

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2019/09/27 15:57:23*

# 1. Input data & parameters (inside of regions)

## 1.1. QualiMap command line

```

qualimap bamqc -bam
/nfs/no_backup/rg/projects/regeneration/pipeline/grape-nf-dm6-
r6.22/work/f6/1ade09b8f0b66c7fd47f1a8b94b35b/H16H00C2_m4_n10_toGe
nome.bam -gff
/nfs/users2/rg/projects/references/Annotation/D.melanogaster/dmel_r6.22/m
RNA_ncRNA/ucsc.dmel-all-
r6.22.mRNA.nRNA.190.length.selection.type.no.Overlapping.Sorted.gtf -nw
400 -hm 3

```

## 1.2. Alignment

Command line:	<pre> STAR --runThreadN 8 --genomeDir genomeDir --readFilesIn C2- dash_R1.fastq.gz C2- dash_R2.fastq.gz -- readFilesCommand pigz -p8 -dc --limitBAMsortRAM 33285996544 -- outSAMtype BAM SortedByCoordinate -- outSAMattributes NH HI AS NM MD --outSAMunmapped Within -- outSAMattrRGline ID:H16H00C2 PU:H16H00C2 SM:H16H00C2 PL:ILLUMINA CN:CRG -- outFilterType BySJout -- outFilterMultimapNmax 10 -- outFilterMismatchNmax 999 -- outFilterMismatchNoverReadLmax 0.04 --alignIntronMin 20 -- alignIntronMax 1000000 -- alignMatesGapMax 1000000 -- alignSJoverhangMin 8 -- alignSJDBoverhangMin 1 -- </pre>
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	quantMode TranscriptomeSAM
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	STAR (STAR_2.4.0j)
Analysis date:	Fri Sep 27 15:57:22 CEST 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/nfs/no_backup/rg/projects/regenerati on/pipeline/grape-nf-dm6- r6.22/work/f6/1ade09b8f0b66c7fd47f 1a8b94b35b/H16H00C2_m4_n10_to Genome.bam

### 1.3. GFF region

Library protocol:	non-strand-specific
Outside statistics:	no
GFF file:	/nfs/users2/rg/projects/references/An notation/D.melanogaster/dmel_r6.22/ mRNA_ncRNA/ucsc.dmel-all- r6.22.mRNA.nRNA.190.length.selecti on.type.no.Overlapping.Sorted.gtf

## 2. Summary (inside of regions)

### 2.1. Globals

Reference size	143,726,002
Number of reads	40,555,738
Mapped reads	37,789,640 / 93.18%
Unmapped reads	2,766,098 / 6.82%
Mapped paired reads	37,789,640 / 93.18%
Mapped reads, first in pair	18,894,820 / 46.59%
Mapped reads, second in pair	18,894,820 / 46.59%
Mapped reads, both in pair	37,789,640 / 93.18%
Mapped reads, singletons	0 / 0%
Read min/max/mean length	76 / 76 / 76
Clipped reads	4,379,848 / 10.8%

### 2.2. Globals (inside of regions)

Regions size/percentage of reference	93,645,580 / 65.16%
Mapped reads	34,853,073 / 85.94%
Mapped reads, only first in pair	17,426,977 / 42.97%
Mapped reads, only second in pair	17,426,096 / 42.97%
Mapped reads, both in pair	34,853,073 / 85.94%
Mapped reads, singletons	0 / 0%
Correct strand reads	0 / 0%
Clipped reads	4,379,848 / 10.8%
Duplicated reads (estimated)	27,092,782 / 77.73%

Duplication rate	52.28%
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### 2.3. ACGT Content (inside of regions)

Number/percentage of A's	642,010,625 / 24.48%
Number/percentage of C's	666,967,103 / 25.44%
Number/percentage of T's	649,128,642 / 24.76%
Number/percentage of G's	663,992,714 / 25.32%
Number/percentage of N's	3,150,264,386 / 120.14%
GC Percentage	50.76%

### 2.4. Coverage (inside of regions)

Mean	61.6449
Standard Deviation	323.3146

### 2.5. Mapping Quality (inside of regions)

Mean Mapping Quality	242.15
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### 2.6. Insert size (inside of regions)

Mean	512.78
Standard Deviation	6,850.13
P25/Median/P75	158 / 209 / 308

### 2.7. Mismatches and indels (inside of regions)

General error rate	0.36%
Mismatches	20,160,812
Insertions	291,431

Mapped reads with at least one insertion	0.77%
Deletions	180,679
Mapped reads with at least one deletion	0.47%
Homopolymer indels	66.93%

## 2.8. Chromosome stats (inside of regions)

Name	Length	Mapped bases	Mean coverage	Standard deviation
chr2L	15854837	1053112778	66.4222	330.7301
chr2R	16880511	1320964753	78.2538	403.4204
chr3L	18005806	1037078633	57.5969	282.012
chr3R	23285070	1282634495	55.084	272.781
chr4	1040043	73441293	70.6137	315.1119
chrM	11009	54430362	4,944.1695	5,943.0238
chrUn_DS485 919v1	0	0	0	0
chrUn_DS483 755v1	0	0	0	0
chrUn_DS485 425v1	0	0	0	0
chrUn_DS484 861v1	0	0	0	0
chrUn_DS484 484v1	0	0	0	0
chrUn_DS483 705v1	0	0	0	0

chrUn_DS485 490v1	0	0	0	0
chrUn_DS485 998v1	0	0	0	0
chrUn_DS483 873v1	0	0	0	0
chrUn_DS485 608v1	0	0	0	0
chrUn_DS485 270v1	0	0	0	0
chrUn_DS485 979v1	0	0	0	0
chrUn_DS485 398v1	0	0	0	0
chrUn_DS484 139v1	0	0	0	0
chrUn_DS483 906v1	0	0	0	0
chrUn_DS485 760v1	0	0	0	0
chrUn_DS484 191v1	0	0	0	0
chrUn_DS485 340v1	0	0	0	0
chrUn_DS484 489v1	0	0	0	0
chrUn_DS485 495v1	0	0	0	0
chrUn_DS484 923v1	0	0	0	0

chrUn_DS484 663v1	0	0	0	0
chrUn_DS485 390v1	0	0	0	0
chrUn_DS485 130v1	0	0	0	0
chrUn_DS485 995v1	0	0	0	0
chrUn_DS484 448v1	0	0	0	0
chrUn_DS484 827v1	0	0	0	0
chrUn_DS485 467v1	0	0	0	0
chrUn_DS485 433v1	0	0	0	0
chrUn_DS484 944v1	0	0	0	0
chrUn_DS485 504v1	0	0	0	0
chrUn_DS484 938v1	0	0	0	0
chrUn_DS485 984v1	0	0	0	0
chrUn_DS484 921v1	0	0	0	0
chrUn_DS485 859v1	0	0	0	0
chrUn_DS485 086v1	0	0	0	0



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chrUn_DS485 294v1	0	0	0	0
chrUn_DS484 855v1	0	0	0	0
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chrUn_DS485 386v1	0	0	0	0
chrUn_DS484 726v1	0	0	0	0
chrUn_DS484 366v1	0	0	0	0
chrUn_DS486 002v1	0	0	0	0
chrUn_DS484 770v1	0	0	0	0
chrUn_DS485 354v1	0	0	0	0
chrUn_DS483 728v1	0	0	0	0
chrUn_DS485 403v1	0	0	0	0
chrUn_DS484 964v1	0	0	0	0
chrUn_DS483 921v1	0	0	0	0

chrUn_DS485 181v1	0	0	0	0
chrUn_DS485 602v1	0	0	0	0
chrUn_DS485 783v1	0	0	0	0
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chrUn_DS484 407v1	0	0	0	0
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chrUn_DS483 748v1	0	0	0	0
chrUn_DS484 460v1	0	0	0	0

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chrUn_DS484 039v1	0	0	0	0
chrUn_DS484 339v1	0	0	0	0
chrUn_DS485 457v1	0	0	0	0
chrUn_DS485 643v1	0	0	0	0
chrUn_DS484 689v1	0	0	0	0
chrUn_DS485 822v1	0	0	0	0
chrUn_DS485 678v1	0	0	0	0
chrUn_DS485 150v1	0	0	0	0
chrUn_DS484 746v1	0	0	0	0
chrUn_DS485 957v1	0	0	0	0
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chrUn_DS484 881v1	0	0	0	0

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chrUn_DS485 337v1	0	0	0	0
chrUn_DS483 700v1	0	0	0	0
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chrUn_DS483 719v1	0	0	0	0
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chrUn_DS485 239v1	0	0	0	0
chrUn_DS485 853v1	0	0	0	0
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chrUn_DS485 381v1	0	0	0	0
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chrUn_DS484 707v1	0	0	0	0
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chrUn_DS485 673v1	0	0	0	0
chrUn_DS483 879v1	0	0	0	0
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chrUn_DS485 891v1	0	0	0	0
chrUn_DS484 329v1	0	0	0	0
chrUn_DS484 653v1	0	0	0	0
chrUn_DS483 692v1	0	0	0	0
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chrUn_DS485 226v1	0	0	0	0
chrUn_DS484 470v1	0	0	0	0
chrUn_DS484 303v1	0	0	0	0
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chrUn_DS485 522v1	0	0	0	0
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chrUn_DS485 623v1	0	0	0	0
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chrUn_DS485 929v1	0	0	0	0
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chrUn_DS484 493v1	0	0	0	0
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chrUn_DS484 866v1	0	0	0	0
chrUn_DS484 772v1	0	0	0	0
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chrUn_DS485 982v1	0	0	0	0

chrUn_DS485 165v1	0	0	0	0
chrUn_DS484 404v1	0	0	0	0
chrUn_DS483 736v1	0	0	0	0
chrUn_DS485 654v1	0	0	0	0
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chrUn_DS484 776v1	0	0	0	0
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chrUn_DS484 920v1	0	0	0	0
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chrUn_DS484 948v1	0	0	0	0
chrUn_DS484 728v1	0	0	0	0

chrUn_DS484 313v1	0	0	0	0
chrUn_DS485 395v1	0	0	0	0
chrUn_DS484 443v1	0	0	0	0
chrUn_DS483 650v1	0	0	0	0
chrUn_DS485 498v1	0	0	0	0
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chrUn_DS484 549v1	0	0	0	0
chrUn_DS484 738v1	0	0	0	0

chrUn_DS484 985v1	0	0	0	0
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chrUn_DS484 154v1	0	0	0	0
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chrX_DS4838 85v1_random	0	0	0	0
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chrX_DS4843 26v1_random	0	0	0	0
chrX_DS4837 45v1_random	0	0	0	0
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chrX_DS4840 61v1_random	0	0	0	0
chrX_DS4843 30v1_random	0	0	0	0
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chrX_DS4840 46v1_random	0	0	0	0
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chrX_DS4839 74v1_random	0	0	0	0
chrX_DS4839 03v1_random	0	0	0	0
chrX_DS4845 38v1_random	0	0	0	0
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chrX_DS4840 60v1_random	0	0	0	0

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chrX_DS4839 69v1_random	0	0	0	0
chrX_DS4840 26v1_random	0	0	0	0
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chrX_CP0071 03v1_random	0	0	0	0
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chrY_DS4848 05v1_random	0	0	0	0
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chrY_DS4857 95v1_random	0	0	0	0
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chrY_DS4839 87v1_random	0	0	0	0

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chrY_DS4855 61v1_random	0	0	0	0
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chrY_DS4844 92v1_random	0	0	0	0
chrY_DS4854 83v1_random	0	0	0	0



chrY_DS4852 50v1_random	0	0	0	0
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chrY_DS4850 14v1_random	0	0	0	0
chrY_DS4847 57v1_random	0	0	0	0
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chrY_DS4846 74v1_random	0	0	0	0
chrY_DS4844 65v1_random	0	0	0	0

chrY_DS4854 36v1_random	0	0	0	0
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chrY_DS4839 88v1_random	0	0	0	0
chrY_DS4848 07v1_random	0	0	0	0
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chrY_DS4854 30v1_random	0	0	0	0
chrY_DS4853 16v1_random	0	0	0	0
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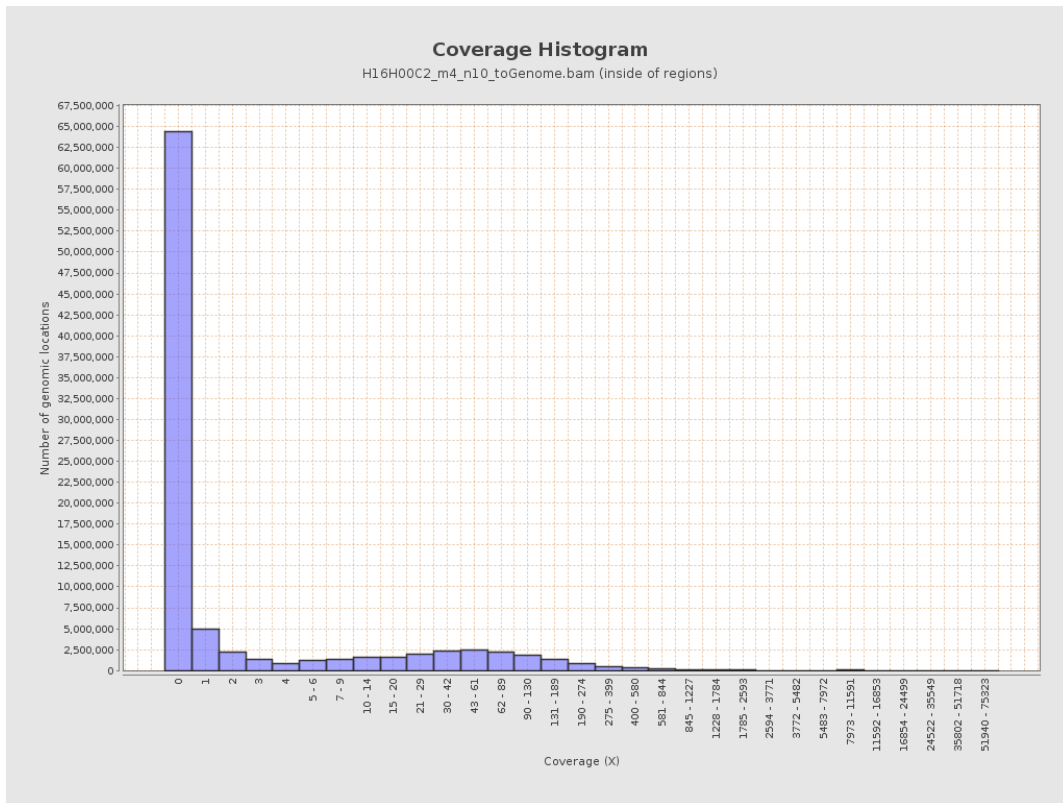
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chrY_DS4841 75v1_random	0	0	0	0
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chrY_DS4840 29v1_random	0	0	0	0
chrY_DS4840 94v1_random	0	0	0	0
chrY_DS4836 77v1_random	0	0	0	0
chrY_DS4837 88v1_random	0	0	0	0

chrY_DS4836 90v1_random	0	0	0	0
chrY_CP0071 09v1_random	0	0	0	0
chrY_CP0071 10v1_random	0	0	0	0
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chrY_CP0071 12v1_random	0	0	0	0
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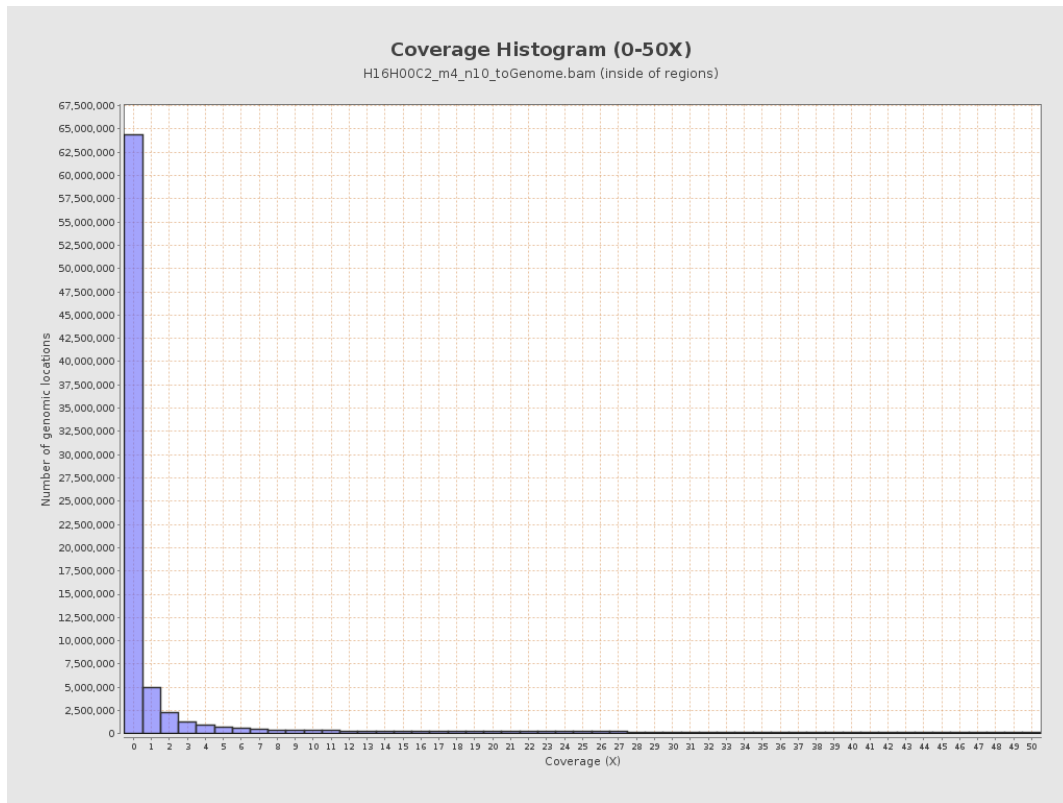
### 3. Results : Coverage across reference (inside of regions)



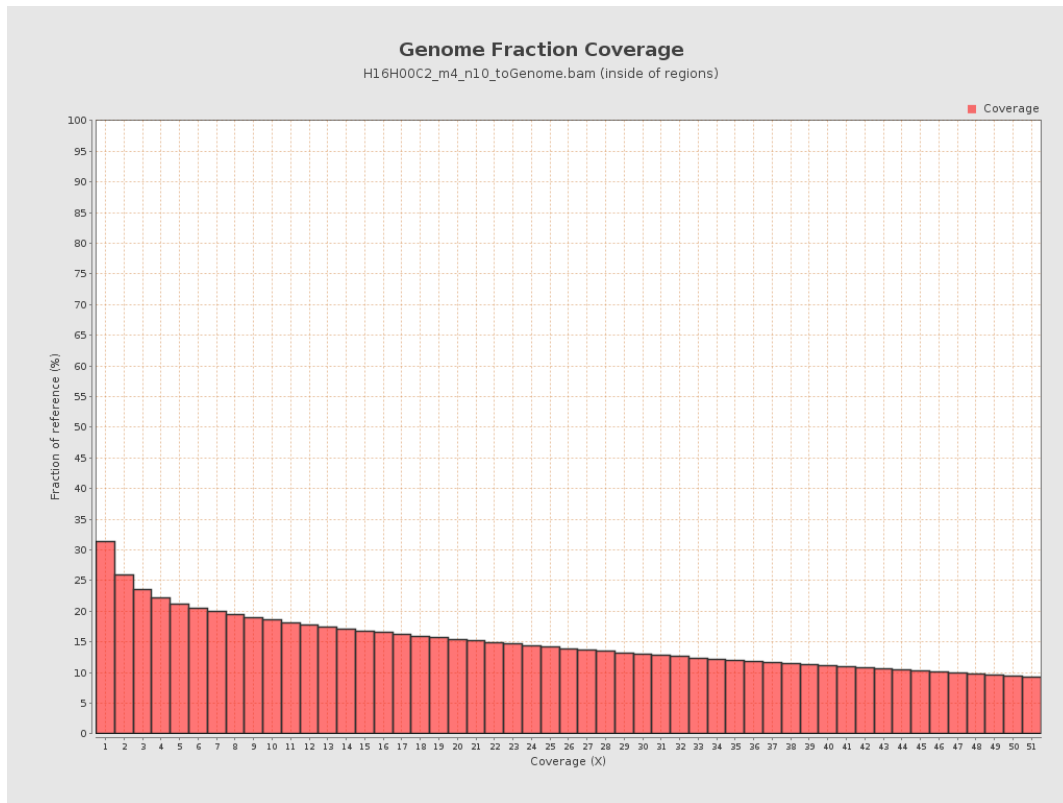
# 4. Results : Coverage Histogram (inside of regions)



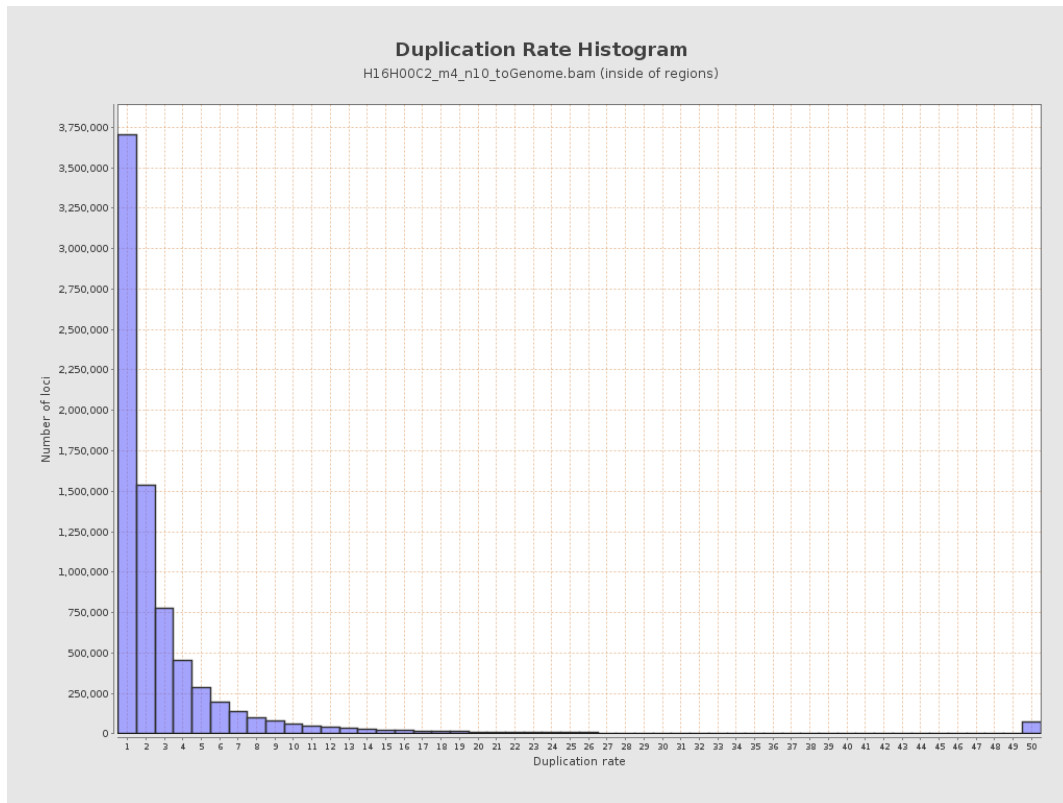
## 5. Results : Coverage Histogram (0-50X) (inside of regions)



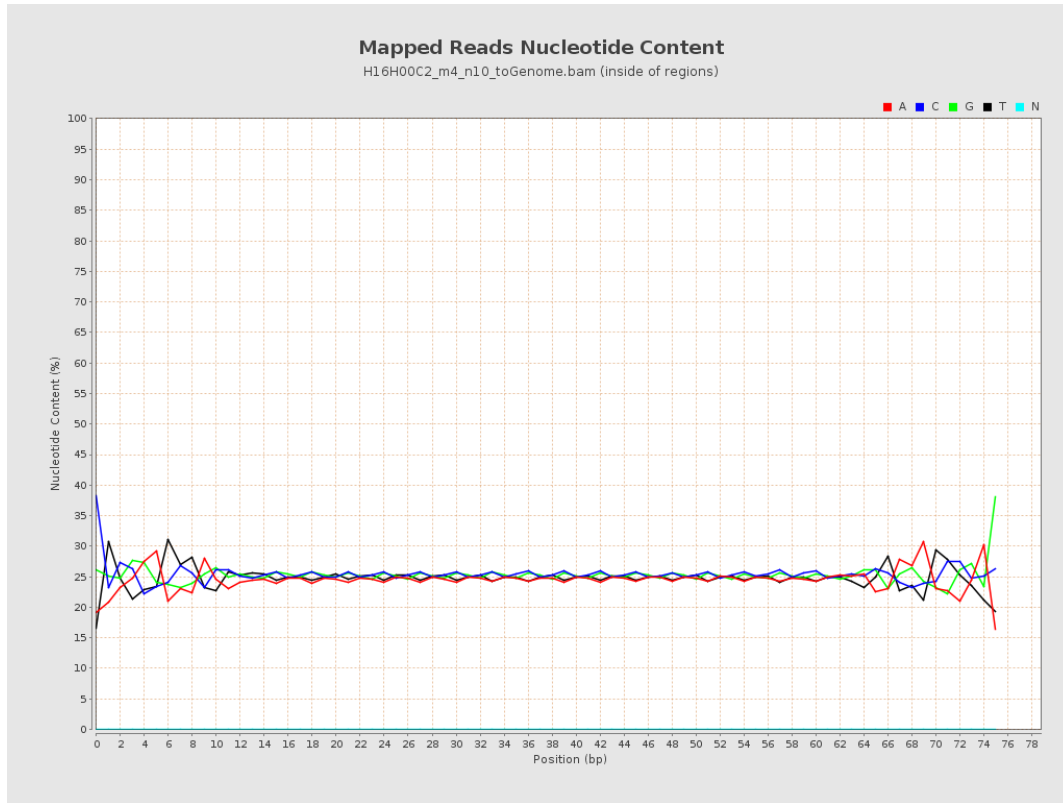
## 6. Results : Genome Fraction Coverage (inside of regions)



## 7. Results : Duplication Rate Histogram (inside of regions)

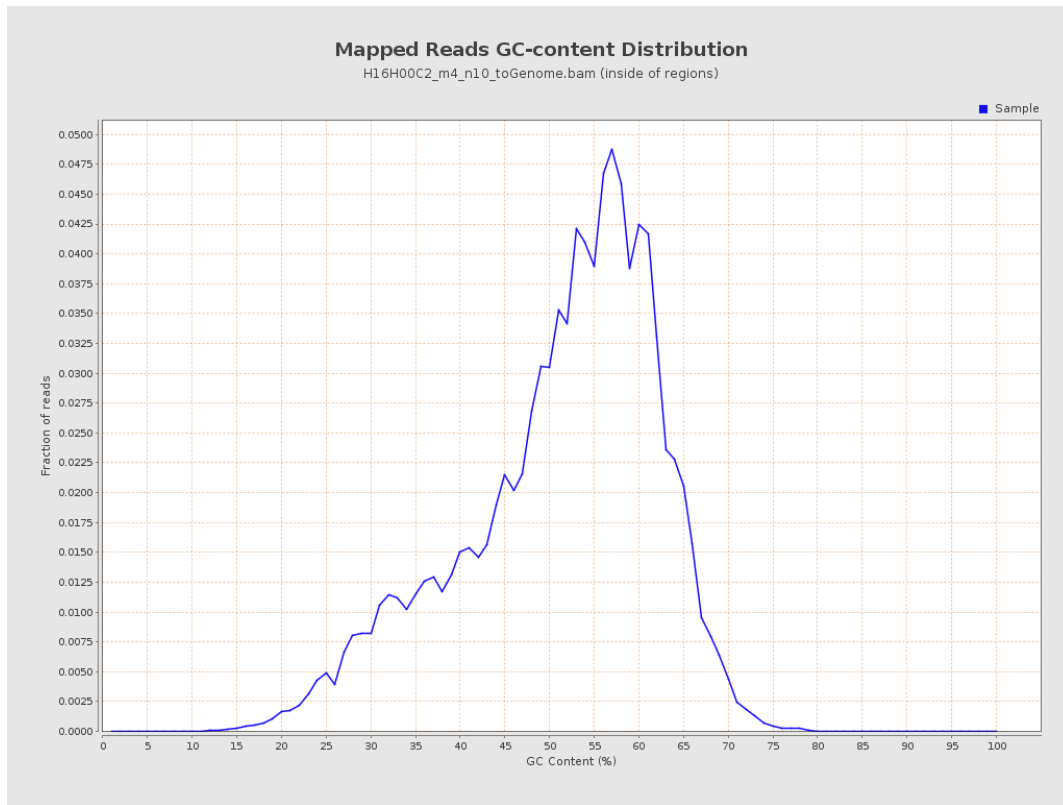


## 8. Results : Mapped Reads Nucleotide Content (inside of regions)

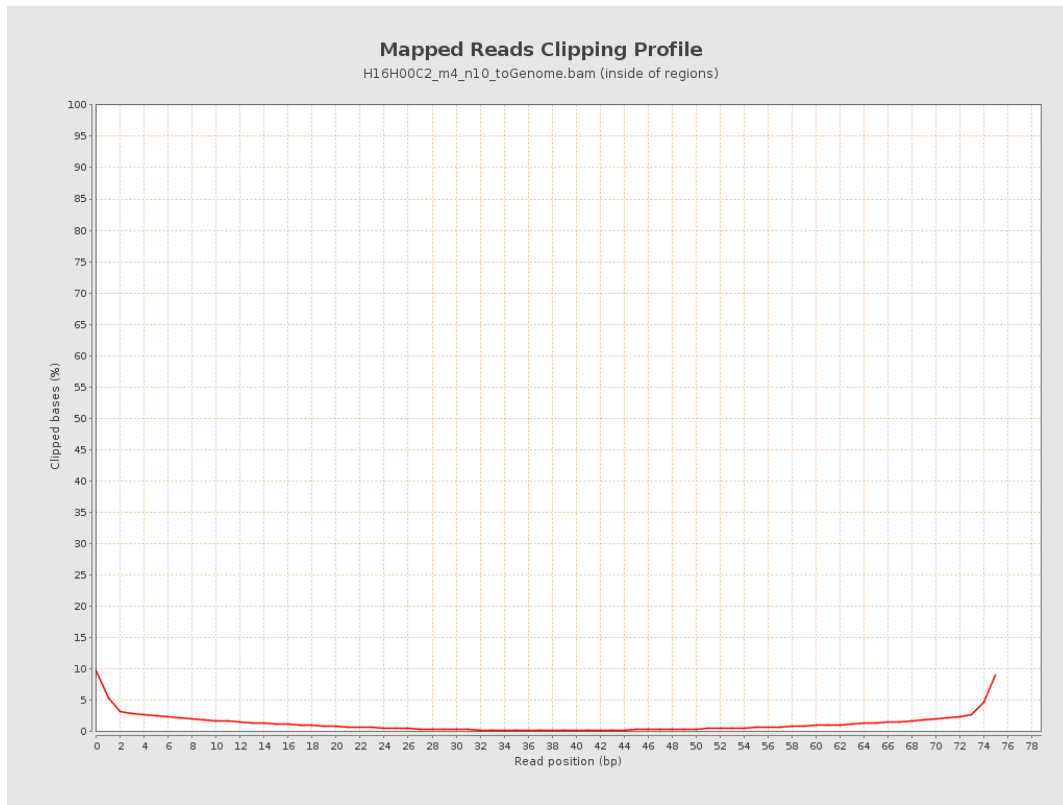




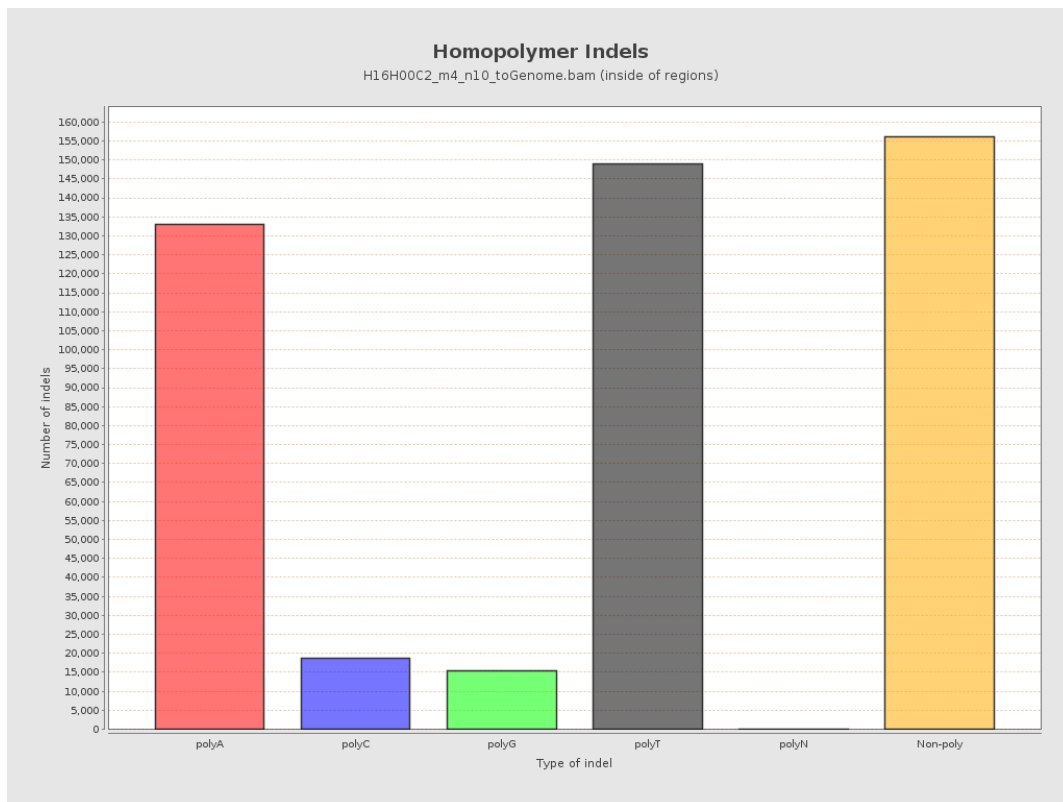
## 9. Results : Mapped Reads GC-content Distribution (inside of regions)



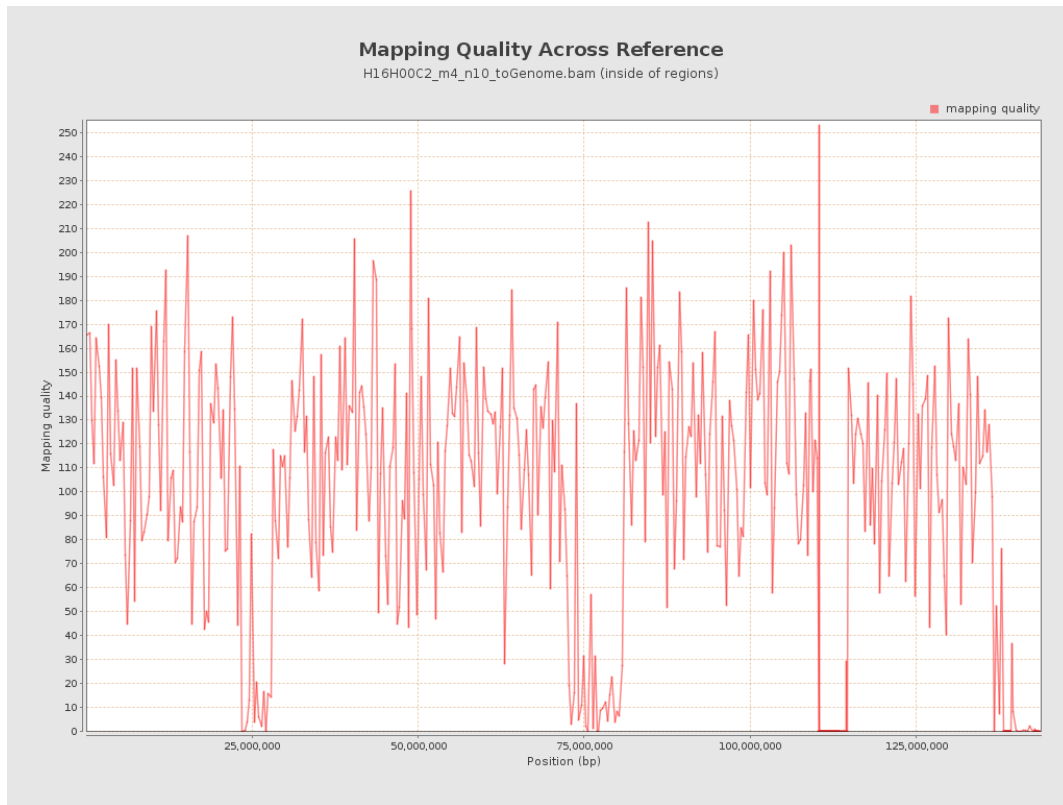
## 10. Results : Mapped Reads Clipping Profile (inside of regions)



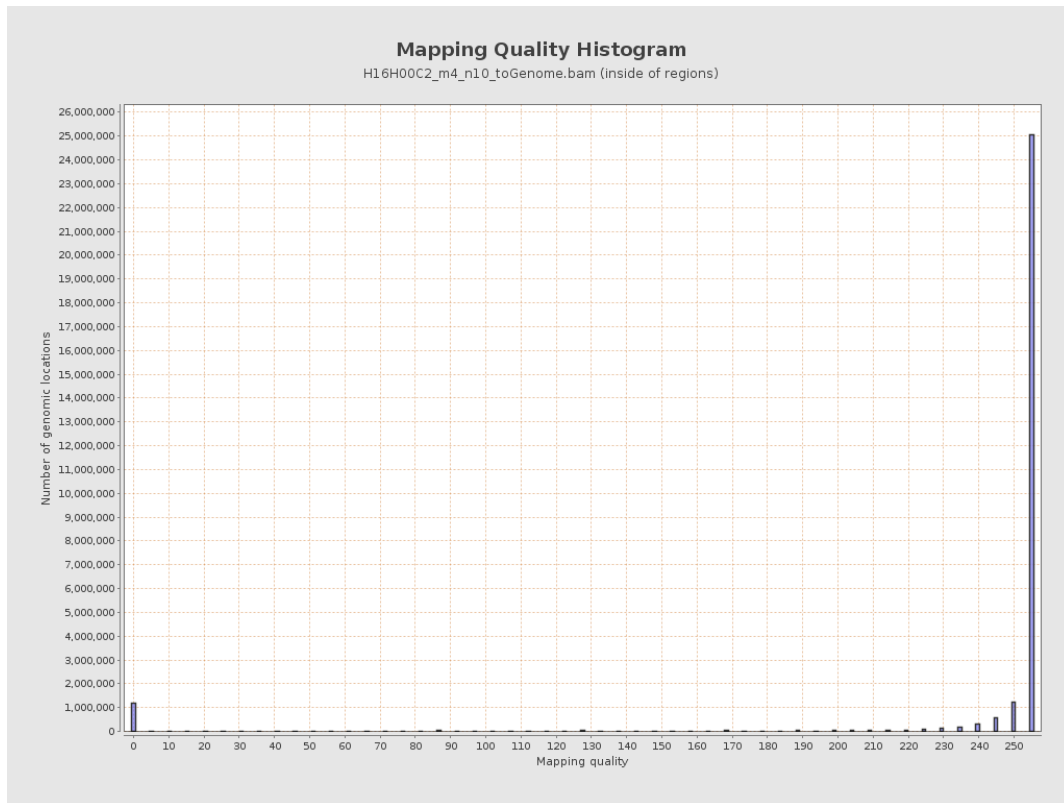
# 11. Results : Homopolymer Indels (inside of regions)



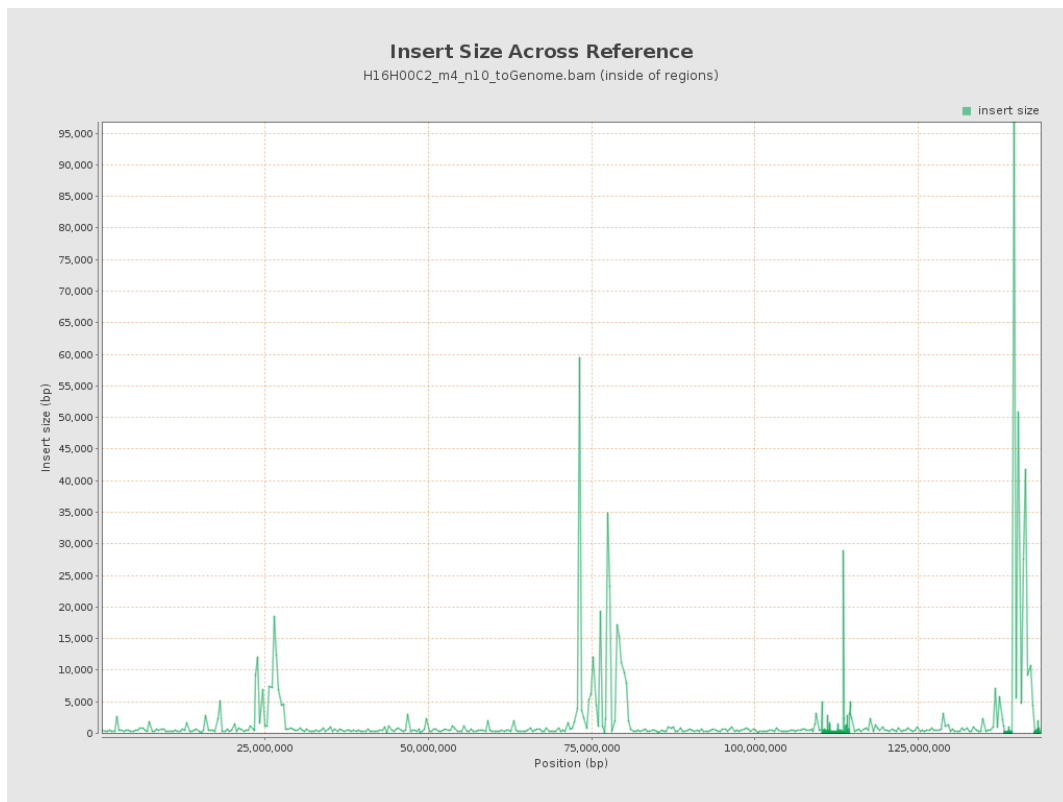
## 12. Results : Mapping Quality Across Reference (inside of regions)



# 13. Results : Mapping Quality Histogram (inside of regions)



# 14. Results : Insert Size Across Reference (inside of regions)



# 15. Results : Insert Size Histogram (inside of regions)

