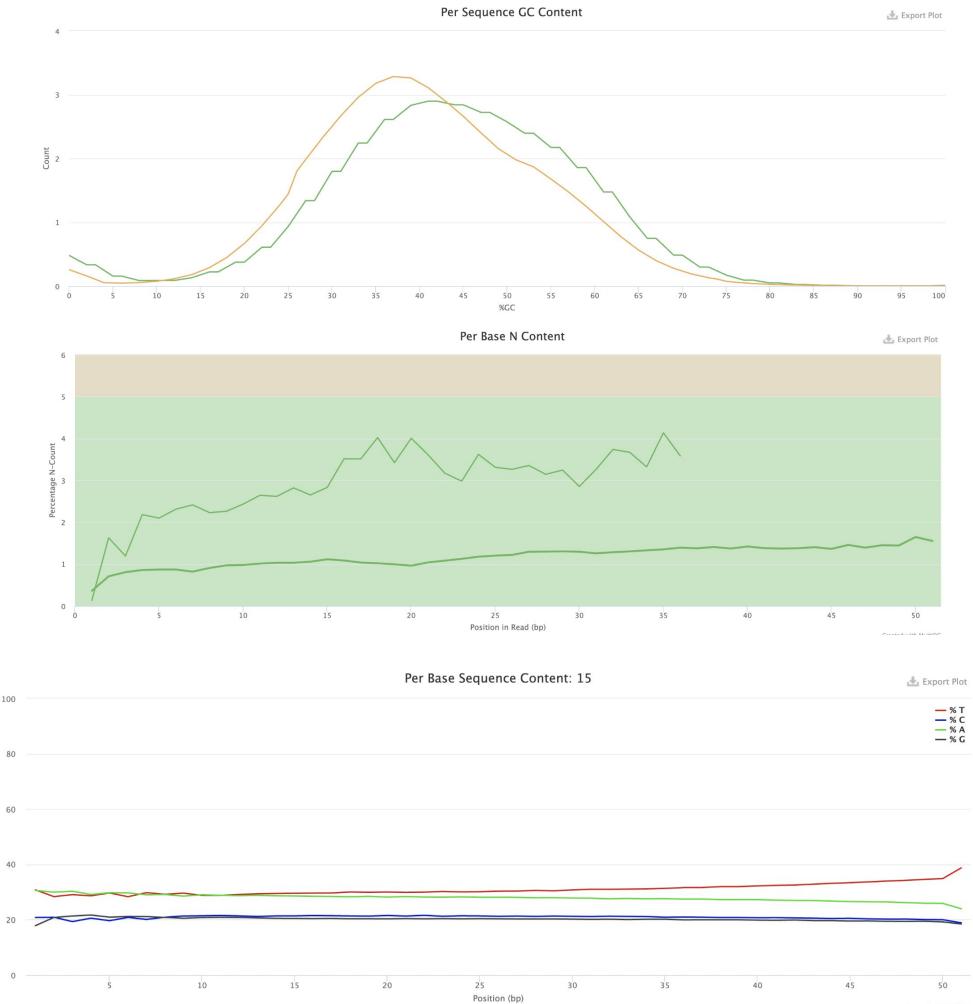


Epigenetics

Konstantin Danilov

ChipSeq

fastq



bam

Bowtie 1 Alignment Scores

[Export Plot](#)

14_bowtie



15_bowtie



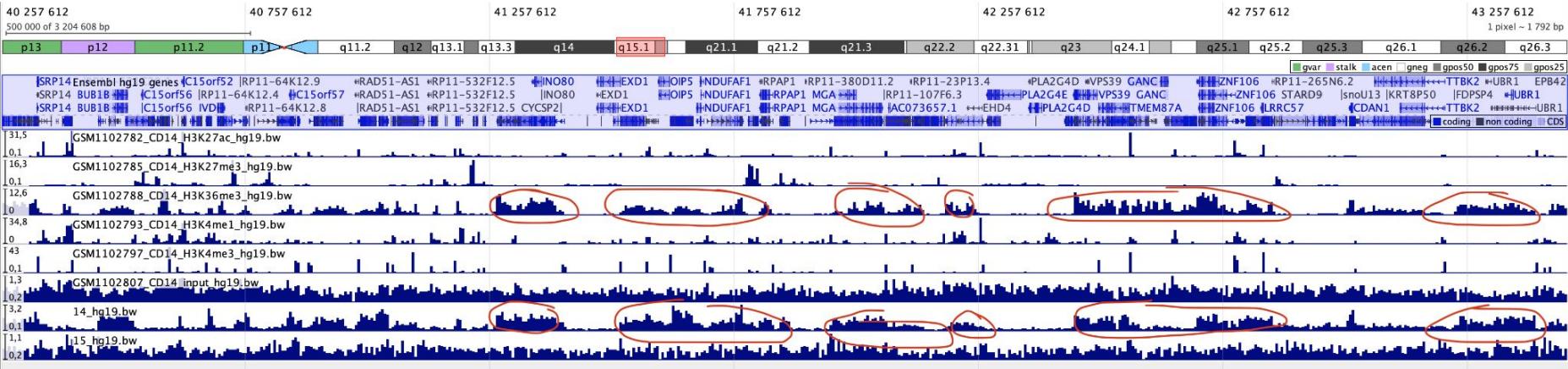
0 1M 2M 3M 4M 5M 6M 7M 8M 9M 10M 11M 12M 13M 14M 15M 16M 17M 18M 19M 20M 21M 22M 23M 24M 25M 26M 27M 28M 2...

Reads

● Aligned ● Multimapped ● Not aligned

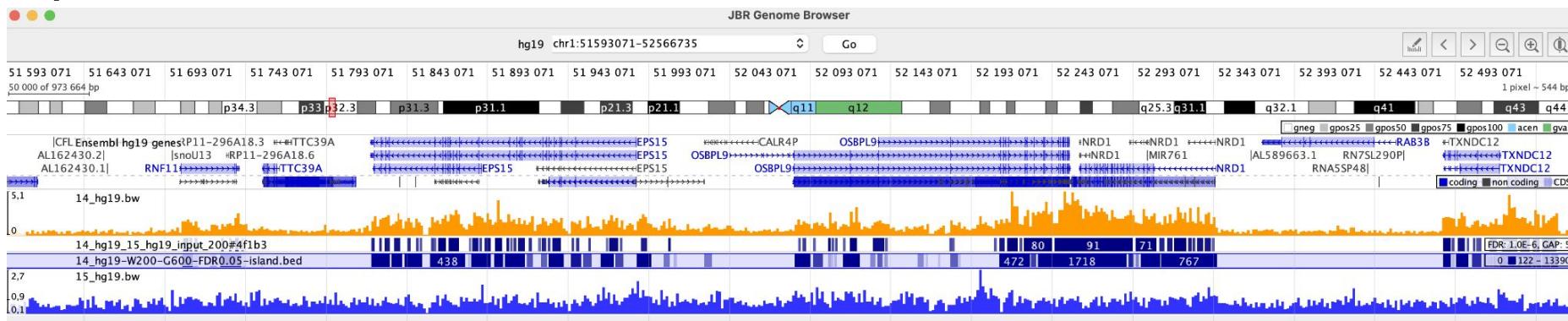
Converted with MultiQC

bw

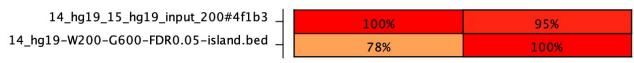


Looks like H3K36me3 => broad peaks => SICER or SPAN

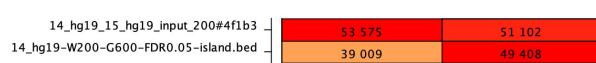
peaks: SPAN & SICER



#	Title	Count	Total length	Genome coverage	Min length	Max length	Mean length	Median length
1	14_hg19_15_hg19_input_200#4f1b3	53 575	145 066 800	0,05%	200	136 600	2 707	1 200
2	14_hg19-W200-G600-FDR0.05-island.bed	49 408	248 097 192	0,08%	199	153 199	5 021	2 999



14_hg19_15_hg19_input_200#4f1b3



14_hg19_15_hg19_input_200#4f1b3

14 hq19-W200-G600-FDR0.05-island.bed

HOMER

Homer Known Motif Enrichment Results (/home/student/chipseq/14_hg19_0.05_5_top500.peak.motif)

[Homer de novo Motif Results](#)

[Gene Ontology Enrichment Results](#)

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

Total Target Sequences = 340, Total Background Sequences = 49895

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	Motif File	SVG
1		TEAD(TEA)/Fibroblast-PU.1-ChIP-Seq(Unpublished)/Homer	1e-2	-4.957e+00	1.0000	32.0	9.41%	2953.8	5.92%	motif file (matrix)	svg

Homer de novo Motif Results (/home/student/chipseq/14_hg19_0.05_5_top500.peak.motif)

[Known Motif Enrichment Results](#)

[Gene Ontology Enrichment Results](#)

If Homer is having trouble matching a motif to a known motif, try copy/pasting the matrix file into [STAMP](#)

More information on motif finding results: [HOMER](#) | [Description of Results](#) | [Tips](#)

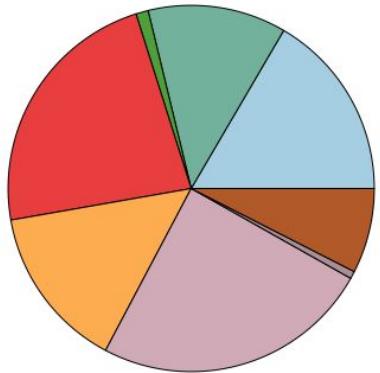
Total target sequences = 340

Total background sequences = 49439

* - possible false positive

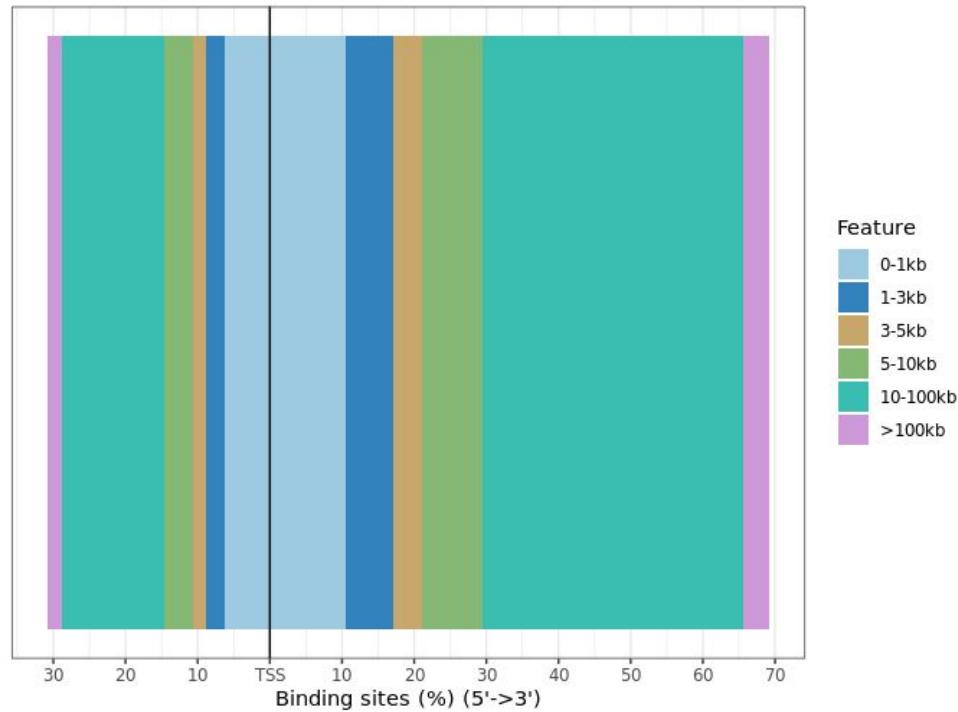
Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1 *		1e-10	-2.341e+01	4.71%	0.52%	50.3bp (58.7bp)	PHO164_1_Six4/Jaspar(0.628) More Information Similar Motifs Found	motif file (matrix)
2 *		1e-8	-2.033e+01	8.53%	2.25%	55.8bp (61.6bp)	Tlx'(NR)/NPC-H3K4me1-ChIP-Seq(GSE16256)/Homer(0.670) More Information Similar Motifs Found	motif file (matrix)
3 *		1e-8	-1.985e+01	3.82%	0.41%	52.1bp (62.0bp)	HOXA1 (Homeobox/mES-Hoxa1-ChIP-Seq(SRP084292)/Homer(0.644) More Information Similar Motifs Found	motif file (matrix)
4 *		1e-8	-1.947e+01	4.12%	0.50%	51.9bp (55.1bp)	PB0121_1_Foxj3_2/Jaspar(0.837) More Information Similar Motifs Found	motif file (matrix)
5 *		1e-8	-1.913e+01	8.24%	2.23%	42.1bp (55.0bp)	PH0100_1_Lmx1a/Jaspar(0.721) More Information Similar Motifs Found	motif file (matrix)
6 *		1e-7	-1.794e+01	2.35%	0.13%	35.9bp (59.5bp)	PB0099_1_Zfp691_1/Jaspar(0.642) More Information Similar Motifs Found	motif file (matrix)
7 *		1e-7	-1.780e+01	10.88%	3.84%	55.1bp (57.3bp)	RORg(NR)/Liver-Rorc-ChIP-Seq(GSE101115)/Homer(0.791) More Information Similar Motifs Found	motif file (matrix)
8 *		1e-7	-1.751e+01	2.94%	0.25%	49.3bp (57.1bp)	Znf281/MA1630_1/Jaspar(0.668) More Information Similar Motifs Found	motif file (matrix)
9 *		1e-7	-1.628e+01	2.06%	0.10%	39.4bp (59.5bp)	Rfx1(HTH)/NPC-H3K4me1-ChIP-Seq(GSE16256)/Homer(0.617) More Information Similar Motifs Found	motif file (matrix)
10 *		1e-6	-1.398e+01	2.35%	0.21%	38.2bp (57.6bp)	Zic1::Zic2/MA1628_1/Jaspar(0.649) More Information Similar Motifs Found	motif file (matrix)

Annotation

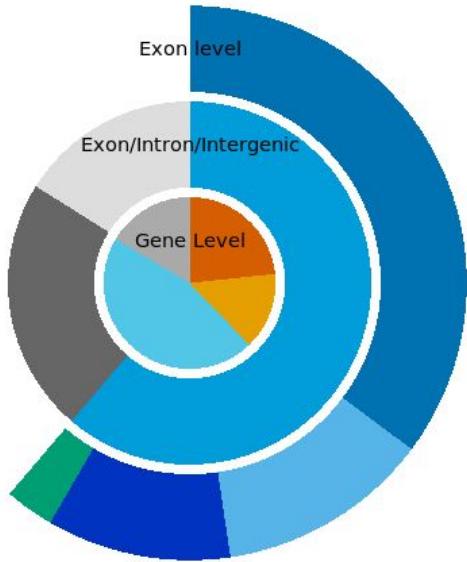


- 5' UTR (16.57%)
- 3' UTR (12.22%)
- 1st Exon (1.09%)
- Other Exon (22.88%)
- 1st Intron (14.49%)
- Other Intron (24.58%)
- Downstream (<=300) (0.66%)
- Distal Intergenic (7.5%)

Distribution wrt to TSS



Annotation



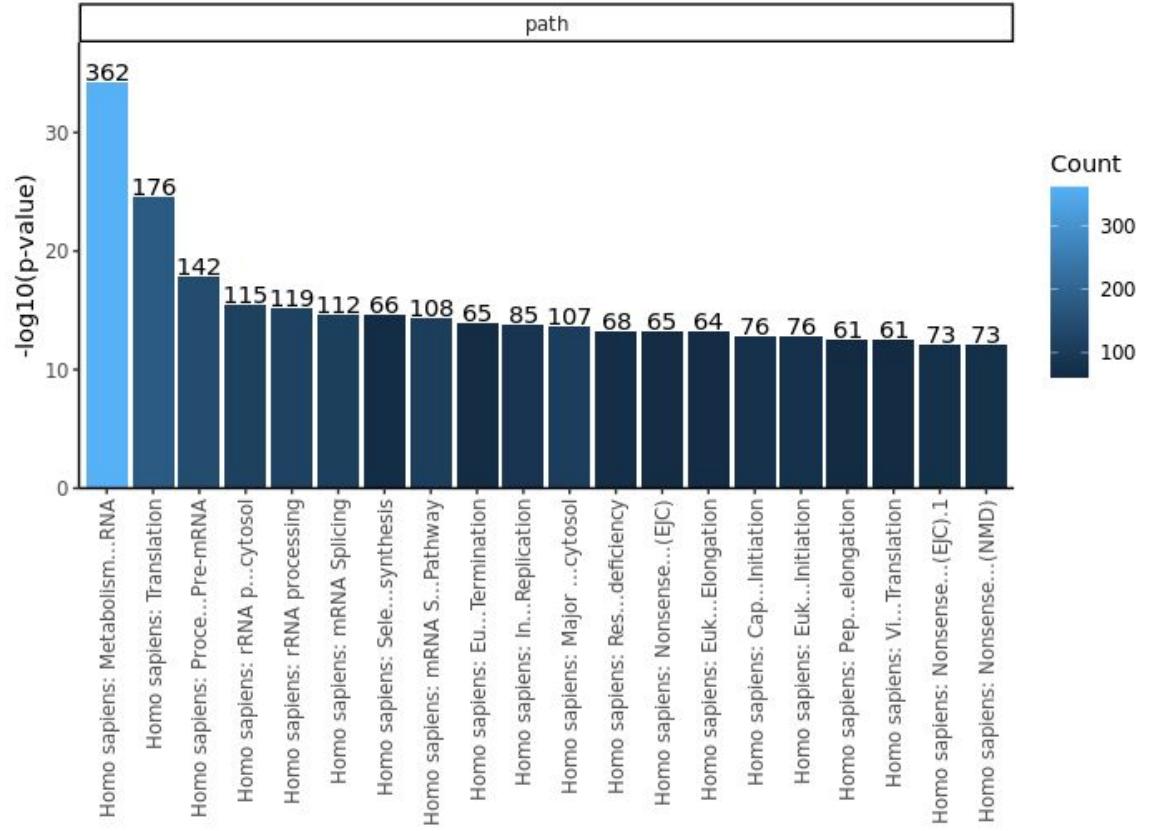
Promoter (23.3%)
Downstream (14.5%)
Gene body (45.7%)
Distal Intergenic (16.5%)
Exon (61.3%)
Intron (22.7%)
Intergenic (16.1%)
5' UTR (35.2%)
3' UTR (12.4%)
CDS (10.7%)
Other exon (2.9%)

GRanges object with 6 ranges and 9 metadata columns:

seqnames	ranges	strand	peak	feature	feature.ranges	feature.strand	distance	<Rle>	<integer>
	<Rle>	<IRanges>	<Rle>	<character>	<character>	<IRanges>			
X1	chr1 753401-761400	*		X1	ENSG00000240453	745489-753092	-	308	
X1	chr1 753401-761400	*		X1	ENSG00000228794	762988-794826	+	1587	
X2	chr1 764401-792600	*		X2	ENSG00000225880	761586-762902	-	1498	
X4	chr1 878401-894800	*		X4	ENSG00000188976	879584-894689	-	0	
X4	chr1 878401-894800	*		X4	ENSG00000187961	895967-901095	+	1166	
X5	chr1 896401-901800	*		X5	ENSG00000188976	879584-894689	-	1711	

insideFeature	distanceToSite			gene_name	entrez_id				
<character>	<integer>	<character>	<character>						
X1	upstream	308	RP11-206L10.10		<NA>				
X1	upstream	1587	LINC01128		643837				
X2	upstream	1498	LINC00115		79854				
X4	includeFeature	0	NOC2L		26155				
X4	upstream	1166	KLHL17		339451				
X5	upstream	1711	NOC2L		26155				

Annotation



Annotation

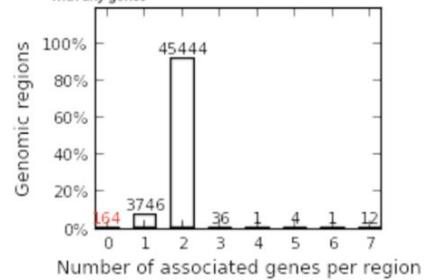
+ Region-Gene Association Graphs

What do these graphs illustrate?

Number of associated genes per region

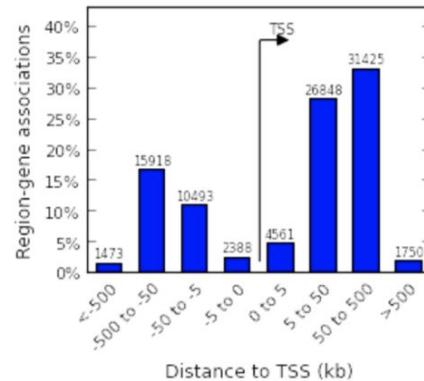
[Download as PDF.](#)

- Genomic regions associated with one or more genes
- Genomic regions not associated with any genes



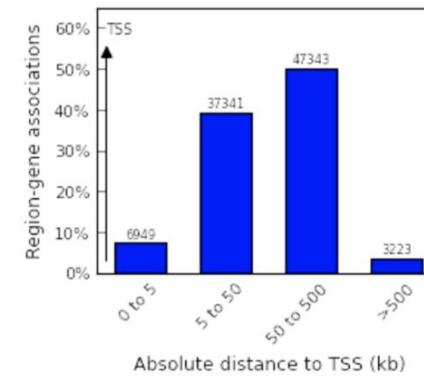
Binned by orientation and distance to TSS

[Download as PDF.](#)



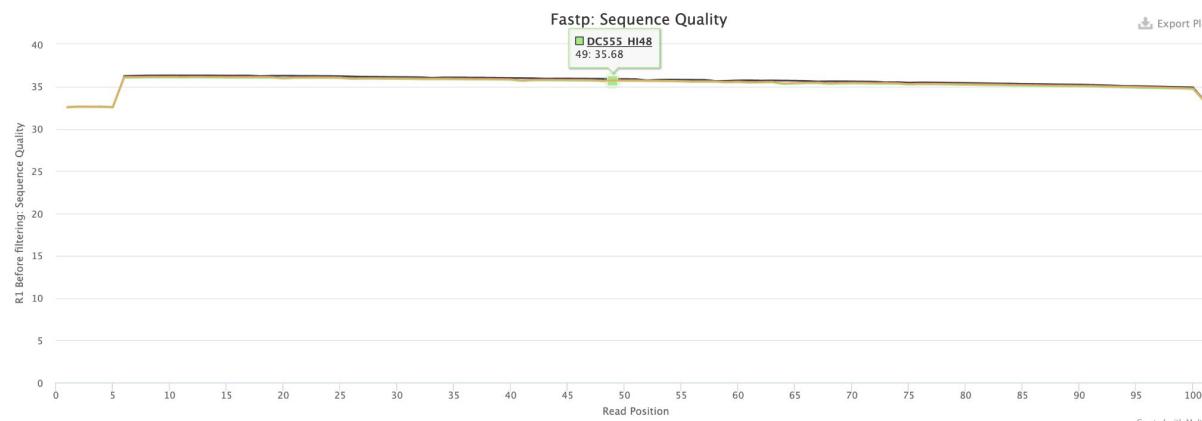
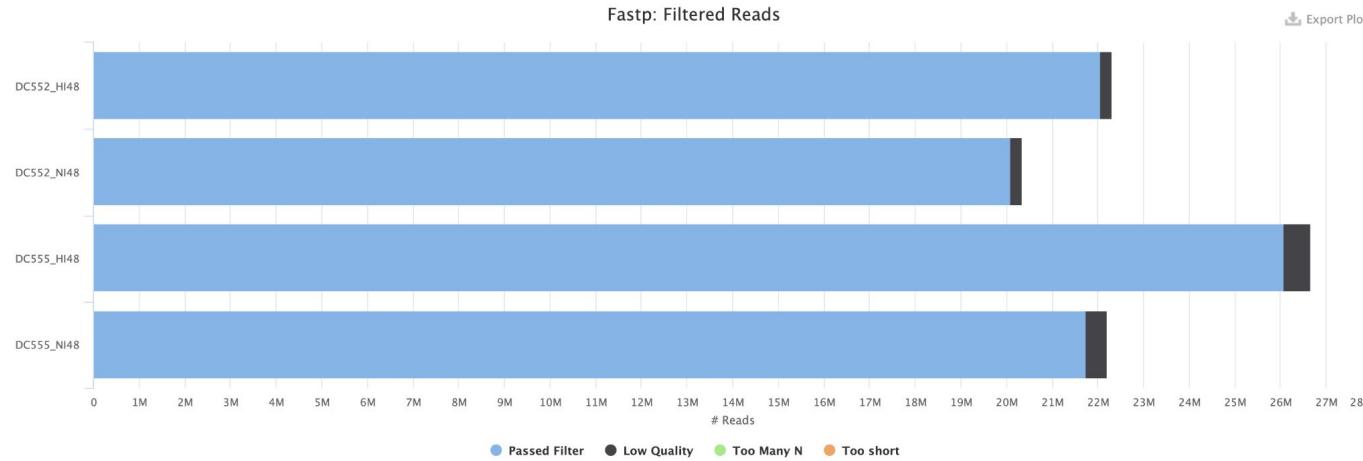
Binned by absolute distance to TSS

[Download as PDF.](#)

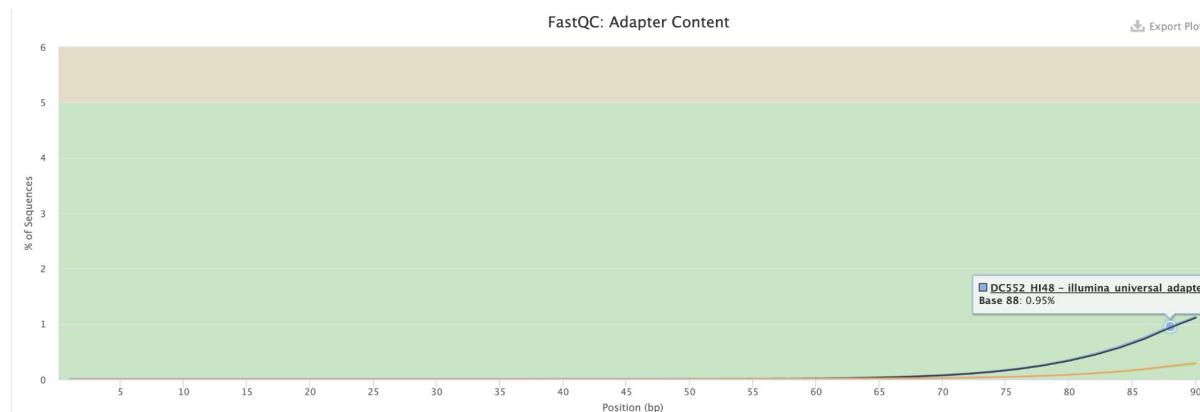
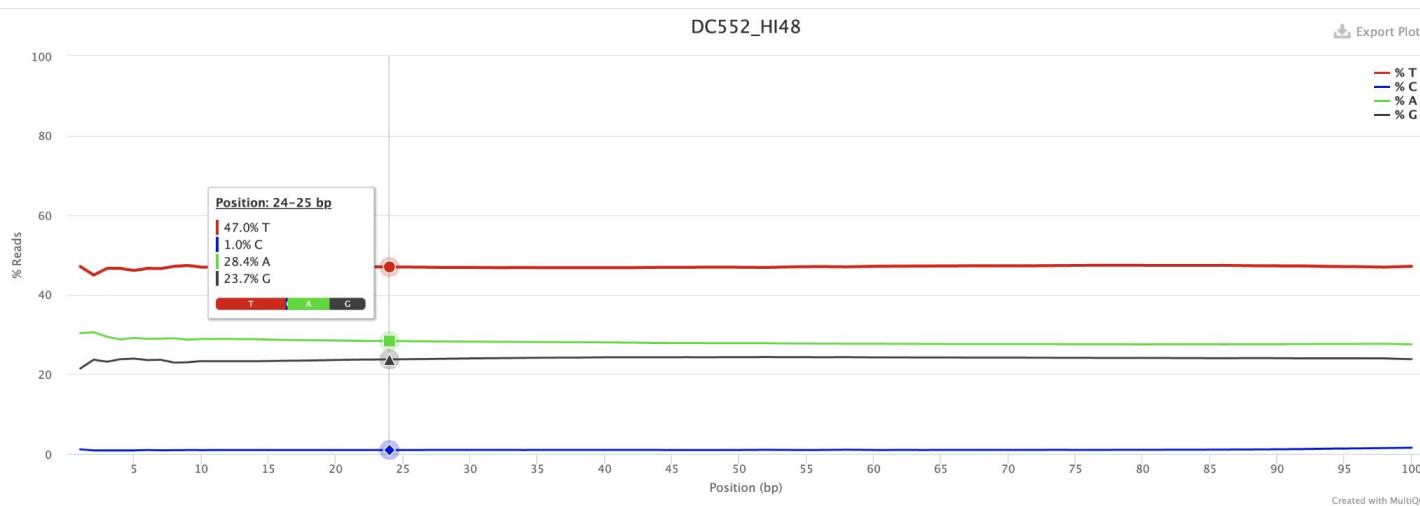


Methylation

QC

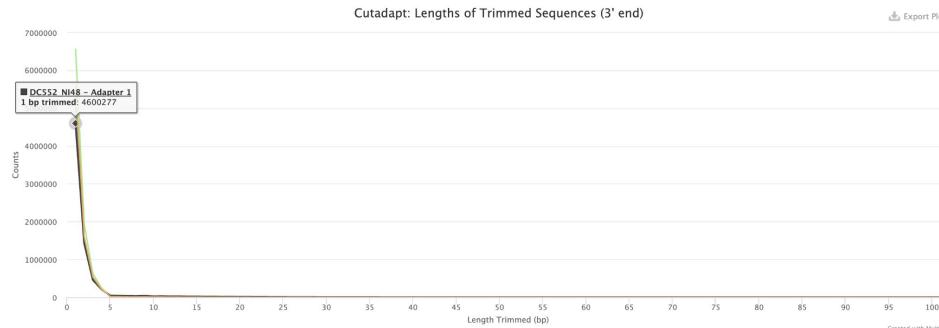


QC



QC after trimming

Sample Name	% BP Trimmed	% Dups	% GC	M Seqs
DC552_HI48	1.5%	46.3%	24%	22.2
DC552_NI48	1.5%	46.6%	24%	20.3
DC555_HI48	1.8%	46.7%	23%	26.4
DC555_NI48	1.8%	42.8%	23%	22.0



Adapter Content

4

Help

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

No samples found with any adapter contamination > 0.1%

Methylome quality

bams/DC555_HI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 0.3%
C methylated in CHG context: 0.5%
C methylated in CHH context: 0.3%
C methylated in Unknown context (CN or CHN): 0.0%
bams/DC552_NI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 0.4%
C methylated in CHG context: 0.5%
C methylated in CHH context: 0.4%
C methylated in Unknown context (CN or CHN): 0.0%
bams/DC555_NI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 0.4%
C methylated in CHG context: 0.5%
C methylated in CHH context: 0.4%
C methylated in Unknown context (CN or CHN): 0.0%
bams/DC552_HI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 0.4%
C methylated in CHG context: 0.5%
C methylated in CHH context: 0.4%
C methylated in Unknown context (CN or CHN): 0.0%

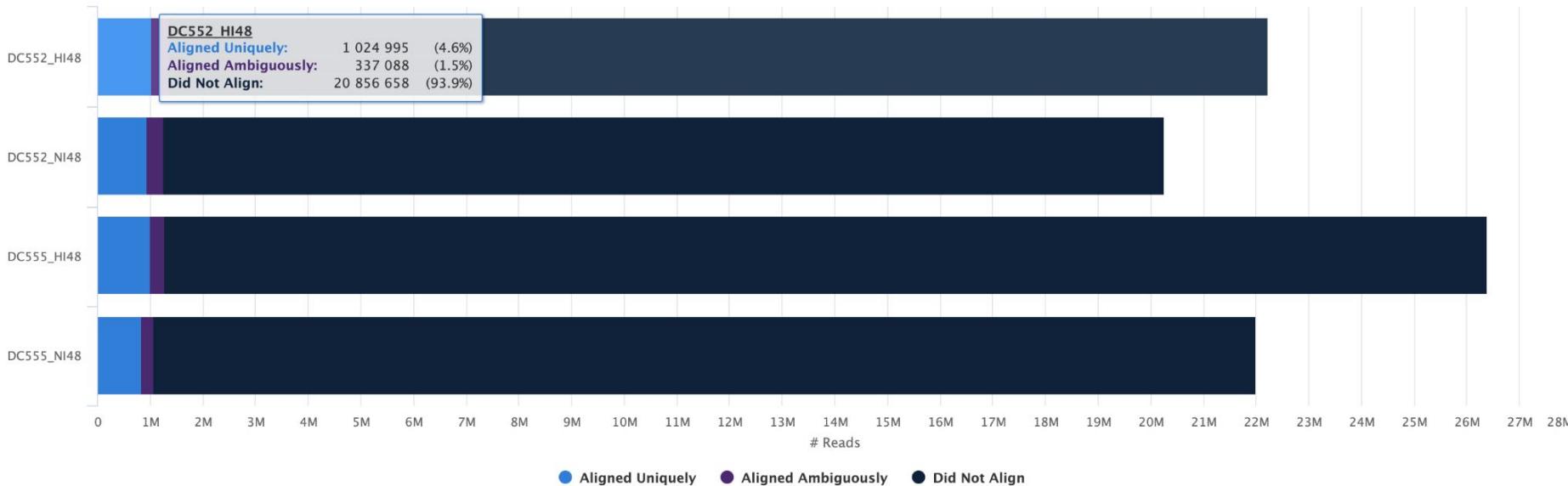
bams/DC555_HI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 51.2%
C methylated in CHG context: 0.6%
C methylated in CHH context: 0.5%
C methylated in Unknown context (CN or CHN): 3.5%
bams/DC552_NI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 51.9%
C methylated in CHG context: 0.7%
C methylated in CHH context: 0.6%
C methylated in Unknown context (CN or CHN): 4.5%
bams/DC555_NI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 53.2%
C methylated in CHG context: 0.6%
C methylated in CHH context: 0.6%
C methylated in Unknown context (CN or CHN): 3.7%
bams/DC552_HI48_trimmed_bismark_bt2_SE_report.txt
C methylated in CpG context: 50.7%
C methylated in CHG context: 0.7%
C methylated in CHH context: 0.6%
C methylated in Unknown context (CN or CHN): 4.2%

Dedup

Sample Name	C Coverage	% Dups	% Aligned	% Dups	% GC	M Seqs
DC552_HI48	1.18X	53.3%	4.6%	1.4%	26%	0.5
DC552_NI48	1.07X	53.4%	4.6%	1.4%	26%	0.4
DC555_HI48	1.12X	49.7%	3.8%	1.0%	25%	0.5
DC555_NI48	0.92X	46.2%	3.8%	0.9%	25%	0.5

Bismark: Alignment Scores

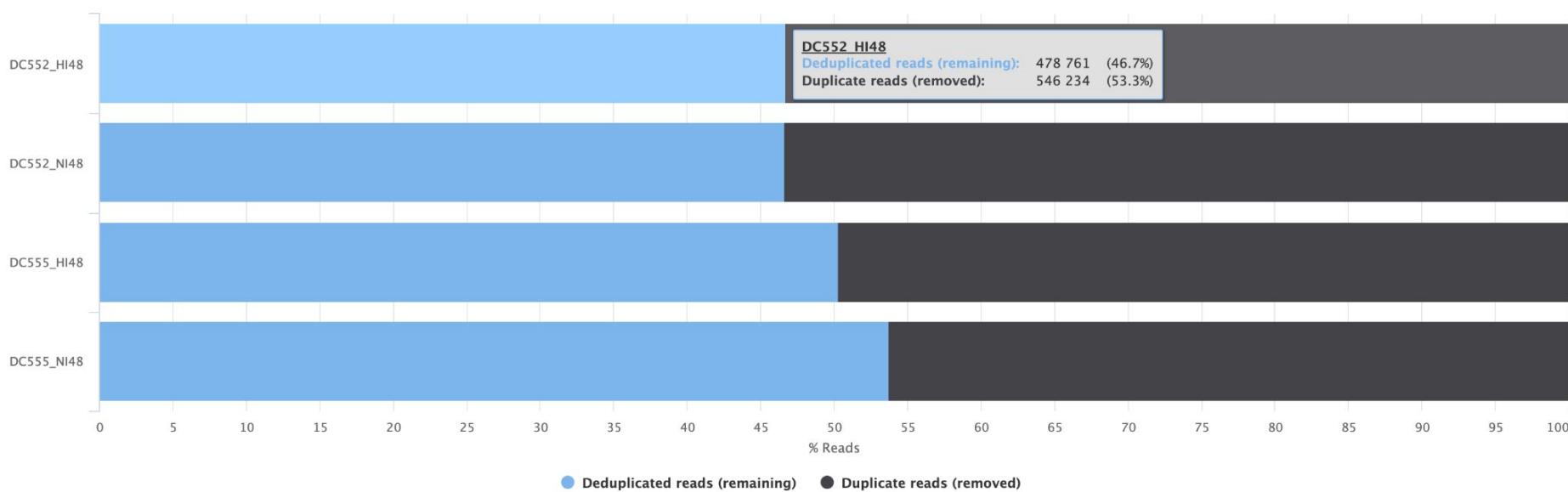
 Export Plot



Dedup

Bismark: Deduplication

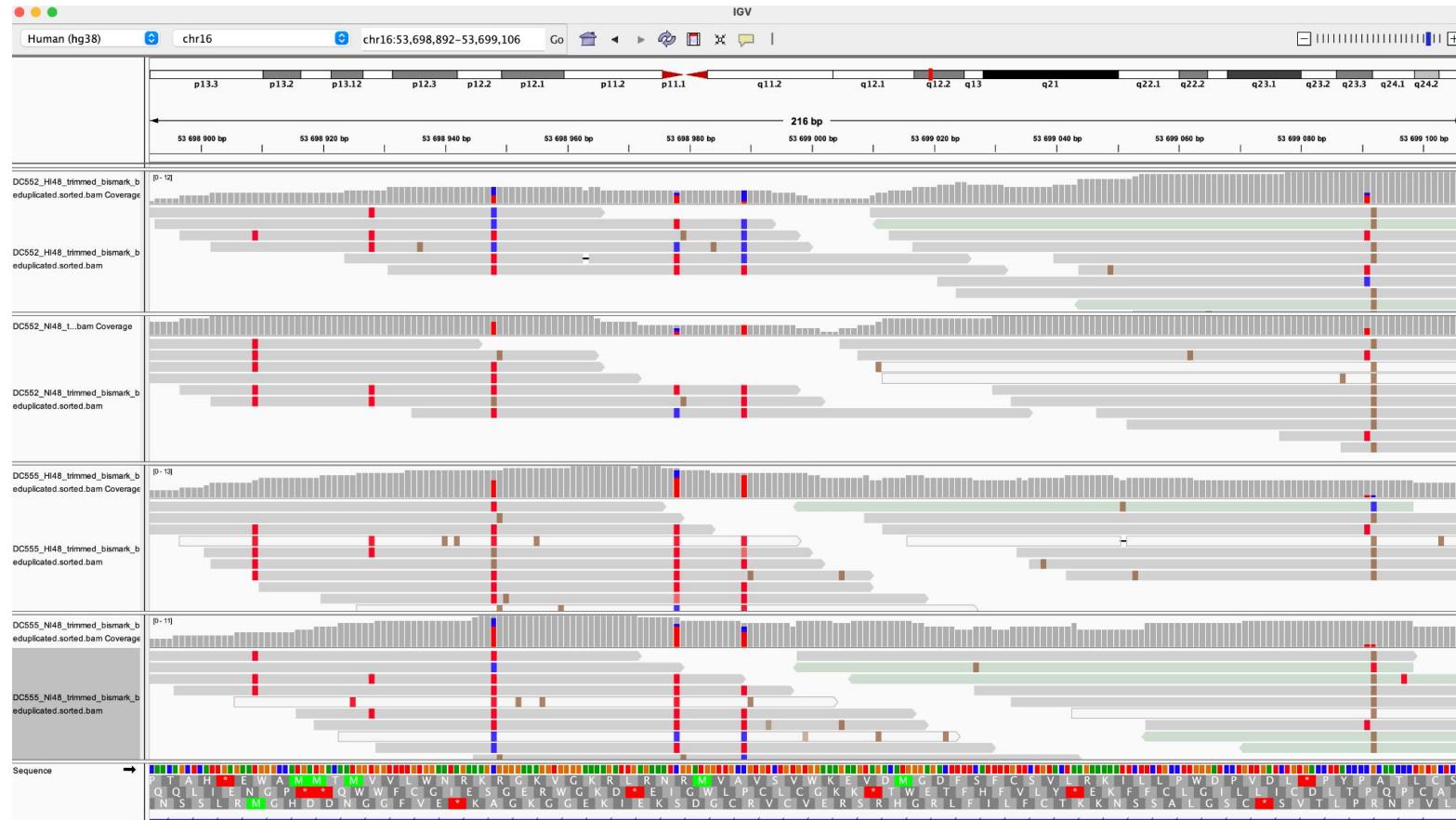
 Export Plot



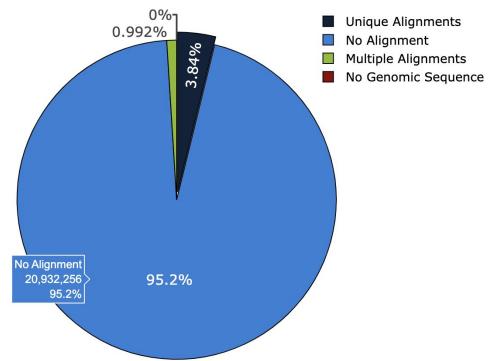
Visualization



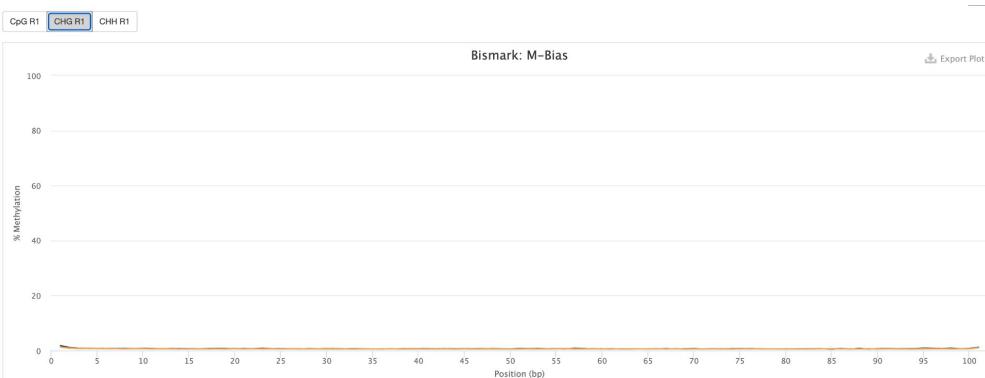
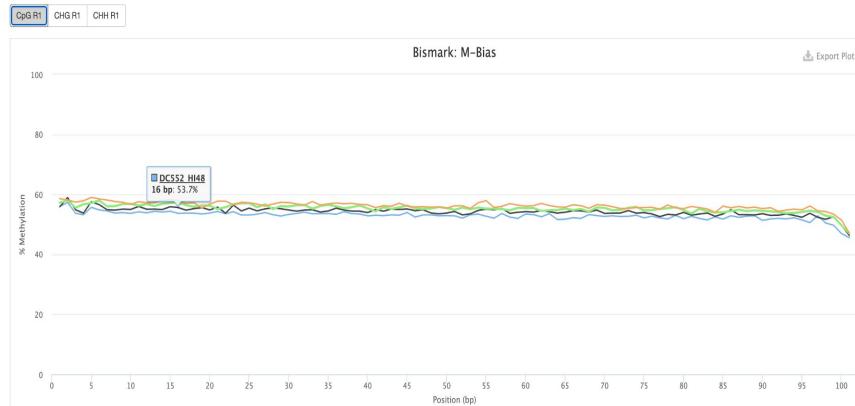
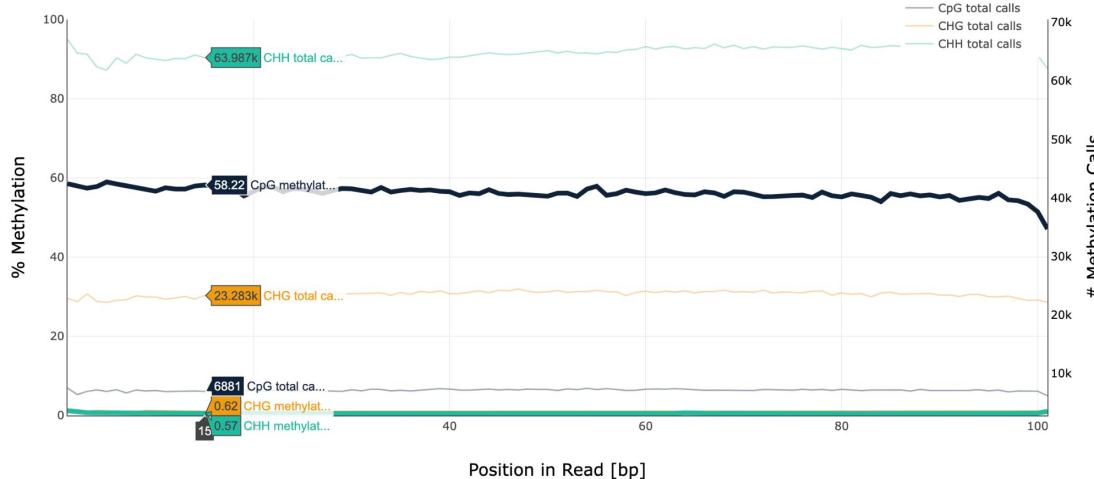
Visualization



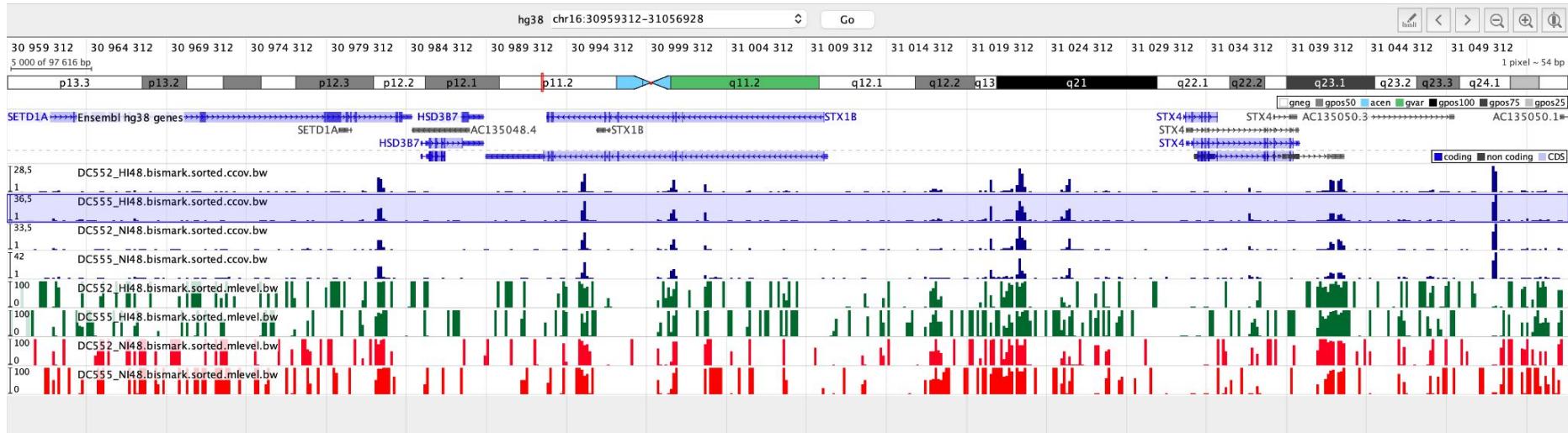
QC



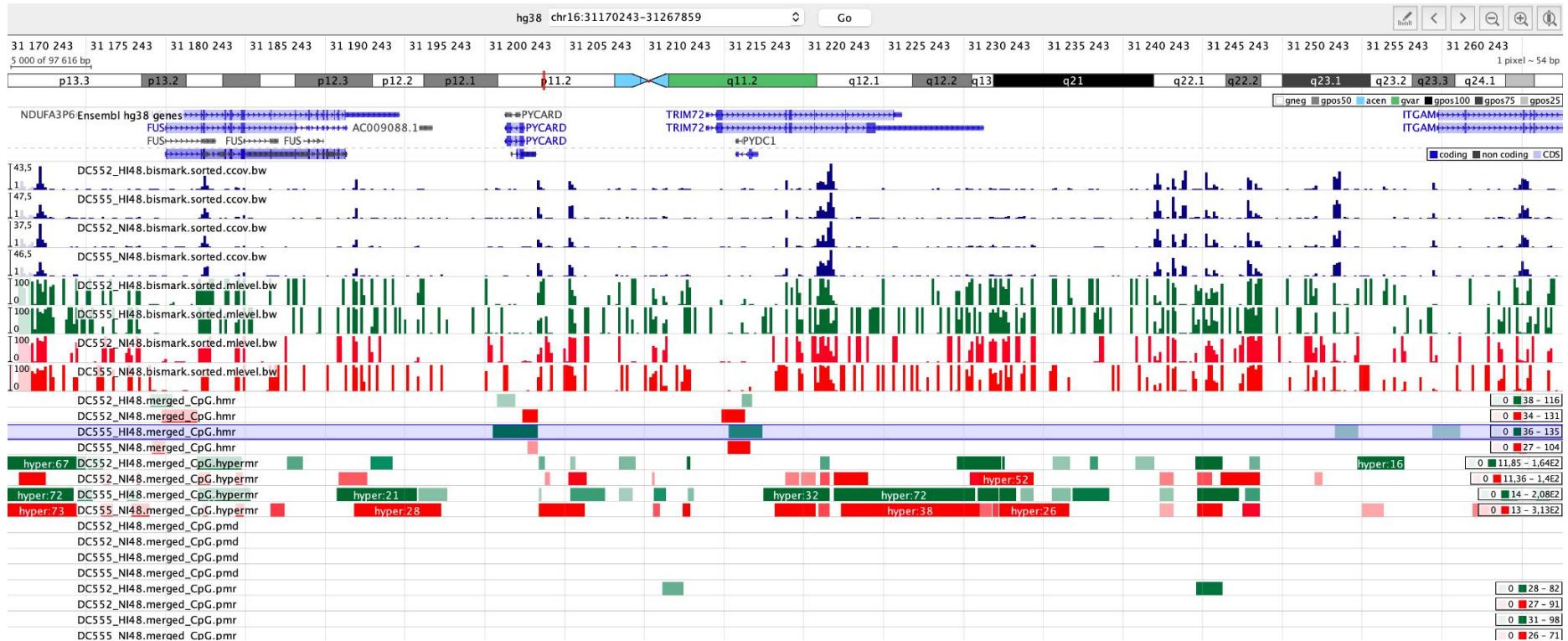
Read 1



bw



regions



df

12 meth_CpG_dmrs/dmrs.bed

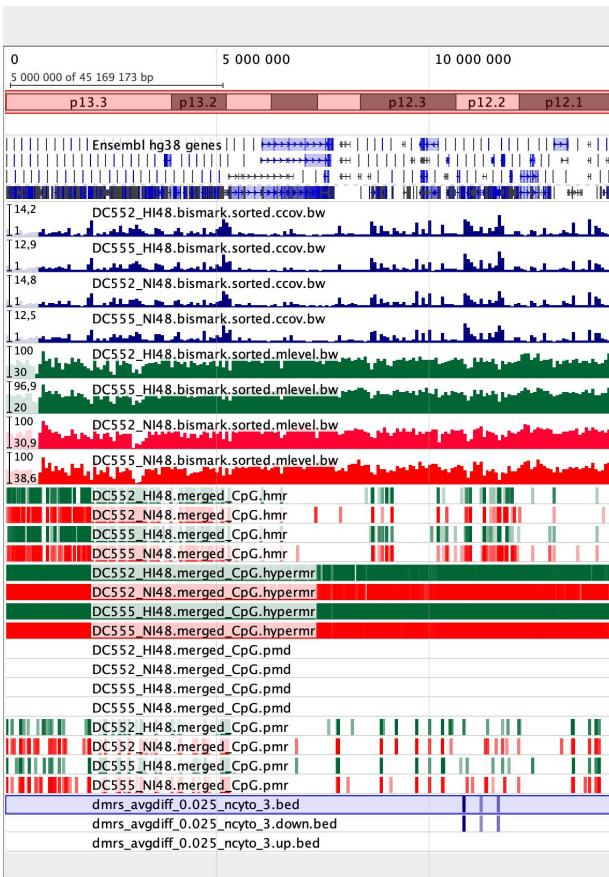
15886 meth_CpG_dmrs/dmc.bed

15886 meth_CpG_dmrs/dmc_adjusted.bed

5 meth_CpG_dmrs/dmrs_avgdiff_0.025_ncyto_3.down.bed

5 meth_CpG_dmrs/dmrs_avgdiff_0.025_ncyto_3.bed

0 meth_CpG_dmrs/dmrs_avgdiff_0.025_ncyto_3.up.bed

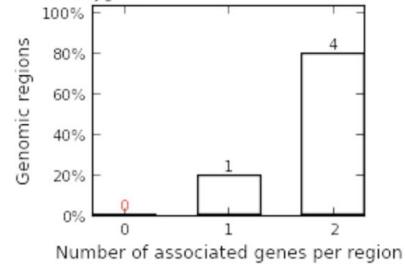


GREAT

Number of associated genes per region

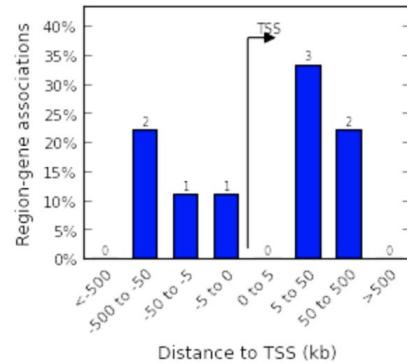
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- Genomic regions associated with one or more genes
- Genomic regions not associated with any genes



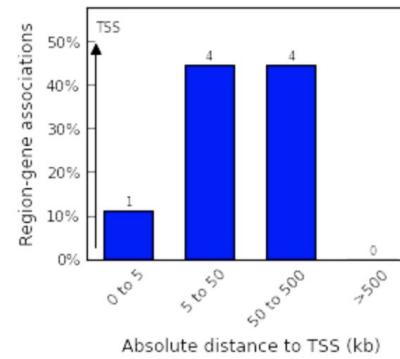
Binned by orientation and distance to TSS

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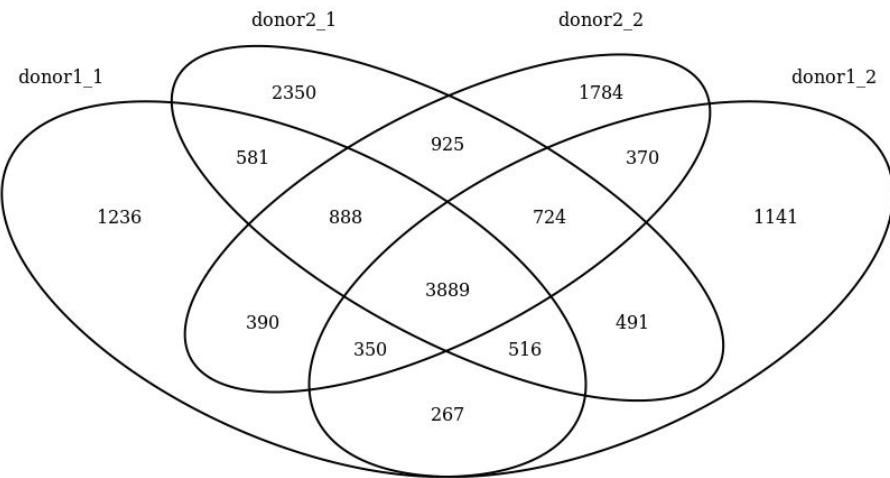
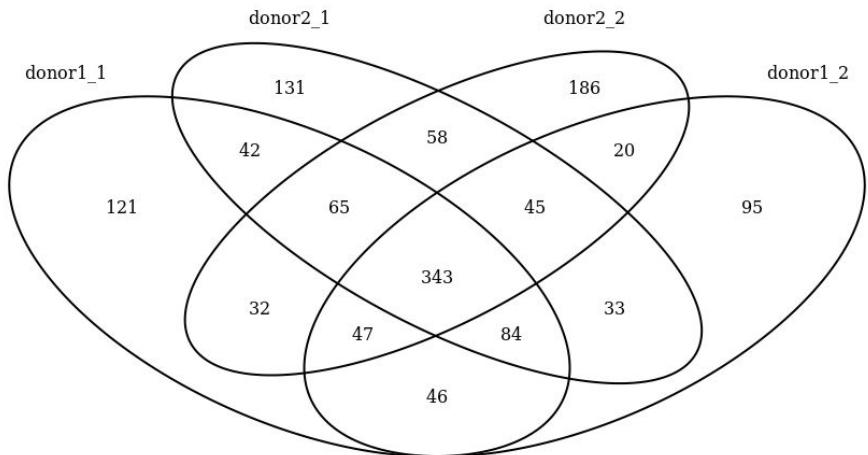


Binned by absolute distance to TSS

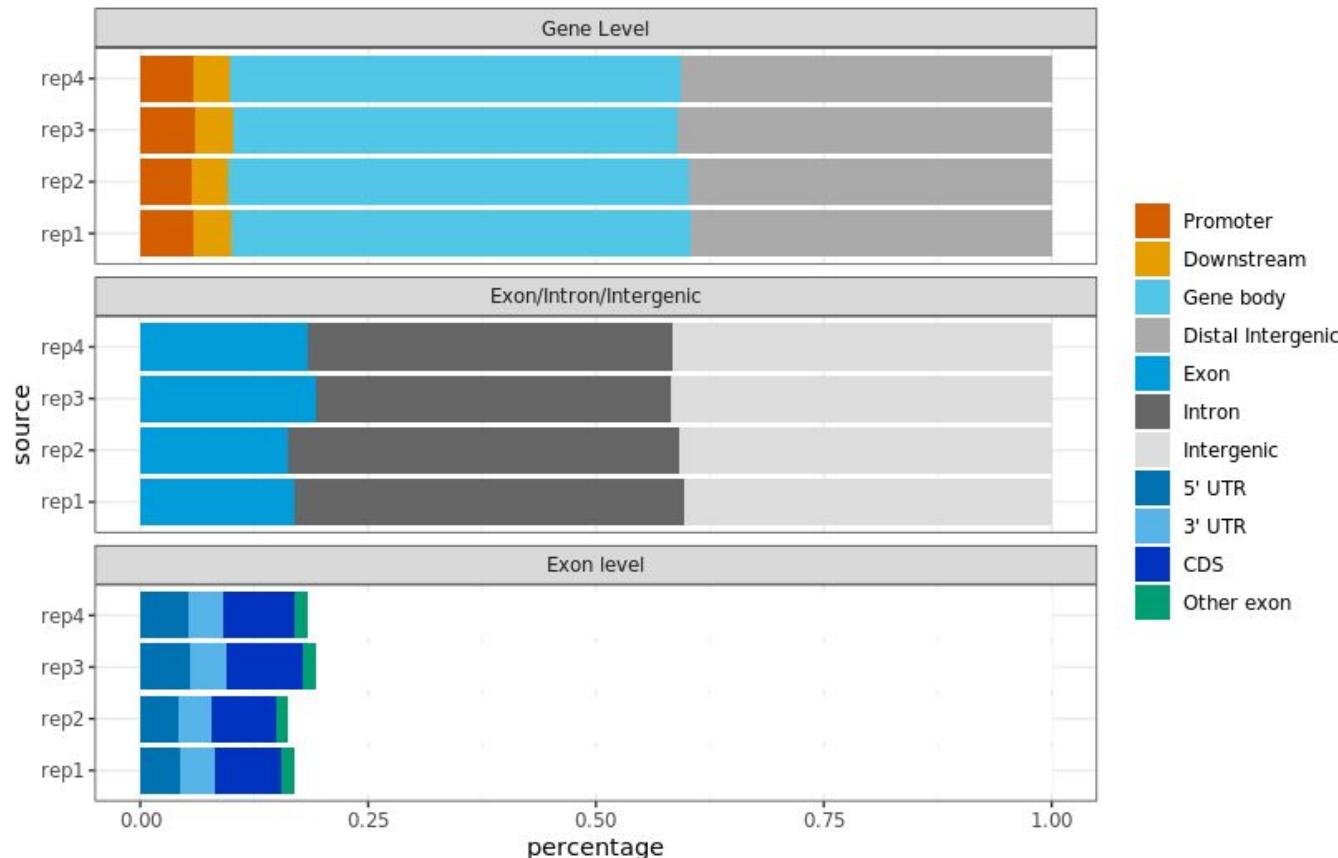
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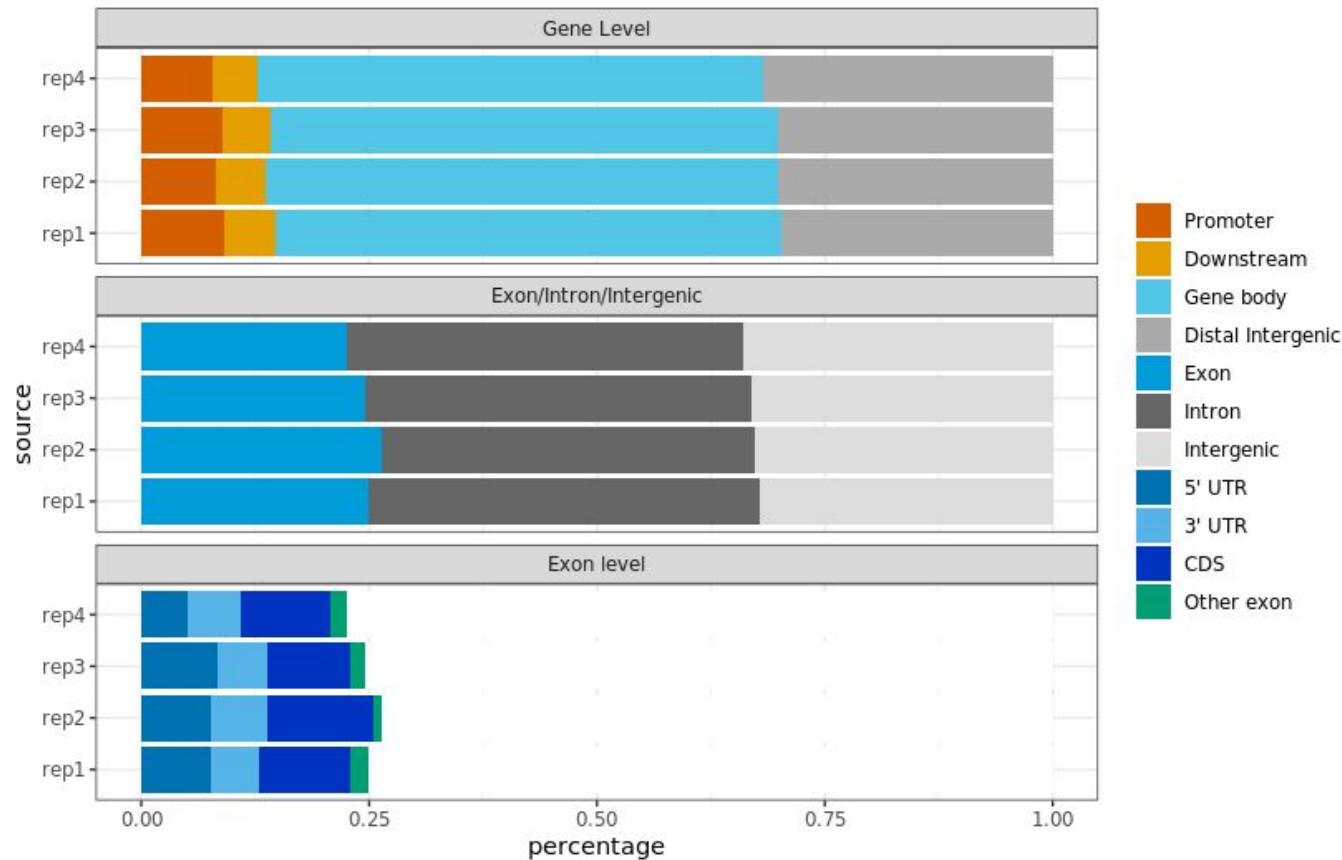
Replicates consistency Hypo and Hyper



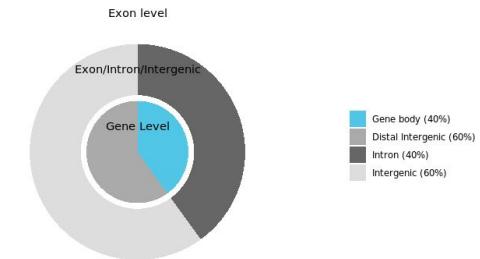
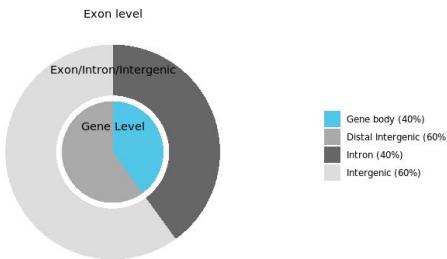
Positional annotation hyper



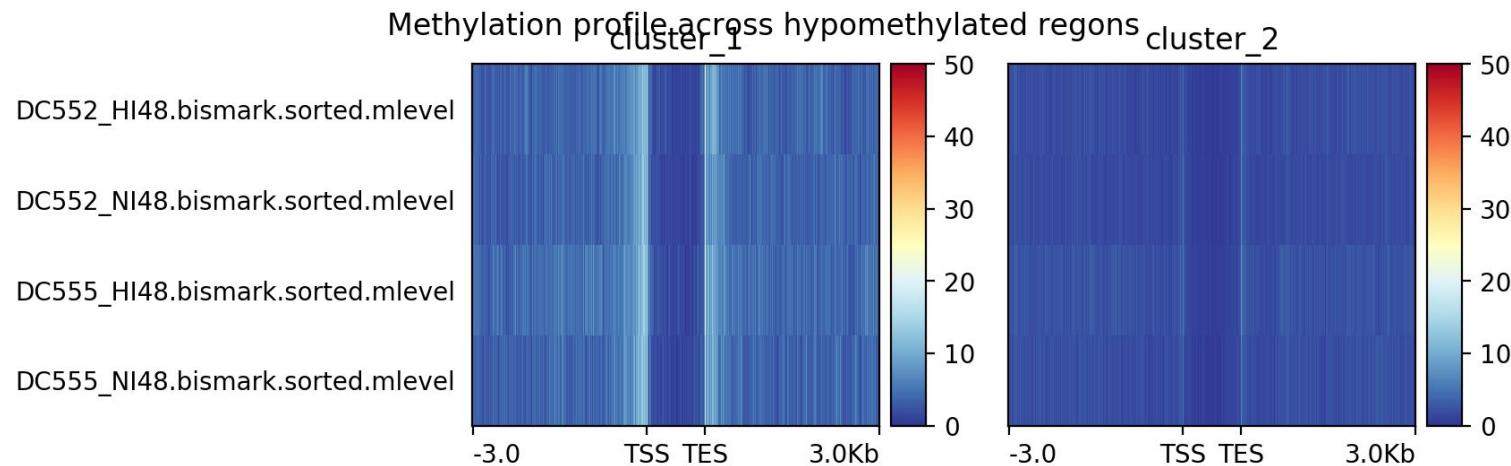
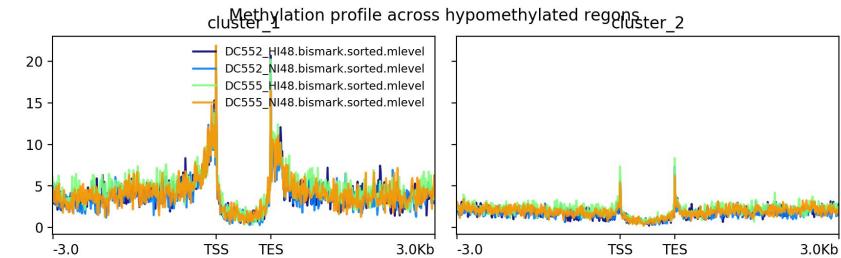
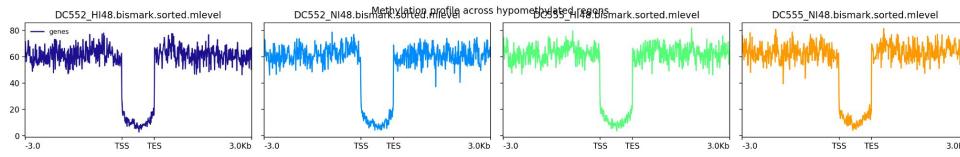
Positional annotation hypo



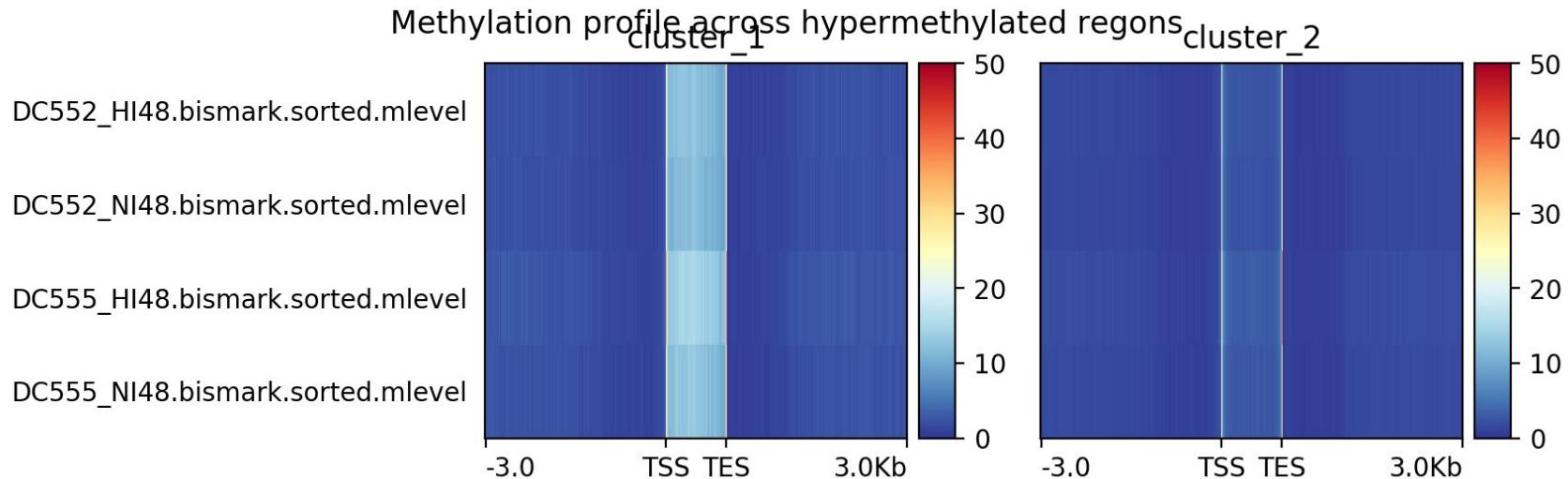
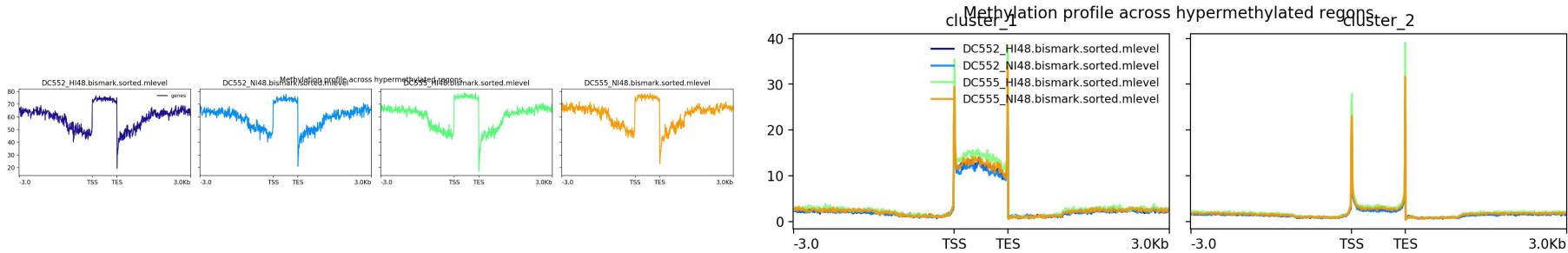
Distribution vs genomic features



Methylation profile across hypomethylated regions



Methylation profile across hypermethylated regions



Methylation profile for DMRs (only down)

