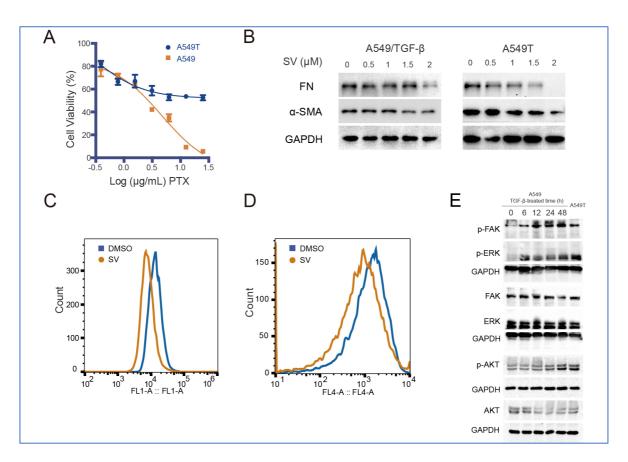
## Targeting Lipid Metabolism to Overcome EMT-Associated Drug

### Resistance Via Integrin $\beta$ 3/FAK Pathway and Tumor-Associated

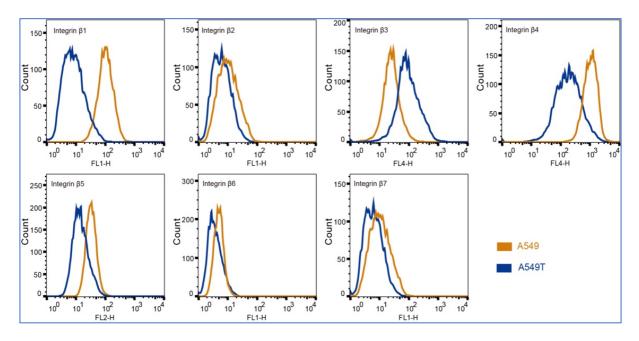
## Macrophage Repolarization Using Legumain-Activatable Delivery

Hongyue Jin <sup>1, 2</sup>, Yang He <sup>1, 2</sup>, Pengfei Zhao <sup>1</sup>, Ying Hu <sup>3, \*</sup>, Jin Tao <sup>3</sup>, Jiang Chen <sup>4</sup>, Yongzhuo Huang <sup>1, 2, \*</sup>



#### **Supplementary Figures**

**Figure S1** (A)\_Cell viability in A549T and A549 cells with PTX treatment. (B) Western blot assay of the mesenchymal markers. (C) Flow cytometry analysis of CTB-488-labeled lipid rafts in A549T cells. (D) Downregulation of integrin  $\beta$ 3 in A549T cells by SV treatment. (E) The phosphorylated FAK/ERK was up-regulated in the TGF- $\beta$ -induced, mesenchymal-type A549 cells; the right lane was the A549T cells with innate EMT nature, showing the activation of FAK/ERK, too.



**Figure S2** Flow cytometry analysis of integrins in A549 and A549T cells. The EMT-type A549T was characterized by the up-regulation of Integrin  $\beta$ 3 expression. Other integrin variants in A549T cells were much lower than those in the A549 cells.

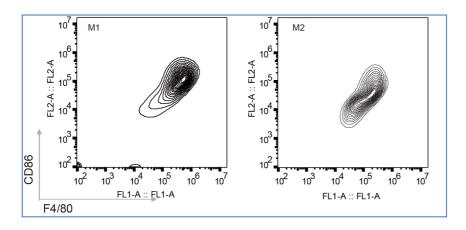
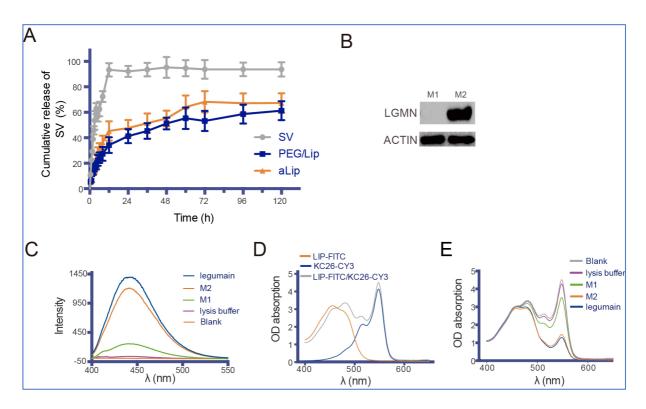
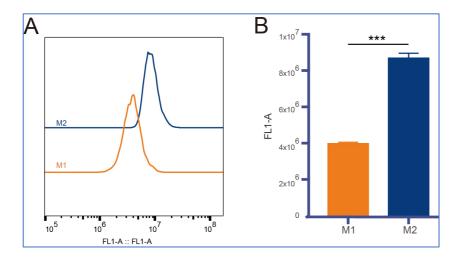


Figure S3 Flow cytometry analysis of BMDM-induced M1 $\Phi$  and M2 $\Phi$ .

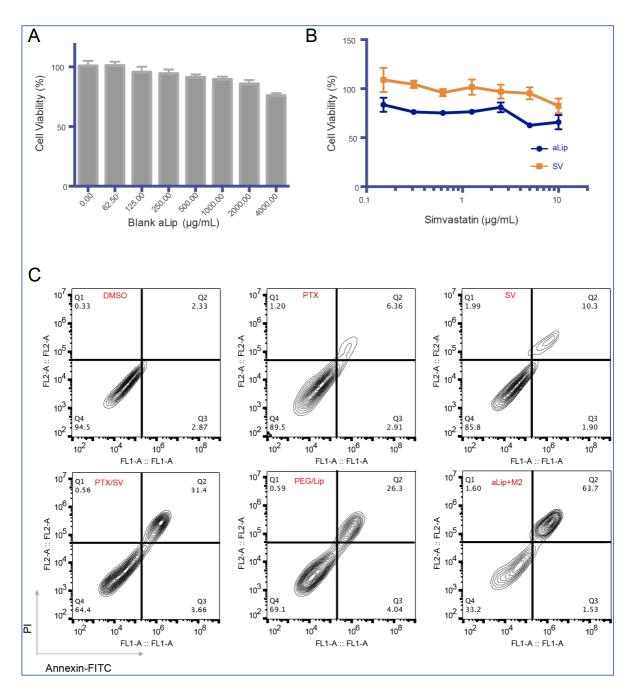


**Figure S4** (A) In vitro release of SV. (B) Legumain expression in M1Φ and M2Φ. (C) Legumain activity in M1Φ and M2Φ was measured by the AAN-AMC probe. (D) The aLip dual labeled with DSPE-PEG-FITC and DSPE-PEG-KC26-CY3 displays two characteristic absorption peaks of FITC and Cy3. (E) After treatment with the M2Φ lysates, the absorbance spectrum shows the intensity of Cy3 reduced, due to the cleavage of the linker KC26 and the consequent detachment of Cy3, but FITC spectra remained the same due to the non-cleavable DSPE-PEG-FITC.

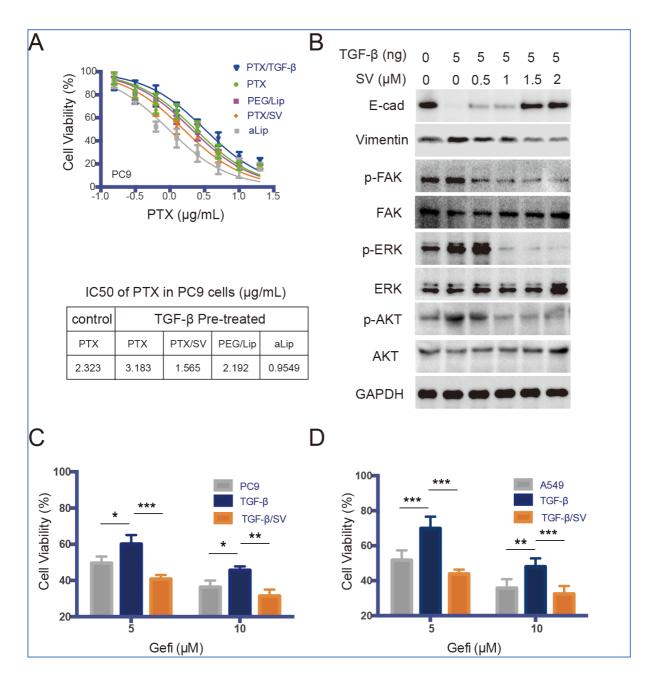


**Figure S5** Uptake of aLip in the BMDM-induced M1 $\Phi$  and M2 $\Phi$ . (A) Flow cytometry analysis of M1 $\Phi$  and M2 $\Phi$ . (B) Quantitative analysis of FACS results.

Supporting Information



**Figure S6** (A) The cytotoxicity of the blank aLip in M2 $\Phi$ . (B) The cytotoxicity of free SV and the drugloaded aLip in in M2 $\Phi$ . (C) Cell apoptosis assay of free drugs and aLip.



**Figure S7** The antitumor efficacy in PC9 cells and the mechanism study. (A) The drug resistance was developed in the PC9 cells treated with TGF- $\beta$ . (B) EMT was induced by exposure to TGF- $\beta$ . However, SV treatment can reverse EMT and repolarize the cells back to epithelial type from the mesenchymal, as characterized by the increased E-cad and reduced vimentin. Meanwhile, the TGF- $\beta$ -induced FAK/ERK/AKT phosphorylation was suppressed by SV treatment. The TGF- $\beta$ -induced mesenchymal PC9 (C) and A549 (D) showed drug resistance to gefitinib but was resensitized by SV.

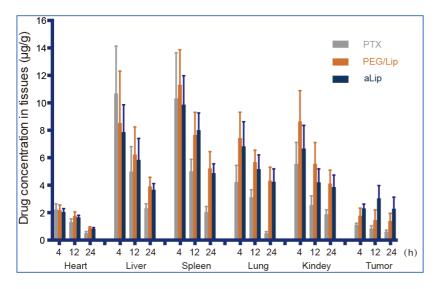
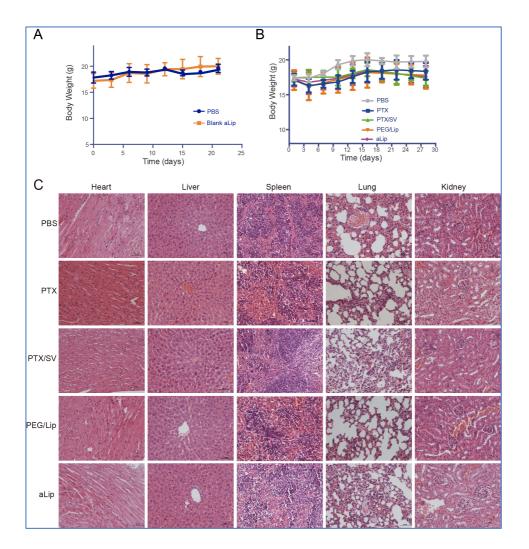
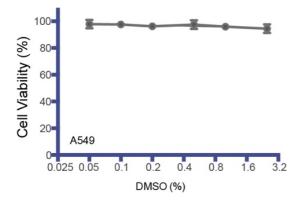


Figure S8 Biodistribution study of the aLip by determining PTX concentration.



**Figure S9** Preliminary biosafety evaluation. (A) The biocompatibility of the blank aLip. (B) Body weight curve during the treatment. (C) Histological examination of the major organs after treatment in the A549T tumor-bearing mice.



**Figure S10** The cytotoxicity test of the solvent DMSO. No cytotoxicity was found at a concentration up to 3%. A safe concentration of 0.2% DMSO was used for the cellular studies.

### **Supplementary Tables**

	A549T	A549	TGF-β induced A549
PTX (µg/mL)	8.19	2.31	5.28
PTX/SV (µg/mL)	1.82	2.10	2.01
SV (µg/mL)	7.9	11.4	9.2

Table S1 The IC  $_{50}$  values measured by MTT test.

#### Table S2 RT-PCR primers.

Name	Primer	Sequence	Size	
Mus GAPDH	Forward	5'- ATGGGTGTGAACCACGAGA -3'	229 bp	
	Reverse	5'- CAGGGATGATGTTCTGGGCA -3'	229 bp	
Mus IL-1b	Forward	5'- TCAGGCAGGCAGTATCACTC -3'	050 k -	
	Reverse	5'- AGCTCATATGGGTCCGACAG -3'	250 bp	
Mus IFN-γ	Forward	Forward 5'- CGCTACACACTGCATCTTGG -3'		
	Reverse	5'- TCCTTTTGCCAGTTCCTCCA -3'	174 bp	
Mus IL-1a	Forward	5'- TGAAGAAGAGACGGCTGAGT -3'	159 bp	
IVIUS IL-TA	Reverse	5'- CAAACTTCTGCCTGACGAGC -3'	109 ph	
Mus CCL-17	Forward	5'- AGAGTGCTGCCTGGATTA -3'	110 bp	
	Reverse	5'- GGACAGTCAGAAACACGATG -3'	no pp	
Mus Arg1	Forward 5'- ACATCAACACTCCCCTGACA -3'		157 bp	
Mus Aig i	Reverse	Reverse 5'- CGCAAGCCAATGTACACGAT -3'		
Mus CD206	Forward	5'- TTGTGGAGCAGATGGAAGGT -3'	200 bp	
Mus CD200	Reverse	5'- TCGTAGTCAGTGGTGGTTCC -3'	200 bp	
Mus CCL-22	Forward	5'- TCTGCTGCCAGGACTACAT -3'	117 bp	
Wids CCL-22	Reverse	5'- CTCGGTTCTTGACGGTTAT -3'	111.55	
Mus II-10	Forward	5'- ACCTGGTAGAAGTGATGCCC -3'	193 bp	
	Reverse	verse 5'- ACACCTTGGTCTTGGAGCTT -3'		
Mus TGF-β1	Forward	5'- AATGGTGGACCGCAACAAC -3'	213 hn	
	Reverse	5'- CCAAGGTAACGCCAGGAAT -3'	213 bp	
	Forward	5'- CGTCAGCCGATTTGCTATCT -3'	000 1	
Mus TNF-α	Reverse	5'- CGGACTCCGCAAAGTCTAAG -3'	206 bp	
	Forward	5'- ACCCGCTGTATGGAAGGAAA -3'	050 hr	
Mus ABCA1	Reverse	5'-TCTGAAGGATGTCTGCGGTT -3'	250 bp	

		A549					
		TGF-β-treated time (h)					
	0	6	12	24	48		
E-CAD/GAPDH	0.2302	0.1887	0.0702	0.0883	0.0350	0.0164	
VIMENTIN/GAPDH	0.2186	0.5834	0.2928	0.3779	0.4216	0.5744	
p-FAK/GAPDH	0.1799	0.2041	0.4851	0.5301	0.5829	0.2873	
p-ERK/GAPDH	0.1777	0.4724	0.4722	0.7363	0.6562	0.7616	
FAK/GAPDH	0.3909	0.4216	0.4371	0.4210	0.3244	0.5433	
ERK/GAPDH	1.1927	1.1037	1.1265	1.1542	1.1503	1.1619	
p-AKT/GAPDH	0.3274	0.3162	0.3673	0.4046	0.5867	0.7126	
AKT/GAPDH	0.4266	0.3960	0.2887	0.3228	0.3209	0.3126	

#### Table S3 Quantification of protein bands on Fig 1A and S1D using densitometry.

Table S4 Quantification of protein bands on Fig 1E using densitometry.

S	V (µM)	0	0.5	1	1.5	2	5
A549/TGF-β	E-CAD/GAPDH	0.2154	0.4044	0.4108	0.5042	0.6256	0.5374
	vimentin/GAPDH	5.6885	8.8112	8.5935	3.3216	2.5216	1.8908
A549T	E-CAD/GAPDH	0.0040	0.0336	0.0552	0.1462	0.2243	0.1925
	vimentin/GAPDH	0.2796	0.2510	0.1623	0.2388	0.1365	0.0901

#### Table S5 Quantification of protein bands on Fig 1H using densitometry.

SV (μM)		0	0.5	1	1.5	2
A549/TGF-β	p-FAK/GAPDH	0.4897	0.2621	0.2825	0.3559	0.1398
	p-ERK/GAPDH	0.9524	0.7923	0.7003	0.7824	0.1731
	FAK/GAPDH	0.7196	0.6567	0.9229	0.6989	0.6411
	ERK/GAPDH	0.9050	1.0342	1.2375	0.8814	1.1212
	p-AKT/GAPDH	1.2653	1.1817	0.8387	0.8252	0.8359
	AKT/GAPDH	2.3602	2.2881	2.5054	2.6453	2.3689
A549T	p-FAK/GAPDH	0.7742	0.9273	0.5137	0.3323	0.2736
	p-ERK/GAPDH	0.5531	0.9290	0.5401	0.3804	0.3122
	FAK/GAPDH	0.9443	0.8529	0.9000	1.2075	0.9897
	ERK/GAPDH	1.7087	1.1479	0.8330	1.2102	1.6117
	p-AKT/GAPDH	1.1151	0.8512	0.9377	0.6288	0.8120
	AKT/GAPDH	1.0569	1.1378	1.0588	0.8321	0.7922