Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:30:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867832.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_SRR9867832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:30:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	964,861
Mapped reads	894,280 / 92.68%
Unmapped reads	70,581 / 7.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,867 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	26,609 / 2.76%
Duplication rate	2.26%
Clipped reads	894,523 / 92.71%

2.2. ACGT Content

Number/percentage of A's	13,762,200 / 25.95%
Number/percentage of C's	10,453,854 / 19.71%
Number/percentage of T's	16,428,823 / 30.98%
Number/percentage of G's	12,379,791 / 23.34%
Number/percentage of N's	6,576 / 0.01%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.1819

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

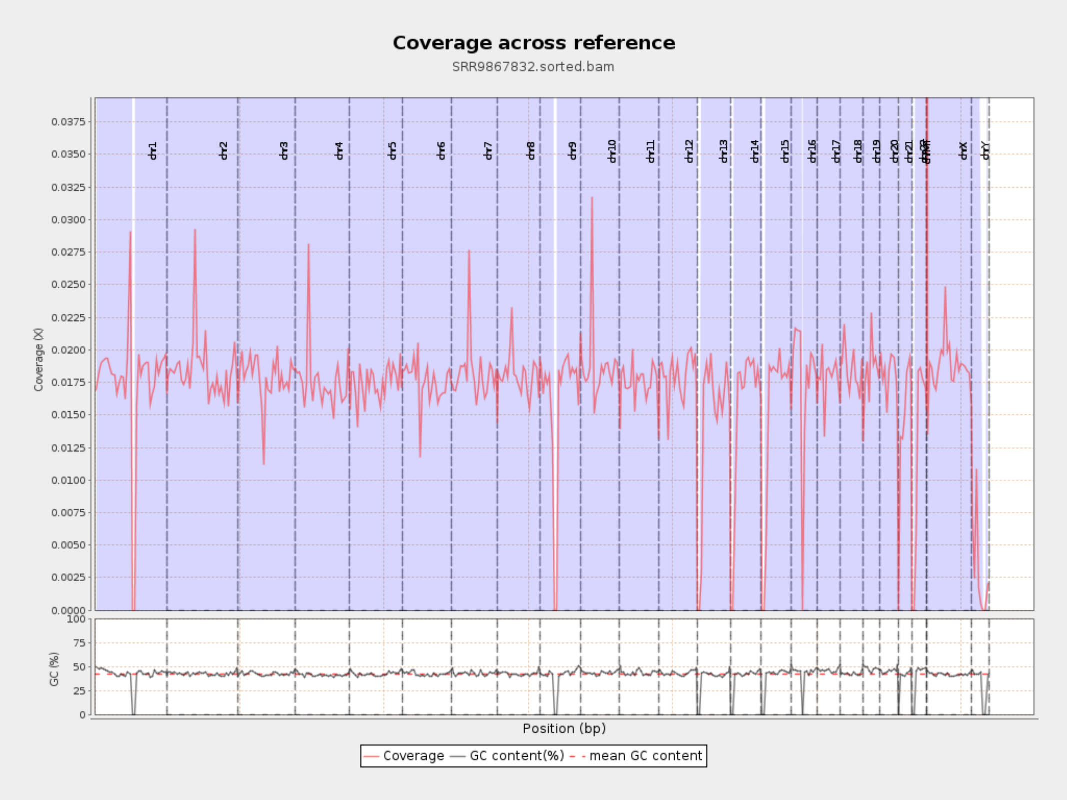
General error rate	0.52%
Mismatches	264,284
Insertions	4,362
Mapped reads with at least one insertion	0.48%
Deletions	10,003
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.36%

2.6. Chromosome stats

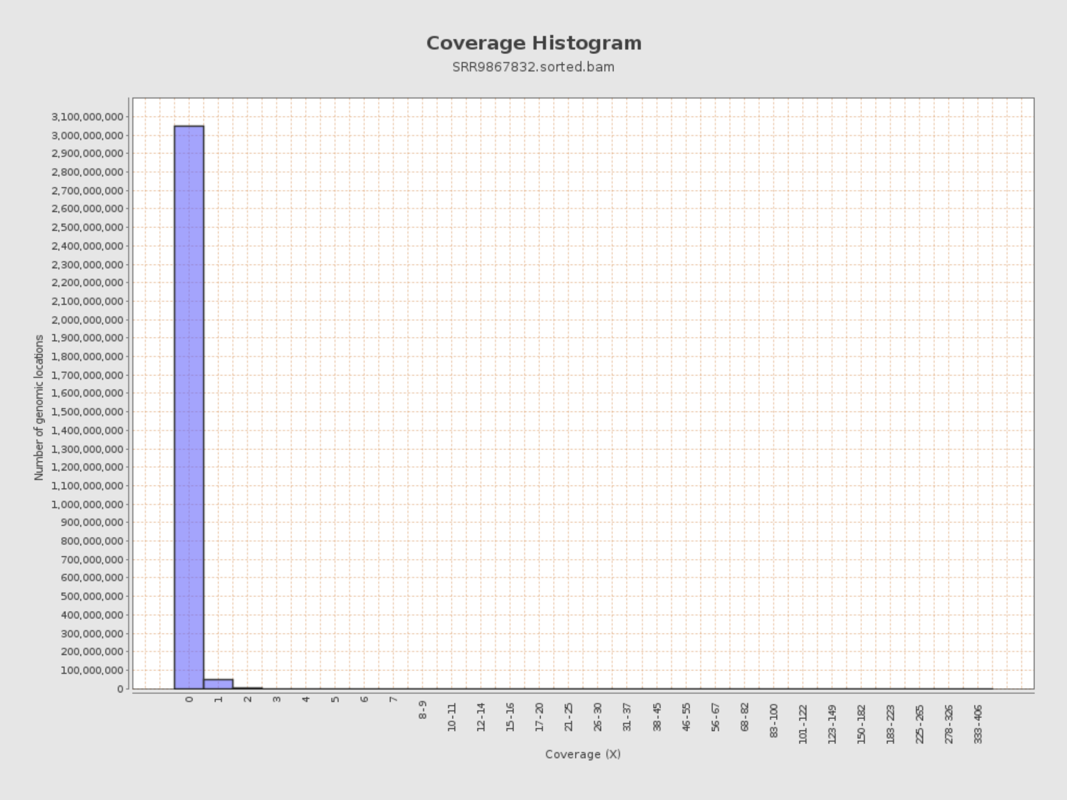
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4340224	0.0174	0.2919
chr2	243199373	4501092	0.0185	0.2303
chr3	198022430	3545721	0.0179	0.1411
chr4	191154276	3372059	0.0176	0.1516
chr5	180915260	3172883	0.0175	0.1403
chr6	171115067	2998654	0.0175	0.1513
chr7	159138663	2912162	0.0183	0.2081

chr8	146364022	2649170	0.0181	0.1967
chr9	141213431	2241370	0.0159	0.1653
chr10	135534747	2551553	0.0188	0.1842
chr11	135006516	2382057	0.0176	0.1669
chr12	133851895	2410755	0.018	0.1428
chr13	115169878	1645227	0.0143	0.1261
chr14	107349540	1623642	0.0151	0.1321
chr15	102531392	1526661	0.0149	0.1297
chr16	90354753	1562682	0.0173	0.1452
chr17	81195210	1453337	0.0179	0.1478
chr18	78077248	1443177	0.0185	0.2607
chr19	59128983	1095754	0.0185	0.229
chr20	63025520	1138642	0.0181	0.1437
chr21	48129895	699927	0.0145	0.138
chr22	51304566	632392	0.0123	0.1169
chrMT	16571	57643	3.4785	2.623
chrX	155270560	2915755	0.0188	0.1518
chrY	59373566	174278	0.0029	0.107

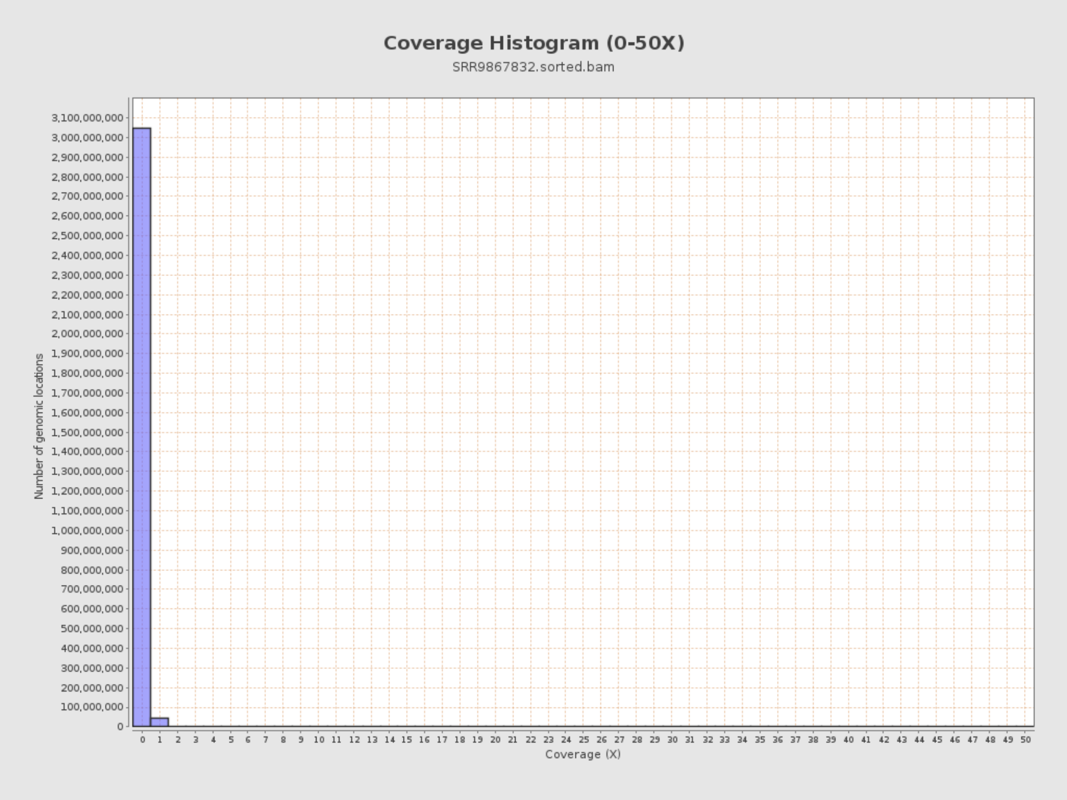
3. Results : Coverage across reference



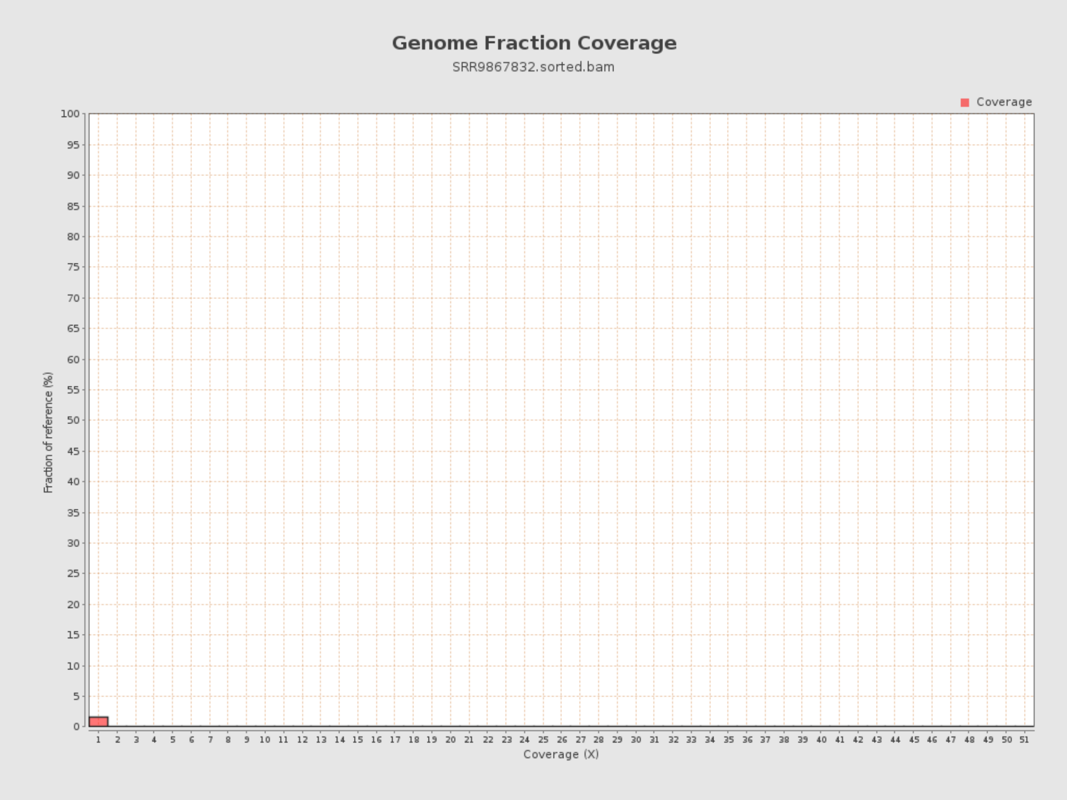
4. Results : Coverage Histogram



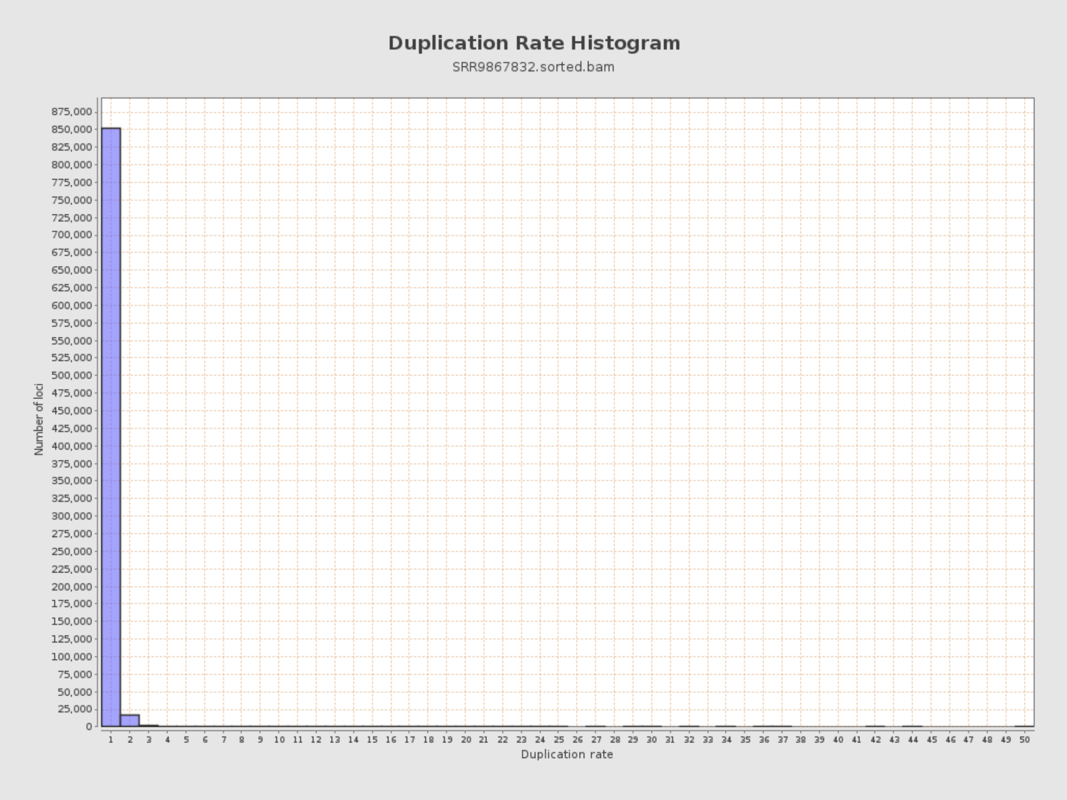
5. Results : Coverage Histogram (0-50X)



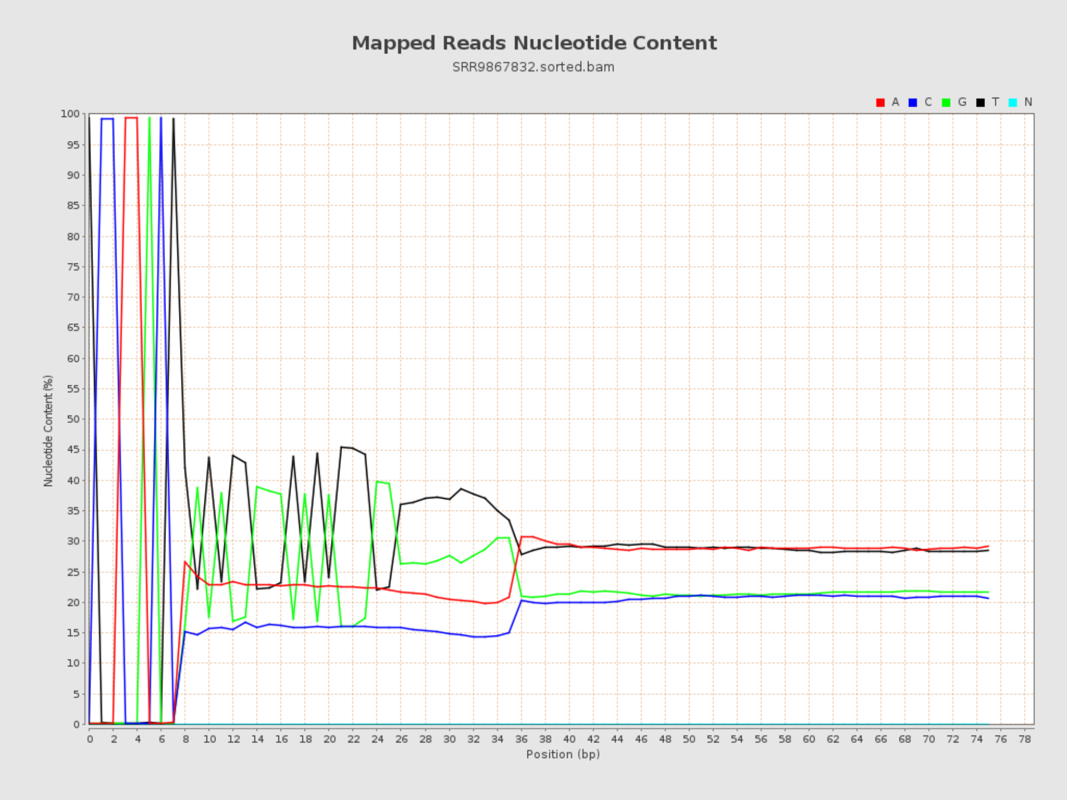
6. Results : Genome Fraction Coverage



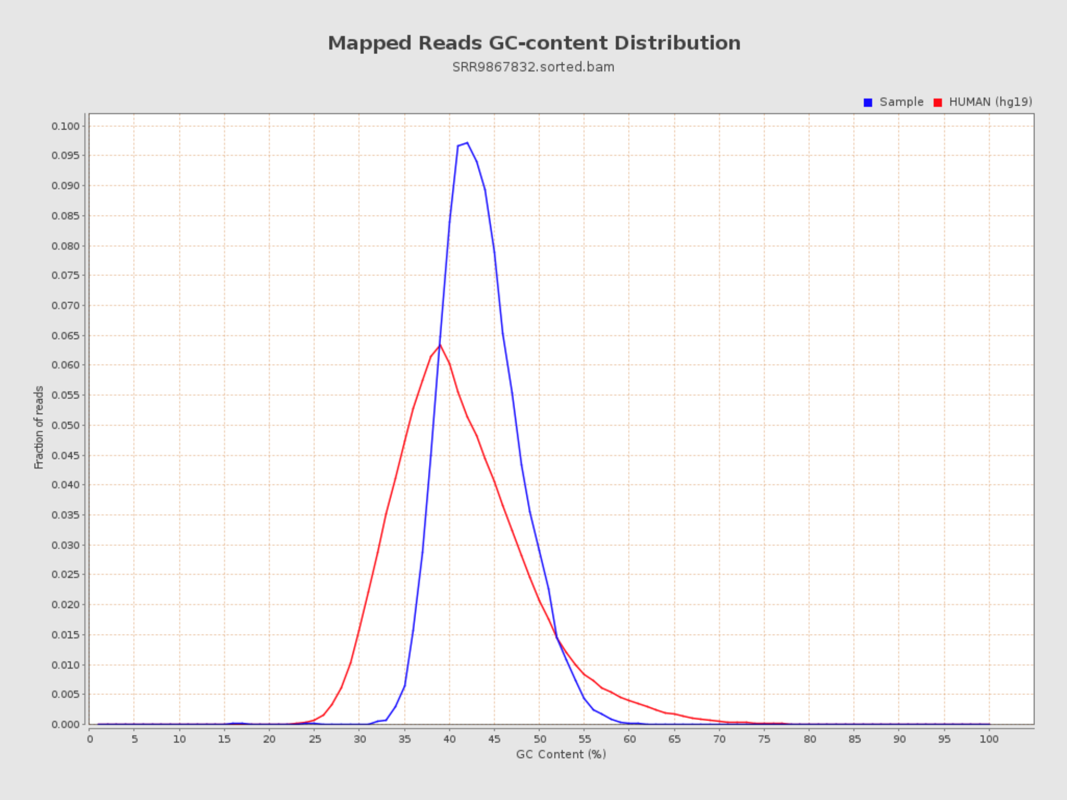
7. Results : Duplication Rate Histogram



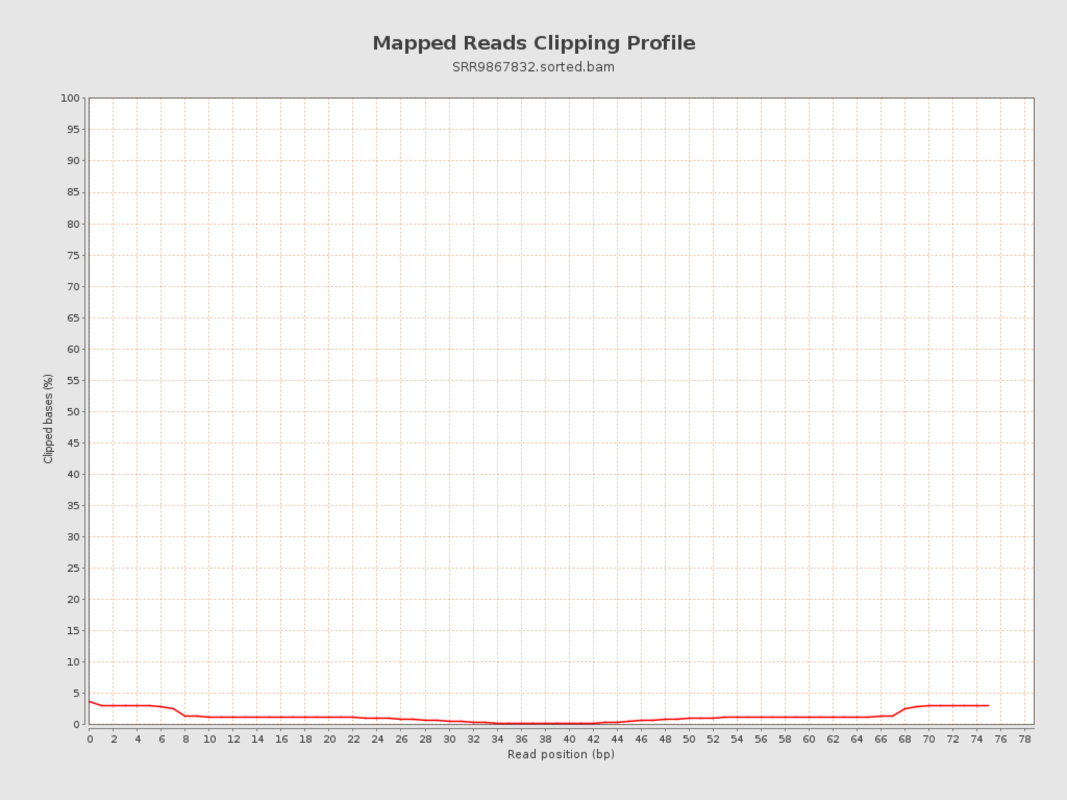
8. Results : Mapped Reads Nucleotide Content



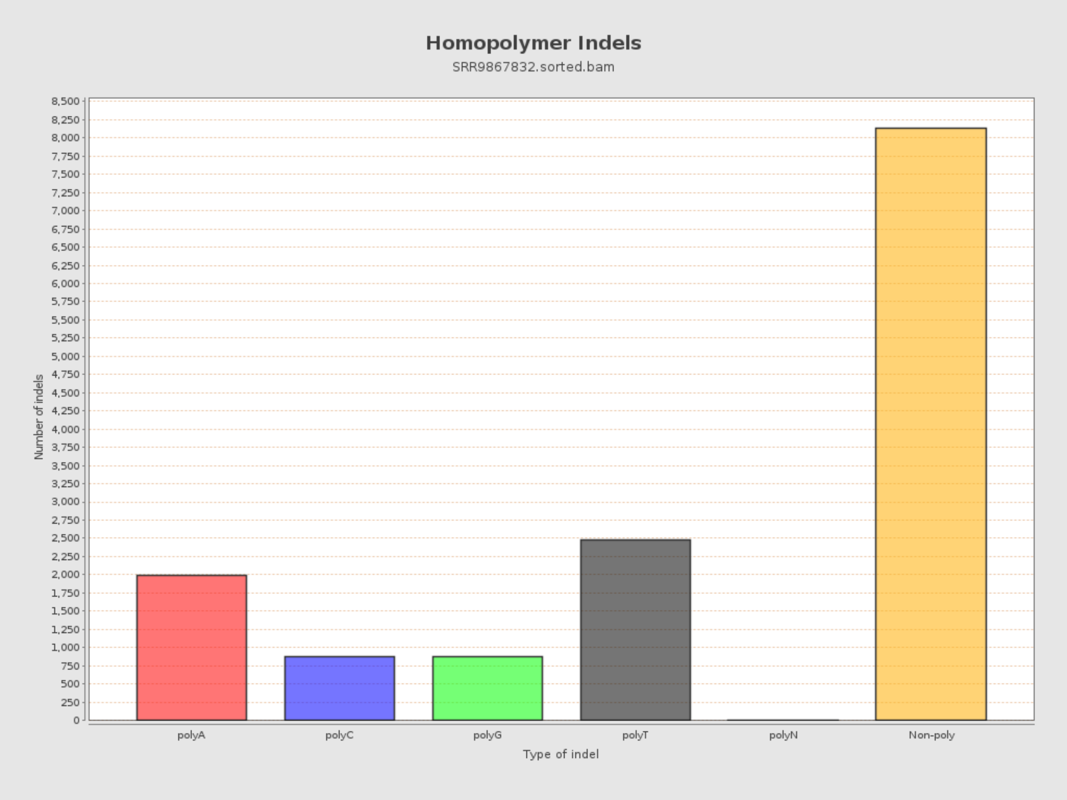
9. Results : Mapped Reads GC-content Distribution



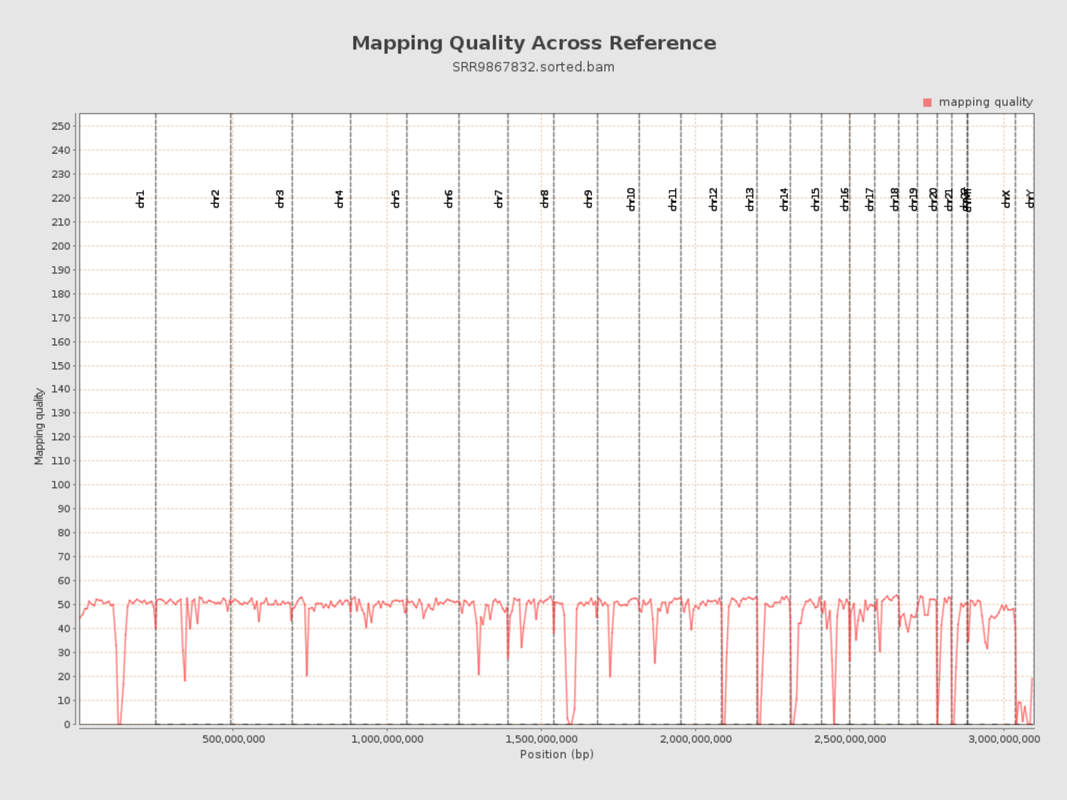
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram