Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:27:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716523.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_SRR9716523 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716523.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:27:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716523.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,013,977
Mapped reads	2,807,503 / 93.15%
Unmapped reads	206,474 / 6.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,337 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	147,652 / 4.9%
Duplication rate	3.99%
Clipped reads	2,817,212 / 93.47%

2.2. ACGT Content

Number/percentage of A's	42,361,115 / 25.74%
Number/percentage of C's	33,746,227 / 20.51%
Number/percentage of T's	49,902,870 / 30.33%
Number/percentage of G's	38,528,399 / 23.42%
Number/percentage of N's	4,553 / 0%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0532

Standard Deviation	0.4359

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

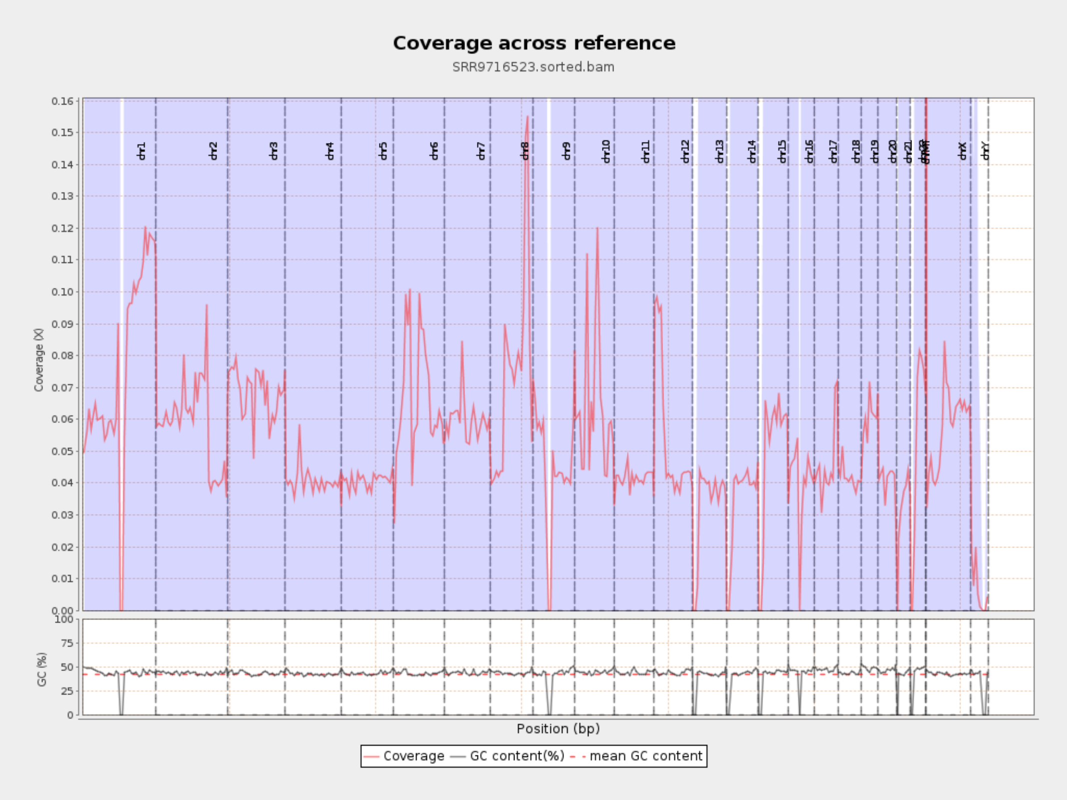
General error rate	0.49%
Mismatches	790,125
Insertions	9,754
Mapped reads with at least one insertion	0.35%
Deletions	29,795
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.72%

2.6. Chromosome stats

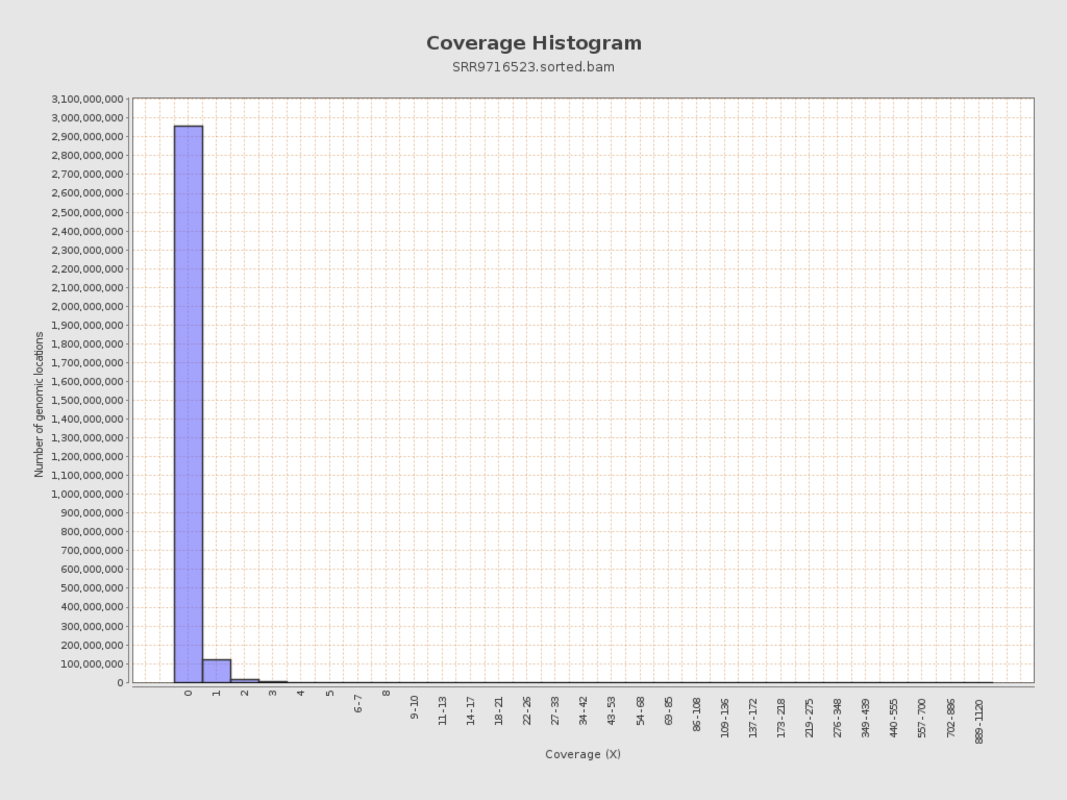
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18845459	0.0756	0.8451
chr2	243199373	14277860	0.0587	0.557
chr3	198022430	13568292	0.0685	0.3072
chr4	191154276	7800789	0.0408	0.2541
chr5	180915260	7382757	0.0408	0.2383
chr6	171115067	11582435	0.0677	0.436
chr7	159138663	9583402	0.0602	0.5555

chr8	146364022	10940094	0.0747	0.3753
chr9	141213431	6198981	0.0439	0.3662
chr10	135534747	8671466	0.064	0.4616
chr11	135006516	5613379	0.0416	0.3391
chr12	133851895	7387716	0.0552	0.2849
chr13	115169878	3787334	0.0329	0.2125
chr14	107349540	3673042	0.0342	0.248
chr15	102531392	5040254	0.0492	0.26
chr16	90354753	3547369	0.0393	0.2744
chr17	81195210	3685975	0.0454	0.2632
chr18	78077248	3270789	0.0419	0.7
chr19	59128983	3545102	0.06	0.5577
chr20	63025520	2601126	0.0413	0.2388
chr21	48129895	1530053	0.0318	0.2379
chr22	51304566	2699900	0.0526	0.2691
chrMT	16571	55002	3.3192	2.6887
chrX	155270560	8909314	0.0574	0.3307
chrY	59373566	392320	0.0066	0.1424

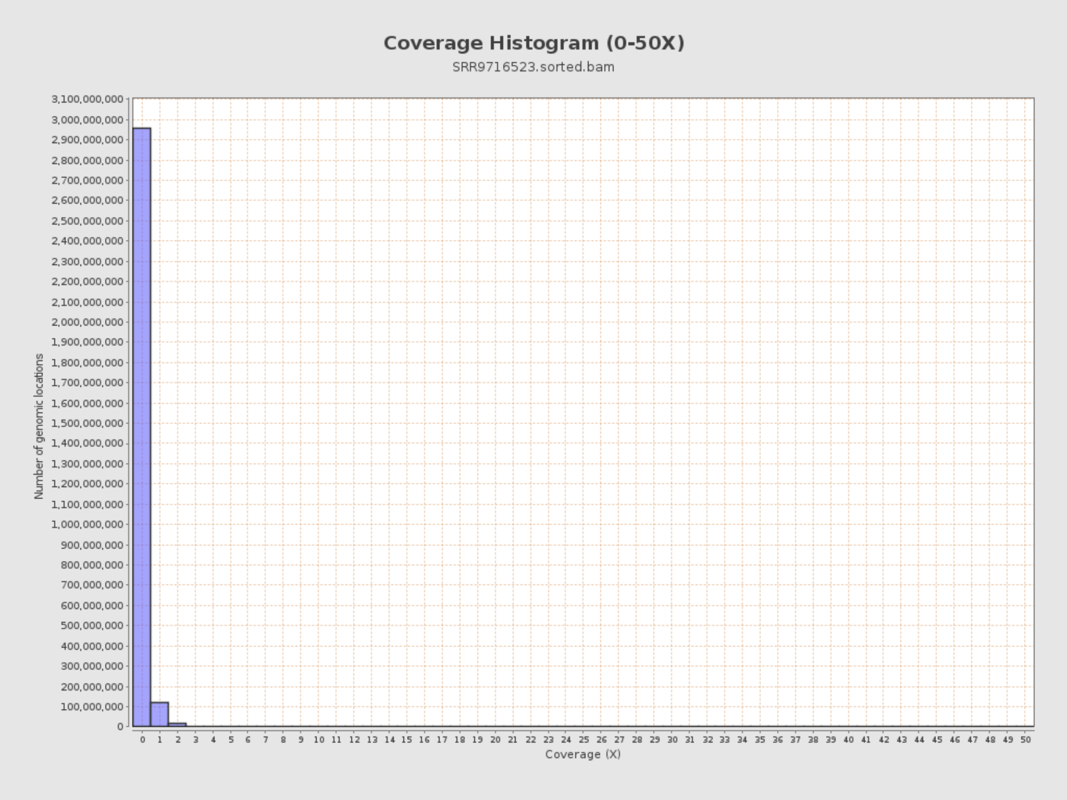
3. Results : Coverage across reference



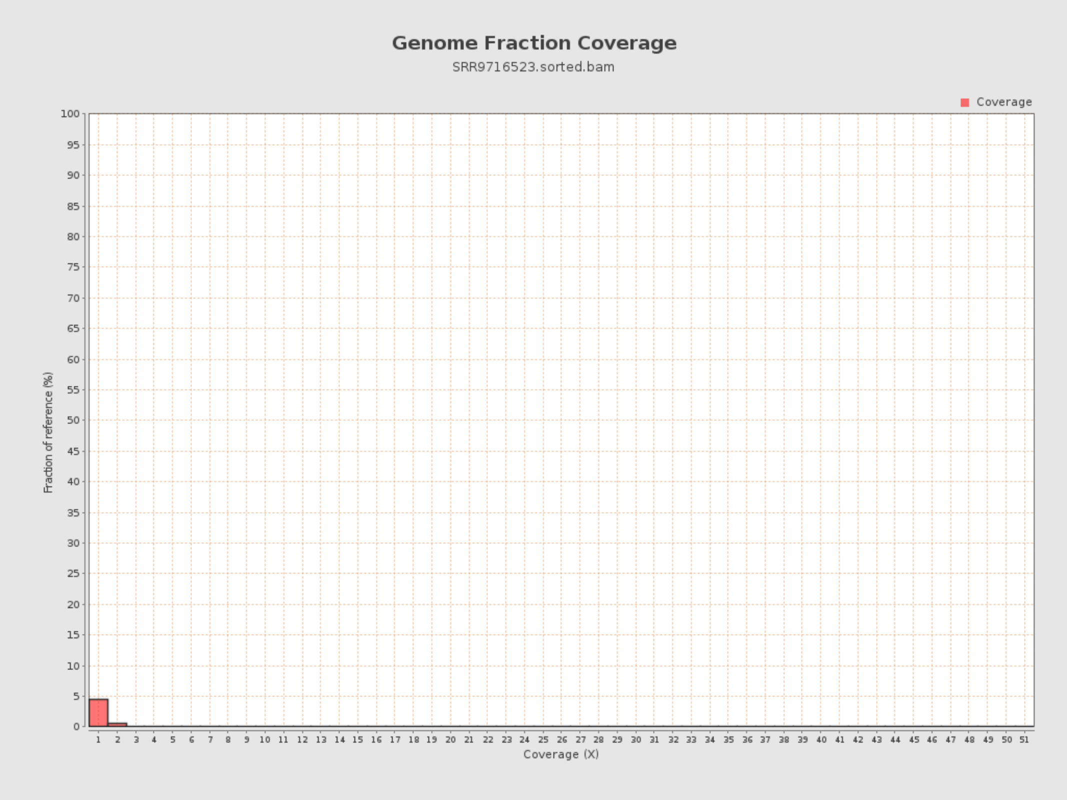
4. Results : Coverage Histogram



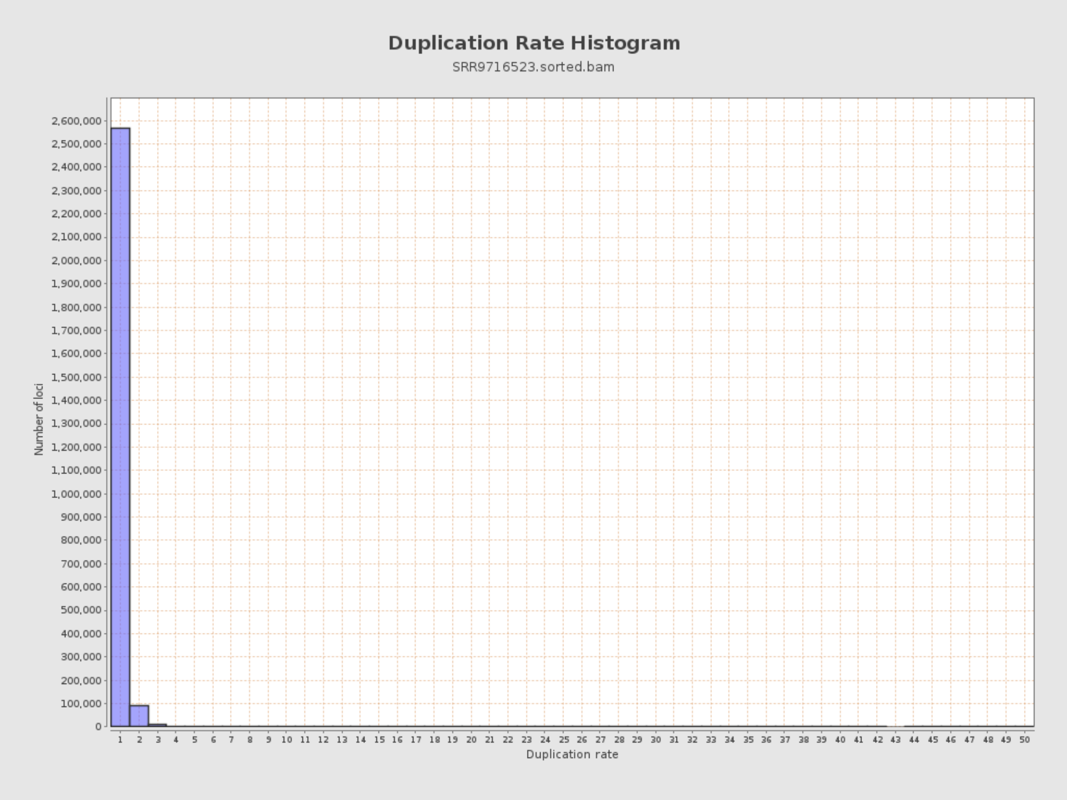
5. Results : Coverage Histogram (0-50X)



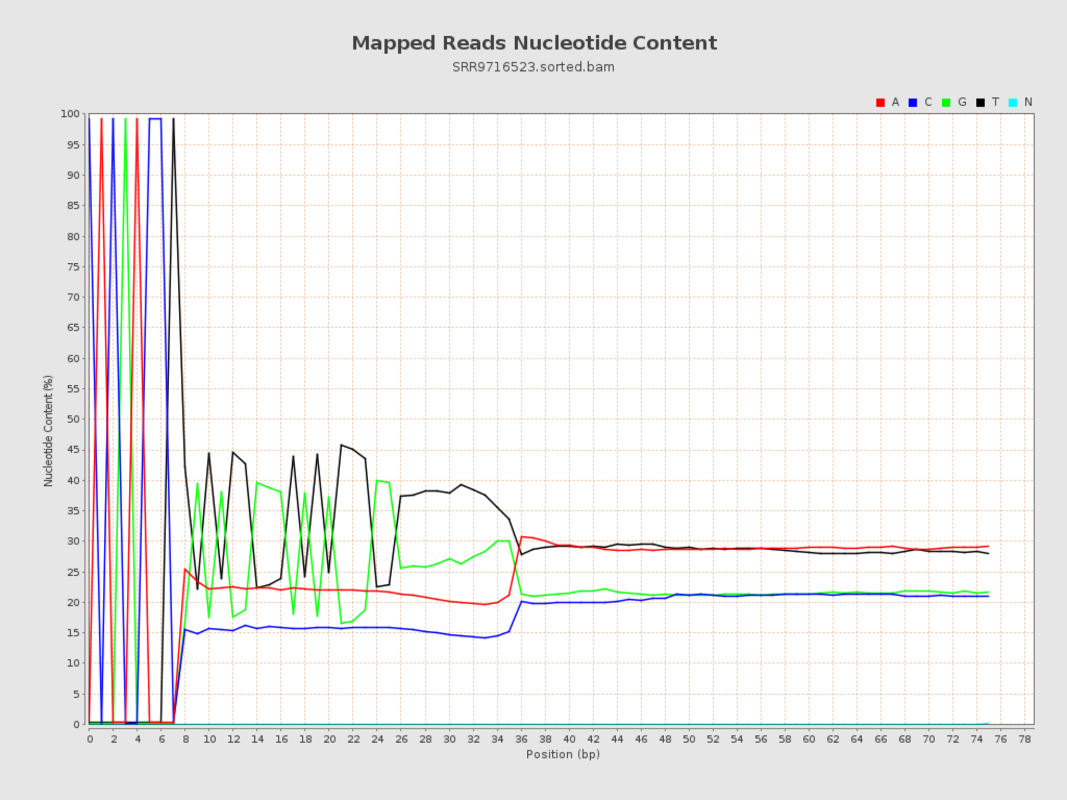
6. Results : Genome Fraction Coverage



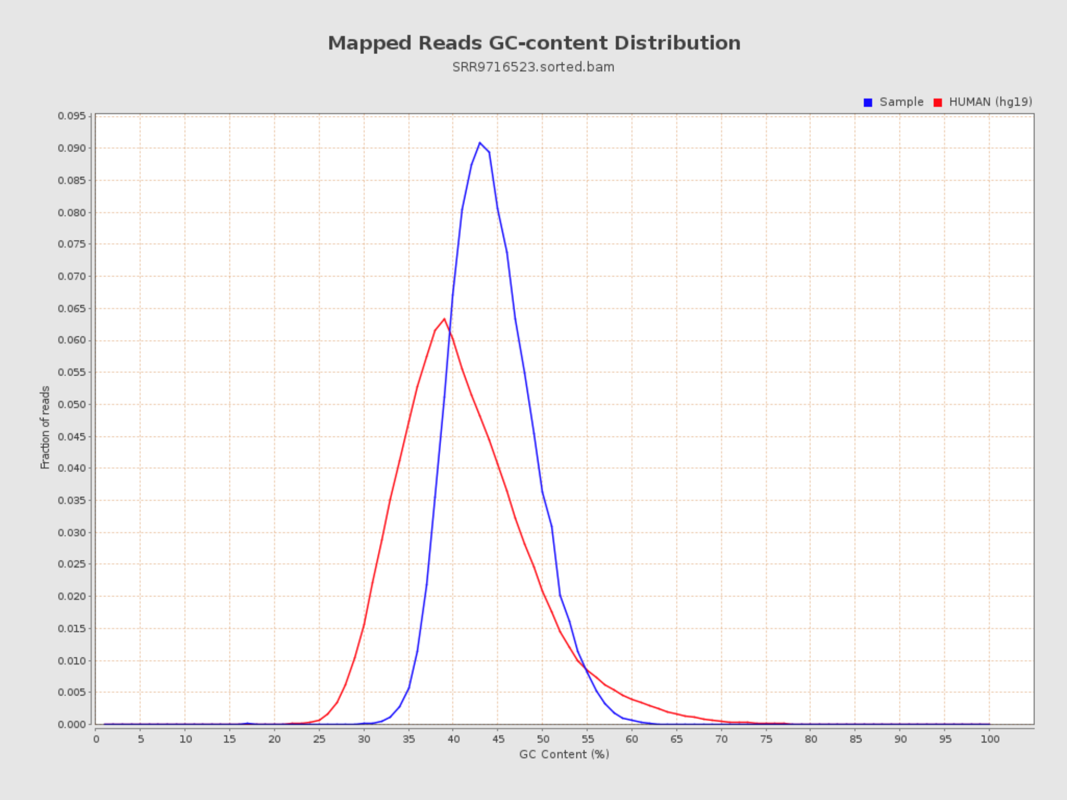
7. Results : Duplication Rate Histogram



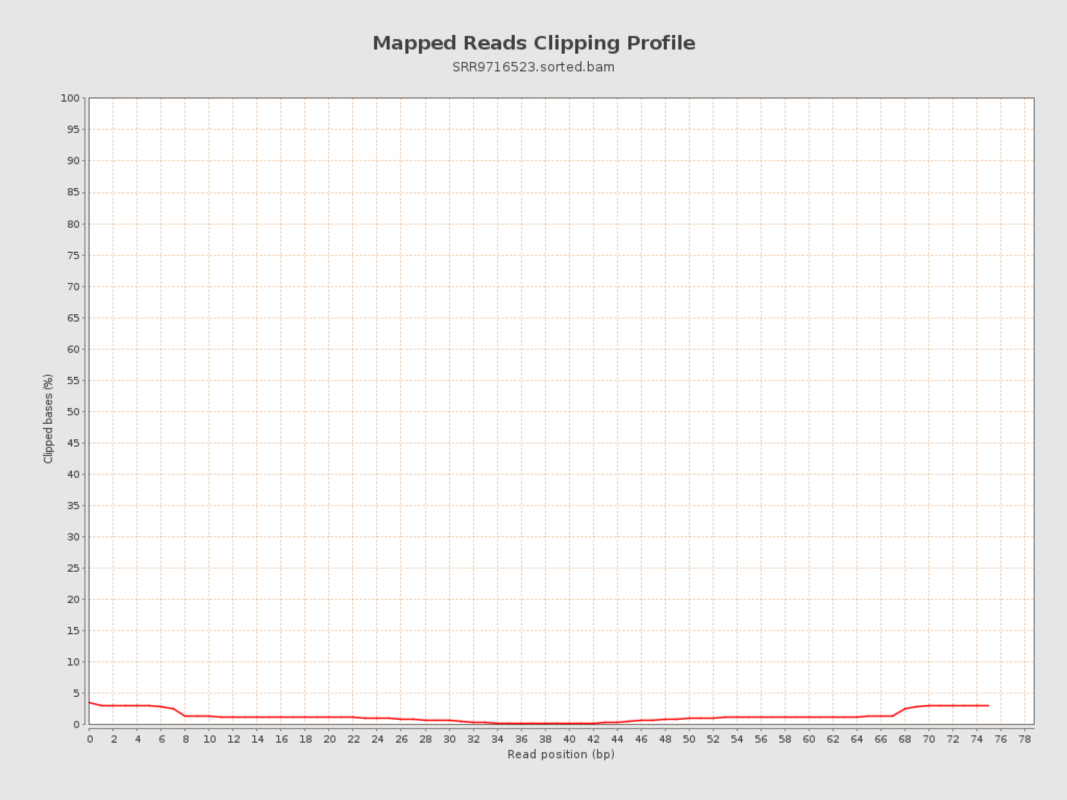
8. Results : Mapped Reads Nucleotide Content



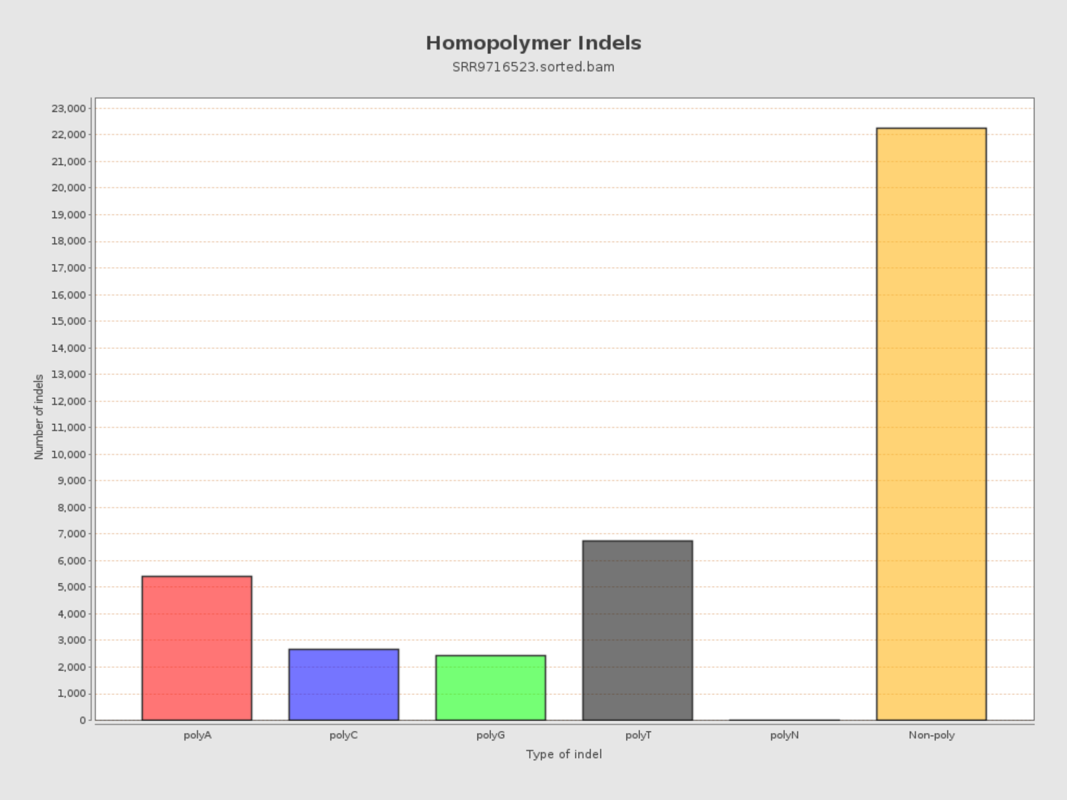
9. Results : Mapped Reads GC-content Distribution



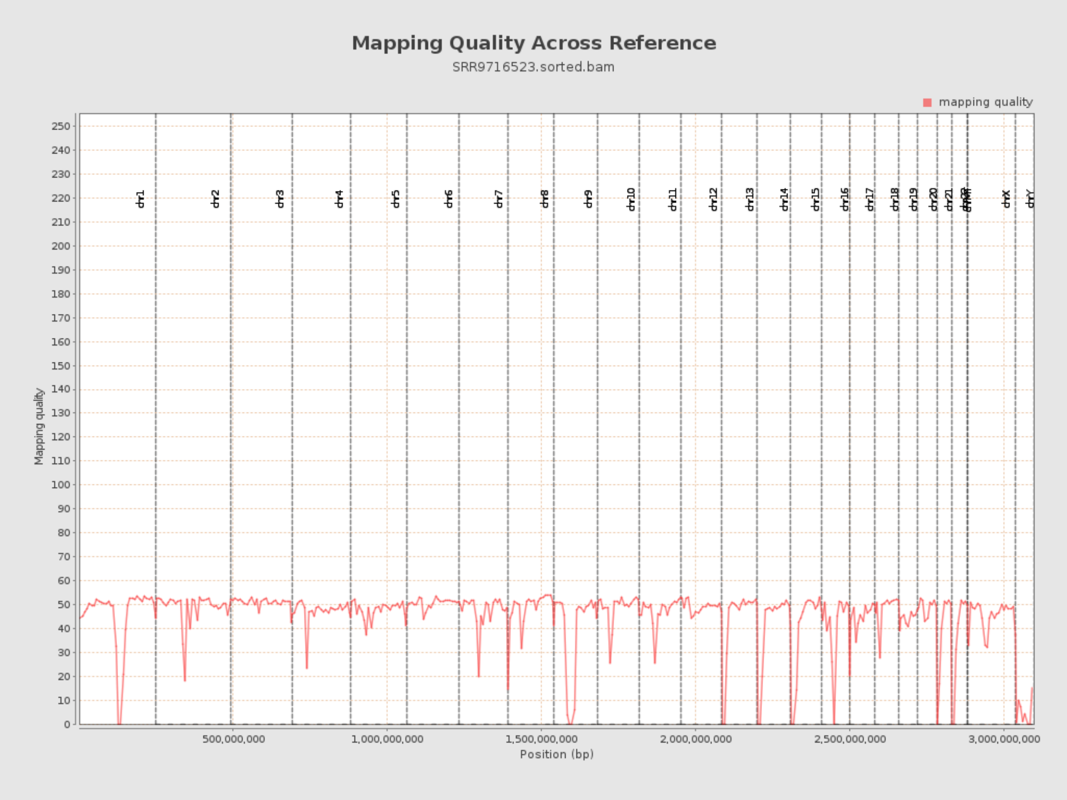
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram