Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:12:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081995.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_SRR3081995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081995.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:12:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081995.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,737,357
Mapped reads	1,544,683 / 88.91%
Unmapped reads	192,674 / 11.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,250 / 1.28%
Read min/max/mean length	30 / 76 / 76.45
Duplicated reads (estimated)	68,237 / 3.93%
Duplication rate	2.52%
Clipped reads	604,167 / 34.78%

2.2. ACGT Content

Number/percentage of A's	30,437,750 / 28.71%
Number/percentage of C's	20,375,002 / 19.22%
Number/percentage of T's	31,473,252 / 29.69%
Number/percentage of G's	23,710,803 / 22.37%
Number/percentage of N's	13,346 / 0.01%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0343

Standard Deviation	0.5047

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

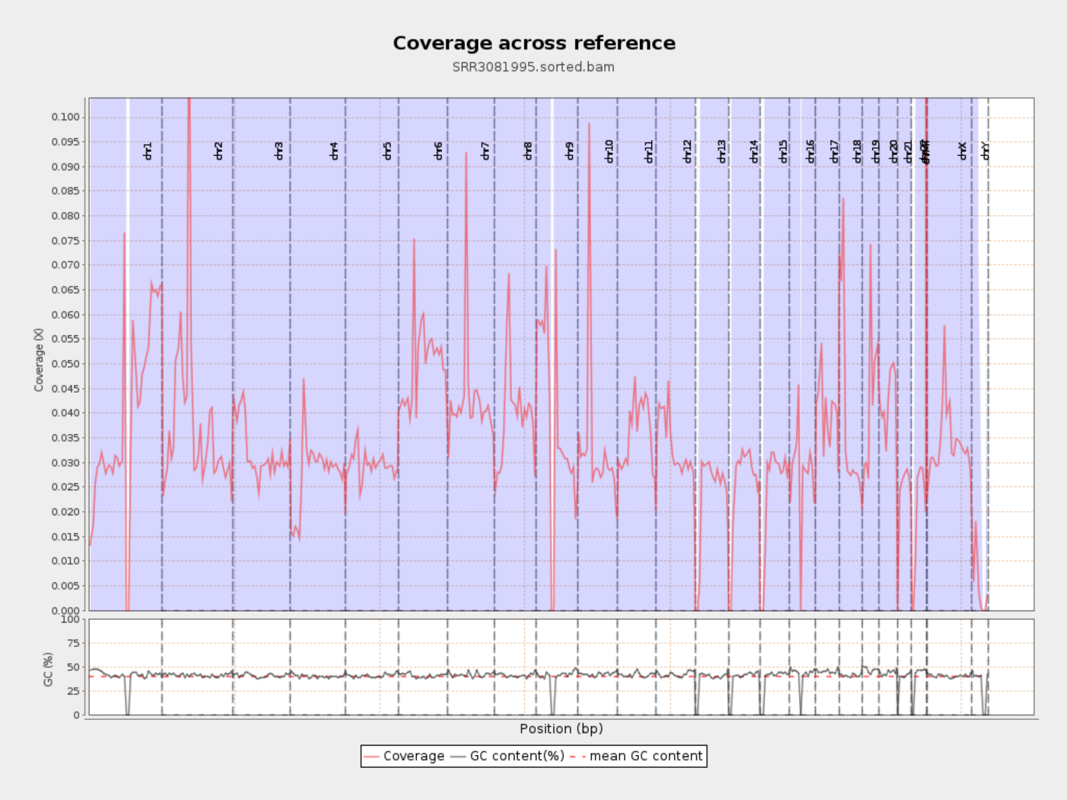
General error rate	0.88%
Mismatches	911,519
Insertions	9,583
Mapped reads with at least one insertion	0.61%
Deletions	21,485
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.06%

2.6. Chromosome stats

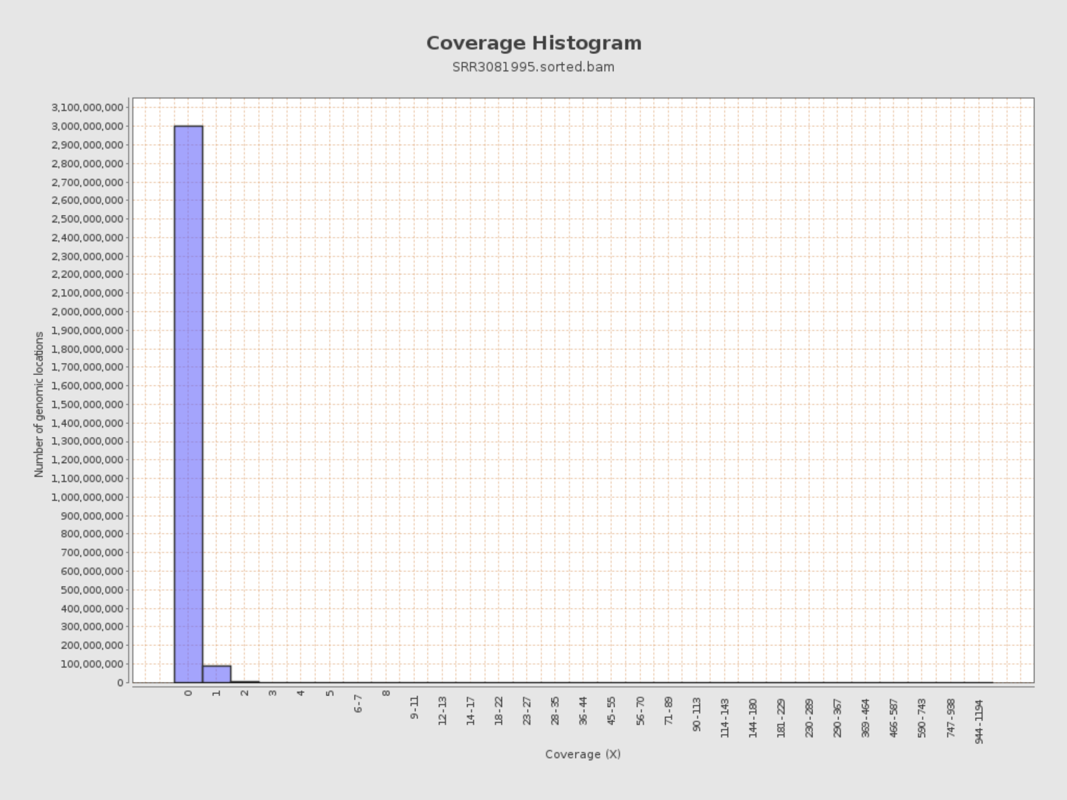
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9721672	0.039	0.9631
chr2	243199373	9311327	0.0383	0.7456
chr3	198022430	6413258	0.0324	0.1987
chr4	191154276	5308519	0.0278	0.219
chr5	180915260	5366834	0.0297	0.1899
chr6	171115067	8529885	0.0498	0.3406
chr7	159138663	6870000	0.0432	0.7278

chr8	146364022	5779099	0.0395	0.531
chr9	141213431	5355190	0.0379	0.5537
chr10	135534747	4505640	0.0332	0.5169
chr11	135006516	4821976	0.0357	0.3458
chr12	133851895	4463760	0.0333	0.2132
chr13	115169878	2659408	0.0231	0.1585
chr14	107349540	2683804	0.025	0.2406
chr15	102531392	2482678	0.0242	0.1708
chr16	90354753	2510727	0.0278	0.2711
chr17	81195210	3264502	0.0402	0.2652
chr18	78077248	3073444	0.0394	0.9984
chr19	59128983	2526119	0.0427	0.6841
chr20	63025520	2661028	0.0422	0.2383
chr21	48129895	1144478	0.0238	0.2367
chr22	51304566	958948	0.0187	0.1428
chrMT	16571	41449	2.5013	2.3293
chrX	155270560	5287688	0.0341	0.2793
chrY	59373566	307305	0.0052	0.1762

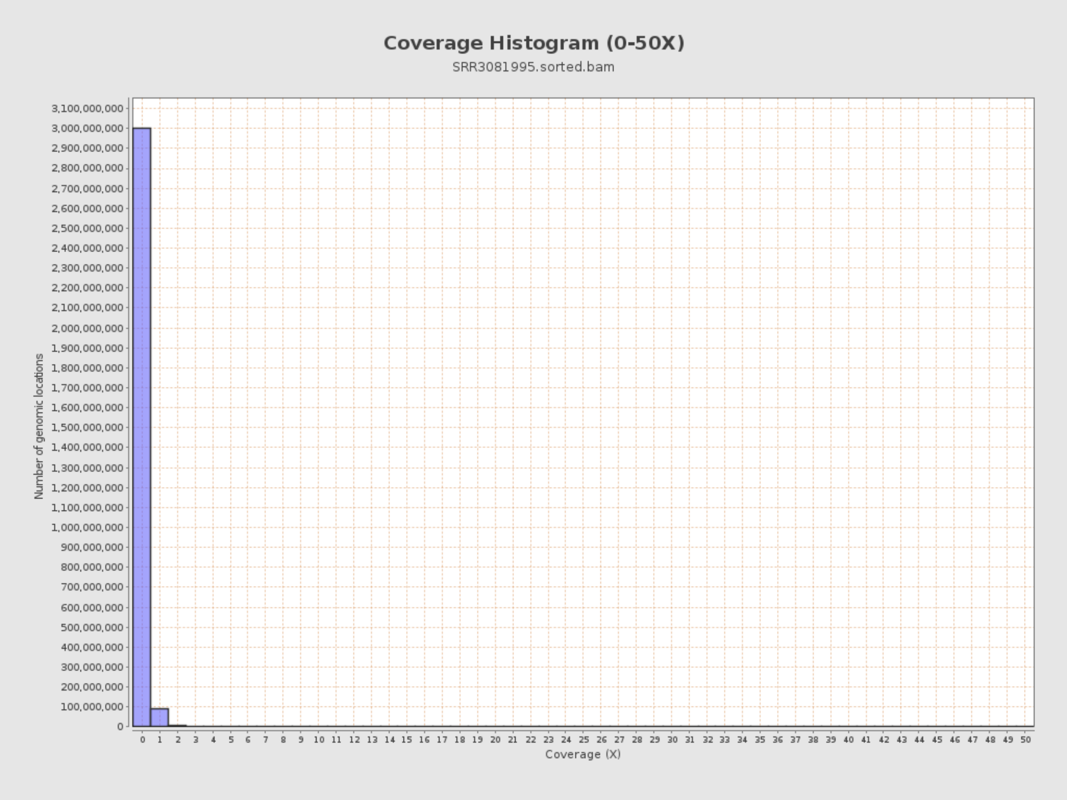
3. Results : Coverage across reference



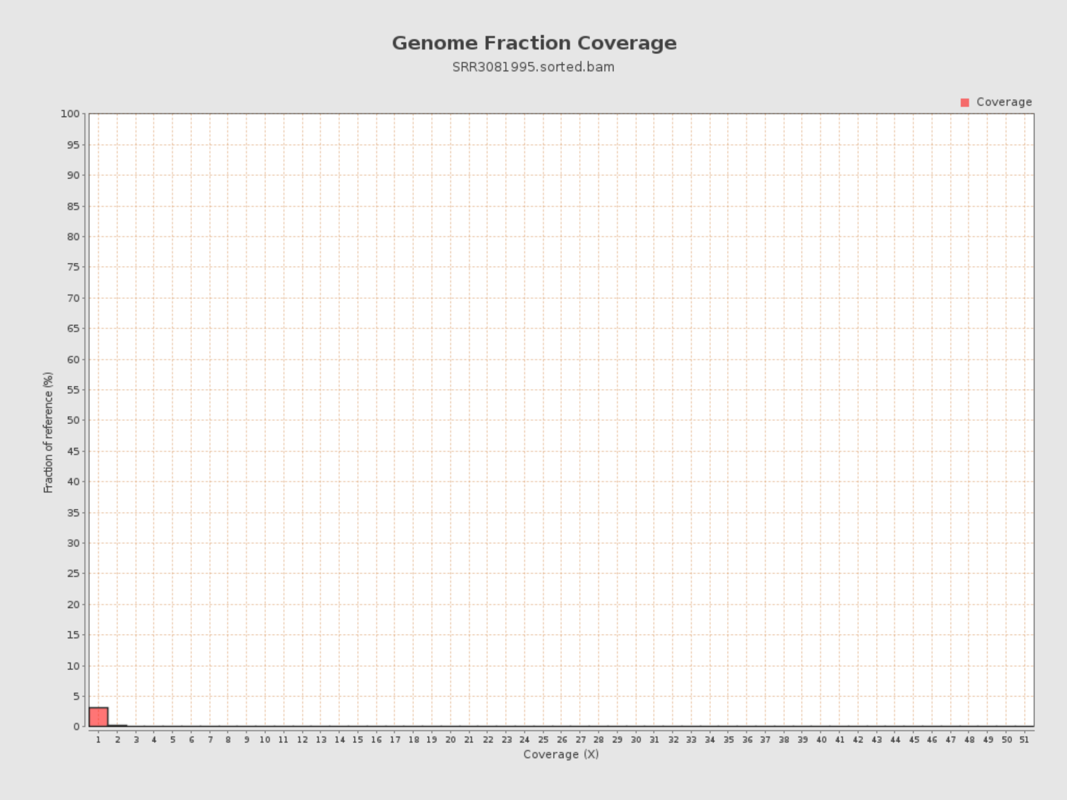
4. Results : Coverage Histogram



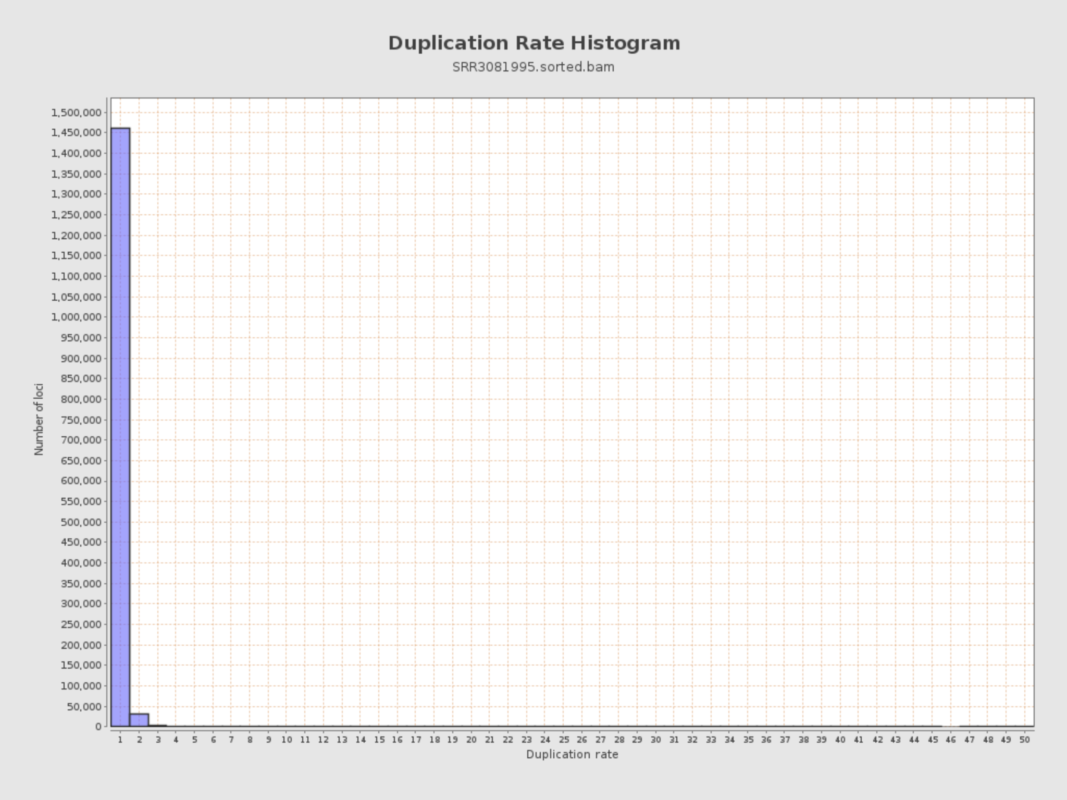
5. Results : Coverage Histogram (0-50X)



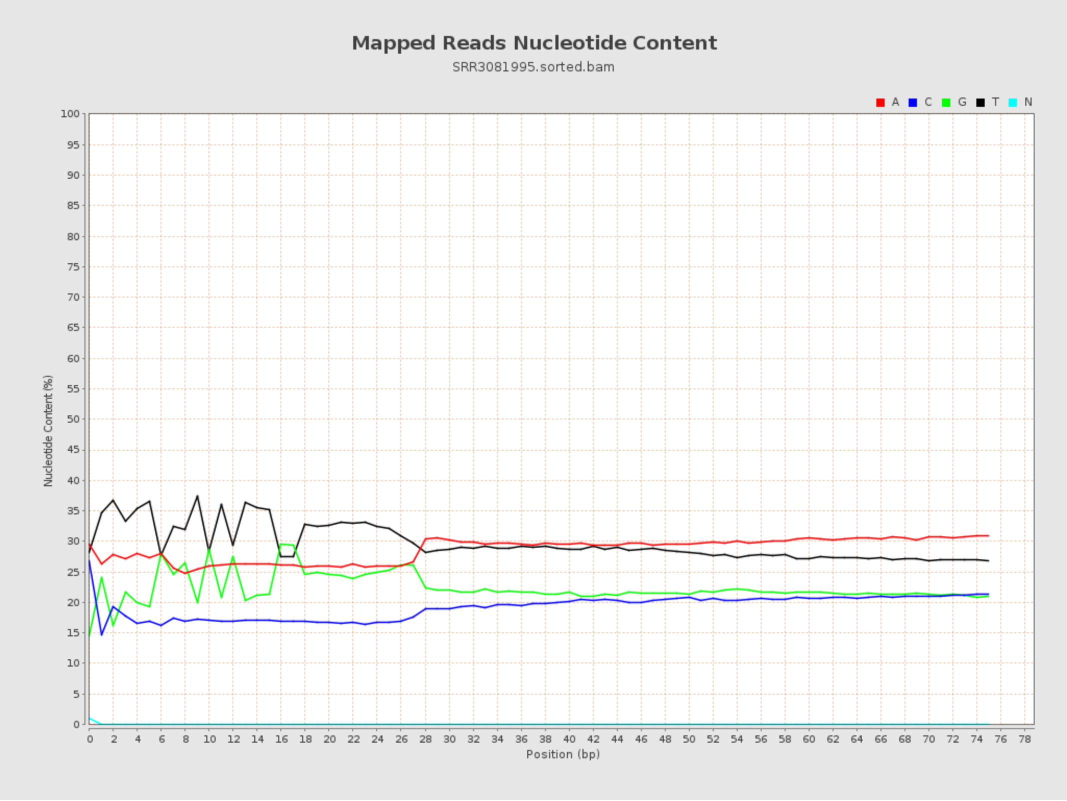
6. Results : Genome Fraction Coverage



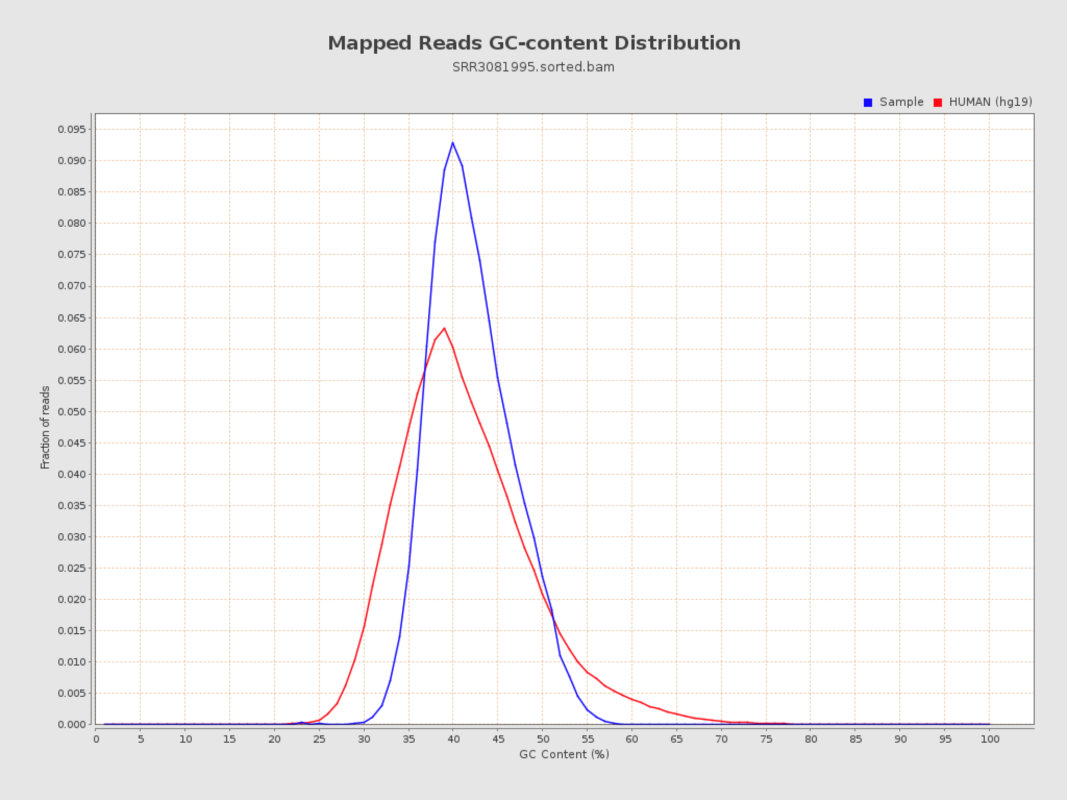
7. Results : Duplication Rate Histogram



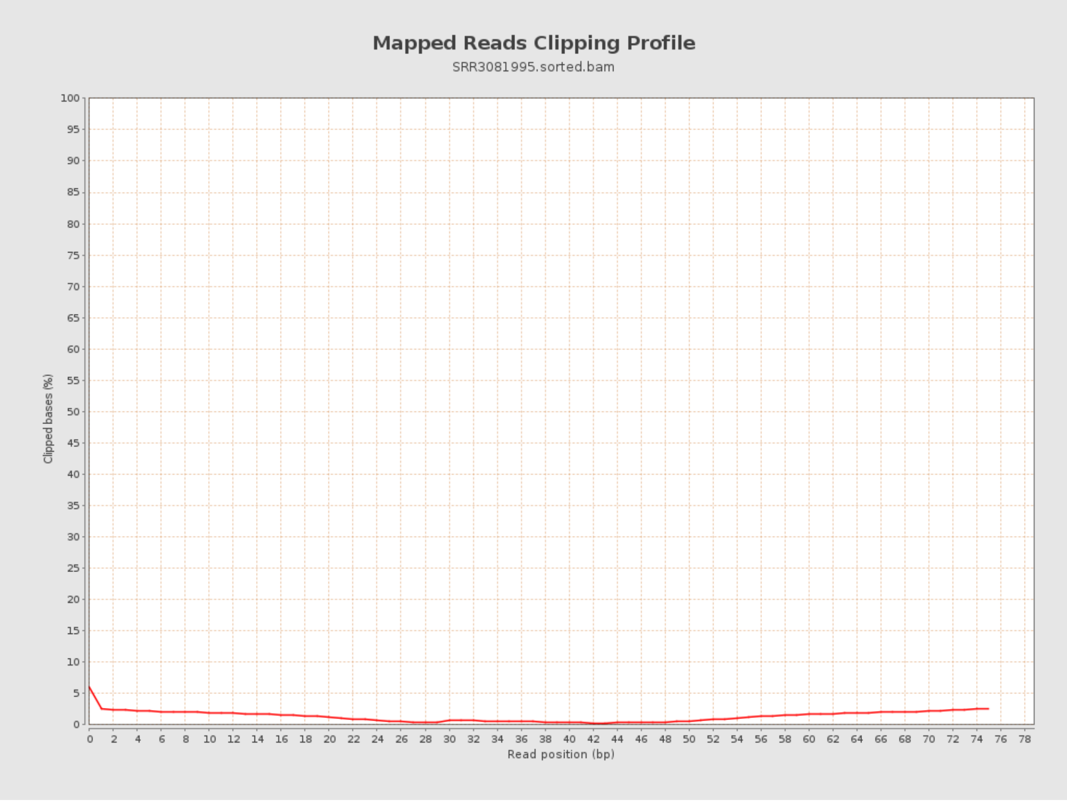
8. Results : Mapped Reads Nucleotide Content



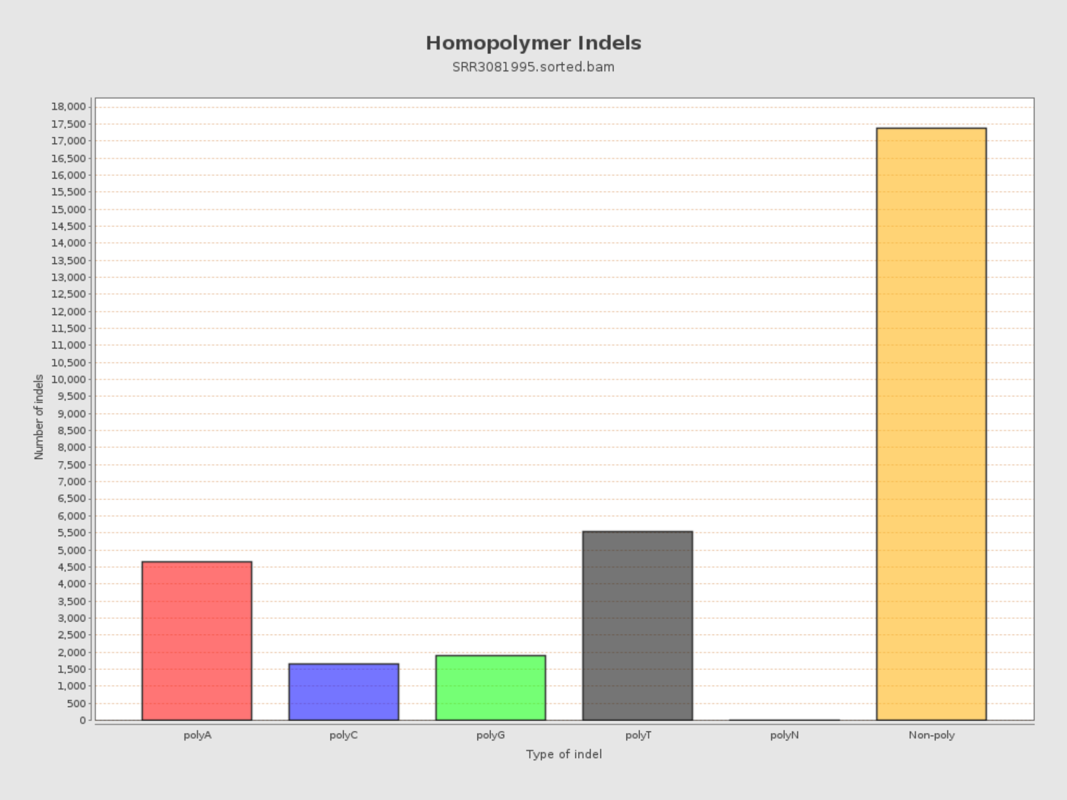
9. Results : Mapped Reads GC-content Distribution



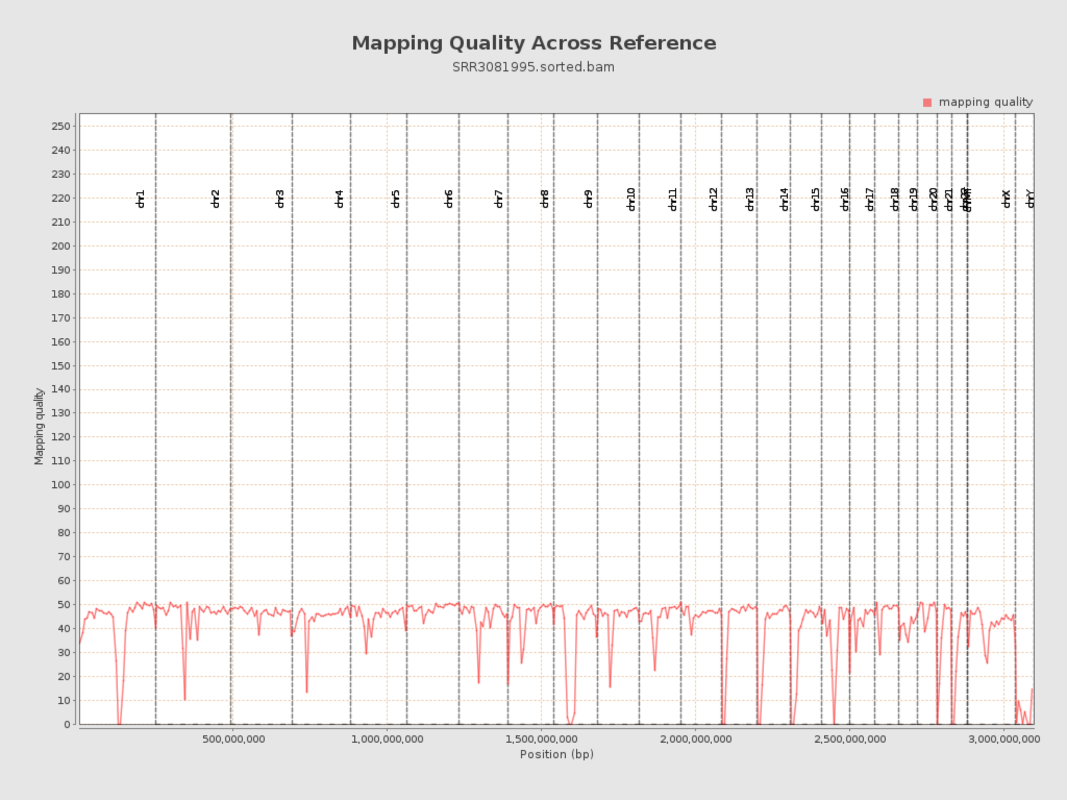
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram