Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:13:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716449.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_SRR9716449 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716449.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:13:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716449.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,443,474
Mapped reads	2,238,372 / 91.61%
Unmapped reads	205,102 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,134 / 1.48%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	120,306 / 4.92%
Duplication rate	3.8%
Clipped reads	2,270,353 / 92.91%

2.2. ACGT Content

Number/percentage of A's	42,674,539 / 24.31%
Number/percentage of C's	33,853,696 / 19.29%
Number/percentage of T's	54,802,962 / 31.22%
Number/percentage of G's	44,184,839 / 25.17%
Number/percentage of N's	9,952 / 0.01%
GC Percentage	44.46%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.5436

2.4. Mapping Quality

Mean Mapping Quality	43.49

2.5. Mismatches and indels

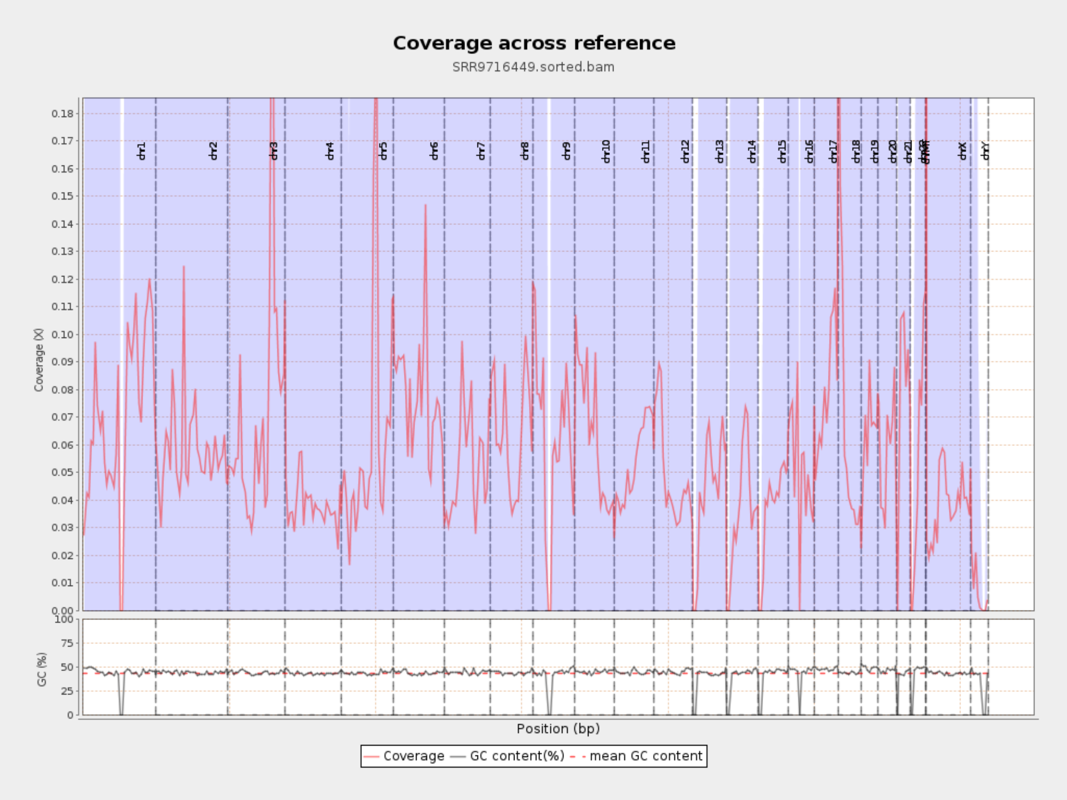
General error rate	0.85%
Mismatches	1,460,581
Insertions	16,145
Mapped reads with at least one insertion	0.71%
Deletions	41,514
Mapped reads with at least one deletion	1.83%
Homopolymer indels	44.89%

2.6. Chromosome stats

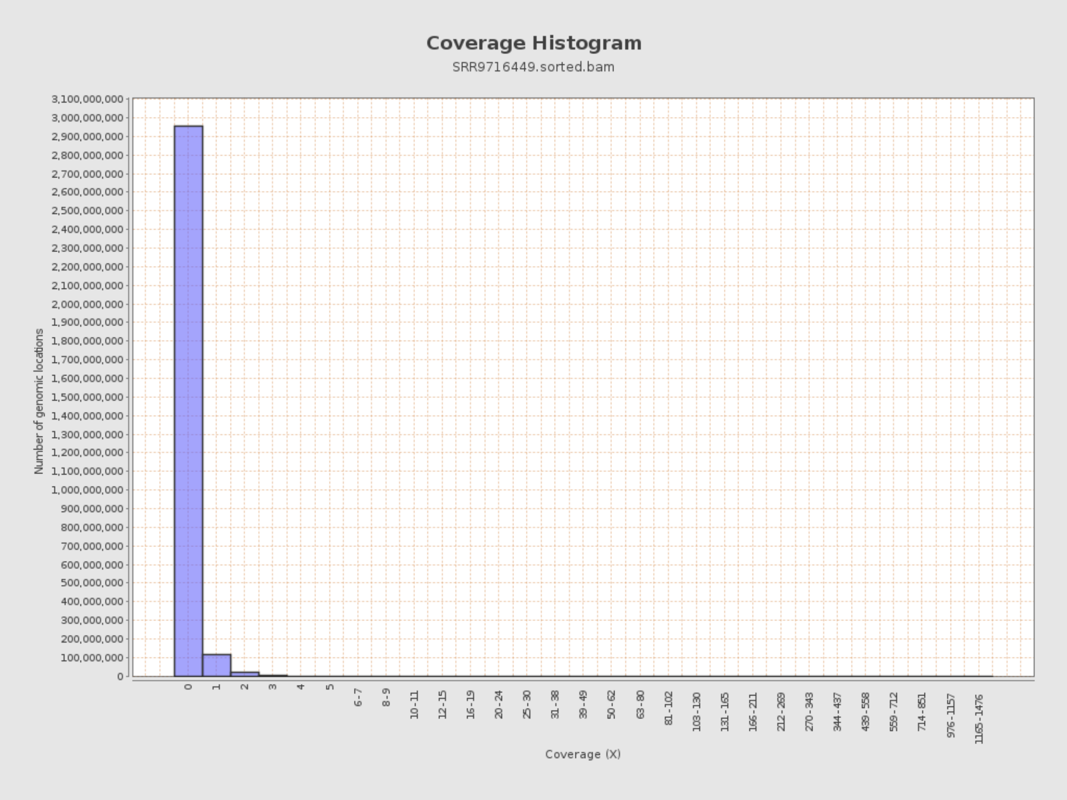
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17406643	0.0698	0.767
chr2	243199373	14247583	0.0586	1.0117
chr3	198022430	13916842	0.0703	0.3361
chr4	191154276	7283892	0.0381	0.2669
chr5	180915260	10988956	0.0607	0.307
chr6	171115067	13320083	0.0778	0.4116
chr7	159138663	8444397	0.0531	0.7034

chr8	146364022	9434882	0.0645	0.6933
chr9	141213431	8620350	0.061	0.4994
chr10	135534747	8768684	0.0647	0.4716
chr11	135006516	7242962	0.0536	0.3795
chr12	133851895	6665371	0.0498	0.277
chr13	115169878	5063804	0.044	0.2513
chr14	107349540	3908514	0.0364	0.2794
chr15	102531392	3666455	0.0358	0.2381
chr16	90354753	4561087	0.0505	0.3143
chr17	81195210	6409815	0.0789	0.3852
chr18	78077248	5442361	0.0697	1.0703
chr19	59128983	3832067	0.0648	0.6556
chr20	63025520	3640305	0.0578	0.3413
chr21	48129895	3644911	0.0757	0.3537
chr22	51304566	2719268	0.053	0.2915
chrMT	16571	28759	1.7355	1.6531
chrX	155270560	5933414	0.0382	0.3087
chrY	59373566	407064	0.0069	0.1973

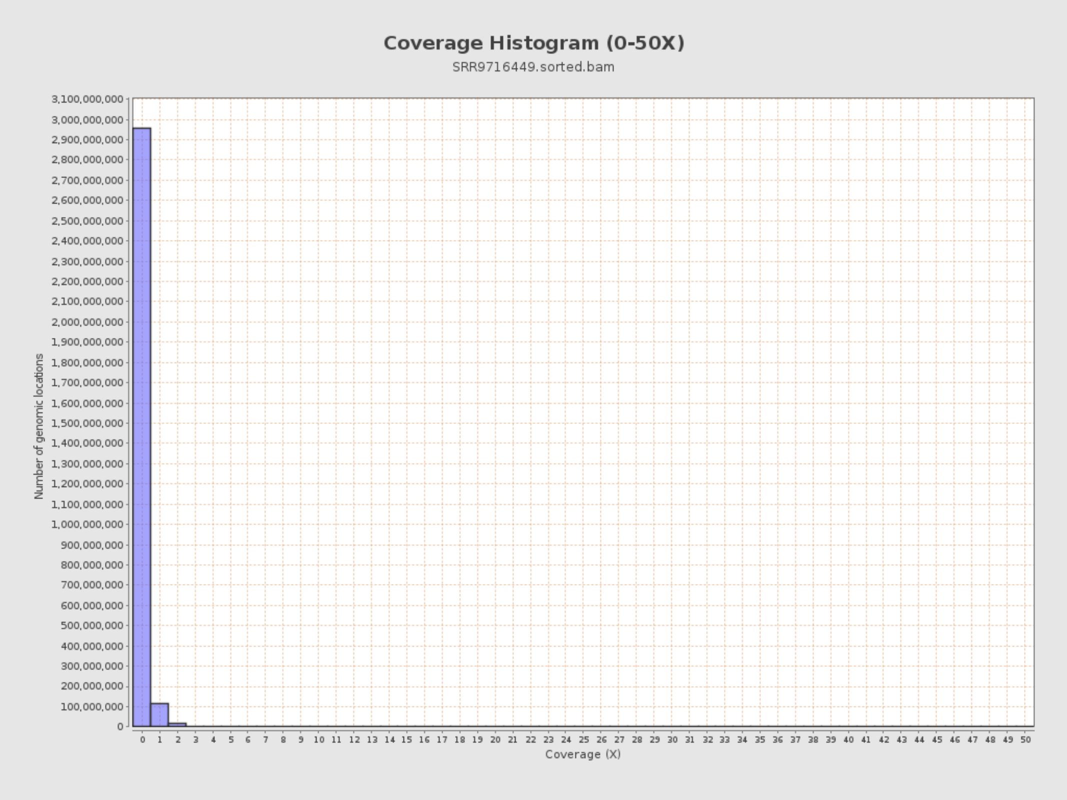
3. Results : Coverage across reference



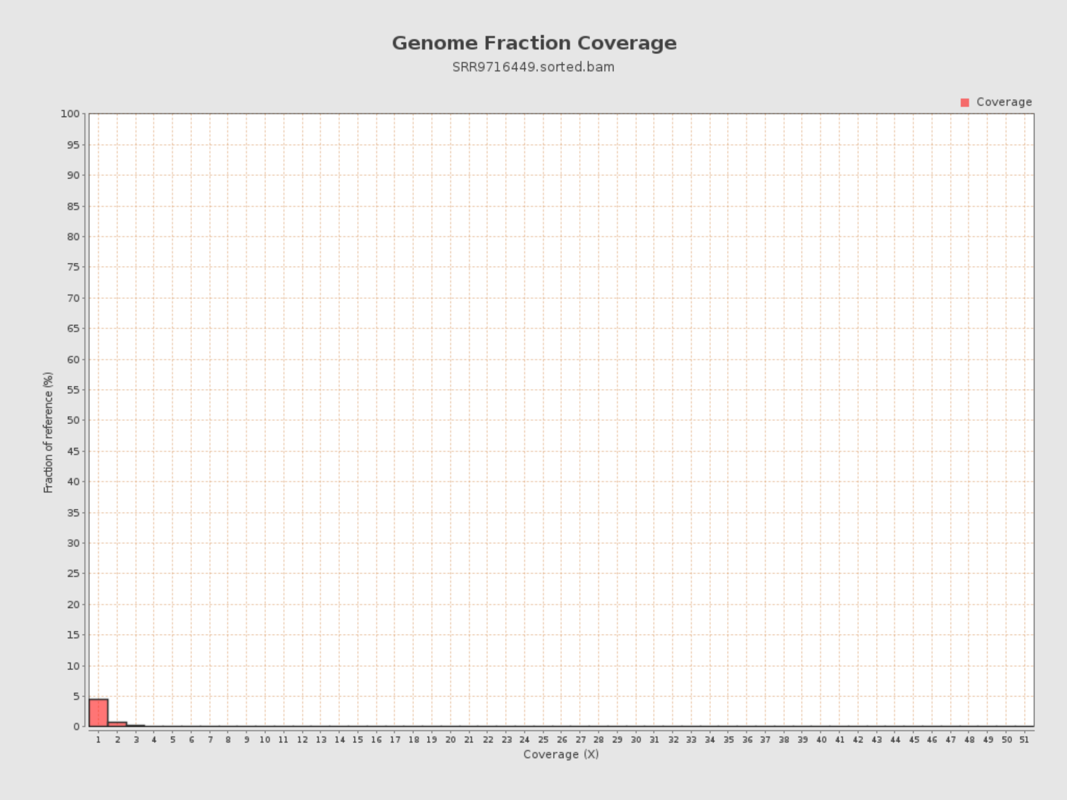
4. Results : Coverage Histogram



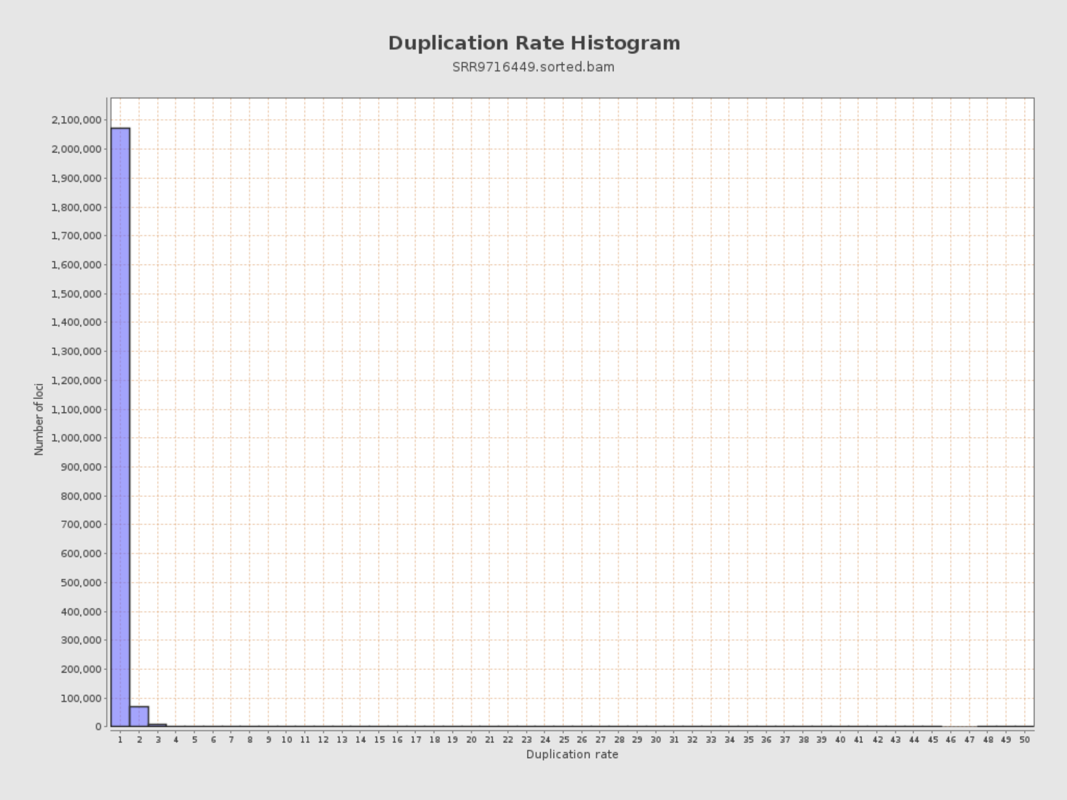
5. Results : Coverage Histogram (0-50X)



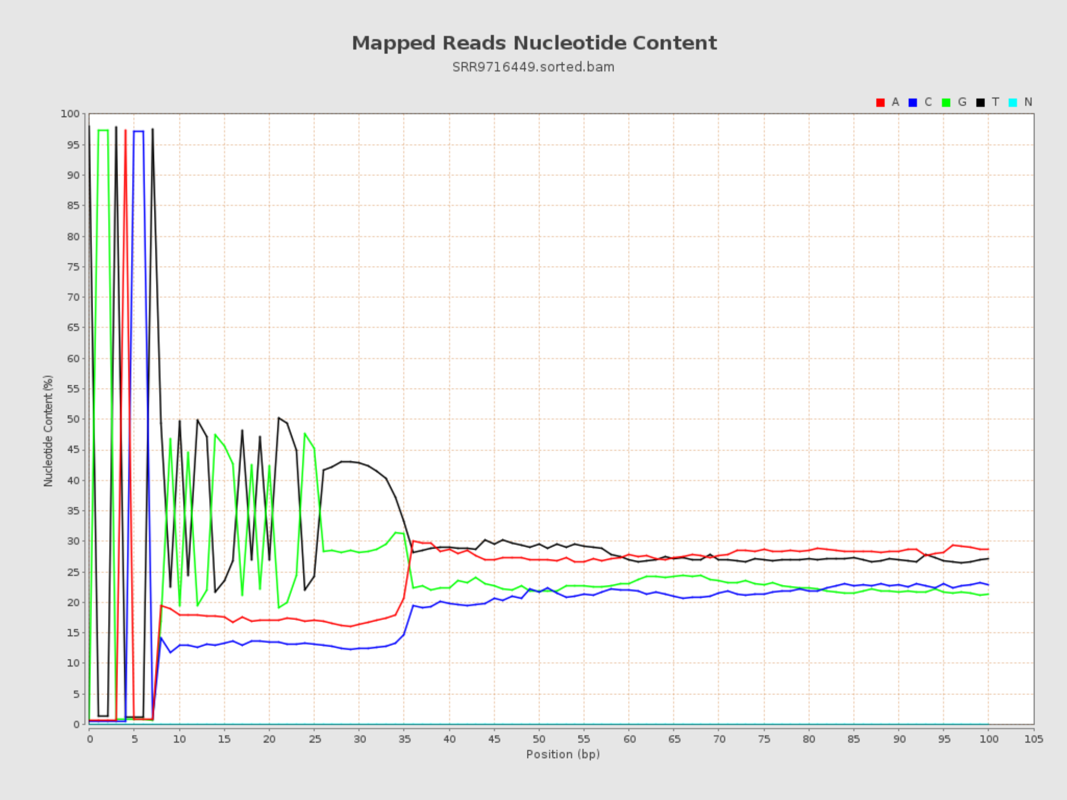
6. Results : Genome Fraction Coverage



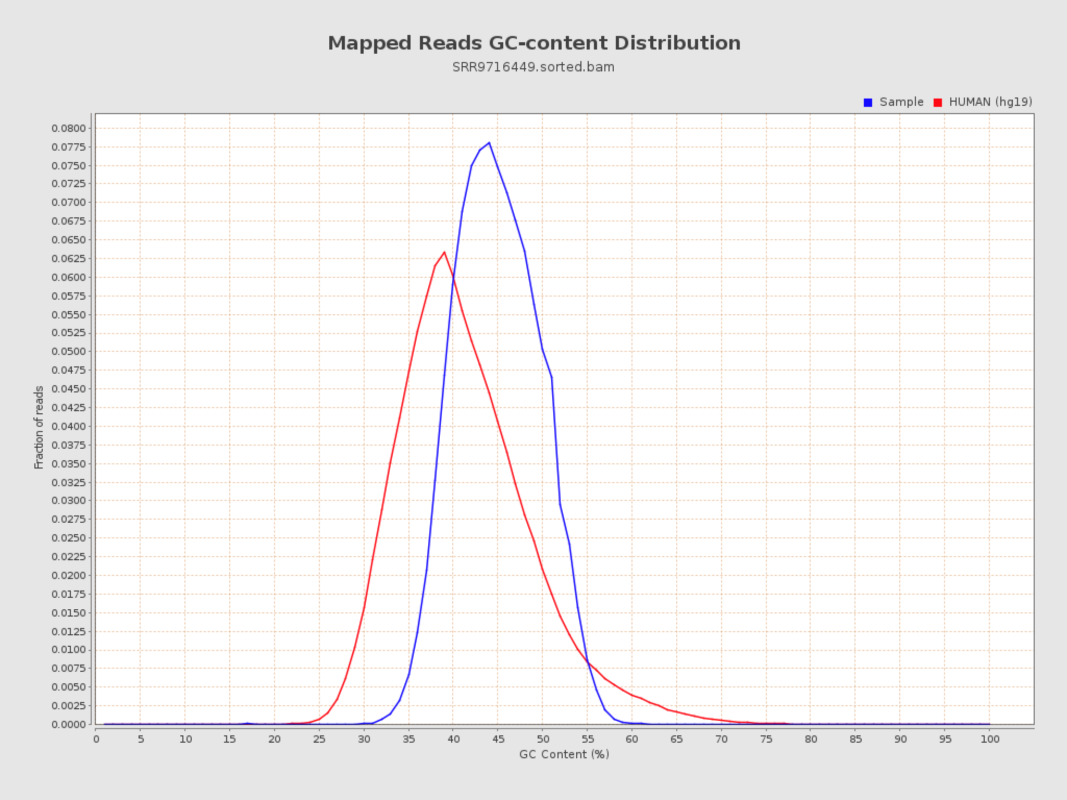
7. Results : Duplication Rate Histogram



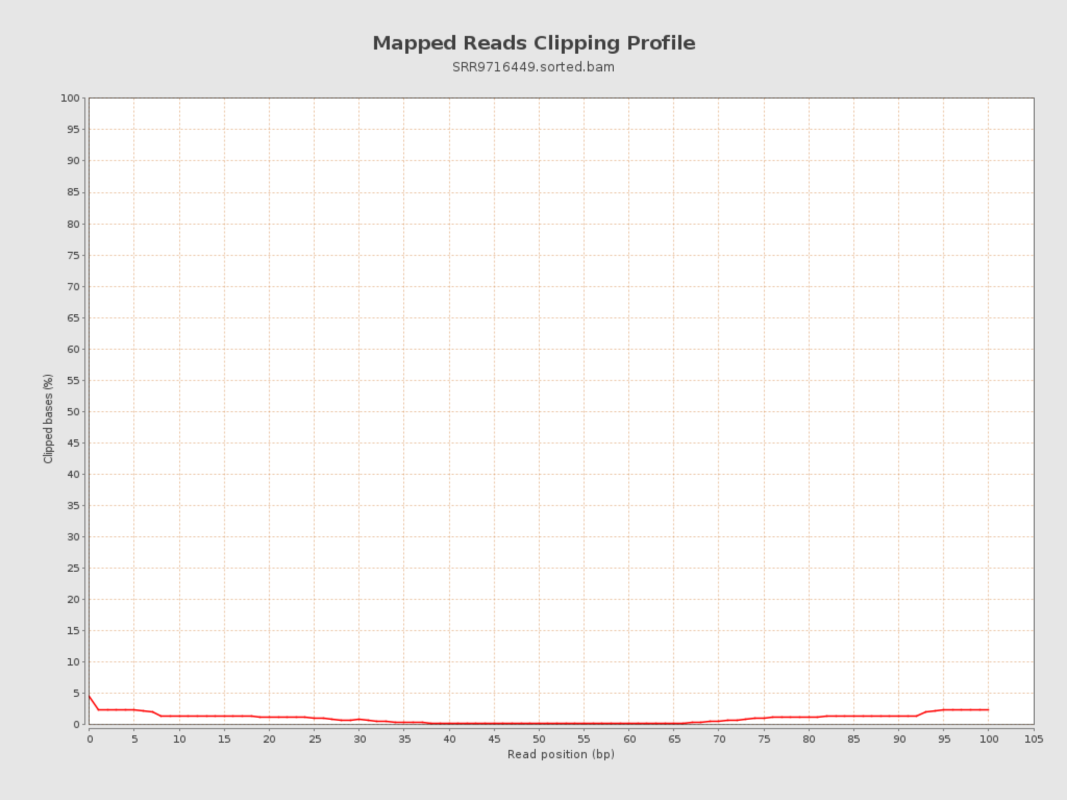
8. Results : Mapped Reads Nucleotide Content



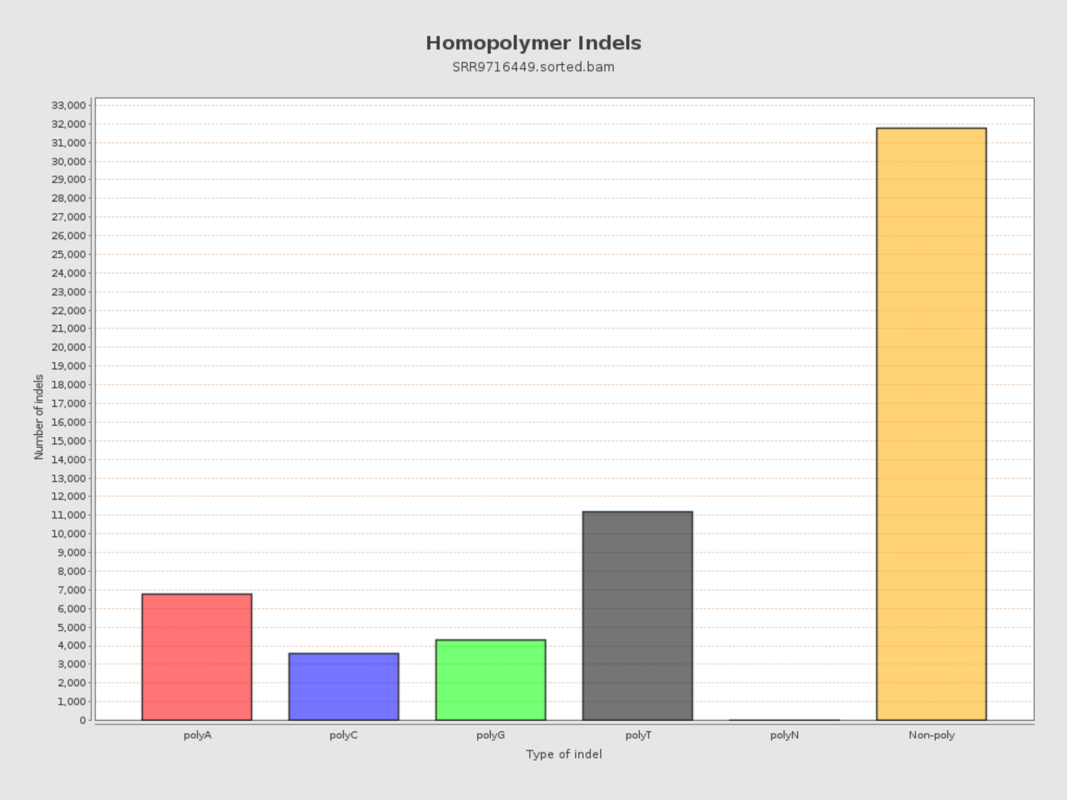
9. Results : Mapped Reads GC-content Distribution



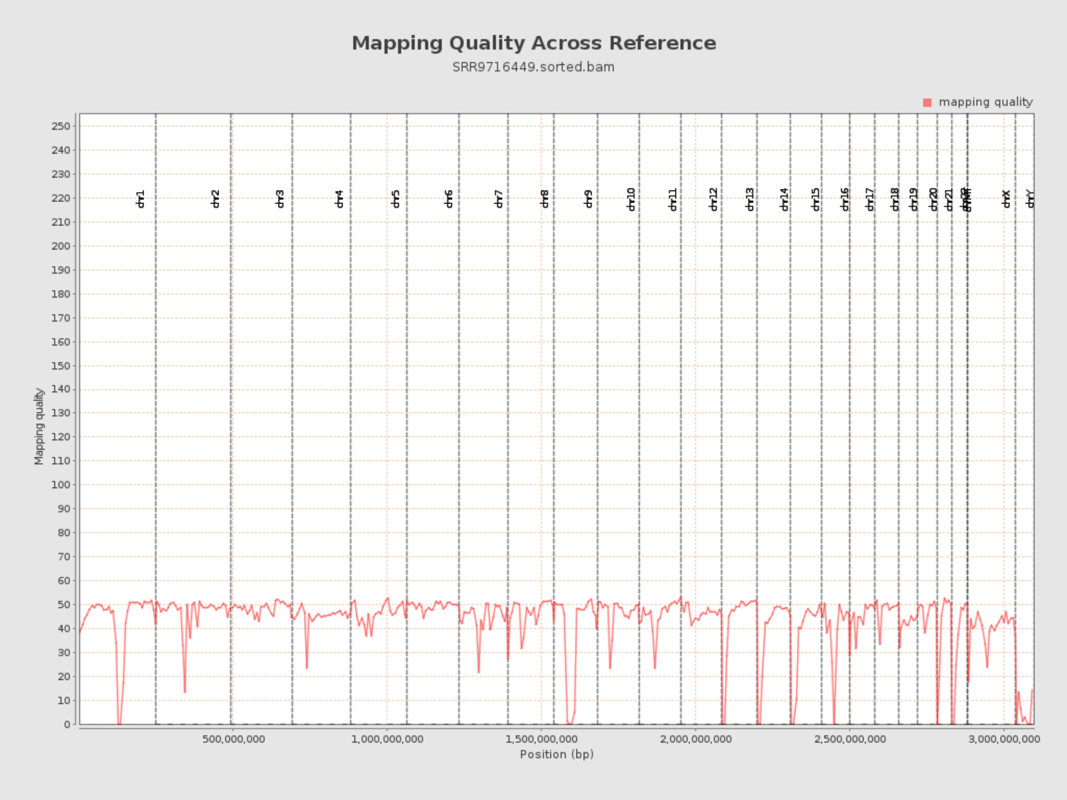
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram