Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:25:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716465.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_SRR9716465 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716465.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:25:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716465.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	626,460
Mapped reads	573,670 / 91.57%
Unmapped reads	52,790 / 8.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,904 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	11,352 / 1.81%
Duplication rate	1.35%
Clipped reads	574,980 / 91.78%

2.2. ACGT Content

Number/percentage of A's	7,839,398 / 23.71%
Number/percentage of C's	5,805,005 / 17.56%
Number/percentage of T's	11,032,595 / 33.37%
Number/percentage of G's	8,388,189 / 25.37%
Number/percentage of N's	719 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1327

2.4. Mapping Quality

Mean Mapping Quality	43.84

2.5. Mismatches and indels

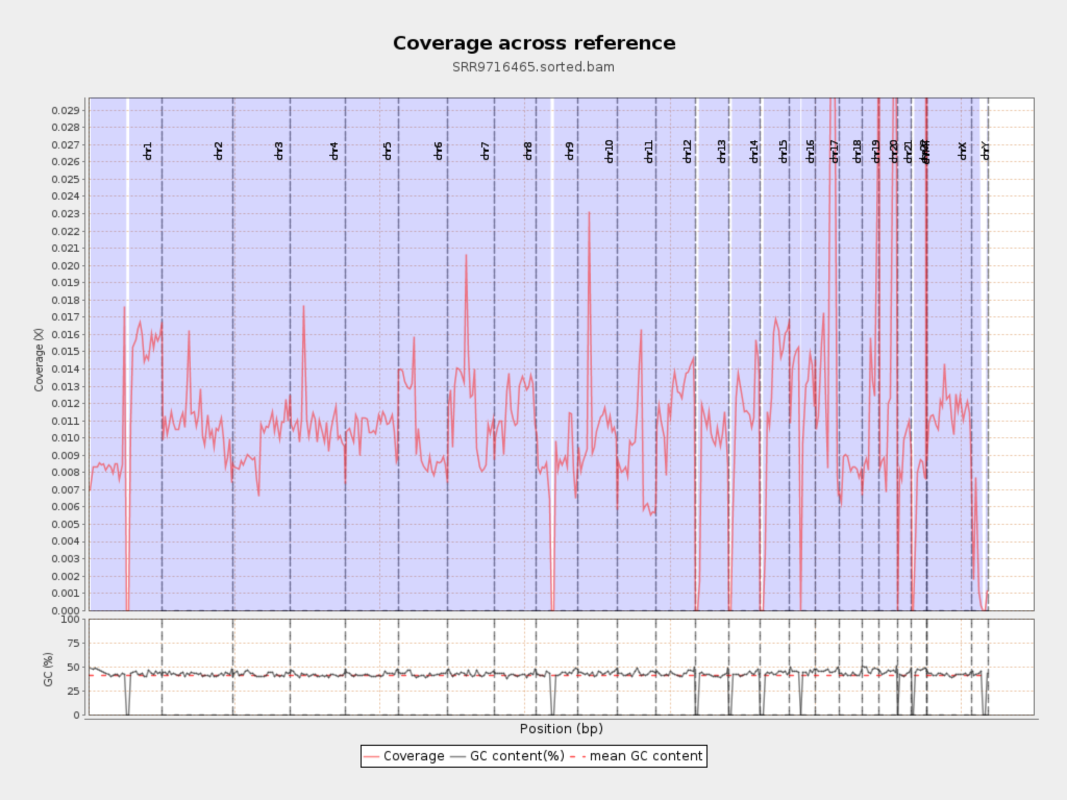
General error rate	0.52%
Mismatches	169,476
Insertions	2,016
Mapped reads with at least one insertion	0.35%
Deletions	6,312
Mapped reads with at least one deletion	1.09%
Homopolymer indels	45.43%

2.6. Chromosome stats

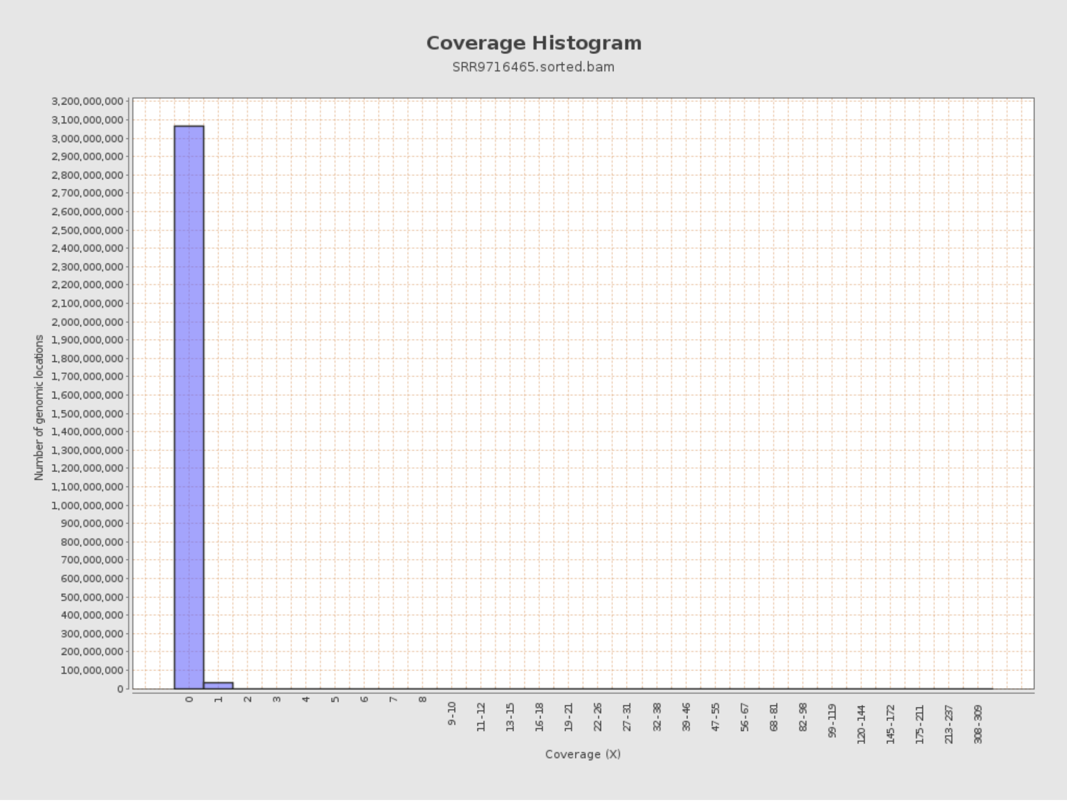
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2768807	0.0111	0.1908
chr2	243199373	2619999	0.0108	0.1669
chr3	198022430	1916098	0.0097	0.1023
chr4	191154276	2063832	0.0108	0.1135
chr5	180915260	1912443	0.0106	0.1065
chr6	171115067	1778641	0.0104	0.1158
chr7	159138663	1906369	0.012	0.1603

chr8	146364022	1738349	0.0119	0.1663
chr9	141213431	1083974	0.0077	0.1003
chr10	135534747	1469168	0.0108	0.1429
chr11	135006516	1158754	0.0086	0.1067
chr12	133851895	1643111	0.0123	0.1147
chr13	115169878	1010874	0.0088	0.097
chr14	107349540	1127194	0.0105	0.1068
chr15	102531392	1203739	0.0117	0.1119
chr16	90354753	1112106	0.0123	0.1174
chr17	81195210	1399718	0.0172	0.1376
chr18	78077248	635192	0.0081	0.1417
chr19	59128983	835672	0.0141	0.166
chr20	63025520	1045589	0.0166	0.1347
chr21	48129895	410664	0.0085	0.103
chr22	51304566	299910	0.0058	0.0786
chrMT	16571	28252	1.7049	1.6346
chrX	155270560	1791772	0.0115	0.1157
chrY	59373566	116027	0.002	0.0876

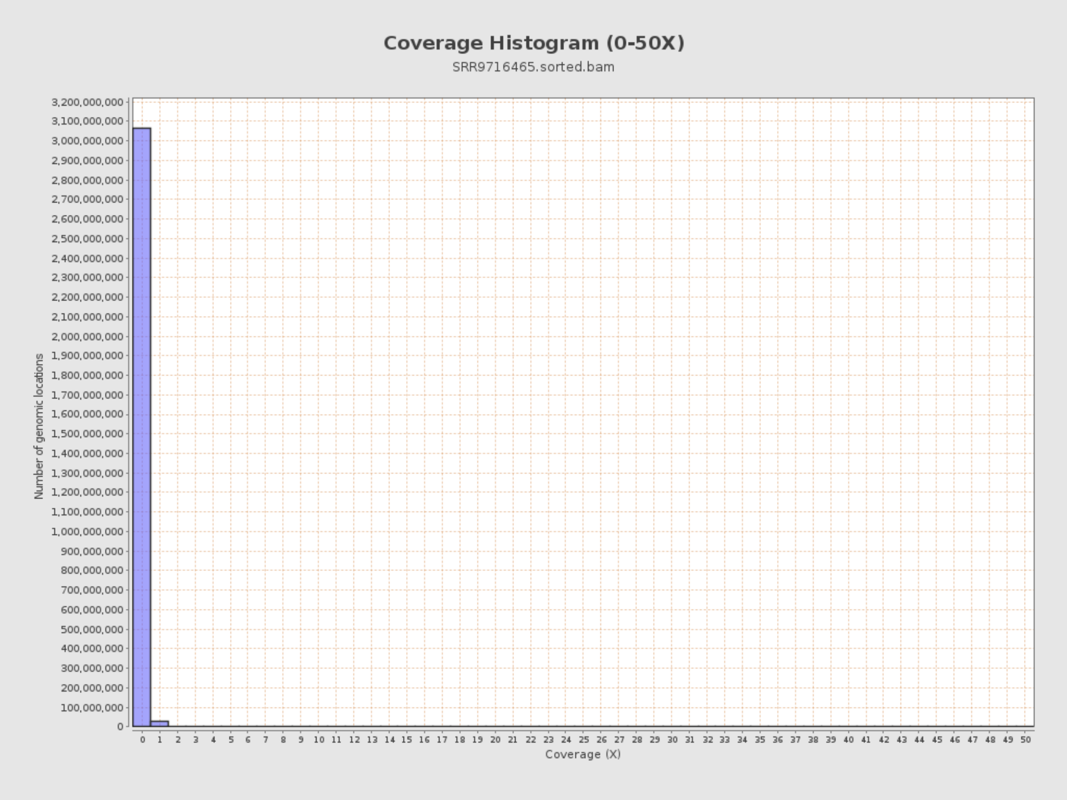
3. Results : Coverage across reference



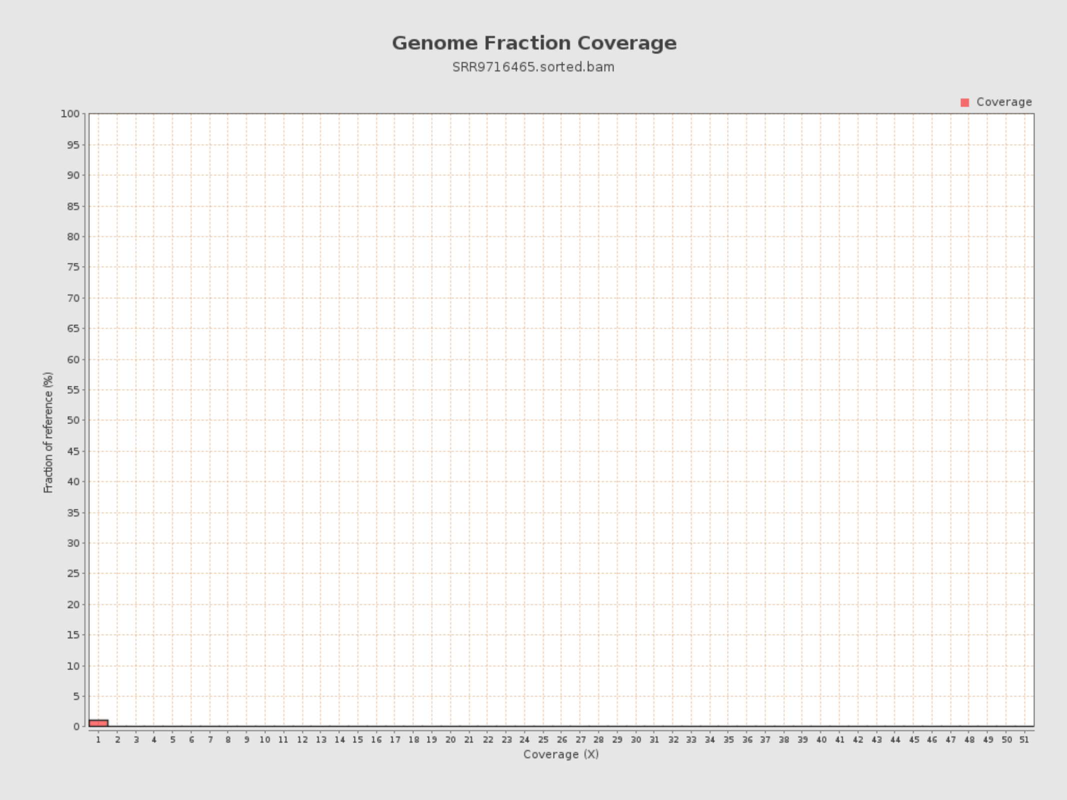
4. Results : Coverage Histogram



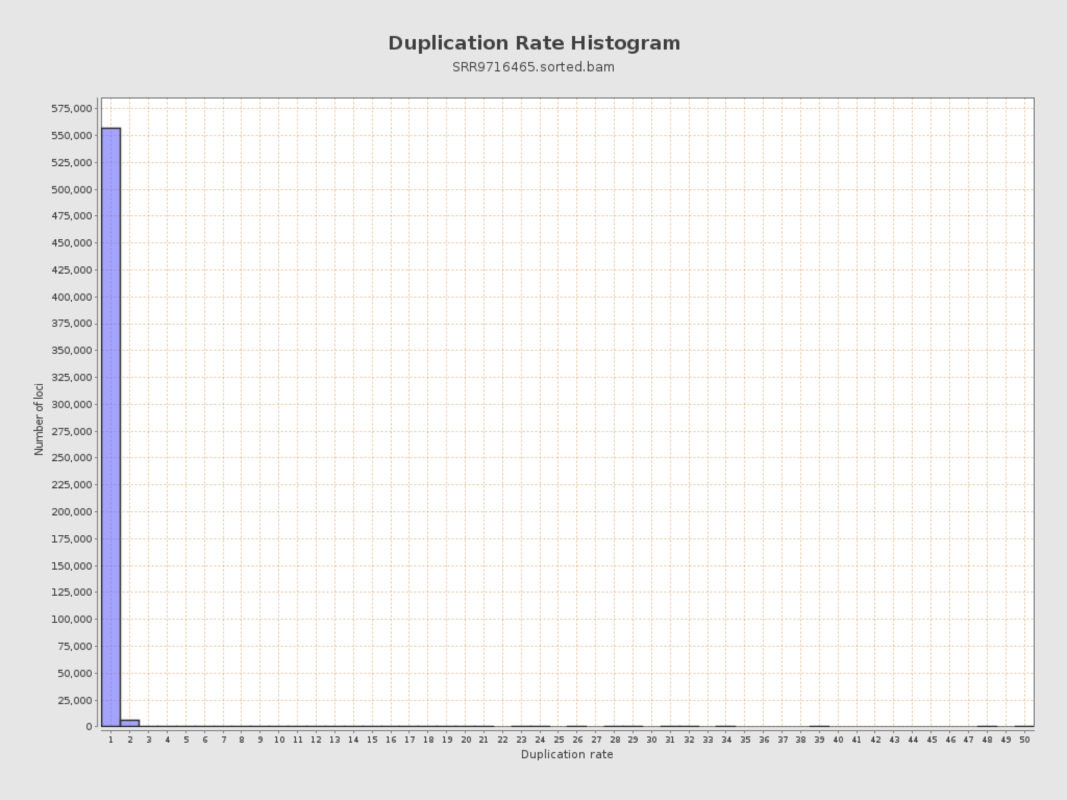
5. Results : Coverage Histogram (0-50X)



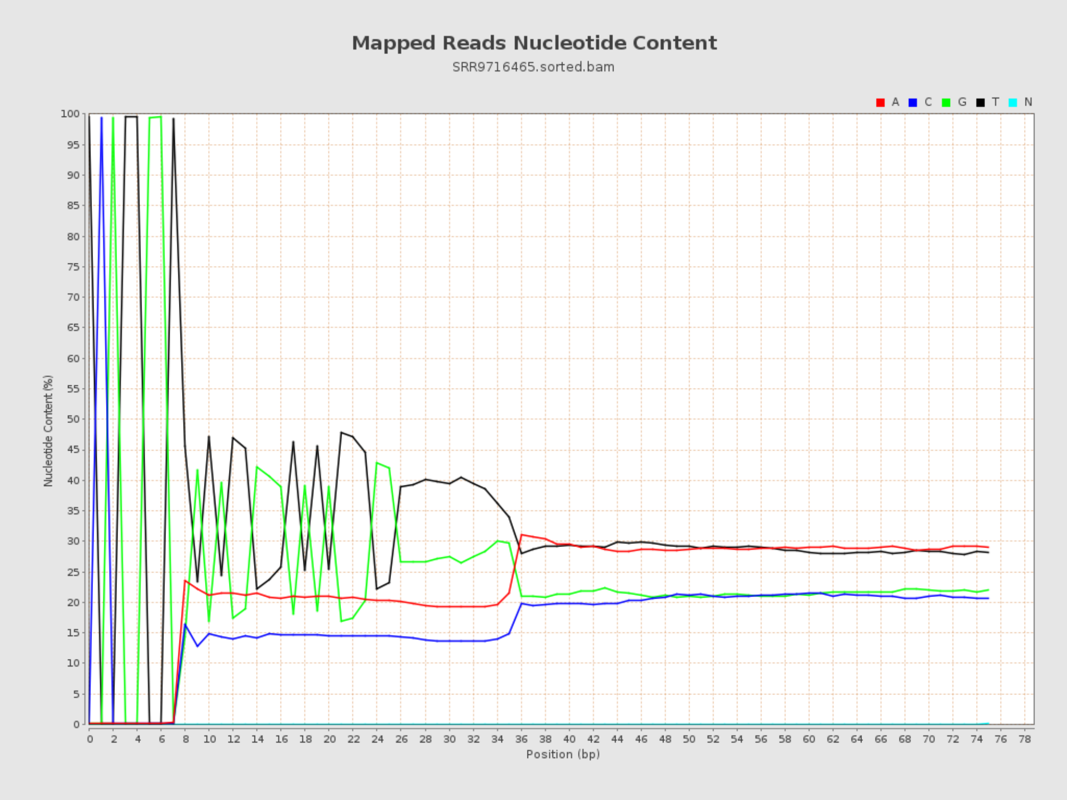
6. Results : Genome Fraction Coverage



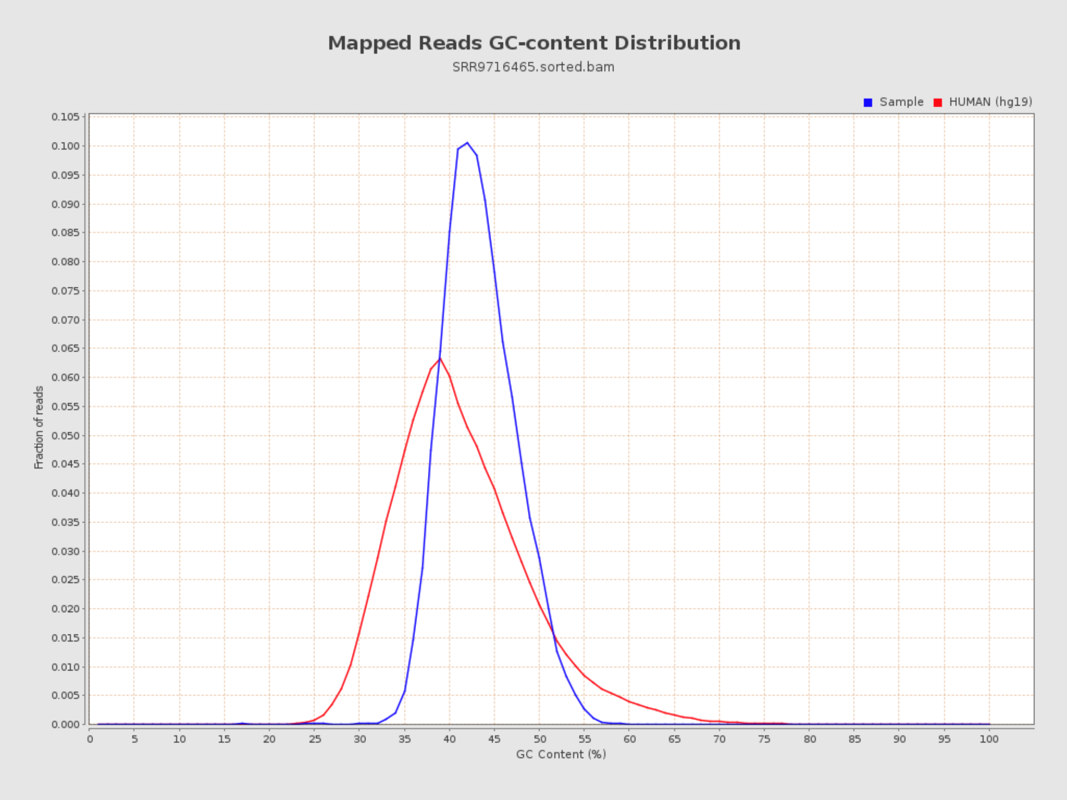
7. Results : Duplication Rate Histogram



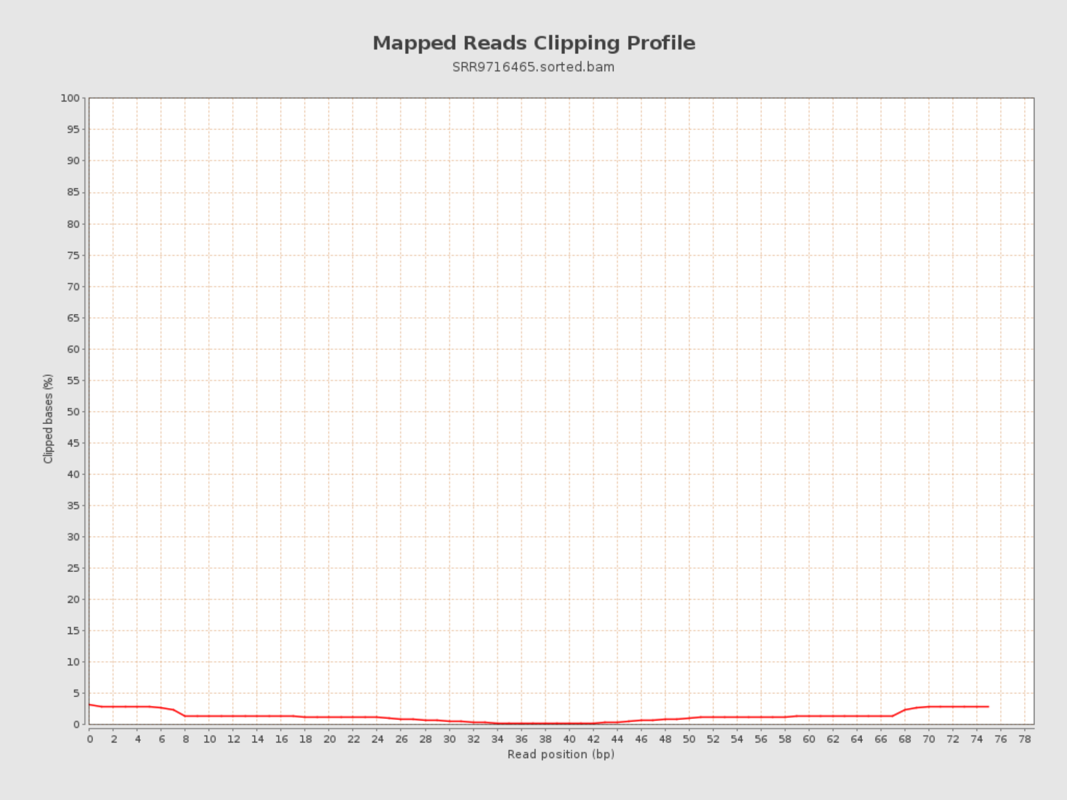
8. Results : Mapped Reads Nucleotide Content



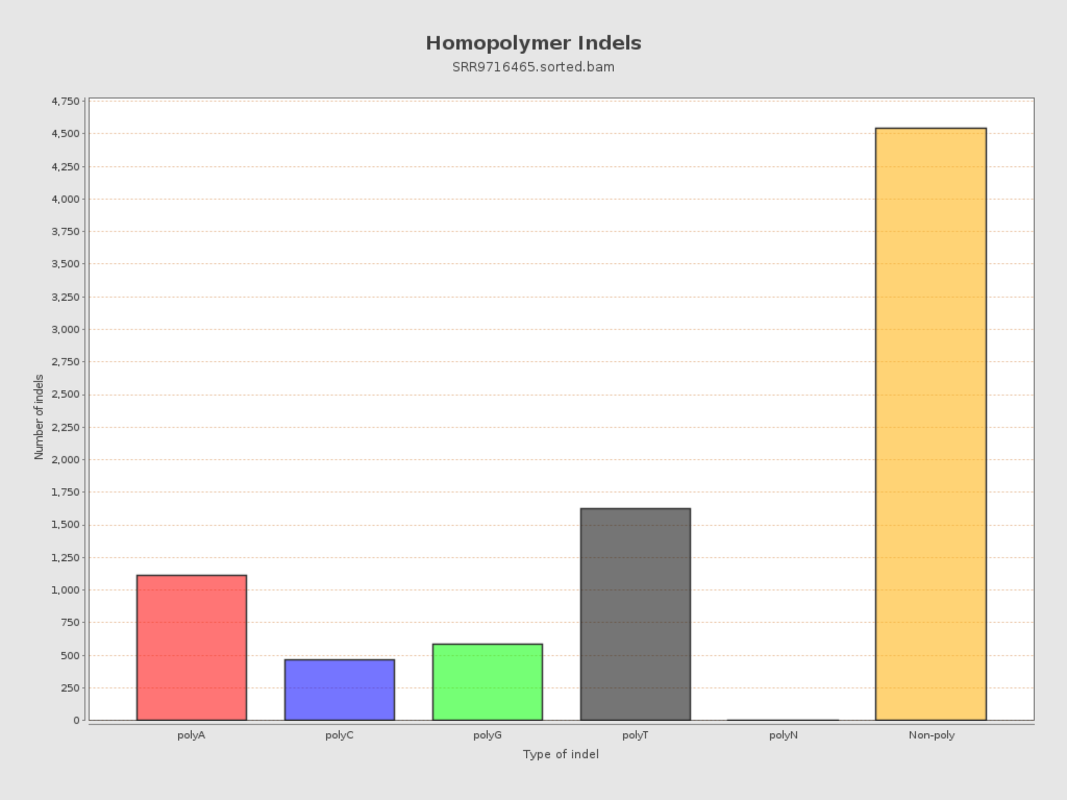
9. Results : Mapped Reads GC-content Distribution



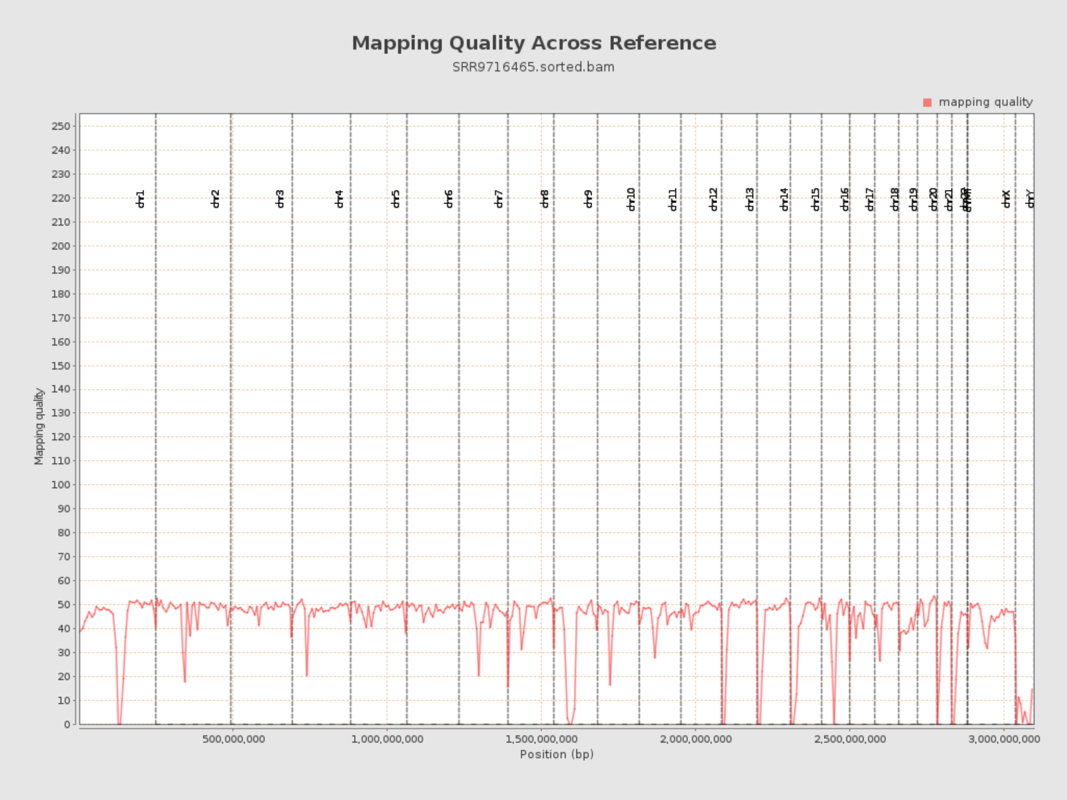
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram