Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:02:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524699.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_SRR10524699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524699.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:02:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,755,890
Mapped reads	1,624,786 / 92.53%
Unmapped reads	131,104 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,753 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	67,457 / 3.84%
Duplication rate	3.03%
Clipped reads	1,626,482 / 92.63%

2.2. ACGT Content

Number/percentage of A's	25,454,166 / 26.35%
Number/percentage of C's	18,136,491 / 18.77%
Number/percentage of T's	30,839,075 / 31.92%
Number/percentage of G's	22,172,166 / 22.95%
Number/percentage of N's	12,768 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.3022

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

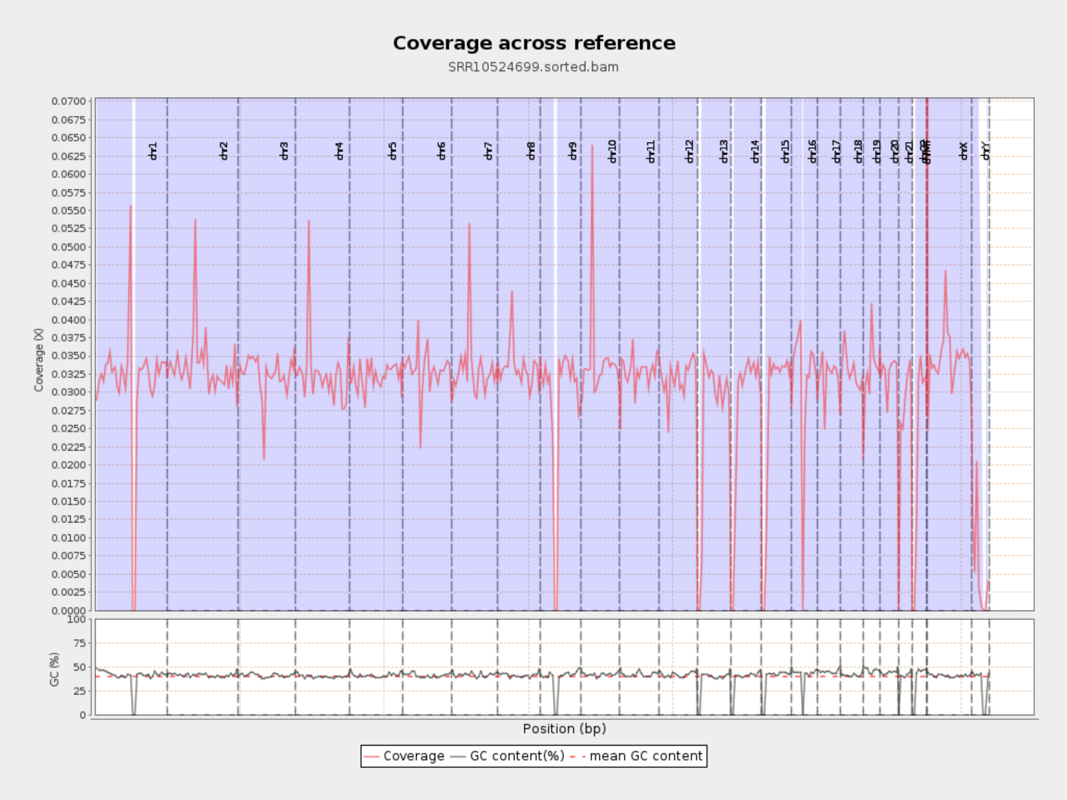
General error rate	0.51%
Mismatches	479,041
Insertions	7,709
Mapped reads with at least one insertion	0.47%
Deletions	18,574
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.99%

2.6. Chromosome stats

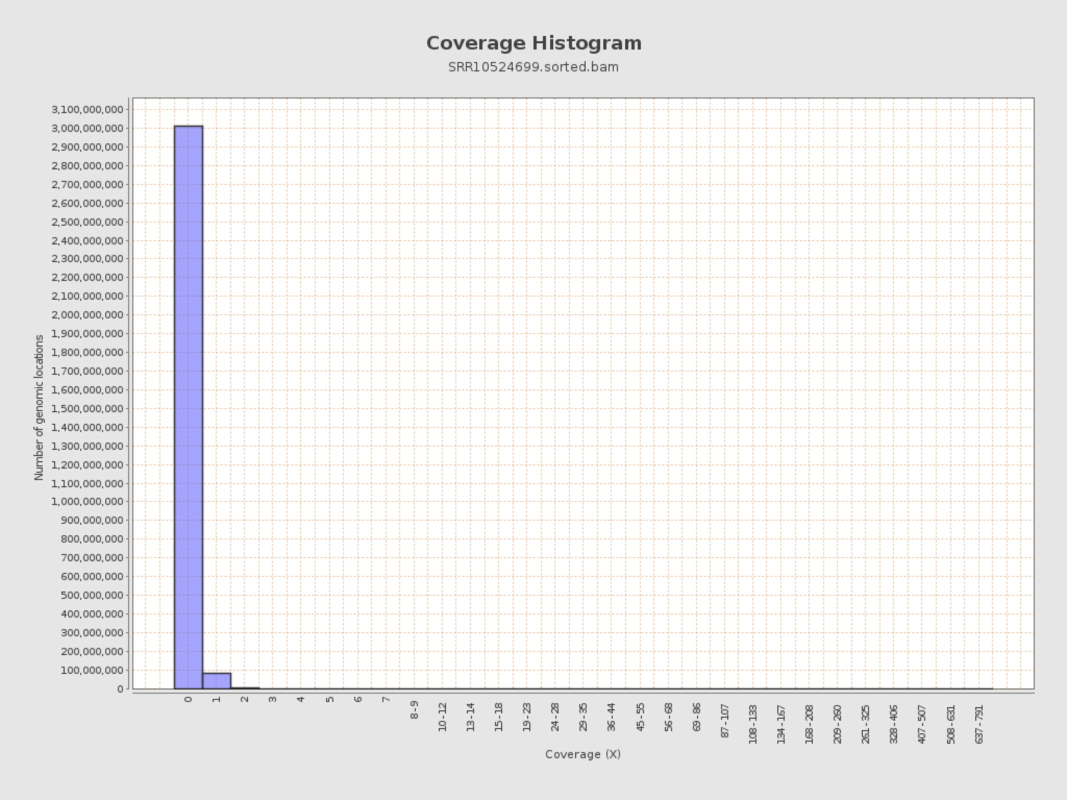
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7777610	0.0312	0.5486
chr2	243199373	8199949	0.0337	0.4063
chr3	198022430	6424633	0.0324	0.1968
chr4	191154276	6238694	0.0326	0.2295
chr5	180915260	5851758	0.0323	0.1975
chr6	171115067	5647885	0.033	0.2243
chr7	159138663	5319462	0.0334	0.3625

chr8	146364022	4911924	0.0336	0.3468
chr9	141213431	4026478	0.0285	0.2479
chr10	135534747	4684985	0.0346	0.3191
chr11	135006516	4444324	0.0329	0.2531
chr12	133851895	4274212	0.0319	0.1968
chr13	115169878	3010848	0.0261	0.1777
chr14	107349540	2906575	0.0271	0.1865
chr15	102531392	2765374	0.027	0.18
chr16	90354753	2784616	0.0308	0.2069
chr17	81195210	2606695	0.0321	0.2067
chr18	78077248	2572416	0.0329	0.445
chr19	59128983	1969274	0.0333	0.397
chr20	63025520	2036884	0.0323	0.198
chr21	48129895	1274095	0.0265	0.21
chr22	51304566	1145816	0.0223	0.1635
chrMT	16571	32583	1.9663	1.824
chrX	155270560	5409712	0.0348	0.2248
chrY	59373566	327397	0.0055	0.2034

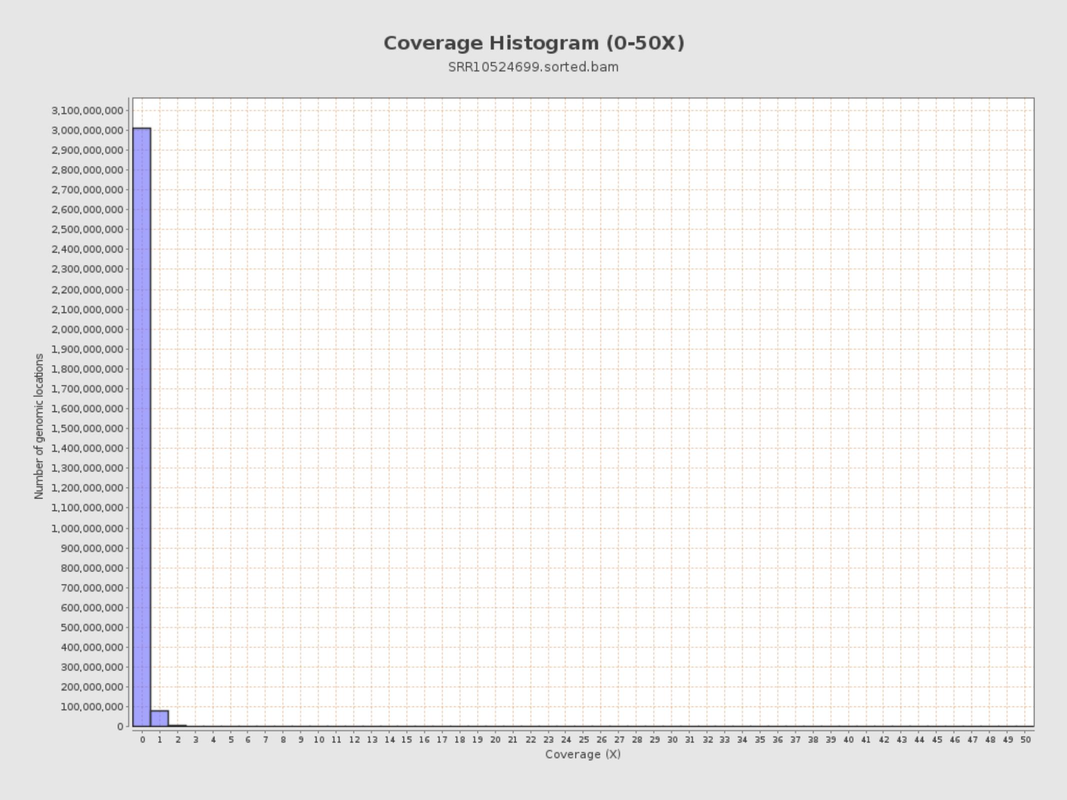
3. Results : Coverage across reference



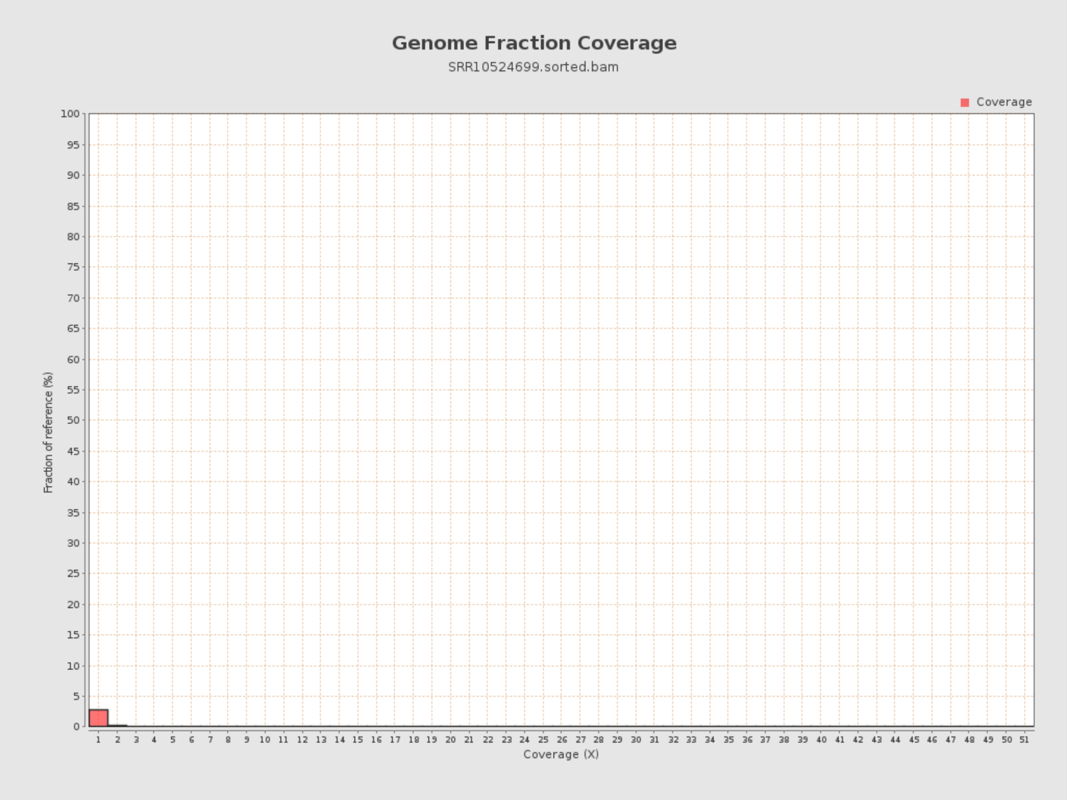
4. Results : Coverage Histogram



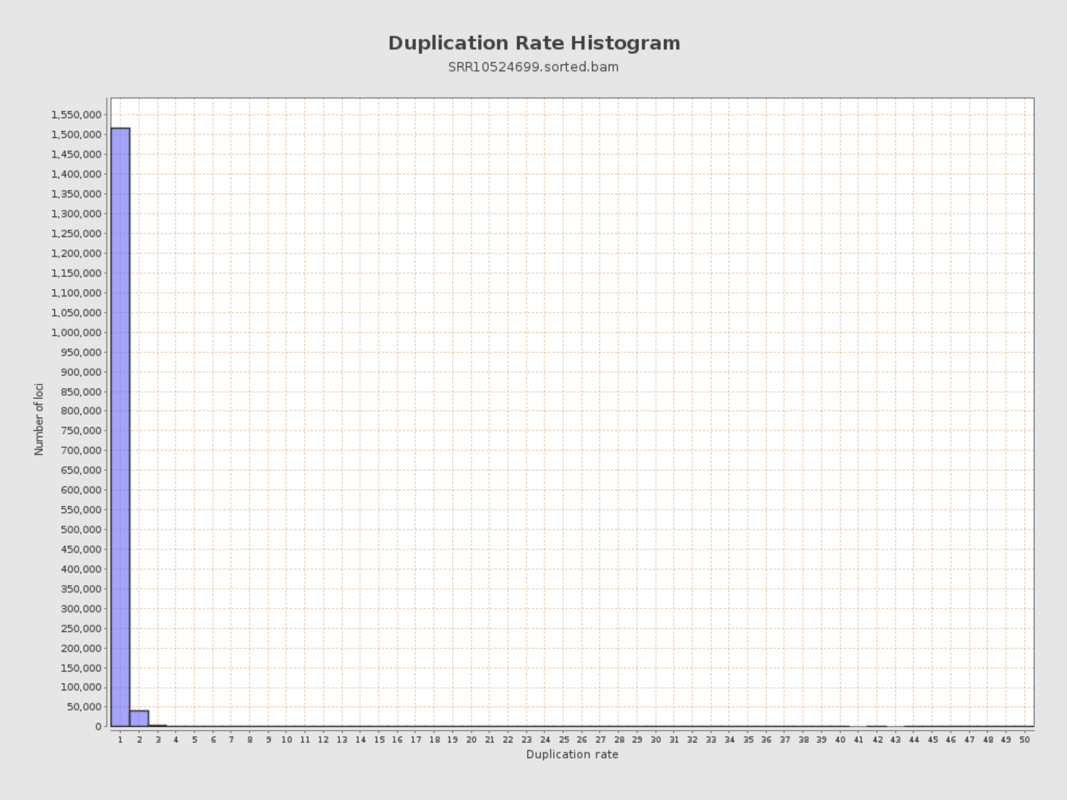
5. Results : Coverage Histogram (0-50X)



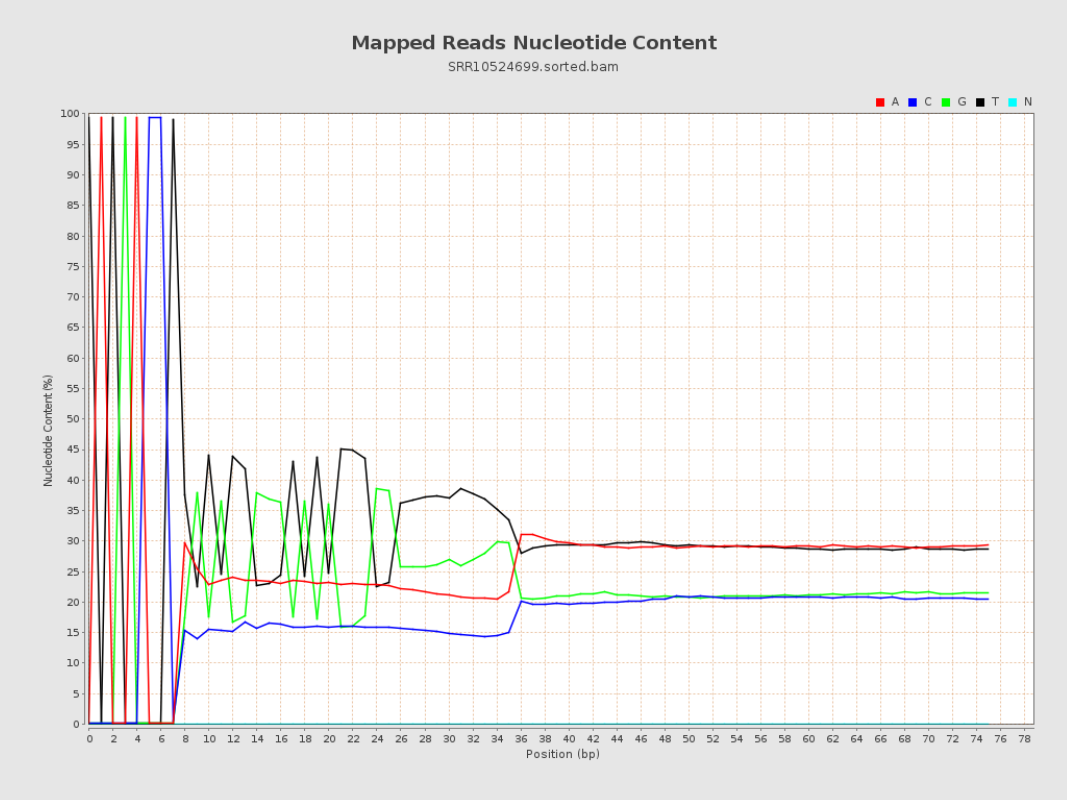
6. Results : Genome Fraction Coverage



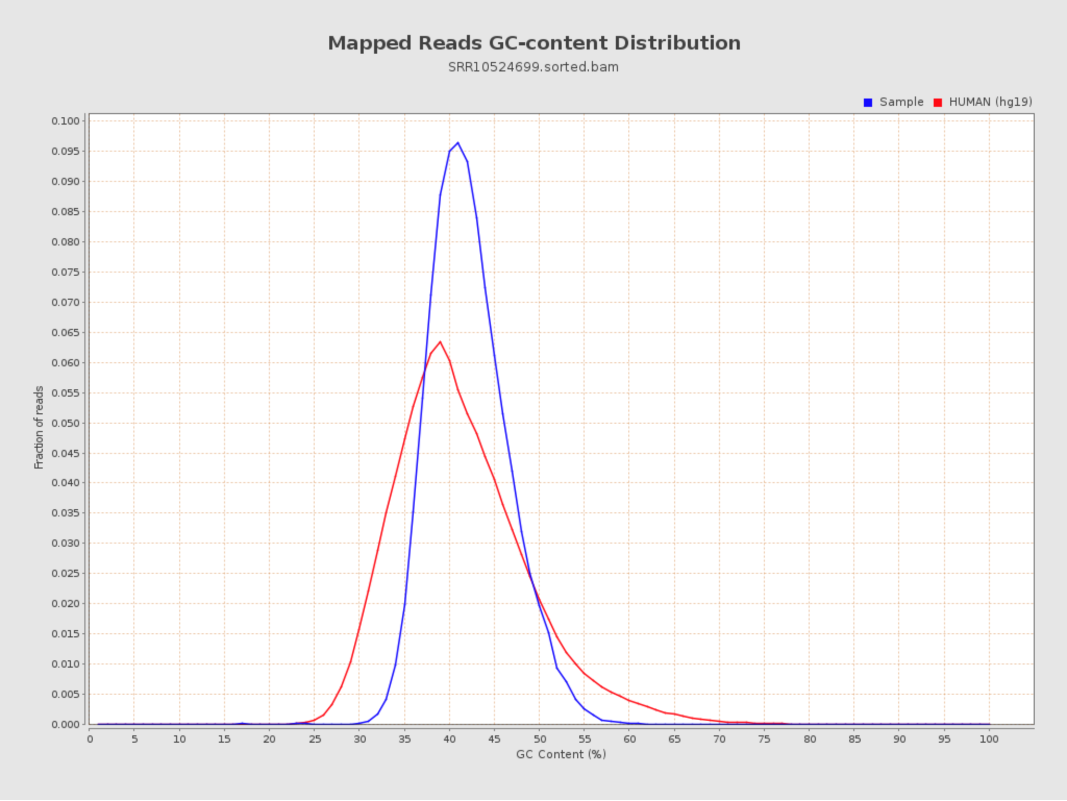
7. Results : Duplication Rate Histogram



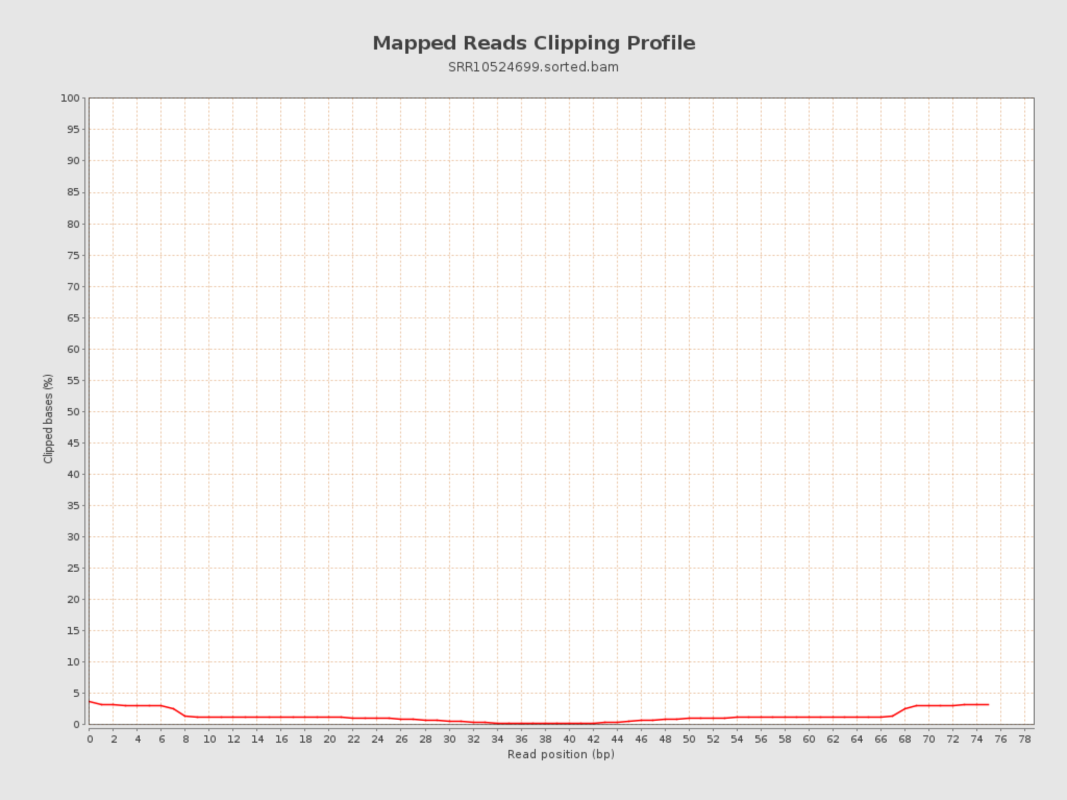
8. Results : Mapped Reads Nucleotide Content



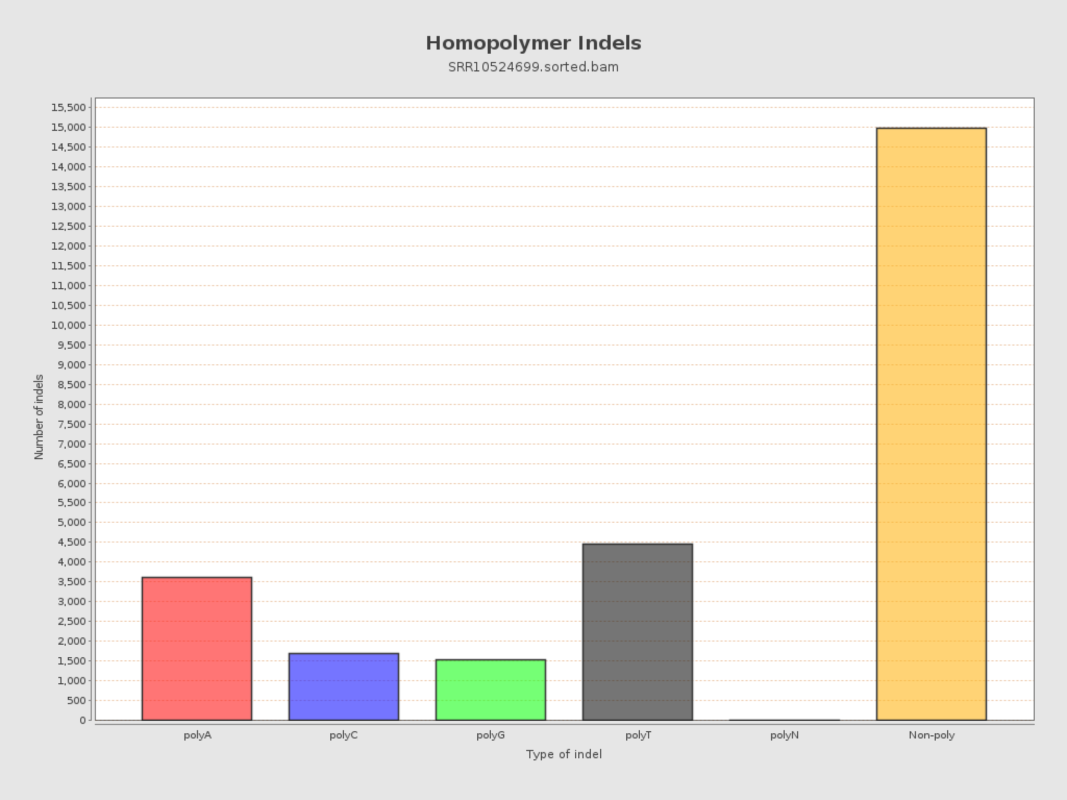
9. Results : Mapped Reads GC-content Distribution



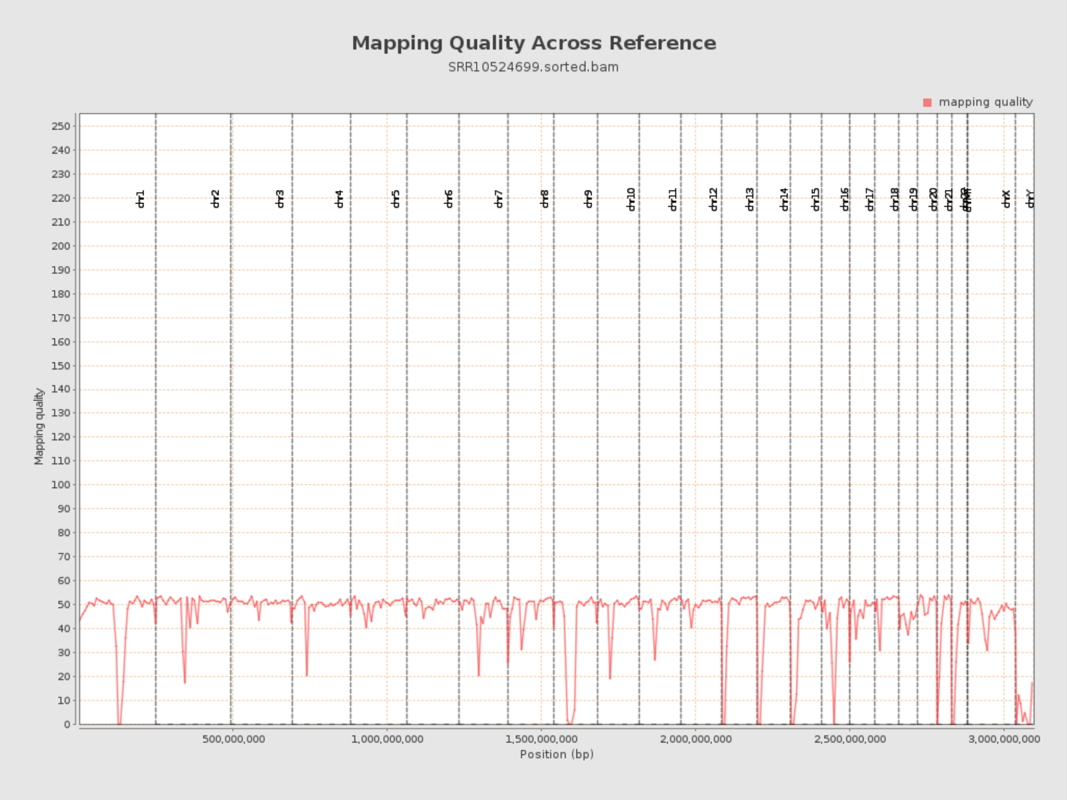
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram