Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:51:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716949.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_SRR9716949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:51:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,921,920
Mapped reads	3,215,567 / 81.99%
Unmapped reads	706,353 / 18.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,172 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	236,447 / 6.03%
Duplication rate	5.5%
Clipped reads	3,221,951 / 82.15%

2.2. ACGT Content

Number/percentage of A's	47,895,094 / 26.05%
Number/percentage of C's	37,639,886 / 20.47%
Number/percentage of T's	55,911,699 / 30.41%
Number/percentage of G's	42,421,740 / 23.07%
Number/percentage of N's	2,614 / 0%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0594

Standard Deviation	0.5458

2.4. Mapping Quality

Mean Mapping Quality	43.36

2.5. Mismatches and indels

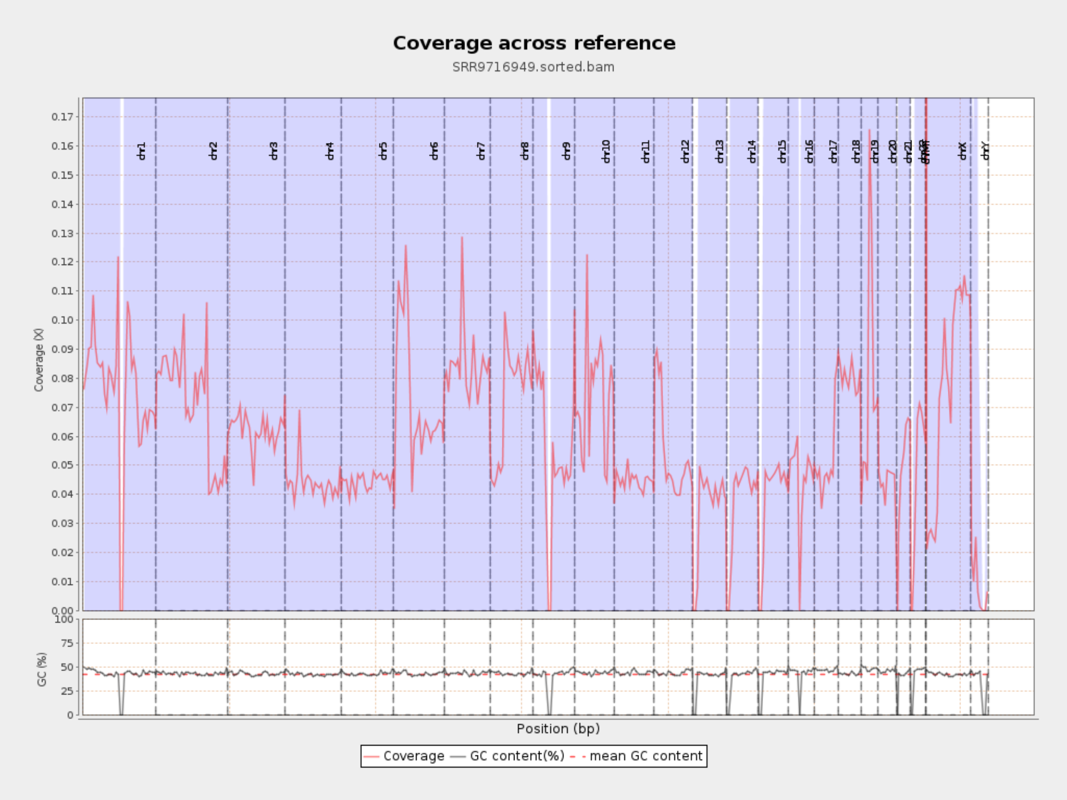
General error rate	0.51%
Mismatches	910,846
Insertions	13,679
Mapped reads with at least one insertion	0.42%
Deletions	30,589
Mapped reads with at least one deletion	0.94%
Homopolymer indels	41.02%

2.6. Chromosome stats

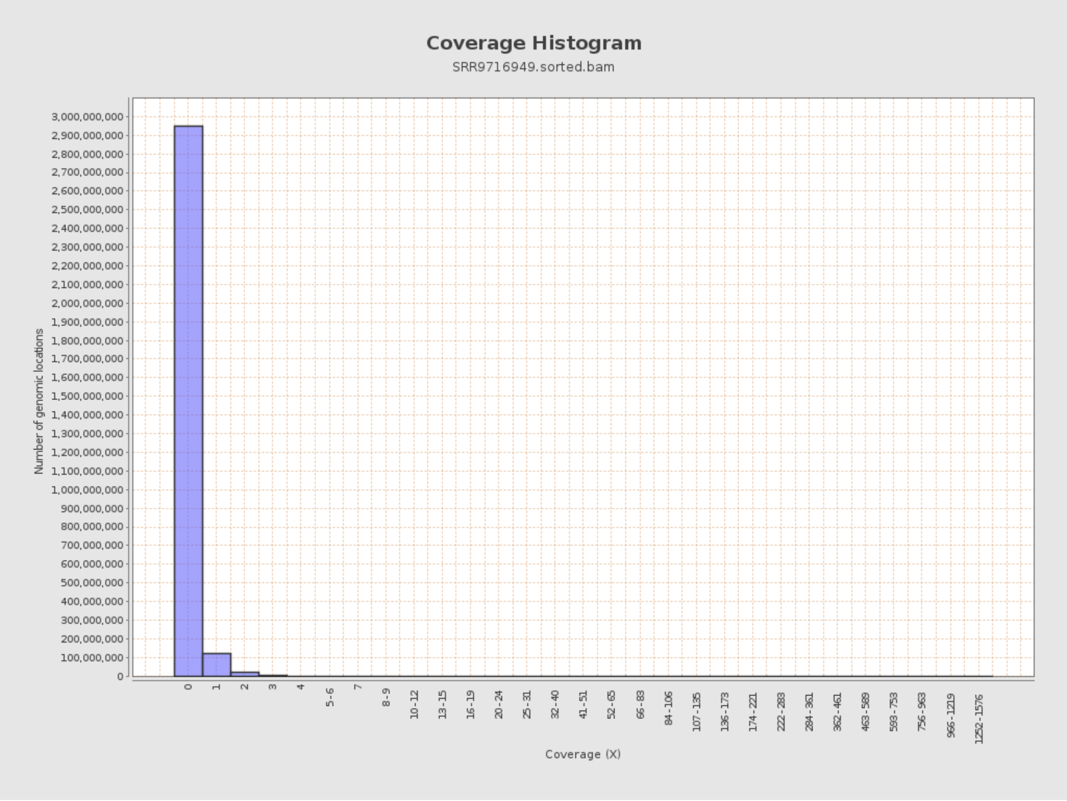
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18860384	0.0757	1.1068
chr2	243199373	17325905	0.0712	0.7522
chr3	198022430	12291544	0.0621	0.3113
chr4	191154276	8436635	0.0441	0.302
chr5	180915260	8037964	0.0444	0.2674
chr6	171115067	12499326	0.073	0.4008
chr7	159138663	13520550	0.085	0.8649

chr8	146364022	10640634	0.0727	0.4185
chr9	141213431	7623610	0.054	0.4228
chr10	135534747	9941456	0.0733	0.5232
chr11	135006516	6043311	0.0448	0.3926
chr12	133851895	7401004	0.0553	0.3022
chr13	115169878	4052528	0.0352	0.2318
chr14	107349540	4027062	0.0375	0.2883
chr15	102531392	3873035	0.0378	0.2592
chr16	90354753	4003406	0.0443	0.2988
chr17	81195210	4137316	0.051	0.3039
chr18	78077248	6284326	0.0805	0.7414
chr19	59128983	4806054	0.0813	0.7354
chr20	63025520	2798209	0.0444	0.2687
chr21	48129895	2321252	0.0482	0.312
chr22	51304566	2356178	0.0459	0.2658
chrMT	16571	265650	16.031	9.3965
chrX	155270560	11895459	0.0766	0.427
chrY	59373566	476059	0.008	0.1881

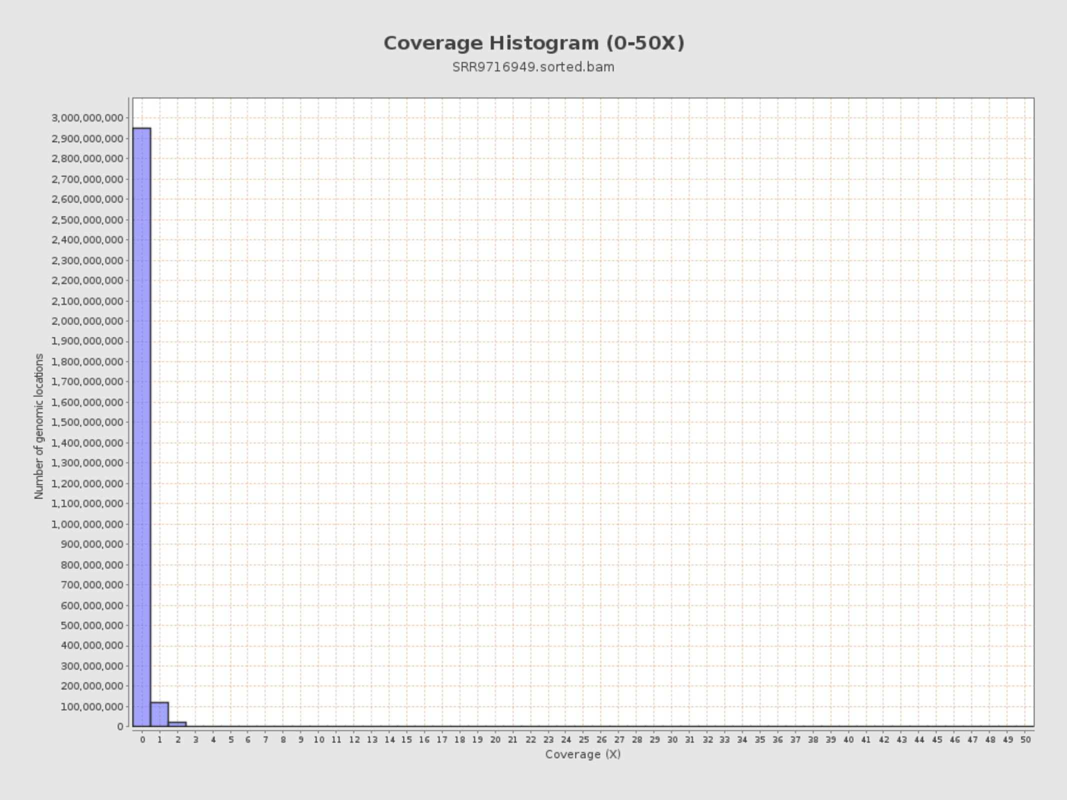
3. Results : Coverage across reference



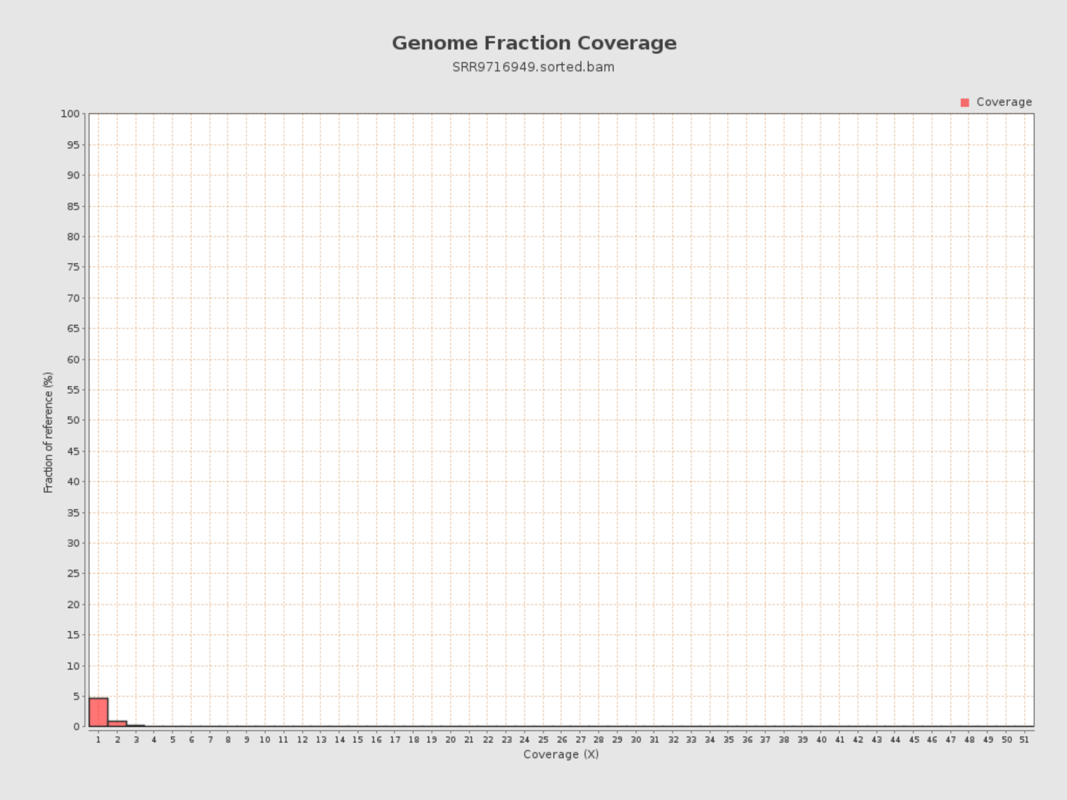
4. Results : Coverage Histogram



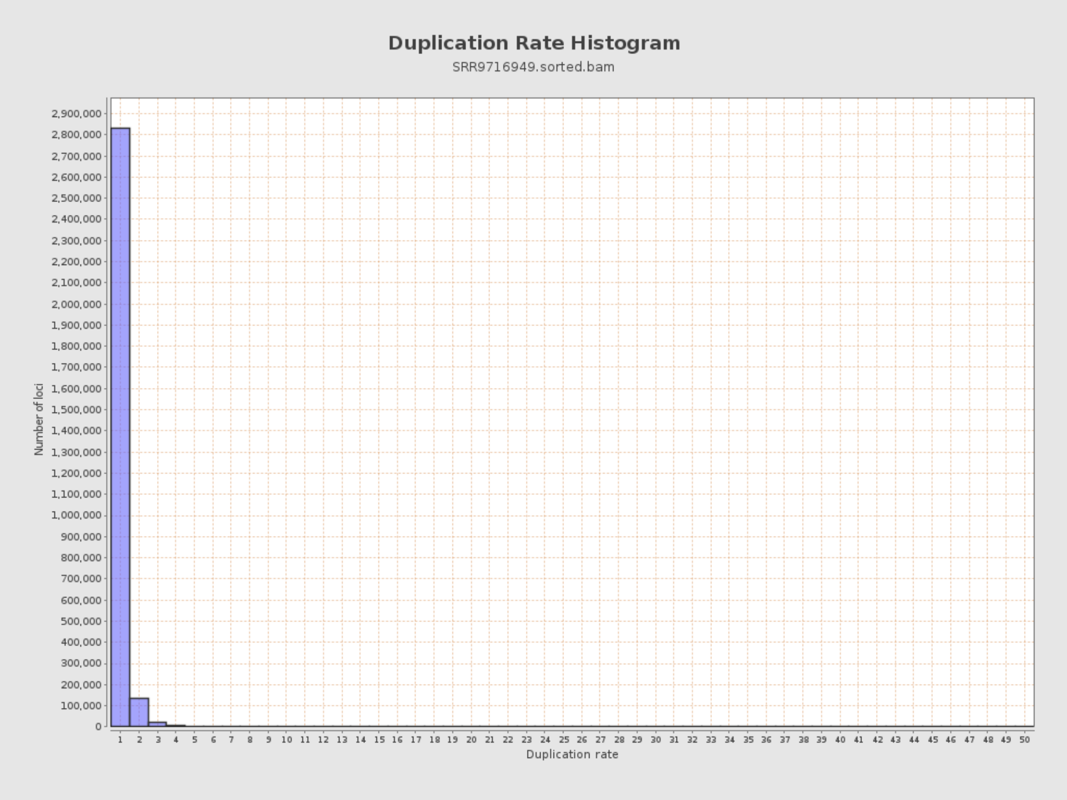
5. Results : Coverage Histogram (0-50X)



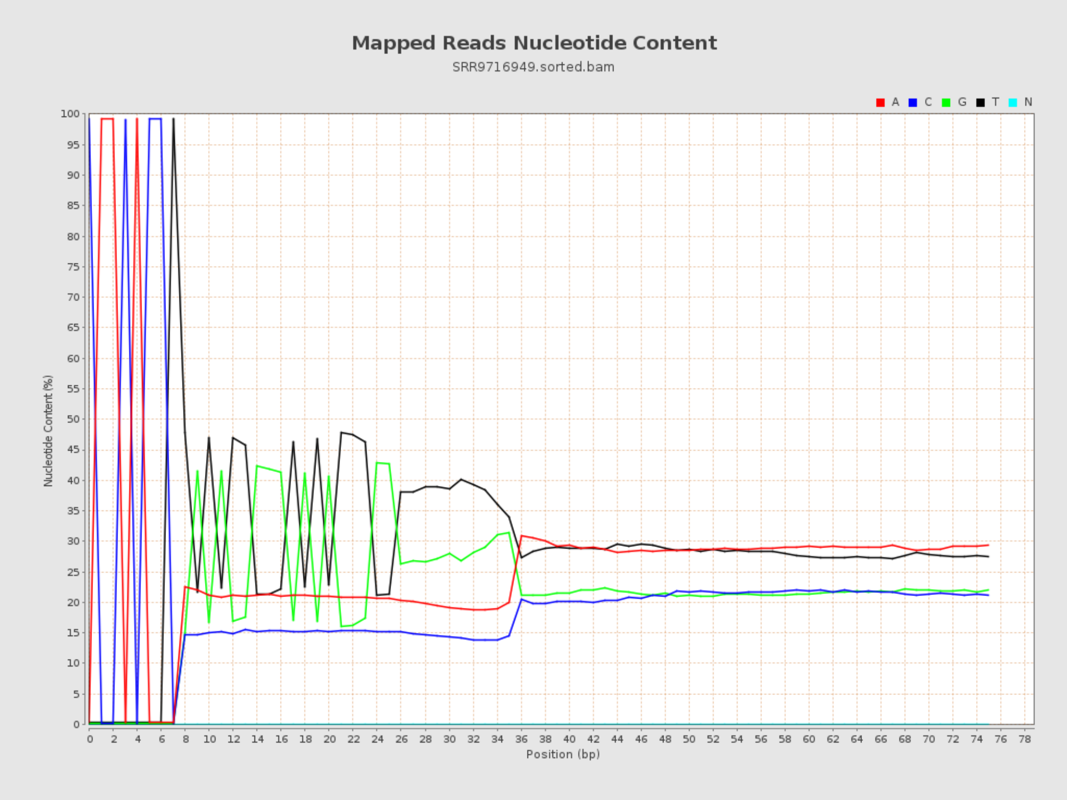
6. Results : Genome Fraction Coverage



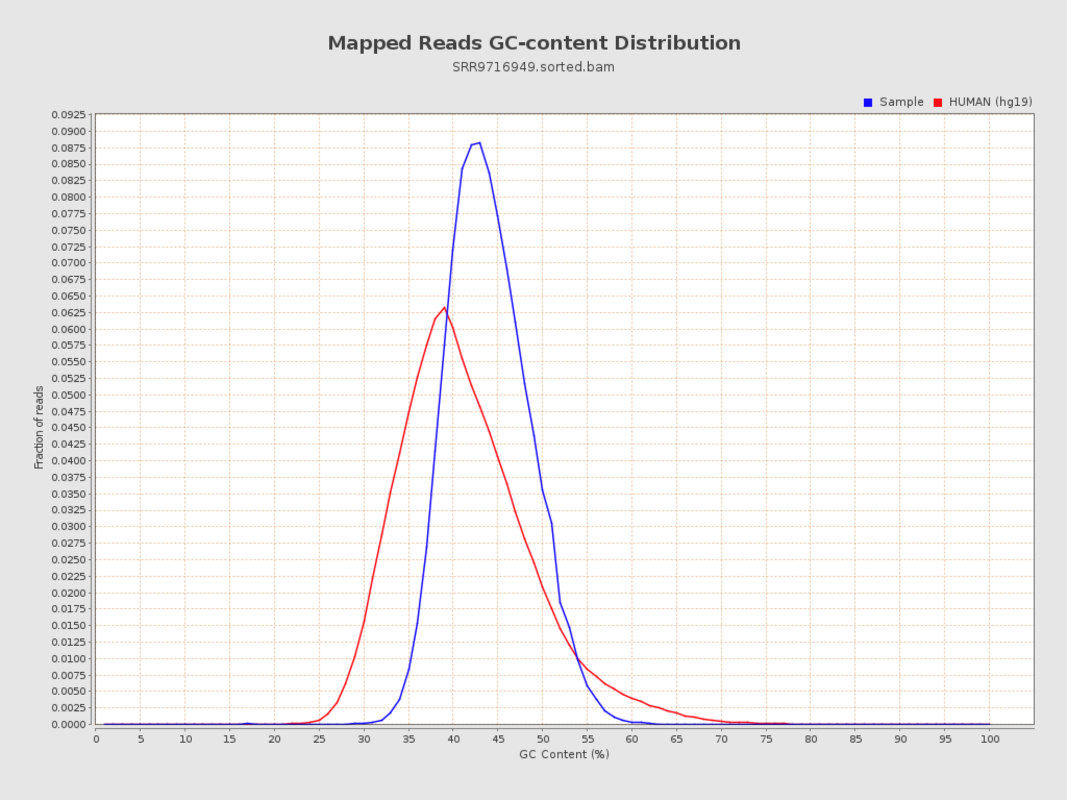
7. Results : Duplication Rate Histogram



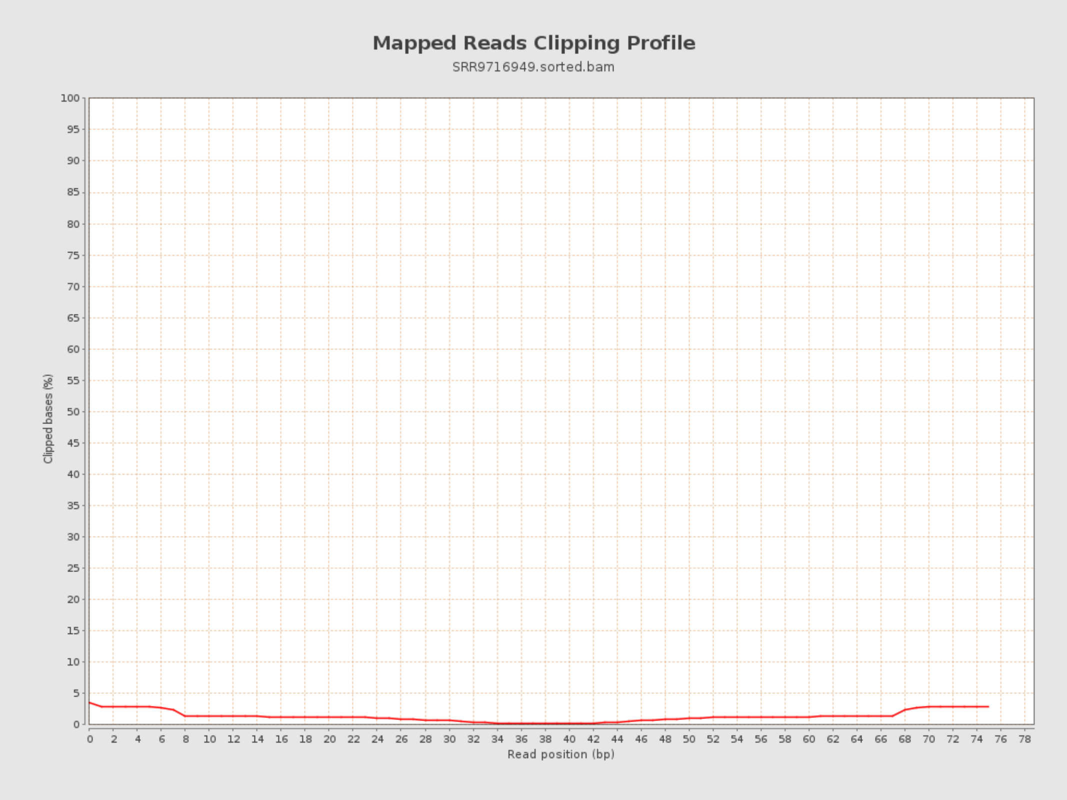
8. Results : Mapped Reads Nucleotide Content



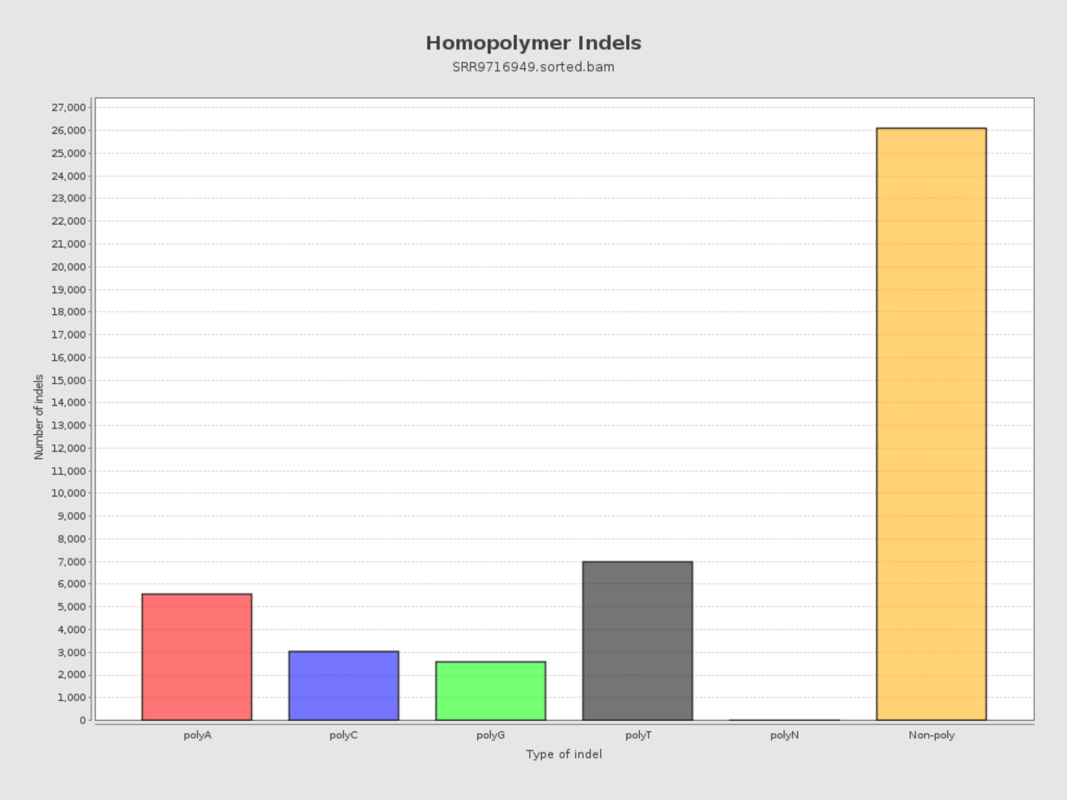
9. Results : Mapped Reads GC-content Distribution



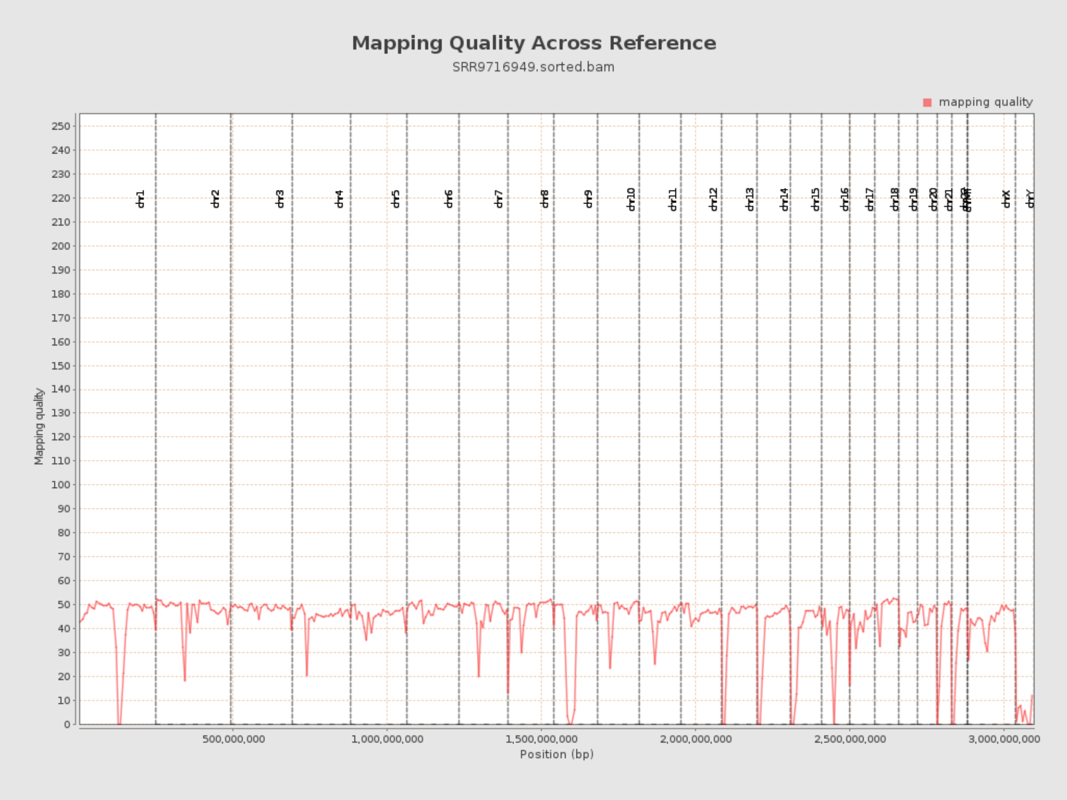
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram