Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:46:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524478.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_SRR10524478 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524478.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:46:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524478.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,567,376
Mapped reads	1,438,447 / 91.77%
Unmapped reads	128,929 / 8.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,055 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	46,117 / 2.94%
Duplication rate	2.28%
Clipped reads	1,440,072 / 91.88%

2.2. ACGT Content

Number/percentage of A's	20,163,976 / 24.24%
Number/percentage of C's	15,371,416 / 18.48%
Number/percentage of T's	26,966,889 / 32.41%
Number/percentage of G's	20,694,526 / 24.87%
Number/percentage of N's	1,562 / 0%
GC Percentage	43.35%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.2476

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

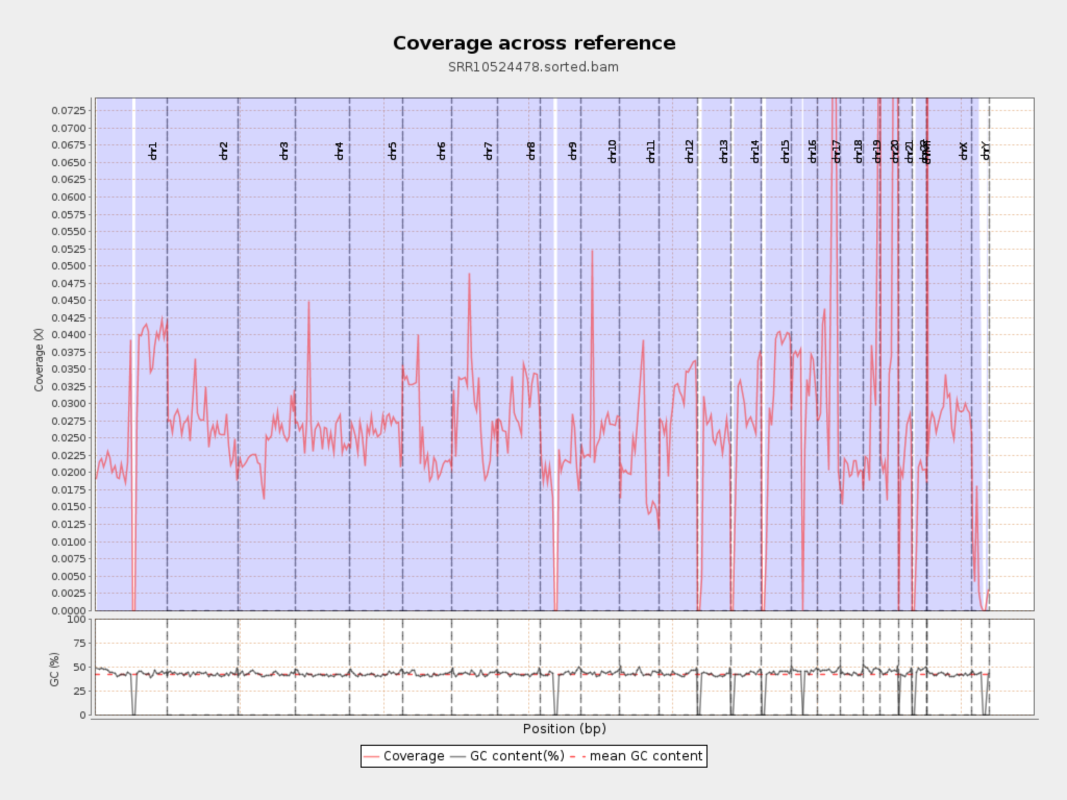
General error rate	0.52%
Mismatches	417,462
Insertions	6,035
Mapped reads with at least one insertion	0.42%
Deletions	16,528
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.58%

2.6. Chromosome stats

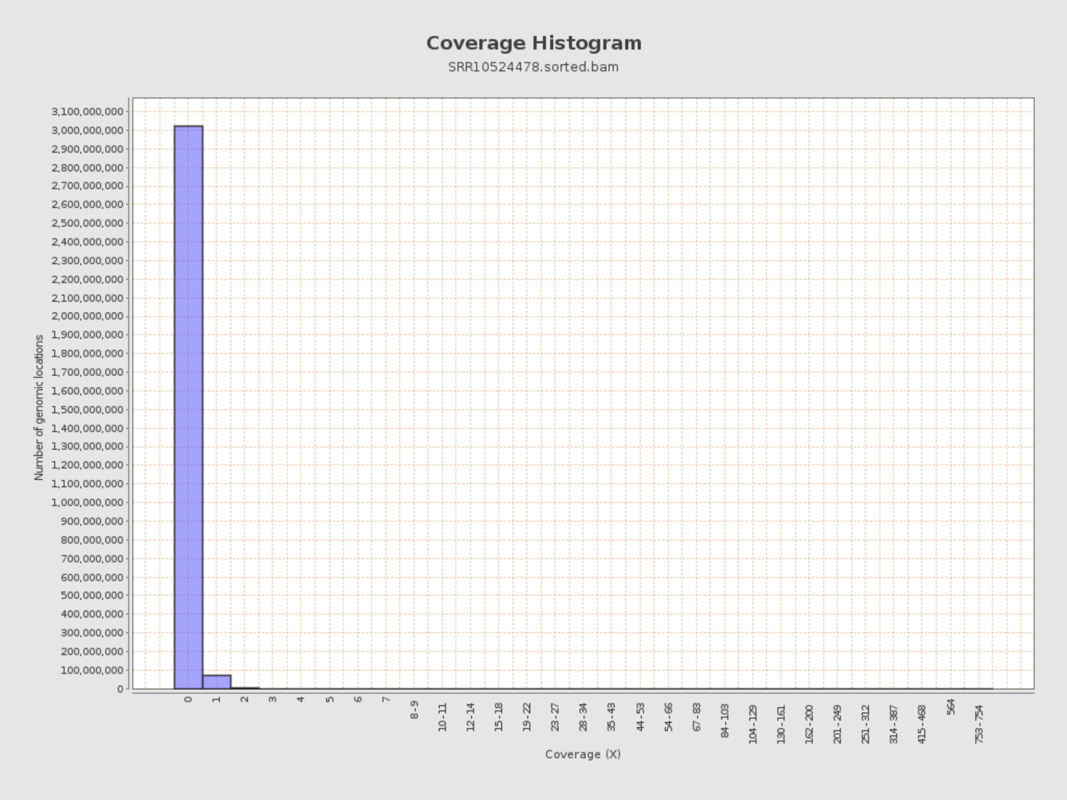
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6968908	0.028	0.3713
chr2	243199373	6533902	0.0269	0.3534
chr3	198022430	4757547	0.024	0.1691
chr4	191154276	5045155	0.0264	0.2012
chr5	180915260	4717259	0.0261	0.1733
chr6	171115067	4422753	0.0258	0.2044
chr7	159138663	4683010	0.0294	0.3247

chr8	146364022	4374063	0.0299	0.294
chr9	141213431	2688051	0.019	0.1819
chr10	135534747	3635273	0.0268	0.2613
chr11	135006516	2928126	0.0217	0.1995
chr12	133851895	4093287	0.0306	0.1896
chr13	115169878	2525656	0.0219	0.1601
chr14	107349540	2746161	0.0256	0.175
chr15	102531392	3017823	0.0294	0.1884
chr16	90354753	2801754	0.031	0.1978
chr17	81195210	3569699	0.044	0.2354
chr18	78077248	1564985	0.02	0.3
chr19	59128983	2302805	0.0389	0.3132
chr20	63025520	3324136	0.0527	0.2605
chr21	48129895	1048587	0.0218	0.1833
chr22	51304566	748069	0.0146	0.1288
chrMT	16571	10596	0.6394	0.9242
chrX	155270560	4439365	0.0286	0.1943
chrY	59373566	277862	0.0047	0.187

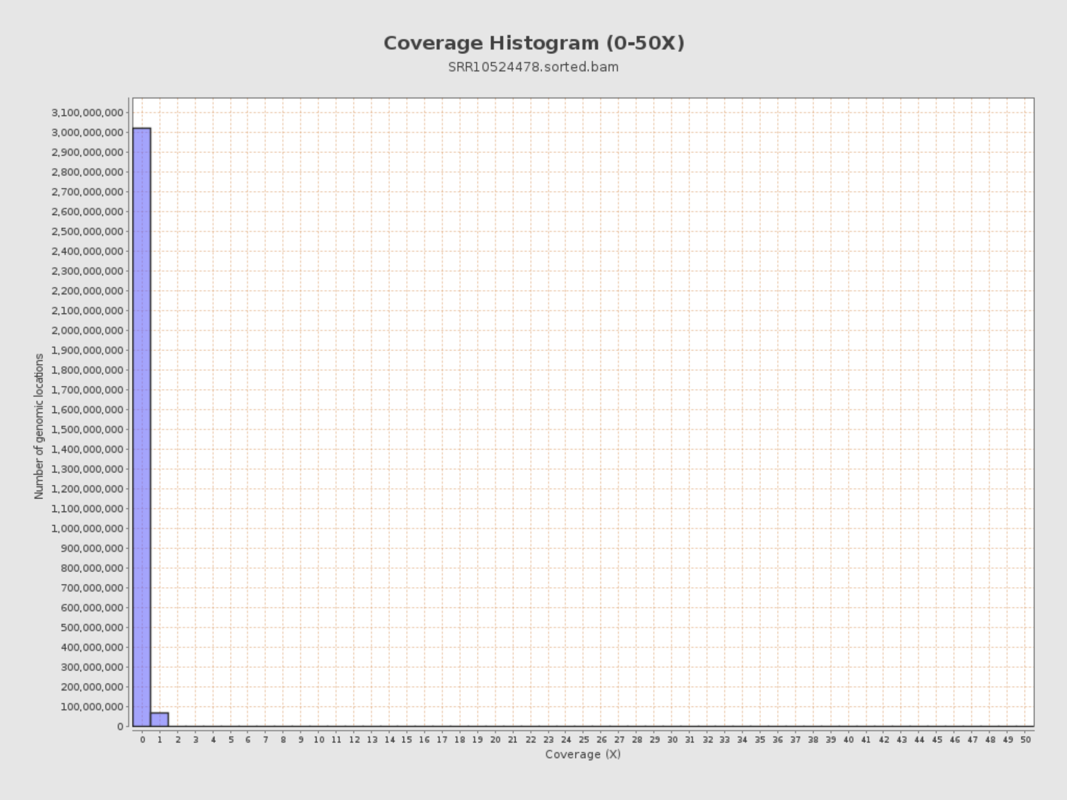
3. Results : Coverage across reference



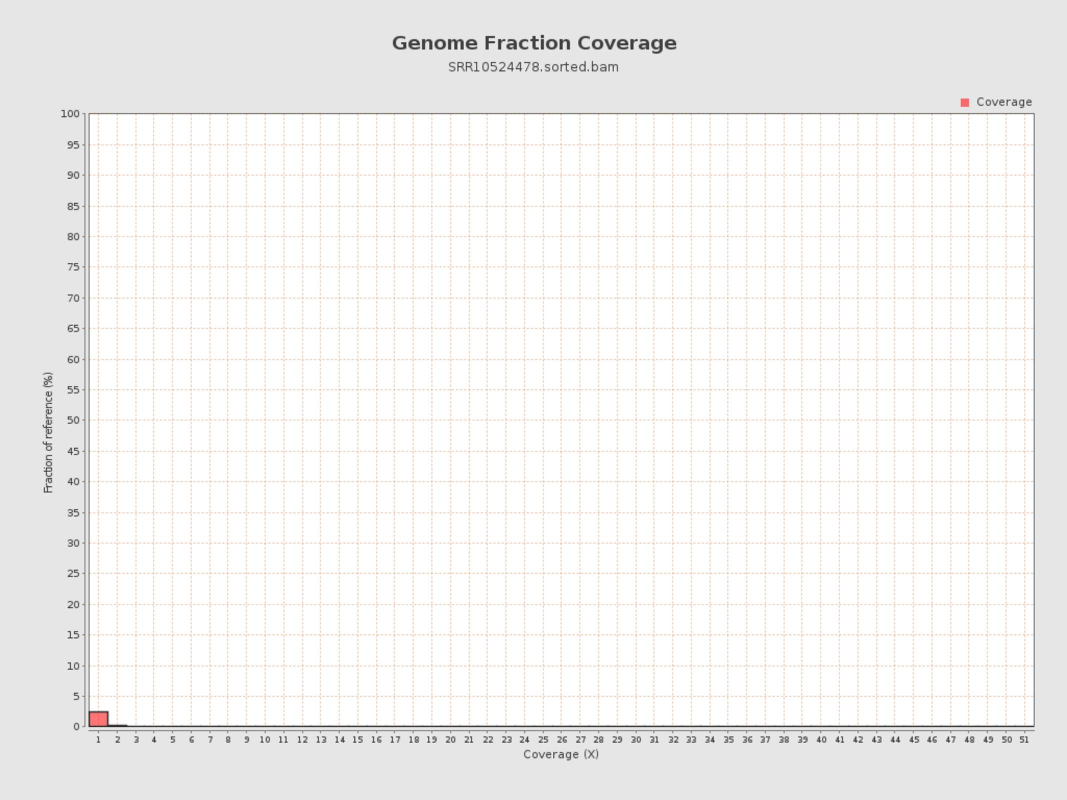
4. Results : Coverage Histogram



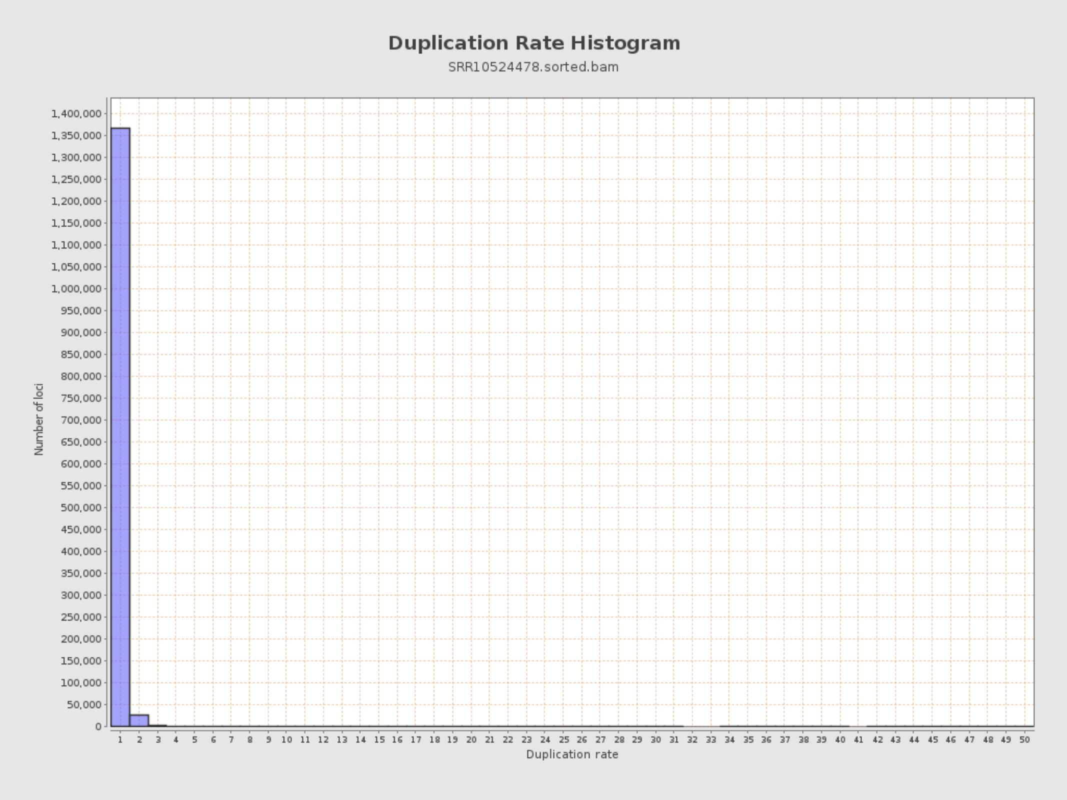
5. Results : Coverage Histogram (0-50X)



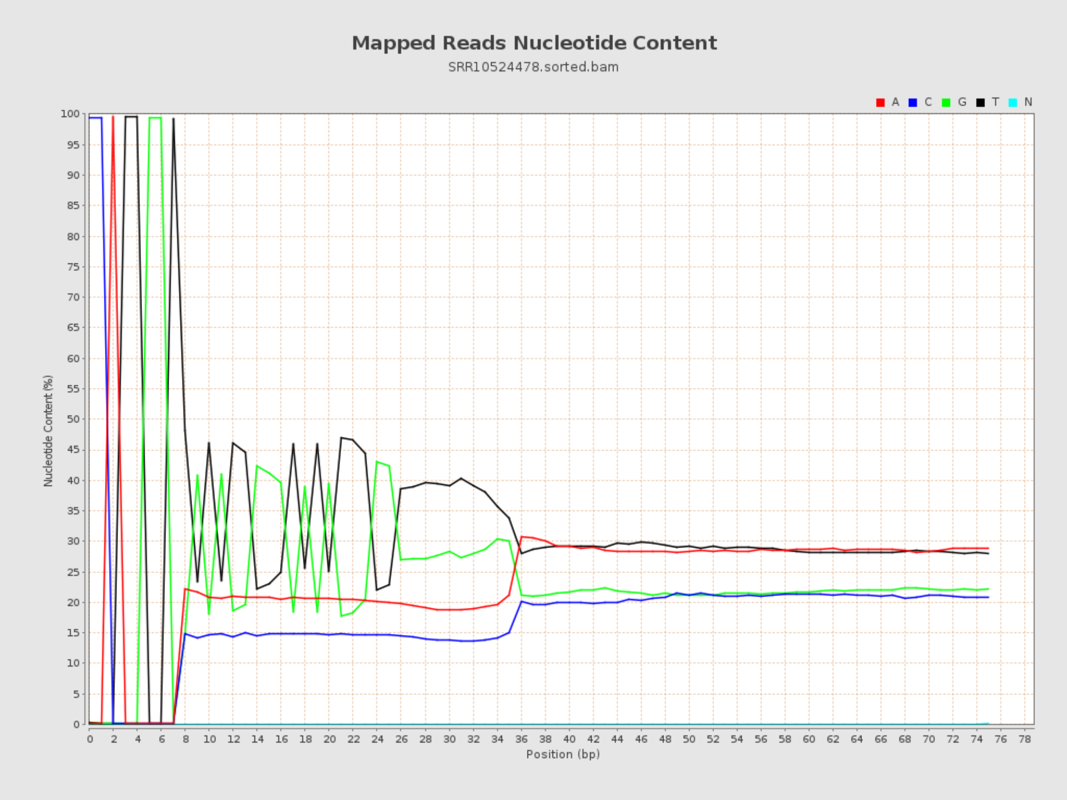
6. Results : Genome Fraction Coverage



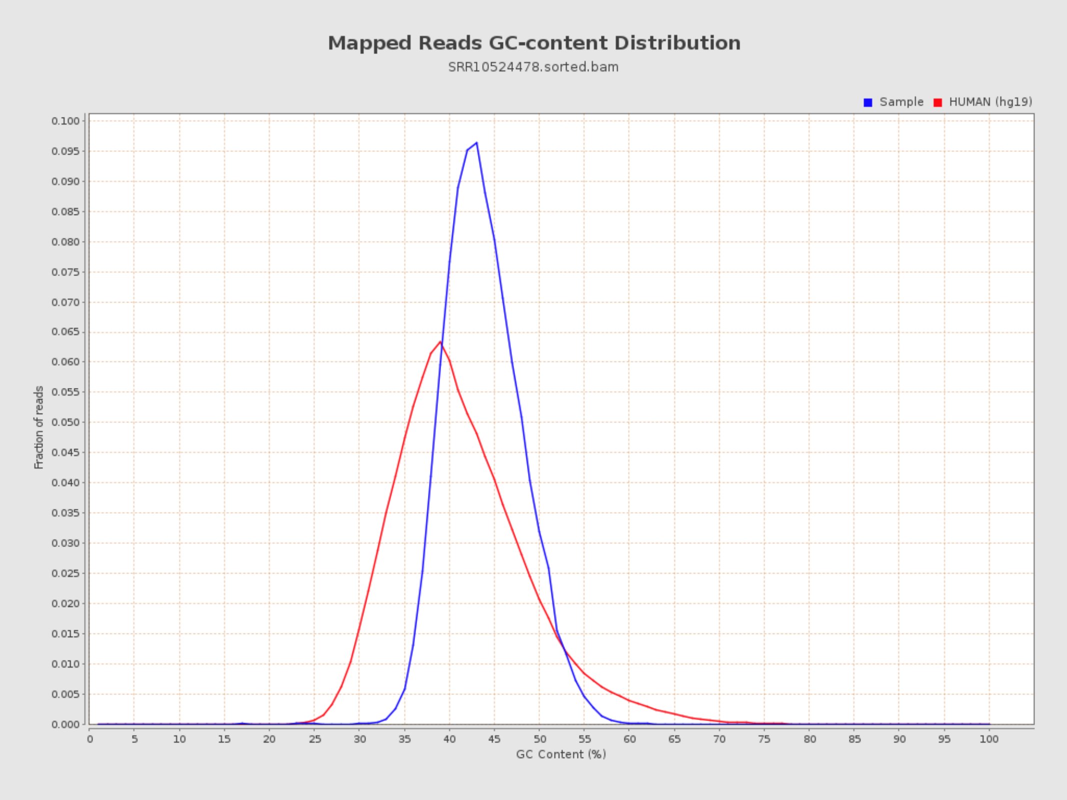
7. Results : Duplication Rate Histogram



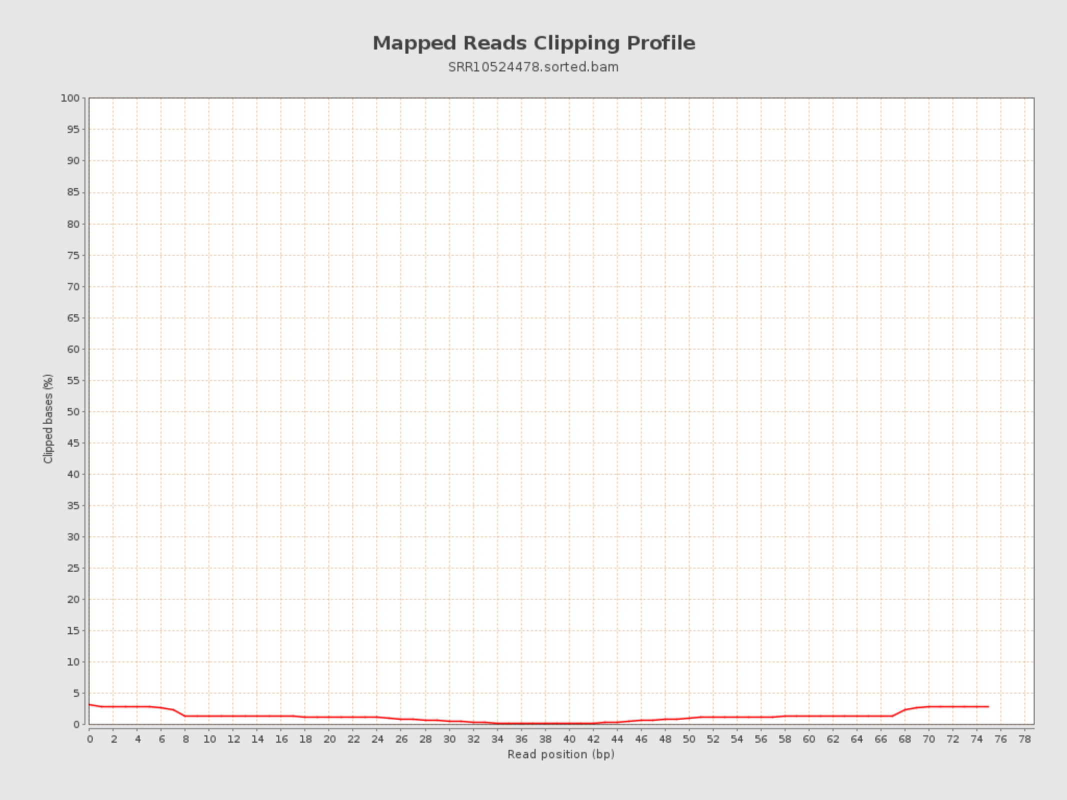
8. Results : Mapped Reads Nucleotide Content



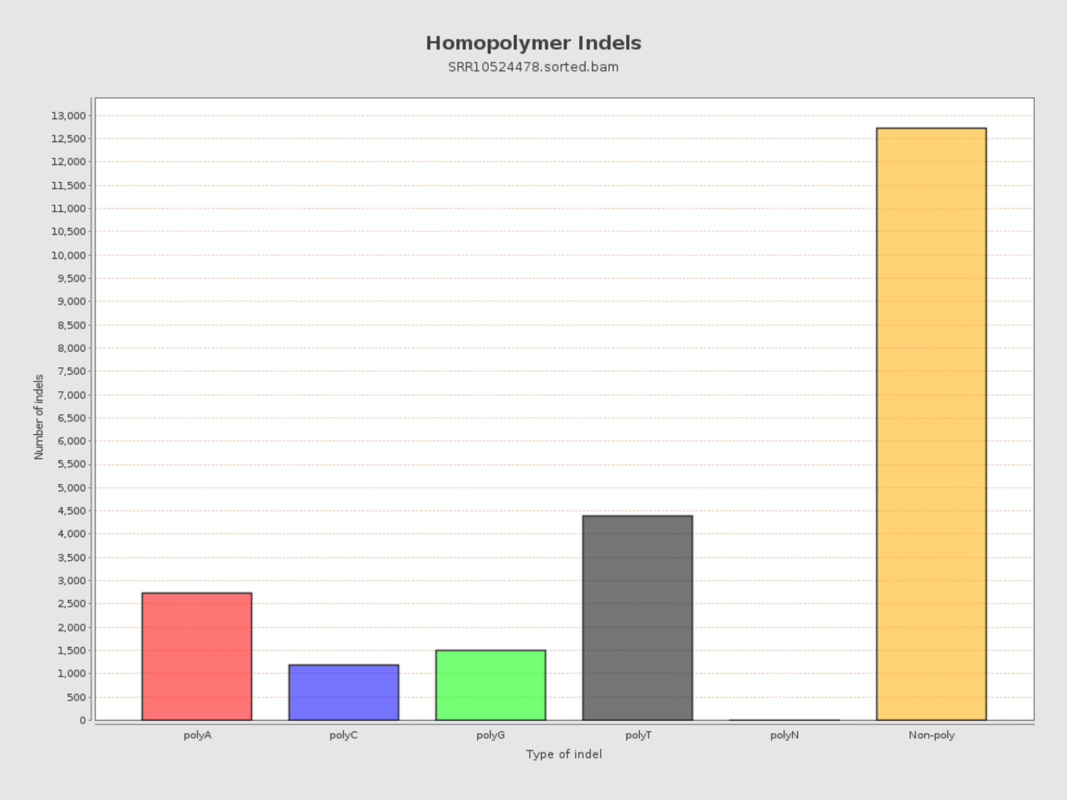
9. Results : Mapped Reads GC-content Distribution



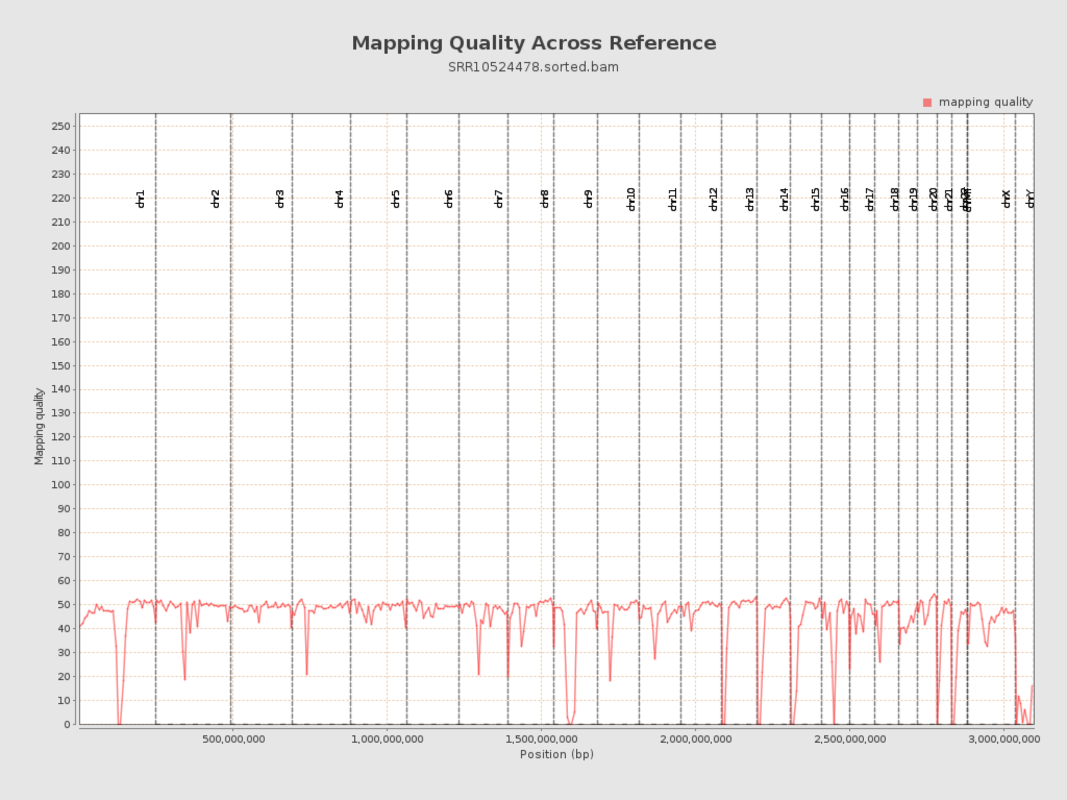
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram