

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/28 14:41:17

1. Input data & parameters (inside of regions)

1.1. QualiMap command line

```
qualimap bamqc -bam blem_22_final_aligned_pacbio_sorted.bam -gff
./Blastocladiaella_emersonii_ATCC_22665.gtf -nw 400 -hm 3
```

1.2. Alignment

Command line:	minimap2 -ax map-hifi -t 112 Blastocladiaella_emersonii_ATCC_22 665.scaffolds.fa ../../raw_reads/demultiplex.bc1012_B AK8A_OA-- bc1012_BAK8A_OA.hifi_reads.filt.fas tq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	minimap2 (2.24-r1122)
Analysis date:	Tue Jun 28 14:41:15 UTC 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	blem_22_final_aligned_pacbio_sort ed.bam

1.3. GFF region

Library protocol:	non-strand-specific
Outside statistics:	no
GFF file:	./Blastocladiaella_emersonii_ATCC_2

2665.gtf

2. Summary (inside of regions)

2.1. Globals

Reference size	32,654,225
Number of reads	605,547
Mapped reads	550,035 / 90.83%
Unmapped reads	55,512 / 9.17%
Mapped paired reads	0 / 0%
Secondary alignments	268,107
Supplementary alignments	4,517 / 0.75%
Read min/max/mean length	0 / 60,944 / 10,594.85
Clipped reads	45,444 / 7.5%

2.2. Globals (inside of regions)

Regions size/percentage of reference	18,908,946 / 57.91%
Mapped reads	474,768 / 78.4%
Duplicated reads (estimated)	43,223 / 9.1%
Duplication rate	3.56%

2.3. ACGT Content (inside of regions)

Number/percentage of A's	469,757,597 / 16.36%
Number/percentage of C's	967,928,212 / 33.7%
Number/percentage of T's	470,336,198 / 16.38%
Number/percentage of G's	963,915,704 / 33.56%
Number/percentage of N's	0 / 0%

GC Percentage	67.27%
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2.4. Coverage (inside of regions)

Mean	153.9974
Standard Deviation	151.0866

2.5. Mapping Quality (inside of regions)

Mean Mapping Quality	59.37
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2.6. Mismatches and indels (inside of regions)

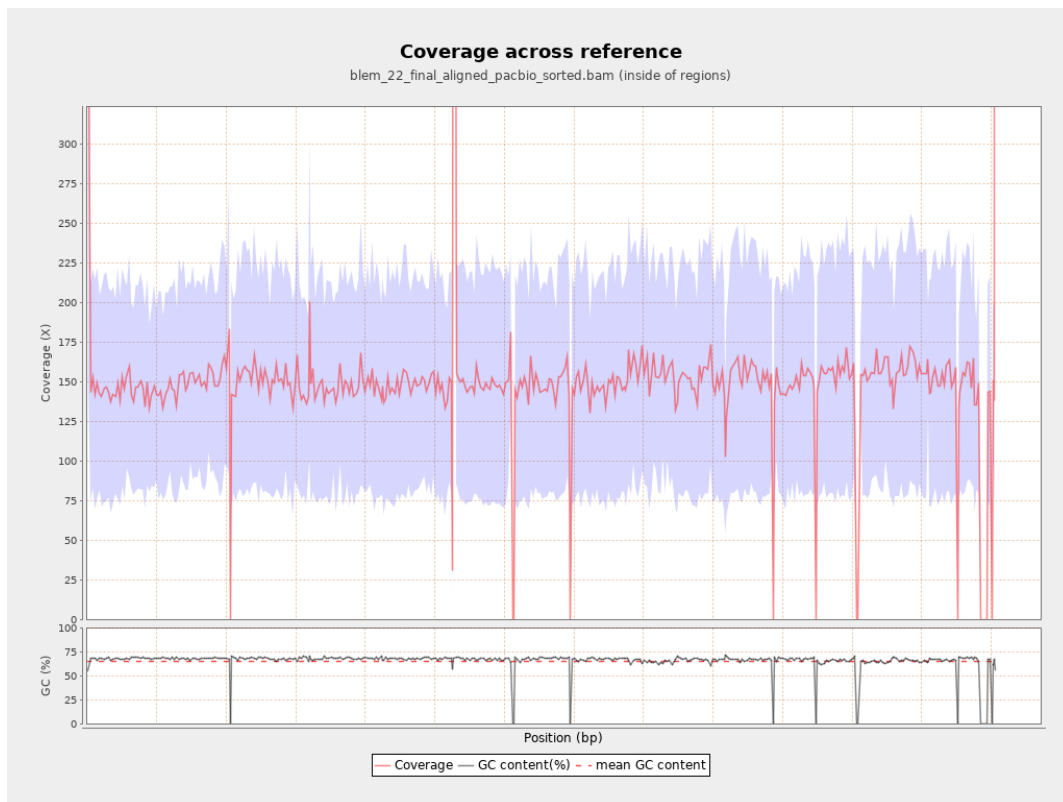
General error rate	5.03%
Insertions	3,914,551
Mapped reads with at least one insertion	51.91%
Deletions	4,478,978
Mapped reads with at least one deletion	63.18%
Homopolymer indels	43.35%

2.7. Chromosome stats (inside of regions)

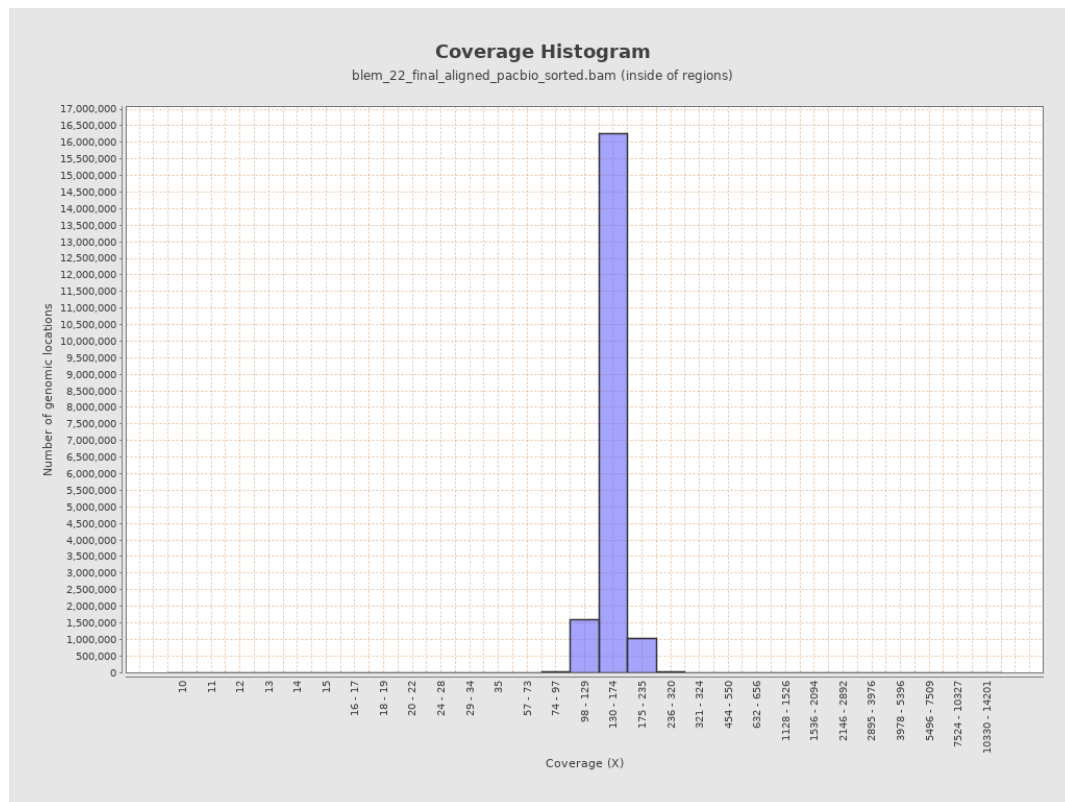
Name	Length	Mapped bases	Mean coverage	Standard deviation
c_be_22_1	3774054	562803548	149.1244	43.6415
c_be_22_2	1841349	276112316	149.9511	15.4401
c_be_22_3	1766176	260850545	147.6923	16.8516
c_be_22_4	1721370	254276009	147.7172	13.9537
c_be_22_5	1155248	209821891	181.625	36.7772

c_be_22_6	1320572	196554278	148.8403	14.1365
c_be_22_7	1210433	177685630	146.7951	14.3068
c_be_22_8	587084	91896823	156.531	16.0696
c_be_22_9	904154	136603963	151.0848	14.9096
c_be_22_10	981880	150530814	153.3088	16.0409
c_be_22_11	822787	122799231	149.2479	13.6127
c_be_22_12	677011	105352327	155.6139	15.3841
c_be_22_13	389119	60672871	155.9237	14.283
c_be_22_14	573396	90200895	157.3099	15.4458
c_be_22_15	544593	82941462	152.2999	15.6654
c_be_22_16	396747	60951528	153.6282	14.8516
c_be_22_17	109013	15092498	138.4468	11.4497
c_be_22_18	96249	13838206	143.7751	11.3996
c_be_22_20	8122	1201655	147.9506	8.0223
c_be_22_22	25542	3520271	137.8228	36.4273
c_be_22_26	4047	38221989	9,444.5241	4,214.7735

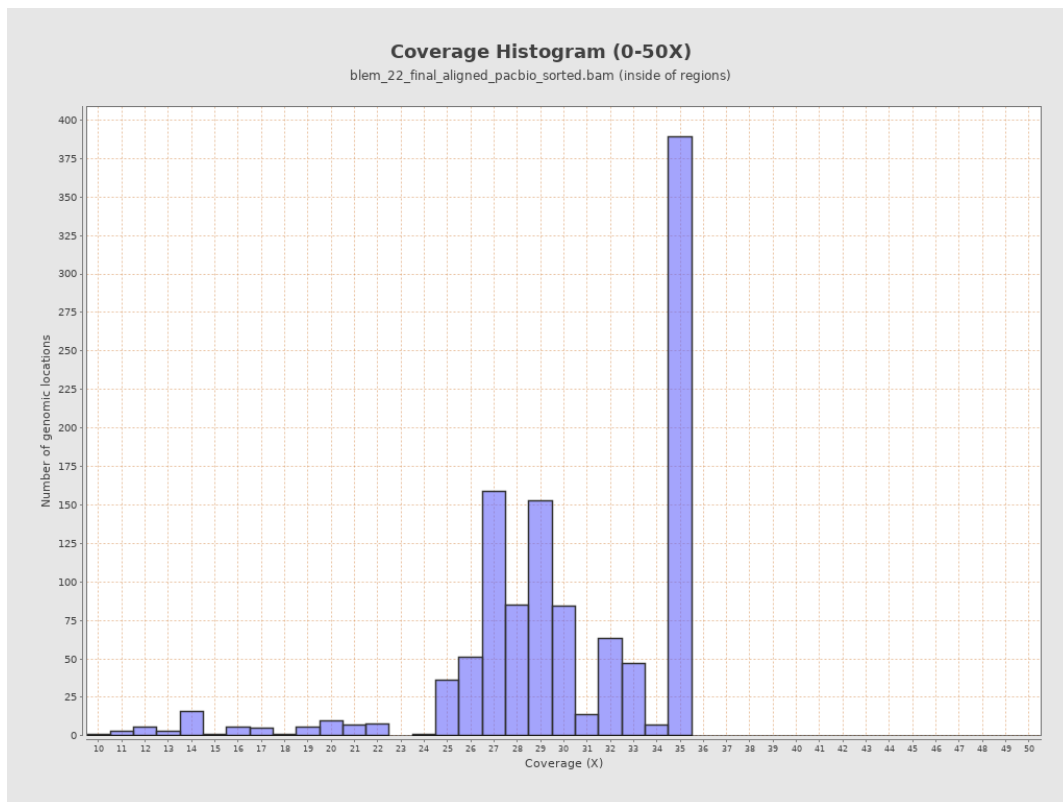
3. Results : Coverage across reference (inside of regions)



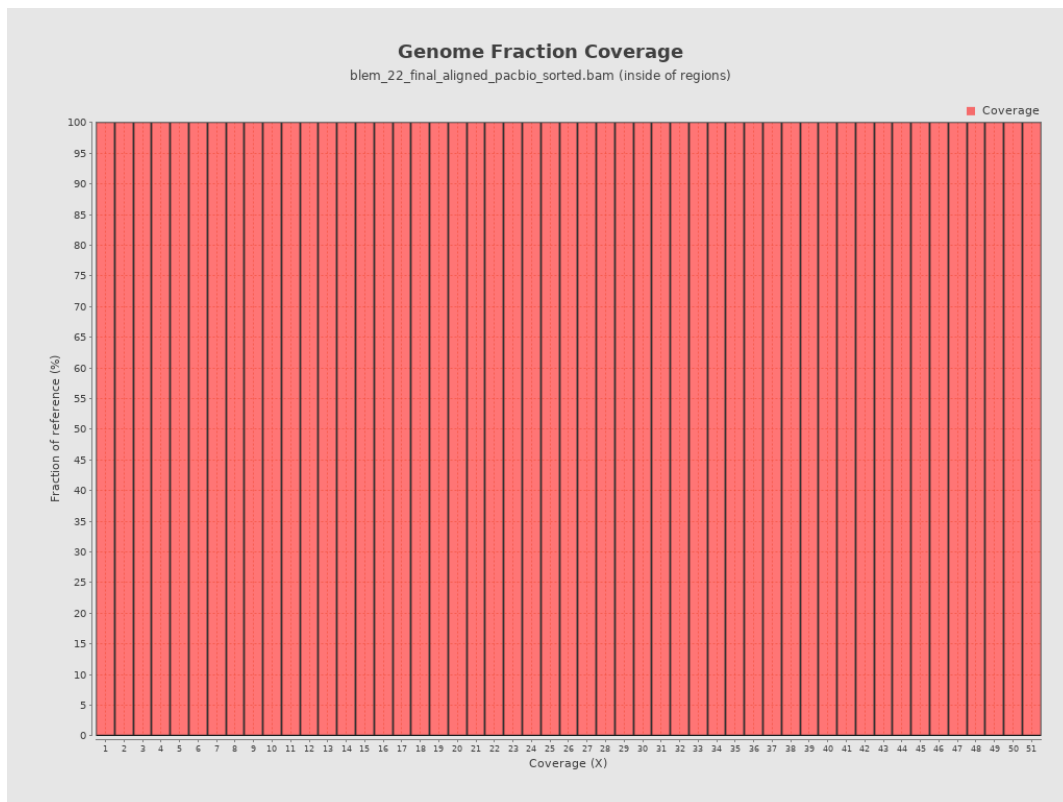
4. Results : Coverage Histogram (inside of regions)



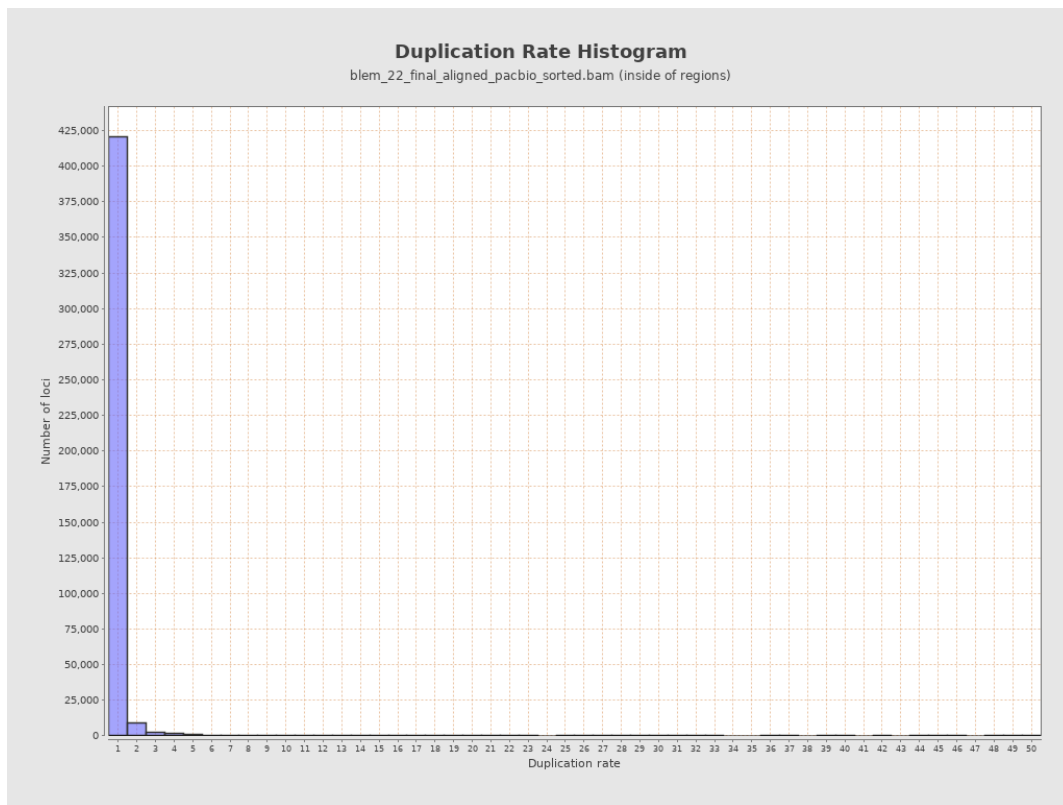
5. Results : Coverage Histogram (0-50X) (inside of regions)



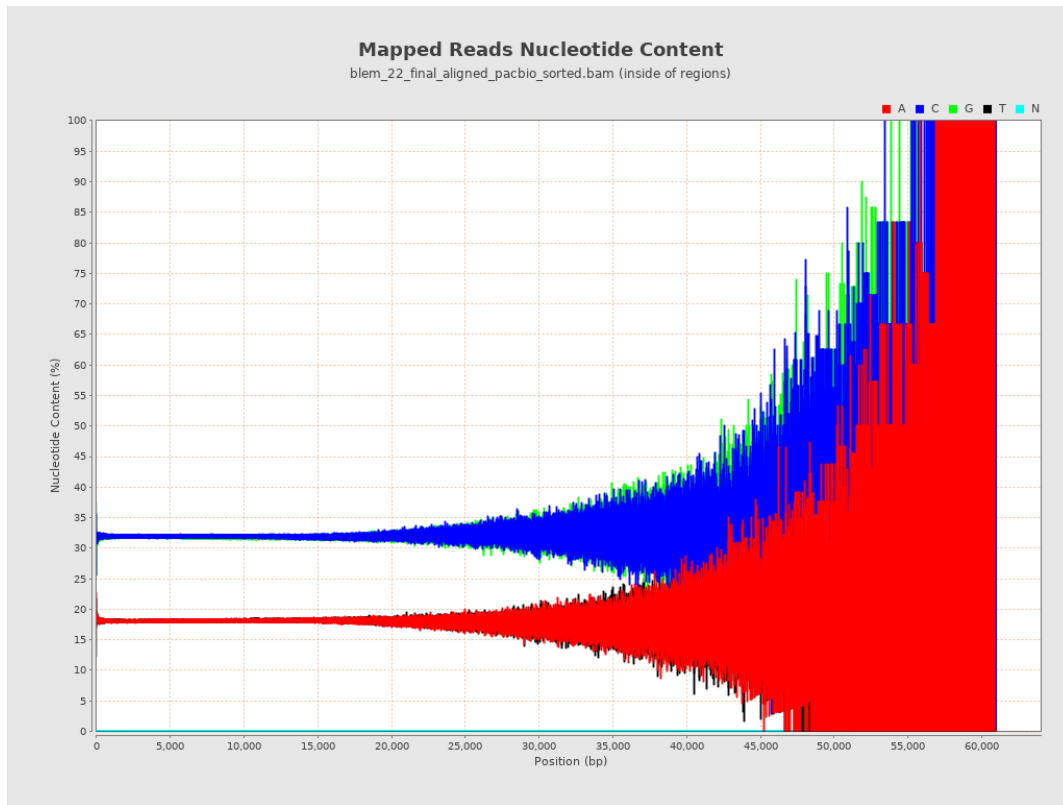
6. Results : Genome Fraction Coverage (inside of regions)



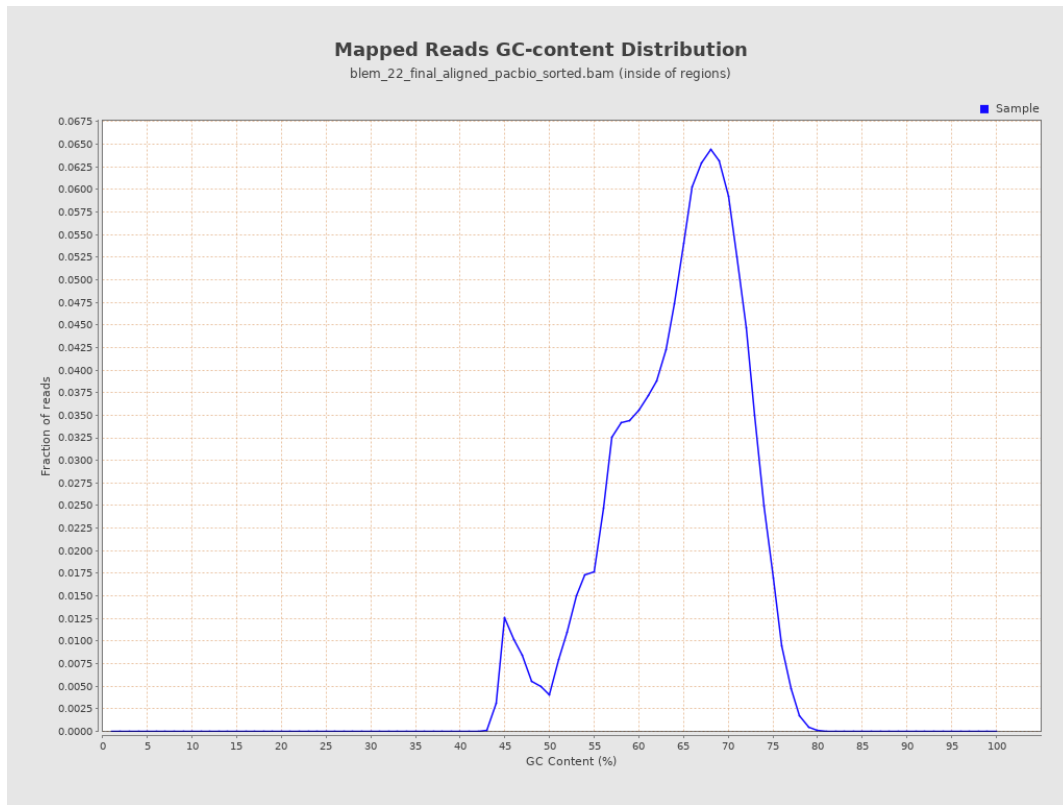
7. Results : Duplication Rate Histogram (inside of regions)



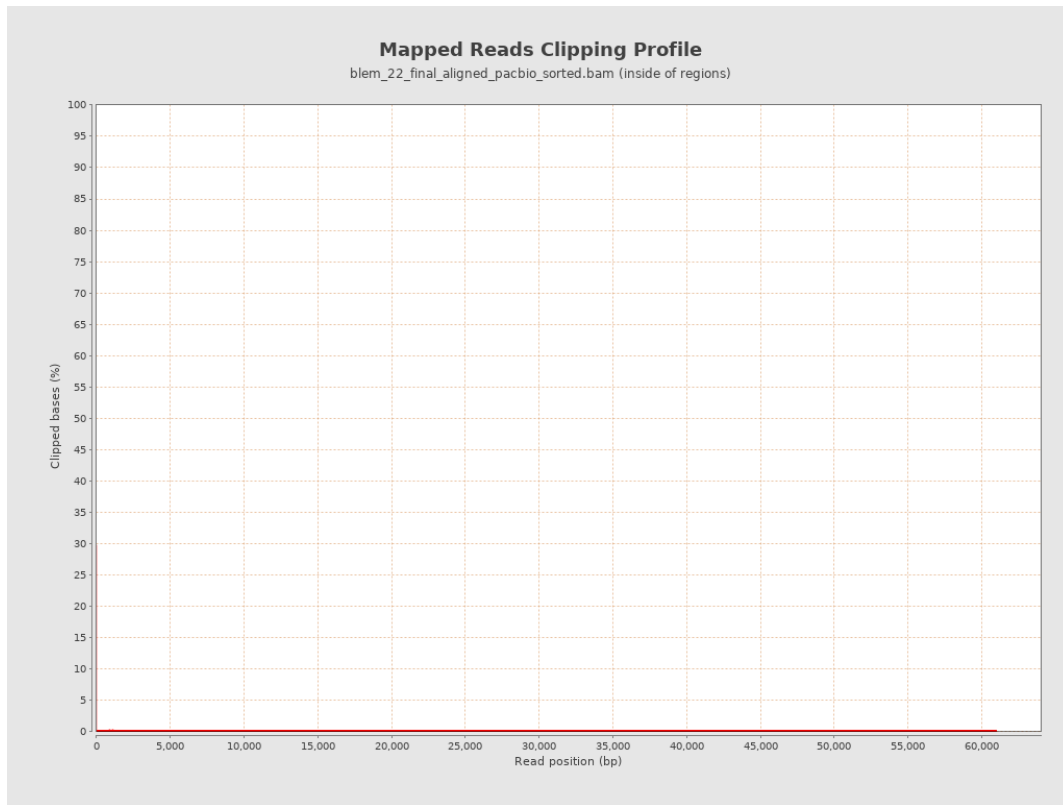
8. Results : Mapped Reads Nucleotide Content (inside of regions)



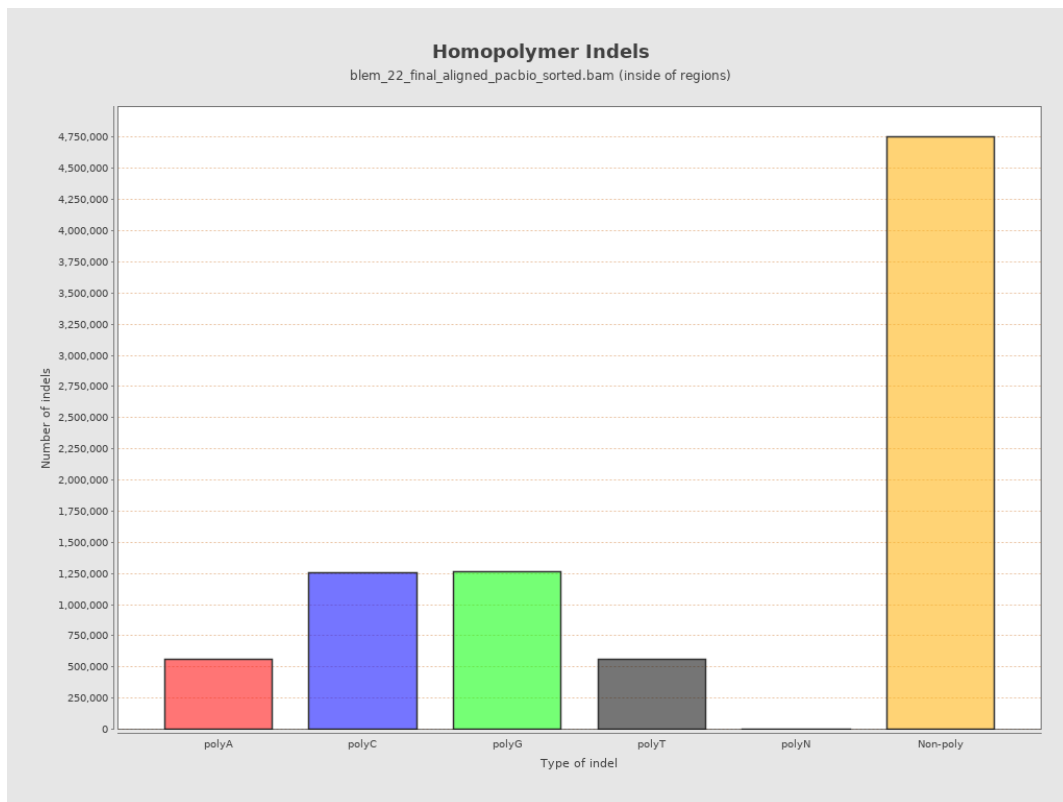
9. Results : Mapped Reads GC-content Distribution (inside of regions)



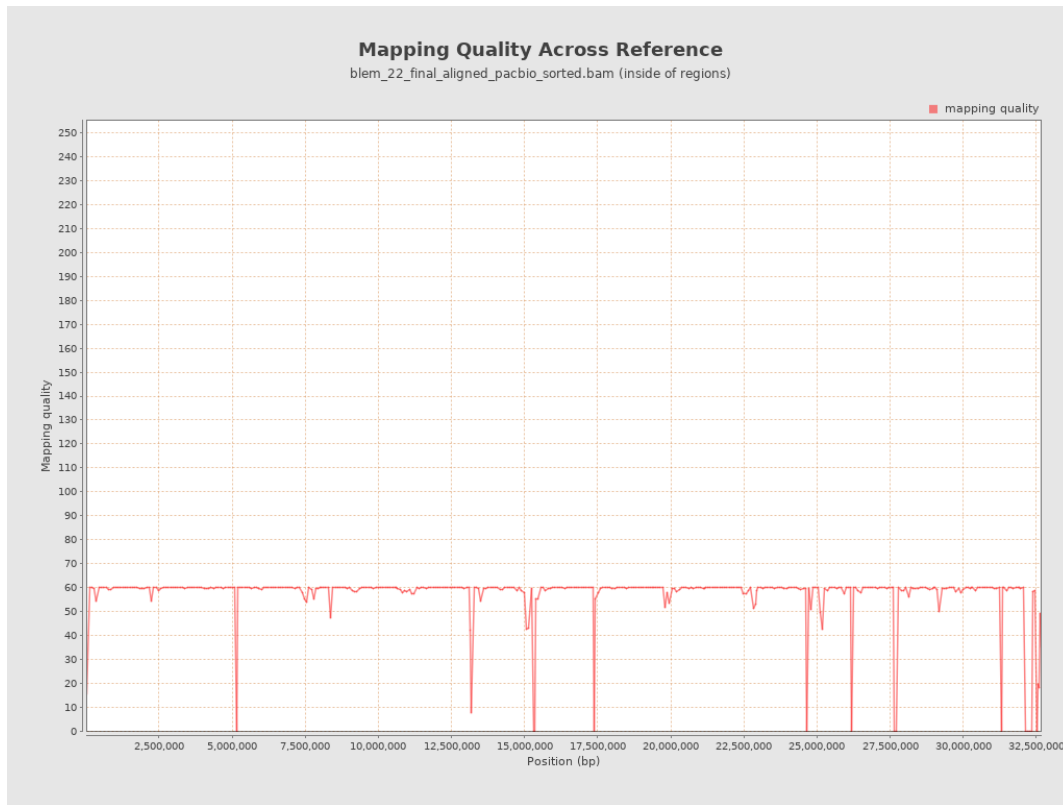
10. Results : Mapped Reads Clipping Profile (inside of regions)



11. Results : Homopolymer Indels (inside of regions)



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



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

