Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:33:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524472.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_SRR10524472 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524472.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:33:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524472.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	992,912
Mapped reads	915,761 / 92.23%
Unmapped reads	77,151 / 7.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,881 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	30,997 / 3.12%
Duplication rate	2.62%
Clipped reads	915,841 / 92.24%

2.2. ACGT Content

Number/percentage of A's	13,311,882 / 24.94%
Number/percentage of C's	9,445,585 / 17.7%
Number/percentage of T's	16,713,444 / 31.31%
Number/percentage of G's	13,905,400 / 26.05%
Number/percentage of N's	1,174 / 0%
GC Percentage	43.75%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.1847

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

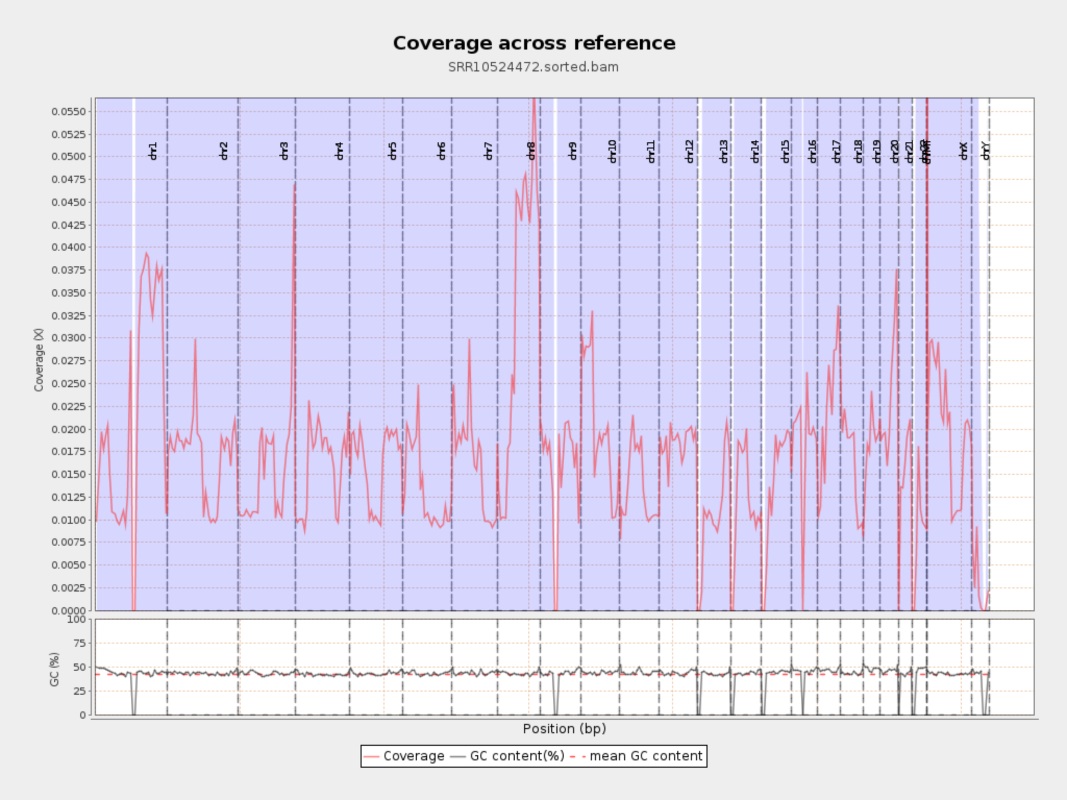
General error rate	0.48%
Mismatches	249,021
Insertions	3,324
Mapped reads with at least one insertion	0.36%
Deletions	9,423
Mapped reads with at least one deletion	1.02%
Homopolymer indels	42.75%

2.6. Chromosome stats

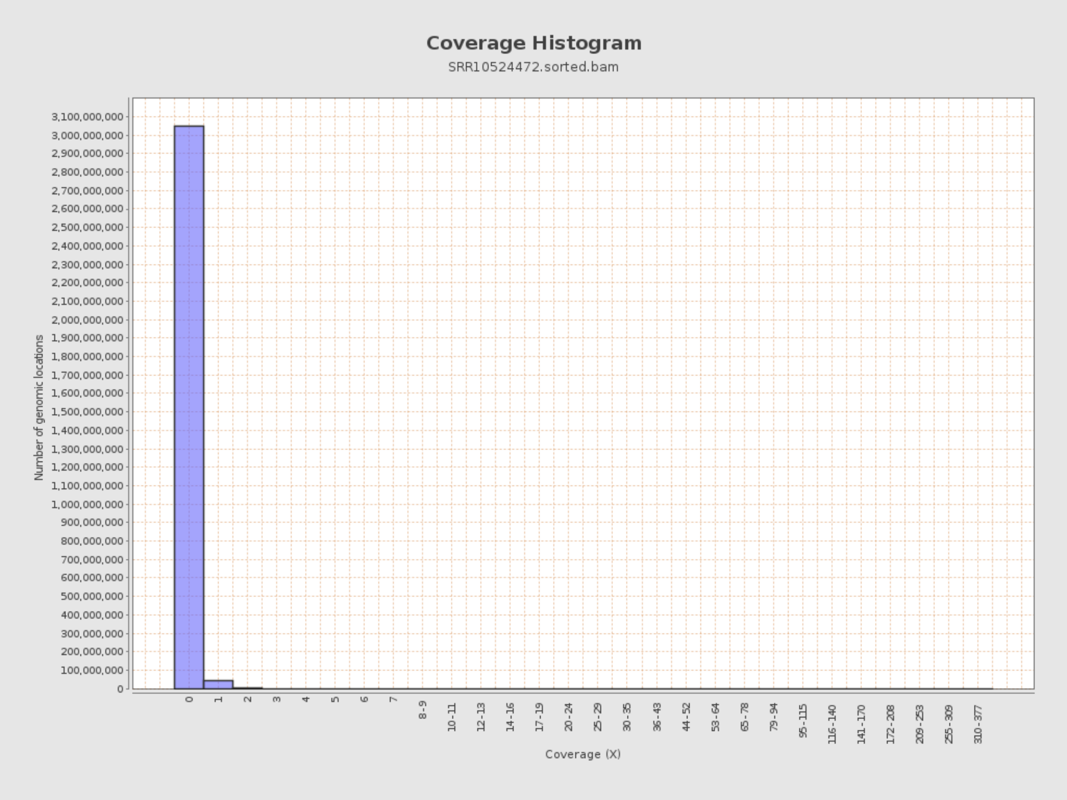
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5300703	0.0213	0.3175
chr2	243199373	4159768	0.0171	0.1981
chr3	198022430	3065079	0.0155	0.1346
chr4	191154276	3045734	0.0159	0.1451
chr5	180915260	2948252	0.0163	0.1373
chr6	171115067	2274549	0.0133	0.1485
chr7	159138663	2631925	0.0165	0.2233

chr8	146364022	4936103	0.0337	0.2177
chr9	141213431	2190966	0.0155	0.1692
chr10	135534747	2811338	0.0207	0.1987
chr11	135006516	1842595	0.0136	0.1685
chr12	133851895	2480237	0.0185	0.1466
chr13	115169878	1217601	0.0106	0.11
chr14	107349540	1260636	0.0117	0.1184
chr15	102531392	1398975	0.0136	0.1272
chr16	90354753	1657171	0.0183	0.1518
chr17	81195210	1800132	0.0222	0.1635
chr18	78077248	1281501	0.0164	0.2621
chr19	59128983	1093578	0.0185	0.228
chr20	63025520	1513774	0.024	0.1671
chr21	48129895	724299	0.015	0.1386
chr22	51304566	436546	0.0085	0.0997
chrMT	16571	3856	0.2327	0.5905
chrX	155270560	3159502	0.0203	0.1654
chrY	59373566	159162	0.0027	0.0791

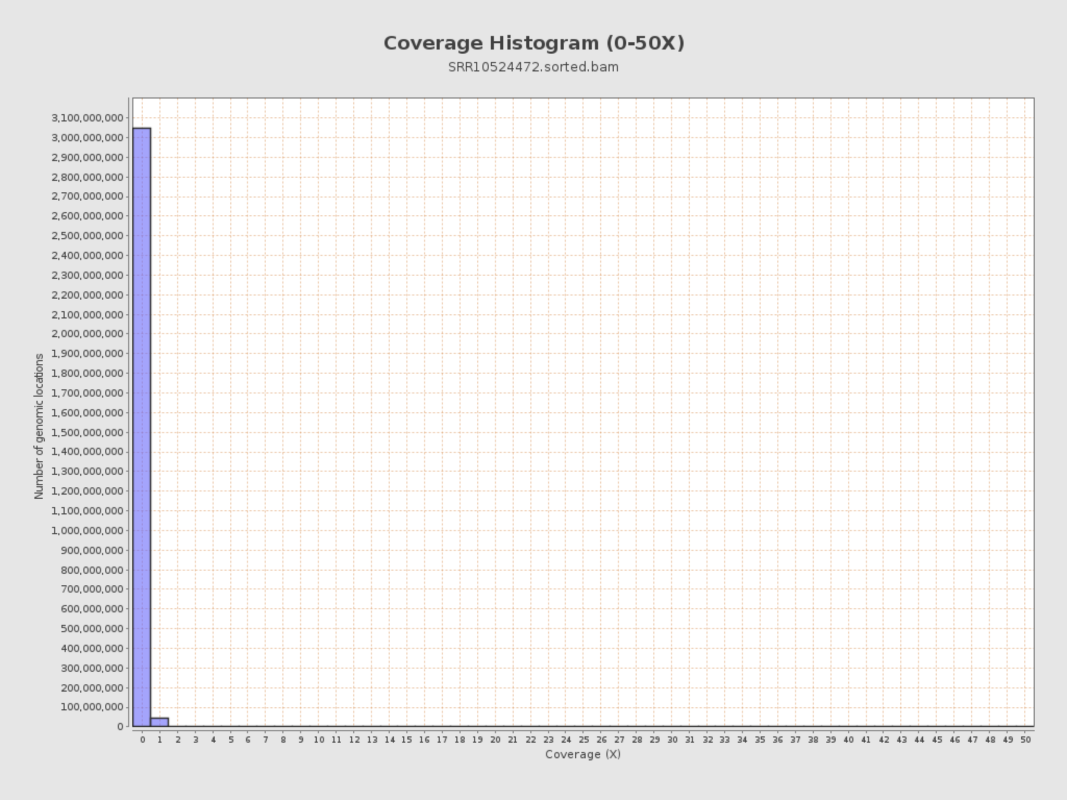
3. Results : Coverage across reference



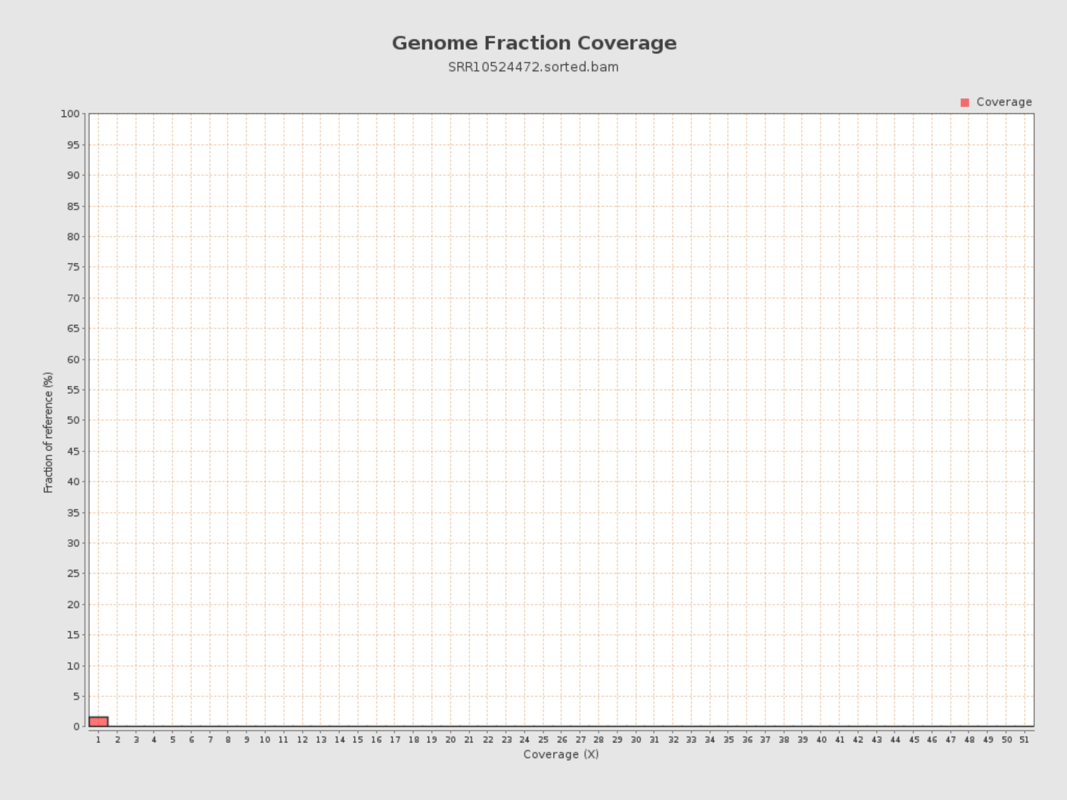
4. Results : Coverage Histogram



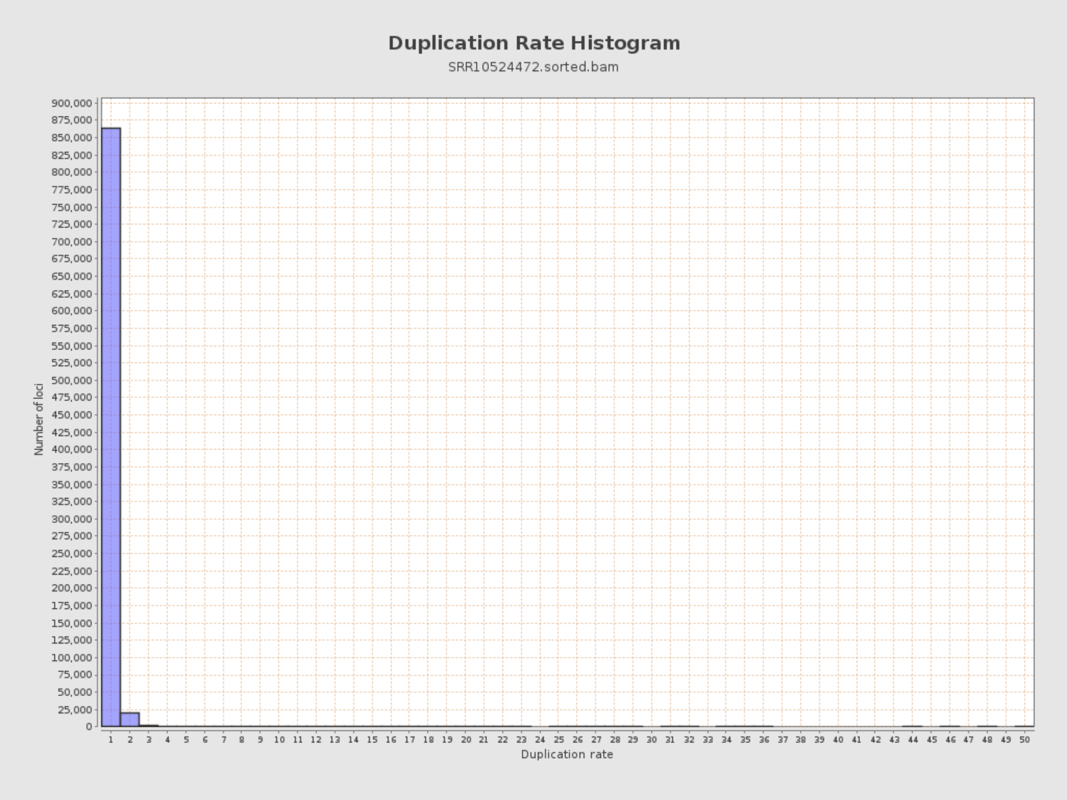
5. Results : Coverage Histogram (0-50X)



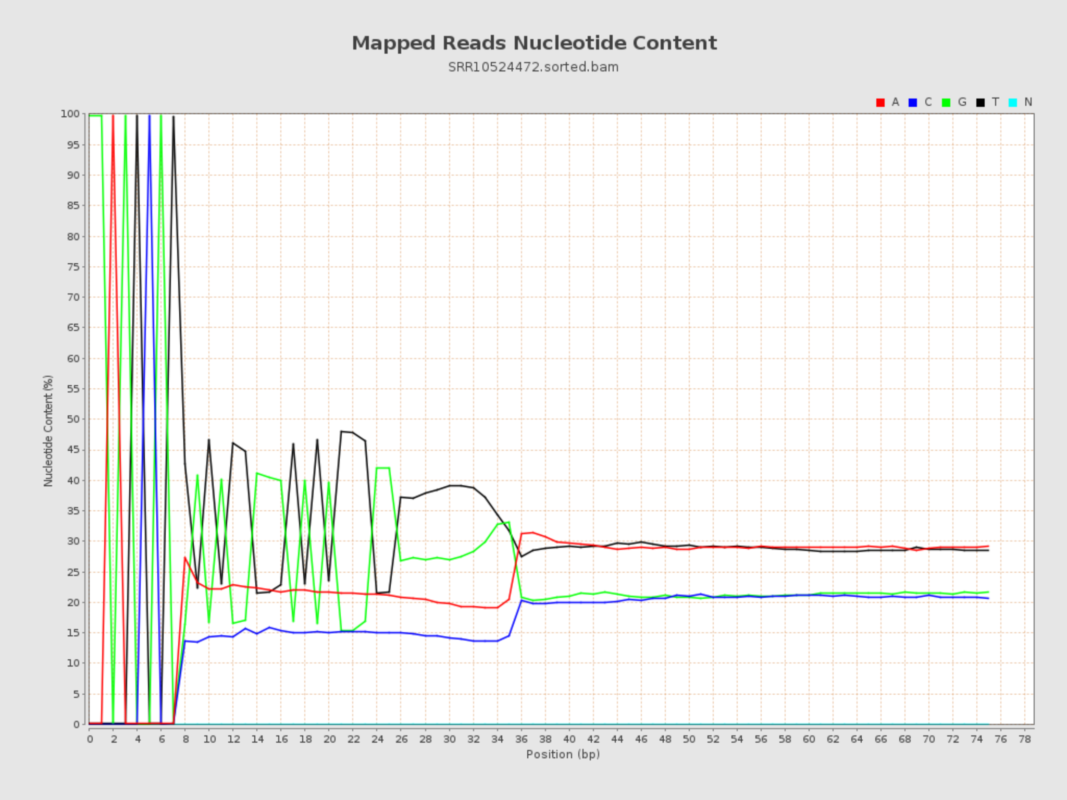
6. Results : Genome Fraction Coverage



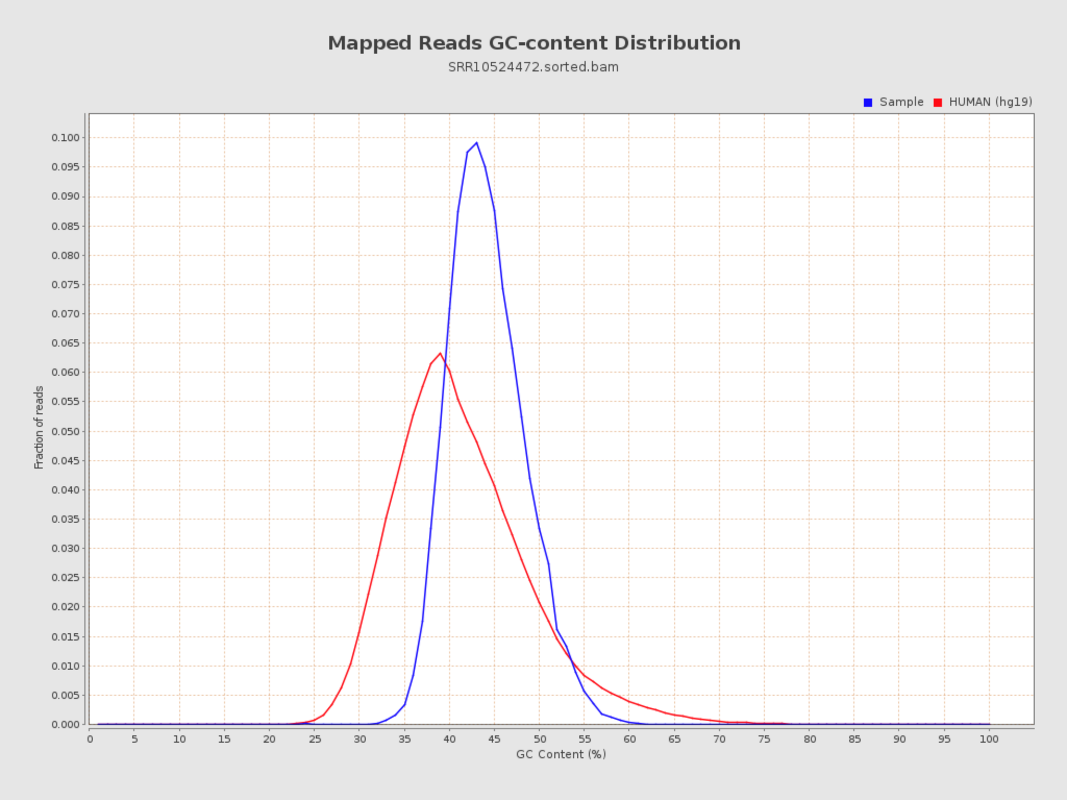
7. Results : Duplication Rate Histogram



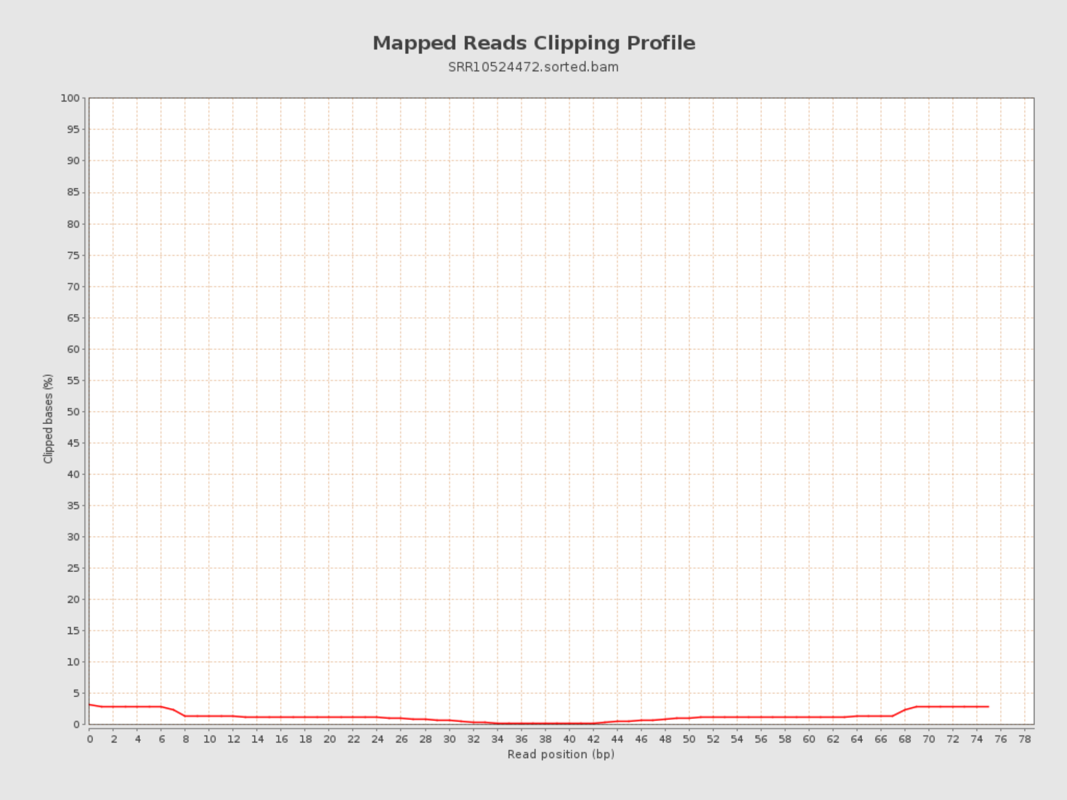
8. Results : Mapped Reads Nucleotide Content



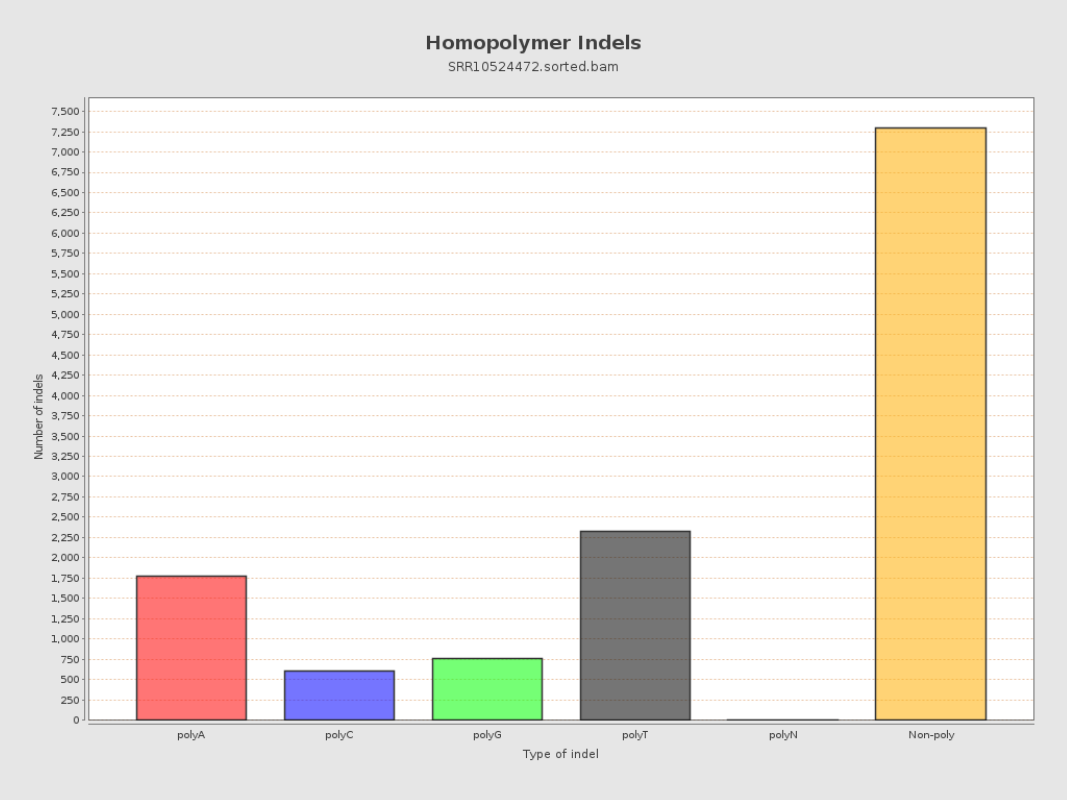
9. Results : Mapped Reads GC-content Distribution



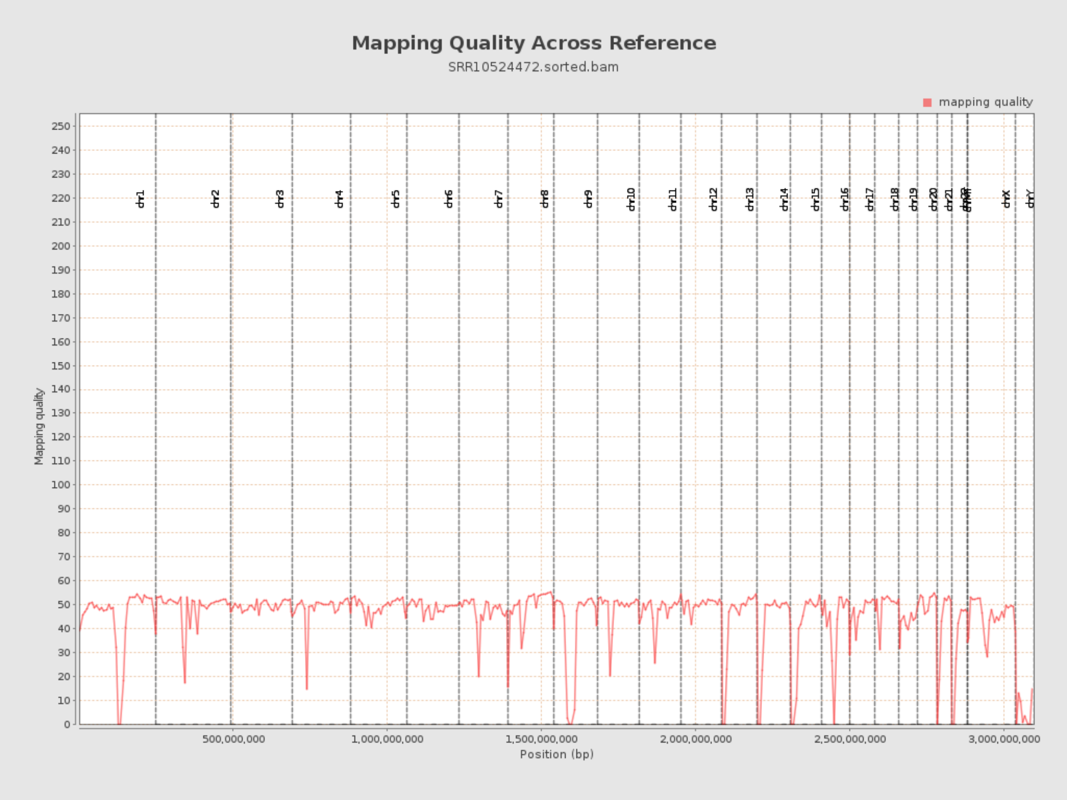
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram