Supporting Information

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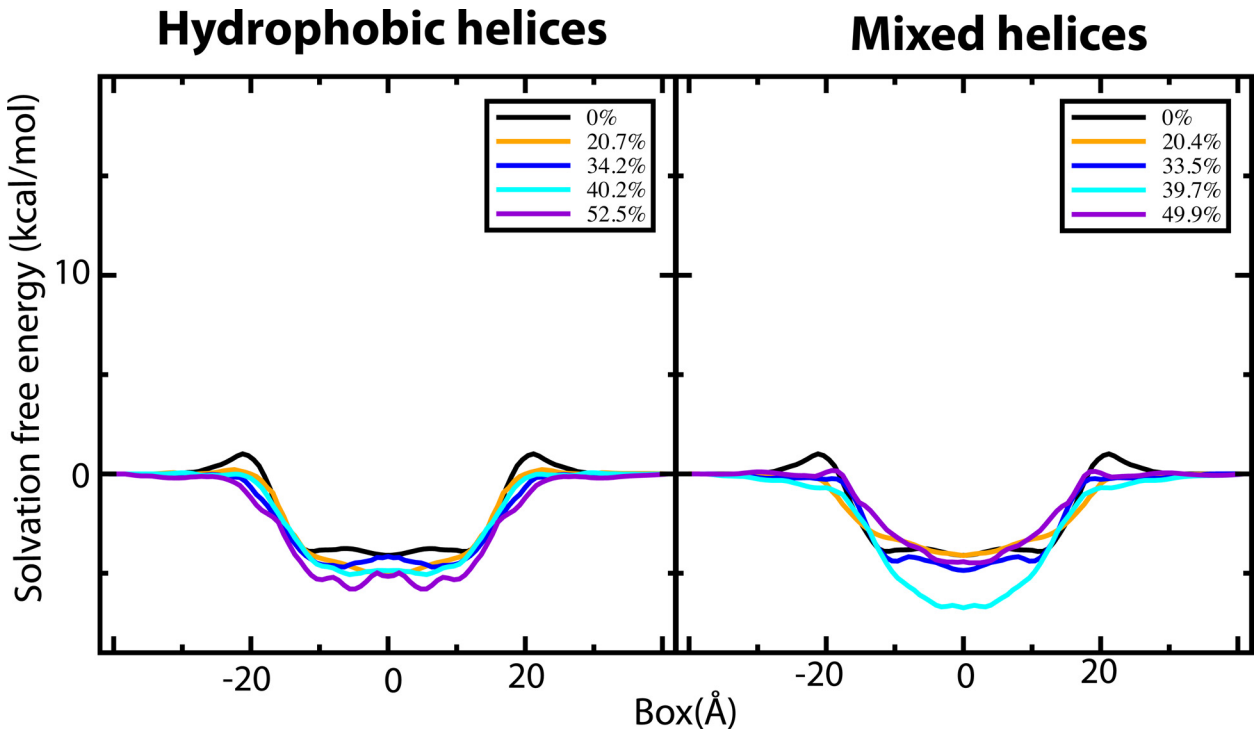

Fig. S1. Spatially resolved free-energy profiles for a leucine analog as a function of distance from the bilayer center along the membrane normal, i.e. the direction perpendicular to the membrane, corresponding to the arginine curves in manuscript Fig. 2. The solvation cost for leucine is almost constant for all tested setups.

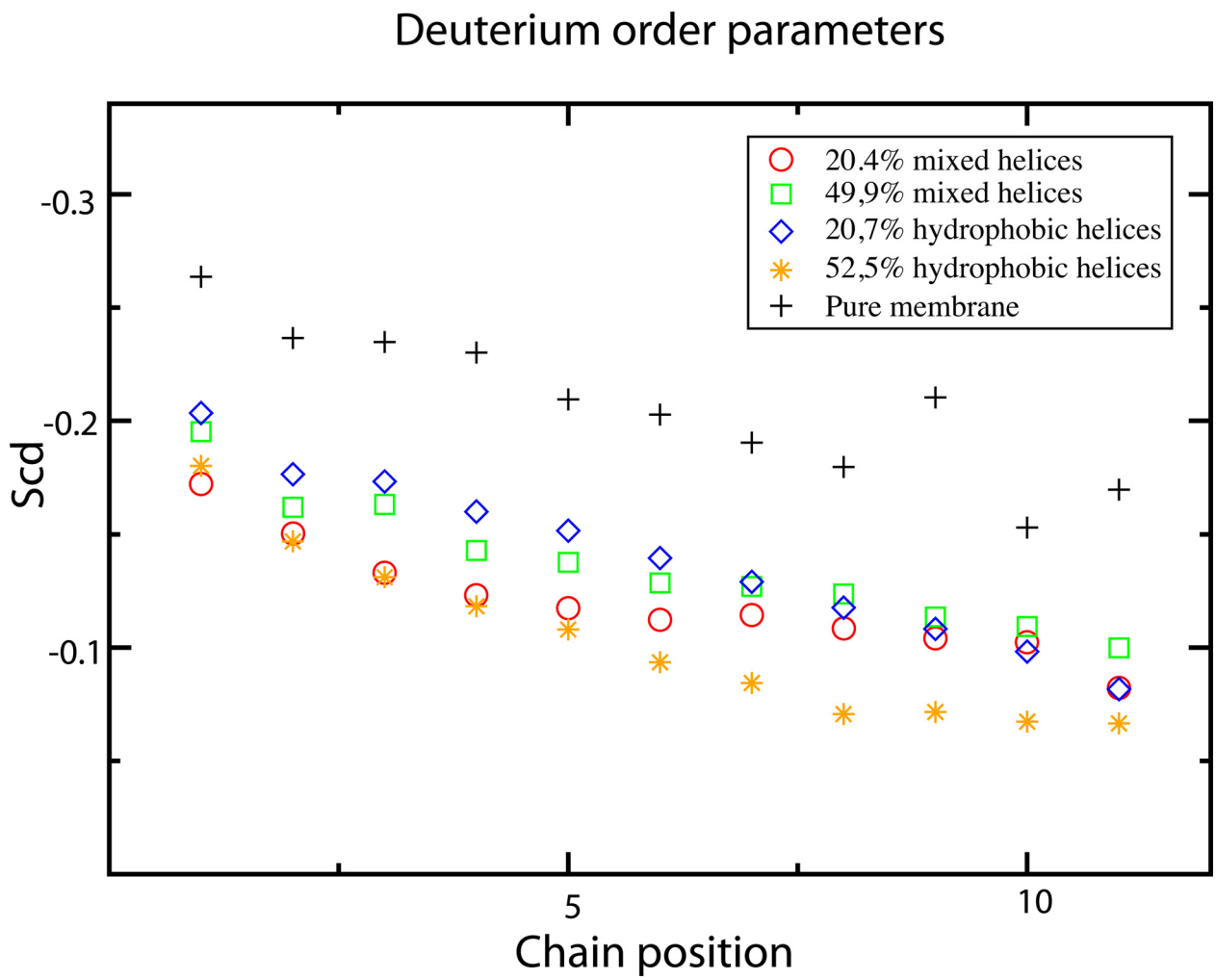

Fig. S2. Deuterium order parameters for the saturated lipid tails of the POPC lipids in the different setups, as a measure of the induced bilayer perturbation. The order in the pure bilayer system corresponds well to experimental values but decreases with inserted helices, although the differences between the systems are still relatively small.

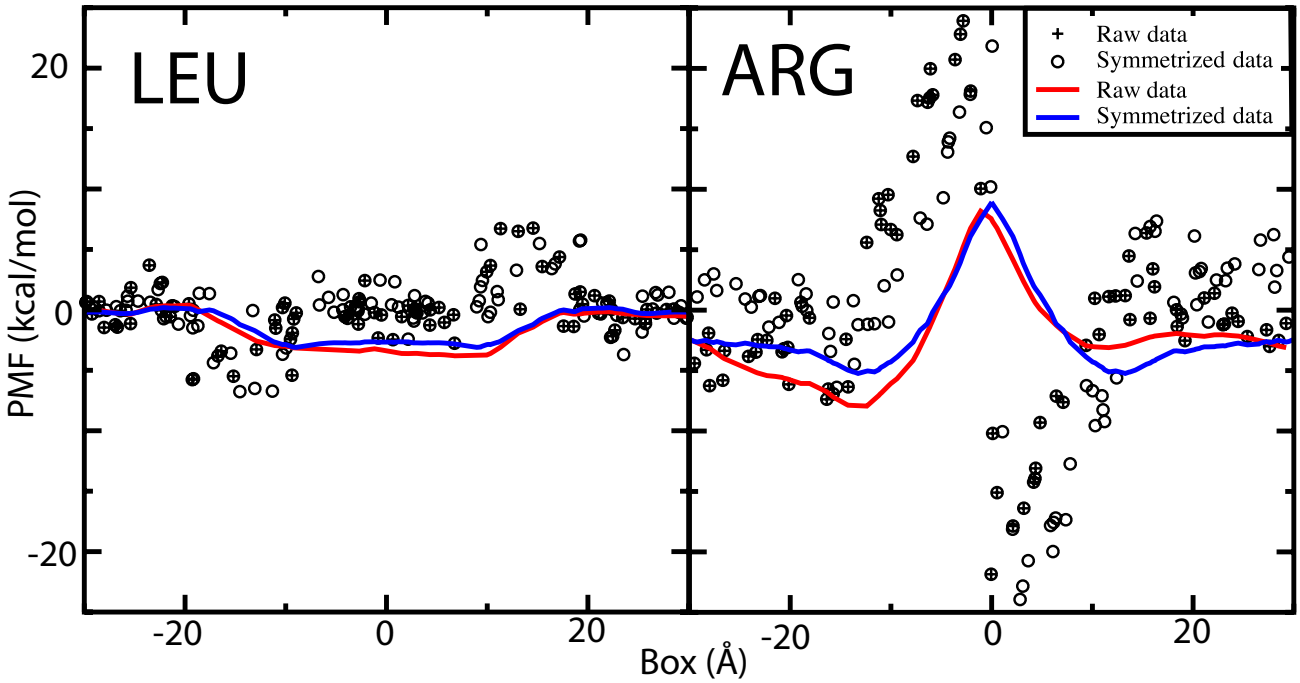

Fig. S3. Illustration of PMF derivation and the difference between raw data (hair-crosses, red potential of mean force profile) and a set where this data has been symmetrized across the membrane (circles, blue potential of mean force profile) for better statistics. This averaging is helpful both to assess accuracy and to further improve the signal-to-noise ratio.