Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:50:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716474.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_SRR9716474 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716474.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:50:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716474.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	714,619
Mapped reads	635,112 / 88.87%
Unmapped reads	79,507 / 11.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,211 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	16,327 / 2.28%
Duplication rate	1.98%
Clipped reads	636,562 / 89.08%

2.2. ACGT Content

Number/percentage of A's	9,464,802 / 25.65%
Number/percentage of C's	6,722,304 / 18.22%
Number/percentage of T's	11,423,607 / 30.96%
Number/percentage of G's	9,288,152 / 25.17%
Number/percentage of N's	274 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.1401

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

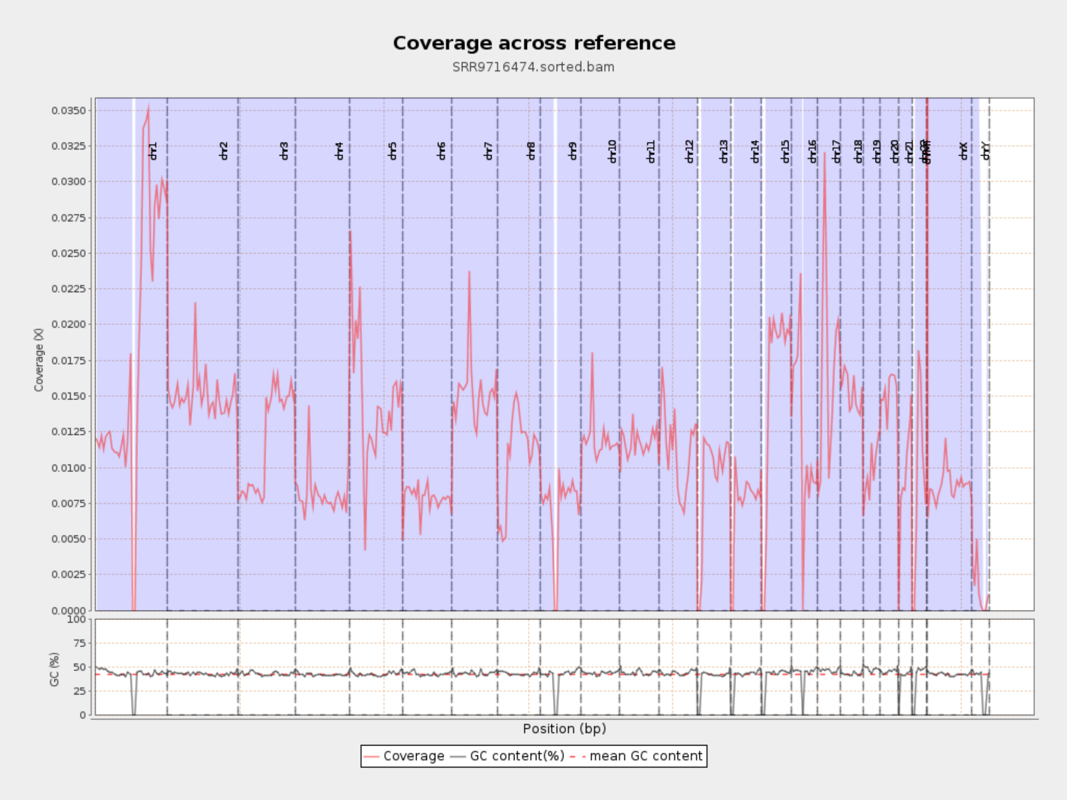
General error rate	0.51%
Mismatches	184,731
Insertions	2,480
Mapped reads with at least one insertion	0.39%
Deletions	6,523
Mapped reads with at least one deletion	1.02%
Homopolymer indels	41.97%

2.6. Chromosome stats

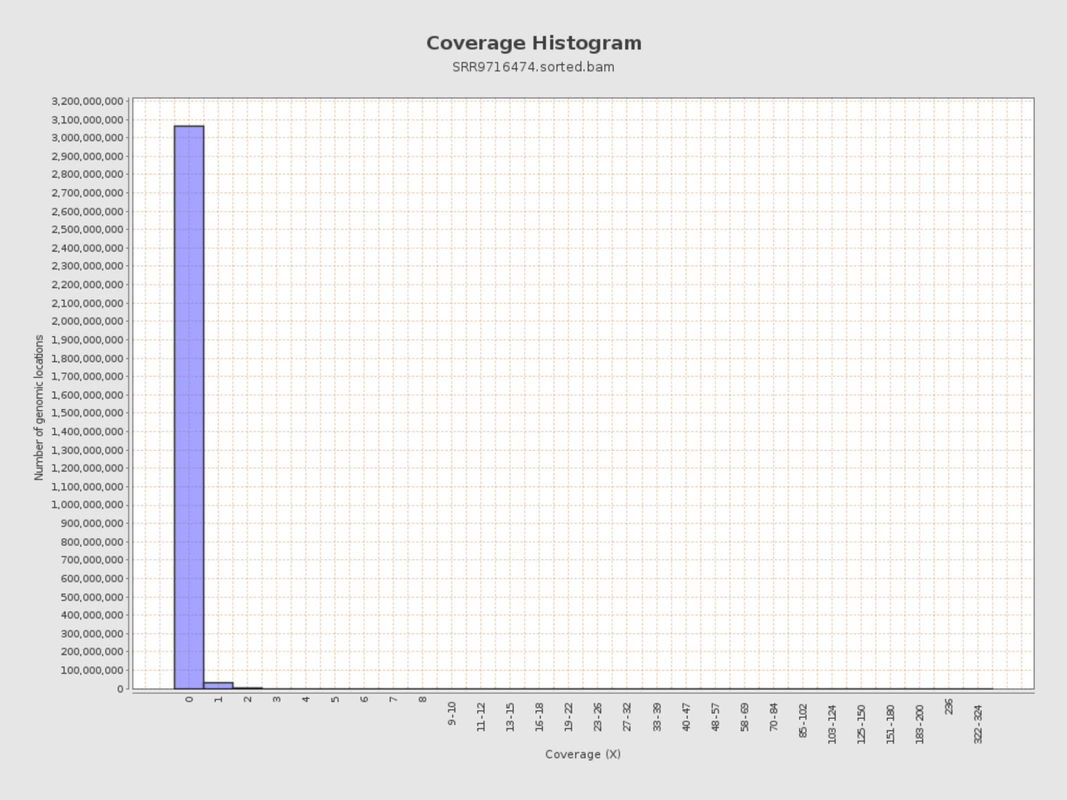
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4477829	0.018	0.2053
chr2	243199373	3658269	0.015	0.1878
chr3	198022430	2338970	0.0118	0.1141
chr4	191154276	1555872	0.0081	0.1024
chr5	180915260	2633050	0.0146	0.1269
chr6	171115067	1341671	0.0078	0.0971
chr7	159138663	2443235	0.0154	0.1928

chr8	146364022	1598550	0.0109	0.126
chr9	141213431	1014748	0.0072	0.1077
chr10	135534747	1631986	0.012	0.1308
chr11	135006516	1598443	0.0118	0.1378
chr12	133851895	1502635	0.0112	0.1117
chr13	115169878	1051091	0.0091	0.1002
chr14	107349540	786066	0.0073	0.0913
chr15	102531392	1617708	0.0158	0.1329
chr16	90354753	1073813	0.0119	0.1178
chr17	81195210	1409069	0.0174	0.143
chr18	78077248	1187073	0.0152	0.2133
chr19	59128983	583525	0.0099	0.1542
chr20	63025520	958753	0.0152	0.1303
chr21	48129895	456081	0.0095	0.1066
chr22	51304566	477011	0.0093	0.1015
chrMT	16571	61625	3.7188	2.8831
chrX	155270560	1363167	0.0088	0.1051
chrY	59373566	89216	0.0015	0.0544

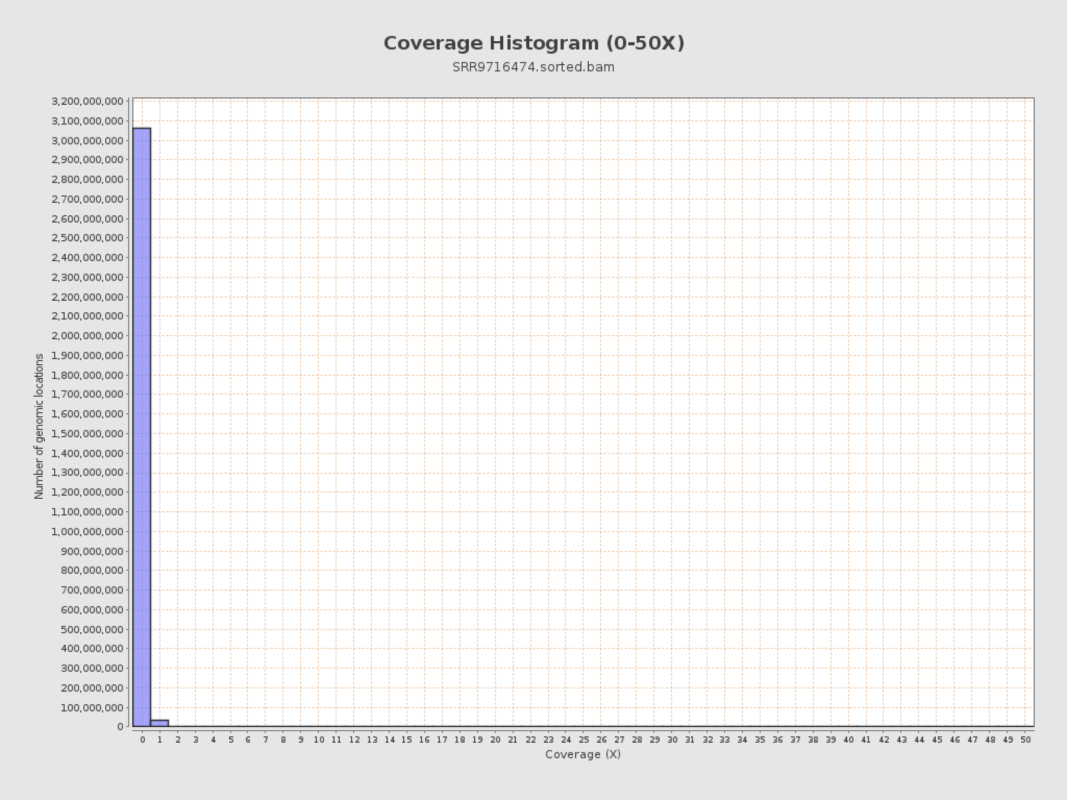
3. Results : Coverage across reference



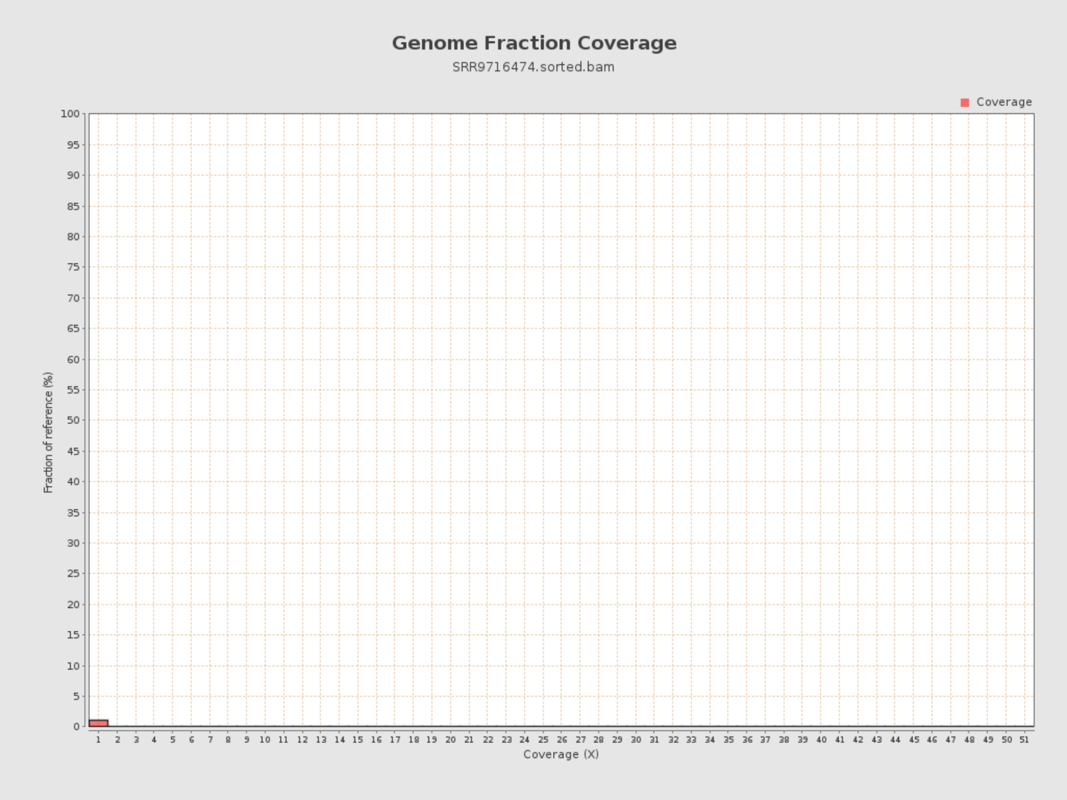
4. Results : Coverage Histogram



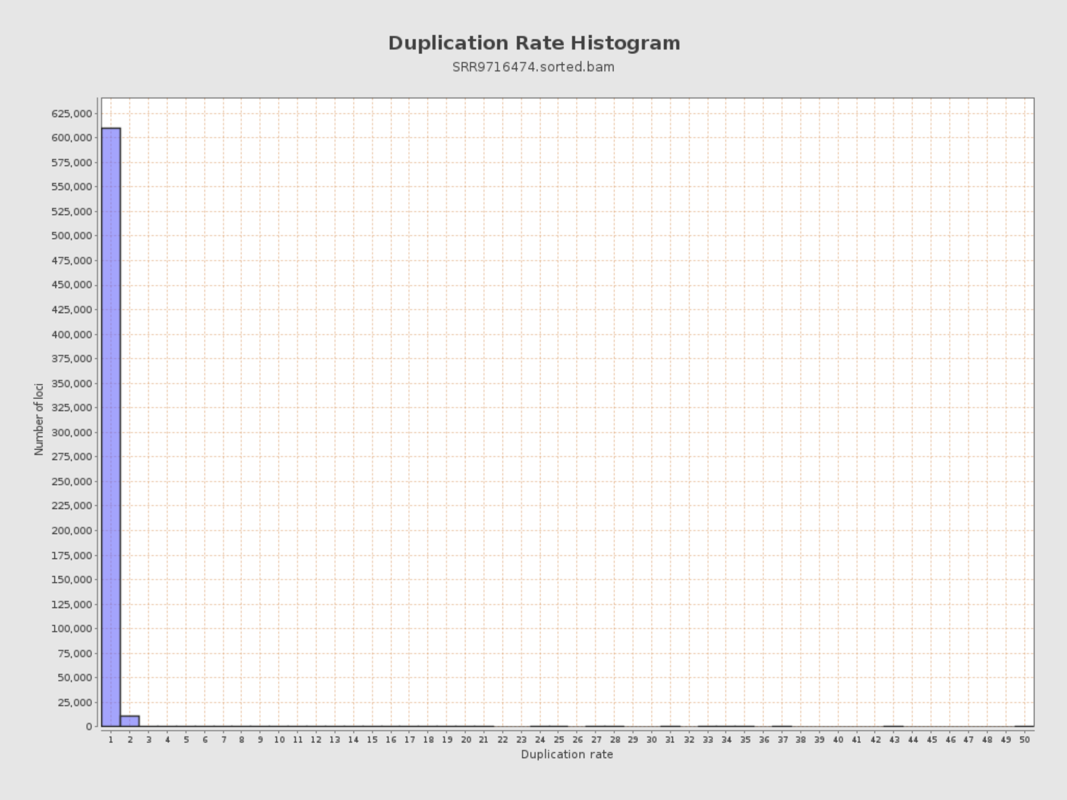
5. Results : Coverage Histogram (0-50X)



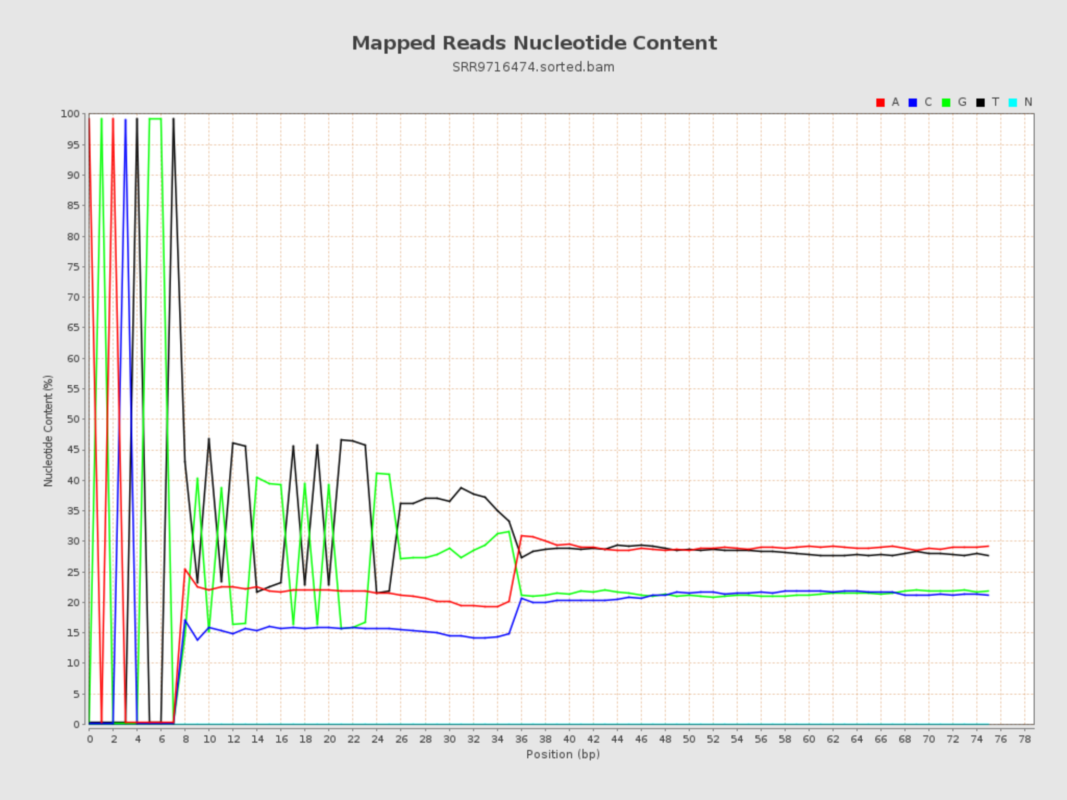
6. Results : Genome Fraction Coverage



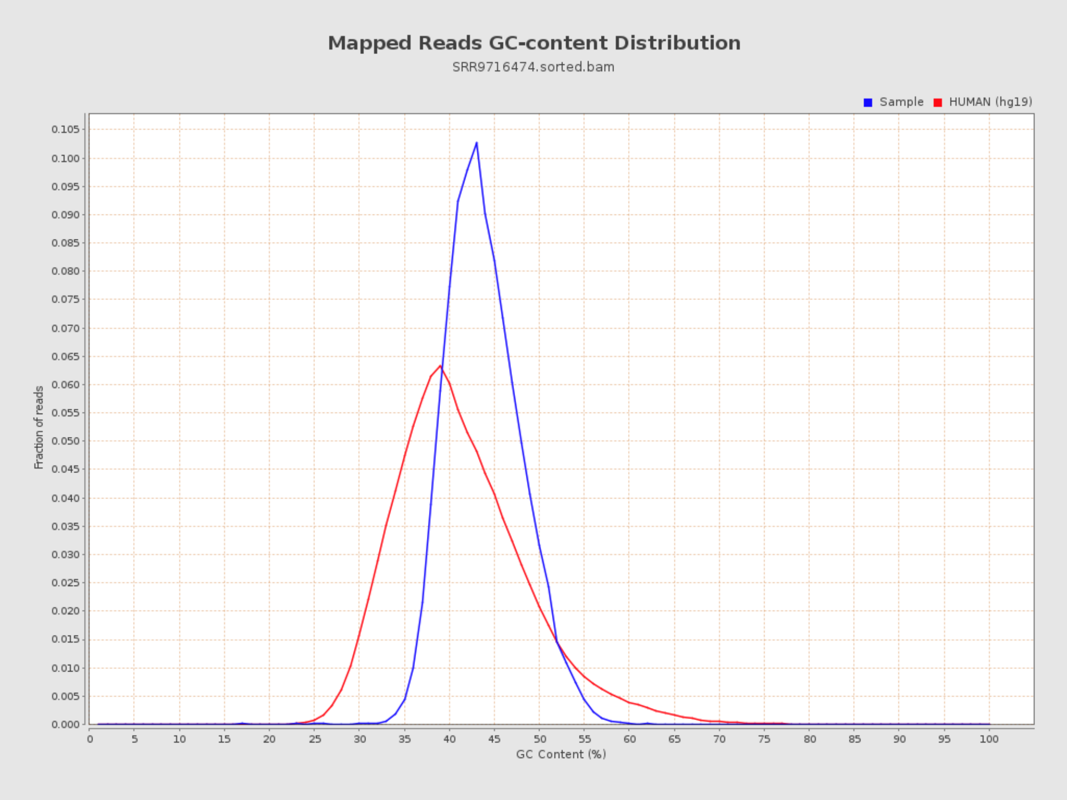
7. Results : Duplication Rate Histogram



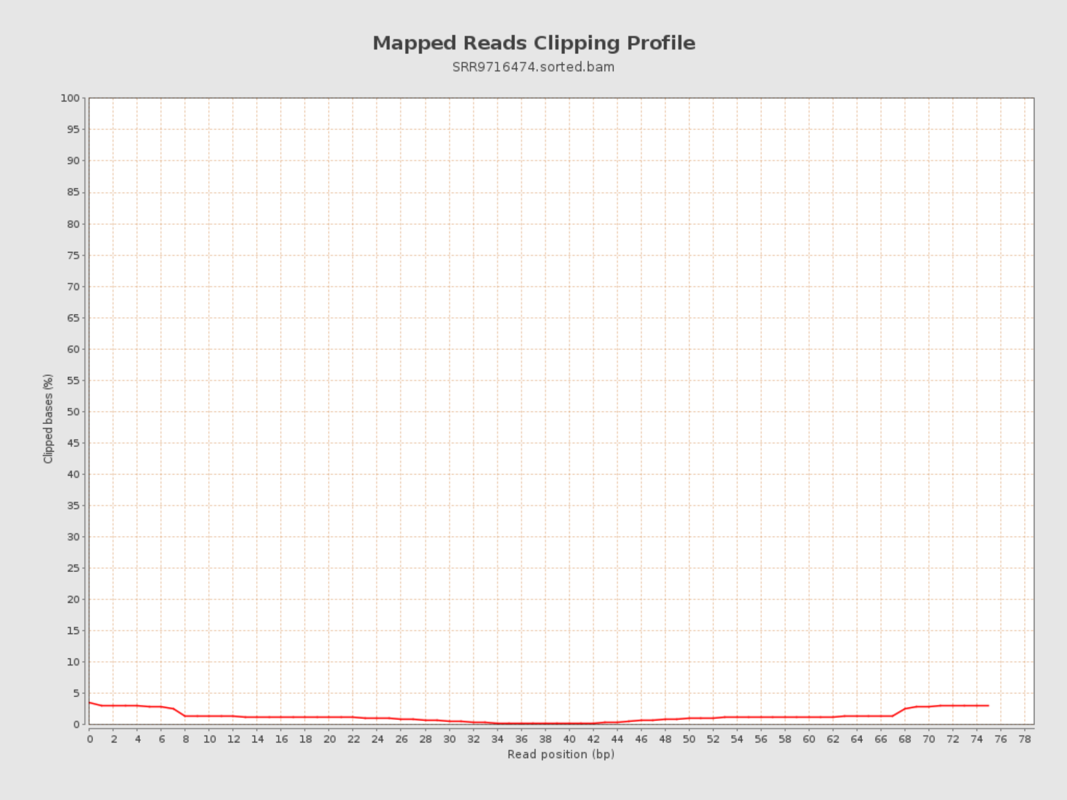
8. Results : Mapped Reads Nucleotide Content



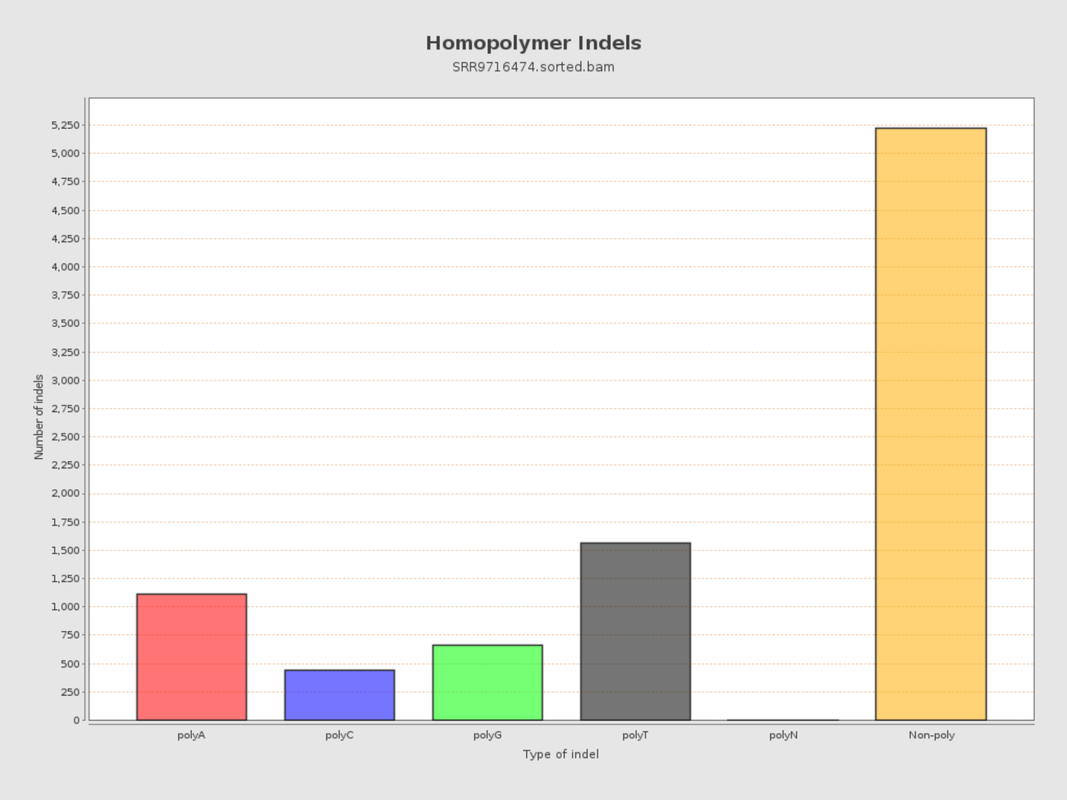
9. Results : Mapped Reads GC-content Distribution



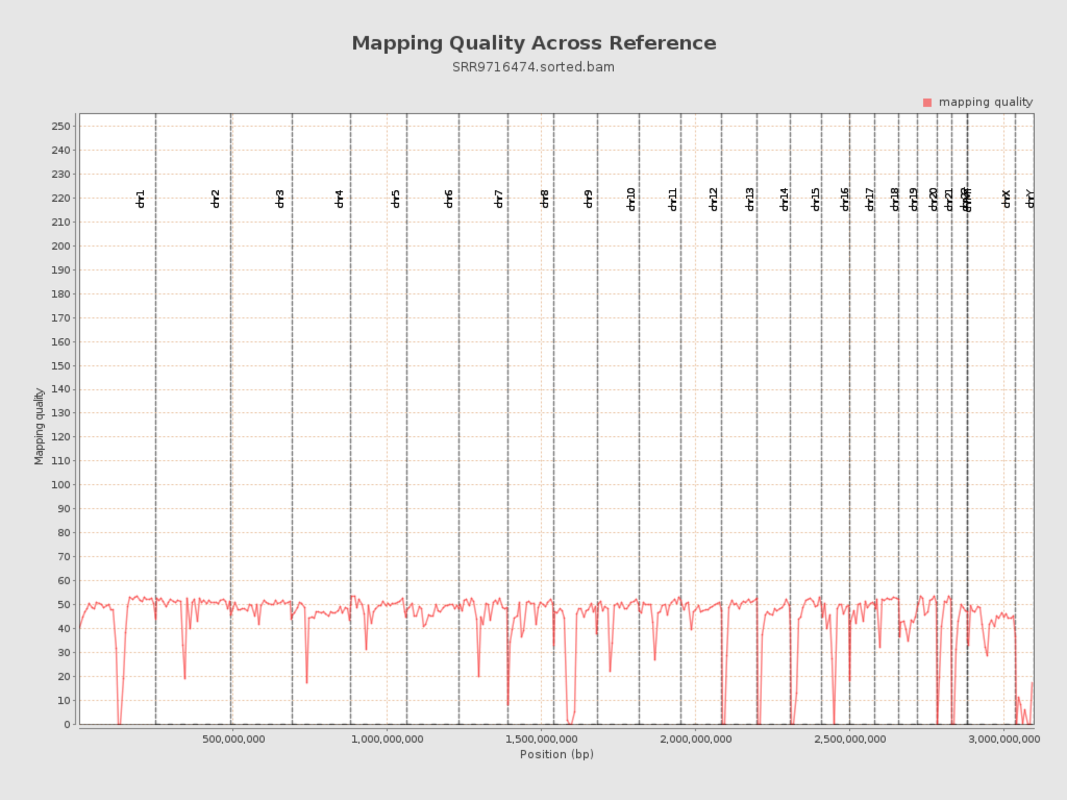
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram