Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:41:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716231.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_SRR9716231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716231.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:41:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,622,632
Mapped reads	1,442,422 / 88.89%
Unmapped reads	180,210 / 11.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,914 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	51,544 / 3.18%
Duplication rate	2.66%
Clipped reads	1,443,730 / 88.97%

2.2. ACGT Content

Number/percentage of A's	20,445,209 / 24.97%
Number/percentage of C's	16,427,225 / 20.07%
Number/percentage of T's	26,279,468 / 32.1%
Number/percentage of G's	18,714,288 / 22.86%
Number/percentage of N's	1,235 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2518

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

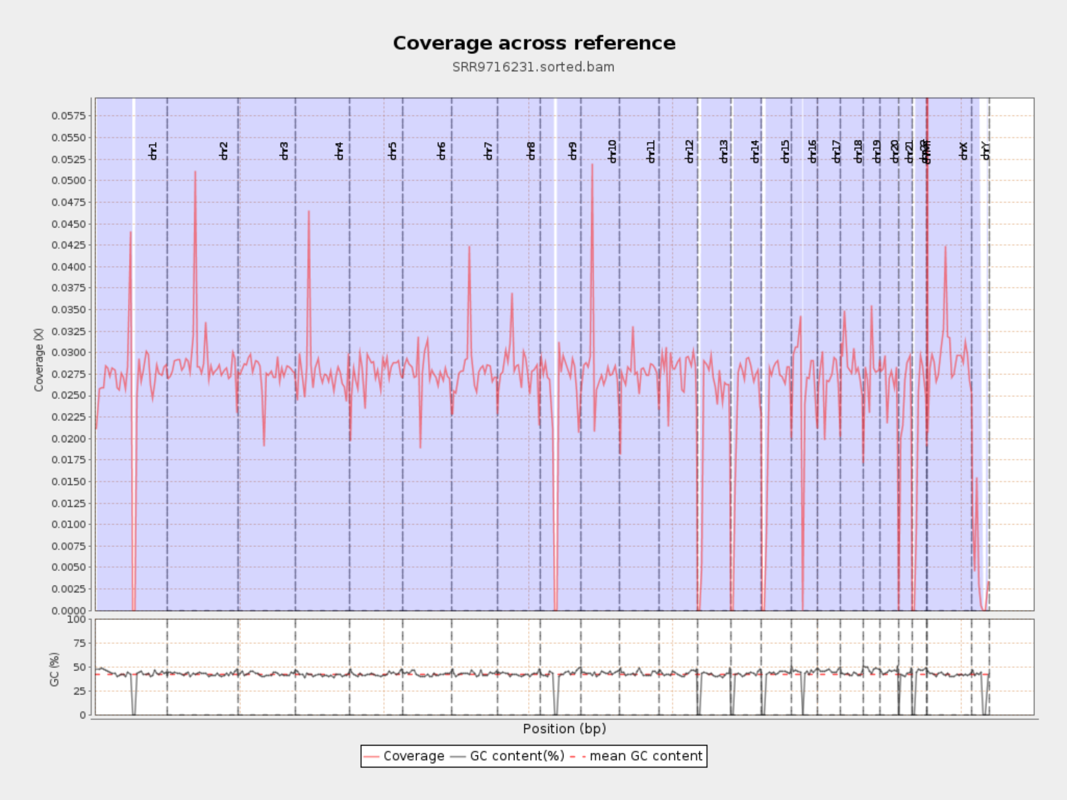
General error rate	0.56%
Mismatches	443,877
Insertions	6,471
Mapped reads with at least one insertion	0.45%
Deletions	14,273
Mapped reads with at least one deletion	0.98%
Homopolymer indels	41.34%

2.6. Chromosome stats

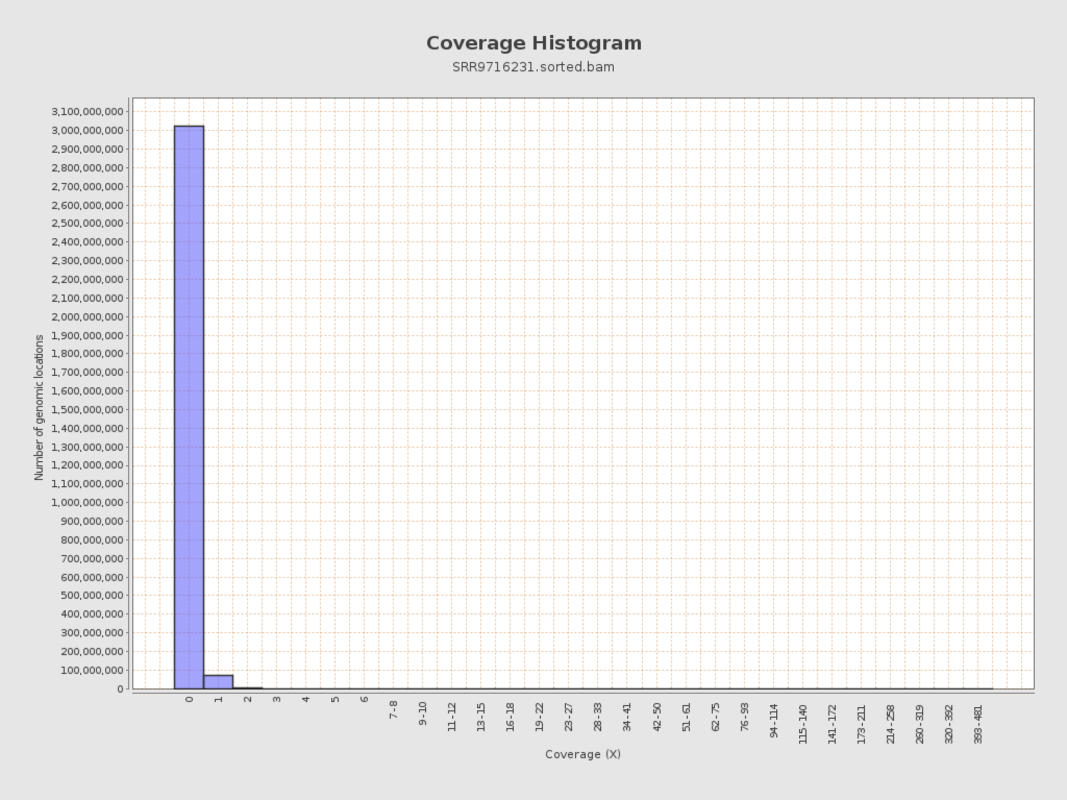
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6468857	0.026	0.4178
chr2	243199373	7083075	0.0291	0.2891
chr3	198022430	5483570	0.0277	0.1798
chr4	191154276	5344226	0.028	0.1992
chr5	180915260	5041280	0.0279	0.1828
chr6	171115067	4724208	0.0276	0.1968
chr7	159138663	4482466	0.0282	0.2815

chr8	146364022	4141791	0.0283	0.2675
chr9	141213431	3437146	0.0243	0.2537
chr10	135534747	3847129	0.0284	0.2646
chr11	135006516	3740571	0.0277	0.2413
chr12	133851895	3758652	0.0281	0.1909
chr13	115169878	2582575	0.0224	0.1599
chr14	107349540	2490667	0.0232	0.1801
chr15	102531392	2301098	0.0224	0.1631
chr16	90354753	2302888	0.0255	0.1885
chr17	81195210	2165982	0.0267	0.1893
chr18	78077248	2258128	0.0289	0.4442
chr19	59128983	1639374	0.0277	0.3471
chr20	63025520	1677334	0.0266	0.1846
chr21	48129895	1093378	0.0227	0.1821
chr22	51304566	952403	0.0186	0.1467
chrMT	16571	11940	0.7205	0.9786
chrX	155270560	4597147	0.0296	0.2255
chrY	59373566	265664	0.0045	0.1171

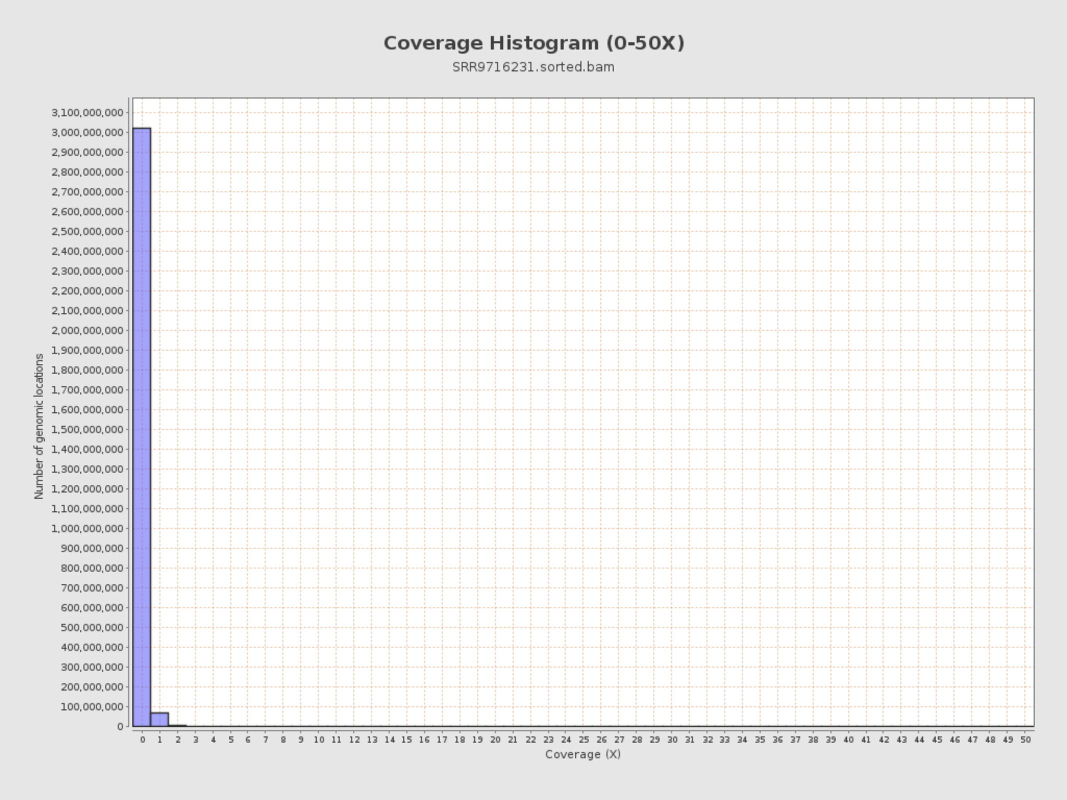
3. Results : Coverage across reference



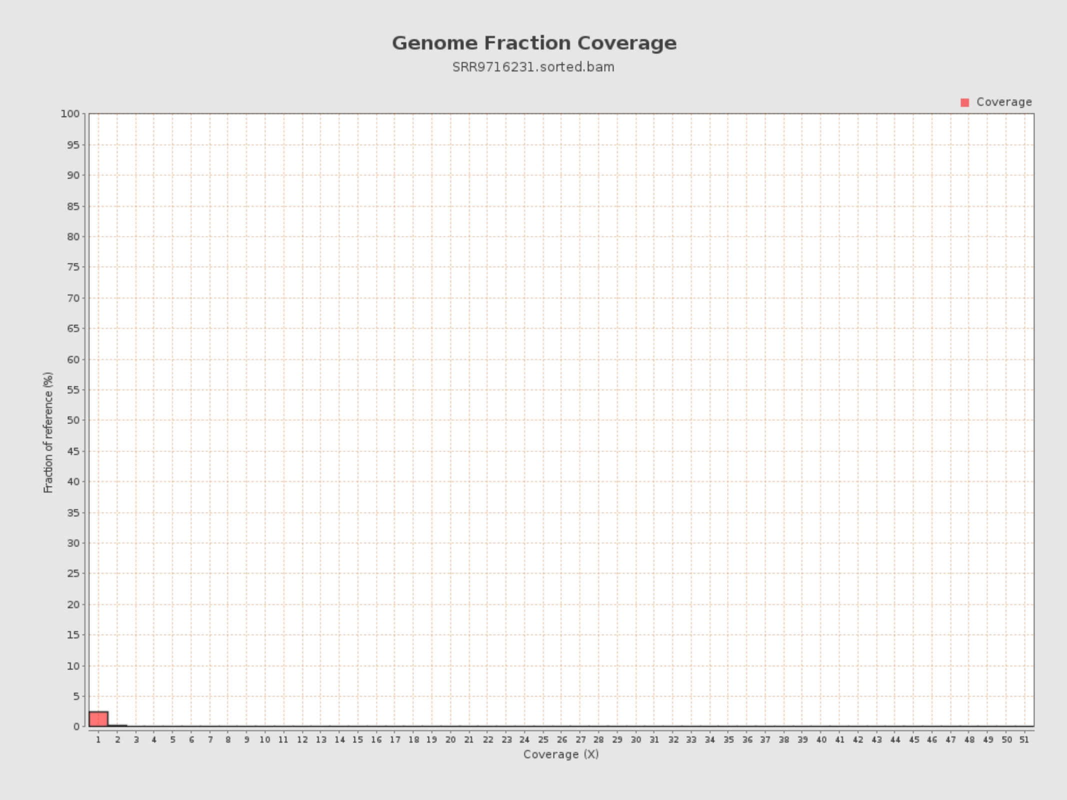
4. Results : Coverage Histogram



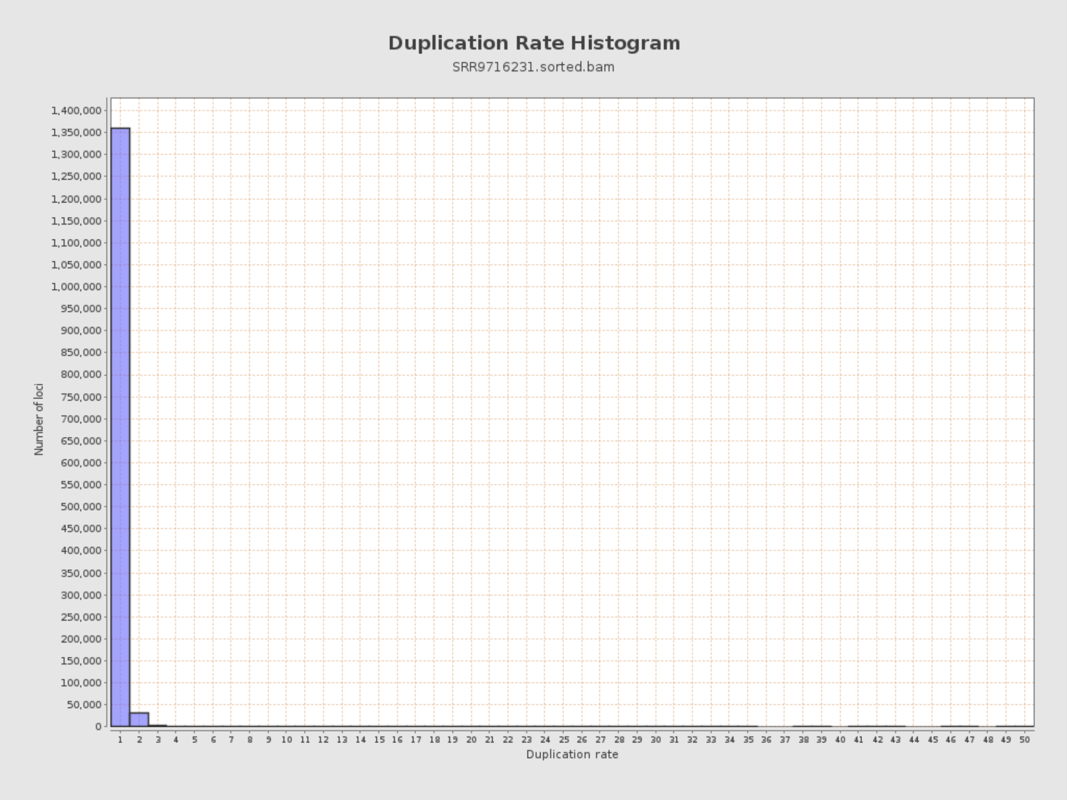
5. Results : Coverage Histogram (0-50X)



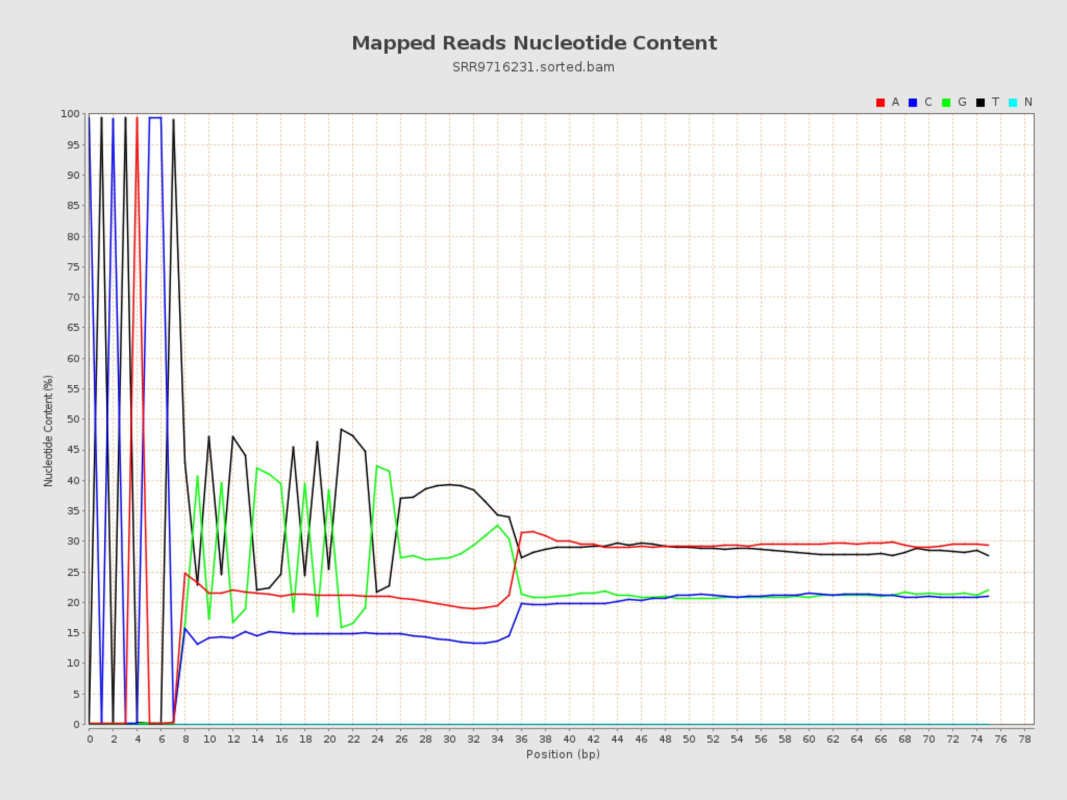
6. Results : Genome Fraction Coverage



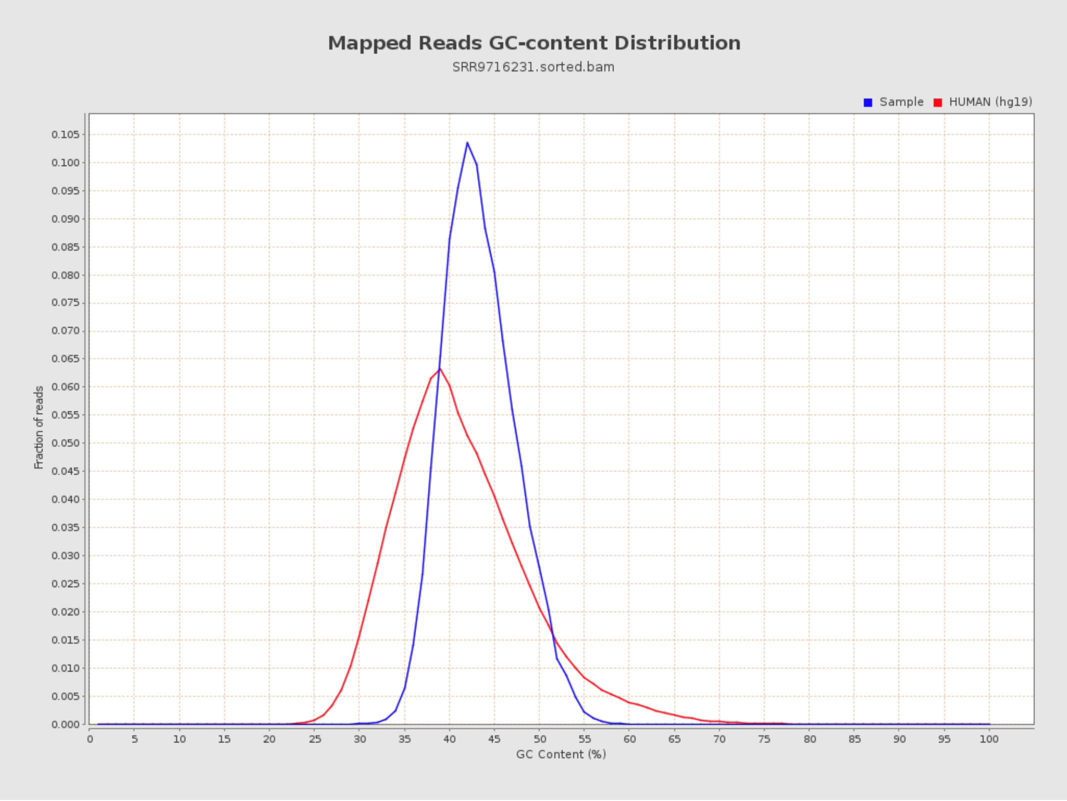
7. Results : Duplication Rate Histogram



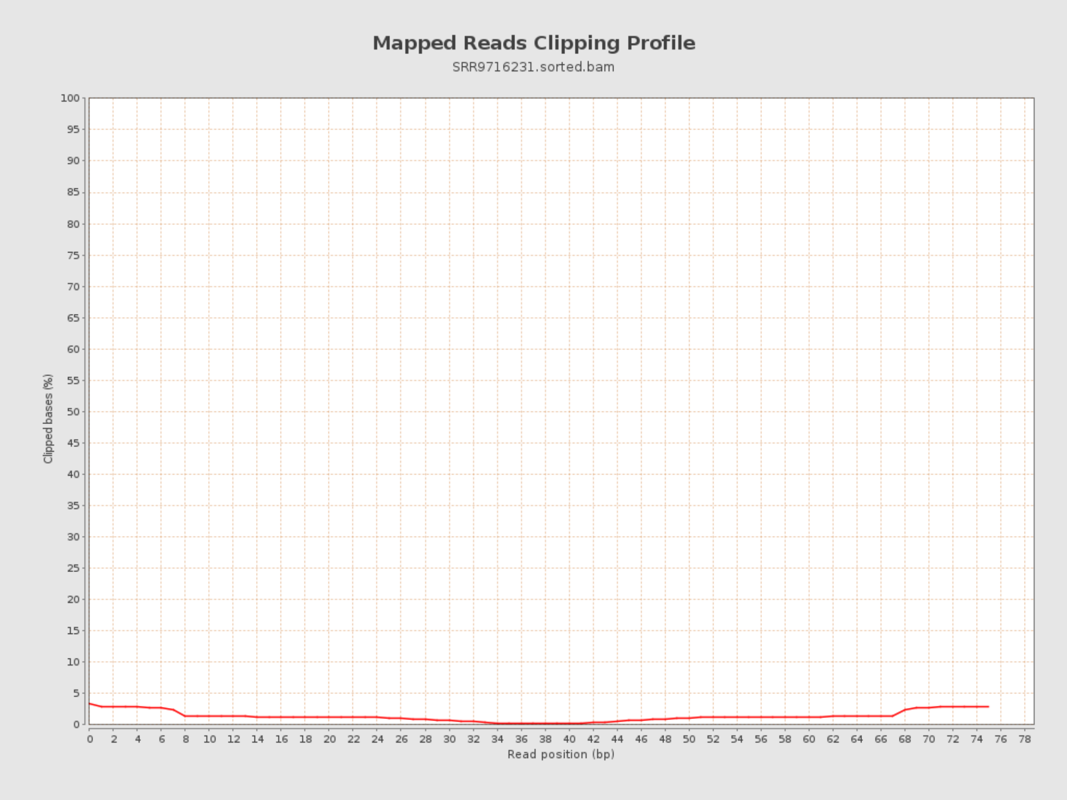
8. Results : Mapped Reads Nucleotide Content



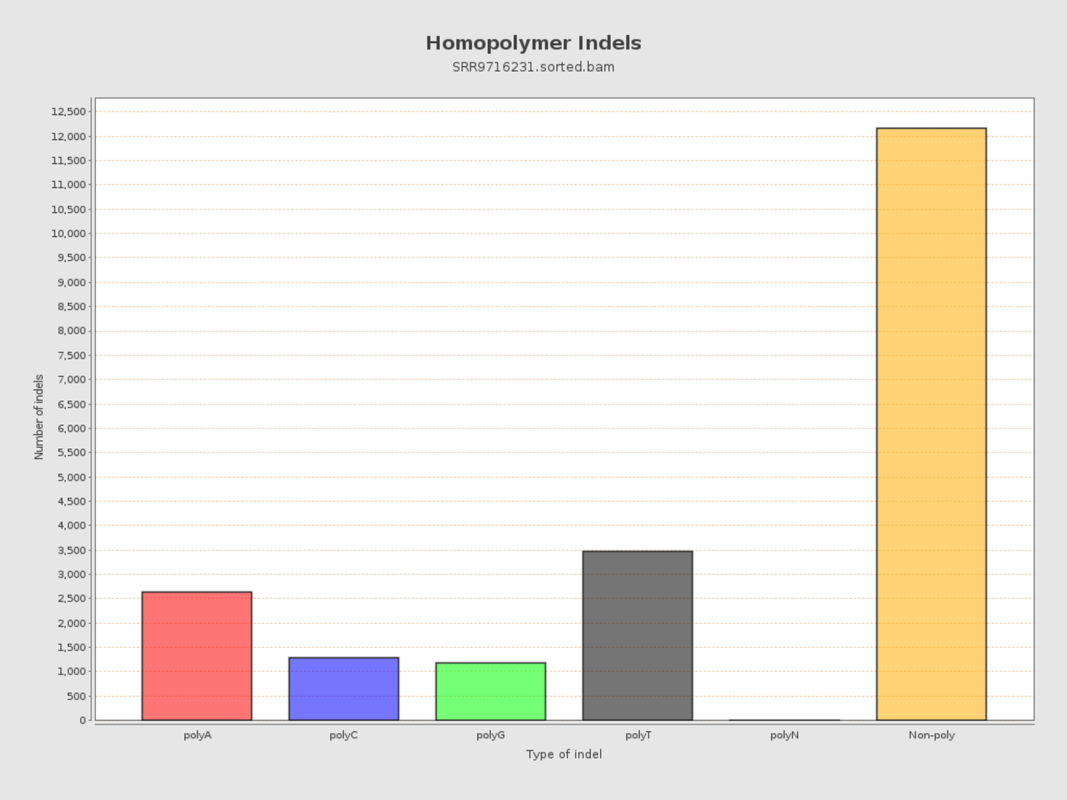
9. Results : Mapped Reads GC-content Distribution



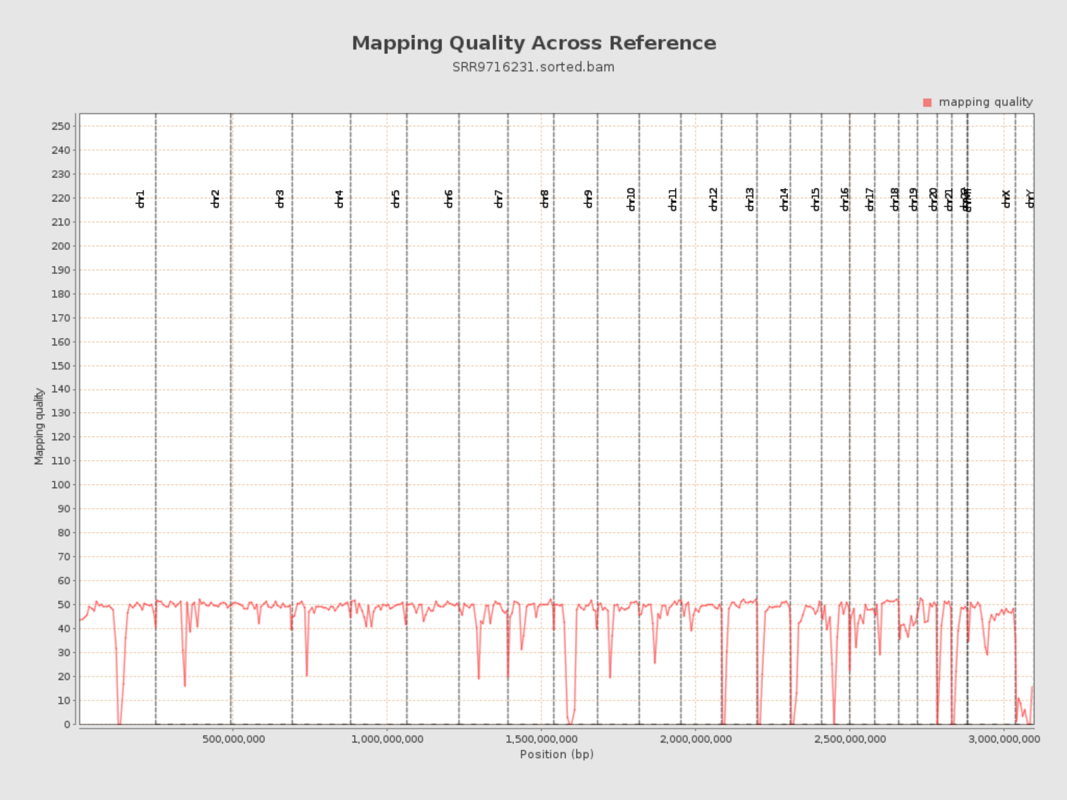
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram