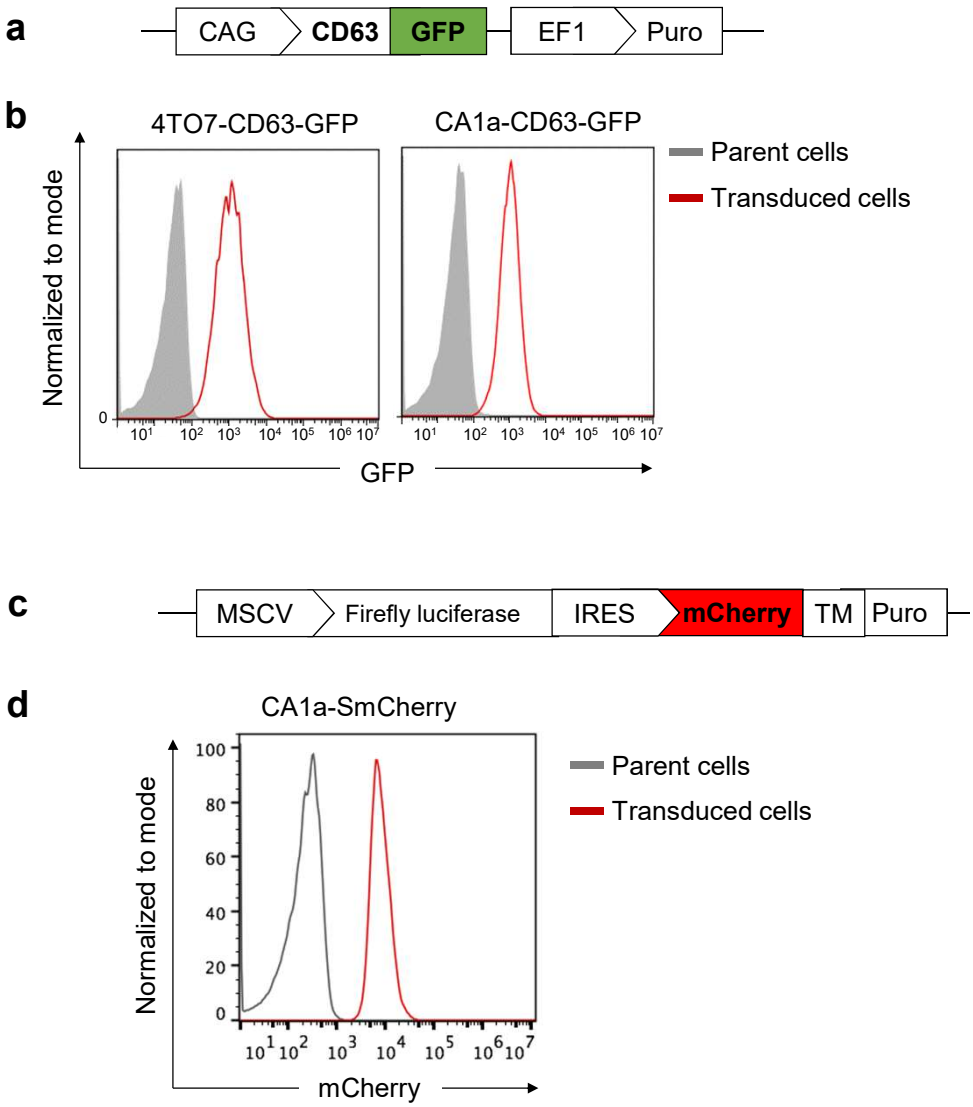
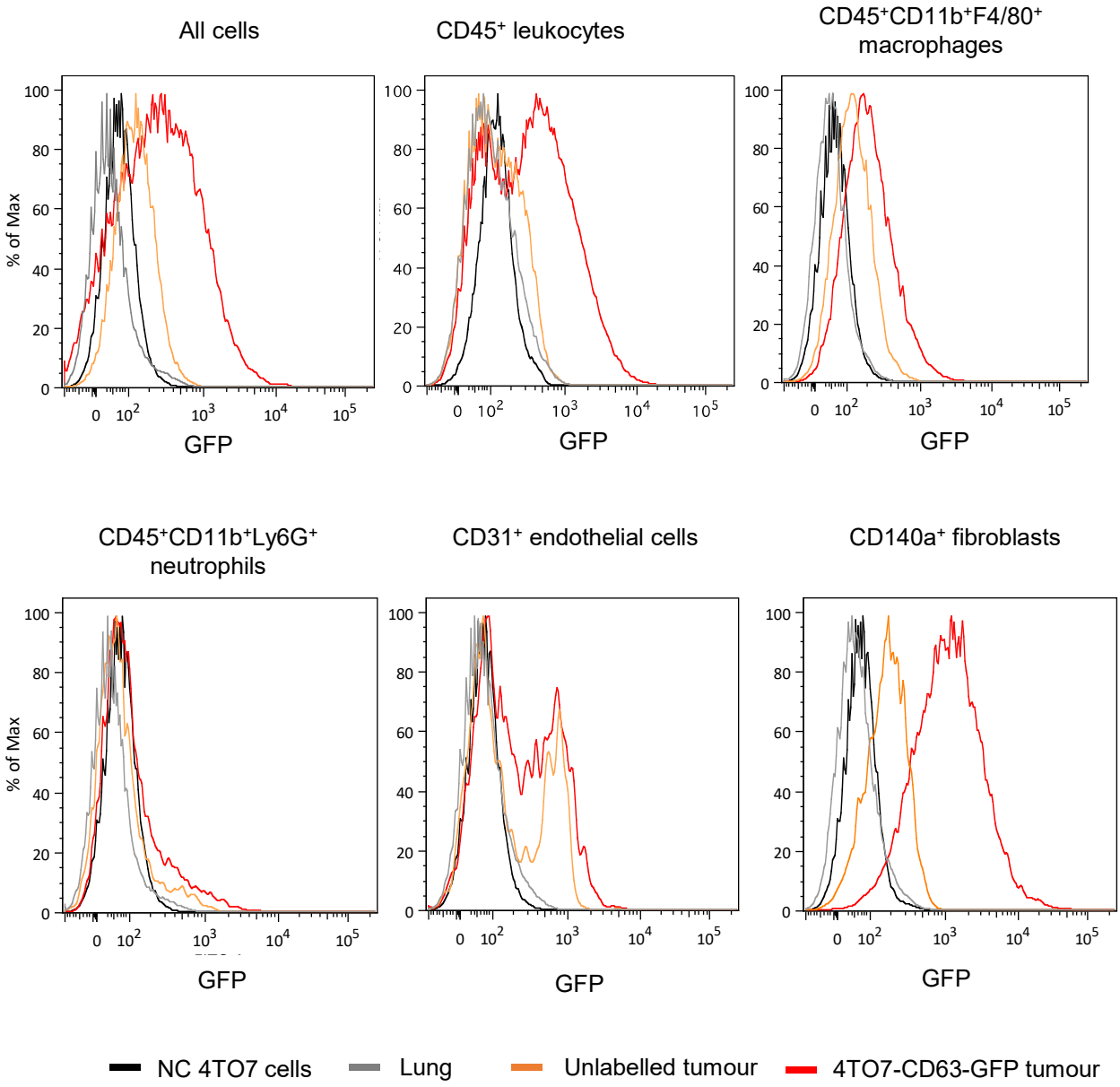
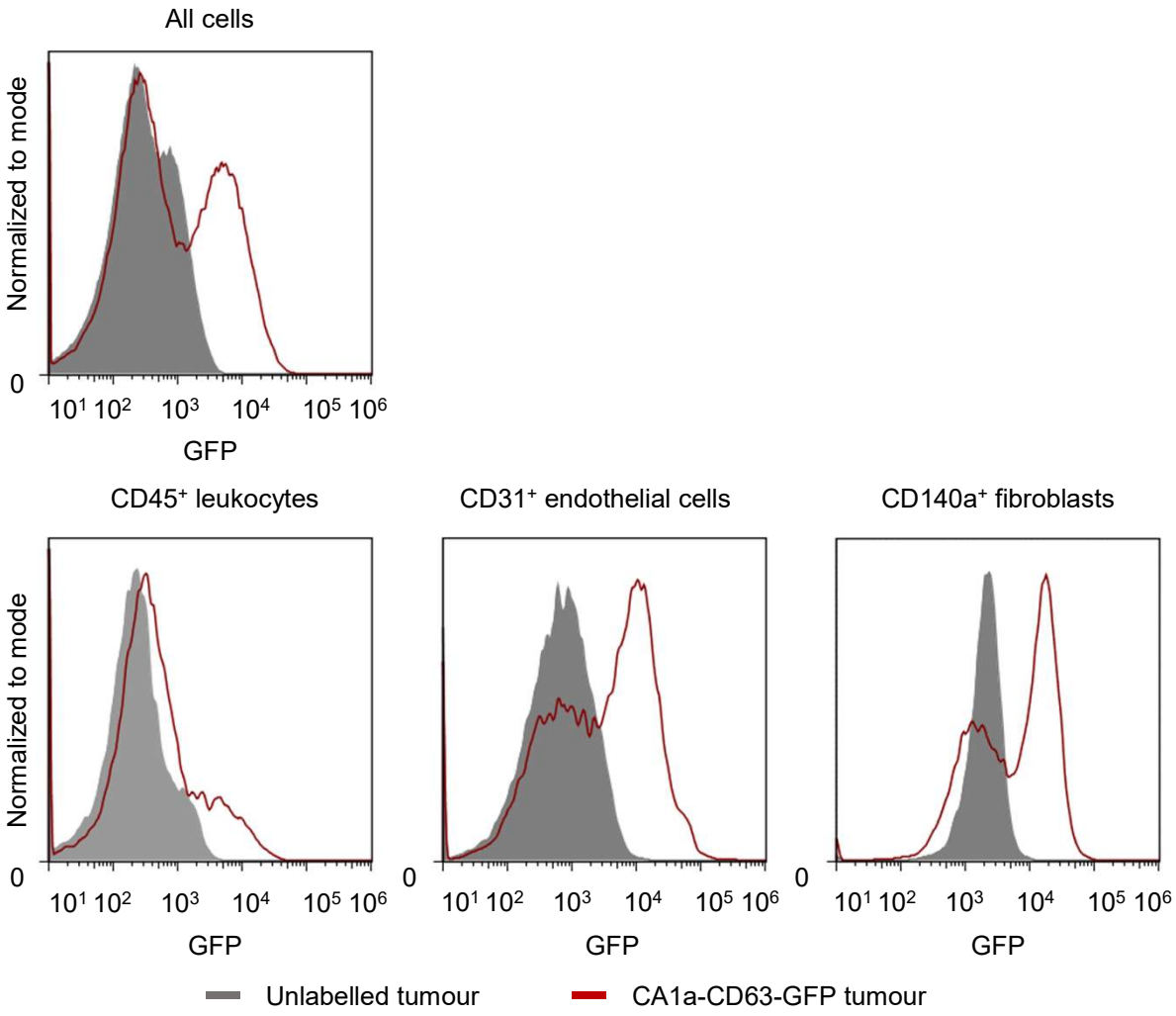


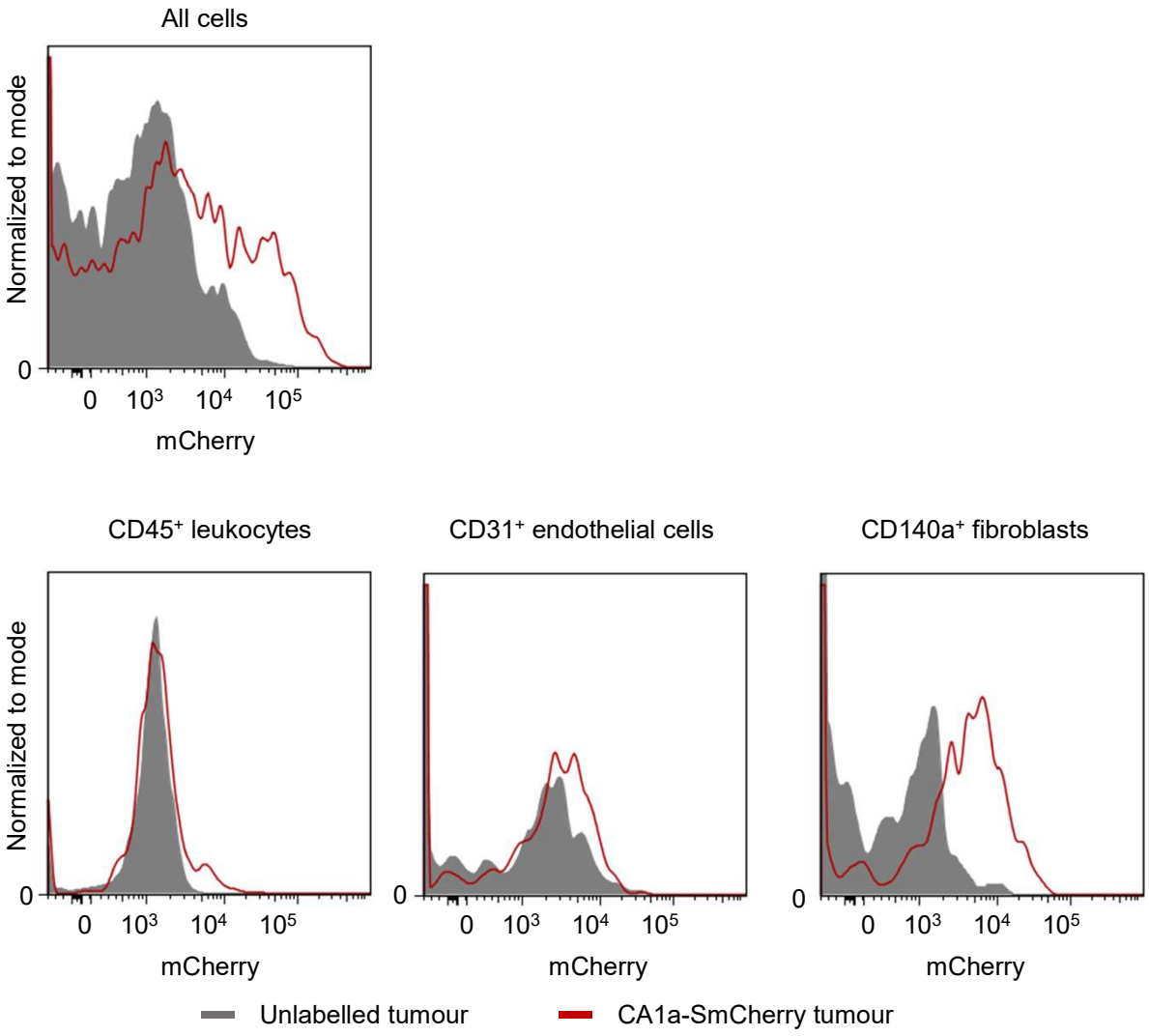
Supplementary Figure 1. Labelling EVs from breast cancer cell lines with fluorescence. **(a)** Schema of CD63 reporter construct: CD63 is expressed as a fusion gene with GFP driven by a CAG promoter. **(b)** FACS analysis of GFP in breast cancer 4TO7, 4T1, and CA1a cells transduced with lentivirus expressing CD63-GFP fusion gene. **(c)** Schema of surface mCherry reporter construct: mCherry was expressed with a transmembrane (TM) domain driven by a MSCV promoter. **(d)** FACS analysis of mCherry in breast cancer CA1a cells transduced with lentivirus expressing TM-mCherry gene.



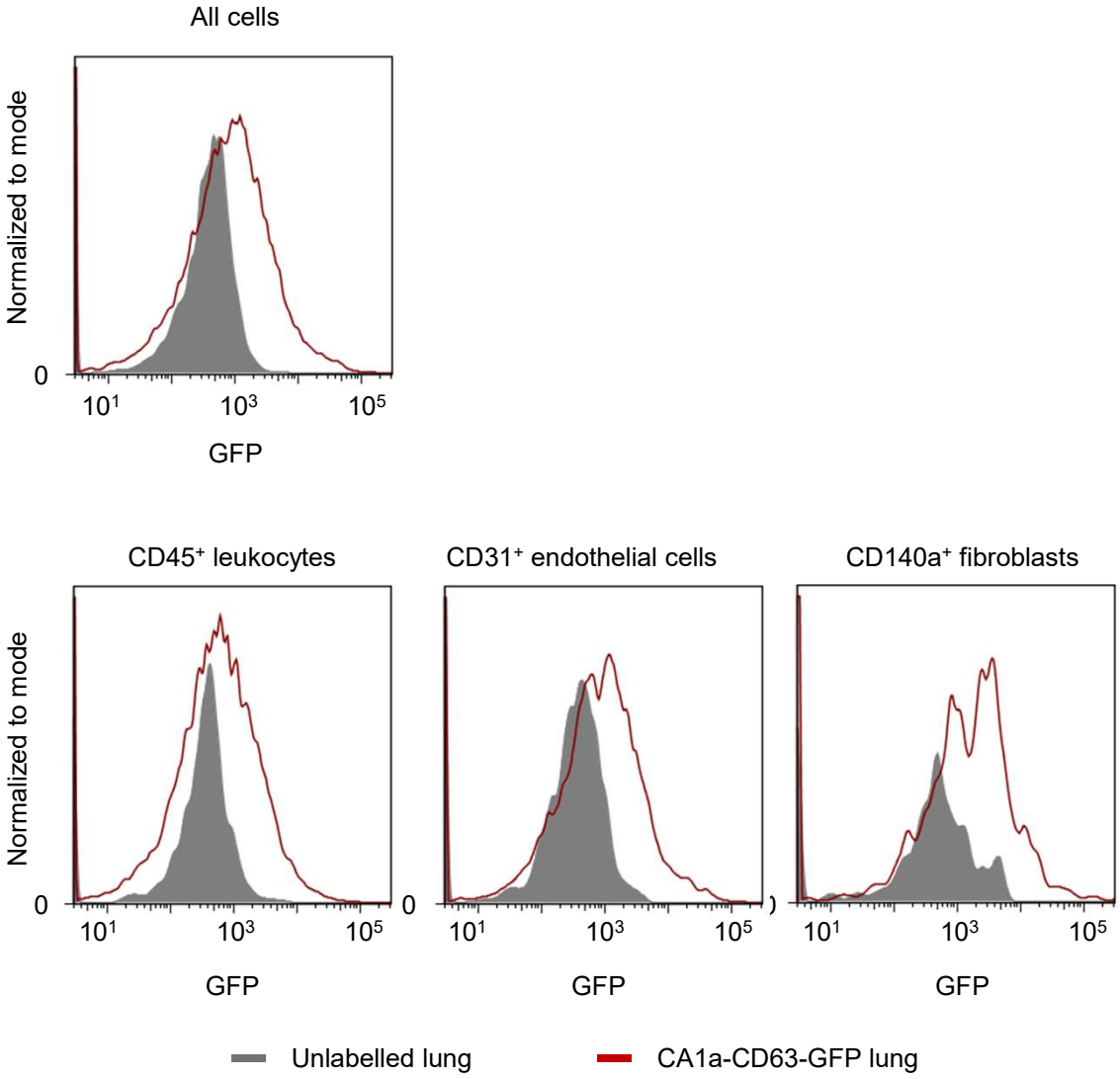
Supplementary Figure 2. FACS analysis of GFP in mouse mammary 4TO7 tumours. 4TO7 cells expressing CD63-GFP and unlabelled 4TO7 cells were implanted in the MFPs of SCID mice. After 2 weeks, cells were dissociated from the tumours and the lungs and analyzed by FACS. The histograms show the GFP intensity in each population of cells dissociated from the lung, the unlabelled tumour and CD63-GFP tumour of the same mouse compared to negative control 4TO7 cells (NC).



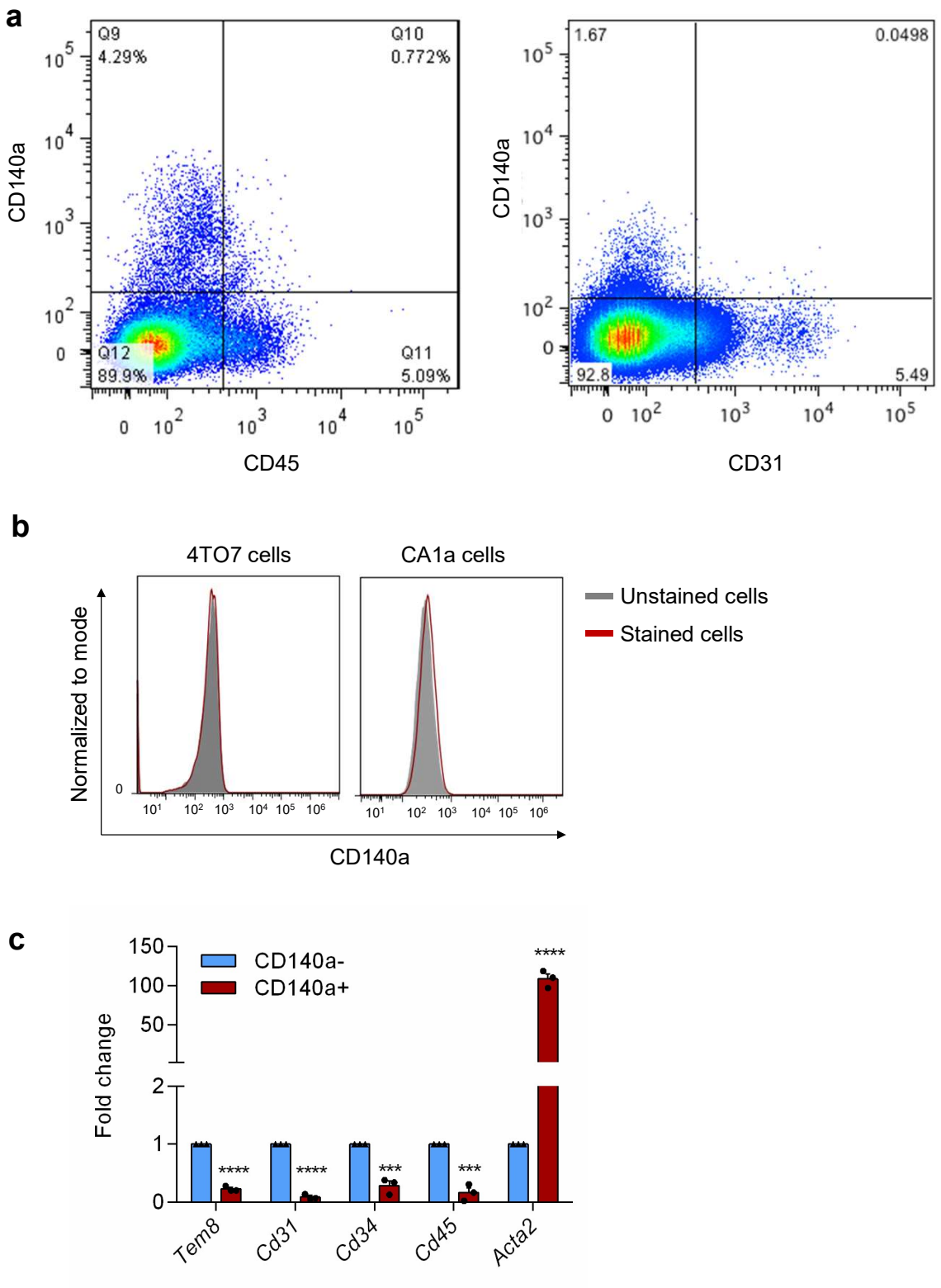
Supplementary Figure 3. FACS analysis of GFP in human mammary CA1a MFP tumours. CA1a cells expressing CD63-GFP and unlabelled CA1a cells were implanted in the MFPs of NSG mice. When the tumours reached 15 mm in diameter (4 weeks), cells were dissociated from the tumours and analyzed by FACS for GFP signals in different lineages of cells including leukocytes (CD45 positive), endothelial cells (CD31 positive), and fibroblasts (CD140a positive).



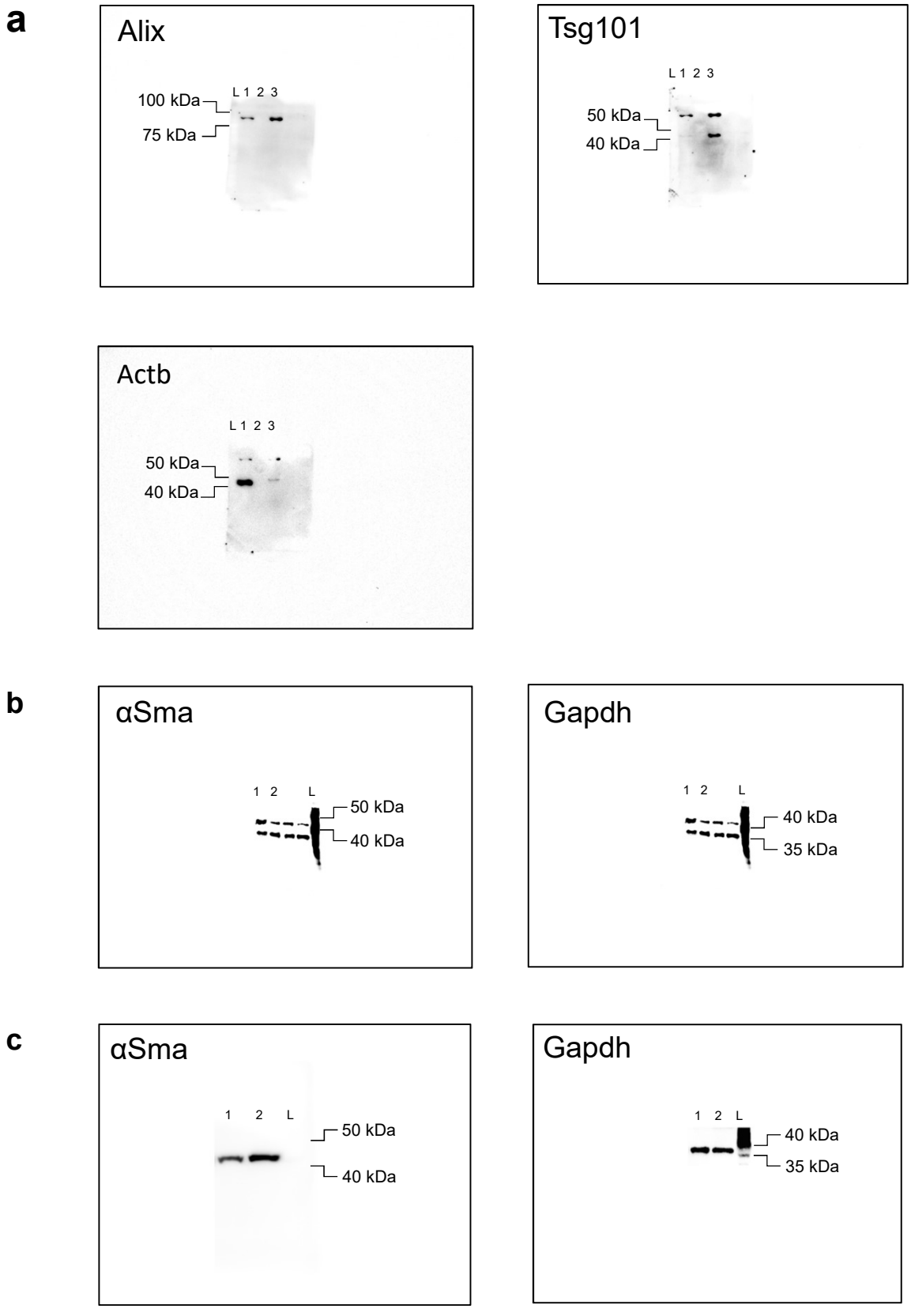
Supplementary Figure 4. FACS analysis of mCherry in human mammary CA1a MFP tumours. CA1a cells expressing surface mCherry and unlabelled CA1a cells were implanted in the MFPs of NSG mice. When the tumours reached 15 mm in diameter (4 weeks), cells were dissociated from the tumours and analyzed by FACS for mCherry signals in different lineages of cells including leukocytes (CD45 positive), endothelial cells (CD31 positive), and fibroblasts (CD140a positive).



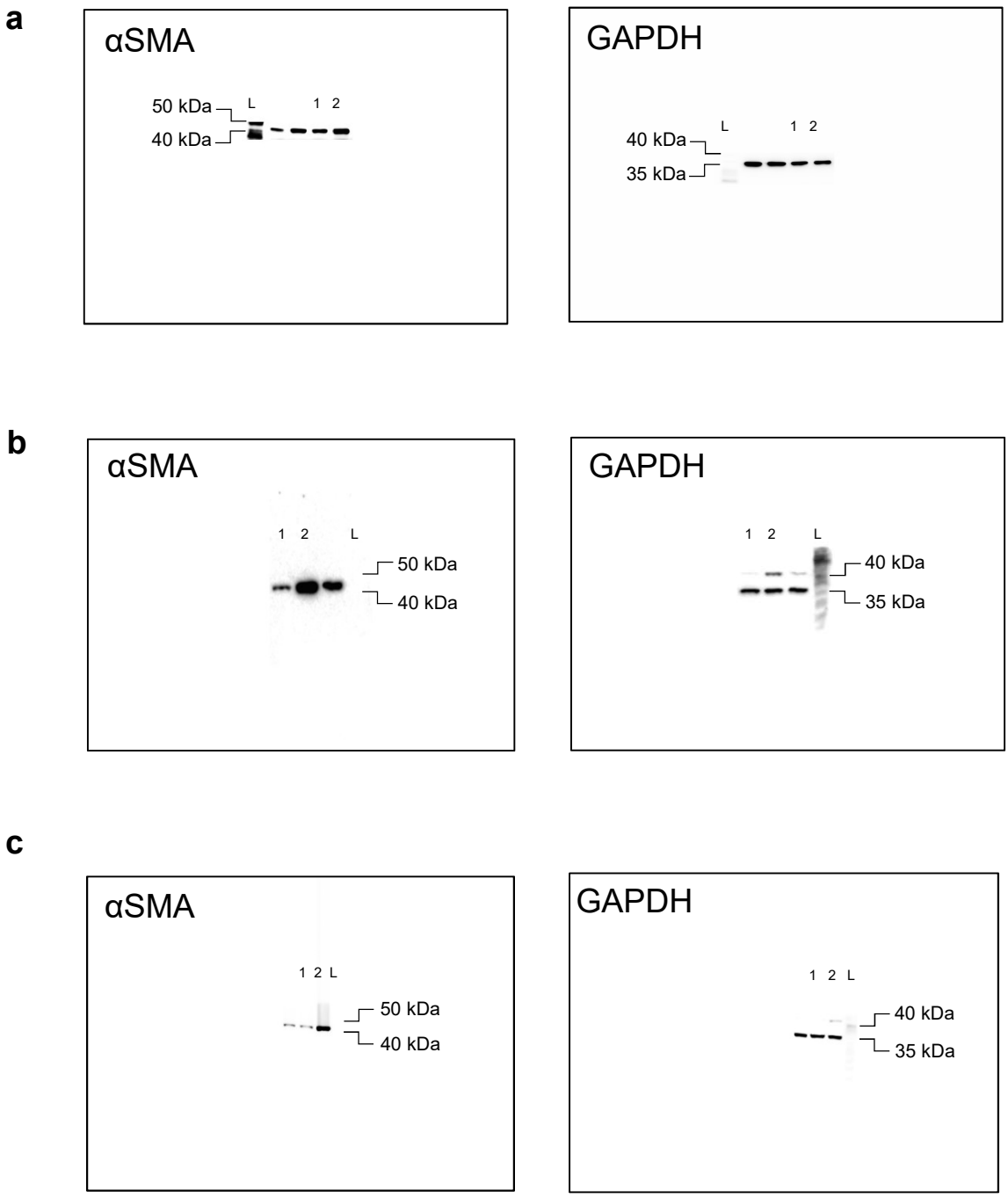
Supplementary Figure 5. FACS analysis of GFP in the lungs with human breast cancer metastasis. CA1a cells expressing CD63-GFP and unlabelled CA1a cells were injected in the tail vein of NSG mice. After 6 weeks, cells were dissociated from the tumours and analyzed by FACS for GFP signals in different lineages of cells including leukocytes (CD45 positive), endothelial cells (CD31 positive), and fibroblasts (CD140a positive).



Supplementary Figure 6. FACS analysis of CD140+ fibroblasts. (a) Staining of CD140a versus CD45 or CD31 of cells in 4TO7 mammary tumours in BALB/c mice. **(b)** Staining of CD140a in 4TO7 or CA1a cells in culture. **(c)** qPCR analysis of endothelial *(Tem8, Cd31, Cd34)*, leukocyte (*Cd45*) and fibroblast (*Acta2*) markers in sorted CD140a- and CD140a+ cells from mammary CA1a tumours (n = 3 replicates) in NSG mice. Bar graphs represent mean ± SEM. *** P < 0.001, and **** P < 0.0001 determined by Student's T-test.



Supplementary Figure 7. Full image of Western blots. (a) Western blot analysis of Alix, Tsg101 and Actb in 4T1 cell lysates (lane 1), SEC fraction 16 to 22 (lane 2) and SEC fraction 7 to 11 (lane 3) from the conditioned medium of 4T1 cells. **(b)** Western blot analysis of αSma and Gapdh in mATFs untreated (lane 1) and transfected with miR-125b mimic (lane 2) for 72 hours. **(c).** Western blot analysis of αSma and Gapdh in mATFs untreated (lane 1) and transfected with *Tp53inp1* siRNA (lane 2) for 72 hours. Protein ladder (L) was loaded to determine the molecular weights.



Supplementary Figure 8. Full image of Western blots. (a) Western blot analysis of αSMA and GAPDH in hFTFs untreated (lane 1) and transfected with miR-125b mimic (lane 2) for 72 hours. **(b)** Western blot analysis of αSMA and GAPDH in hFTFs untreated (lane 1) and transfected with *TP53* siRNA (lane 2) for 72 hours. **(c)** Western blot analysis of αSMA and GAPDH in hFTFs untreated (lane 1) and transfected with *TP53INP1* siRNA (lane 2) for 72 hours. Protein ladder (L) was loaded to determine the molecular weights.

Supplementary table 1. List of primers

Genes	F/R	Mouse	Human
GAPDH	F	AGGTCGGTGTGAACGGATTTG	GGAGCGAGATCCCTCCAAAAT
	R	TGTAGACCATGTAGTTGAGGTCA	GGCTGTTGTCATACTTCTCATGG
ACTA2	F	TGATCACCATTGGAAACGAA	CTATGAGGGCTATGCCTTGCC
	R	CCCCTGACAGGACGTTGTTA	GCTCAGCAGTAGTAACGAAGGA
CXCL12	F	GCTCTGCATCAGTGACGGTA	ATTCTCAACACTCCAAACTGTGC
	R	TAATTTCGGGTCAATGCACA	ACTTTAGCTTCGGGTCAATGC
PLAUR	F	CGCCACAAACCTCTGCAAC	TGTAAGACCAACGGGGATTGC
	R	CTCTGTAGGATAGCGGCATTG	AGCCAGTCCGATAGCTCAGG
CAV1	F	GGGAACAGGGCAACATCTAC	GCGACCCTAAACACCTCAAC
	R	TCCCTTCTGGTTCTGCAATC	ATGCCGTCAAAACTGTGTGTC
FGF2	F	AGCGGCTCTACTGCAAGAAC	AGTGTGTGCTAACCGTTACCT
	R	GCCGTCCATCTTCCTTCATA	ACTGCCCAGTTCGTTTCAGTG
MMP2	F	GGACAAGTGGTCCGCGTAAA	CCCACTGCGGTTTTCTCGAAT
	R	CCGACCGTTGAACAGGAAGG	CAAAGGGGTATCCATCGCCAT
MMP3	F	TGGAGATGCTCACTTTGACG	CGGTTCCGCCTGTCTCAAG
	R	ATGGAAACGGGACAAGTCTG	CGCCAAAAGTGCCTGTCTT
TFGB1	F	CTTCAATACGTCAGACATTCGGG	CTAATGGTGGAAACCCACAACG
	R	GTAACGCCAGGAATTGTTGCTA	TATCGCCAGGAATTGTTGCTG
HGF1	F	TAGGAGCCACAAGGATCTGG	TTTGTCAGCGCTGGGATCAT
	R	ACATGAAGCAGGAGGAGGTG	CAGCCTCTGTCACTCACCAG
P53	F	GTCACGCTTCTCCGAAGACT	GGAAACATTTTCAGACCTATGGA
	R	ATCCGACTGTGACTCCTCCA	ATTCTGGGAGCTTCATCTGG
BAK-1	F	CTGGACAAGGACCAGGTCCC	TGGTCACCTTACCTCTGCAA
	R	TAGCTTCGAAAGACCTCCTCTG	TCATAGCGTCGGTTGATGTC
TP53INP1	F	AGGCGAGTTGTGGAAATGAT	CCACCCGTGGGACTGATGAAT
	R	GTGAATGTGCTTCCCCATTT	GAGCAGCAAGAGCTGCAACATA
PPP1CA	F	AACCTGGACTCCATCATCG	
	R	ACAGACCACGGATCTCGTTC	
PPP2CA	F	CTCTCACTGCCTTGGTGGAT	
	R	TCGGATGTGATCCAGTGTGT	
PRKRA	F	GCCCACTTTCACCTTCAGAG	
	R	GTGCTTCGCCAGCTTCTTAC	
CD45	F	ATGGTCCTCTGAATAAAGCCCA	
	R	TCAGCACTATTGGTAGGCTCC	
CD31	F	AGGCTTGCATAGAGCTCCAG	
	R	TTCTTGGTTTCCAGCTATGG	
CD34	F	GAAGACCCTTATTACACGGA	
	R	GCTGAATGGCCGTTTCT	

TEM8	F	CCGGAGCAGGAATATGAATT	
	R	GACCCACAAGGCATCGA	
pri-miR-125b	F	TCTCAAGAAAGAATGAAGGAATCG	
	R	AGCGATGCAAAGGCACGACCCG	