Supporting information for

Cholesterol flipflop in heterogeneous membranes

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Figure S1. Convergence of molecular dynamics simulations. Trajectories of the simulations at (A) 310 K and (B) 290 K were divided in blocks of 1 μs and the DPPC-DOPC radical distribution function (RDF) profiles were calculated for each block. Results are shown for the two leaflets respectively (left column and right column).
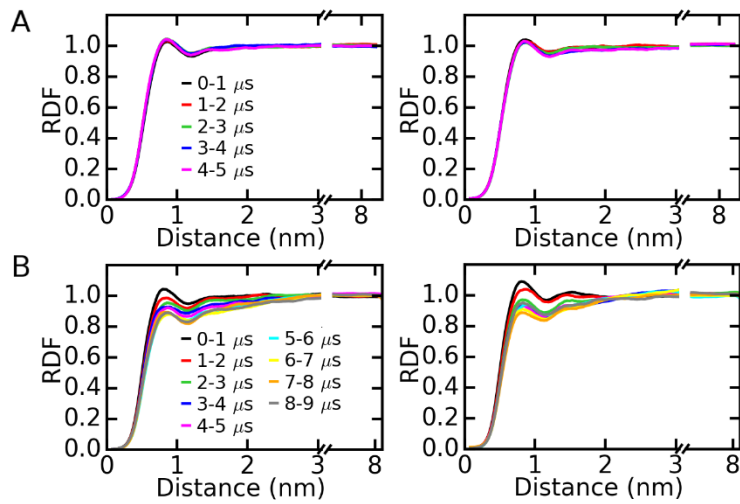
Figure S2. Dependence of cholesterol flipflop on the local environment. (A) Histograms of DPPC enrichment values in the local environment of all cholesterol in the simulation box, and the flipflopped cholesterol (before and after the flipflop event), respectively. Results at 310 K and 290 K are shown. (B) Cholesterol flipflop rate as a function of DPPC enrichment value (before and after the flipflop event) of the local environment.
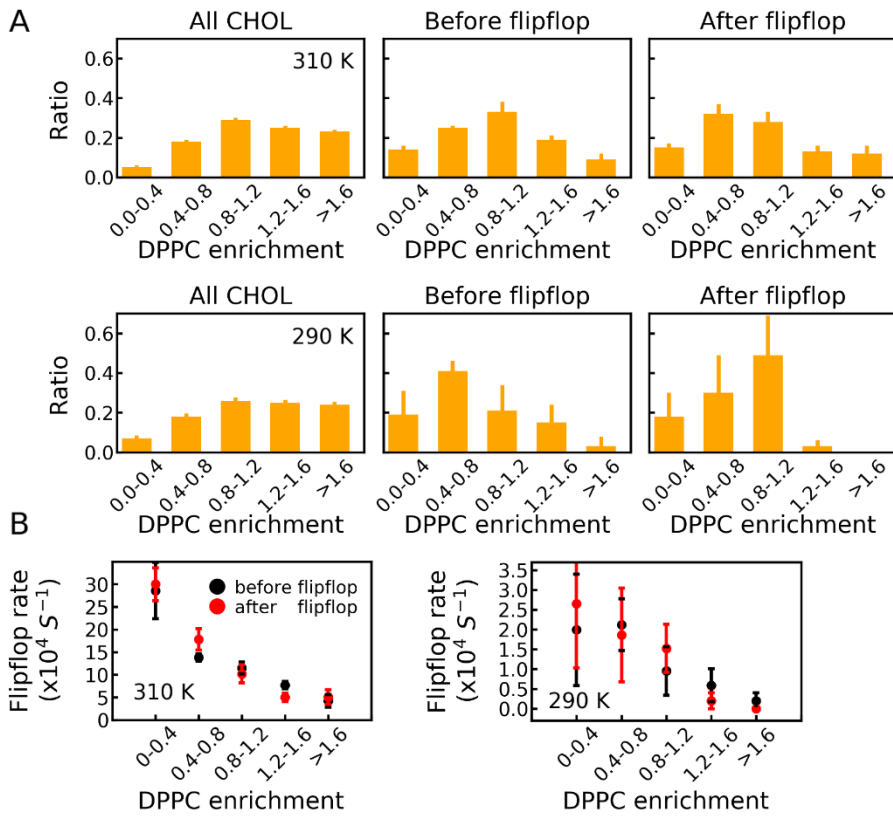
Figure S3. Overlap of disordered clusters facilitates cholesterol flipflop. 2D histogram of DOPC enrichment values of two opposite leaflets associated with the same position along the bilayer, at (A) 310 K and (B) 290 K. The x and y axes are the DOPC enrichment in the upper and lower leaflets, respectively. Results are compared for the whole bilayer, the aborted and successful flipflop attempts.