Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:55:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231779.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_SRR6231779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:55:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,152,148
Mapped reads	1,005,448 / 87.27%
Unmapped reads	146,700 / 12.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,498 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	67,741 / 5.88%
Duplication rate	1.99%
Clipped reads	499,781 / 43.38%

2.2. ACGT Content

Number/percentage of A's	19,294,709 / 29.17%
Number/percentage of C's	12,352,060 / 18.67%
Number/percentage of T's	18,119,793 / 27.39%
Number/percentage of G's	16,380,145 / 24.76%
Number/percentage of N's	4,538 / 0.01%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0214

Standard Deviation	5.289

2.4. Mapping Quality

Mean Mapping Quality	43.18

2.5. Mismatches and indels

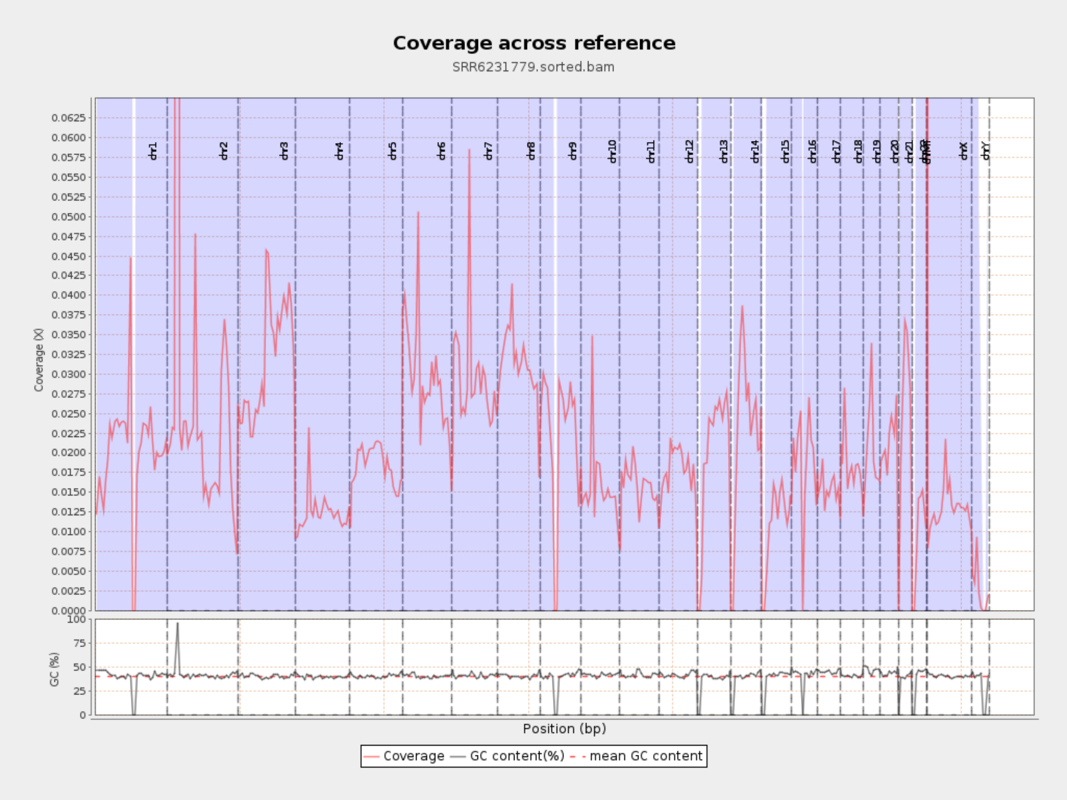
General error rate	0.74%
Mismatches	478,455
Insertions	5,965
Mapped reads with at least one insertion	0.58%
Deletions	15,581
Mapped reads with at least one deletion	1.53%
Homopolymer indels	42.34%

2.6. Chromosome stats

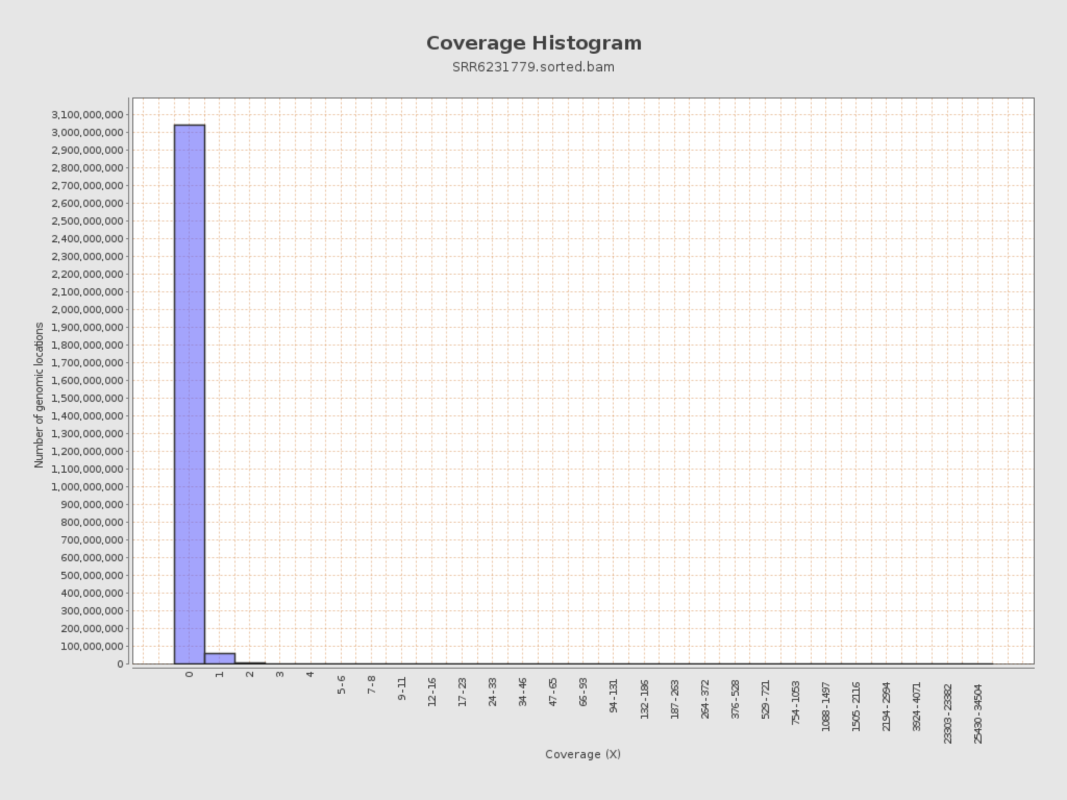
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4999626	0.0201	0.5617
chr2	243199373	8162052	0.0336	18.8471
chr3	198022430	6319223	0.0319	0.1865
chr4	191154276	2364462	0.0124	0.1254
chr5	180915260	3363345	0.0186	0.1441
chr6	171115067	5116225	0.0299	0.2281
chr7	159138663	4703843	0.0296	0.4504

chr8	146364022	4593532	0.0314	0.324
chr9	141213431	3167876	0.0224	0.2107
chr10	135534747	2109315	0.0156	0.2166
chr11	135006516	2161198	0.016	0.2281
chr12	133851895	2379516	0.0178	0.1425
chr13	115169878	2297324	0.0199	0.1469
chr14	107349540	2471516	0.023	0.1994
chr15	102531392	1103619	0.0108	0.1088
chr16	90354753	1656294	0.0183	0.1622
chr17	81195210	1246398	0.0154	0.138
chr18	78077248	1451626	0.0186	0.4068
chr19	59128983	1234103	0.0209	0.3339
chr20	63025520	1337431	0.0212	0.1573
chr21	48129895	1223541	0.0254	0.1768
chr22	51304566	498164	0.0097	0.1017
chrMT	16571	26278	1.5858	1.5074
chrX	155270560	2033053	0.0131	0.1343
chrY	59373566	157963	0.0027	0.0725

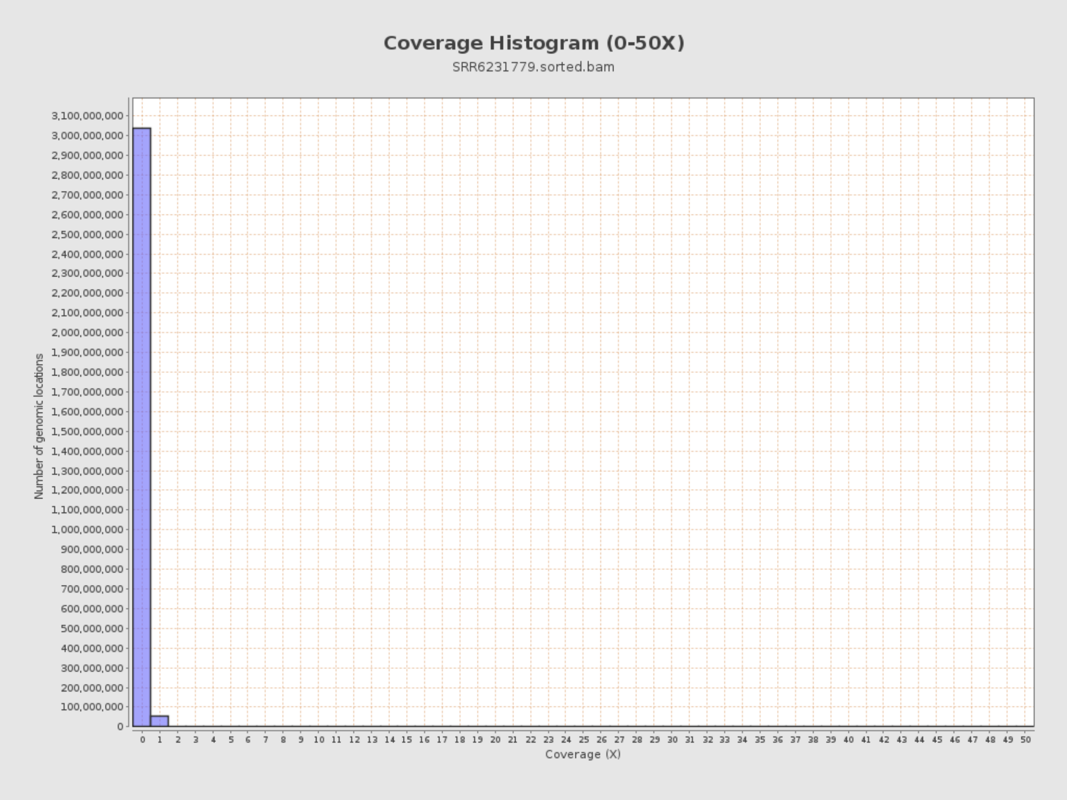
3. Results : Coverage across reference



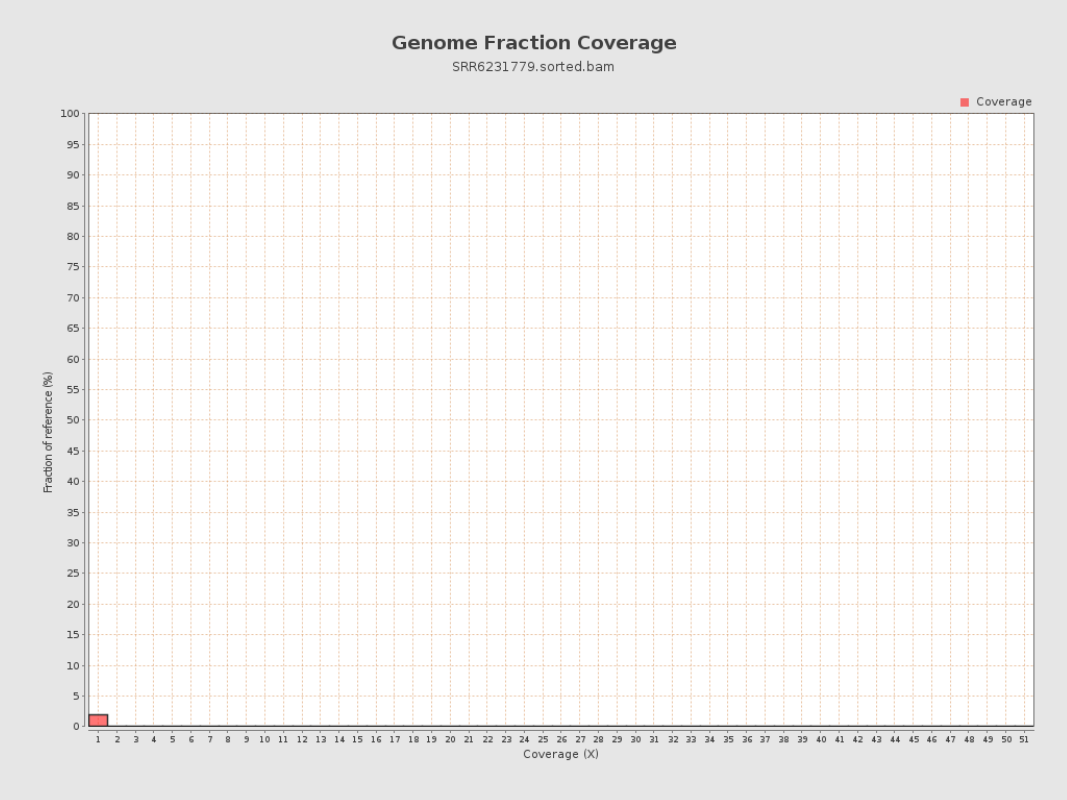
4. Results : Coverage Histogram



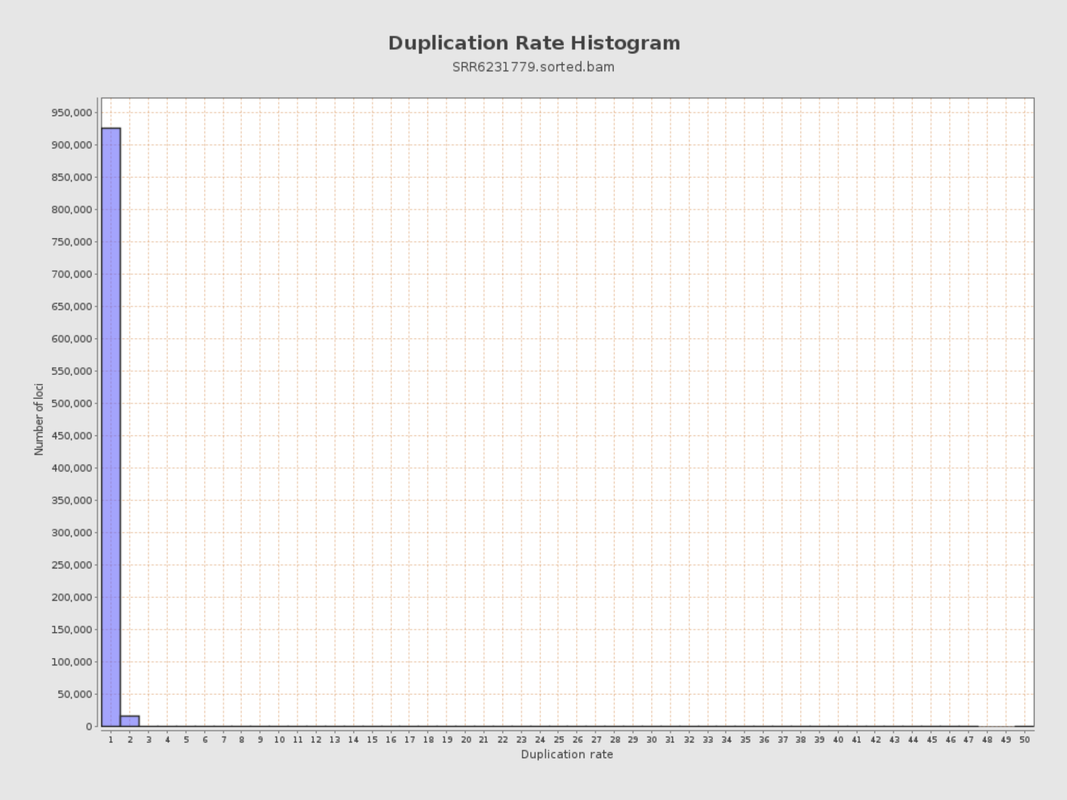
5. Results : Coverage Histogram (0-50X)



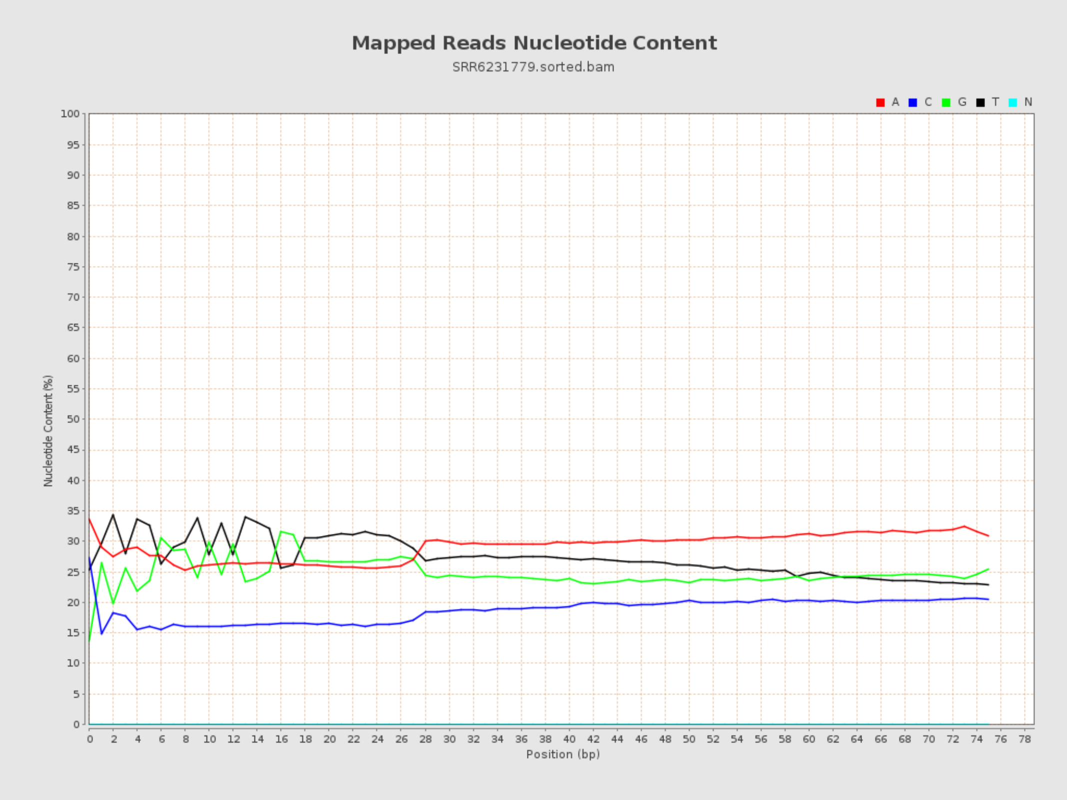
6. Results : Genome Fraction Coverage



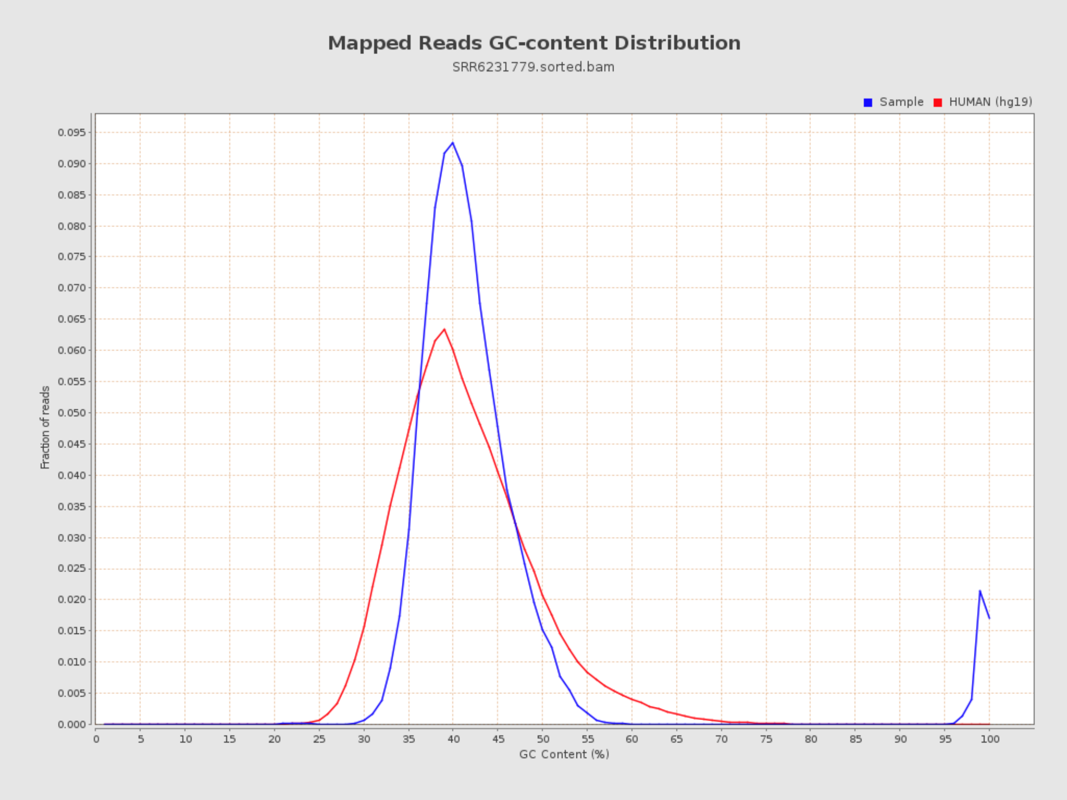
7. Results : Duplication Rate Histogram



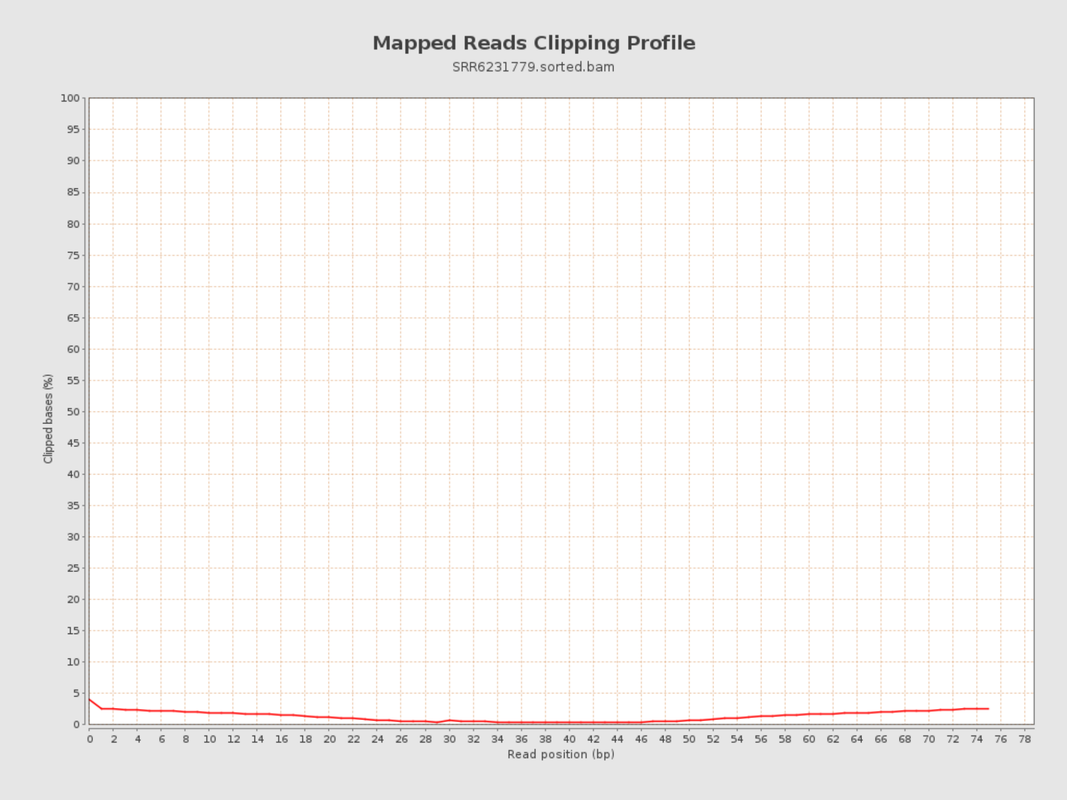
8. Results : Mapped Reads Nucleotide Content



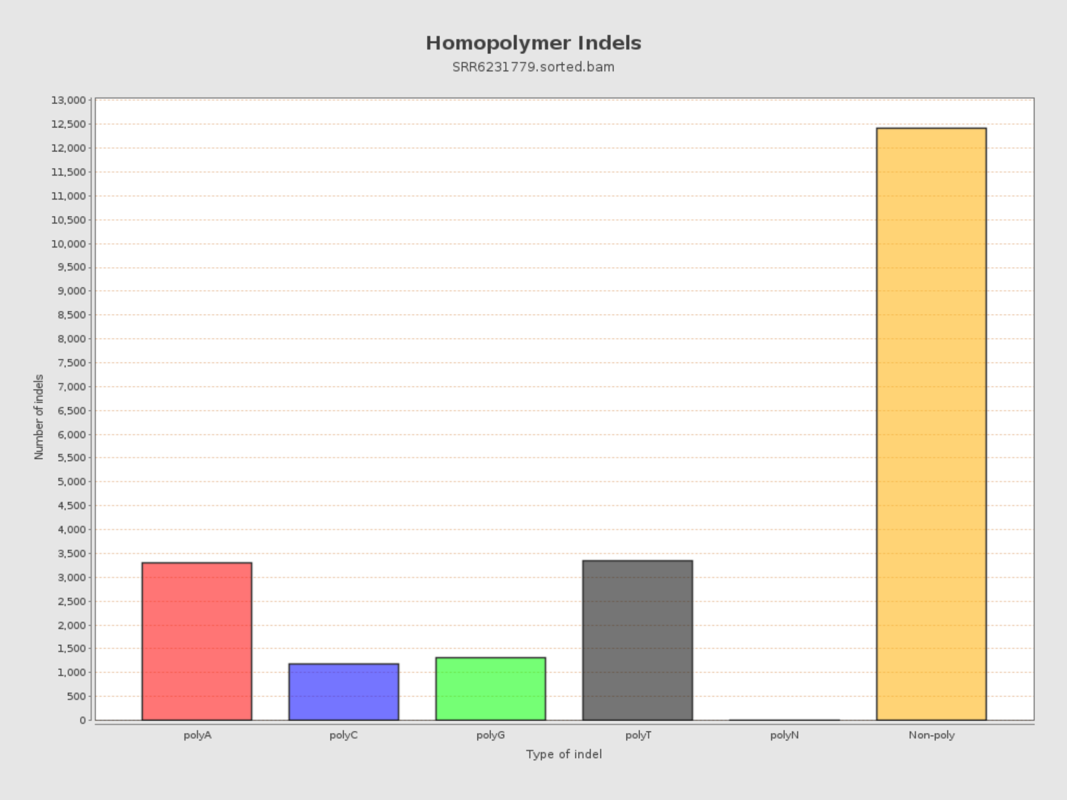
9. Results : Mapped Reads GC-content Distribution



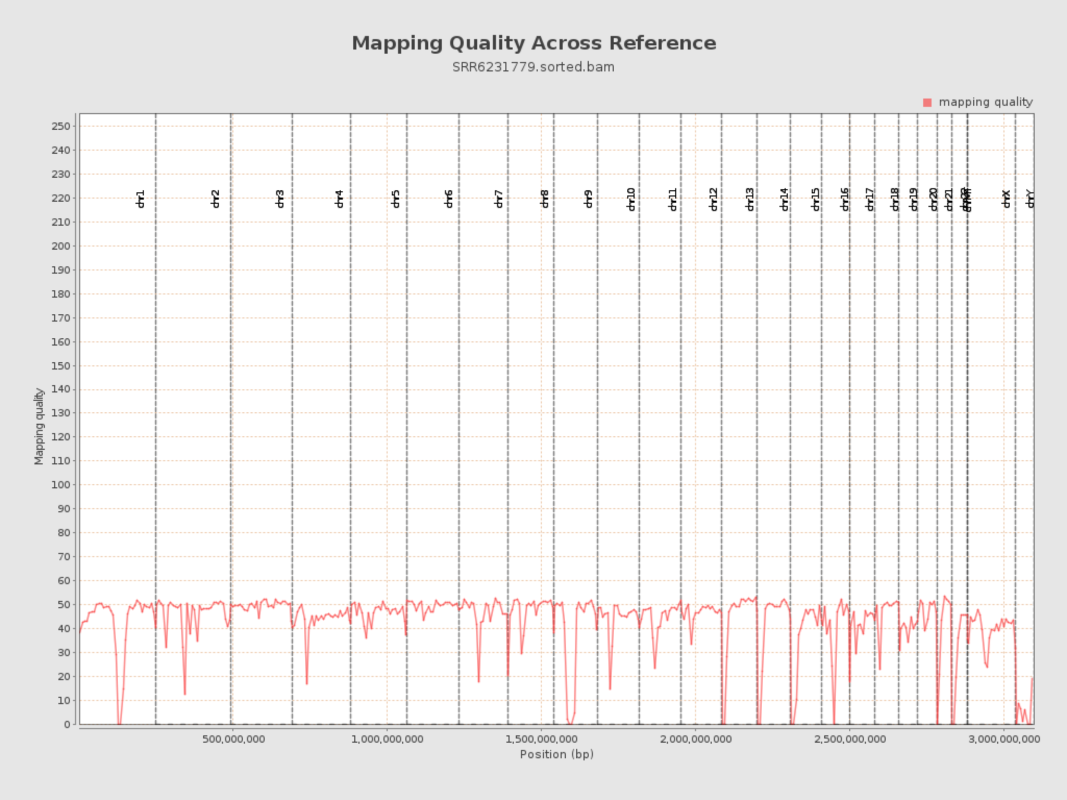
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram