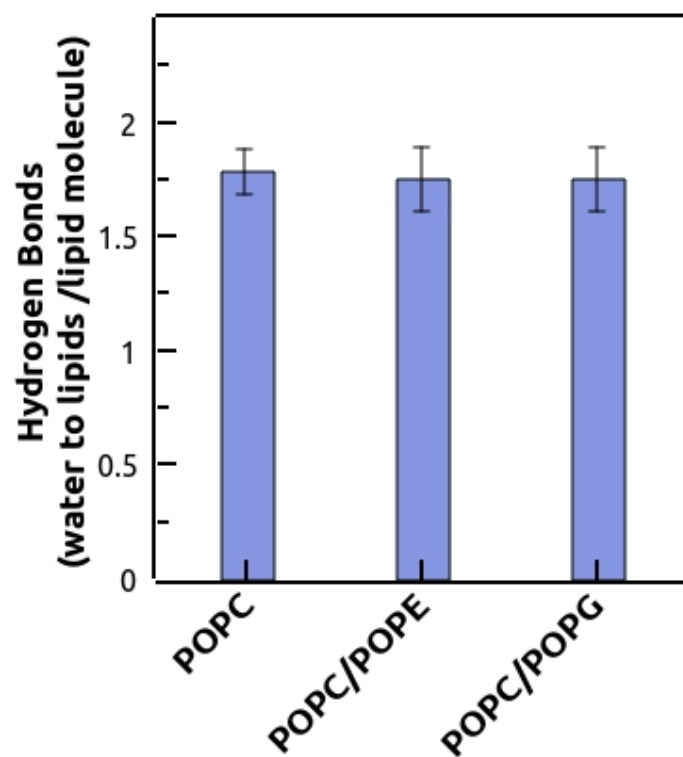**Figure S1**. Area per lipid. Surface area per lipid vs. time of a single replica simulation of POPC/TMX (32:11) (black), POPC/POPE/TMX (24:8:11) (blue) and POPC/POPG/TMX (24:8:11) (red).

Figure S2. Carbonyl hydrogen bonding. Hydrogen bonds between water and phospholipid carbonyl groups in the different simulated phospholipid bilayers. Error bars represent the s.d. of the trajectories analyzed.
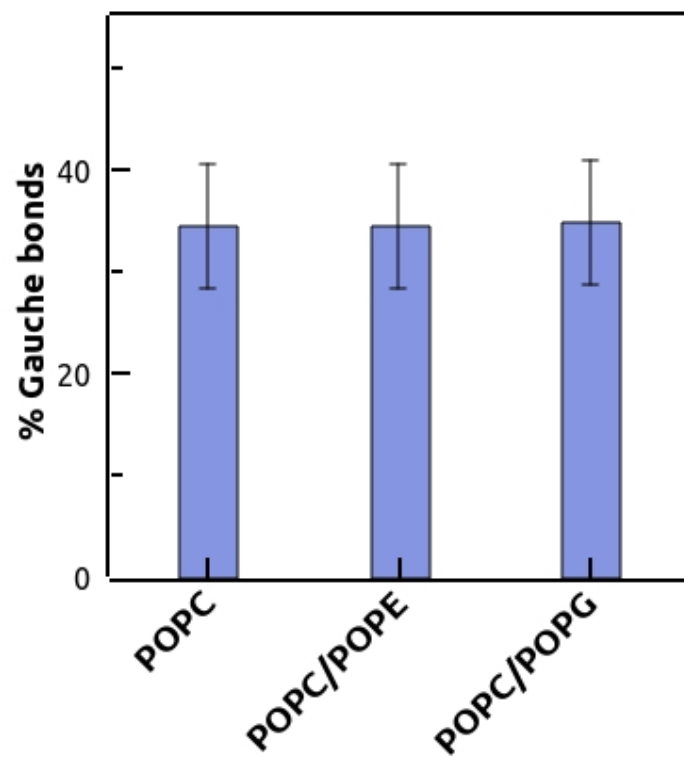
Figure S3. *Gauche* conformers. The proportion of *gauche* conformers in the different simulated phospholipid bilayers. Error bars represent the s.d. of the trajectories analyzed.