Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:31:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716962.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_SRR9716962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716962.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:31:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	573,042
Mapped reads	535,118 / 93.38%
Unmapped reads	37,924 / 6.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,232 / 2.48%
Read min/max/mean length	30 / 101 / 101.92
Duplicated reads (estimated)	11,396 / 1.99%
Duplication rate	1.68%
Clipped reads	548,229 / 95.67%

2.2. ACGT Content

Number/percentage of A's	10,400,555 / 25.06%
Number/percentage of C's	8,485,068 / 20.44%
Number/percentage of T's	12,416,112 / 29.91%
Number/percentage of G's	10,204,446 / 24.58%
Number/percentage of N's	1,606 / 0%
GC Percentage	45.03%

2.3. Coverage

Mean	0.0134

Standard Deviation	0.1403

2.4. Mapping Quality

Mean Mapping Quality	46.44

2.5. Mismatches and indels

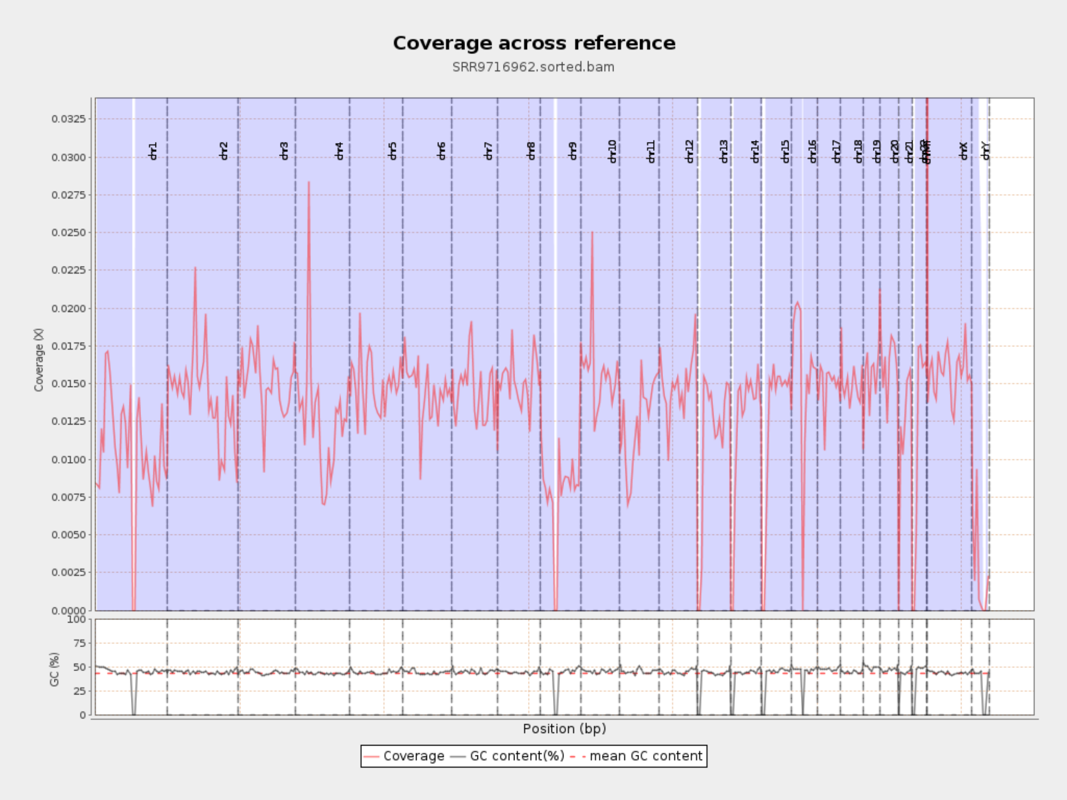
General error rate	0.68%
Mismatches	274,856
Insertions	3,658
Mapped reads with at least one insertion	0.67%
Deletions	7,724
Mapped reads with at least one deletion	1.42%
Homopolymer indels	38.96%

2.6. Chromosome stats

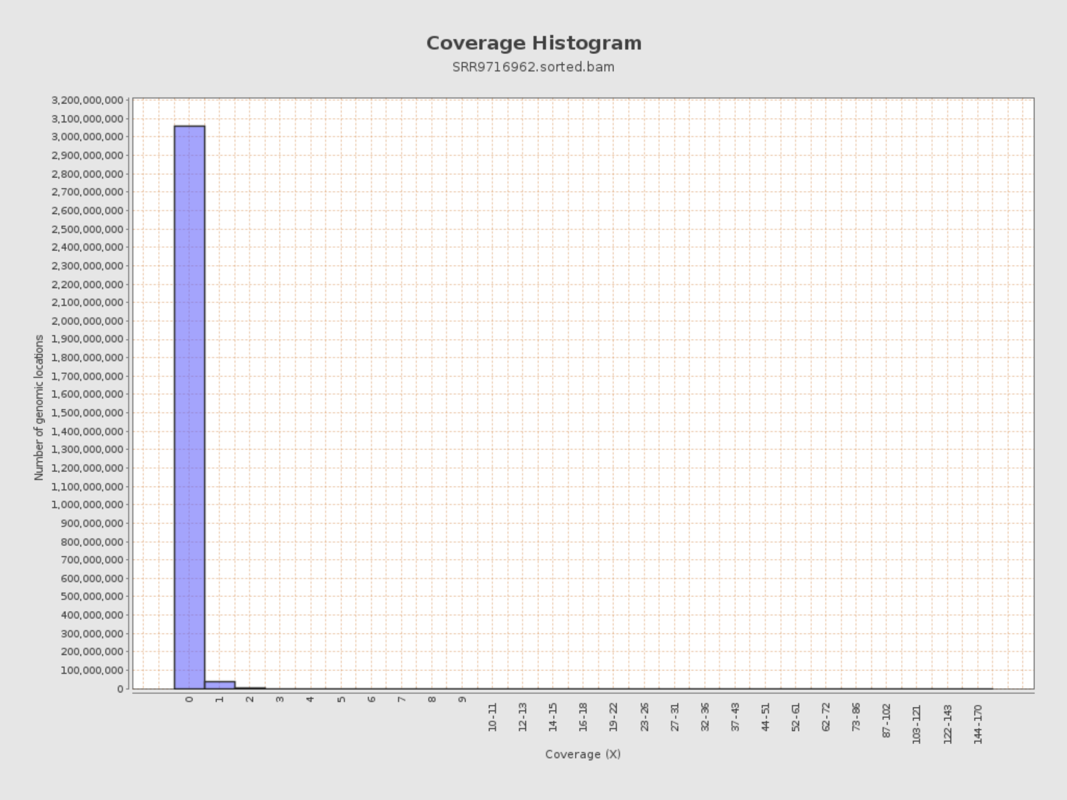
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2605632	0.0105	0.1733
chr2	243199373	3471163	0.0143	0.1522
chr3	198022430	2989806	0.0151	0.1292
chr4	191154276	2456344	0.0129	0.1345
chr5	180915260	2719202	0.015	0.1292
chr6	171115067	2471383	0.0144	0.1295
chr7	159138663	2318710	0.0146	0.1615

chr8	146364022	2220321	0.0152	0.1503
chr9	141213431	1103804	0.0078	0.1139
chr10	135534747	2137635	0.0158	0.1589
chr11	135006516	1675195	0.0124	0.1382
chr12	133851895	1995742	0.0149	0.1292
chr13	115169878	1302204	0.0113	0.1119
chr14	107349540	1306246	0.0122	0.121
chr15	102531392	1267936	0.0124	0.1173
chr16	90354753	1380873	0.0153	0.134
chr17	81195210	1203942	0.0148	0.1335
chr18	78077248	1164248	0.0149	0.1801
chr19	59128983	926647	0.0157	0.1598
chr20	63025520	1022926	0.0162	0.1391
chr21	48129895	581964	0.0121	0.1243
chr22	51304566	597612	0.0116	0.1154
chrMT	16571	11614	0.7009	1.0126
chrX	155270560	2446056	0.0158	0.1373
chrY	59373566	146783	0.0025	0.0867

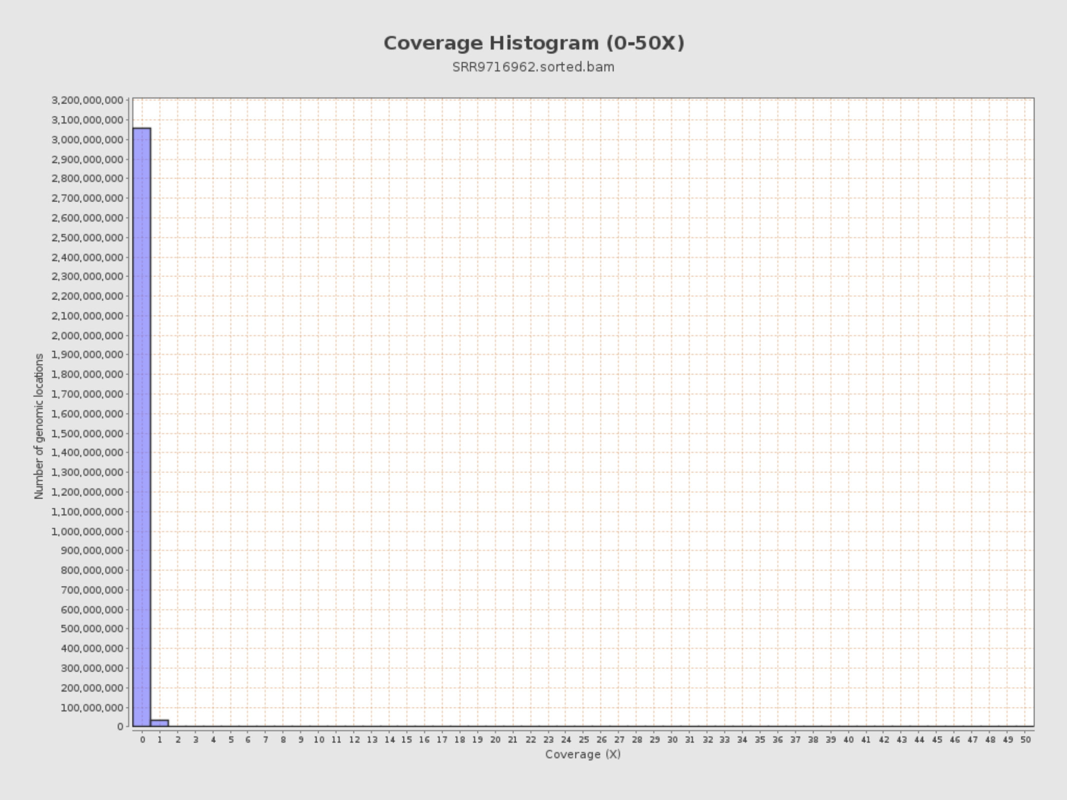
3. Results : Coverage across reference



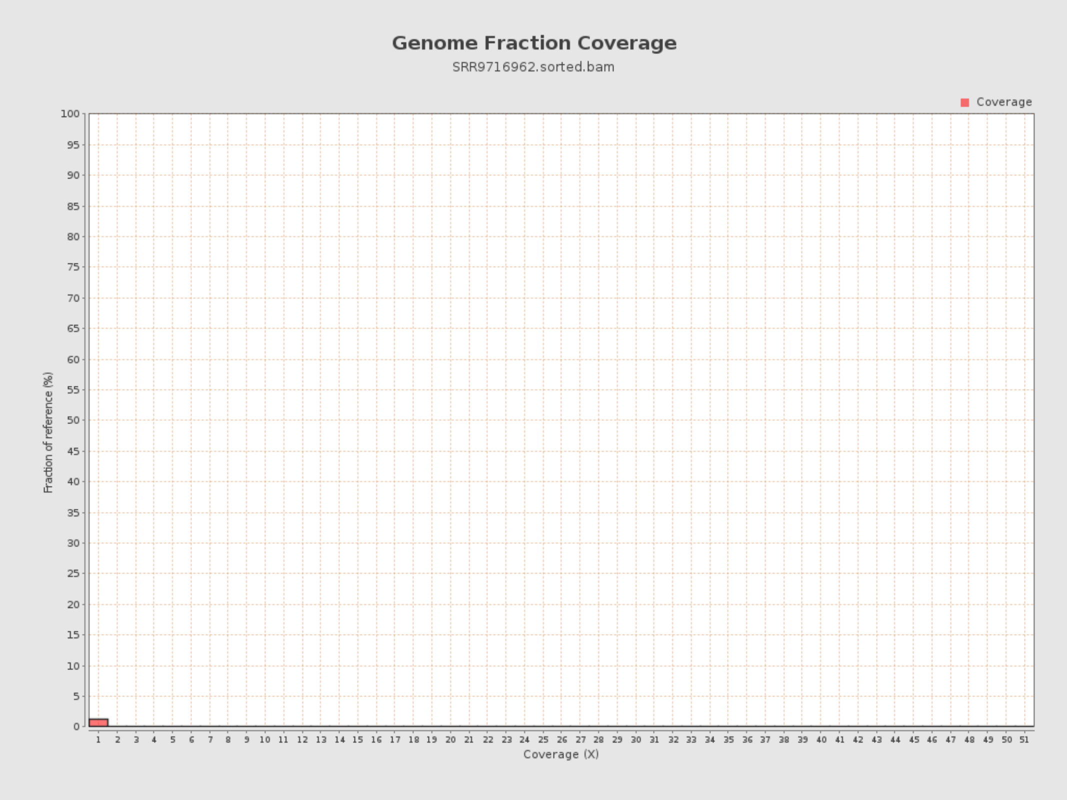
4. Results : Coverage Histogram



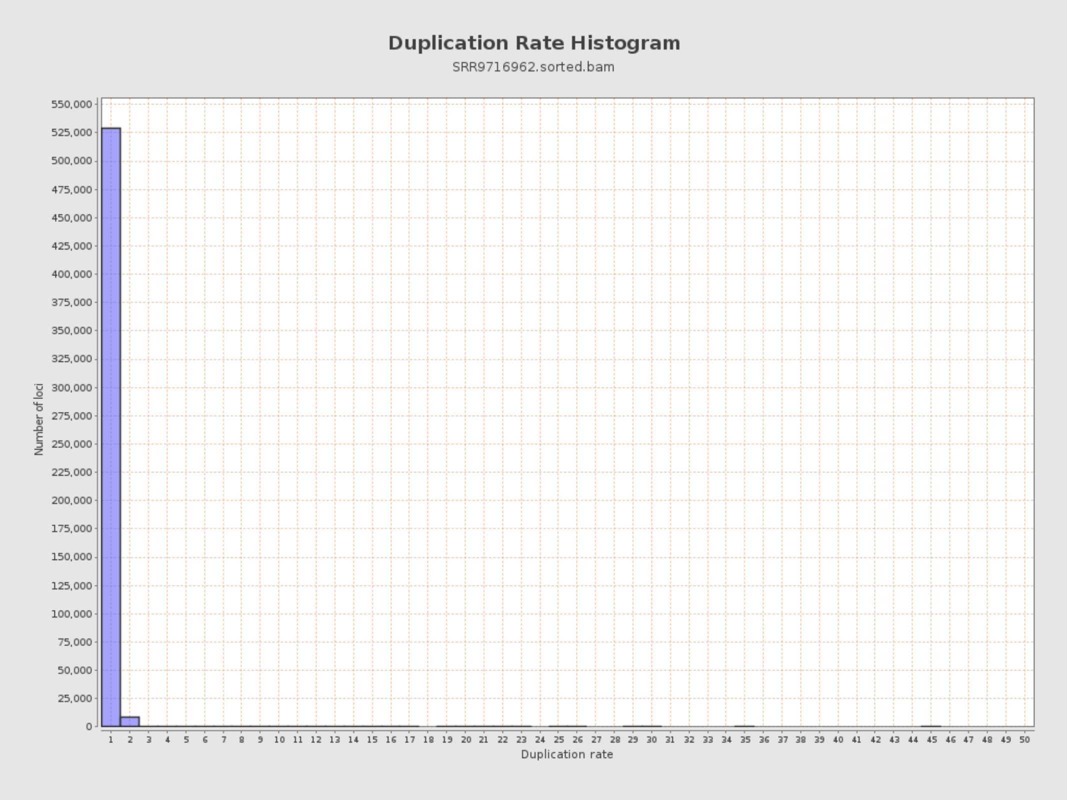
5. Results : Coverage Histogram (0-50X)



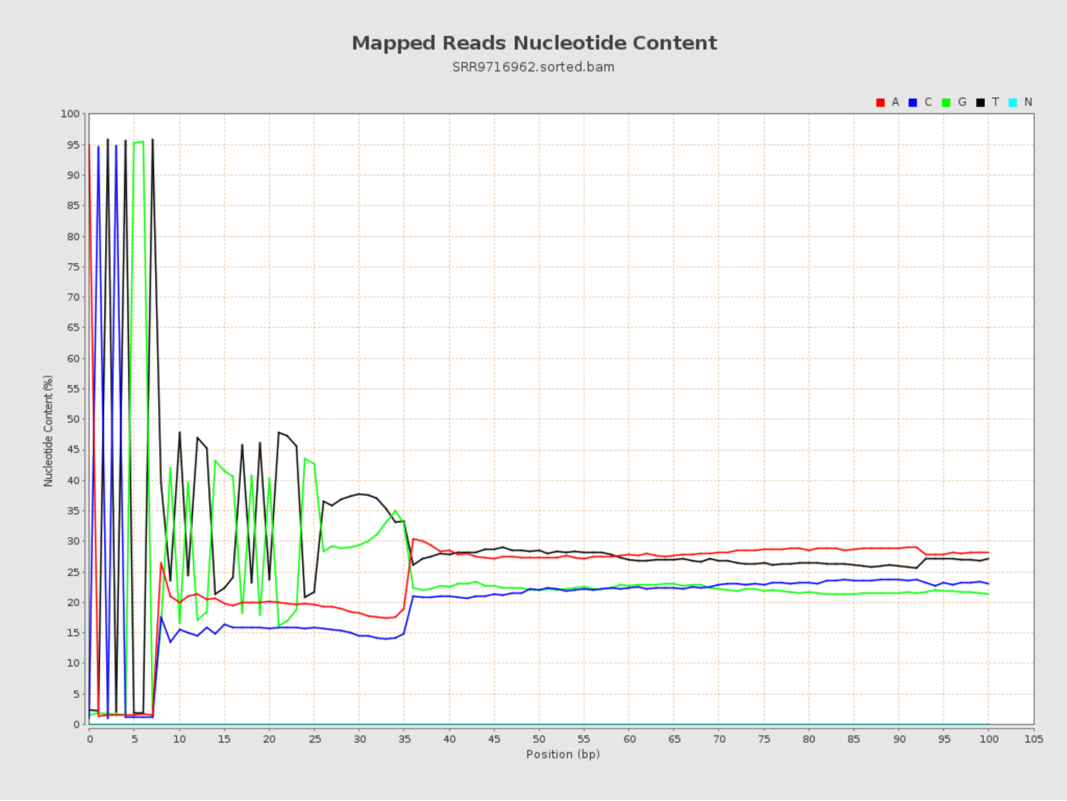
6. Results : Genome Fraction Coverage



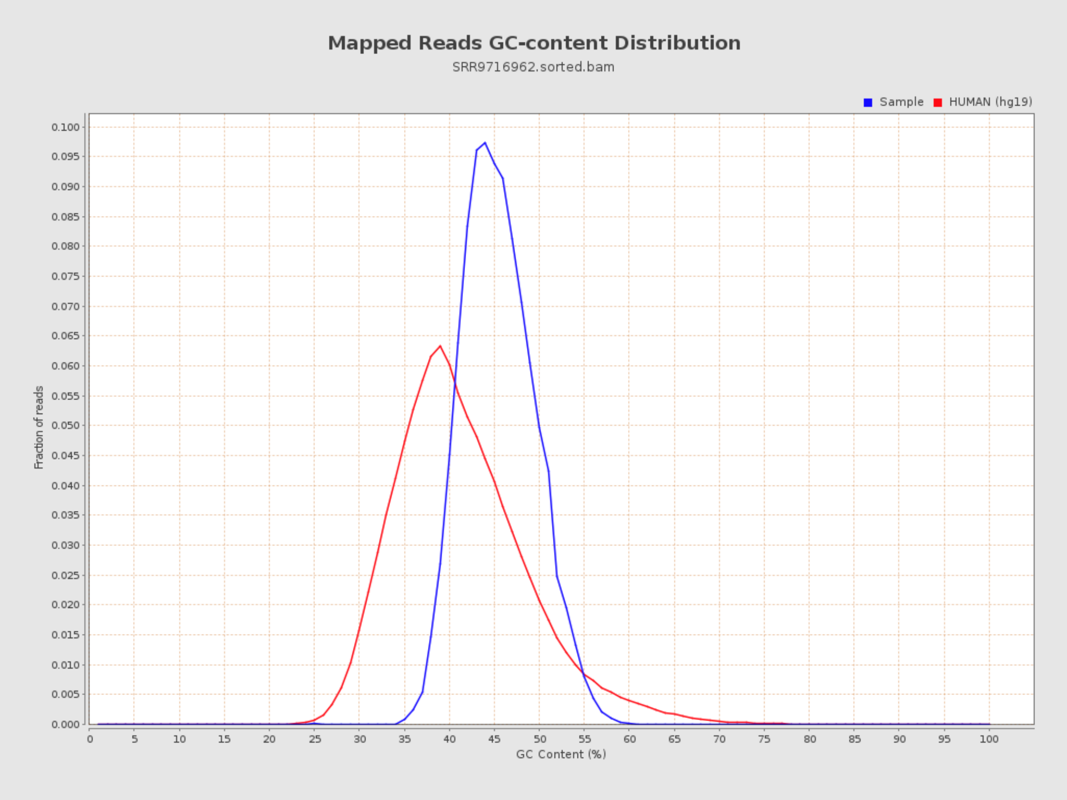
7. Results : Duplication Rate Histogram



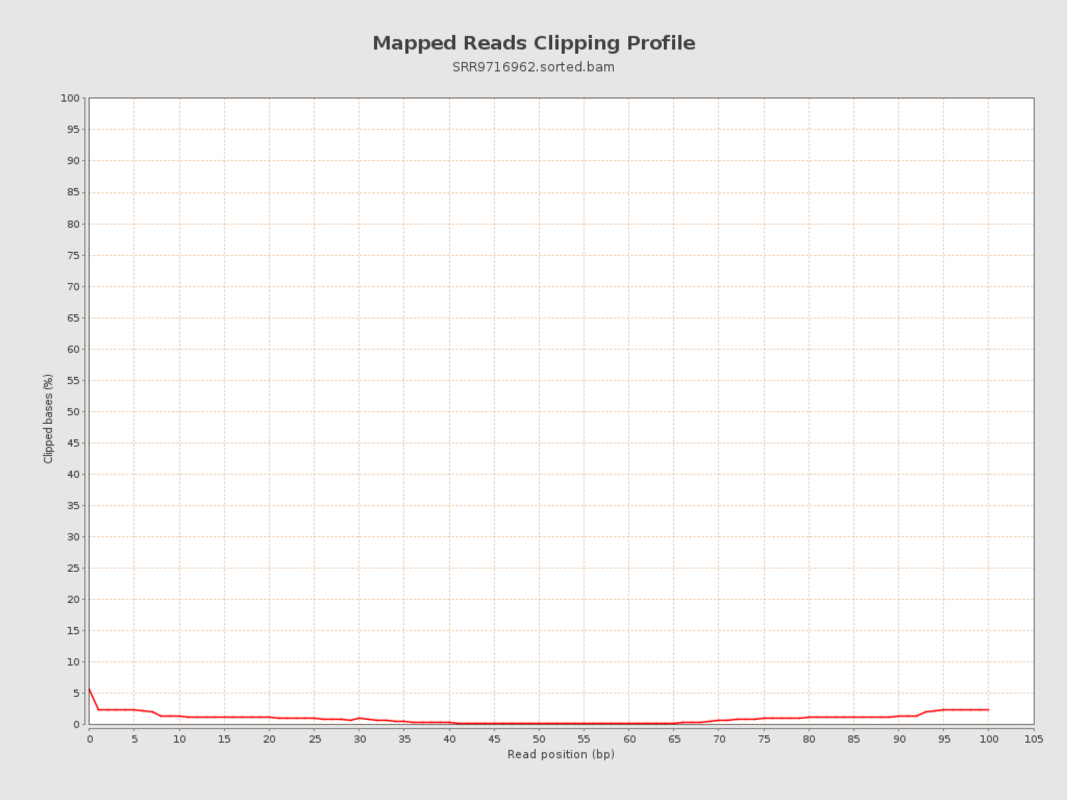
8. Results : Mapped Reads Nucleotide Content



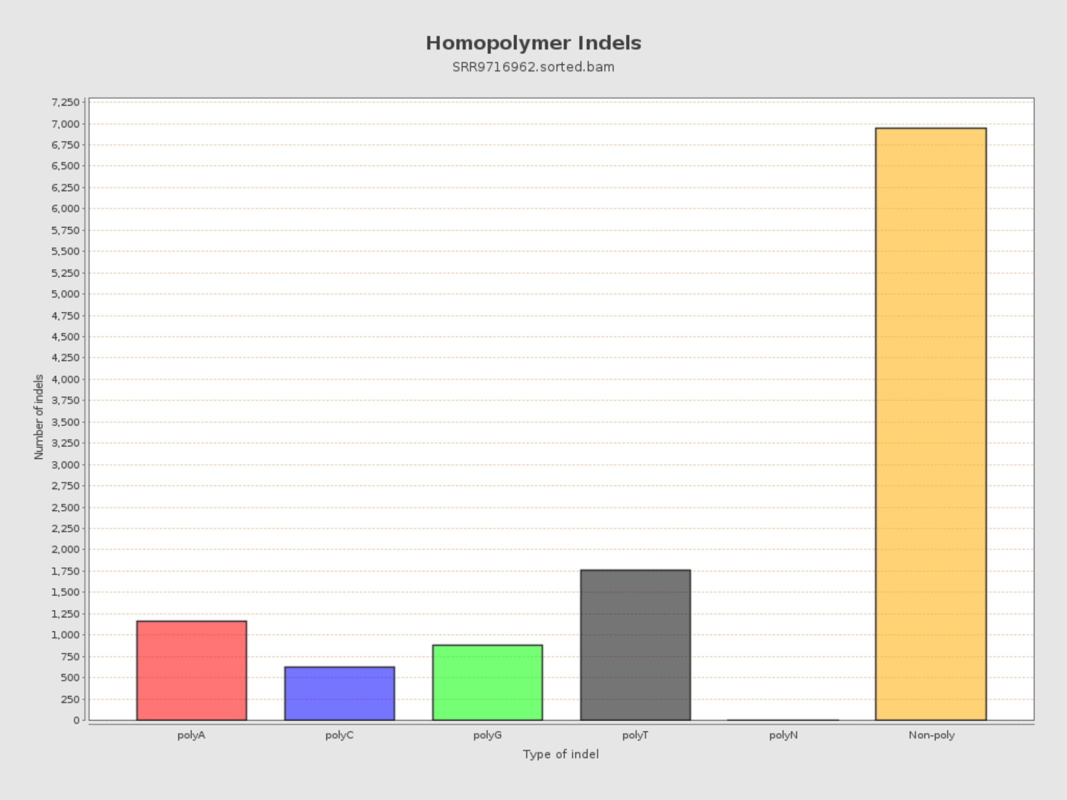
9. Results : Mapped Reads GC-content Distribution



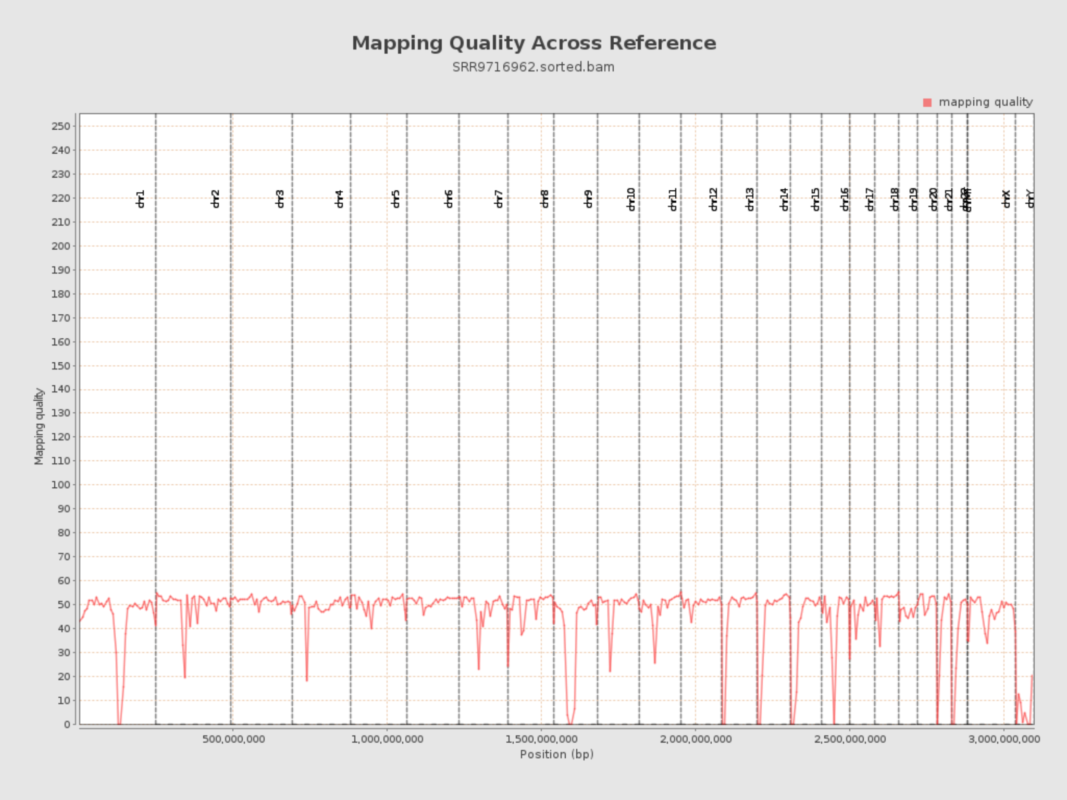
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram