Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:03:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231883.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_SRR6231883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231883.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:03:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,461,523
Mapped reads	1,165,293 / 79.73%
Unmapped reads	296,230 / 20.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,199 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	150,896 / 10.32%
Duplication rate	10.78%
Clipped reads	718,279 / 49.15%

2.2. ACGT Content

Number/percentage of A's	19,261,302 / 26.1%
Number/percentage of C's	12,766,774 / 17.3%
Number/percentage of T's	24,622,977 / 33.37%
Number/percentage of G's	17,142,153 / 23.23%
Number/percentage of N's	3,239 / 0%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.2539

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

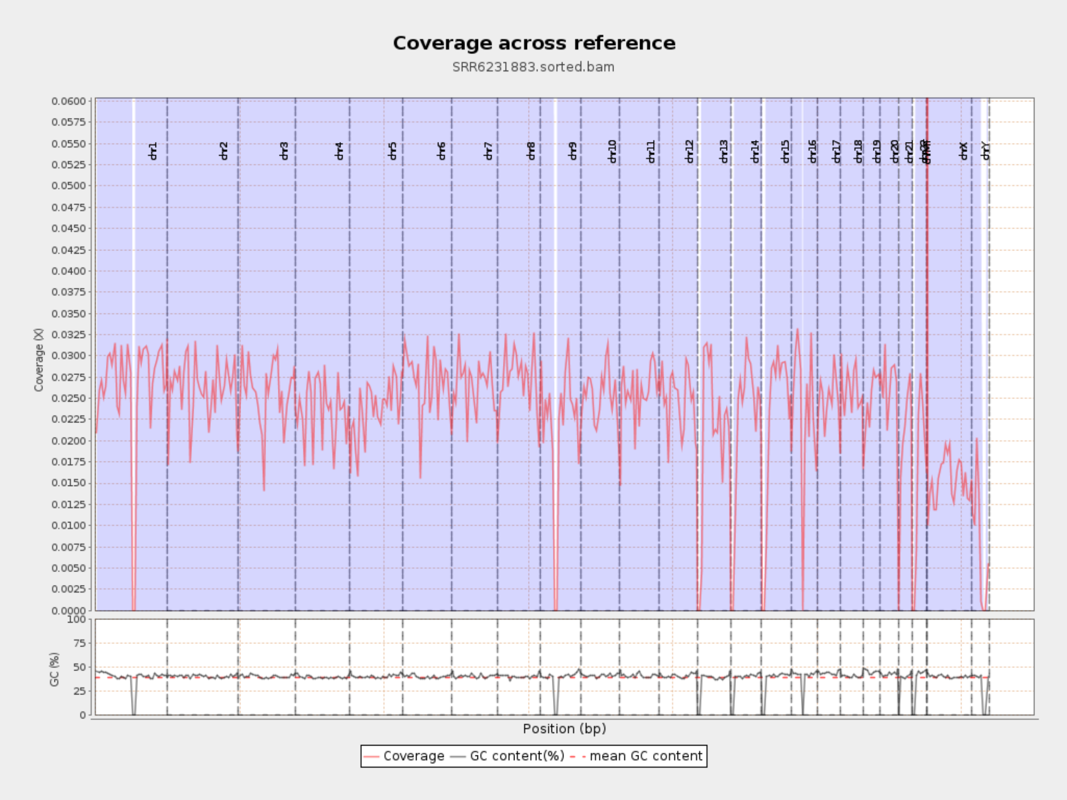
General error rate	0.82%
Mismatches	594,494
Insertions	6,087
Mapped reads with at least one insertion	0.52%
Deletions	24,607
Mapped reads with at least one deletion	2.09%
Homopolymer indels	49.63%

2.6. Chromosome stats

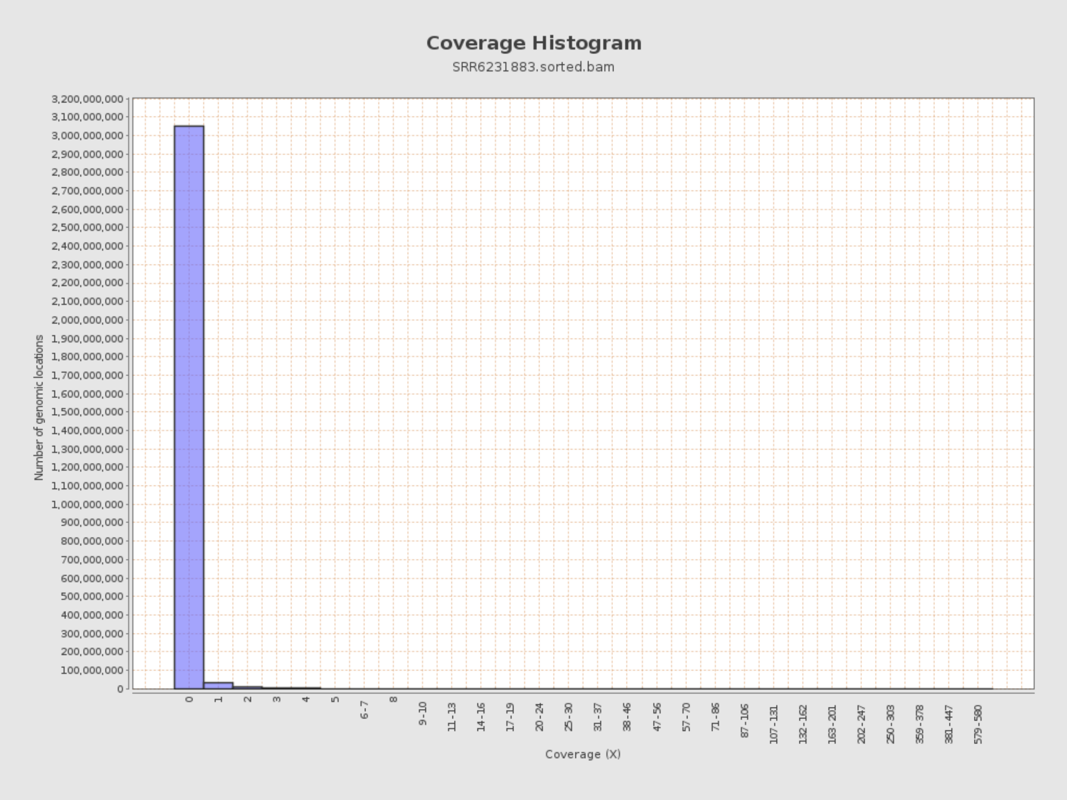
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6509234	0.0261	0.2651
chr2	243199373	6418204	0.0264	0.3405
chr3	198022430	5091917	0.0257	0.2353
chr4	191154276	4520935	0.0237	0.2365
chr5	180915260	4311156	0.0238	0.2272
chr6	171115067	4610952	0.0269	0.2582
chr7	159138663	4221799	0.0265	0.284

chr8	146364022	3984679	0.0272	0.3418
chr9	141213431	3031732	0.0215	0.229
chr10	135534747	3440902	0.0254	0.2473
chr11	135006516	3498864	0.0259	0.2817
chr12	133851895	3305636	0.0247	0.2319
chr13	115169878	2352874	0.0204	0.211
chr14	107349540	2352424	0.0219	0.2186
chr15	102531392	2273507	0.0222	0.2253
chr16	90354753	2086061	0.0231	0.2213
chr17	81195210	2027871	0.025	0.2412
chr18	78077248	2040210	0.0261	0.2825
chr19	59128983	1469859	0.0249	0.2397
chr20	63025520	1647153	0.0261	0.2387
chr21	48129895	970041	0.0202	0.2087
chr22	51304566	810083	0.0158	0.1779
chrMT	16571	28950	1.747	2.3943
chrX	155270560	2380368	0.0153	0.1822
chrY	59373566	455153	0.0077	0.1287

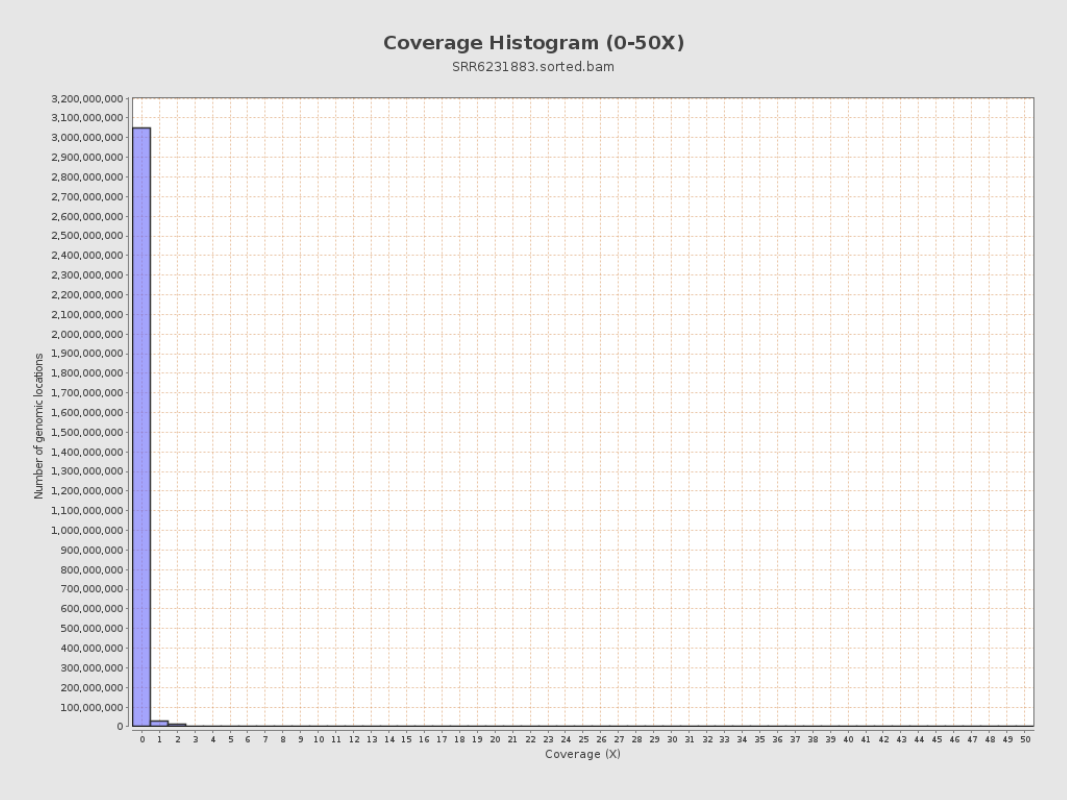
3. Results : Coverage across reference



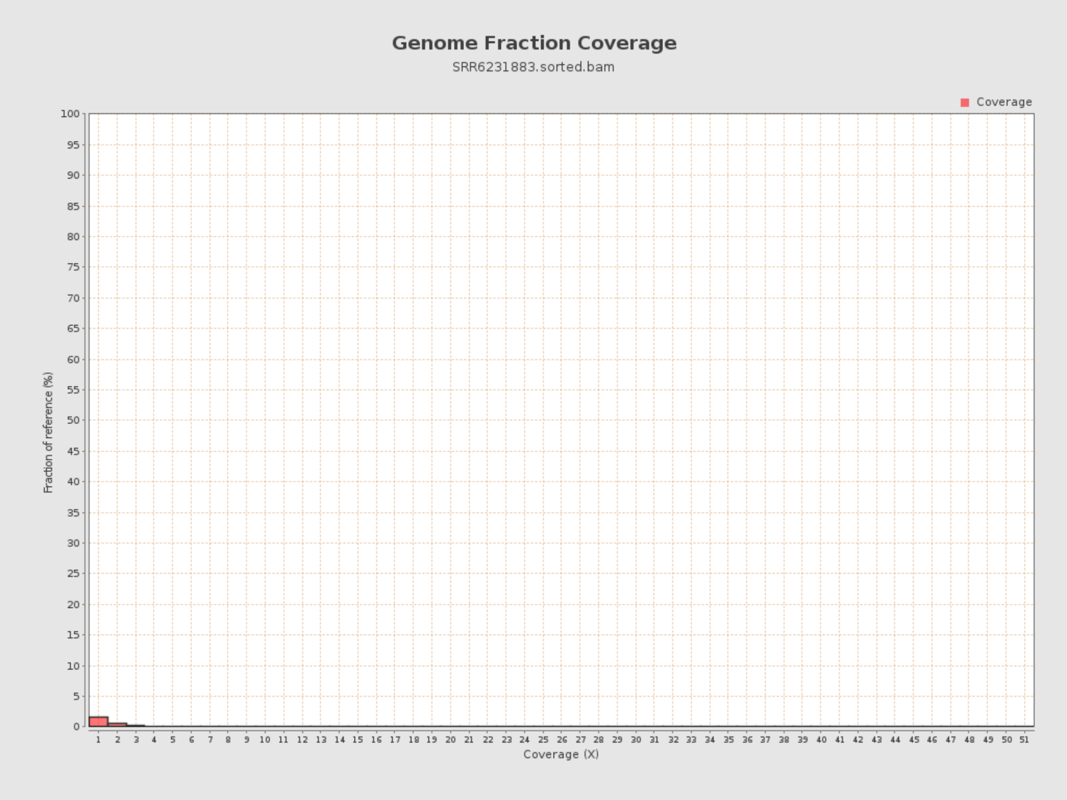
4. Results : Coverage Histogram



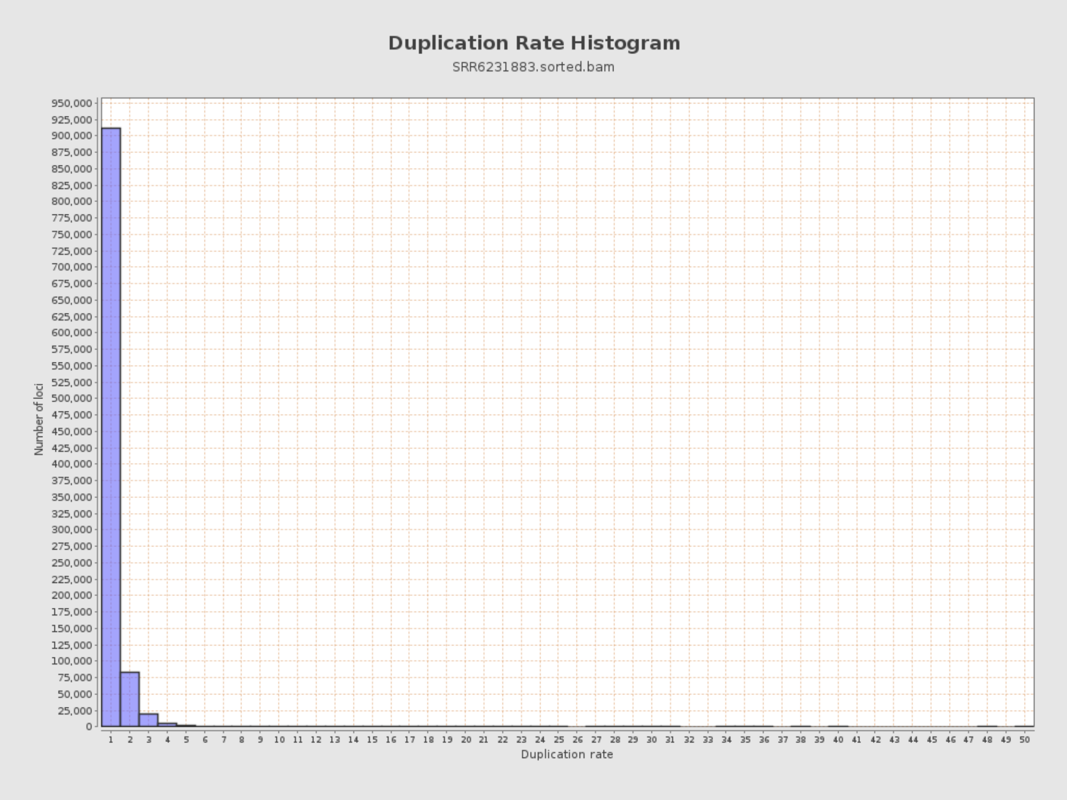
5. Results : Coverage Histogram (0-50X)



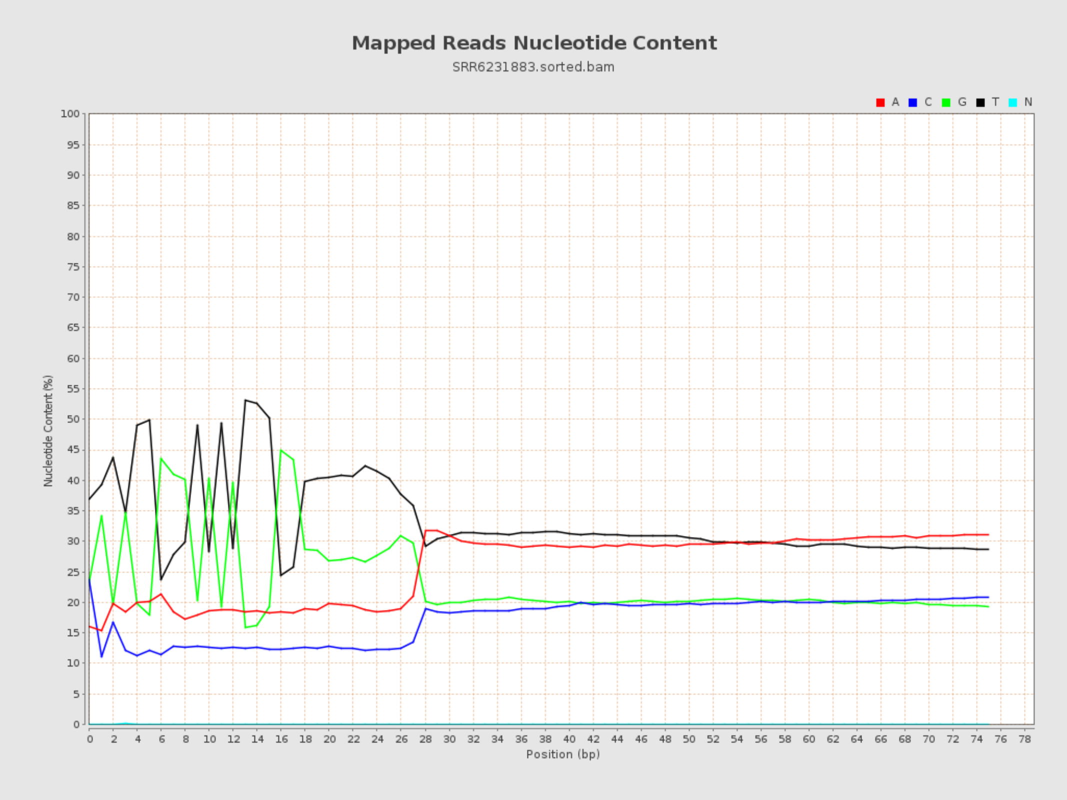
6. Results : Genome Fraction Coverage



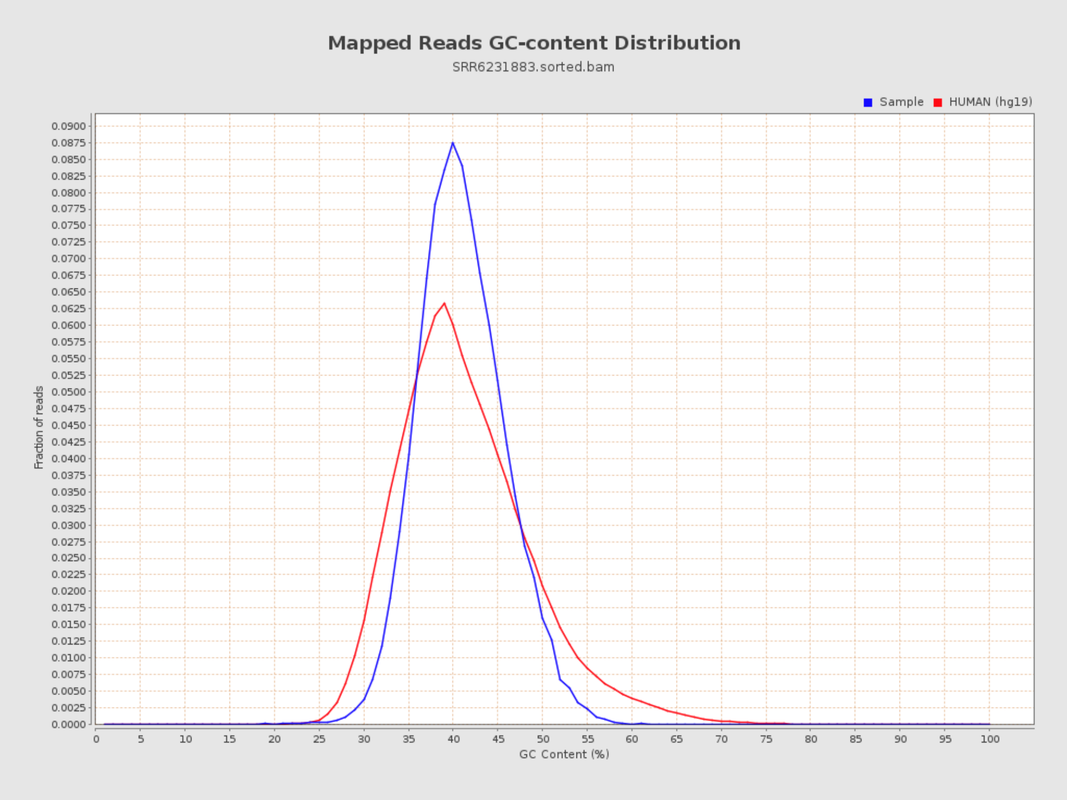
7. Results : Duplication Rate Histogram



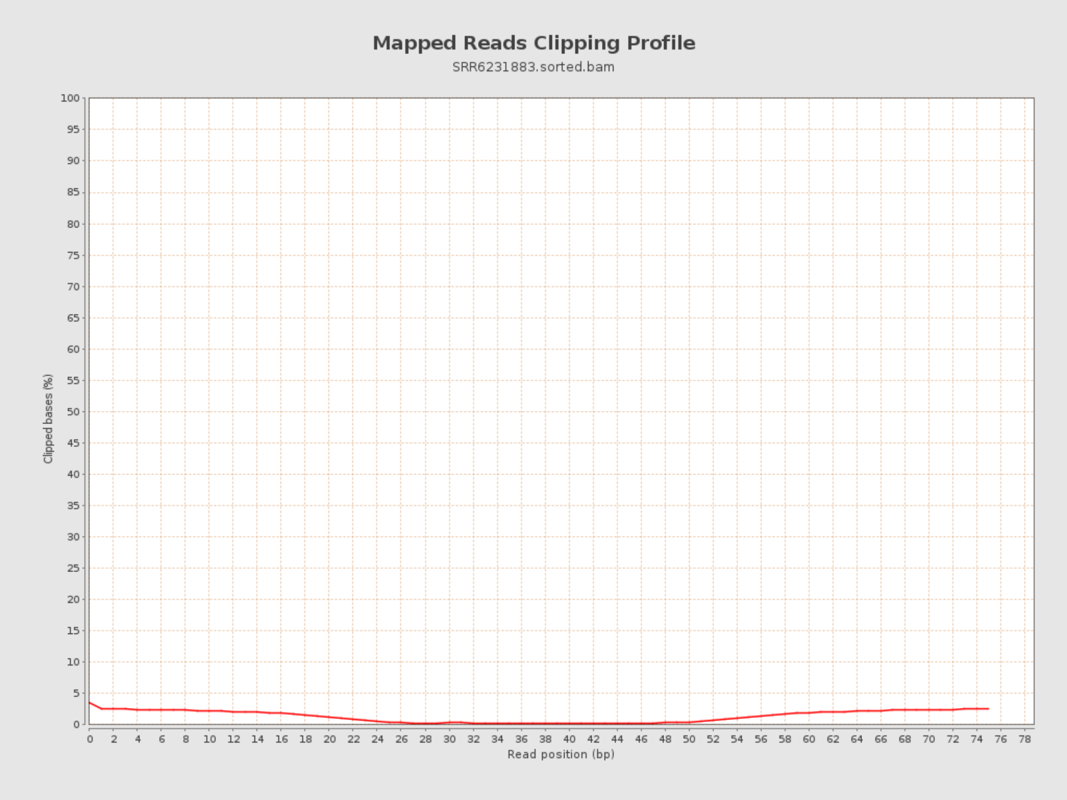
8. Results : Mapped Reads Nucleotide Content



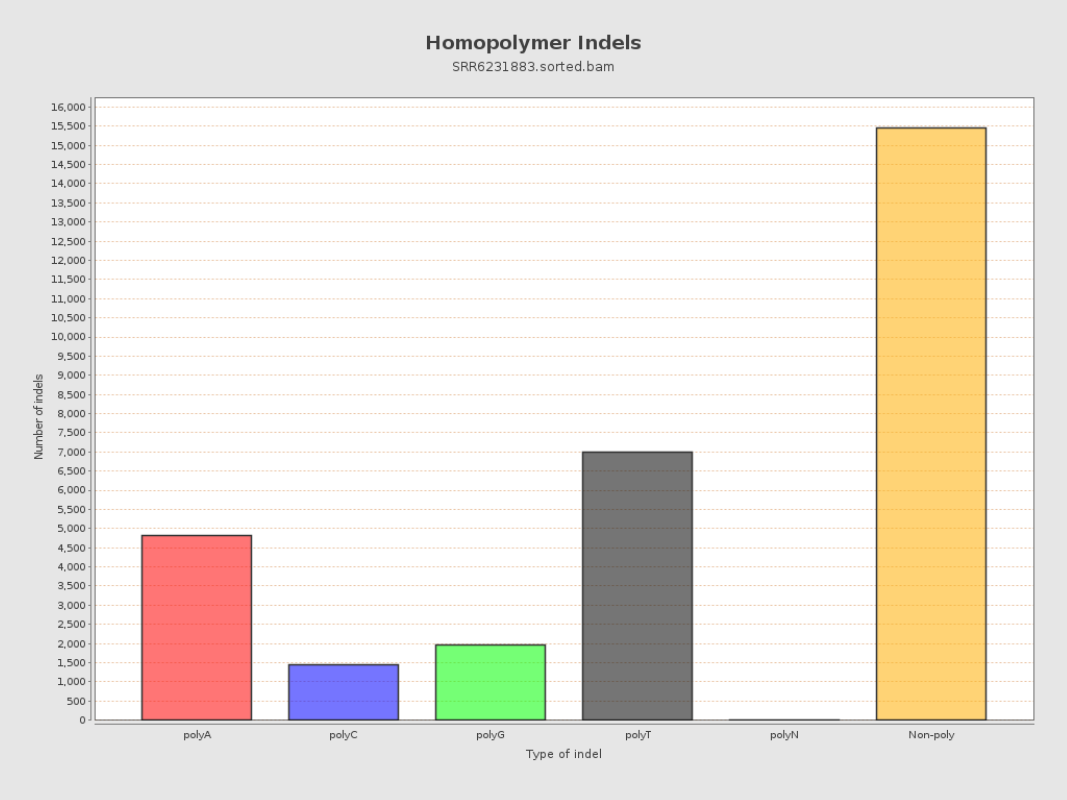
9. Results : Mapped Reads GC-content Distribution



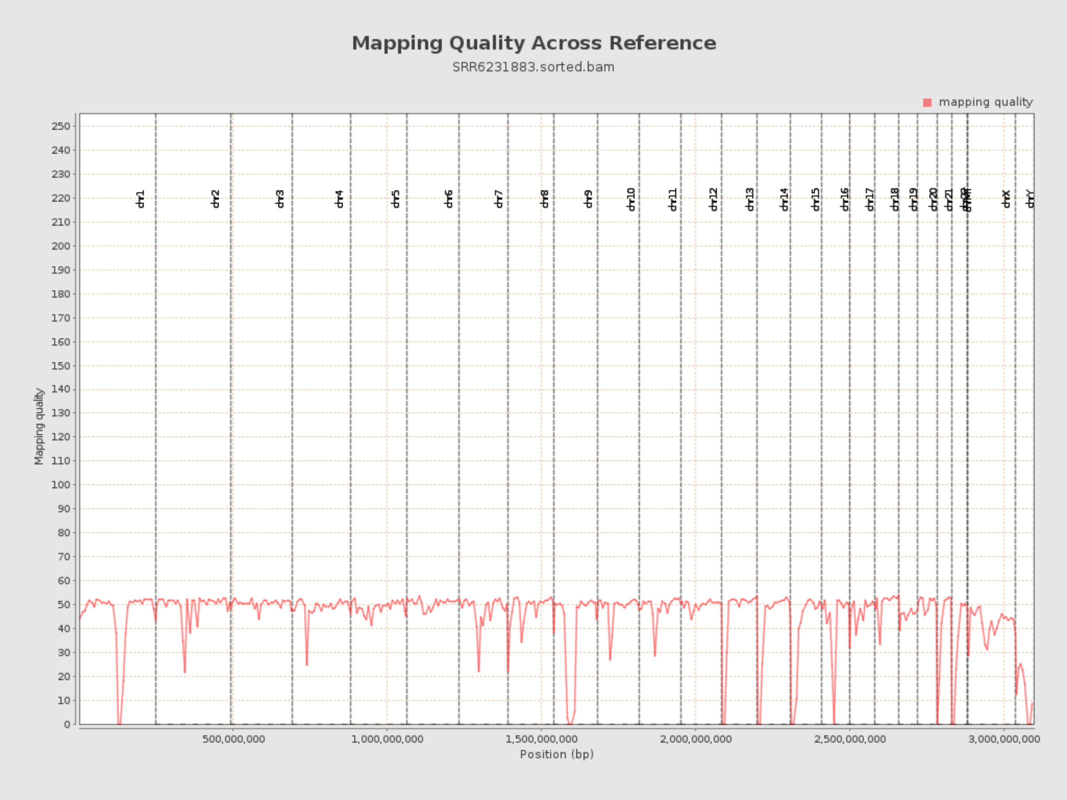
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram