

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/09/27 16:01:31

1. Input data & parameters (inside of regions)

1.1. QualiMap command line

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qualimap bamqc -bam
/nfs/no_backup/rg/projects/regeneration/pipeline/grape-nf-dm6-
r6.22/work/f3/ddaf58945435f74323f644fec37af3/CRGH16H25C1_m4_n10_t
oGenome.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

<p>Command line:</p>	<pre> STAR --runThreadN 8 --genomeDir genomeDir --readFilesIn EV2_13004_GCCAAT_read1.fastq.g z EV2_13004_GCCAAT_read2.fastq.g z --readFilesCommand pigz -p8 -dc --limitBAMsortRAM 33285996544 --outSAMtype BAM SortedByCoordinate -- outSAMattributes NH HI AS NM MD --outSAMunmapped Within -- outSAMattrRGline ID:CRGH16H25C1 PU:CRGH16H25C1 SM:CRGH16H25C1 PL:ILLUMINA CN:CRG --outFilterType BySJout --outFilterMultimapNmax 10 -- outFilterMismatchNmax 999 -- outFilterMismatchNoverReadLmax 0.04 --alignIntronMin 20 -- alignIntronMax 1000000 -- alignMatesGapMax 1000000 -- </pre>
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	alignSJoverhangMin 8 -- alignSJDBoverhangMin 1 -- quantMode TranscriptomeSAM
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	STAR (STAR_2.4.0j)
Analysis date:	Fri Sep 27 16:01:30 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/f3/ddaf58945435f74323f6 44fec37af3/CRGH16H25C1_m4_n10 _toGenome.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	136,724,040
Mapped reads	130,897,384 / 95.74%
Unmapped reads	5,826,656 / 4.26%
Mapped paired reads	130,897,384 / 95.74%
Mapped reads, first in pair	65,448,692 / 47.87%
Mapped reads, second in pair	65,448,692 / 47.87%
Mapped reads, both in pair	130,897,384 / 95.74%
Mapped reads, singletons	0 / 0%
Read min/max/mean length	50 / 50 / 50
Clipped reads	5,285,325 / 3.87%

2.2. Globals (inside of regions)

Regions size/percentage of reference	93,645,580 / 65.16%
Mapped reads	101,895,089 / 74.53%
Mapped reads, only first in pair	50,872,356 / 37.21%
Mapped reads, only second in pair	51,022,733 / 37.32%
Mapped reads, both in pair	101,895,089 / 74.53%
Mapped reads, singletons	0 / 0%
Correct strand reads	0 / 0%
Clipped reads	5,285,325 / 3.87%
Duplicated reads (estimated)	91,489,118 / 89.79%

Duplication rate	65.37%
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2.3. ACGT Content (inside of regions)

Number/percentage of A's	1,270,804,900 / 25.05%
Number/percentage of C's	1,254,169,950 / 24.72%
Number/percentage of T's	1,300,417,959 / 25.64%
Number/percentage of G's	1,247,298,166 / 24.59%
Number/percentage of N's	7,292,493,640 / 143.76%
GC Percentage	49.31%

2.4. Coverage (inside of regions)

Mean	132.0466
Standard Deviation	1,095.1024

2.5. Mapping Quality (inside of regions)

Mean Mapping Quality	241.88
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2.6. Insert size (inside of regions)

Mean	932.36
Standard Deviation	13,691.06
P25/Median/P75	204 / 278 / 412

2.7. Mismatches and indels (inside of regions)

General error rate	0.17%
Mismatches	20,680,664
Insertions	344,348

Mapped reads with at least one insertion	0.26%
Deletions	224,777
Mapped reads with at least one deletion	0.17%
Homopolymer indels	73.07%

2.8. Chromosome stats (inside of regions)

Name	Length	Mapped bases	Mean coverage	Standard deviation
chr2L	15854837	1943972226	122.6107	886.763
chr2R	16880511	3191471622	189.0625	1,608.3227
chr3L	18005806	2612006387	145.0647	870.3675
chr3R	23285070	2423167070	104.0653	645.0383
chr4	1040043	222165144	213.6115	1,045.5908
chrM	11009	302701720	27,495.8416	38,564.7444
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

chrUn_DS484 058v1	0	0	0	0
chrUn_DS485 294v1	0	0	0	0
chrUn_DS484 855v1	0	0	0	0
chrUn_DS485 356v1	0	0	0	0
chrUn_DS485 246v1	0	0	0	0
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 972v1	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_DS485 296v1	0	0	0	0
chrUn_DS485 337v1	0	0	0	0
chrUn_DS483 700v1	0	0	0	0
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chrUn_DS485 973v1	0	0	0	0
chrUn_DS483 719v1	0	0	0	0
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chrUn_DS485 733v1	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 065v1	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 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
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chrUn_DS485 810v1	0	0	0	0
chrUn_DS485 982v1	0	0	0	0

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chrUn_DS484 710v1	0	0	0	0

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chrUn_DS484 369v1	0	0	0	0
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
chrUn_DS485 668v1	0	0	0	0
chrUn_DS485 751v1	0	0	0	0
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chrUn_DS485 545v1	0	0	0	0
chrUn_DS485 076v1	0	0	0	0
chrUn_DS484 394v1	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 324v1	0	0	0	0
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chrUn_DS484 979v1	0	0	0	0
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chrUn_DS483 680v1	0	0	0	0
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chrUn_DS484 456v1	0	0	0	0
chrUn_DS485 488v1	0	0	0	0
chrUn_DS484 479v1	0	0	0	0
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chrX_DS4846 22v1_random	0	0	0	0
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chrX_DS4859 94v1_random	0	0	0	0
chrX_DS4852 35v1_random	0	0	0	0
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chrX_DS4845 07v1_random	0	0	0	0
chrX_DS4840 74v1_random	0	0	0	0

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chrX_DS4857 97v1_random	0	0	0	0
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chrX_DS4849 65v1_random	0	0	0	0
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chrX_DS4851 12v1_random	0	0	0	0
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chrX_DS4857 98v1_random	0	0	0	0
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chrX_DS4857 78v1_random	0	0	0	0

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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_DS4841 85v1_random	0	0	0	0
chrX_DS4855 50v1_random	0	0	0	0
chrX_DS4837 95v1_random	0	0	0	0
chrX_DS4846 66v1_random	0	0	0	0
chrX_DS4836 66v1_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
chrX_DS4837 45v1_random	0	0	0	0
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_DS4845 86v1_random	0	0	0	0
chrX_DS4842 78v1_random	0	0	0	0
chrX_DS4840 46v1_random	0	0	0	0
chrX_DS4841 33v1_random	0	0	0	0

chrX_DS4839 09v1_random	0	0	0	0
chrX_DS4844 88v1_random	0	0	0	0
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
chrX_DS4838 51v1_random	0	0	0	0
chrX_DS4839 26v1_random	0	0	0	0
chrX_DS4845 63v1_random	0	0	0	0
chrX_DS4839 23v1_random	0	0	0	0
chrX_DS4841 66v1_random	0	0	0	0
chrX_DS4843 41v1_random	0	0	0	0
chrX_DS4840 99v1_random	0	0	0	0
chrX_DS4840 60v1_random	0	0	0	0

chrX_DS4841 32v1_random	0	0	0	0
chrX_DS4838 21v1_random	0	0	0	0
chrX_DS4838 18v1_random	0	0	0	0
chrX_DS4845 62v1_random	0	0	0	0
chrX_DS4839 69v1_random	0	0	0	0
chrX_DS4840 26v1_random	0	0	0	0
chrX_CP0071 04v1_random	0	0	0	0
chrX_CP0071 03v1_random	0	0	0	0
chrY	1063129	6173148	5.8066	17.5316
chrY_DS4851 13v1_random	0	0	0	0
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chrY_DS4849 92v1_random	0	0	0	0
chrY_DS4855 94v1_random	0	0	0	0
chrY_DS4848 05v1_random	0	0	0	0
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chrY_DS4841 84v1_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_DS4837 78v1_random	0	0	0	0
chrY_DS4846 81v1_random	0	0	0	0
chrY_DS4859 27v1_random	0	0	0	0
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chrY_DS4841 64v1_random	0	0	0	0
chrY_DS4855 34v1_random	0	0	0	0
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chrY_DS4839 87v1_random	0	0	0	0

chrY_DS4851 59v1_random	0	0	0	0
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chrY_DS4855 61v1_random	0	0	0	0
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chrY_DS4852 50v1_random	0	0	0	0
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chrY_DS4848 18v1_random	0	0	0	0
chrY_DS4855 75v1_random	0	0	0	0
chrY_DS4856 96v1_random	0	0	0	0
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chrY_DS4845 74v1_random	0	0	0	0
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chrY_DS4842 49v1_random	0	0	0	0
chrY_DS4859 38v1_random	435	0	0	0
chrY_DS4853 29v1_random	0	0	0	0
chrY_DS4845 23v1_random	0	0	0	0

chrY_DS4850 42v1_random	0	0	0	0
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chrY_DS4843 36v1_random	0	0	0	0
chrY_DS4851 78v1_random	0	0	0	0
chrY_DS4854 09v1_random	0	0	0	0
chrY_DS4857 64v1_random	0	0	0	0
chrY_DS4841 28v1_random	0	0	0	0
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chrY_DS4854 52v1_random	0	0	0	0
chrY_DS4849 09v1_random	1356	0	0	0

chrY_DS4856 41v1_random	0	0	0	0
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chrY_DS4850 48v1_random	0	0	0	0
chrY_DS4853 63v1_random	0	0	0	0

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 18v1_random	0	0	0	0
chrY_DS4859 63v1_random	0	0	0	0

chrY_DS4857 76v1_random	0	0	0	0
chrY_DS4851 37v1_random	0	0	0	0
chrY_DS4853 15v1_random	0	0	0	0
chrY_DS4846 96v1_random	0	0	0	0
chrY_DS4837 42v1_random	654	0	0	0
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chrY_DS4841 71v1_random	0	0	0	0
chrY_DS4850 97v1_random	0	0	0	0
chrY_DS4841 81v1_random	0	0	0	0
chrY_CP0071 19v1_random	0	0	0	0
chrY_DS4858 88v1_random	0	0	0	0
chrY_DS4845 31v1_random	0	0	0	0
chrY_DS4854 70v1_random	0	0	0	0
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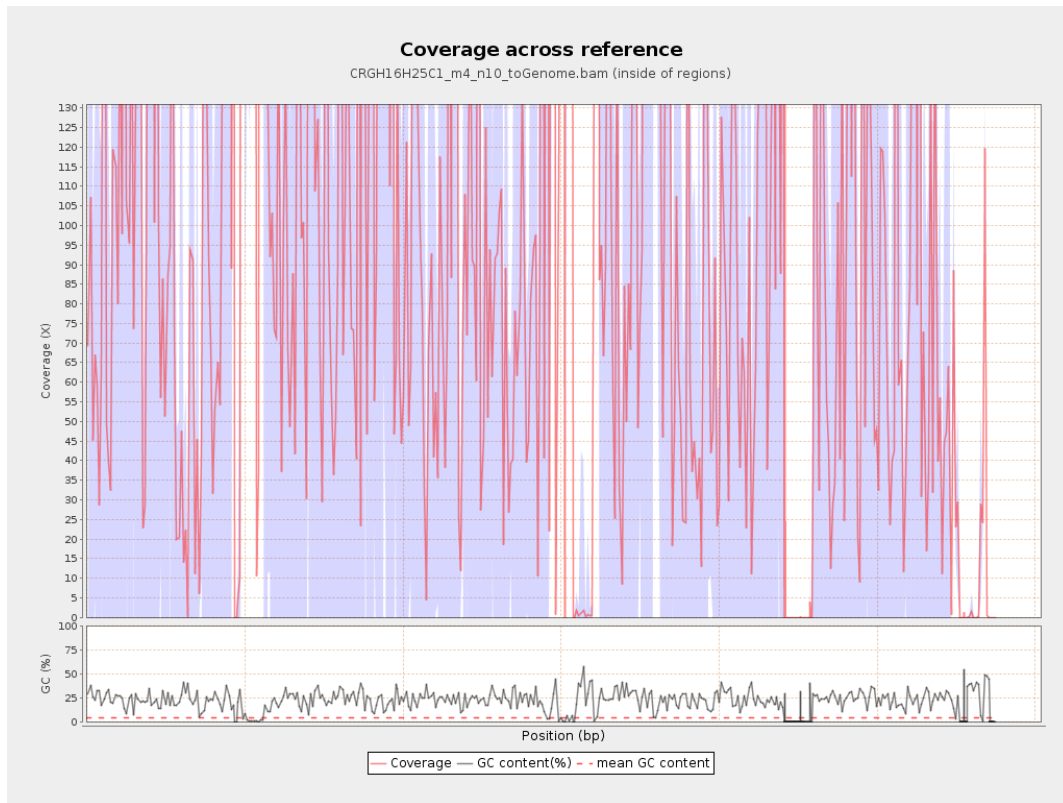
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chrY_DS4852 88v1_random	0	0	0	0
chrY_DS4850 14v1_random	0	0	0	0
chrY_DS4847 57v1_random	0	0	0	0
chrY_DS4848 20v1_random	0	0	0	0
chrY_DS4854 22v1_random	0	0	0	0
chrY_DS4848 76v1_random	0	0	0	0
chrY_DS4858 58v1_random	0	0	0	0
chrY_DS4855 12v1_random	0	0	0	0
chrY_DS4851 43v1_random	0	0	0	0
chrY_DS4843 90v1_random	0	0	0	0
chrY_DS4854 16v1_random	0	0	0	0
chrY_DS4846 74v1_random	0	0	0	0
chrY_DS4844 65v1_random	0	0	0	0

chrY_DS4854 36v1_random	0	0	0	0
chrY_DS4854 50v1_random	0	0	0	0
chrY_DS4848 30v1_random	0	0	0	0
chrY_DS4839 88v1_random	0	0	0	0
chrY_DS4848 07v1_random	0	0	0	0
chrY_DS4859 56v1_random	0	0	0	0
chrY_DS4852 83v1_random	0	0	0	0
chrY_DS4853 35v1_random	0	0	0	0
chrY_DS4856 98v1_random	0	0	0	0
chrY_DS4846 41v1_random	0	0	0	0
chrY_DS4854 30v1_random	0	0	0	0
chrY_DS4853 16v1_random	0	0	0	0
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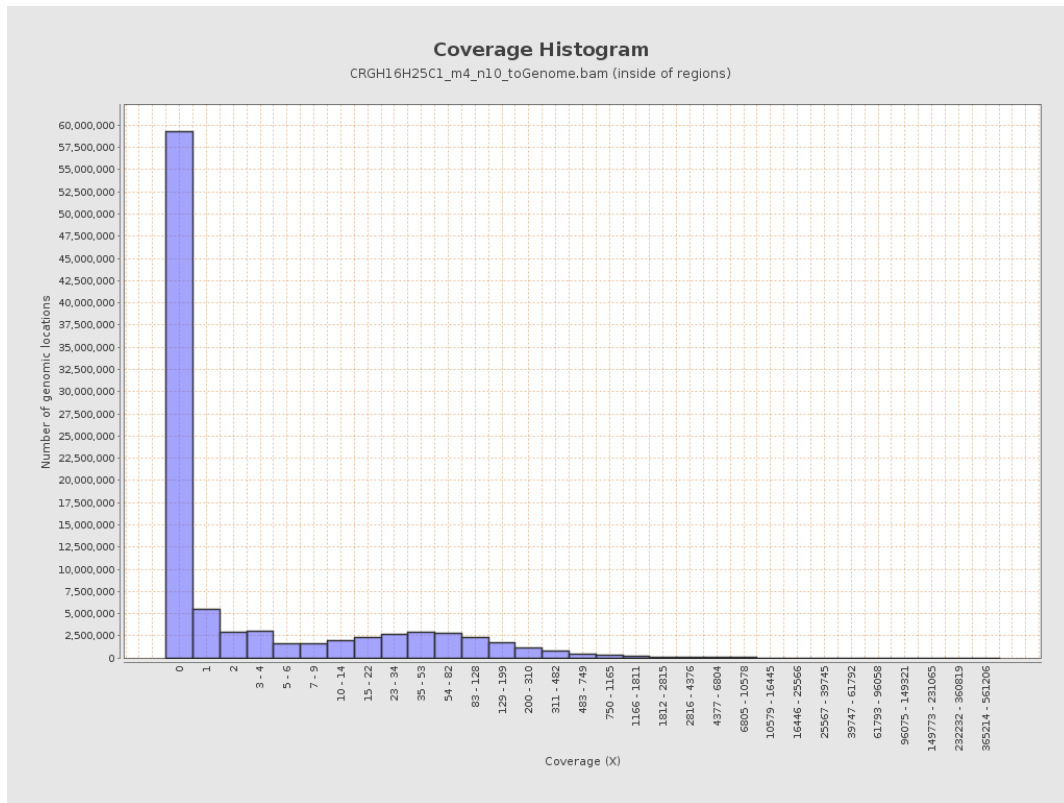
chrY_DS4858 85v1_random	0	0	0	0
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chrY_DS4852 19v1_random	0	0	0	0
chrY_DS4848 75v1_random	0	0	0	0
chrY_DS4841 75v1_random	0	0	0	0
chrY_DS4850 28v1_random	0	0	0	0
chrY_DS4837 25v1_random	0	0	0	0
chrY_DS4839 31v1_random	1190	0	0	0
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chrY_DS4838 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
chrY_CP0071 13v1_random	0	0	0	0
chrY_CP0071 14v1_random	0	0	0	0
chrY_CP0071 15v1_random	0	0	0	0
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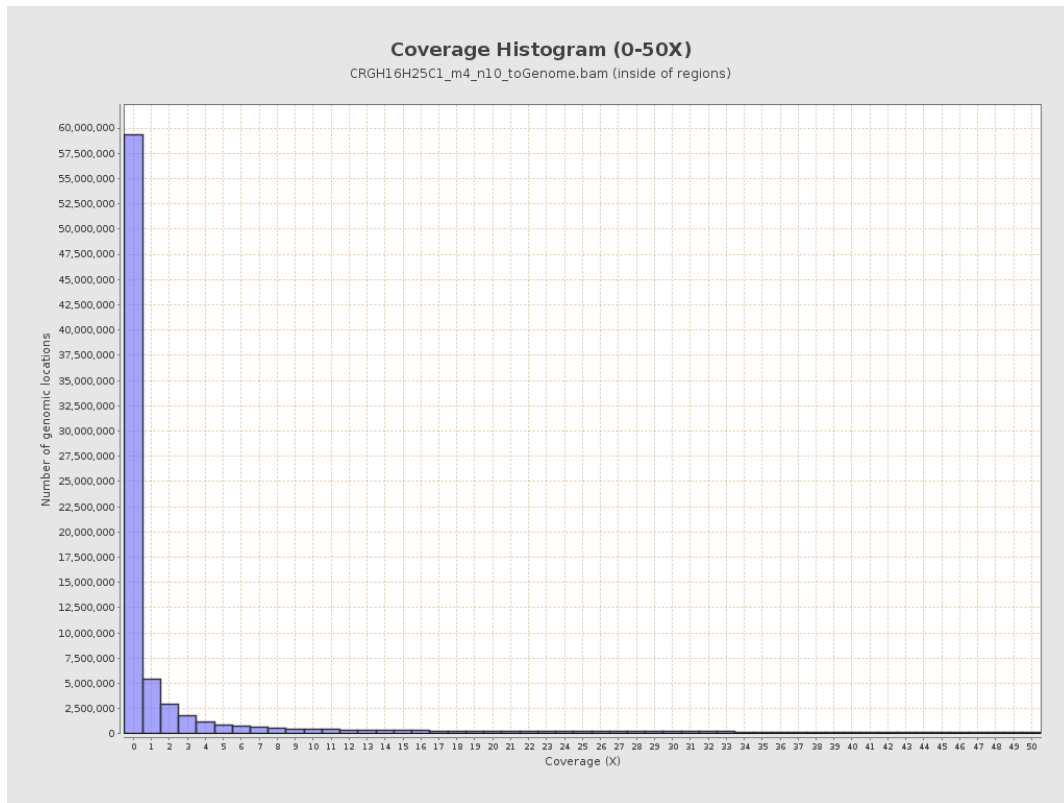
3. Results : Coverage across reference (inside of regions)



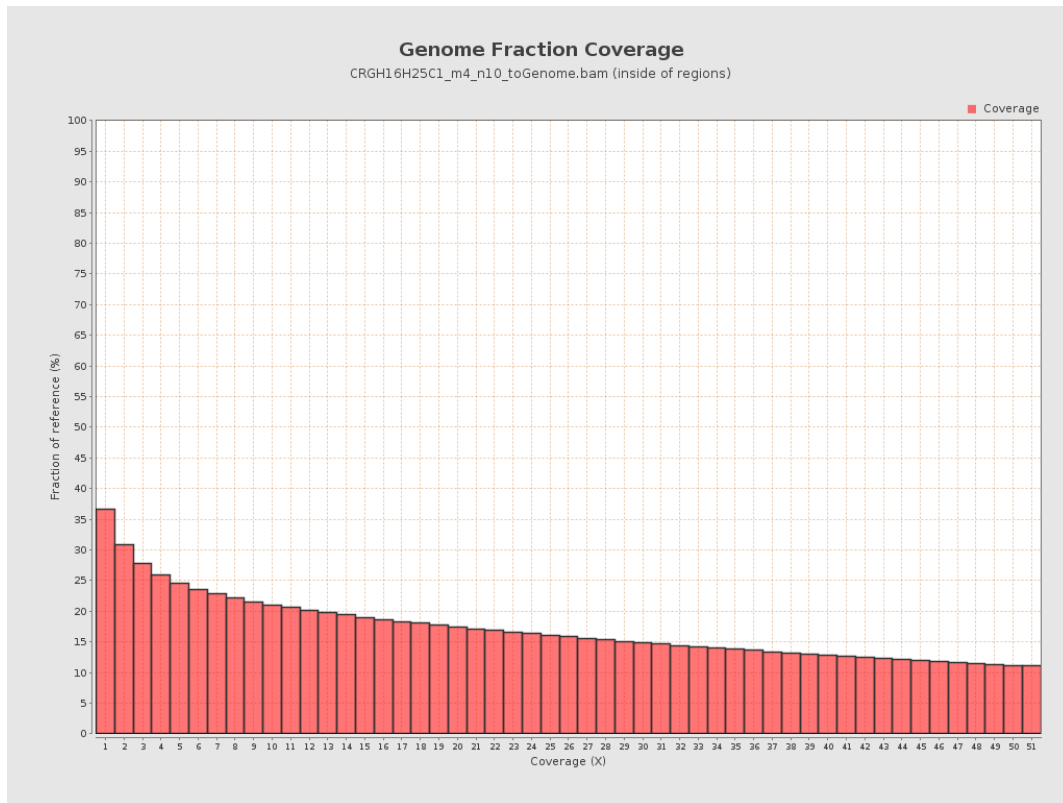
4. Results : Coverage Histogram (inside of regions)



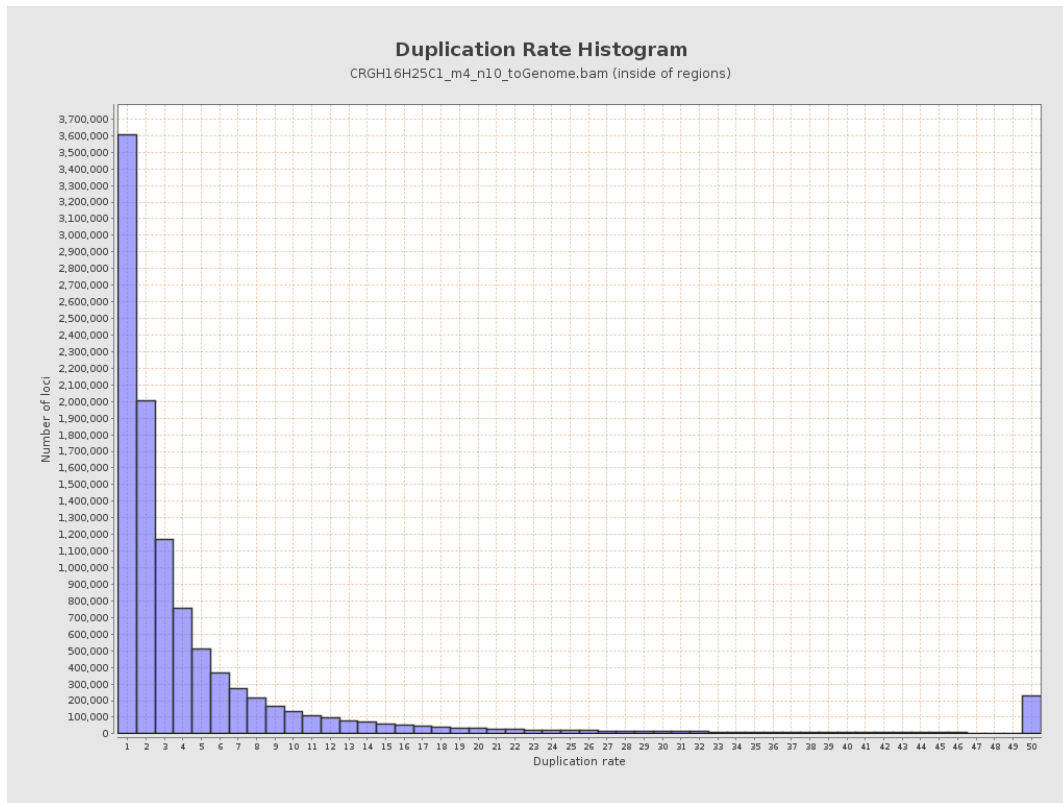
5. Results : Coverage Histogram (0-50X) (inside of regions)



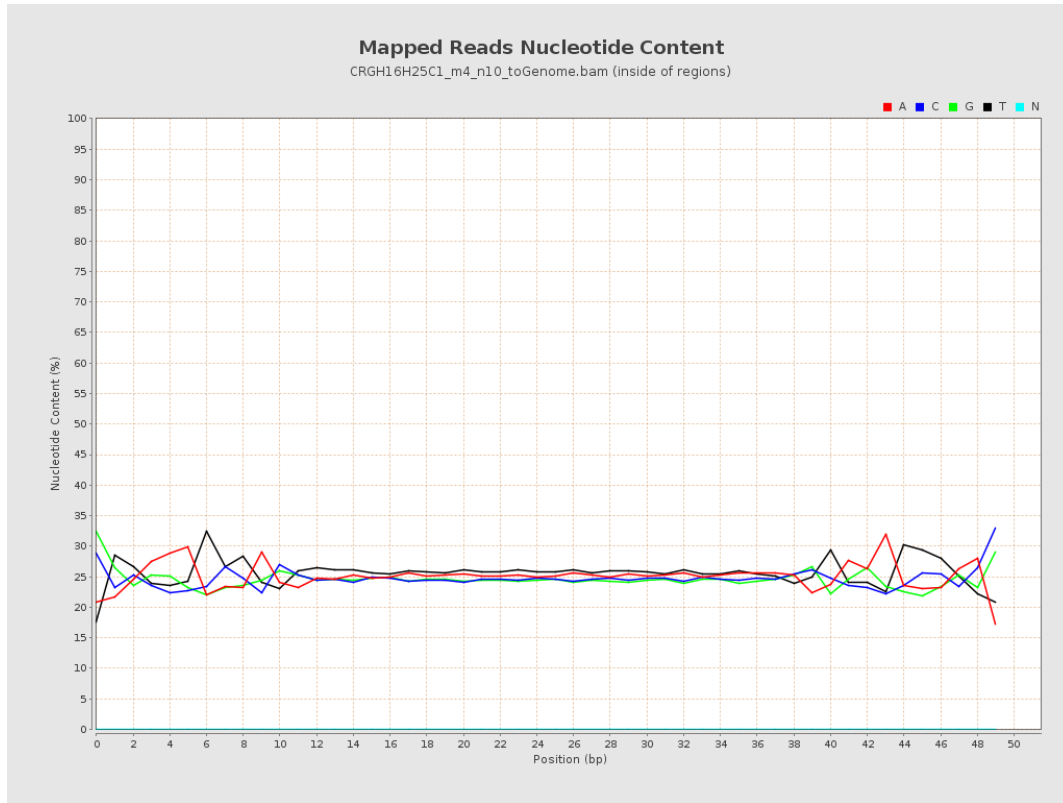
6. Results : Genome Fraction Coverage (inside of regions)



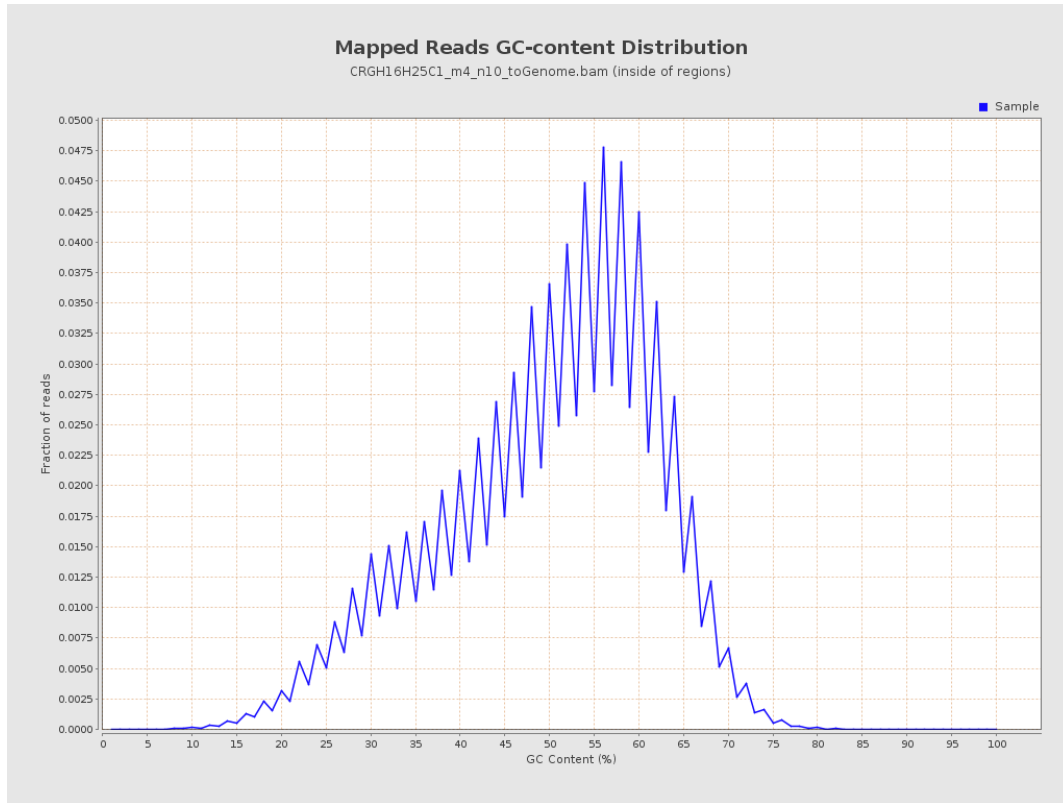
7. Results : Duplication Rate Histogram (inside of regions)



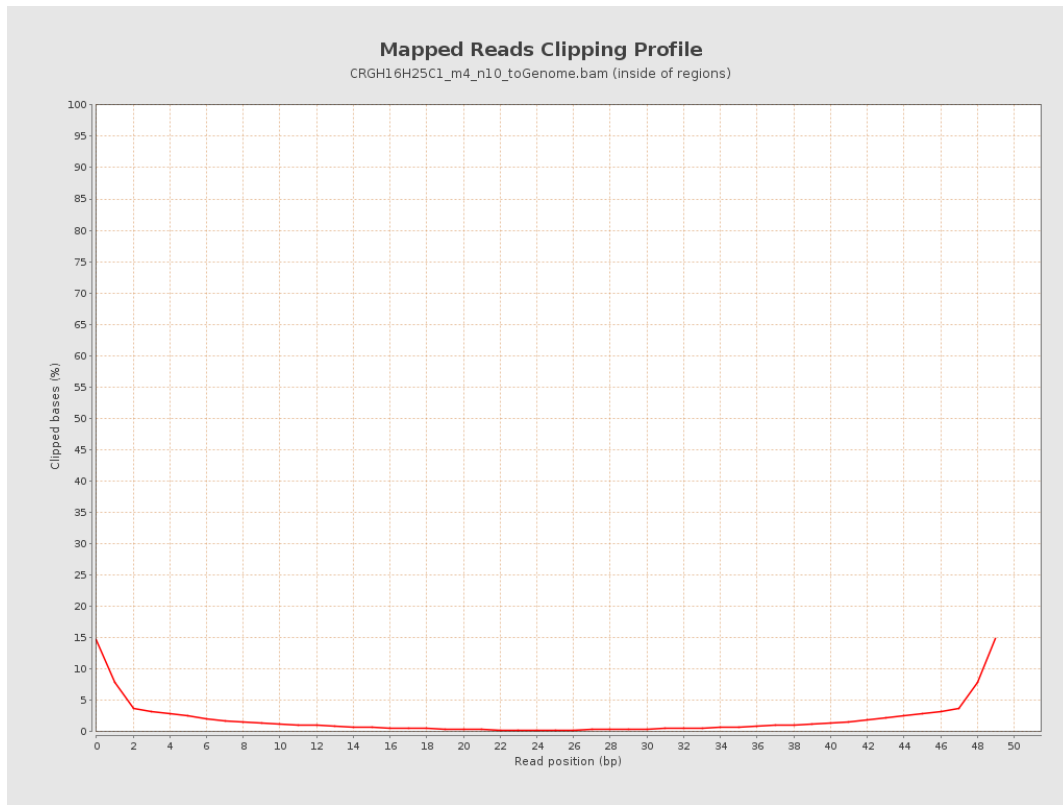
8. Results : Mapped Reads Nucleotide Content (inside of regions)



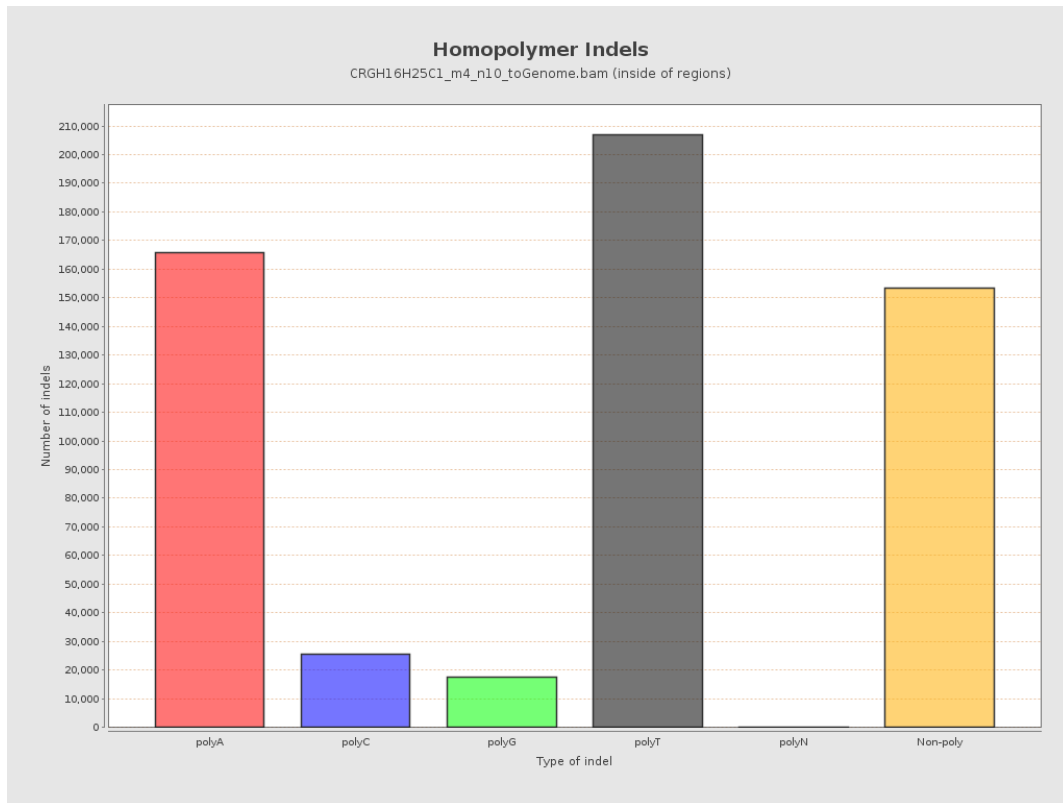
9. Results : Mapped Reads GC-content Distribution (inside of regions)



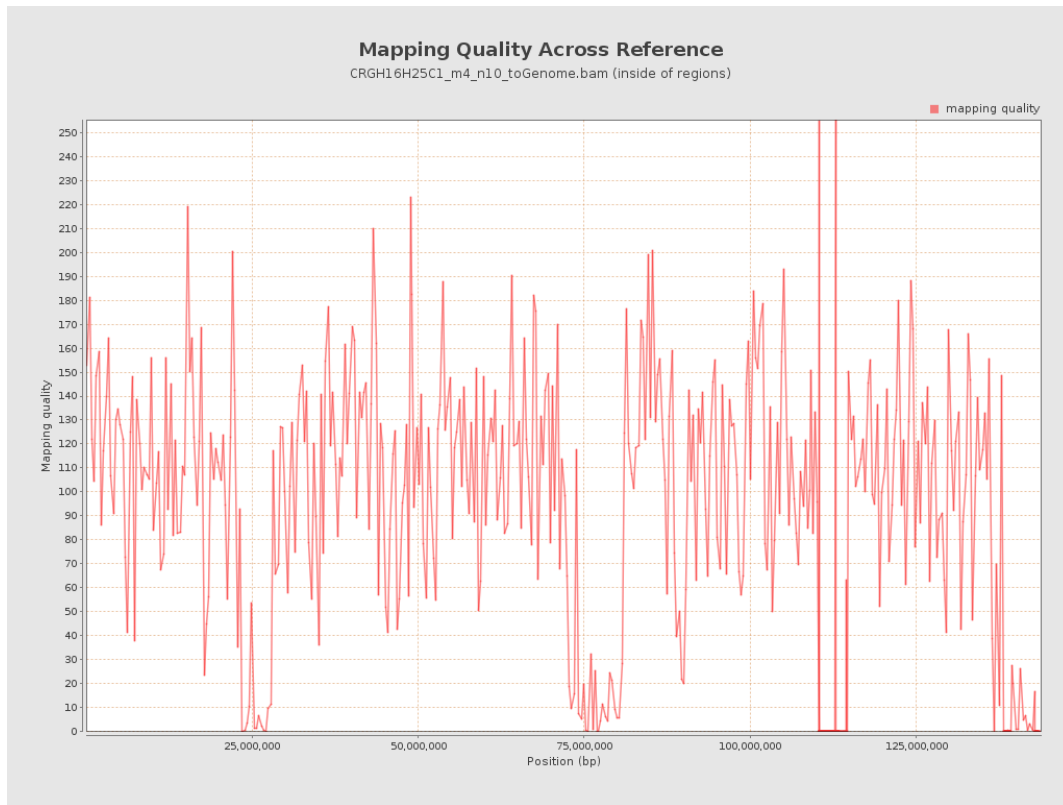
10. Results : Mapped Reads Clipping Profile (inside of regions)



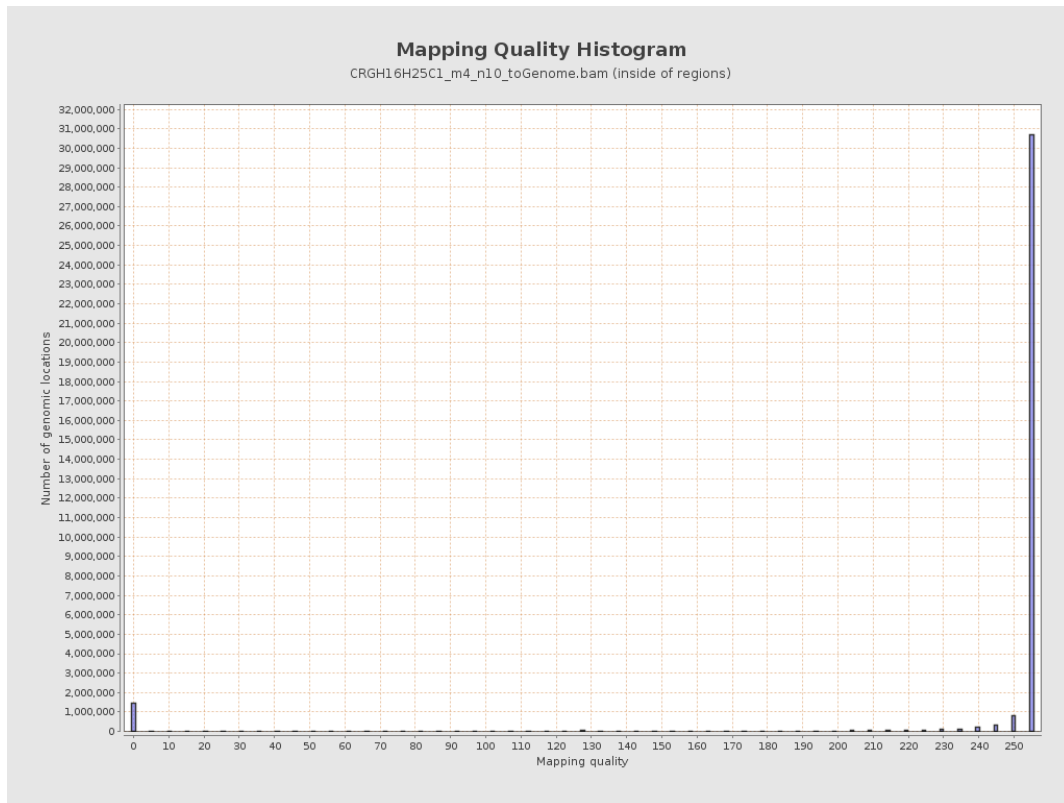
11. Results : Homopolymer Indels (inside of regions)



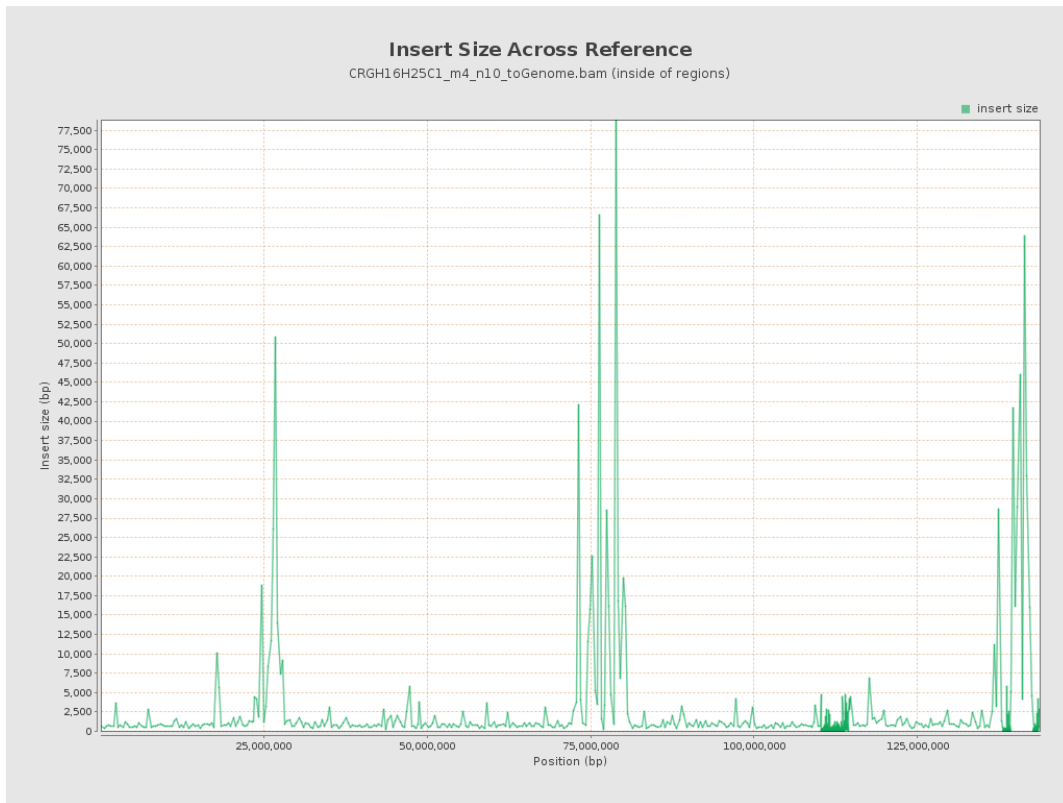
12. Results : Mapping Quality Across Reference (inside of regions)



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)

