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An energy-blocking nanoparticle decorated with anti-VEGF antibody to reverse chemotherapeutic drug resistance

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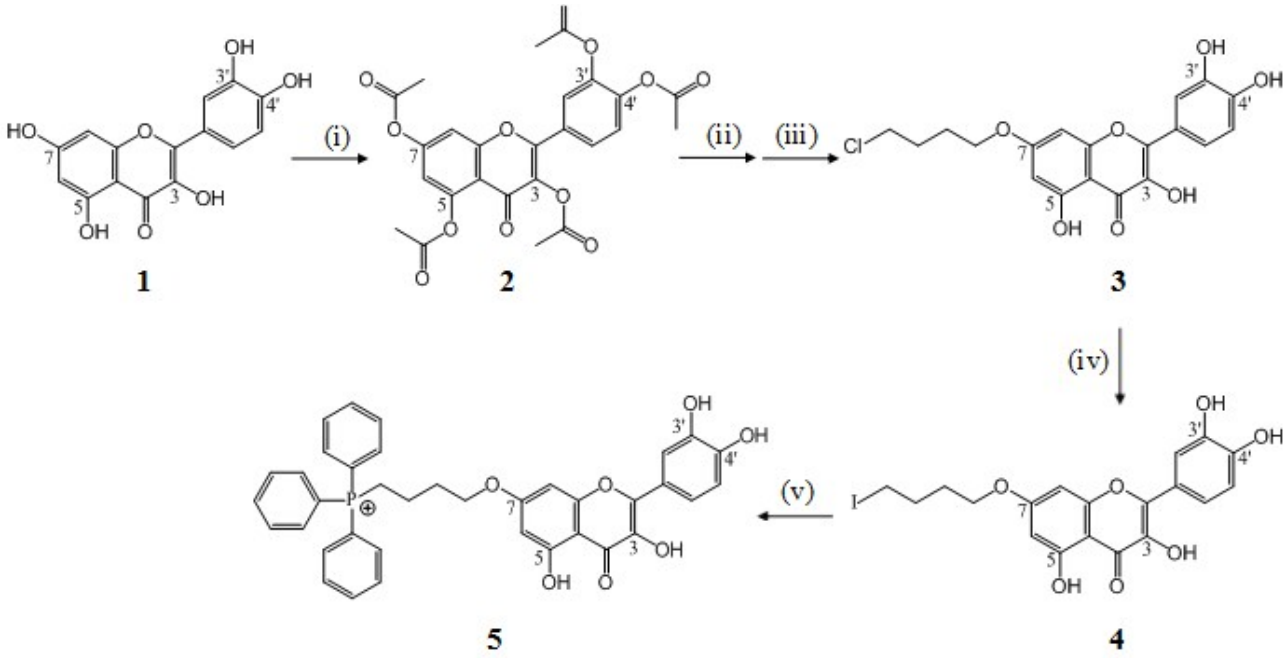


Figure S1. Synthesis route of TQ.

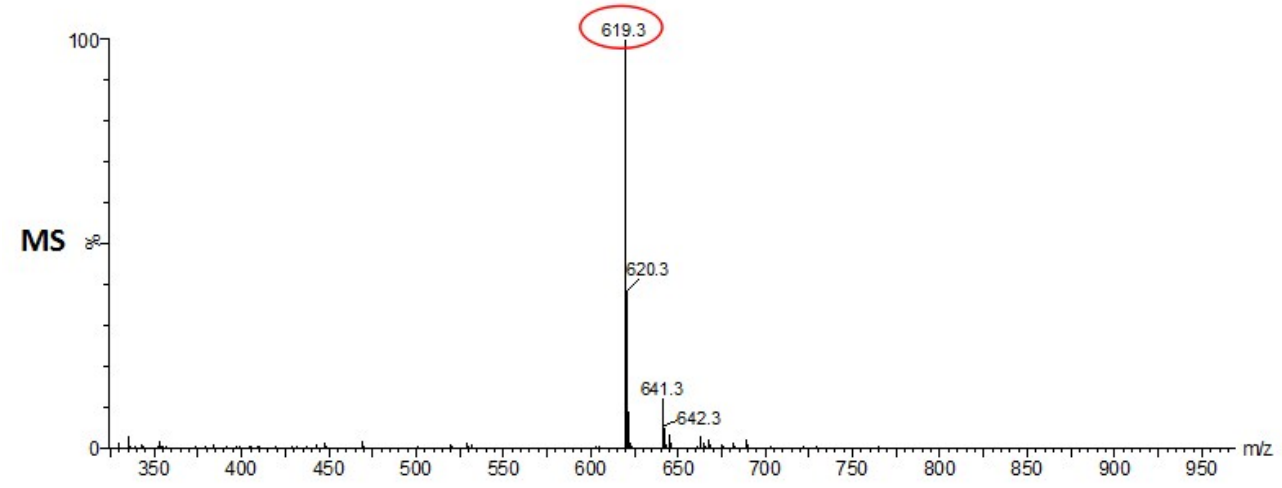


Figure S2. Mass spectrum analysis of TQ.

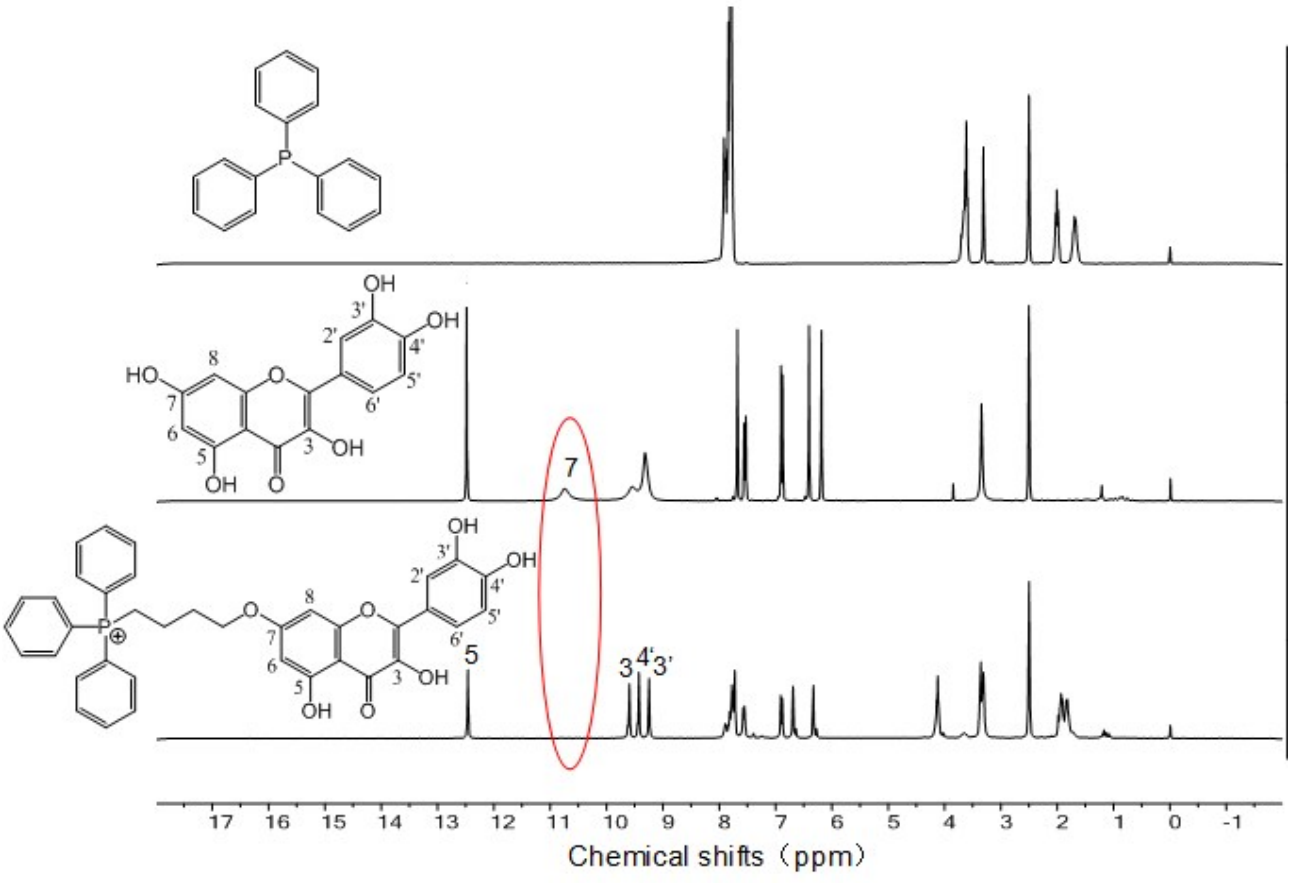


Figure S3. ^{1}H-NMR spectra of TPP, Que and TQ dissolved in DMSO-d6. ^{1}H-NMR of TQ (300 MHz, DMSO-d6): δ (ppm) = 1.58-2.13 (m, 4H, -CH_2×2), 3.96-4.32 (m, 4H, -CH_2×2), 6.35 (s, 1H, 6-H), 6.71 (s, 1H, 8-H), 6.91 (s, 1H, 5'-H), 7.49 (s, 1H, 6'-H), 7.63-7.96 (m, 16H, 15H = PPh_3, 1H = 2'-H).

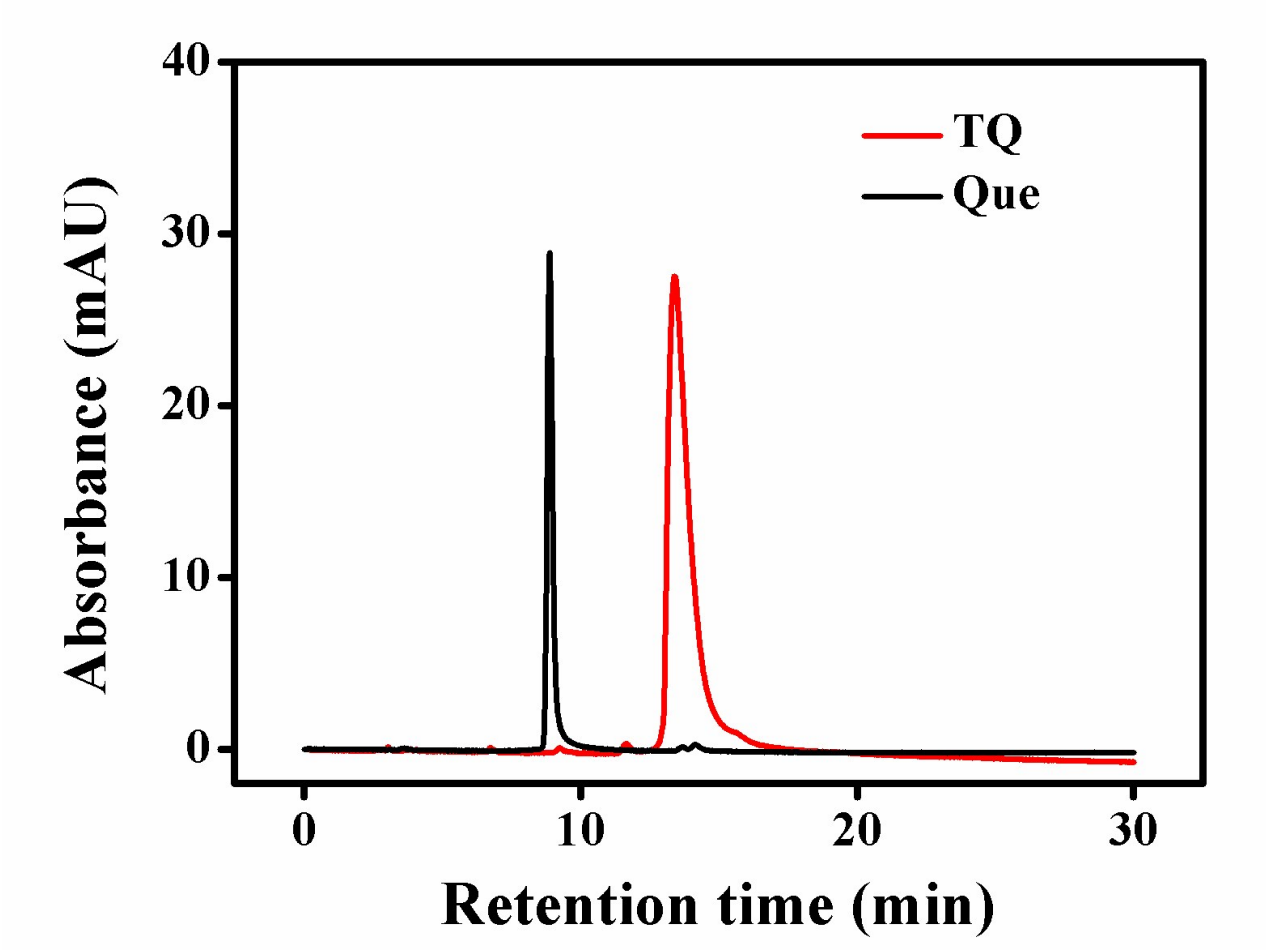


Figure S4. HPLC spectra of TQ and Que.

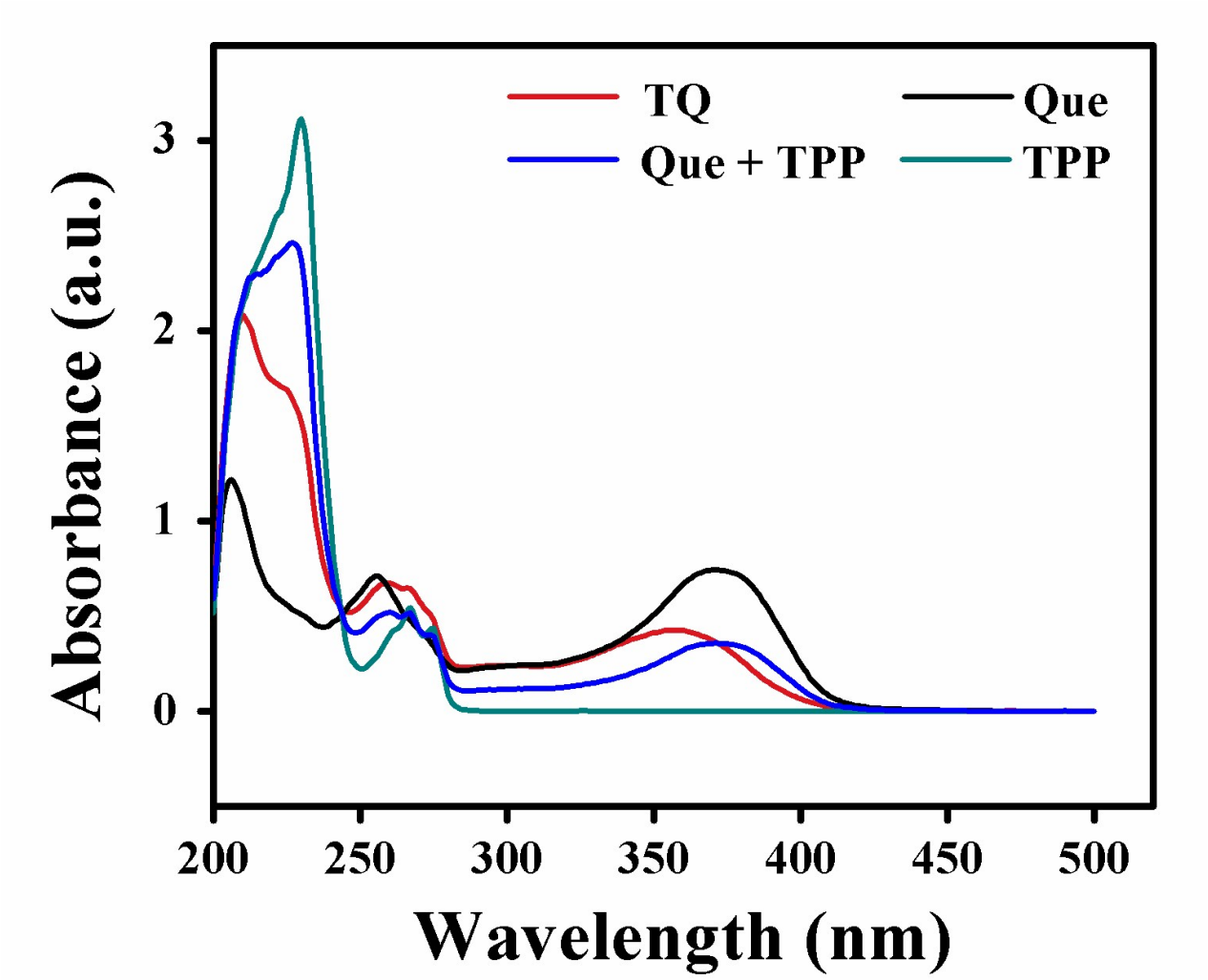


Figure S5. UV-Vis spectrum of Que, TPP, Que + TPP and TQ in DMSO.

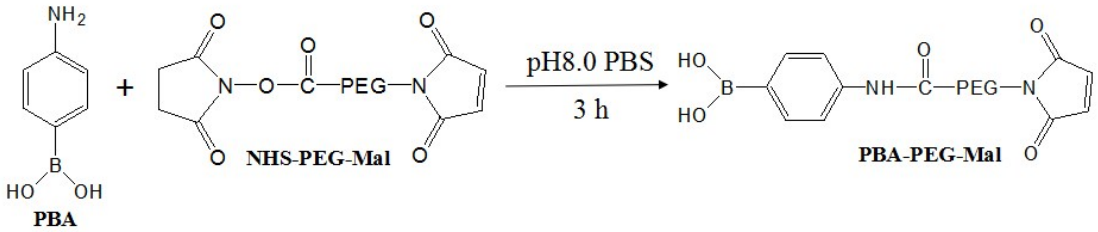


Figure S6. Synthesis route of PBA-PEG-Mal.

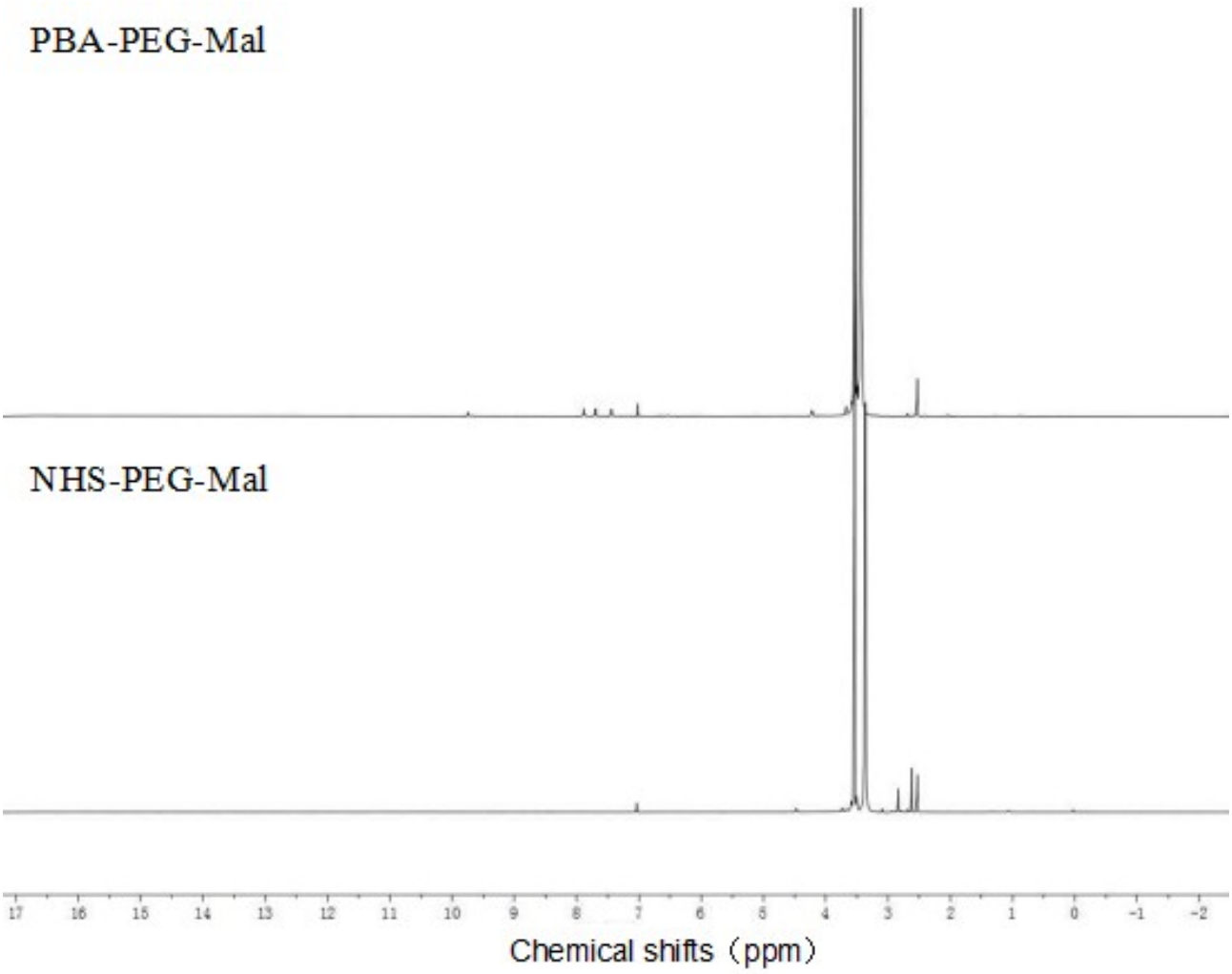


Figure S7. ^{1}H-NMR spectrum of PBA-PEG-Mal and NHS-PEG-Mal in DMSO-d6. ^{1}H-NMR spectrum of PBA-PEG-Mal (300 MHz, DMSO-d6): δ (ppm) = 9.8 (s, -NH-), δ (ppm) = 7.5-8.5 (m, 6H, -PhB$(OH)_2$), δ (ppm) = 6.9 (s, 2H, Mal), δ (ppm) = 3.4-3.6 (m,180H, -CH_2CH_2O-).

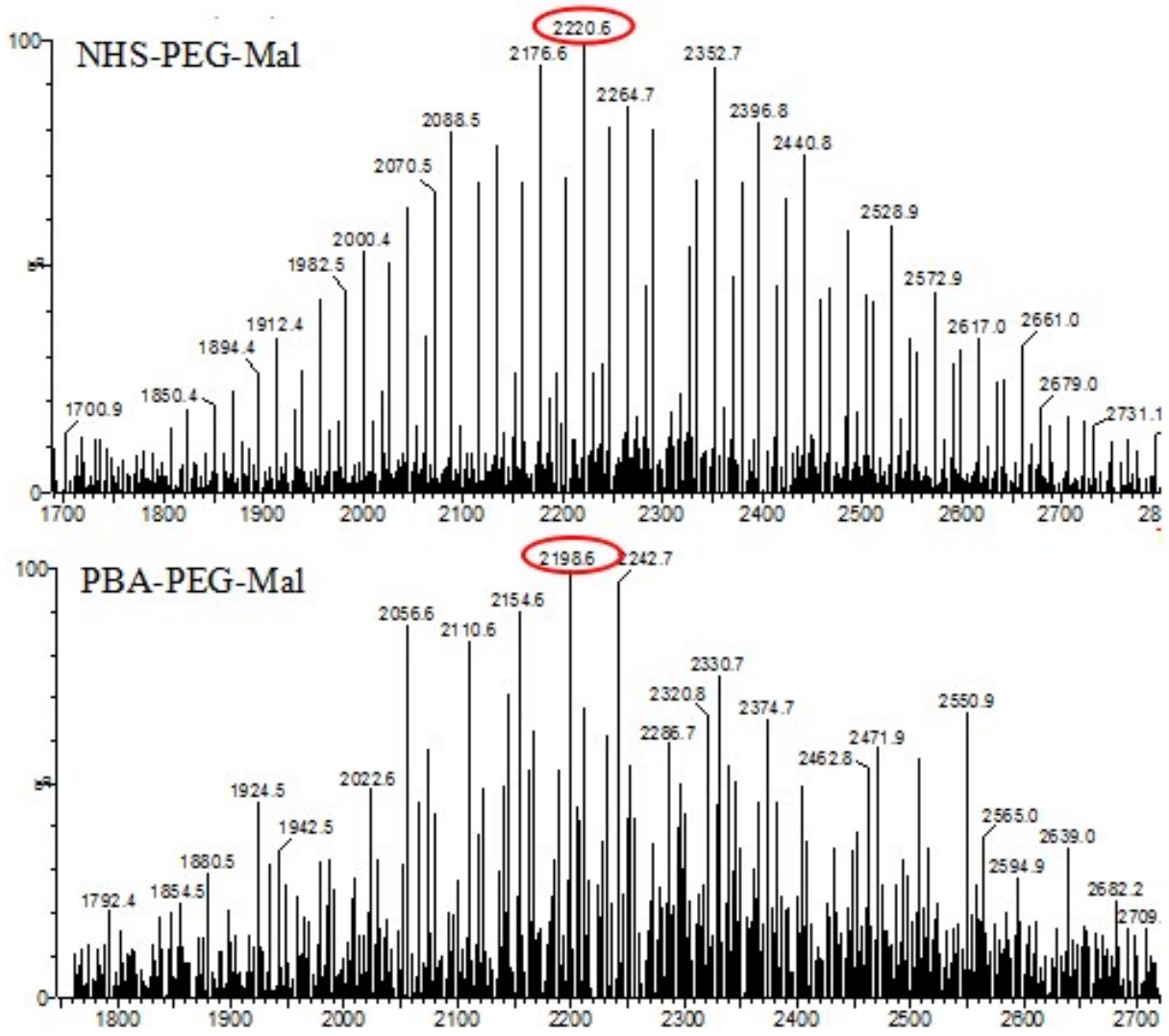


Figure S8. Mass spectrum analysis of PBA-PEG-Mal and NHS-PEG-Mal.

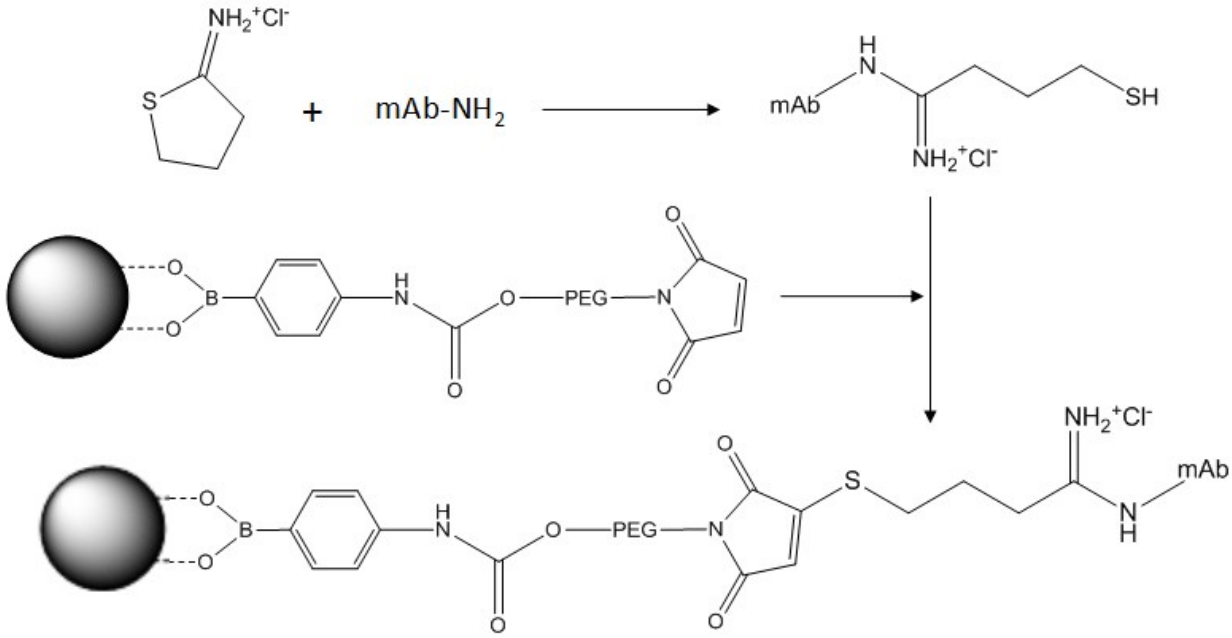


Figure S9. Synthesis scheme of anti-VEGF mAb conjugation to the surface of TQ/DOX-PEG.

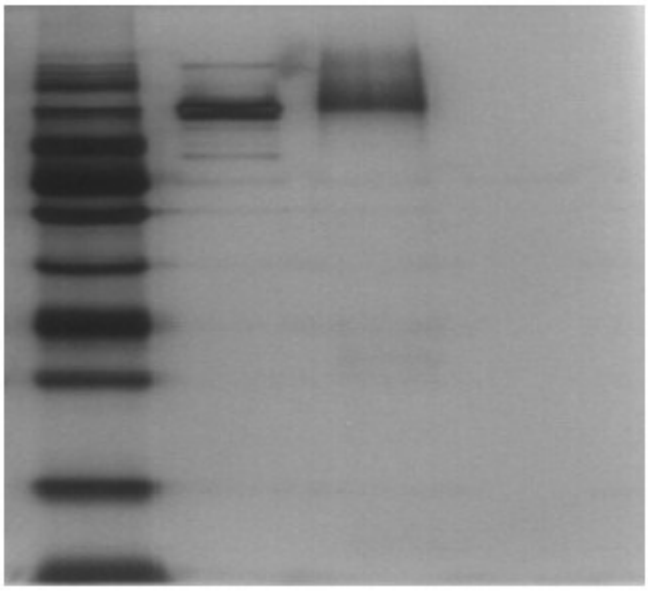
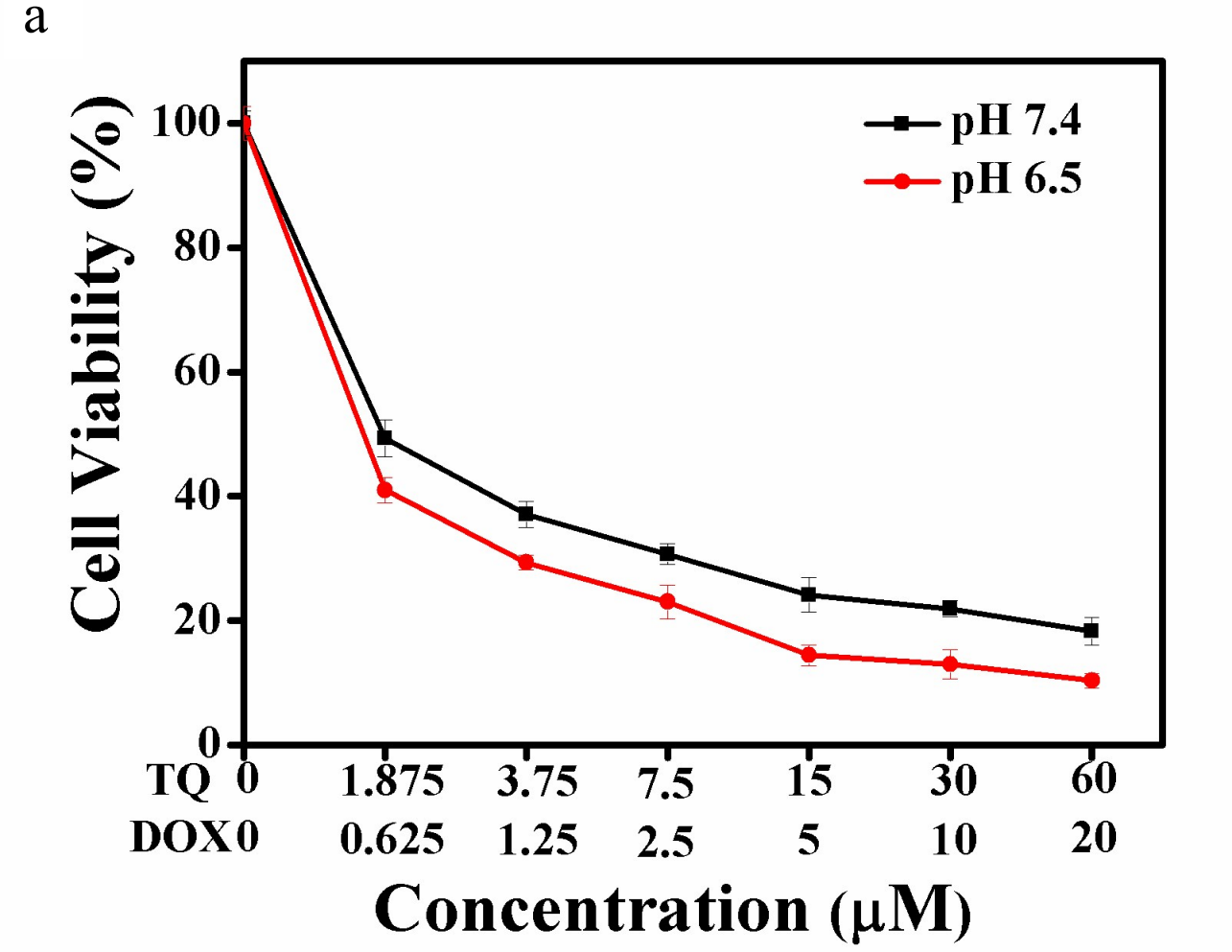


Figure S10. SDS-PAGE of anti-VEGF mAb, TQ/DOX-PEG-mAb and TQ/DOX-PEG (12%). Lane 1: protein marker; lane 2: anti-VEGF mAb; lane 3: TQ/DOX-PEG-mAb; lane 4: TQ/DOX-PEG.

a


Cell Viability (%)
100
80
60
40
20
0
pH 7.4
pH 6.5
TQ 0 1.875 3.75 7.5 15 30 60
DOX 0 0.625 1.25 2.5 5 10 20
Concentration (μM)

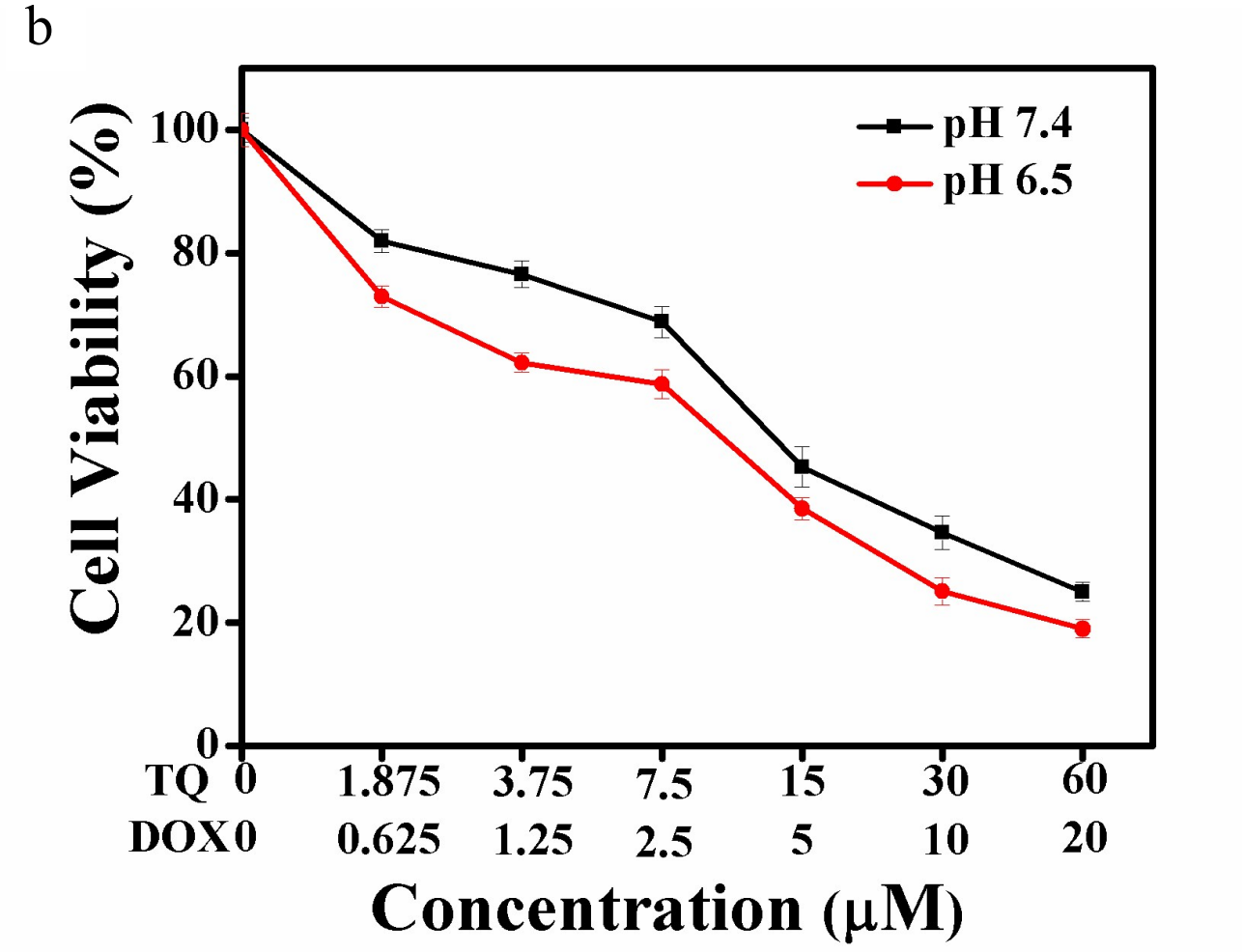


Figure S11. Cell viability of (a) MCF-7 cells and (b) MCF-7/ADR cells after 48h incubation TQ/DOX-PEG-mAb under pHs of 6.5 and 7.4.

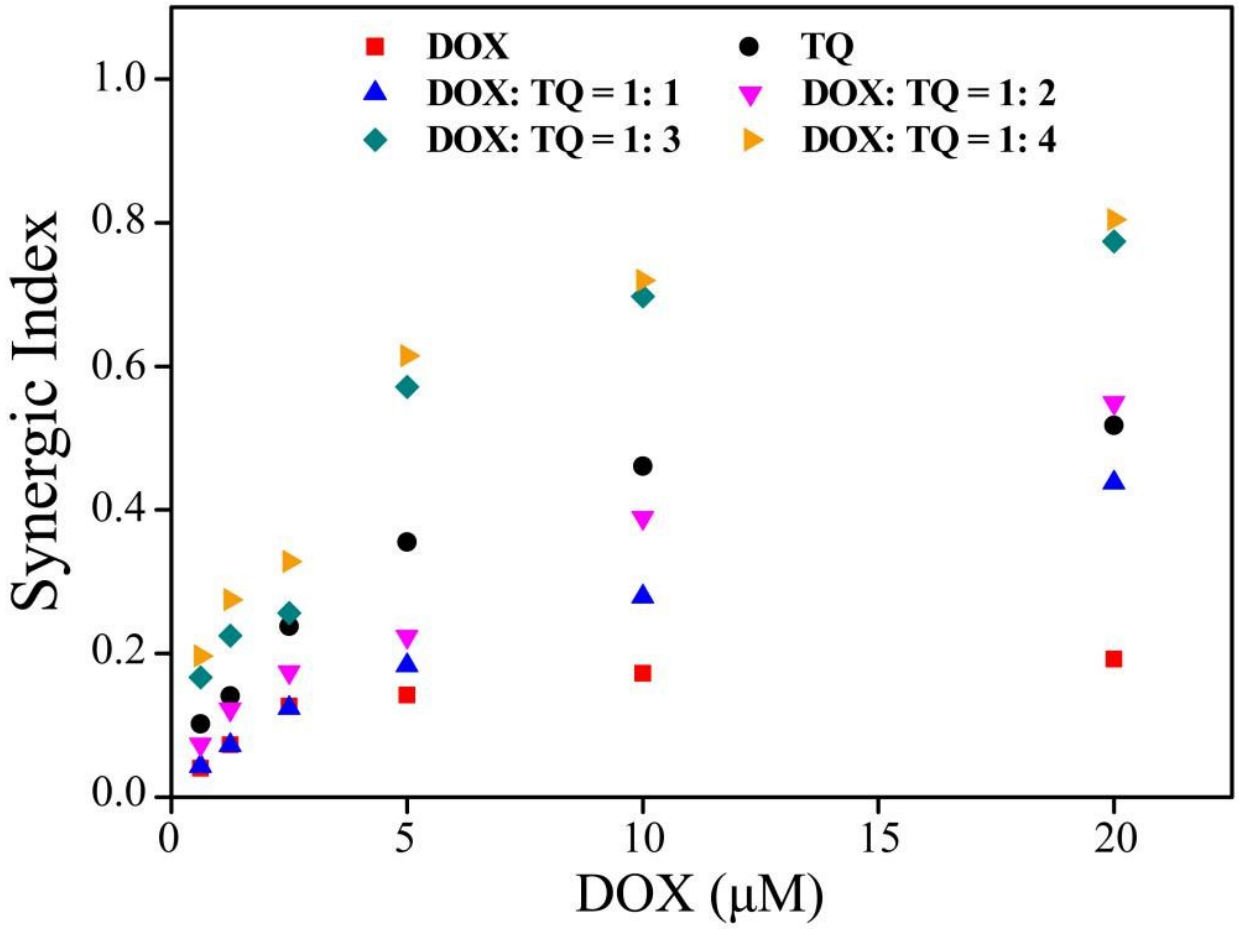


Figure S12. Synergic index (SI) of different molar ratios between TQ and DOX (1: 1, 2: 1, 3: 1 and 4: 1, respectively) was calculated by CompuSyn software. The concentration of DOX was at 0.625, 1.25, 2.5, 5, 10 and 20 μM, respectively.

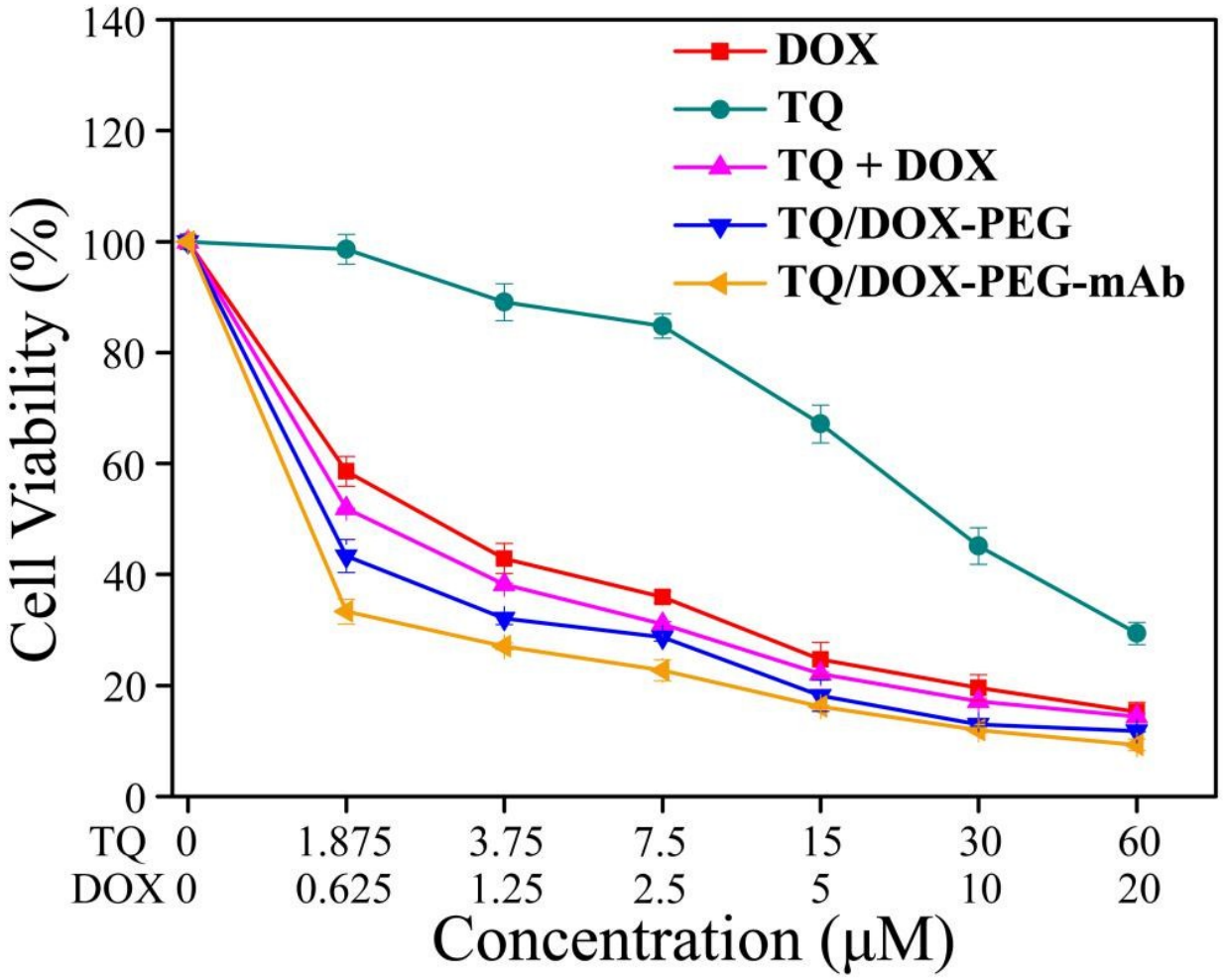


Figure S13. Cell viability of MDA-MB-231 cells after 48h incubation with DOX, TQ, TQ + DOX, TQ/DOX-PEG and TQ/DOX-PEG-mAb.

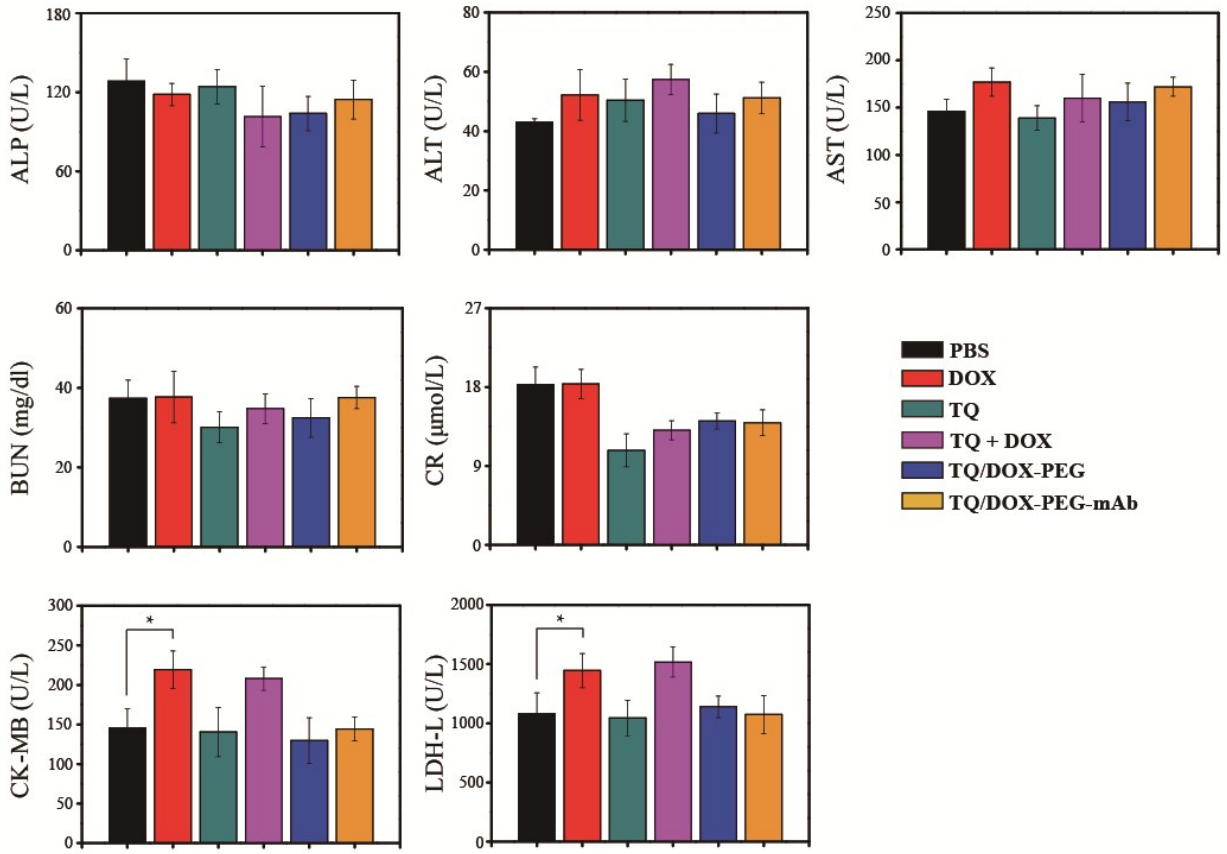


Figure S14. Blood biochemistry assessment of mice after treatment (n = 5), including liver function markers (ALP, ALT and AST), kidney function markers (BUN and CR) and heart function markers (CK-MB and LDH).

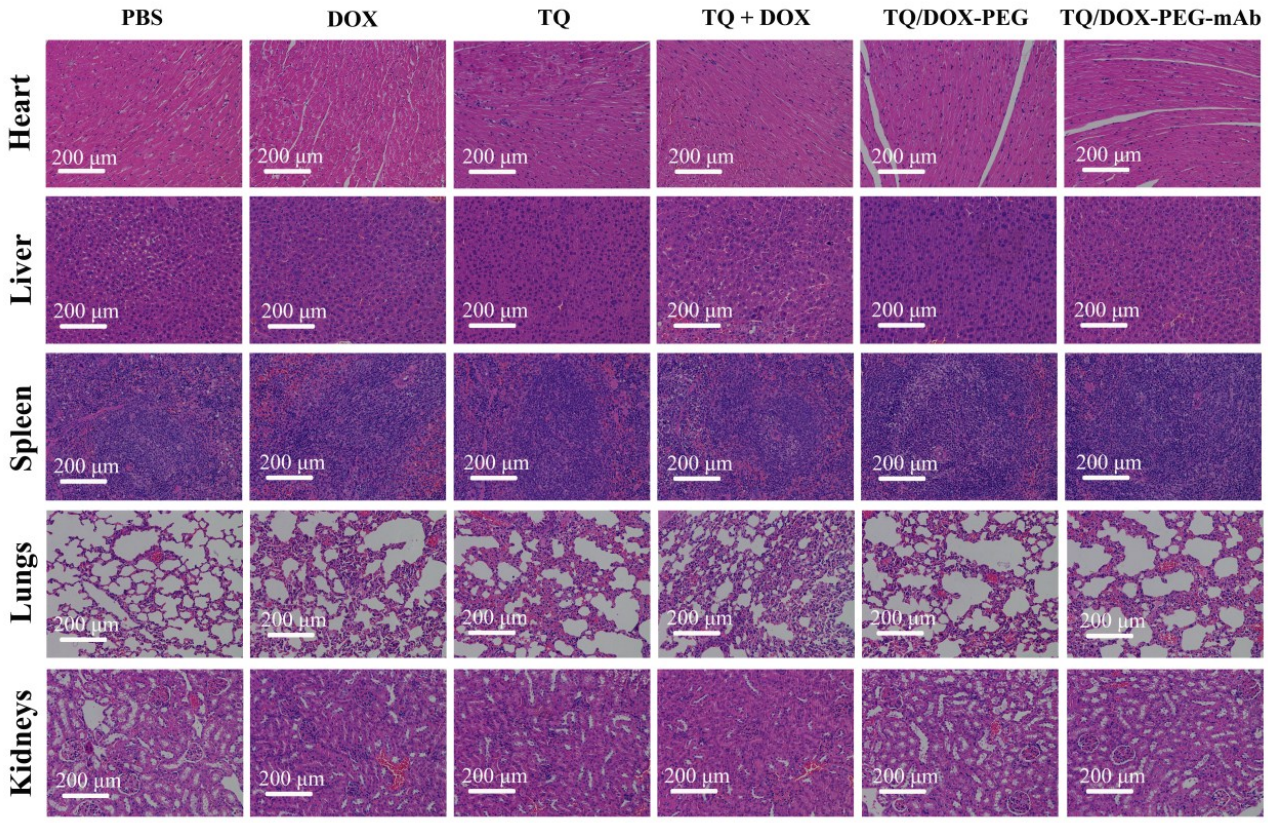


Figure S15. H&E staining of major organs after treatment with different groups (n = 5), scale bar = 200 μm.

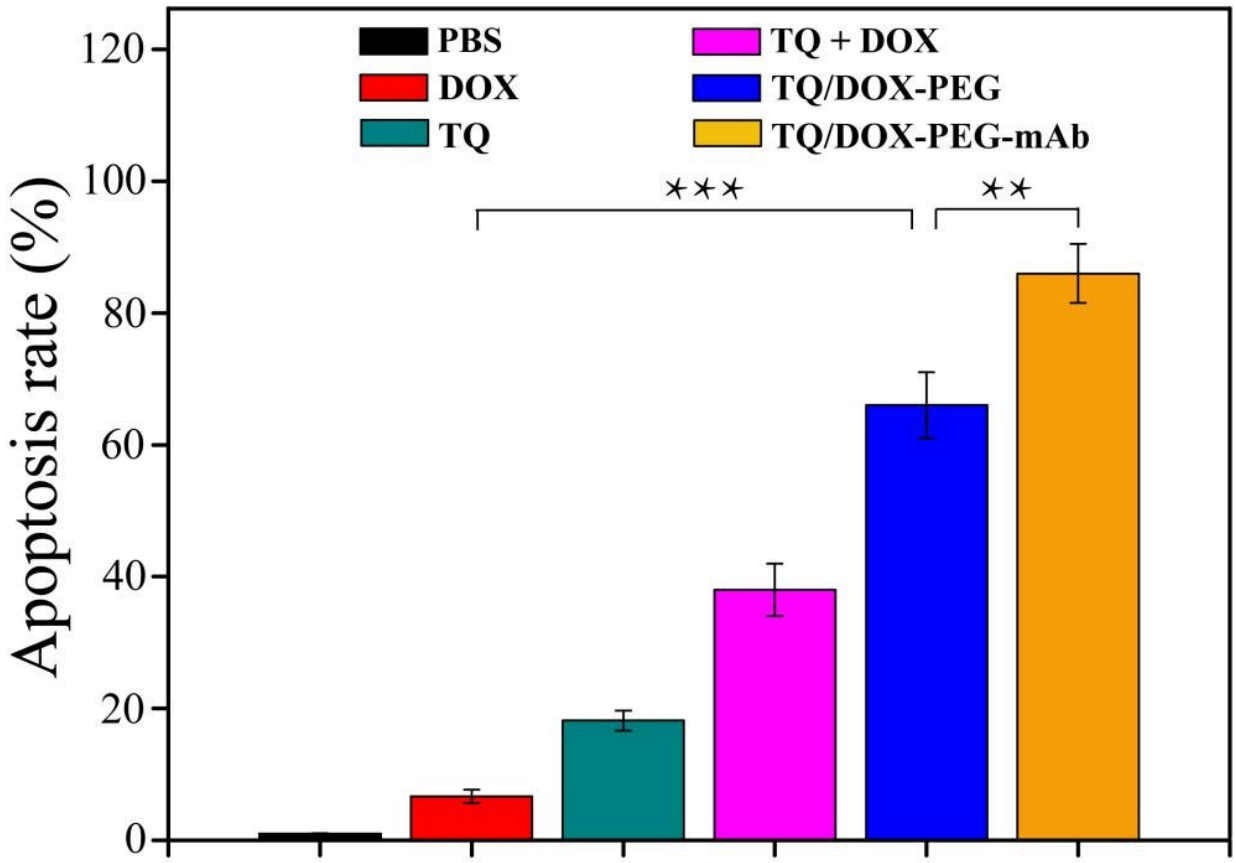


Figure S16. Quantitative analysis of TUNEL staining by ImageJ software. **p < 0.01, ***p < 0.001 were measured by One-Way ANOVA.

Table S1. The characterization of TQ/DOX-PEG and TQ/DOX-PEG-mAb.

	TQ/DOX-PEG	TQ/DOX-PEG-mAb
Particle size (nm)	89.3 ± 2.5	109.6 ± 3.3
Zeta potential (mV)	10.3 ± 0.4	1.5 ± 0.2
PDI	0.169 ± 0.024	0.182 ± 0.019

Table S2. The encapsulation efficiency of TQ and DOX in TQ/DOX-PEG-mAb.

	TQ	DOX
Encapsulation efficiency (%)	89.3 ± 0.23	94.7 ± 0.19

Table S3. The IC_{50} of different formulations on MCF-7 and MCF-7/ADR cells.

	MCF-7	MCF-7/ADR
DOX	4.05 μM	462.97 μM
TQ	11.32 μM	20.14 μM
TQ + DOX	1.70 μM	9.16 μM
TQ/DOX-PEG	0.77 μM	5.47 μM
TQ/DOX-PEG-mAb	0.084 μM	2.00 μM