Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:00:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716549.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_SRR9716549 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716549.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:00:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716549.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,393,308
Mapped reads	2,209,384 / 92.32%
Unmapped reads	183,924 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,089 / 0.55%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	90,310 / 3.77%
Duplication rate	2.95%
Clipped reads	2,219,875 / 92.75%

2.2. ACGT Content

Number/percentage of A's	31,043,319 / 24.05%
Number/percentage of C's	27,024,070 / 20.93%
Number/percentage of T's	40,573,093 / 31.43%
Number/percentage of G's	30,454,500 / 23.59%
Number/percentage of N's	1,818 / 0%
GC Percentage	44.52%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.362

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

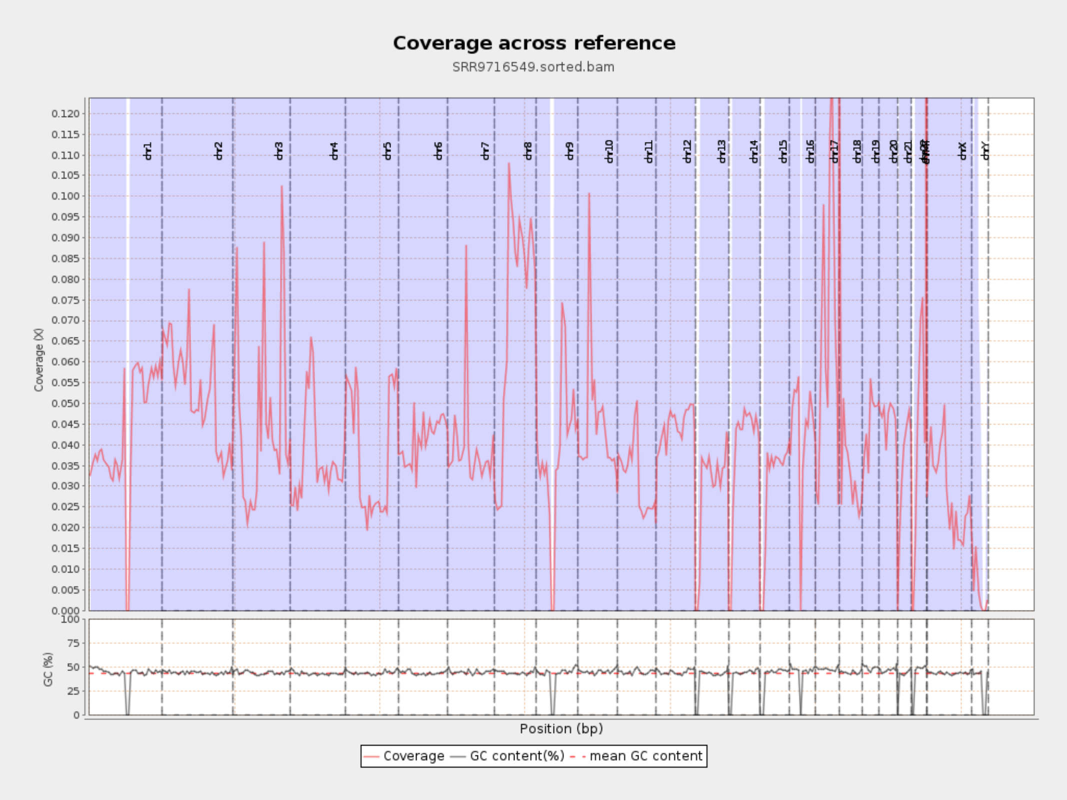
General error rate	0.51%
Mismatches	644,733
Insertions	7,545
Mapped reads with at least one insertion	0.34%
Deletions	23,637
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.53%

2.6. Chromosome stats

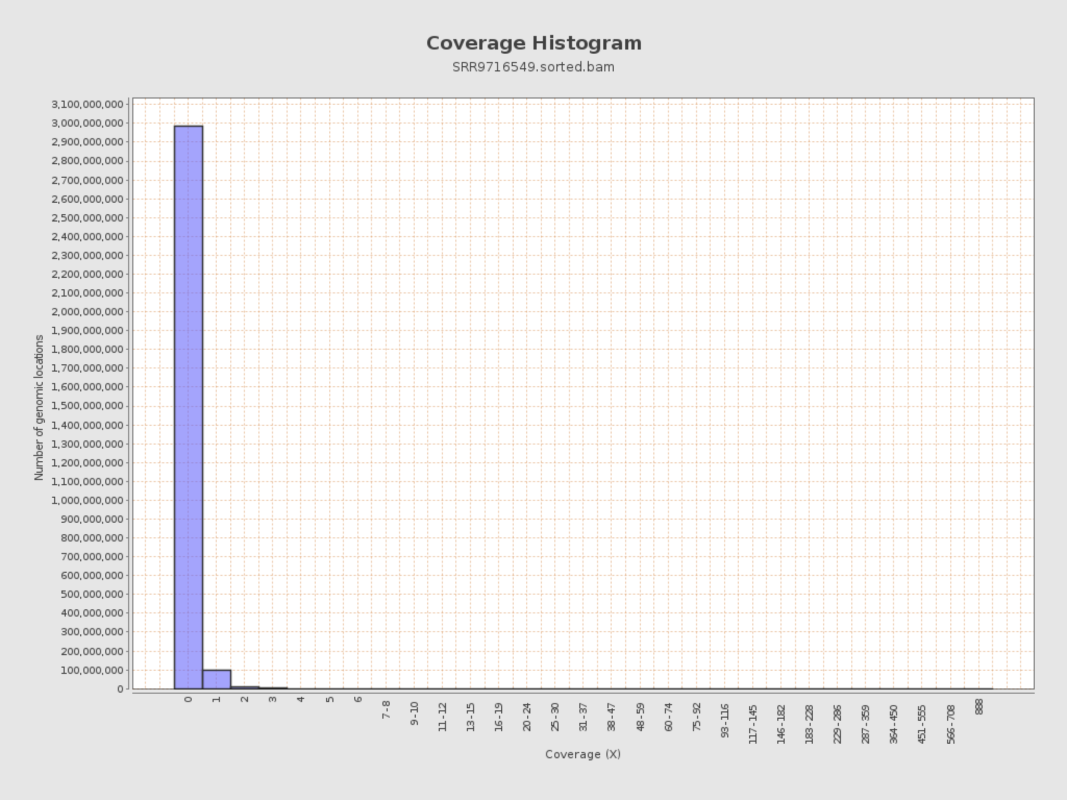
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10624431	0.0426	0.554
chr2	243199373	12887070	0.053	0.4678
chr3	198022430	9112643	0.046	0.2507
chr4	191154276	7049737	0.0369	0.2359
chr5	180915260	6857789	0.0379	0.2172
chr6	171115067	7070569	0.0413	0.2546
chr7	159138663	6264145	0.0394	0.7035

chr8	146364022	10651572	0.0728	0.4087
chr9	141213431	5320758	0.0377	0.2653
chr10	135534747	6088688	0.0449	0.4557
chr11	135006516	4308156	0.0319	0.2588
chr12	133851895	5968173	0.0446	0.2561
chr13	115169878	3347650	0.0291	0.1933
chr14	107349540	4105464	0.0382	0.2246
chr15	102531392	3047914	0.0297	0.1933
chr16	90354753	3921089	0.0434	0.2495
chr17	81195210	5495698	0.0677	0.3089
chr18	78077248	2905380	0.0372	0.4255
chr19	59128983	2655888	0.0449	0.4915
chr20	63025520	2923909	0.0464	0.2523
chr21	48129895	1631297	0.0339	0.2175
chr22	51304566	1993194	0.0389	0.2208
chrMT	16571	94159	5.6822	3.9832
chrX	155270560	4523598	0.0291	0.2273
chrY	59373566	285377	0.0048	0.1191

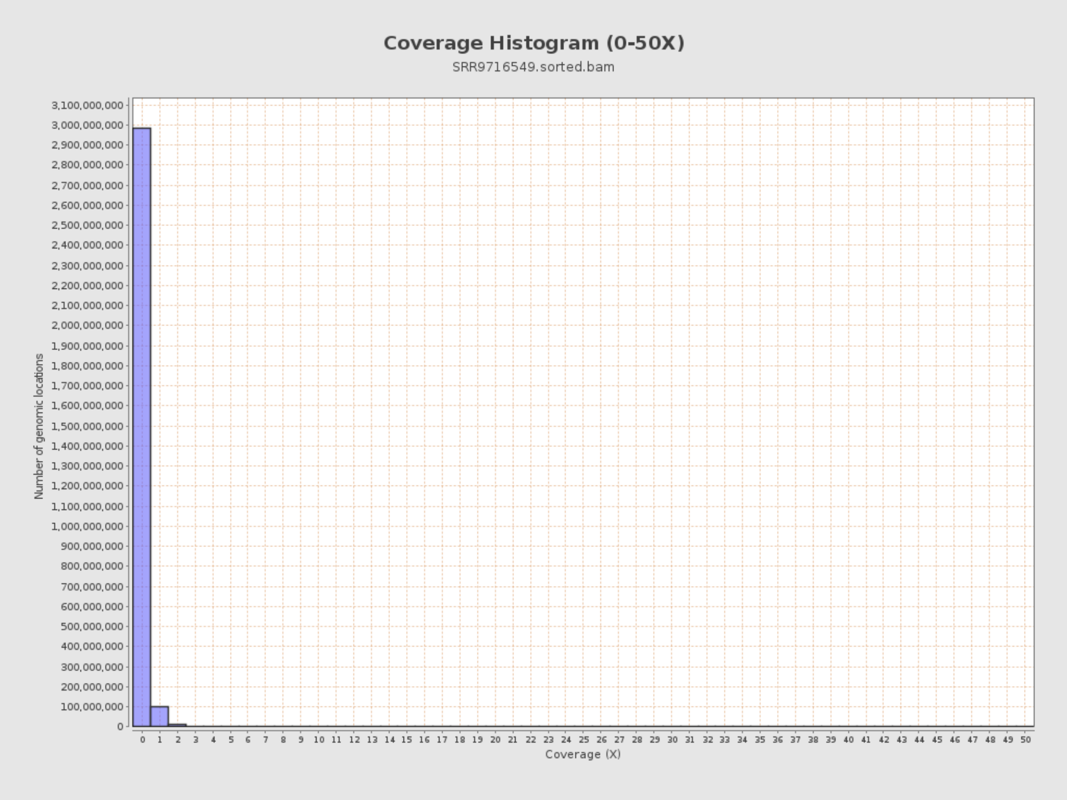
3. Results : Coverage across reference



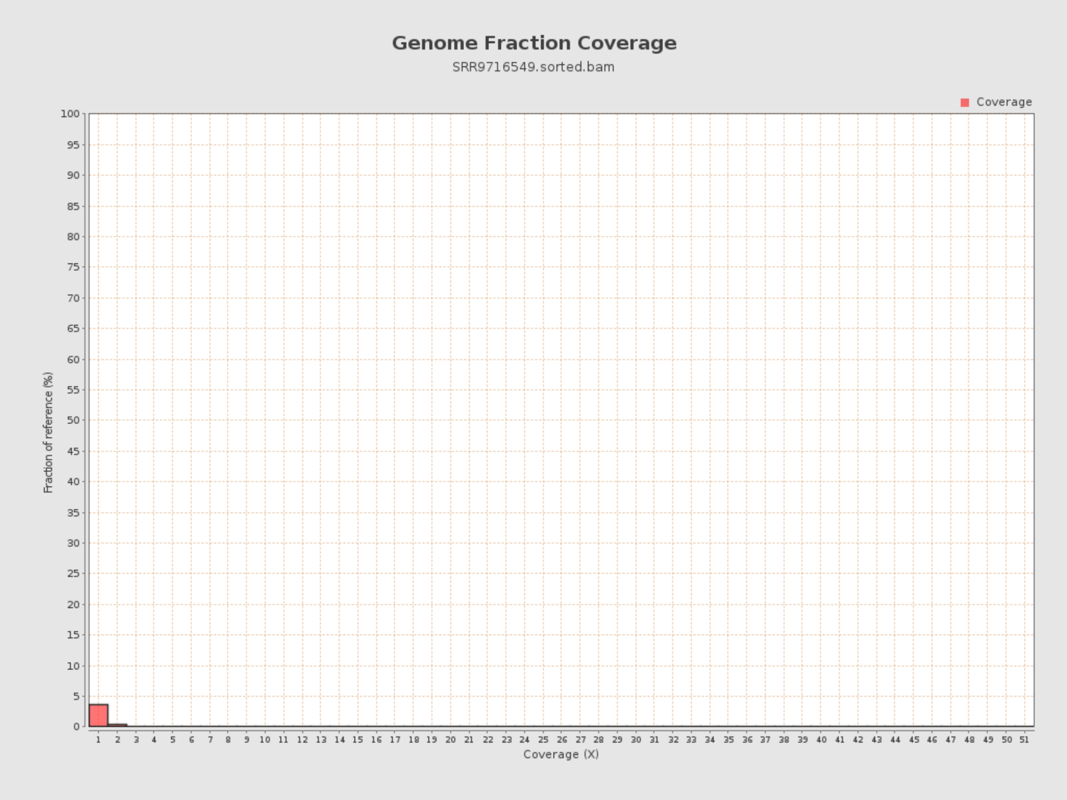
4. Results : Coverage Histogram



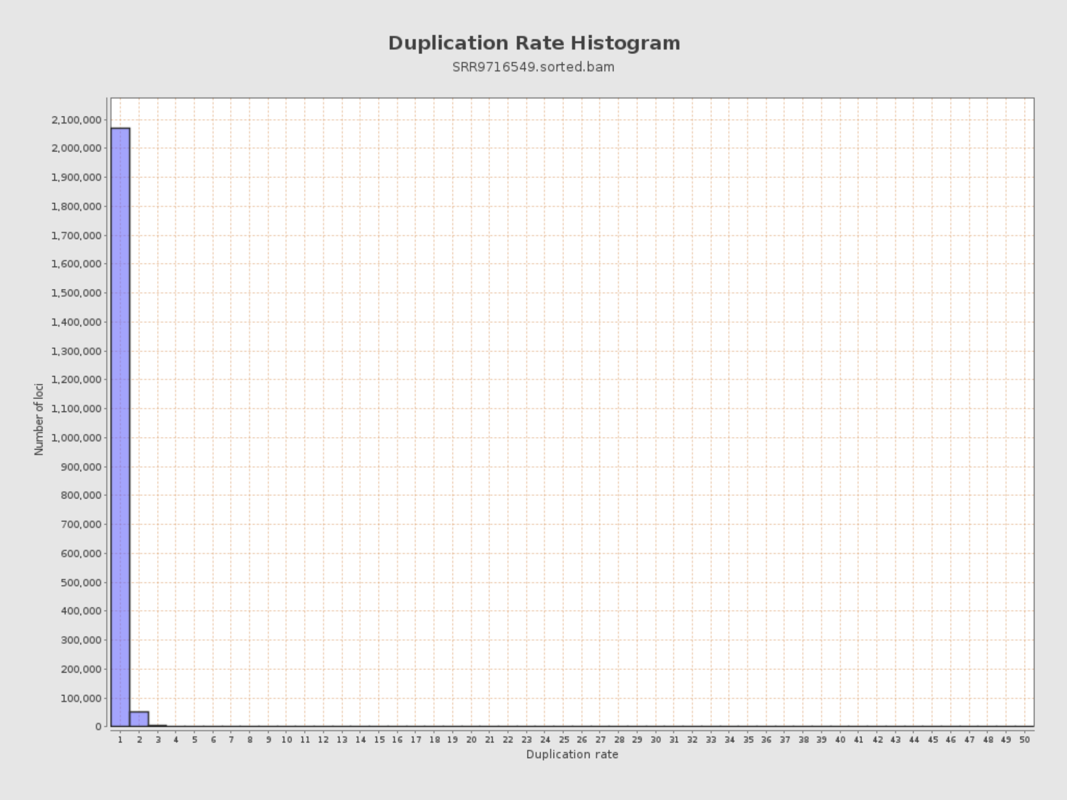
5. Results : Coverage Histogram (0-50X)



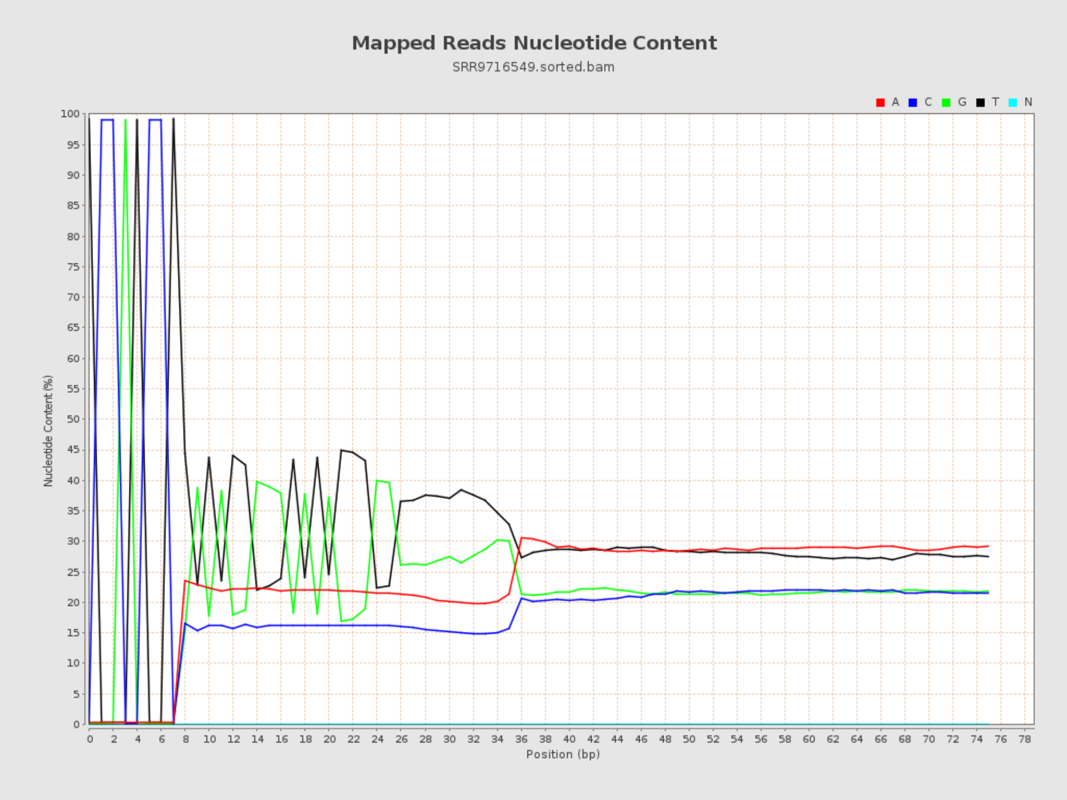
6. Results : Genome Fraction Coverage



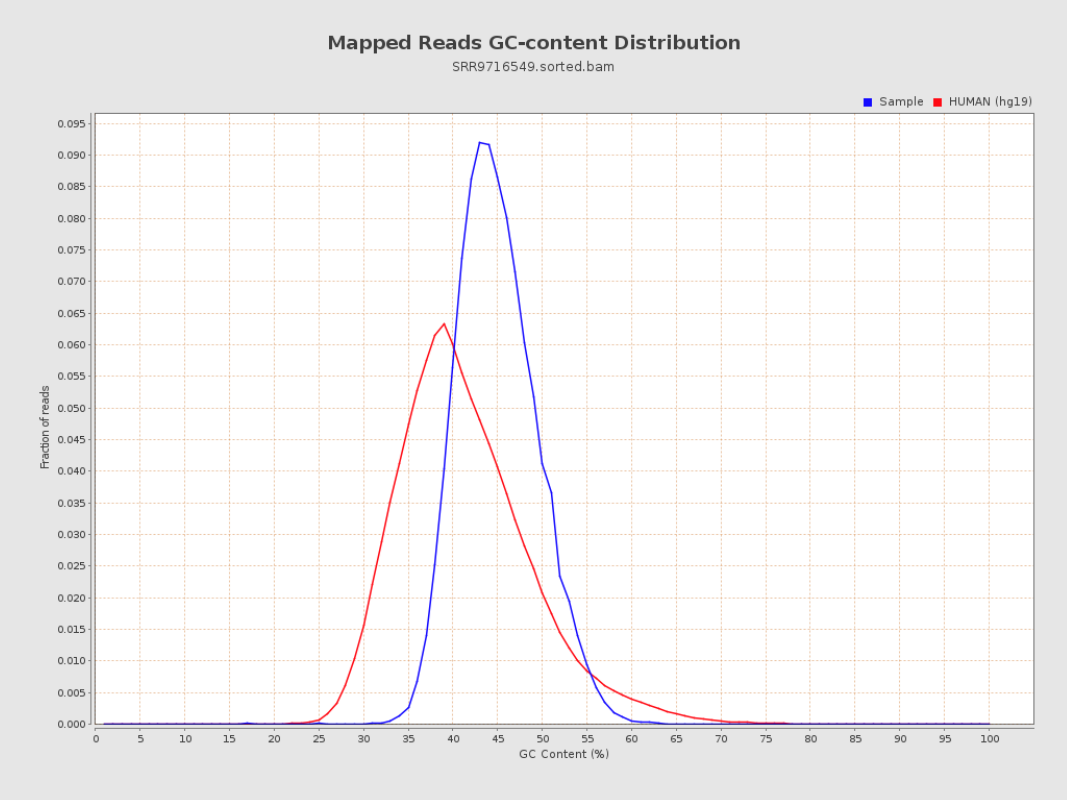
7. Results : Duplication Rate Histogram



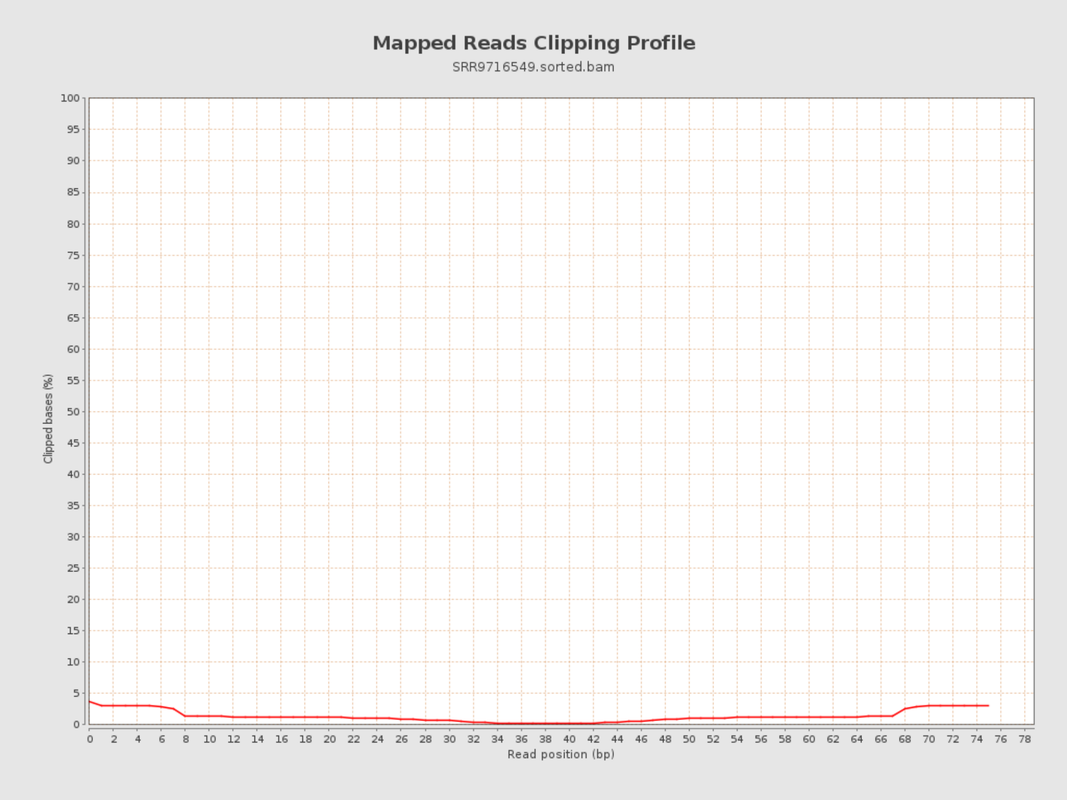
8. Results : Mapped Reads Nucleotide Content



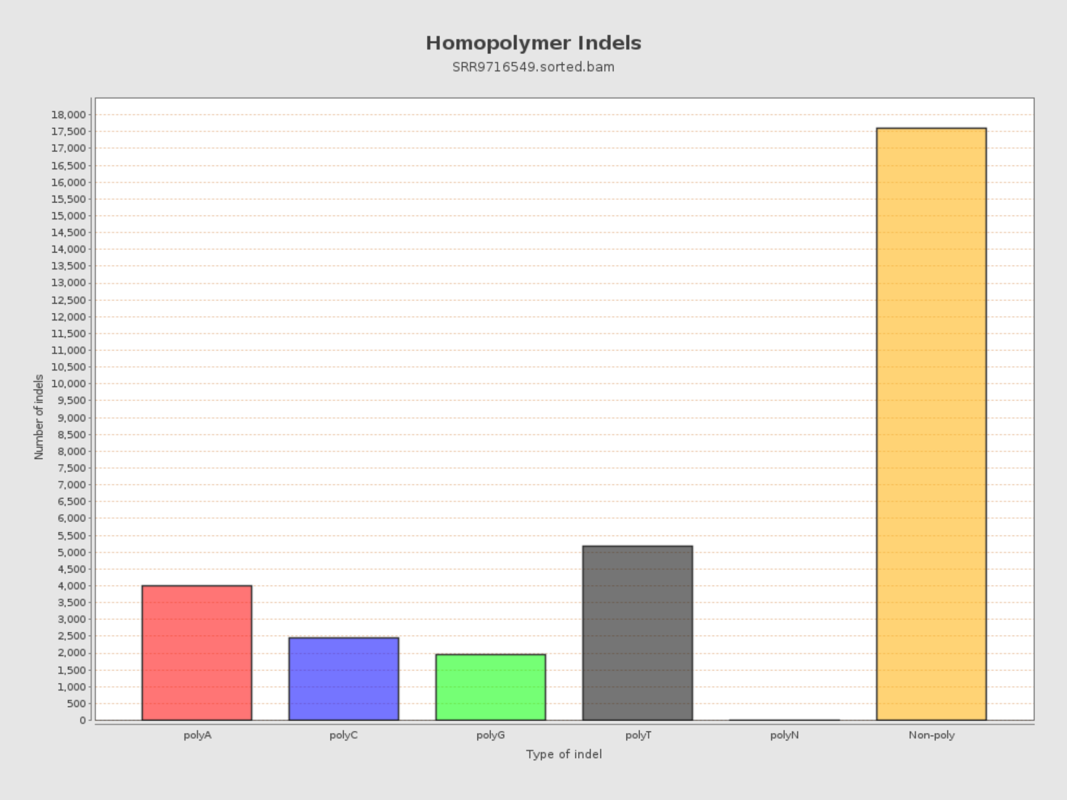
9. Results : Mapped Reads GC-content Distribution



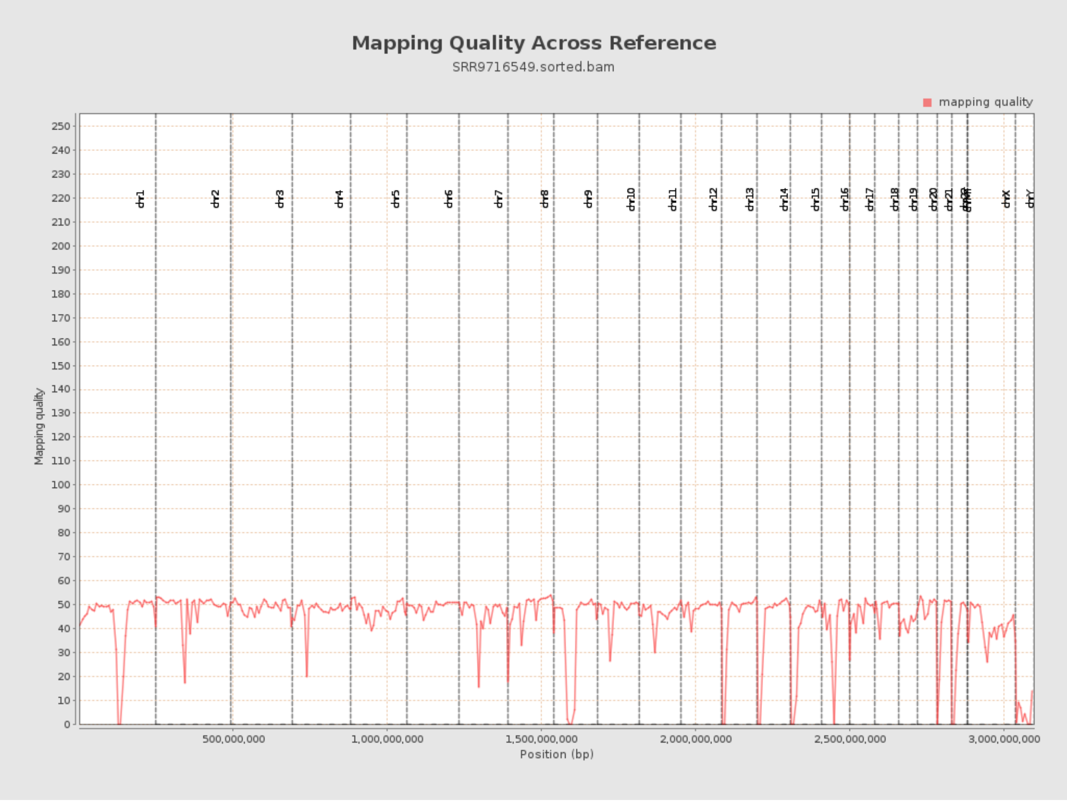
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram