Single-Cell Analysis of the 3D Topologies of Genomic Loci Using Genome Architecture Mapping

We will study the Histone Locus Body (HLB), which resides in the nucleus and plays an important role in the production of histone genes. The HLB is formed at specific times during the cell cycle when histone genes are needed. At other times, the HLB is deconstructed. The HLB is formed by the coalescing of portions of the genome that contain the histone genes (which are contained on chromosomes 13, 3, 11, and 6 of the mouse). We will study on the largest portion of the HLB – the HIST1 region.

HIST1 is located on mouse chromosome 13 at the following coordinates:

Start:21.7 Mb

Stop: 24.1 Mb

Extract the HIST1 region from the segmentation table.

Extract relevant NPs for HIST1 (NPs which contain at least one window in the region of interest).

Calculate basic statistics for the HIST1 region:

1. Number of genomic windows
2. Number of NPs
3. On average, how many windows are present in an NP?
4. What is the smallest number of windows present in any NP? The largest?
5. On average, what is the number of NPs in which a window is detected? The smallest? The largest?

What are the most common radial positions of the HIST1 region? (Based on the NPs that captured the region.)

What are the typical compactions of the windows within the HIST1 region?