

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:19:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236075.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_SRR6236075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:19:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,556,160
Mapped reads	1,241,843 / 79.8%
Unmapped reads	314,317 / 20.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,952 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	93,401 / 6%
Duplication rate	6.25%
Clipped reads	598,384 / 38.45%

2.2. ACGT Content

Number/percentage of A's	22,173,629 / 27.21%
Number/percentage of C's	14,440,239 / 17.72%
Number/percentage of T's	26,577,163 / 32.62%
Number/percentage of G's	18,247,954 / 22.4%
Number/percentage of N's	41,330 / 0.05%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0263

Standard Deviation	0.2857
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.03
----------------------	-------

2.5. Mismatches and indels

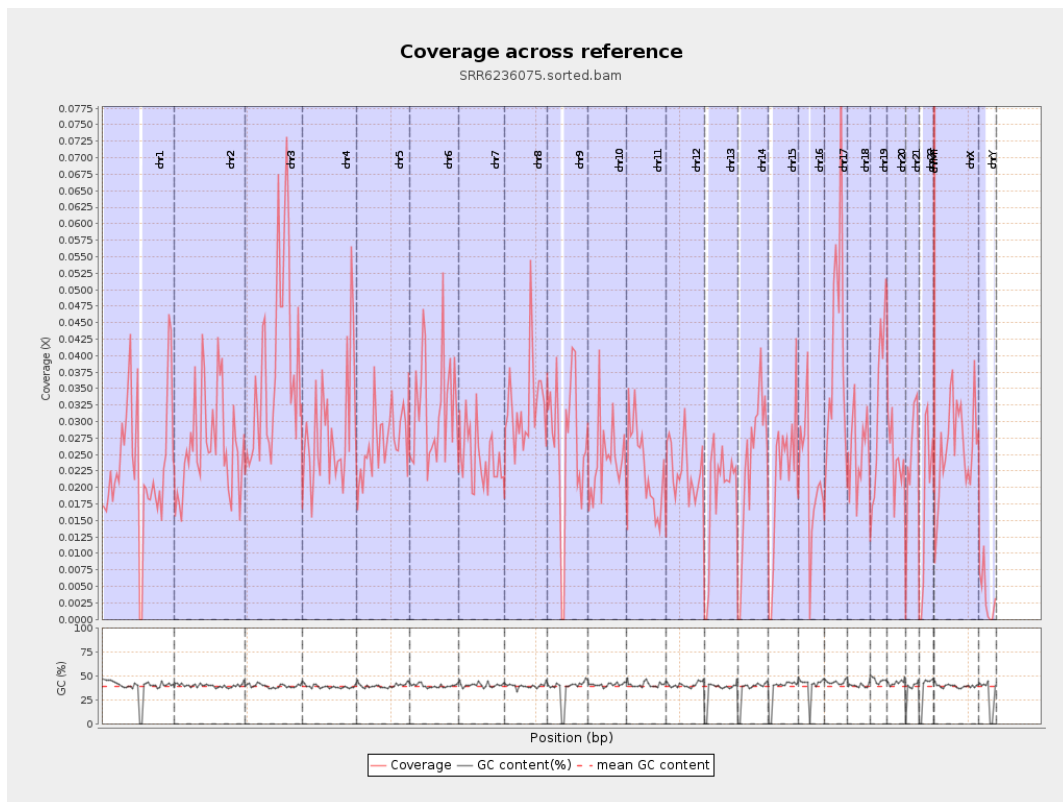
General error rate	0.83%
Mismatches	665,877
Insertions	6,094
Mapped reads with at least one insertion	0.49%
Deletions	20,735
Mapped reads with at least one deletion	1.65%
Homopolymer indels	48.92%

2.6. Chromosome stats

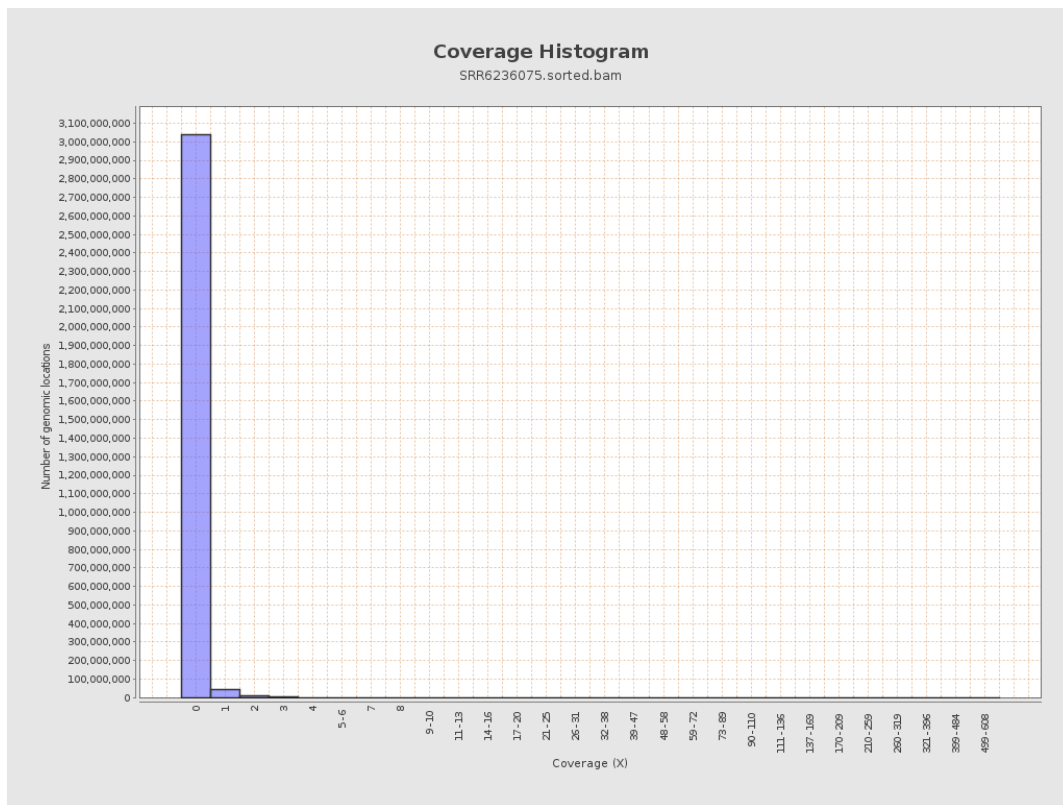
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5739729	0.023	0.4398
chr2	243199373	6462433	0.0266	0.296
chr3	198022430	7548258	0.0381	0.2558
chr4	191154276	5428547	0.0284	0.2273
chr5	180915260	4880732	0.027	0.215
chr6	171115067	5446384	0.0318	0.2543
chr7	159138663	3907316	0.0246	0.274

chr8	146364022	4735132	0.0324	0.4422
chr9	141213431	3677611	0.026	0.2664
chr10	135534747	3261129	0.0241	0.2594
chr11	135006516	3090901	0.0229	0.2403
chr12	133851895	3025500	0.0226	0.1993
chr13	115169878	2165860	0.0188	0.1786
chr14	107349540	2517109	0.0234	0.2085
chr15	102531392	2230870	0.0218	0.192
chr16	90354753	1885229	0.0209	0.1944
chr17	81195210	3301544	0.0407	0.2839
chr18	78077248	1978830	0.0253	0.4499
chr19	59128983	1955132	0.0331	0.3381
chr20	63025520	1543111	0.0245	0.2078
chr21	48129895	1195868	0.0248	0.2132
chr22	51304566	944810	0.0184	0.1723
chrMT	16571	311123	18.7751	12.0449
chrX	155270560	4076543	0.0263	0.2277
chrY	59373566	207318	0.0035	0.0977

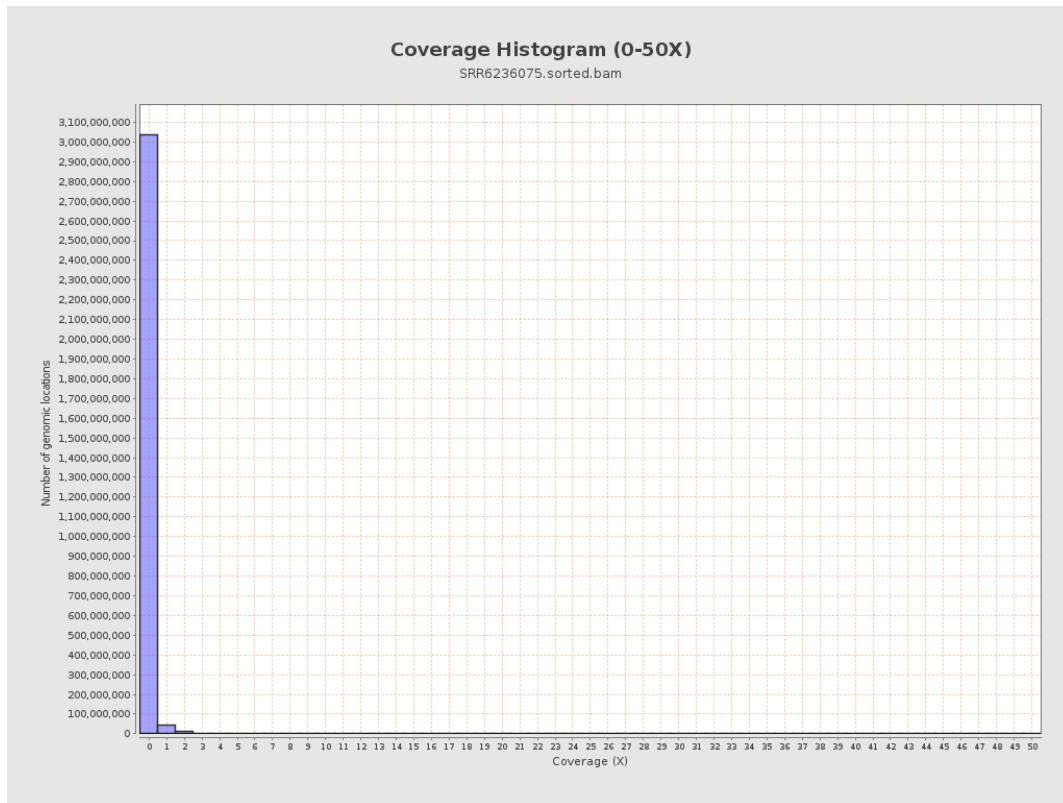
3. Results : Coverage across reference



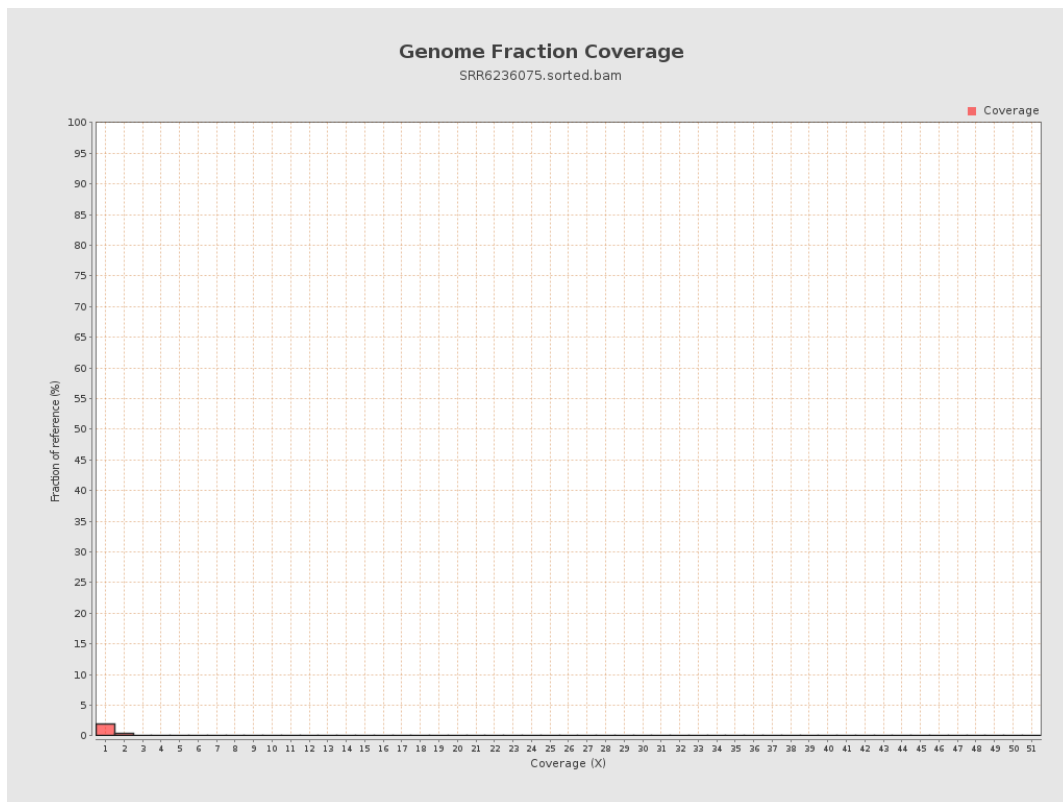
4. Results : Coverage Histogram



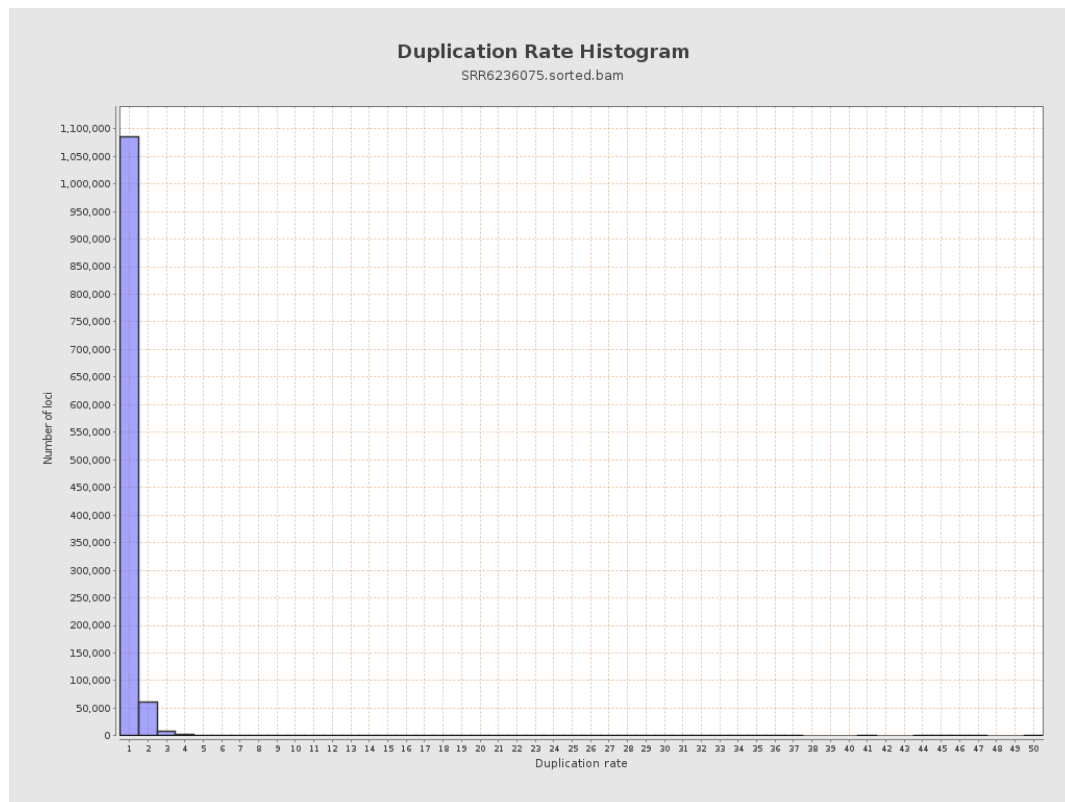
5. Results : Coverage Histogram (0-50X)



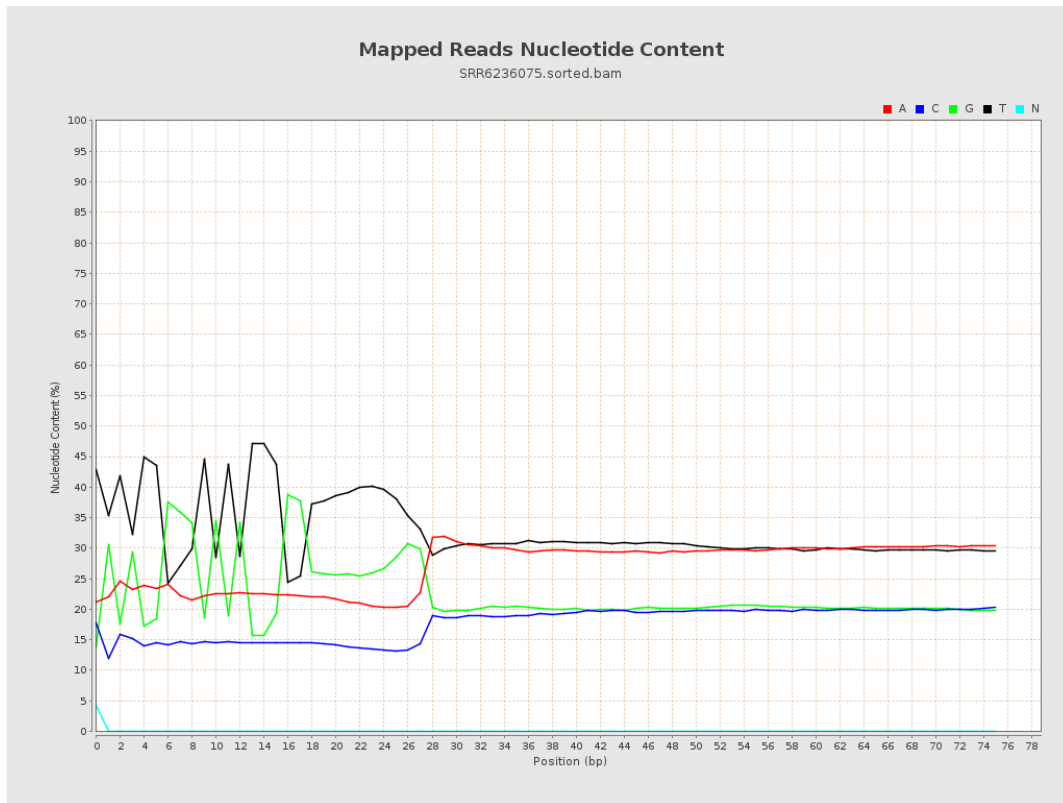
6. Results : Genome Fraction Coverage



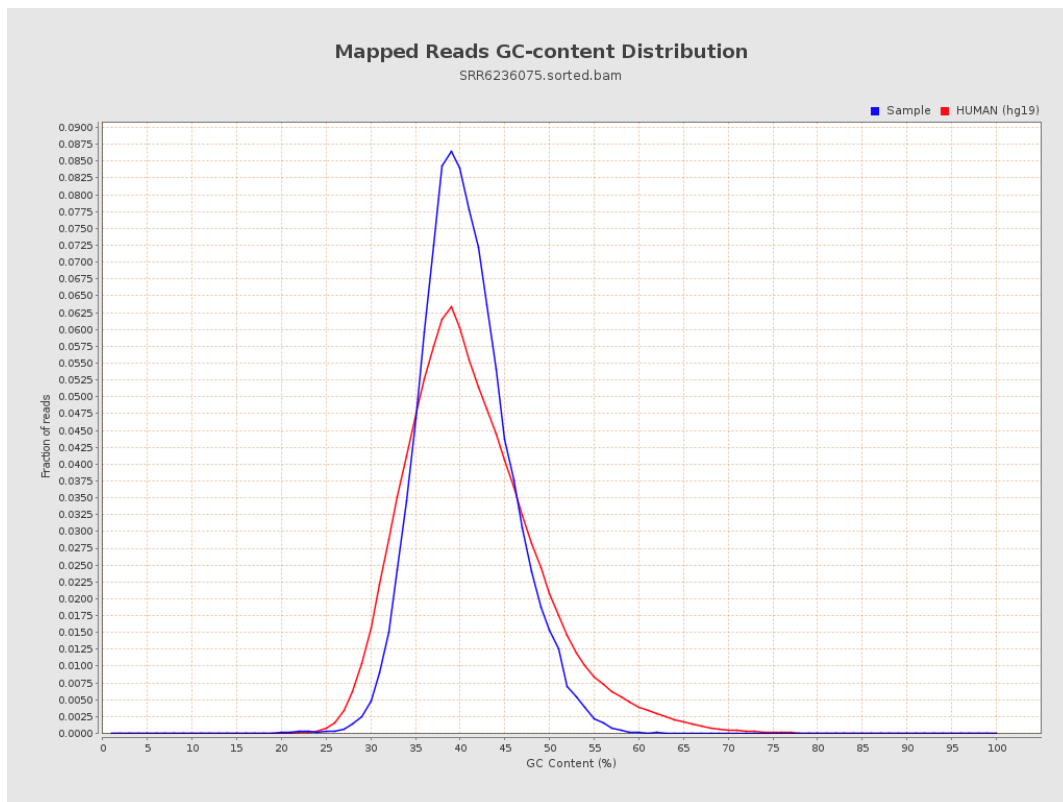
7. Results : Duplication Rate Histogram



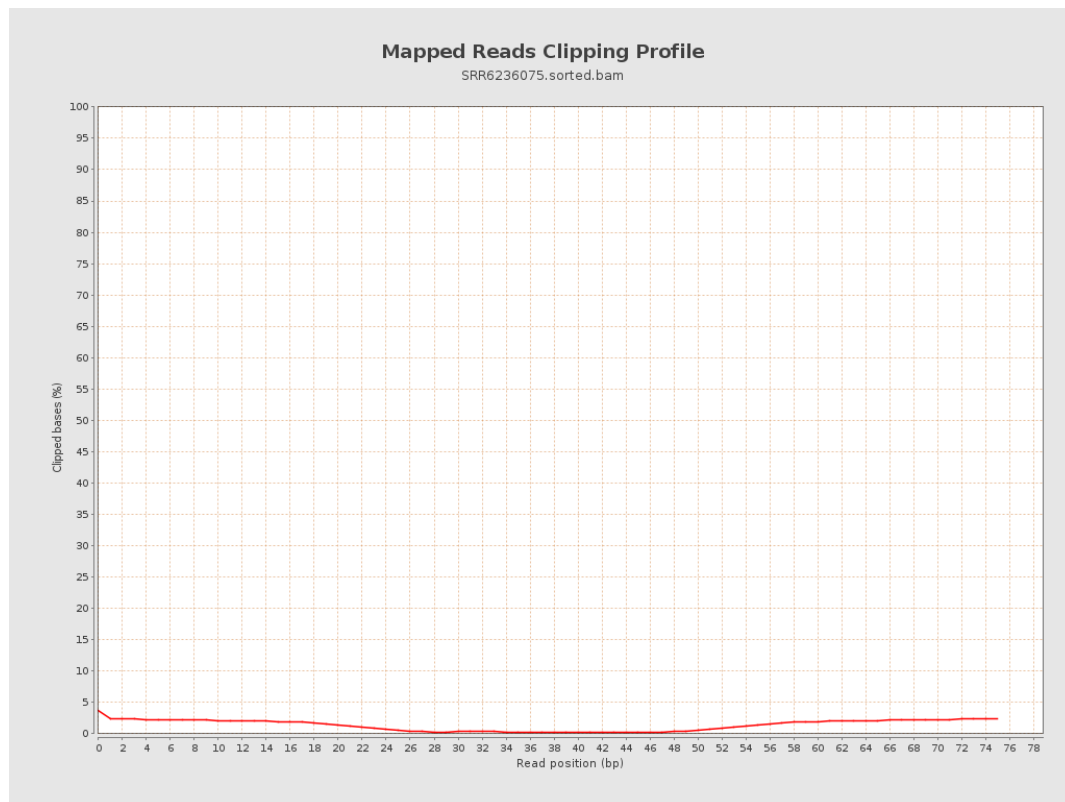
8. Results : Mapped Reads Nucleotide Content



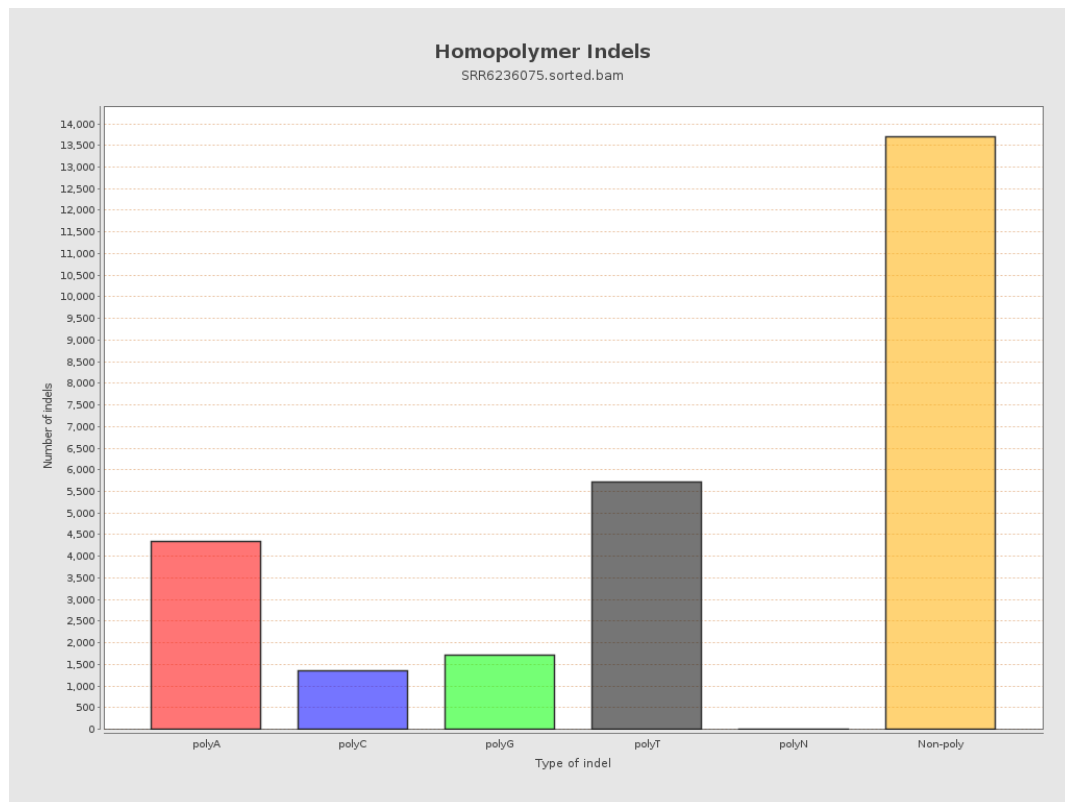
9. Results : Mapped Reads GC-content Distribution



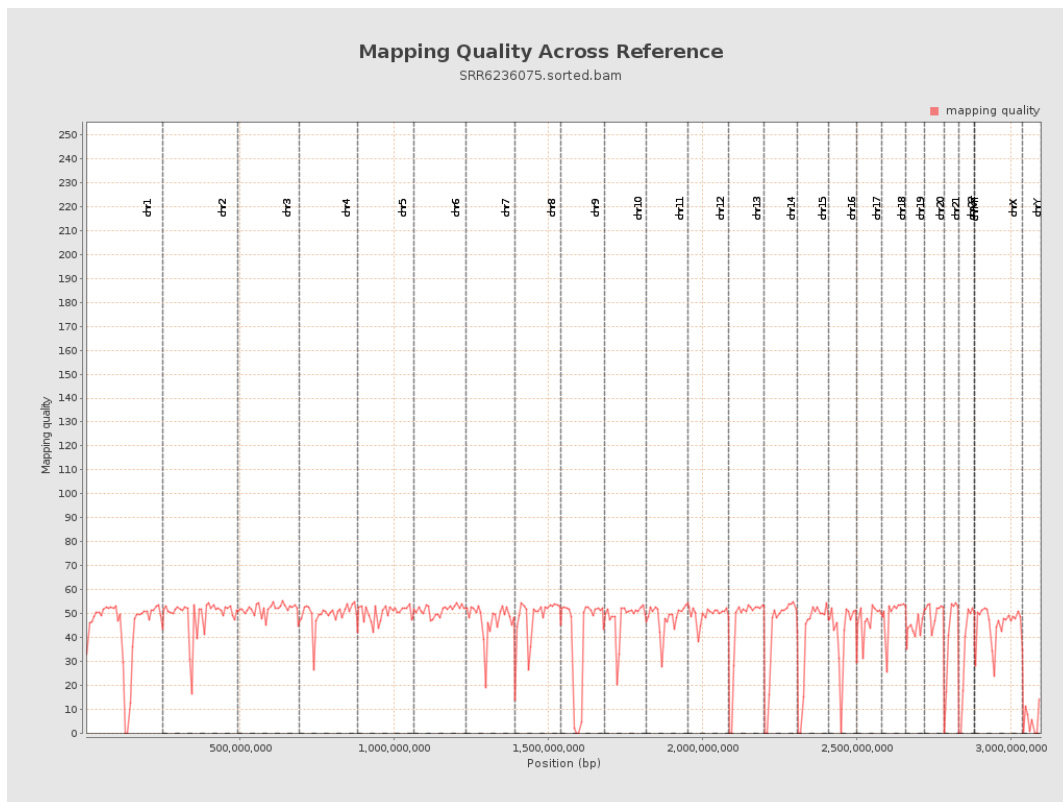
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

