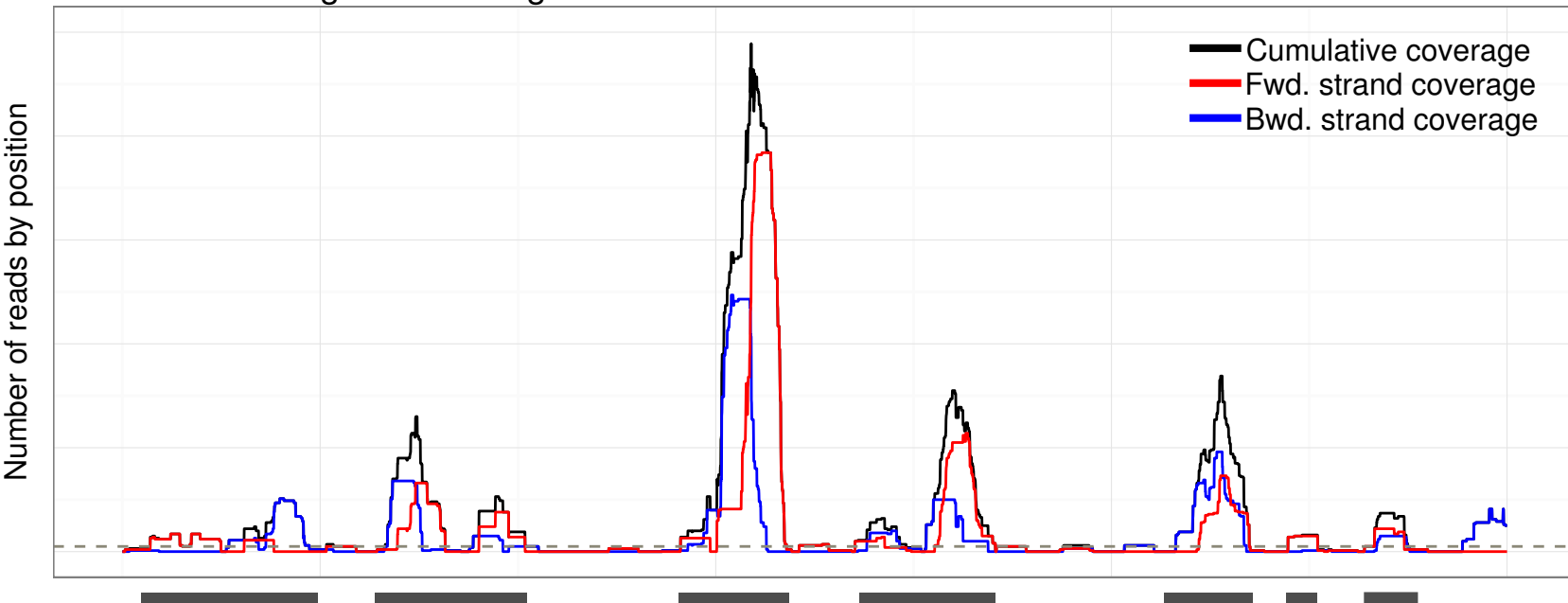


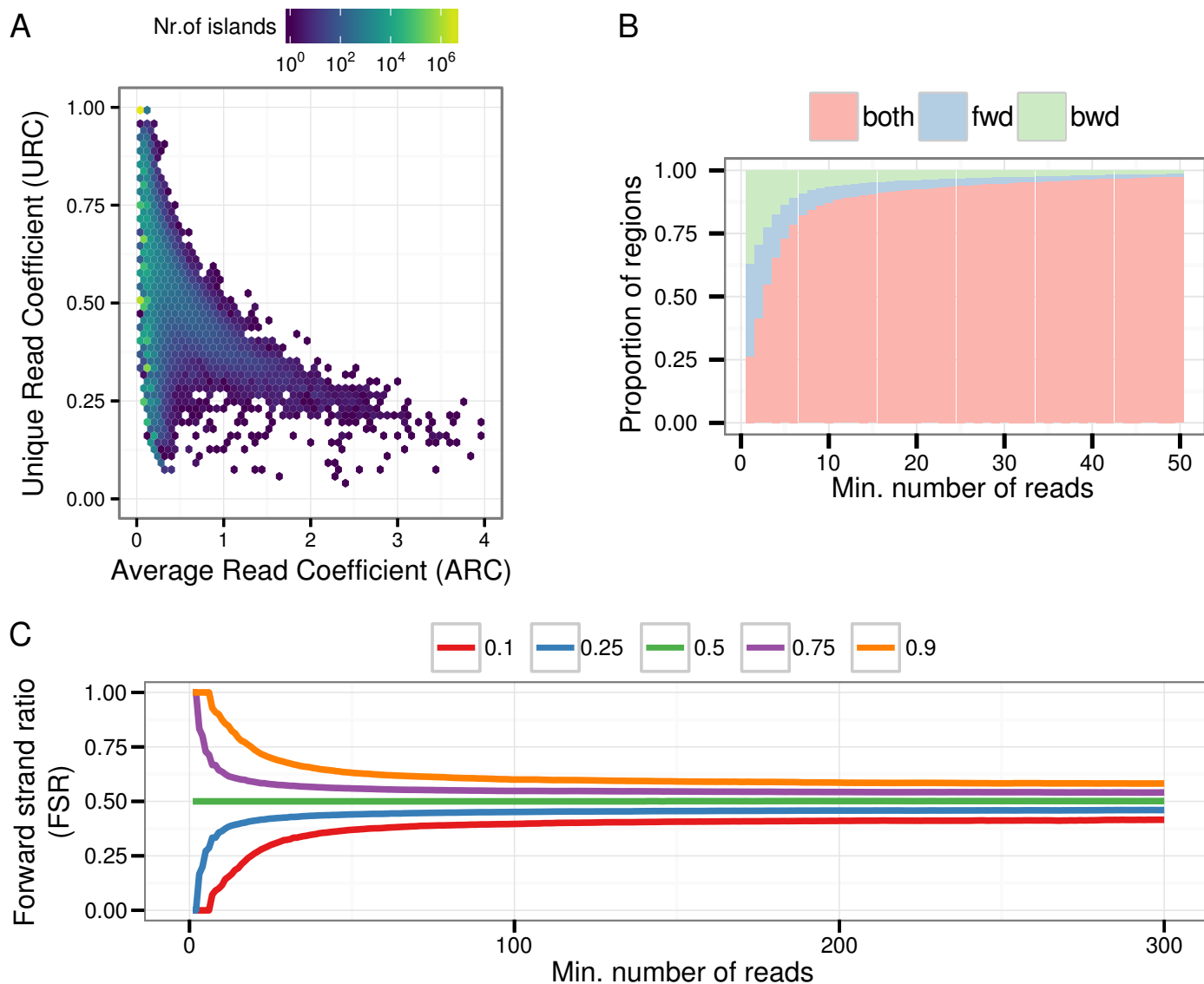
1 - Partitions the genome and generate ChIP-exo islands.



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:



4 - Generate quantitative summaries of these diagnostics plots.