

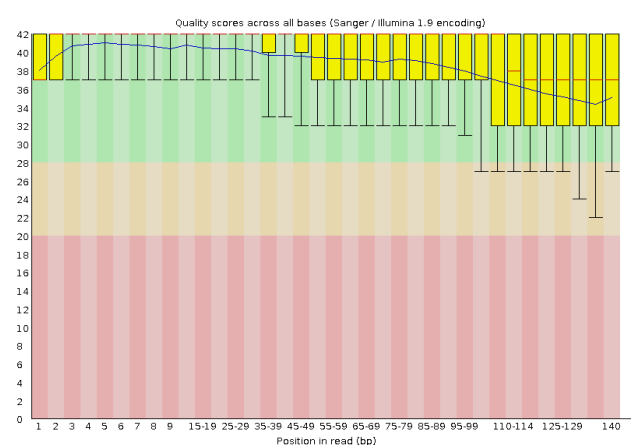
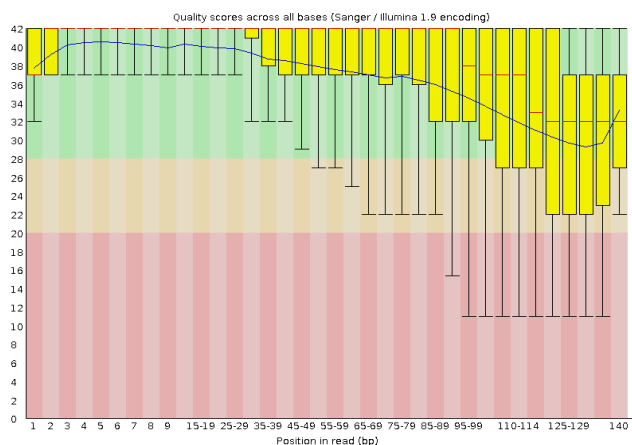
Report WGBS Methylation

Used Sequences and chromosome:

- Chromosome 17 of Genome mm10 has been used.
- This report describes the Methylation analysis performed on 8cell, ICM and Epiblast sequences.

FastQC analysis:

Replicate	Reads	Sequences		GC%		Sequence Lenght	
		Before Trimming	After Trimming	Before Trimming	After Trimming	Before Trimming	After Trimming
Replicate 1	8cell R1	105515878	102224948	36	35	19-140	20-140
	8cell R2	105515878	102224948	37	33	19-140	20-140
	Epiblast R1	163183367	159250949	22	22	19-140	20-140
	Epiblast R2	163183367	159250949	22	22	19-140	20-140
	ICM R1	108333570	105557539	26	25	19-140	20-140
	ICM R2	108333570	105557539	27	25	19-140	20-140
Replicate 2	8cell R1	38756007	38087730	26	26	19-140	20-140
	8cell R2	38756007	38087730	27	26	19-140	20-140
	Epiblast R1	210268052	207324742	22	22	19-140	20-140
	Epiblast R2	210268052	207324742	22	22	19-140	20-140
	ICM R1	98895869	98895869	26	26	19-140	20-140
	ICM R2	98976468	98895869	26	27	19-140	20-140



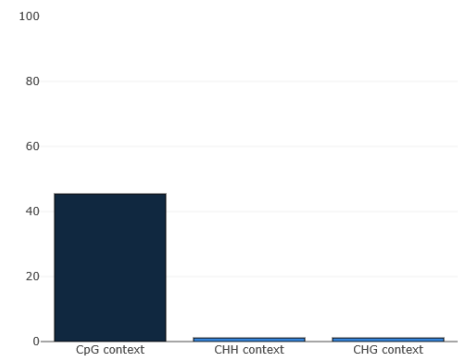
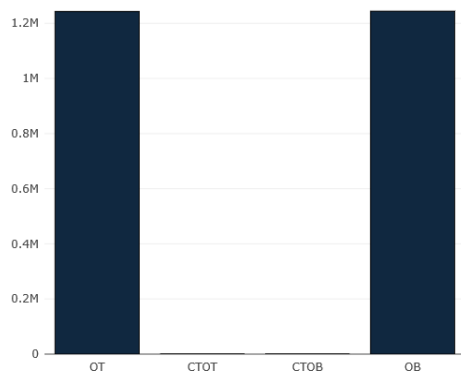
QC Analysis between 8cell rep2 samples before and after QC

For more Bismark images, kindly visit: https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/tree/master/Bismark_png

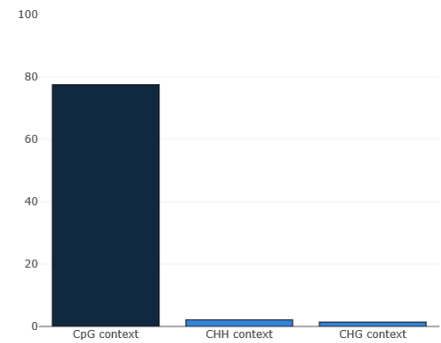
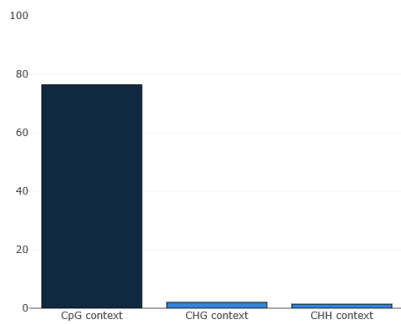
Bismark:

<p>8cell Methylation rep_1: Reads uniquely mapped to genome: No. of reads: 2487182 % of reads: 2.43% Before extraction: Methylated C's in CpG context: 3362279 Unmethylated C's in CpG context: 3633266 Percentage Methylation CpG context: 48.1% After extraction: Methylated C's in CpG context: 2180365 Unmethylated C's in CpG context: 2617263 Percentage Methylation CpG context: 45.4%</p> <p>ICM Methylation rep_1: Reads uniquely mapped to genome: No. of reads: 3609359 % of reads: 3.42% Before extraction: Methylated C's in CpG context: 2619172 Unmethylated C's in CpG context: 7027390 Percentage Methylation CpG context: 27.2% After extraction: Methylated C's in CpG context: 1891361 Unmethylated C's in CpG context: 5671490 Percentage Methylation CpG context: 25.0%</p> <p>Epiblast Methylation rep_1: Reads uniquely mapped to genome: No. of reads: 6108122 % of reads: 3.84% Before extraction: Methylated C's in CpG context: 11887344 Unmethylated C's in CpG context: 3674642 Percentage Methylation CpG context: 76.4% After extraction: Methylated C's in CpG context: 10083697 Unmethylated C's in CpG context: 2929285 Percentage Methylation CpG context: 77.5%</p>	<p>8cell Methylation rep_2: Reads uniquely mapped to genome: No. of reads: 7463936 % of reads: 3.55% Before extraction: Methylated C's in CpG context: 15412262 Unmethylated C's in CpG context: 4622857 Percentage Methylation CpG context: 76.9% After extraction: Methylated C's in CpG context: 1507564 Unmethylated C's in CpG context: 4636189 Percentage Methylation CpG context: 24.5%</p> <p>ICM Methylation rep_2: Reads uniquely mapped to genome: No. of reads: 3300806 % of reads: 3.34% Before extraction: Methylated C's in CpG context: 2449585 Unmethylated C's in CpG context: 6804858 Percentage Methylation CpG context: 26.5% After extraction: Methylated C's in CpG context: 1768898 Unmethylated C's in CpG context: 5362350 Percentage Methylation CpG context: 25.0%</p> <p>Epiblast Methylation rep_2: Reads uniquely mapped to genome: No. of reads: 7463936 % of reads: 3.55% Before extraction: Methylated C's in CpG context: 15412262 Unmethylated C's in CpG context: 4622857 Percentage Methylation CpG context: 76.9% After extraction: Methylated C's in CpG context: 14278956 Unmethylated C's in CpG context: 3876432 Percentage Methylation CpG context: 78.2%</p>
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Bismark reports:



8cell rep 1 R1



8cell rep 1 R2

Fig:- Bismark reports: Before Bismark Methylation extraction (left) and after Bismark Methylation Extraction (right).

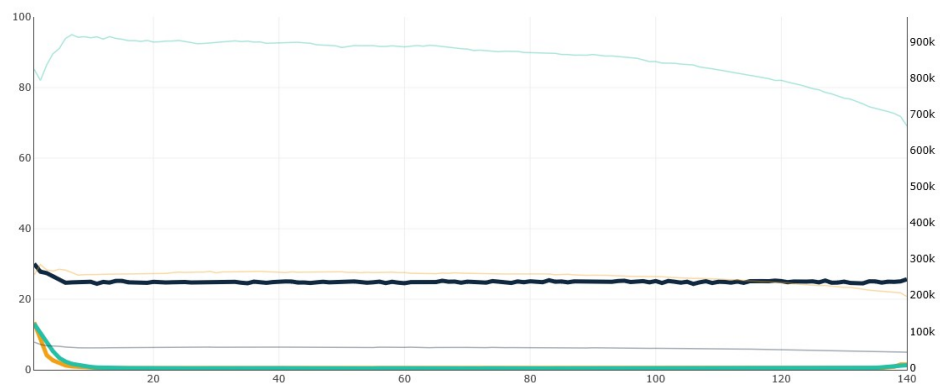


Fig: ICM rep 1 M-Bias plot

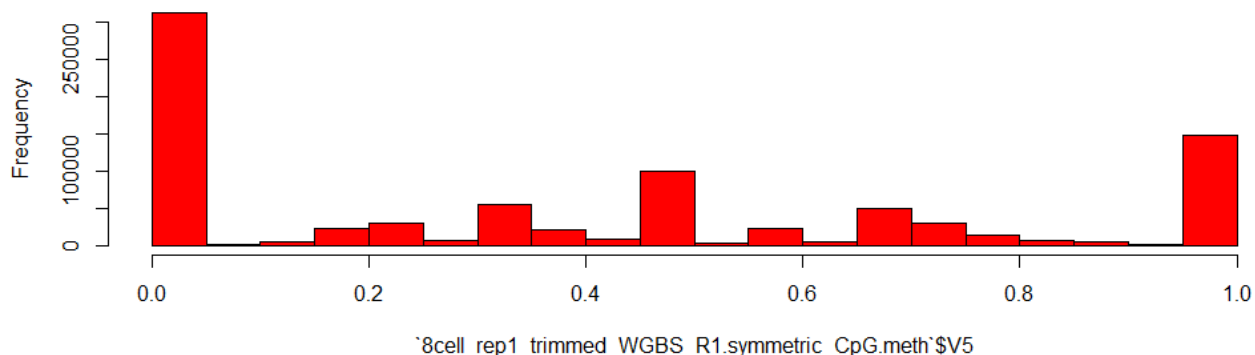
For more Bismark images, kindly visit: https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/tree/master/Bismark_png

Commands list can be found [here](https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/blob/master/Methylation%20Assignment%20Commands.pdf). All the commands are for rep2, and later rep1 combined. Same commands have been modified to be used for rep1. Please follow the link:

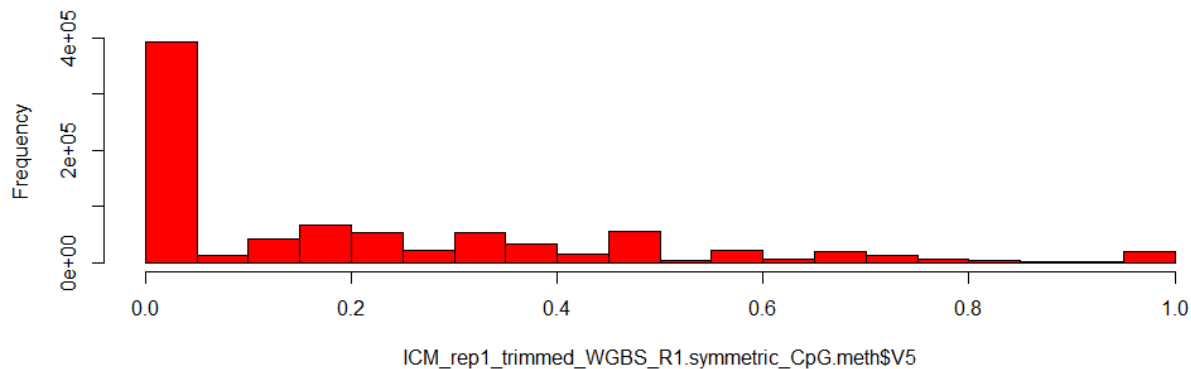
<https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/blob/master/Methylation%20Assignment%20Commands.pdf>

CpG Cytosine Methylation Levels Histograms:

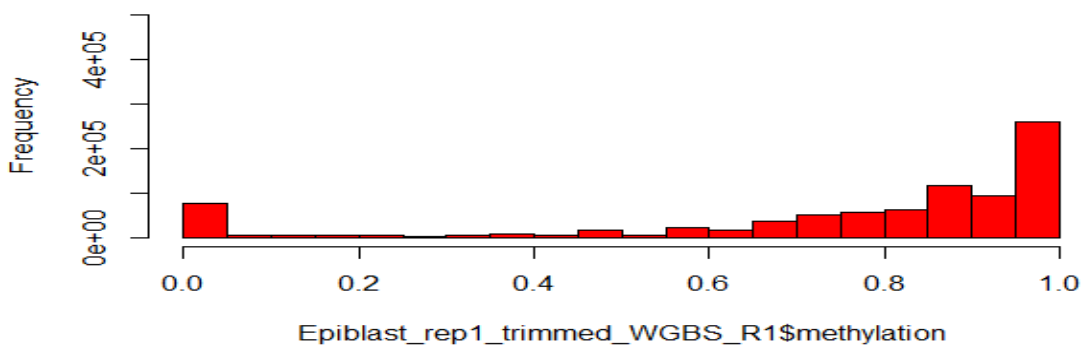
Histogram of `8cell_rep1_trimmed_WGBS_R1.symmetric_CpG.meth`\$V5



Histogram of ICM_rep1_trimmed_WGBS_R1.symmetric_CpG.meth\$V5



Histogram of Epiblast_rep1_trimmed_WGBS_R1\$methylation



Genome Browser Tracks:

Methylation and CpG analysis:

```
track type=bigWig visibility=full
name="8cell_rep1_trimmed_WGBS_R1.methylation.bigWig" color=197,172,24
maxHeightPixels=24 viewLimits=0:10 autoScale=off alwaysZero=on
bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/
raw/master/8cell\_rep1\_trimmed\_WGBS\_R1.methylation.bigWig
```

```
track type=bigWig visibility=full
name="8cell_rep1_trimmed_WGBS_R1_genomecov.coverage.bigWig"
color=0,0,0 maxHeightPixels=24 viewLimits=0:20 autoScale=off
alwaysZero=on bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/
\*8cell\_rep1\_trimmed\_WGBS\_R1\_genomecov.coverage.bigWig
```

```
track type=bigWig visibility=full
name="Epiblast_rep1_trimmed_WGBS_R1.methylation.bigWig"
color=197,172,24 maxHeightPixels=24 viewLimits=0:10 autoScale=off
alwaysZero=on bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/
Epiblast\_rep1\_trimmed\_WGBS\_R1.methylation.bigWig
```

```
track type=bigWig visibility=full
name="Epiblast_rep1_trimmed_WGBS_R1_genomecov.coverage.bigWig"
color=0,0,0 maxHeightPixels=24 viewLimits=0:20 autoScale=off
alwaysZero=on bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/
\*Epiblast\_rep1\_trimmed\_WGBS\_R1\_genomecov.coverage.bigWig
```

```
track type=bigWig visibility=full
name="ICM_rep1_trimmed_WGBS_R1.methylation.bigWig" color=197,172,24
maxHeightPixels=24 viewLimits=0:10 autoScale=off alwaysZero=on
bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/
raw/master/ICM\_rep1\_trimmed\_WGBS\_R1.methylation.bigWig
```

```
track type=bigWig visibility=full
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maxHeightPixels=24 viewLimits=0:20 autoScale=off alwaysZero=on
bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/
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```

```
track type=bigWig visibility=full
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maxHeightPixels=24 viewLimits=0:10 autoScale=off alwaysZero=on
```

bigDataUrl=[https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/
raw/master/v1/*8cell_rep2_trimmed_WGBS_R1.methylation.bigWig](https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/*8cell_rep2_trimmed_WGBS_R1.methylation.bigWig)

track type=bigWig visibility=full
name="8cell_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig"
color=0,0,0 maxHeightPixels=24 viewLimits=0:20 autoScale=off
alwaysZero=on bigDataUrl=[https://github.com/SarmadAK/Files-for-UCSC-
Genome-Browser/raw/master/v1/
*8cell_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig](https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/*8cell_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig)

track type=bigWig visibility=full
name="Epiblast_rep2_trimmed_WGBS_R1.methylation.bigWig"
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Genome-Browser/raw/master/v1/
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track type=bigWig visibility=full
name="Epiblast_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig"
color=0,0,0 maxHeightPixels=24 viewLimits=0:20 autoScale=off
alwaysZero=on bigDataUrl=[https://github.com/SarmadAK/Files-for-UCSC-
Genome-Browser/raw/master/v1/
*Epiblast_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig](https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/*Epiblast_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig)

track type=bigWig visibility=full
name="ICM_rep2_trimmed_WGBS_R1.methylation.bigWig" color=197,172,24
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raw/master/v1/*ICM_rep2_trimmed_WGBS_R1.methylation.bigWig](https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/*ICM_rep2_trimmed_WGBS_R1.methylation.bigWig)

track type=bigWig visibility=full
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raw/master/v1/*ICM_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig](https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/*ICM_rep2_trimmed_WGBS_R1_genomecov.coverage.bigWig)

Session Link: https://genome.ucsc.edu/s/sarmadak/mm10_Methylation

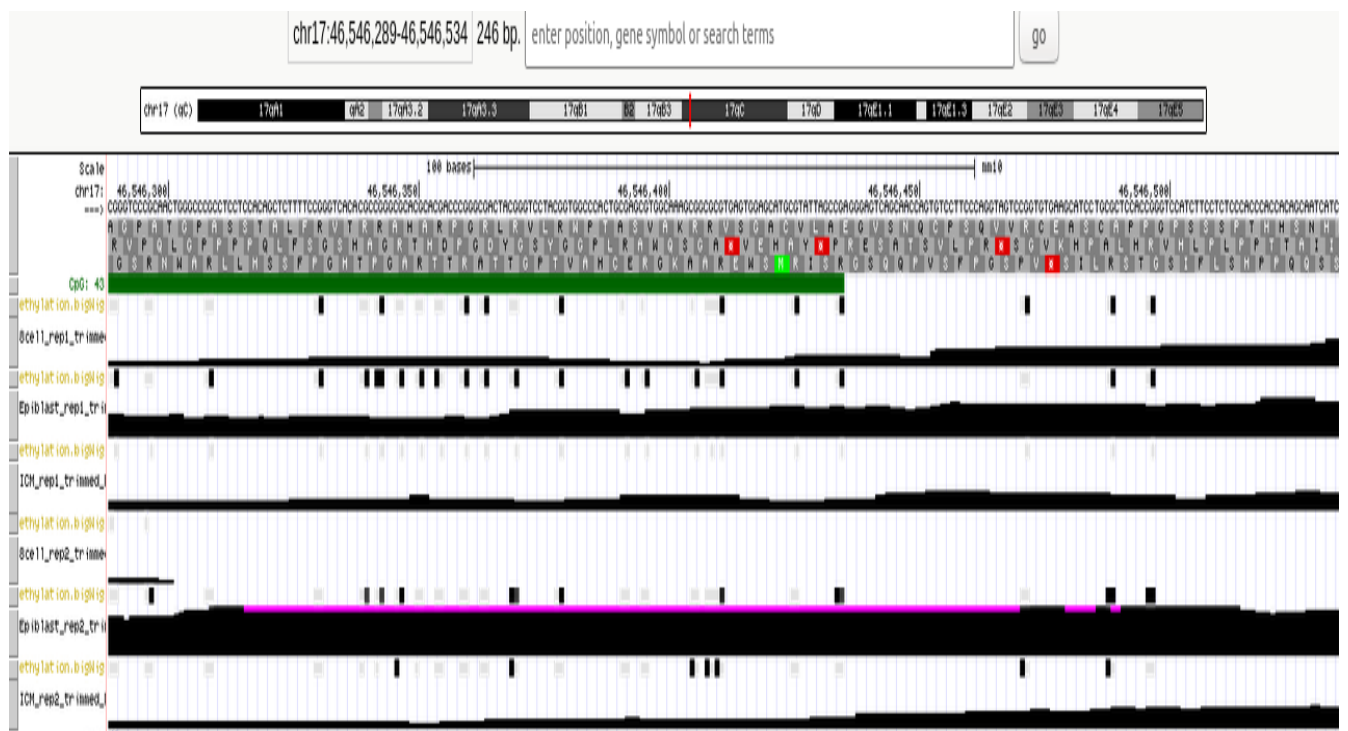
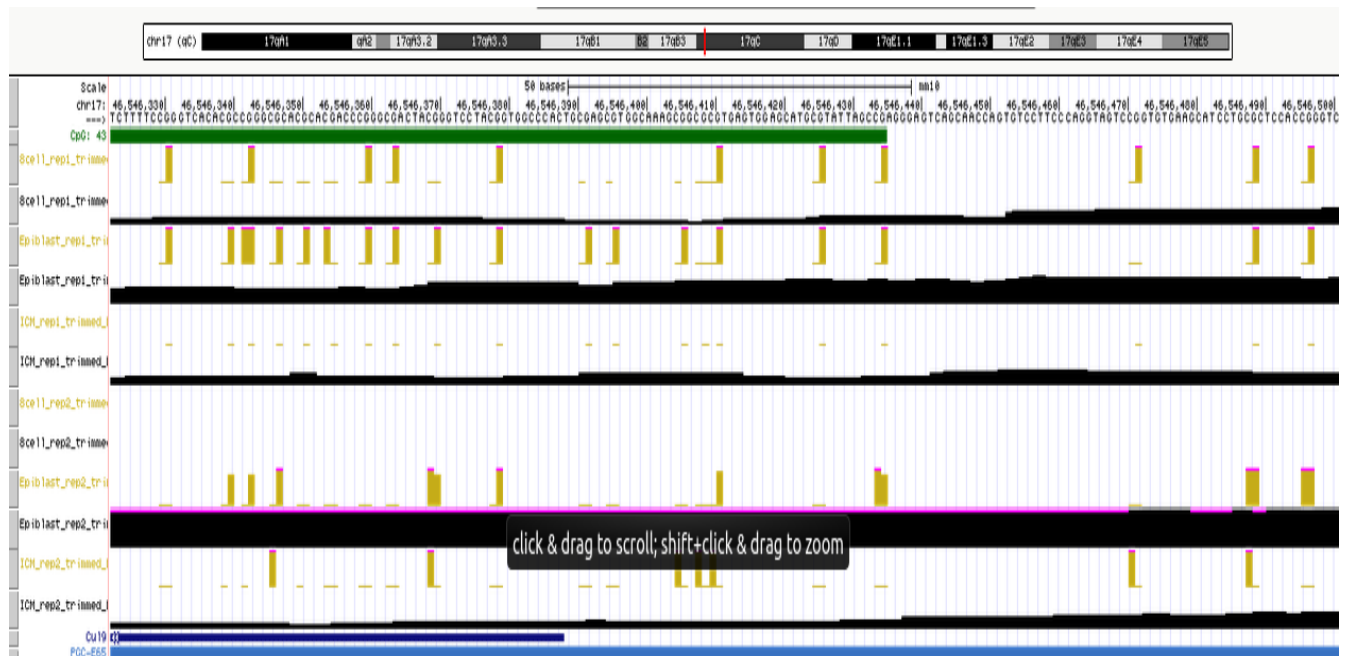


Fig:UCSC Genome Browser, cytosine Methylation and coverage overview at position chromosome 17.

DMR Analysis:

```
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alwaysZero=on bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/raw/master/v1/\*Epiblast.dmr.bb
```

```
track type=bigBed visibility=full name="ICM.dmr.bb" color=0,0,0
maxHeightPixels=24 viewLimits=0:20 autoScale=off alwaysZero=on
bigDataUrl=https://github.com/SarmadAK/Files-for-UCSC-Genome-Browser/
raw/masterv1/\*ICM.dmr.bb
```

Session Link: <https://genome.ucsc.edu/s/sarmadak/mm10>

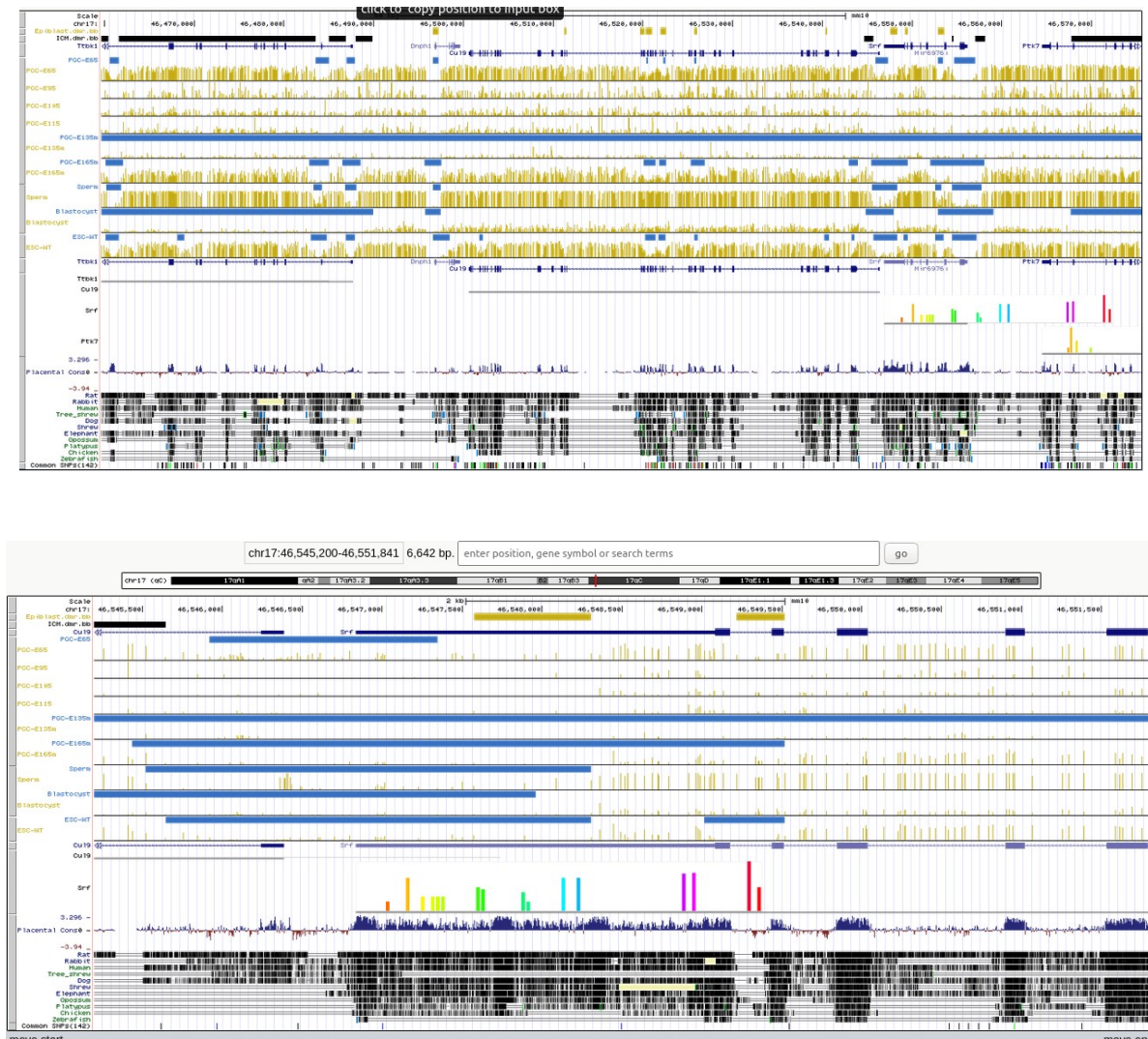


Fig: Differentially Methylated Regions illustrated in UCSC Genome Browser

