Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:16:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524919.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_SRR10524919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:16:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	792,139
Mapped reads	729,327 / 92.07%
Unmapped reads	62,812 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,101 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,218 / 2.93%
Duplication rate	2.49%
Clipped reads	730,499 / 92.22%

2.2. ACGT Content

Number/percentage of A's	10,764,505 / 25.37%
Number/percentage of C's	8,288,336 / 19.54%
Number/percentage of T's	13,332,513 / 31.42%
Number/percentage of G's	10,040,896 / 23.67%
Number/percentage of N's	387 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0137

Standard Deviation	0.1551

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

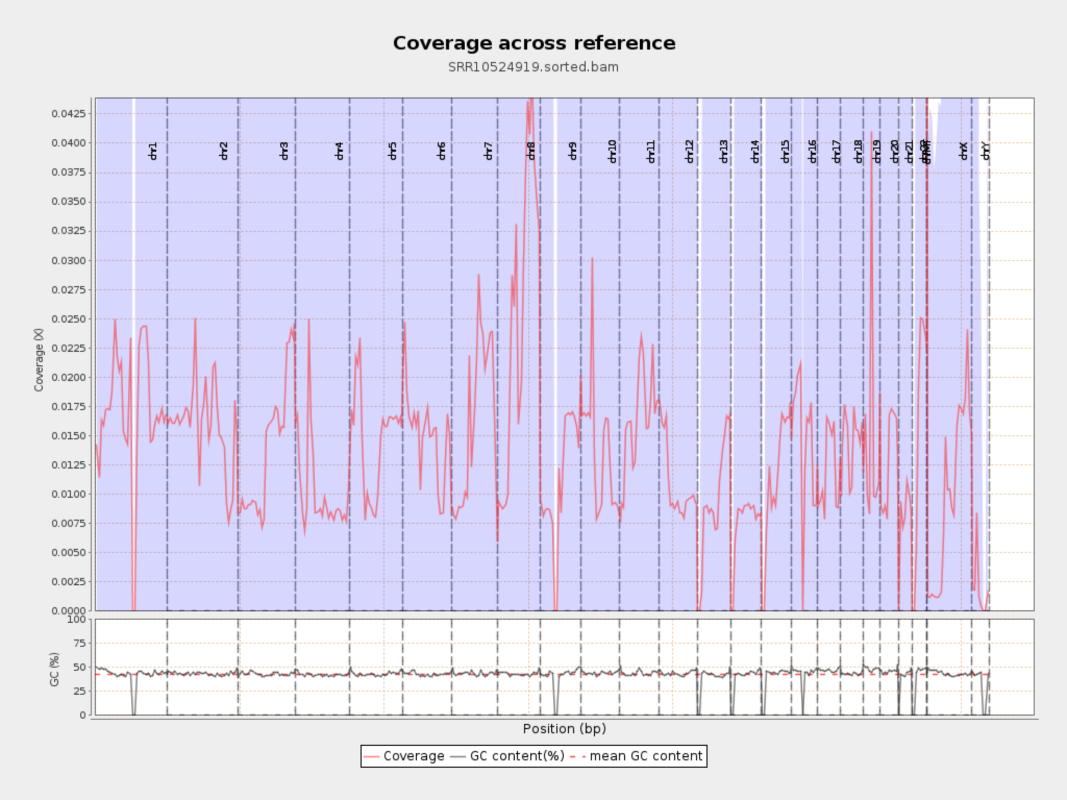
General error rate	0.53%
Mismatches	219,087
Insertions	3,086
Mapped reads with at least one insertion	0.42%
Deletions	8,218
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.72%

2.6. Chromosome stats

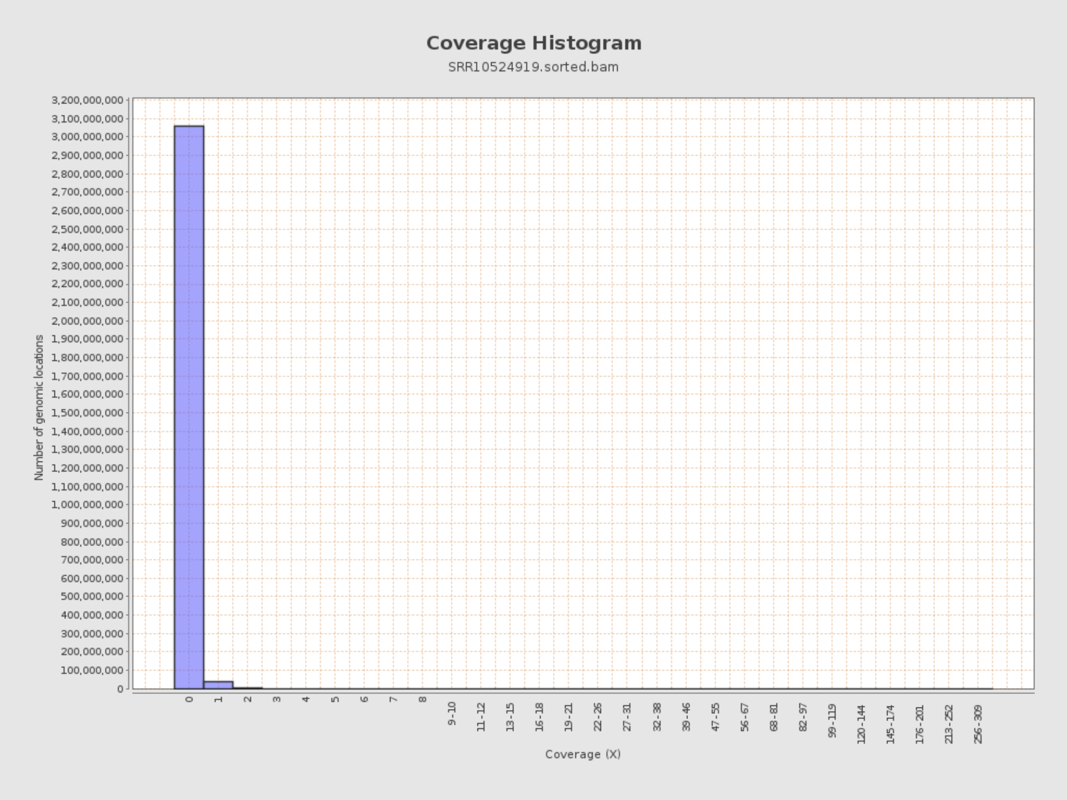
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4229965	0.017	0.2488
chr2	243199373	3865934	0.0159	0.187
chr3	198022430	2716572	0.0137	0.1245
chr4	191154276	1976848	0.0103	0.1228
chr5	180915260	2656949	0.0147	0.1284
chr6	171115067	2584831	0.0151	0.1352
chr7	159138663	2586548	0.0163	0.1795

chr8	146364022	3789881	0.0259	0.2085
chr9	141213431	1558310	0.011	0.1305
chr10	135534747	1887990	0.0139	0.168
chr11	135006516	2216825	0.0164	0.1515
chr12	133851895	1454963	0.0109	0.1125
chr13	115169878	1053607	0.0091	0.1013
chr14	107349540	789090	0.0074	0.0916
chr15	102531392	1126056	0.011	0.1118
chr16	90354753	1301400	0.0144	0.1316
chr17	81195210	965210	0.0119	0.1168
chr18	78077248	1126721	0.0144	0.1941
chr19	59128983	896009	0.0152	0.1898
chr20	63025520	809695	0.0128	0.1222
chr21	48129895	387836	0.0081	0.1075
chr22	51304566	803558	0.0157	0.1333
chrMT	16571	1258	0.0759	0.2804
chrX	155270560	1540864	0.0099	0.1115
chrY	59373566	113544	0.0019	0.0836

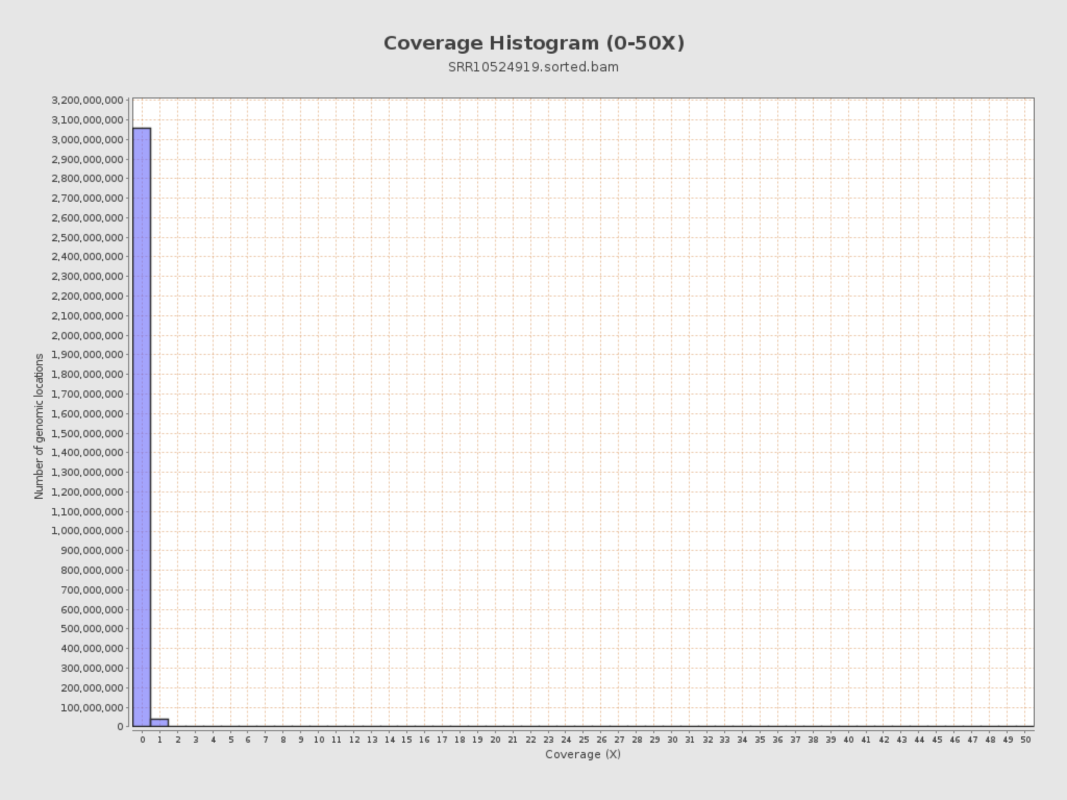
3. Results : Coverage across reference



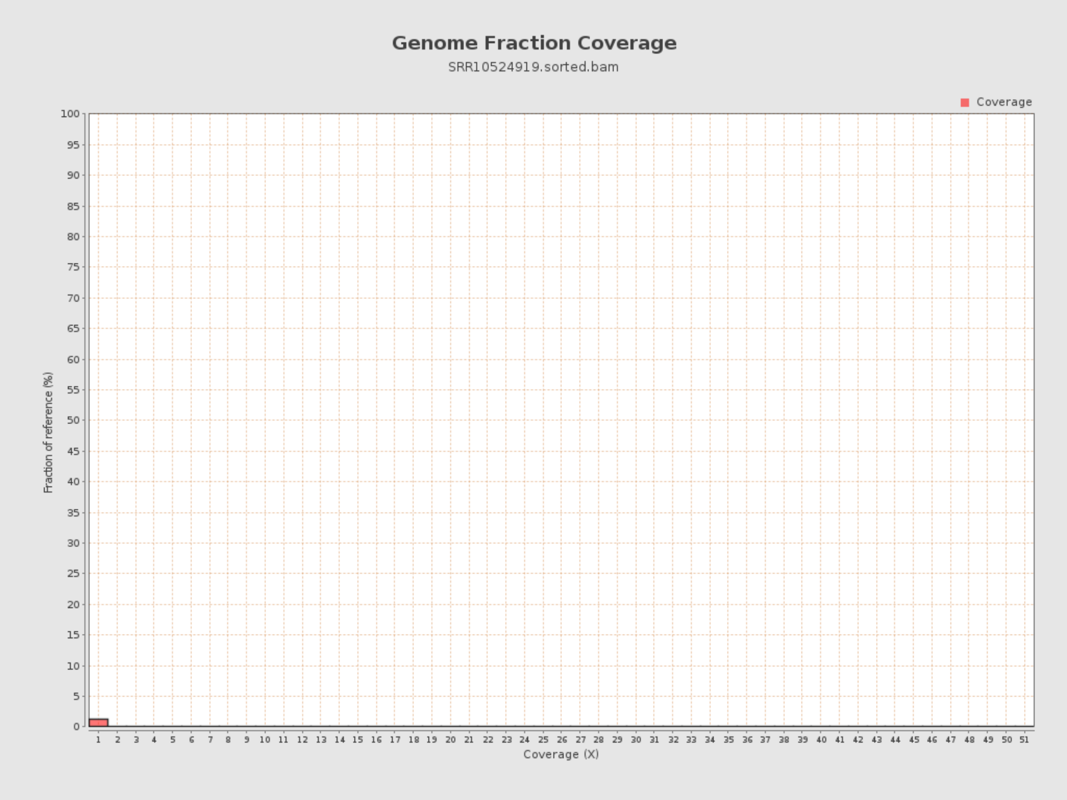
4. Results : Coverage Histogram



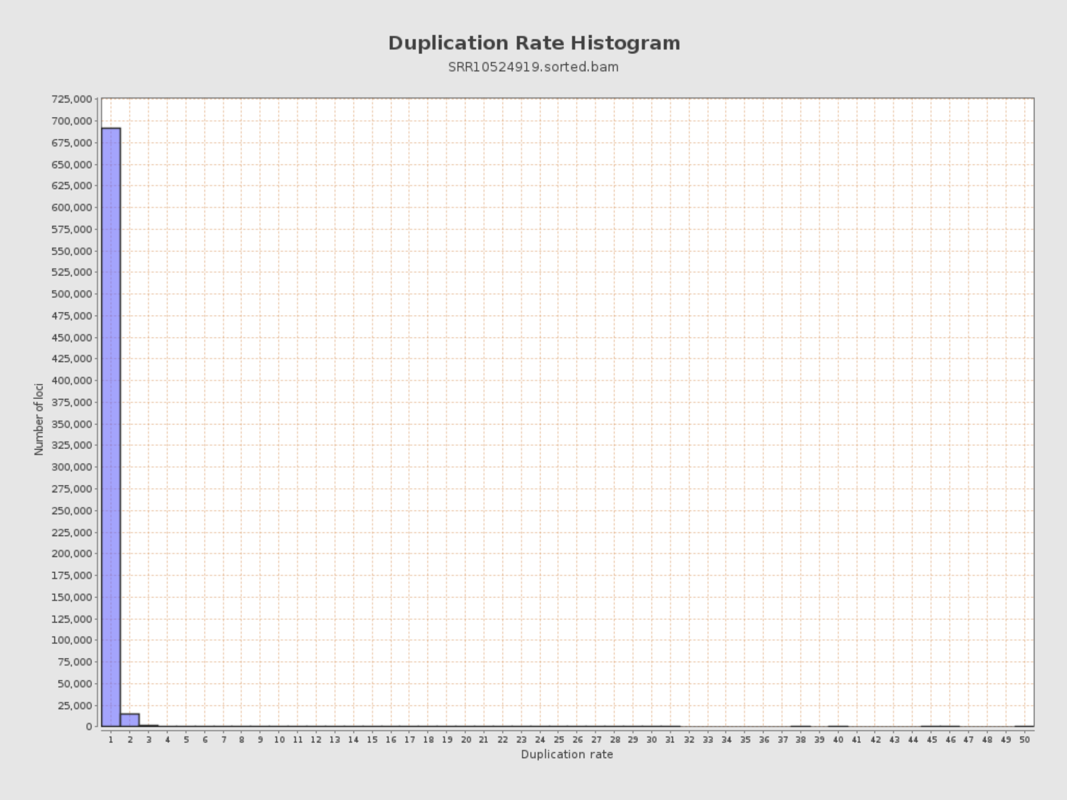
5. Results : Coverage Histogram (0-50X)



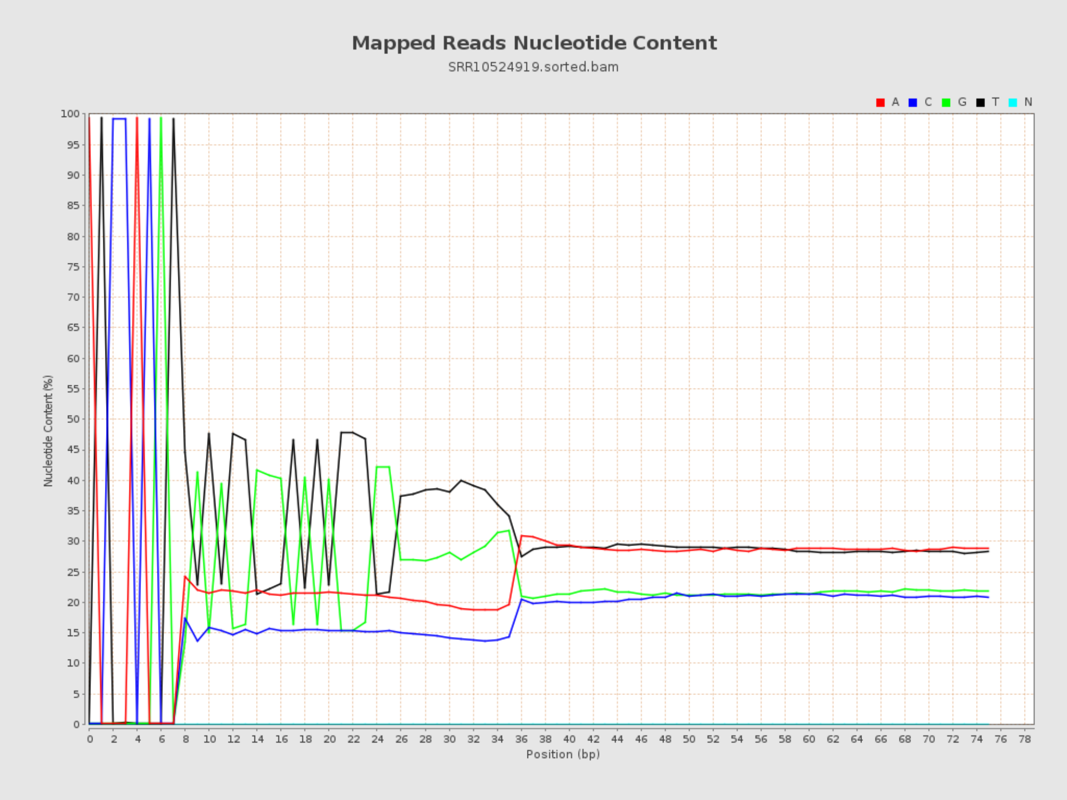
6. Results : Genome Fraction Coverage



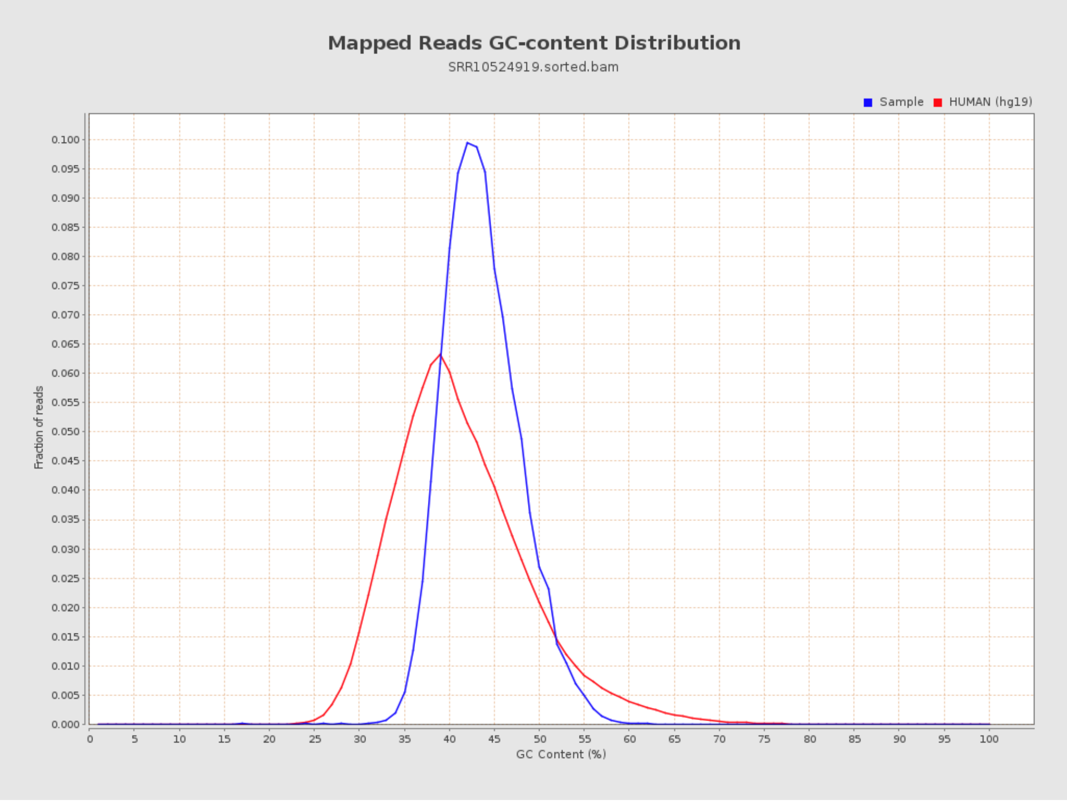
7. Results : Duplication Rate Histogram



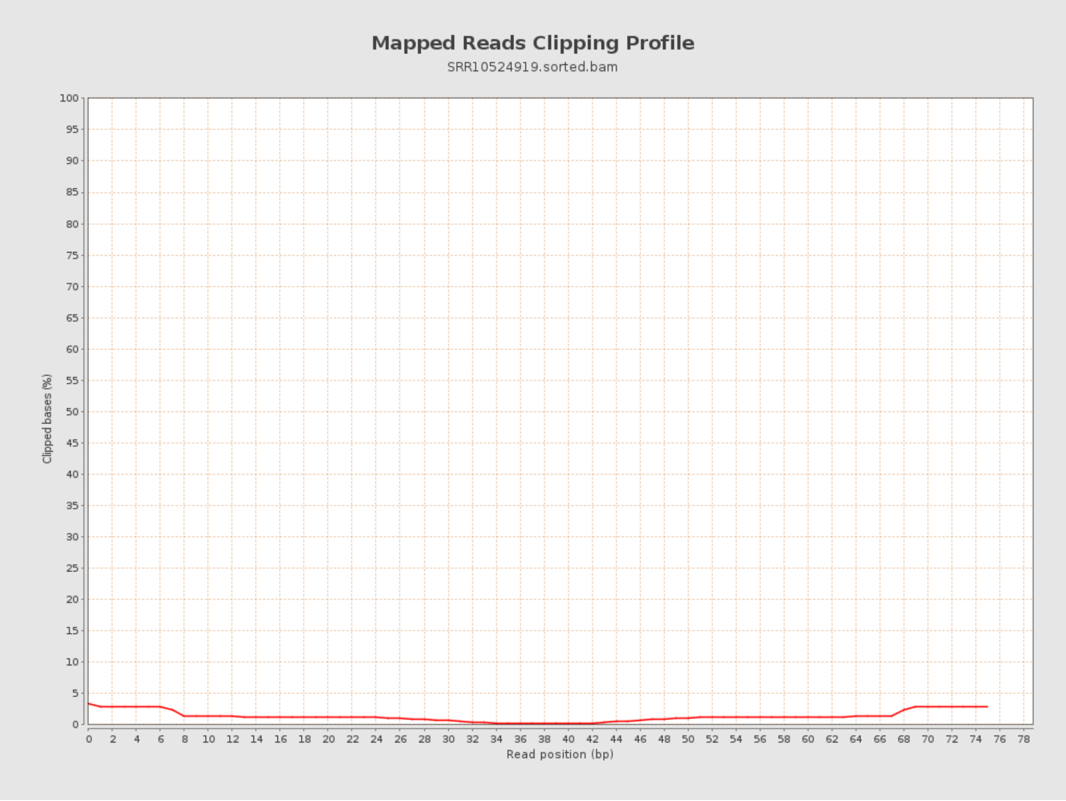
8. Results : Mapped Reads Nucleotide Content



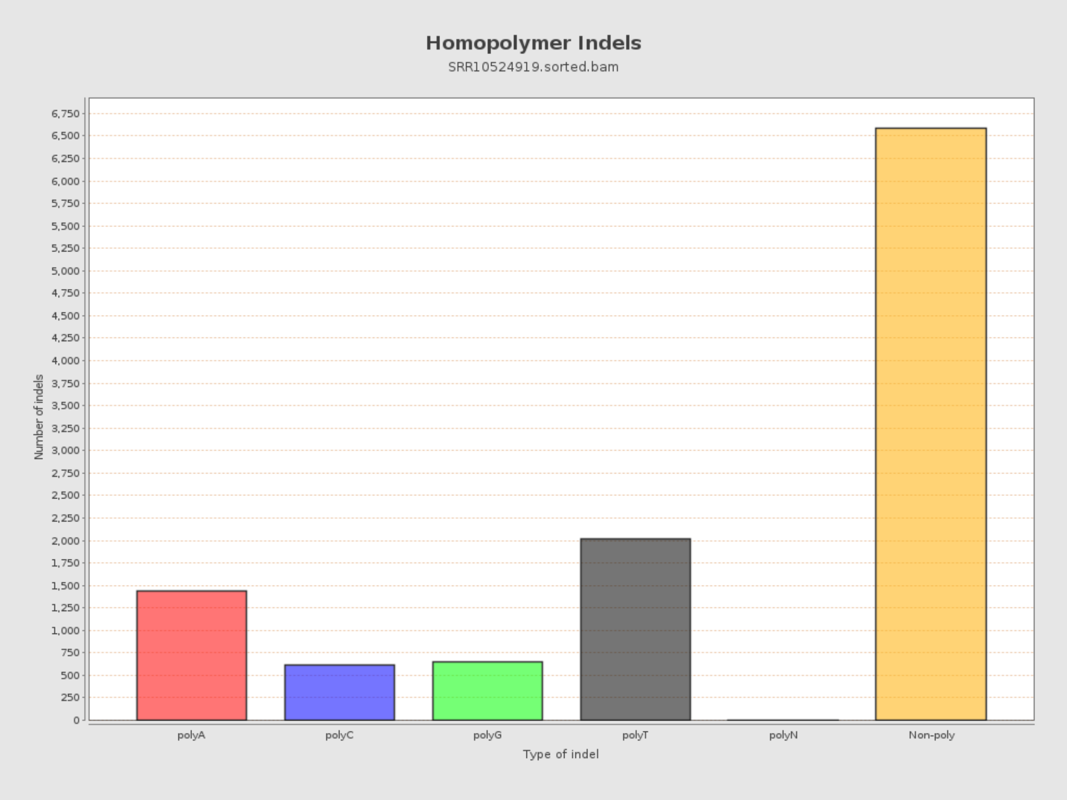
9. Results : Mapped Reads GC-content Distribution



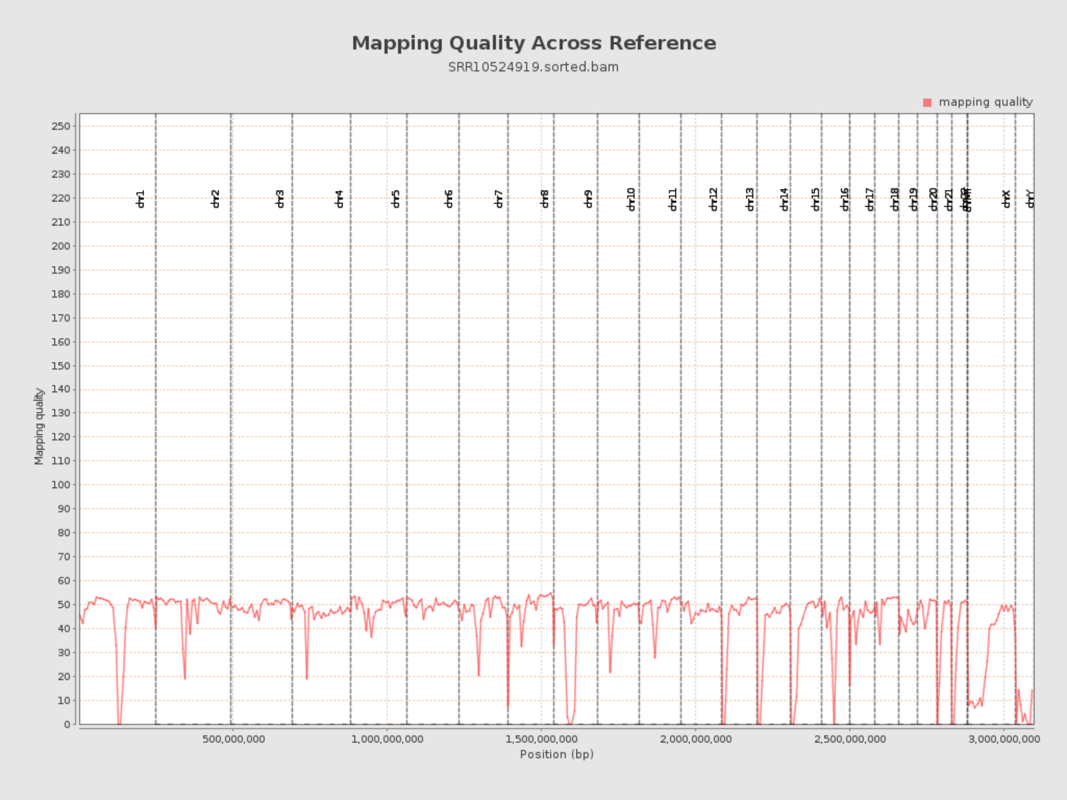
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram