### Supplementary Table S1. Primers used in gene amplification

| Gene names | Primer sequence                  |
|------------|----------------------------------|
|            | Sense (5′→3′) | Anti-sense (5′→3′) |
| Mouse NCAM-180 | AGCCCTTTAGCAGCATGAGCGG | CTGCCTCAGGGTGTTTCTGAC |
| Mouse NCAM-140 | GCTGACAGAACCCGAAAGG | CCCATCATGCTTTGCTCTCAT |
| Mouse NCAM-120 | GGCACCCCCTATTCTACCTA | GCAAAGGCTTTGCTTTGAGC |
| Human NCAM  | TTGTTTTTCTCGGAACTGC | TAGCTTTGGCATCTCCTGAC |
| Mouse ST8SiaII | TCAGAATCAGAACCCCGCA | CGACAGTCAGTTTCTCAATGCC |
| Mouse ST8SiaIV | ACTGAAAGTGCGAACTGCCT | GAGAACCTGTGCTTTGAGC |
| Human ST8SiaII | TCAGAACCAAGAACCCAGTC | CGACAGTCAGTTTCTCAAGCC |
| Human ST8SiaIV | ACTGAAAGTGCGAACTGCCT | GAGAACCTGTGCTTTGAGC |
| Mouse c-Myc | AGAGCTCCTCGAGCATGTTT | ACCGAAGTCATGAGCTGAGT |
| Mouse Wnt3a | ACTACGTGGAGATCATGCC | GGTGCTTTGCTCCAGAAGAG |
| Mouse slug | ATCTGTGCGAGGCTTCTCTC | GATGTGCGCTCAGGTCTGAT |
| Mouse GSK-3β | GCAGCCCTCATGTTTGGTA | AACTGACTTTGCTGGGCTG |
| Mouse Fzd7 | CCAGCGGCATGGAACAATCA | CGAGGAGAGGGATGACAGG |
| Mouse cyclin D1 | AGACCTTTTGTGCGCCCTCT | GCAGGAGAGGGATGACAGG |
| Mouse CK1α | CATCCCAGTGTGTGACT | GTCCAGAGGATCATGTAG |
| Mouse axin2 | TATGCTTTGCGACGACCA | TGGATCTCTTCTGAGACTG |
| Mouse APC | GCCAGGCTTTTACAGCCGCC | GTTGGCTTTTCTGCACCTCC |
| Human β-actin | CTTCTGTGGGCGATGAGTC | GCGATACACAGGAGATA |
| Mouse γ-tubulin | ATCTACCTGTGAGCATGAC | GCCTCCCGATCTGATGAC |
Supplementary Table S2. NCAM levels in normal and malignant breast tissue samples

| Diagnosis         | LN(P) | LN | Stage          | D | NCAM (fd) |
|-------------------|-------|----|----------------|---|-----------|
| 1 N               | -     | -  | -              | - | 0.81±0.02 |
| 2 N               | -     | -  | -              | - | 1.13±0.10 |
| 3 N               | -     | -  | -              | - | 0.50±0.07 |
| 4 N               | -     | -  | -              | - | 1.00±0.00 |
| 5 IDC             | 28    | 33 | T2N3M0 IIIc    | U | 1.2±0.32  |
| 6 IDC             | 22    | 24 | T1N3M0 IIIc    | 2 | 5.6±0.05  |
| 7 IDC             | 16    | 16 | T2N3M0 IIIc    | 2.1| 13.00±0.21|
| 8 IDC             | 3     | 14 | T4N1M0 IIIb    | 6 | 3.98±0.14 |
| 9 IDC             | 2     | 25 | T4N1M0 IIIb    | 6.5| 2.45±0.06 |
| 10 IC             | U     | U  | T2N2M0 IIIa    | 3.4| 7.11±0.43 |
| 11 SMC            | 1     | 28 | T2N1M0 IIb     | 4 | 3.21±0.03 |
| 12 IDC            | 2     | 18 | T2N1M0 IIb     | 2.3| 1.51±0.02 |
| 13 ILC            | 3     | 22 | T2N1M0 IIb     | 2.5| 1.50±0.03 |
| 14 IDLC           | 0     | 23 | T2N0M0 IIa     | 2.5| 0.50±0.01 |
| 15 MC             | 0     | 19 | T2N0M0 IIa     | 2.3| 1.42±0.06 |
| 16 IDC-NS         | 1     | 25 | T1N1M0 IIa     | 2 | 5.00±0.11 |
| 17 IDLC           | 1     | 24 | T1N1M0 IIa     | 2 | 0.98±0.02 |
| 18 IDC            | 0     | 20 | T2N0M0 IIa     | 2.8| 0.81±0.03 |
| 19 IDC            | 0     | 12 | T1N0M0 I       | 1.6| 1.45±0.04 |
| 20 IDC            | 0     | U  | T1N0M0 I       | 1.2| 1.04±0.00 |
| 21 IDC            | 0     | U  | T1N0M0 I       | U | 1.92±0.01 |
| 22 IDC            | 0     | U  | T1N0M0 I       | U | 1.10±0.01 |
| 23 IDC            | 0     | U  | T1N0M0 I       | 1.5| 0.66±0.02 |
| 24 IDC            | 0     | U  | T1N0M0 I       | U | 0.74±0.05 |

LN(P), lymph node positivity; D, diameter (cm); fd, fold change; N, normal; IDC, infiltrating ductal carcinoma; IC, infiltrating carcinoma; SMC, squamous metaplastic carcinoma; ILC, infiltrating lobular carcinoma; IDLC, infiltrating ductal-lobular carcinoma; MC, mucinous carcinoma; IDC-NS, infiltrating ductal carcinoma with neural secretion; U, unknown. NCAM level was determined by quantitative RT-PCR and normalized relative to sample 4 (fold change) (see M&M). Values are shown as the mean±SEM.
Supplementary Table S3. Association of disease characteristics with NCAM gene expression in malignant BC patients

| Characteristics         | TNM Stage |   |   |   | Total |
|-------------------------|-----------|---|---|---|-------|
| No. of patients         | I         | II| III|   |       |
| Site:                   |           |   |   |   | 20    |
| Left                    | 6         | 8 | 6 |   | 20    |
| Right                   | 4         | 6 | 3 |   | 13    |
| Histology               |           |   |   |   | 13    |
| Invasive/Infil.         | 6         | 2 | 5 |   | 13    |
| Invasive/Infil.         | 0         | 1 | 0 |   | 1     |
| Invasive/Infil.         | 0         | 2 | 0 |   | 2     |
| Others                  | 0         | 3 | 1 |   | 4     |
| Lymph node involvement  |           |   |   |   |       |
| Absent                  | 6         | 3 | 0 |   | 9     |
| Present                 | 0         | 5 | 6 |   | 11    |
| Unknown                 | 0         | 0 | 0 |   | 0     |
| NCAM positive           | 1/6 (17%) | 4/8 (50%) | 5/6 (83%) | 10/20 (50%) |

fd=fold change;  fd>1.5=NCAM positive.
Supplementary Figure S1. Verification of EMT cell model and NCAM overexpressing cell lines
(A) Western blot analysis of EMT markers. Aliquots from control cells or TGF-β1 treated cells were
immunoblotted with specific antibodies. (B) Testing of NCAM overexpressing cell lines by flow
cytometric analysis using anti-NCAM antibody. (C) Morphological changes induced by NCAM.
Cells were cultured for 2 or 4 days and photos were taken. Magnification: 200×.
Supplementary Figure S2. Verification of polysialylated NCAM in transfected cell lines and cell adhesion assay  (a) Western blot analysis of ST8SiaII expression in transfected cells using β-tubulin as the loading control. (b) mRNA levels of ST8SiaII genes in transfected cell lines were assessed by RT-qPCR, with γ-tubulin as the control. ***P<0.001. (c) Cell adhesion to FN, LN, collagen IV, matrigel or BSA solution was determined as described in M&M, and phase-contrast images were taken. (d) Down-regulation of ST8SiaII by siRNA. Cultured NMuMG and transfected cells were transfected with siRNA-targeting mouse ST8SiaII or with negative control RNA (NC). Quantitative RT-PCR was performed for ST8SiaII. **P<0.01.