Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:40:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716542.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_SRR9716542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716542.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:40:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	450,011
Mapped reads	410,552 / 91.23%
Unmapped reads	39,459 / 8.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,477 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	8,308 / 1.85%
Duplication rate	1.59%
Clipped reads	411,060 / 91.34%

2.2. ACGT Content

Number/percentage of A's	5,931,945 / 24.89%
Number/percentage of C's	4,659,819 / 19.56%
Number/percentage of T's	7,480,352 / 31.39%
Number/percentage of G's	5,755,681 / 24.15%
Number/percentage of N's	811 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0077

Standard Deviation	0.1067

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

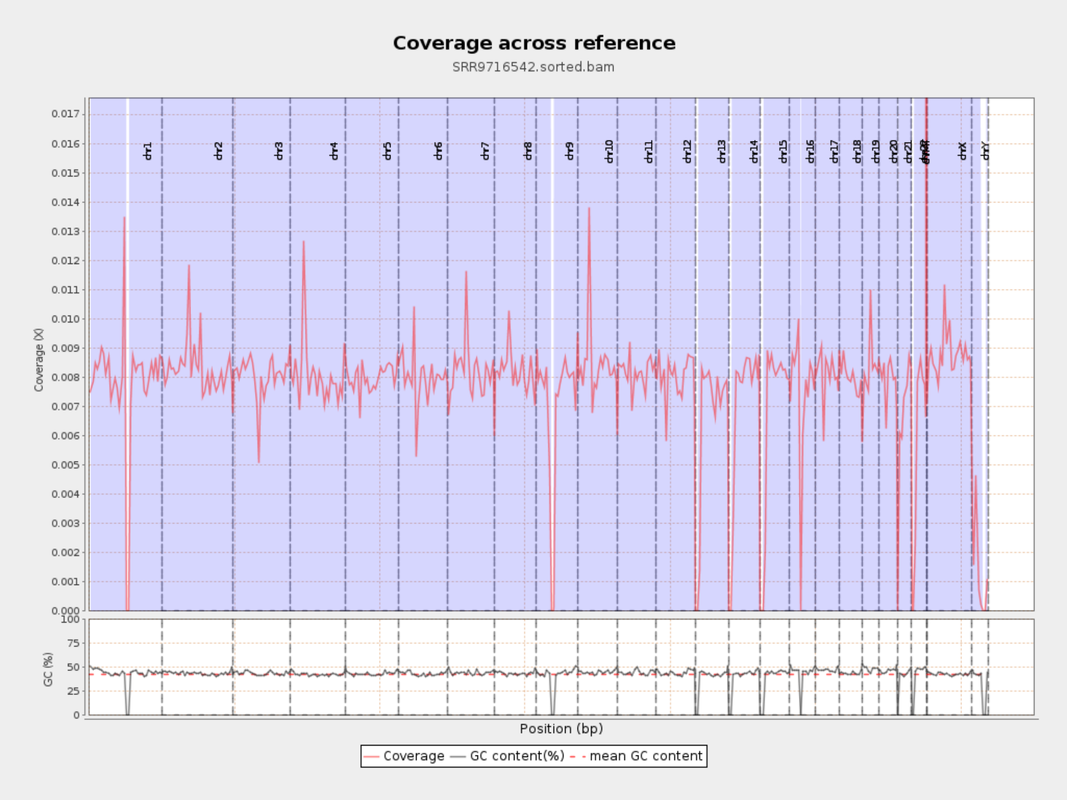
General error rate	0.52%
Mismatches	121,094
Insertions	1,686
Mapped reads with at least one insertion	0.41%
Deletions	4,553
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.53%

2.6. Chromosome stats

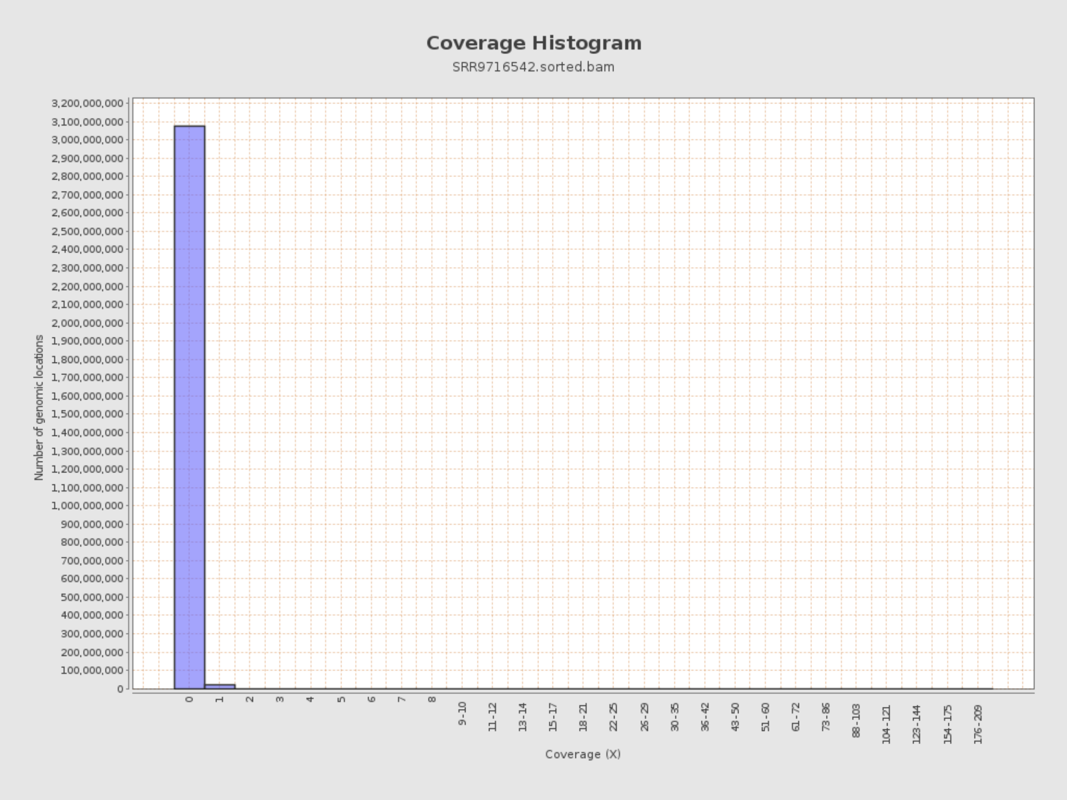
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1933001	0.0078	0.1683
chr2	243199373	2027626	0.0083	0.1218
chr3	198022430	1585023	0.008	0.0924
chr4	191154276	1536788	0.008	0.095
chr5	180915260	1441217	0.008	0.0923
chr6	171115067	1367052	0.008	0.0973
chr7	159138663	1311637	0.0082	0.1136

chr8	146364022	1202324	0.0082	0.1095
chr9	141213431	972944	0.0069	0.0943
chr10	135534747	1148246	0.0085	0.1065
chr11	135006516	1097317	0.0081	0.0996
chr12	133851895	1073061	0.008	0.093
chr13	115169878	737753	0.0064	0.0829
chr14	107349540	728566	0.0068	0.0857
chr15	102531392	686665	0.0067	0.0851
chr16	90354753	669597	0.0074	0.0909
chr17	81195210	655552	0.0081	0.0944
chr18	78077248	625444	0.008	0.1289
chr19	59128983	492764	0.0083	0.1258
chr20	63025520	499857	0.0079	0.0928
chr21	48129895	317753	0.0066	0.0864
chr22	51304566	280734	0.0055	0.0766
chrMT	16571	7743	0.4673	0.7263
chrX	155270560	1359033	0.0088	0.0992
chrY	59373566	78052	0.0013	0.0489

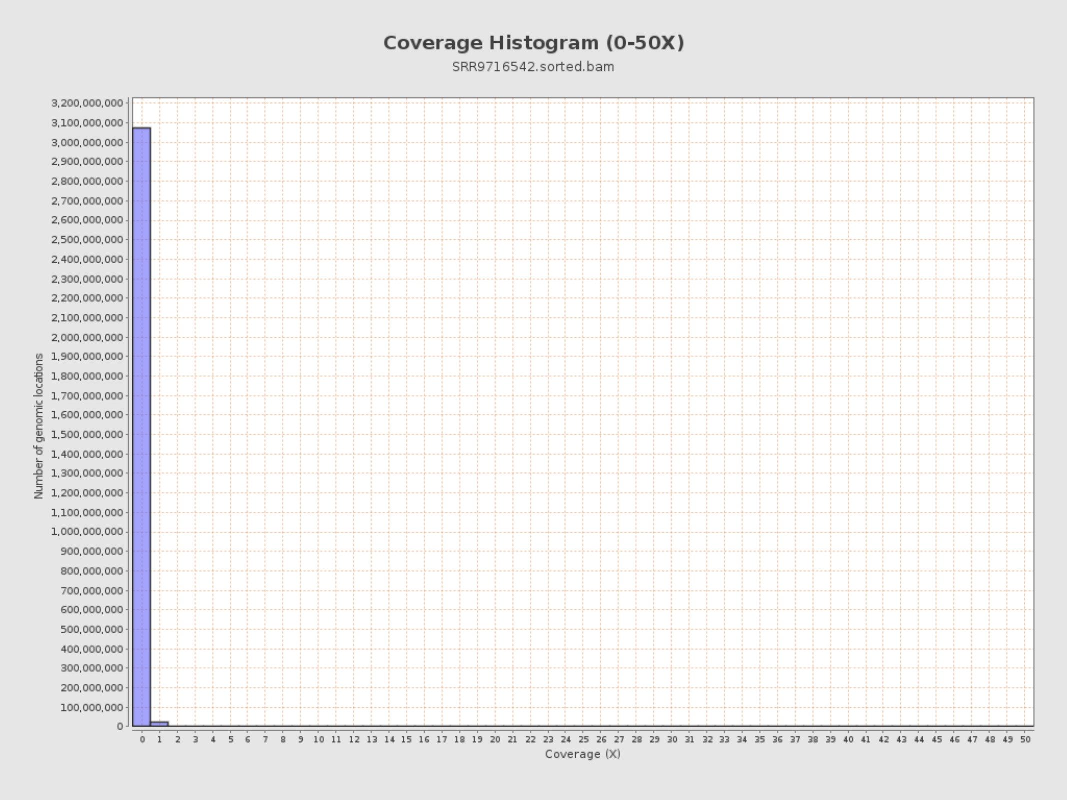
3. Results : Coverage across reference



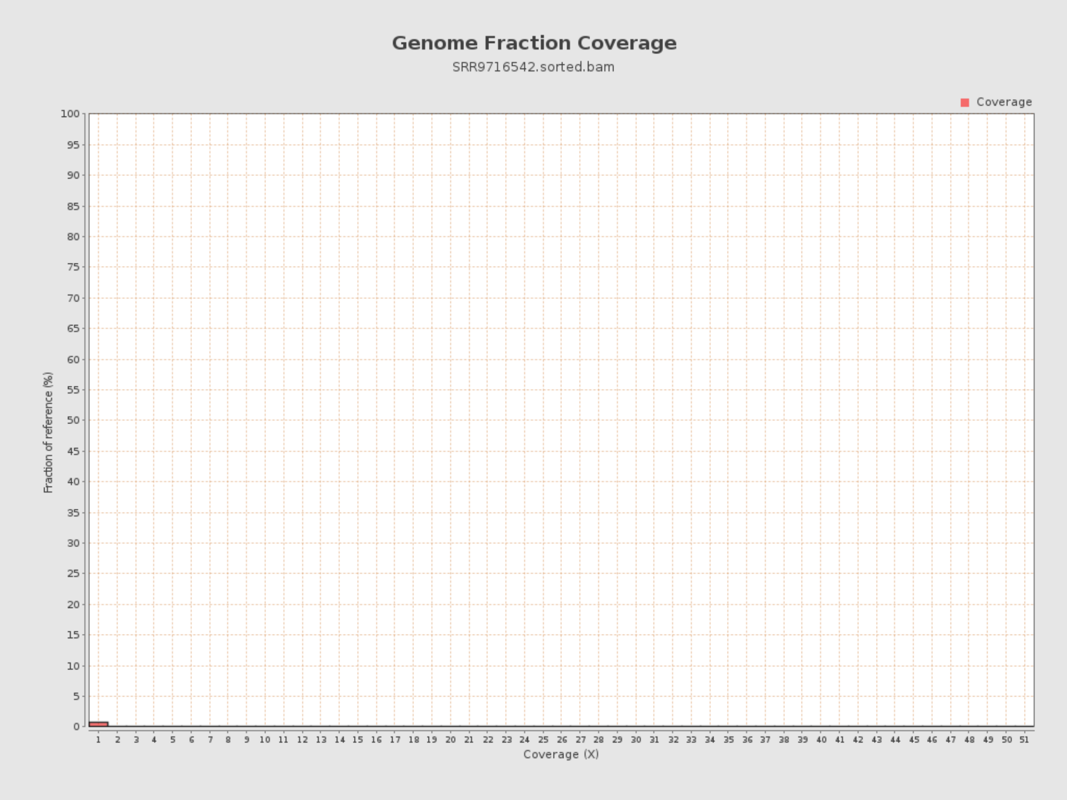
4. Results : Coverage Histogram



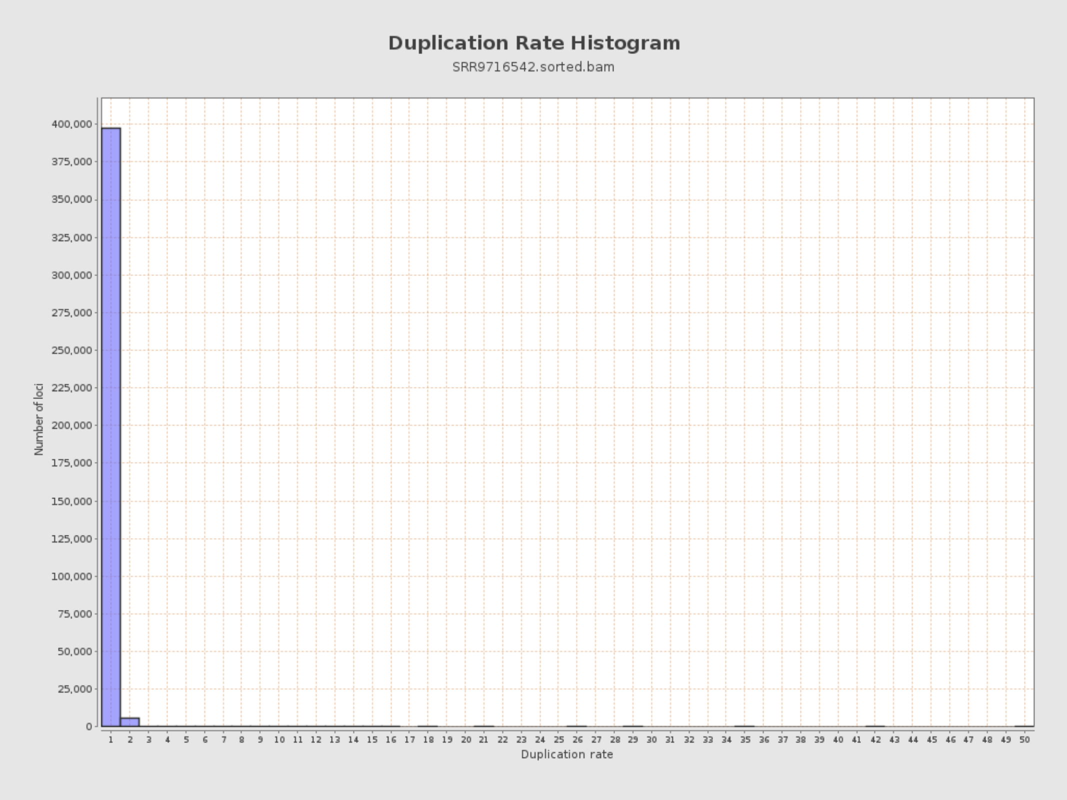
5. Results : Coverage Histogram (0-50X)



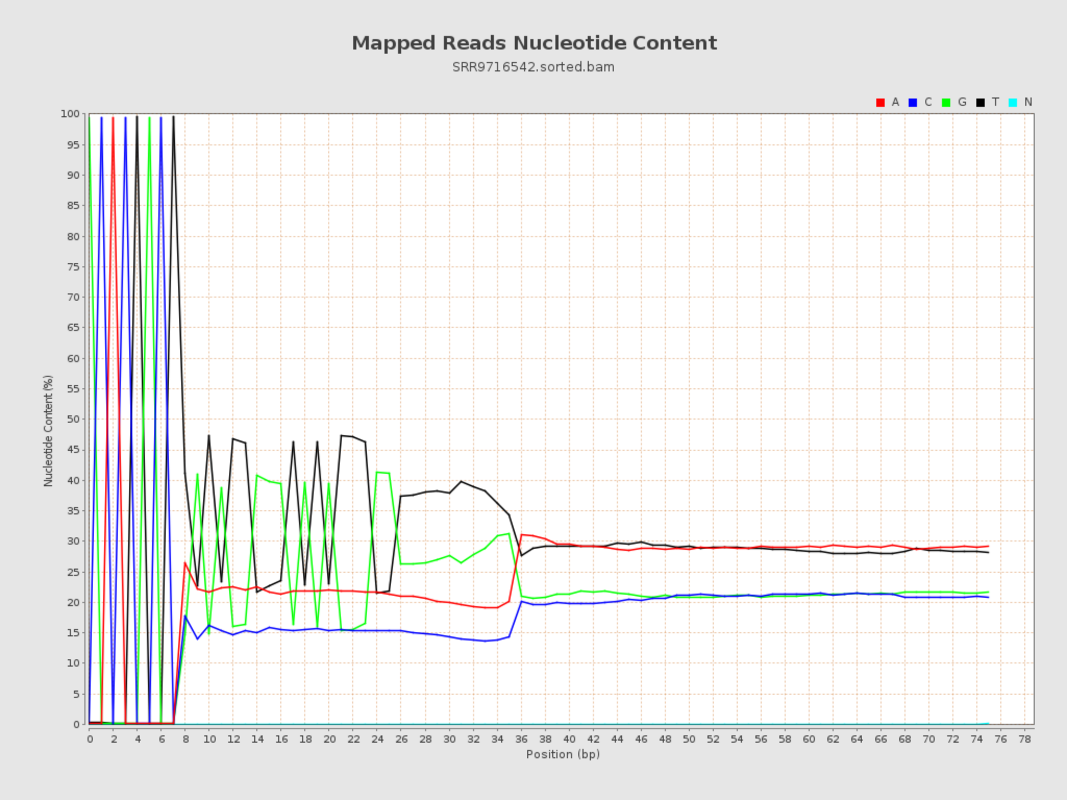
6. Results : Genome Fraction Coverage



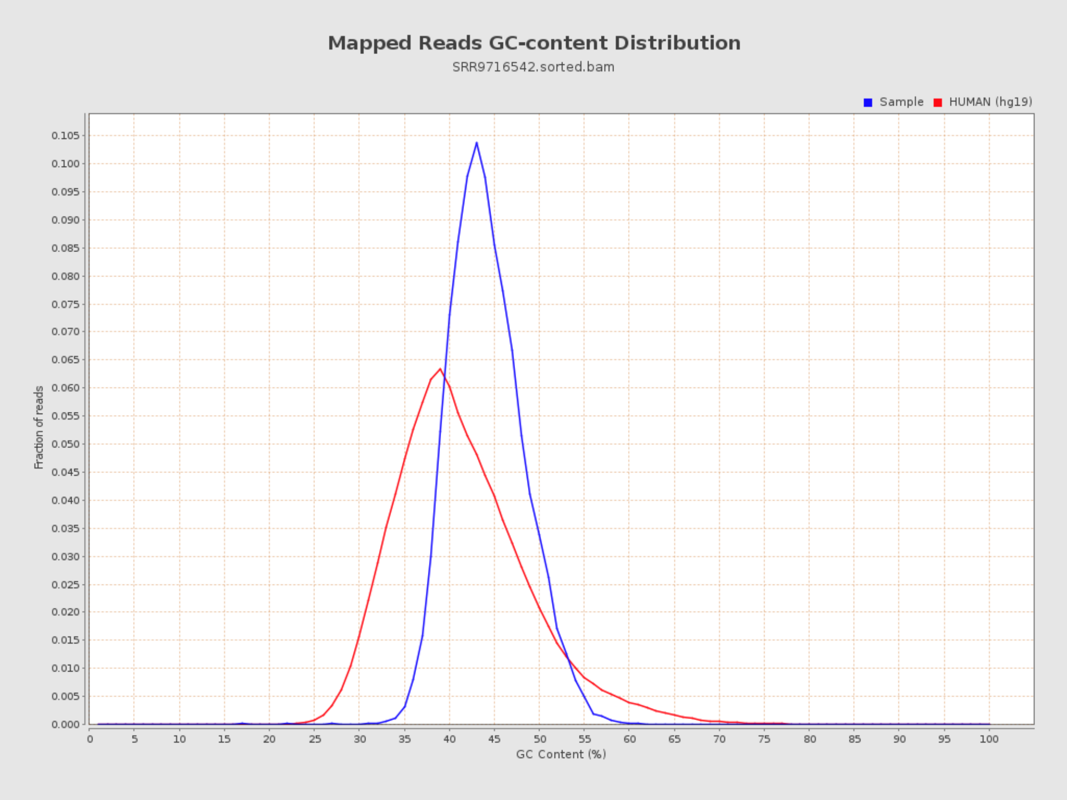
7. Results : Duplication Rate Histogram



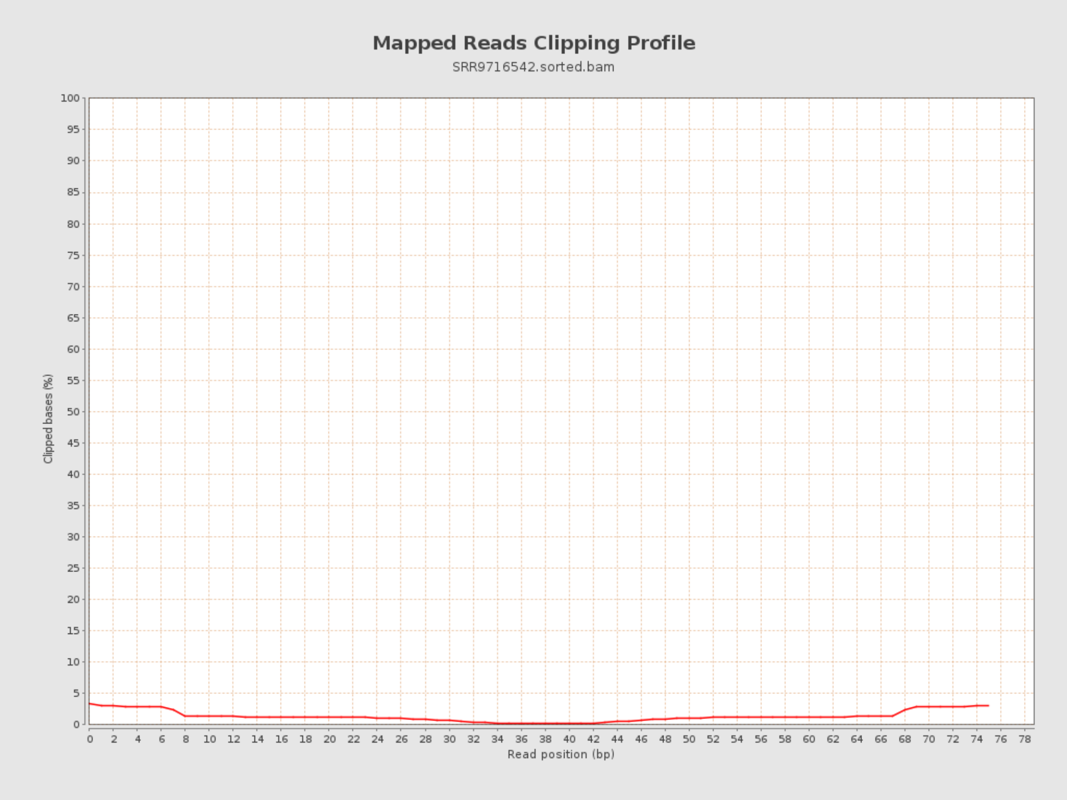
8. Results : Mapped Reads Nucleotide Content



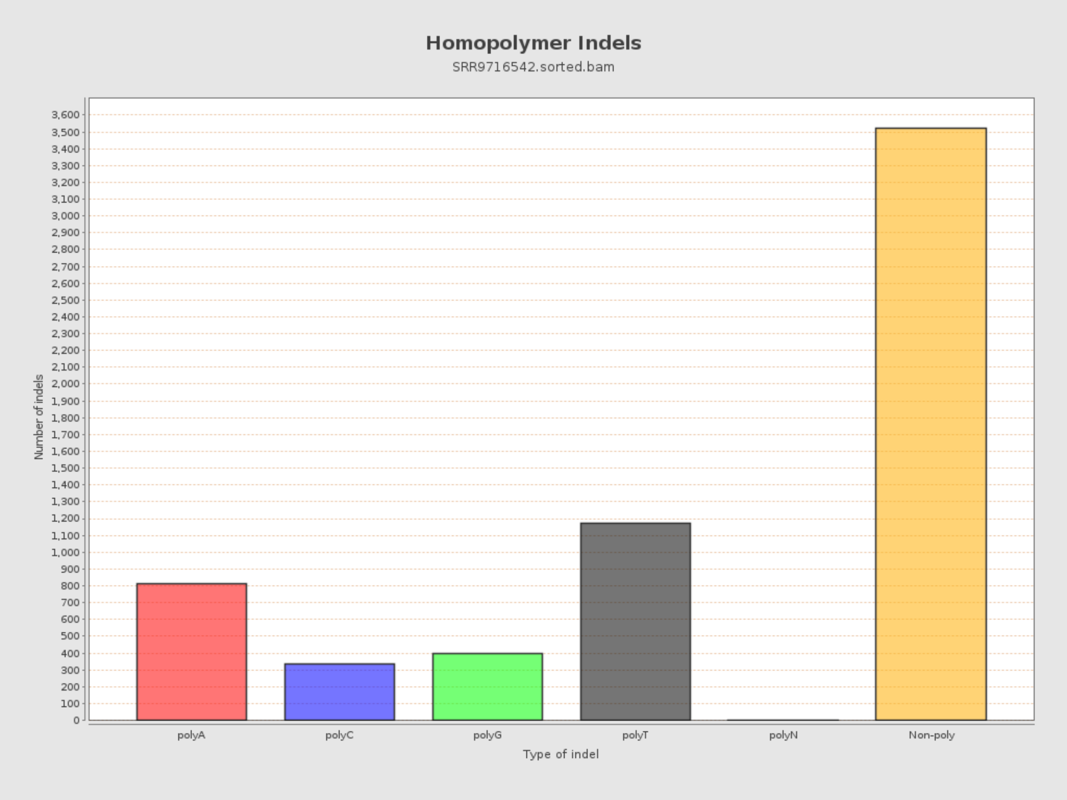
9. Results : Mapped Reads GC-content Distribution



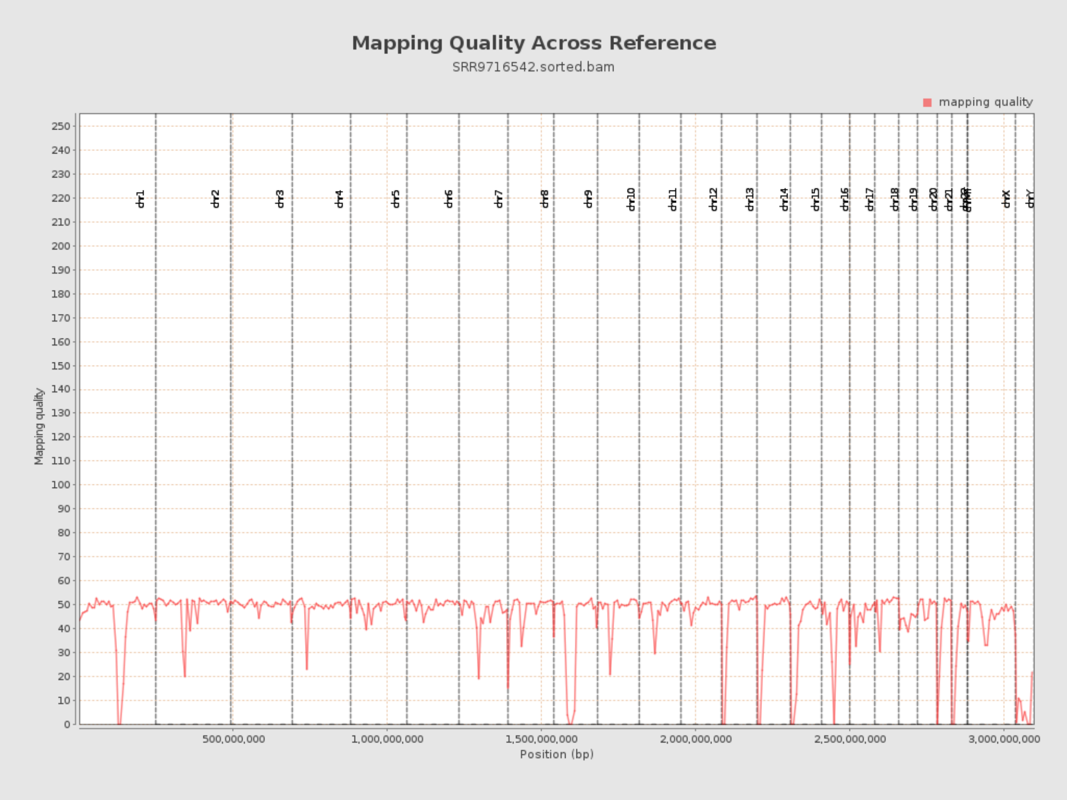
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram