Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:05:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524967.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_SRR10524967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:05:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,107,823
Mapped reads	1,017,711 / 91.87%
Unmapped reads	90,112 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,608 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	22,173 / 2%
Duplication rate	1.52%
Clipped reads	1,018,789 / 91.96%

2.2. ACGT Content

Number/percentage of A's	14,799,518 / 25.2%
Number/percentage of C's	11,057,338 / 18.83%
Number/percentage of T's	18,712,290 / 31.86%
Number/percentage of G's	14,160,555 / 24.11%
Number/percentage of N's	1,772 / 0%
GC Percentage	42.94%

2.3. Coverage

Mean	0.019

Standard Deviation	0.1912

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

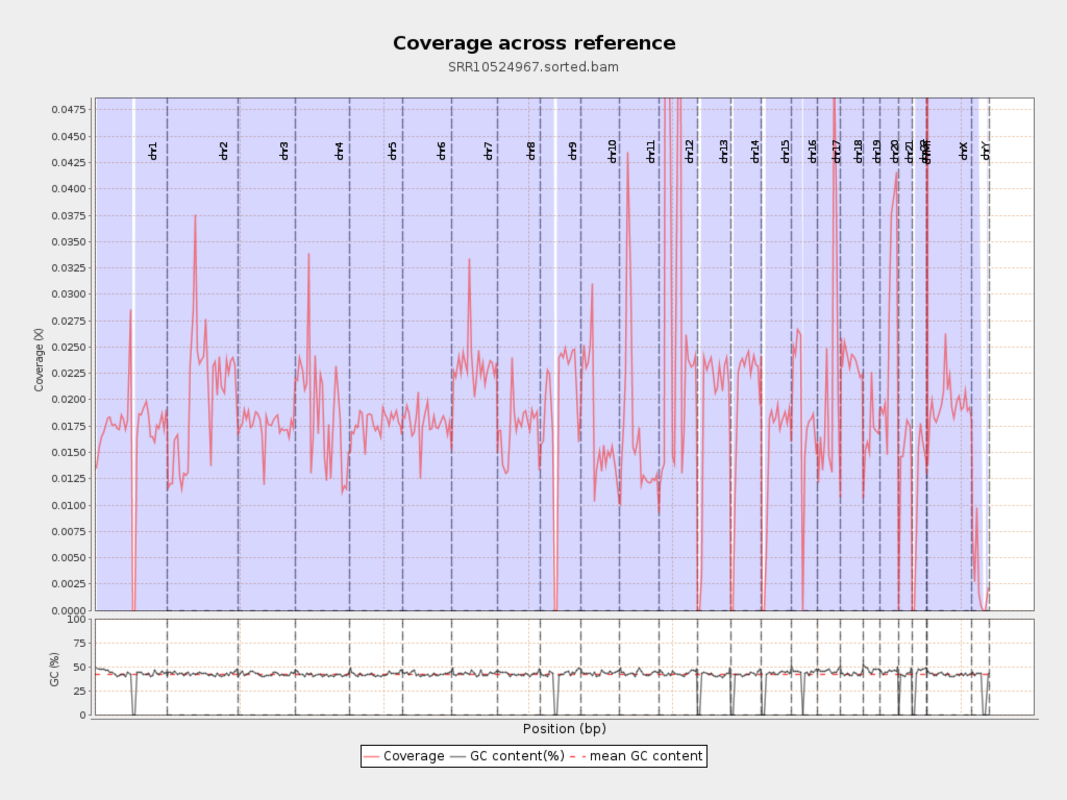
General error rate	0.49%
Mismatches	279,591
Insertions	3,894
Mapped reads with at least one insertion	0.38%
Deletions	9,404
Mapped reads with at least one deletion	0.92%
Homopolymer indels	41.66%

2.6. Chromosome stats

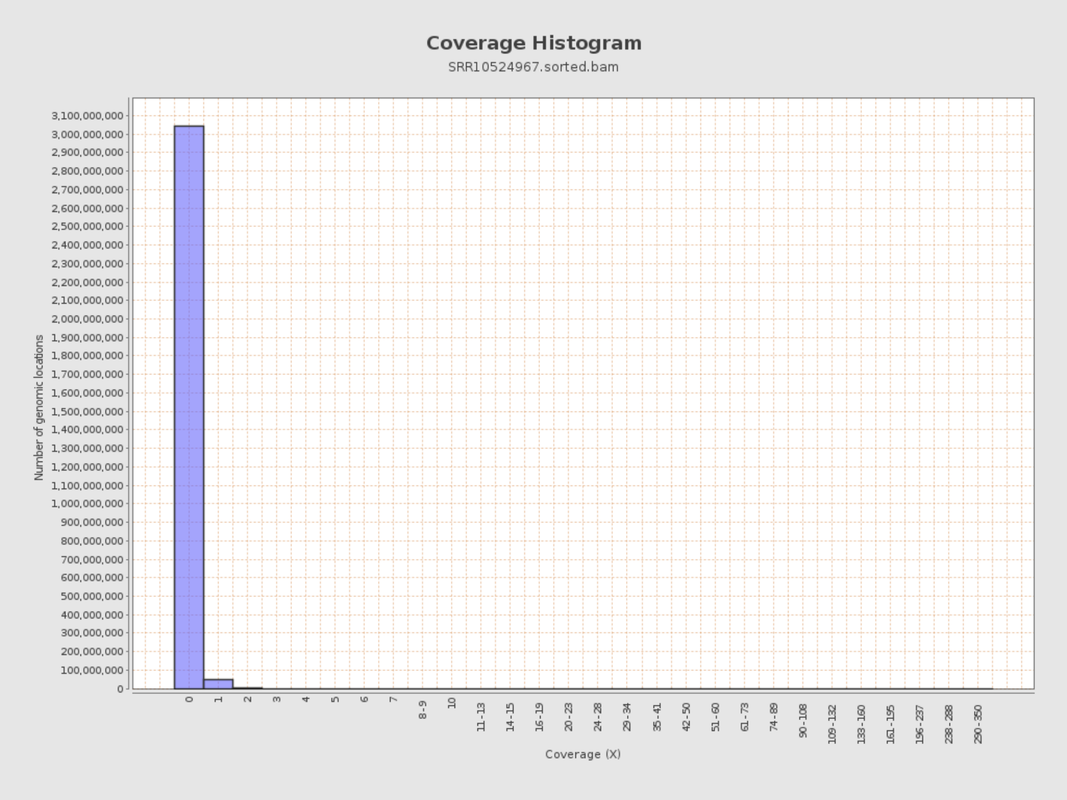
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4186127	0.0168	0.3001
chr2	243199373	4939041	0.0203	0.2076
chr3	198022430	3484481	0.0176	0.1392
chr4	191154276	3587654	0.0188	0.1576
chr5	180915260	3226574	0.0178	0.1414
chr6	171115067	3040111	0.0178	0.1469
chr7	159138663	3717153	0.0234	0.2471

chr8	146364022	2538255	0.0173	0.1759
chr9	141213431	2704922	0.0192	0.2035
chr10	135534747	2369767	0.0175	0.1919
chr11	135006516	2287093	0.0169	0.1645
chr12	133851895	4390090	0.0328	0.2047
chr13	115169878	2160728	0.0188	0.1433
chr14	107349540	2079014	0.0194	0.1542
chr15	102531392	1516575	0.0148	0.1277
chr16	90354753	1661795	0.0184	0.1492
chr17	81195210	1767313	0.0218	0.1588
chr18	78077248	1849408	0.0237	0.3246
chr19	59128983	998705	0.0169	0.2242
chr20	63025520	1747098	0.0277	0.1785
chr21	48129895	698456	0.0145	0.1387
chr22	51304566	573504	0.0112	0.1104
chrMT	16571	9443	0.5699	0.8637
chrX	155270560	3048302	0.0196	0.1626
chrY	59373566	165443	0.0028	0.0772

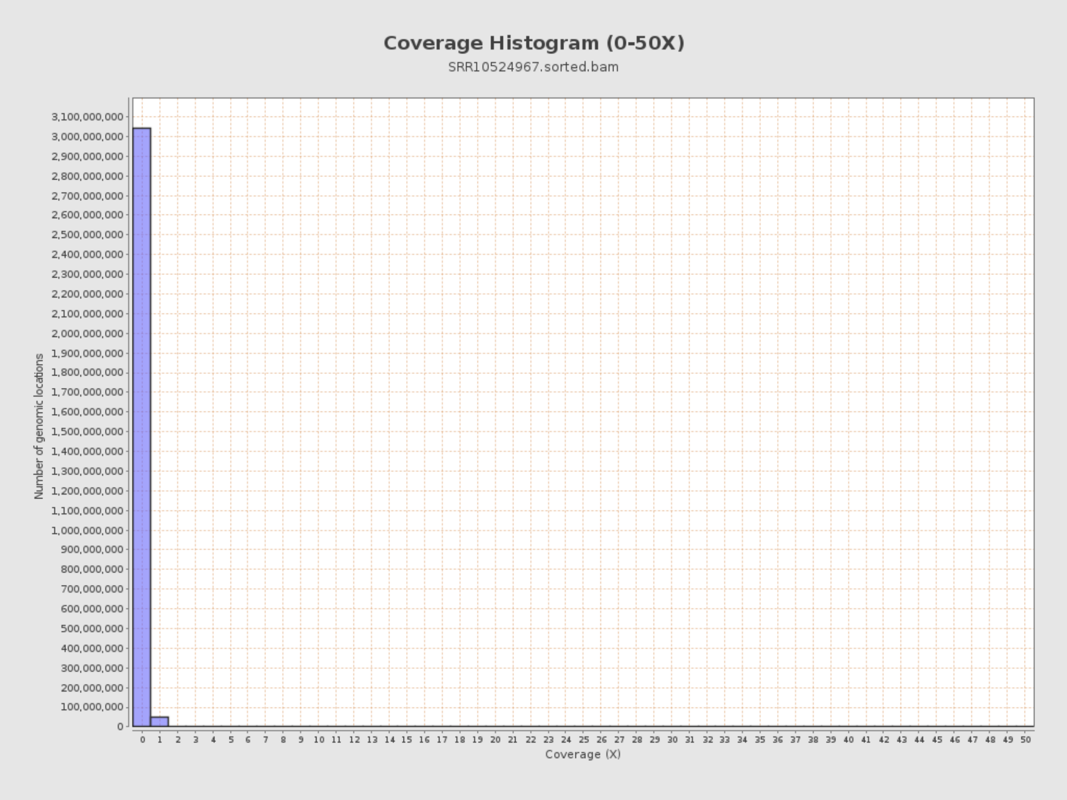
3. Results : Coverage across reference



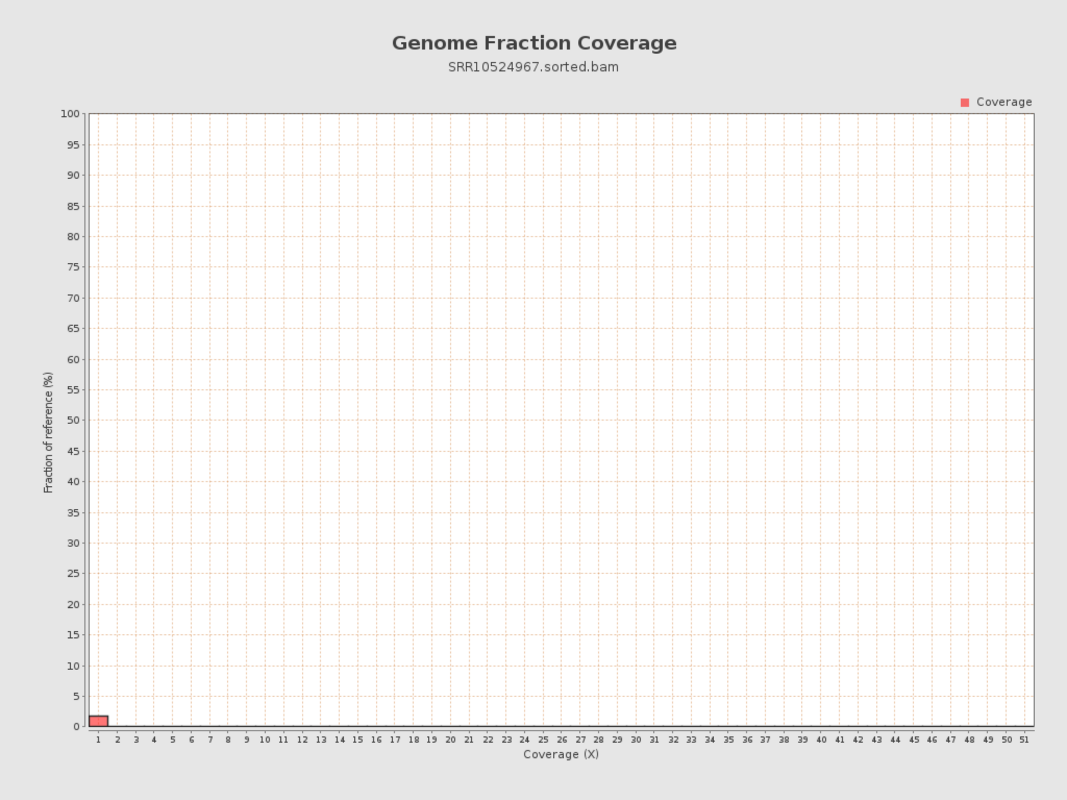
4. Results : Coverage Histogram



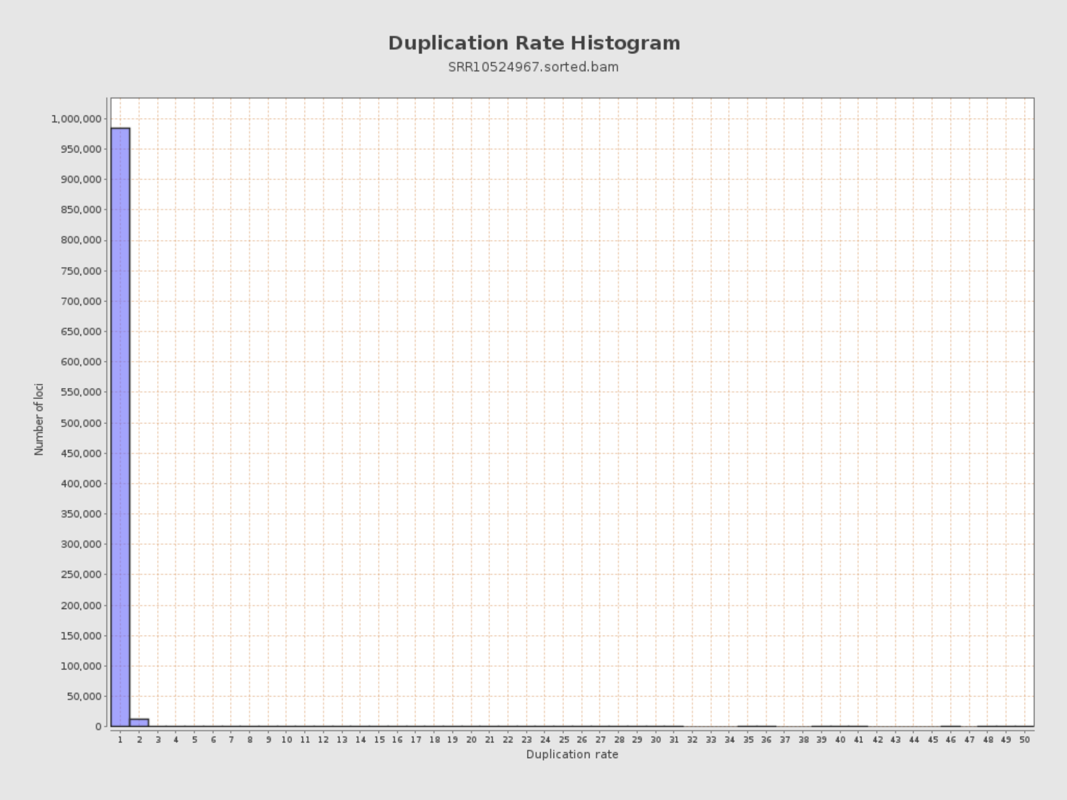
5. Results : Coverage Histogram (0-50X)



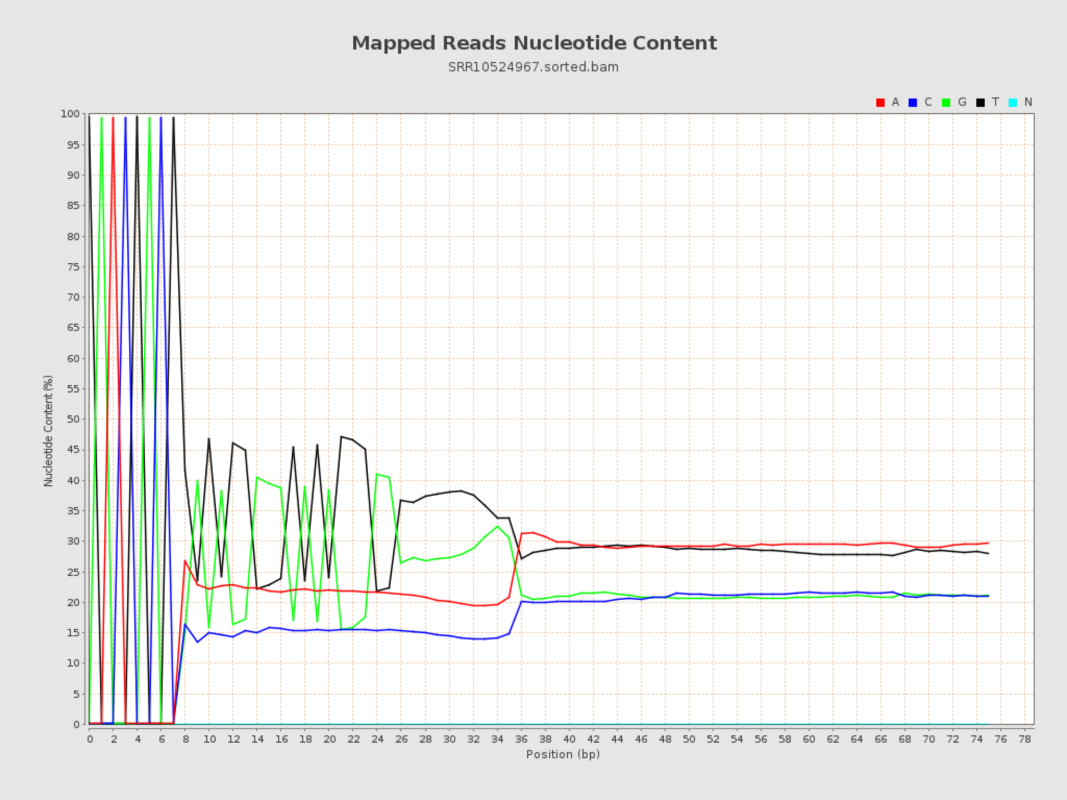
6. Results : Genome Fraction Coverage



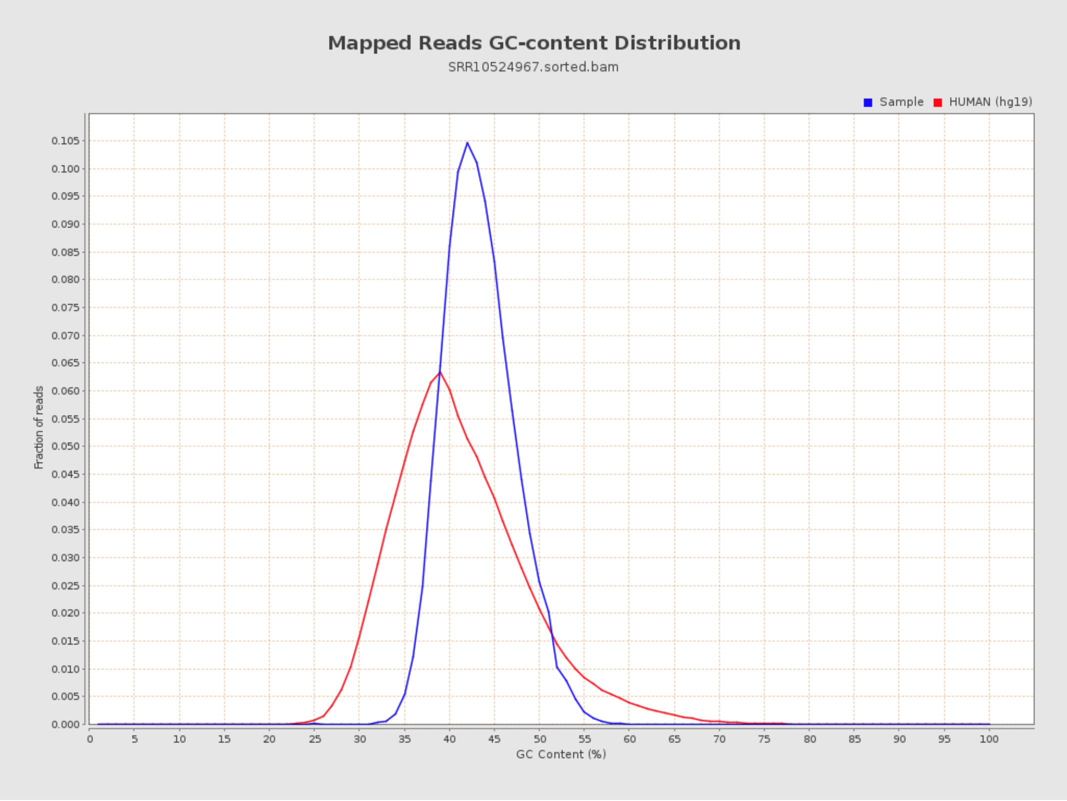
7. Results : Duplication Rate Histogram



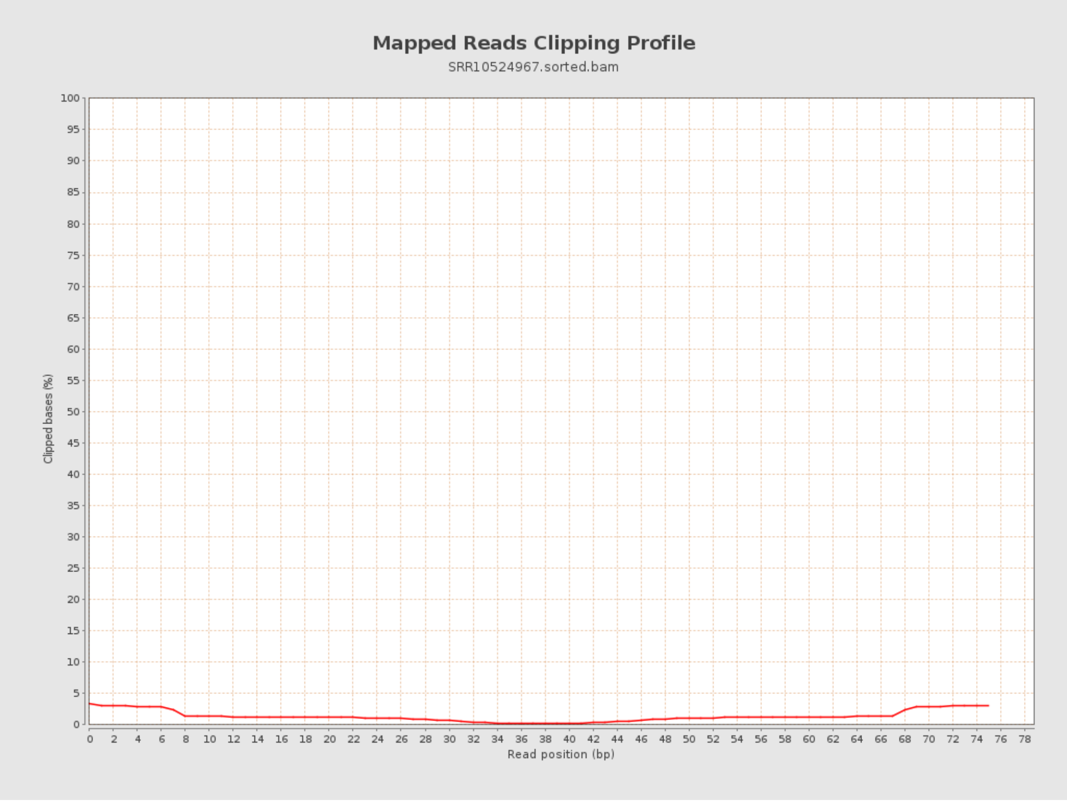
8. Results : Mapped Reads Nucleotide Content



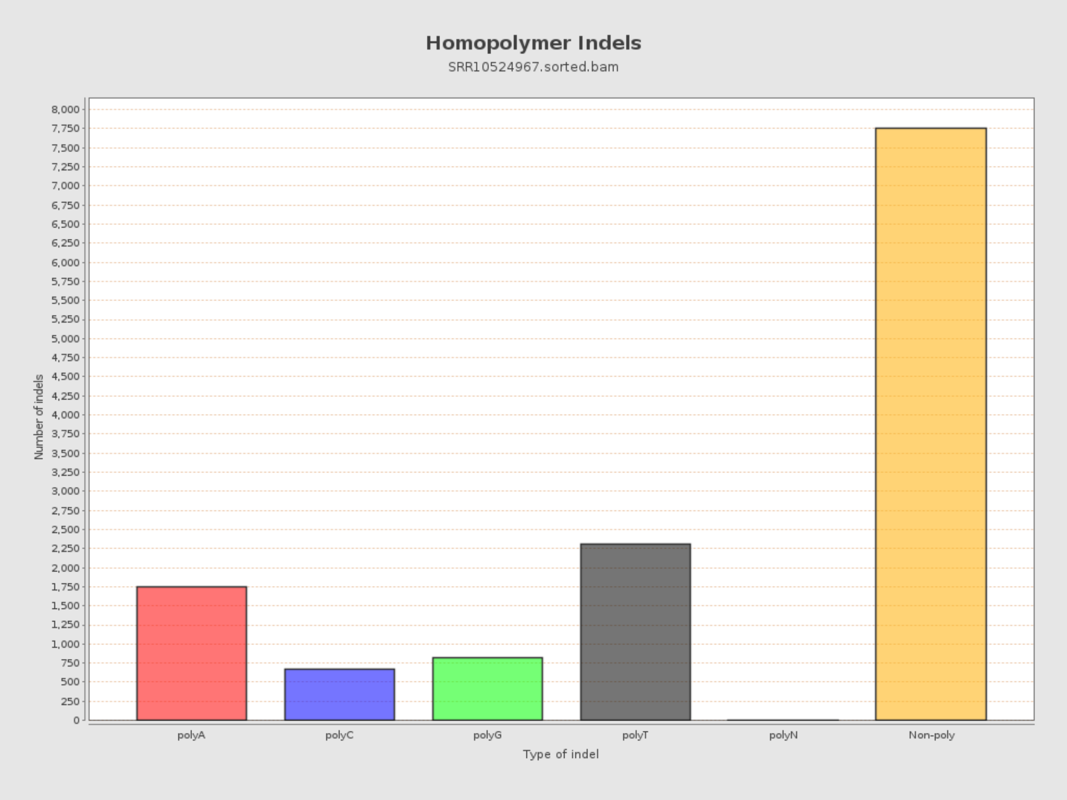
9. Results : Mapped Reads GC-content Distribution



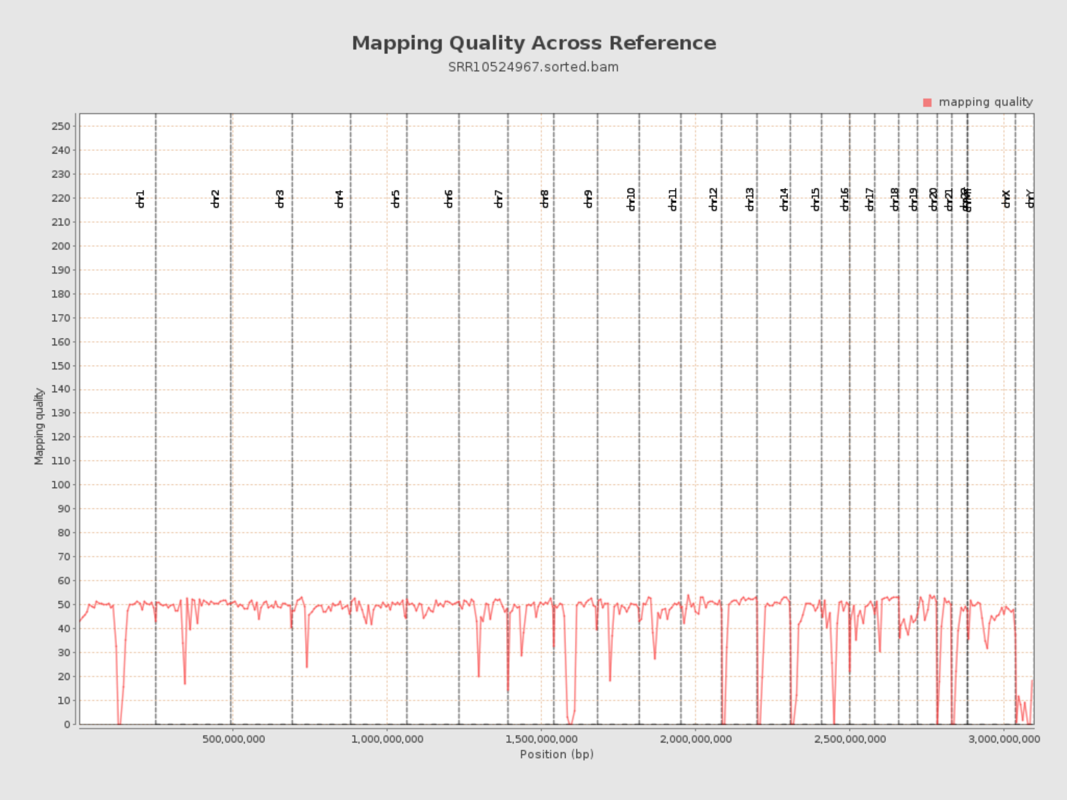
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram