Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:11:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231854.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_SRR6231854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231854.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:11:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,254,531
Mapped reads	4,890,826 / 93.08%
Unmapped reads	363,705 / 6.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,437 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	518,442 / 9.87%
Duplication rate	8.62%
Clipped reads	2,685,105 / 51.1%

2.2. ACGT Content

Number/percentage of A's	82,689,738 / 26.42%
Number/percentage of C's	55,965,417 / 17.88%
Number/percentage of T's	102,441,424 / 32.73%
Number/percentage of G's	71,808,613 / 22.94%
Number/percentage of N's	120,344 / 0.04%
GC Percentage	40.82%

2.3. Coverage

Mean	0.1012

Standard Deviation	1.1142

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

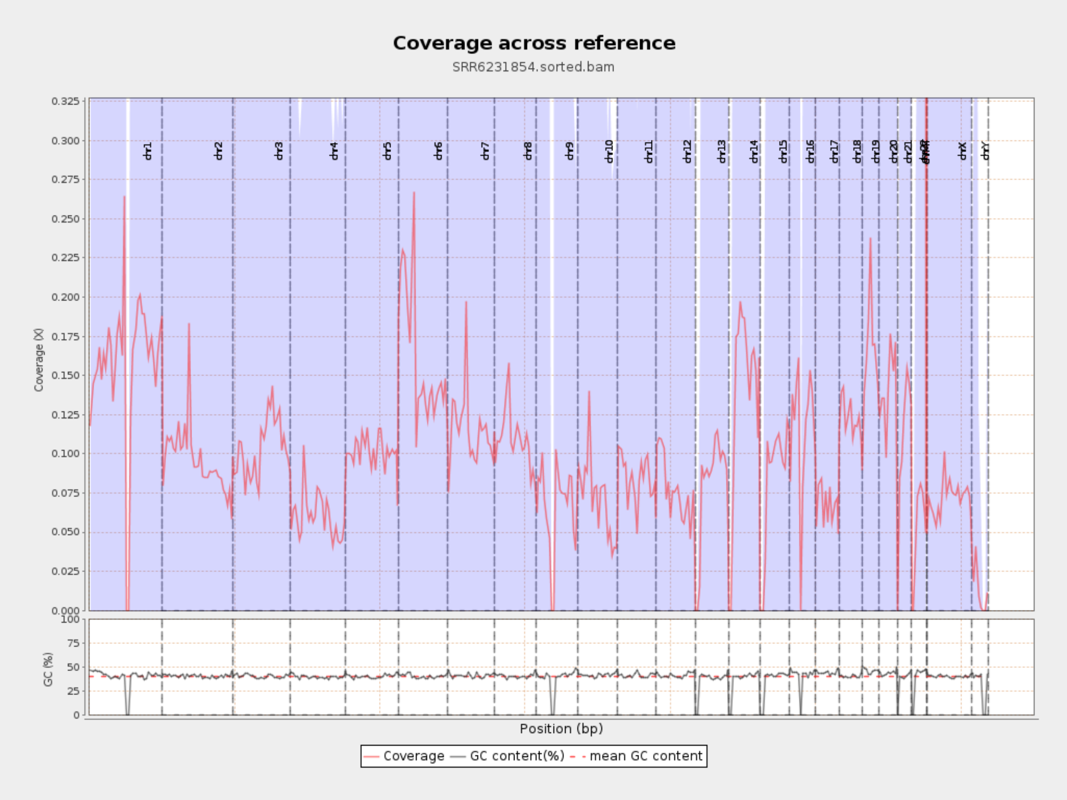
General error rate	0.64%
Mismatches	1,979,182
Insertions	20,545
Mapped reads with at least one insertion	0.42%
Deletions	68,428
Mapped reads with at least one deletion	1.39%
Homopolymer indels	44.49%

2.6. Chromosome stats

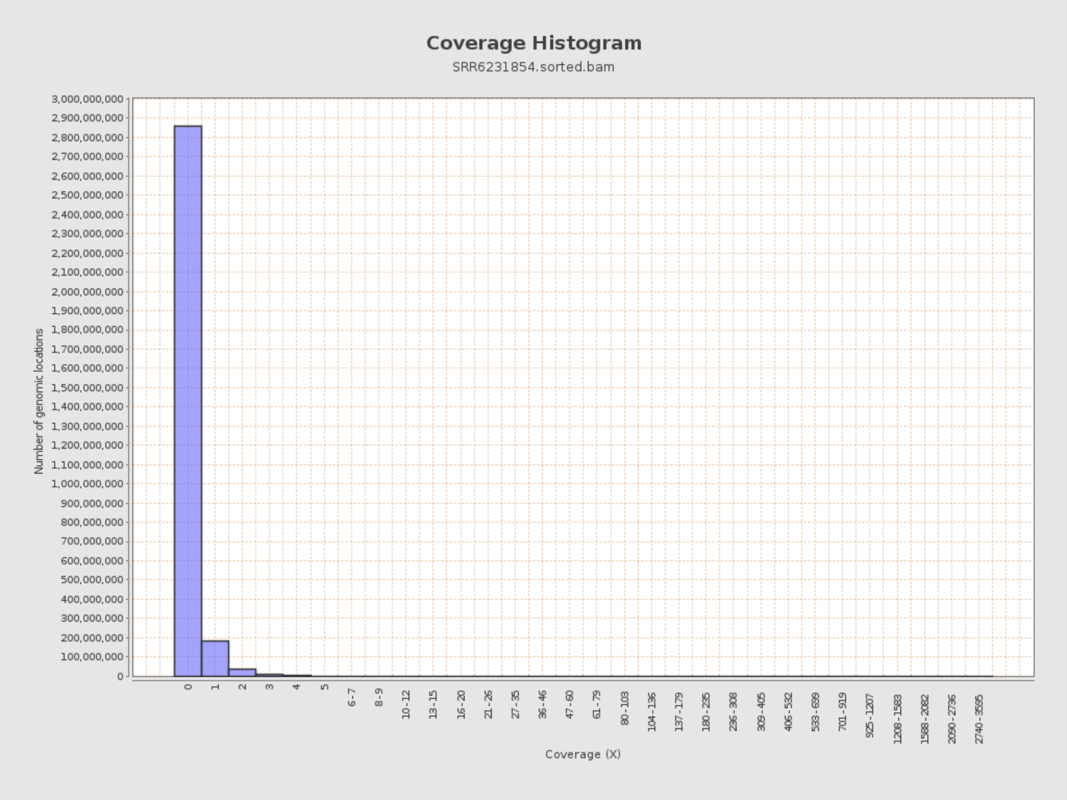
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39268491	0.1575	2.7542
chr2	243199373	23444865	0.0964	1.4008
chr3	198022430	20621584	0.1041	0.4107
chr4	191154276	11404324	0.0597	0.3624
chr5	180915260	18415221	0.1018	0.426
chr6	171115067	27808908	0.1625	0.8669
chr7	159138663	18435809	0.1158	1.2887

chr8	146364022	15970596	0.1091	1.3326
chr9	141213431	9377103	0.0664	0.6916
chr10	135534747	9764291	0.072	0.6465
chr11	135006516	11292559	0.0836	0.6745
chr12	133851895	10251395	0.0766	0.3805
chr13	115169878	9153597	0.0795	0.3909
chr14	107349540	14770461	0.1376	0.4986
chr15	102531392	8553080	0.0834	0.4153
chr16	90354753	10547063	0.1167	0.5107
chr17	81195210	5445186	0.0671	0.3946
chr18	78077248	9636660	0.1234	1.6597
chr19	59128983	9853214	0.1666	1.4874
chr20	63025520	8838337	0.1402	0.4889
chr21	48129895	5324420	0.1106	0.4538
chr22	51304566	2632290	0.0513	0.2774
chrMT	16571	379976	22.9302	12.7157
chrX	155270560	11189457	0.0721	0.4649
chrY	59373566	765745	0.0129	0.2732

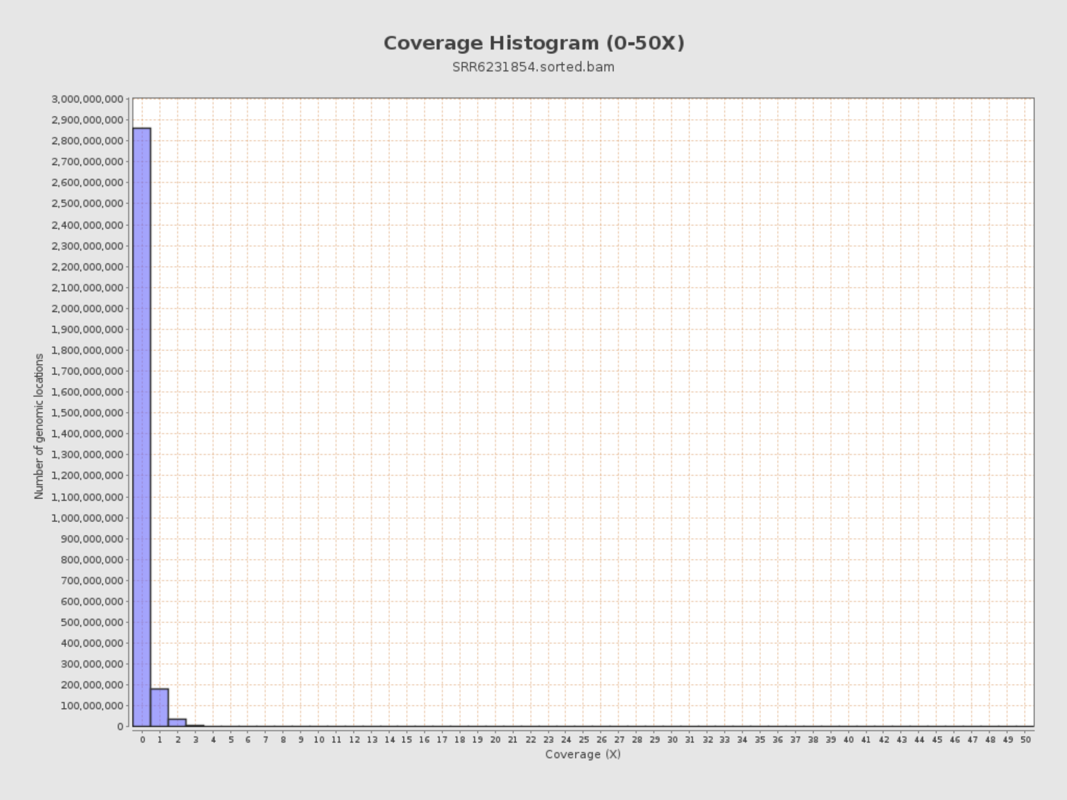
3. Results : Coverage across reference



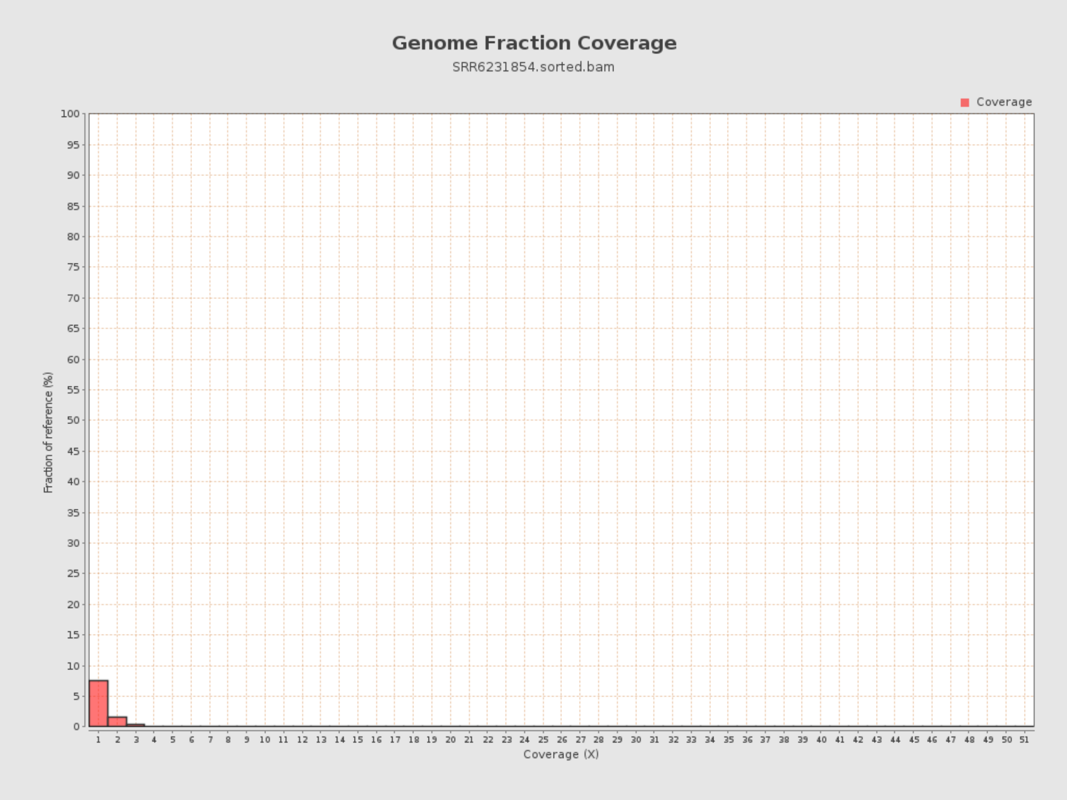
4. Results : Coverage Histogram



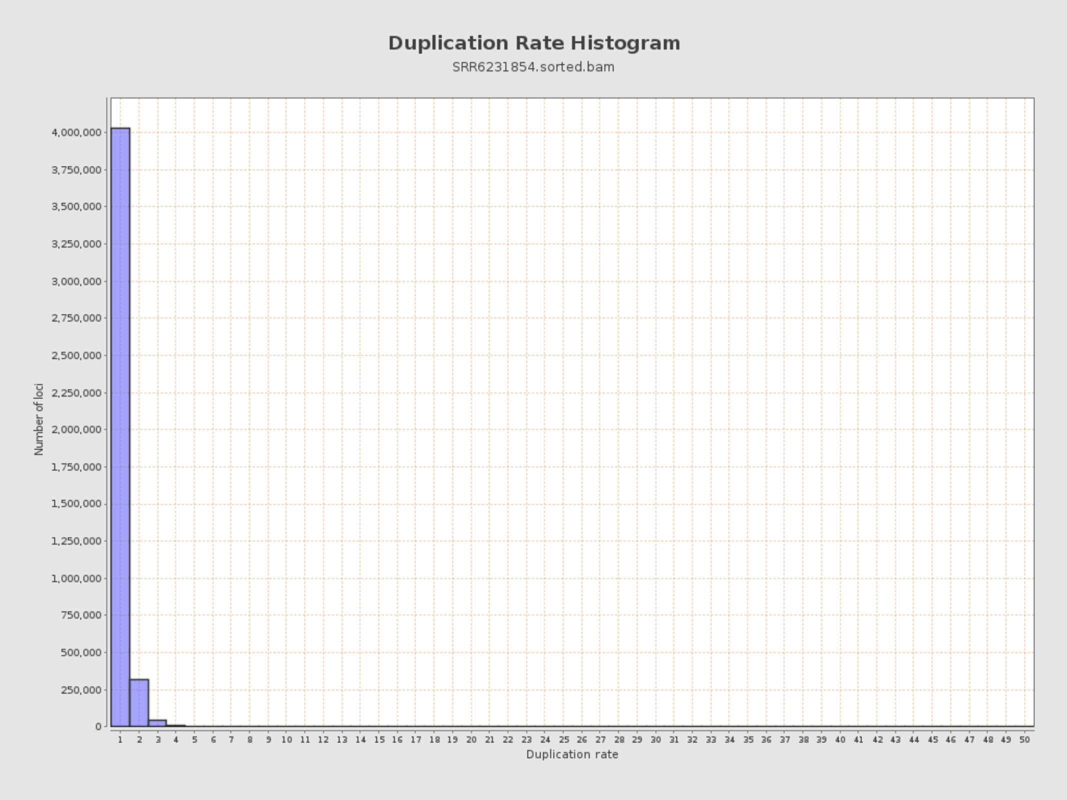
5. Results : Coverage Histogram (0-50X)



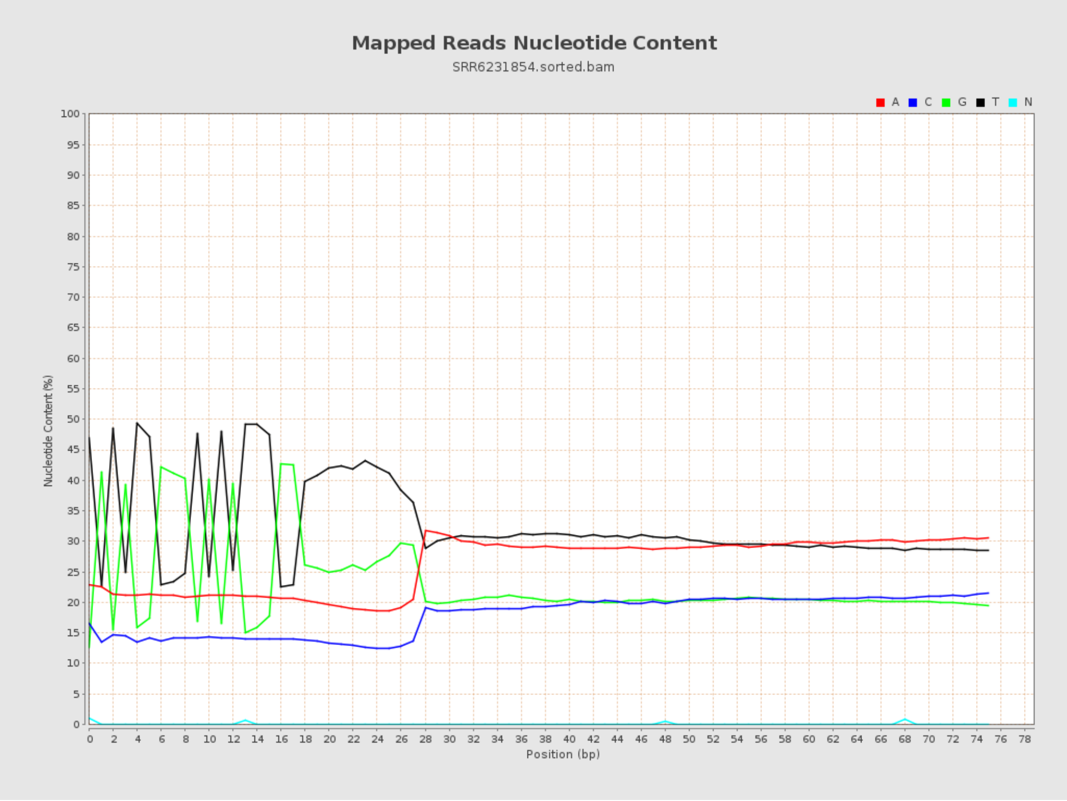
6. Results : Genome Fraction Coverage



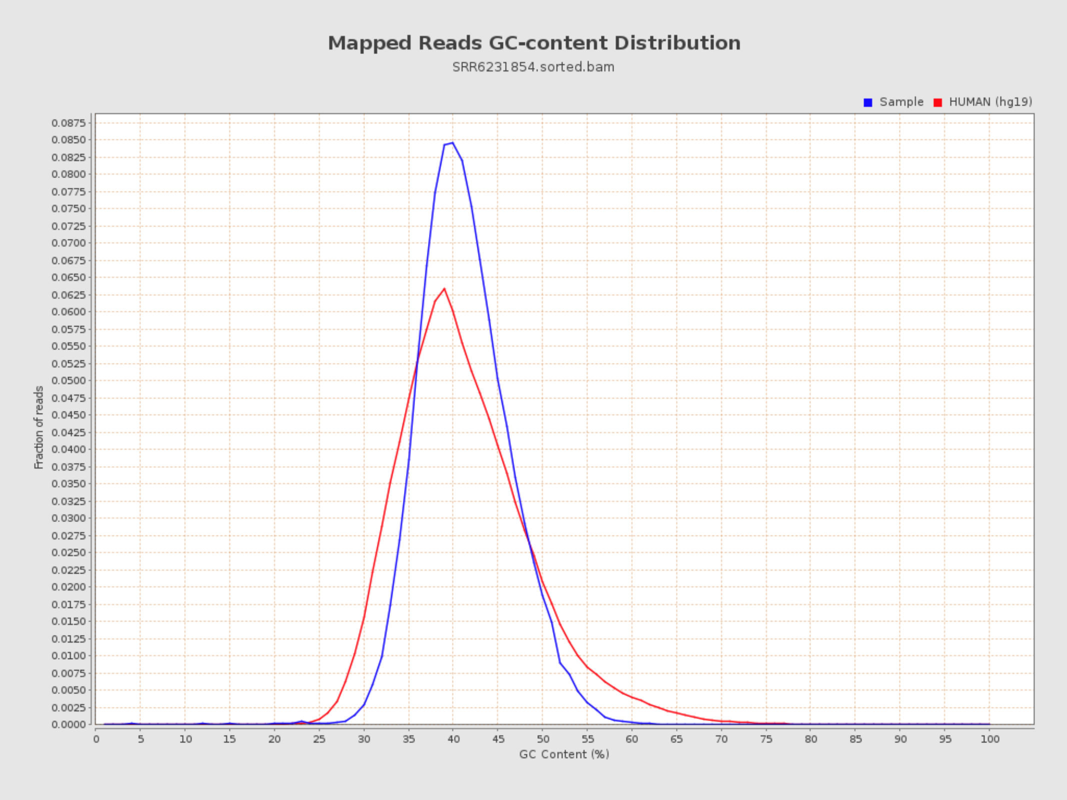
7. Results : Duplication Rate Histogram



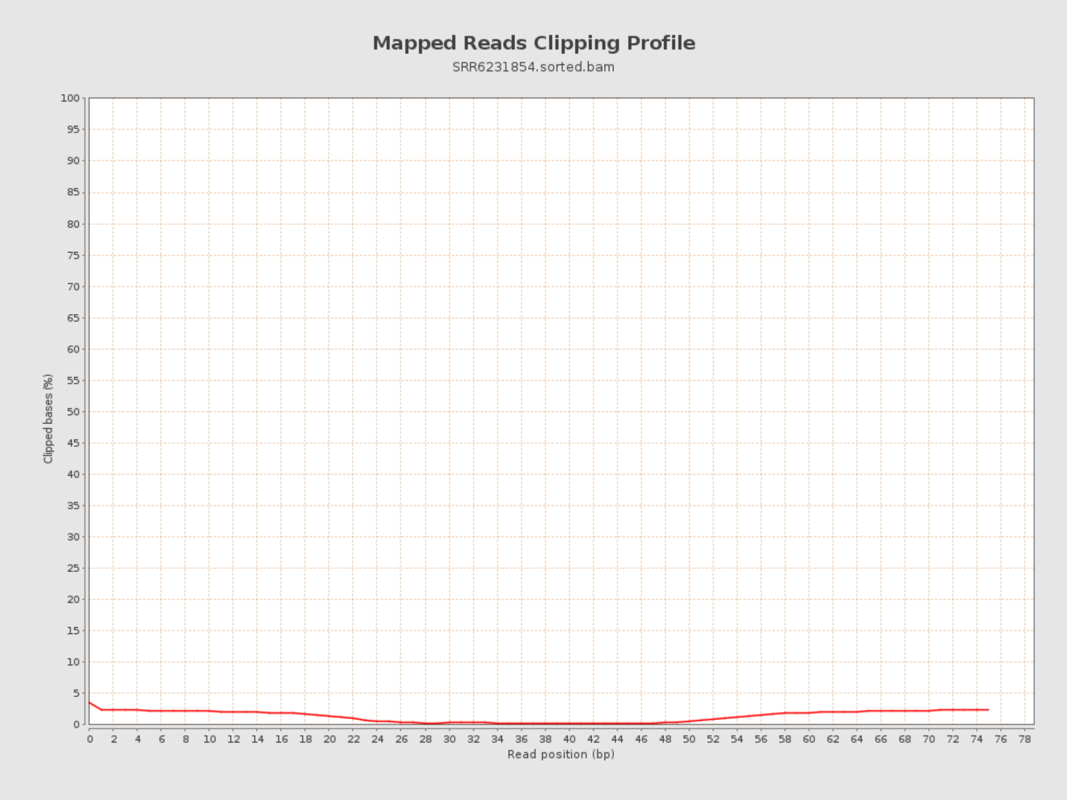
8. Results : Mapped Reads Nucleotide Content



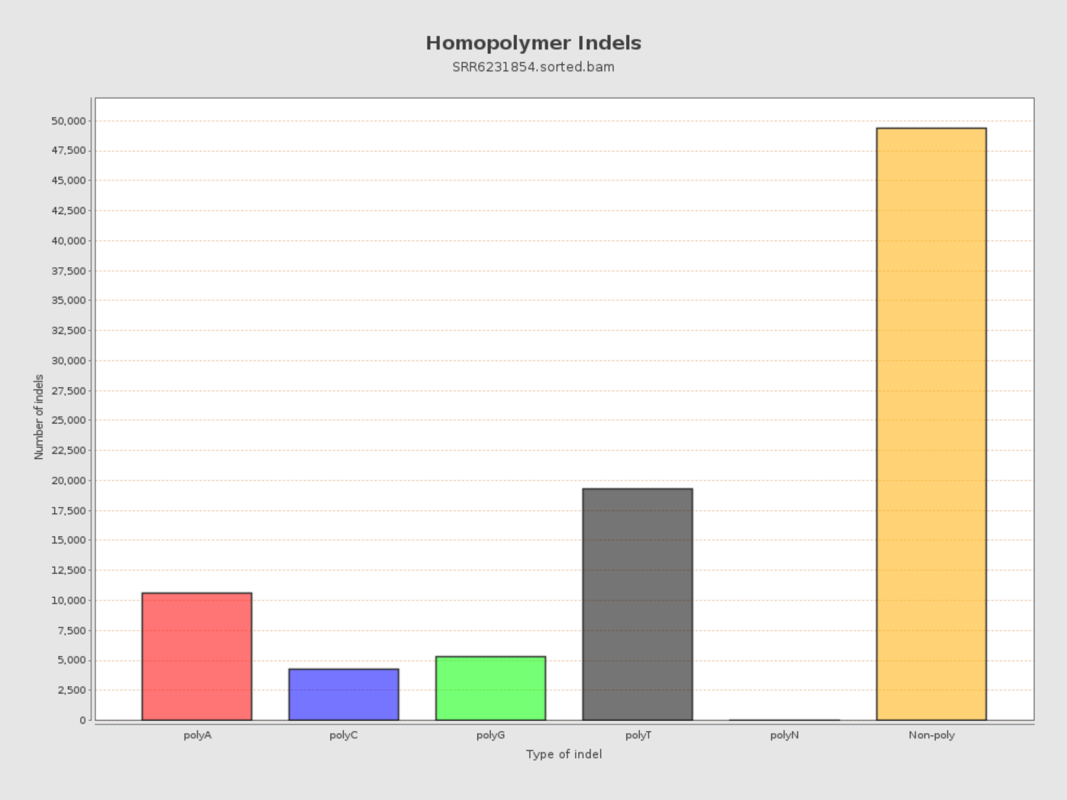
9. Results : Mapped Reads GC-content Distribution



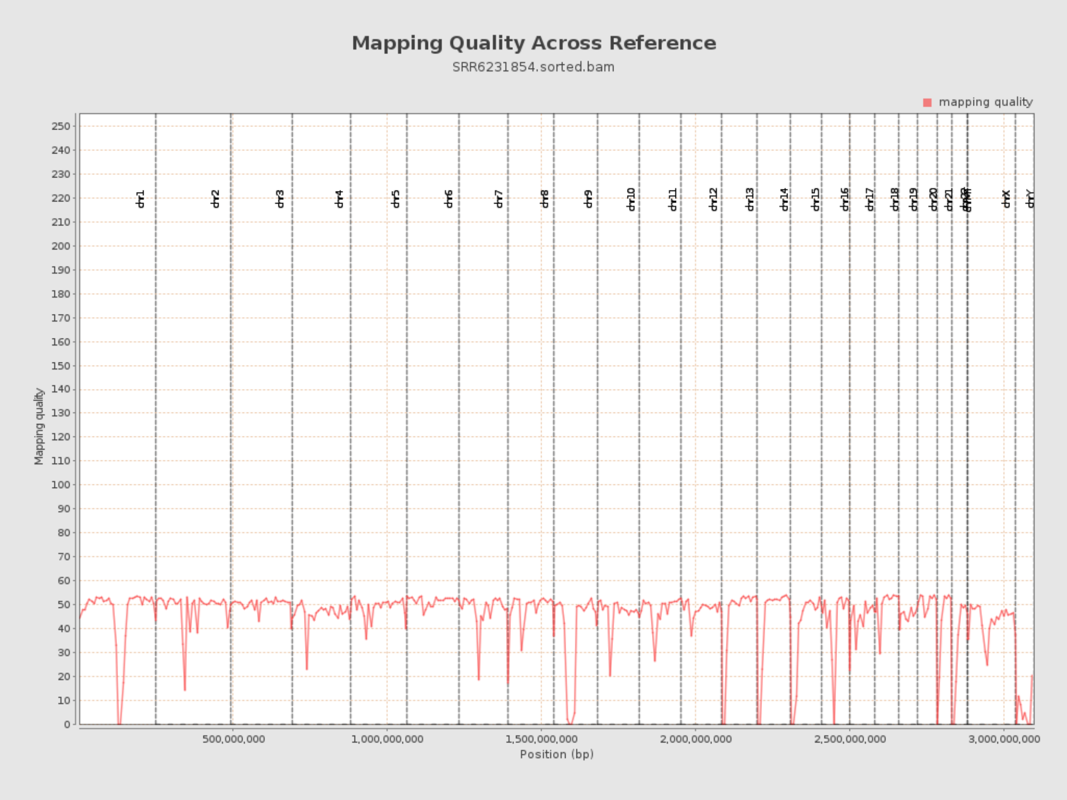
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram