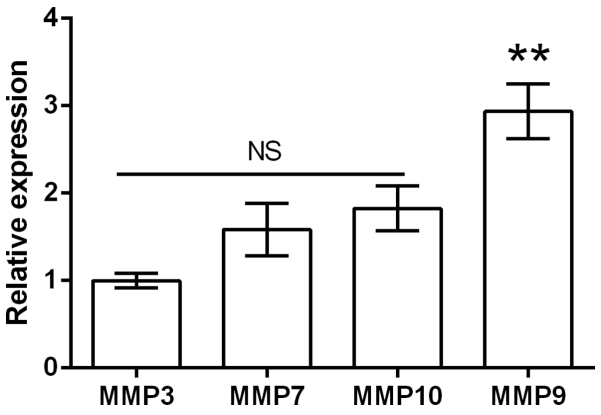

Figure S4. Quantitative analysis of semi-quantitative PCR results in Fig. 5A. The band intensity of each lane was determined using ImageJ software, and the pixel density was calculated. The pixel density of MMP9 was first normalized to GAPDH, and then normalized to the values of the corresponding untreated Unc5C-shCtrl. The minus sign indicates the addition of DMSO reagent only. *P<0.05, **P<0.01 vs. no inhibitors. UNC5C, Unc-5 Netrin Receptor C; sh, short hairpin; Ctrl, control.

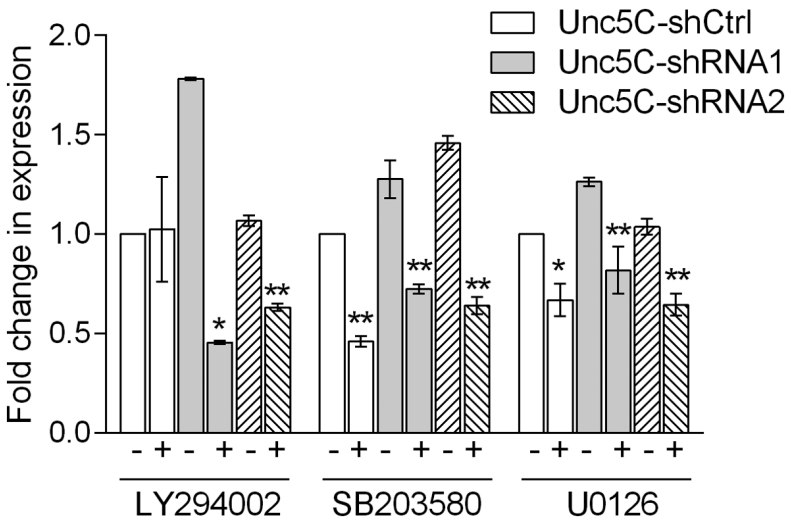

Figure S5. Quantitative analysis of the western blot results in Fig. 6D. The expression of p-ILK, p-FAK and p-Src was assessed using the following formula: (Phosphorylated protein shRNA/control)/(total protein shRNA/control). The expression of integrin α6 was assessed using the following formula: (ITGA6 shRNA/control)/(tubulin shRNA/control). *P<0.05, **P<0.01. NS, not significant; UNC5C, Unc-5 Netrin Receptor C; sh, short hairpin; Ctrl, control; ITGA6, integrin α6; p, phosphorylated; ILK, integrin-linked kinase.

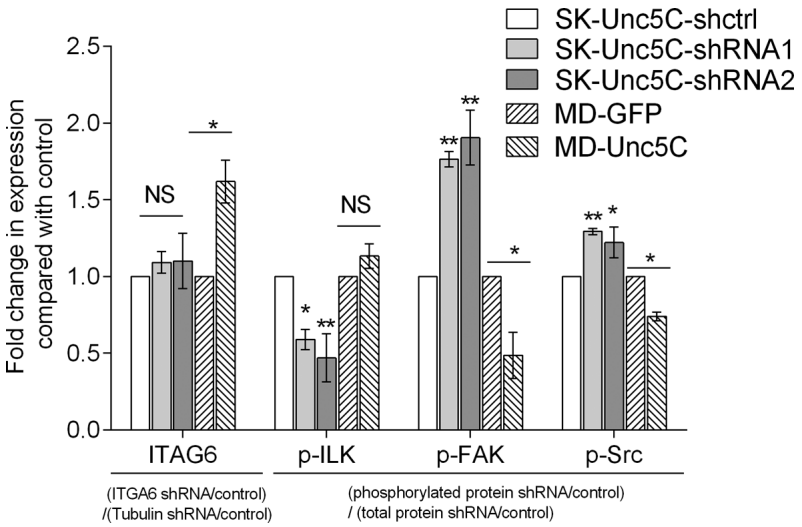

Table SI. Primers for reverse transcription-quantitative PCR and semi-quantitative PCR.

A, Primers for reverse transcription-quantitative PCR

Primer	Sequence (5'-3')
MMP2-F	TTTGACGGTAAGGACGGACTC
MMP2-R	TTGGTGTAGGTGTAAATGGGTG
MMP3-F	TCAGTCCCTCTATGGACCTC
MMP3-R	GAGGGAAACCTAGGGTGTGG
MMP7-F	GGGAACAGGCTCAGGACTATC
MMP7-R	GTGAGCATCTCCTCCGAGAC
MMP9-F	CGGAGCACGGAGACGGGTAT
MMP9-R	GCCGCCACGAGGAACAAACT
MMP10-F	AGTTTGGCTCATGCCTACCC
MMP10-R	GGCCCAGAACTCATTTCCTTT
GAPDH-F	ACCACAGTCCATGCCATCAC
GAPDH-R	TCCACCACCCTGTTGCTGTA

B, Primers for reverse transcription-semi-quantitative PCR

Primer	Sequence (5'-3')
MMP2-F	CAAGGACCGGTTCATTTGGC
MMP2-R	GGCCTCGTATACCGCATCAA
MMP3-F	GTCCCTCTATGGACCTCCCC
MMP3-R	AGGGATTTGCGCCAAAAGTG
MMP7-F	GTCTCTGGACGGCAGCTATG
MMP7-R	GATAGTCCTGAGCCTGTTCCC
MMP9-F	GATCATTCCTCAGTGCCGGA
MMP9-R	TTCAGGGCGAGGACCATAGA
MMP10-F	GACAGAAGATGCATCAGGCAC
MMP10-R	CATCTTGCGAAAGGCGGAAC
β-actin-F	CATCCTCACCCTGAAGTACCC
β-actin-R	AGCCTGGATAGCAACGTACATG'

F, forward; R, reverse; MMP, matrix metalloproteinase.