Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:32:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231821.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_SRR6231821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:32:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,477,018
Mapped reads	710,888 / 48.13%
Unmapped reads	766,130 / 51.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,235 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	112,189 / 7.6%
Duplication rate	11.6%
Clipped reads	348,786 / 23.61%

2.2. ACGT Content

Number/percentage of A's	12,834,068 / 27.82%
Number/percentage of C's	8,148,145 / 17.66%
Number/percentage of T's	15,070,939 / 32.67%
Number/percentage of G's	10,069,193 / 21.82%
Number/percentage of N's	15,389 / 0.03%
GC Percentage	39.48%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.2473

2.4. Mapping Quality

Mean Mapping Quality	46.8

2.5. Mismatches and indels

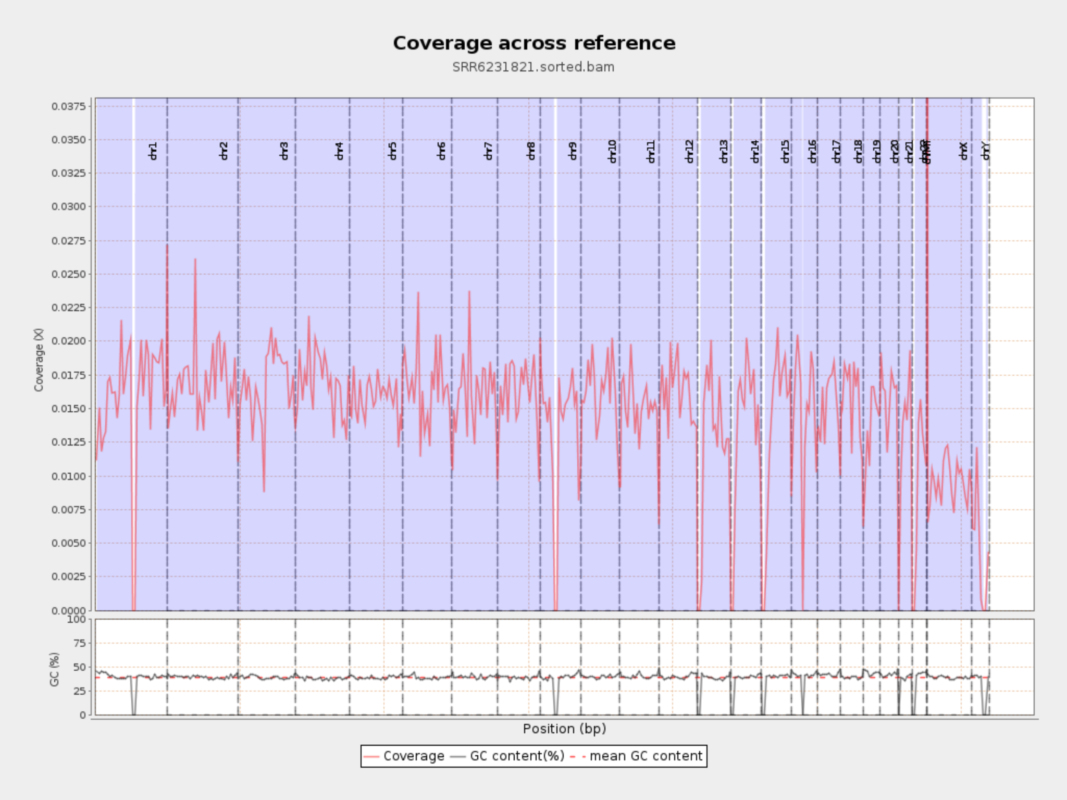
General error rate	0.93%
Mismatches	419,079
Insertions	4,138
Mapped reads with at least one insertion	0.57%
Deletions	14,558
Mapped reads with at least one deletion	2.02%
Homopolymer indels	48.14%

2.6. Chromosome stats

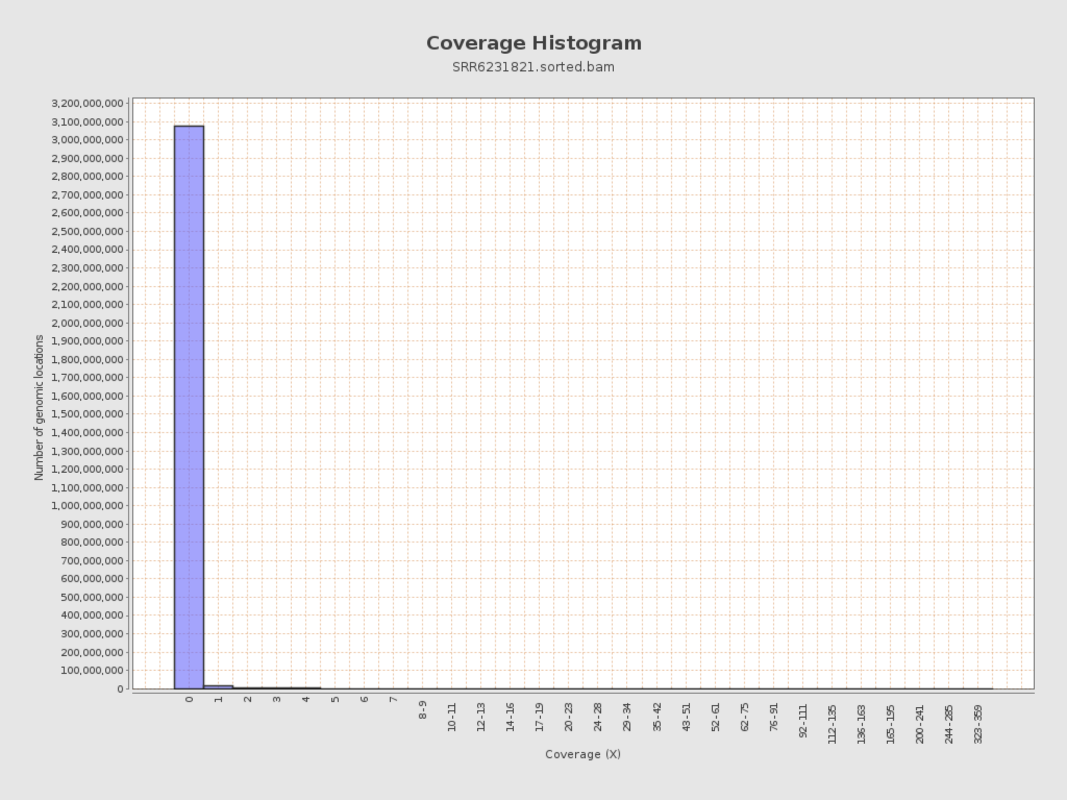
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3934389	0.0158	0.2576
chr2	243199373	4125273	0.017	0.2655
chr3	198022430	3313999	0.0167	0.2728
chr4	191154276	3216364	0.0168	0.2519
chr5	180915260	2857753	0.0158	0.274
chr6	171115067	2838100	0.0166	0.2516
chr7	159138663	2567011	0.0161	0.2785

chr8	146364022	2362481	0.0161	0.3143
chr9	141213431	1891155	0.0134	0.2275
chr10	135534747	2209605	0.0163	0.2494
chr11	135006516	2056261	0.0152	0.2387
chr12	133851895	2177733	0.0163	0.2374
chr13	115169878	1394360	0.0121	0.2066
chr14	107349540	1427337	0.0133	0.2164
chr15	102531392	1379451	0.0135	0.2183
chr16	90354753	1278591	0.0142	0.2247
chr17	81195210	1237067	0.0152	0.2241
chr18	78077248	1245727	0.016	0.3209
chr19	59128983	800898	0.0135	0.2129
chr20	63025520	993682	0.0158	0.2231
chr21	48129895	629510	0.0131	0.2166
chr22	51304566	473400	0.0092	0.1653
chrMT	16571	6579	0.397	0.9252
chrX	155270560	1483067	0.0096	0.1768
chrY	59373566	263256	0.0044	0.1132

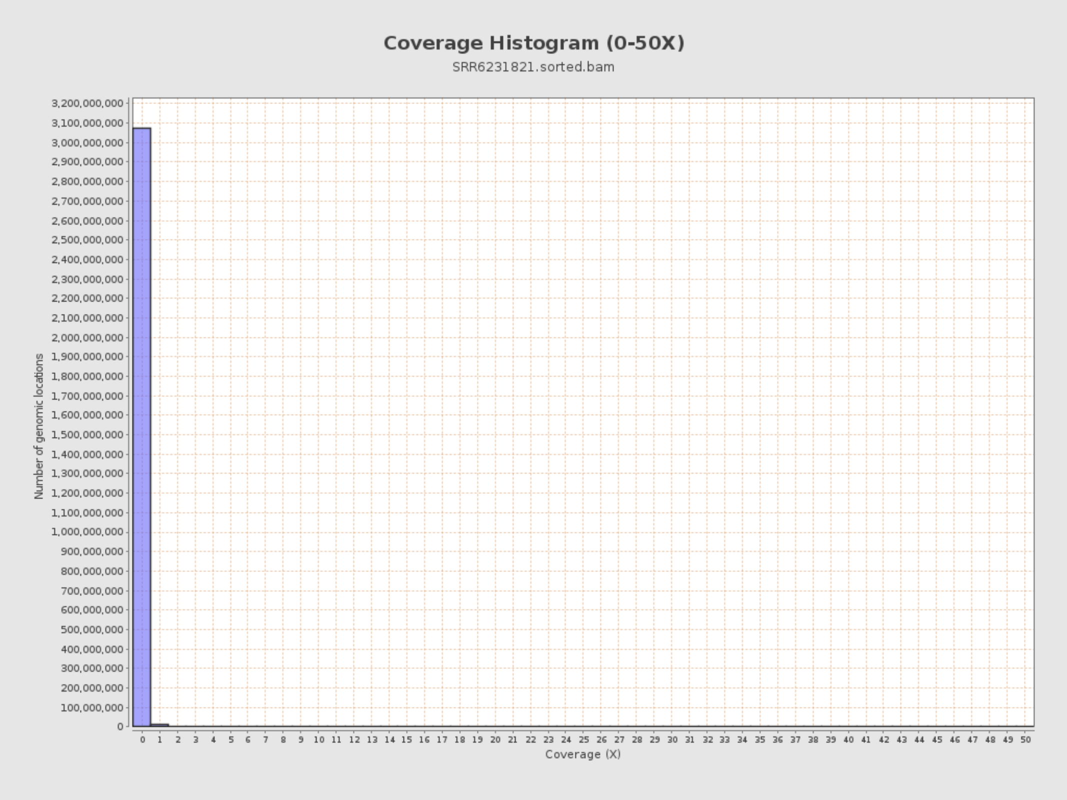
3. Results : Coverage across reference



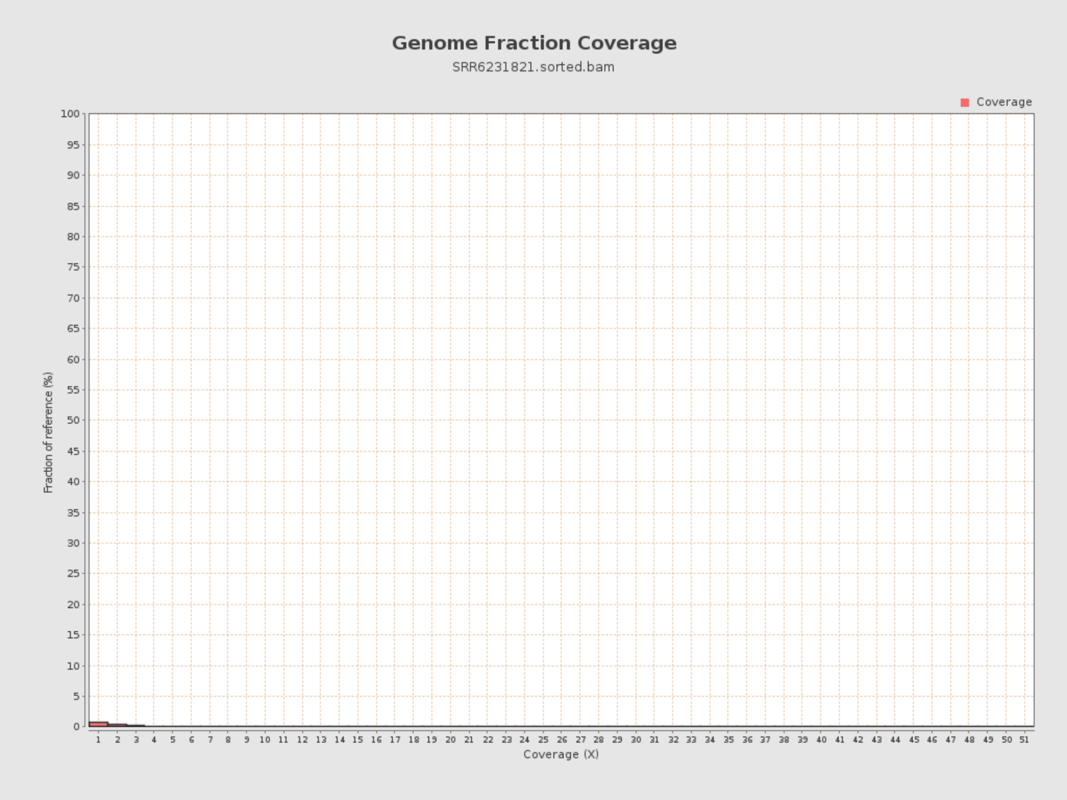
4. Results : Coverage Histogram



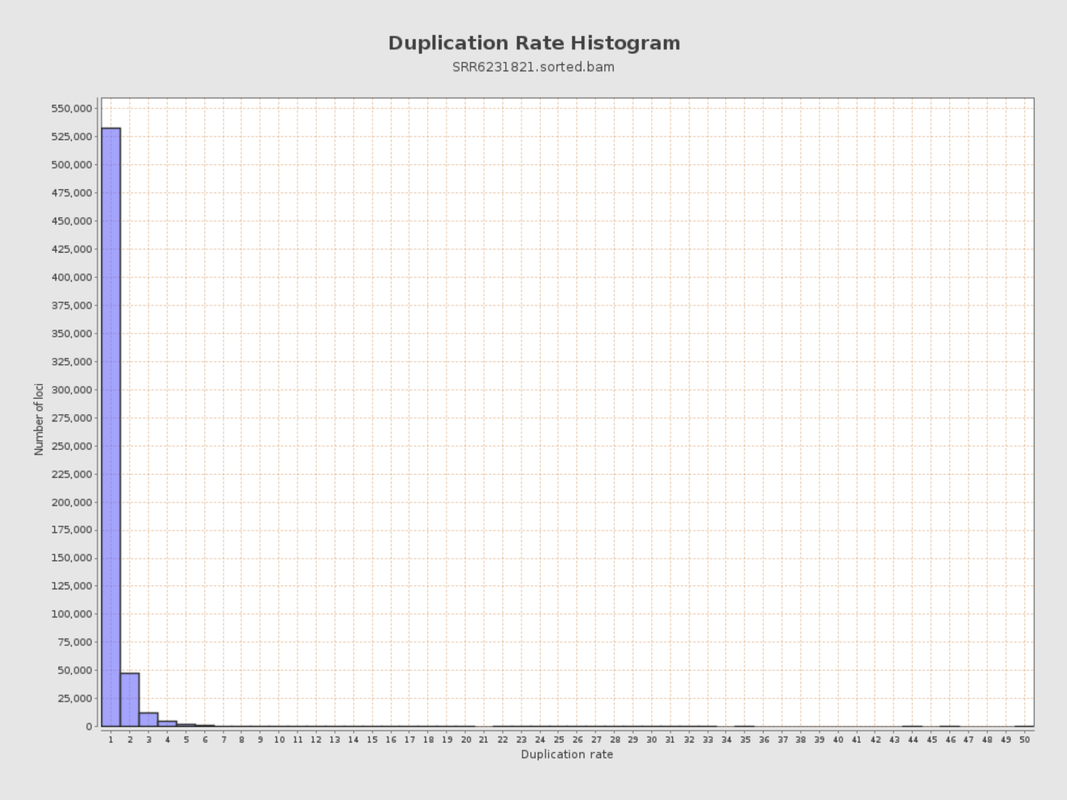
5. Results : Coverage Histogram (0-50X)



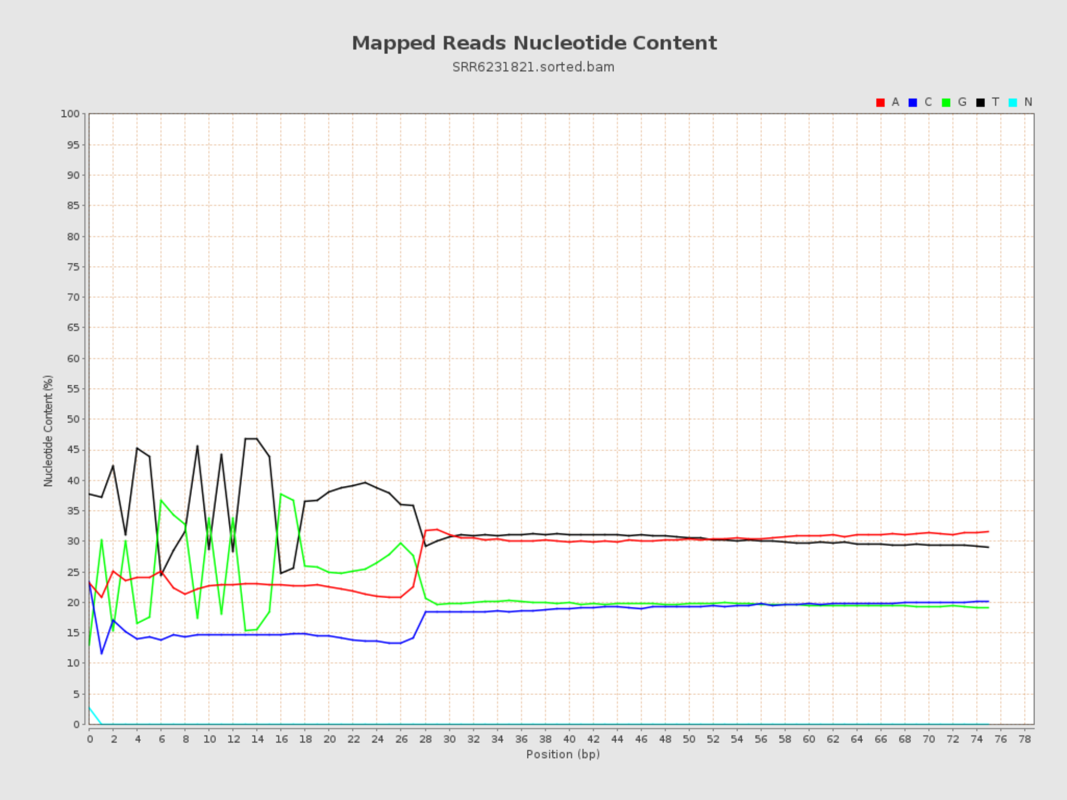
6. Results : Genome Fraction Coverage



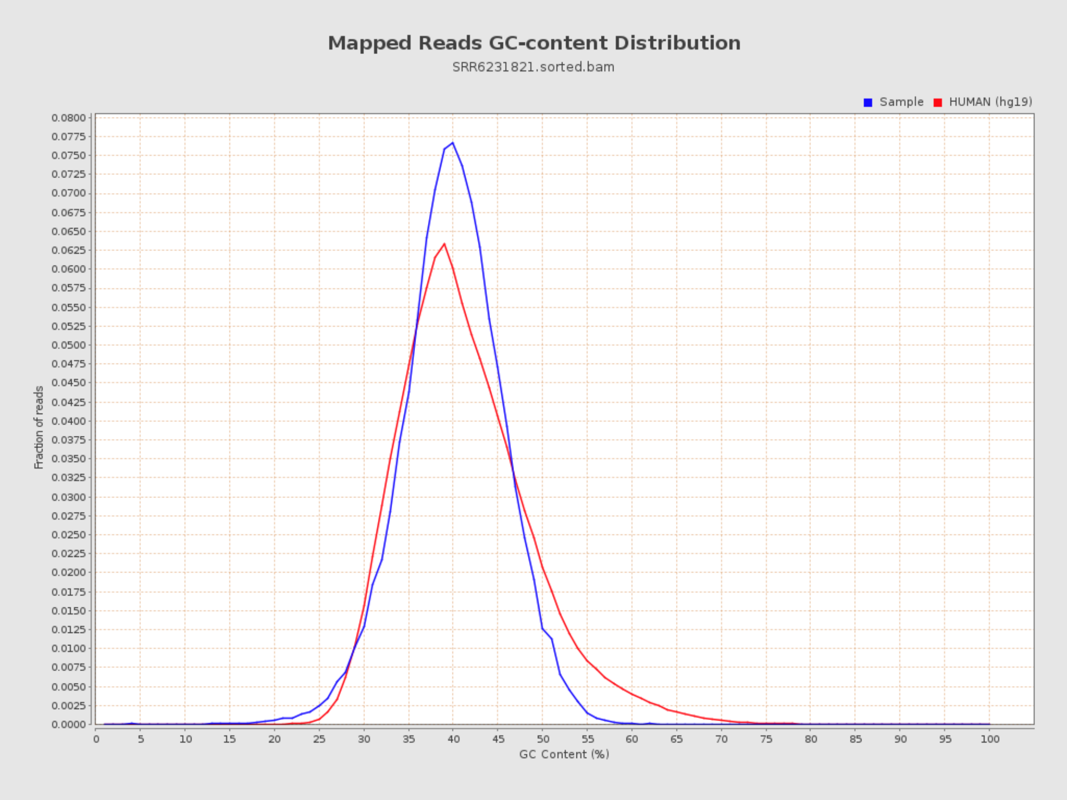
7. Results : Duplication Rate Histogram



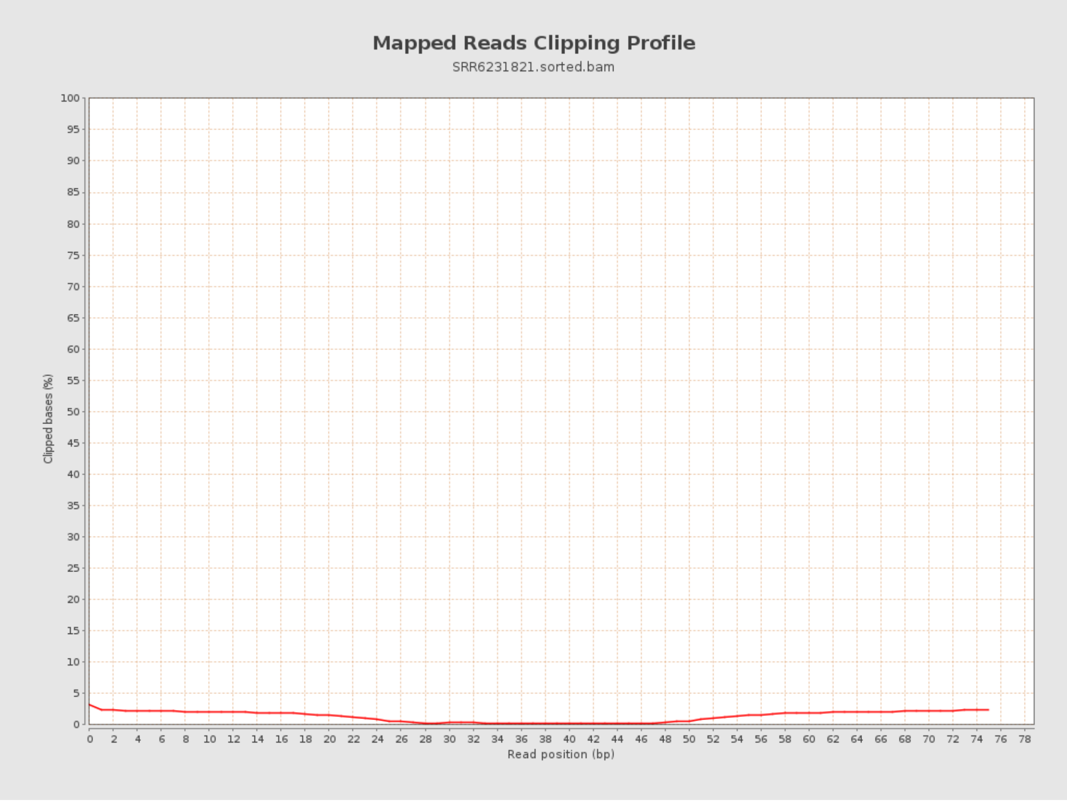
8. Results : Mapped Reads Nucleotide Content



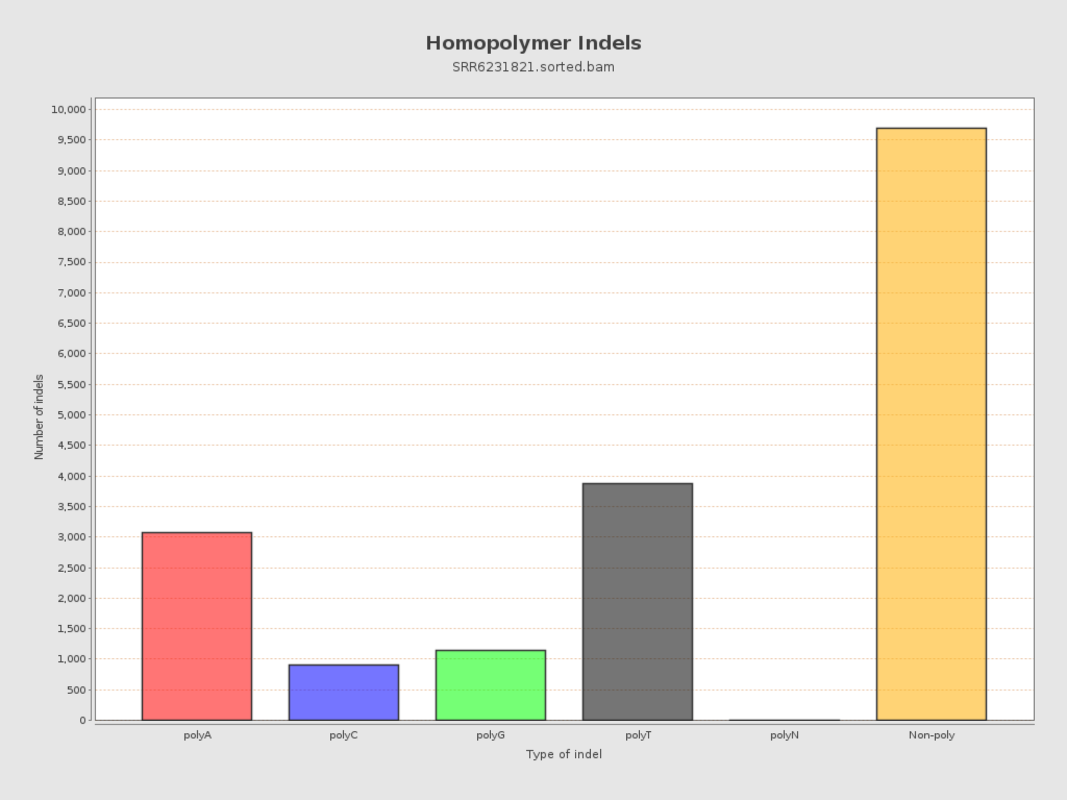
9. Results : Mapped Reads GC-content Distribution



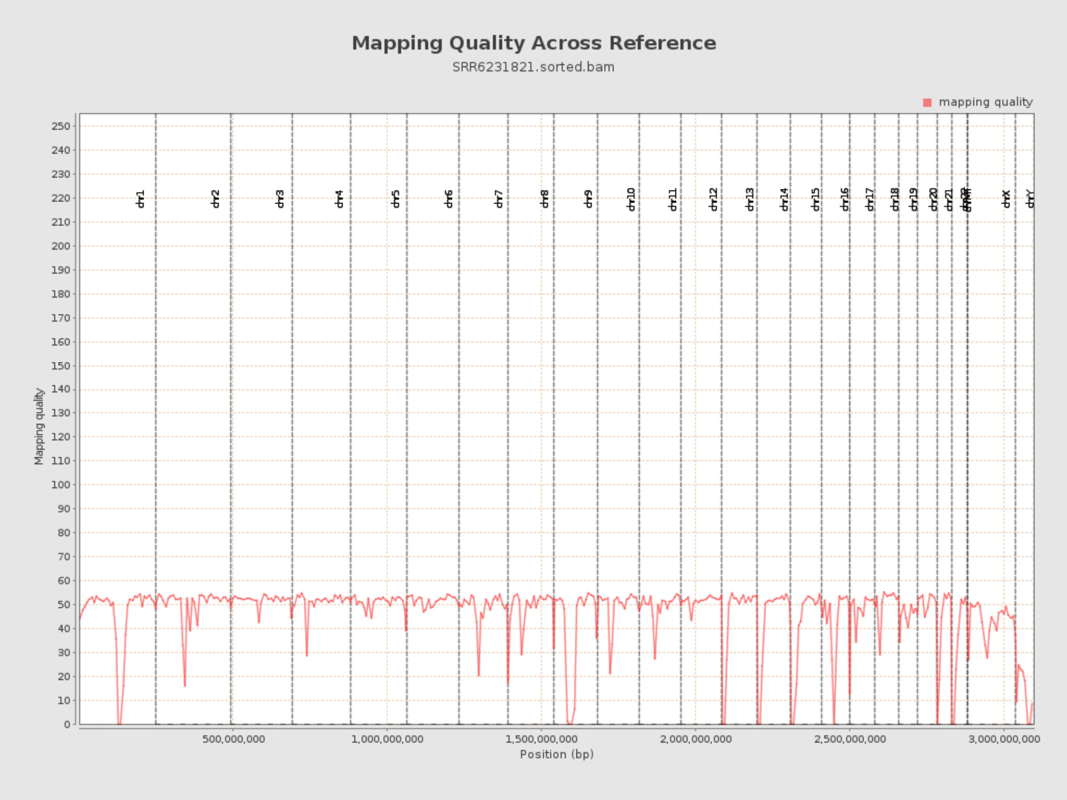
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram