

Supplementary Information

Lipoprotein particles interact with membranes and transfer their cargo without receptors

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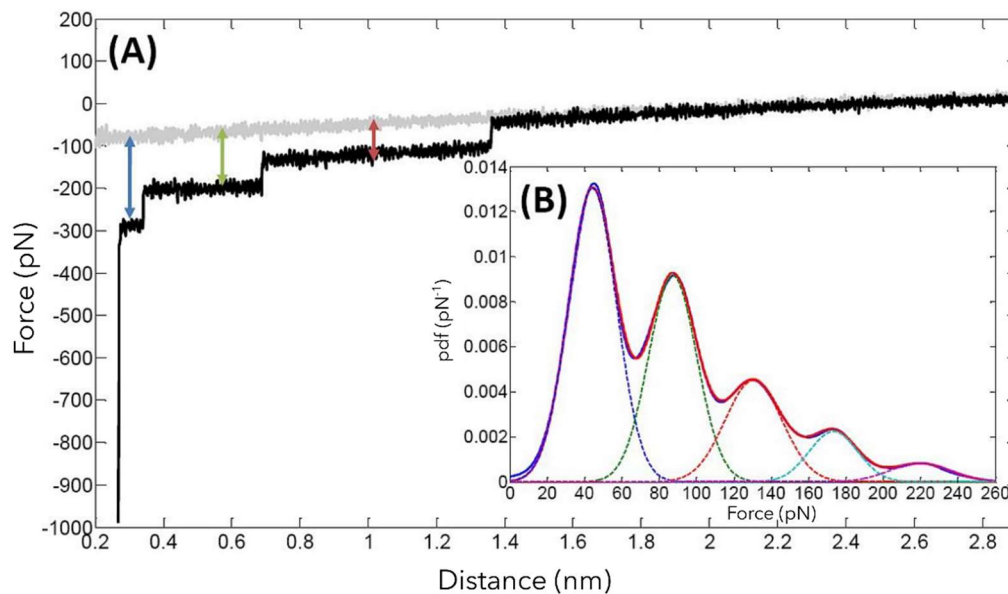


Figure S1. Evaluation of the force steps. A) Represents a force-distance cycle and assuming three force steps. The force for each step was determined between the respective plateaus (blue - first step; green - second step; red - second step) and the baseline (grey - approach curve). B) Probability density function of measured forces: The resulting value μ_i describes the force for the respective step, which was calculated with the provided formula. The plot shows the summarized data of 500 force distance cycles.

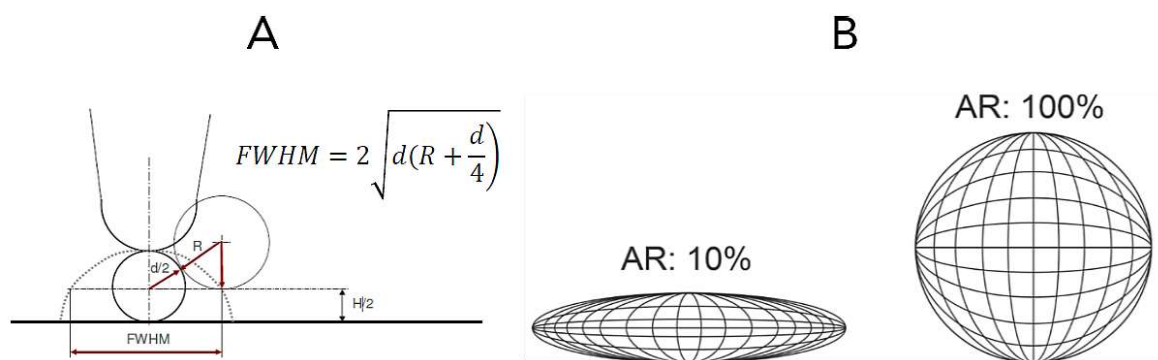


Figure S2. Theoretical Aspects (A) Model for the AFM tip convolution: The dotted line represents the height information of a spherical object, which is detected by an AFM tip if the diameters of both objects are nearly identical (diameter AFM tip apex (R) \sim diameter spherical particle (d)). By measuring the Full Width at Half Maximum (FWHM) of the AFM images and solving the equation (see Figure S1 (A)) for the parameter d , the deconvoluted particle width is obtained. (B) Two representations of particles with an Aspect Ratio ($AR = \text{Height/Width} * 100\%$) of 10% and 100%.

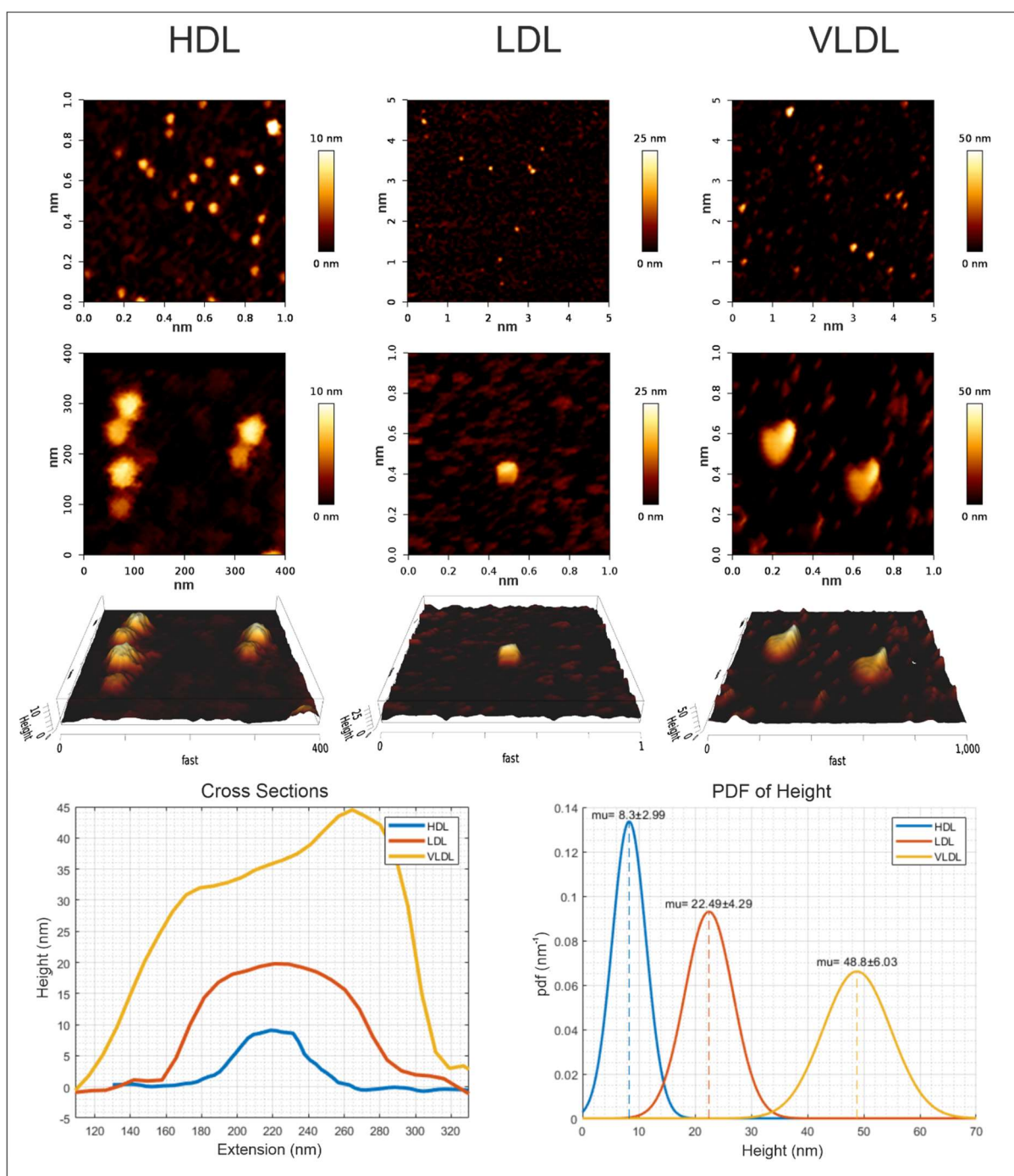


Figure S3. AFM height image overview (first row), increased magnification (second row) and 3D display of magnified HDL, LDL and VLDL particles (third row) on adsorbed on glass cover slip. Cross section figure of magnified HDL, LDL, and VLDL particles. Probability Density Function (PDF) of analyzed HDL, LDL and VLDL particle heights. The population average of the PDF functions of the respective particles are: HDL= 8.3 ± 3.0 nm, LDL= 22.5 ± 4.3 nm and VLDL= 48.8 ± 6.0 nm ($\mu \pm \sigma$) $n=10$.

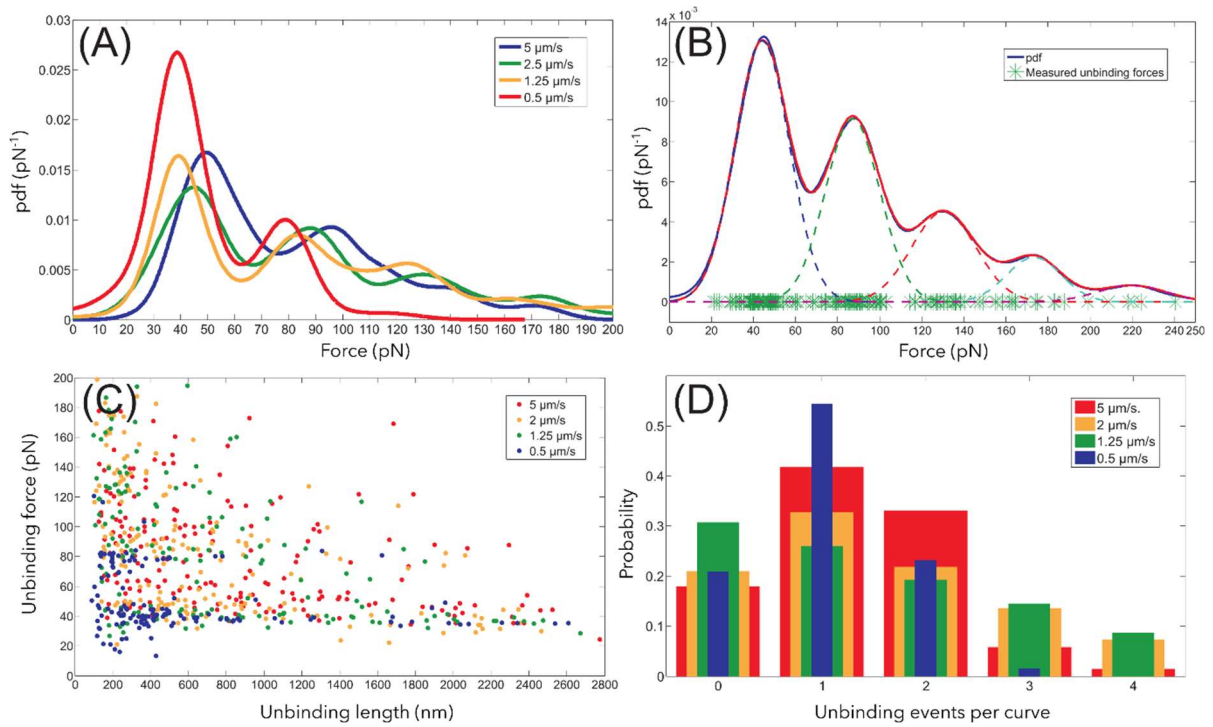


Figure S4. Dependence of force of individual steps on the pulling velocity. The retraction velocity ranges from 0.5 - 5 $\mu\text{m/s}$. Colors are consistent for all images: red 0.5 $\mu\text{m/s}$, yellow 1.25 $\mu\text{m/s}$, green 2.5 $\mu\text{m/s}$, blue 5 $\mu\text{m/s}$. A) Force pdf for varying retraction speeds. B) The exact forces were extracted via a Gaussian fit. C) Force versus length: Independent on the adjusted pulling velocity well defined force steps were measured. D) Probability of unbinding events: Up to four unbinding events were detected.

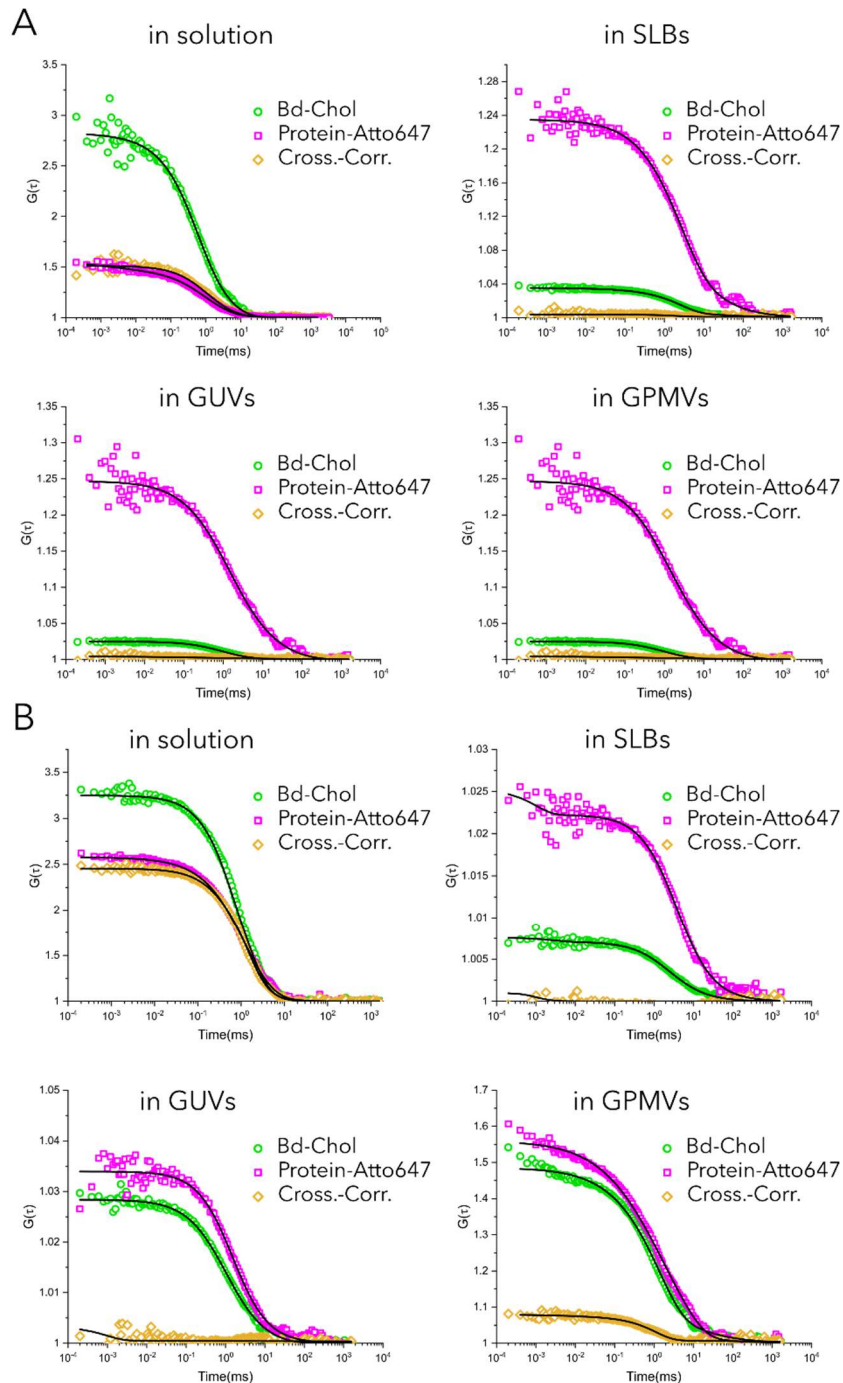


Figure S5. Fluorescence cross-correlation spectroscopy of Bd-Chol and proteins measured in solution (intact lipoprotein particles) as well as in target membranes (GUVs, GPMVs and SLBs – as labeled) for A) HDL and B) LDL. In solution, high cross-correlation of Bd-Chol and protein signals is detected which suggests co-diffusion. In target membrane, cross-correlation curve amplitude is close to zero which suggests that Bd-Chol and protein molecules diffuse in the target membrane independently.

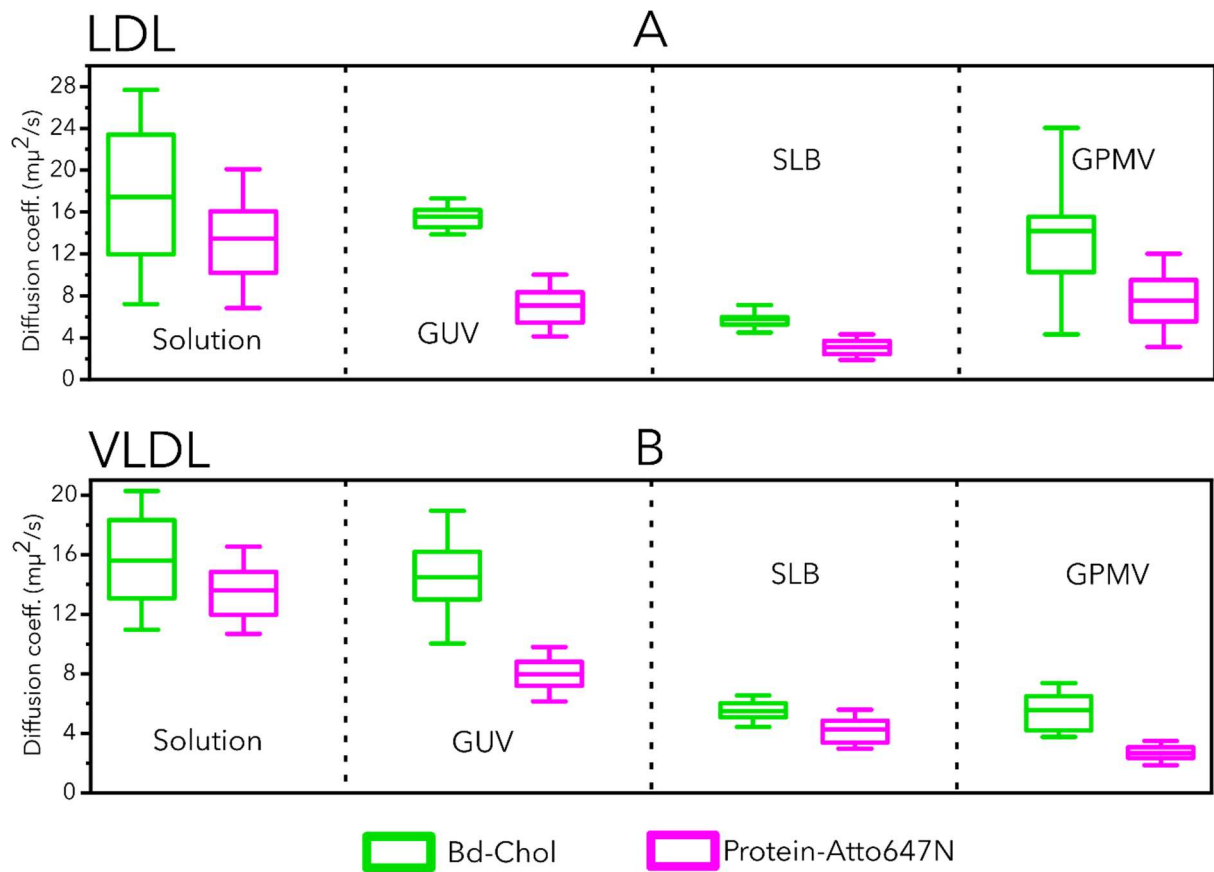


Figure S6: Diffusion coefficients of Bd-Chol and Protein-Atto647N measured in solution (intact lipoprotein particles) as well as in target membranes (GUVs, GPMVs and SLBs – as labeled) for A) LDL and B) VLDL. In solution, diffusion coefficients of Bd-Chol and Protein-Atto647N are similar, because they diffuse together as intact lipoprotein particle. In all target membranes, Bd-Chol diffuses faster than Protein-Atto647N