ChIP-seq data analysis

1.1 Reads downloading

I used Dataset #3 that contains
Yng (H3K27me3/Input) and **Old** (H3K27me3/Input) samples

They corresponding SRA ids are as follows:
SRR6116838, SRR6116863, SRR6116844, SRR6116875

I downloaded `.fastq` files in the `~/chipseq/fastq` using `fastq-dump` tool from `sra-toolkit`, which is installed in `meth` conda environment on the machine.

`~/chipseq/fastq`
`fastq-dump >>> .fastq`

```
#####################################################################
#1. Download fastq
sra_ids="SRR6116838 SRR6116863 SRR6116844 SRR6116875"

mkdir -p fastq
cd fastq

conda activate meth
for sra_id in ${sra_ids}; do
    echo "${sra_id}"
    fastq-dump --gzip ${sra_id}
done
conda deactivate
```

1.2 Reads downsampling

H3K27me3 is a broad mark,

Broad Marks	H3F3A	H3K27me3	H3K36me3	H3K4me1	H3K79me2	H3K79me3	H3K9me1	H3K9me2	H4K20me1
Narrow Marks	H2AFZ	H3ac	H3K27ac	H3K4me2	H3K4me3	H3K9ac			
Exceptions	H3K9me3								

and for broad-peak histone experiments each replicate should have at least 45 million usable fragments (size recommended for the ChIP-seq type from Encode guidelines)

So I set `K=45000000` and obtain **`_45000000.fastq`** in the **`~/chipseq/fastq`** folder

`~/chipseq/fastq`

`awk >>> _45000000.fastq`

```
#####################################################################
#1.2 Downsample fastq

K=45000000

for sra_id in $sra_ids
do
    INPUT="${sra_id}.fastq.gz"
    OUTPUT="${sra_id}_${K}.fastq.gz"

    zcat "$INPUT" | awk '{ printf("%s",$0); n++; if(n%4==0) {printf("\n");} else {
printf("\t");} }' | \
    awk -v k=$K 'BEGIN{srand(systime() +
PROCINFO["pid"]);}{s=x++<k?x-1:int(rand()*x);if(s<k)R[s]=$0} END{for(i in R)print
R[i]}' | \
    awk -F"\t" '{print $1"\n"$2"\n"$3"\n"$4}' | gzip - > "$OUTPUT"

    echo "Processed $INPUT and saved to $OUTPUT"
done

find /home/user/chipseq/fastq -name '*.gz' -exec gunzip {} \;
```

2 Reads QC

I prepared reads QC using `fastqc` and summarize results with `multiqc`.

```
~/chipseq/fastqc
fastqc >>> _fastqc.html + _fastqc.zip + _fastqc.log
multiqc >>> multiqc_report.html
```

```
######################################################################
#2 Reads QC

mkdir -p ~/chipseq/fastqc
conda activate chipseq

for FILE in $(find /home/user/chipseq/fastq -name '*.f*q')
do :
 FILE_NAME=${FILE##*/}
 NAME=${FILE_NAME%%.f*q} # file name without extension
 fastqc --outdir ~/chipseq/fastqc "${FILE}" 2>&1 | tee ${NAME}_fastqc.log
done
mv ~/chipseq/fastq/*_fastqc.log ~/chipseq/fastqc/

multiqc -f -o ~/chipseq/fastqc ~/chipseq/fastqc
```

2 Reads QC

1. Per base sequence quality shows appropriate results - quality at all positions in a green zone.

2. Per sequence quality score also shows good results with one peak near 30-39

3. Per base sequence content also good, small fluctuations at the start probably corresponds to 10-12 bases result from non fully random priming during library preparation.

4. Per base sequence GC content - mean values are around 41, that is equal mean human GC content, but reads not fully random distributed and a little peak arises on each plot. In bad case it could be contamination or maybe it relates with library preparation/downsampling.

5. Sequence duplication level shows a little peak near >10. I assume that possible reasons for it is many cycles of PCR amplification/too little starting material/downsampling consequences

3 Reads alignment

Reads were aligned using bowtie (`.sam files` + `_bowtie.log`), then using `samtools view` and `sort` binary files were created (`.bam files`) and saved in `~/chipseq/bam`

~/chipseq/bam

bowtie >>> .sam + **_bowtie.log**
samtools view >>> _not_sorted.bam
samtools sort >>> **.bam**

```
######################################################################
#3. Reads alignment

GENOME=hg19
export BOWTIE_INDEXES=/mnt/chipseq/index/${GENOME}/
for FILE in $(find ~/chipseq/fastq -name '*.f*q')
do :
 NAME=$(basename ${FILE%%.fastq})
 ID=${NAME}_${GENOME}
 BAM_NAME="${ID}.bam"
 if [[ ! -f "${BAM_NAME}" ]]; then
   bowtie -p 6 -St -m 1 -v 3 --best --strata ${GENOME} ${FILE} ${ID}.sam 2>&1 |\
      tee ${NAME}_bowtie.log
   samtools view -bS ${ID}.sam -o ${ID}_not_sorted.bam
   samtools sort ${ID}_not_sorted.bam -o ${BAM_NAME}
   rm ${ID}.sam ${ID}_not_sorted.bam
 fi
done

mkdir -p ~/chipseq/bam
mv ~/chipseq/fastq/*.bam ~/chipseq/bam/
mv ~/chipseq/fastq/*_bowtie.log ~/chipseq/bam/
```

4 Reads alignment QC

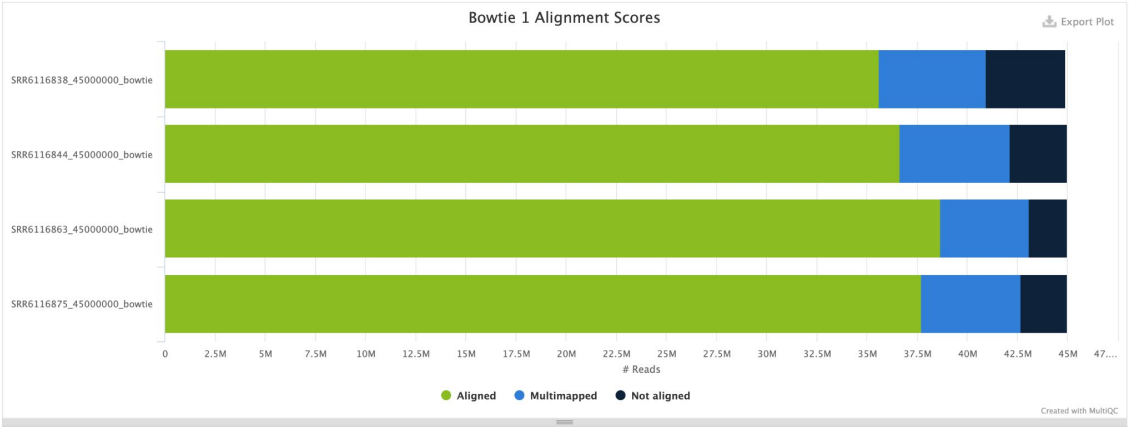
Common alignment QC were aggregated with `multiqc` as in previous case.

```
~/chipseq/bams_qc
multiqc >>> multiqc_report.html
```

```
######################################################################
#4 Reads alignment QC

multiqc -f -o ~/chipseq/bams_qc ~/chipseq/bam/*_bowtie.log
```

4 Reads alignment QC

Majority of reads were successfully aligned, ~10% of reads were multimapped and ~5% was not aligned at all. I assume that it is appropriate result and we can proceed.



5 Coverage

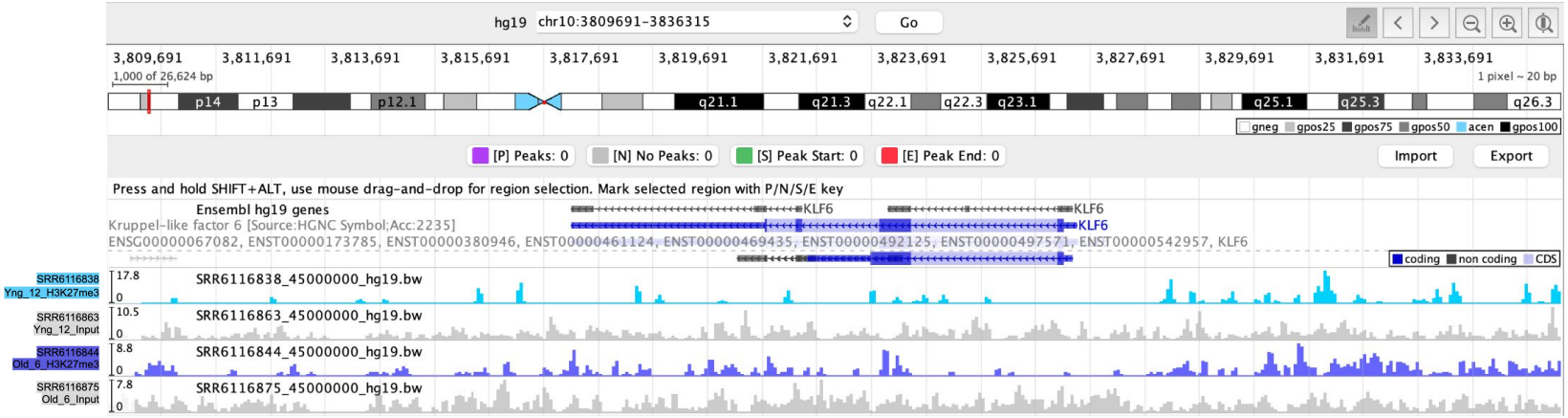
Coverage `.bw` files were prepared using `bamCoverage` and saved in `~/chipseq/bw`. Now we can explore them in genome browser.

`~/chipseq/bw`

`bamCoverage >>> .bw + _bw.log`

```
#####################################################################
#5 Coverage

for FILE in $(find ~/chipseq/bam -name '*.bam')
do :
   NAME=$(basename ${FILE%%.bam})
   BW=${NAME}.bw
   if [[ ! -f ${BW} ]]; then
       samtools index ${FILE}
       bamCoverage --bam ${FILE} -o ${BW} 2>&1 | tee ${NAME}_bw.log
   fi
done

mkdir ~/chipseq/bw
mv ~/chipseq/fastq/*.bw ~/chipseq/bw
mv ~/chipseq/fastq/*_bw.log ~/chipseq/bw
```

6 Analyze coverage profile



I've loaded results in JBR browser so now we can see Yng and Old samples with corresponding Inputs. We know in advance that H3K27me3 is a broad mark so list of possible tools is: MACS2 in broad option (but in general MACS2 is not so good for broad marks), SICER that is especially useful in this case and SPAN. Due to problems with SICER launching I decided at least do analysis using MACS2_broad and SPAN. Also just out of curiosity I repeat analysis with MACS2 in narrow peaks regimen. Honestly it is not easy to conclude unambiguously that profiles contains broad peaks only. It seems like some positions rather contains narrow peaks so I wanted to check how MACS will work with them.

So my final list if MACS2, MACS2_broad and SPAN.

However in original article MACS2 broad peak calling was used for H3K27me3 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7080409/)

7 Peak calling (MACS2)

Peak calling was done using
-MACS in narrow regimen,
-MACS in broad regimen,
-SPAN

Each tool was launched twice for Yng and Old samples

~/chipseq/macs2

macs2 >>> **.narrowPeak** + **_macs2.log**

```
######################################################################
#7 Peak calling
#7.1 MACS Narrow
SUFFIX="q0.05"
PARAMS="-q 0.05"

# Yng
INPUT=~/chipseq/bam/SRR6116863_45000000_hg19.bam
FILE=~/chipseq/bam/SRR6116838_45000000_hg19.bam
# Old
INPUT=~/chipseq/bam/SRR6116875_45000000_hg19.bam
FILE=~/chipseq/bam/SRR6116844_45000000_hg19.bam

NAME=$(basename ${FILE%%.bam})  # File name without extension
ID=${NAME}_${SUFFIX}
if [[ -z $(find . -name "${ID}*.*Peak") ]]; then  # Peaks file is not created yet
    TMP_DIR=$(mktemp -d macs2.XXXXXXXX)
    mkdir -p ${TMP_DIR}
    echo "Macs2 TMP_DIR: ${TMP_DIR}"
        macs2 callpeak --tempdir ${TMP_DIR} -t ${FILE} -c ${INPUT} -f BAM -g hs -n
${ID} ${PARAMS} 2>&1 |\
            tee ${ID}_macs2.log
    # Cleanup
    rm -rf ${TMP_DIR}
fi
```

7 Peak calling (MACS2_broad)

Peak calling was done using
-MACS in narrow regimen,
-MACS in broad regimen,
-SPAN

Each tool was launched twice for Yng and Old samples

```
~/chipseq/macs2_broad
macs2 >>> .broadPeak + _macs2.log
```

```
######################################################################
#7 Peak calling
#7.2 MACS Broad
SUFFIX="broad_0.1"
PARAMS="--broad --broad-cutoff 0.1"

# Yng
INPUT=~/chipseq/bam/SRR6116863_45000000_hg19.bam
FILE=~/chipseq/bam/SRR6116838_45000000_hg19.bam
# Old
INPUT=~/chipseq/bam/SRR6116875_45000000_hg19.bam
FILE=~/chipseq/bam/SRR6116844_45000000_hg19.bam

NAME=$(basename ${FILE%%.bam})  # File name without extension
ID=${NAME}_${SUFFIX}
if [[ -z $(find . -name "${ID}*.*Peak") ]]; then  # Peaks file is not created yet
    TMP_DIR=$(mktemp -d macs2.XXXXXXXX)
    mkdir -p ${TMP_DIR}
    echo "Macs2 TMP_DIR: ${TMP_DIR}"
        macs2 callpeak --tempdir ${TMP_DIR} -t ${FILE} -c ${INPUT} -f BAM -g hs -n
${ID} ${PARAMS} 2>&1 |\
            tee ${ID}_macs2.log
    # Cleanup
    rm -rf ${TMP_DIR}
fi
```

7 Peak calling (SPAN)

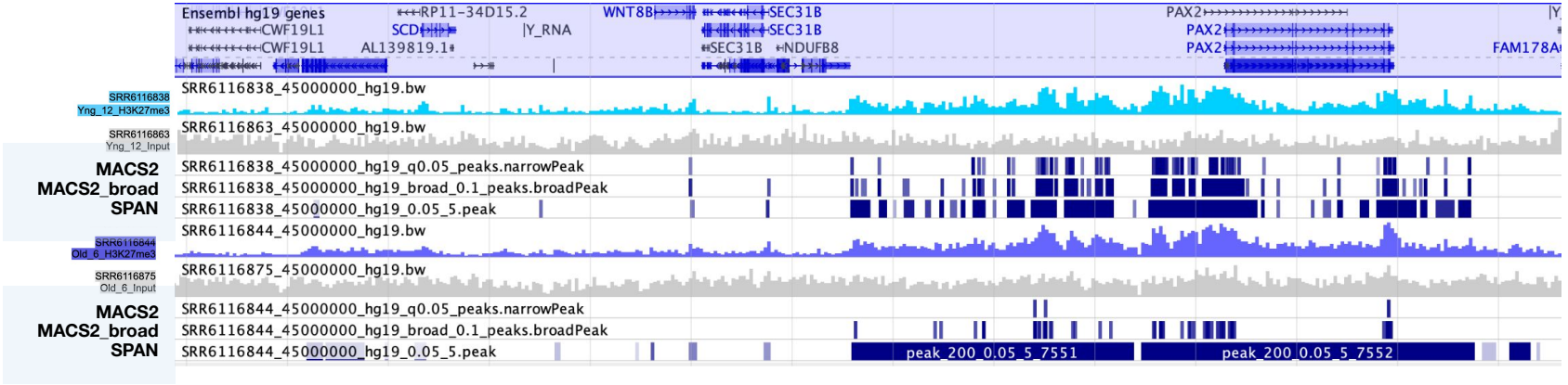
Peak calling was done using
-MACS in narrow regimen,
-MACS in broad regimen,
-SPAN

Each tool was launched twice for Yng and Old samples

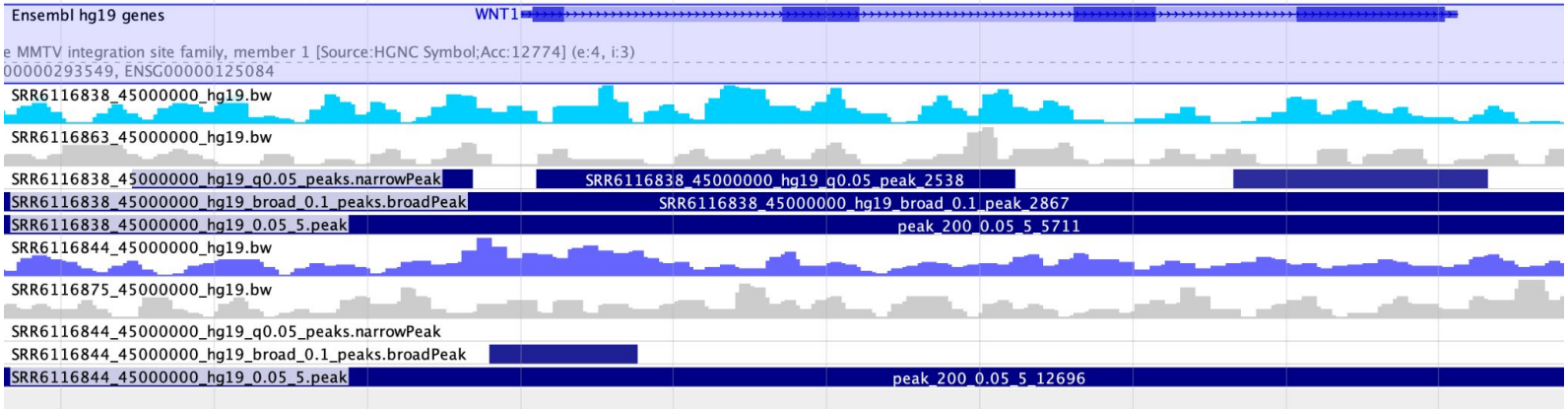
```
~/chipseq/macs2_broad
span >>> .peak + _span.log
```

```
######################################################################
#7 Peak calling
#7.3 SPAN
BIN=200
FDR=0.05
GAP=5

# Young
INPUT=~/chipseq/bam/SRR6116863_45000000_hg19.bam
FILE=~/chipseq/bam/SRR6116838_45000000_hg19.bam
# Old
INPUT=~/chipseq/bam/SRR6116875_45000000_hg19.bam
FILE=~/chipseq/bam/SRR6116844_45000000_hg19.bam

NAME=$(basename ${FILE%%.bam})  # File name without extension
ID=${NAME}_${FDR}_${GAP}
if [[ ! -f ${ID}.peak ]]; then # Not created yet
  java -Xmx16G -jar /mnt/chipseq/span-1.1.5628.jar analyze -t ${FILE} -c ${INPUT} \
    --chrom.sizes /mnt/chipseq/hg19.chrom.sizes \
    --bin ${BIN} --fdr ${FDR} --gap ${GAP} \
    --peaks ${ID}.peak \
    --threads 6 2>&1 | tee ${NAME}_span.log
fi
```

8 Peak calling visualization



8 Peak calling visualization



As an example I decided to explore **WNT1** gene, protooncogene. Also modifications in WNT signaling were mentioned in the original article. On the figure above you can see H3K27me3 peaks in Yng sample which disappear during aging. This modification associated with gene downregulation and formation of heterochromatic regions. Maybe this could lead to cancer progression during aging..

9 Peak calling summary

#	Title	Bed format	Count	Total length	Genome coverage	Min length	Max length	Mean length	Median length
1	SRR6116838_45000000_hg19_q0.05_peaks.narrowPeak	(bed6+, '\t')	13041	6724654	0.0021435474411748315	295	12145	515	404
2	SRR6116838_45000000_hg19_broad_0.1_peaks.broadPeak	(bed6+, '\t')	13280	27166863	0.008659696048063915	295	67797	2045	1159
3	SRR6116838_45000000_hg19_0.05_5.peak	(bed6+, '\t')	26063	73437331	0.023408847942475424	200	143800	2817	1400
4	SRR6116844_45000000_hg19_q0.05_peaks.narrowPeak	(bed6+, '\t')	1030	77728	2.4776539507852345E-5	52	320	75	67
5	SRR6116844_45000000_hg19_broad_0.1_peaks.broadPeak	(bed6+, '\t')	7417	1544089	4.921930592854598E-4	52	3129	208	170
6	SRR6116844_45000000_hg19_0.05_5.peak	(bed6+, '\t')	64306	549864441	0.17527452200493573	200	427600	8550	5000

In general SPAN found more peaks and peaks are much longer. There is especially prominent result for Old sample (highlighted). It looks uncommonly.. maybe it will good to adjust the settings for SPAN another time (?)

10-11 Common and differential peaks

Using `bedtools intersect -u` I`ve obtained common peaks and with `bedtools intersect -v` I obtain differential peaks.

To explore changes that occurs during aging I compare Old sample with Yng.
`-a` is an Old sample peaks
`-b` is an Yng sample peaks

So I found peaks that (i) **Old shares** with Yng samples and (ii) peaks that are founded in **Old sample only**

~/chipseq/intersect
bedtools intersect >>> .bed

```
#####################################################################
# 10 Common peaks
mkdir ~/chipseq/intersect

bedtools intersect -u -a
~/chipseq/macs2_broad/SRR6116844_45000000_hg19_broad_0.1_peaks.broadPeak \
  -b ~/chipseq/macs2_broad/SRR6116838_45000000_hg19_broad_0.1_peaks.broadPeak >
~/chipseq/intersect/macs2_broad_common.bed

#####################################################################
# 11 Differential peaks
bedtools intersect -v -a
~/chipseq/macs2_broad/SRR6116844_45000000_hg19_broad_0.1_peaks.broadPeak \
  -b ~/chipseq/macs2_broad/SRR6116838_45000000_hg19_broad_0.1_peaks.broadPeak >
~/chipseq/intersect/macs2_broad_differential.bed
```

12 Functional annotation

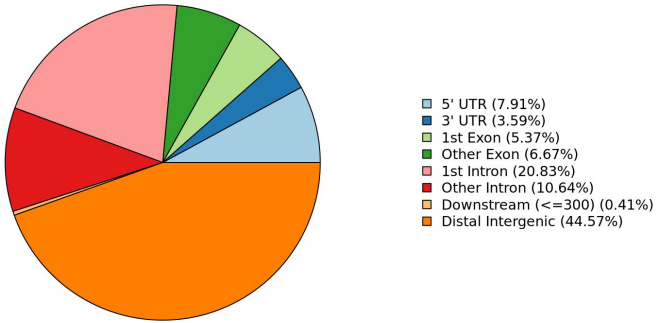
Firstly I prepared `.bed3` files and then switched to R console..

```
~/chipseq/intersect
cat >>> .bed3 >>> R console
```

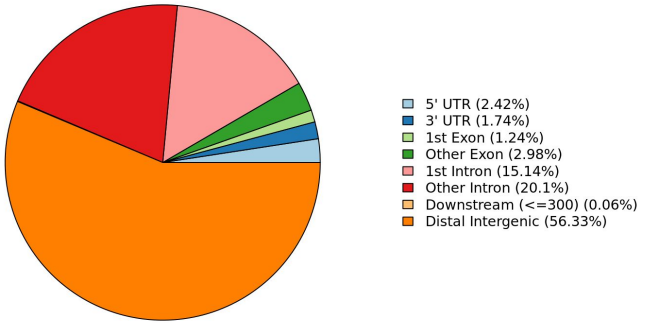
```
######################################################################
# 12 Functional annotation using ChIPpeakAnno R package

cat ~/chipseq/intersect/macs2_broad_common.bed | awk -v OFS='\t' '{N+=1; print
$1,$2,$3,N}' >\
 ~/chipseq/intersect/macs2_broad_common.bed3
cat ~/chipseq/intersect/macs2_broad_differential.bed | awk -v OFS='\t' '{N+=1; print
$1,$2,$3,N}' >\
 ~/chipseq/intersect/macs2_broad_differential.bed3
```

12 Functional annotation

Old_shared (common)



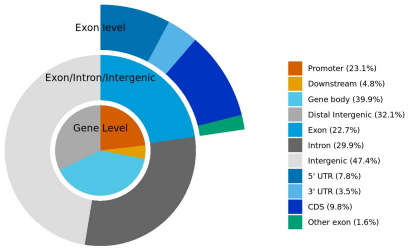
Old_only (differential)



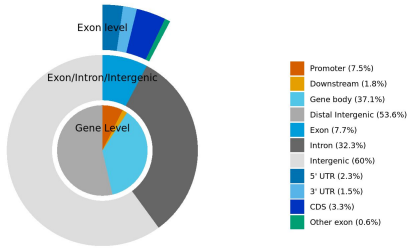
Peaks that occurs in Old sample are more often located in distal intergenic region..

12 Functional annotation

Old_shared (common)



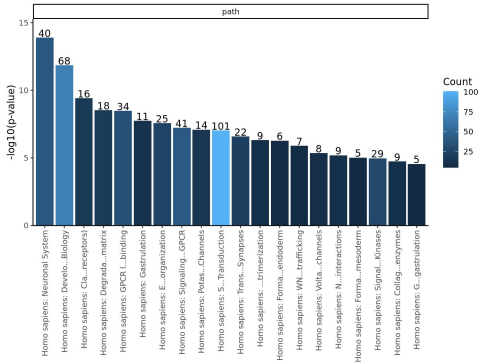
Old_only (differential)



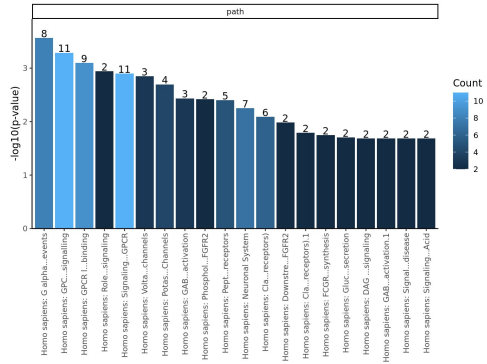
This plots support the previous one, and we can see that peaks are typical for Old sample are rarely found in Exons..

12 Functional annotation

Old_shared (common)



Old_only (differential)



Reactome db shows that common peaks are associated with pathways related with Neuronal system, Development, Gastrulation..
Peaks founded in Old sample only (differential) are related with signaling (G alpha signalling events, Signaling by GPCR, DAG and IP3 signaling), Potassium Channels and GABA receptor activation.

13 Motif analysis with Homer

To find motifs across common and differential peaks I firstly sorted and filtered previously founded peak sets and save only top-500 in each group in **_top500.bed**, then obtain **homer** output in **homerResults.html**

~/chipseq/intersect
sort >>> **_top500.bed**
homer >>> **homerResults.html**

```
######################################################################
# 13 Motif analysis with Homer

sort -k 9,9nr ~/chipseq/intersect/macs2_broad_common.bed | head -n 500 | sort -k1,1
-k2,2n |\
 awk -v OFS='\t' '{print($1, int(($3+$2)/2)-100, int(($3+$2)/2)+100)}' >\
 ~/chipseq/intersect/macs2_broad_common_top500.bed
sort -k 9,9nr ~/chipseq/intersect/macs2_broad_differential.bed | head -n 500 | sort
-k1,1 -k2,2n |\
 awk -v OFS='\t' '{print($1, int(($3+$2)/2)-100, int(($3+$2)/2)+100)}' >\
 ~/chipseq/intersect/macs2_broad_differential_top500.bed

perl /opt/conda/envs/chipseq/share/homer/bin/findMotifsGenome.pl \
 ~/chipseq/intersect/macs2_broad_common_top500.bed hg19 \
 ~/chipseq/macs2_broad_common_top500.narrowPeak.motif -size 200 -mask
perl /opt/conda/envs/chipseq/share/homer/bin/findMotifsGenome.pl \
 ~/chipseq/intersect/macs2_broad_differential_top500.bed hg19 \
 ~/chipseq/macs2_broad_differential_top500.narrowPeak.motif -size 200 -mask
```

13 Motif analysis with Homer

Old_shared (common)

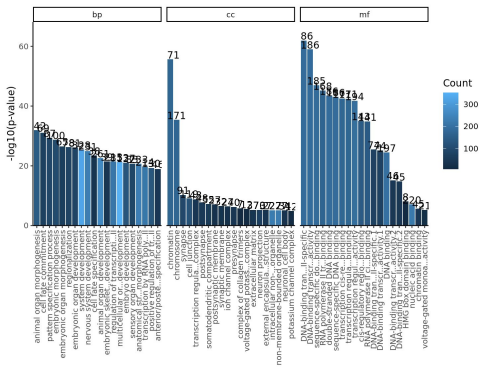
Rank	Motif	P-value	log P-pvalue	% of Targets
1		1e-17	-4.107e+01	2.83%
2		1e-12	-2.896e+01	1.29%
3 *		1e-11	-2.697e+01	3.08%
4 *		1e-11	-2.550e+01	1.29%
5 *		1e-11	-2.547e+01	2.06%

Old_only (differential)

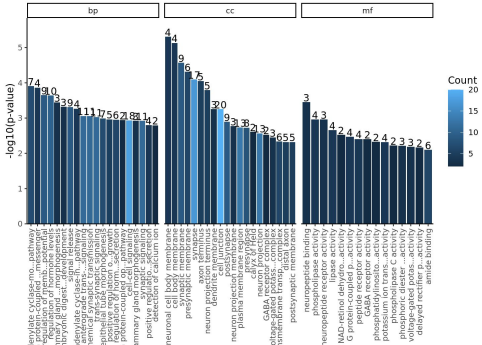
Rank	Motif	P-value	log P-pvalue	% of Targets
1		1e-12	-2.897e+01	5.56%
2 *		1e-11	-2.592e+01	6.86%
3 *		1e-9	-2.284e+01	1.96%
4 *		1e-9	-2.246e+01	4.90%
5 *		1e-9	-2.141e+01	1.96%

14 Gene set enrichment analysis

Old_shared (common)



Old_only (differential)



Gene enrichment shows that common peaks are associated with organ morphogenesis, regionalization, system development (Biological processes)
Peaks founded in Old sample only (differential) are related with G-proteins, regulation of membrane potential signal release, trans-synaptic signaling.

15 Related datasets (common peaks)

Then I've download .bed files to find related datasets in ChIP-Atlas. Results contains datasets from various classes (Blood, Stem cells, Placenta..) and H3K4me3/H3K27me3 Antigens

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

My project

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / dataset	common	Overlaps / Control	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX2018542	Histone	H3K27me3	Blood	Neutrophil progenitors	20231	294/5793		32/5793	-54.8	-50.3	9.19	TRUE
SRX2018544	Histone	H3K27me3	Blood	Neutrophil progenitors	20376	292/5793		33/5793	-53.5	-49.3	8.85	TRUE
SRX386200	Histone	H3K27me3	Blood	CD34+	29643	285/5793		32/5793	-52.4	-48.3	8.91	TRUE
SRX646123	Histone	H3K27me3	Blood	Erythroblasts	24690	255/5793		22/5793	-51.8	-47.8	11.59	TRUE
SRX2018543	Histone	H3K27me3	Blood	Neutrophil progenitors	16796	262/5793		25/5793	-51.3	-47.5	10.48	TRUE
SRX2018541	Histone	H3K27me3	Blood	Neutrophil progenitors	15575	258/5793		24/5793	-51.0	-47.3	10.75	TRUE
SRX2018540	Histone	H3K27me3	Blood	Neutrophil progenitors	17089	272/5793		30/5793	-50.4	-46.7	9.07	TRUE
SRX1089821	Histone	H3K27me3	Blood	Erythroblasts	24739	251/5793		23/5793	-49.9	-46.3	10.91	TRUE
SRX2018538	Histone	H3K27me3	Blood	CD34+	11870	207/5793		13/5793	-46.1	-42.5	15.92	TRUE
SRX2018539	Histone	H3K27me3	Blood	CD34+	15021	215/5793		18/5793	-44.0	-40.5	11.94	TRUE
SRX480621	Histone	H3K27me3	Pluripotent stem cell	hESC H9	15403	225/5793		22/5793	-43.6	-40.1	10.23	TRUE
SRX1008493	Histone	H3K4me1	Epidermis	NHEK	248649	552/5793		194/5793	-42.4	-39.0	2.85	TRUE
SRX547407	Histone	H3K4me3	Pluripotent stem cell	iPS cells	37420	282/5793		48/5793	-41.8	-38.4	5.88	TRUE
SRX9621856	Histone	H3K4me3	Pluripotent stem cell	hESC H9	33435	282/5793		49/5793	-41.2	-37.9	5.76	TRUE
SRX480623	Histone	H3K27me3	Pluripotent stem cell	hESC H9	19239	212/5793		21/5793	-40.9	-37.5	10.10	TRUE
SRX547409	Histone	H3K4me3	Pluripotent stem cell	iPS cells	34098	275/5793		47/5793	-40.6	-37.3	5.85	TRUE
SRX8406468	Histone	H3K27me3	Prostate	Prostate	46194	331/5793		74/5793	-40.4	-37.1	4.47	TRUE
SRX13466354	Histone	H3K4me3	Pluripotent stem cell	ES cells	32234	275/5793		48/5793	-40.1	-36.8	5.73	TRUE
SRX480610	Histone	H3K27me3	Pluripotent stem cell	hESC H9	15488	203/5793		19/5793	-40.0	-36.7	10.68	TRUE
SRX547411	Histone	H3K4me3	Pluripotent stem cell	iPS cells	39332	298/5793		59/5793	-39.9	-36.7	5.05	TRUE
SRX547405	Histone	H3K4me3	Pluripotent stem cell	iPS cells	36340	302/5793		61/5793	-39.9	-36.7	4.95	TRUE
SRX480611	Histone	H3K27me3	Pluripotent stem cell	hESC H9	25730	247/5793		37/5793	-39.4	-36.2	6.68	TRUE
SRX480622	Histone	H3K27me3	Pluripotent stem cell	hESC H9	13785	195/5793		17/5793	-39.4	-36.2	11.47	TRUE
SRX9621855	Histone	H3K4me3	Pluripotent stem cell	hESC H9	38136	285/5793		54/5793	-39.4	-36.2	5.28	TRUE
SRX6608388	Histone	H3K27me3	Blood	RCH-ACV	13360	201/5793		20/5793	-38.7	-35.6	10.05	TRUE
SRX480609	Histone	H3K27me3	Pluripotent stem cell	hESC H9	15618	209/5793		23/5793	-38.6	-35.5	9.09	TRUE
SRX8997966	Histone	H3K4me3	Pluripotent stem cell	iPS cells	41220	337/5793		82/5793	-38.3	-35.2	4.11	TRUE
SRX5931557	Histone	H3K27me3	Blood	CD34+	9900	185/5793		16/5793	-37.4	-34.4	11.56	TRUE

15 Related datasets (differential peaks)

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

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ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / dataset A	Overlaps / Control	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX2586644	Histone	H3K4me3	Pluripotent stem cell	iPSC derived neural cells	34697	39/1624	8/1624	-5.3	-1.4	4.88	TRUE
SRX16711619	Histone	H3K4me3	Placenta	Placenta	35628	48/1624	13/1624	-5.2	-1.4	3.69	TRUE
SRX2586643	Histone	H3K4me3	Pluripotent stem cell	iPSC derived neural cells	38128	41/1624	10/1624	-4.9	-1.4	4.10	TRUE
SRX1089821	Histone	H3K27me3	Blood	Erythroblasts	24739	33/1624	6/1624	-4.9	-1.4	5.50	TRUE
SRX16711622	Histone	H3K4me3	Placenta	Placenta	33897	48/1624	14/1624	-4.8	-1.4	3.43	TRUE
SRX16711620	Histone	H3K4me3	Placenta	Placenta	38043	46/1624	13/1624	-4.8	-1.4	3.54	TRUE
SRX19194555	Histone	H3K27me3	Blood	PBMC	15394	23/1624	2/1624	-4.7	-1.4	11.50	TRUE
SRX5931554	Histone	H3K4me3	Blood	HUDEP-2	26590	42/1624	11/1624	-4.7	-1.4	3.82	TRUE
SRX16711601	Histone	H3K4me3	Placenta	Placenta	32741	40/1624	10/1624	-4.7	-1.4	4.00	TRUE
SRX10606493	Histone	H3K4me3	Kidney	293	22804	38/1624	9/1624	-4.7	-1.4	4.22	TRUE
SRX646123	Histone	H3K27me3	Blood	Erythroblasts	24690	32/1624	6/1624	-4.7	-1.4	5.33	TRUE
SRX3288598	Histone	H3K4me3	Pluripotent stem cell	hESC H9	38173	36/1624	8/1624	-4.6	-1.4	4.50	TRUE
SRX12982841	Histone	H3K27me3	Blood	Peripheral blood	14505	25/1624	3/1624	-4.6	-1.4	8.33	TRUE
SRX16711623	Histone	H3K4me3	Placenta	Placenta	32948	45/1624	13/1624	-4.6	-1.4	3.46	TRUE
SRX16711606	Histone	H3K4me3	Placenta	Placenta	33498	43/1624	12/1624	-4.5	-1.3	3.58	TRUE
SRX16711608	Histone	H3K4me3	Placenta	Placenta	31066	41/1624	11/1624	-4.5	-1.3	3.73	TRUE
SRX3468015	Histone	H3K4me3	Others	Aska	27445	39/1624	10/1624	-4.5	-1.3	3.90	TRUE
SRX8150290	Histone	H3K4me1	Others	SCC-25	109192	56/1624	20/1624	-4.4	-1.3	2.80	TRUE
SRX2636082	Histone	H3K4me3	Neural	Fetal neural cells	32517	37/1624	9/1624	-4.4	-1.3	4.11	TRUE
SRX16711607	Histone	H3K4me3	Placenta	Placenta	31852	44/1624	13/1624	-4.4	-1.3	3.38	TRUE
SRX8150293	Histone	H3K4me1	Others	SCC-25	127775	55/1624	20/1624	-4.3	-1.2	2.75	TRUE
SRX3088201	Histone	H3K27ac	Neural	Entorhinal Cortex	42689	36/1624	9/1624	-4.2	-1.2	4.00	TRUE
SRX386200	Histone	H3K27me3	Blood	CD34+	29643	36/1624	9/1624	-4.2	-1.2	4.00	TRUE
SRX5392486	Histone	H3K27ac	Neural	Wilms Tumor	89095	61/1624	24/1624	-4.2	-1.2	2.54	TRUE
SRX11354207	Histone	H3K4me3	Digestive tract	SW 480	29988	34/1624	8/1624	-4.2	-1.2	4.25	TRUE
SRX16500387	Histone	H3K27me3	Blood	Dendritic Cells	19322	21/1624	2/1624	-4.2	-1.2	10.50	TRUE
SRX16711617	Histone	H3K4me3	Placenta	Placenta	33260	43/1624	13/1624	-4.2	-1.2	3.31	TRUE
SRX2636167	Histone	H3K4me3	Pluripotent stem cell	iPS cells	41981	44/1624	14/1624	-4.1	-1.1	3.14	TRUE
SRX14410413	Histone	H3K4me3	Pluripotent stem cell	iPS cells	28841	33/1624	8/1624	-4.0	-1.1	4.12	TRUE