

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/06/28 15:24:42*

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

## 1.1. QualiMap command line

```
qualimap bamqc -bam blem_22_final_aligned_gaiix_sorted.bam -gff
./Blastocladiaella_emersonii_ATCC_22665.gtf -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	bwa sampe Blastocladiaella_emersonii_ATCC_22665.scaffolds.fa blem_22_final_vs_s_1_1.sai blem_22_final_vs_s_1_2.sai /sequencing/before_oxford/blastocladiaella/illumina_gaii/trimmed/s_1_1_trimmed_paired.fastq.gz /sequencing/before_oxford/blastocladiaella/illumina_gaii/trimmed/s_1_2_trimmed_paired.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jun 28 15:24:41 UTC 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	blem_22_final_aligned_gaiix_sorted.bam

## 1.3. GFF region

Library protocol:	non-strand-specific
Outside statistics:	no
GFF file:	./Blastocladiella_emersonii_ATCC_2665.gtf

## 2. Summary (inside of regions)

### 2.1. Globals

Reference size	32,654,225
Number of reads	34,499,850
Mapped reads	28,358,716 / 82.2%
Unmapped reads	6,141,134 / 17.8%
Mapped paired reads	28,358,716 / 82.2%
Mapped reads, first in pair	14,186,663 / 41.12%
Mapped reads, second in pair	14,172,053 / 41.08%
Mapped reads, both in pair	27,863,594 / 80.76%
Mapped reads, singletons	495,122 / 1.44%
Secondary alignments	0
Read min/max/mean length	40 / 66 / 63.35
Clipped reads	17,618 / 0.05%

### 2.2. Globals (inside of regions)

Regions size/percentage of reference	18,908,946 / 57.91%
Mapped reads	9,613,400 / 27.87%
Mapped reads, only first in pair	4,803,574 / 13.92%
Mapped reads, only second in pair	4,809,826 / 13.94%
Mapped reads, both in pair	9,438,314 / 27.36%
Mapped reads, singletons	175,086 / 0.51%
Correct strand reads	0 / 0%
Clipped reads	17,618 / 0.05%

Duplicated reads (estimated)	3,521,055 / 36.63%
Duplication rate	35.25%

### 2.3. ACGT Content (inside of regions)

Number/percentage of A's	98,554,054 / 17.54%
Number/percentage of C's	183,027,226 / 32.57%
Number/percentage of T's	96,858,565 / 17.24%
Number/percentage of G's	183,180,262 / 32.6%
Number/percentage of N's	298,014 / 0.05%
GC Percentage	65.17%

### 2.4. Coverage (inside of regions)

Mean	29.7172
Standard Deviation	36.9466

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

Mean Mapping Quality	50.7
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### 2.6. Insert size (inside of regions)

Mean	4,122.3
Standard Deviation	84,175.54
P25/Median/P75	252 / 357 / 443

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

General error rate	0.41%
Mismatches	2,297,110

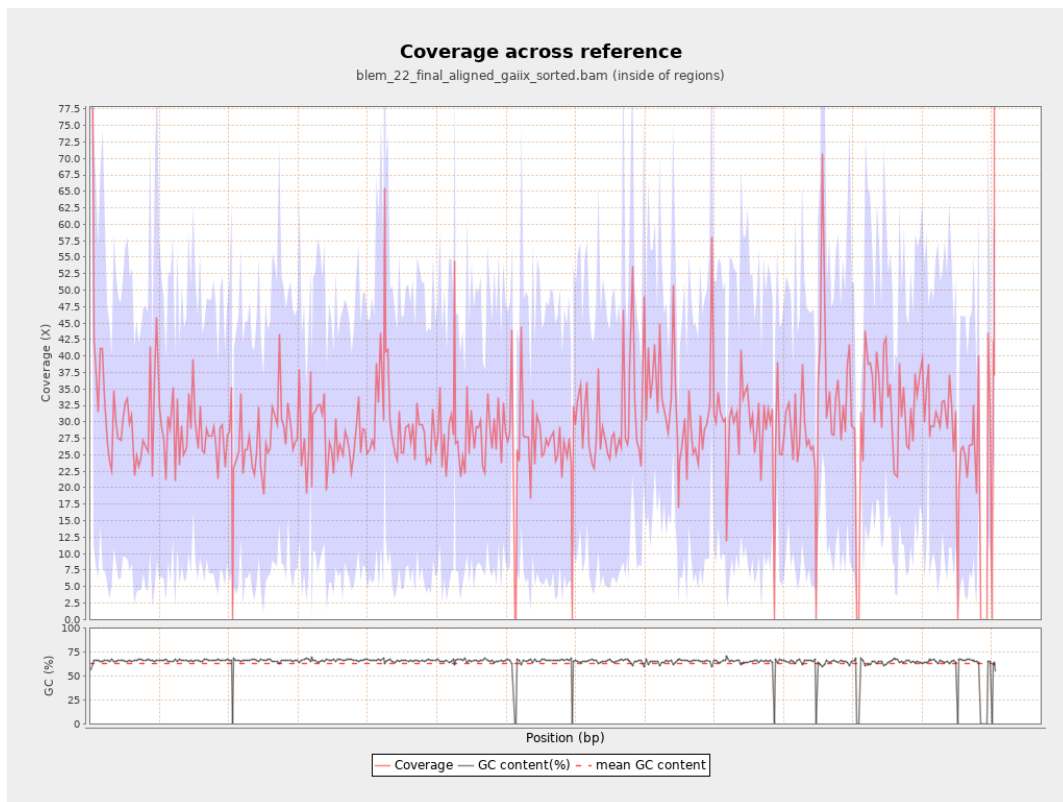
Insertions	1,814
Mapped reads with at least one insertion	0.01%
Deletions	3,131
Mapped reads with at least one deletion	0.01%
Homopolymer indels	27.44%

## 2.8. Chromosome stats (inside of regions)

Name	Length	Mapped bases	Mean coverage	Standard deviation
c_be_22_1	3774054	112380408	29.7771	23.2257
c_be_22_2	1841349	50018361	27.164	19.8766
c_be_22_3	1766176	50482619	28.583	21.0823
c_be_22_4	1721370	49001364	28.4665	21.2131
c_be_22_5	1155248	32203810	27.8761	19.8743
c_be_22_6	1320572	35457015	26.8497	20.384
c_be_22_7	1210433	35361907	29.2143	22.0579
c_be_22_8	587084	20843910	35.5041	22.6403
c_be_22_9	904154	25927512	28.676	20.4053
c_be_22_10	981880	29498803	30.0432	21.772
c_be_22_11	822787	22795333	27.705	20.6409
c_be_22_12	677011	23836769	35.2088	26.1212
c_be_22_13	389119	13808098	35.4855	24.409
c_be_22_14	573396	17733381	30.9269	20.9947
c_be_22_15	544593	16693273	30.6527	21.8634

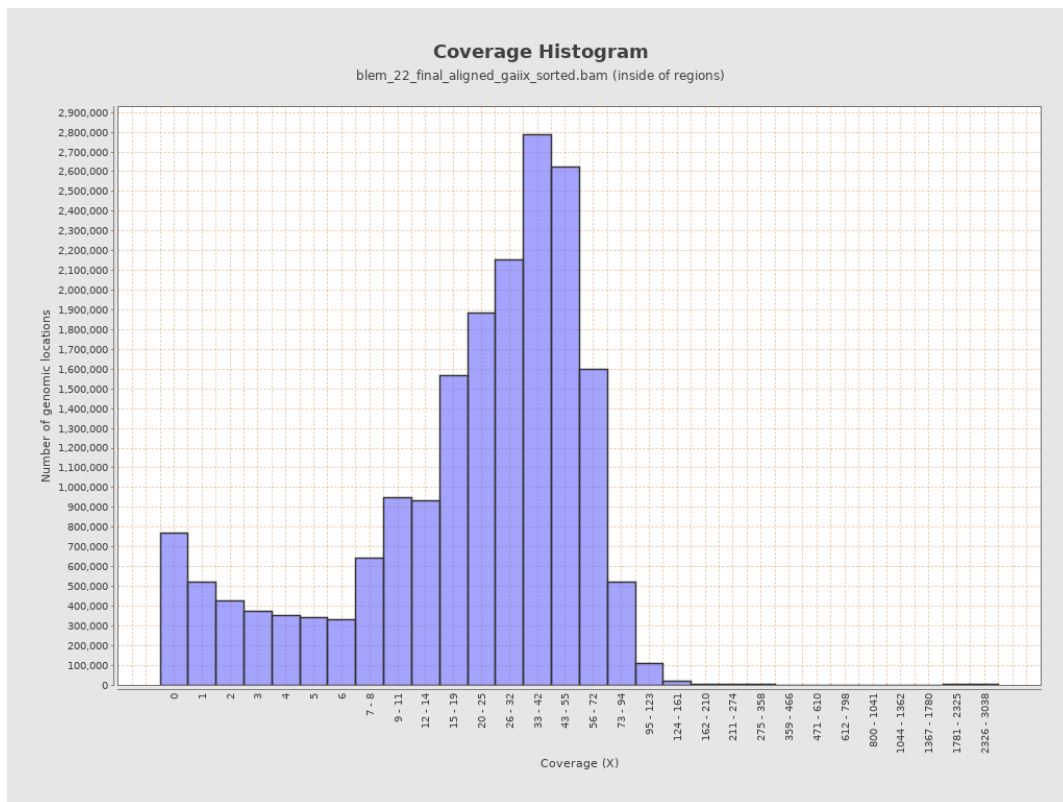
c_be_22_16	396747	10114695	25.4941	19.2275
c_be_22_17	109013	2741215	25.1458	20.3825
c_be_22_18	96249	3675496	38.1874	24.6907
c_be_22_20	8122	338245	41.6455	26.7146
c_be_22_22	25542	945251	37.0077	21.4277
c_be_22_26	4047	8063269	1,992.4065	550.6858

### 3. Results : Coverage across reference (inside of regions)

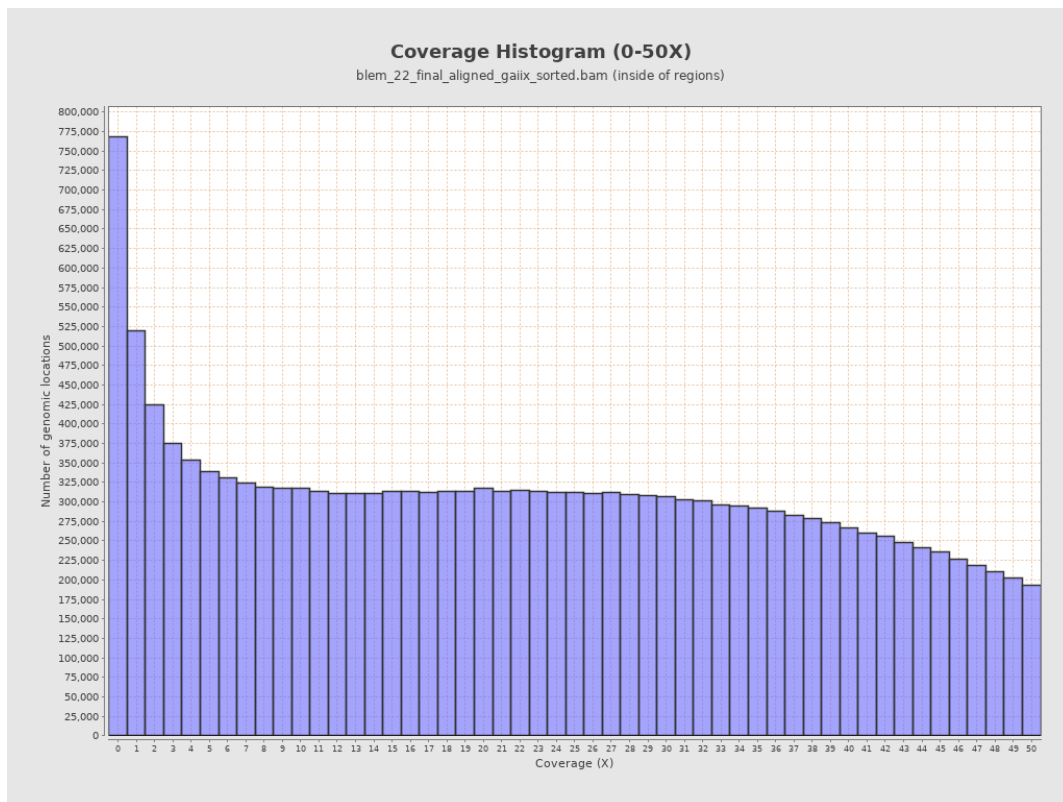




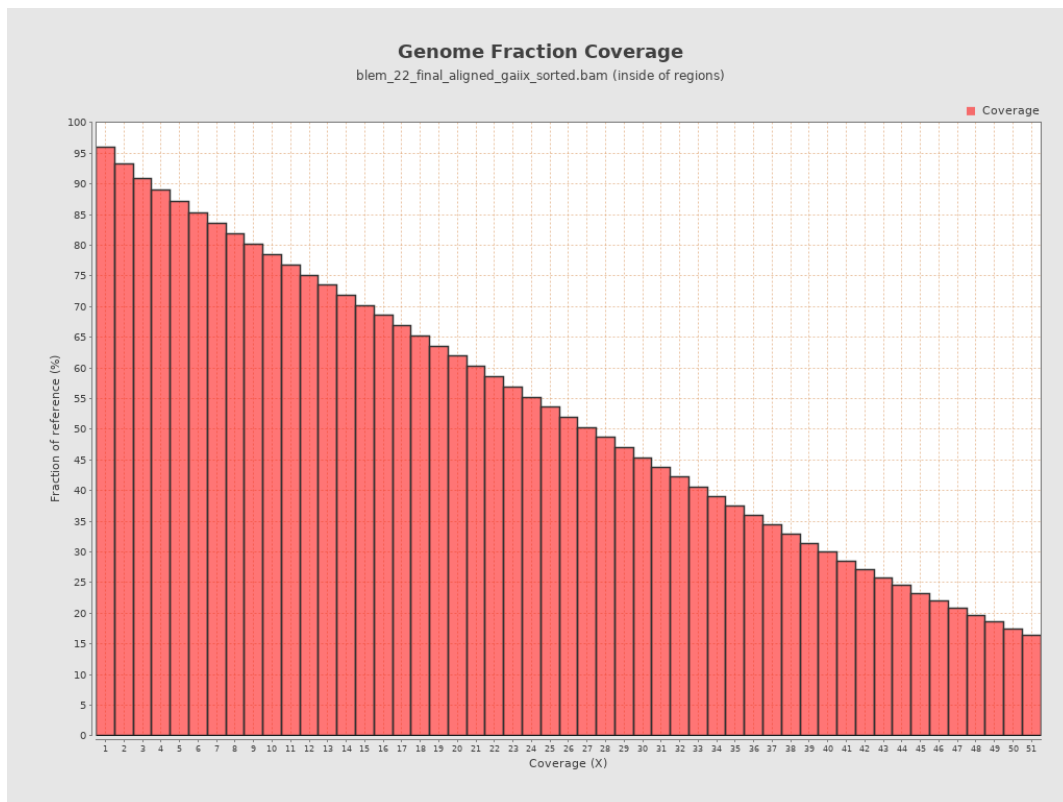
## 4. Results : Coverage Histogram (inside of regions)



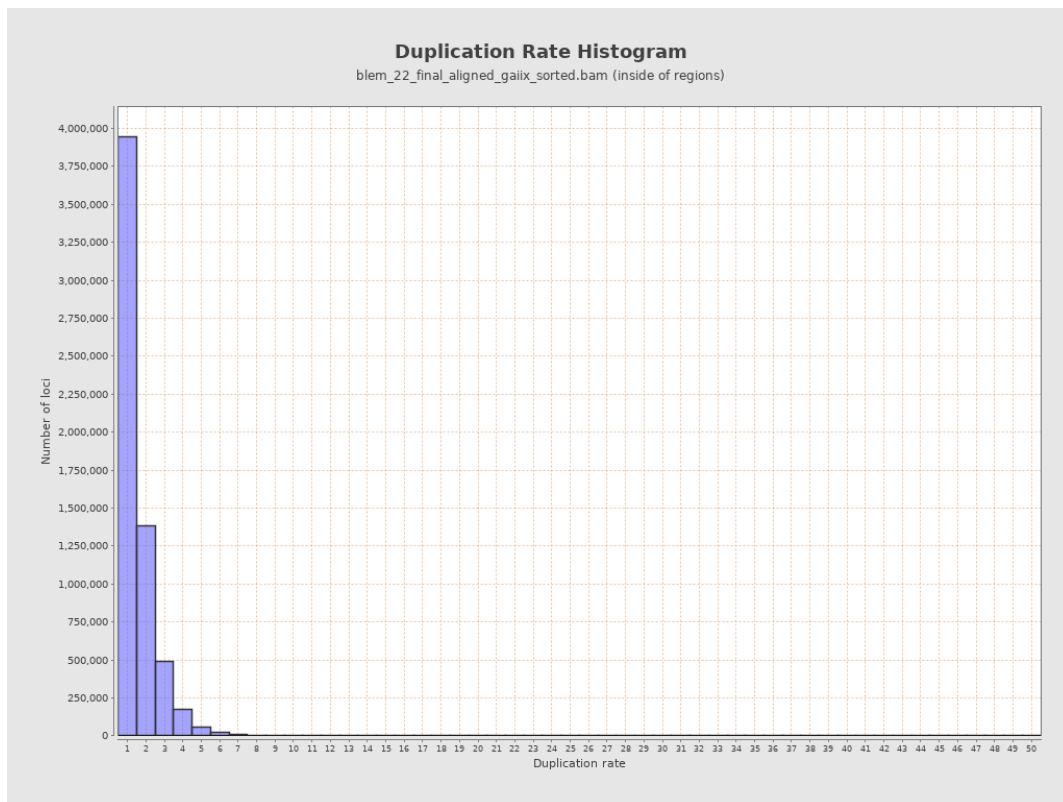
## 5. Results : Coverage Histogram (0-50X) (inside of regions)



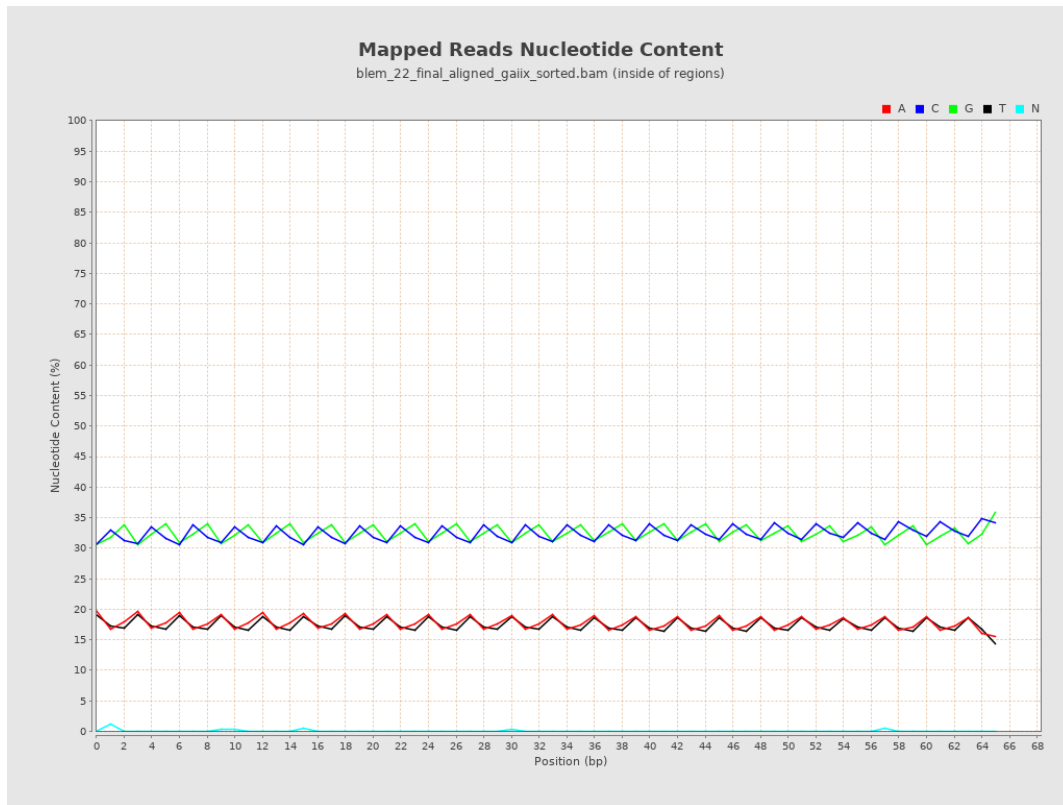
## 6. Results : Genome Fraction Coverage (inside of regions)



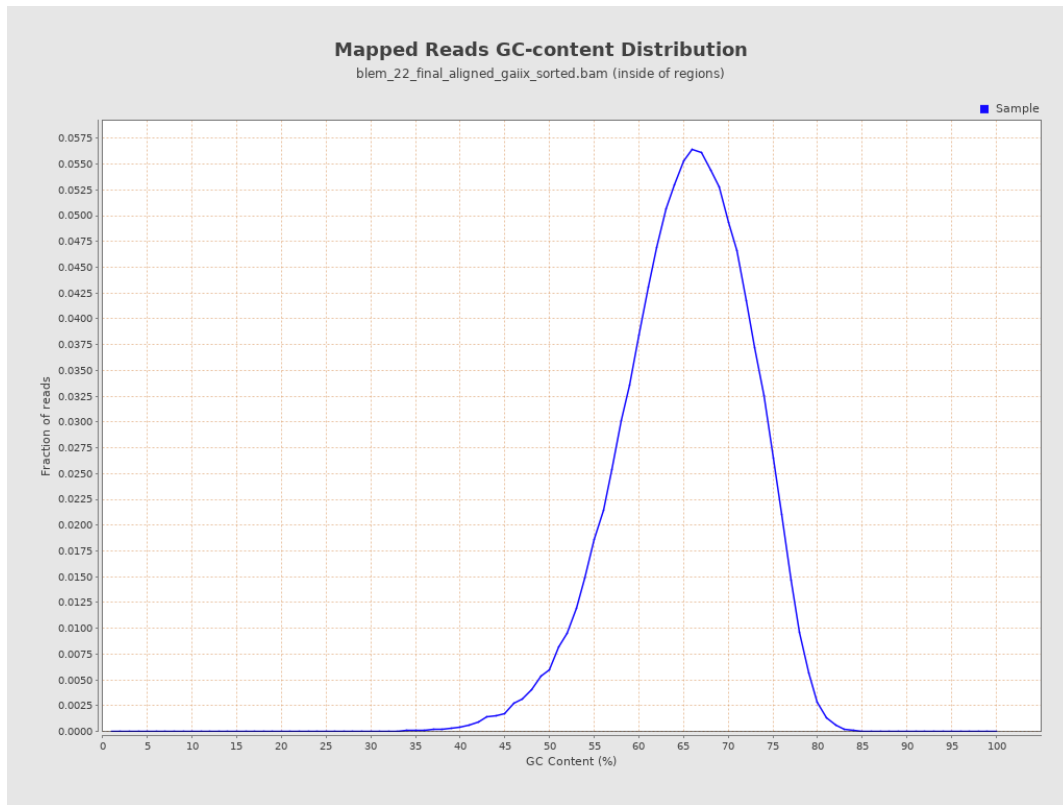
## 7. Results : Duplication Rate Histogram (inside of regions)



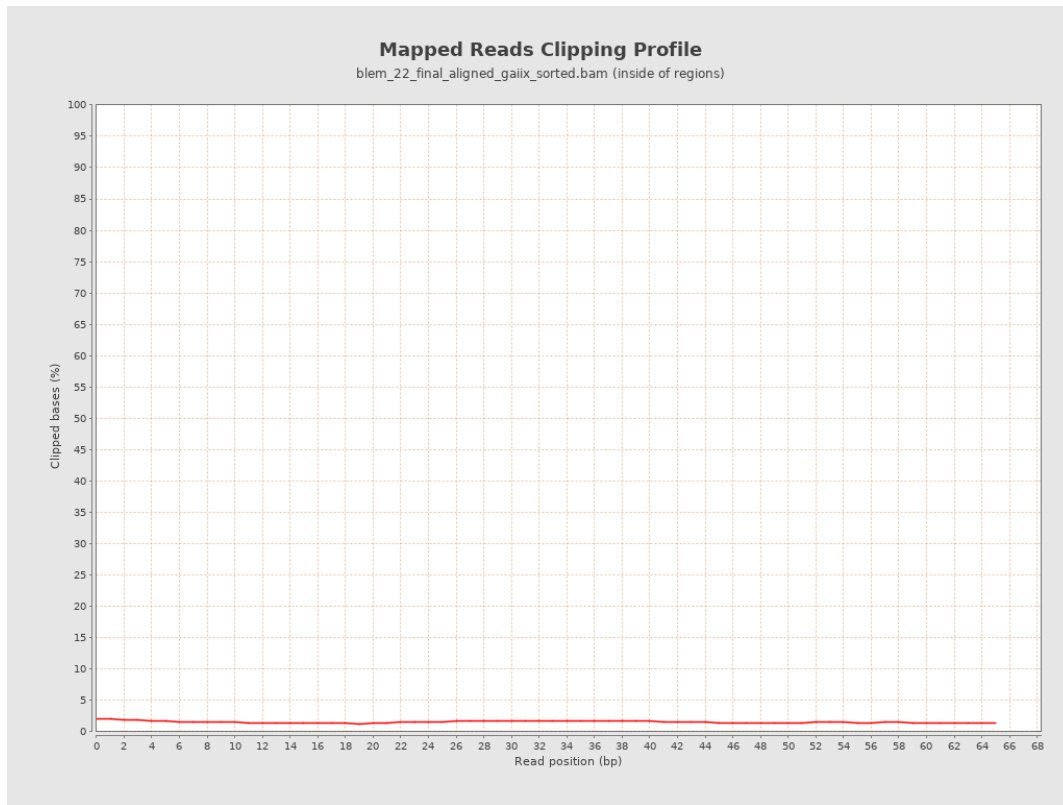
## 8. Results : Mapped Reads Nucleotide Content (inside of regions)



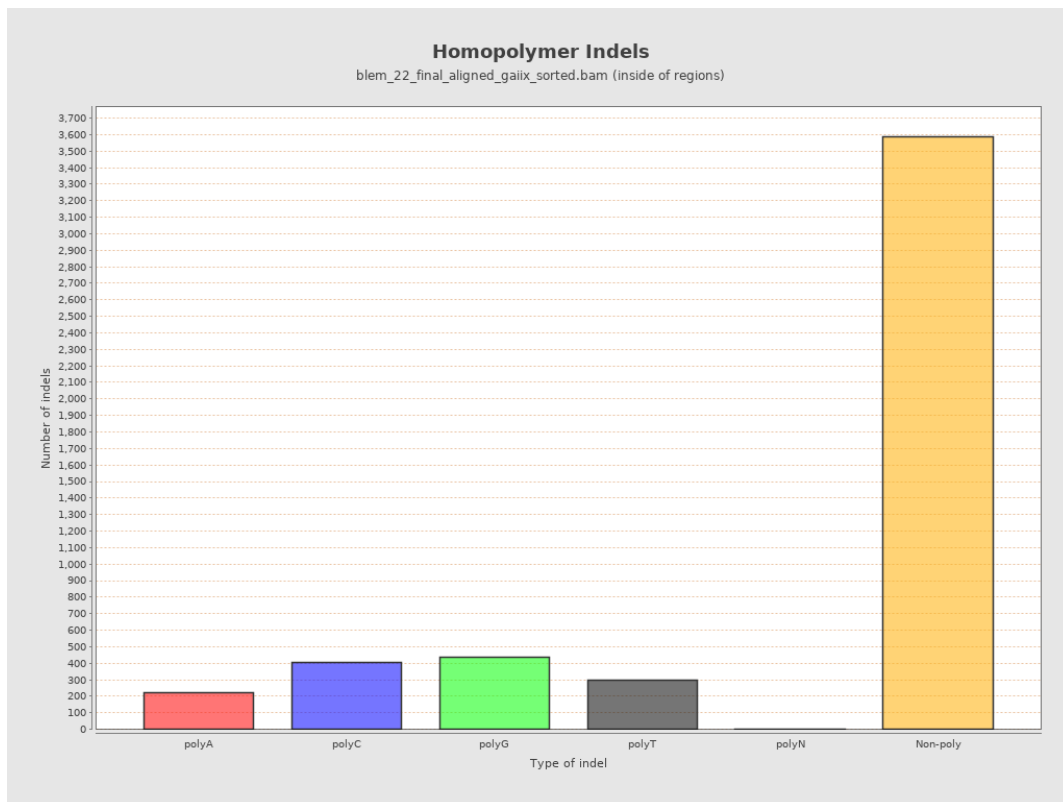
## 9. Results : Mapped Reads GC-content Distribution (inside of regions)



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

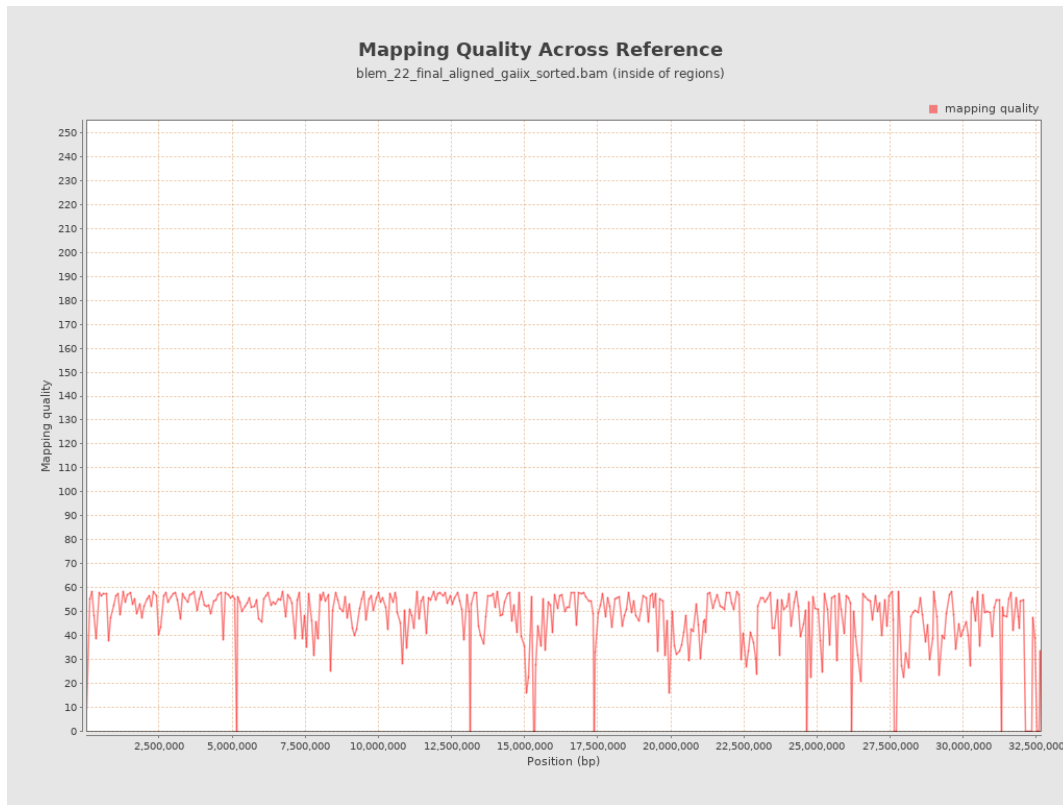


## 11. Results : Homopolymer Indels (inside of regions)

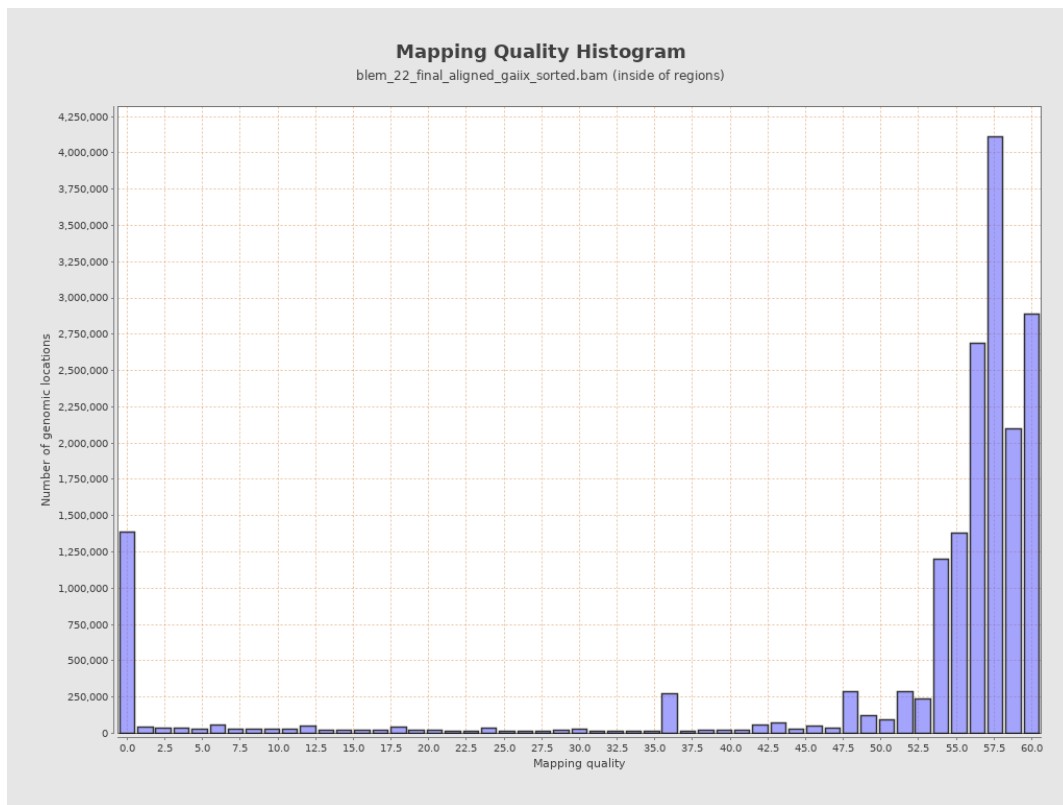




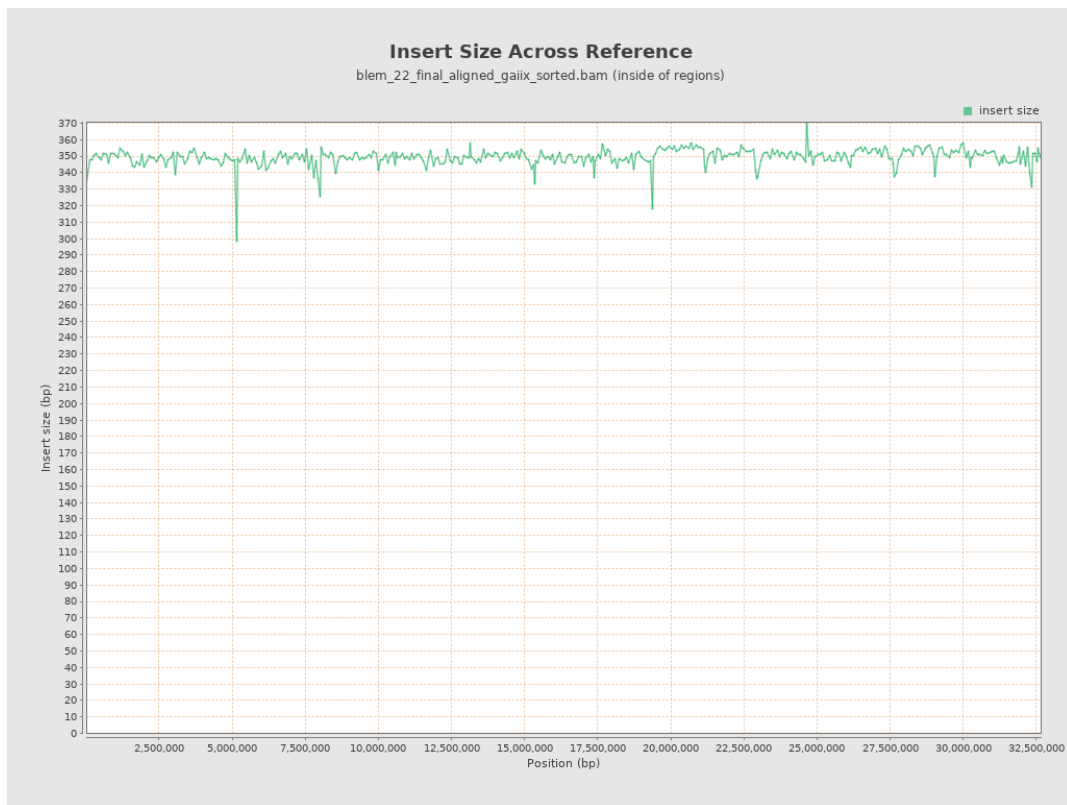
## 12. Results : Mapping Quality Across Reference (inside of regions)



## 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)

