

Differential binding analysis

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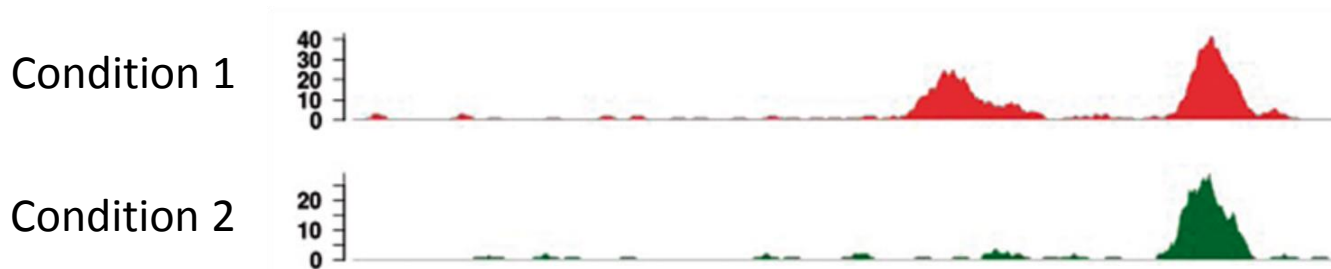
Sergio Martinez Cuesta sermarcue@gmail.com

Ashley Sawle Ashley.Sawle@cruk.cam.ac.uk

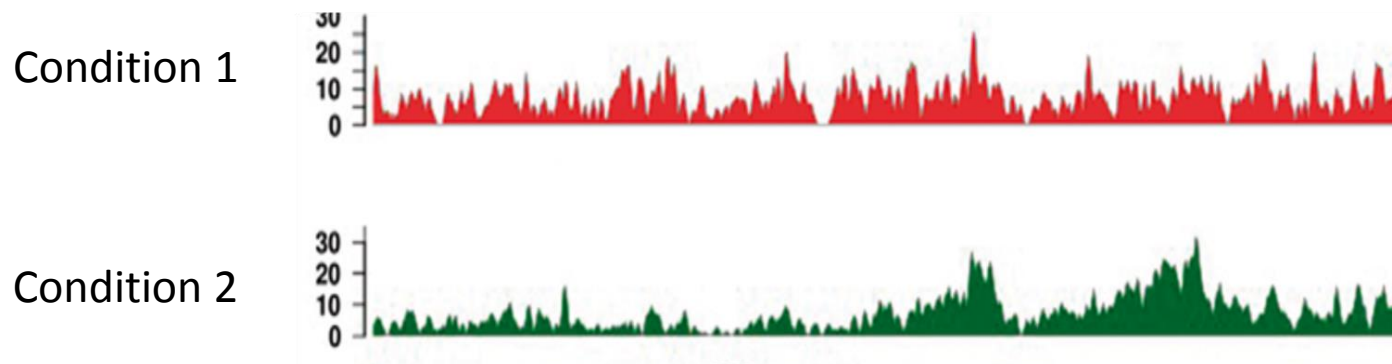
Denis Seyres Denis.seyres@bioresource.nihr.ac.uk

Why differential binding analysis?

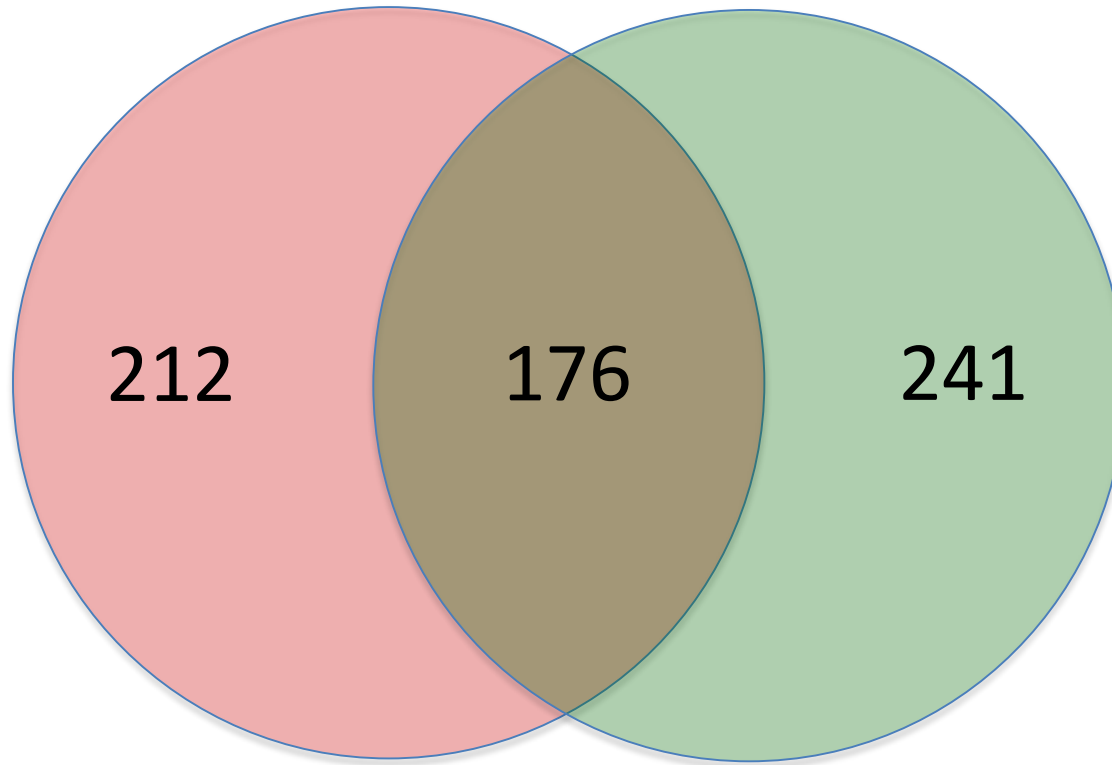
- The same **transcription factor** has *different binding profiles* in different conditions



- The same **histone modification** has *different patterns of occurrence* in different conditions



Why differential binding analysis?



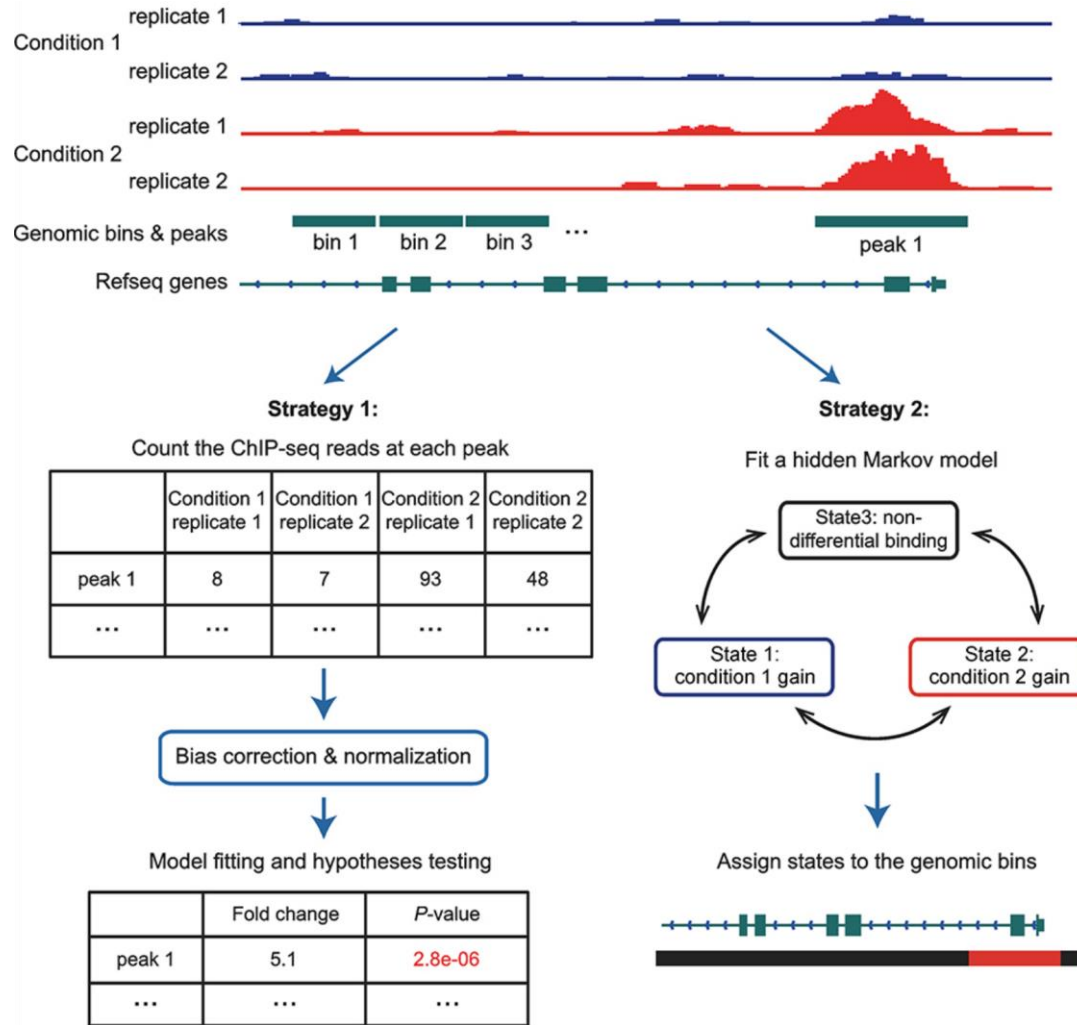
Condition 1



Condition 2



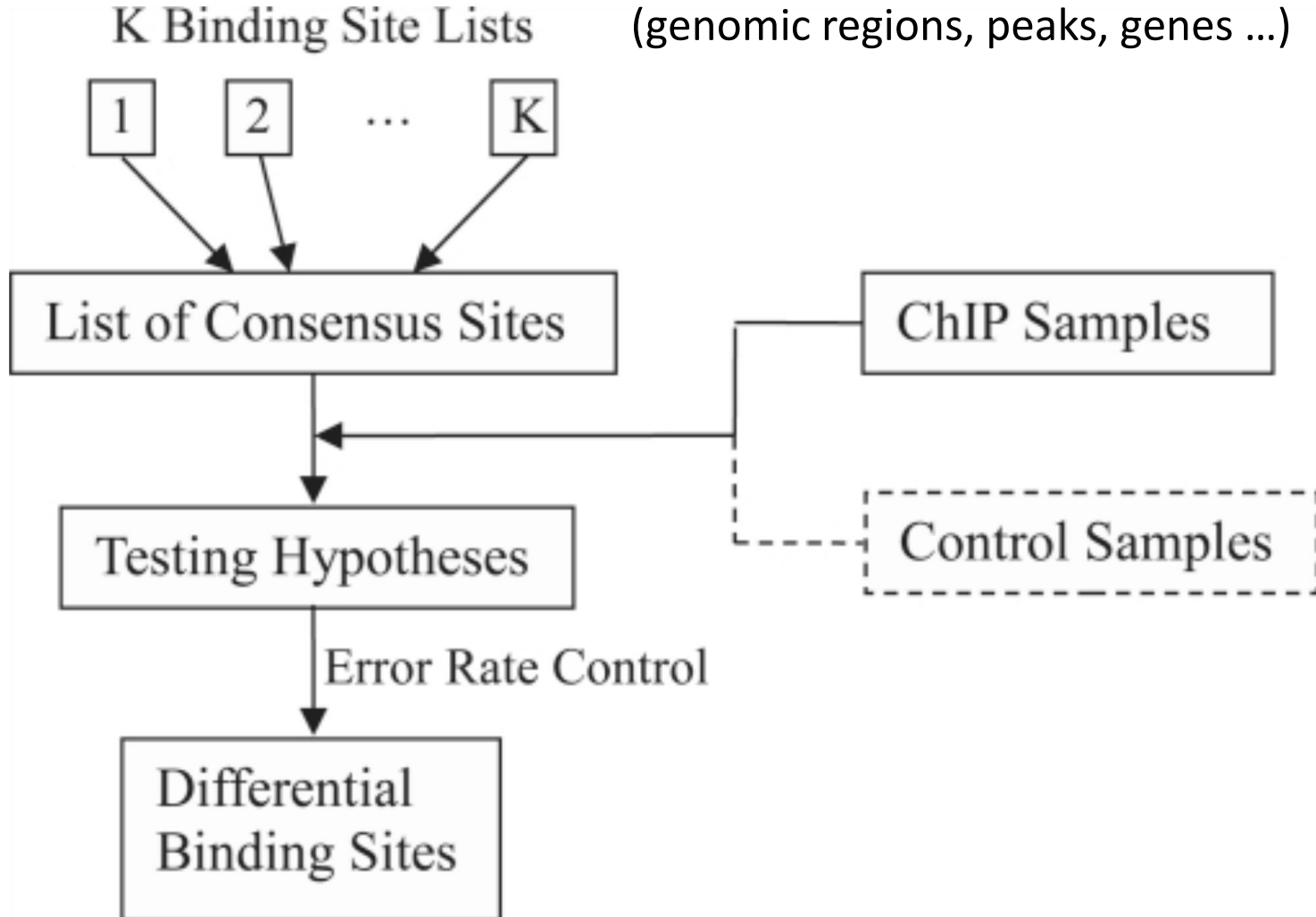
Strategies



Count-based

Hidden Markov Model

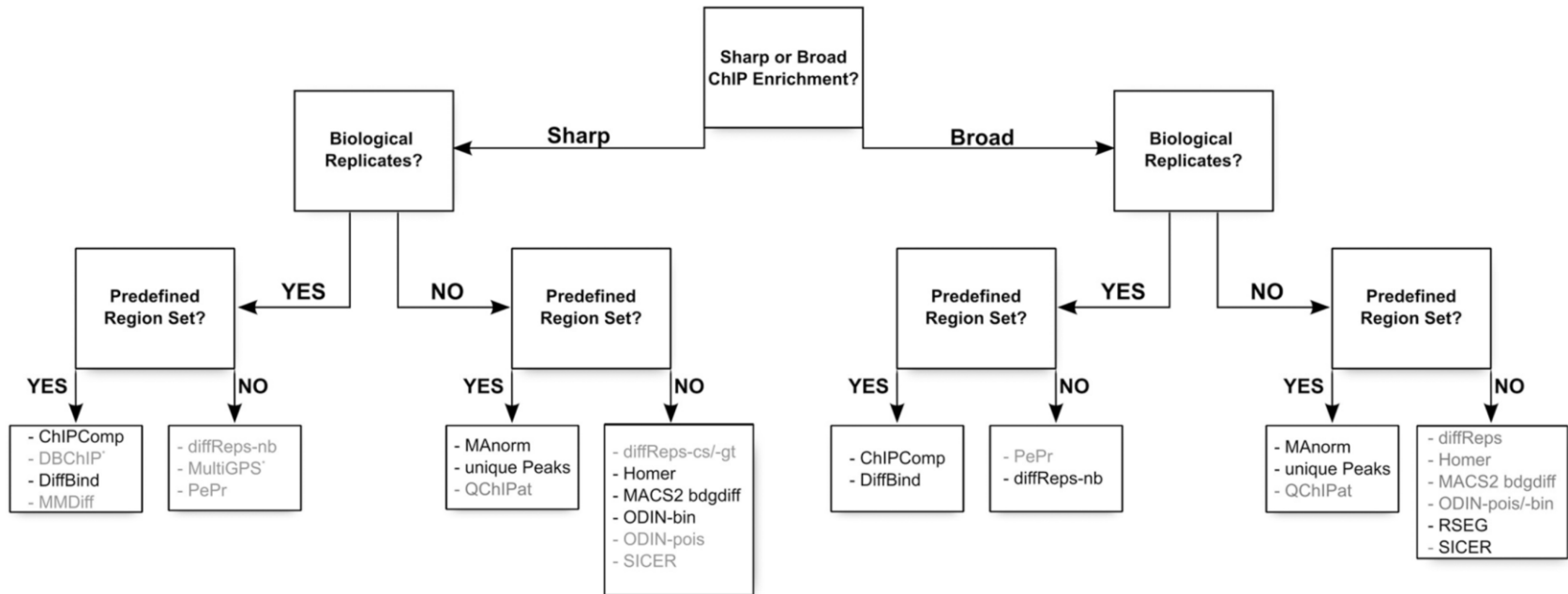
Count-based methods



Tools

Transcription factors

Histone modifications

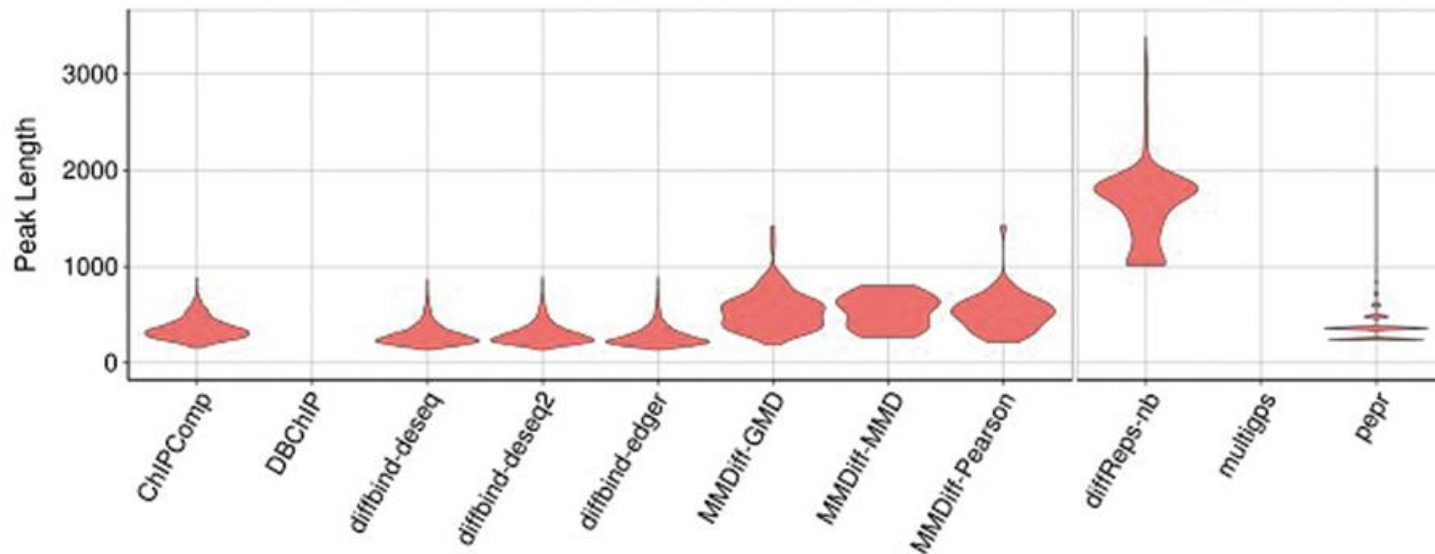
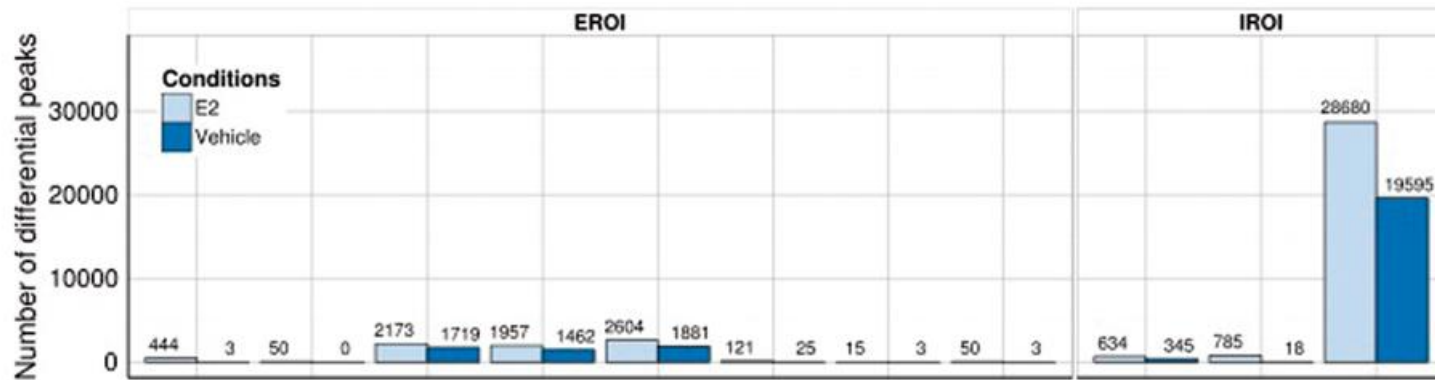


Tools

Transcription factors (FoxA1)

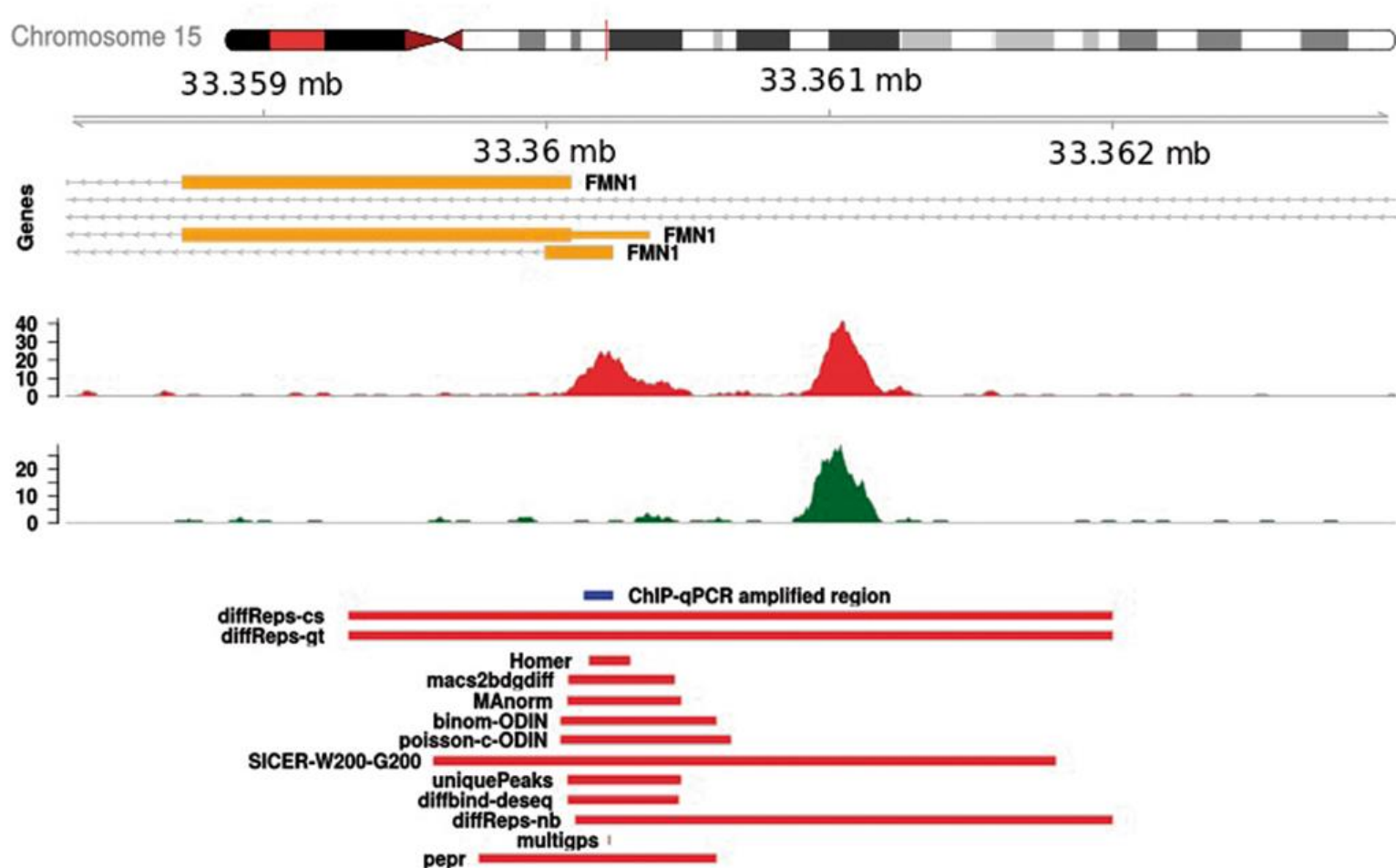
EROI – External Regions Of Interest

IROI – Internal Regions Of Interest



Tools

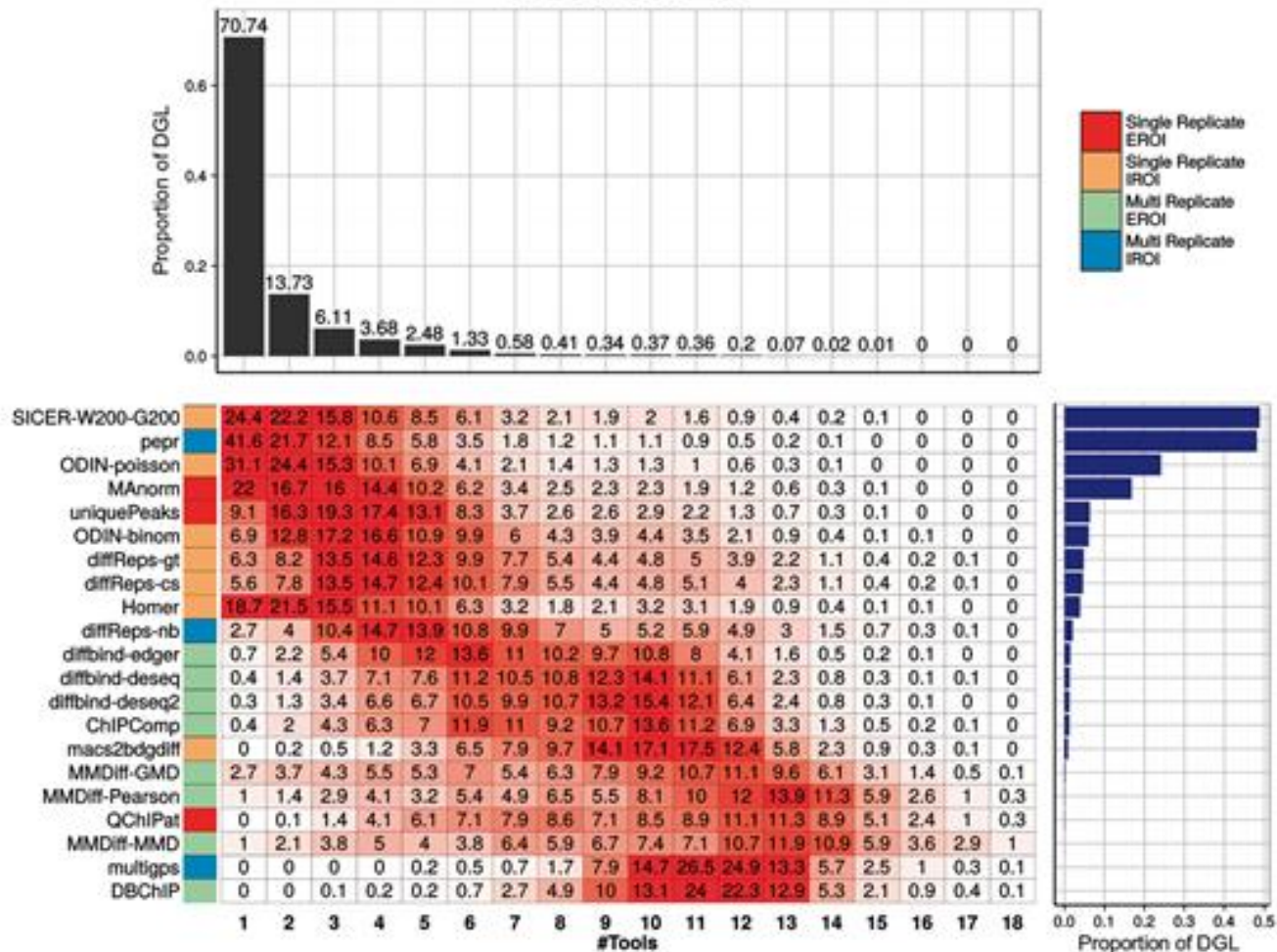
Transcription factors (FoxA1)



Tools

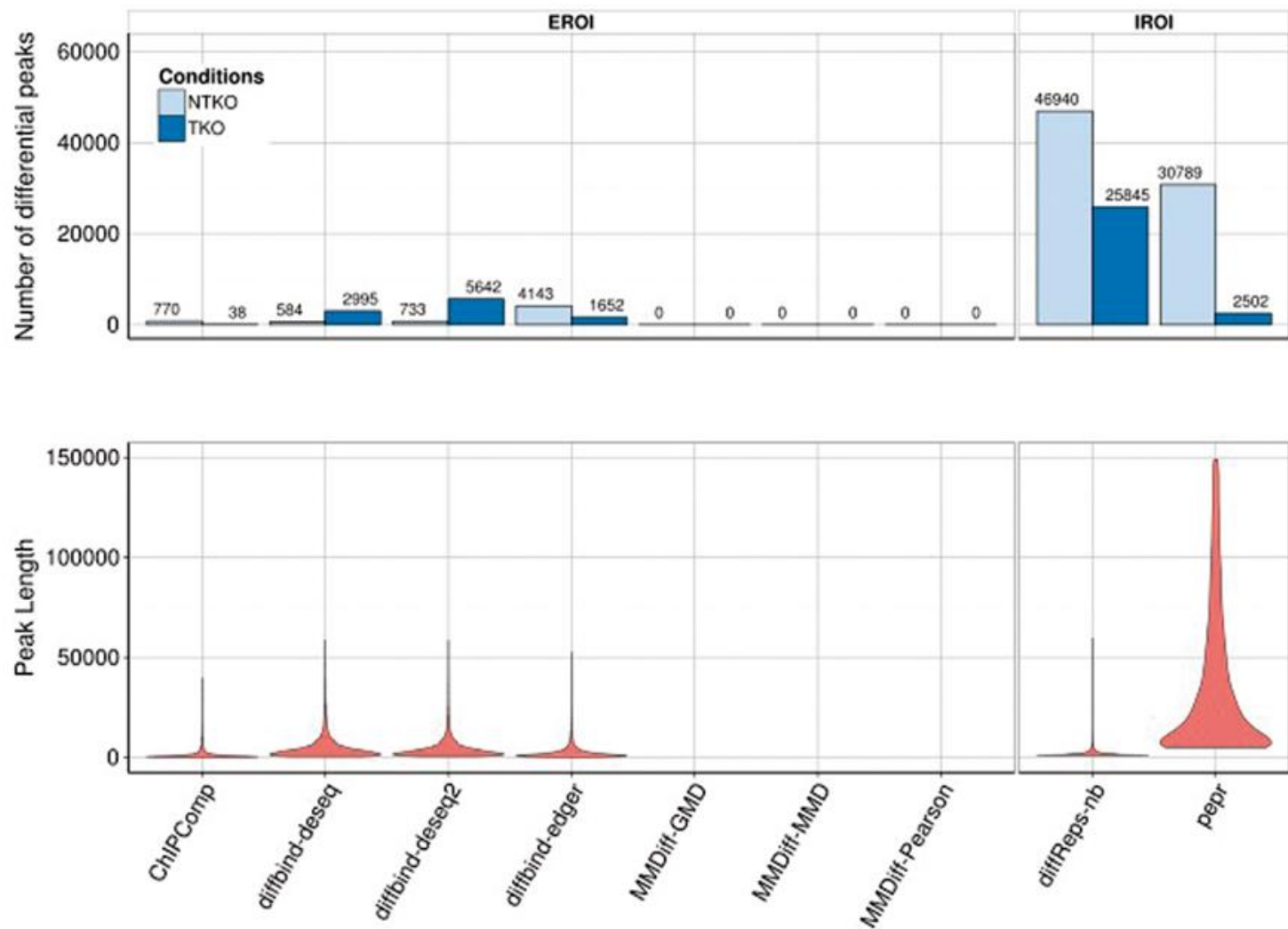
Transcription factors (FoxA1)

FoxA1 E2



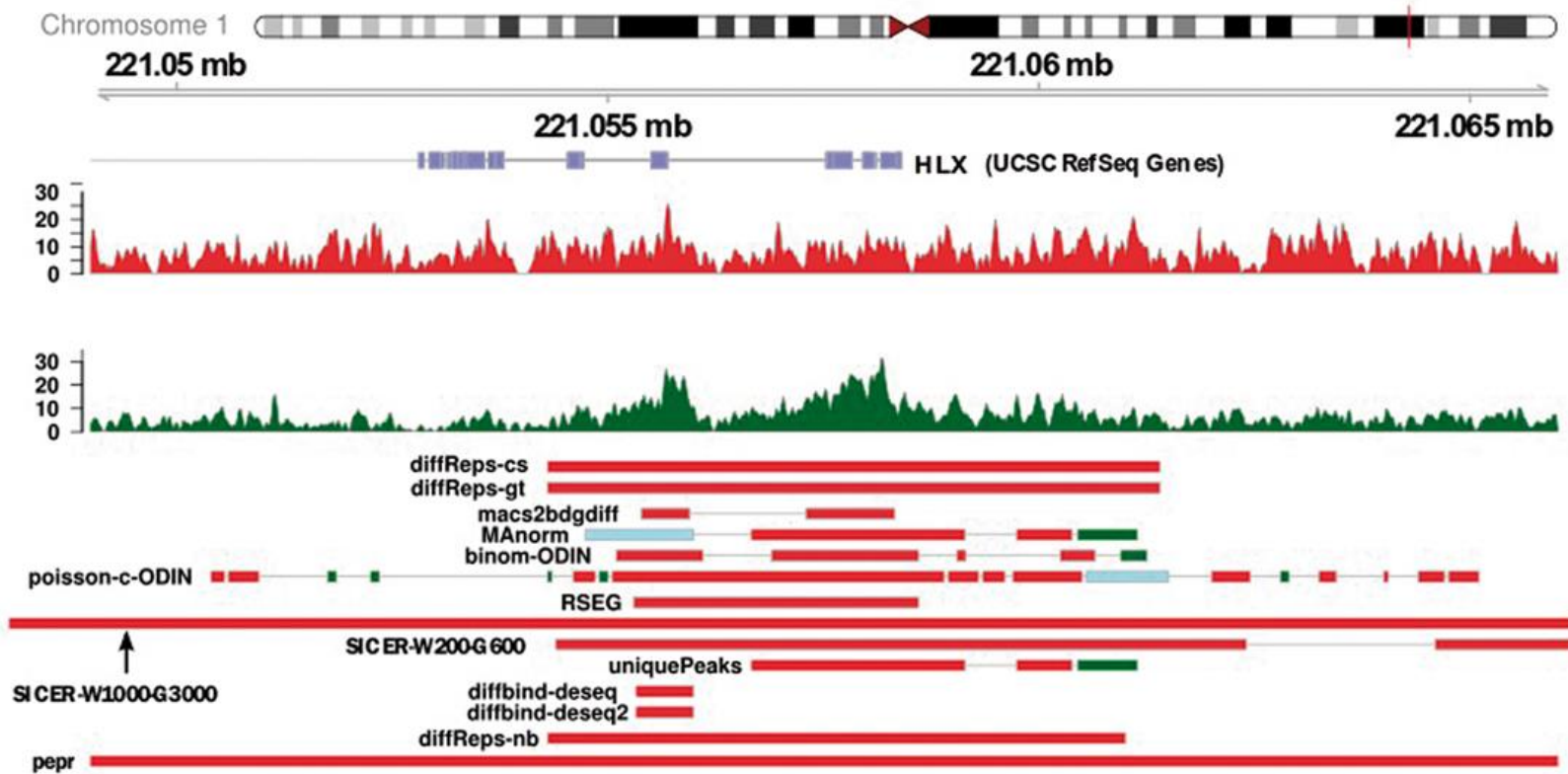
Tools

Histone modifications (H3K36me3)

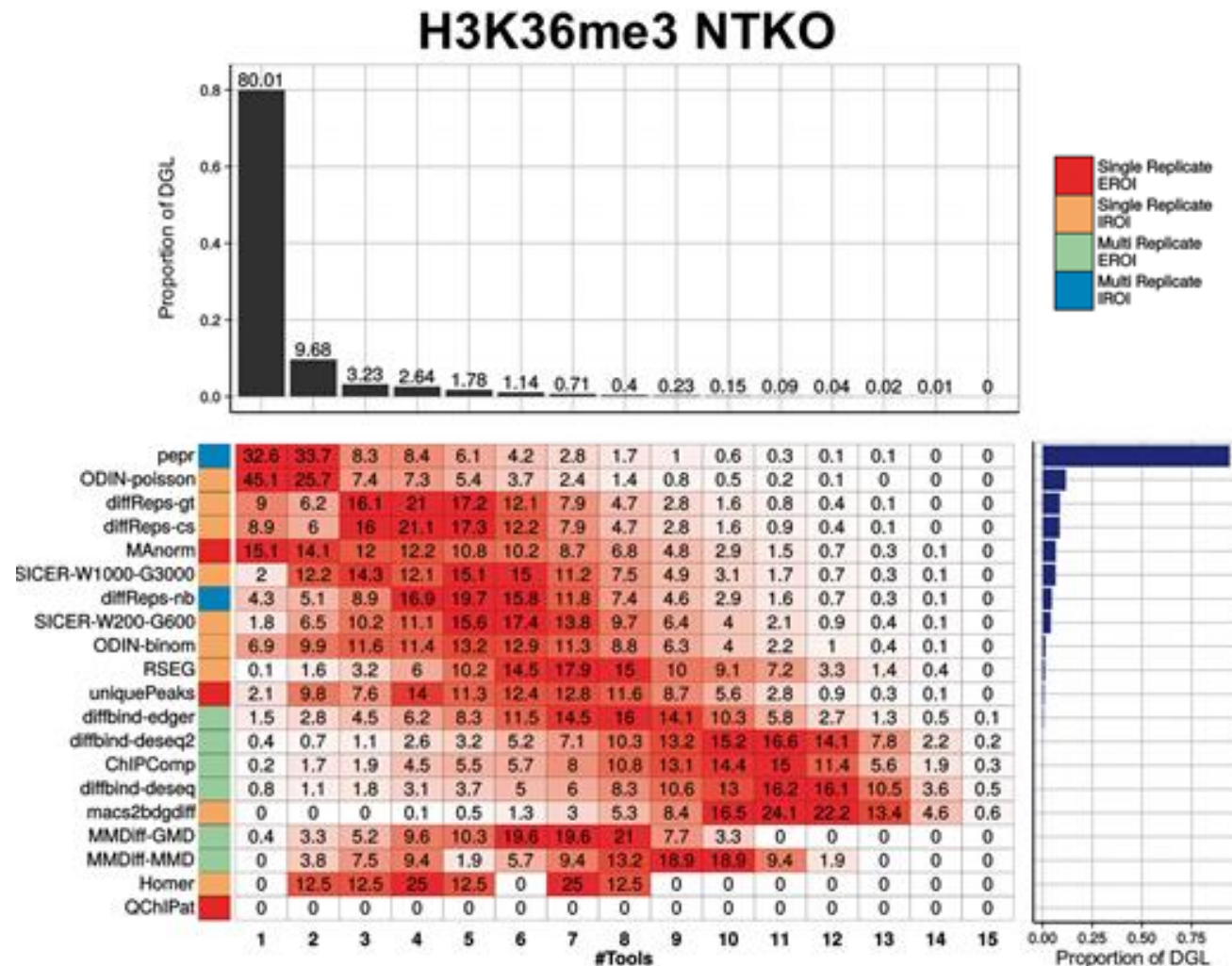


Tools

Histone modifications (H3K36me3)



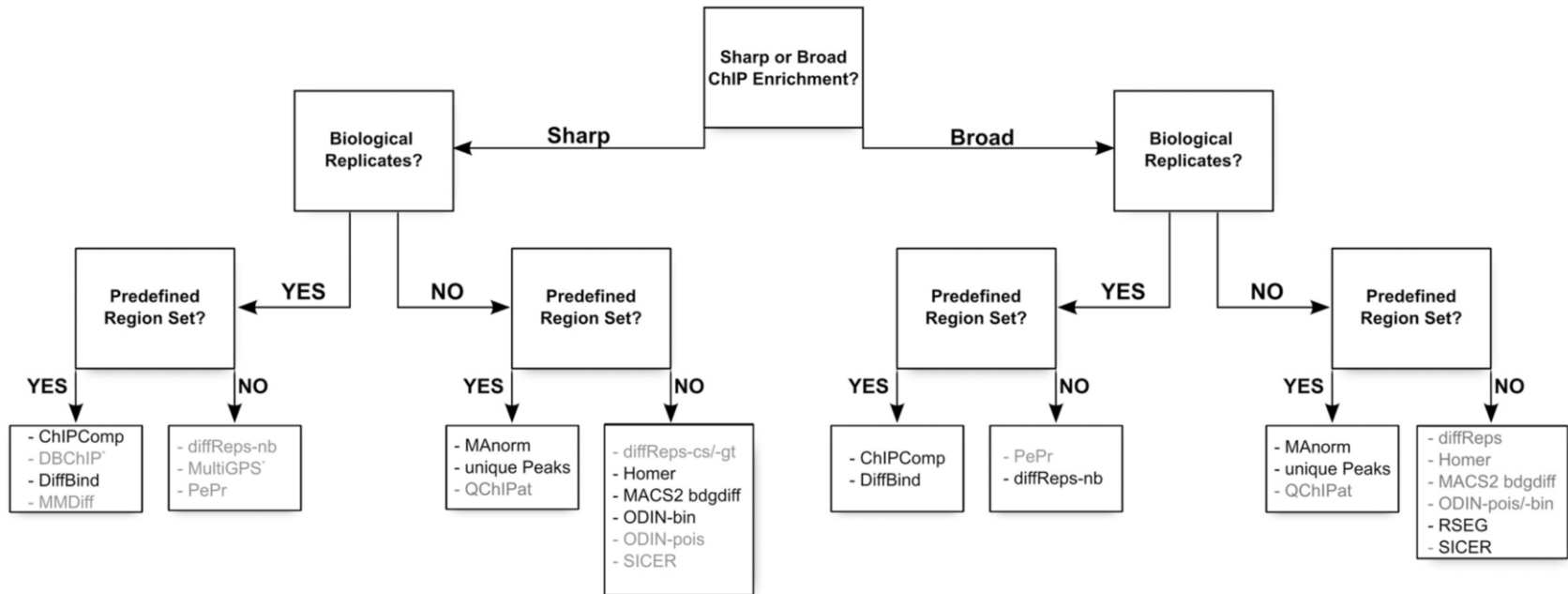
Histone modifications (H3K36me3)



Tools

Transcription factors

Histone modifications



Key points

There are **differences** between the tools to perform differential binding analysis

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Methods considering **replicates** are more robust than those considering single data sets only

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Key points

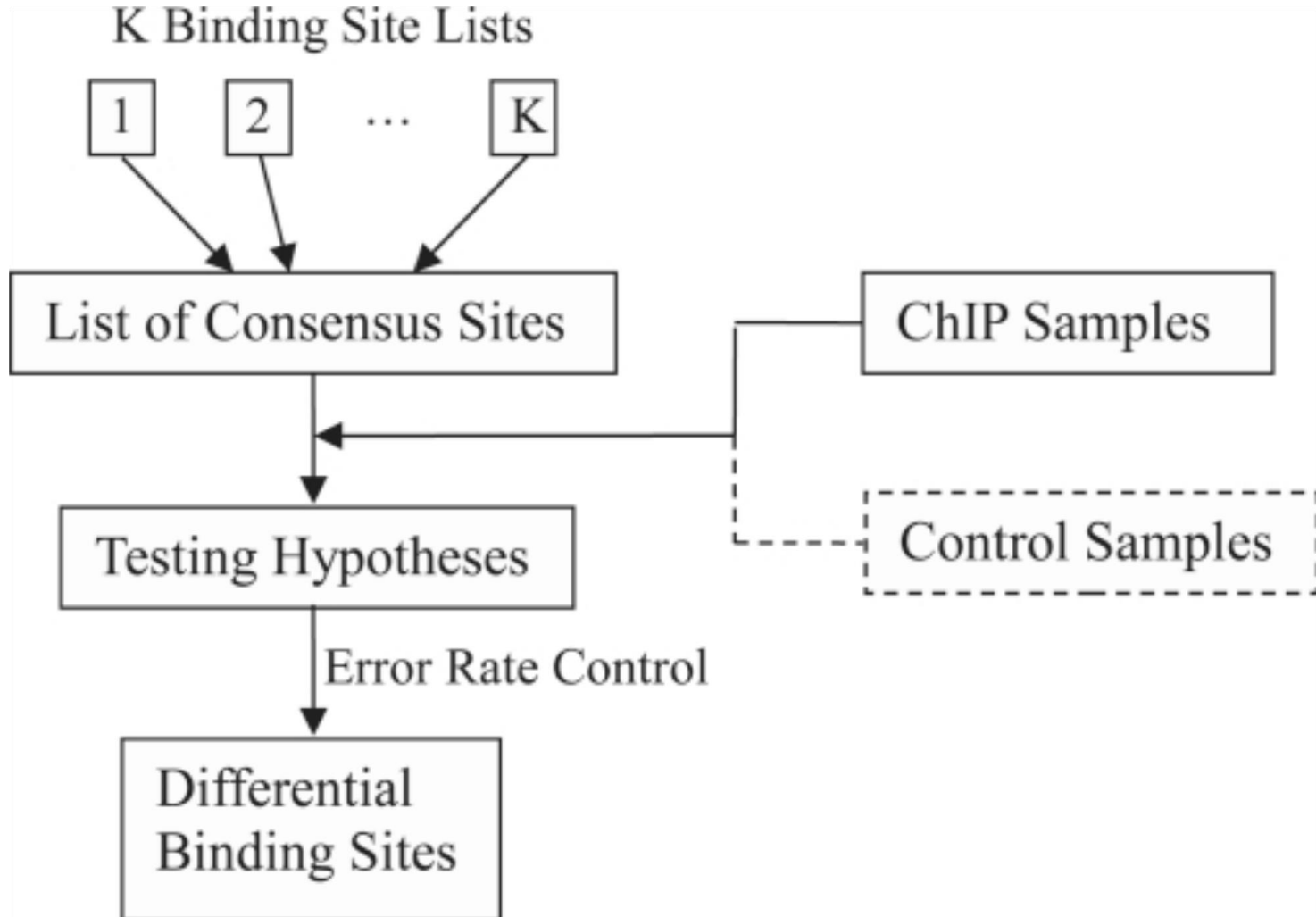
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Methods considering **replicates** are more robust than those considering single data sets only

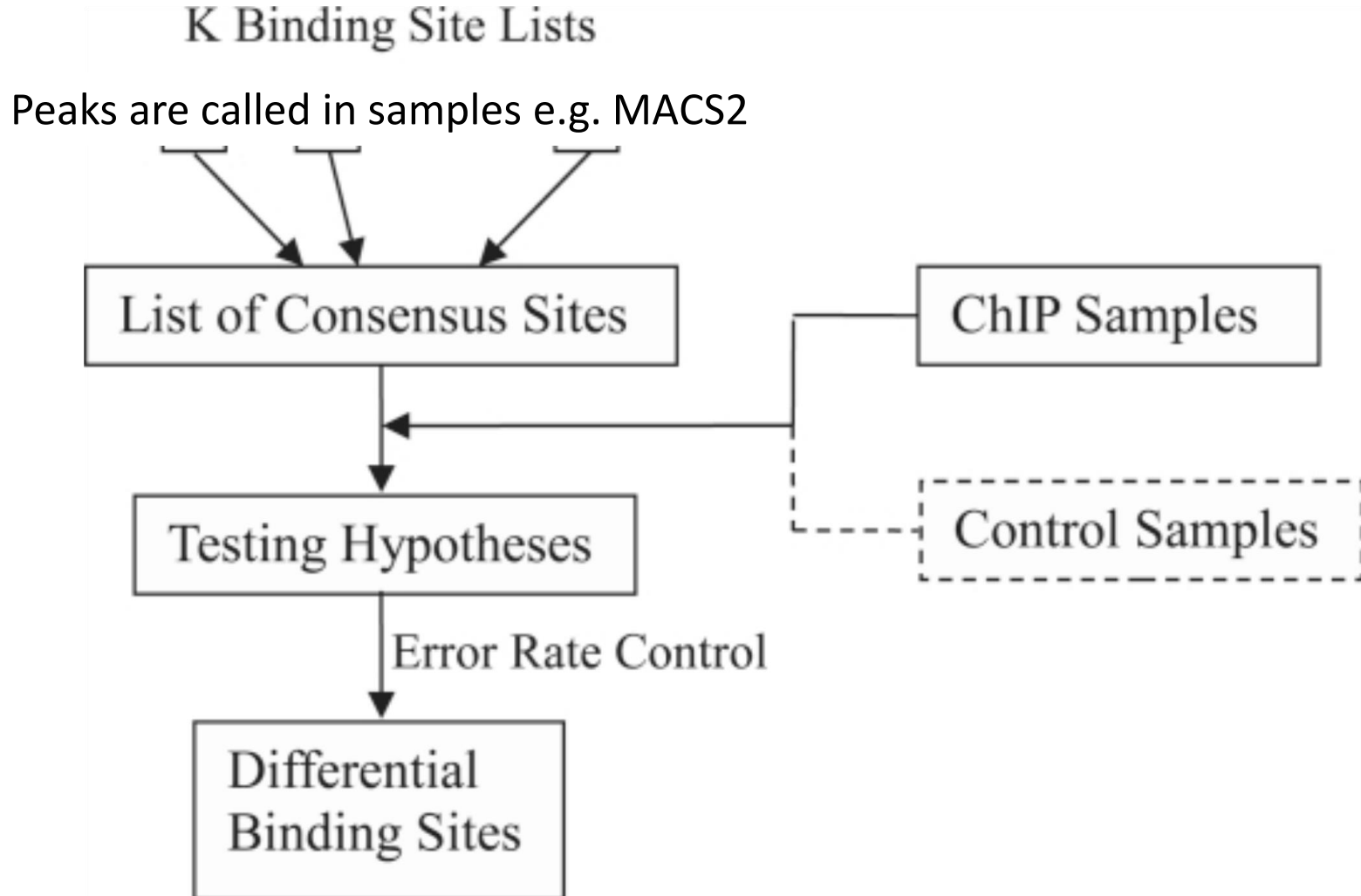
Some tools give good results with default parameters e.g. **ChIPComp** and **diffBind** when replicates are available

The other tools require more extensive fine-tuning of parameters to achieve satisfactory results

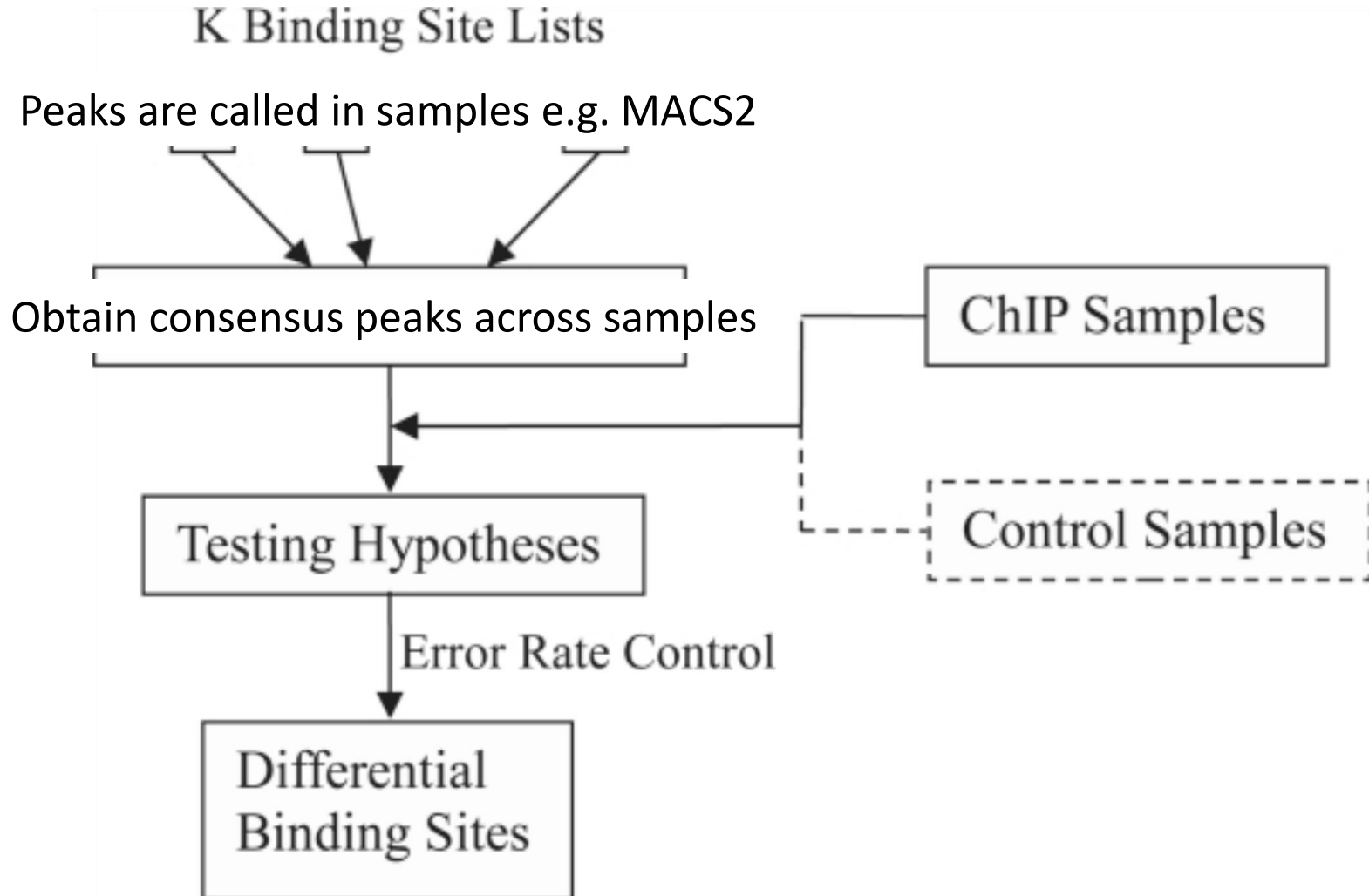
diffBind workflow



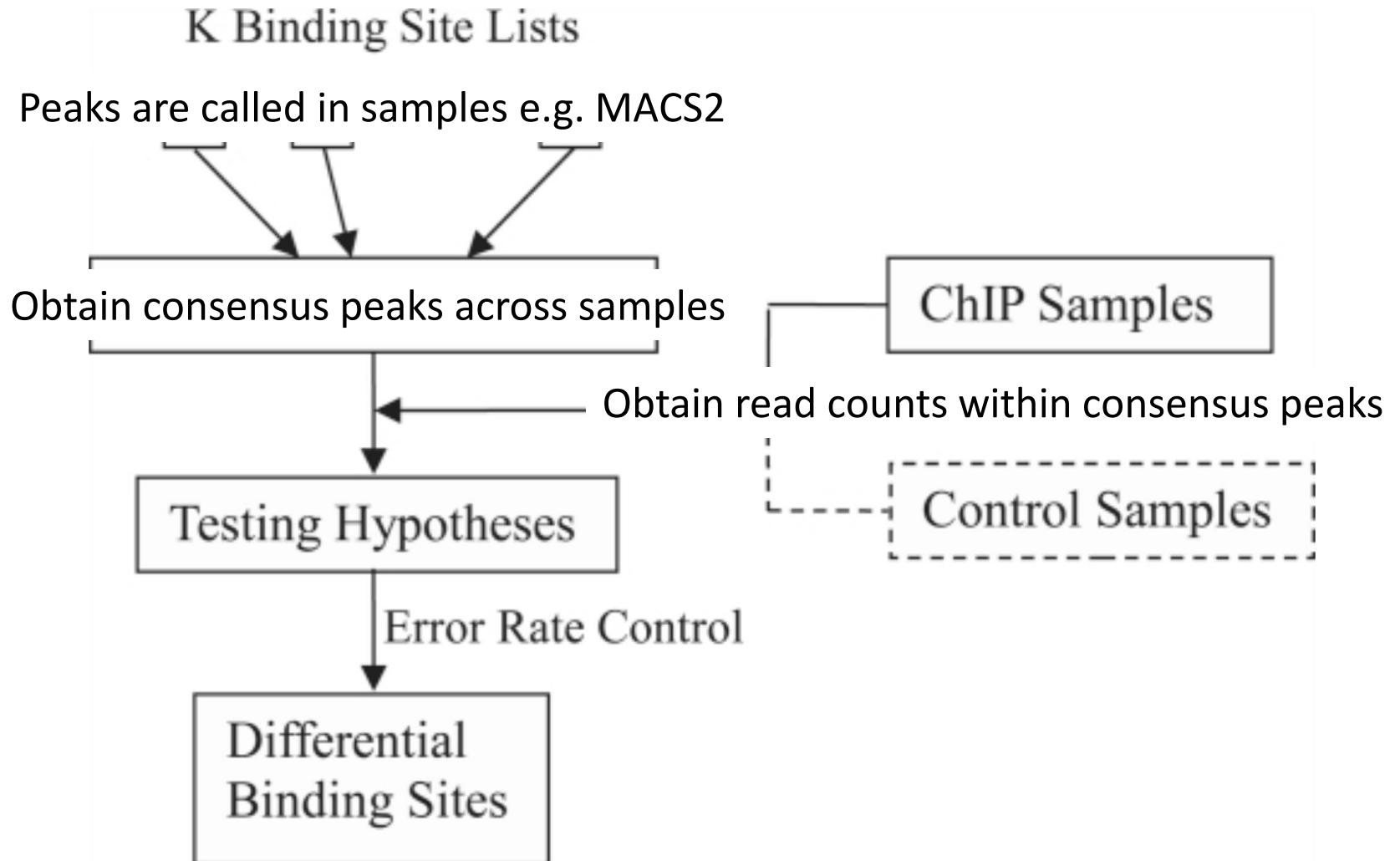
diffBind workflow



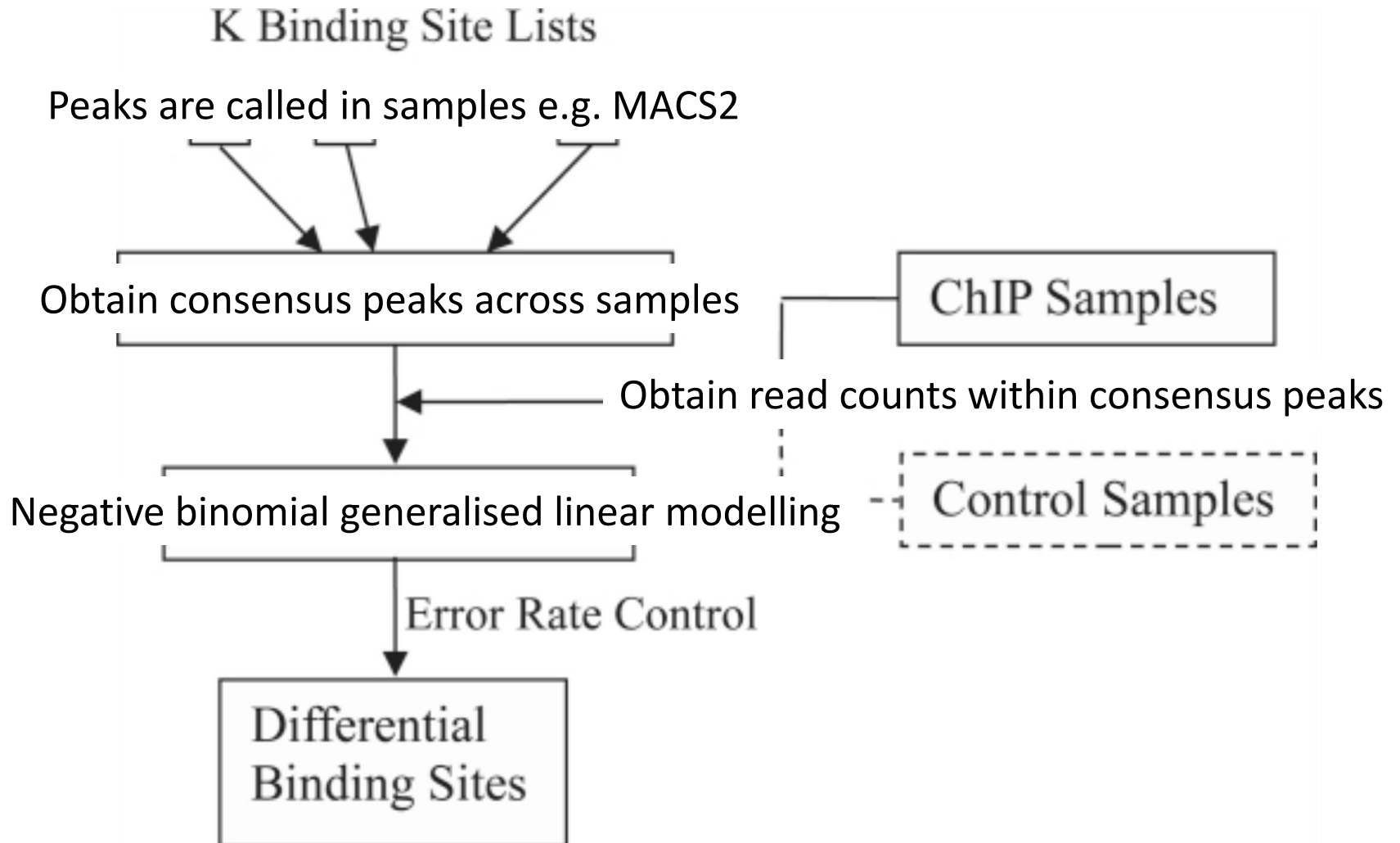
diffBind workflow



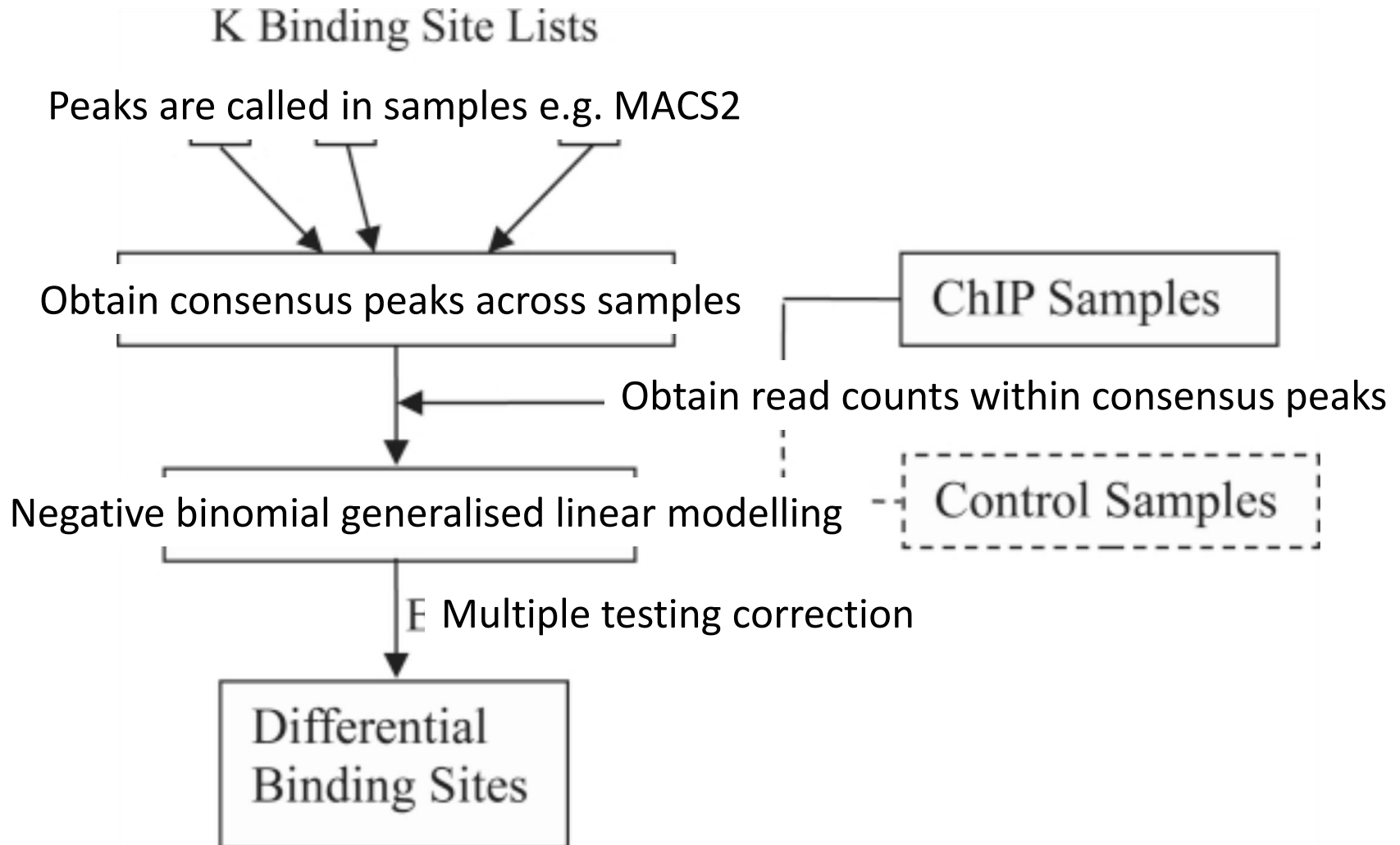
diffBind workflow



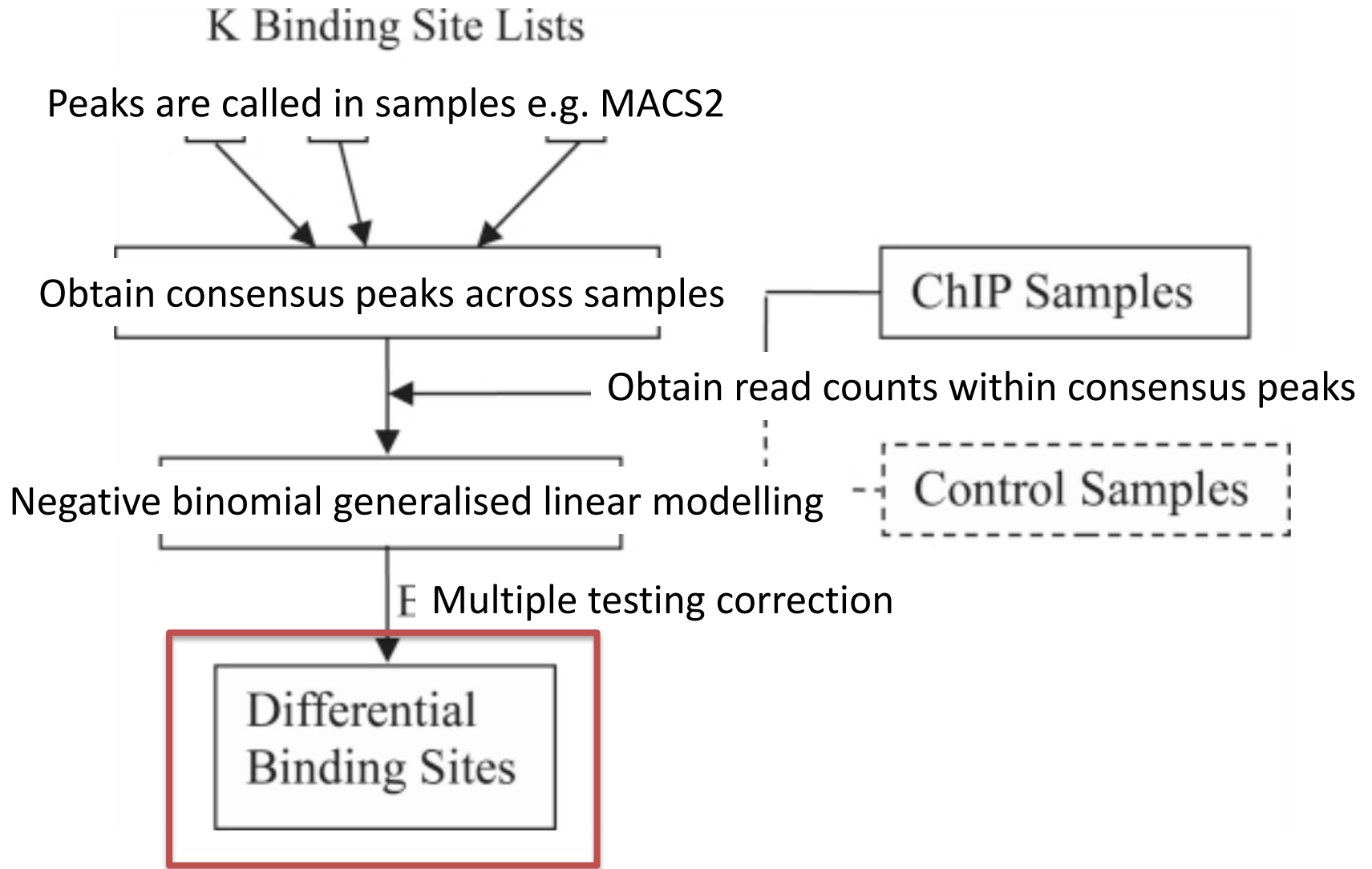
diffBind workflow



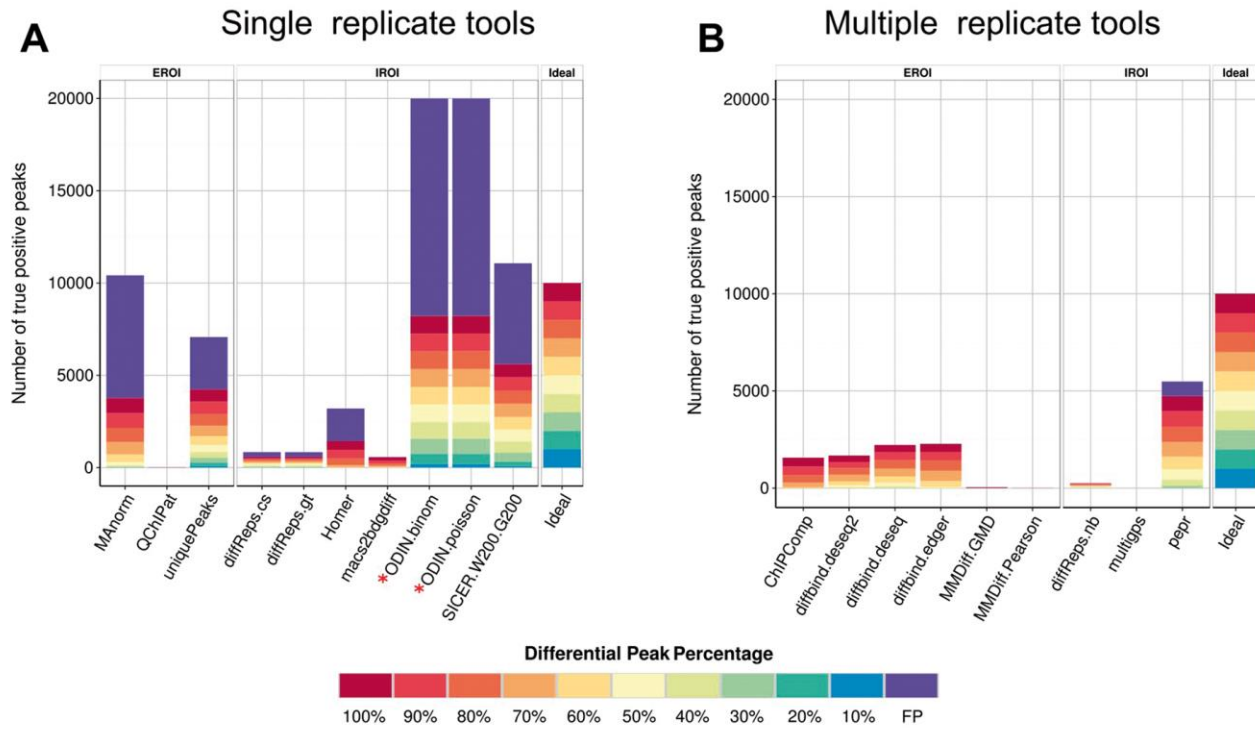
diffBind workflow



diffBind workflow



Sharp ChIP-seq signal: FoxA1



Broad ChIP-seq signal: H3K36me3

