Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:19:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716414.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_SRR9716414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716414.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:19:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	994,065
Mapped reads	822,344 / 82.73%
Unmapped reads	171,721 / 17.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,247 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	18,079 / 1.82%
Duplication rate	1.6%
Clipped reads	824,168 / 82.91%

2.2. ACGT Content

Number/percentage of A's	12,176,644 / 25.3%
Number/percentage of C's	8,546,700 / 17.76%
Number/percentage of T's	15,081,314 / 31.33%
Number/percentage of G's	12,328,019 / 25.61%
Number/percentage of N's	701 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0156

Standard Deviation	0.1655

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

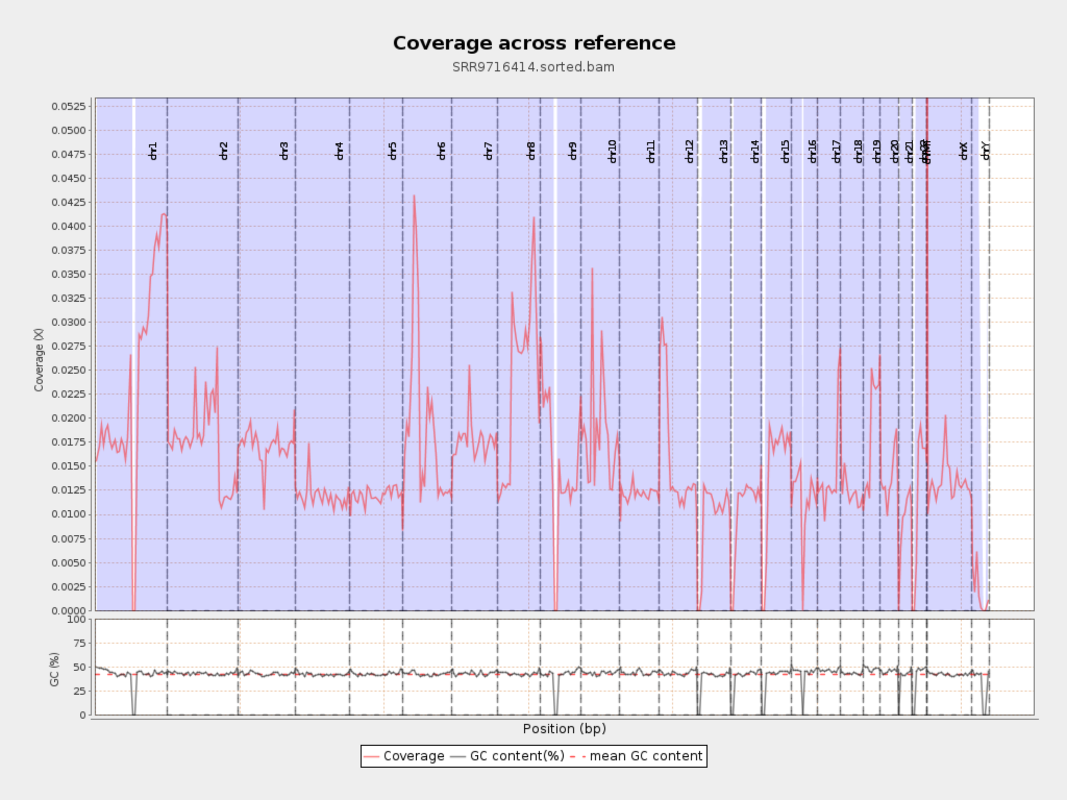
General error rate	0.5%
Mismatches	234,084
Insertions	3,254
Mapped reads with at least one insertion	0.39%
Deletions	8,635
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.68%

2.6. Chromosome stats

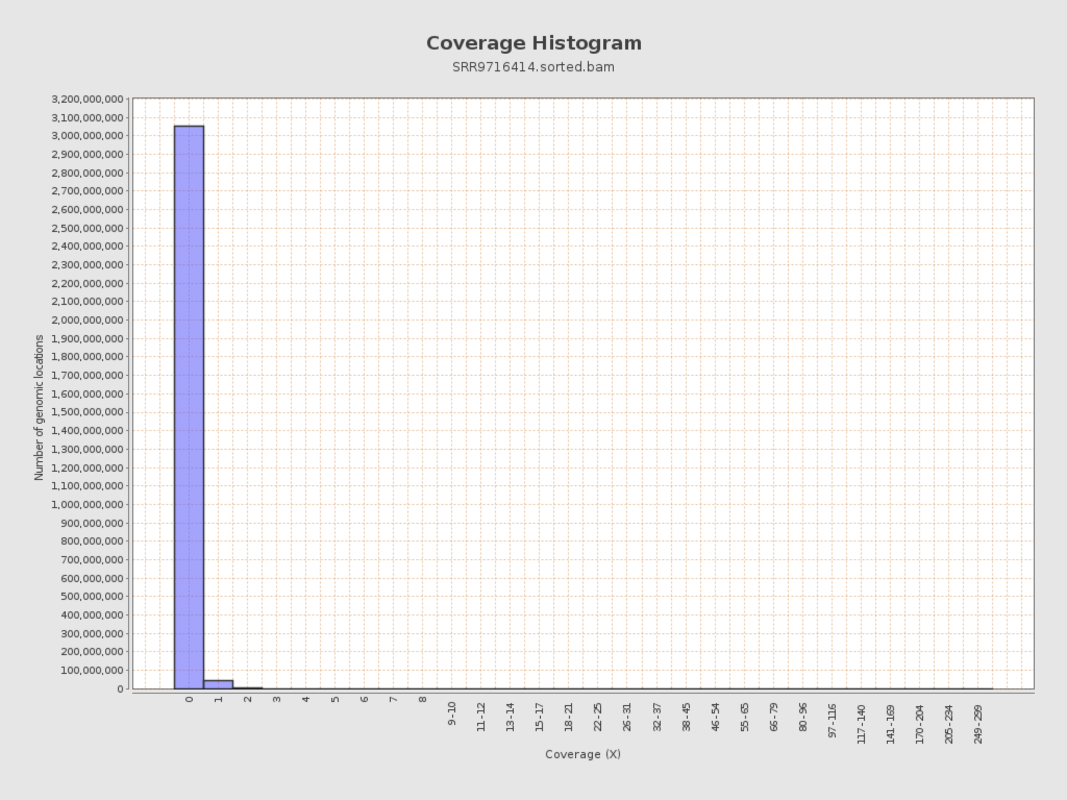
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5929479	0.0238	0.2757
chr2	243199373	4214104	0.0173	0.1904
chr3	198022430	3394916	0.0171	0.139
chr4	191154276	2284554	0.012	0.1196
chr5	180915260	2182880	0.0121	0.1167
chr6	171115067	3252246	0.019	0.1742
chr7	159138663	2839067	0.0178	0.1953

chr8	146364022	3540084	0.0242	0.1727
chr9	141213431	2087815	0.0148	0.1544
chr10	135534747	2524984	0.0186	0.1899
chr11	135006516	1645387	0.0122	0.1424
chr12	133851895	2179115	0.0163	0.136
chr13	115169878	1101570	0.0096	0.1026
chr14	107349540	1104567	0.0103	0.1197
chr15	102531392	1473605	0.0144	0.1261
chr16	90354753	1026053	0.0114	0.1208
chr17	81195210	1157892	0.0143	0.1302
chr18	78077248	953506	0.0122	0.229
chr19	59128983	1113030	0.0188	0.2057
chr20	63025520	875769	0.0139	0.1245
chr21	48129895	448953	0.0093	0.1082
chr22	51304566	618207	0.012	0.1152
chrMT	16571	2527	0.1525	0.4243
chrX	155270560	2087713	0.0134	0.1327
chrY	59373566	109189	0.0018	0.0567

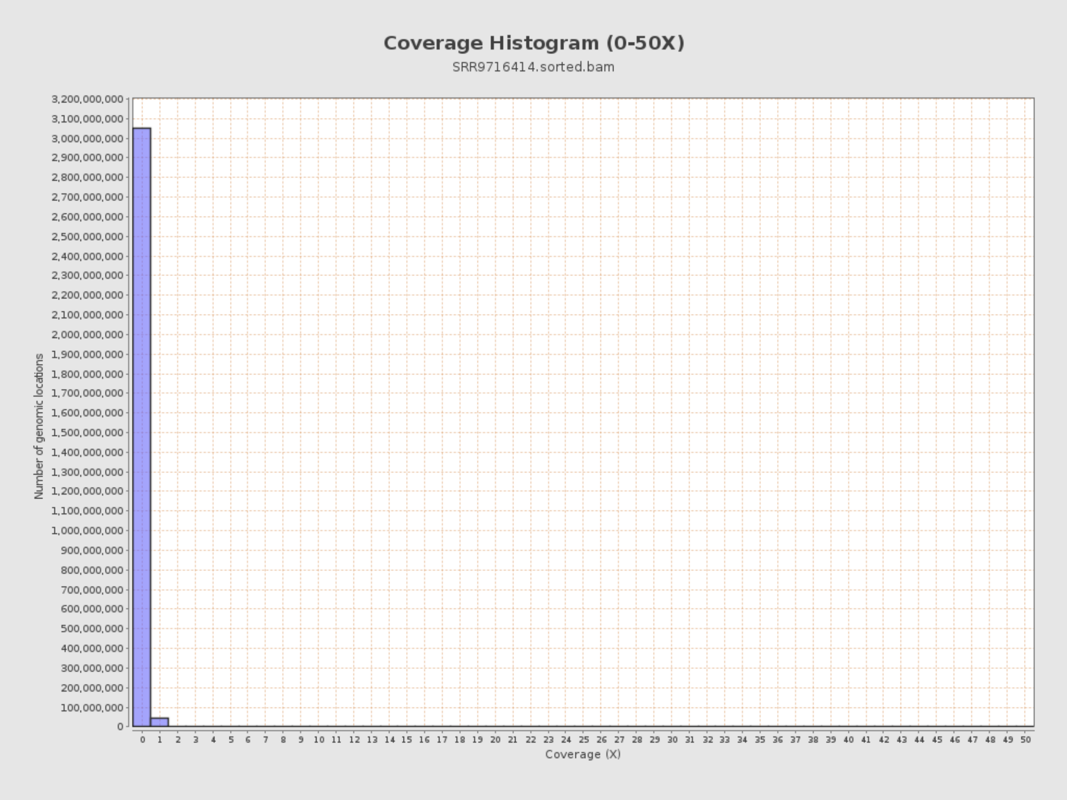
3. Results : Coverage across reference



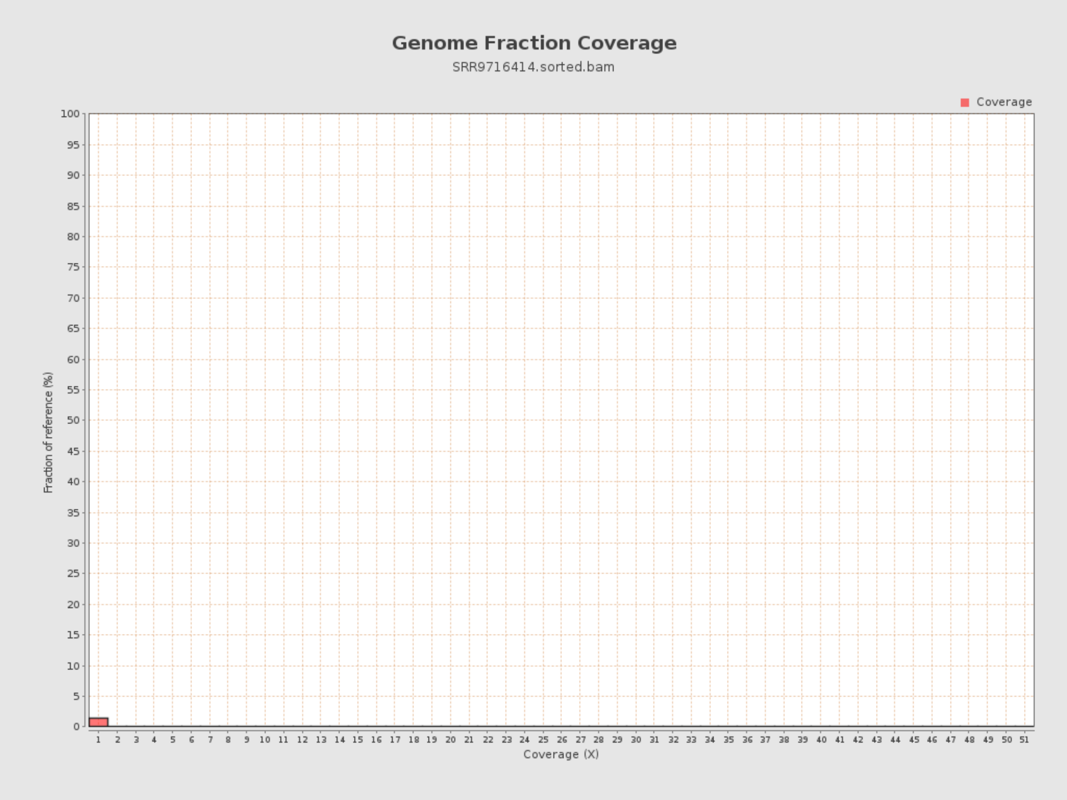
4. Results : Coverage Histogram



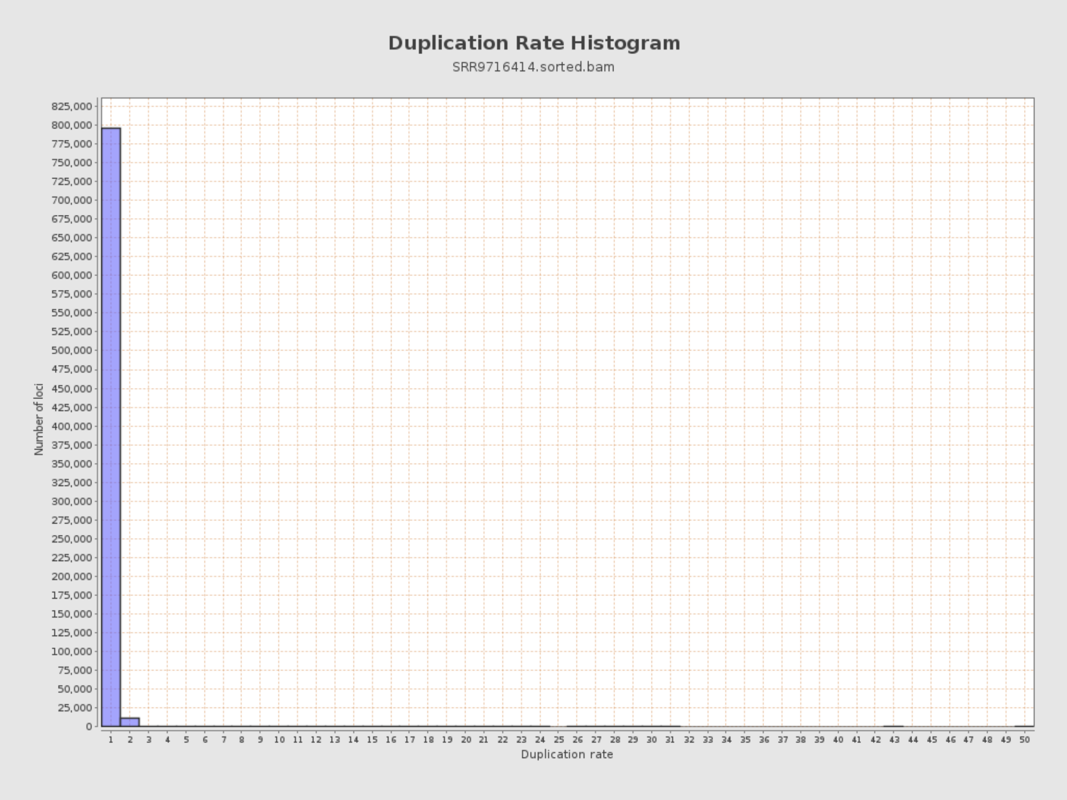
5. Results : Coverage Histogram (0-50X)



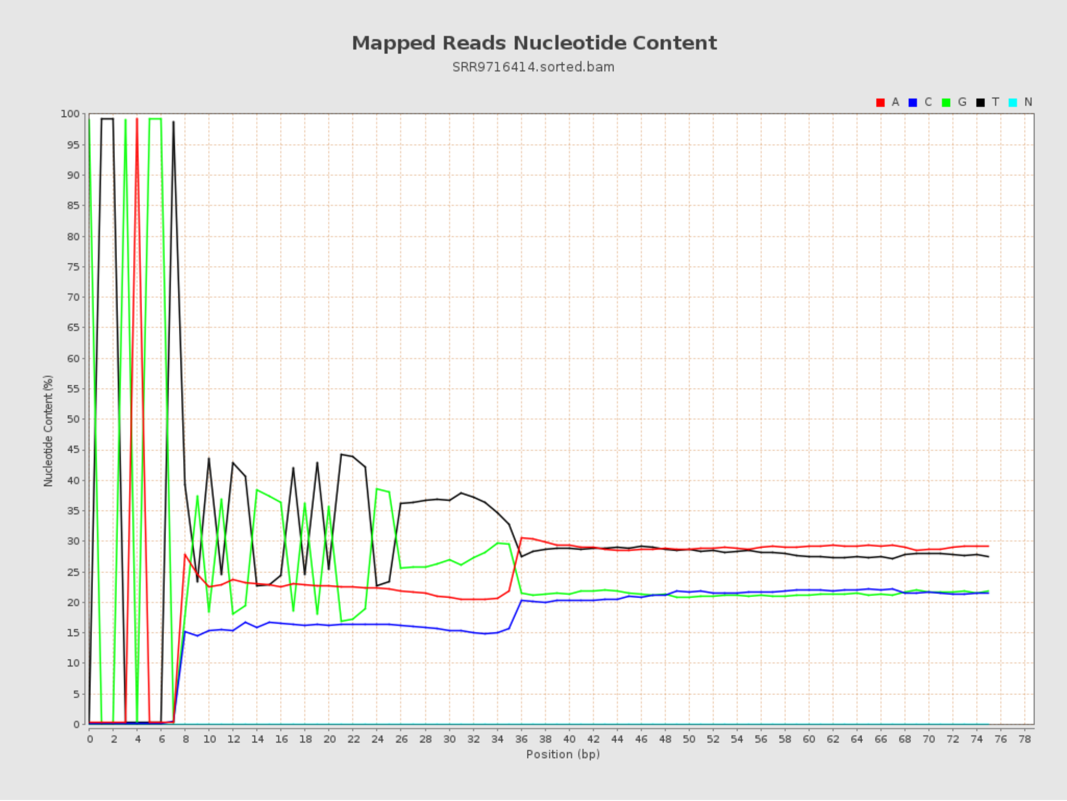
6. Results : Genome Fraction Coverage



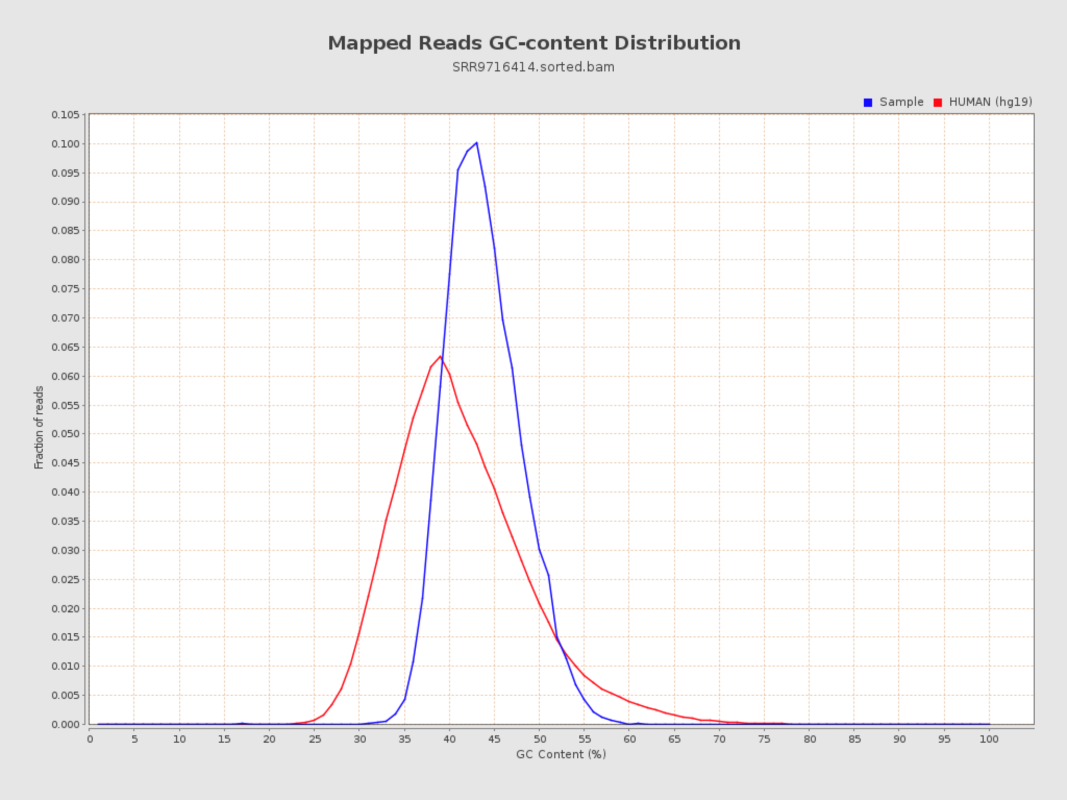
7. Results : Duplication Rate Histogram



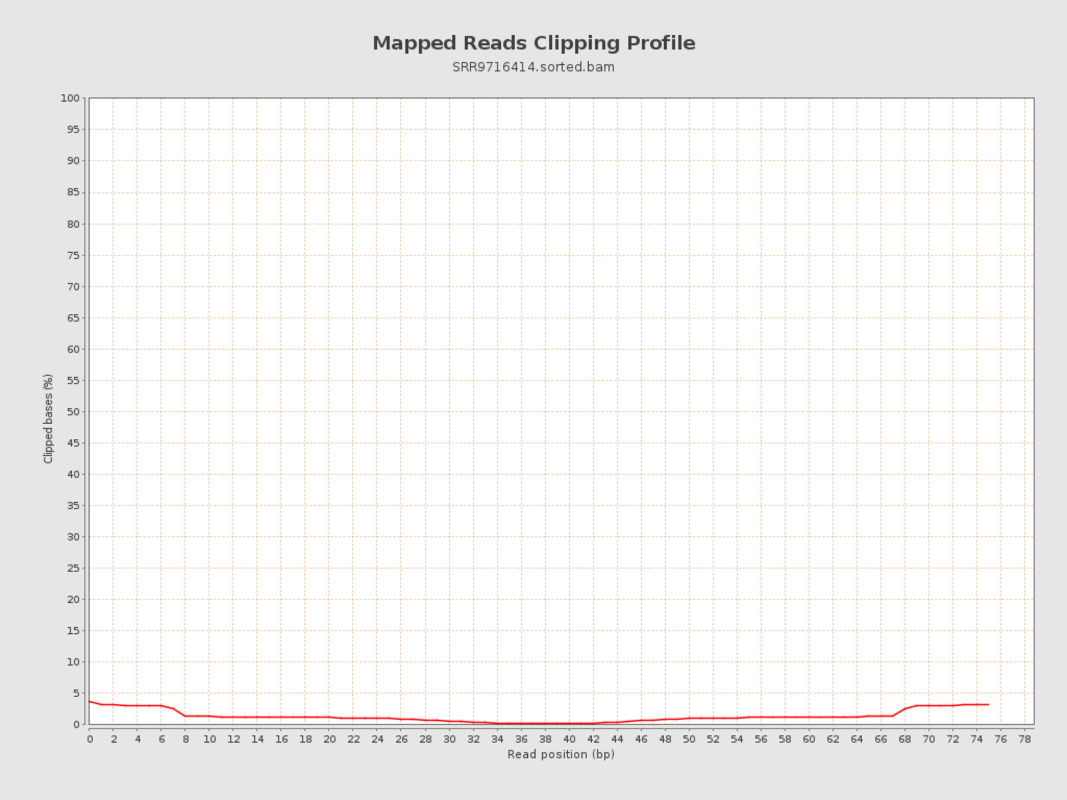
8. Results : Mapped Reads Nucleotide Content



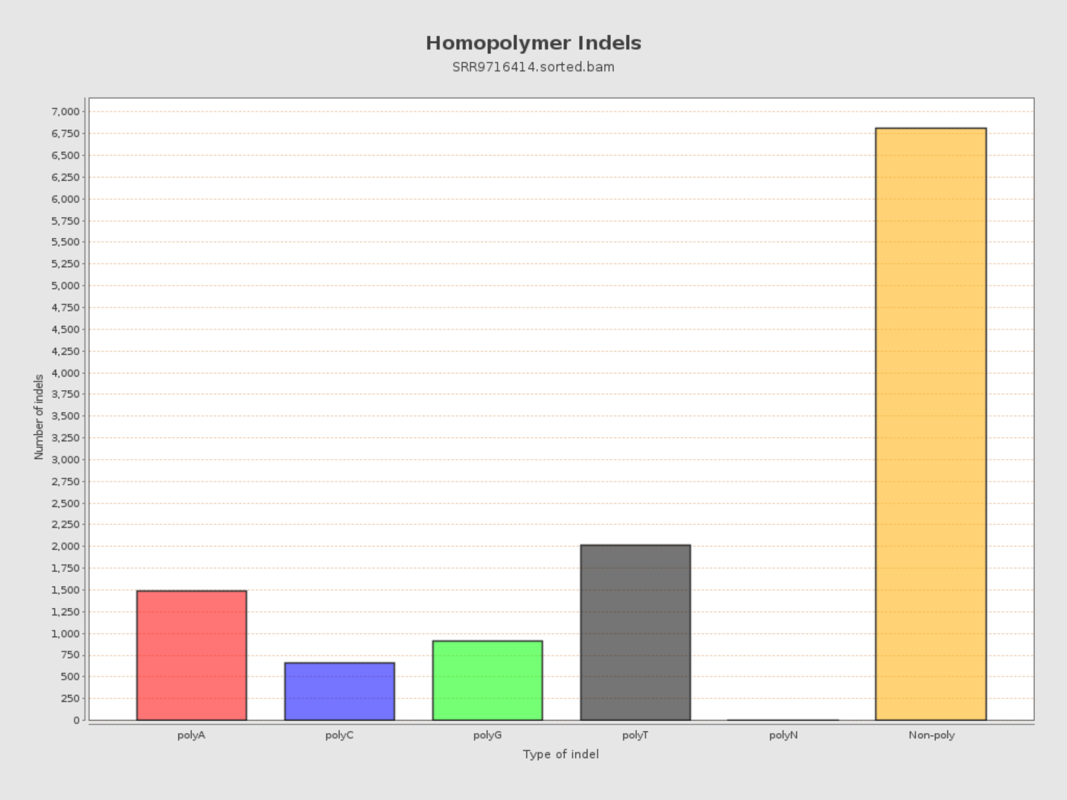
9. Results : Mapped Reads GC-content Distribution



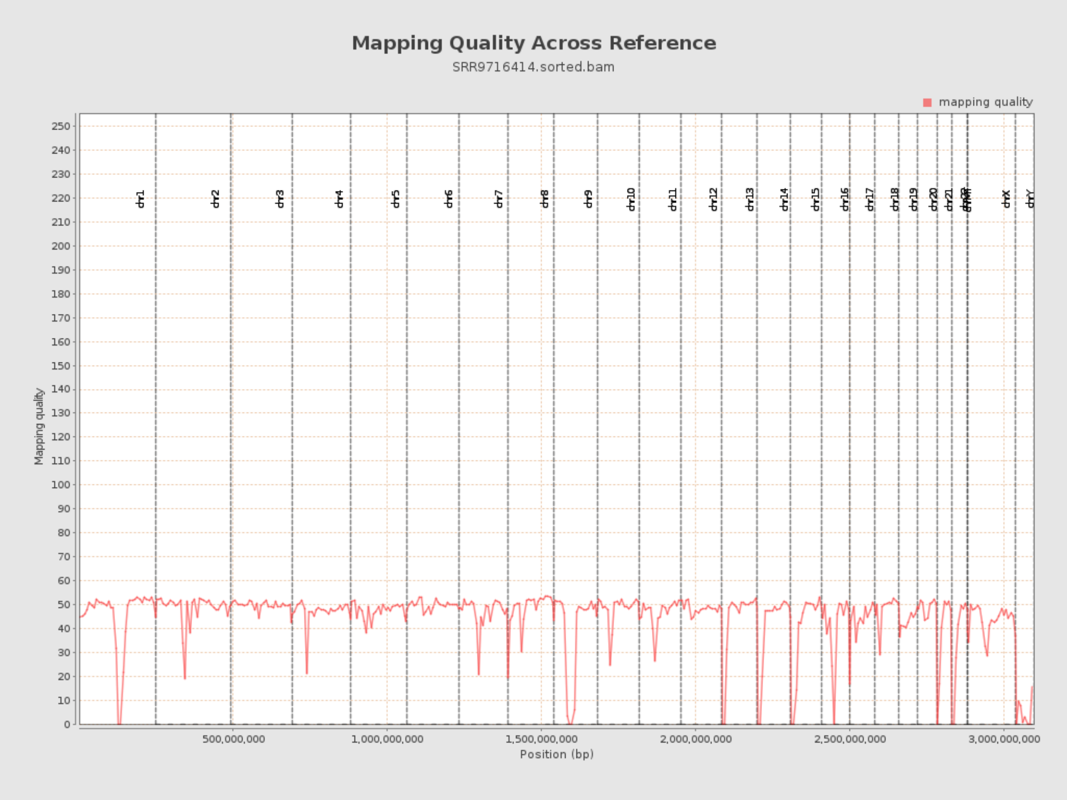
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram