

# A Quality Control pipeline for ChIP-exo and ChIP-nexus data.

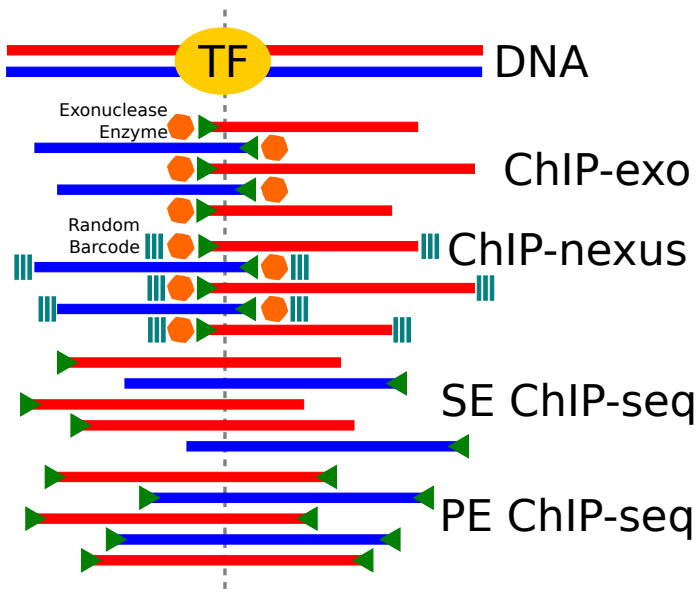
Rene Welch & Sündüz Keleş

Department of Statistics  
University of Wisconsin - Madison

June 24, 2016

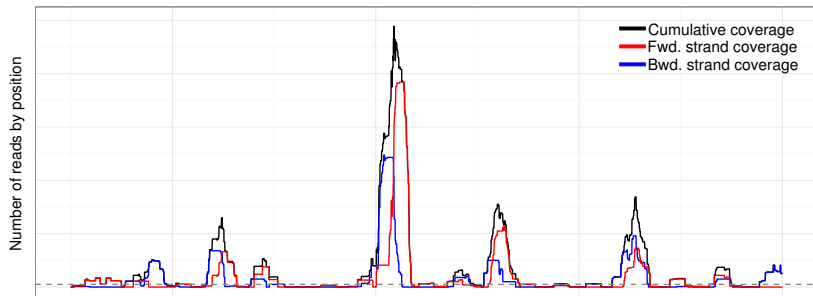
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# What is ChIP-exo and ChIP-nexus.



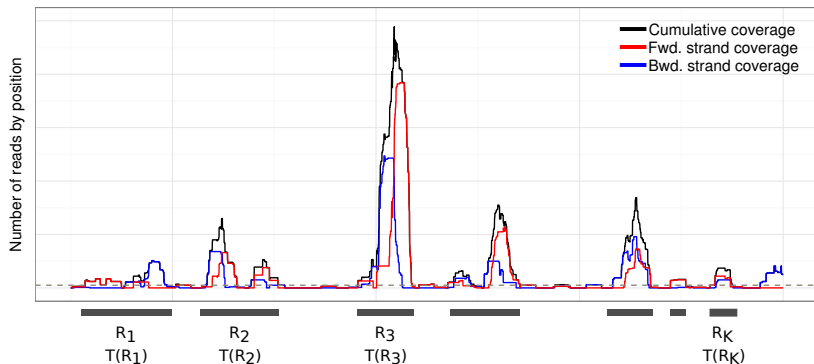
# Overview of the pipeline.

1. Partition the genome and generate ChIP-exo/nexus islands.



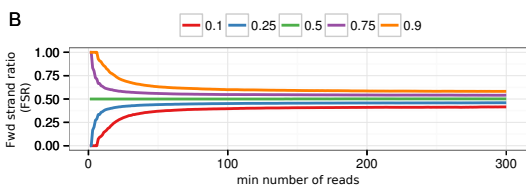
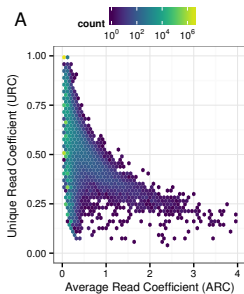
# Overview of the pipeline.

2. Calculate a vector of summary statistics for each island.



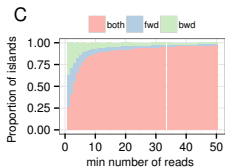
# Overview of the pipeline.

## 3. Visualize all islands together and calculate quality scores.



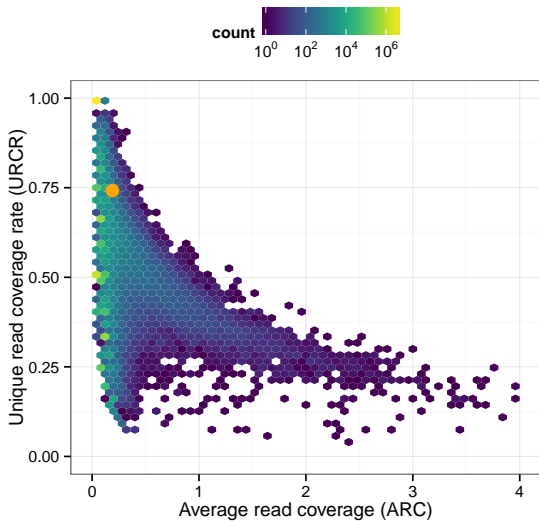
3A - ARC vs. URC - This plot presents a global view of the balance between library complexity and enrichment. There are two arms, one with low ARC, which corresponds to regions formed by few aligned positions, and the other where the URC decreases as the ARC increases.

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.

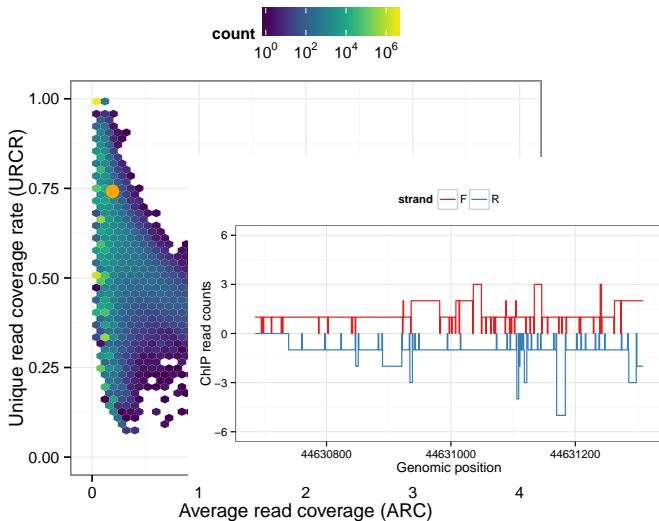


3C - Min depth vs. Proportion of Islands - This plot provides a more detailed view of the FSR. Islands with low depth then to have reads only from one strand. Hence, the plot compares the percentage of islands that contain at least one read of each strand vs. the regions that consist of only reads with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

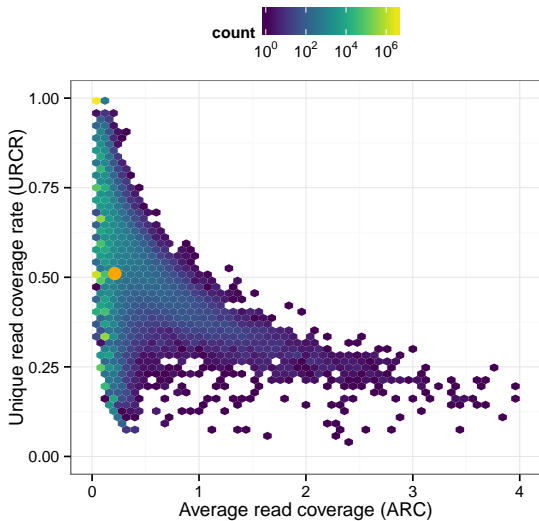
# ARC vs. URCR exploration



# ARC vs. URCCR exploration

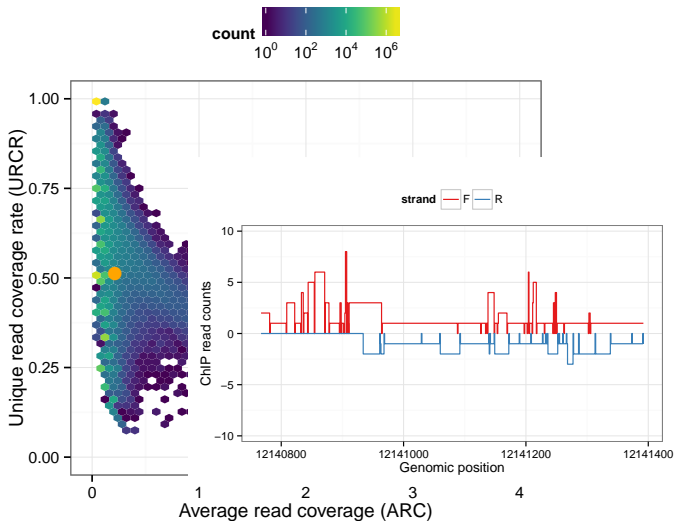


# ARC vs. URCR exploration

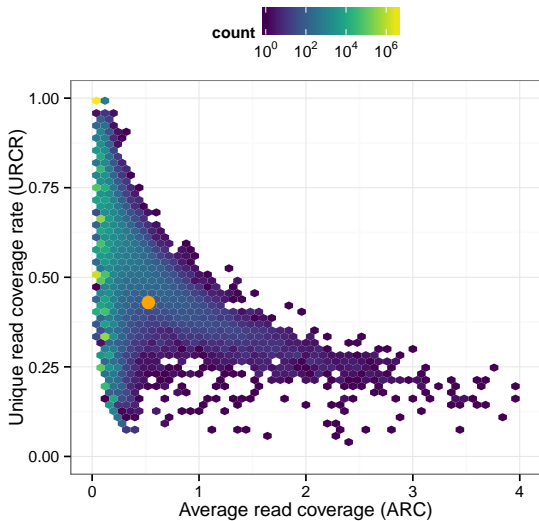




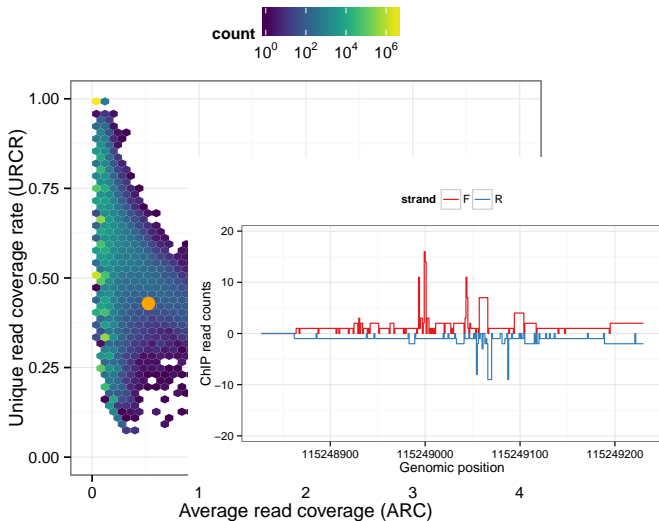
# ARC vs. URCCR exploration



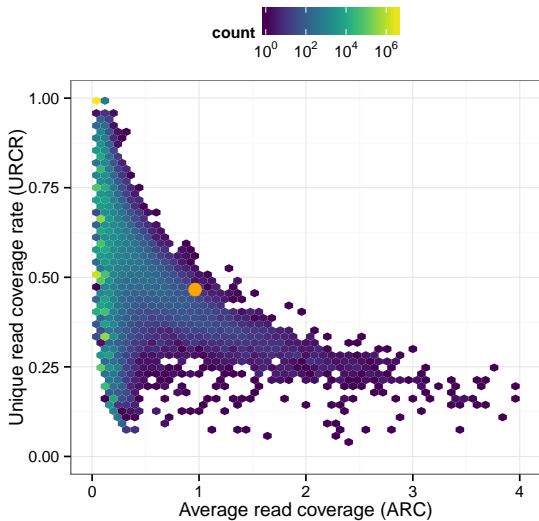
# ARC vs. URCR exploration



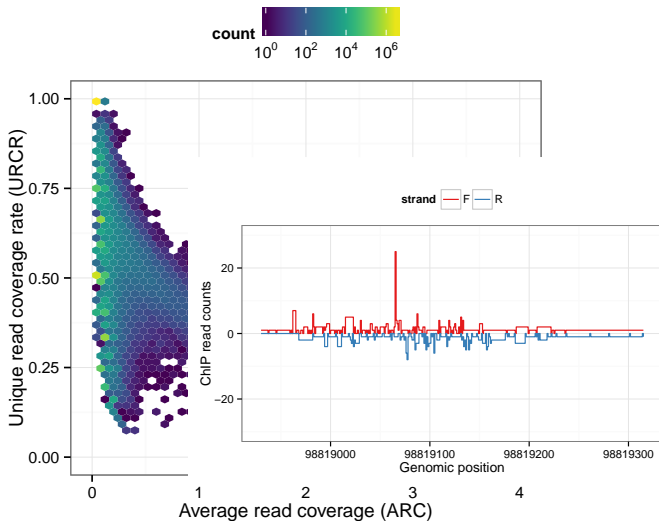
# ARC vs. URCCR exploration



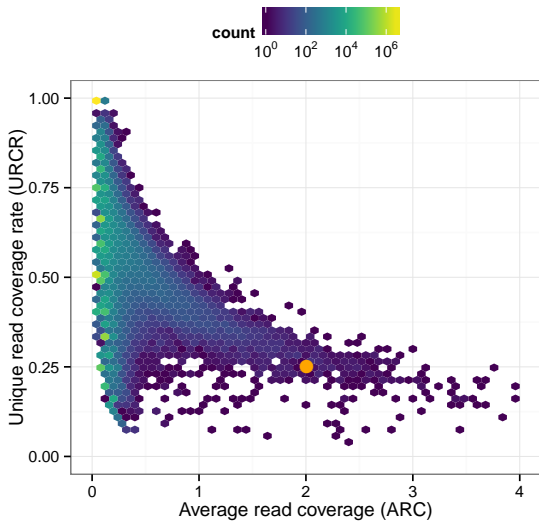
# ARC vs. URCR exploration



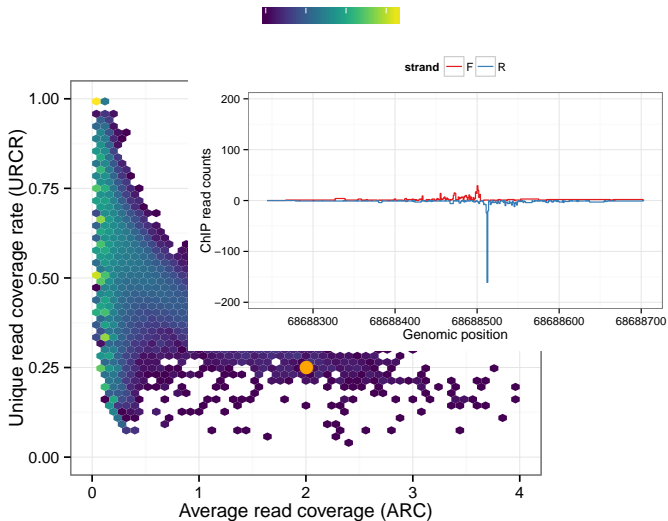
# ARC vs. URCCR exploration



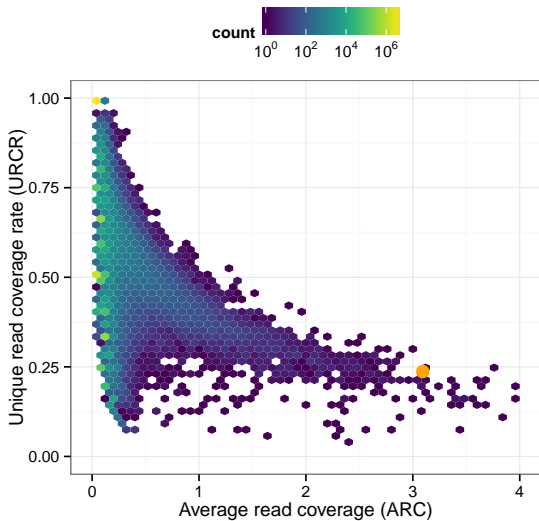
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# ARC vs. URCCR exploration

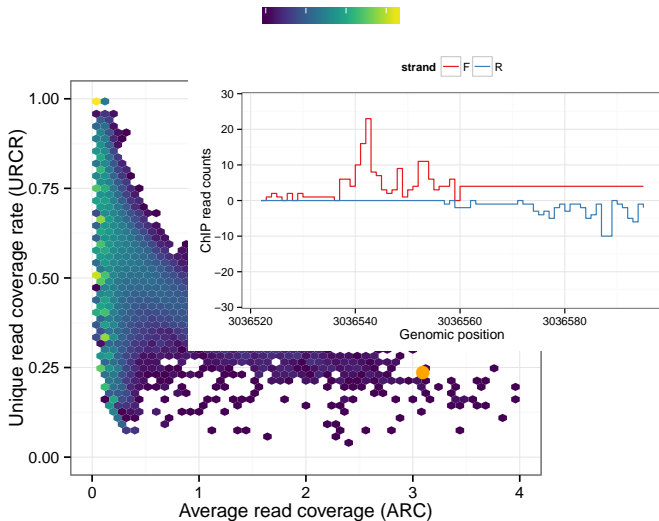


# ARC vs. URCR exploration

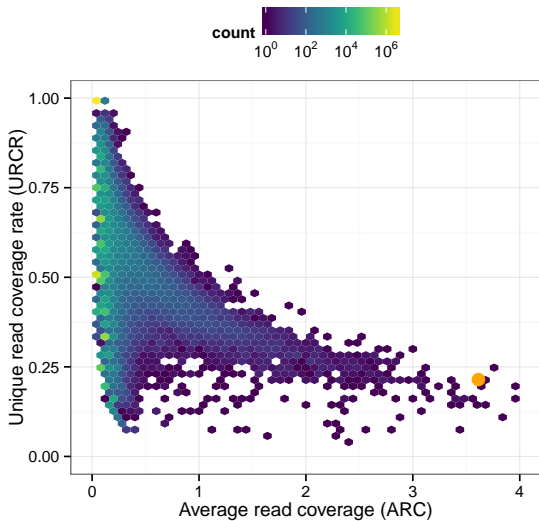




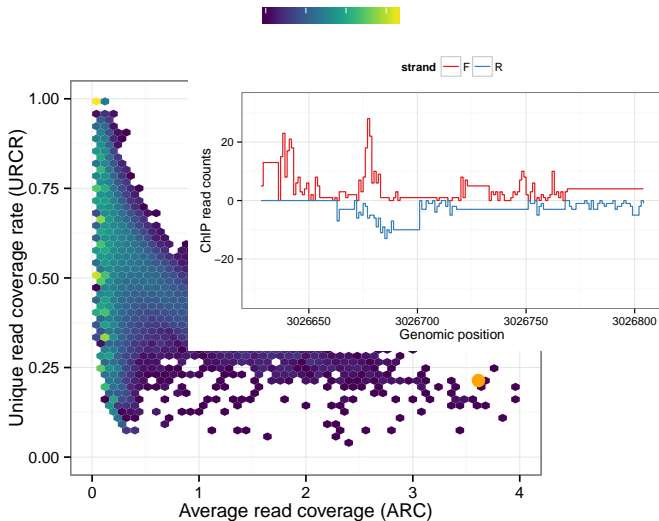
# ARC vs. URCR exploration



# ARC vs. URCR exploration

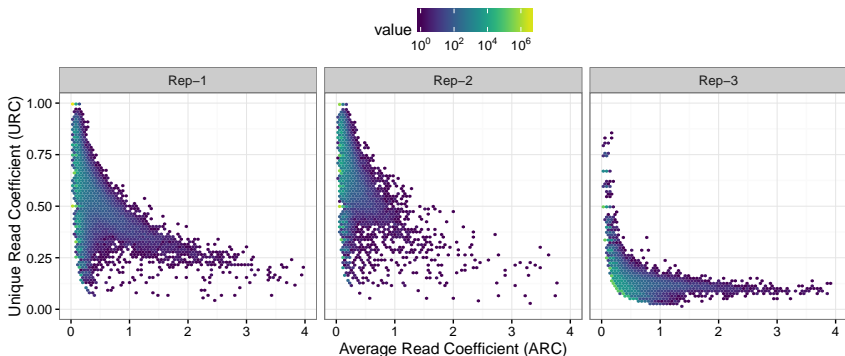


# ARC vs. URCCR exploration



# Case of Study: FoxA1 on mouse liver.

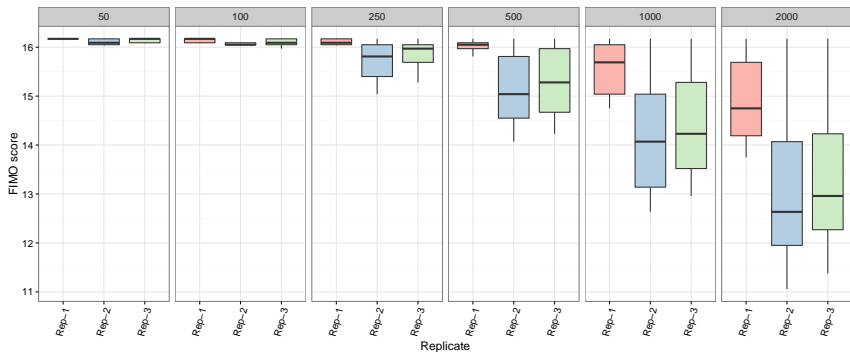
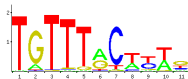
## Enrichment and library complexity



- ▶ Rep-1 shows the highest quality.
- ▶ Rep-2 is not sufficiently enriched.
- ▶ Rep-3 exhibits low library complexity.

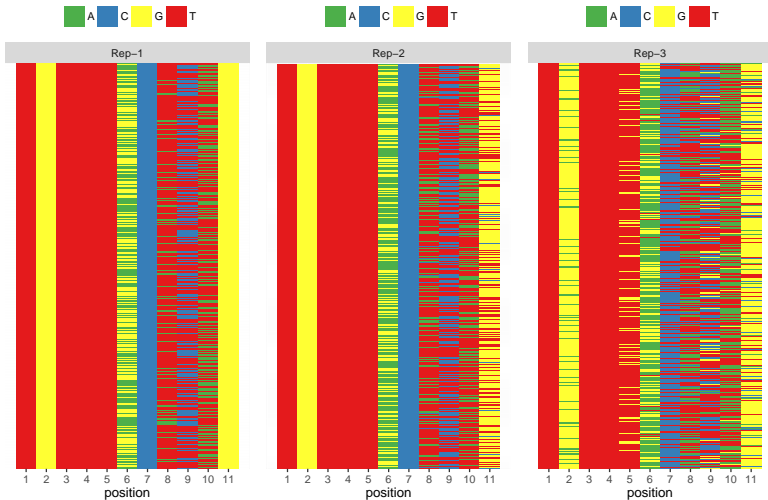
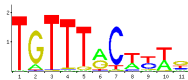
# Comparison of samples with FIMO analysis.

We searched for the FoxA1 motif using FIMO.



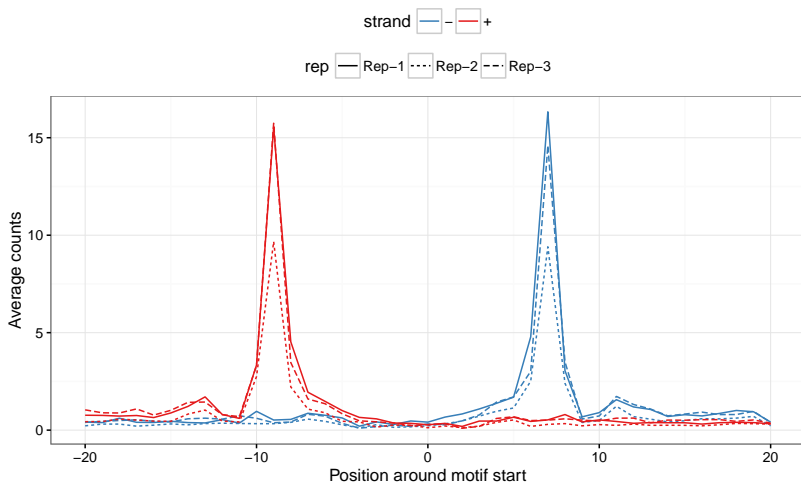
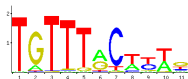
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Thank you very much!