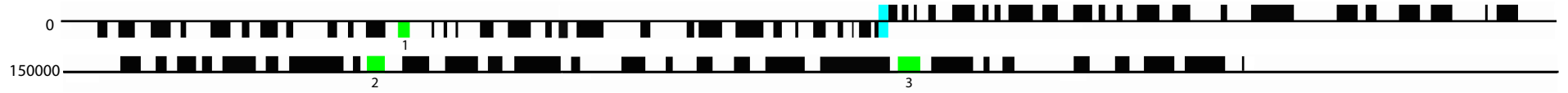
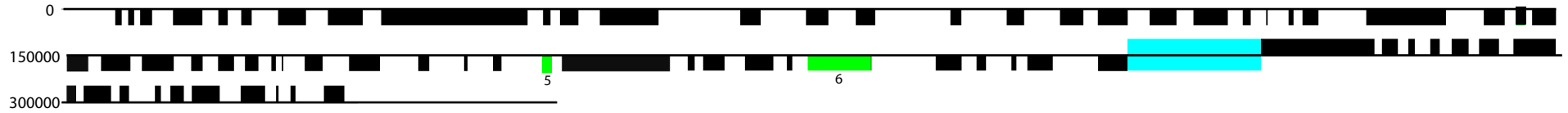


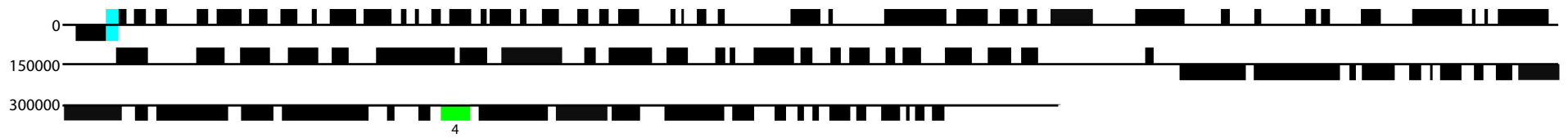
### Chromosome 1



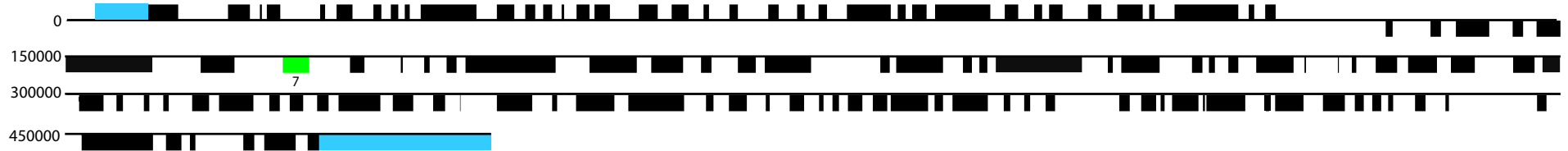
### Chromosome 2



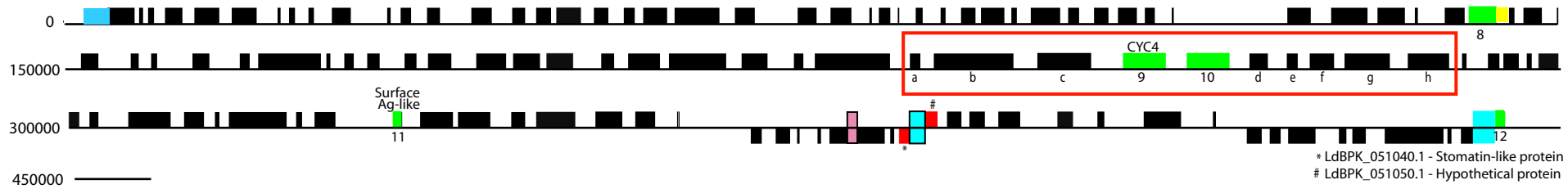
### Chromosome 3



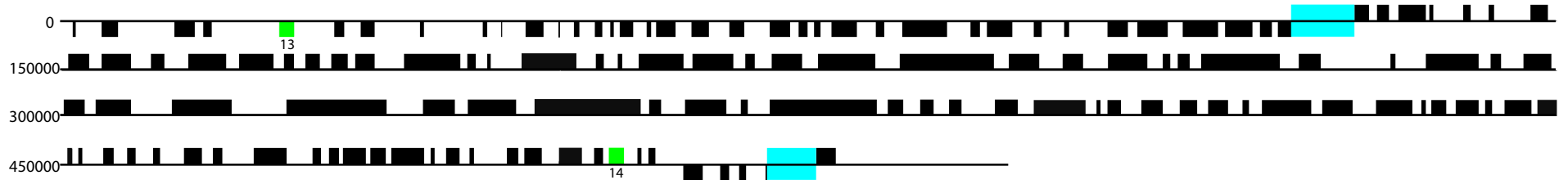
### Chromosome 4



### Chromosome 5



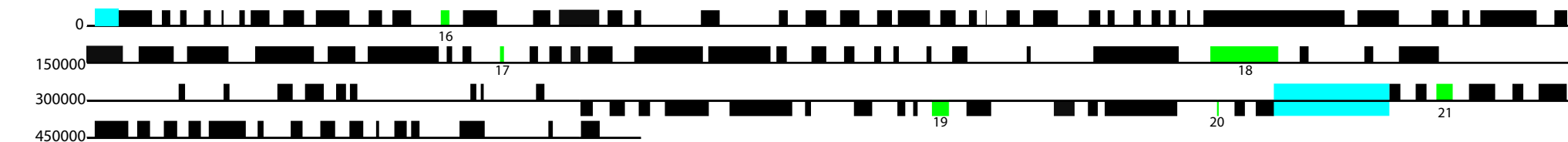
### Chromosome 6



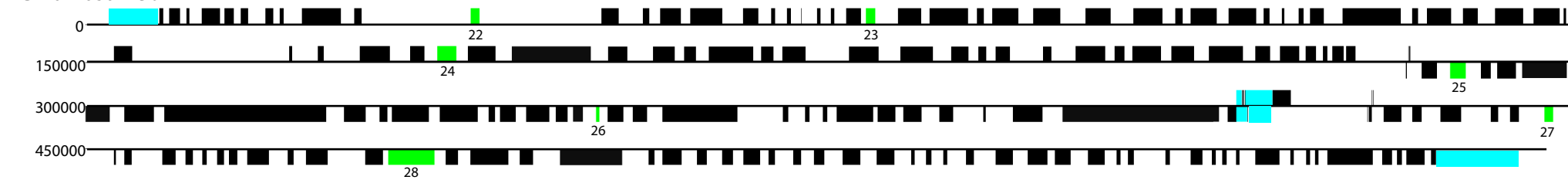
### Chromosome 7



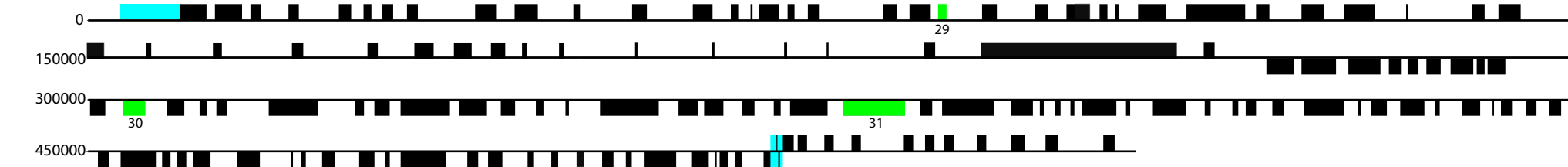
### Chromosome 8



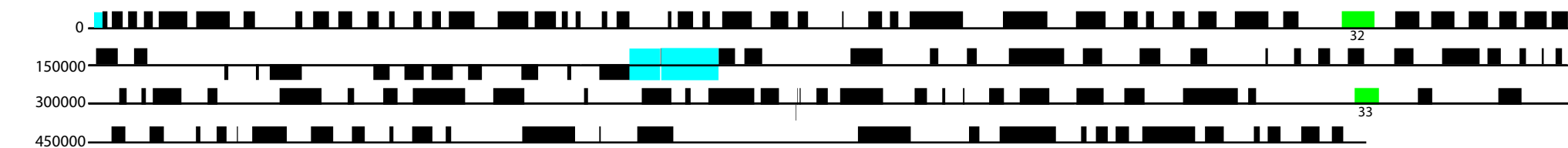
### Chromosome 9



### Chromosome 10



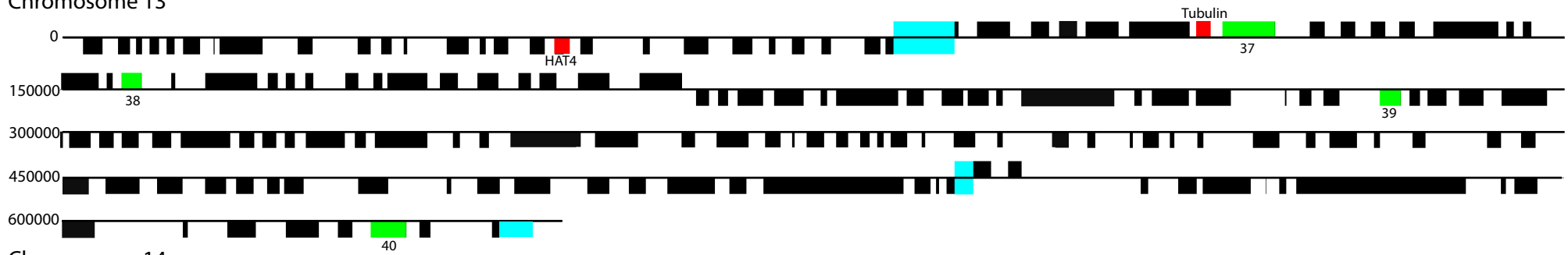
### Chromosome 11



### Chromosome 12



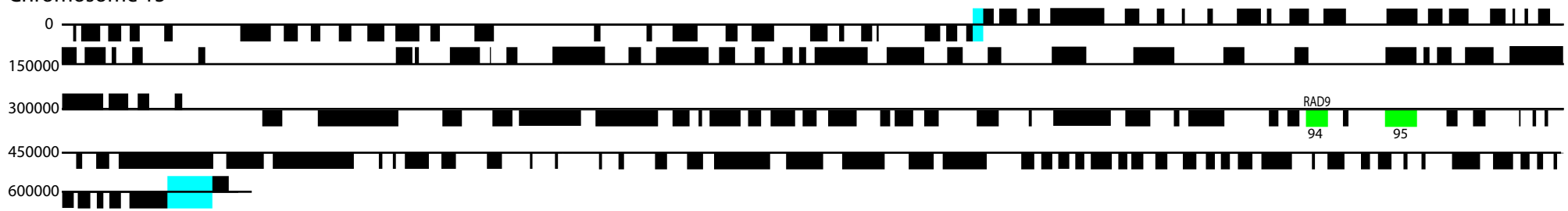
### Chromosome 13



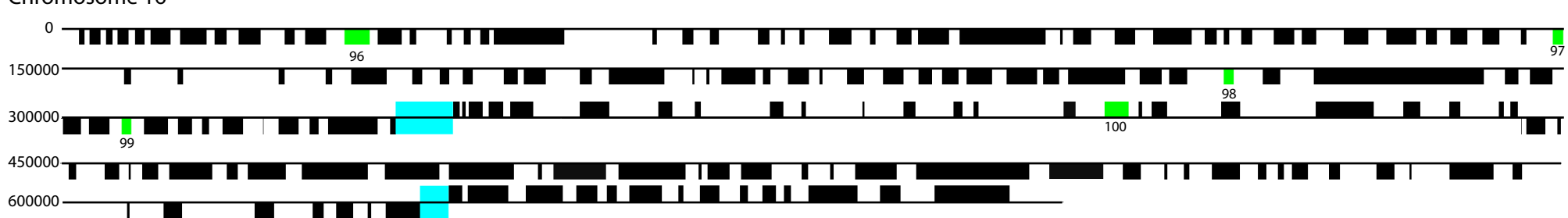
### Chromosome 14



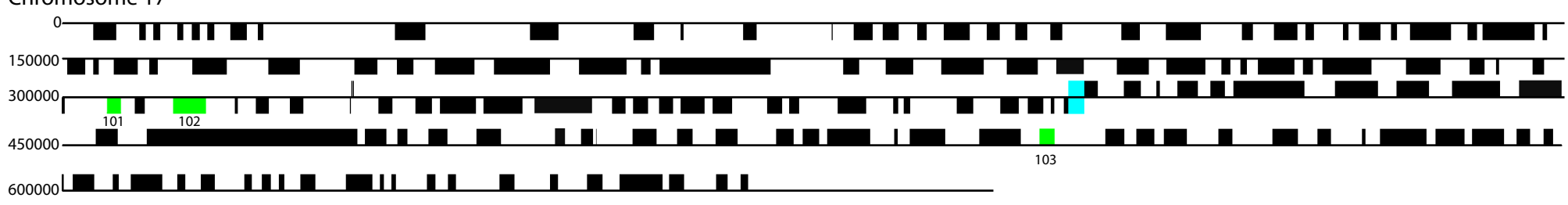
### Chromosome 15



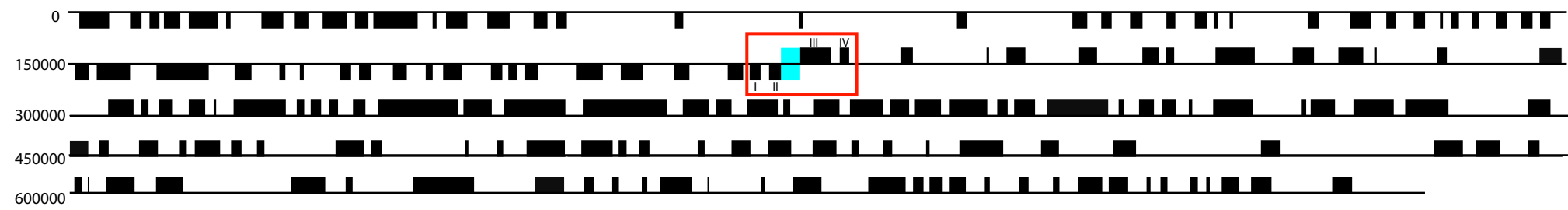
### Chromosome 16



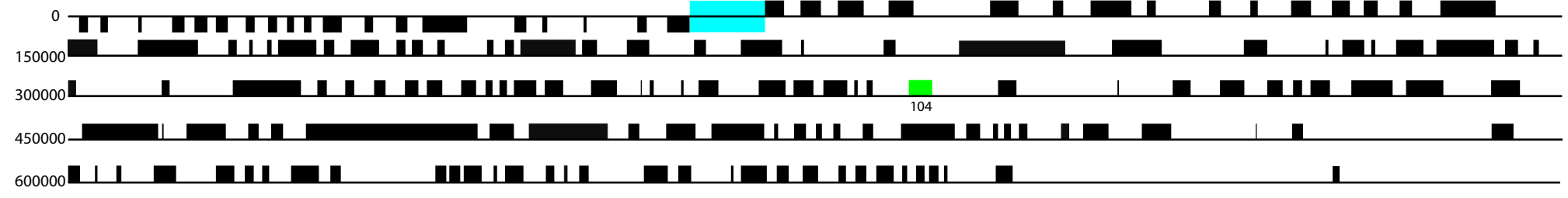
### Chromosome 17



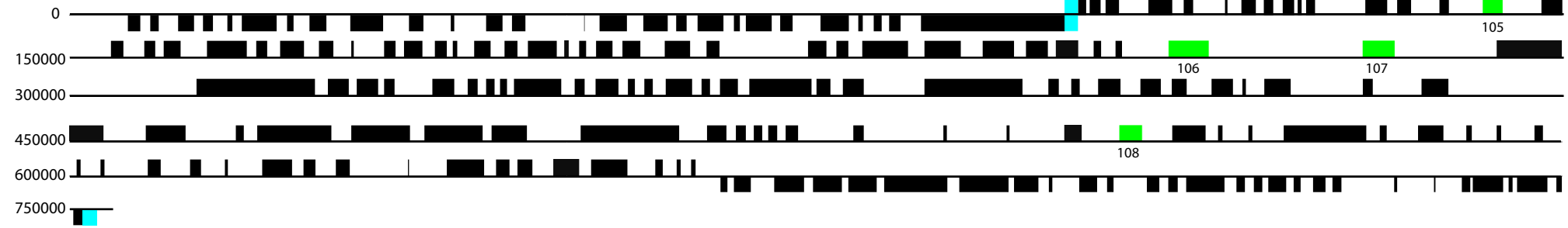
### Chromosome 18



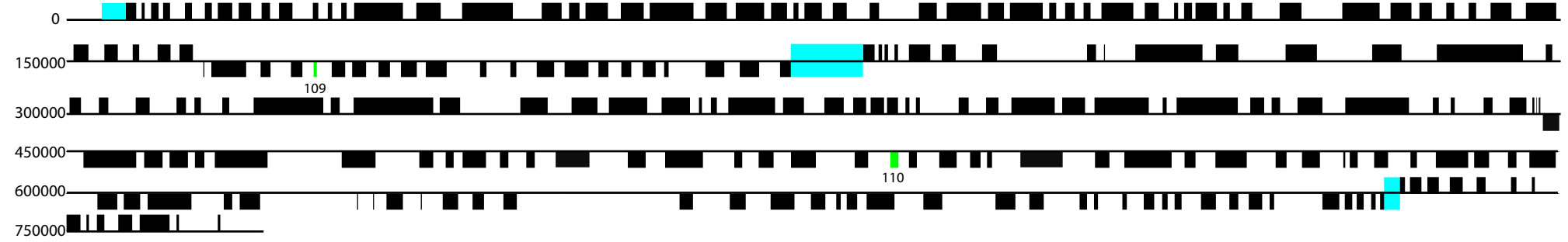
### Chromosome 19



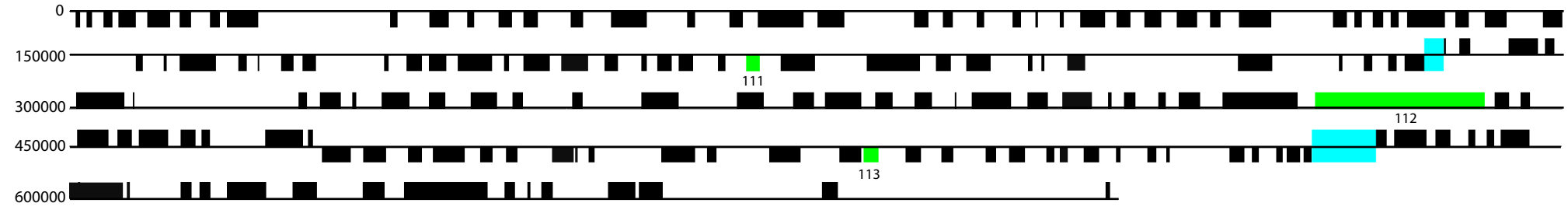
### Chromosome 20

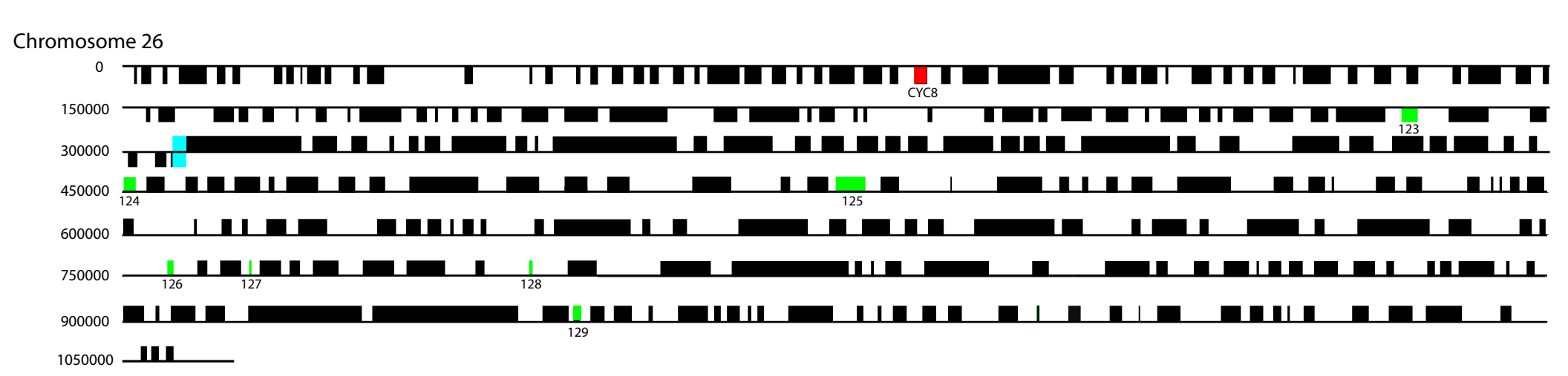
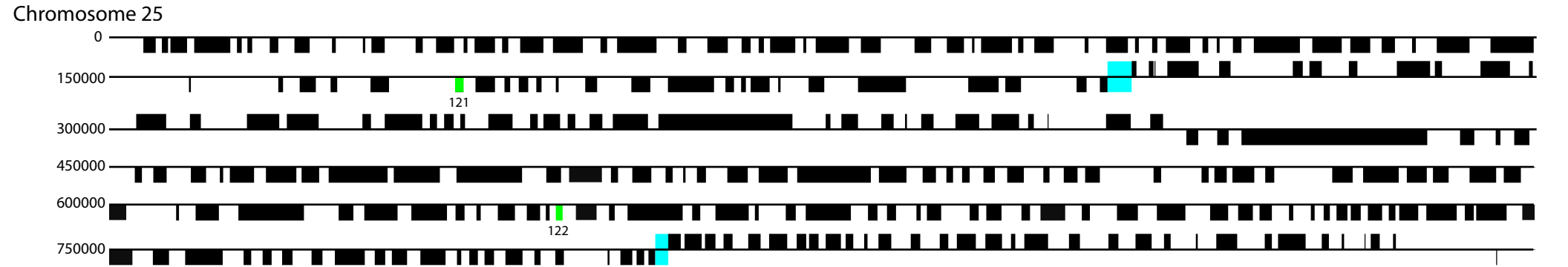
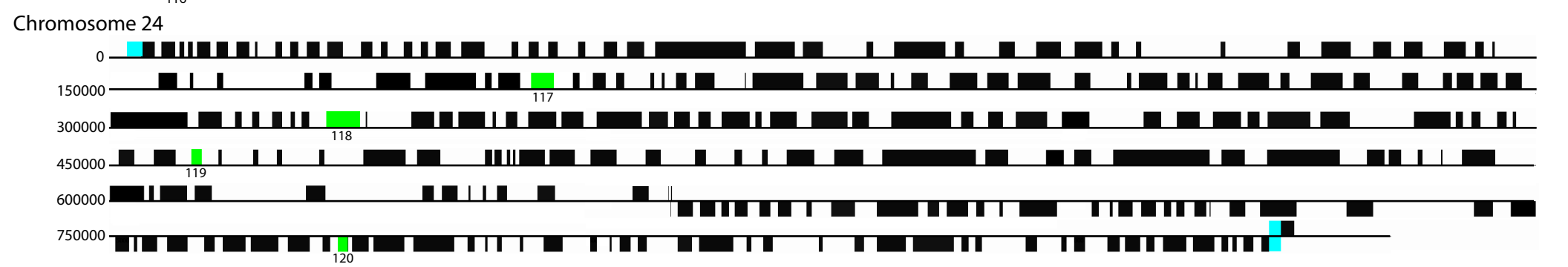
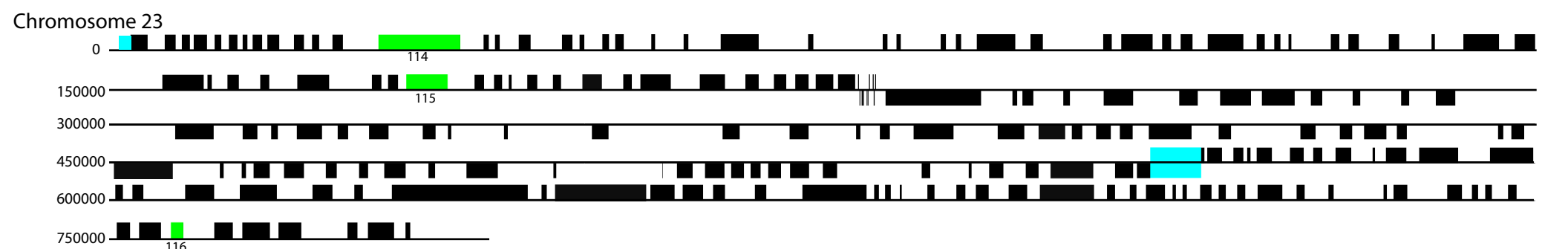


### Chromosome 21

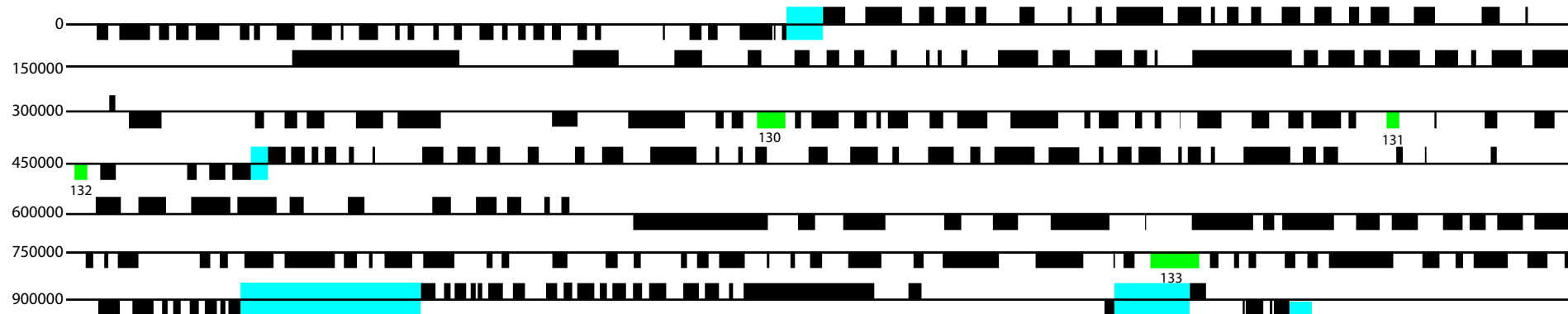


### Chromosome 22

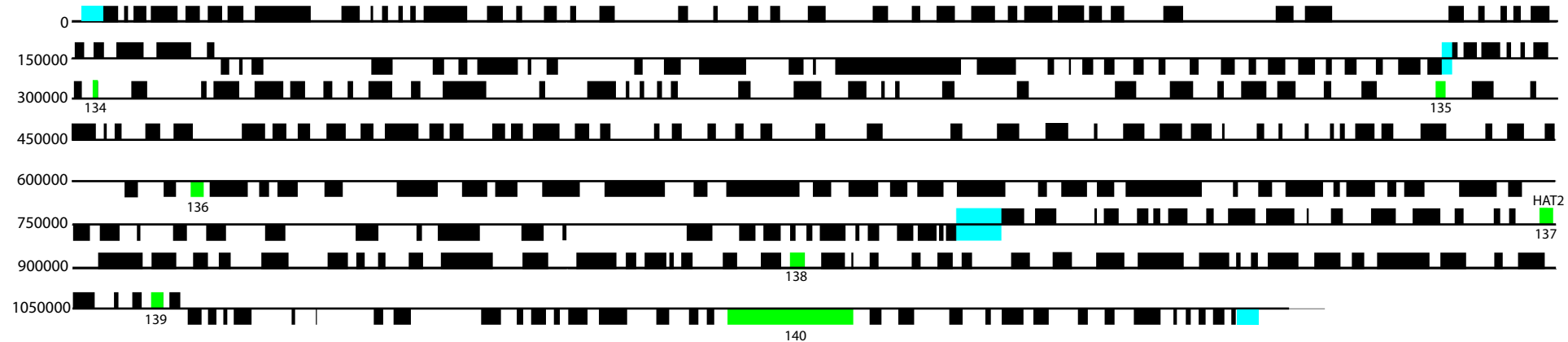




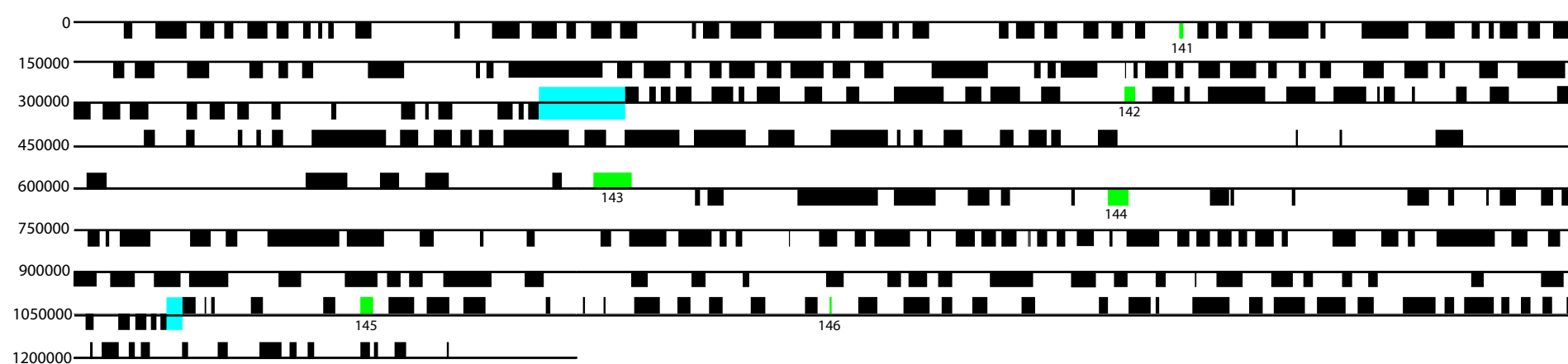
### Chromosome 27



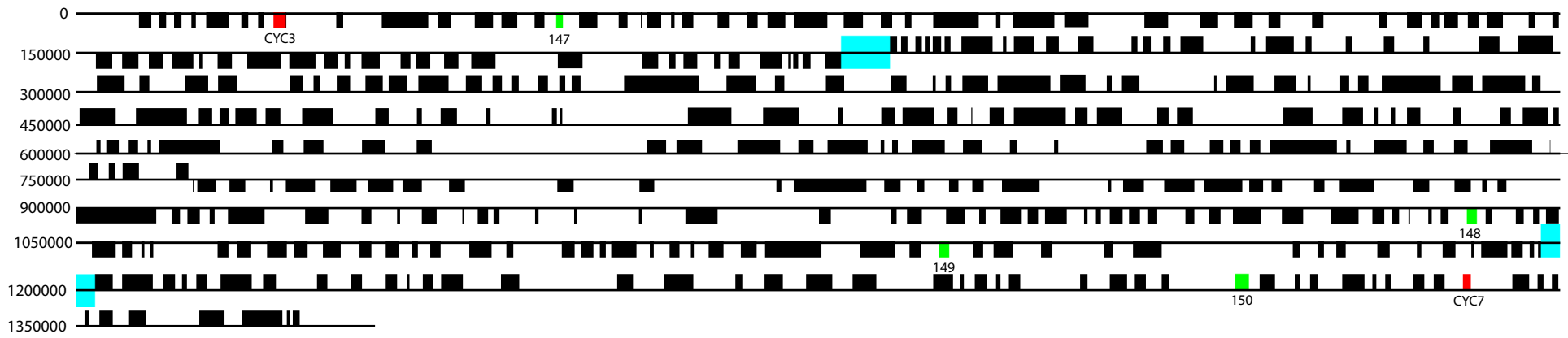
### Chromosome 28



### Chromosome 29



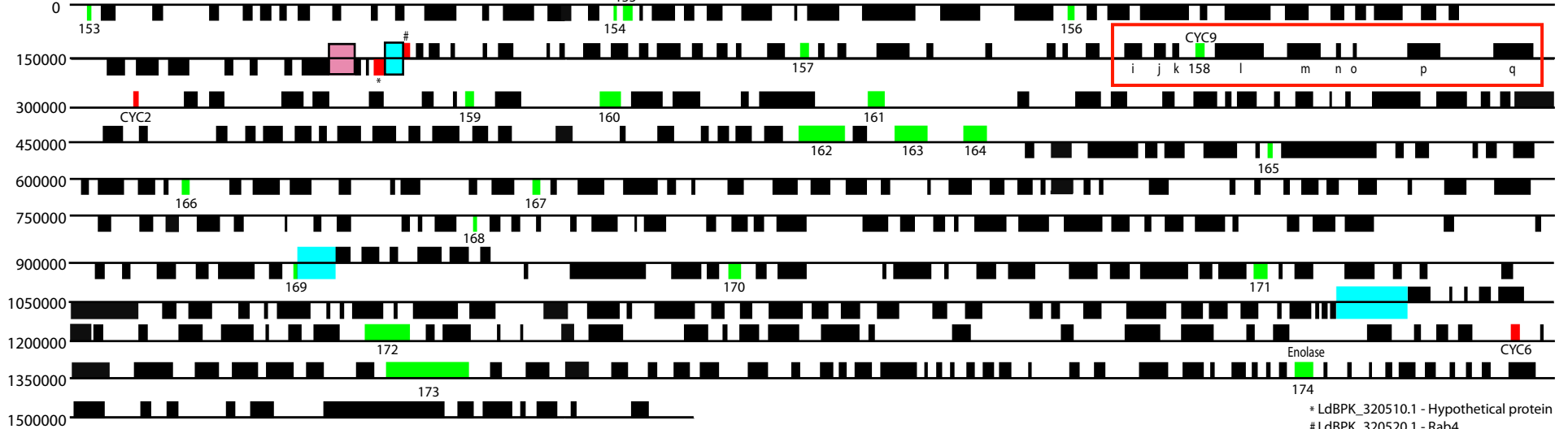
### Chromosome 30



### Chromosome 31

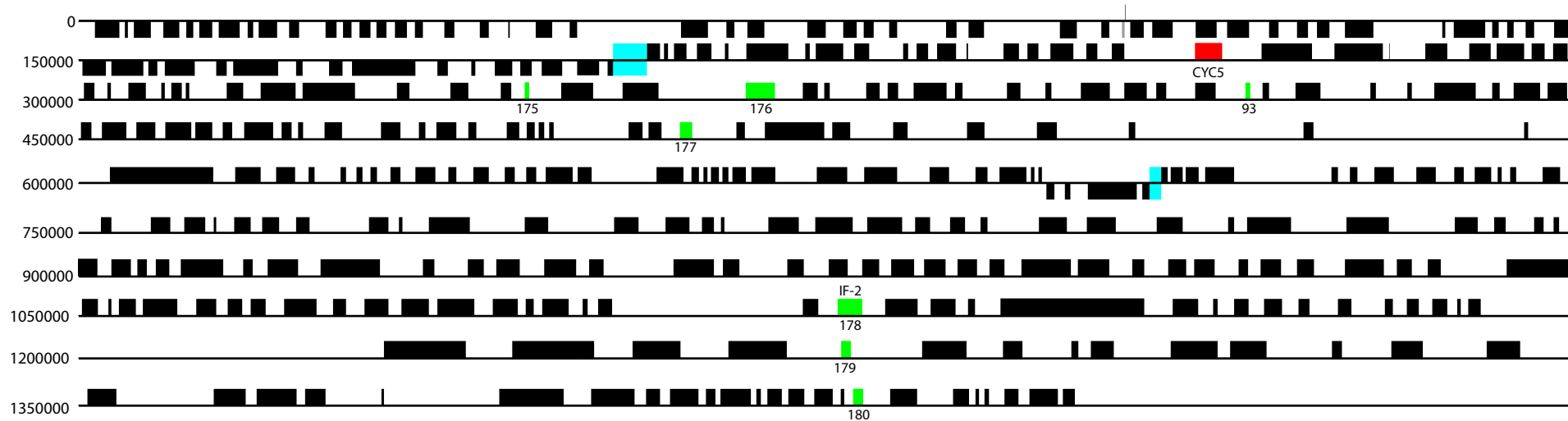


### Chromosome 32

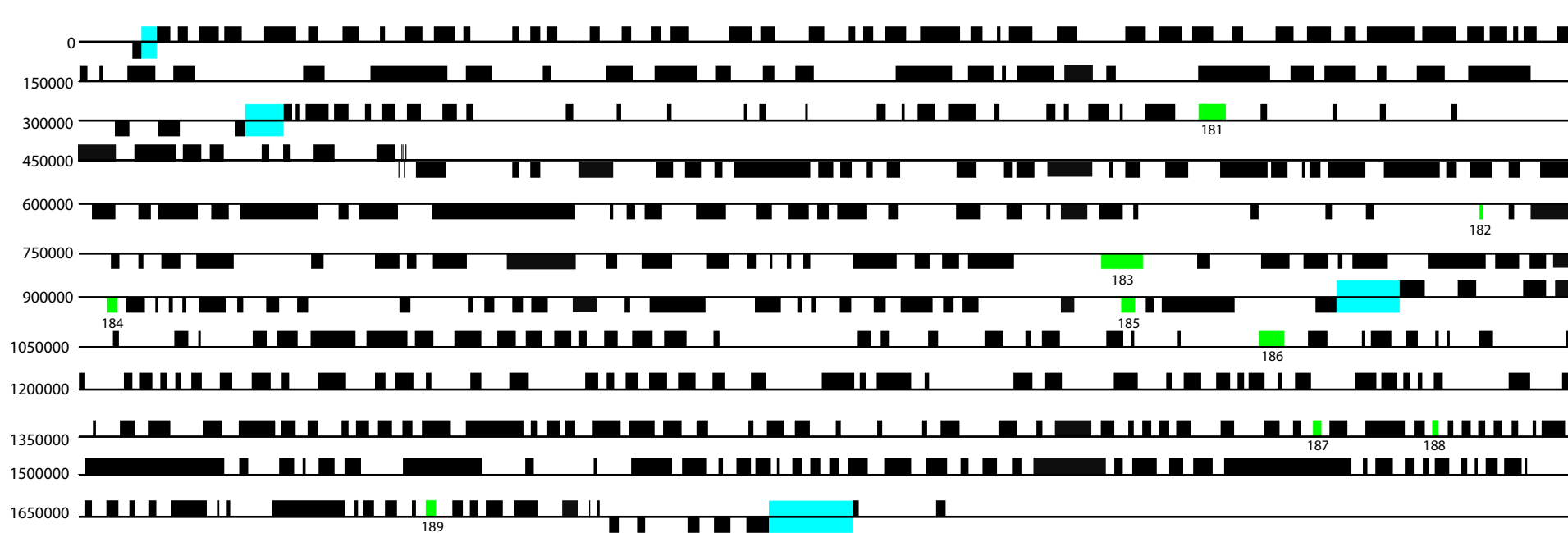


\* LdBPK\_320510.1 - Hypothetical protein  
# LdBPK\_320520.1 - Rab4

### Chromosome 33

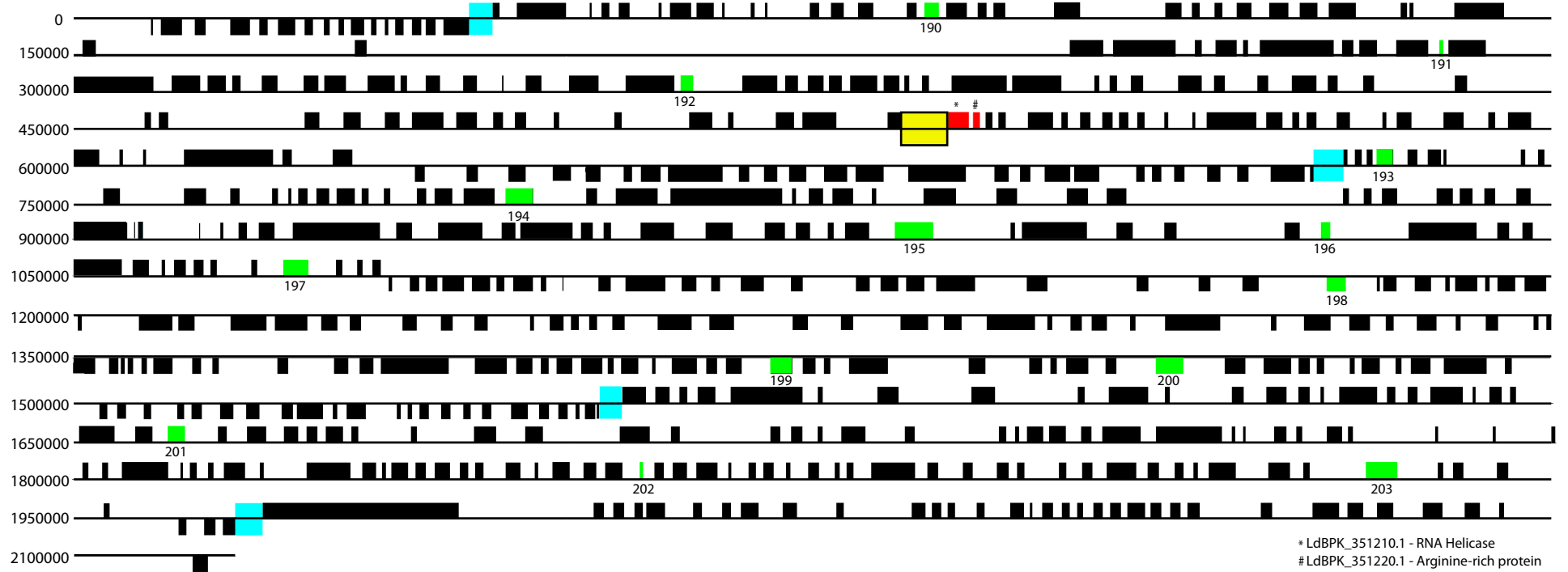


### Chromosome 34

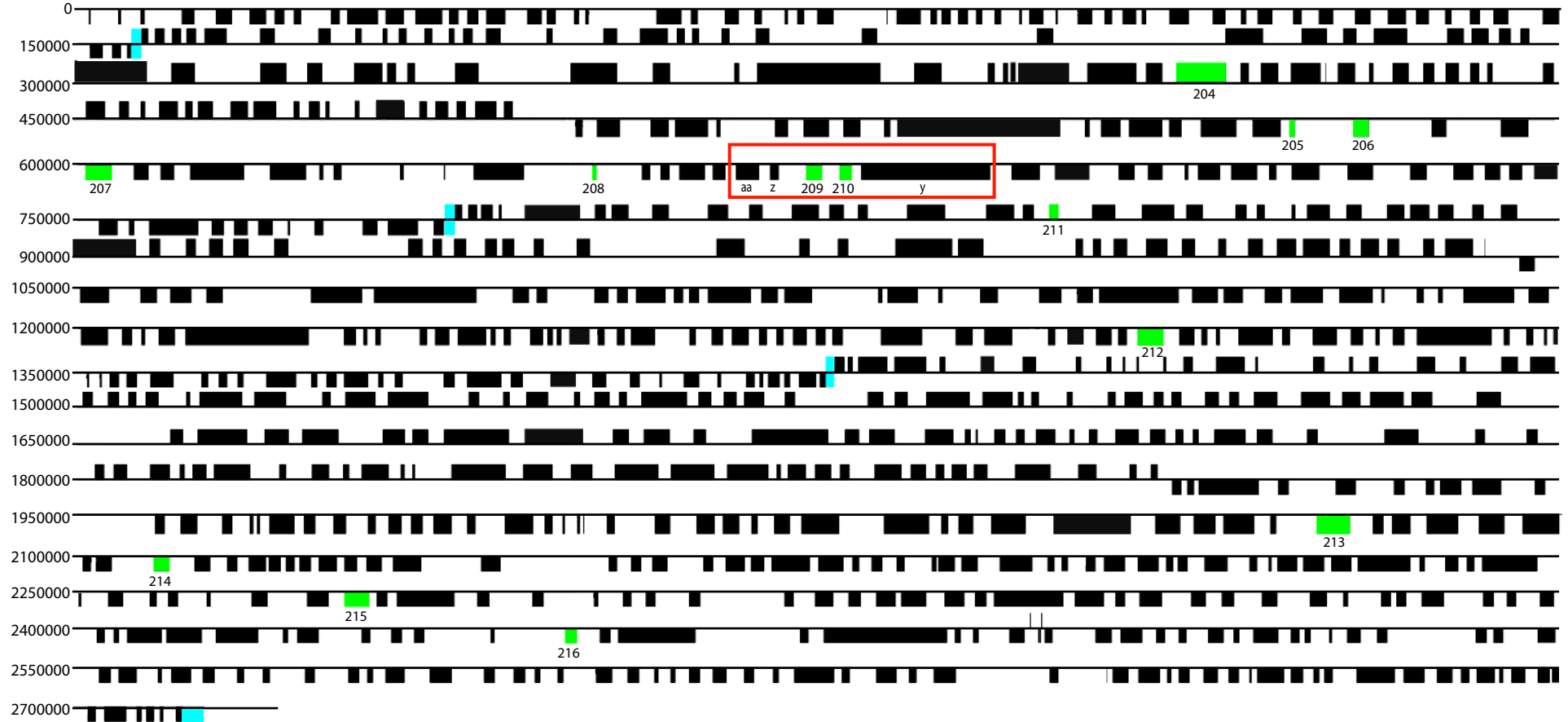




Chromosome 35



## Chromosome 36



S4 Fig: Genome map adapted from the *Leishmania donovani* genome map in the GeneDB ([www.genedb.org](http://www.genedb.org)). Genes that are downregulated in HAT2-depleted cells (based on microarray data) are depicted as green boxes and assigned an arabic numeral corresponding to their serial number in S4 Table. Predicted dSSRs and TSRs (transcription start sites) at chromosome ends are shaded light blue and ChIP-analyzed dSSRs are boxed; HT sites on chromosomes 5 and 35 shaded yellow; non-dSSR intergenic regions on chromosomes 5 and 32 that were analyzed in ChIPs are shaded pink. All analyzed S phase and mitotic cyclin genes (except CYC4 and CYC9), tubulin, HAT4, are depicted as red boxes. Analyzed genes coupled to chromosome 5 and chromosome 32 dSSRs as well as to chromosome 35 HT site are also depicted as red boxes. Gene clusters analyzed in run-ons are demarcated by red boxes.