Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 21:46:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716562.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_SRR9716562 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716562.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 21:46:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716562.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,446,765
Mapped reads	3,057,936 / 88.72%
Unmapped reads	388,829 / 11.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,909 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	120,771 / 3.5%
Duplication rate	2.93%
Clipped reads	3,060,868 / 88.8%

2.2. ACGT Content

Number/percentage of A's	41,003,222 / 23.6%
Number/percentage of C's	34,975,749 / 20.13%
Number/percentage of T's	55,838,423 / 32.14%
Number/percentage of G's	41,927,051 / 24.13%
Number/percentage of N's	3,743 / 0%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0561

Standard Deviation	0.3834

2.4. Mapping Quality

Mean Mapping Quality	43.49

2.5. Mismatches and indels

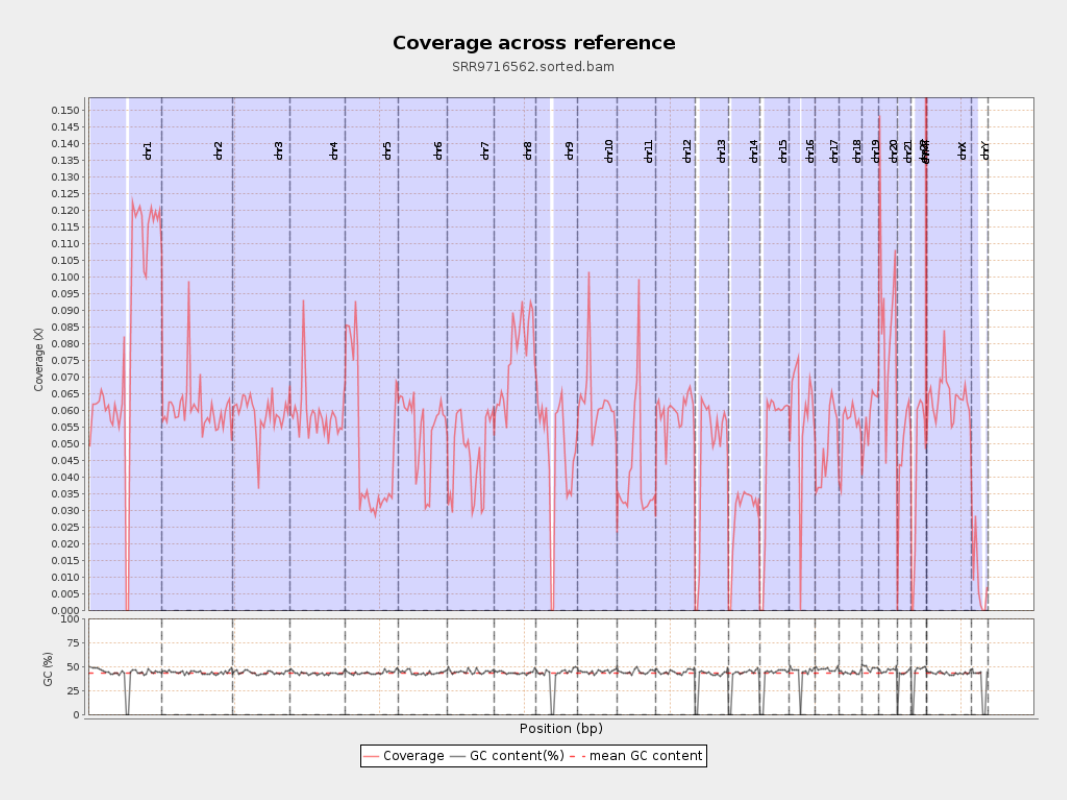
General error rate	0.51%
Mismatches	857,664
Insertions	12,378
Mapped reads with at least one insertion	0.4%
Deletions	27,807
Mapped reads with at least one deletion	0.9%
Homopolymer indels	40.24%

2.6. Chromosome stats

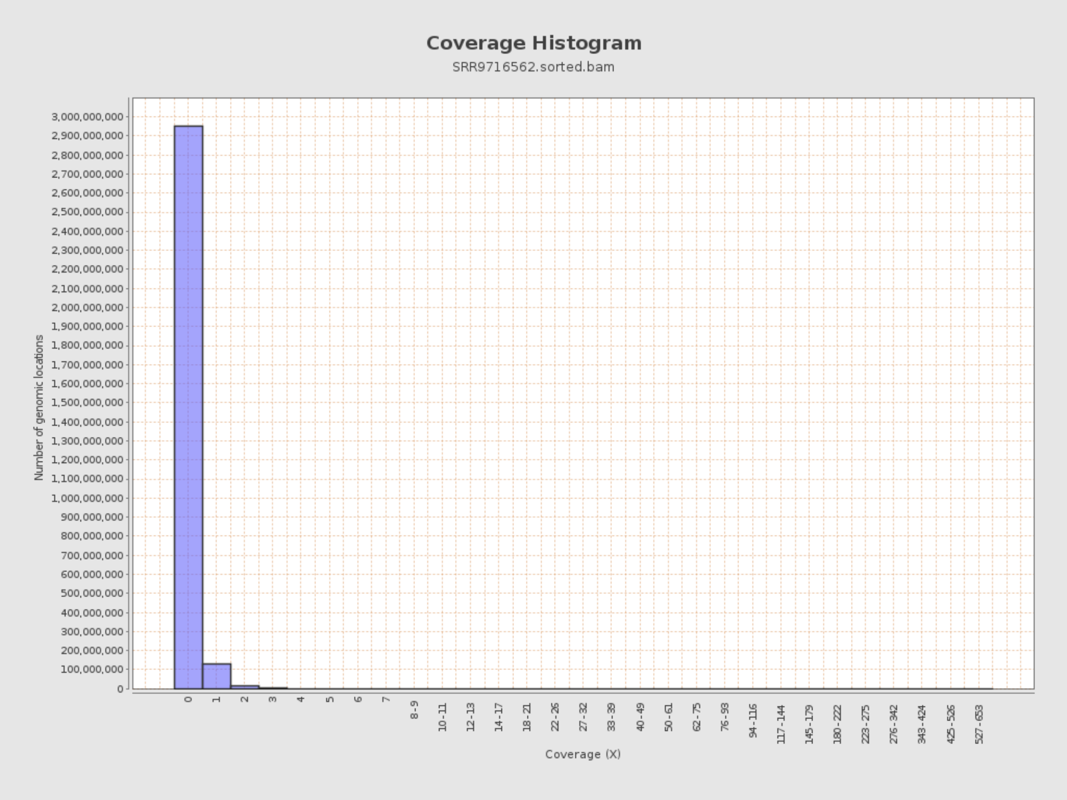
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20088377	0.0806	0.6047
chr2	243199373	14749584	0.0606	0.4702
chr3	198022430	11662777	0.0589	0.2833
chr4	191154276	11220196	0.0587	0.3239
chr5	180915260	8777996	0.0485	0.2606
chr6	171115067	9301733	0.0544	0.2967
chr7	159138663	7380748	0.0464	0.3326

chr8	146364022	11133392	0.0761	0.3812
chr9	141213431	6518122	0.0462	0.3946
chr10	135534747	8465202	0.0625	0.4643
chr11	135006516	5548079	0.0411	0.3428
chr12	133851895	8011583	0.0599	0.2928
chr13	115169878	5456575	0.0474	0.2492
chr14	107349540	3006741	0.028	0.2425
chr15	102531392	5067116	0.0494	0.2586
chr16	90354753	5324665	0.0589	0.326
chr17	81195210	3970234	0.0489	0.2676
chr18	78077248	4307024	0.0552	0.7447
chr19	59128983	3450411	0.0584	0.4687
chr20	63025520	5498572	0.0872	0.3574
chr21	48129895	2288580	0.0476	0.3038
chr22	51304566	2112589	0.0412	0.2348
chrMT	16571	32788	1.9786	1.8689
chrX	155270560	9902646	0.0638	0.35
chrY	59373566	519380	0.0087	0.1933

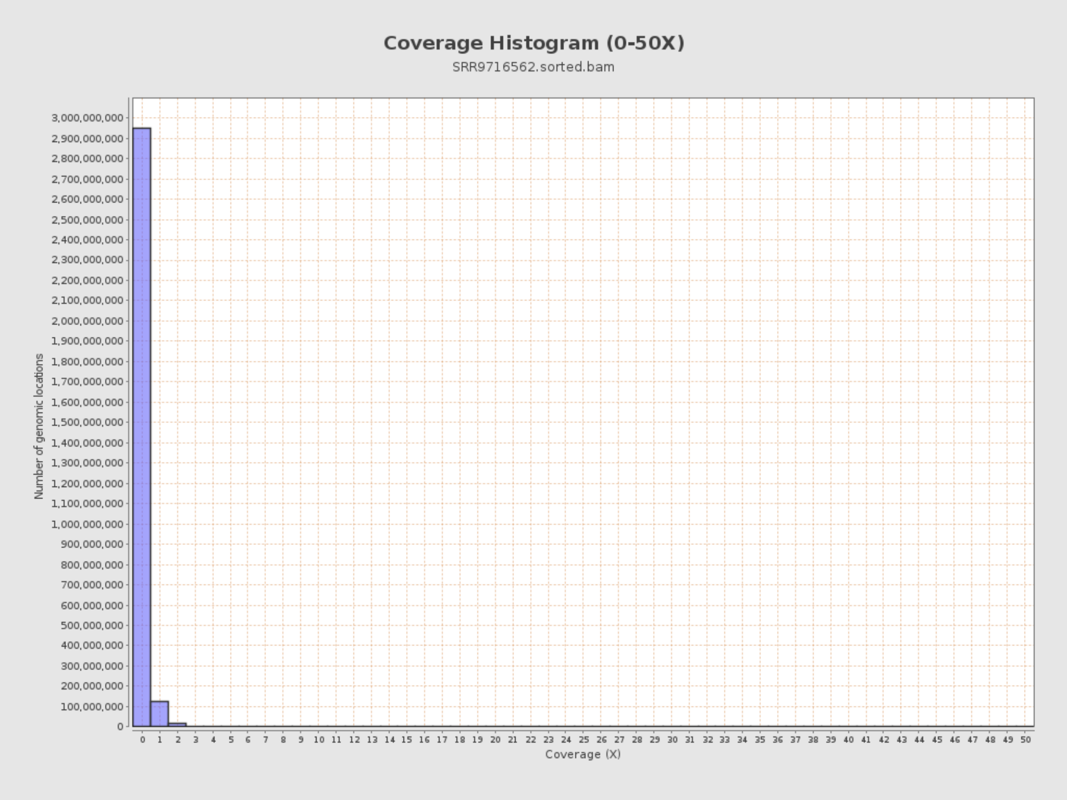
3. Results : Coverage across reference



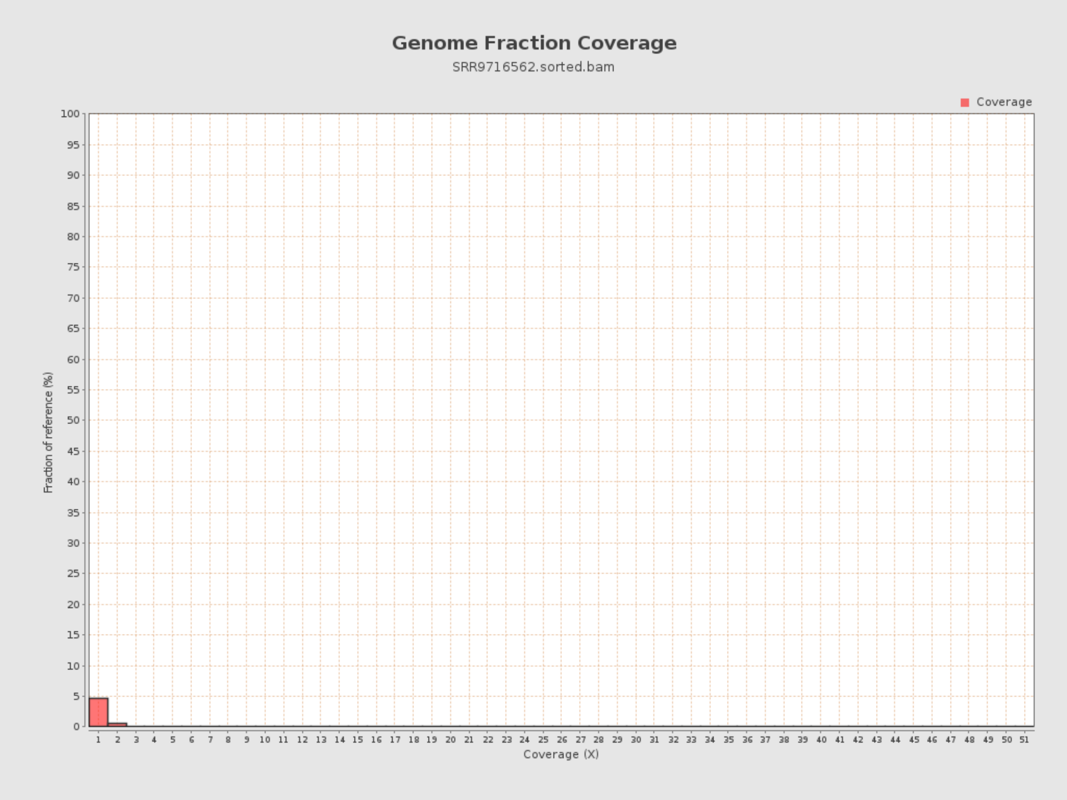
4. Results : Coverage Histogram



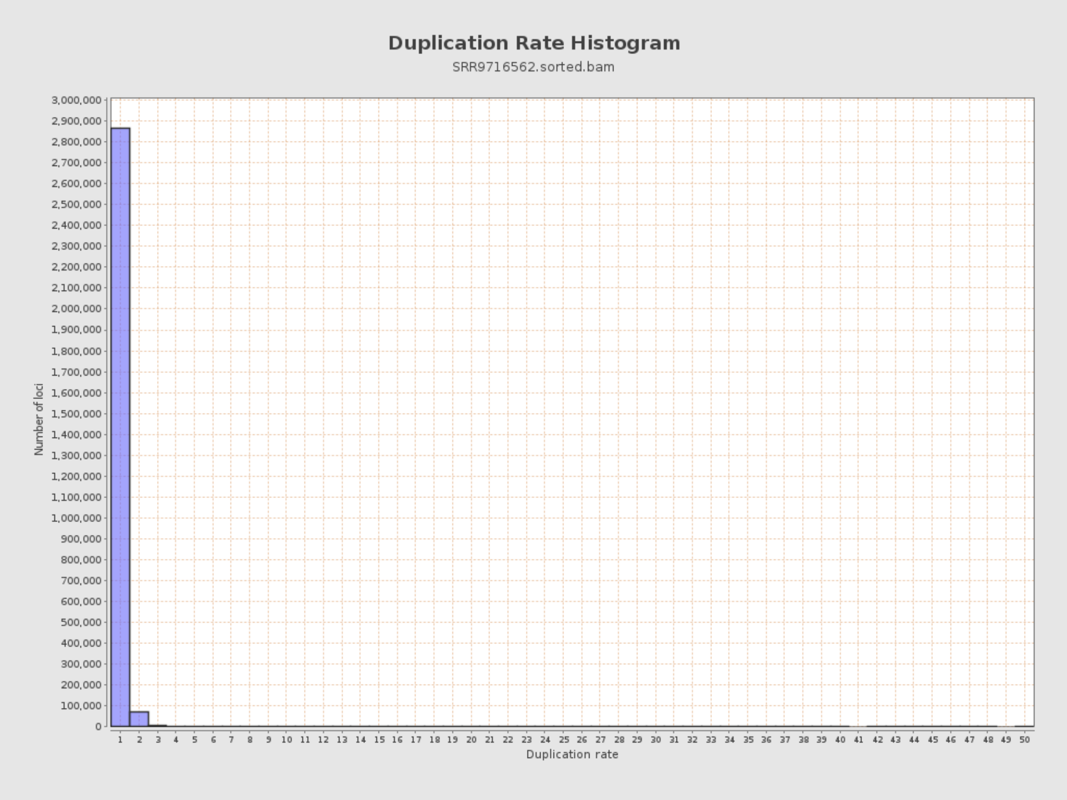
5. Results : Coverage Histogram (0-50X)



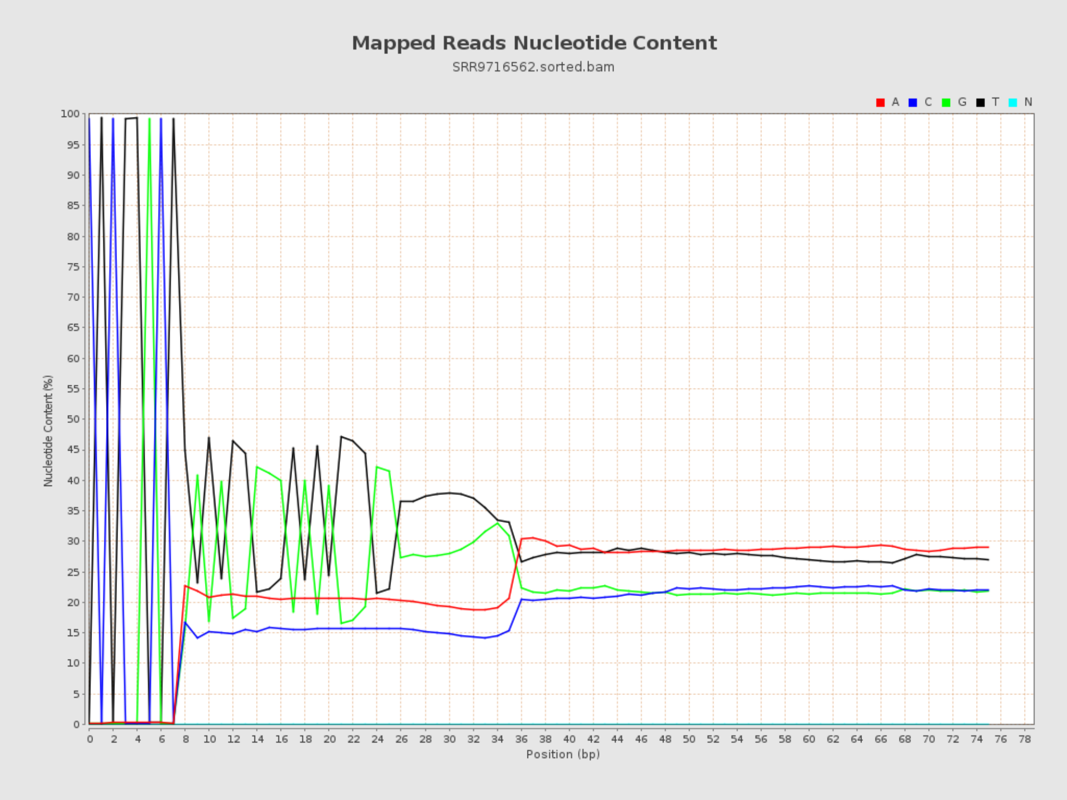
6. Results : Genome Fraction Coverage



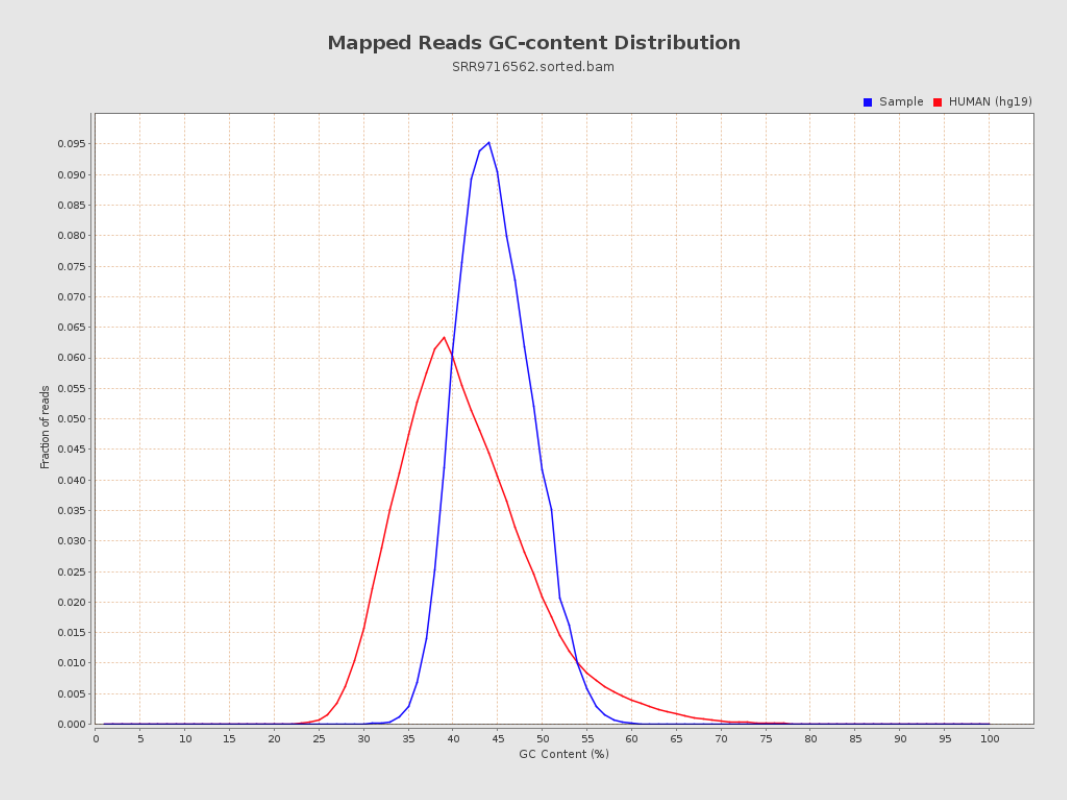
7. Results : Duplication Rate Histogram



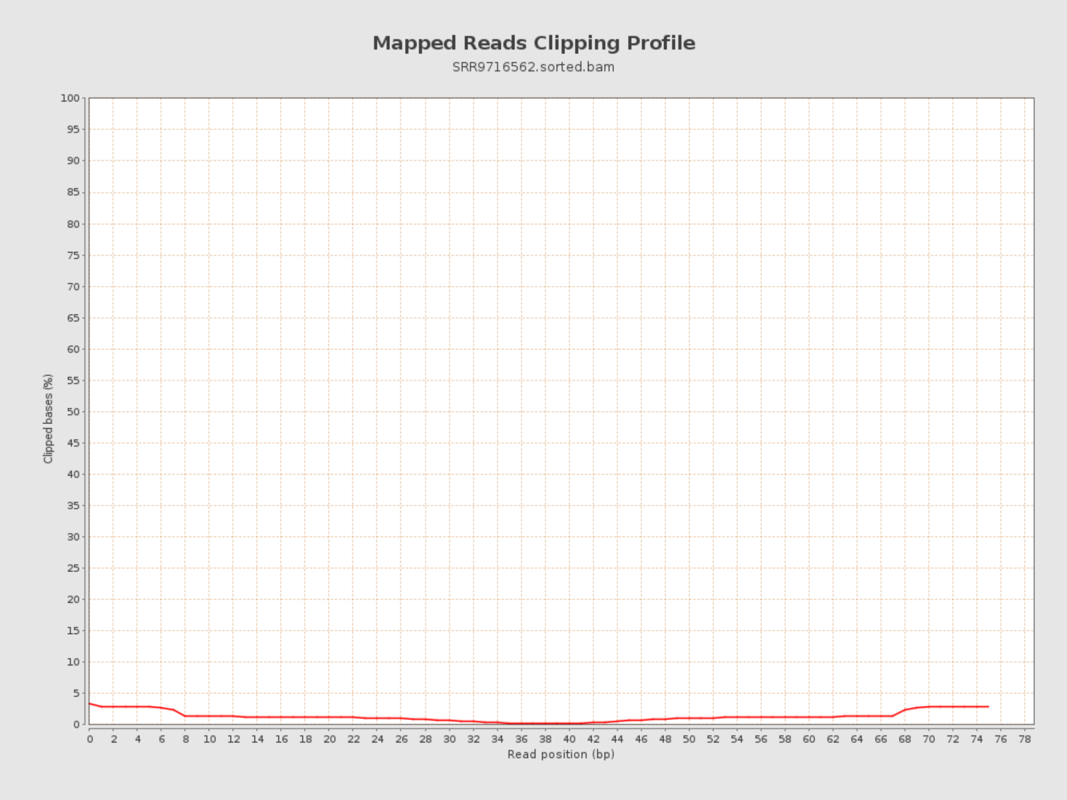
8. Results : Mapped Reads Nucleotide Content



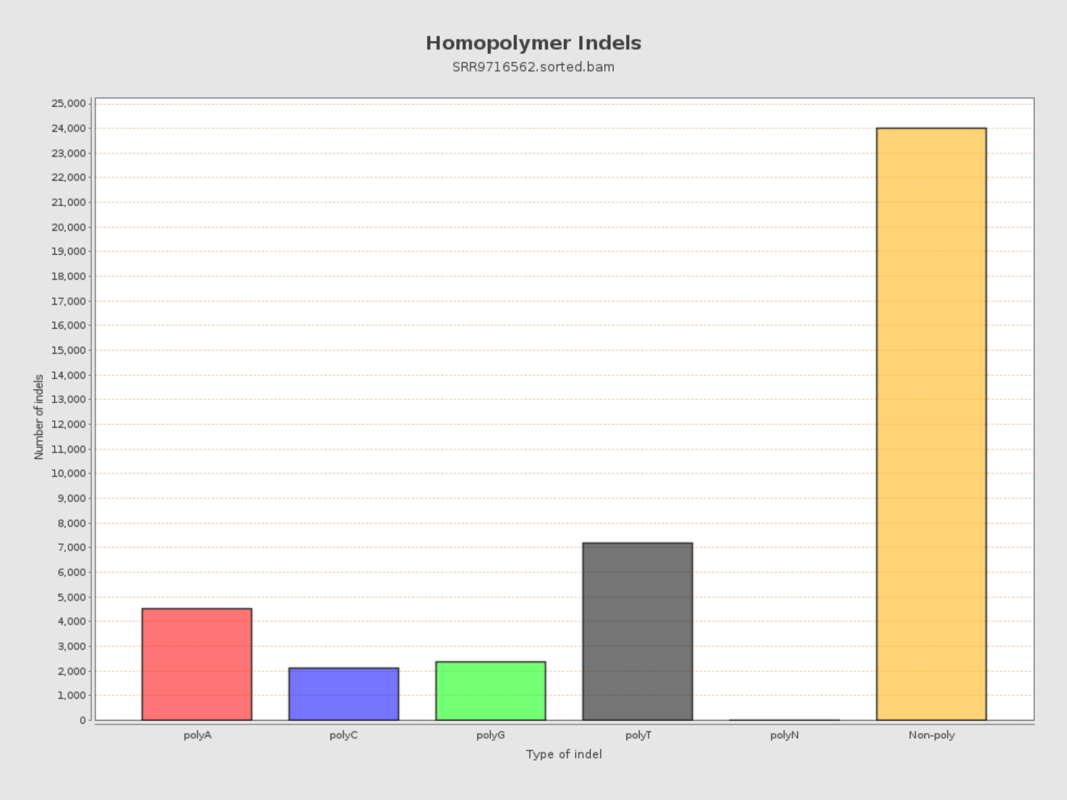
9. Results : Mapped Reads GC-content Distribution



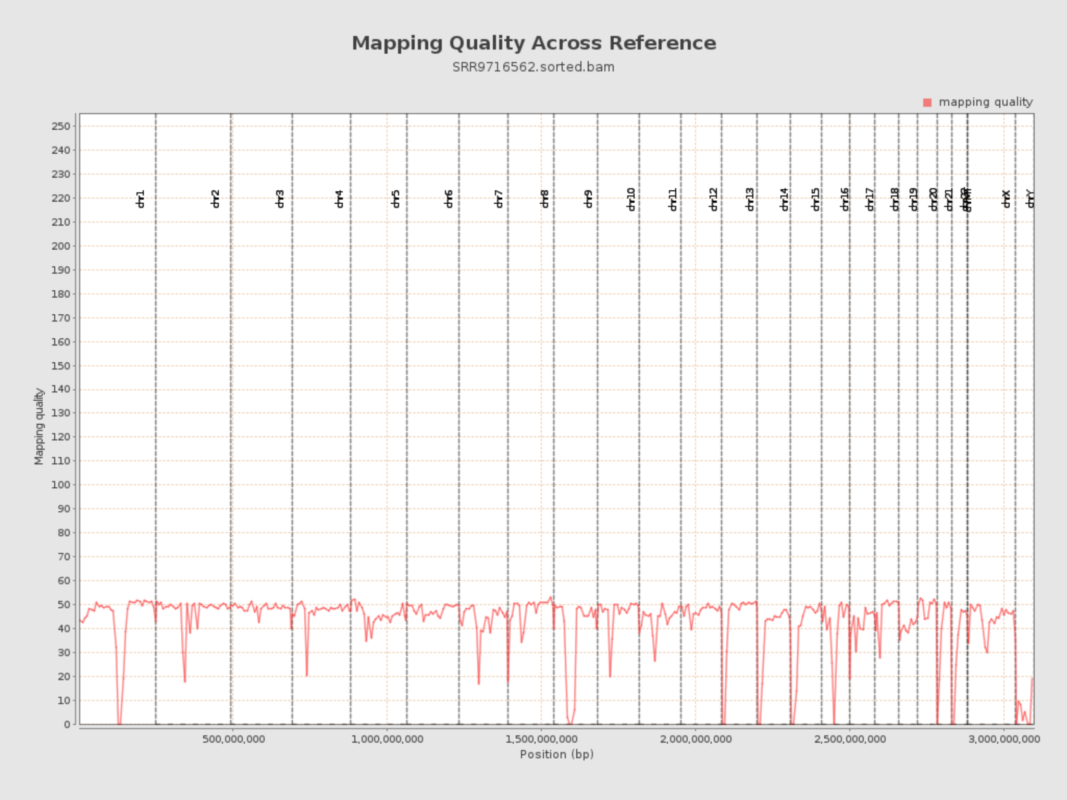
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram