Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:11:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231752.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_SRR6231752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:11:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,508,495
Mapped reads	5,152,024 / 93.53%
Unmapped reads	356,471 / 6.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,716 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	601,980 / 10.93%
Duplication rate	5.38%
Clipped reads	1,916,048 / 34.78%

2.2. ACGT Content

Number/percentage of A's	92,186,488 / 26.21%
Number/percentage of C's	65,073,811 / 18.5%
Number/percentage of T's	100,341,868 / 28.53%
Number/percentage of G's	94,017,608 / 26.73%
Number/percentage of N's	75,591 / 0.02%
GC Percentage	45.24%

2.3. Coverage

Mean	0.1136

Standard Deviation	38.8126

2.4. Mapping Quality

Mean Mapping Quality	41.18

2.5. Mismatches and indels

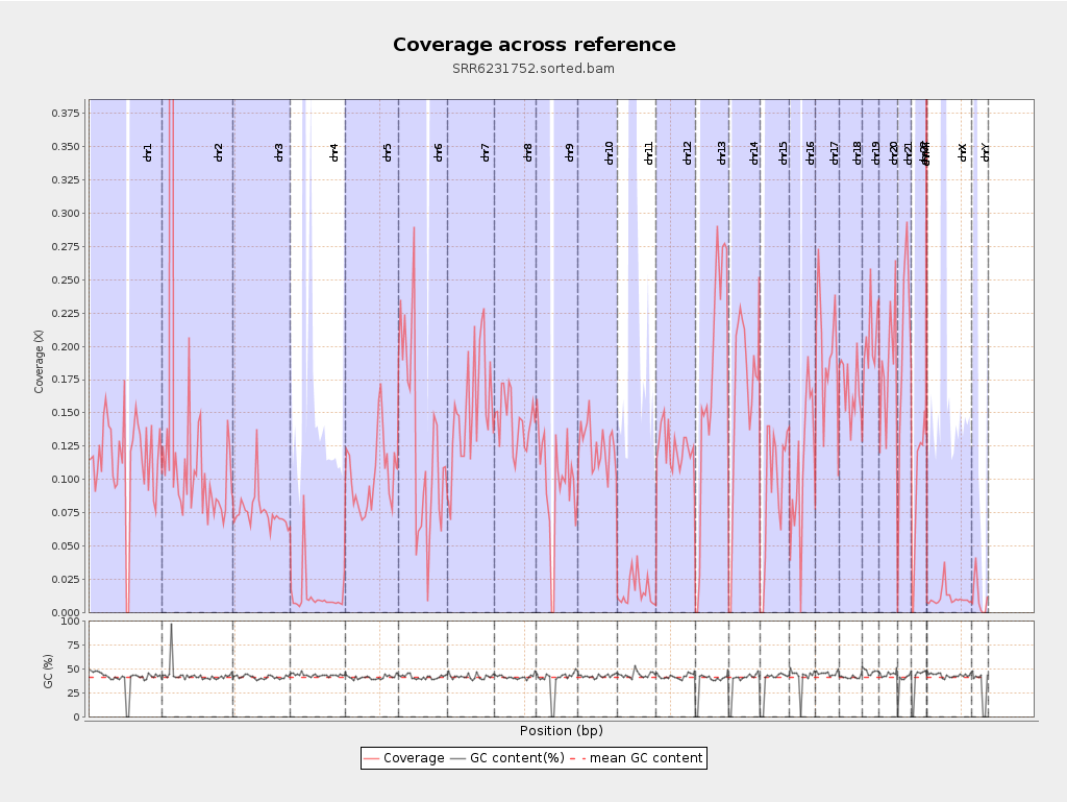
General error rate	0.67%
Mismatches	2,313,972
Insertions	24,419
Mapped reads with at least one insertion	0.47%
Deletions	76,542
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.86%

2.6. Chromosome stats

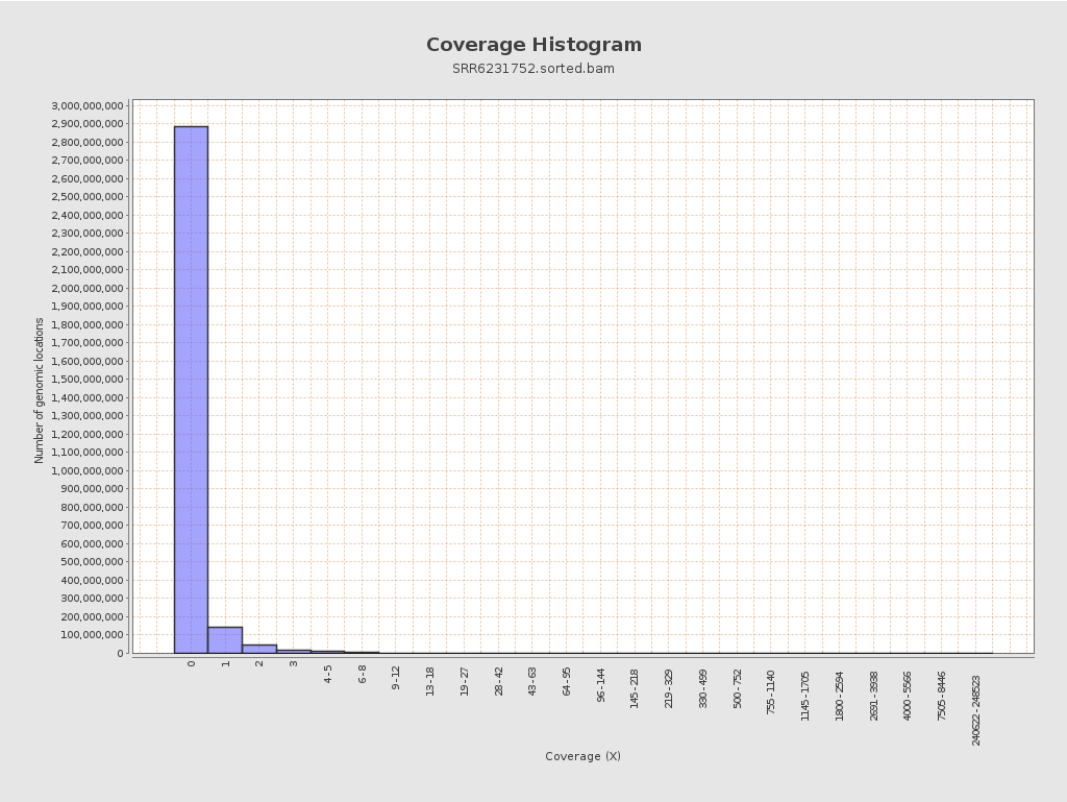
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28249074	0.1133	1.5113
chr2	243199373	44529881	0.1831	138.4452
chr3	198022430	15096354	0.0762	0.3956
chr4	191154276	2334384	0.0122	0.2512
chr5	180915260	18551436	0.1025	0.4744
chr6	171115067	22077902	0.129	0.7729
chr7	159138663	24465464	0.1537	1.1193

chr8	146364022	21013104	0.1436	0.8485
chr9	141213431	13457034	0.0953	0.8675
chr10	135534747	16996058	0.1254	0.7799
chr11	135006516	2191805	0.0162	0.5974
chr12	133851895	16515808	0.1234	0.5187
chr13	115169878	20182129	0.1752	0.6244
chr14	107349540	17295442	0.1611	0.742
chr15	102531392	9630117	0.0939	0.4457
chr16	90354753	10012663	0.1108	0.6106
chr17	81195210	15696575	0.1933	0.7104
chr18	78077248	13162950	0.1686	1.9428
chr19	59128983	12100800	0.2047	1.0994
chr20	63025520	11641134	0.1847	0.6695
chr21	48129895	9395251	0.1952	0.7267
chr22	51304566	4845765	0.0945	0.4565
chrMT	16571	12091	0.7296	1.1576
chrX	155270560	1707109	0.011	0.3914
chrY	59373566	662251	0.0112	0.2594

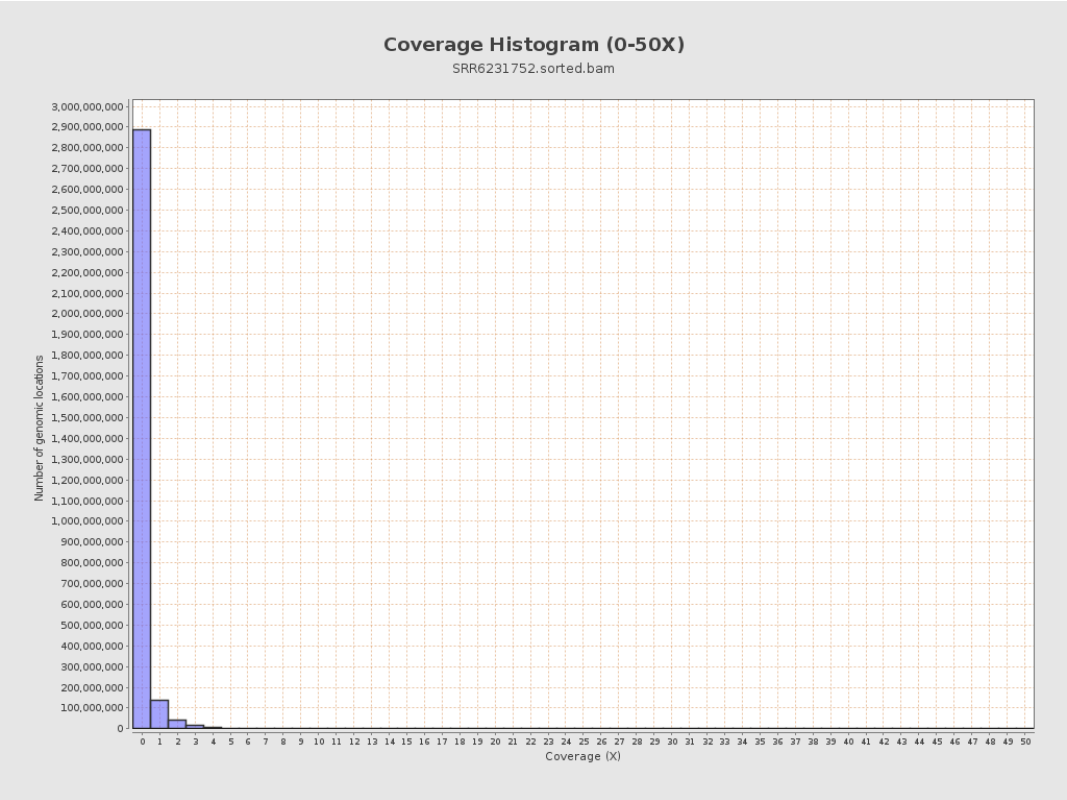
3. Results : Coverage across reference



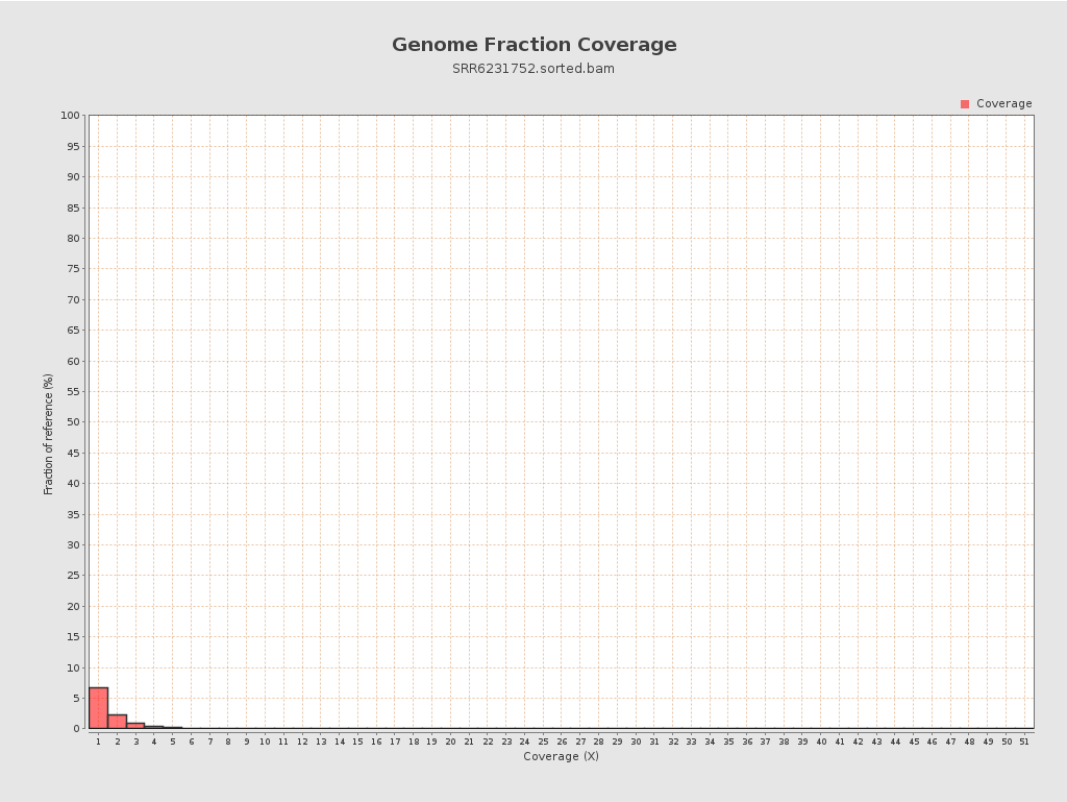
4. Results : Coverage Histogram



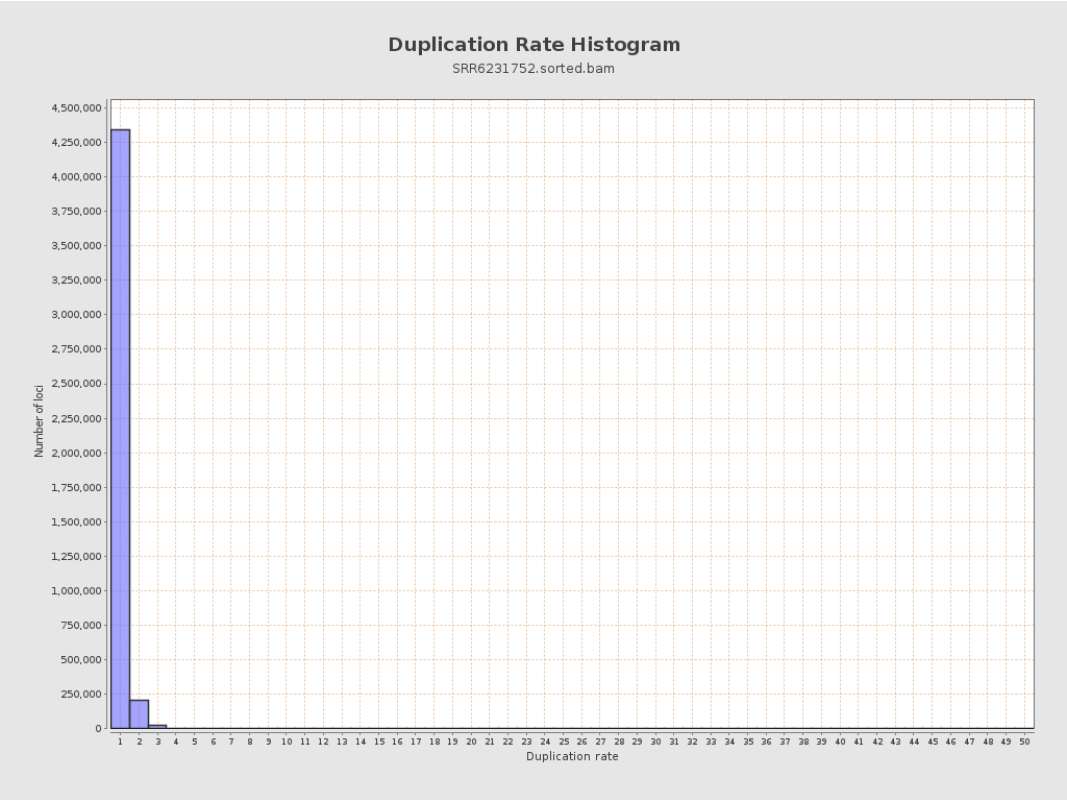
5. Results : Coverage Histogram (0-50X)



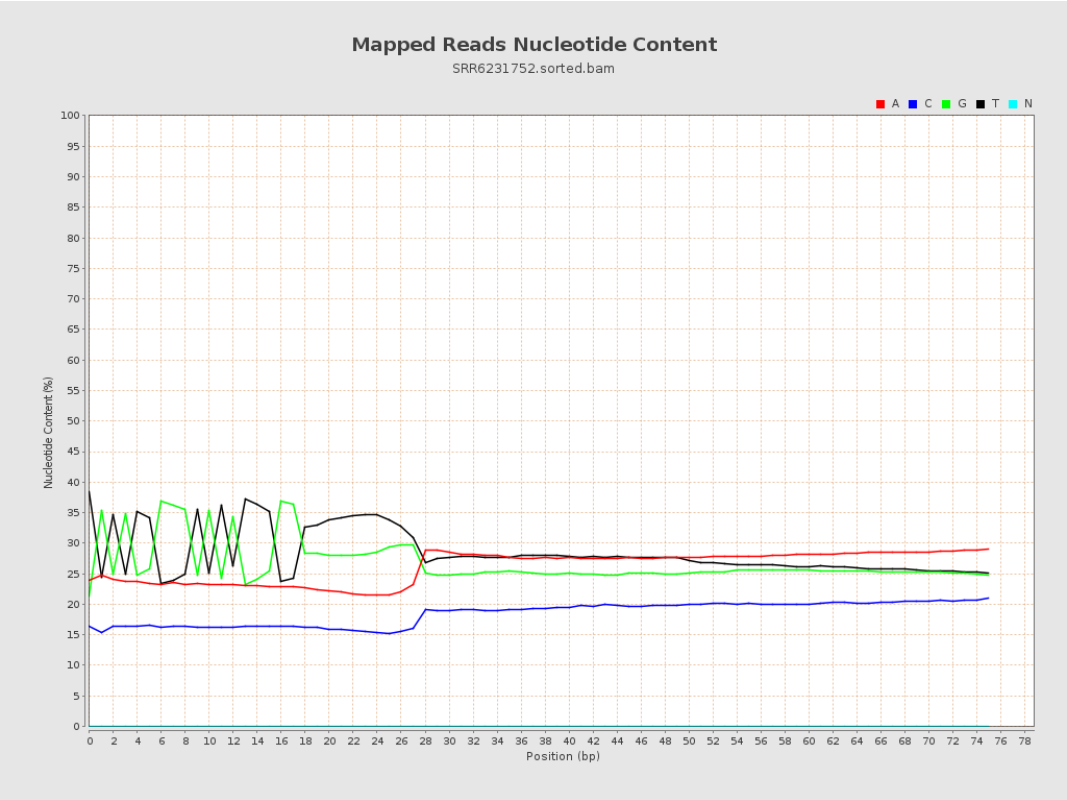
6. Results : Genome Fraction Coverage



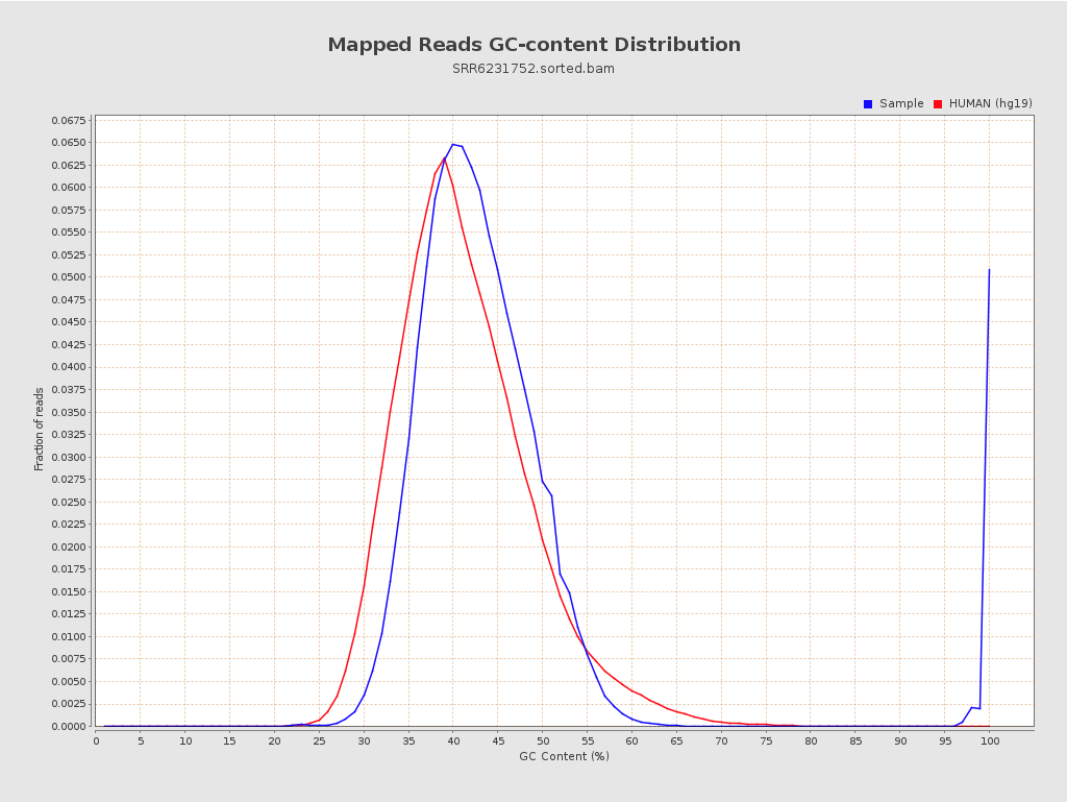
7. Results : Duplication Rate Histogram



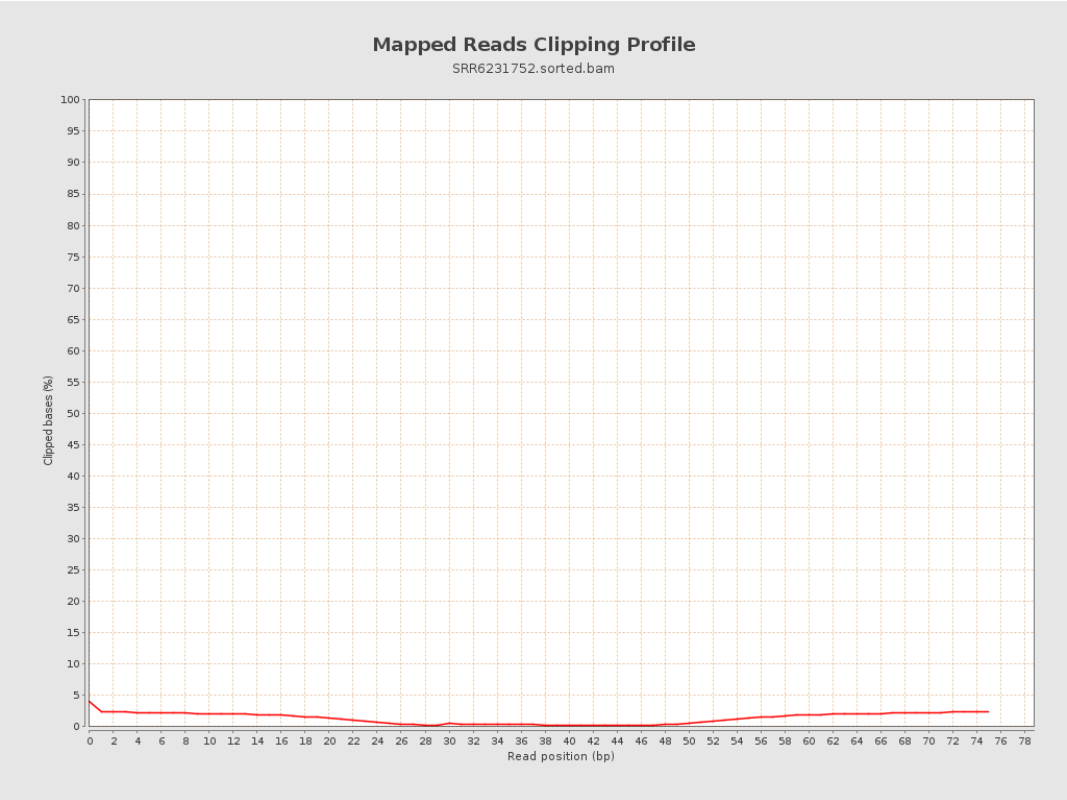
8. Results : Mapped Reads Nucleotide Content



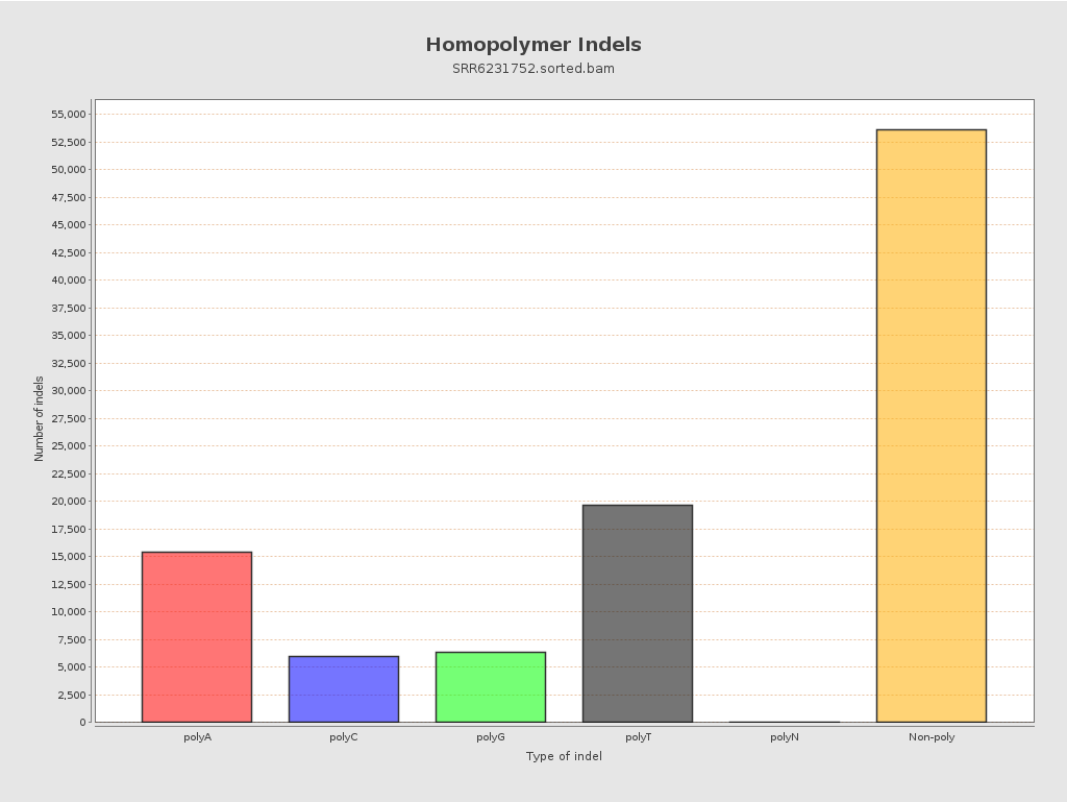
9. Results : Mapped Reads GC-content Distribution



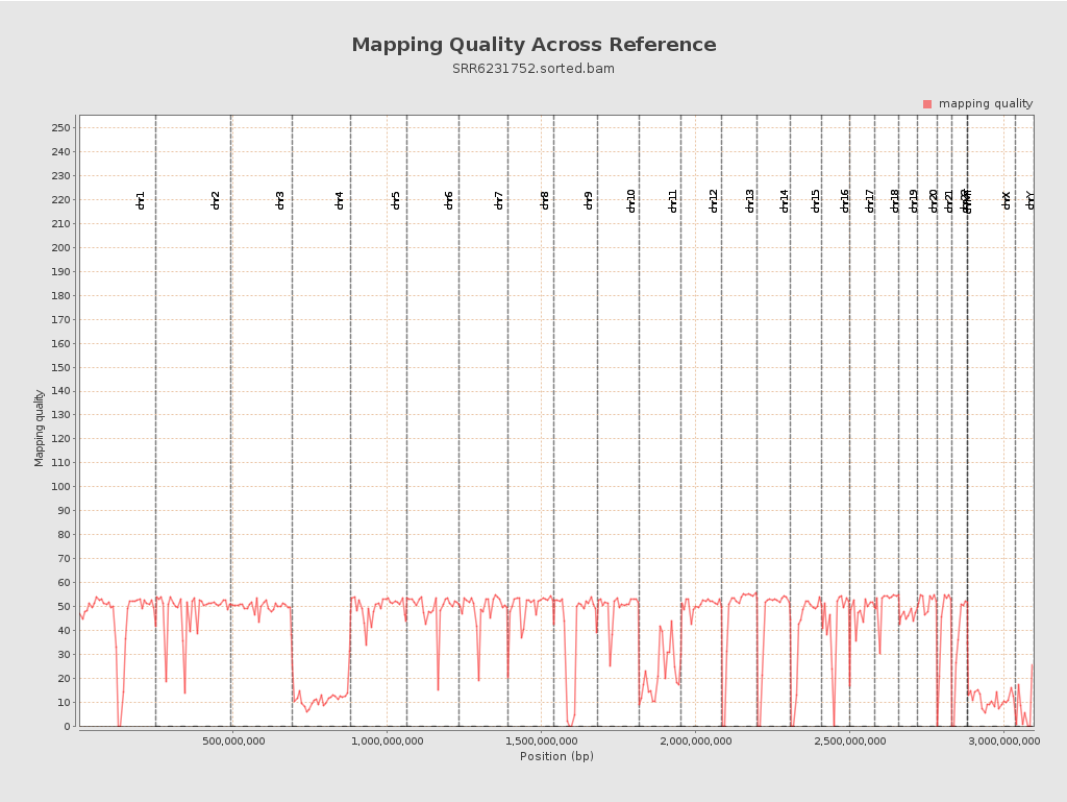
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram