Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:18:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082795.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_SRR3082795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:18:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,598,100
Mapped reads	3,147,425 / 87.47%
Unmapped reads	450,675 / 12.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,698 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	165,462 / 4.6%
Duplication rate	4.33%
Clipped reads	1,201,027 / 33.38%

2.2. ACGT Content

Number/percentage of A's	61,934,007 / 28.75%
Number/percentage of C's	39,013,914 / 18.11%
Number/percentage of T's	70,141,874 / 32.56%
Number/percentage of G's	44,333,226 / 20.58%
Number/percentage of N's	12,082 / 0.01%
GC Percentage	38.69%

2.3. Coverage

Mean	0.0696

Standard Deviation	0.5189

2.4. Mapping Quality

Mean Mapping Quality	47.57

2.5. Mismatches and indels

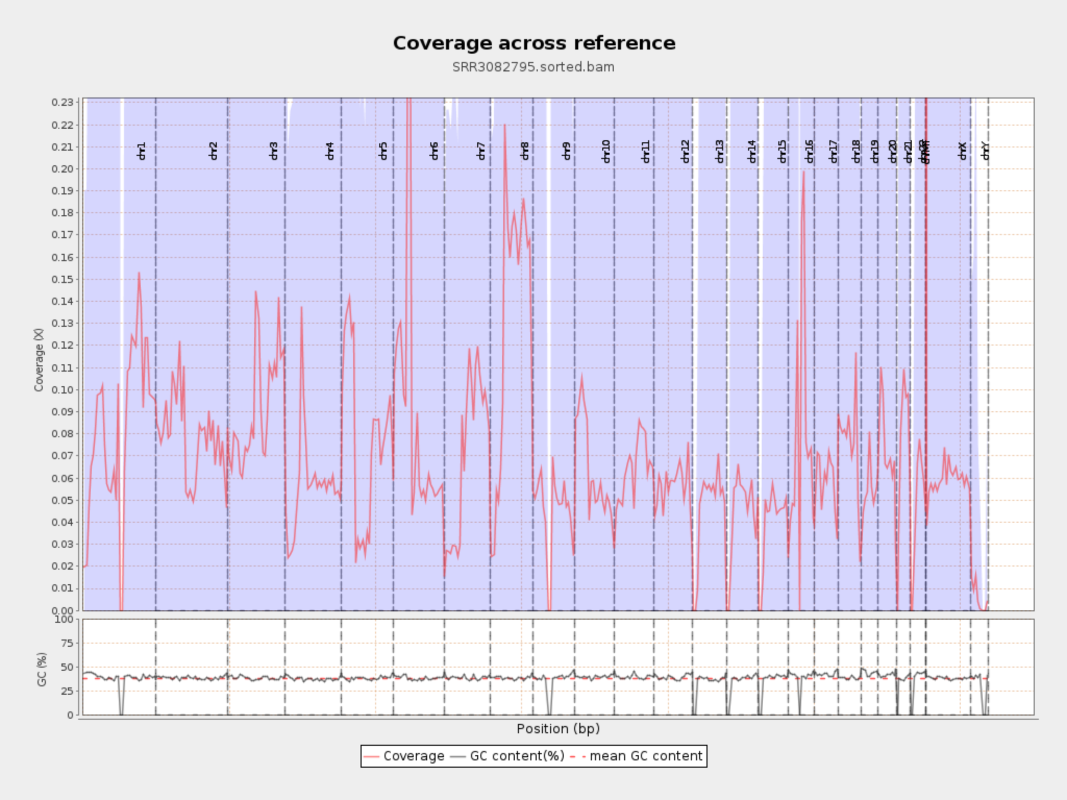
General error rate	0.89%
Mismatches	1,876,667
Insertions	17,188
Mapped reads with at least one insertion	0.54%
Deletions	46,031
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.76%

2.6. Chromosome stats

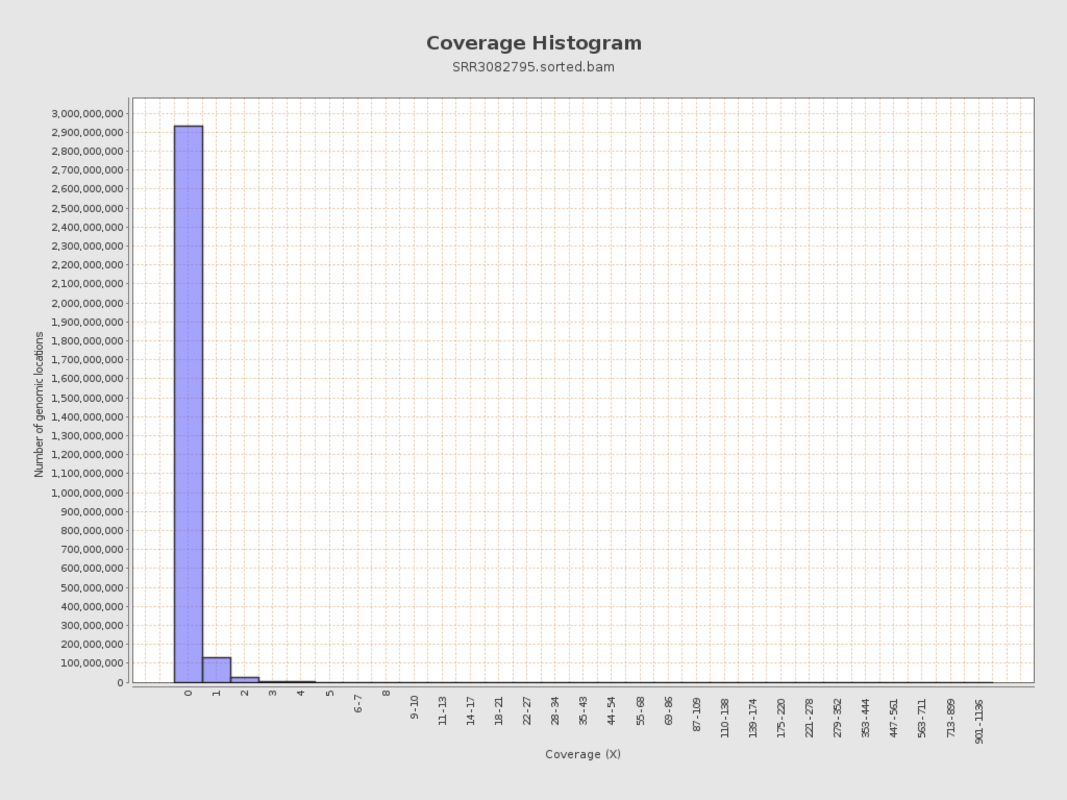
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20476791	0.0822	1.0182
chr2	243199373	19129624	0.0787	0.5502
chr3	198022430	18013376	0.091	0.3743
chr4	191154276	10948715	0.0573	0.3031
chr5	180915260	13898206	0.0768	0.3473
chr6	171115067	15802285	0.0923	0.5725
chr7	159138663	11251469	0.0707	0.4876

chr8	146364022	19415219	0.1327	0.7551
chr9	141213431	6380879	0.0452	0.426
chr10	135534747	8708472	0.0643	0.439
chr11	135006516	8625223	0.0639	0.4089
chr12	133851895	7532544	0.0563	0.2979
chr13	115169878	5243914	0.0455	0.2629
chr14	107349540	4757895	0.0443	0.2835
chr15	102531392	3975219	0.0388	0.2415
chr16	90354753	7137282	0.079	0.4141
chr17	81195210	4818418	0.0593	0.3682
chr18	78077248	6034720	0.0773	0.8874
chr19	59128983	3237766	0.0548	0.6297
chr20	63025520	4684491	0.0743	0.3472
chr21	48129895	3520260	0.0731	0.3424
chr22	51304566	2379173	0.0464	0.2611
chrMT	16571	62149	3.7505	2.9842
chrX	155270560	9134481	0.0588	0.3333
chrY	59373566	345554	0.0058	0.1188

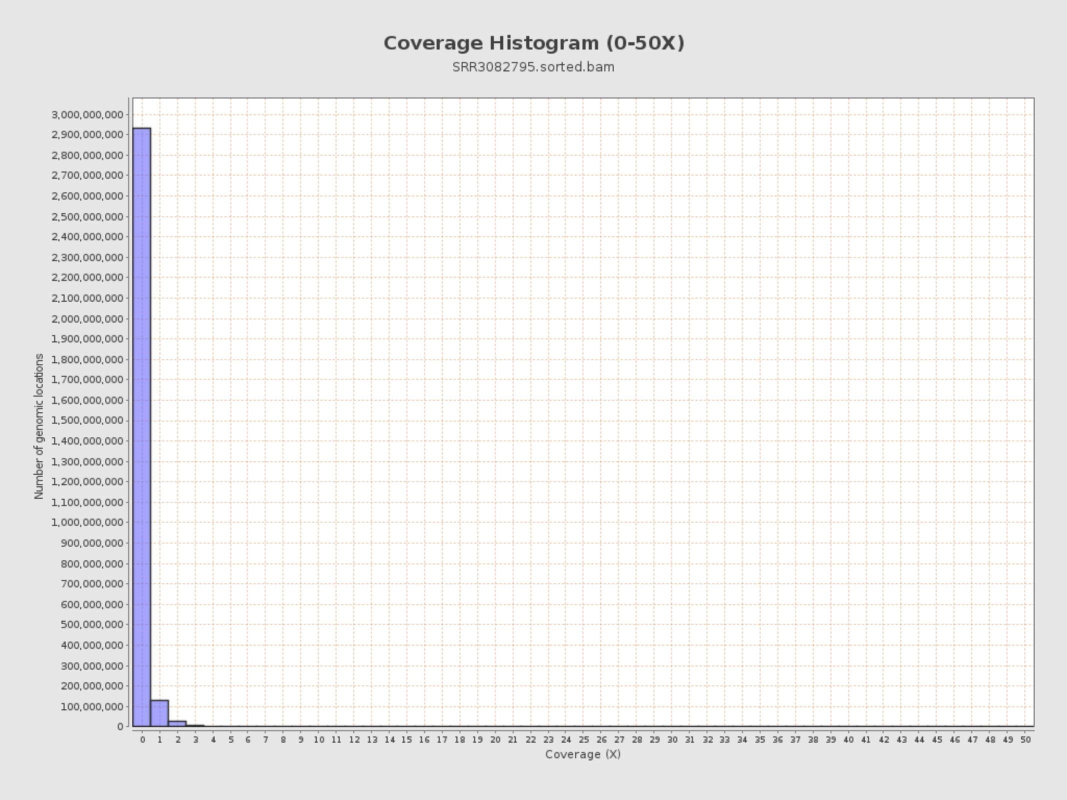
3. Results : Coverage across reference



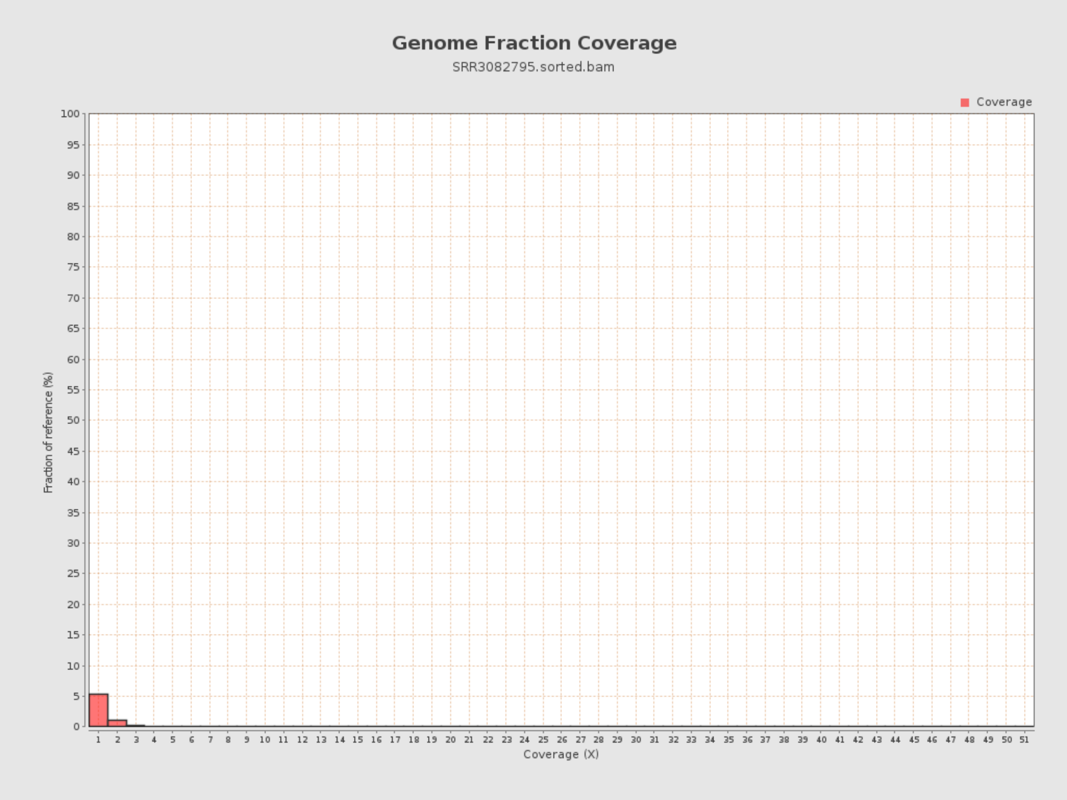
4. Results : Coverage Histogram



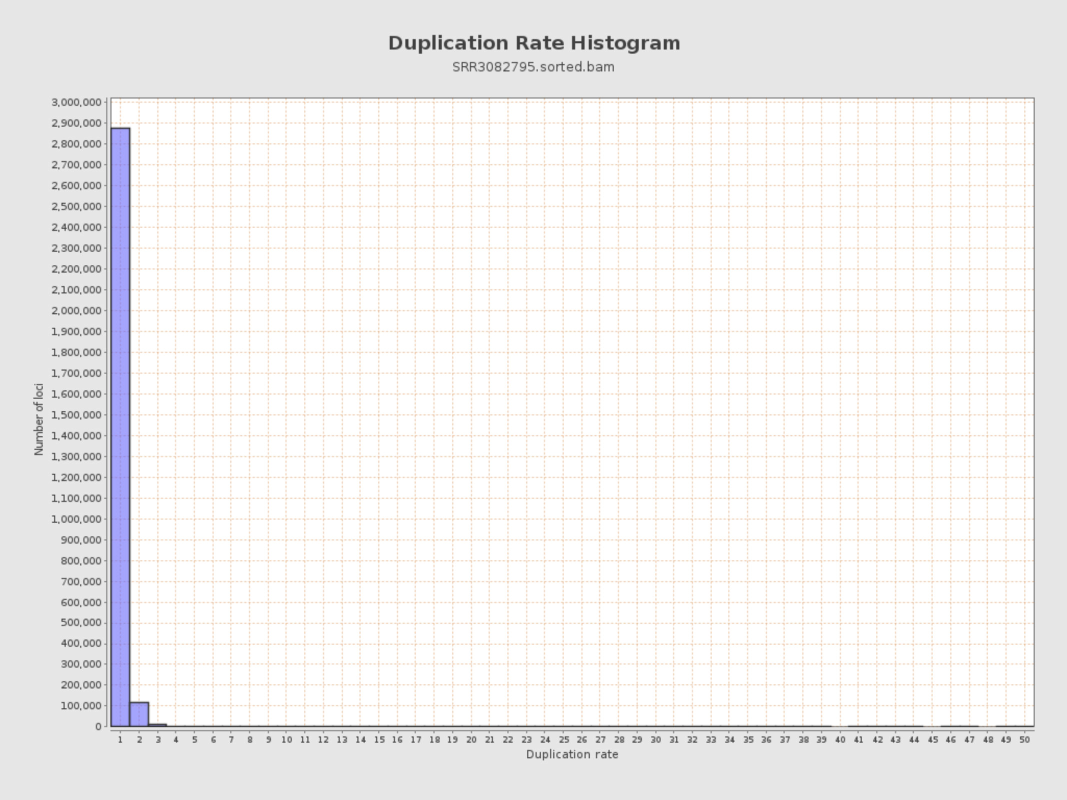
5. Results : Coverage Histogram (0-50X)



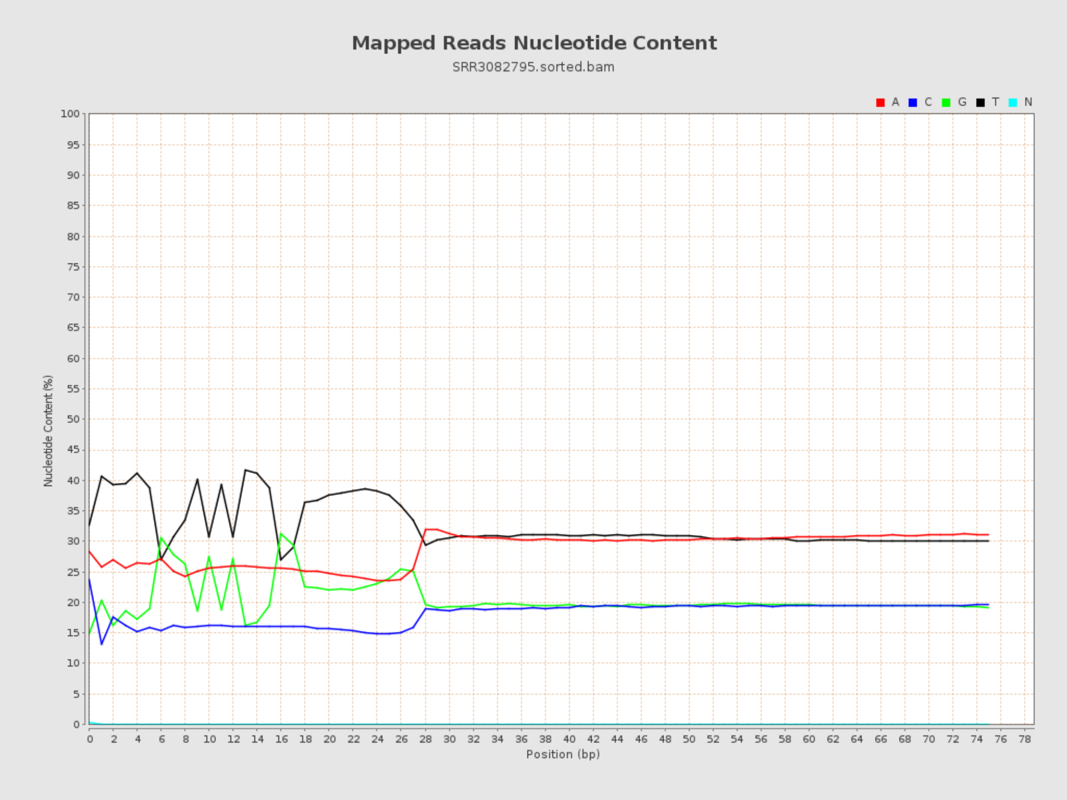
6. Results : Genome Fraction Coverage



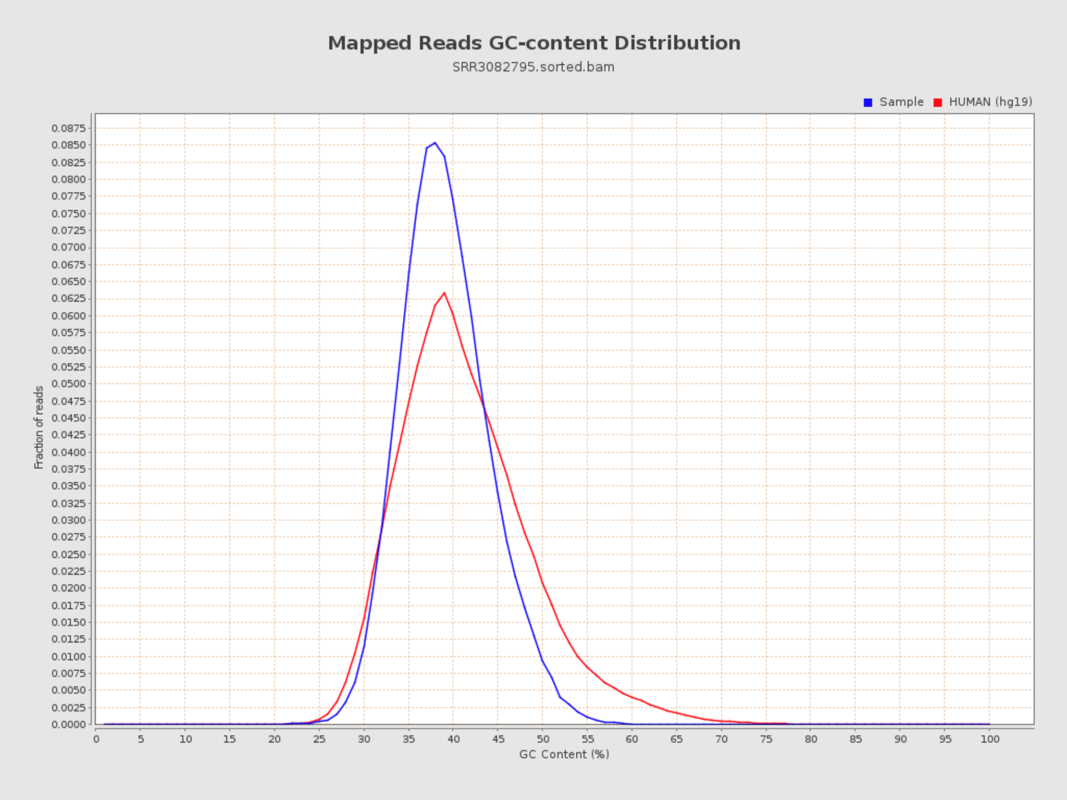
7. Results : Duplication Rate Histogram



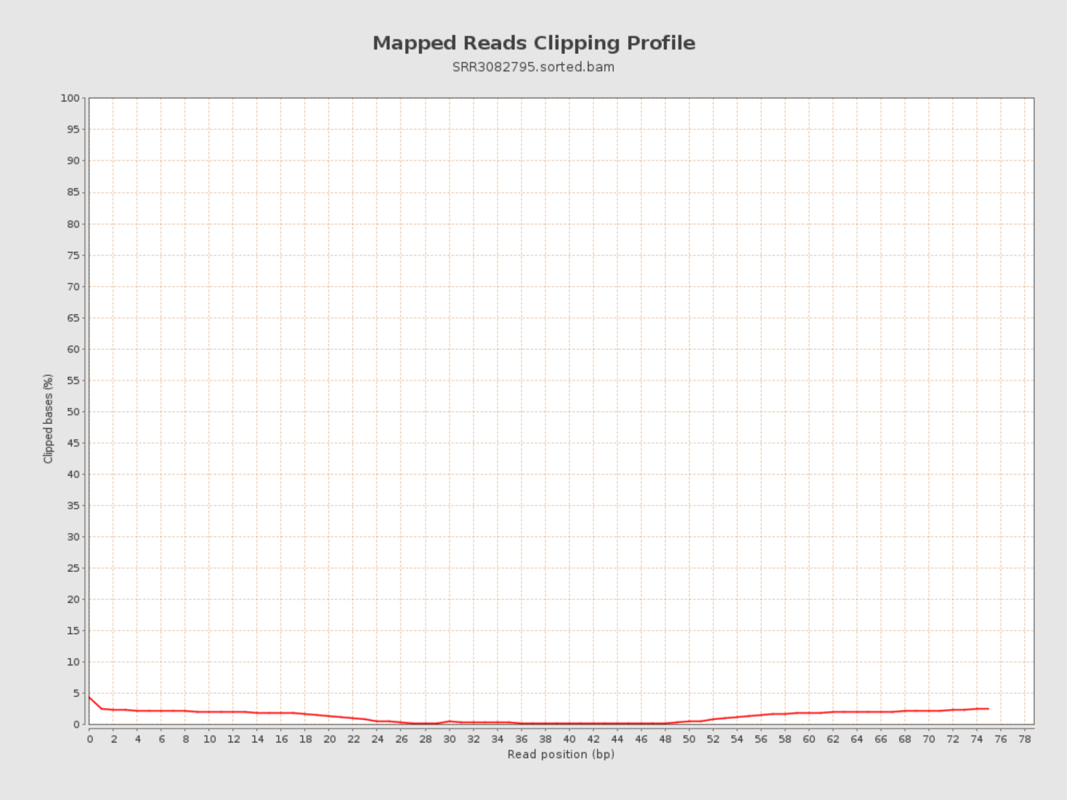
8. Results : Mapped Reads Nucleotide Content



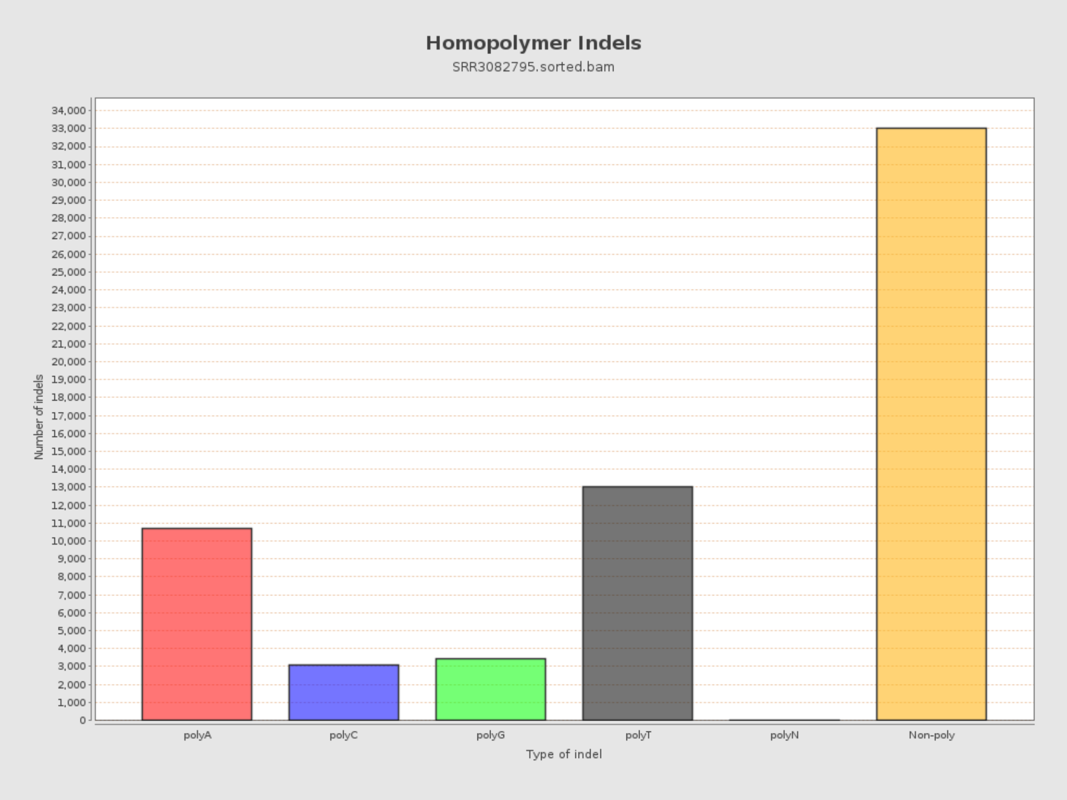
9. Results : Mapped Reads GC-content Distribution



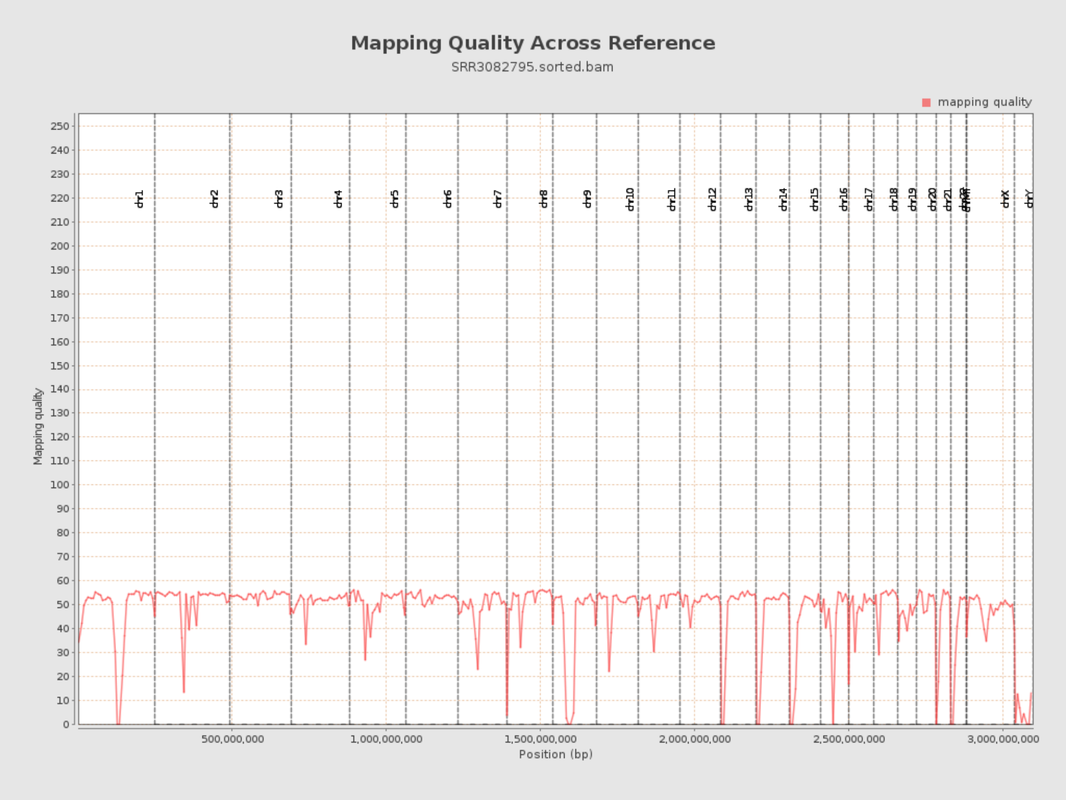
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram