Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:52:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524767.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_SRR10524767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524767.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:52:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,419,786
Mapped reads	1,306,591 / 92.03%
Unmapped reads	113,195 / 7.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,568 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	38,185 / 2.69%
Duplication rate	2%
Clipped reads	1,306,351 / 92.01%

2.2. ACGT Content

Number/percentage of A's	18,676,580 / 24.61%
Number/percentage of C's	14,020,429 / 18.48%
Number/percentage of T's	24,605,368 / 32.42%
Number/percentage of G's	18,581,089 / 24.49%
Number/percentage of N's	1,581 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2397

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

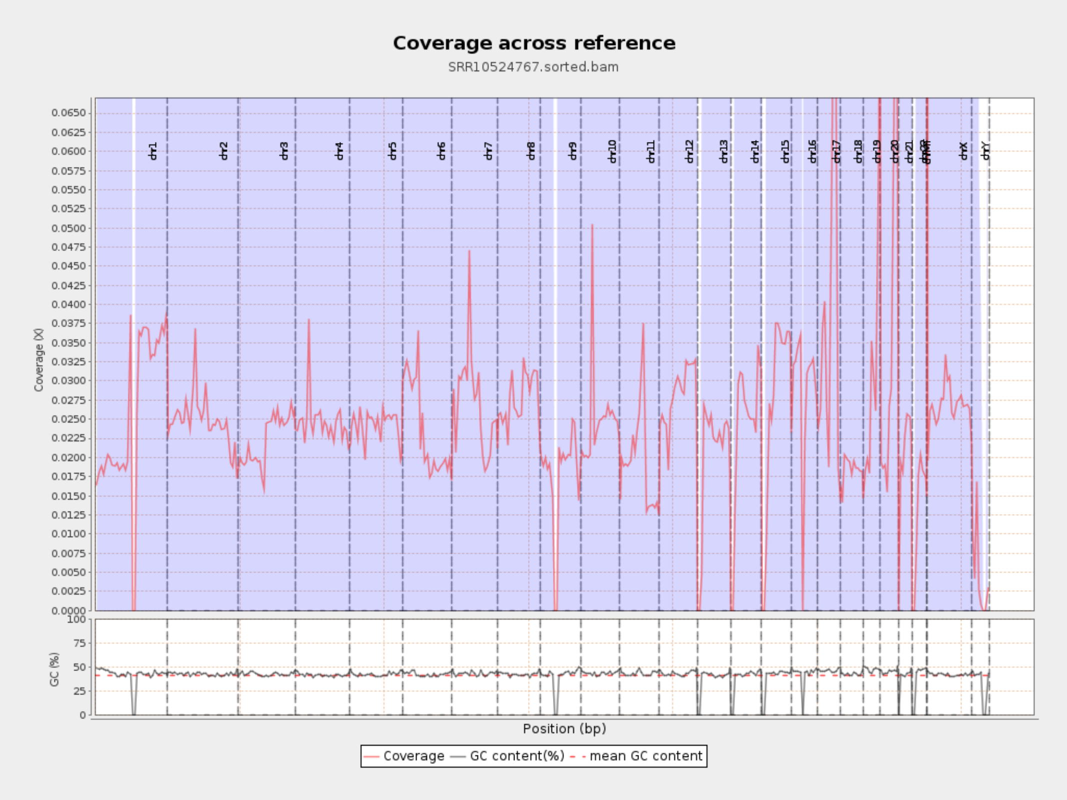
General error rate	0.52%
Mismatches	385,663
Insertions	6,141
Mapped reads with at least one insertion	0.47%
Deletions	15,188
Mapped reads with at least one deletion	1.16%
Homopolymer indels	40.9%

2.6. Chromosome stats

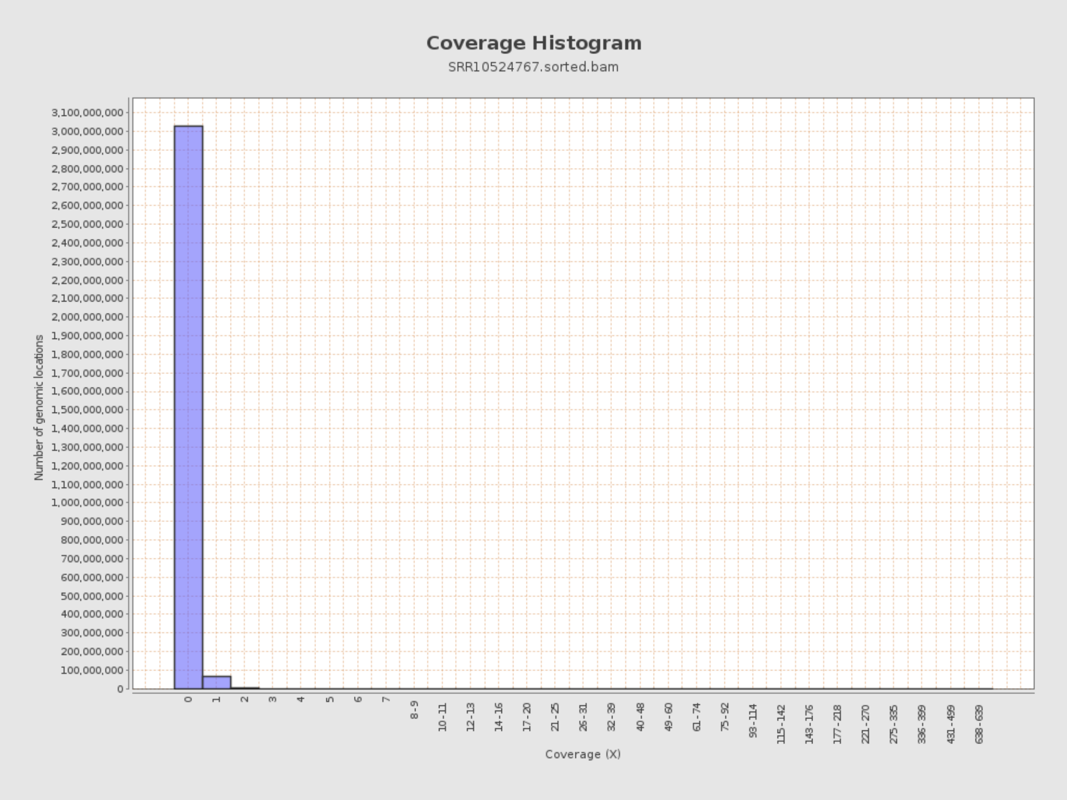
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6341918	0.0254	0.389
chr2	243199373	6044013	0.0249	0.3164
chr3	198022430	4418913	0.0223	0.1608
chr4	191154276	4711057	0.0246	0.1853
chr5	180915260	4398754	0.0243	0.1666
chr6	171115067	4056907	0.0237	0.1904
chr7	159138663	4335547	0.0272	0.3281

chr8	146364022	4064799	0.0278	0.2964
chr9	141213431	2489297	0.0176	0.1716
chr10	135534747	3384945	0.025	0.2584
chr11	135006516	2680915	0.0199	0.1921
chr12	133851895	3771223	0.0282	0.1797
chr13	115169878	2288023	0.0199	0.1514
chr14	107349540	2544538	0.0237	0.1656
chr15	102531392	2757674	0.0269	0.1775
chr16	90354753	2547976	0.0282	0.1901
chr17	81195210	3216595	0.0396	0.2209
chr18	78077248	1433857	0.0184	0.2814
chr19	59128983	1872150	0.0317	0.2974
chr20	63025520	2383400	0.0378	0.2152
chr21	48129895	974026	0.0202	0.1677
chr22	51304566	664021	0.0129	0.1207
chrMT	16571	84339	5.0896	3.4775
chrX	155270560	4180656	0.0269	0.1876
chrY	59373566	263584	0.0044	0.1694

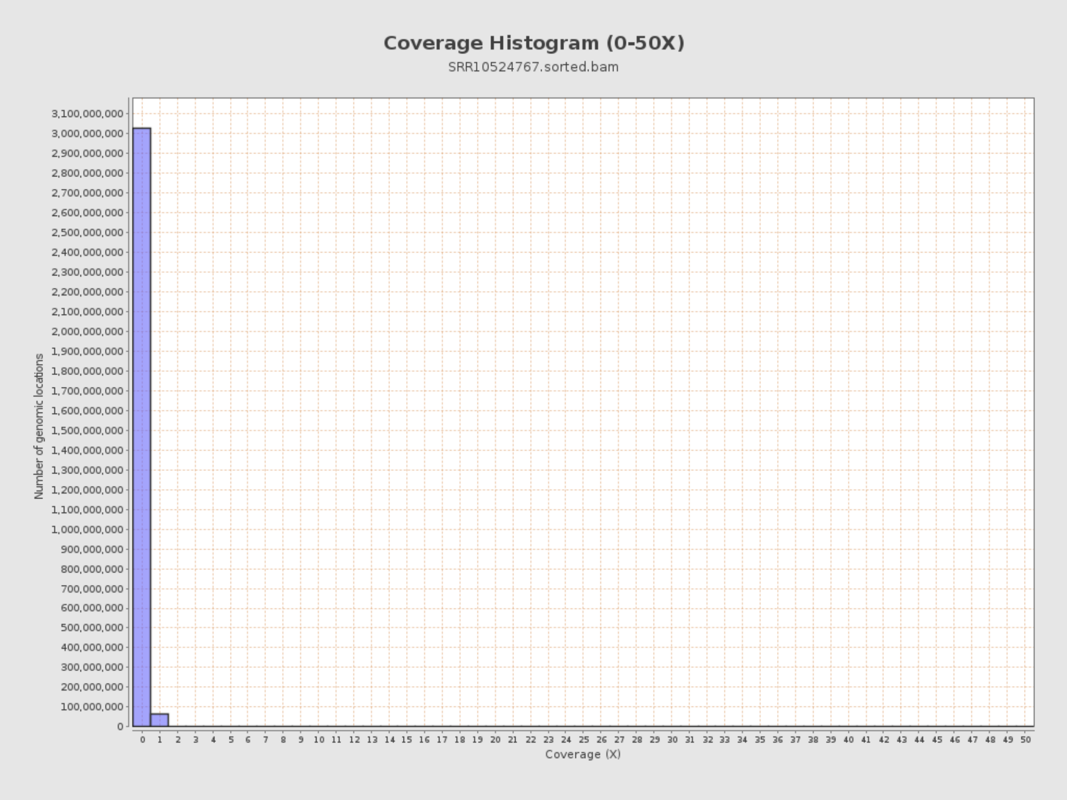
3. Results : Coverage across reference



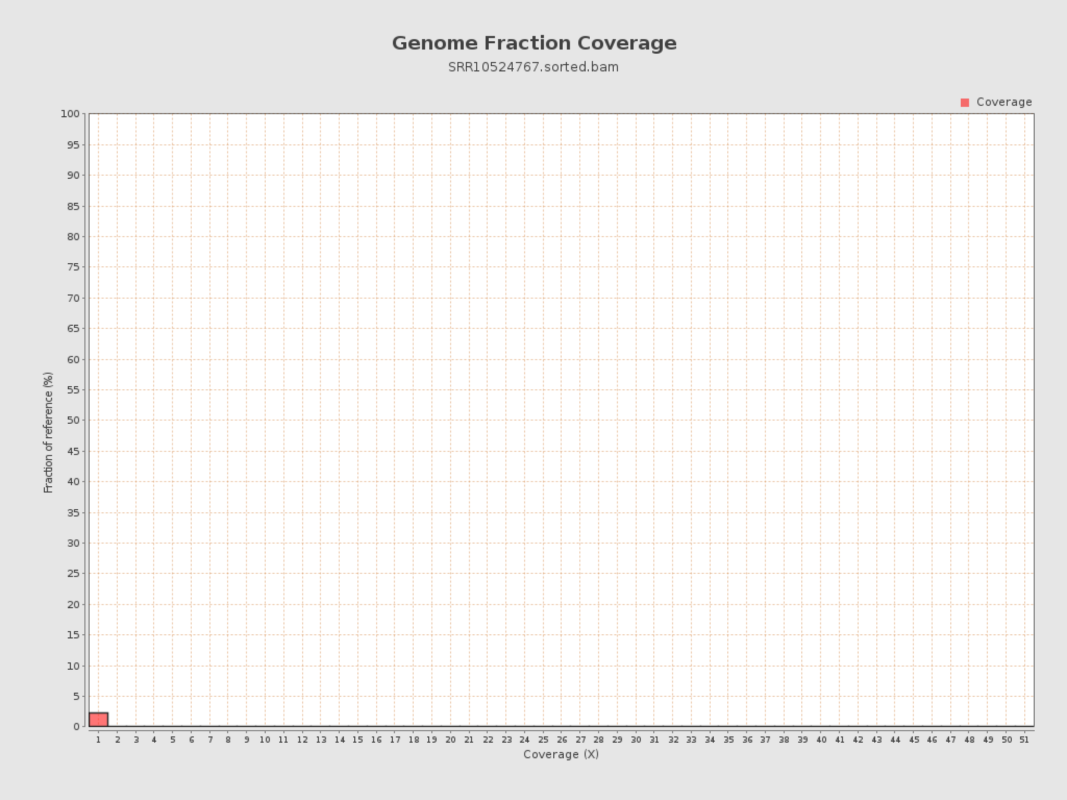
4. Results : Coverage Histogram



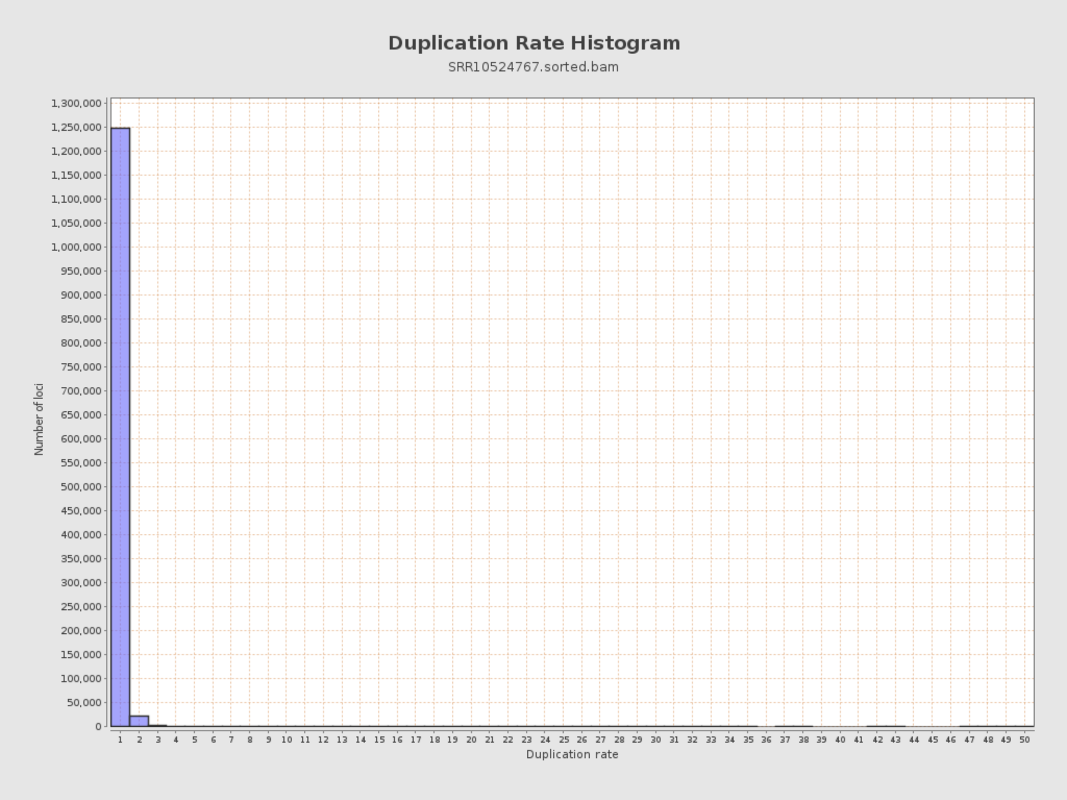
5. Results : Coverage Histogram (0-50X)



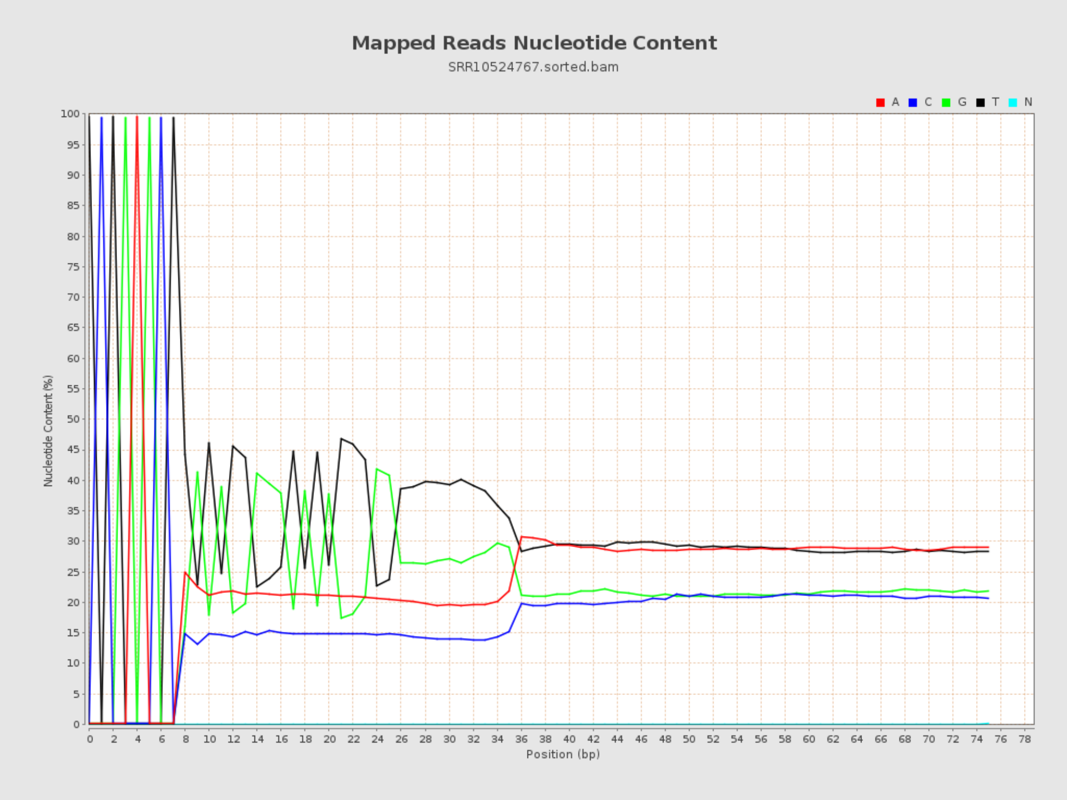
6. Results : Genome Fraction Coverage



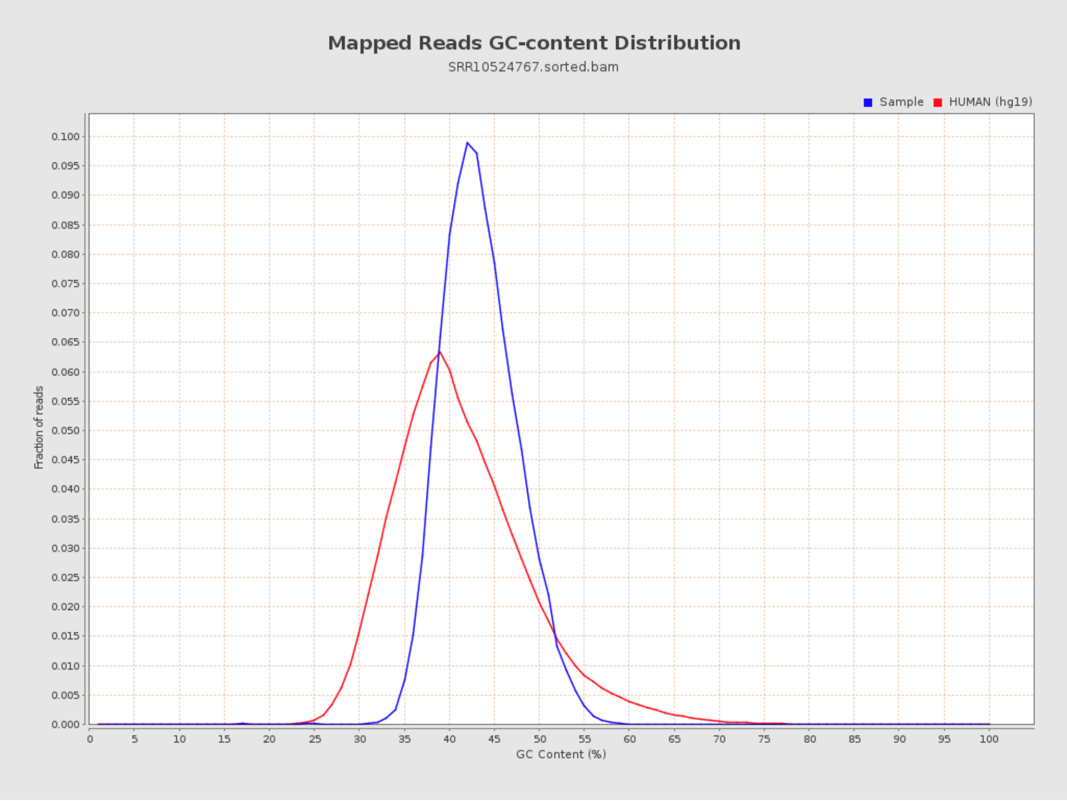
7. Results : Duplication Rate Histogram



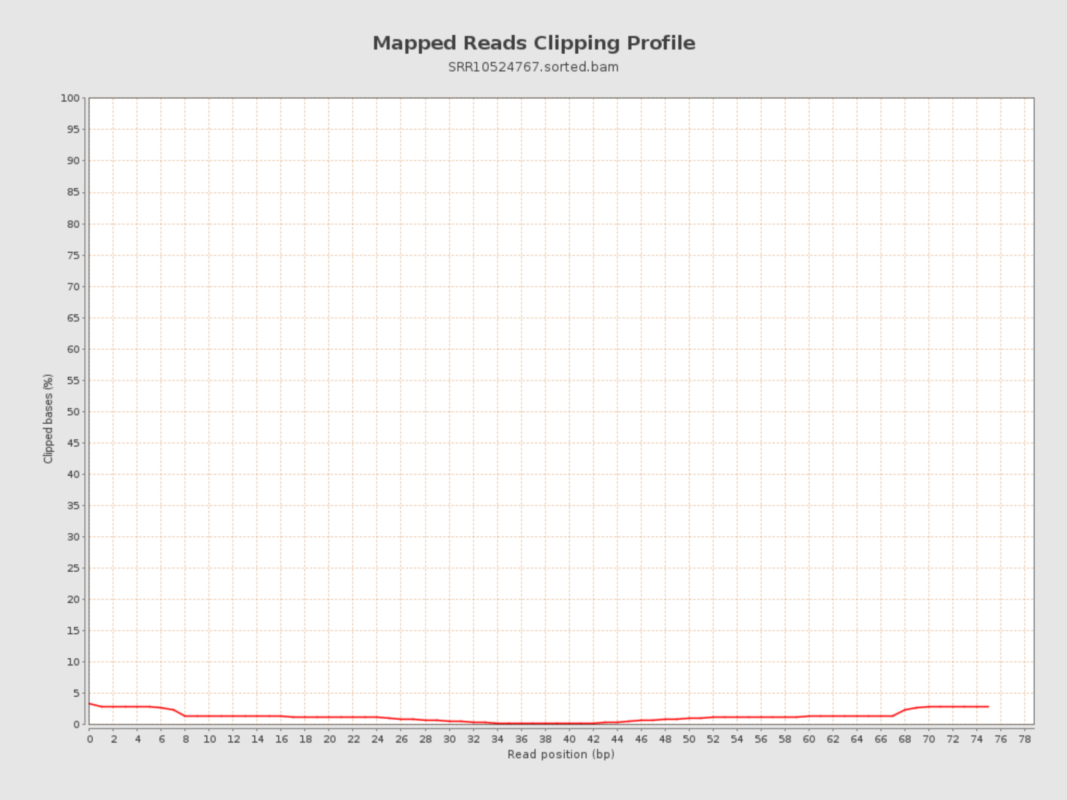
8. Results : Mapped Reads Nucleotide Content



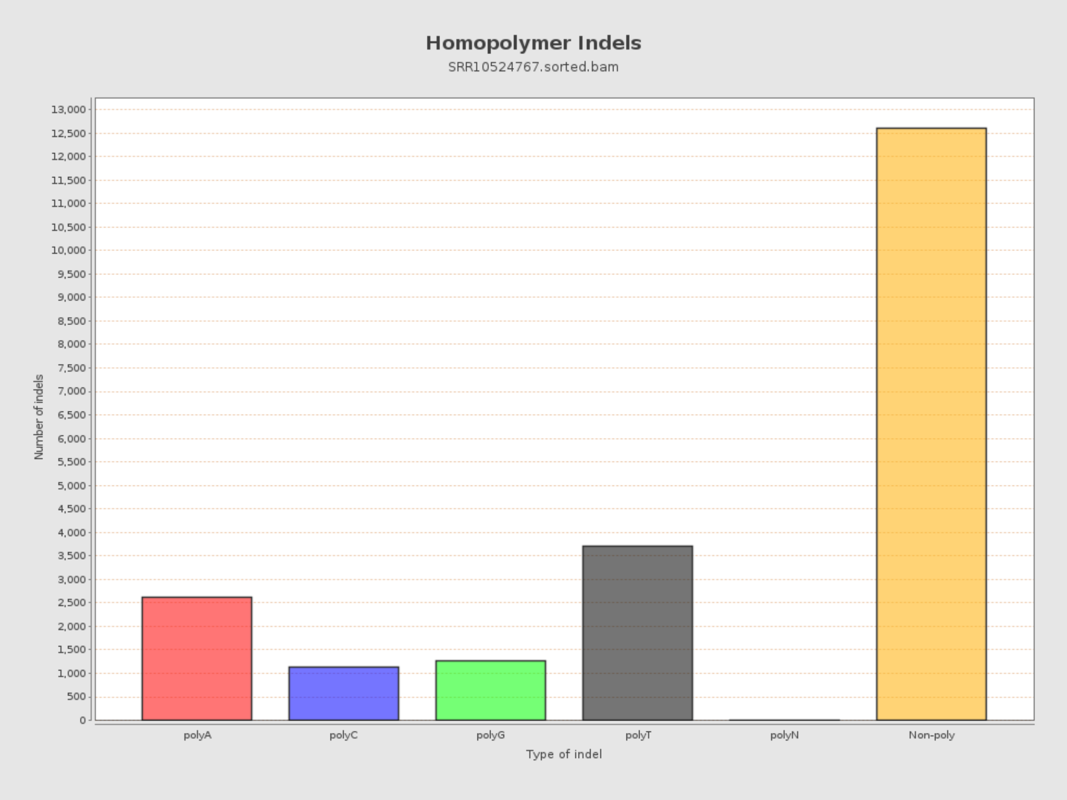
9. Results : Mapped Reads GC-content Distribution



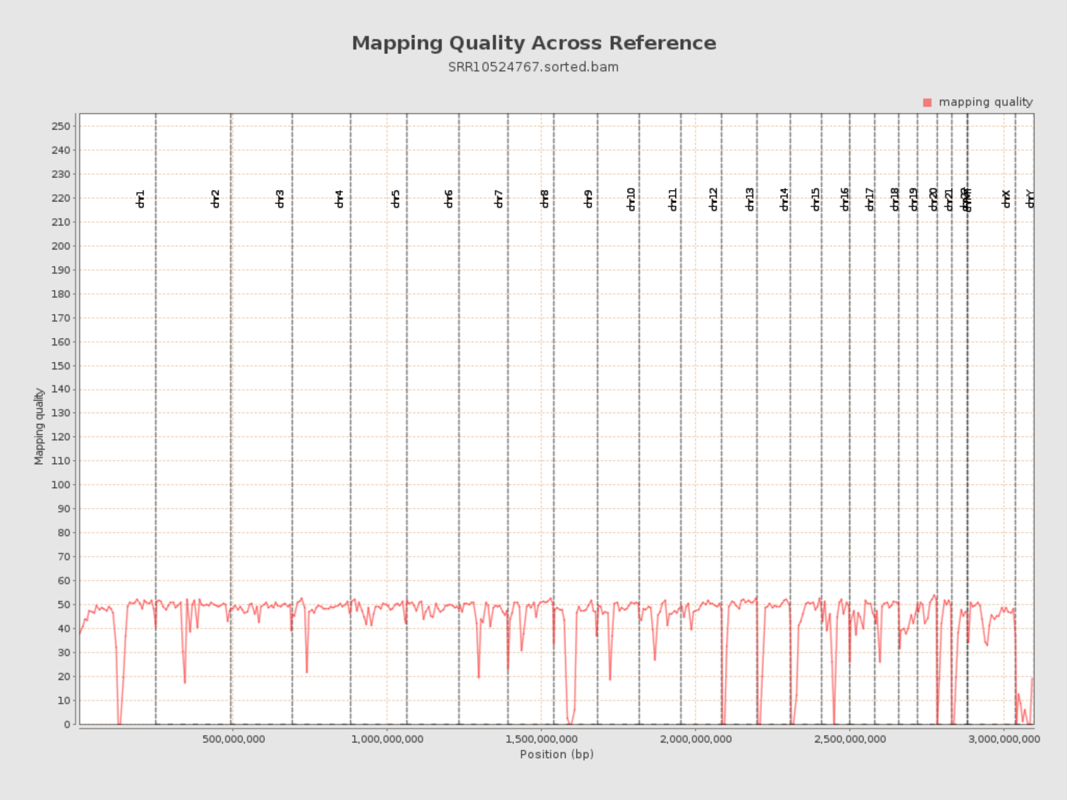
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram