Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:56:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231851.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_SRR6231851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231851.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:56:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,135,278
Mapped reads	3,794,868 / 91.77%
Unmapped reads	340,410 / 8.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,710 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	295,393 / 7.14%
Duplication rate	6.39%
Clipped reads	2,247,024 / 54.34%

2.2. ACGT Content

Number/percentage of A's	57,159,043 / 24%
Number/percentage of C's	43,552,785 / 18.28%
Number/percentage of T's	77,173,016 / 32.4%
Number/percentage of G's	60,238,534 / 25.29%
Number/percentage of N's	85,683 / 0.04%
GC Percentage	43.57%

2.3. Coverage

Mean	0.077

Standard Deviation	0.7189

2.4. Mapping Quality

Mean Mapping Quality	40.93

2.5. Mismatches and indels

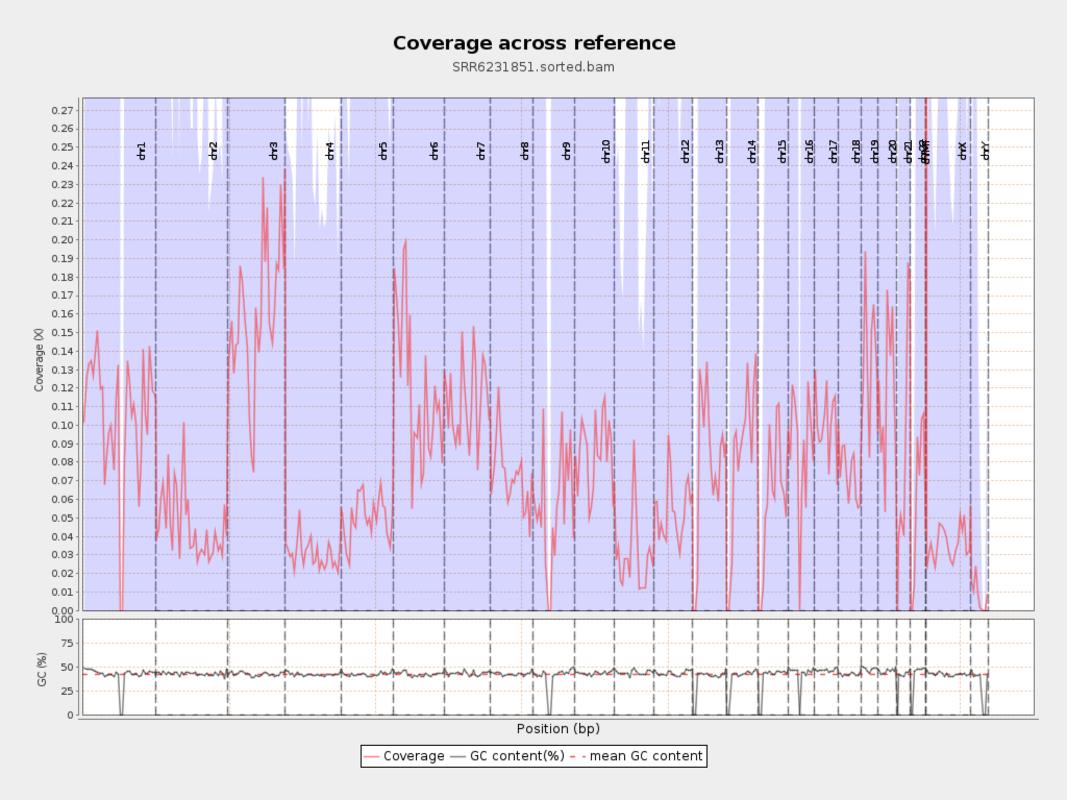
General error rate	0.64%
Mismatches	1,496,803
Insertions	15,920
Mapped reads with at least one insertion	0.42%
Deletions	58,537
Mapped reads with at least one deletion	1.53%
Homopolymer indels	43.64%

2.6. Chromosome stats

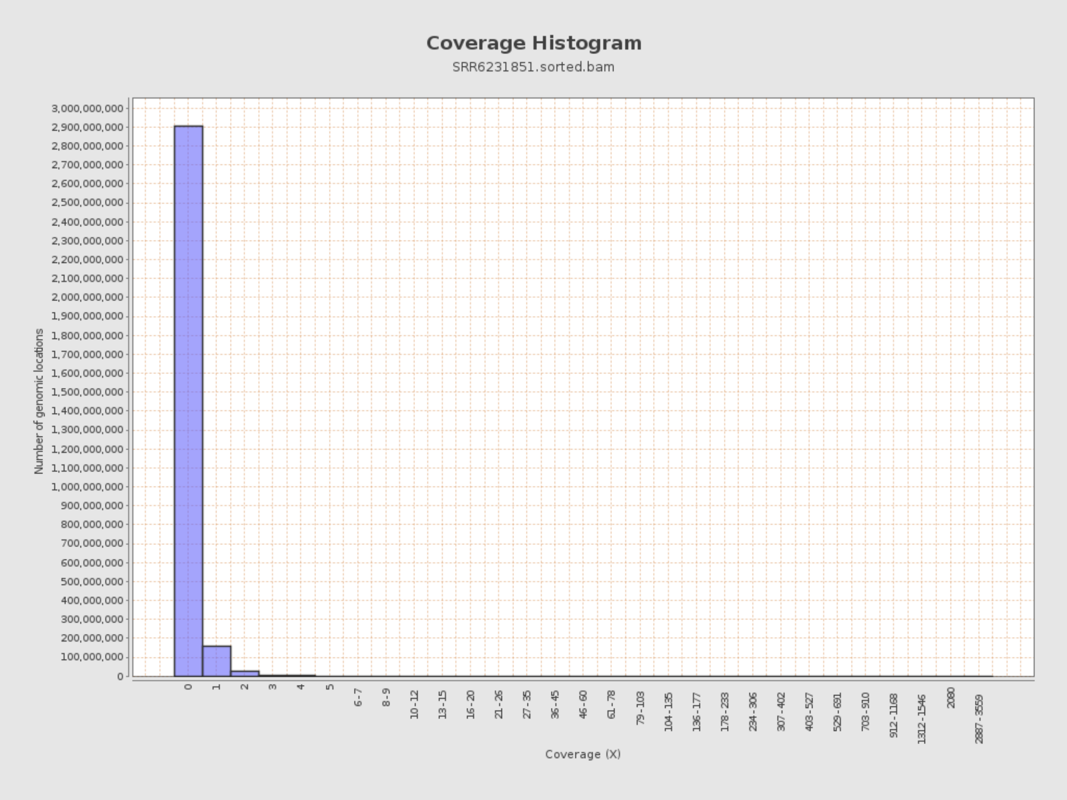
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26021327	0.1044	1.1528
chr2	243199373	11207878	0.0461	1.5874
chr3	198022430	31431359	0.1587	0.4961
chr4	191154276	5838220	0.0305	0.2366
chr5	180915260	9183118	0.0508	0.2793
chr6	171115067	20293249	0.1186	0.6826
chr7	159138663	18043997	0.1134	1.0158

chr8	146364022	10644642	0.0727	0.5061
chr9	141213431	7762715	0.055	0.3752
chr10	135534747	11577331	0.0854	0.5227
chr11	135006516	4105267	0.0304	0.2669
chr12	133851895	7341140	0.0548	0.2916
chr13	115169878	8979866	0.078	0.3885
chr14	107349540	9005361	0.0839	0.362
chr15	102531392	6051886	0.059	0.3569
chr16	90354753	7715702	0.0854	0.3863
chr17	81195210	8323430	0.1025	0.3999
chr18	78077248	5766559	0.0739	0.9531
chr19	59128983	8027403	0.1358	0.7595
chr20	63025520	7353587	0.1167	0.4329
chr21	48129895	4150880	0.0862	0.376
chr22	51304566	3100724	0.0604	0.2988
chrMT	16571	264316	15.9505	9.3081
chrX	155270560	5620952	0.0362	0.2739
chrY	59373566	501851	0.0085	0.1958

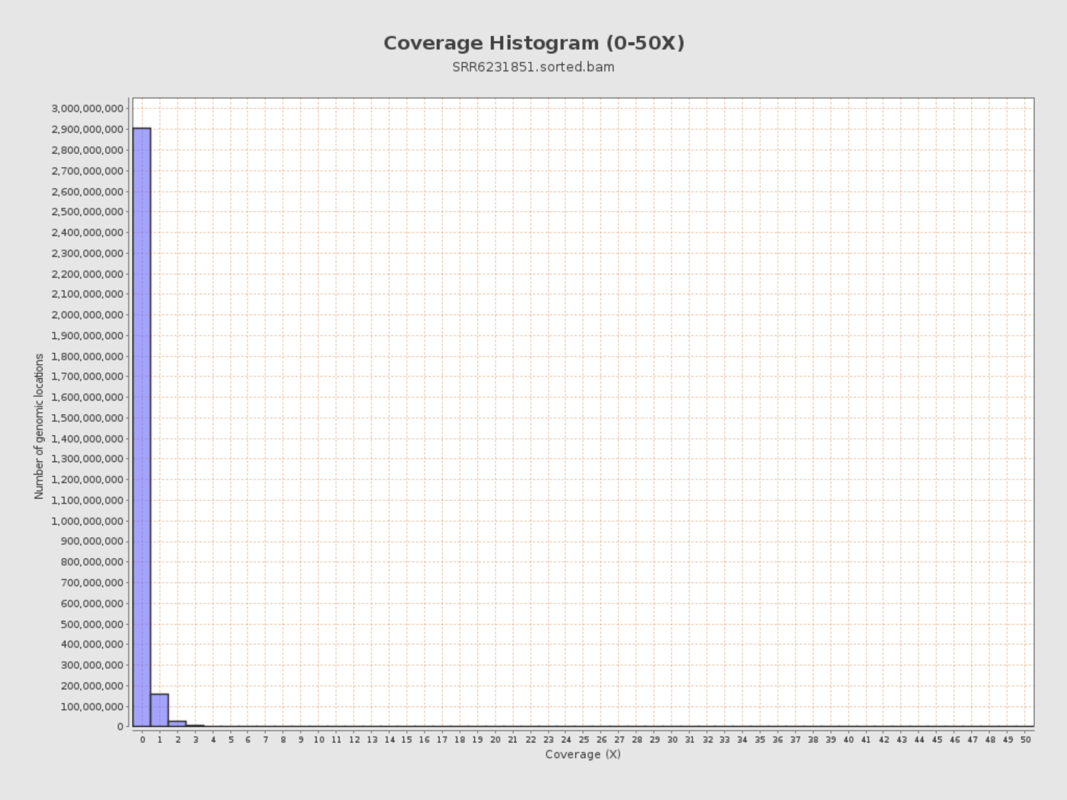
3. Results : Coverage across reference



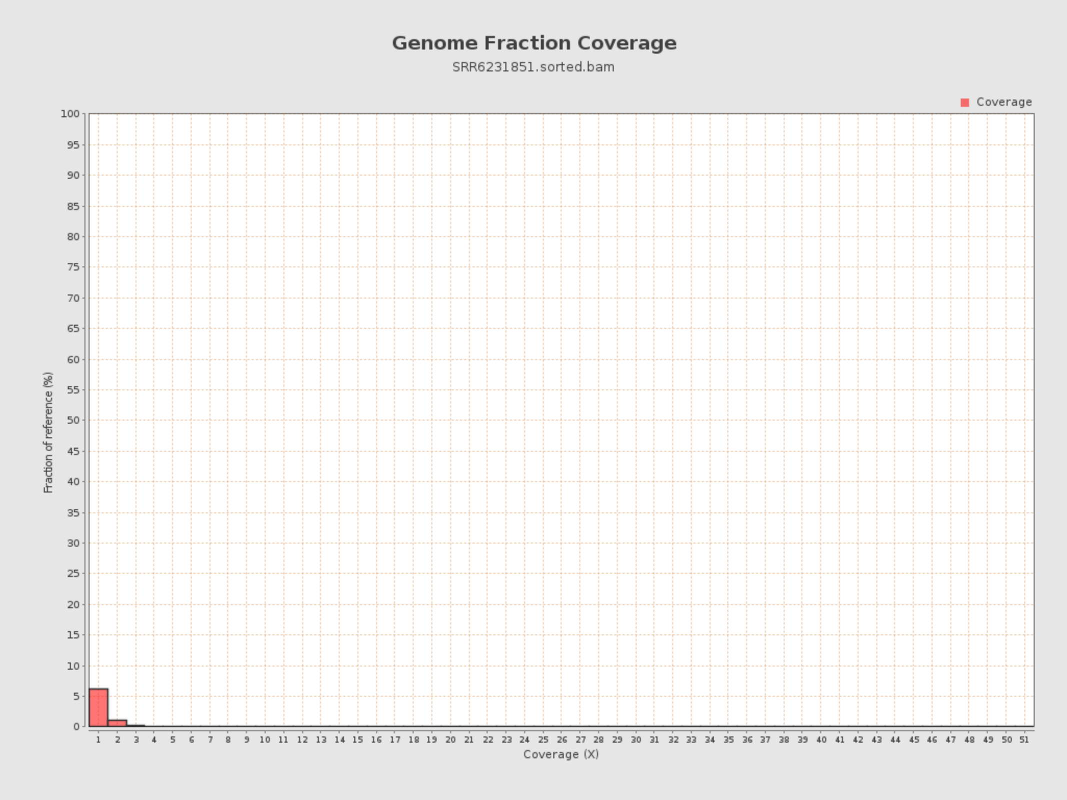
4. Results : Coverage Histogram



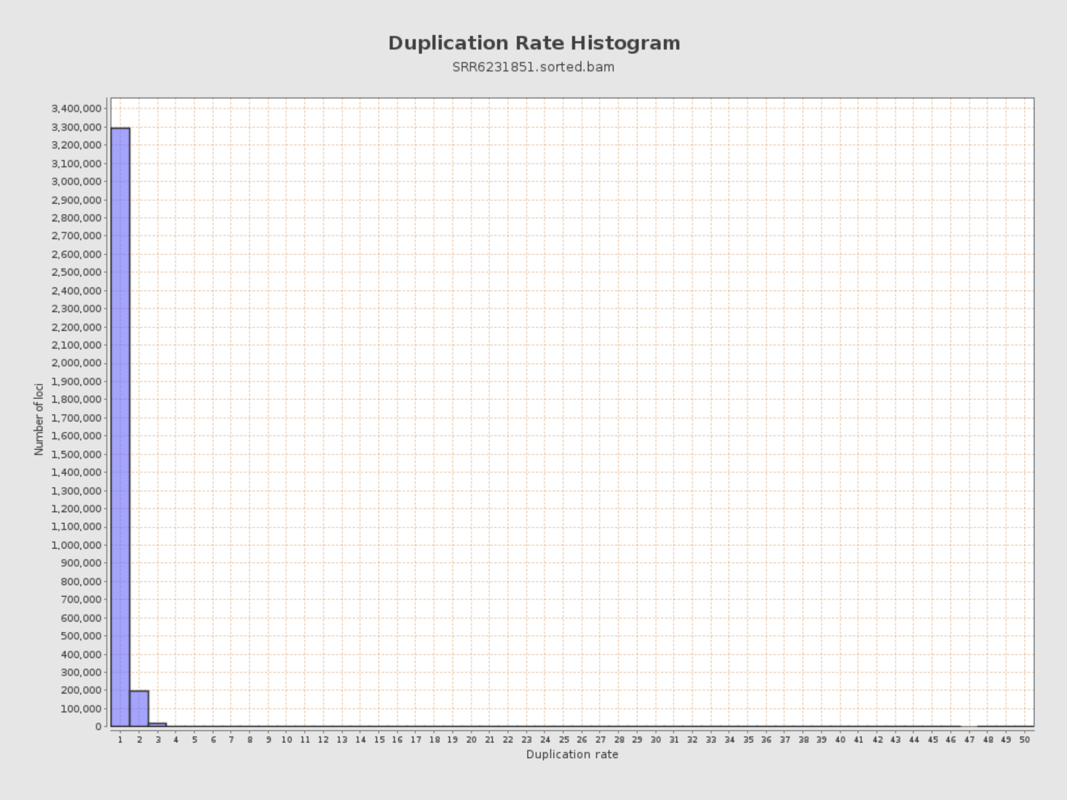
5. Results : Coverage Histogram (0-50X)



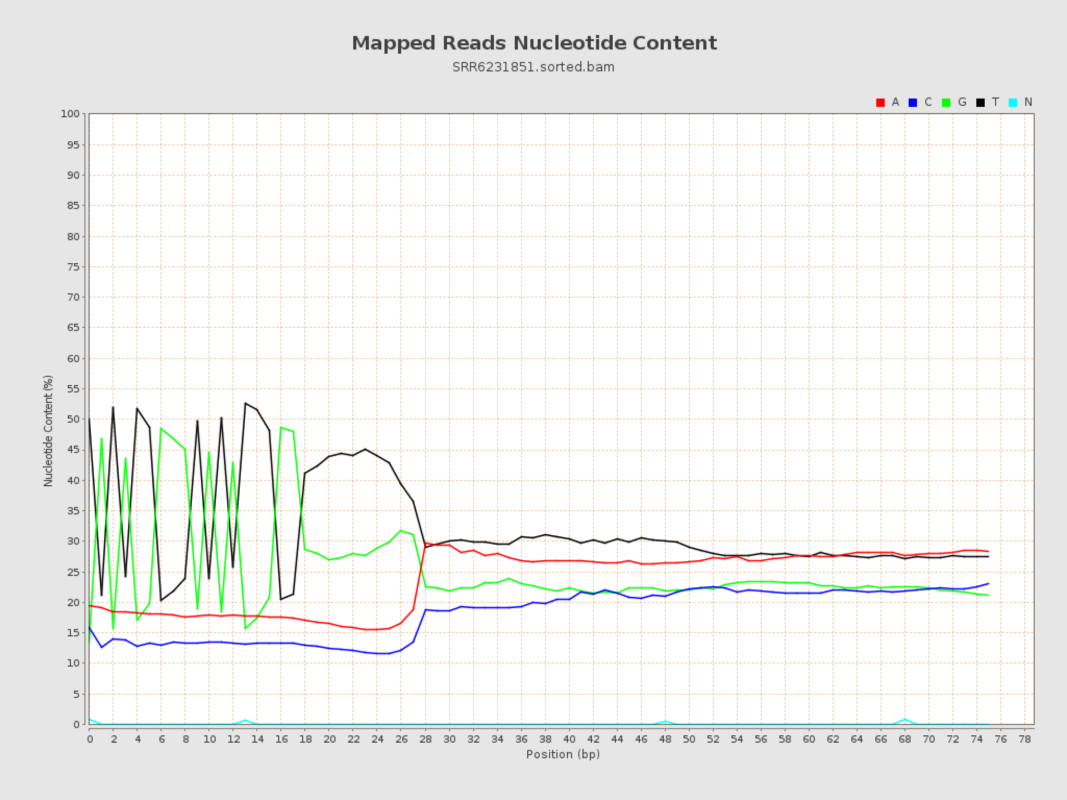
6. Results : Genome Fraction Coverage



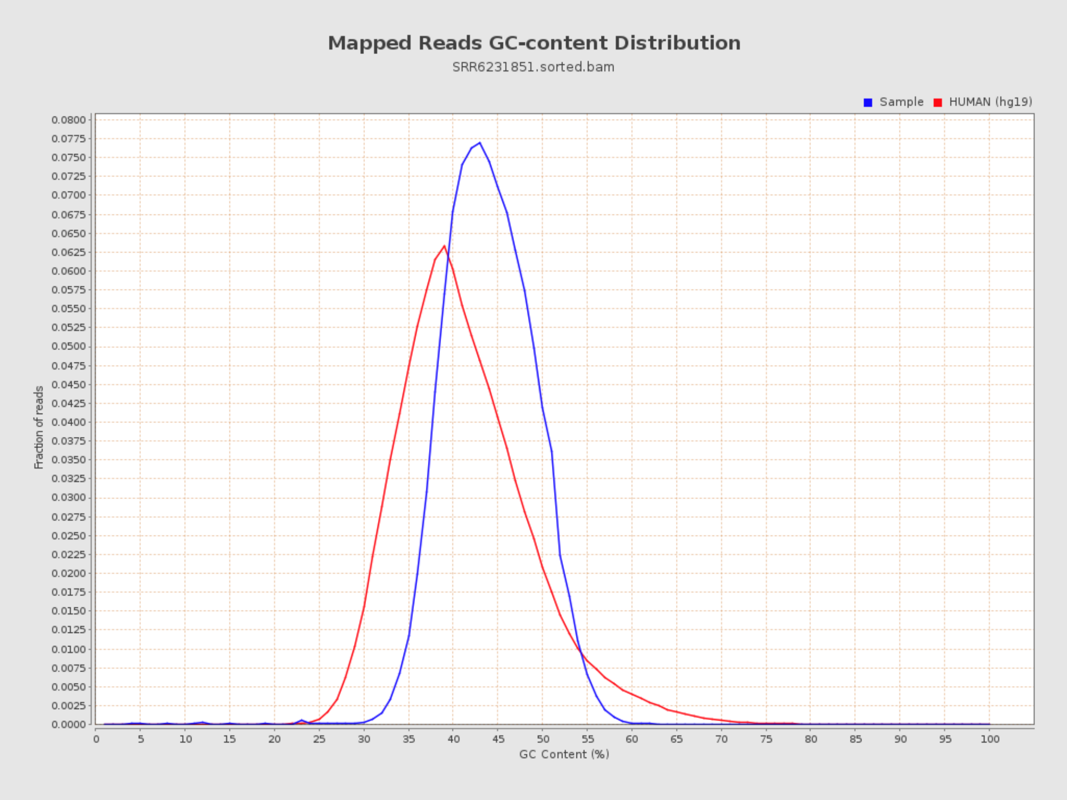
7. Results : Duplication Rate Histogram



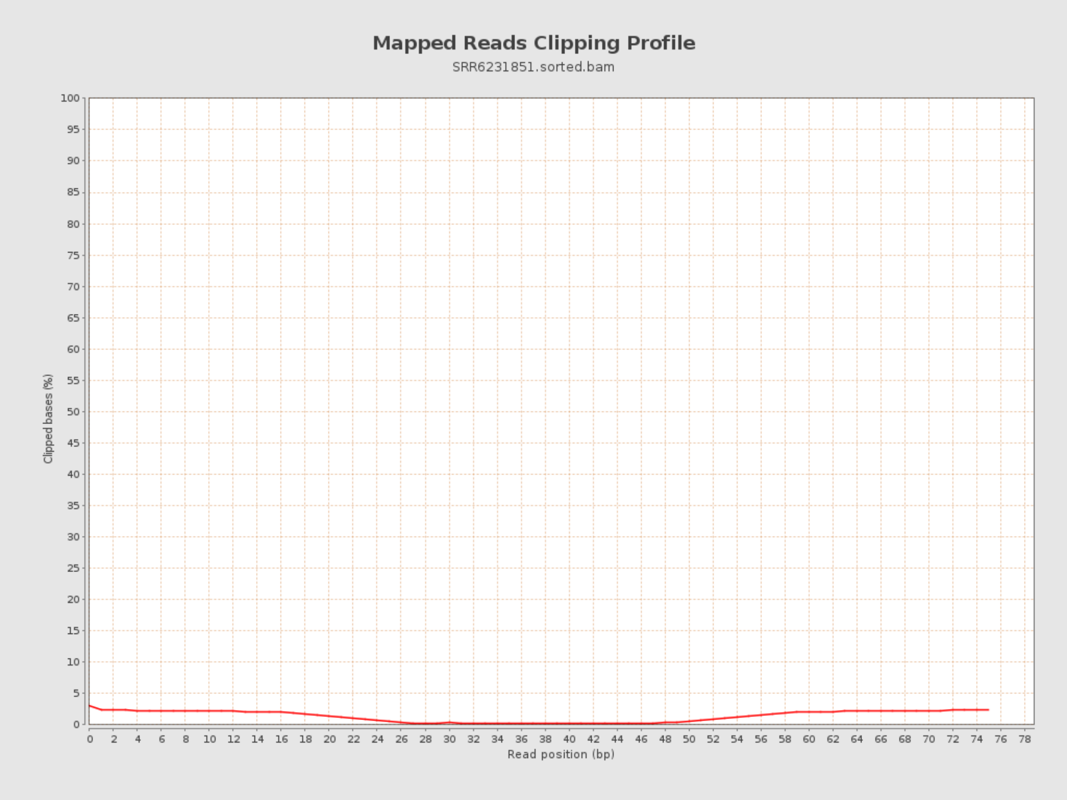
8. Results : Mapped Reads Nucleotide Content



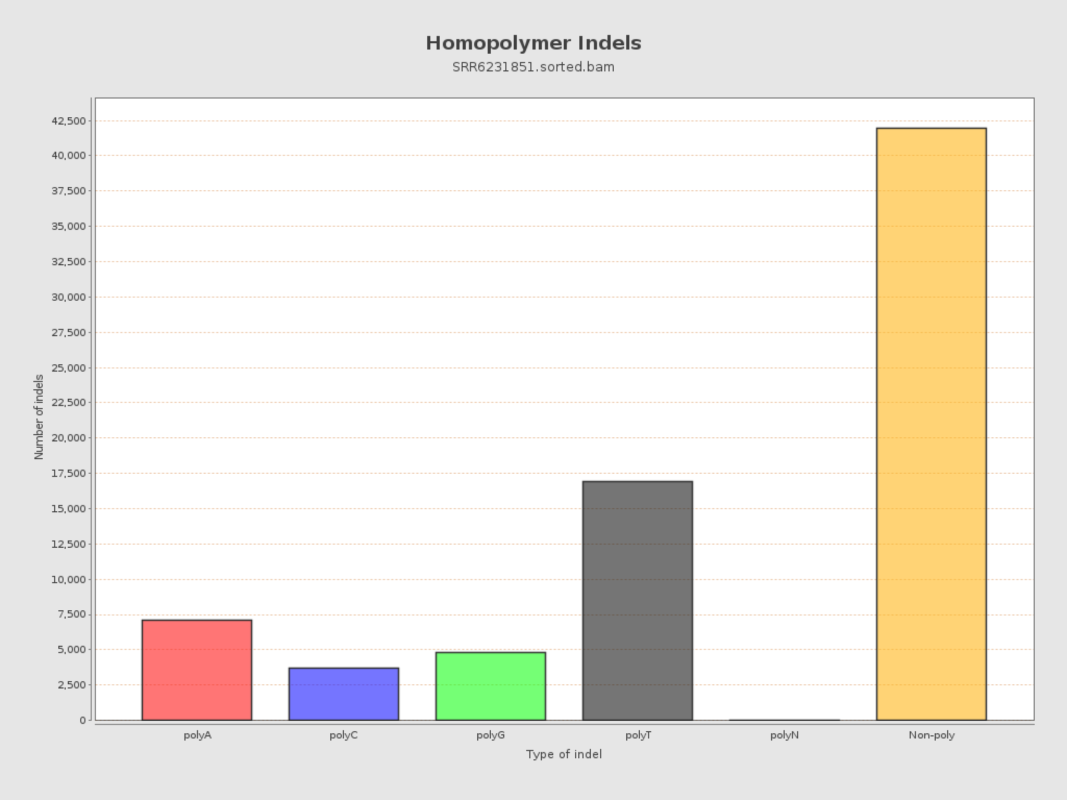
9. Results : Mapped Reads GC-content Distribution



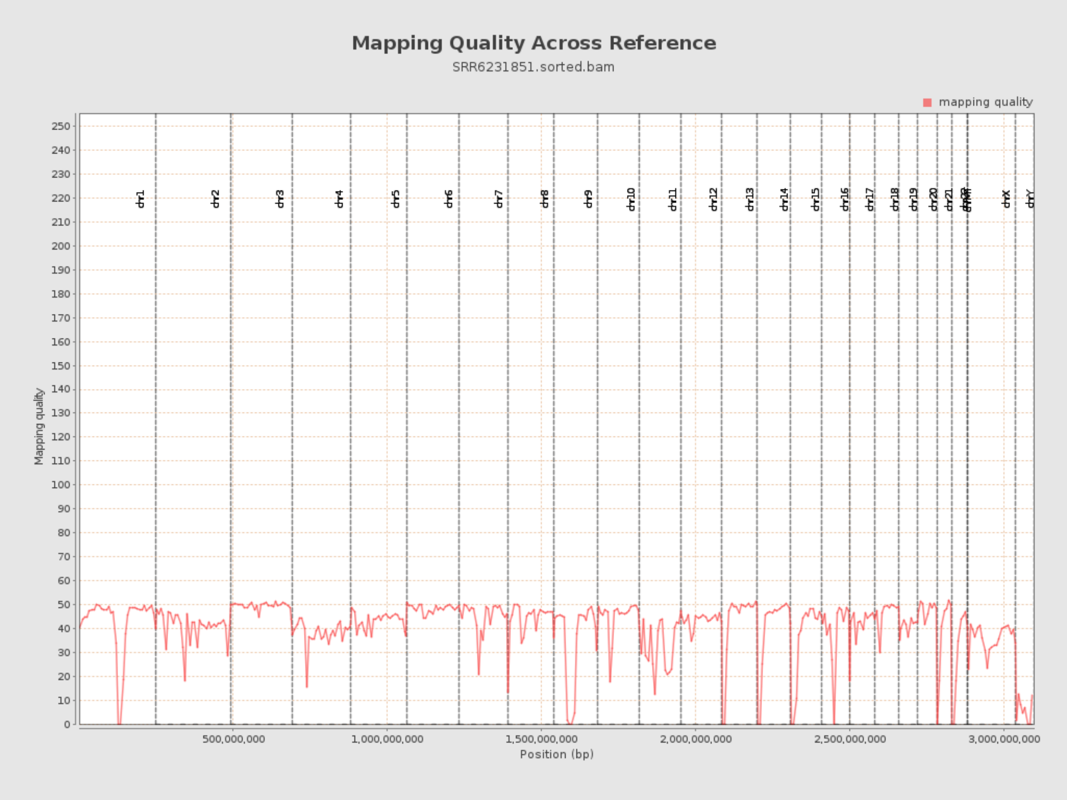
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram