Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:09:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716498.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_SRR9716498 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716498.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:09:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,661,860
Mapped reads	2,242,787 / 84.26%
Unmapped reads	419,073 / 15.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,633 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	97,312 / 3.66%
Duplication rate	3.3%
Clipped reads	2,248,135 / 84.46%

2.2. ACGT Content

Number/percentage of A's	34,169,407 / 26.43%
Number/percentage of C's	22,858,597 / 17.68%
Number/percentage of T's	40,747,818 / 31.52%
Number/percentage of G's	31,509,811 / 24.37%
Number/percentage of N's	3,748 / 0%
GC Percentage	42.05%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.3491

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

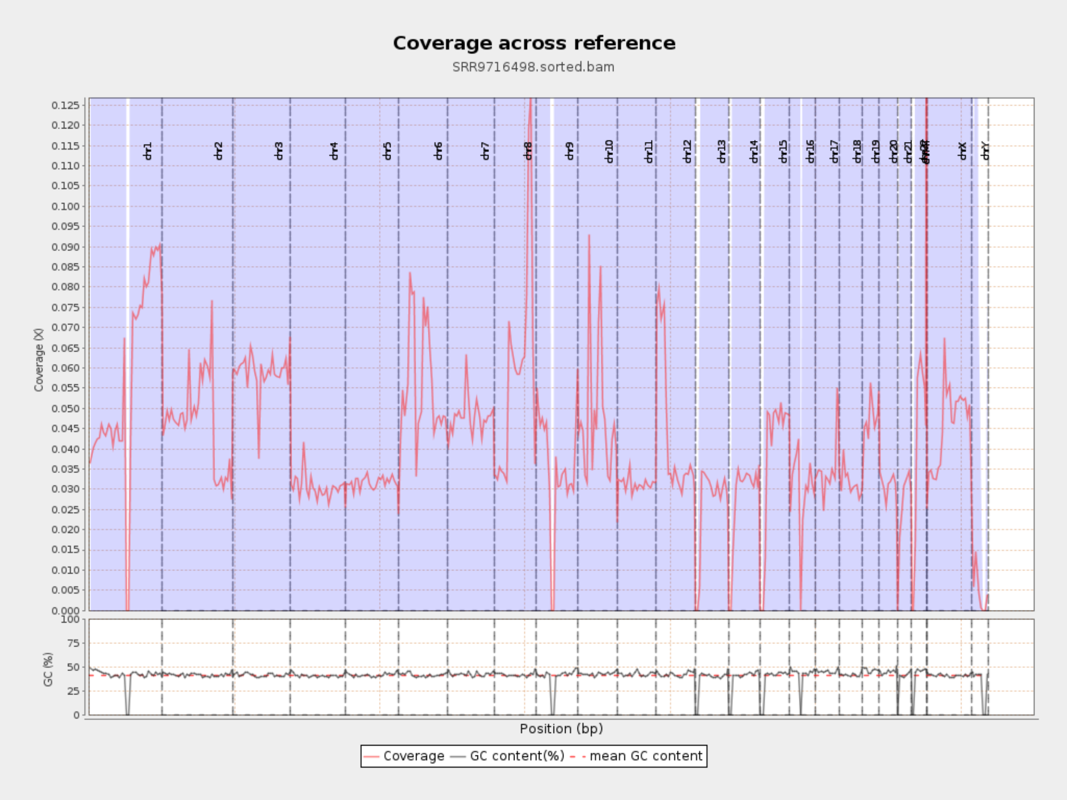
General error rate	0.5%
Mismatches	623,139
Insertions	9,328
Mapped reads with at least one insertion	0.41%
Deletions	21,794
Mapped reads with at least one deletion	0.97%
Homopolymer indels	43%

2.6. Chromosome stats

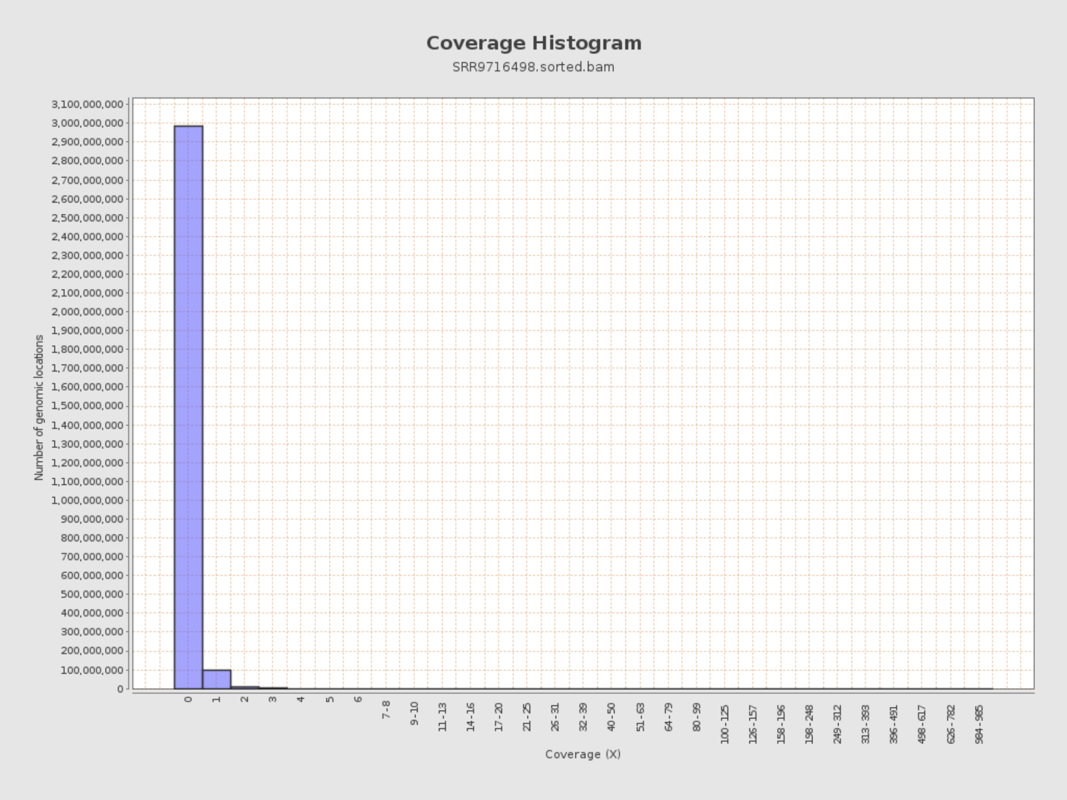
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14154221	0.0568	0.631
chr2	243199373	11376441	0.0468	0.4726
chr3	198022430	11651527	0.0588	0.2756
chr4	191154276	5830816	0.0305	0.2077
chr5	180915260	5738224	0.0317	0.2035
chr6	171115067	9527353	0.0557	0.3623
chr7	159138663	7657365	0.0481	0.4121

chr8	146364022	8733873	0.0597	0.3098
chr9	141213431	4743705	0.0336	0.2868
chr10	135534747	6583987	0.0486	0.4246
chr11	135006516	4211117	0.0312	0.2717
chr12	133851895	5851651	0.0437	0.2411
chr13	115169878	2981466	0.0259	0.1817
chr14	107349540	2911021	0.0271	0.2081
chr15	102531392	3943710	0.0385	0.2237
chr16	90354753	2694250	0.0298	0.2343
chr17	81195210	2885645	0.0355	0.224
chr18	78077248	2475230	0.0317	0.5118
chr19	59128983	2795585	0.0473	0.4533
chr20	63025520	1951371	0.031	0.2002
chr21	48129895	1230769	0.0256	0.2
chr22	51304566	2040741	0.0398	0.2259
chrMT	16571	5929	0.3578	0.6502
chrX	155270560	7044714	0.0454	0.2787
chrY	59373566	302826	0.0051	0.1152

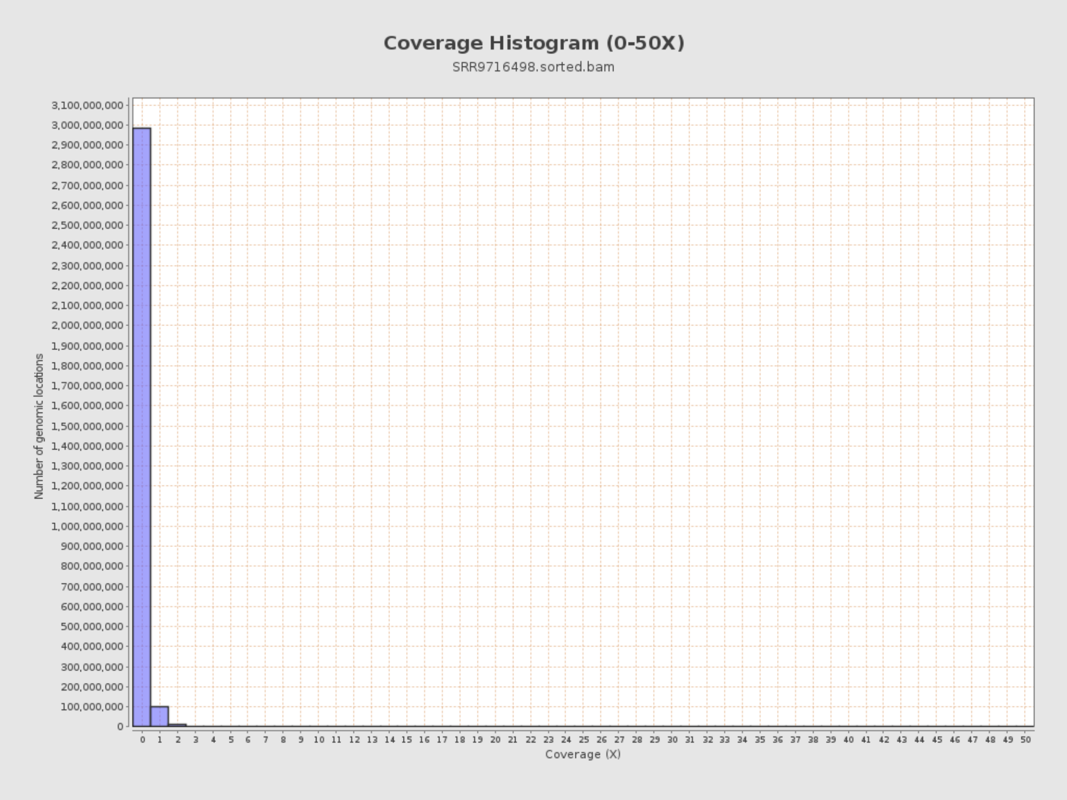
3. Results : Coverage across reference



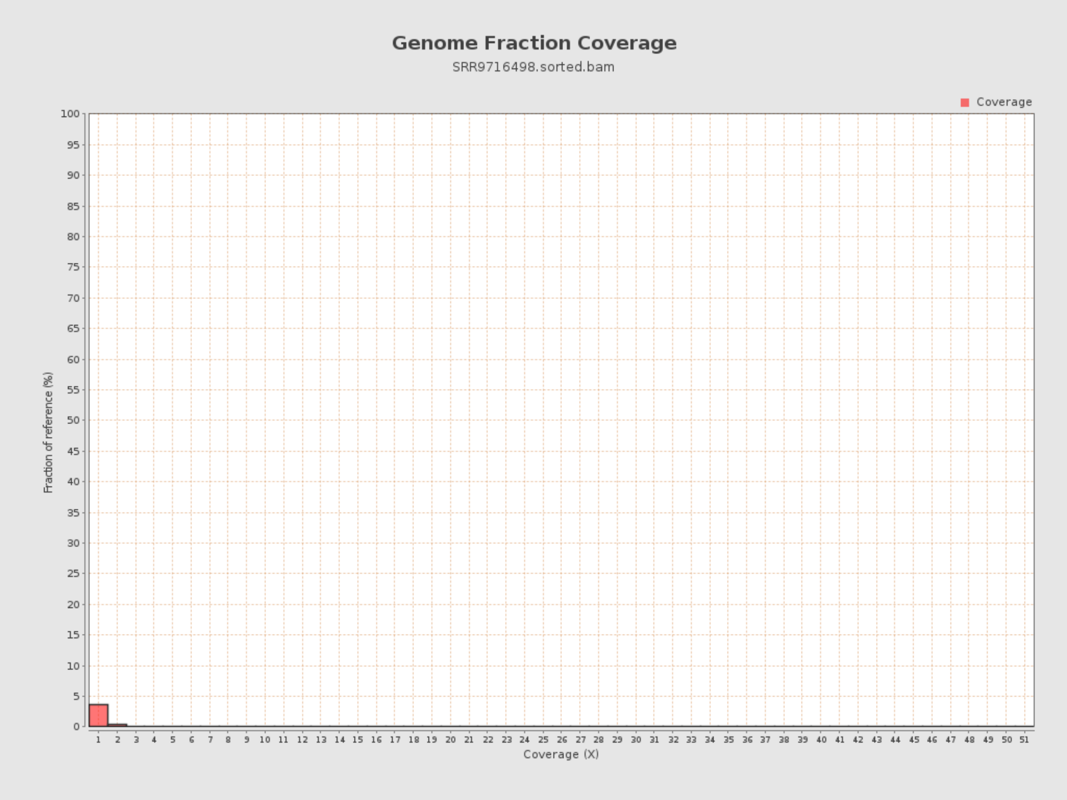
4. Results : Coverage Histogram



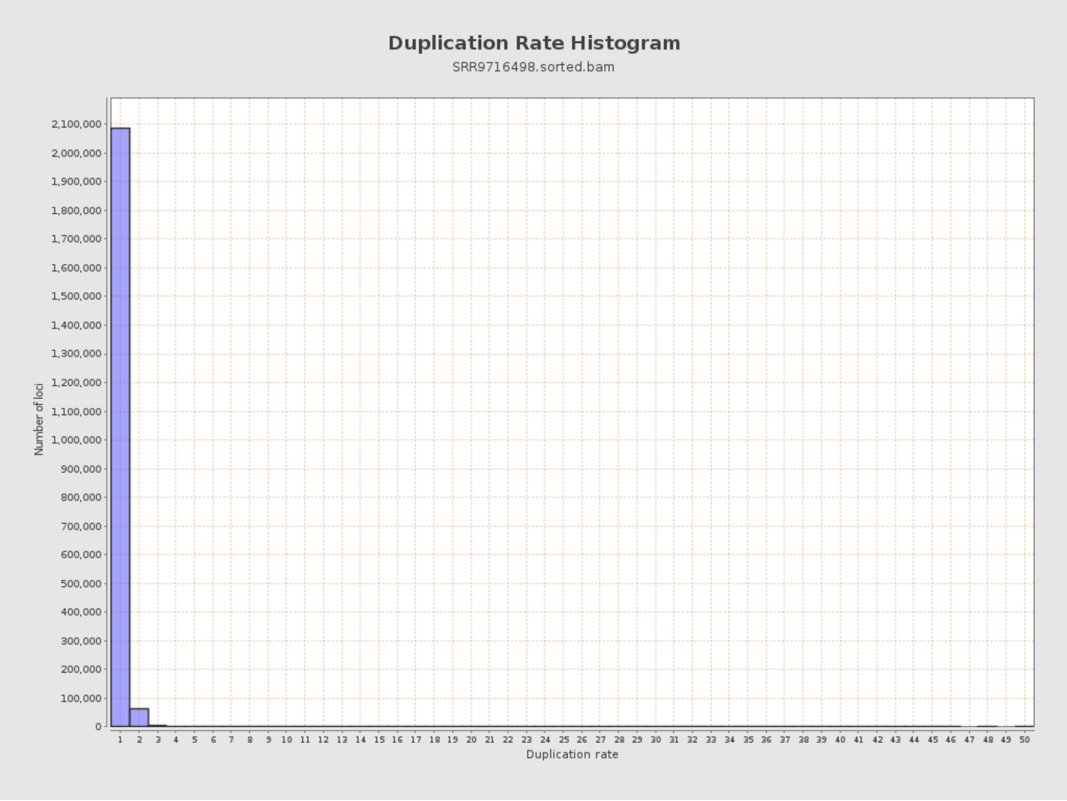
5. Results : Coverage Histogram (0-50X)



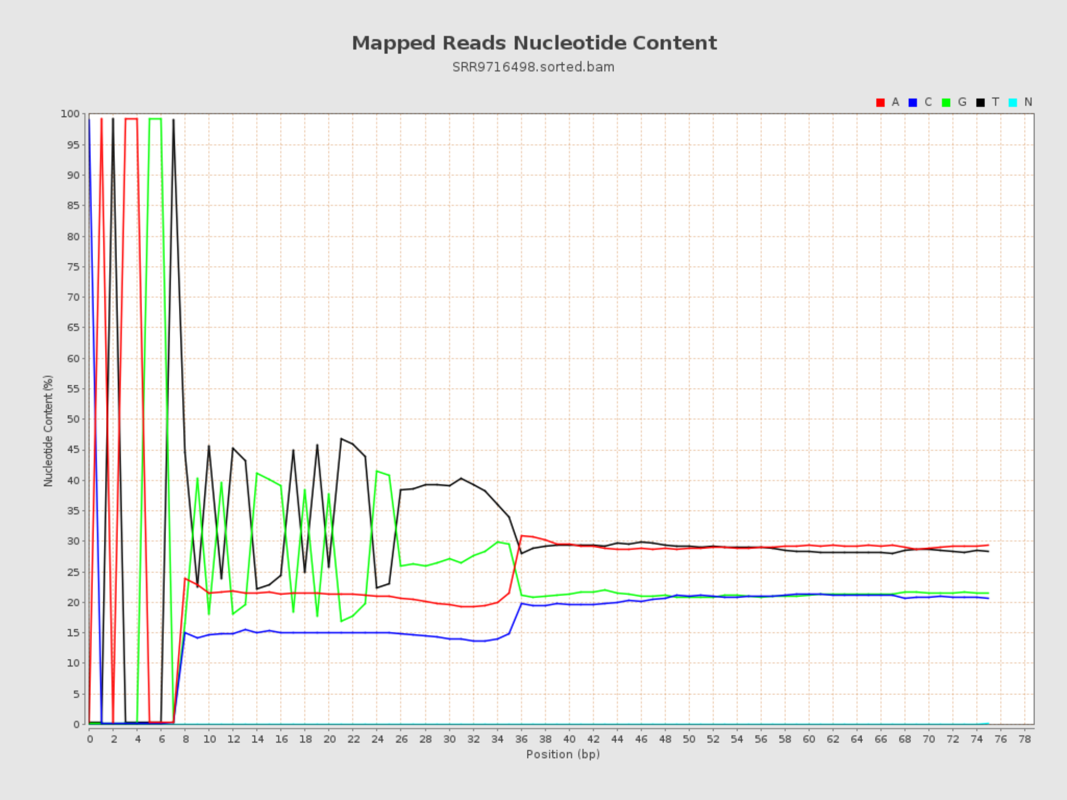
6. Results : Genome Fraction Coverage



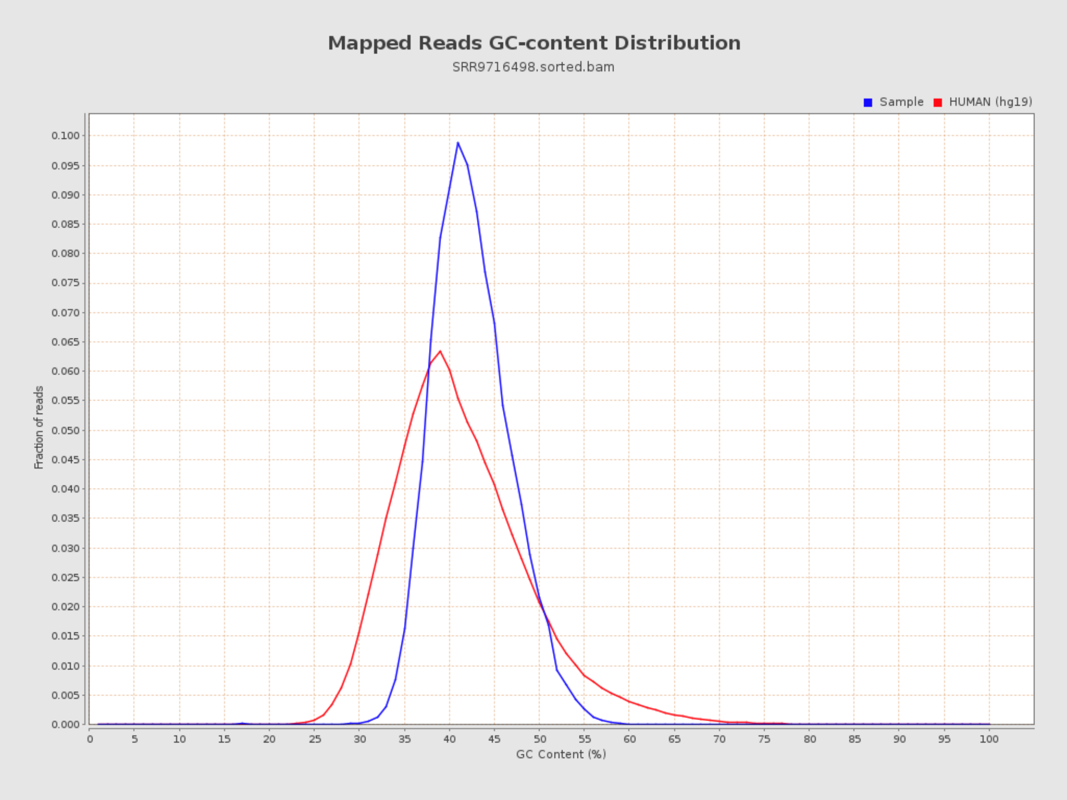
7. Results : Duplication Rate Histogram



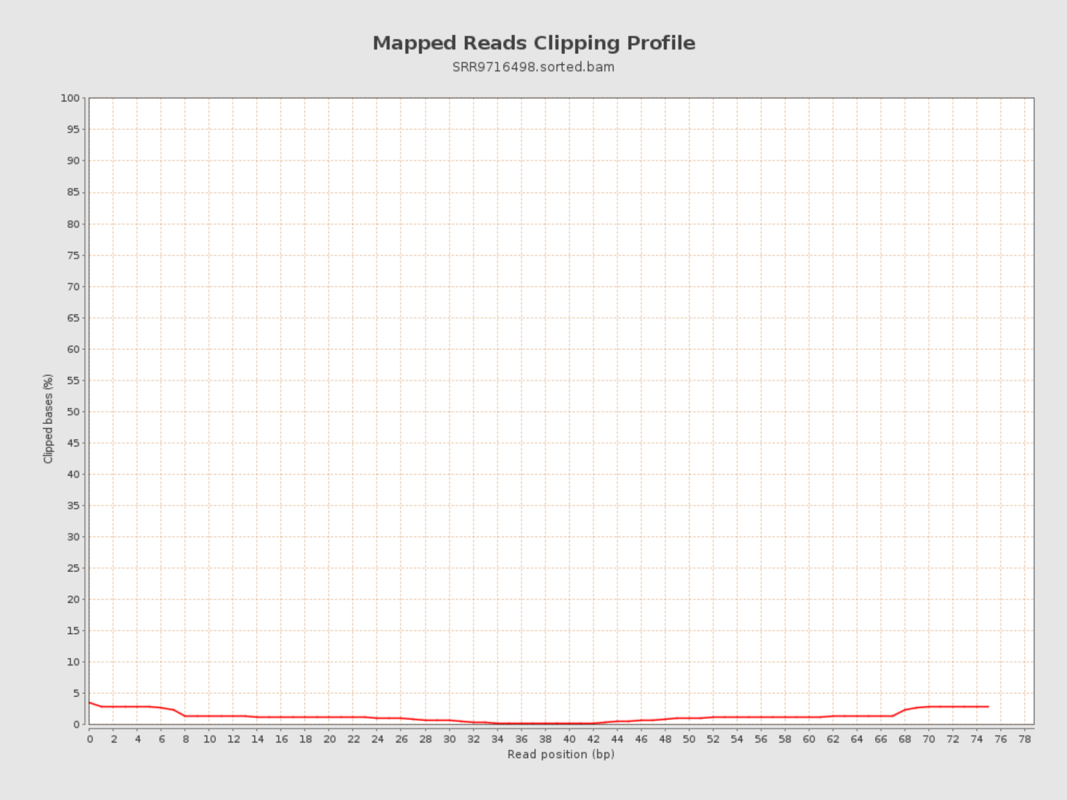
8. Results : Mapped Reads Nucleotide Content



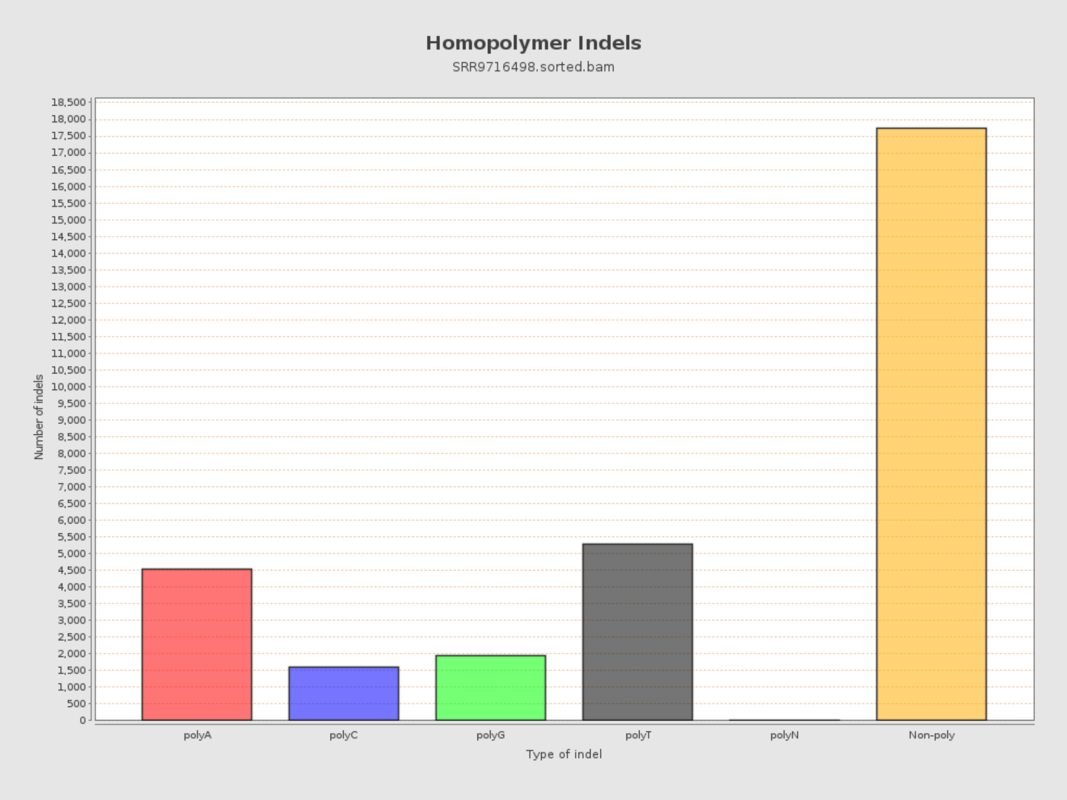
9. Results : Mapped Reads GC-content Distribution



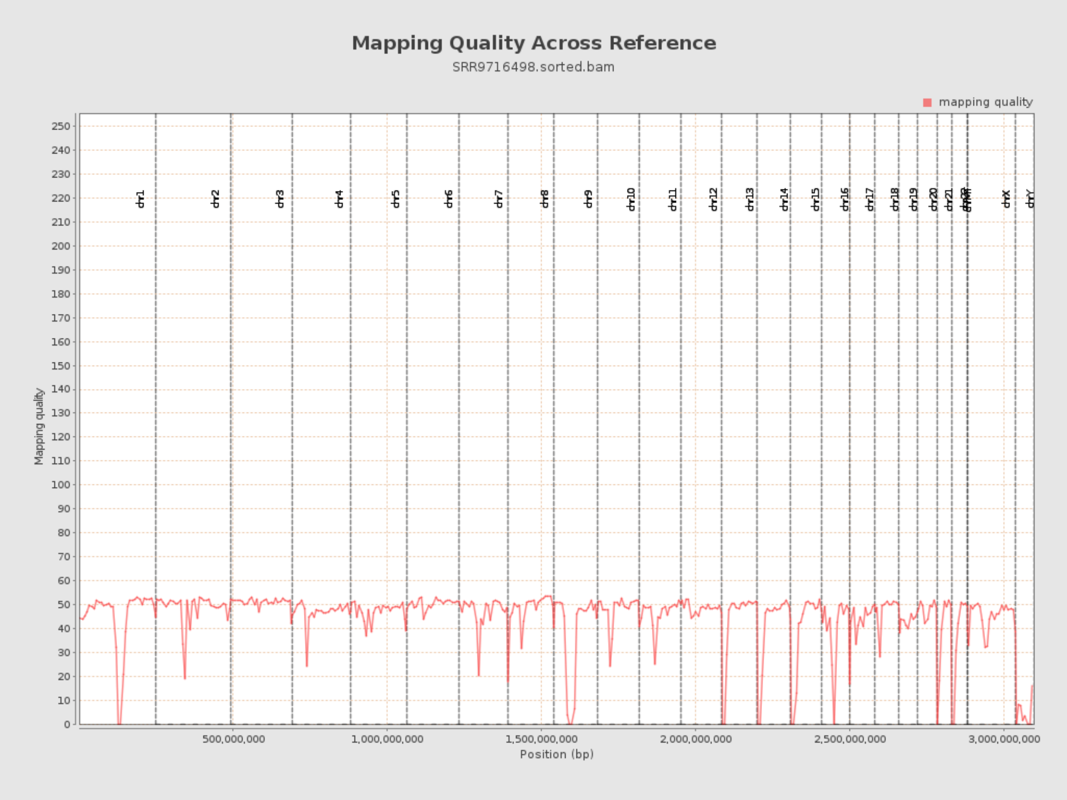
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram