1 - Partitions the genome and generate ChIP-exo islands.

Legend:
- Cumulative coverage (black)
- Fwd. strand coverage (red)
- Bwd. strand coverage (blue)

Number of reads by position
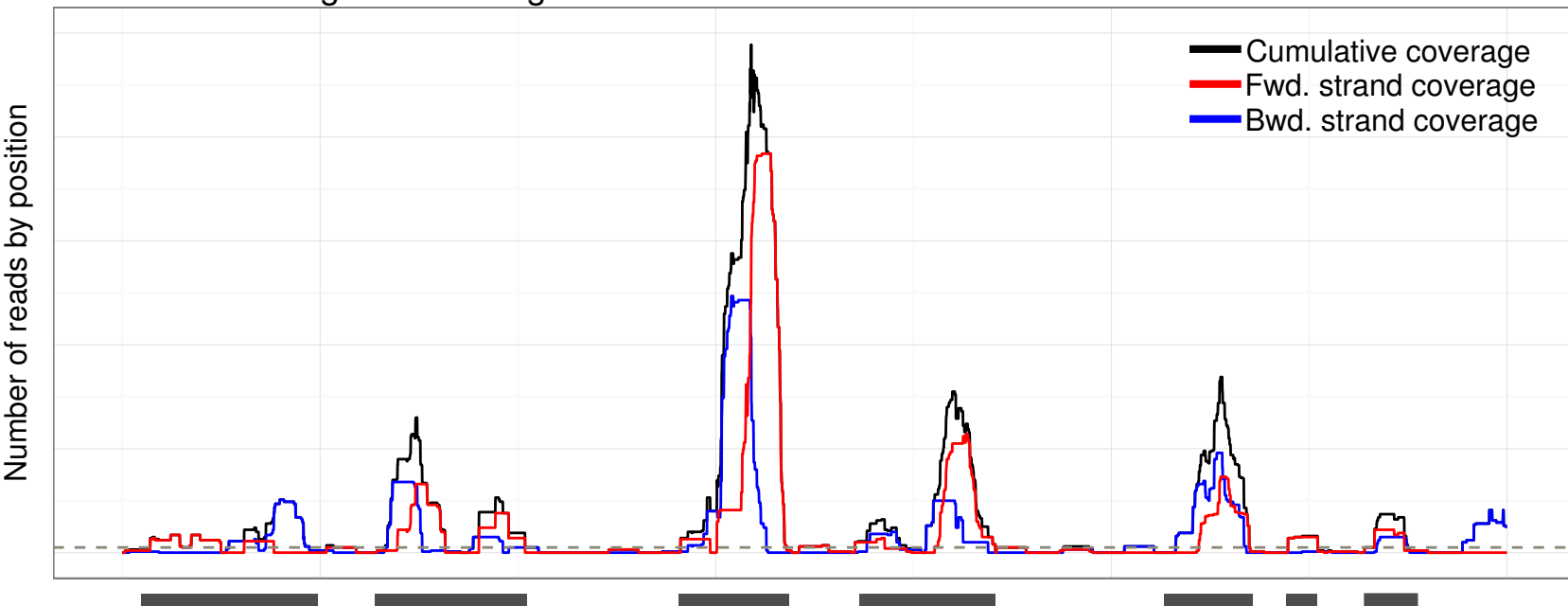
2 - Calculate a vector of summary statistics for each island

R_1 R_2 R_3 R_K

$T(R_1)$ $T(R_2)$ $T(R_3)$ $T(R_K)$

3 - Visualize all islands together:

A

Nr. of islands: 10^0 10^2 10^4 10^6

Unique read coverage rate (URCR)

Average read coverage (ARC)

B

Legend: both, fwd, bwd

Proportion of regions

Min. number of reads

C

Legend: 0.1, 0.25, 0.5, 0.75, 0.9

Forward strand ratio (FSR)

Min. number of reads