Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:37:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716526.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_SRR9716526 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716526.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:37:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716526.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,174,620
Mapped reads	2,985,707 / 94.05%
Unmapped reads	188,913 / 5.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	58,429 / 1.84%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	158,615 / 5%
Duplication rate	3.9%
Clipped reads	3,039,532 / 95.74%

2.2. ACGT Content

Number/percentage of A's	59,399,580 / 25.2%
Number/percentage of C's	46,290,857 / 19.64%
Number/percentage of T's	72,071,123 / 30.57%
Number/percentage of G's	57,947,680 / 24.58%
Number/percentage of N's	16,282 / 0.01%
GC Percentage	44.22%

2.3. Coverage

Mean	0.0762

Standard Deviation	0.5869

2.4. Mapping Quality

Mean Mapping Quality	47.43

2.5. Mismatches and indels

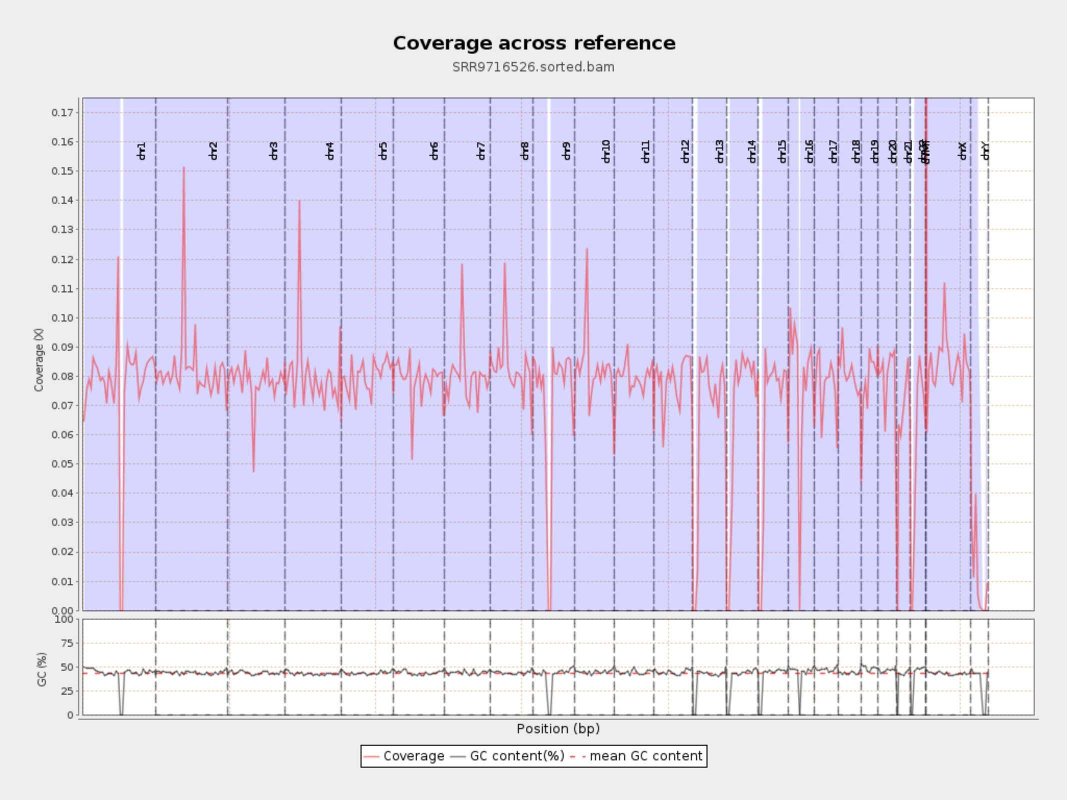
General error rate	0.64%
Mismatches	1,458,460
Insertions	18,560
Mapped reads with at least one insertion	0.61%
Deletions	52,894
Mapped reads with at least one deletion	1.74%
Homopolymer indels	43.38%

2.6. Chromosome stats

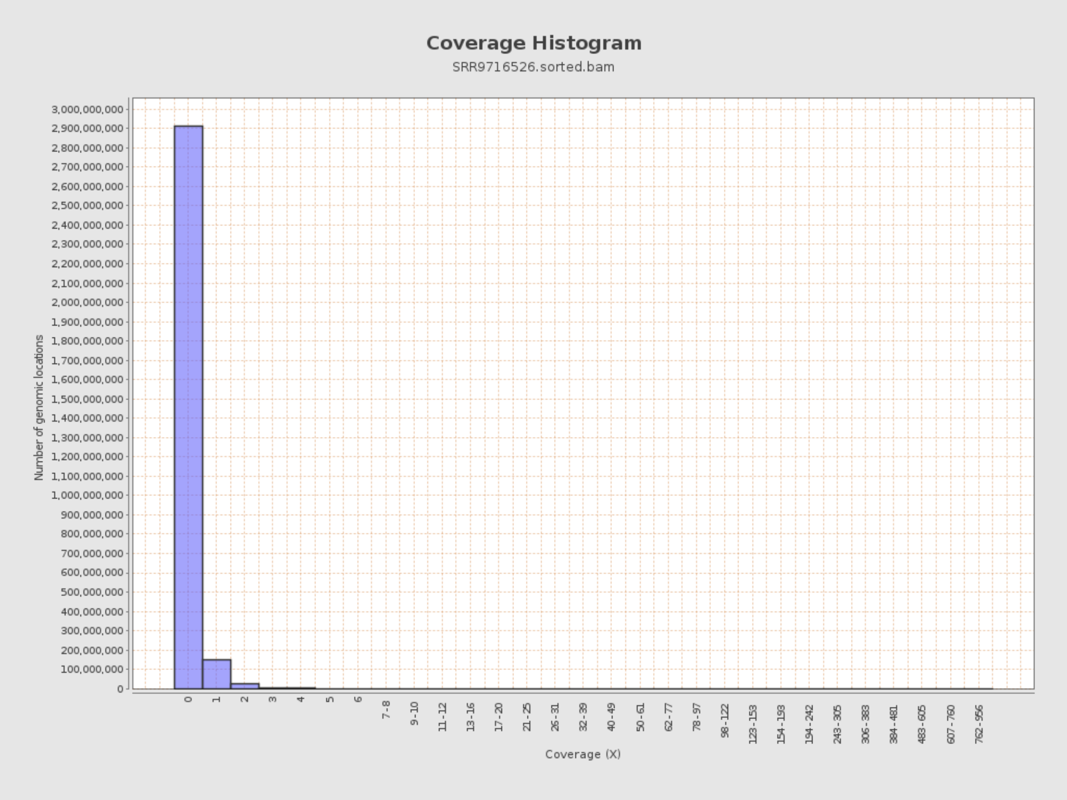
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19081003	0.0766	0.9248
chr2	243199373	20141763	0.0828	0.7873
chr3	198022430	15461306	0.0781	0.3379
chr4	191154276	15454585	0.0808	0.4493
chr5	180915260	14469404	0.08	0.3525
chr6	171115067	13509851	0.079	0.3936
chr7	159138663	12761704	0.0802	0.8324

chr8	146364022	12068529	0.0825	0.7621
chr9	141213431	9993396	0.0708	0.598
chr10	135534747	11231566	0.0829	0.5767
chr11	135006516	10709182	0.0793	0.619
chr12	133851895	10599871	0.0792	0.3489
chr13	115169878	7492960	0.0651	0.3081
chr14	107349540	7315398	0.0681	0.3643
chr15	102531392	6676013	0.0651	0.3141
chr16	90354753	6847713	0.0758	0.3749
chr17	81195210	6313911	0.0778	0.4096
chr18	78077248	6355731	0.0814	1.0355
chr19	59128983	4646618	0.0786	0.71
chr20	63025520	5055058	0.0802	0.3739
chr21	48129895	3087585	0.0642	0.3758
chr22	51304566	2780435	0.0542	0.2924
chrMT	16571	25570	1.5431	1.5114
chrX	155270560	13075512	0.0842	0.4504
chrY	59373566	672663	0.0113	0.3245

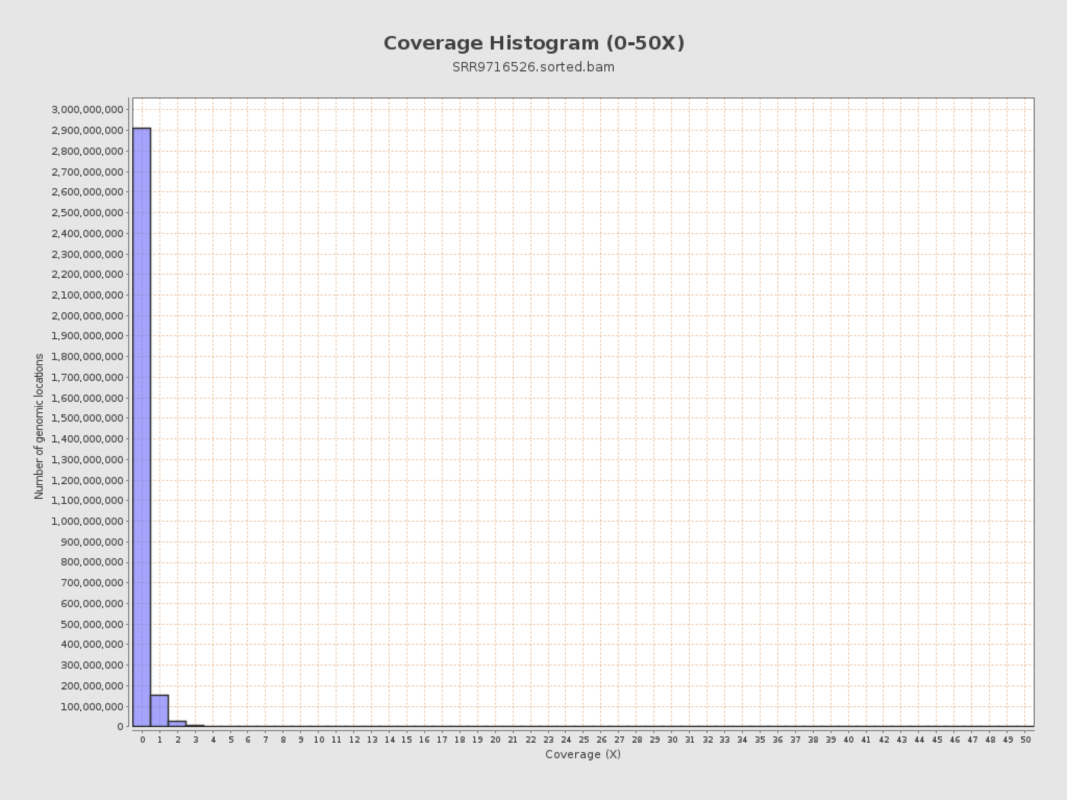
3. Results : Coverage across reference



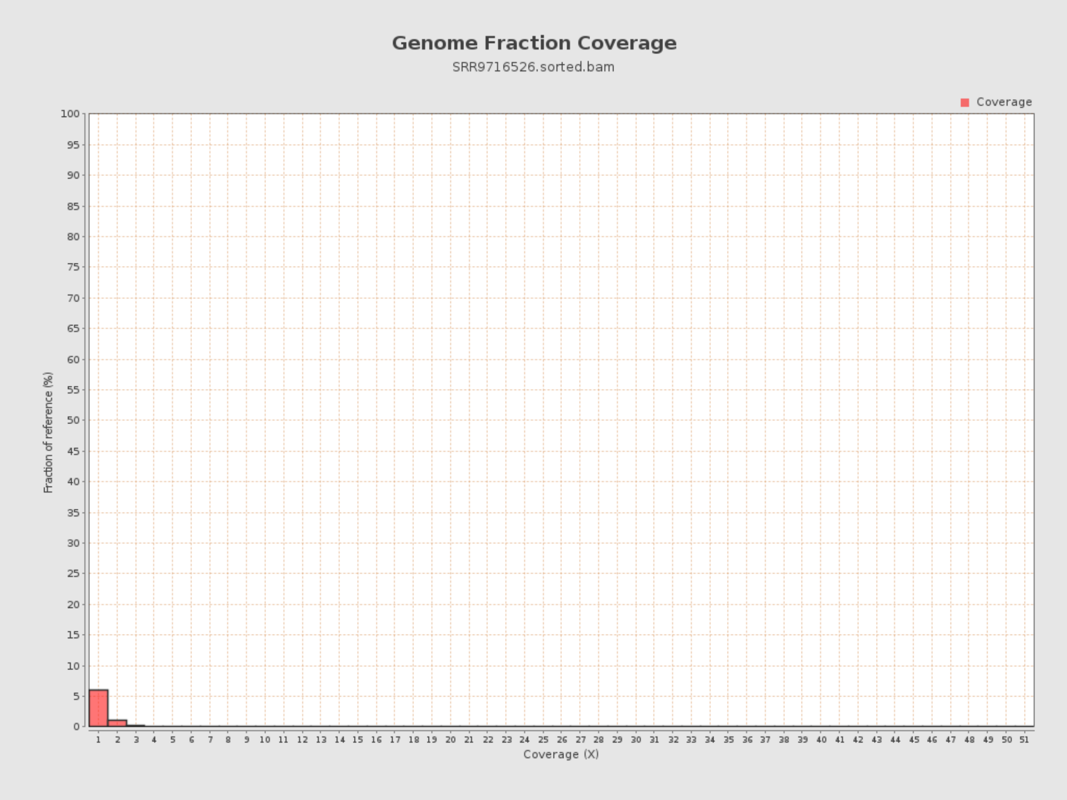
4. Results : Coverage Histogram



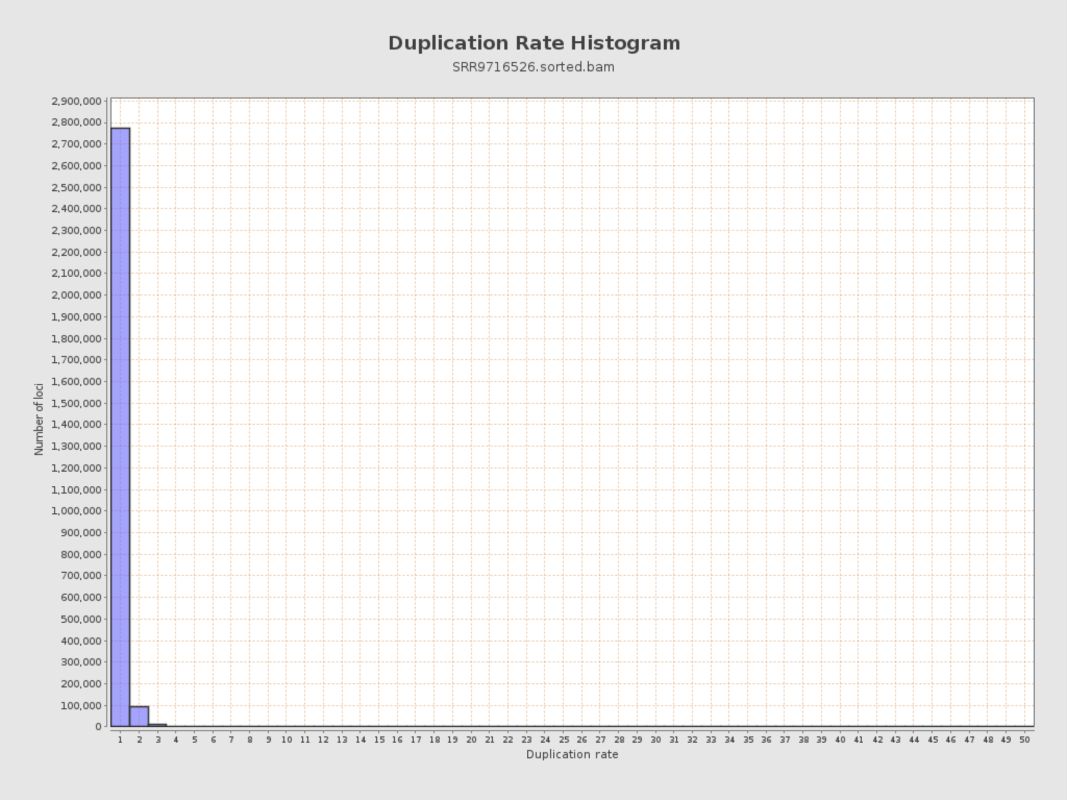
5. Results : Coverage Histogram (0-50X)



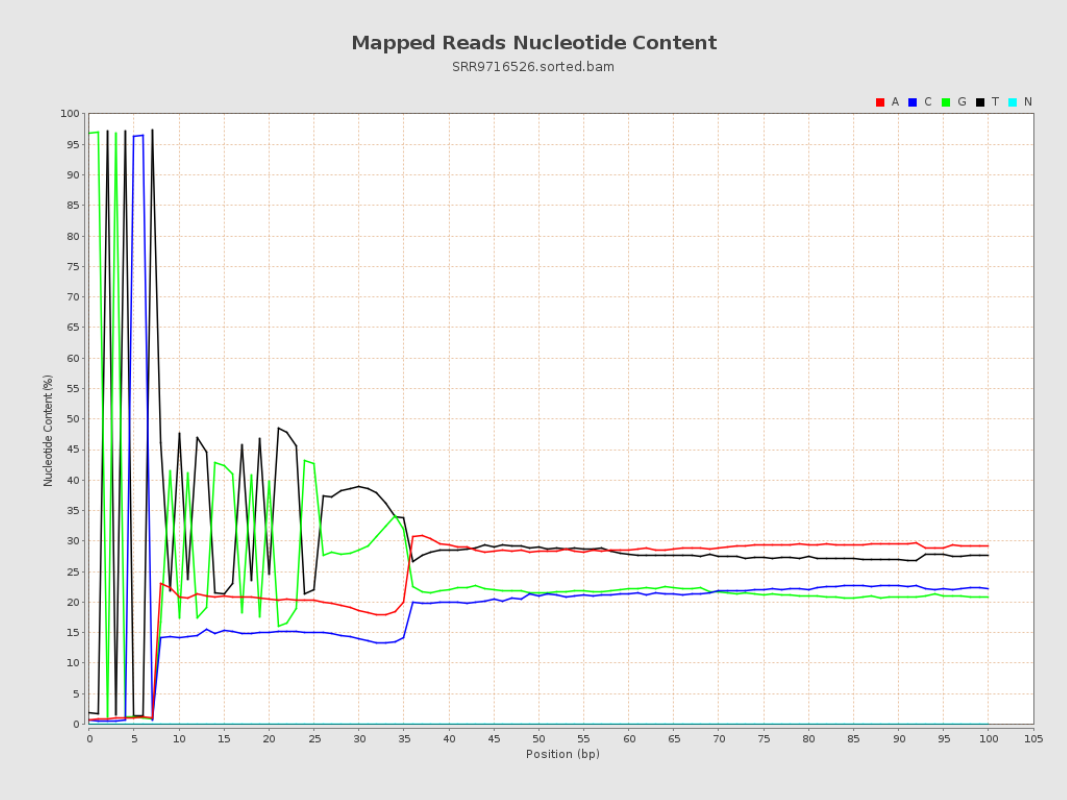
6. Results : Genome Fraction Coverage



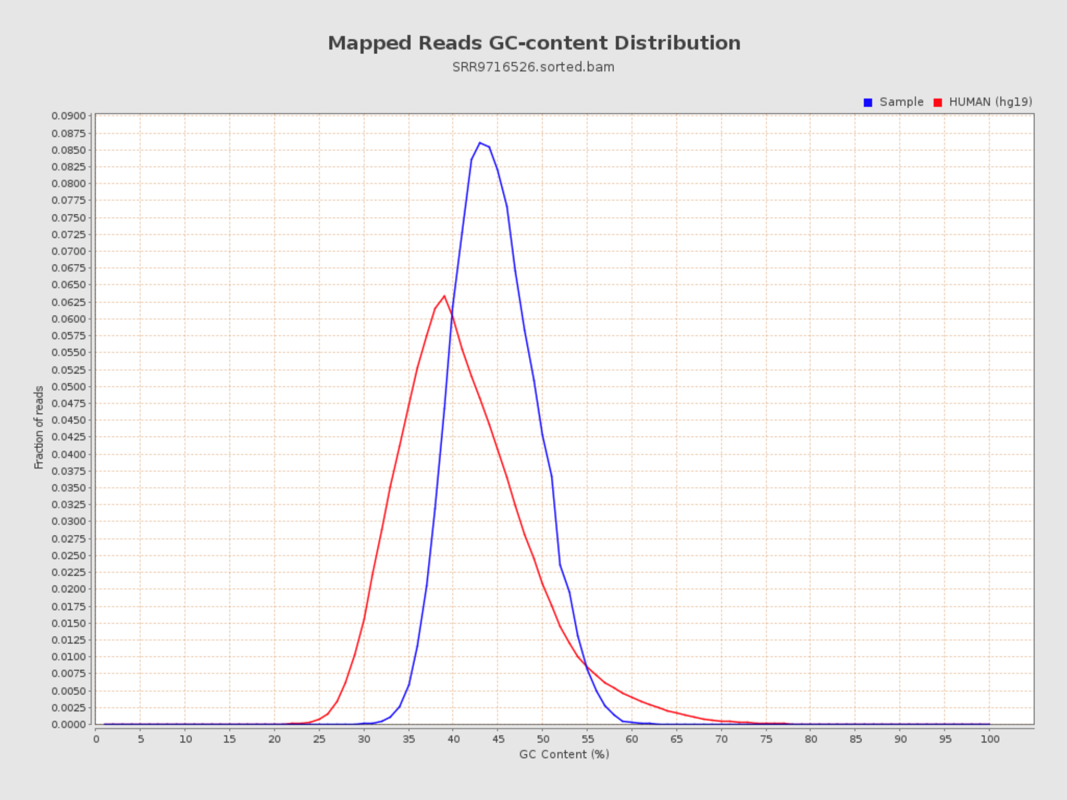
7. Results : Duplication Rate Histogram



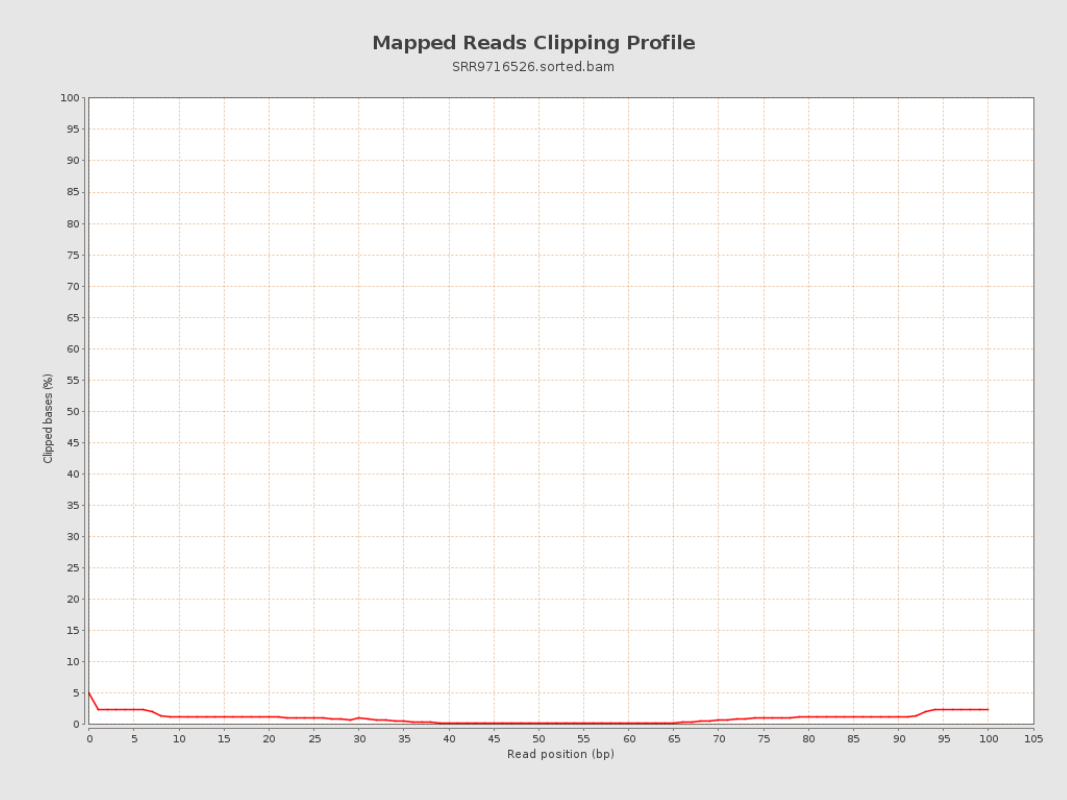
8. Results : Mapped Reads Nucleotide Content



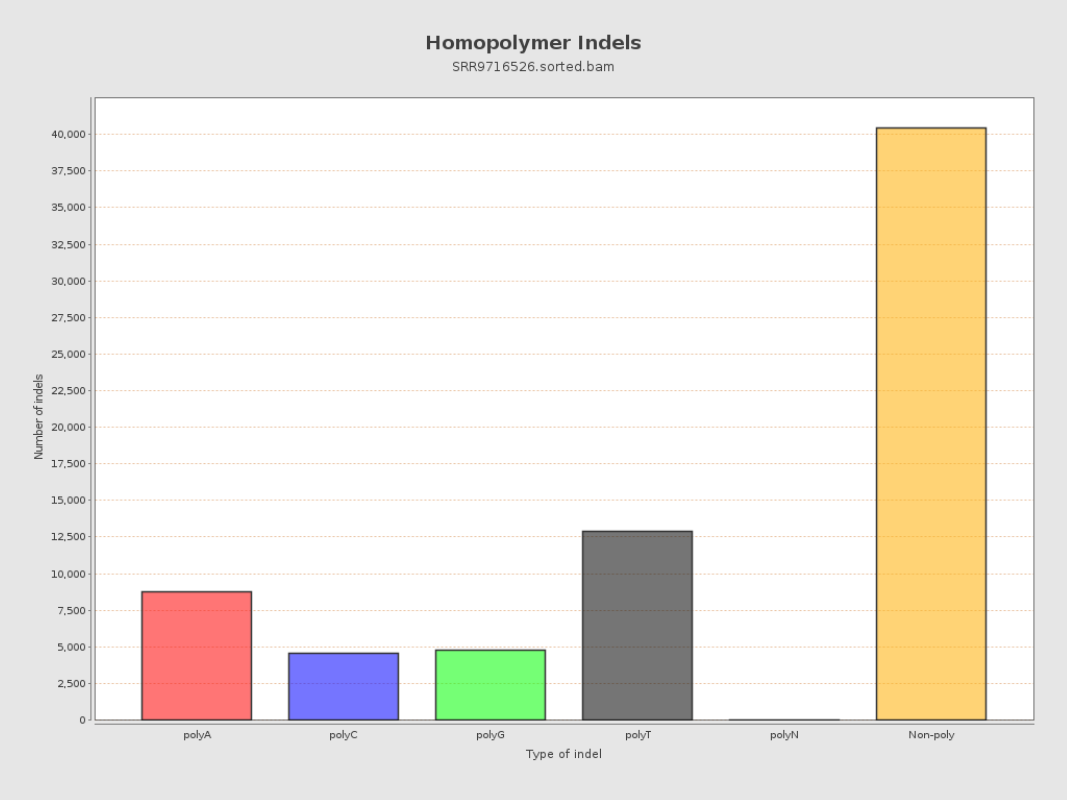
9. Results : Mapped Reads GC-content Distribution



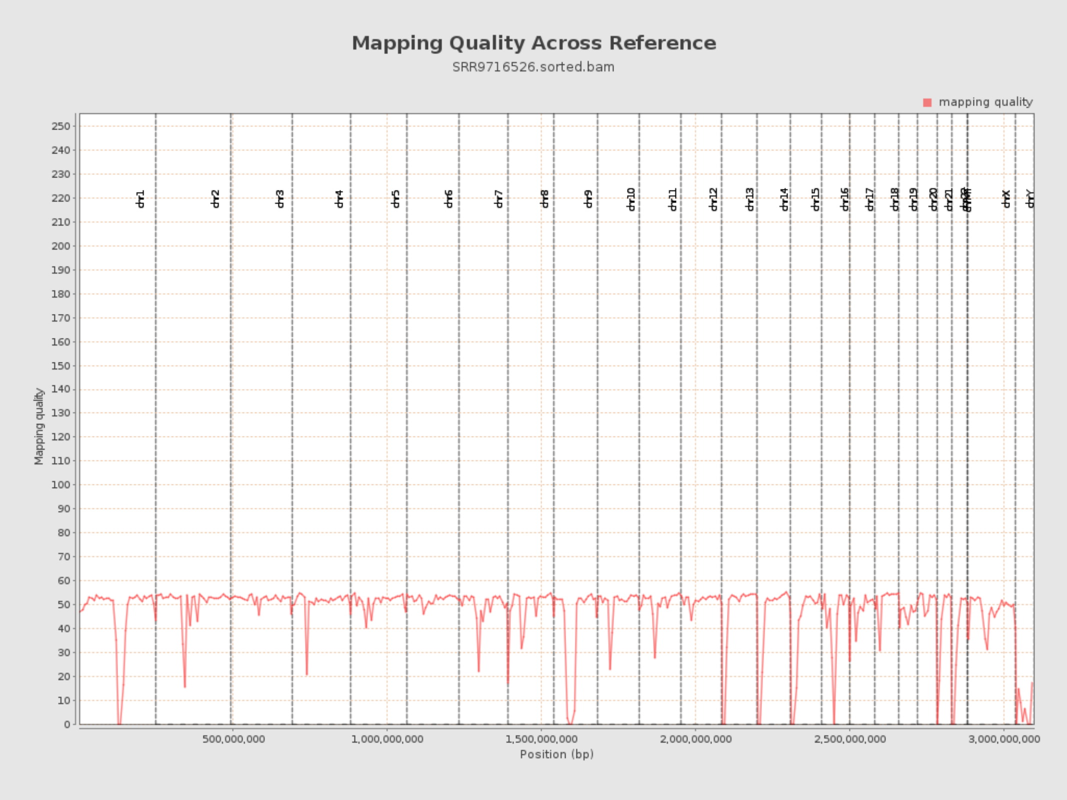
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram