Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:32:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231771.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_SRR6231771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231771.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:32:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231771.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,760,883
Mapped reads	1,100,590 / 62.5%
Unmapped reads	660,293 / 37.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,662 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	119,025 / 6.76%
Duplication rate	8.74%
Clipped reads	634,304 / 36.02%

2.2. ACGT Content

Number/percentage of A's	18,442,426 / 26.37%
Number/percentage of C's	13,322,113 / 19.05%
Number/percentage of T's	21,780,753 / 31.14%
Number/percentage of G's	16,373,928 / 23.41%
Number/percentage of N's	16,845 / 0.02%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2687

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

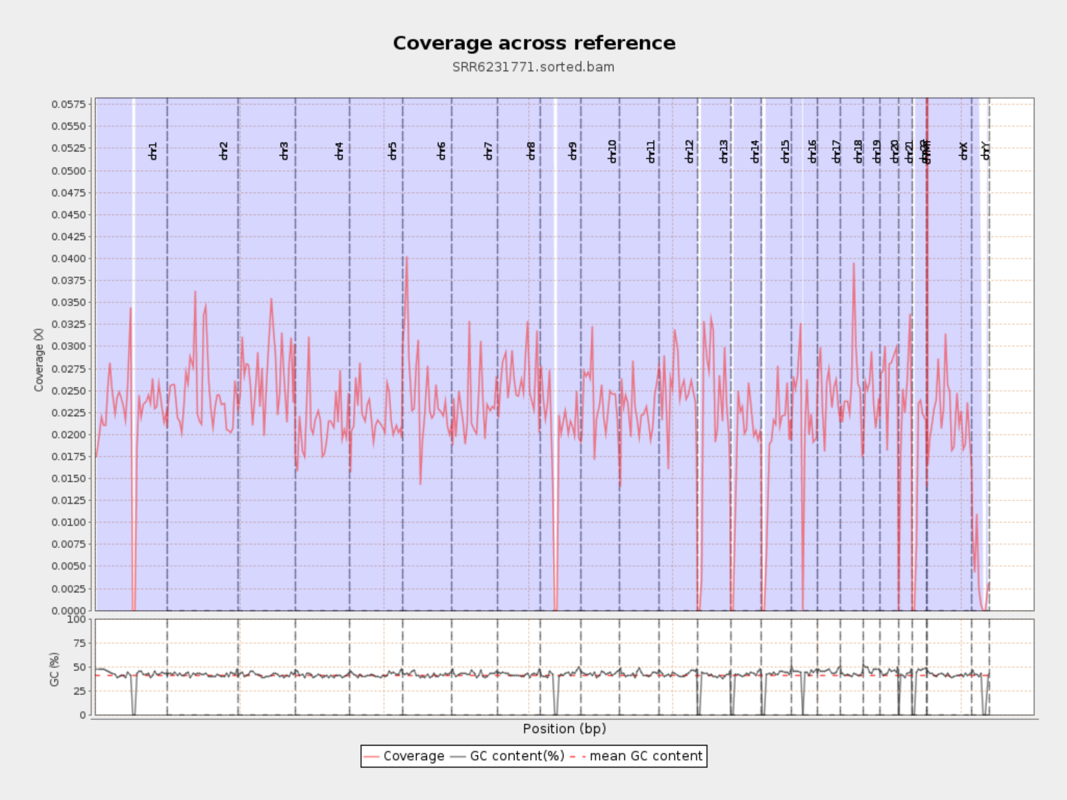
General error rate	0.91%
Mismatches	628,802
Insertions	5,803
Mapped reads with at least one insertion	0.52%
Deletions	23,592
Mapped reads with at least one deletion	2.11%
Homopolymer indels	45.24%

2.6. Chromosome stats

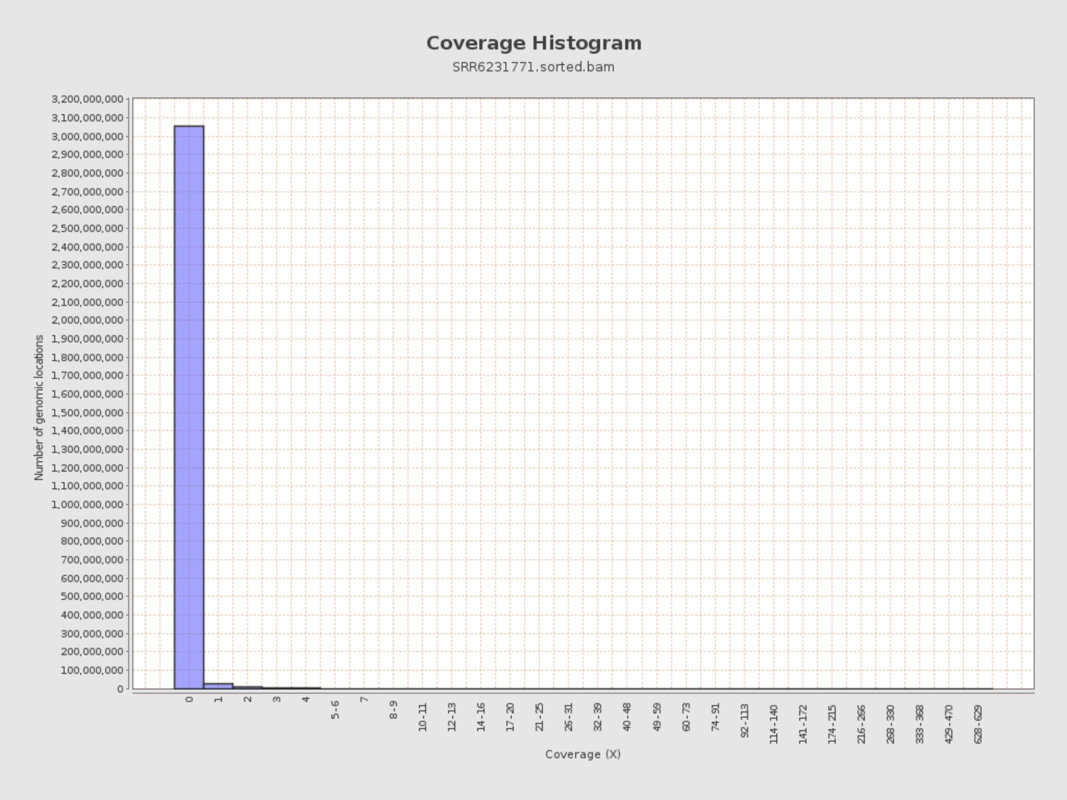
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5497200	0.0221	0.3793
chr2	243199373	5985640	0.0246	0.3623
chr3	198022430	5304879	0.0268	0.2479
chr4	191154276	4048228	0.0212	0.2253
chr5	180915260	4007335	0.0222	0.2239
chr6	171115067	4216773	0.0246	0.268
chr7	159138663	3686705	0.0232	0.2708

chr8	146364022	3832039	0.0262	0.2767
chr9	141213431	2769116	0.0196	0.235
chr10	135534747	3221336	0.0238	0.2602
chr11	135006516	3075384	0.0228	0.2458
chr12	133851895	3356374	0.0251	0.2422
chr13	115169878	2500332	0.0217	0.2291
chr14	107349540	1960918	0.0183	0.2097
chr15	102531392	1806830	0.0176	0.2031
chr16	90354753	1948867	0.0216	0.2265
chr17	81195210	2006012	0.0247	0.2483
chr18	78077248	2011397	0.0258	0.3401
chr19	59128983	1449610	0.0245	0.2983
chr20	63025520	1705377	0.0271	0.2567
chr21	48129895	1092350	0.0227	0.2367
chr22	51304566	790596	0.0154	0.186
chrMT	16571	46082	2.7809	3.466
chrX	155270560	3444145	0.0222	0.228
chrY	59373566	211490	0.0036	0.1022

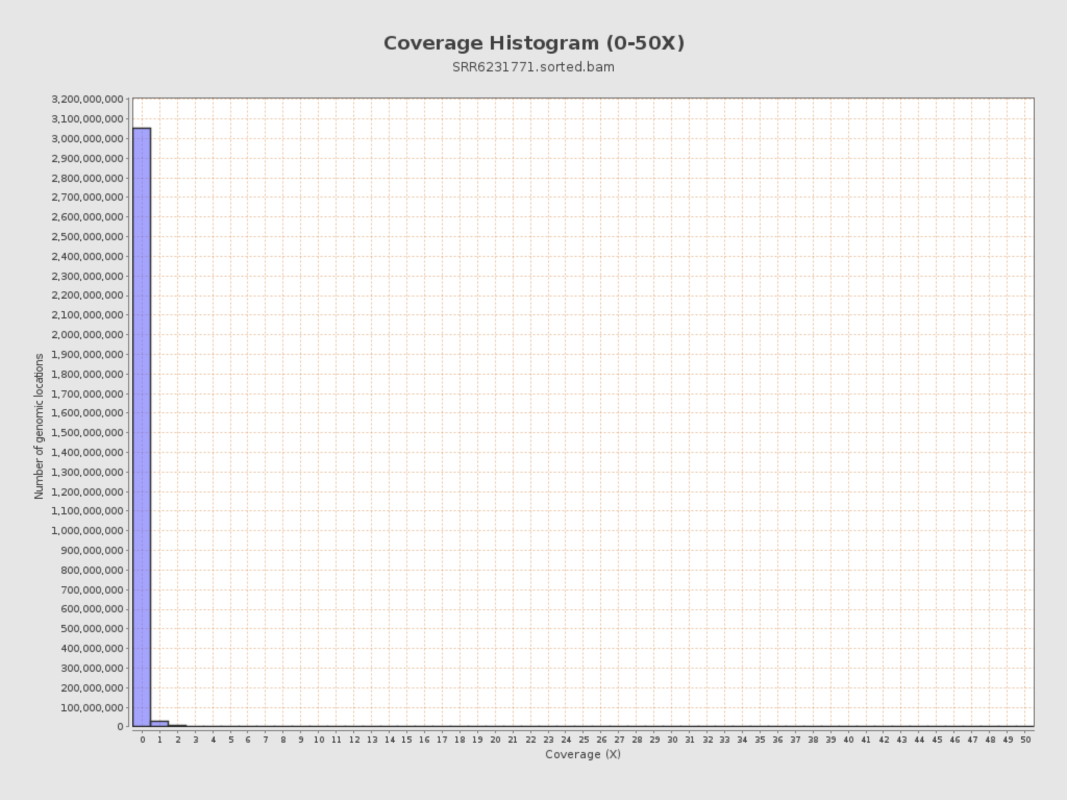
3. Results : Coverage across reference



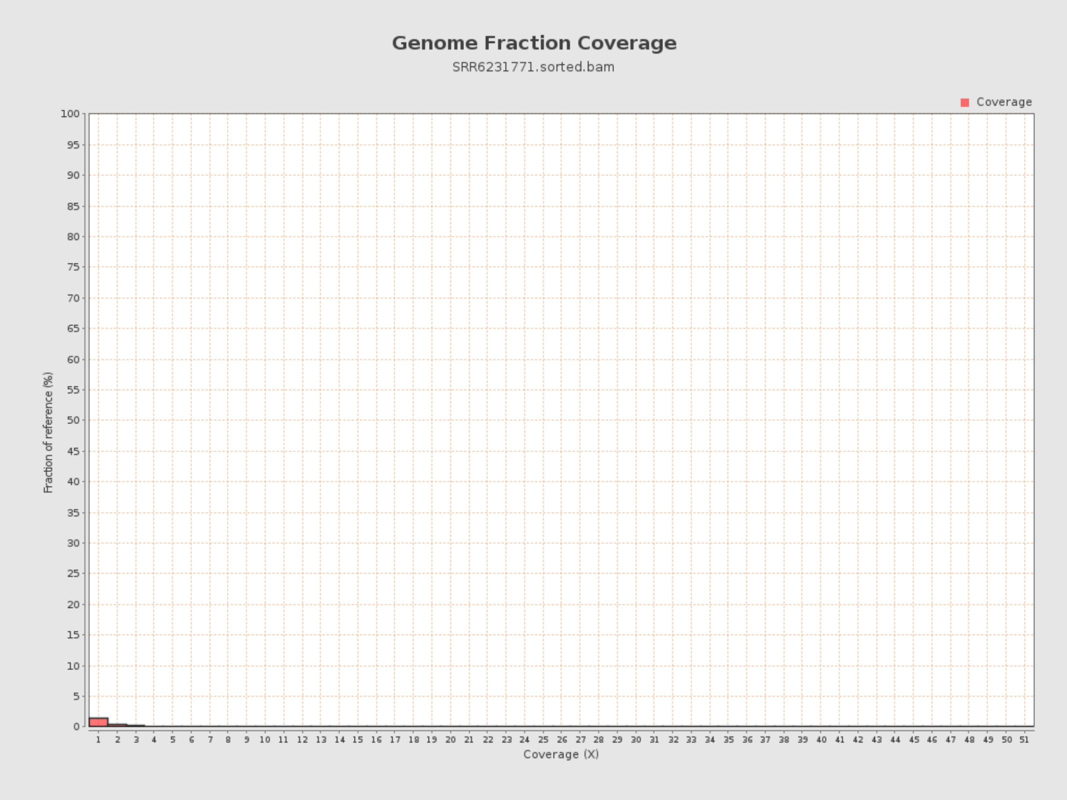
4. Results : Coverage Histogram



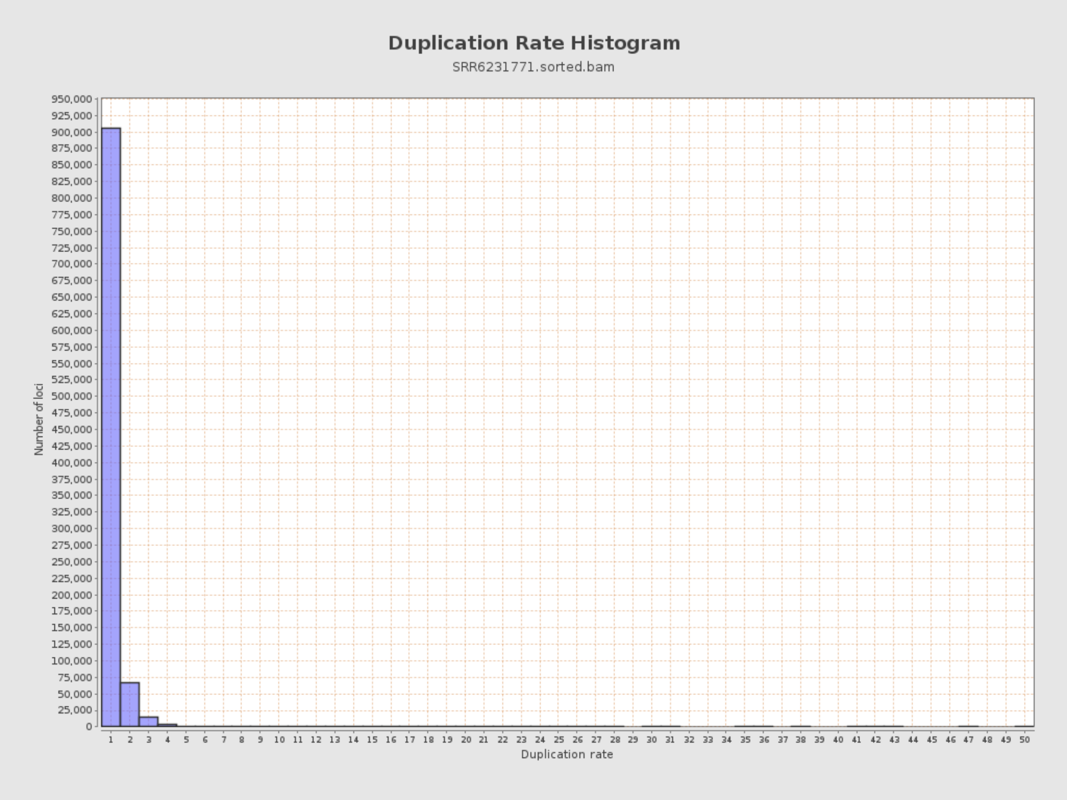
5. Results : Coverage Histogram (0-50X)



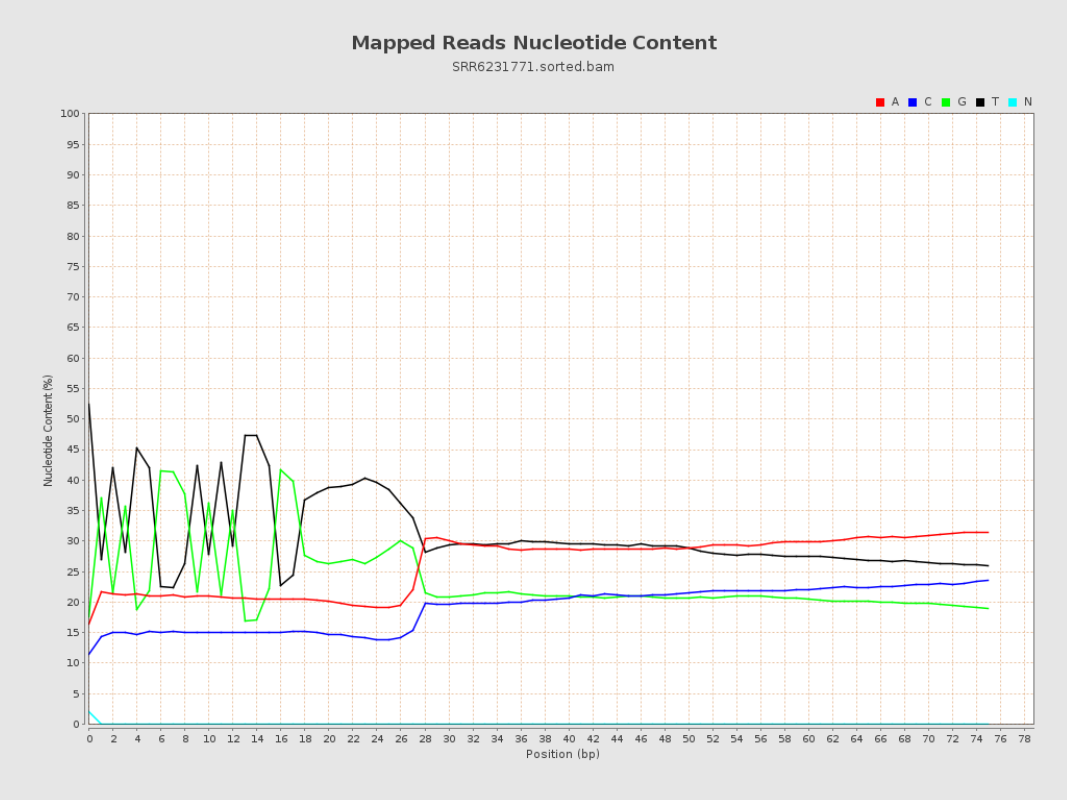
6. Results : Genome Fraction Coverage



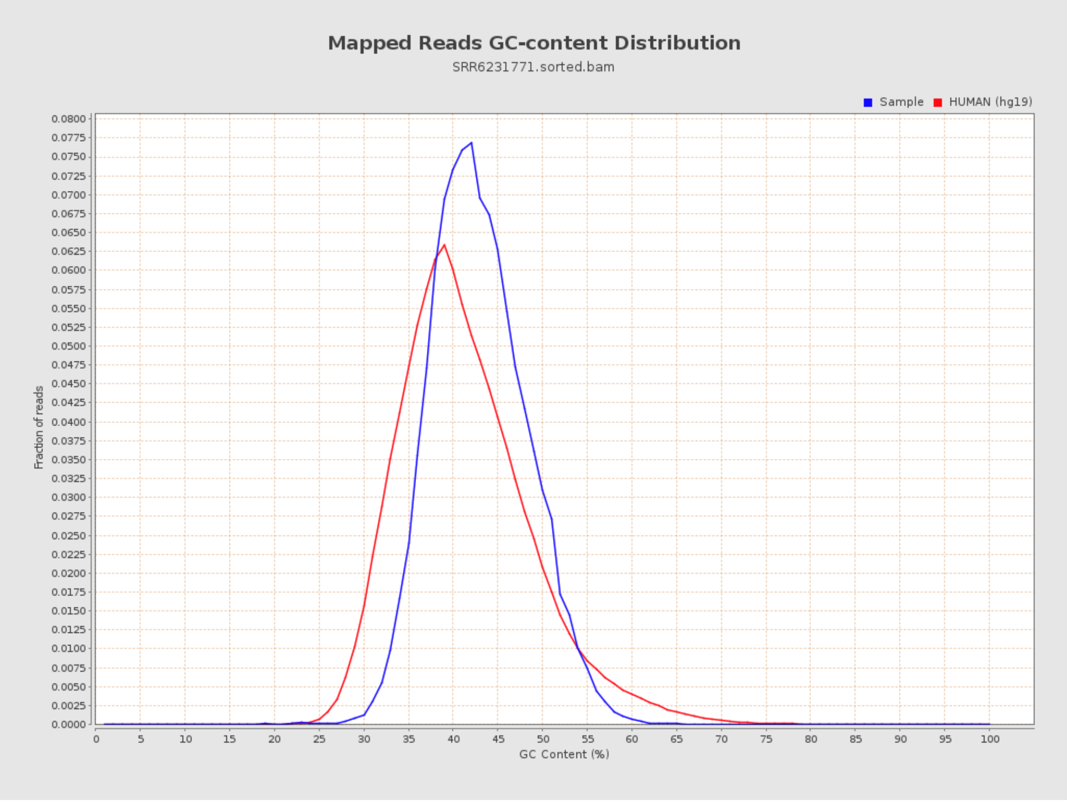
7. Results : Duplication Rate Histogram



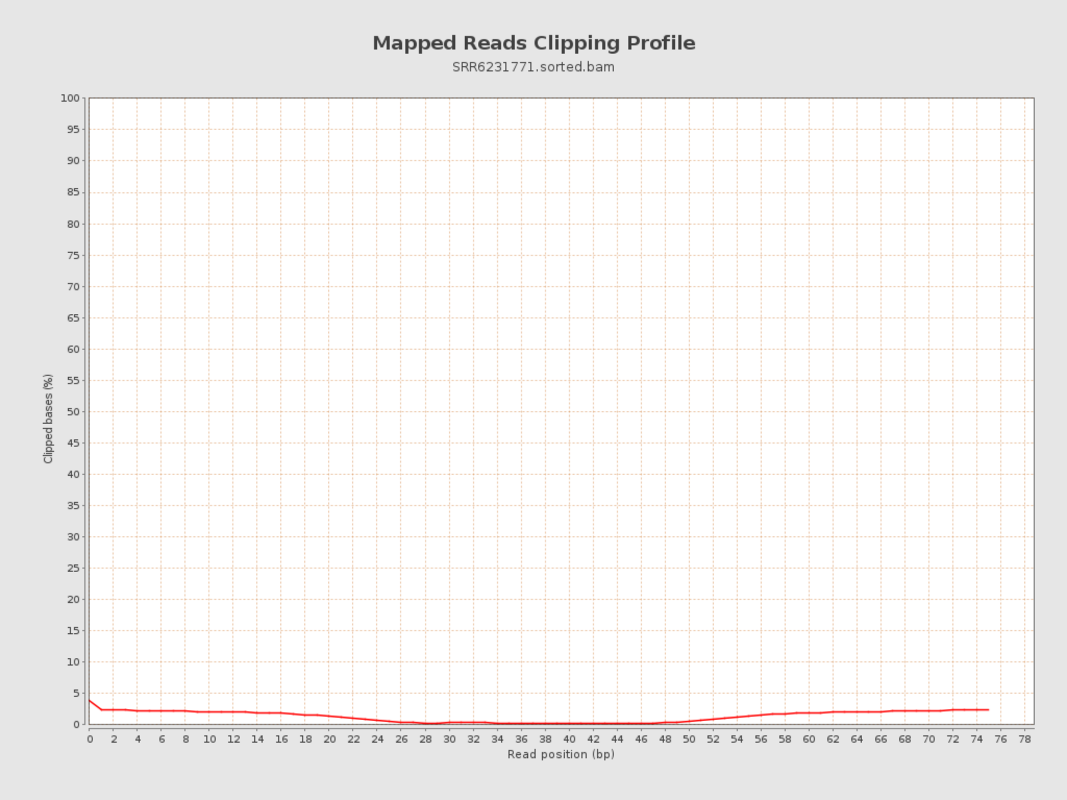
8. Results : Mapped Reads Nucleotide Content



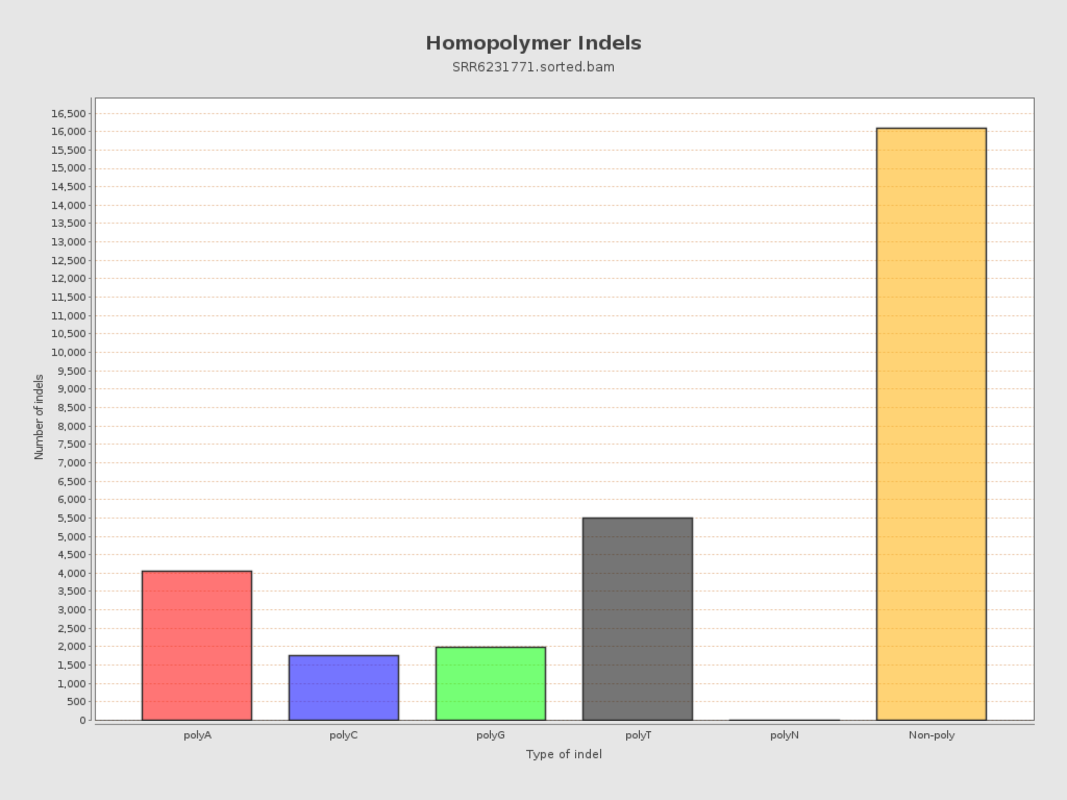
9. Results : Mapped Reads GC-content Distribution



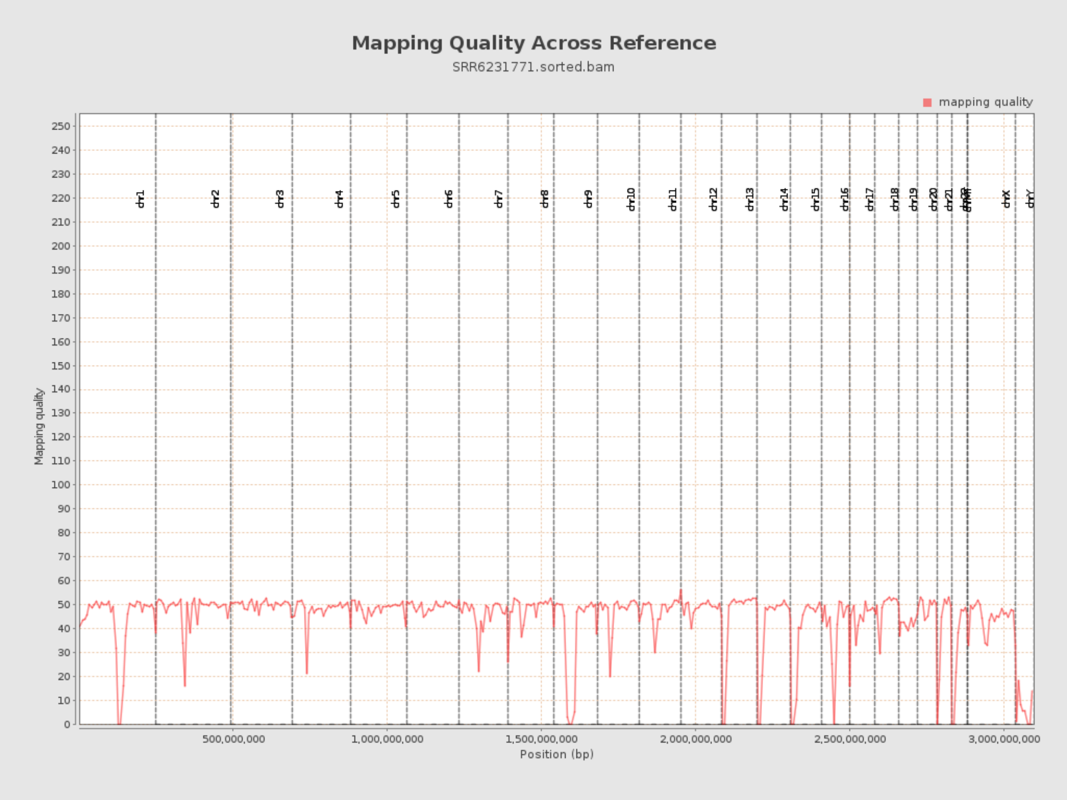
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram