## **Supporting Information**

## Statistical versus block fluoropolymers in gene delivery

Echuan Tan,<sup>a</sup> Jia Lv,<sup>a</sup> Jingjing Hu,<sup>a</sup> Wanwan Shen,<sup>a</sup> Hui Wang,<sup>a</sup> Yiyun Cheng<sup>\*a</sup>

<sup>a</sup> Shanghai Key Laboratory of Regulatory Biology, School of Life Sciences, East China Normal University, Shanghai, 200241, P.R. China.

\*E-mail: yycheng@mail.ustc.edu.cn



**Figure S1.** <sup>1</sup>H NMR spectra of the monomer solutions after RAFT polymerization. The number under each peak represents the relative integrated area. The peak labeled "a" represents the vinyl protons on DMAEMA monomer, "A" represents the methylene protons on pDMAEMA. The peak labeled "b" represents the vinyl protons on HFMA monomer, "B" represents the methylene protons on pHFMA. The peak labeled "c<sub>1</sub>" and "c<sub>2</sub>" represent the vinyl protons on BMA and HMA monomers, respectively, while "C<sub>1</sub>" and "C<sub>2</sub>" represent the methylene protons on pBMA and pHMA, respectively. The monomer conversion and theoretical molecular weight of pDMAEMA can be calculated by following formula:

$$Conv_{DMAEMA} (\%) = \frac{I_A}{(I_A + 2I_a)} \times 100\%$$

 $M_{n,th} = M_{n,DMAEMA} \times Conv_{DMAEMA} \times m + M_{n,CPADB}$ 

Where *m* represents the molar ratio of monomer to CTA.  $I_A$  and  $I_a$  represent the relative integrated areas for peak A and a, respectively. The monomer conversion and theoretical molecular weight the block and statistical copolymers were calculated by the similar method.



**Figure S2.** DLS and TEM images of the prepared pDMAEMA<sub>40</sub> micelles. The scale bar is 500 nm.



**Figure S3.** A plot of light scattered intensity (kilo counts per second) versus polymer concentrations for pDMAEMA<sub>42</sub>-*st*-pHFMA<sub>12</sub> (a) and pDMAEMA<sub>42</sub>-*b*-pHFMA<sub>13</sub> (b) nanomicelles prepared in deionized water. The intersection of the two lines represents the critical micelle concentration (CMC). Both fluoropolymers showed a similar and low CMC value around 4  $\mu$ g/mL.



**Figure S4.** Agarose gel electrophoresis analysis of pDMAEMA<sub>40</sub>, pDMAEMA<sub>42</sub>-*st*-pHFMA<sub>12</sub>, pDMAEMA<sub>42</sub>-*b*-pHFMA<sub>13</sub>, pDMAEMA<sub>42</sub>-*st*-pBMA<sub>12</sub>, pDMAEMA<sub>44</sub>-*st*-pHMA<sub>10</sub> nanomicelle complexes with luciferase DNA. The nanomicelle/DNA complexes were prepared at N/P ratios of 4:1, 6:1, 8:1 and 10:1, respectively.



**Figure S5.** Flow cytometry analysis of 293T cells transfected with pDMAEMA<sub>40</sub>/DNA complexes prepared at N/P ratios from 6:1 to 12:1 for 48 h.



**Figure S6.** Flow cytometry analysis of 293T cells transfected with pDMAEMA<sub>42</sub>-*st*-pHFMA<sub>12</sub>/DNA complexes prepared at N/P ratios from 6:1 to 12:1 for 48 h.



**Figure S7.** Flow cytometry analysis of 293T cells transfected with pDMAEMA<sub>42</sub>-*b*-pHFMA<sub>13</sub>/DNA complexes prepared at N/P ratios from 6:1 to 12:1 for 48 h.



**Figure S8.** Flow cytometry analysis of 293T cells transfected with pDMAEMA<sub>42</sub>-*st*-pBMA<sub>12</sub>/DNA complexes prepared at N/P ratios from 6:1 to 12:1 for 48 h.



**Figure S9.** Flow cytometry analysis of 293T cells transfected with  $pDMAEMA_{44}$ -*st*- $pHMA_{10}/DNA$  complexes prepared at N/P ratios from 6:1 to 12:1 for 48 h.



**Figure S10.** Flow cytometry analysis of untreated 293T cells and cells transfected with Lipo 2000/DNA lipoplexes for 48 h.



**Figure S11.** Cytotoxicity of polymers on 293T cells without plasmid (a) or with luciferase plasmid (b, N/P is 8:1) for 48 h. The polymer concentrations are equal to those in gene transfection experiments at an N/P ratio of 8:1. The data are analyzed by Student's t-test, (\*) p < 0.05, (\*\*) p < 0.01, and (\*\*\*) p < 0.001, respectively.



**Figure S12.** Confocal images of 293T cells treated with YOYO-1 labeled plasmid/pDMAEMA<sub>42</sub>-*b*-pHFMA<sub>13</sub> complex for 6 h and 12 h, respectively. The scale bar is 20  $\mu$ m.