Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:42:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716491.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_SRR9716491 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716491.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:42:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	794,018
Mapped reads	660,031 / 83.13%
Unmapped reads	133,987 / 16.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,284 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	15,915 / 2%
Duplication rate	1.93%
Clipped reads	661,839 / 83.35%

2.2. ACGT Content

Number/percentage of A's	9,768,847 / 25.96%
Number/percentage of C's	7,578,312 / 20.14%
Number/percentage of T's	11,499,604 / 30.56%
Number/percentage of G's	8,786,346 / 23.35%
Number/percentage of N's	483 / 0%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.1372

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

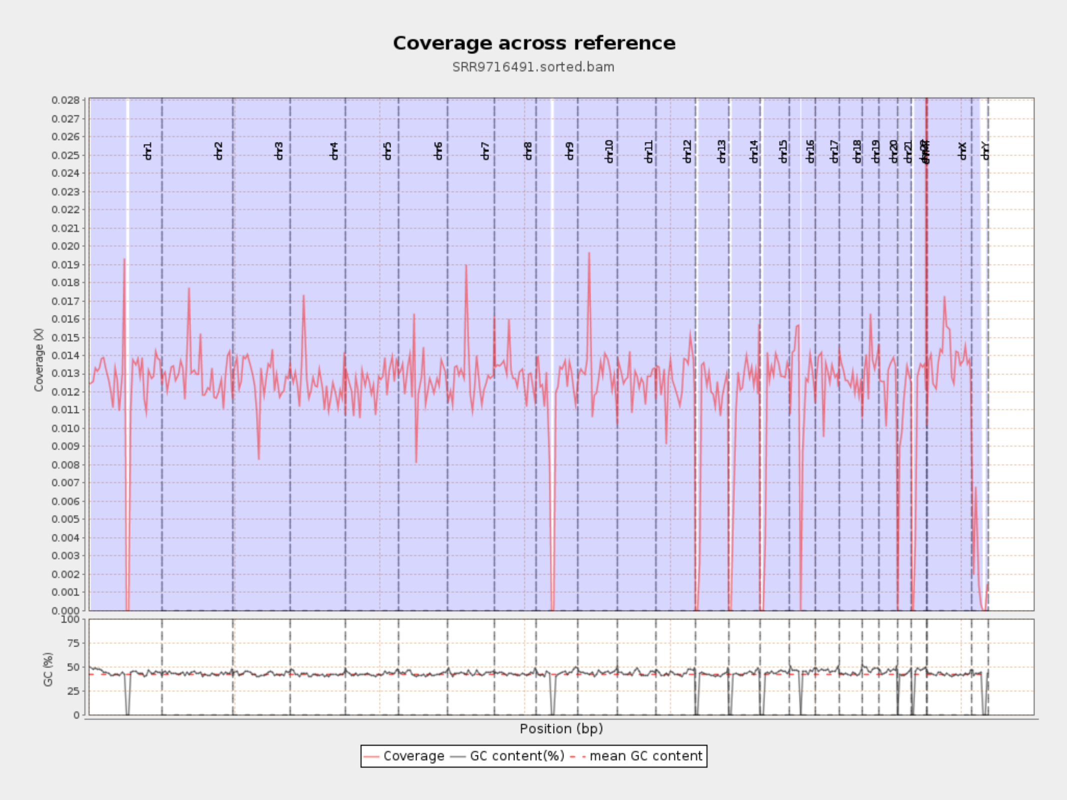
General error rate	0.52%
Mismatches	189,802
Insertions	2,794
Mapped reads with at least one insertion	0.42%
Deletions	6,535
Mapped reads with at least one deletion	0.98%
Homopolymer indels	39.66%

2.6. Chromosome stats

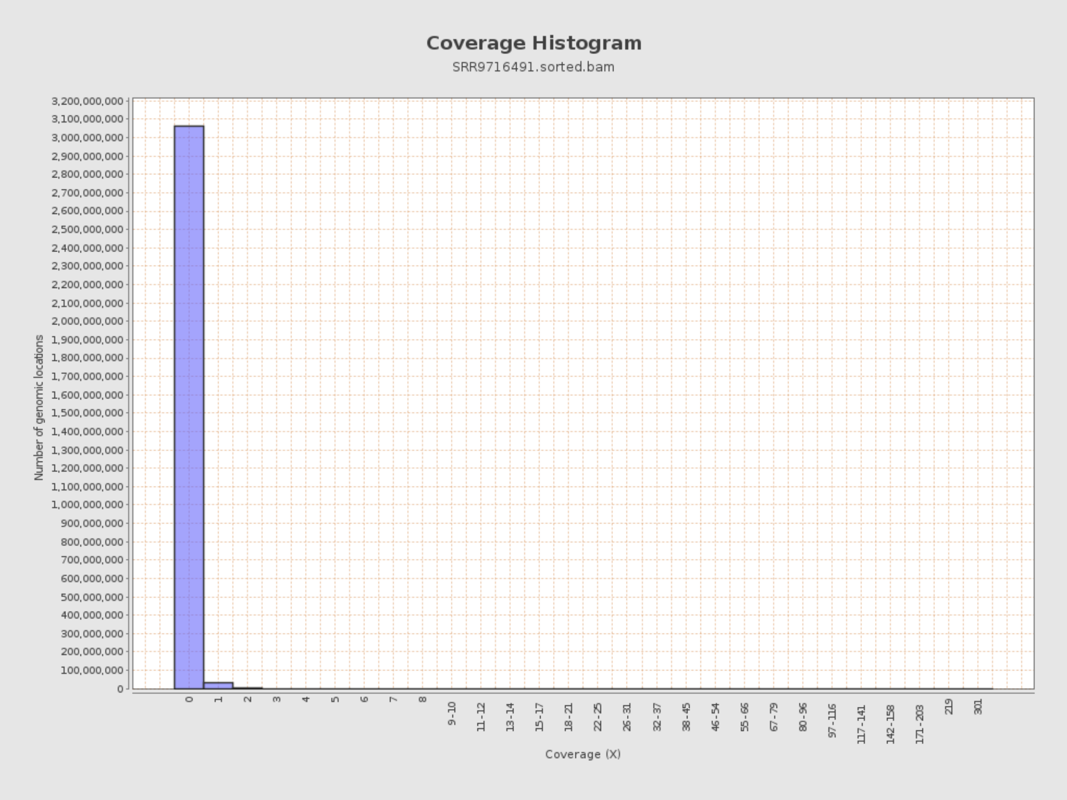
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3059207	0.0123	0.1944
chr2	243199373	3152491	0.013	0.1718
chr3	198022430	2509218	0.0127	0.1184
chr4	191154276	2381487	0.0125	0.1217
chr5	180915260	2261650	0.0125	0.1181
chr6	171115067	2175377	0.0127	0.1273
chr7	159138663	2050328	0.0129	0.1537

chr8	146364022	1905724	0.013	0.1382
chr9	141213431	1558583	0.011	0.1231
chr10	135534747	1788557	0.0132	0.1399
chr11	135006516	1713963	0.0127	0.1348
chr12	133851895	1709901	0.0128	0.1194
chr13	115169878	1190167	0.0103	0.1074
chr14	107349540	1130880	0.0105	0.1111
chr15	102531392	1096505	0.0107	0.1102
chr16	90354753	1088210	0.012	0.118
chr17	81195210	1044097	0.0129	0.122
chr18	78077248	993356	0.0127	0.1695
chr19	59128983	806000	0.0136	0.17
chr20	63025520	794862	0.0126	0.1186
chr21	48129895	500437	0.0104	0.1106
chr22	51304566	465958	0.0091	0.1004
chrMT	16571	1959	0.1182	0.3576
chrX	155270560	2145549	0.0138	0.1284
chrY	59373566	119450	0.002	0.0608

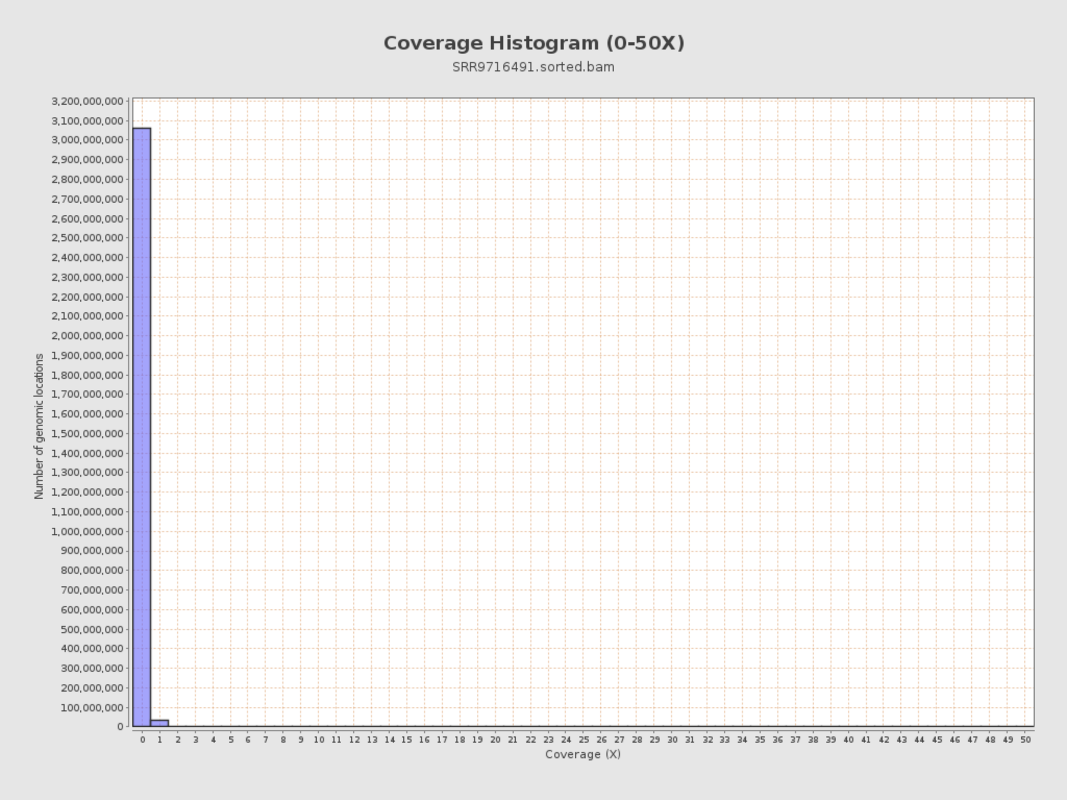
3. Results : Coverage across reference



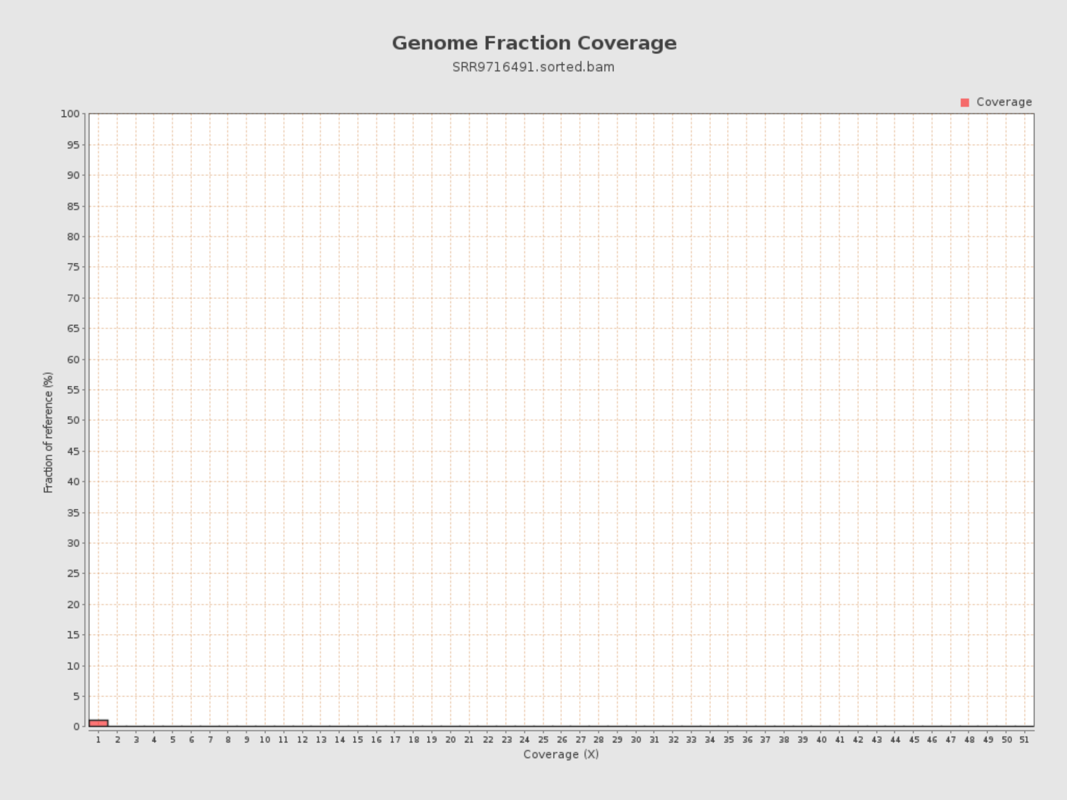
4. Results : Coverage Histogram



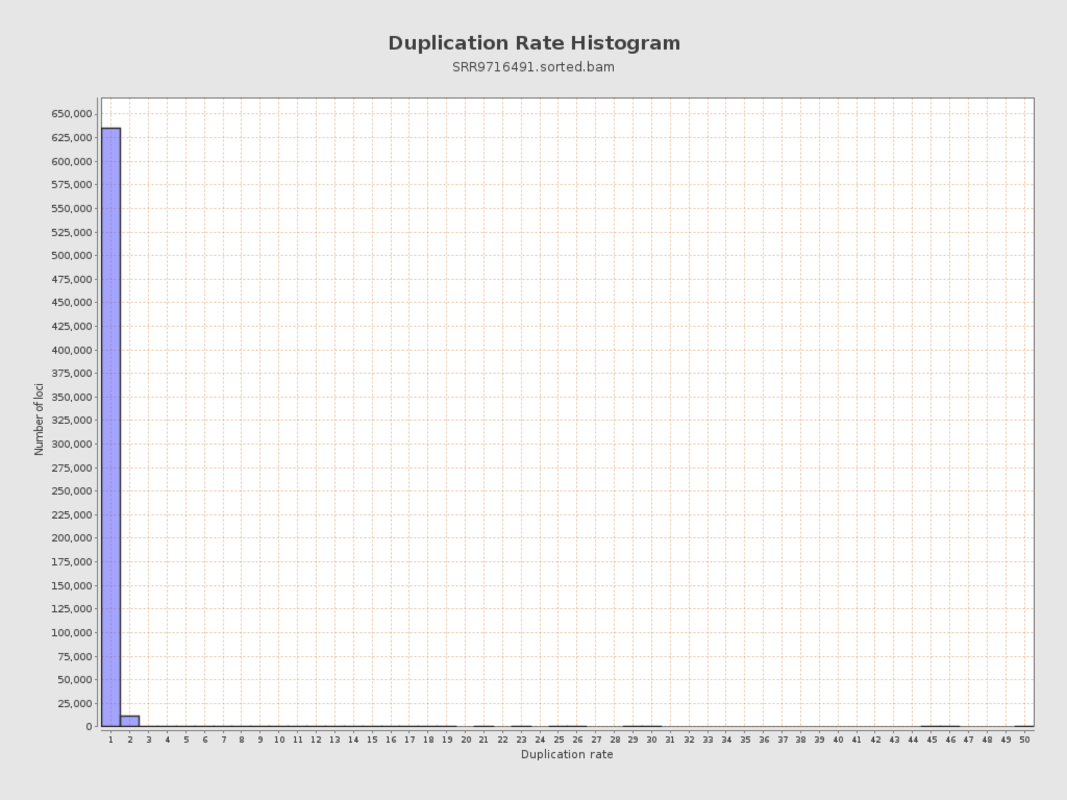
5. Results : Coverage Histogram (0-50X)



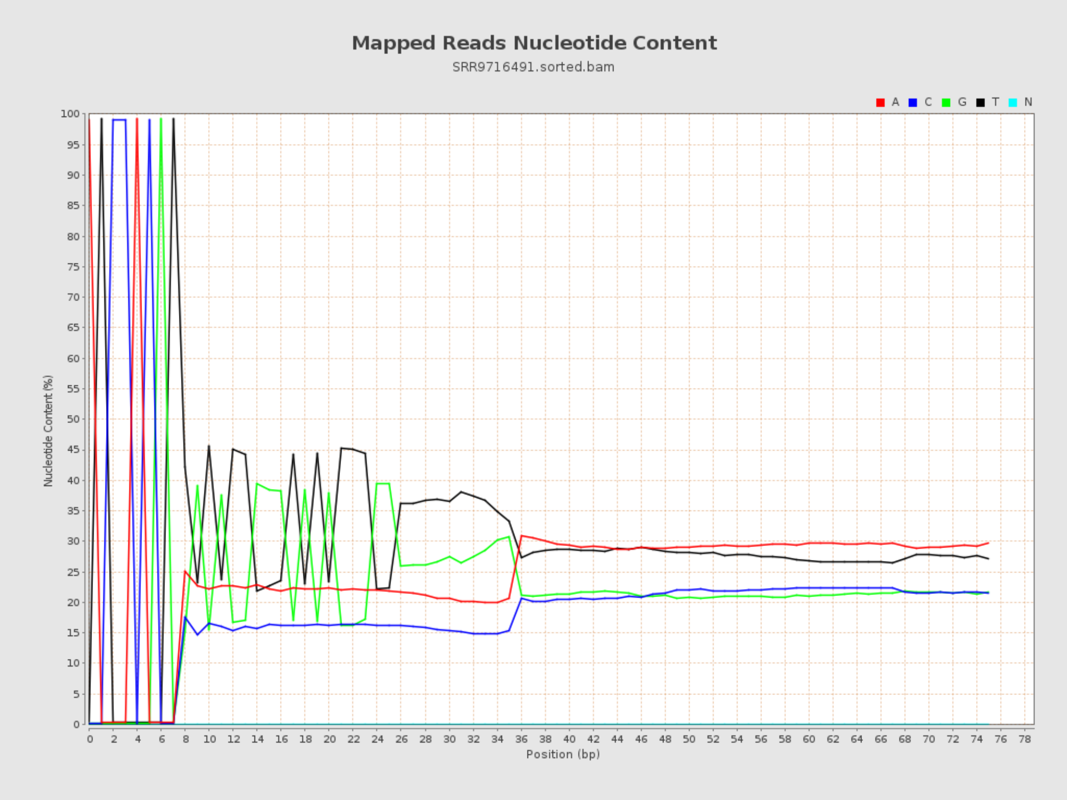
6. Results : Genome Fraction Coverage



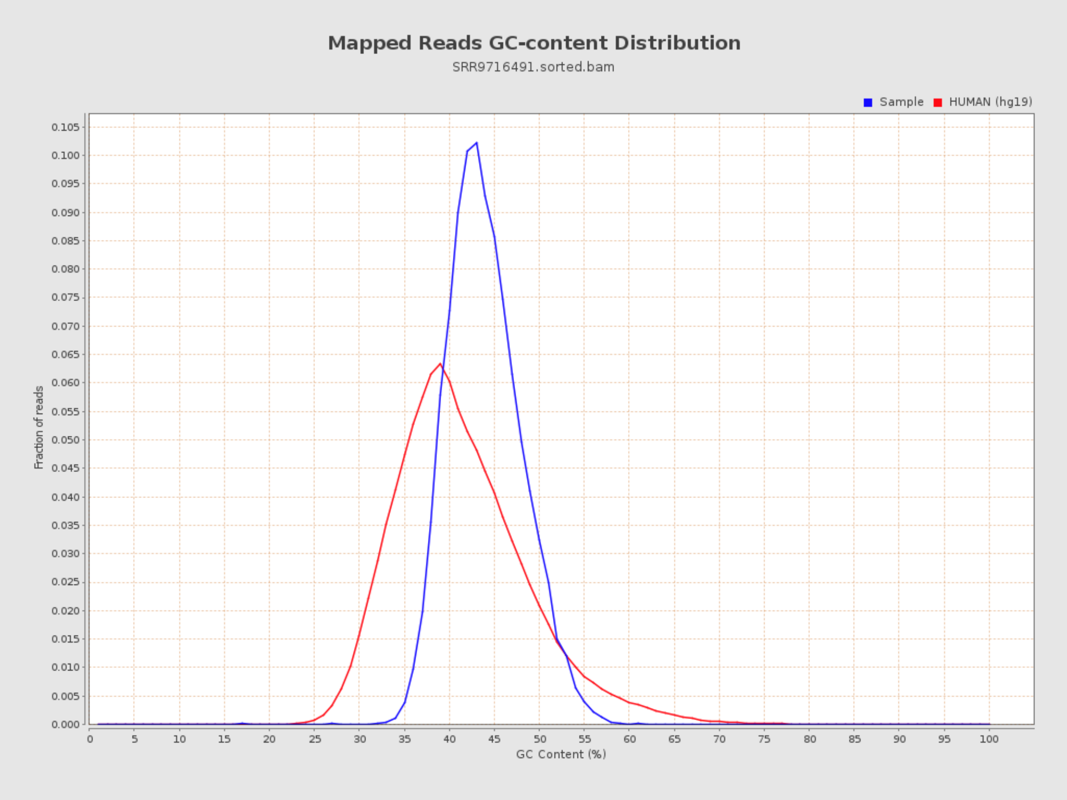
7. Results : Duplication Rate Histogram



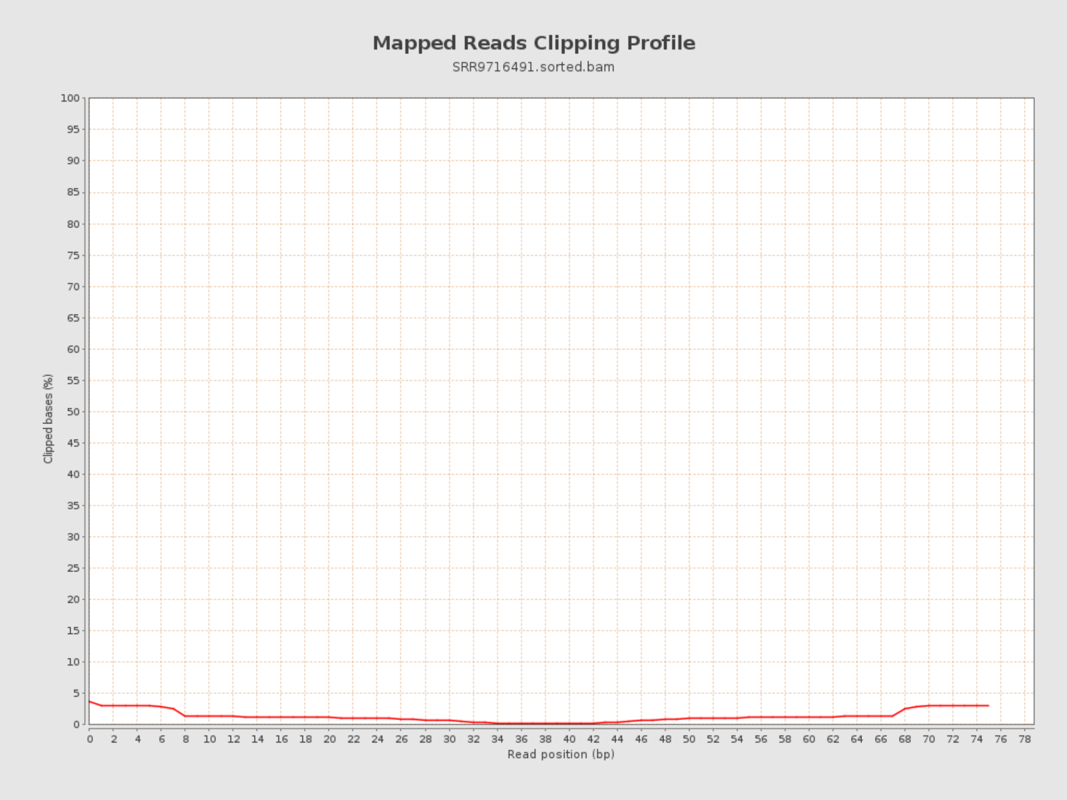
8. Results : Mapped Reads Nucleotide Content



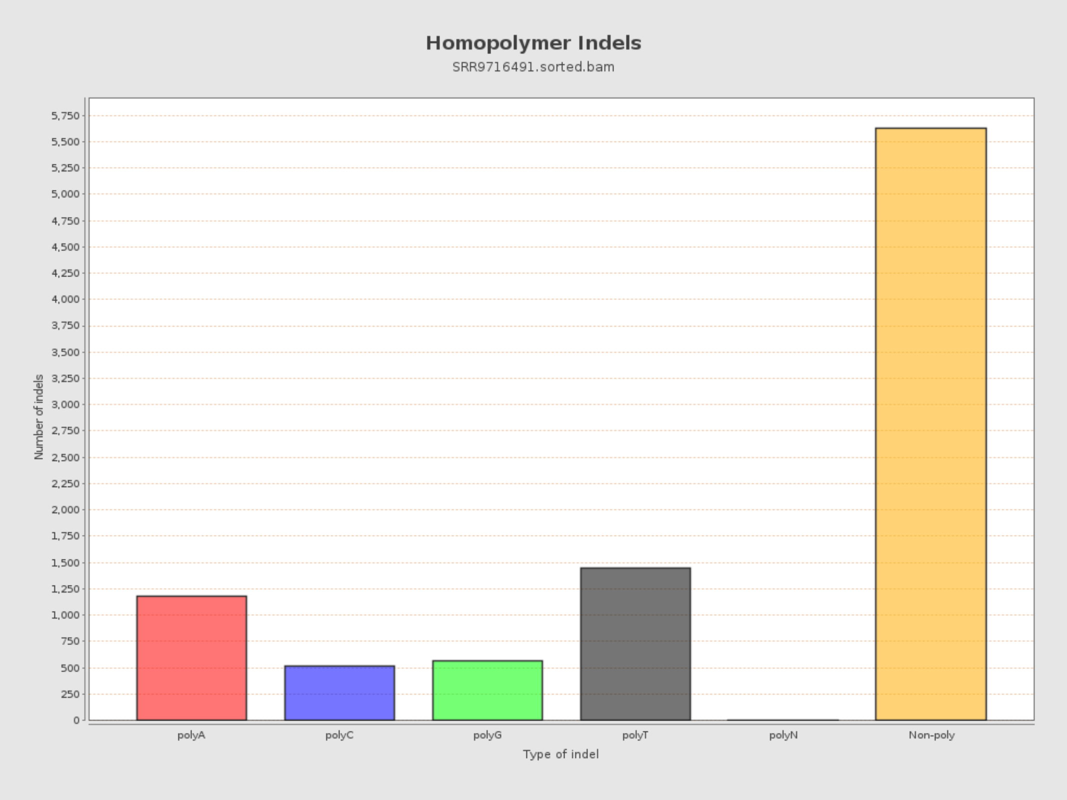
9. Results : Mapped Reads GC-content Distribution



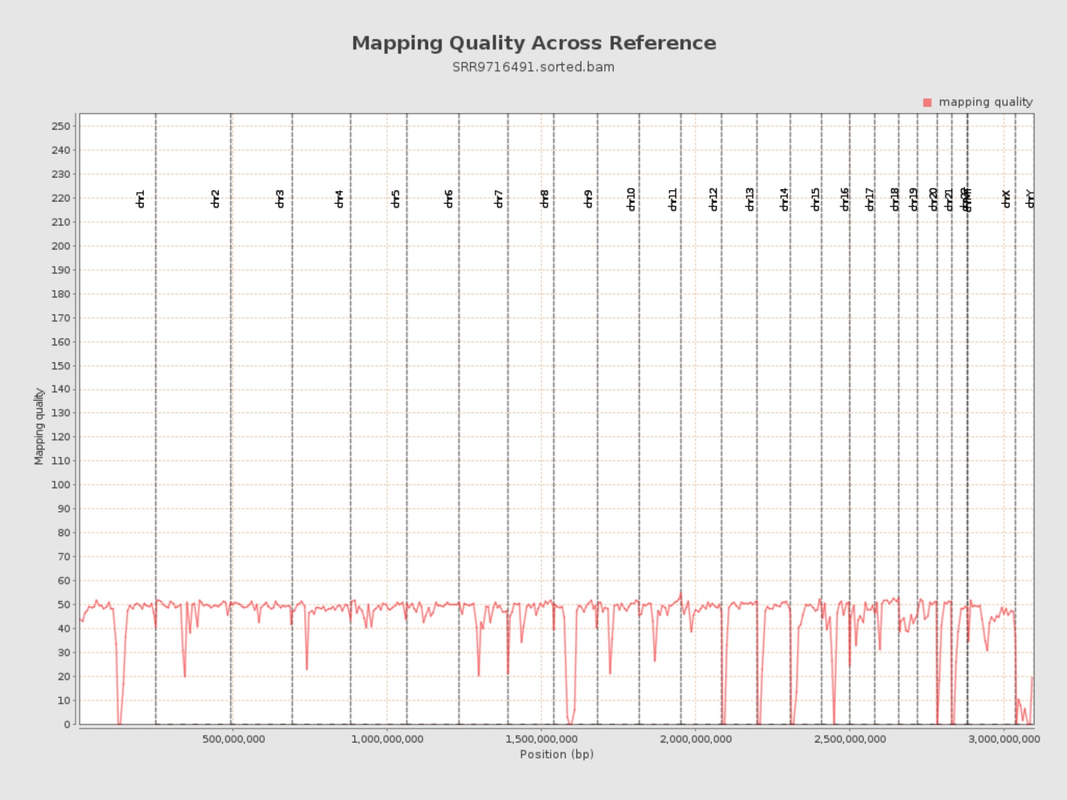
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram