Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:45:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524692.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_SRR10524692 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524692.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:45:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524692.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,730,947
Mapped reads	2,521,092 / 92.32%
Unmapped reads	209,855 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,601 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	125,657 / 4.6%
Duplication rate	3.62%
Clipped reads	2,523,423 / 92.4%

2.2. ACGT Content

Number/percentage of A's	39,147,637 / 26.24%
Number/percentage of C's	25,358,546 / 17%
Number/percentage of T's	47,802,954 / 32.04%
Number/percentage of G's	36,854,743 / 24.7%
Number/percentage of N's	20,557 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0482

Standard Deviation	0.4213

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

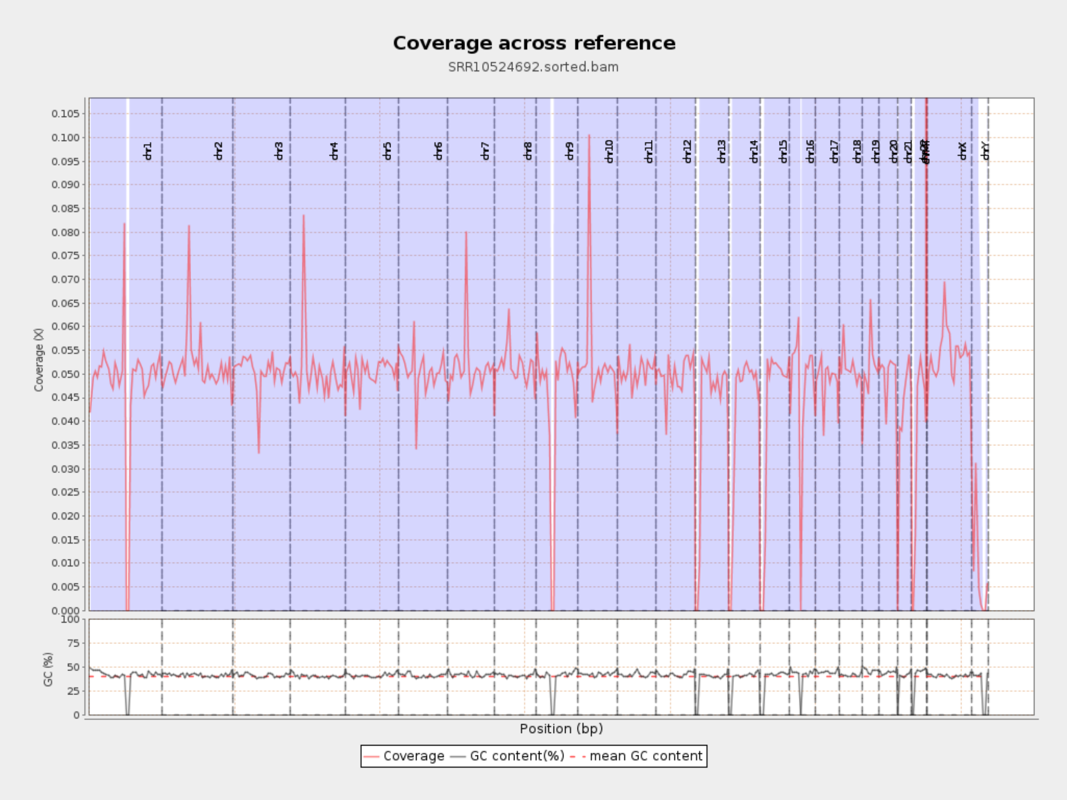
General error rate	0.51%
Mismatches	741,710
Insertions	11,393
Mapped reads with at least one insertion	0.45%
Deletions	28,364
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.4%

2.6. Chromosome stats

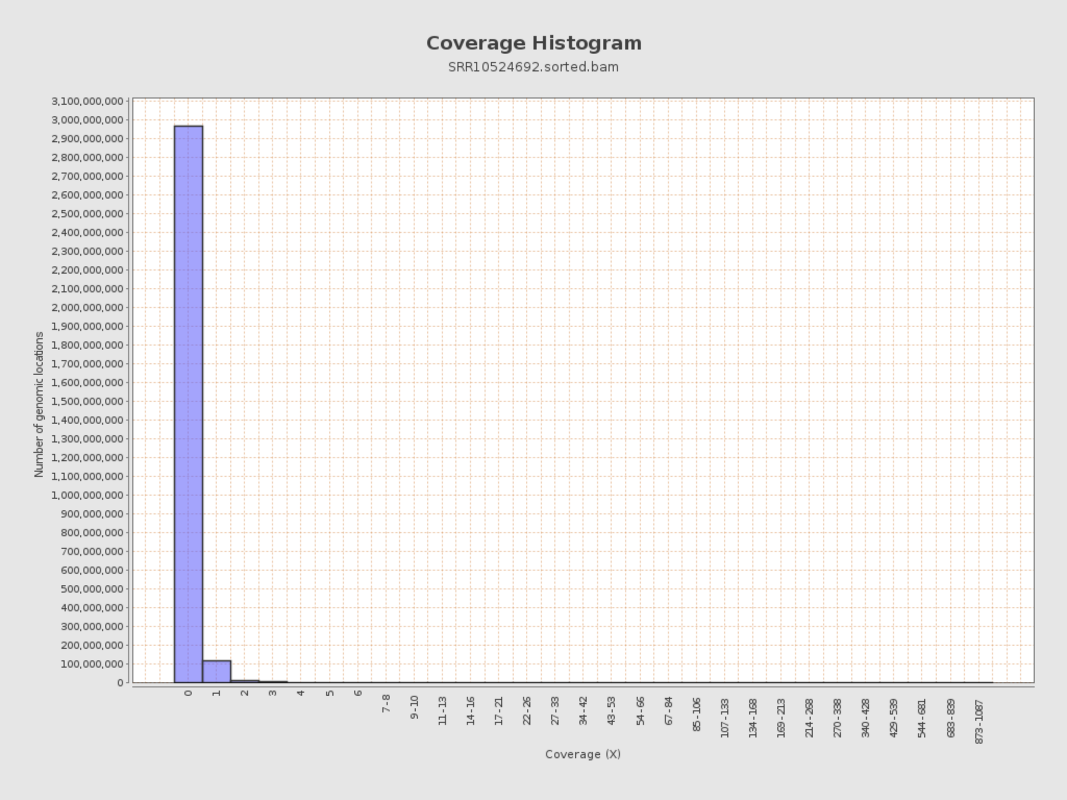
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11931067	0.0479	0.7878
chr2	243199373	12662564	0.0521	0.5639
chr3	198022430	10001061	0.0505	0.2539
chr4	191154276	9688541	0.0507	0.3026
chr5	180915260	9142673	0.0505	0.2558
chr6	171115067	8651651	0.0506	0.3007
chr7	159138663	8247107	0.0518	0.5229

chr8	146364022	7565835	0.0517	0.4525
chr9	141213431	6275631	0.0444	0.3412
chr10	135534747	7160001	0.0528	0.4554
chr11	135006516	6819994	0.0505	0.3557
chr12	133851895	6662999	0.0498	0.2553
chr13	115169878	4756472	0.0413	0.23
chr14	107349540	4420938	0.0412	0.2371
chr15	102531392	4229289	0.0412	0.2335
chr16	90354753	4259285	0.0471	0.2818
chr17	81195210	3934085	0.0485	0.2683
chr18	78077248	4019040	0.0515	0.6828
chr19	59128983	3048431	0.0516	0.5815
chr20	63025520	3118628	0.0495	0.2599
chr21	48129895	1987631	0.0413	0.2748
chr22	51304566	1730935	0.0337	0.2063
chrMT	16571	37374	2.2554	1.7907
chrX	155270560	8386386	0.054	0.2943
chrY	59373566	492381	0.0083	0.2935

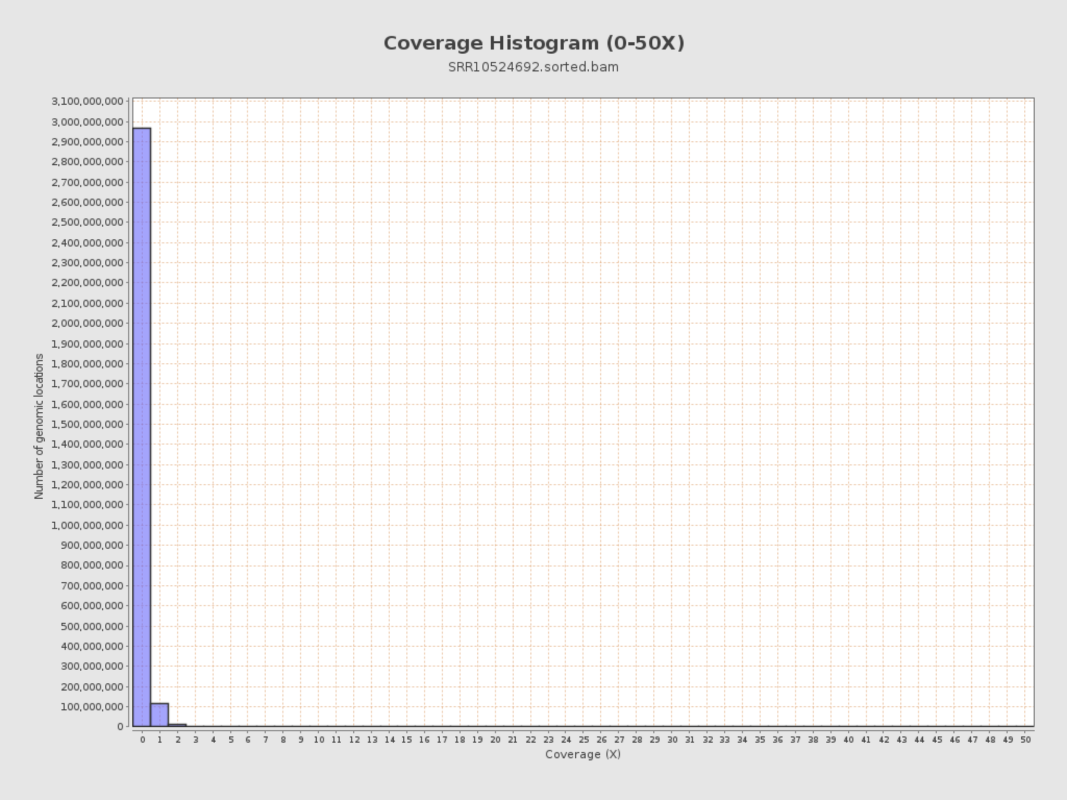
3. Results : Coverage across reference



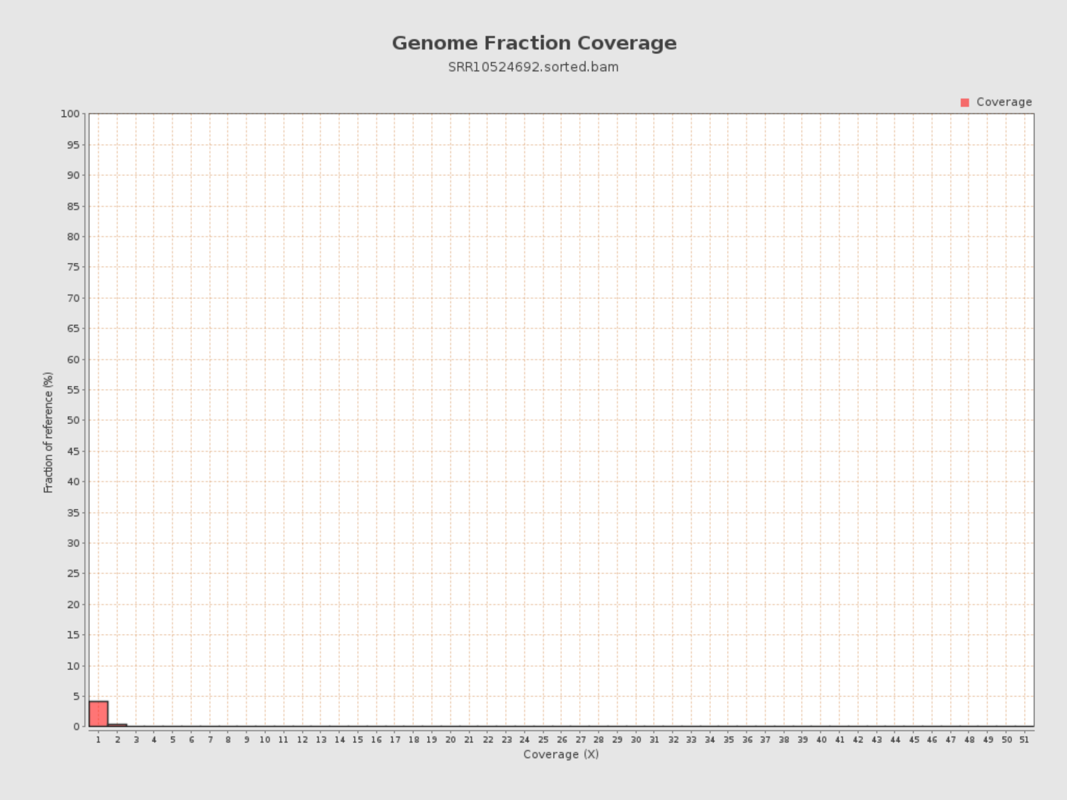
4. Results : Coverage Histogram



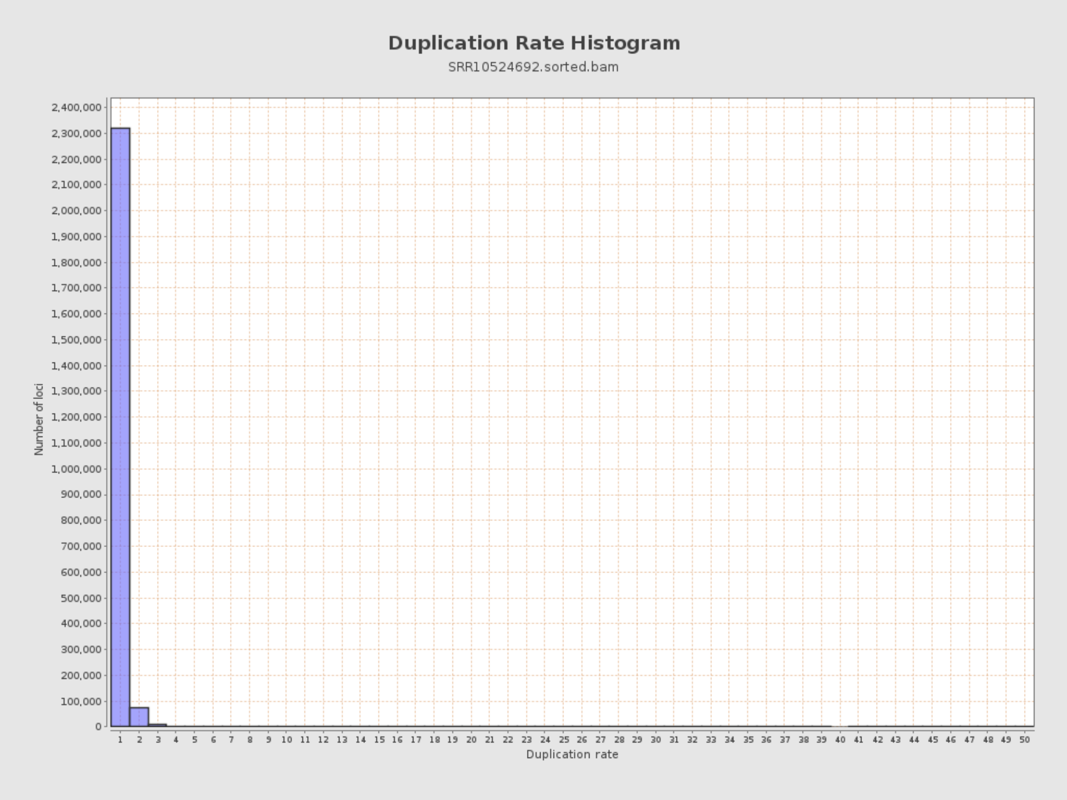
5. Results : Coverage Histogram (0-50X)



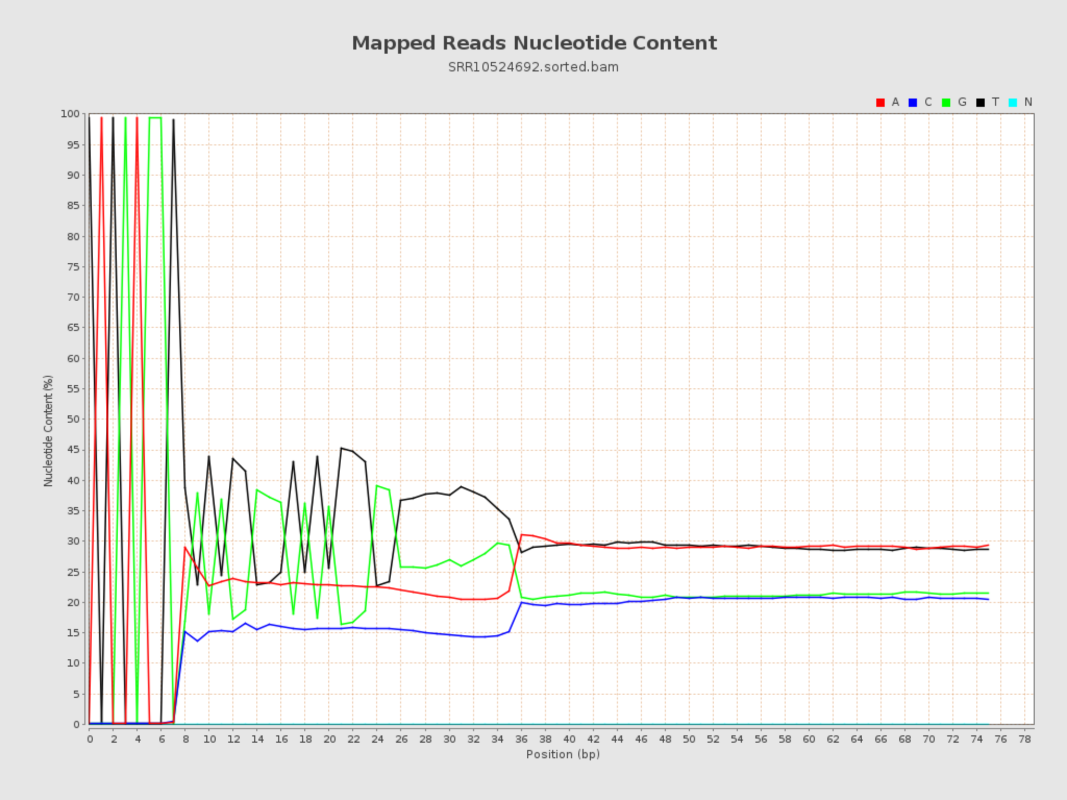
6. Results : Genome Fraction Coverage



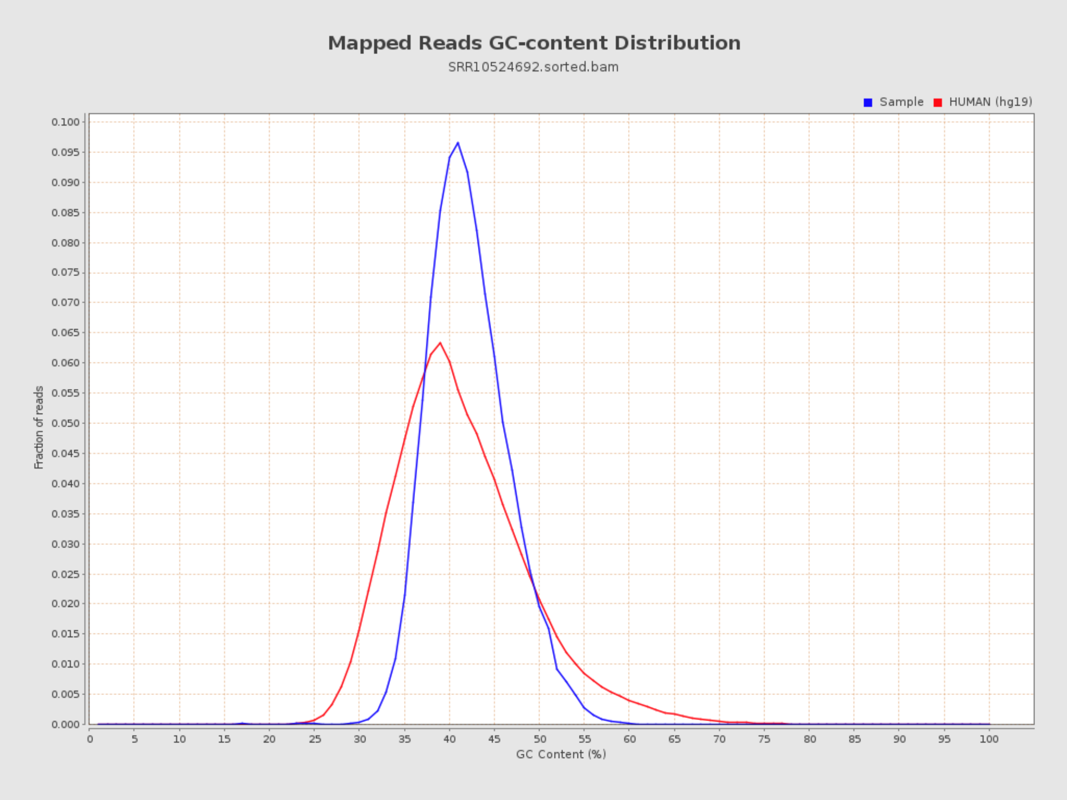
7. Results : Duplication Rate Histogram



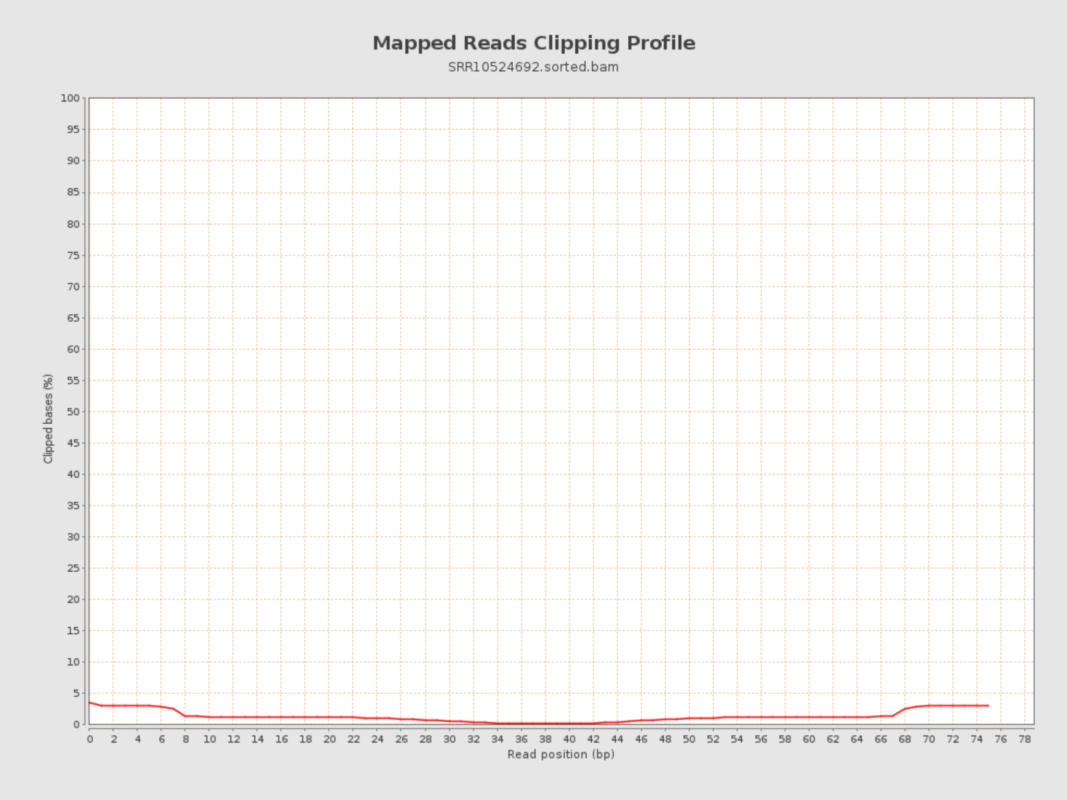
8. Results : Mapped Reads Nucleotide Content



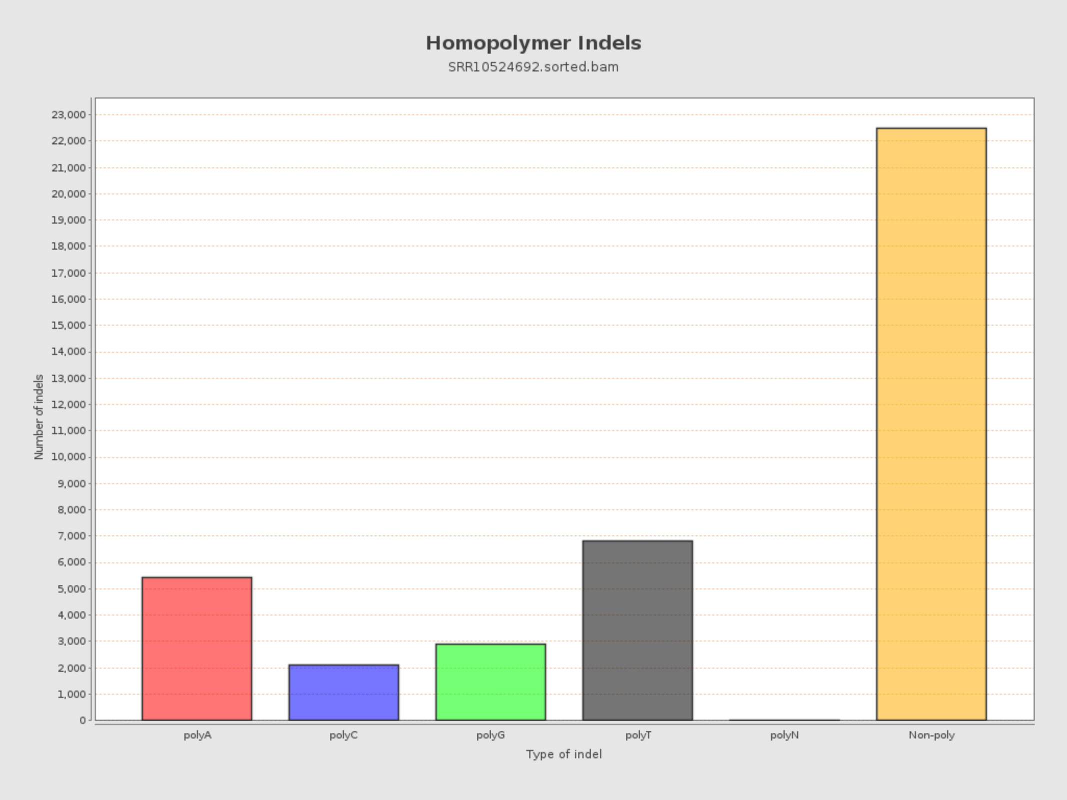
9. Results : Mapped Reads GC-content Distribution



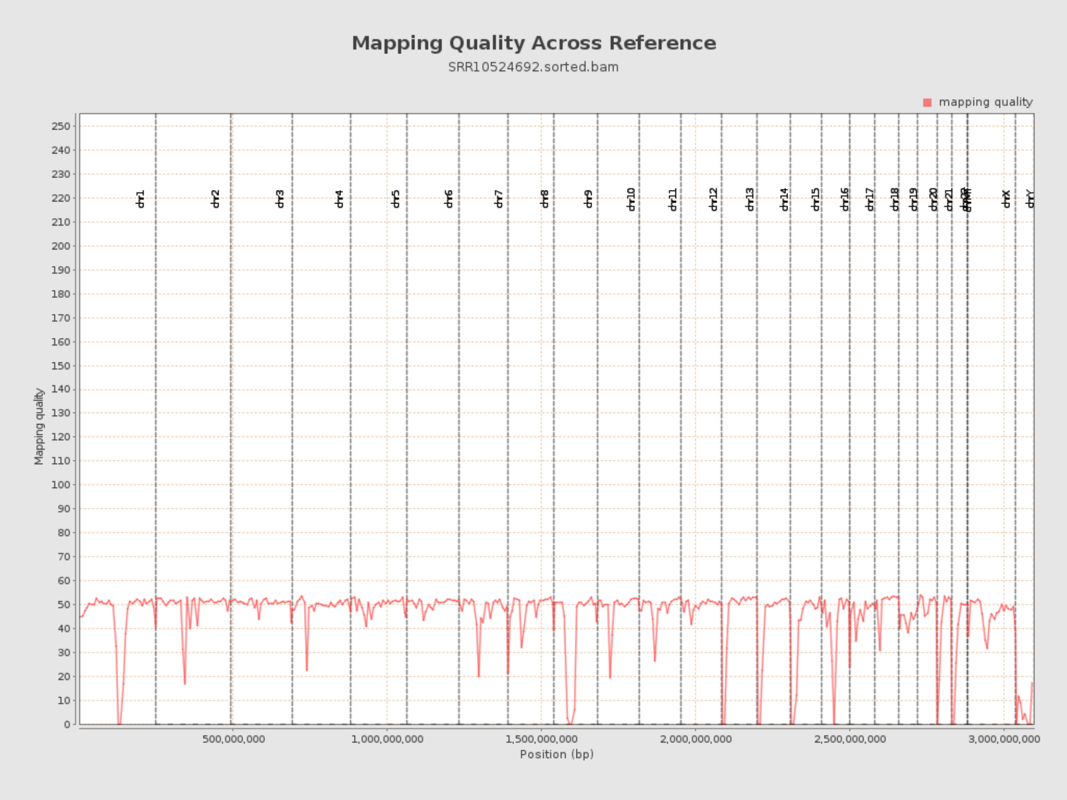
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram