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SUPPLEMENTARY INFORMATION

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Combined expansion microscopy with structured illumination microscopy for analyzing protein complexes

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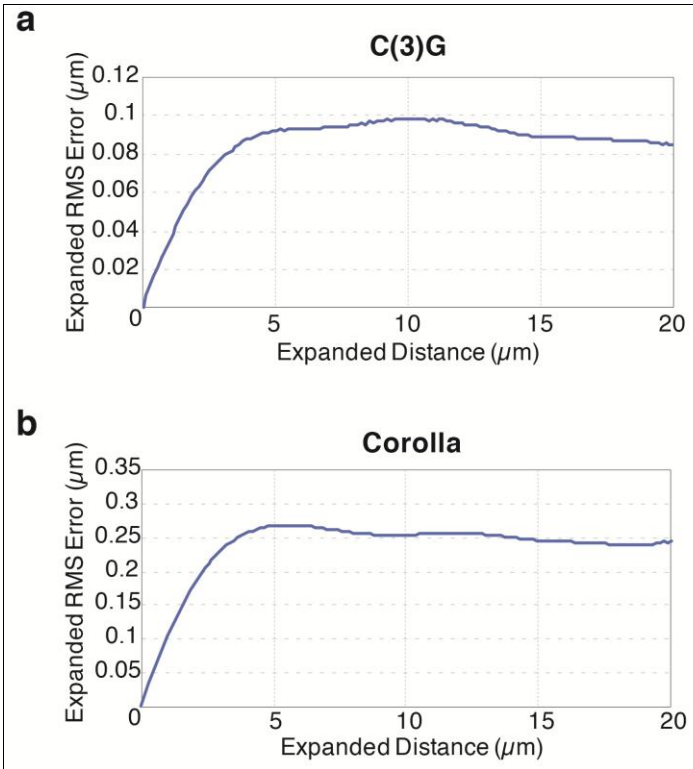
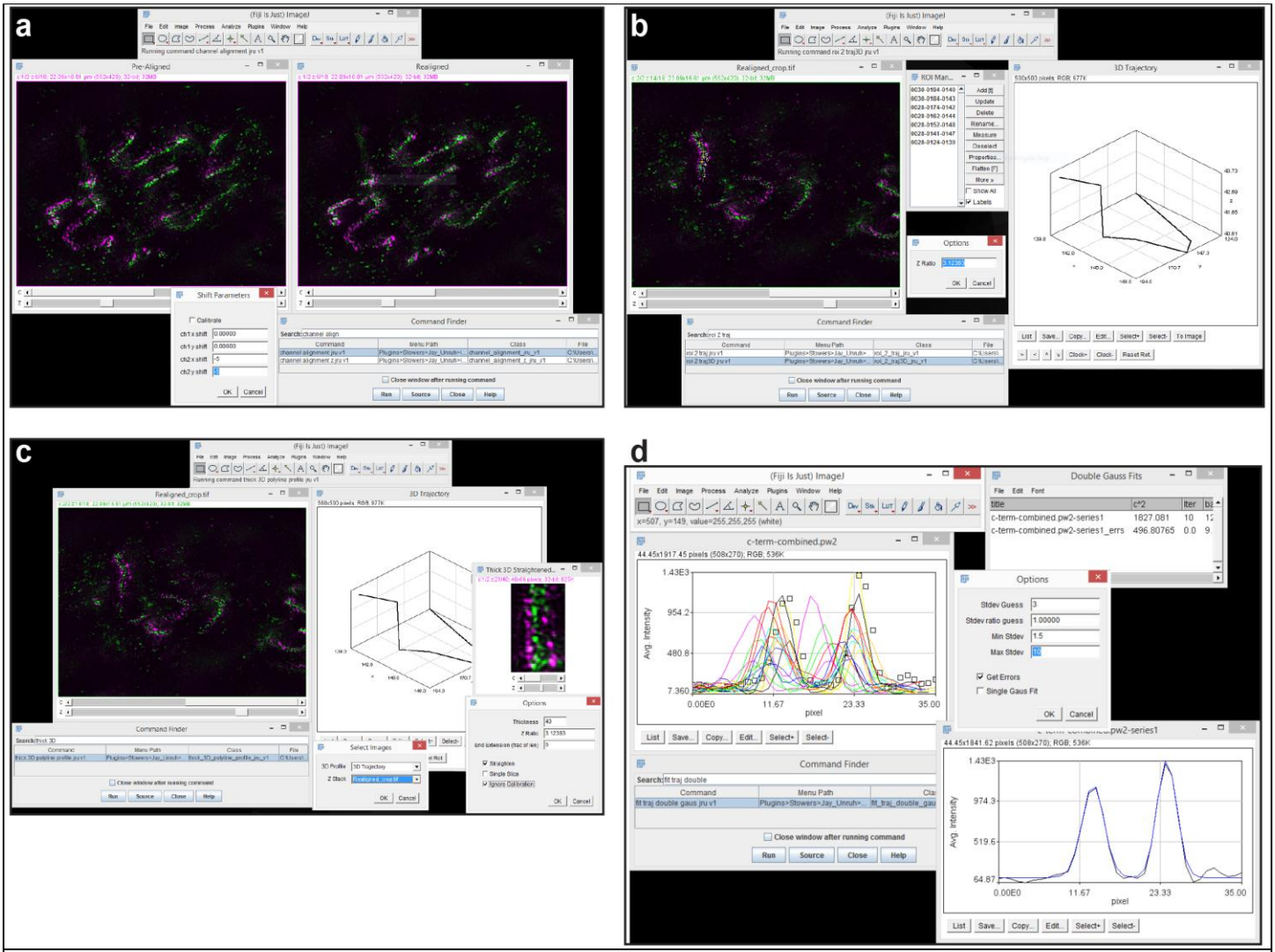


Supplementary Figure 1

Quantification of expansion distortion.

The plot shows the average RMS distance error for all pairs of points as a function of distance in an overlaid SIM and expanded confocal image of C(3)G in Box 3 panels a–c (a) and of Corolla in Box 3 panels d–f (b). Both distances are in expanded units. The distance errors in each subregion were determined by cross-correlation analysis as opposed to feature comparison as in Chen et al.[3]. Note that given the sample manipulations in our protocol (for example: slicing, relabeling), this error represents both expansion distortion and changes in local labeling density.



Supplementary Figure 2

Screenshots of the single particle averaging analysis.

Screenshots illustrating the details of steps (a) 65—color alignment, (b) 68—making an interpolated three-dimensional line profile, (c) 69—computational straightening of the SC along the *Y* axis, and (d) 75–76—Gaussian fitting.