### Table S1

**Antibodies (Ab) applied for flow cytometry (FC), fluorescence microscopy (FM) and Western blotting (WB)**

| Primary Ab against | Clone | Epitope | Host/Clonality | Isotype | Conjugation | Specificity | Distributor | Application | Working conc. (µg/mL) | Incubation conditions | Terminology in manuscript |
|--------------------|-------|---------|----------------|---------|-------------|------------|-------------|-------------|----------------------|-----------------------|--------------------------|
| CD44               | MEM-85| n.d.    | Ms/m           | IgG2b   | APC or PE   | human      | Immunotools | FC, FM      | 1:5           | 45 min, 4 °C (FC) | CD44-APC                 |
| CD133              | AC133 | CD133/1 | Ms/m           | IgG1    | PE         | human      | Miltienny Biotec | FC          | 16.5          | 45 min, 4 °C | CD133-PE                |
| CD326              | HEA-125| n.d.    | Ms/m           | IgG1    | FITC       | human      | Miltienny Biotec | FC          | 1:20          | 45 min, 4 °C | CD326-FITC              |
| CD44v9             | RV3   | n.d.    | Rt/m           | IgG2a   | -          | human      | Abnova      | FC          | 10            | 1 h, 4 °C   | CD44v9                  |
| CD44pan            | EPR1013Y| aa153-171 of hCD44 | Rb/m | IgG | - | human | Abcam | WB | 1:1000 | O/N, 4°C | αCD44 (1)           |
| CD44pan²           | 156-3C11| constant part of hCD44 | Ms/m | IgG2a | - | human | Cell Signaling | WB | 1:1000 | O/N, 4°C | αCD44 (2)           |
| CD31               | MEC 13.3| n.d.    | Rt/m           | IgG2a   | -          | mouse      | G. Breier, TU Dresden | FM          | 1000          | 2 h, RT    | CD31                   |
| β-actin            | AC-15 | aa1-15  | Ms/m           | IgG1    | - various  | Abcam | WB | 3100 | O/N, 4 °C | β-Actin               |
| α-tubulin          | DM1A 426-450| n.d.    | Ms/m           | IgG1    | - various  | Millipore | WB | 1000 | O/N, 4 °C | α-Tub                 |
| MHCI+HLA B         | EP2624| n.d.    | Rb/m           | IgG     | -          | human      | Abcam | WB | 2000 | O/N, 4 °C | HLA-B                 |
| Pimonidazole       | n.d.  | n.d.    | Rb/p           | IgG     | -          | hpi        | FM | 200  | 2 h, RT   | pimonidazole          |

#### Isotype Ab

| Ab                | Clone | Epitope | Host/Clonality | Isotype | Conjugation | Specificity | Distributor | Application | Working conc. (µg/mL) | Incubation conditions | Terminology in manuscript |
|-------------------|-------|---------|----------------|---------|-------------|------------|-------------|-------------|----------------------|-----------------------|--------------------------|
| IgG1              | IS5-21F5| n.d.    | Ms/m           | IgG1    | FITC       | n.d.       | Miltienny Biotec | FC          | 1:100          | 45 min, 4 °C | Isotype                |
| IgG1              | IS5-21F5| n.d.    | Ms/m           | IgG1    | PE         | n.d.       | Miltienny Biotec | FC          | 22            | 45 min, 4 °C | Isotype                |
| IgG2b             | RTK2758| n.d.    | Rt/m           | IgG2a   | -          | n.d.       | Abcam | FC       | 10           | 45 min, 4 °C | Isotype                |
| IgG2b             | PLRV219| n.d.    | Ms/m           | IgG2b   | APC or PE  | n.d.       | Immunotools | FC          | 1:100         | 45 min, 4 °C (FC) | Isotype                |

#### Secondary Ab against

| Ab against | Host/Clonality | Isotype | Conjugation | Specificity | Distributor | Application | Working conc. (µg/mL) | Incubation conditions | Terminology in manuscript |
|------------|----------------|---------|-------------|------------|-------------|-------------|----------------------|-----------------------|--------------------------|
| Ms IgG     | n.d.           | n.d.    | Gt/p        | IgG        | A488 mouse | Invitrogen | FC                 | 10                  | 30 min, 4 °C             |
| Ms IgG     | n.d.           | n.d.    | Rb/p        | IgG        | HRP mouse  | Dako       | WB                 | 1300                | 1 h, RT                  |
| Rb IgG     | n.d.           | n.d.    | Sw/p        | IgG        | HRP rabbit | Dako       | WB                 | 340                 | 1 h, RT                  |
| Rt IgG     | n.d.           | n.d.    | Gt/p        | IgG        | A405 rat   | Abcam      | FC                 | 1:2000              | 30 min, 4 °C             |
| Rt IgG     | n.d.           | n.d.    | Gt/p        | IgG        | A488 rat   | Life Technologies | FM | 2000 | 2 h, RT |                 |
| Rt IgG     | n.d.           | n.d.    | Gt/p        | IgG        | A594 rat   | Life Technologies | FM | 2000 | 2 h, RT |                 |
Table S2

Primers used for the detection of CD44, its splice variants and the housekeeping genes ACTB (β-Actin) and B2M (β2-microglobulin); primers were designed for human specificity

| Target gene  | Primer sequence  | Number of cycles | Product size (bp) |
|--------------|------------------|------------------|-------------------|
| ACTB         | Forward - CACCCTGAA GTACCCCCATCG  
               Reverse - GCTGGGGGTGTTGAAGGCTCT | 20               | 199               |
| B2M          | Forward - AGGCTATCCAGCGTACTCCA  
               Reverse - TCAATGCGGATGGATGAAAA | 20               | 112               |
| CD133        | Forward - GGATTATTCTATGCTGTCTCTG  
               Reverse - TGCCACAAAAACCATAGAAGAT | -                | 215               |
| CTNNB1       | Forward - ATTTGATGGAGTTGGACATGGC  
               Reverse - TGAGTGAAGGACTGAGAAATCCC | -                | 211               |
| ESRP1        | Forward - ACAGAATGCGGTGAGGAAGC  
               Reverse - AGAGGGGCCGAGGAGAAT | -                | 120               |
| ESRP2        | Forward - AGGAGATGAGCCGAGTGCT  
               Reverse - GCTTGGAAAGGTTGGTAGGT | -                | 108               |
| MMP2         | Forward - GTGACGGAAAGATGGGTGT  
               Reverse - CCAAATGAAACCGGTCTTGGA | -                | 365               |
| MMP9         | Forward - GGCTTAGATCATCTCTCAGTG  
               Reverse - CTGGCGGTTGTTGGTTGGTG | -                | 365               |
| SNAI1        | Forward - GAAAGGCCTTCAAACTGCAAA  
               Reverse - TGACATCTGAGTTGGTCTGG | -                | 159               |
| SNAI2        | Forward - TCGGACCCACACATTACCTT  
               Reverse - TGAGCCCTCAGATTTGACCT | -                | 159               |
| TWIST1       | Forward - CTCGGTCTGAGGATGAGGAG  
               Reverse - CCACGCCCTGTGTTCTTGAA | -                | 228               |
| VIM          | Forward - CAGGCTCAGATTCAGGAACAG  
               Reverse - GGCGTCATTGTTCCGTTG | -                | 191               |
| ZEB1         | Forward - GGCCCCACACTCAACTACGG  
               Reverse - TGGGCGGTTGAGATCCAGTCC | -                | 155               |
| ZEB2         | Forward - AAGCCCCATCAACCCATACAAAG  
               Reverse - AAATTCCTGAGGAGGCACAGC | -                | 124               |
| CD44 total*  | A, Forward - GTGATCAACAGTGGAATGGG  
               B, Reverse - CCACATTCTGCGGTCTCTTT | 27               | 163               |
| CD44 isoforms | C, Forward - GAAAGGAGCAGCAGTCAGCTCAGG  
                    D, Reverse - TGGAATTTGGGTTGGTCCTTA | 30               | 1392              |
| CD44 v9exon  | C, Forward - GAAAGGAGCAGCAGCTTCAGG  
               E, Reverse - CAAGCCTTCATGATGCTAAG | 30               | 1009              |

*Note: This primer set detects all CD44 transcript variants except for Tr. variant 8 (RefSeq: NM_001202557.1)
Table S3

Fractions of CD133* and CD44* cells in exponentially growing CRC cell lines with fluorescence signals above isotype controls determined in 3 independent experiments as representatively shown in Figures 1 and S1.

The list is arranged according to an increasing CD133* cell fraction. The CD133 signal was selectively enhanced by a two-step FASER protocol (see Materials & Methods). CD24* cell fractions were also analyzed and are given for completeness.

| Cell line | Organ of origin | MSI/MSS status | CD133* ± SD (%) | CD44* ± SD (%) | CD133*/CD44* ± SD (%) | CD24* ± SD (%) | CD133*/ CD24* ± SD (%) |
|-----------|----------------|----------------|-----------------|----------------|------------------------|----------------|------------------------|
| RKO       | colon          | MSI            | 0.0 ± 0.0       | 99.9 ± 0.2     | 0.0 ± 0.1              | 0.0 ± 0.0      | 0.0 ± 0.0              |
| SW480     | colon          | MSS            | 0.2 ± 0.2 †     | 98.2 ± 2.7     | 0.6 ± 0.3              | 0.1 ± 0.2      | 0.2 ± 0.2              |
| SW837     | rectum         | MSS            | 0.3 ± 0.2       | 86.4 ± 4.7     | 0.8 ± 0.9              | 0.2 ± 0.1      | 0.2 ± 0.1              |
| HCT-8     | colon          | MSI            | 0.6 ± 0.5       | 88.9 ± 4.9     | 0.6 ± 0.4              | 0.8 ± 0.7      | 0.3 ± 0.2              |
| NCI-H716  | cecum          | MSS            | 0.6 ± 0.3       | 77.2 ± 6.6     | 0.7 ± 0.3              | 25.2 ± 2.5     | 0.7 ± 0.3              |
| LS180     | colon          | MSI            | 1.0 ± 0.3       | 99.7 ± 0.1     | 0.8 ± 0.2              | 10.8 ± 4.7     | 0.3 ± 0.1              |
| Colo-320 HSR | colon      | MSS            | 1.7 ± 1.1       | 94.0 ± 7.7     | 2.0 ± 1.2              | 0.9 ± 0.5      | 0.4 ± 0.5              |
| Colo-320 DM | colon         | MSS            | 3.1 ± 0.6       | 61.6 ± 9.4     | 1.5 ± 1.0              | 1.1 ± 0.9      | 0.0 ± 0.1              |
| SNU-C1    | colon          | MSS            | 3.1 ± 1.5       | 98.2 ± 0.9     | 3.3 ± 0.9              | 42.3 ± 13.8    | 4.7 ± 0.0              |
| LS1034    | cecum          | MSS            | 38.5 ± 10.9 †   | 0.2 ± 0.1      | 0.1 ± 0.2              | 87.6 ± 7.3     | 37.2 ± 11.6            |
| NCI-H630  | rectum         | MSI            | 46.5 ± 4.5      | 37.8 ± 11.6    | 13.0 ± 6.0             | 77.8 ± 8.8     | 36.6 ± 5.9             |
| SW403     | colon          | MSS            | 41.9 ± 4.7      | 97.0 ± 1.7     | 40.9 ± 4.5             | 0.3 ± 0.3      | 0.6 ± 0.1              |
| SW1417    | colon          | MSS            | 69.7 ± 9.1 †    | 92.4 ± 3.6     | 52.7 ± 4.8             | 63.3 ± 7.4     | 33.6 ± 10.0            |
| SW620     | colon          | MSS            | 73.5 ± 3.0 †    | 70.1 ± 1.5     | 51.2 ± 8.6             | 36.1 ± 6.6     | 26.9 ± 8.9             |
| HCT-116   | colon          | MSI            | 78.0 ± 4.4 †    | 99.4 ± 1.6     | 80.5 ± 3.6             | 0.2 ± 0.1      | 0.1 ± 0.1              |
| Colo-201  | colon          | MSS            | 89.2 ± 7.9      | 58.7 ± 14.0    | 58.8 ± 13.9            | 75.2 ± 16.6    | 72.5 ± 24.6            |
| CaCo2     | colon          | MSS            | 94.9 ± 1.3      | 57.5 ± 3.5     | 59.9 ± 16.6            | 5.9 ± 3.7      | 4.6 ± 0.7              |
| HT29      | colon          | MSS            | 97.3 ± 1.3 †    | 99.8 ± 0.2     | 96.5 ± 1.6             | 77.0 ± 7.5     | 82.1 ± 6.5             |
| LS513     | cecum          | MSS            | 96.0 ± 0.7      | 94.0 ± 1.4     | 89.9 ± 1.0             | 8.7 ± 3.6      | 3.2 ± 2.3              |
| LS411N    | cecum          | MSS            | 98.9 ± 0.2      | 99.0 ± 0.3     | 98.1 ± 0.8             | 83.7 ± 4.5     | 82.0 ± 7.2             |

* Note: Membrane-defect (PI-positive) cells were excluded in the analysis and polynomial gates were applied to best distinguish marker-positive from putatively negative cells. However, it is important to emphasize that all cell fractions are defined relative to cells stained with an isotype control antibody and neither necessarily nor always represent distinct subpopulations as often stated in the literature. For example, only 39% ± 11% of the LS1034 cells express a CD133* fluorescence signal higher than the isotype control; however, the fluorescence distribution of the entire population is shifted to the right (see Fig. S1) indicating that - based on flow cytometry best practice - there is only one population, and in principle all LS1034 cells might be slightly positive for CD133. This is invisible without (multiple) FASER amplification steps.

† The CD133 (but not CD44) data have been published earlier in Peickert et al. [33]

‡ CD133 subpopulations resemble previous measurements in the respective cell line using the advanced CD133 staining protocol [23,33]
Table S4

Significance levels (p values) for differences in the engraftment (tumor take rates, TTR) of cell lines (A) and cell line subpopulations defined by their CD44/CD133 surface expression profiles (B-D)

Statistical significance was evaluated by a bootstrapping approach as detailed in the Materials and Methods section; *control = run-through sorter original cells (processed according to the respective subpopulations)

(A) Comparison of cell line-specific TTR after injection of 10-10,000 in vitro grown cells (data documented in Figure 1B)

| Cell line 1 | Cell line 2 | p     |
|-------------|-------------|-------|
| SW480       | SW620       | <0.01 |
| SW480       | LS1034      | n.s.  |
| SW620       | LS1034      | <0.001|

(B) Comparison of TTR after injection of 10-100 in vitro grown SW620 cells sorted according to their CD133/CD44 surface expression pattern (data documented in Figure 2B)

| Subpopulation 1 vs. | Subpopulation 2 | p     |
|---------------------|-----------------|-------|
| CD133+/CD44-        | CD133+/CD44+    | n.s.  |
| CD133-/CD44-        | CD133+/CD44-    | n.s.  |
| CD133+/CD44-        | CD133+/CD44+    | n.s.  |
| CD133-/CD44-        | CD133+/CD44+    | n.s.  |
| CD133+/CD44-        | CD133+/CD44-    | n.s.  |
| Control*            | any CD133/CD44-defined subpopulation | n.s.  |

(C) Comparison of TTR after injection of 10-100 in vitro grown (CD44-negative) LS1034 cells sorted according to their CD133 surface expression (data documented in Figure 3B)

| Subpopulation 1 | Subpopulation 2 | p     |
|-----------------|-----------------|-------|
| CD133           | CD133+          | n.s.  |
| Control*        | CD133-          | 0.057 (trend) |
| Control*        | CD133+          | n.s.  |

(D) Comparison of TTR after injection of 500-10,000 LS1034 cells derived from xenografts and sorted according to their CD133/CD44 surface expression pattern (data documented in Figure 4B)

| Subpopulation 1 vs. | Subpopulation 2 | p     |
|---------------------|-----------------|-------|
| CD133+/CD44-        | CD133+/CD44-    | <0.02 |
| CD133-/CD44-        | CD133+/CD44+    | <0.001|
| CD133+/CD44-        | CD133+/CD44+    | <0.01 |
| Control*            | CD133-/CD44-    | <0.01 |
| Control*            | CD133+/CD44+    | n.s.  |
| Control*            | CD133+/CD44-    | <0.01 |
Figure S1 A

Representative flow cytometric dot blot diagrams and histograms showing the CD133 and CD44 surface pattern in various exponentially growing CRC cell lines kept under identical 2-D in vitro conditions. Cell lines are listed in alphabetical order; immunofluorescence stainings were performed with the antibodies and conditions given in Table S1. Notably, the CD133 (AC133) fluorescence signal was enhanced by a two step FASER series as detailed earlier [23,33].
Stain index \(= \frac{\text{median FL}_{\text{stained sample}} - \text{median FL}_{\text{isotype}}}{2 \times \text{SD of FL}_{\text{isotype}}} \)

FL - fluorescence signal
SD - standard deviation

Figure S1 B

Stain index (SI) for CD133 and CD44 fluorescence signals in cell line subpopulations that could be clearly distinguished in the dot blot diagrams as representatively shown in (A). The graphs document average values +SD from N\(\geq 3\) independent experiments. On the left, results are illustrated for cell lines alphabetically ordered according to Figure S1A; the right graphs display the data ordered by (i) an increasing SI which quantitatively reflects biomarker surface expression and (ii) the presence of one or two distinct populations.

Note: Populations can be categorized as follows: SI<1 = equivalent to the marker-negative isotype controls, SI>1 to 2 = marginal; SI>2 to 5 = low, SI>5 to 20 = intermediate, SI>20 to 100 = high, and SI>100 = exceptionally high marker expression.
**Figure S2 A/B**

SW620 cell populations with distinct CD133/CD44 surface pattern in vitro do not differ in growth kinetics or cell morphology but differentially re-adapt their surface expression profile in culture.

**A** Growth behavior and modifications in mean cell diameter of SW620 subpopulations cultured up to 18 days after FACS sorting; one experiment with intraexperimental variation is documented (N=1, n=3).

**B** Fractions of cells with CD133⁺, CD44⁺ and CD133⁻/CD44⁻ surface expression in cultures grown from the respective FACS sorted SW620 subpopulations; average values ± SD from three independent experiments are shown (N=3; n=1-2).
Figure S2 C

Representative flow cytometric CD133/CD44 dot blot diagrams from one experimental series included in the analyses shown in Figure S2B.
Figure S3

Flow cytometric dot blot diagrams showing the CD133/CD44 surface pattern in SW480 cell suspensions prepared from three individual xenografts. The samples were pre-gated to exclude non-human and membrane-defect (PI-positive) cells. Aliquots exposed to isotype control antibodies required for analyses of cell fractions are documented in the upper row. For comparison with (i) CD133/CD44 expression in SW480 monolayer culture (cf. Figure 1) and (ii) CD133/CD44 profile in SW620 xenograft cells (cf. Figure 2). Notably, in all SW480 xenograft preparations a minor proportion (0.1-1%) of cells stained with the isotype antibody shows FC signals beyond the major isotype gate limiting the sensitivity of quantitation.
Figure S4 A/B

Median frozen sections (10 µm) of two additional LS1034 xenografts co-stained for CD44, CD31 (endothelial cells), pimonidazole (hypoxia) and DAPI (nuclei) and imaged with a magnification of 200x support the finding highlighted in Figure 5 in spite of histomorphological heterogeneity and staining variations. Whole tumor sections (stitched from >1,000 single images - top) as well as selected regions at higher magnification (bottom) are displayed as four-channel overlay; bars represent 1,000 µm in whole tumor sections and 100 µm in all other images.
Median section of 1ˢᵗ generation LS1034 xenograft (#3)

Figure S4 A/B (continued)

Representative parts of sections stained with isotype antibodies and DAPI are shown as controls (multi-channel).
In (A), single fluorescence channel images of the magnified region are also depicted (right).
**Figure S5**

Heterologous CD44 protein expression in CRC cell lines as detected by Western blotting (WB); 40 µg (A) and 25 µg (C) of total protein was loaded per lane. No WB bands were detected with any of the antibodies and illumination times for LS1034 cells grown under diverse conditions (negative blots not shown). Flow cytometric analyses (FC) reveal CD44 surface presentation on SW620 cells.

(A) Representative WB of CD44 pattern in whole cell protein extracts of various CRC cell lines as detected with the pan-αCD44(1) antibody (Ab); *two independently prepared protein lysates of SW620 monolayer cells (L1, L2) were loaded on this specific SDS-PAGE.

(B) CD44 surface presentation in SW620 monolayer cells as detected by FC (cf. Figures 1, 2 and S1) is confirmed with a second pan-αCD44 (αCD44(2)).

(C) Representative WBs showing the main CD44 protein band at ~100-110 kDa via two different pan-αCD44 Abs (αCD44(1) and αCD44(2)) in SW480 and SW620 cells grown for 24-144 h in DMEM or stem cell medium (SC2) with and without serum.
### Figure S6 A-C

**A** Overview of human CD44 transcript variants 1-8 with their constant and variable exons. Notably, our PCR design and primers (cf. Figure 5C-F) allowed to detect all variants except for Tr. variant 8 while the sequencing could not discriminate Tr. variants 4 and 8. The product of Tr. variant 4 is CD44s which is likely to be expressed in CRC cells; Tr. variant 8 supposedly translates into a more rare short-tail or tail-less CD44 isoform (CD44st) as exon 18 contains a stop codon that originates a truncated cytoplasmic tail, consequently leading to the loss of intracellular protein domains and signaling motifs necessary for the interaction with cytoskeletal components [46]; function and relevance of this isoform are unclear and thus not further discussed.

(B/C) CD44 product sequence chromatograms and sequences, respectively, for PCR products obtained with primer pairs C/D (645 bp and 249 bp) and C/E (262 bp) according to Figure 5E/F (see next 3 pages)

*monoallelic mutation in exon v8 (c.689T>C [p.Ile230Thr] identified in the 645 bp (primer pair C/D) and the 262 bp (primer pair C/E) sequence products according to CD44 transcript mRNA isoform 3 (RefSeq: NM_001001390.1)*
Sequence of CD44 645 bp PCR product from sequencing experiments
(RefSeq: NM_001001390.1; BLAST Alignment 987..1631 bp)

GAAAGGAGCAGCAGCTTCAAGGAGGTTACATCTTTTACACCTTTTCTACTGTACACCCCA
TCCCCAGACGAAGACAGTCCCTGGATCACCAGACAGACAGACAGAAATCCCTCTGCTACC
AATATGCCACTCCAGCTCATAGTANAAACGGTTCTCAGCCTACTGCAATCCAAACACAGGTT
TGGTGGAAGATTGGACAGGACAGGACCTCCTTCTCAATGACAAAGCGACAGGTATT
CTCAGAGCTTCTCTACATCATGAAGGCTTGGAAGAAGATAAAGACCATCCAACAC
TTCTACTTGTACATCAAGCAATAGGAATGATGTCACAGGGTAGGAAGAGGACCAAAAT
CATTCTGAAGGCTCAACTCTTTACTGGAAGGTTACCTCTCTCTACATTCCCACACAGGA
AGGAACAGCAAGACCTTCCACCTCAGTGAACCTCAGCTAAGACTGGGTCTTGTGAGTTA
CTGCAATTTACTGTGGGAGATTCACAATCTAATGTCAATCGTTCCTTTACAGGAGACCA
AGACACATTCCACCCAGTGGGGGTCCCATACACCACCTCATGGATCTGAATGGC
ACACTCACATTGGAGTCAAGAAGGAGTGAGCAGAAACACCAACCTCTGAGTCCTATAGGAC
ACCCCAAATTCCA
B continued

*CD44* 249 bp product sequence chromatogram: reading with forward primer C

*CD44* 249 bp product sequence chromatogram: reading with reverse primer D

Sequence of *CD44* 249 bp PCR product from sequencing experiments (RefSeq: NM_001001391.1 and NM_001202557.1; BLAST Alignment 987..1235 bp)

```
GAAAGGAGCAAGCACAATTTCAGGAGTTACATCTTTTTACACCTTTTCTACTGTACACCCCA
TCCAGACGAAGAGCCGTCCTGGATCAGGCACAGCAGACAGACAGATCCCTGCTACC
AGAACCAAAGAGACATTCACCCACCAGTGAGGAGGTCCTACCCATGCACTATGGATCTGAA
TCAGATGGACACTCAGGAGCTCAAGAAGGTGGAGCAAACACAACCTCTGGTCC
TATAAGGACACCCCCAAATTCCA
```
CD44 262 bp product sequence chromatogram: reading with forward primer C

CD44 262 bp product sequence chromatogram: reading with reverse primer E

Sequence of CD44 262 bp PCR product from sequencing experiments (RefSeq: NM_001001390.1; BLAST Alignment 987..1248 bp)

GAAAGGAGCAGCAGTTCAGGAGTTACATCTTTTATACCTTTTCTACTGTACACCCCA TCCAGAGAAGAGCATCCCTGGATCACCAGACAGCAGGAGAGGACAATTCCCTGCTACC AATATGGACTTTAGATAGTAGAAGTACGCTTTACCTACTGCAAATCCAAACAGGTT TGGTGGAGAATTTGGACAGCAGGACAGGACCTTTTCAATGACAACGCAGCAGAGTAATT CTCAGAGCTTTCTCTACATCATGAAGGCTTGG
Figure S7

Schematic representation of inverse transcript expression of CD44 tv4 (st) and CD44 tv3 (v8-10) in primary normal colon epithelium and colon adenocarcinoma tissue based on the TCGA (n=308) and GTEX (n=331) databases.

(A) Visualization of the CD44 tv3 and CD44 tv4 transcript structures and density plots showing the expression range in the tissues of interest.

(B) Heatmap of CD44 tv3 and CD44 tv4 transcript-specific expression (% of isoform) in colon adenocarcinoma and primary normal colon epithelium.