Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:38:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231876.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_SRR6231876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231876.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:38:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,035,739
Mapped reads	694,826 / 34.13%
Unmapped reads	1,340,913 / 65.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,823 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	137,556 / 6.76%
Duplication rate	14.48%
Clipped reads	426,342 / 20.94%

2.2. ACGT Content

Number/percentage of A's	11,471,266 / 26.8%
Number/percentage of C's	7,129,645 / 16.66%
Number/percentage of T's	14,503,836 / 33.89%
Number/percentage of G's	9,682,813 / 22.62%
Number/percentage of N's	10,434 / 0.02%
GC Percentage	39.28%

2.3. Coverage

Mean	0.0138

Standard Deviation	0.2334

2.4. Mapping Quality

Mean Mapping Quality	43.62

2.5. Mismatches and indels

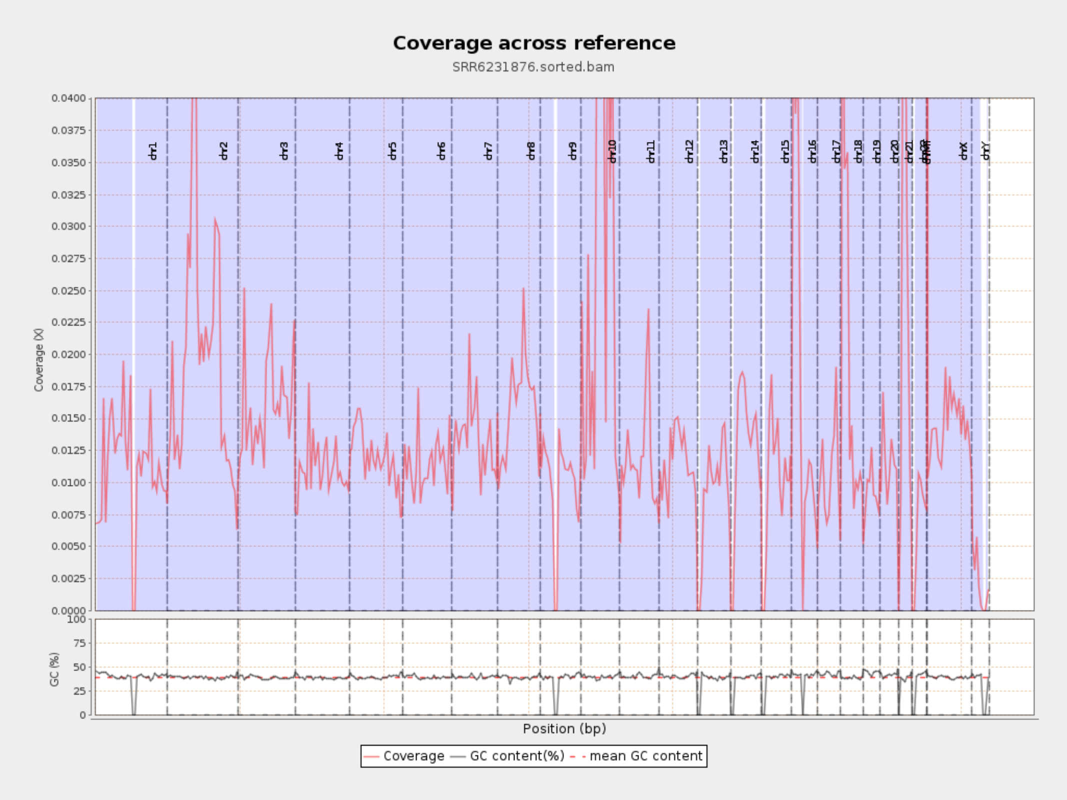
General error rate	0.96%
Mismatches	399,483
Insertions	4,450
Mapped reads with at least one insertion	0.63%
Deletions	14,414
Mapped reads with at least one deletion	2.05%
Homopolymer indels	45.79%

2.6. Chromosome stats

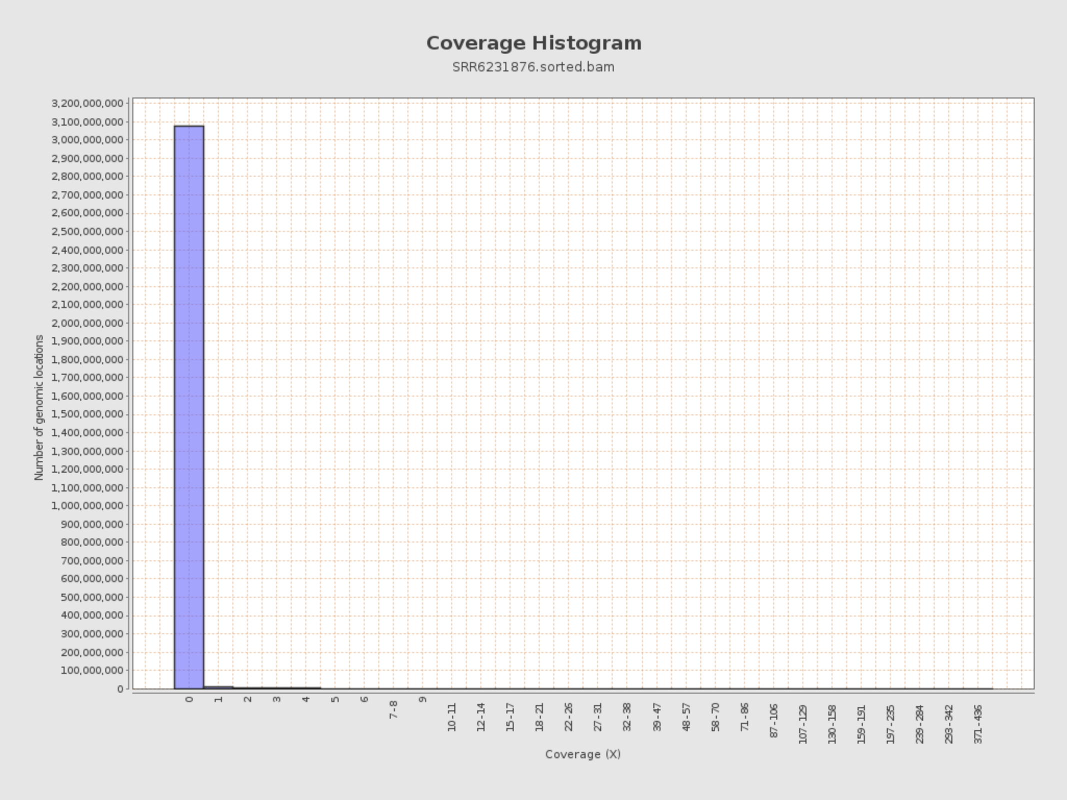
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2799969	0.0112	0.2343
chr2	243199373	4896565	0.0201	0.3116
chr3	198022430	3166596	0.016	0.2242
chr4	191154276	2109395	0.011	0.1959
chr5	180915260	2183436	0.0121	0.1949
chr6	171115067	1948340	0.0114	0.2076
chr7	159138663	2133721	0.0134	0.2363

chr8	146364022	2345044	0.016	0.3452
chr9	141213431	1393538	0.0099	0.1812
chr10	135534747	3886817	0.0287	0.3098
chr11	135006516	1610210	0.0119	0.1988
chr12	133851895	1548650	0.0116	0.1887
chr13	115169878	1047302	0.0091	0.2
chr14	107349540	1362808	0.0127	0.2051
chr15	102531392	1028106	0.01	0.176
chr16	90354753	1626275	0.018	0.2336
chr17	81195210	870655	0.0107	0.1785
chr18	78077248	1652182	0.0212	0.3417
chr19	59128983	551568	0.0093	0.1767
chr20	63025520	716369	0.0114	0.1856
chr21	48129895	1187810	0.0247	0.2903
chr22	51304566	345575	0.0067	0.1344
chrMT	16571	39567	2.3877	3.2034
chrX	155270560	2244938	0.0145	0.2134
chrY	59373566	126210	0.0021	0.0735

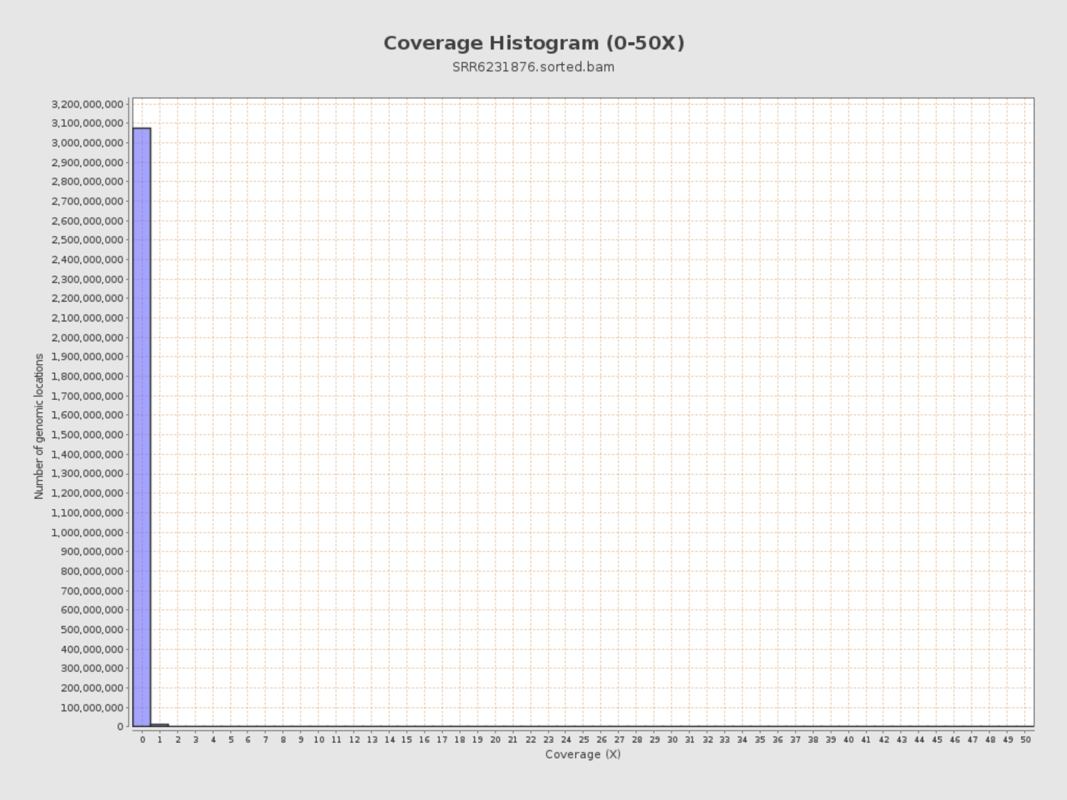
3. Results : Coverage across reference



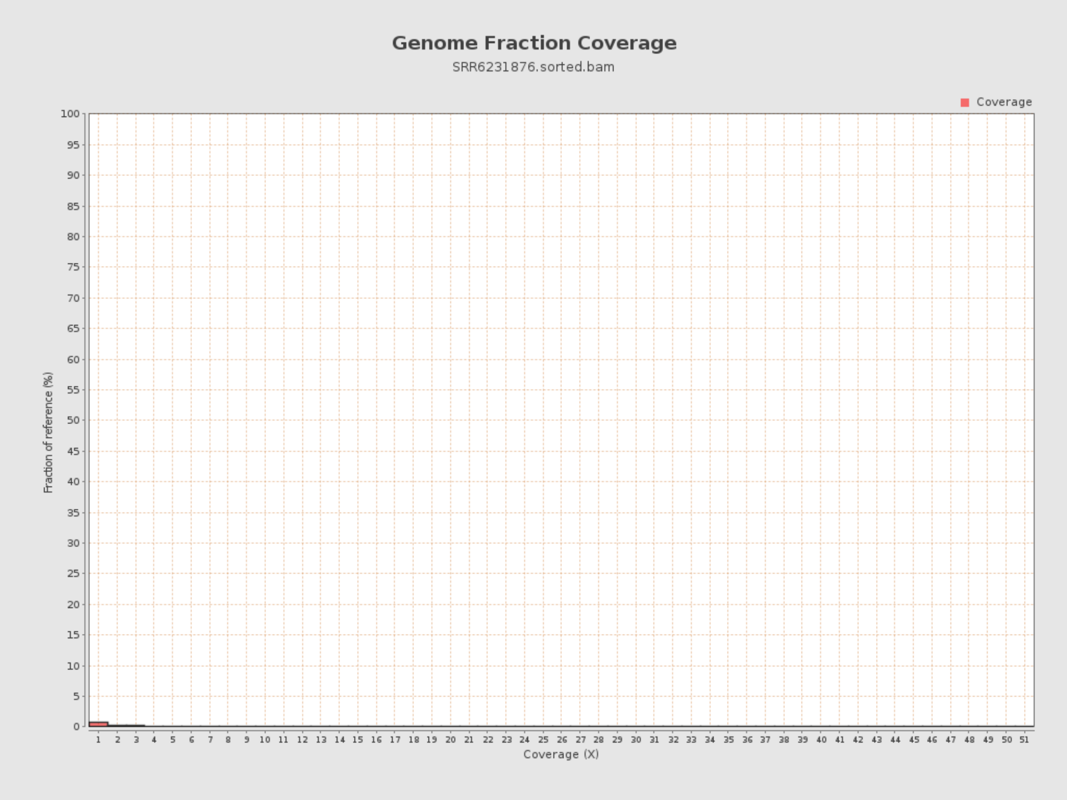
4. Results : Coverage Histogram



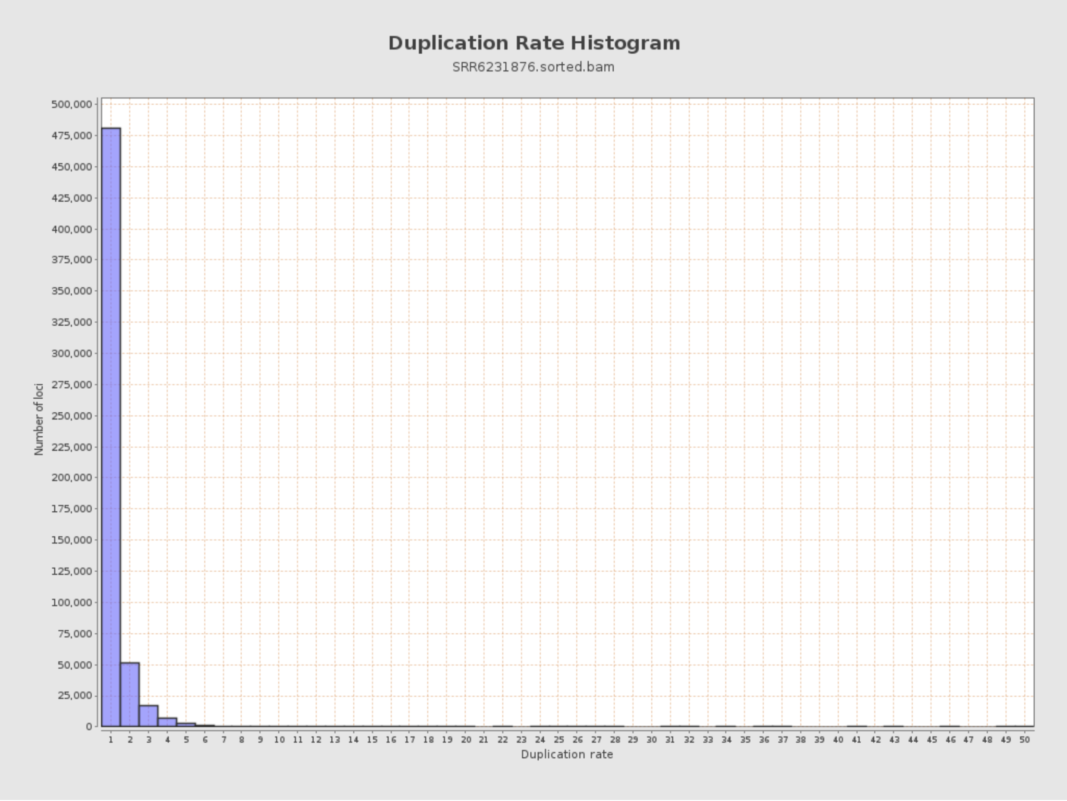
5. Results : Coverage Histogram (0-50X)



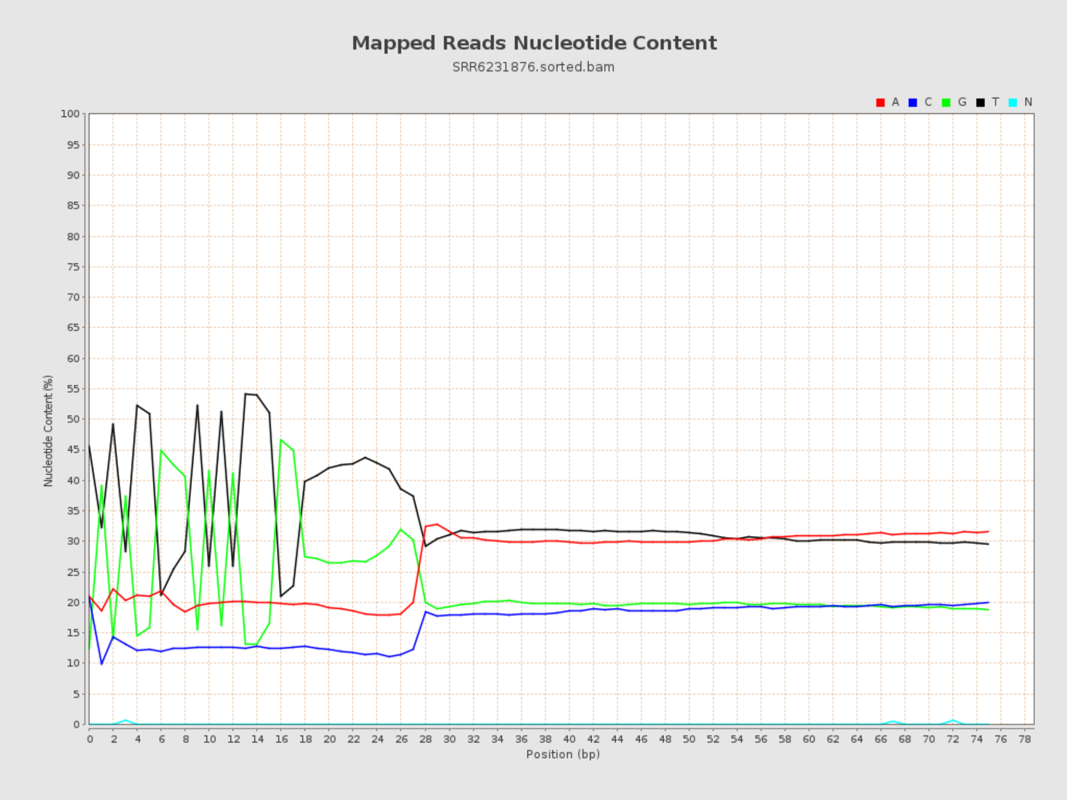
6. Results : Genome Fraction Coverage



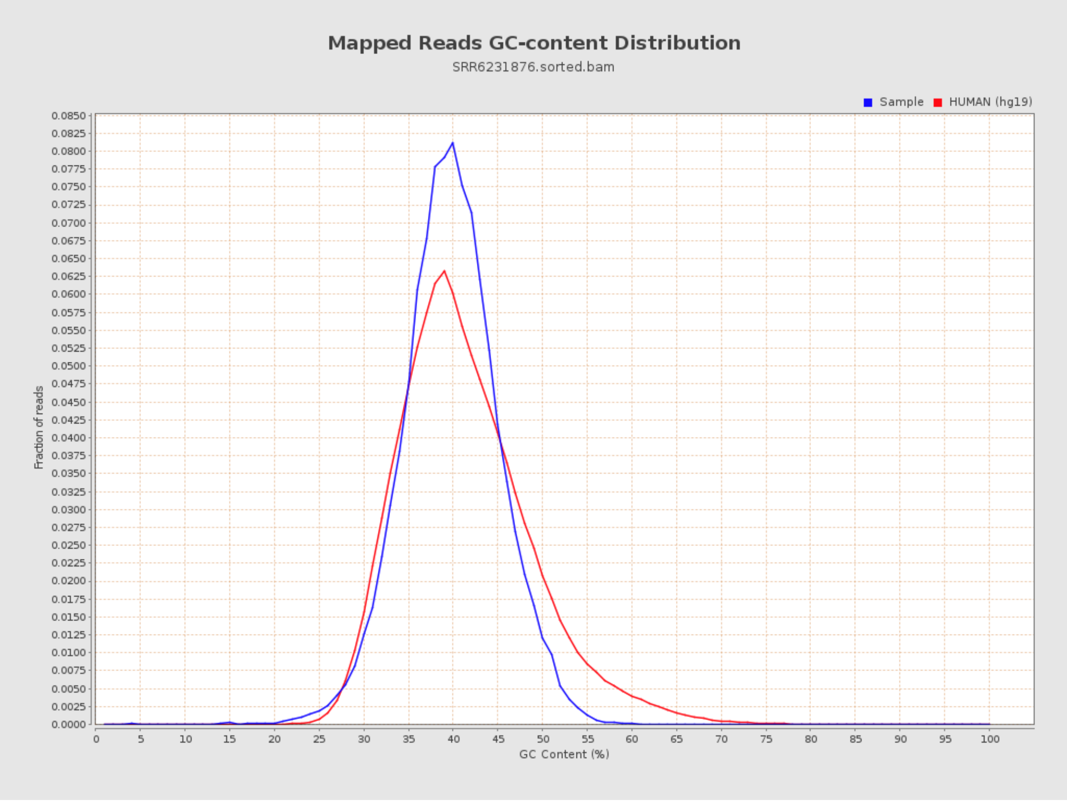
7. Results : Duplication Rate Histogram



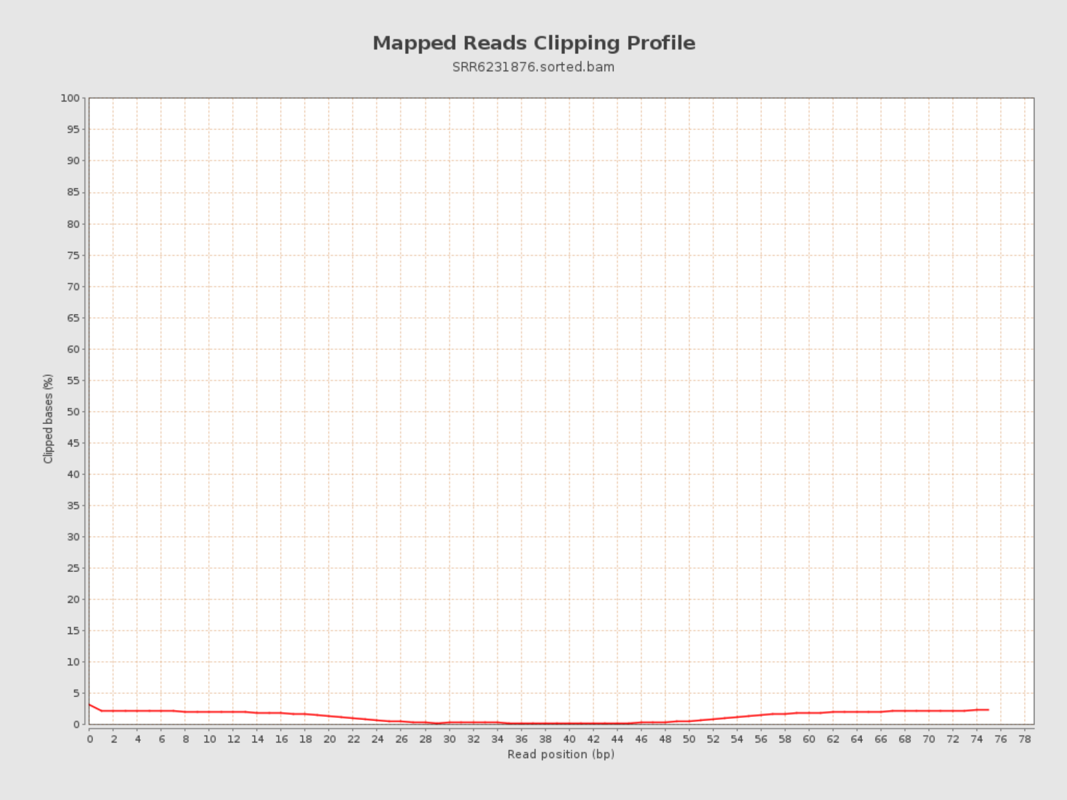
8. Results : Mapped Reads Nucleotide Content



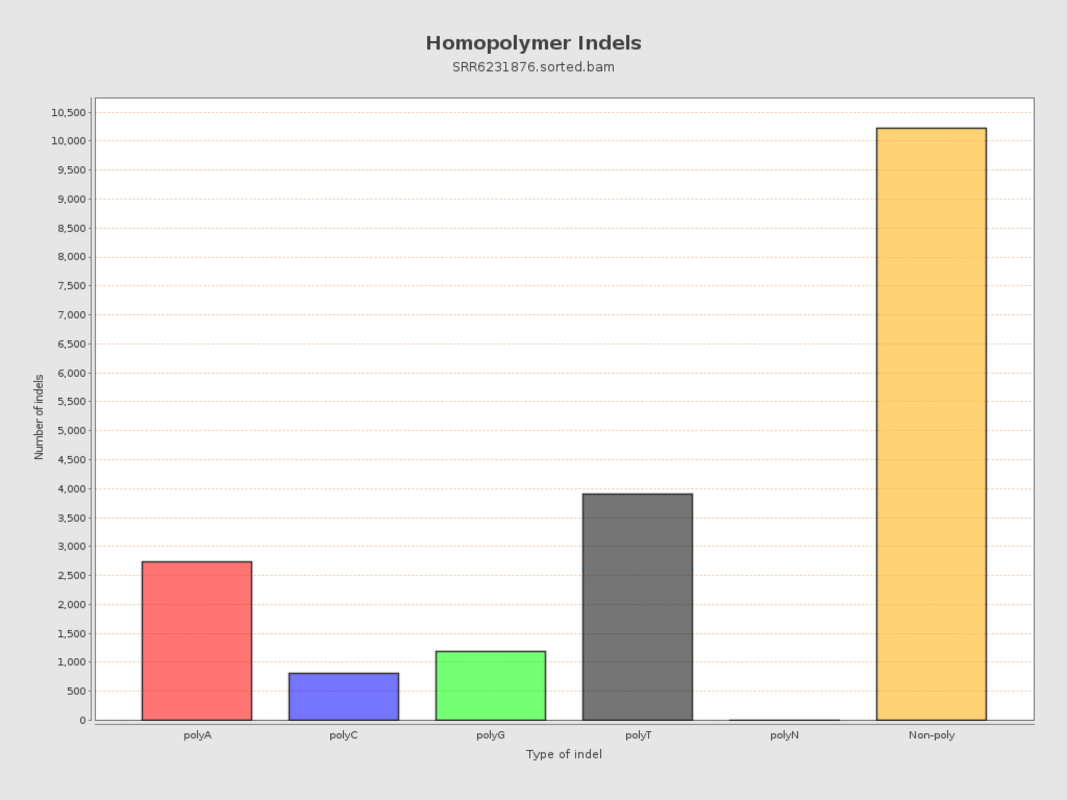
9. Results : Mapped Reads GC-content Distribution



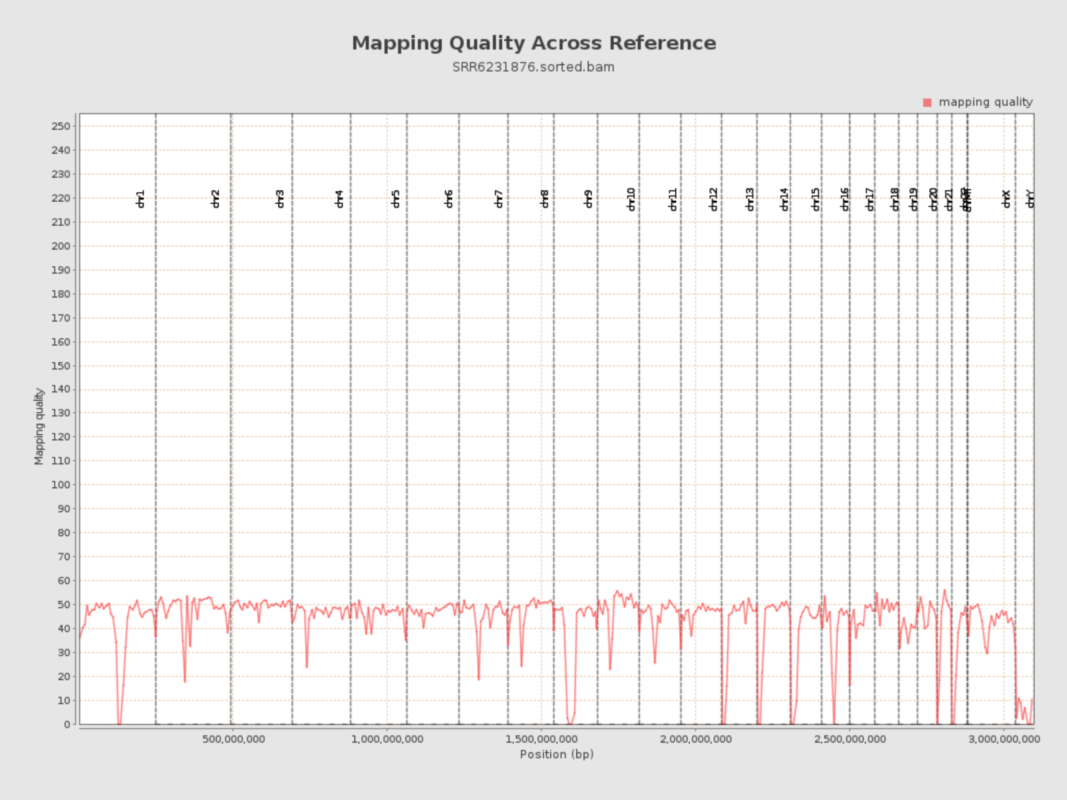
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram