Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:56:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524796.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_SRR10524796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524796.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:56:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,319,069
Mapped reads	1,195,032 / 90.6%
Unmapped reads	124,037 / 9.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,028 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	42,789 / 3.24%
Duplication rate	2.74%
Clipped reads	1,195,971 / 90.67%

2.2. ACGT Content

Number/percentage of A's	16,633,654 / 24.65%
Number/percentage of C's	11,086,470 / 16.43%
Number/percentage of T's	22,118,382 / 32.78%
Number/percentage of G's	17,637,308 / 26.14%
Number/percentage of N's	8,045 / 0.01%
GC Percentage	42.56%

2.3. Coverage

Mean	0.0218

Standard Deviation	0.2077

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

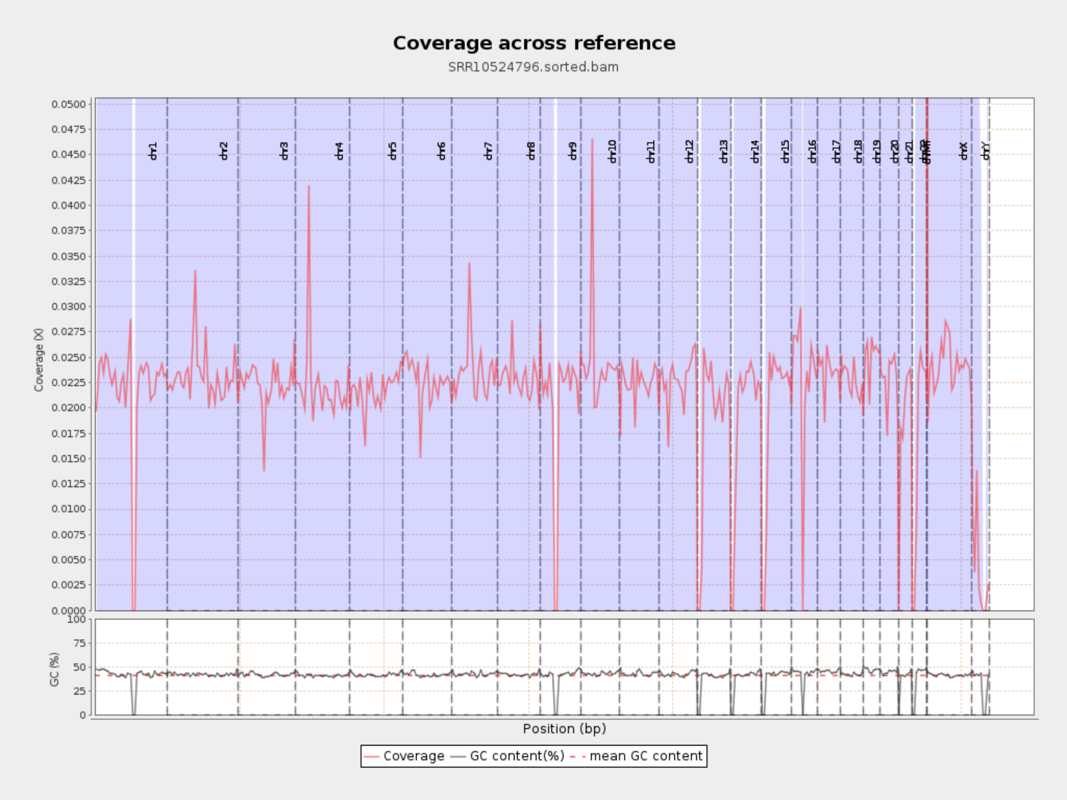
General error rate	0.53%
Mismatches	344,412
Insertions	4,885
Mapped reads with at least one insertion	0.41%
Deletions	13,317
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.33%

2.6. Chromosome stats

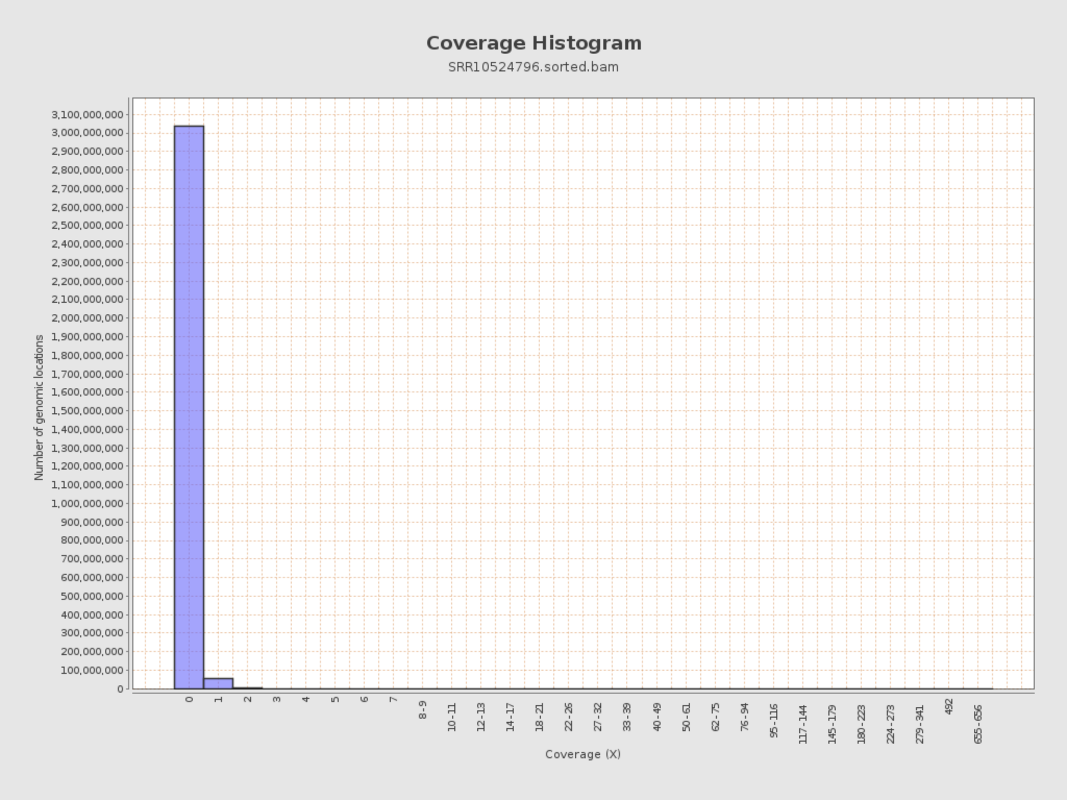
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5393353	0.0216	0.2709
chr2	243199373	5650573	0.0232	0.3251
chr3	198022430	4400602	0.0222	0.1644
chr4	191154276	4277463	0.0224	0.1865
chr5	180915260	3959882	0.0219	0.1603
chr6	171115067	3877817	0.0227	0.178
chr7	159138663	3784564	0.0238	0.2463

chr8	146364022	3340742	0.0228	0.1945
chr9	141213431	2861447	0.0203	0.1803
chr10	135534747	3327140	0.0245	0.2453
chr11	135006516	3057273	0.0226	0.1885
chr12	133851895	3056748	0.0228	0.1656
chr13	115169878	2114395	0.0184	0.1471
chr14	107349540	2024140	0.0189	0.1532
chr15	102531392	1960648	0.0191	0.1519
chr16	90354753	2046312	0.0226	0.1783
chr17	81195210	1921520	0.0237	0.1727
chr18	78077248	1774238	0.0227	0.2643
chr19	59128983	1477281	0.025	0.2274
chr20	63025520	1437134	0.0228	0.1723
chr21	48129895	906337	0.0188	0.1599
chr22	51304566	851559	0.0166	0.1418
chrMT	16571	13302	0.8027	1.0457
chrX	155270560	3760783	0.0242	0.1797
chrY	59373566	230072	0.0039	0.1122

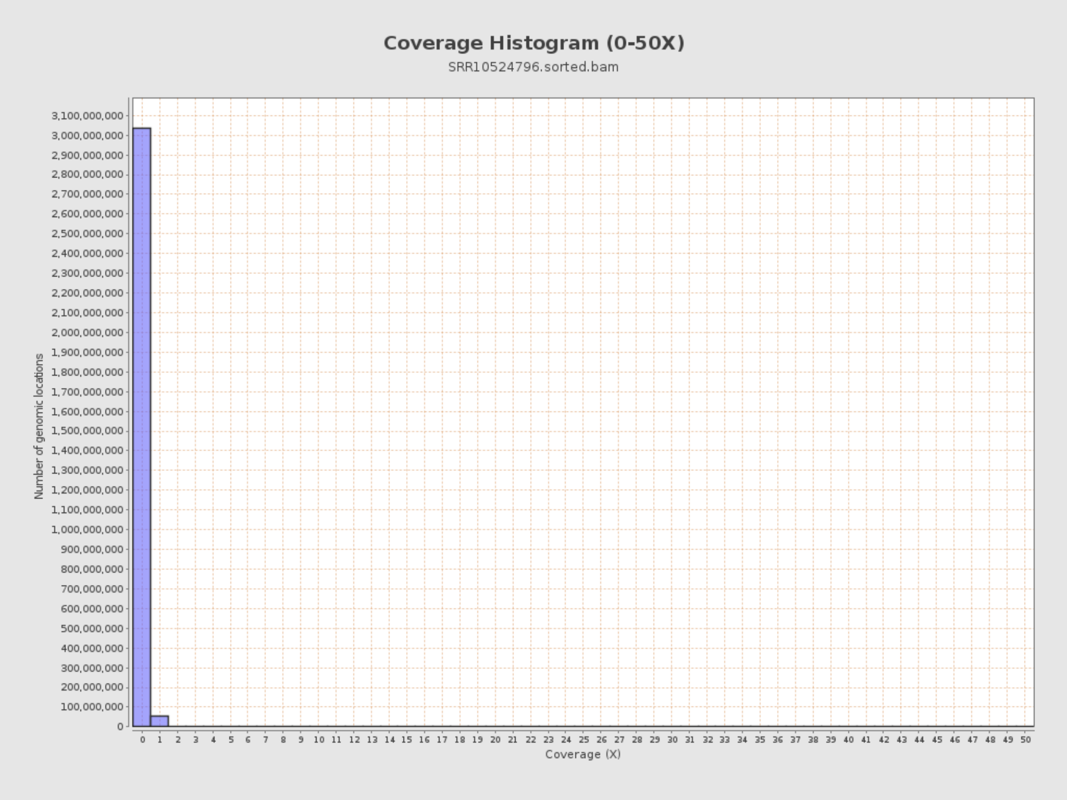
3. Results : Coverage across reference



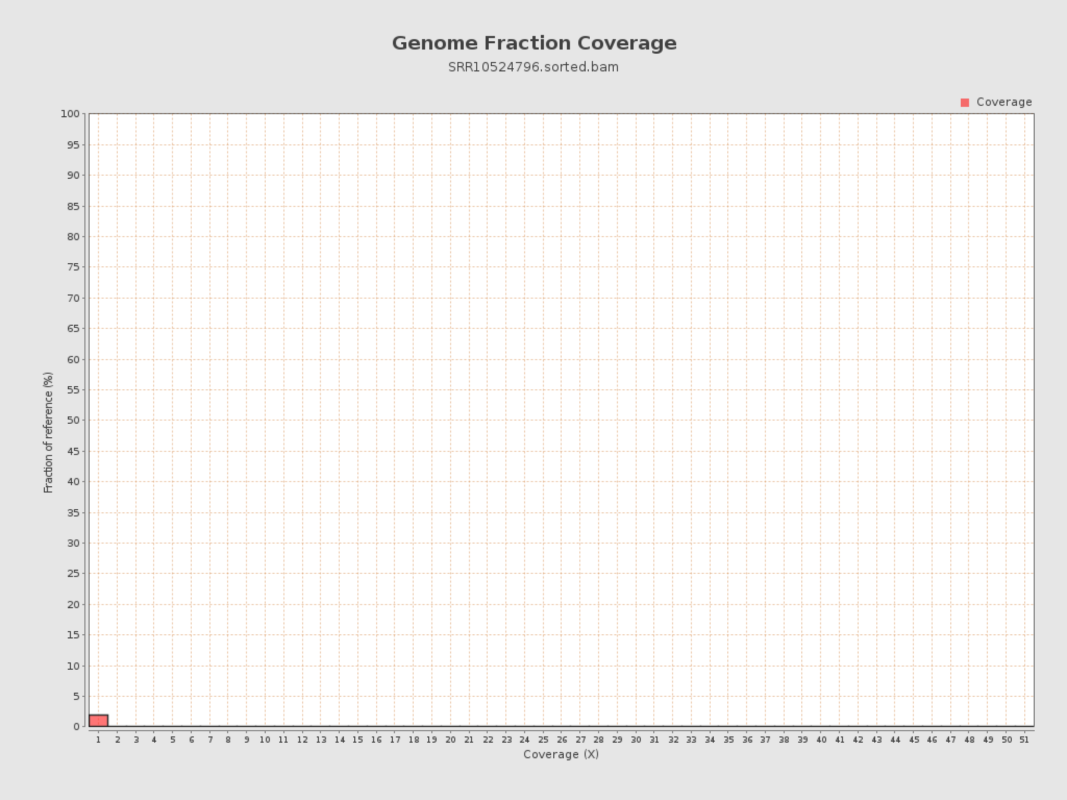
4. Results : Coverage Histogram



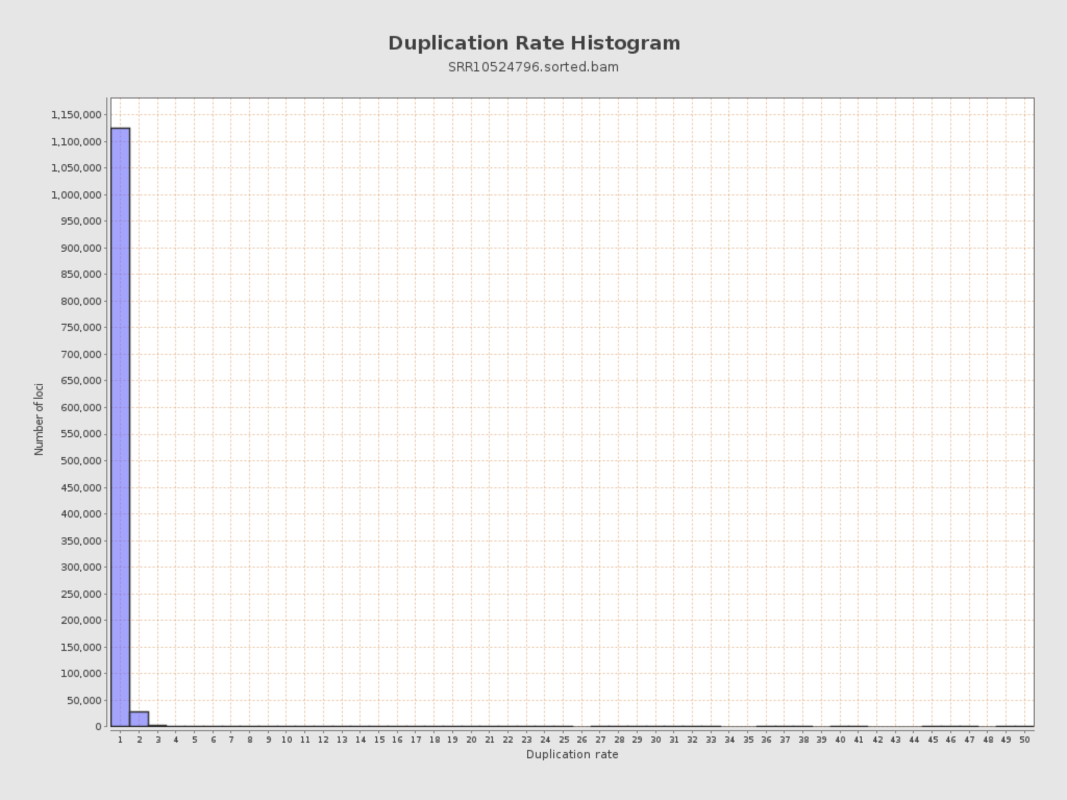
5. Results : Coverage Histogram (0-50X)



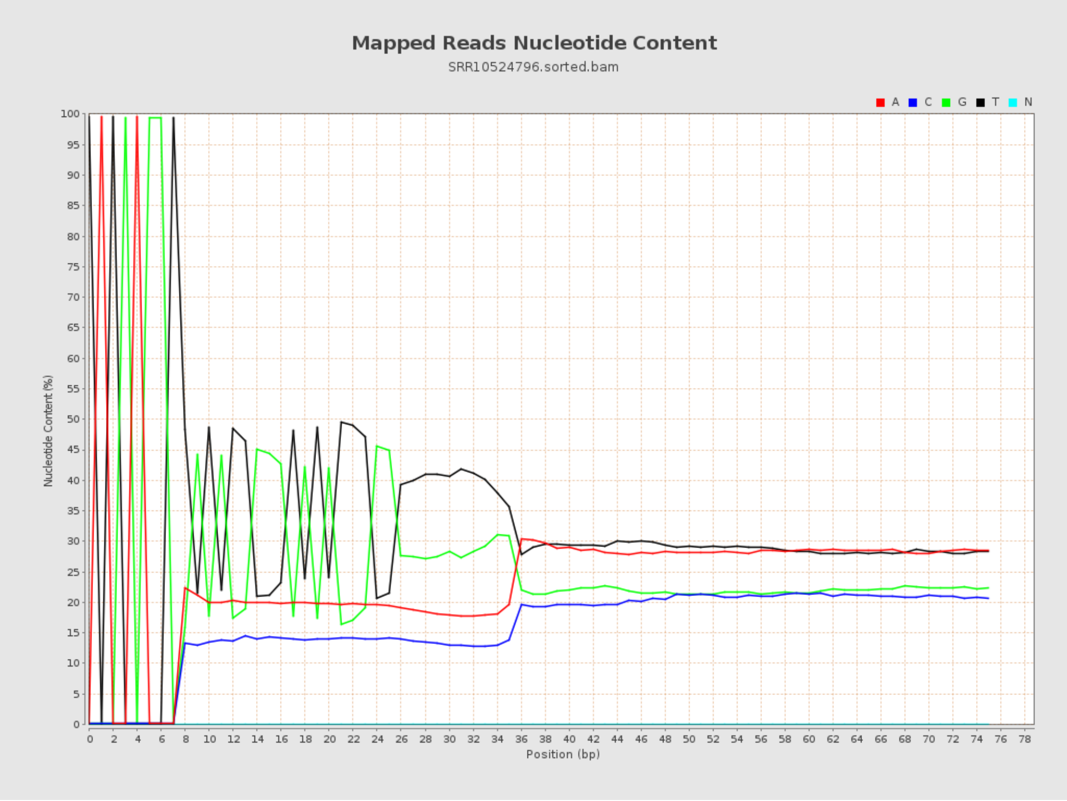
6. Results : Genome Fraction Coverage



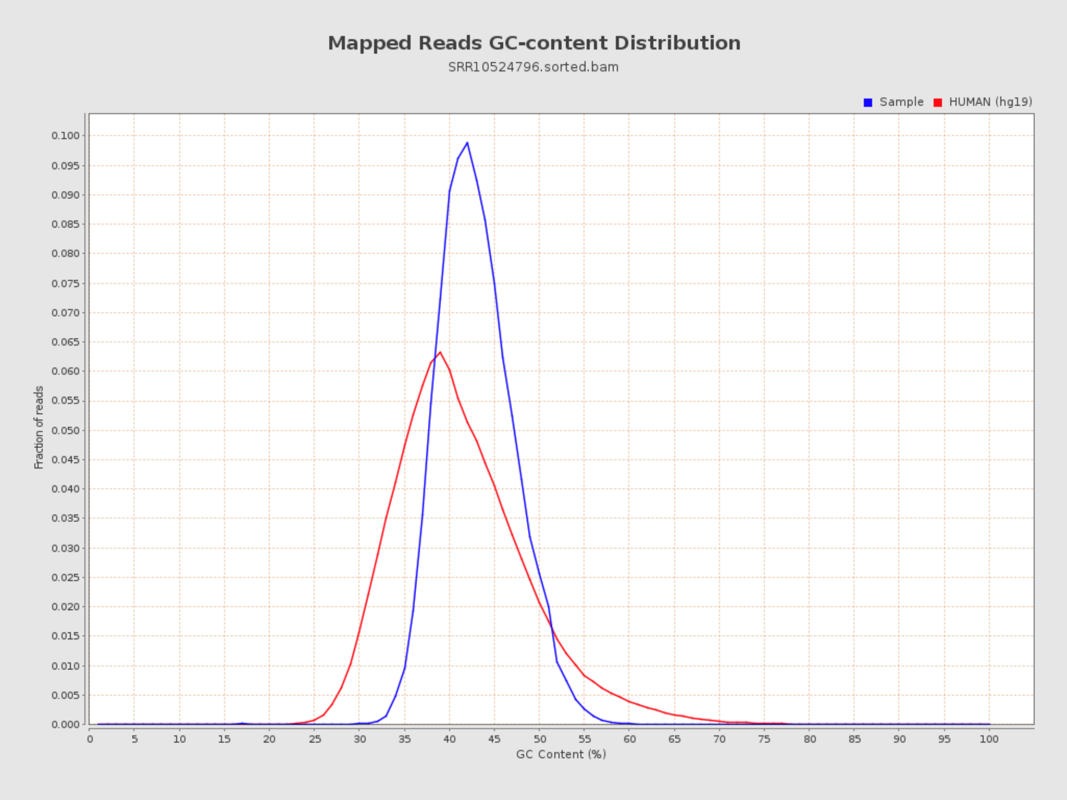
7. Results : Duplication Rate Histogram



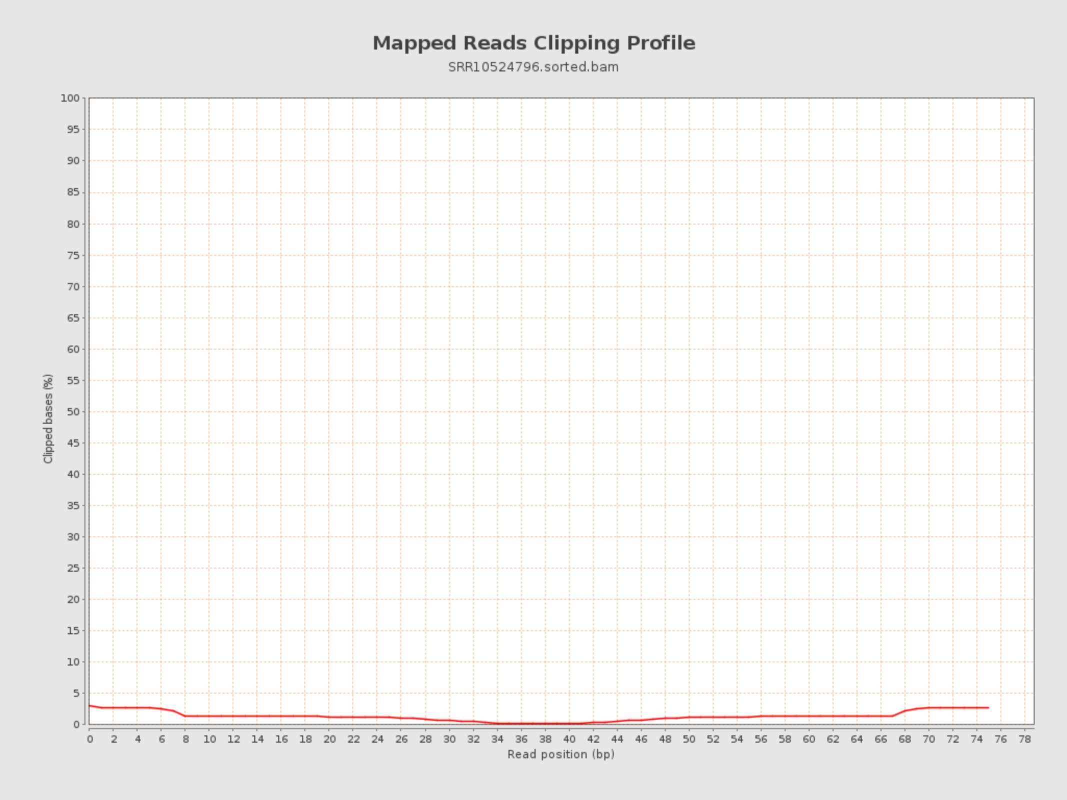
8. Results : Mapped Reads Nucleotide Content



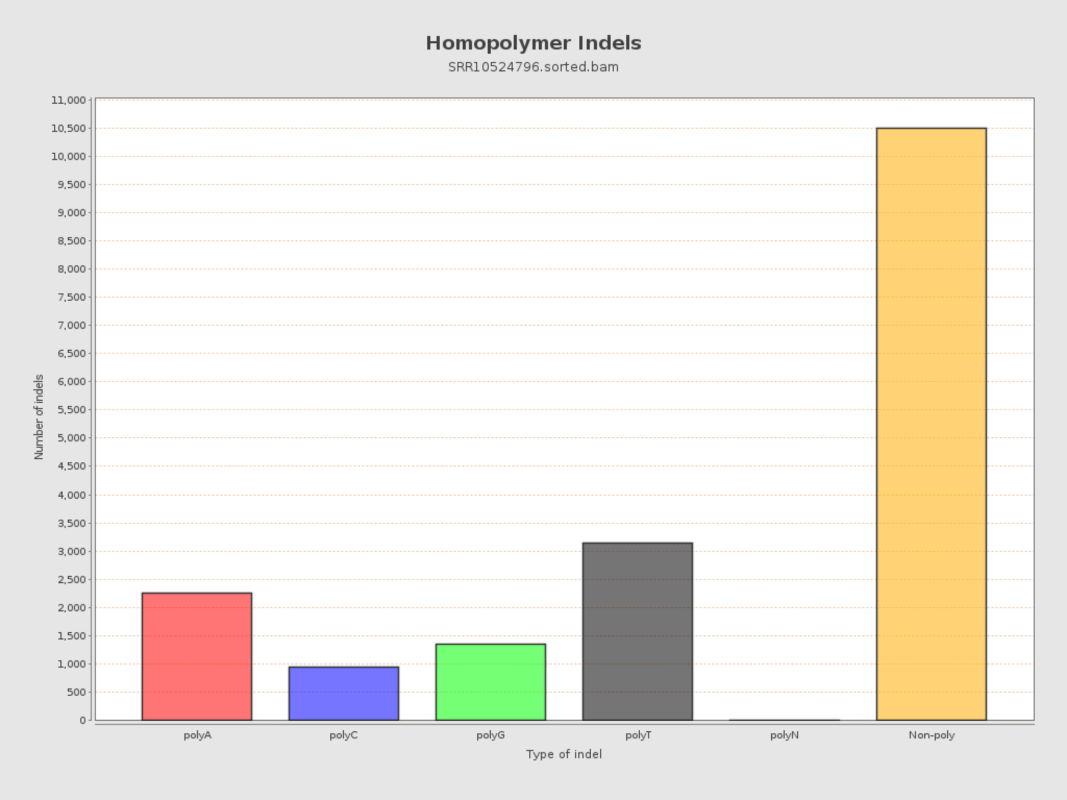
9. Results : Mapped Reads GC-content Distribution



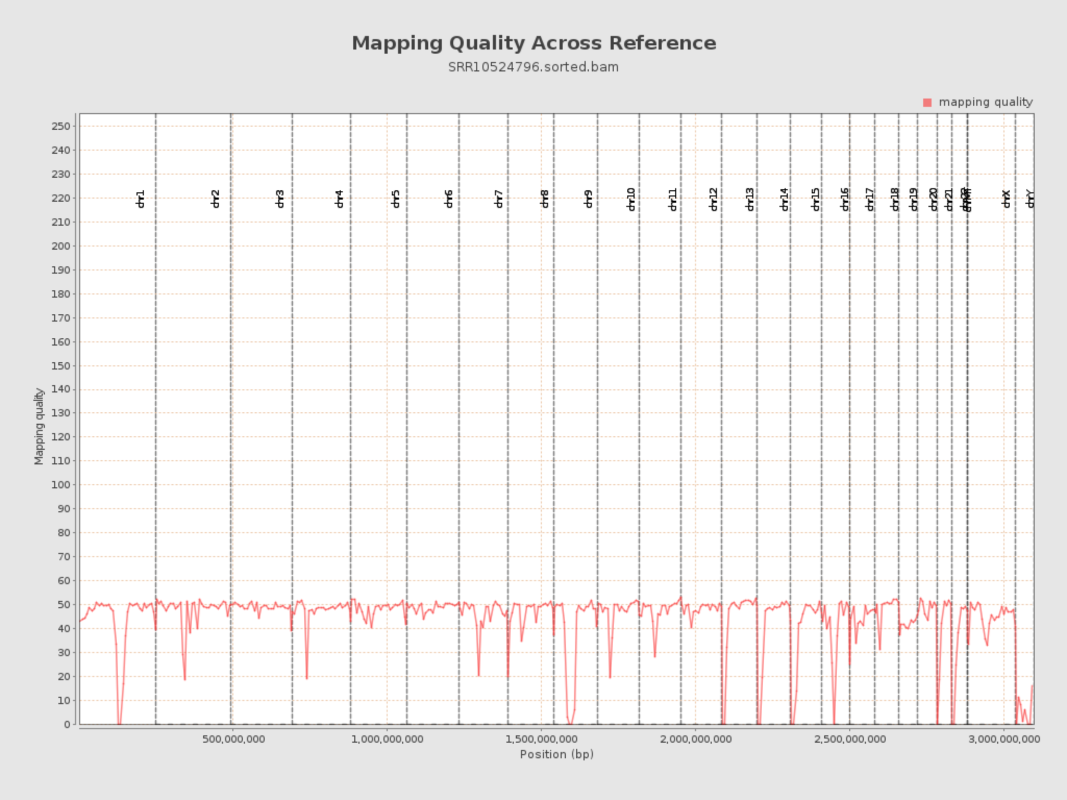
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram