Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:37:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524559.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_SRR10524559 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524559.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:37:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524559.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,139,065
Mapped reads	1,802,537 / 84.27%
Unmapped reads	336,528 / 15.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,282 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	307,823 / 14.39%
Duplication rate	11.58%
Clipped reads	1,807,149 / 84.48%

2.2. ACGT Content

Number/percentage of A's	23,463,860 / 23.52%
Number/percentage of C's	19,833,629 / 19.88%
Number/percentage of T's	32,805,931 / 32.89%
Number/percentage of G's	23,647,350 / 23.71%
Number/percentage of N's	1,339 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.3738

2.4. Mapping Quality

Mean Mapping Quality	43.51

2.5. Mismatches and indels

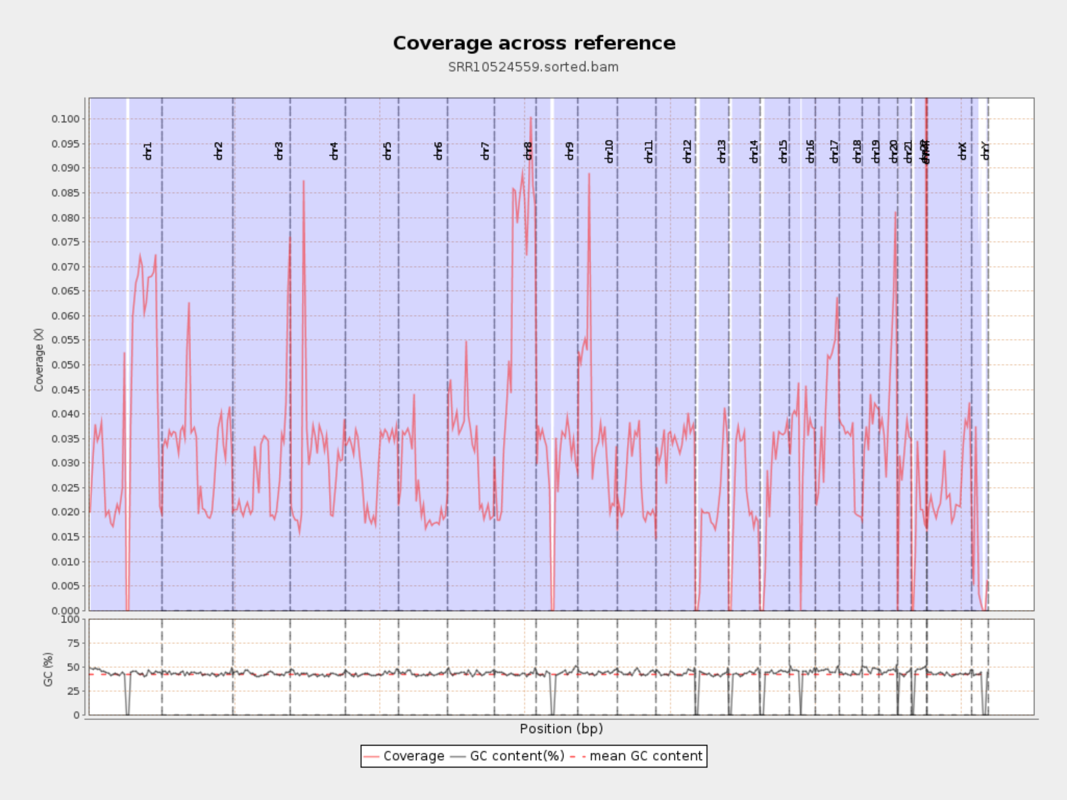
General error rate	0.65%
Mismatches	630,424
Insertions	6,741
Mapped reads with at least one insertion	0.37%
Deletions	27,912
Mapped reads with at least one deletion	1.53%
Homopolymer indels	41.76%

2.6. Chromosome stats

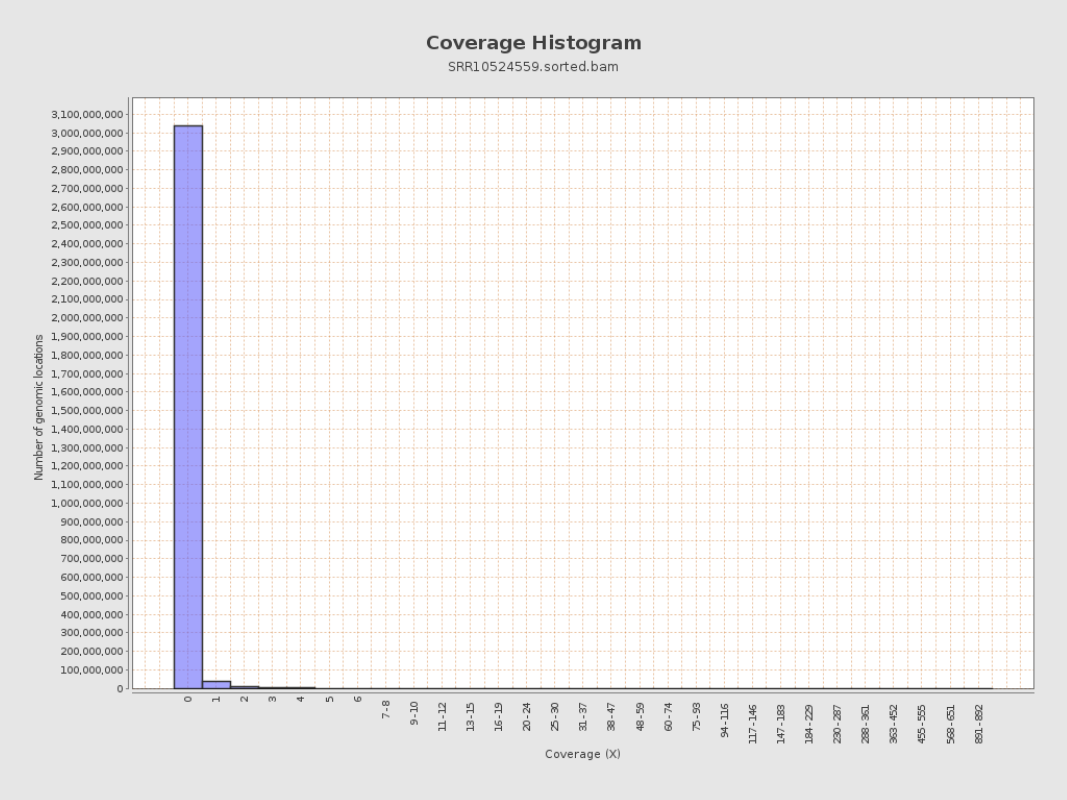
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9941640	0.0399	0.5292
chr2	243199373	8119271	0.0334	0.529
chr3	198022430	5548173	0.028	0.2633
chr4	191154276	5934074	0.031	0.3733
chr5	180915260	5482639	0.0303	0.2691
chr6	171115067	4198843	0.0245	0.2804
chr7	159138663	5234191	0.0329	0.399

chr8	146364022	9118521	0.0623	0.4577
chr9	141213431	4218462	0.0299	0.3068
chr10	135534747	5373896	0.0396	0.5051
chr11	135006516	3476407	0.0257	0.3041
chr12	133851895	4618605	0.0345	0.2937
chr13	115169878	2321895	0.0202	0.2214
chr14	107349540	2418881	0.0225	0.2359
chr15	102531392	2695443	0.0263	0.2533
chr16	90354753	3177567	0.0352	0.3142
chr17	81195210	3513924	0.0433	0.3498
chr18	78077248	2399842	0.0307	0.4667
chr19	59128983	2213804	0.0374	0.4075
chr20	63025520	2964857	0.047	0.3567
chr21	48129895	1434342	0.0298	0.3236
chr22	51304566	844503	0.0165	0.2074
chrMT	16571	157709	9.5172	7.4227
chrX	155270560	3927256	0.0253	0.2626
chrY	59373566	463953	0.0078	0.352

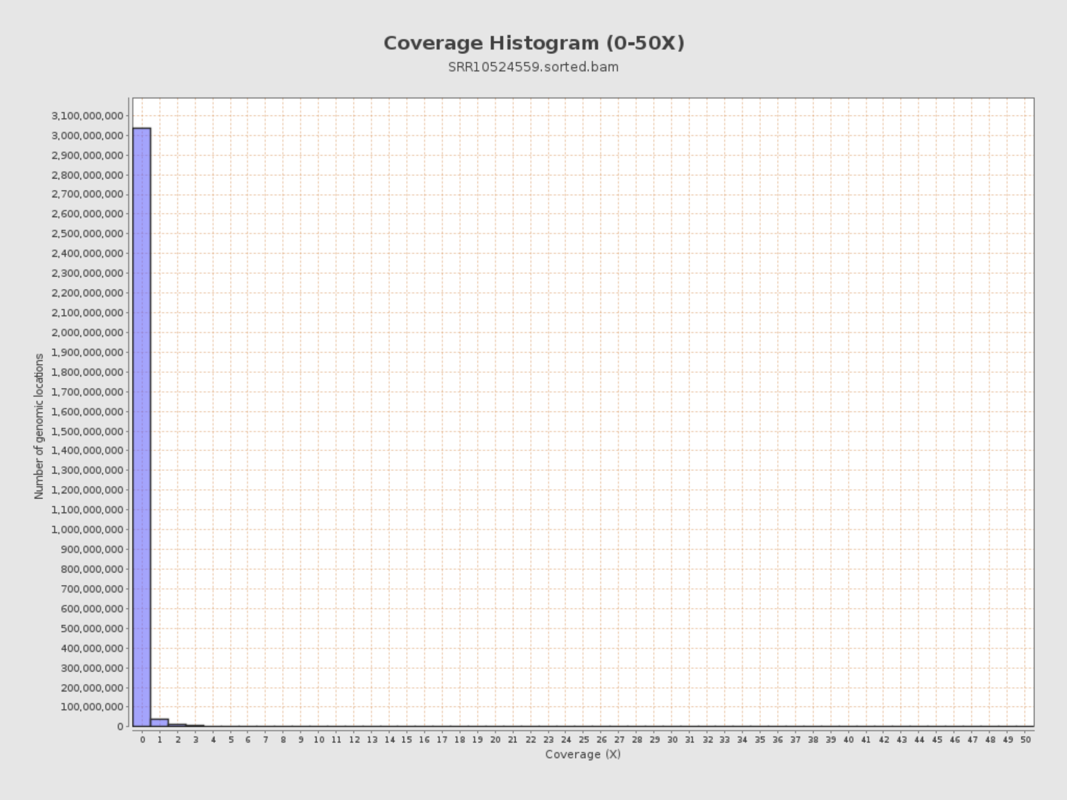
3. Results : Coverage across reference



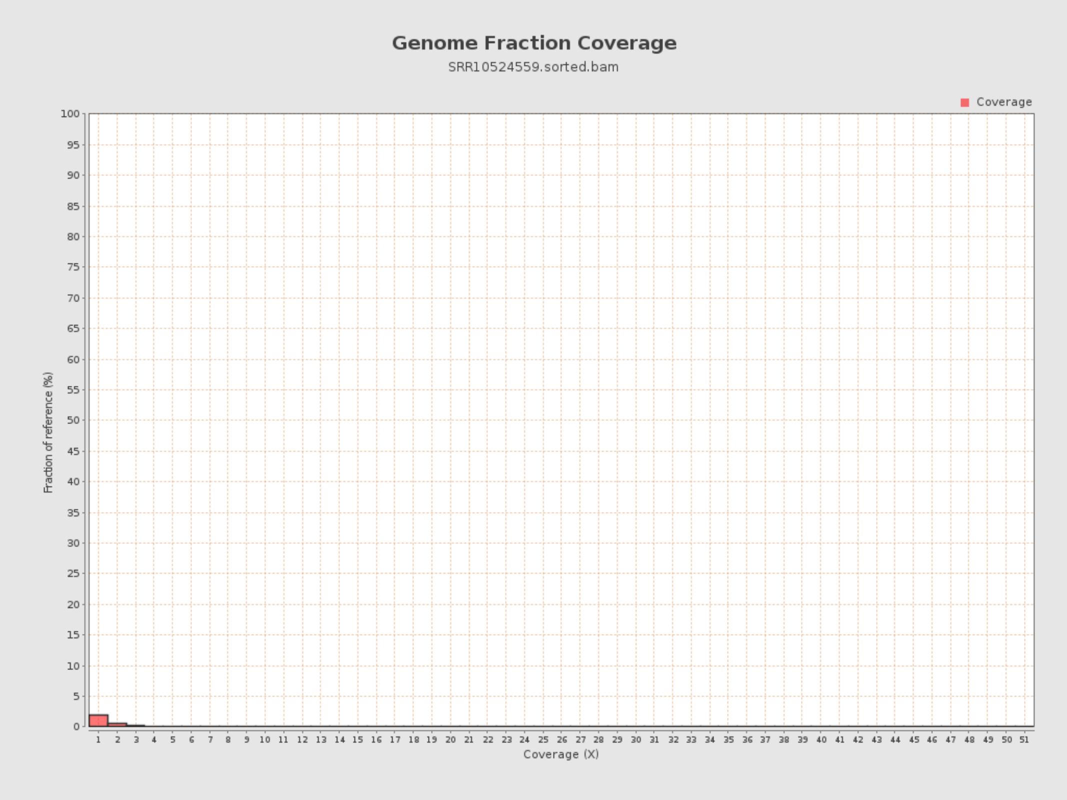
4. Results : Coverage Histogram



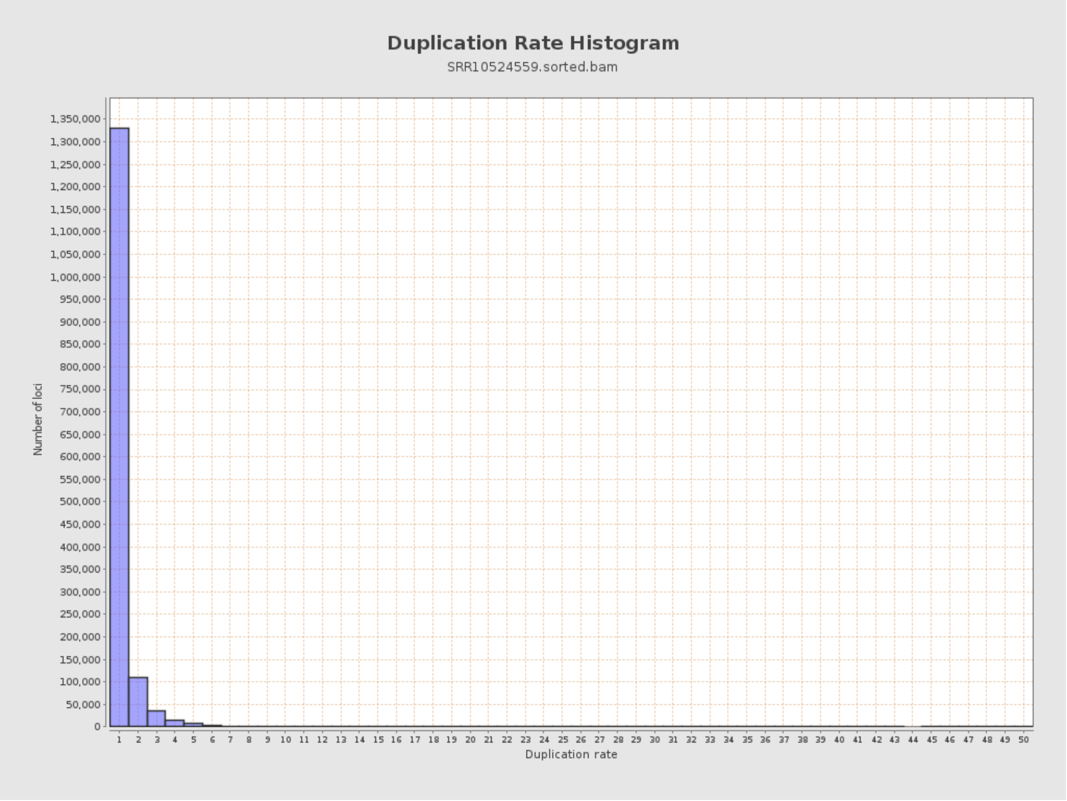
5. Results : Coverage Histogram (0-50X)



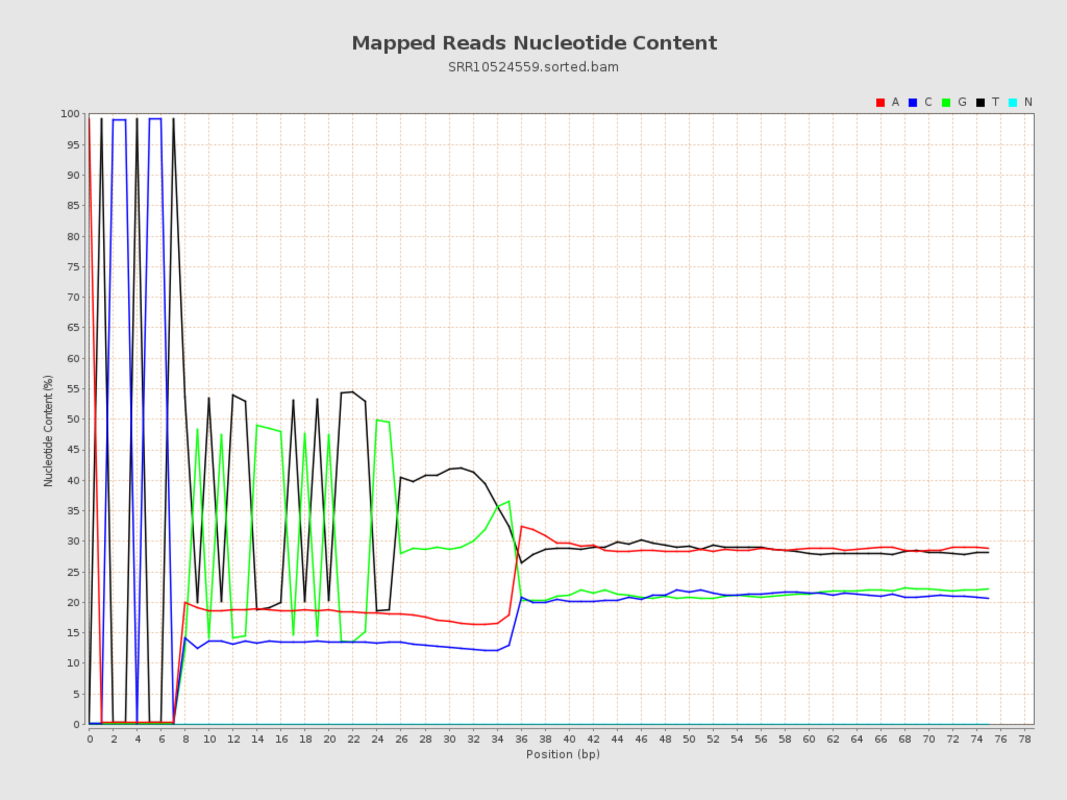
6. Results : Genome Fraction Coverage



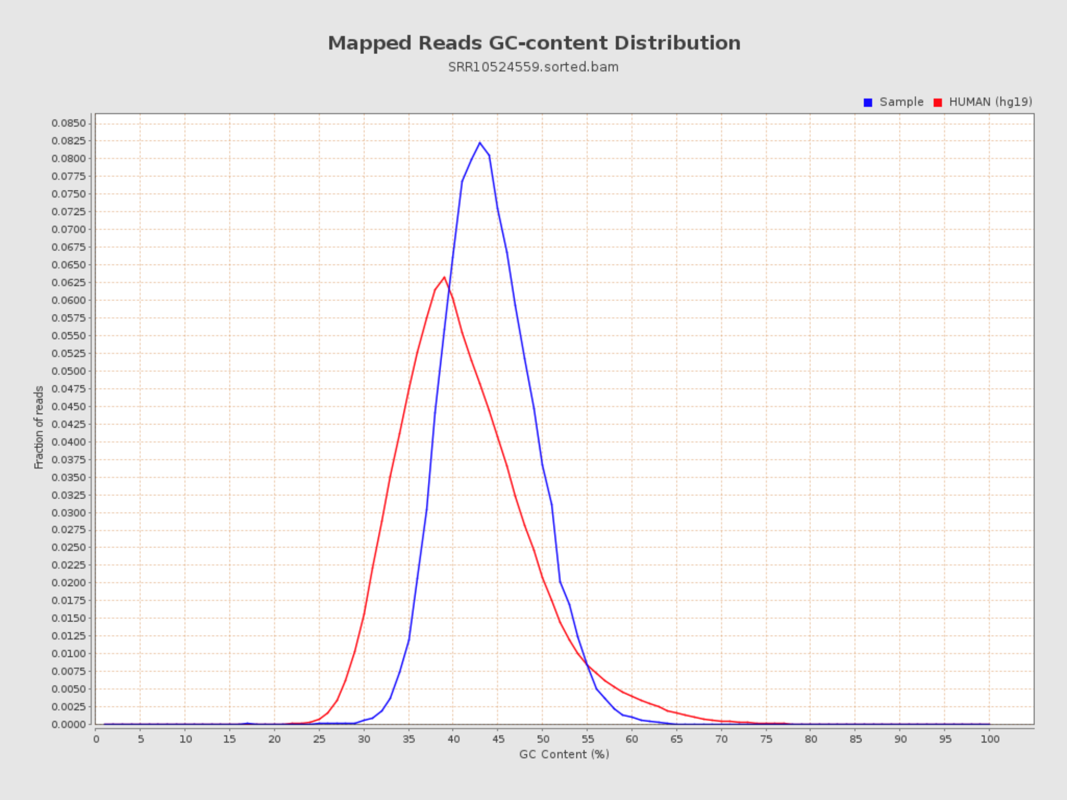
7. Results : Duplication Rate Histogram



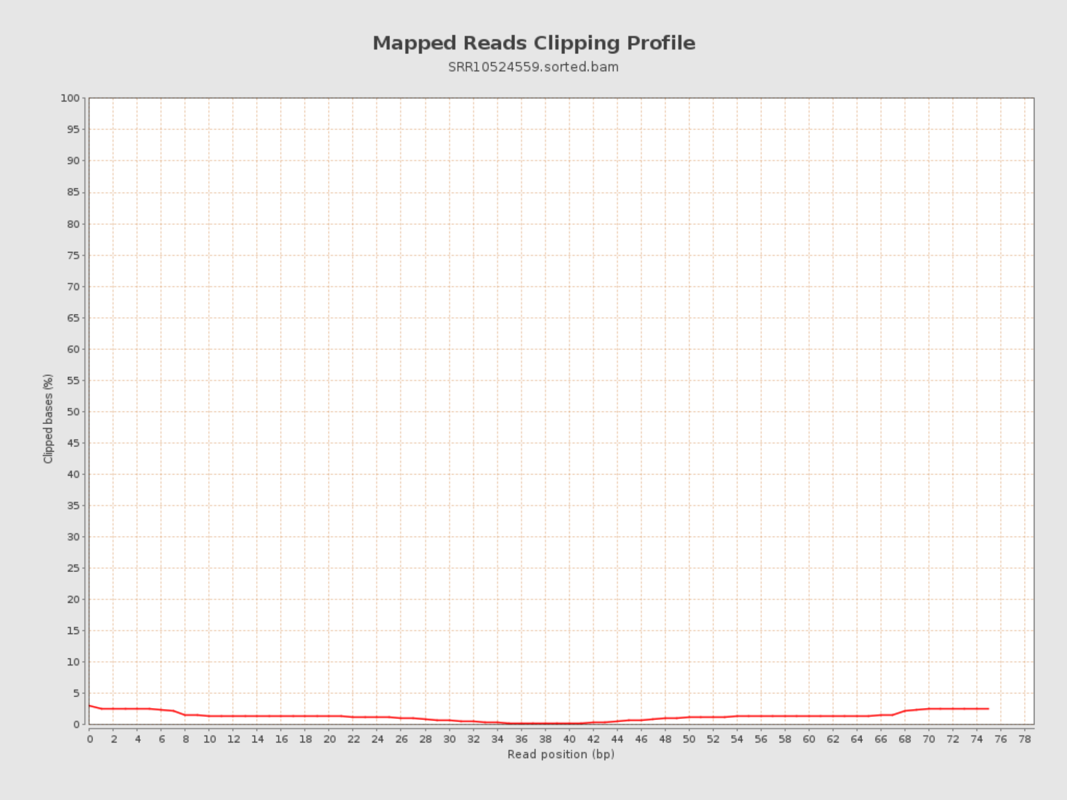
8. Results : Mapped Reads Nucleotide Content



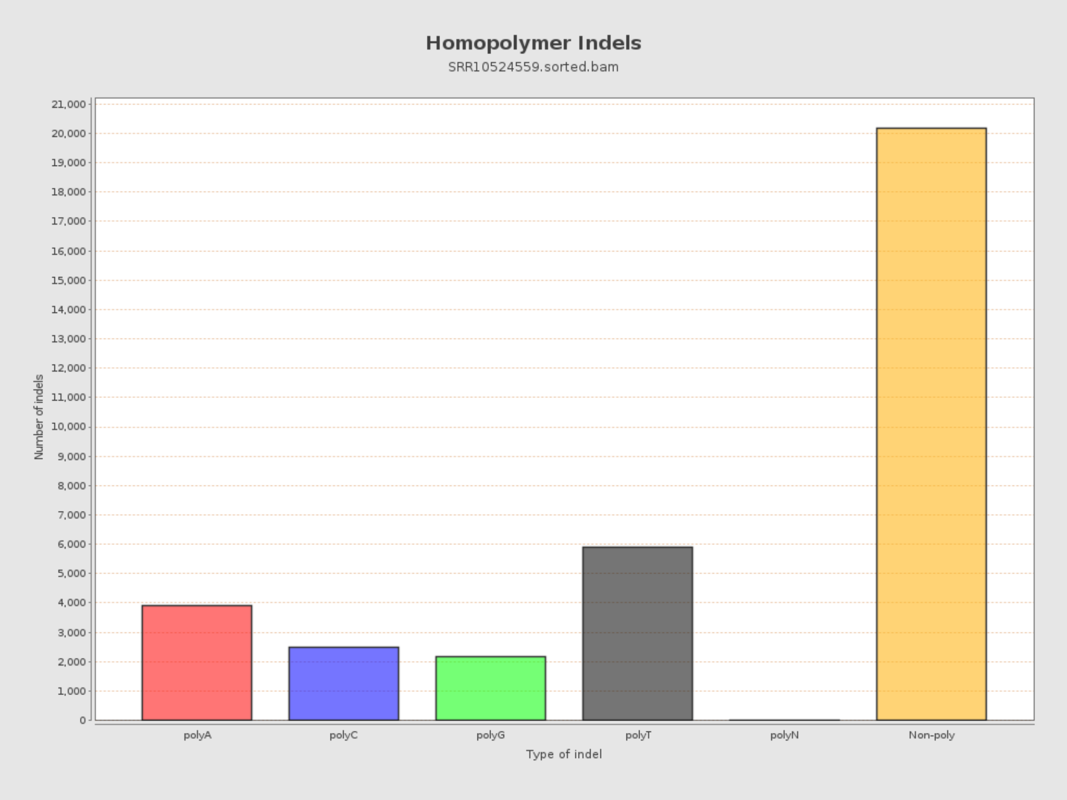
9. Results : Mapped Reads GC-content Distribution



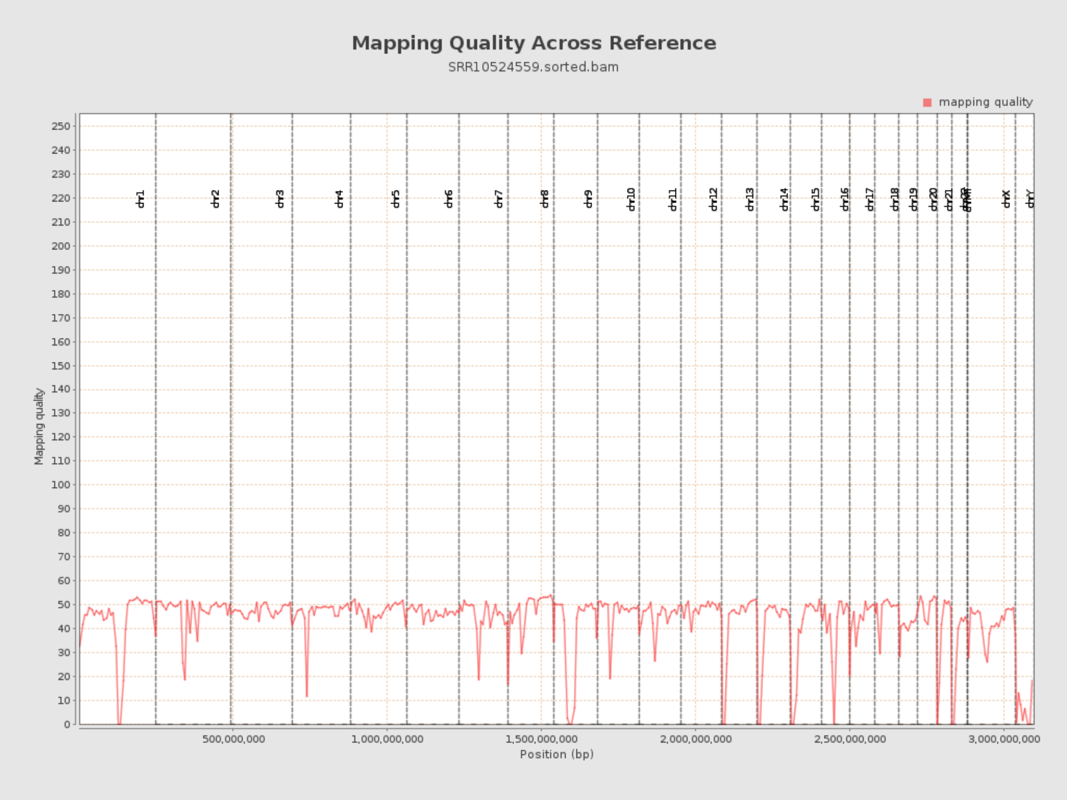
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram