Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:56:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524484.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_SRR10524484 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524484.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:56:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524484.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	889,545
Mapped reads	809,090 / 90.96%
Unmapped reads	80,455 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,905 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	25,576 / 2.88%
Duplication rate	2.47%
Clipped reads	809,180 / 90.97%

2.2. ACGT Content

Number/percentage of A's	11,829,142 / 25.3%
Number/percentage of C's	8,606,481 / 18.41%
Number/percentage of T's	15,109,784 / 32.32%
Number/percentage of G's	11,209,583 / 23.97%
Number/percentage of N's	952 / 0%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1639

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

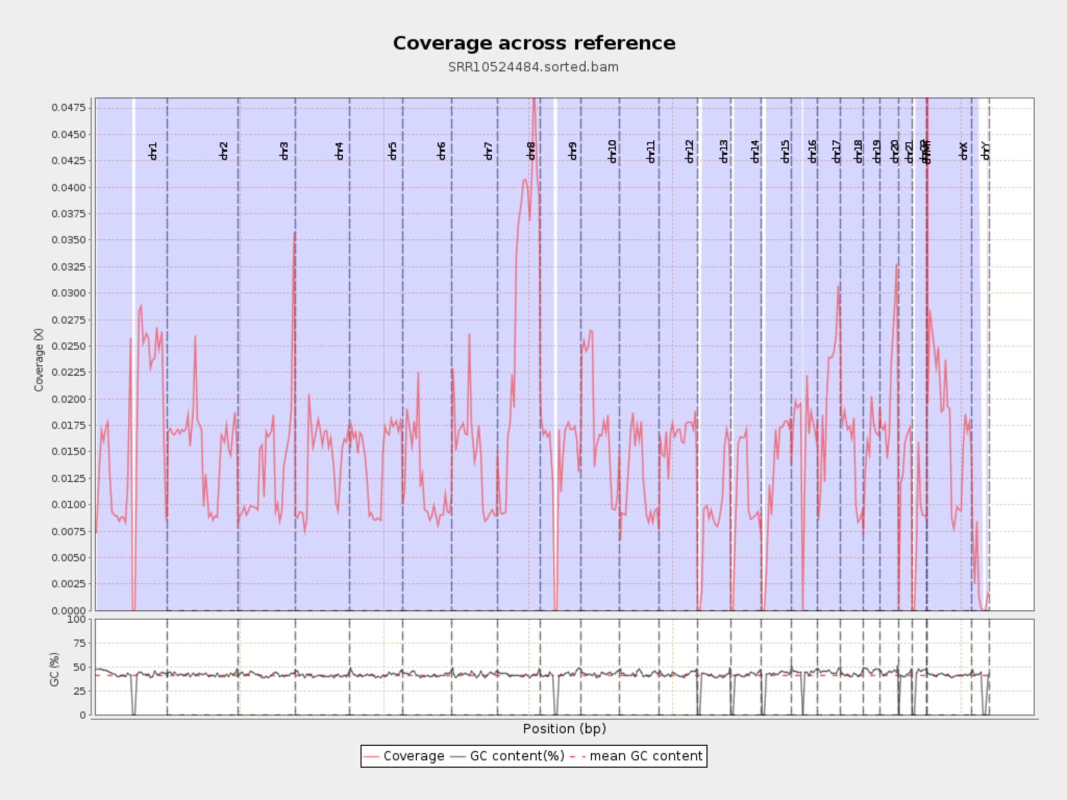
General error rate	0.48%
Mismatches	219,285
Insertions	3,066
Mapped reads with at least one insertion	0.38%
Deletions	8,460
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.56%

2.6. Chromosome stats

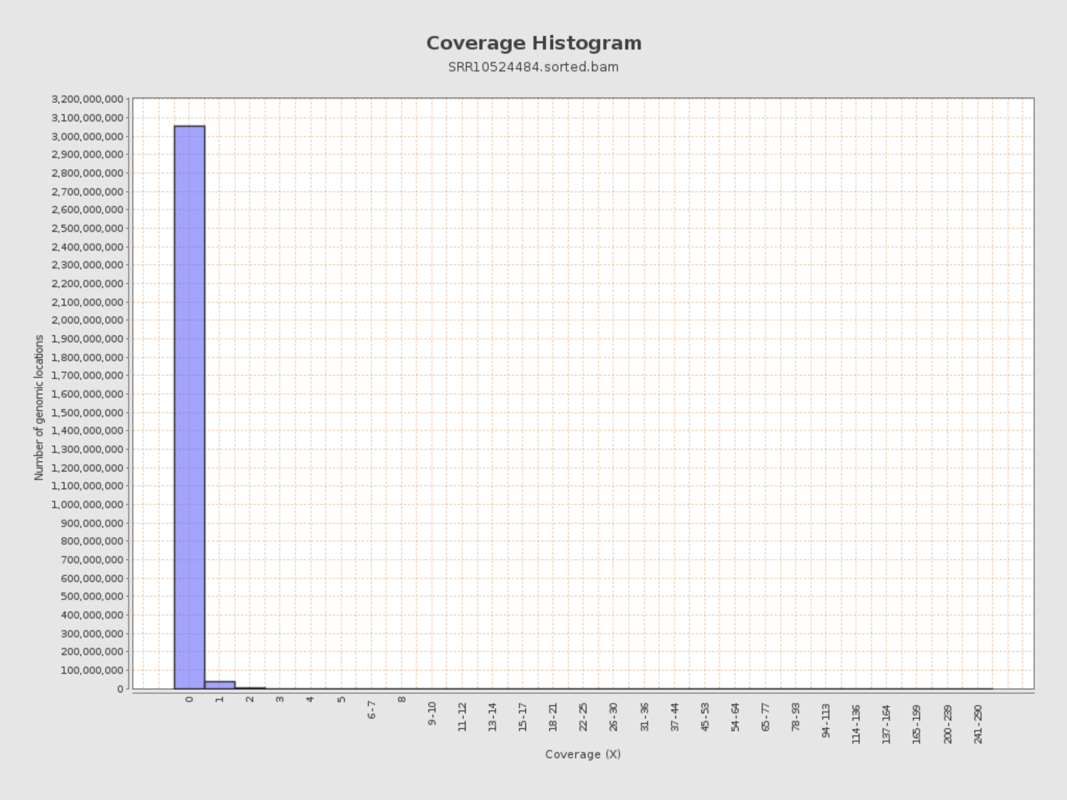
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4073300	0.0163	0.2525
chr2	243199373	3761429	0.0155	0.188
chr3	198022430	2636214	0.0133	0.1231
chr4	191154276	2676613	0.014	0.1348
chr5	180915260	2618837	0.0145	0.1283
chr6	171115067	2069253	0.0121	0.1339
chr7	159138663	2354402	0.0148	0.2026

chr8	146364022	4261689	0.0291	0.1978
chr9	141213431	2019792	0.0143	0.1508
chr10	135534747	2460855	0.0182	0.1656
chr11	135006516	1642808	0.0122	0.1559
chr12	133851895	2209713	0.0165	0.1377
chr13	115169878	1052471	0.0091	0.1029
chr14	107349540	1106552	0.0103	0.1097
chr15	102531392	1265912	0.0123	0.124
chr16	90354753	1472419	0.0163	0.1392
chr17	81195210	1651077	0.0203	0.1565
chr18	78077248	1136144	0.0146	0.2324
chr19	59128983	955160	0.0162	0.1995
chr20	63025520	1342753	0.0213	0.1562
chr21	48129895	650522	0.0135	0.127
chr22	51304566	399394	0.0078	0.0939
chrMT	16571	4809	0.2902	0.6133
chrX	155270560	2796781	0.018	0.1523
chrY	59373566	151517	0.0026	0.0756

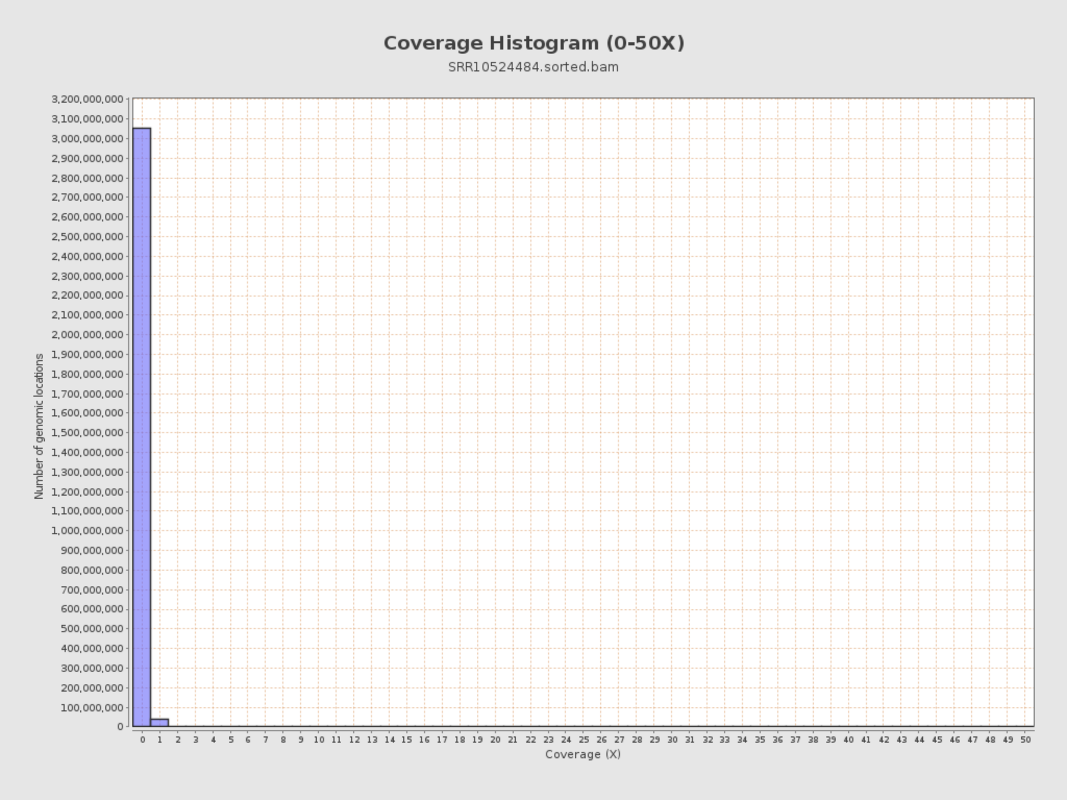
3. Results : Coverage across reference



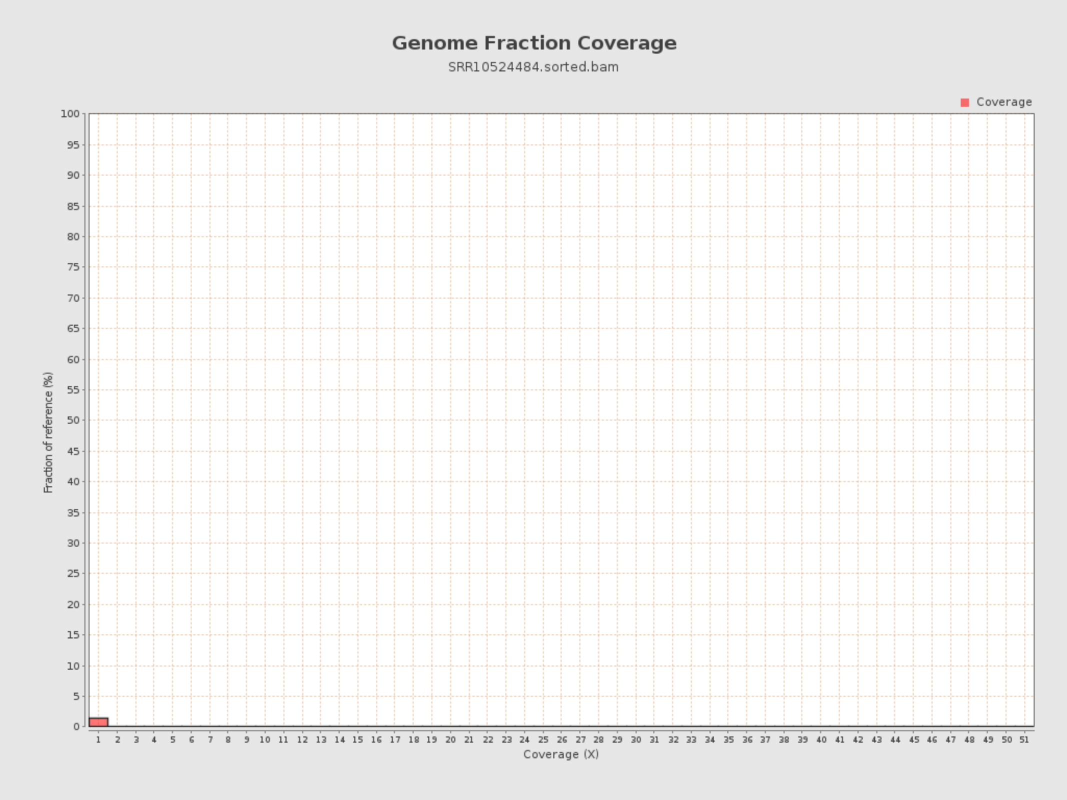
4. Results : Coverage Histogram



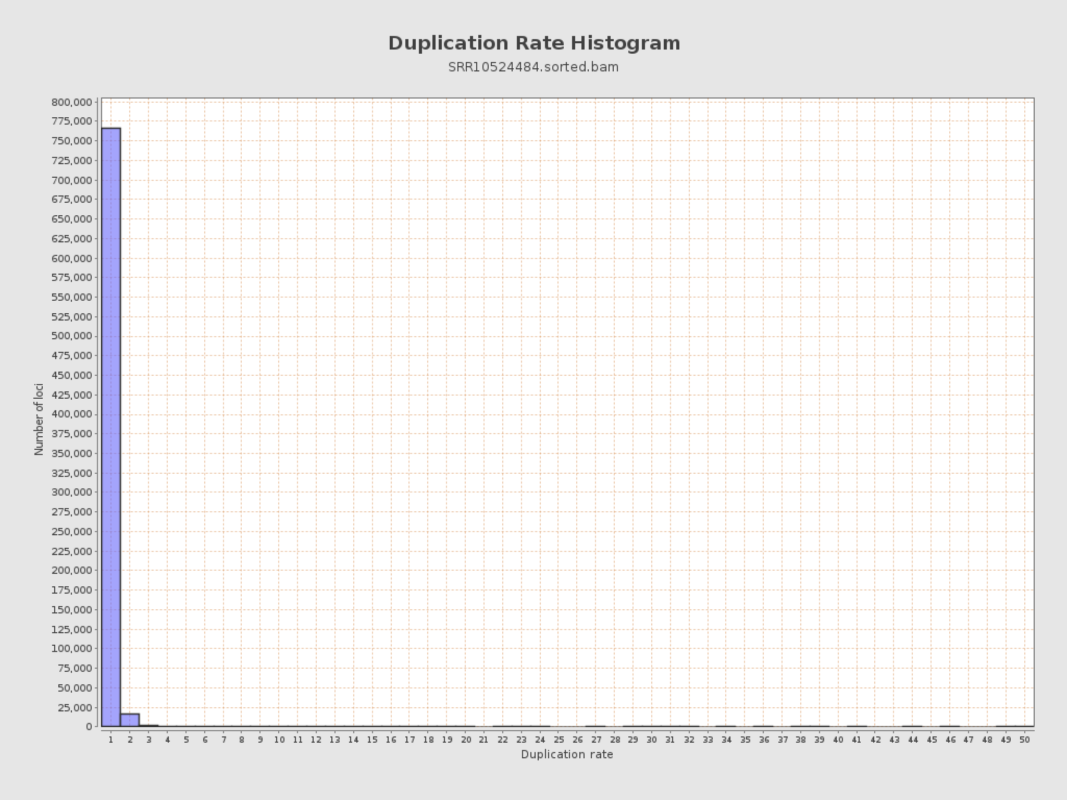
5. Results : Coverage Histogram (0-50X)



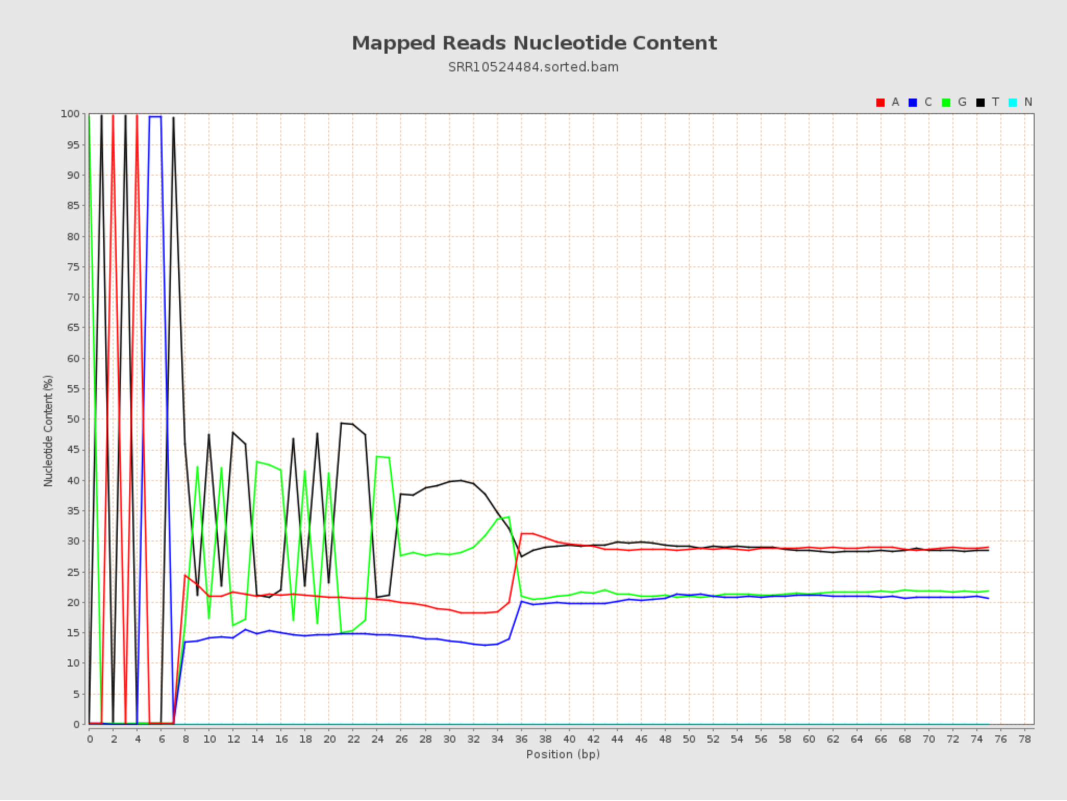
6. Results : Genome Fraction Coverage



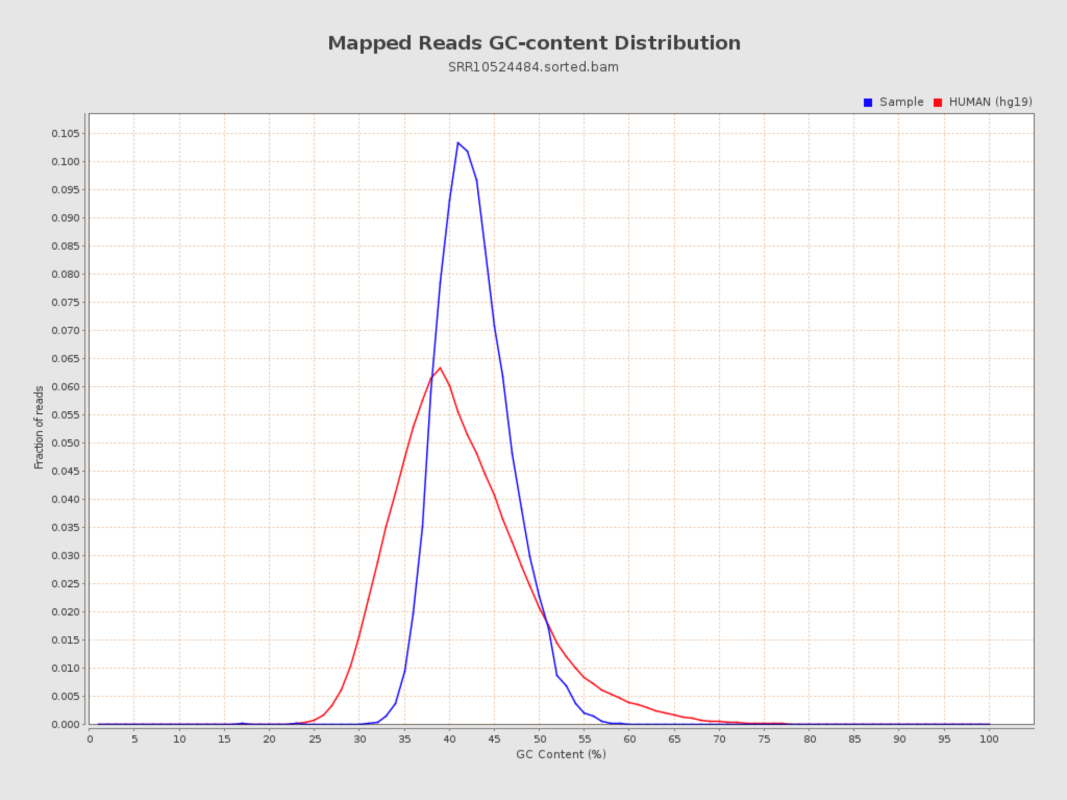
7. Results : Duplication Rate Histogram



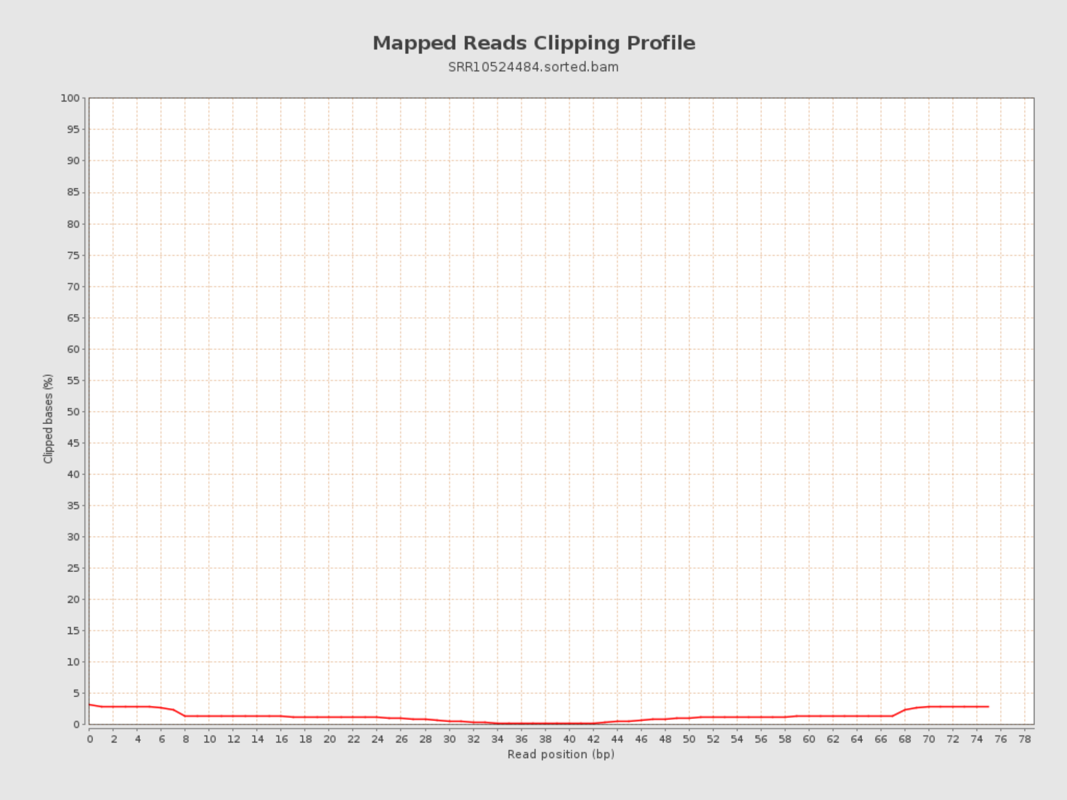
8. Results : Mapped Reads Nucleotide Content



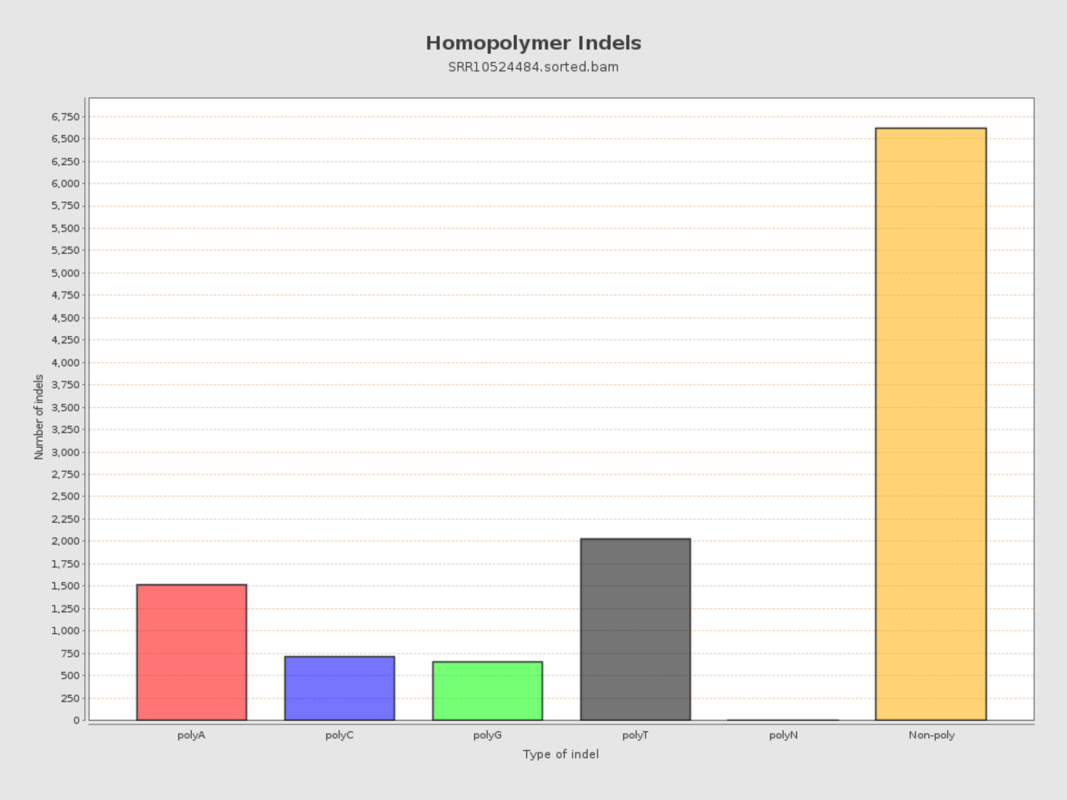
9. Results : Mapped Reads GC-content Distribution



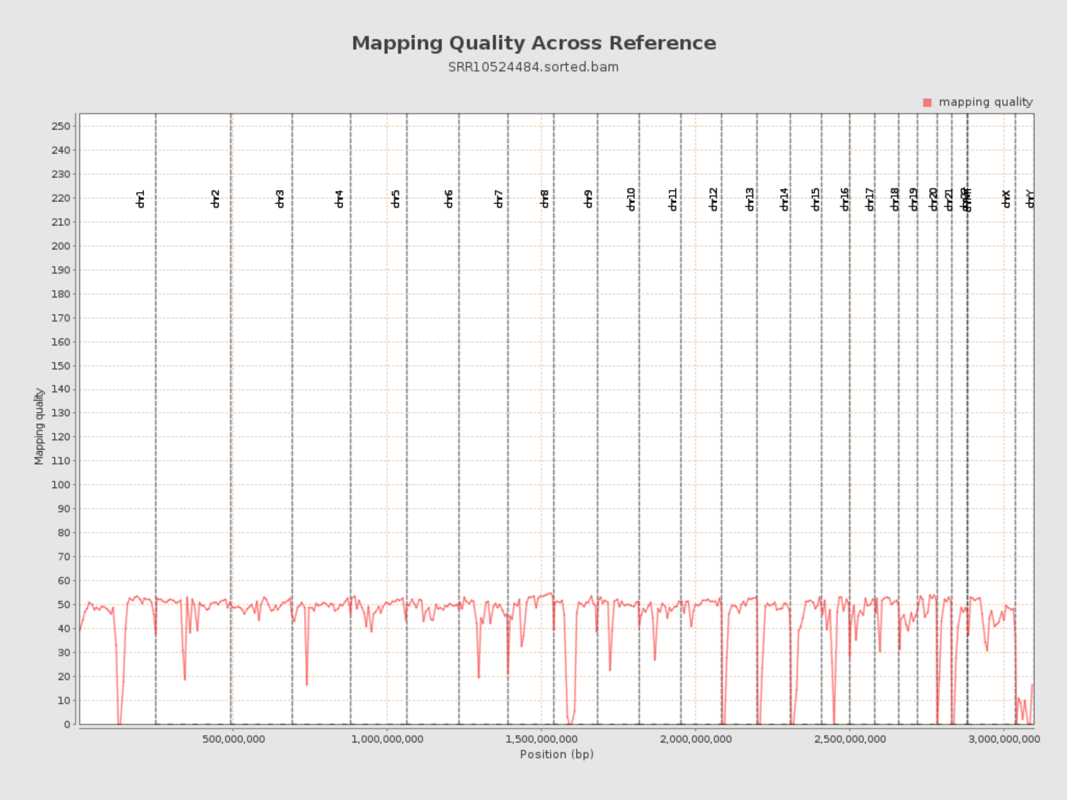
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram