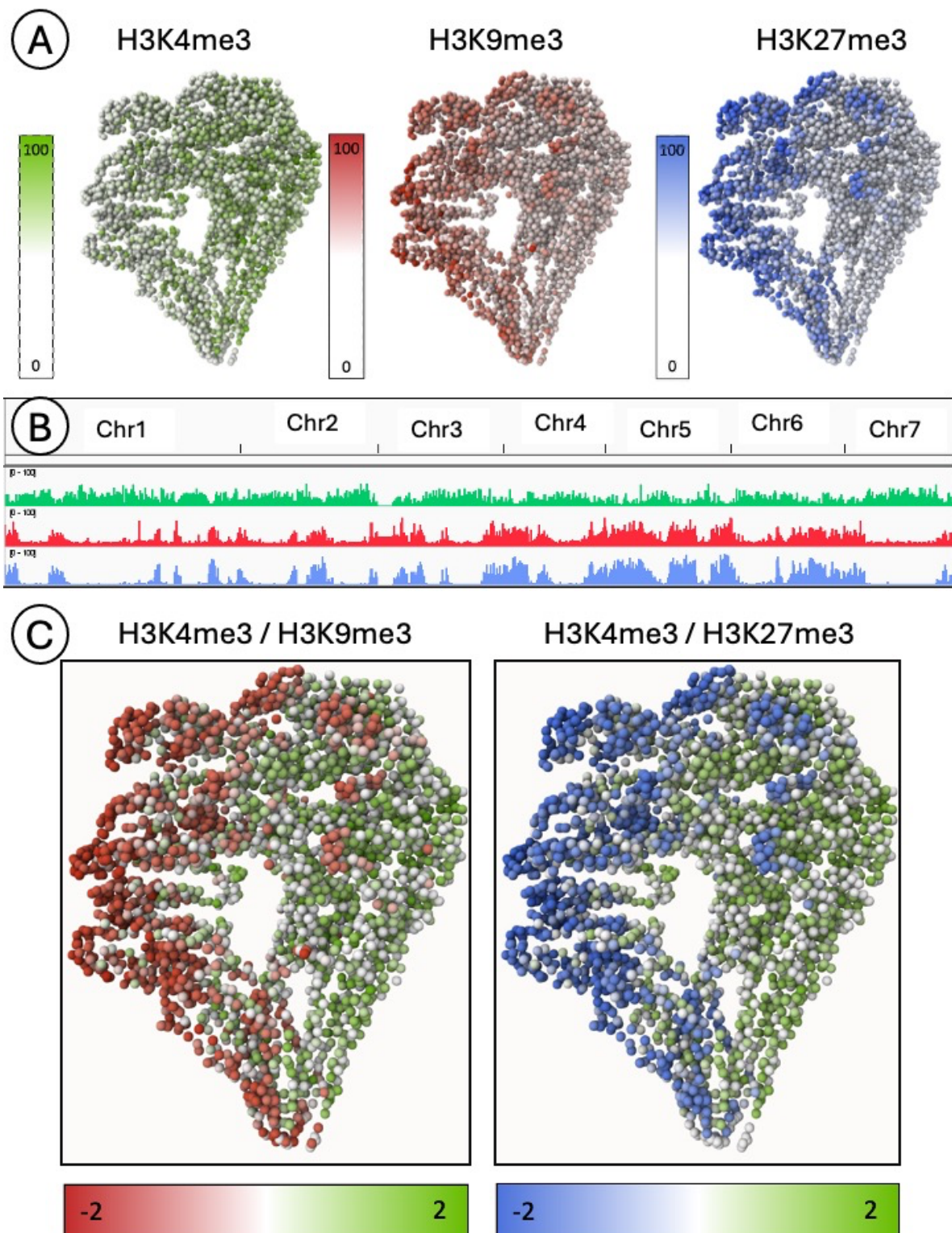


DataFile 7



Genome-wide patterns of three post-translational histone modifications, relating to open euchromatin (H3K4me3) and compact heterochromatin (H3K9me3 and H3K27me3). The ChIP-seq data were collected from (1) and analysed using the

pipeline available <https://src.koda.cnrs.fr/AnakimGualdoni/3dgb-chipseq-analysis>. **(A)** ChIP-seq signal intensities were calculated for each bead in the 3D model ('per bin') and used to colour the beads according to relative colour scales ranging from 0 (no signal) to 100 (very strong signal). **(B)** A linear representation of the same ChIP-seq signals is shown using a standard genome browser. Green, red and blue correspond to the histone marks H3K4me3, H3K9me3 and H3K27me3, respectively. **(C)** Representation of the relative intensities of the H3K4me3 and H3K9me3 or H3K27me3 signals is shown here. Positive values correspond to H3K4me3-specific regions (green), while negative values correspond to H3K9me3-specific (red) or H3K27me3-specific (blue) regions.

Reference

1. Carlier,F., Li,M., Maroc,L., Debuchy,R., Souaid,C., Noordermeer,D., Grognet,P. and Malagnac,F. (2021) Loss of EZH2-like or SU(VAR)3-9-like proteins causes simultaneous perturbations in H3K27 and H3K9 tri-methylation and associated developmental defects in the fungus *Podospora anserina*. *Epigenetics Chromatin*, **14**, 22.