Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:35:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231823.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_SRR6231823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231823.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:35:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	762,505
Mapped reads	584,758 / 76.69%
Unmapped reads	177,747 / 23.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,224 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	38,130 / 5%
Duplication rate	5.01%
Clipped reads	304,803 / 39.97%

2.2. ACGT Content

Number/percentage of A's	10,630,586 / 28.11%
Number/percentage of C's	6,260,916 / 16.56%
Number/percentage of T's	12,853,960 / 33.99%
Number/percentage of G's	8,069,823 / 21.34%
Number/percentage of N's	1,888 / 0%
GC Percentage	37.89%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.3545

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

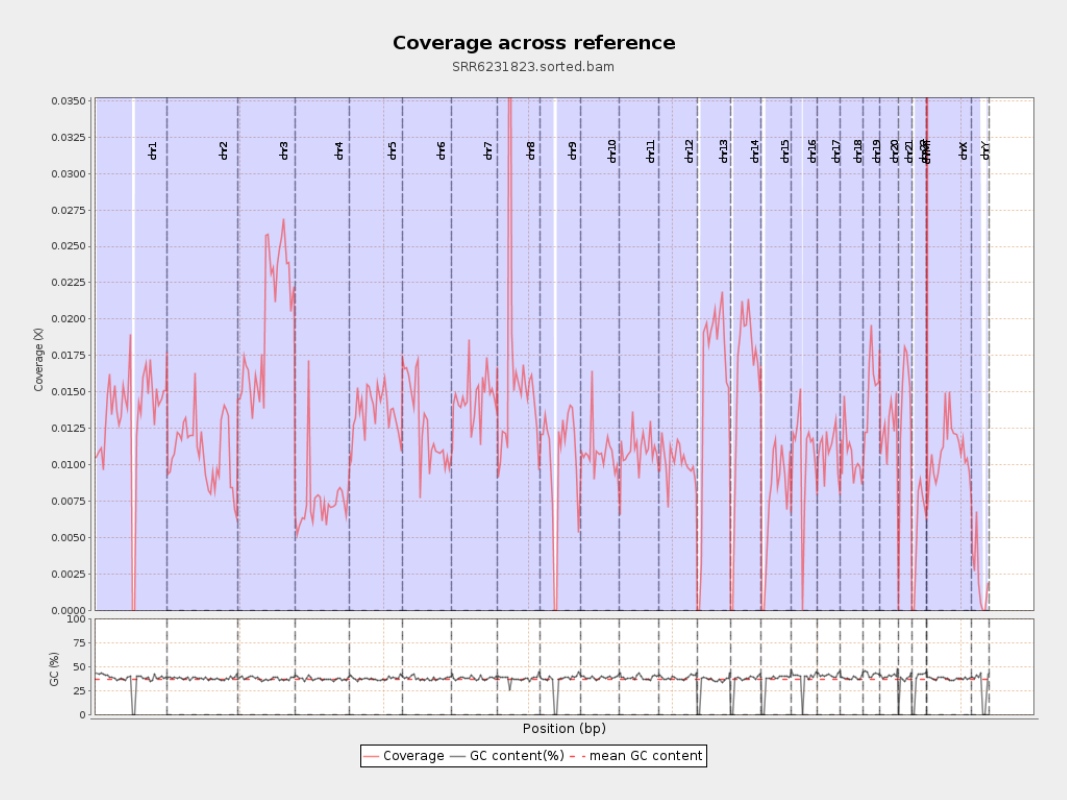
General error rate	0.91%
Mismatches	336,449
Insertions	3,496
Mapped reads with at least one insertion	0.59%
Deletions	11,483
Mapped reads with at least one deletion	1.93%
Homopolymer indels	46.71%

2.6. Chromosome stats

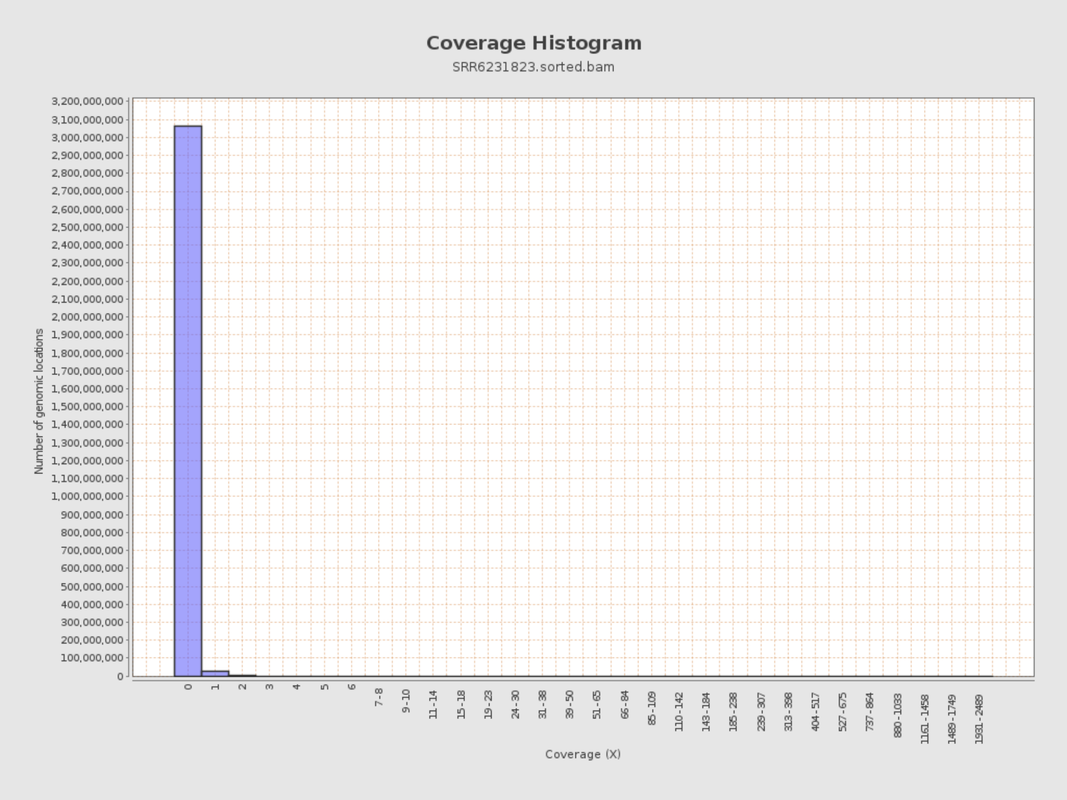
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3309308	0.0133	0.2026
chr2	243199373	2643351	0.0109	0.1494
chr3	198022430	3919497	0.0198	0.1652
chr4	191154276	1425114	0.0075	0.1042
chr5	180915260	2478865	0.0137	0.142
chr6	171115067	2168564	0.0127	0.1334
chr7	159138663	2312683	0.0145	0.1616

chr8	146364022	2384718	0.0163	1.4943
chr9	141213431	1460749	0.0103	0.1283
chr10	135534747	1463457	0.0108	0.1352
chr11	135006516	1495453	0.0111	0.135
chr12	133851895	1364772	0.0102	0.1171
chr13	115169878	1802883	0.0157	0.1479
chr14	107349540	1658565	0.0155	0.1471
chr15	102531392	778357	0.0076	0.0997
chr16	90354753	931375	0.0103	0.1227
chr17	81195210	891609	0.011	0.1235
chr18	78077248	826172	0.0106	0.2193
chr19	59128983	904212	0.0153	0.1653
chr20	63025520	782746	0.0124	0.1322
chr21	48129895	669752	0.0139	0.1392
chr22	51304566	289976	0.0057	0.0835
chrMT	16571	47831	2.8864	3.2629
chrX	155270560	1700519	0.011	0.1234
chrY	59373566	126770	0.0021	0.06

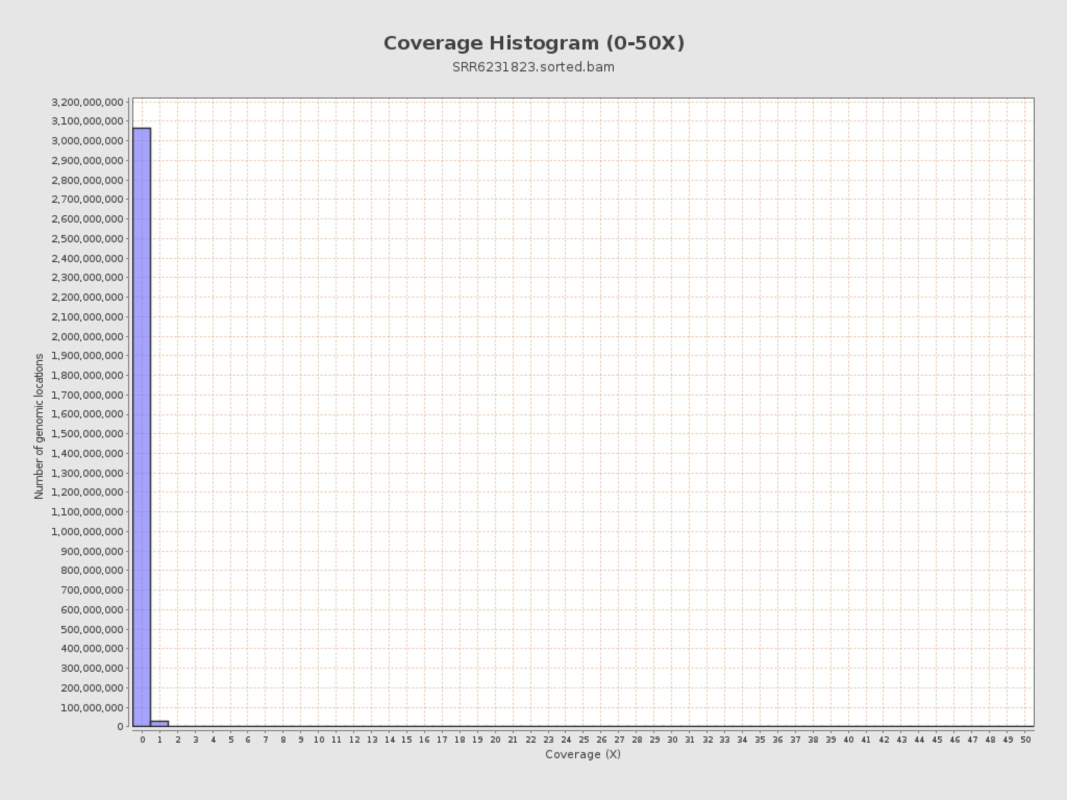
3. Results : Coverage across reference



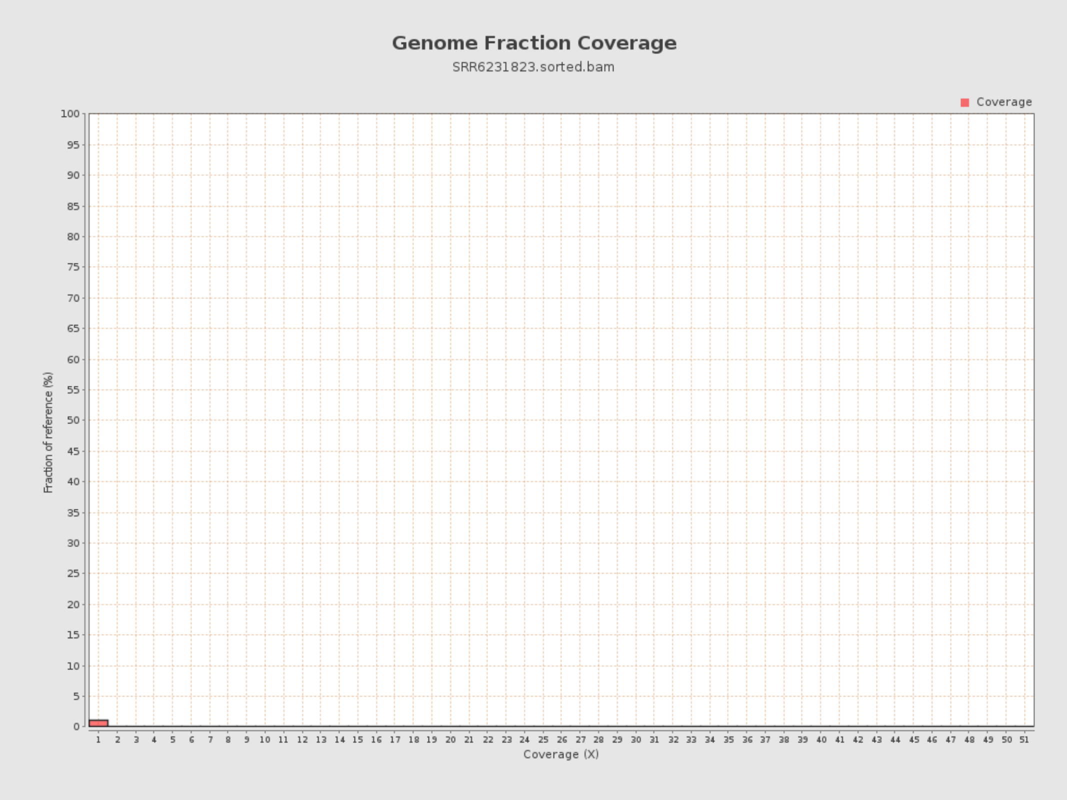
4. Results : Coverage Histogram



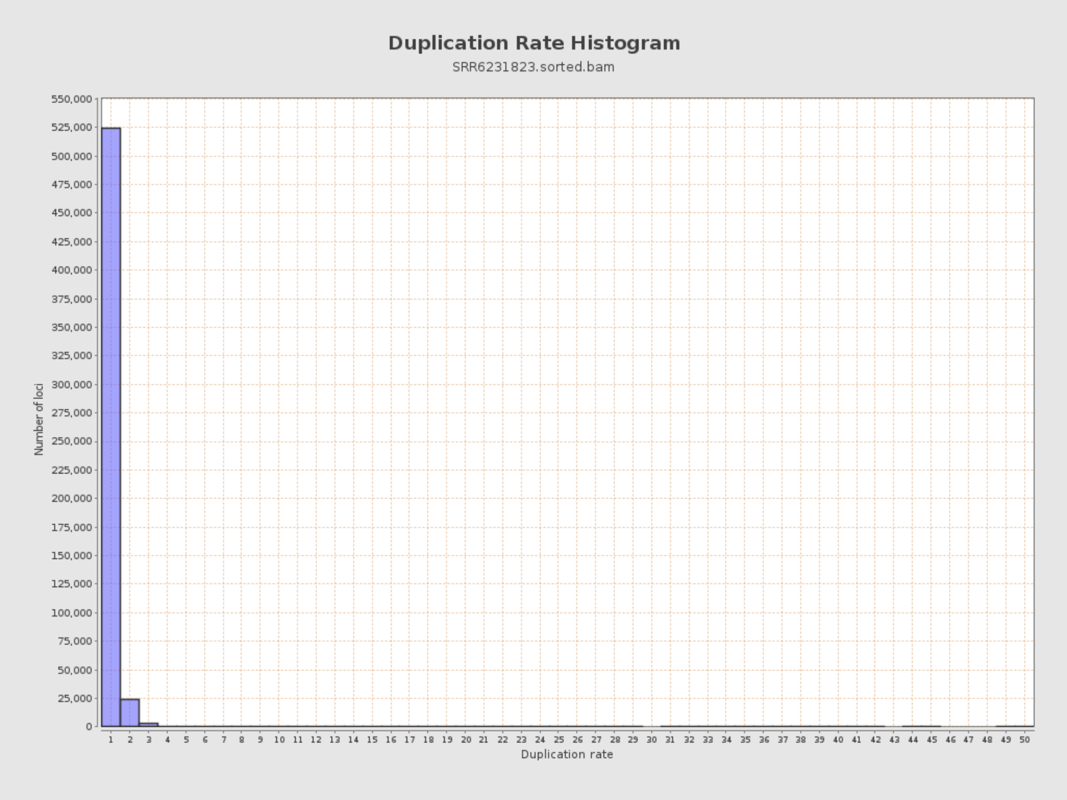
5. Results : Coverage Histogram (0-50X)



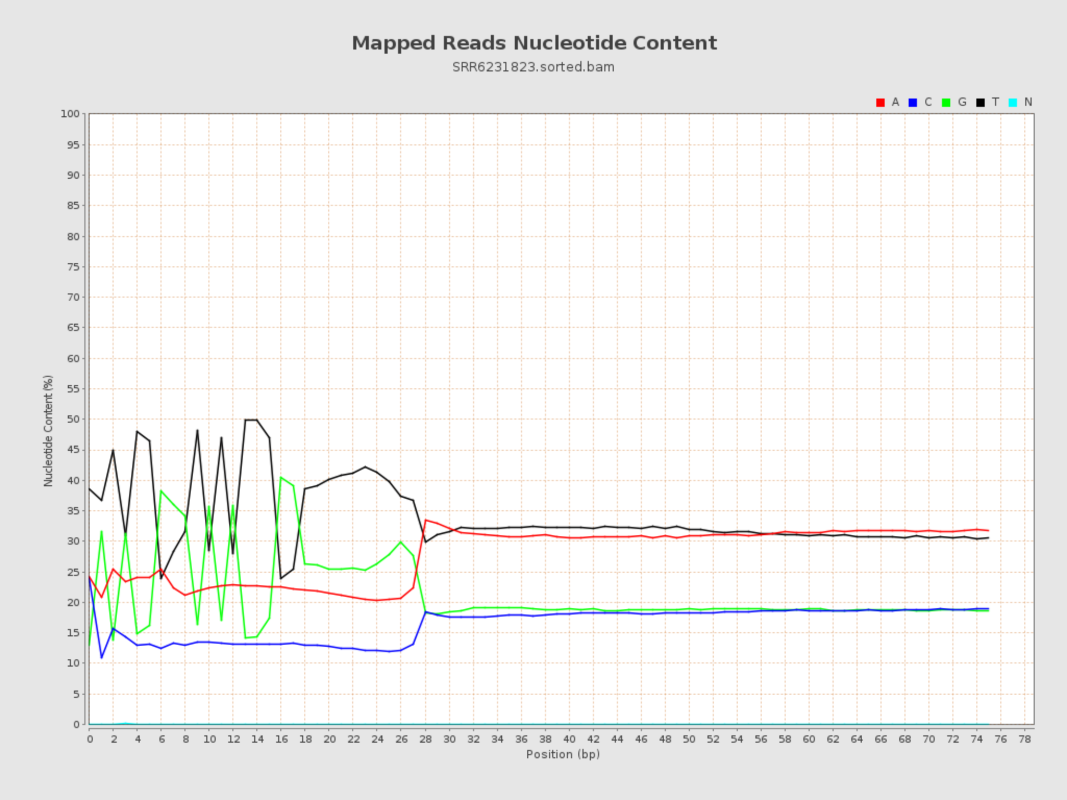
6. Results : Genome Fraction Coverage



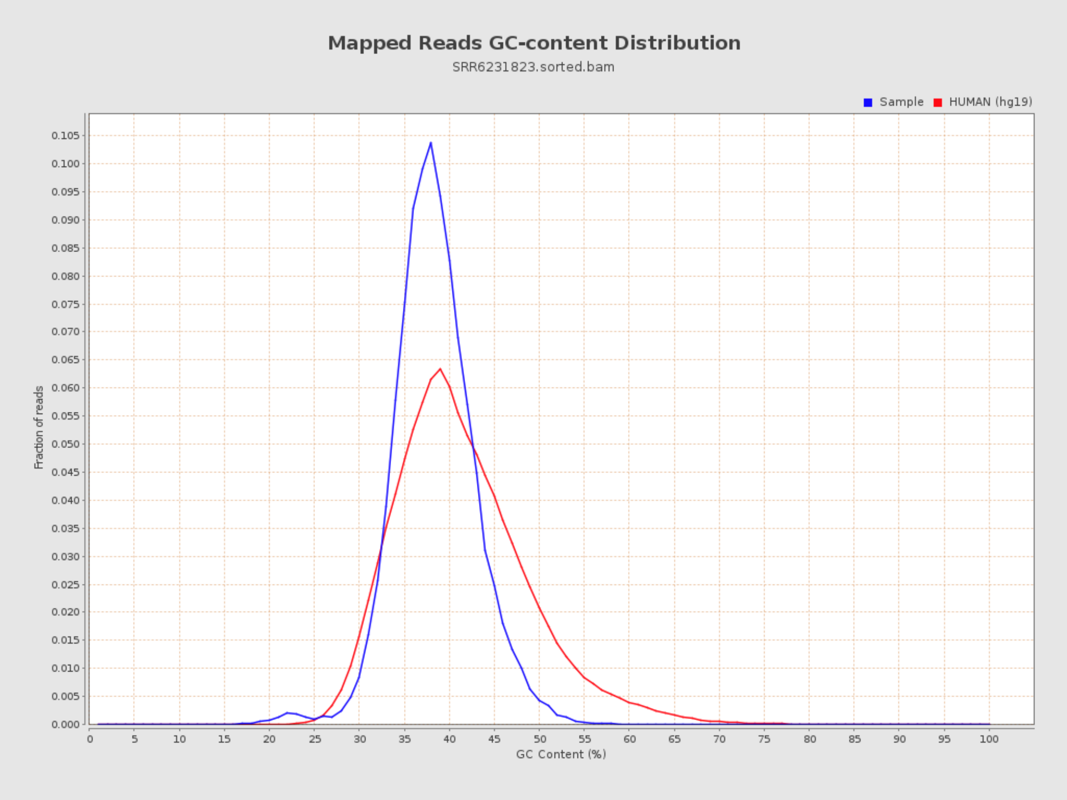
7. Results : Duplication Rate Histogram



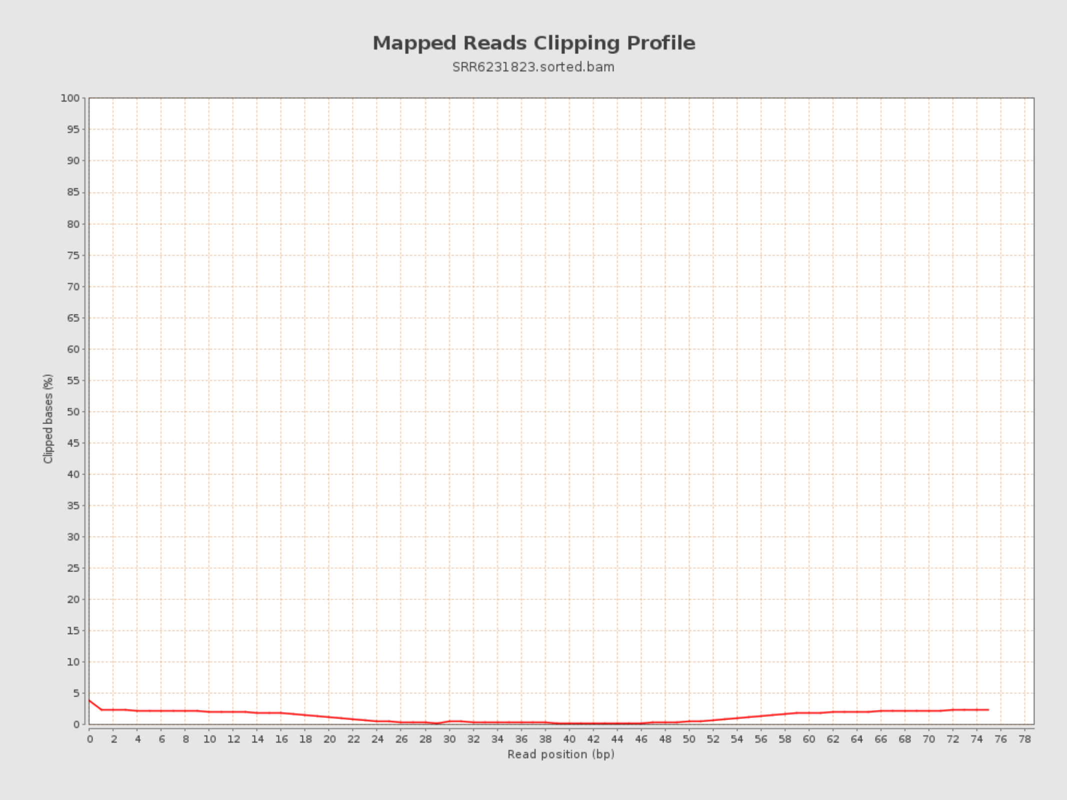
8. Results : Mapped Reads Nucleotide Content



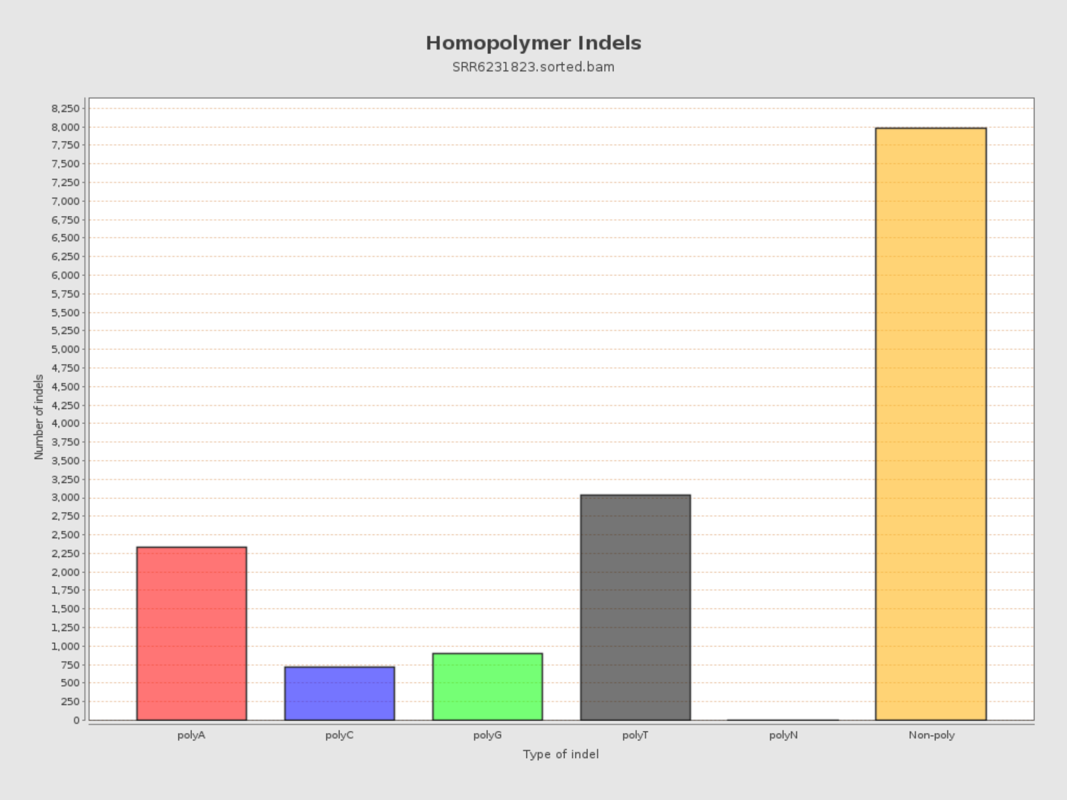
9. Results : Mapped Reads GC-content Distribution



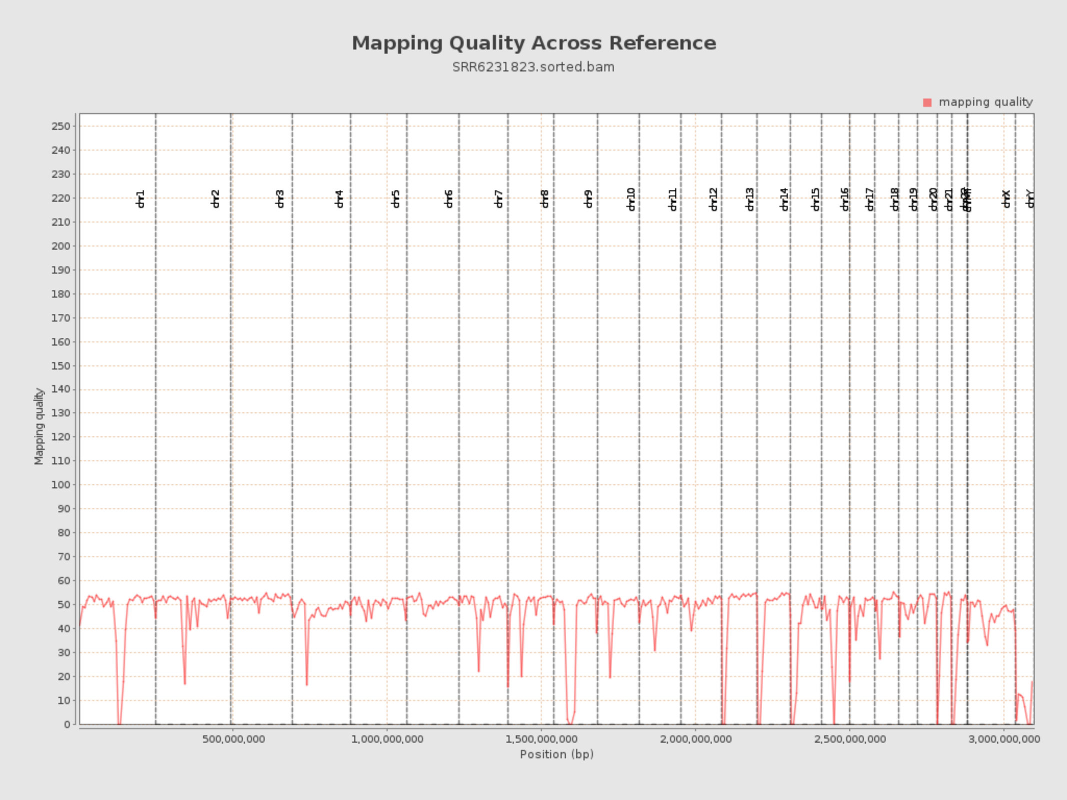
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram