Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:07:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524678.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_SRR10524678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524678.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:07:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524678.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	821,879
Mapped reads	748,976 / 91.13%
Unmapped reads	72,903 / 8.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,608 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	18,873 / 2.3%
Duplication rate	1.82%
Clipped reads	749,304 / 91.17%

2.2. ACGT Content

Number/percentage of A's	10,305,010 / 23.91%
Number/percentage of C's	8,119,807 / 18.84%
Number/percentage of T's	14,557,422 / 33.77%
Number/percentage of G's	10,124,833 / 23.49%
Number/percentage of N's	862 / 0%
GC Percentage	42.32%

2.3. Coverage

Mean	0.0139

Standard Deviation	0.1652

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

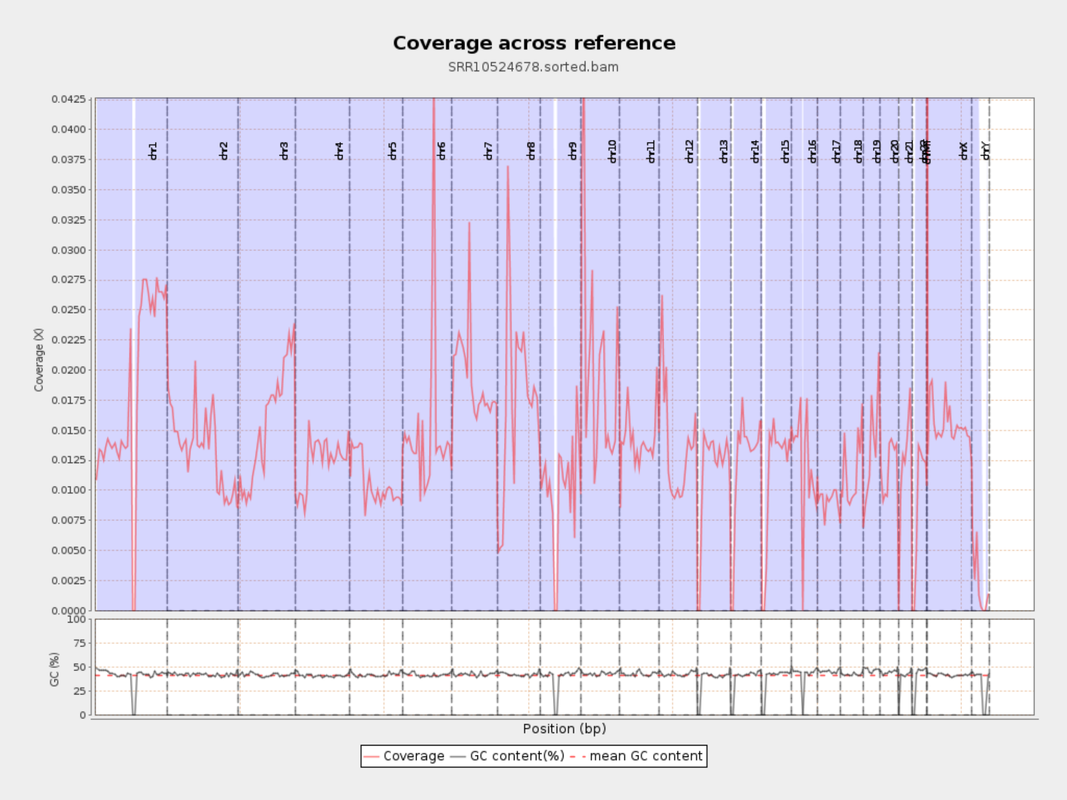
General error rate	0.53%
Mismatches	221,317
Insertions	3,090
Mapped reads with at least one insertion	0.41%
Deletions	9,099
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.85%

2.6. Chromosome stats

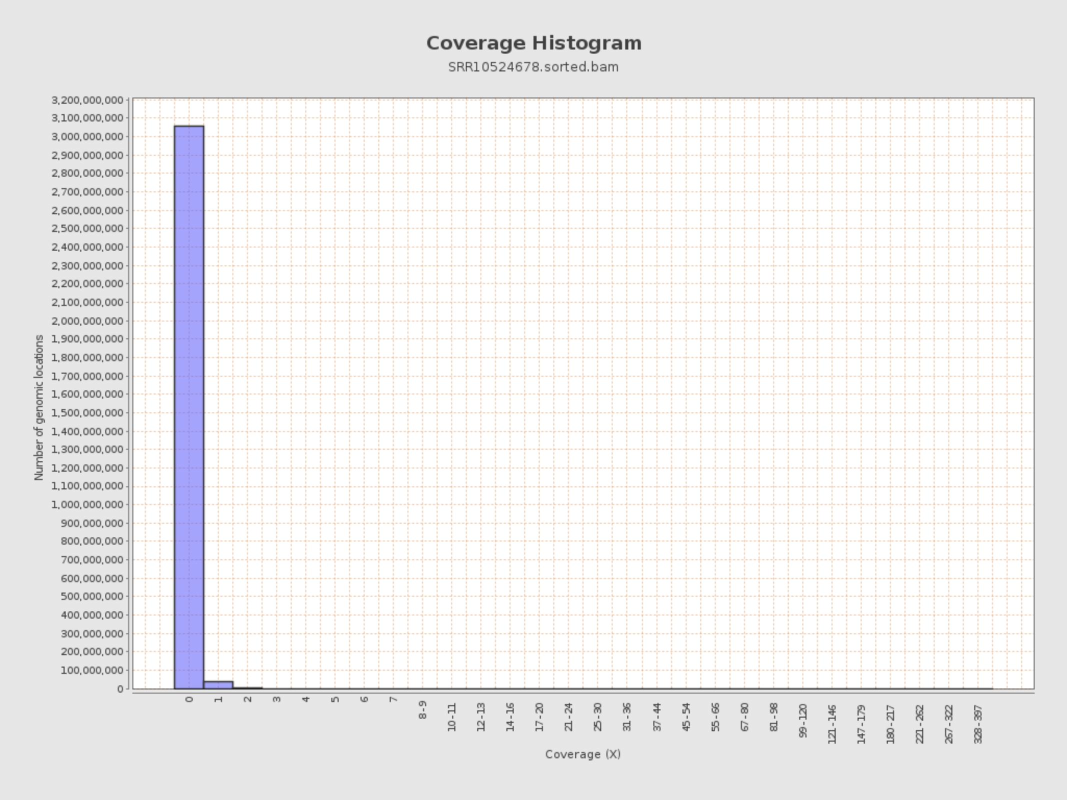
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4531736	0.0182	0.2647
chr2	243199373	3265994	0.0134	0.2016
chr3	198022430	3065188	0.0155	0.1309
chr4	191154276	2375114	0.0124	0.12
chr5	180915260	1929658	0.0107	0.108
chr6	171115067	2585837	0.0151	0.1362
chr7	159138663	3090859	0.0194	0.2742

chr8	146364022	2601659	0.0178	0.1741
chr9	141213431	1438873	0.0102	0.1256
chr10	135534747	2770451	0.0204	0.1821
chr11	135006516	1911968	0.0142	0.1485
chr12	133851895	1844088	0.0138	0.1227
chr13	115169878	1326907	0.0115	0.1134
chr14	107349540	1316263	0.0123	0.1173
chr15	102531392	1154628	0.0113	0.1139
chr16	90354753	1105287	0.0122	0.1234
chr17	81195210	741475	0.0091	0.1012
chr18	78077248	887235	0.0114	0.2141
chr19	59128983	802106	0.0136	0.1905
chr20	63025520	743230	0.0118	0.1136
chr21	48129895	597509	0.0124	0.1192
chr22	51304566	460269	0.009	0.0991
chrMT	16571	43314	2.6138	2.1021
chrX	155270560	2406406	0.0155	0.1368
chrY	59373566	126263	0.0021	0.0654

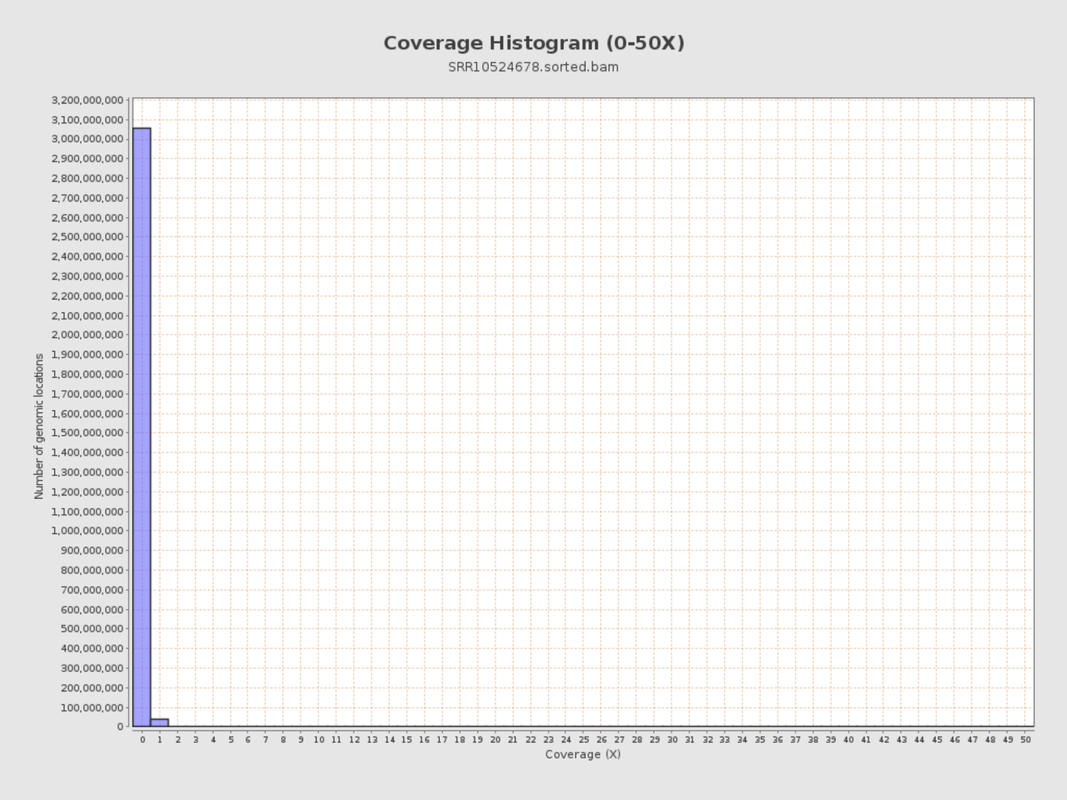
3. Results : Coverage across reference



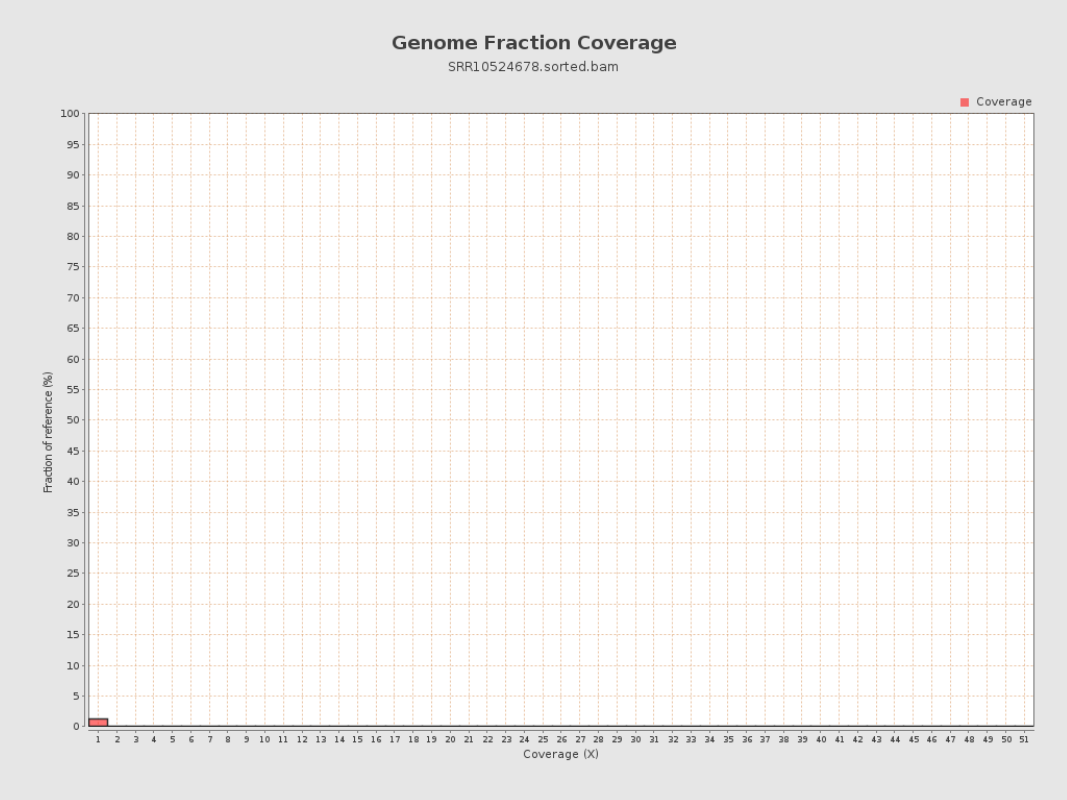
4. Results : Coverage Histogram



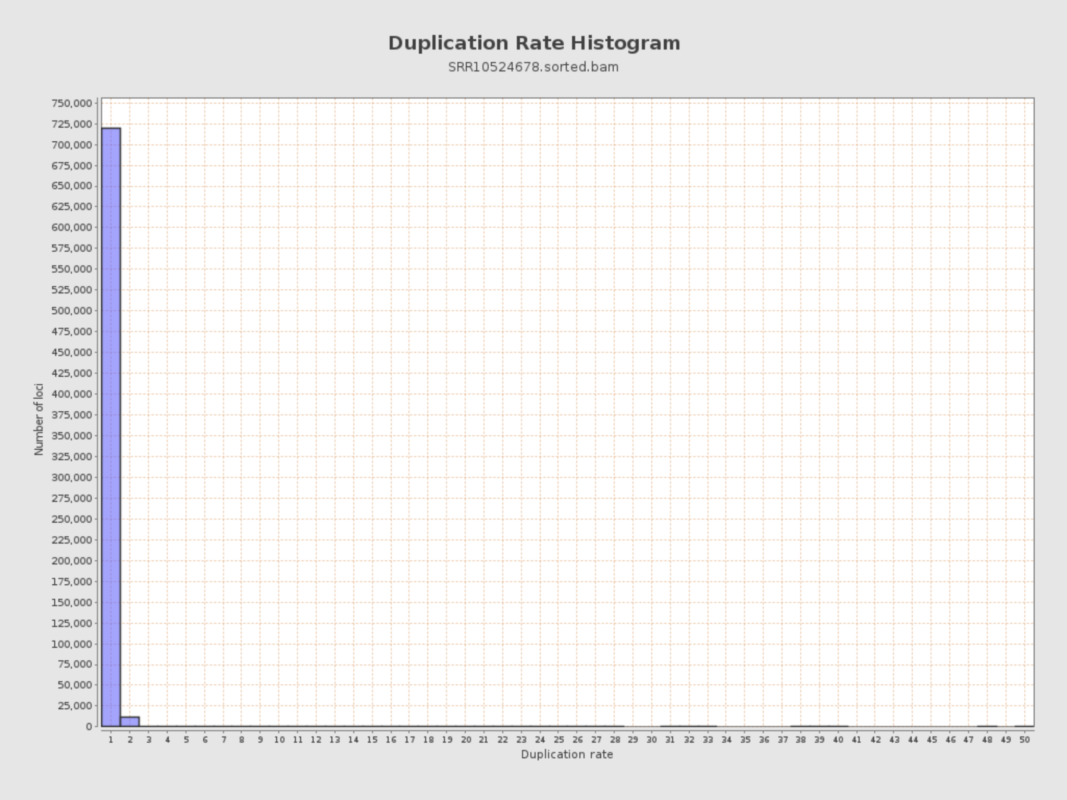
5. Results : Coverage Histogram (0-50X)



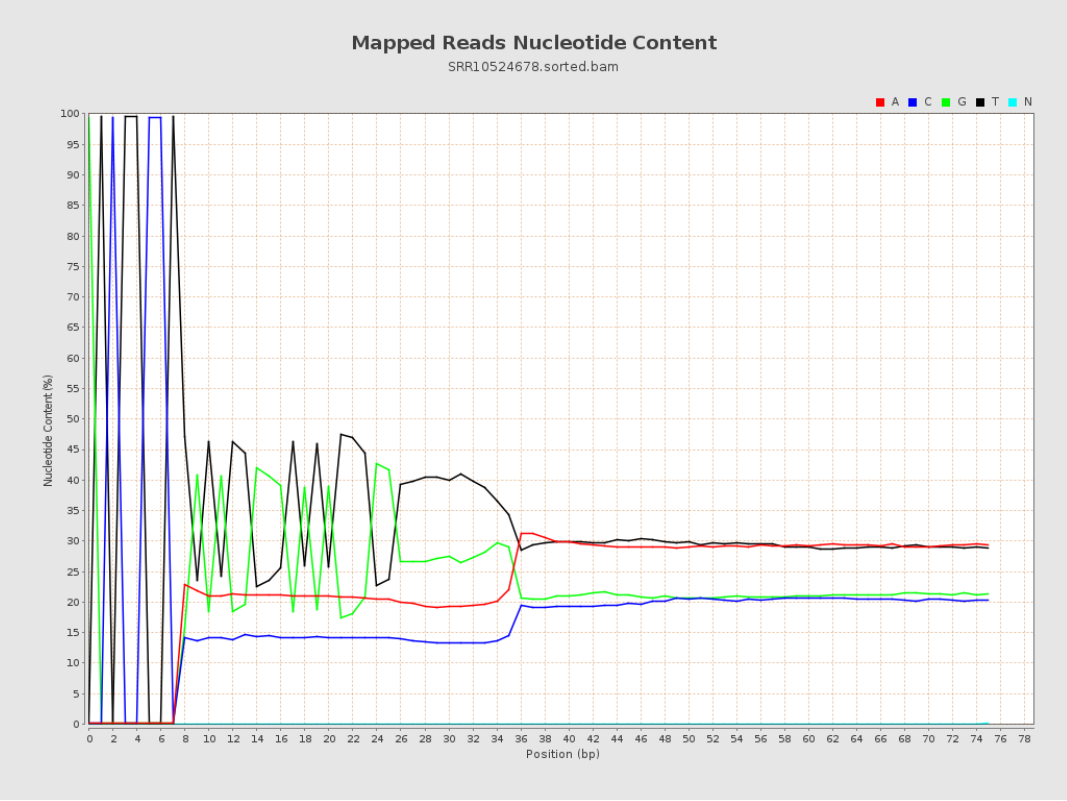
6. Results : Genome Fraction Coverage



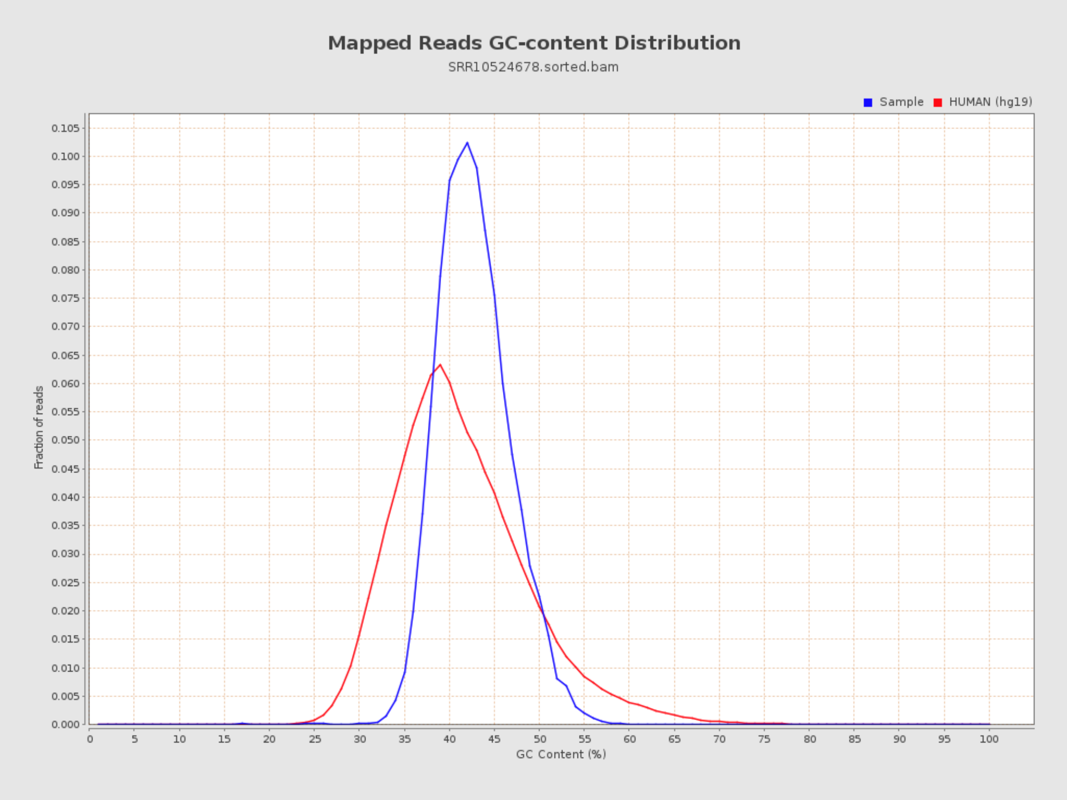
7. Results : Duplication Rate Histogram



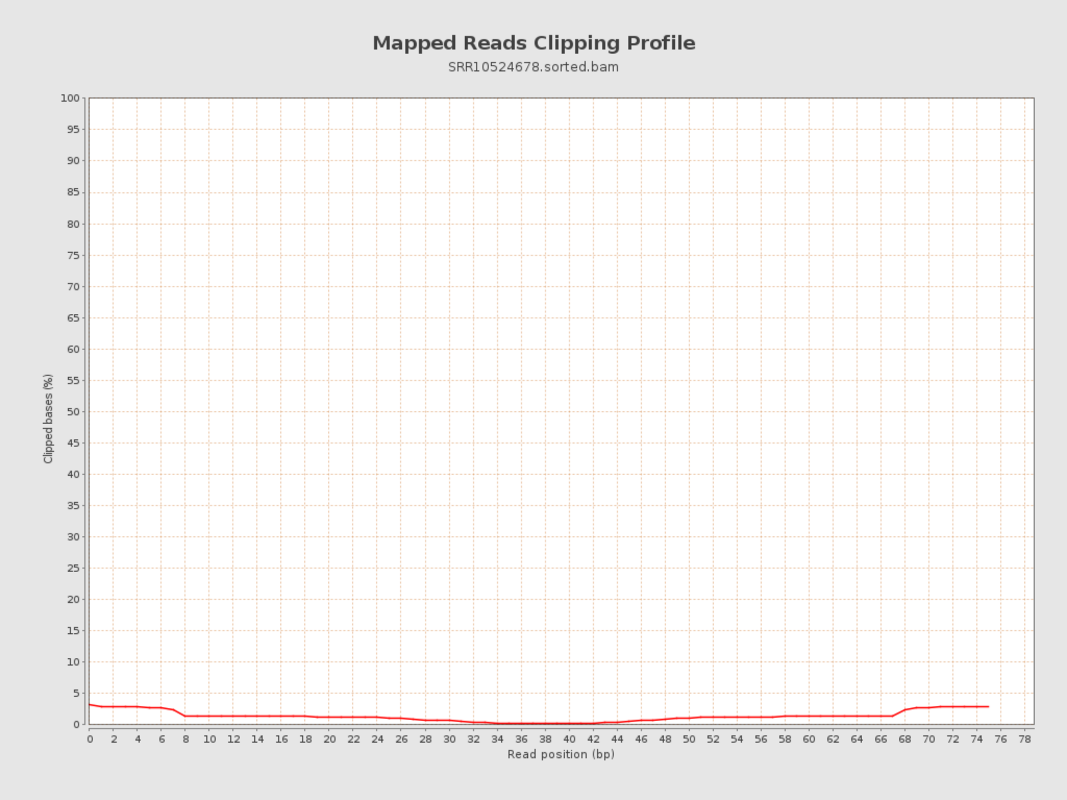
8. Results : Mapped Reads Nucleotide Content



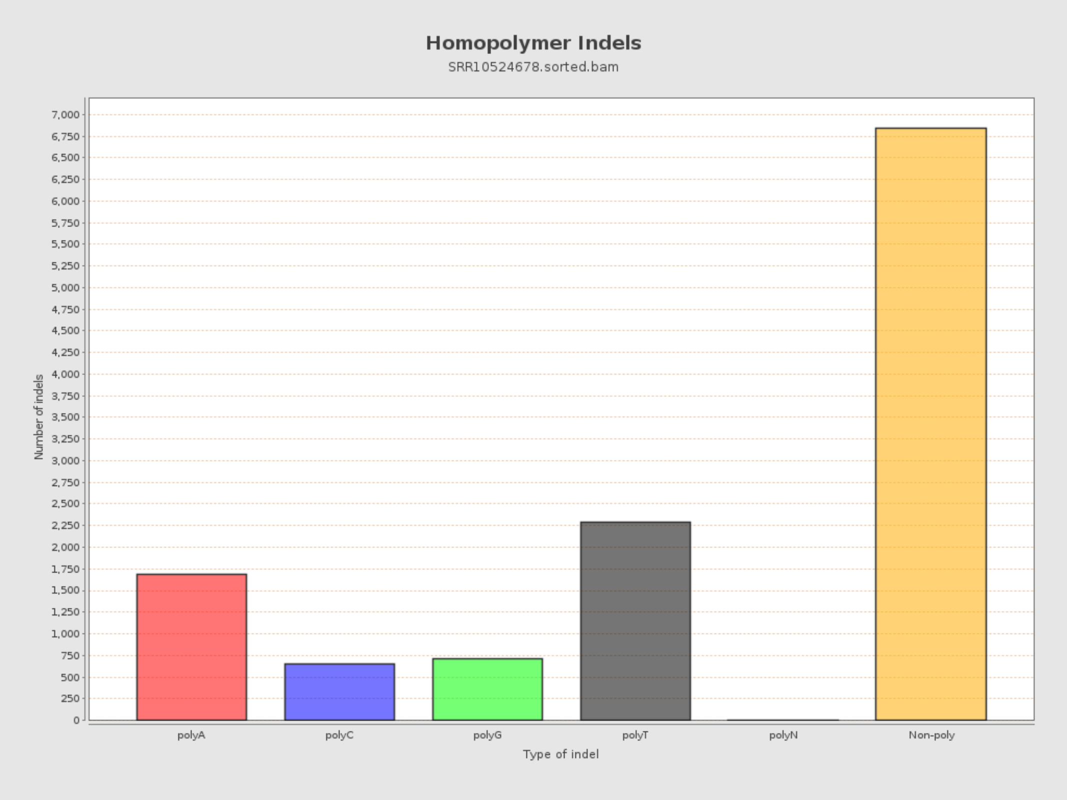
9. Results : Mapped Reads GC-content Distribution



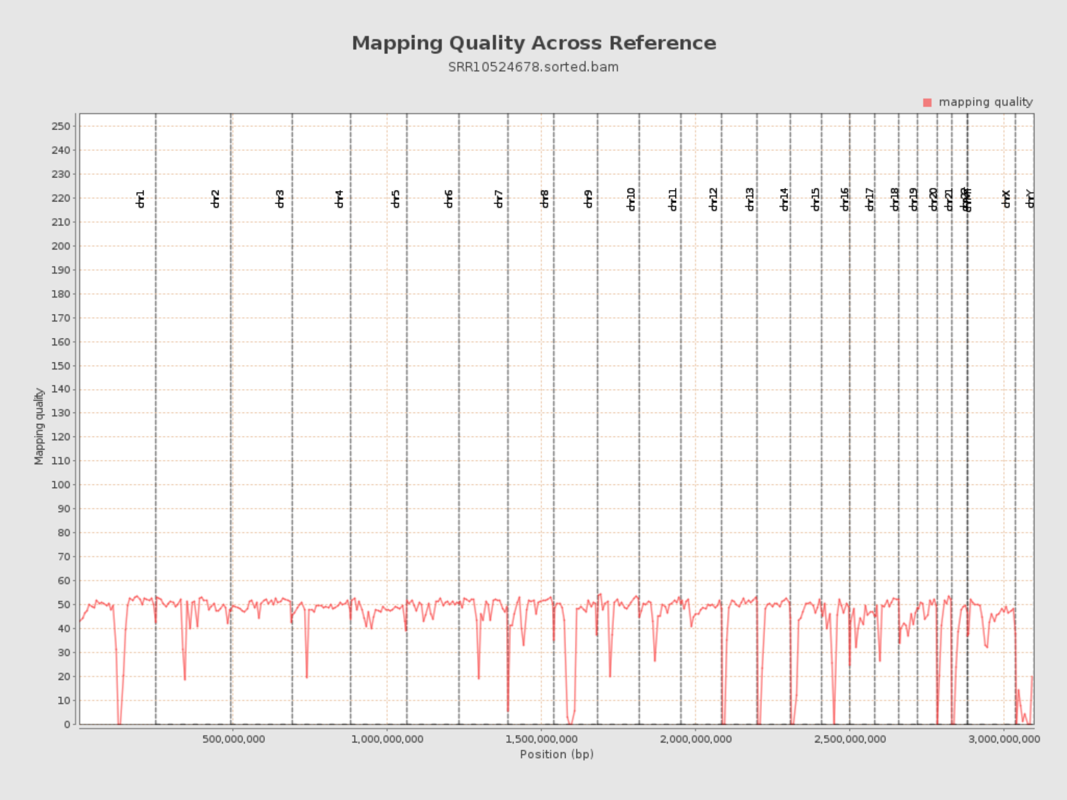
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram