Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:14:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080791.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_SRR3080791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:14:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,382,445
Mapped reads	2,130,042 / 89.41%
Unmapped reads	252,403 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,921 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	84,495 / 3.55%
Duplication rate	3.26%
Clipped reads	1,059,548 / 44.47%

2.2. ACGT Content

Number/percentage of A's	40,105,364 / 28.59%
Number/percentage of C's	26,864,998 / 19.15%
Number/percentage of T's	43,055,578 / 30.69%
Number/percentage of G's	30,270,779 / 21.58%
Number/percentage of N's	2,847 / 0%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0453

Standard Deviation	0.3503

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

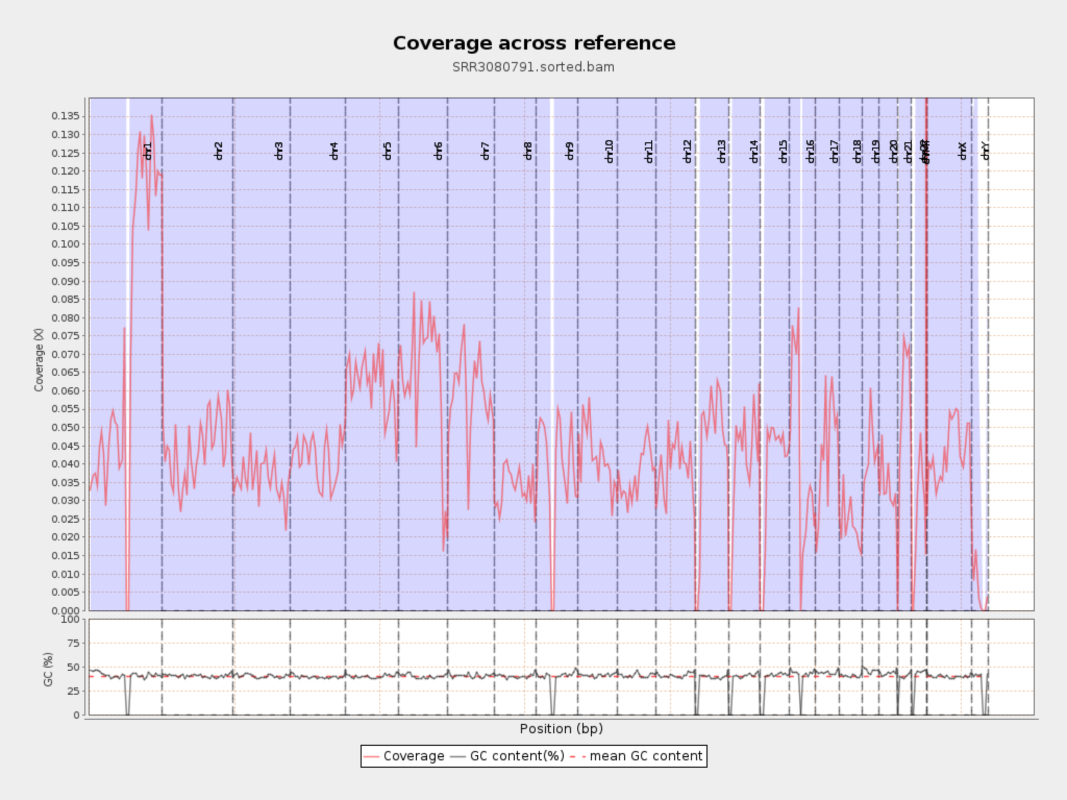
General error rate	0.78%
Mismatches	1,070,639
Insertions	10,496
Mapped reads with at least one insertion	0.49%
Deletions	30,557
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.17%

2.6. Chromosome stats

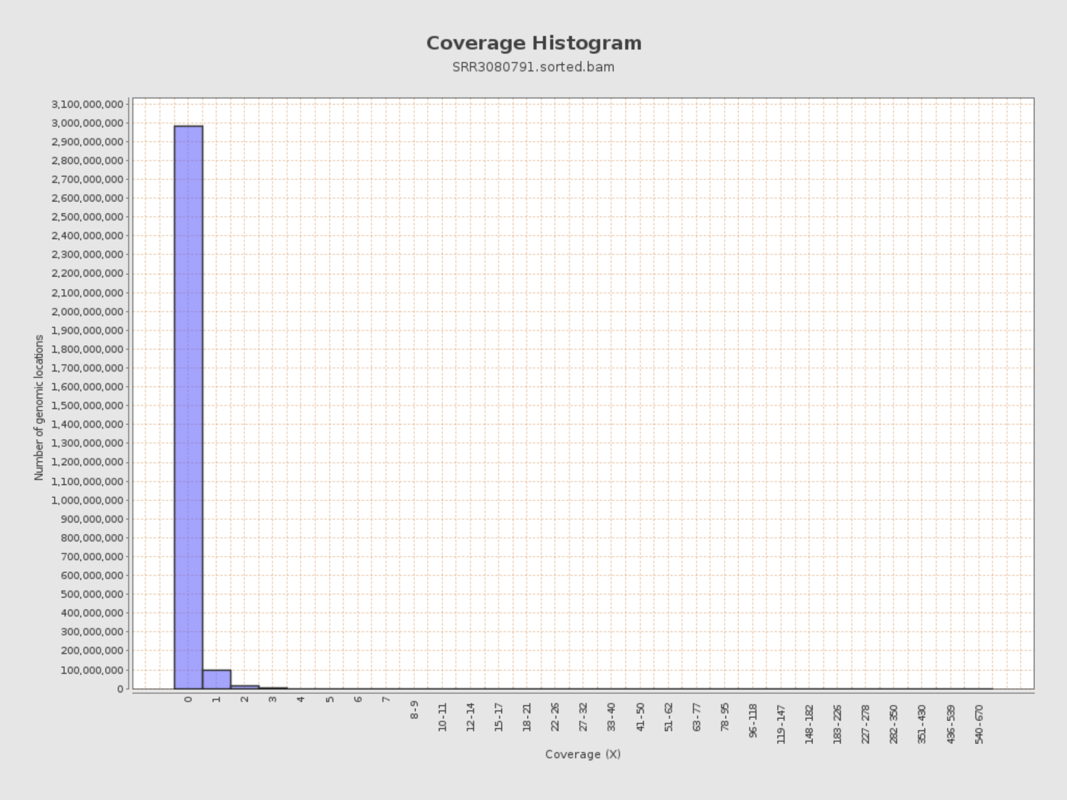
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18392333	0.0738	0.6695
chr2	243199373	10724634	0.0441	0.3639
chr3	198022430	7137453	0.036	0.2211
chr4	191154276	7990994	0.0418	0.2467
chr5	180915260	11126824	0.0615	0.2919
chr6	171115067	11034842	0.0645	0.3625
chr7	159138663	9450789	0.0594	0.392

chr8	146364022	4901779	0.0335	0.4066
chr9	141213431	5526353	0.0391	0.3027
chr10	135534747	5736882	0.0423	0.3104
chr11	135006516	5006920	0.0371	0.2594
chr12	133851895	5259191	0.0393	0.2345
chr13	115169878	5054140	0.0439	0.2452
chr14	107349540	4204617	0.0392	0.2434
chr15	102531392	3875195	0.0378	0.237
chr16	90354753	3816294	0.0422	0.2619
chr17	81195210	3597109	0.0443	0.2561
chr18	78077248	1835236	0.0235	0.5296
chr19	59128983	2531198	0.0428	0.4633
chr20	63025520	2133533	0.0339	0.2213
chr21	48129895	2633144	0.0547	0.2828
chr22	51304566	1268346	0.0247	0.1853
chrMT	16571	56610	3.4162	2.6573
chrX	155270560	6735040	0.0434	0.2561
chrY	59373566	318776	0.0054	0.1119

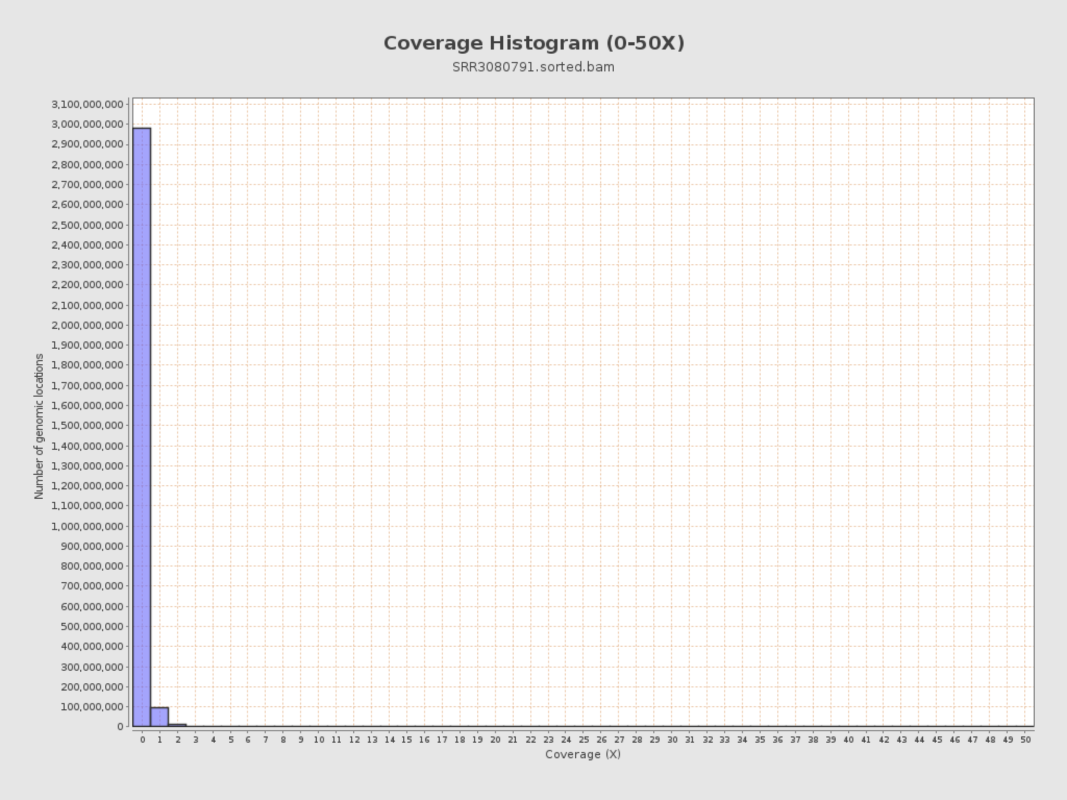
3. Results : Coverage across reference



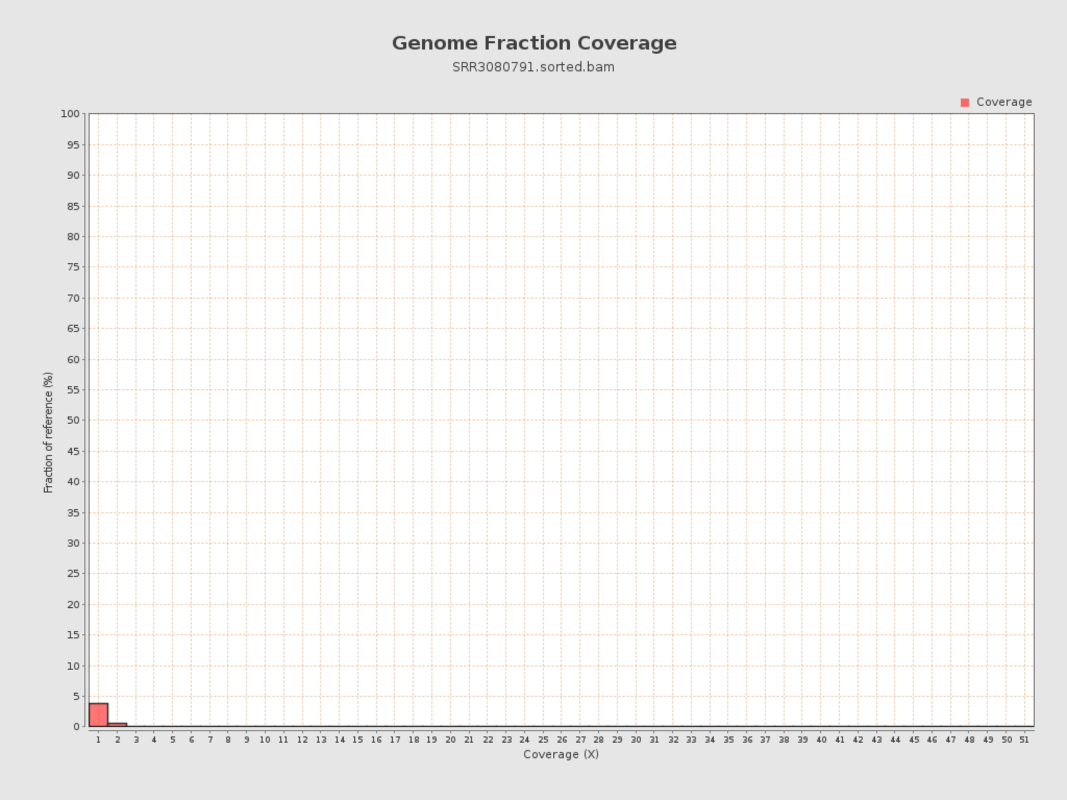
4. Results : Coverage Histogram



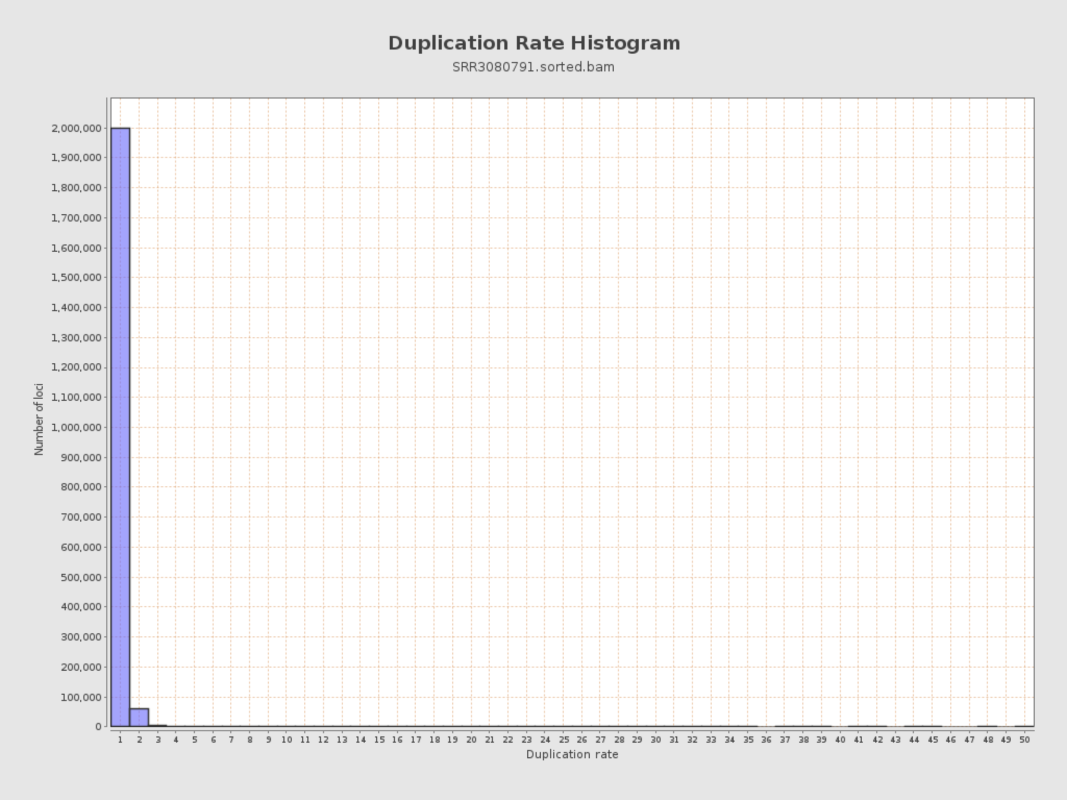
5. Results : Coverage Histogram (0-50X)



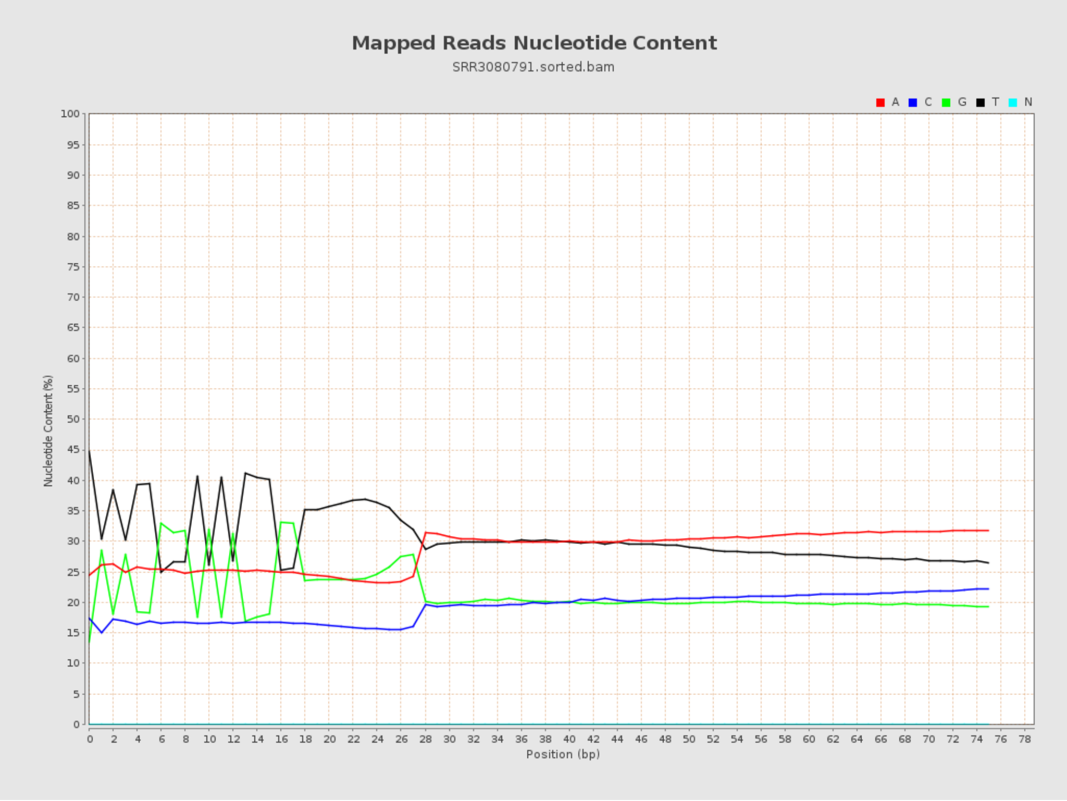
6. Results : Genome Fraction Coverage



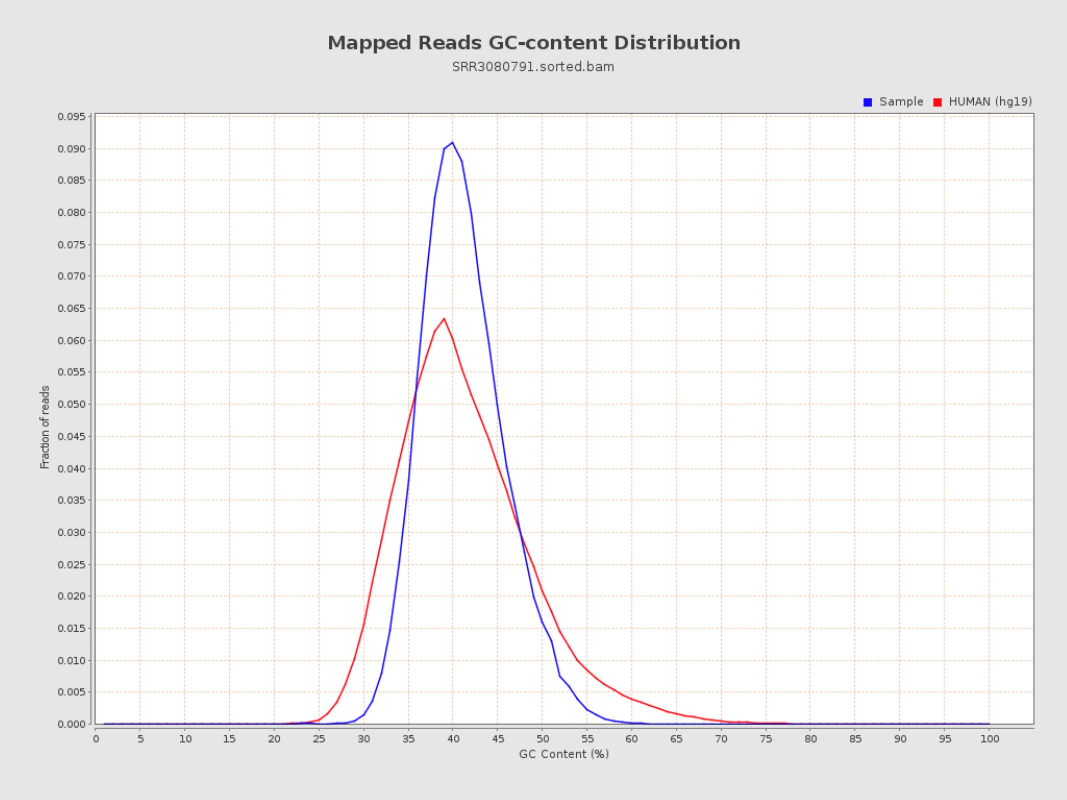
7. Results : Duplication Rate Histogram



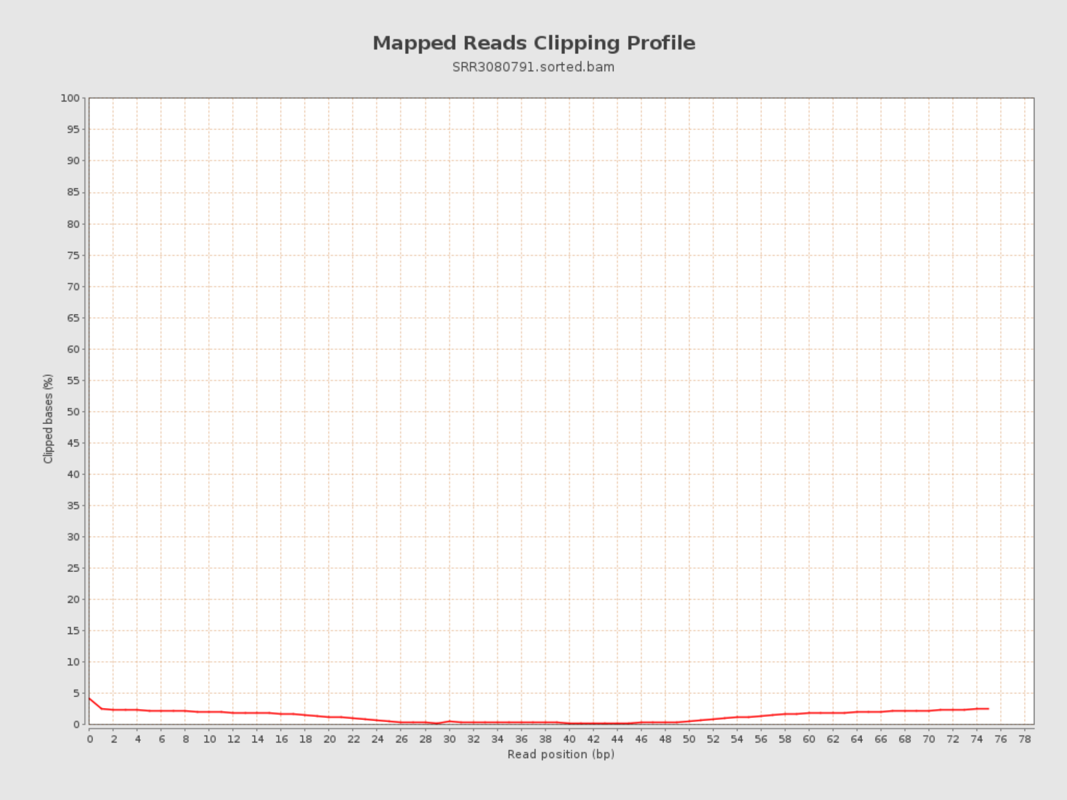
8. Results : Mapped Reads Nucleotide Content



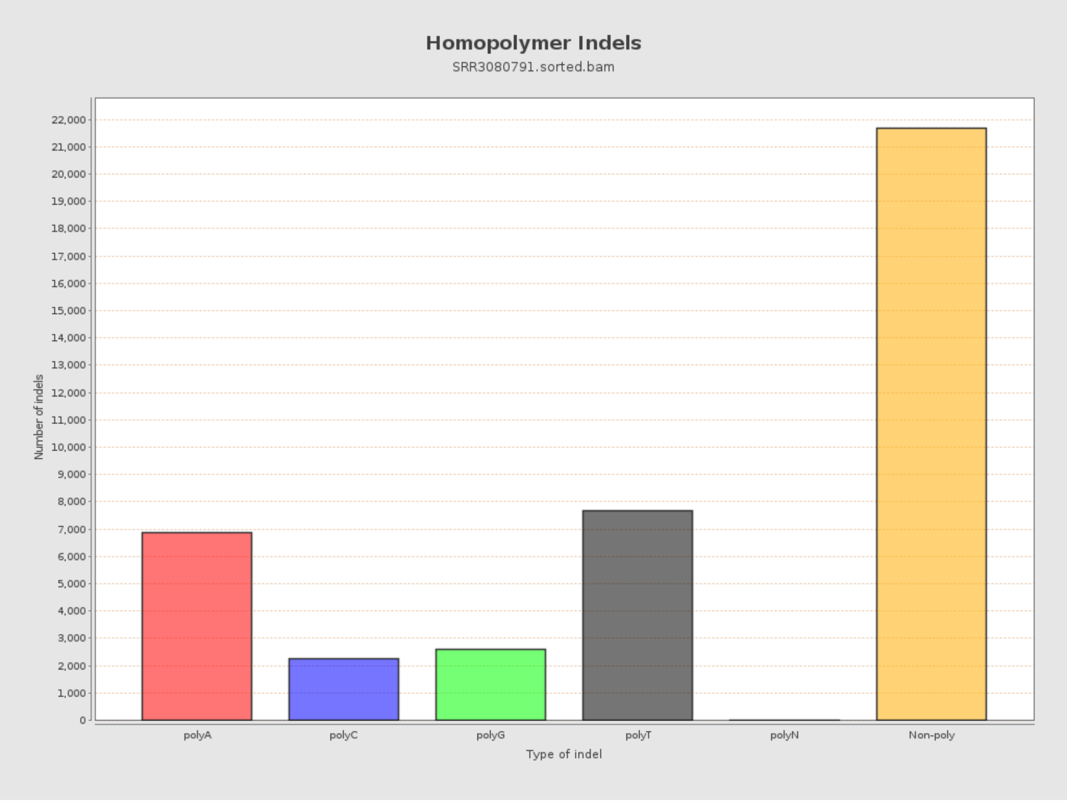
9. Results : Mapped Reads GC-content Distribution



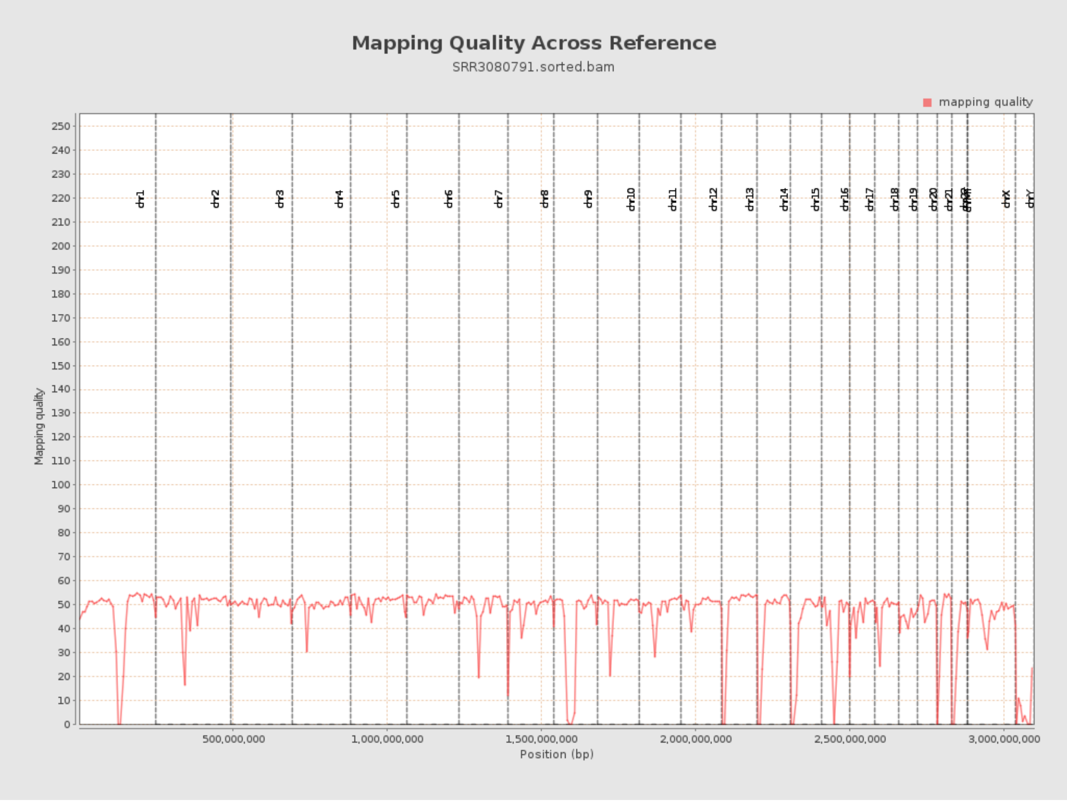
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram