

Visualisation of genomic data with the Hilbert curve

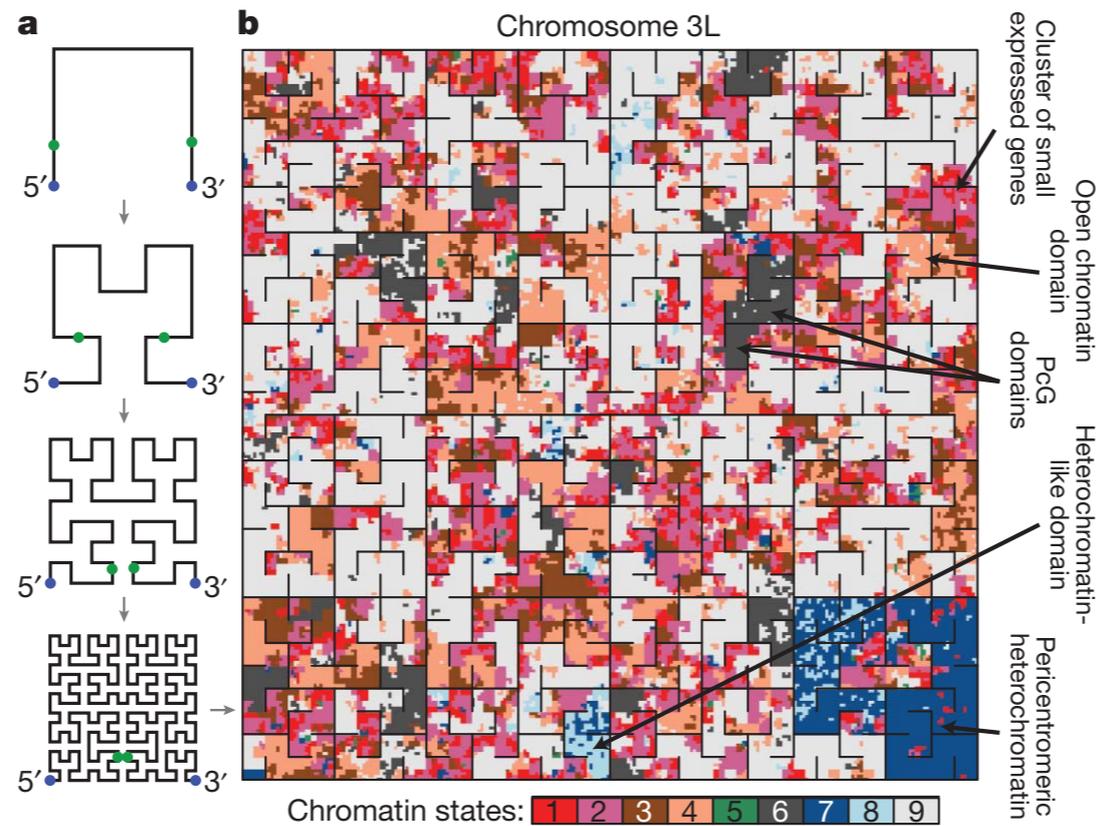


Figure 2 | Visualization of spatial scales and organization using compact folding. a, The chromosome is folded using a geometric pattern (Hilbert space-

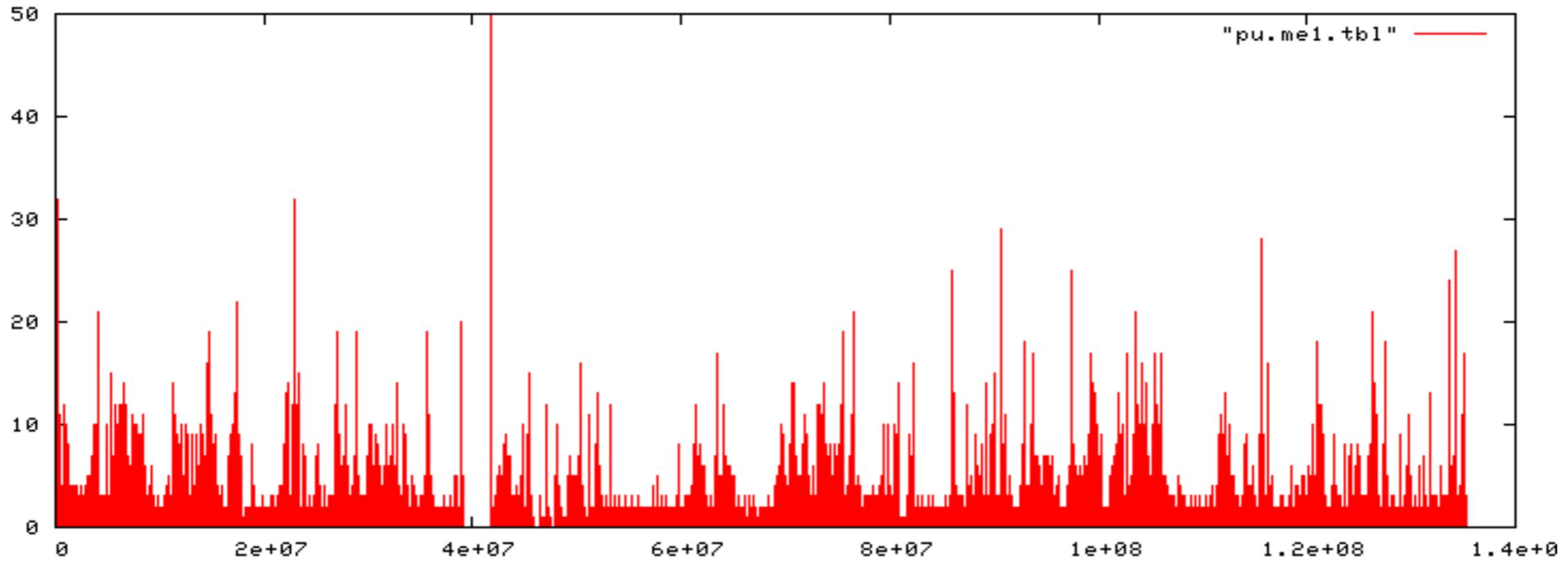
Wolfgang Huber

Brixen 2011

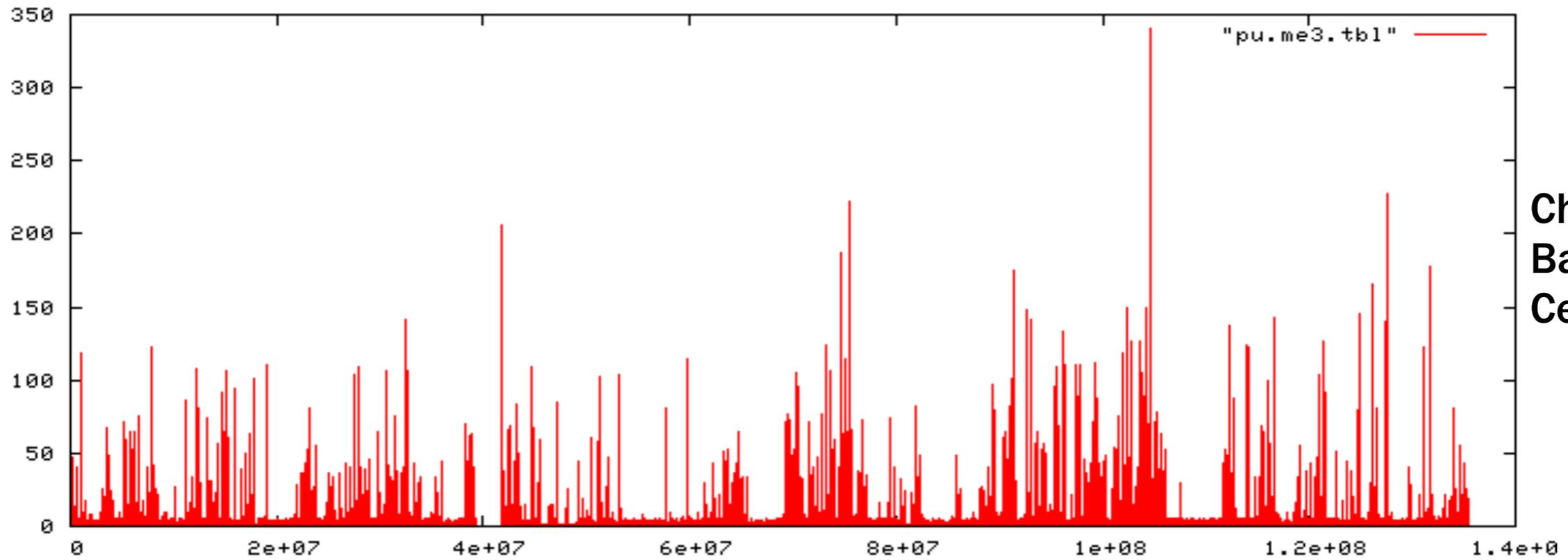
with slides from Simon Anders

Pile-up plot for chromosome 10

H3K4me1



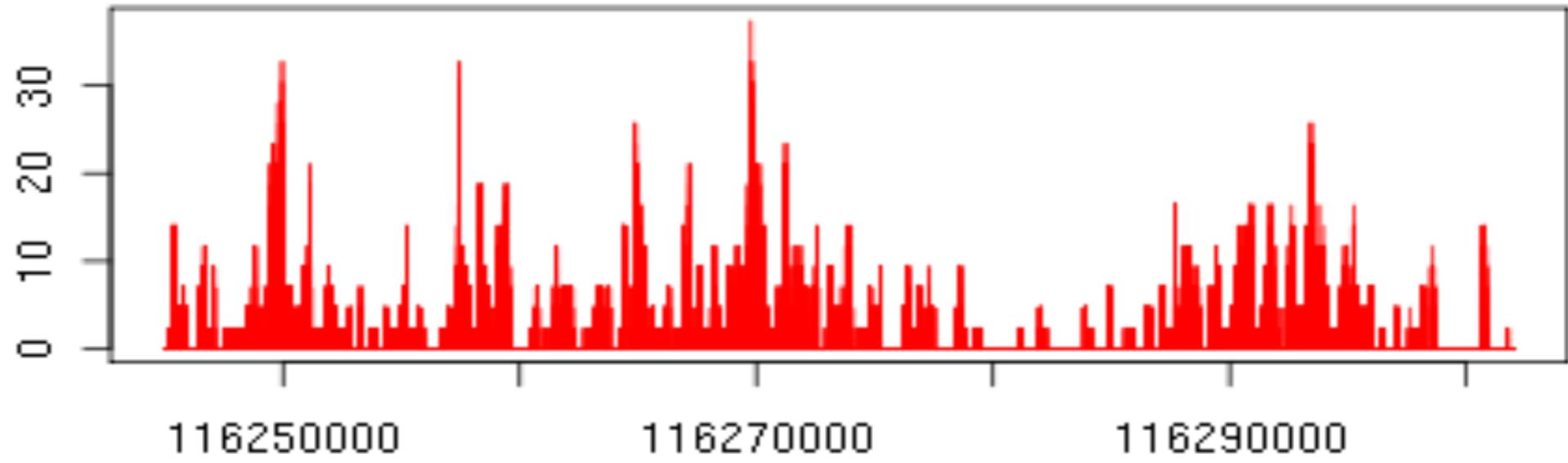
H3K4me3



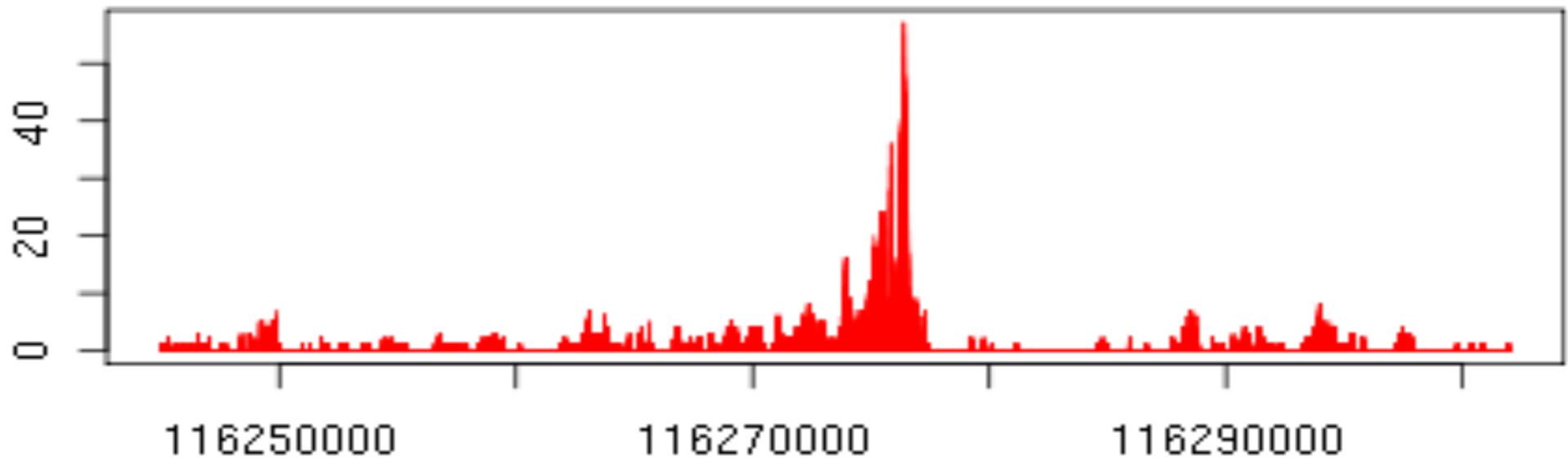
ChIP-Seq
Barski et al.
Cell 2007

Zoom-in

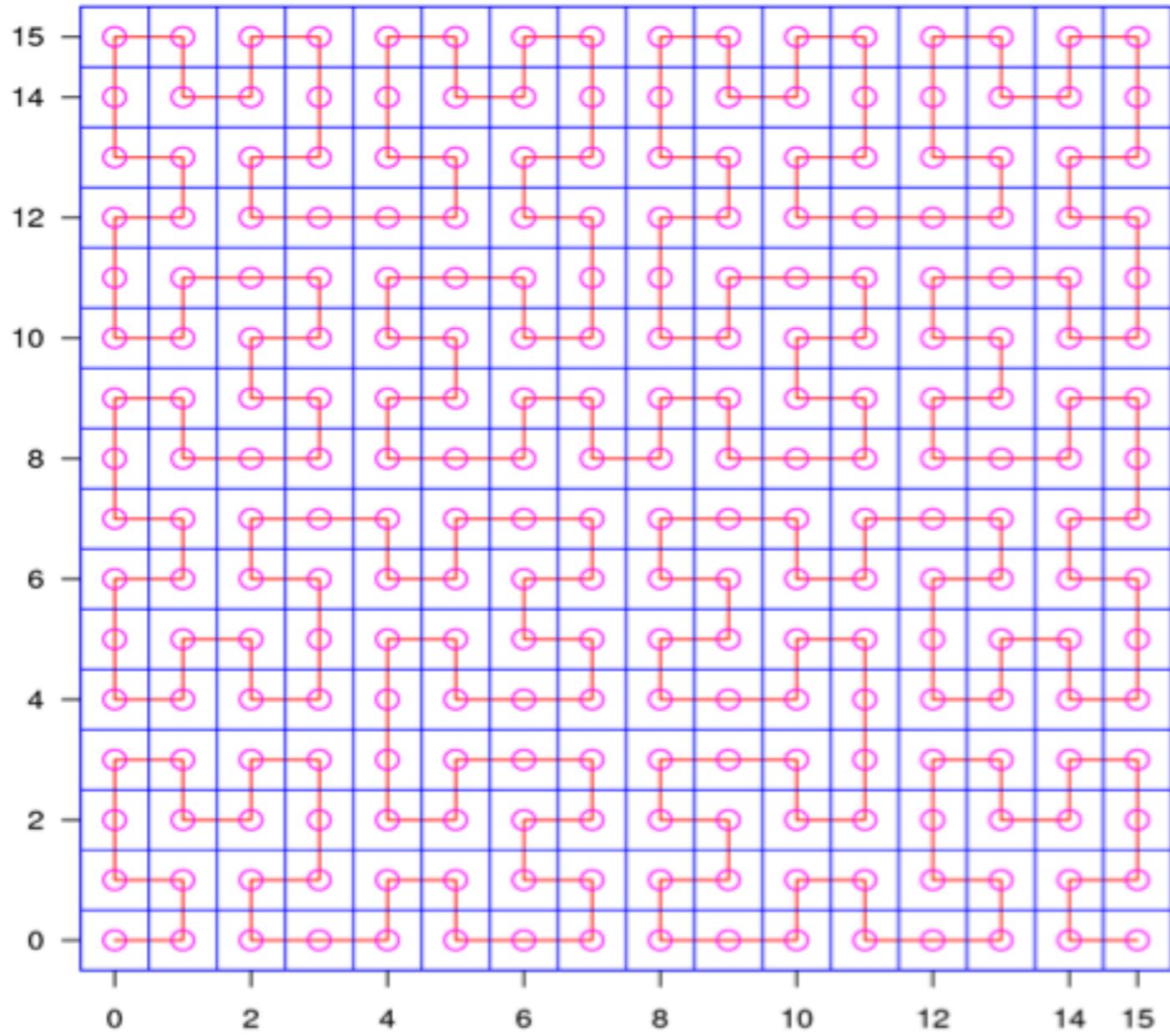
H3K4me1



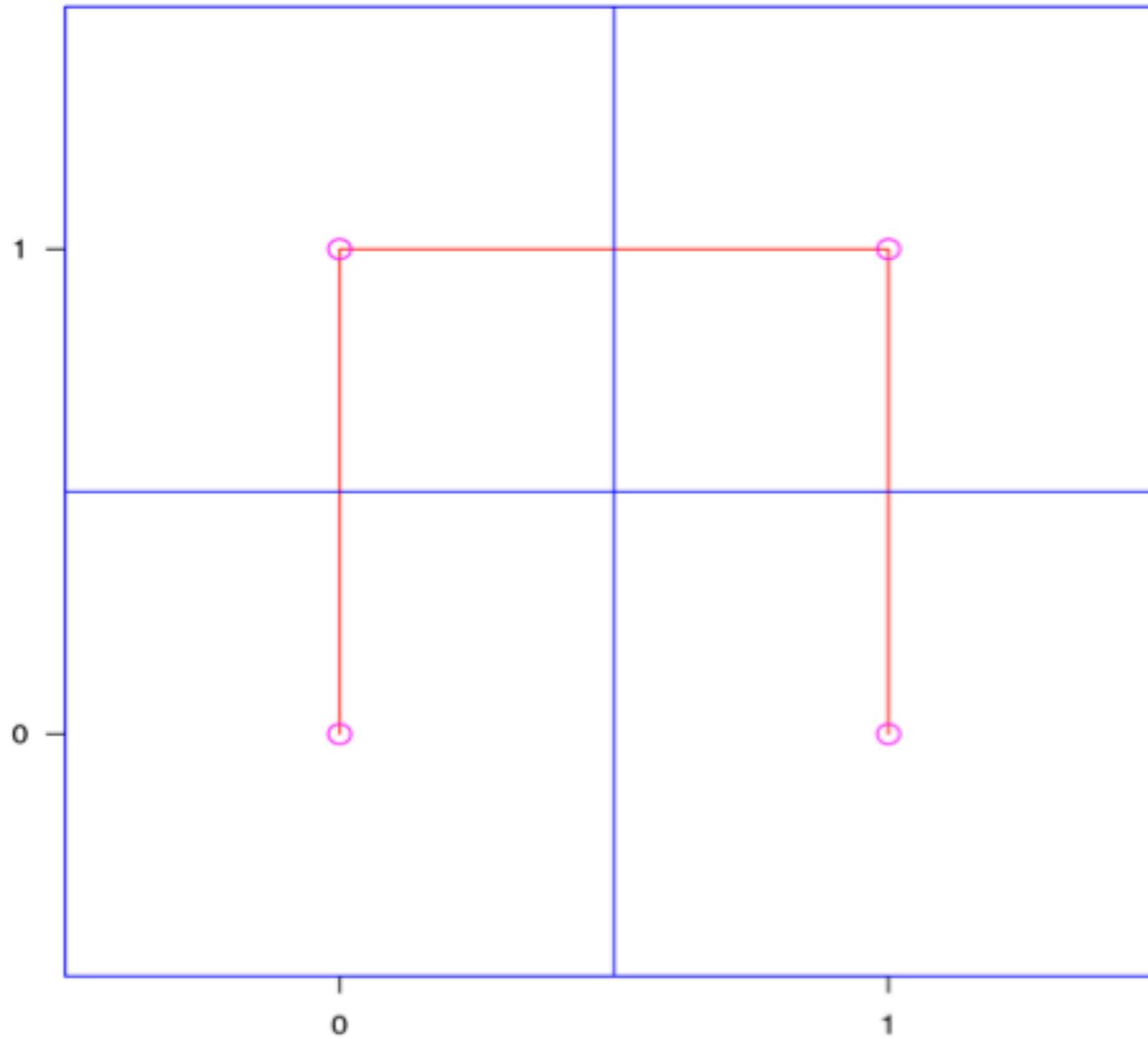
H3K4me3



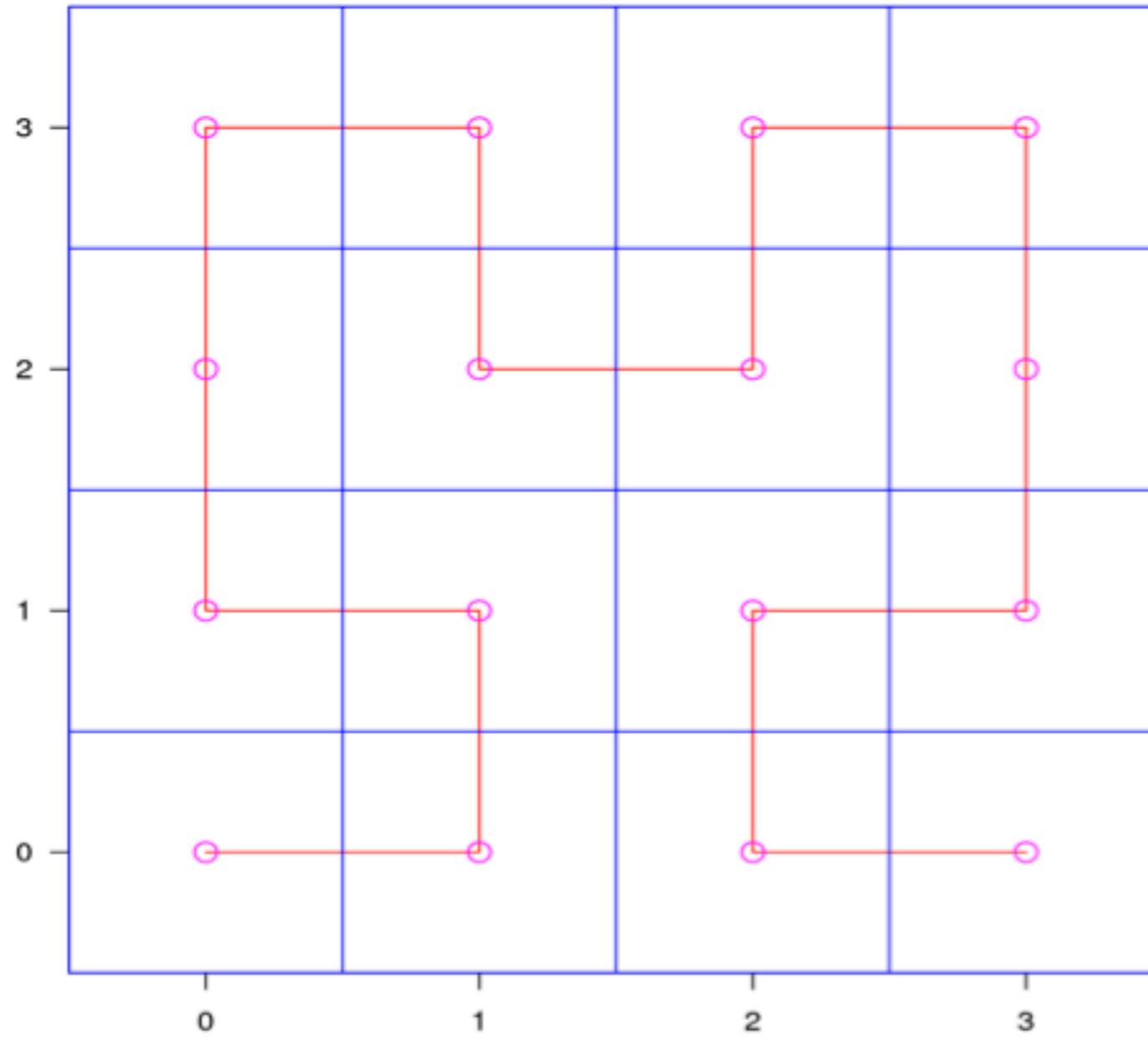
Hilbert curve



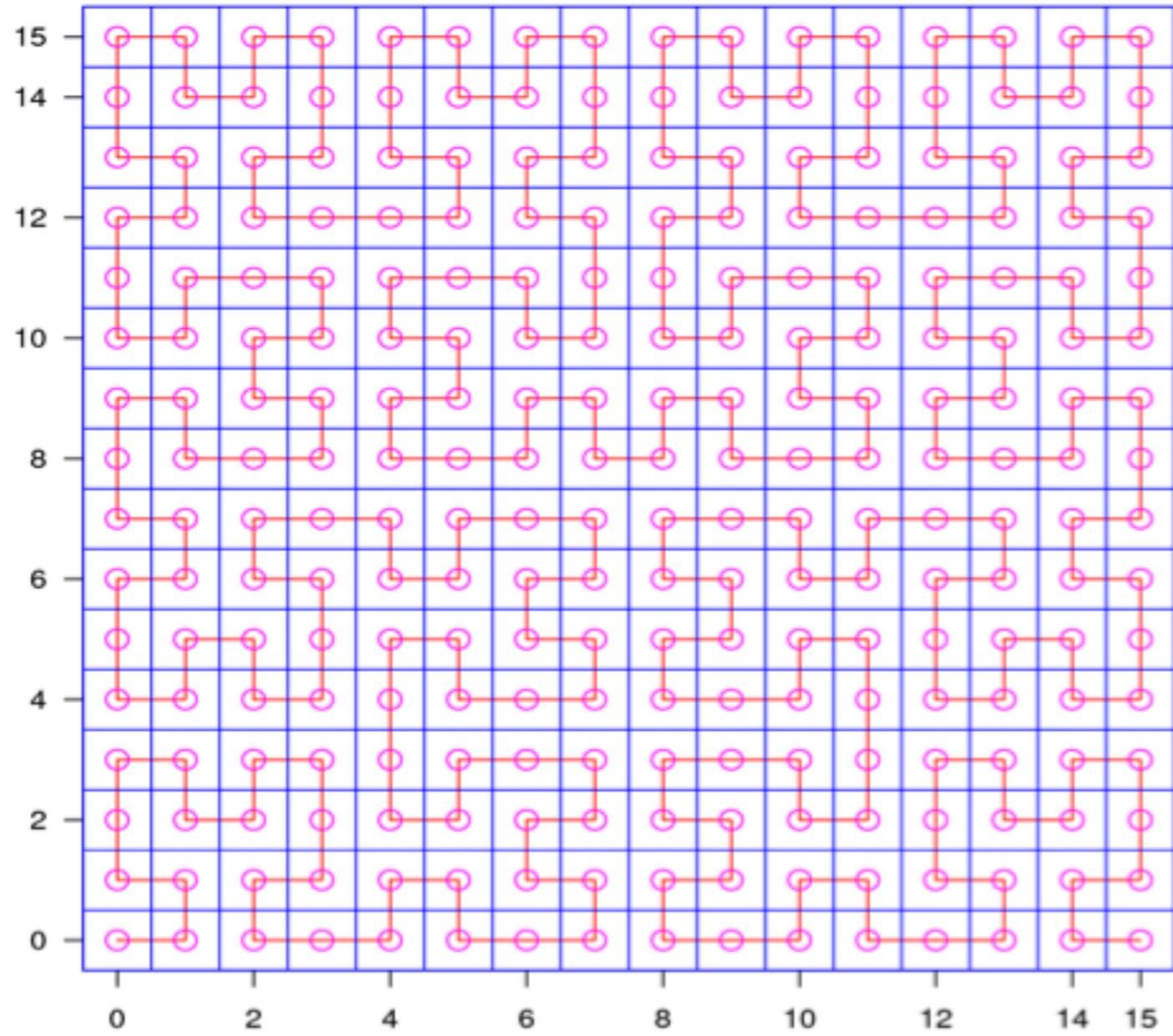
Hilbert curve, iteration 1



Hilbert curve, iteration 2

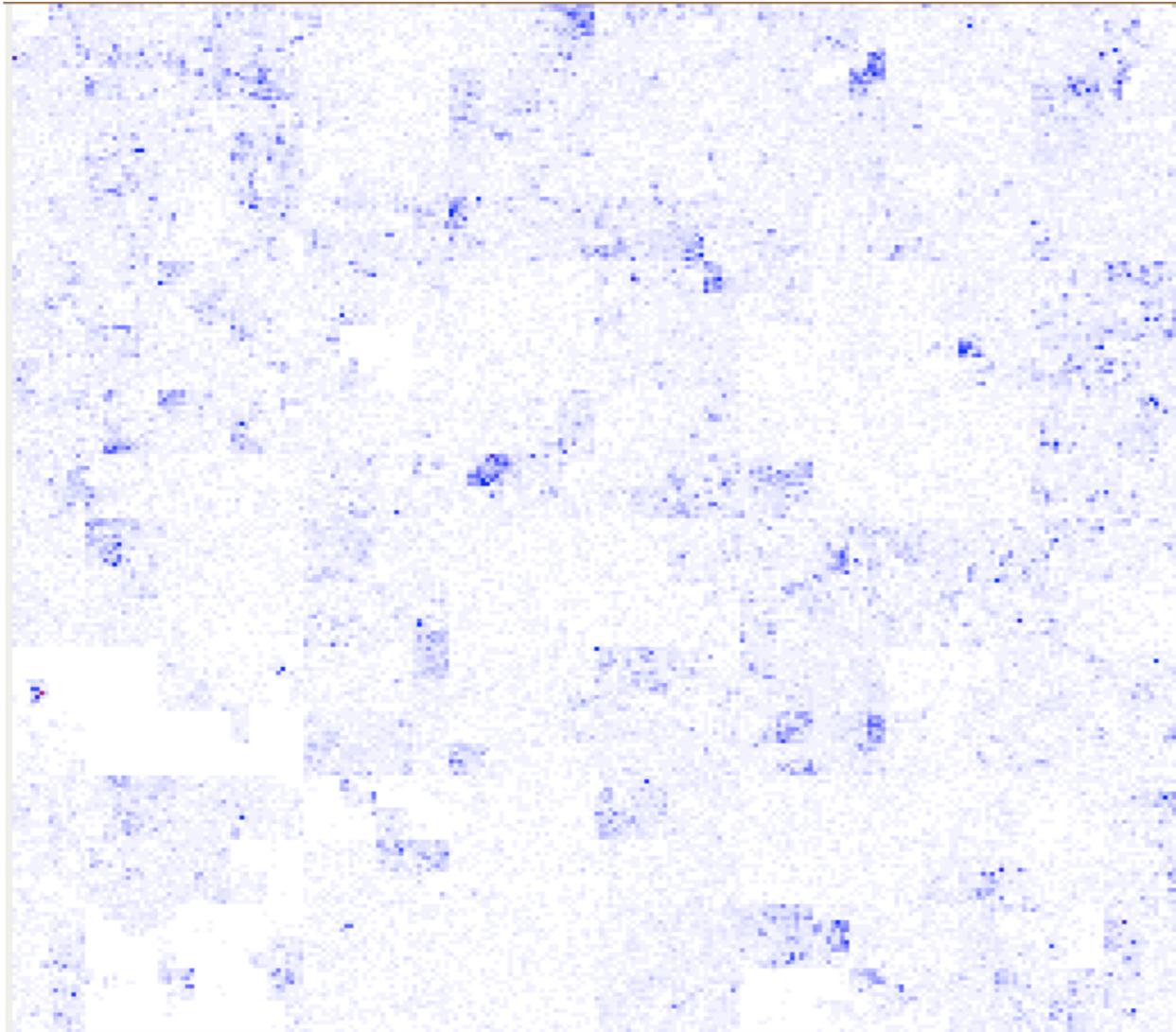


Hilbert curve, iteration 4

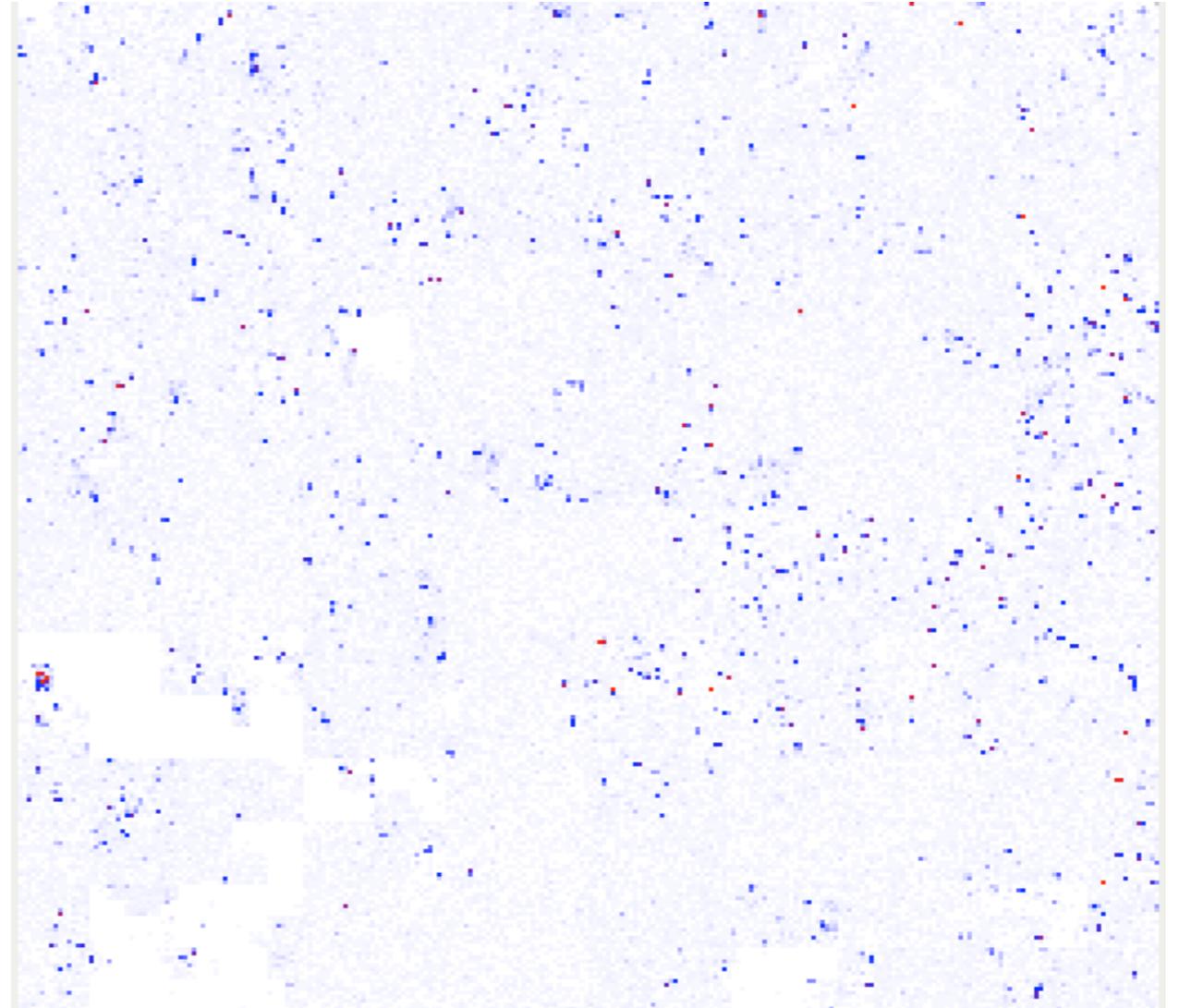


Hilbert plots of chromosome 10

H3K4me1



H3K4me3

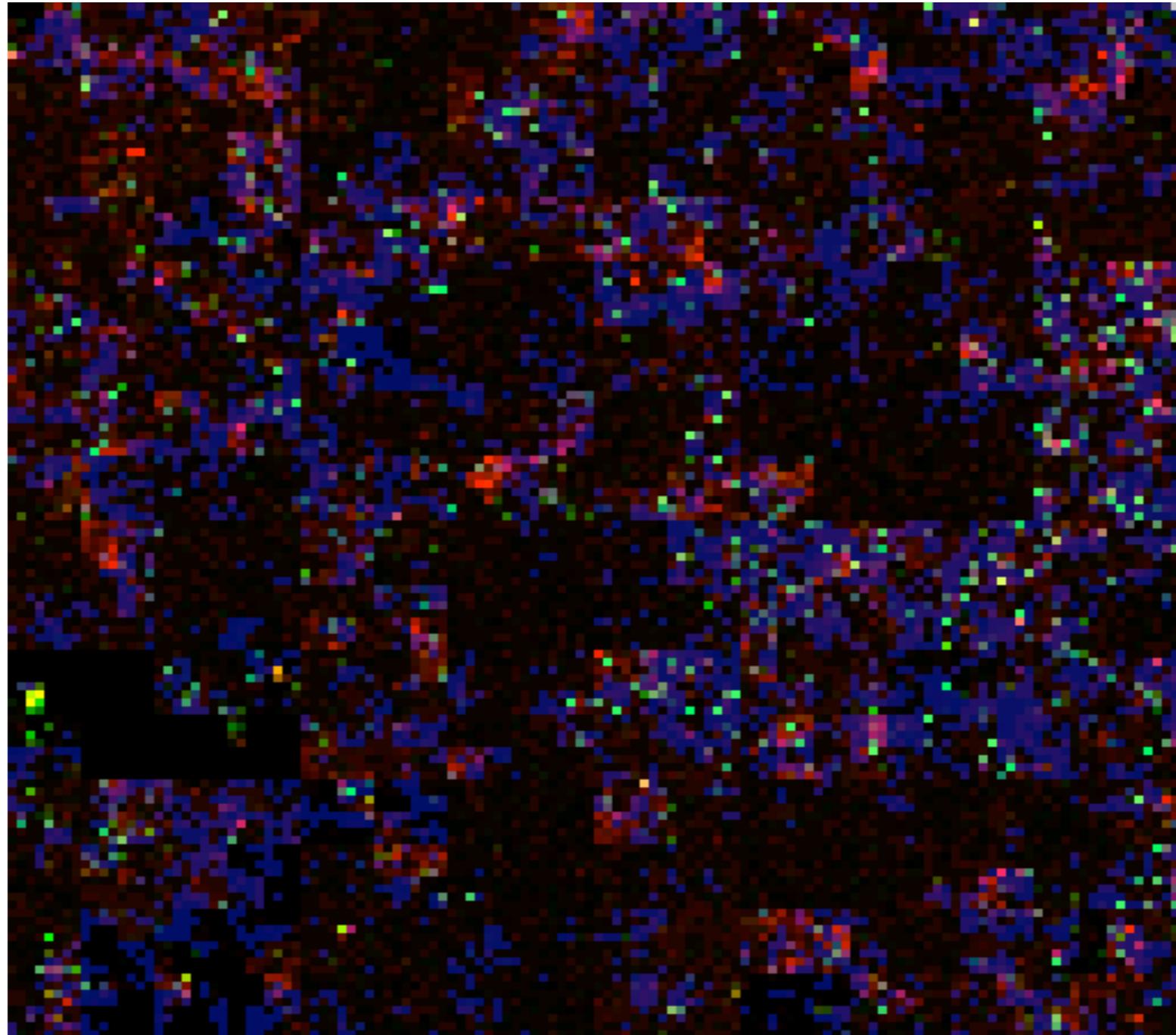


3-colour Hilbert plot

red: H3K4me1

green: H3K4me3

blue: exons



History

The concept of space-filling curves is due to Giuseppe Peano (1890).

This specific curve has been invented by David Hilbert (1891).

The idea to use these curves for visualization was first published by Daniel Keim (1996) for economics data.

Comprehensive analysis of the chromatin landscape in *Drosophila melanogaster*

Peter V. Kharchenko et al. (modEncode) Nature 2010

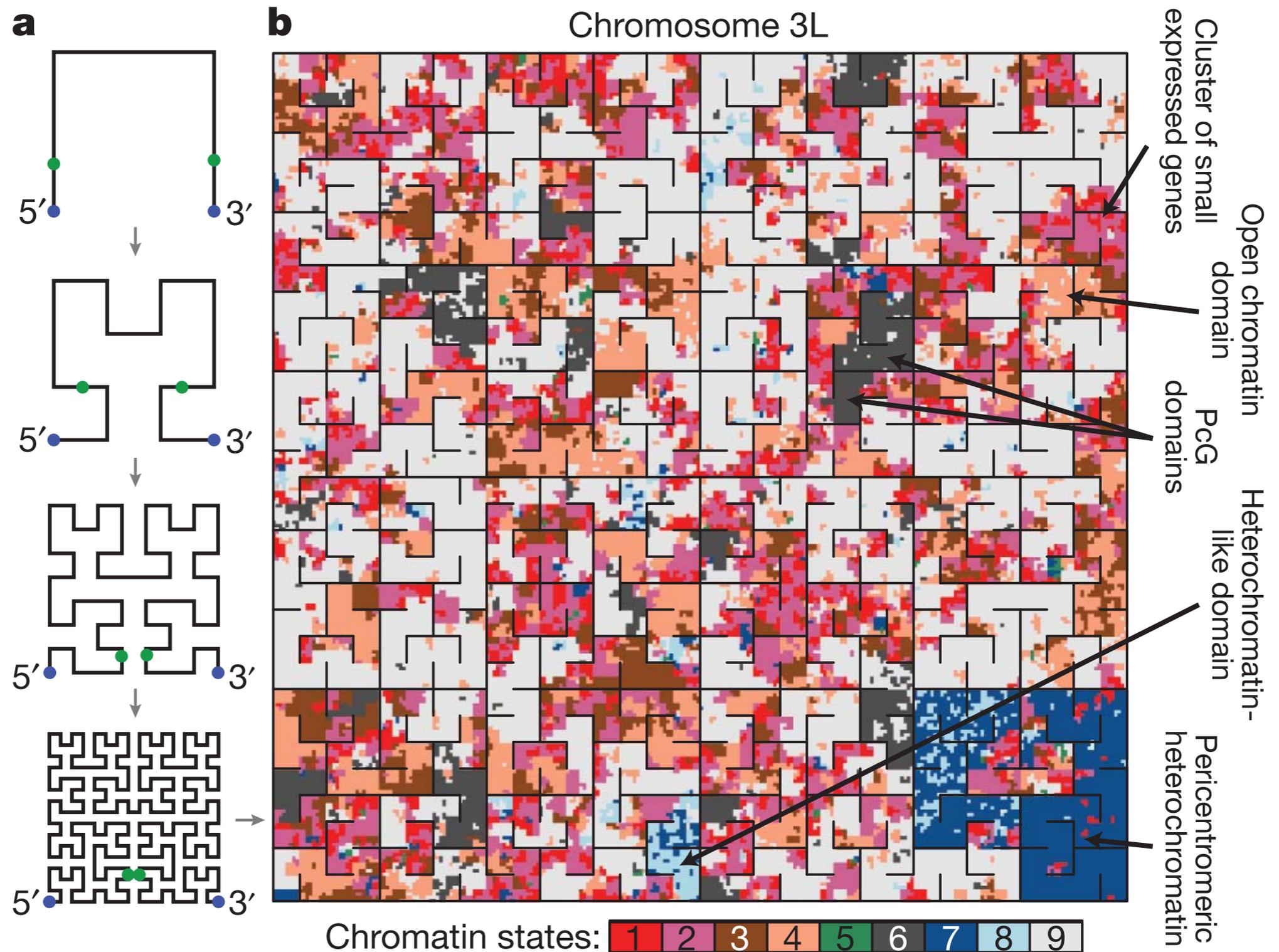


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Bioconductor packages HilbertVis & HilbertVisGUI



Simon
Anders

**Stand-alone application:
reads GFF and wiggle track
files (incl. BED)**

