Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 04:10:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231805.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_SRR6231805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 04:10:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,860,469
Mapped reads	7,705,871 / 78.15%
Unmapped reads	2,154,598 / 21.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	99,677 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	990,375 / 10.04%
Duplication rate	8.63%
Clipped reads	4,221,278 / 42.81%

2.2. ACGT Content

Number/percentage of A's	148,252,260 / 29.64%
Number/percentage of C's	99,249,476 / 19.85%
Number/percentage of T's	146,044,648 / 29.2%
Number/percentage of G's	106,526,530 / 21.3%
Number/percentage of N's	38,151 / 0.01%
GC Percentage	41.15%

2.3. Coverage

Mean	0.1616

Standard Deviation	7.0542

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

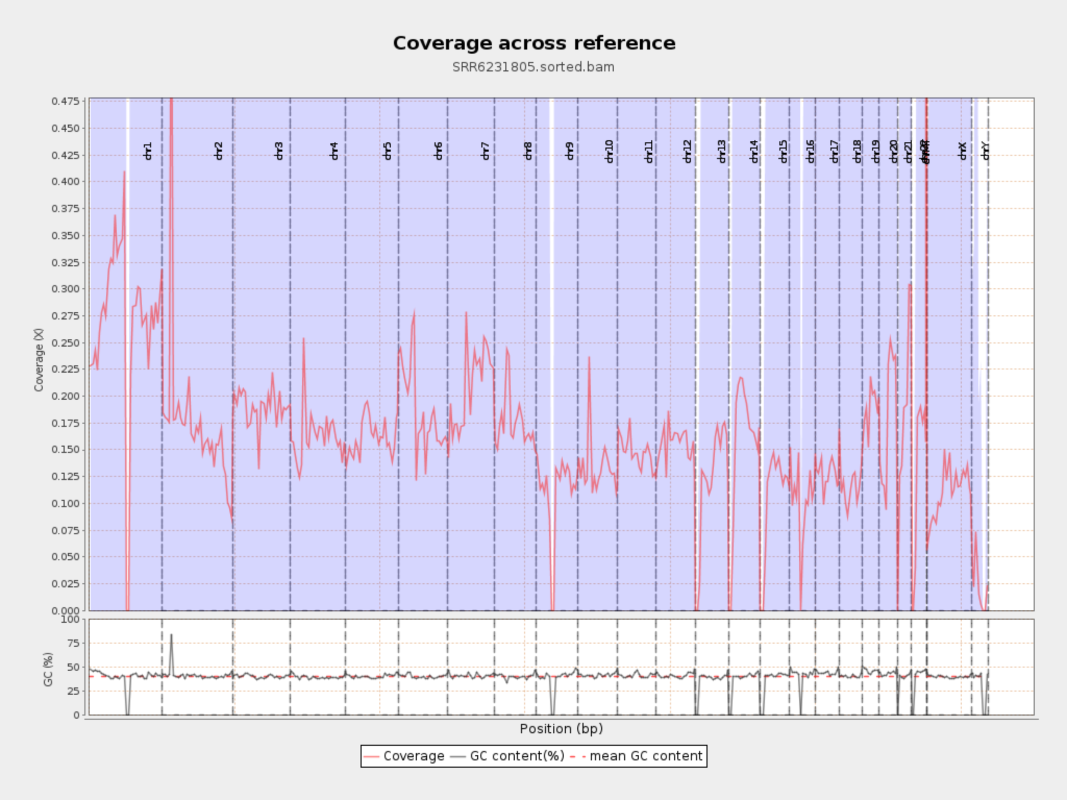
General error rate	0.58%
Mismatches	2,819,651
Insertions	36,180
Mapped reads with at least one insertion	0.47%
Deletions	103,023
Mapped reads with at least one deletion	1.32%
Homopolymer indels	47.15%

2.6. Chromosome stats

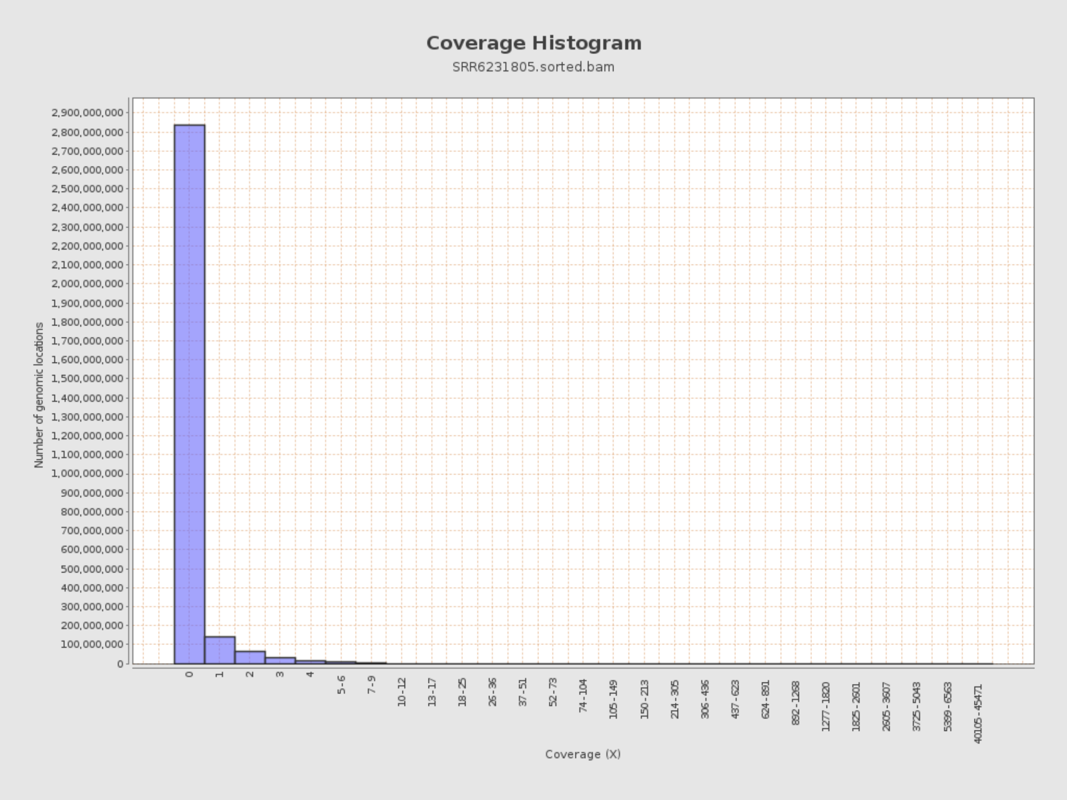
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	67224600	0.2697	2.8471
chr2	243199373	42975105	0.1767	24.6286
chr3	198022430	37691530	0.1903	0.7984
chr4	191154276	31038641	0.1624	0.7968
chr5	180915260	29228584	0.1616	0.6724
chr6	171115067	32110640	0.1877	0.8561
chr7	159138663	33426442	0.21	1.6369

chr8	146364022	25614119	0.175	3.9411
chr9	141213431	15291279	0.1083	0.7861
chr10	135534747	18224289	0.1345	1.2684
chr11	135006516	19844712	0.147	0.9501
chr12	133851895	20912996	0.1562	0.6607
chr13	115169878	13867711	0.1204	0.5892
chr14	107349540	16540149	0.1541	0.7186
chr15	102531392	10863511	0.106	0.5236
chr16	90354753	9153417	0.1013	0.6284
chr17	81195210	10266382	0.1264	0.6822
chr18	78077248	9005403	0.1153	1.548
chr19	59128983	11107244	0.1878	1.7803
chr20	63025520	11262045	0.1787	0.7508
chr21	48129895	8814856	0.1831	0.7867
chr22	51304566	6289251	0.1226	0.5707
chrMT	16571	1151676	69.4995	55.3028
chrX	155270560	17122445	0.1103	0.6417
chrY	59373566	1258068	0.0212	0.4874

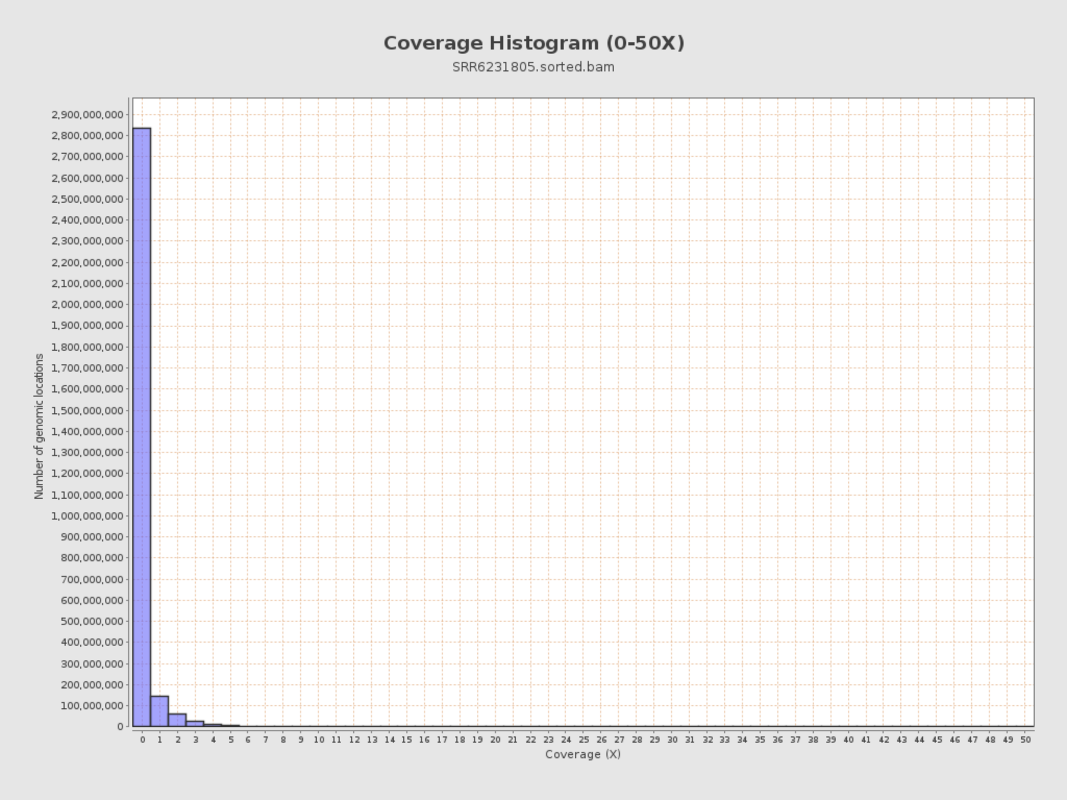
3. Results : Coverage across reference



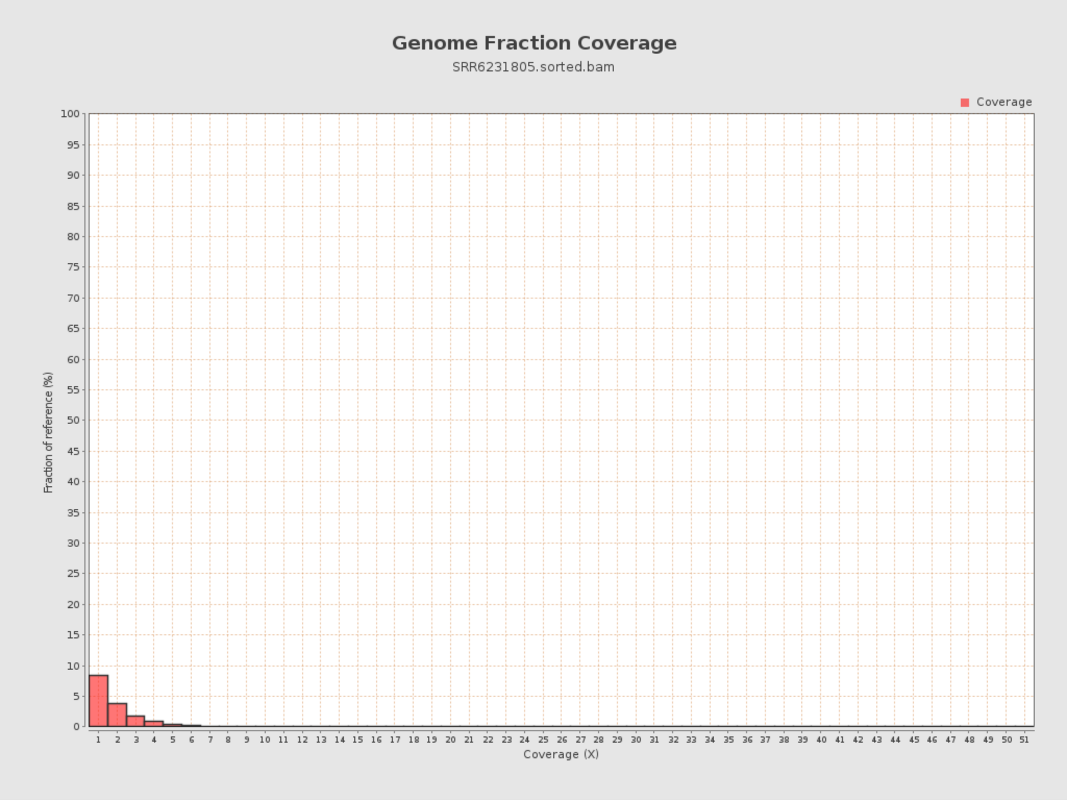
4. Results : Coverage Histogram



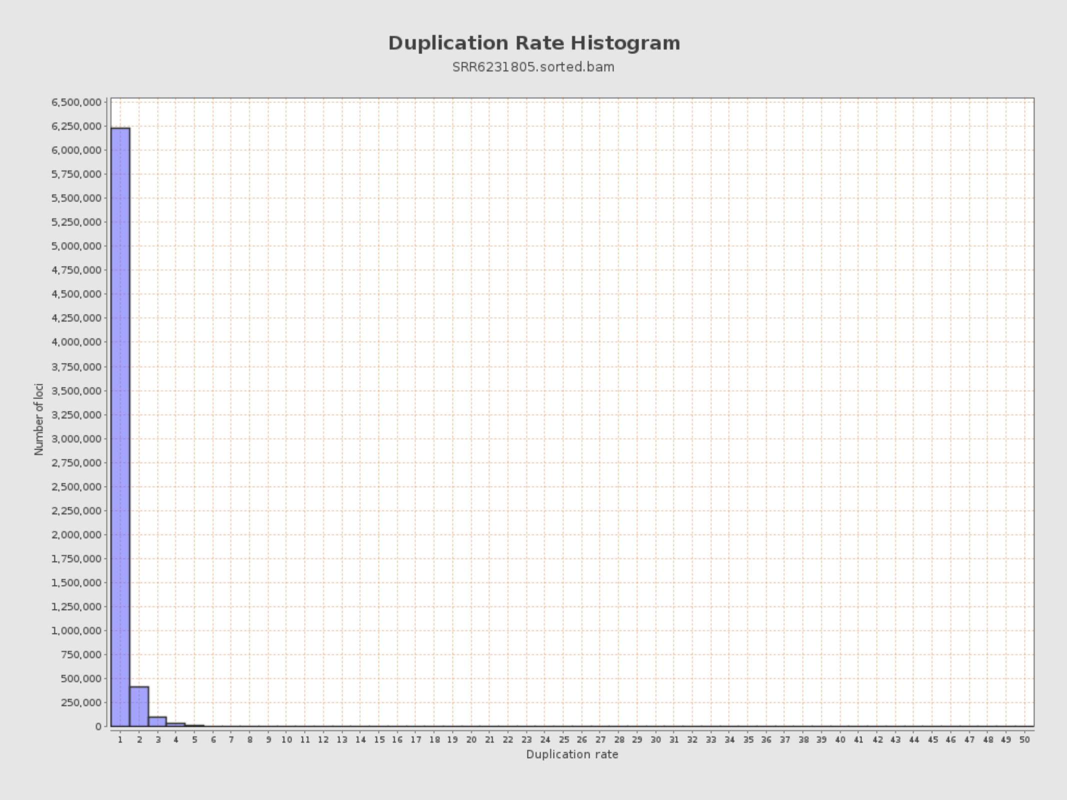
5. Results : Coverage Histogram (0-50X)



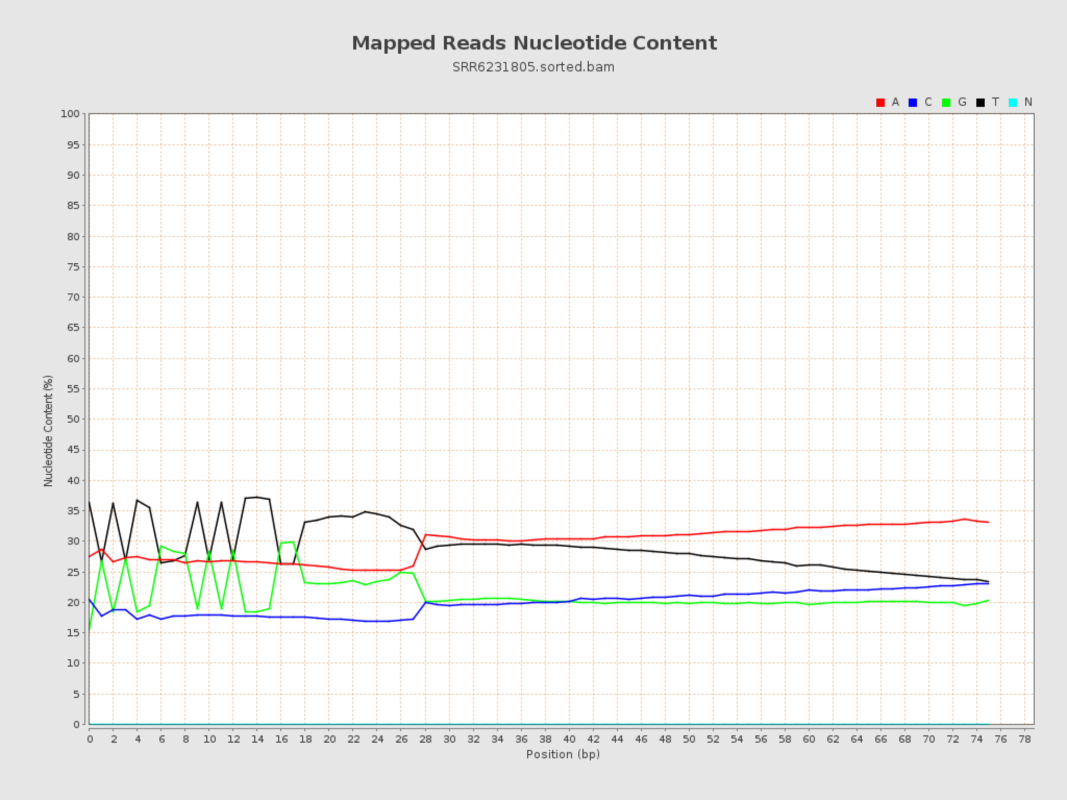
6. Results : Genome Fraction Coverage



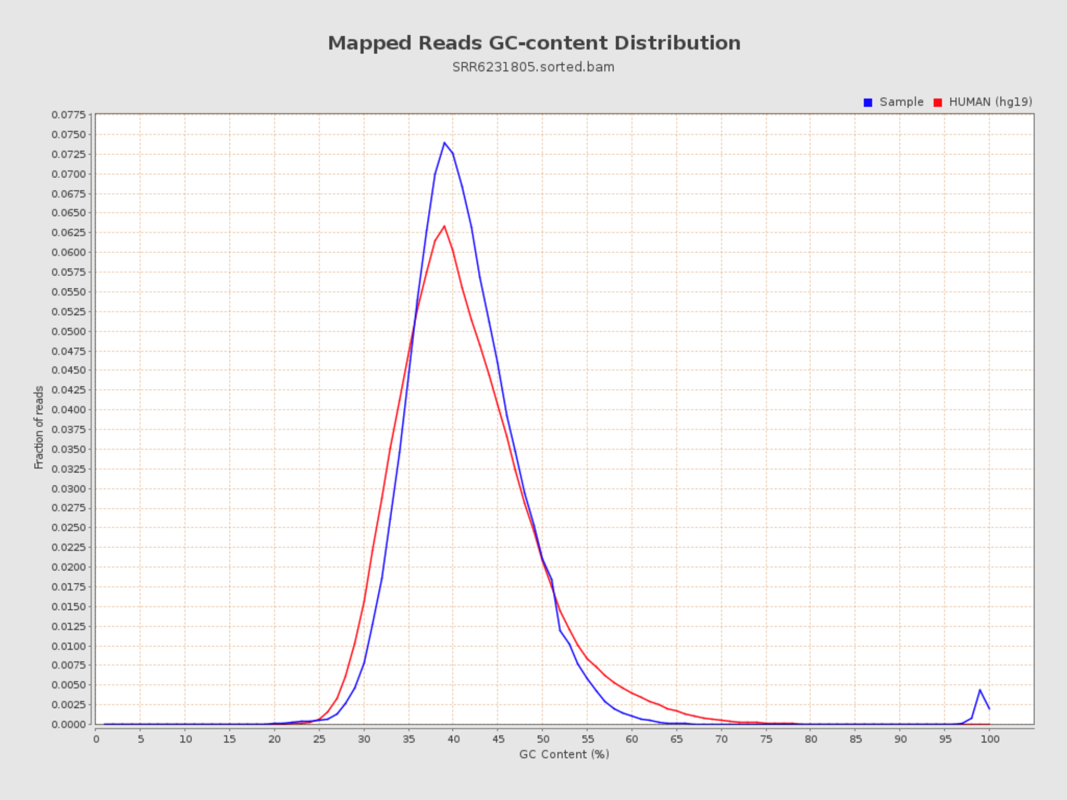
7. Results : Duplication Rate Histogram



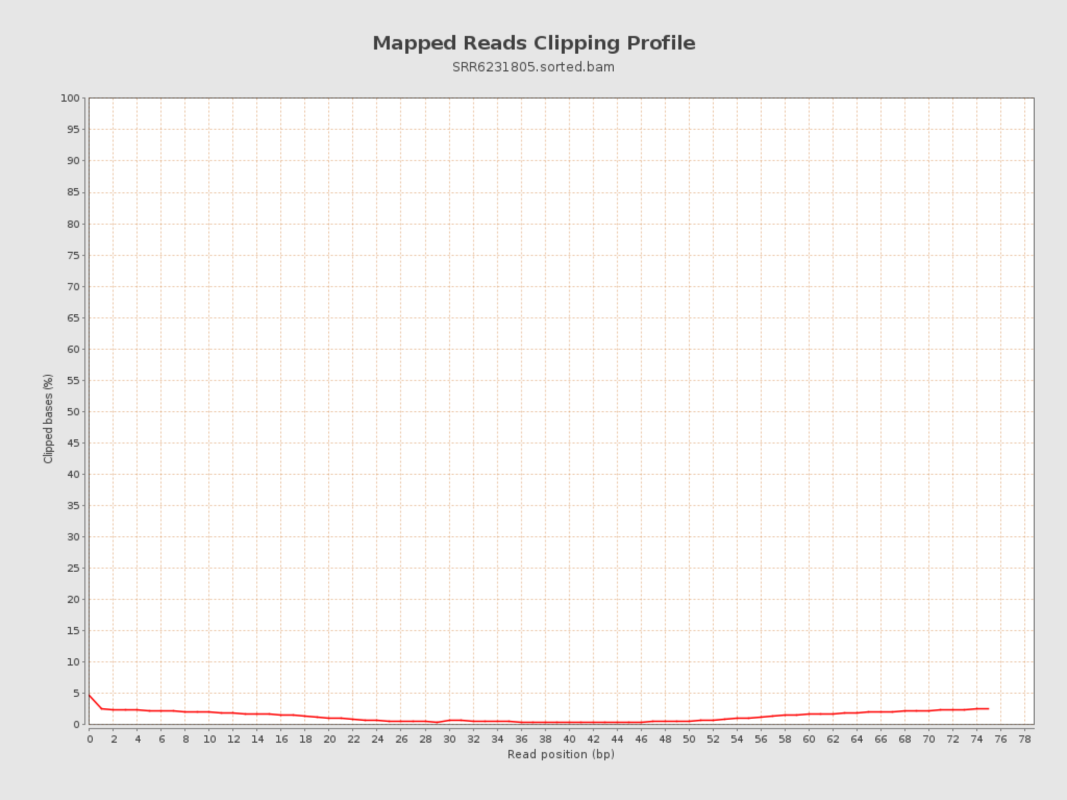
8. Results : Mapped Reads Nucleotide Content



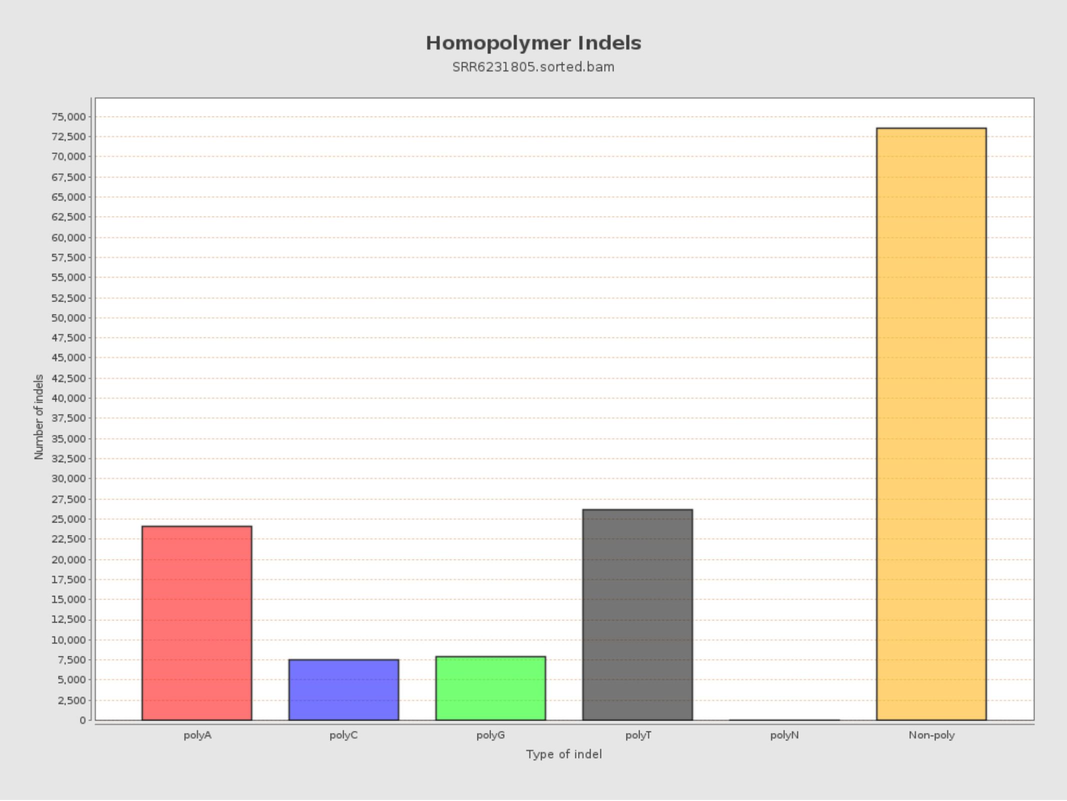
9. Results : Mapped Reads GC-content Distribution



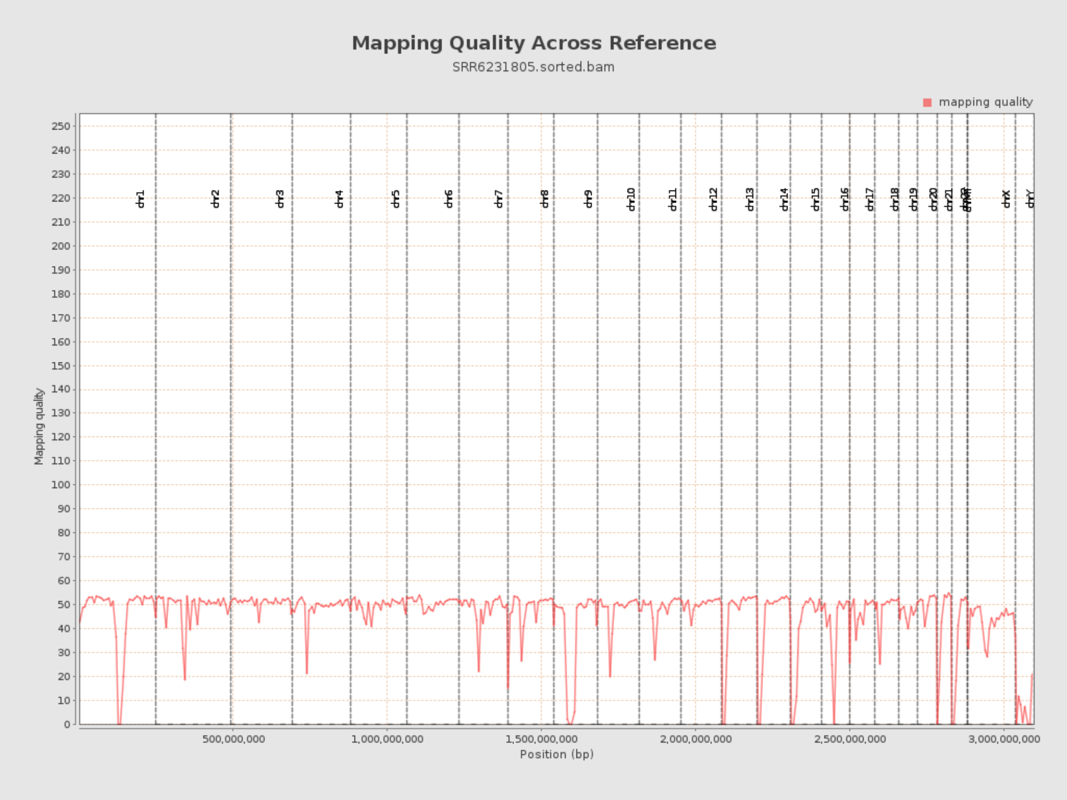
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram