Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:00:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524698.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_SRR10524698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524698.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:00:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	99,097
Mapped reads	91,014 / 91.84%
Unmapped reads	8,083 / 8.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	299 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	740 / 0.75%
Duplication rate	0.66%
Clipped reads	91,032 / 91.86%

2.2. ACGT Content

Number/percentage of A's	1,330,828 / 24.79%
Number/percentage of C's	951,469 / 17.72%
Number/percentage of T's	1,765,434 / 32.88%
Number/percentage of G's	1,320,525 / 24.6%
Number/percentage of N's	653 / 0.01%
GC Percentage	42.32%

2.3. Coverage

Mean	0.0017

Standard Deviation	0.0439

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

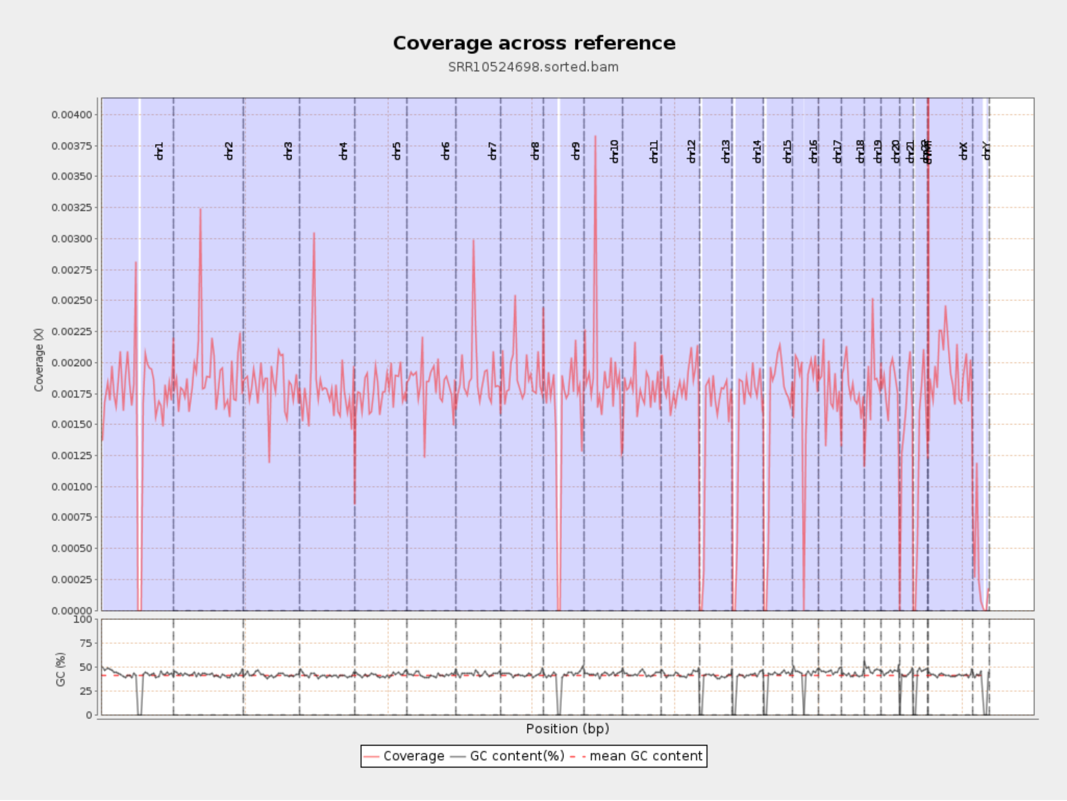
General error rate	0.51%
Mismatches	26,754
Insertions	381
Mapped reads with at least one insertion	0.42%
Deletions	1,000
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.32%

2.6. Chromosome stats

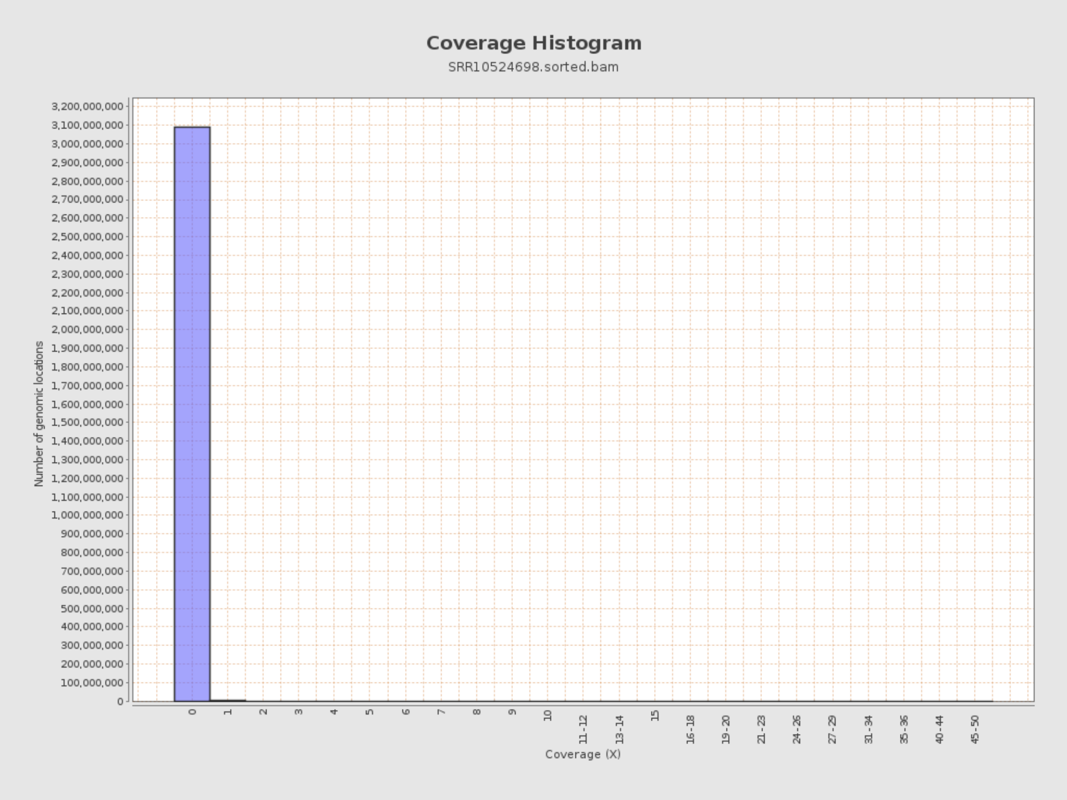
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	425384	0.0017	0.0501
chr2	243199373	459979	0.0019	0.0486
chr3	198022430	359042	0.0018	0.0429
chr4	191154276	340727	0.0018	0.0428
chr5	180915260	320908	0.0018	0.0425
chr6	171115067	311341	0.0018	0.0433
chr7	159138663	302916	0.0019	0.0468

chr8	146364022	277393	0.0019	0.0457
chr9	141213431	224667	0.0016	0.0414
chr10	135534747	262076	0.0019	0.0464
chr11	135006516	241153	0.0018	0.0431
chr12	133851895	246477	0.0018	0.0433
chr13	115169878	167889	0.0015	0.0385
chr14	107349540	159450	0.0015	0.0388
chr15	102531392	155734	0.0015	0.0394
chr16	90354753	155780	0.0017	0.0421
chr17	81195210	143180	0.0018	0.0426
chr18	78077248	139763	0.0018	0.0487
chr19	59128983	109196	0.0018	0.048
chr20	63025520	113130	0.0018	0.0427
chr21	48129895	72497	0.0015	0.0392
chr22	51304566	62455	0.0012	0.0351
chrMT	16571	295	0.0178	0.1322
chrX	155270560	299722	0.0019	0.0446
chrY	59373566	19299	0.0003	0.0203

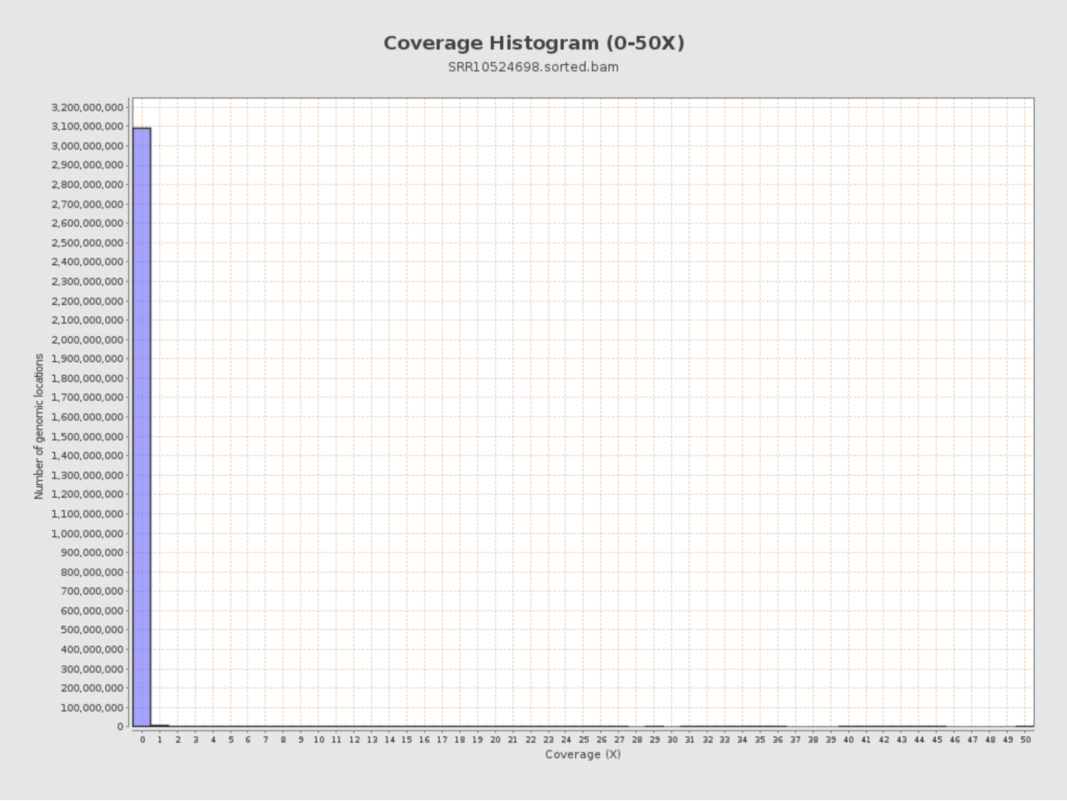
3. Results : Coverage across reference



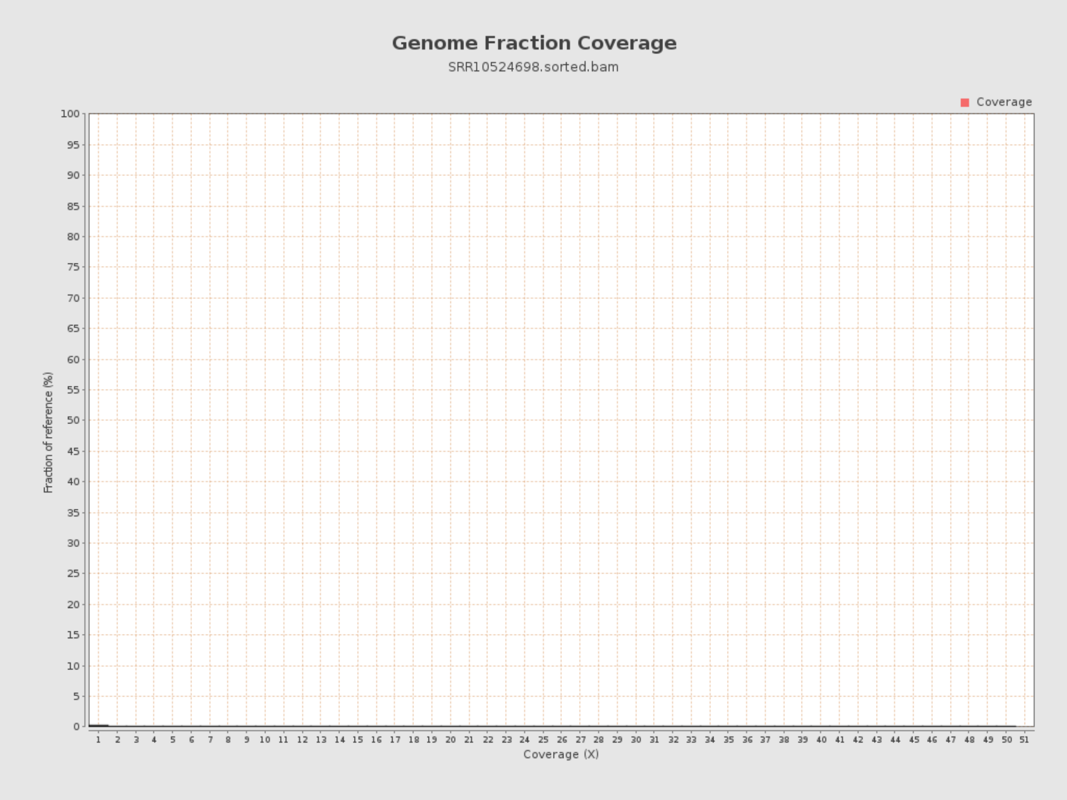
4. Results : Coverage Histogram



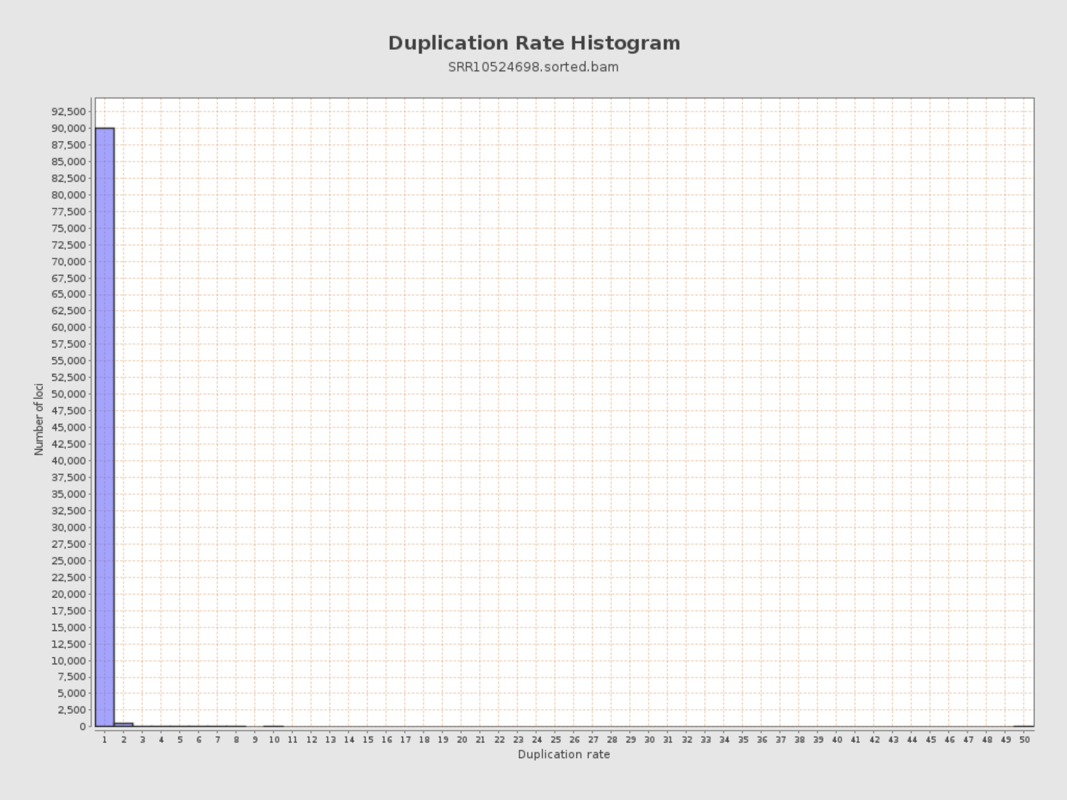
5. Results : Coverage Histogram (0-50X)



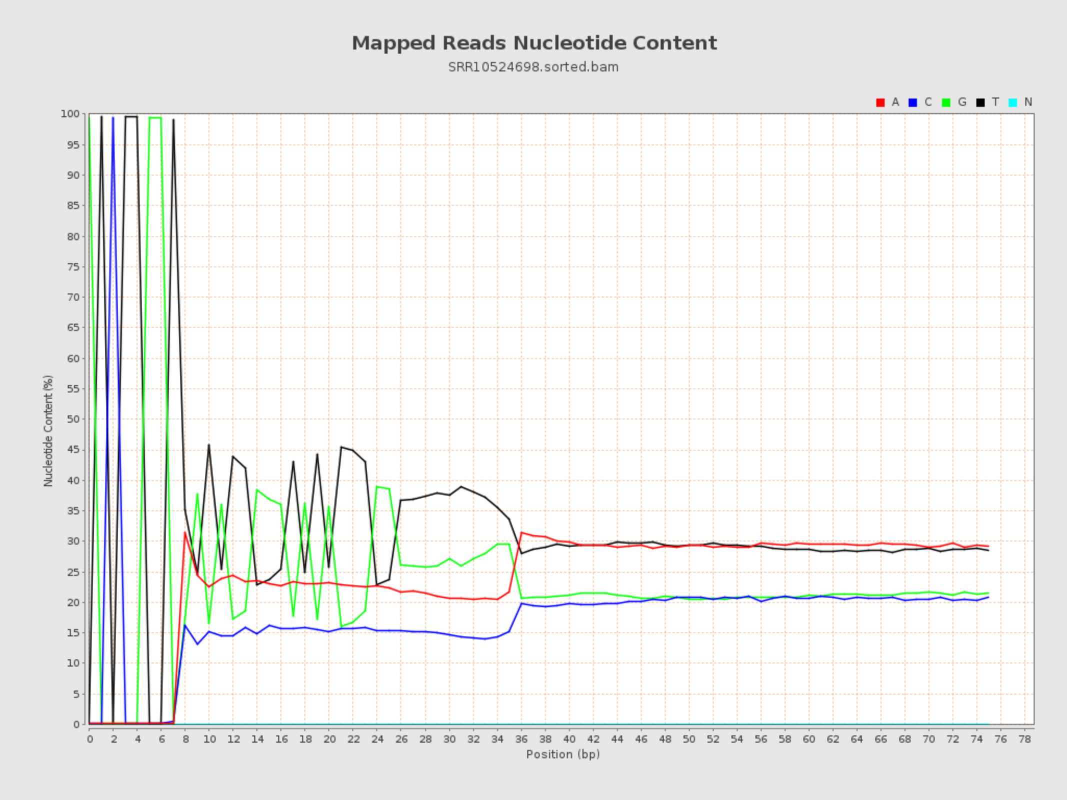
6. Results : Genome Fraction Coverage



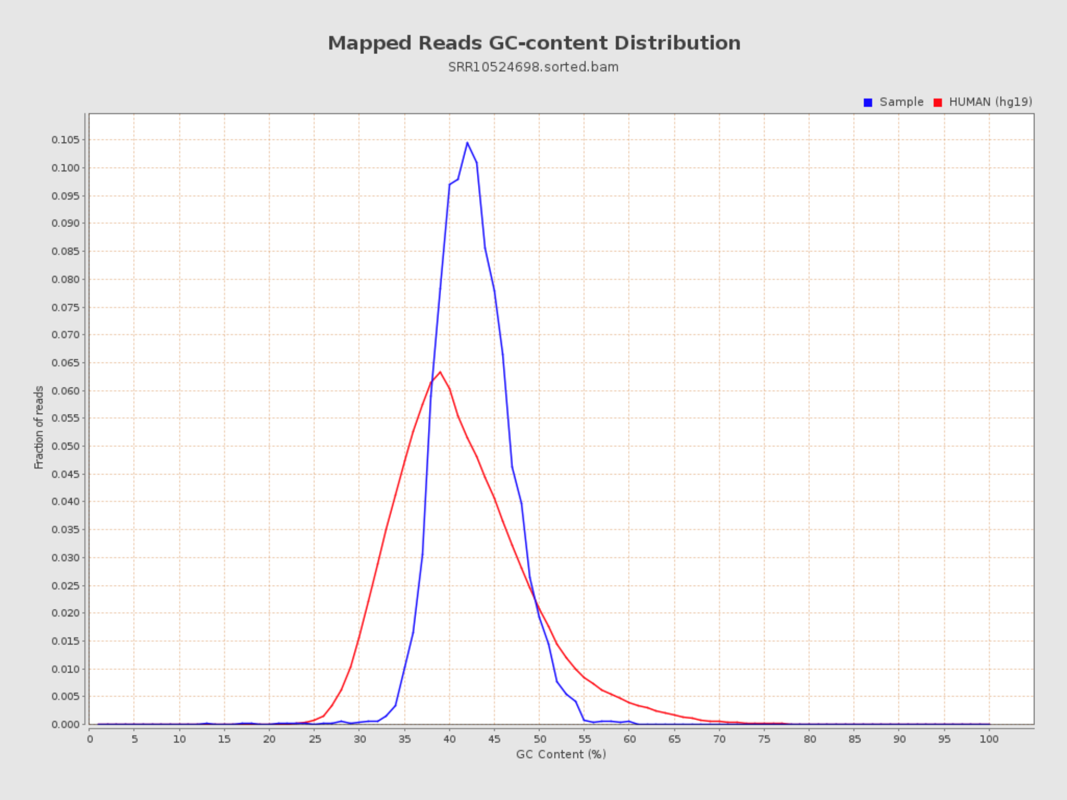
7. Results : Duplication Rate Histogram



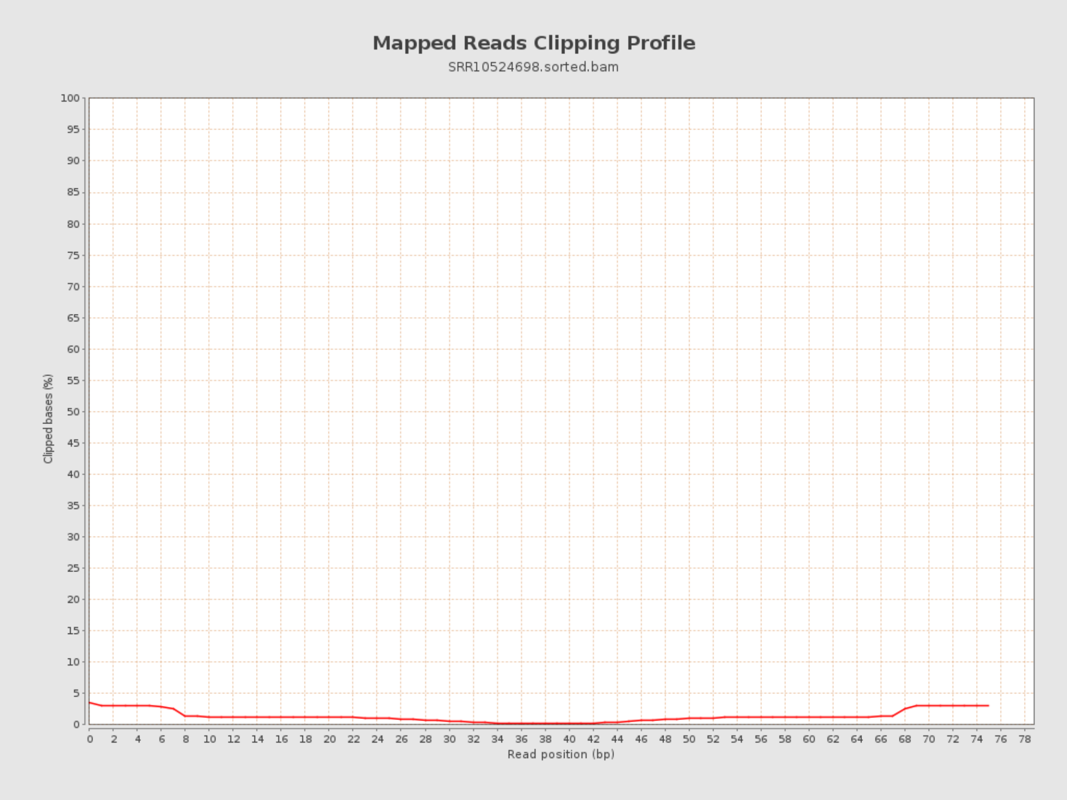
8. Results : Mapped Reads Nucleotide Content



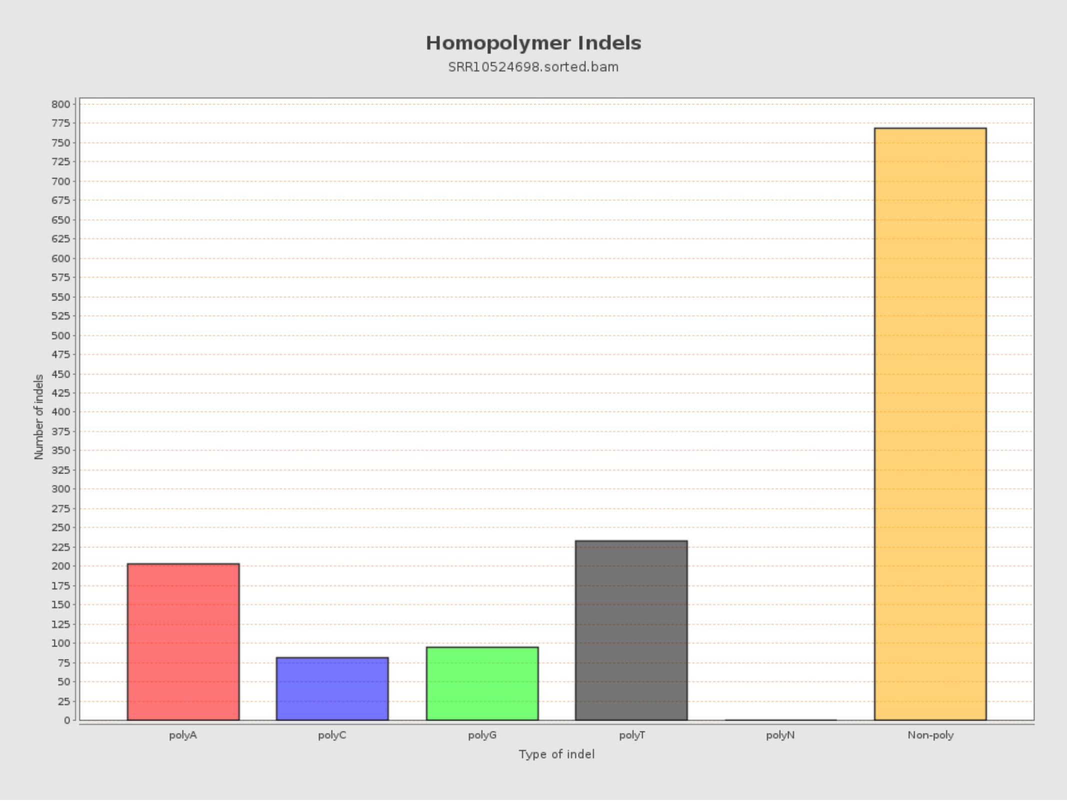
9. Results : Mapped Reads GC-content Distribution



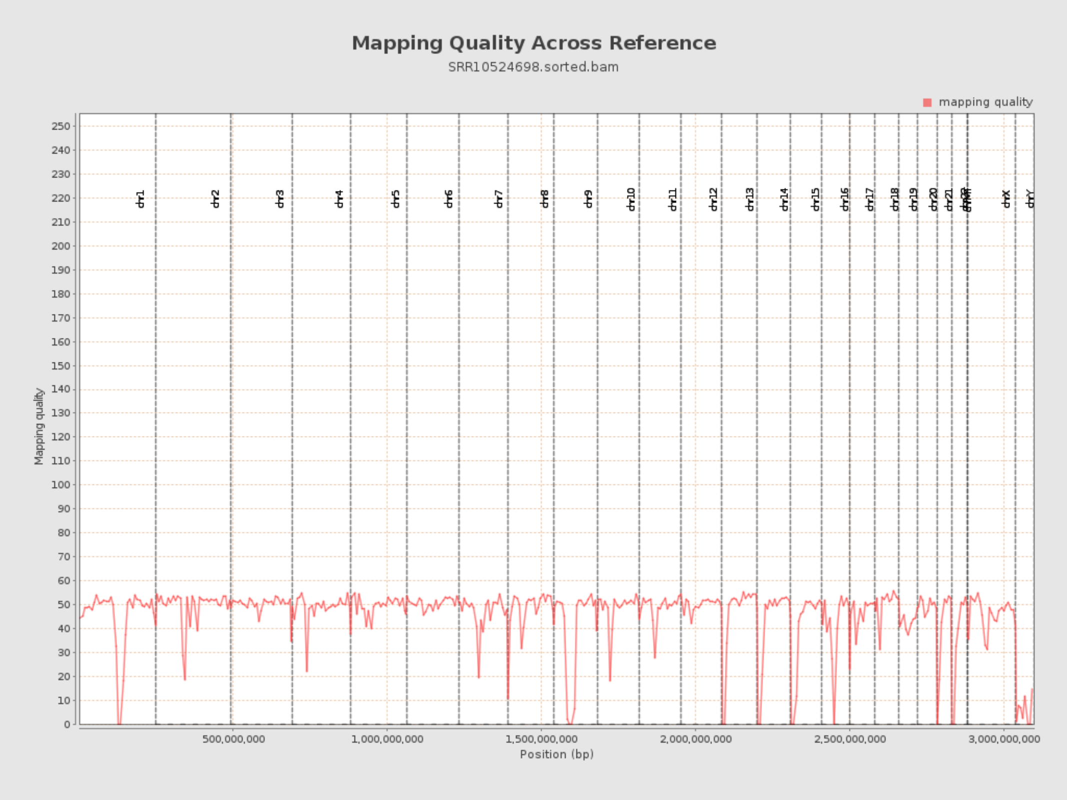
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram