Supporting Information

Cell Contact and Pressure Control of YAP Localization and Clustering Revealed by Super-resolution Imaging

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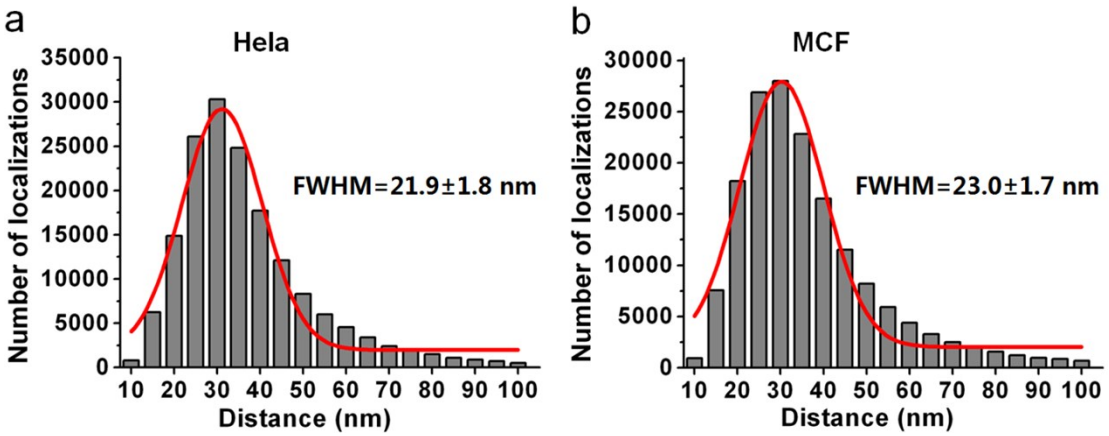
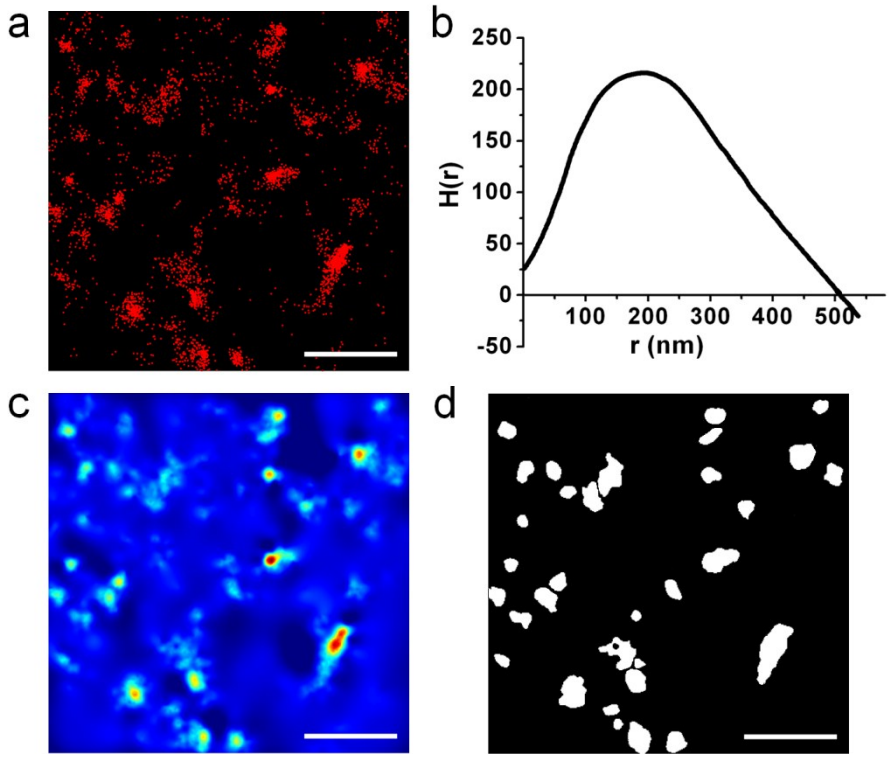
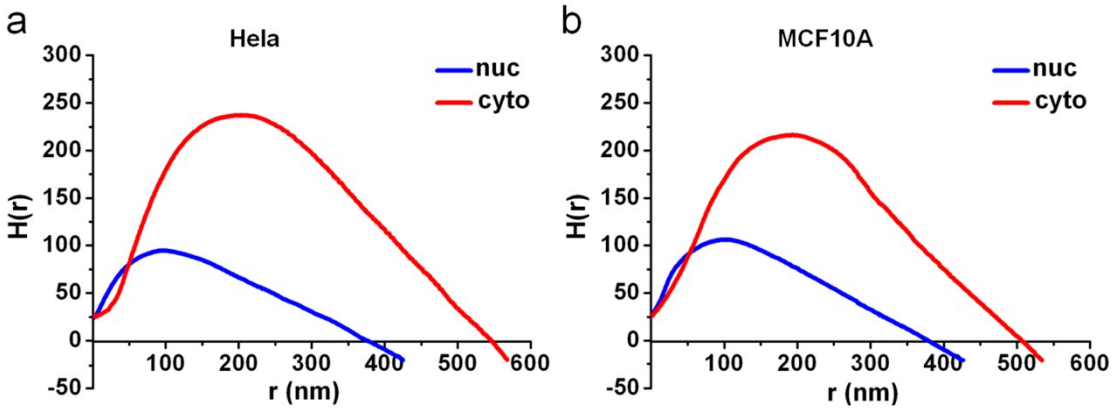


FigS1. The resolution of dSTORM images of YAP in different cells. (a) Quantitative analysis of localizations in a Hela cell at a low cell density from a collection of 5000 frames. The histogram of localizations was fitted to a Gaussian function to determine the imaging resolution, which is described as a full width at half-maximum (FWHM) value of 21.9±1.8 nm. (b) Measurement of the imaging resolution in a MCF10A cell using the same method. The FWHM is 23.0±1.7 nm.



FigS2. An example of YAP clustering analysis by Ripley's K-function. (a) A 4×4 μm^2 region of the reconstructed dSTORM image of YAP in the cytoplasm of a Hela cell at the high cell density. (b) The corresponding Ripley's K-function plot showing that the radius of maximal aggregation is 190 nm and clustering range on length scales at 510 nm. (c) The interpolated cluster map based on Ripley's K-function analysis. (d) The binary cluster image generated from the color-coded cluster map, from which the cluster number, size and shape can be extracted. Scale bars are 1 μm.



FigS3. Ripley's K-function plots of YAP clustering under the pressure. Hela and MCF10A cells were cultured sparsely, and then 2 mm-thick PDMS (p≈24Pa) was pressed on cells for 2 h. After that, cells were fixed, permeablized and stained to image by dSTORM. Ripley's K function was processed in 4×4 μm^2 regions of reconstructed dSTORM images of YAP in the cytoplasm (cyto) and nucleus (nuc) of Hela and MCF10A cells. Each plot shown is the representative of 300 analyzed regions from 100 cells in ten independent experiments.