CLIP-Explorer: CLIP-Seq data analysis in Galaxy

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Me*In*Bio - Bio*In*Me Research Training Group
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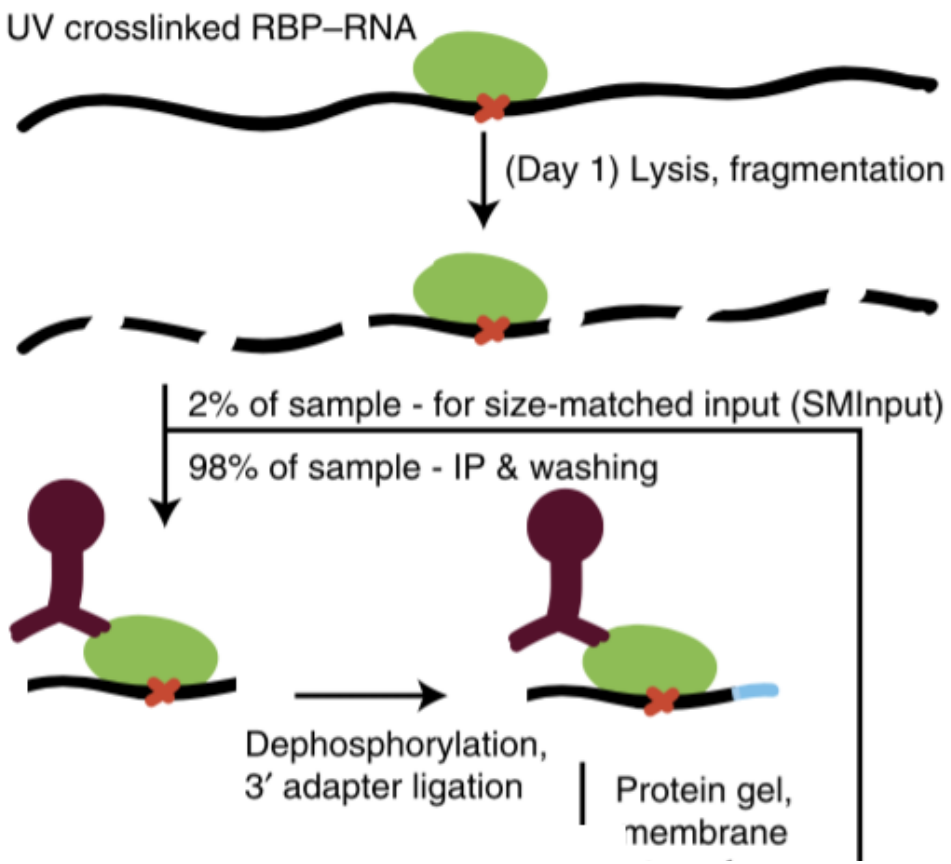
1.1 CLIP-Seq in a Nutshell



[Nostrand *et al.* 2016]

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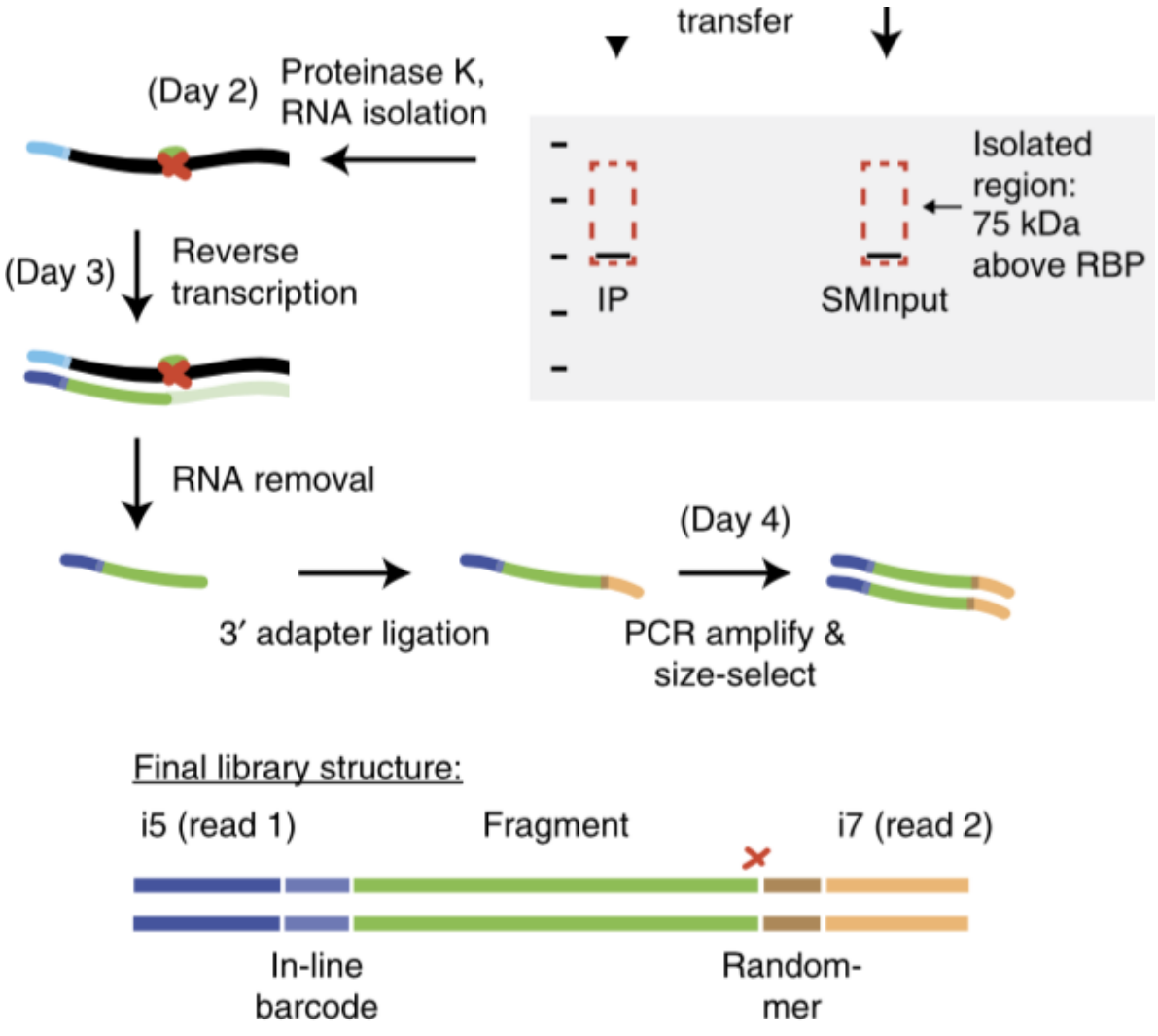

[Nostrand *et al.* 2016]

1.2 Problems of a Data Analysis Pipeline

[https://www.wikihow.com/Play-Jenga]

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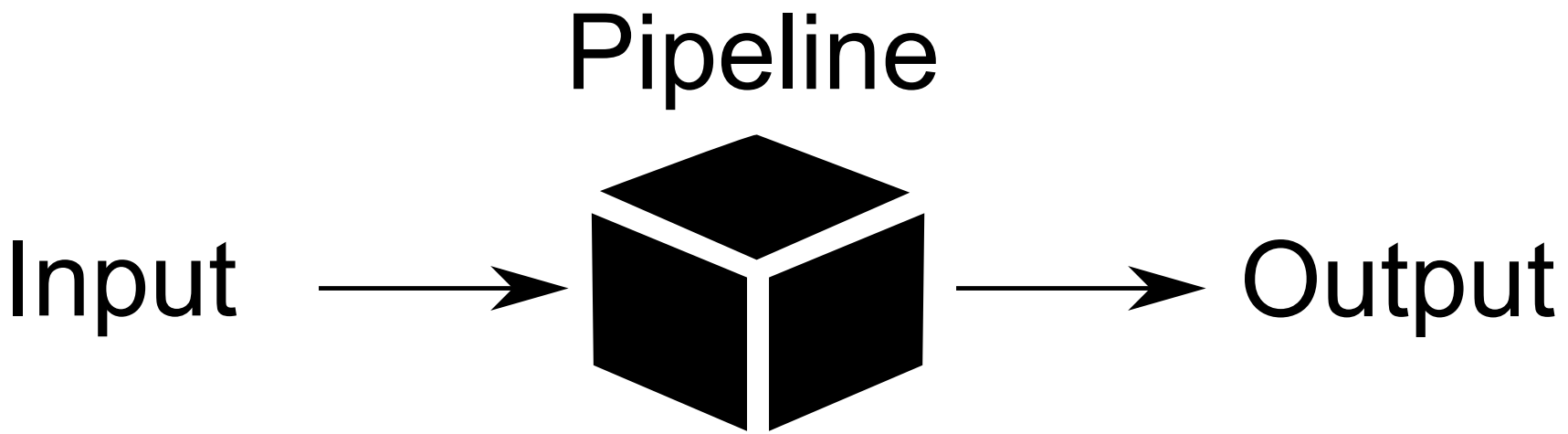
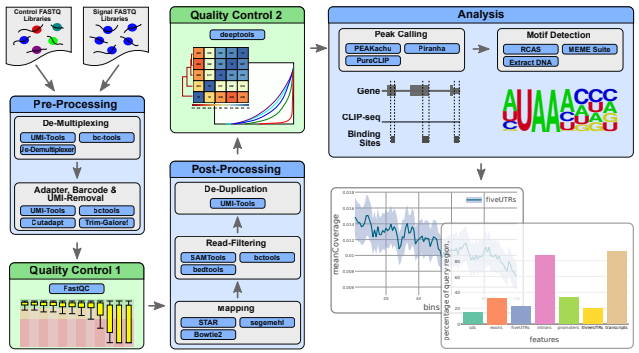


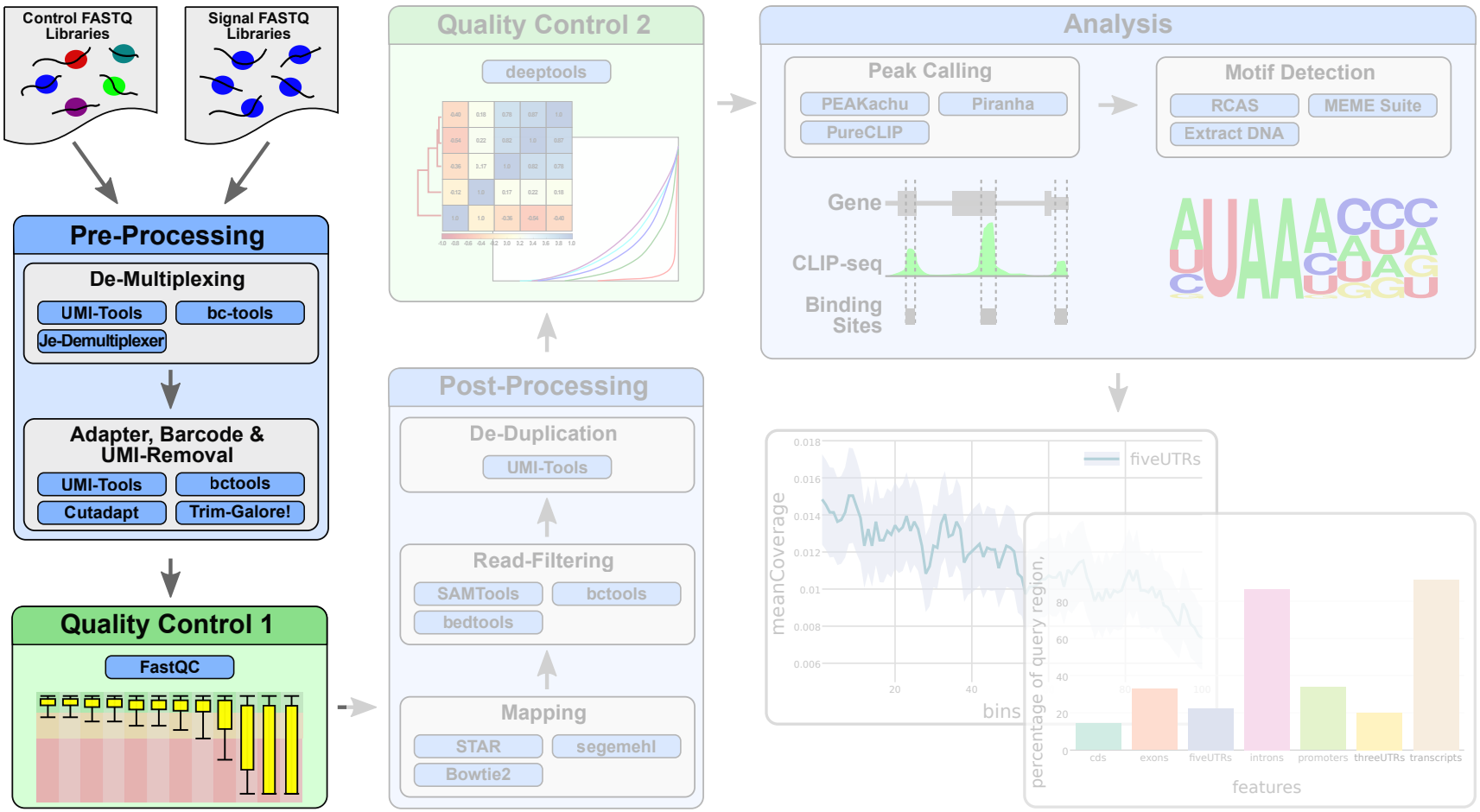
1.2 Problems of a Data Analysis Pipeline

Galaxy Pipeline

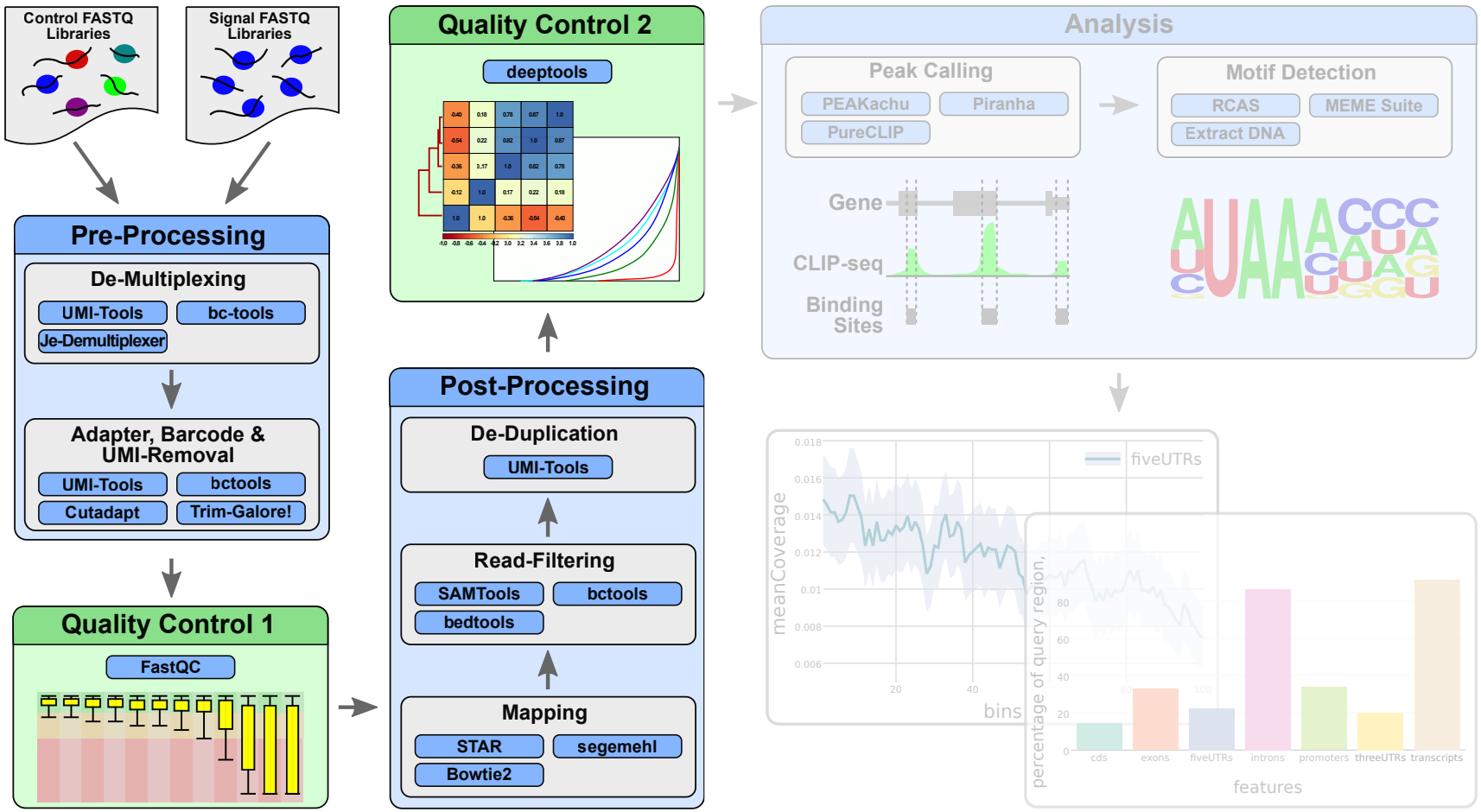


Input → Output

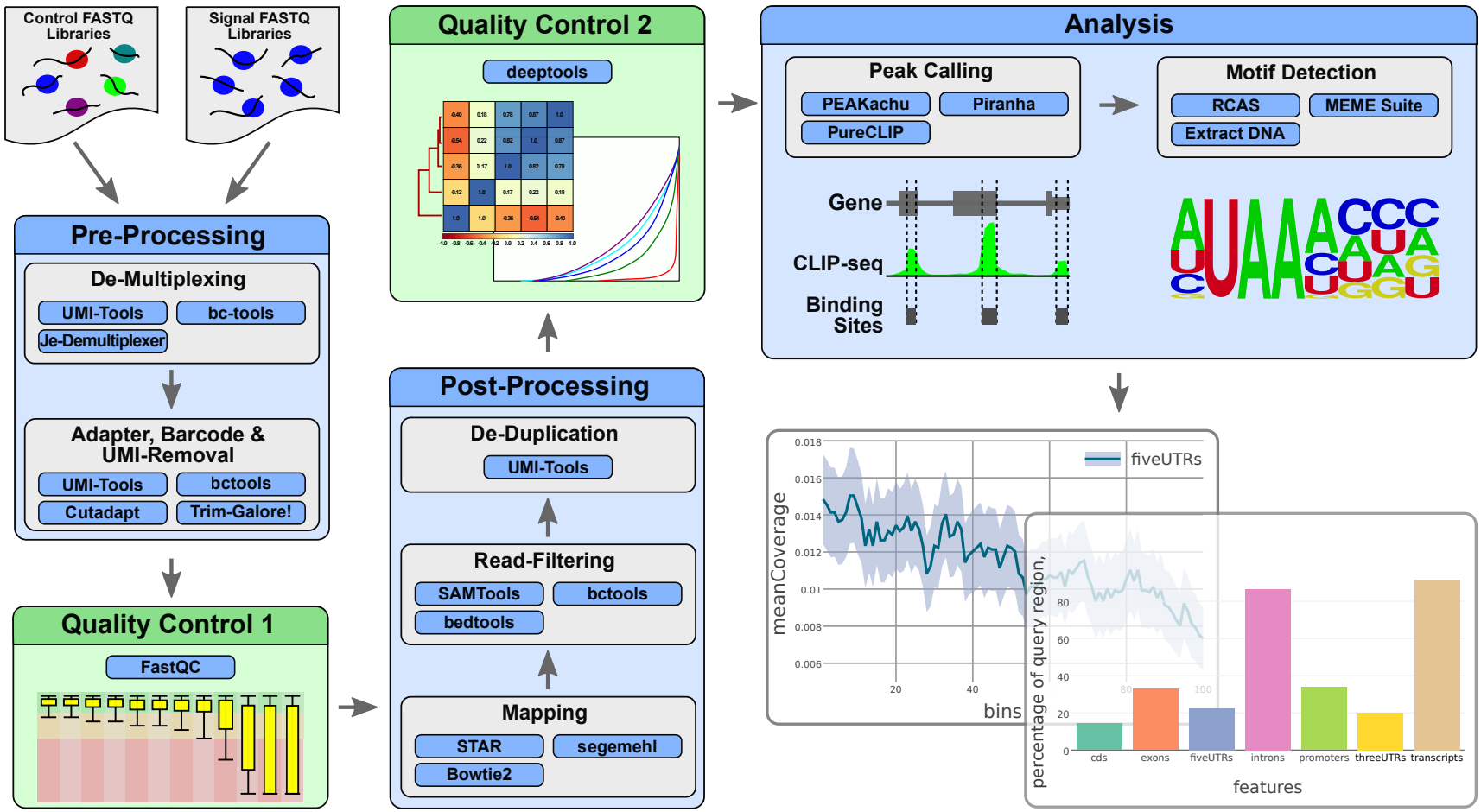
1.3 CLIP-Explorer



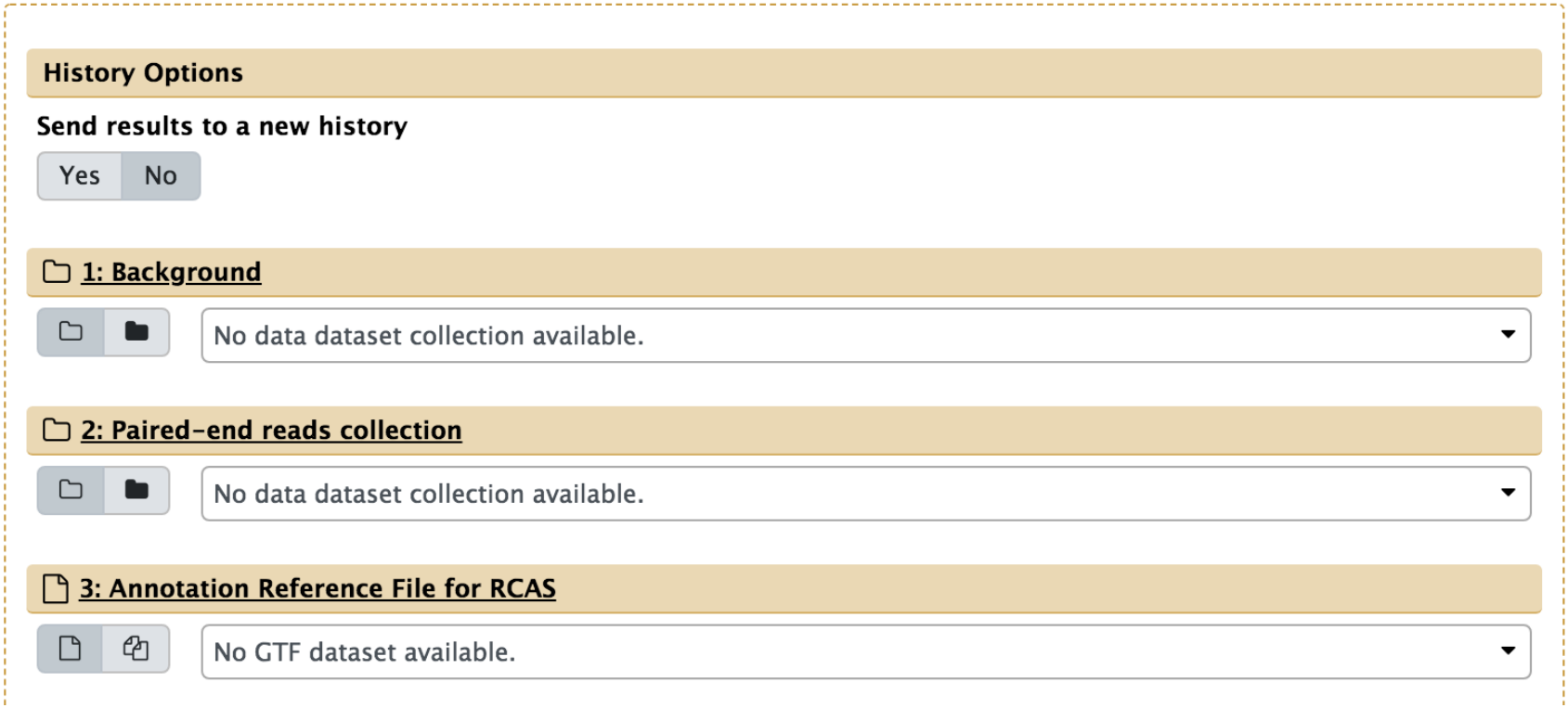
1.3 CLIP-Explorer



1.3 CLIP-Explorer

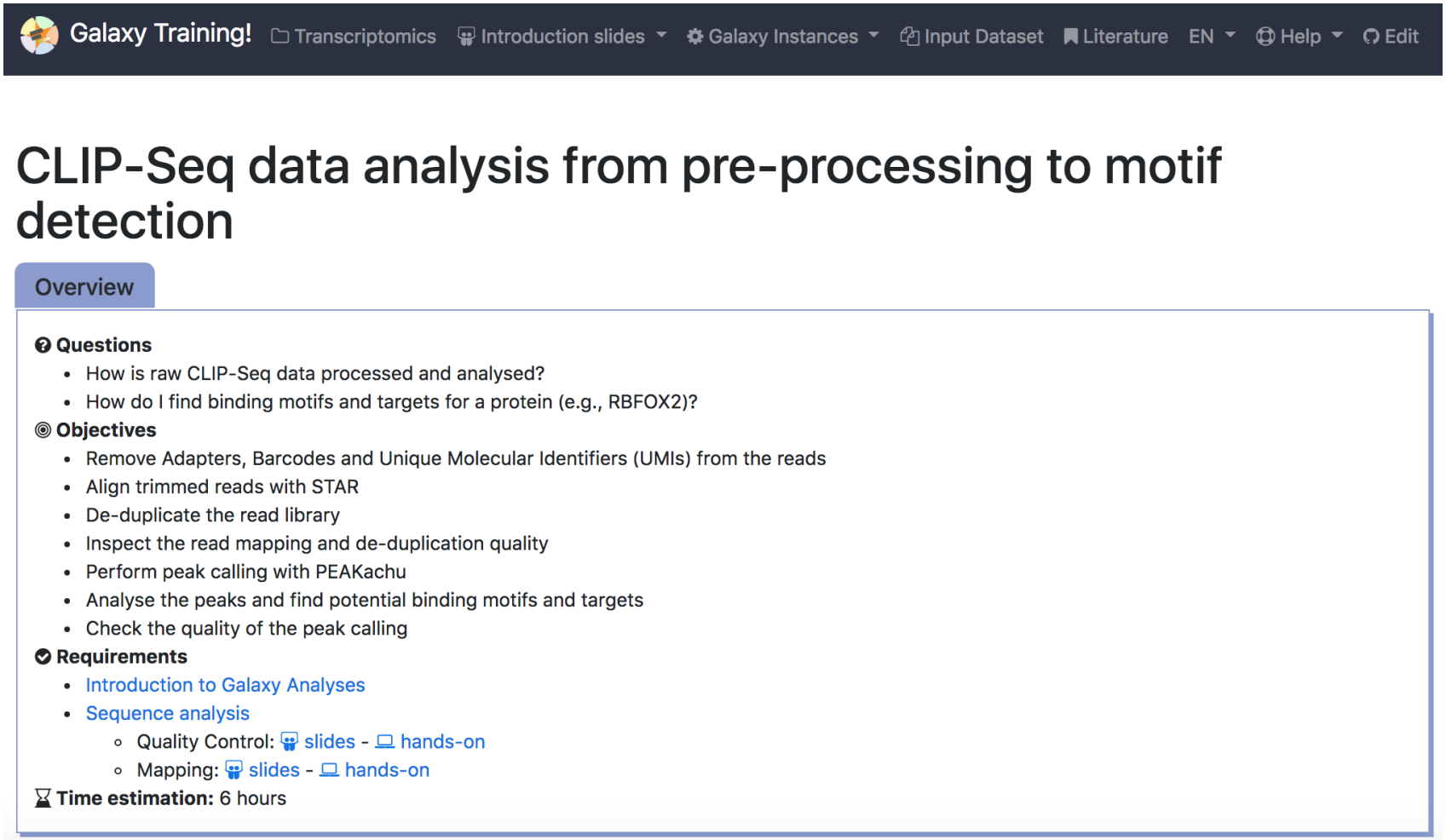


1.4 CLIP-Explorer Available Under



https://clipseq.usegalaxy.eu/

1.5 Galaxy Training Material for CLIP-Explorer



https://galaxyproject.github.io/training-material/topics/transcriptomics/tutorials/clipseq

1.6 Analysis of RBFOX2

- Mainly binds to introns adjacent to differentially spliced exons
- Development and tissue-specific splicing factor
- Main motif: TGCATG

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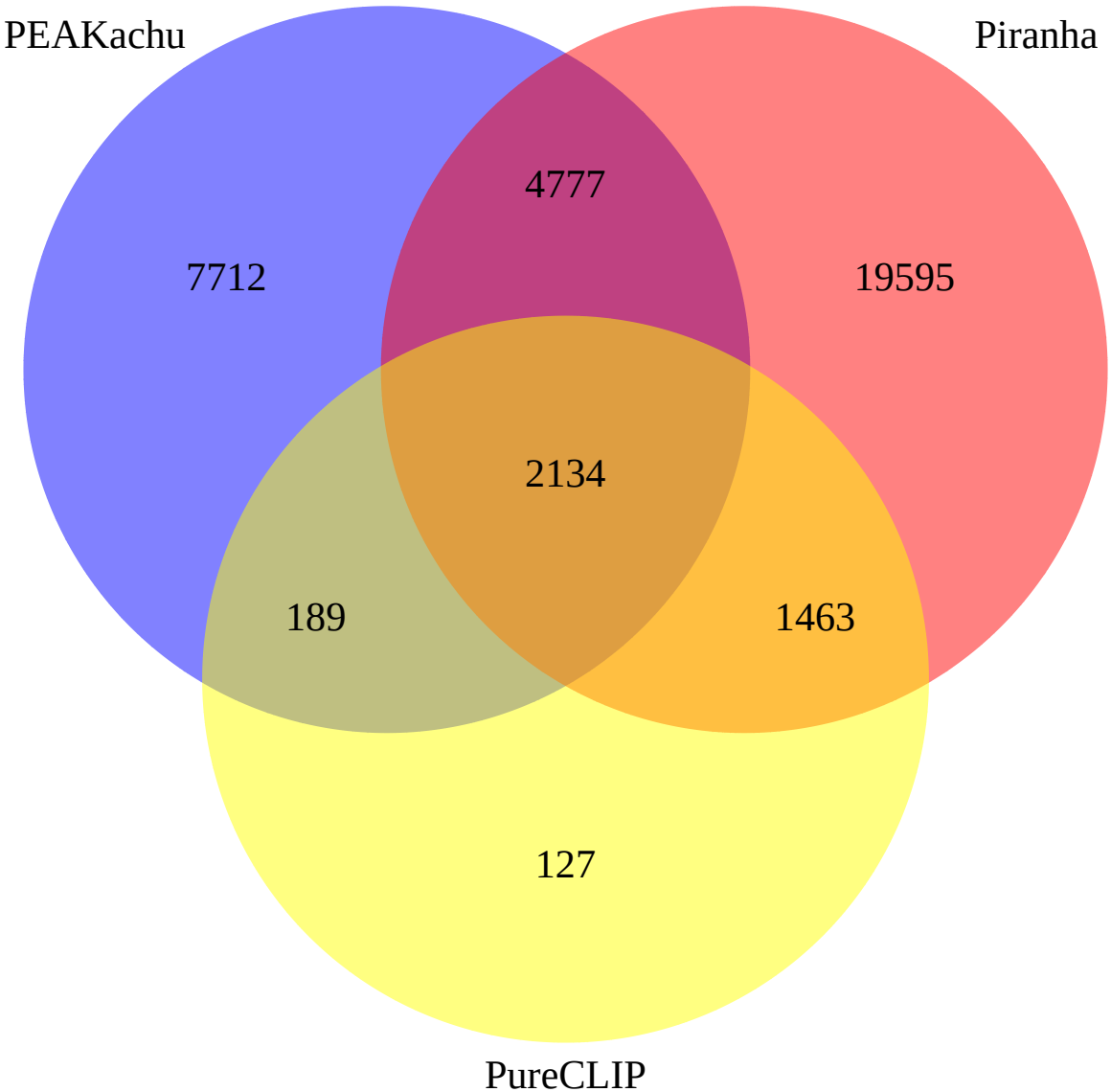
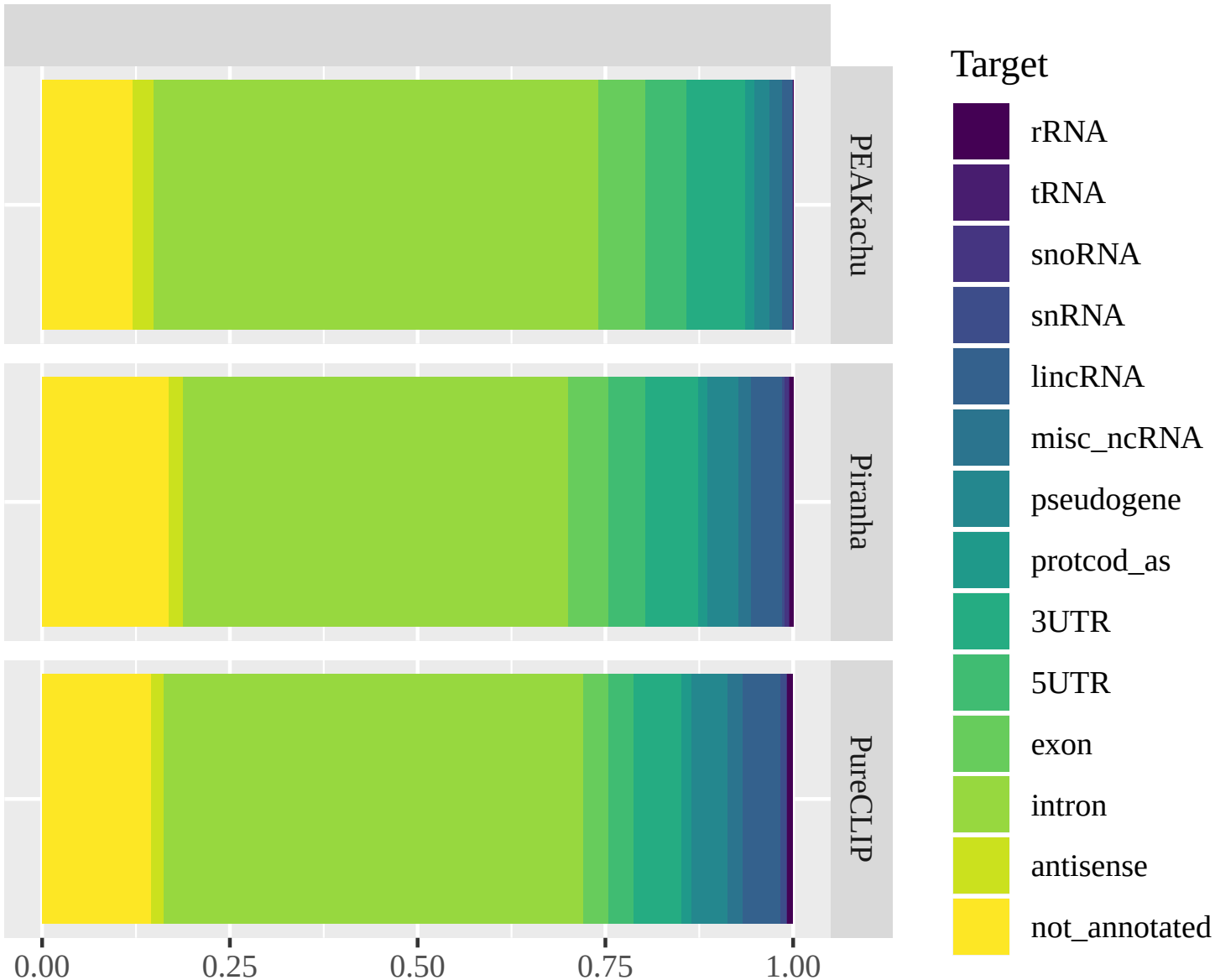


1.6 Analysis of RBFOX2



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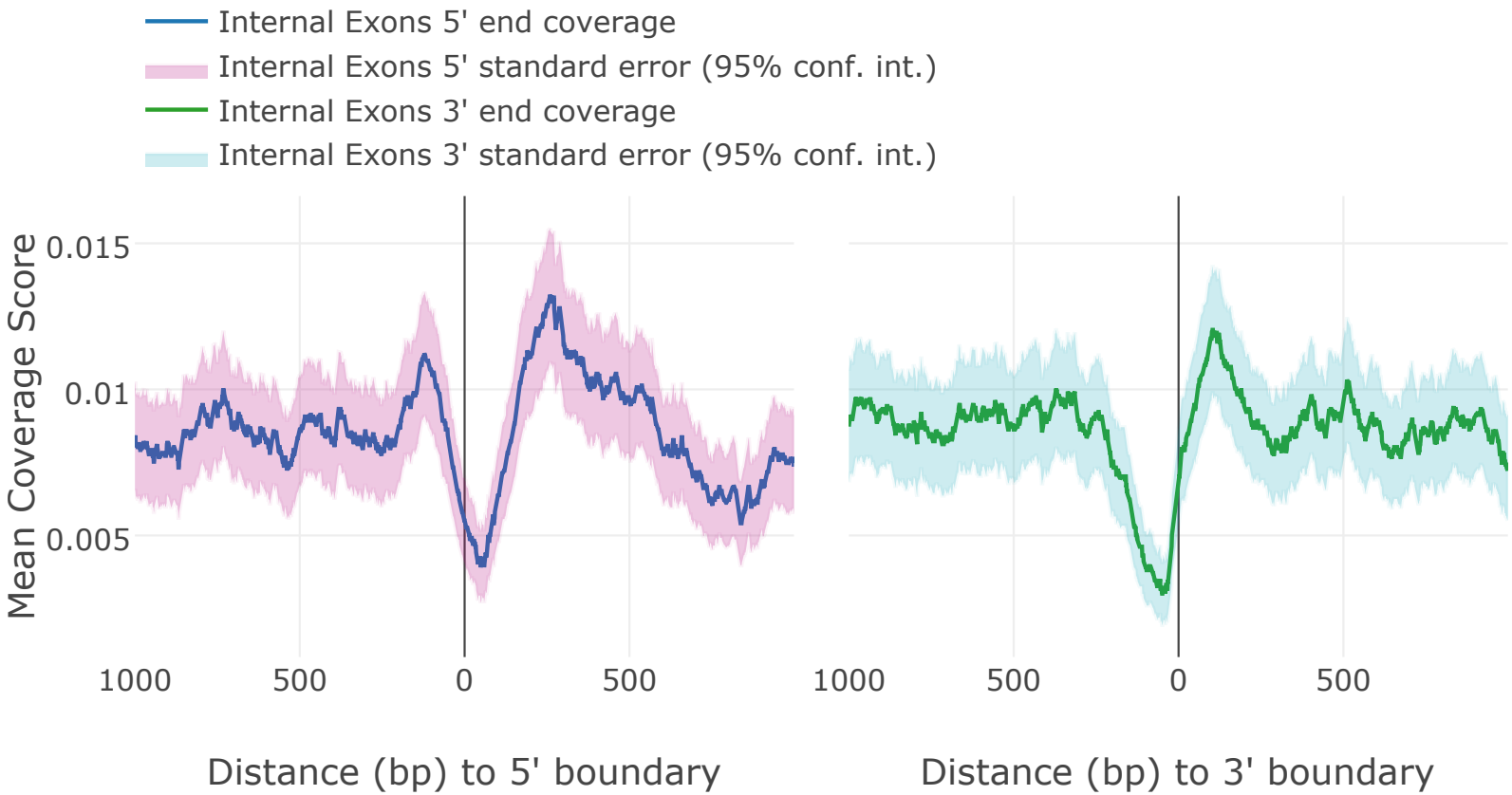

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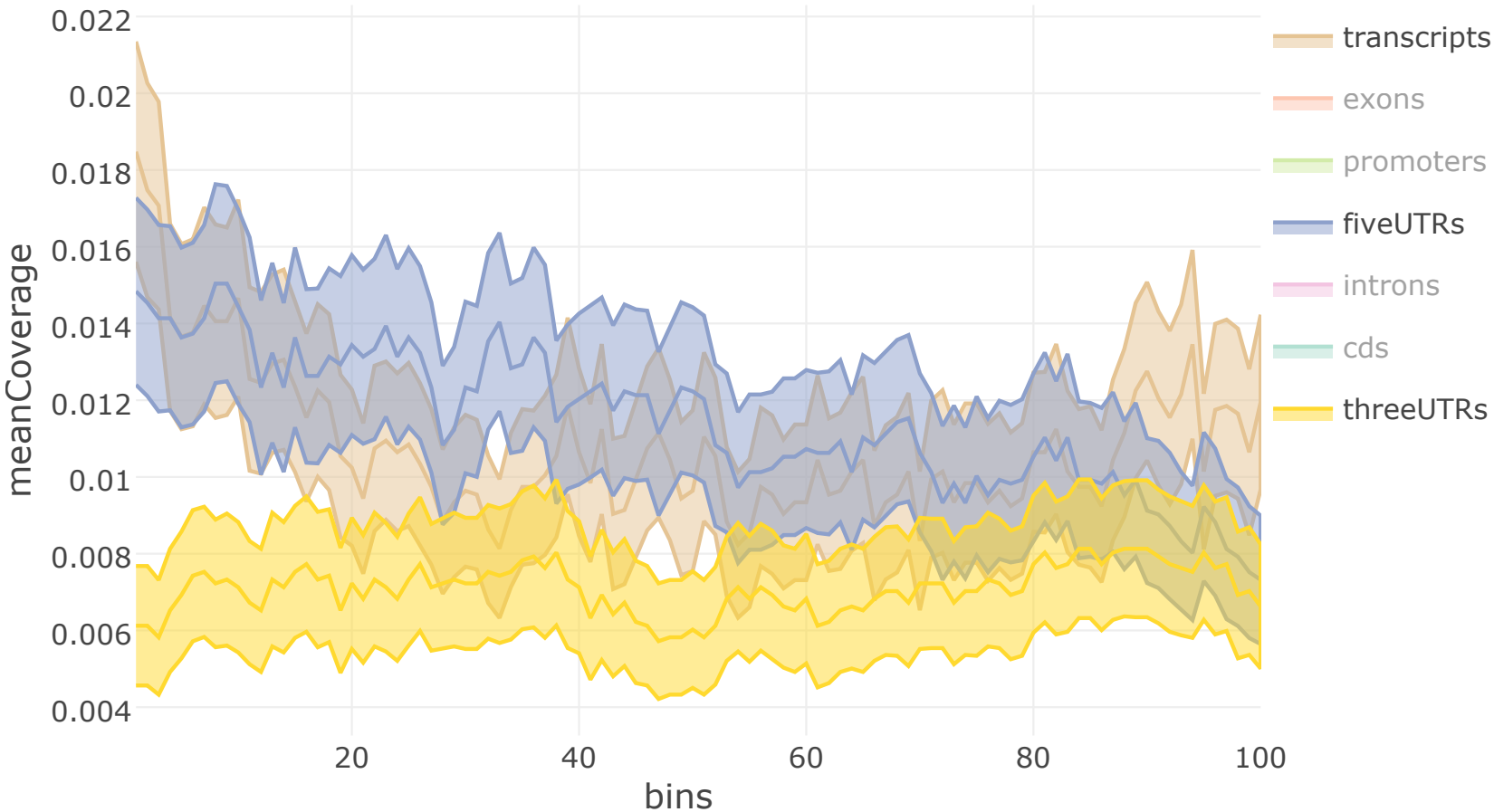

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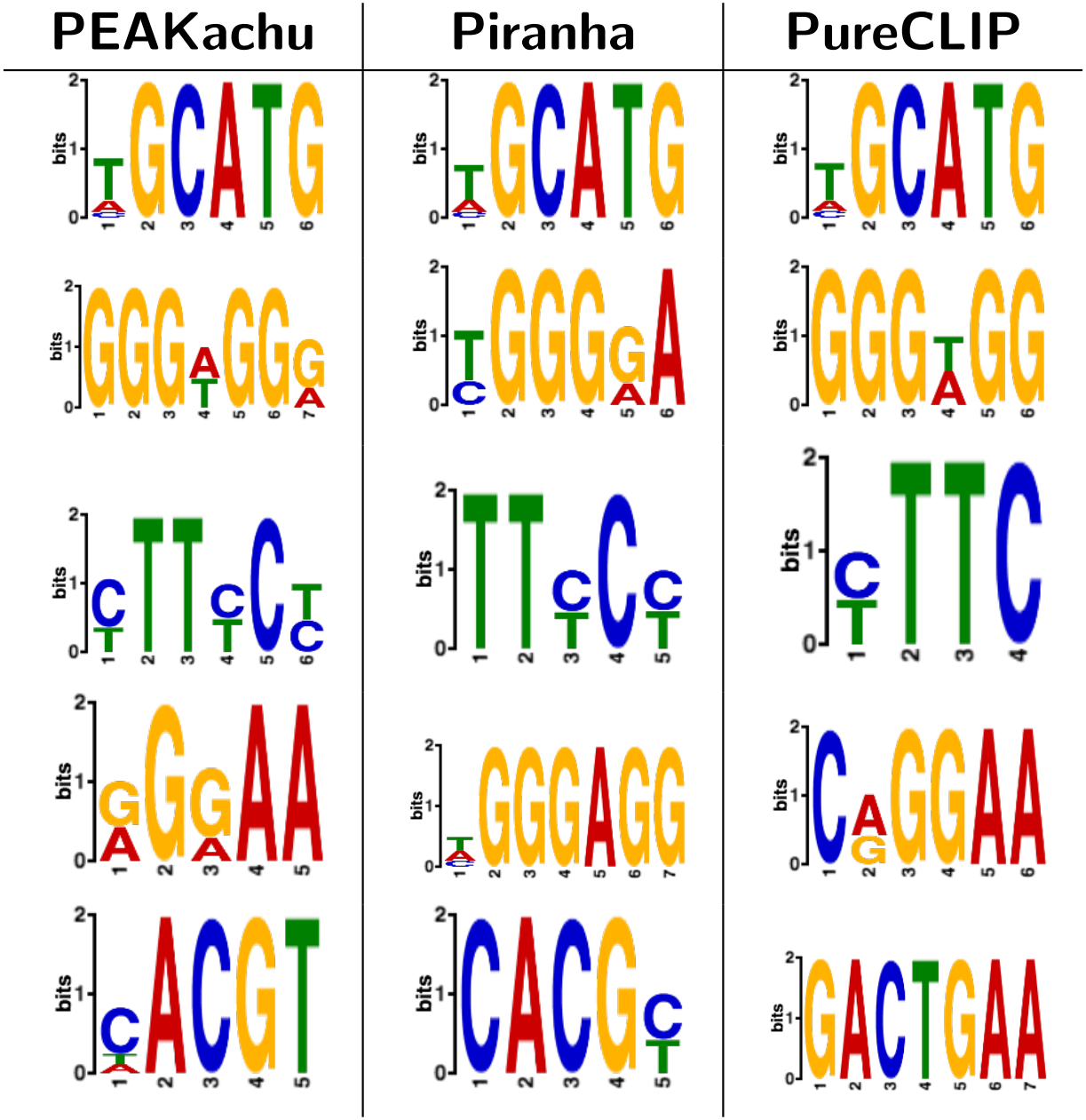

2. THANKS

Thanks to my group:

- Rolf Backofen
- Daniel Maticzka := Florian Eggenhofer
- Galaxy team
- Everybody Else

Thanks to: