Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:19:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231795.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_SRR6231795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:19:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,884,312
Mapped reads	4,408,700 / 90.26%
Unmapped reads	475,612 / 9.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,383 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	399,721 / 8.18%
Duplication rate	7.43%
Clipped reads	2,760,629 / 56.52%

2.2. ACGT Content

Number/percentage of A's	64,413,150 / 23.36%
Number/percentage of C's	51,920,122 / 18.83%
Number/percentage of T's	87,984,770 / 31.91%
Number/percentage of G's	71,317,492 / 25.86%
Number/percentage of N's	100,350 / 0.04%
GC Percentage	44.69%

2.3. Coverage

Mean	0.0891

Standard Deviation	0.9035

2.4. Mapping Quality

Mean Mapping Quality	37.57

2.5. Mismatches and indels

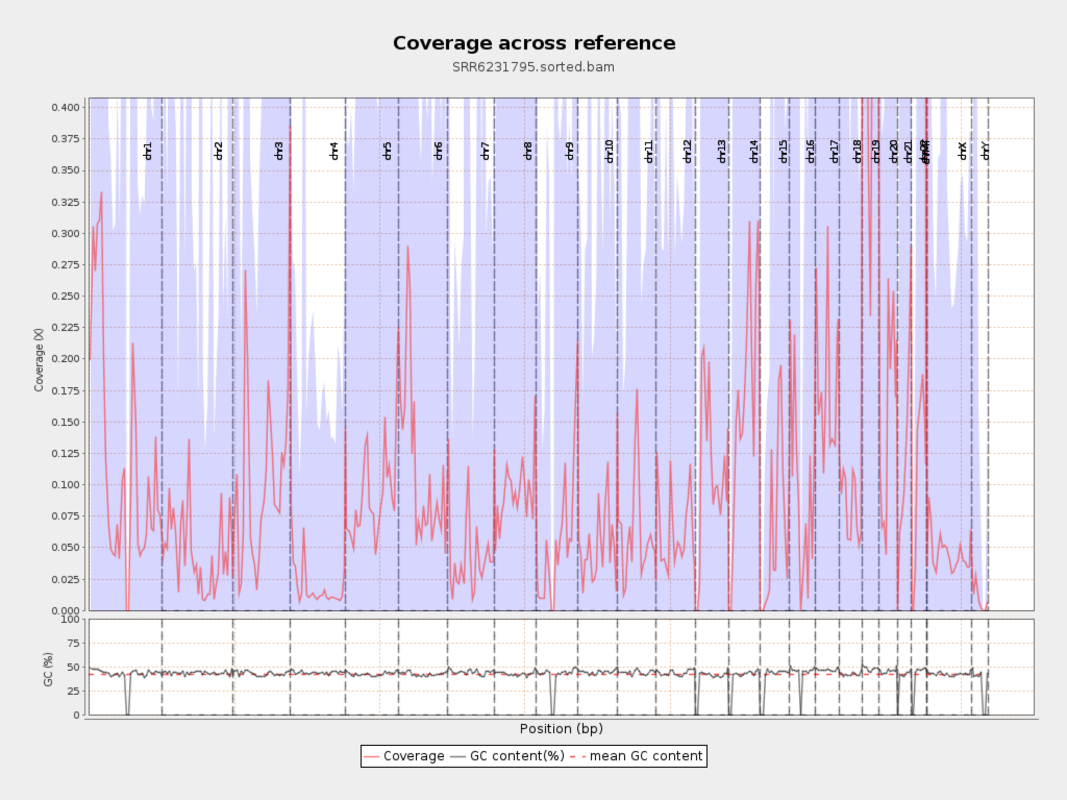
General error rate	0.76%
Mismatches	2,052,650
Insertions	22,873
Mapped reads with at least one insertion	0.51%
Deletions	83,863
Mapped reads with at least one deletion	1.88%
Homopolymer indels	42.9%

2.6. Chromosome stats

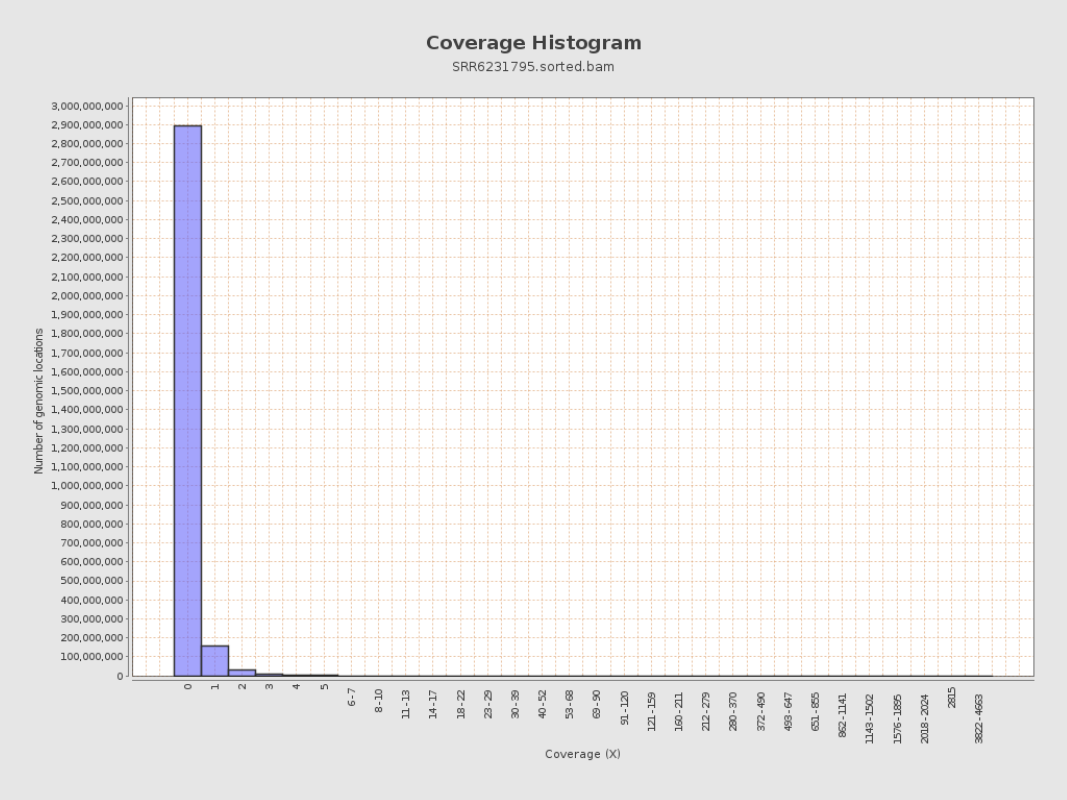
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29653072	0.119	1.4704
chr2	243199373	11577631	0.0476	2.1005
chr3	198022430	19822092	0.1001	0.426
chr4	191154276	3549022	0.0186	0.2396
chr5	180915260	16367653	0.0905	0.3976
chr6	171115067	19568911	0.1144	0.8038
chr7	159138663	6541293	0.0411	0.5417

chr8	146364022	13564405	0.0927	0.617
chr9	141213431	7165149	0.0507	0.4984
chr10	135534747	6831004	0.0504	0.3715
chr11	135006516	8650298	0.0641	0.5625
chr12	133851895	8660513	0.0647	0.3298
chr13	115169878	12306459	0.1069	0.528
chr14	107349540	17585461	0.1638	0.5626
chr15	102531392	6494594	0.0633	0.4306
chr16	90354753	8413974	0.0931	0.4828
chr17	81195210	14839574	0.1828	0.585
chr18	78077248	6630977	0.0849	1.5897
chr19	59128983	28634720	0.4843	1.2337
chr20	63025520	9565914	0.1518	0.5484
chr21	48129895	5966387	0.124	0.4801
chr22	51304566	5539434	0.108	0.4263
chrMT	16571	281097	16.9632	19.5168
chrX	155270560	7100063	0.0457	0.3988
chrY	59373566	564714	0.0095	0.2839

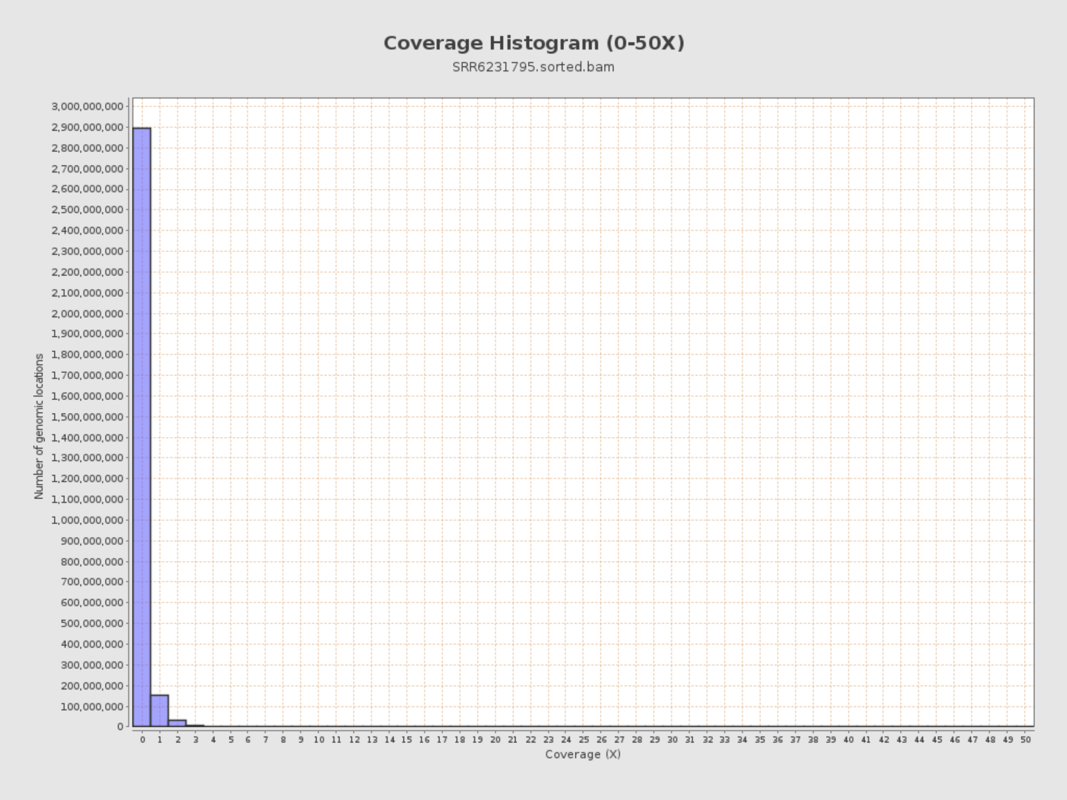
3. Results : Coverage across reference



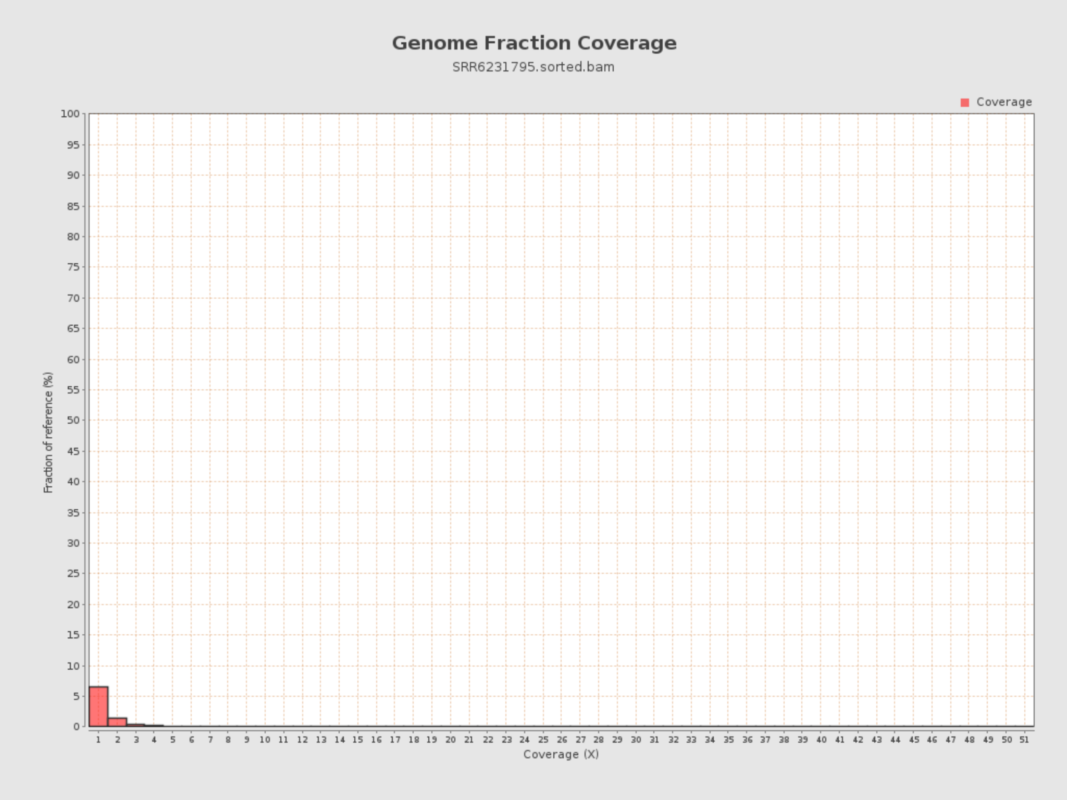
4. Results : Coverage Histogram



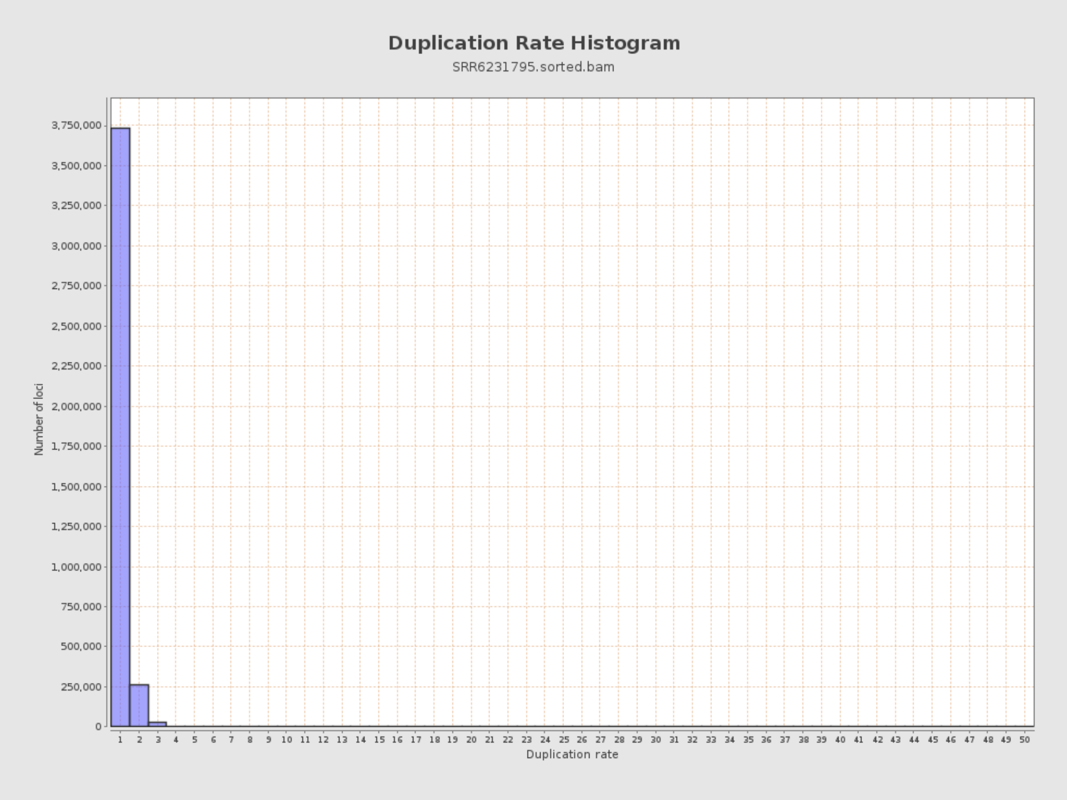
5. Results : Coverage Histogram (0-50X)



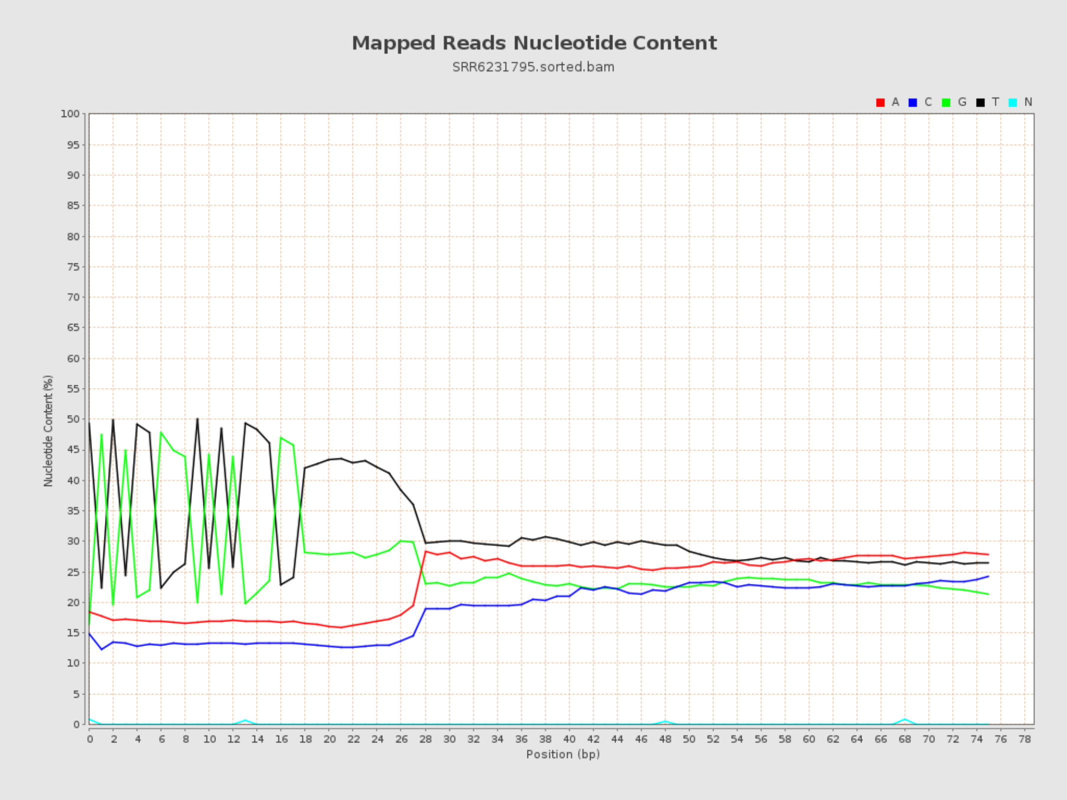
6. Results : Genome Fraction Coverage



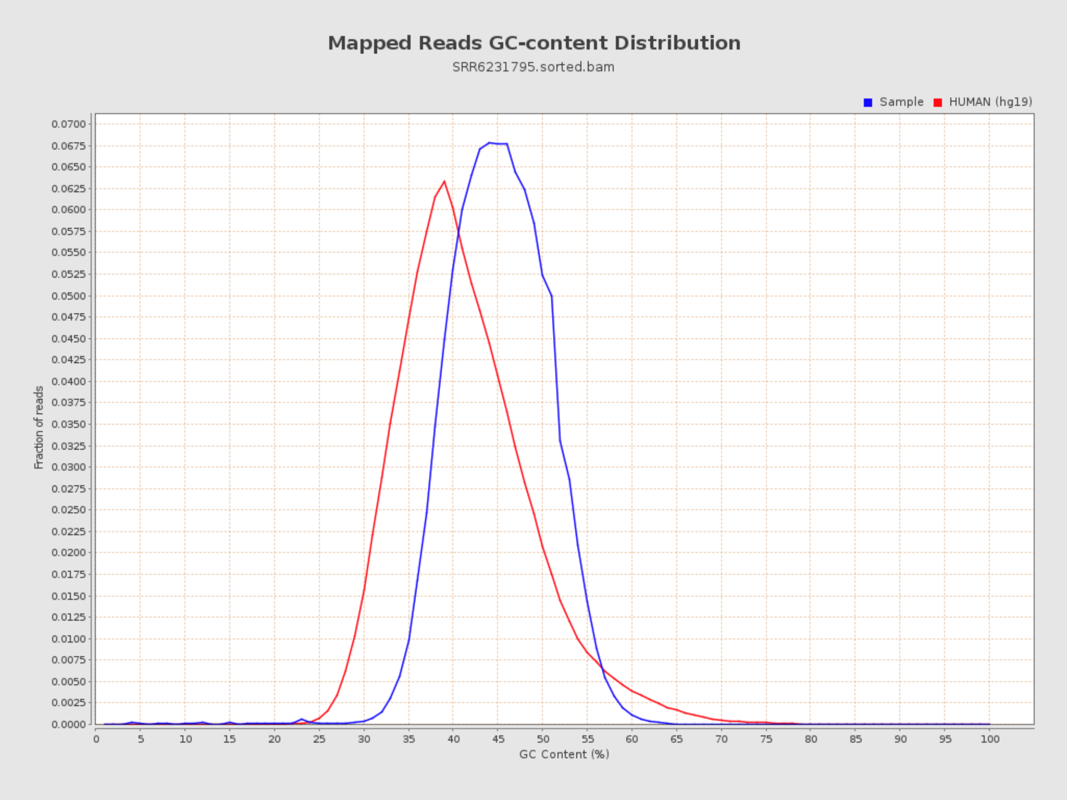
7. Results : Duplication Rate Histogram



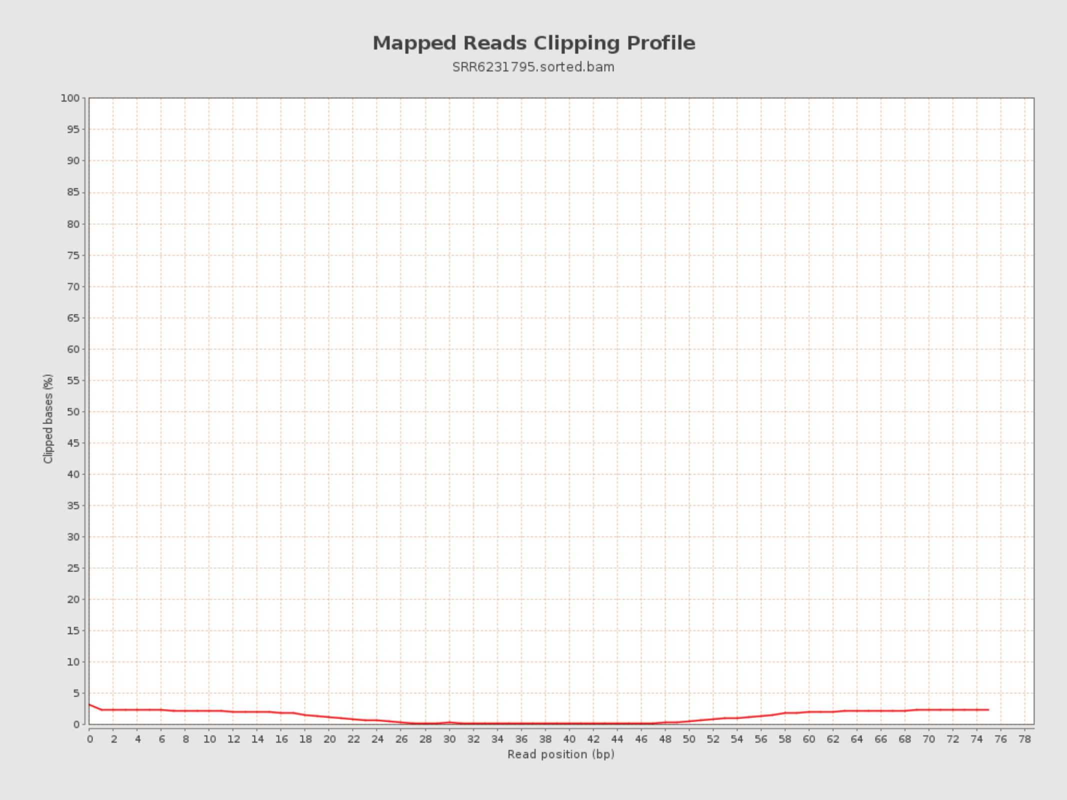
8. Results : Mapped Reads Nucleotide Content



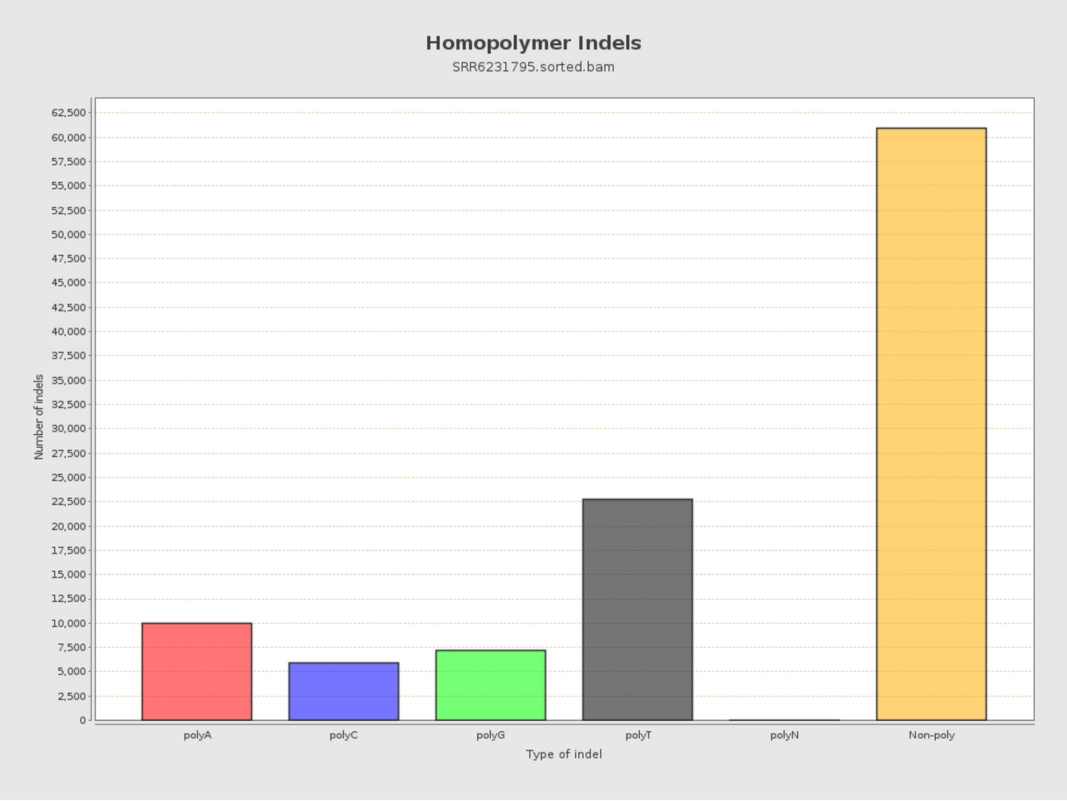
9. Results : Mapped Reads GC-content Distribution



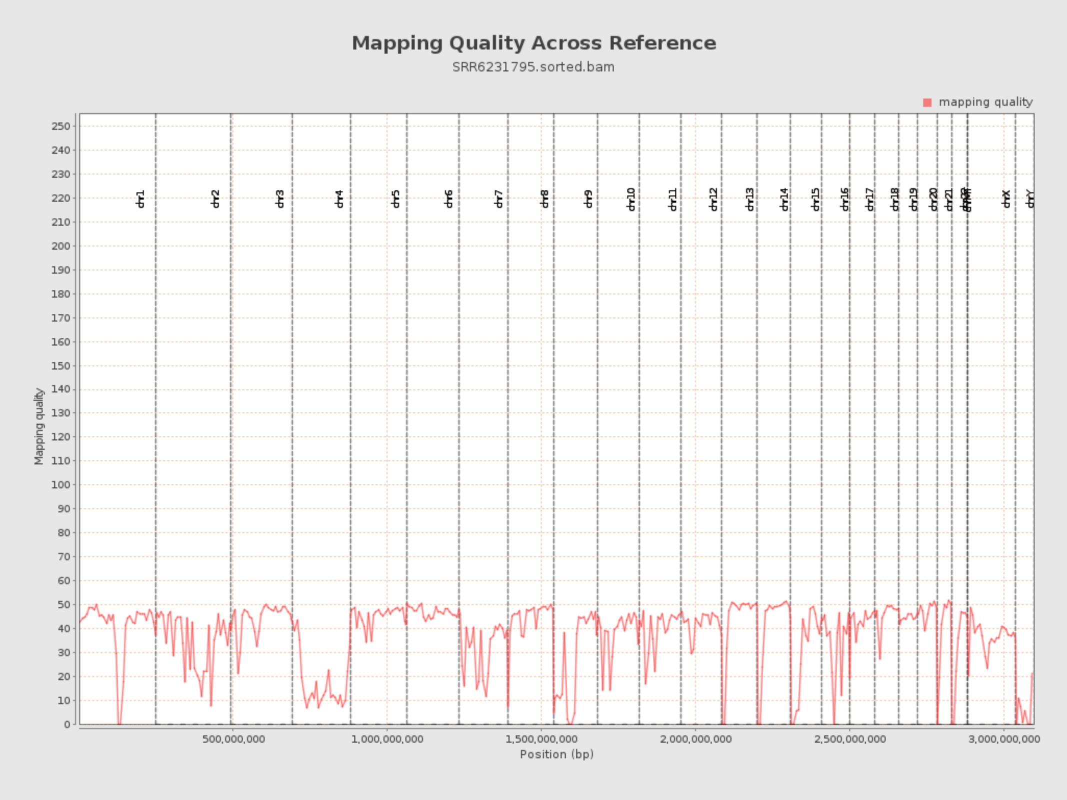
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram