Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:24:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717025.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_SRR9717025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717025.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:24:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	845,470
Mapped reads	768,159 / 90.86%
Unmapped reads	77,311 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,211 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	14,485 / 1.71%
Duplication rate	1.41%
Clipped reads	770,975 / 91.19%

2.2. ACGT Content

Number/percentage of A's	10,686,604 / 24.35%
Number/percentage of C's	8,125,920 / 18.51%
Number/percentage of T's	13,423,379 / 30.58%
Number/percentage of G's	11,655,383 / 26.55%
Number/percentage of N's	881 / 0%
GC Percentage	45.07%

2.3. Coverage

Mean	0.0142

Standard Deviation	0.1456

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Mismatches and indels

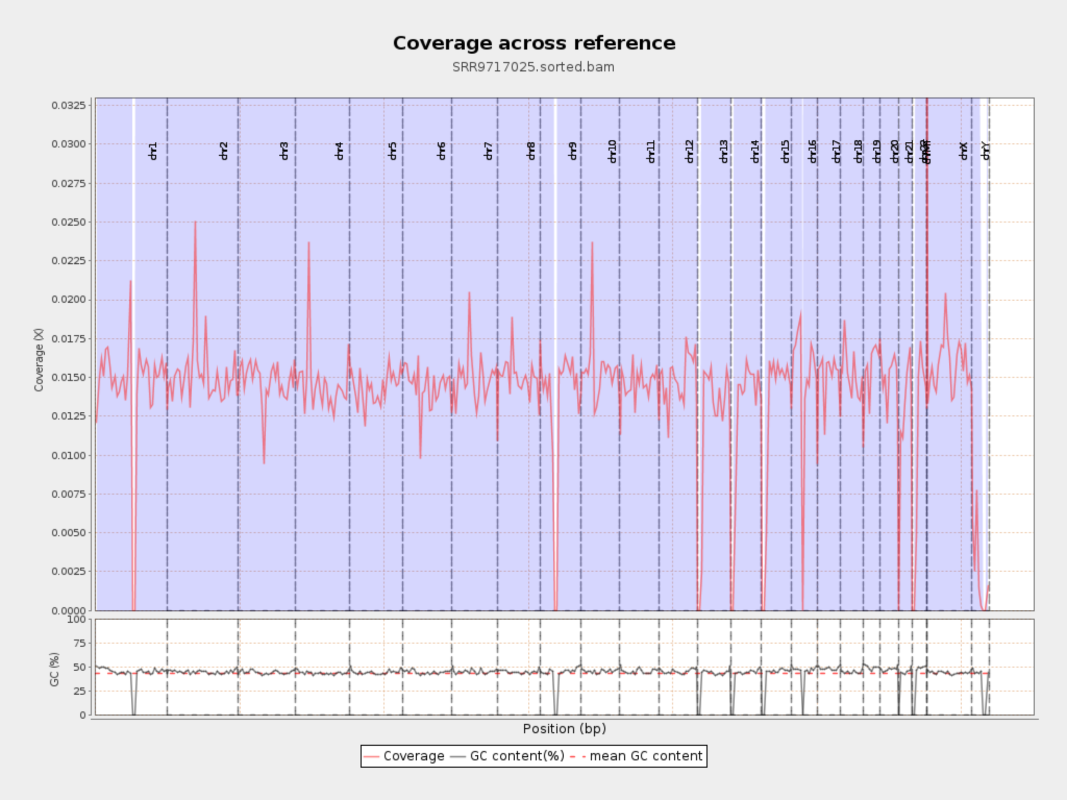
General error rate	0.51%
Mismatches	220,941
Insertions	2,686
Mapped reads with at least one insertion	0.35%
Deletions	7,029
Mapped reads with at least one deletion	0.91%
Homopolymer indels	41.1%

2.6. Chromosome stats

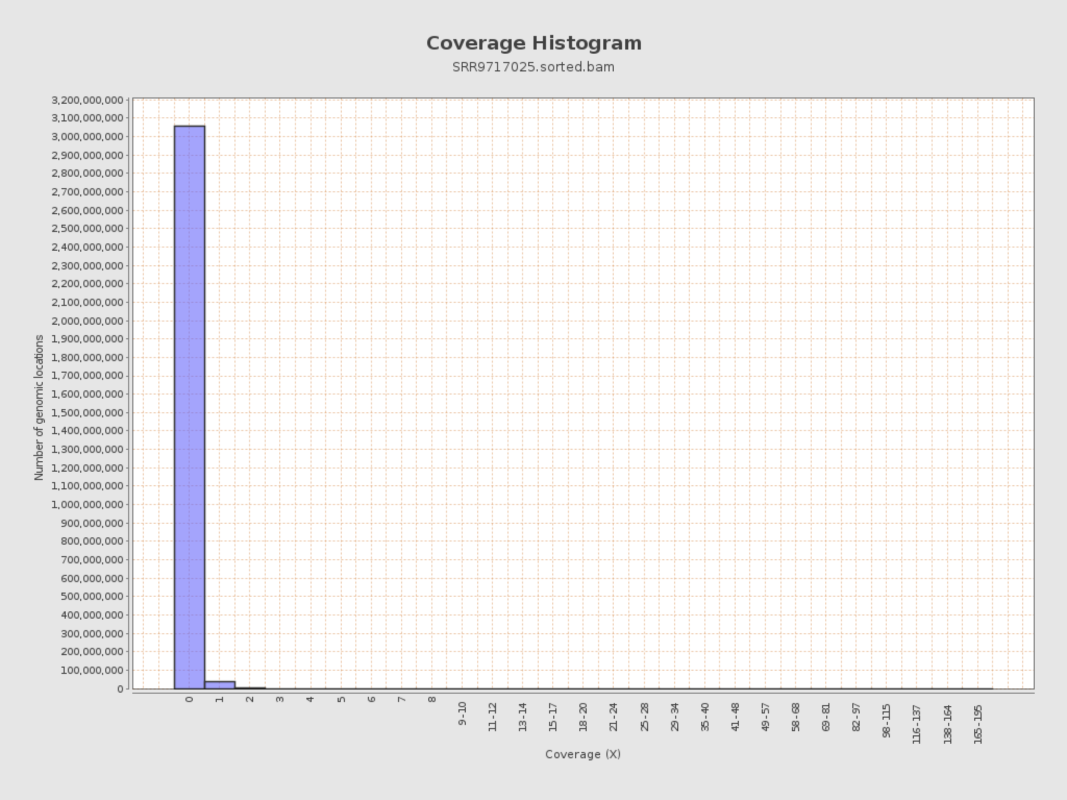
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3566943	0.0143	0.1987
chr2	243199373	3707897	0.0152	0.1611
chr3	198022430	2916190	0.0147	0.1265
chr4	191154276	2798925	0.0146	0.1328
chr5	180915260	2603478	0.0144	0.1259
chr6	171115067	2468140	0.0144	0.1292
chr7	159138663	2389253	0.015	0.1603

chr8	146364022	2204247	0.0151	0.1398
chr9	141213431	1857860	0.0132	0.1449
chr10	135534747	2112687	0.0156	0.1493
chr11	135006516	1982608	0.0147	0.1457
chr12	133851895	2002142	0.015	0.1292
chr13	115169878	1357289	0.0118	0.1128
chr14	107349540	1311843	0.0122	0.1201
chr15	102531392	1275483	0.0124	0.1173
chr16	90354753	1323584	0.0146	0.1314
chr17	81195210	1230812	0.0152	0.1331
chr18	78077248	1183658	0.0152	0.2398
chr19	59128983	924685	0.0156	0.1604
chr20	63025520	944500	0.015	0.1297
chr21	48129895	596721	0.0124	0.1234
chr22	51304566	547132	0.0107	0.1078
chrMT	16571	836	0.0504	0.2315
chrX	155270560	2461219	0.0159	0.1411
chrY	59373566	135877	0.0023	0.0645

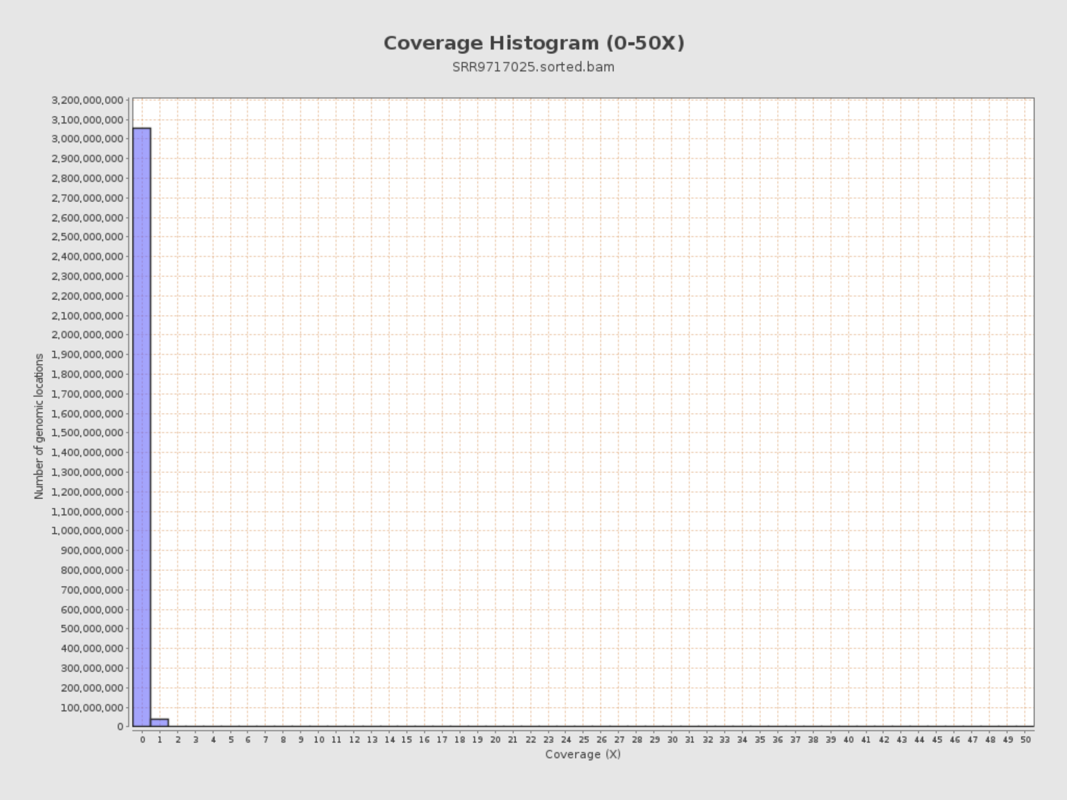
3. Results : Coverage across reference



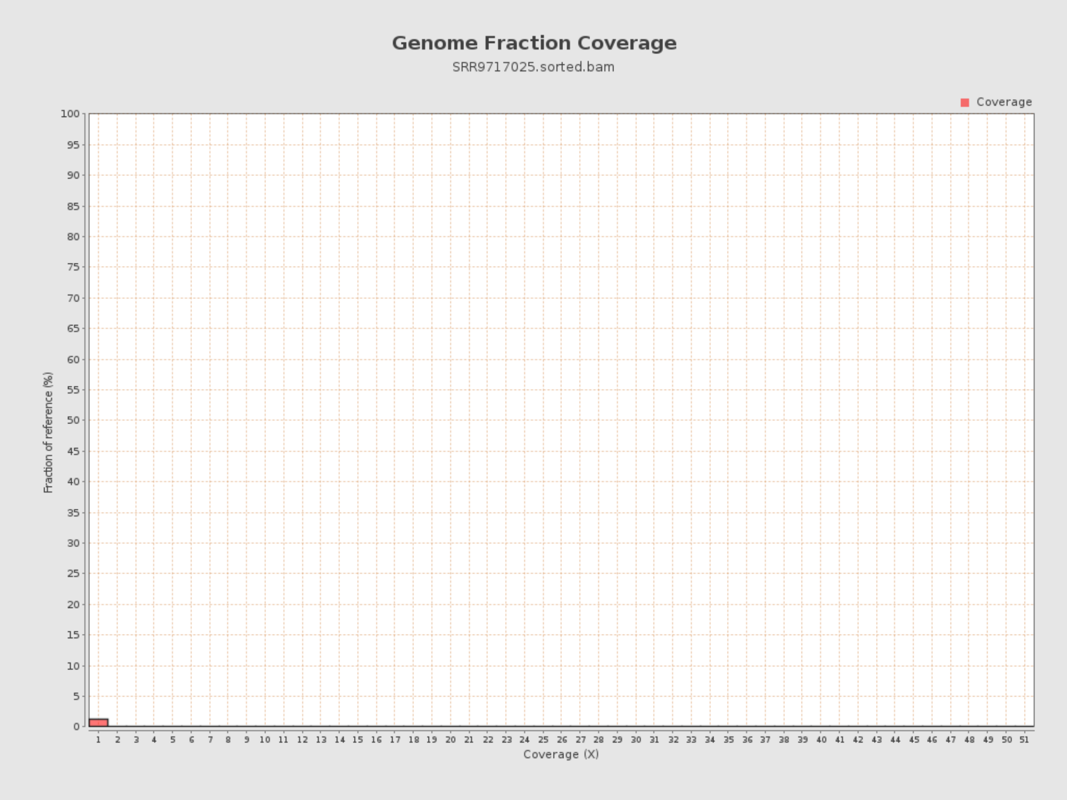
4. Results : Coverage Histogram



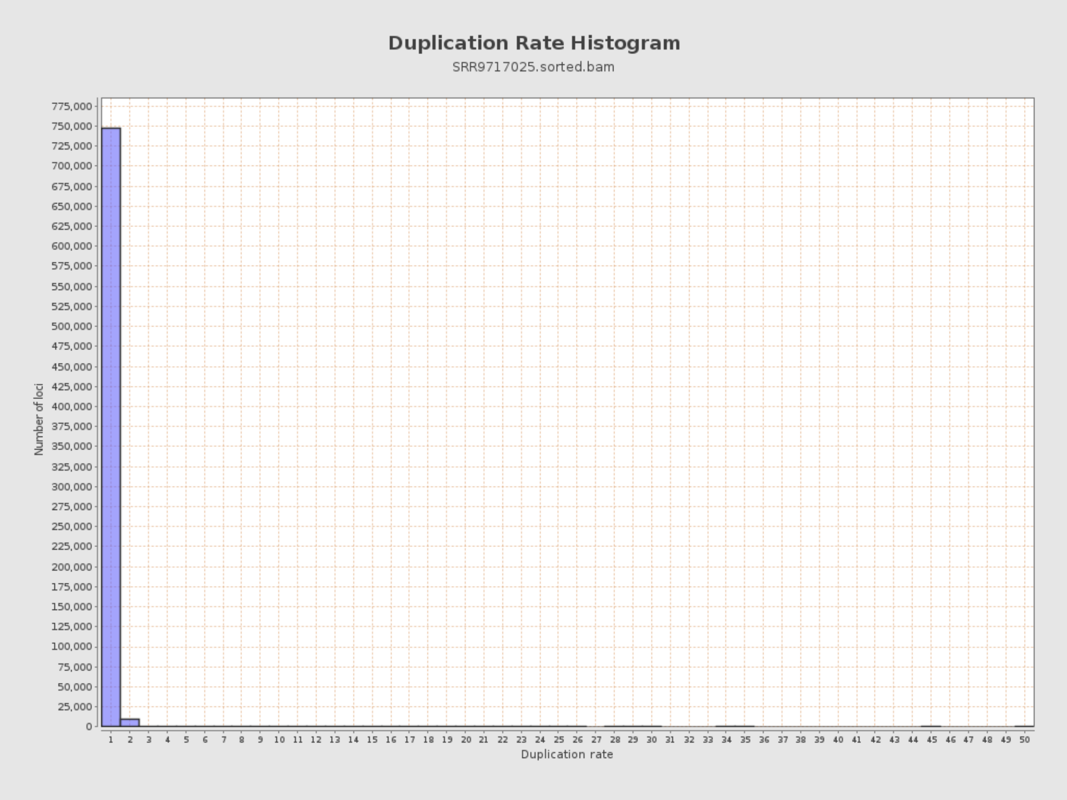
5. Results : Coverage Histogram (0-50X)



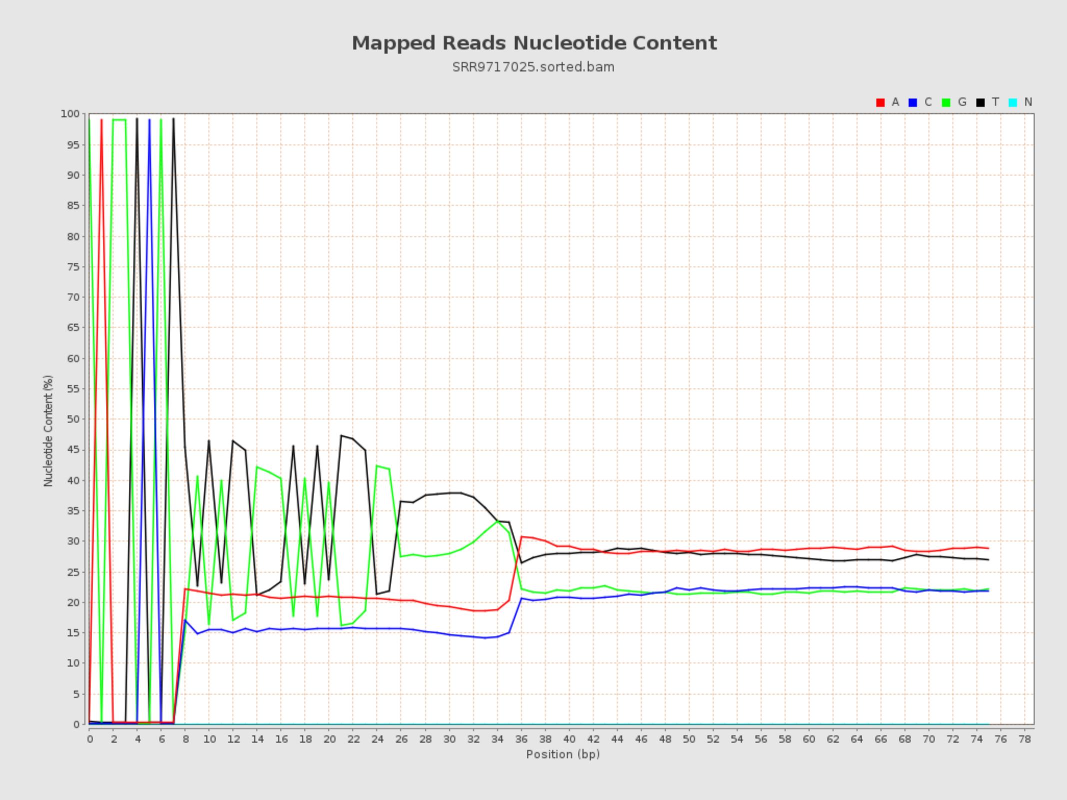
6. Results : Genome Fraction Coverage



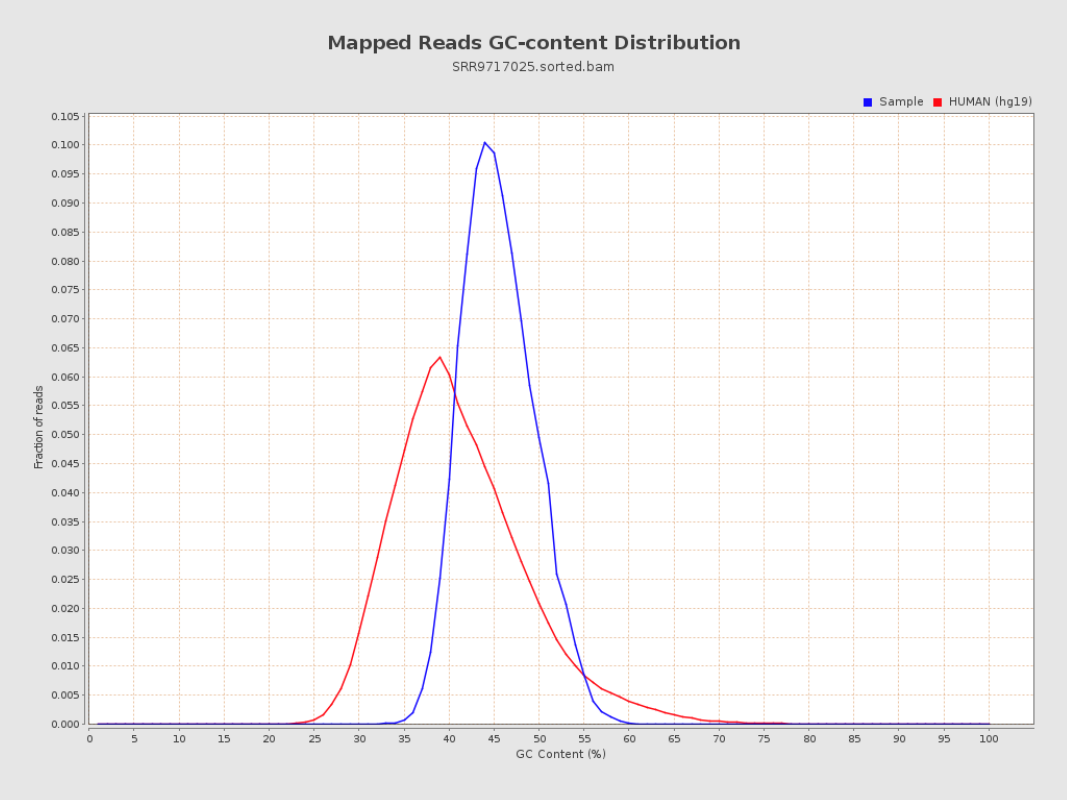
7. Results : Duplication Rate Histogram



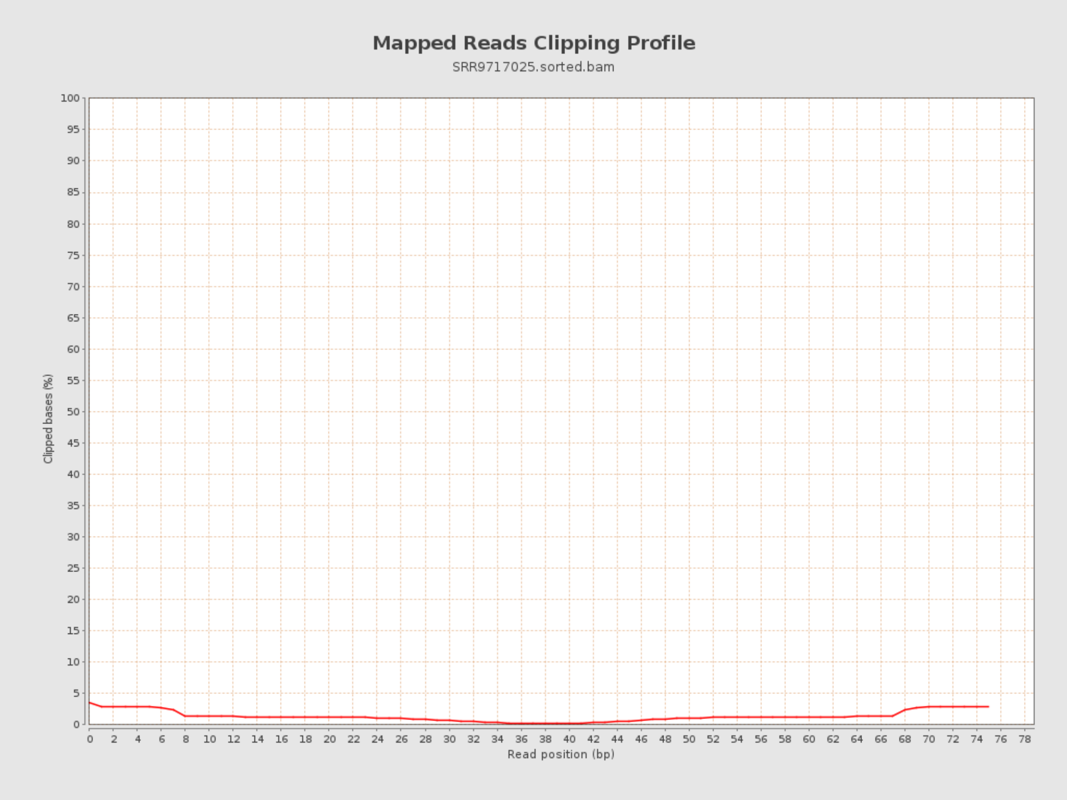
8. Results : Mapped Reads Nucleotide Content



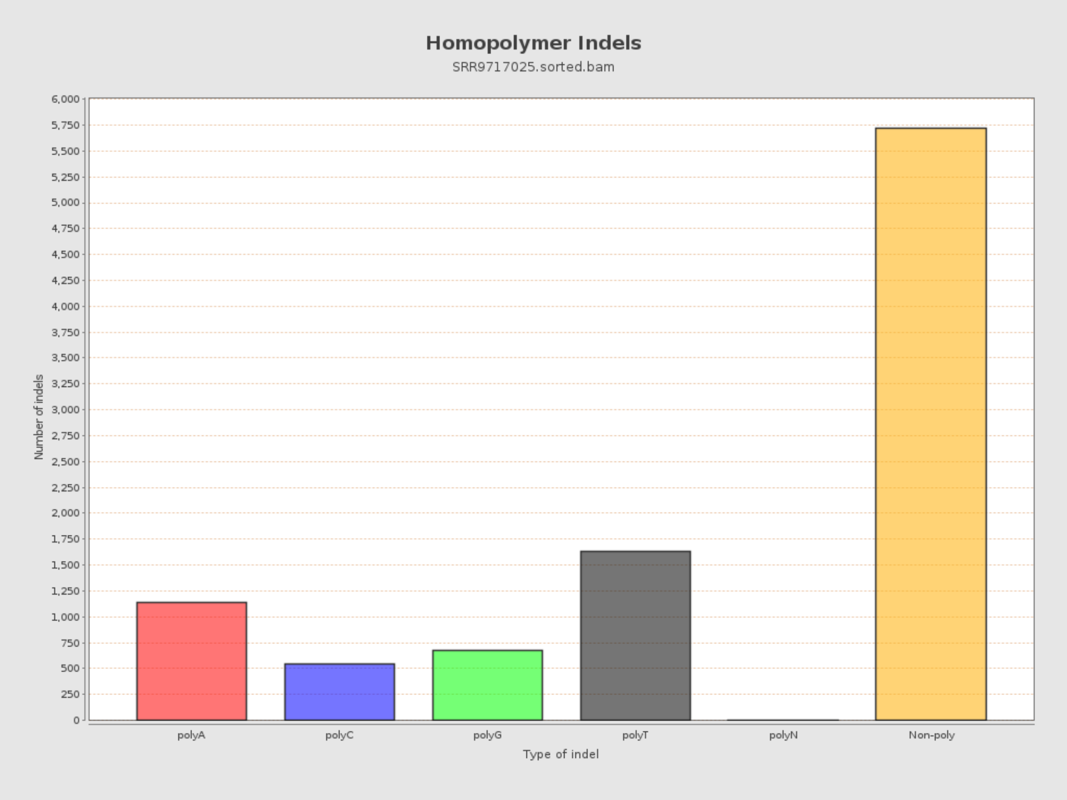
9. Results : Mapped Reads GC-content Distribution



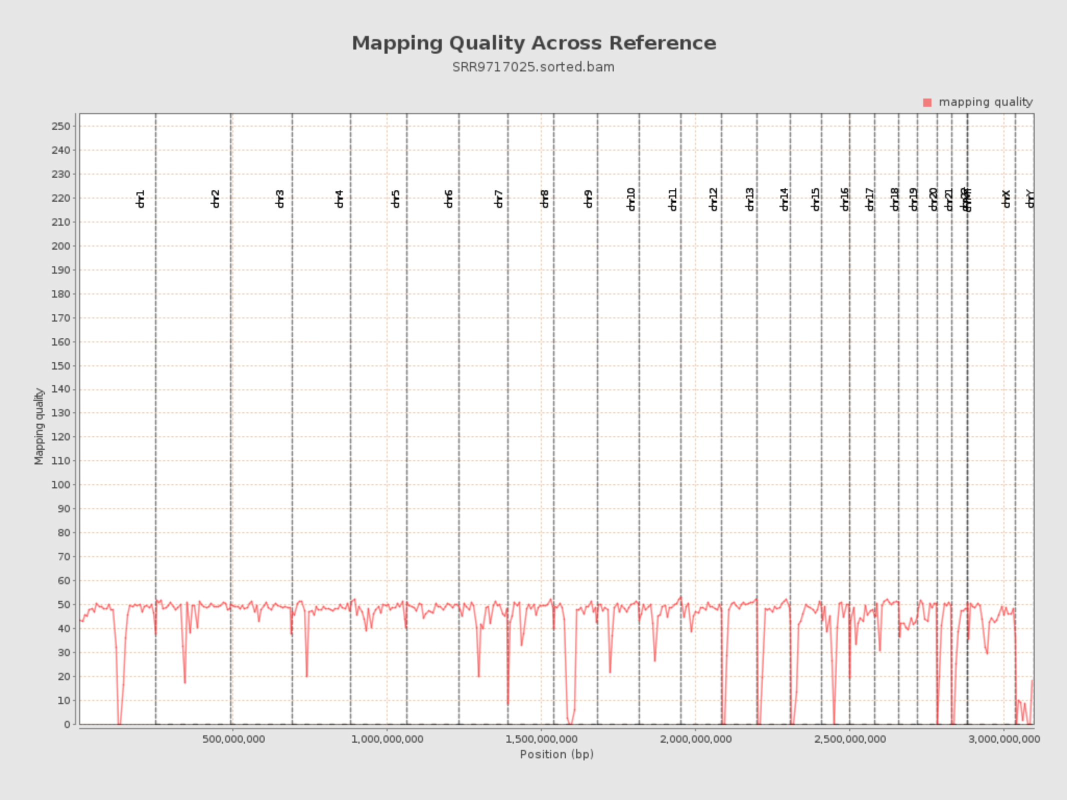
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram