Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:42:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717032.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_SRR9717032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:42:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	602,914
Mapped reads	555,314 / 92.11%
Unmapped reads	47,600 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,713 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	9,482 / 1.57%
Duplication rate	1.18%
Clipped reads	556,388 / 92.28%

2.2. ACGT Content

Number/percentage of A's	8,155,356 / 24.75%
Number/percentage of C's	6,167,044 / 18.72%
Number/percentage of T's	10,479,363 / 31.8%
Number/percentage of G's	8,148,138 / 24.73%
Number/percentage of N's	406 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.135

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

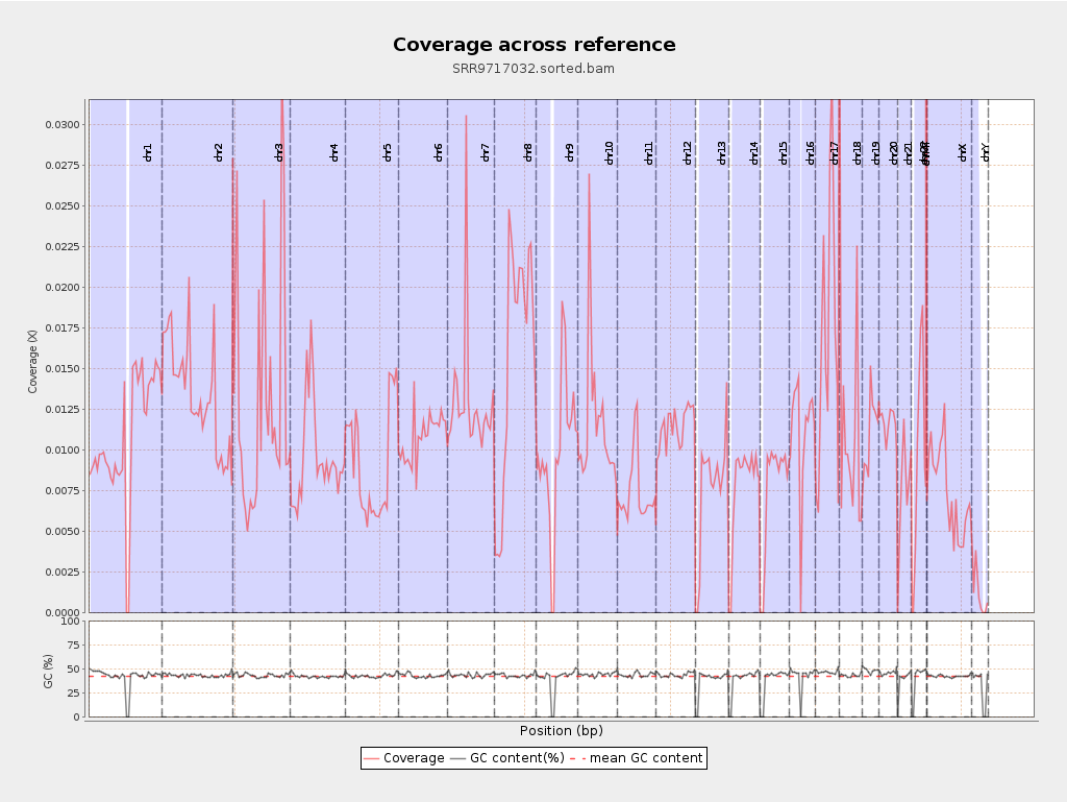
General error rate	0.51%
Mismatches	163,959
Insertions	2,368
Mapped reads with at least one insertion	0.42%
Deletions	6,104
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.32%

2.6. Chromosome stats

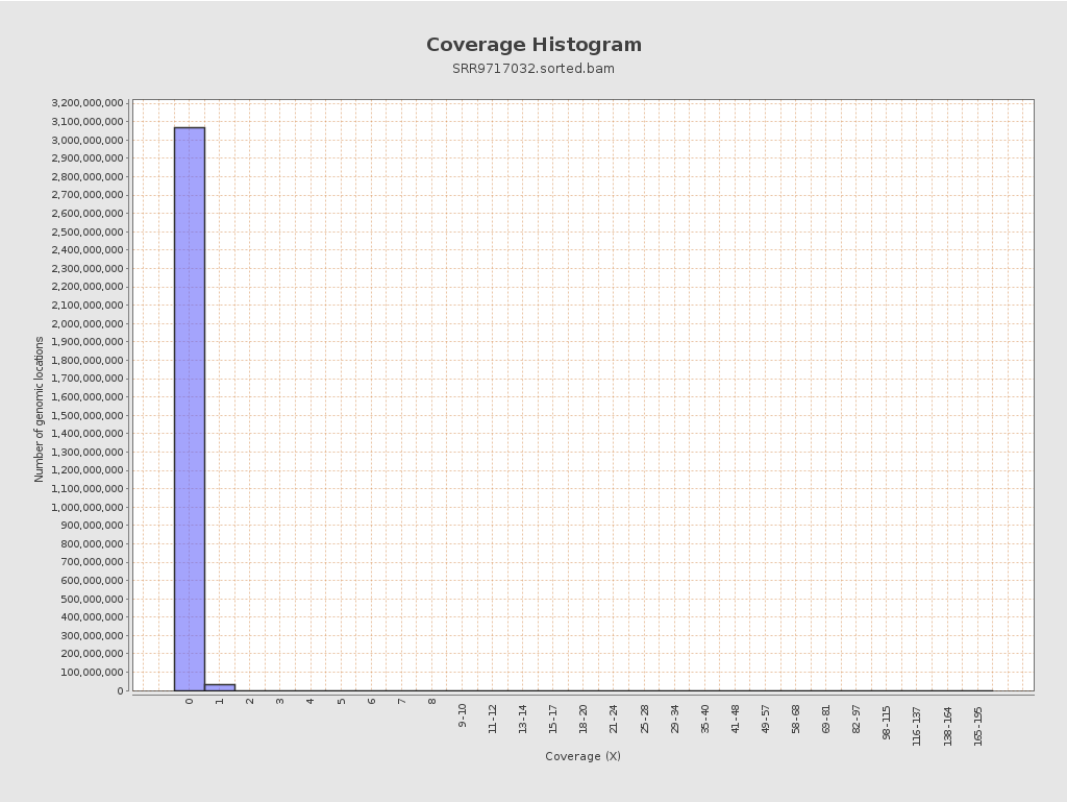
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2687727	0.0108	0.1655
chr2	243199373	3279787	0.0135	0.1496
chr3	198022430	2590964	0.0131	0.1206
chr4	191154276	1822593	0.0095	0.1039
chr5	180915260	1648052	0.0091	0.0984
chr6	171115067	1847349	0.0108	0.1109
chr7	159138663	2066456	0.013	0.2685

chr8	146364022	2308470	0.0158	0.1513
chr9	141213431	1379382	0.0098	0.1101
chr10	135534747	1549157	0.0114	0.1626
chr11	135006516	986265	0.0073	0.1009
chr12	133851895	1529674	0.0114	0.1161
chr13	115169878	878453	0.0076	0.0899
chr14	107349540	826110	0.0077	0.0911
chr15	102531392	777852	0.0076	0.0909
chr16	90354753	1013888	0.0112	0.1116
chr17	81195210	1365925	0.0168	0.1351
chr18	78077248	906611	0.0116	0.1473
chr19	59128983	656621	0.0111	0.1669
chr20	63025520	732780	0.0116	0.1138
chr21	48129895	360611	0.0075	0.0919
chr22	51304566	476436	0.0093	0.0993
chrMT	16571	38113	2.3	2.0987
chrX	155270560	1161416	0.0075	0.0956
chrY	59373566	69511	0.0012	0.0418

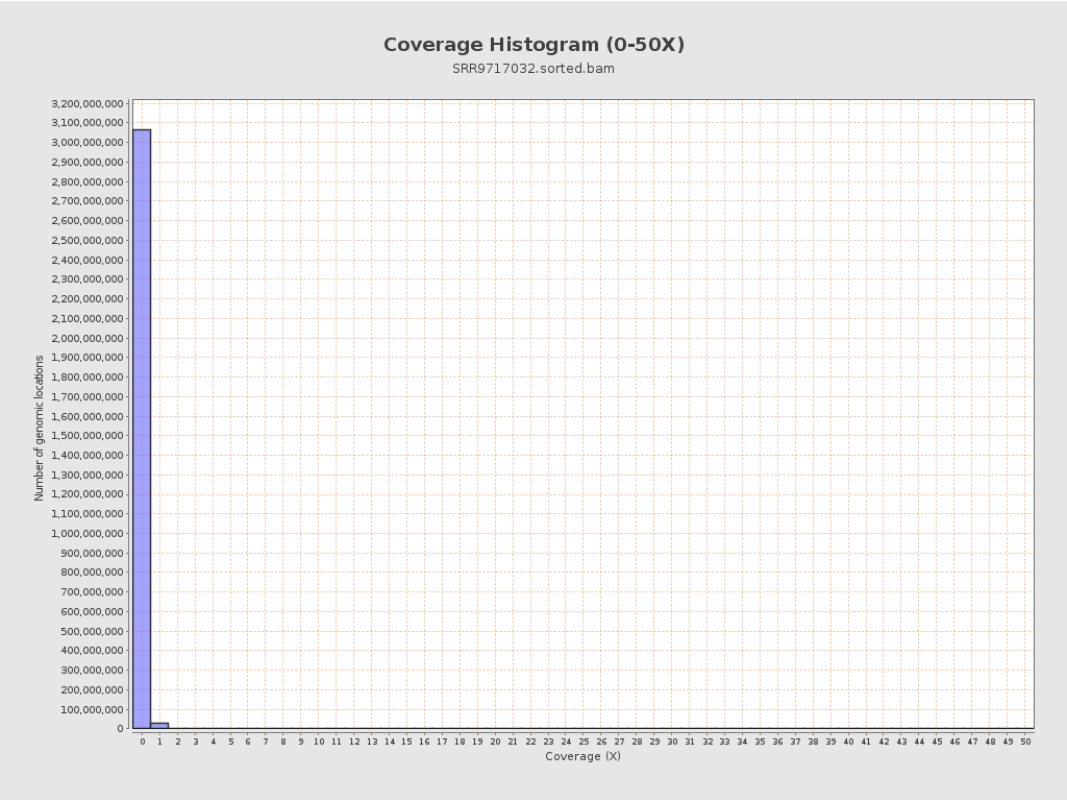
3. Results : Coverage across reference



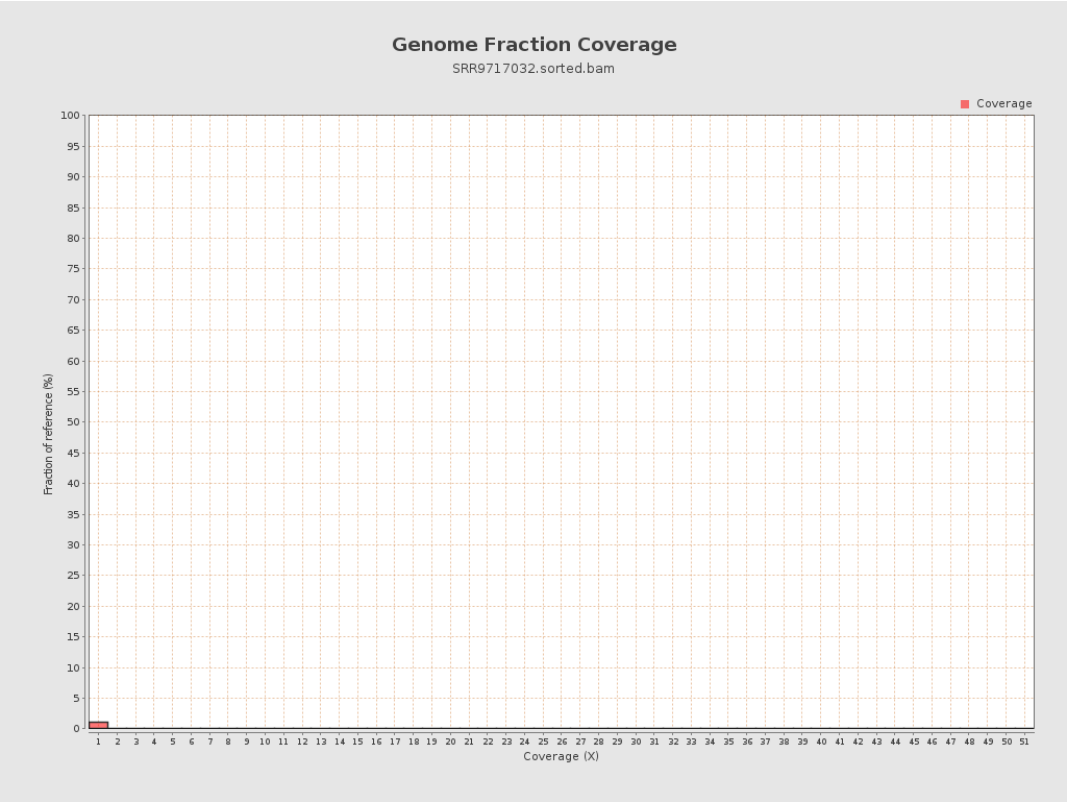
4. Results : Coverage Histogram



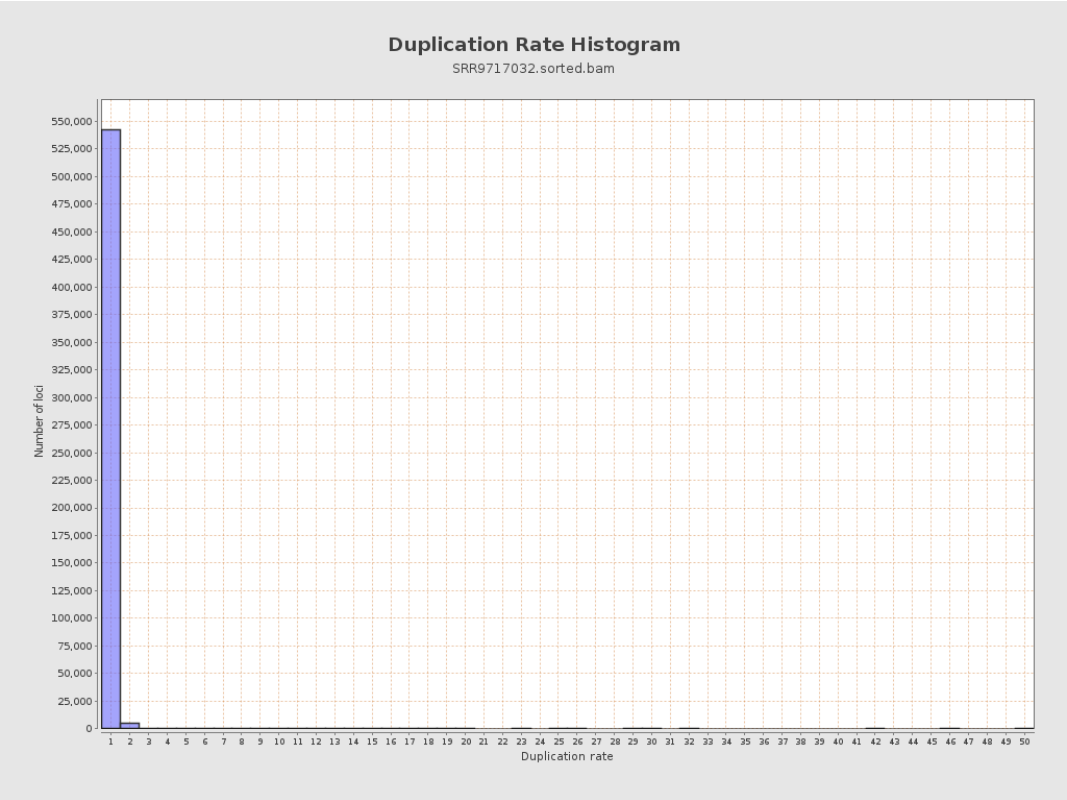
5. Results : Coverage Histogram (0-50X)



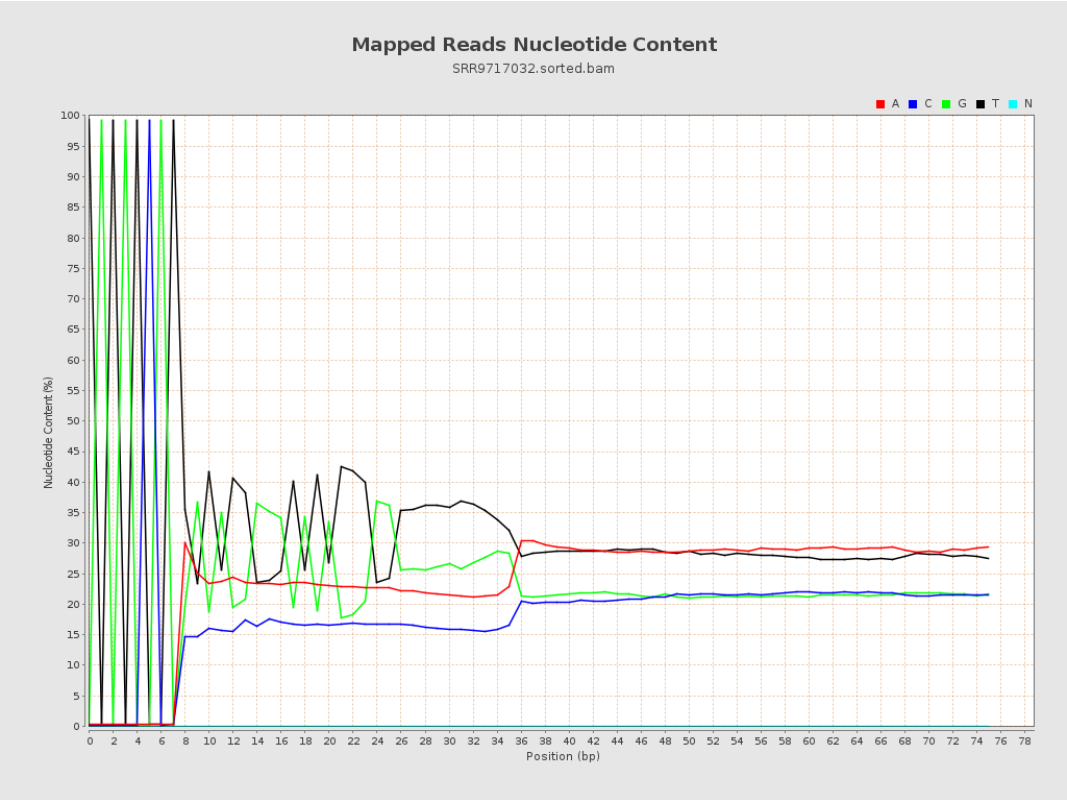
6. Results : Genome Fraction Coverage



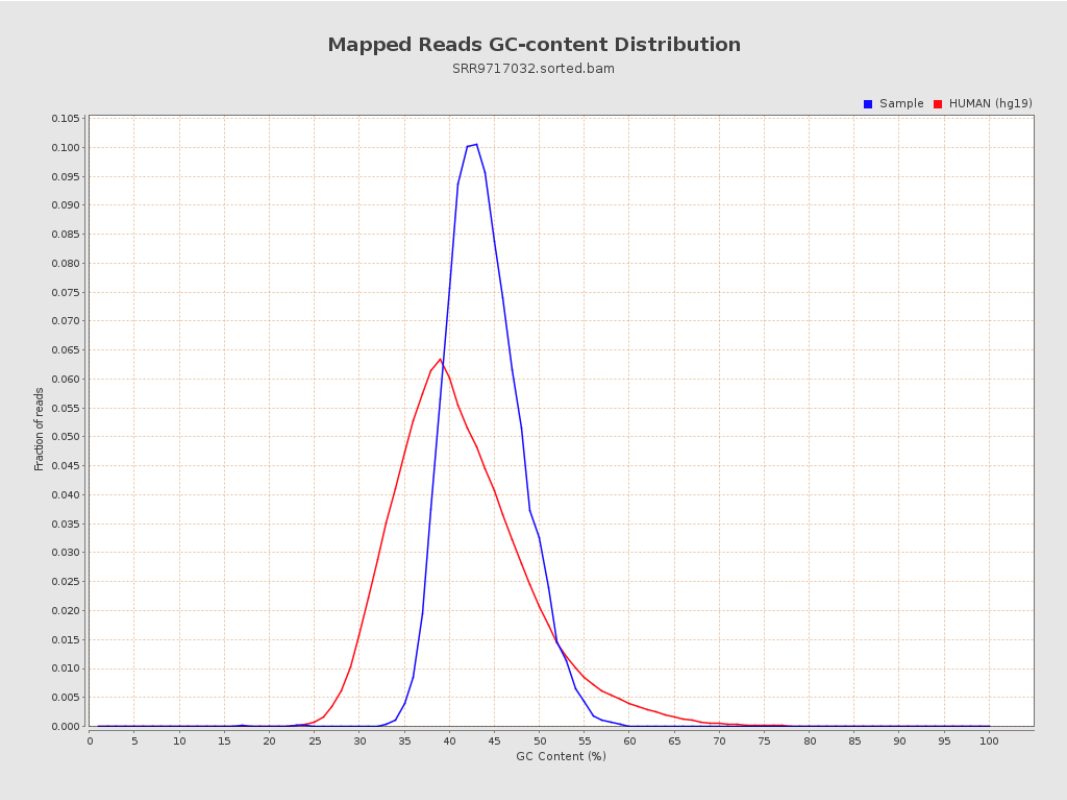
7. Results : Duplication Rate Histogram



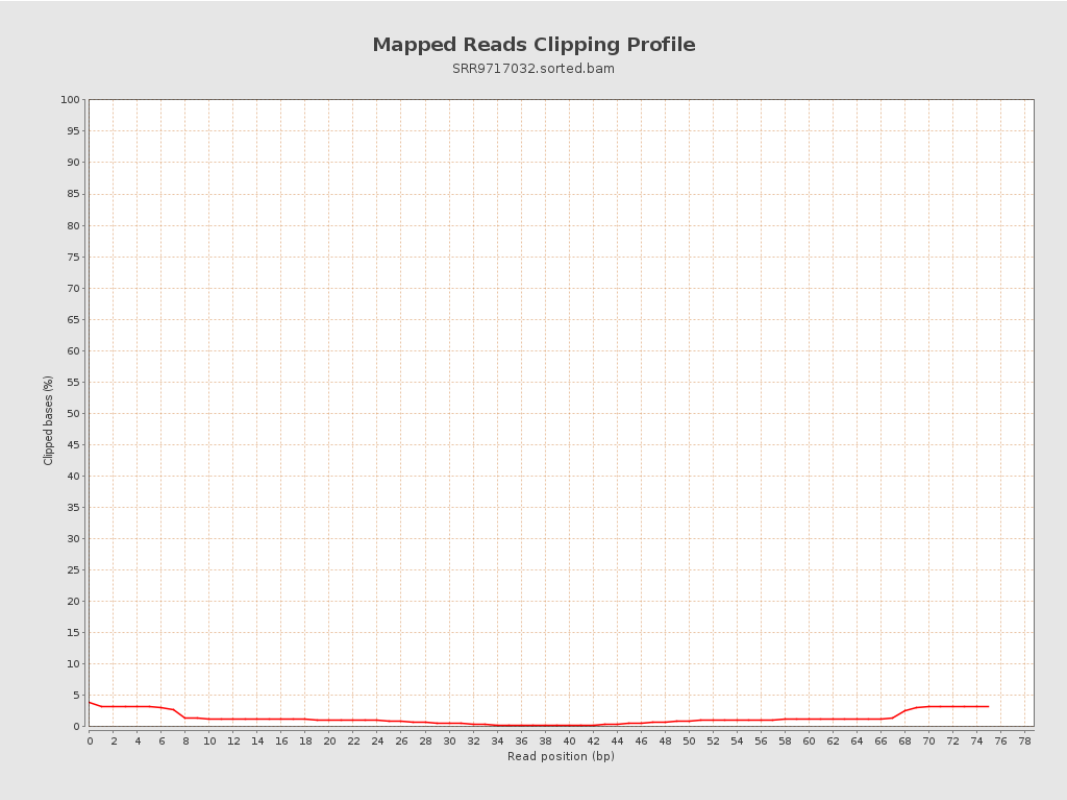
8. Results : Mapped Reads Nucleotide Content



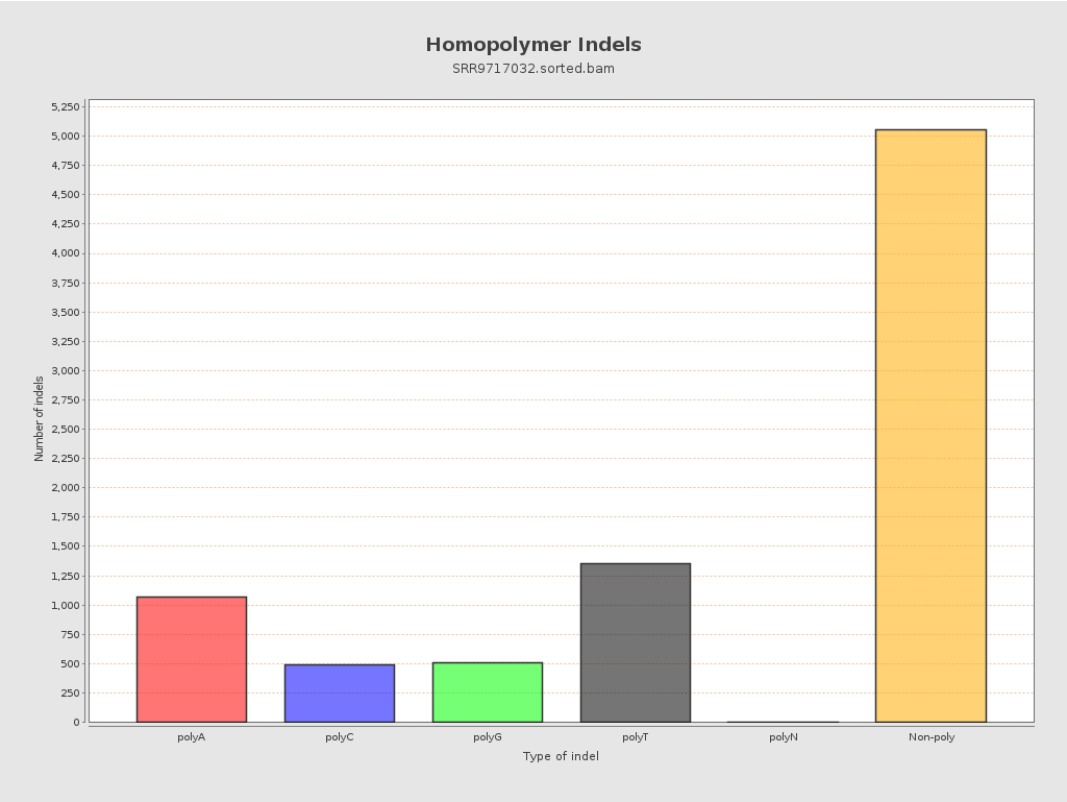
9. Results : Mapped Reads GC-content Distribution



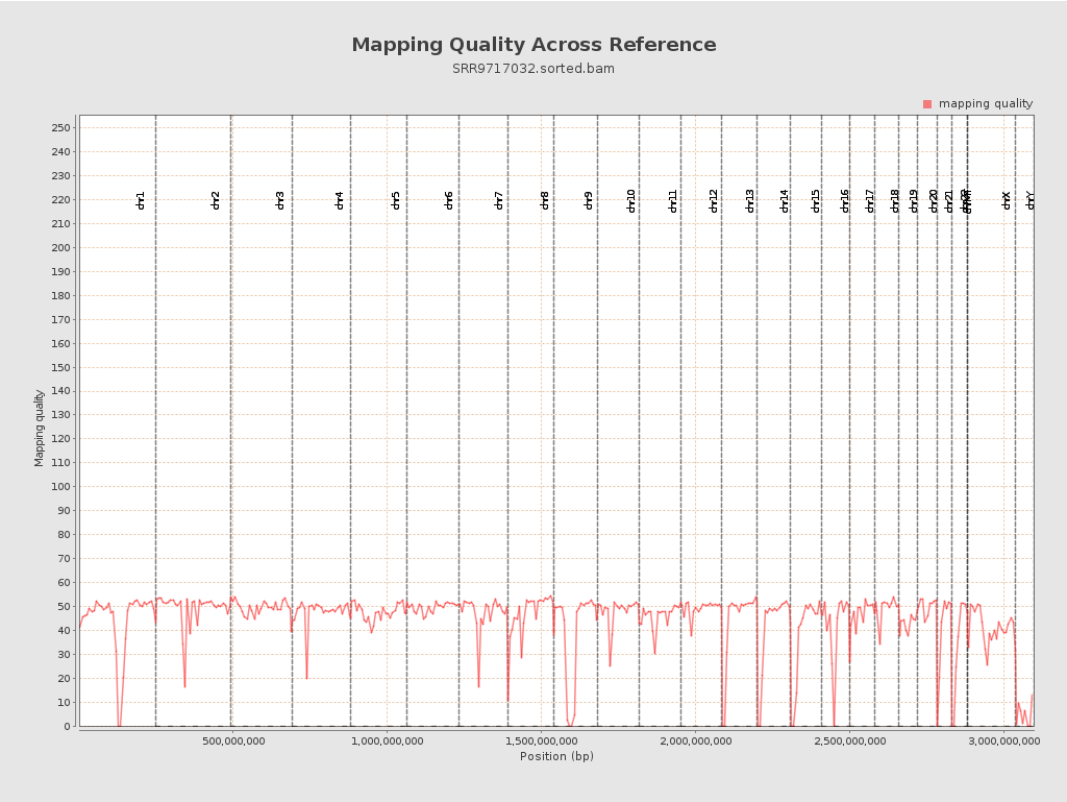
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram