Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:14:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717021.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_SRR9717021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:14:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	899,994
Mapped reads	771,735 / 85.75%
Unmapped reads	128,259 / 14.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,466 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	13,482 / 1.5%
Duplication rate	1.35%
Clipped reads	773,621 / 85.96%

2.2. ACGT Content

Number/percentage of A's	10,826,486 / 24.83%
Number/percentage of C's	8,115,951 / 18.61%
Number/percentage of T's	13,951,183 / 31.99%
Number/percentage of G's	10,711,217 / 24.56%
Number/percentage of N's	949 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.141

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Mismatches and indels

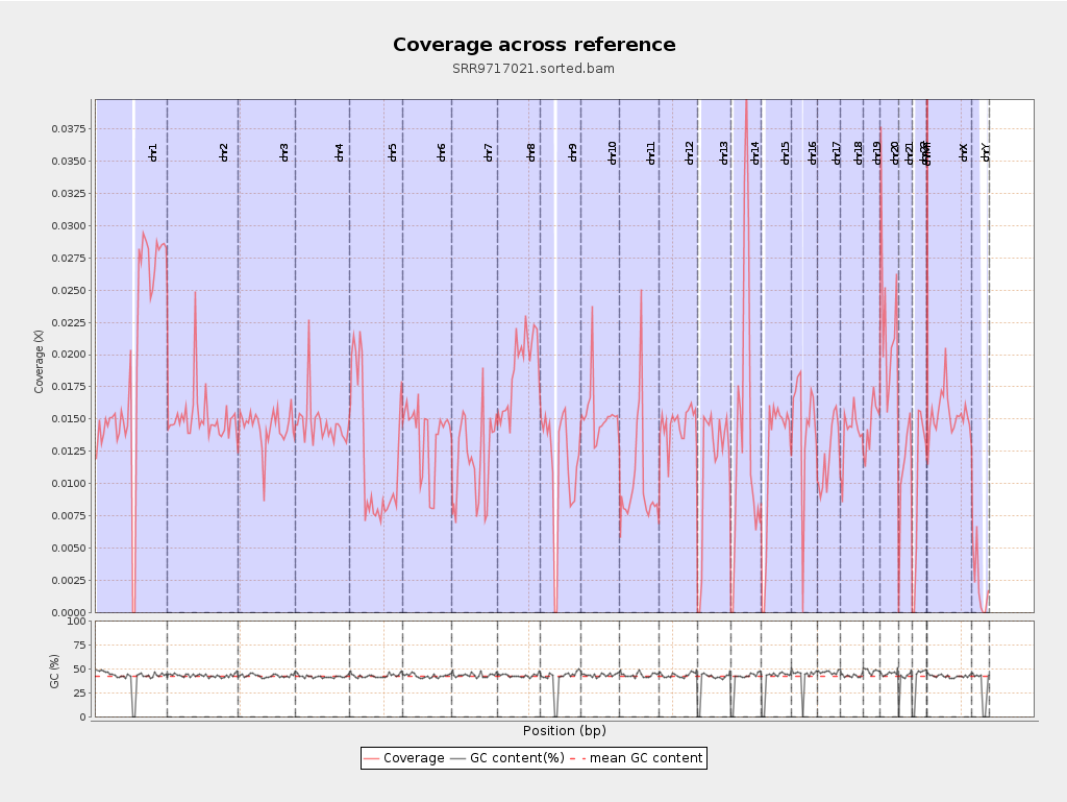
General error rate	0.51%
Mismatches	216,644
Insertions	2,652
Mapped reads with at least one insertion	0.34%
Deletions	6,882
Mapped reads with at least one deletion	0.88%
Homopolymer indels	41.25%

2.6. Chromosome stats

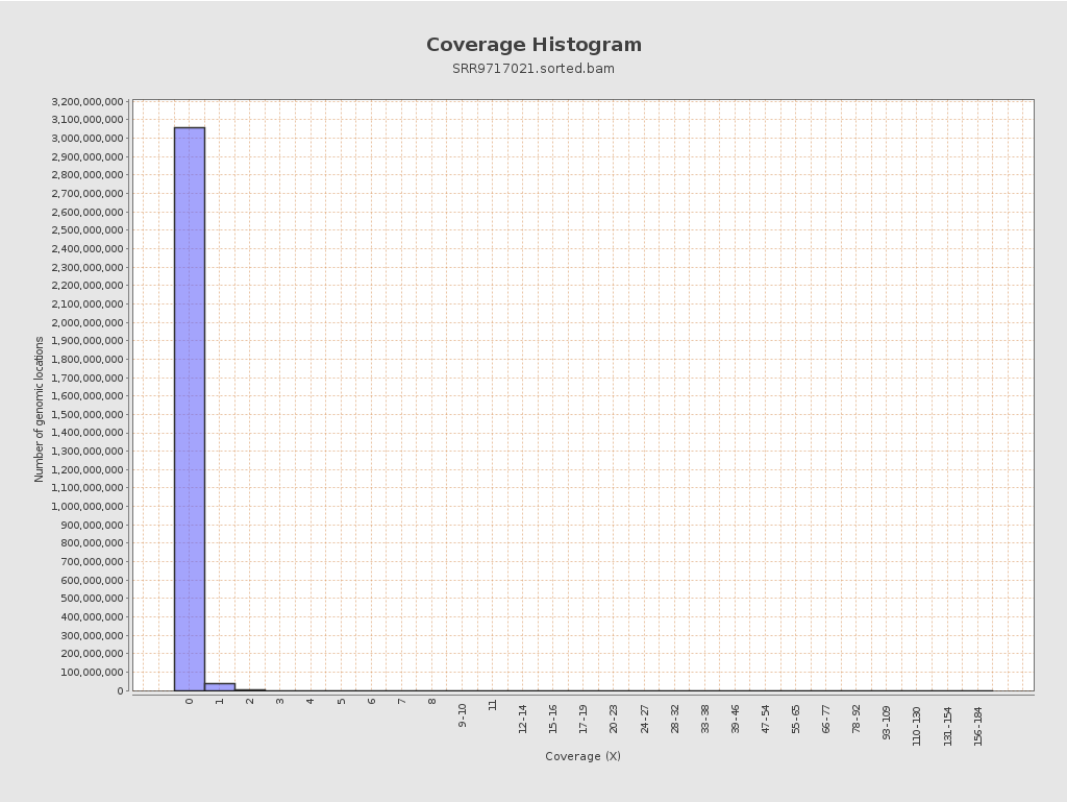
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4794600	0.0192	0.1968
chr2	243199373	3678356	0.0151	0.157
chr3	198022430	2847407	0.0144	0.1252
chr4	191154276	2798600	0.0146	0.1312
chr5	180915260	2164663	0.012	0.1148
chr6	171115067	2326472	0.0136	0.1271
chr7	159138663	1906100	0.012	0.1241

chr8	146364022	2752823	0.0188	0.1539
chr9	141213431	1607664	0.0114	0.1338
chr10	135534747	2077981	0.0153	0.1521
chr11	135006516	1388453	0.0103	0.1236
chr12	133851895	1949555	0.0146	0.127
chr13	115169878	1327027	0.0115	0.1115
chr14	107349540	1534423	0.0143	0.1295
chr15	102531392	1247470	0.0122	0.1157
chr16	90354753	1299525	0.0144	0.1319
chr17	81195210	989519	0.0122	0.1169
chr18	78077248	1082484	0.0139	0.2245
chr19	59128983	866613	0.0147	0.1542
chr20	63025520	1400754	0.0222	0.1584
chr21	48129895	541961	0.0113	0.1151
chr22	51304566	518811	0.0101	0.1045
chrMT	16571	2449	0.1478	0.403
chrX	155270560	2386940	0.0154	0.1373
chrY	59373566	126731	0.0021	0.0581

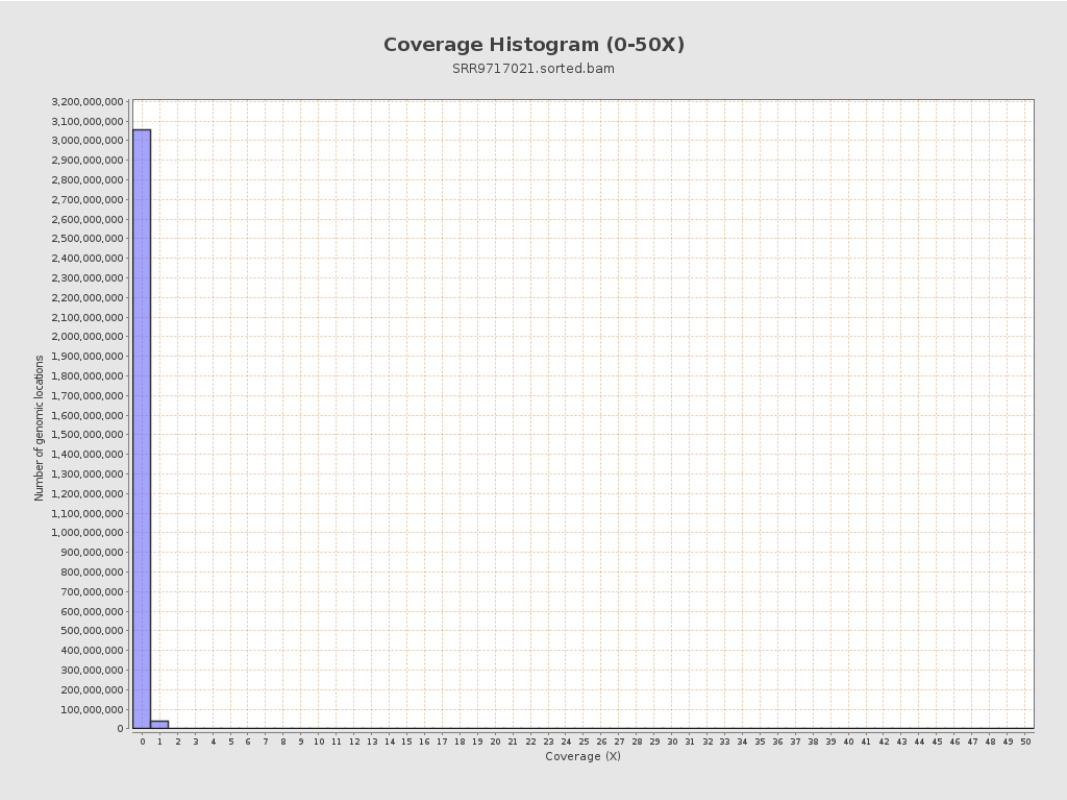
3. Results : Coverage across reference



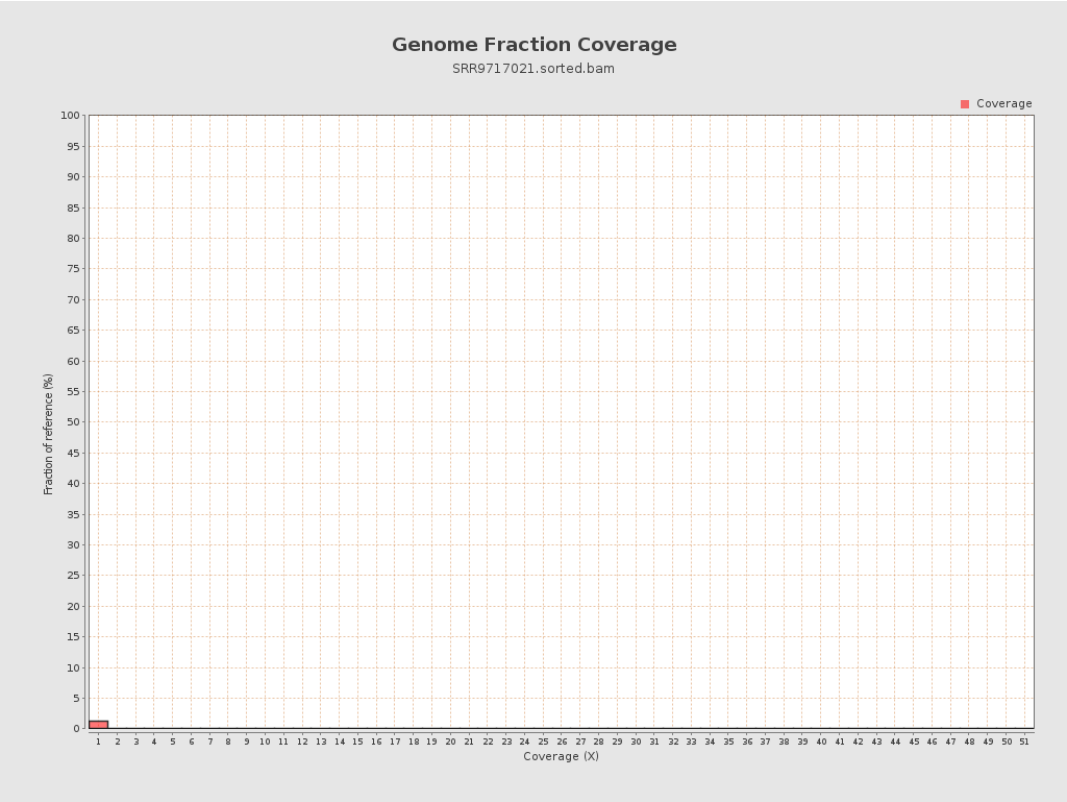
4. Results : Coverage Histogram



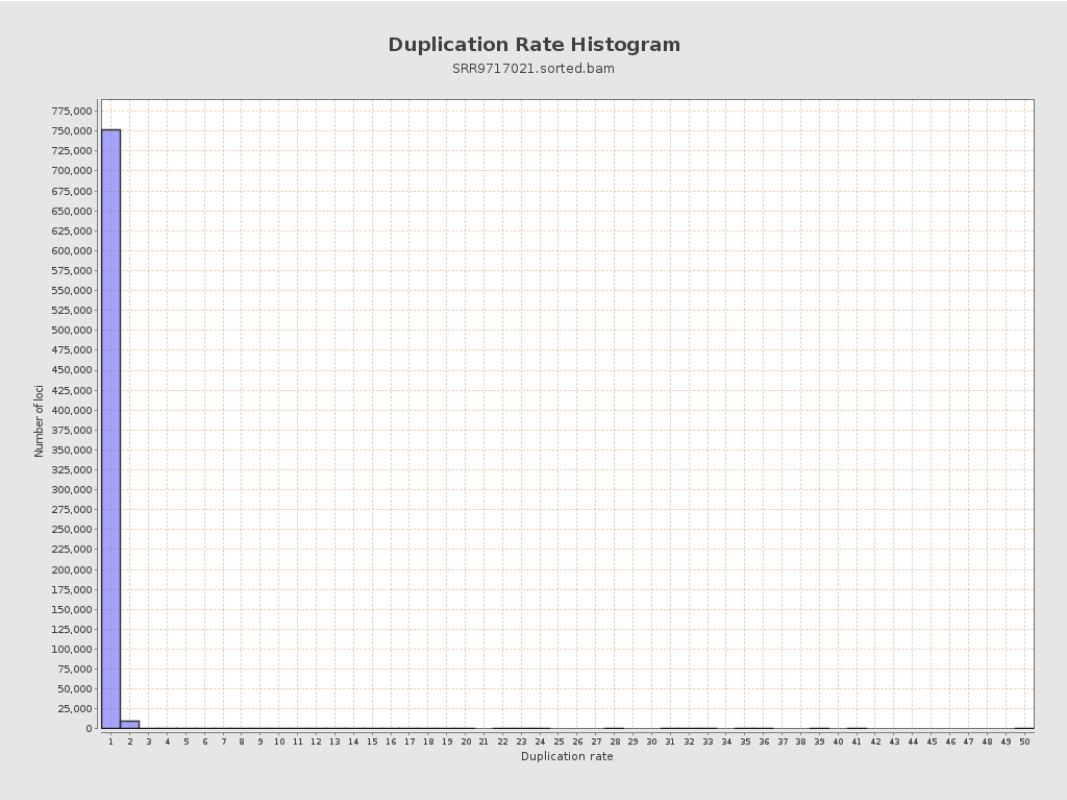
5. Results : Coverage Histogram (0-50X)



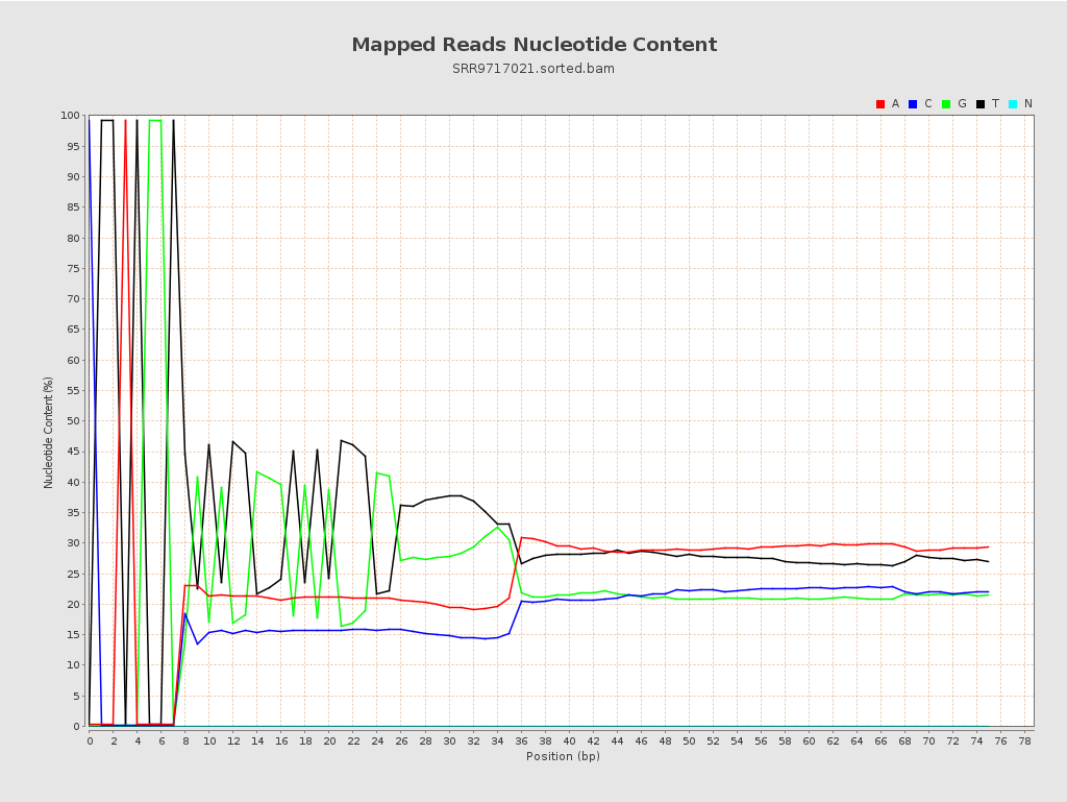
6. Results : Genome Fraction Coverage



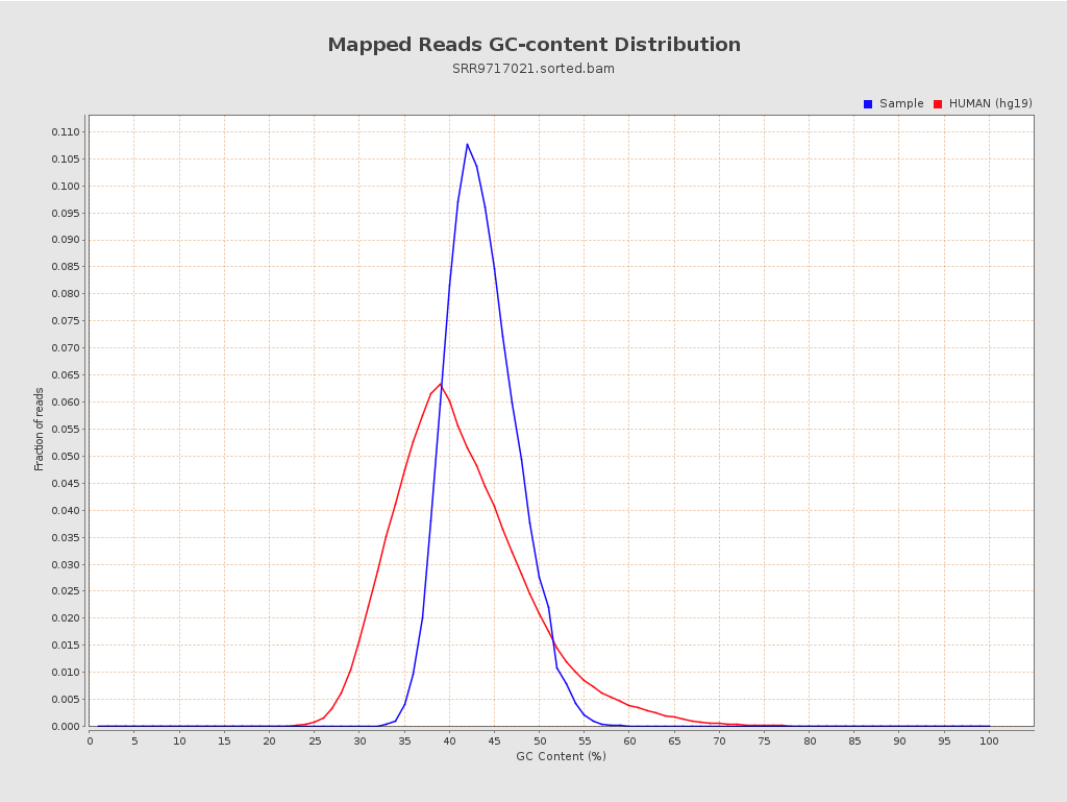
7. Results : Duplication Rate Histogram



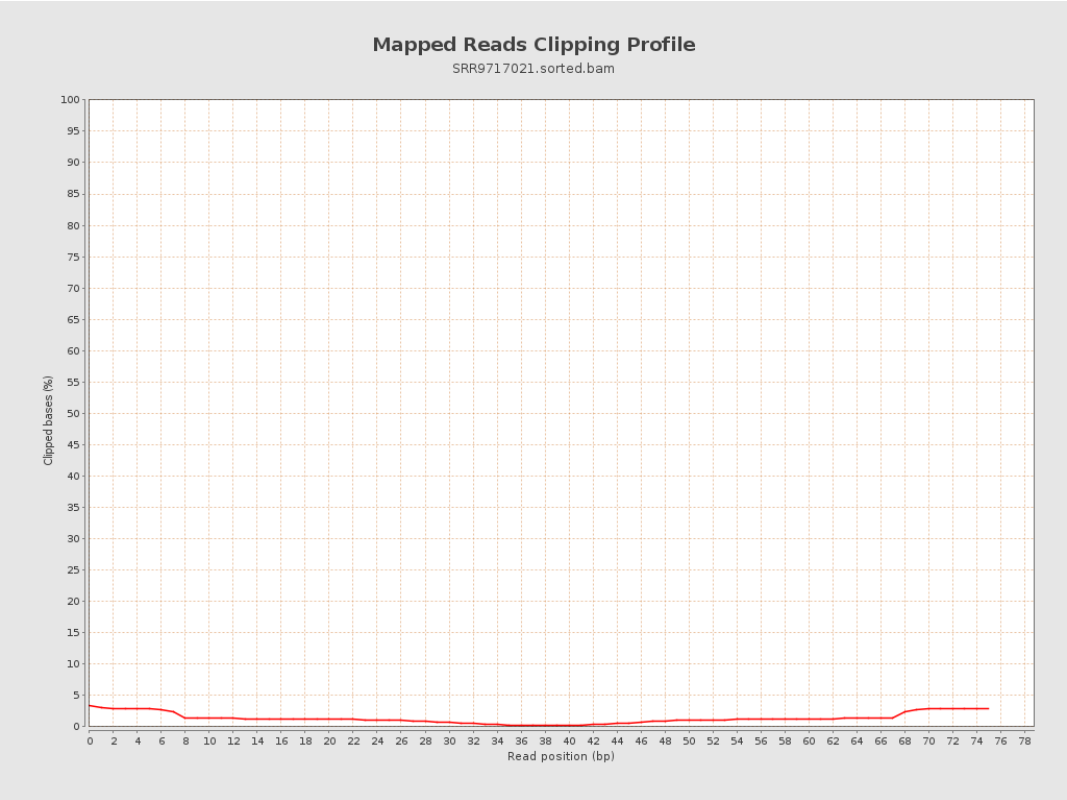
8. Results : Mapped Reads Nucleotide Content



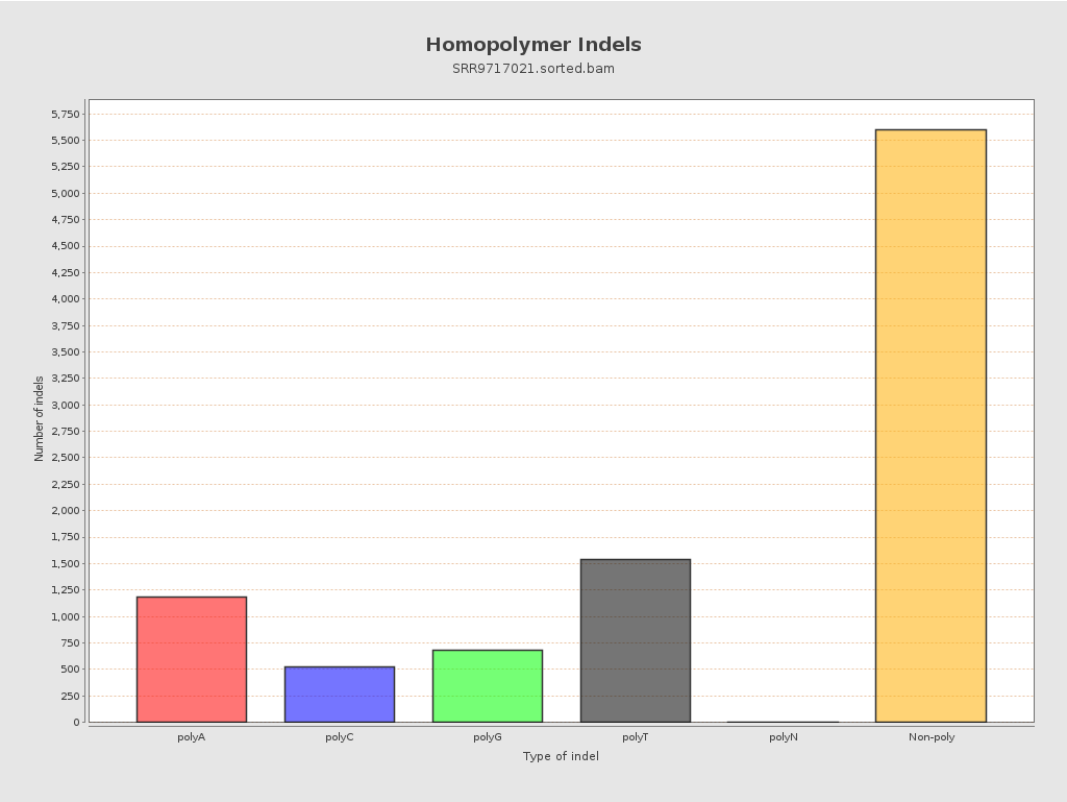
9. Results : Mapped Reads GC-content Distribution



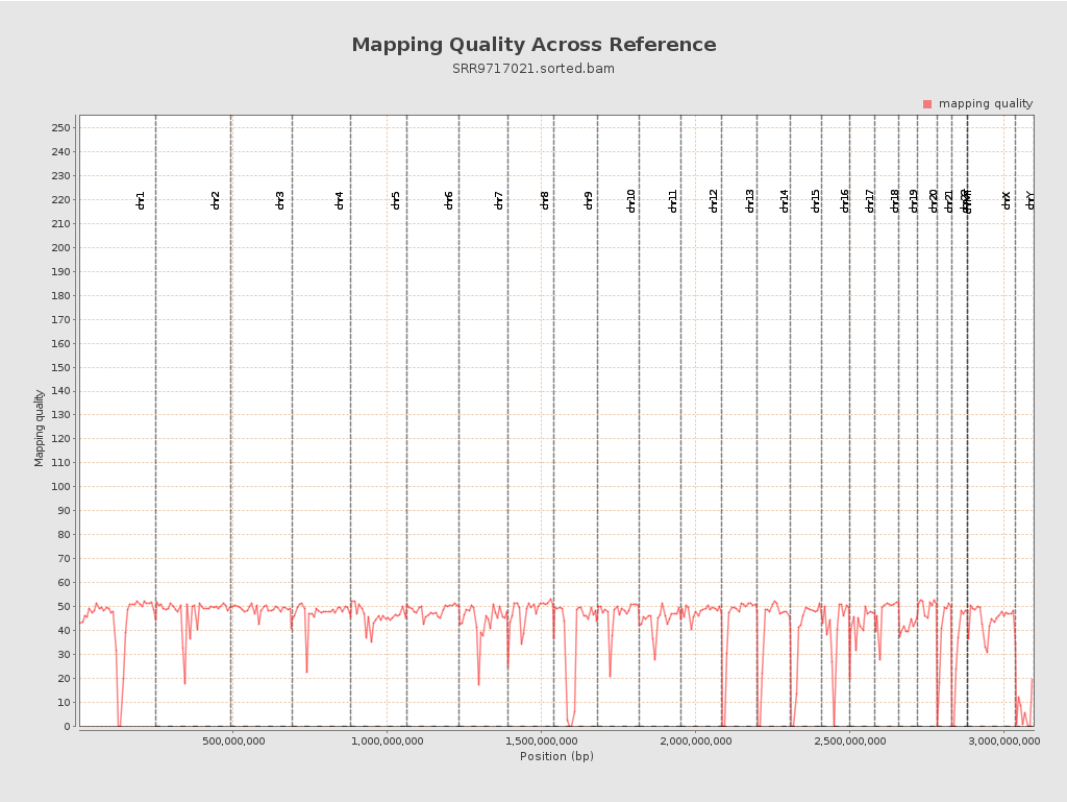
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram