Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:51:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716546.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_SRR9716546 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716546.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:51:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716546.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	709,303
Mapped reads	640,323 / 90.27%
Unmapped reads	68,980 / 9.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,286 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	18,042 / 2.54%
Duplication rate	2.22%
Clipped reads	640,670 / 90.32%

2.2. ACGT Content

Number/percentage of A's	8,782,877 / 23.79%
Number/percentage of C's	7,163,645 / 19.4%
Number/percentage of T's	12,232,503 / 33.14%
Number/percentage of G's	8,736,647 / 23.67%
Number/percentage of N's	1,049 / 0%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.143

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

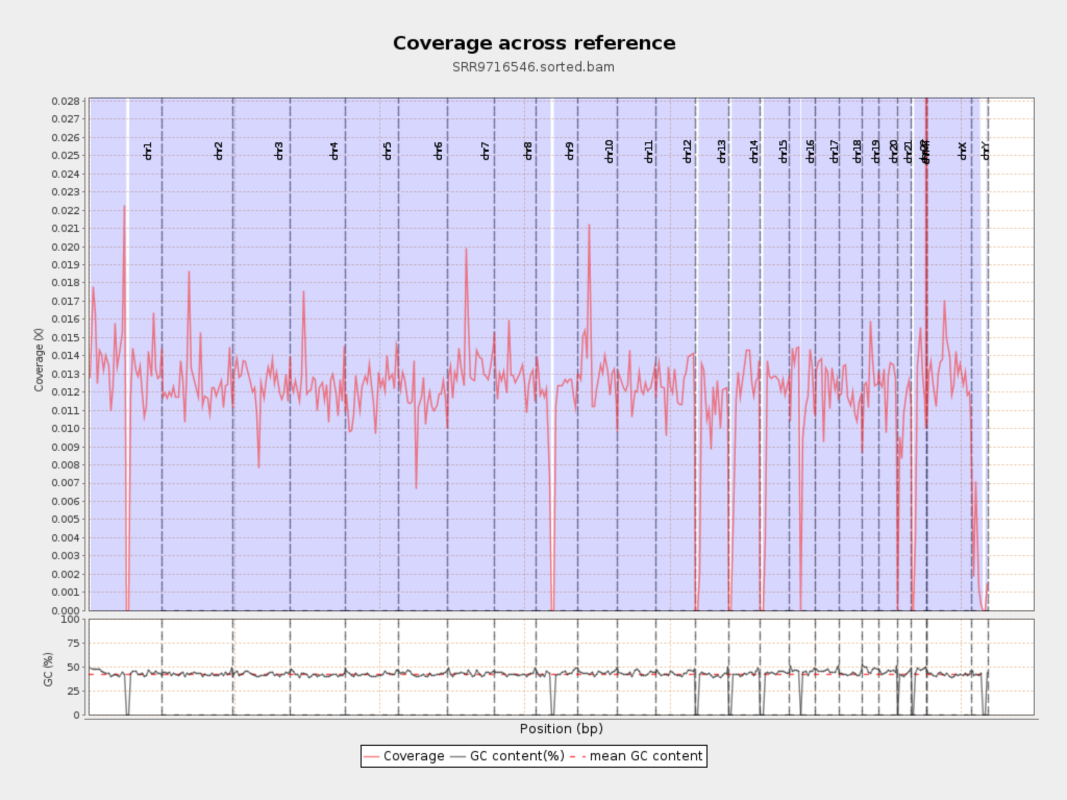
General error rate	0.52%
Mismatches	186,833
Insertions	2,606
Mapped reads with at least one insertion	0.41%
Deletions	7,000
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.07%

2.6. Chromosome stats

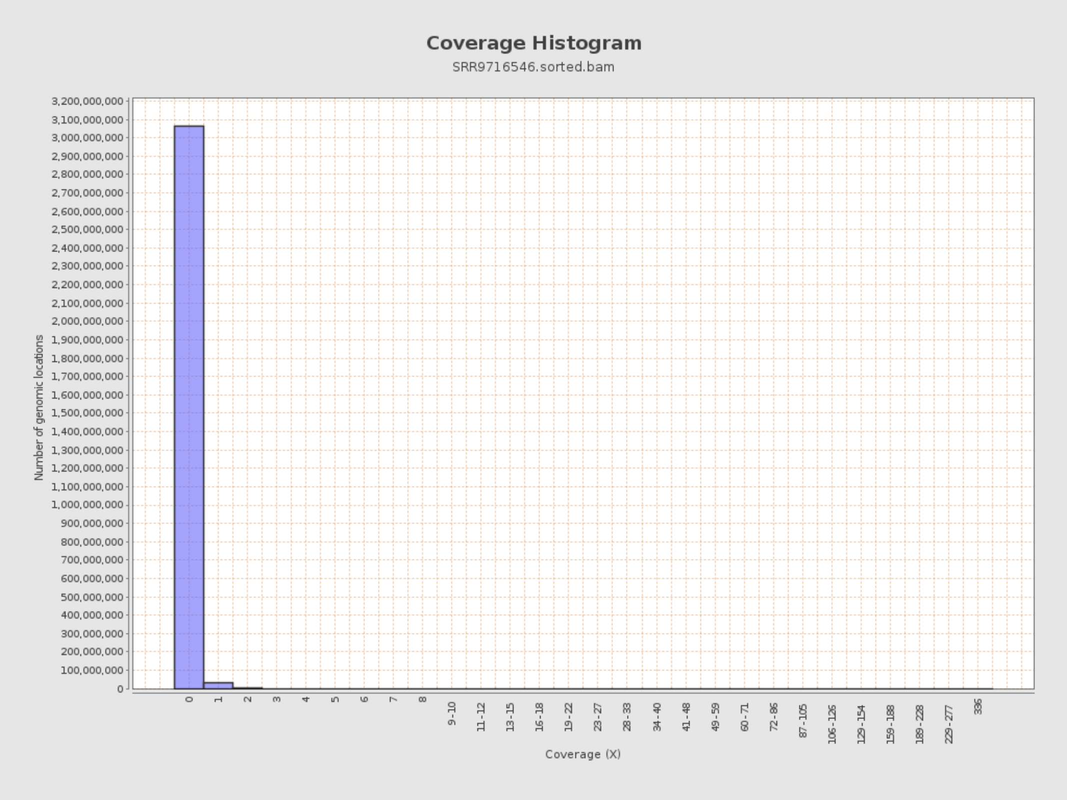
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3231850	0.013	0.2373
chr2	243199373	3024935	0.0124	0.1815
chr3	198022430	2462878	0.0124	0.1172
chr4	191154276	2367511	0.0124	0.1211
chr5	180915260	2204438	0.0122	0.1165
chr6	171115067	1987190	0.0116	0.1209
chr7	159138663	2172057	0.0136	0.158

chr8	146364022	1872697	0.0128	0.1392
chr9	141213431	1500786	0.0106	0.1199
chr10	135534747	1827591	0.0135	0.1407
chr11	135006516	1672257	0.0124	0.1266
chr12	133851895	1676621	0.0125	0.119
chr13	115169878	1115024	0.0097	0.1029
chr14	107349540	1136539	0.0106	0.1107
chr15	102531392	1047996	0.0102	0.1069
chr16	90354753	1046140	0.0116	0.1165
chr17	81195210	1016870	0.0125	0.1222
chr18	78077248	924476	0.0118	0.176
chr19	59128983	754198	0.0128	0.1769
chr20	63025520	782288	0.0124	0.1179
chr21	48129895	470073	0.0098	0.1075
chr22	51304566	464854	0.0091	0.1001
chrMT	16571	17225	1.0395	1.2095
chrX	155270560	2031260	0.0131	0.1269
chrY	59373566	119793	0.002	0.0685

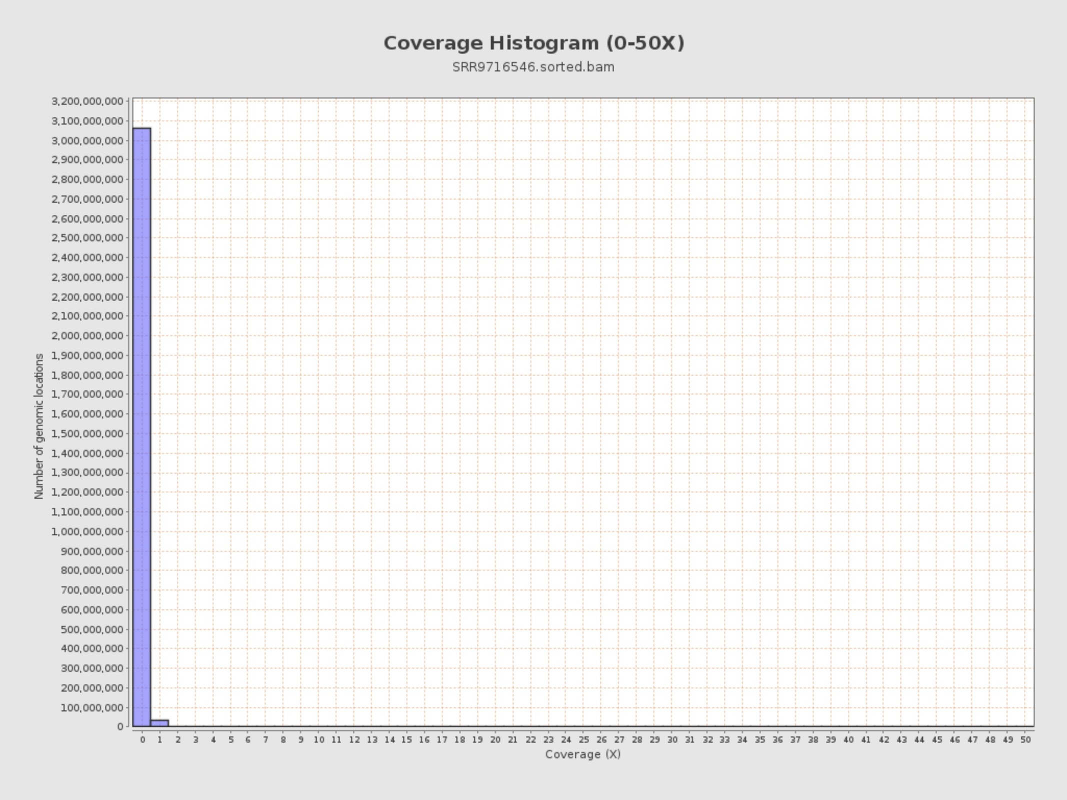
3. Results : Coverage across reference



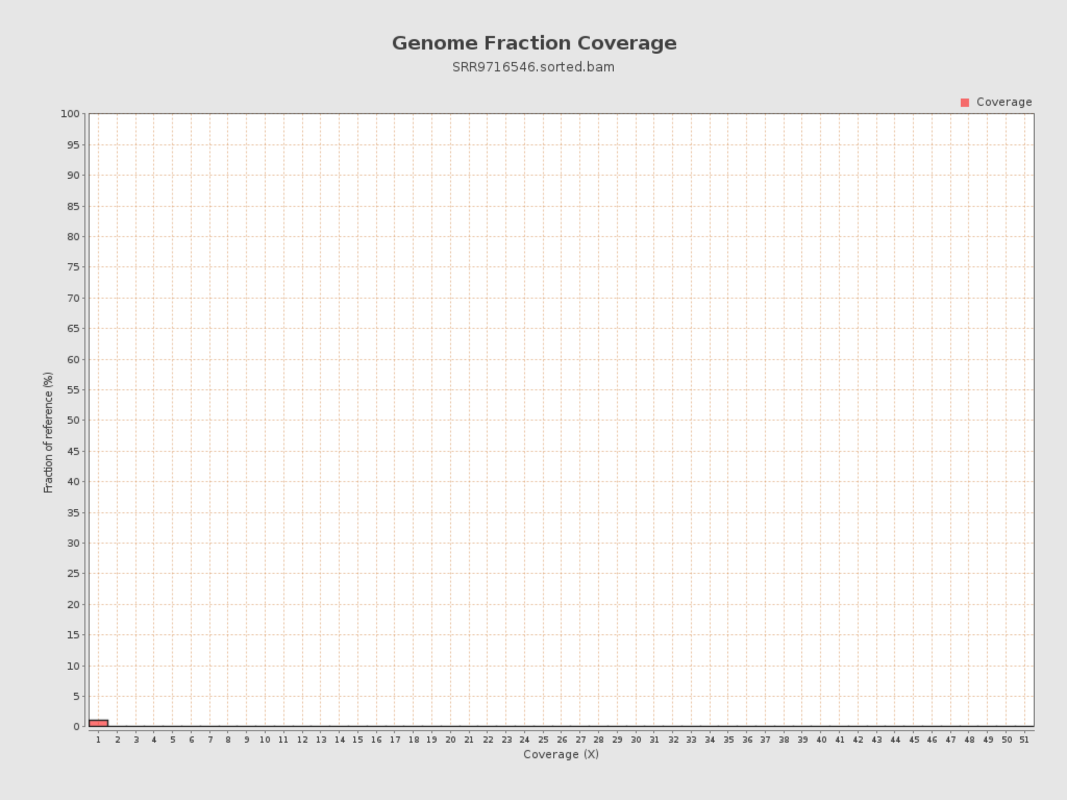
4. Results : Coverage Histogram



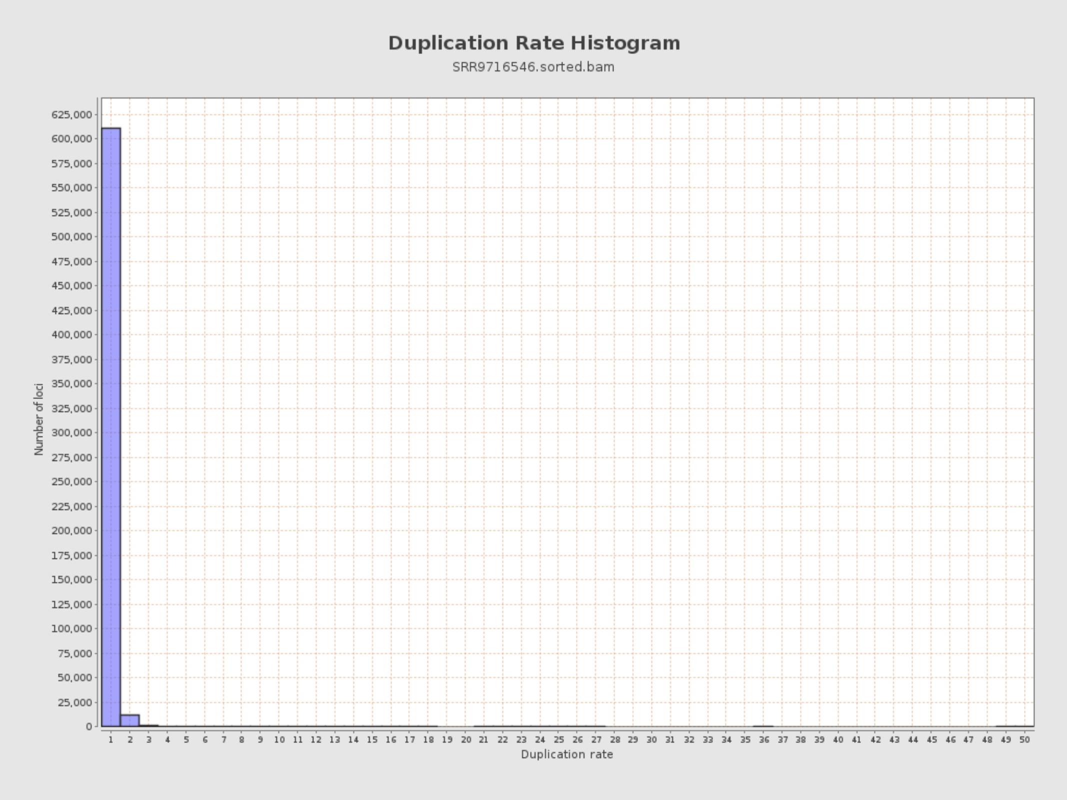
5. Results : Coverage Histogram (0-50X)



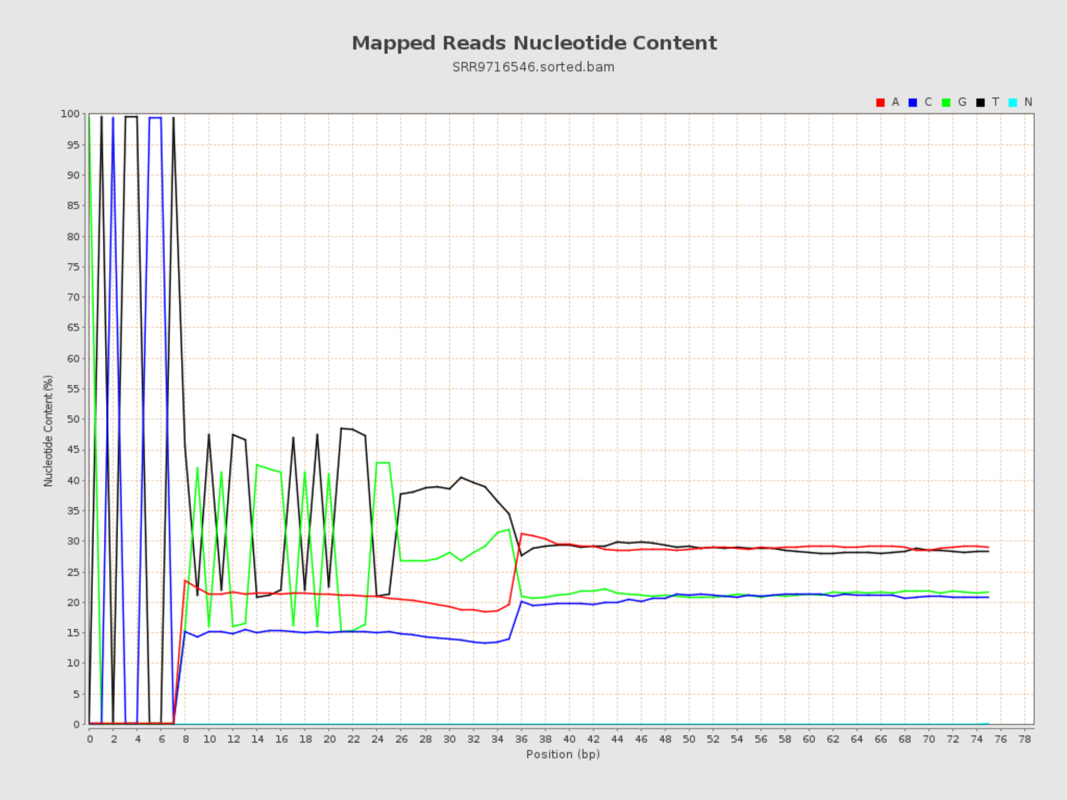
6. Results : Genome Fraction Coverage



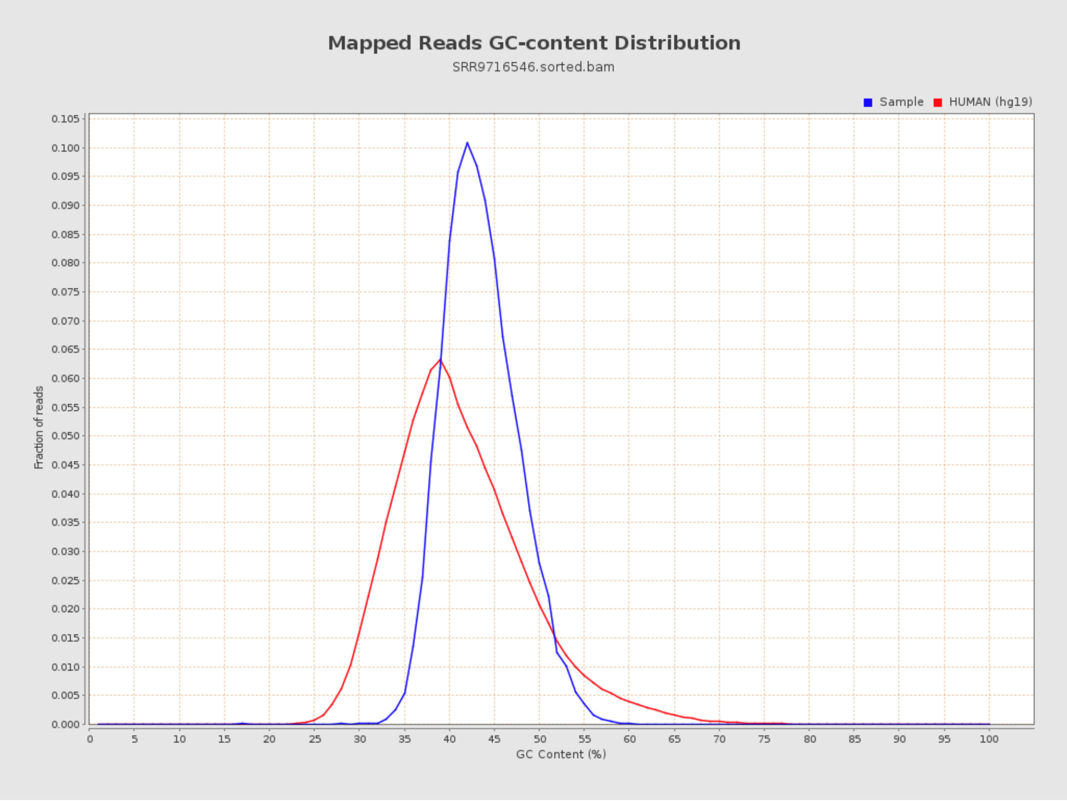
7. Results : Duplication Rate Histogram



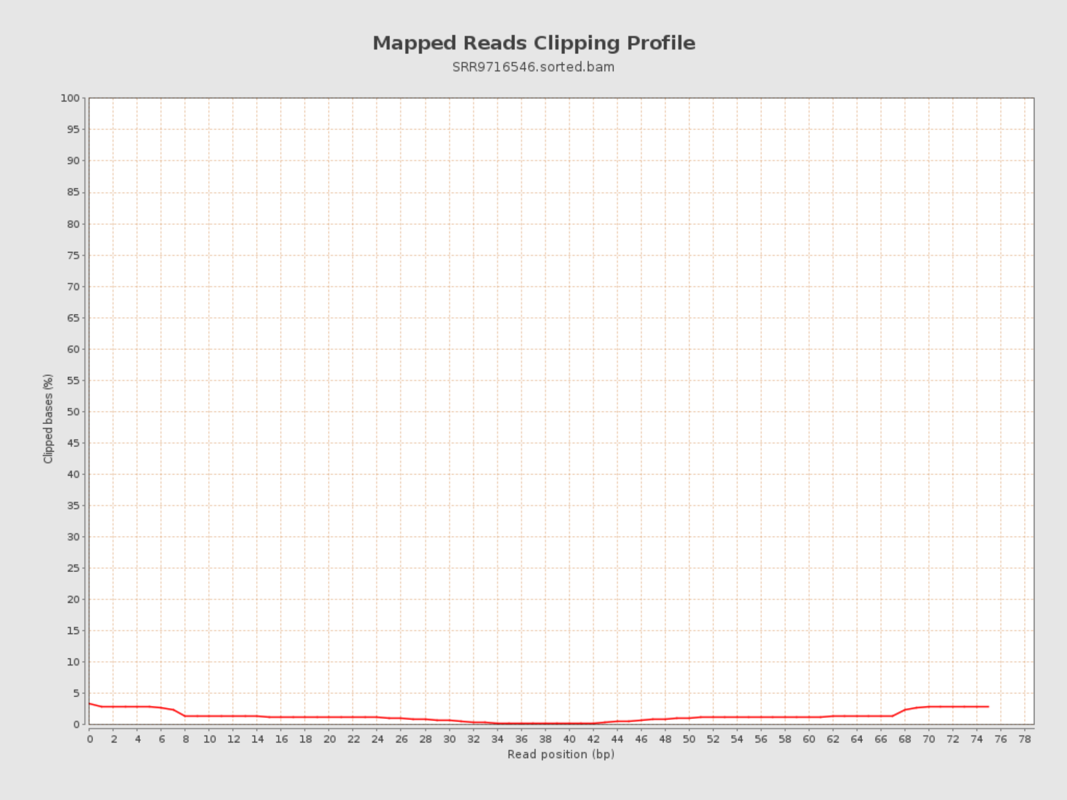
8. Results : Mapped Reads Nucleotide Content



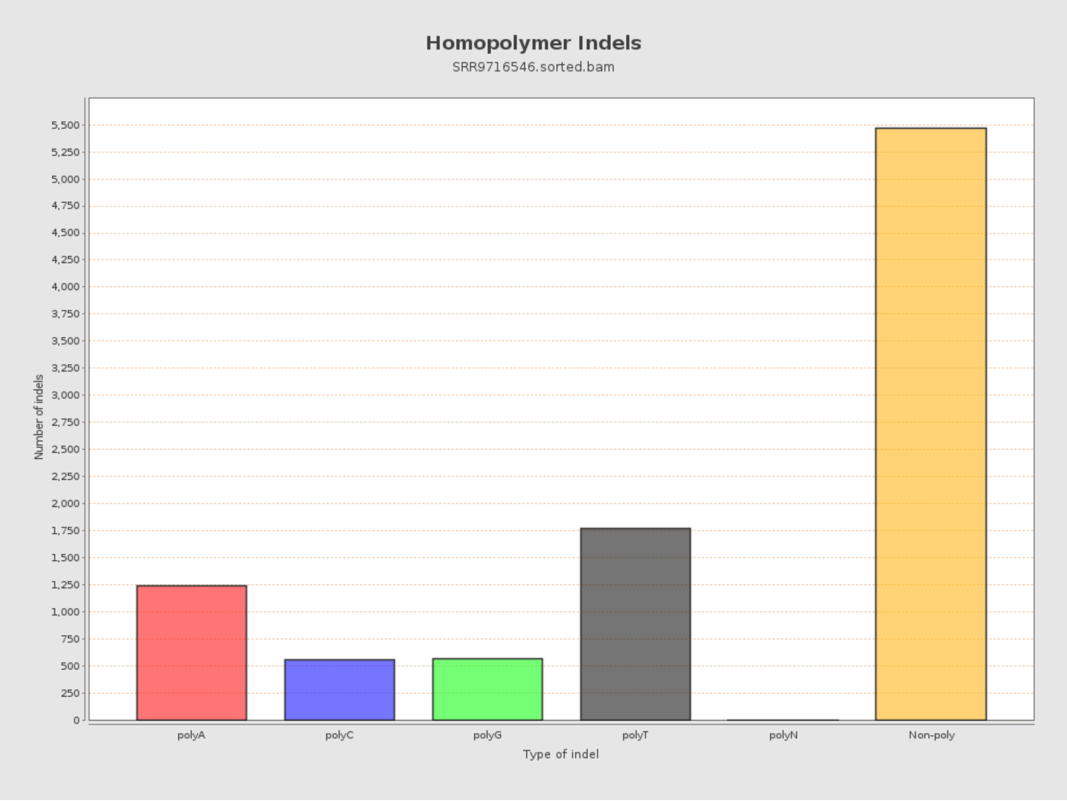
9. Results : Mapped Reads GC-content Distribution



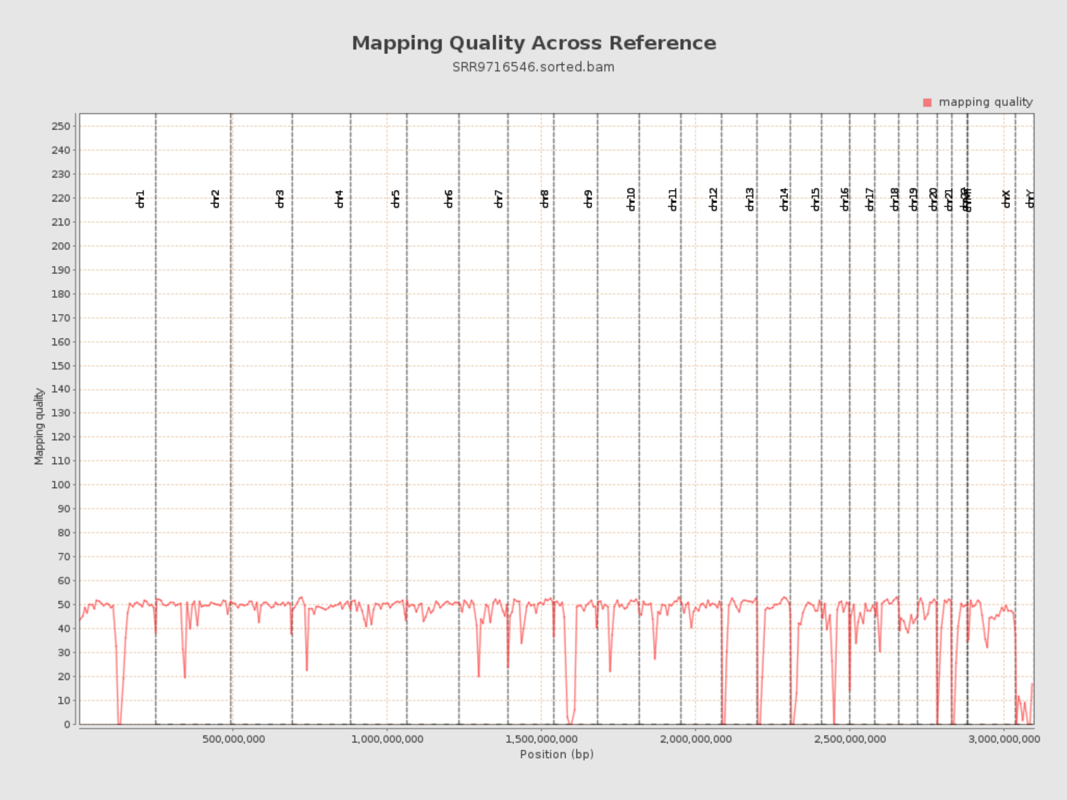
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram