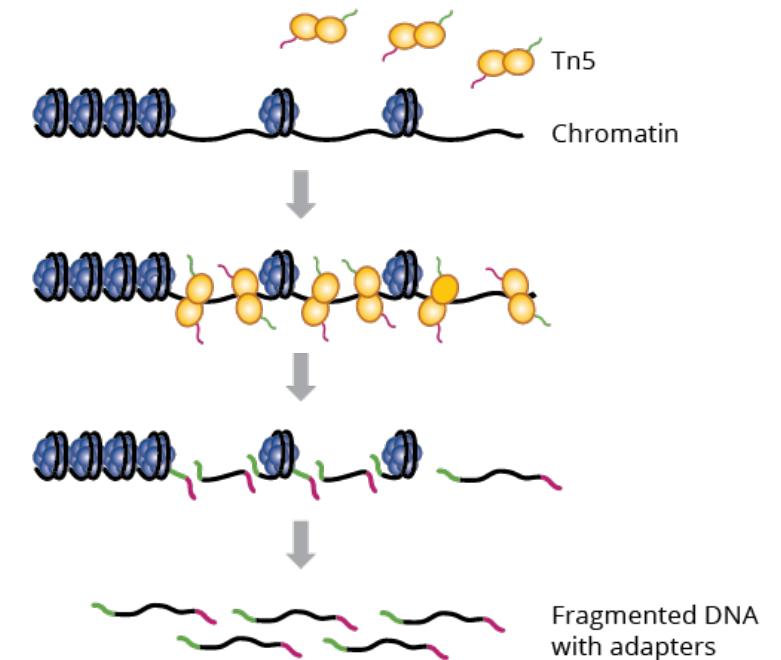
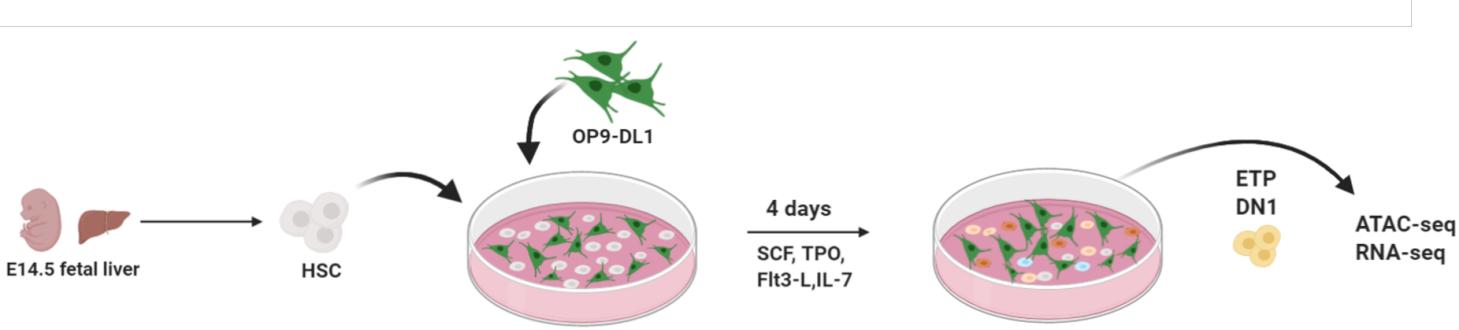
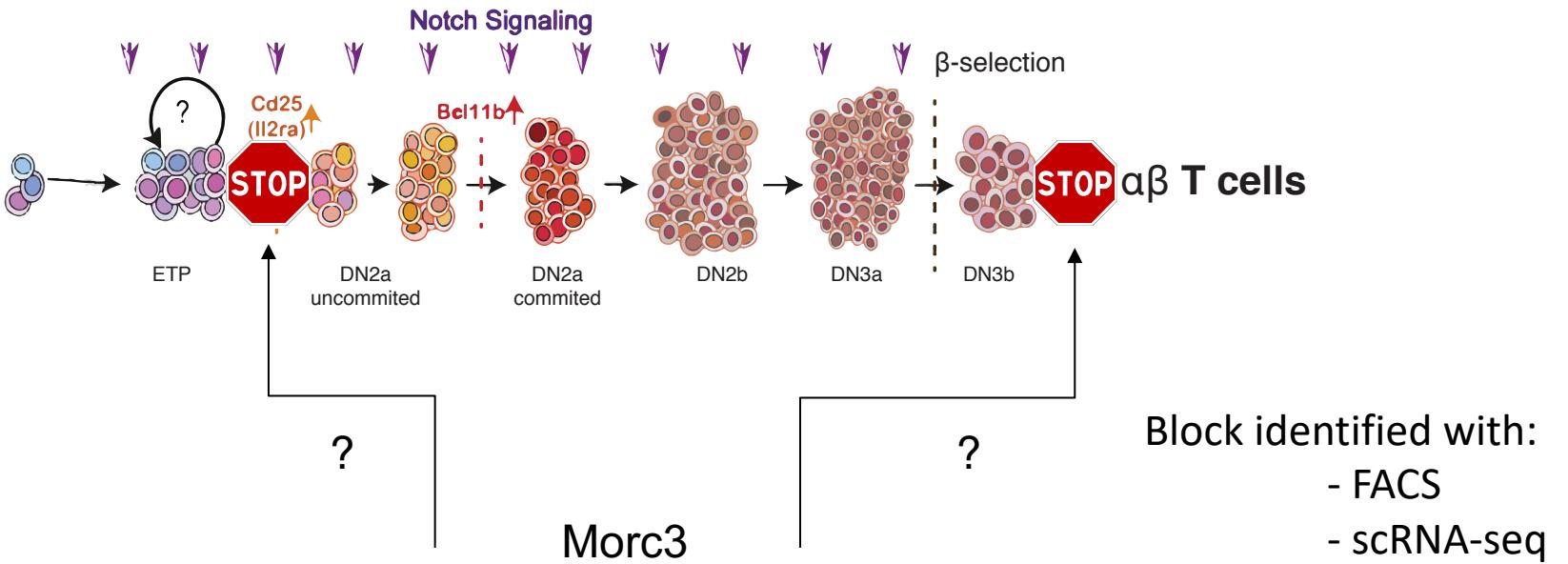


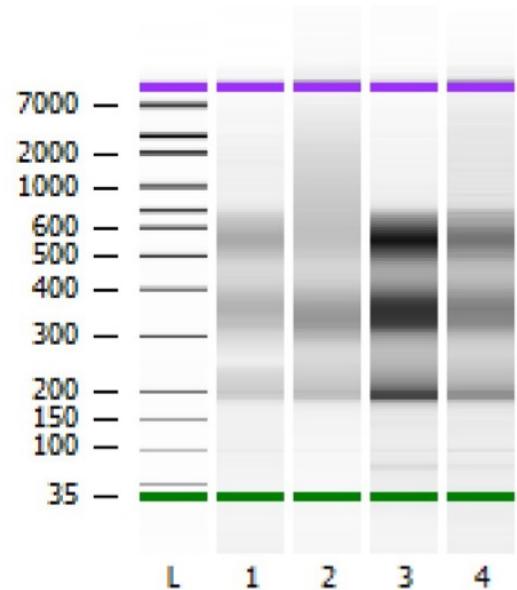
# DN1 ATAC-seq

Veronica

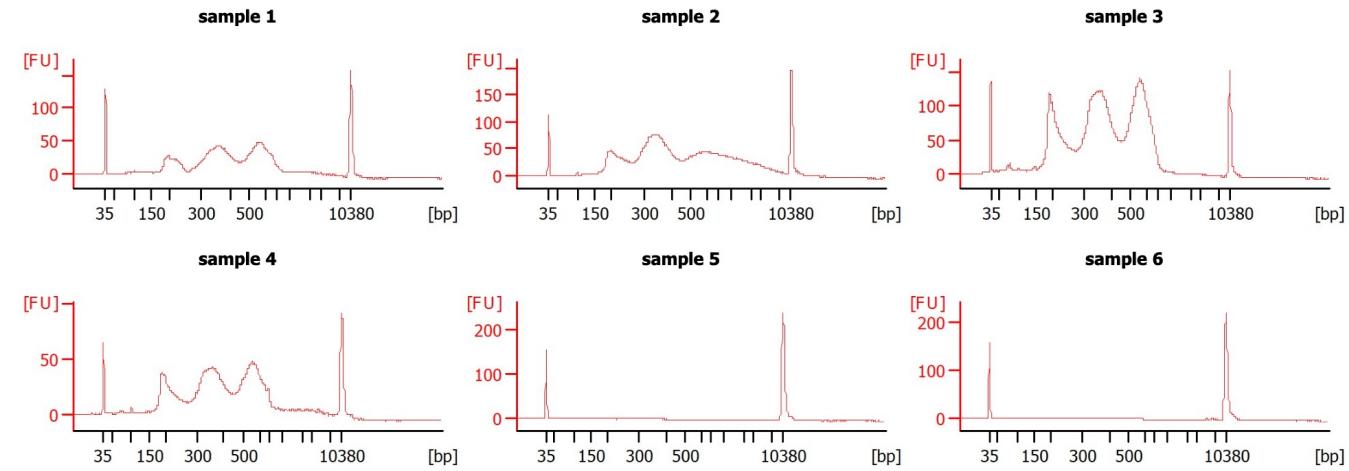
# Background



- 50000 DN1 cells from OP9:
  - 2 x WT
  - 2 x KO

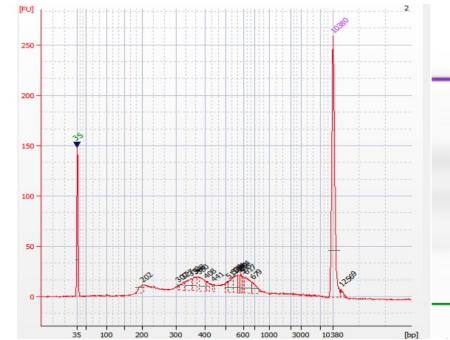


sample nb	name	primer 1	primer 2	Concentration Qubit	Cycles added to second PCR
1	WT1	S507	N702	1,28	12
2	WT2	S507	N704	1,98	13
3	KO1	S507	N705	3,15	10
4	KO2	S507	N707	1,97	8

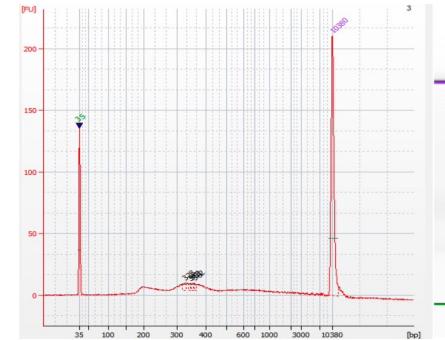


#	Library Name	Library Type	Conc. (ng/uL)	Conc. (nM)	Size (bp)	Result*	
1	DN1_WT_rep1	ETC	0.2	0.72	434	Fail	Low Quantity to (Run or Capture)
2	DN1_WT_rep2	ETC	0.26	0.97	409	Fail	Low Quantity to (Run or Capture)
3	DN1_KO_rep1	ETC	0.85	3.26	403	Fail	Low Quantity to (Run or Capture)
4	DN1_KO_rep2	ETC	0.24	0.88	417	Fail	Low Quantity to (Run or Capture)

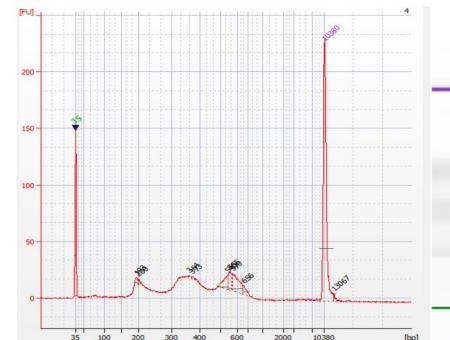
[Click to Enlarge =>1:Library : DN1\\_WT\\_rep1](#)



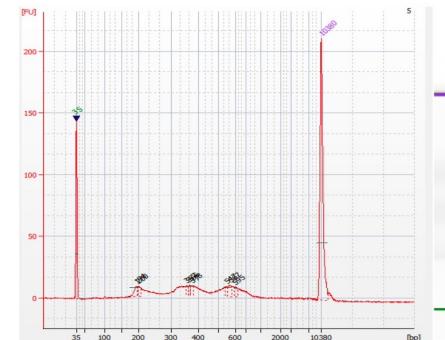
[Click to Enlarge =>2:Library : DN1\\_WT\\_rep2](#)



[Click to Enlarge =>3:Library : DN1\\_KO\\_rep1](#)



[Click to Enlarge =>4:Library : DN1\\_KO\\_rep2](#)



# QC reports provided by Macrogen

Client Name	Macrogen Europe
Company / Institution	Macrogen Europe
Order Number	HN00155645
Type of Read	Paired-end
Read Length	151
Number of Samples	3
Type of Sequencer	Illumina platform

Download link	File size	md5sum
<a href="#">DN1_KO_rep1_1.fastq.gz</a>	1.0G	c2095e9bc993755383be9247d830e2e3
<a href="#">DN1_KO_rep1_2.fastq.gz</a>	991.1M	8d654303f1407119a14ccf671cd4d375
<a href="#">DN1_WT_rep1_1.fastq.gz</a>	347.0M	31260d4e330390984afb1aabf1f39e60
<a href="#">DN1_WT_rep1_2.fastq.gz</a>	322.8M	ff40f5e78e477fc6632206f1cc6ece8f
<a href="#">DN1_WT_rep2_1.fastq.gz</a>	295.6M	339faea0788651328629e0dd3722b12f
<a href="#">DN1_WT_rep2_2.fastq.gz</a>	283.9M	ee417d9b45ea135496b10b6edebf49ce

Sample ID	Total read bases (bp)	Total reads	GC(%)	AT(%)	Q20(%)	Q30(%)
DN1_KO_rep1	5,031,883,230	33,323,730	51.04	48.96	94.66	89.32
DN1_WT_rep1	1,474,346,182	9,763,882	51.46	48.54	94.92	89.57
DN1_WT_rep2	1,013,035,444	6,708,844	51.28	48.72	89.67	77.98

Table 1. Raw data Stats (maximum 20 samples)

Sample ID	Total read bases (bp)	Total reads	GC(%)	AT(%)	Q20(%)	Q30(%)
DN1_KO_rep1	5,031,883,230	33,323,730	51.04	48.96	94.66	89.32
DN1_WT_rep1	1,474,346,182	9,763,882	51.46	48.54	94.92	89.57
DN1_WT_rep2	1,013,035,444	6,708,844	51.28	48.72	89.67	77.98

# Analysis

- Done with our [Snakemake-ATAC-seq pipeline](#)

# Quality controls

## General Statistics

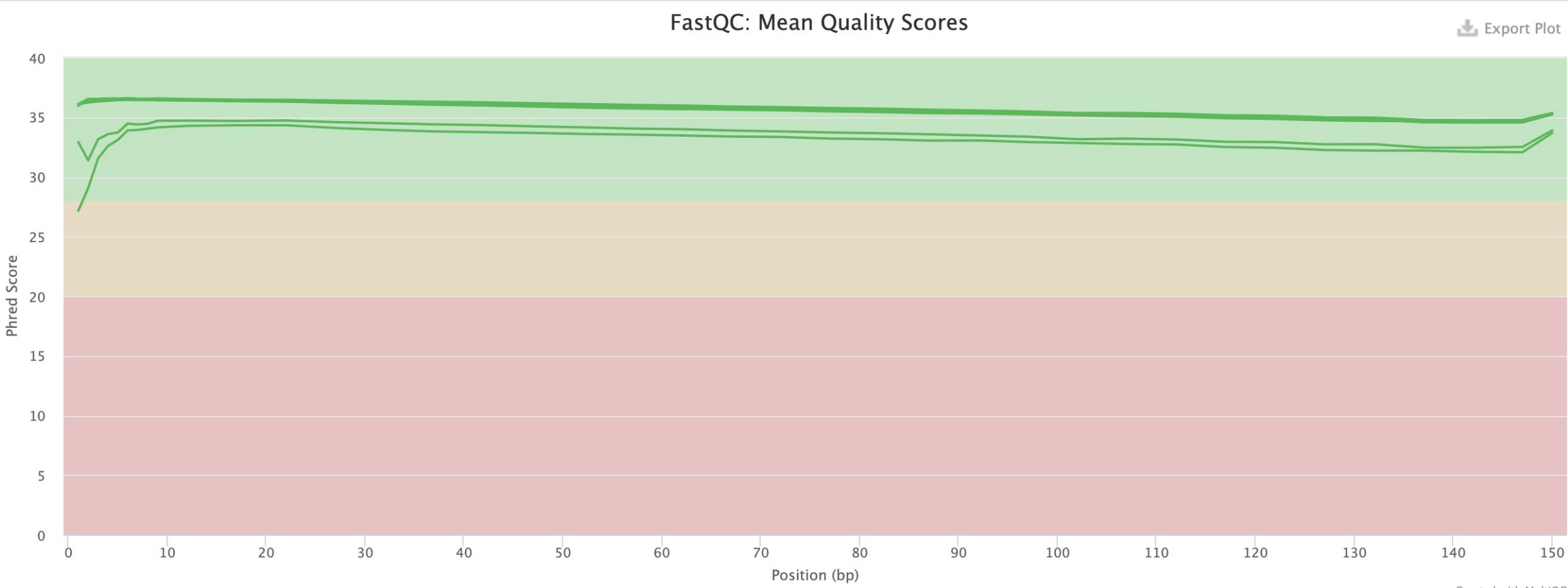
Copy table   Configure Columns   Plot   Showing 9/9 rows and 7/9 columns.

Sample Name	% Aligned	Insert Size	% Dups	% Dups	% GC	Length	M Seqs
DN1KO1	92%	168 bp	23.4%				
DN1KO1_R1				25.3%	47%	111 bp	16.6
DN1KO1_R2				25.7%	47%	111 bp	16.6
DN1WT1	93%	148 bp	19.8%				
DN1WT1_R1				18.2%	48%	110 bp	4.9
DN1WT1_R2				18.6%	48%	110 bp	4.9
DN1WT2	95%	178 bp	11.2%				
DN1WT2_R1				6.9%	49%	123 bp	3.4
DN1WT2_R2				6.9%	49%	123 bp	3.4

# Quality controls

FastQC: Mean Quality Scores

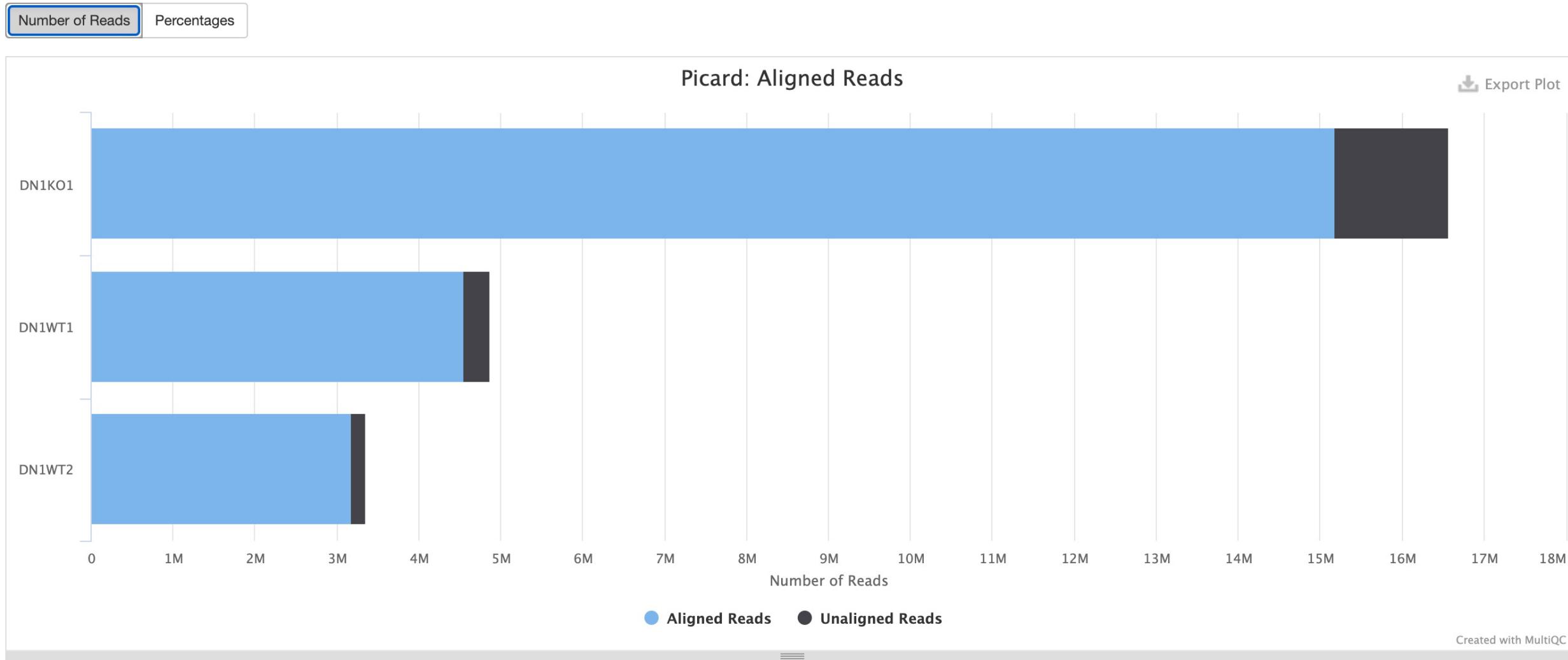
 Export Plot



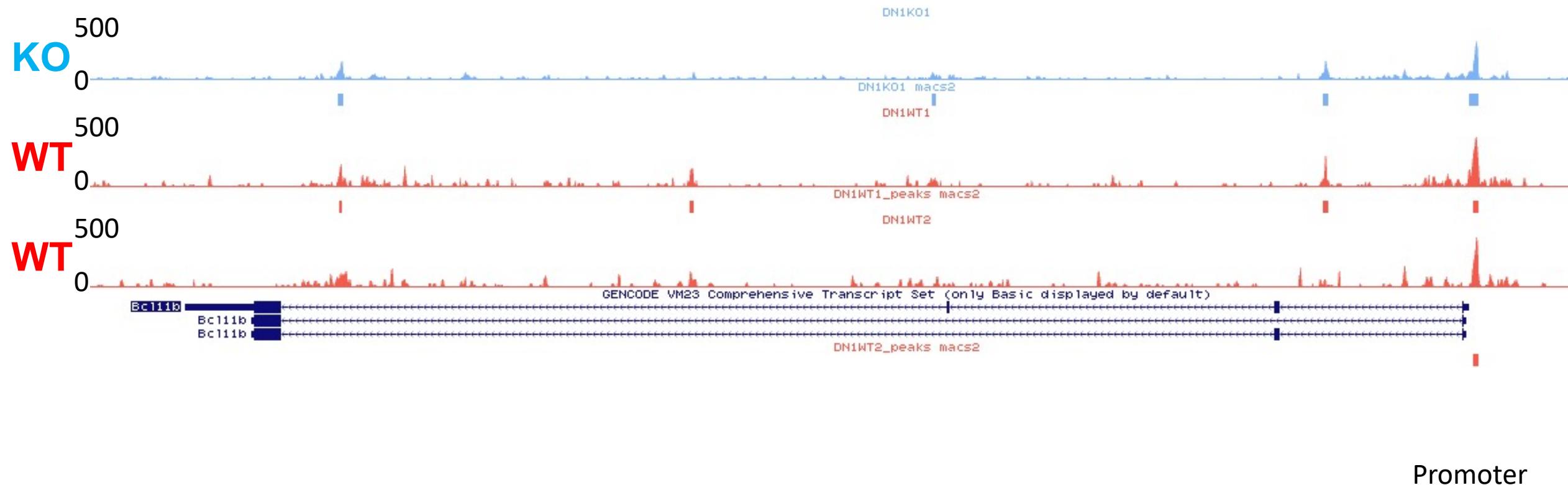
# Quality controls

## Alignment Summary

Please note that Picard's read counts are divided by two for paired-end data.

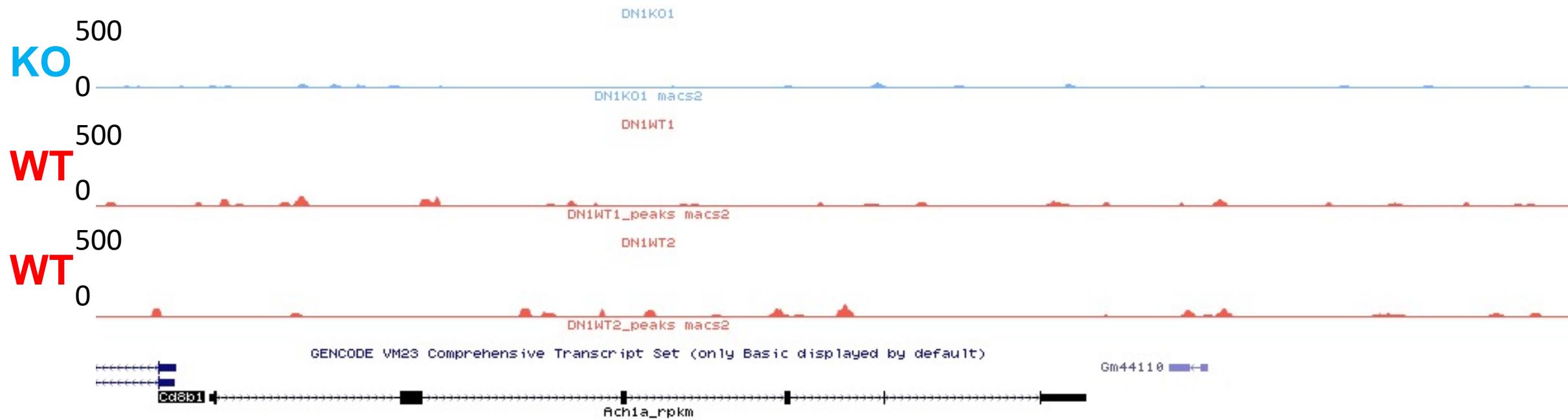


# *Bcl11b*



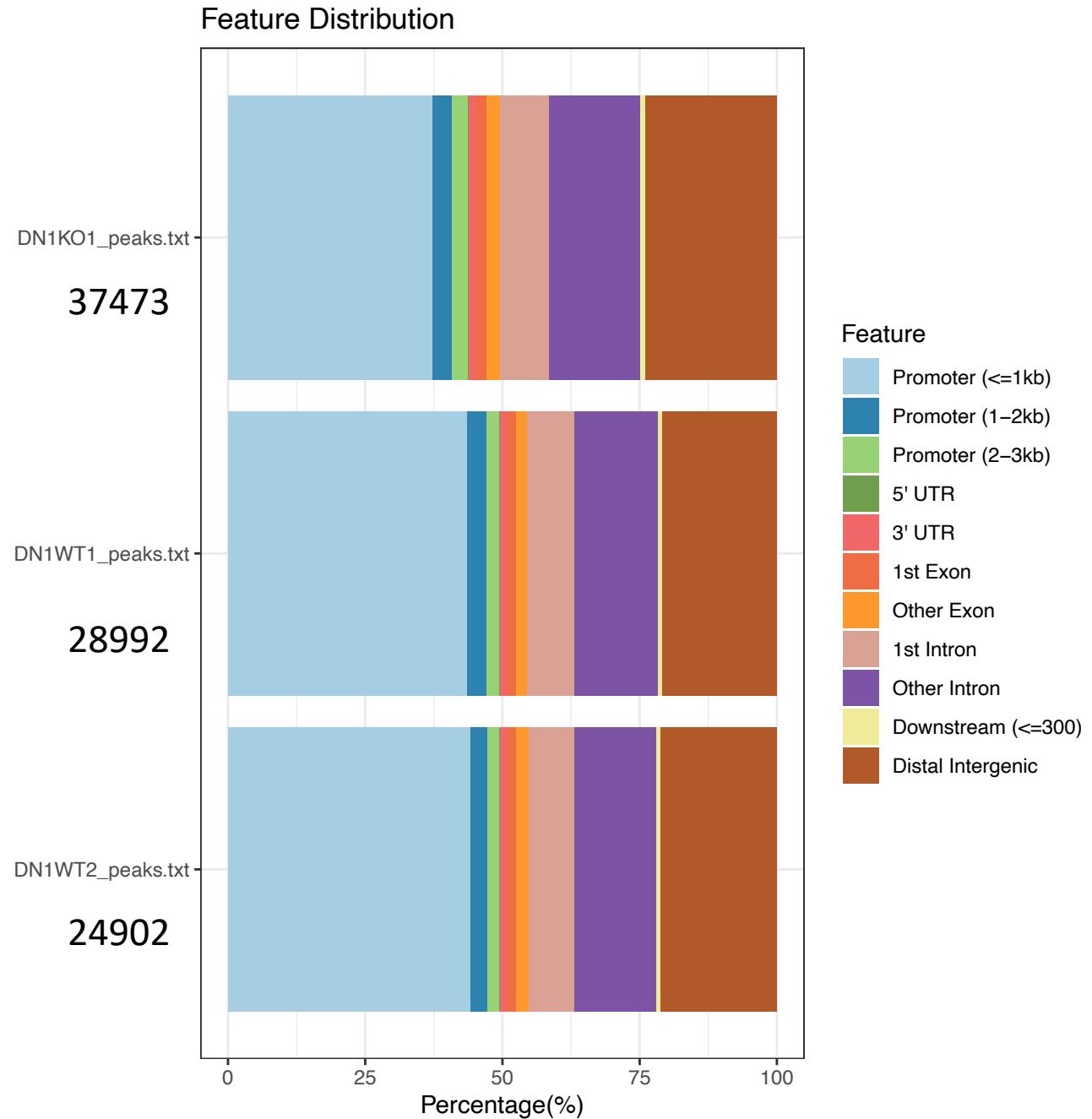
Promoter

# *Cd8b1*



# Peak calling: MACS2

name	peaks
WT1	28992
WT2	24902
KO1	37473



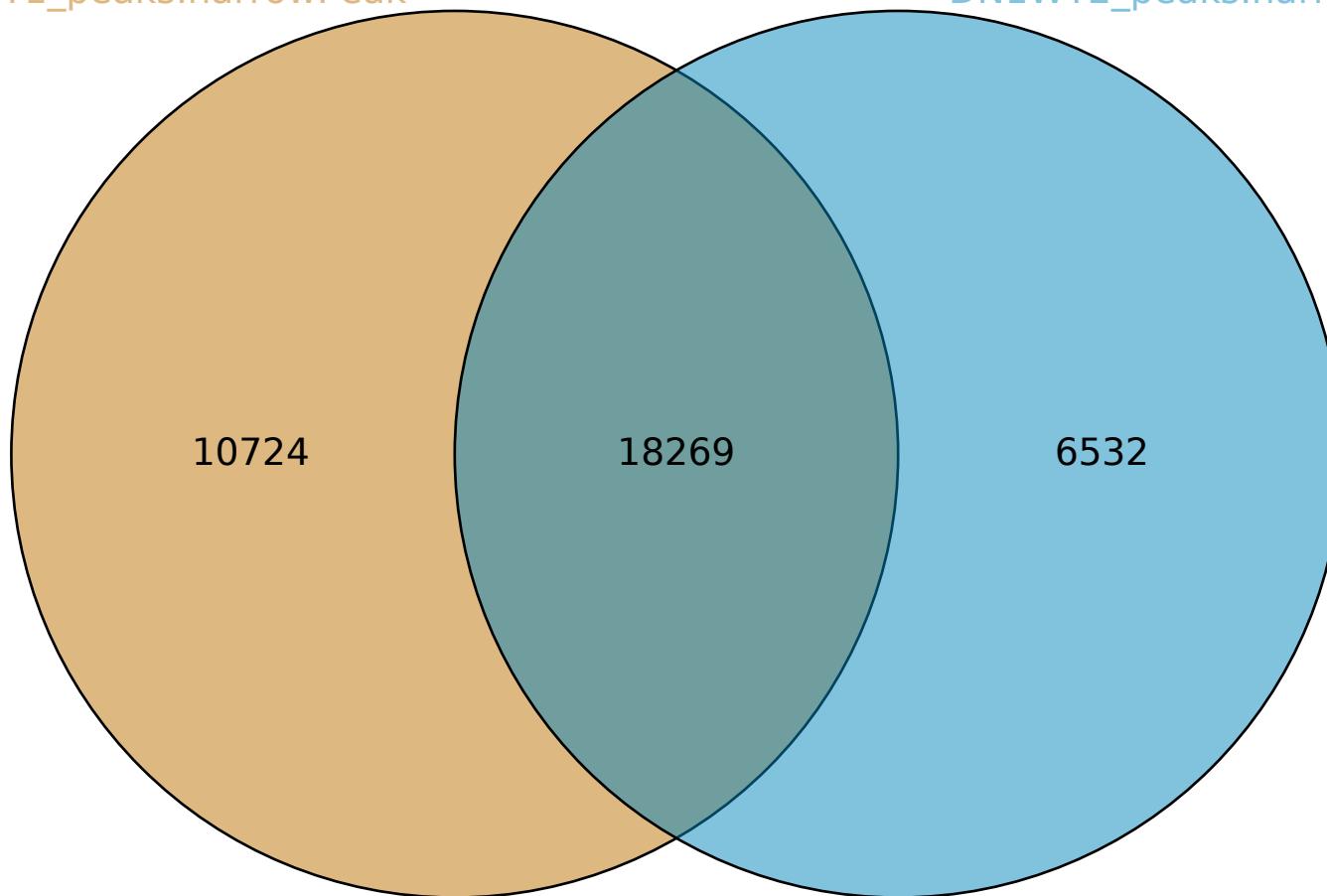
# Overlap WT1 and WT2

DN1WT1\_peaks.narrowPeak  
DN1WT2\_peaks.narrowPeak

DN1WT1\_peaks.narrowPeak      DN1WT2\_peaks.narrowPeak

63% of WT1 peaks overlap  
with WT2

73% of WT2 peaks overlap  
with WT1



# Differential peak analysis

2xWT versus 1xKO

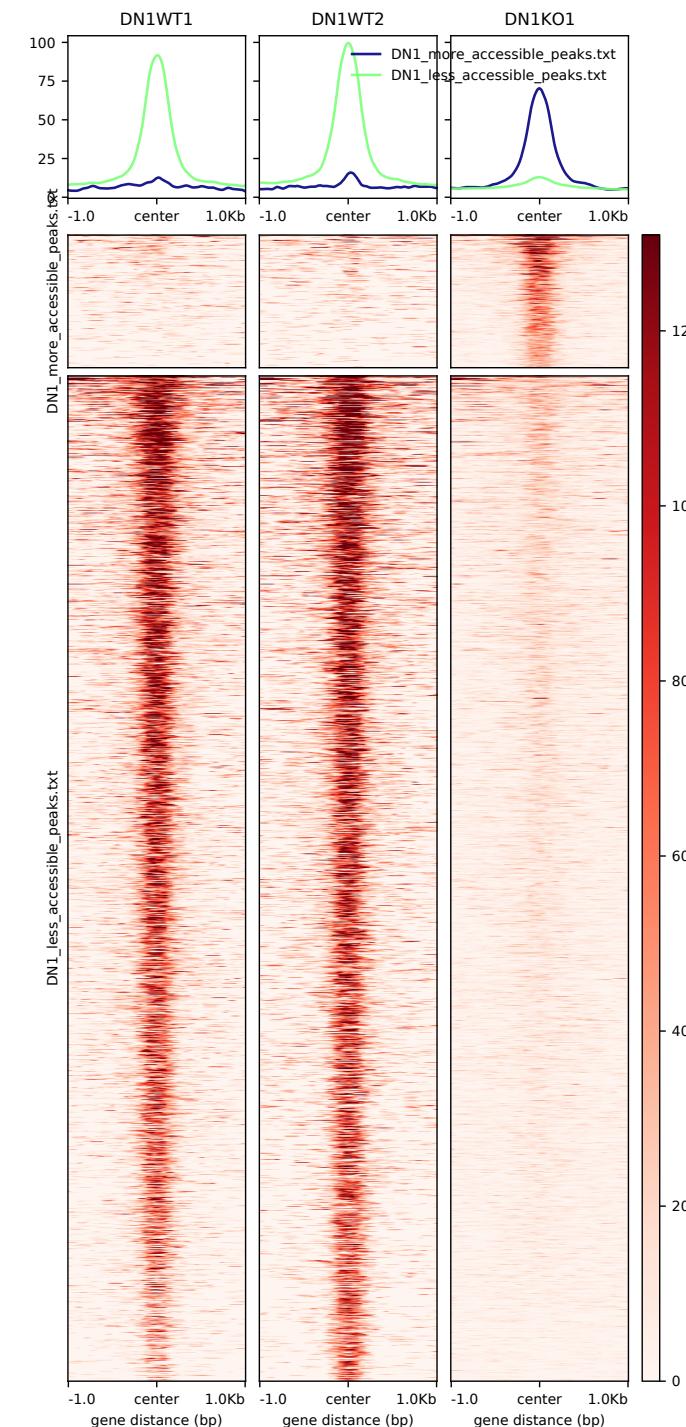
Homer **getDifferentialPeaks FC > 4 / p-value <0.05**

Relative to WT:

Less accessible in KO	2046
More accessible in KO	269

Average size less accessible peaks: 320bp  
(SD=113bp)

Average size more accessible peaks: 284bp  
(SD=145bp)



# The *cis*-Regulatory Atlas of the Mouse Immune System

2x DN1 analyzed

99% Aligned reads (10M reads)

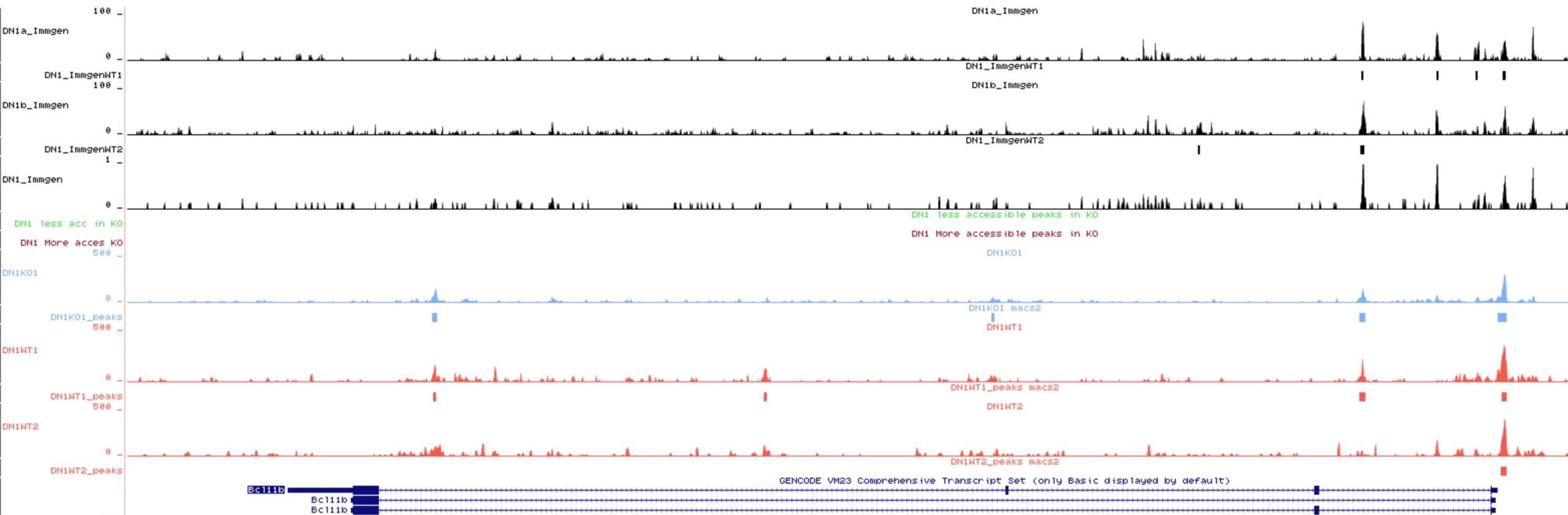
Phred > 35

Samples	Peaks
ImmgenWT1	58066
ImmgenWT2	42862

## Authors

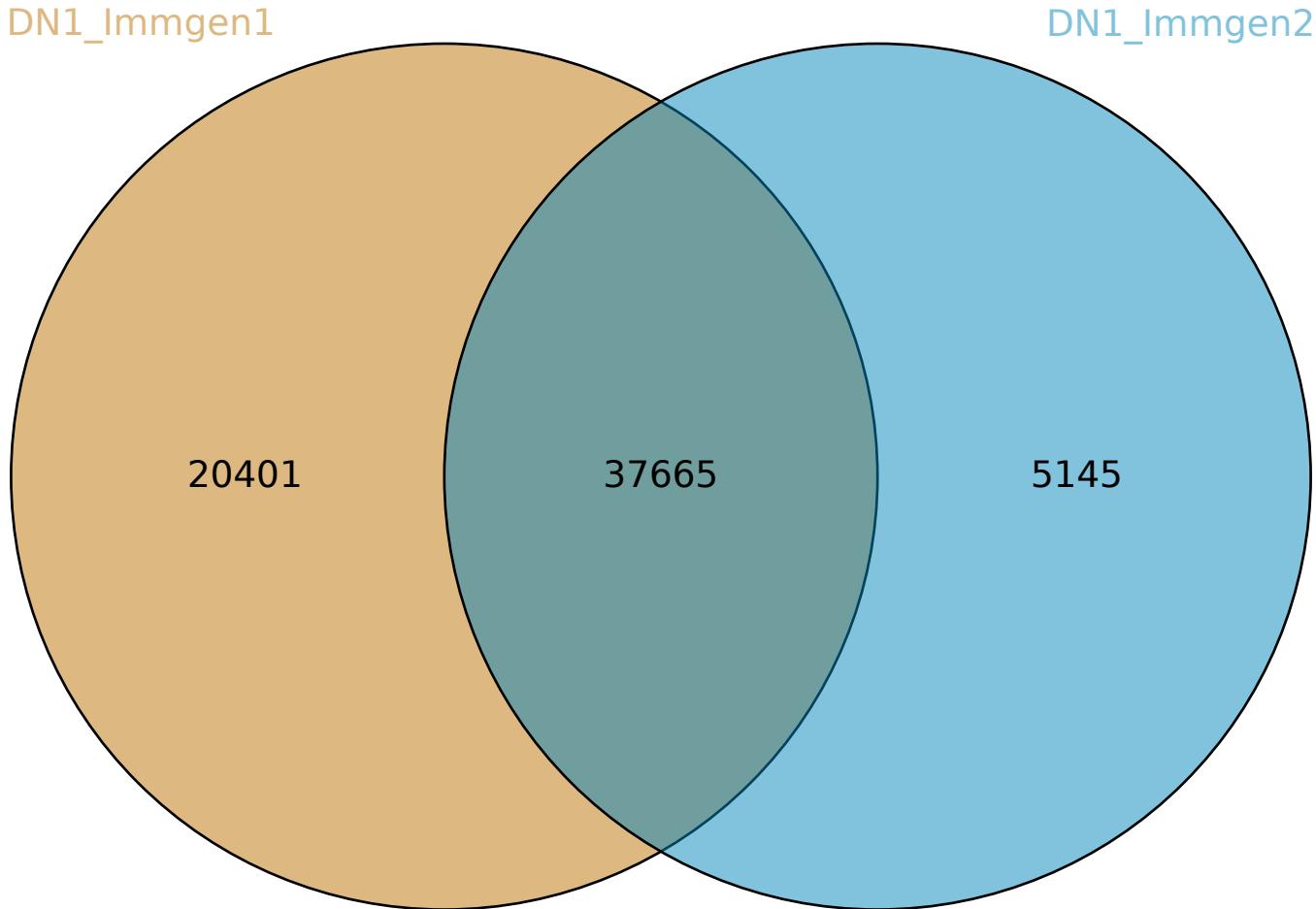
Hideyuki Yoshida, Caleb A. Lareau,  
Ricardo N. Ramirez, ...,  
Jason D. Buenrostro, Christophe Benoist,  
the Immunological Genome Project

# *Bcl11b*



# Overlap Immgen Replicates

DN1\_Immgen1  
DN1\_Immgen2

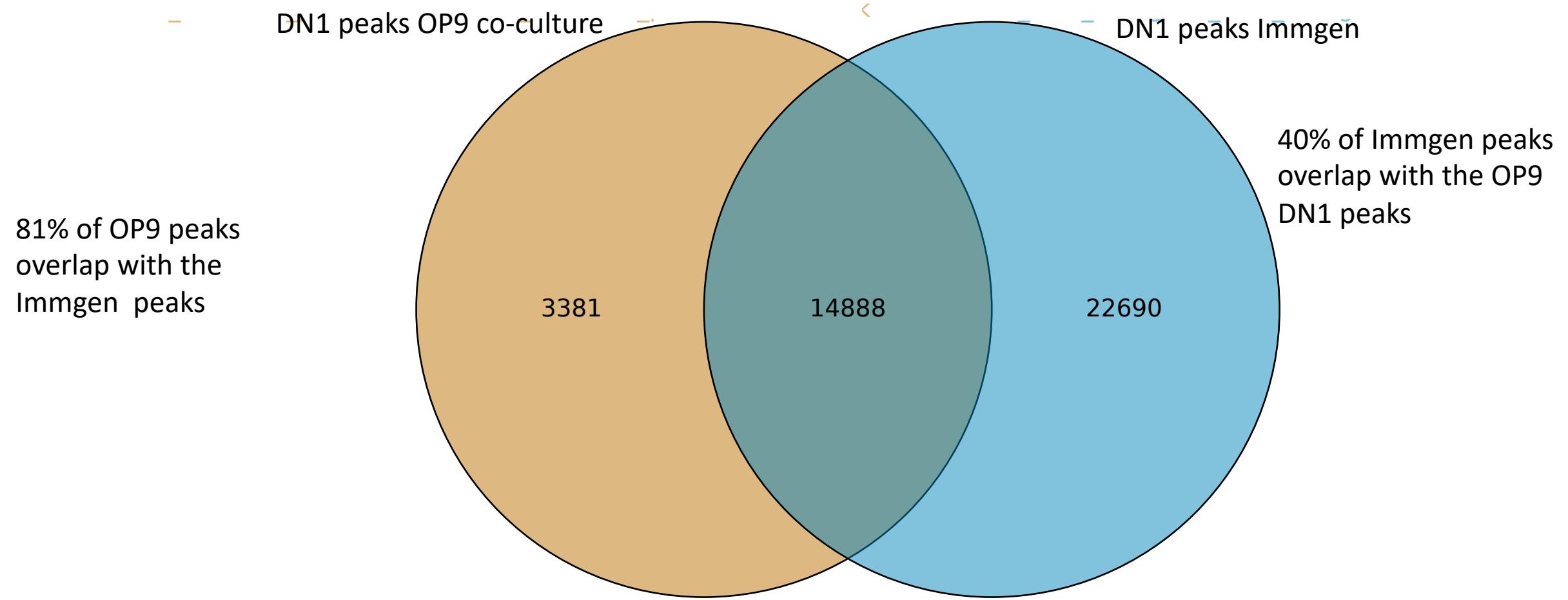


64% of WT1 overlaps with WT2

88% of WT2 overlaps with WT1

# Overlap Immgen and OP9 peaks

11\_DN1WT1\_peaks.narrowPeak\_DN1WT2\_peaks.narrowPeak  
11\_DN1\_Immgen1\_DN1\_Immgen2



81% of OP9 peaks overlap with the Immgen peaks

40% of Immgen peaks overlap with the OP9 DN1 peaks

The OP9 ATAC-seq detects less peaks than the Immgen DN1 but most of them are overlap. With our dataset we might be missing some change in accessibility at certain loci.

## Motif analysis

Differential peaks are mostly found away from the gene promoters

### Number of Peaks

### Feature Distribution

2046

DN1\_less\_accessible\_peaks.txt

269

DN1\_more\_accessible\_peaks.txt

37473

DN1KO1\_peaks.txt

28992

DN1WT1\_peaks.txt

24902

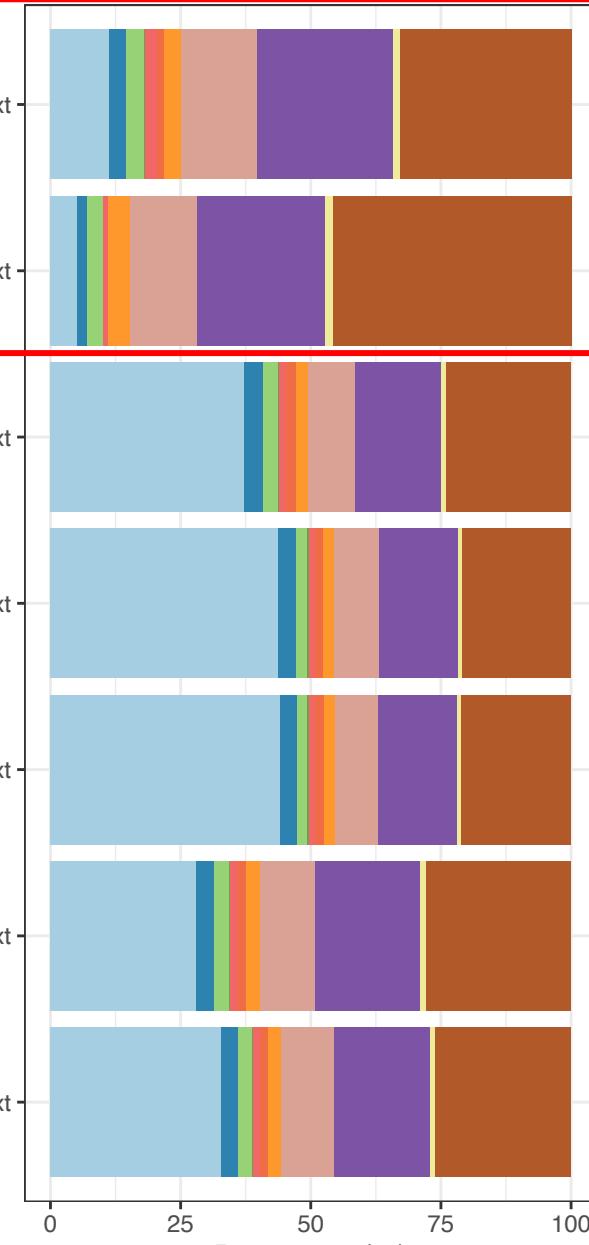
DN1WT2\_peaks.txt

58065

ImmegenDN1A\_peaks.txt

42861

ImmegenDN1B\_peaks.txt

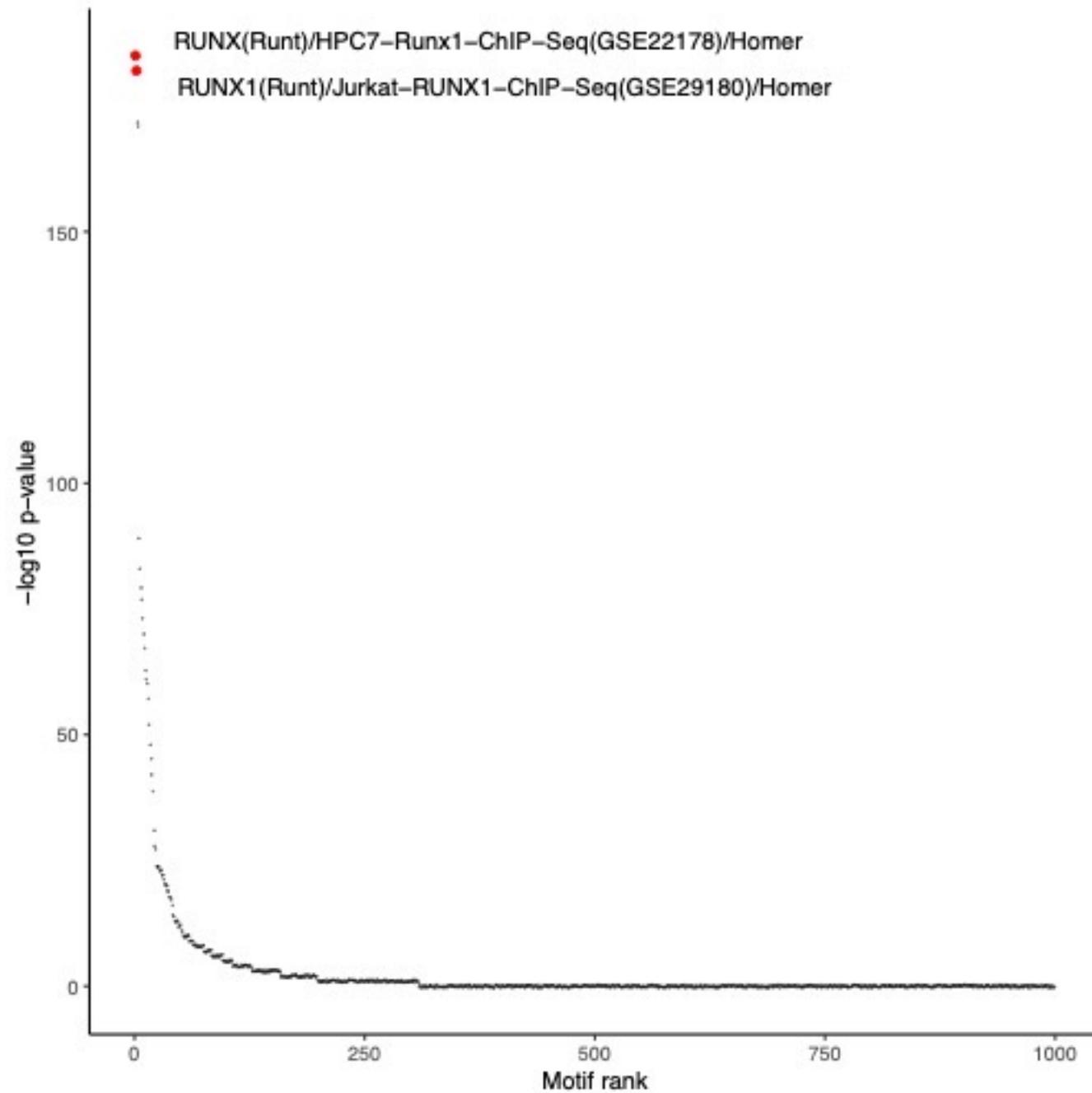


### Feature

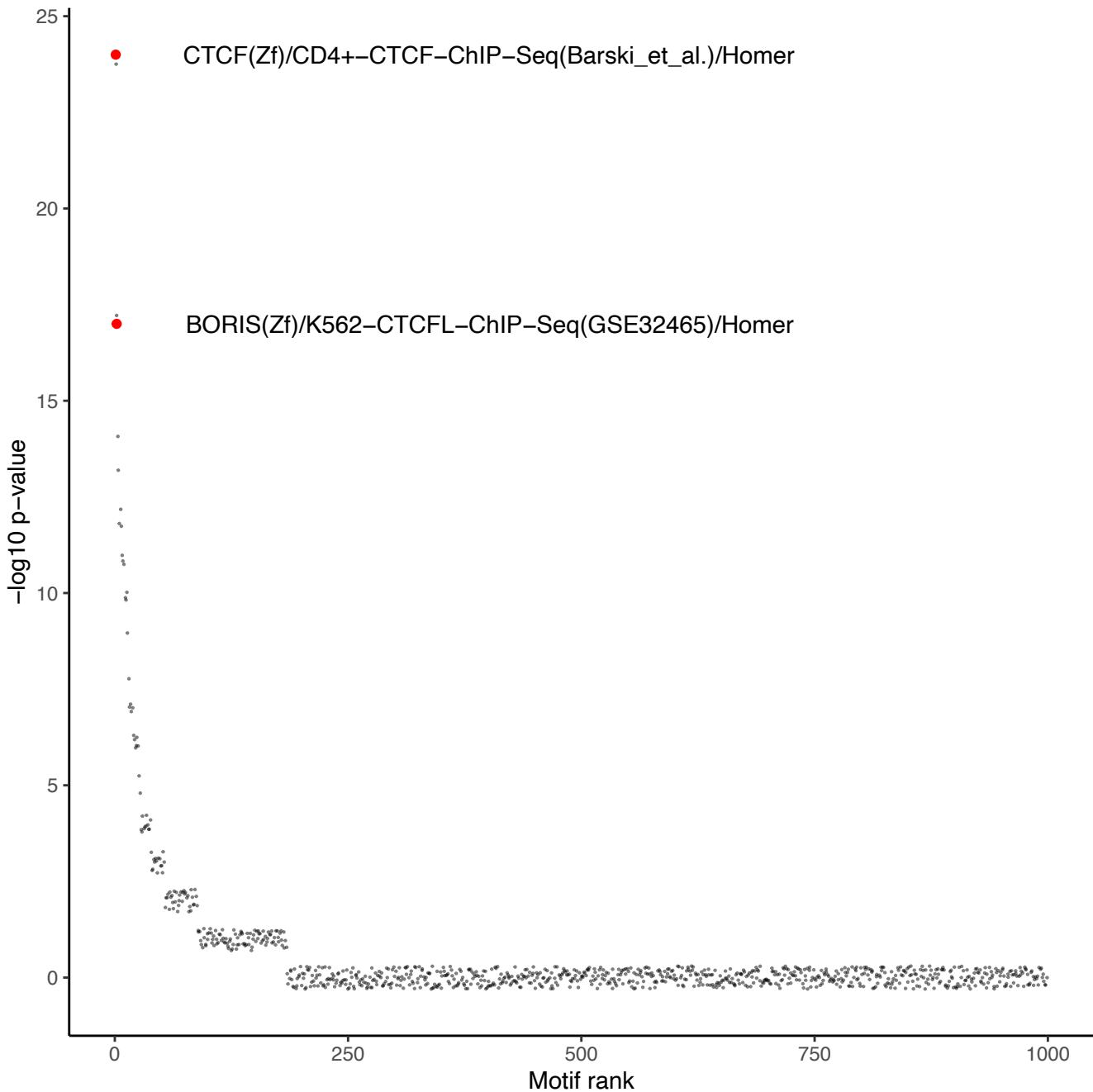
- Promoter (<=1kb)
- Promoter (1-2kb)
- Promoter (2-3kb)
- 5' UTR
- 3' UTR
- 1st Exon
- Other Exon
- 1st Intron
- Other Intron
- Downstream (<=300)
- Distal Intergenic

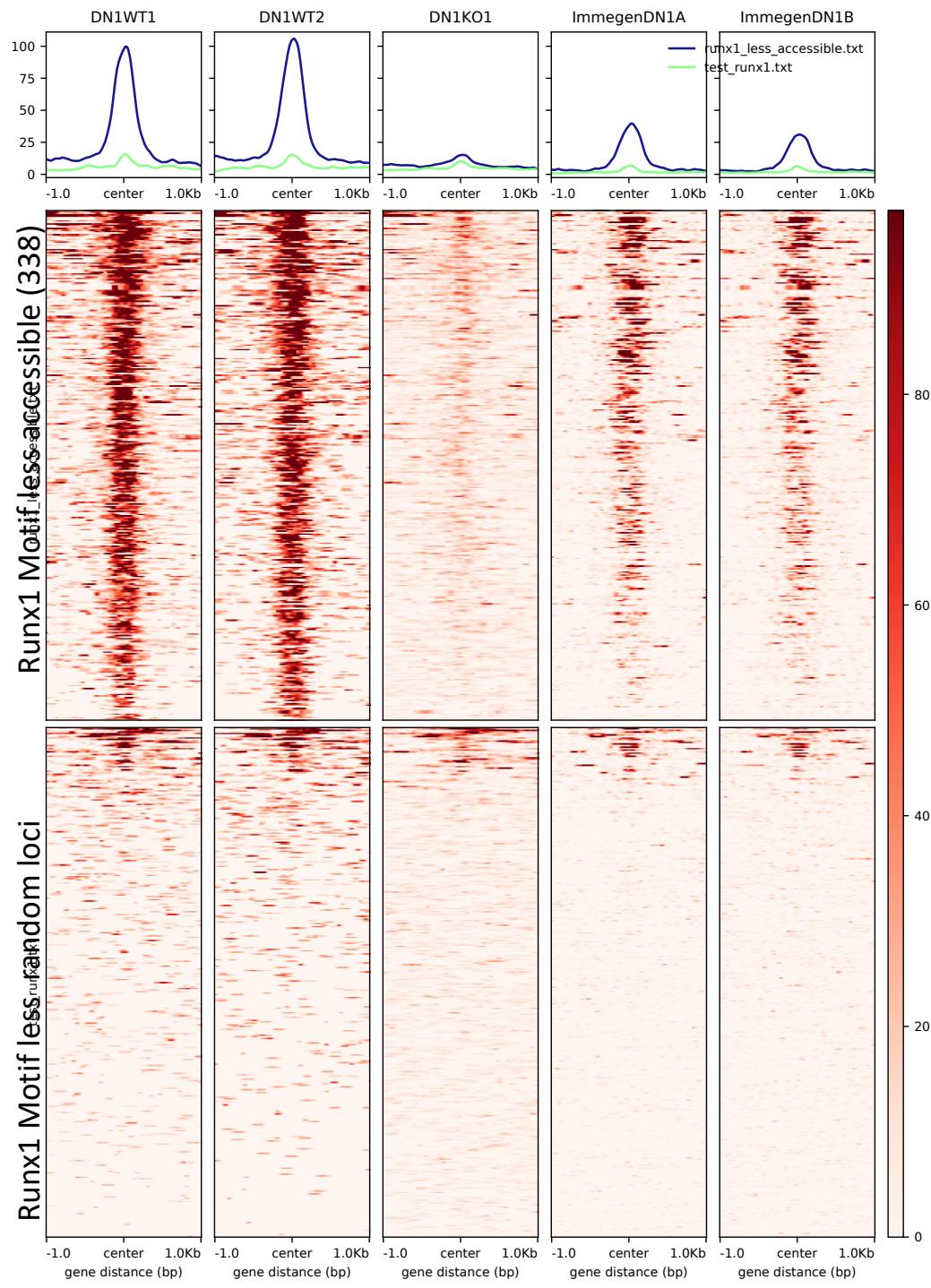
Percentage(%)

**2046 LESS accessible loci in the mutant compared to the WT**



**269 MORE accessible loci in the mutant compared to the WT**

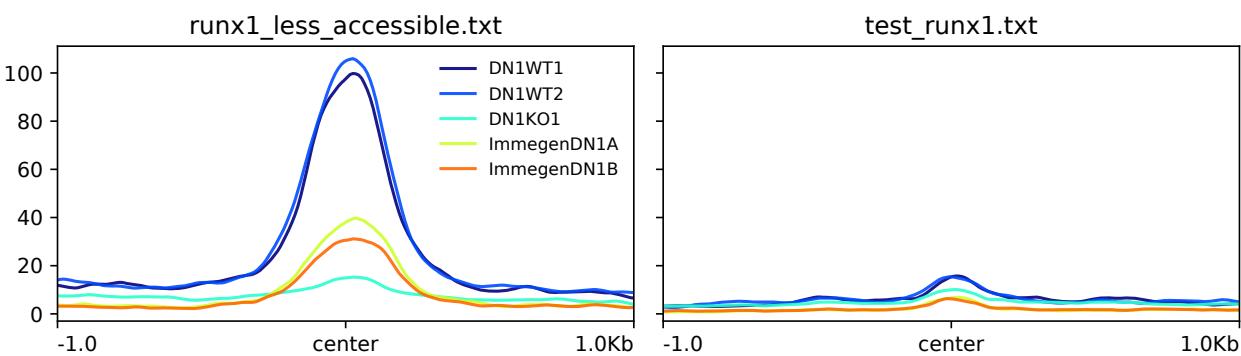




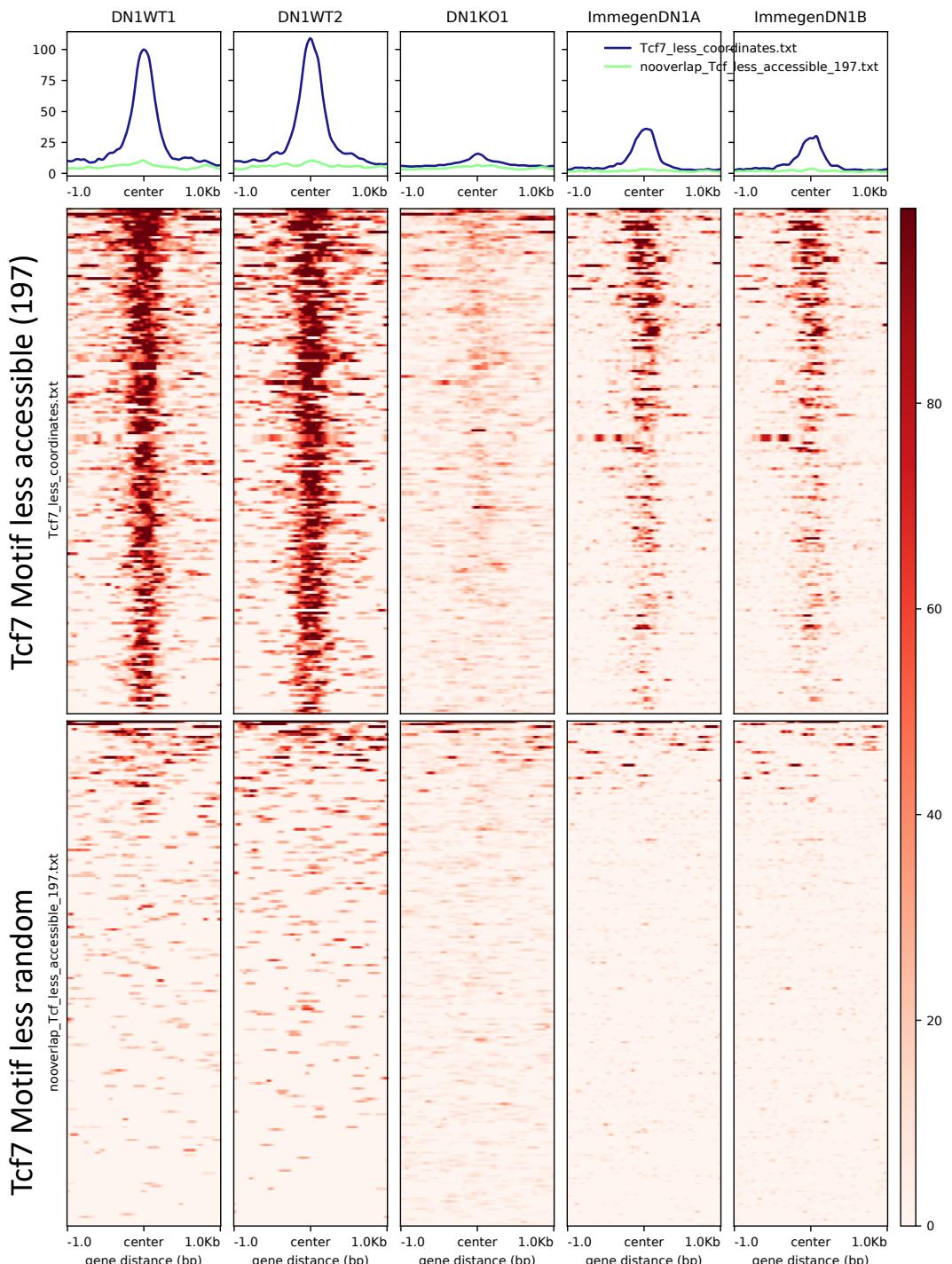
Runx1 motif: CWAACCACAR

Occurrence genome-wide :85689

Overlap with Less accessible peaks: 338 (17%)



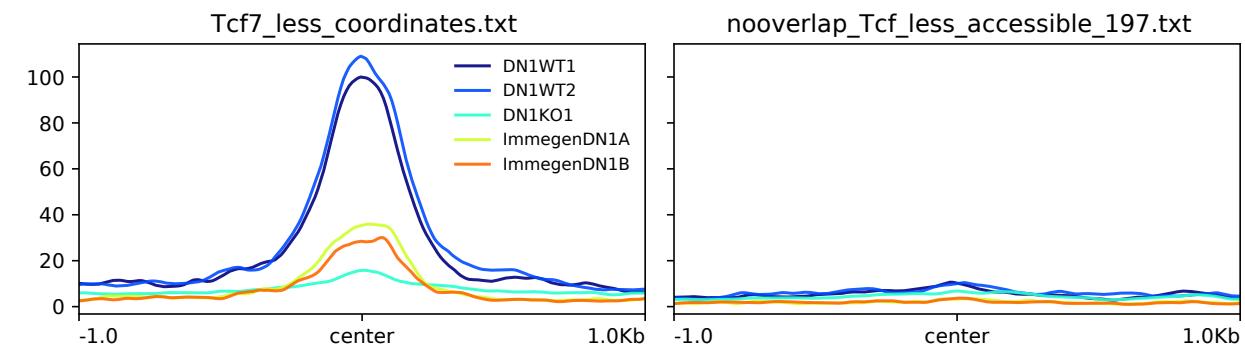
Runx1 motif are more accessible in WT than in mutant.  
Also true from Immgen



Tcf7 motif: CCACATCAAAGG

Occurrence genome-wide : 70110

Overlap with Less accessible peaks: 197 (10%)



# Summary

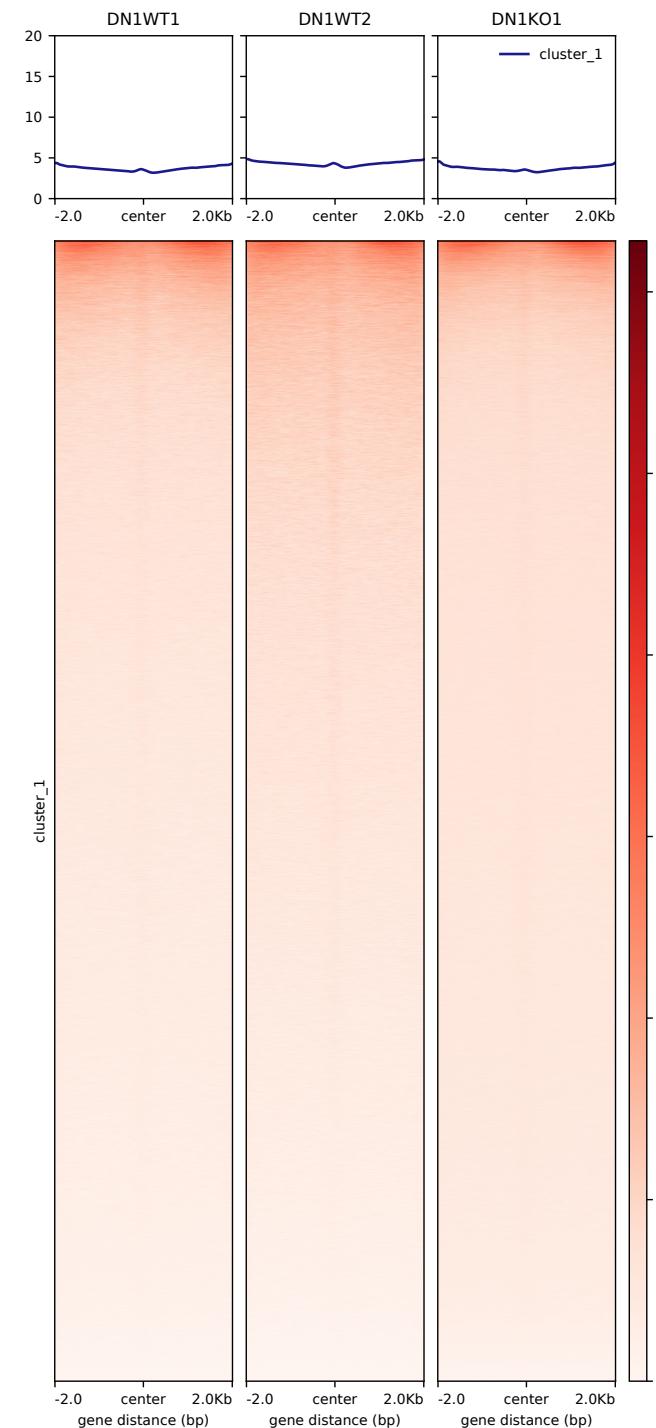
- Despite low coverage, we can identify accessible chromatin in OP-9 ATAC-seq
- Most peaks identified are located in promoter region
- Identification of Differentially accessible loci (DALs):
  - 2046 are less accessible in the mutant than in WT
  - 269 are more accessible in the mutant than in WT
- The motif analysis shows that potential binding sites for important TF regulators of T-cell commitment are impacted
- Are those DALs enhancers?
- To do: Differential peak analysis between WT OP9 and WT Immgen.

## Analysis of coverage at TEs

Coverage at **LTR**

Coverage at LTR does not change between WT and KO

Both are lowly covered with ATAC-seq reads.

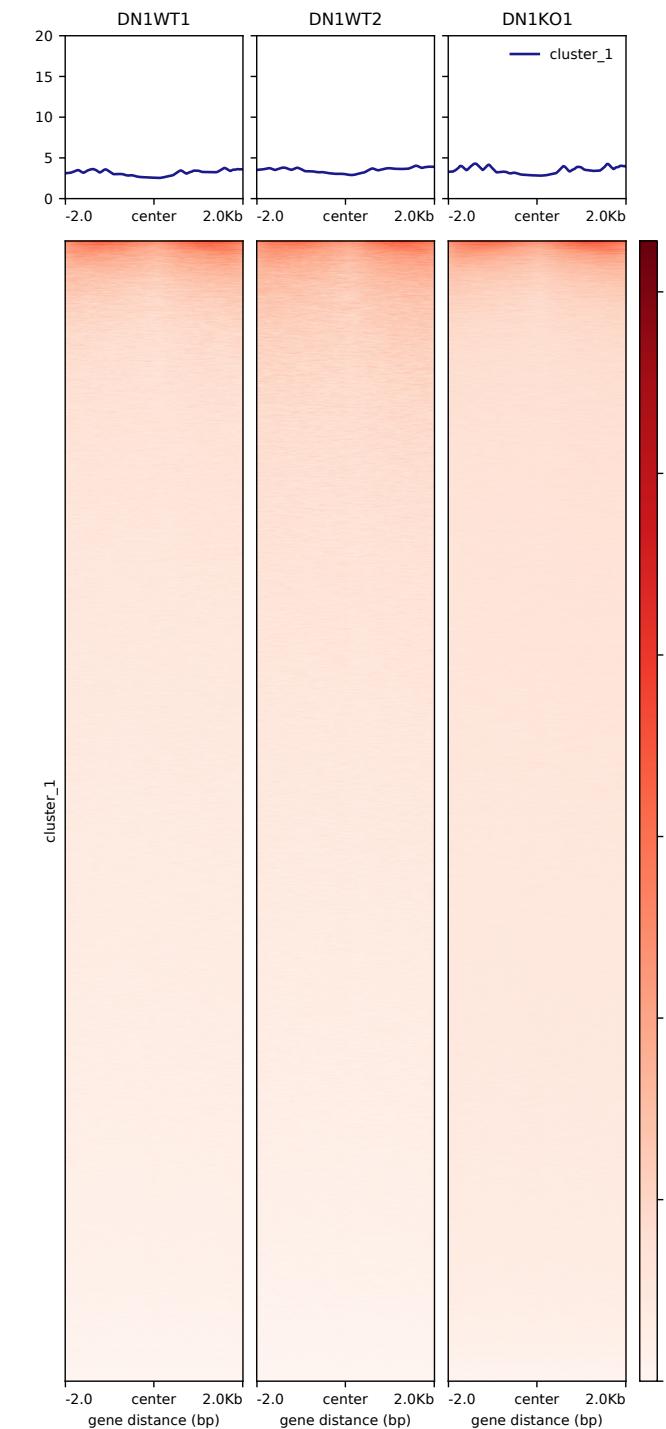


# Analysis of coverage at TEs

Coverage at **LINE**

Coverage does not change between WT and KO

Both are lowly covered with ATAC-seq reads.

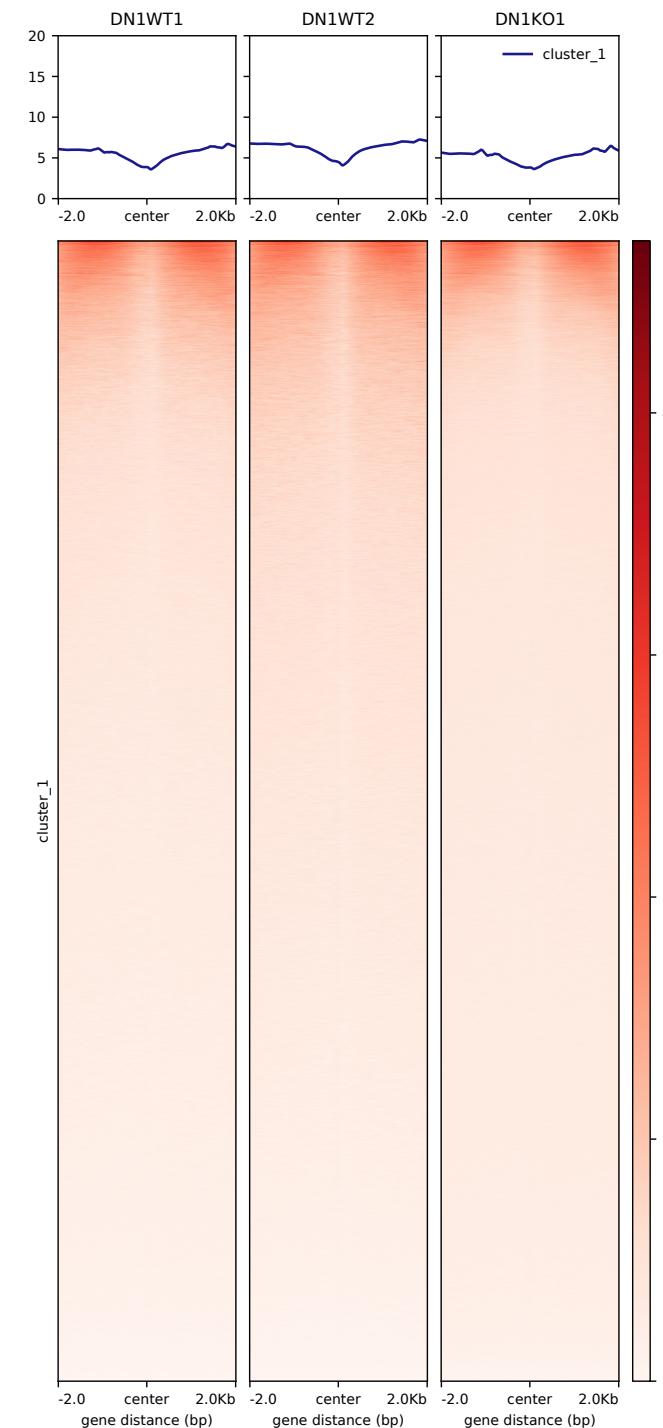


# Analysis of coverage at TEs

Coverage at **SINE**

Coverage does not change between WT and KO

Both are lowly covered with ATAC-seq reads.

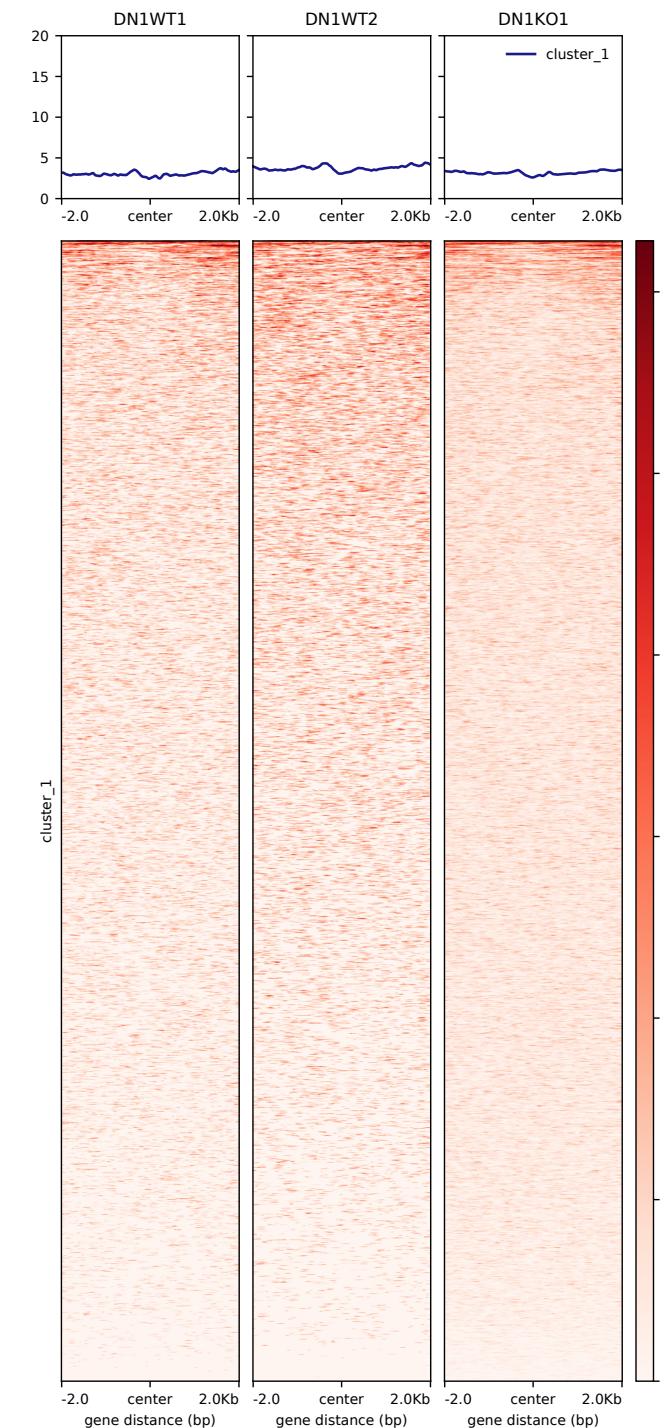


## Analysis of coverage at TEs

Coverage at **MERVL**

Coverage does not change between WT and KO

Both are lowly covered with ATAC-seq reads.

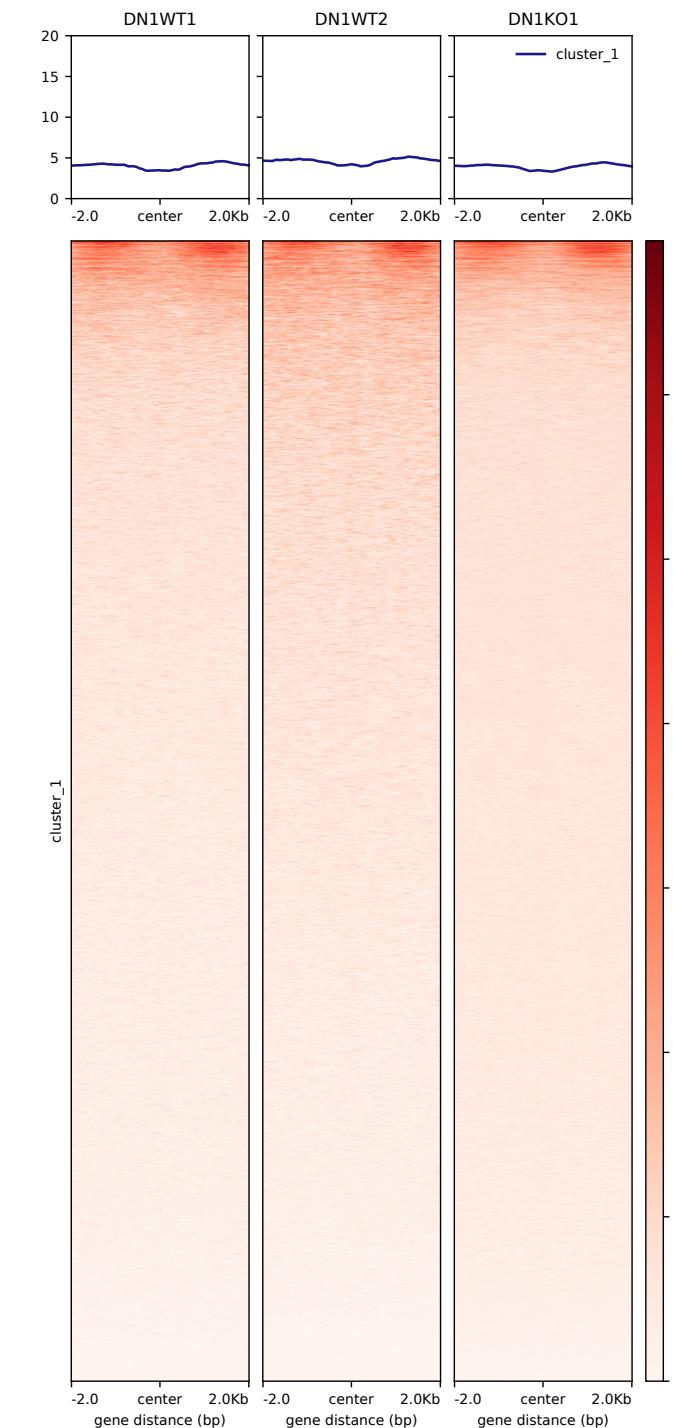


## Analysis of coverage at TEs

Coverage at **ERV1**

Coverage does not change between WT and KO

Both are lowly covered with ATAC-seq reads.

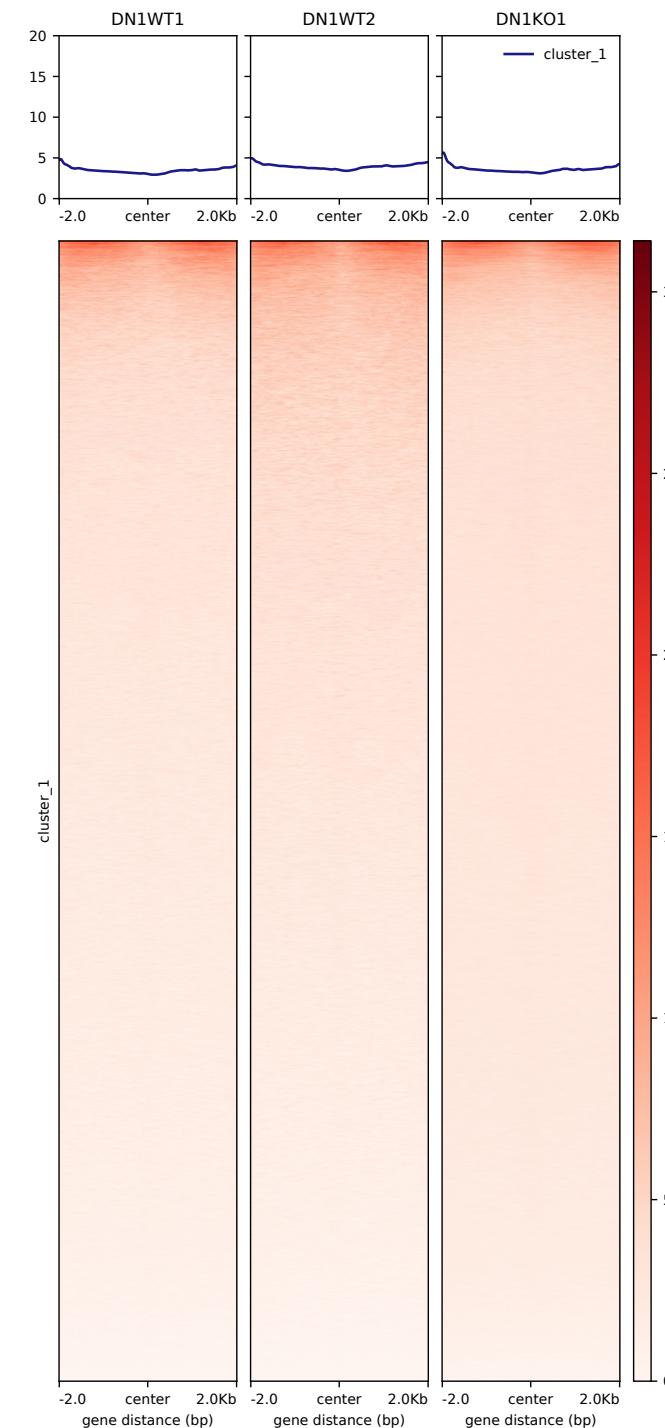


# Analysis of coverage at TEs

Coverage at **ERVK**

Coverage does not change between WT and KO

Both are lowly covered with ATAC-seq reads.

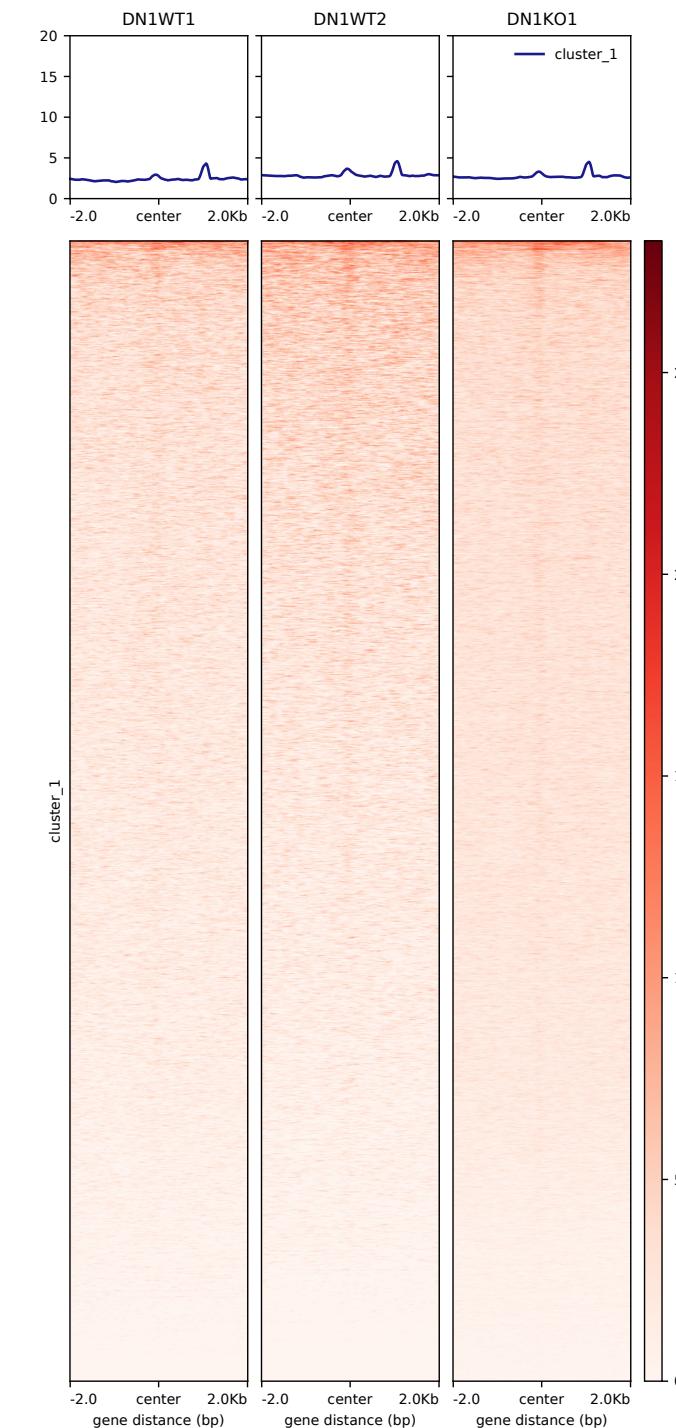


# Analysis of coverage at TEs

Coverage at **IAP**

Coverage does not change between WT and KO

Both are lowly covered with ATAC-seq reads.



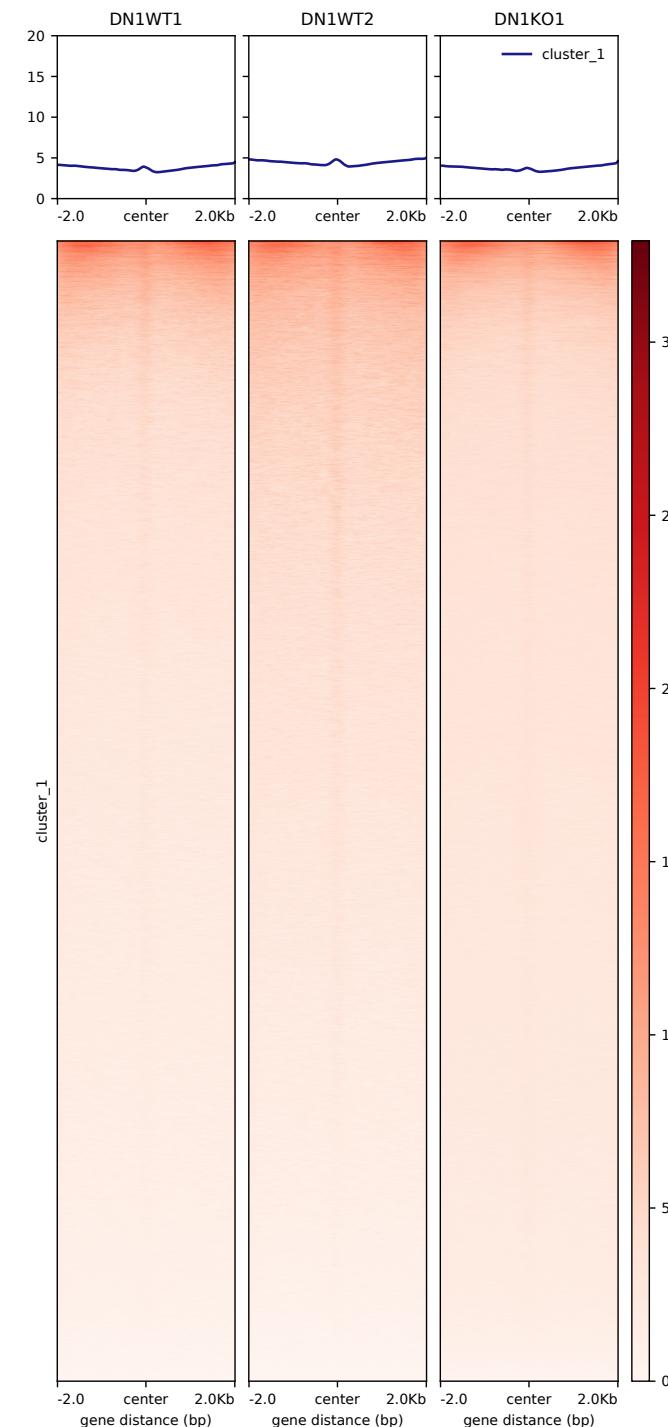
# Analysis of coverage at TEs

Coverage at **ERVL**

Coverage does not change between WT and KO

Both are lowly covered with ATAC-seq reads.

ERVL show a slight coverage of accessibility in the center of the element

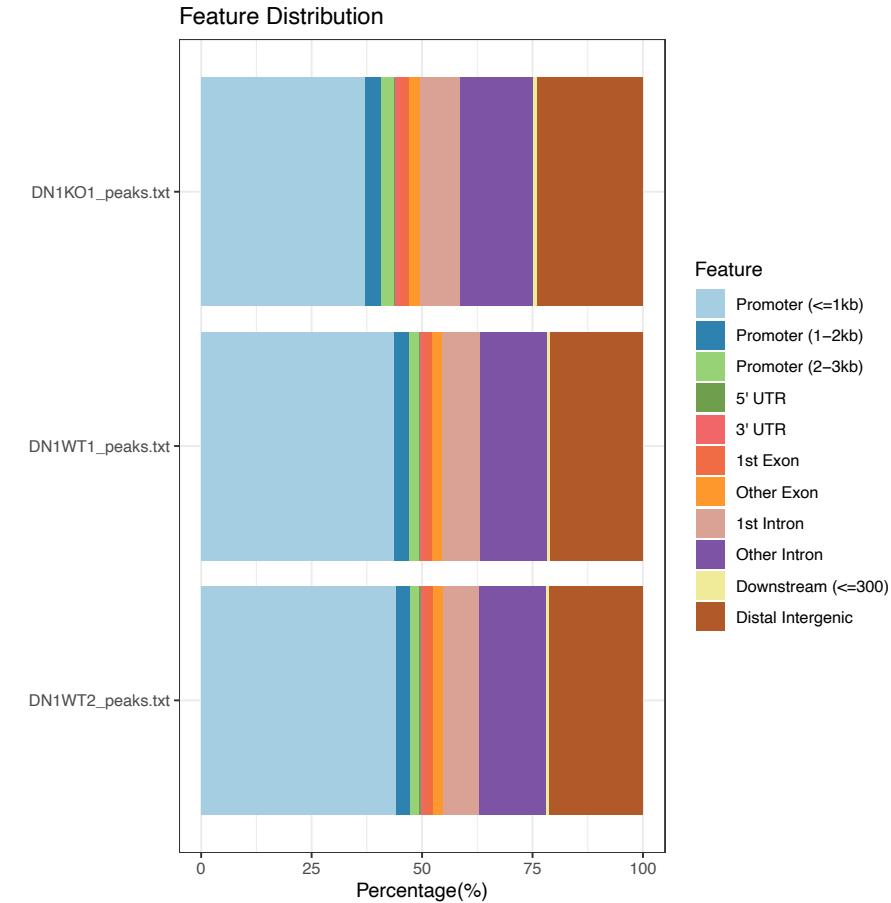


Does Morc3 affect chromatin accessibility in thymus development?

# Results DN1 ATAC-seq July 2021

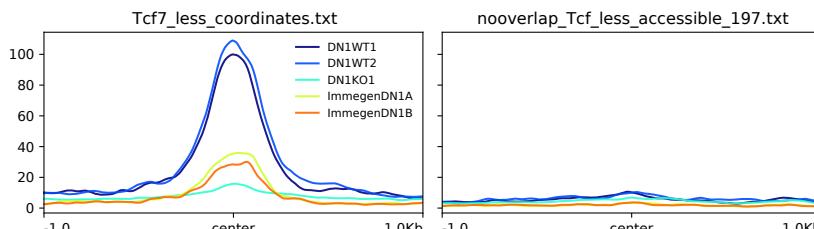
- Sequenced 2xWT and 1x mutant
- Despite low coverage, we can identify accessible chromatin in OP-9 ATAC-seq
- Most peaks identified are in promoter region

name	peaks
WT1	28992
WT2	24902
KO1	37473



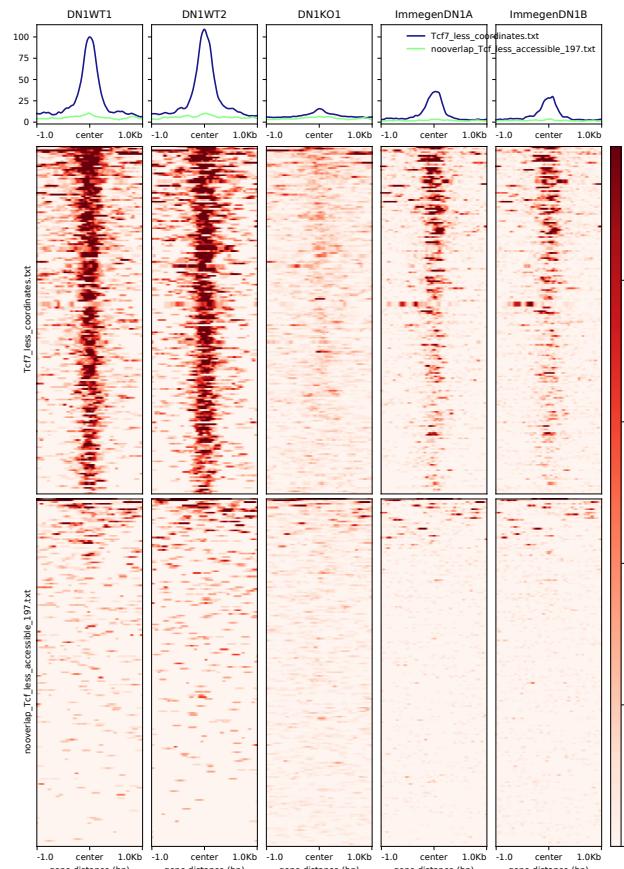
# Results DN1 ATAC-seq July 2021

- Identification of Differentially accessible loci (DALs):
  - 2046 are less accessible in the mutant than in WT
  - 269 are more accessible in the mutant than in WT
- The motif analysis shows that potential binding sites for important TF regulators of T-cell commitment are impacted
- E.g Specific Tcf7 potential binding sites are less accessible in Morc3 mutant than in WT at DN1 (Similar for Runx1)



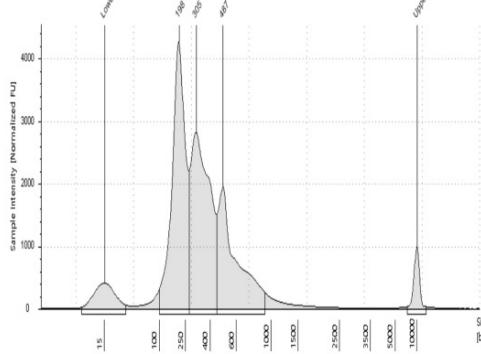
Occurrence genome-wide : 70110

Overlap with Less accessible peaks: 197 (10%)

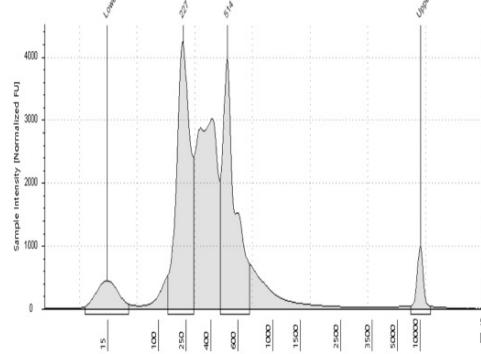


# Overview DN1 ATAC 2nd experiment

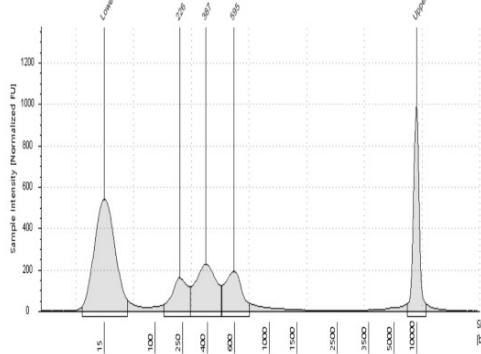
[Click to Enlarge =>1:Library : DN1\\_WT\\_Dec1](#)



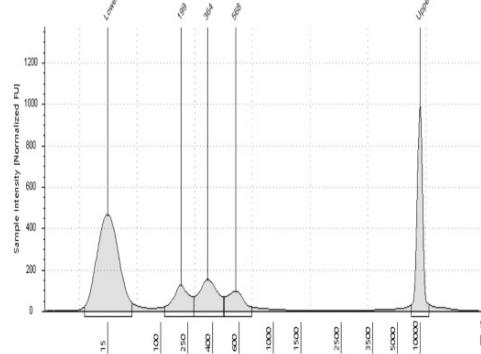
[Click to Enlarge =>2:Library : DN1\\_KO\\_Dec1](#)



[Click to Enlarge =>3:Library : DN1\\_KO\\_Jul1](#)



[Click to Enlarge =>4:Library : DN1\\_KO\\_Jul2](#)



SampleID	p5 Adapter	i5 Index	p7 Adapter	i7 Index	Sample Conc. (ng/ul)	Volume (uL)
DN1_WT_Dec1	S522	TTATGCGA	N714	TCATGAGC	5,168	12
DN1_KO_Dec1	S522	TTATGCGA	N715	CCTGAGAT	6,144	12
DN1_KO_Jul1	S505	GTAAGGAG	N705	AGGAGTCC	1,12	10
DN1_KO_Jul2	S505	GTAAGGAG	N707	GTAGAGAG	1,52	10

150bp  
PE sequencing  
Macrogen

### Fastp: Filtered Reads

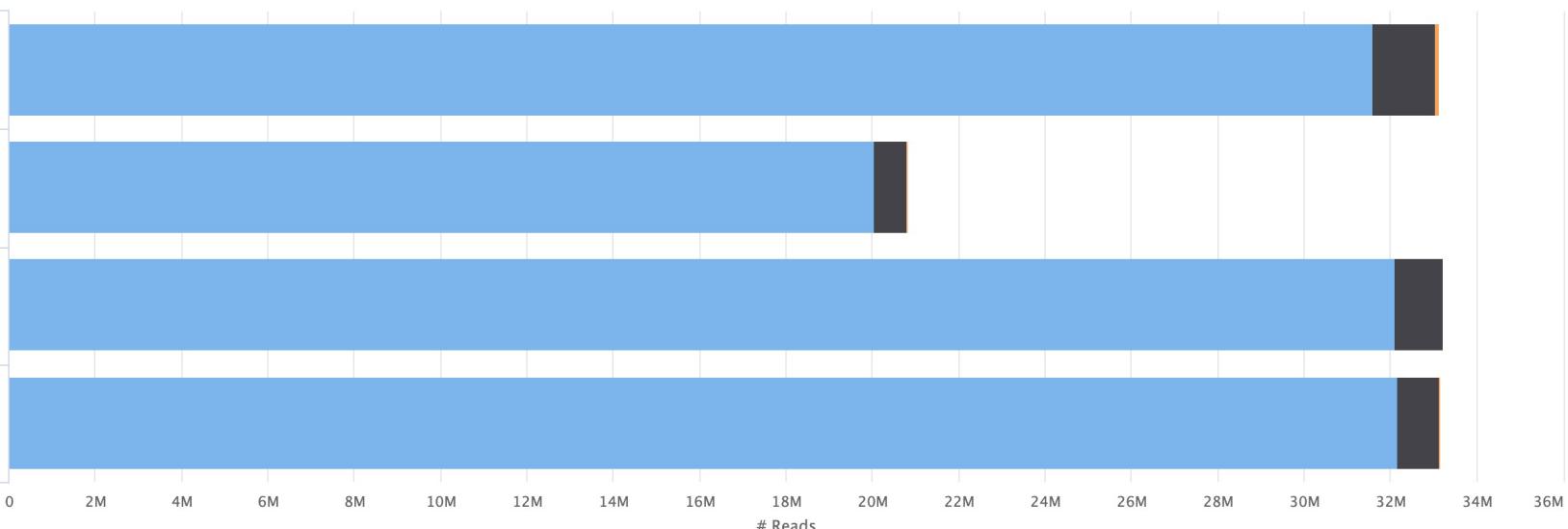
[Export Plot](#)

DN1KO1Jul\_fastp

DN1KO2Jul\_fastp

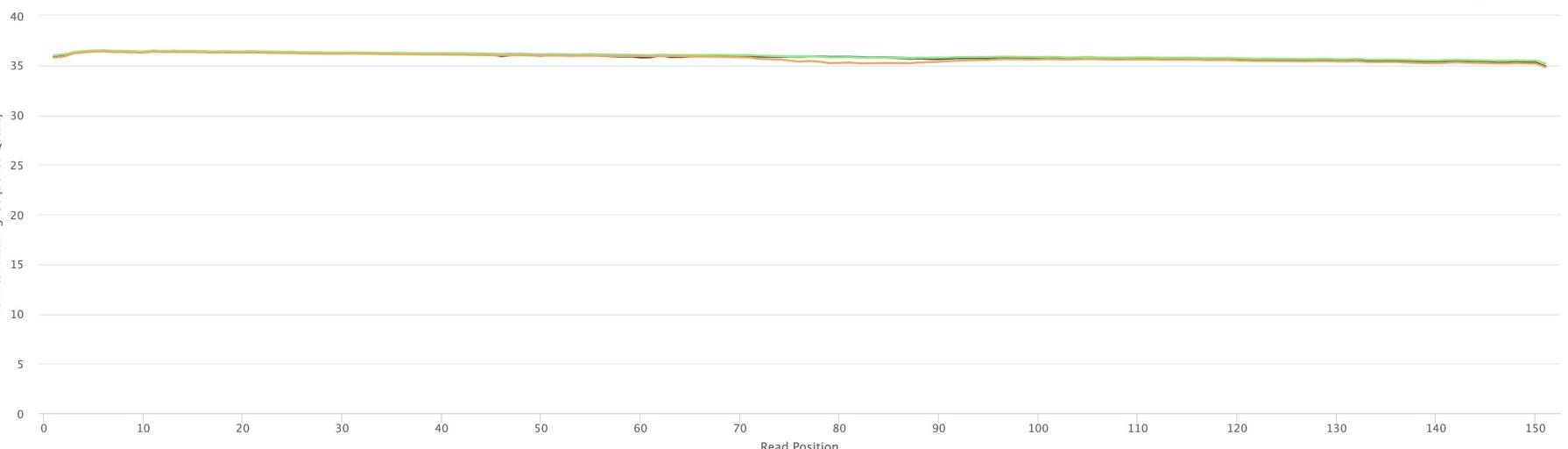
DN1KODec1\_fastp

DN1WTDec1\_fastp

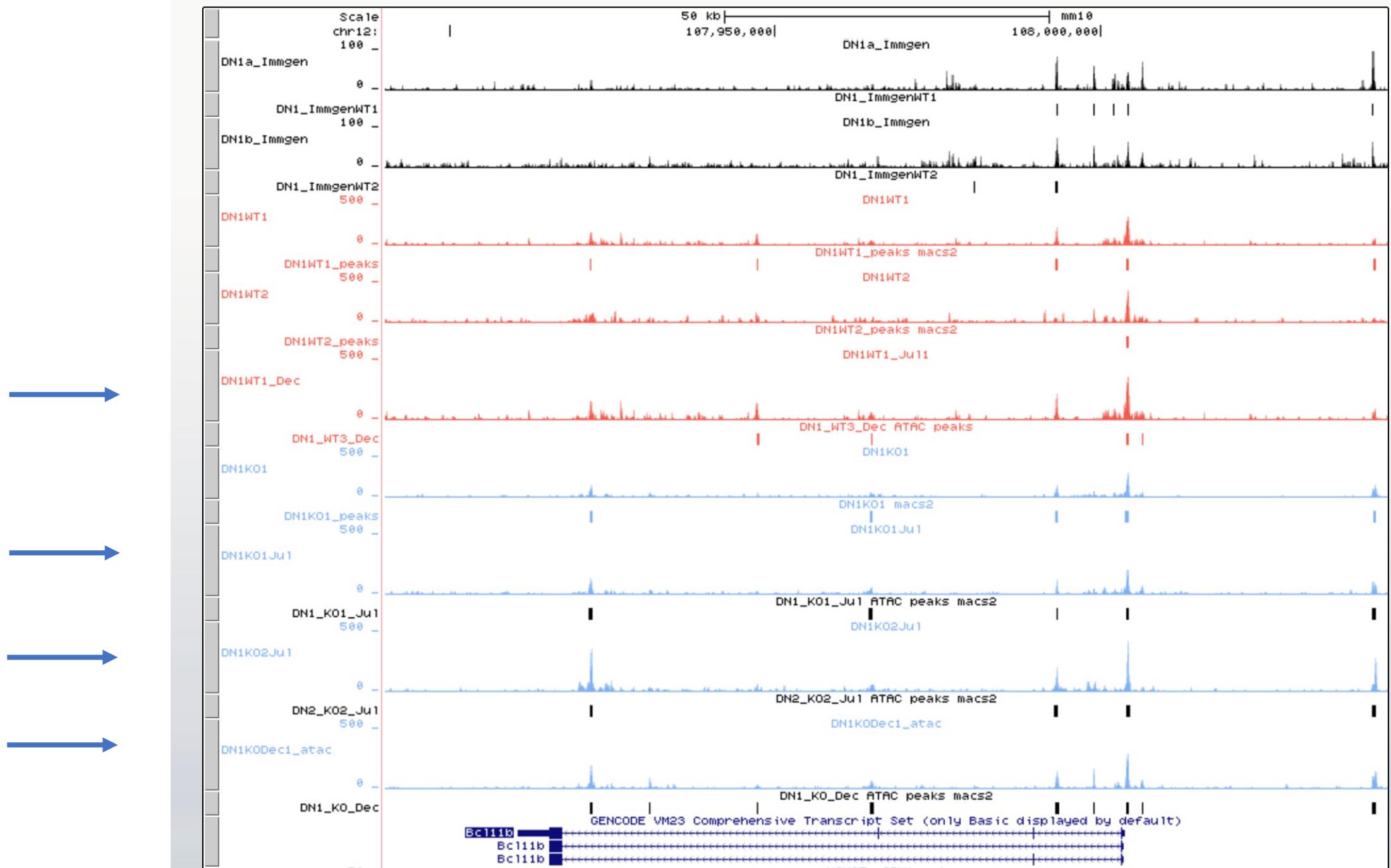


Created with MultiQC

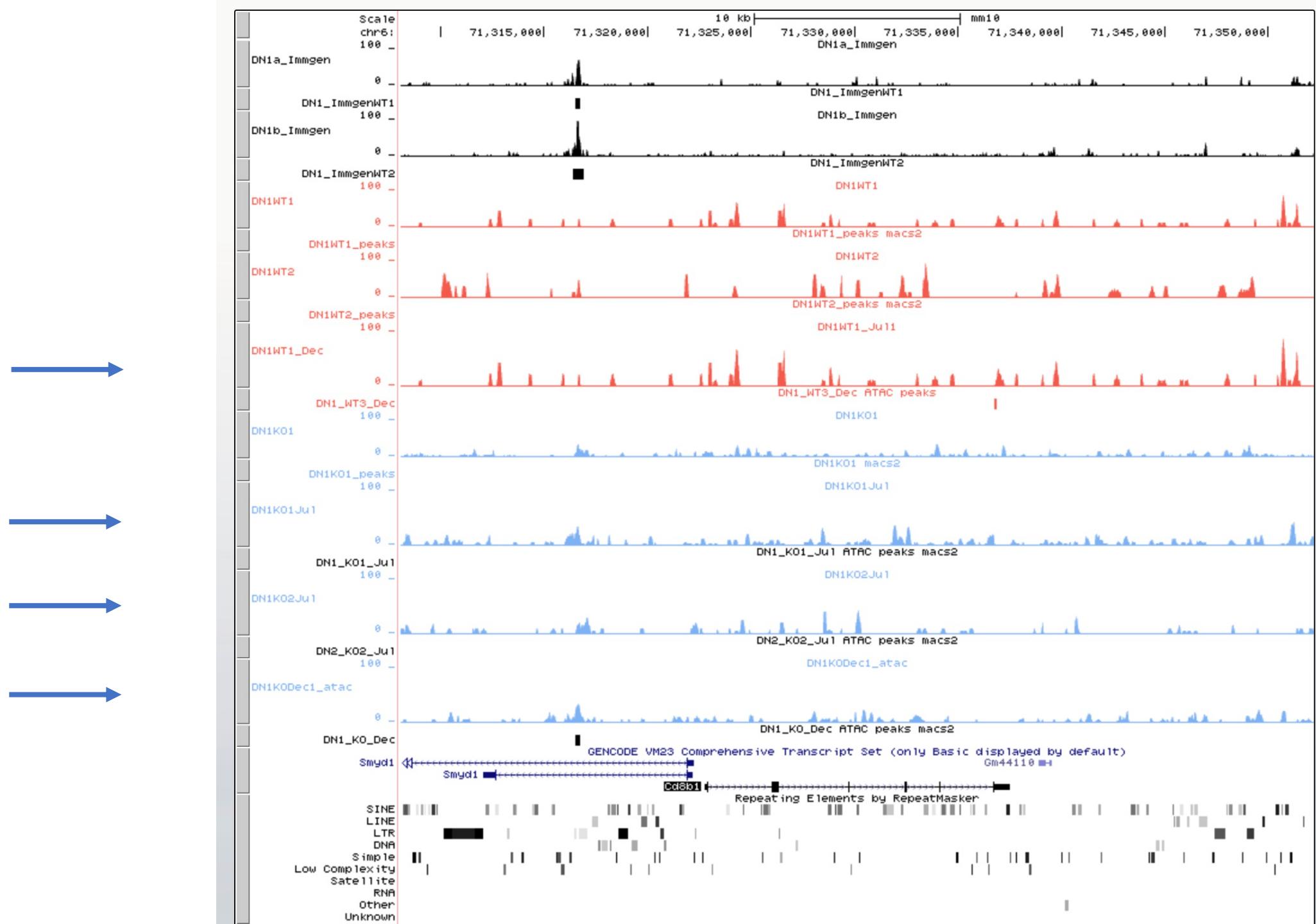
### Fastp: Sequence Quality

[Export Plot](#)

# *Bcl11b*



# Cd8b1

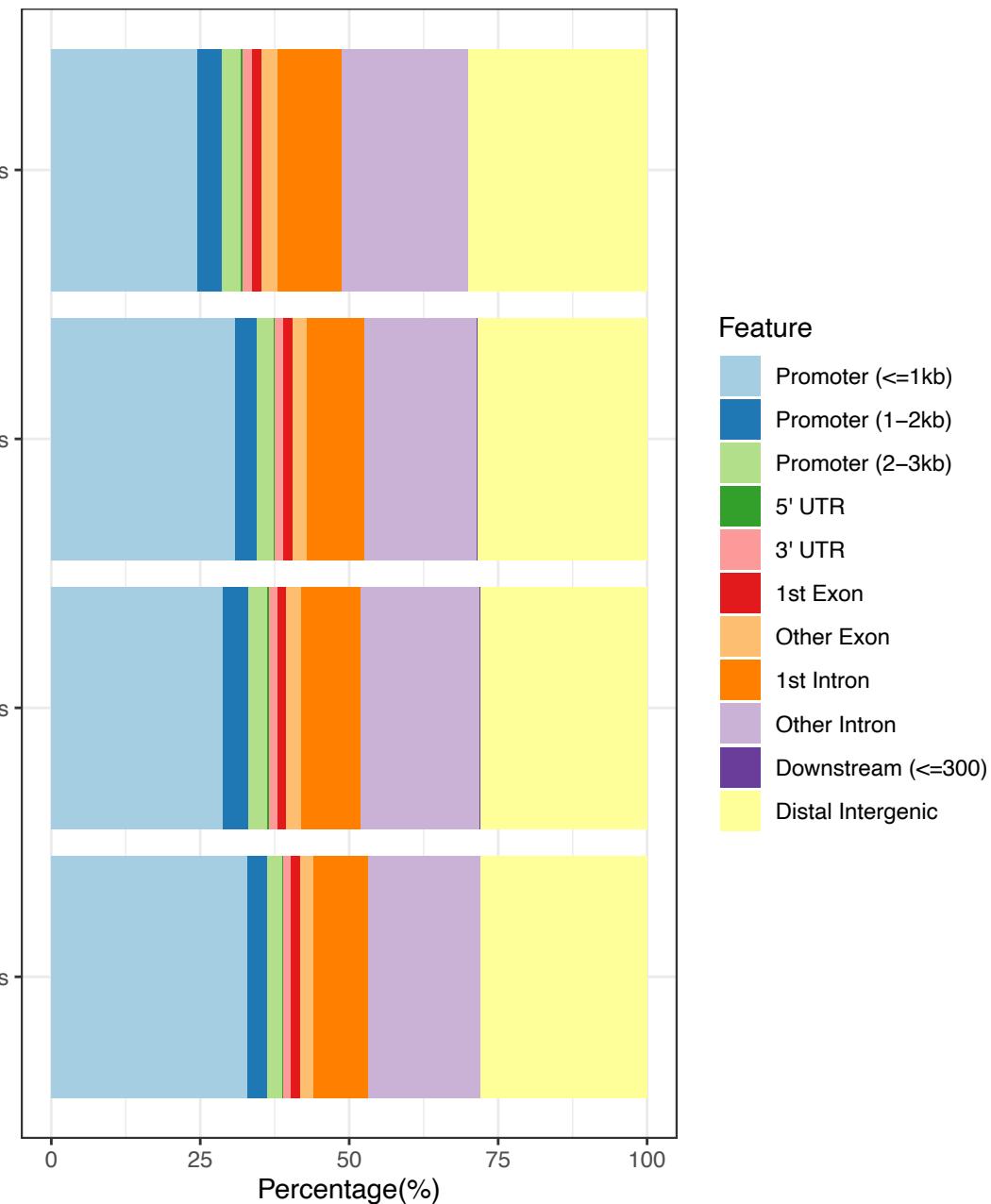


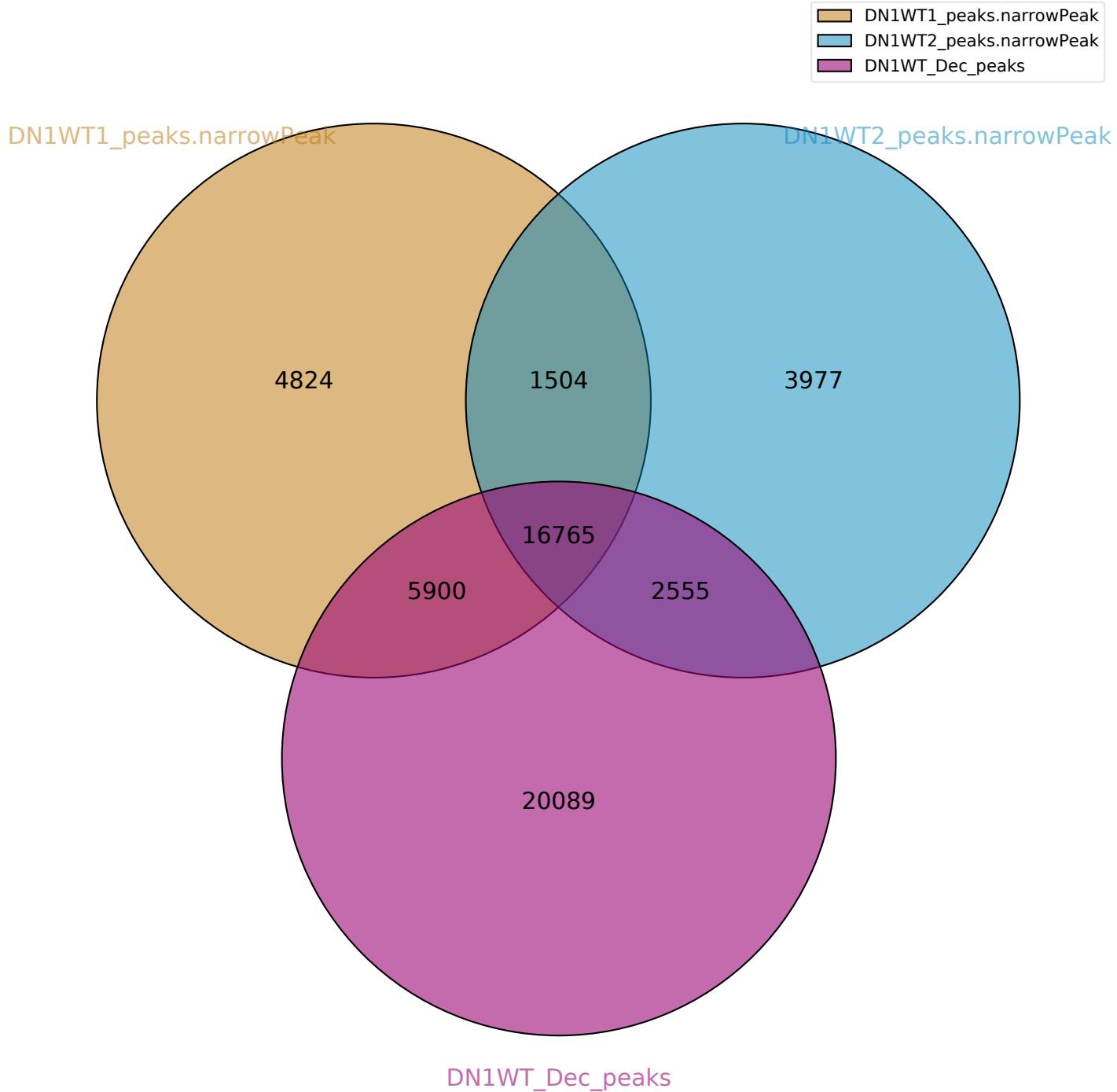
# Annotation peaks DN1 ATAC Dec 2021

name	peaks	Experiment
WT1	28992	July 2021
WT2	24902	
KO1	37473	
WTDec	46140	
KODec	76930	Dec 2021
KOJul1	45832	
KOJul2	49211	

With a higher coverage we detect more peaks.  
 Peaks are mostly at promoters or distal intergenic regions

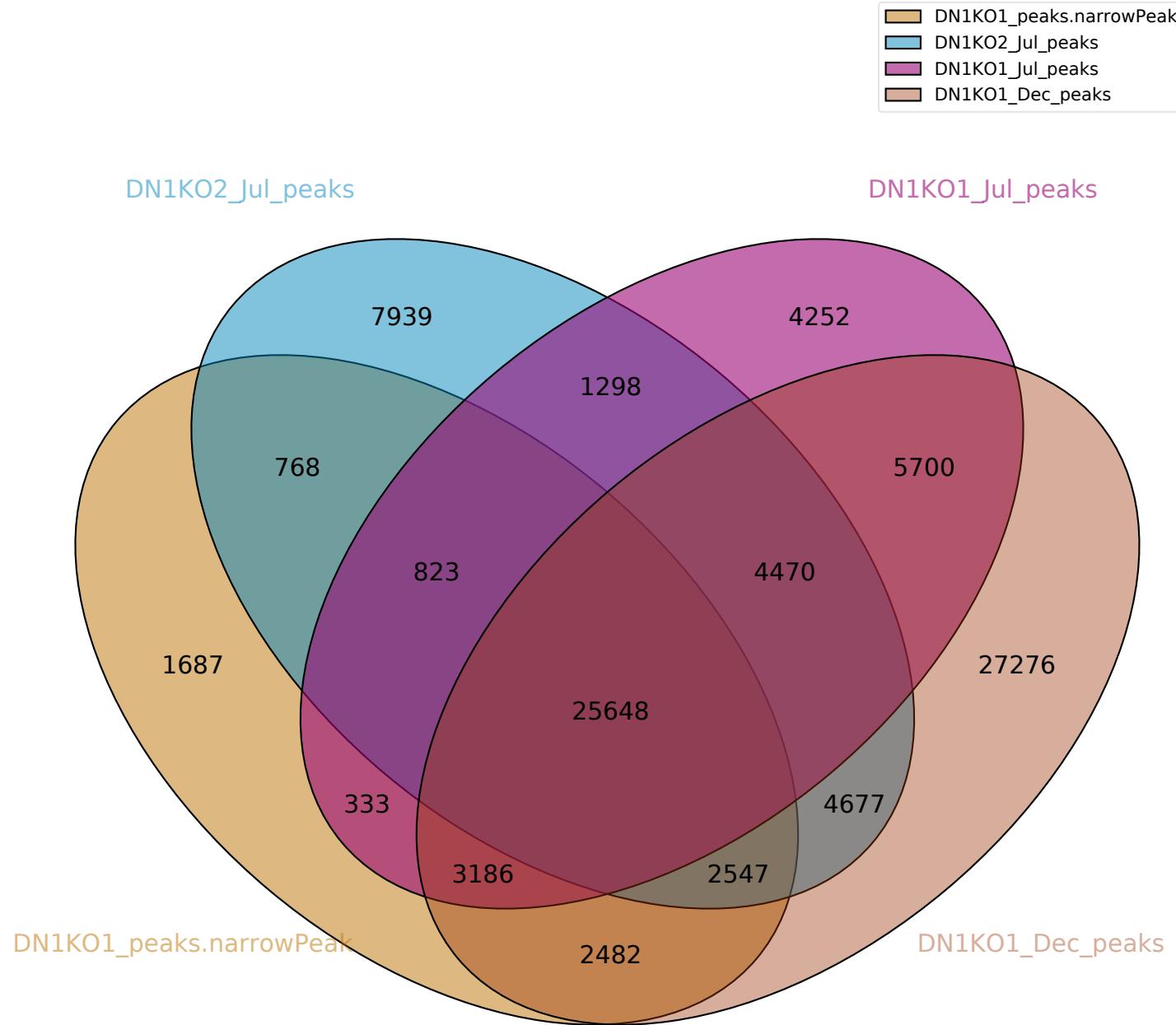
Feature Distribution





The ATAC-seq of december get many peaks that were not detected previously

I have the coordinates of those peaks and can annotate them.



The ATAC-seq of december get many peaks that were not detected previously

I have the coordinates of those peaks and can annotate them.

name	peaks	Experiment
WT1	28992	
WT2	24902	
KO1	37473	July 2021
WTDec	46140	
KODec	76930	
KOJul1	45832	
KOJul2	49211	Dec 2021

Male

Female

# Annotation of the peaks identified for ATAC DN1

44699 peaks

45832 peaks

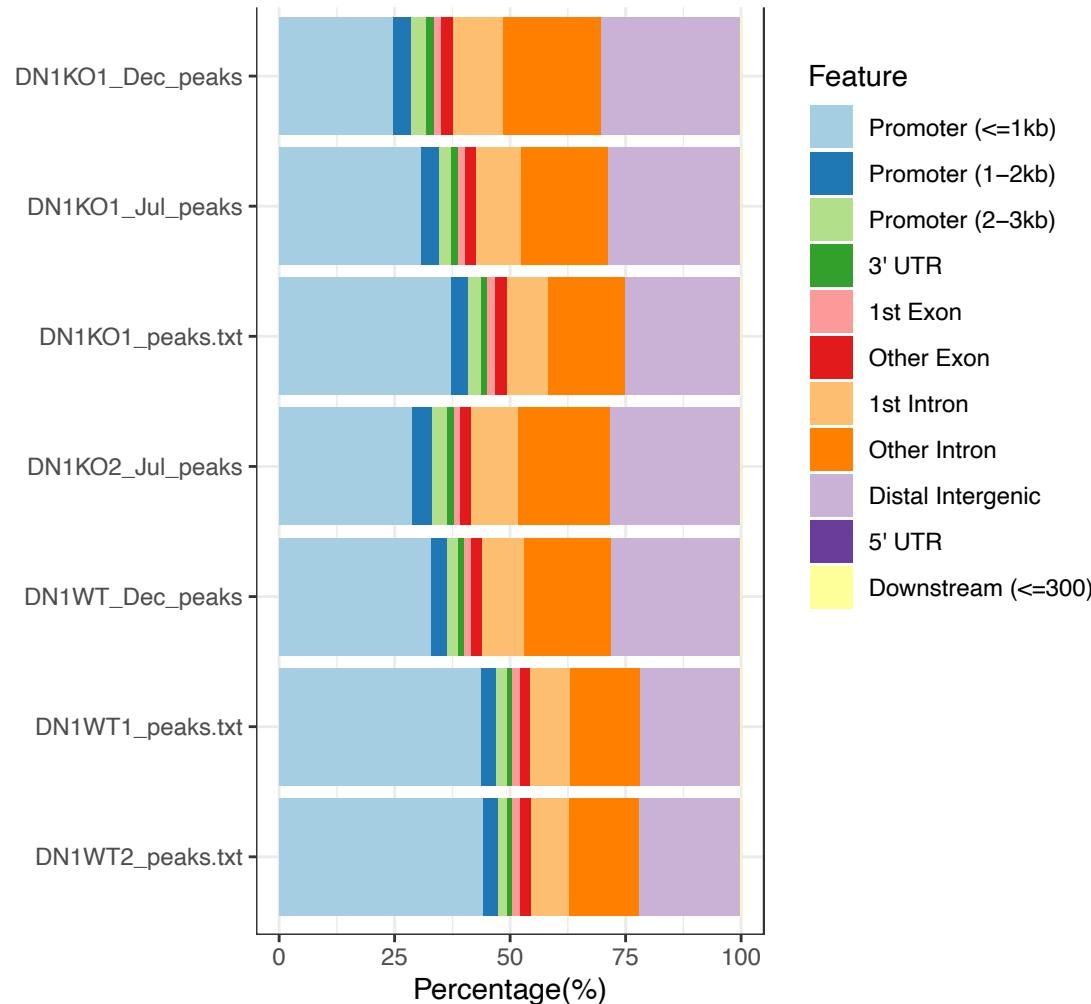
36436 peaks

47935 peaks

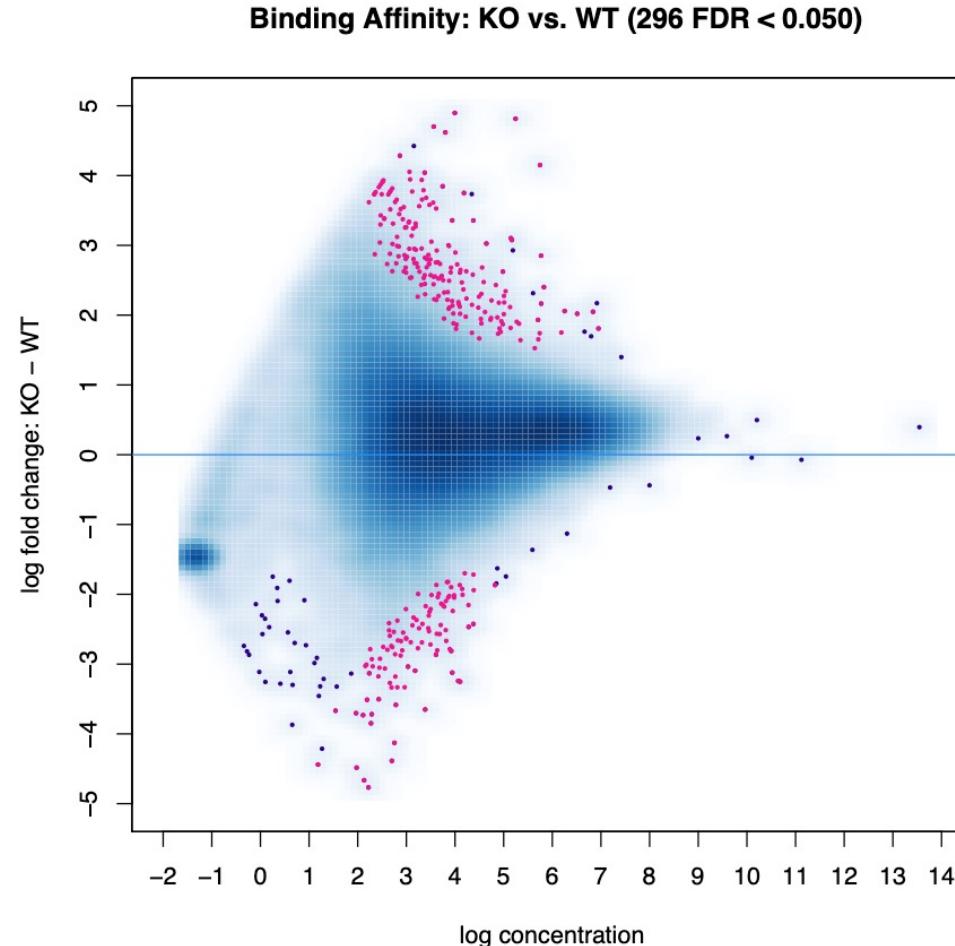
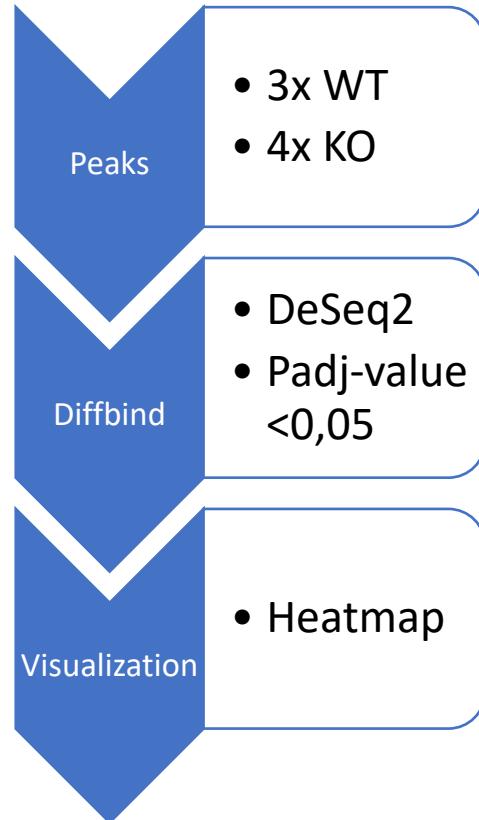
44699 peaks

28288 peaks

24902 peaks



# Differential peak analysis



More accessible in KO

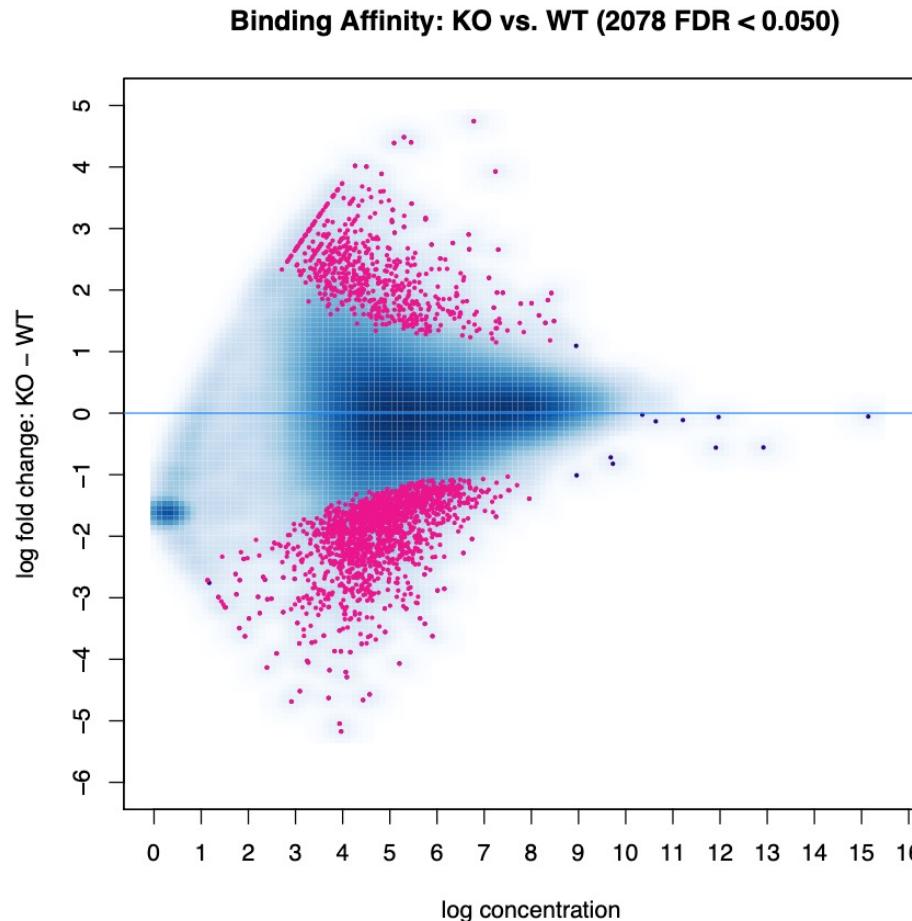
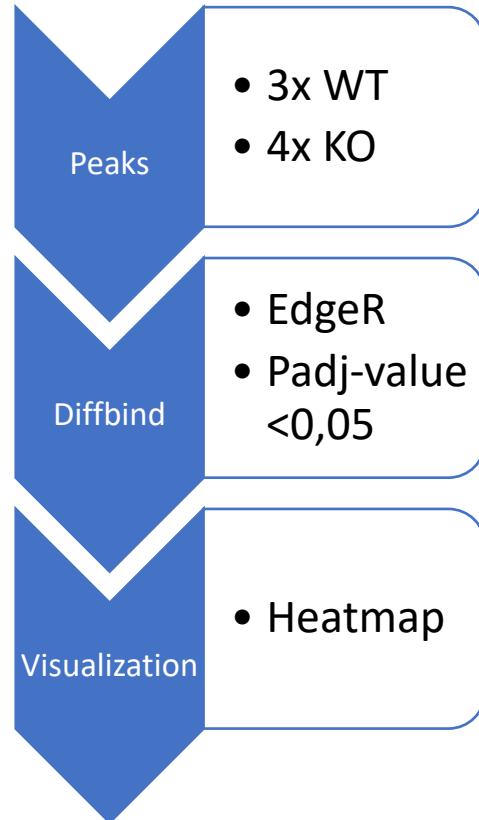
(194)

Less accessible in KO

(103)

Across 7 samples, it measured the difference of accessibility at 58465 peaks. There were found in common in at least 1 WT and 1 KO sample

# Differential peak analysis

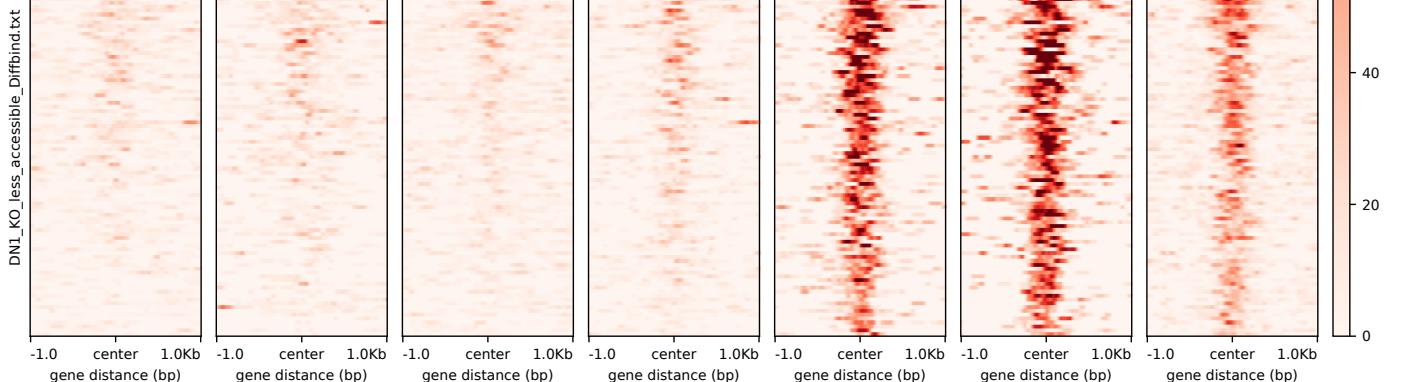


More accessible in KO

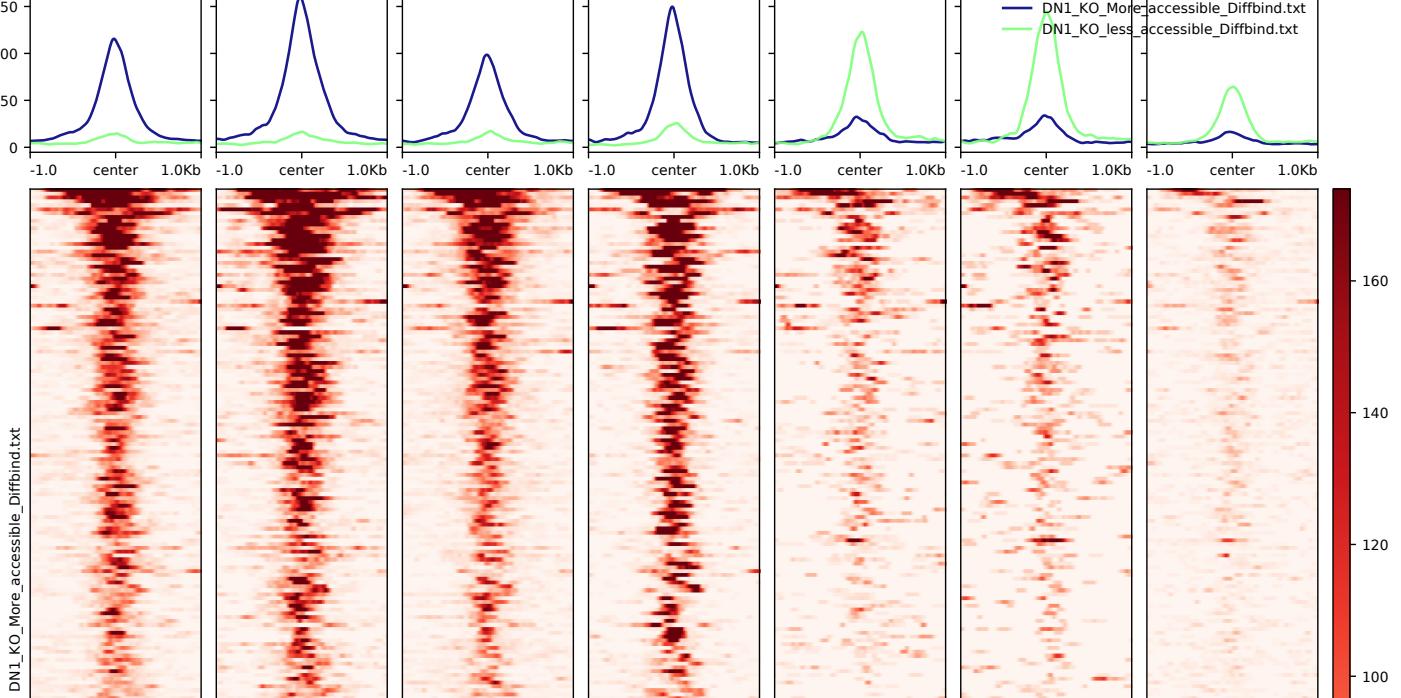
Less accessible in KO

As usual EdgeR is less constraining than DESEQ2 for differential peak analysis. We usually choose DESEQ2.

## Less accessible peaks in KO (103)



## More accessible peaks in KO (194)



Less accessible peaks seem consistent between replicates

Most peaks that are more accessible in the KO are also accessible in the WT

Most difference in accessibility between mutant and WT occur in the distal intergenic region and introns.

The differences are smaller than with the previous set of samples

103 peaks

194 peaks

44699 peaks

45832 peaks

36436 peaks

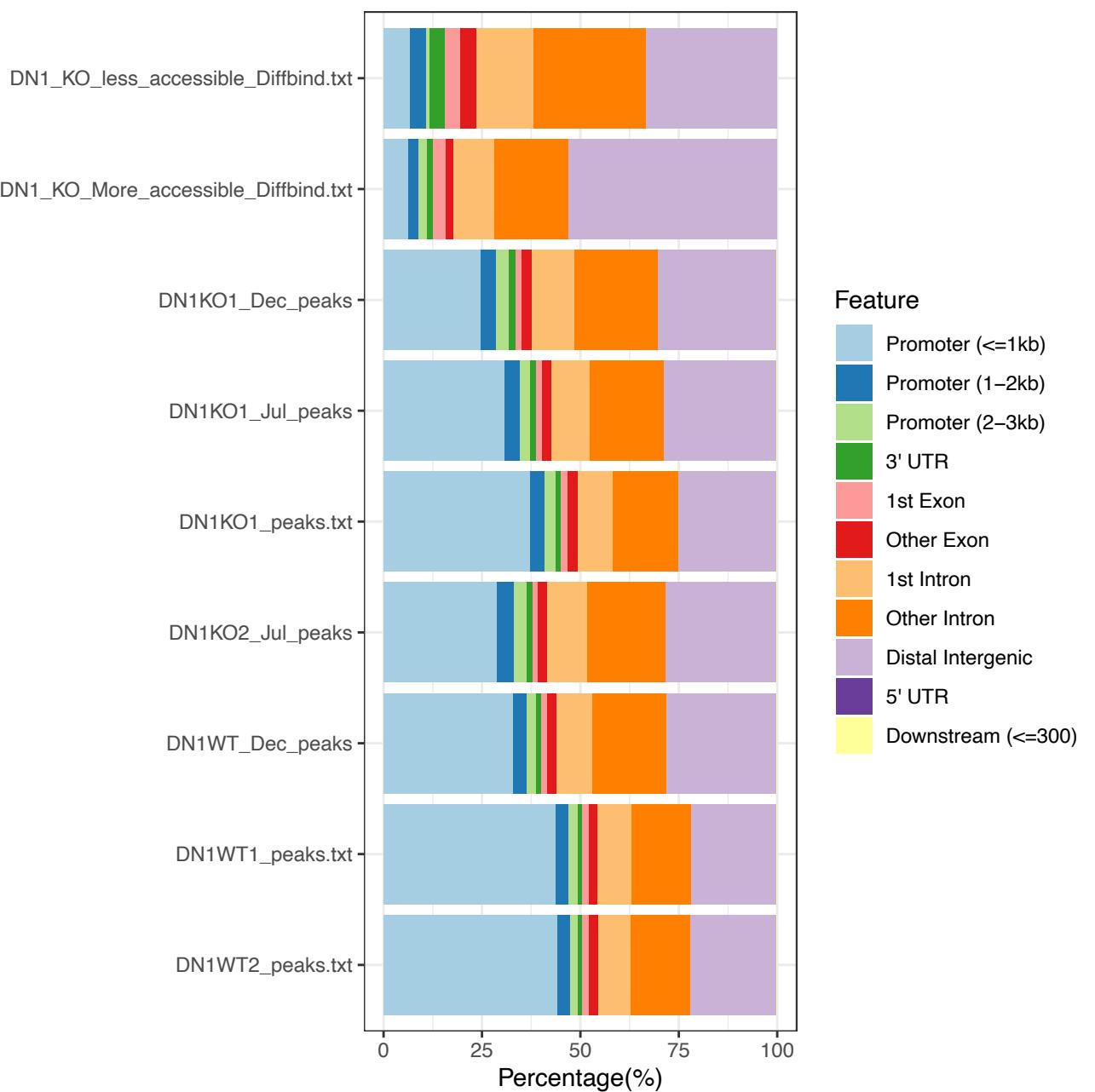
47935 peaks

44699 peaks

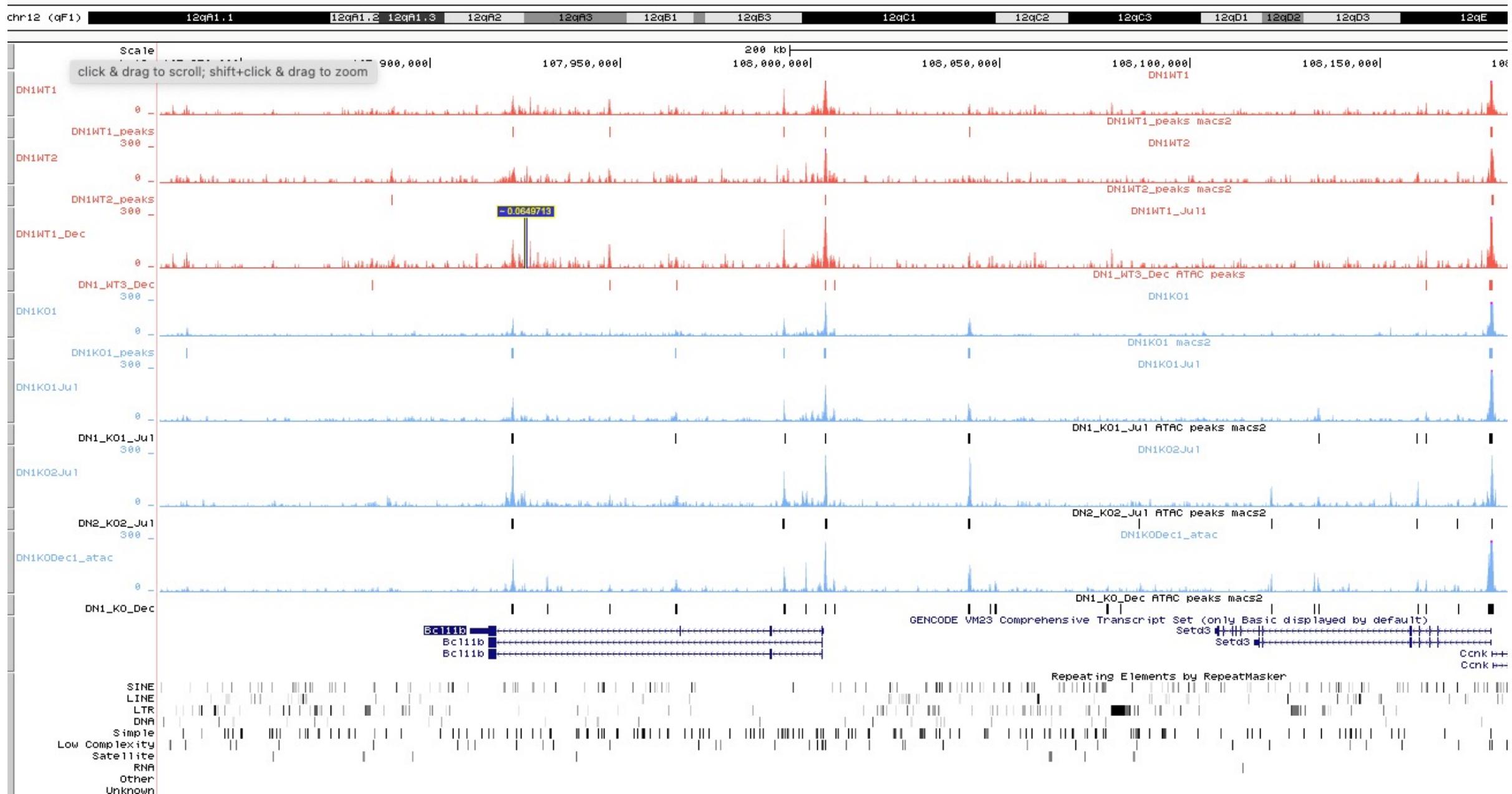
28288 peaks

24902 peaks

Feature Distribution



## *Bcl11b* possess an more accessible loci upstream of the promoter in the KO



# ATAC-seq (*Bcl11b*)

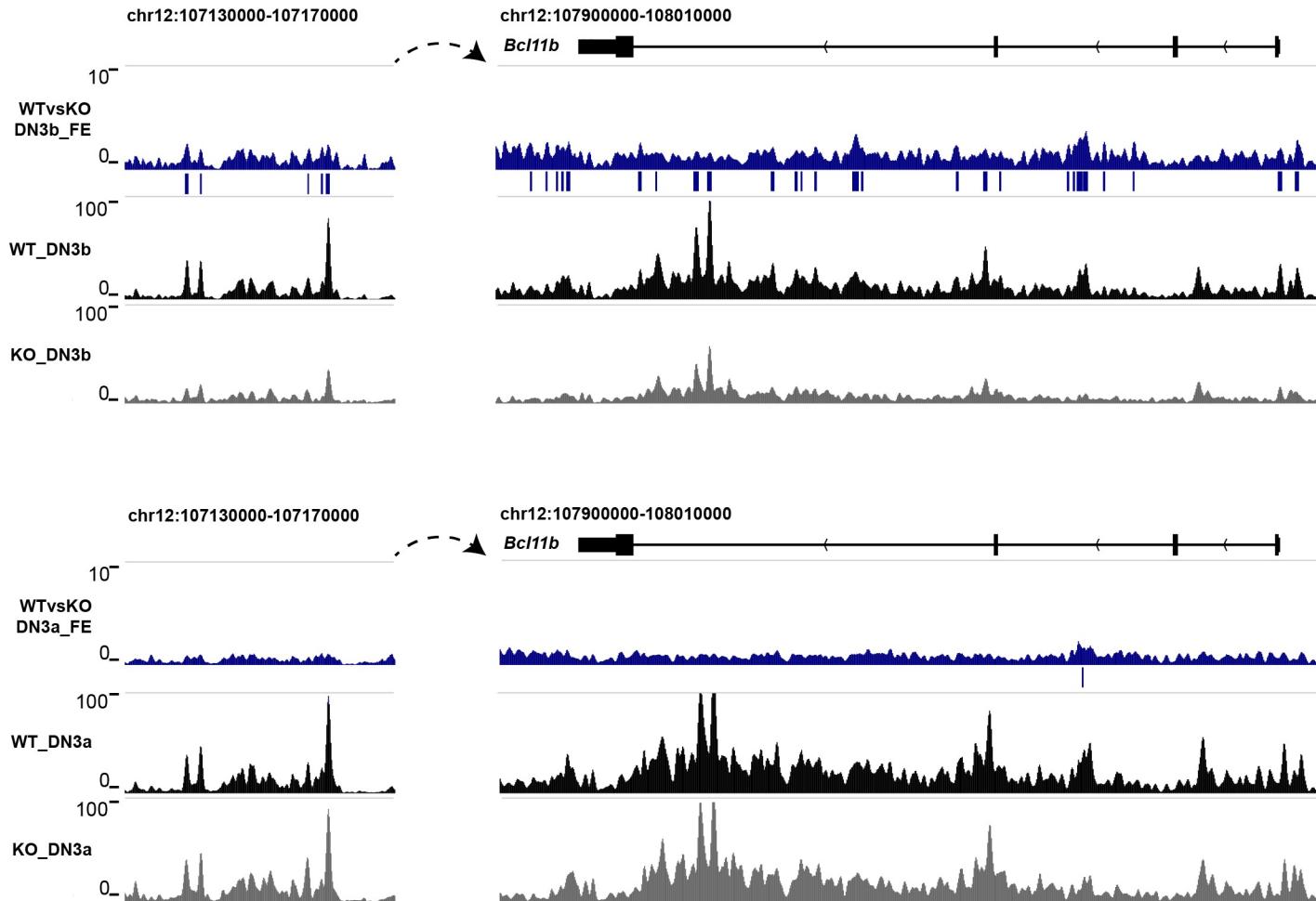
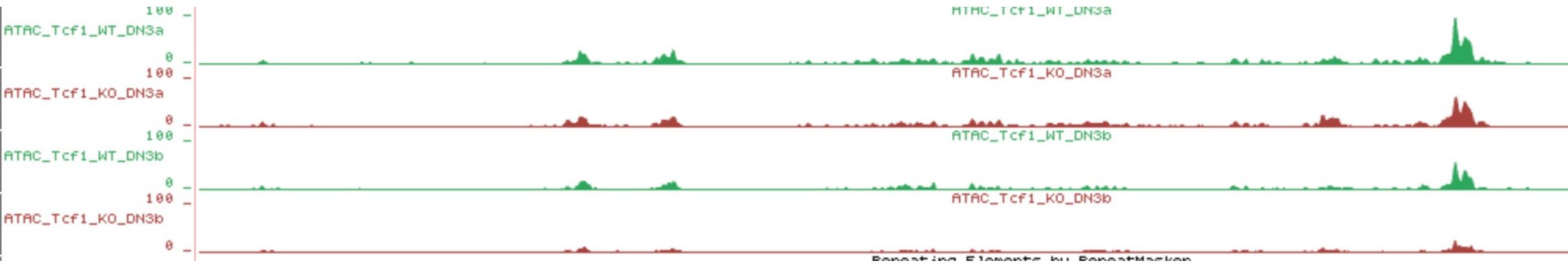


Fig: ATAC-seq tracks in *Bcl11b* gene locus and predicted enhancer which is about 800kb downstream of *Bcl11b*, black and gray tracks are from normalized combined WT and KO(DN3b on the top and DN3a at the bottom) datasets. Blue tracks shows the Fold Enrichment(FE) comparing WT to KO. Blue bars show the peaks called by MACS2 using WT against KO dataset.

More open chromatin state is found from WT DN3b compared to KO in both gene body region and predicted enhancer locus, but there is no change from DN3a.

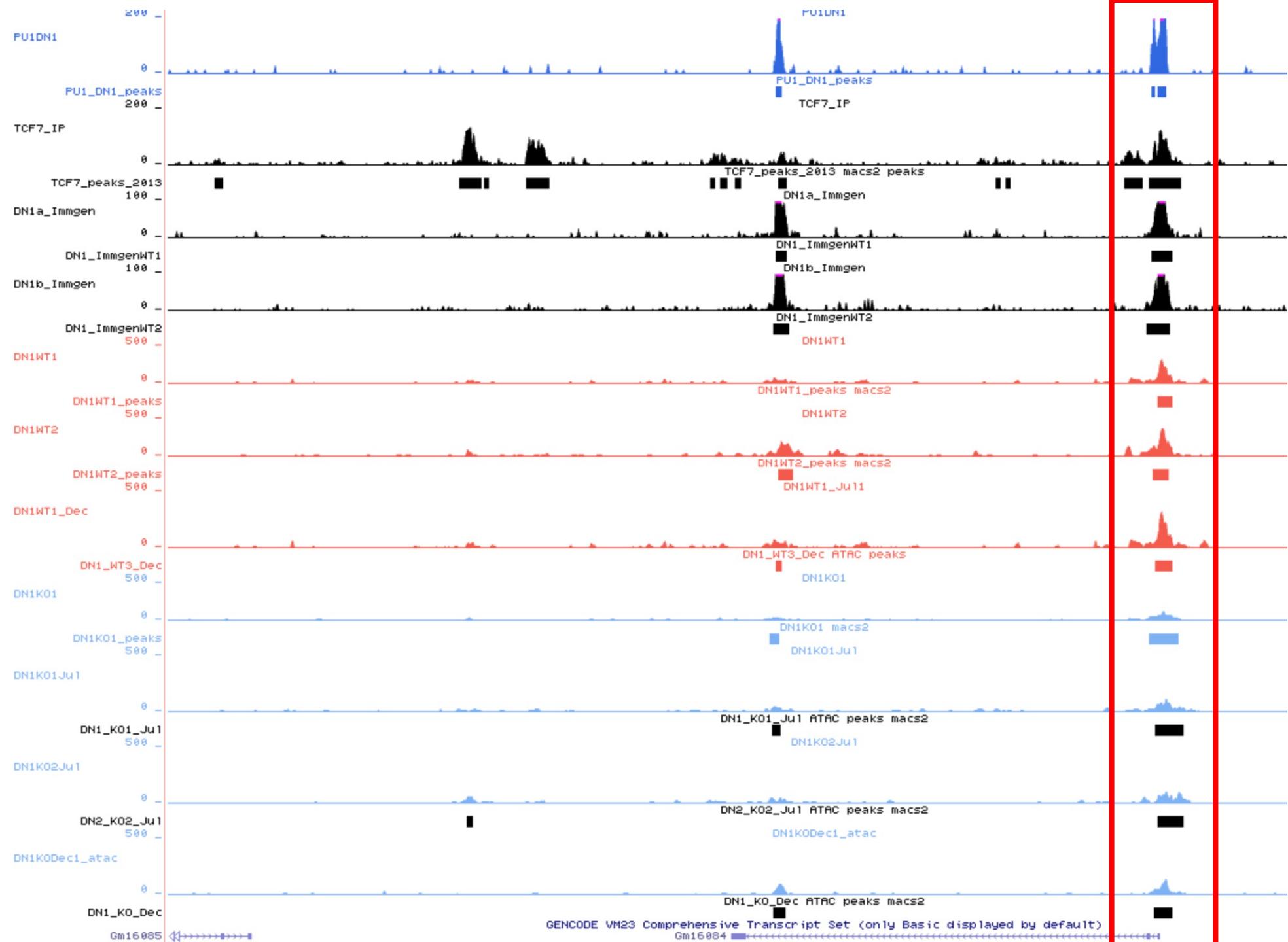
chr12:107,130,001-107,170,000



As Hoayu showed, the Bcl11b enhancer has less accessibility in Tcf1 KO at DN3b stage

The differential peak I identified using homer is not the same as the known enhancer.

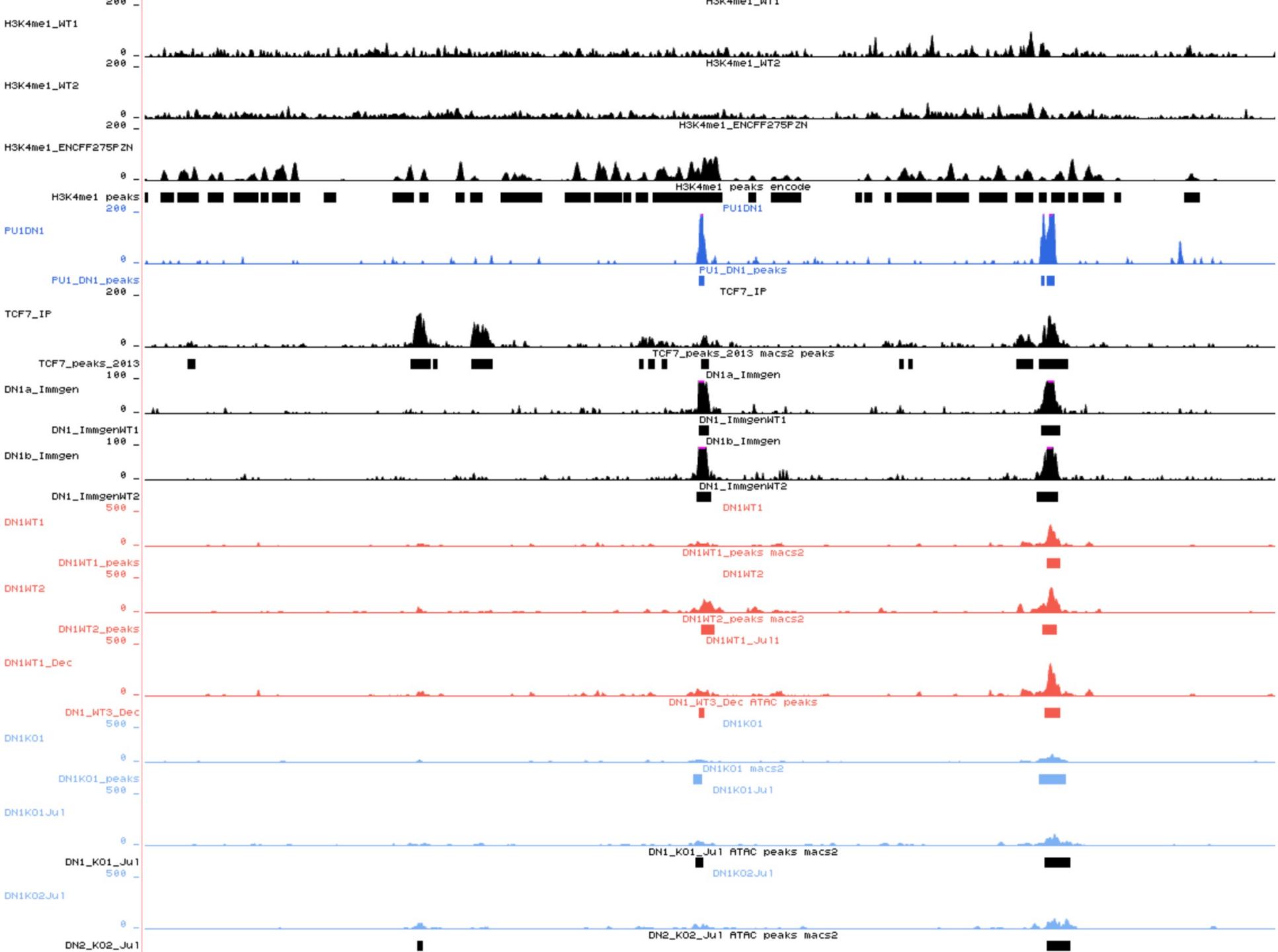
Bcl11b known enhancer  
seems to be less  
accessible at DN1 in the  
MORC3 KO samples



## H3K4me1 ChIP-seq in thymus

We do not observe a clear H3K4me1 peak at the known enhancer.

Need to produce the H3K4me1 ChIP-seq at DN1 to confirm or infirm the enhancer.



# Differential peak analysis – July samples

2xWT versus 1xKO

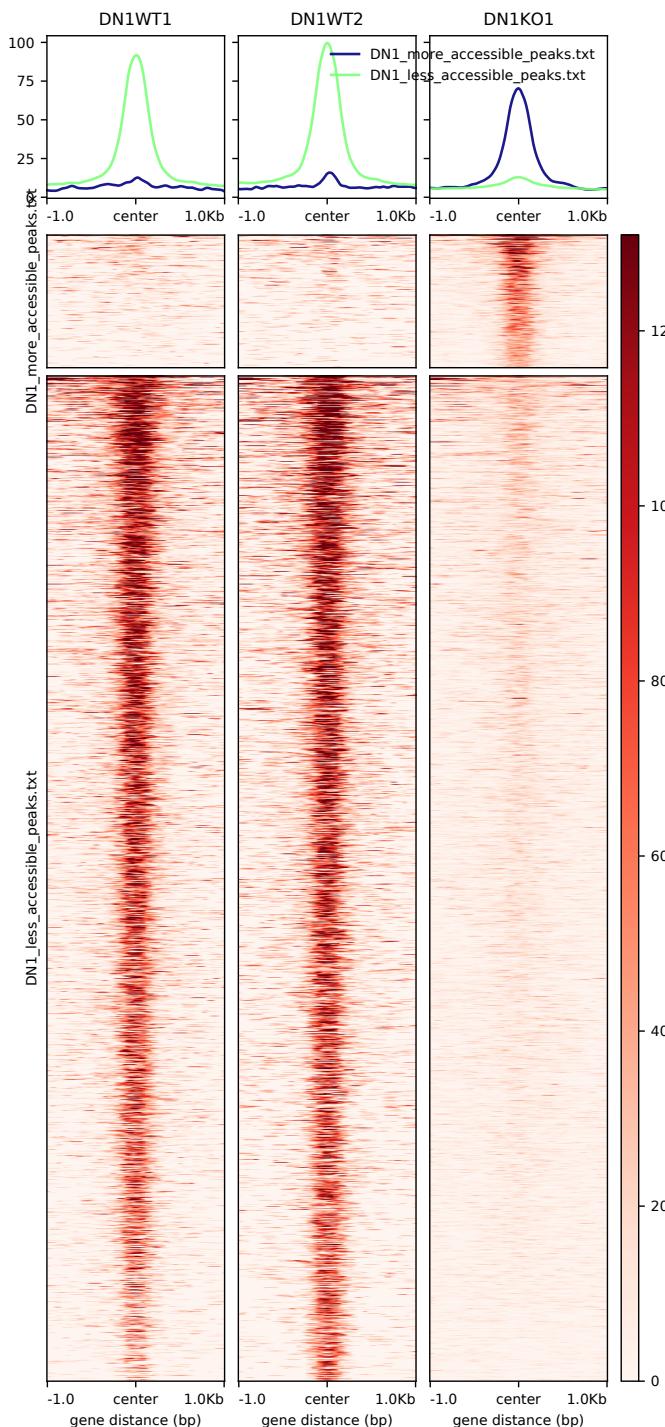
Homer `getDifferentialPeaks FC > 4 / p-value <0.05`

Relative to WT:

Less accessible in KO	2046
More accessible in KO	269

Average size less accessible peaks: 320bp  
(SD=113bp)

Average size more accessible peaks: 284bp  
(SD=145bp)



# Differential peak analysis

3xWT versus 4xKO → Merge peaks function of HOMER

How many peaks? 107610

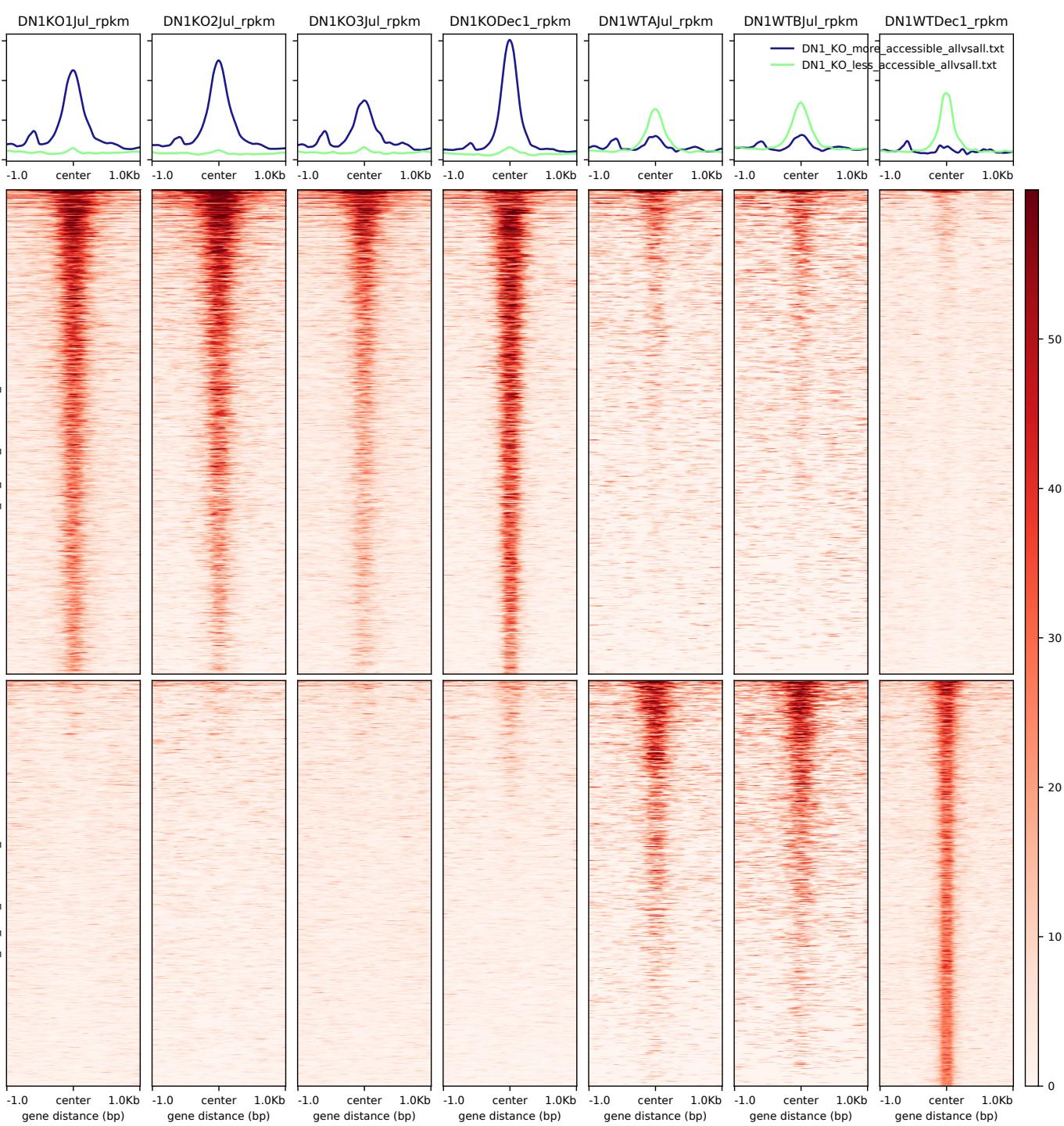
Homer getDifferentialPeaks FC > 4 / p-value <0.05

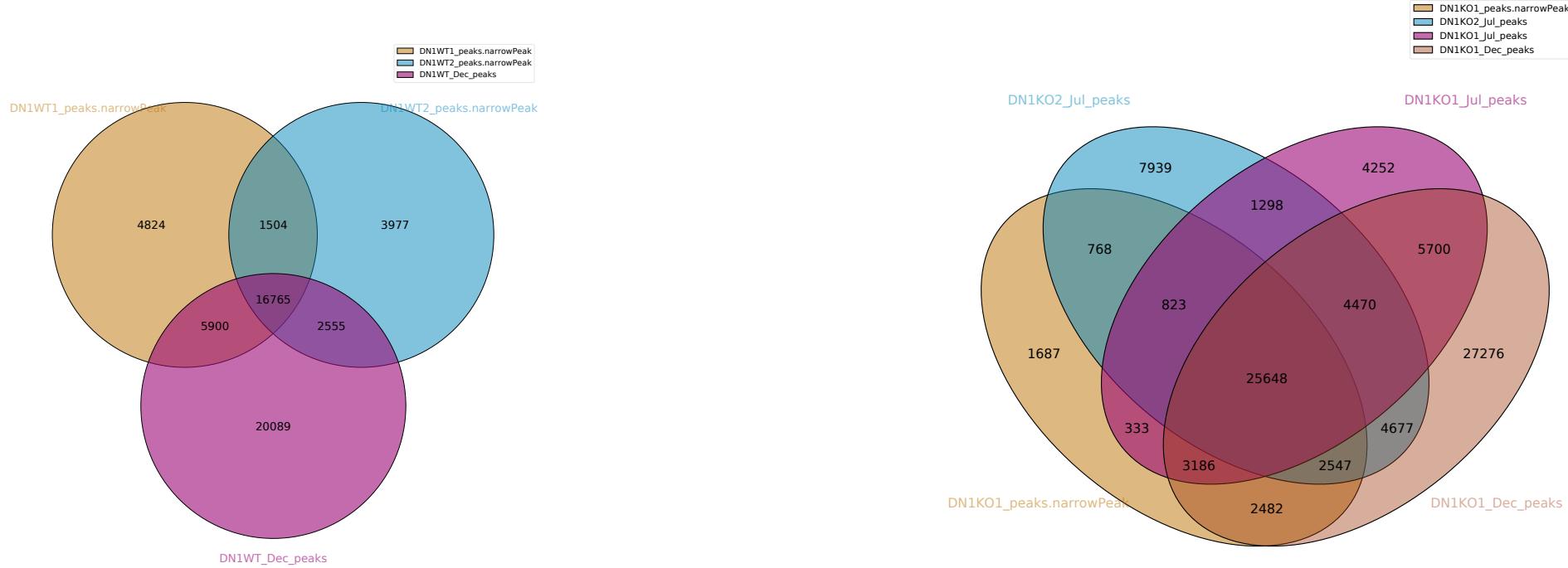
relative to WT	
Less accessible in KO	1658
More accessible in KO	1879

I should try by merging only the peaks that are consistent between the July and Dec experiment for WT and KO.

Average size less accessible peaks: 413bp  
(SD=153bp)

Average size more accessible peaks: 606bp  
(SD=272bp)





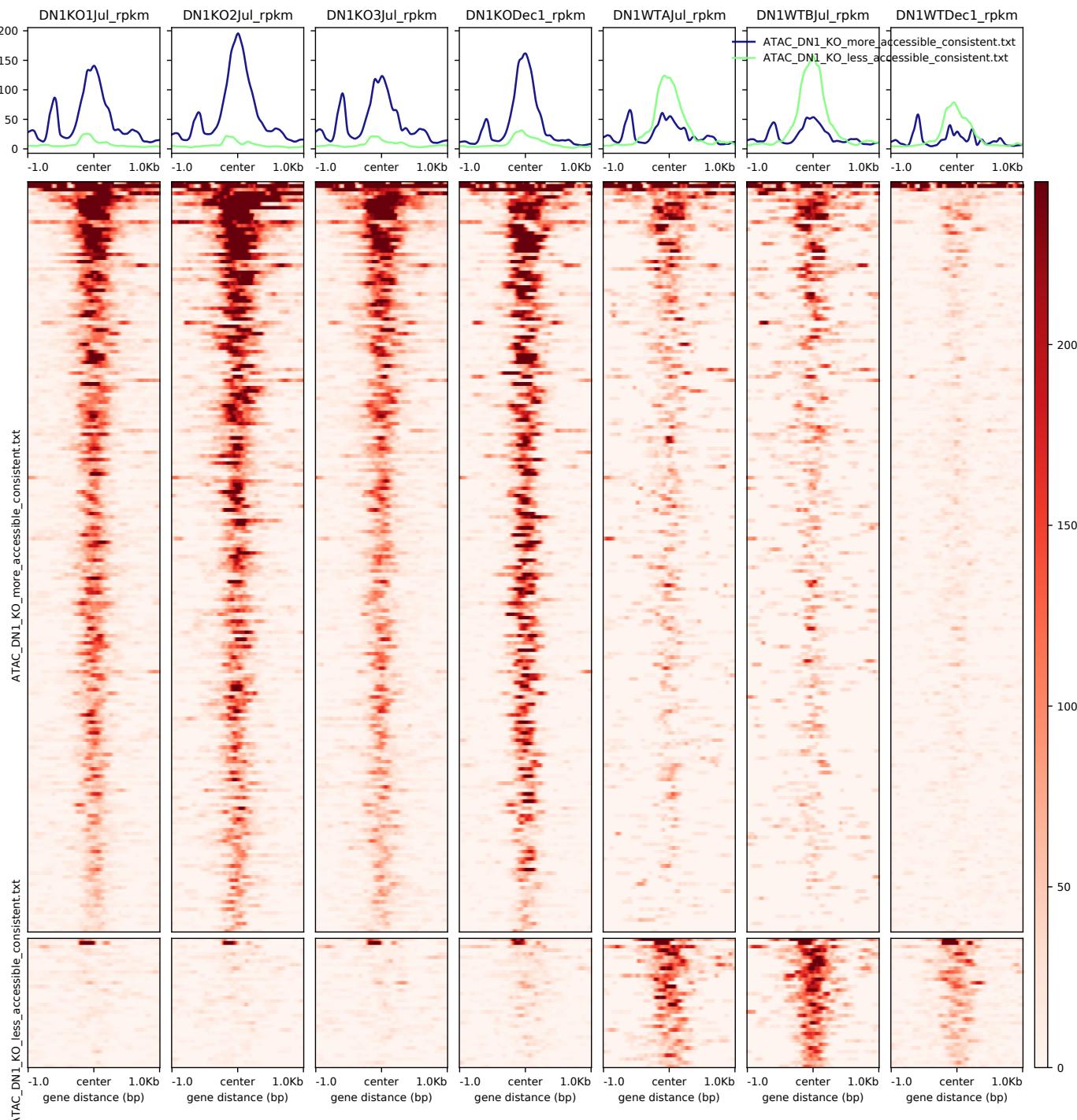
MergePeaks (found in all replicates)

Differential peaks

Less accessible in KO	36	
More accessible in KO	209	Homer consistent

**Less accessible  
peaks in KO  
(36)**

**More accessible peaks in KO  
(209)**



- How many differential peaks are overlapping between the different methods?
- What are the motifs at the differentially accessible loci?
- Accessibility at TE → Running

# Motif analysis on Diffbind all vs all

Are T-cell regulators TF motifs still present with our new set of samples?

# 1879 more accessible loci

Homer all peaks

Rank	Motif	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences with Motif	% of Targets Sequences with Motif	# Background Sequences with Motif	% of Background Sequences with Motif
1		Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-171	-3.960e+02	0.0000	805.0	40.68%	7025.8	14.72%
2		ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-170	-3.926e+02	0.0000	953.0	48.16%	9595.4	20.10%
3		ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-167	-3.847e+02	0.0000	1057.0	53.41%	11660.1	24.43%
4		Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-165	-3.822e+02	0.0000	825.0	41.69%	7517.2	15.75%
5		ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-156	-3.593e+02	0.0000	802.0	40.53%	7422.1	15.55%
6		PU.1(ETS)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	1e-155	-3.579e+02	0.0000	571.0	28.85%	3961.4	8.30%
7		SpiB(ETS)/OCILY3-SPIB-ChIP-Seq(GSE56857)/Homer	1e-154	-3.557e+02	0.0000	373.0	18.85%	1659.7	3.48%
8		Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-153	-3.539e+02	0.0000	760.0	38.40%	6802.7	14.25%
9		GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-143	-3.304e+02	0.0000	688.0	34.77%	5943.3	12.45%
10		ELF5(ETS)/T47D-ELF5-ChIP-Seq(GSE30407)/Homer	1e-135	-3.118e+02	0.0000	657.0	33.20%	5681.4	11.90%

Several ETS transcription factors (includind Pu.1) could bind to the more accessible sites.

ETS TF regulates immune development

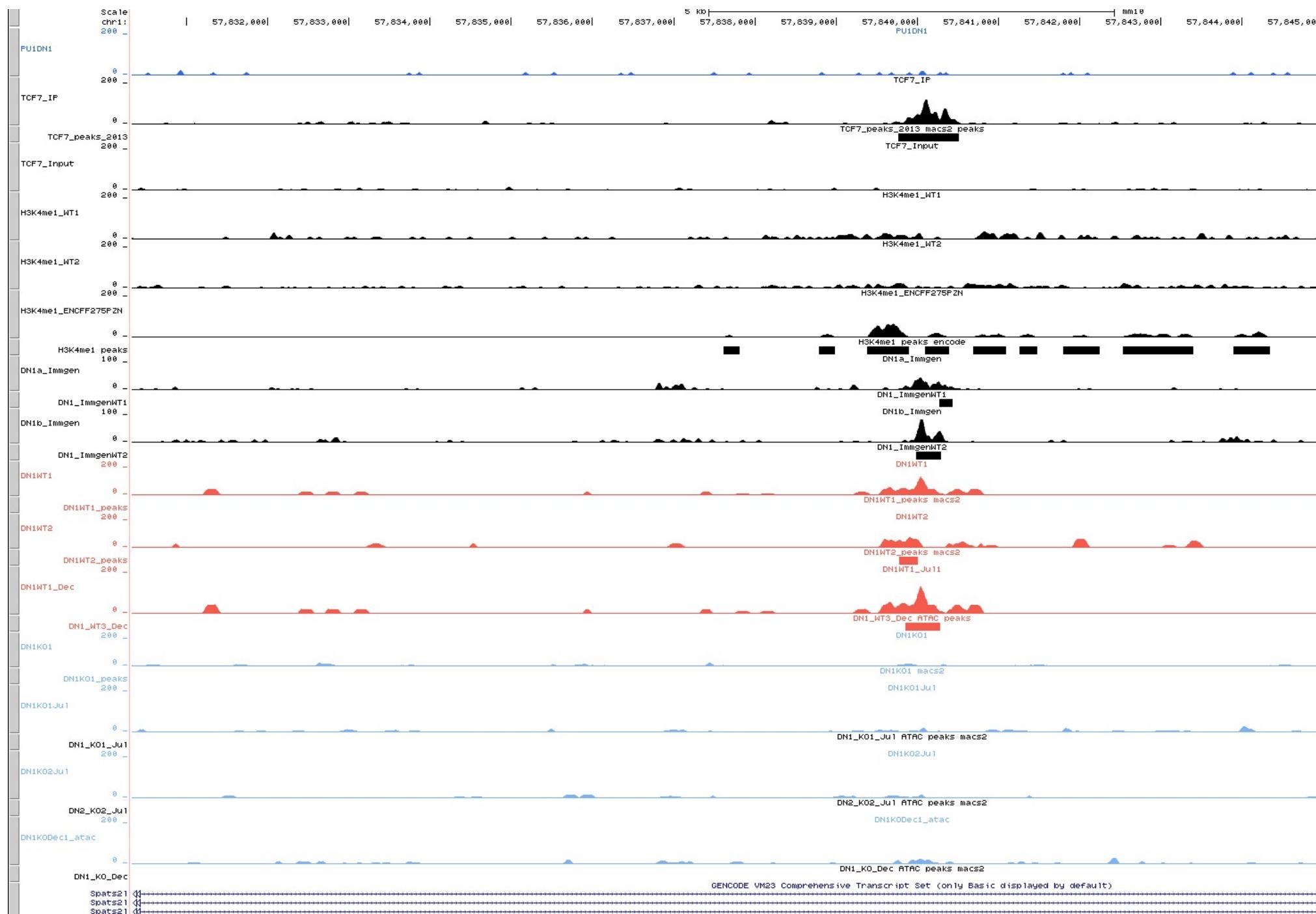
# 1658 less accessible loci

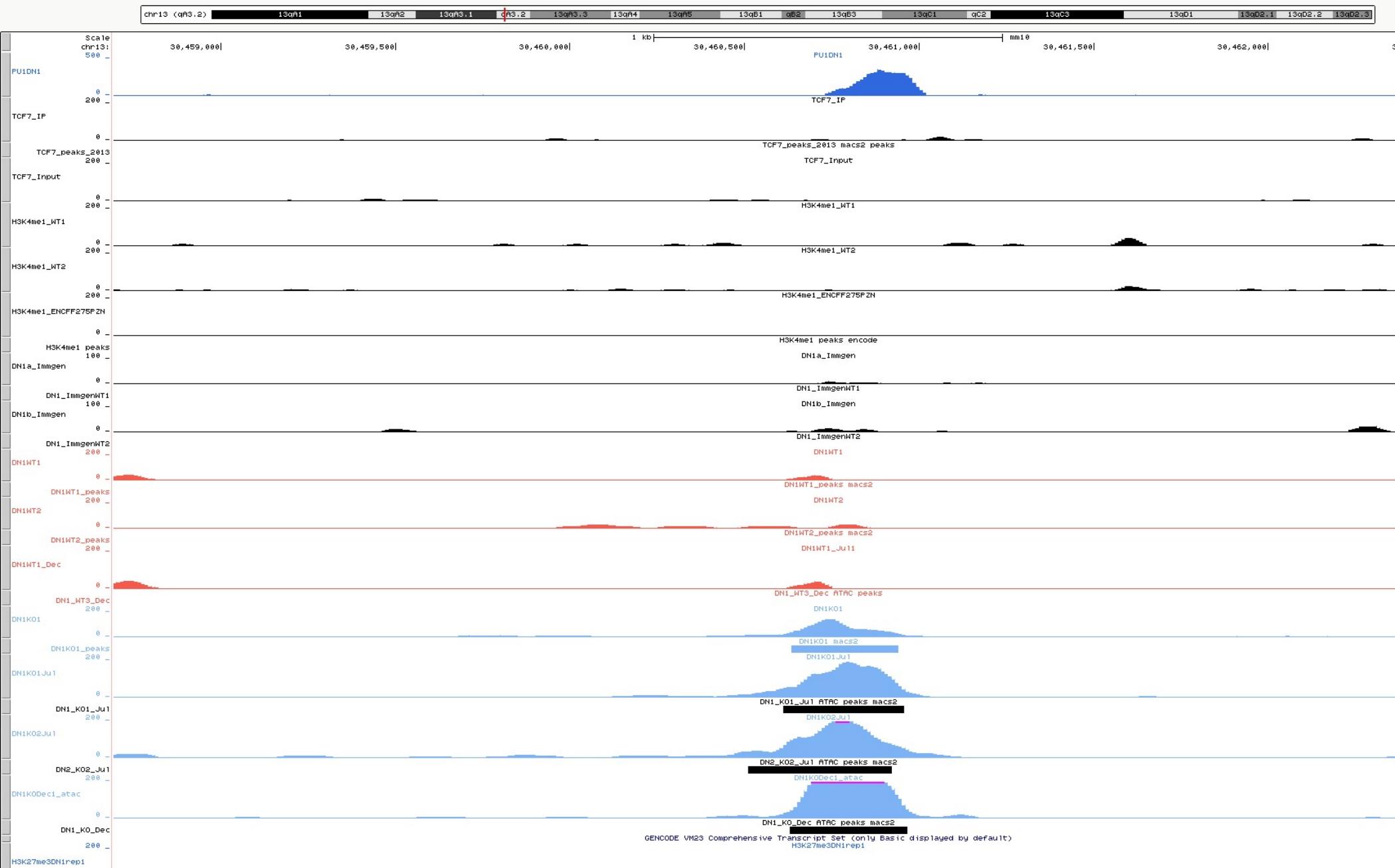
Homer all peaks

Rank	Motif	Name	P-value	log P-pvalue	q-value (Benjamini)	# Target Sequences with Motif	% of Targets Sequences with Motif	# Background Sequences with Motif	% of Background Sequences with Motif
1		RUNX-AML(Runt)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer	1e-28	-6.657e+01	0.0000	257.0	15.50%	3524.5	7.31%
2		RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer	1e-27	-6.326e+01	0.0000	289.0	17.43%	4274.2	8.87%
3		RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer	1e-24	-5.695e+01	0.0000	325.0	19.60%	5247.1	10.89%
4		RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer	1e-23	-5.399e+01	0.0000	242.0	14.60%	3534.8	7.33%
5		Tcf7(HMG)/GM12878-TCF7-ChIP-Seq(Encode)/Homer	1e-10	-2.402e+01	0.0000	97.0	5.85%	1356.4	2.81%
6		Tcf3(HMG)/mES-Tcf3-ChIP-Seq(GSE11724)/Homer	1e-9	-2.112e+01	0.0000	82.0	4.95%	1131.2	2.35%
7		E2A(bHLH)/proBcell-E2A-ChIP-Seq(GSE21978)/Homer	1e-7	-1.750e+01	0.0000	375.0	22.62%	8358.9	17.34%
8		Ascl2(bHLH)/ESC-Ascl2-ChIP-Seq(GSE97712)/Homer	1e-7	-1.736e+01	0.0000	296.0	17.85%	6325.2	13.12%
9		Ascl1(bHLH)/NeuralTubes-Ascl1-ChIP-Seq(GSE55840)/Homer	1e-6	-1.499e+01	0.0000	396.0	23.88%	9117.3	18.92%
10		ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-6	-1.460e+01	0.0000	224.0	13.51%	4689.9	9.73%

Runx and Tcf7 could bind to the less accessible sites.

Runx1 and Tcf7 are regulators of the Immune development.

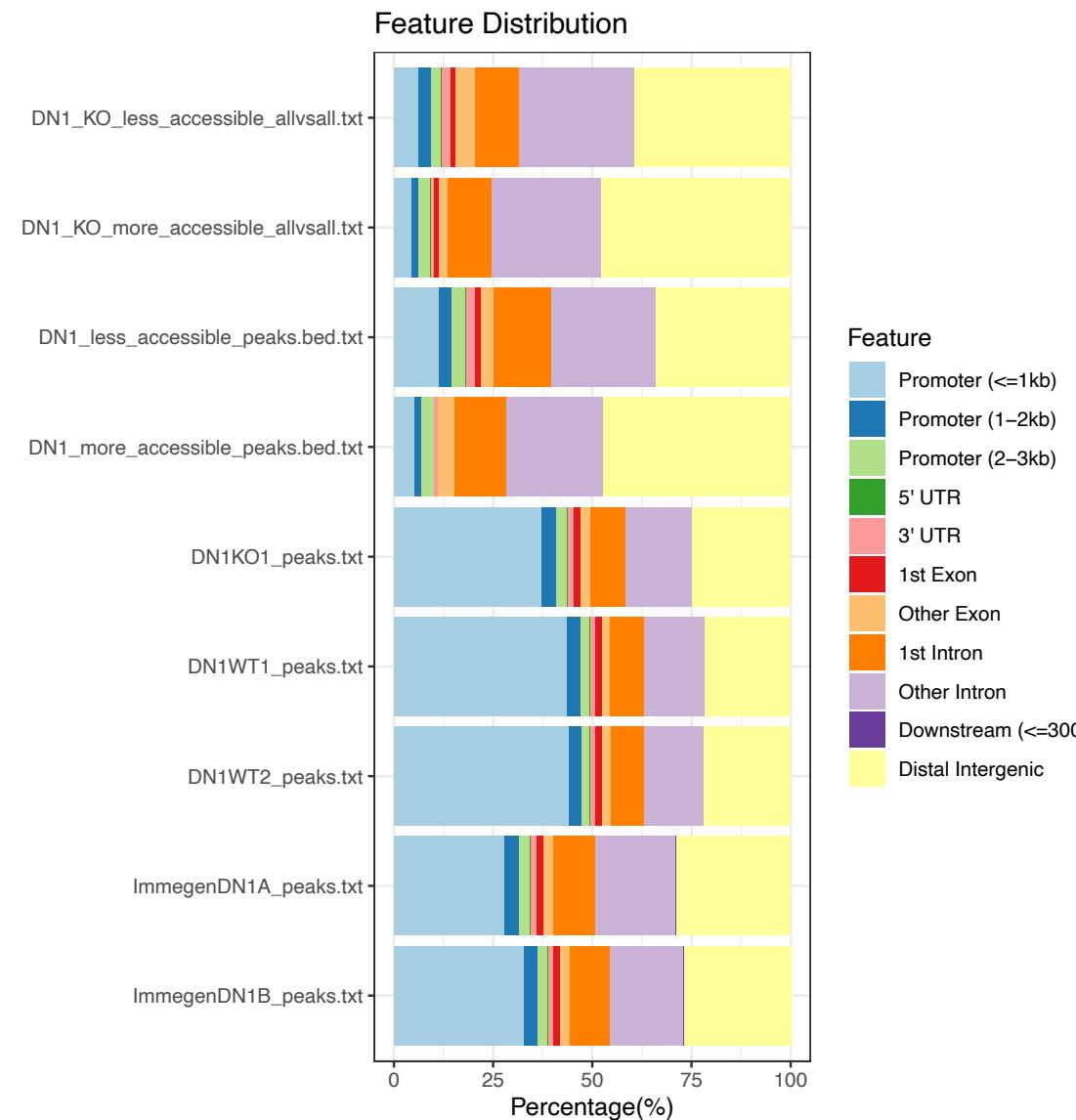




# Summary (25/01/22)

- MORC3 affects chromatin accessibility at DN1
- Accessibility is changed at immune development potential binding sites
  - What is their effect on development? → Veronica will make a summary of what
- Seems that accessibility change might affect enhancer sites (eg. *Bcl11b*)
  - We need H3K4me1 in DN1 to validate
- Is there a change in the expression of the TF regulators?
  - RNA-seq on DN1 will give us this answer.

relative to WT	
Less accessible in KO	1658
More accessible in KO	1879



# 194 more accessible loci

[Homer de novo Motif Results](#)

[Gene Ontology Enrichment Results](#)

[Known Motif Enrichment Results \(txt file\)](#)

Total Target Sequences = 193, Total Background Sequences = 49505

Rank	Motif	Name	P-value	log P-pvalue	q-value (Benjamini)	# Target Sequences with Motif	% of Targets Sequences with Motif	# Background Sequences with Motif	% of Background Sequences with Motif
1		Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-25	-5.862e+01	0.0000	121.0	62.69%	13029.7	26.32%
2		ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-22	-5.285e+01	0.0000	118.0	61.14%	13204.0	26.67%
3		PU.1(ETS)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	1e-21	-4.912e+01	0.0000	83.0	43.01%	7080.3	14.30%
4		Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-20	-4.780e+01	0.0000	109.0	56.48%	12061.9	24.36%
5		RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer	1e-20	-4.668e+01	0.0000	100.0	51.81%	10429.4	21.06%
6		GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-20	-4.630e+01	0.0000	102.0	52.85%	10872.8	21.96%
7		ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-19	-4.502e+01	0.0000	112.0	58.03%	13109.1	26.48%
8		ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-19	-4.462e+01	0.0000	130.0	67.36%	17256.2	34.85%
9		ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-19	-4.429e+01	0.0000	140.0	72.54%	19820.5	40.03%
10		RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer	1e-19	-4.415e+01	0.0000	121.0	62.69%	15231.2	30.76%

# 103 less accessible loci

[Homer de novo Motif Results](#)

[Gene Ontology Enrichment Results](#)

[Known Motif Enrichment Results \(txt file\)](#)

Total Target Sequences = 103, Total Background Sequences = 48408

Rank	Motif	Name	P-value	log P-pvalue	q-value (Benjamini)	# Target Sequences with Motif	% of Targets Sequences with Motif	# Background Sequences with Motif	% of Background Sequences with Motif
1		RUNX-AML(Runt)/CD4+PolII-ChIP-Seq(Barski_et_al.)/Homer	1e-20	-4.796e+01	0.0000	60.0	58.25%	8035.8	16.60%
2		RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer	1e-19	-4.538e+01	0.0000	63.0	61.17%	9412.9	19.44%
3		RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer	1e-17	-4.072e+01	0.0000	55.0	53.40%	7688.2	15.88%
4		RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer	1e-16	-3.778e+01	0.0000	64.0	62.14%	11233.3	23.20%
5		Tcf7(HMG)/GM12878-TCF7-ChIP-Seq(Encode)/Homer	1e-13	-3.081e+01	0.0000	30.0	29.13%	2716.0	5.61%
6		Tcf4(HMG)/Hct116-Tcf4-ChIP-Seq(SRA012054)/Homer	1e-10	-2.414e+01	0.0000	31.0	30.10%	3782.1	7.81%
7		Tcf3(HMG)/mES-Tcf3-ChIP-Seq(GSE11724)/Homer	1e-9	-2.254e+01	0.0000	23.0	22.33%	2175.6	4.49%
8		Ascl1(bHLH)/NeuralTubes-Ascl1-ChIP-Seq(GSE55840)/Homer	1e-9	-2.209e+01	0.0000	73.0	70.87%	19411.1	40.09%
9		LEF1(HMG)/H1-LEF1-ChIP-Seq(GSE64758)/Homer	1e-9	-2.122e+01	0.0000	35.0	33.98%	5360.9	11.07%
10		E2A(bHLH)/proBcell-E2A-ChIP-Seq(GSE21978)/Homer	1e-8	-1.860e+01	0.0000	67.0	65.05%	17963.7	37.10%

# Motifs identified homer differentially accessible loci – consistent peaks

Less accessible in KO	36
More accessible in KO	209

Homer consistent

> Proc Natl Acad Sci U S A. 2011 Dec 13;108(50):20060-5. doi: 10.1073/pnas.1110230108.  
Epub 2011 Nov 22.

## T-cell factor 1 is a gatekeeper for T-cell specification in response to Notch signaling

Kristine Germar<sup>1</sup>, Marei Dose, Tassos Konstantinou, Jiangwen Zhang, Hongfang Wang,  
Camille Lobry, Kelly L Arnett, Stephen C Blacklow, Iannis Aifantis, Jon C Aster, Fotini Gounari

Affiliations + expand

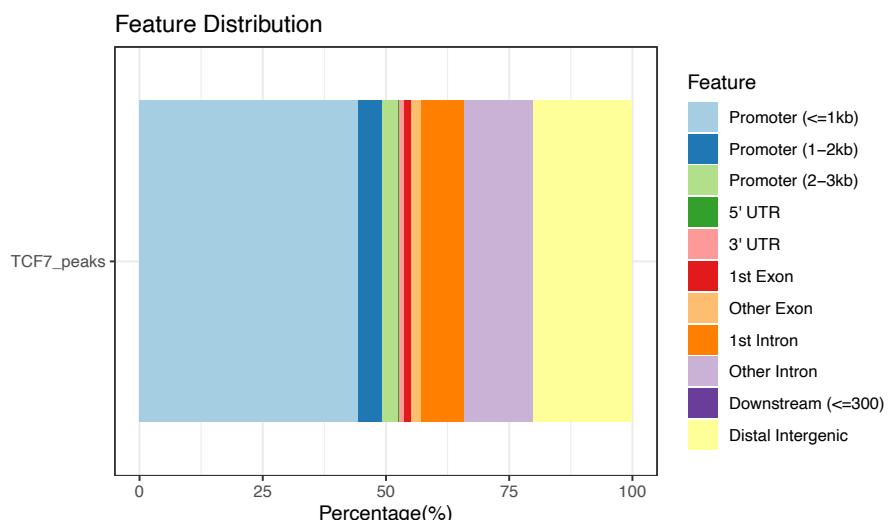
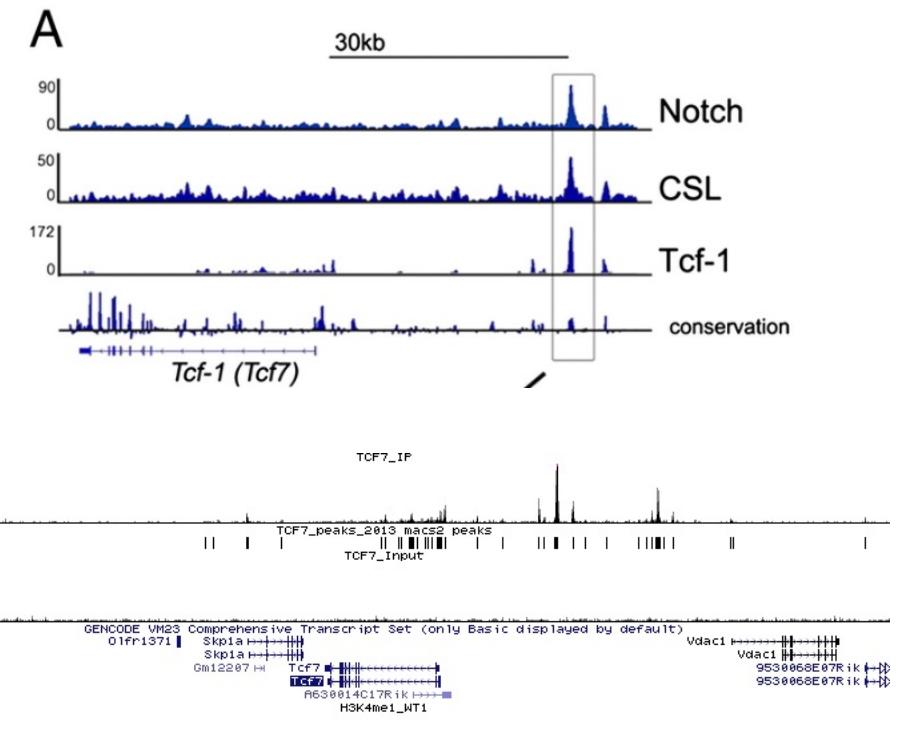
PMID: 22109558 PMCID: PMC3250146 DOI: 10.1073/pnas.1110230108

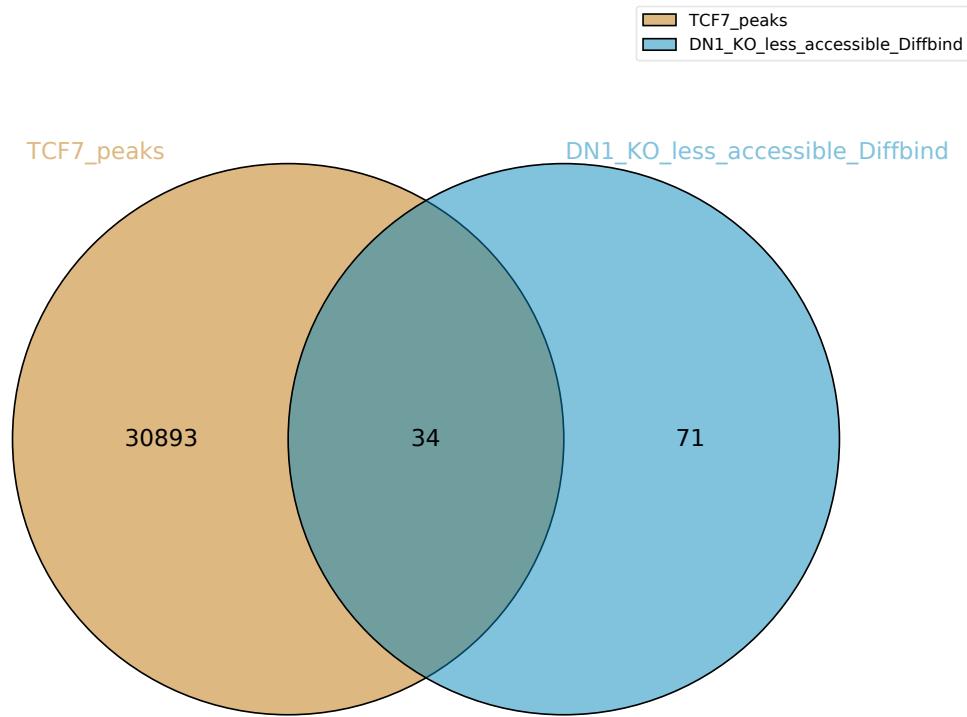
Free PMC article

ChIP	peaks
TCF7	30527

ChIP performed on primary thymocytes

Has an input sample to normalize

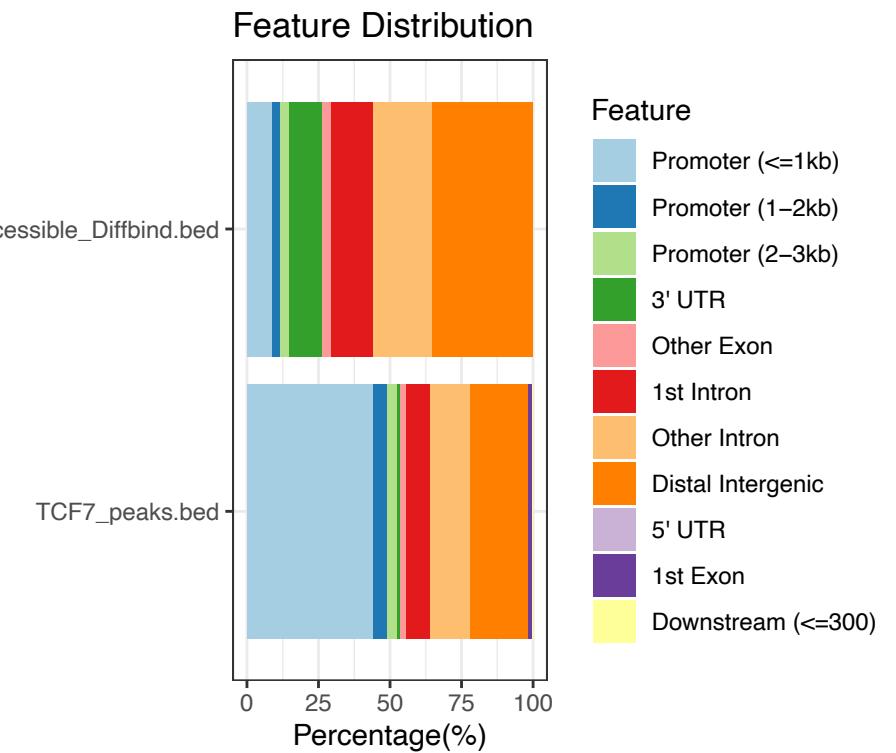




The 34 loci that show less accessibility in MORC3-/-, where TCF7 binds, are mainly intron-distal intergenic region?

Are they enhancers?  
TCF7 and H3K4me1 are from another tissue.

11\_TCF7\_peaks\_DN1\_KO\_less\_accessible\_Diffbind.bed



An example of the overlap between TCF7 ChIP-seq and DAL (less accessible)

