Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:30:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717091.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_SRR9717091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:30:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	713,522
Mapped reads	657,400 / 92.13%
Unmapped reads	56,122 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,094 / 1.41%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	19,858 / 2.78%
Duplication rate	1.79%
Clipped reads	667,268 / 93.52%

2.2. ACGT Content

Number/percentage of A's	12,892,840 / 24.86%
Number/percentage of C's	10,106,170 / 19.49%
Number/percentage of T's	16,088,407 / 31.03%
Number/percentage of G's	12,762,414 / 24.61%
Number/percentage of N's	2,749 / 0.01%
GC Percentage	44.1%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.2245

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

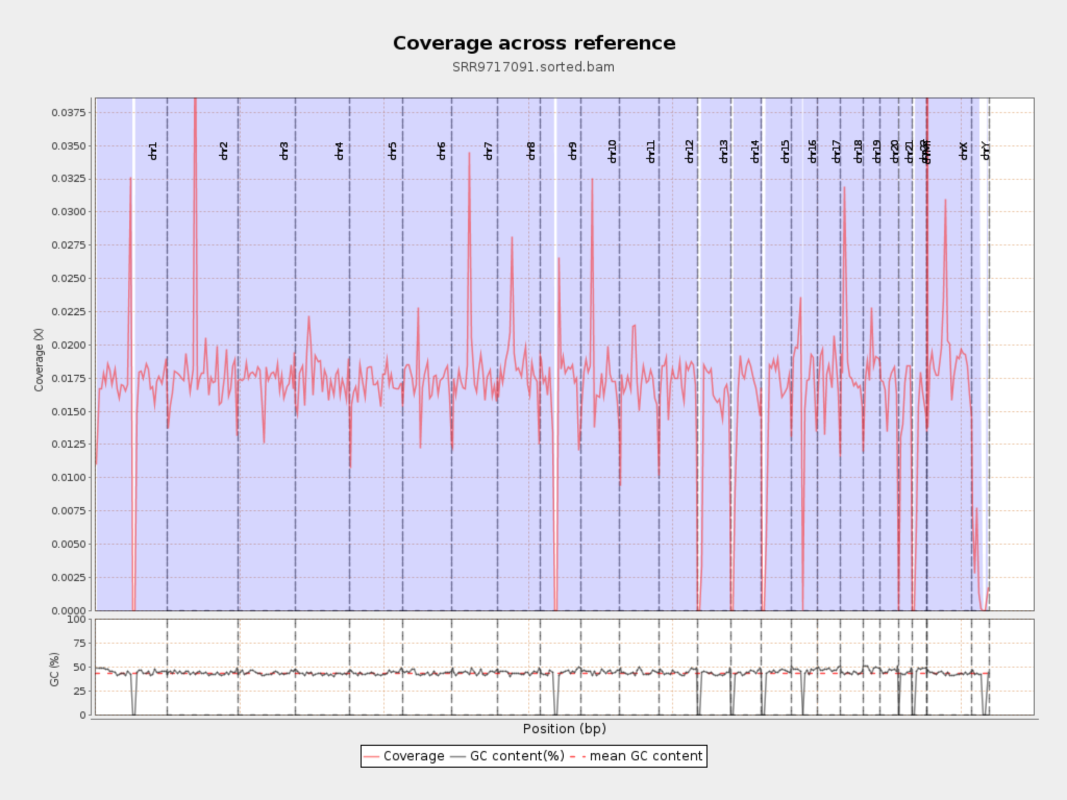
General error rate	0.84%
Mismatches	428,930
Insertions	4,520
Mapped reads with at least one insertion	0.68%
Deletions	12,961
Mapped reads with at least one deletion	1.94%
Homopolymer indels	44.56%

2.6. Chromosome stats

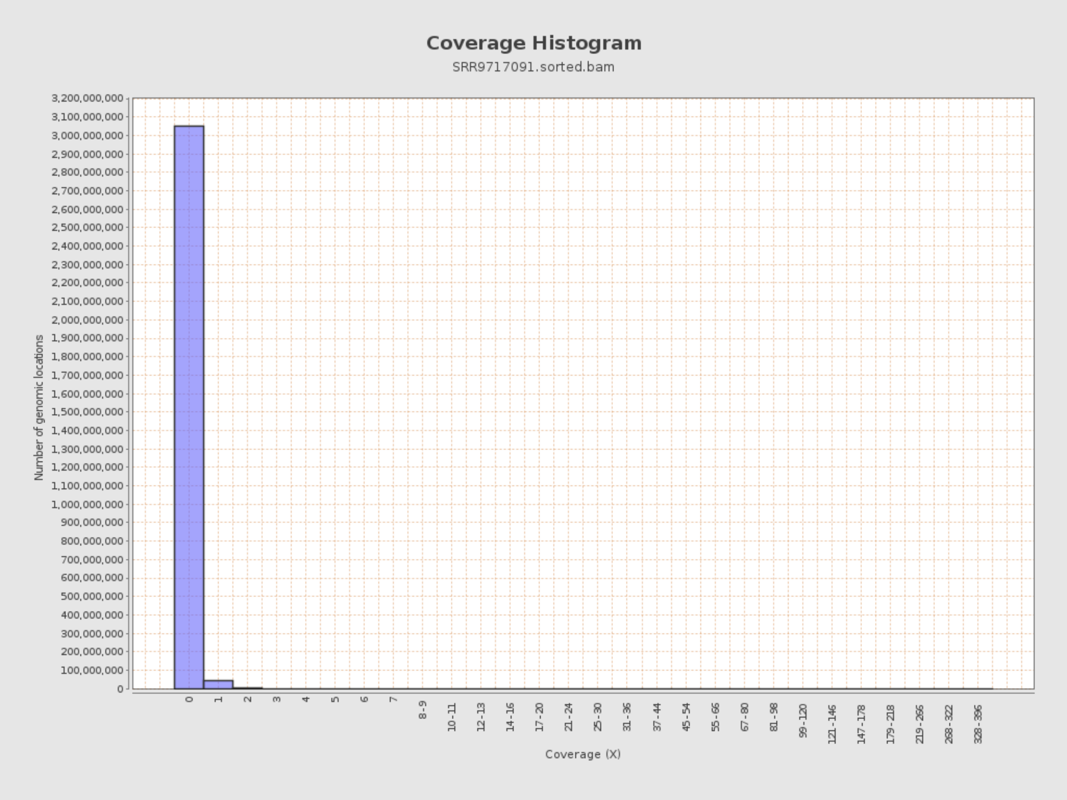
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4105398	0.0165	0.3461
chr2	243199373	4454429	0.0183	0.3188
chr3	198022430	3435108	0.0173	0.139
chr4	191154276	3361859	0.0176	0.1471
chr5	180915260	3099227	0.0171	0.1394
chr6	171115067	2952038	0.0173	0.161
chr7	159138663	2877555	0.0181	0.2876

chr8	146364022	2704432	0.0185	0.2958
chr9	141213431	2237431	0.0158	0.243
chr10	135534747	2425016	0.0179	0.2065
chr11	135006516	2334203	0.0173	0.2179
chr12	133851895	2339300	0.0175	0.1418
chr13	115169878	1597415	0.0139	0.1235
chr14	107349540	1567439	0.0146	0.1596
chr15	102531392	1460072	0.0142	0.1272
chr16	90354753	1492742	0.0165	0.1485
chr17	81195210	1420139	0.0175	0.1502
chr18	78077248	1470375	0.0188	0.4222
chr19	59128983	1101216	0.0186	0.2635
chr20	63025520	1034715	0.0164	0.14
chr21	48129895	696171	0.0145	0.1325
chr22	51304566	575119	0.0112	0.1113
chrMT	16571	6411	0.3869	0.7031
chrX	155270560	2983957	0.0192	0.1833
chrY	59373566	143066	0.0024	0.0743

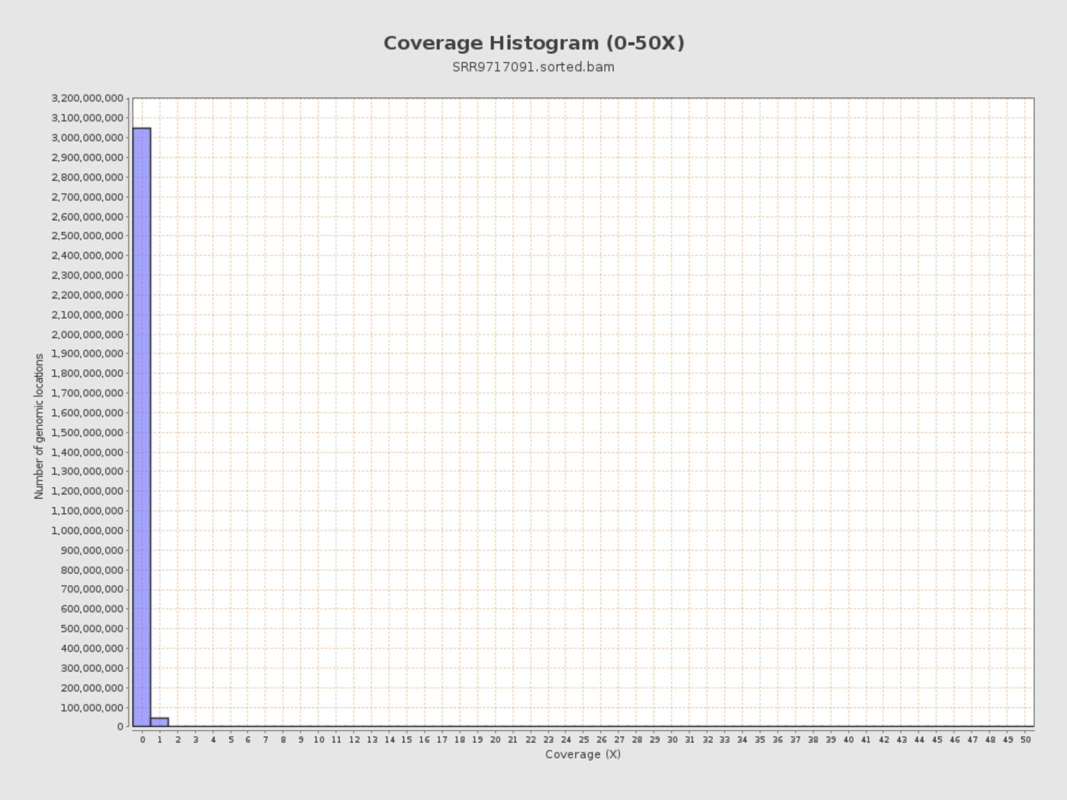
3. Results : Coverage across reference



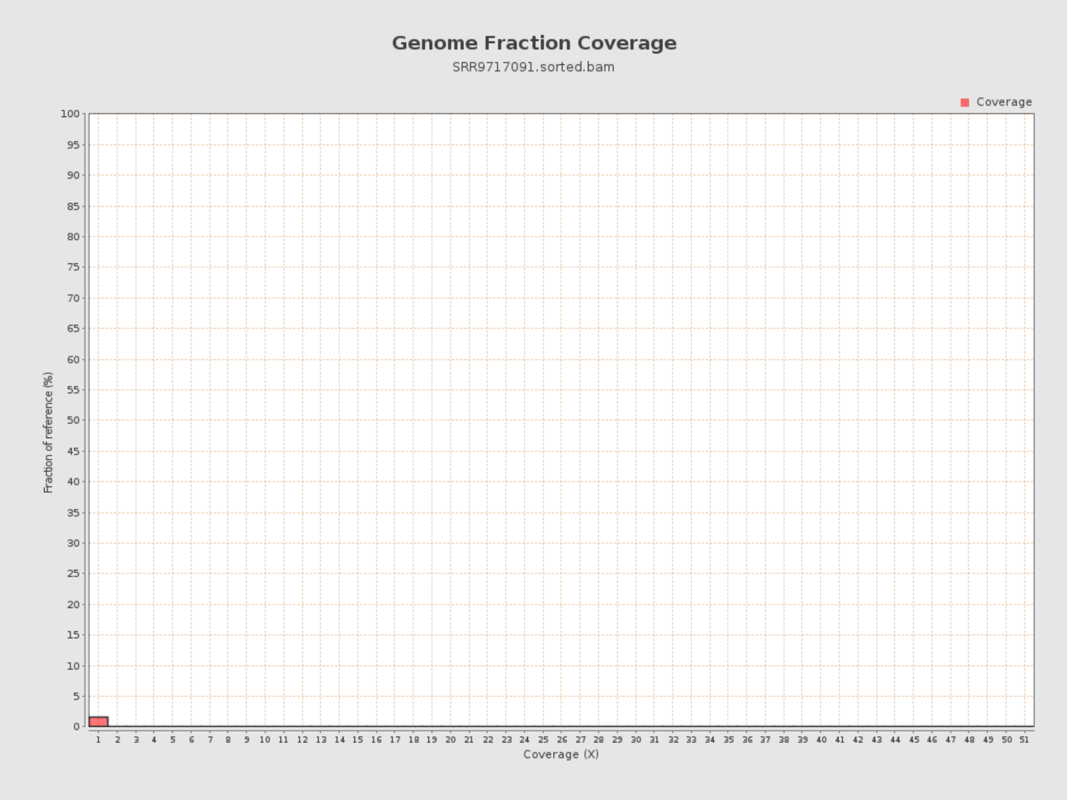
4. Results : Coverage Histogram



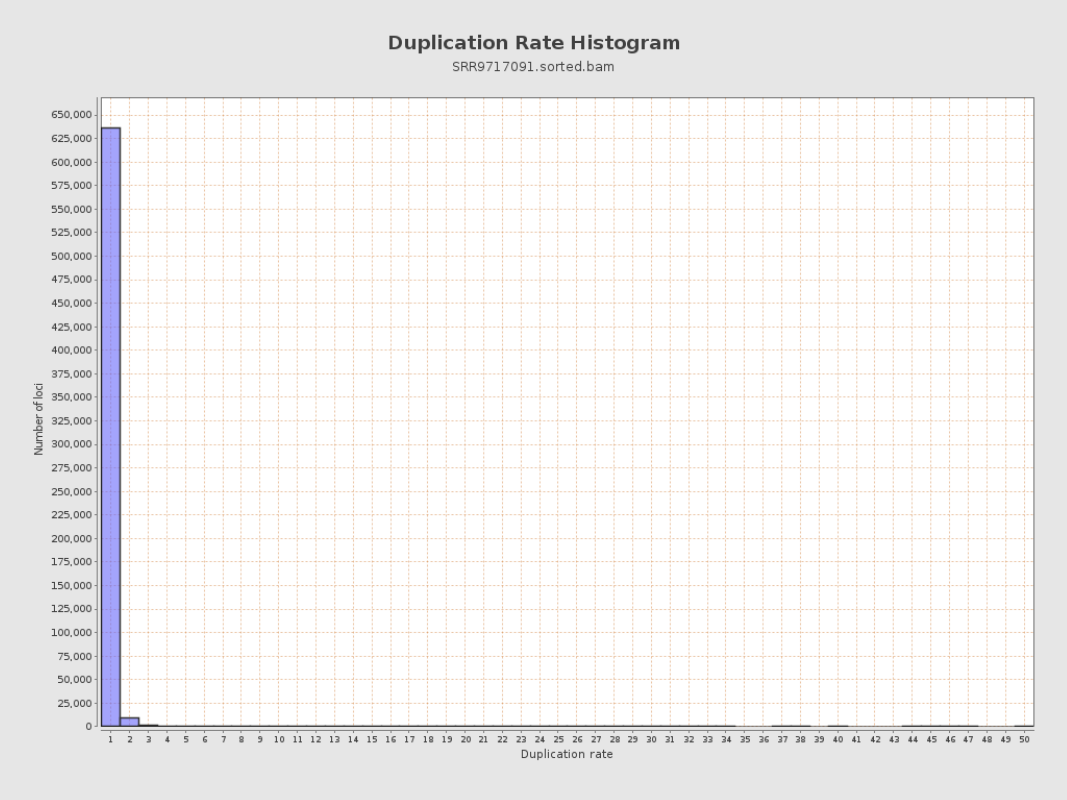
5. Results : Coverage Histogram (0-50X)



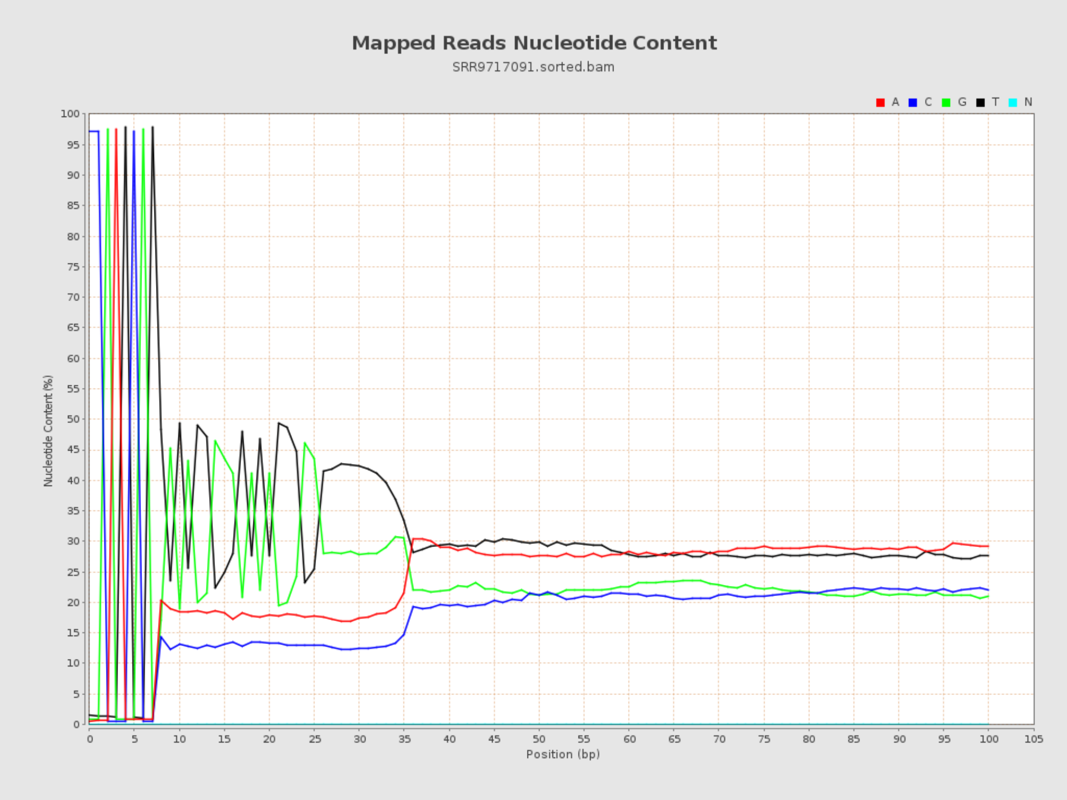
6. Results : Genome Fraction Coverage



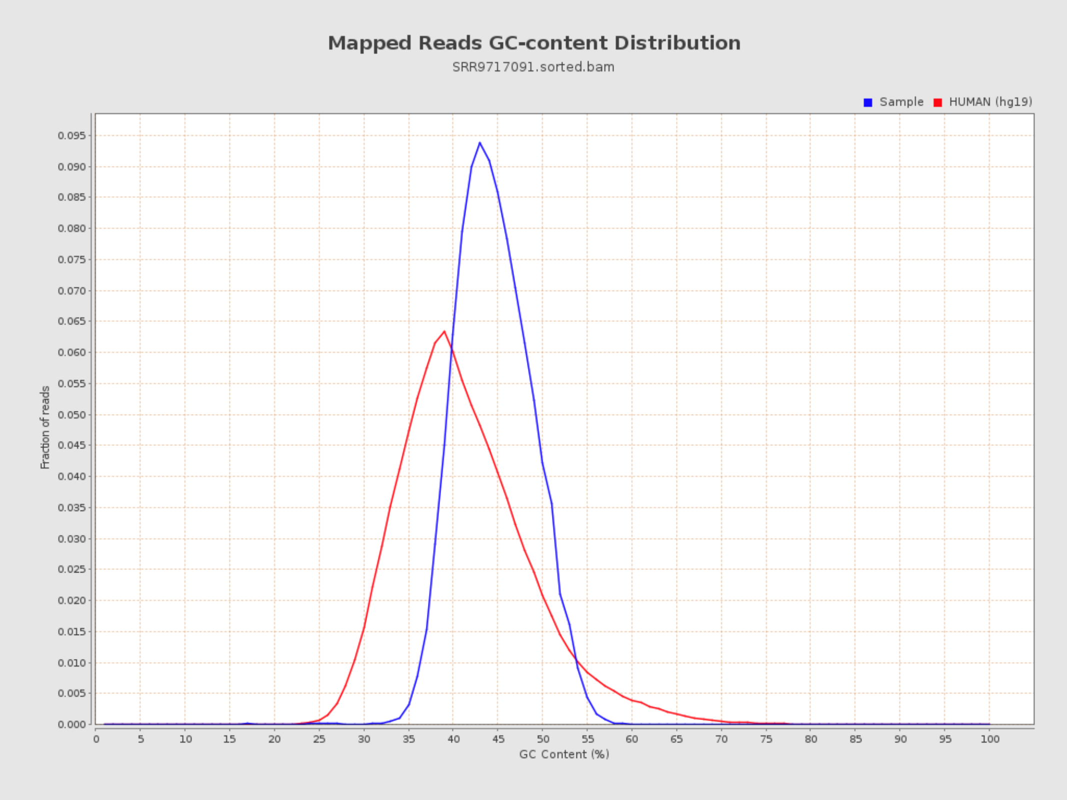
7. Results : Duplication Rate Histogram



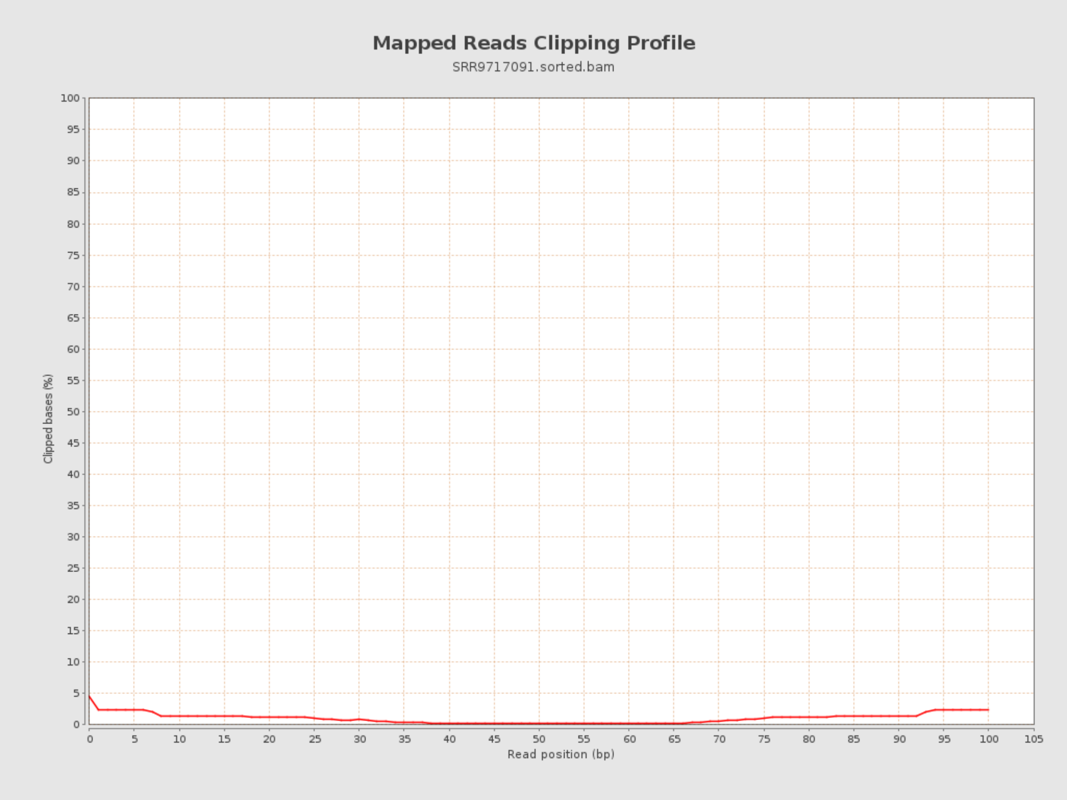
8. Results : Mapped Reads Nucleotide Content



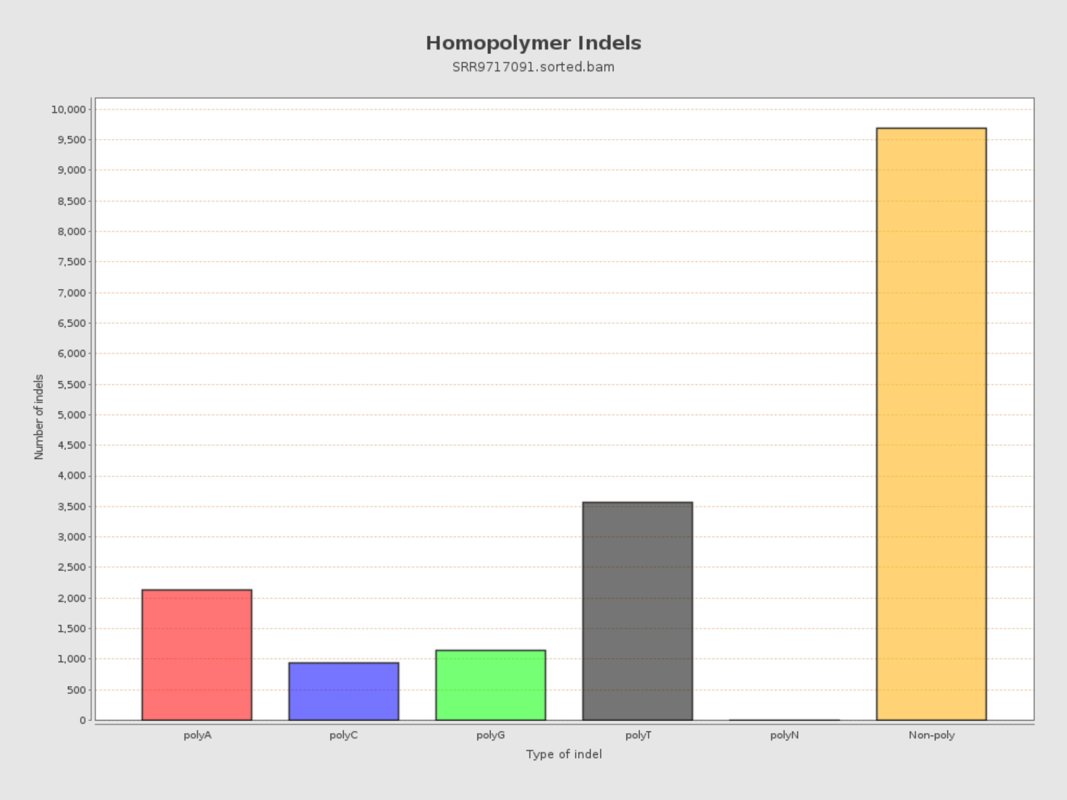
9. Results : Mapped Reads GC-content Distribution



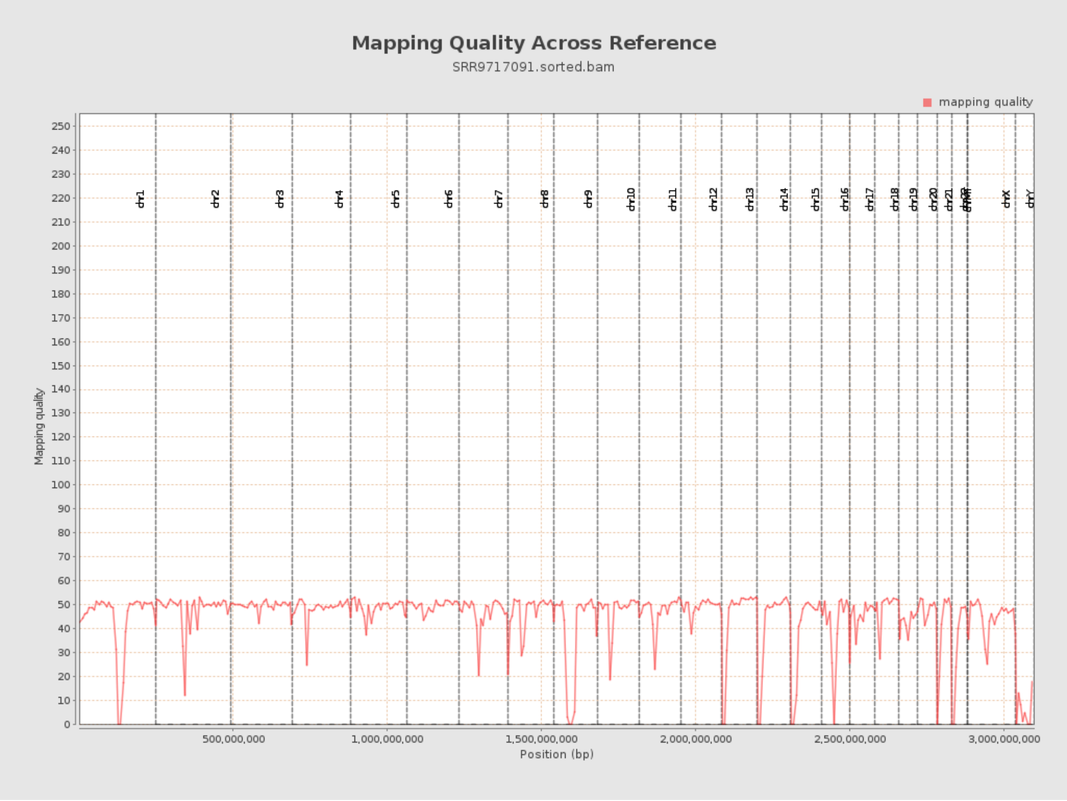
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram