Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:54:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524795.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_SRR10524795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:54:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,069,258
Mapped reads	977,866 / 91.45%
Unmapped reads	91,392 / 8.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,587 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	29,928 / 2.8%
Duplication rate	2.33%
Clipped reads	980,438 / 91.69%

2.2. ACGT Content

Number/percentage of A's	13,088,246 / 23.34%
Number/percentage of C's	9,880,210 / 17.62%
Number/percentage of T's	18,623,592 / 33.21%
Number/percentage of G's	14,475,262 / 25.81%
Number/percentage of N's	6,545 / 0.01%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0181

Standard Deviation	0.1804

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

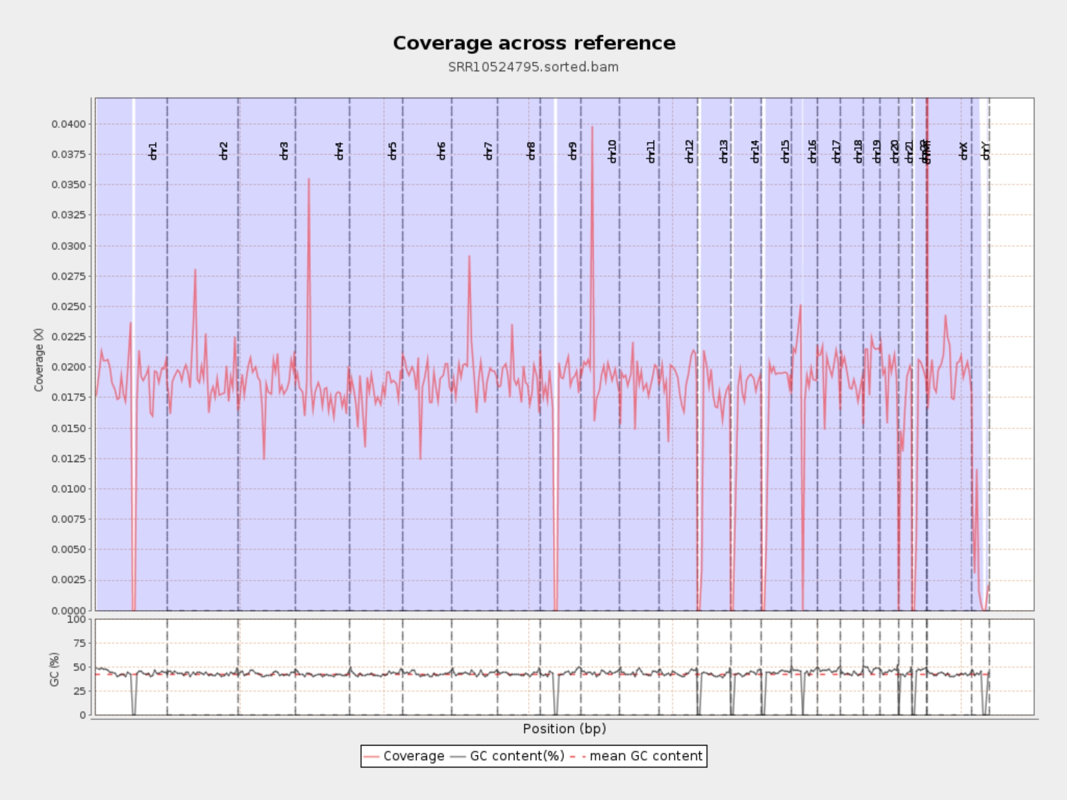
General error rate	0.52%
Mismatches	285,369
Insertions	3,376
Mapped reads with at least one insertion	0.34%
Deletions	11,308
Mapped reads with at least one deletion	1.15%
Homopolymer indels	44.17%

2.6. Chromosome stats

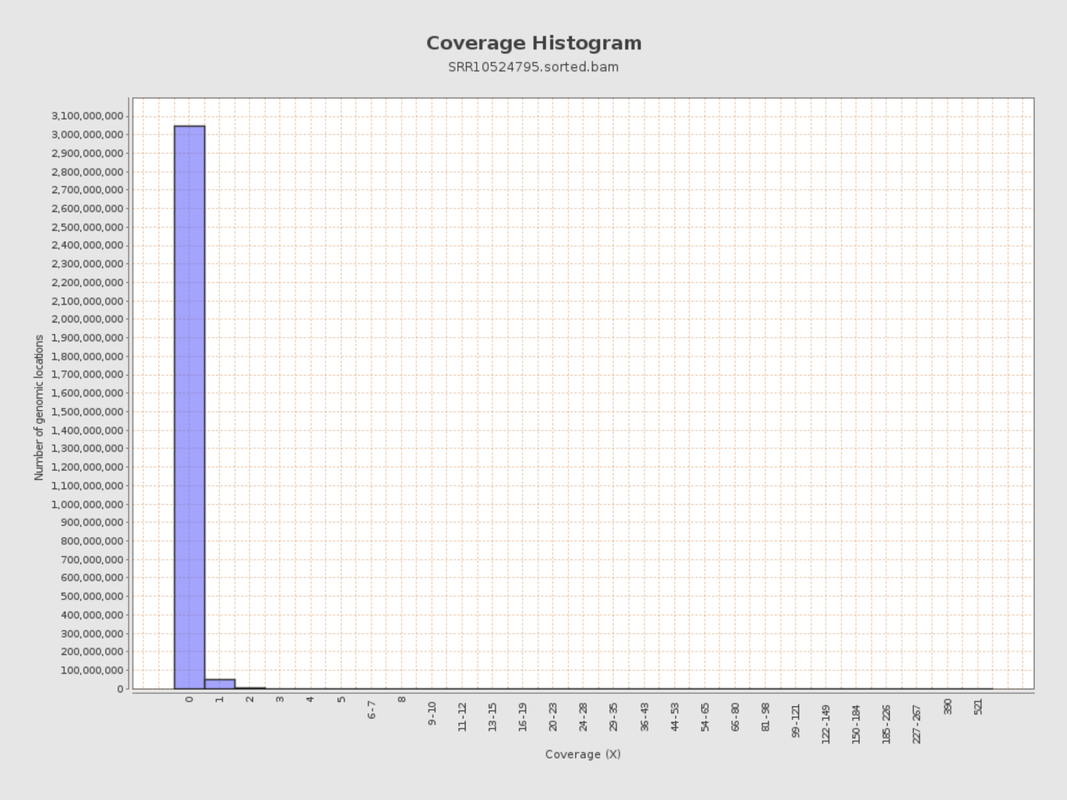
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4493896	0.018	0.2372
chr2	243199373	4700400	0.0193	0.2665
chr3	198022430	3716712	0.0188	0.1486
chr4	191154276	3535084	0.0185	0.1614
chr5	180915260	3263310	0.018	0.1435
chr6	171115067	3232800	0.0189	0.1567
chr7	159138663	3144261	0.0198	0.2183

chr8	146364022	2769076	0.0189	0.1691
chr9	141213431	2388115	0.0169	0.1571
chr10	135534747	2759221	0.0204	0.2113
chr11	135006516	2564432	0.019	0.1628
chr12	133851895	2531471	0.0189	0.1491
chr13	115169878	1751123	0.0152	0.1324
chr14	107349540	1670534	0.0156	0.1357
chr15	102531392	1614272	0.0157	0.1338
chr16	90354753	1668396	0.0185	0.1592
chr17	81195210	1616559	0.0199	0.1561
chr18	78077248	1483182	0.019	0.2238
chr19	59128983	1232346	0.0208	0.2022
chr20	63025520	1220333	0.0194	0.155
chr21	48129895	744319	0.0155	0.1451
chr22	51304566	702238	0.0137	0.126
chrMT	16571	11355	0.6852	0.9734
chrX	155270560	3089188	0.0199	0.1591
chrY	59373566	189657	0.0032	0.1003

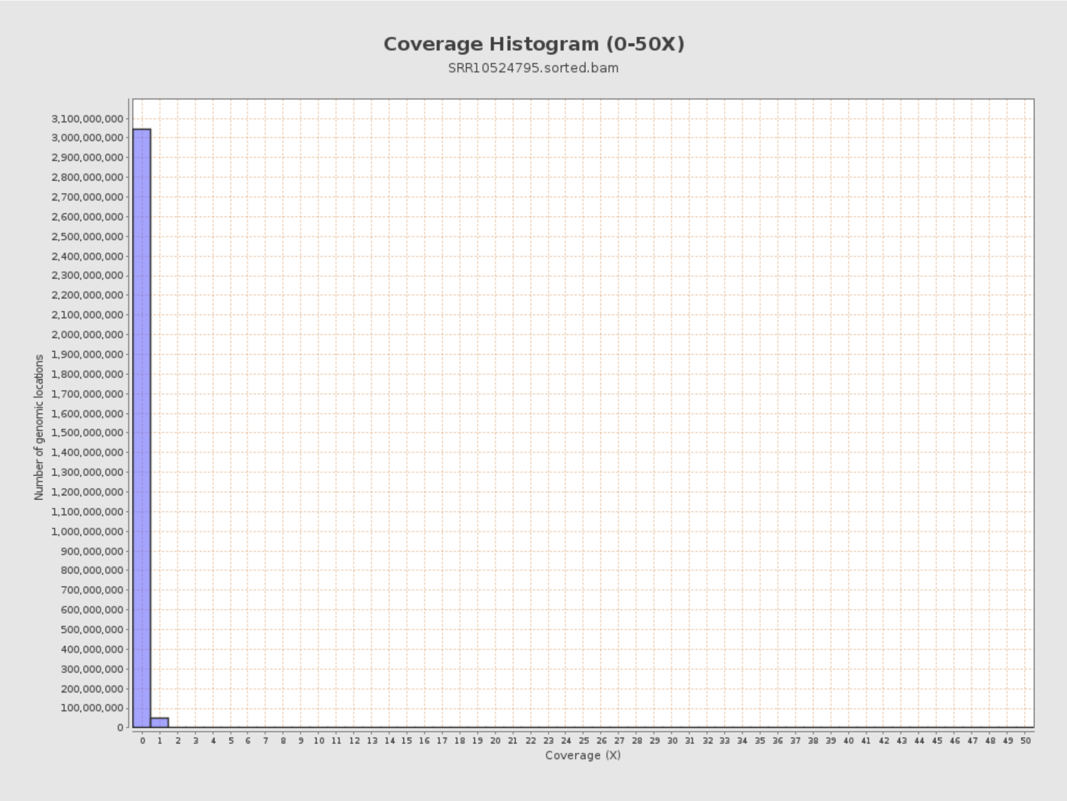
3. Results : Coverage across reference



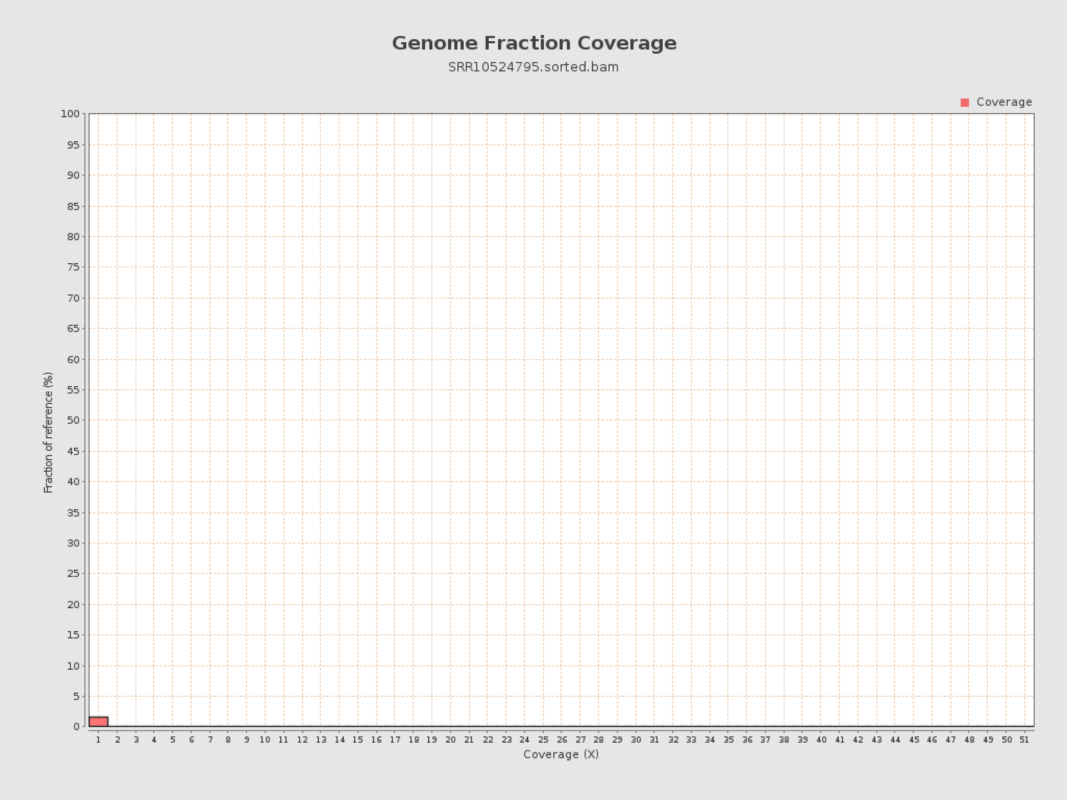
4. Results : Coverage Histogram



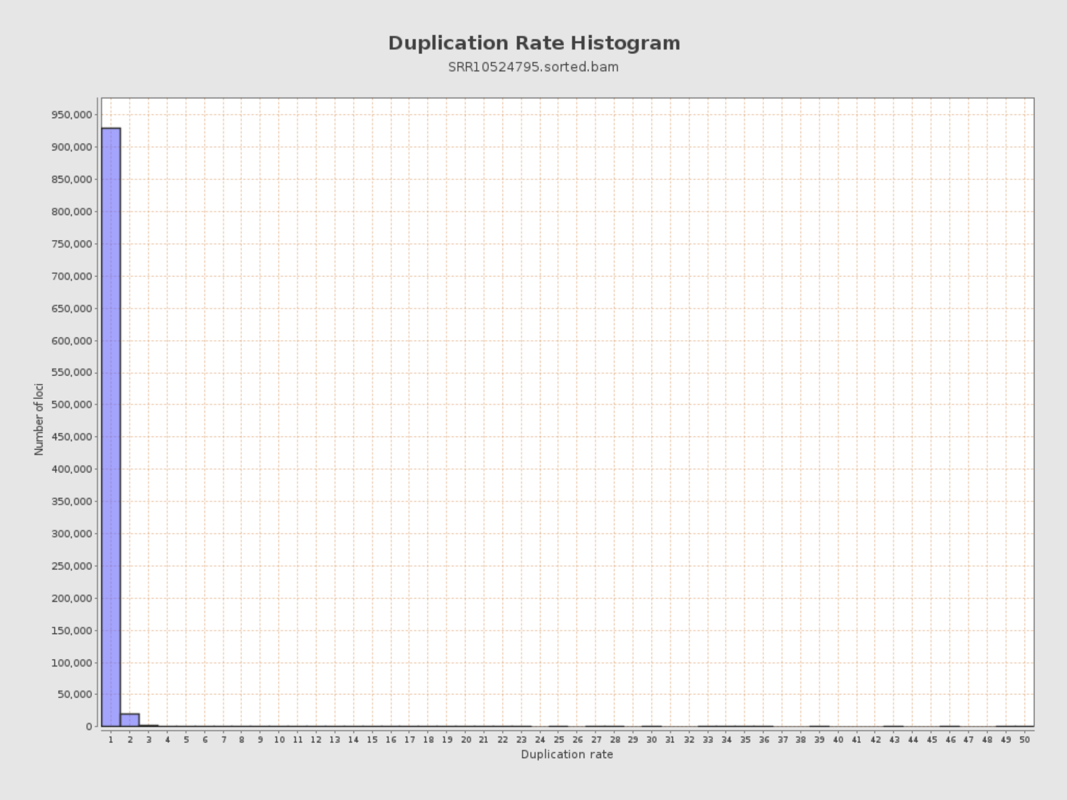
5. Results : Coverage Histogram (0-50X)



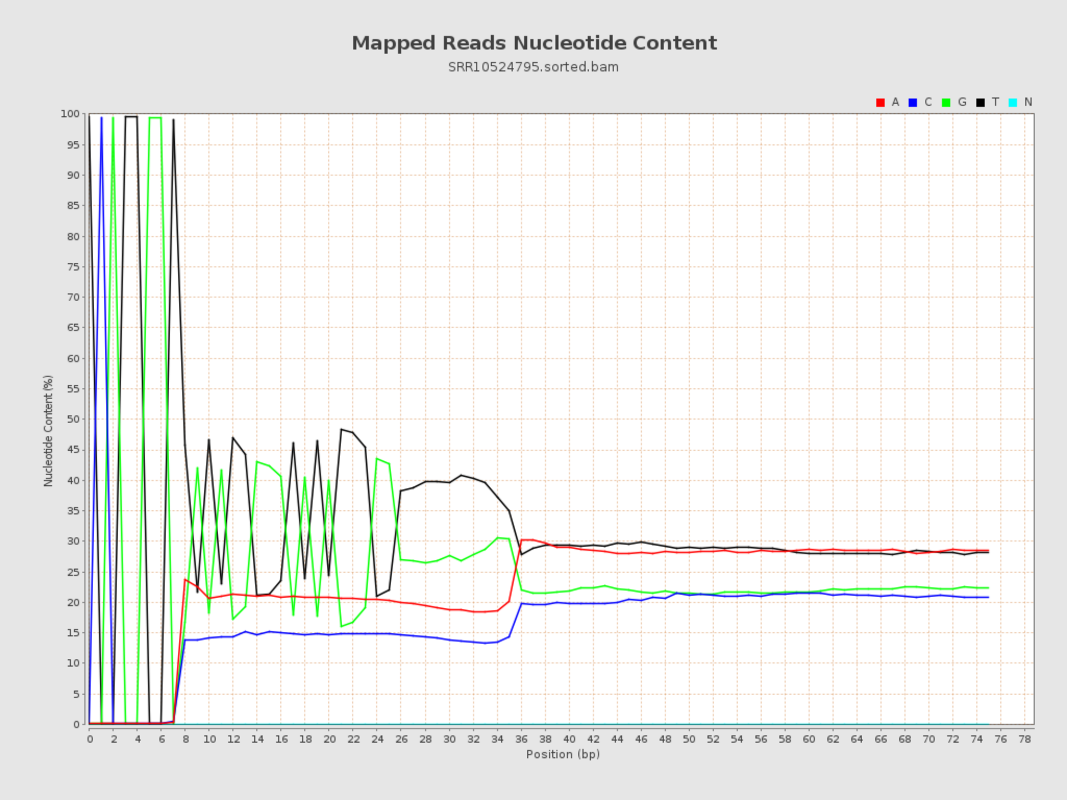
6. Results : Genome Fraction Coverage



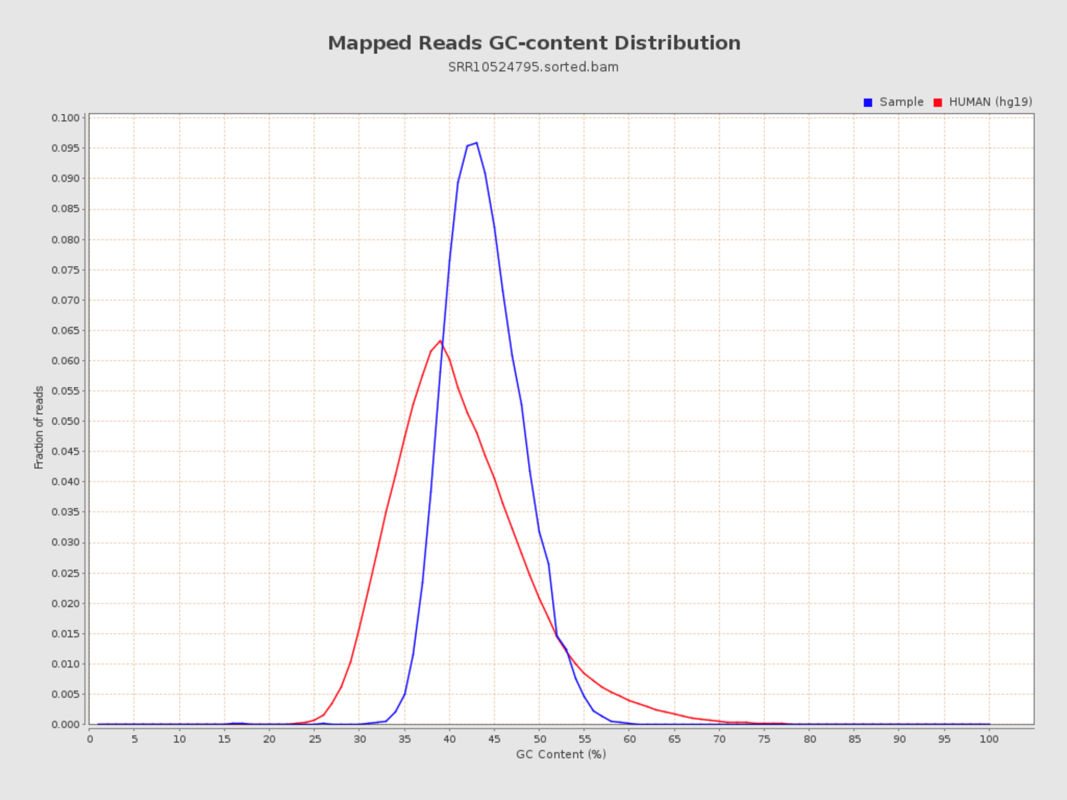
7. Results : Duplication Rate Histogram



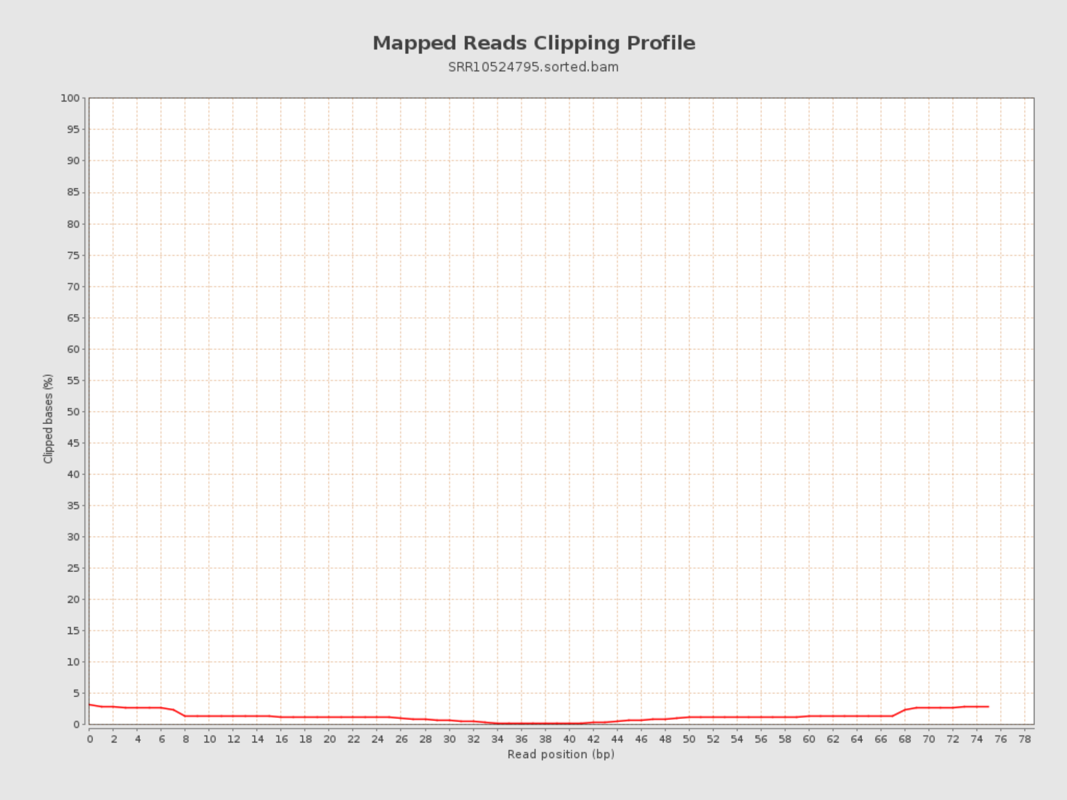
8. Results : Mapped Reads Nucleotide Content



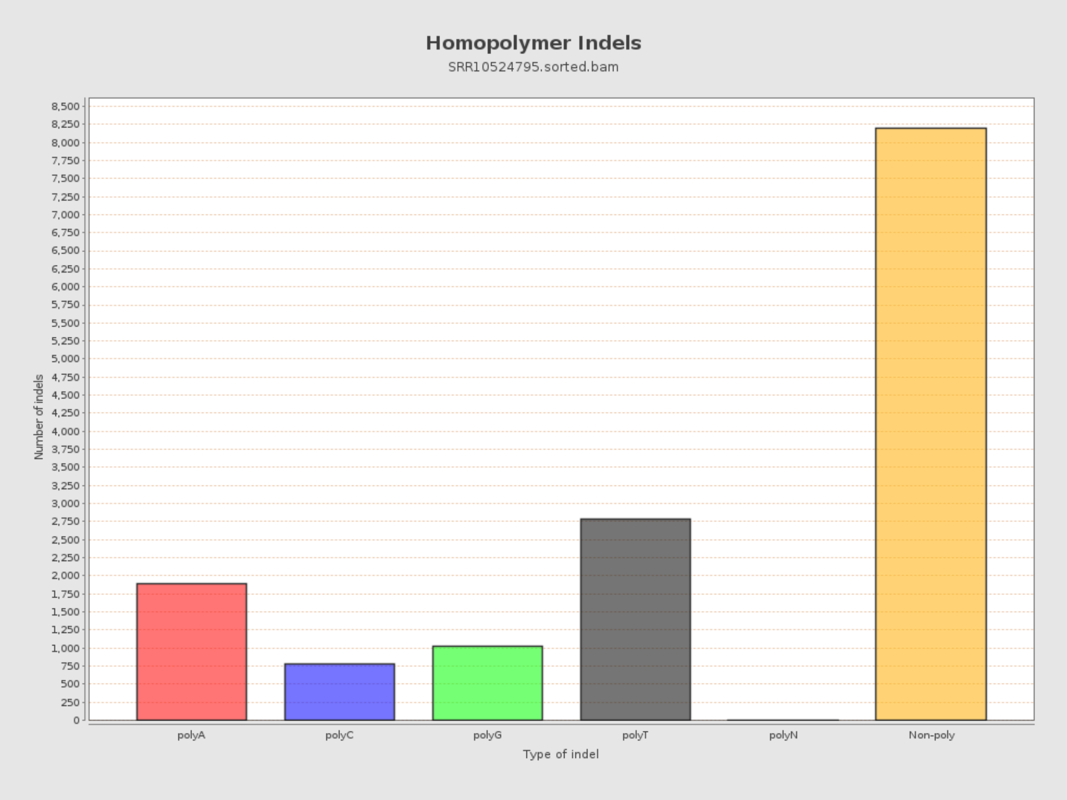
9. Results : Mapped Reads GC-content Distribution



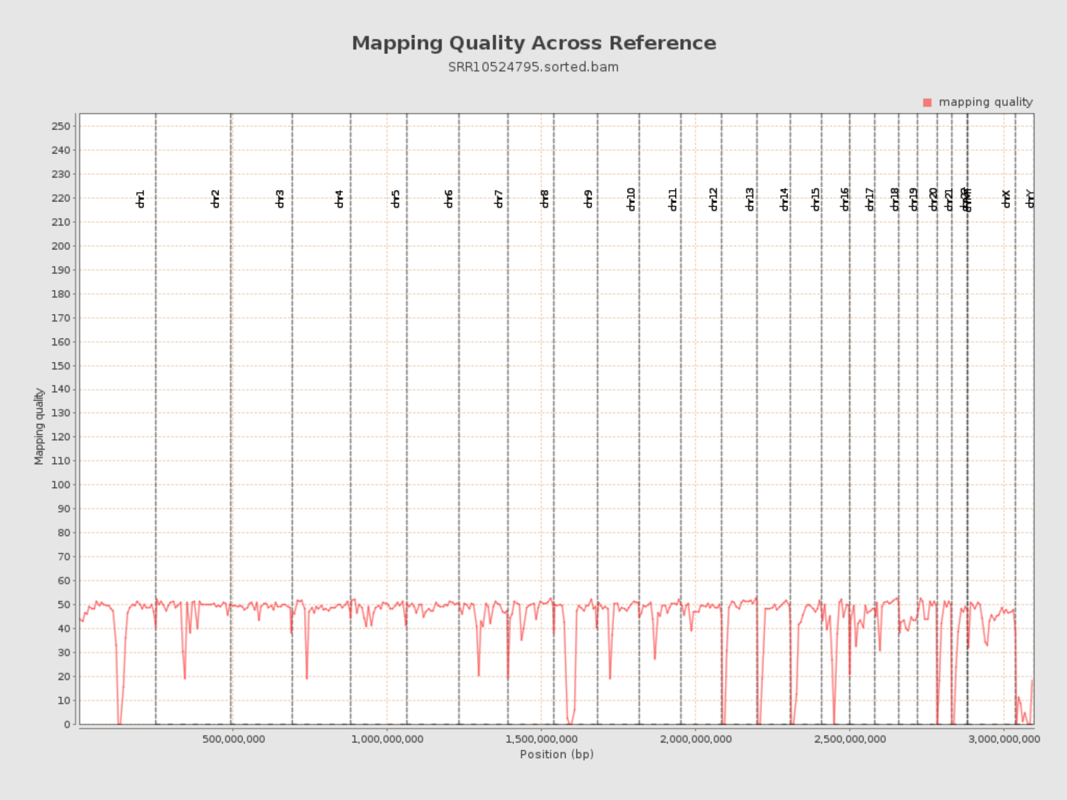
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram