

Characterization of epigenetic and transcriptional landscape in heat stressed-rats using ATAC-seq and RNA-seq



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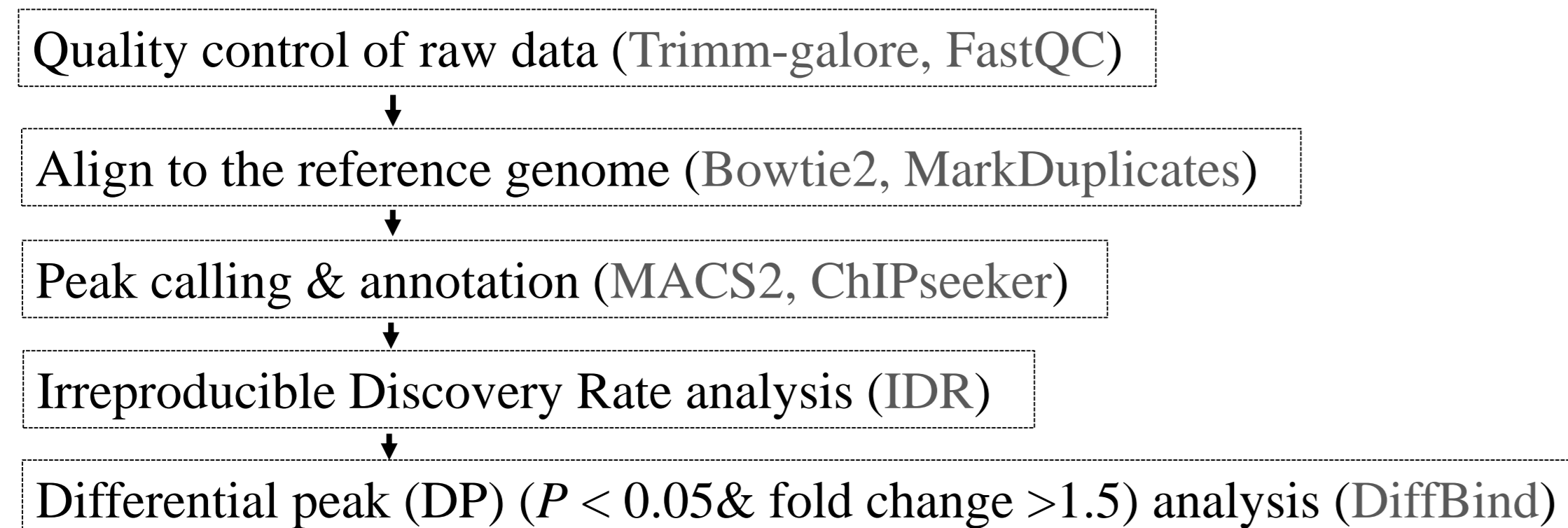
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Introduction

- Understanding animal physiology and identifying reliable biomarkers may help to establish effective management strategies for prevention of heat stress (HS)
- Little is known about the molecular mechanism of mammal tolerance to high temperature
- In a previous study with Sprague-Dawley rats, we performed RNA-seq assays on liver of rats in control check (CK; 22 °C, n = 5) and heat stress (H120; 42 °C for 120 min, n=5) groups. A total of 3,909 differential expression genes (DEGs, $Q < 0.05$) were observed

Materials and Methods

- Animals:** Female Sprague Dawley rats weighing 205 ± 7.16 g (8 weeks old)
- Methods:** Three liver tissues were selected from the RNA-seq samples in the CK and H120 groups and had an Assay for Transpose Accessible Chromatin sequencing (ATAC-seq) performed
- Bioinformatics analysis:**

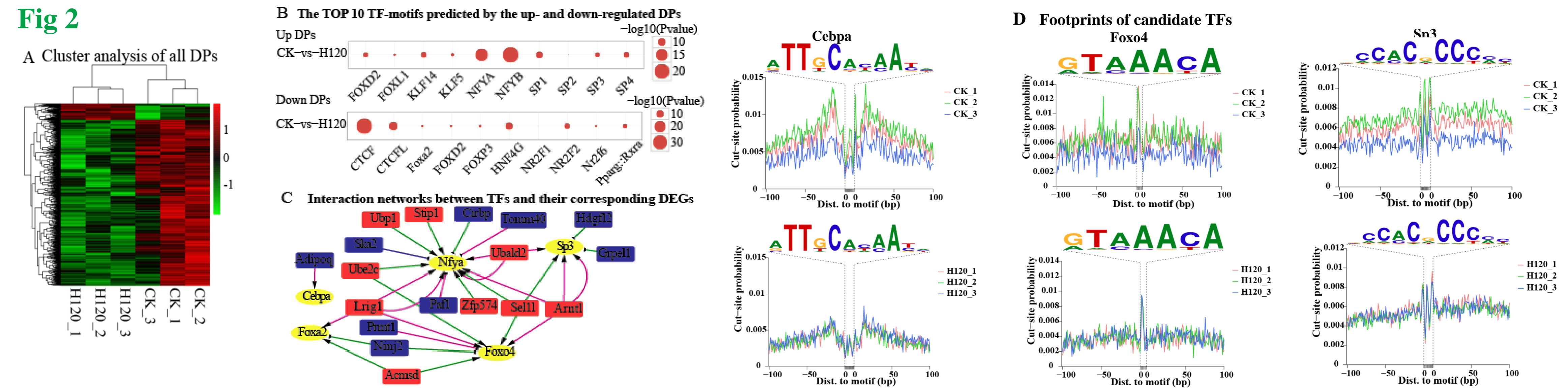
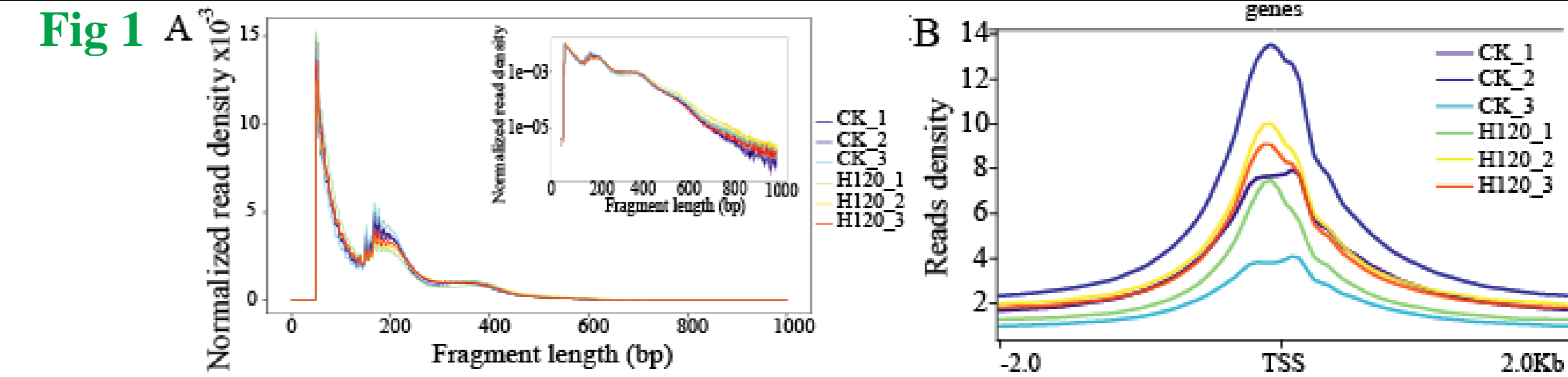


Functional annotation (GO, KEGG)

* DPGs: Differential peaks related genes
DPEGs: Differential peaks related genes that were differentially expressed in RNA-seq data

Results and Discussion

- All ATAC-seq libraries generated an expected distribution of the insert fragment lengths, with the majority of fragments being small and progressively fewer fragments of larger size (Fig 1A)
- The accessibility of transcriptional start sites (TSS) was significantly enriched (Fig 1B)
- A total of 2,586 DPs were identified comparing of CK vs. H120, including 230 up regulated DPs and 2,356 down regulated DPs, which mapped to 571 DEGs (Fig 2A)
- Thirty six and 22 TF-motifs were predicted by the up- and down-regulated DPs in CK vs. H120 (Fig 2B)
- Based on the literature and integration of ATAC-seq and RNA-seq analyses, *Cebpa*, *Foxo4* and *Sp3* involving in the process of oxidative stress were proposed as candidate TFs (Fig 2C-D)



Conclusions

- The nuclear chromatin in the liver of heat stressed-rats was less open than that of control rats
- It is suggested that TFs, including *Cebpa*, *Foxo4* and *Sp3*, and their corresponding DEGs may be involved in the physiological mechanism of HS regulation

Acknowledgements

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