Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:39:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716284.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_SRR9716284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716284.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:39:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,774,918
Mapped reads	1,622,782 / 91.43%
Unmapped reads	152,136 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,813 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	49,951 / 2.81%
Duplication rate	2.41%
Clipped reads	1,624,461 / 91.52%

2.2. ACGT Content

Number/percentage of A's	23,719,295 / 25.39%
Number/percentage of C's	18,831,253 / 20.16%
Number/percentage of T's	28,541,903 / 30.55%
Number/percentage of G's	22,329,105 / 23.9%
Number/percentage of N's	2,073 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.2365

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

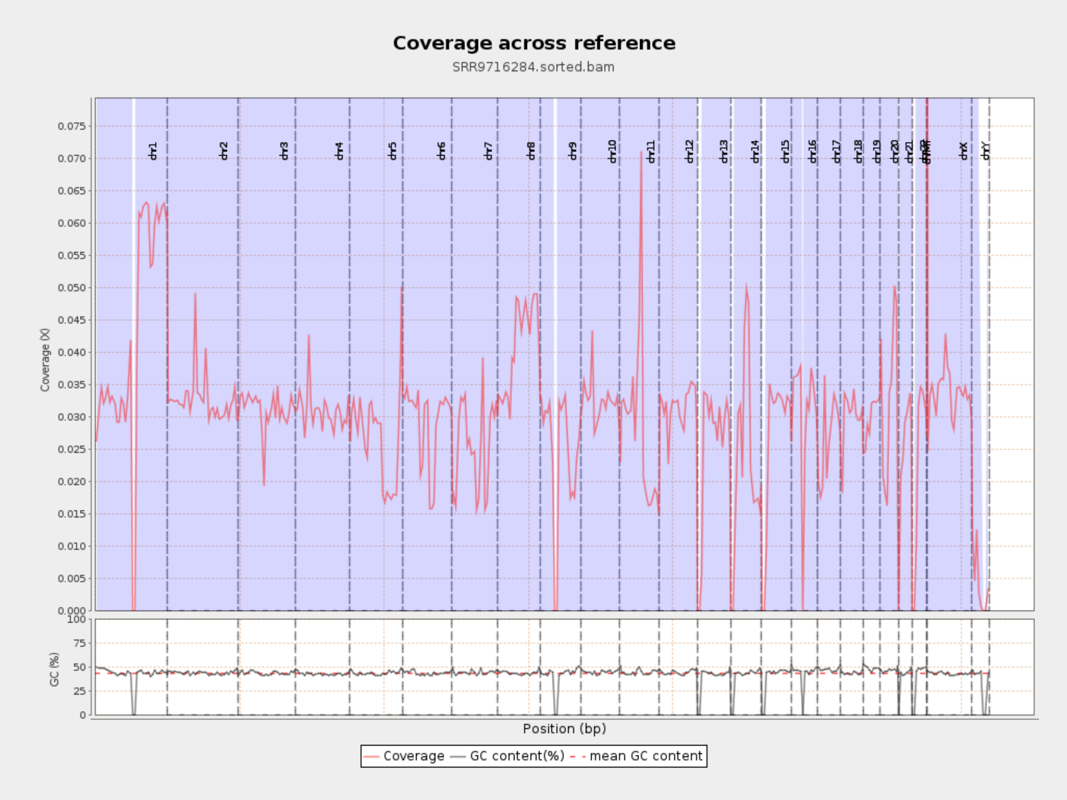
General error rate	0.5%
Mismatches	453,173
Insertions	7,026
Mapped reads with at least one insertion	0.43%
Deletions	14,535
Mapped reads with at least one deletion	0.89%
Homopolymer indels	39.7%

2.6. Chromosome stats

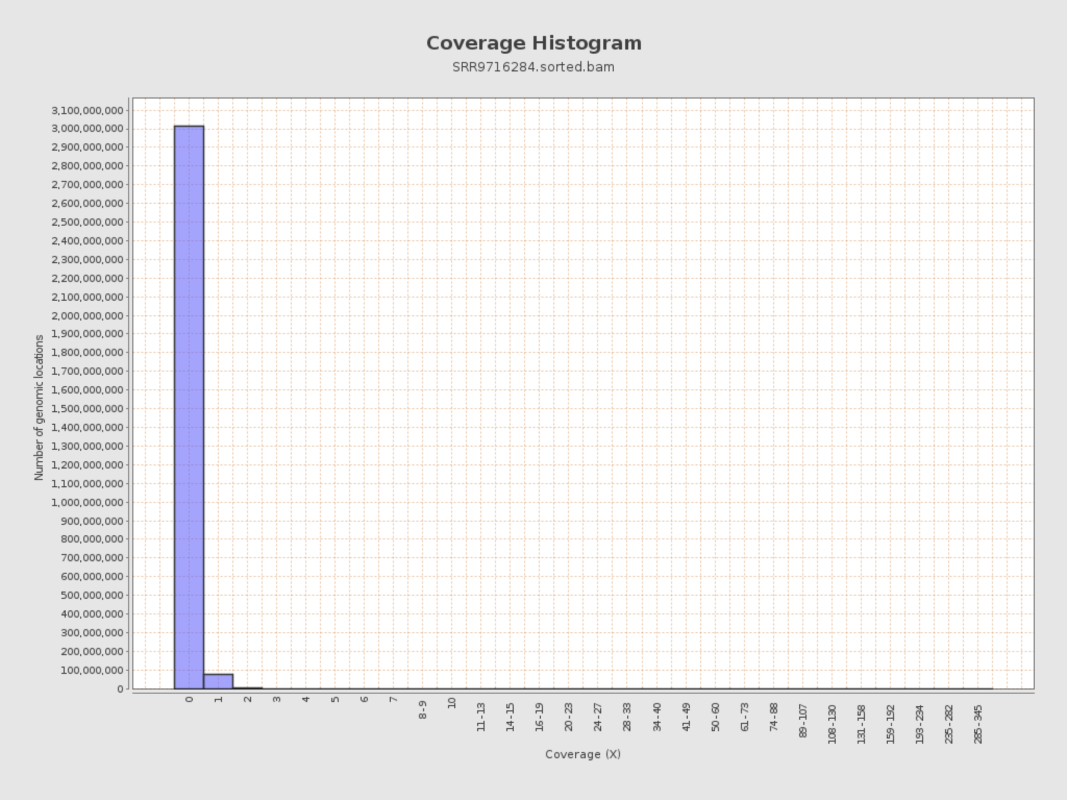
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10503894	0.0421	0.3497
chr2	243199373	7955390	0.0327	0.268
chr3	198022430	6167046	0.0311	0.1931
chr4	191154276	5924771	0.031	0.2049
chr5	180915260	4798858	0.0265	0.1802
chr6	171115067	4971826	0.0291	0.1989
chr7	159138663	4082447	0.0257	0.2127

chr8	146364022	6005479	0.041	0.2502
chr9	141213431	3427376	0.0243	0.25
chr10	135534747	4415486	0.0326	0.2392
chr11	135006516	3926737	0.0291	0.2437
chr12	133851895	4235287	0.0316	0.1967
chr13	115169878	2910131	0.0253	0.1733
chr14	107349540	2540267	0.0237	0.176
chr15	102531392	2710319	0.0264	0.1777
chr16	90354753	2757404	0.0305	0.2065
chr17	81195210	2161393	0.0266	0.1865
chr18	78077248	2311081	0.0296	0.4422
chr19	59128983	1766414	0.0299	0.2893
chr20	63025520	2017986	0.032	0.2023
chr21	48129895	1211562	0.0252	0.1861
chr22	51304566	1154046	0.0225	0.164
chrMT	16571	6125	0.3696	0.6822
chrX	155270560	5242781	0.0338	0.2242
chrY	59373566	244011	0.0041	0.0972

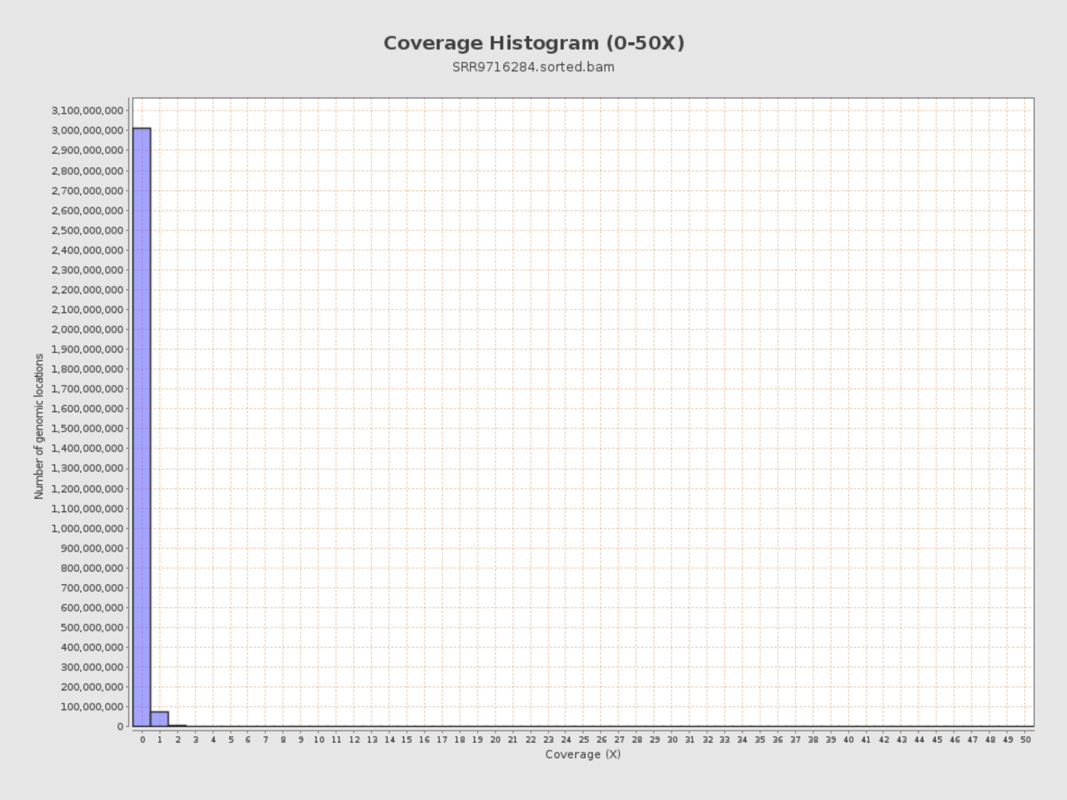
3. Results : Coverage across reference



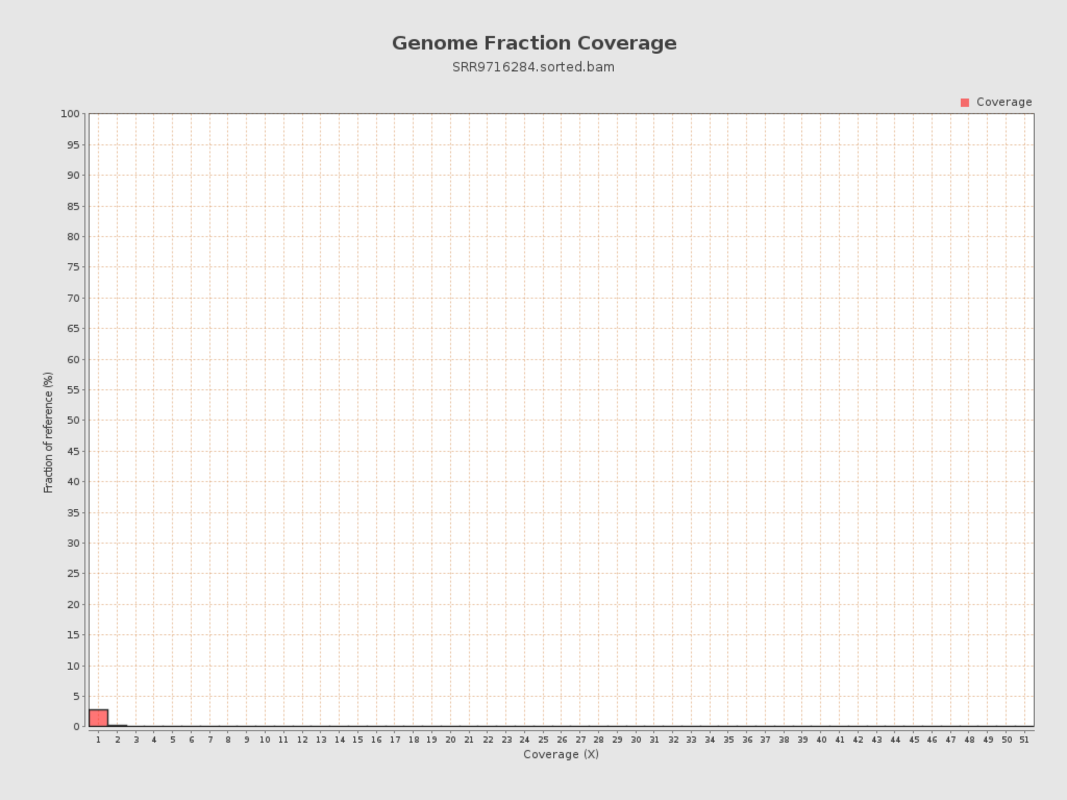
4. Results : Coverage Histogram



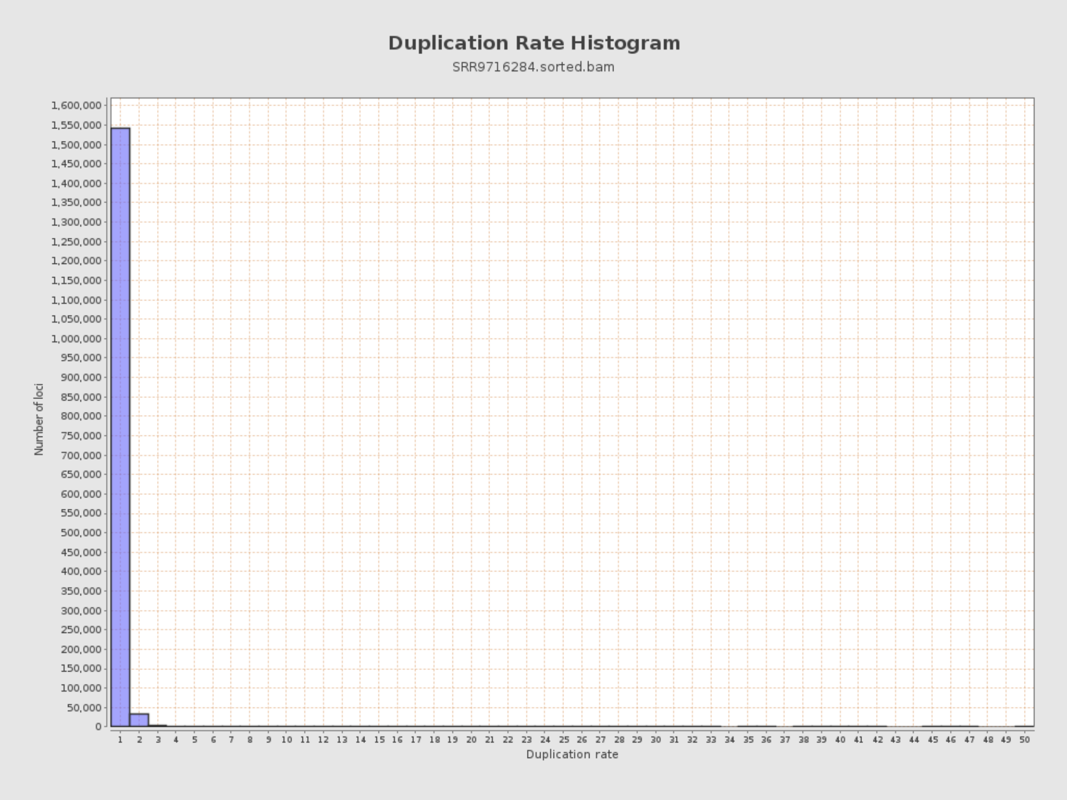
5. Results : Coverage Histogram (0-50X)



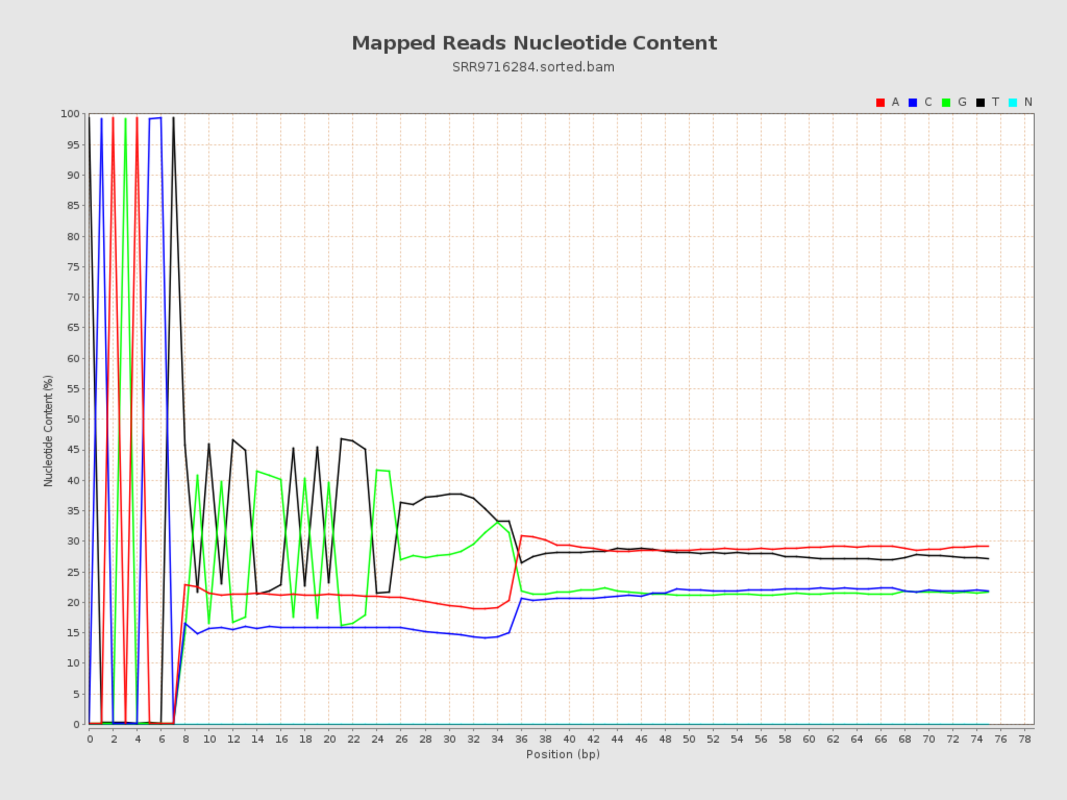
6. Results : Genome Fraction Coverage



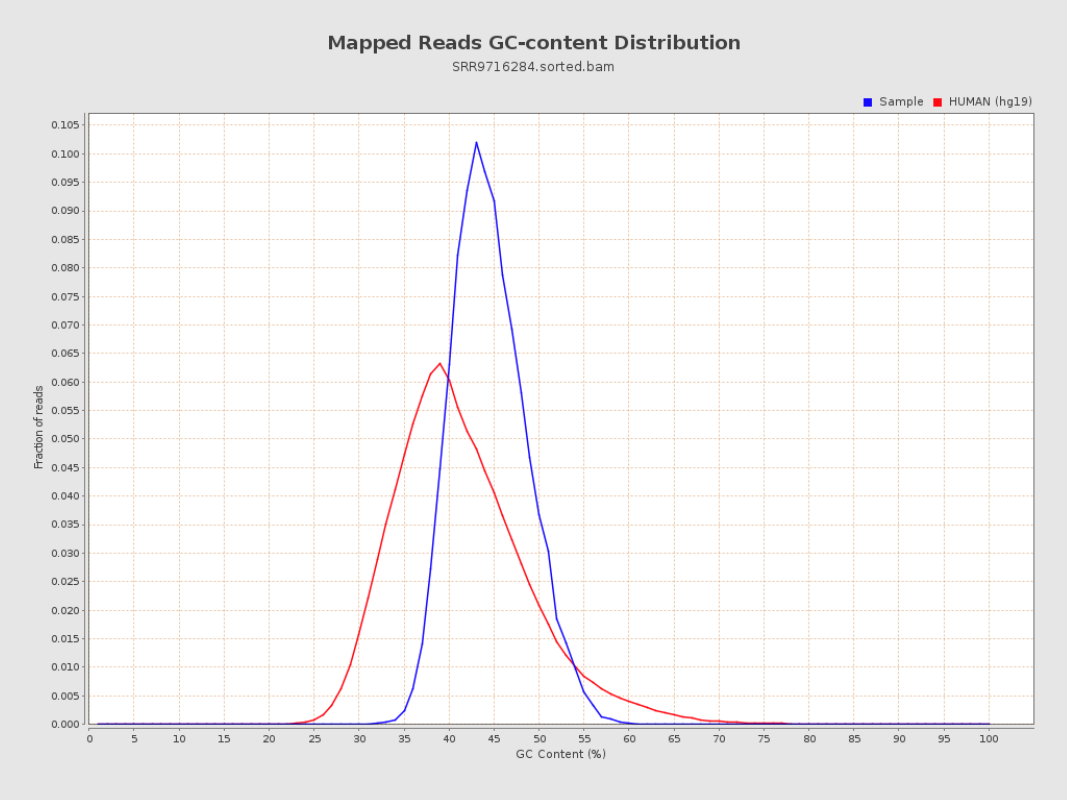
7. Results : Duplication Rate Histogram



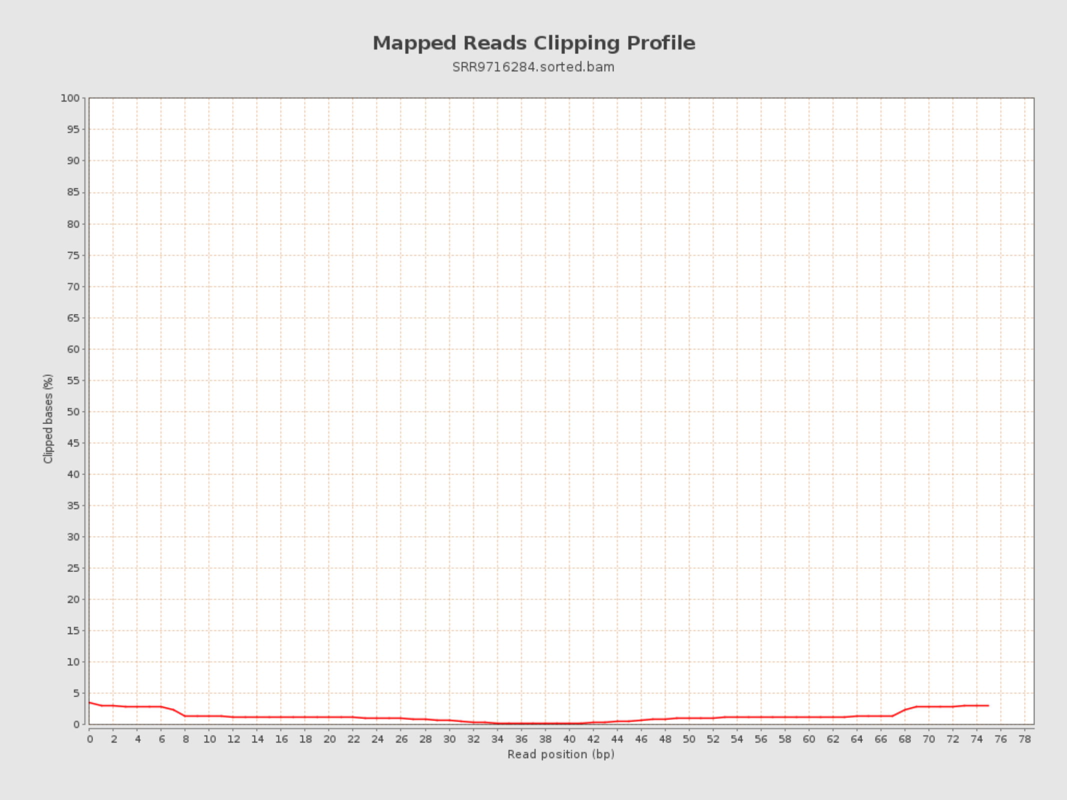
8. Results : Mapped Reads Nucleotide Content



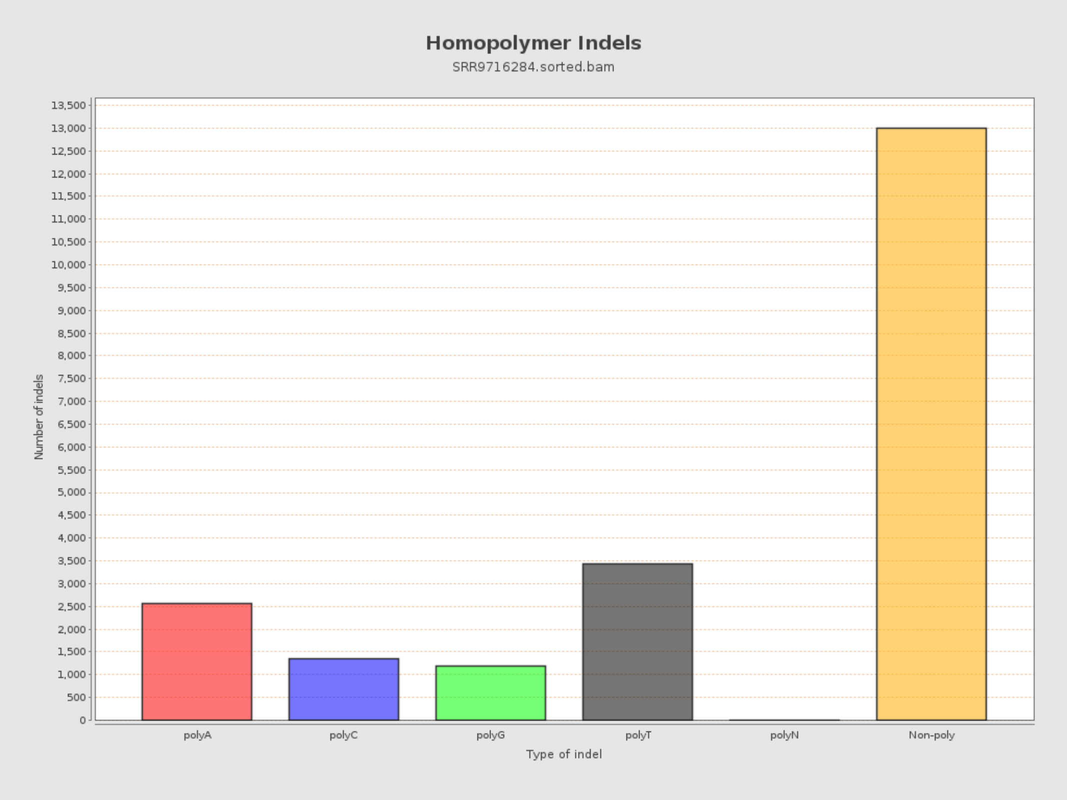
9. Results : Mapped Reads GC-content Distribution



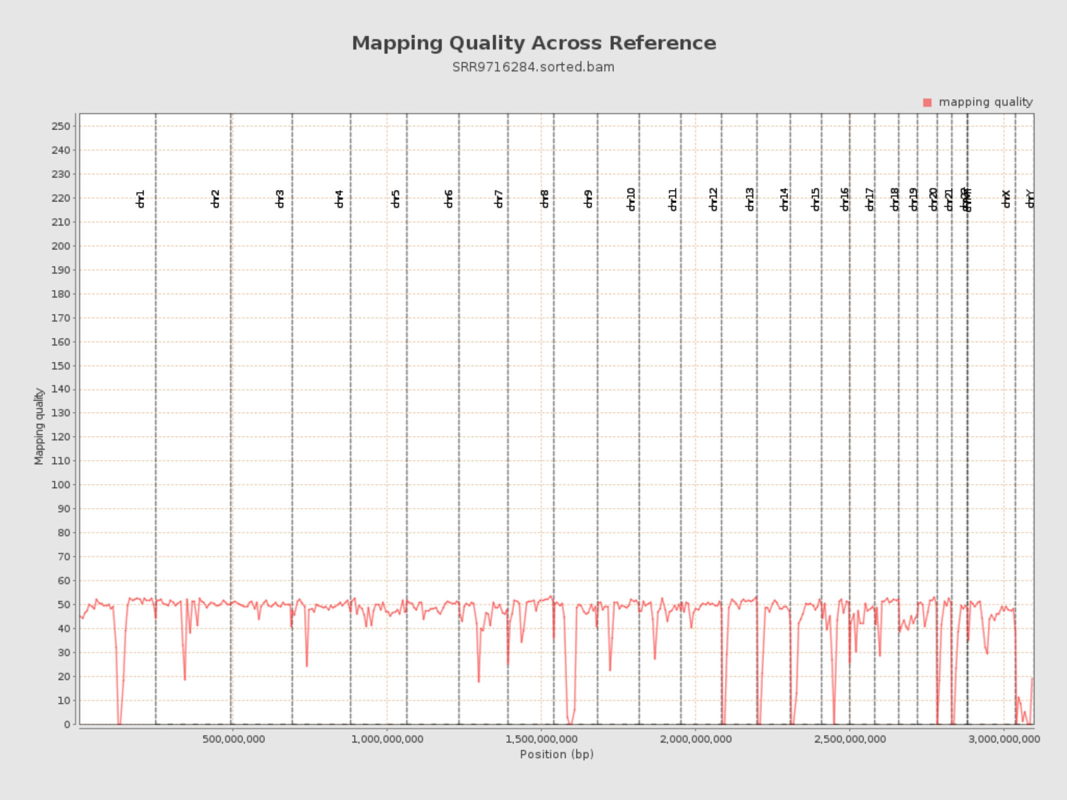
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram