Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:19:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524995.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_SRR10524995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524995.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:19:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524995.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,405,635
Mapped reads	1,282,640 / 91.25%
Unmapped reads	122,995 / 8.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,525 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	38,650 / 2.75%
Duplication rate	2.18%
Clipped reads	1,282,484 / 91.24%

2.2. ACGT Content

Number/percentage of A's	18,317,292 / 24.62%
Number/percentage of C's	13,843,854 / 18.61%
Number/percentage of T's	24,001,415 / 32.26%
Number/percentage of G's	18,245,318 / 24.52%
Number/percentage of N's	829 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2315

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

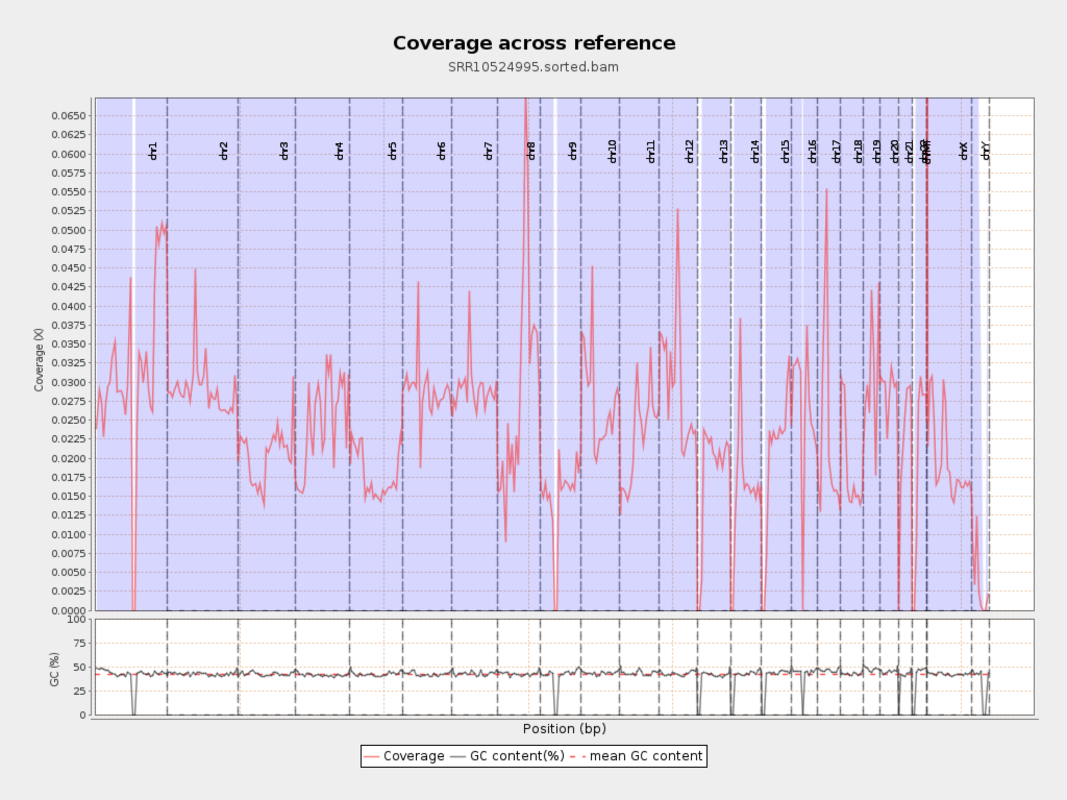
General error rate	0.5%
Mismatches	364,635
Insertions	5,565
Mapped reads with at least one insertion	0.43%
Deletions	14,629
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.07%

2.6. Chromosome stats

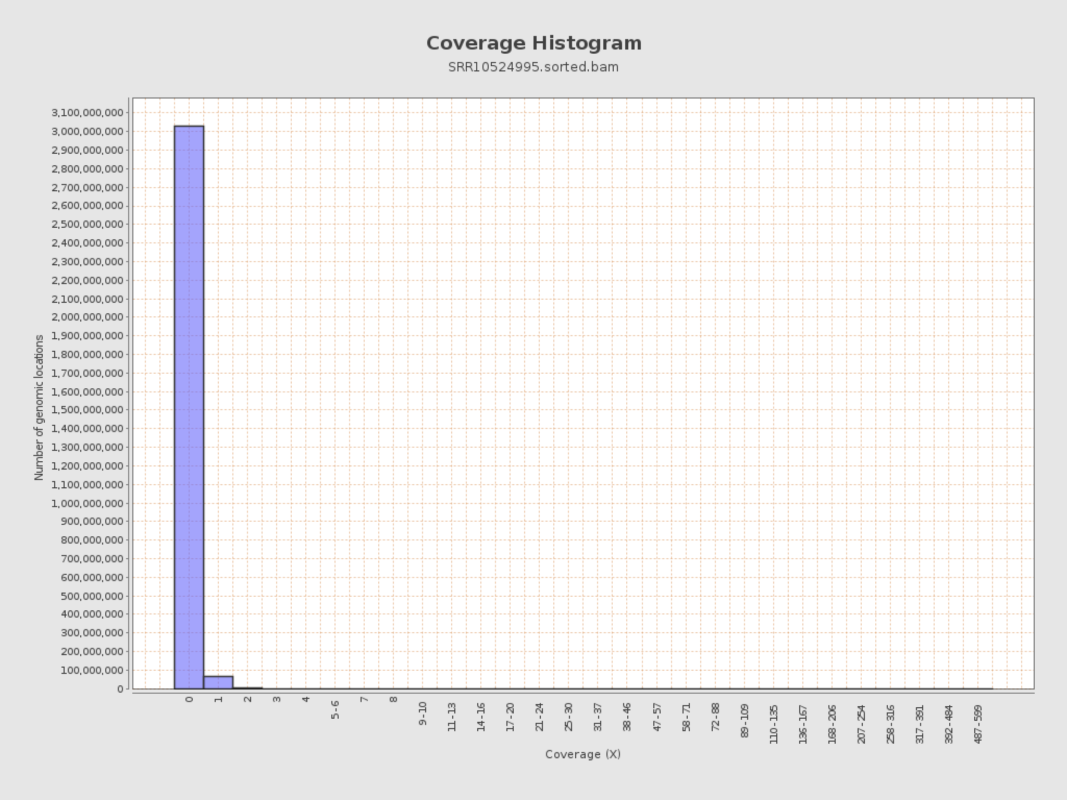
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7816677	0.0314	0.4404
chr2	243199373	7076496	0.0291	0.2639
chr3	198022430	4073139	0.0206	0.1533
chr4	191154276	4755618	0.0249	0.1803
chr5	180915260	3243880	0.0179	0.1461
chr6	171115067	4950651	0.0289	0.2416
chr7	159138663	4653811	0.0292	0.2818

chr8	146364022	4354786	0.0298	0.2358
chr9	141213431	2079532	0.0147	0.1735
chr10	135534747	3755953	0.0277	0.2244
chr11	135006516	3104395	0.023	0.2068
chr12	133851895	3990950	0.0298	0.1846
chr13	115169878	2045535	0.0178	0.1436
chr14	107349540	1700876	0.0158	0.1378
chr15	102531392	2061973	0.0201	0.1567
chr16	90354753	2370401	0.0262	0.1786
chr17	81195210	1916592	0.0236	0.21
chr18	78077248	1453499	0.0186	0.279
chr19	59128983	1825378	0.0309	0.2785
chr20	63025520	1809662	0.0287	0.1814
chr21	48129895	1076106	0.0224	0.1698
chr22	51304566	1007100	0.0196	0.1486
chrMT	16571	4269	0.2576	0.5807
chrX	155270560	3097137	0.0199	0.1687
chrY	59373566	208717	0.0035	0.0965

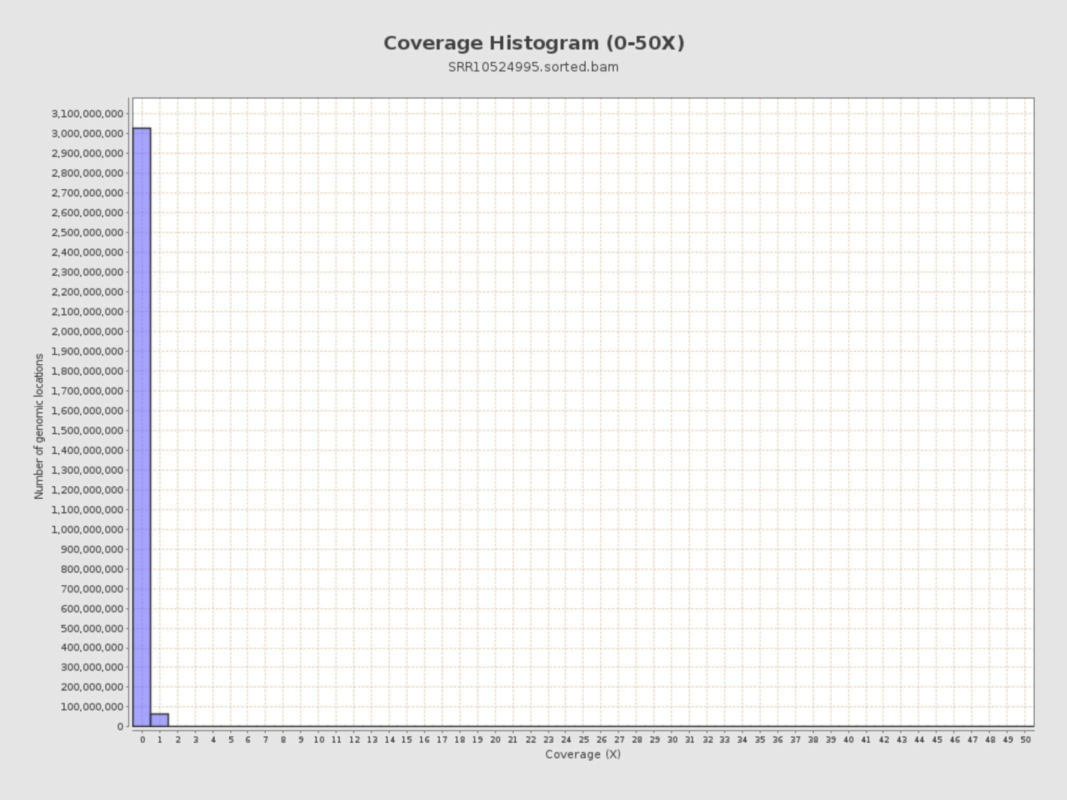
3. Results : Coverage across reference



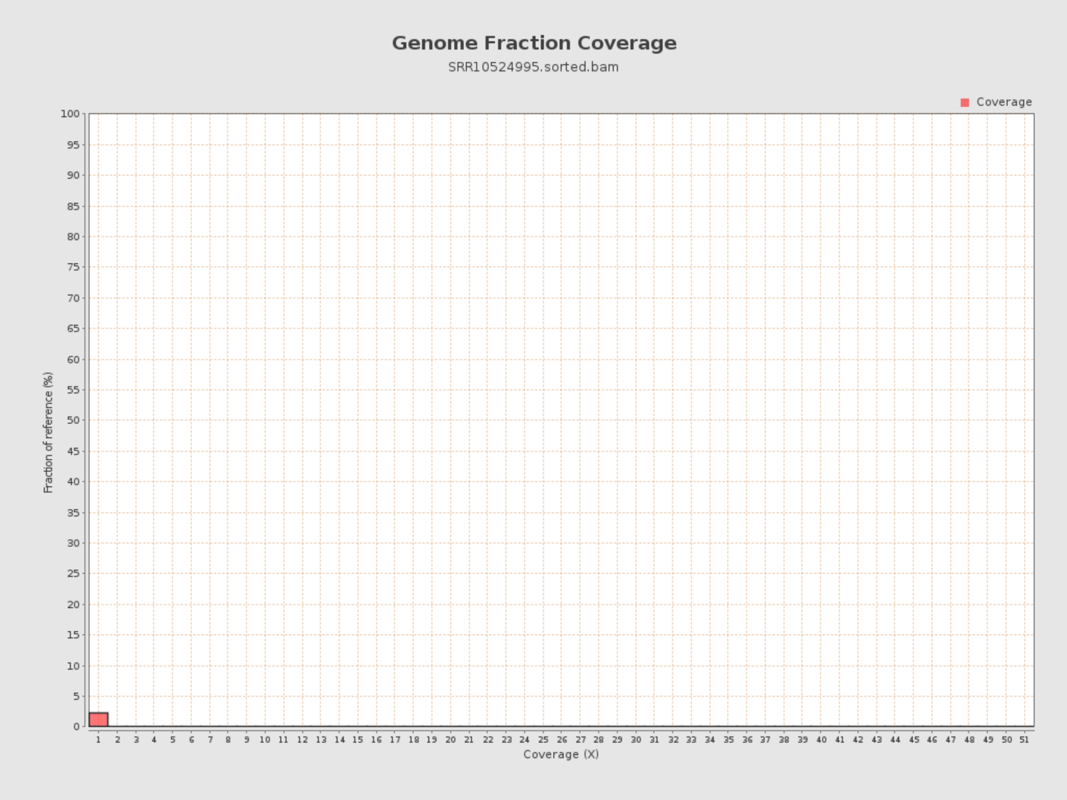
4. Results : Coverage Histogram



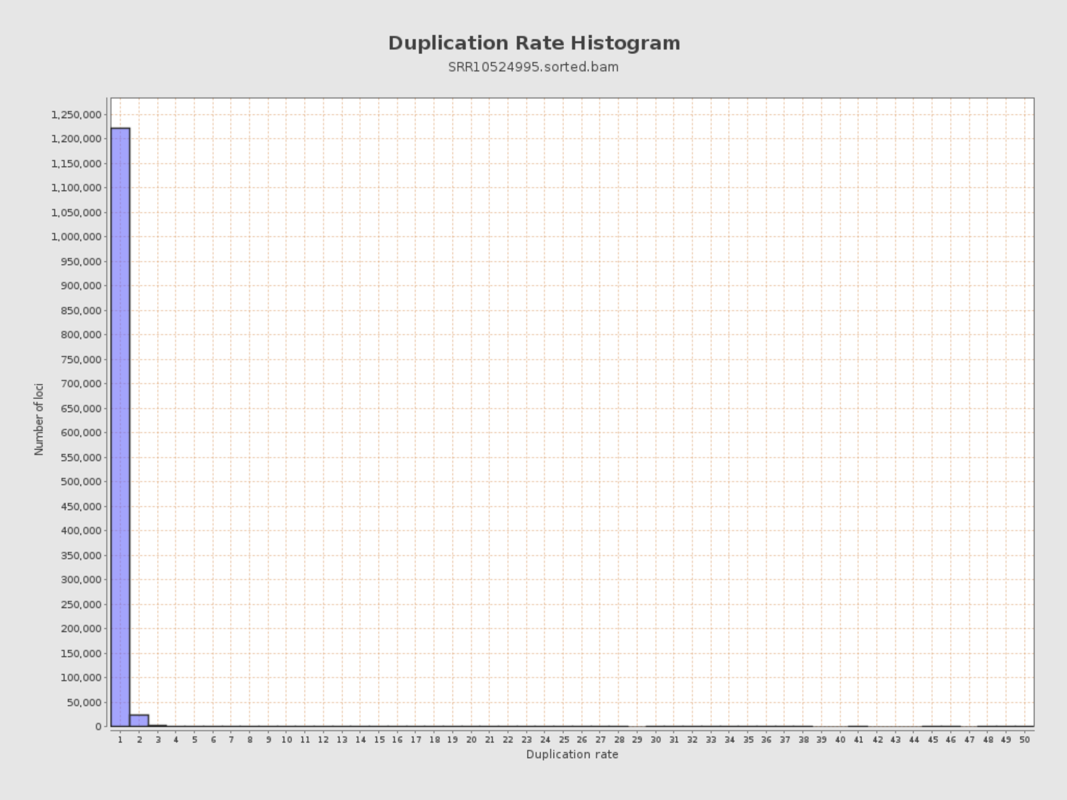
5. Results : Coverage Histogram (0-50X)



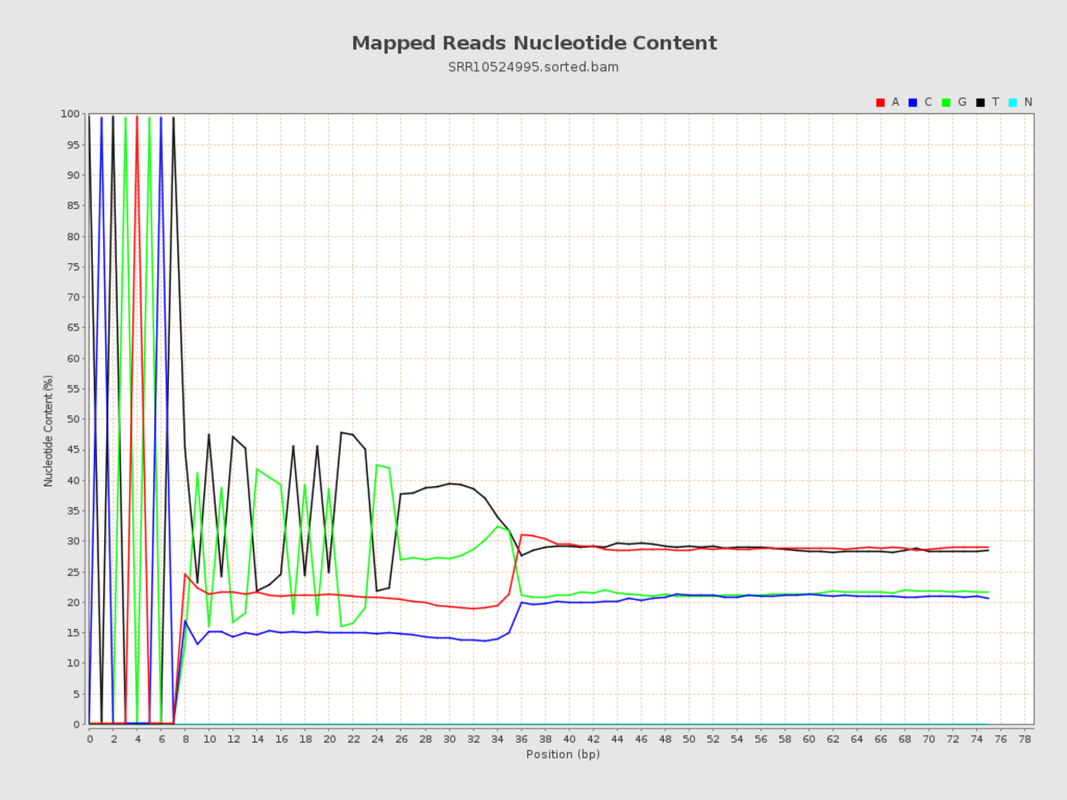
6. Results : Genome Fraction Coverage



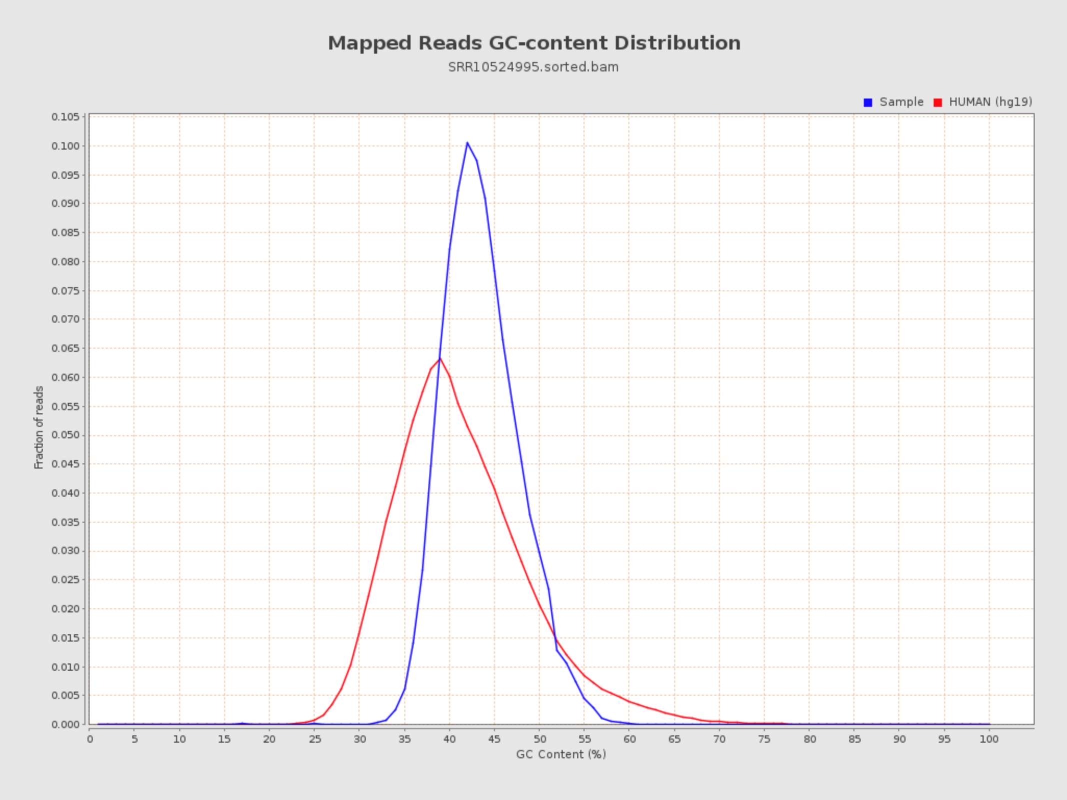
7. Results : Duplication Rate Histogram



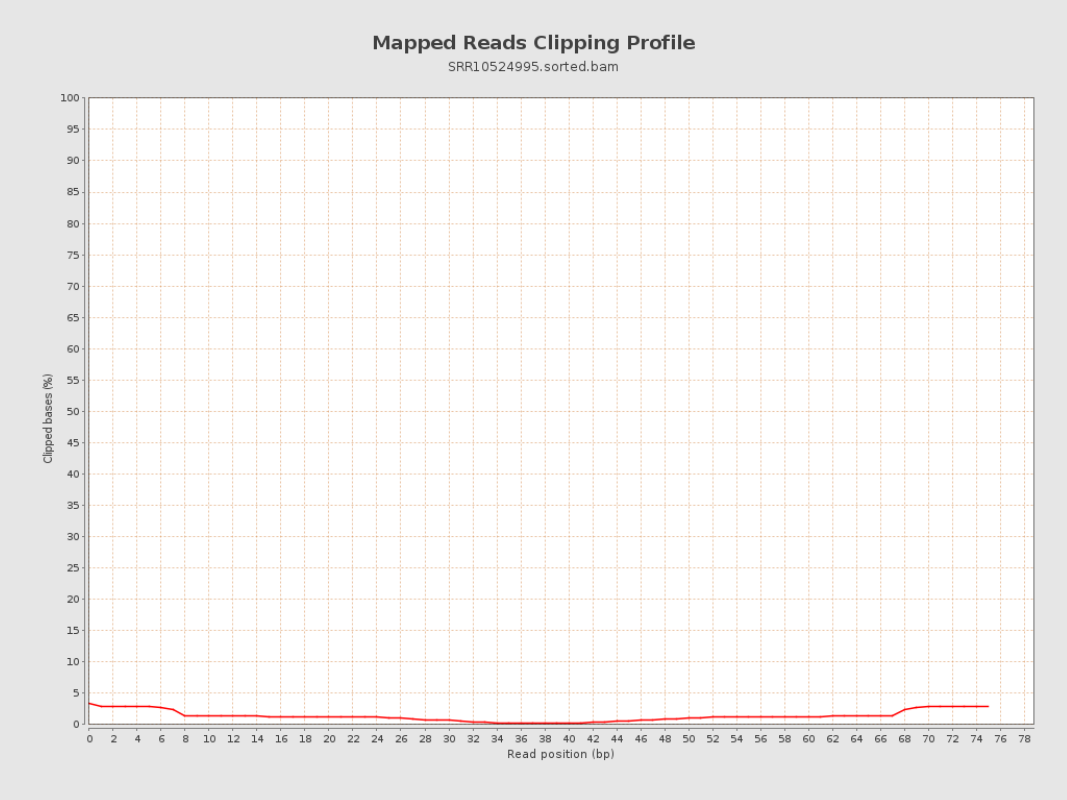
8. Results : Mapped Reads Nucleotide Content



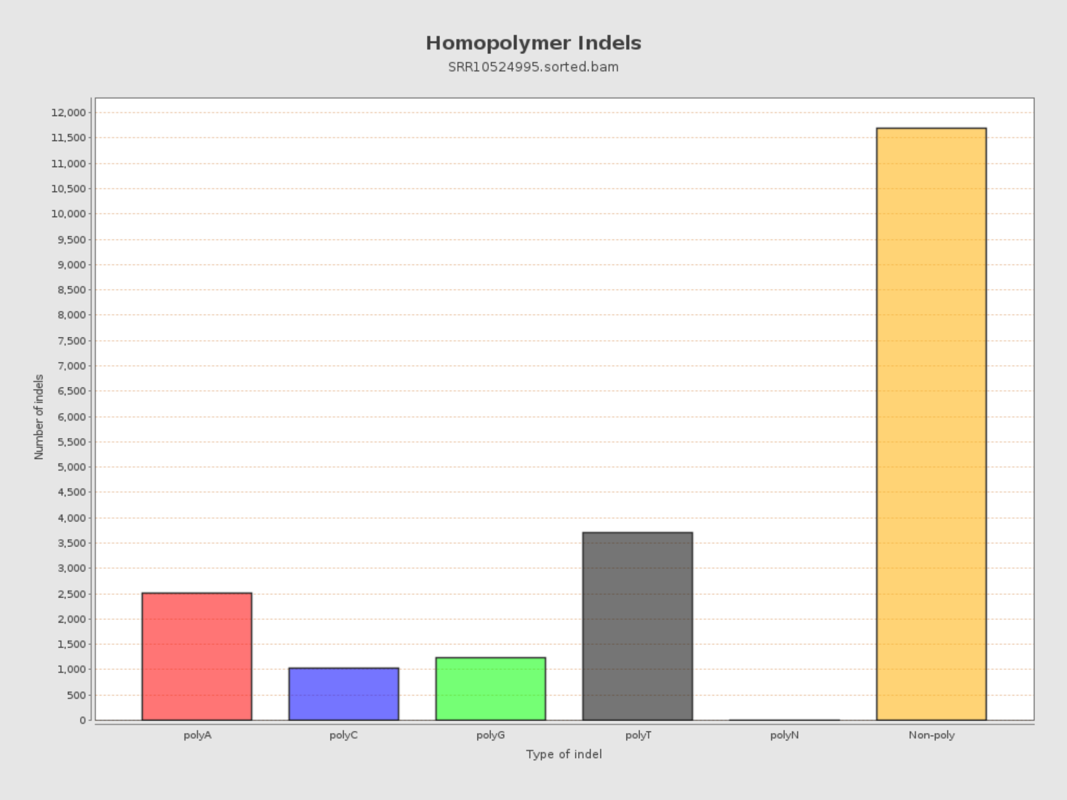
9. Results : Mapped Reads GC-content Distribution



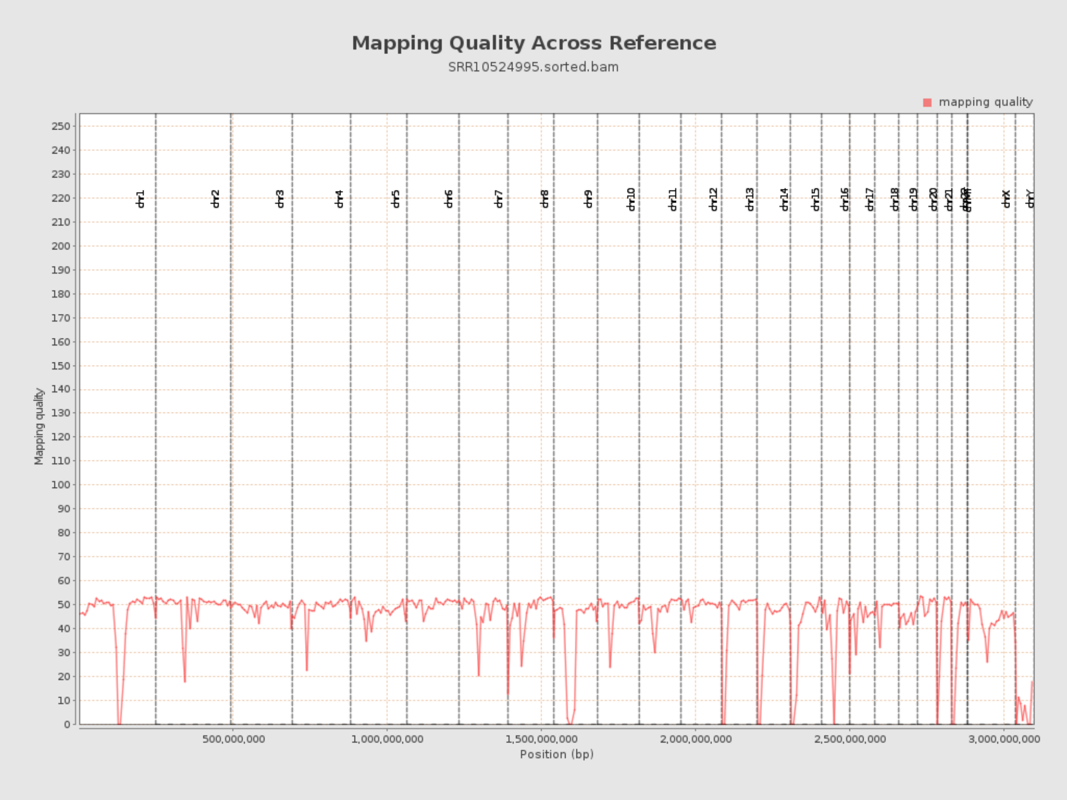
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram