Supporting Information

Elaboration on the Distribution of Hydrophobic Segments in the Chains of Amphiphilic Cationic Polymers for siRNA Delivery

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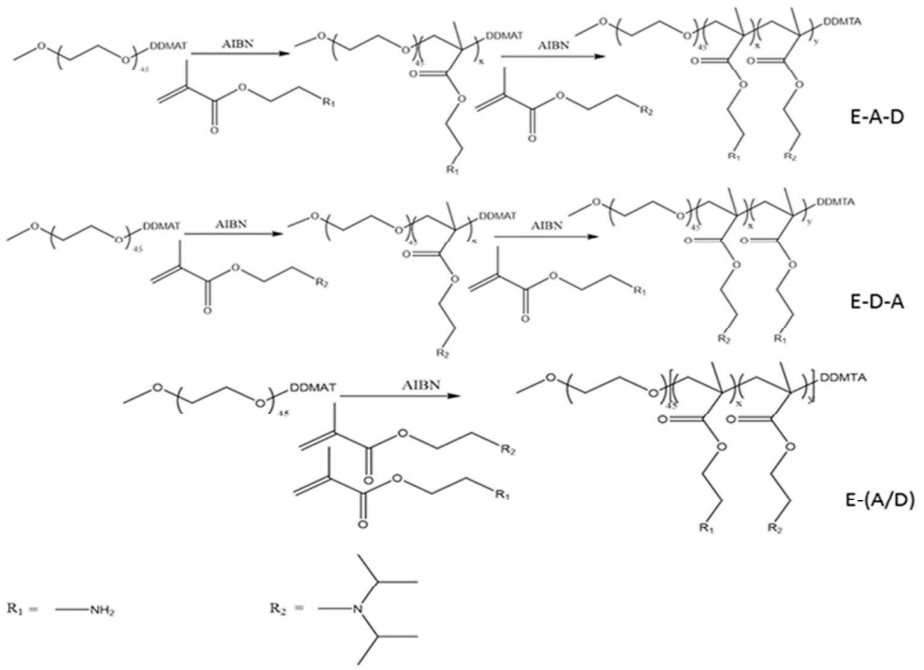

Scheme S1. The synthetic routes of E-A-D, E-D-A and E-(A/D).

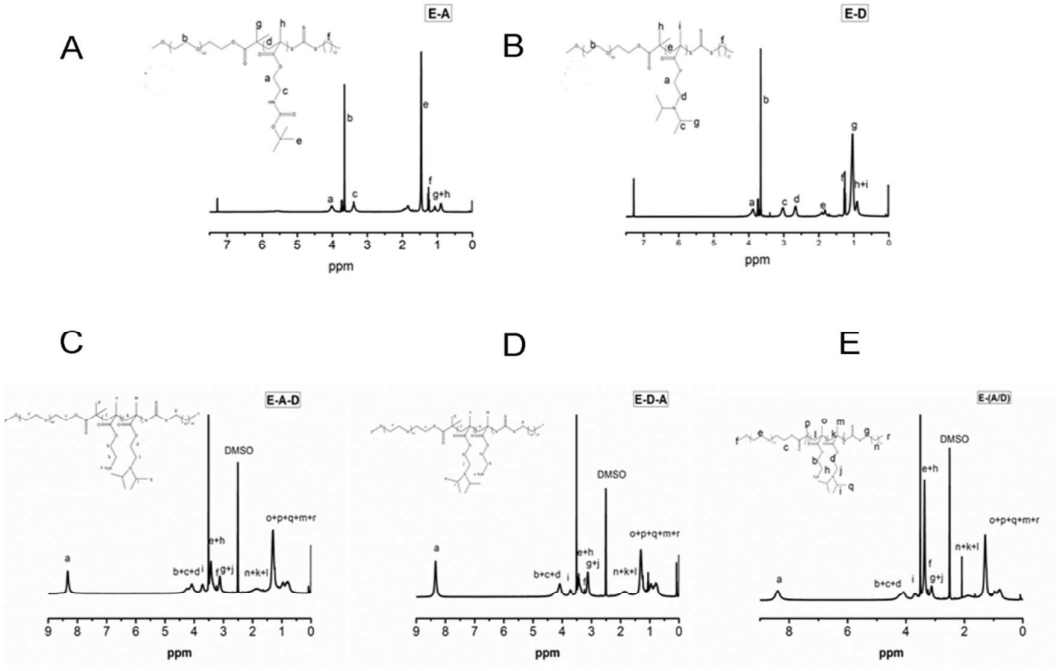

Figure S1. [1]H-NMR spectroscopies of E-A, E-D, E-A-D, E-D-A and E-(A/D).

Table S1. The molecular structure, molecular weight and PDI of three polymers.

Sample	The molecular structure of the polymer[a]	M_n[b](10^4 g/mol)	PDI[c]
E-A-D	PEG_{45}-PAM_{46}-PDP_{45}	2.21	1.67
E-D-A	PEG_{45}-PDP_{45}-PAM_{44}	2.17	1.68
E-(A/D)	PEG_{45}-P(AM_{42}/DP_{42})	2.06	1.57

[a] The molecular structure of the polymer was determined by ^{1}H NMR.
[b] The mean molecular weight (M_n) of copolymers was estimated by ^{1}H NMR.
[c] PDI=M_w/M_n measured by GPC.

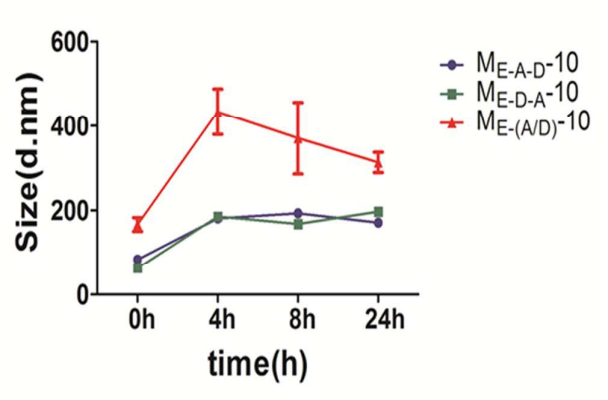

Figure S2. The stability of siRNA-loaded micelles at N/P=10 in PBS.

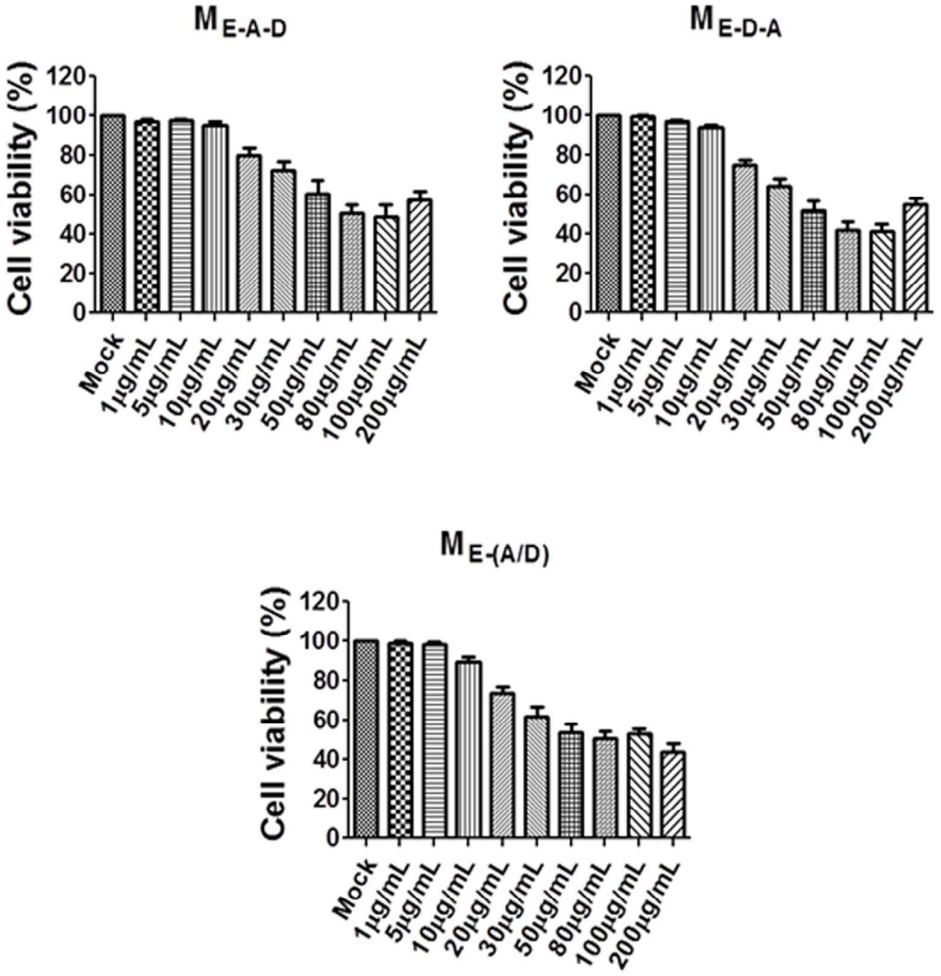

Figure S3. Cell cytotoxicity of $M_{E\text{-}A\text{-}D}$, $M_{E\text{-}D\text{-}A}$ and $M_{E\text{-}(A/D)}$ at different concentrations.

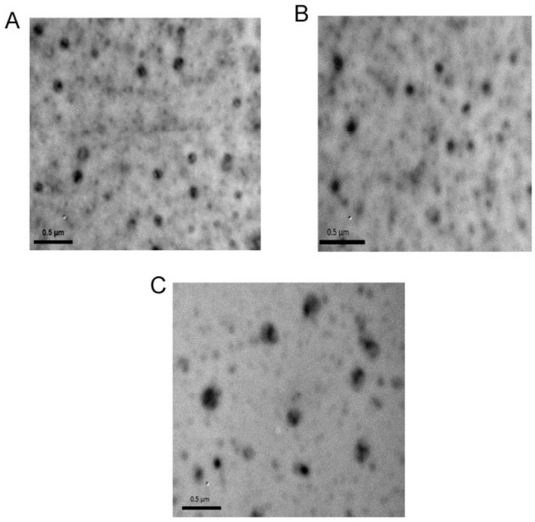

Figure S4. TEM images of $M_{E\text{-}A\text{-}D}$ (A), $M_{E\text{-}D\text{-}A}$ (B) and $M_{E\text{-}(A/D)}$ (C).

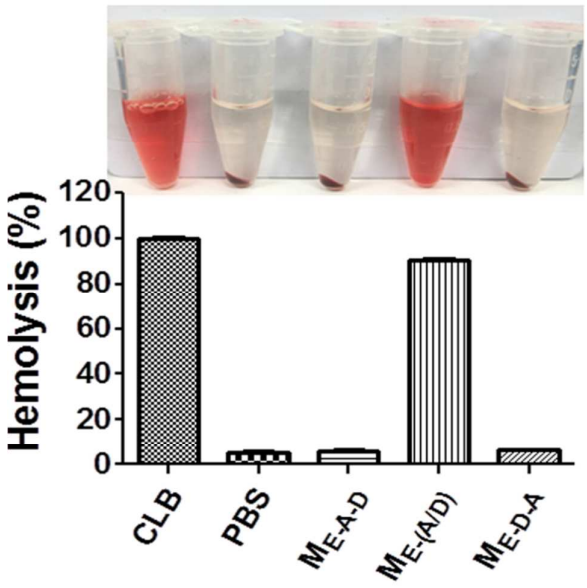

Figure S5. Hemolysis assay of 5 mM micelles in 1 mL PBS at pH=7.4. Cell lysis buffer was used as positive control and PBS was used as negative control.

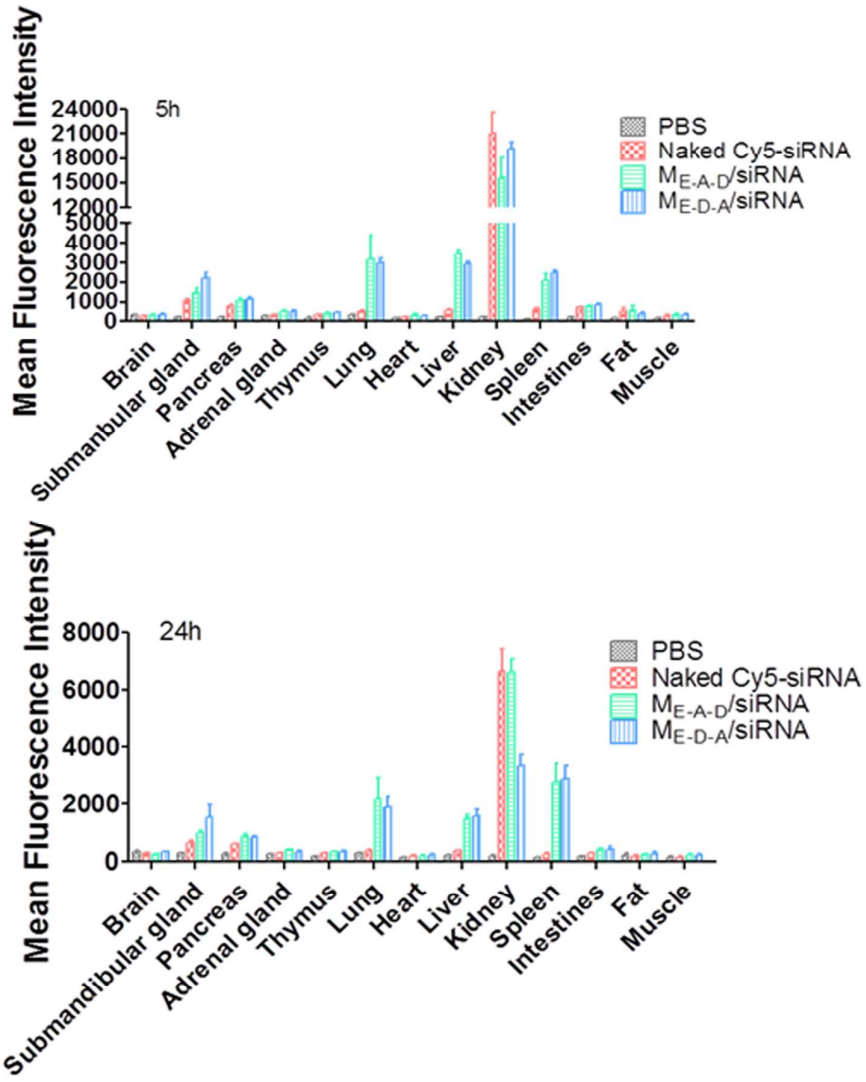

Figure S6. Quantitative analysis of different organs using a molecular imaging software package at 5 h and 24 h. Data were normalized to corresponding tissues from saline-treated animals. Each bar represents the mean±S.E. of three different experiments.

Table S2. The sequences of the siRNA used in this work.

siRNA Name	Sequences
Cy5-siRNA	sense: 5'-Cy5-CCUUGAGGCAUACUUCAAAdTdT-3'
	anti-sense: 5'-UUUGAAGUAUGCCUCAAGGdTdT-3'
siFL	sense: 5'-CCCUAUUCUCCUUCUUCGCdTdT-3'
	anti-sense: 5'-GCGAAGAAGGAGAAUAGGGdTdT-3'
siApoB	sense: 5'-GUCAUCACACUGAAUACCAAUdTdT-3'
	anti-sense: 5'-AUUGGUAUUCAGUGUGAUGACACdTdT-3'
siPLK1	sense: 5'-UGAAGAAGAUCACCCUCCUUAdTdT-3'
	anti-sense: 5'-UAAGGAGGGUGAUCUUCUUCAdTdT-3'
siRRM2	sense: 5'-GCGAUUUAGCCAAGAAGUUCA-3'
	anti-sense: 5'-UAGCGACUAAACACAUCAAUU-3'