Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:00:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234131.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_SRR6234131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:00:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,327,598
Mapped reads	1,019,563 / 76.8%
Unmapped reads	308,035 / 23.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,662 / 0.13%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	792,935 / 59.73%
Duplication rate	6.66%
Clipped reads	216,105 / 16.28%

2.2. ACGT Content

Number/percentage of A's	3,378,742 / 4.65%
Number/percentage of C's	2,293,718 / 3.16%
Number/percentage of T's	4,865,607 / 6.69%
Number/percentage of G's	62,141,044 / 85.49%
Number/percentage of N's	7,156 / 0.01%
GC Percentage	88.65%

2.3. Coverage

Mean	0.0235

Standard Deviation	118.521

2.4. Mapping Quality

Mean Mapping Quality	36.56

2.5. Mismatches and indels

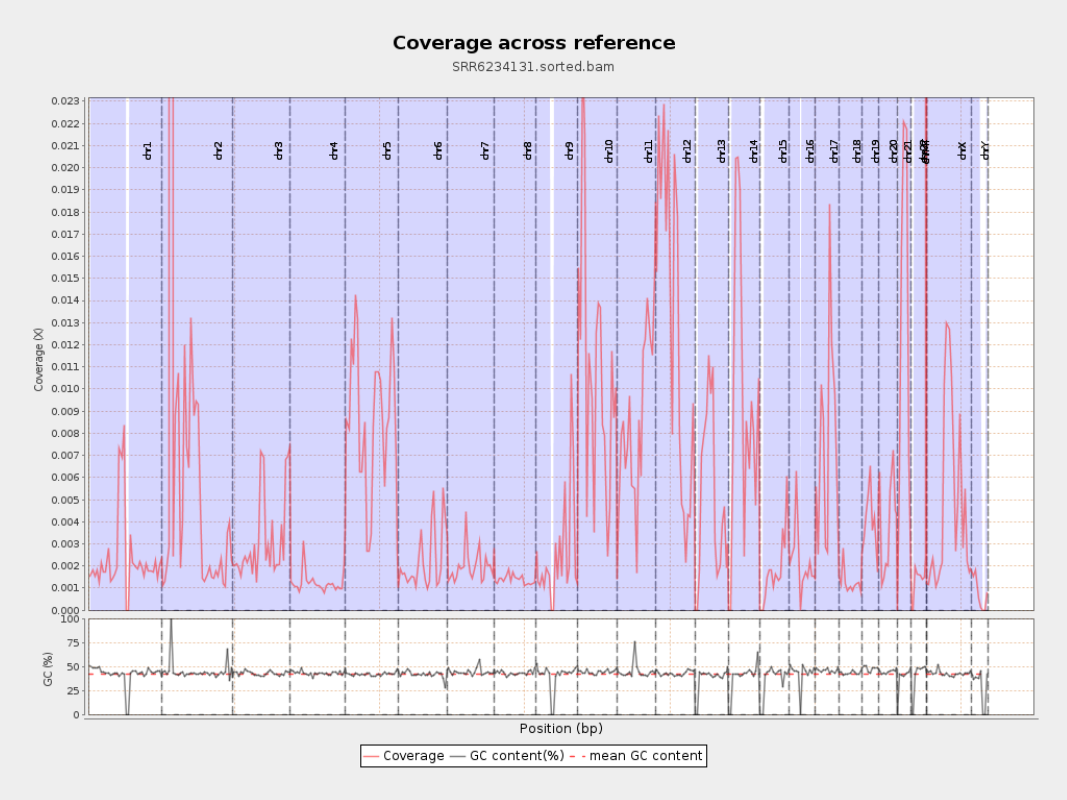
General error rate	0.39%
Mismatches	276,214
Insertions	2,343
Mapped reads with at least one insertion	0.22%
Deletions	3,079
Mapped reads with at least one deletion	0.3%
Homopolymer indels	37.81%

2.6. Chromosome stats

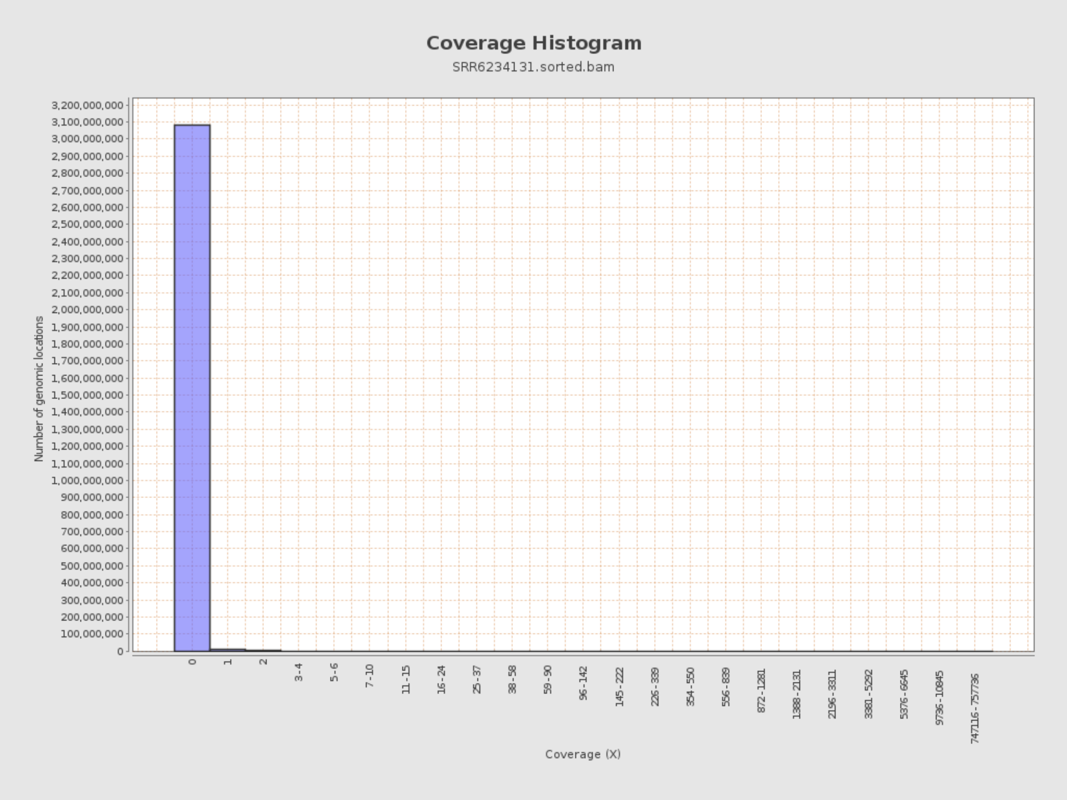
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	573578	0.0023	0.0697
chr2	243199373	59520283	0.2447	422.8563
chr3	198022430	614069	0.0031	0.068
chr4	191154276	236016	0.0012	0.0437
chr5	180915260	1553316	0.0086	0.1105
chr6	171115067	380659	0.0022	0.1368
chr7	159138663	313783	0.002	0.1495

chr8	146364022	202668	0.0014	0.0509
chr9	141213431	361875	0.0026	0.0642
chr10	135534747	1484763	0.011	0.1395
chr11	135006516	1160476	0.0086	0.3745
chr12	133851895	1679229	0.0125	0.1604
chr13	115169878	586689	0.0051	0.0939
chr14	107349540	988819	0.0092	0.4168
chr15	102531392	192363	0.0019	0.1326
chr16	90354753	202219	0.0022	0.0605
chr17	81195210	621958	0.0077	0.1124
chr18	78077248	99429	0.0013	0.0514
chr19	59128983	243093	0.0041	0.0878
chr20	63025520	234021	0.0037	0.0726
chr21	48129895	575236	0.012	0.1332
chr22	51304566	67198	0.0013	0.0401
chrMT	16571	13373	0.807	2.5312
chrX	155270560	739275	0.0048	0.0872
chrY	59373566	46408	0.0008	0.042

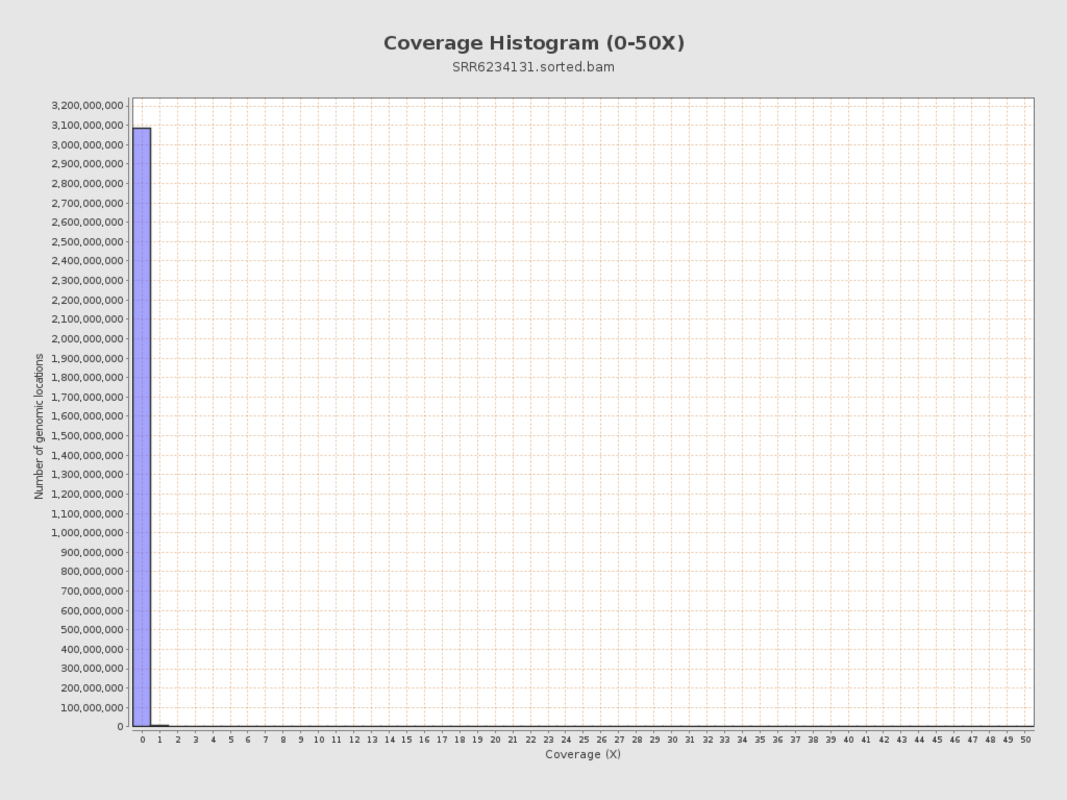
3. Results : Coverage across reference



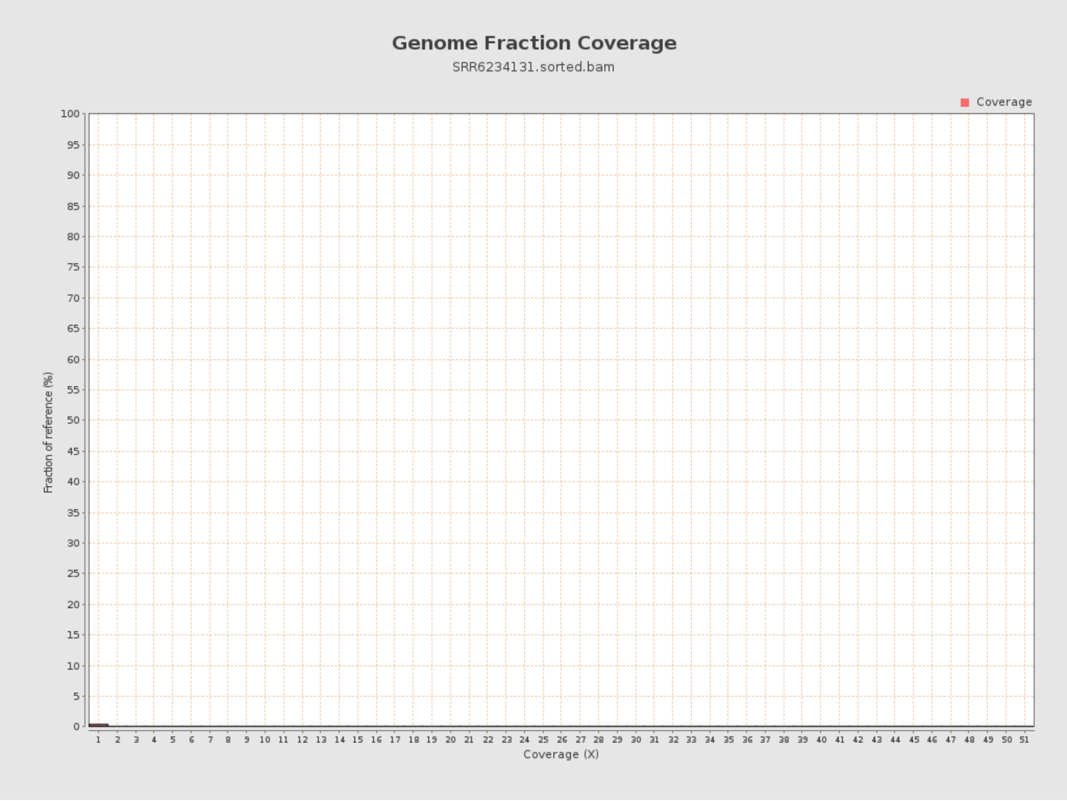
4. Results : Coverage Histogram



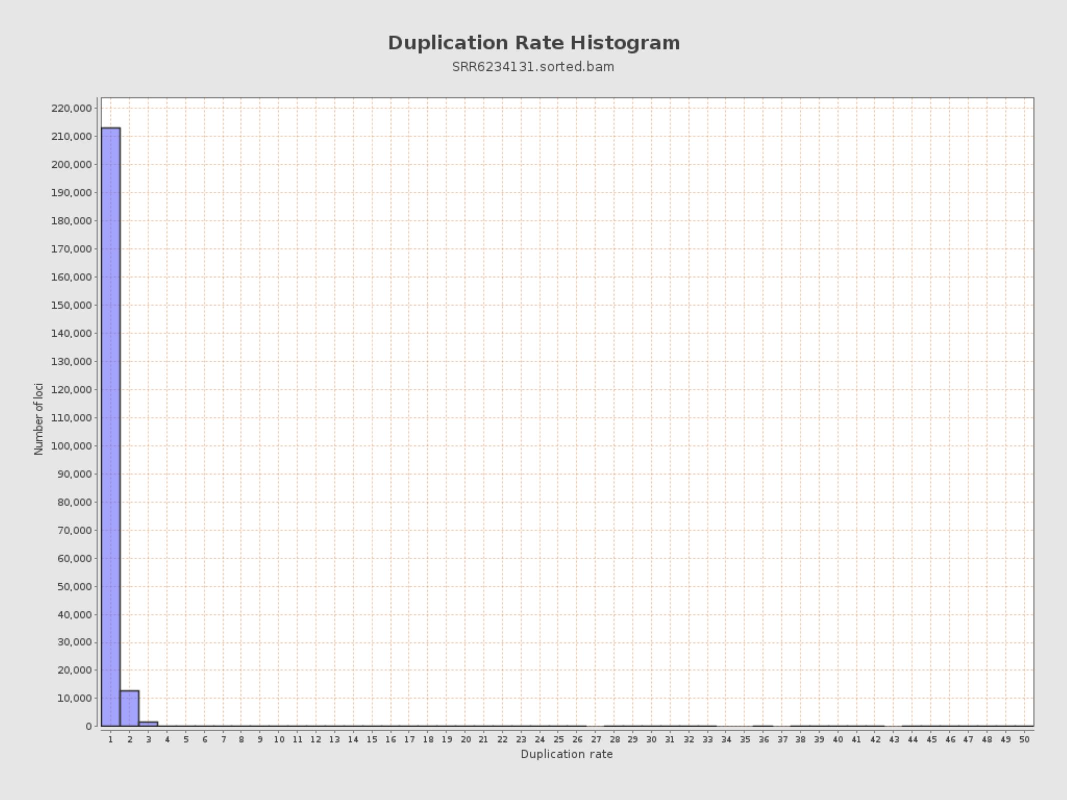
5. Results : Coverage Histogram (0-50X)



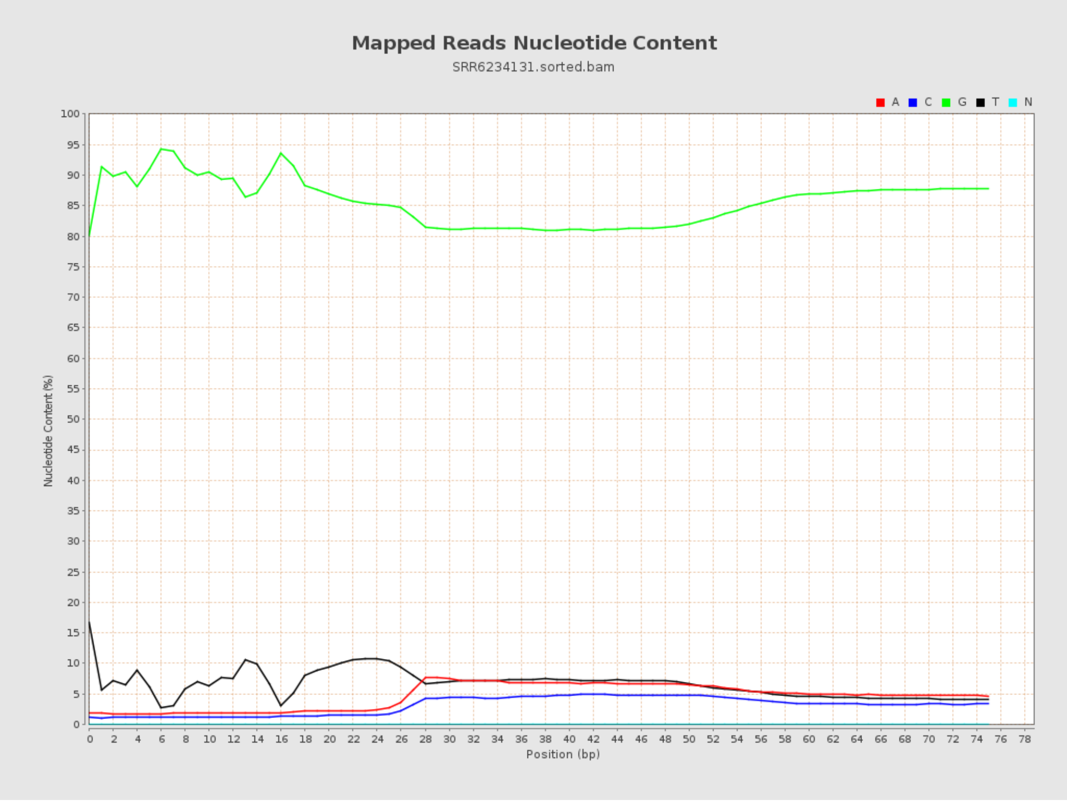
6. Results : Genome Fraction Coverage



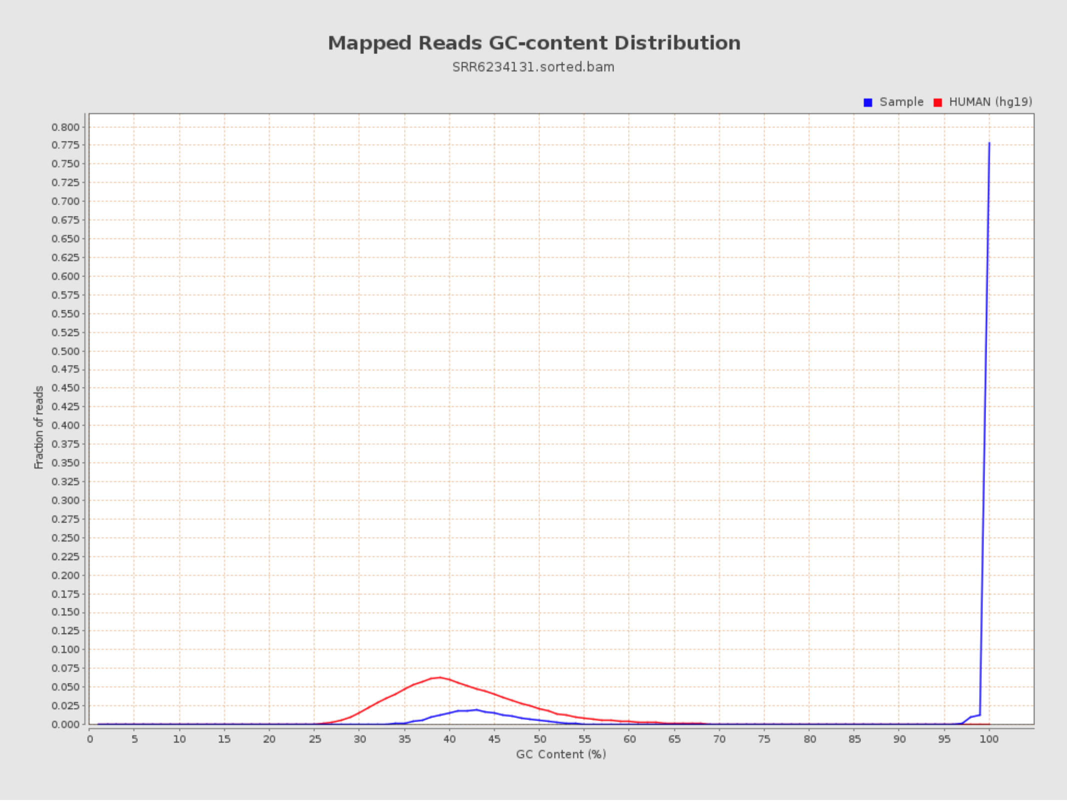
7. Results : Duplication Rate Histogram



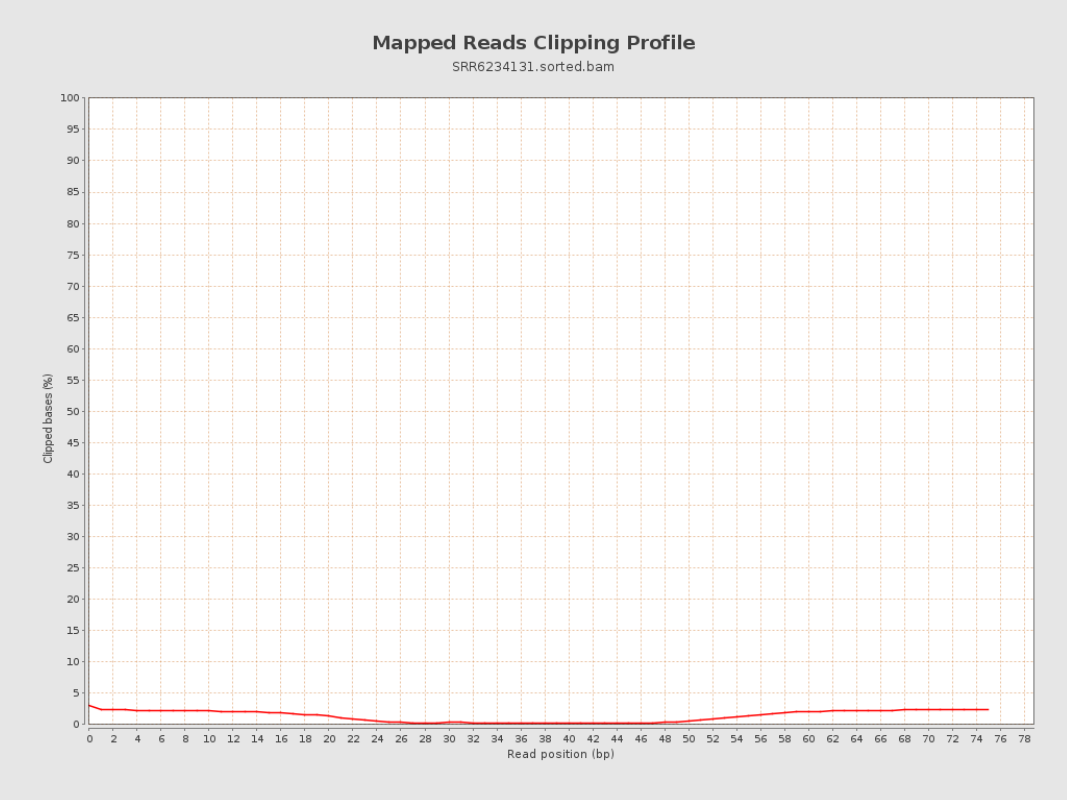
8. Results : Mapped Reads Nucleotide Content



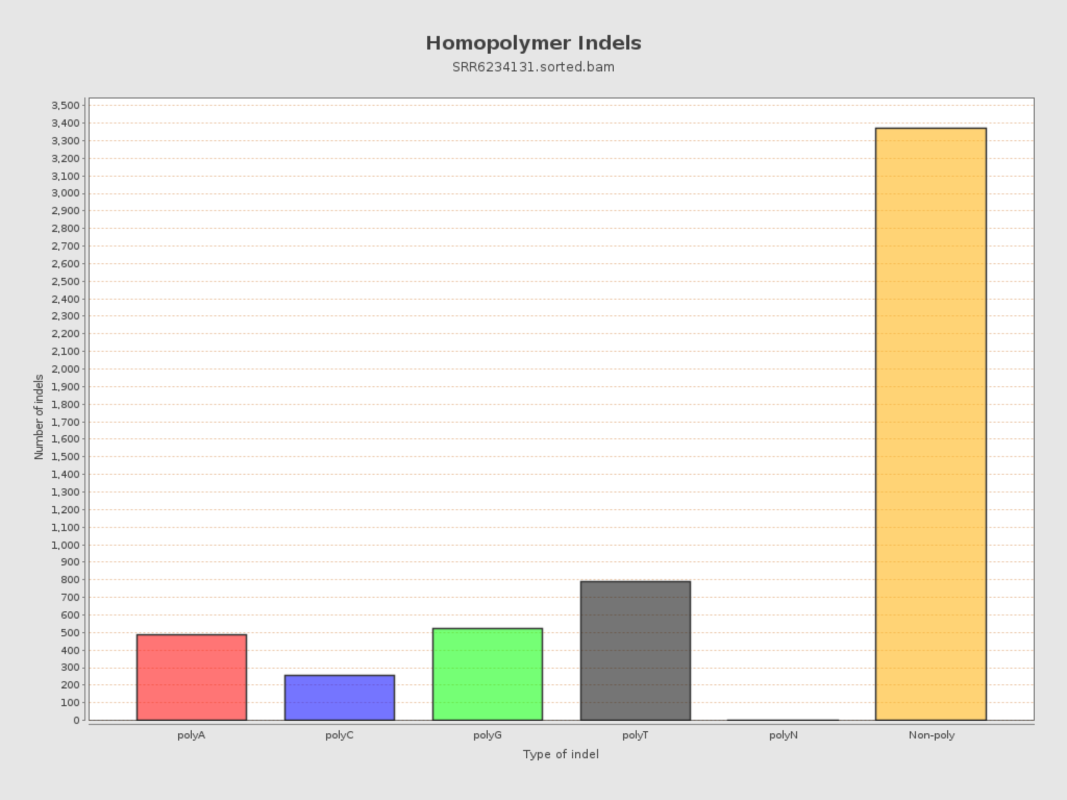
9. Results : Mapped Reads GC-content Distribution



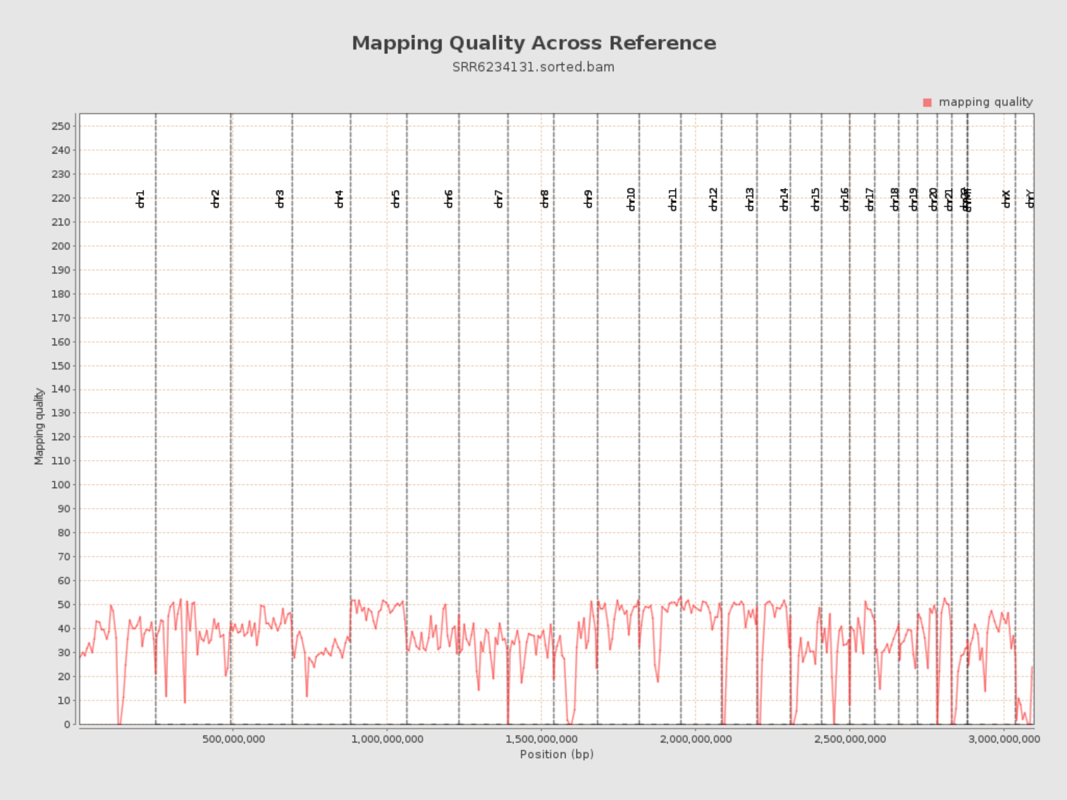
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram