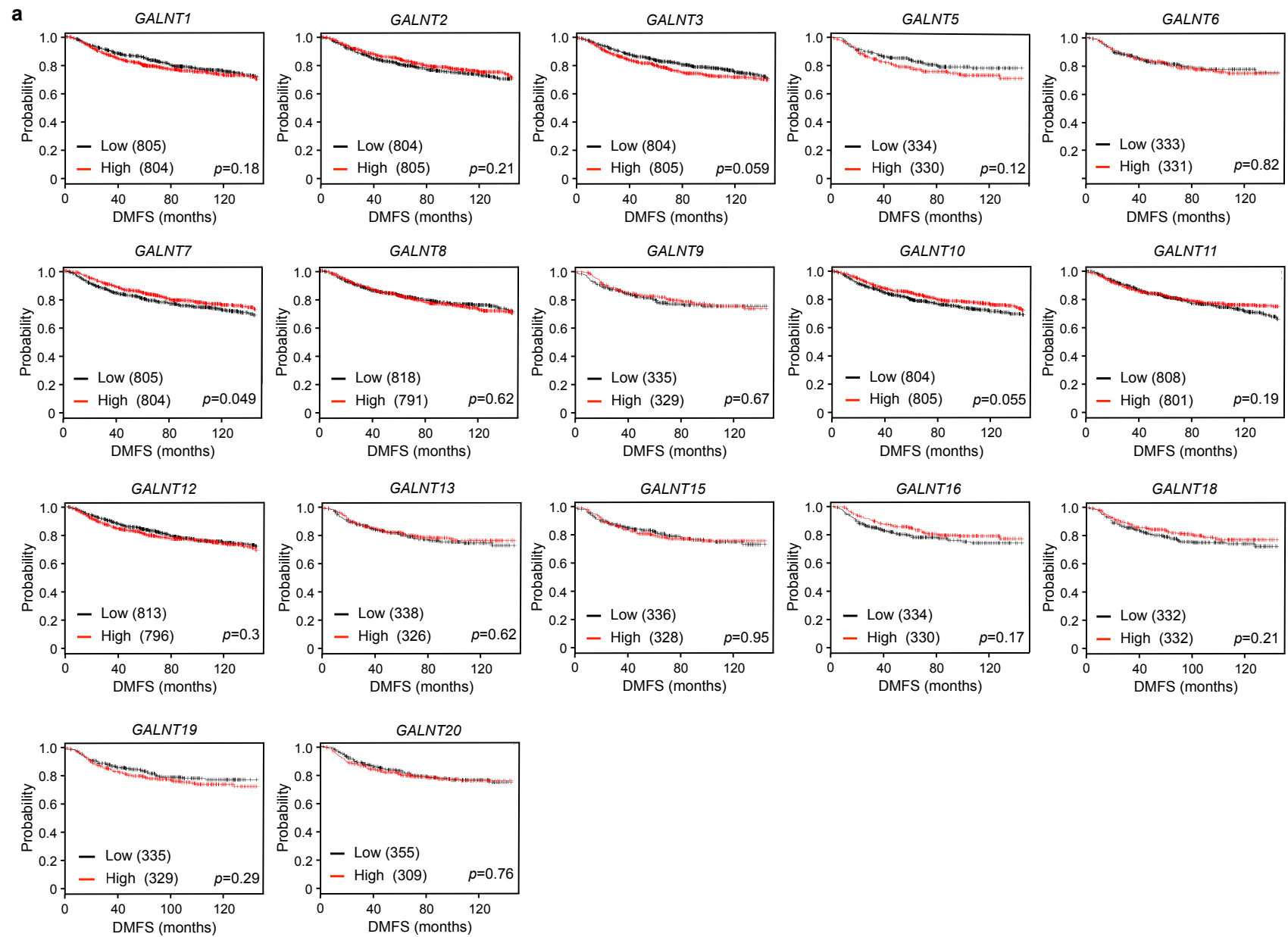
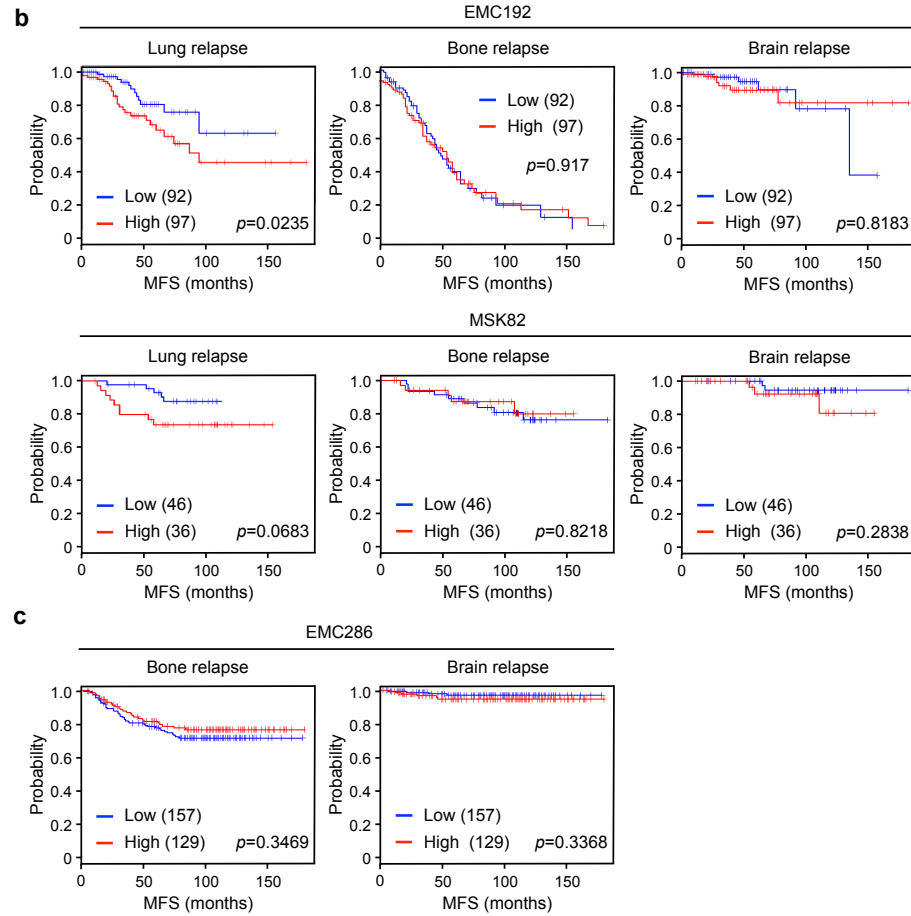






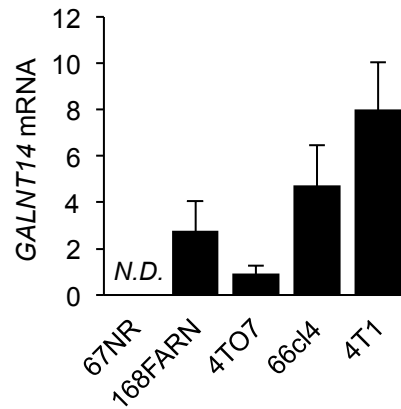
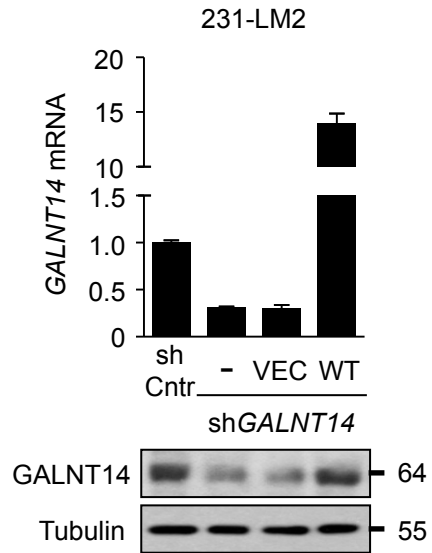
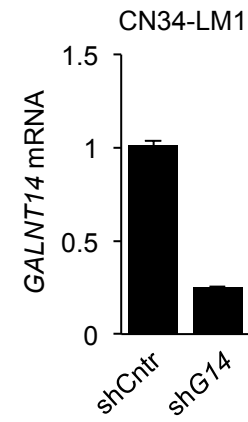
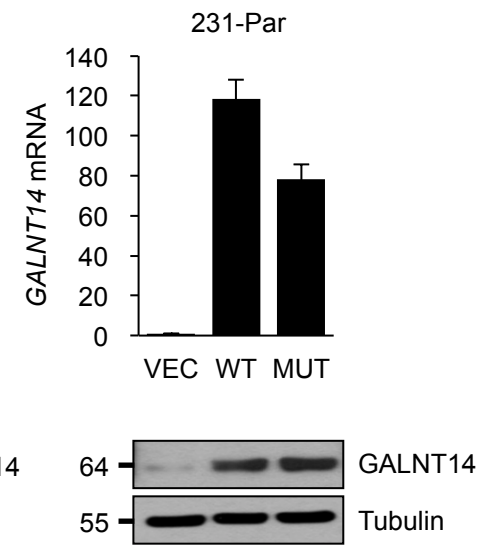
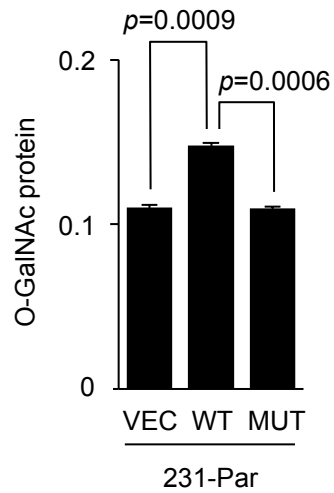
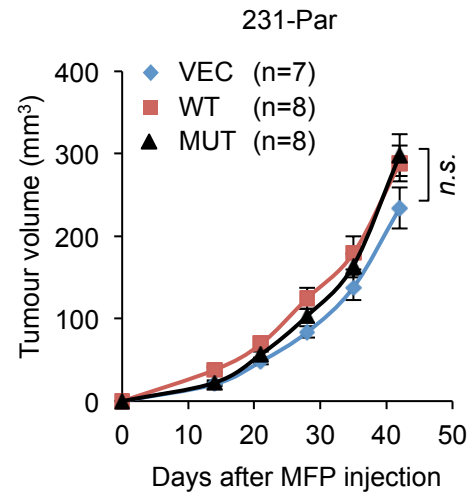
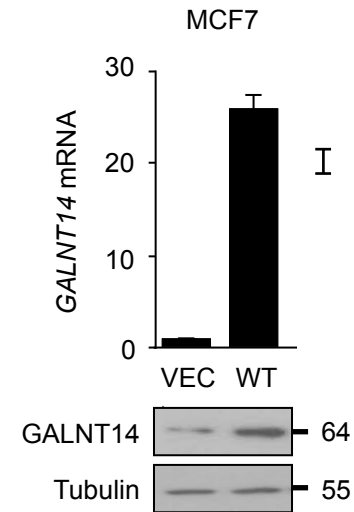
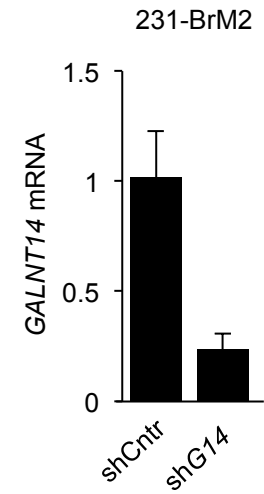
Supplementary Figure 1 Expression of *GALNT14*, but not other *GALNT* members, is associated with poor distant metastasis-free survival in breast cancer patients.

(a) Kaplan-Meier curve representation of distant metastasis-free survival (DMFS) in breast cancer patients by using “KM plotter”. Detailed methods are described in Methods section. Patients were categorized into two groups according to the median expression of the indicated *GALNT* members in their primary tumours. 18 *GALNT* family members whose expression data was available were analyzed.

(b) Similar analysis as in Fig. 1c except that EMC192 (top) and MSK82 (bottom) were analyzed separately. $p=0.0427$ by the Wilcoxon test. $p=0.0683$ by the log-rank test.

(c) Bone or brain metastasis-free survival (MFS) rates were analyzed in EMC286 cohort.

P-values were calculated using a log rank test unless indicated otherwise.

a**b****c****d****e****f****g****h**

Supplementary Figure 2 GALNT14 selectively promotes lung metastasis.

(a) Relative *GALNT14* mRNA levels in mouse breast cancer cells with varying lung metastasis activities. 67NR, non-metastatic; 168FARN and 4T07, weakly metastatic to lymph nodes; 66cl4, weakly lung metastatic; 4T1, highly metastatic to the lung and bones. *N.D.*: not detected.

(b) Relative *GALNT14* mRNA (top) or protein (bottom) levels in control, *GALNT14*-silenced, and rescued 231-LM2 cells. shCntr: non-targeting control shRNA, sh*GALNT14*: shRNA against *GALNT14*, VEC: control vector for a *GALNT14* expression vector, WT: wild-type *GALNT14* expression vector.

(c) Similar experiments as in **b** except that CN34-LM1 cells are used. sh*G14* indicates sh*GALNT14*.

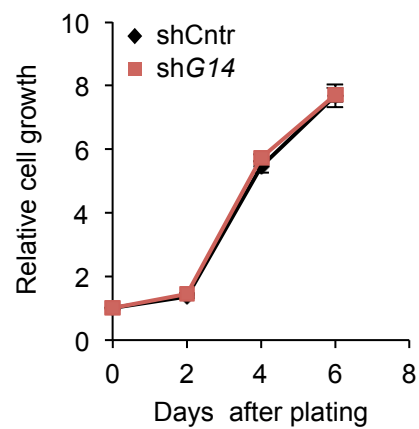
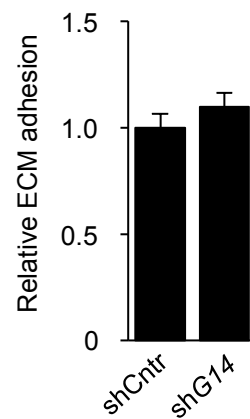
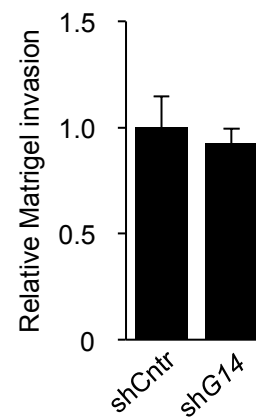
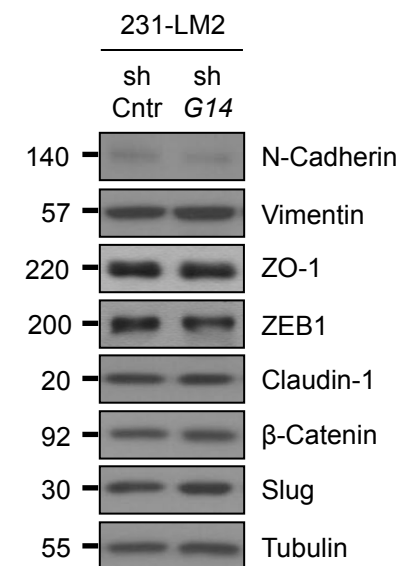
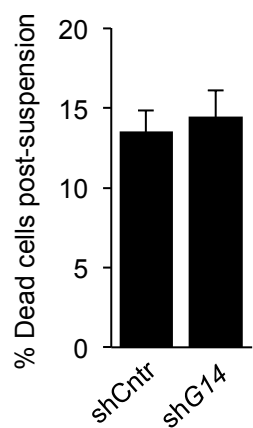
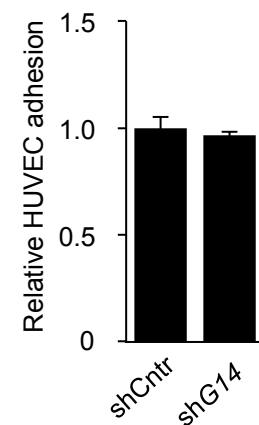
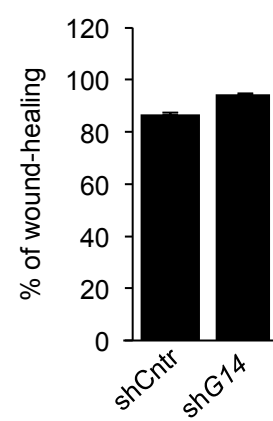
(d,e) Relative mRNA (top) and protein (bottom) of *GALNT14* (**d**) and O-GalNAc-glycosylated protein levels (**e**) in 231-Par cells expressing control vector (VEC), wild-type (WT) and catalytic mutant (MUT) *GALNT14*.

(f) The indicated 231-Par cells (5×10^5) were implanted into the mammary fat pads and tumour growth rates were measured.

(g) Relative *GALNT14* mRNA (top) and protein levels (bottom) of MCF7 cells expressing control vector or wild-type *GALNT14* were analyzed.

(h) Relative expression of *GALNT14* in control and *GALNT14*-silenced 231-BrM2 cells.

P-values were calculated using two-tailed unpaired Student's *t* test except (f) using one-tailed Mann-Whitney test. Data are mean $\pm$ SEM (error bars). Western blot results in **b,c,d** and **g** are representative and were replicated at least two times. qRT-PCR data are representative of two independent experiments, each with triplicate samples.

a**c****e****g****b****d****f**

Supplementary Figure 3 GALNT14 is not required for cell proliferation, resistance to anoikis, motility or EMT.

(a) Comparison of growth rates between control and *GALNT14*-knockdown (shG14) 231-LM2 cells. $n=6$.

(b) Relative anoikis resistance of the indicated 231-LM2 cells. Cells were grown under suspension conditions for 3 days in media containing 0.5% FBS and the number of dead or viable cells were counted by using trypan blue dye. The percentages of dead cells are shown. $n=4$.

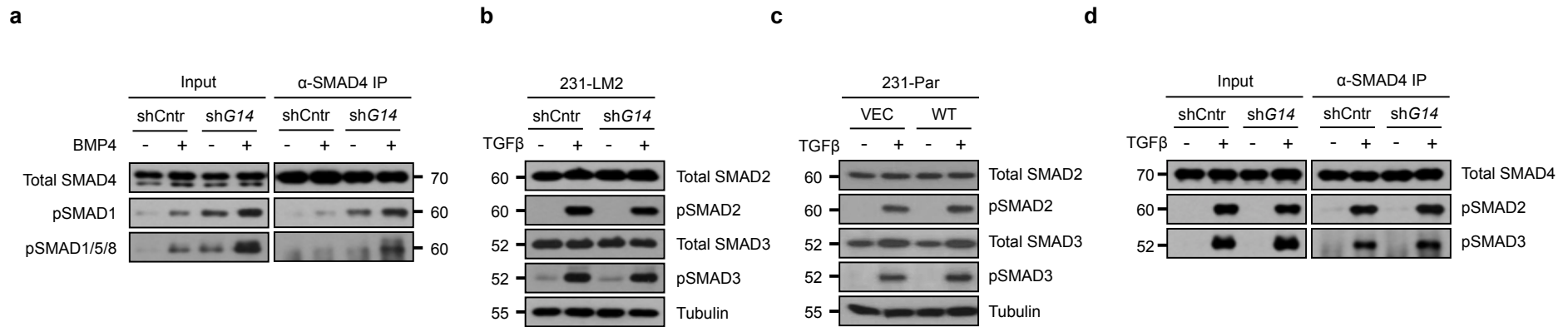
(c,d) Comparative adhesion abilities of the indicated 231-LM2 cells to extra cellular matrix (ECM) or Human umbilical vein endothelial cell (HUVEC). Cells were seeded onto the plates coated with matrigel (c) or HUVEC monolayer (d) and numbers of adhered cancer cells were assessed by measuring the luminescent signals. $n=6$.

(e) Invasion abilities of the indicated 231-LM2 cells. Cells were labeled with cell tracker dye and plated onto matrigel-coated trans-well inserts. Images of migrating cells were captured at X10 magnification and quantified with Image J software. $n=6$.

(f) Relative migration of the indicated 231-LM2 cells. Wound healing motility assays were performed measuring wound closure following by scratching the cell monolayer. Images of migrating cells were captured at X4 magnification. $n=9$.

(g) Analysis of EMT markers in the indicated 231-LM2 cells by western blotting analysis.

Data are mean $\pm$ SEM (error bars).



Supplementary Figure 4 Analysis of BMP and TGF signaling pathways upon changes in *GALNT14* expression.

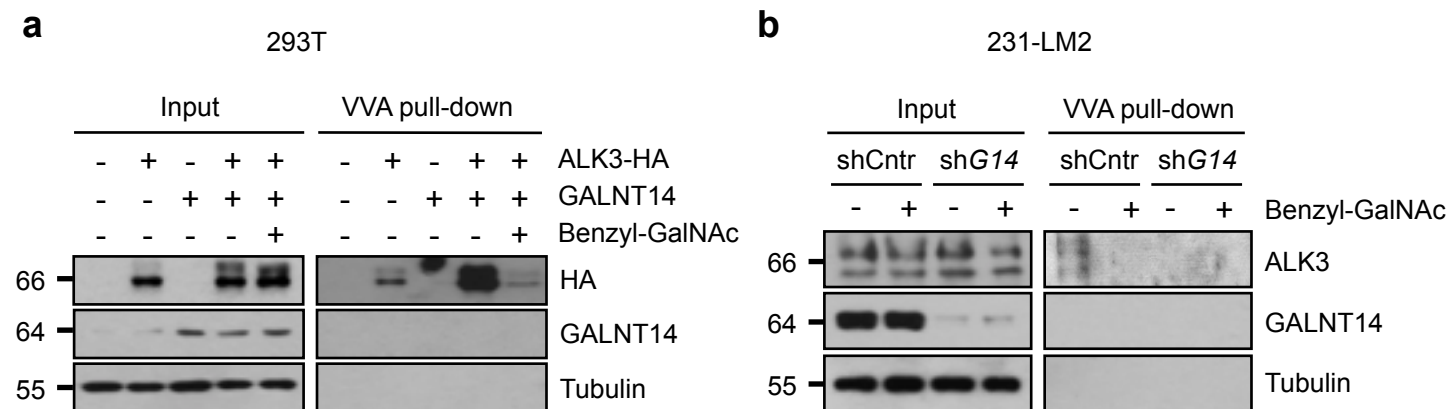
(a) Control and shG14-expressing 231-LM2 cells were treated with vehicle or BMP4 (10 ng ml⁻¹ for 15 minutes).

Nuclear extract was isolated and subjected to immuno-precipitation with an antibody against SMAD4 and co-immunoprecipitated pSMAD1 and pSMAD1/5/8 were analyzed by immunoblotting.

(b,c) The indicated 231-LM2 (b) and 231-Par (c) cells were treated with TGFβ (100 pM for 15 minutes) and total and phosphorylated levels of the indicated SMADs were analyzed by western blotting.

(d) Similar experiments as in a except that interaction between pSMAD 2/3 and SMAD4 was analyzed in the presence of TGFβ (100 pM for 15 minutes).

Western blot images are representative of three independent experiments.

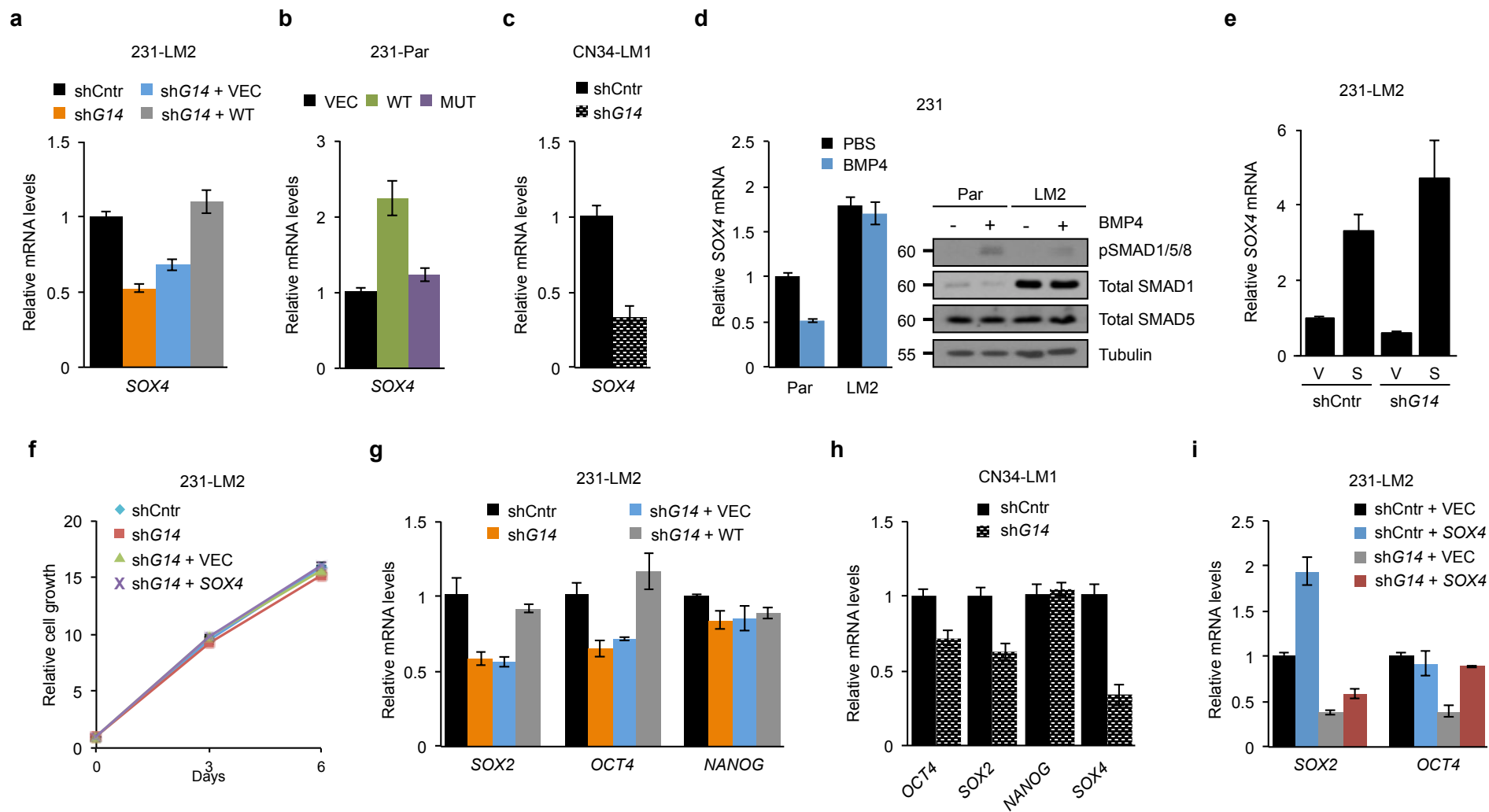


Supplementary Figure 5 BMPR 1A (ALK3) is O-GalNAcylated by GALNT14.

(a) Pull-down assays with VVA-agarose were performed as shown in Fig. 4f using 293T cells transfected with the indicated construct. 1mM benzyI-GalNAc (BG) was added to the media 24 hours prior to IP in lane 5.

(b) Similar experiments as in a except that O-GalNAcylation of endogenous ALK3 in shCntr and shG14-expressing 231-LM2 cells were analysed.

Western blot images are representative of three independent experiments.



Supplementary Figure 6 GALNT14 alleviates the BMP-mediated suppression of SOX4 expression.

(a-c) Relative expression of SOX4 in the indicated 231-LM2 (a), 231-Par (b) and CN34 (c) cells. shG14 indicates shGALNT14. *n*=6.

(d) BMP-responsiveness of 231-Par and LM2 cells. Relative SOX4 mRNA levels upon the addition of 10 ng ml⁻¹ of BMP4 (left). Cell lysates were subjected to immunoblotting analyses with antibodies against the indicated proteins (right). *n*=6.

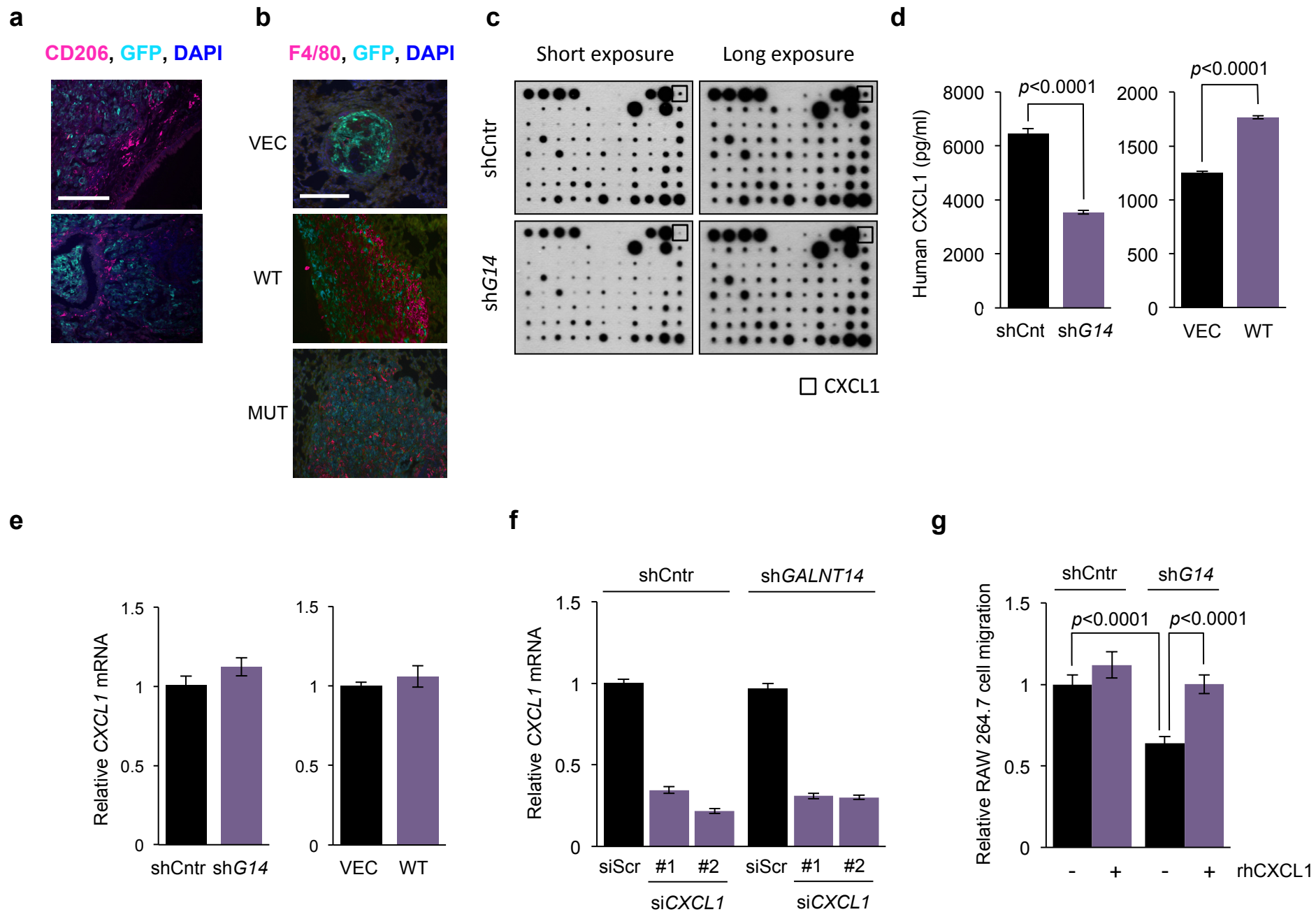
(e) Relative SOX4 mRNA levels in the indicated 231-LM2 cells. V: control vector, S: SOX4 expression vector. *n*=6.

(f) Comparative cell growth of the indicated 231-LM2 cells. *n*=6.

(g,h) Relative expression levels of SOX4, SOX2, OCT4, and NANOG in the indicated 231-LM2 (g) and CN34-LM1 (h) cells. *n*=6.

(i) Relative SOX4 expression levels in the indicated 231-LM2 cells. *n*=6.

Data are mean ± SEM (error bars). Western blot images in d are representatives of two independent experiments.



Supplementary Figure 7 GALNT14 endows BCCs with an ability to modify the lung microenvironment.

(a) CD206 immunofluorescent staining of frozen lung sections from mice injected with the 231-LM2 expressing shCntr. Two representative areas of lung nodules are shown. GFP-positive cells represent cancer cells. Scale bar, 100 μ m.

(b) F4/80 Representative immunofluorescent staining of frozen lung sections from mice injected with the indicated 231-Par cells. Representative images are shown. GFP-positive cells represent cancer cells. Scale bar, 100 μ m.

(c) Conditioned media collected from shCntr or sh*G14*-expressing 231-LM2 cells were subjected to cytokine array (Ray Biotech).

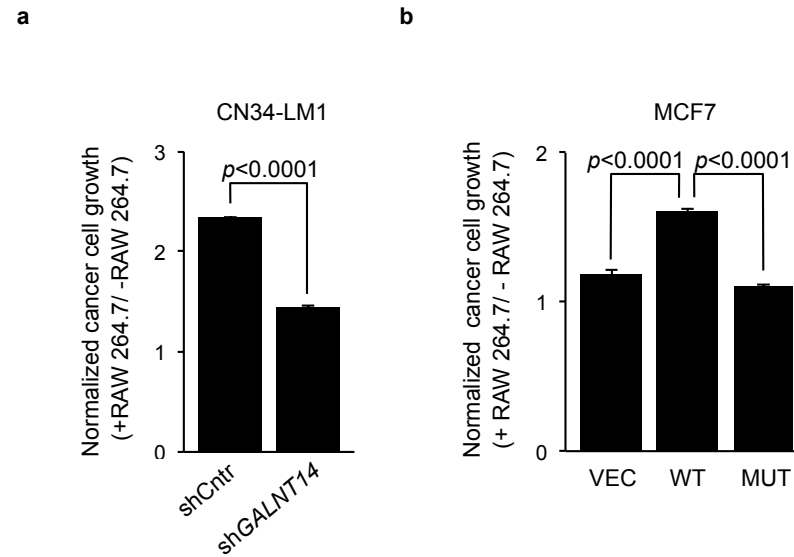
(d) Conditioned media (CM) from the indicated 231-LM2 (left) and 231-Par (right) cells were subjected to CXCL1 ELISA. $n=6$.

(e) Relative CXCL1 mRNA levels in the indicated 231-LM2 (left) and 231-Par (right) cells. $n=6$.

(f) The shCntr or sh*GALNT14*-expressing 231-LM2 cells were transfected with two independent siRNAs against CXCL1. Relative expression levels of CXCL1 were analyzed by qRT-PCR. $n=6$.

(g) RAW 264.7 cell transwell migration assay as in Fig. 6c except that recombinant human CXCL1 (5 ng ml⁻¹) was added to CM from the indicated 231-LM2 cells. $n=9$.

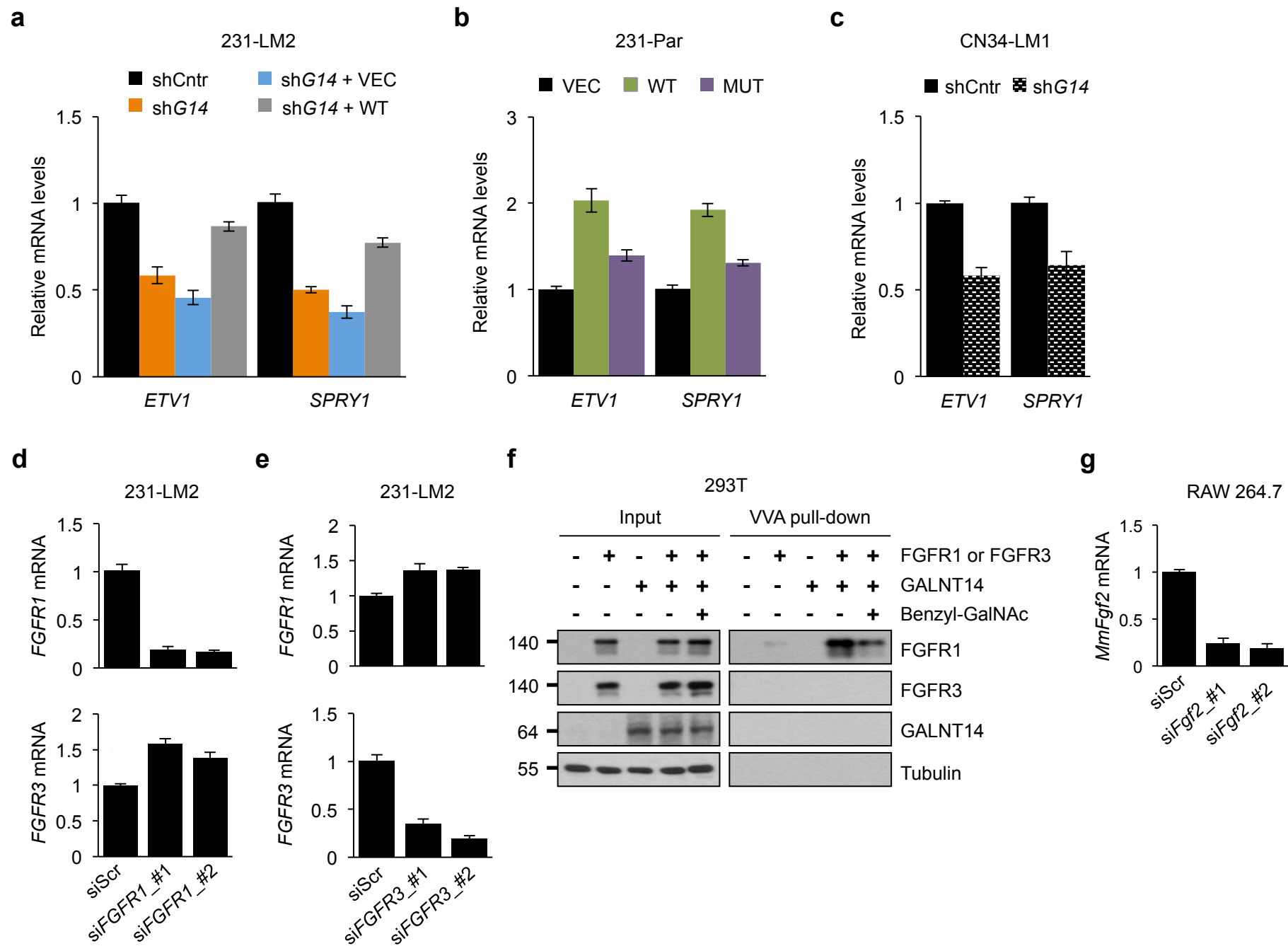
P-values were calculated using two-tailed unpaired Student's *t* test. Data are mean $\pm$ SEM (error bars).



Supplementary Figure 8 GALNT14 enhances macrophage-stimulated growth of BCCs.

Relative growth of the indicated CN34-LM1 (**a**) and MCF7 (**b**) cells in the absence or presence of RAW 264.7 macrophage cells. $n=6$.

P -values were calculated using two-tailed unpaired Student's t test. Data are mean $\pm$ SEM (error bars).



Supplementary Figure 9 GALNT14 activates FGF signaling in BCCs.

(a-c) Relative mRNA levels of FGF-responsive genes *ETV1* and *SPRY1* in the indicated 231-LM2 (a), 231-Par (b) and CN34-LM1 (c) cells. *n*=6.

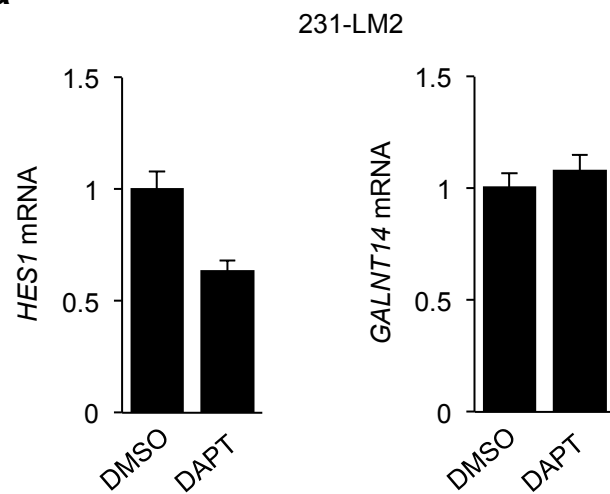
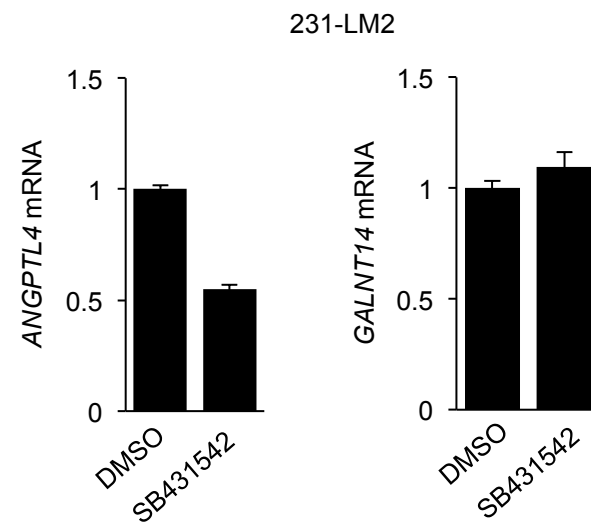
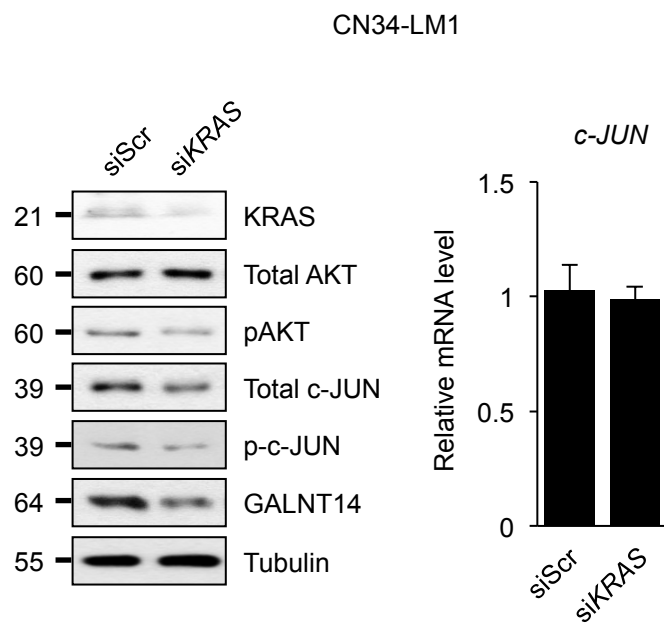
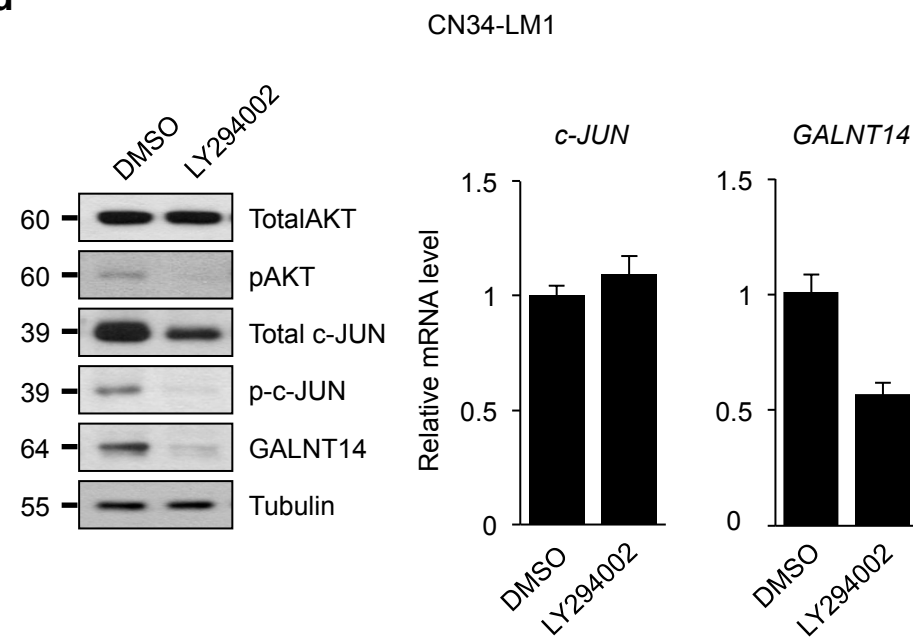
(d) Relative mRNA levels of *FGFR1* (top) and *FGFR3* (bottom) in 231-LM2, transfected with scrambled (siScr) or two independent siRNAs against *FGFR1*. *n*=6.

(e) Similar experiment as in d except that siRNAs against *FGFR3* were used. *n*=6.

(f) O-glycosylation of FGF receptors. Similar experiments as in Fig. 4f except that HEK 293T cells were transfected with *FGFR1* or *FGFR3* expression vectors. 1 mM benzyl-GalNAc was added to the media 24 hours prior to IP where indicated. Western blot images are representative of three independent experiments.

(g) Relative expression of *MmFgf2* in RAW264.7 cells transfected with two independent siRNAs against this gene. *n*=6.

Data are mean $\pm$ SEM (error bars).

a**b****c****d**

Supplementary Figure 10 Activated KRAS-PI3K-c-JUN, but not NOTCH or TGF β signaling pathways, increases *GALNT14* transcription in lung metastatic BCCs.

(a,b) Relative *GALNT14* mRNA levels in the presence of NOTCH inhibitor DAPT (5 μ M) (a) and TGF β inhibitor SB431542 (30 μ M) (b). *HES1* and *Angiopoietin-like 4* (*ANGPTL4*) were used as a positive control for DAPT and SB431542, respectively. $n=6$.

(c) Changes in total and phosphorylated c-JUN and AKT and *GALNT14* protein (left) and *c-JUN* mRNA (right) levels in CN34-LM1 cells upon *KRAS* knockdown. $n=6$.

(d) Left: Comparison of total and phosphorylated c-JUN and AKT as well as *GALNT14* protein level in the absence or presence of LY294002 (30 μ M). Right: *GALNT14* and *c-JUN* mRNA levels under the same condition. $n=6$.

Data are mean $\pm$ SEM (error bars). Western blot images in c and d are representative and were replicated at least two times.

Fig. 2a

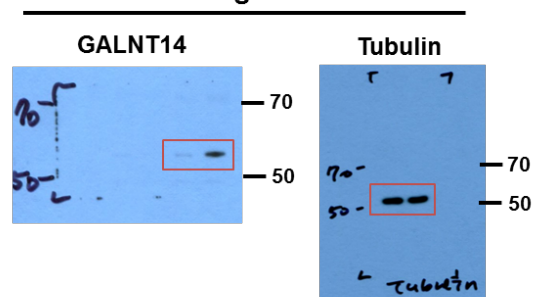
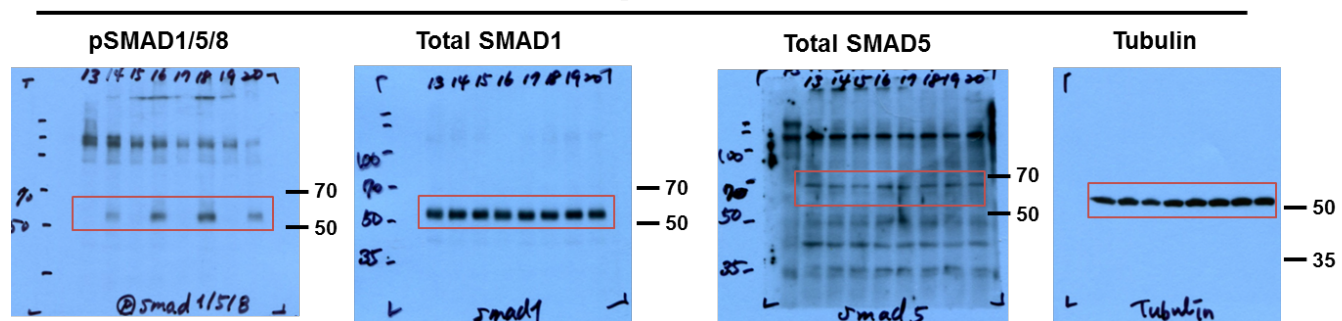


Fig. 4d



Supplementary Figure 11 Unprocessed scans of western blots.

Fig. 4e

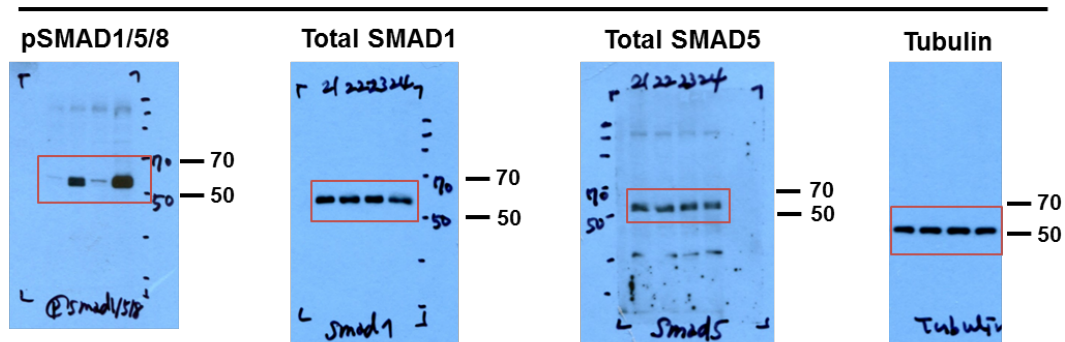
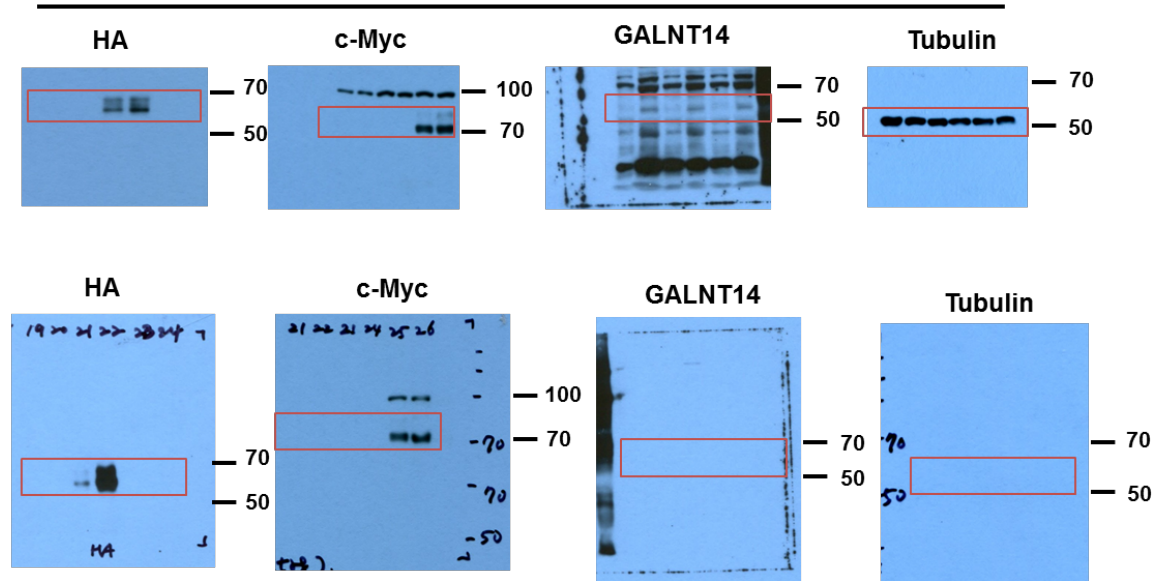


Fig. 4f



Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Fig. 6d

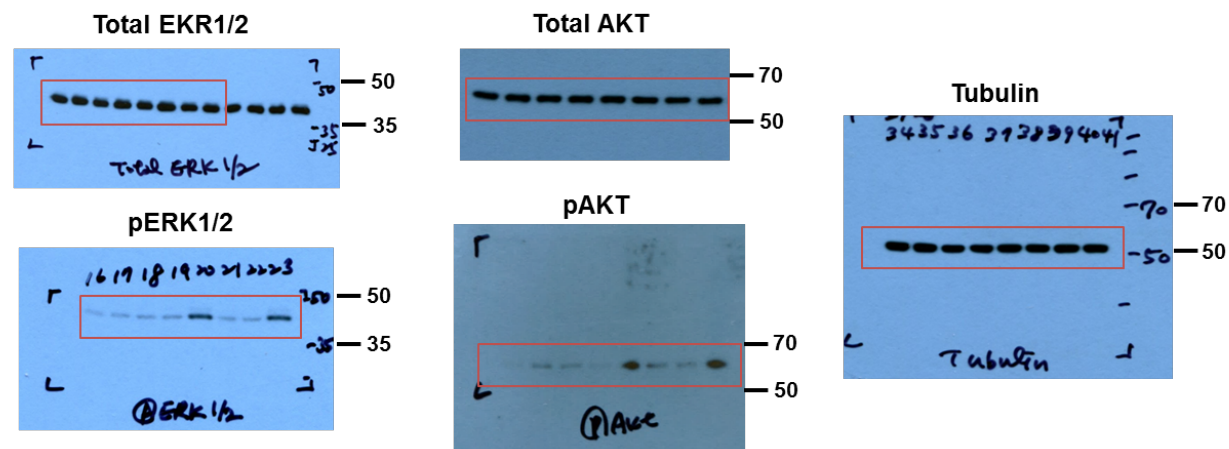
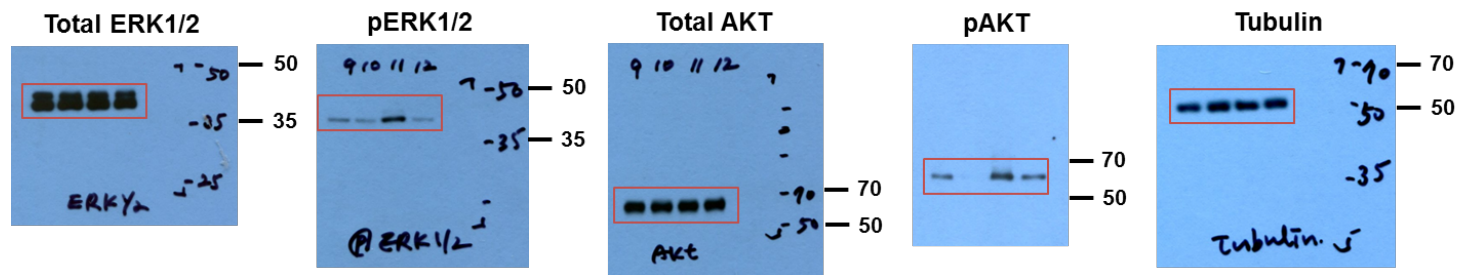


Fig. 7c



Supplementary Figure 11 Unprocessed scans of western blots.

Fig. 7e

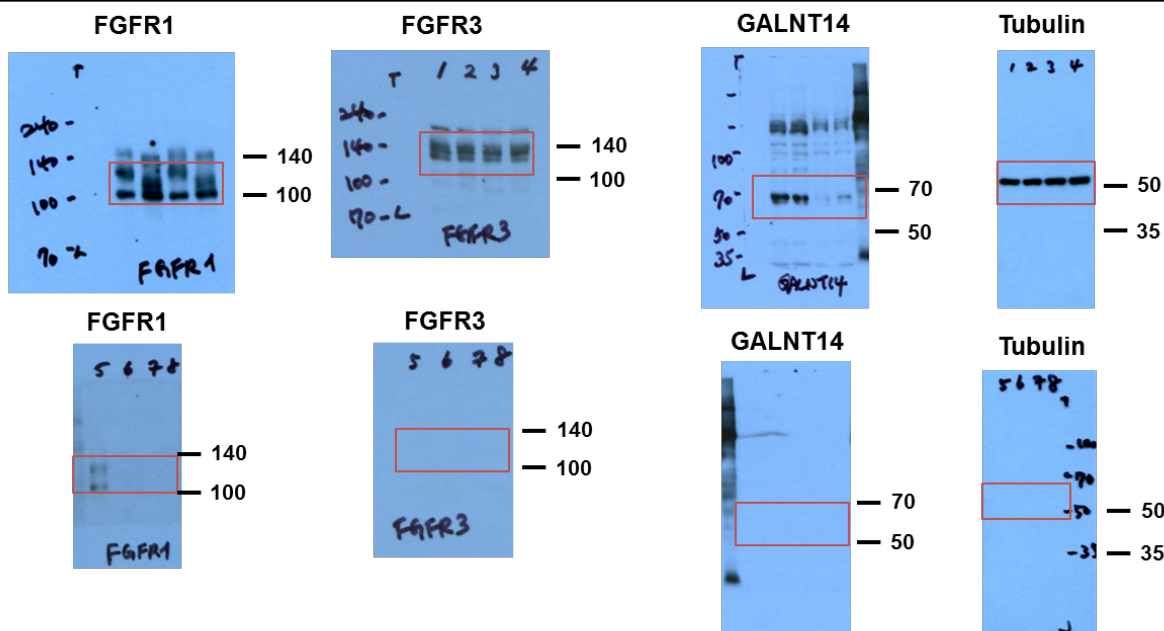


Fig. 8a

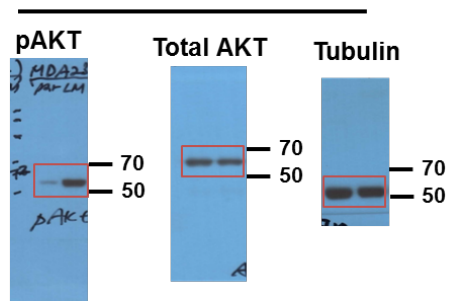
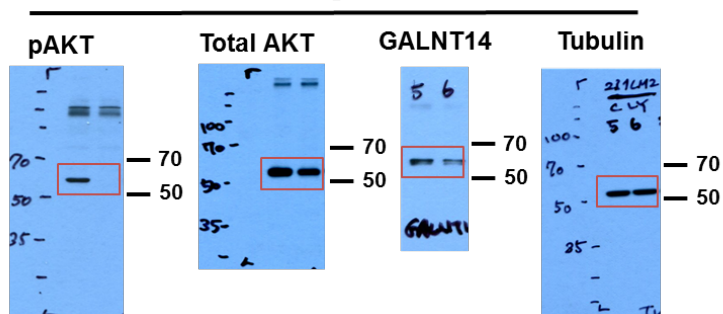


Fig. 8b



Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Fig. 8c

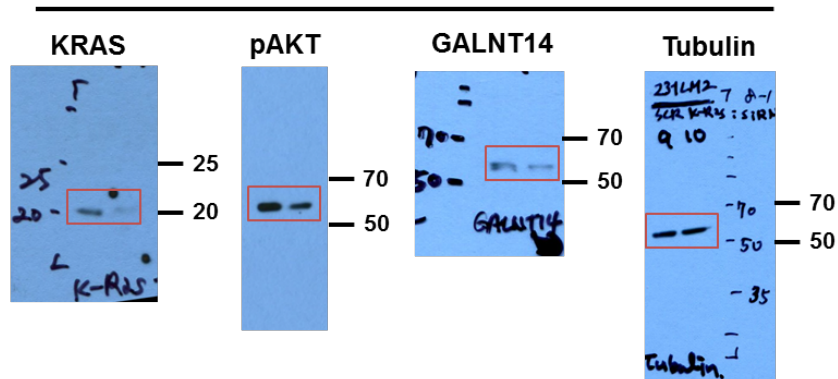


Fig. 8e

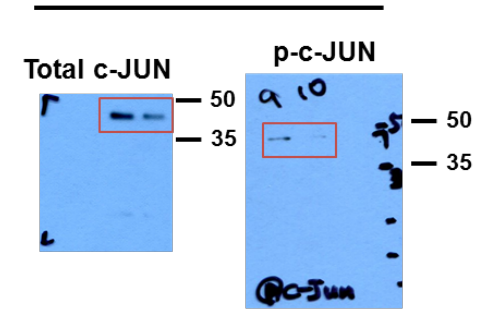
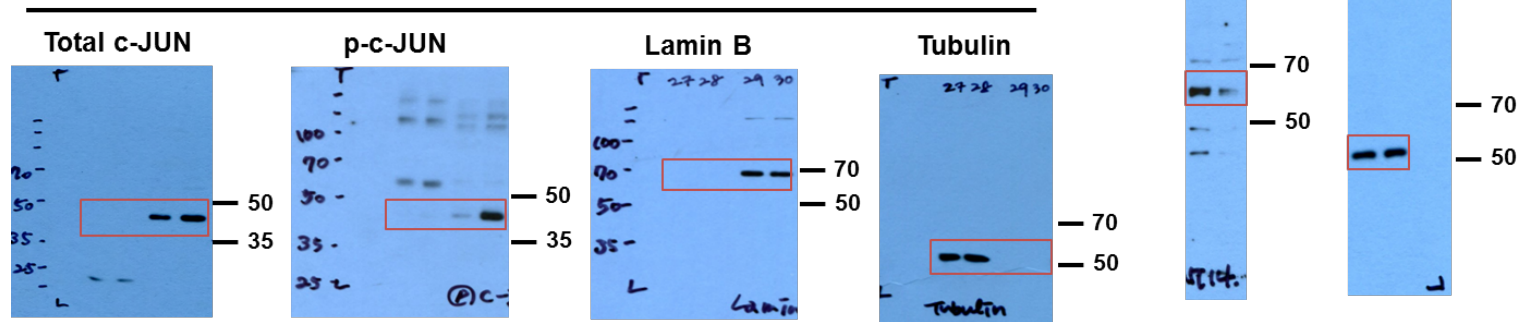


Fig. 8d



Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Fig. 8f

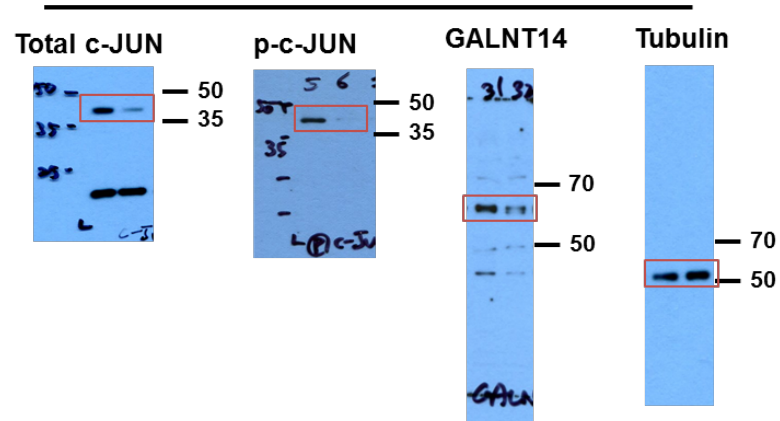


Fig. 8h

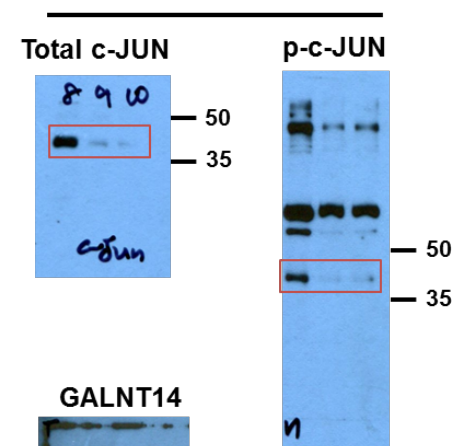
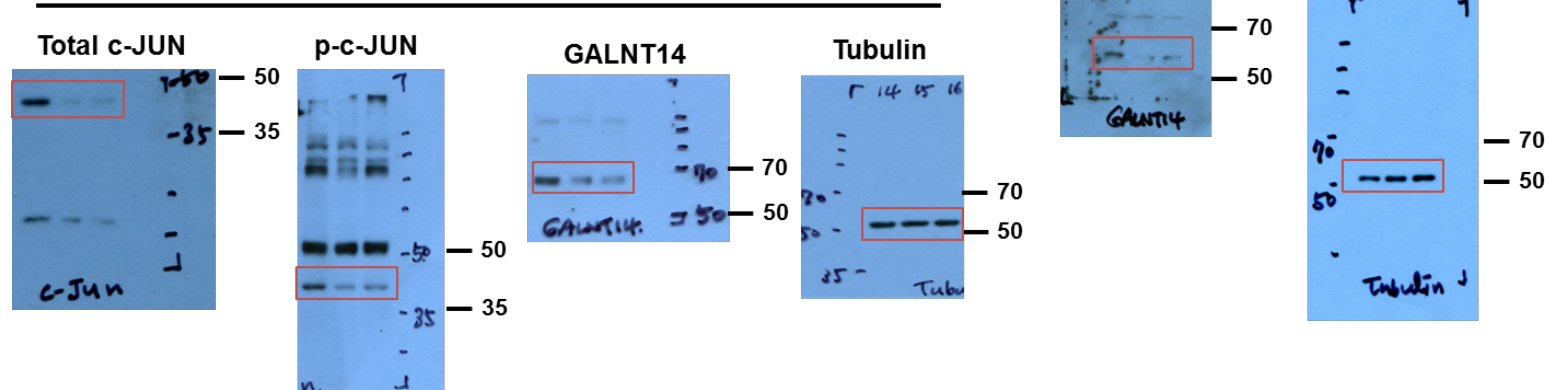
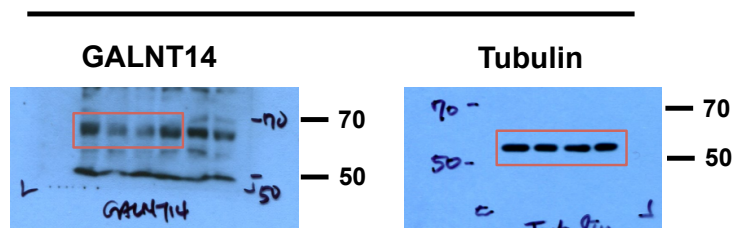


Fig. 8g

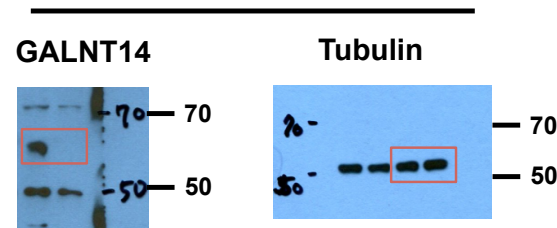


Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

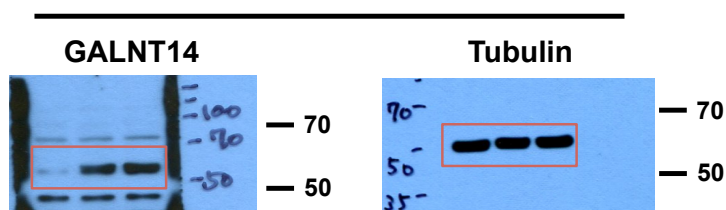
Supplementary Fig. 2b



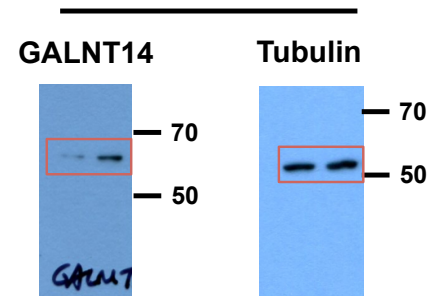
Supplementary Fig. 2c



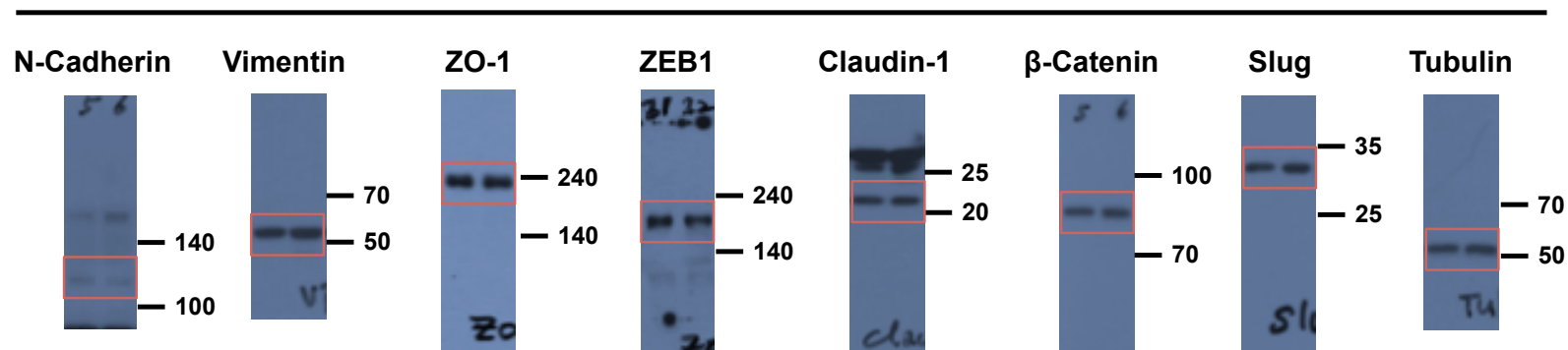
Supplementary Fig. 2d



Supplementary Fig. 2g

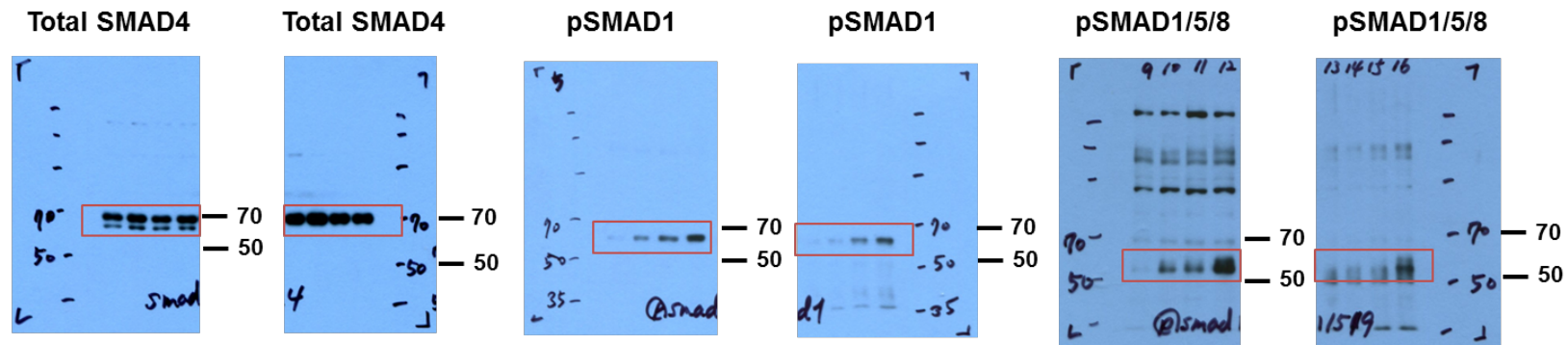


Supplementary Fig. 3g

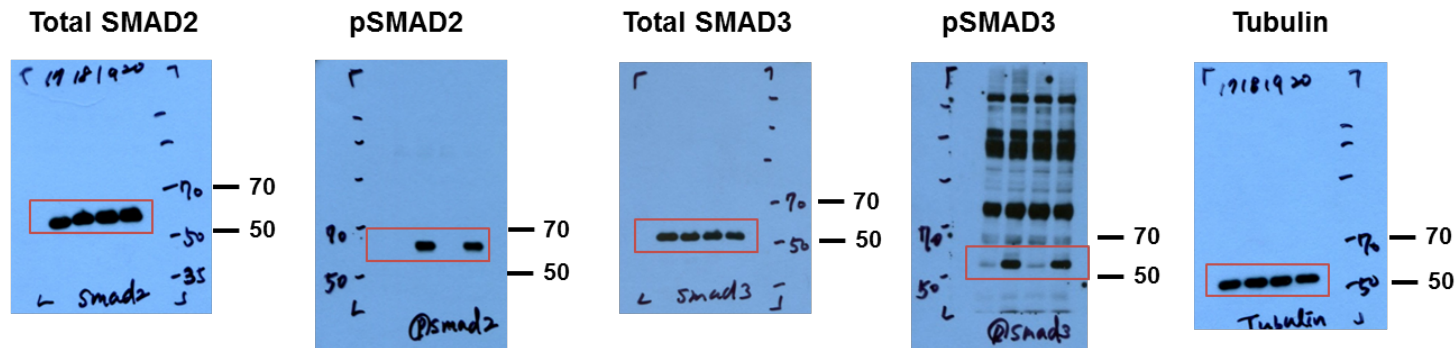


Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Supplementary Fig. 4a

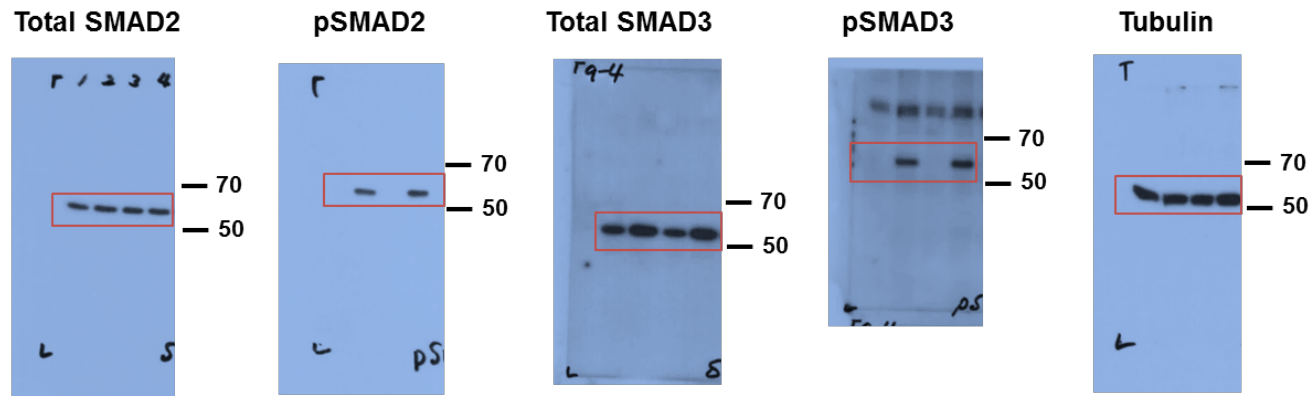


Supplementary Fig. 4b

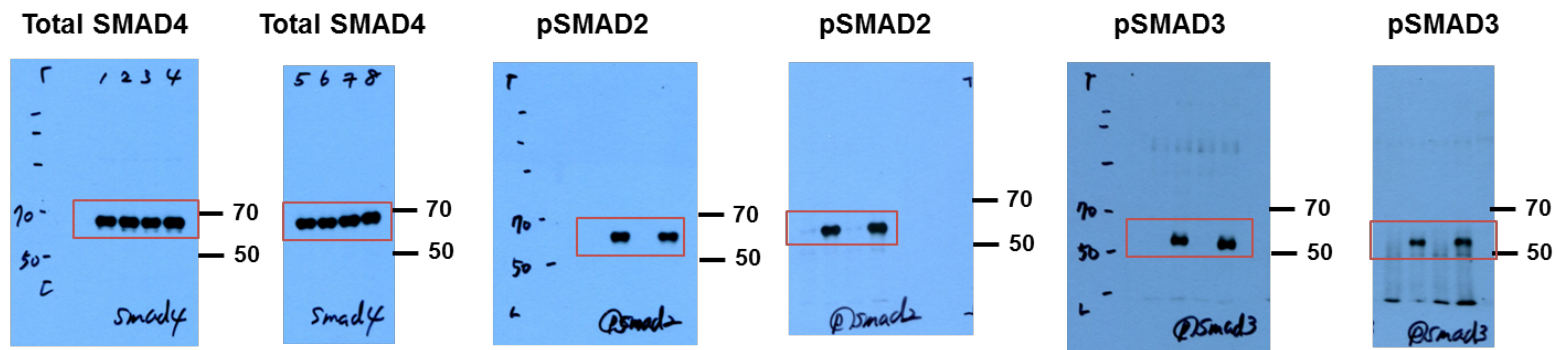


Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Supplementary Fig. 4c

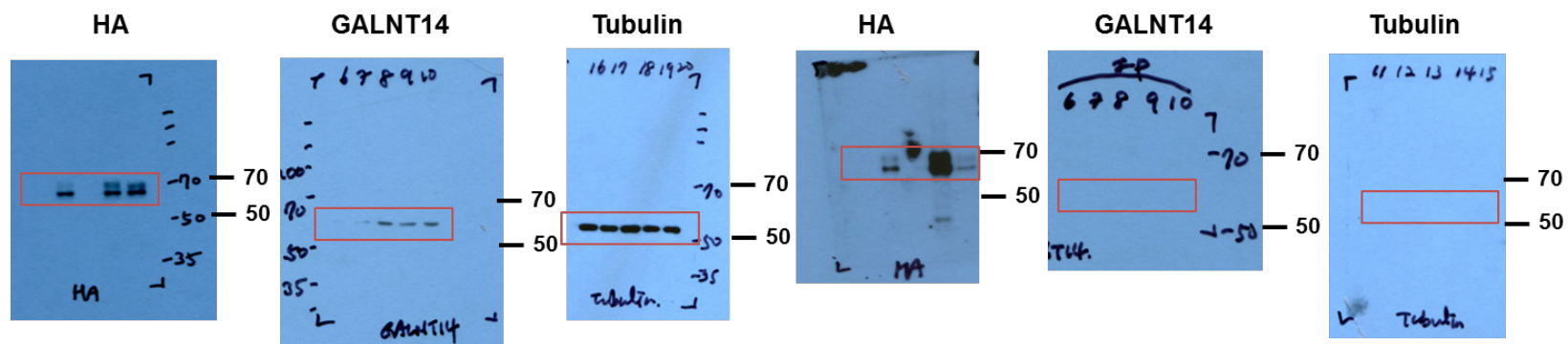


Supplementary Fig. 4d

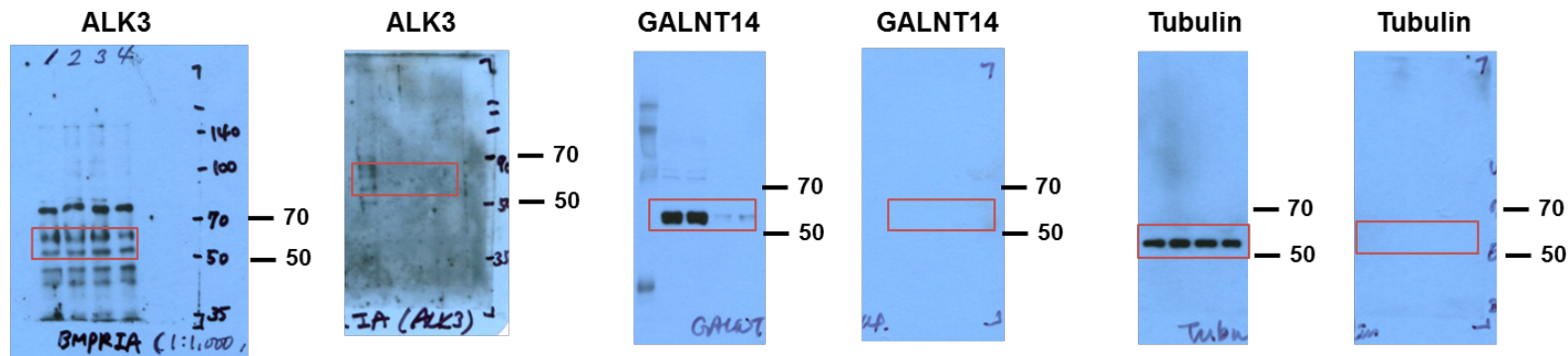


Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Supplementary Fig. 5a



Supplementary Fig. 5b



Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Supplementary Fig. 6d

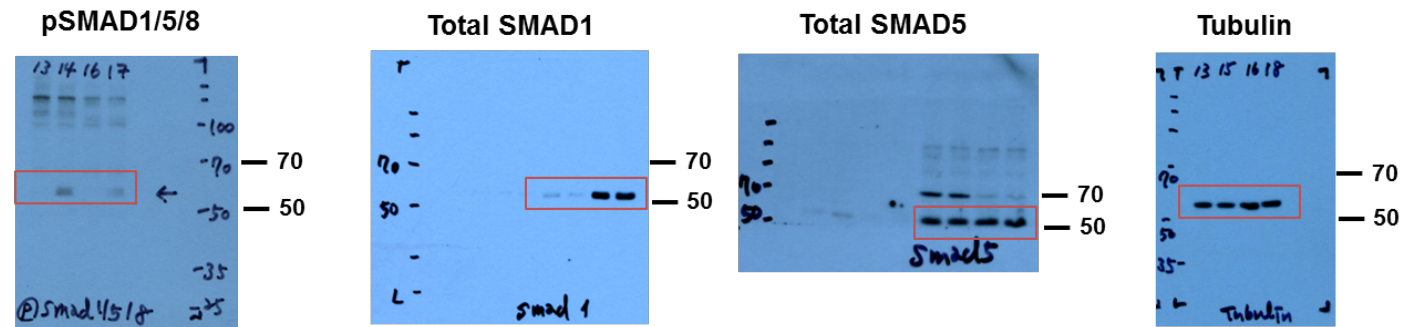
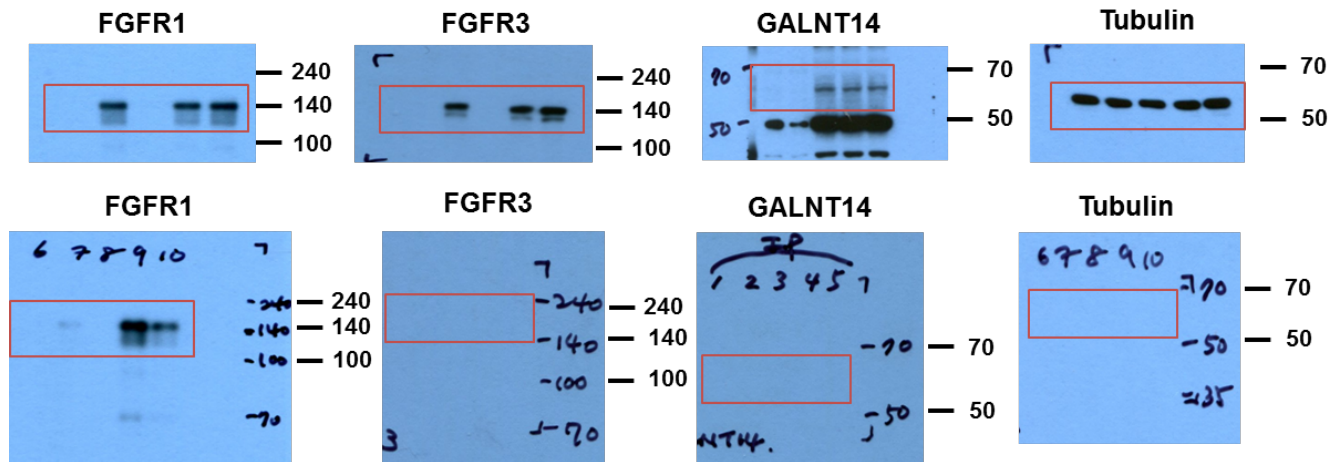
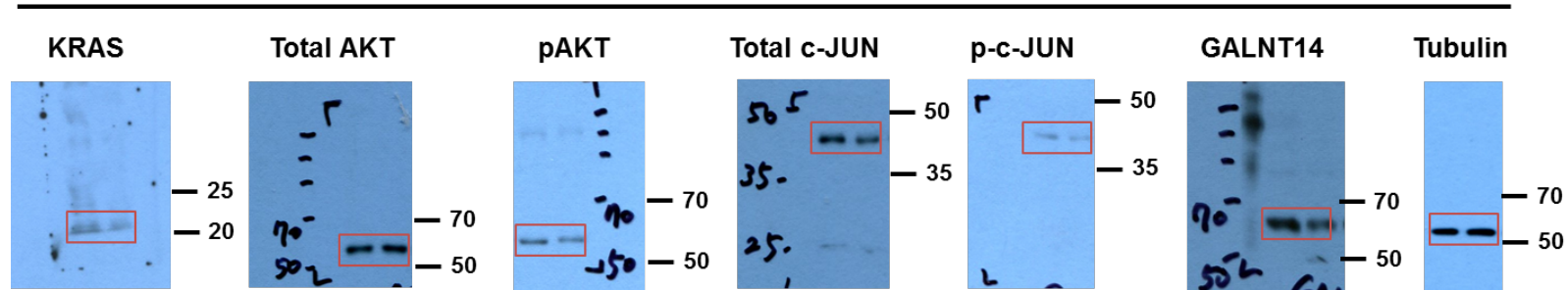


Fig. 9f

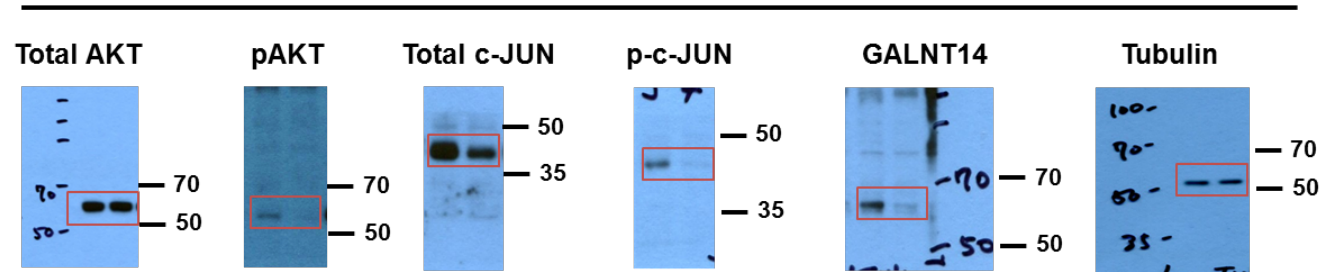


Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Supplementary Fig. 10c



Supplementary Fig. 10d



Supplementary Figure 11 Unprocessed scans of western blots. (Continued)

Supplementary Table 1 Recurrence rates according to *GALNT14* expression level in combined cohorts of EMC192 and MSK82, Related to Fig. 1c.

<i>GALNT14</i> Expression	Relapse Rate		
	Lung	Bone	Brain
<i>GALNT14</i> Low (138)	17/138 (12.3%)	59/138 (42.8%)	8/138 (5.8%)
<i>GALNT14</i> High (133)	34/133 (25.6%)	57/133 (42.9%)	10/133 (7.5%)

Supplementary Table 2 A list of differentially expressed genes upon depletion or ectopic expression of *GALNT14*, Related to Fig. 5a.

17 up- and 13 down-regulated genes by GALNT 14 are listed. Fold-changes (shCntr/sh*GALNT14* and WT/VEC) are shown. The details are described in the text.

Gene Symbol	shCntr /sh <i>GALNT14</i>	WT/VEC	Gene Description
<i>GALNT14</i>	5.09	686.15	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)
<i>SOX4</i>	3.27	4.04	SRY (sex determining region Y)-box 4
<i>SLCO4A1</i>	2.21	1.29	solute carrier organic anion transporter family, member 4A1
<i>PTGES</i>	1.83	1.39	prostaglandin E synthase
<i>RP11-93B14.5</i>	1.83	1.78	ribosomal protein L11
<i>SPRY1</i>	1.66	1.27	sprouty homolog 1, antagonist of FGF signaling (Drosophila)
<i>MARCH2</i>	1.55	1.35	membrane-associated ring finger (C3HC4) 2
<i>KLF9</i>	1.54	1.44	Kruppel-like factor 9
<i>GGT5</i>	1.52	1.74	gamma-glutamyltransferase 5
<i>CDK15</i>	1.47	1.32	PFTAIRE protein kinase 2
<i>SAT1</i>	1.47	1.31	spermidine/spermine N1-acetyltransferase 1
<i>BDH2</i>	1.42	1.43	3-hydroxybutyrate dehydrogenase, type 2
<i>NR2F1-AS1</i>	1.39	1.32	NR2F1 Antisense RNA
<i>DNAJB5</i>	1.39	1.28	DnaJ (Hsp40) homolog, subfamily B, member 5
<i>ETV1 (ER81)</i>	1.36	1.20	ets variant 1
<i>TTC8</i>	1.30	1.23	tetratricopeptide repeat domain 8
<i>ARMCX2</i>	1.28	1.30	armadillo repeat containing, X-linked 2
<i>CLK4</i>	1.27	1.22	CDC-like kinase 4
<i>ATG101</i>	0.72	0.78	autophagy related 101

<i>CDC42EP2</i>	0.70	0.84	CDC42 effector protein (Rho GTPase binding) 2
<i>FJX1</i>	0.72	0.81	four jointed box 1 (Drosophila)
<i>INO80D</i>	0.74	0.80	INO80 complex subunit D
<i>KLF15</i>	0.57	0.69	Kruppel-like factor 15
<i>MARCH4</i>	0.71	0.79	membrane-associated ring finger (C3HC4) 4
<i>MSRA</i>	0.79	0.75	methionine sulfoxide reductase A
<i>PHLDB3</i>	0.66	0.64	pleckstrin homology-like domain, family B, member 3
<i>SH2D3A</i>	0.69	0.76	SH2 domain containing 3A
<i>SLC9A1</i>	0.78	0.83	solute carrier family 9 (sodium/hydrogen exchanger), member 1
<i>TGFB1</i>	0.79	0.84	transforming growth factor, beta 1
<i>TSC22D4</i>	0.70	0.83	TSC22 domain family, member 4
<i>WASH1</i>	0.33	0.52	similar to WAS protein family homolog 1

Supplementary Table 3 List of shRNA and siRNAs used in this study.

Gene	Sense sequence (5'-3')	Ref.
<i>c-JUN</i> _#1	UCCUGAAACAGAGCAUGACCCUAGA	1
<i>c-JUN</i> _#2	GAUGGAAACGACCUUCUAAUUU	2
<i>CXCL1</i> _#1	GCACAUCUGUUUUGUAACU	3
<i>CXCL1</i> _#2	CAGUGUUUCUGGCUUAGAA	4
<i>FGFR1</i> _#1	GCCACACUCUGCACCGCUA	5
<i>FGFR1</i> _#2	CCACAGAAUUGGAGGCUAC	6
<i>FGFR3</i> _#1	CGCCAAGCCUGUCACCGUA	7
<i>FGFR3</i> _#2	GACCGUGUCCUUACCGUGA	7
<i>MmFgf2</i> _#1	GUGUUUCUUCUUUGAACGACU	8
<i>MmFgf2</i> _#2	GCACUGAAACGAACUGGGCAGUAU	9
<i>KRAS</i>	SMARTpool: siGENOME (M-005069-00)	
<i>GALNT14</i>	Mission shRNA TRC Number: TRCN0000421183	

Supplementary Table 4 List of gene constructs used in this study.

Gene	Vector	Tag / Fusion protein	Source	Ref.
<i>ActRIIB</i>	pCS2	5'-c-Myc	Dr. Oelgeschläger	10
<i>ALK3</i>	pCS2	5'-HA	Dr. Oelgeschläger	10
<i>c-JUN</i>	pMIEG3	3'-IRES eGFP	Addgene (#40348)	11
<i>FGFR1</i>	pCMV	3'-EGFP	Dr. Heo	
<i>FGFR3</i>	pCMV	3'-mCit	Dr. Heo	
<i>GALNT14</i>	pBABE-hygro	5'-FLAG	Sinobiologicals	
<i>SOX4</i>	pBABE-hygro	5'-FLAG	Addgene (#36984)	12

Supplementary Table 5 List of qRT-PCR primers used in this study.

Gene		Sequence (5'-3')
<i>c-JUN</i>	Forward	GGCTACAGTAACCCCAAGA
	Reverse	GTGAGGAGGTCCGAGTTC
<i>CXCL1</i>	Forward	ACCCCAAGTTAGTTCAATCTG
	Reverse	GATCCGCCAGCCTCTATC
<i>ETV1</i>	Forward	AAGAGGAGAATTTGATTAGACTAAGT
	Reverse	CCATAACAATAGCCACGGTATA
<i>FGFR1</i>	Forward	ATCTTGGCTTCTTACAGTTCTT
	Reverse	CTTAGTGAGGACAGTGATGAC
<i>FGFR3</i>	Forward	CCAAGCCTGTCACCGTAG
	Reverse	ATCATCTTCATCATCTCCATCTCA
<i>GALNT1</i>	Forward	TGATATGTAGAGCAGTCTGTTG
	Reverse	GCAGTGAAAGTCCTTGATAATC'
<i>GALNT2</i>	Forward	TTACTGCGGTTGCGTTAG
	Reverse	CGAAGGGCTCTTAGGAAAG
<i>GALNT3</i>	Forward	GCTCAAGGTCTCGTTCAG
	Reverse	TCCCATATCTGCTCTCCA
<i>GALNT4</i>	Forward	AGCAGCCTTAAAGTTTATCAAA
	Reverse	GAGAAGTGGGTGGGTTTAG
<i>GALNT5</i>	Forward	AATGTGGAGAATGGTGTATAGC
	Reverse	CTGGATGAAAGACTGATGTTGA
<i>GALNT6</i>	Forward	CCTTGCTATTATTACCTGAAGTCT
	Reverse	GTTTCTGTCCTGTCTTTCTCA
<i>GALNT7</i>	Forward	GCTGCTGCCATAATGACT
	Reverse	AGTGATATTACCAACTTACAAAGC
<i>GALNT9</i>	Forward	AGCCTTCTTGCCTGACTC
	Reverse	CCACATCCTCACACTTCTTC
<i>GALNT10</i>	Forward	GCACTCTGGCATTGTCAT
	Reverse	AGTCAAGTTCTGTCCTTCCT
<i>GALNT11</i>	Forward	GGTGAAGAAGTGAGTGTCC
	Reverse	GATACTGTGGTTTGCCTCTAT
<i>GALNT12</i>	Forward	ATGTTATGAAGCCTCGTGTATC
	Reverse	TTTGGTGGGTTCTGGTCA
<i>GALNT13</i>	Forward	TCTGTTTCAACTCTCGTCTAATC
	Reverse	GTGGATATGGTGGCAAGTC
<i>GALNT14</i> (3'UTR)	Forward	TCATTCCCTGATTGGTATCTG
	Reverse	AGAGACTGCTTCCTTTGTAG
<i>GALNT14</i> (ORF)	Forward	TGTCAGTCATCACCTTGTTT
	Reverse	CATTGCTGTCGGTCATCT
<i>GALNT16</i>	Forward	AACCTCTGCTCTGGATTGAA

	Reverse	AGACACTTGGCTGCTGAC
	Forward	CCAGAACCGCAAGTCTAAGC
<i>GALNT18</i>	Reverse	CACTAACCTGGTTCCCCAGA
	Forward	CCTCTGGTTAGGGTGCACAT
<i>GALNT19</i>	Reverse	GCTAGGTCAGCATCGTCACA
	Forward	CATGGGGAAGGTGAAGGTCG
<i>GAPDH</i>	Reverse	GTTGAGGTCAATGAAGGGGT
	Forward	CACAGAAAGTCATCAAAGCCTAT
<i>HES1</i>	Reverse	TCCAGAATGTCCGCCTTC
	Forward	TGACCTTGATTTATTTTGCATACC
<i>HPRT</i>	Reverse	CGAGCAAGACGTTCAAGTCCT
	Forward	GGCTGAATCCTTCCTCTC
<i>NANOG</i>	Reverse	GCTCCAACCATACTCCAC
	Forward	AACTGGTGTGTTTATGTTCTTAC
<i>OCT4</i>	Reverse	CCTCTTCTGCTTCAGGAG
	Forward	TAGTCTCCAAGCGACGAA
<i>SOX2</i>	Reverse	AGCAAGAAGCCTCTCCTT
	Forward	ACTCCTCCTCTTCCTCCT
<i>SOX4</i>	Reverse	CAGGGACATGCTCTCAAAG
	Forward	TTCCCTGTTTCCCACCTT
<i>SPRY1</i>	Reverse	GCTTCCCAGTCCACTCTT
	Forward	GAGAAGAGCGACCCACAC
<i>MmFgf2</i>	Reverse	ACACACTTAGAAGCCAGCAG
	Forward	AGCCAAATACAAAGCCTAAGAT
<i>MmHPRT</i>	Reverse	ACAGTAACATTCATAGAAGGTTCA
<i>ANGPTL4</i>	Assay ID	Hs01101127
<i>B2M</i>	Assay ID	Hs00984230
<i>GALNT8</i>	Assay ID	Hs00213610
<i>GALNT15</i>	Assay ID	Hs00365065
<i>GALNT17</i>	Assay ID	Hs01391759
<i>GALNT20</i>	Assay ID	Hs00377152
<i>MmB2M</i>	Assay ID	Mm00437762
<i>MmGALNT14</i>	Assay ID	Mm01233030

Supplementary Table 6 List of antibodies used in this study.

Antibody	Company	Catalog no.	Source	kDa	Dilution
AKT	Cell signaling	4691	Rabbit	60	1:2,000
pAKT (S473)	Cell signaling	4060	Rabbit	60	1:1,000
BMPR-1A	Santa Cruz Biotechnology	20736	Rabbit	66	1:3,000
β -Catenin	Cell signaling	8480	Rabbit	92	1:1,000
Claudin-1	Cell signaling	13255	Rabbit	20	1:1,000
c-JUN	Santa Cruz Biotechnology	44	Rabbit	39	1:1,000
p-c-JUN (S63/73)	Santa Cruz Biotechnology	16312	Rabbit	39	1:1,000
c-Myc-Tag	Abcam	9106	Rabbit		1:5,000
ERK1/2	Cell signaling	4695	Rabbit	42, 44	1:2,000
pERK1/2 (T202/Y204)	Cell signaling	9101	Rabbit	42, 44	1:2,000
FGFR1	Cell signaling	9740	Rabbit	92, 120, 145	1:1,000
FGFR3	Cell signaling	4574	Rabbit	125, 145, 165	1:1,000
GALNT14	GeneTex	122371	Rabbit	64	1:5,000
HA-Tag	Cell signaling	3724	Rabbit		1:1,000
KRAS	Santa Cruz Biotechnology	30	Mouse	21	1:1,000
Lamin B	Santa Cruz Biotechnology	6217	Goat	67	1:1,000
N-Cadherin	Cell signaling	13116	Rabbit	140	1:1,000
Slug	Cell signaling	9585	Rabbit	30	1:1,000
SMAD1	Cell signaling	6944	Rabbit	60	1:1,000
SMAD2	Cell signaling	5339	Rabbit	60	1:1,000
SMAD3	Cell signaling	9523	Rabbit	52	1:1,000
SMAD4	Cell signaling	9515	Rabbit	70	1:1,000
SMAD4 (also used for IP)	Santa Cruz Biotechnology	7966	Mouse	70	1:1,000
SMAD5	Cell signaling	12534	Rabbit	60	1:1,000
pSMAD2 (S465/467)	Cell signaling	3108	Rabbit	60	1:1,000
pSMAD3 (S423/425)	Cell signaling	9520	Rabbit	52	1:1,000
pSMAD1/5 (S463/465) /8 (S426/428)	Cell signaling	9511	Rabbit	60	1:1,000
pSMAD1/5 (S463/465) /9 (S465/467)	Cell signaling	13820	Rabbit	60	1:1,000
Tubulin	Millipore	05-829	Mouse	55	1:10,000

Vimentin	Cell signaling	5741	Rabbit	57	1:1,000
ZEB1	Cell signaling	3396	Rabbit	200	1:1,000
ZO-1	Cell signaling	8193	Rabbit	220	1:1,000

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