

## Additional File 1

### Linker histone epitopes are hidden by in situ higher-order chromatin structure

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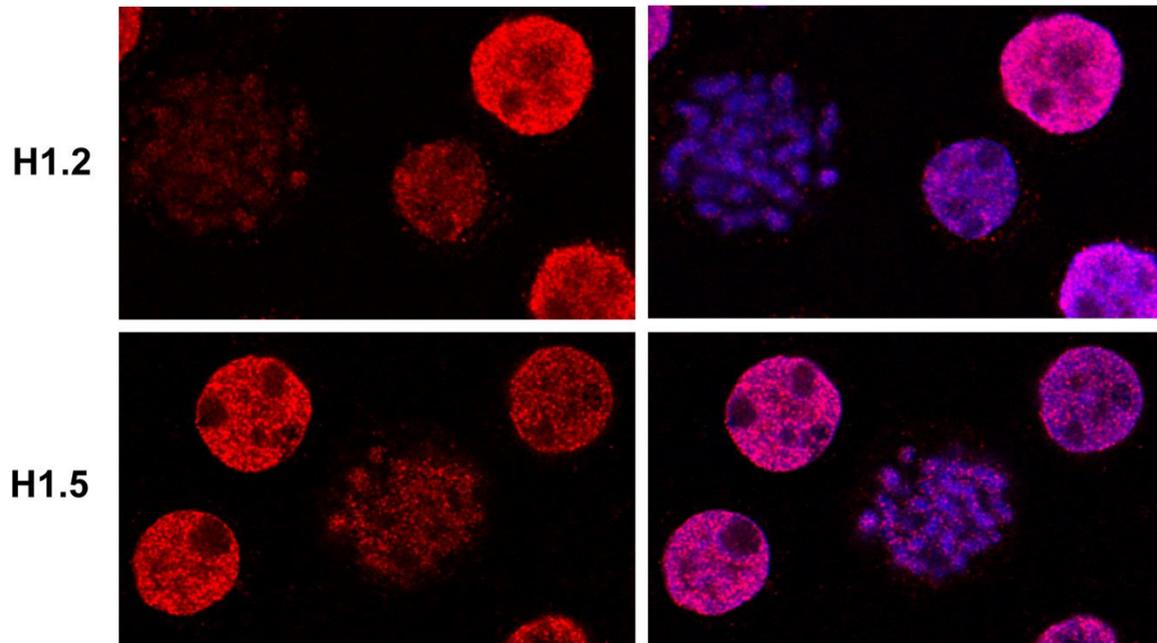


Figure S1. Confocal imaging of interphase and mitotic undifferentiated HL-60/S4 cells stained with anti-H1.2 (top row) including DAPI (right column) or with anti-H1.5 (bottom row) including DAPI (right column). Note that anti-H1.2 stains the mitotic chromosomes weaker than does anti-H1.5; but the staining of interphase nuclei are comparable.

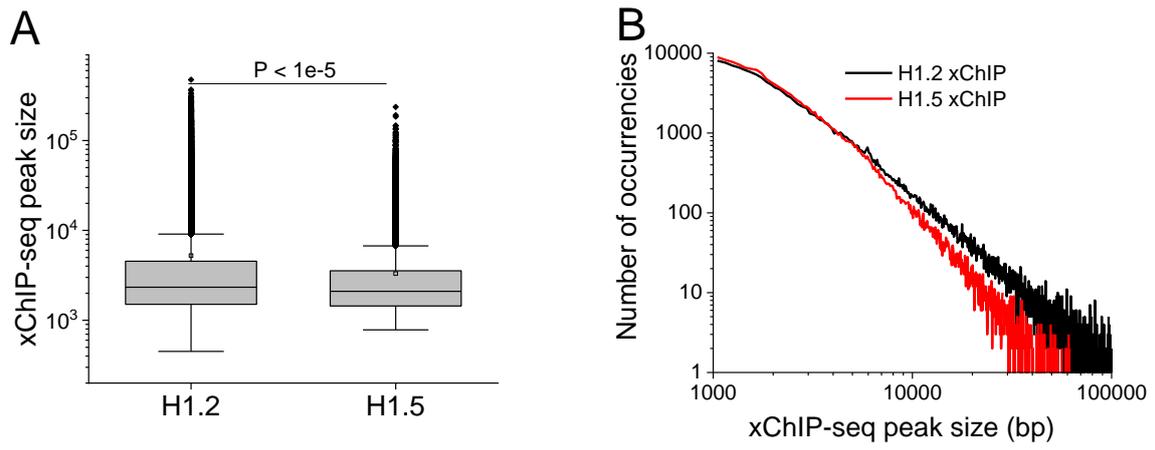


Figure S2. Analysis of the size (bp) distribution of chromatin peaks enriched with anti-H1.2 and anti-H1.5 based on xChIP-seq. Peak calling was performed using MUSIC.

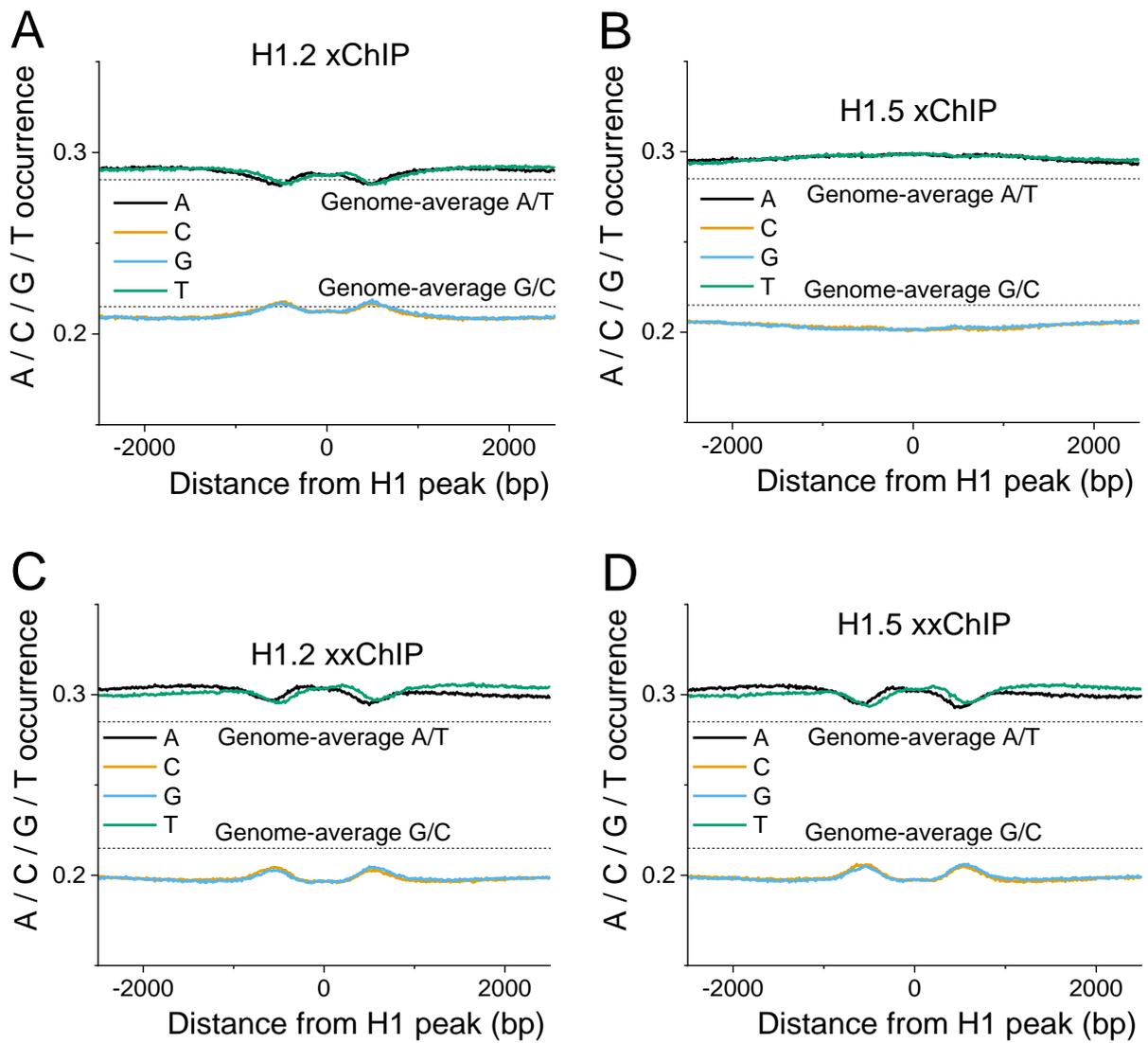


Figure S3. Nucleotide content around MUSIC-called peaks enriched for H1 variants.

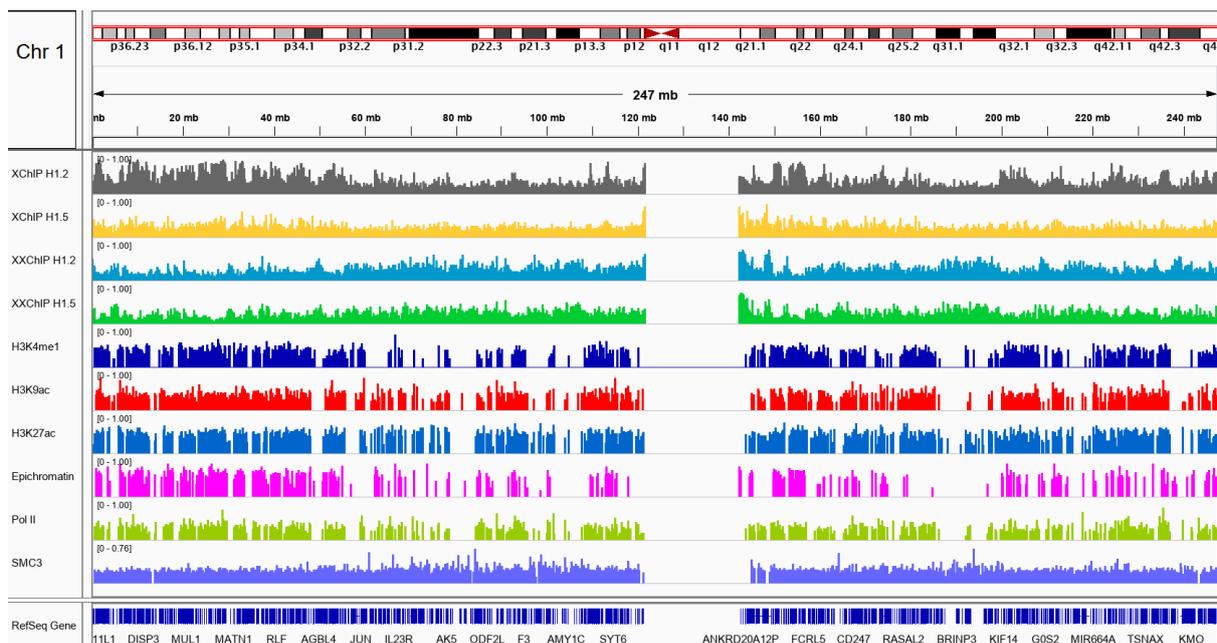


Figure S4. Large-scale (low resolution) comparisons between xChIP and xxChIP sequencing strategies for all the human chromosomes. H1 epitope “exposure” peak densities are measured by scanning with a window of 1000 base pairs: for xChIP H1.2 (black), xChIP H1.5 (orange), xxChIP H1.2 (blue) and xxChIP H1.5 (green). Also indicated are cytogenetic road marks, chromosome coordinates (mb), the epichromatin track (Olins et al., 2014), and tracks showing the density of peaks enriched with H3K4me1, H3K9ac, H3K27ac, Pol II and SMC3.

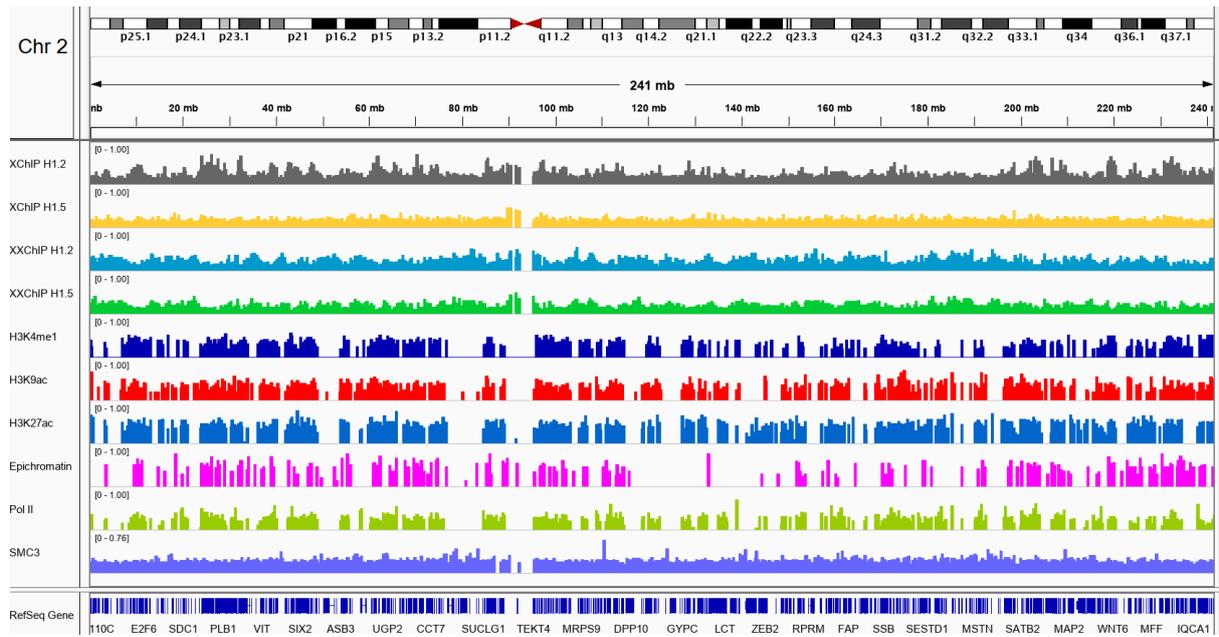


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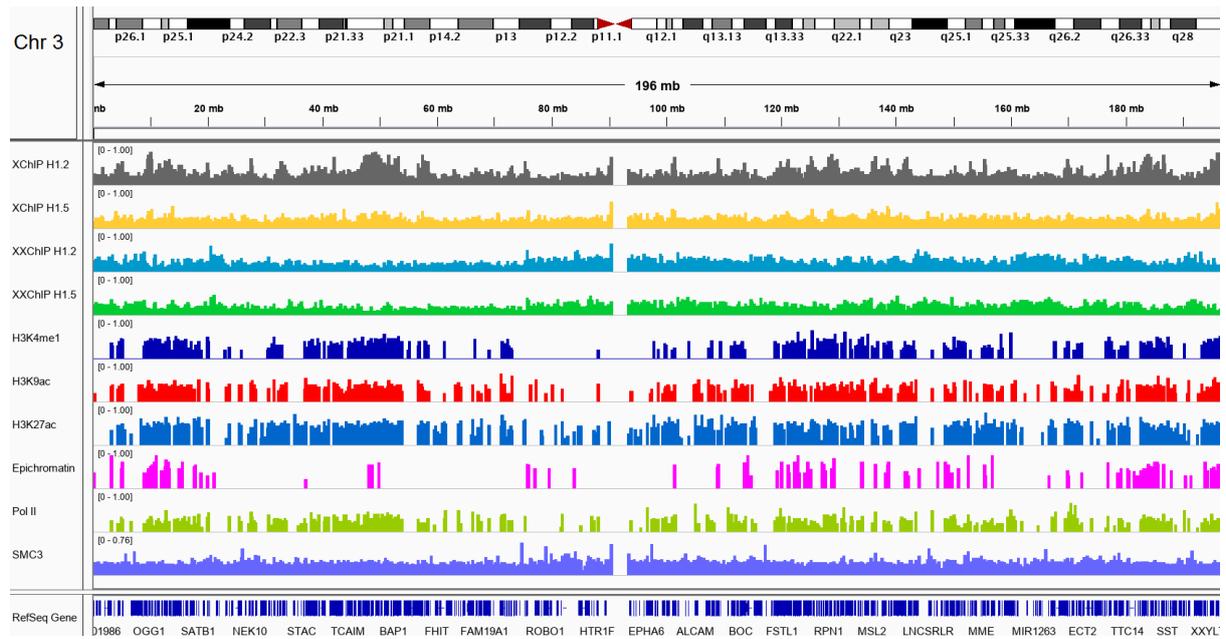


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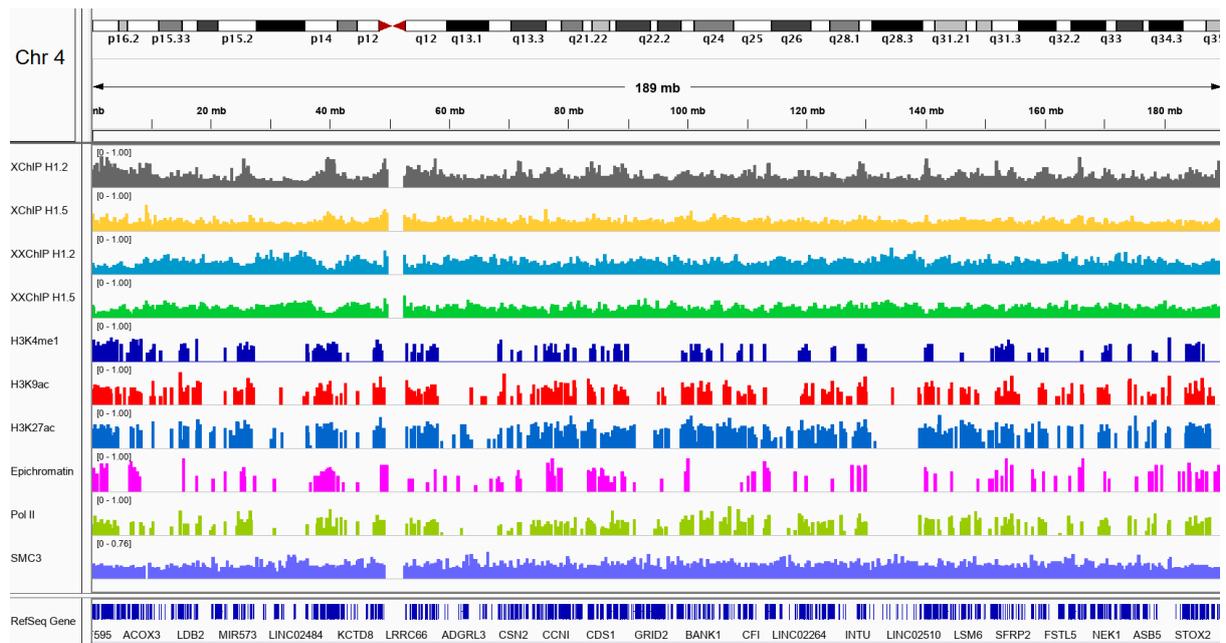


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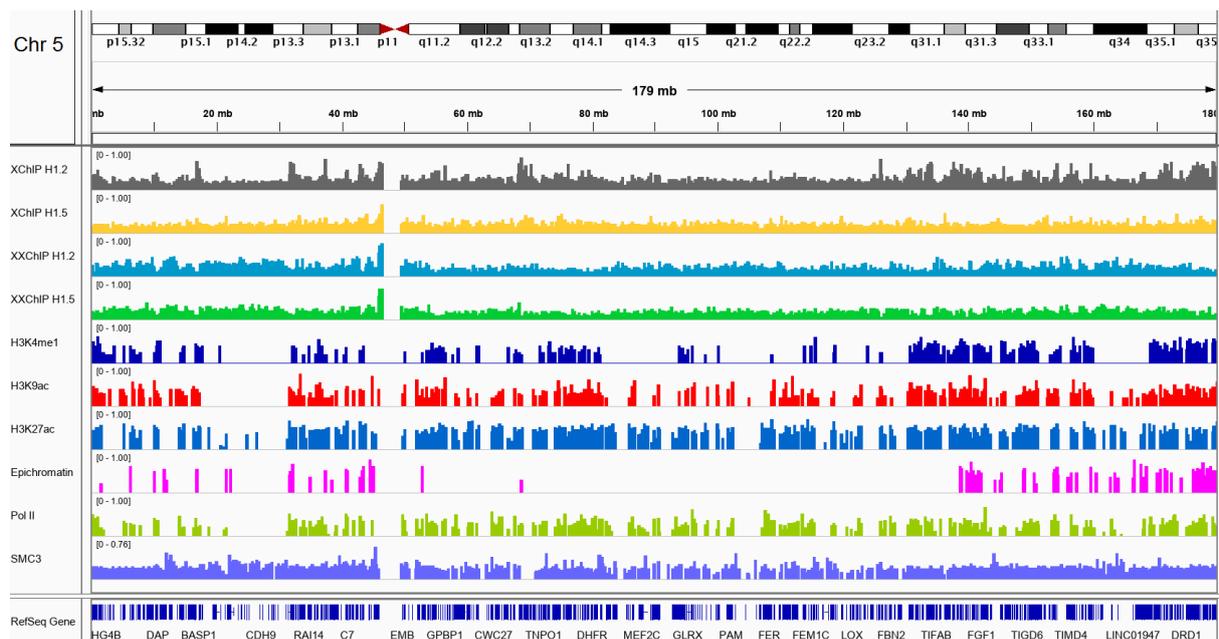


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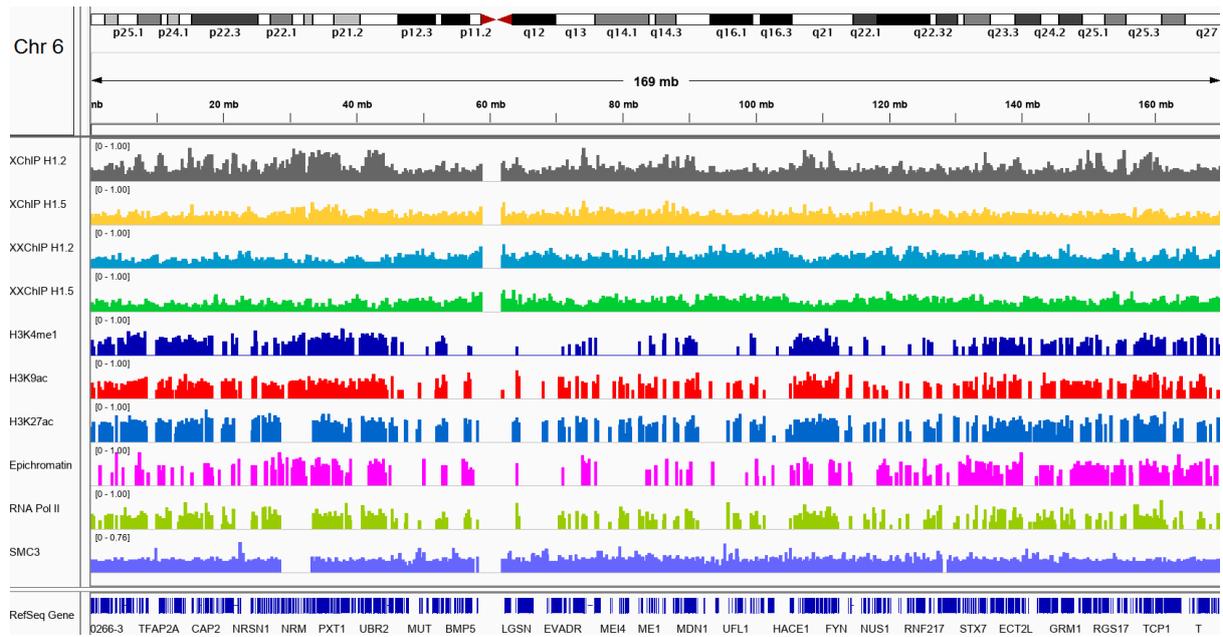


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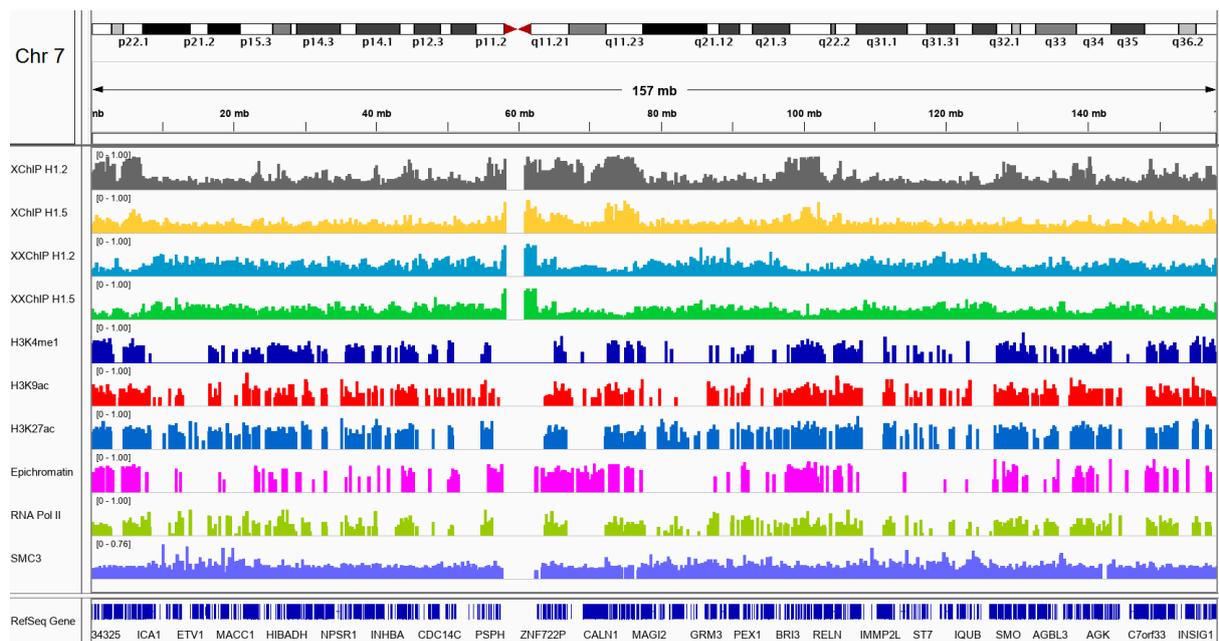


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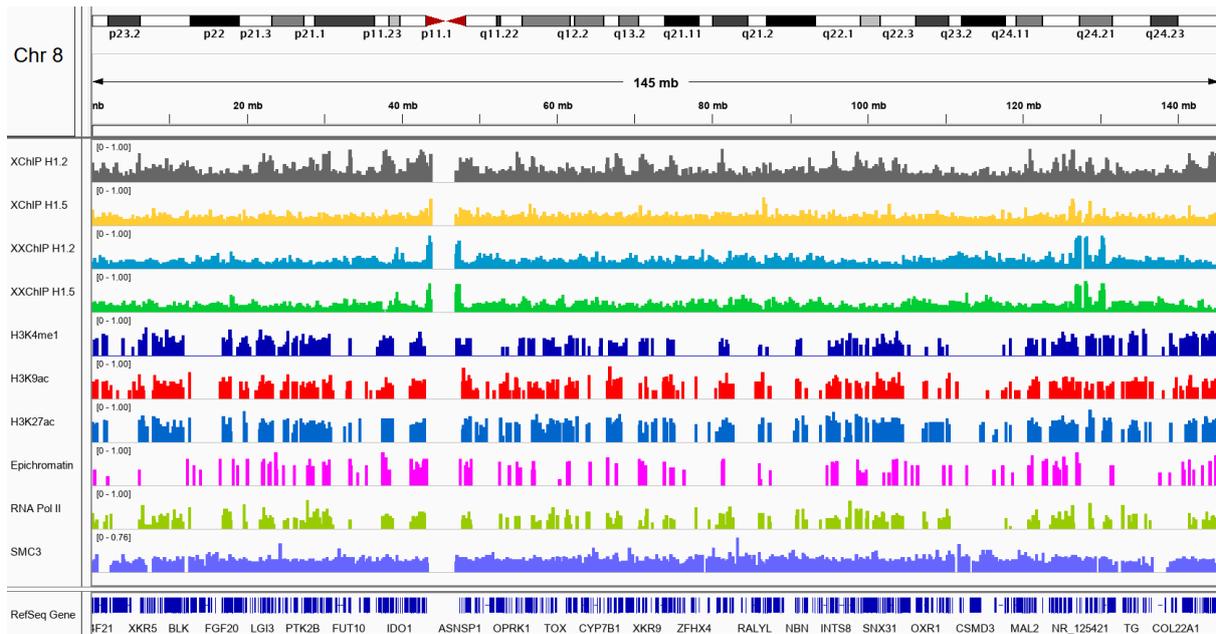


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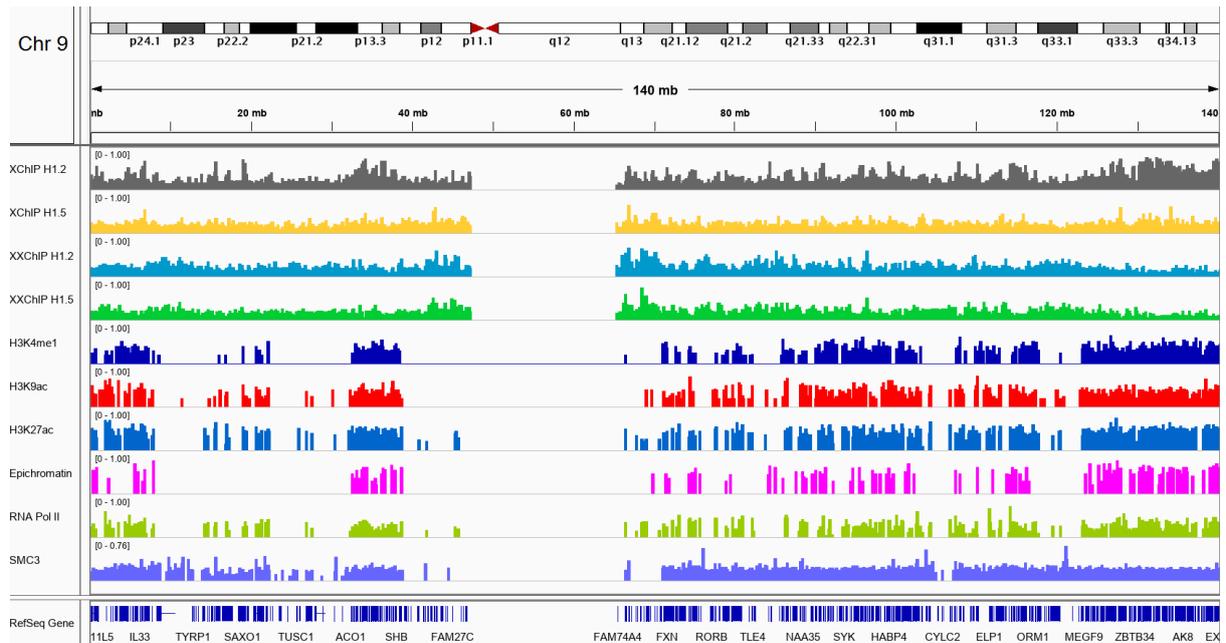


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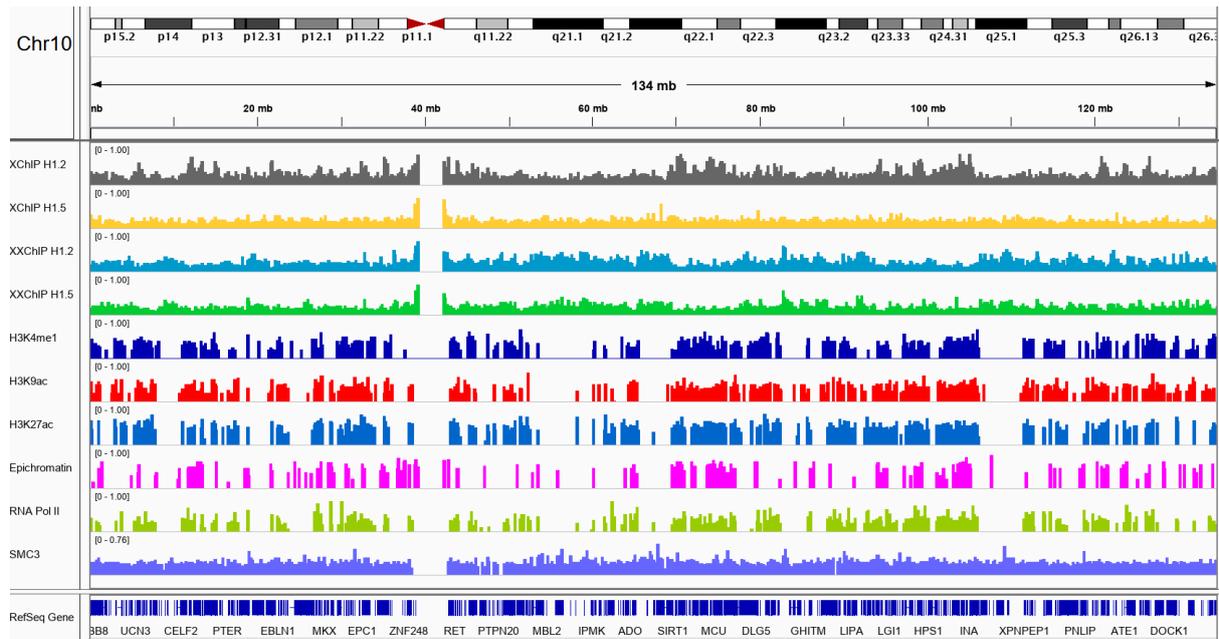


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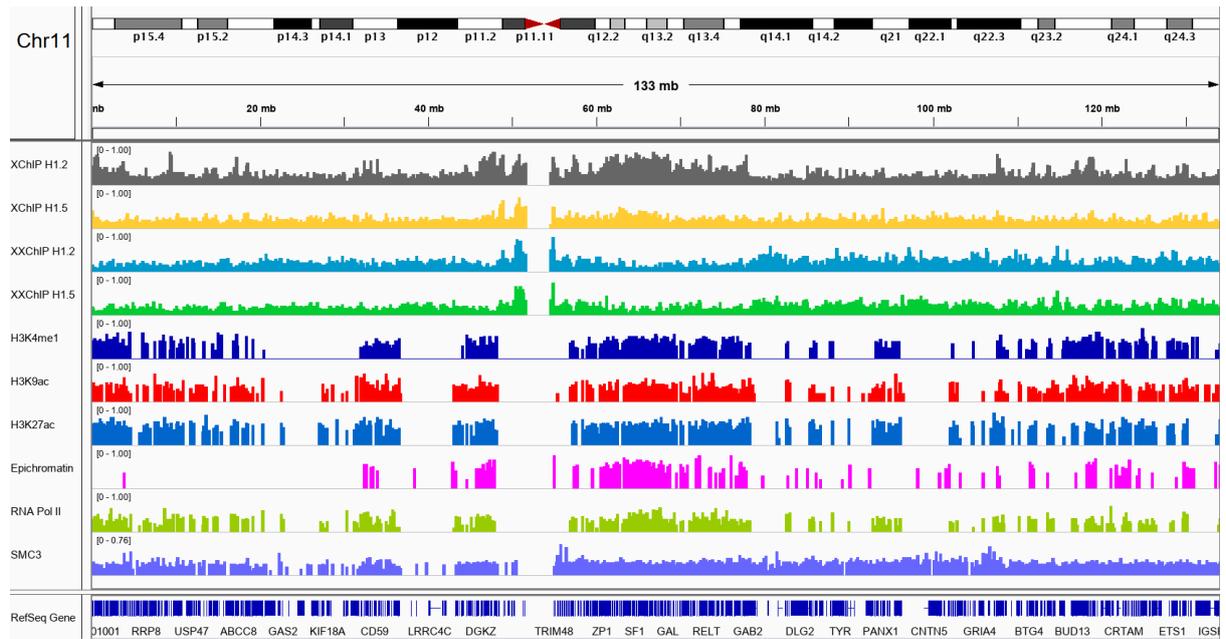


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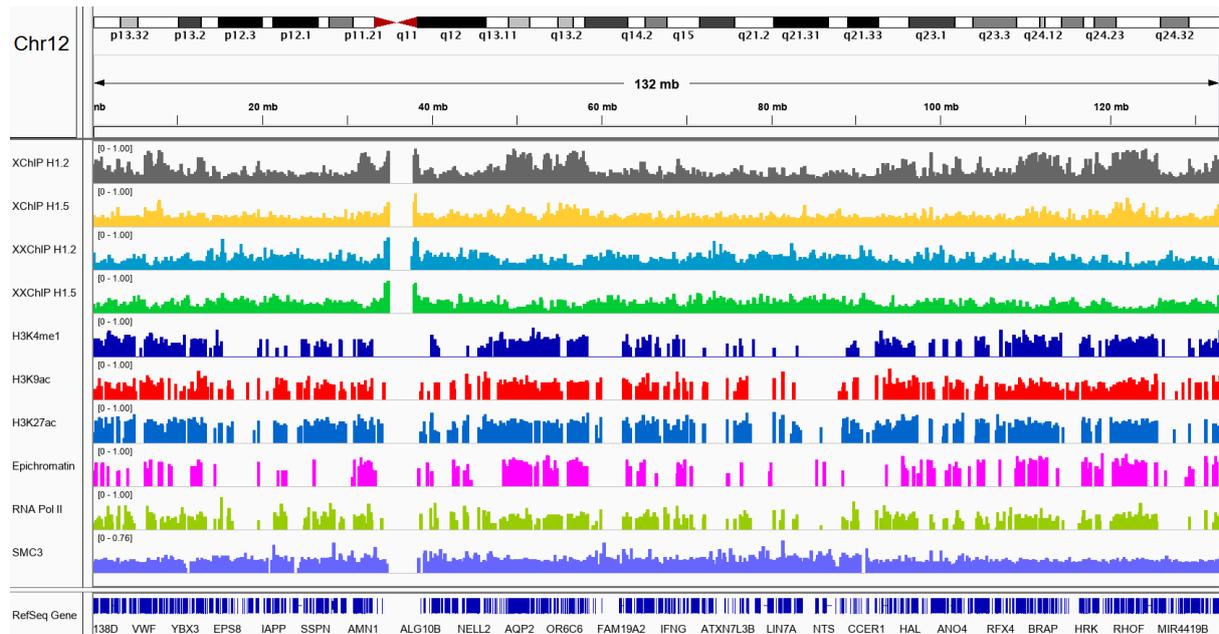


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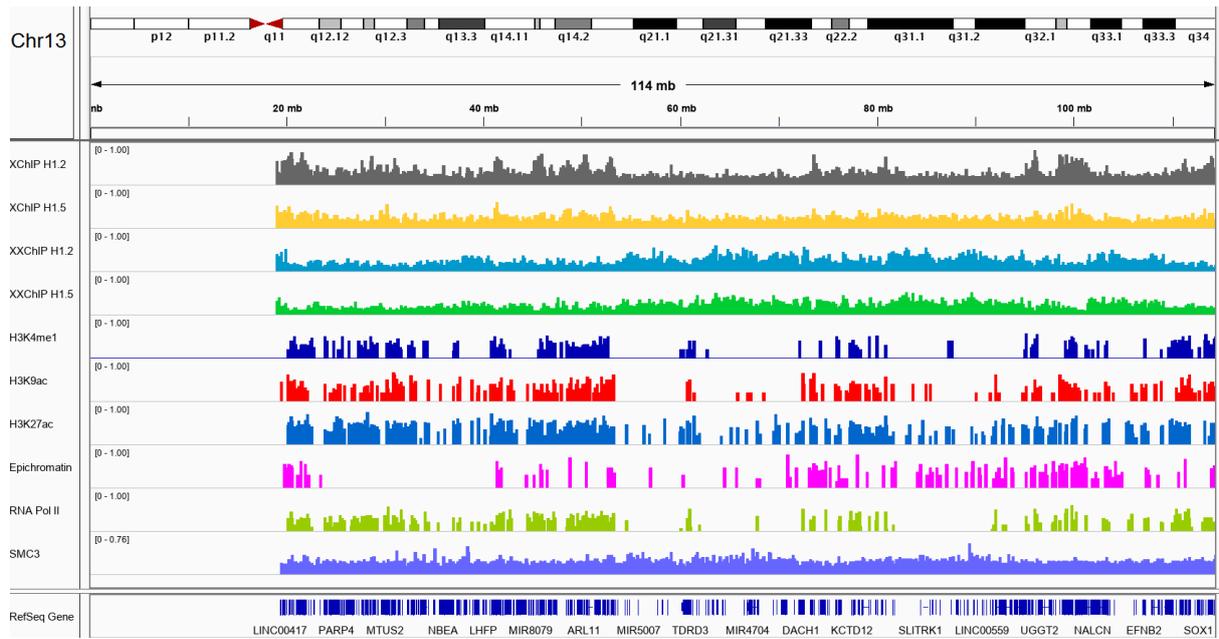


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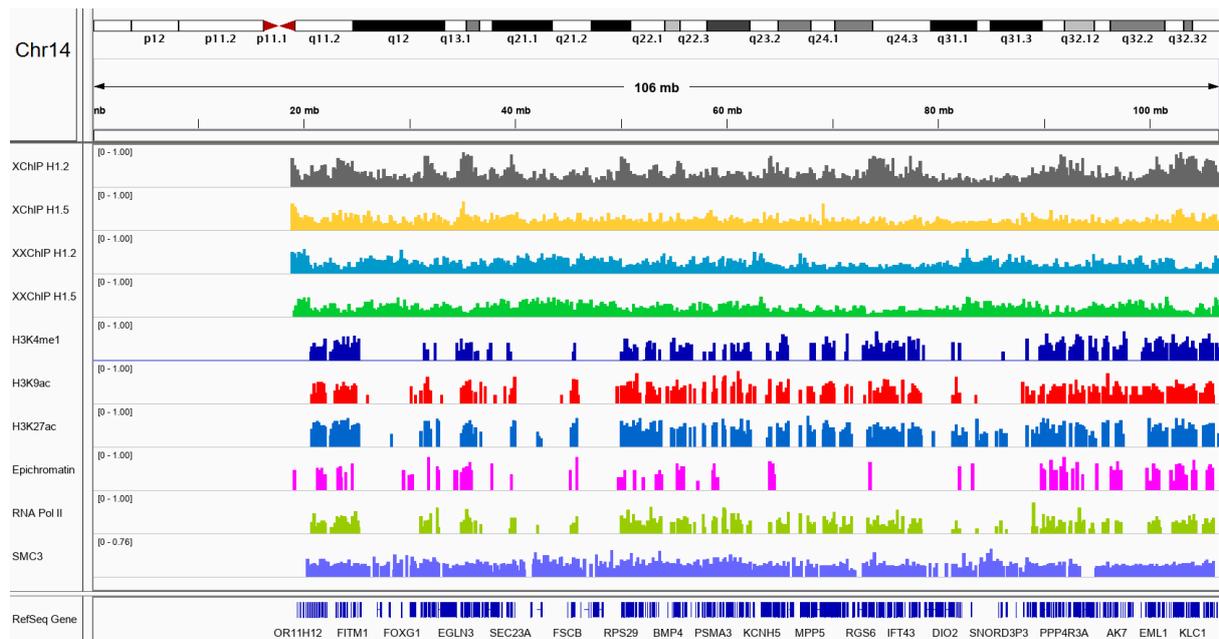


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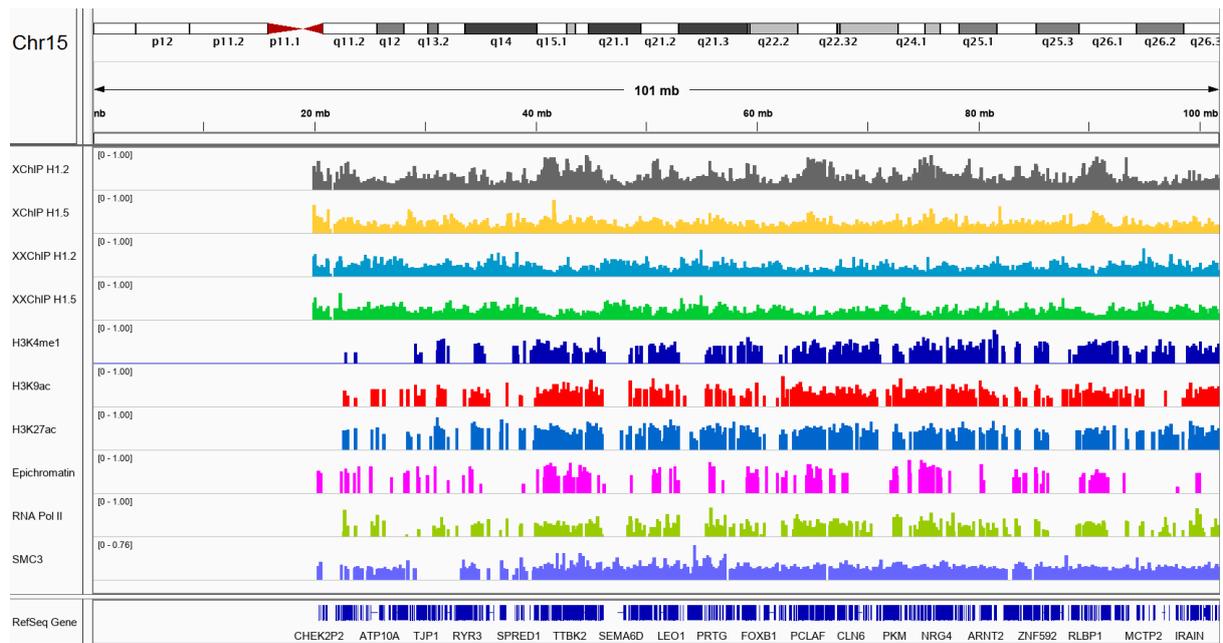


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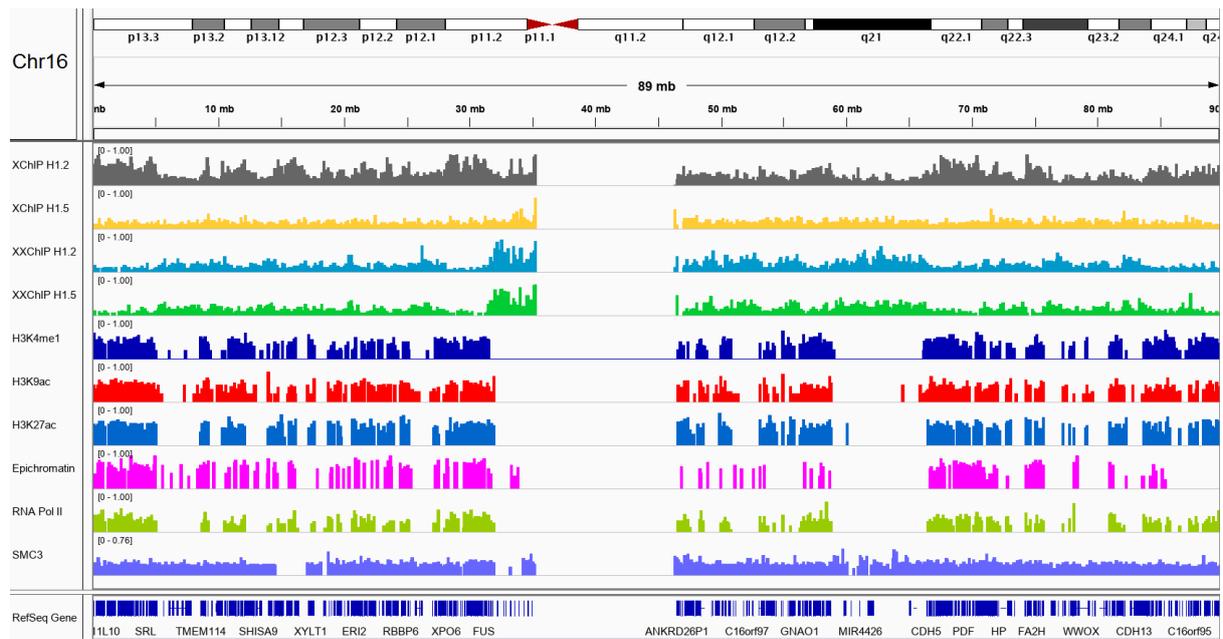


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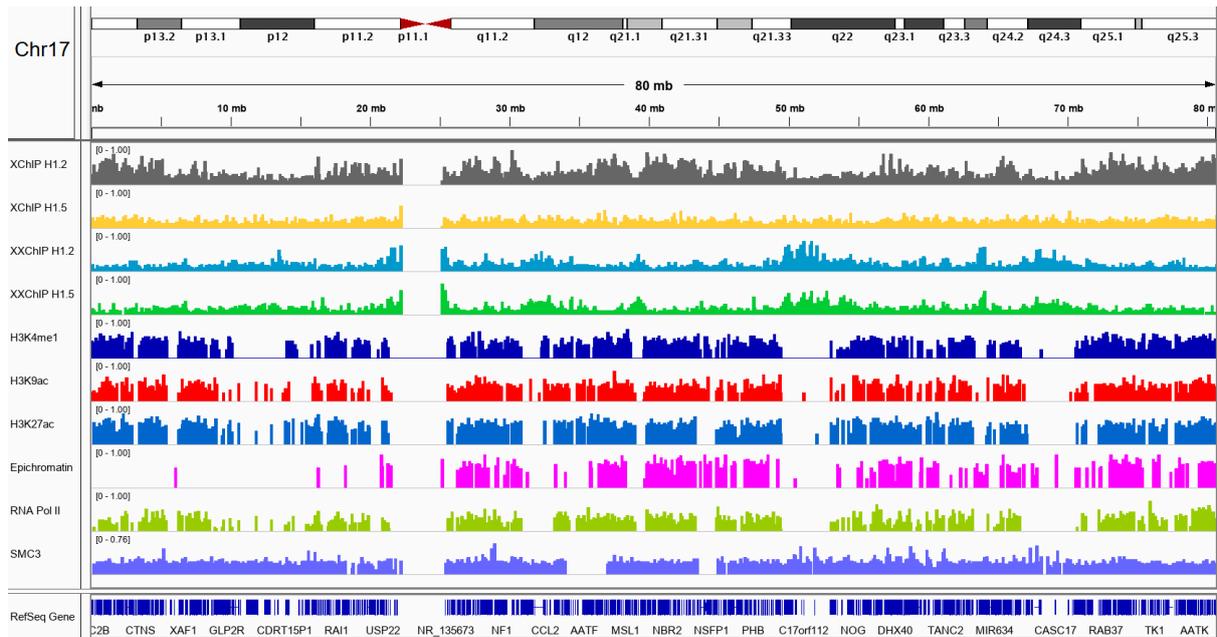


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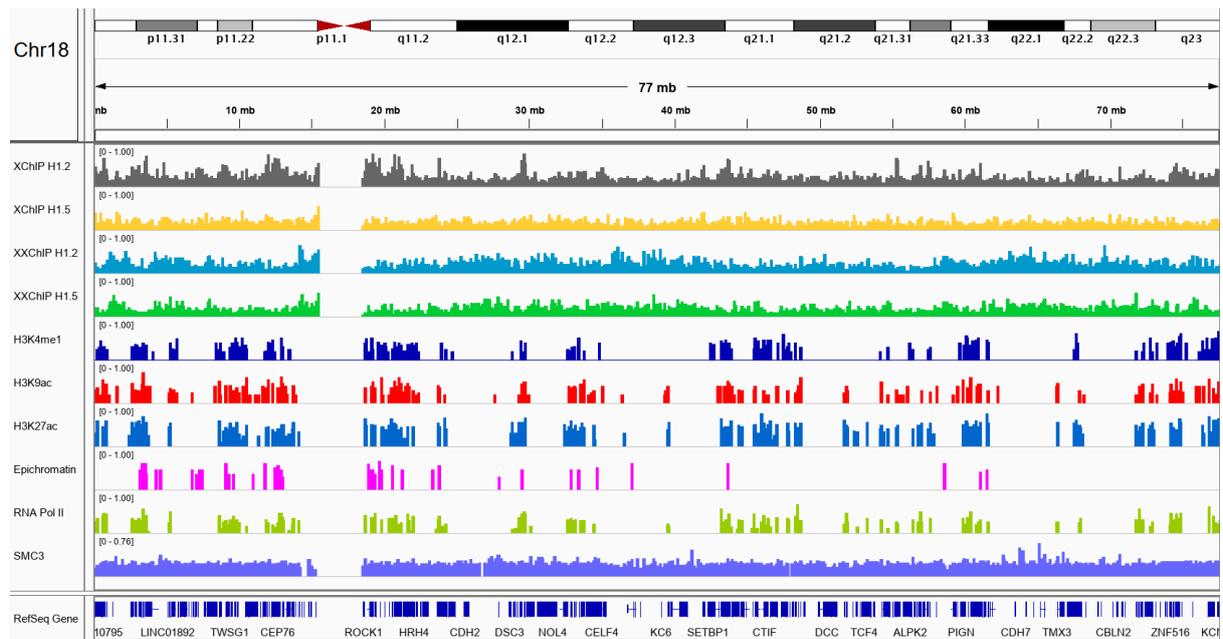


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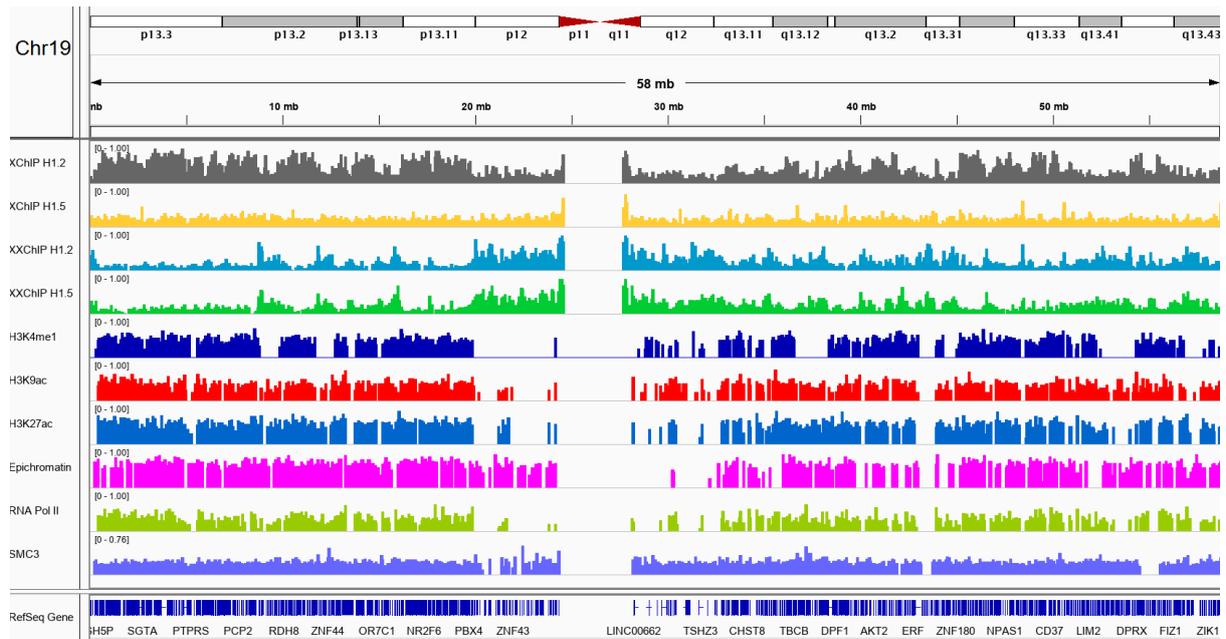


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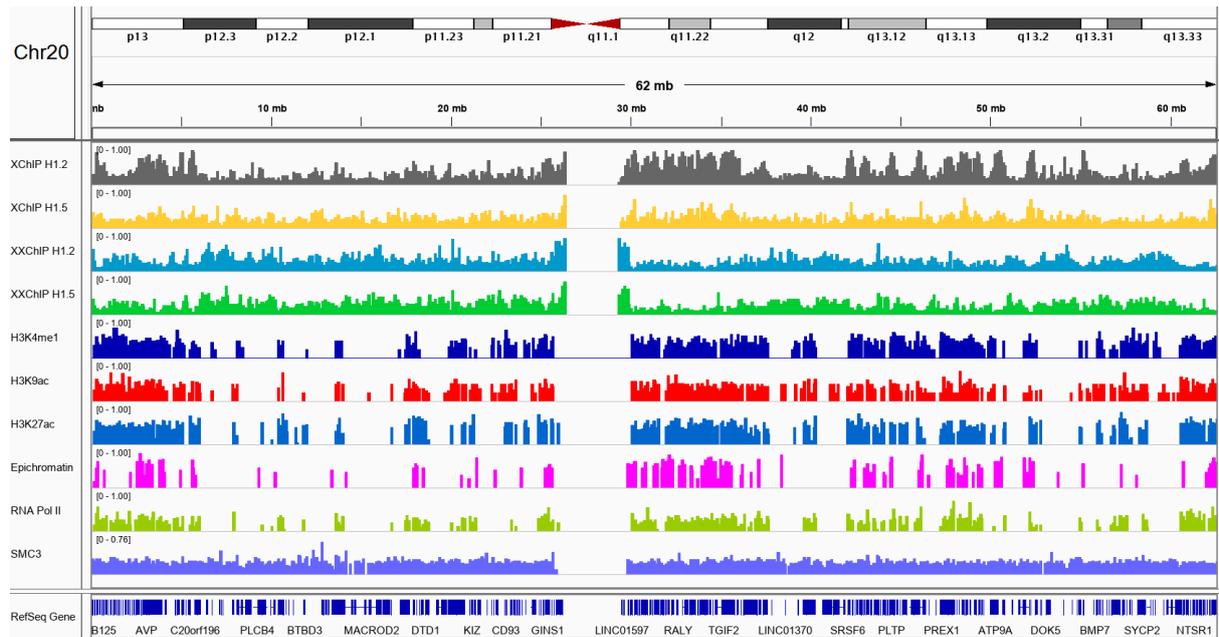


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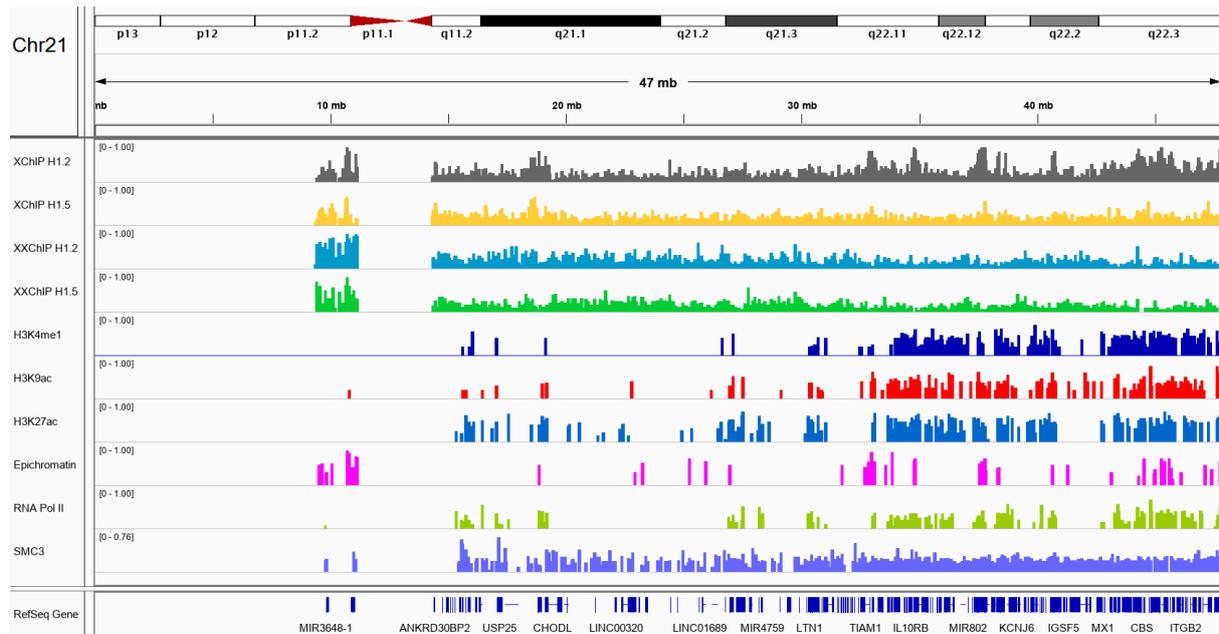


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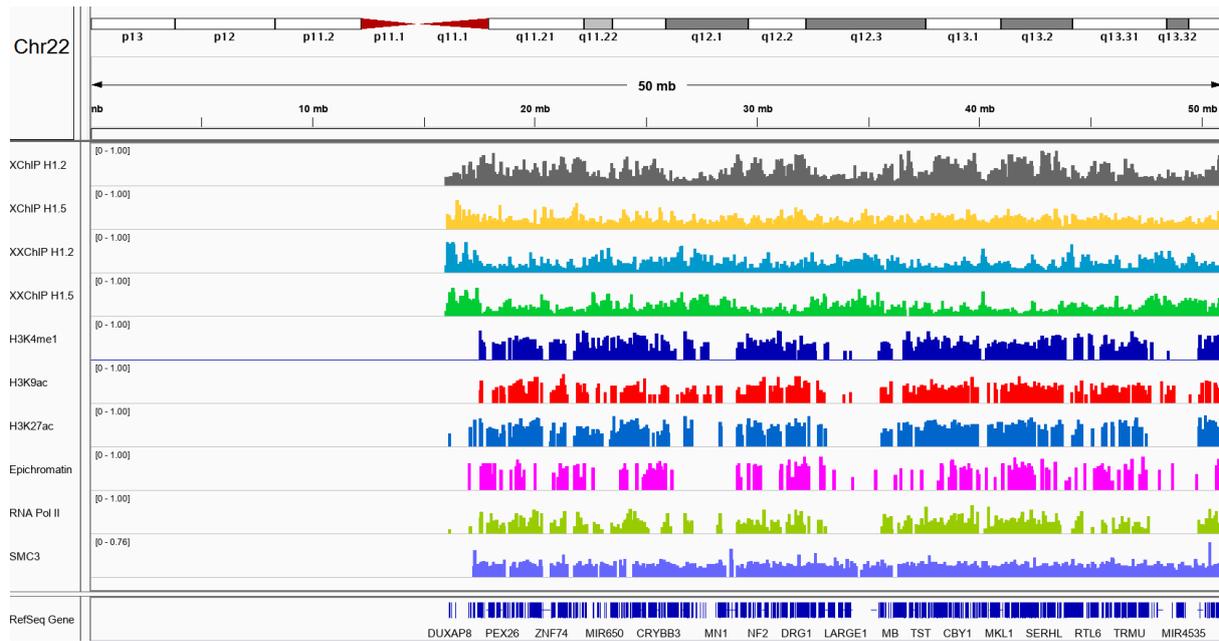


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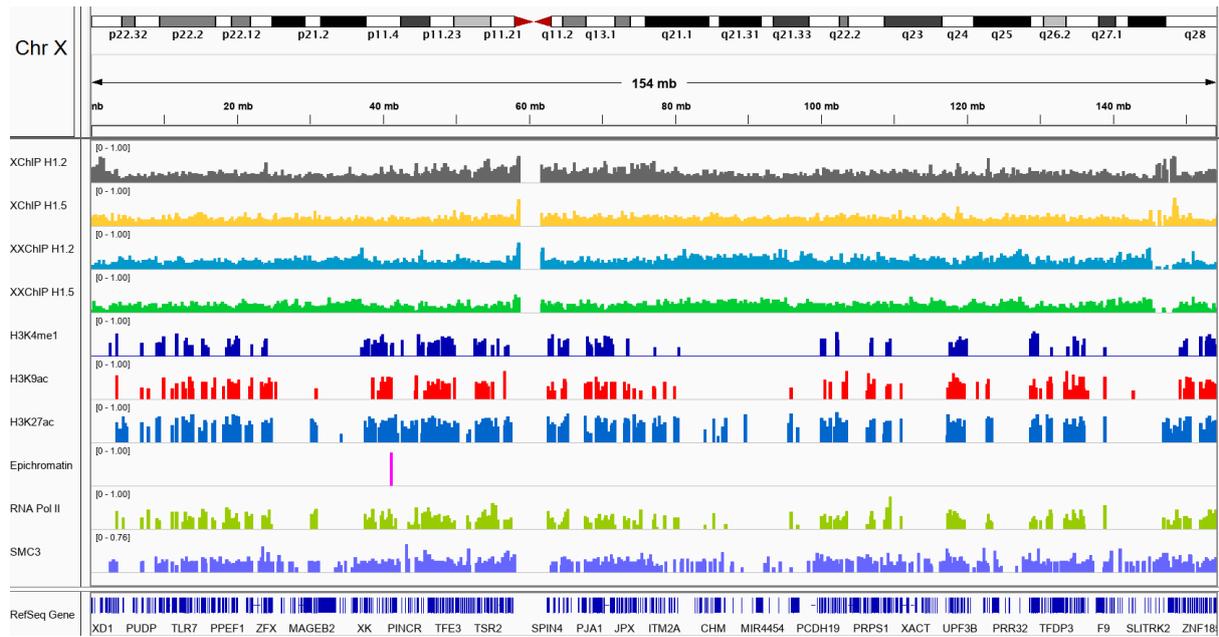


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