Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:17:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716413.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_SRR9716413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716413.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:17:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	849,261
Mapped reads	719,271 / 84.69%
Unmapped reads	129,990 / 15.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,107 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	16,131 / 1.9%
Duplication rate	1.73%
Clipped reads	720,527 / 84.84%

2.2. ACGT Content

Number/percentage of A's	10,763,643 / 26.19%
Number/percentage of C's	7,864,482 / 19.14%
Number/percentage of T's	12,406,980 / 30.19%
Number/percentage of G's	10,055,555 / 24.47%
Number/percentage of N's	653 / 0%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1432

2.4. Mapping Quality

Mean Mapping Quality	43.8

2.5. Mismatches and indels

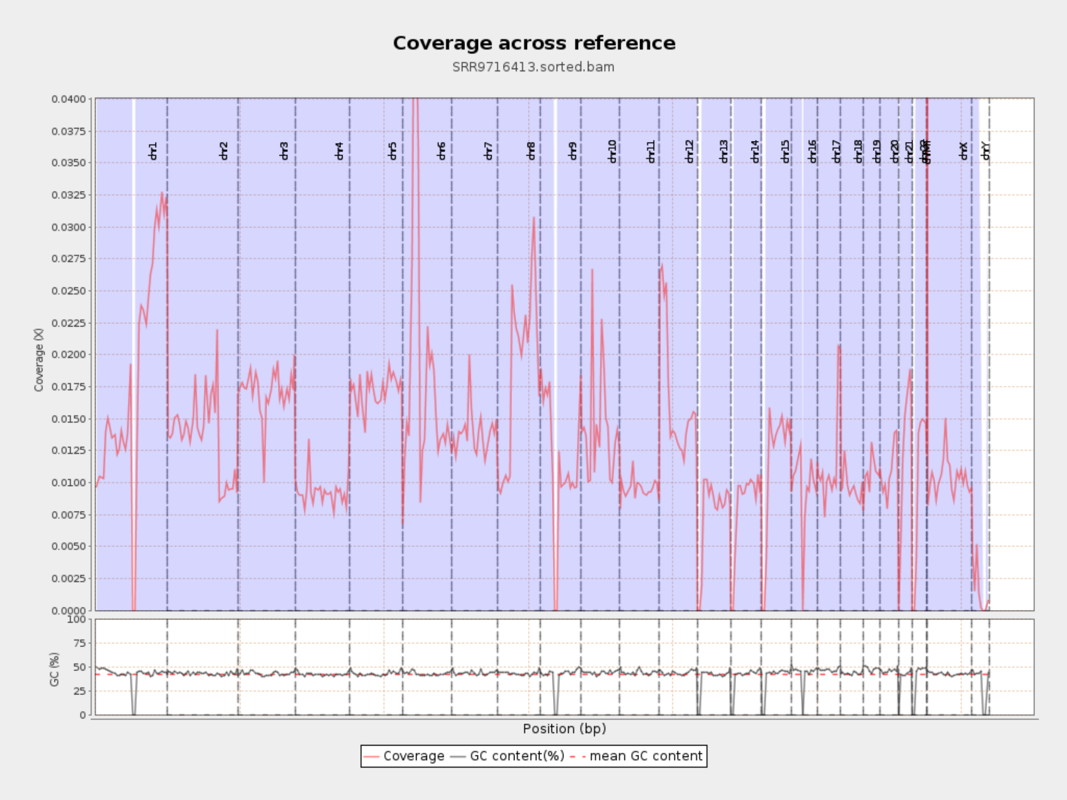
General error rate	0.51%
Mismatches	202,464
Insertions	3,041
Mapped reads with at least one insertion	0.42%
Deletions	6,960
Mapped reads with at least one deletion	0.96%
Homopolymer indels	39.99%

2.6. Chromosome stats

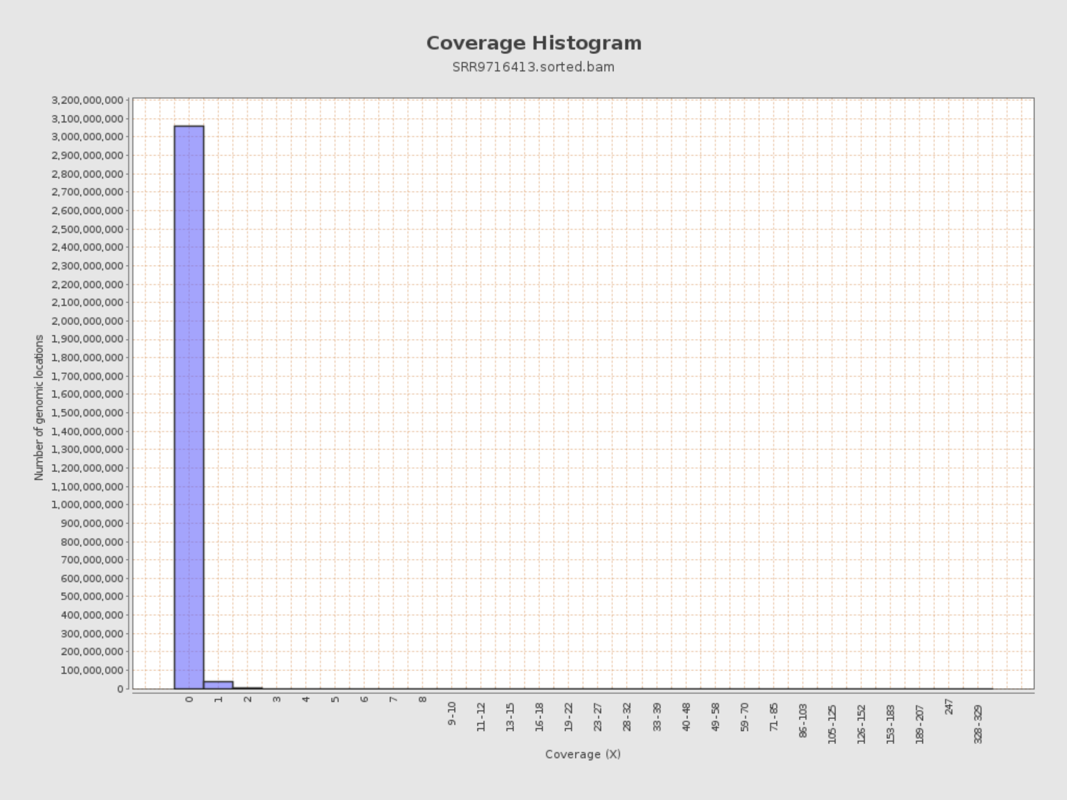
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4534066	0.0182	0.2012
chr2	243199373	3315650	0.0136	0.18
chr3	198022430	3392148	0.0171	0.1372
chr4	191154276	1775746	0.0093	0.1045
chr5	180915260	3123630	0.0173	0.138
chr6	171115067	3259474	0.019	0.1716
chr7	159138663	2226447	0.014	0.1695

chr8	146364022	2754273	0.0188	0.1499
chr9	141213431	1614657	0.0114	0.1301
chr10	135534747	1956639	0.0144	0.1525
chr11	135006516	1298816	0.0096	0.115
chr12	133851895	2246162	0.0168	0.1374
chr13	115169878	869880	0.0076	0.0913
chr14	107349540	867433	0.0081	0.1023
chr15	102531392	1174355	0.0115	0.1134
chr16	90354753	853714	0.0094	0.1078
chr17	81195210	931931	0.0115	0.1136
chr18	78077248	749709	0.0096	0.1799
chr19	59128983	642362	0.0109	0.1477
chr20	63025520	683087	0.0108	0.1099
chr21	48129895	609189	0.0127	0.1204
chr22	51304566	506293	0.0099	0.1046
chrMT	16571	2438	0.1471	0.4003
chrX	155270560	1620441	0.0104	0.114
chrY	59373566	93625	0.0016	0.0495

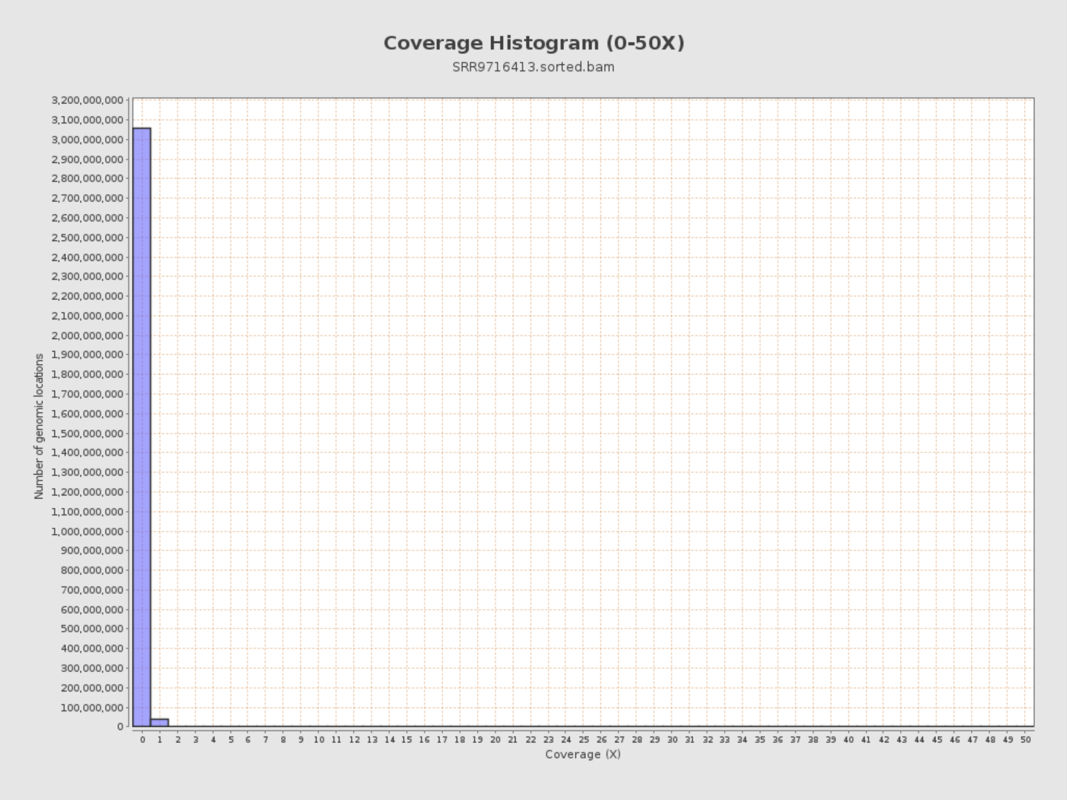
3. Results : Coverage across reference



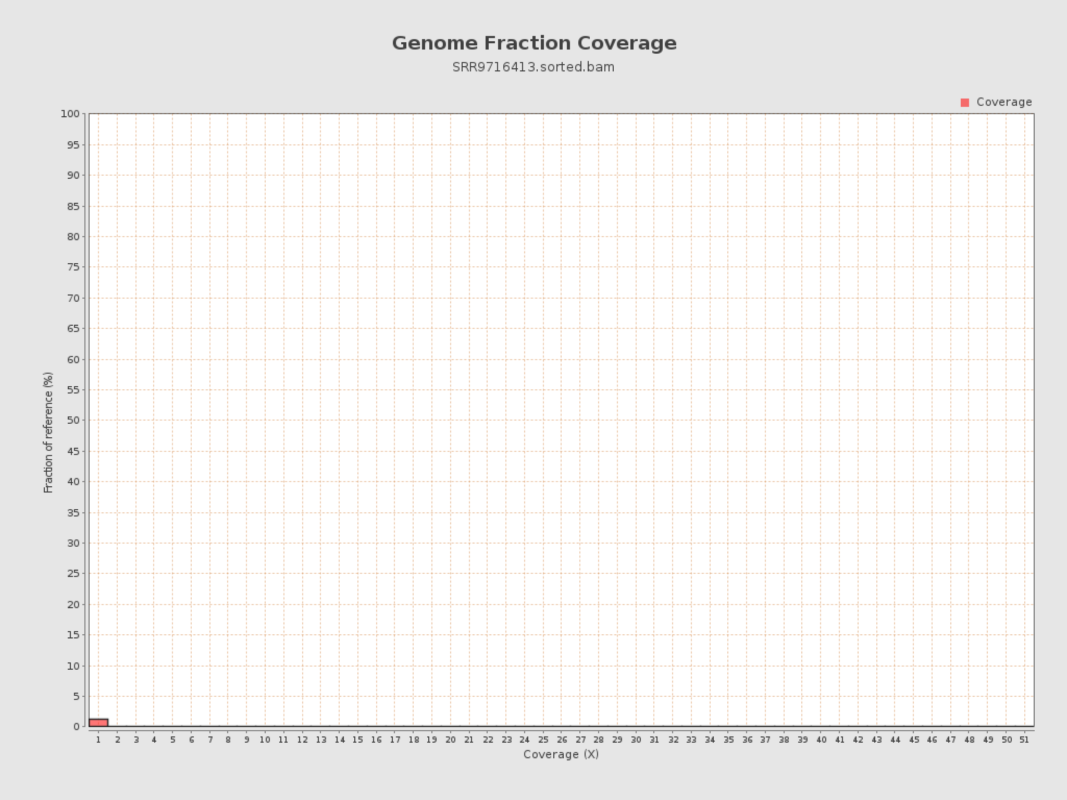
4. Results : Coverage Histogram



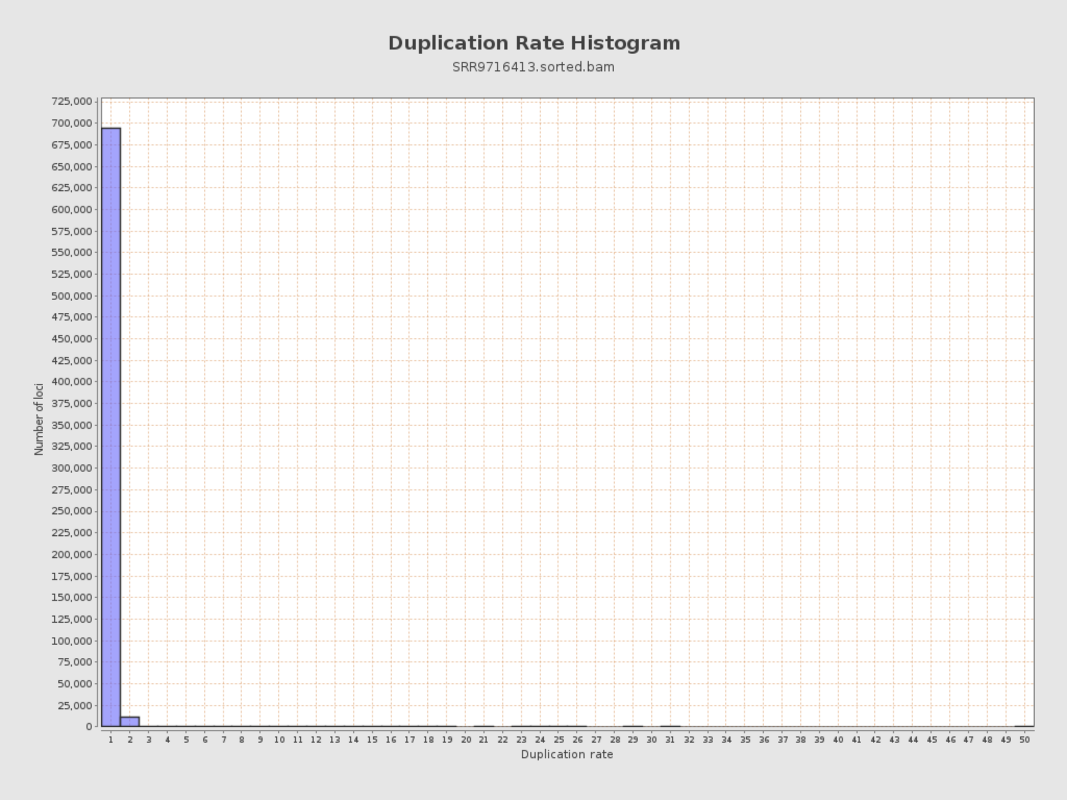
5. Results : Coverage Histogram (0-50X)



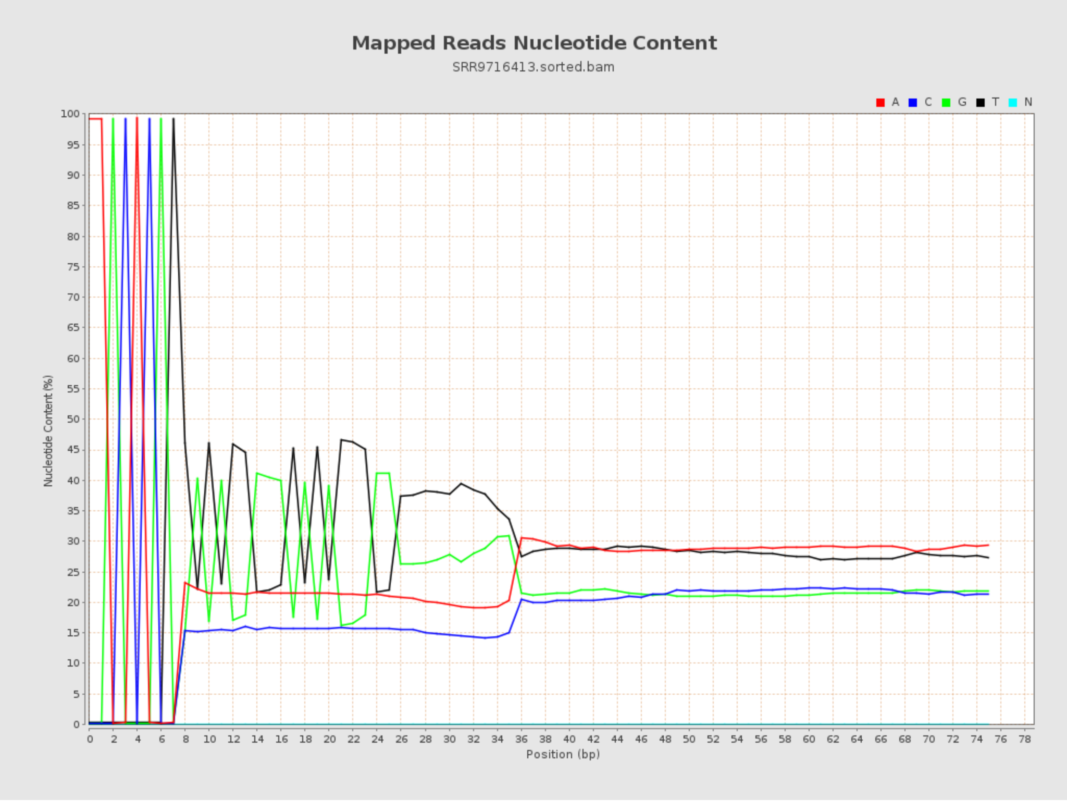
6. Results : Genome Fraction Coverage



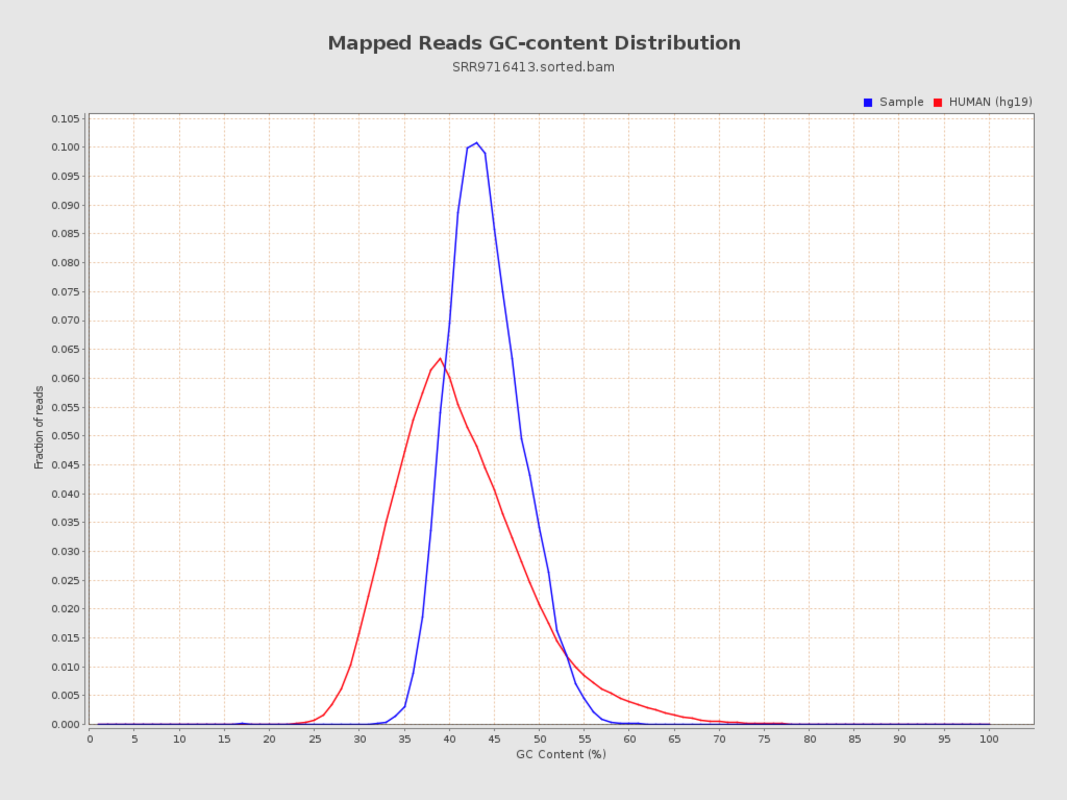
7. Results : Duplication Rate Histogram



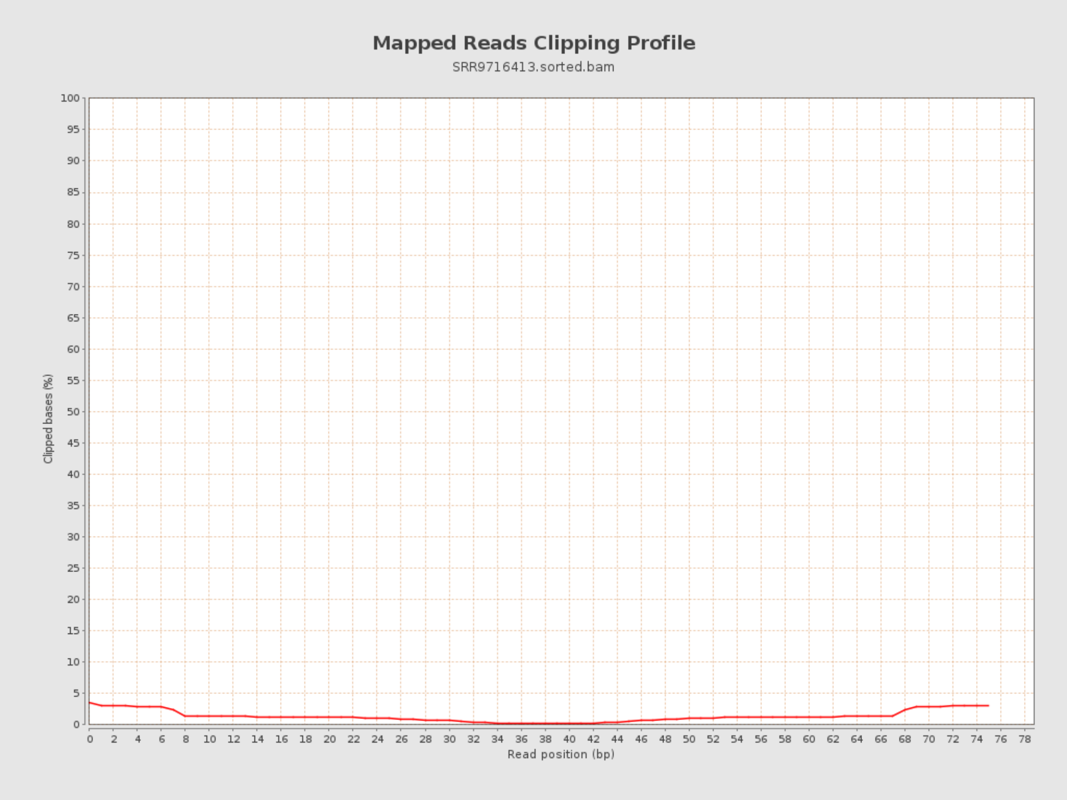
8. Results : Mapped Reads Nucleotide Content



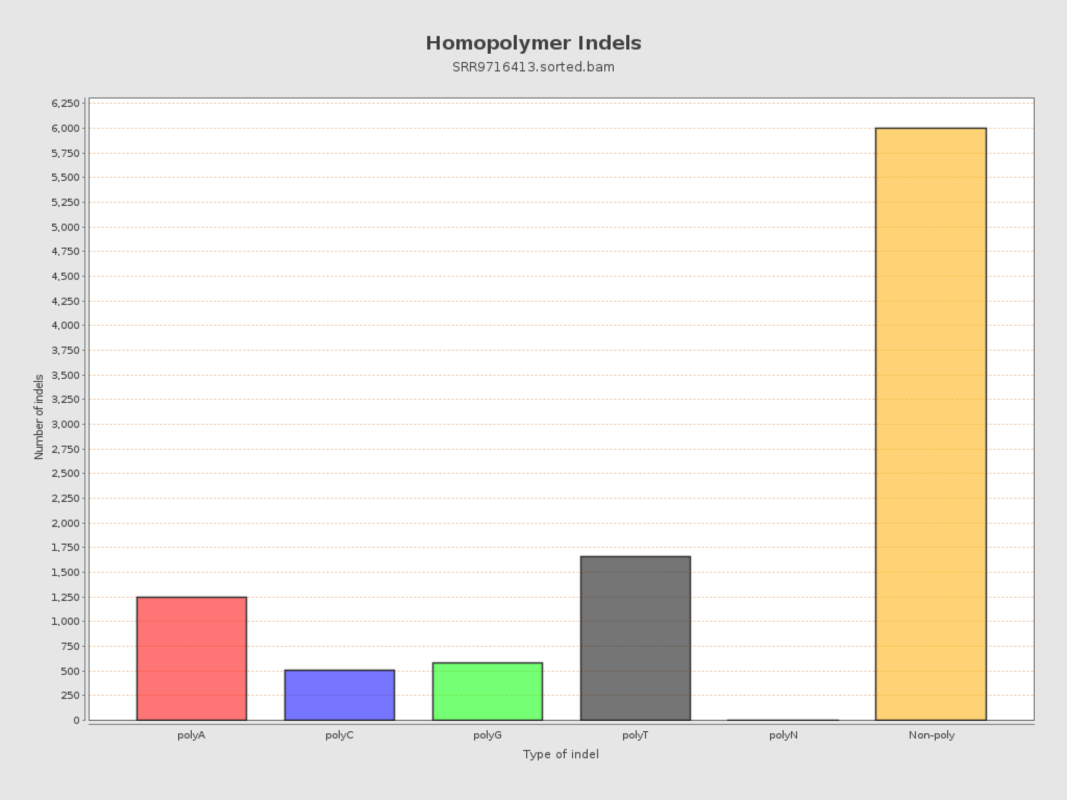
9. Results : Mapped Reads GC-content Distribution



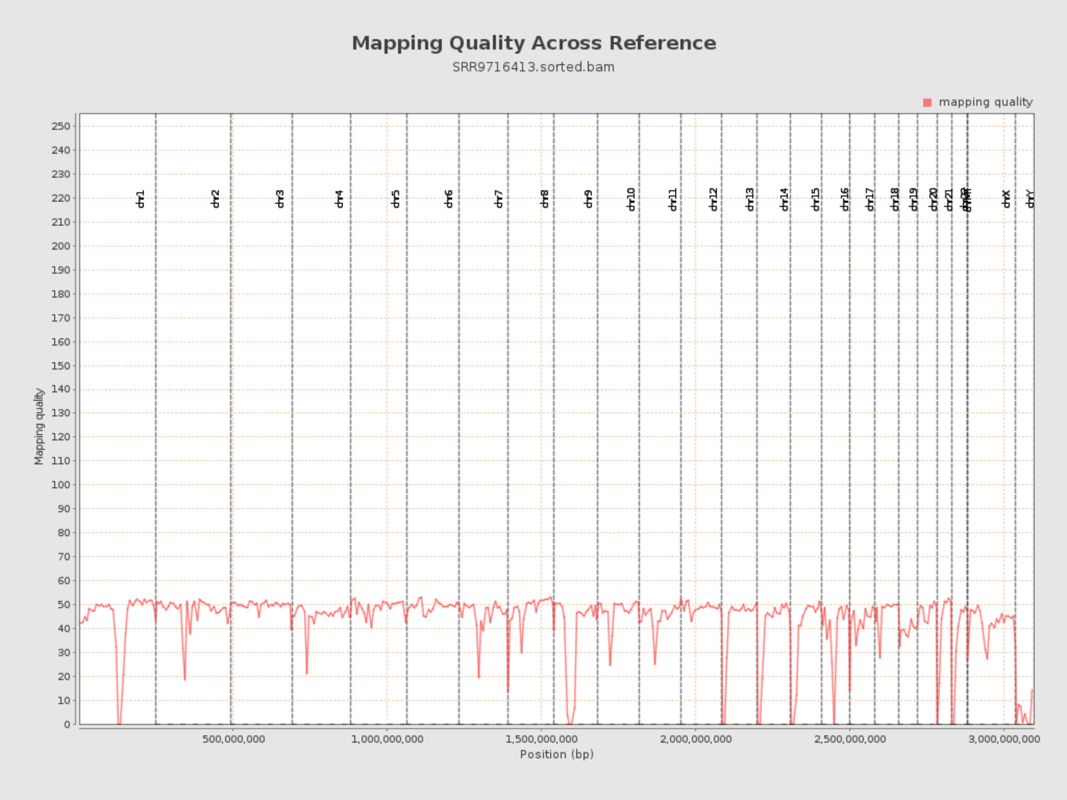
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram