

Identify Human Alpha Satellite Higher-Order Repeats with HMMER (HumAS-HMMER HOR module)

Human genome assembly (hg38)

HMM profiles for centromeric alpha satellite HOR monomers

Identify each monomer (nhmmer)

Convert tabular output to BED format with a color coding and a threshold of score to length ratio ( $> 0.7$ )

Sort target regions according to coordinates

Select monomers with the highest score from overlapping elements in BED file (bedmap)

Reduce multiple descriptions of the best hit to a single one

Annotation track of HOR monomers (BED format)

Analyse Structural Variants of Alpha Satellite Higher-Order Repeats (SVASHOR)

BED file with UCSC hg38 assembly fragments coordinates

Human alpha satellite SF annotation track for hg38 assembly (PERCON)

Reports with information on SF classes and a copy number of each structural HOR variant and a full text map

