Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:00:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524399.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_SRR10524399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524399.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:00:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	681,136
Mapped reads	631,925 / 92.78%
Unmapped reads	49,211 / 7.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,242 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	13,718 / 2.01%
Duplication rate	1.6%
Clipped reads	632,191 / 92.81%

2.2. ACGT Content

Number/percentage of A's	9,612,130 / 25.86%
Number/percentage of C's	6,984,843 / 18.79%
Number/percentage of T's	11,245,990 / 30.25%
Number/percentage of G's	9,323,505 / 25.08%
Number/percentage of N's	5,175 / 0.01%
GC Percentage	43.87%

2.3. Coverage

Mean	0.012

Standard Deviation	0.1489

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

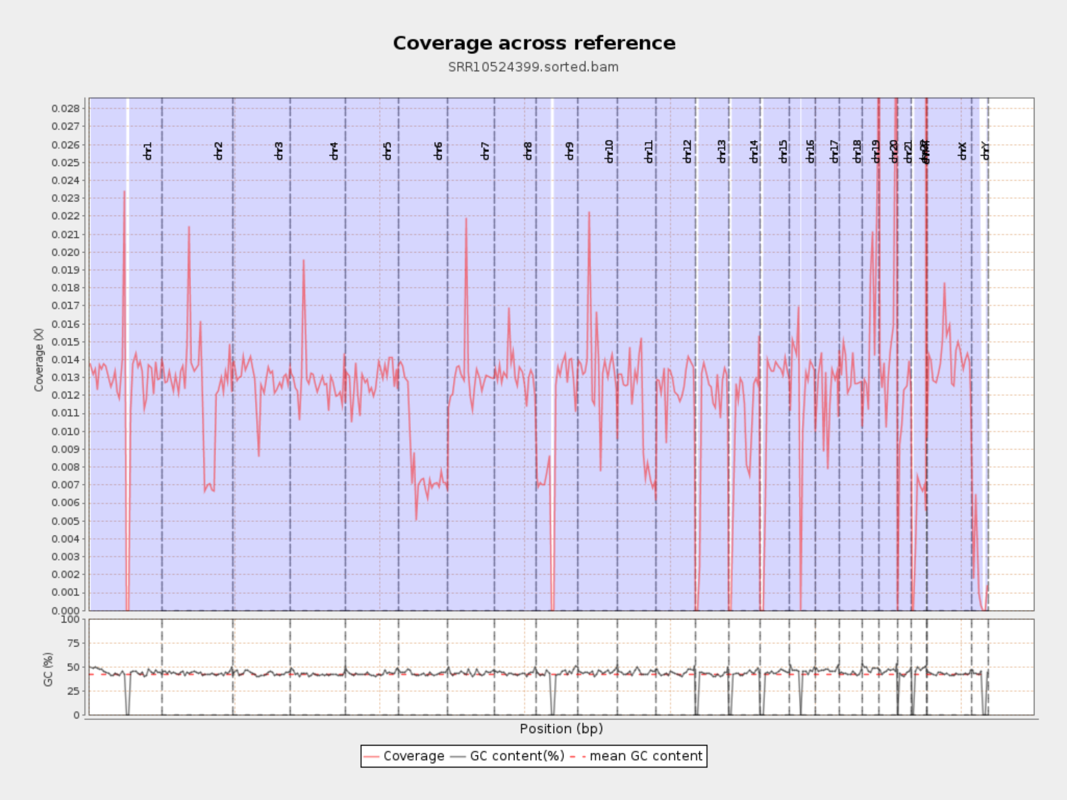
General error rate	0.5%
Mismatches	180,263
Insertions	2,884
Mapped reads with at least one insertion	0.45%
Deletions	6,875
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.86%

2.6. Chromosome stats

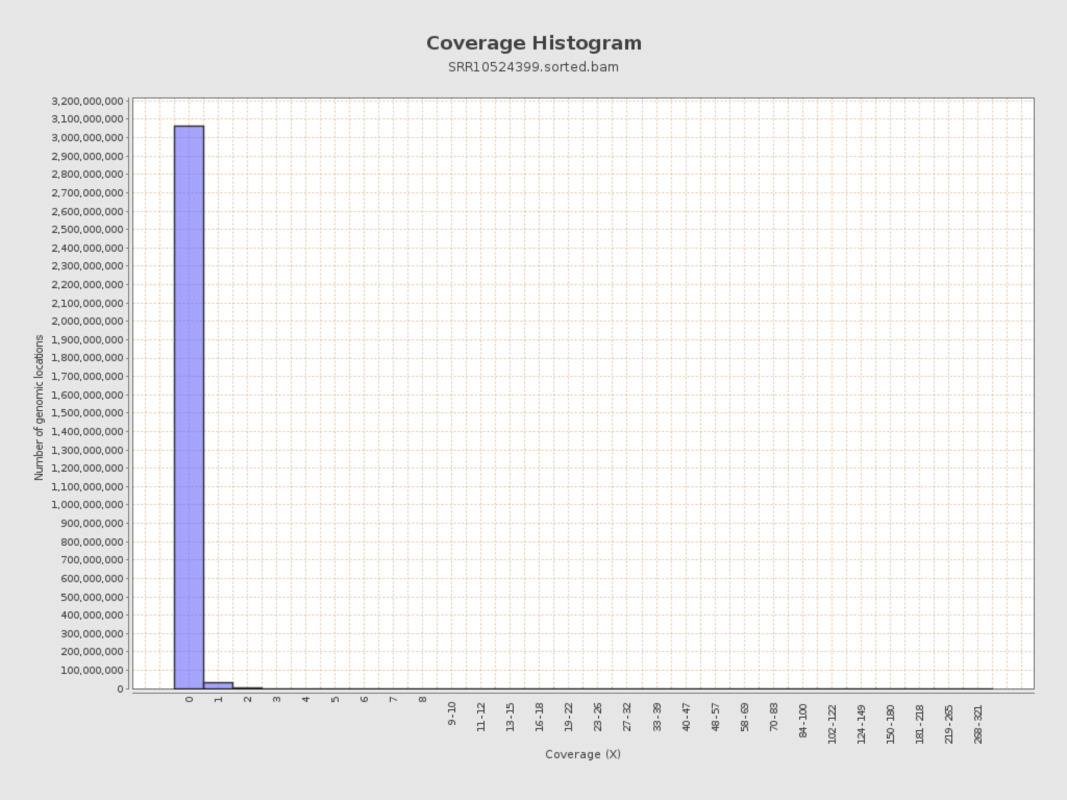
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3138294	0.0126	0.2658
chr2	243199373	3018940	0.0124	0.1586
chr3	198022430	2542498	0.0128	0.117
chr4	191154276	2450876	0.0128	0.1235
chr5	180915260	2314506	0.0128	0.1175
chr6	171115067	1459155	0.0085	0.1
chr7	159138663	2096451	0.0132	0.1909

chr8	146364022	1943415	0.0133	0.1382
chr9	141213431	1384876	0.0098	0.1233
chr10	135534747	1857802	0.0137	0.1426
chr11	135006516	1514300	0.0112	0.1252
chr12	133851895	1694773	0.0127	0.1186
chr13	115169878	1213508	0.0105	0.1063
chr14	107349540	1027149	0.0096	0.1032
chr15	102531392	1133490	0.0111	0.1091
chr16	90354753	1126848	0.0125	0.1181
chr17	81195210	968550	0.0119	0.1172
chr18	78077248	1038753	0.0133	0.1778
chr19	59128983	1023030	0.0173	0.1994
chr20	63025520	1035800	0.0164	0.1349
chr21	48129895	511349	0.0106	0.1122
chr22	51304566	253560	0.0049	0.0725
chrMT	16571	148319	8.9505	5.5696
chrX	155270560	2175818	0.014	0.1296
chrY	59373566	110575	0.0019	0.0633

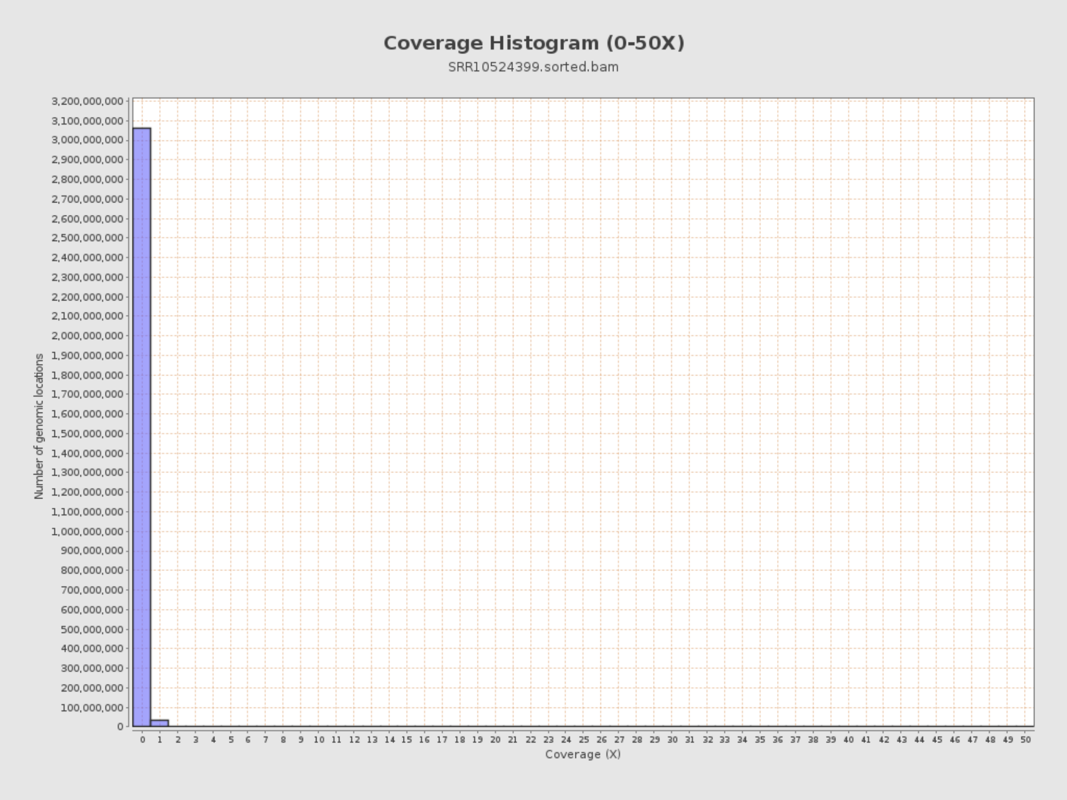
3. Results : Coverage across reference



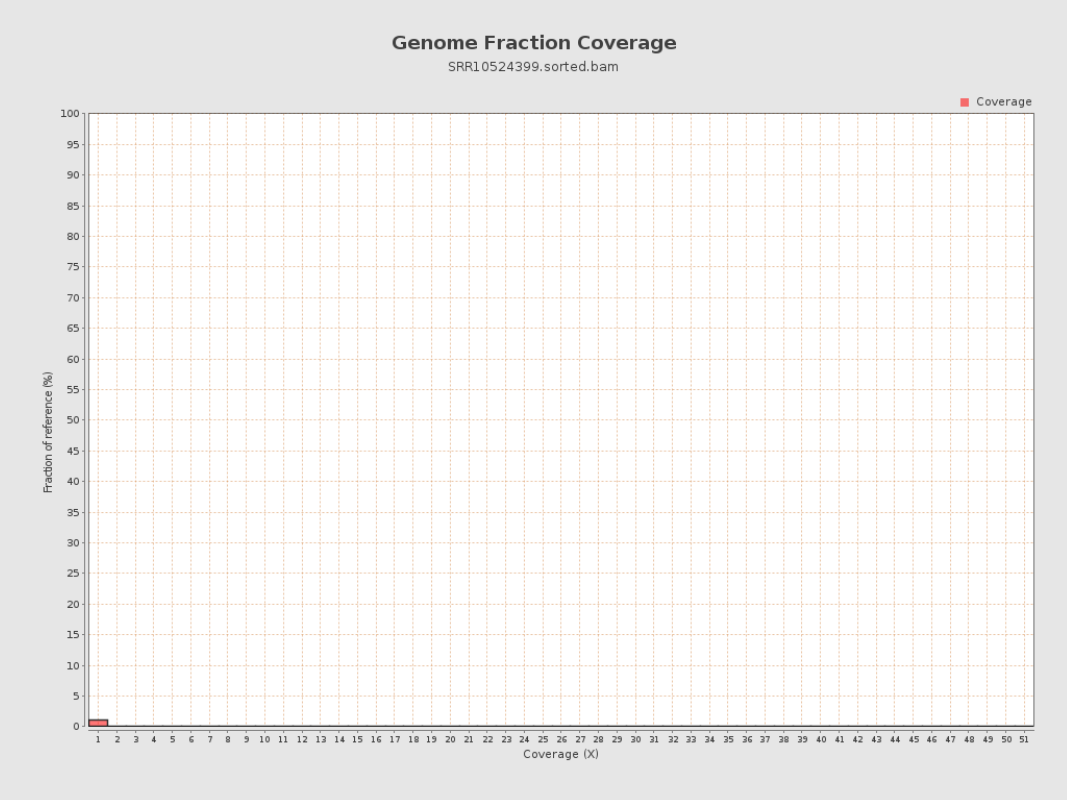
4. Results : Coverage Histogram



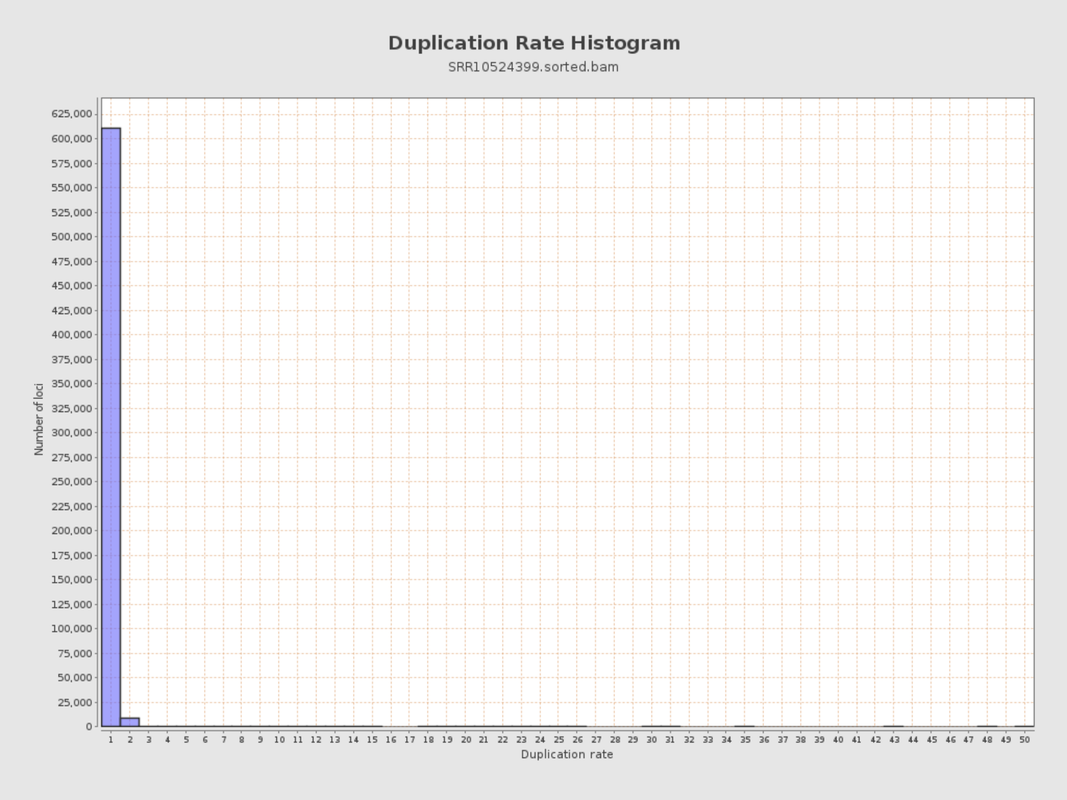
5. Results : Coverage Histogram (0-50X)



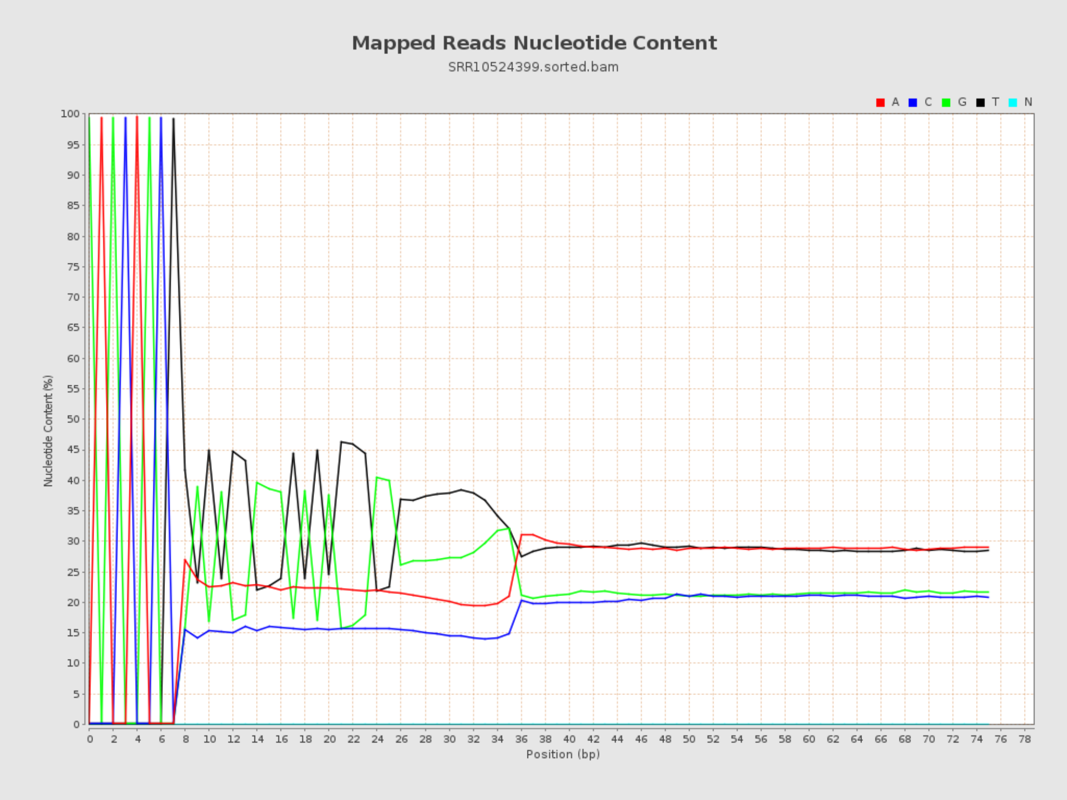
6. Results : Genome Fraction Coverage



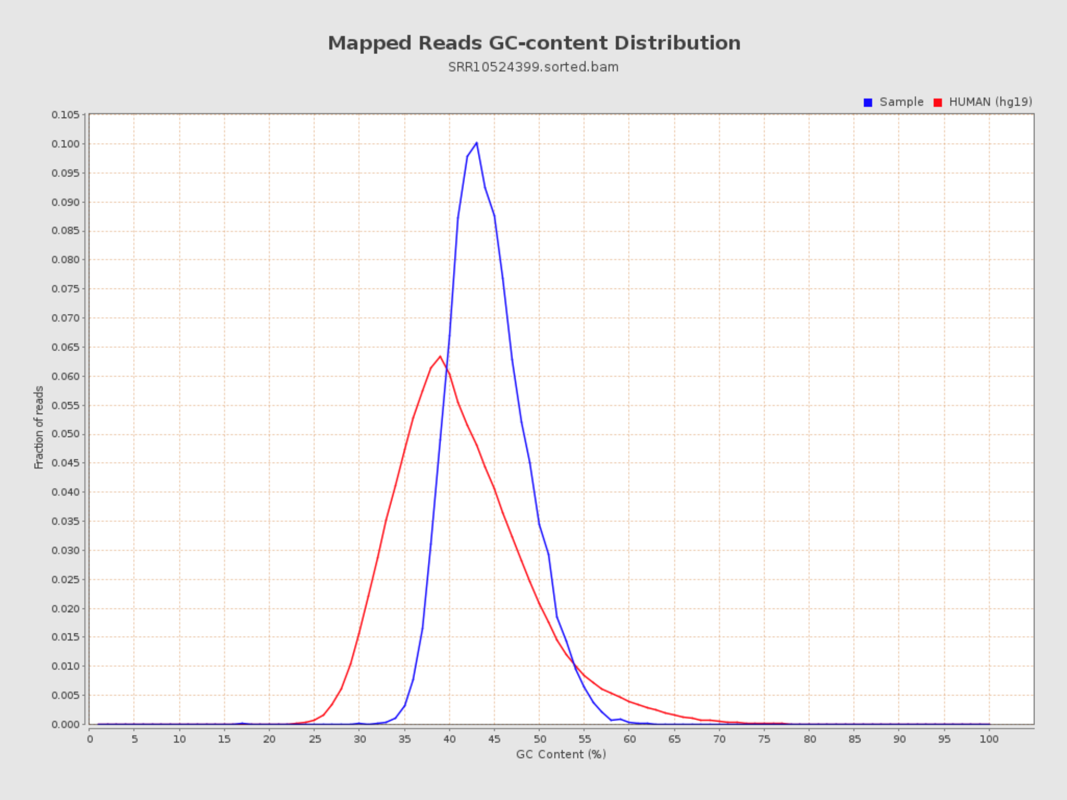
7. Results : Duplication Rate Histogram



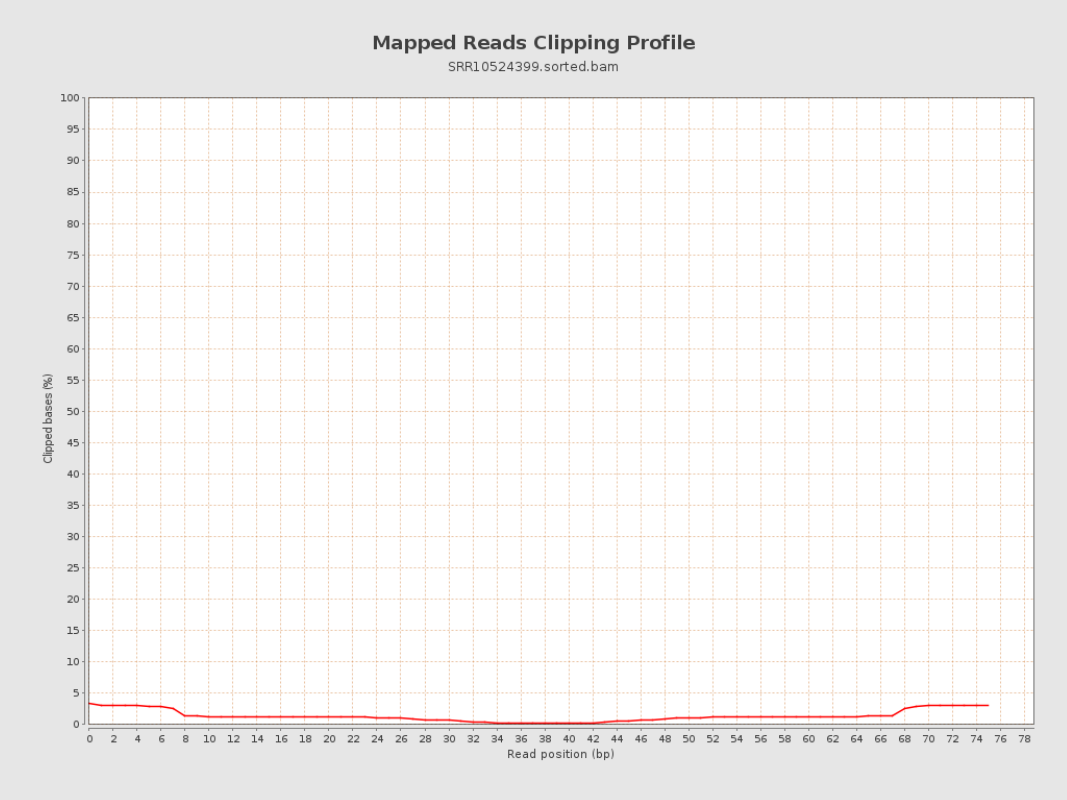
8. Results : Mapped Reads Nucleotide Content



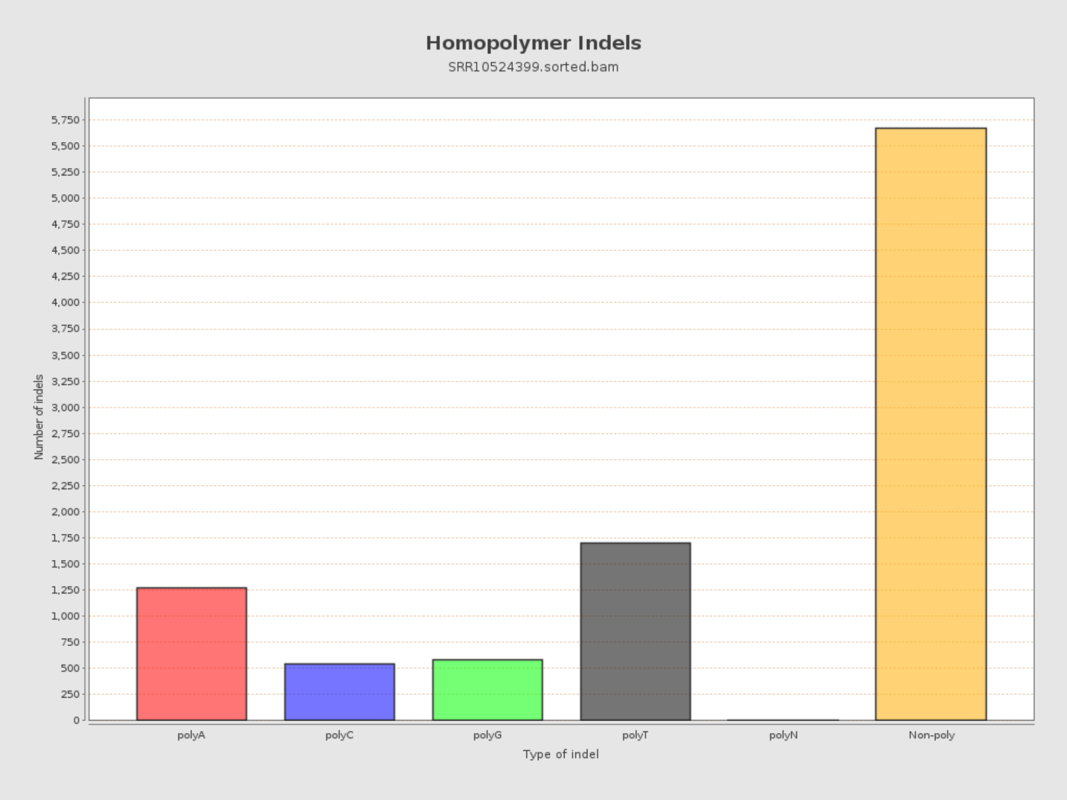
9. Results : Mapped Reads GC-content Distribution



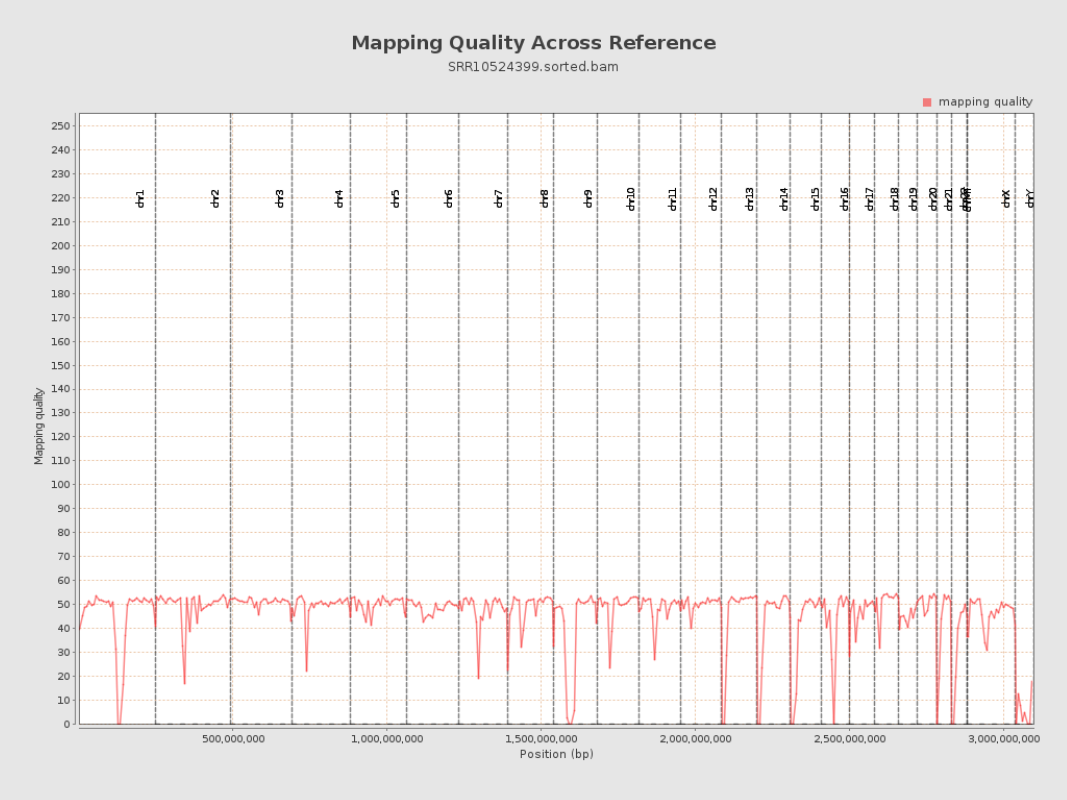
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram