Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:26:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524386.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_SRR10524386 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524386.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:26:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524386.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	947,201
Mapped reads	879,265 / 92.83%
Unmapped reads	67,936 / 7.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,617 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,341 / 2.46%
Duplication rate	1.94%
Clipped reads	881,863 / 93.1%

2.2. ACGT Content

Number/percentage of A's	12,460,858 / 24.12%
Number/percentage of C's	9,260,471 / 17.93%
Number/percentage of T's	16,897,952 / 32.71%
Number/percentage of G's	13,027,970 / 25.22%
Number/percentage of N's	6,697 / 0.01%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0167

Standard Deviation	0.1863

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

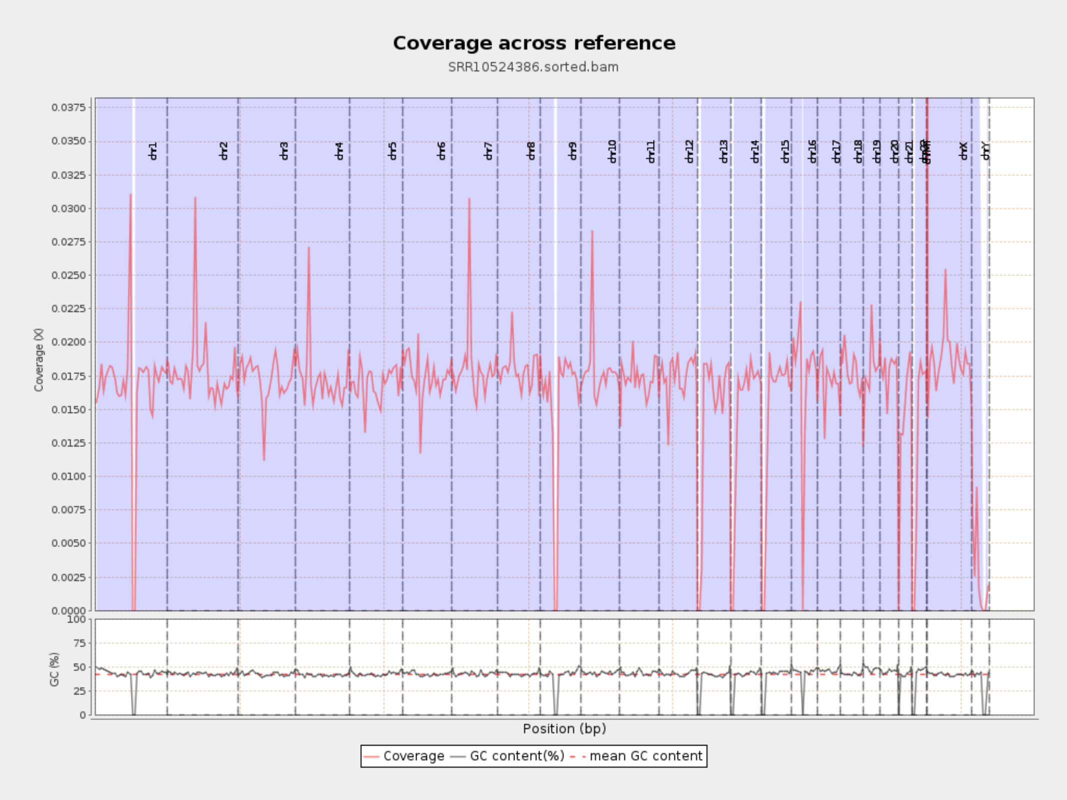
General error rate	0.49%
Mismatches	249,325
Insertions	2,969
Mapped reads with at least one insertion	0.34%
Deletions	9,074
Mapped reads with at least one deletion	1.03%
Homopolymer indels	45.45%

2.6. Chromosome stats

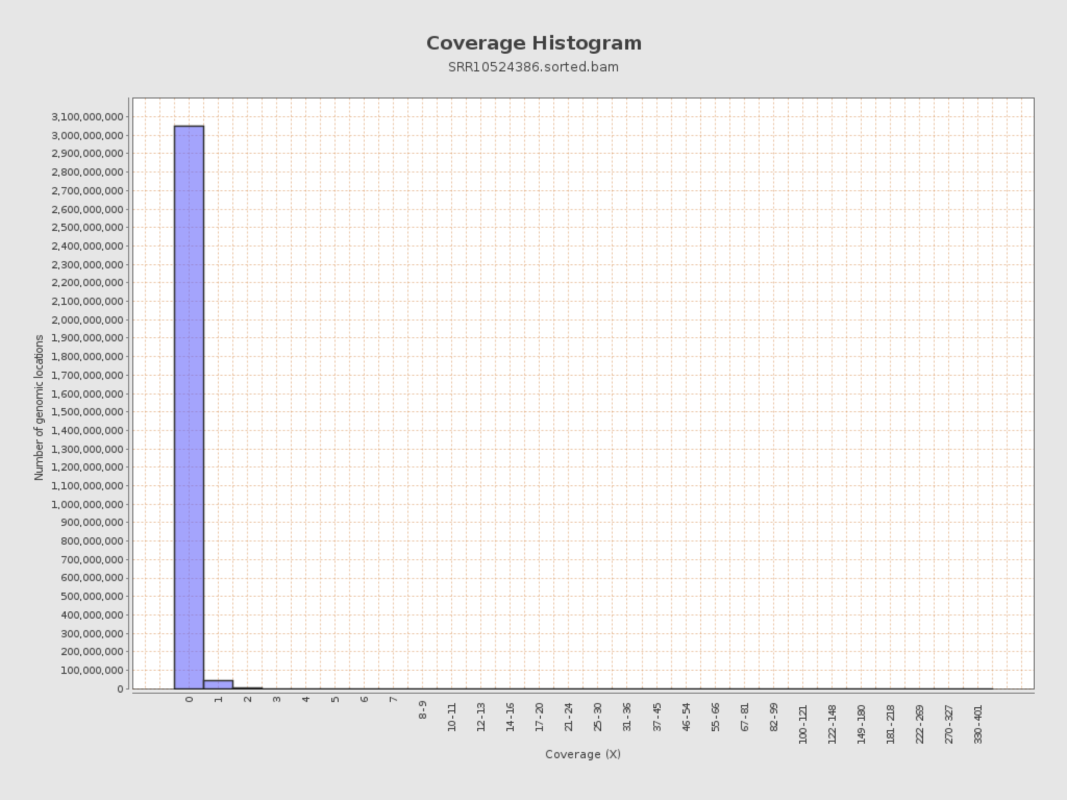
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4121575	0.0165	0.345
chr2	243199373	4330195	0.0178	0.2002
chr3	198022430	3423679	0.0173	0.1381
chr4	191154276	3320314	0.0174	0.1483
chr5	180915260	3070640	0.017	0.1369
chr6	171115067	2983871	0.0174	0.148
chr7	159138663	2896157	0.0182	0.2487

chr8	146364022	2626903	0.0179	0.171
chr9	141213431	2163962	0.0153	0.1587
chr10	135534747	2436816	0.018	0.1692
chr11	135006516	2351698	0.0174	0.1696
chr12	133851895	2343090	0.0175	0.1413
chr13	115169878	1647462	0.0143	0.125
chr14	107349540	1546625	0.0144	0.1287
chr15	102531392	1478749	0.0144	0.1263
chr16	90354753	1541261	0.0171	0.1417
chr17	81195210	1392422	0.0171	0.144
chr18	78077248	1398234	0.0179	0.2658
chr19	59128983	1071037	0.0181	0.2414
chr20	63025520	1116983	0.0177	0.1419
chr21	48129895	694243	0.0144	0.135
chr22	51304566	630265	0.0123	0.1162
chrMT	16571	7488	0.4519	0.7411
chrX	155270560	2917369	0.0188	0.1573
chrY	59373566	157573	0.0027	0.0819

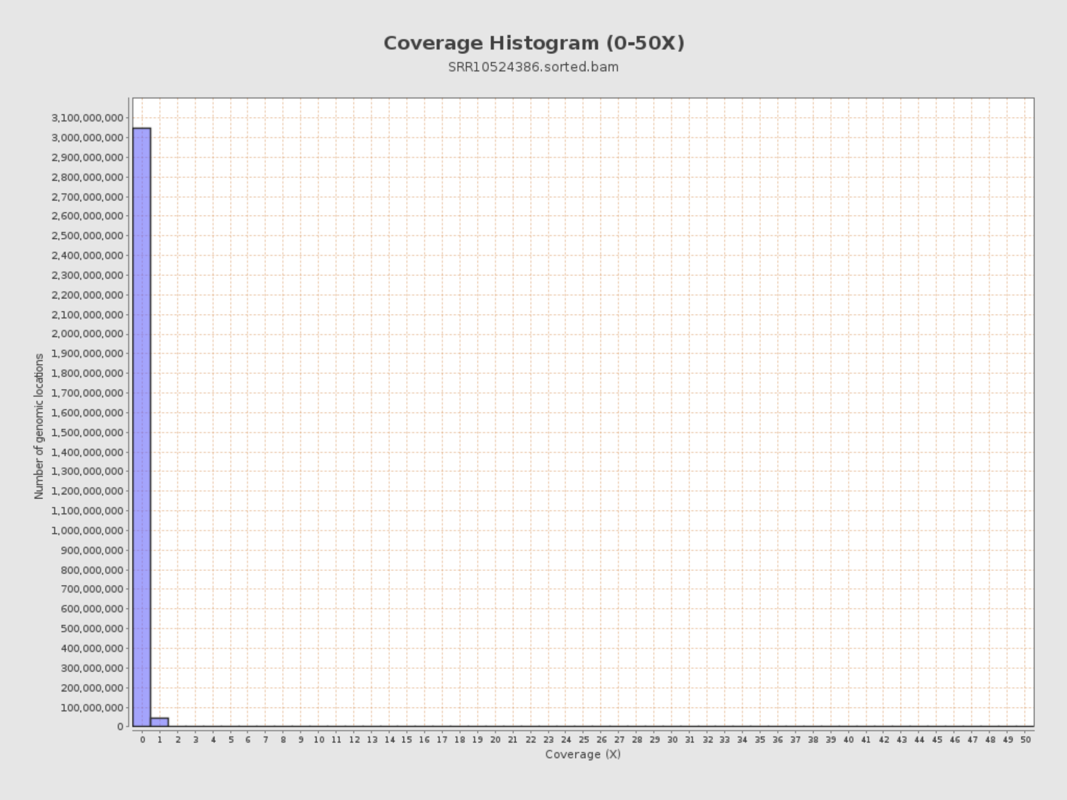
3. Results : Coverage across reference



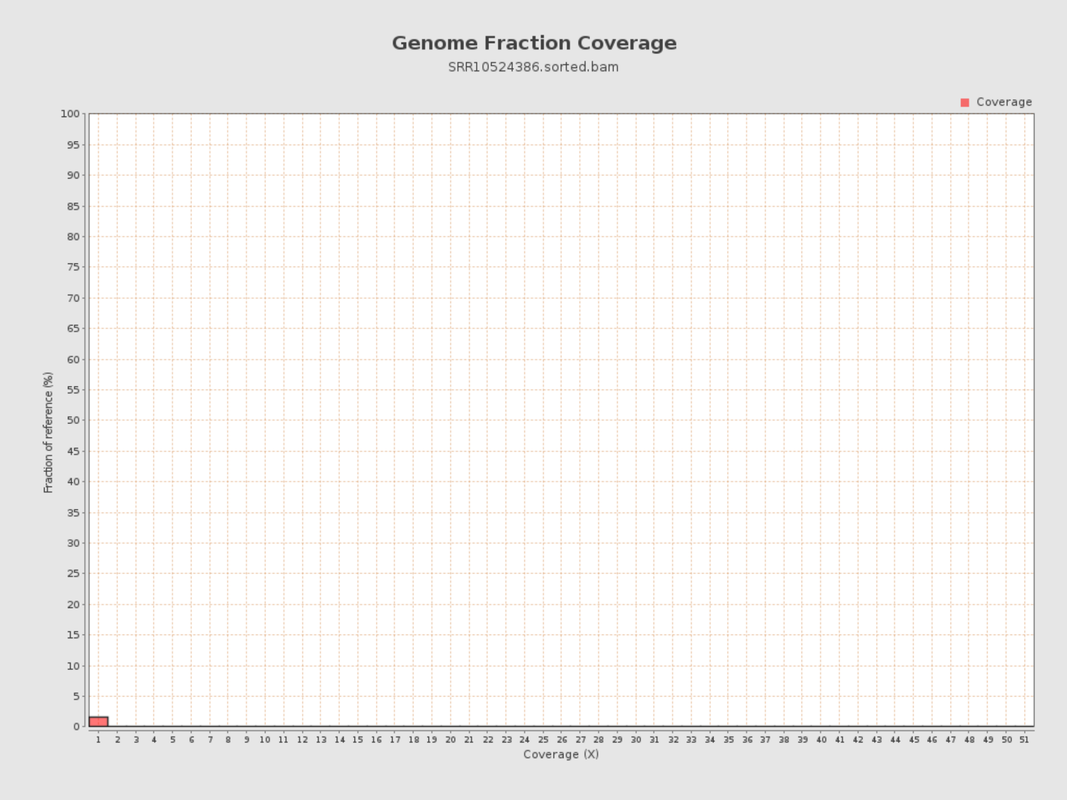
4. Results : Coverage Histogram



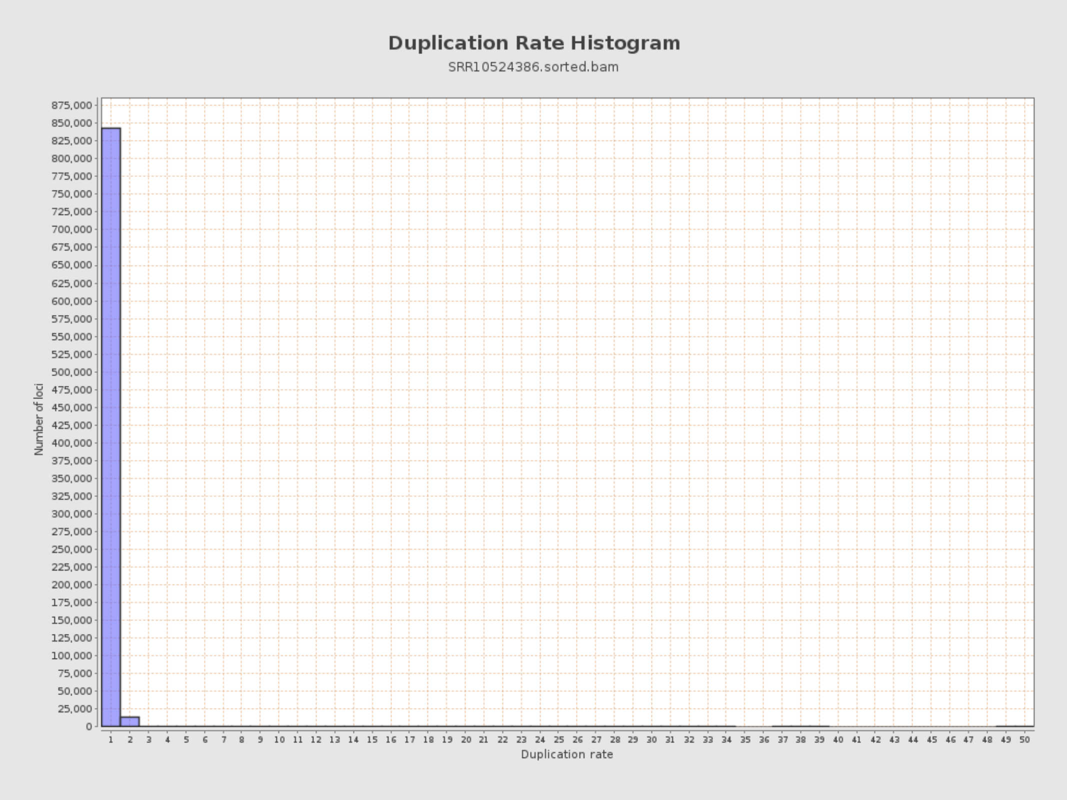
5. Results : Coverage Histogram (0-50X)



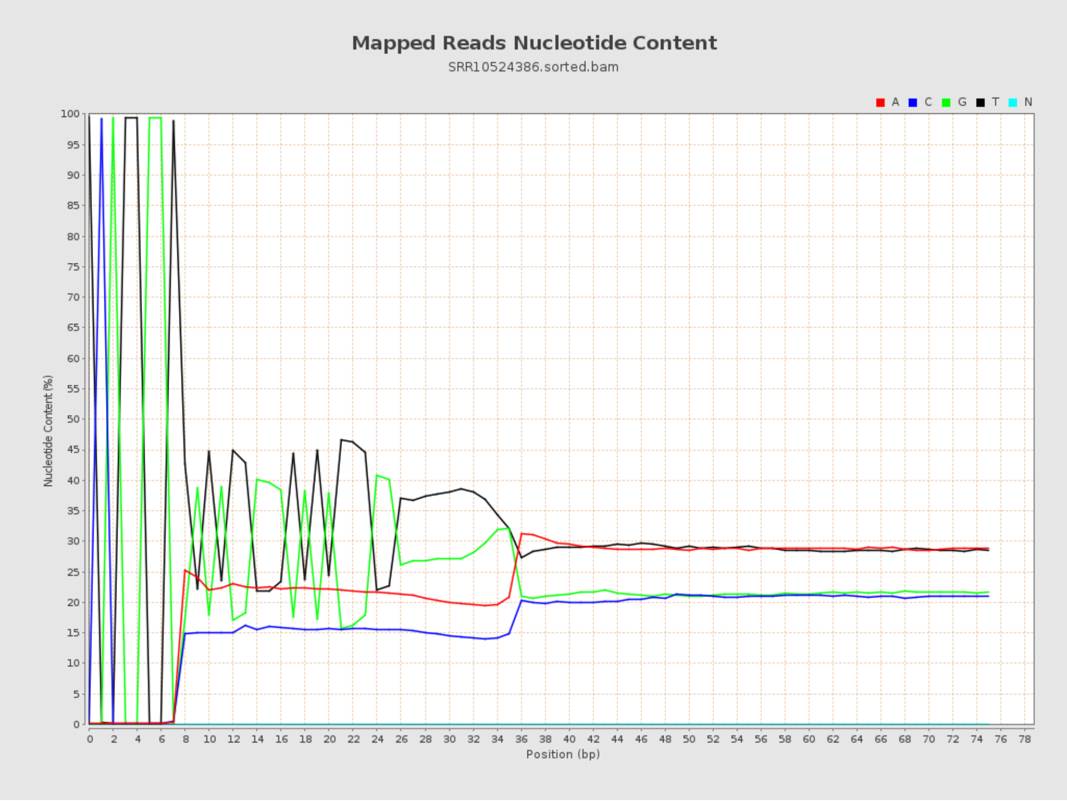
6. Results : Genome Fraction Coverage



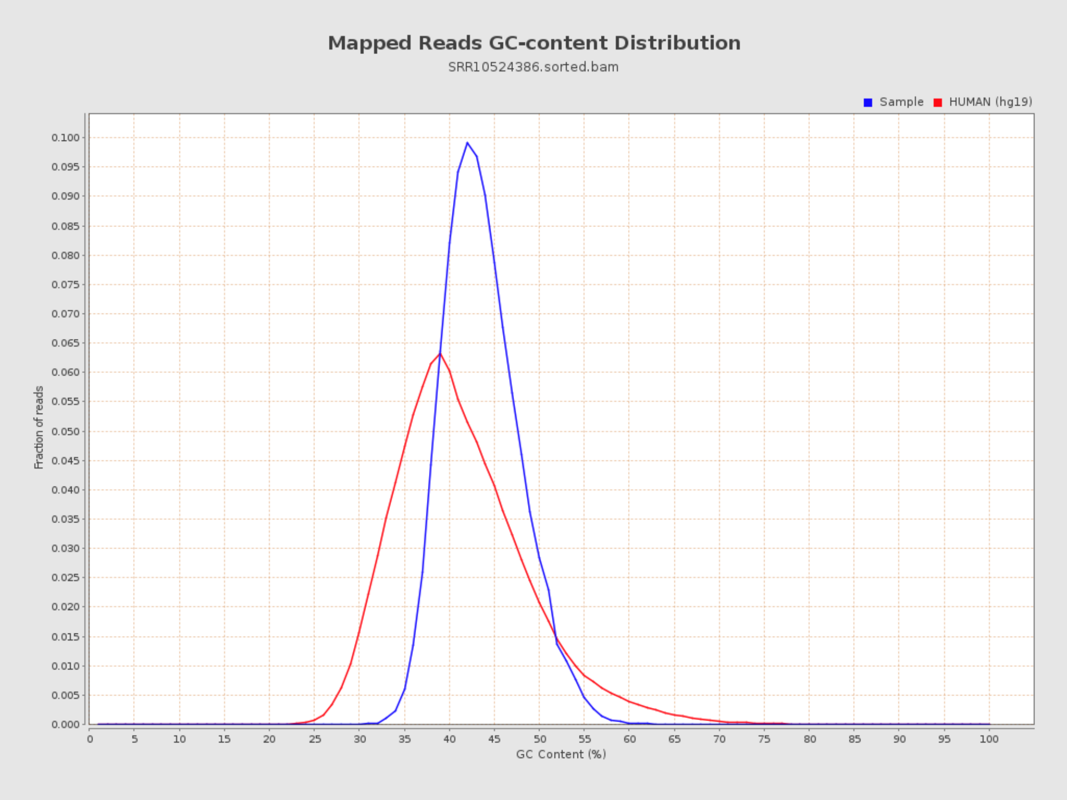
7. Results : Duplication Rate Histogram



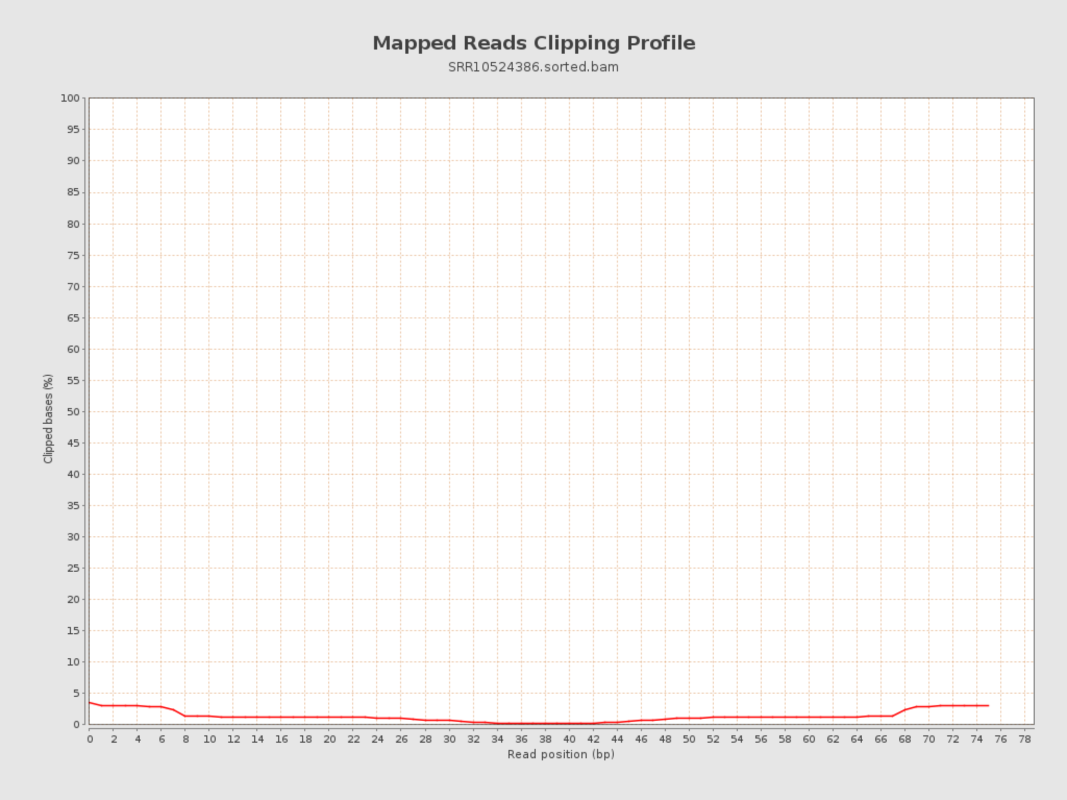
8. Results : Mapped Reads Nucleotide Content



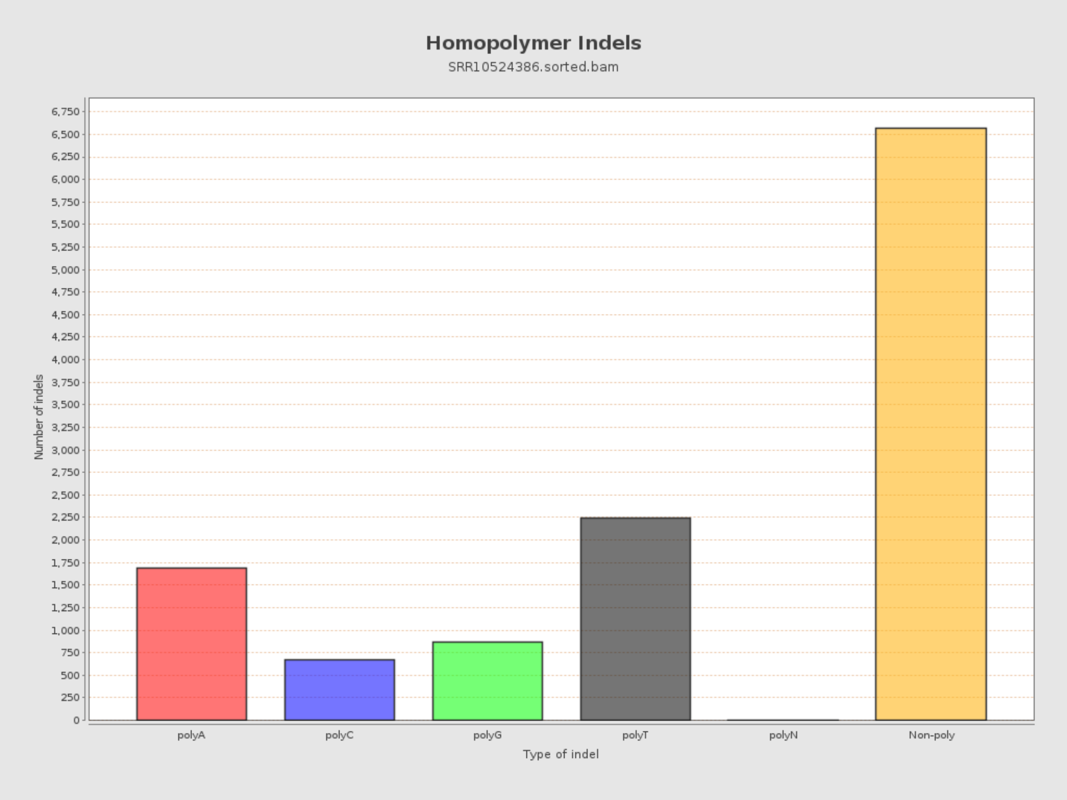
9. Results : Mapped Reads GC-content Distribution



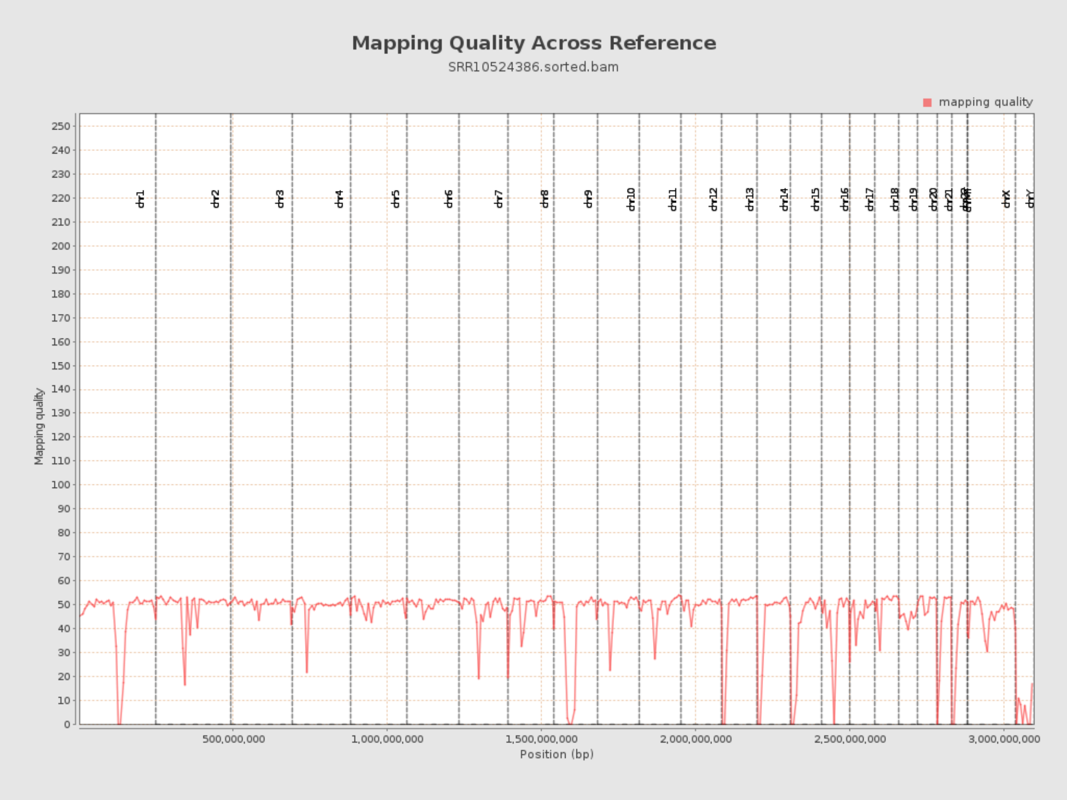
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram