

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/09/27 15:56:27

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/9d/99786d37a1742b4d55c025cffe4137/H16H15S1_m4_n10_toG
enome.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 S3_R1.fastq.gz S3_R2.fastq.gz - -readFilesCommand pigz -p8 -dc --limitBAMsortRAM 33285996544 - -outSAMtype BAM SortedByCoordinate -- outSAMattributes NH HI AS NM MD --outSAMunmapped Within -- outSAMattrRGline ID:H16H15S1 PU:H16H15S1 SM:H16H15S1 PL:ILLUMINA CN:CRG -- outFilterType BySJout -- outFilterMultimapNmax 10 -- outFilterMismatchNmax 999 -- outFilterMismatchNoverReadLmax 0.04 --alignIntronMin 20 -- alignIntronMax 1000000 -- alignMatesGapMax 1000000 -- alignSJoverhangMin 8 -- alignSJDBoverhangMin 1 -- quantMode TranscriptomeSAM </pre>

Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	STAR (STAR_2.4.0j)
Analysis date:	Fri Sep 27 15:56:27 CEST 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/nfs/no_backup/rg/projects/regeneration/pipeline/grape-nf-dm6-r6.22/work/9d/99786d37a1742b4d55c025cffe4137/H16H15S1_m4_n10_to Genome.bam

1.3. GFF region

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

2. Summary (inside of regions)

2.1. Globals

Reference size	143,726,002
Number of reads	20,980,136
Mapped reads	18,882,276 / 90%
Unmapped reads	2,097,860 / 10%
Mapped paired reads	18,882,276 / 90%
Mapped reads, first in pair	9,441,138 / 45%
Mapped reads, second in pair	9,441,138 / 45%
Mapped reads, both in pair	18,882,276 / 90%
Mapped reads, singletons	0 / 0%
Read min/max/mean length	76 / 76 / 76
Clipped reads	9,041,027 / 43.09%

2.2. Globals (inside of regions)

Regions size/percentage of reference	93,645,580 / 65.16%
Mapped reads	17,179,305 / 81.88%
Mapped reads, only first in pair	8,589,820 / 40.94%
Mapped reads, only second in pair	8,589,485 / 40.94%
Mapped reads, both in pair	17,179,305 / 81.88%
Mapped reads, singletons	0 / 0%
Correct strand reads	0 / 0%
Clipped reads	9,041,027 / 43.09%
Duplicated reads (estimated)	13,010,739 / 75.73%

Duplication rate	40.98%
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2.3. ACGT Content (inside of regions)

Number/percentage of A's	300,086,529 / 23.45%
Number/percentage of C's	336,736,945 / 26.32%
Number/percentage of T's	306,631,700 / 23.97%
Number/percentage of G's	335,972,163 / 26.26%
Number/percentage of N's	1,379,944,858 / 107.86%
GC Percentage	52.58%

2.4. Coverage (inside of regions)

Mean	28.3998
Standard Deviation	291.6582

2.5. Mapping Quality (inside of regions)

Mean Mapping Quality	245.13
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2.6. Insert size (inside of regions)

Mean	485.69
Standard Deviation	7,322.65
P25/Median/P75	145 / 186 / 265

2.7. Mismatches and indels (inside of regions)

General error rate	0.38%
Mismatches	9,931,623
Insertions	93,426

Mapped reads with at least one insertion	0.49%
Deletions	64,820
Mapped reads with at least one deletion	0.34%
Homopolymer indels	59.09%

2.8. Chromosome stats (inside of regions)

Name	Length	Mapped bases	Mean coverage	Standard deviation
chr2L	15854837	454869999	28.6897	277.6494
chr2R	16880511	697050571	41.2932	485.4268
chr3L	18005806	535021617	29.7138	228.864
chr3R	23285070	521596464	22.4005	197.7144
chr4	1040043	34891145	33.5478	175.5979
chrM	11009	22433877	2,037.7761	2,329.5629
chrUn_DS485919v1	0	0	0	0
chrUn_DS483755v1	0	0	0	0
chrUn_DS485425v1	0	0	0	0
chrUn_DS484861v1	0	0	0	0
chrUn_DS484484v1	0	0	0	0
chrUn_DS483705v1	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_DS485 457v1	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
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chrUn_DS483 719v1	0	0	0	0
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chrUn_DS485 733v1	0	0	0	0
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chrUn_DS485 675v1	0	0	0	0
chrUn_DS485 065v1	0	0	0	0

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chrUn_DS484 716v1	0	0	0	0
chrUn_DS485 907v1	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
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chrUn_DS485 585v1	0	0	0	0
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

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chrUn_DS485 904v1	0	0	0	0
chrUn_DS484 979v1	0	0	0	0
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chrUn_DS484 479v1	0	0	0	0
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chrUn_DS484 251v1	0	0	0	0

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chrX_DS4845 26v1_random	0	0	0	0
chrX_DS4859 94v1_random	0	0	0	0
chrX_DS4852 35v1_random	0	0	0	0
chrX_DS4847 45v1_random	0	0	0	0
chrX_DS4845 07v1_random	0	0	0	0
chrX_DS4840 74v1_random	0	0	0	0

chrX_DS4856 18v1_random	0	0	0	0
chrX_DS4857 97v1_random	0	0	0	0
chrX_DS4843 67v1_random	0	0	0	0
chrX_DS4848 09v1_random	0	0	0	0
chrX_DS4849 65v1_random	0	0	0	0
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chrX_DS4845 29v1_random	0	0	0	0
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chrX_DS4845 94v1_random	0	0	0	0
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chrX_DS4850 74v1_random	0	0	0	0
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chrX_DS4858 52v1_random	0	0	0	0
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chrX_DS4851 12v1_random	0	0	0	0
chrX_DS4845 06v1_random	0	0	0	0
chrX_DS4853 36v1_random	0	0	0	0
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chrX_DS4850 80v1_random	0	0	0	0
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chrX_DS4857 98v1_random	0	0	0	0
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chrX_DS4857 90v1_random	0	0	0	0
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chrX_DS4847 02v1_random	0	0	0	0
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chrX_DS4839 71v1_random	0	0	0	0
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chrX_DS4857 78v1_random	0	0	0	0

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chrX_DS4857 07v1_random	0	0	0	0
chrX_DS4838 09v1_random	0	0	0	0
chrX_DS4848 57v1_random	0	0	0	0
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chrX_DS4856 51v1_random	0	0	0	0
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chrX_DS4855 50v1_random	0	0	0	0
chrX_DS4837 95v1_random	0	0	0	0
chrX_DS4846 66v1_random	0	0	0	0
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chrX_DS4843 71v1_random	0	0	0	0
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chrX_DS4843 87v1_random	0	0	0	0
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chrX_DS4838 85v1_random	0	0	0	0
chrX_DS4839 28v1_random	0	0	0	0

chrX_DS4843 26v1_random	0	0	0	0
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chrX_DS4838 92v1_random	0	0	0	0
chrX_DS4840 61v1_random	0	0	0	0
chrX_DS4843 30v1_random	0	0	0	0
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chrX_DS4839 09v1_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
chrX_DS4839 46v1_random	0	0	0	0
chrX_DS4845 56v1_random	0	0	0	0
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chrX_DS4839 26v1_random	0	0	0	0
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chrX_DS4843 41v1_random	0	0	0	0
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chrX_DS4839 69v1_random	0	0	0	0
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chrX_CP0071 03v1_random	0	0	0	0
chrY	1063129	1115496	1.0493	4.1263
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chrY_DS4855 94v1_random	0	0	0	0
chrY_DS4848 05v1_random	0	0	0	0
chrY_DS4840 21v1_random	0	0	0	0

chrY_DS4841 84v1_random	0	0	0	0
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chrY_DS4853 75v1_random	0	0	0	0
chrY_DS4842 33v1_random	0	0	0	0
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chrY_DS4858 65v1_random	0	0	0	0
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chrY_DS4841 46v1_random	0	0	0	0
chrY_DS4839 59v1_random	0	0	0	0

chrY_DS4857 95v1_random	0	0	0	0
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chrY_DS4859 27v1_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_DS4841 03v1_random	0	0	0	0
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chrY_DS4849 42v1_random	0	0	0	0
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chrY_DS4846 80v1_random	0	0	0	0
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chrY_DS4853 15v1_random	0	0	0	0
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chrY_DS4857 55v1_random	0	0	0	0

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chrY_DS4852 88v1_random	0	0	0	0
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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_DS4848 30v1_random	0	0	0	0
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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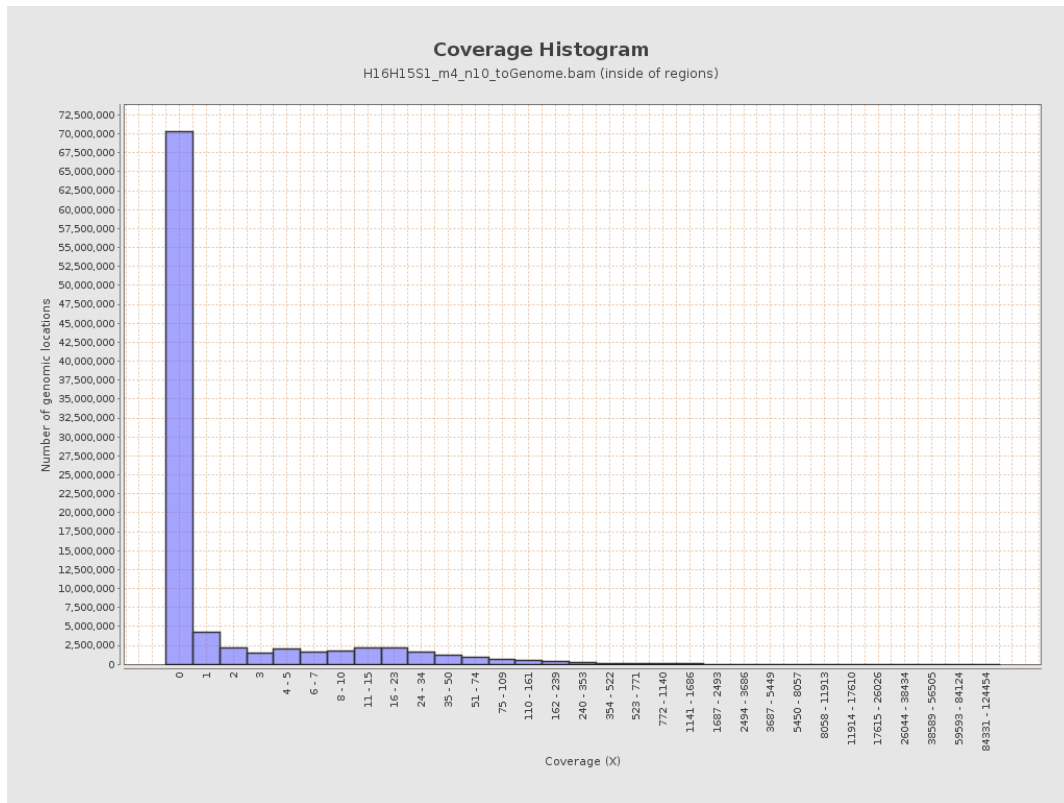
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chrY_DS4848 75v1_random	0	0	0	0
chrY_DS4841 75v1_random	0	0	0	0
chrY_DS4850 28v1_random	0	0	0	0
chrY_DS4837 25v1_random	0	0	0	0
chrY_DS4839 31v1_random	1190	0	0	0
chrY_DS4839 96v1_random	0	0	0	0
chrY_DS4838 75v1_random	2770	0	0	0
chrY_DS4838 89v1_random	0	0	0	0
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
chrY_CP0071 11v1_random	0	0	0	0
chrY_CP0071 12v1_random	0	0	0	0
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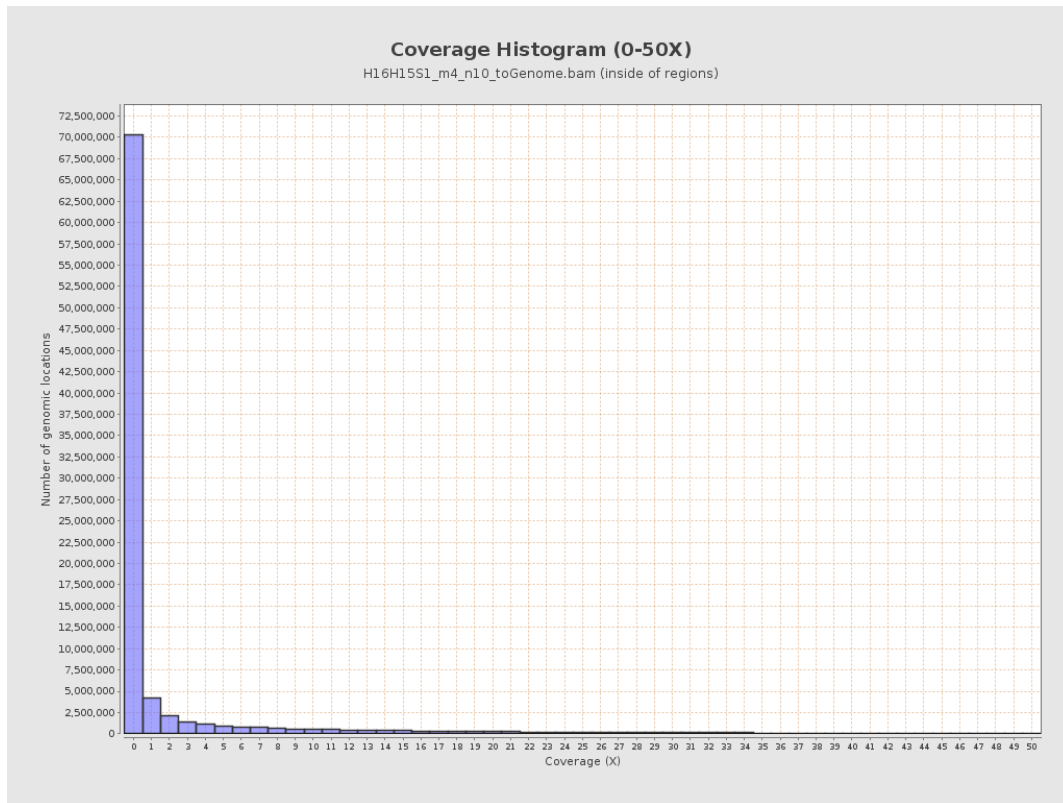
3. Results : Coverage across reference (inside of regions)



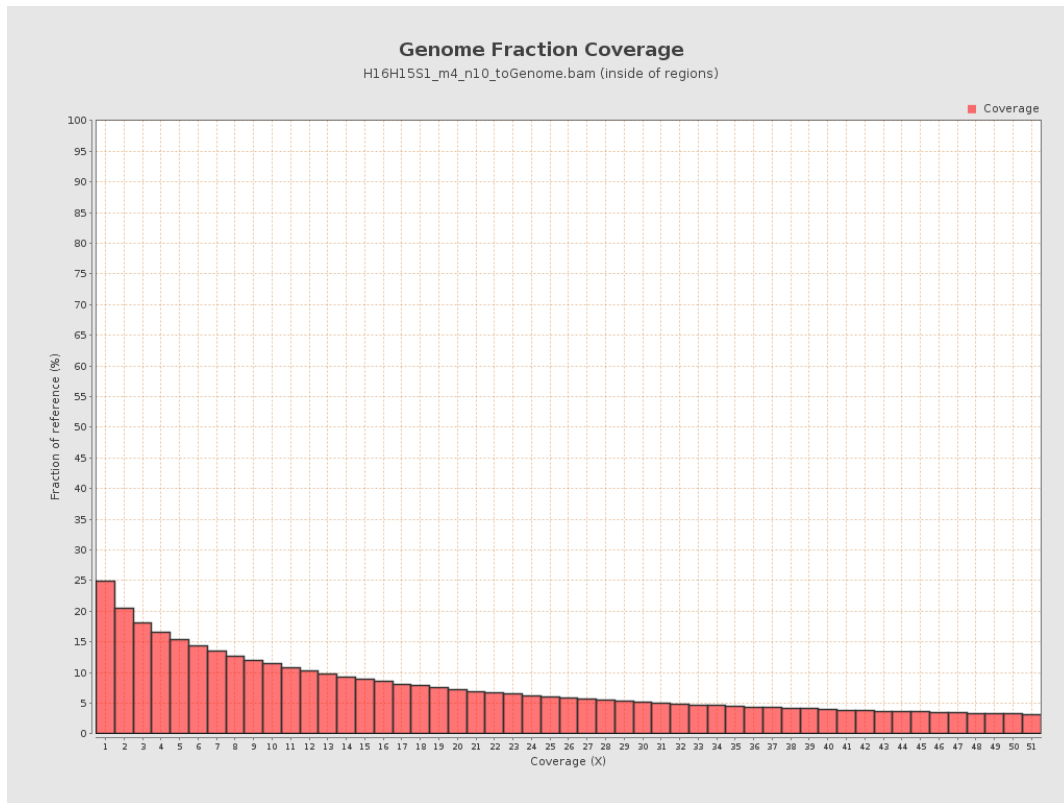
4. Results : Coverage Histogram (inside of regions)



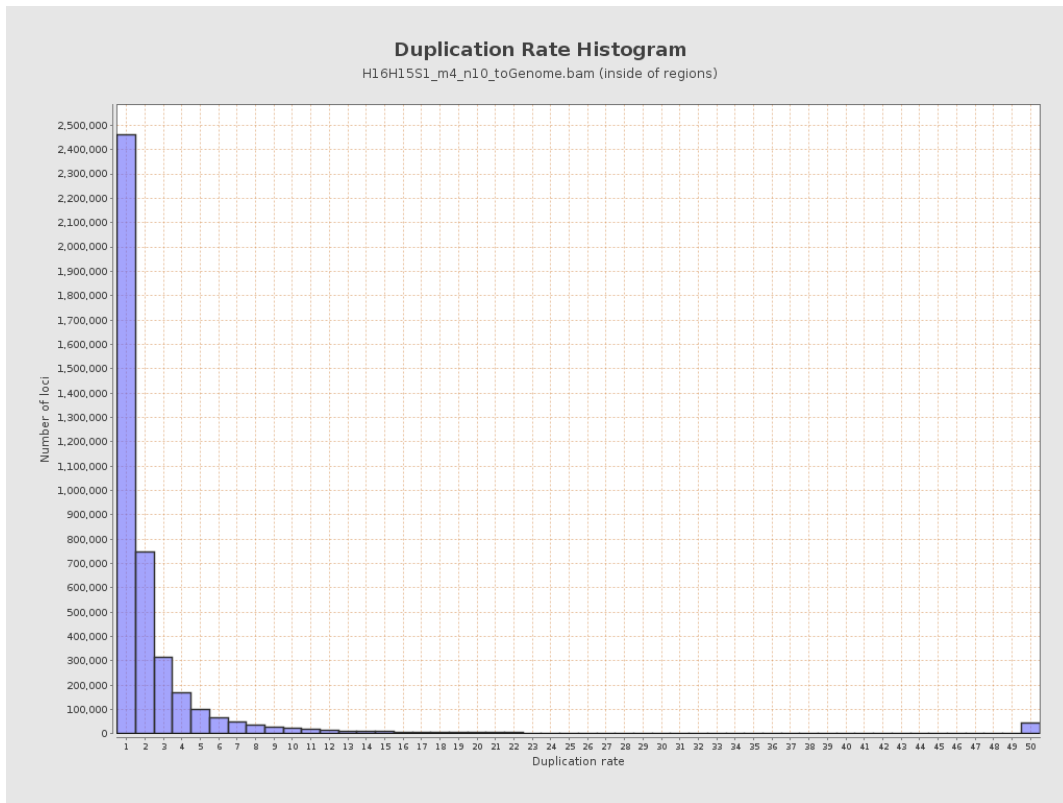
5. Results : Coverage Histogram (0-50X) (inside of regions)



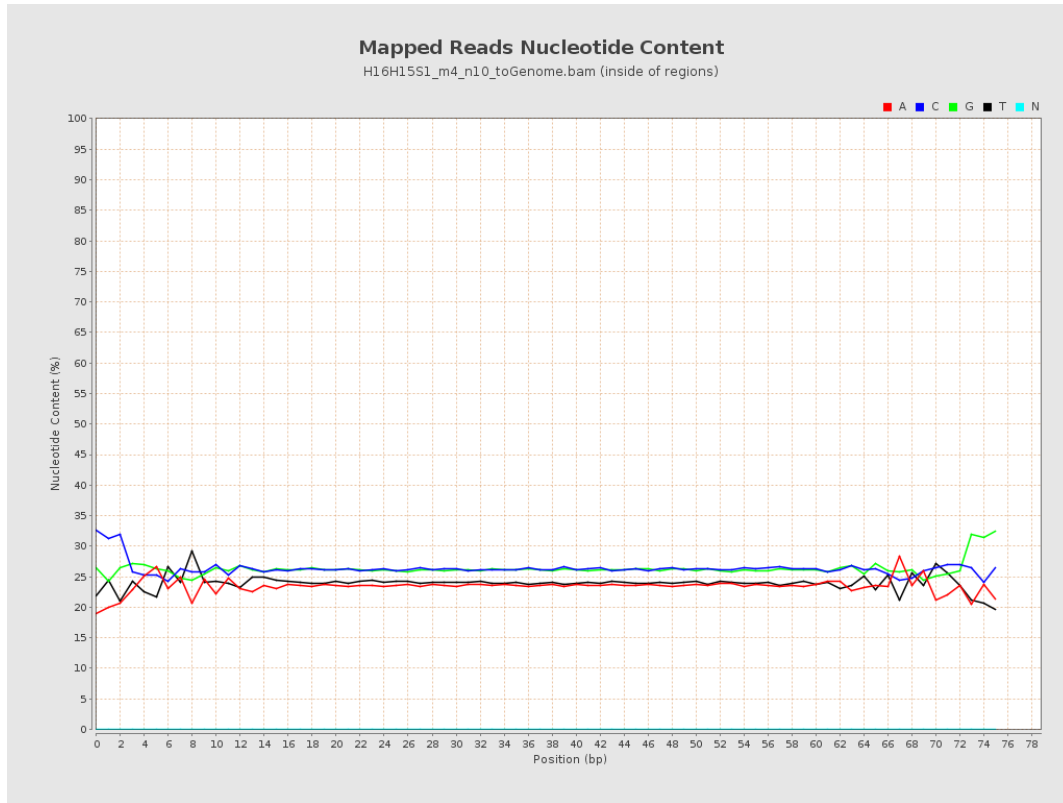
6. Results : Genome Fraction Coverage (inside of regions)



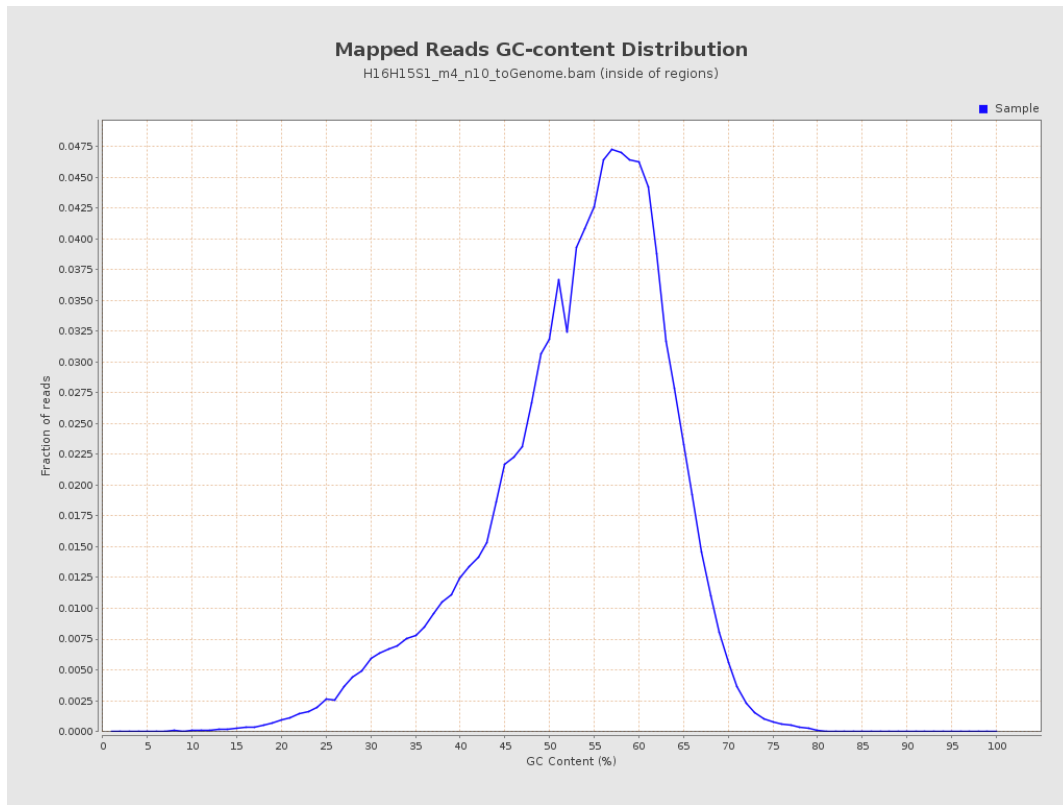
7. Results : Duplication Rate Histogram (inside of regions)



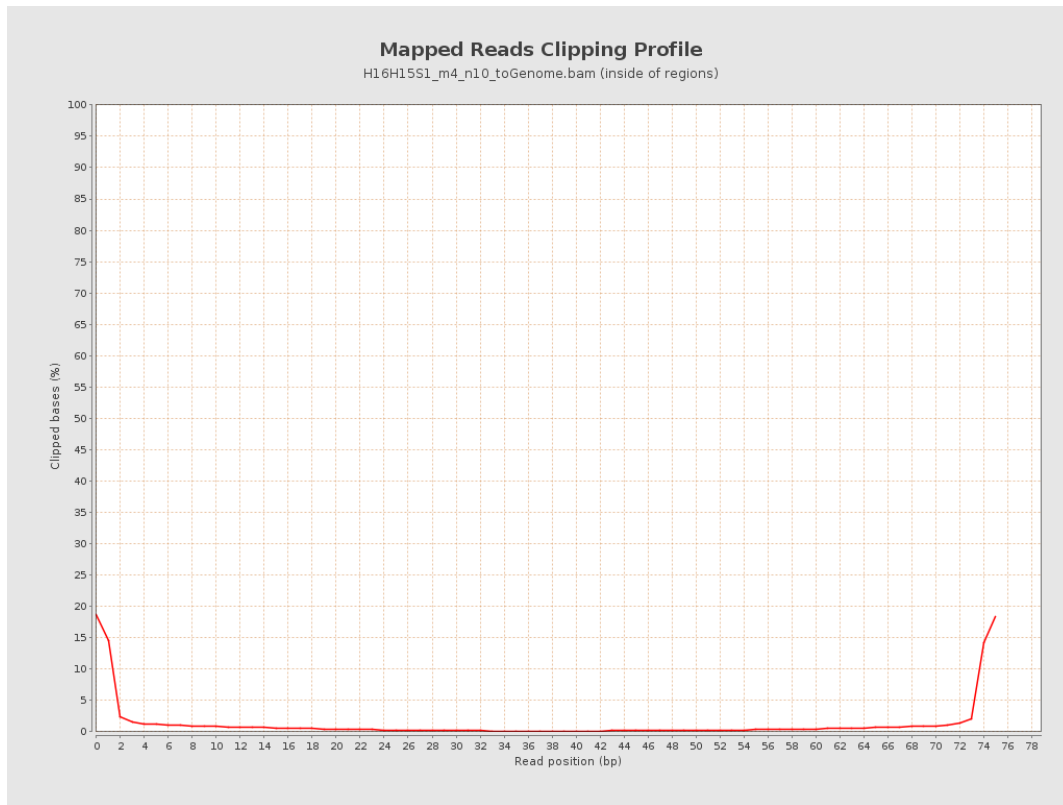
8. Results : Mapped Reads Nucleotide Content (inside of regions)



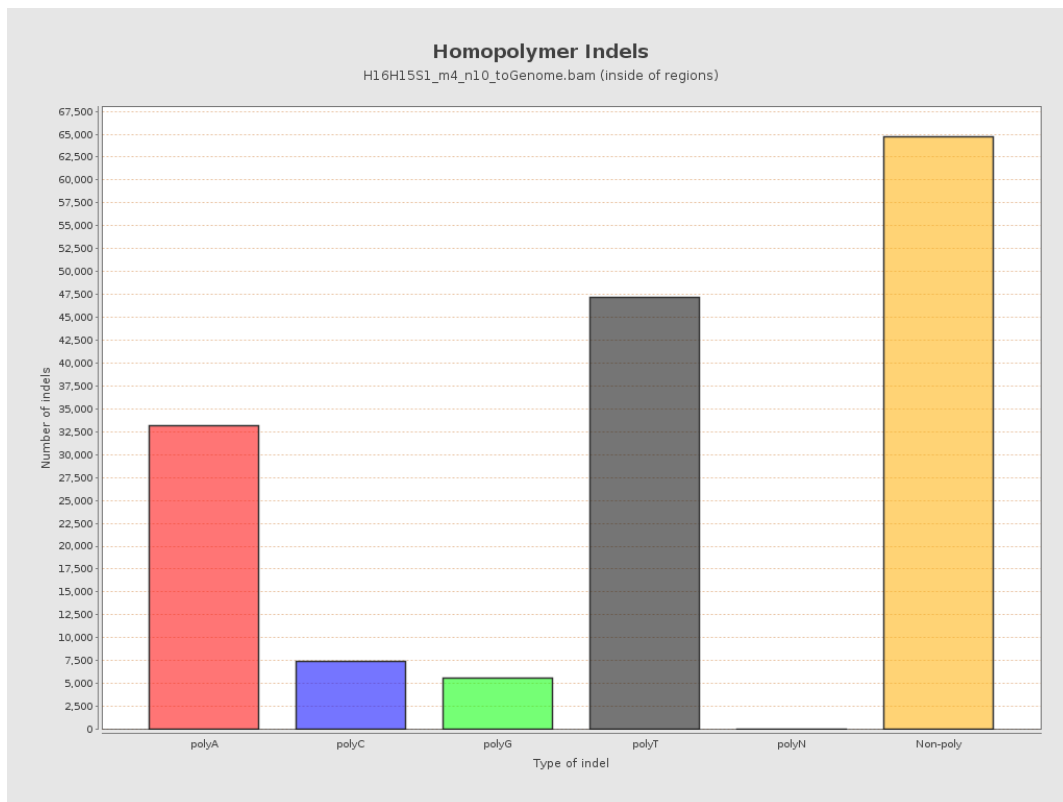
9. Results : Mapped Reads GC-content Distribution (inside of regions)



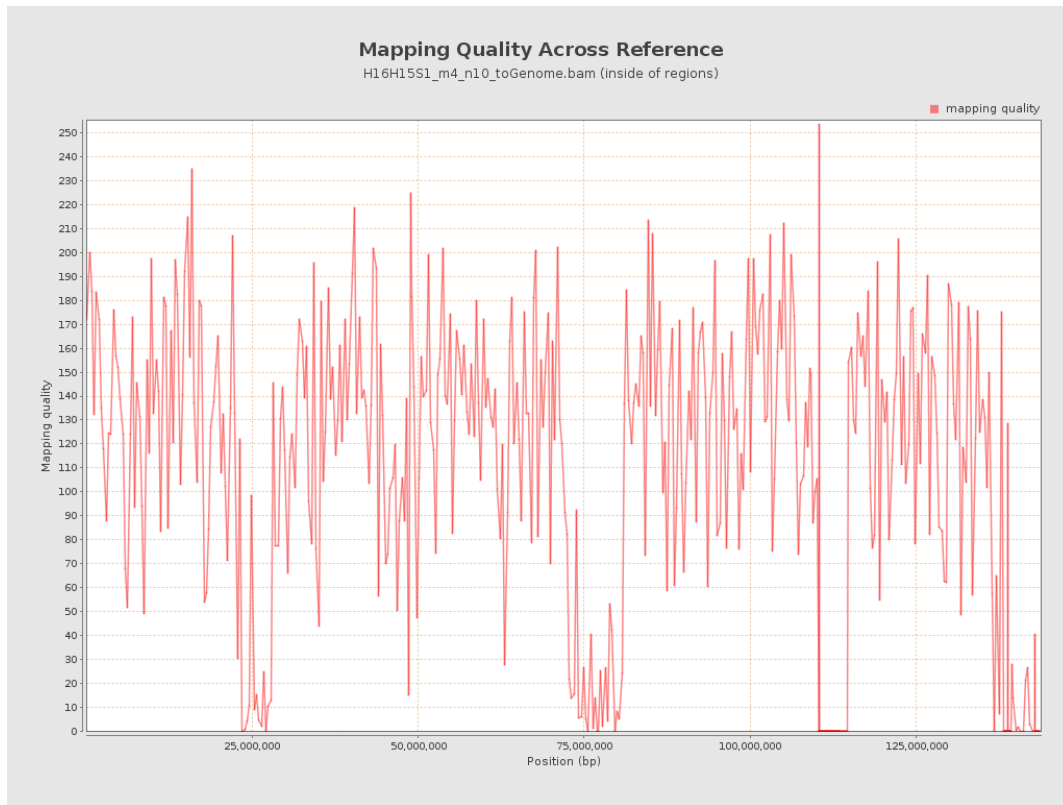
10. Results : Mapped Reads Clipping Profile (inside of regions)



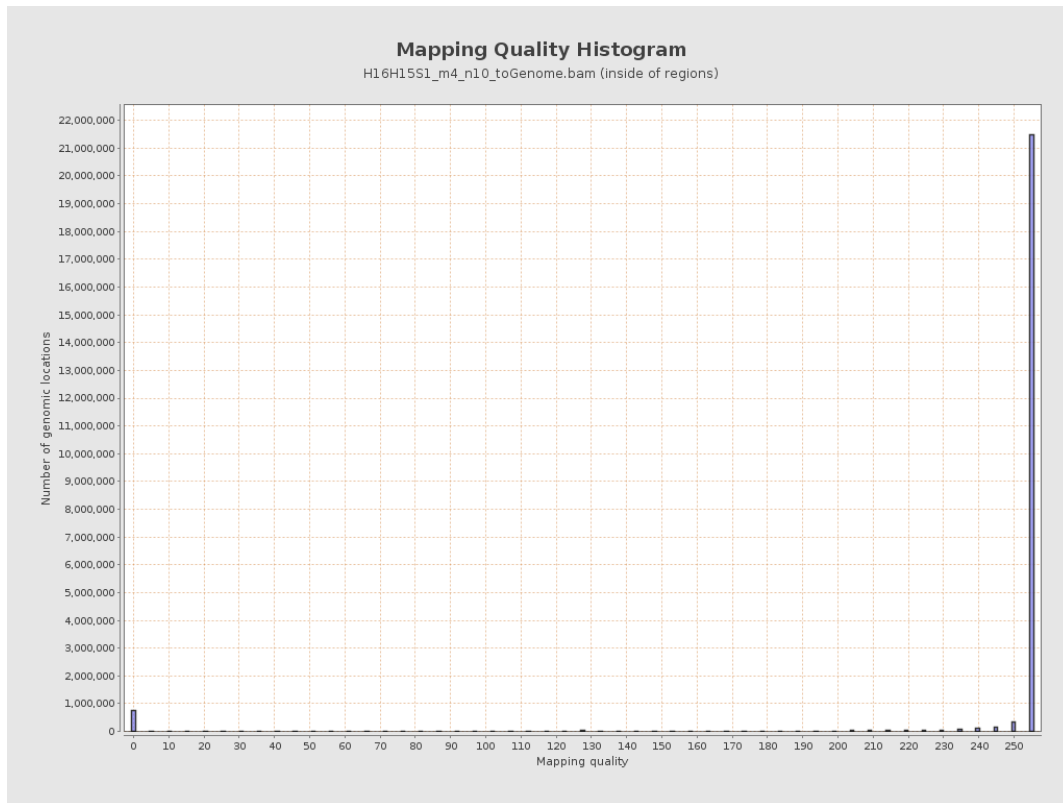
11. Results : Homopolymer Indels (inside of regions)



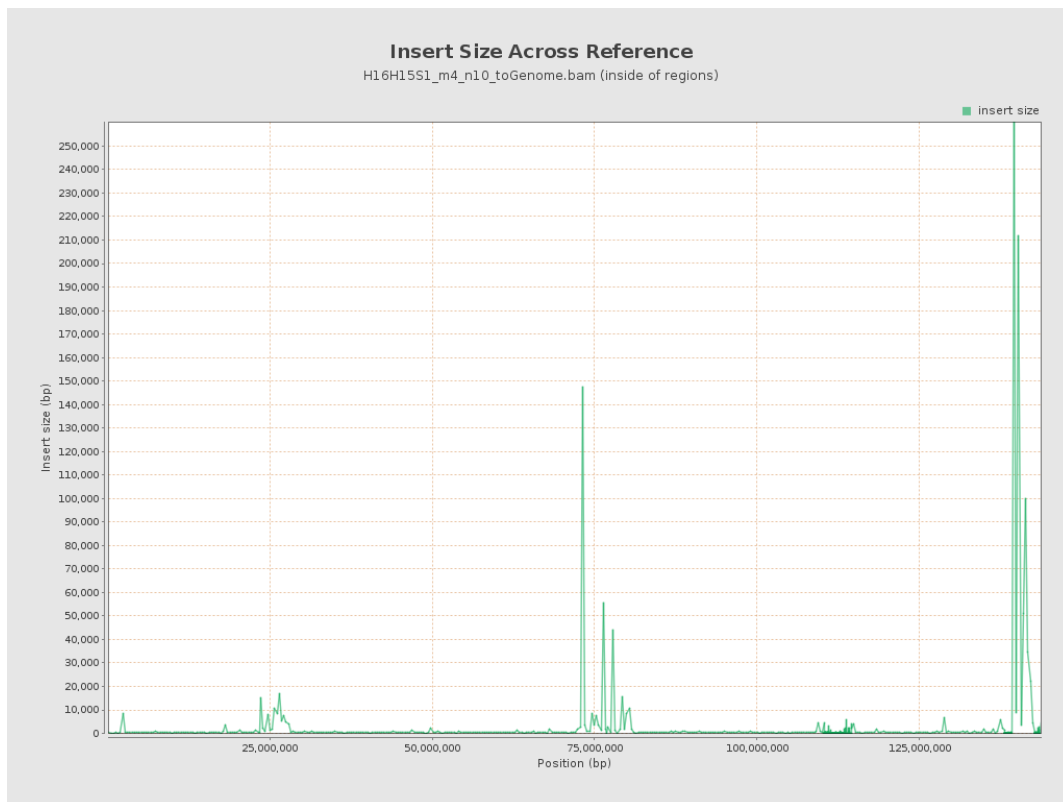
12. Results : Mapping Quality Across Reference (inside of regions)



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)

