Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:34:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231822.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_SRR6231822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:34:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,037,386
Mapped reads	500,477 / 48.24%
Unmapped reads	536,909 / 51.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,896 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	39,360 / 3.79%
Duplication rate	6.15%
Clipped reads	274,709 / 26.48%

2.2. ACGT Content

Number/percentage of A's	8,948,105 / 28.21%
Number/percentage of C's	5,205,801 / 16.41%
Number/percentage of T's	10,802,090 / 34.06%
Number/percentage of G's	6,758,352 / 21.31%
Number/percentage of N's	1,243 / 0%
GC Percentage	37.72%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.248

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

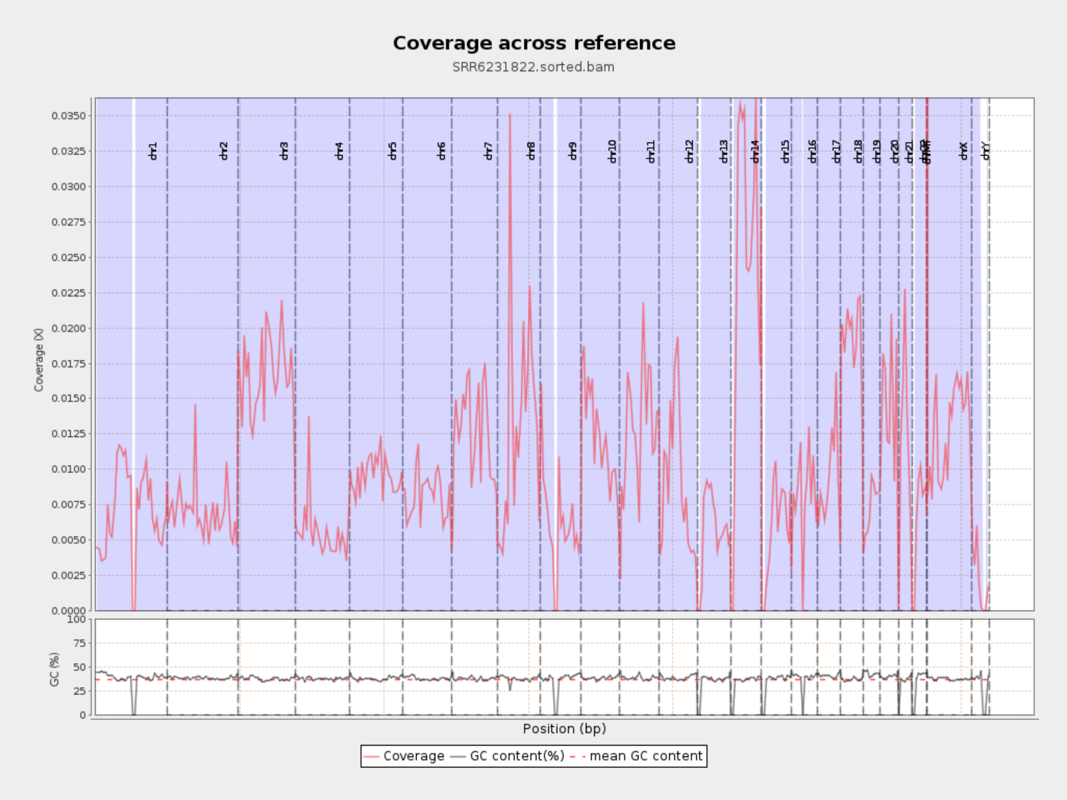
General error rate	0.97%
Mismatches	301,015
Insertions	3,023
Mapped reads with at least one insertion	0.6%
Deletions	11,383
Mapped reads with at least one deletion	2.24%
Homopolymer indels	43.61%

2.6. Chromosome stats

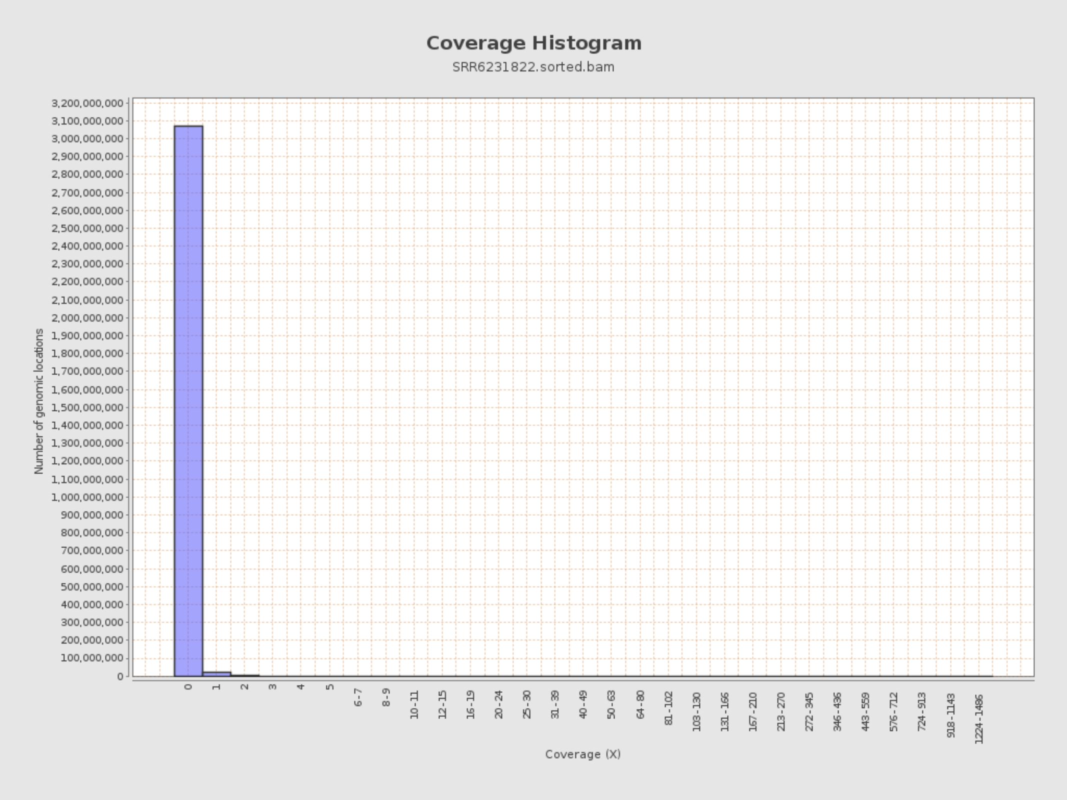
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1750771	0.007	0.1246
chr2	243199373	1703019	0.007	0.1377
chr3	198022430	3341580	0.0169	0.1605
chr4	191154276	1058924	0.0055	0.0946
chr5	180915260	1736387	0.0096	0.1218
chr6	171115067	1401974	0.0082	0.1267
chr7	159138663	2024721	0.0127	0.1764

chr8	146364022	1958346	0.0134	0.9375
chr9	141213431	886573	0.0063	0.1101
chr10	135534747	1672322	0.0123	0.1478
chr11	135006516	1734522	0.0128	0.1515
chr12	133851895	1196972	0.0089	0.1333
chr13	115169878	644179	0.0056	0.0946
chr14	107349540	2599096	0.0242	0.1989
chr15	102531392	583747	0.0057	0.1122
chr16	90354753	719681	0.008	0.1116
chr17	81195210	753490	0.0093	0.1201
chr18	78077248	1532470	0.0196	0.3579
chr19	59128983	436760	0.0074	0.1137
chr20	63025520	924985	0.0147	0.1487
chr21	48129895	580421	0.0121	0.139
chr22	51304566	344389	0.0067	0.0987
chrMT	16571	26813	1.6181	1.7171
chrX	155270560	1996756	0.0129	0.1427
chrY	59373566	126582	0.0021	0.058

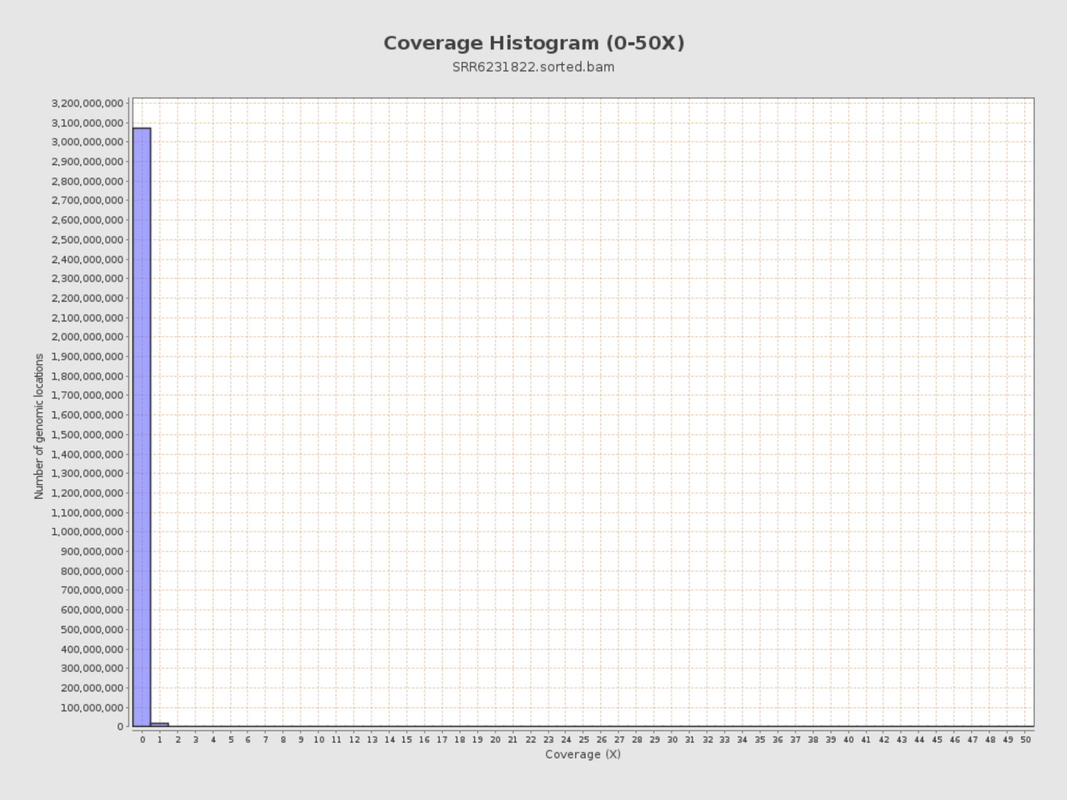
3. Results : Coverage across reference



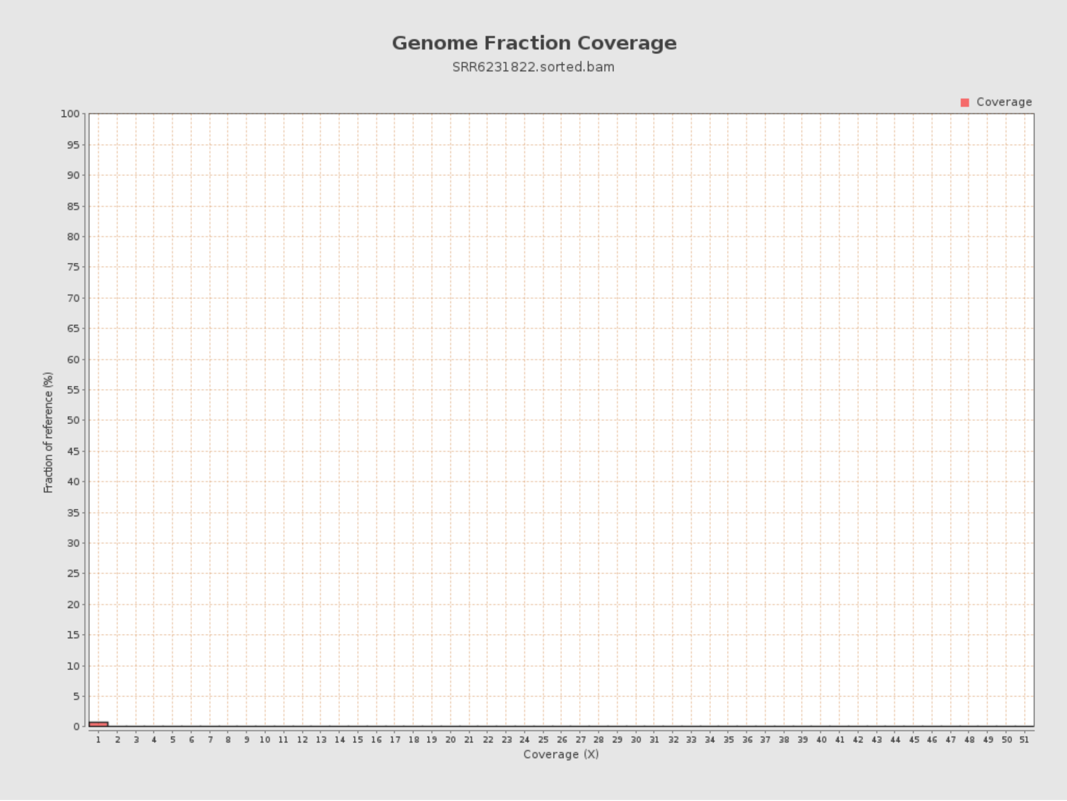
4. Results : Coverage Histogram



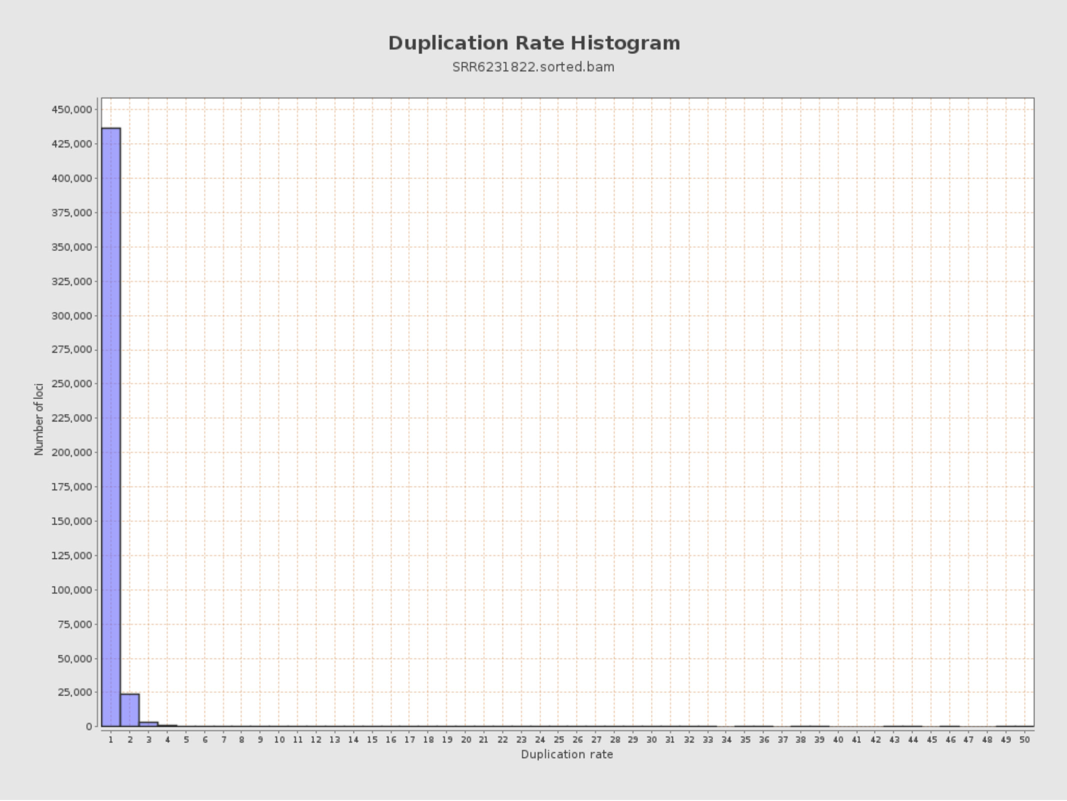
5. Results : Coverage Histogram (0-50X)



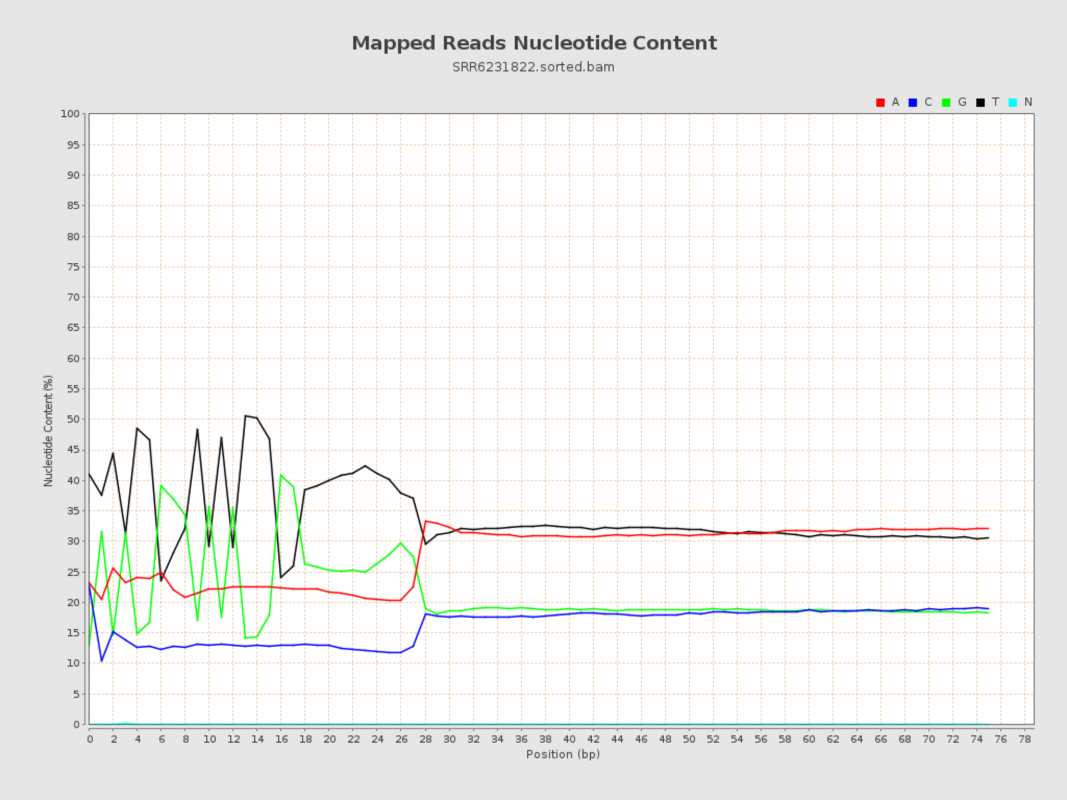
6. Results : Genome Fraction Coverage



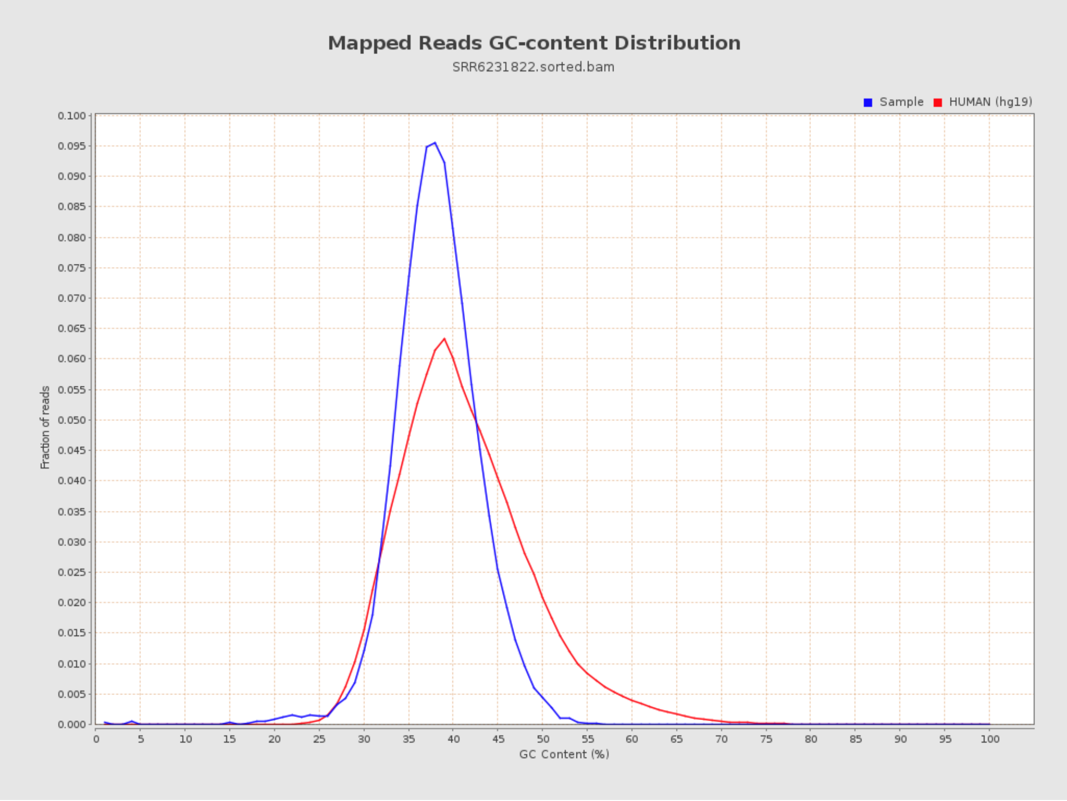
7. Results : Duplication Rate Histogram



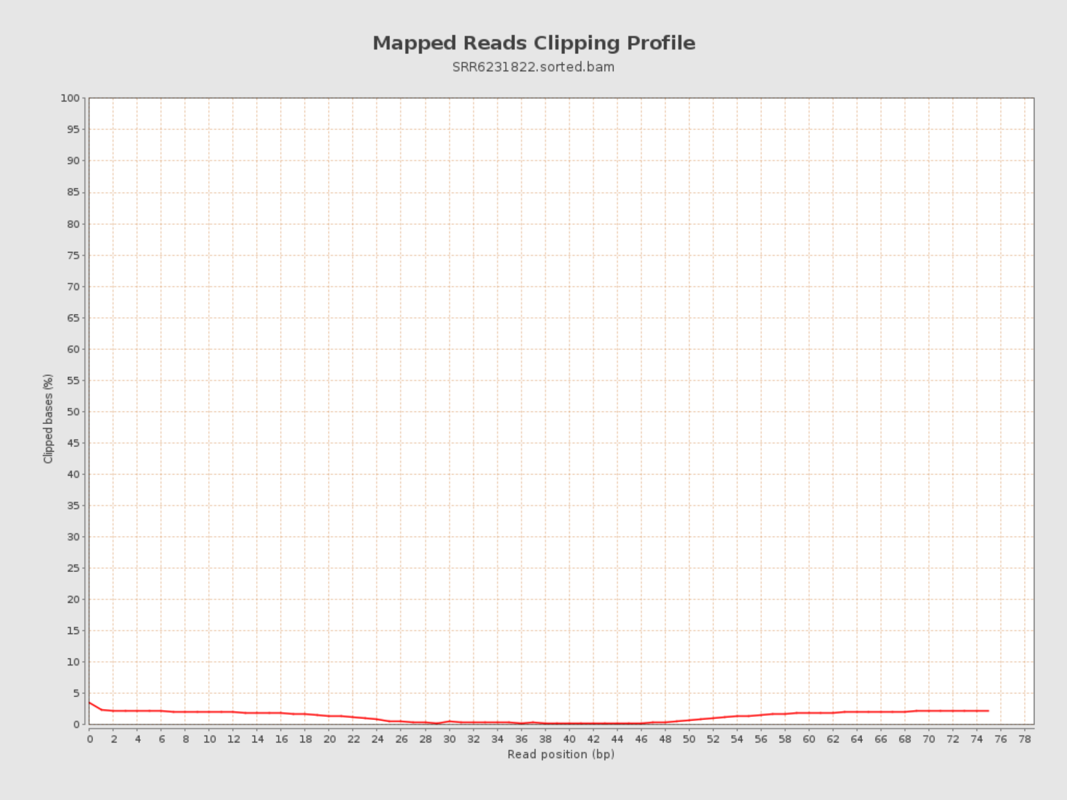
8. Results : Mapped Reads Nucleotide Content



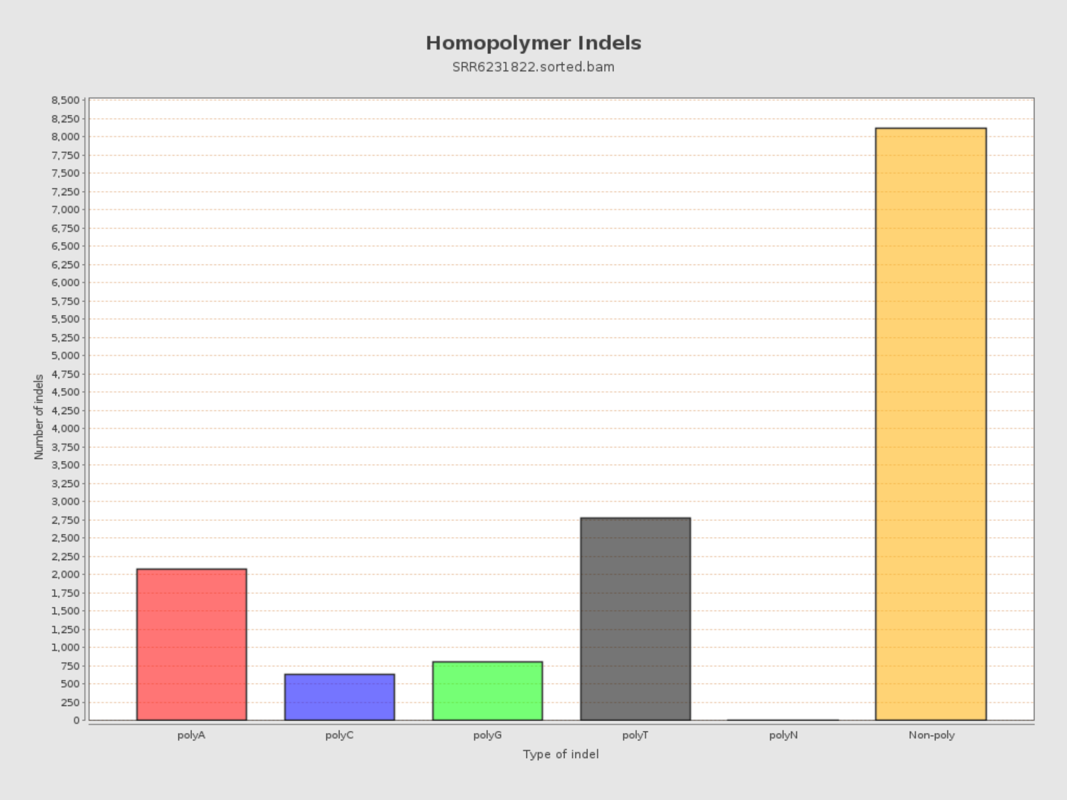
9. Results : Mapped Reads GC-content Distribution



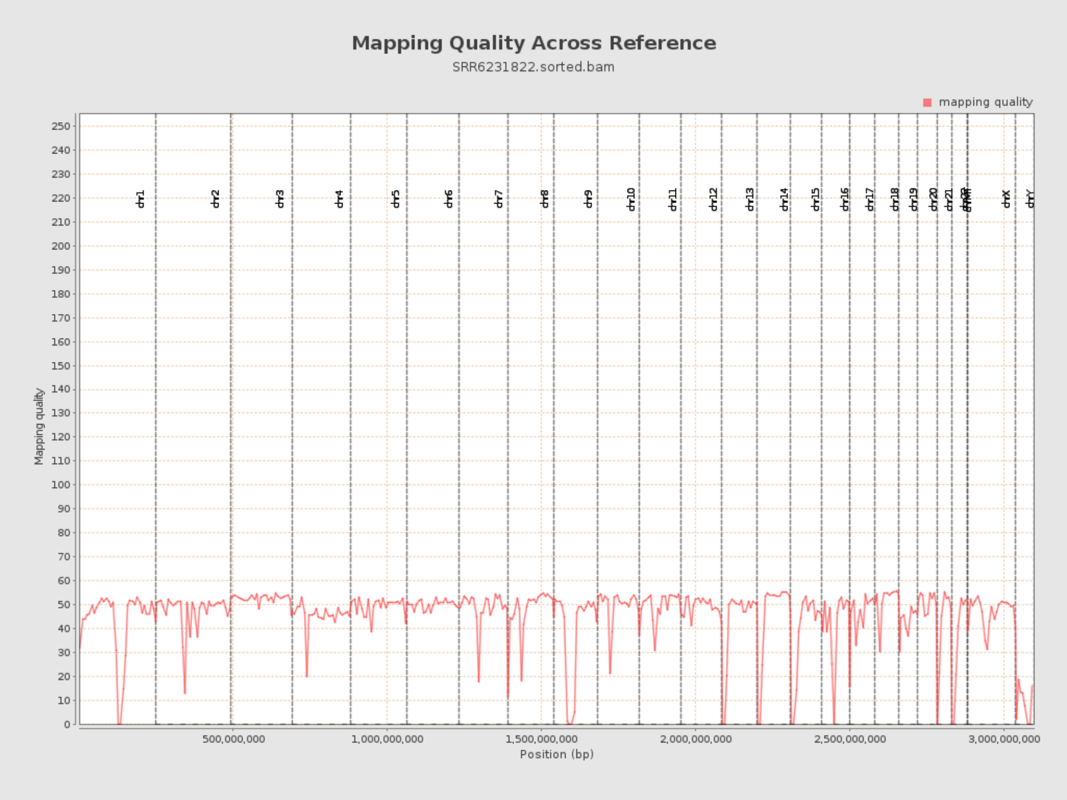
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram