Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:38:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524476.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_SRR10524476 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524476.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:38:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524476.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	472,877
Mapped reads	434,399 / 91.86%
Unmapped reads	38,478 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	934 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	9,306 / 1.97%
Duplication rate	1.71%
Clipped reads	433,824 / 91.74%

2.2. ACGT Content

Number/percentage of A's	6,604,598 / 26.22%
Number/percentage of C's	4,661,624 / 18.51%
Number/percentage of T's	7,707,728 / 30.6%
Number/percentage of G's	6,215,146 / 24.67%
Number/percentage of N's	486 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0081

Standard Deviation	0.1085

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

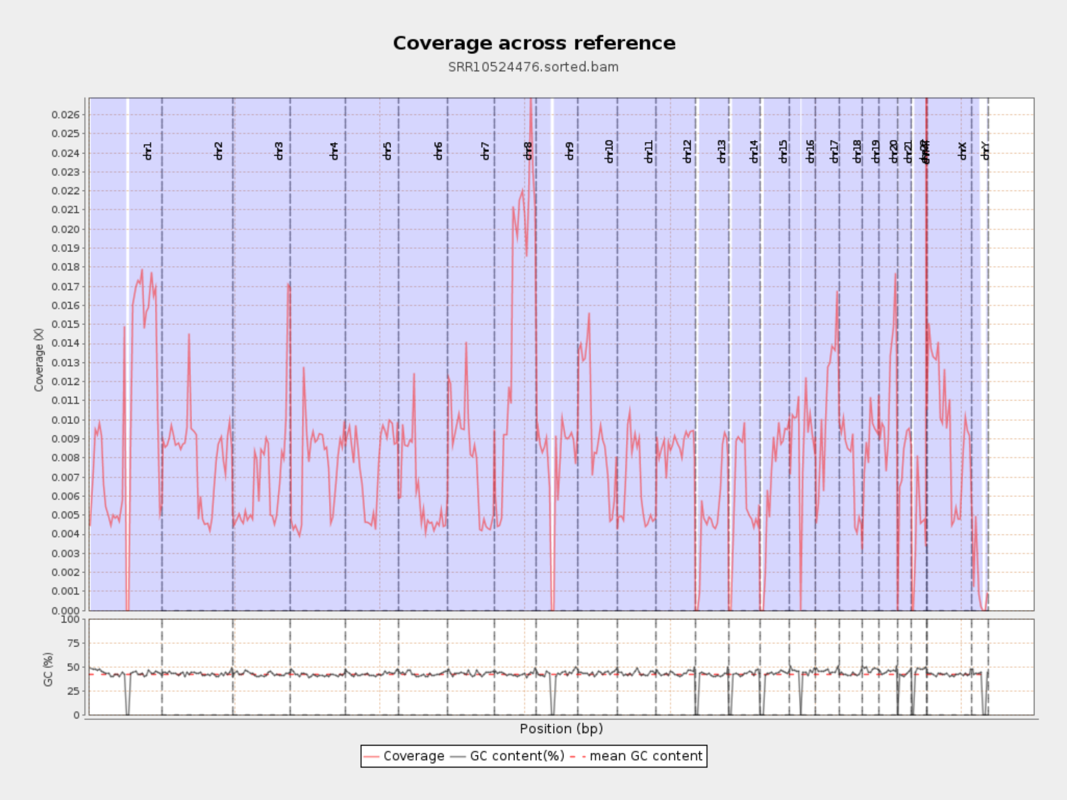
General error rate	0.48%
Mismatches	117,496
Insertions	1,984
Mapped reads with at least one insertion	0.46%
Deletions	4,529
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.67%

2.6. Chromosome stats

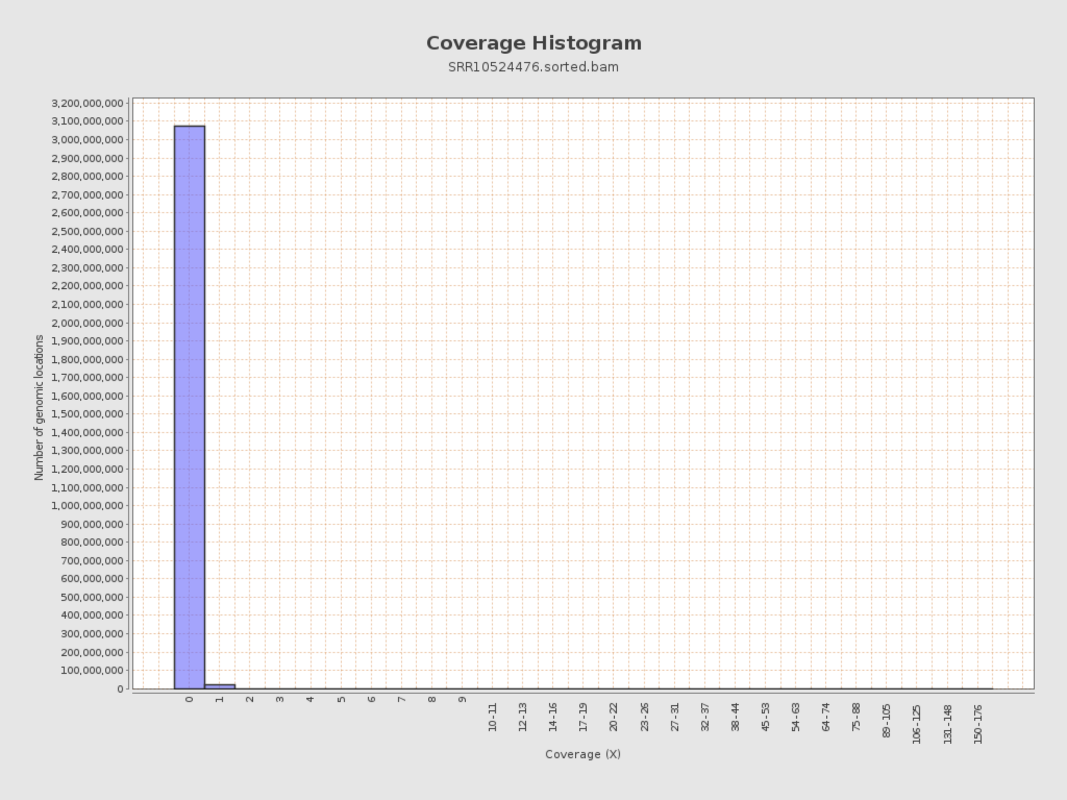
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2471741	0.0099	0.1607
chr2	243199373	1960455	0.0081	0.1165
chr3	198022430	1354330	0.0068	0.0861
chr4	191154276	1431077	0.0075	0.0939
chr5	180915260	1402335	0.0078	0.0914
chr6	171115067	1070206	0.0063	0.0904
chr7	159138663	1270839	0.008	0.1218

chr8	146364022	2288529	0.0156	0.1361
chr9	141213431	1074513	0.0076	0.1016
chr10	135534747	1310218	0.0097	0.1162
chr11	135006516	876659	0.0065	0.098
chr12	133851895	1162842	0.0087	0.0968
chr13	115169878	578165	0.005	0.0735
chr14	107349540	607388	0.0057	0.0786
chr15	102531392	679321	0.0066	0.0857
chr16	90354753	802015	0.0089	0.0997
chr17	81195210	879081	0.0108	0.1101
chr18	78077248	581395	0.0074	0.1383
chr19	59128983	525220	0.0089	0.1286
chr20	63025520	725209	0.0115	0.1114
chr21	48129895	358301	0.0074	0.0915
chr22	51304566	200235	0.0039	0.0647
chrMT	16571	1499	0.0905	0.3286
chrX	155270560	1502805	0.0097	0.106
chrY	59373566	82798	0.0014	0.0488

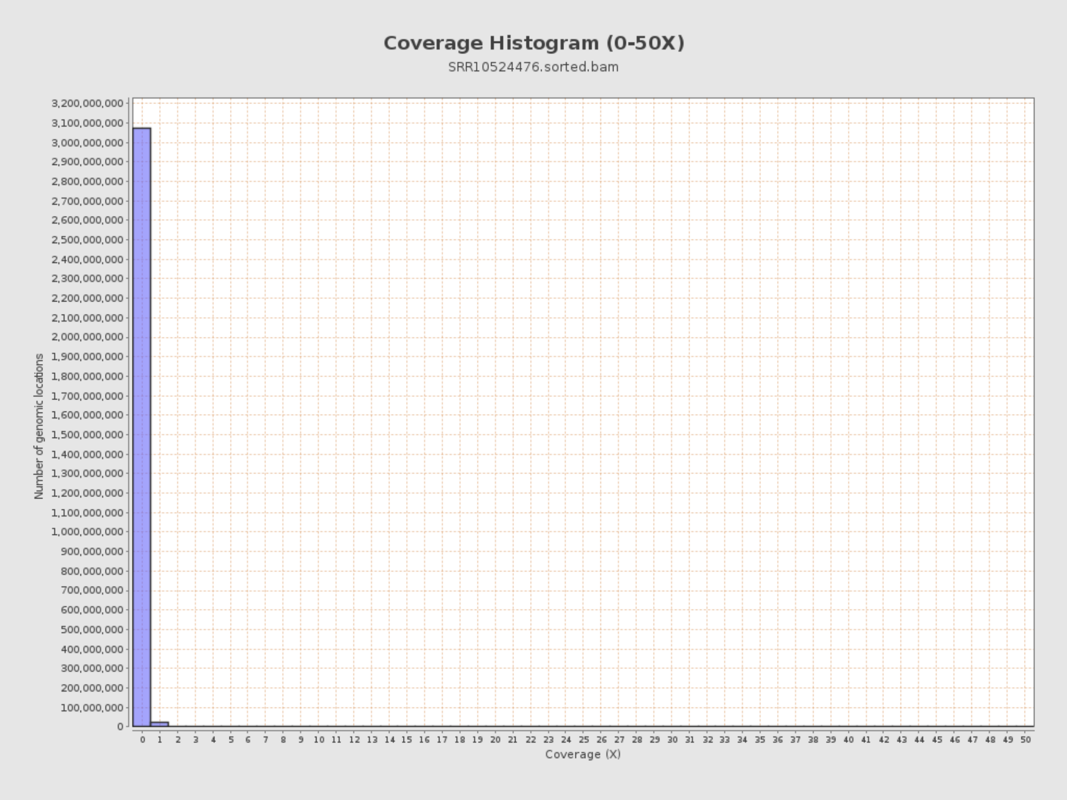
3. Results : Coverage across reference



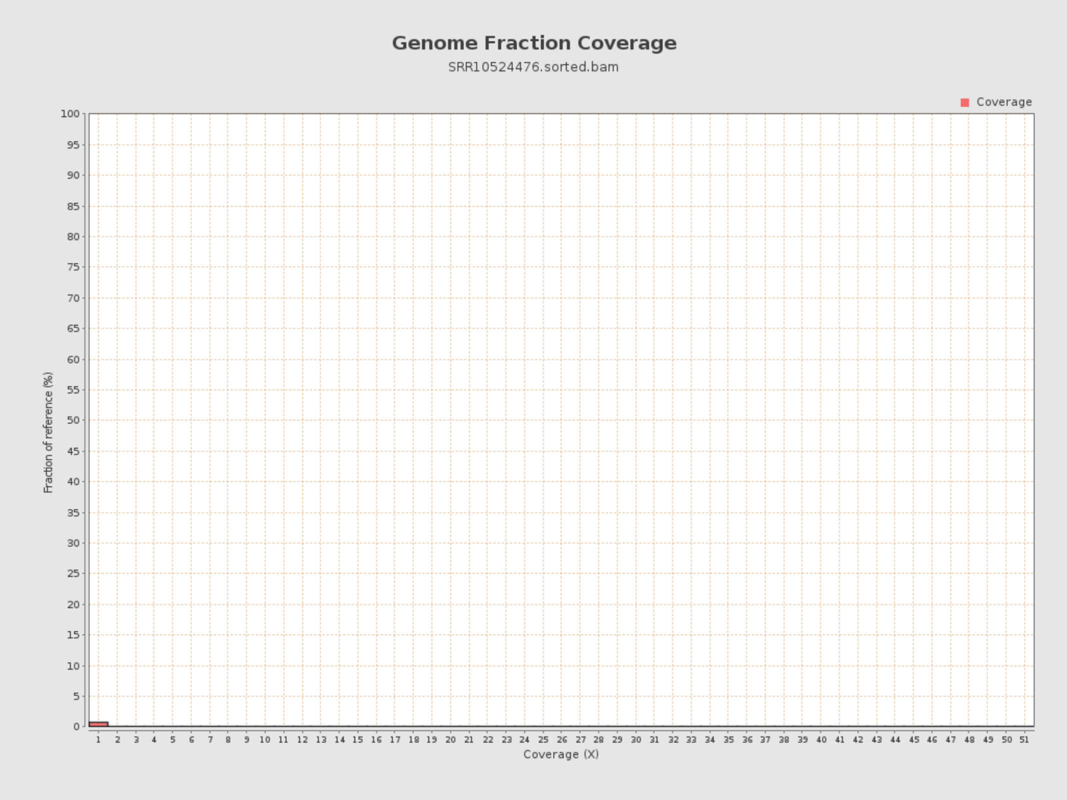
4. Results : Coverage Histogram



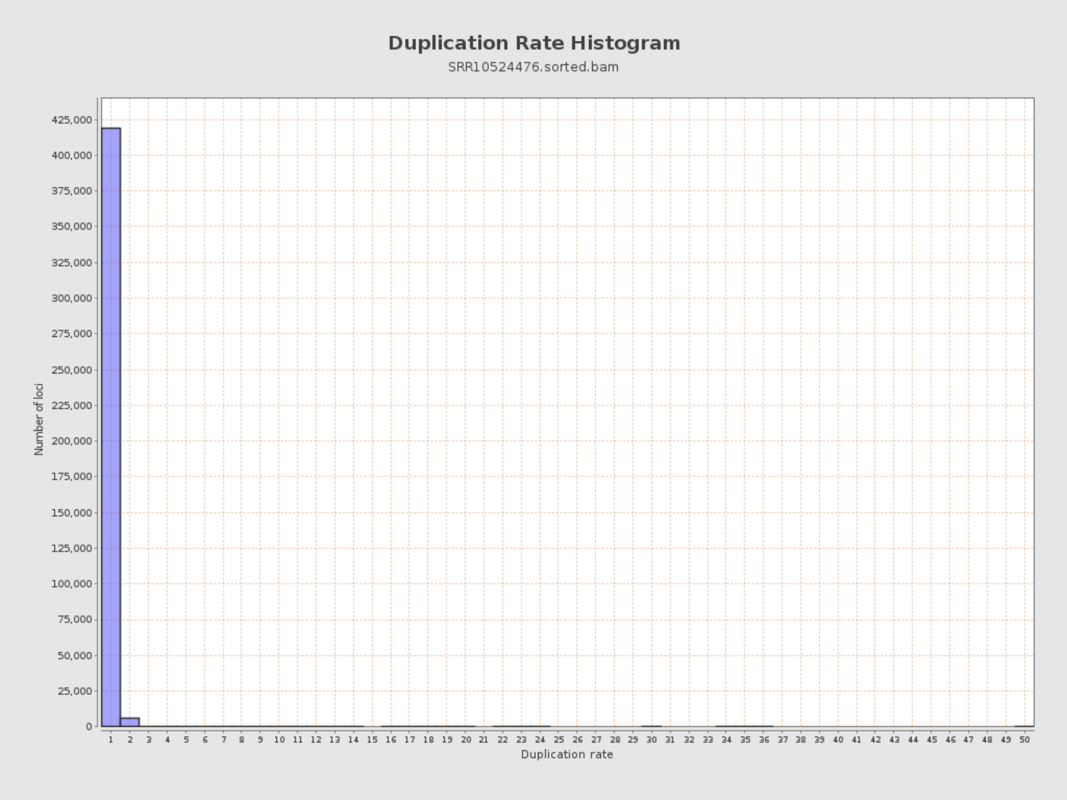
5. Results : Coverage Histogram (0-50X)



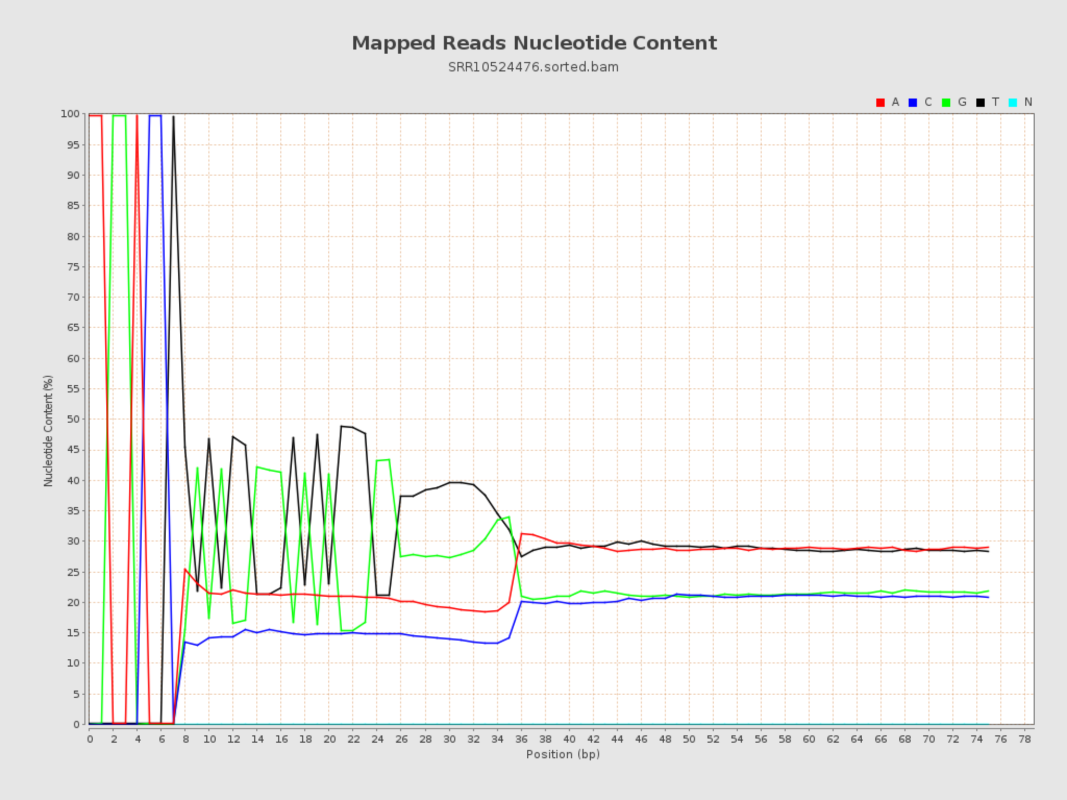
6. Results : Genome Fraction Coverage



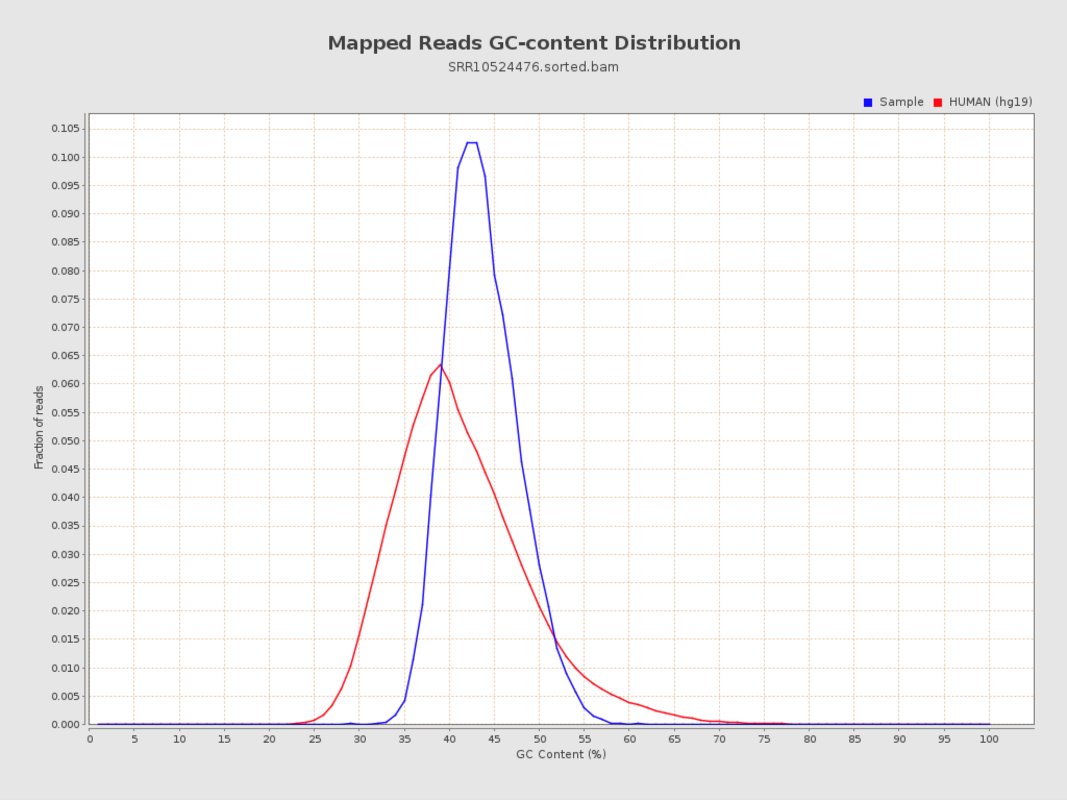
7. Results : Duplication Rate Histogram



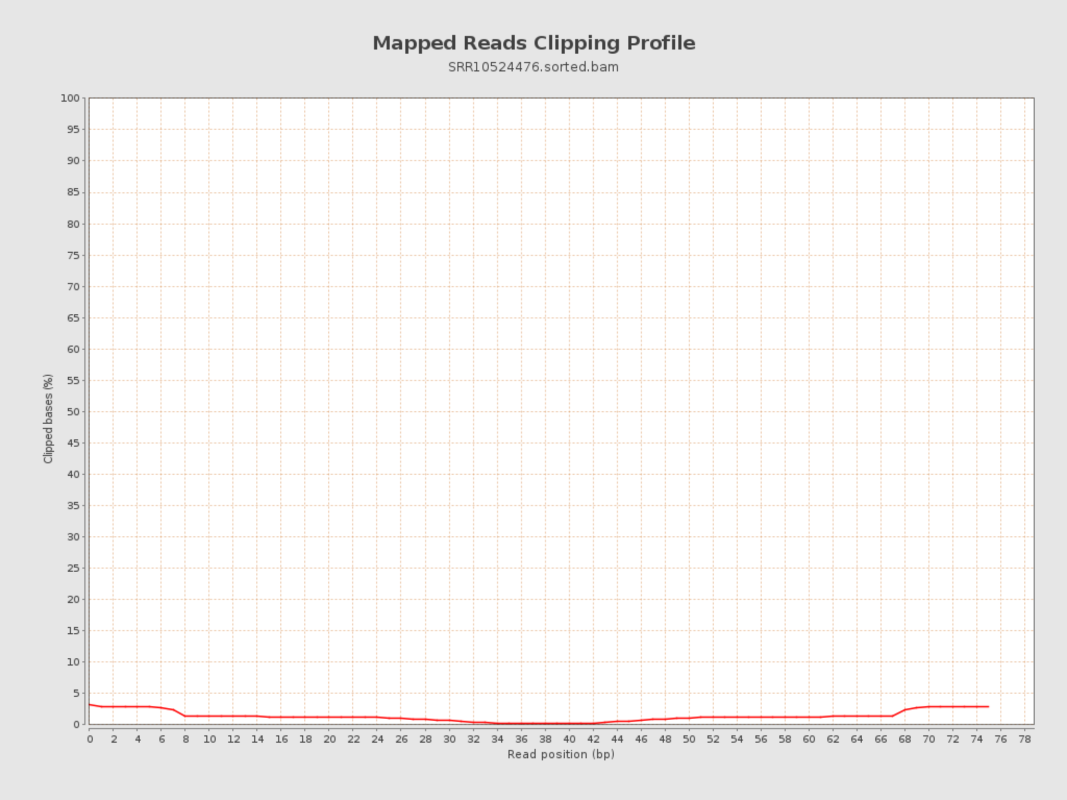
8. Results : Mapped Reads Nucleotide Content



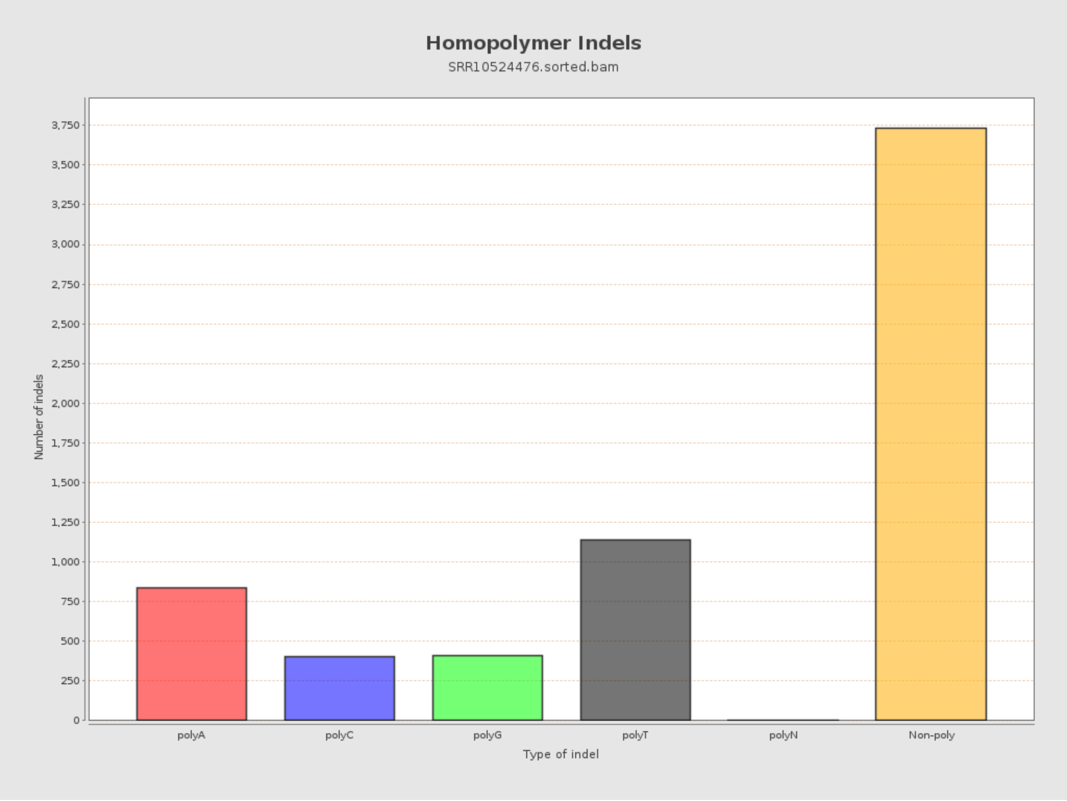
9. Results : Mapped Reads GC-content Distribution



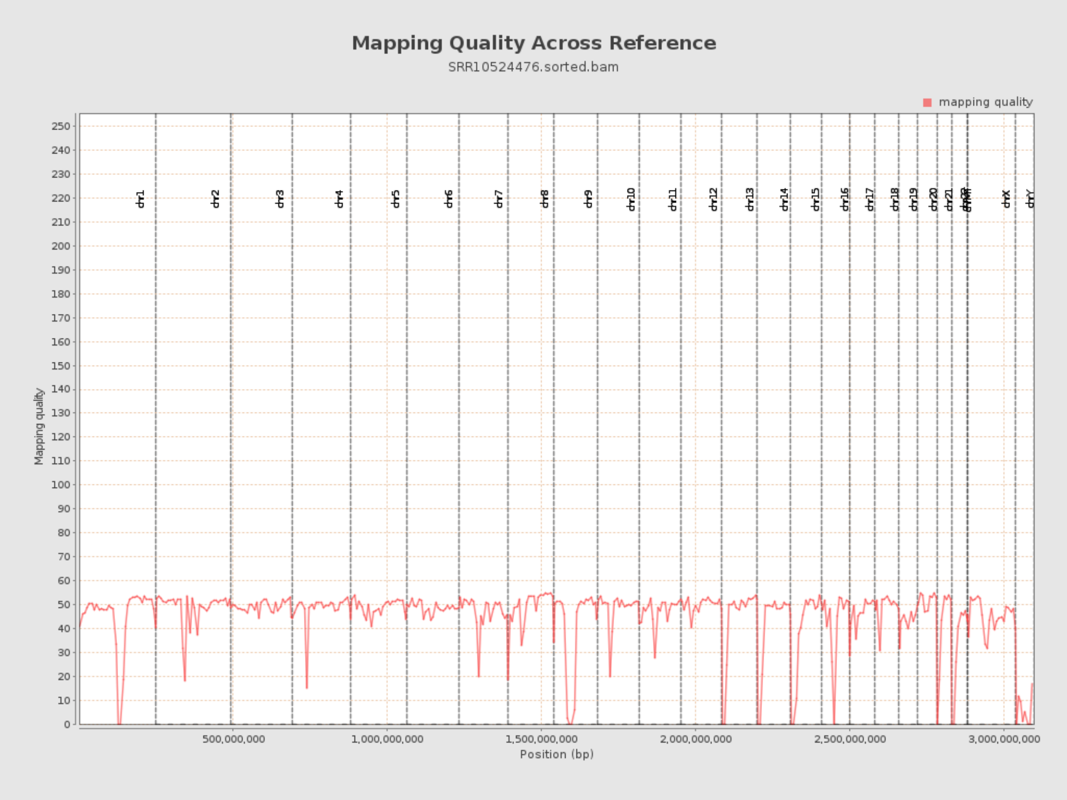
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram