Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:45:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716798.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_SRR9716798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:45:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	832,062
Mapped reads	632,699 / 76.04%
Unmapped reads	199,363 / 23.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	735 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	31,370 / 3.77%
Duplication rate	4.46%
Clipped reads	632,403 / 76%

2.2. ACGT Content

Number/percentage of A's	6,981,174 / 20.85%
Number/percentage of C's	6,250,135 / 18.67%
Number/percentage of T's	10,781,828 / 32.2%
Number/percentage of G's	9,465,324 / 28.27%
Number/percentage of N's	547 / 0%
GC Percentage	46.94%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1244

2.4. Mapping Quality

Mean Mapping Quality	42.9

2.5. Mismatches and indels

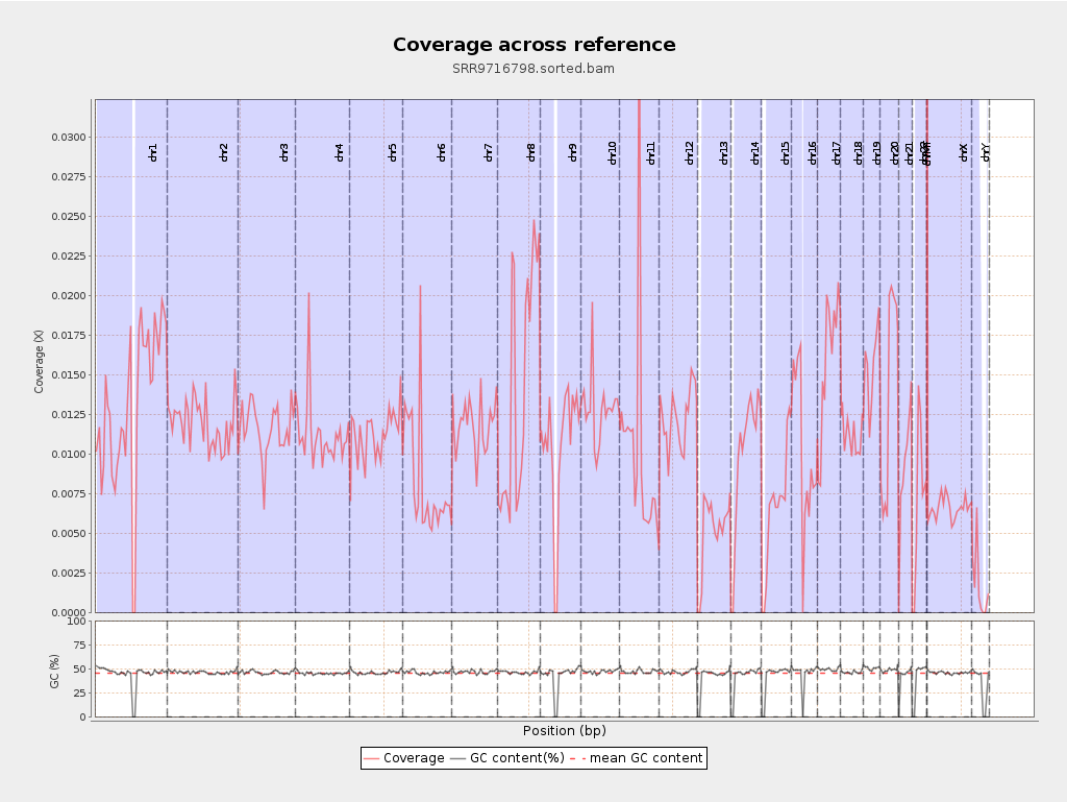
General error rate	0.68%
Mismatches	224,095
Insertions	1,827
Mapped reads with at least one insertion	0.29%
Deletions	5,278
Mapped reads with at least one deletion	0.83%
Homopolymer indels	39.76%

2.6. Chromosome stats

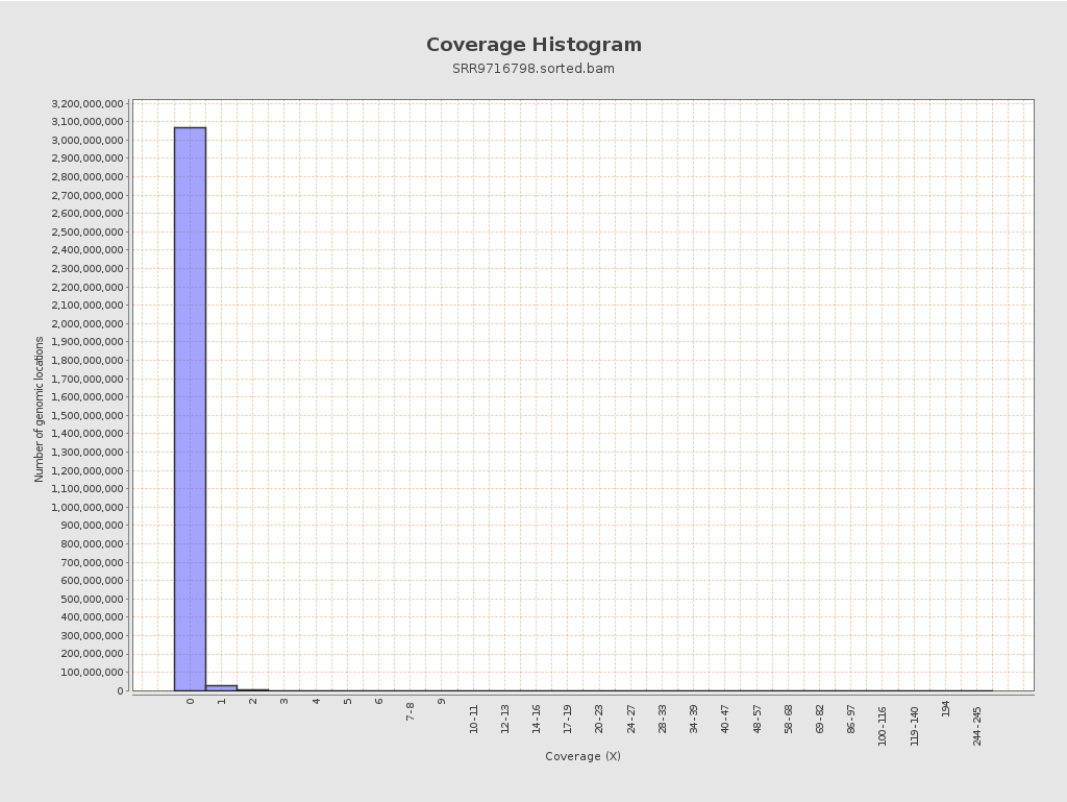
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3270546	0.0131	0.1524
chr2	243199373	2905243	0.0119	0.1597
chr3	198022430	2294141	0.0116	0.1176
chr4	191154276	2158737	0.0113	0.1204
chr5	180915260	2061486	0.0114	0.1162
chr6	171115067	1406668	0.0082	0.1085
chr7	159138663	1887024	0.0119	0.1327

chr8	146364022	2079551	0.0142	0.1322
chr9	141213431	1477963	0.0105	0.1155
chr10	135534747	1743553	0.0129	0.1411
chr11	135006516	1413114	0.0105	0.1202
chr12	133851895	1648068	0.0123	0.1216
chr13	115169878	583834	0.0051	0.0785
chr14	107349540	1072267	0.01	0.1092
chr15	102531392	680576	0.0066	0.0892
chr16	90354753	907687	0.01	0.1152
chr17	81195210	1296981	0.016	0.1417
chr18	78077248	869758	0.0111	0.1287
chr19	59128983	911225	0.0154	0.1605
chr20	63025520	868064	0.0138	0.1301
chr21	48129895	450679	0.0094	0.1094
chr22	51304566	375037	0.0073	0.0945
chrMT	16571	1403	0.0847	0.3108
chrX	155270560	1024680	0.0066	0.0906
chrY	59373566	99585	0.0017	0.0603

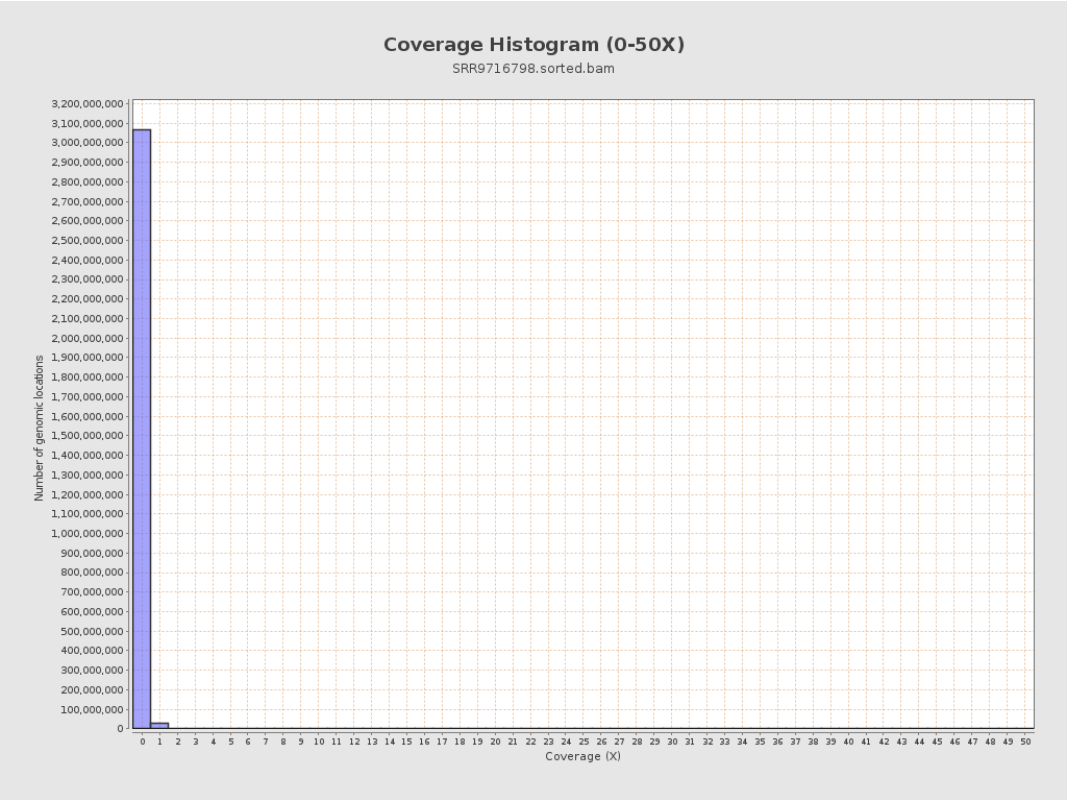
3. Results : Coverage across reference



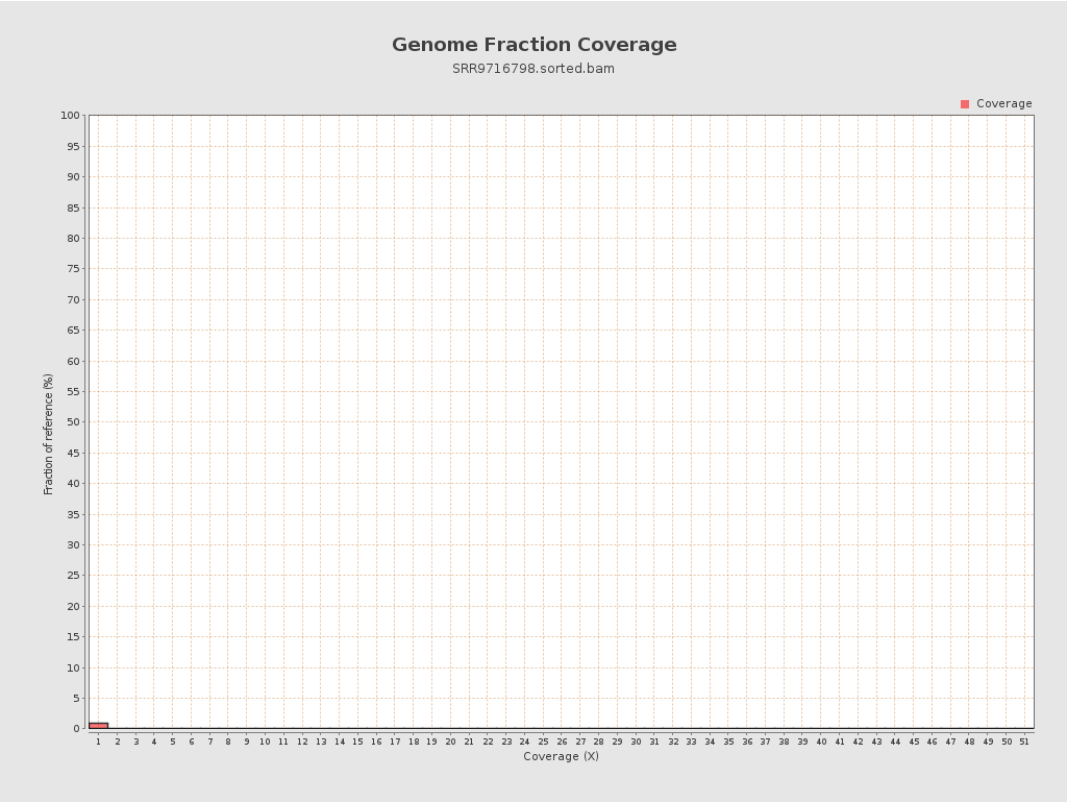
4. Results : Coverage Histogram



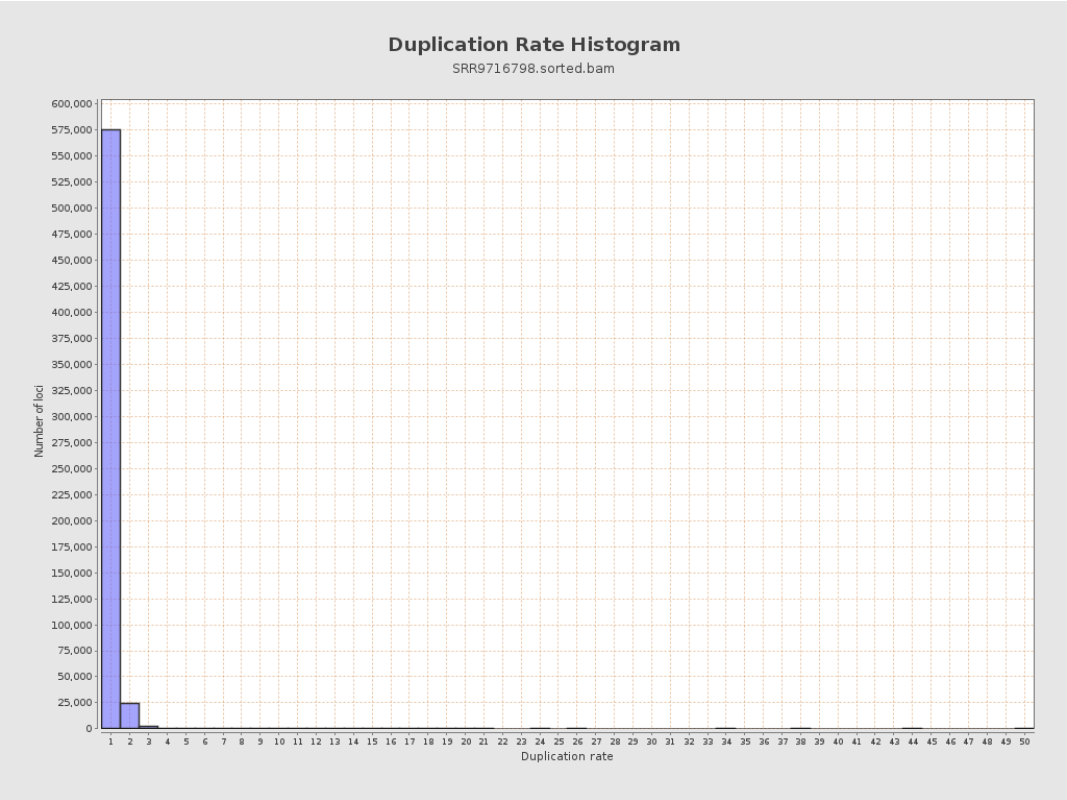
5. Results : Coverage Histogram (0-50X)



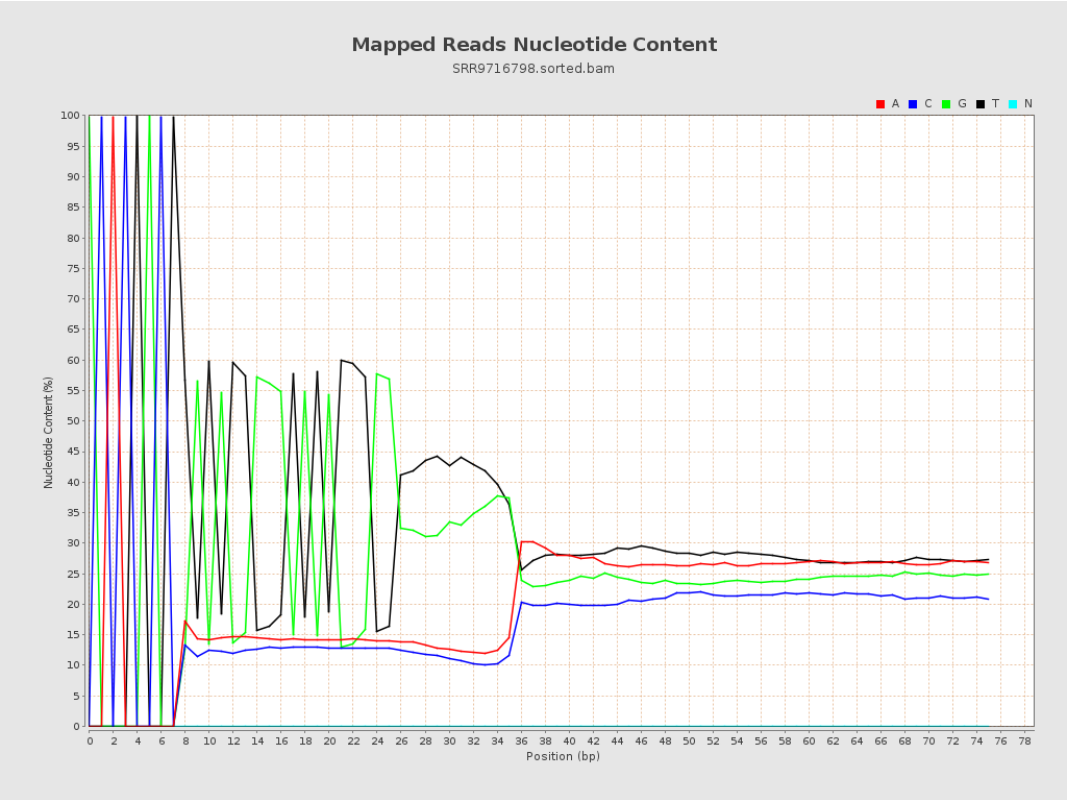
6. Results : Genome Fraction Coverage



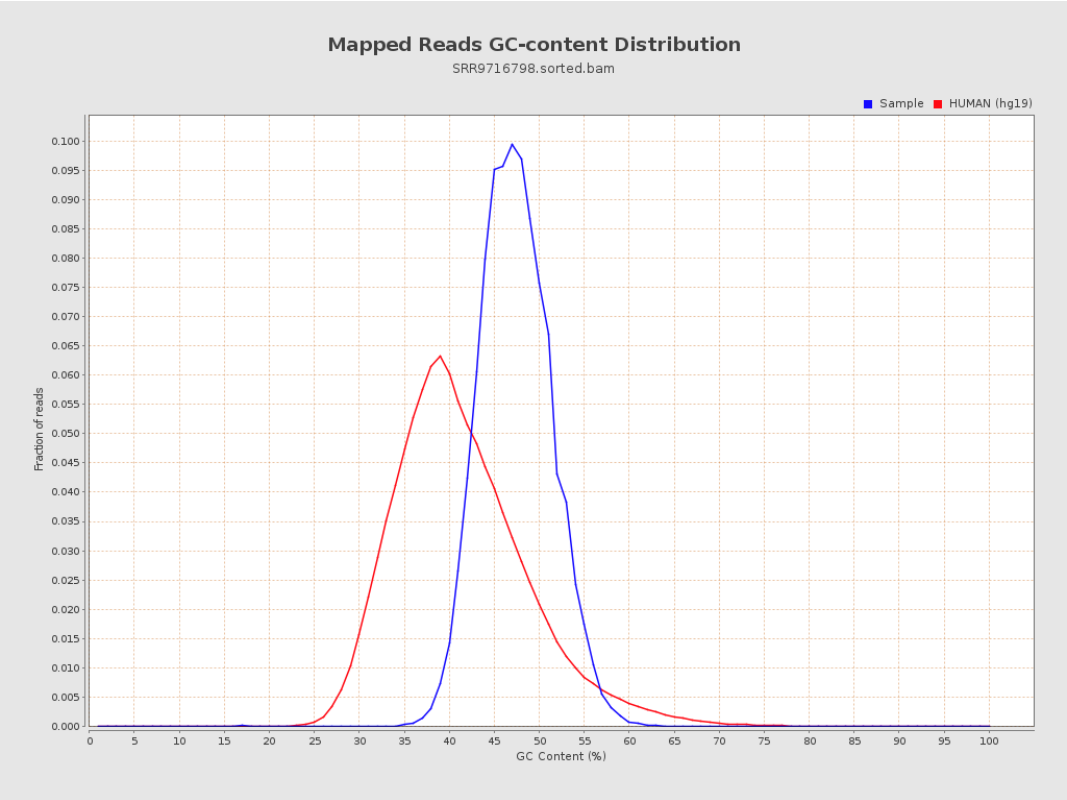
7. Results : Duplication Rate Histogram



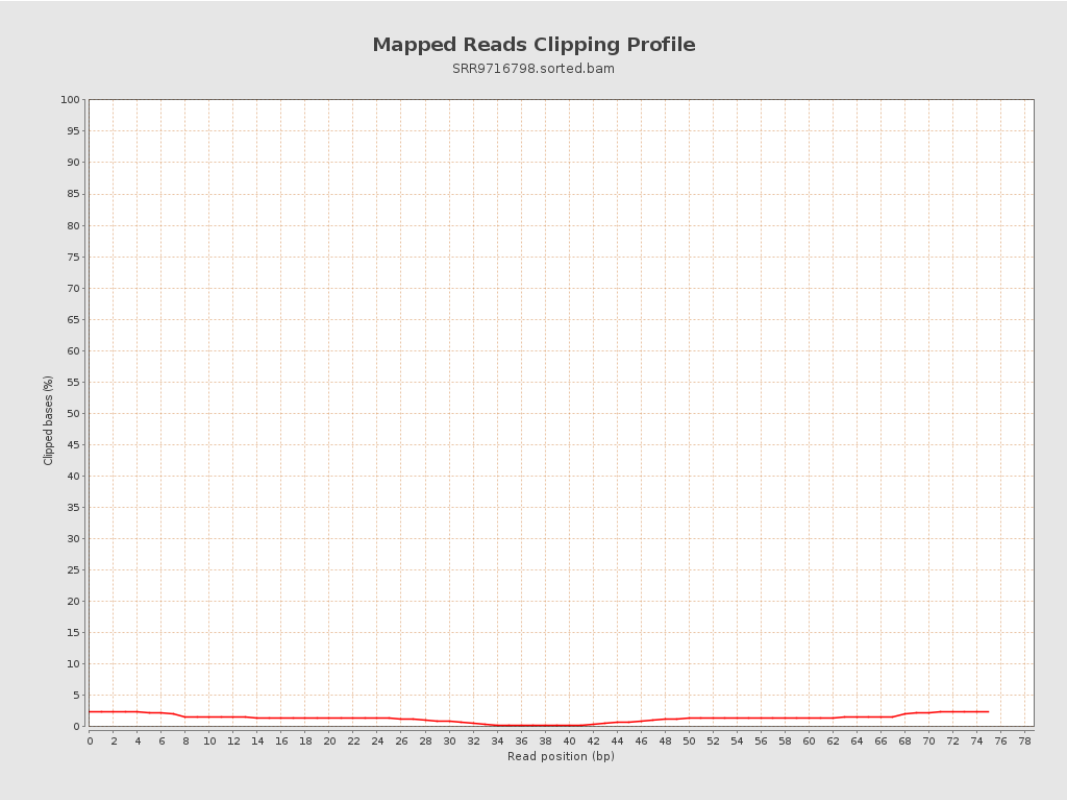
8. Results : Mapped Reads Nucleotide Content



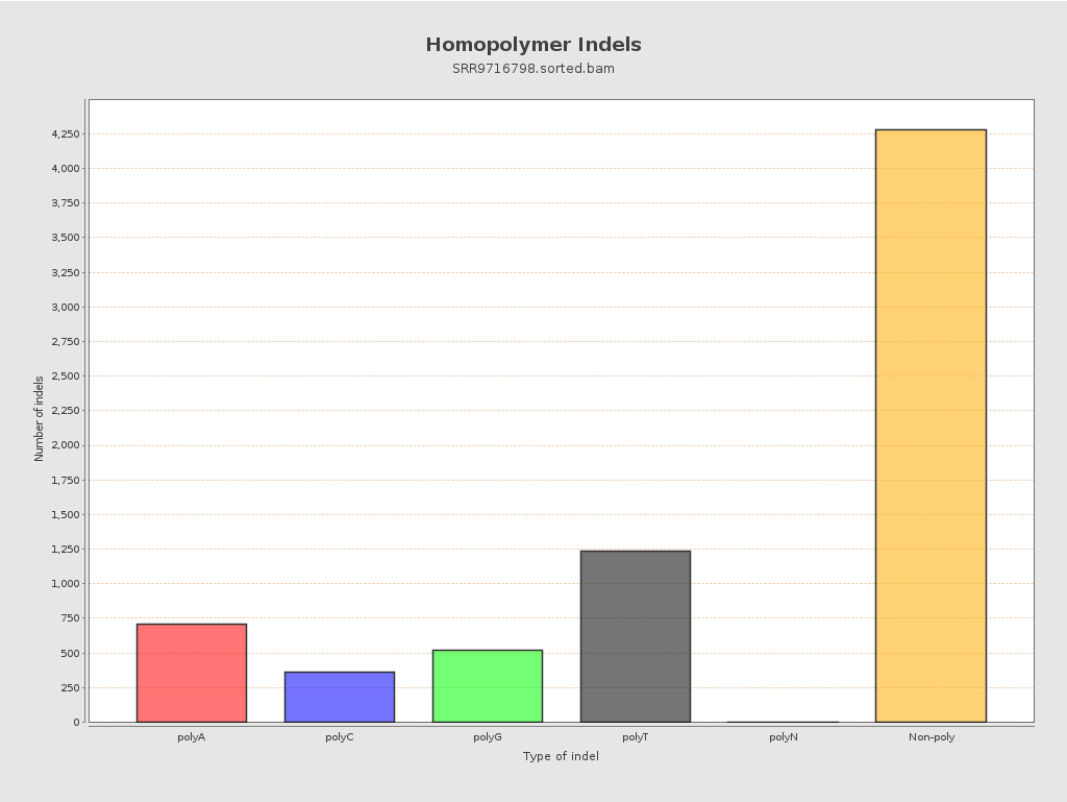
9. Results : Mapped Reads GC-content Distribution



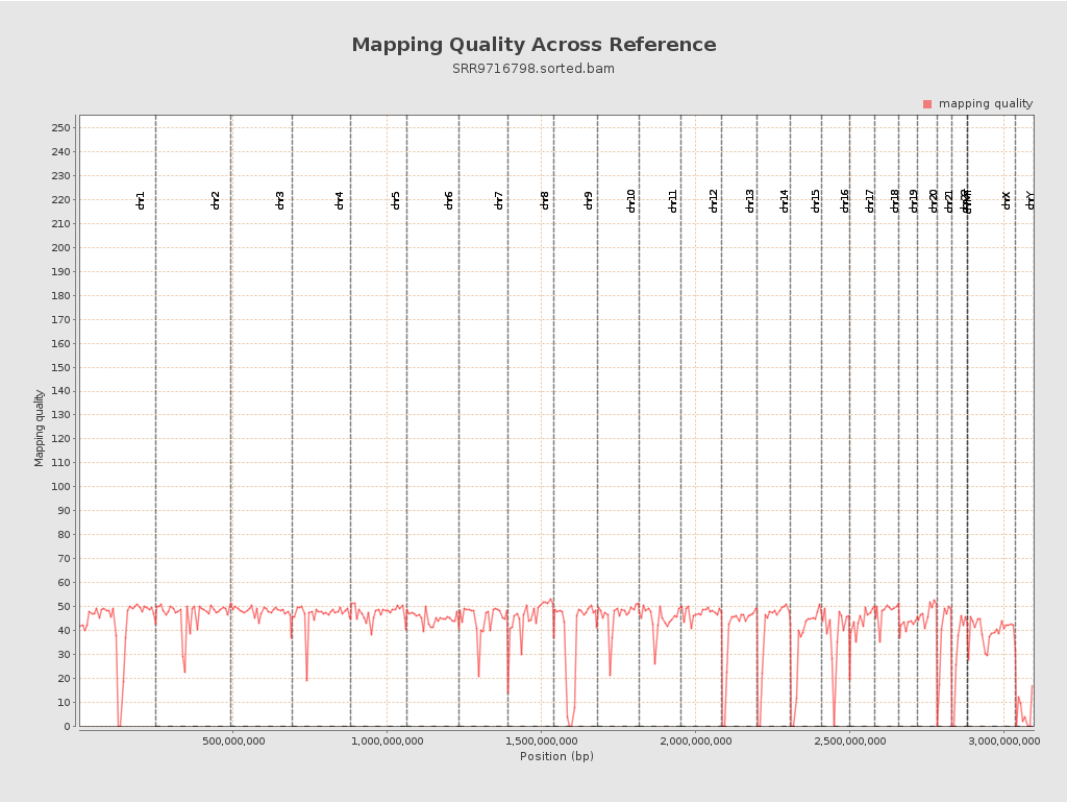
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram