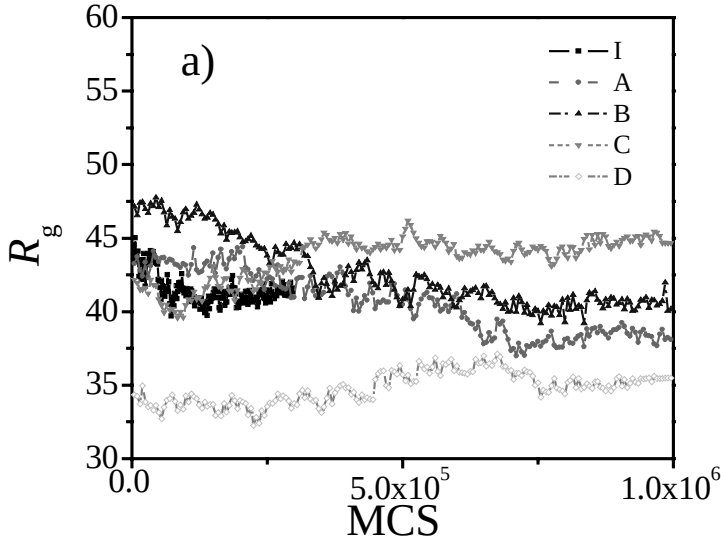
Supporting Information

"Effects of Polar Group Saturation on Physical Gelation of Amphiphilic Polymer Solutions"



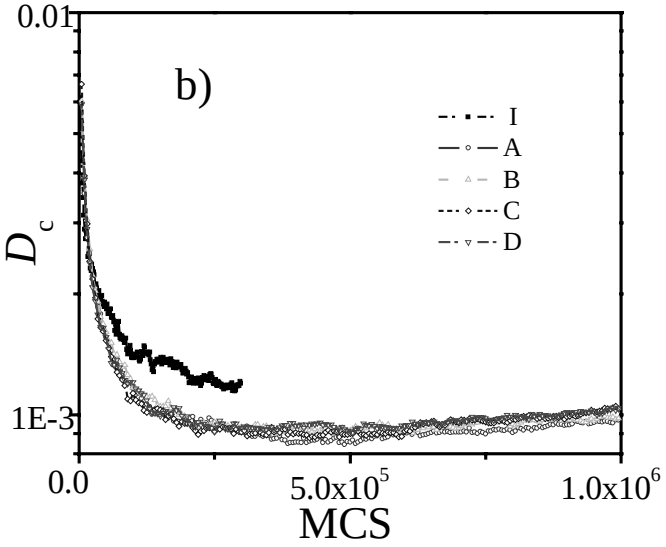


Figure S1. The simulation time dependence of the root-mean square radius of gyration (R_g) a) and the diffusion coefficient D_c (k_{sa} = 0.36, ϕ = 0.15) b). Both of the two parameters level off as the simulation time increases in the typical time profiles for all simulation data. Here the labels I, A, B, C, D represent the initial 3×10^5 MCS Monte Carlos simulation without any interactions, and the four different solvent conditions running for a total of 1×10^6 MCS respectively.

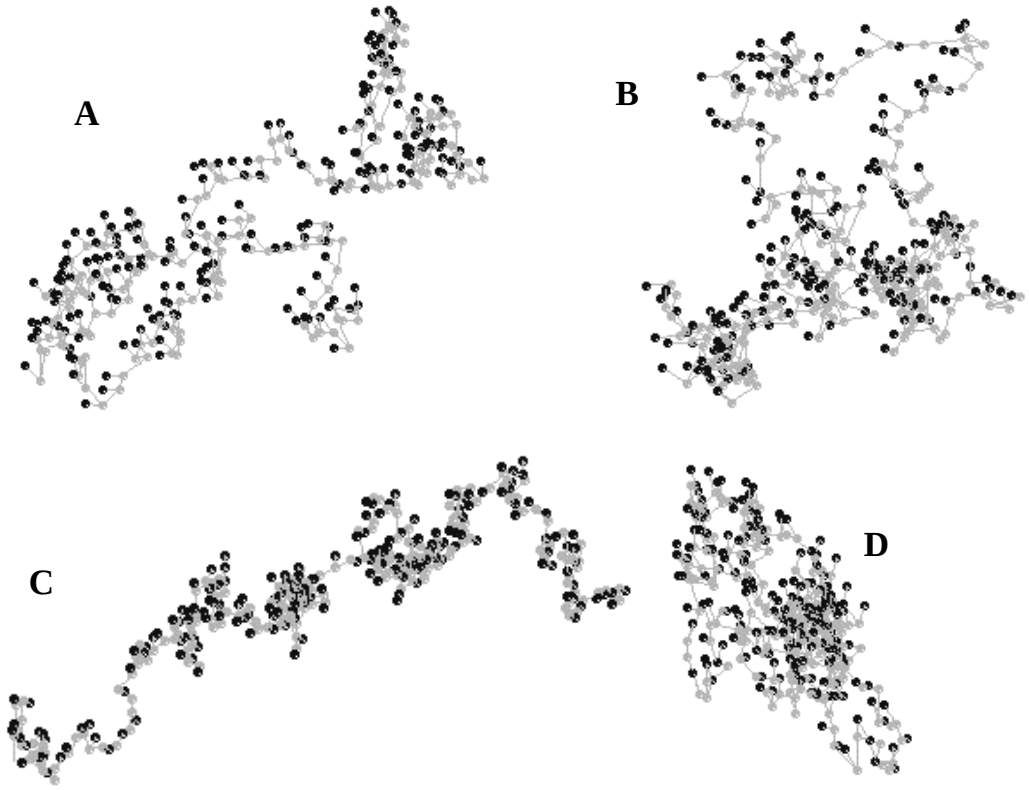


Figure S2. Snapshots of the single chain conformation picked up from the final simulation configurations ($k_{sa} = 0.36$, $\phi = 0.15$) under four different solvent conditions described in Table 1. The dark and grey dots are the side-chain P monomers and the backbone N monomers respectively.