intermediate investigation on parchment data

2022-10-02

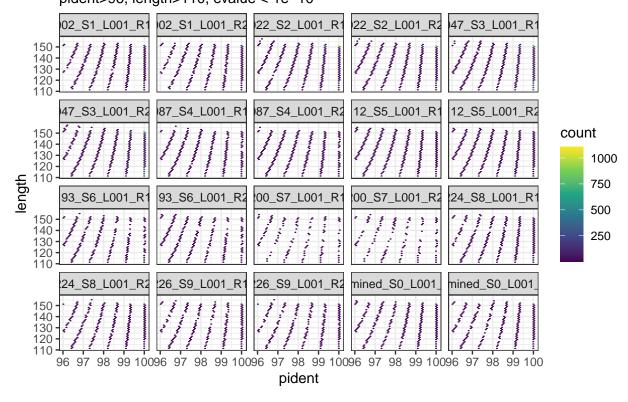
Reference file name

Genome assembly ARS-LIC_NZ_Holstein-Friesian_1 $\,$

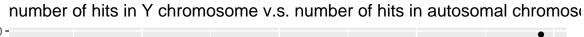
percentage of identity V.S. coverage among 22 samples.

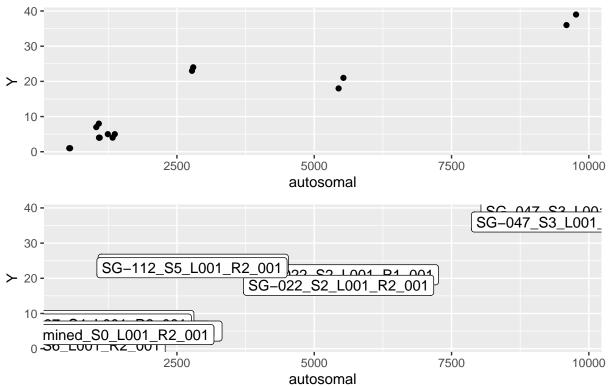
sample SG-LibNeg_S10_L001_R1_001 and SG-LibNeg_S10_L001_R2_001 have few hits that are not informative. Therefore, they are removed

percentage of identity v.s. coverage pident>96, length>110, evalue < 1e-10



Number of autosomal chromosome hits V.S. number of Y chromosome hits





map of hits in Y chromosome reference sequence

x dots are projections of the curve on **x** axis

