Supplementary Material (ESI) for *Soft Matter*

Electronic Supplementary Information

1. Formation of substrate-supported lipid monolayer

Supported lipid monolayers are prepared by the vesicle fusion method. The formation of the monolayer is monitored using X-ray reflectivity measurements, with representative data shown in Figure S1. It is clear that monolayer formation completes within minutes. To ensure complete monolayer coverage on the substrate, we always start subsequent steps in sample preparation at least 30 minutes after the injection of vesicle solution. Details of these X-ray reflectivity measurements and the data analysis have been described elsewhere (ref 6 from the text). Figure S2 shows the results of modeling the data from the final measurement (at 270min).

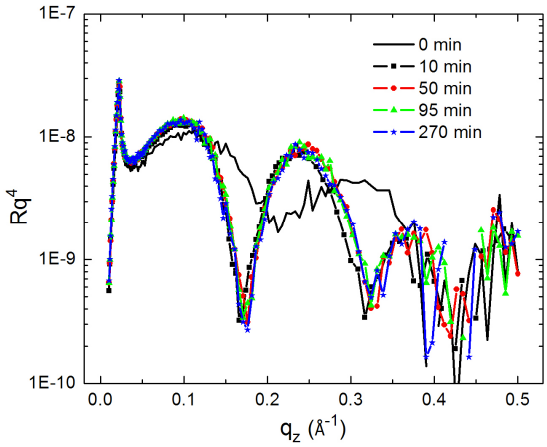

Figure S1. X-ray reflectivity curves obtained at time t=0 (just before adding lipid solution), 10, 50, 95 and 270 minutes after injecting the 21:4 DOPC/DOTAP lipid solution in 10mM MES into the sample cell.

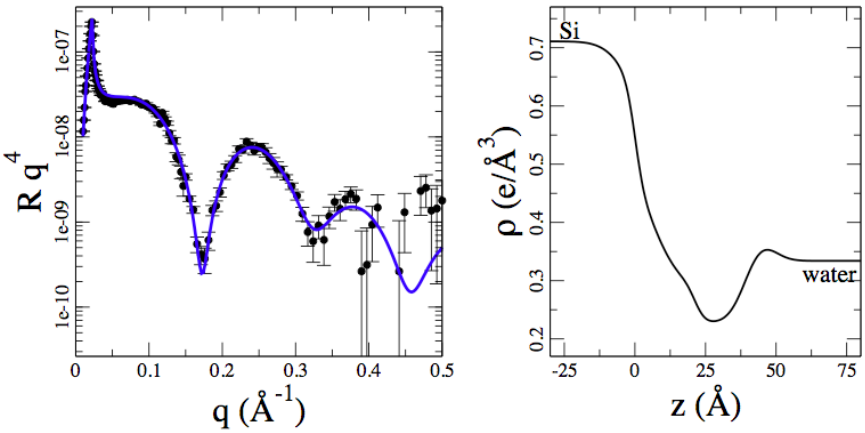

Figure S2. Left: fitting results (blue solid line) for the data collected at 270min (black symbols). The data have been corrected to account for partially reflected X-ray beam at small q when the beam overfills the sample. See ref.6 for details on the fitting procedure. Right: the electron density obtained from the fit.

2. Additional AFM images

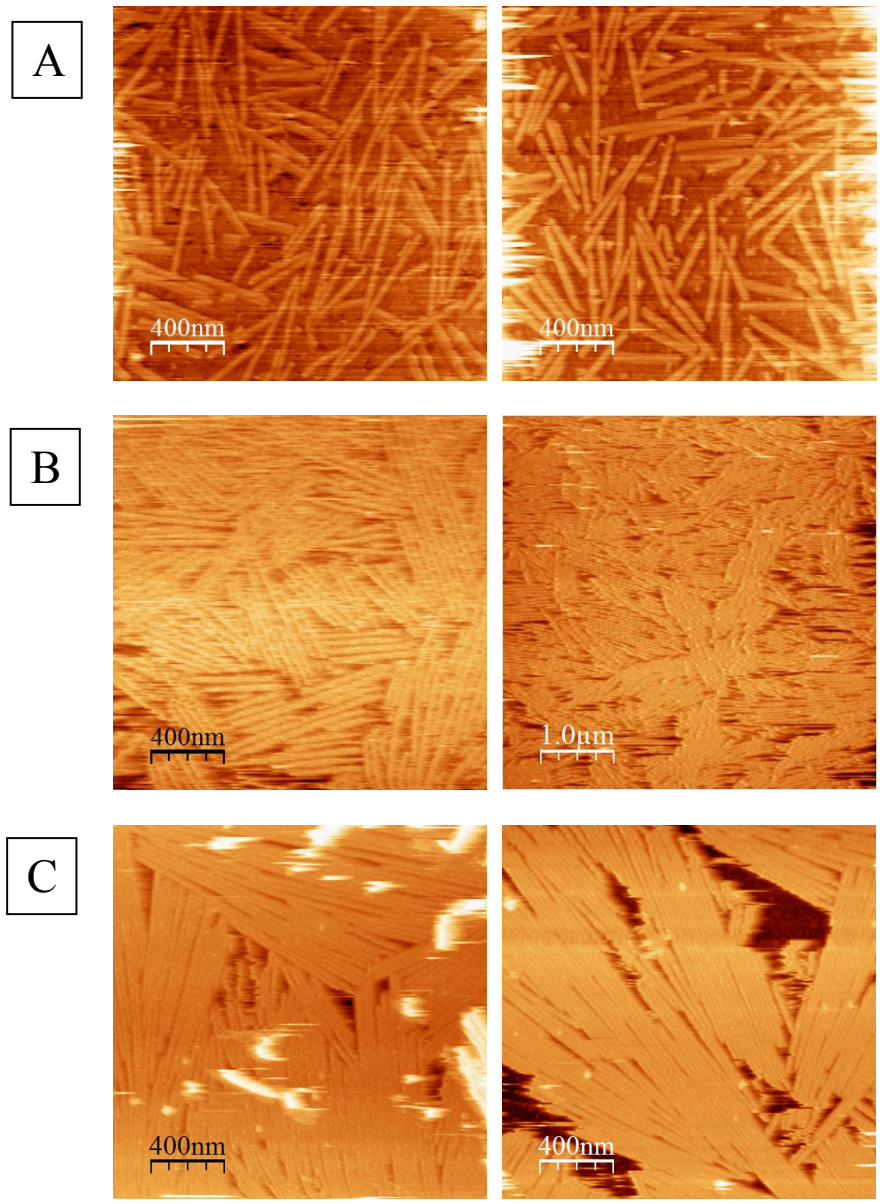

Figure S3 AFM topography images of (A) TMVs adsorbed on a bare silicon substrate under 10mM MES with 100mM $CaCl_2$, (B) TMVs adsorbed on a supported 21:4 DOPC/DOTAP lipid monolayer under 10mM MES without $CaCl_2$, and (C) TMVs adsorbed on a supported 21:4 DOPC/DOTAP lipid monolayer under 10mM MES with 100mM $CaCl_2$. In each case, the images shown here are consistent with those included in the text, indicating that the structures observed are representative of the actual structures in the sample.

3. Monte Carlo simulation of structure factor

The Monte Carlo simulations are carried out using a 1D model system of particles (NTV ensemble). The system evolves following a standard Metropolis method previously described (Yang et.al., Biophys. J. 1999 77:2648–2656). The periodic boundary condition is imposed. All particles have the diameter of unity. The size of the simulation box is fixed to 100 and the number of particles is determined by requiring the average density of the system to match the input parameter.

In order to eliminate artifacts due to the initial particle positions, the system contained no particle at the start of the simulation and the particles are added into the system one by one as the system is evolving. Once all the particles have entered the simulation, the sampling for the pair correlation function begins. The distances between all possible particle pairs are histogrammed periodically. The distance histogram is then normalized to give the pair correlation function g(r), from which the structure factor is calculated by Fourier transform.

3.1 simulation results of particles in 1D interacting via screened Coulomb repulsion

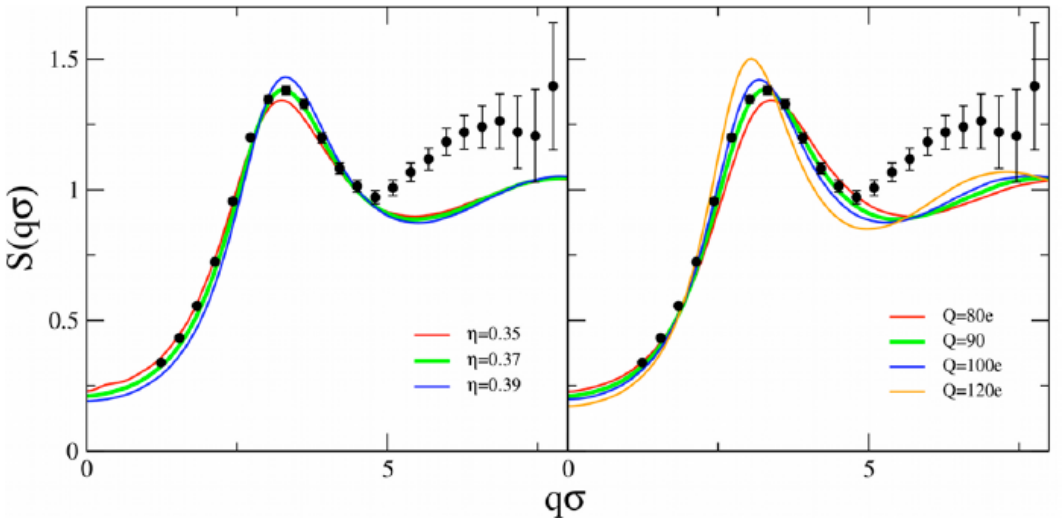

Figure S4A. The structure factors obtained from Monte Carlo simulations based on screened Coulomb repulsion (4.5nm Debye length) and hardwall repulsion at short inter-particle spacings. The radius of the hardwall part of the inter-particle interaction is σ=18nm. The results on the left correspond to various particle packing fractions and the total rod charge of 90e. The results on the right correspond to various total charges per rod and the constant packing fraction of η=0.37. The "experimental" structure factor (Figure 8 in the text) is shown as symbols.

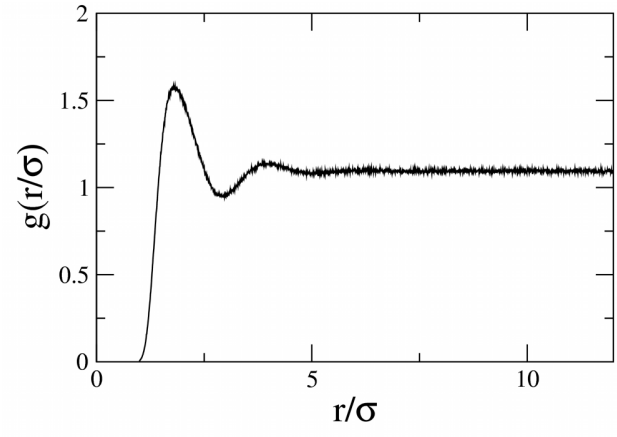

Figure S4B. The pair distribution function corresponding to η=0.37 and Q=90e.

3.2 simulation results of particles in 1D interacting via square well interaction

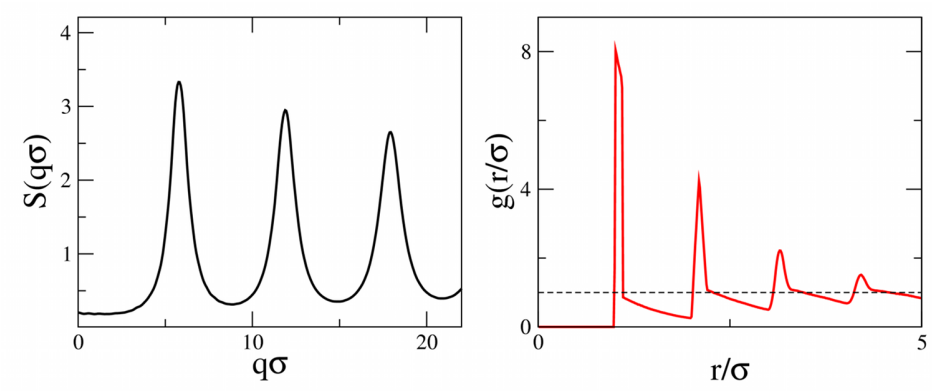

Figure S5. The structure factor obtained from Monte Carlo simulations of 1D rods with a packing fraction of η=0.72 and interacting via a square well potential beyond hard wall exclusion, together with the corresponding pair correlation functions. The square well width is 10% of the hard wall radius and its depth is 2.1k_BT. These two parameters combine to give the same stickiness parameter obtained from the fit shown in Figure 10.

4. Additional X-ray scattering data from bulk solutions of TMVs at different Ca^{2+} concentrations

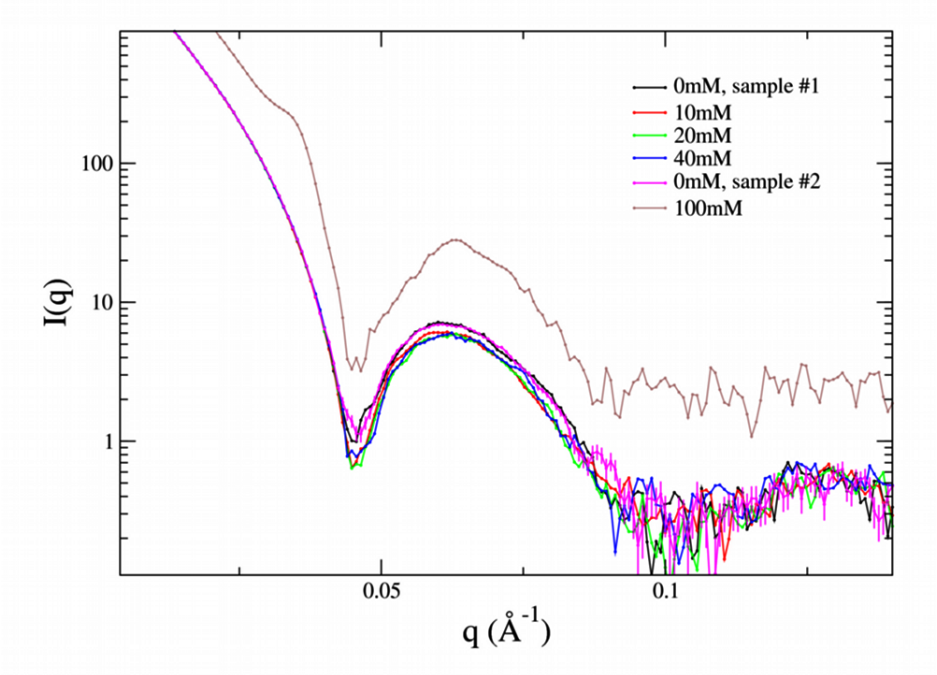

Figure S6. Data collected from 1mg/ml TMV solutions in 10mM MES and various $CaCl_2$ concentrations. All curves are scaled so that their low q ends match. For clarity, the data for 100mM $CaCl_2$ has been shifted and only the error bars for one of the 0mM curves are shown. An additional peak at q~0.034 Å^{-1} is clearly seen in the 100mM $CaCl_2$ data. The 0mM data were reproduced by two different samples. Their amplitudes at q~0.06 Å^{-1} are consistently higher than those in the data collected for samples with 10mM, 20mM and 40mM $CaCl_2$ concentrations. Note that the 0mM and 40mM scattering data shown in the text correspond to longer X-ray exposure times (150s vs. 30s) and therefore have better signal-to-noise ratios compared to data shown here.