

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:18:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234031.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6234031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234031.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:18:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,656,825
Mapped reads	2,184,233 / 82.21%
Unmapped reads	472,592 / 17.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,564 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	99,868 / 3.76%
Duplication rate	3.58%
Clipped reads	1,115,795 / 42%

2.2. ACGT Content

Number/percentage of A's	37,602,323 / 26.65%
Number/percentage of C's	26,984,256 / 19.13%
Number/percentage of T's	43,226,461 / 30.64%
Number/percentage of G's	33,242,015 / 23.56%
Number/percentage of N's	24,835 / 0.02%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.3838
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2.4. Mapping Quality

Mean Mapping Quality	43.9
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2.5. Mismatches and indels

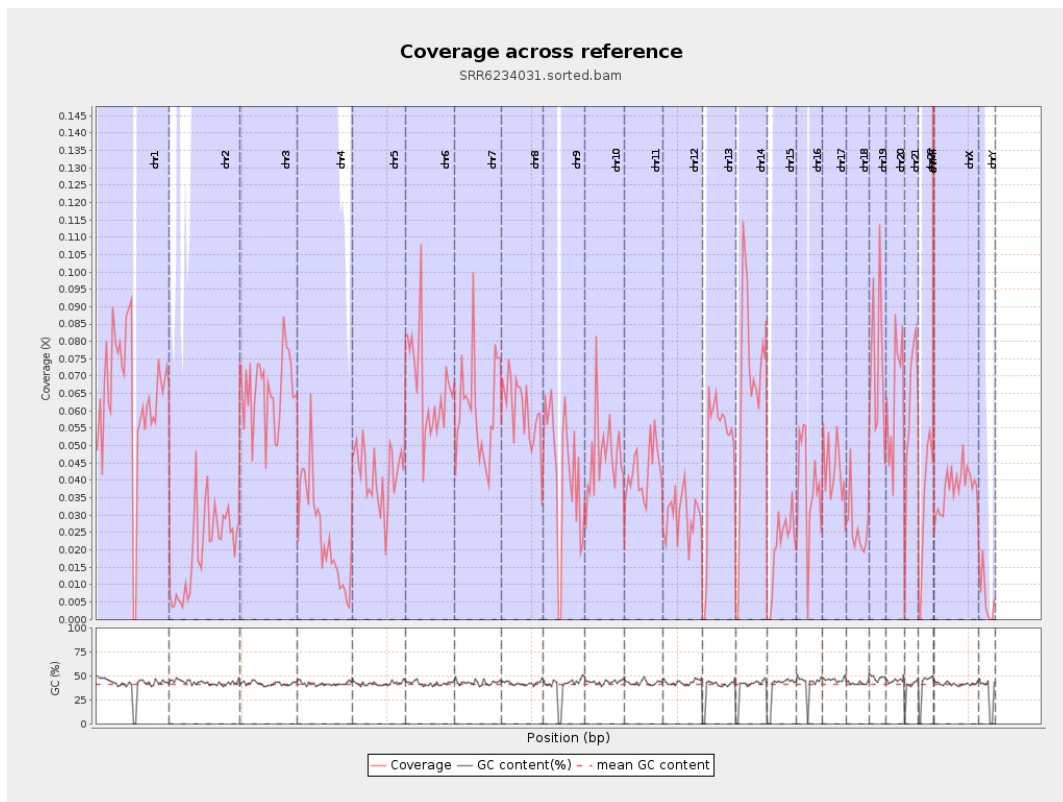
General error rate	0.75%
Mismatches	1,046,629
Insertions	9,604
Mapped reads with at least one insertion	0.43%
Deletions	31,796
Mapped reads with at least one deletion	1.44%
Homopolymer indels	44.88%

2.6. Chromosome stats

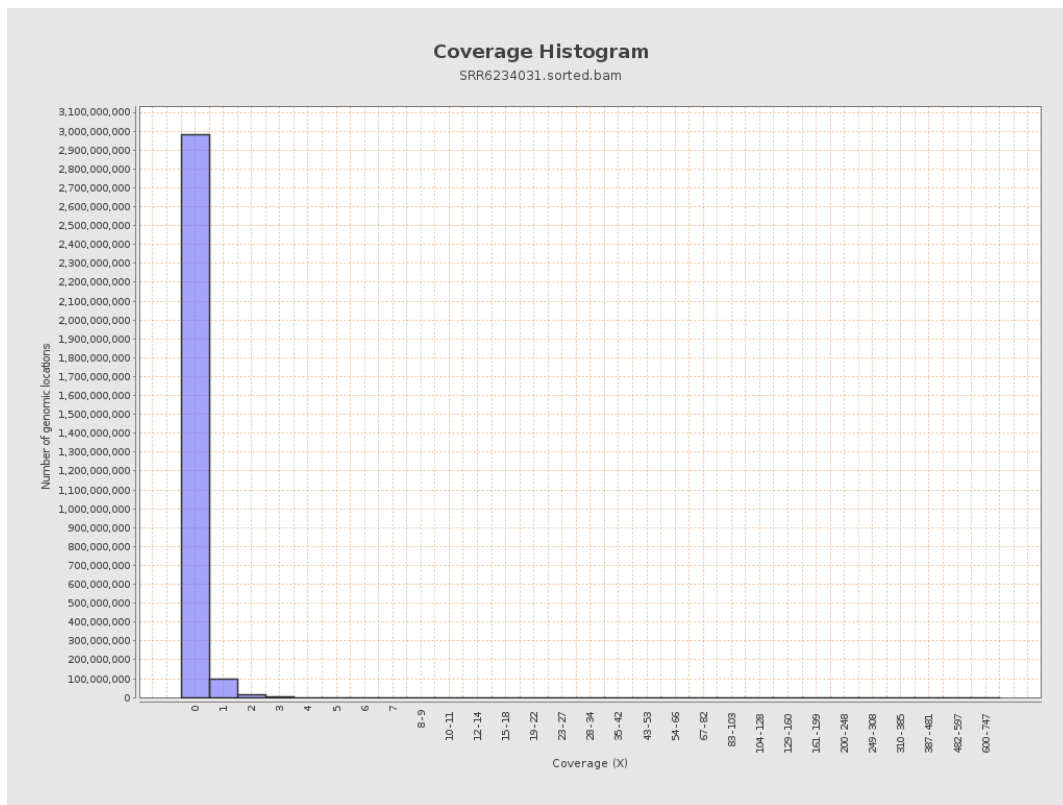
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15865658	0.0637	0.6051
chr2	243199373	4969650	0.0204	0.4069
chr3	198022430	13033594	0.0658	0.3006
chr4	191154276	4620540	0.0242	0.2042
chr5	180915260	7500347	0.0415	0.2367
chr6	171115067	11462843	0.067	0.4107
chr7	159138663	9580162	0.0602	0.6504

chr8	146364022	8802785	0.0601	0.377
chr9	141213431	5989150	0.0424	0.3505
chr10	135534747	6363822	0.047	0.3939
chr11	135006516	5696949	0.0422	0.3282
chr12	133851895	4002601	0.0299	0.2094
chr13	115169878	5549957	0.0482	0.2568
chr14	107349540	7155888	0.0667	0.3302
chr15	102531392	2118655	0.0207	0.1681
chr16	90354753	3468285	0.0384	0.2799
chr17	81195210	3502352	0.0431	0.2695
chr18	78077248	2039748	0.0261	0.68
chr19	59128983	4347590	0.0735	0.4896
chr20	63025520	4052588	0.0643	0.3074
chr21	48129895	2905598	0.0604	0.3132
chr22	51304566	1712810	0.0334	0.2127
chrMT	16571	152996	9.2328	6.5157
chrX	155270560	5882920	0.0379	0.2558
chrY	59373566	357979	0.006	0.1347

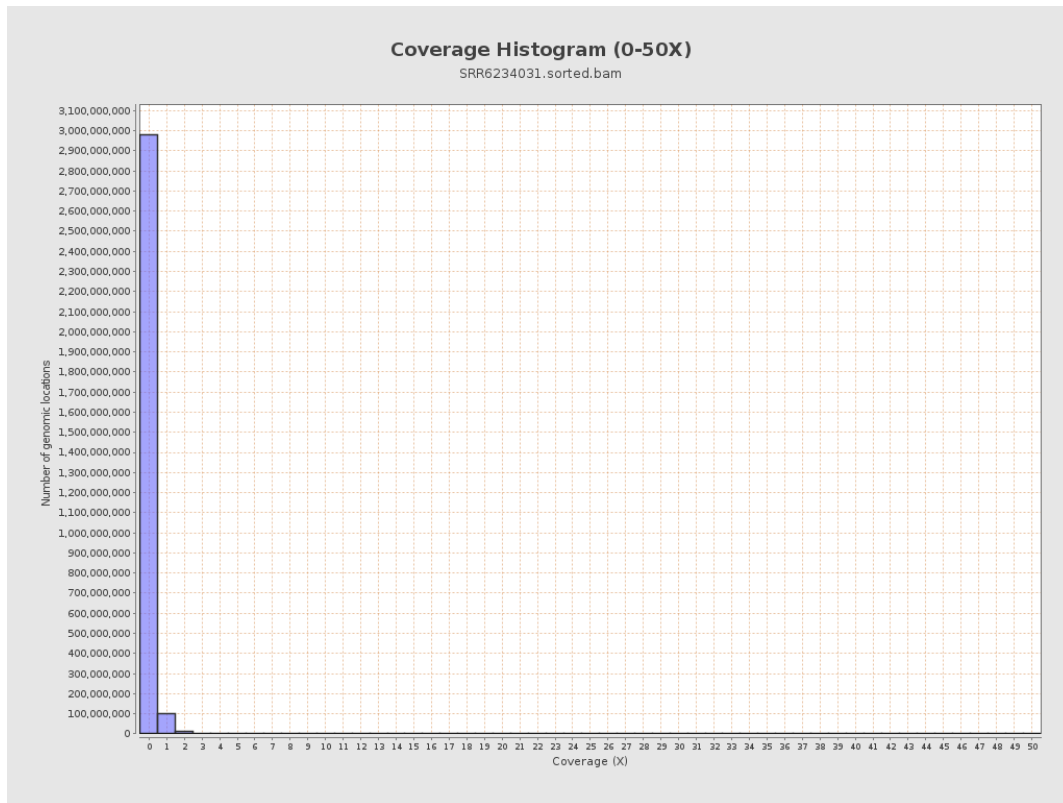
3. Results : Coverage across reference



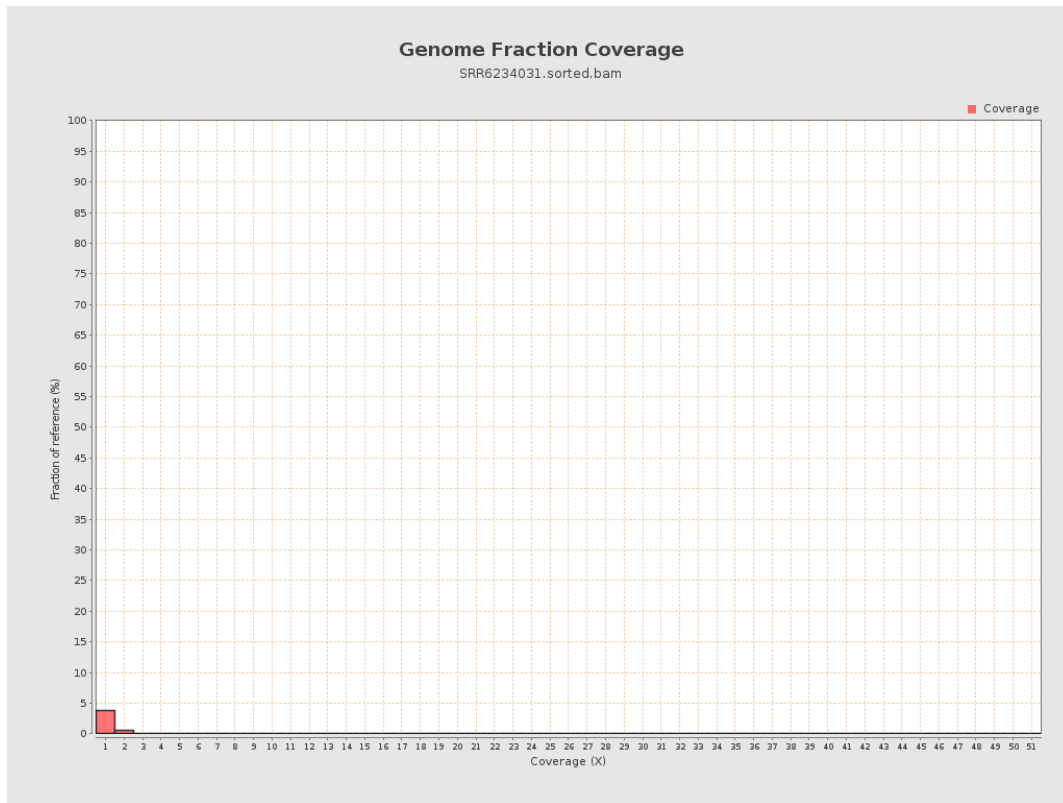
4. Results : Coverage Histogram



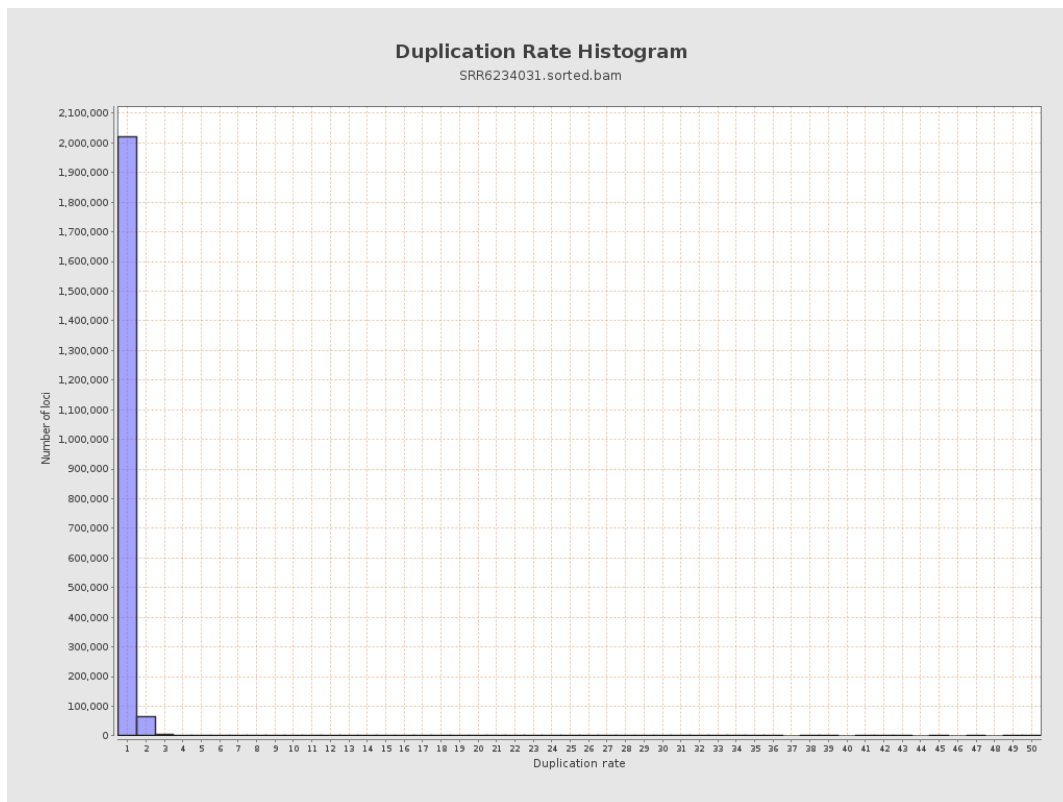
5. Results : Coverage Histogram (0-50X)



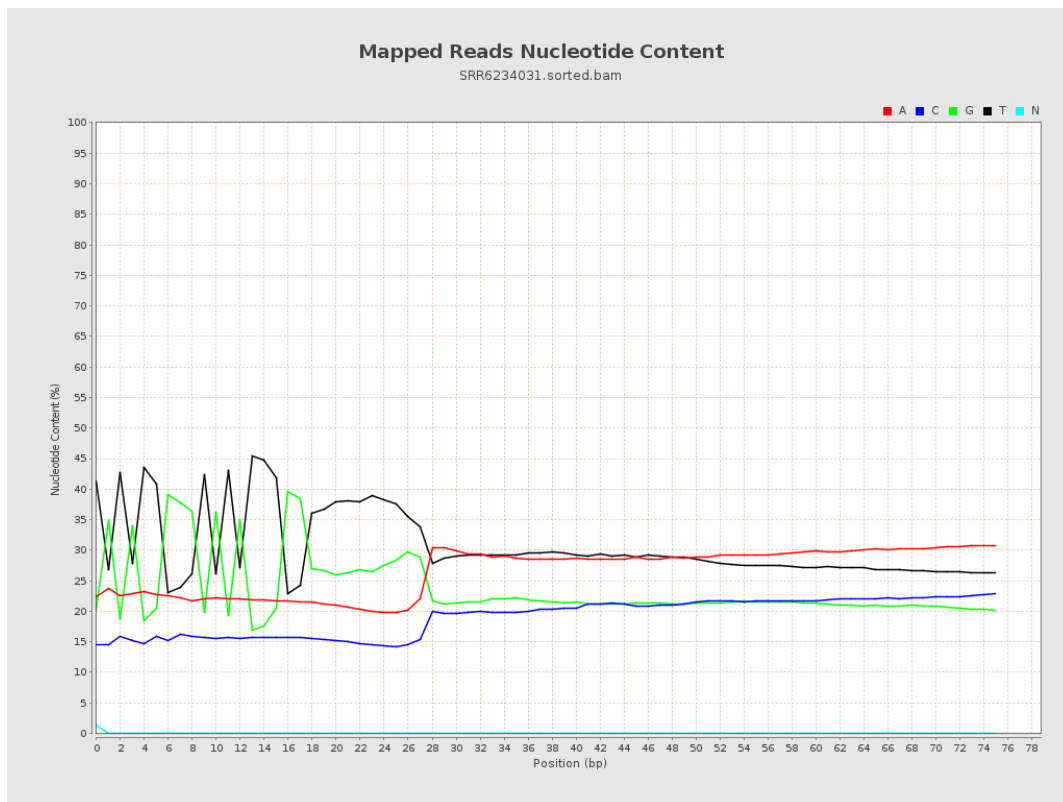
6. Results : Genome Fraction Coverage



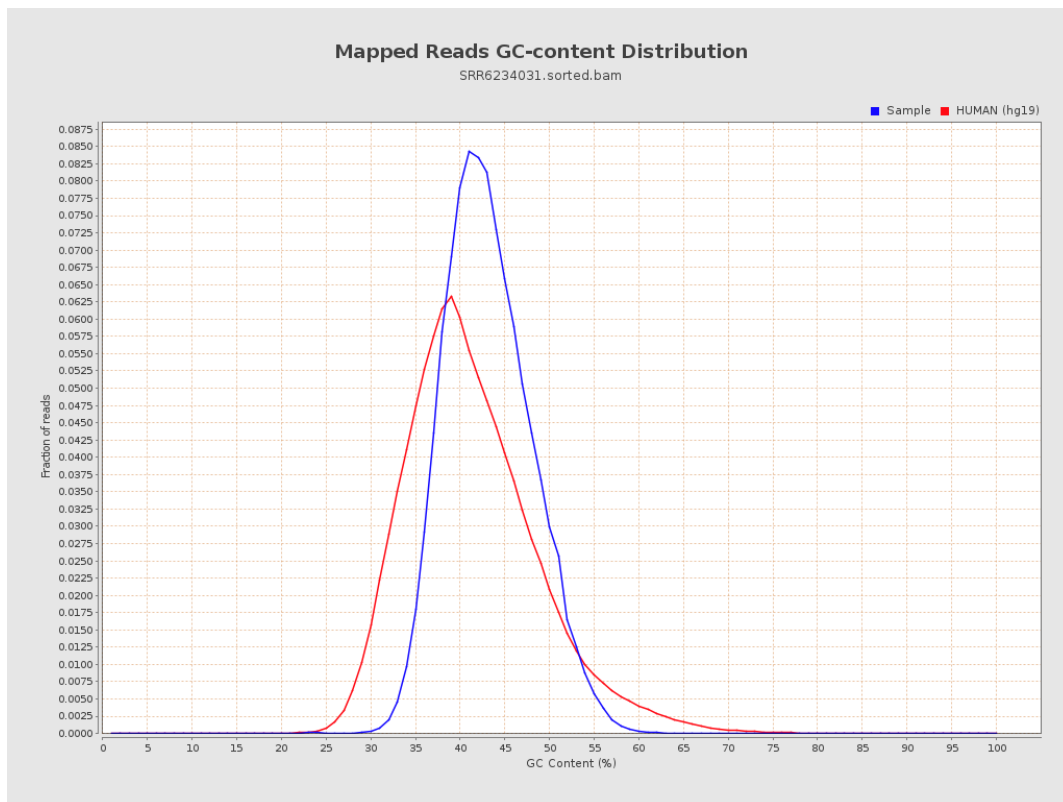
7. Results : Duplication Rate Histogram



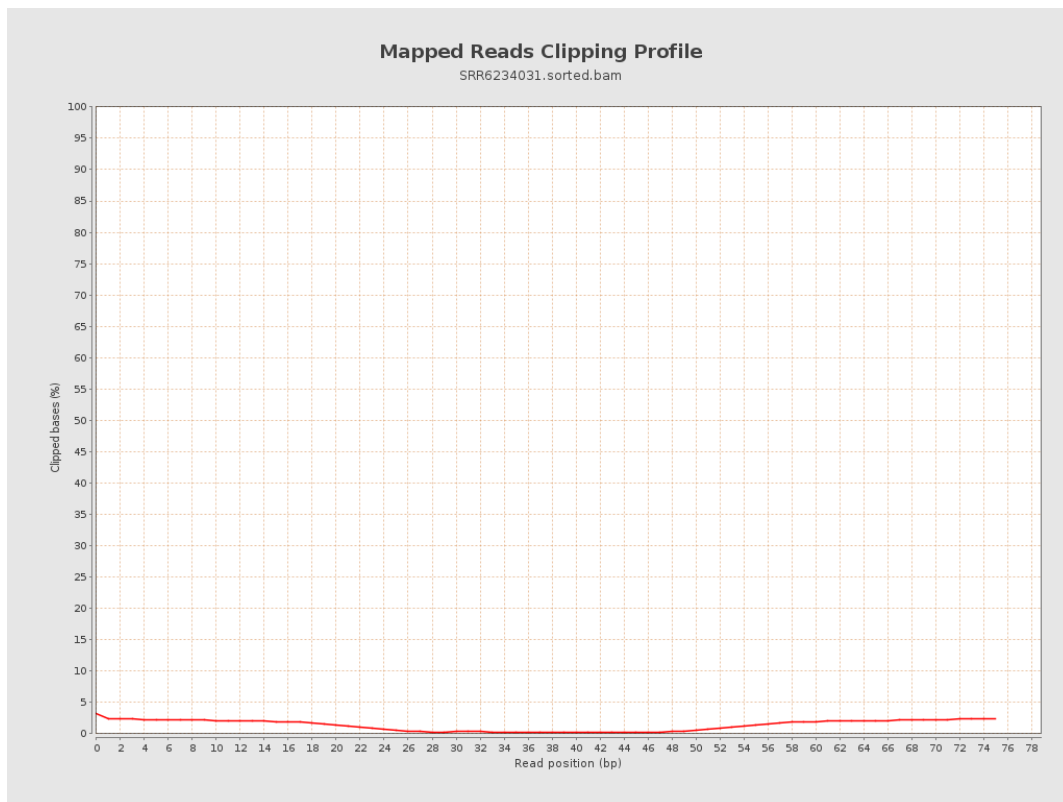
8. Results : Mapped Reads Nucleotide Content



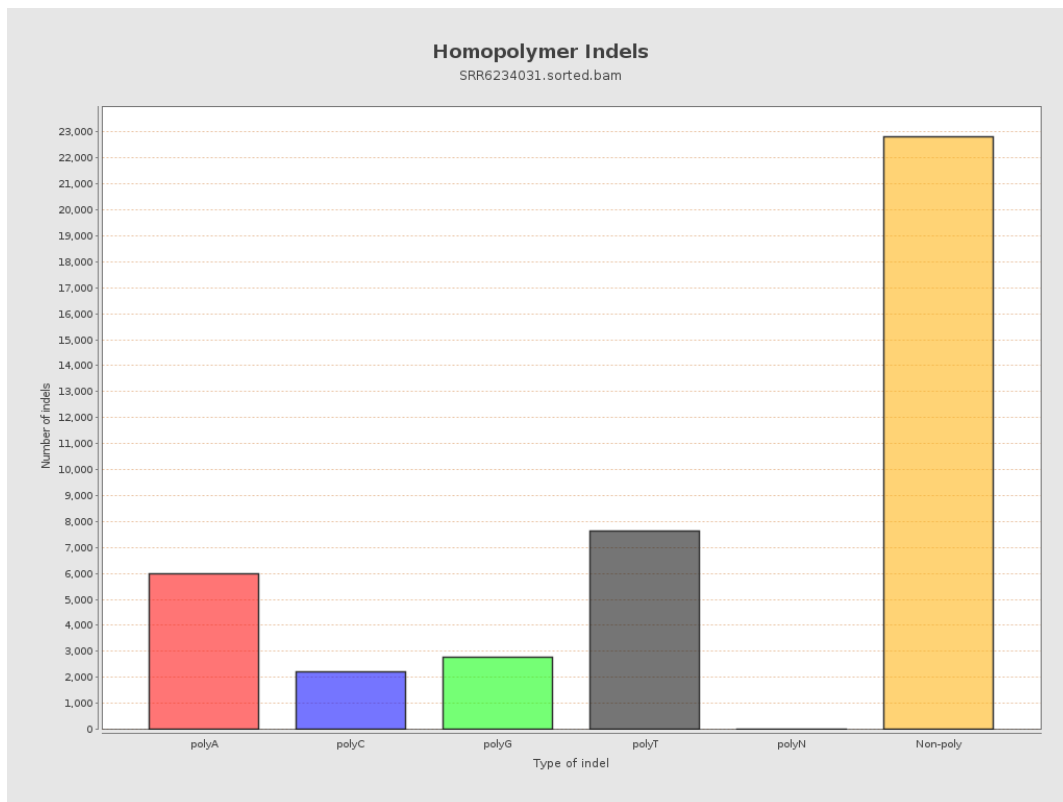
9. Results : Mapped Reads GC-content Distribution



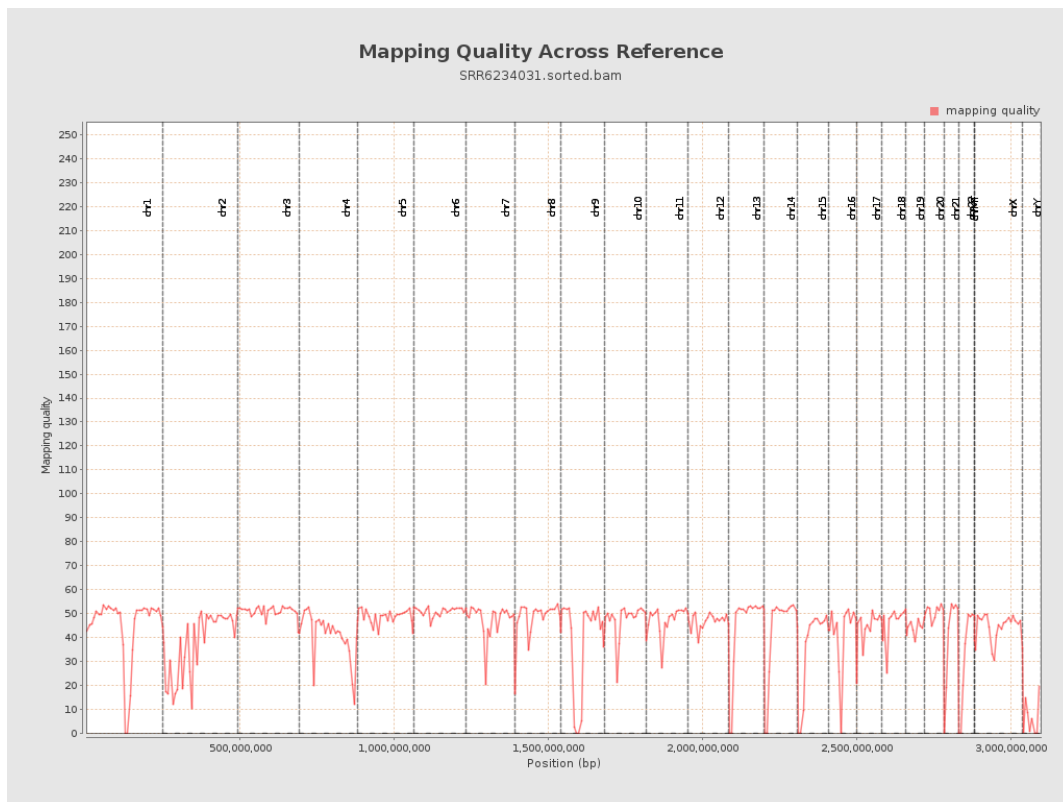
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

