Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:18:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231872.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_SRR6231872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231872.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:18:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,582,463
Mapped reads	5,274,314 / 94.48%
Unmapped reads	308,149 / 5.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,465 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	653,576 / 11.71%
Duplication rate	10.3%
Clipped reads	2,493,238 / 44.66%

2.2. ACGT Content

Number/percentage of A's	93,948,724 / 27.09%
Number/percentage of C's	62,750,014 / 18.09%
Number/percentage of T's	112,542,623 / 32.45%
Number/percentage of G's	77,450,622 / 22.33%
Number/percentage of N's	139,677 / 0.04%
GC Percentage	40.42%

2.3. Coverage

Mean	0.1121

Standard Deviation	1.0952

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

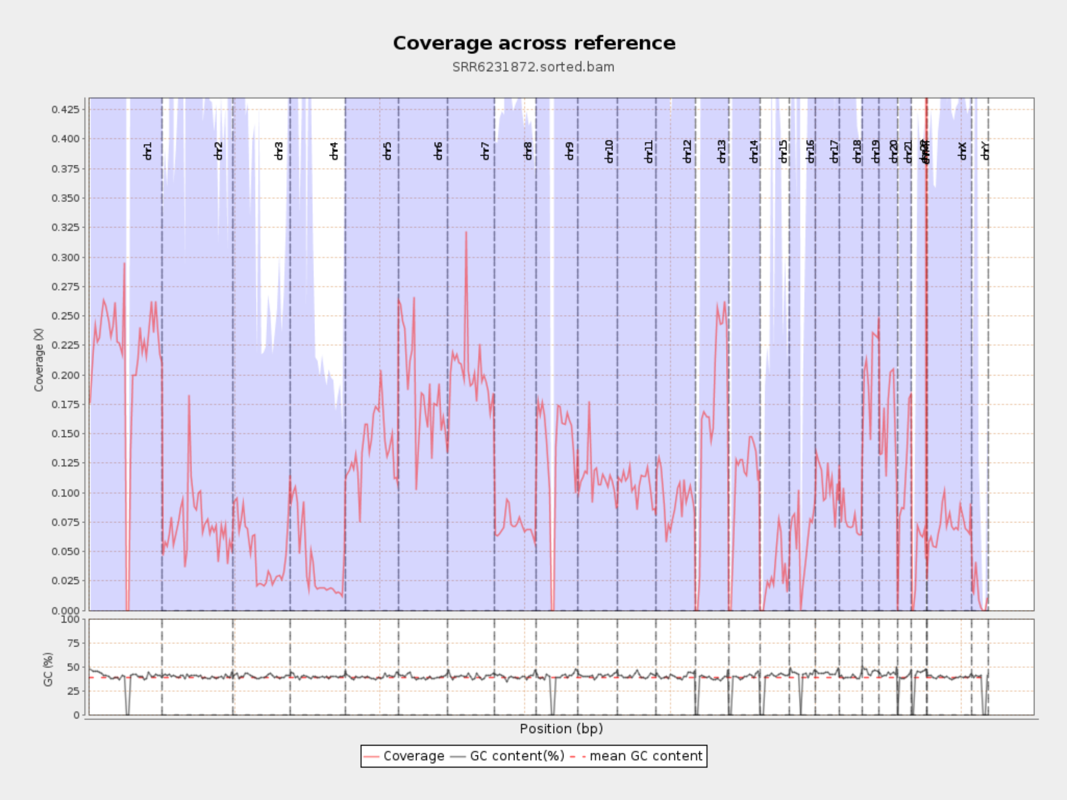
General error rate	0.62%
Mismatches	2,117,259
Insertions	23,640
Mapped reads with at least one insertion	0.44%
Deletions	77,722
Mapped reads with at least one deletion	1.46%
Homopolymer indels	45.65%

2.6. Chromosome stats

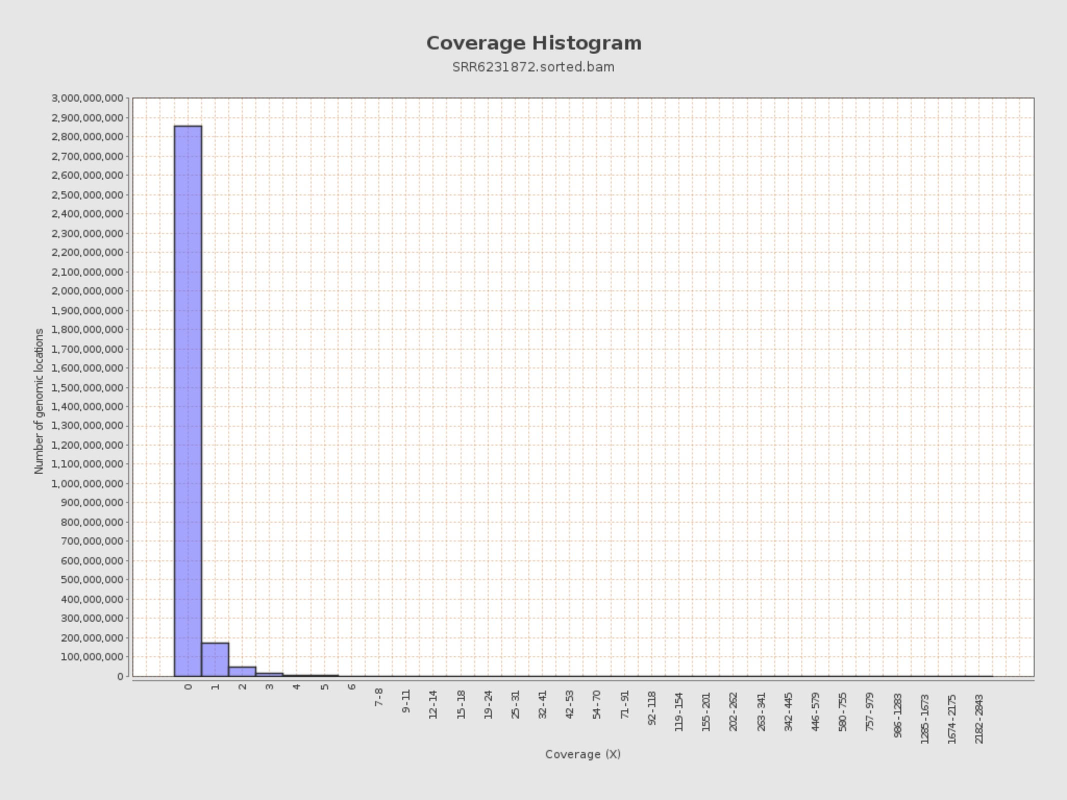
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	53900383	0.2162	2.414
chr2	243199373	17792742	0.0732	1.1843
chr3	198022430	9681394	0.0489	0.3111
chr4	191154276	7718600	0.0404	0.3324
chr5	180915260	25141456	0.139	0.5105
chr6	171115067	31974165	0.1869	0.8636
chr7	159138663	32398609	0.2036	2.1732

chr8	146364022	10443108	0.0714	1.117
chr9	141213431	19321263	0.1368	0.7587
chr10	135534747	15350915	0.1133	0.7756
chr11	135006516	14409414	0.1067	0.6344
chr12	133851895	12658261	0.0946	0.4455
chr13	115169878	19266727	0.1673	0.5731
chr14	107349540	11483920	0.107	0.5016
chr15	102531392	3025149	0.0295	0.2673
chr16	90354753	5651869	0.0626	0.4504
chr17	81195210	8750736	0.1078	0.4971
chr18	78077248	6026483	0.0772	1.5602
chr19	59128983	12147573	0.2054	1.3924
chr20	63025520	9952842	0.1579	0.5633
chr21	48129895	5302406	0.1102	0.4892
chr22	51304566	2306447	0.045	0.2716
chrMT	16571	635743	38.3648	19.7975
chrX	155270560	10947981	0.0705	0.4401
chrY	59373566	681517	0.0115	0.2708

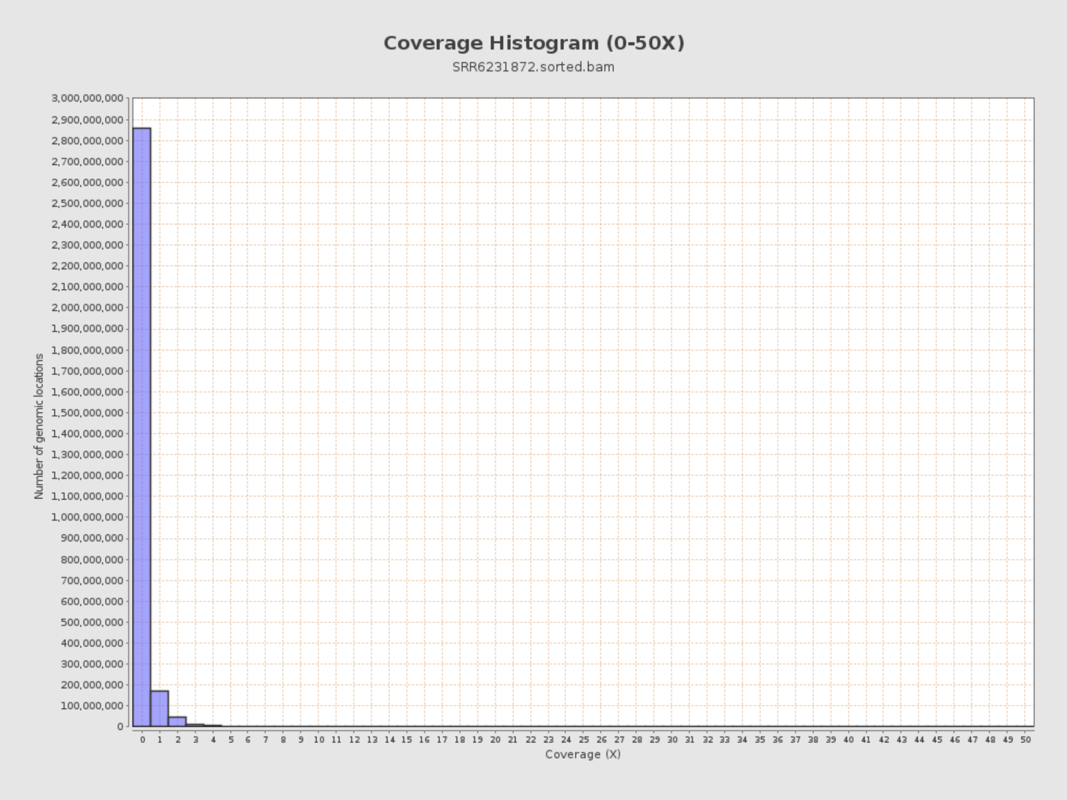
3. Results : Coverage across reference



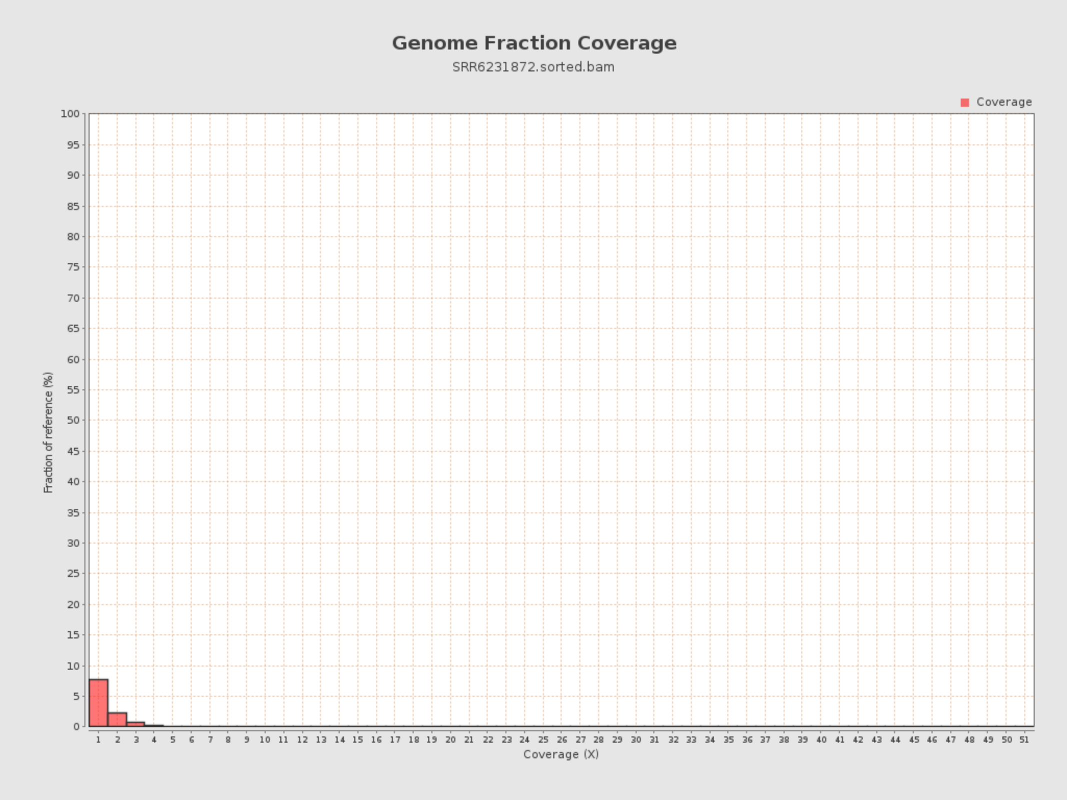
4. Results : Coverage Histogram



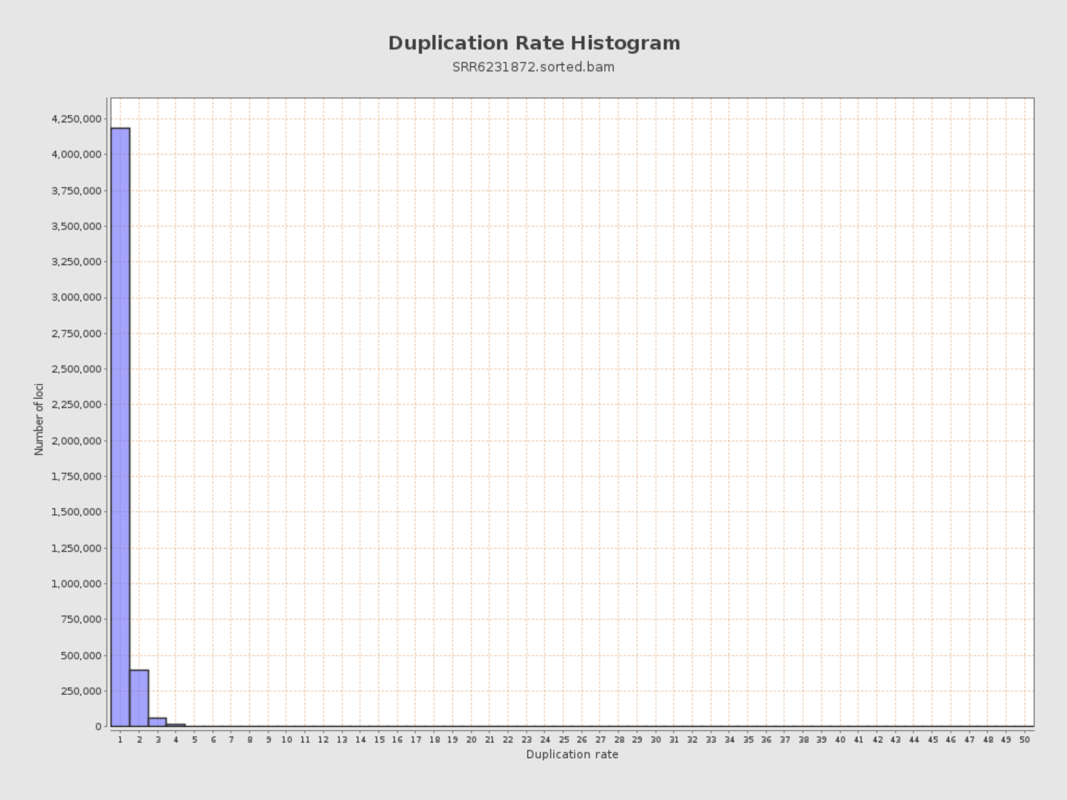
5. Results : Coverage Histogram (0-50X)



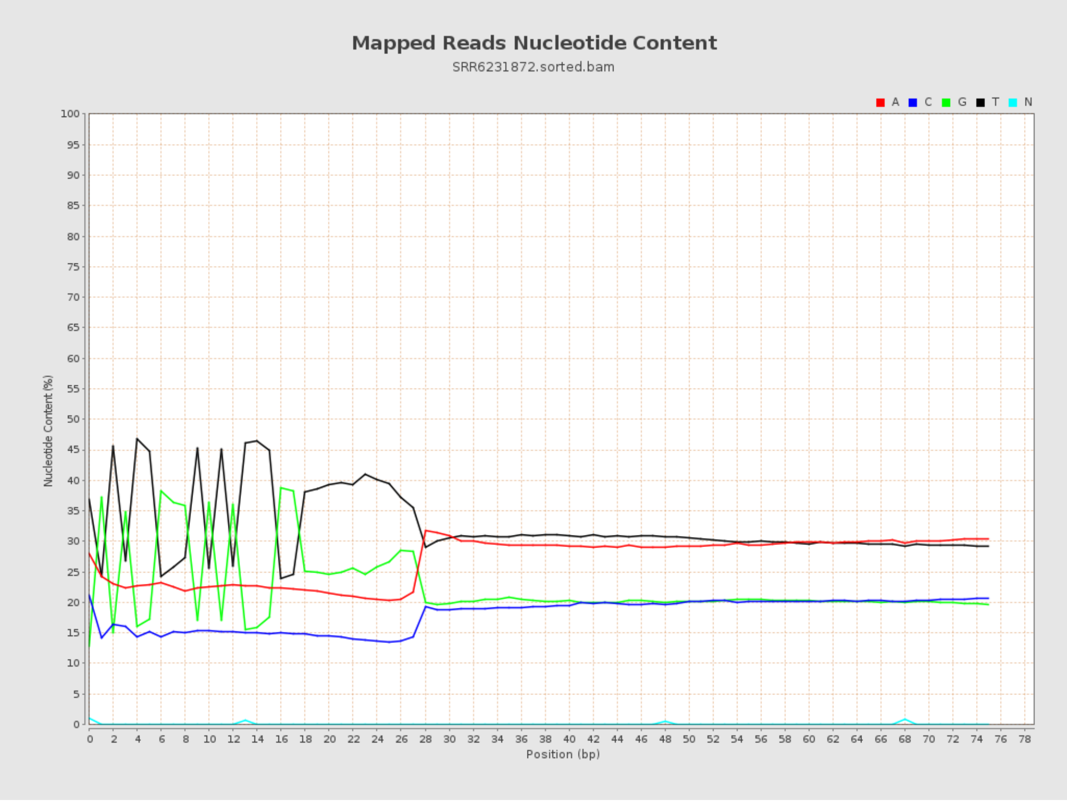
6. Results : Genome Fraction Coverage



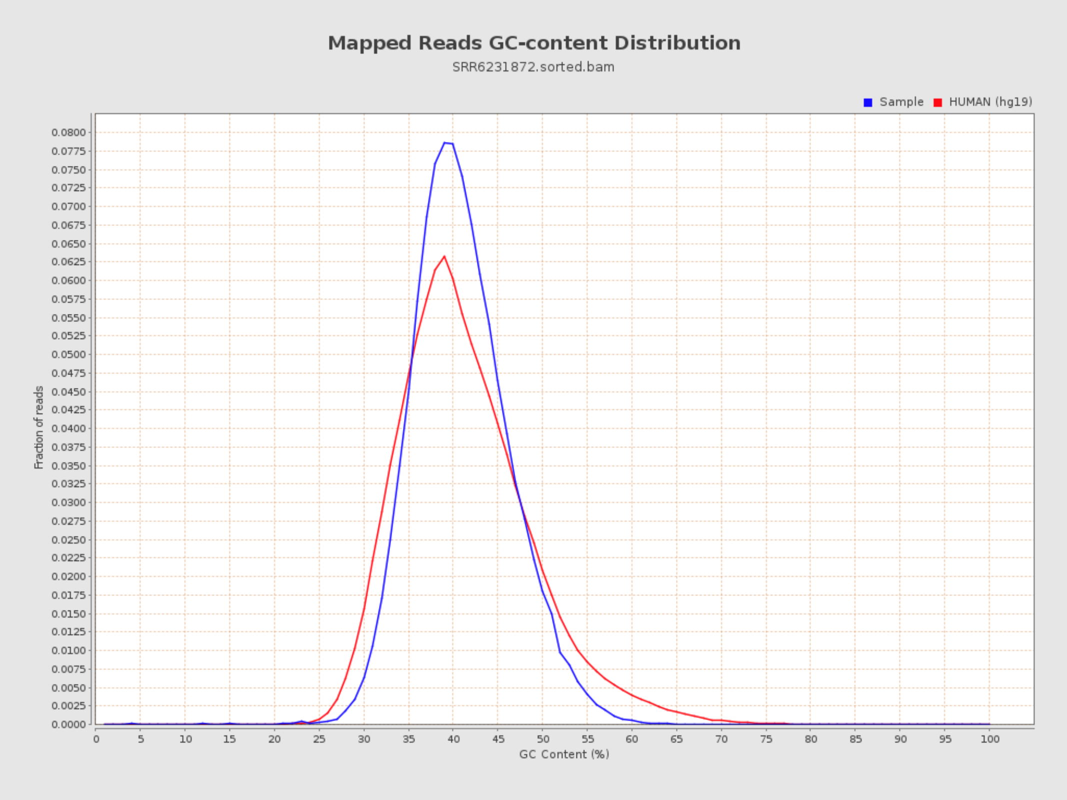
7. Results : Duplication Rate Histogram



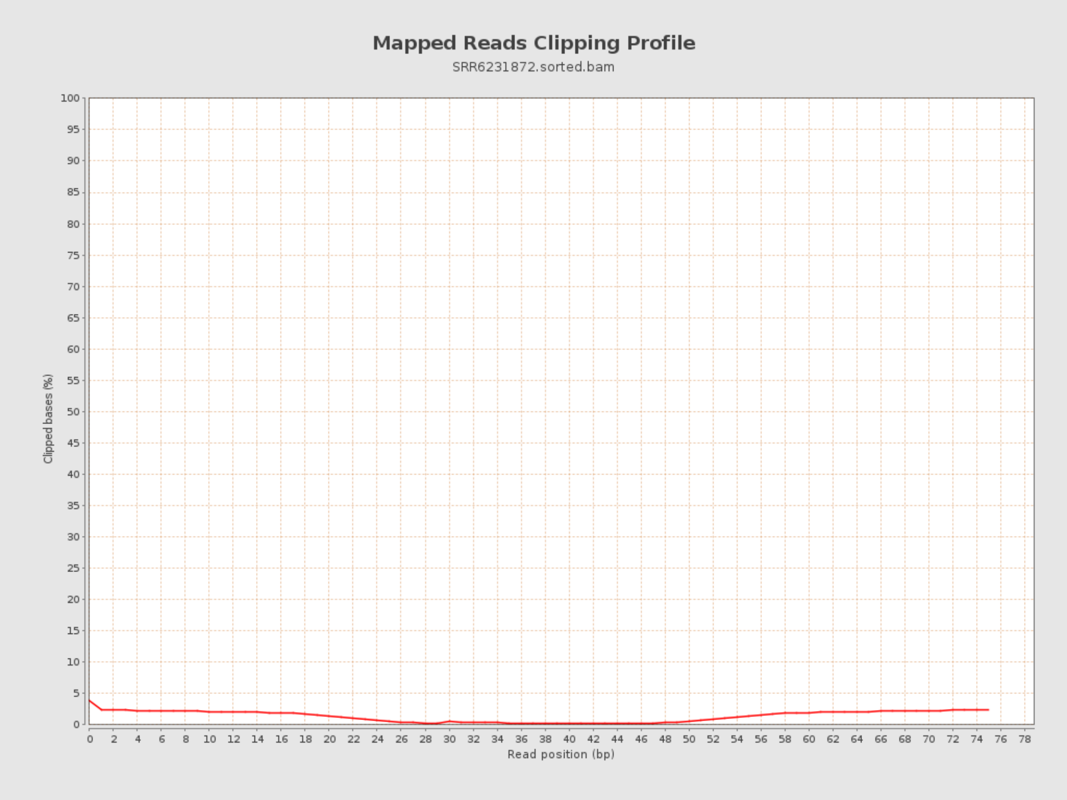
8. Results : Mapped Reads Nucleotide Content



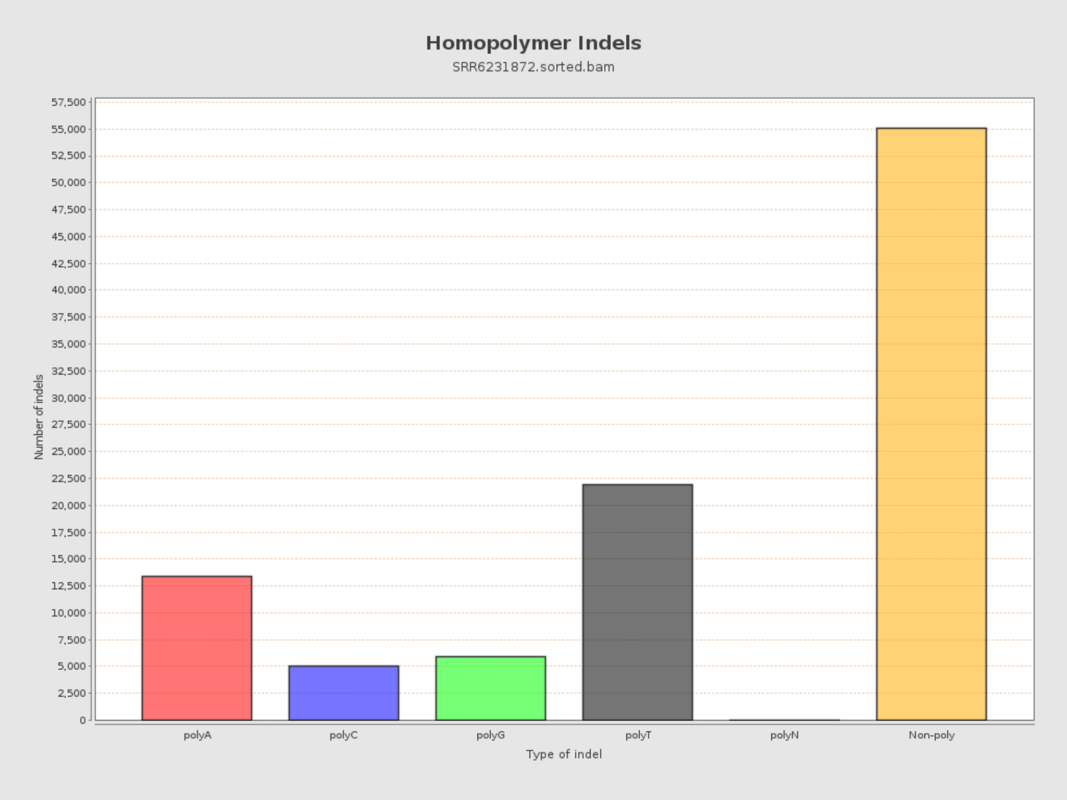
9. Results : Mapped Reads GC-content Distribution



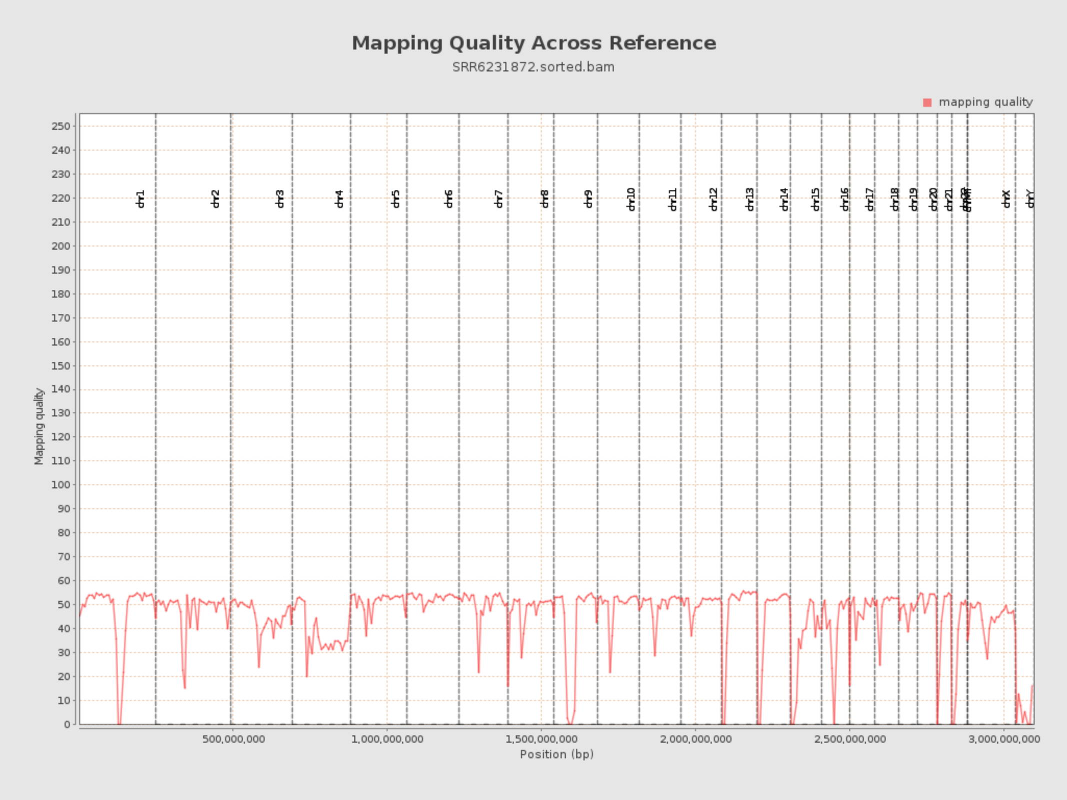
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram