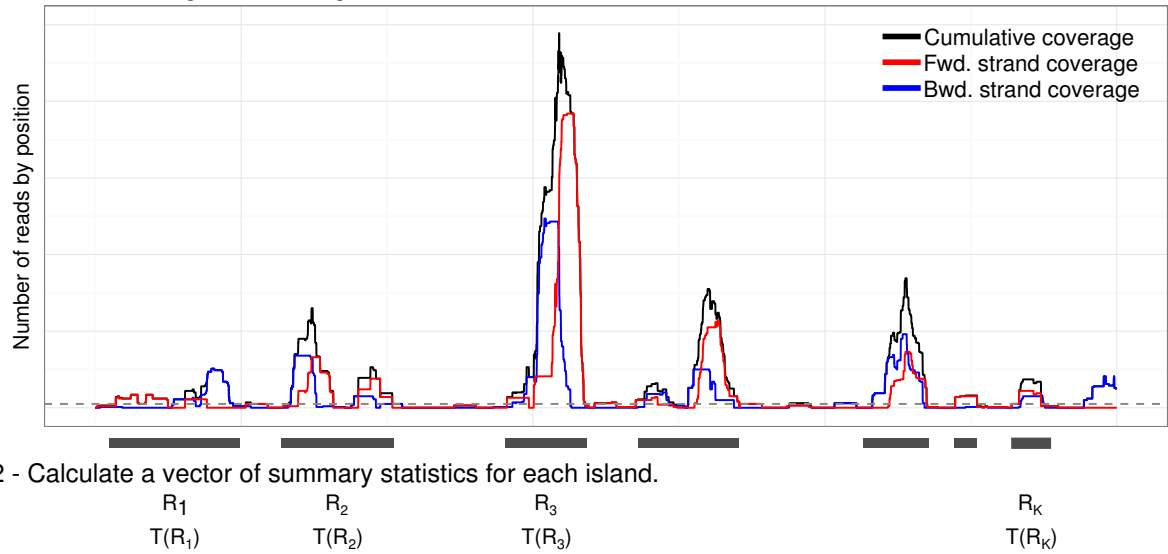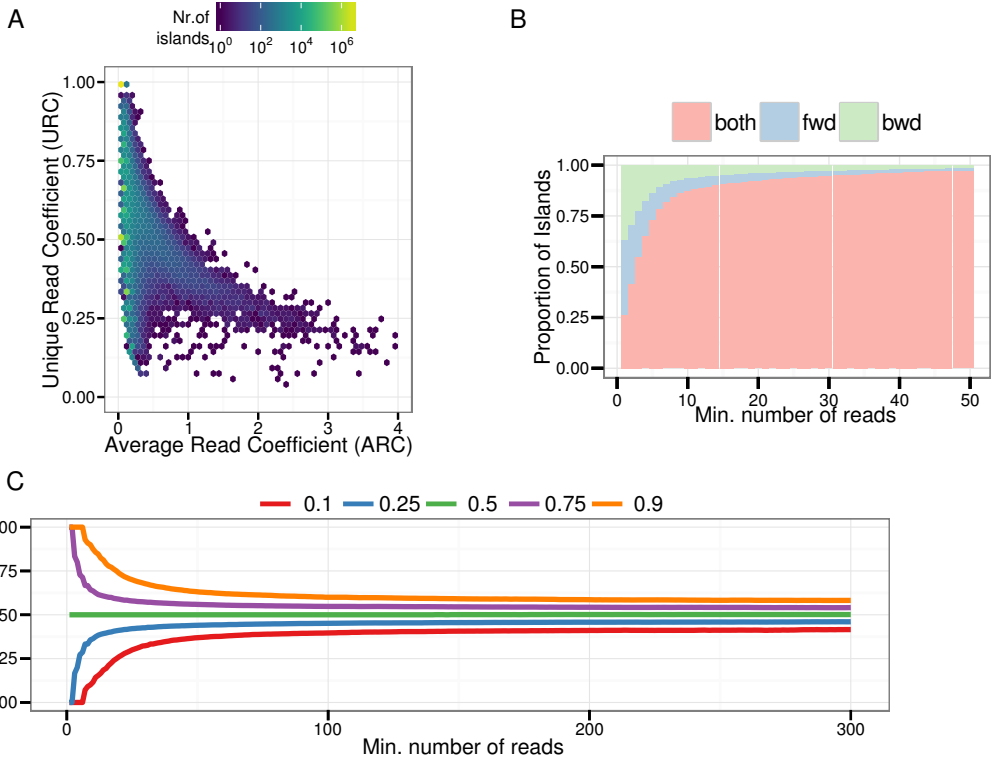1 - Partitions the genome and generate ChIP-exo islands.

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 diagnostic plots.