Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:32:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081743.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_SRR3081743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:32:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,349,272
Mapped reads	2,119,424 / 90.22%
Unmapped reads	229,848 / 9.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,025 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	81,944 / 3.49%
Duplication rate	3.15%
Clipped reads	915,807 / 38.98%

2.2. ACGT Content

Number/percentage of A's	39,576,959 / 27.96%
Number/percentage of C's	26,810,859 / 18.94%
Number/percentage of T's	43,820,655 / 30.95%
Number/percentage of G's	31,356,063 / 22.15%
Number/percentage of N's	1,507 / 0%
GC Percentage	41.09%

2.3. Coverage

Mean	0.0457

Standard Deviation	0.3312

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

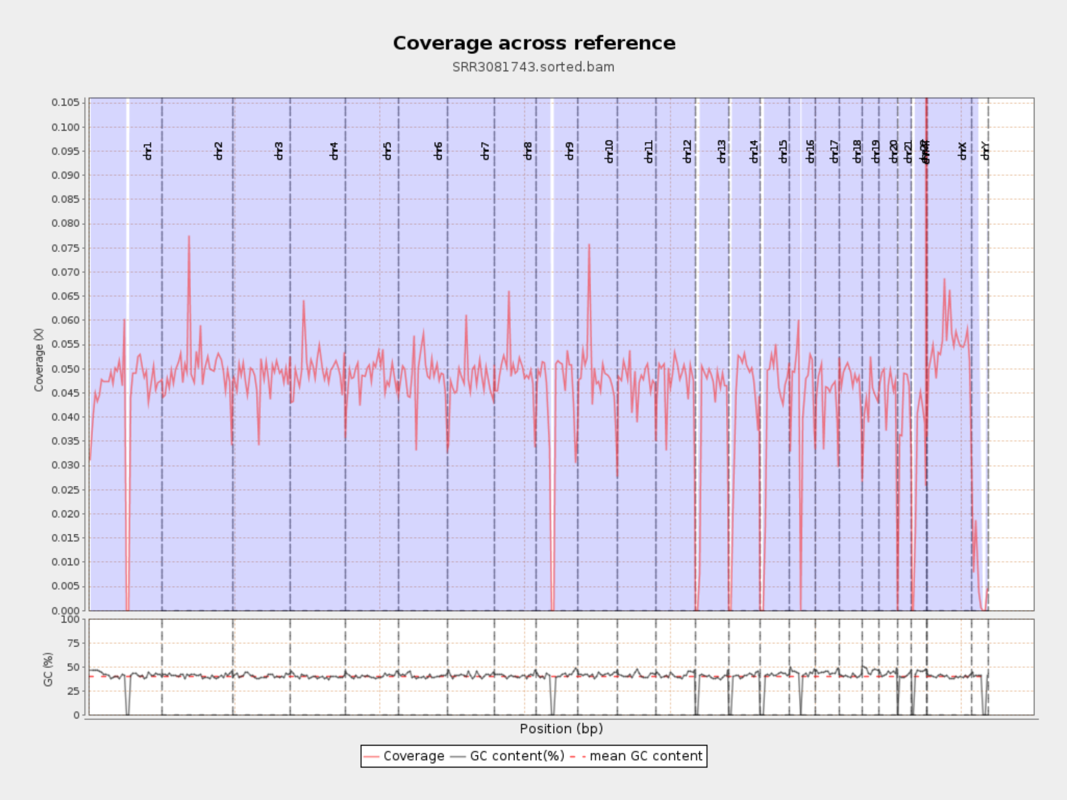
General error rate	0.79%
Mismatches	1,105,135
Insertions	10,272
Mapped reads with at least one insertion	0.48%
Deletions	29,520
Mapped reads with at least one deletion	1.38%
Homopolymer indels	47.06%

2.6. Chromosome stats

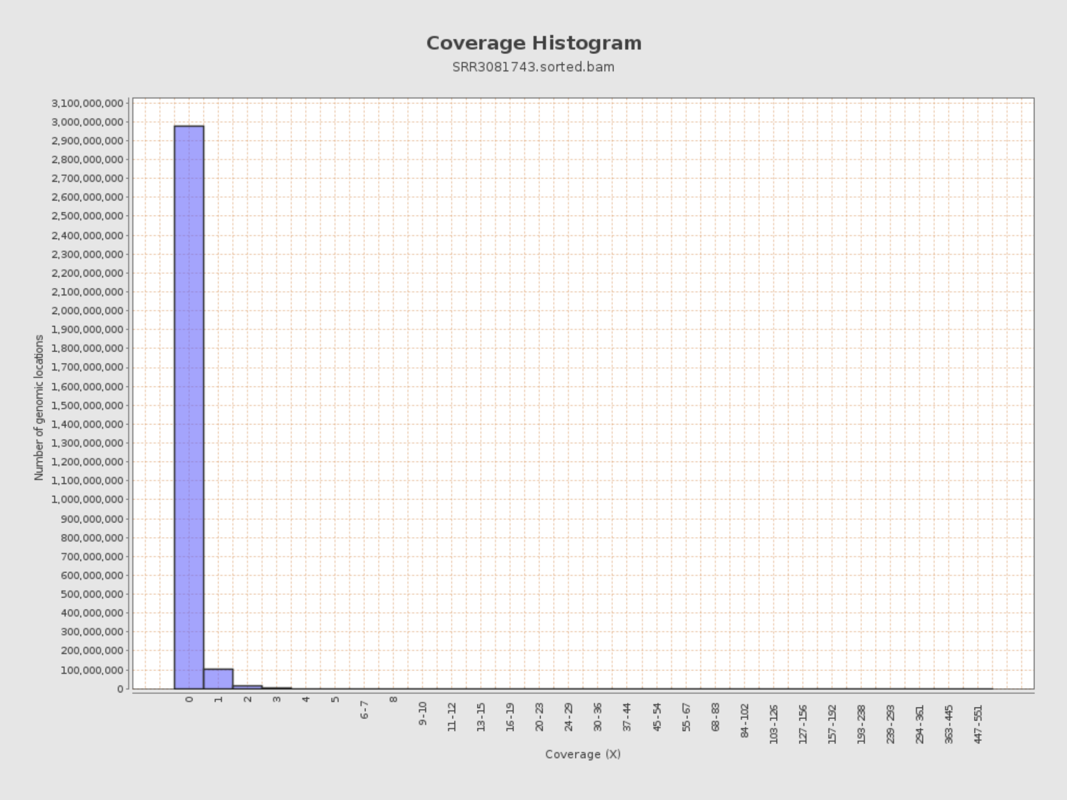
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11109382	0.0446	0.4783
chr2	243199373	12207325	0.0502	0.4078
chr3	198022430	9536687	0.0482	0.2502
chr4	191154276	9525232	0.0498	0.2718
chr5	180915260	8804132	0.0487	0.2514
chr6	171115067	8291598	0.0485	0.2751
chr7	159138663	7612940	0.0478	0.3859

chr8	146364022	7221508	0.0493	0.4293
chr9	141213431	5967998	0.0423	0.3303
chr10	135534747	6691724	0.0494	0.3932
chr11	135006516	6388753	0.0473	0.2991
chr12	133851895	6387541	0.0477	0.2503
chr13	115169878	4567804	0.0397	0.2267
chr14	107349540	4332368	0.0404	0.2413
chr15	102531392	4044921	0.0395	0.2317
chr16	90354753	3969481	0.0439	0.2678
chr17	81195210	3568928	0.044	0.2532
chr18	78077248	3766245	0.0482	0.5325
chr19	59128983	2568452	0.0434	0.3938
chr20	63025520	2864498	0.0454	0.2491
chr21	48129895	1839310	0.0382	0.2405
chr22	51304566	1467457	0.0286	0.19
chrMT	16571	9647	0.5822	0.8497
chrX	155270560	8501471	0.0548	0.2903
chrY	59373566	372450	0.0063	0.1492

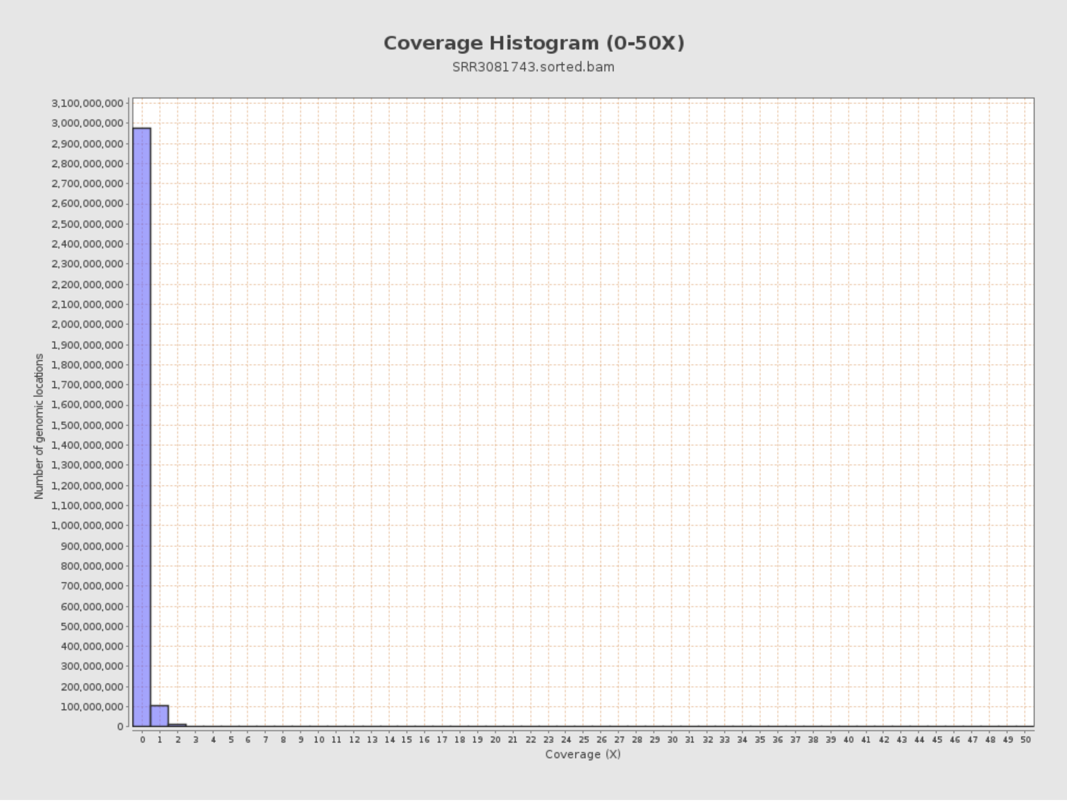
3. Results : Coverage across reference



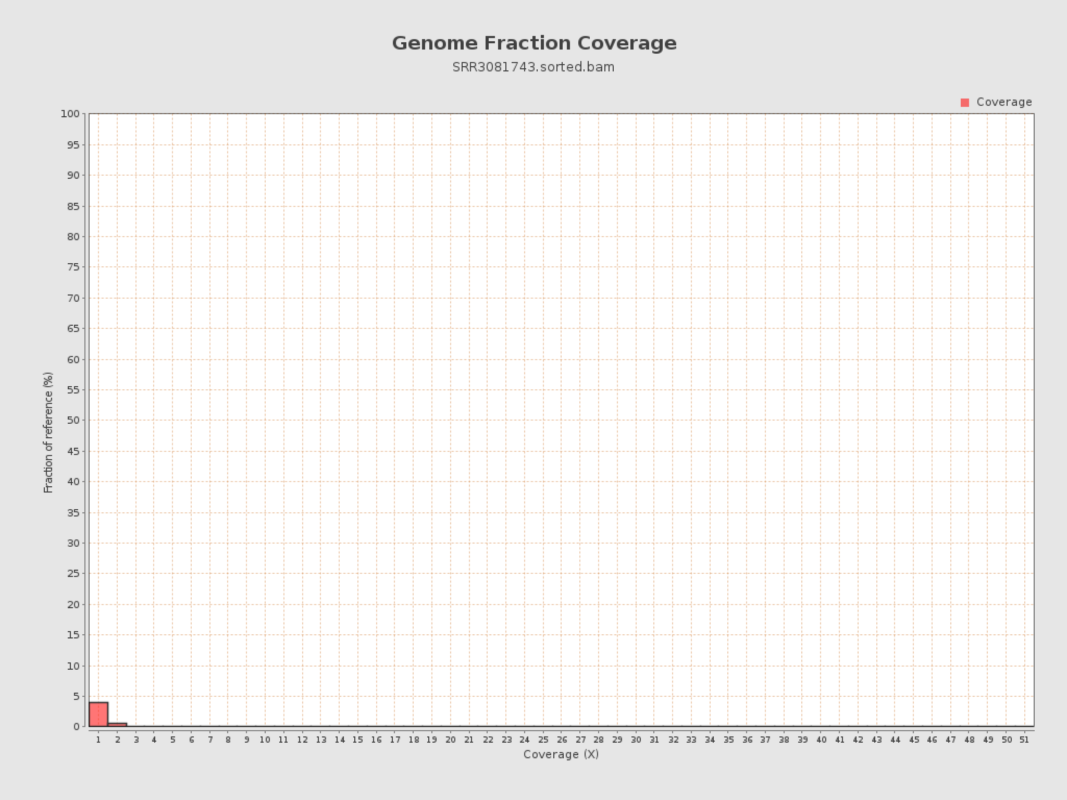
4. Results : Coverage Histogram



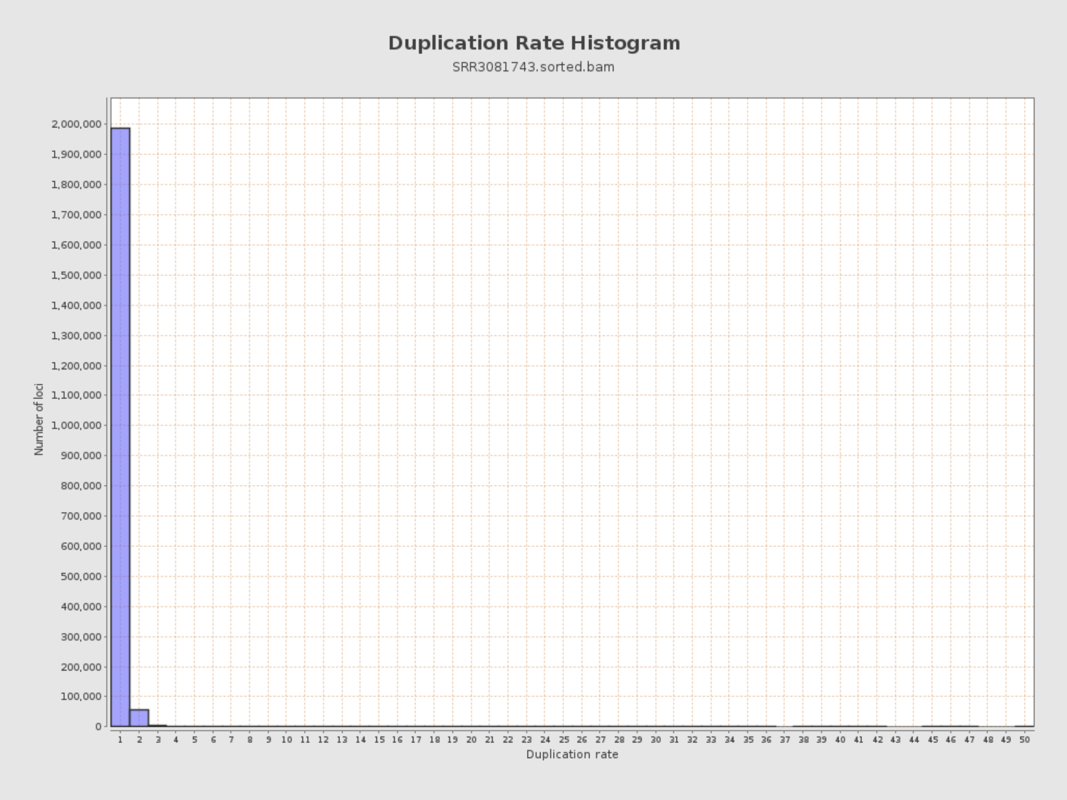
5. Results : Coverage Histogram (0-50X)



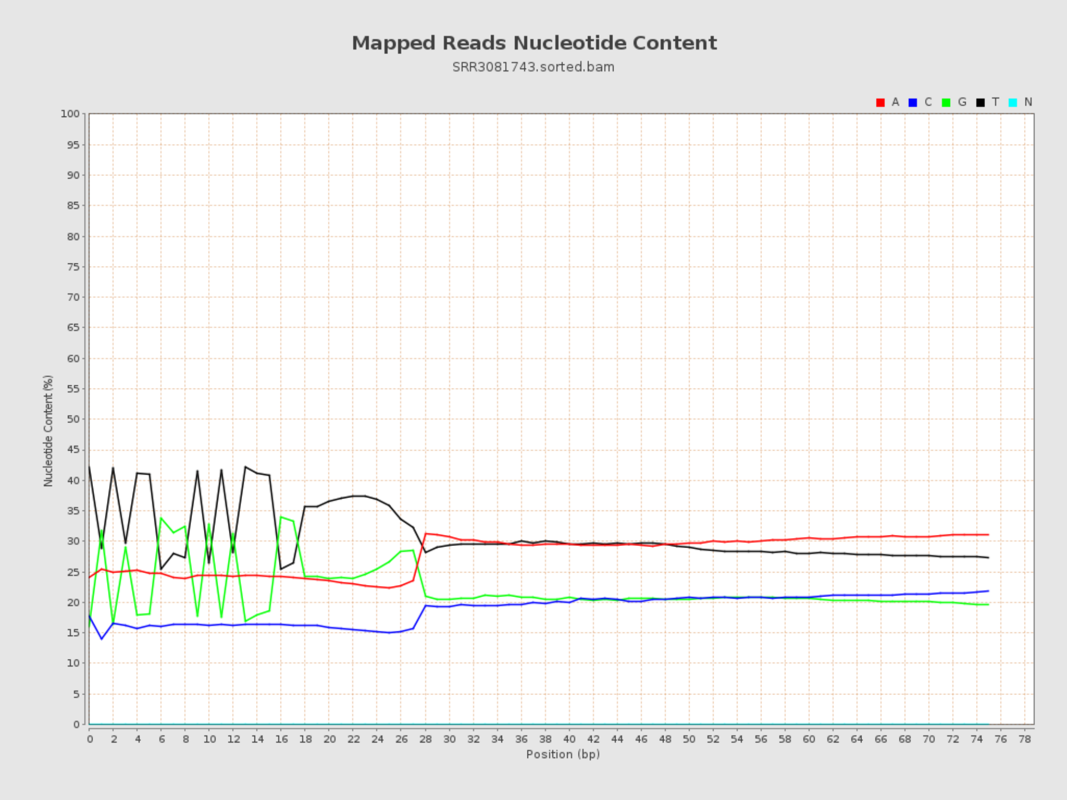
6. Results : Genome Fraction Coverage



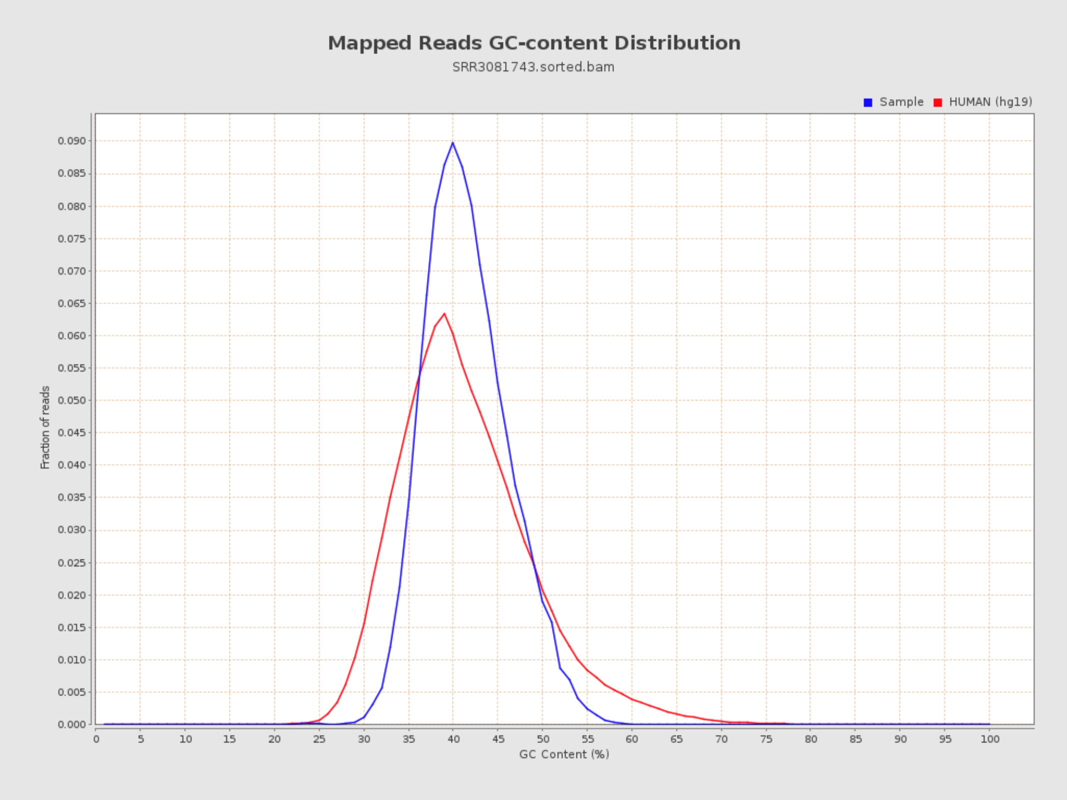
7. Results : Duplication Rate Histogram



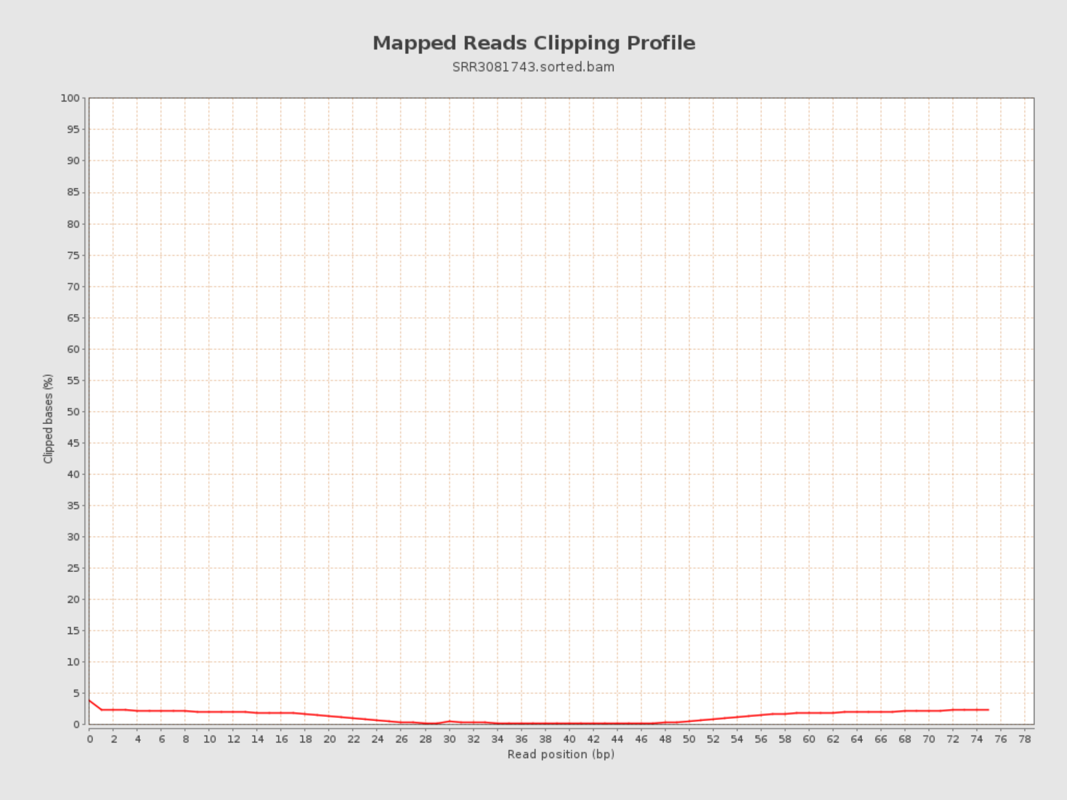
8. Results : Mapped Reads Nucleotide Content



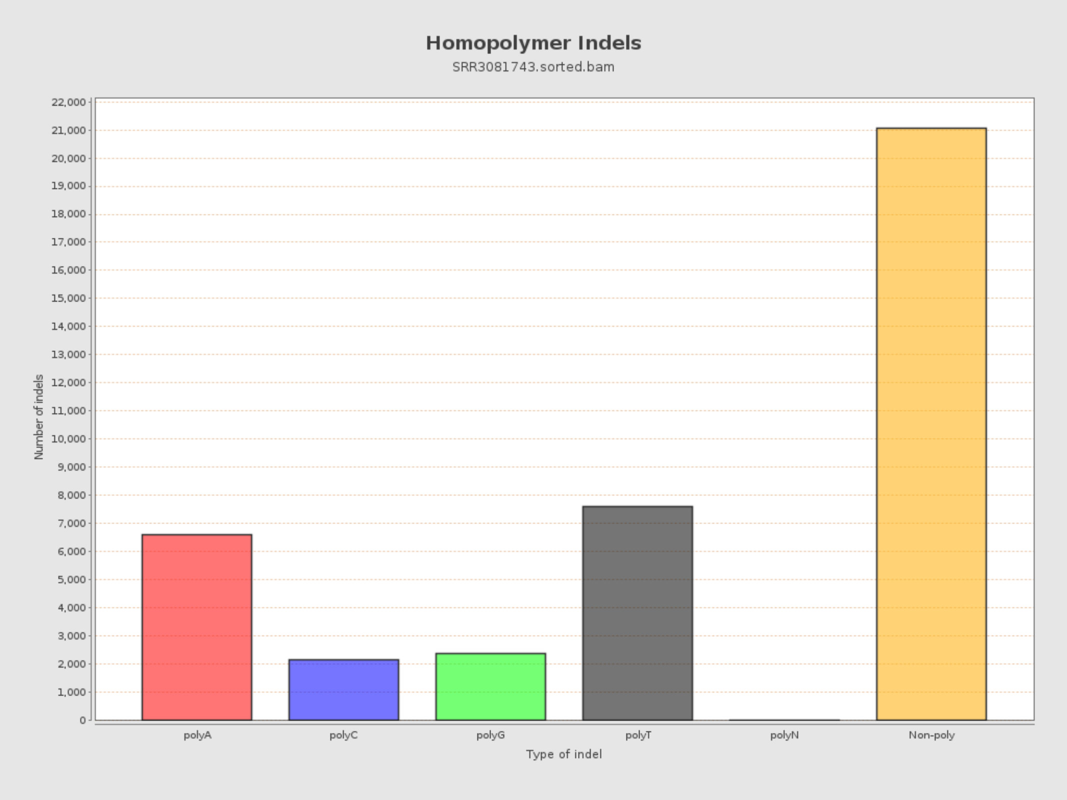
9. Results : Mapped Reads GC-content Distribution



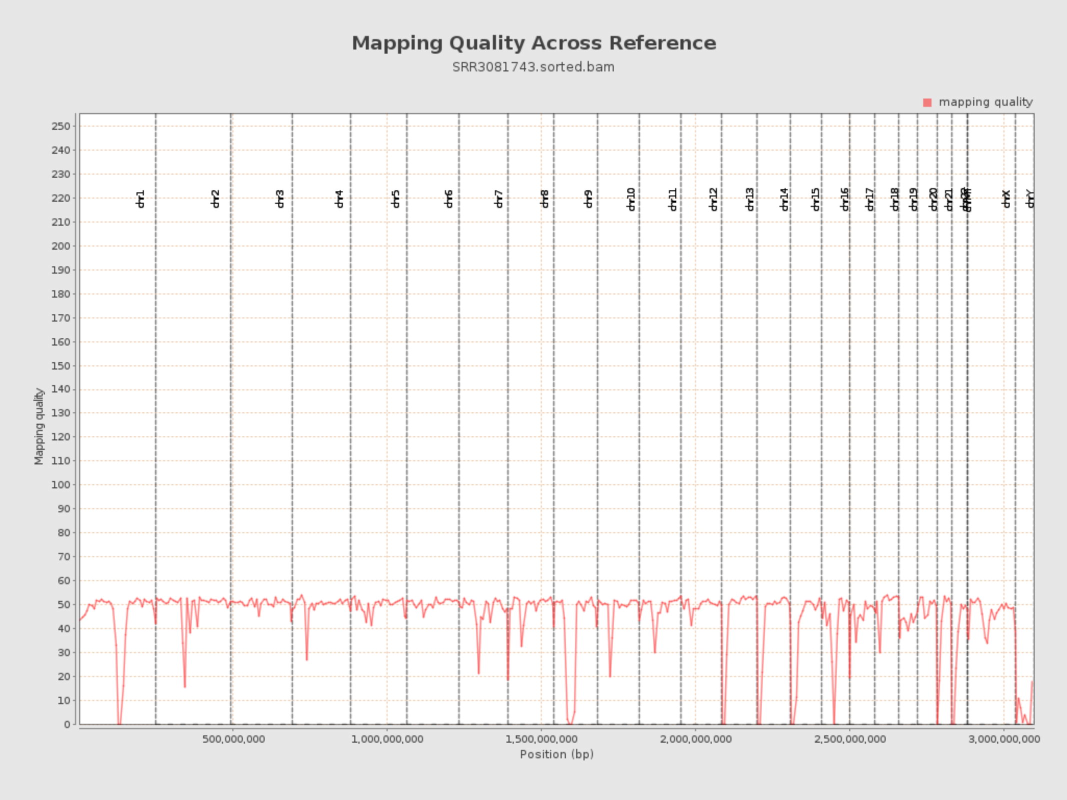
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram