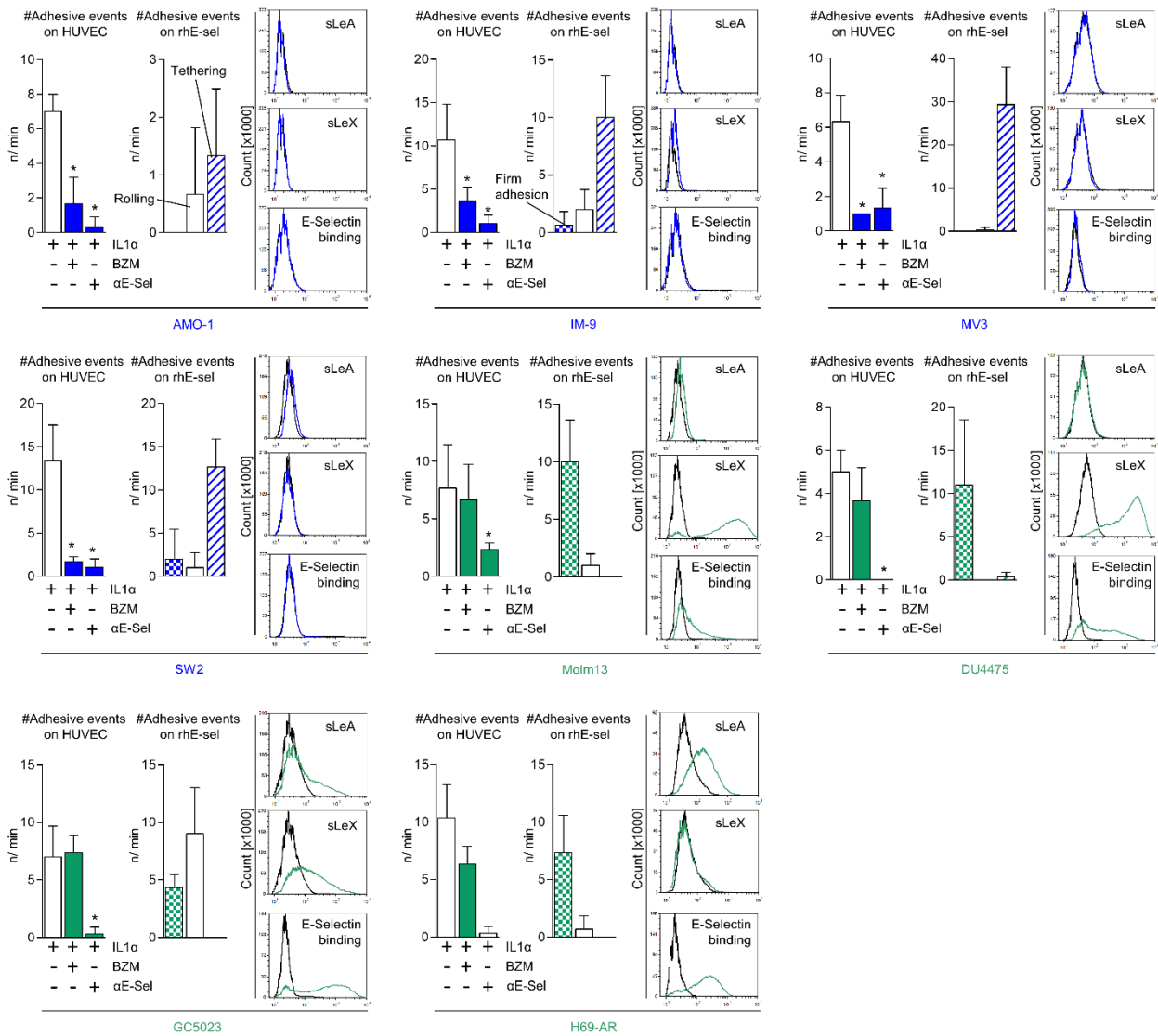


## **Supplemental Information**

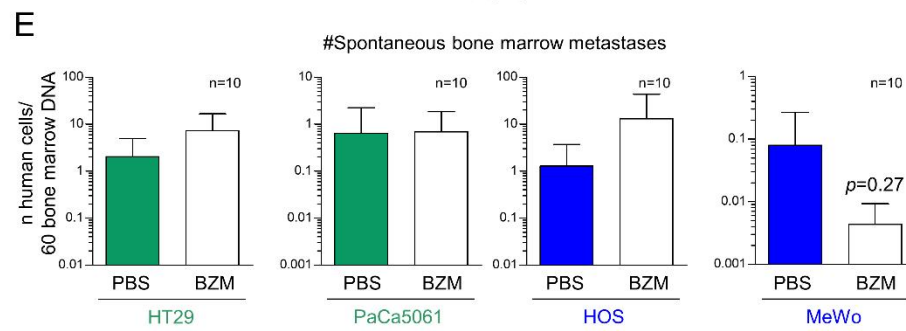
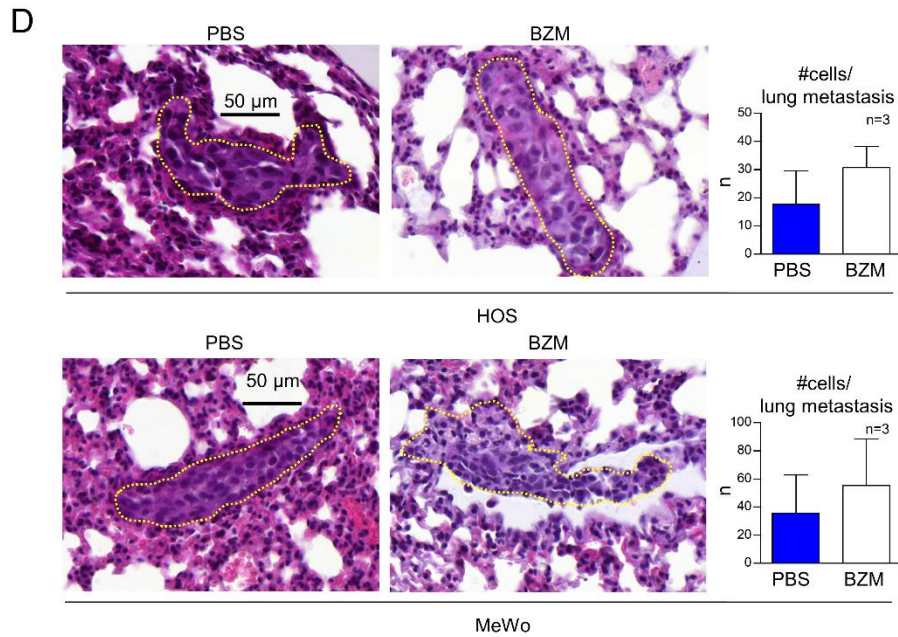
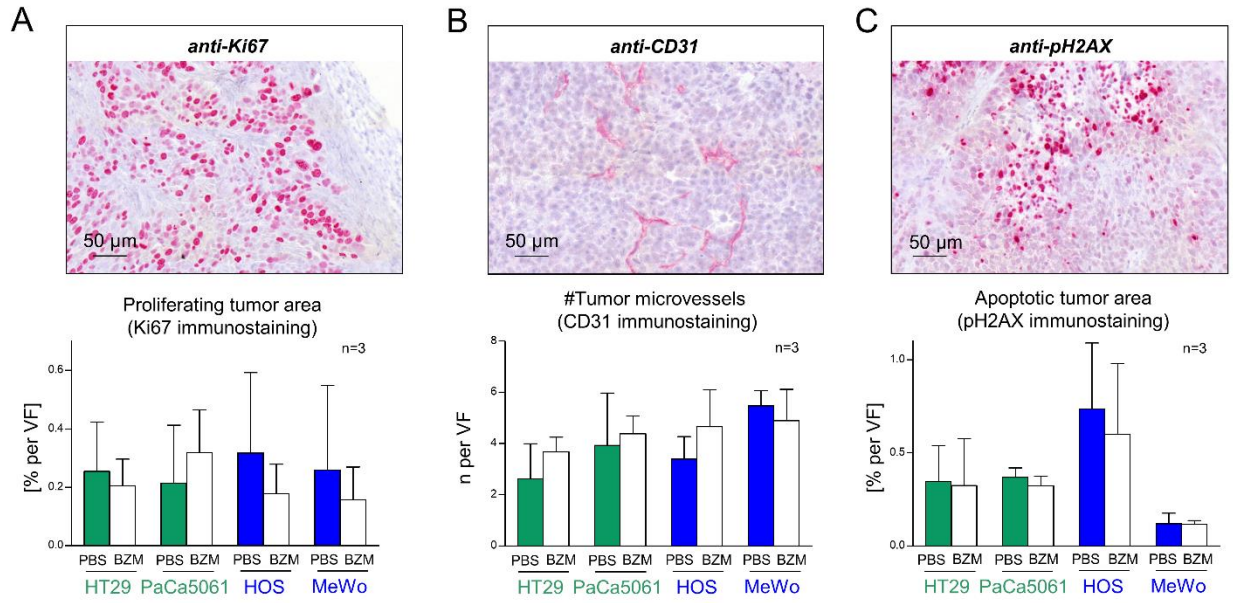
### **Tumor cell E-selectin ligands determine partial efficacy of bortezomib on spontaneous lung metastasis formation of solid human tumors *in vivo***

**Tobias Lange, Ursula Valentiner, Daniel Wicklein, Hanna Maar, Vera Labitzky, Ann-Kristin Ahlers, Sarah Starzonek, Sandra Genduso, Lisa Staffeldt, Carolin Pahlow, Anna-Maria Dück, Christine Stürken, Anke Baranowsky, Alexander T. Bauer, Etmar Bulk, Albrecht Schwab, Kristoffer Riecken, Christian Börnchen, Rainer Kiefmann, Valsamma Abraham, Horace M. DeLisser, Timo Gemoll, Jens K. Habermann, Andreas Block, Klaus Pantel, and Udo Schumacher**

# 1 Supplemental Figures and Legends



2  
3 **Figure S1: Verification of the relationship between adhesive properties of the tumor cells**  
4 **and anti-adhesive efficacy of BZM by further human tumor cell lines.** Numbers of adhesive  
5 events of indicated tumor cells under flow conditions on ECs treated +/-IL-1α +/-BZM +/-E-  
6 selectin-blocking antibody as well as on immobilized rhE-selectin. Representative histograms of  
7 tumor cell surface sLeA/X expression and static E-selectin binding capacity. Bar charts represent  
8 mean ± SD of three replicates; black lines in histograms represent isotype controls (sLeA, sLeX)  
9 or binding of IgG1-Fc (rhE-selectin binding); \* $p < 0.05$ .



11 **Figure S2: Exclusion of potential ‘off-target’ effects of BZM.** Immunostaining-based  
12 quantification of Ki67-positive xenograft primary tumor cells (A), CD31-positive xenograft  
13 primary tumor microvessels (B) and p2H2AX-positive xenograft primar tumor cells in the  
14 indicated xenograft models and treatment groups (C). Number of cells per lung metastasis in PBS  
15 vs. BZM-treated mice carrying the annotated s.c. xenografts (D). Number of spontaneous bone  
16 marrow metastases in PBS vs. BZM-treated mice bearing the indicated s.c. xenografts (E). Bone  
17 marrow endothelium is known to constitutively express E-selectin <sup>17</sup>. Bar charts in (A-C) represent  
18 mean  $\pm$  SD from n=3, each containing up to 27 viewing fields per tumor. Bar charts in (D) represent  
19 mean  $\pm$  SD of n=3. Bar charts in (E) represent mean  $\pm$  SD of n=10.

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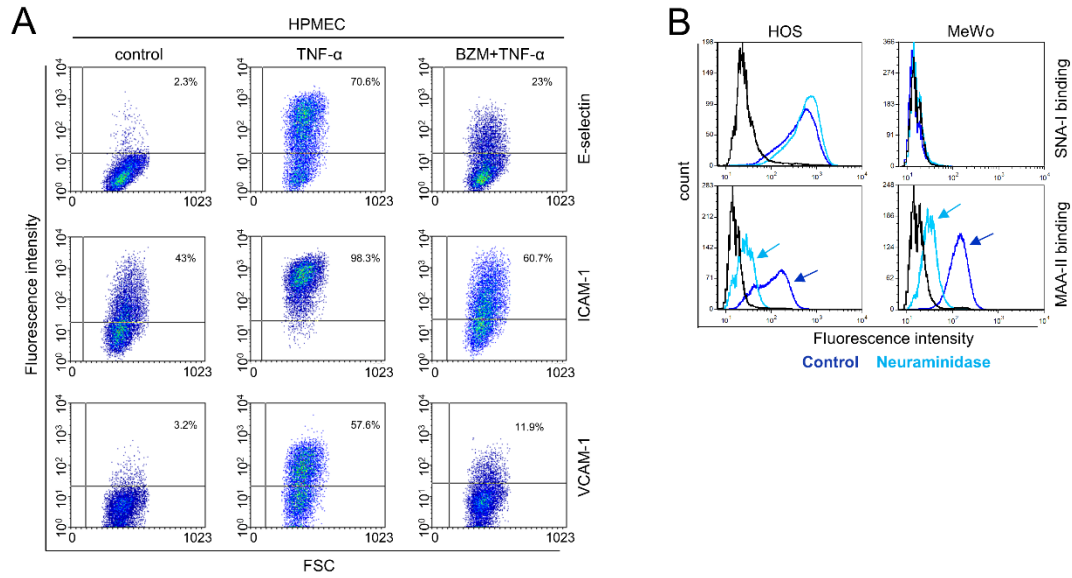
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32 **Figure S3: BZM effects on cytokine-mediated induction of CAMs in HPMEC and detection**

33 **of  $\alpha$ -2,3- and  $\alpha$ -2,6-sialic acid on sLeA/X-negative tumor cells. Flow cytometric analyses of E-**

34 **selectin, ICAM-1 and VCAM-1 after TNF- $\alpha$  stimulation and pre-incubation with BZM in HPMEC**

35 **(A). MAA-II and SNA-I lectin binding towards HOS and MeWo cells before (dark blue) and after**

36 **(light blue) neuraminidase treatment as indicated (B).**

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48 groups (PBS vs. BZM), only single cells could be found in the lungs (visualized by anti-NCAM  
49 immunostaining) (A). Other than SKOV3 (Fig. 6D), HOS, MeWo and SW2 xenografts fail to  
50 upregulate sLeA or sLeX *in vivo* (B). Detection of differential sLeA levels in primary patient  
51 material of colon and ovarian cancer by IHC (B).

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**Table S1:** qPCR profiler array human glycosylation/ glucosidase genes, see Fig. 4E.

Gene symbol	2 <sup>-</sup> ΔCt			Fold Regulation	
	HT29	HOS	MeWo	HOS vs. HT29	MeWo vs. HT29
A4GNT	2.2E-04	5.4E-05	5.8E-04	-4.04	2.65
AGA	1.5E-02	3.7E-03	2.0E-02	-3.95	1.34
B3GALTL	2.5E-02	9.1E-03	2.8E-02	-2.68	1.13
B3GNT2	8.1E-02	2.5E-02	7.5E-02	-3.28	-1.08
B3GNT3	4.3E-02	1.7E-03	2.4E-03	-24.84	-17.9
B3GNT4	7.1E-04	6.3E-04	1.1E-03	-1.11	1.55
B3GNT8	5.7E-04	2.7E-04	1.5E-03	-2.09	2.58
B4GALT1	1.6E-01	3.2E-02	1.0E-01	-5.08	-1.6
B4GALT2	6.5E-02	4.2E-02	1.1E-01	-1.56	1.62
B4GALT3	5.8E-02	2.6E-02	6.1E-02	-2.19	1.05
B4GALT5	7.8E-02	5.3E-02	1.5E-01	-1.47	1.91
C1GALT1	1.2E-01	4.5E-02	9.7E-02	-2.66	-1.24
C1GALT1C1	5.2E-02	4.1E-02	4.9E-02	-1.27	-1.05
EDEM1	2.3E-02	5.7E-02	1.1E-01	2.45	4.91
EDEM2	2.5E-02	1.9E-02	3.4E-02	-1.29	1.39
EDEM3	4.7E-02	3.4E-02	3.4E-02	-1.38	-1.38
FUCA1	5.3E-02	3.9E-03	1.6E-02	-13.68	-3.27
FUCA2	9.8E-02	9.5E-02	2.9E-01	-1.02	2.98
FUT11	2.4E-02	2.1E-02	7.9E-02	-1.12	3.26
FUT8	4.5E-03	1.6E-01	3.9E-02	34.89	8.67
GALNT1	2.3E-02	8.2E-02	1.6E-01	3.56	6.9
GALNT10	7.8E-03	4.8E-02	7.9E-03	6.12	1.01
GALNT11	1.5E-02	5.9E-03	5.4E-02	-2.59	3.52
GALNT12	1.1E-01	2.6E-03	7.7E-03	-41.49	-14.24
GALNT13	5.7E-05	2.9E-05	4.1E-05	-1.99	-1.38
GALNT14	5.5E-02	1.6E-02	3.7E-05	-3.42	-1491.45
GALNT2	2.4E-02	3.7E-02	2.2E-01	1.51	9.11
GALNT3	1.8E-01	2.1E-05	1.4E-01	-8569.52	-1.26
GALNT4	1.5E-02	6.0E-03	6.9E-03	-2.52	-2.19
GALNT6	1.4E-03	1.1E-02	4.0E-04	7.33	-3.56
GALNT7	4.6E-02	3.3E-02	2.2E-02	-1.38	-2.05
GALNT8	2.0E-04	1.6E-05	3.7E-05	-12.25	-5.43
GALNT9	1.8E-04	1.4E-04	5.6E-04	-1.31	3.15
GALNTL1	1.1E-04	3.7E-03	1.3E-04	34.41	1.15
GALNTL5	4.9E-05	1.9E-05	8.3E-05	-2.54	1.7
GALNTL6	2.1E-05	1.6E-05	6.9E-05	-1.3	3.22
GANAB	5.0E-01	4.3E-01	6.5E-01	-1.16	1.29
GCNT1	1.2E-03	1.5E-03	3.4E-03	1.21	2.72
C2GNT2	9.2E-01	1.7E-04	1.1E-03	-5499.17	-856.61
GCNT4	2.9E-04	6.3E-04	3.9E-04	2.16	1.32
GLB1	6.8E-02	5.2E-02	5.5E-02	-1.3	-1.24



GNPTAB	2.3E-02	1.2E-02	2.4E-01	-1.87	10.46
GNPTG	3.3E-02	1.7E-02	8.8E-02	-1.91	2.68
HEXA	7.7E-03	1.1E-02	1.3E-01	1.46	16.53
HEXB	1.3E-01	6.5E-02	3.1E-01	-1.91	2.47
MAN1A1	5.9E-02	4.1E-02	6.8E-04	-1.45	-86.97
MAN1A2	3.3E-02	1.1E-02	4.6E-02	-3.06	1.42
MAN1B1	6.2E-02	2.9E-02	8.4E-02	-2.15	1.35
MAN1C1	1.6E-04	2.3E-03	7.4E-04	14.57	4.68
MAN2A1	4.2E-02	1.9E-02	3.6E-02	-2.19	-1.16
MAN2A2	2.4E-02	4.3E-03	4.6E-02	-5.59	1.91
MAN2B1	1.6E-02	2.1E-02	1.7E-02	1.3	1.09
MANBA	1.9E-02	5.0E-03	2.3E-02	-3.71	1.24
MGAT1	2.8E-02	1.5E-02	7.9E-02	-1.83	2.86
MGAT2	6.8E-03	2.2E-02	1.6E-02	3.17	2.34
MGAT3	3.7E-03	1.2E-04	3.7E-05	-29.54	-98.53
MGAT4A	3.6E-03	1.5E-04	1.3E-02	-23.34	3.54
MGAT4B	1.8E-01	5.7E-02	1.1E-01	-3.08	-1.66
MGAT4C	2.1E-05	1.6E-05	3.7E-05	-1.3	1.72
MGAT5	9.0E-02	2.2E-02	7.4E-02	-4.09	-1.21
MGAT5B	1.6E-04	1.0E-02	1.0E-01	63.77	638.03
MOGS	4.6E-02	3.0E-02	6.3E-02	-1.54	1.36
NAGPA	1.4E-03	1.3E-03	3.2E-03	-1.08	2.21
NEU1	9.2E-02	4.1E-02	1.7E-01	-2.27	1.83
NEU2	4.1E-04	1.2E-04	7.9E-04	-3.37	1.94
NEU3	9.8E-03	6.6E-03	6.8E-02	-1.47	6.95
NEU4	2.5E-04	8.9E-05	2.4E-04	-2.83	-1.03
OGT	7.9E-02	4.7E-02	4.9E-02	-1.67	-1.6
POFUT1	3.6E-02	3.0E-02	2.0E-02	-1.19	-1.8
POFUT2	2.6E-02	1.8E-02	1.0E-02	-1.42	-2.64
POMGNT1	5.0E-02	3.9E-02	7.8E-02	-1.27	1.56
POMT1	8.2E-04	6.5E-04	2.7E-02	-1.25	32.84
POMT2	1.0E-02	2.2E-02	5.1E-02	2.16	5.16
PRKCSH	2.0E-01	1.8E-01	3.0E-01	-1.09	1.54
ST3GAL1	2.0E-01	9.9E-03	1.1E-02	-20.46	-17.78
ST3GAL2	4.7E-02	2.0E-02	4.3E-02	-2.35	-1.1
ST6GAL1	9.5E-03	1.9E-02	1.2E-03	2.02	-8.06
ST6GALNAC1	2.2E-03	1.6E-05	6.1E-05	-132.05	-35.81
ST8SIA2	2.2E-05	2.4E-05	8.8E-05	1.11	4.04
ST8SIA3	9.2E-05	1.2E-04	6.2E-05	1.27	-1.48
ST8SIA4	2.1E-05	6.2E-04	7.6E-03	28.94	353.97
ST8SIA6	2.1E-05	3.2E-05	2.3E-03	1.48	105.96
UGCGL1	5.3E-02	6.2E-02	1.2E-01	1.16	2.32
UGCGL2	3.1E-02	1.1E-02	2.6E-02	-2.79	-1.17

## 69 **Supplemental Methods**

### 70 *Human tumor cell lines*

71 HT29 human colorectal cancer cells and DU4475 human breast cancer cells were purchased from  
72 ECACC (Porton Down, UK). HOS osteosarcoma<sup>1</sup> as well as MeWo and MV3 melanoma<sup>2</sup> cells  
73 were kindly provided by the Dept. of Pediatric Hematology and Oncology (University Medical  
74 Center Hamburg-Eppendorf, UKE) and the Dept. of Dermatology at UKE, respectively. The  
75 human pancreatic cancer cell line PaCa5061<sup>3</sup> and gastric cancer cell line GC5023<sup>4</sup> were  
76 established in the Dept. of General, Visceral and Thoracic Surgery at UKE. The human small cell  
77 lung cancer cell lines SW2 and H69-AR were kind gifts from Prof. Zangemeister-Wittke (Institute  
78 of Pharmacology, University of Bern, Switzerland). The human multiple myeloma cell lines  
79 AMO-1 and IM-9 were kindly provided by Prof. M. Binder (Dept. of Oncology and Hematology,  
80 UKE). The human acute myeloid leukemia cell line Molm13 was provided by Dr. J. Wellbrock  
81 (Dept. of Oncology and Hematology, UKE). Human SKOV3 ovarian cancer cells were obtained  
82 from ATCC (Manassas, USA) and cultured in McCoy's 5A + L-glutamine supplemented with  
83 10% FCS and 1% penicillin/ streptomycin (Gibco). All other human tumor cell lines were cultured  
84 in RPMI-1640 + L-glutamine (Gibco), supplemented with 10% FCS and 1% penicillin/  
85 streptomycin and were kept under standard conditions (37°C, 95% H<sub>2</sub>O-saturated atmosphere, 5%  
86 CO<sub>2</sub>).

87

### 88 *Human primary tumor models*

89 The primary human colon cancer model PT457 was derived from a primary adenocarcinoma of  
90 the colon which was surgically resected from a male Caucasian in 2014. The PT1003 model was

91 established from a surgically resected, chemo-naïve liver metastasis of a colon sigmoideum  
92 adenocarcinoma from a 73 years-old male Caucasian. For spheroid culture, the protocol published  
93 by Jeppesen et al. was used.<sup>5</sup> Slight modifications of this protocol were the use of a 100 µm mesh  
94 size cell strainer for preparation and the use of Matrigel-coated 24-well plates for subsequent  
95 cultivation. Tumoroids were growing in 30-50µm domes surrounded by 1 mL stem cell medium.  
96 The use of patient material for research purposes was approved by the local ethics committee  
97 (Ärztchamber Hamburg, project PV4753, Sept 2<sup>nd</sup>, 2014).

98

#### 99 *Primary endothelial cells*

100 Human umbilical vein endothelial cells (HUVEC) and human pulmonary microvascular  
101 endothelial cells (HPMEC) were obtained from PromoCell and cultured as described.<sup>6,7</sup> Murine  
102 pulmonary endothelial cells (MPEC) were freshly isolated as illustrated in Fig. 2D and previously  
103 described.<sup>8</sup> All experiments with primary cells were performed within the first six passages.

104

#### 105 *qRT-PCR for pulmonary *Sele*, *Vcam1* and *Icam1* expression*

106 To analyze effects of the BZM treatment on pulmonary *Sele*, *Vcam1* and *Icam1* expression,  
107 xenograft tumor-bearing mice treated with PBS or BZM were sacrificed, lungs were resected and  
108 total RNA was extracted using a standard phenol/chloroform protocol and transcribed to cDNA  
109 using the cDNA RT<sup>2</sup> Easy First Strand Synthesis Kit (Qiagen). cDNA was used for qRT-PCR in  
110 a StepOnePlus system (Applied Biosystems, Thermo Fisher). *Gapdh* was used as housekeeping  
111 control. Nucleotide sequences of SYBR® Green primers were as follows:

112 *Sele*-fwd GGCTTTAGCTTGCATGGCTC, *Sele*-rev CATCTTTCCCGGGACGTCAA;  
113 *Icam1*-fwd CCATCCATCCCAGAGAAGCC, *Icam1*-rev CACTGAGTCTCCAAGCCCAG;  
114 *Vcam1*-fwd GTCACGGTCAAGTGTTTGGC, *Vcam1*-rev TGTTTCATGAGCTGGTCACCC.

115

#### 116 *Ex vivo lung perfusion model*

117 SCID mice were left untreated (control) or treated with 1  $\mu$ g rmTNF $\alpha$  i.p. (Peprotech) for 4h.  
118 TNF $\alpha$ -treated mice were pretreated with PBS (solvent control) or 1.25 mg/kg BZM 24h and 1h  
119 before TNF $\alpha$  injection. 4h after TNF $\alpha$  injection, mice were narcotized and the cardiorespiratory  
120 system was resected and extracorporeally perfused as described<sup>9</sup> and illustrated in Fig. 2E. In short,  
121 12 weeks old mice were narcotized and a cannula was placed into the trachea, by which the lungs  
122 were held under static inflation with a gas mixture of 30 % O<sub>2</sub>, 5% CO<sub>2</sub> and 65 % N<sub>2</sub>. Hence,  
123 normoxic conditions were maintained during the experiment, but ventilatory lung excursions were  
124 concomitantly avoided. Afterwards, the Vv. cavae were ligated, cannulae were inserted into the  
125 pulmonary artery and the left atrium, and the cardiorespiratory system was resected *en bloc*. The  
126 lung vasculature was then perfused through the cannulae with a HEPES-buffered perfusate at  
127 37°C. Under these conditions, the lung periphery was examined using real-time epifluorescent  
128 video microscopy (Zeiss AxioTech with a Zeiss 40x water emission objective [NA: 0.8],  
129 Photometrics CoolSnap HQ camera). Physiological blood flow conditions in the lung  
130 microvasculature were controlled by adding isolated red blood cells (RBC) to the perfusate.  
131 Afterwards, 1x10<sup>6</sup> HOS cells (labeled with Calcein RedOrange) were added to the perfusate and  
132 their adhesive behavior was analyzed in each compartment of the pulmonary microcirculation,  
133 namely precapillary arterioles, capillaries and post-capillary venules. RBC velocity and HOS

134 tumor cell adhesion or arrest was analyzed from the digital recordings using image analysis  
135 software (MetaMorph, Molecular Devices).

136

### 137 *Single cell force spectroscopy*

138 To measure the adhesion force [nN] between cancer and endothelial cells, we applied single cell  
139 force spectroscopy (SCFS). As described earlier,<sup>10-12</sup> this method is based on atomic force  
140 microscopy (AFM) and allows to quantify the adhesion force (nN) between single cancer cells and  
141 endothelial cells. The CellHesion® software (JPK, SPM, version 4) directed the experiment.  
142 Analysis of the data was performed using JPK Data Processing (software version 4.3.18). Briefly,  
143  $1.5 \times 10^5$  human umbilical vein endothelial cells (HUVECs) were seeded overnight in a well of an  
144 ibidi Culture-Insert (Culture-Insert 2 well, #80209, ibidi, Germany). The next day, the Culture-  
145 Inserts were removed and the cells were supplemented for 4 h with fresh medium, with or without  
146 IL-1 $\alpha$  (10 ng/ml). Tipless cantilevers (#ARROW-TL1x48-10, NanoWorld AG) were preincubated  
147 for 20 min in PBS containing 1 mg/ml wheat germ agglutinin (WGA; #L-9640, Sigma-Aldrich).  
148 Before starting the experiment, HUVECs were rinsed 3x with Ringer's solution (in mmol/l: NaCl  
149 122.5, KCl 5.4, CaCl<sub>2</sub> 1.2, MgCl<sub>2</sub> 0.8, HEPES 10, and D-glucose 5.5, adjusted to pH 7.4 with 1 M  
150 NaOH) and maintained in this solution. Afterwards, 2  $\mu$ l of a cancer cell suspension (~100 cells/  
151  $\mu$ l) were added to a cell-free area within the dish containing the HUVECs. Next, the WGA-coated  
152 cantilever was guided under optical control over a single cancer cell and brought into contact with  
153 this cell for 6 s by pressing the cantilever onto the cell with a maximal loading force of 2 nN. To  
154 ensure that the cancer cells were attached to the cantilever and always had the same mechanical  
155 properties, we standardized this picking procedure.

156 For measuring the cell-cell adhesion forces, the parameters were changed to 2 s contact time with  
157 a maximum loading force of 1 nN. This time, the cantilever with the attached cancer cell was  
158 lowered under optical control onto a single HUVEC within the endothelial cell layer and after 2 s  
159 contact time the cantilever was lifted back to its starting position. The maximal adhesion force was  
160 determined from the resulting force-distance curve. Each cancer cell was brought into contact with  
161 20 individual HUVECs (n=1). At least three independent experiments were performed for each  
162 condition (n≥3). Further parameters for the measurements were as follows: pulling length (z-  
163 length) was set to 100 μm (to ensure a complete separation of cells), velocity during approach and  
164 retraction was set to 5 μm/s. The spring constant was 0.03 N/m and had been corrected by the  
165 Standardized Nanomechanical AFM Procedure (SNAP).<sup>13</sup>

166

#### 167 *shRNA-mediated depletion of CD44, E-selectin, C2GNT2 and MGAT5*

168 To test the functional importance of CD44 and MGAT5 (HOS and MeWo cells), E-selectin  
169 (HUVECs) and C2GNT2 (HT29 and PaCa5061 cells) the mRNAs of interest were stably depleted  
170 by lentiviral transduction of corresponding shRNAs. In case of the CD44 knockdown, a pLVX-  
171 puro vector was used and continuous selection with puromycin, FACS and limiting dilution  
172 cloning were performed. Finally, at least 5 clones showing the strongest depletion were pooled to  
173 avoid clonal effects. In case of the E-selectin and C2GNT2 knockdowns, cells were transduced  
174 with a pLVX-puro vector containing the shRNA of interest and subsequently selected with  
175 puromycin, but without FACS or limiting dilution cloning. In case of MGAT5, knockdown cells  
176 were transduced and selected in the same way, but additionally FACS-sorted based on cell surface  
177 PHA-L binding. In parallel, the 'shControl' cell lines were generated by transducing parental cells  
178 with a pLVX-puro vector containing a nonsense sequence (without mRNA target in mammalian



179 cells). The nucleotide sequences of the used shRNAs were: shCD44: 5'-  
180 GGCGCAGATCGATTTGAAT-3'; shE-selectin: 5'-CACACACCTGGTTGCAATT-3';  
181 shC2GNT2 (GCNT3): 5'-CCGGGCTTAGAA-  
182 GAATACCTACGTTCTCGAGAACGTAGGTATTCTTCTAAGCTTTTTG-3'; shMGAT5: 5'-  
183 GATCCGGCGGAAATTCGTACAGATTTCAAGAGAATCTGTACGAATTTCCGCCTTTTT  
184 TACGCGTG-3'.

185

### 186 *CAM and glycosyltransferase expression in human tumor cell lines*

187 Commonly described E-selectin ligand carrier glycoproteins were tested on HT29, PaCa5061,  
188 HOS, and MeWo cells by flow cytometry using commercial antibodies against CD44 (B-F24),  
189 CD44v3 (3G5), CD24 (eBioSN3), CD43 (eBio84-3C1), ESL-1 (AE-6), MUC-1 (SantaCruz),  
190 PSGL-1 (FLEG), LGALS3BP (3G8). Isotype controls were used as appropriate. Tumor cells were  
191 marked dead or alive by propidium iodide staining immediately before flow cytometry.

192 RNA was extracted from HT29, HOS and MeWo cells and human glycosyltransferase qPCR  
193 profiler arrays performed as described.<sup>14</sup> In short, RNA concentrations were quantified using a  
194 NanoDrop spectrophotometer and 1 mg was processed to cDNA with RT2 First Strand Kit (SA  
195 Biosciences). Expression levels of 84 human glycosylation genes were determined with the Human  
196 Glycosylation RT<sup>2</sup> Profiler PCR Array (SA Biosciences) in a LightCycler 480 (Roche).  
197 Housekeeping genes for normalization and internal controls for genomic DNA contamination,  
198 RNA quality, and general PCR performance were included as well. Differences in C2GNT2  
199 (GCNT3) expression as indicated by the qPCR profiler array were validated by WB as described.<sup>15</sup>

200 Total protein extraction was made with RIPA lysis buffer. For protein detection, the following

201 antibodies were used: polyclonal rabbit anti-GCNT3 (C2GNT2), mouse monoclonal anti-HSC70  
202 (B-6) (SantaCruz).

203

#### 204 *Lectin flow cytometry*

205  $\alpha$ -2,3- and  $\alpha$ -2,6-sialic acid residues within the human tumor cell glycocalyx were determined  
206 using biotinylated *Maackia amurensis* (MAA-II) and *Sambucus nigra* (SNA-I) lectin (Vector  
207 Labs.) at 10  $\mu$ g/mL in lectin buffer (Tris-buffered saline +Ca<sup>2+</sup>/ +Mg<sup>2+</sup>) for 30 min at 4°C. As  
208 ‘isotype’ controls, lectins were applied after treating the tumor cells with periodic acid. Lectins  
209 were labeled with streptavidin-APC (Sigma) for flow cytometry. Tumor cells were treated with  
210 neuraminidase (see methods of main text) or left untreated prior to the lectin binding assay.

211

#### 212 *CD44 WB, enzymatic treatments and lectin pulldown assays*

213 HOS and MeWo cell protein extracts from parental cell lines as well as MGAT5 control and  
214 knockdown derivatives were generated by scraping the cells in RIPA buffer (supplemented with  
215 protease inhibitor cocktail (Calbiochem) and x M vanadate, 30 min at 4°C, then 30 min centrifuged  
216 at 14,000 g at 4°C). Protein extracts were left untreated or treated with PNGase F (*Flavobacterium*  
217 *meningosepticum*, recombinant from *E. coli*; 1 U/ 10  $\mu$ g protein overnight at 37°C) or sialidase  
218 (*Arthrobacter ureafaciens*, 1.25 mU/ 10  $\mu$ g protein for 45 min at 37°C) before protein bands were  
219 separated using SDS-PAGE followed by anti-CD44 western blot analysis. Briefly, proteins were  
220 transferred to PVDF membranes and unspecific binding sites were blocked with blocking solution  
221 (StartingBlock™ Blocking Buffer) + 0.05% Tween 20 for 1h at RT. Primary antibody (R&D  
222 systems, clone 2C5, 1  $\mu$ g/mL) was incubated for 1 h at RT. HRP-conjugated goat-anti-mouse was

223 used as secondary antibody and binding was detected using a chemiluminescence kit (Thermo  
224 Fisher). Additional tumor cell samples were treated with 2  $\mu$ M synthetic swainsonine for 72 h prior  
225 to protein extraction (control: methanol). In addition, some protein extracts (+/- swainsonine or  
226 from MGAT5 control and knockdown derivatives) were incubated with DSL-agarose or PHA-L  
227 agarose (both from Vector Labs.) in a protein: lectin ratio of 10: 1 overnight at 4°C (rolling). After  
228 centrifugation and washing five times, the precipitated proteins were subjected to SDS-PAGE and  
229 CD44 WB as described above.

230

### 231 *Immunohistochemistry*

232 Immunohistochemistry for hNCAM was carried out on 4  $\mu$ m lung tissue sections (FFPE) from  
233 SW2 xenograft mice. After de-paraffinization, antigen retrieval was performed with Dako S1699  
234 Retrieval Solution at pH 6 in a microwave for 2 x 4 min. Final concentration of the primary  
235 antibody (Leica #NCL-CD56-1B6) was 0.88  $\mu$ g/ml and visualization of bound antibody was  
236 performed with the Dako Real Detection System K5005.

237 5  $\mu$ m sections of HT29, PaCa5061, HOS and MeWo xenograft tumors (FFPE) were stained with  
238 anti-Ki67 (Dako S1699 Retrieval Solution at pH 6, 85°C overnight; primary antibody: Dako  
239 #M7240, final concentration: 1.1  $\mu$ g/ml; visualization with the Vectastain ABC-AP kit from  
240 Vector Labs.), anti-pH2AX (Dako S1699 Retrieval Solution at pH 6, 121°C, 10 min; primary  
241 antibody: abcam #ab81299, final concentration: 0.07  $\mu$ g/ml; visualization with ABC-AP), and  
242 anti-CD31 (Dako S2367 Retrieval Solution at pH 9, 121°C, 10 min; primary antibody: abcam  
243 #ab28364, final concentration: 0.8  $\mu$ g/ml, visualization with ABC-AP). For quantification of the  
244 Ki67 and pH2AX staining, the stained area was determined using Image J software (Color

245 Threshold Plugin) analyzing up to 27 viewing fields (200-fold magnification) depending on the  
246 entire size of the respective xenograft tumor section. Three samples per group (PBS vs. BZM)  
247 were considered per xenograft tumor entity (HT29, PaCa5061, HOS, MeWo). For quantification  
248 of the CD31 staining, the number of microvessels (CD31-positive) was counted in up to 20  
249 viewing fields (200-fold magnification) per tumor depending on the tumor size and three samples  
250 were considered per group.

251 Immunohistochemistry for sLeA was performed on 5 µm sections of agar-embedded SKOV3 cells  
252 as well as SKOV3, HOS and MeWo xenograft tumors (FFPE). In addition, sLeA was stained on  
253 colon cancer and ovarian cancer surgical specimens. In short, sections were de-paraffinized and  
254 pre-treated with trypsin 0.1% in a water bath at 37°C for 10 min. The primary antibody was  
255 121SLE from abcam (#ab3982) diluted 1:750 and bound antibody was visualized using the Dako  
256 Real Detection System K5005. Counterstaining of nuclei was performed with Mayer's hemalum  
257 solution for 3-5 s.

258

### 259 *Patient material*

260 Clinical colorectal cancer and ovarian cancer specimens were collected from surgically removed  
261 tissues adhering to guidelines of the local ethical review board and after written informed consent  
262 of the patients (ethics committee of the Universität zu Lübeck, approval #07-124). For sLeA  
263 immunohistochemistry, tissues of 60 colorectal cancers as well as 30 corresponding adjacent  
264 normal mucosa specimens from the same patients were selected. Tissue cores (diameter 1.5 mm)  
265 were implemented into a tissue microarray by using a semiautomated arrayer (TMArrayer,  
266 Pathology Devices, San Diego, USA) as described<sup>16</sup>. The ovarian cancer specimens were provided

267 by Professor Johannes Dietl (Department of Obstetrics and Gynecology, Würzburg University  
268 Hospital).

269

#### 270 *Statistics*

271 Data are presented as means  $\pm$  SD unless otherwise indicated. Student's t and Mann-Whitney-U  
272 tests were performed as appropriate to assess associations between variables. Statistical  
273 significance was assigned at 2-tailed *p*-values less than 0.05. Numbers of lung metastases were  
274 also evaluated by an analysis of covariance (ANCOVA) with the tumor weight (Fig. 6A) or growth  
275 period (Fig. 2B) as covariates. These statistical tests were carried out using IBM SPSS software  
276 (SPSS version 21.0 for Windows, IBM). All data were visualized using Graph Pad Prism 5.0  
277 (Graph Pad Software, San Diego).

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287 **Supplemental References**

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