Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:14:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524493.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_SRR10524493 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524493.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:14:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524493.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	559,264
Mapped reads	513,143 / 91.75%
Unmapped reads	46,121 / 8.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,217 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	16,448 / 2.94%
Duplication rate	2.66%
Clipped reads	514,105 / 91.93%

2.2. ACGT Content

Number/percentage of A's	7,176,586 / 24.21%
Number/percentage of C's	5,743,474 / 19.38%
Number/percentage of T's	9,299,283 / 31.38%
Number/percentage of G's	7,418,265 / 25.03%
Number/percentage of N's	640 / 0%
GC Percentage	44.41%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1198

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

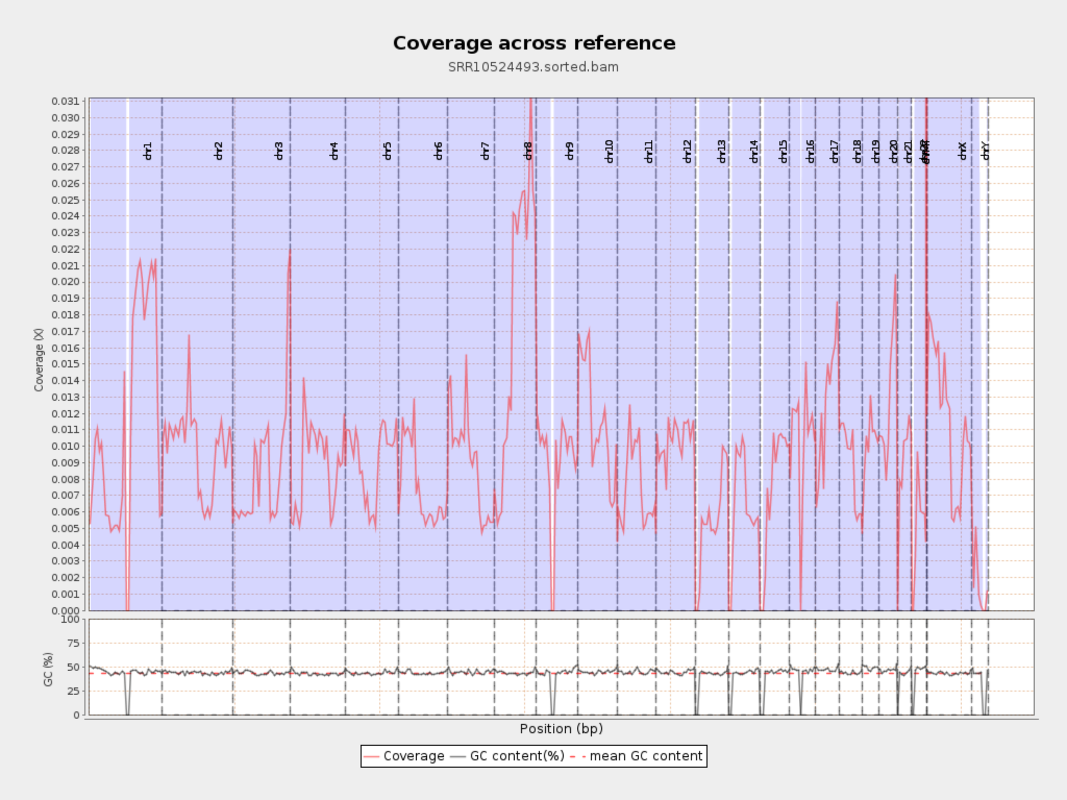
General error rate	0.48%
Mismatches	140,087
Insertions	1,519
Mapped reads with at least one insertion	0.29%
Deletions	5,538
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.94%

2.6. Chromosome stats

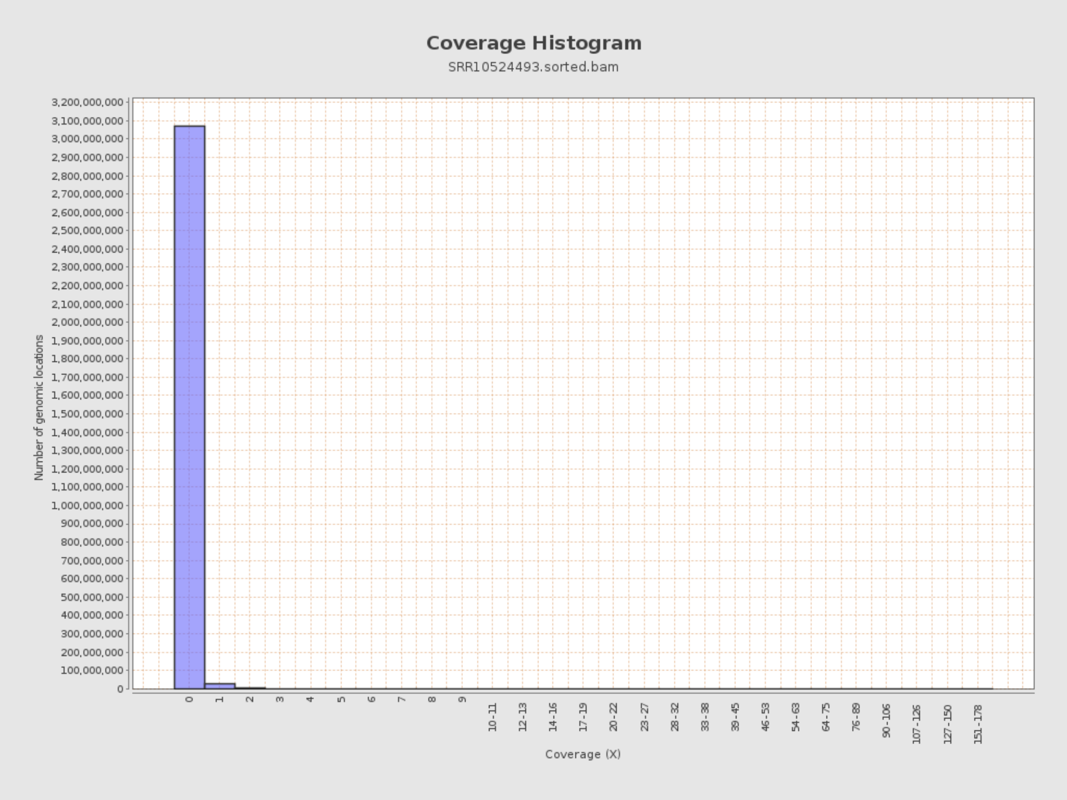
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2862494	0.0115	0.163
chr2	243199373	2412632	0.0099	0.1382
chr3	198022430	1652784	0.0083	0.0975
chr4	191154276	1681857	0.0088	0.1059
chr5	180915260	1661607	0.0092	0.1022
chr6	171115067	1280299	0.0075	0.1002
chr7	159138663	1438965	0.009	0.14

chr8	146364022	2657191	0.0182	0.1526
chr9	141213431	1246910	0.0088	0.1119
chr10	135534747	1583636	0.0117	0.1293
chr11	135006516	1009609	0.0075	0.109
chr12	133851895	1394309	0.0104	0.109
chr13	115169878	629896	0.0055	0.0788
chr14	107349540	677811	0.0063	0.0857
chr15	102531392	761863	0.0074	0.0948
chr16	90354753	945083	0.0105	0.1109
chr17	81195210	1036062	0.0128	0.1232
chr18	78077248	700554	0.009	0.1485
chr19	59128983	606886	0.0103	0.1316
chr20	63025520	823855	0.0131	0.1228
chr21	48129895	425145	0.0088	0.1038
chr22	51304566	246333	0.0048	0.0733
chrMT	16571	10060	0.6071	0.908
chrX	155270560	1811205	0.0117	0.1211
chrY	59373566	90904	0.0015	0.0532

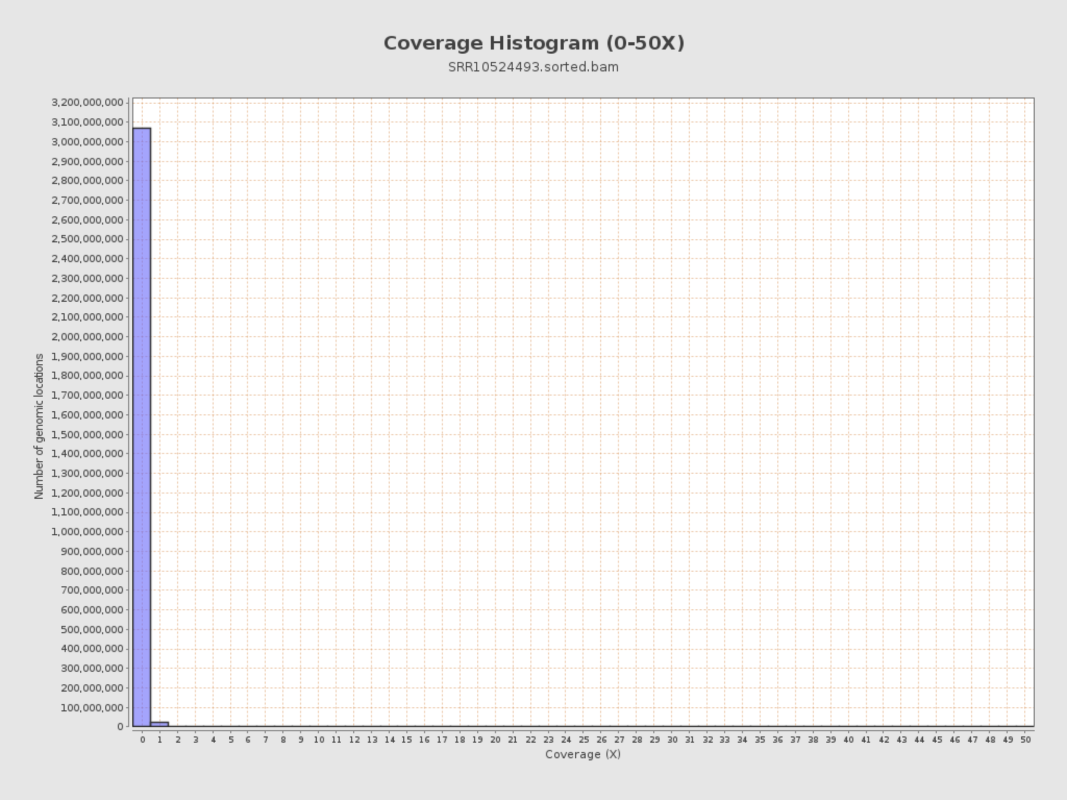
3. Results : Coverage across reference



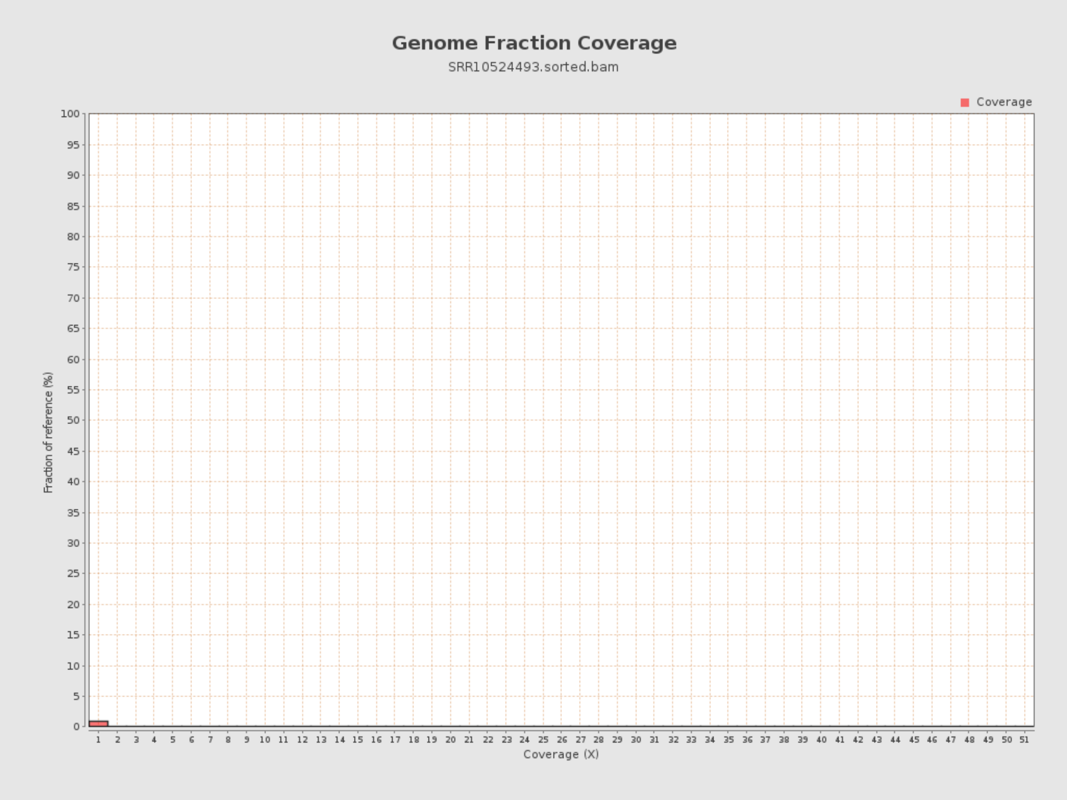
4. Results : Coverage Histogram



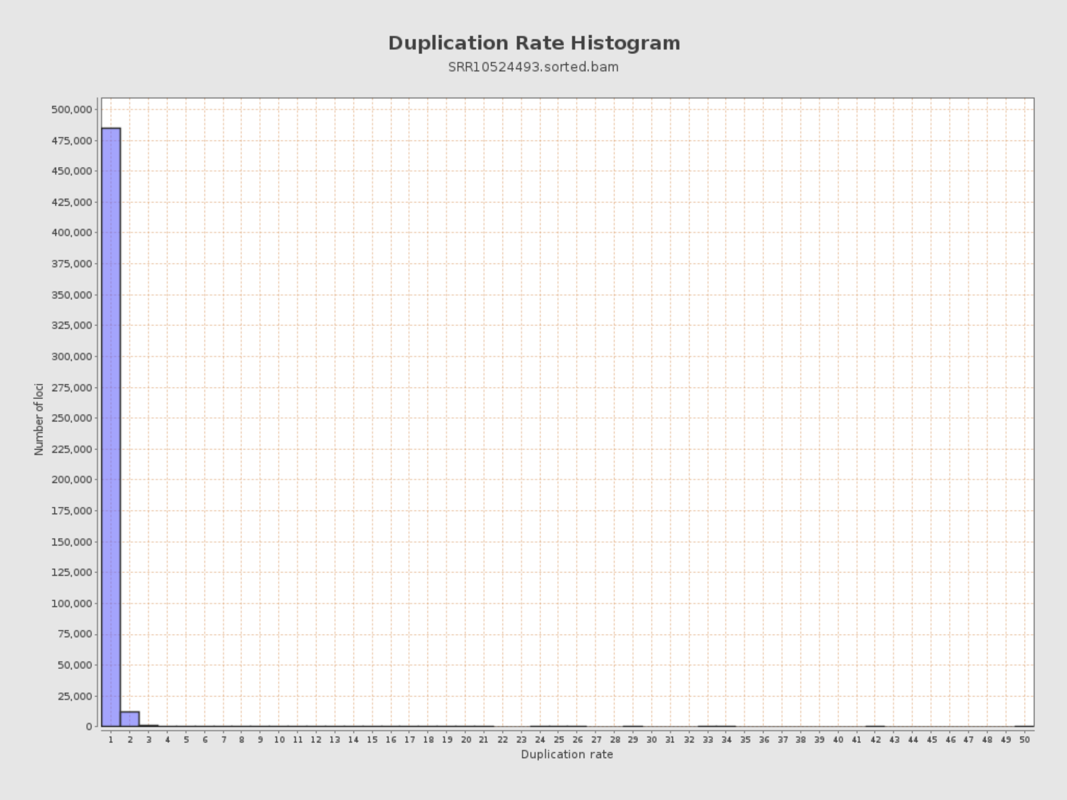
5. Results : Coverage Histogram (0-50X)



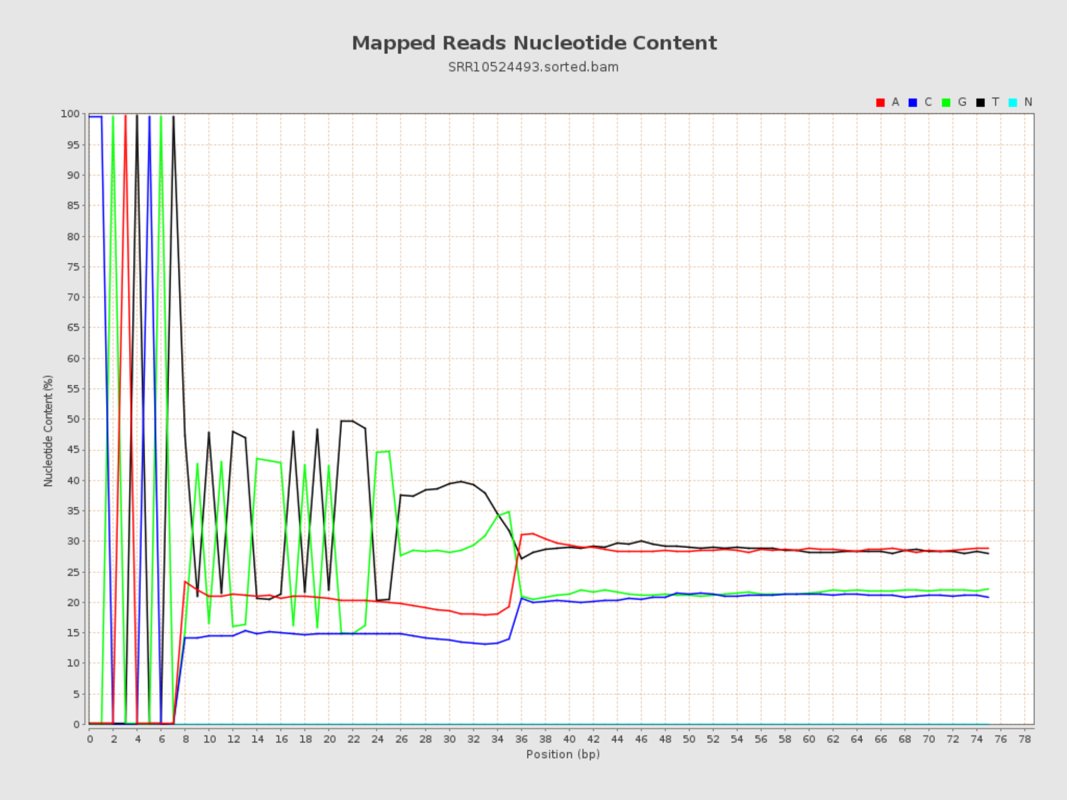
6. Results : Genome Fraction Coverage



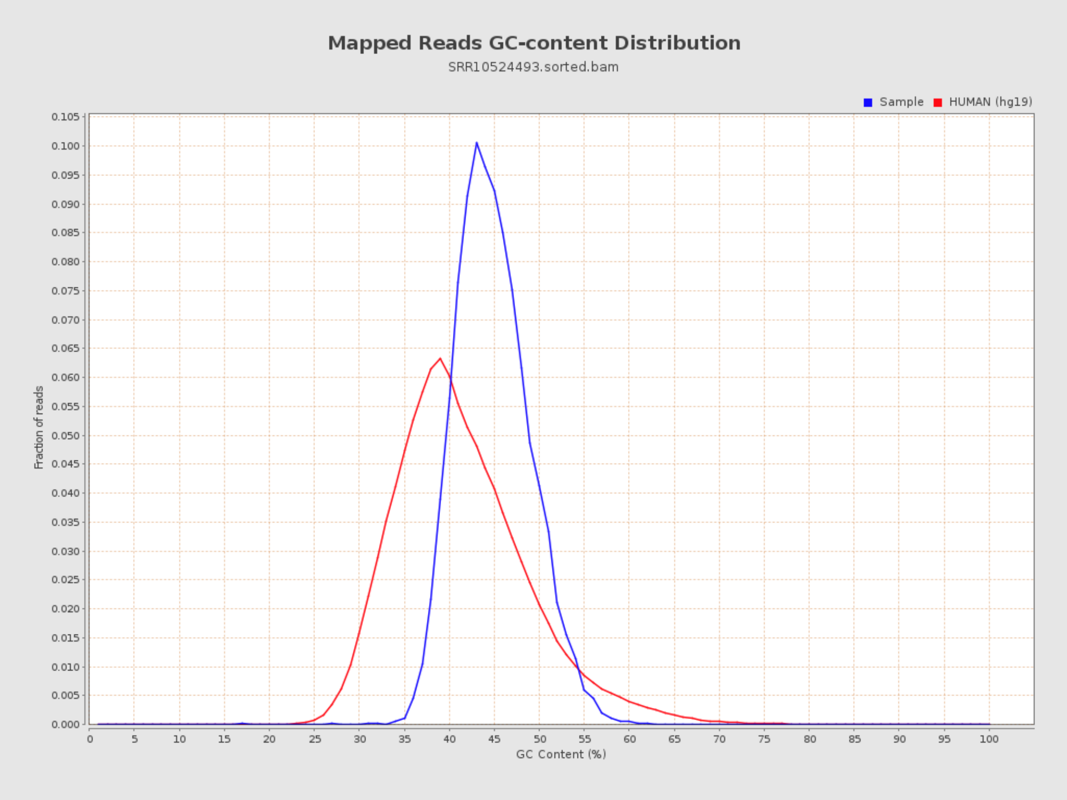
7. Results : Duplication Rate Histogram



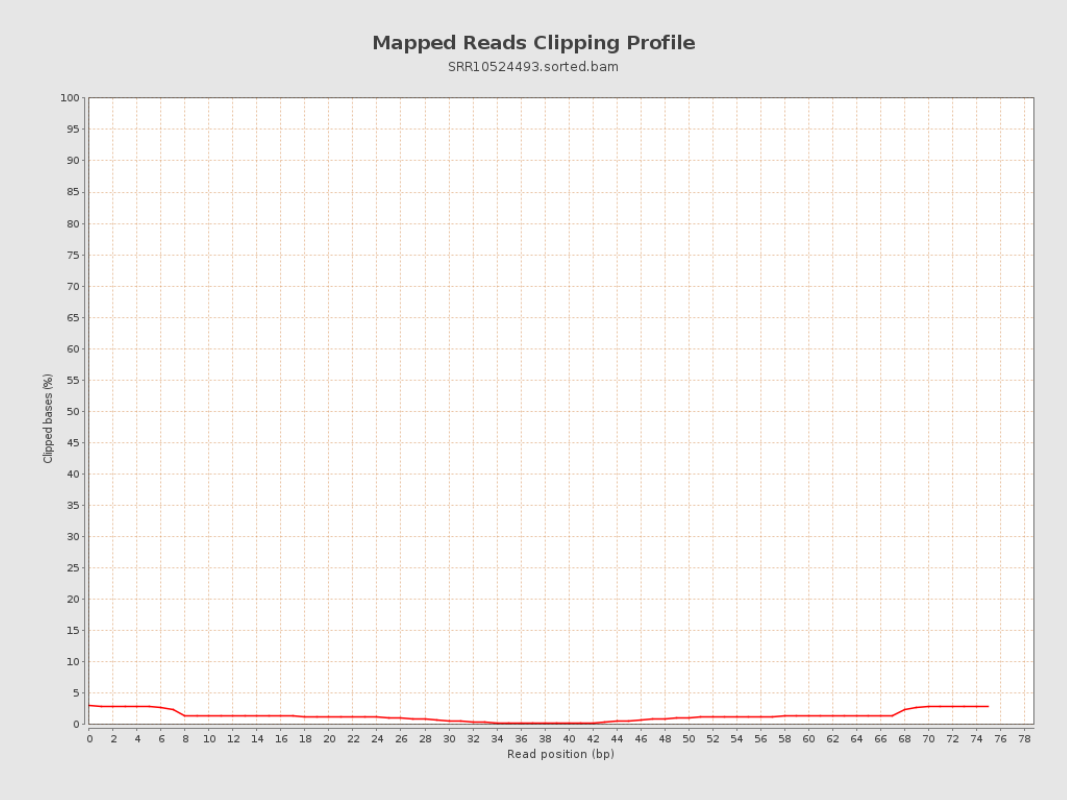
8. Results : Mapped Reads Nucleotide Content



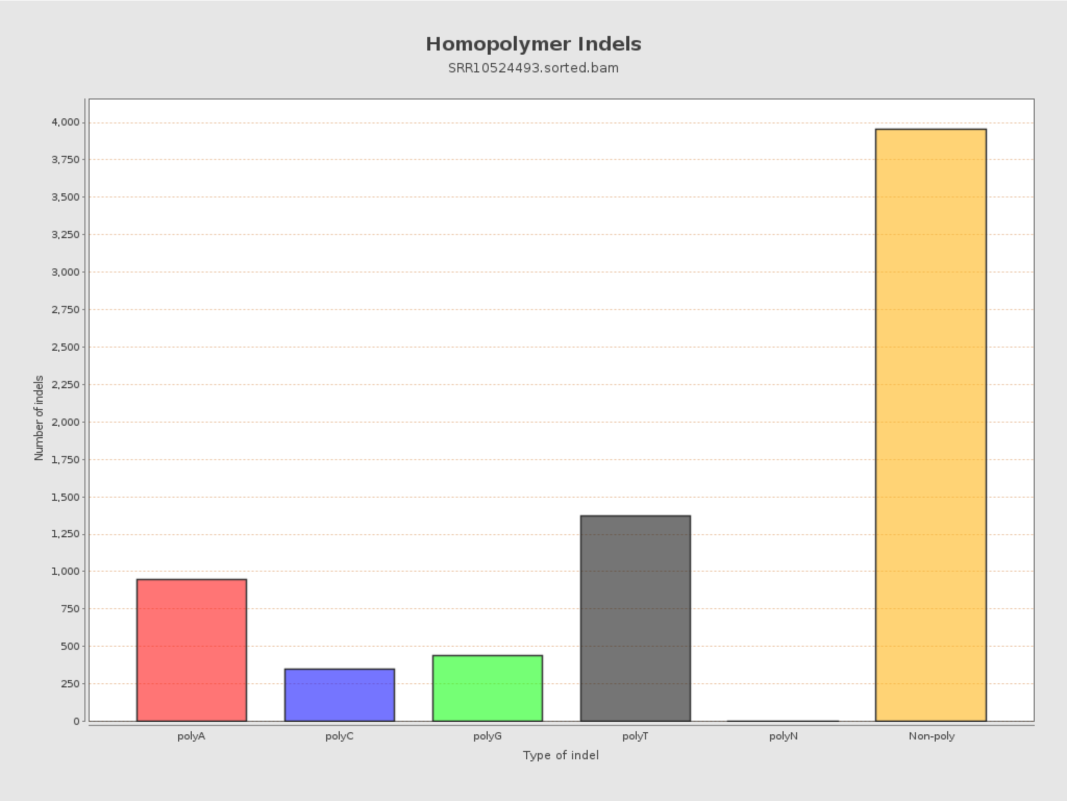
9. Results : Mapped Reads GC-content Distribution



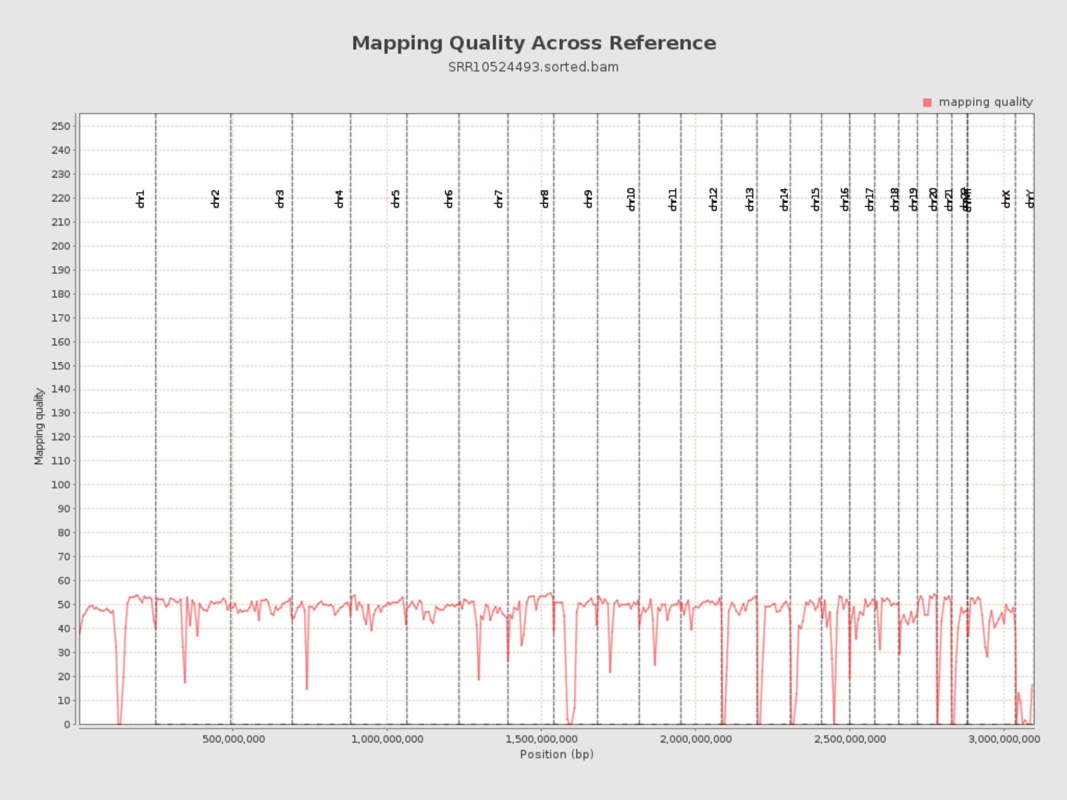
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram