Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:52:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716372.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_SRR9716372 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716372.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:52:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716372.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,545,004
Mapped reads	2,377,339 / 93.41%
Unmapped reads	167,665 / 6.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,524 / 1.83%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	120,759 / 4.74%
Duplication rate	3.68%
Clipped reads	2,418,574 / 95.03%

2.2. ACGT Content

Number/percentage of A's	49,272,004 / 26.12%
Number/percentage of C's	37,636,372 / 19.95%
Number/percentage of T's	57,324,658 / 30.38%
Number/percentage of G's	44,417,829 / 23.54%
Number/percentage of N's	13,647 / 0.01%
GC Percentage	43.49%

2.3. Coverage

Mean	0.061

Standard Deviation	0.5436

2.4. Mapping Quality

Mean Mapping Quality	47.53

2.5. Mismatches and indels

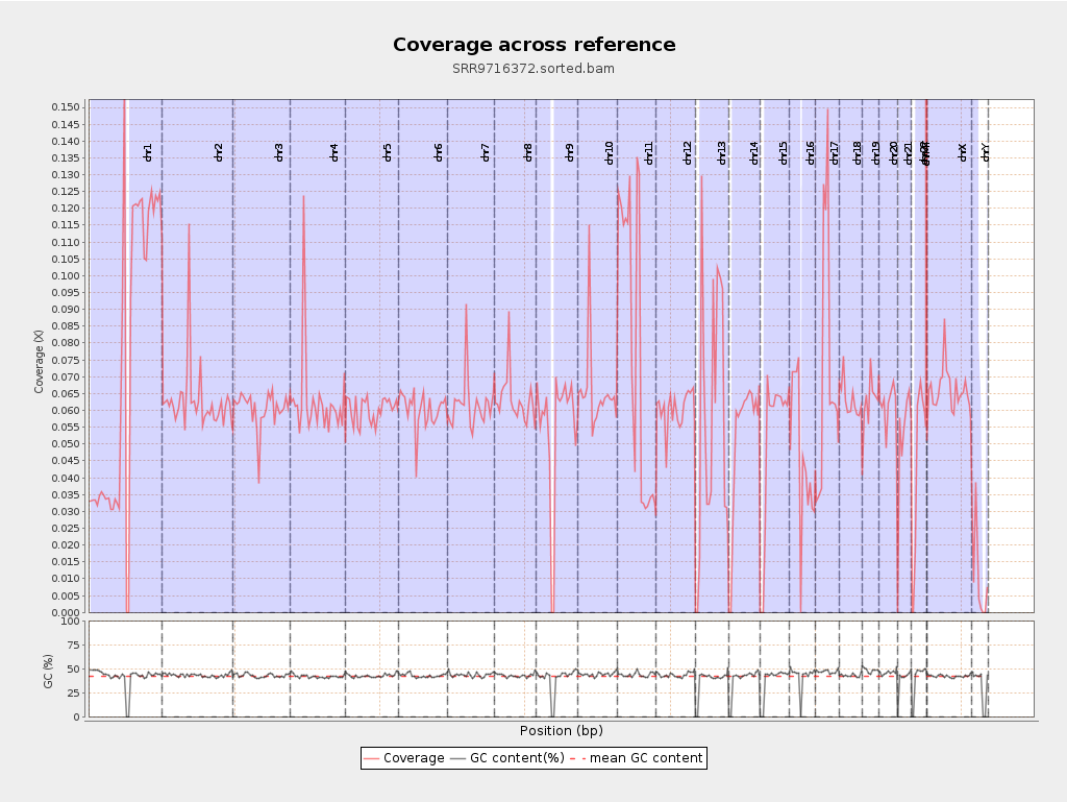
General error rate	0.68%
Mismatches	1,245,253
Insertions	15,990
Mapped reads with at least one insertion	0.66%
Deletions	47,107
Mapped reads with at least one deletion	1.95%
Homopolymer indels	42.91%

2.6. Chromosome stats

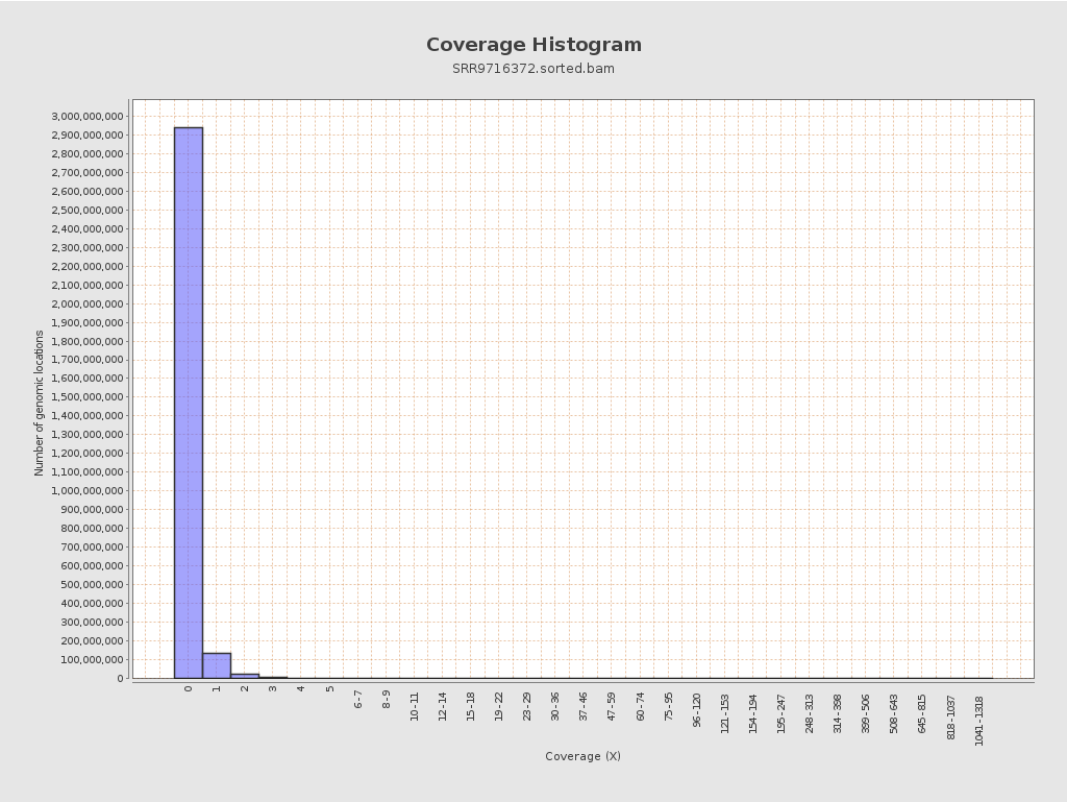
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18444709	0.074	1.1767
chr2	243199373	15319739	0.063	0.5781
chr3	198022430	11975953	0.0605	0.2853
chr4	191154276	11938033	0.0625	0.3908
chr5	180915260	10882814	0.0602	0.2862
chr6	171115067	10318854	0.0603	0.3142
chr7	159138663	9829888	0.0618	0.638

chr8	146364022	9221604	0.063	0.5871
chr9	141213431	7689814	0.0545	0.4404
chr10	135534747	8827754	0.0651	0.5441
chr11	135006516	10560204	0.0782	0.5869
chr12	133851895	8076280	0.0603	0.2873
chr13	115169878	6545674	0.0568	0.2791
chr14	107349540	5514860	0.0514	0.2869
chr15	102531392	5301340	0.0517	0.2628
chr16	90354753	4193883	0.0464	0.2856
chr17	81195210	5978561	0.0736	0.3963
chr18	78077248	4938261	0.0632	0.7945
chr19	59128983	3739924	0.0633	0.7663
chr20	63025520	3858010	0.0612	0.3069
chr21	48129895	2507857	0.0521	0.3304
chr22	51304566	2214671	0.0432	0.2425
chrMT	16571	68822	4.1532	2.9279
chrX	155270560	10224475	0.0658	0.3641
chrY	59373566	581866	0.0098	0.3289

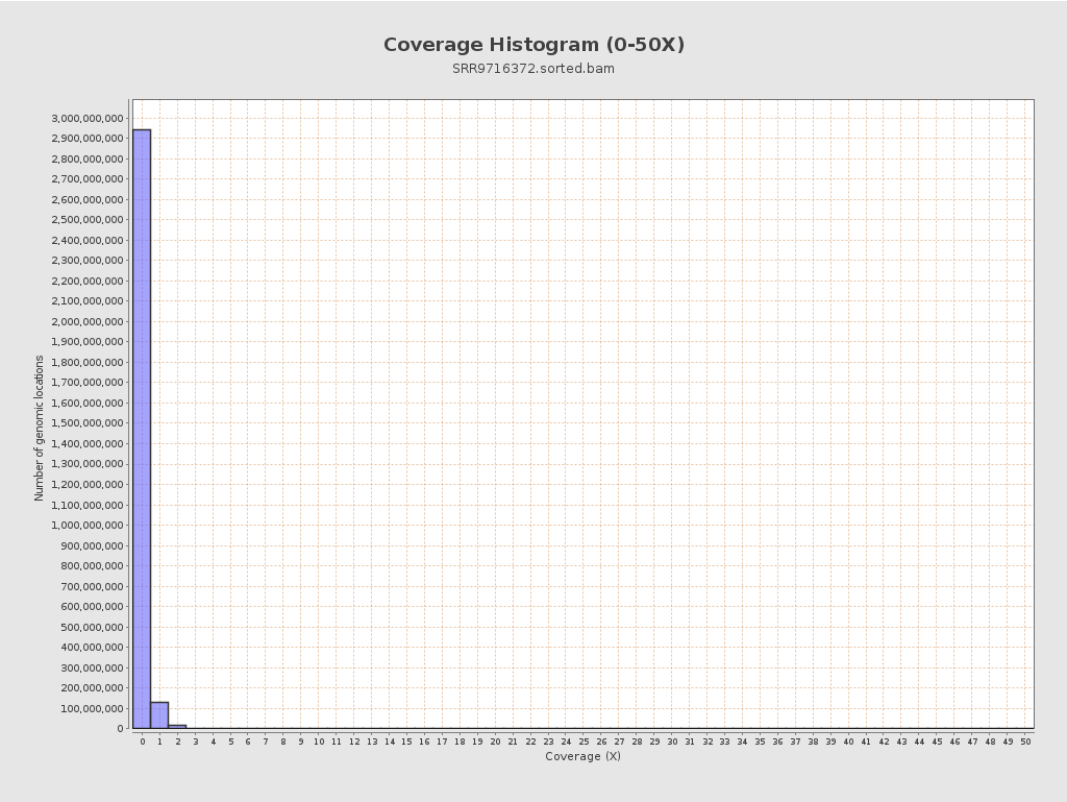
3. Results : Coverage across reference



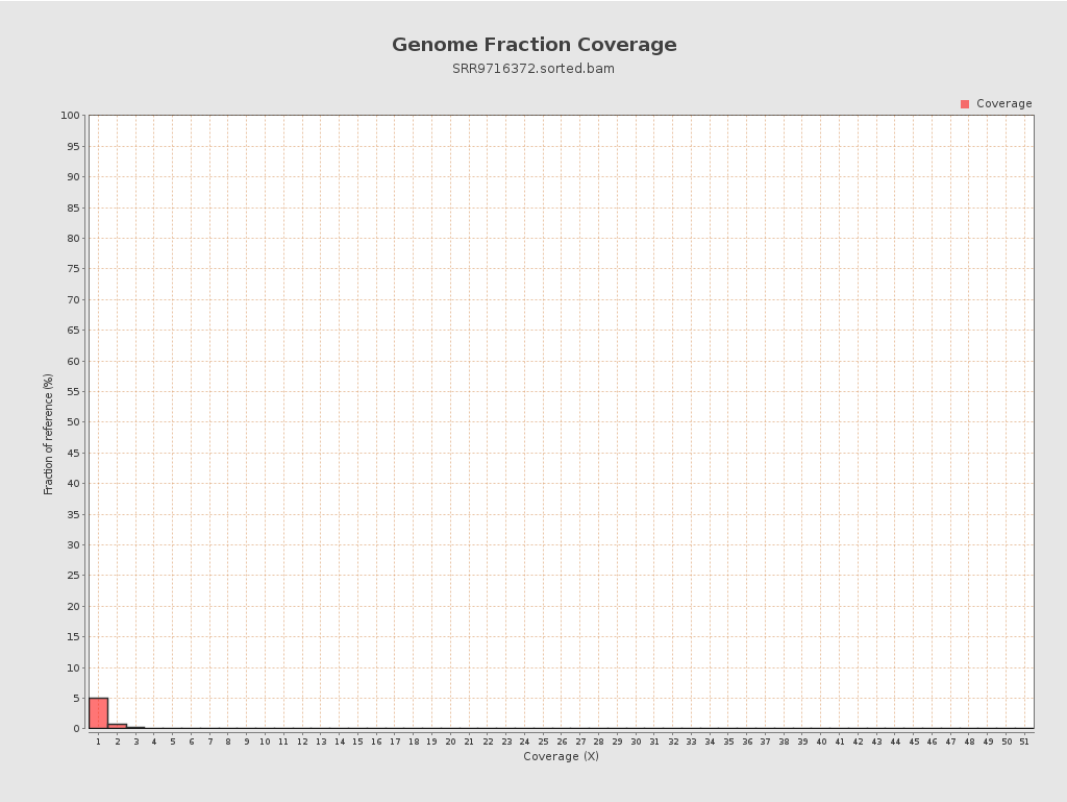
4. Results : Coverage Histogram



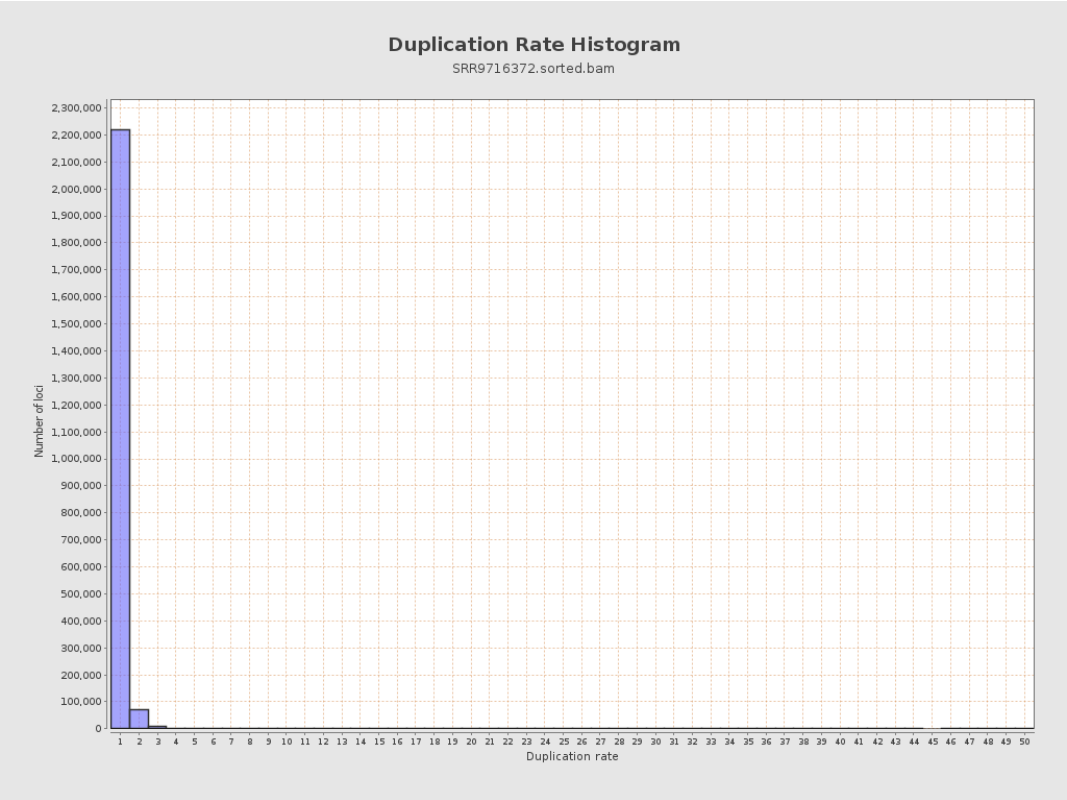
5. Results : Coverage Histogram (0-50X)



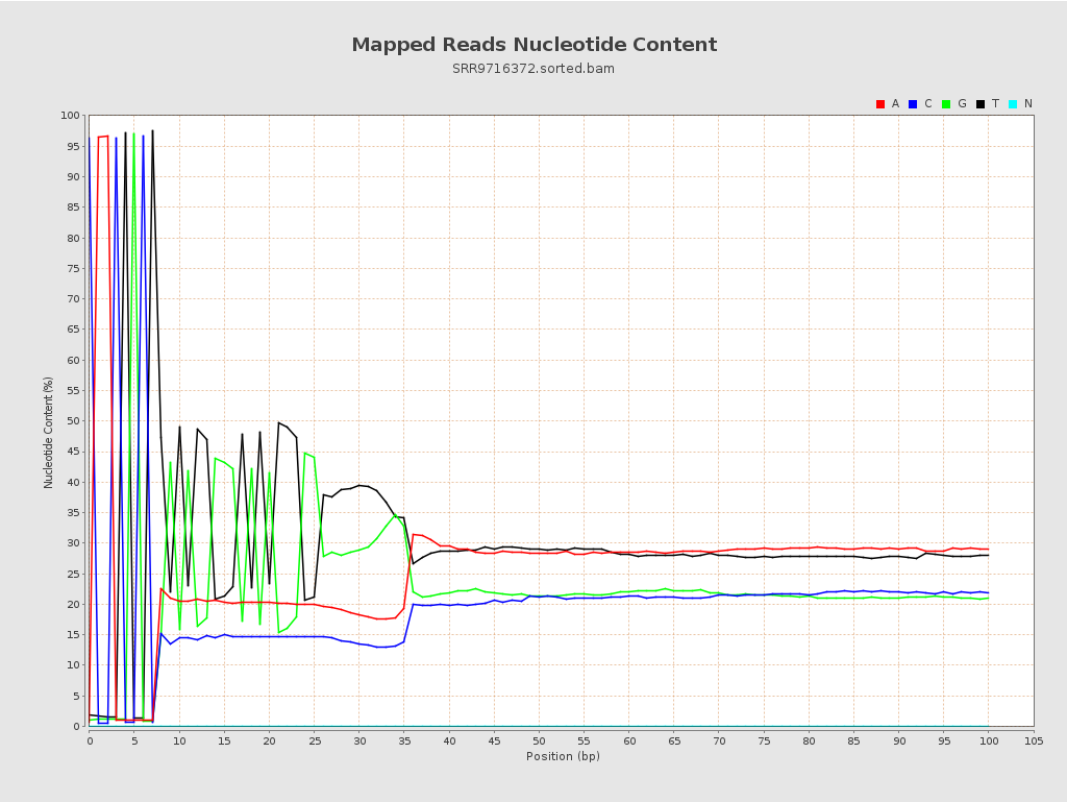
6. Results : Genome Fraction Coverage



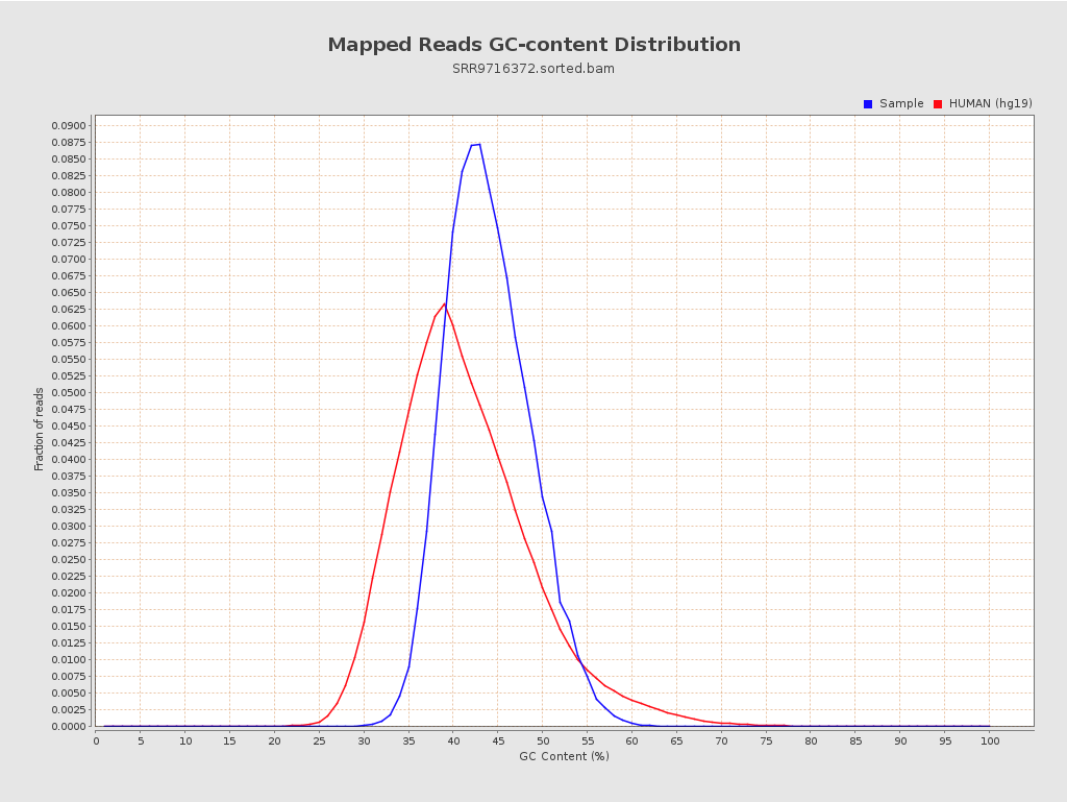
7. Results : Duplication Rate Histogram



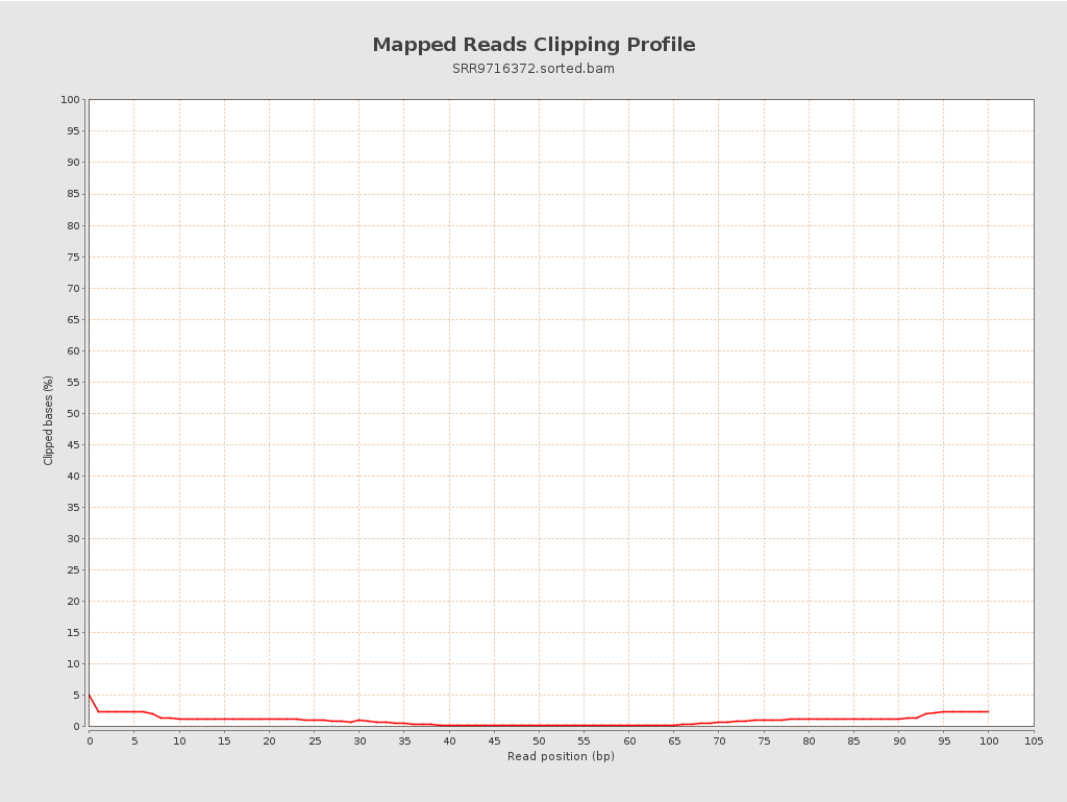
8. Results : Mapped Reads Nucleotide Content



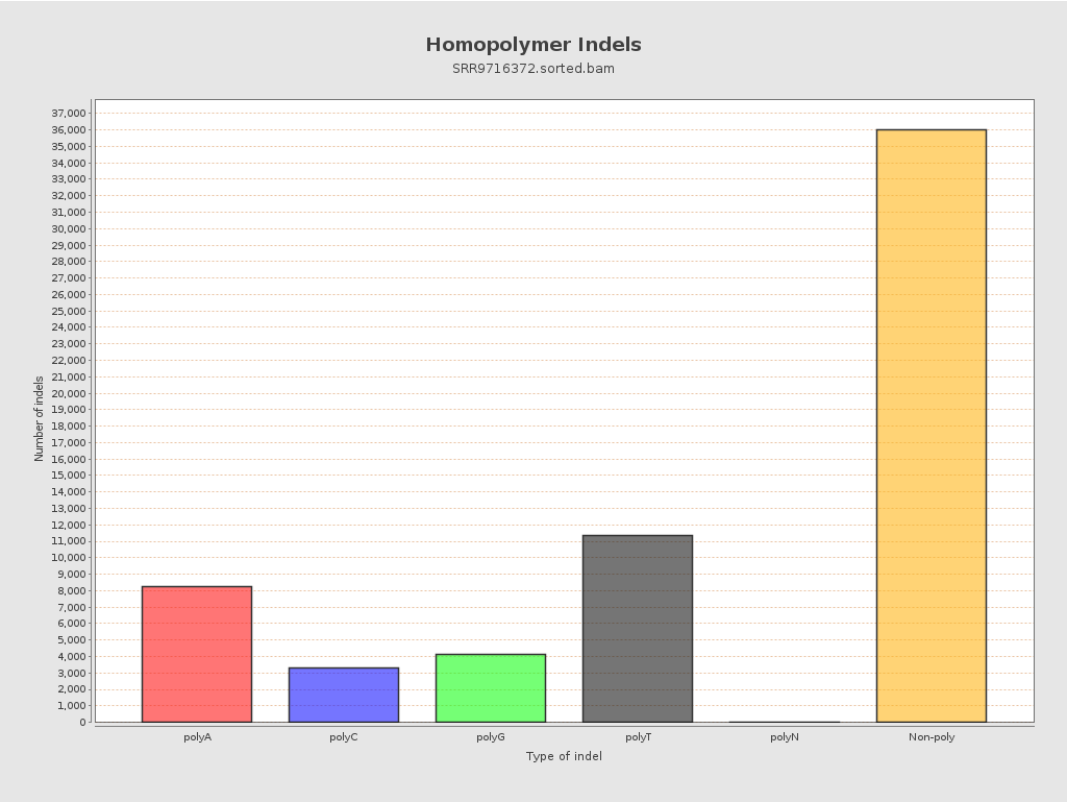
9. Results : Mapped Reads GC-content Distribution



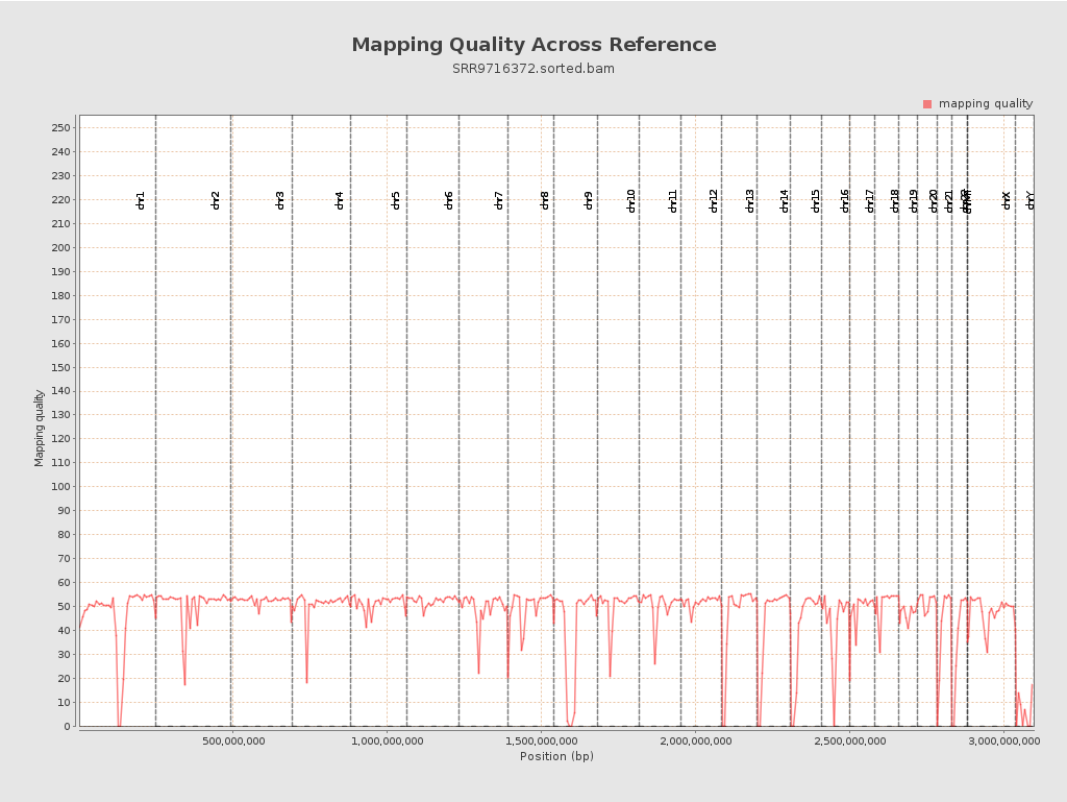
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram