

***Super-resolution imaging reveals distinct chromatin folding for different epigenetic states***

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**Abstract:**

Over the last century, improved microscopic approaches have enabled the study of chromosome organization at increasing resolution. The authors investigate the 3D organization of chromatin in different epigenetic states using super-resolution imaging. They classified genomic domains in *Drosophila* cells into transcriptionally active, inactive or Polycomb-repressed states, and observed distinct chromatin organizations for each state. All three types of chromatin domains exhibit power-law scaling between their physical sizes in 3D and their domain lengths, but each type has a distinct scaling exponent. Polycomb-repressed domains show the densest packing and are characterized by a high degree of chromatin intermixing within the domain. Moreover, compared to inactive domains, Polycomb-repressed domains spatially exclude neighbouring active chromatin to a much stronger degree. Computational modelling and knockdown experiments suggest that reversible chromatin interactions mediated by Polycomb-group proteins play an important role in these packaging properties of the repressed chromatin.

**References:**

1. Boettiger A. N., et al. (2016) Super-resolution imaging reveals distinct chromatin folding for different epigenetic state. *Nature*, **529**, 418-422, doi:10.1038/nature16496.