

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:19:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234105.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_SRR6234105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:19:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,848,640
Mapped reads	4,582,614 / 94.51%
Unmapped reads	266,026 / 5.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,566 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	547,189 / 11.29%
Duplication rate	9.97%
Clipped reads	2,404,001 / 49.58%

2.2. ACGT Content

Number/percentage of A's	76,374,336 / 25.85%
Number/percentage of C's	53,566,417 / 18.13%
Number/percentage of T's	95,945,209 / 32.47%
Number/percentage of G's	69,574,687 / 23.55%
Number/percentage of N's	28,837 / 0.01%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0955

Standard Deviation	0.9456
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2.4. Mapping Quality

Mean Mapping Quality	45.96
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2.5. Mismatches and indels

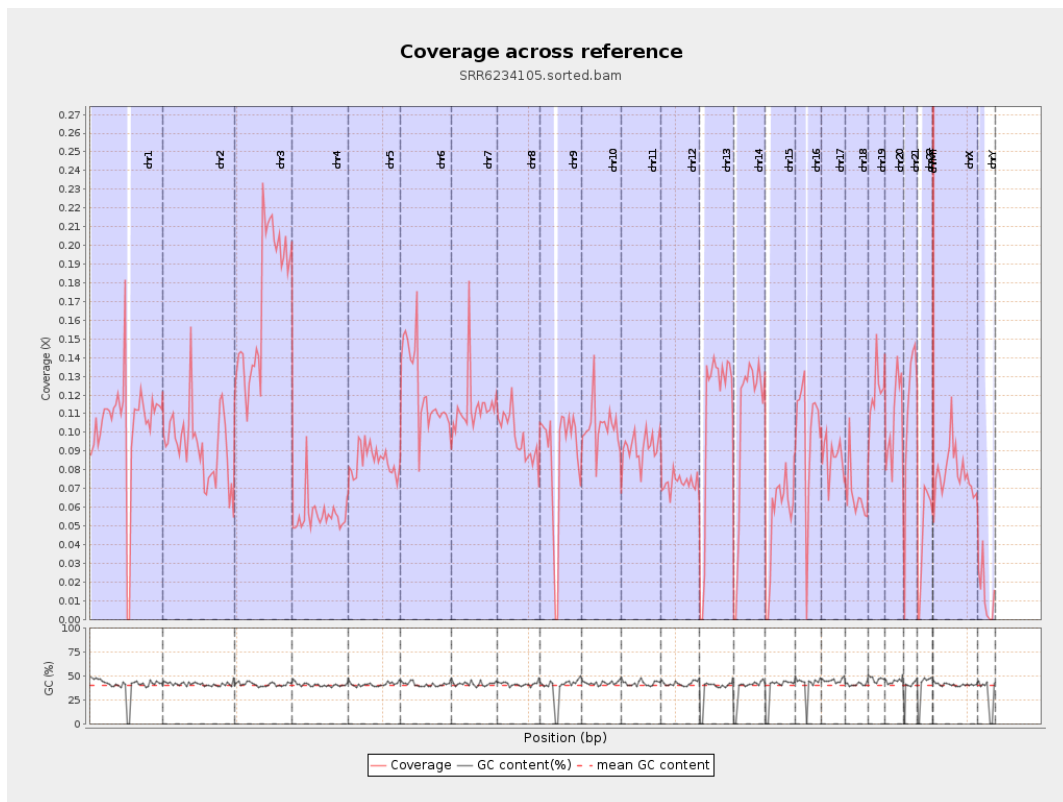
General error rate	0.55%
Mismatches	1,578,569
Insertions	18,617
Mapped reads with at least one insertion	0.4%
Deletions	64,080
Mapped reads with at least one deletion	1.39%
Homopolymer indels	44.49%

2.6. Chromosome stats

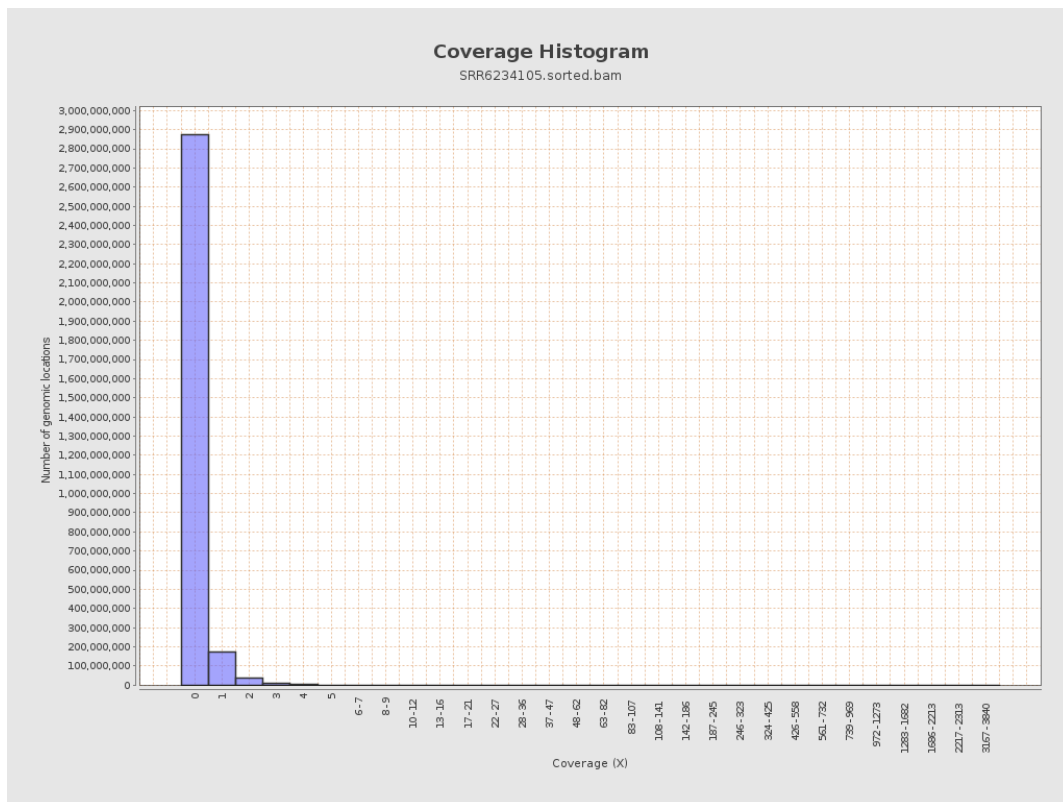
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26029994	0.1044	1.8501
chr2	243199373	22493084	0.0925	1.7573
chr3	198022430	33499903	0.1692	0.5308
chr4	191154276	10729354	0.0561	0.3718
chr5	180915260	15382923	0.085	0.381
chr6	171115067	20960167	0.1225	0.7156
chr7	159138663	18077727	0.1136	1.1866

chr8	146364022	14175684	0.0969	0.9514
chr9	141213431	12271929	0.0869	0.6212
chr10	135534747	13976143	0.1031	0.7125
chr11	135006516	12369440	0.0916	0.6423
chr12	133851895	9755090	0.0729	0.3672
chr13	115169878	12721132	0.1105	0.4828
chr14	107349540	11373574	0.1059	0.4613
chr15	102531392	5502096	0.0537	0.3334
chr16	90354753	9013454	0.0998	0.4968
chr17	81195210	7081323	0.0872	0.4574
chr18	78077248	5209694	0.0667	1.4982
chr19	59128983	7230972	0.1223	1.0583
chr20	63025520	6726708	0.1067	0.4655
chr21	48129895	5434699	0.1129	0.4606
chr22	51304566	2400864	0.0468	0.2681
chrMT	16571	255613	15.4253	9.0552
chrX	155270560	12135722	0.0782	0.4624
chrY	59373566	793547	0.0134	0.2505

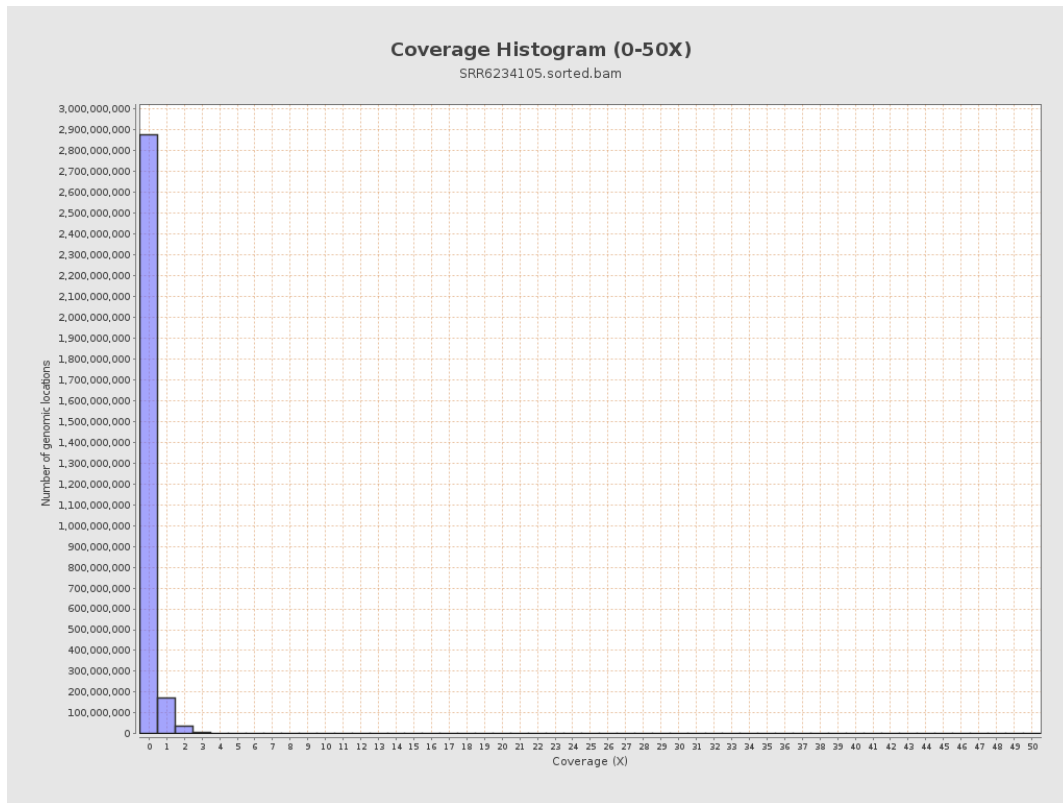
3. Results : Coverage across reference



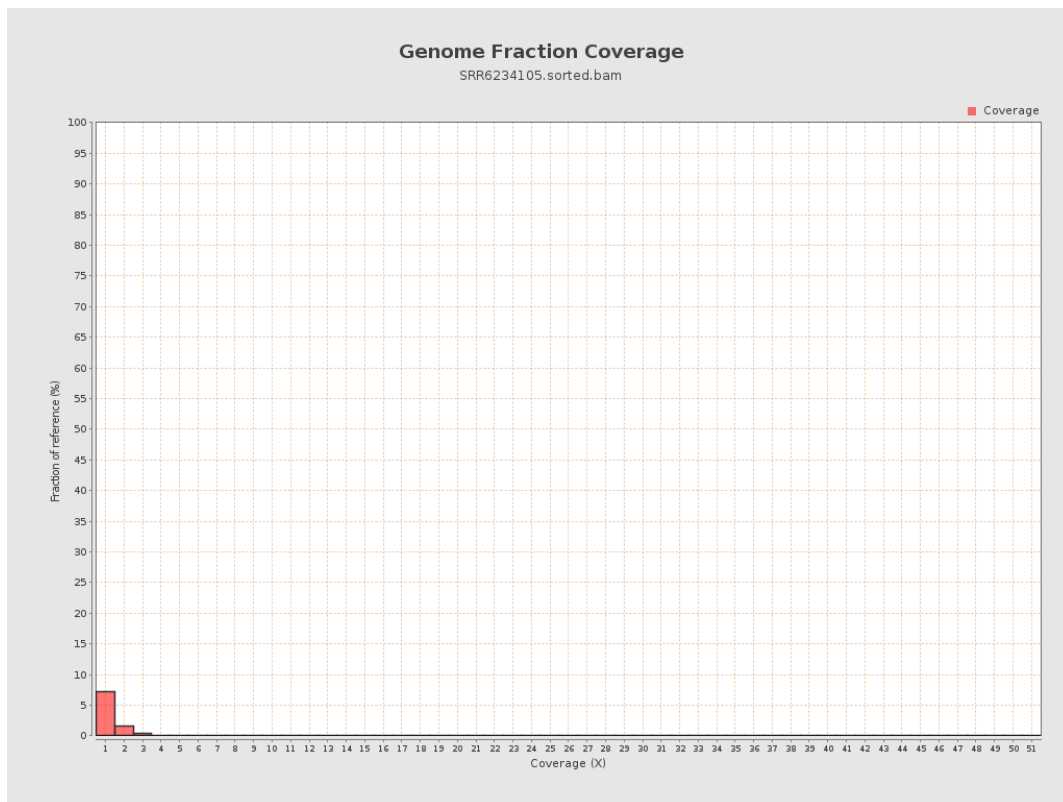
4. Results : Coverage Histogram



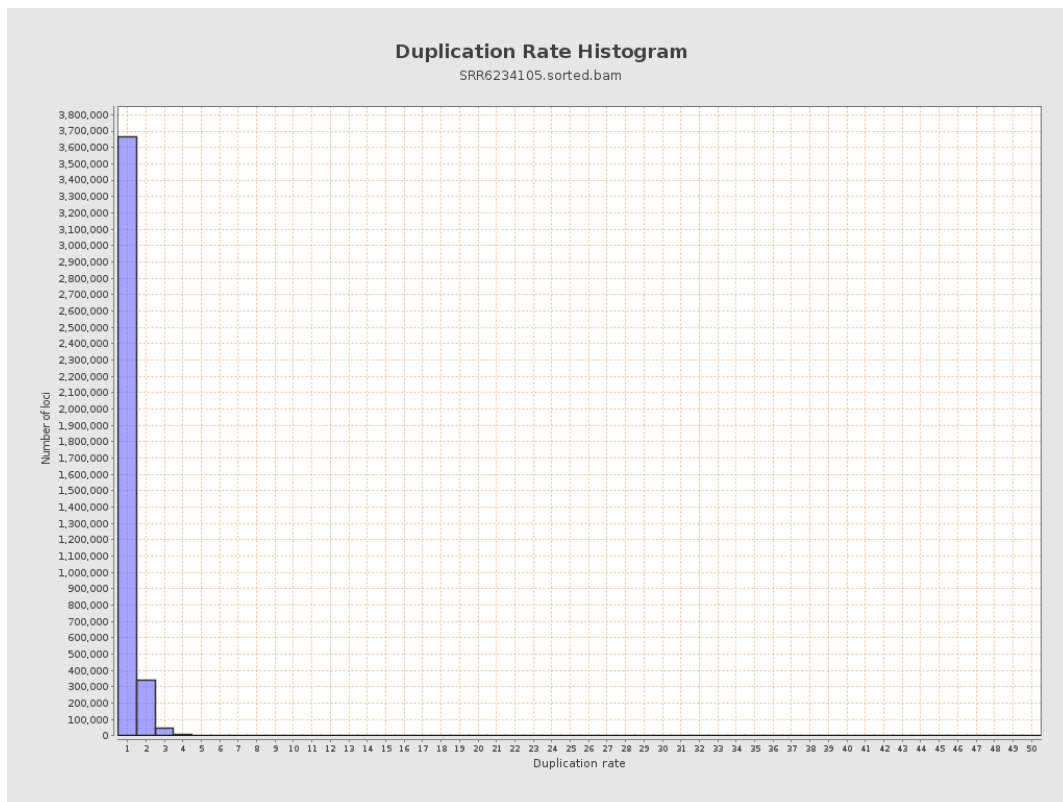
5. Results : Coverage Histogram (0-50X)



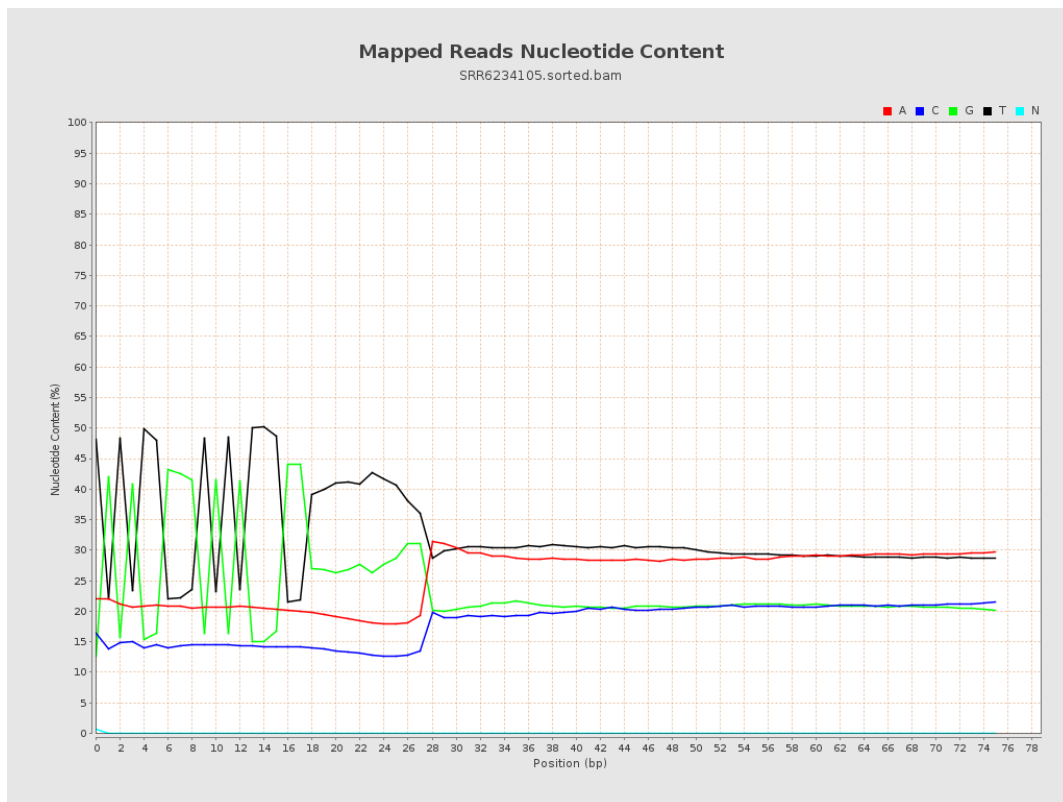
6. Results : Genome Fraction Coverage



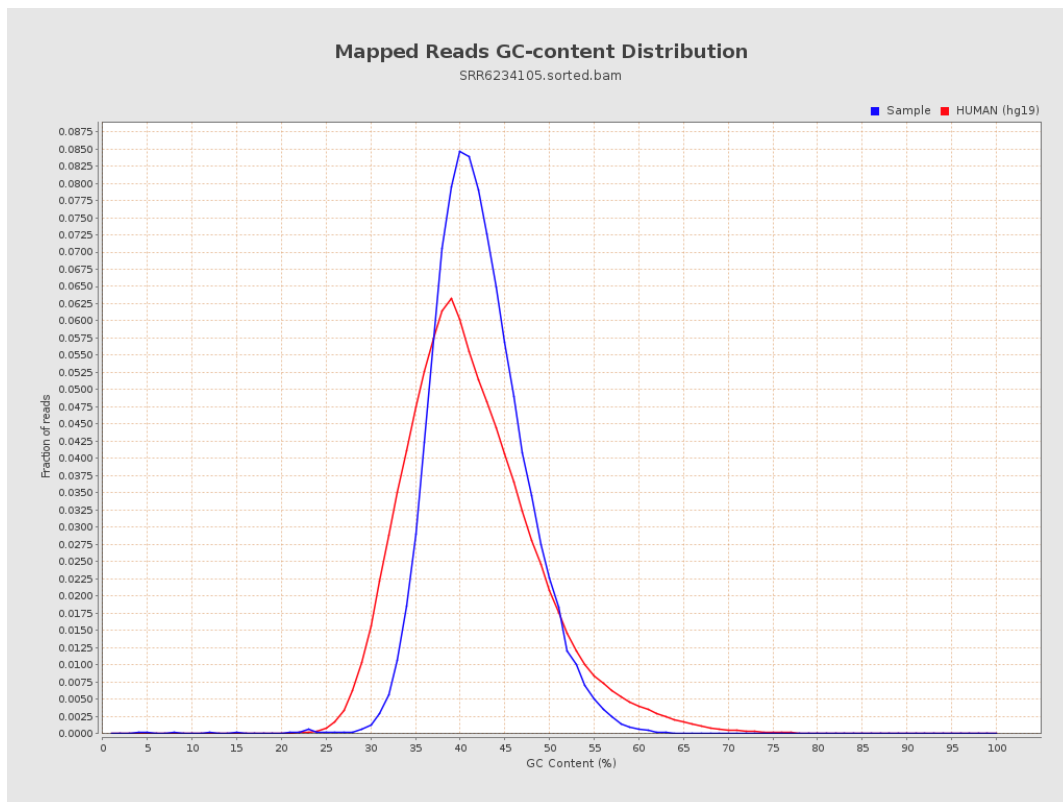
7. Results : Duplication Rate Histogram



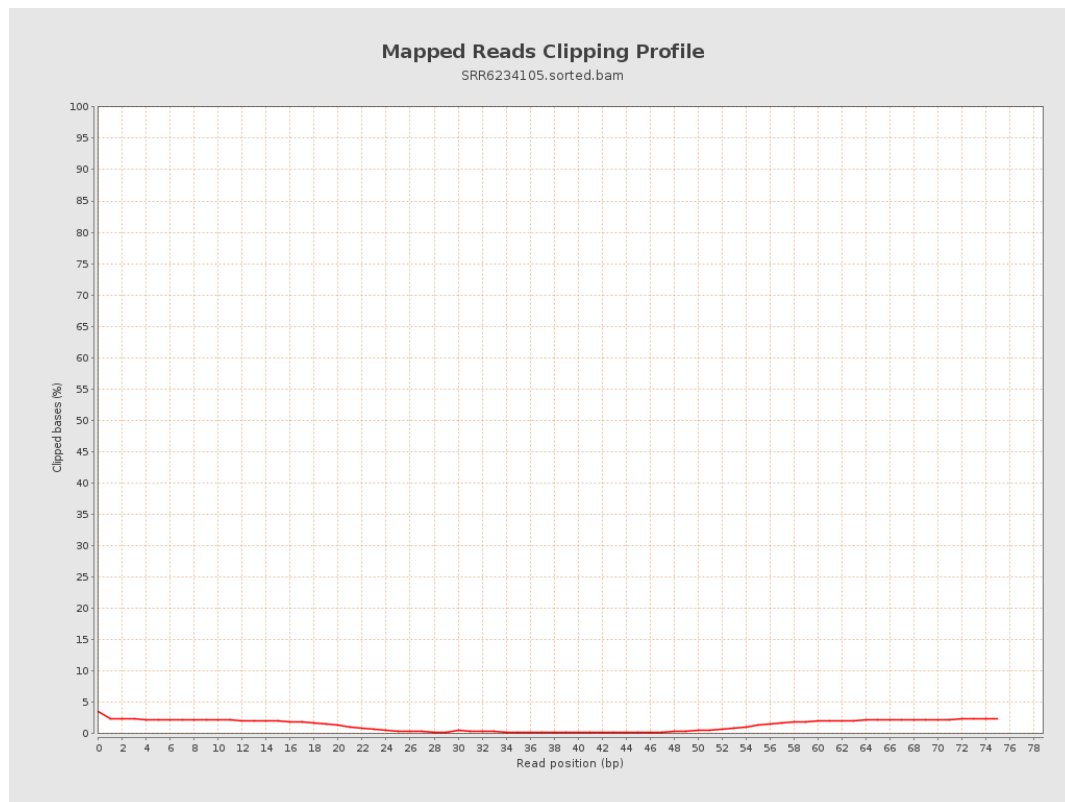
8. Results : Mapped Reads Nucleotide Content



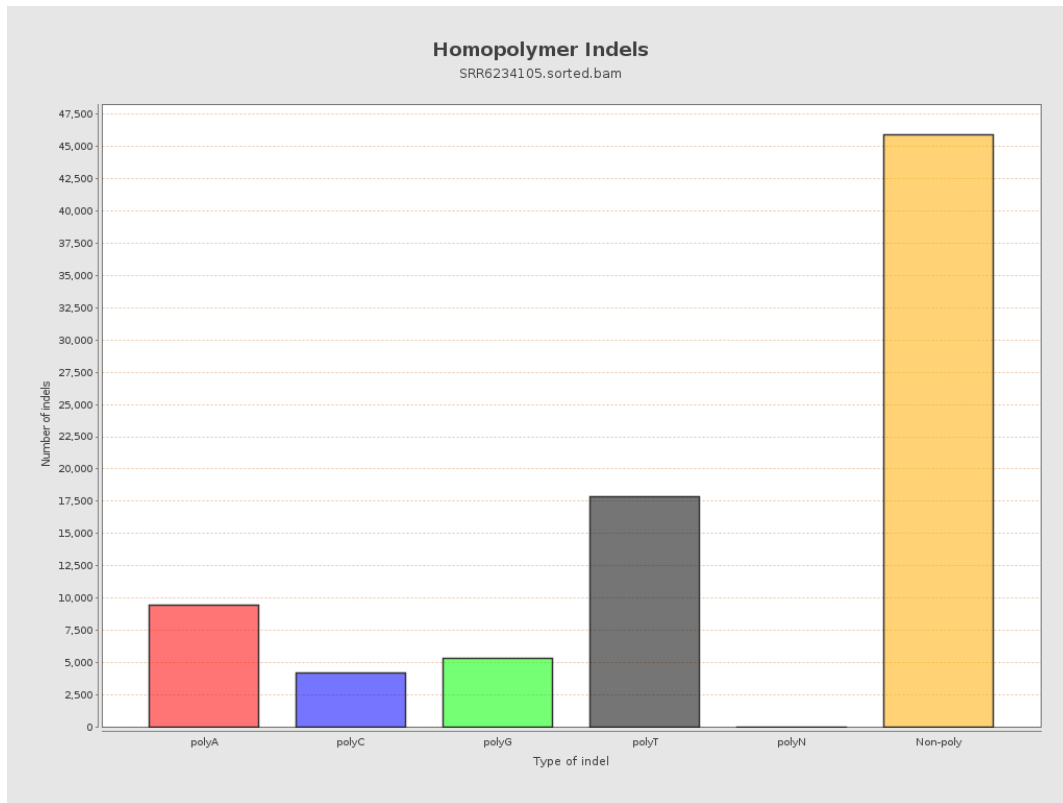
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

