Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:42:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524556.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_SRR10524556 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524556.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:42:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524556.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,380,560
Mapped reads	1,263,504 / 91.52%
Unmapped reads	117,056 / 8.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,504 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	44,454 / 3.22%
Duplication rate	2.62%
Clipped reads	1,265,848 / 91.69%

2.2. ACGT Content

Number/percentage of A's	18,013,602 / 24.59%
Number/percentage of C's	13,701,420 / 18.7%
Number/percentage of T's	23,541,269 / 32.13%
Number/percentage of G's	18,004,805 / 24.58%
Number/percentage of N's	1,060 / 0%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2325

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

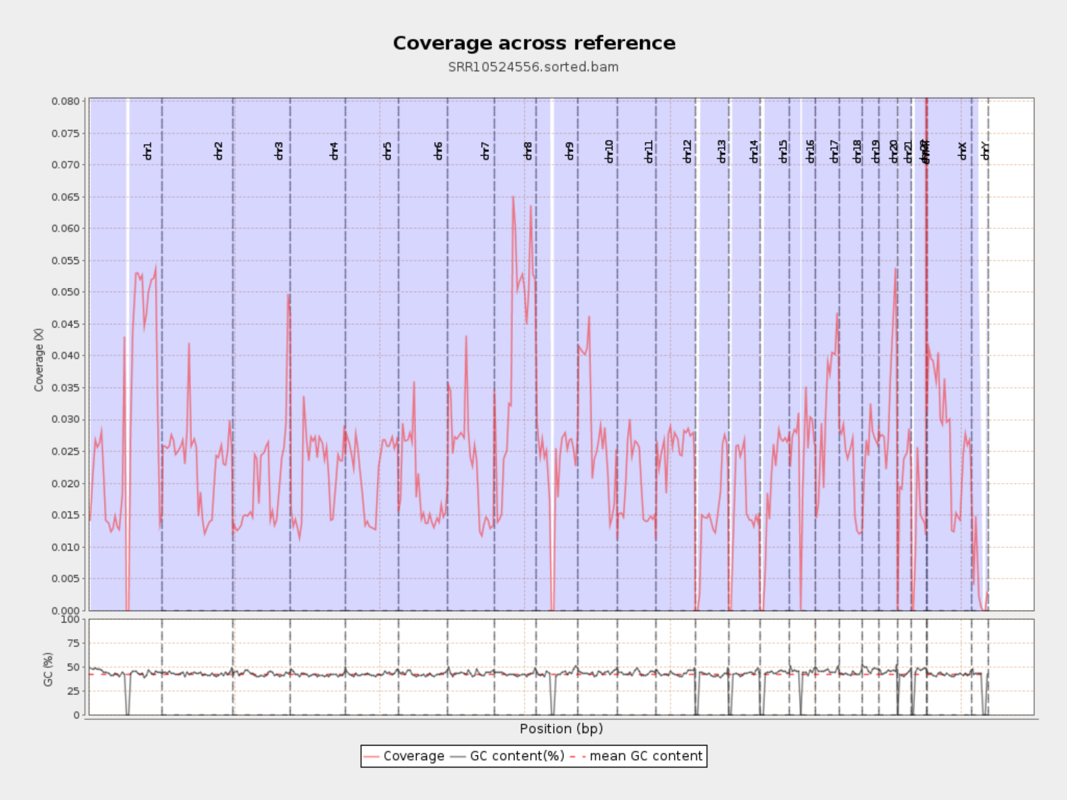
General error rate	0.51%
Mismatches	368,801
Insertions	4,420
Mapped reads with at least one insertion	0.35%
Deletions	13,751
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.06%

2.6. Chromosome stats

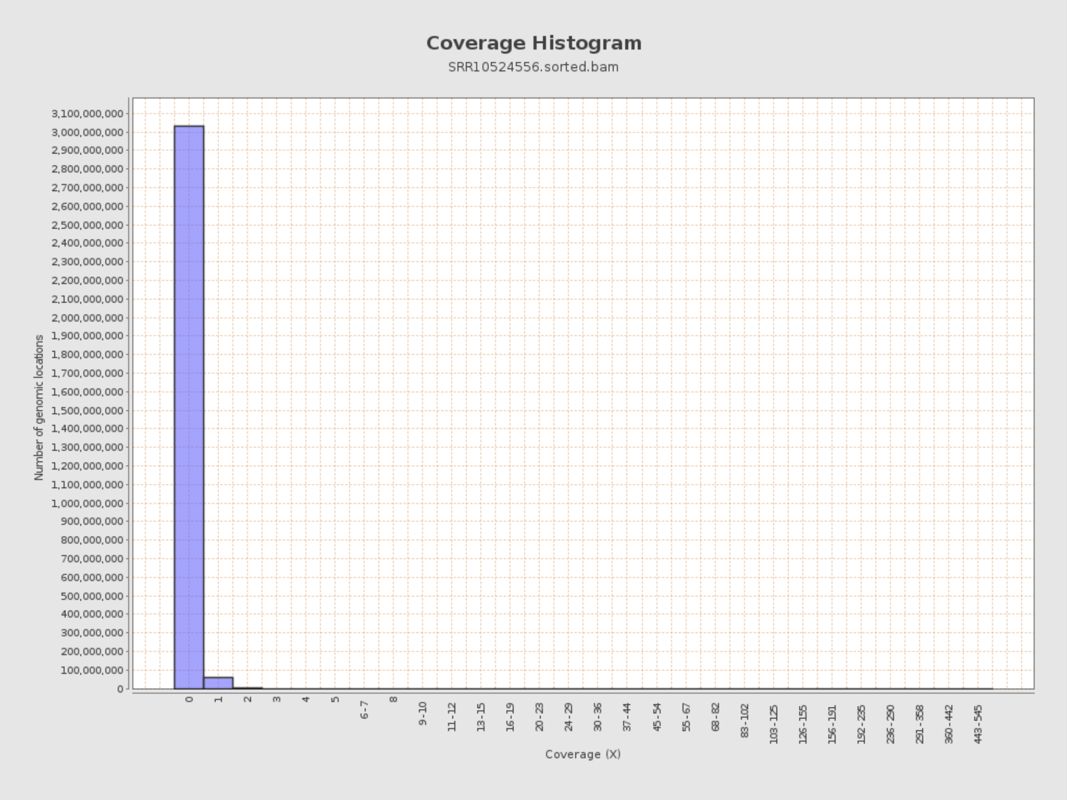
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7351539	0.0295	0.4171
chr2	243199373	5715254	0.0235	0.2574
chr3	198022430	3981070	0.0201	0.1541
chr4	191154276	4167694	0.0218	0.1773
chr5	180915260	3993973	0.0221	0.1607
chr6	171115067	3273902	0.0191	0.1816
chr7	159138663	3691609	0.0232	0.3032

chr8	146364022	6010304	0.0411	0.249
chr9	141213431	3111826	0.022	0.2015
chr10	135534747	3924275	0.029	0.244
chr11	135006516	2604254	0.0193	0.2174
chr12	133851895	3496549	0.0261	0.1749
chr13	115169878	1706707	0.0148	0.1318
chr14	107349540	1746754	0.0163	0.1411
chr15	102531392	1976823	0.0193	0.1527
chr16	90354753	2295889	0.0254	0.186
chr17	81195210	2607456	0.0321	0.2056
chr18	78077248	1697313	0.0217	0.338
chr19	59128983	1538861	0.026	0.2925
chr20	63025520	2150273	0.0341	0.2006
chr21	48129895	1008494	0.021	0.1678
chr22	51304566	623229	0.0121	0.1193
chrMT	16571	48892	2.9505	2.3691
chrX	155270560	4312881	0.0278	0.1966
chrY	59373566	249266	0.0042	0.1203

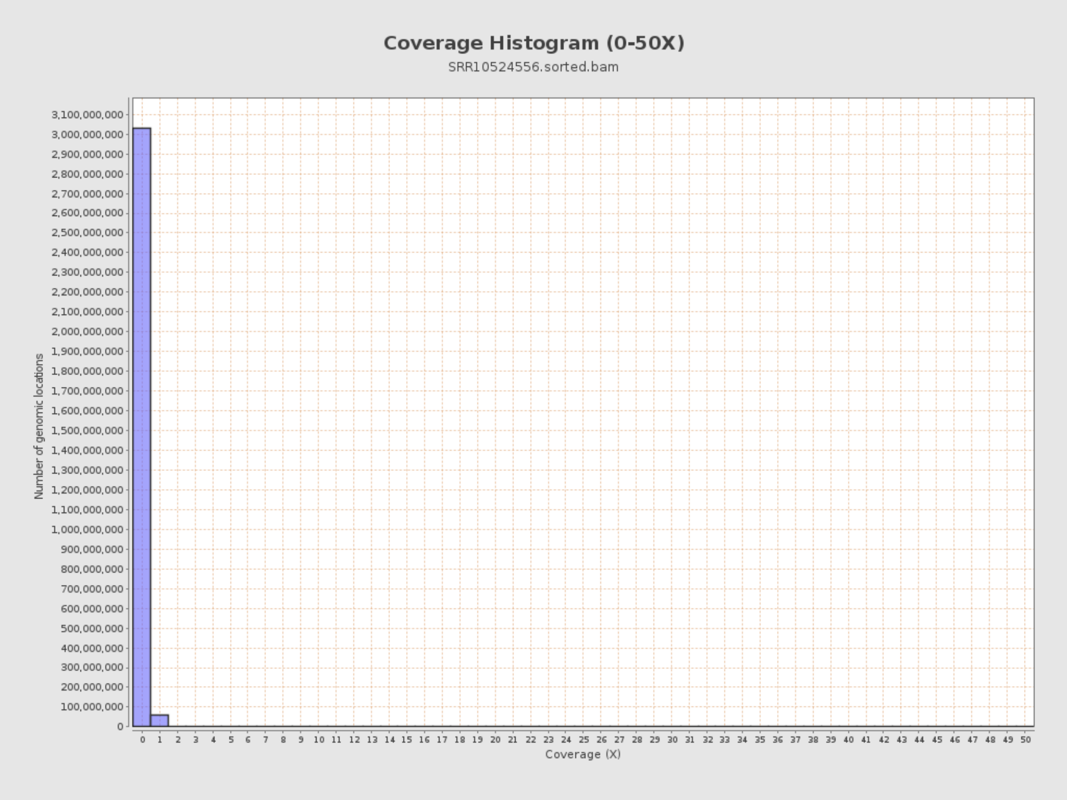
3. Results : Coverage across reference



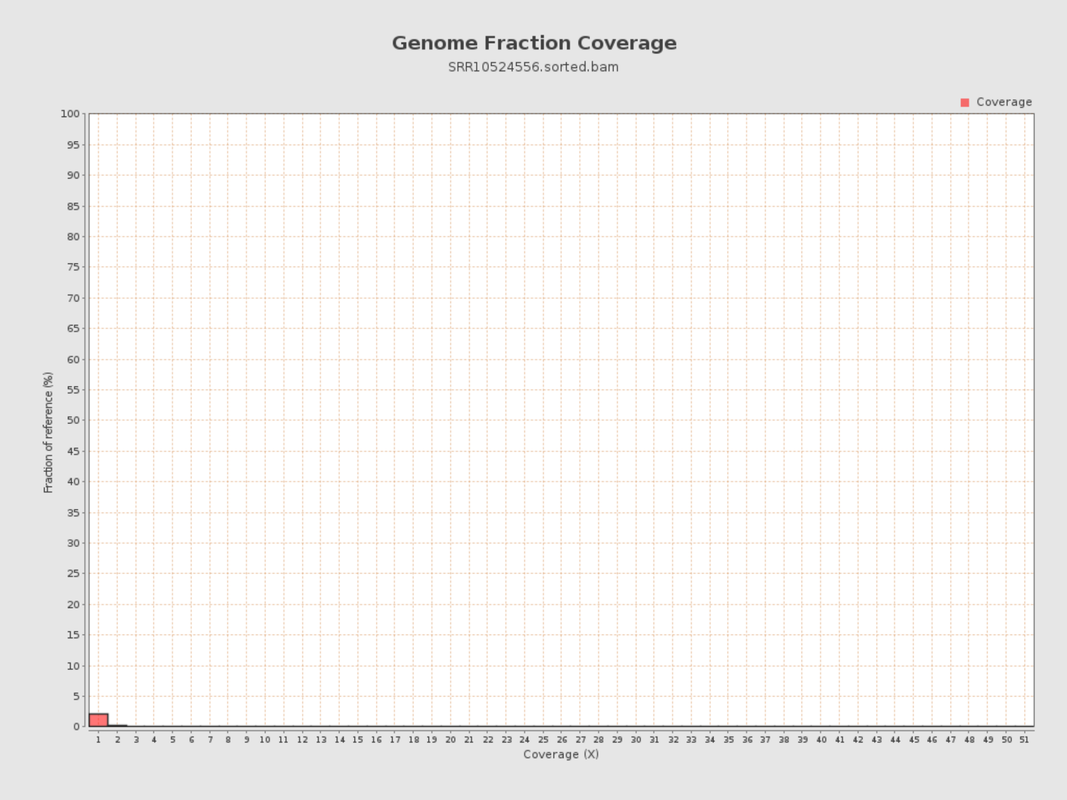
4. Results : Coverage Histogram



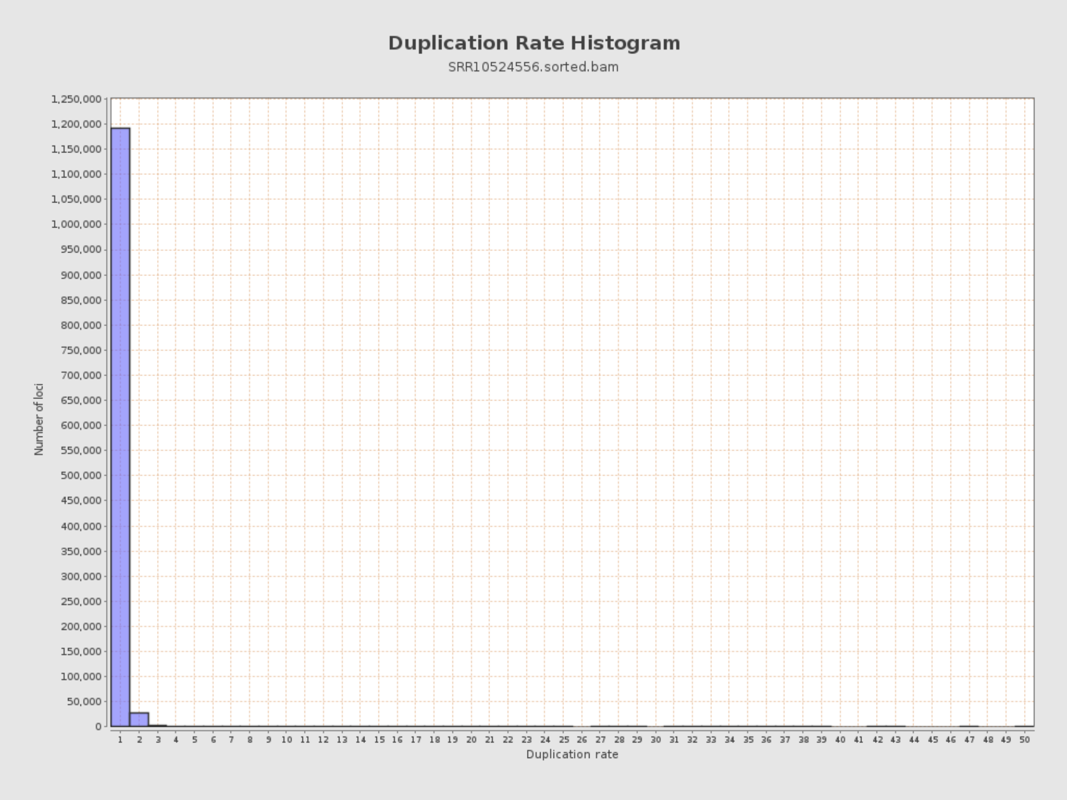
5. Results : Coverage Histogram (0-50X)



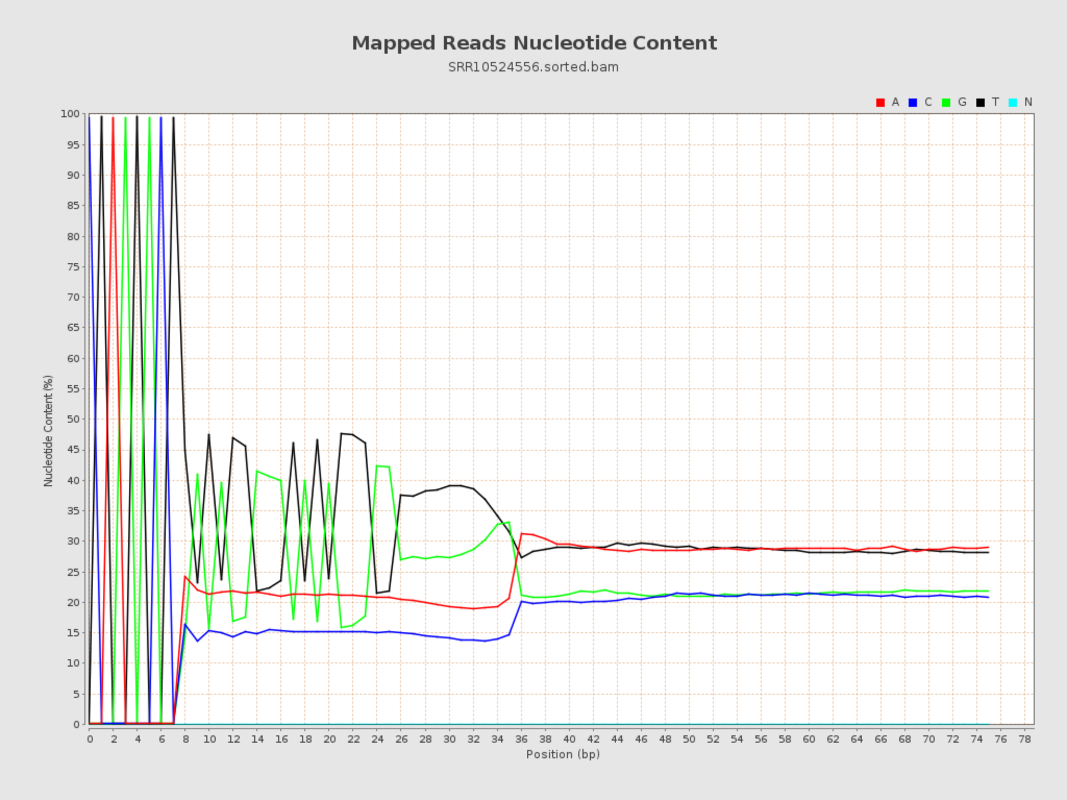
6. Results : Genome Fraction Coverage



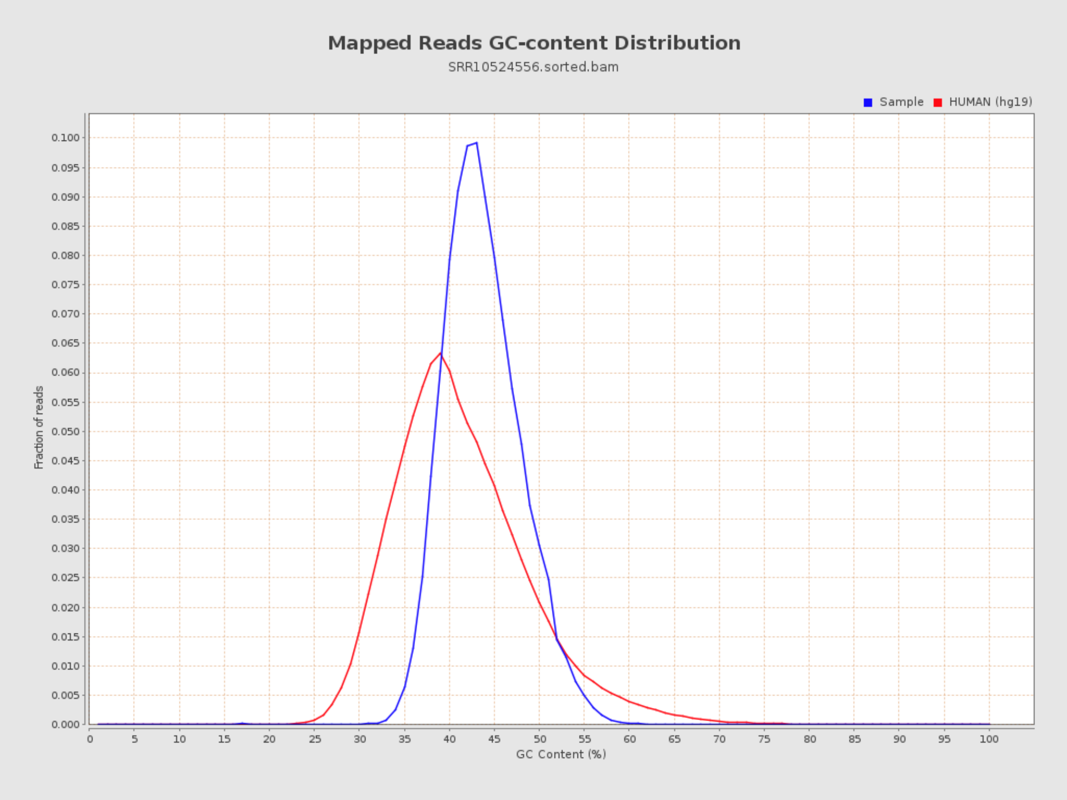
7. Results : Duplication Rate Histogram



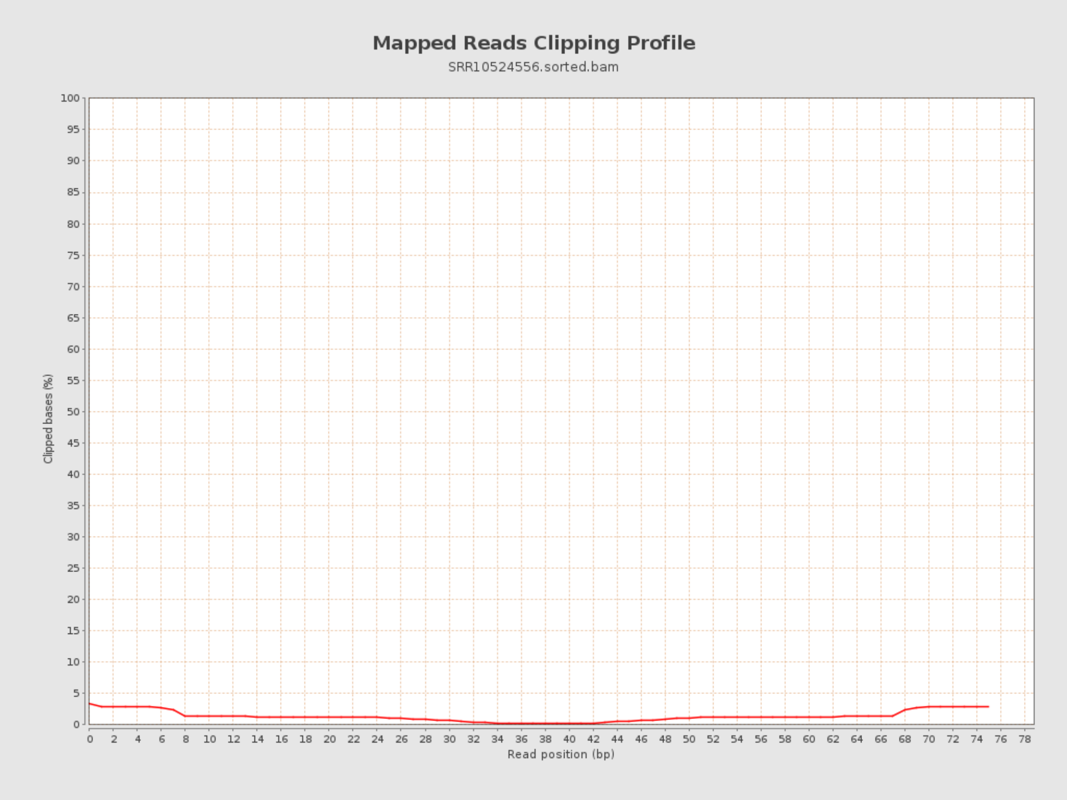
8. Results : Mapped Reads Nucleotide Content



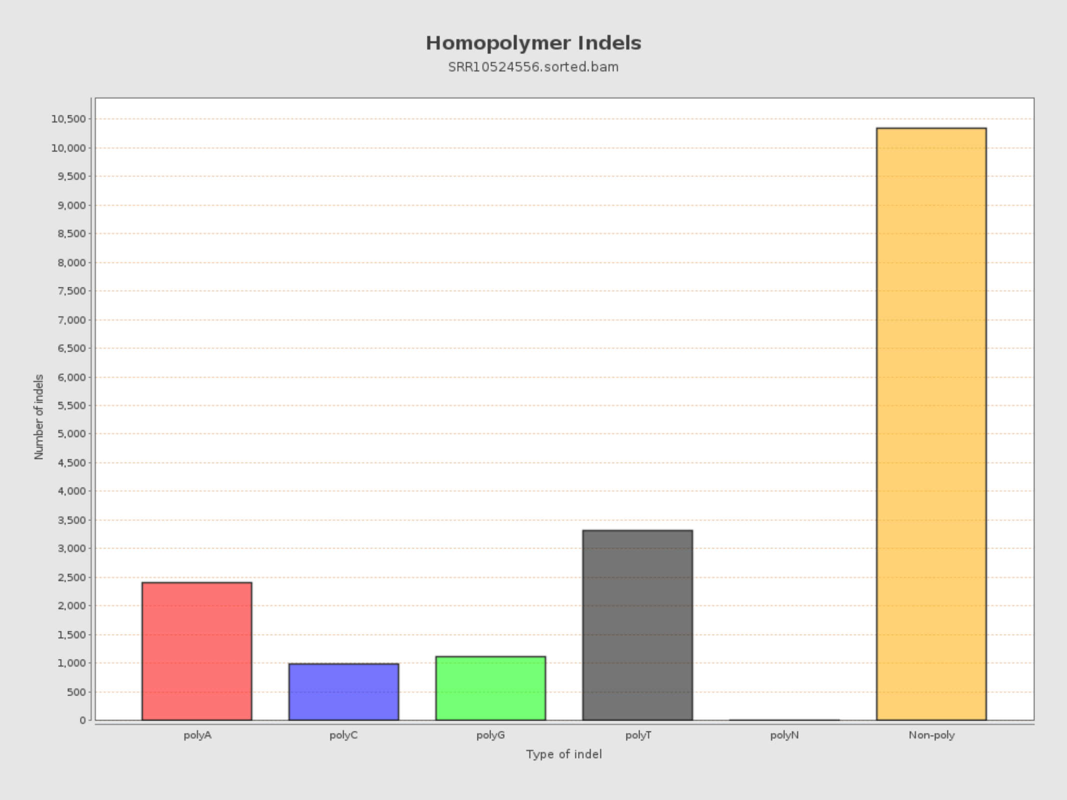
9. Results : Mapped Reads GC-content Distribution



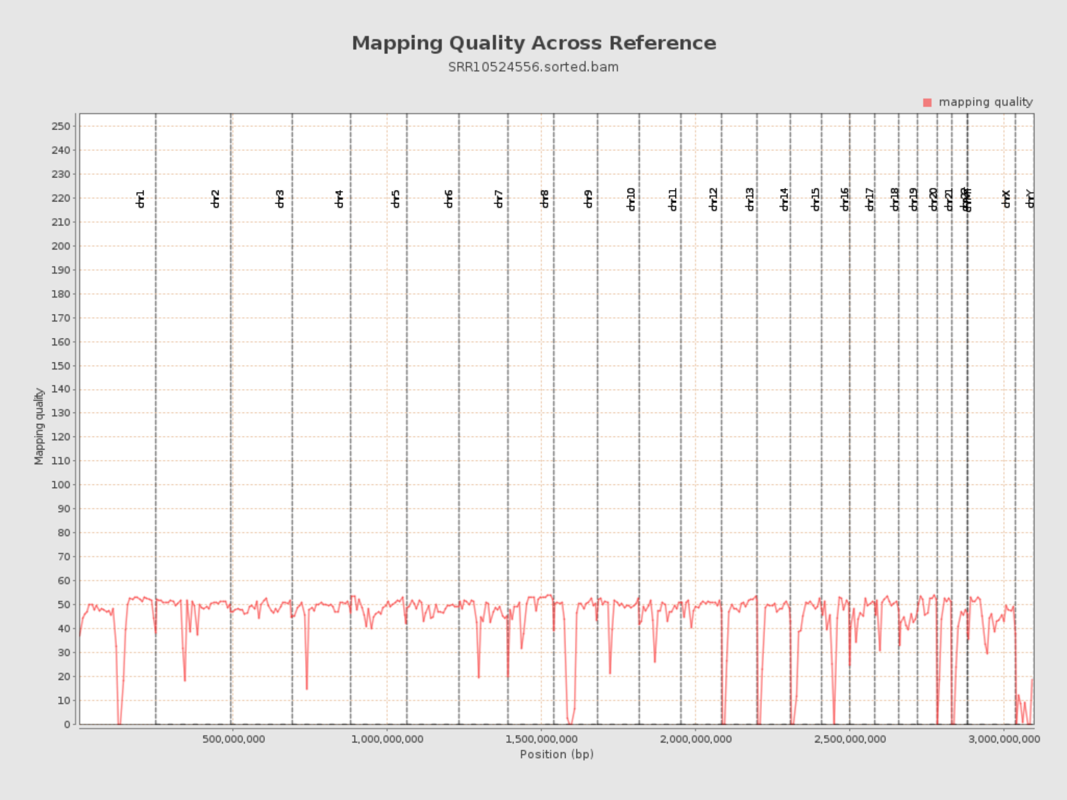
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram