Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:30:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716593.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_SRR9716593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716593.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:30:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716593.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,504,531
Mapped reads	1,350,036 / 89.73%
Unmapped reads	154,495 / 10.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,301 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	49,088 / 3.26%
Duplication rate	2.82%
Clipped reads	1,353,035 / 89.93%

2.2. ACGT Content

Number/percentage of A's	18,864,610 / 24.01%
Number/percentage of C's	15,716,841 / 20%
Number/percentage of T's	25,461,134 / 32.41%
Number/percentage of G's	18,525,206 / 23.58%
Number/percentage of N's	1,041 / 0%
GC Percentage	43.58%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2354

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

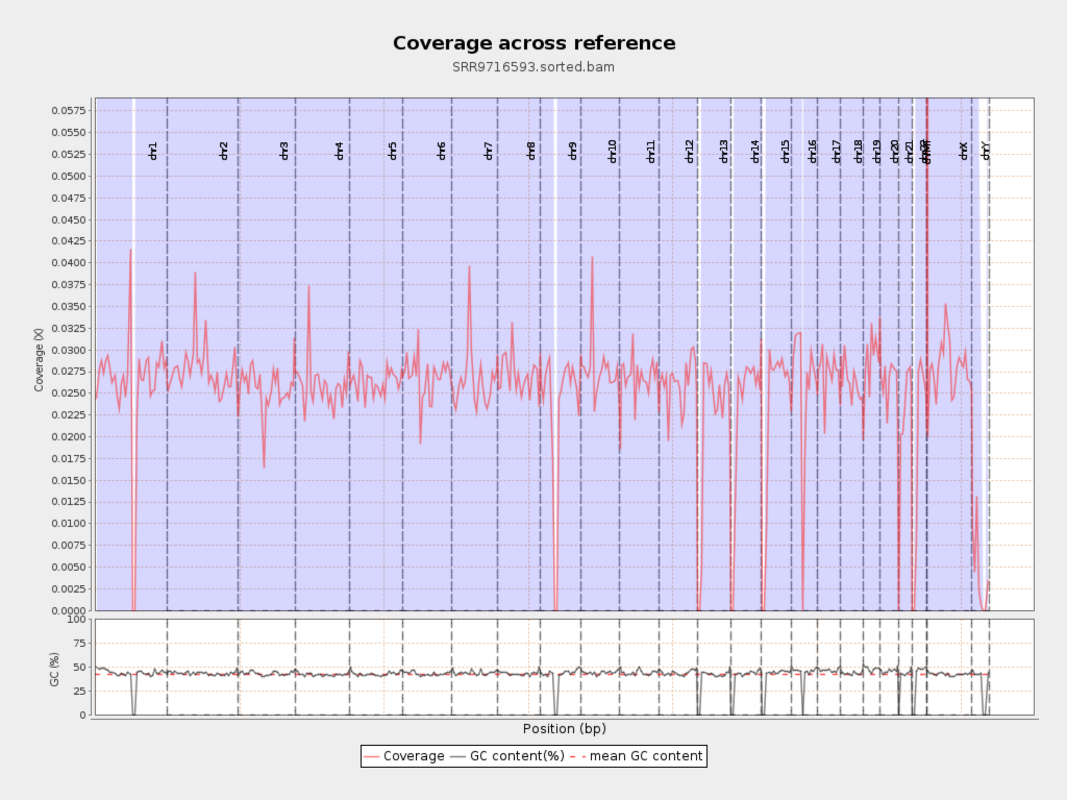
General error rate	0.51%
Mismatches	390,730
Insertions	5,542
Mapped reads with at least one insertion	0.41%
Deletions	14,128
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.1%

2.6. Chromosome stats

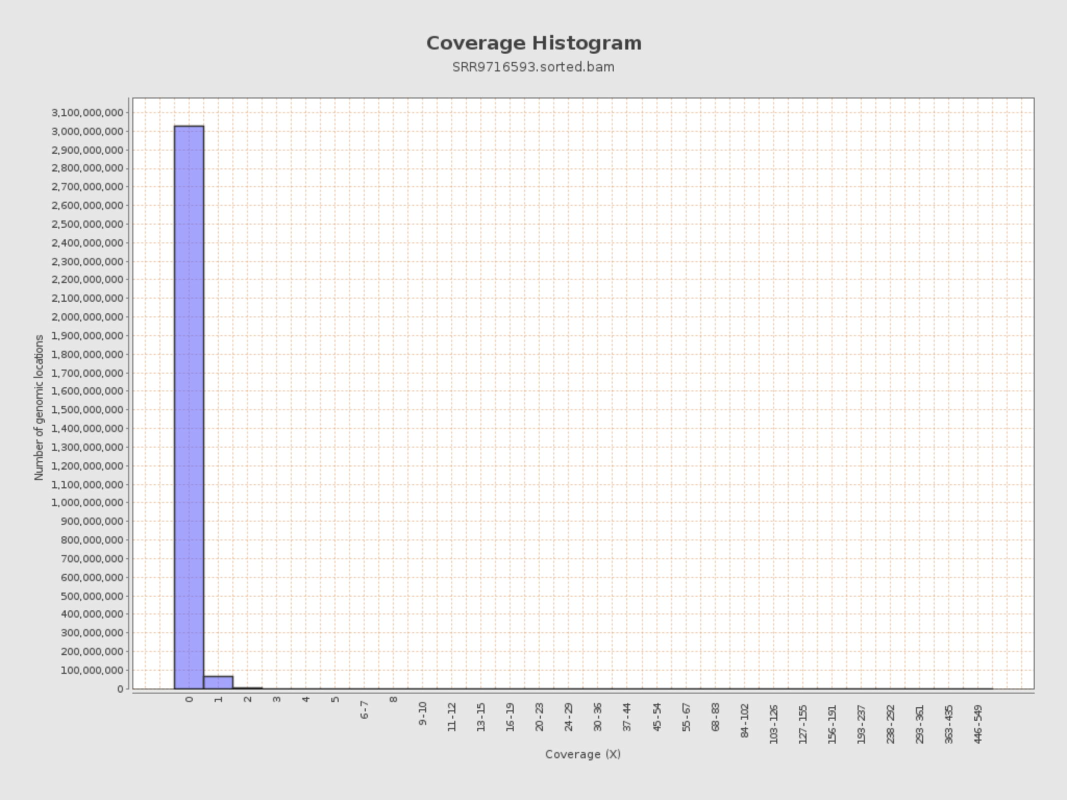
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6420333	0.0258	0.4098
chr2	243199373	6741351	0.0277	0.3015
chr3	198022430	5037241	0.0254	0.1733
chr4	191154276	4971498	0.026	0.1852
chr5	180915260	4766393	0.0263	0.1776
chr6	171115067	4597363	0.0269	0.2039
chr7	159138663	4222953	0.0265	0.2771

chr8	146364022	3948415	0.027	0.2185
chr9	141213431	3260731	0.0231	0.1995
chr10	135534747	3759463	0.0277	0.2269
chr11	135006516	3639530	0.027	0.2083
chr12	133851895	3510410	0.0262	0.1795
chr13	115169878	2465216	0.0214	0.1595
chr14	107349540	2393547	0.0223	0.1703
chr15	102531392	2306167	0.0225	0.1659
chr16	90354753	2286431	0.0253	0.1826
chr17	81195210	2222360	0.0274	0.1916
chr18	78077248	2052061	0.0263	0.3282
chr19	59128983	1714056	0.029	0.3074
chr20	63025520	1659749	0.0263	0.1804
chr21	48129895	1052792	0.0219	0.1748
chr22	51304566	950778	0.0185	0.1483
chrMT	16571	19152	1.1558	1.2322
chrX	155270560	4358757	0.0281	0.1964
chrY	59373566	234474	0.0039	0.1051

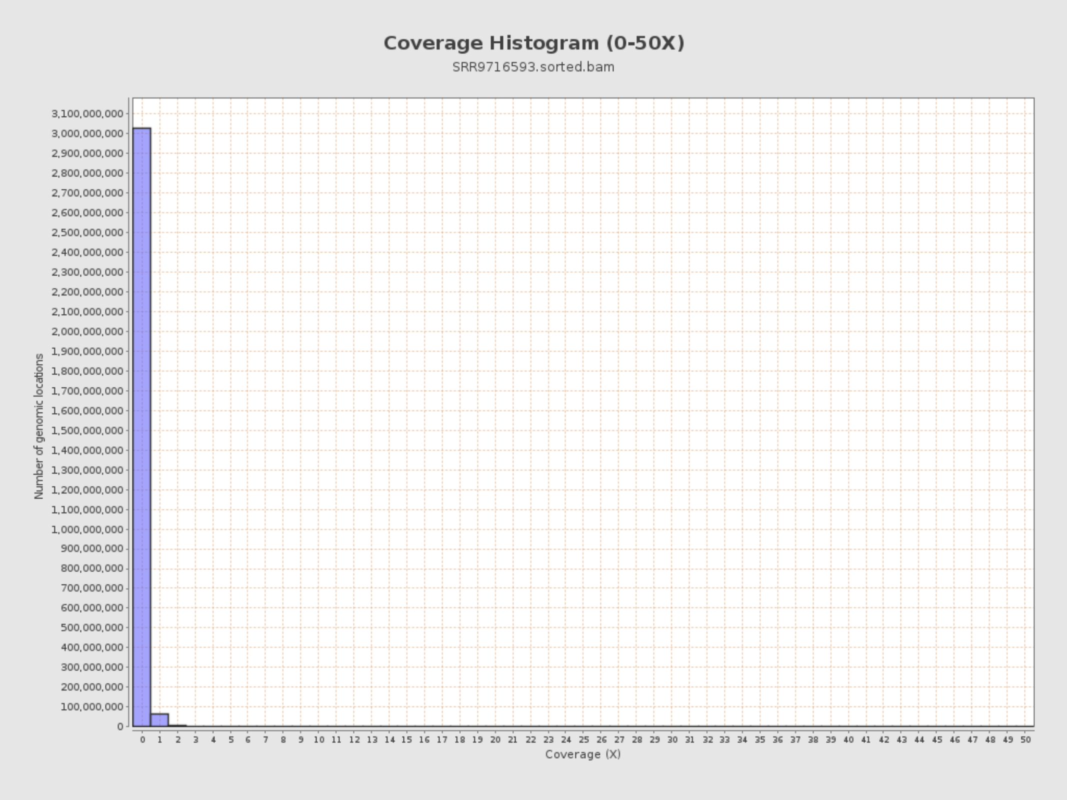
3. Results : Coverage across reference



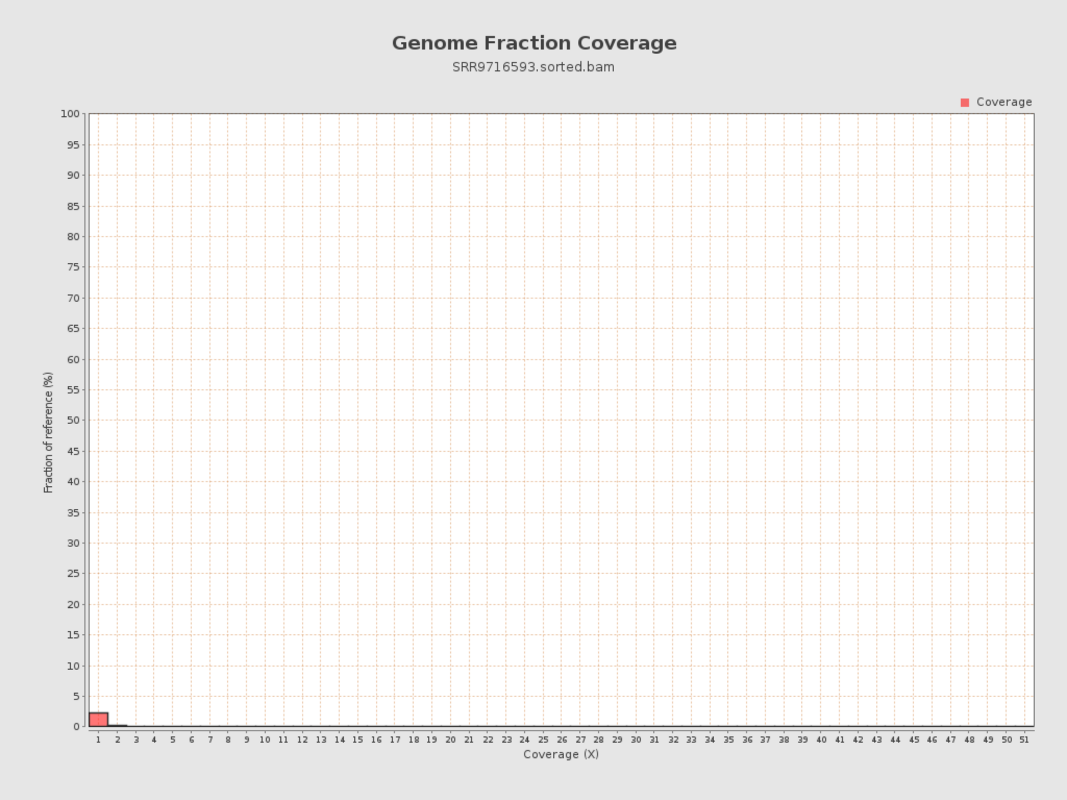
4. Results : Coverage Histogram



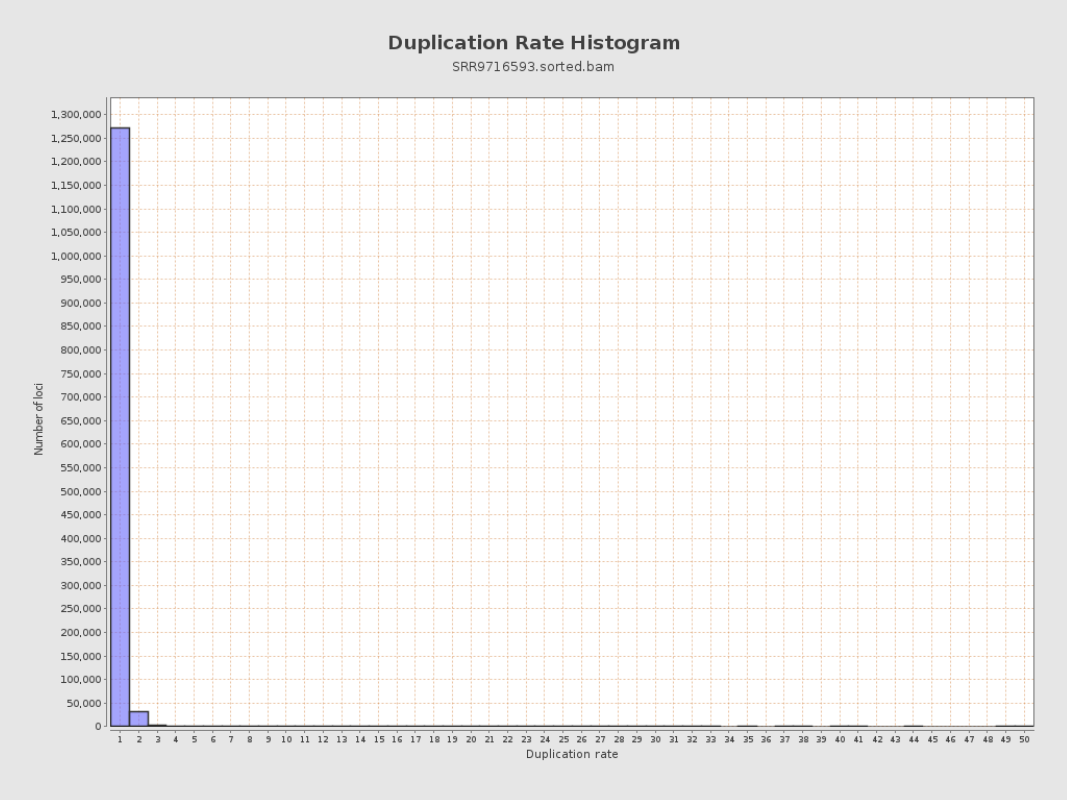
5. Results : Coverage Histogram (0-50X)



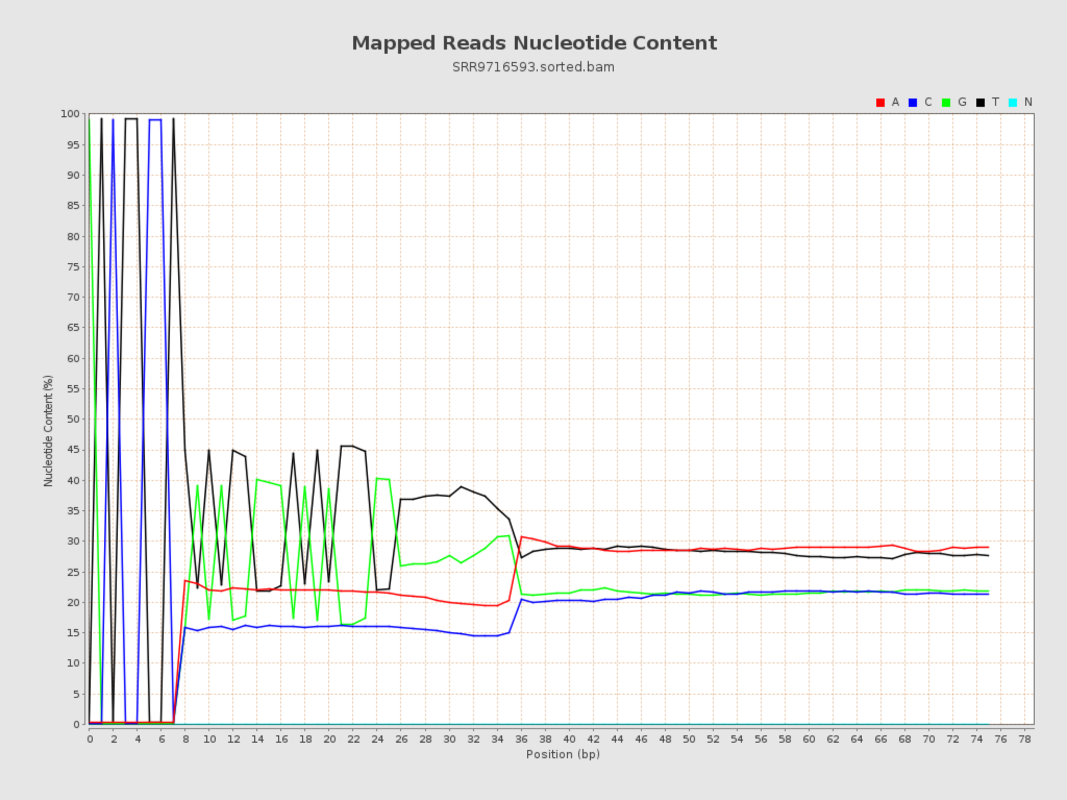
6. Results : Genome Fraction Coverage



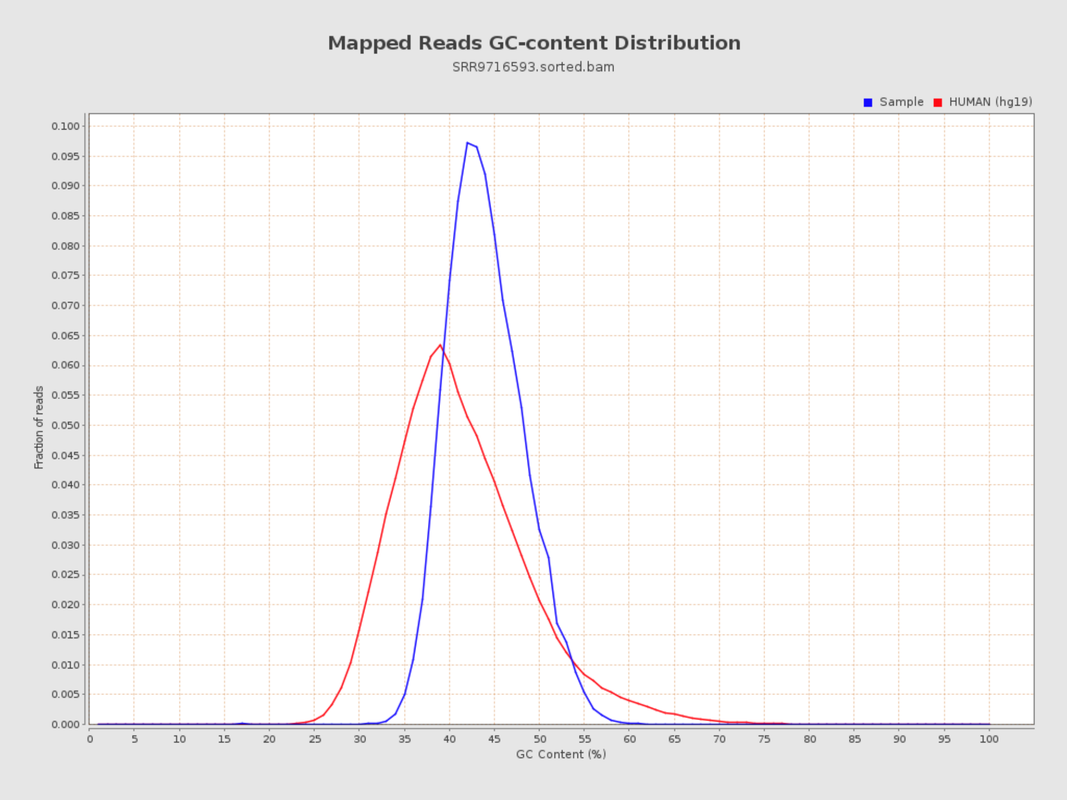
7. Results : Duplication Rate Histogram



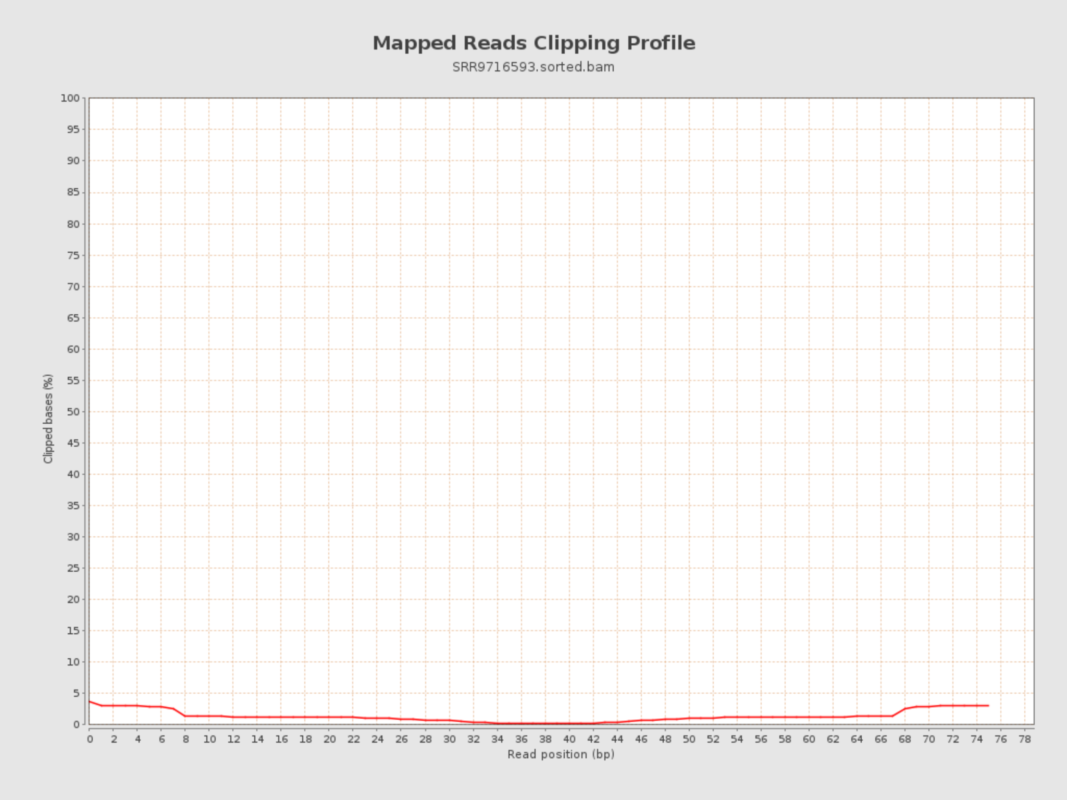
8. Results : Mapped Reads Nucleotide Content



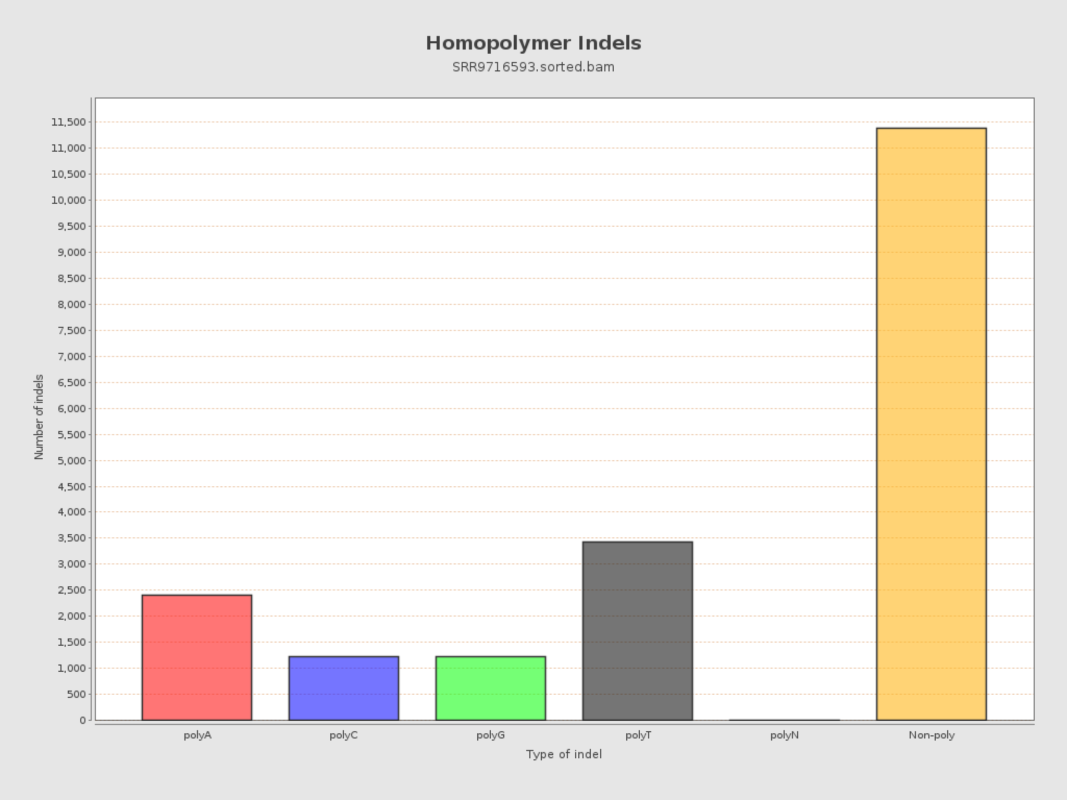
9. Results : Mapped Reads GC-content Distribution



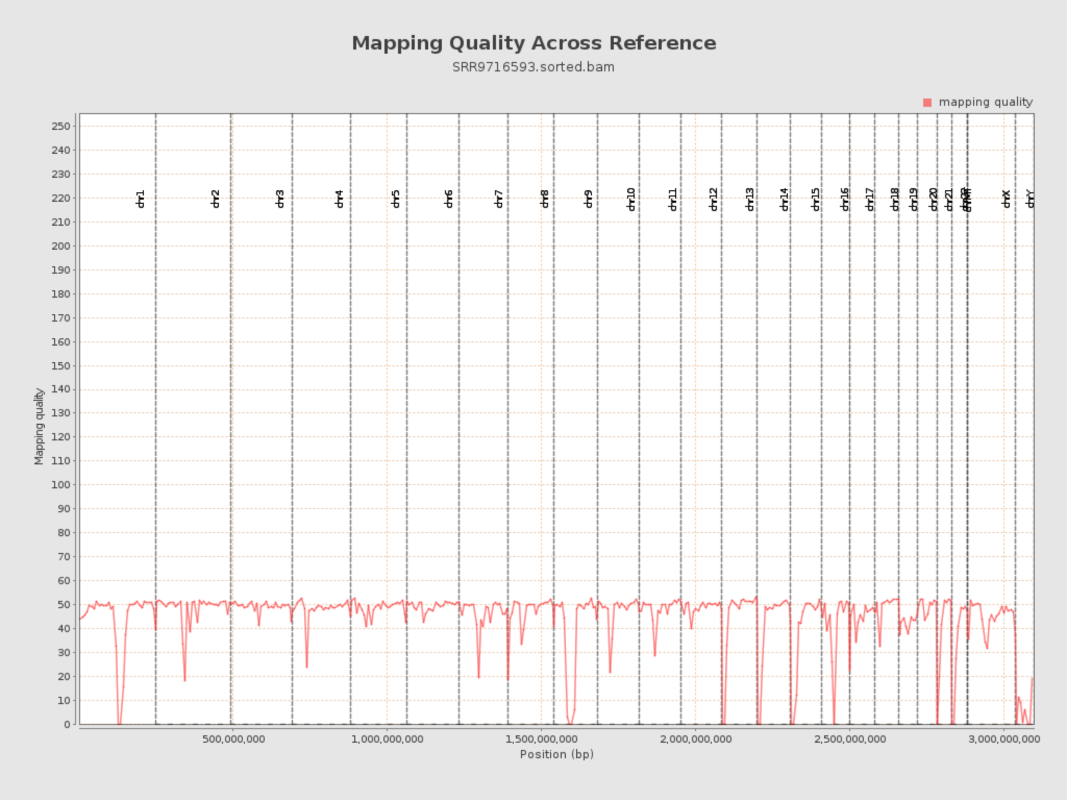
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram