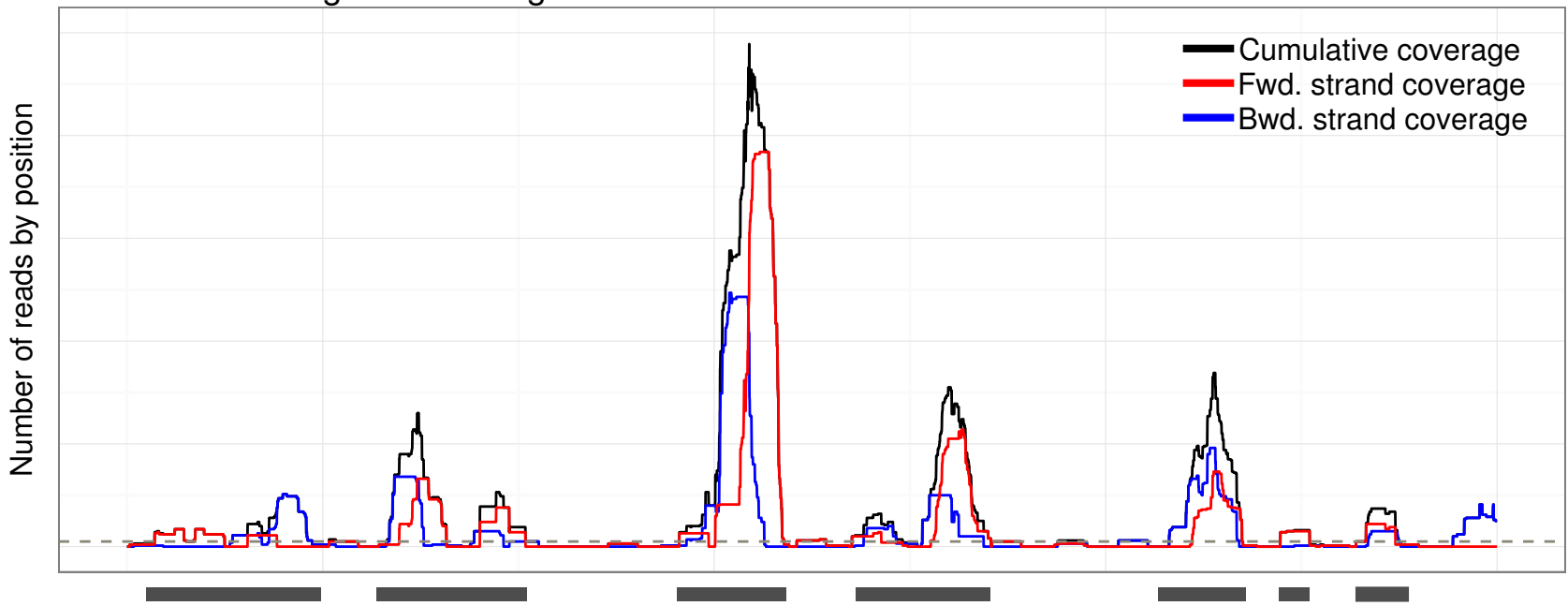


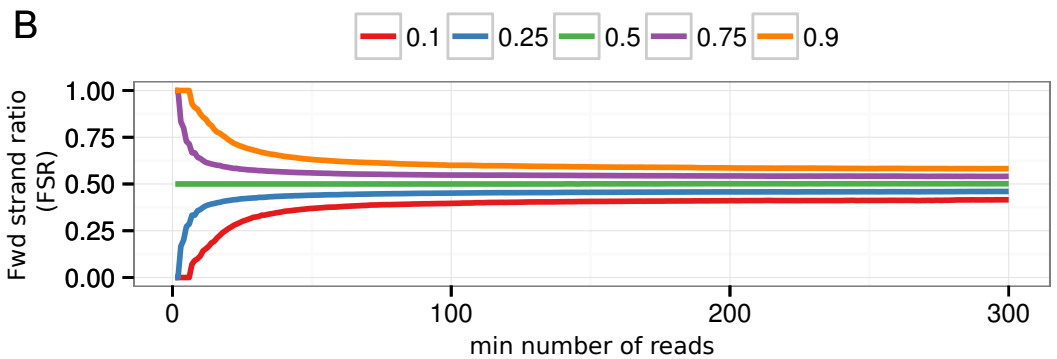
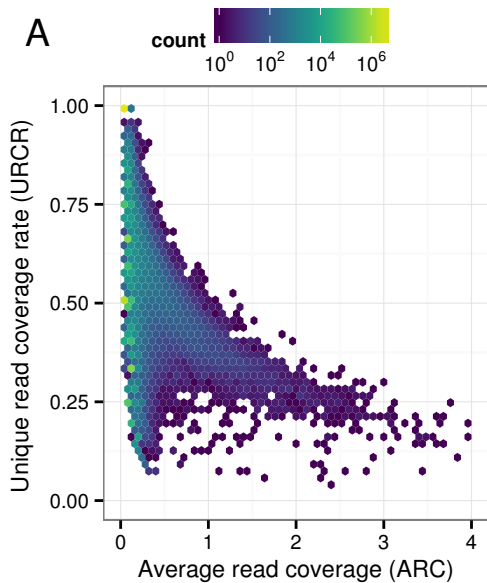
## 1 - Partitions the genome and generate ChIP-exo islands.



## 2 - Calculate a vector of summary statistics for each island

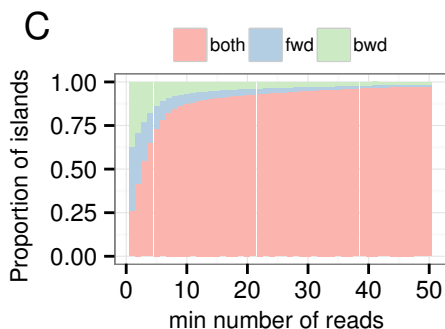
$R_1$   $R_2$   $R_3$   $R_K$   
 $T(R_1)$   $T(R_2)$   $T(R_3)$   $T(R_K)$

## 3 - Visualize all islands together:



3A - ARC vs. URCR - This plot presents a global view of the balance between library complexity and enrichment. There are two arms, one with low ARC, which corresponds to regions formed by few aligned positions, and the other where the URCR decreases as the ARC increases.

3B - Min depth vs. FSR - This plot depicts how quickly the distribution of the FSR approximates the median. In a high quality dataset sample, the median is around 0.5, and the other quantiles reach that value quickly.



3C - Min depth vs. Proportion of Islands - This plot provides a more detailed view of the FSR. Islands with low depth then to have reads only from one strand. Hence, the plot compares the percentage of islands that contain at least one read of each strand vs the regions that consist of only reads with only one strand.