Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:46:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085131.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_SRR3085131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:46:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,257,972
Mapped reads	2,029,009 / 89.86%
Unmapped reads	228,963 / 10.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,504 / 0.82%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	71,617 / 3.17%
Duplication rate	2.64%
Clipped reads	889,188 / 39.38%

2.2. ACGT Content

Number/percentage of A's	38,117,076 / 27.97%
Number/percentage of C's	25,375,841 / 18.62%
Number/percentage of T's	42,711,674 / 31.34%
Number/percentage of G's	30,062,677 / 22.06%
Number/percentage of N's	21,801 / 0.02%
GC Percentage	40.68%

2.3. Coverage

Mean	0.044

Standard Deviation	0.3841

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

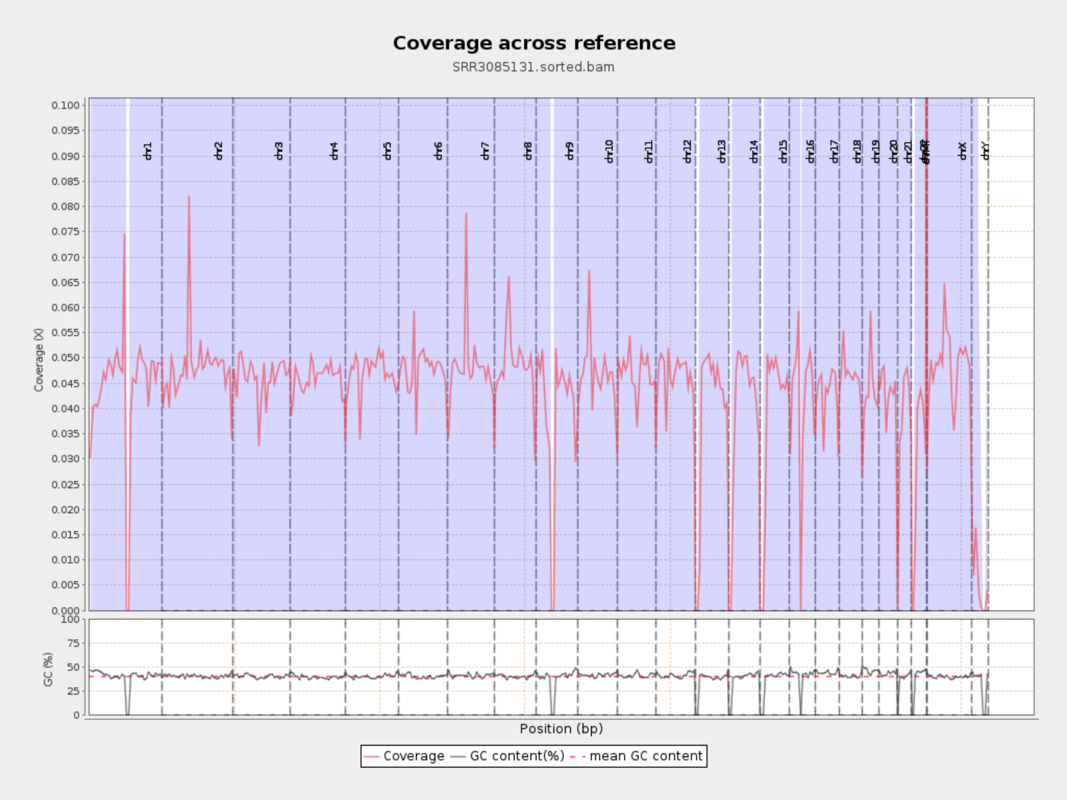
General error rate	0.93%
Mismatches	1,246,151
Insertions	10,972
Mapped reads with at least one insertion	0.54%
Deletions	34,304
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.35%

2.6. Chromosome stats

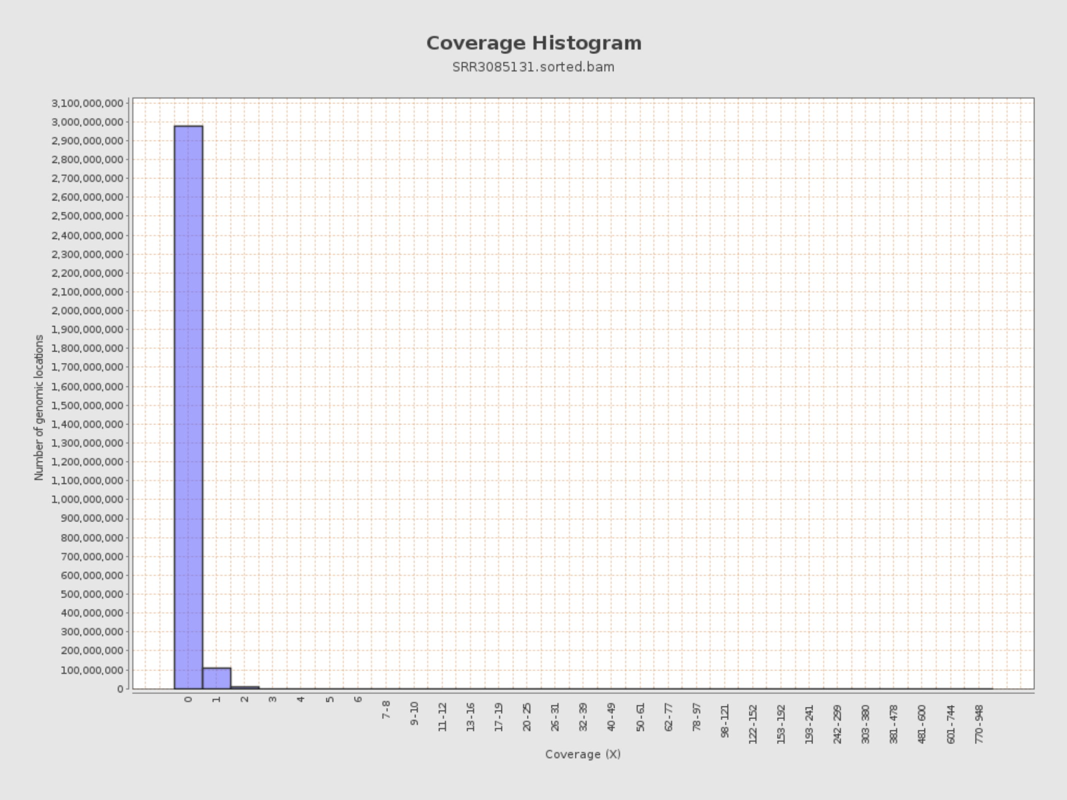
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10981079	0.0441	0.6772
chr2	243199373	11737637	0.0483	0.4474
chr3	198022430	9152404	0.0462	0.2347
chr4	191154276	8793372	0.046	0.24
chr5	180915260	8508647	0.047	0.2388
chr6	171115067	8177889	0.0478	0.2825
chr7	159138663	7744182	0.0487	0.5368

chr8	146364022	7123557	0.0487	0.6158
chr9	141213431	5506494	0.039	0.3384
chr10	135534747	6391354	0.0472	0.3339
chr11	135006516	6313501	0.0468	0.3376
chr12	133851895	6211602	0.0464	0.2403
chr13	115169878	4424799	0.0384	0.215
chr14	107349540	4185044	0.039	0.2326
chr15	102531392	3909115	0.0381	0.2179
chr16	90354753	3780863	0.0418	0.2479
chr17	81195210	3462145	0.0426	0.2534
chr18	78077248	3667625	0.047	0.6146
chr19	59128983	2588529	0.0438	0.5224
chr20	63025520	2694461	0.0428	0.2329
chr21	48129895	1776758	0.0369	0.2186
chr22	51304566	1423740	0.0278	0.1799
chrMT	16571	10226	0.6171	0.8809
chrX	155270560	7467647	0.0481	0.2696
chrY	59373566	312704	0.0053	0.1166

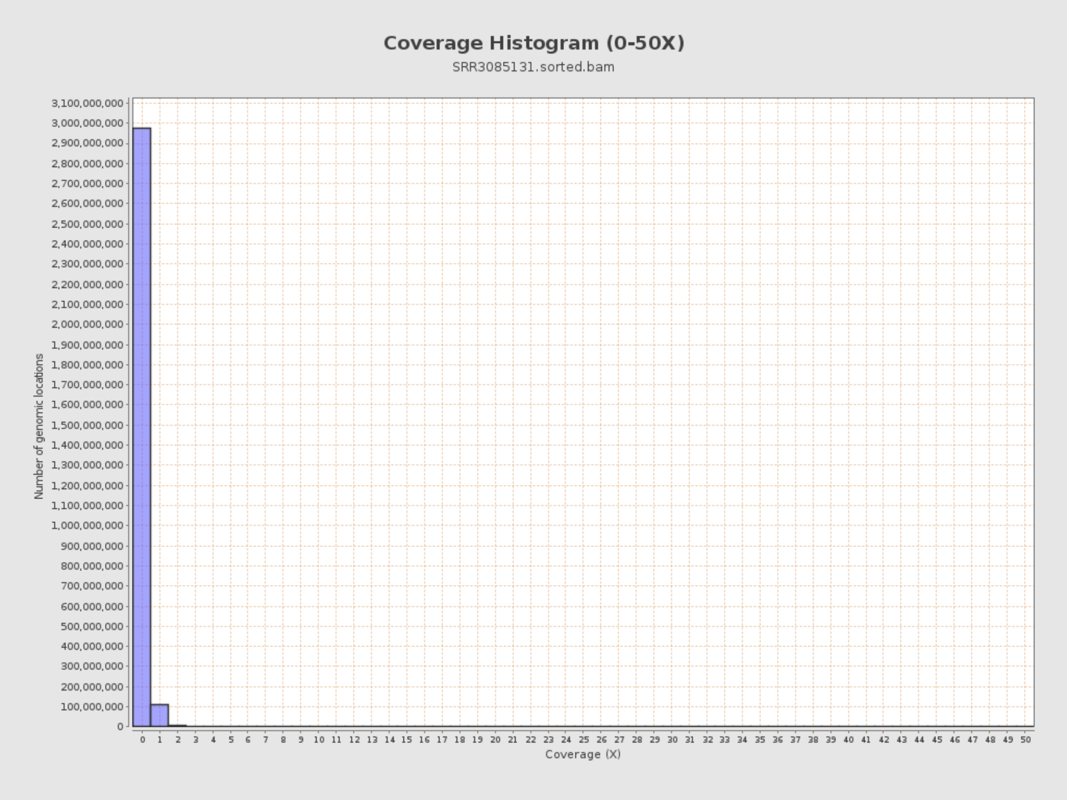
3. Results : Coverage across reference



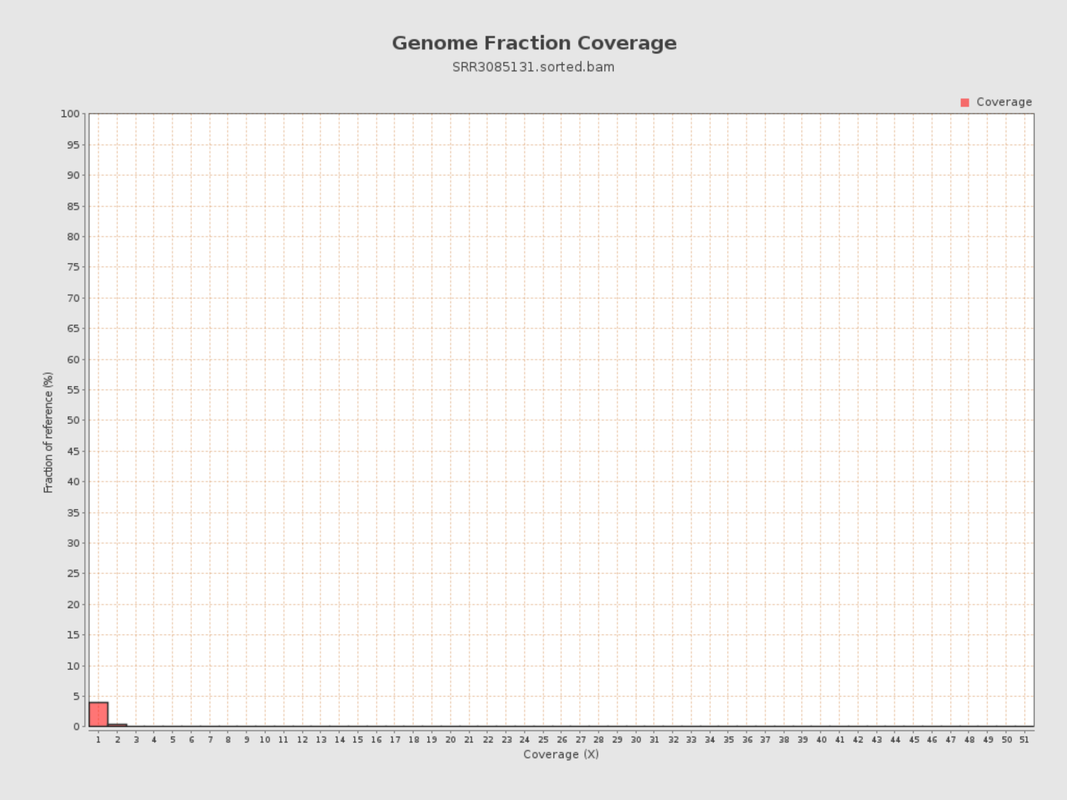
4. Results : Coverage Histogram



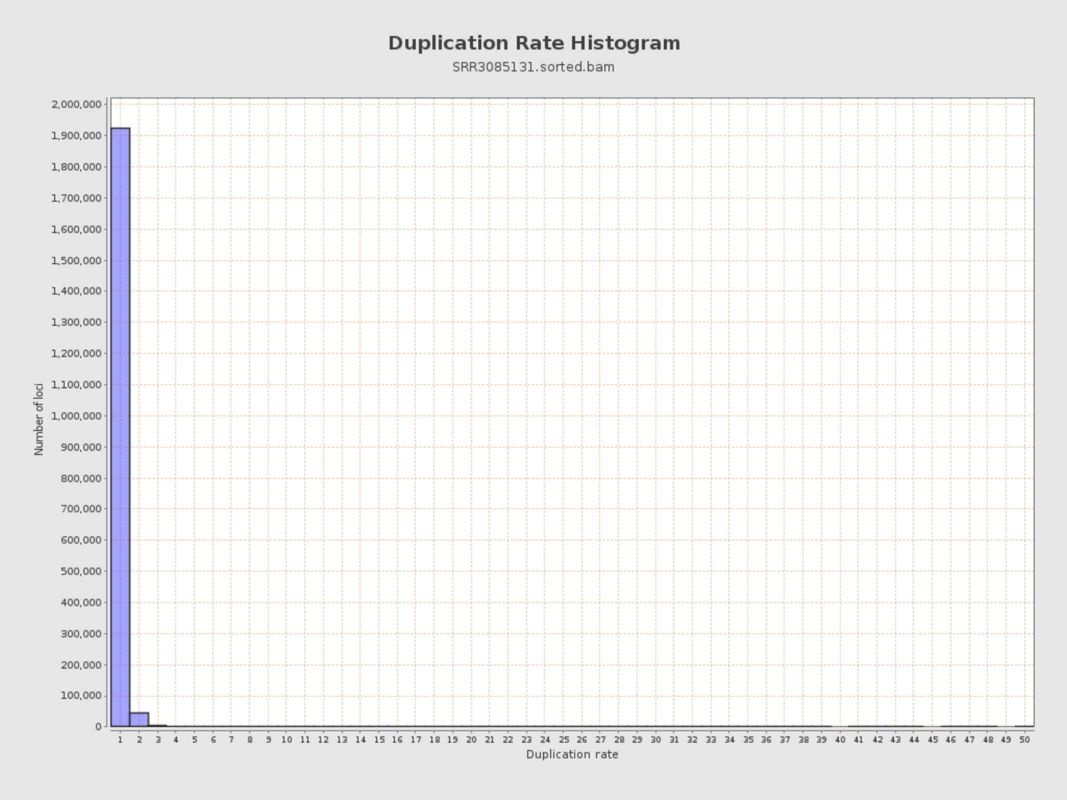
5. Results : Coverage Histogram (0-50X)



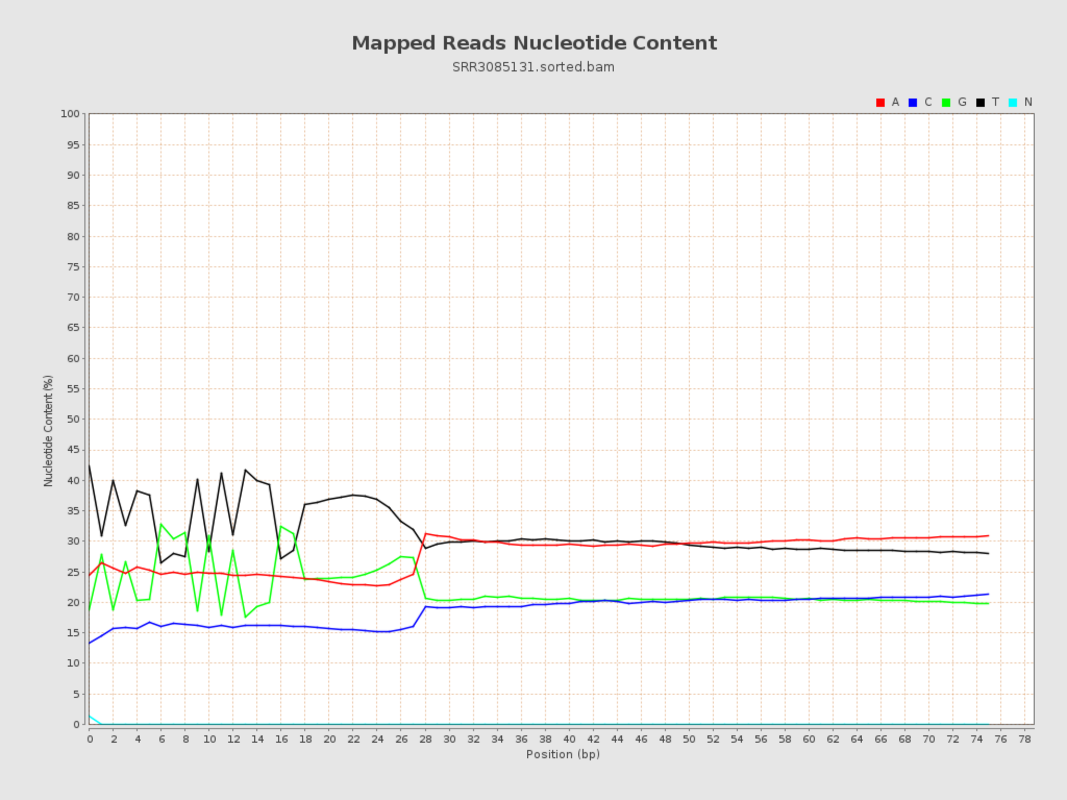
6. Results : Genome Fraction Coverage



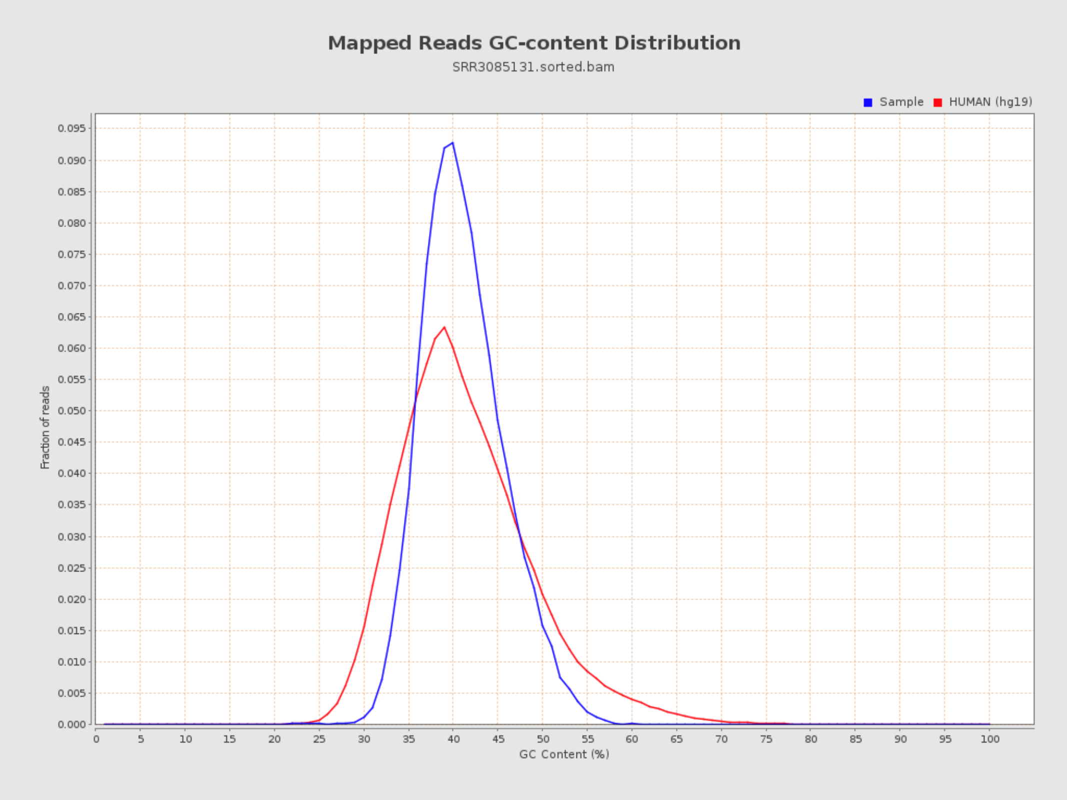
7. Results : Duplication Rate Histogram



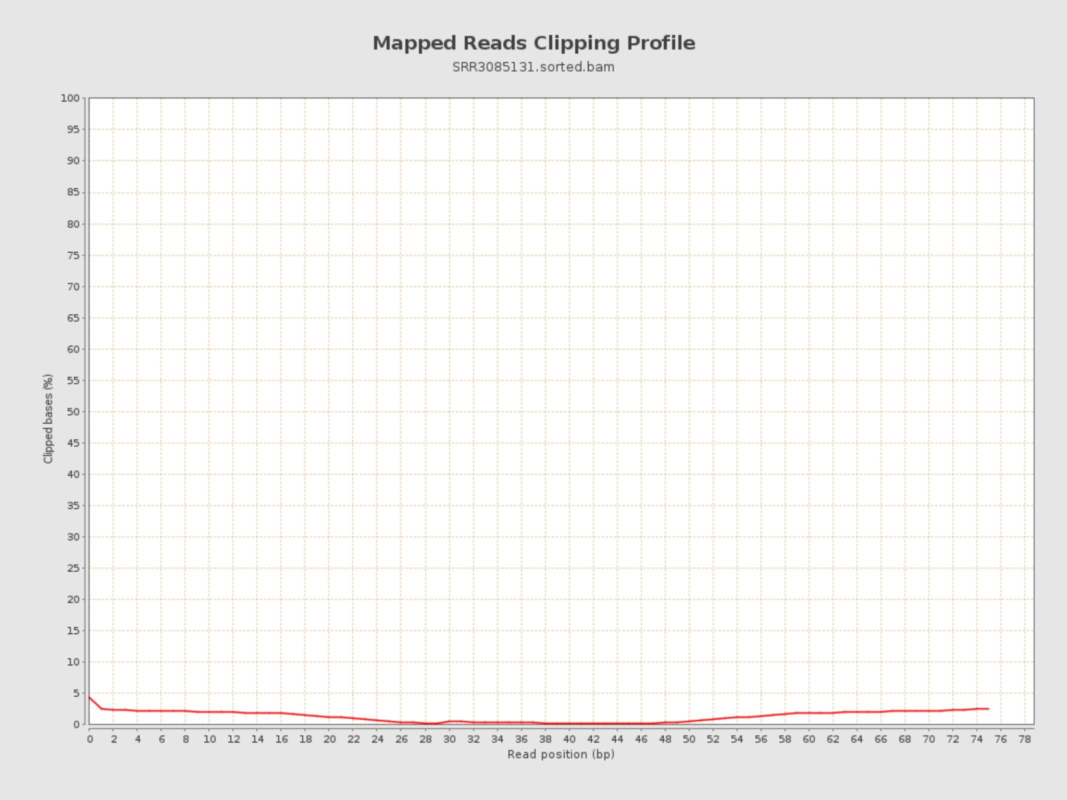
8. Results : Mapped Reads Nucleotide Content



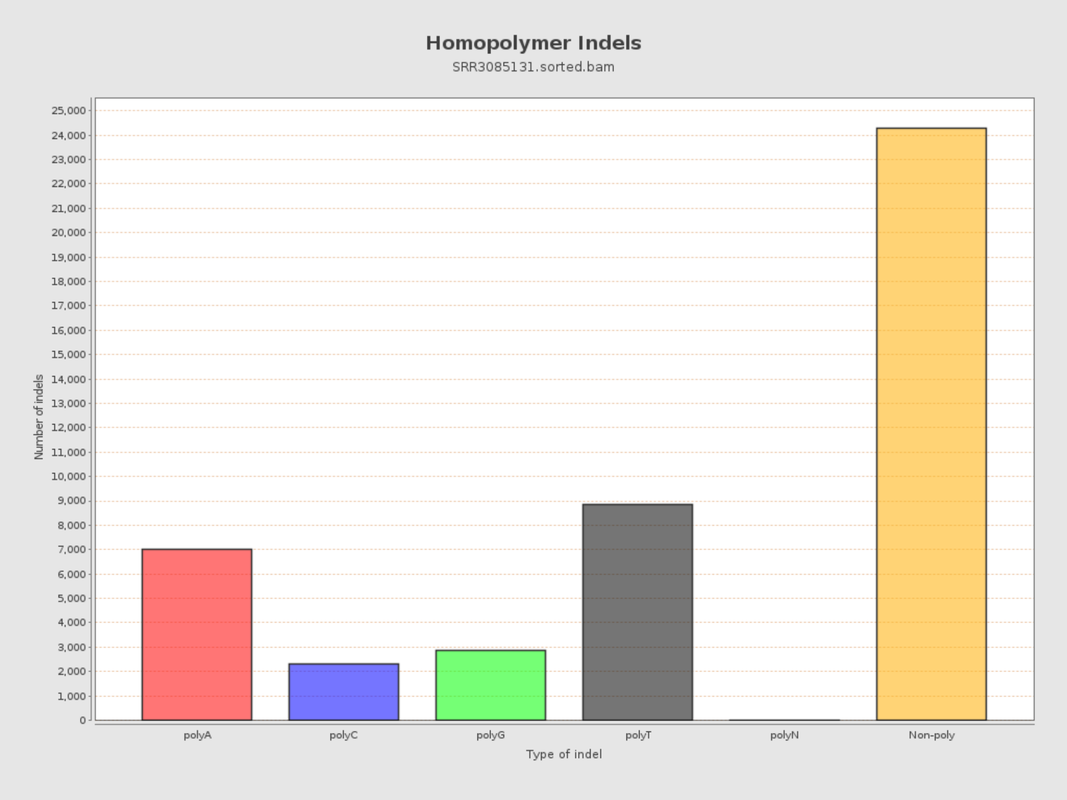
9. Results : Mapped Reads GC-content Distribution



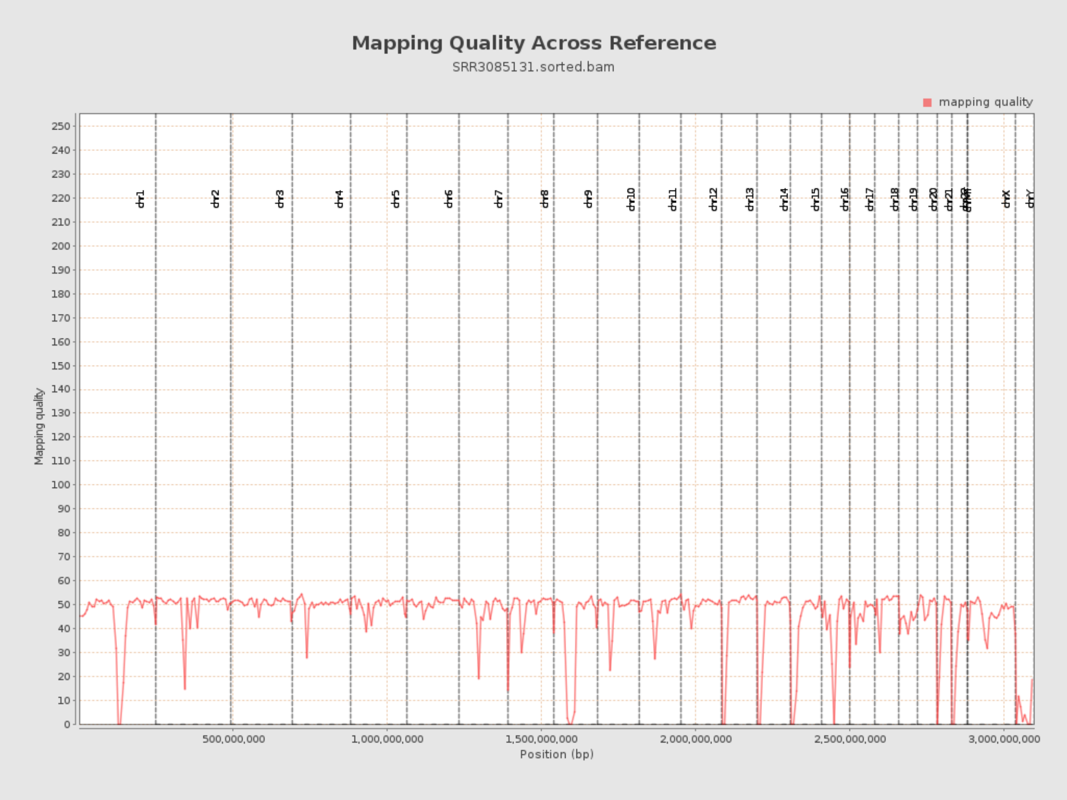
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram