Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:16:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716393.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_SRR9716393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716393.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:16:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,371,990
Mapped reads	2,128,648 / 89.74%
Unmapped reads	243,342 / 10.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,630 / 1.38%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	114,273 / 4.82%
Duplication rate	3.44%
Clipped reads	2,157,886 / 90.97%

2.2. ACGT Content

Number/percentage of A's	42,026,187 / 25.32%
Number/percentage of C's	31,943,154 / 19.25%
Number/percentage of T's	52,065,651 / 31.37%
Number/percentage of G's	39,914,385 / 24.05%
Number/percentage of N's	9,603 / 0.01%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.5897

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

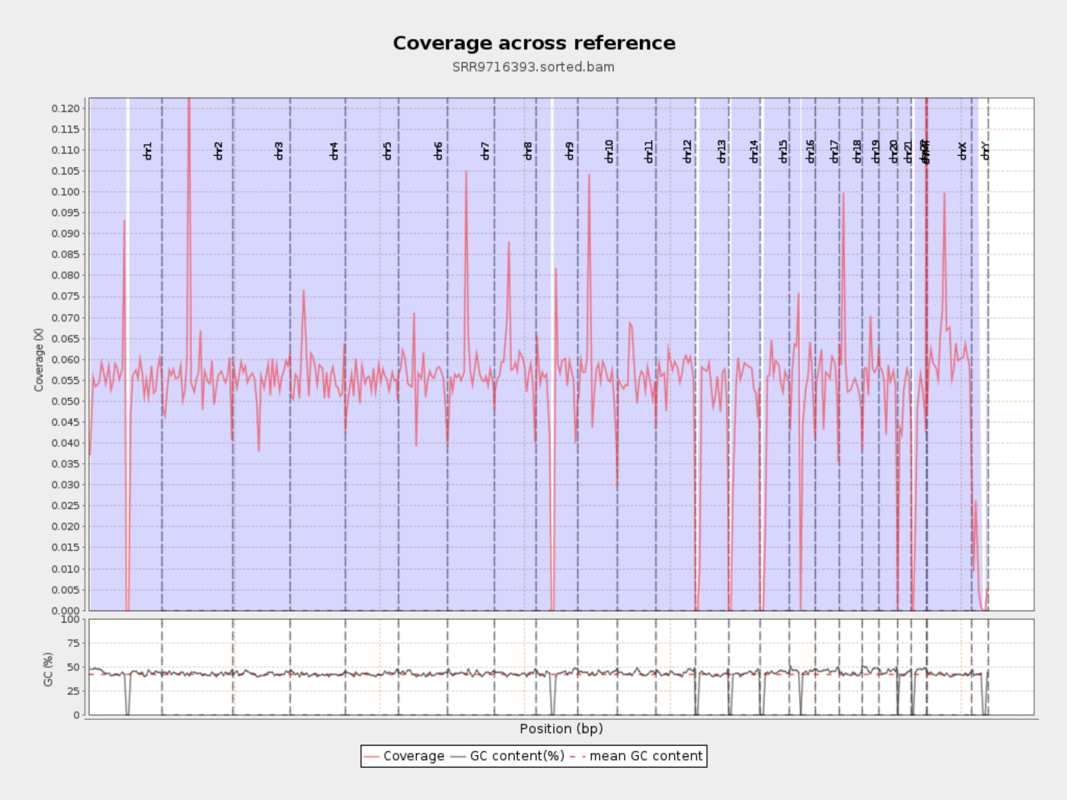
General error rate	0.91%
Mismatches	1,482,936
Insertions	15,225
Mapped reads with at least one insertion	0.71%
Deletions	42,630
Mapped reads with at least one deletion	1.97%
Homopolymer indels	44.36%

2.6. Chromosome stats

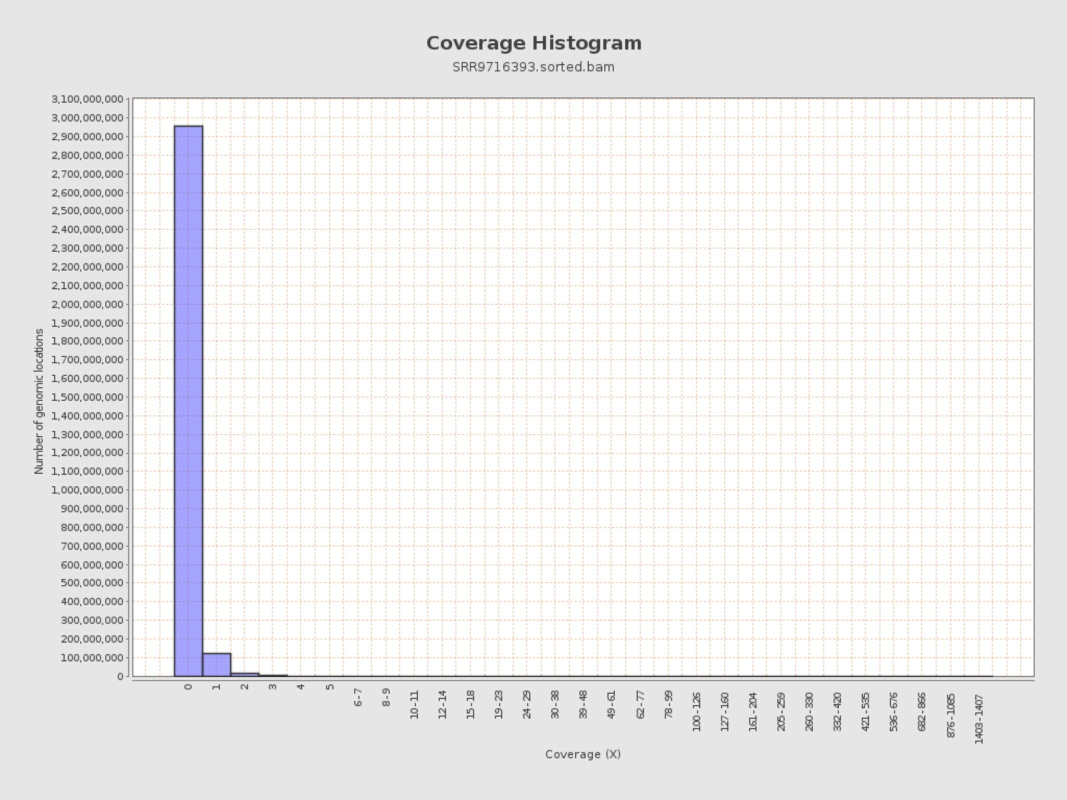
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13144134	0.0527	0.8921
chr2	243199373	14005162	0.0576	0.9314
chr3	198022430	10973209	0.0554	0.2746
chr4	191154276	10802117	0.0565	0.308
chr5	180915260	9900542	0.0547	0.2829
chr6	171115067	9552421	0.0558	0.3648
chr7	159138663	9299239	0.0584	0.7835

chr8	146364022	8603649	0.0588	0.7982
chr9	141213431	7151093	0.0506	0.662
chr10	135534747	7820089	0.0577	0.5386
chr11	135006516	7461726	0.0553	0.5716
chr12	133851895	7646213	0.0571	0.2908
chr13	115169878	5210950	0.0452	0.2442
chr14	107349540	5009283	0.0467	0.3852
chr15	102531392	4717319	0.046	0.2581
chr16	90354753	4711154	0.0521	0.3234
chr17	81195210	4432573	0.0546	0.3132
chr18	78077248	4628622	0.0593	1.2873
chr19	59128983	3420289	0.0578	0.6851
chr20	63025520	3355547	0.0532	0.2975
chr21	48129895	2162560	0.0449	0.2776
chr22	51304566	1828995	0.0356	0.2184
chrMT	16571	15530	0.9372	1.2358
chrX	155270560	9708755	0.0625	0.4401
chrY	59373566	472265	0.008	0.2253

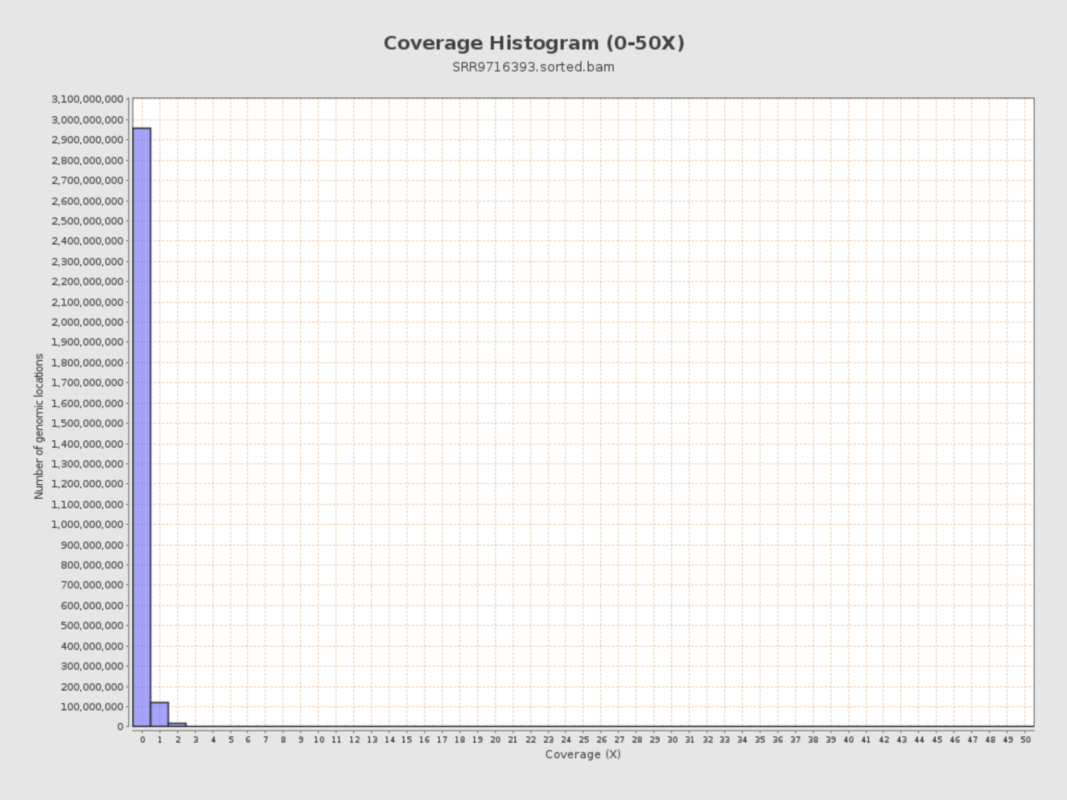
3. Results : Coverage across reference



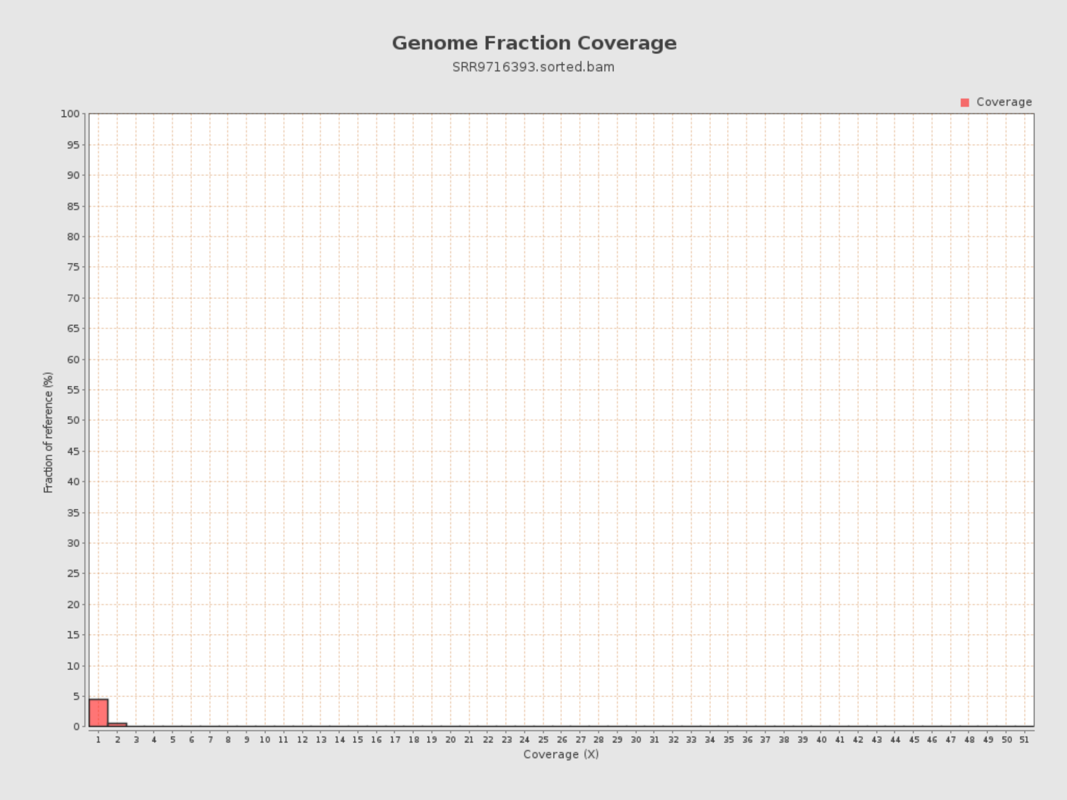
4. Results : Coverage Histogram



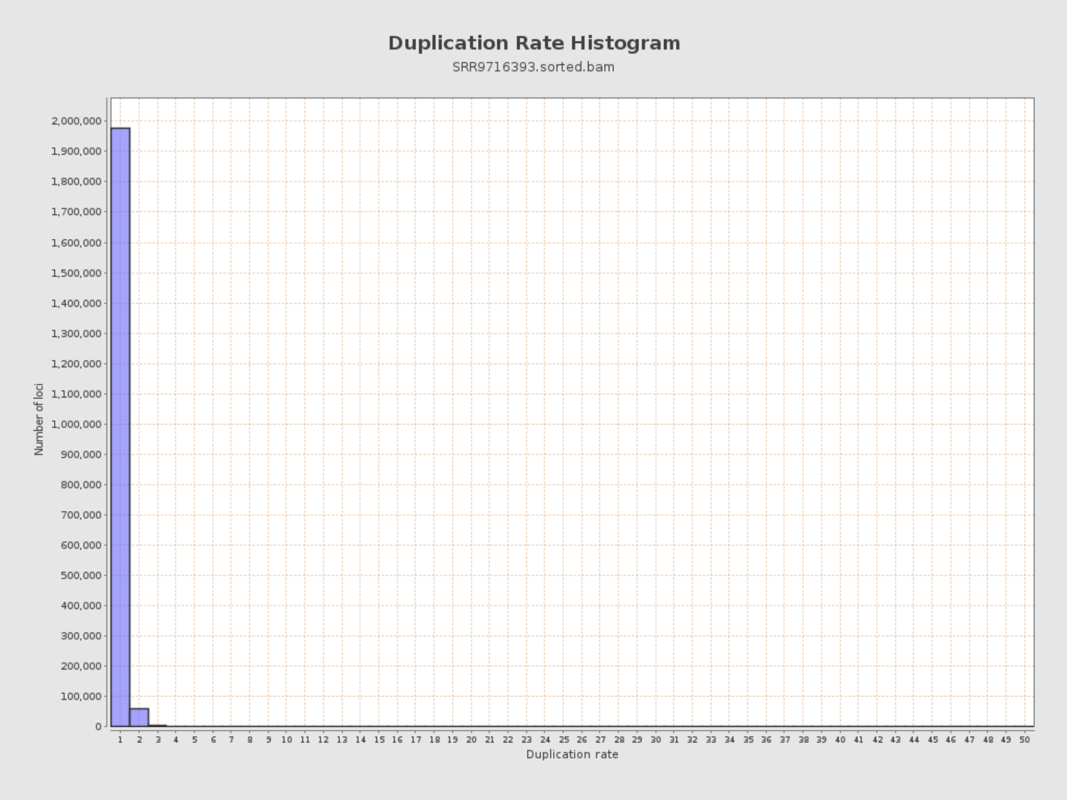
5. Results : Coverage Histogram (0-50X)



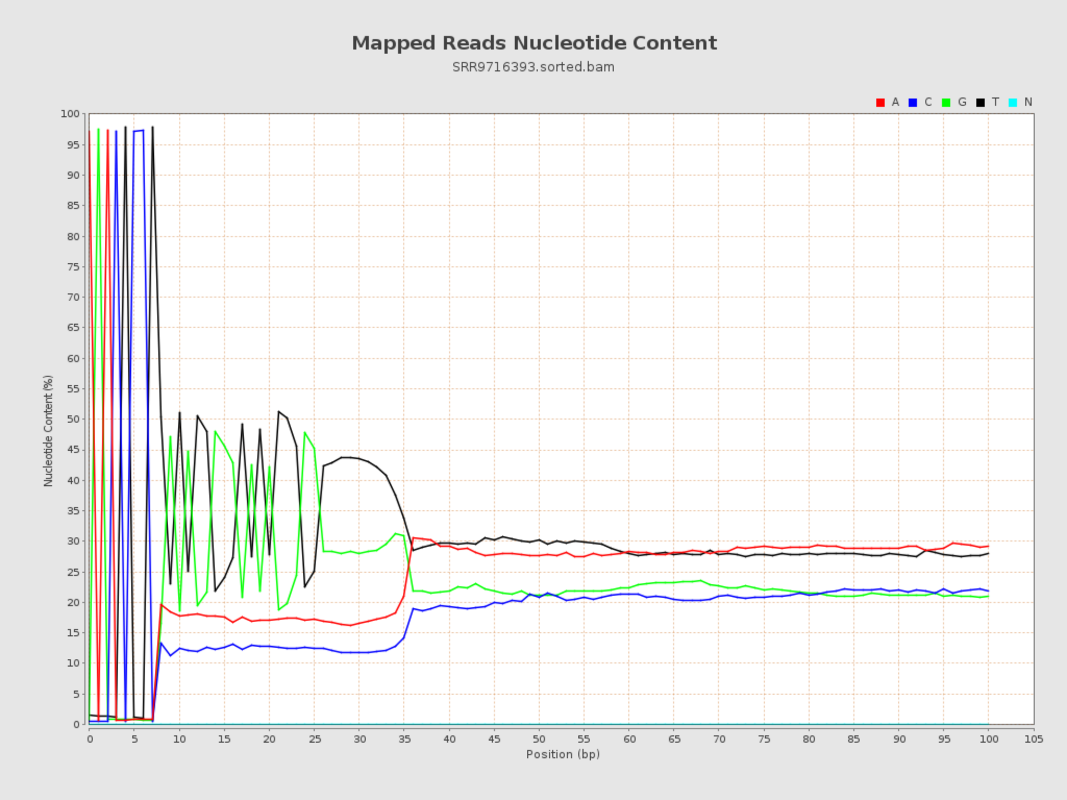
6. Results : Genome Fraction Coverage



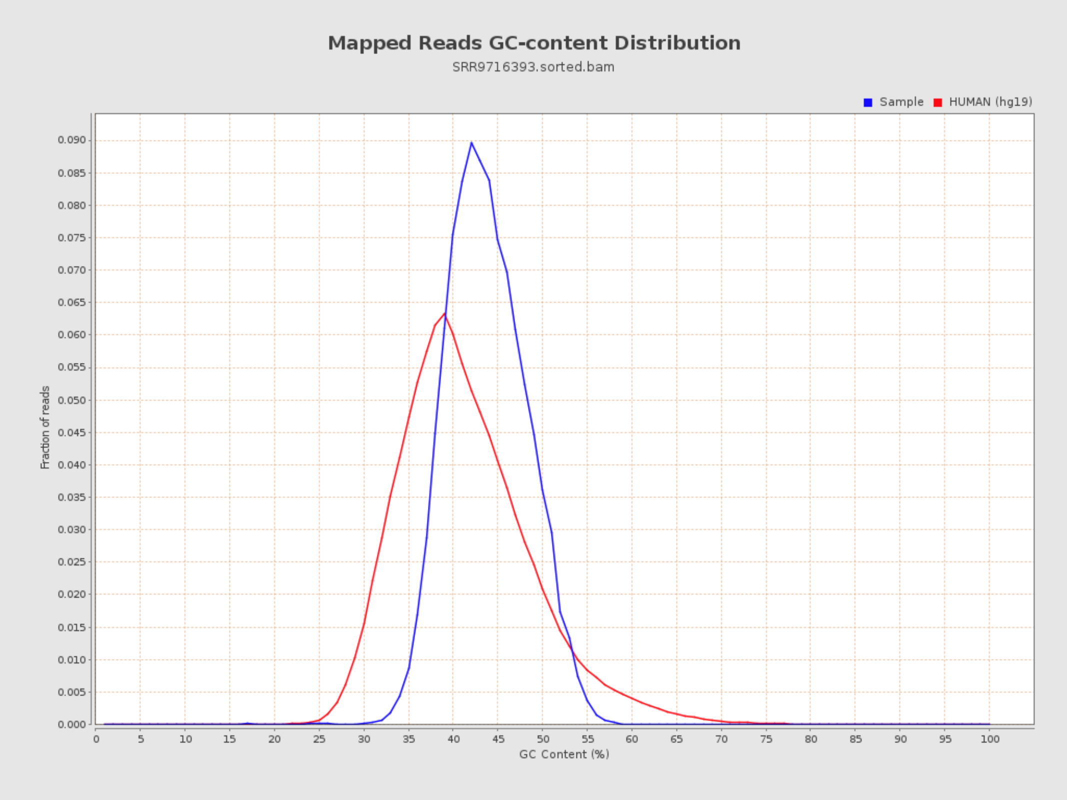
7. Results : Duplication Rate Histogram



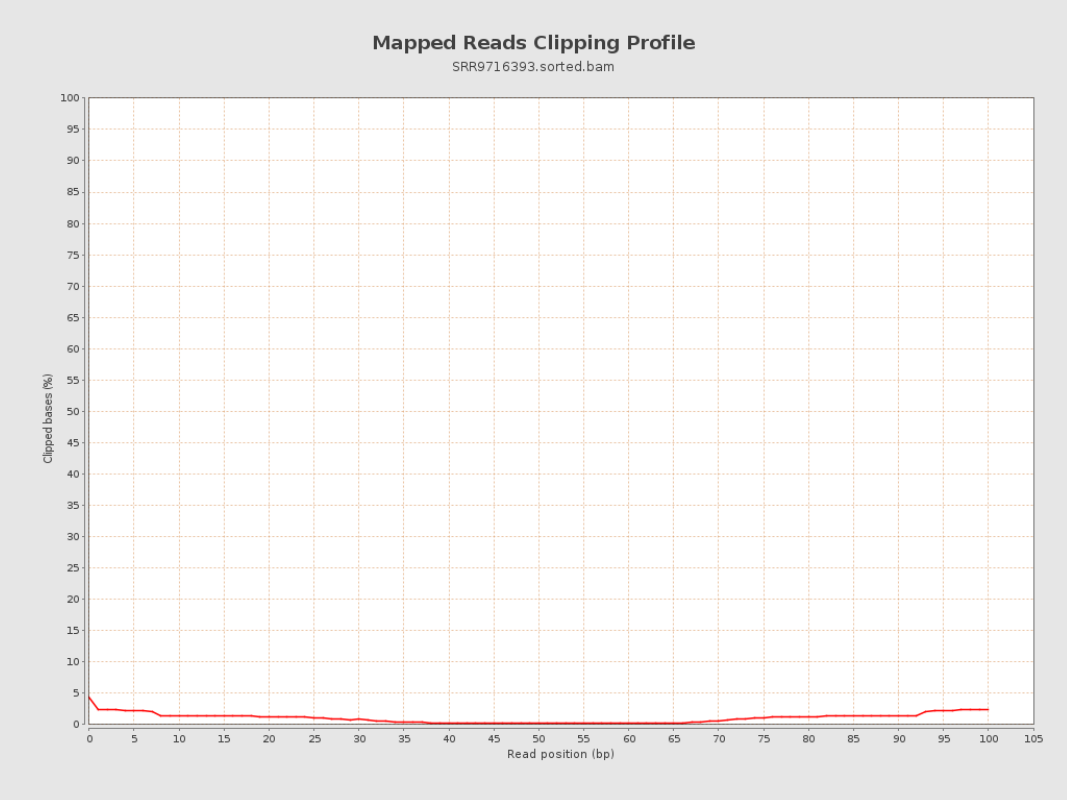
8. Results : Mapped Reads Nucleotide Content



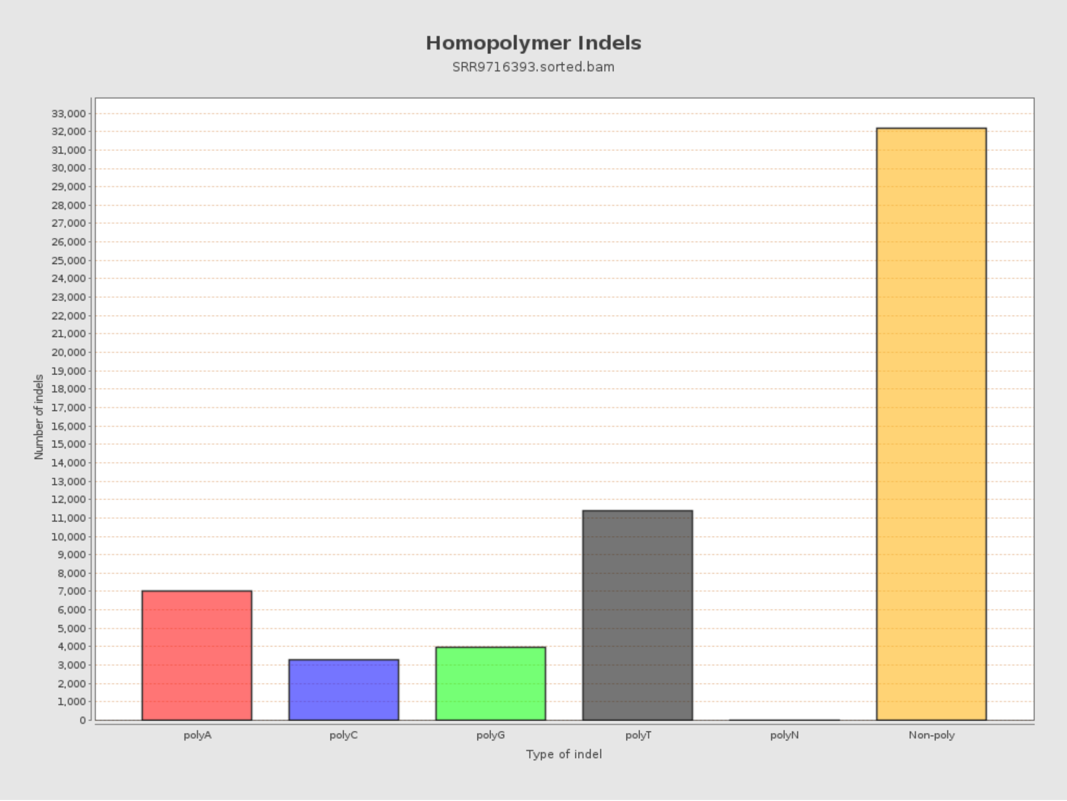
9. Results : Mapped Reads GC-content Distribution



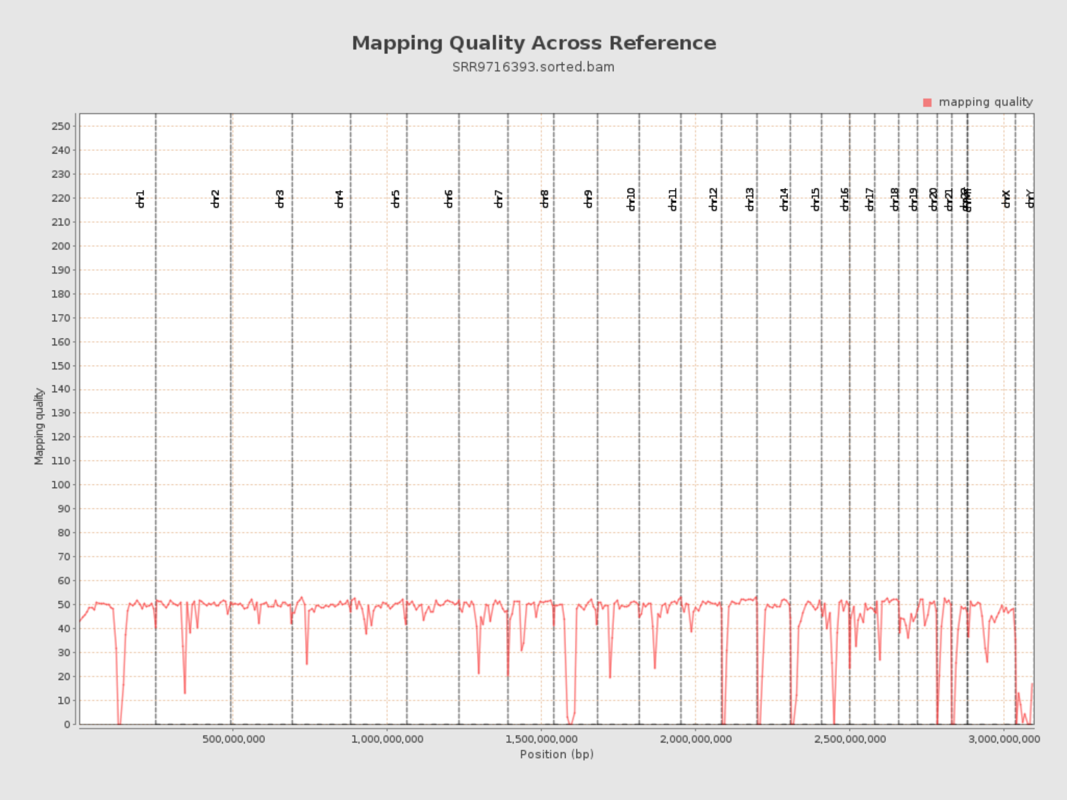
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram