Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:17:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524596.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_SRR10524596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524596.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:17:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,174,310
Mapped reads	1,092,019 / 92.99%
Unmapped reads	82,291 / 7.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,294 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	40,916 / 3.48%
Duplication rate	2.93%
Clipped reads	1,090,854 / 92.89%

2.2. ACGT Content

Number/percentage of A's	16,284,161 / 25.65%
Number/percentage of C's	11,625,026 / 18.31%
Number/percentage of T's	20,605,519 / 32.46%
Number/percentage of G's	14,973,149 / 23.58%
Number/percentage of N's	374 / 0%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0205

Standard Deviation	0.2018

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

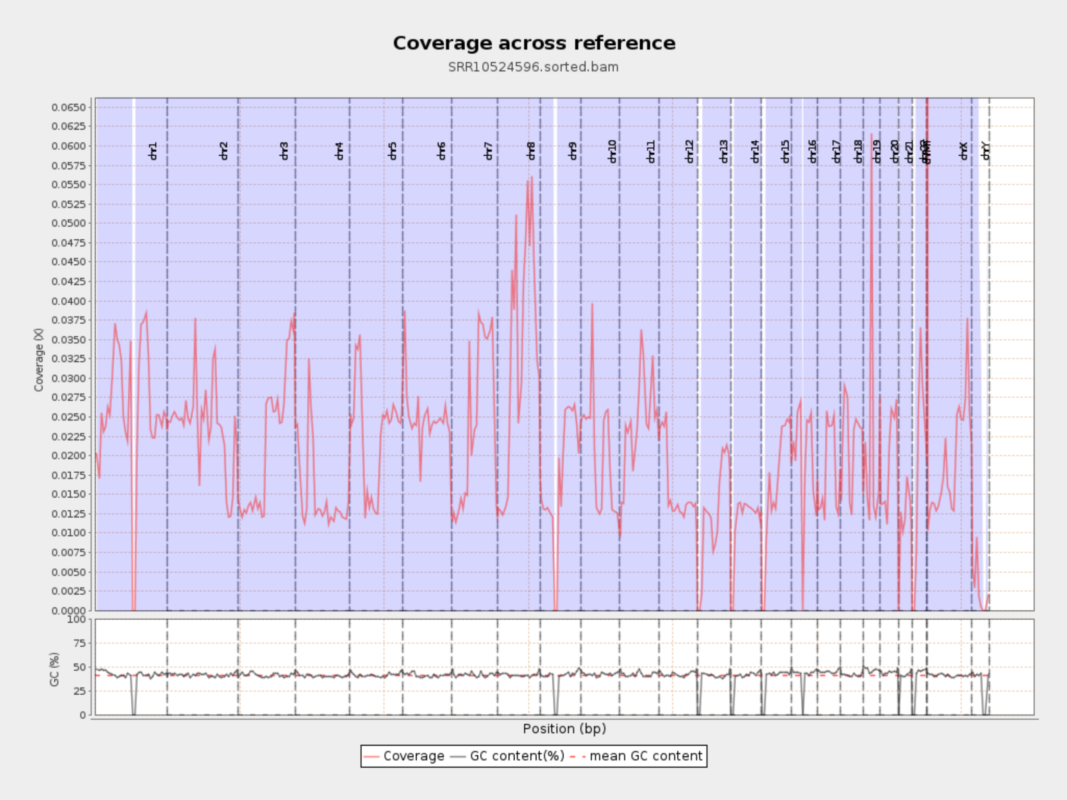
General error rate	0.49%
Mismatches	298,572
Insertions	4,745
Mapped reads with at least one insertion	0.43%
Deletions	11,882
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.45%

2.6. Chromosome stats

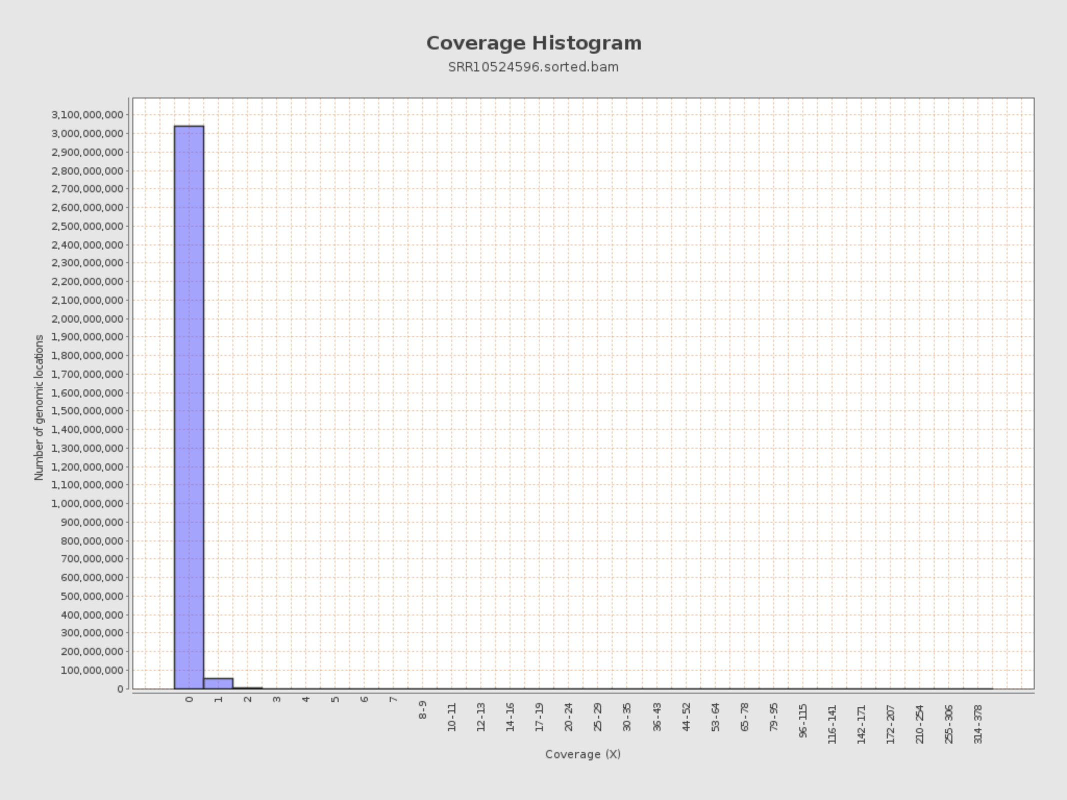
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6429384	0.0258	0.3282
chr2	243199373	5804597	0.0239	0.2328
chr3	198022430	4257432	0.0215	0.1597
chr4	191154276	2934694	0.0154	0.1533
chr5	180915260	4098322	0.0227	0.1634
chr6	171115067	4259365	0.0249	0.1799
chr7	159138663	3866097	0.0243	0.264

chr8	146364022	4910893	0.0336	0.2553
chr9	141213431	2418152	0.0171	0.1797
chr10	135534747	2791416	0.0206	0.2073
chr11	135006516	3281204	0.0243	0.2013
chr12	133851895	2112015	0.0158	0.1402
chr13	115169878	1416946	0.0123	0.1211
chr14	107349540	1215696	0.0113	0.12
chr15	102531392	1629312	0.0159	0.1405
chr16	90354753	1748645	0.0194	0.1584
chr17	81195210	1442846	0.0178	0.1491
chr18	78077248	1712645	0.0219	0.2805
chr19	59128983	1266265	0.0214	0.2392
chr20	63025520	1208345	0.0192	0.1524
chr21	48129895	566555	0.0118	0.1303
chr22	51304566	979310	0.0191	0.1491
chrMT	16571	15816	0.9544	1.1779
chrX	155270560	2984469	0.0192	0.1635
chrY	59373566	157939	0.0027	0.0827

3. Results : Coverage across reference



4. Results : Coverage Histogram



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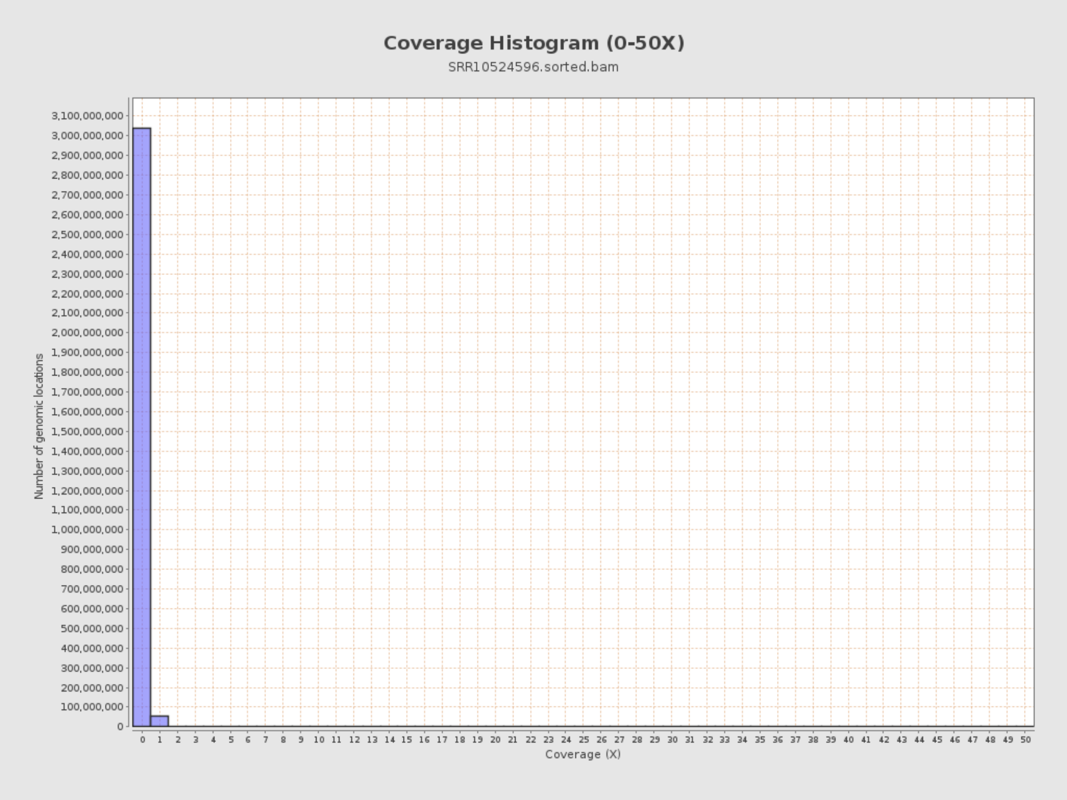
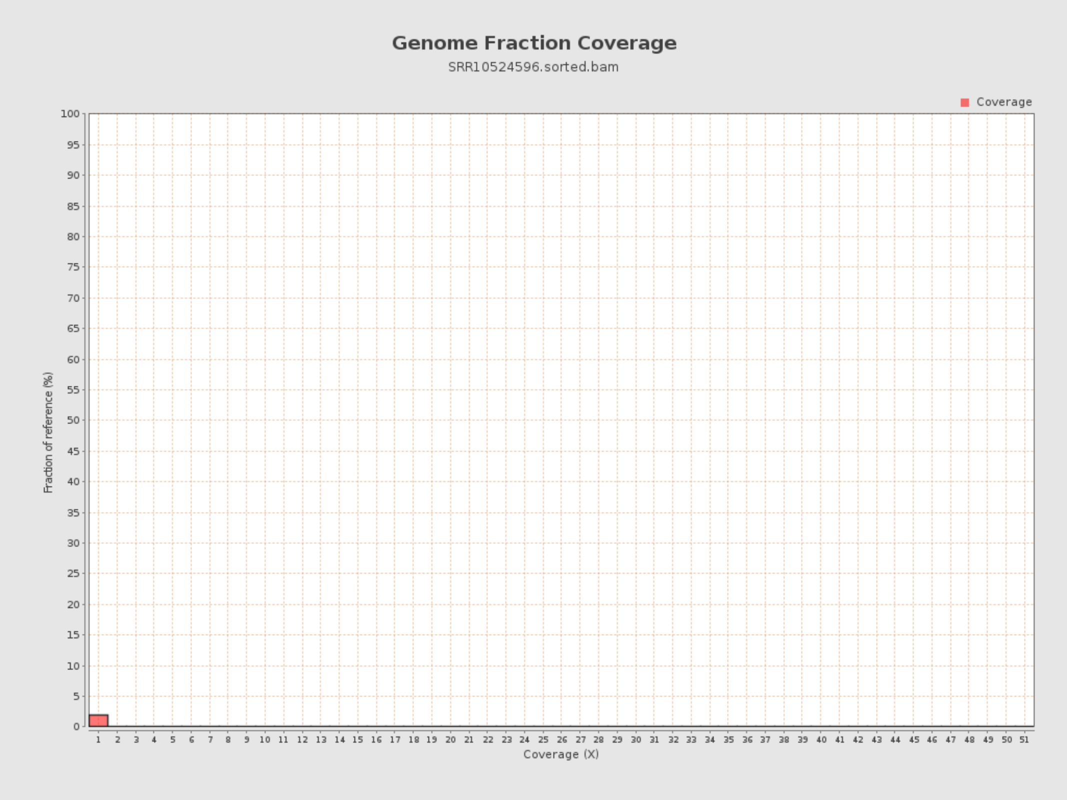
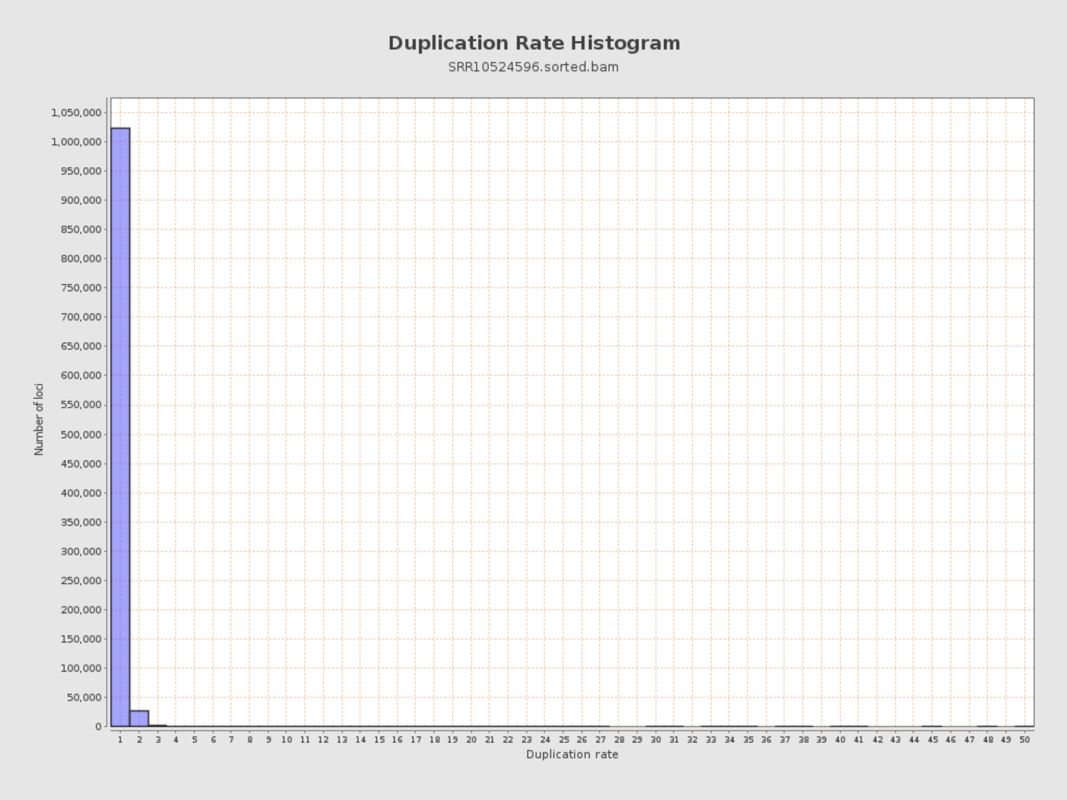
5. Results : Coverage Histogram (0-50X)



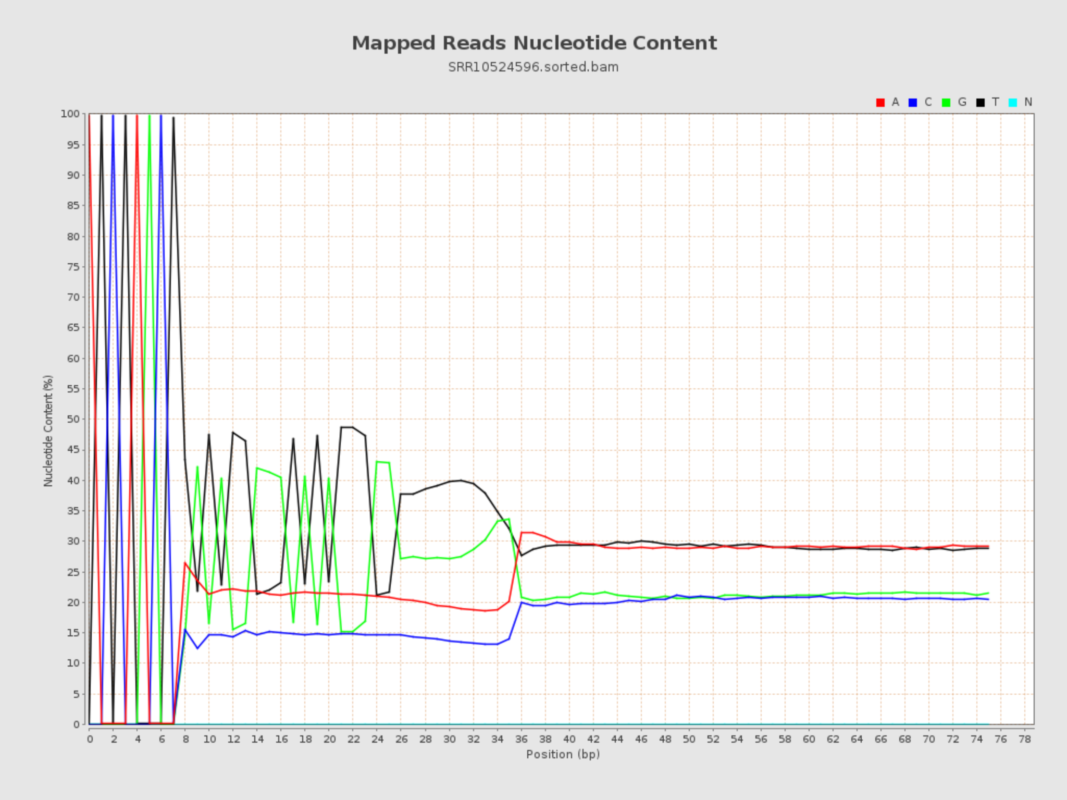
6. Results : Genome Fraction Coverage



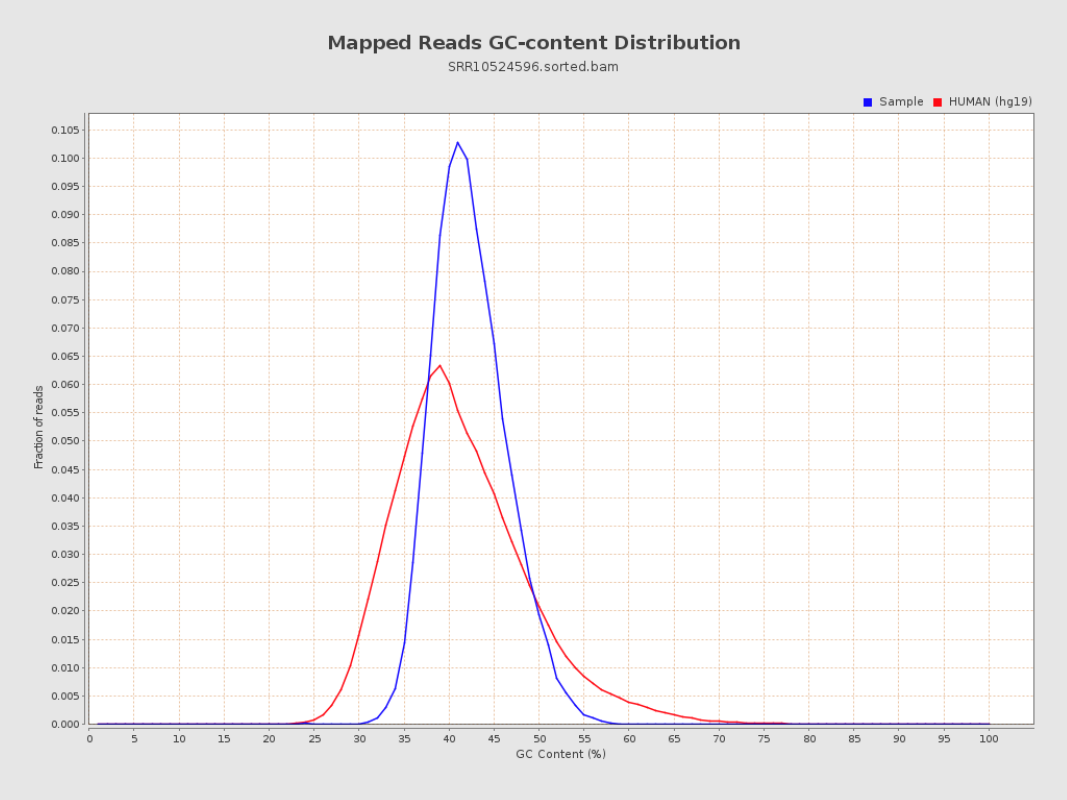
7. Results : Duplication Rate Histogram



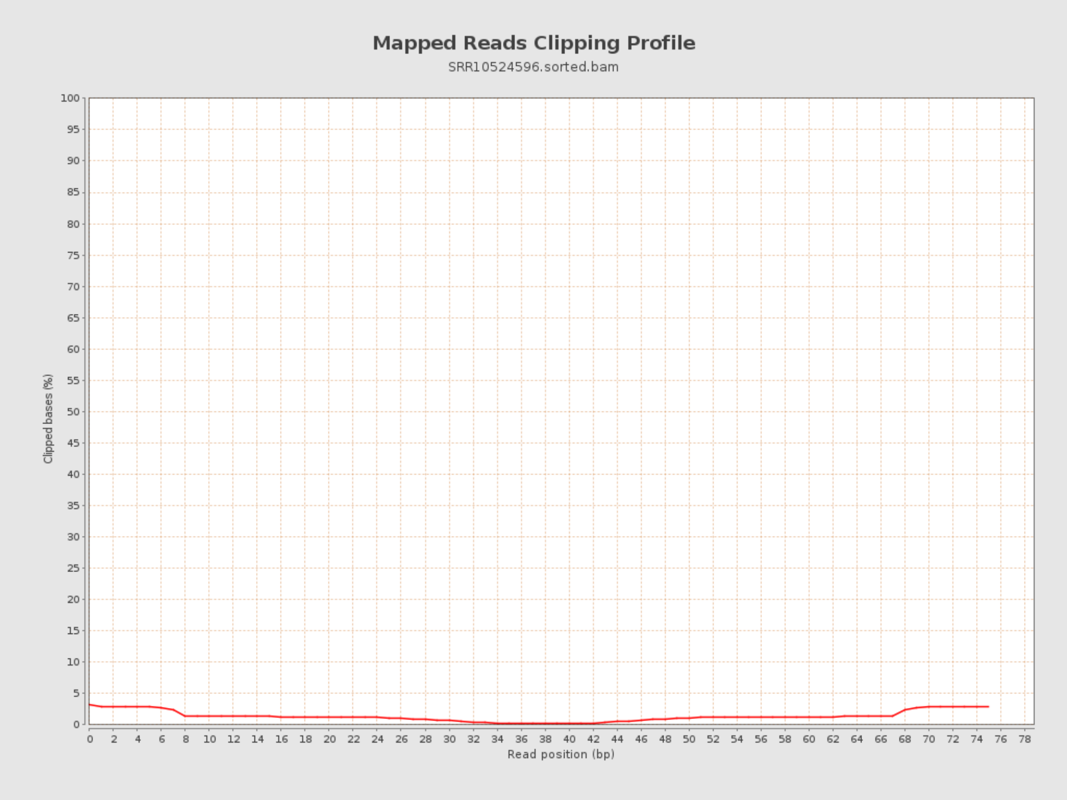
8. Results : Mapped Reads Nucleotide Content



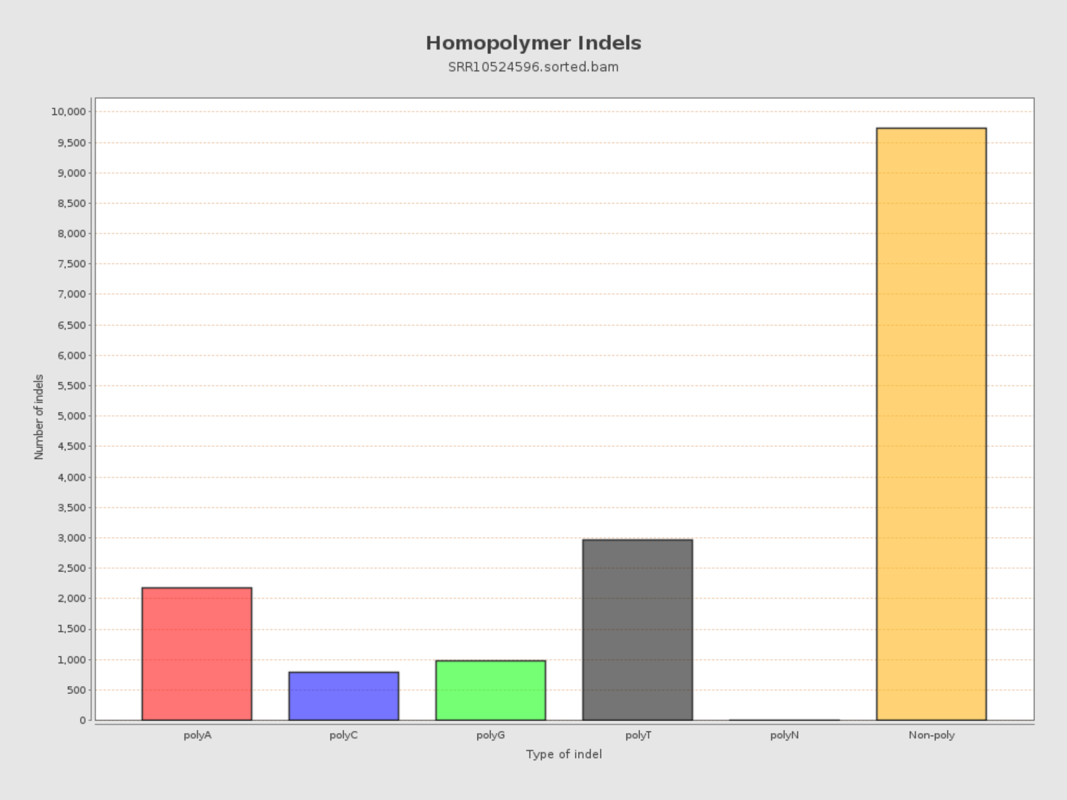
9. Results : Mapped Reads GC-content Distribution



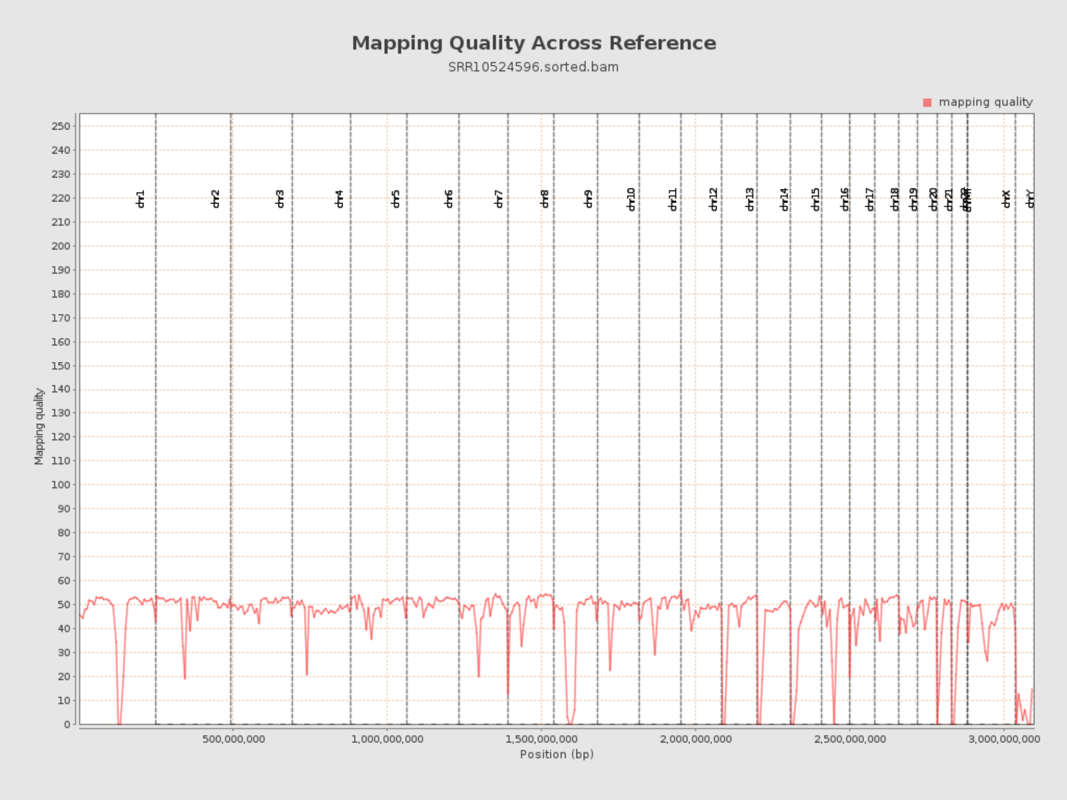
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram