Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:16:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716461.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_SRR9716461 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716461.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:16:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716461.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	566,260
Mapped reads	515,679 / 91.07%
Unmapped reads	50,581 / 8.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,710 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	10,117 / 1.79%
Duplication rate	1.34%
Clipped reads	516,056 / 91.13%

2.2. ACGT Content

Number/percentage of A's	7,185,554 / 24.38%
Number/percentage of C's	5,147,574 / 17.46%
Number/percentage of T's	9,856,258 / 33.44%
Number/percentage of G's	7,288,518 / 24.72%
Number/percentage of N's	533 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.125

2.4. Mapping Quality

Mean Mapping Quality	43.3

2.5. Mismatches and indels

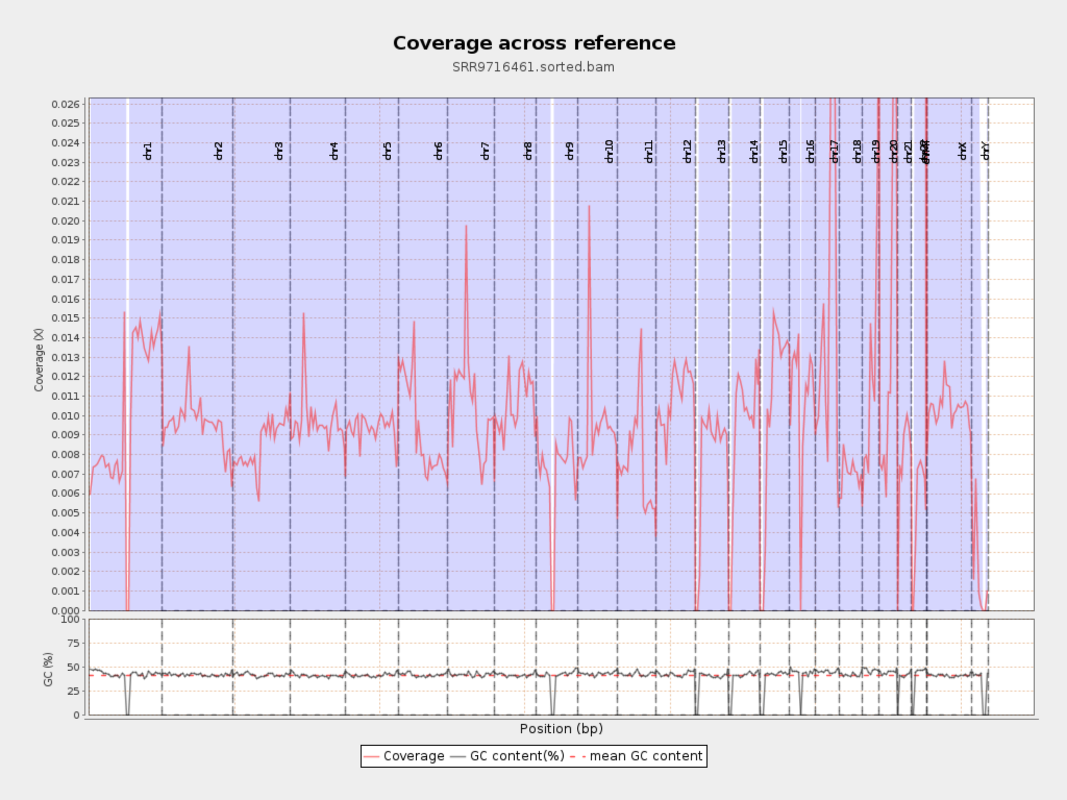
General error rate	0.53%
Mismatches	152,968
Insertions	2,299
Mapped reads with at least one insertion	0.44%
Deletions	5,643
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.33%

2.6. Chromosome stats

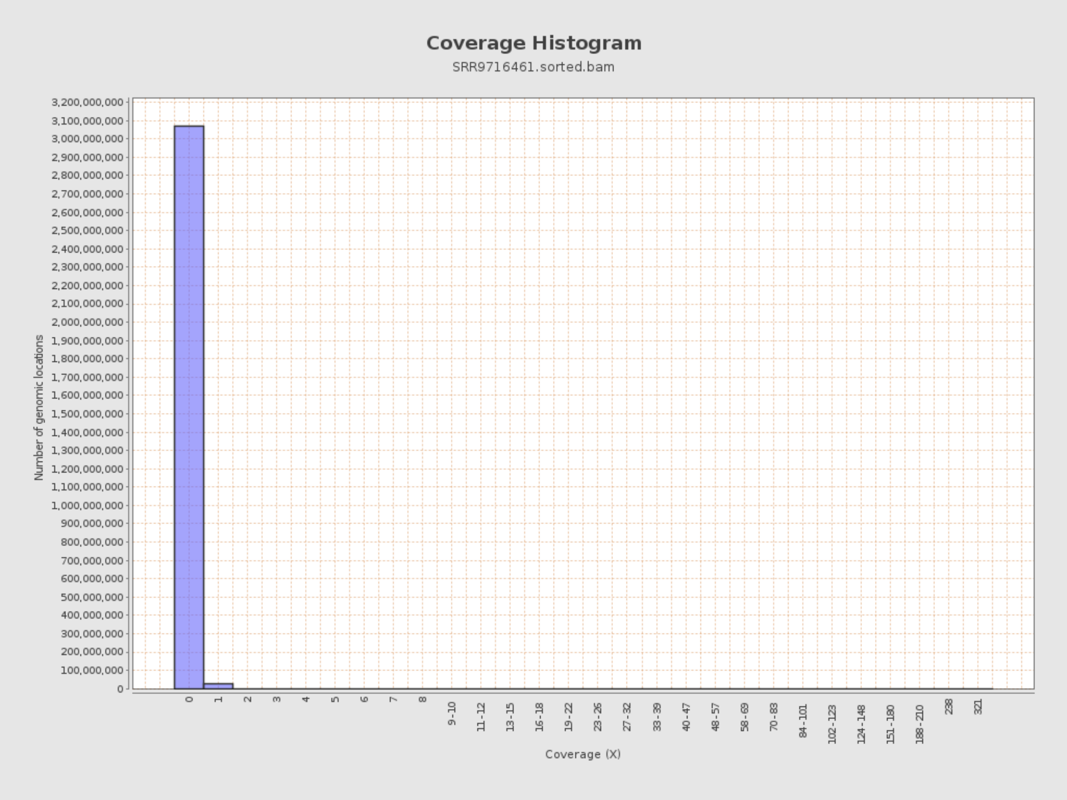
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2475749	0.0099	0.1749
chr2	243199373	2341878	0.0096	0.1627
chr3	198022430	1682111	0.0085	0.0959
chr4	191154276	1849846	0.0097	0.1066
chr5	180915260	1693524	0.0094	0.0997
chr6	171115067	1598328	0.0093	0.1077
chr7	159138663	1711529	0.0108	0.1644

chr8	146364022	1560951	0.0107	0.148
chr9	141213431	979520	0.0069	0.0957
chr10	135534747	1287625	0.0095	0.1278
chr11	135006516	1040257	0.0077	0.1014
chr12	133851895	1472501	0.011	0.1088
chr13	115169878	895100	0.0078	0.0916
chr14	107349540	989425	0.0092	0.1001
chr15	102531392	1059637	0.0103	0.1066
chr16	90354753	980850	0.0109	0.1102
chr17	81195210	1244124	0.0153	0.1292
chr18	78077248	552674	0.0071	0.1326
chr19	59128983	750725	0.0127	0.158
chr20	63025520	963469	0.0153	0.1292
chr21	48129895	371953	0.0077	0.0959
chr22	51304566	258520	0.005	0.0735
chrMT	16571	8780	0.5298	0.8154
chrX	155270560	1616213	0.0104	0.11
chrY	59373566	102191	0.0017	0.0766

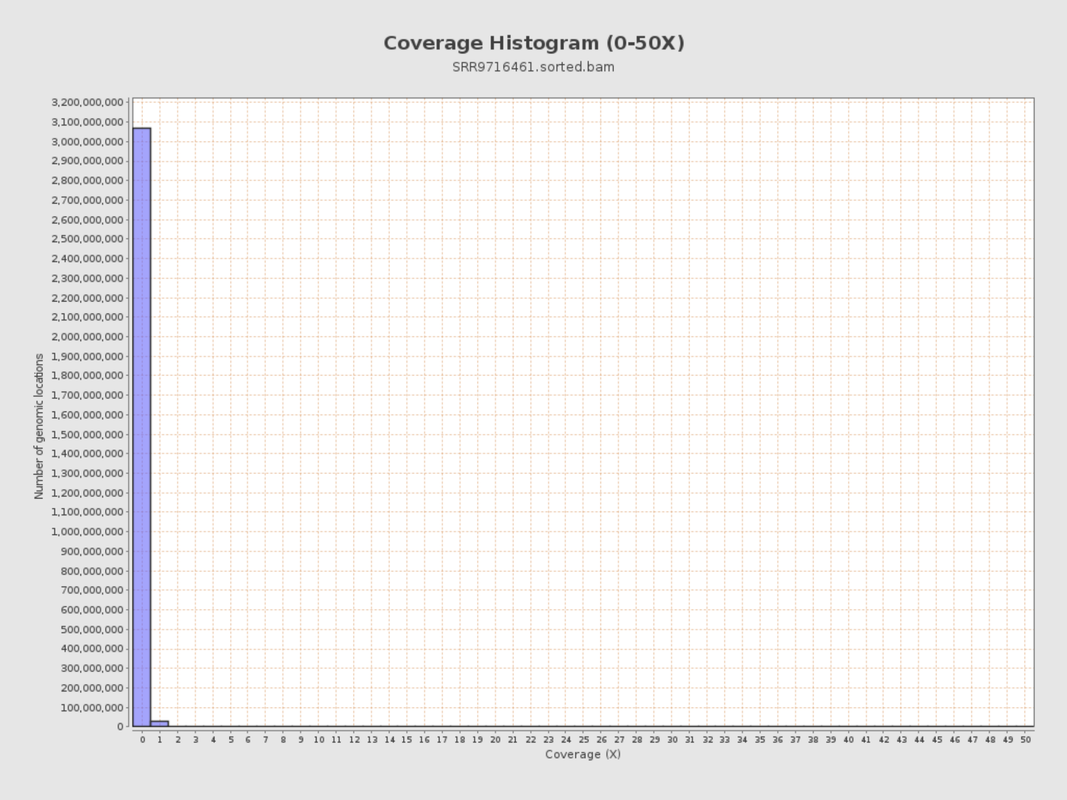
3. Results : Coverage across reference



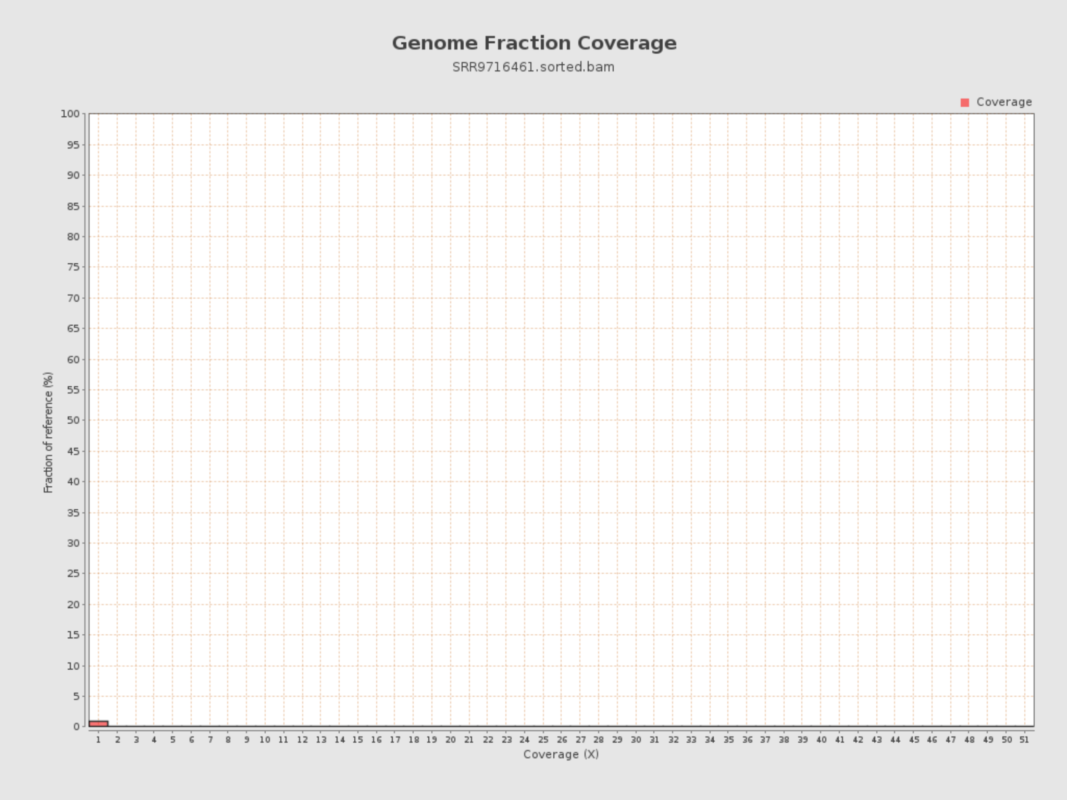
4. Results : Coverage Histogram



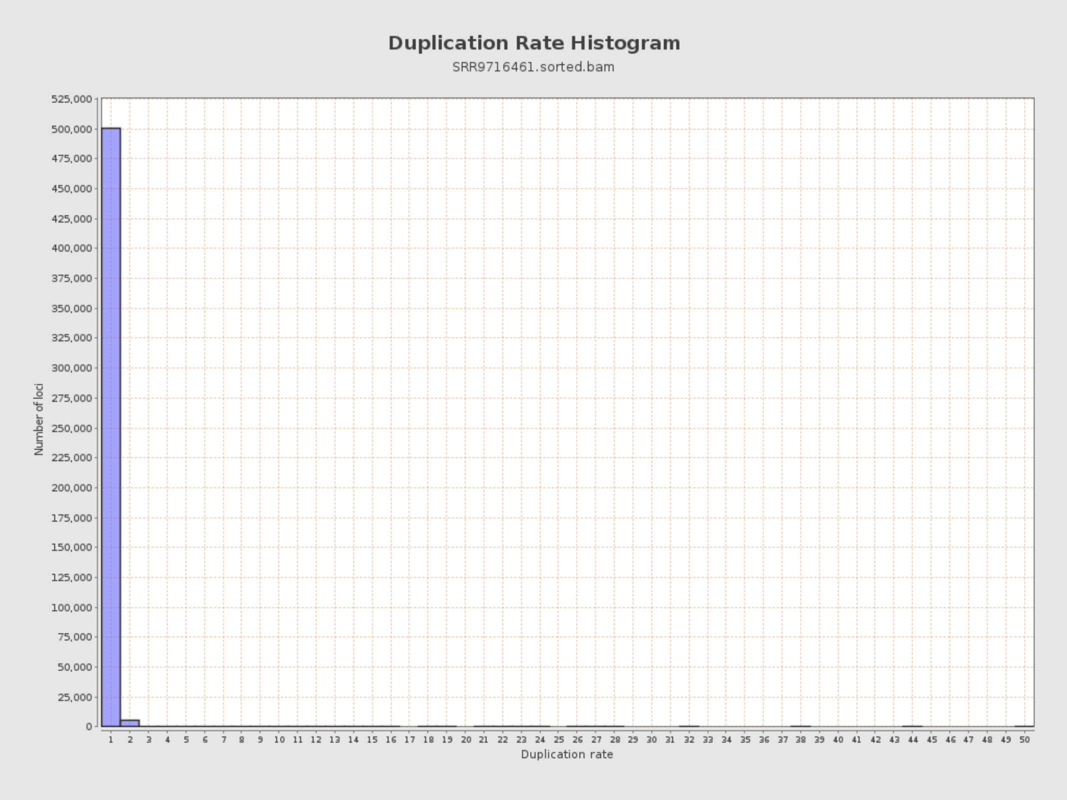
5. Results : Coverage Histogram (0-50X)



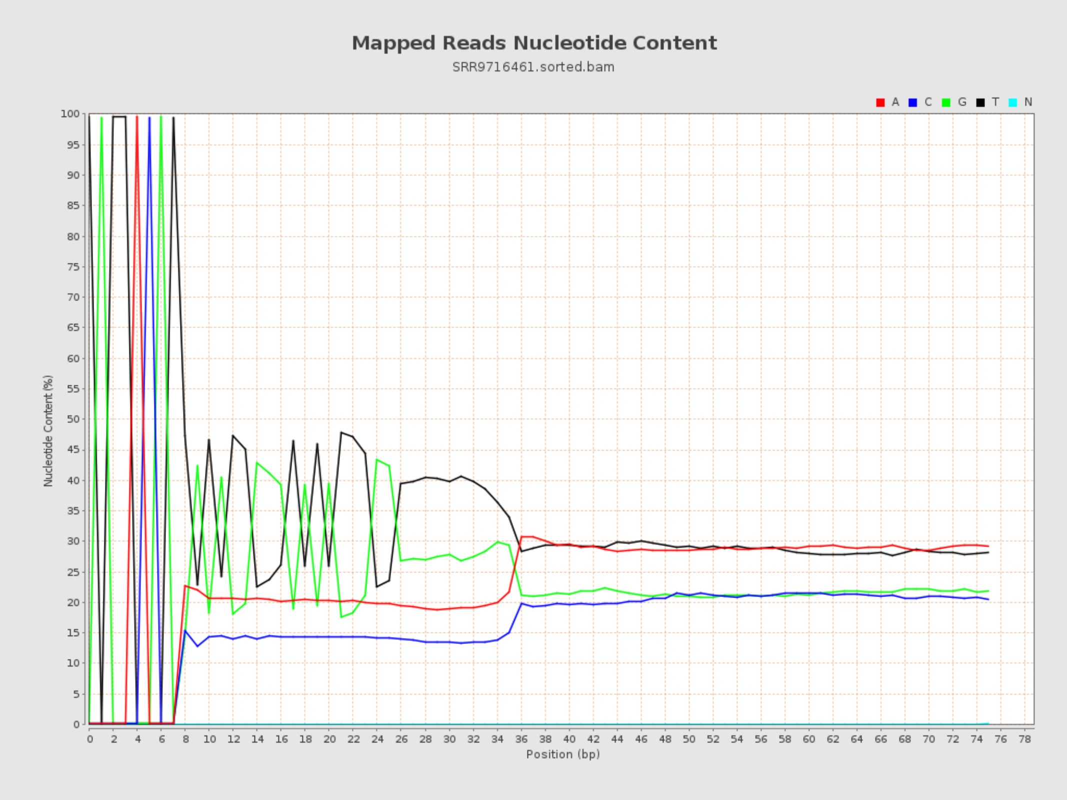
6. Results : Genome Fraction Coverage



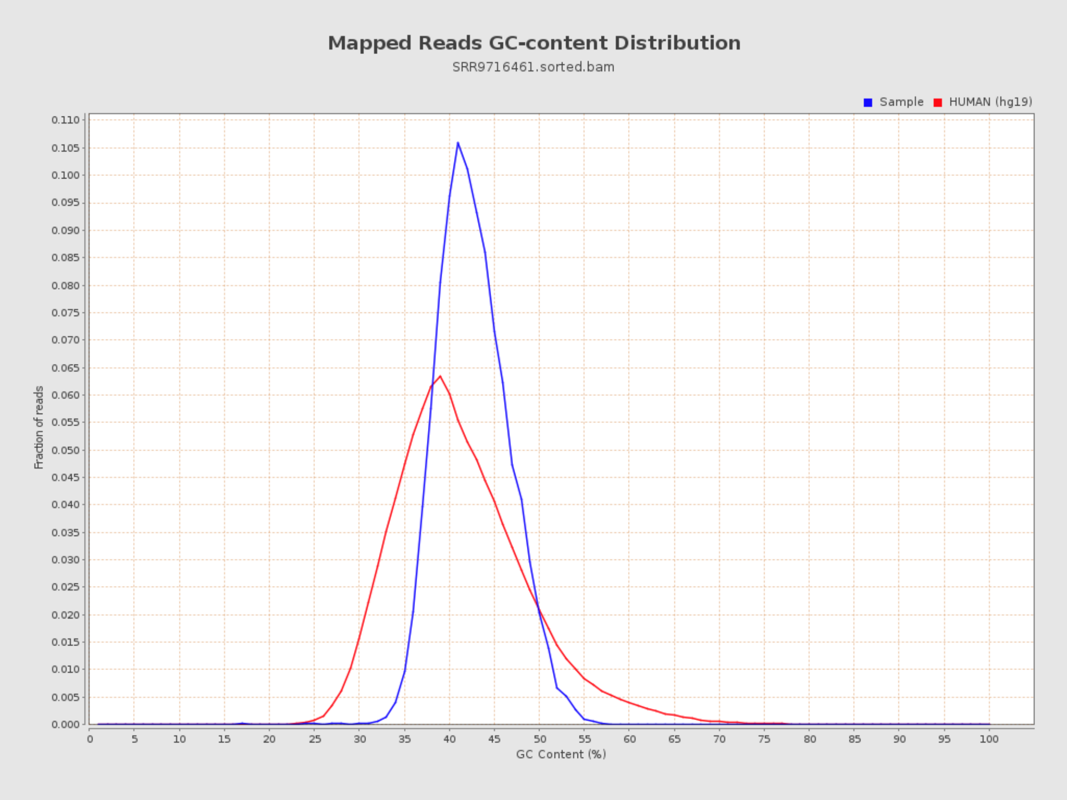
7. Results : Duplication Rate Histogram



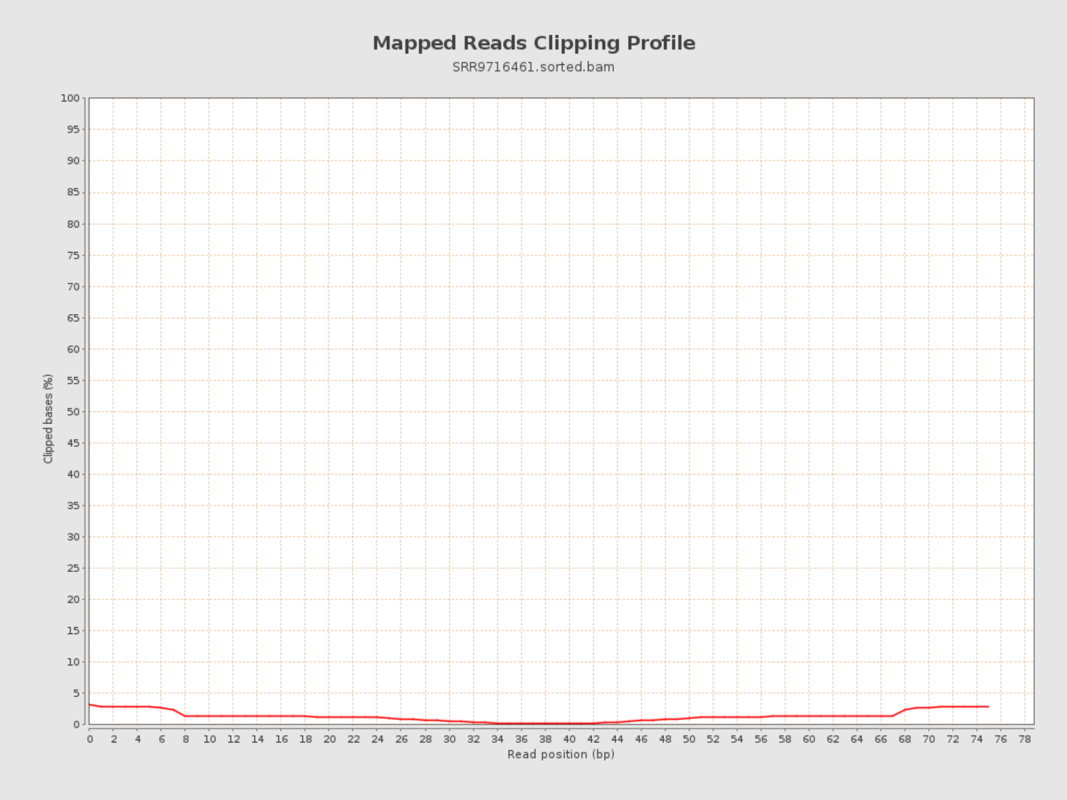
8. Results : Mapped Reads Nucleotide Content



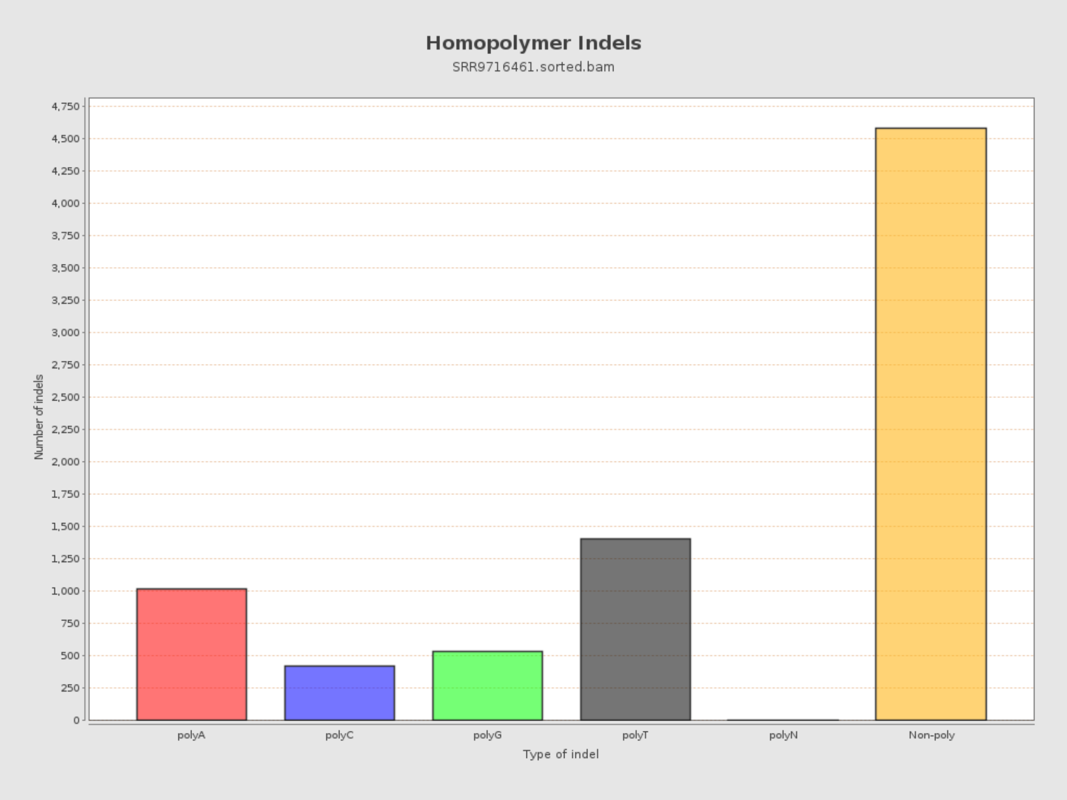
9. Results : Mapped Reads GC-content Distribution



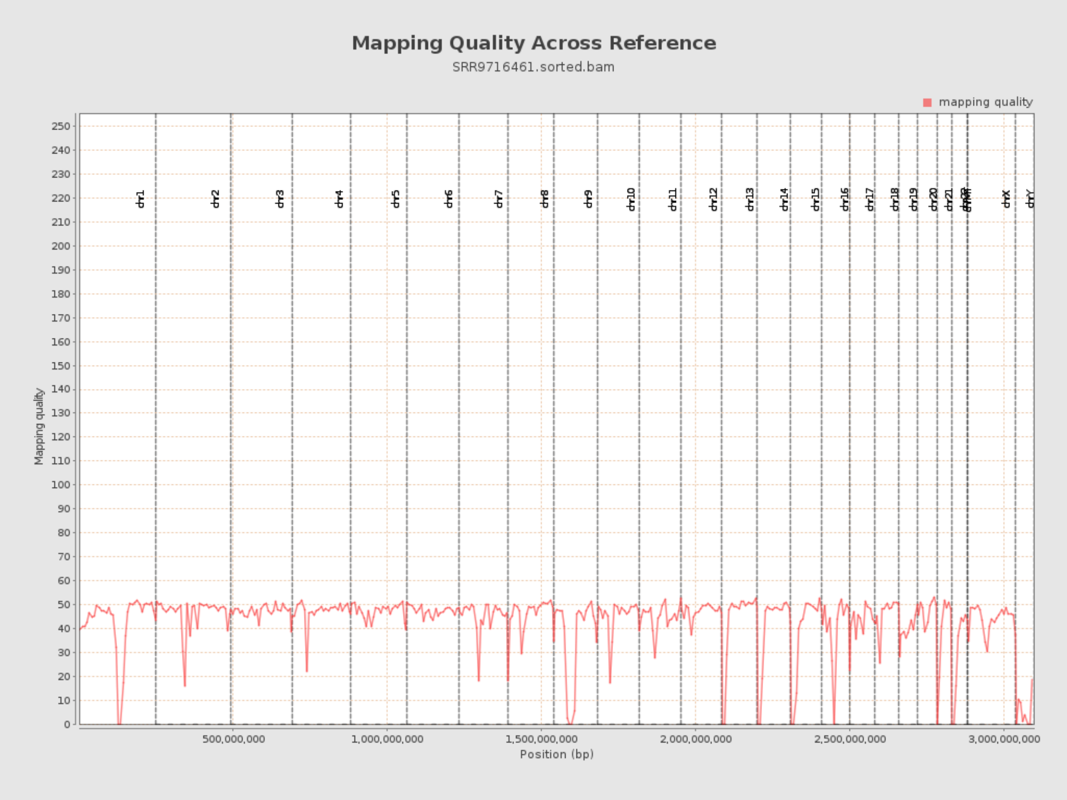
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram