Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:27:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080795.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_SRR3080795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:27:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,237,708
Mapped reads	2,863,993 / 88.46%
Unmapped reads	373,715 / 11.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,808 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	181,275 / 5.6%
Duplication rate	5.06%
Clipped reads	814,448 / 25.16%

2.2. ACGT Content

Number/percentage of A's	62,174,889 / 30.62%
Number/percentage of C's	37,574,262 / 18.51%
Number/percentage of T's	62,921,626 / 30.99%
Number/percentage of G's	40,329,288 / 19.86%
Number/percentage of N's	29,177 / 0.01%
GC Percentage	38.37%

2.3. Coverage

Mean	0.0656

Standard Deviation	0.7187

2.4. Mapping Quality

Mean Mapping Quality	47.86

2.5. Mismatches and indels

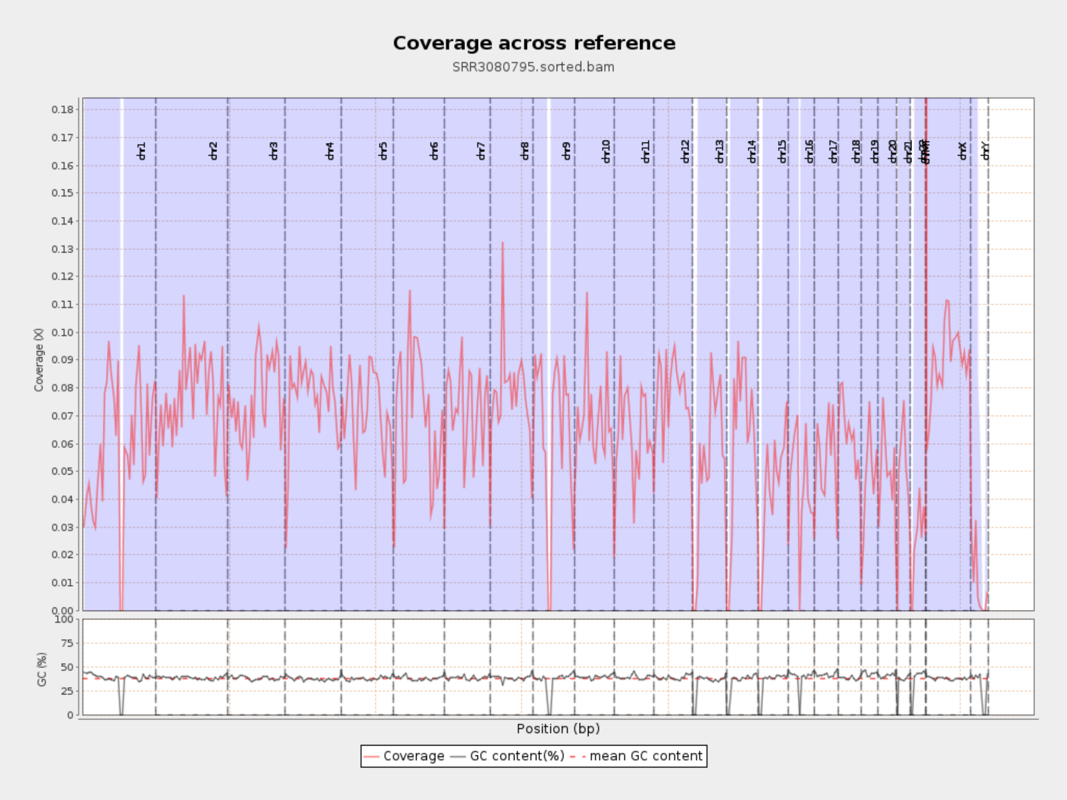
General error rate	0.83%
Mismatches	1,652,086
Insertions	16,356
Mapped reads with at least one insertion	0.57%
Deletions	42,500
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.02%

2.6. Chromosome stats

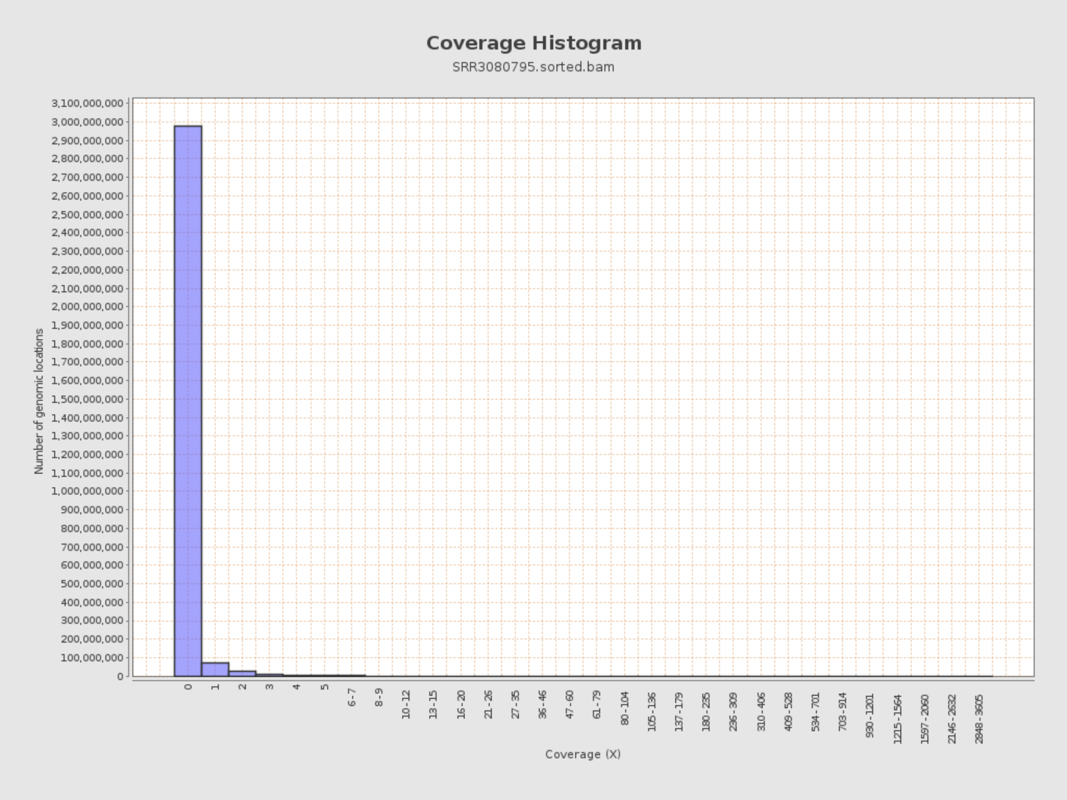
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14498332	0.0582	0.7922
chr2	243199373	18540499	0.0762	0.5861
chr3	198022430	15080726	0.0762	0.4303
chr4	191154276	14605073	0.0764	0.4768
chr5	180915260	12836031	0.071	0.4161
chr6	171115067	12167888	0.0711	0.5007
chr7	159138663	11471117	0.0721	0.6283

chr8	146364022	11468860	0.0784	2.3366
chr9	141213431	9221924	0.0653	0.5105
chr10	135534747	9233301	0.0681	0.6596
chr11	135006516	8600914	0.0637	0.4563
chr12	133851895	10432142	0.0779	0.439
chr13	115169878	6174746	0.0536	0.3648
chr14	107349540	6579599	0.0613	0.3969
chr15	102531392	4434438	0.0432	0.3182
chr16	90354753	3986259	0.0441	0.3485
chr17	81195210	4536052	0.0559	0.3896
chr18	78077248	4978012	0.0638	0.7986
chr19	59128983	2868389	0.0485	0.5471
chr20	63025520	3224735	0.0512	0.3566
chr21	48129895	2290420	0.0476	0.3742
chr22	51304566	1288924	0.0251	0.2327
chrMT	16571	102765	6.2015	4.4237
chrX	155270560	13918178	0.0896	0.4796
chrY	59373566	566481	0.0095	0.2837

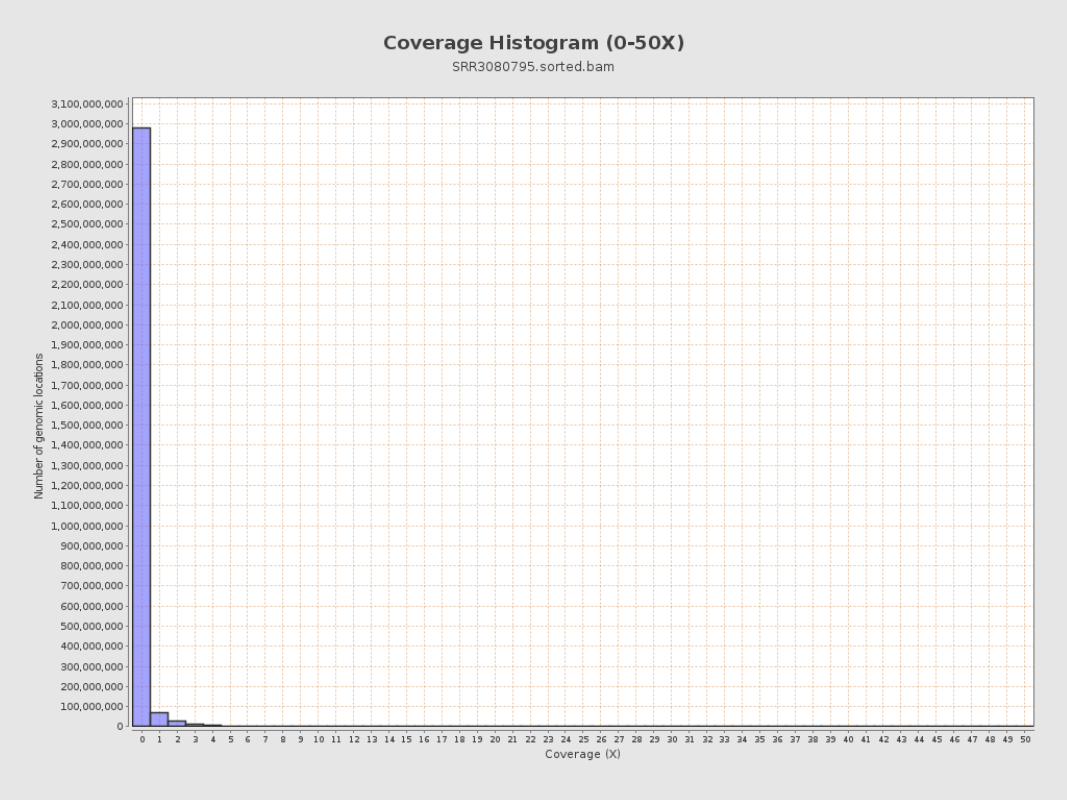
3. Results : Coverage across reference



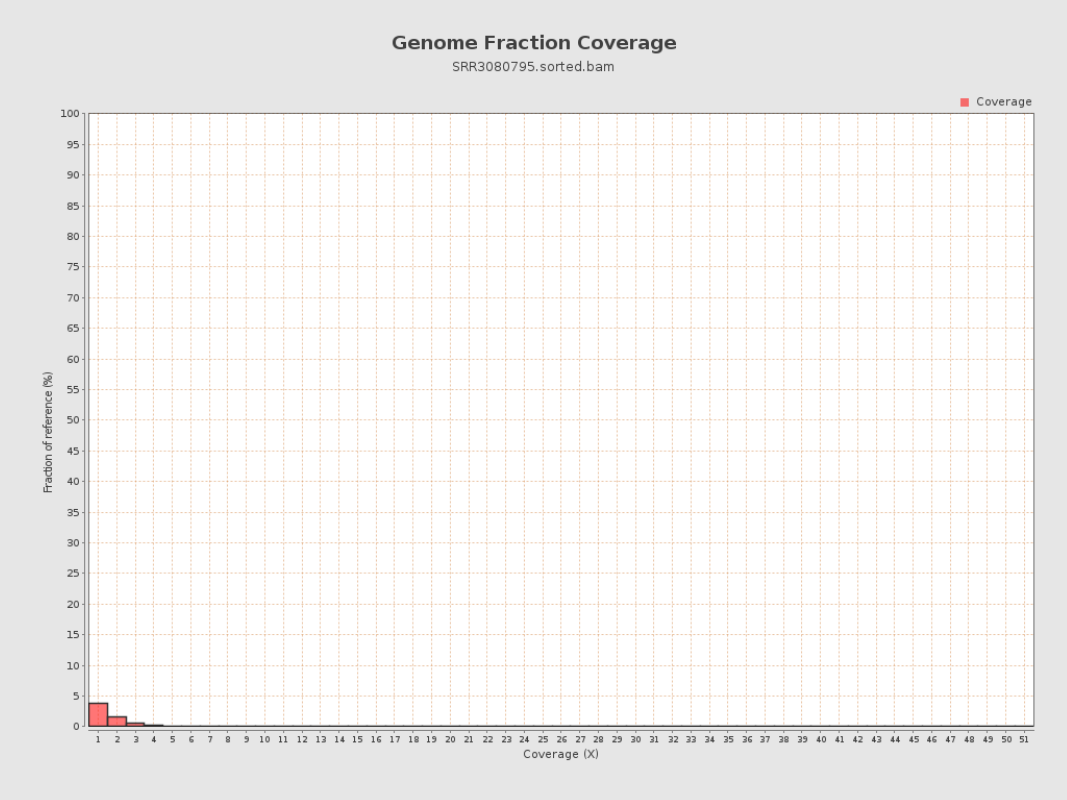
4. Results : Coverage Histogram



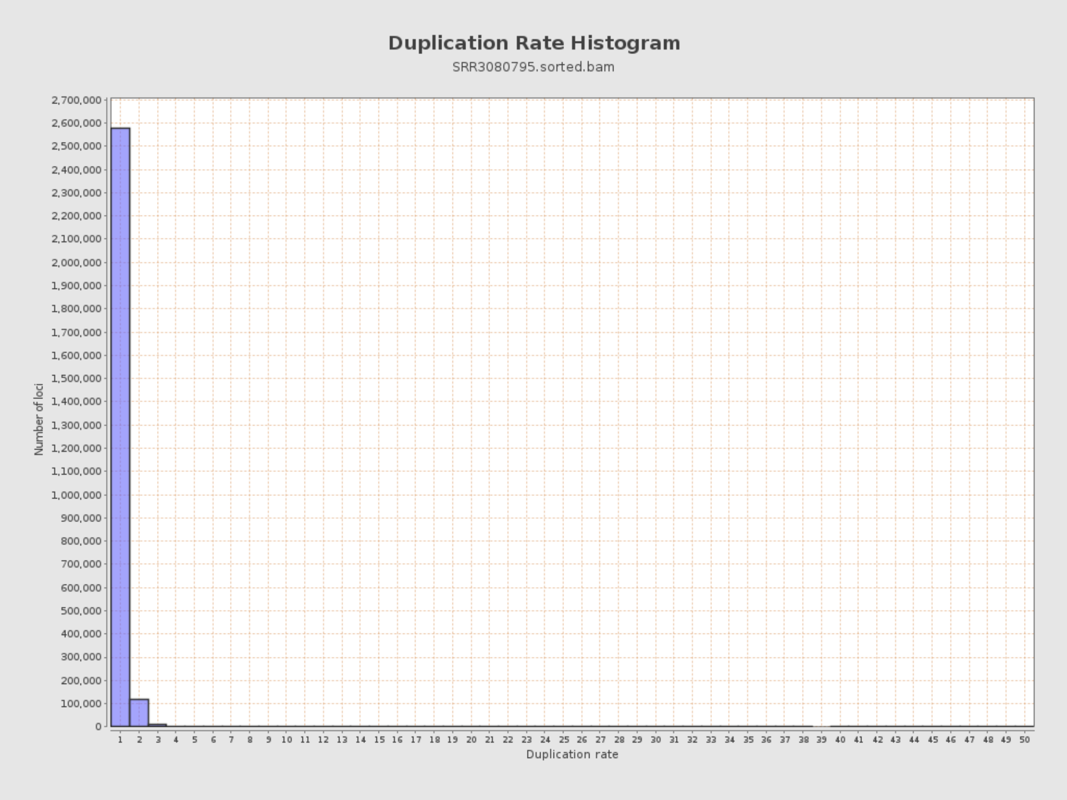
5. Results : Coverage Histogram (0-50X)



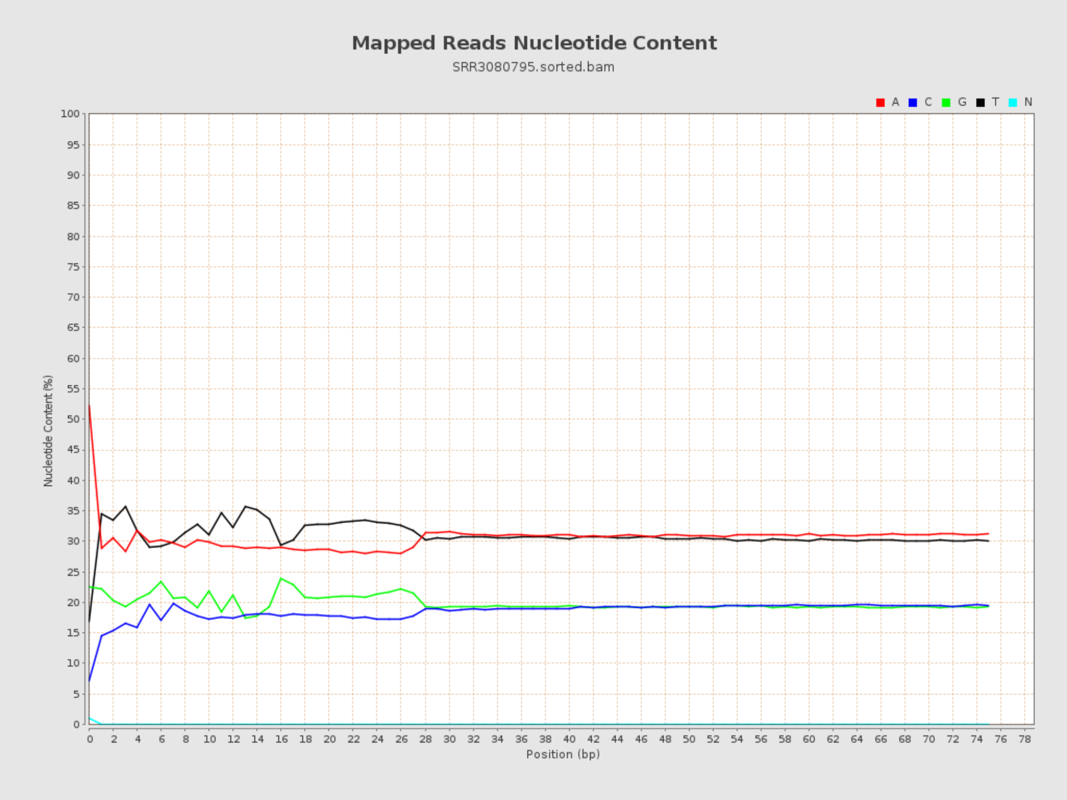
6. Results : Genome Fraction Coverage



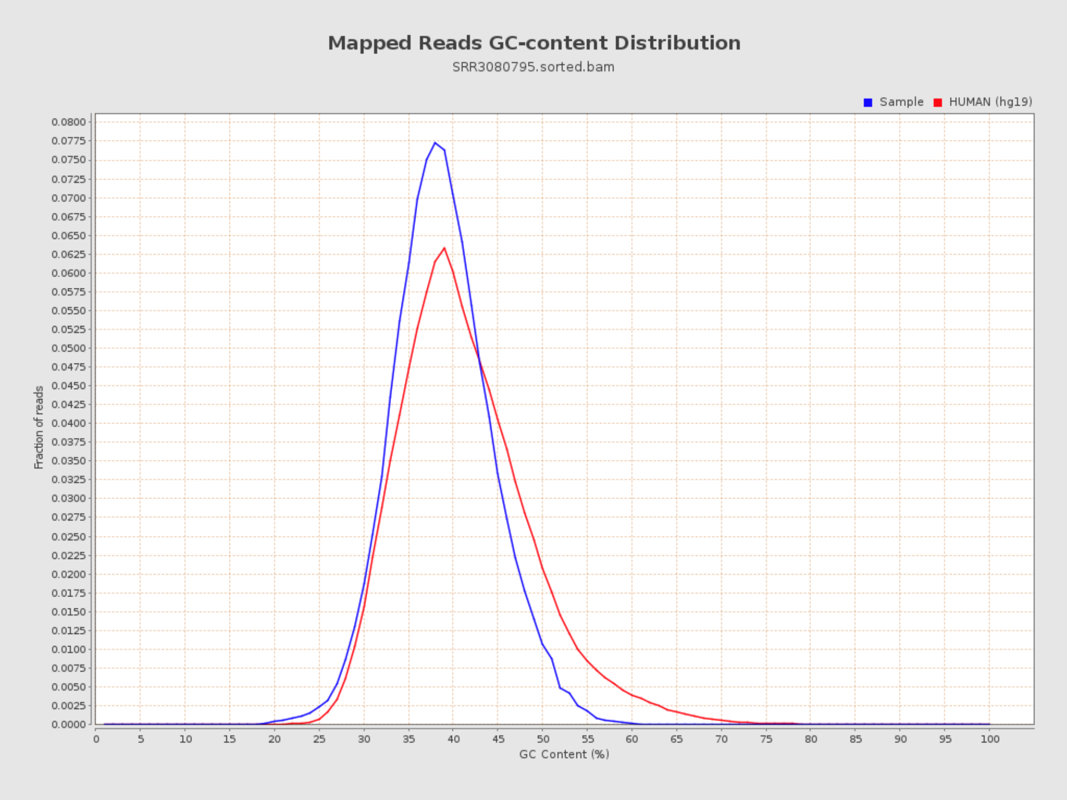
7. Results : Duplication Rate Histogram



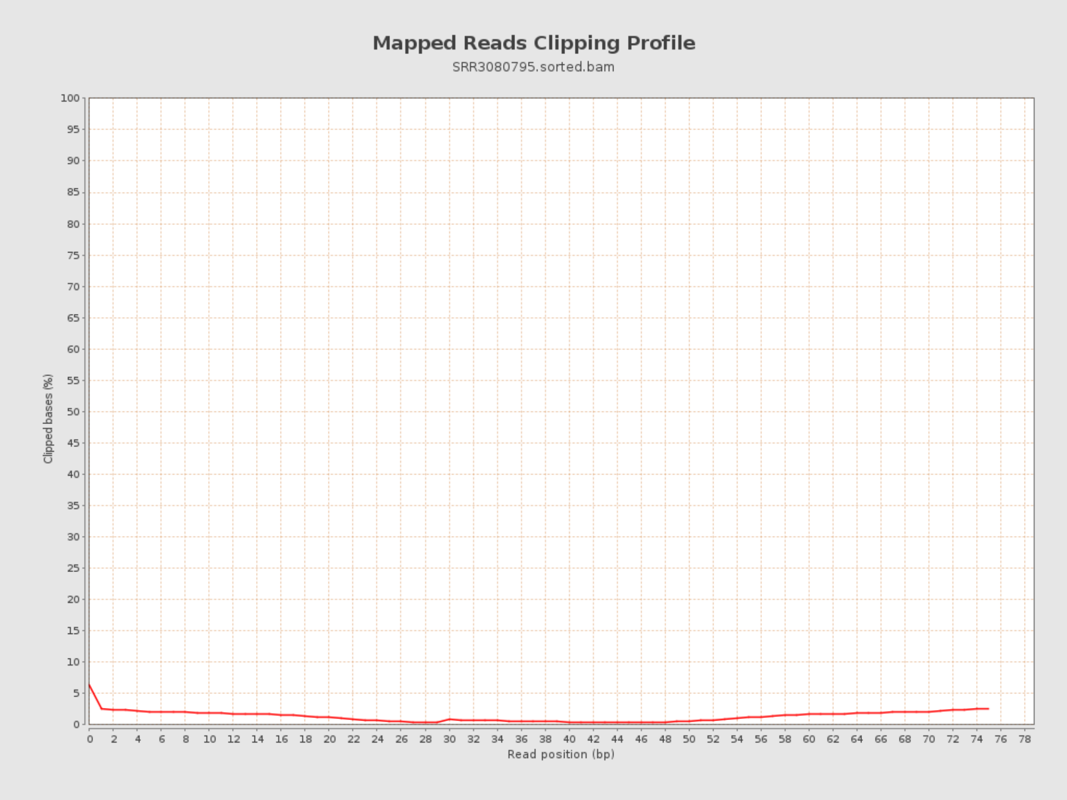
8. Results : Mapped Reads Nucleotide Content



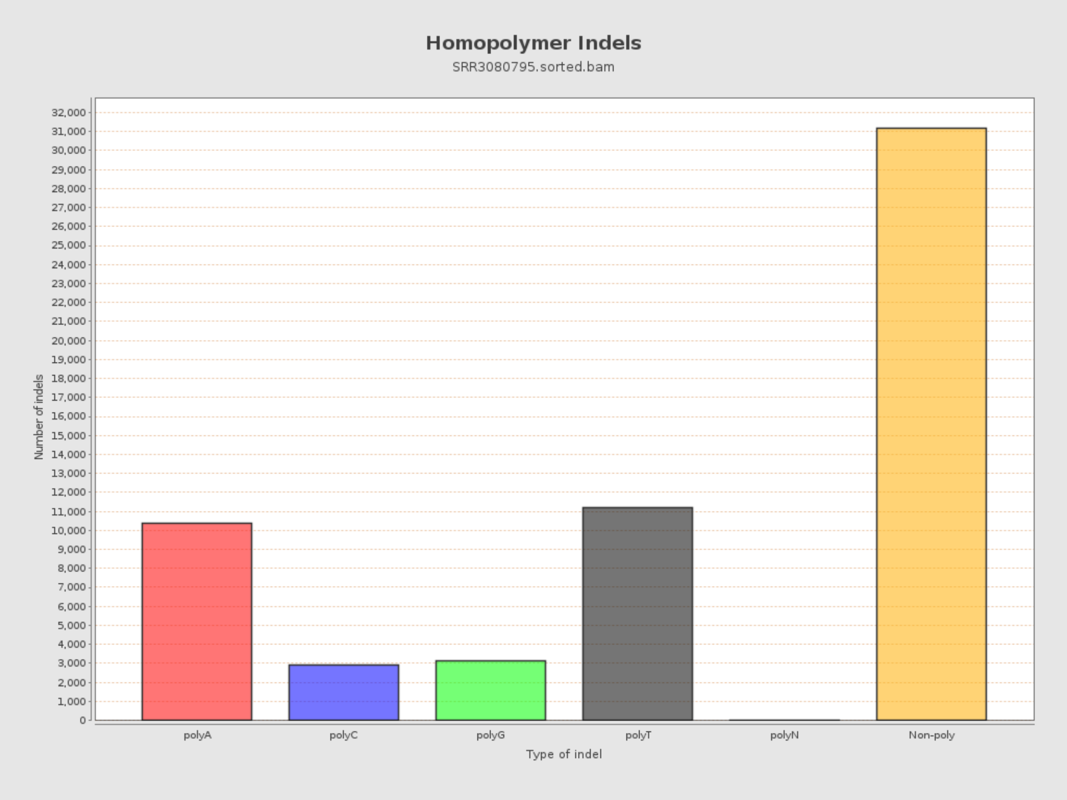
9. Results : Mapped Reads GC-content Distribution



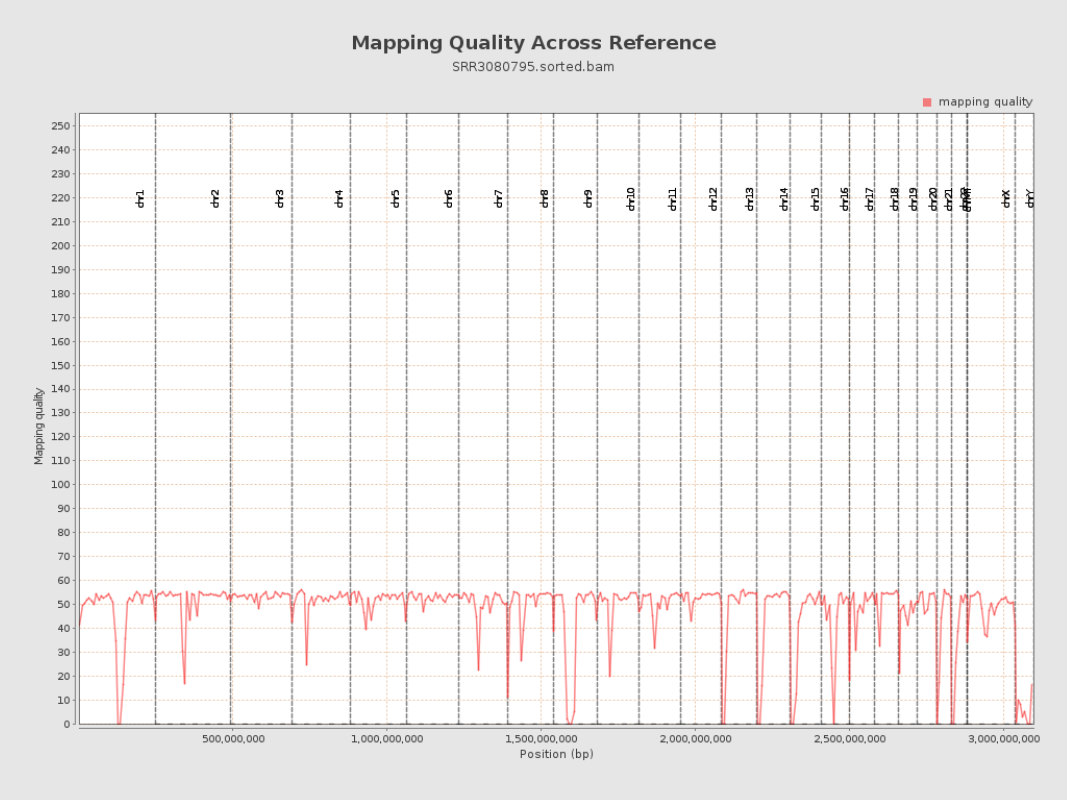
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram