Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:55:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524695.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_SRR10524695 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524695.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:55:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524695.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,806,431
Mapped reads	1,664,973 / 92.17%
Unmapped reads	141,458 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,393 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	71,391 / 3.95%
Duplication rate	3.16%
Clipped reads	1,670,318 / 92.47%

2.2. ACGT Content

Number/percentage of A's	24,852,063 / 25.29%
Number/percentage of C's	19,194,593 / 19.53%
Number/percentage of T's	30,627,185 / 31.16%
Number/percentage of G's	23,596,753 / 24.01%
Number/percentage of N's	13,298 / 0.01%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.3078

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

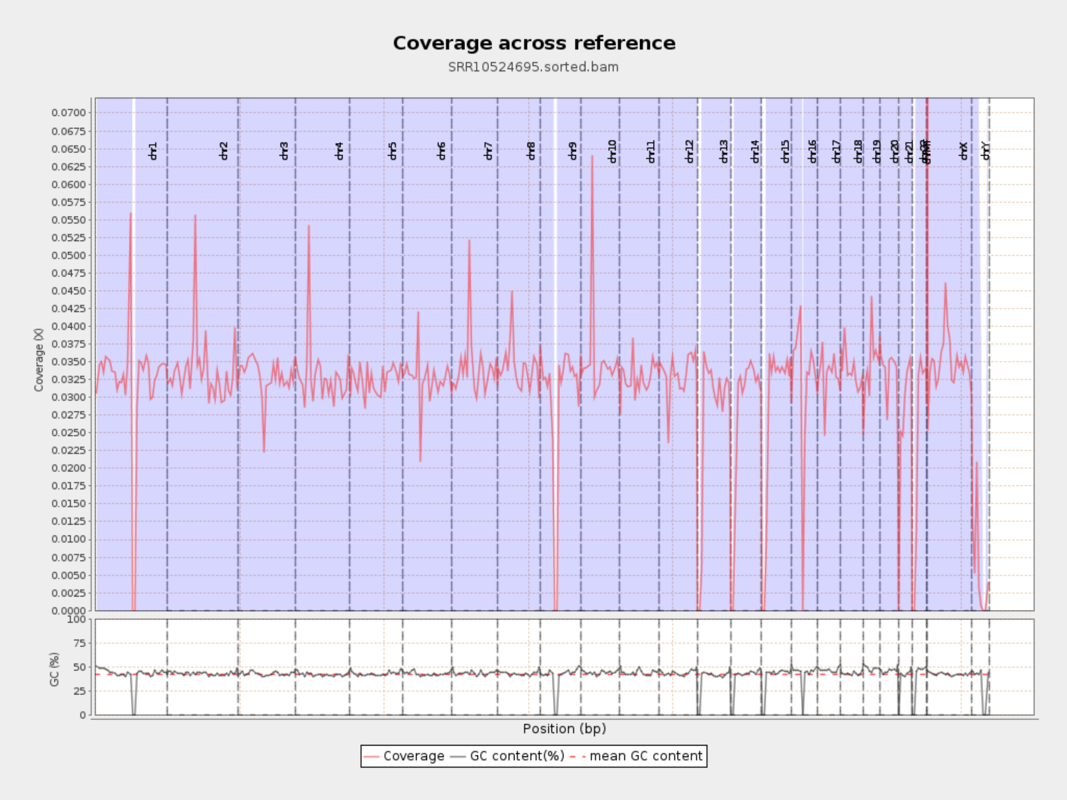
General error rate	0.51%
Mismatches	489,409
Insertions	6,037
Mapped reads with at least one insertion	0.36%
Deletions	18,196
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.01%

2.6. Chromosome stats

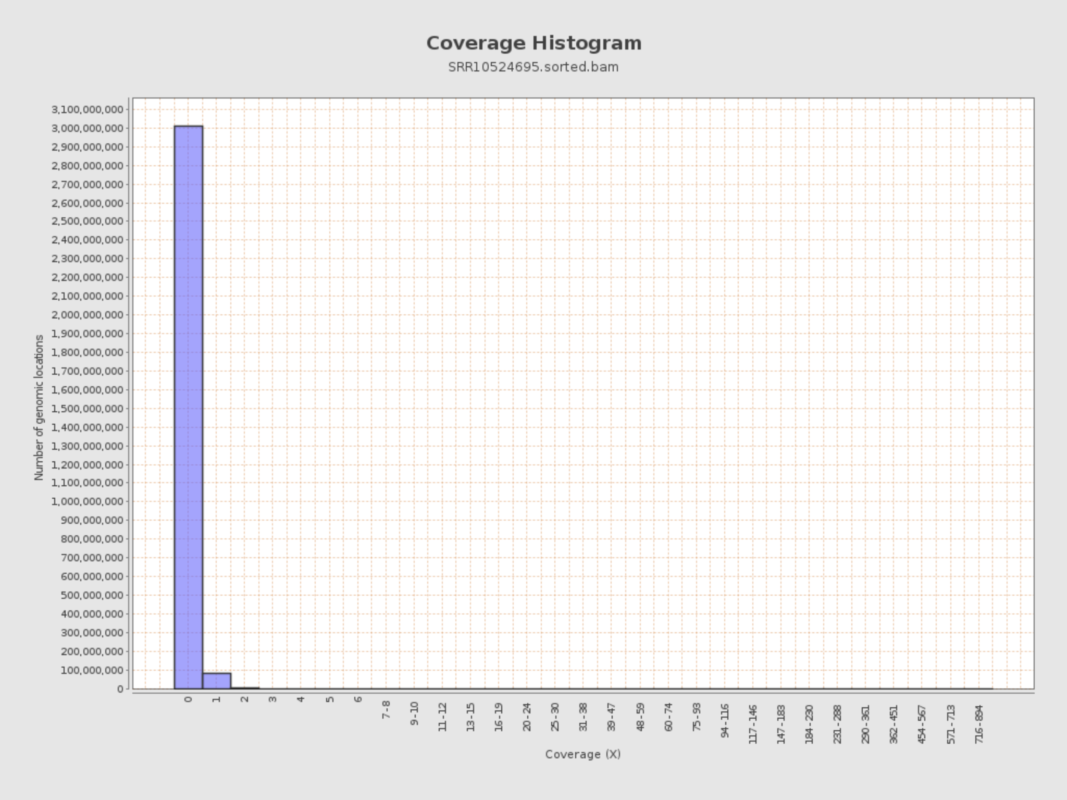
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7973593	0.032	0.5604
chr2	243199373	8198724	0.0337	0.4364
chr3	198022430	6530592	0.033	0.1985
chr4	191154276	6333308	0.0331	0.2277
chr5	180915260	5899204	0.0326	0.1988
chr6	171115067	5574055	0.0326	0.23
chr7	159138663	5459768	0.0343	0.3477

chr8	146364022	5019195	0.0343	0.3375
chr9	141213431	4134753	0.0293	0.245
chr10	135534747	4796571	0.0354	0.3191
chr11	135006516	4451264	0.033	0.2542
chr12	133851895	4446301	0.0332	0.2033
chr13	115169878	3078418	0.0267	0.1804
chr14	107349540	2929543	0.0273	0.1881
chr15	102531392	2832712	0.0276	0.1835
chr16	90354753	2869762	0.0318	0.212
chr17	81195210	2689688	0.0331	0.2143
chr18	78077248	2632552	0.0337	0.463
chr19	59128983	2067600	0.035	0.4253
chr20	63025520	2107427	0.0334	0.2046
chr21	48129895	1318602	0.0274	0.2042
chr22	51304566	1200256	0.0234	0.1679
chrMT	16571	7510	0.4532	0.759
chrX	155270560	5432976	0.035	0.2248
chrY	59373566	328889	0.0055	0.191

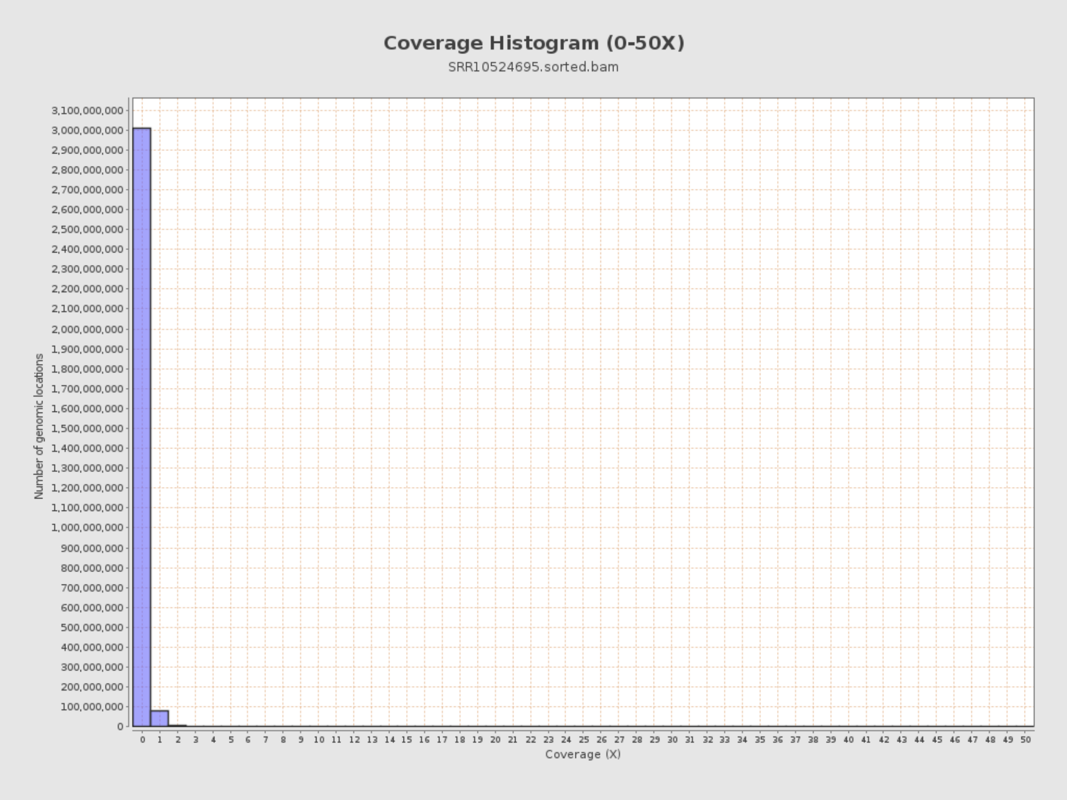
3. Results : Coverage across reference



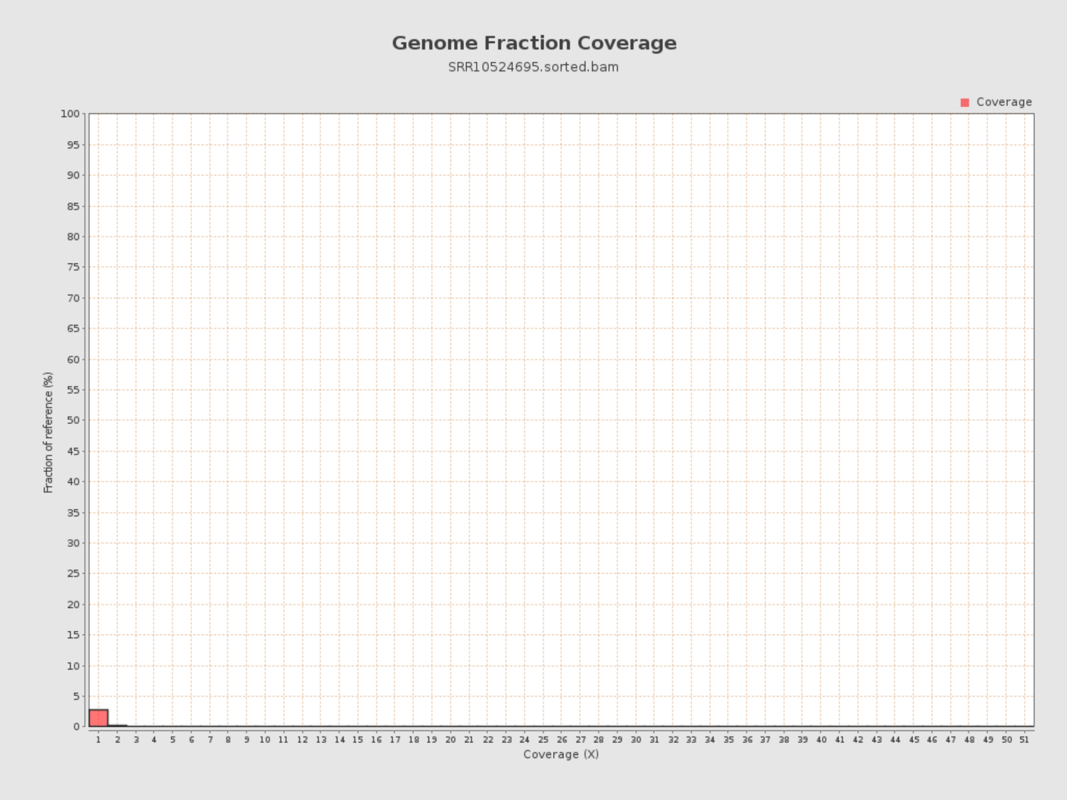
4. Results : Coverage Histogram



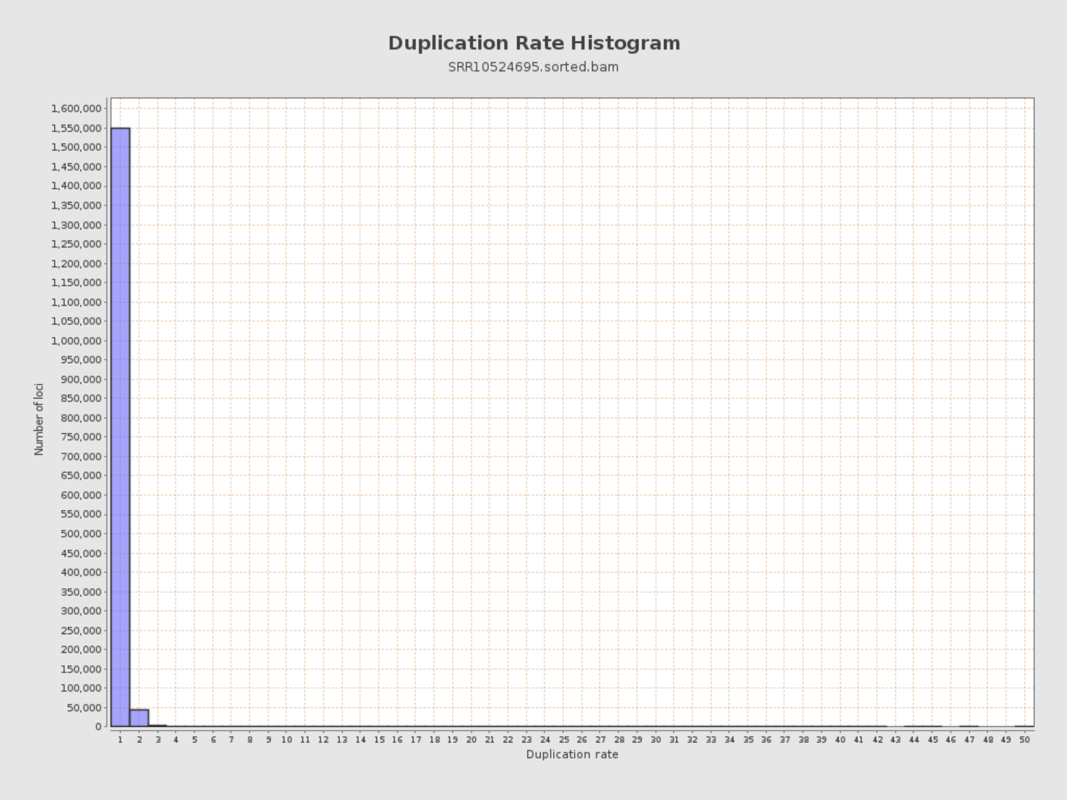
5. Results : Coverage Histogram (0-50X)



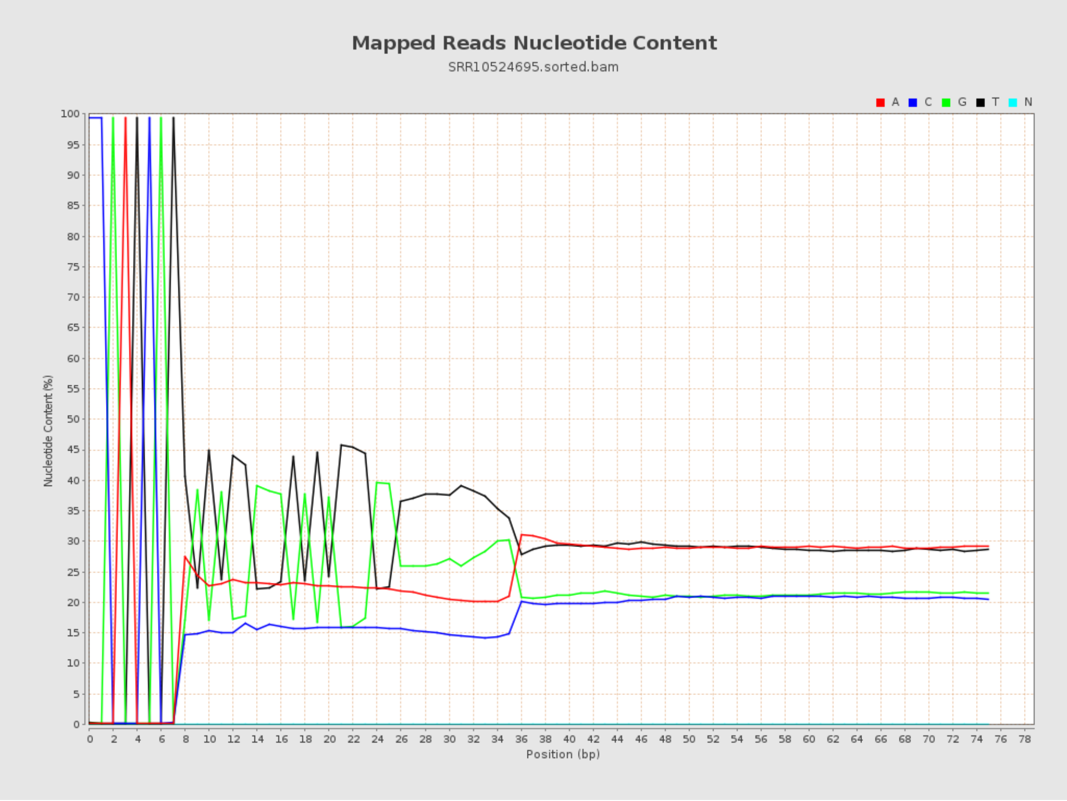
6. Results : Genome Fraction Coverage



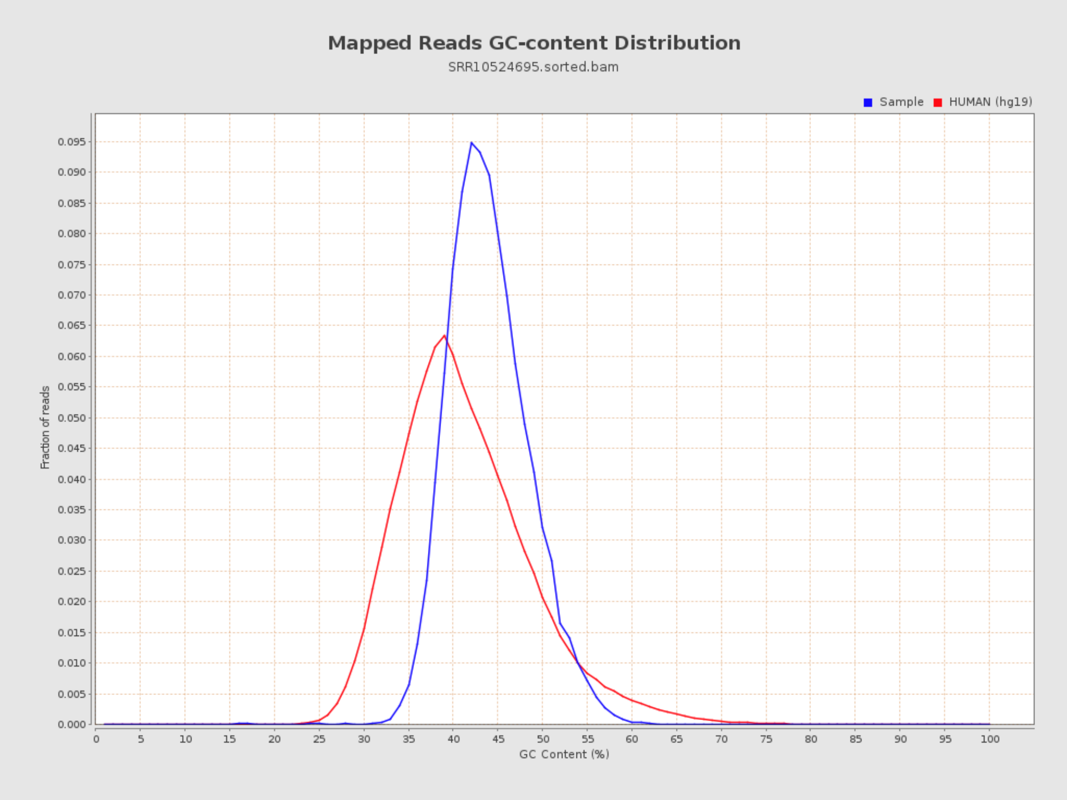
7. Results : Duplication Rate Histogram



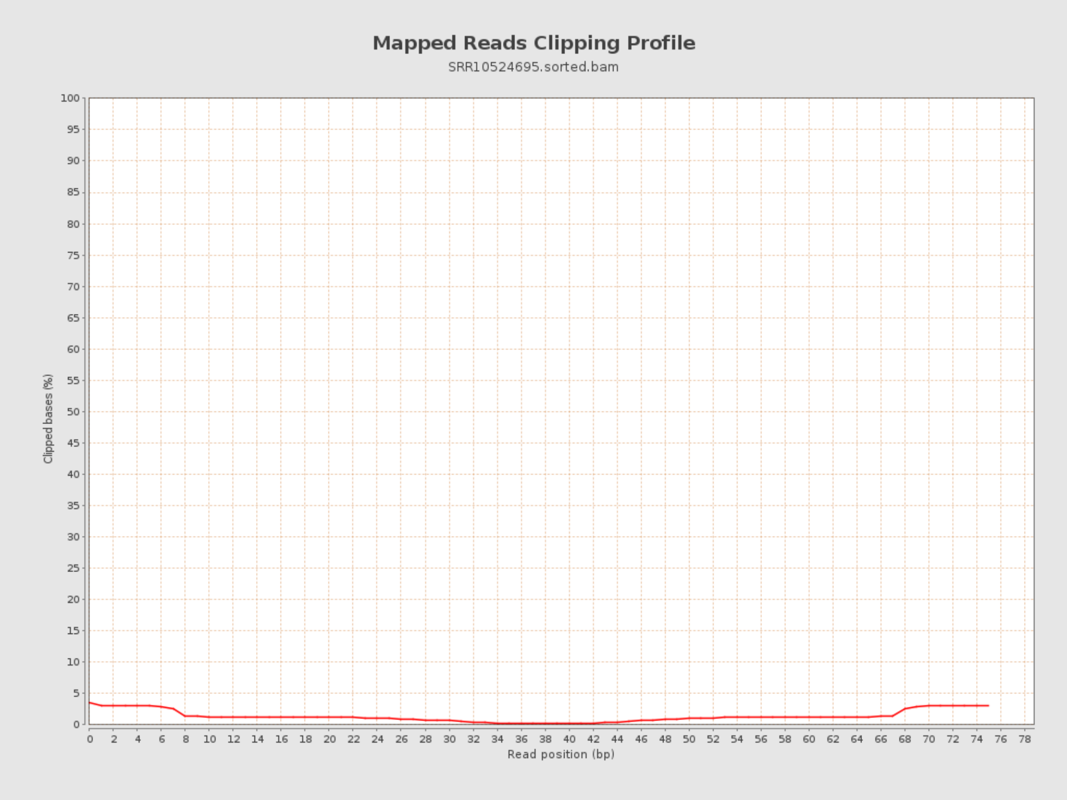
8. Results : Mapped Reads Nucleotide Content



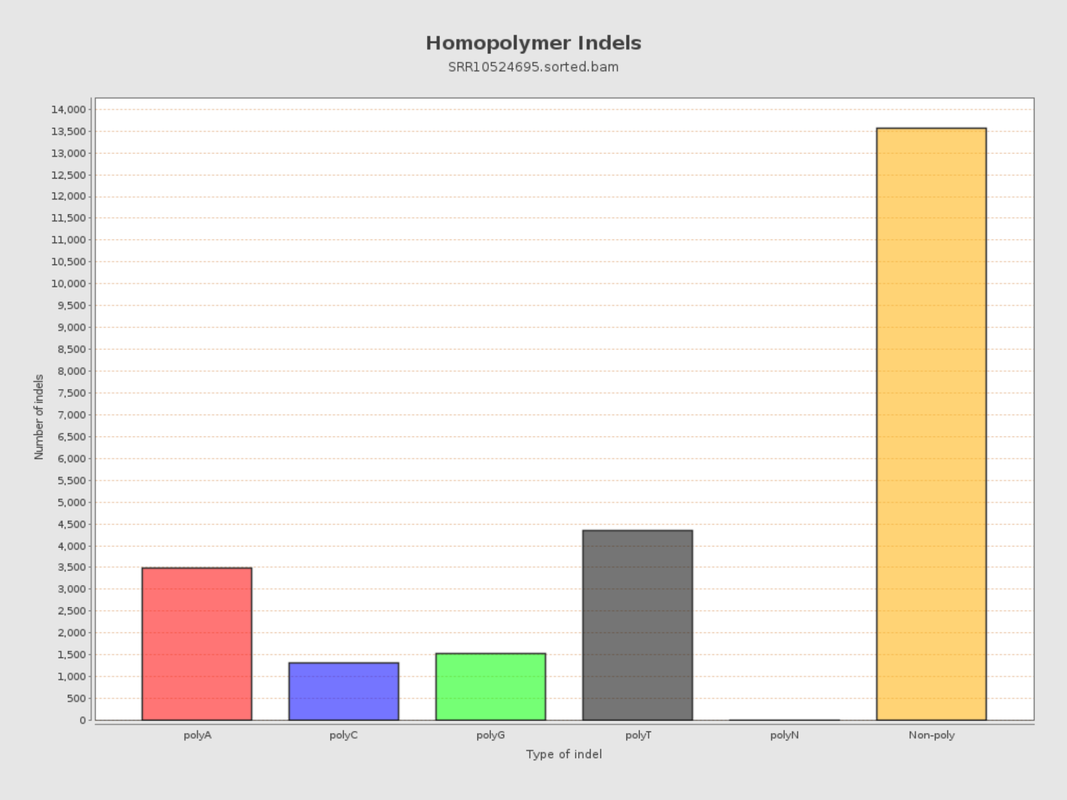
9. Results : Mapped Reads GC-content Distribution



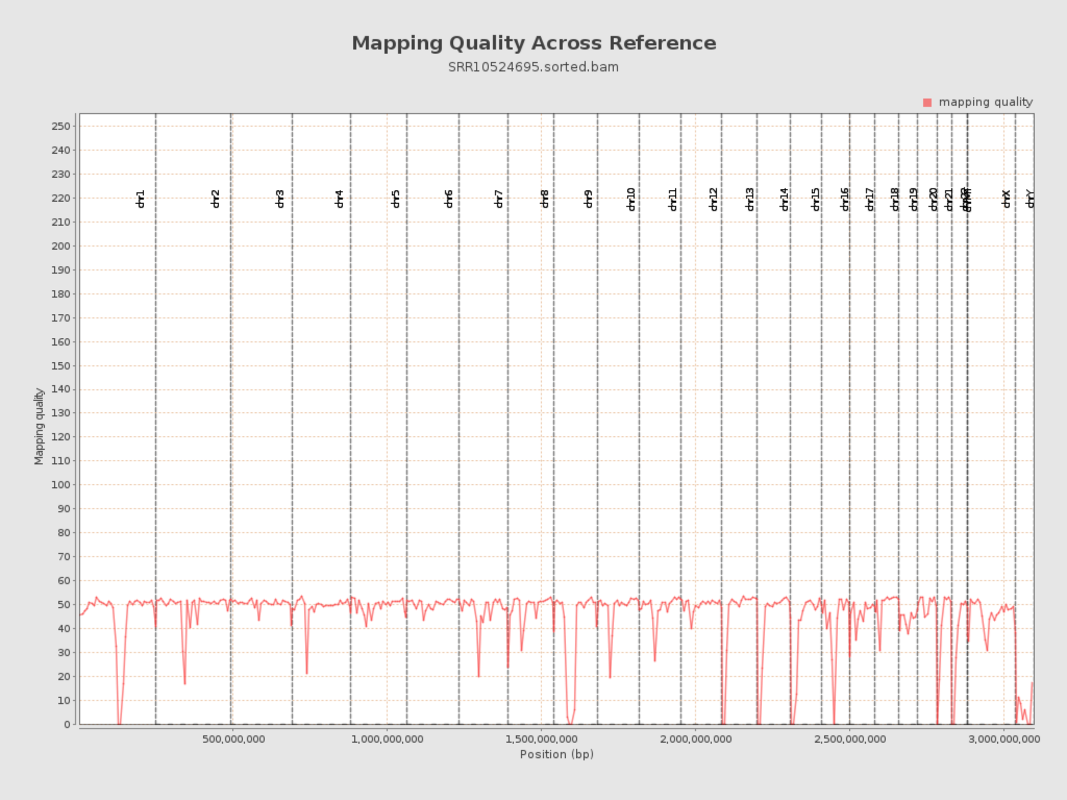
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram