Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:22:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524407.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_SRR10524407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524407.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:22:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	541,821
Mapped reads	507,121 / 93.6%
Unmapped reads	34,700 / 6.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,344 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	8,969 / 1.66%
Duplication rate	1.26%
Clipped reads	508,280 / 93.81%

2.2. ACGT Content

Number/percentage of A's	8,109,044 / 26.22%
Number/percentage of C's	6,007,577 / 19.42%
Number/percentage of T's	9,528,447 / 30.81%
Number/percentage of G's	7,281,272 / 23.54%
Number/percentage of N's	4,413 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	0.01

Standard Deviation	0.1346

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

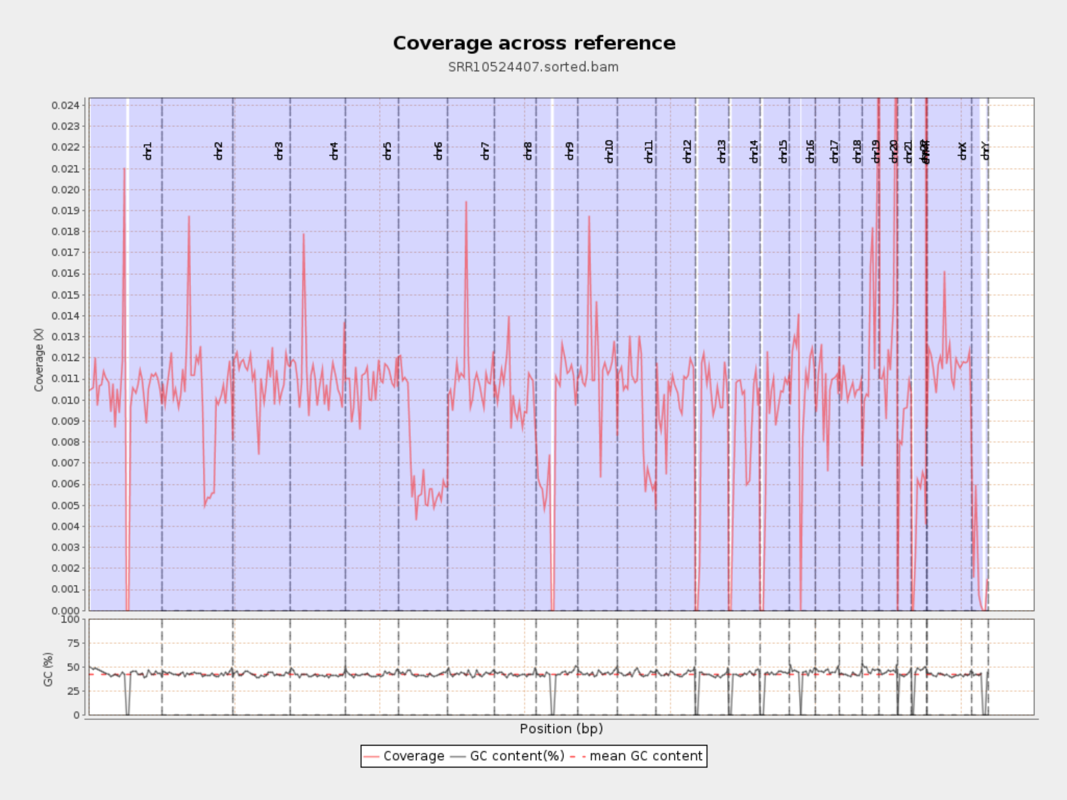
General error rate	0.49%
Mismatches	145,752
Insertions	2,321
Mapped reads with at least one insertion	0.46%
Deletions	5,420
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.61%

2.6. Chromosome stats

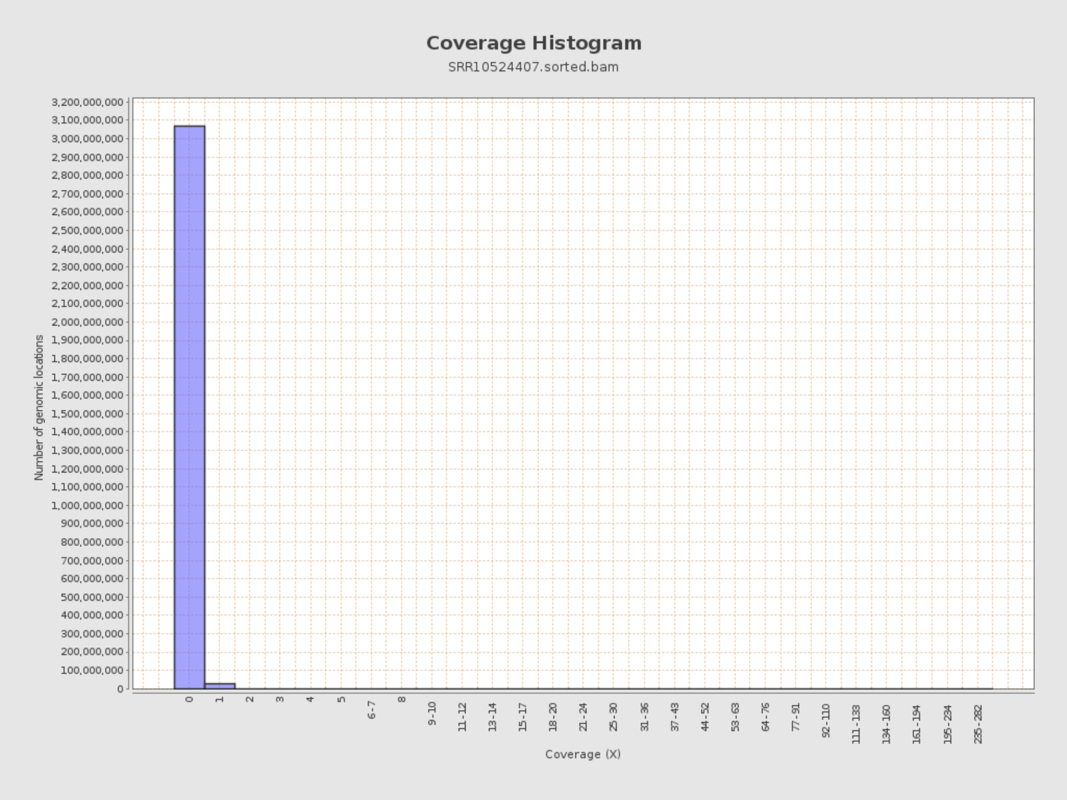
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2550834	0.0102	0.2551
chr2	243199373	2492313	0.0102	0.1301
chr3	198022430	2185127	0.011	0.1081
chr4	191154276	2129209	0.0111	0.1158
chr5	180915260	1952693	0.0108	0.1073
chr6	171115067	1180614	0.0069	0.0876
chr7	159138663	1782589	0.0112	0.1721

chr8	146364022	1514888	0.0104	0.1316
chr9	141213431	1163415	0.0082	0.106
chr10	135534747	1587489	0.0117	0.1294
chr11	135006516	1293206	0.0096	0.1184
chr12	133851895	1376004	0.0103	0.1061
chr13	115169878	1028329	0.0089	0.0975
chr14	107349540	868641	0.0081	0.094
chr15	102531392	876458	0.0085	0.0954
chr16	90354753	967177	0.0107	0.1081
chr17	81195210	836485	0.0103	0.1103
chr18	78077248	832095	0.0107	0.1587
chr19	59128983	862249	0.0146	0.1797
chr20	63025520	895791	0.0142	0.1249
chr21	48129895	407691	0.0085	0.1014
chr22	51304566	219629	0.0043	0.0672
chrMT	16571	7717	0.4657	0.75
chrX	155270560	1830695	0.0118	0.1168
chrY	59373566	98320	0.0017	0.0597

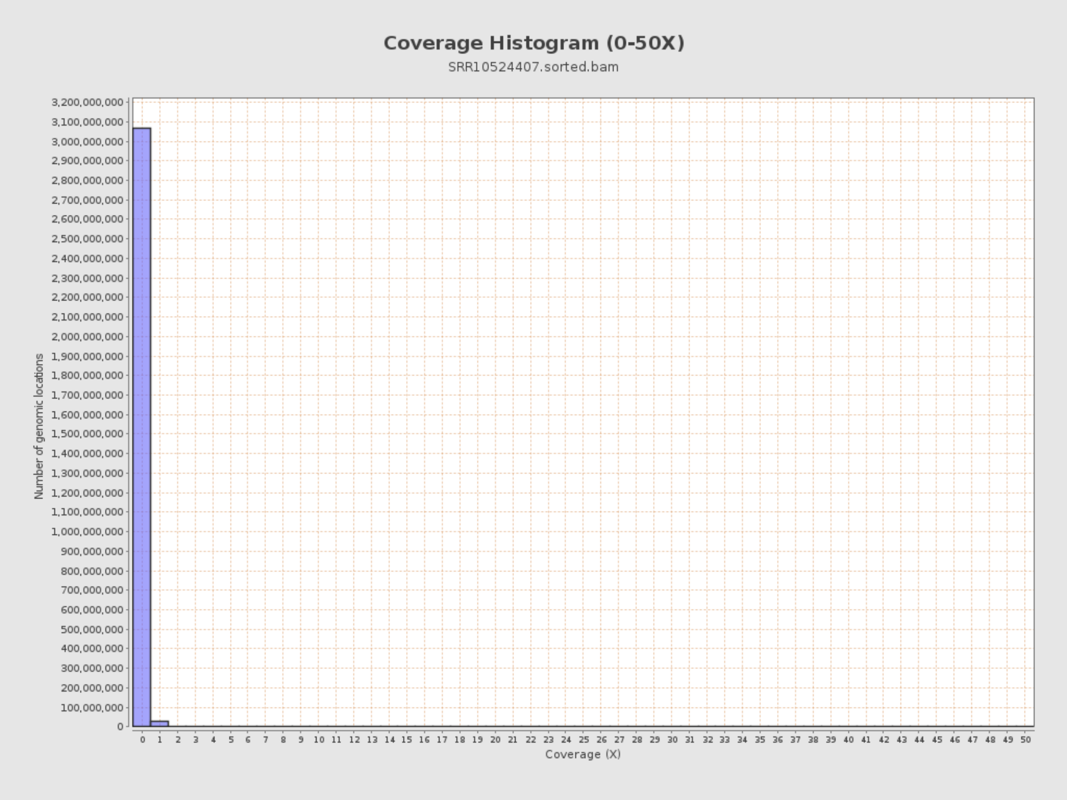
3. Results : Coverage across reference



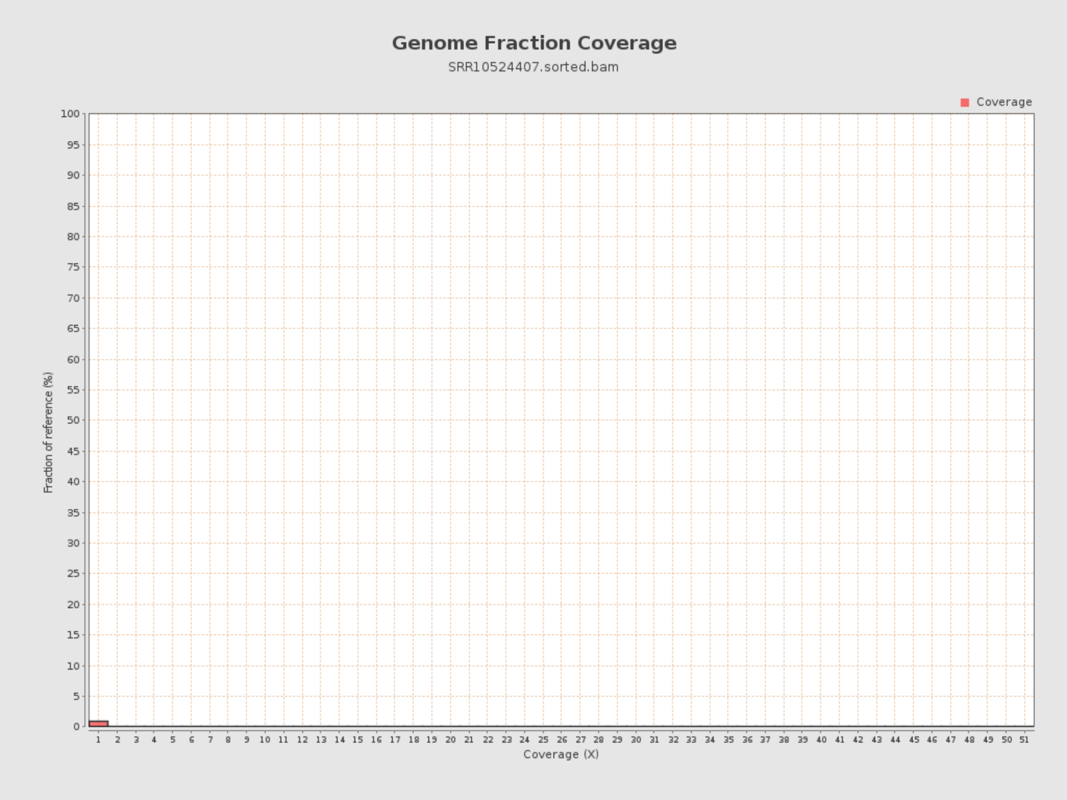
4. Results : Coverage Histogram



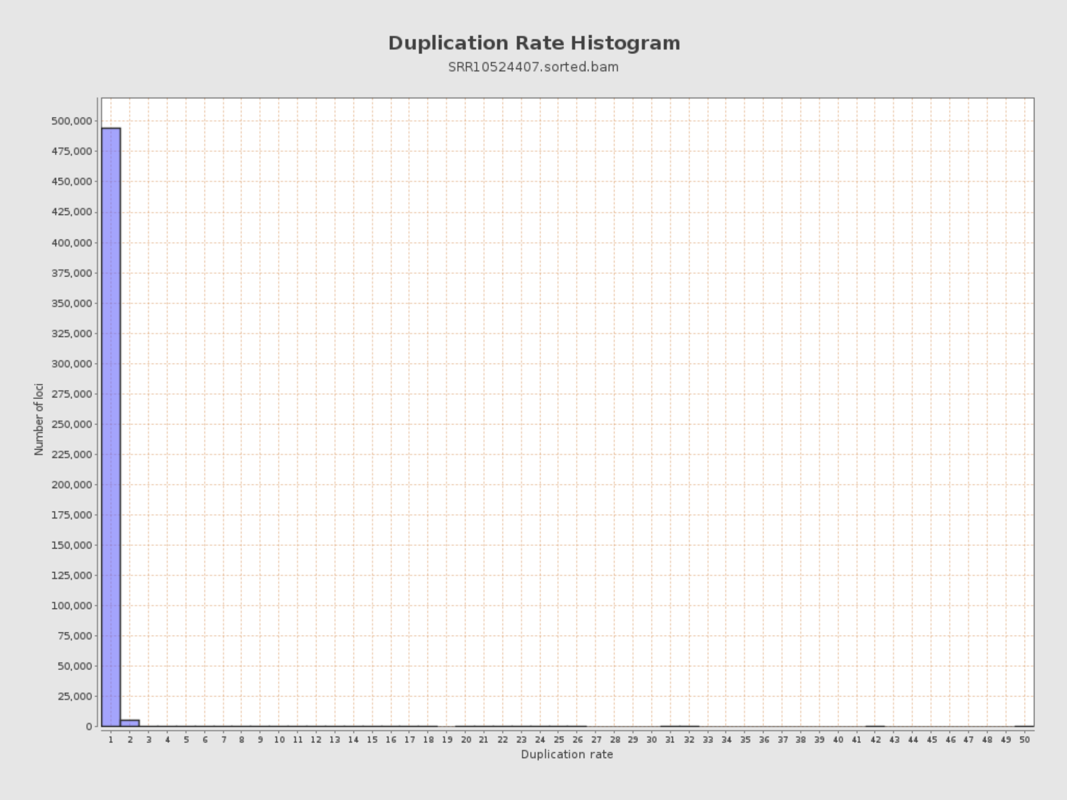
5. Results : Coverage Histogram (0-50X)



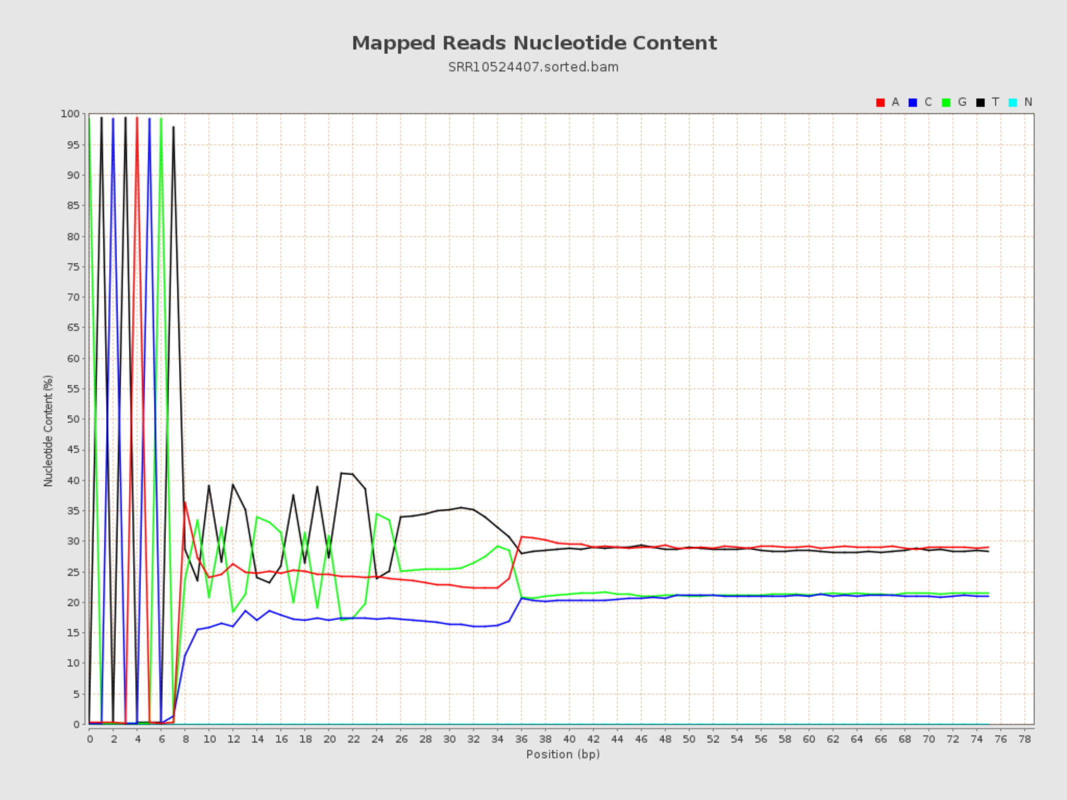
6. Results : Genome Fraction Coverage



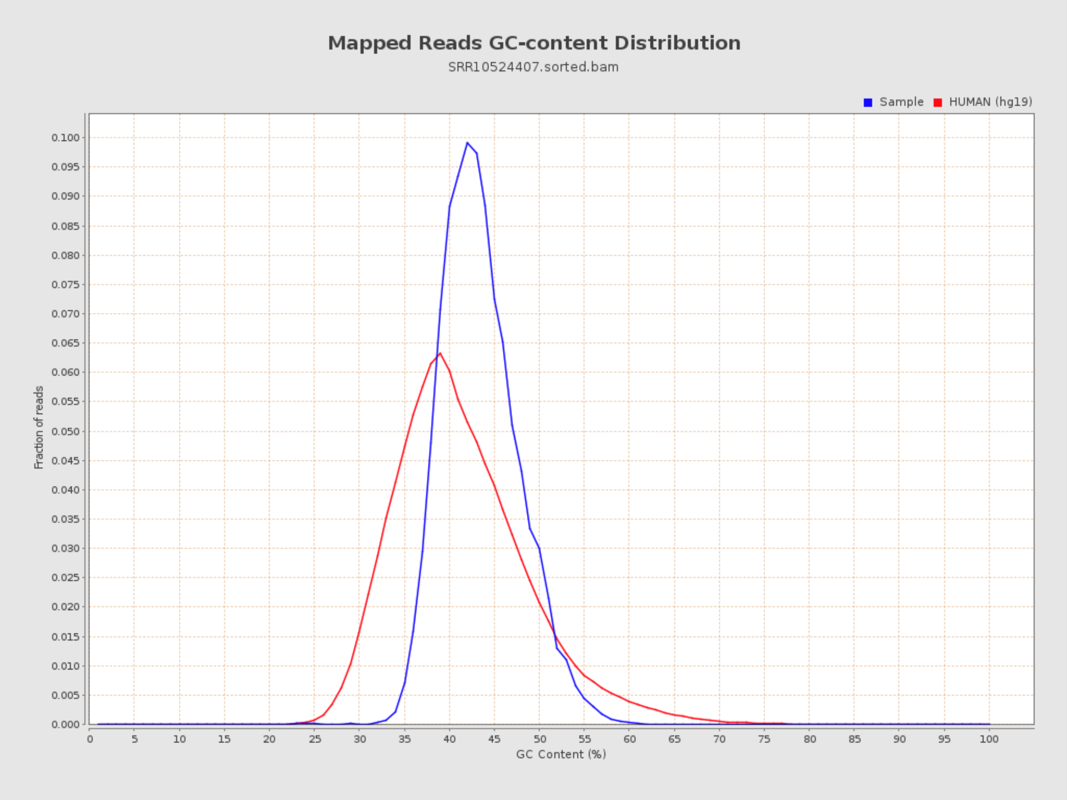
7. Results : Duplication Rate Histogram



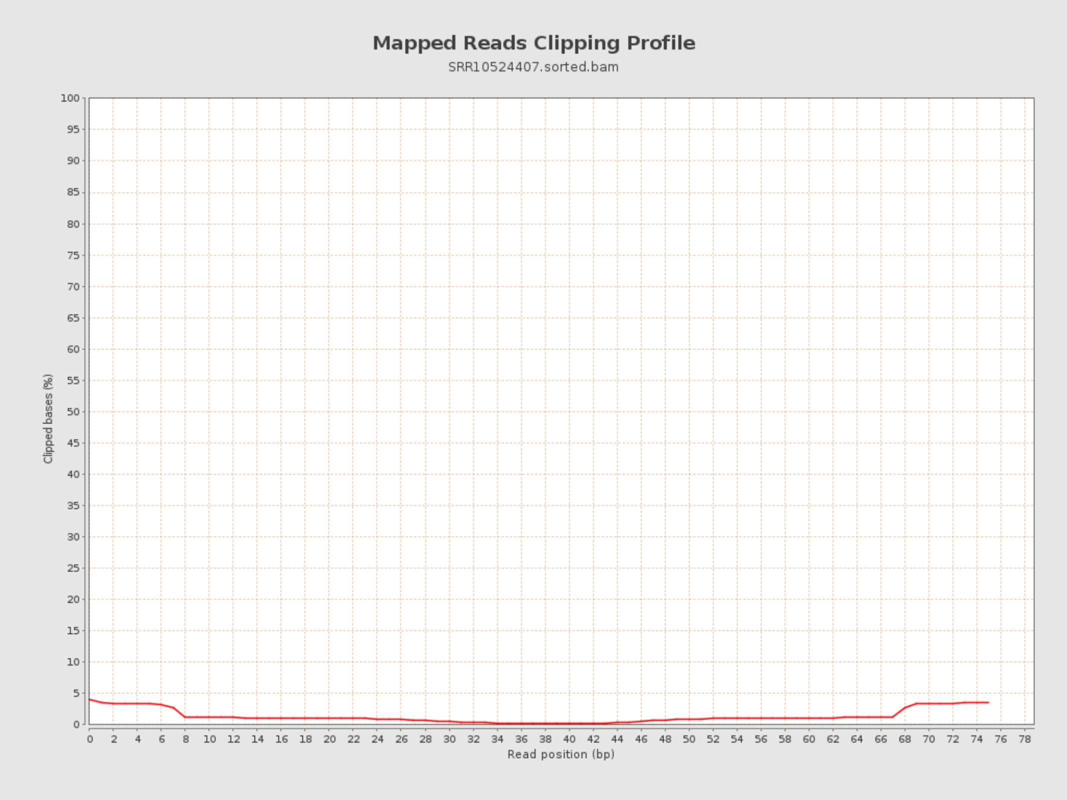
8. Results : Mapped Reads Nucleotide Content



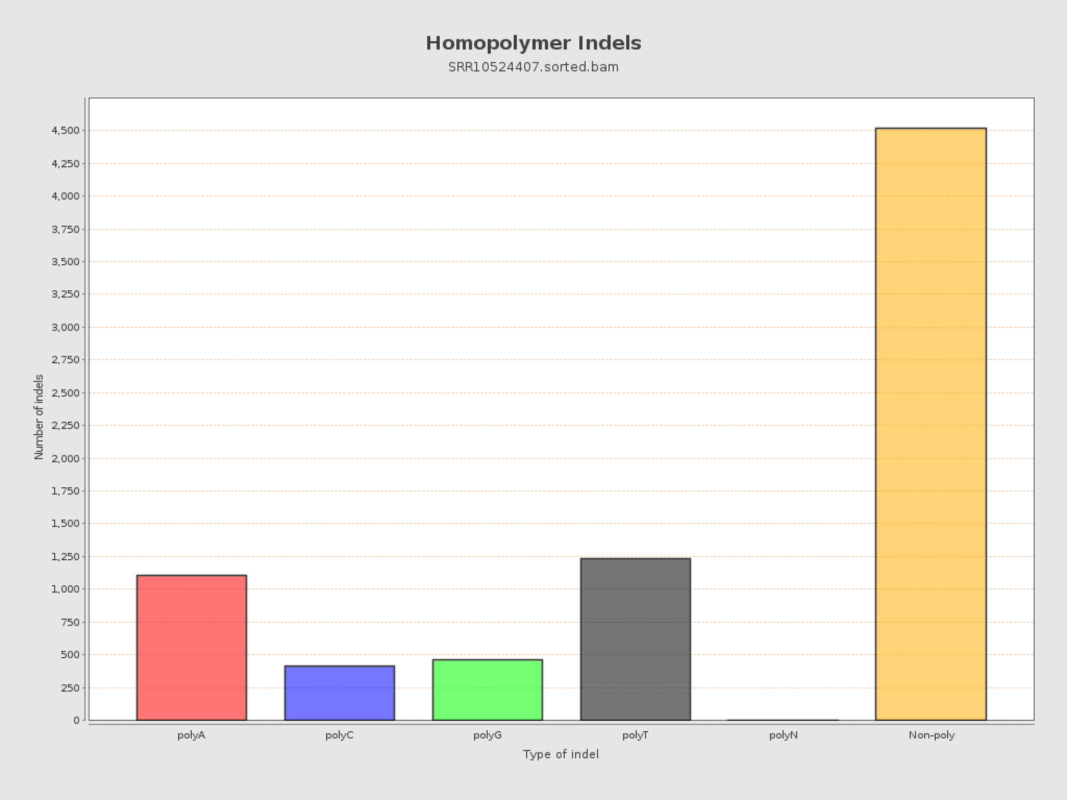
9. Results : Mapped Reads GC-content Distribution



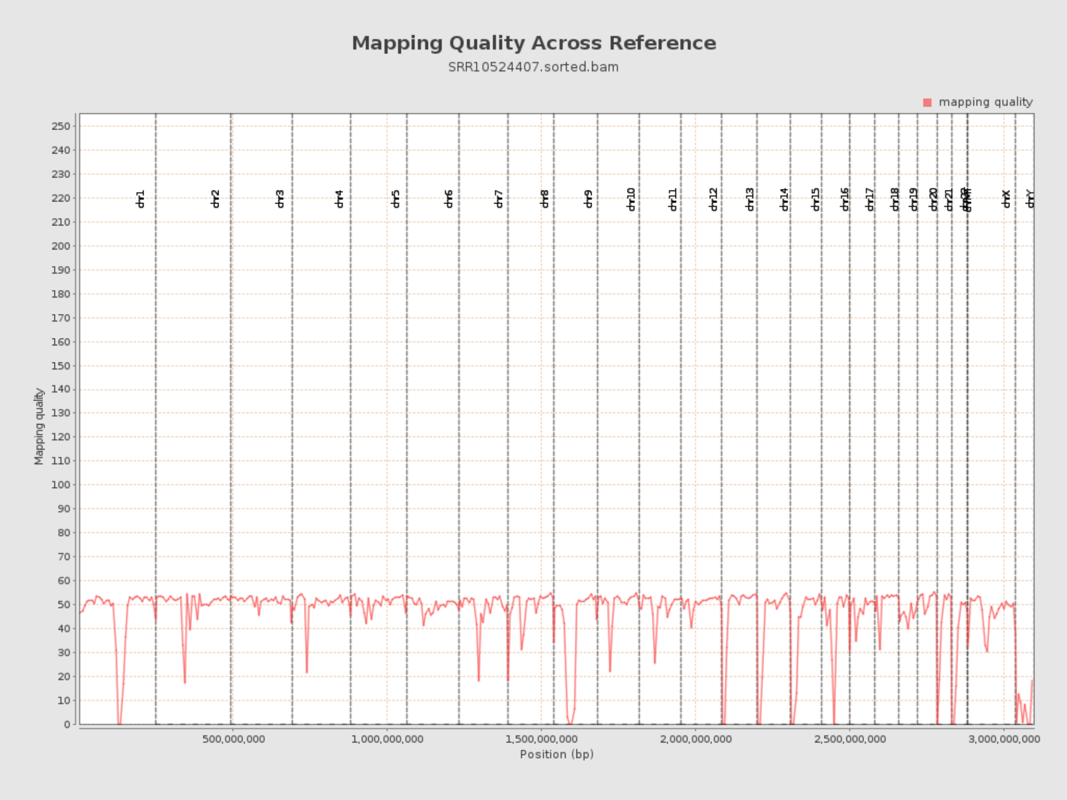
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram