

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:56:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236067.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_SRR6236067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:56:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,909,123
Mapped reads	1,676,148 / 87.8%
Unmapped reads	232,975 / 12.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,325 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	123,064 / 6.45%
Duplication rate	5.83%
Clipped reads	699,023 / 36.61%

2.2. ACGT Content

Number/percentage of A's	31,926,846 / 28.18%
Number/percentage of C's	21,035,853 / 18.57%
Number/percentage of T's	35,864,833 / 31.66%
Number/percentage of G's	24,456,275 / 21.59%
Number/percentage of N's	1,143 / 0%
GC Percentage	40.16%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.4635
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2.4. Mapping Quality

Mean Mapping Quality	46.5
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2.5. Mismatches and indels

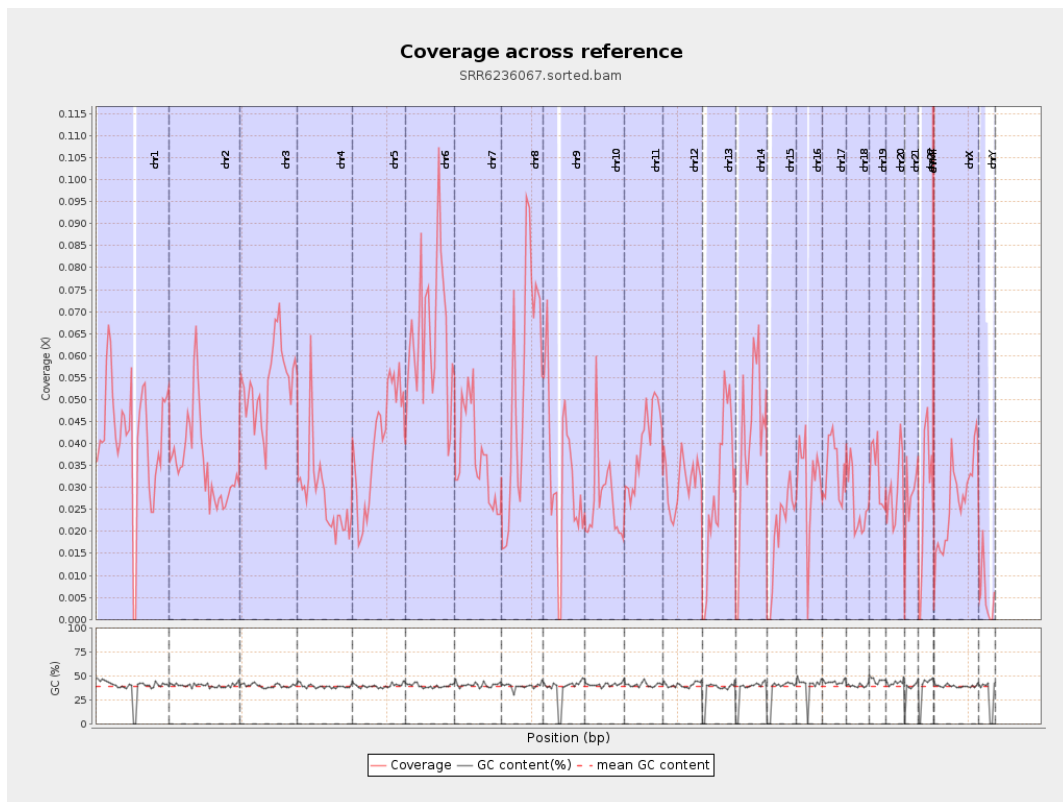
General error rate	0.77%
Mismatches	849,772
Insertions	9,631
Mapped reads with at least one insertion	0.57%
Deletions	30,776
Mapped reads with at least one deletion	1.81%
Homopolymer indels	47.45%

2.6. Chromosome stats

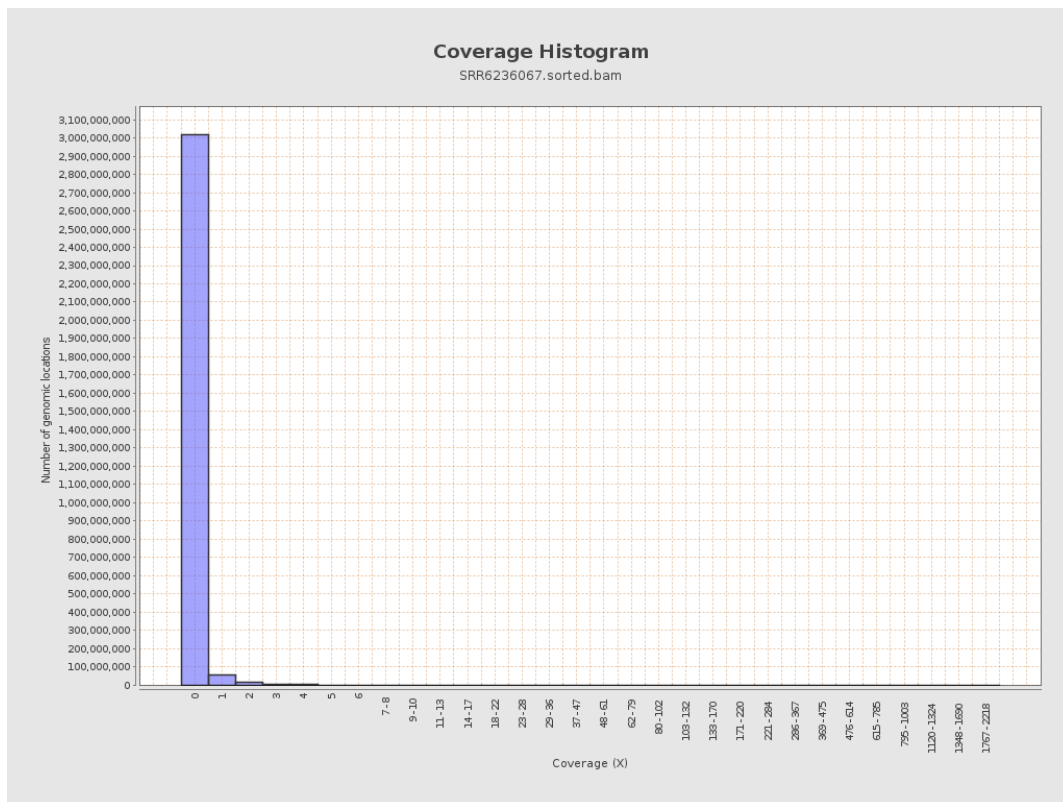
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10342389	0.0415	0.5331
chr2	243199373	8682105	0.0357	0.3955
chr3	198022430	10692517	0.054	0.319
chr4	191154276	5345242	0.028	0.2775
chr5	180915260	7285282	0.0403	0.2763
chr6	171115067	10995739	0.0643	0.4104
chr7	159138663	5875352	0.0369	0.3923

chr8	146364022	7673662	0.0524	1.4601
chr9	141213431	4614278	0.0327	0.3295
chr10	135534747	3668741	0.0271	0.3447
chr11	135006516	5341788	0.0396	0.3536
chr12	133851895	4167481	0.0311	0.2455
chr13	115169878	3414803	0.0297	0.2375
chr14	107349540	4295509	0.04	0.2848
chr15	102531392	2057715	0.0201	0.1921
chr16	90354753	2867673	0.0317	0.257
chr17	81195210	2818798	0.0347	0.2894
chr18	78077248	2069661	0.0265	0.5486
chr19	59128983	1969817	0.0333	0.3579
chr20	63025520	1837189	0.0291	0.241
chr21	48129895	1339532	0.0278	0.2593
chr22	51304566	1404111	0.0274	0.2205
chrMT	16571	148565	8.9654	9.3944
chrX	155270560	4124018	0.0266	0.2361
chrY	59373566	306585	0.0052	0.1637

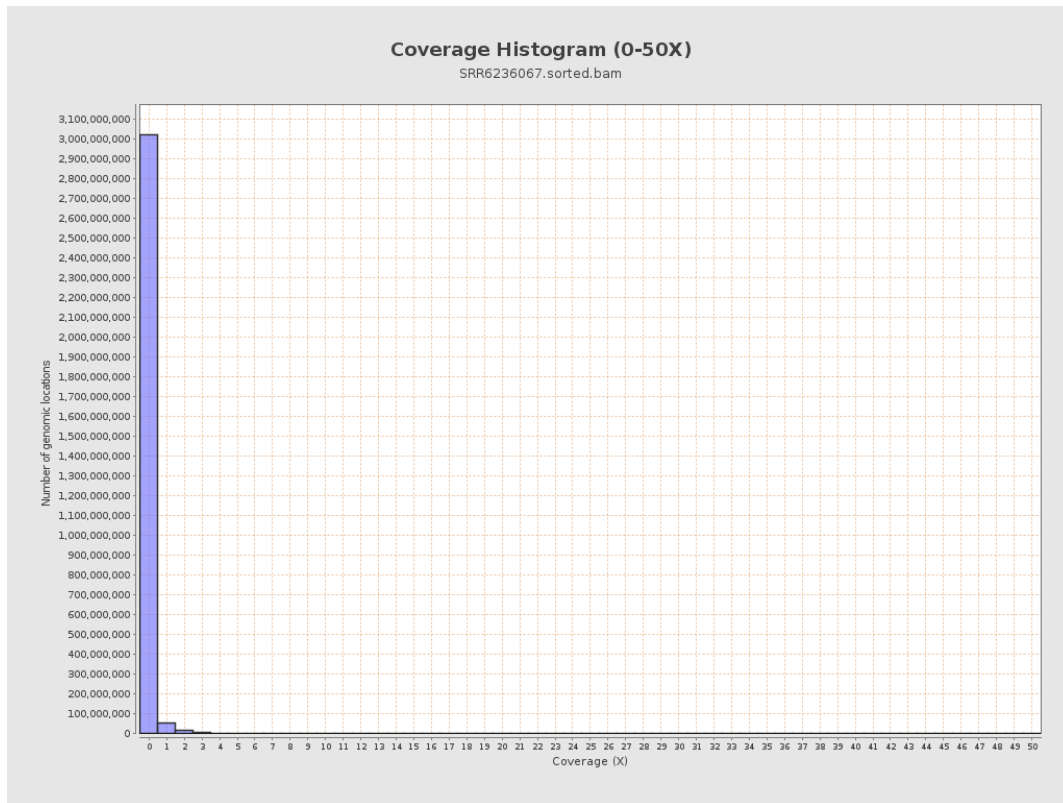
3. Results : Coverage across reference



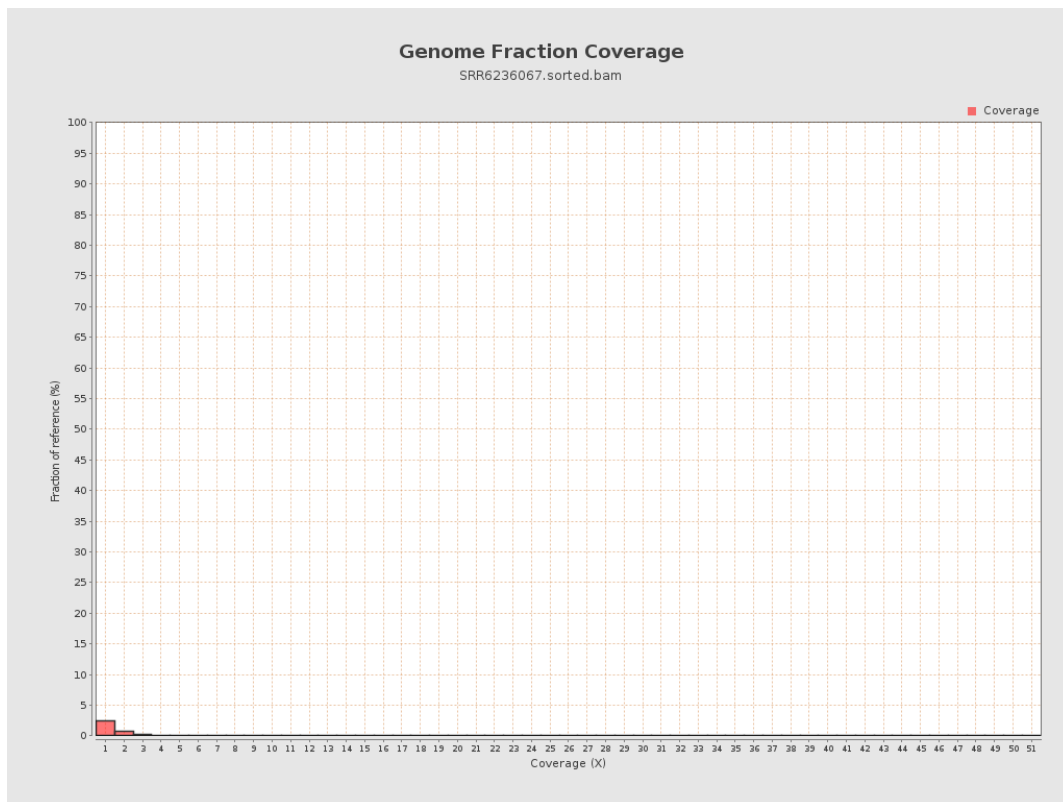
4. Results : Coverage Histogram



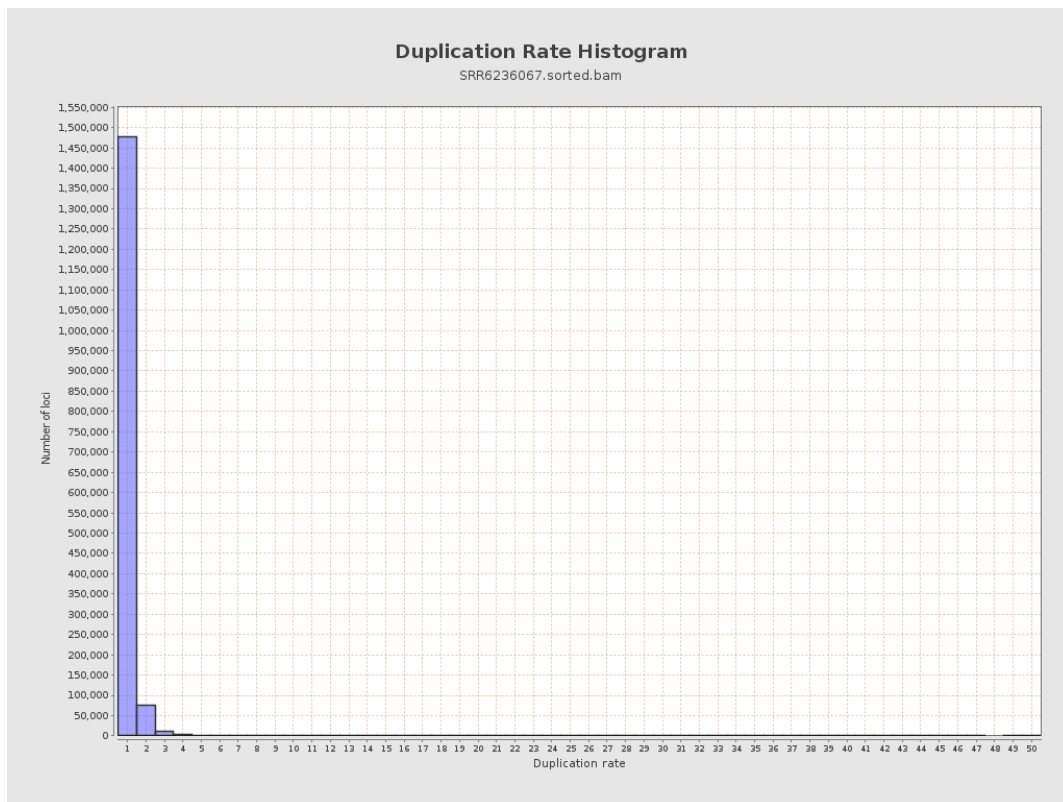
5. Results : Coverage Histogram (0-50X)



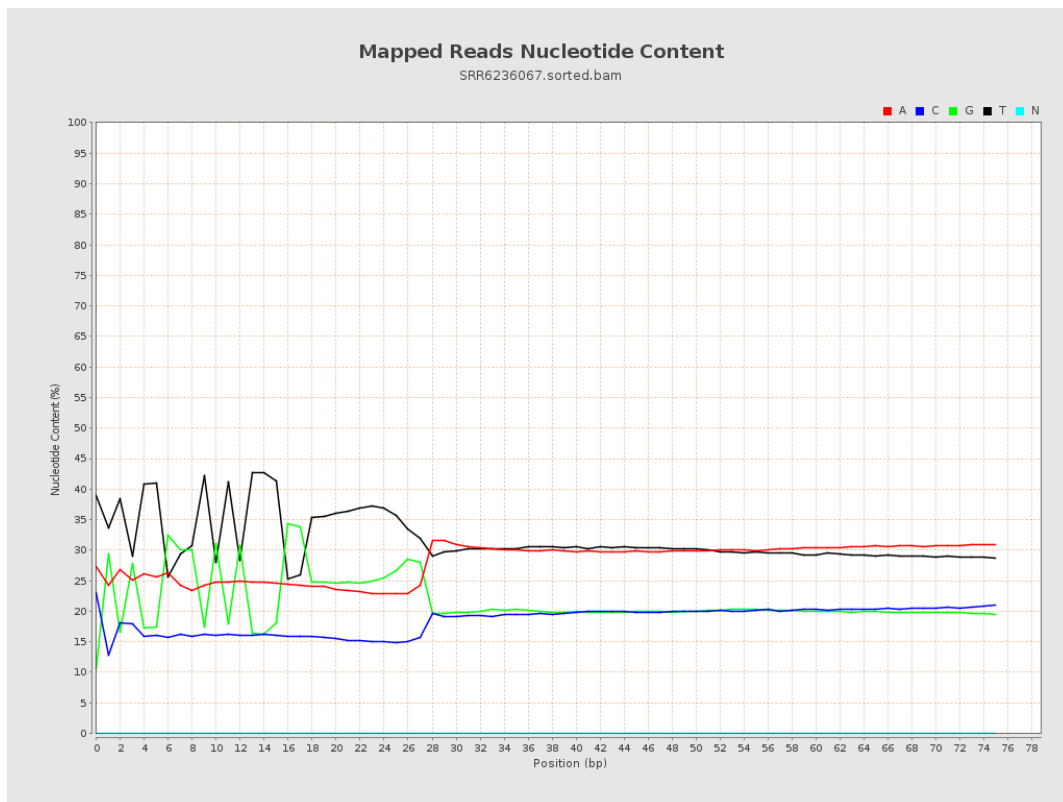
6. Results : Genome Fraction Coverage



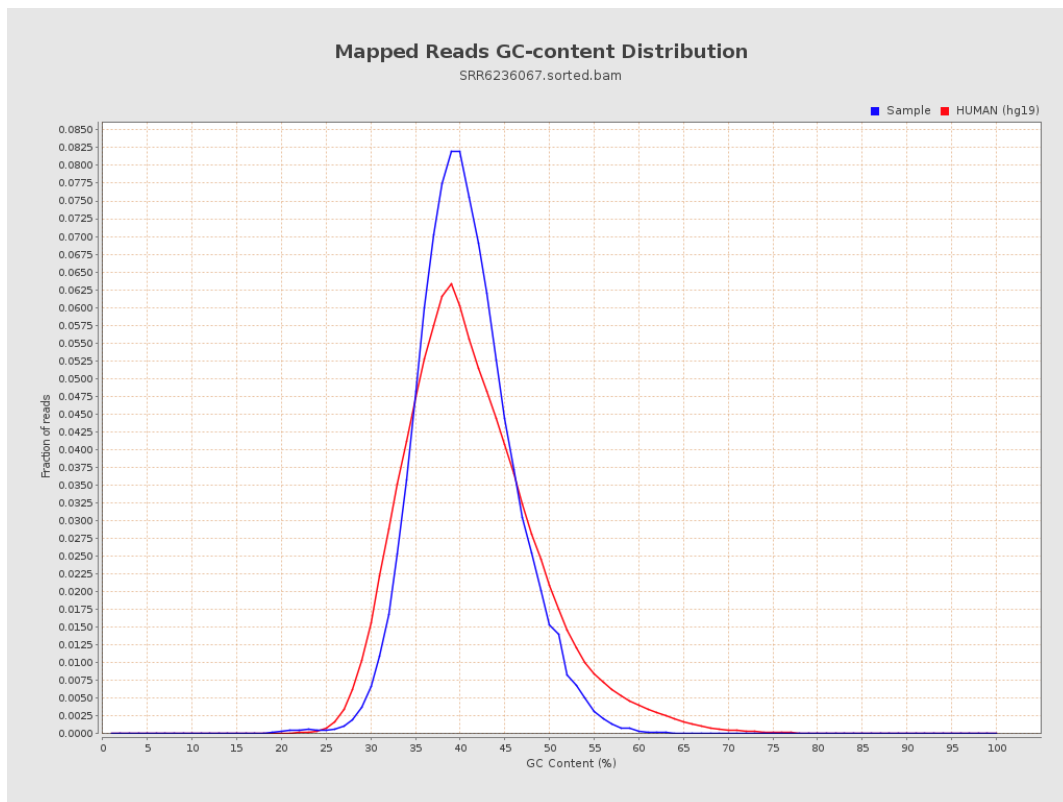
7. Results : Duplication Rate Histogram



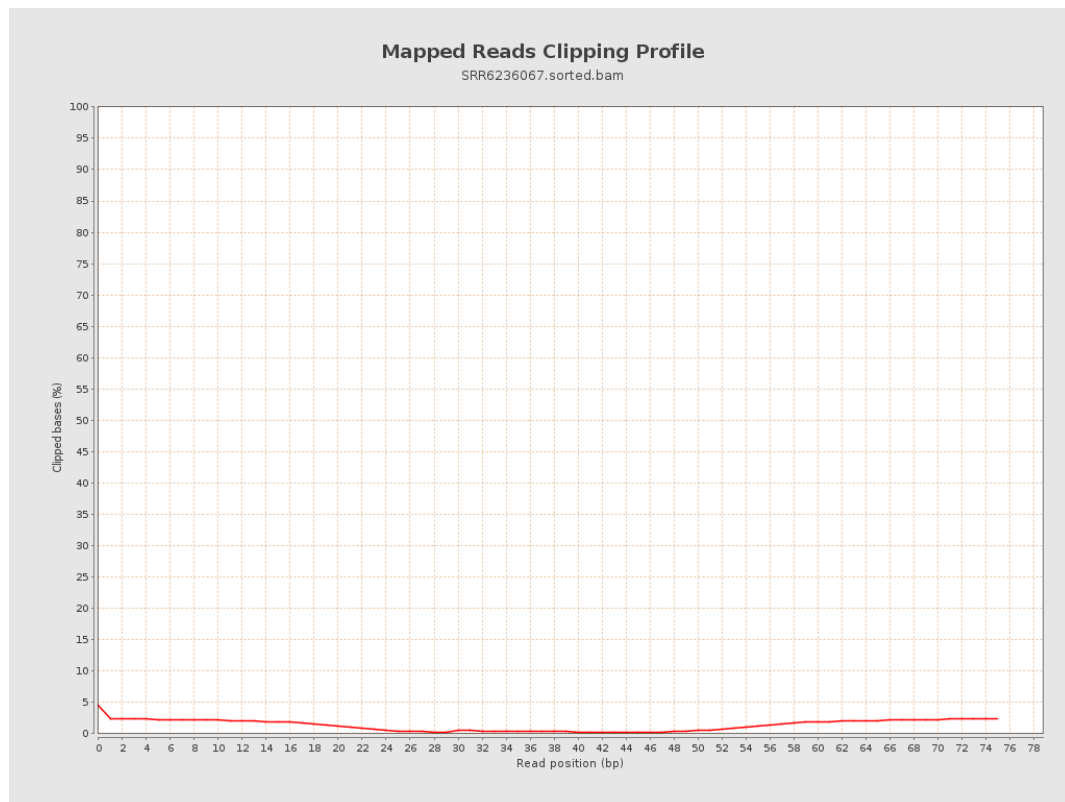
8. Results : Mapped Reads Nucleotide Content



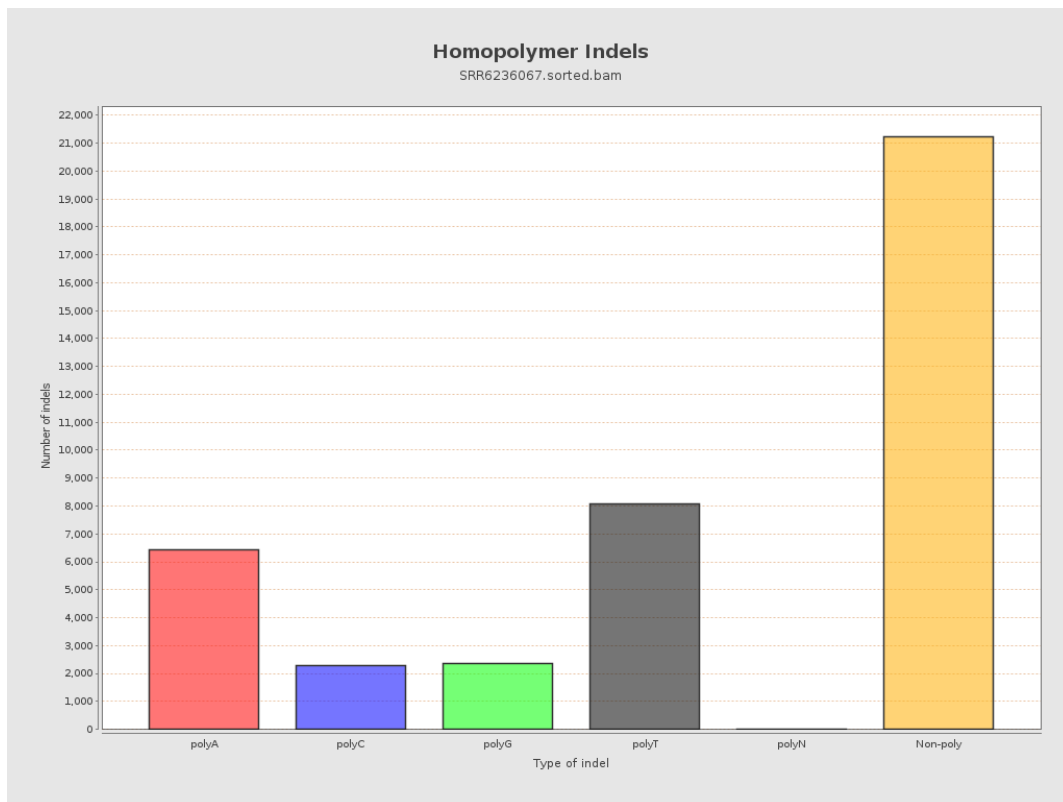
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

