Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:58:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081956.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_SRR3081956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081956.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:58:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,080,173
Mapped reads	2,794,909 / 90.74%
Unmapped reads	285,264 / 9.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,746 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	125,139 / 4.06%
Duplication rate	3.05%
Clipped reads	892,840 / 28.99%

2.2. ACGT Content

Number/percentage of A's	56,880,106 / 29.22%
Number/percentage of C's	36,211,763 / 18.6%
Number/percentage of T's	61,164,380 / 31.42%
Number/percentage of G's	40,383,657 / 20.75%
Number/percentage of N's	25,531 / 0.01%
GC Percentage	39.35%

2.3. Coverage

Mean	0.0629

Standard Deviation	0.6608

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

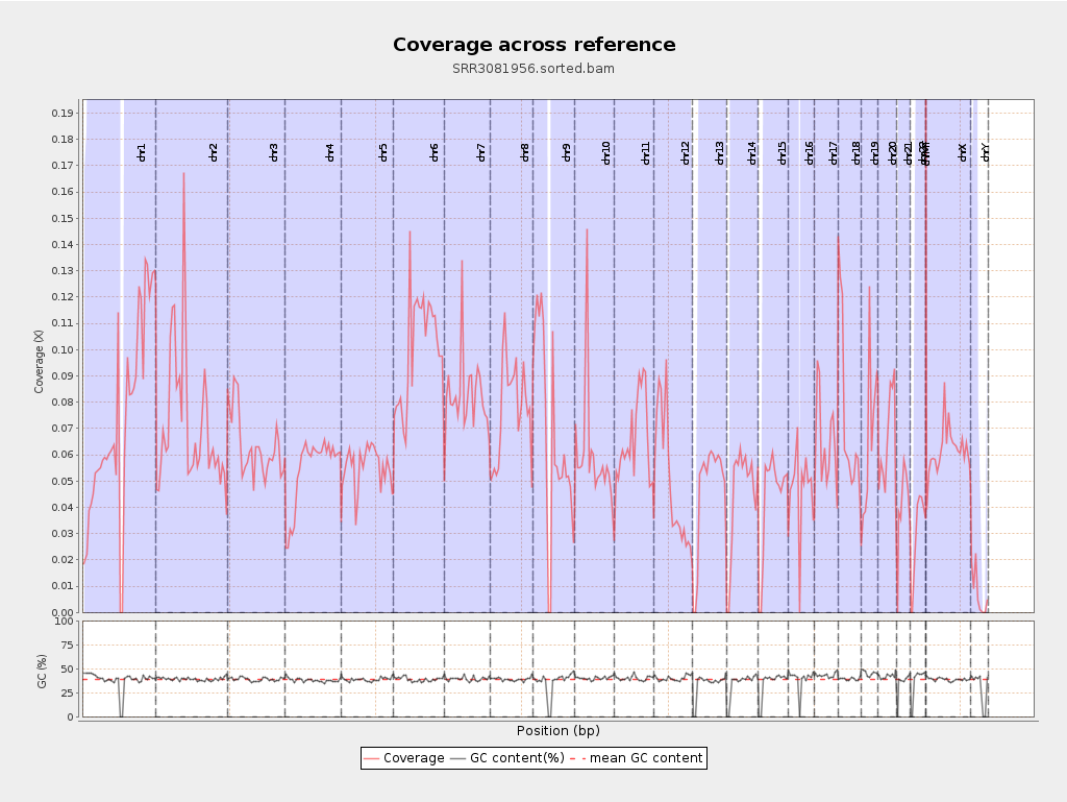
General error rate	0.82%
Mismatches	1,566,835
Insertions	14,503
Mapped reads with at least one insertion	0.52%
Deletions	47,684
Mapped reads with at least one deletion	1.69%
Homopolymer indels	47.03%

2.6. Chromosome stats

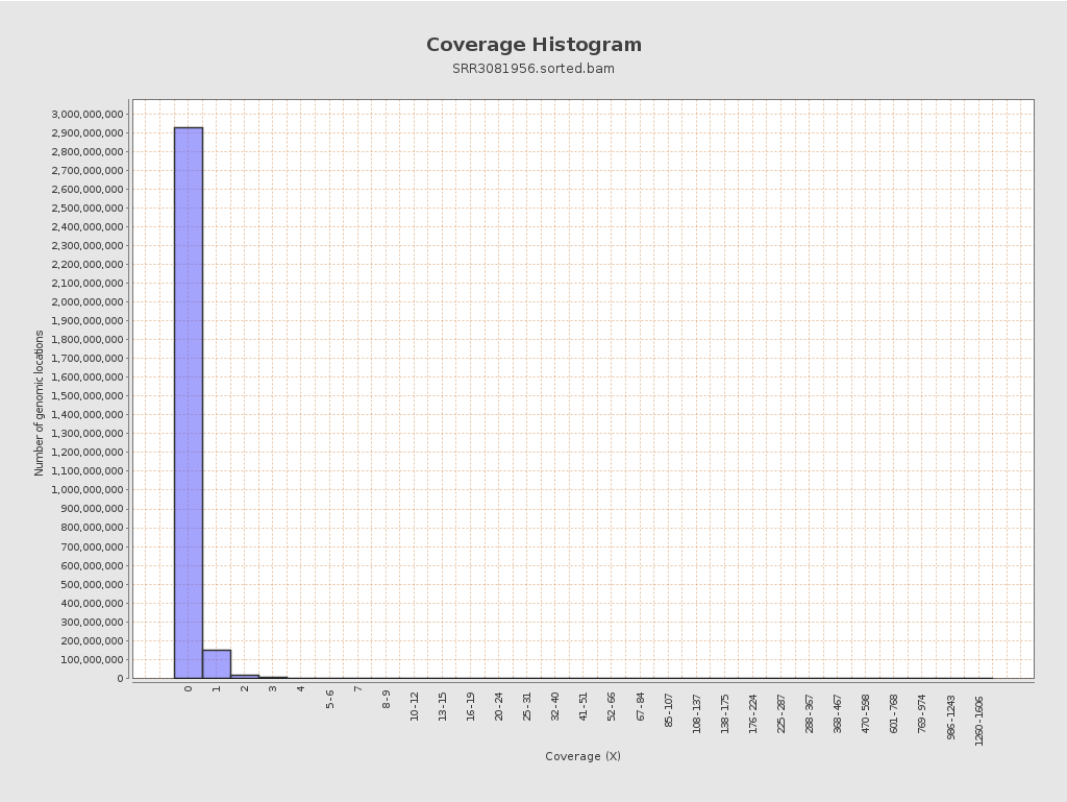
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18226394	0.0731	1.3568
chr2	243199373	17431007	0.0717	0.8002
chr3	198022430	12582486	0.0635	0.2927
chr4	191154276	10419342	0.0545	0.2843
chr5	180915260	9974675	0.0551	0.2695
chr6	171115067	17223734	0.1007	0.519
chr7	159138663	13085819	0.0822	0.8913

chr8	146364022	11358888	0.0776	0.976
chr9	141213431	9536321	0.0675	0.6316
chr10	135534747	8076357	0.0596	0.7016
chr11	135006516	8876217	0.0657	0.42
chr12	133851895	6549400	0.0489	0.274
chr13	115169878	5392712	0.0468	0.2391
chr14	107349540	4861159	0.0453	0.291
chr15	102531392	4394766	0.0429	0.2316
chr16	90354753	4148455	0.0459	0.3416
chr17	81195210	5316526	0.0655	0.3215
chr18	78077248	5718487	0.0732	1.0892
chr19	59128983	3929888	0.0665	0.9861
chr20	63025520	4167863	0.0661	0.3003
chr21	48129895	1955295	0.0406	0.2741
chr22	51304566	1513822	0.0295	0.1875
chrMT	16571	3743	0.2259	0.4614
chrX	155270560	9579411	0.0617	0.3464
chrY	59373566	426338	0.0072	0.1849

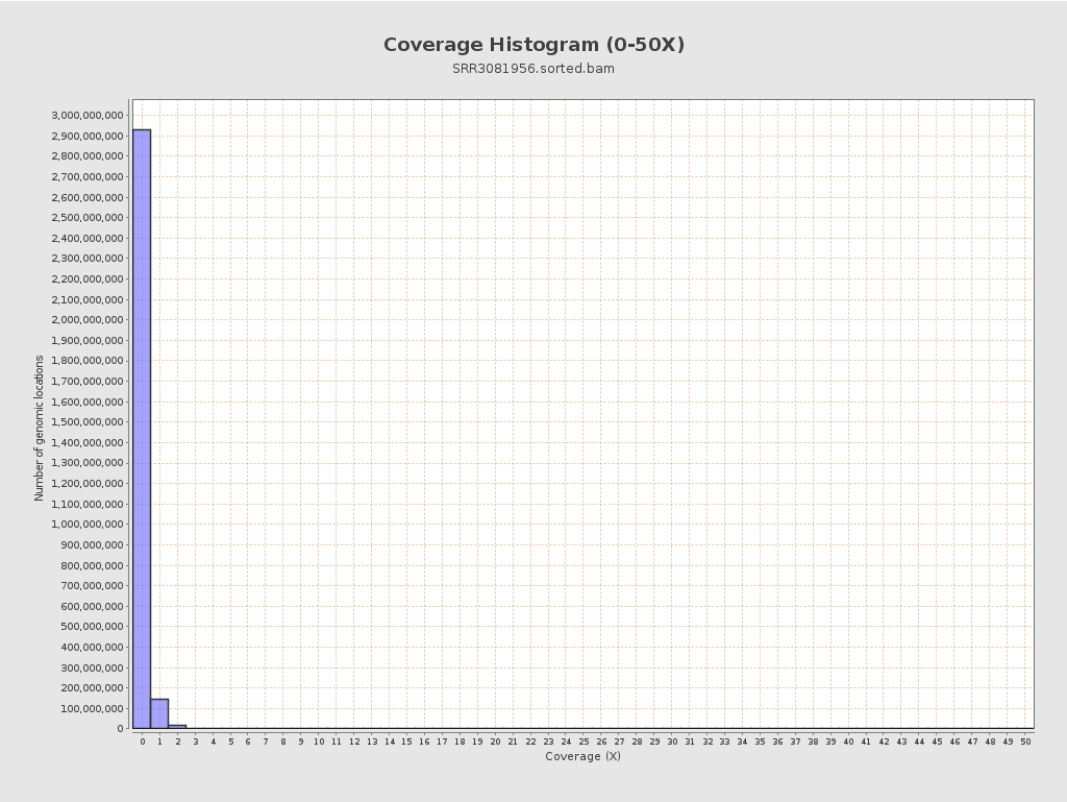
3. Results : Coverage across reference



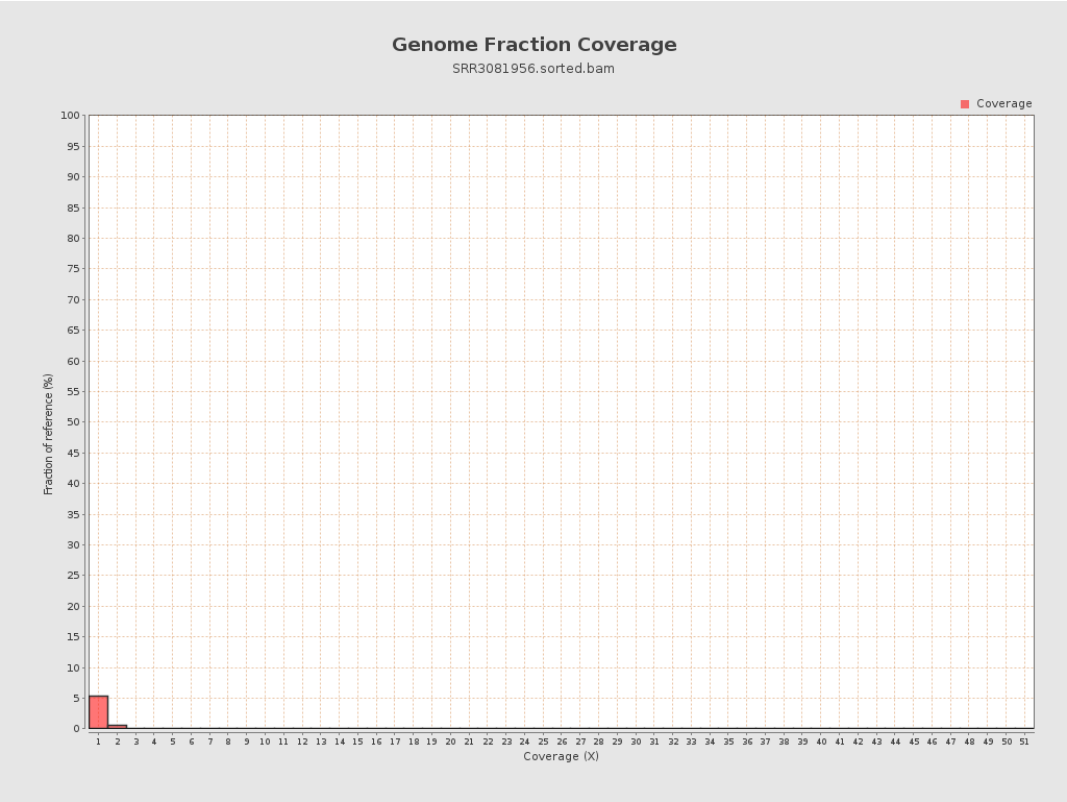
4. Results : Coverage Histogram



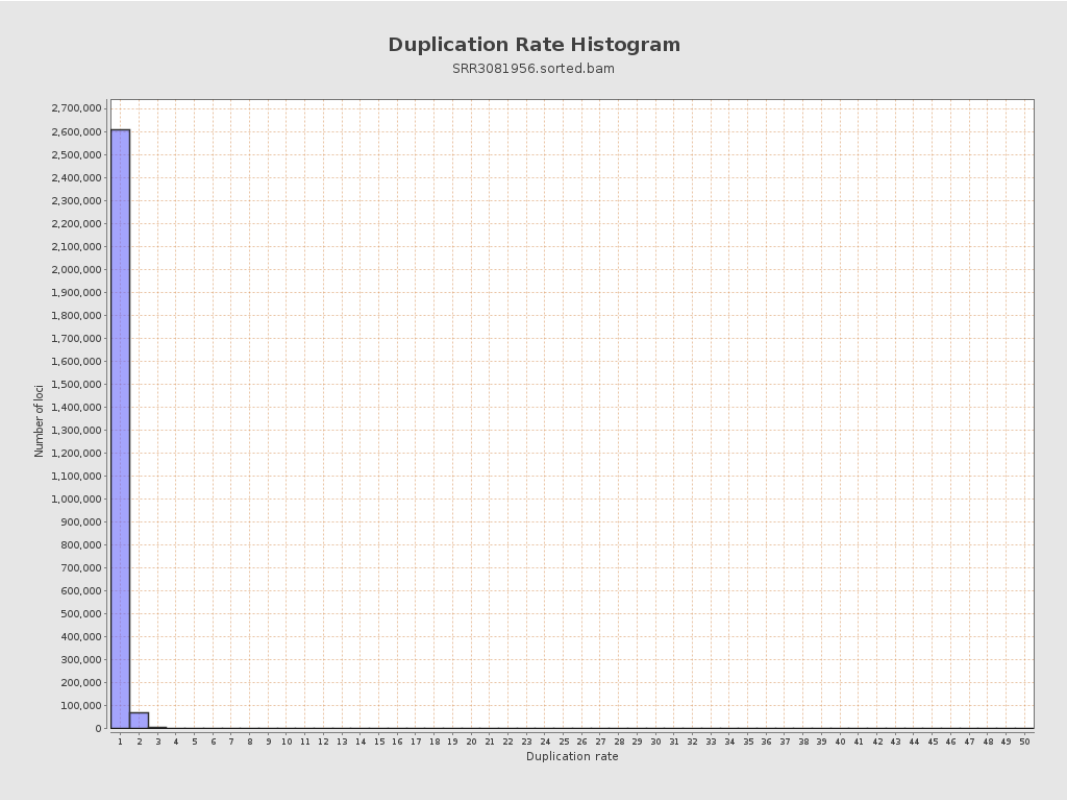
5. Results : Coverage Histogram (0-50X)



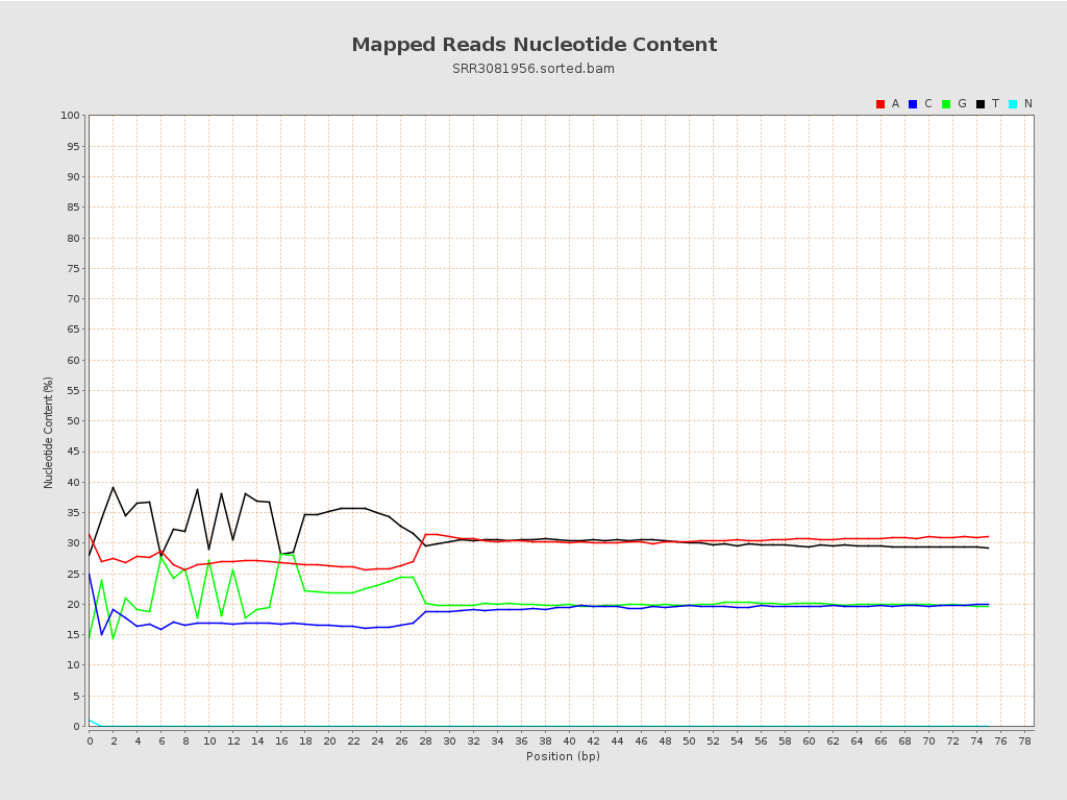
6. Results : Genome Fraction Coverage



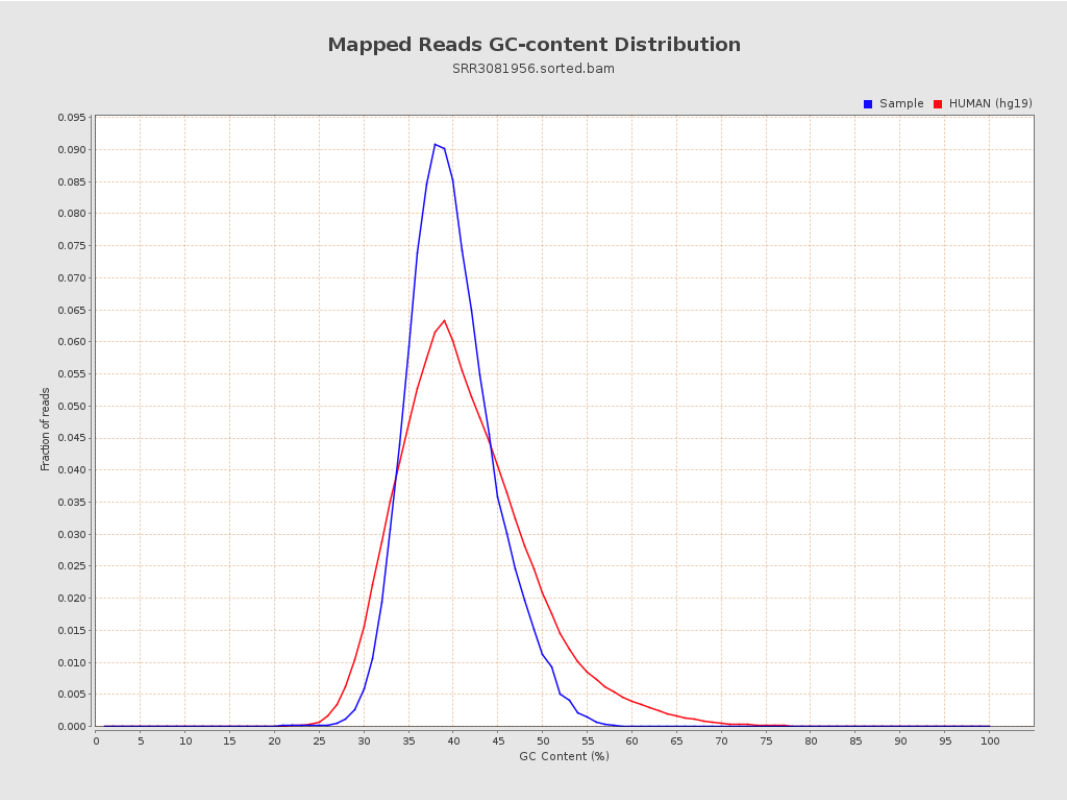
7. Results : Duplication Rate Histogram



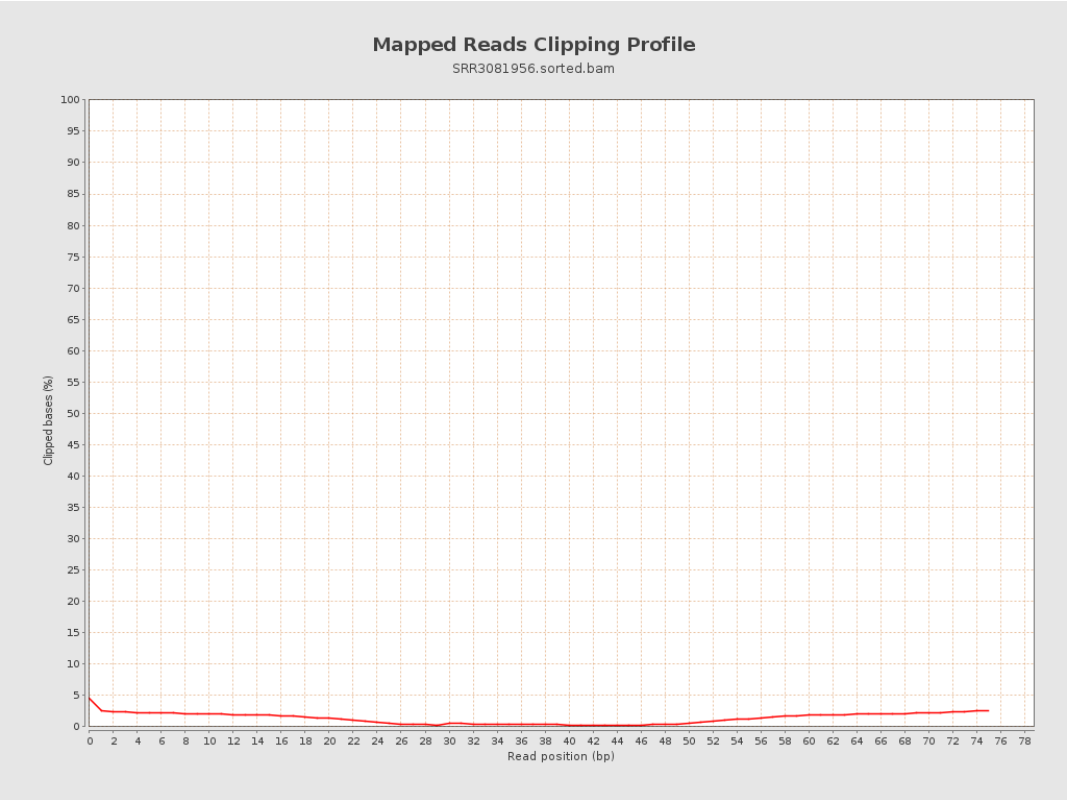
8. Results : Mapped Reads Nucleotide Content



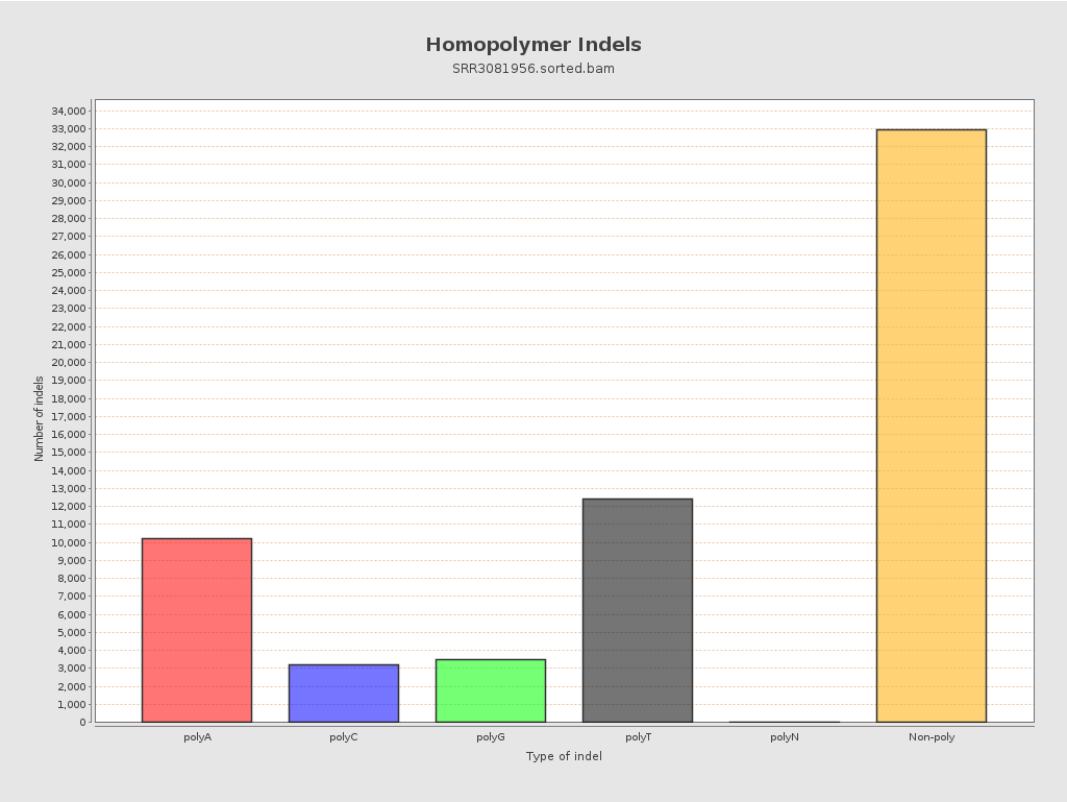
9. Results : Mapped Reads GC-content Distribution



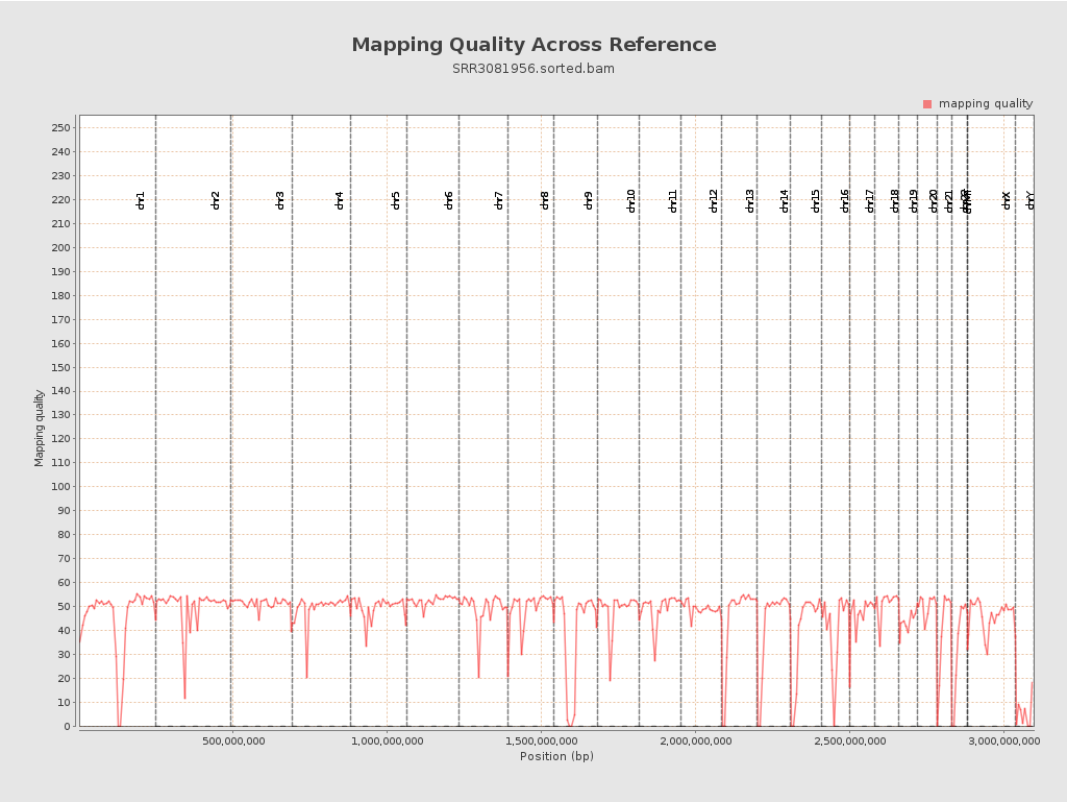
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram