

SUPPORTING INFORMATION:

**Denoising Autoencoder Trained on
Simulation-Derived Structures for Noise
Reduction in Chromatin Scanning Transmission
Electron Microscopy**

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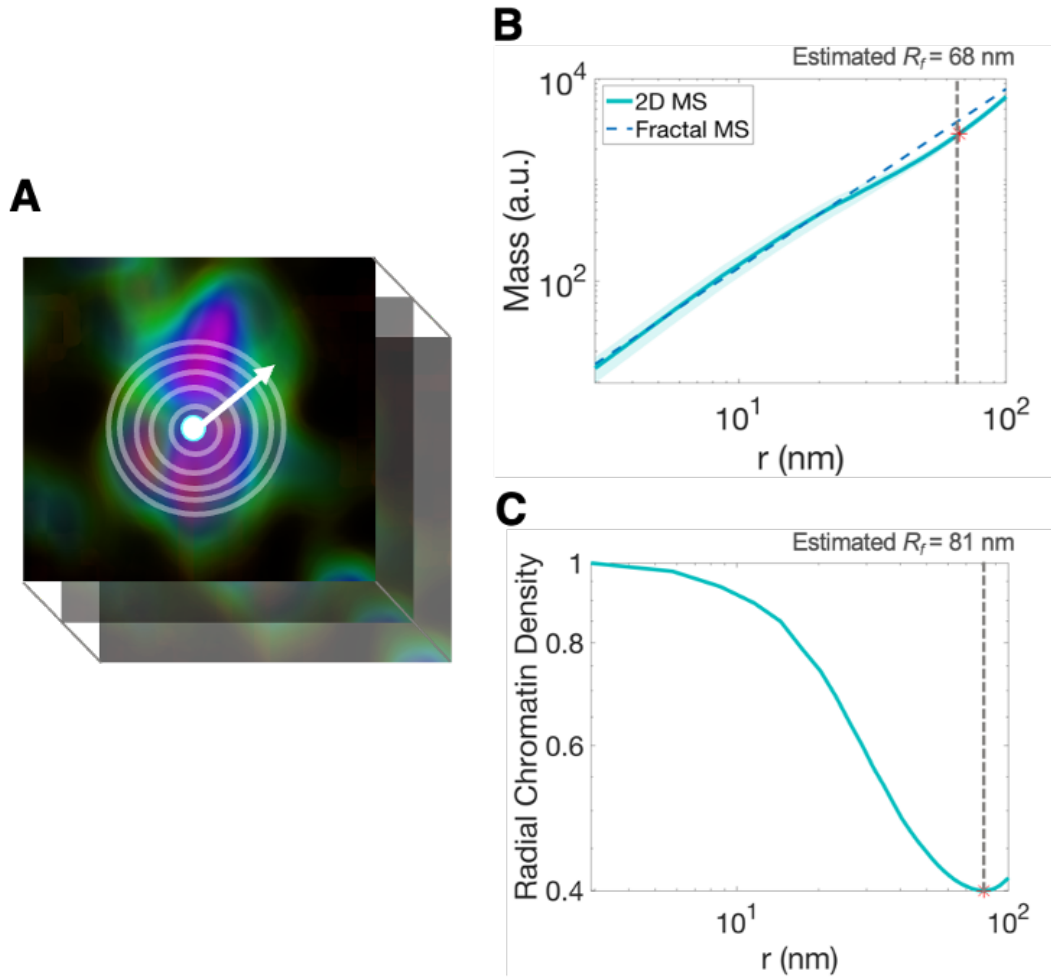


Figure S1: Mass scaling and density analysis originating from the domain centers. A) Mass and radial chromatin density are evaluated starting from the center of a domain (white circle with cyan outline) in concentric circles with increasing distance, r . B) Mass scaling of an individual domain in the log-log scale. We performed linear regression on the mass scaling curve and obtained a slope, $D < 3$ for r up to 68 nm (blue dashed line). Beyond the red asterisk, a more significant divergence ($>5\%$ error) in the mass scaling behavior is observed. Further, as r increases, there is a sharp transition to the supra-domain regime with D approaching 3. C) Radial chromatin density of an individual domain in the log-log scale. Radial chromatin density of a domain initially is almost constantly high, roughly near the center of the domain. The density then decreases rapidly at moderate distances from the domain center. After a given large distance shown as a red asterisk at 81 nm, radial density increases again. This increase is potentially due to the end of one domain boundary and the interactions with neighboring domains.

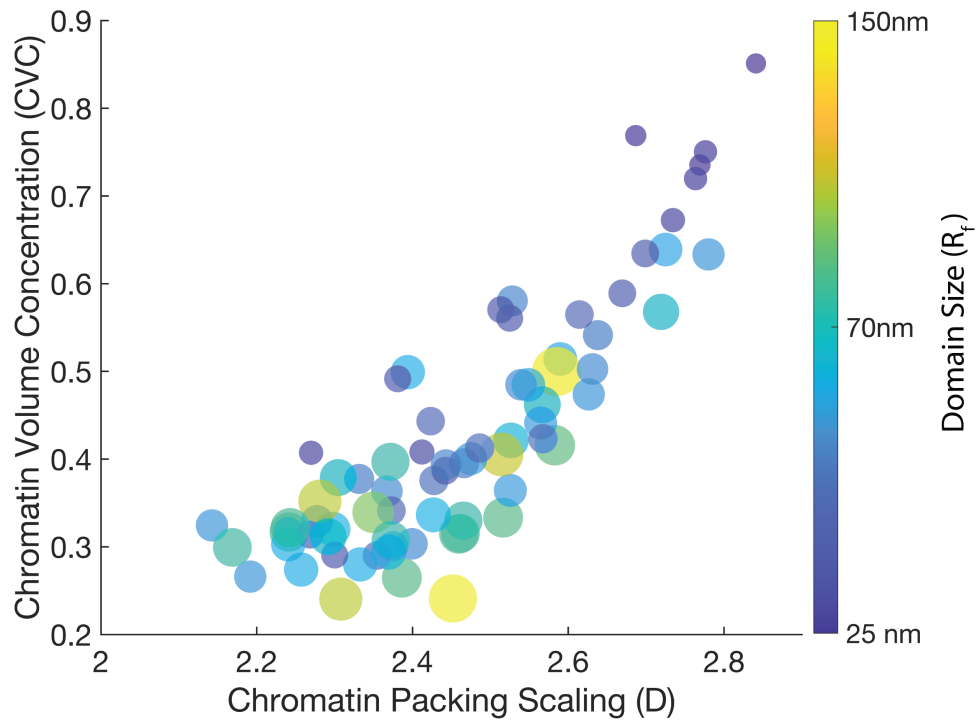


Figure S2: Characterization of morphological properties of original higher-noise tomograph of A549 cells. Statistical distribution of chromatin packing scaling D , cluster volume concentration CVC , and domain size R_f .

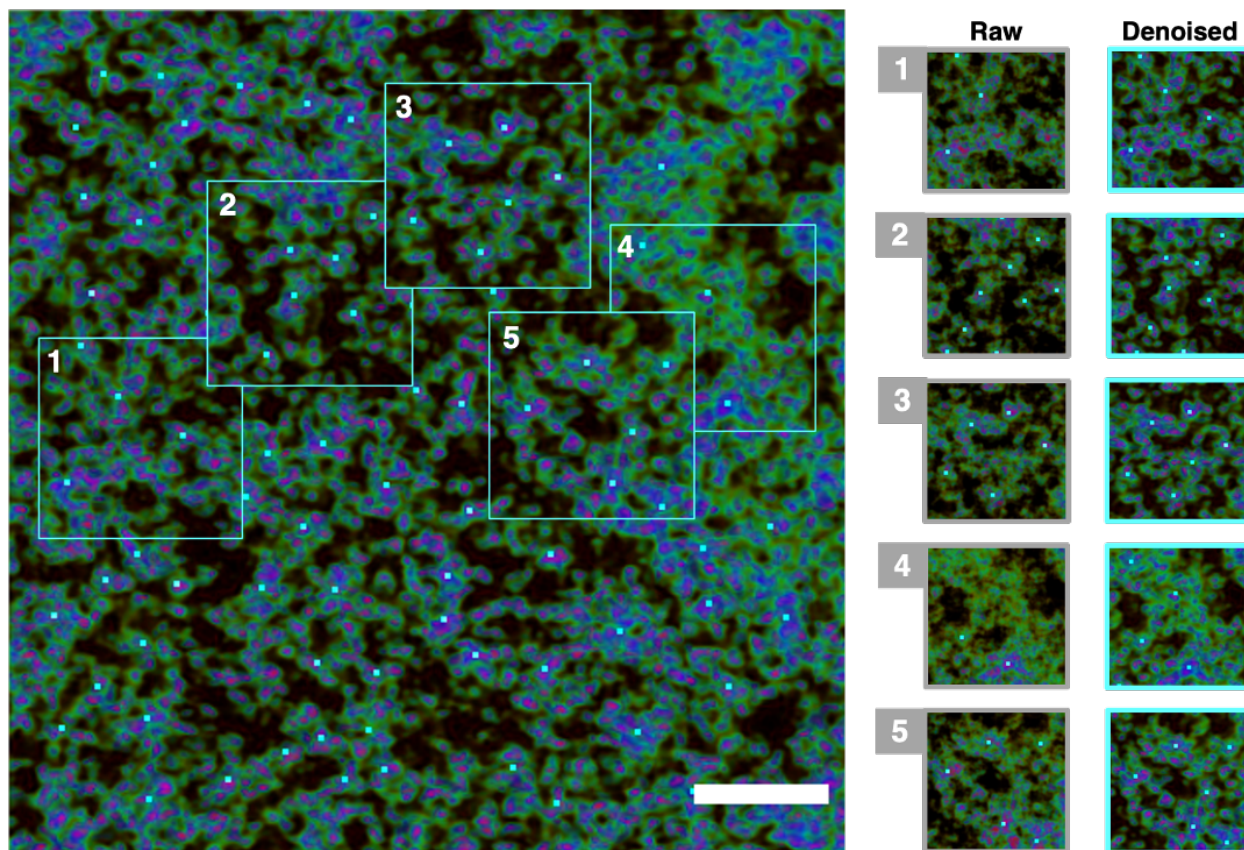


Figure S3: Denoising can resolve domains that are closer in space. Left: Domain centers were estimated from denoised tomograms. Right: Five representative regions of the raw and the denoised tomograms show that more domains were identified in the denoised tomogram. Centers are indicated in cyan.