Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:14:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716553.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_SRR9716553 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716553.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:13:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716553.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,128,373
Mapped reads	1,812,292 / 85.15%
Unmapped reads	316,081 / 14.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,547 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	50,155 / 2.36%
Duplication rate	1.95%
Clipped reads	1,817,180 / 85.38%

2.2. ACGT Content

Number/percentage of A's	25,993,897 / 25.38%
Number/percentage of C's	19,953,840 / 19.48%
Number/percentage of T's	32,158,385 / 31.4%
Number/percentage of G's	24,322,636 / 23.75%
Number/percentage of N's	801 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.2705

2.4. Mapping Quality

Mean Mapping Quality	42.22

2.5. Mismatches and indels

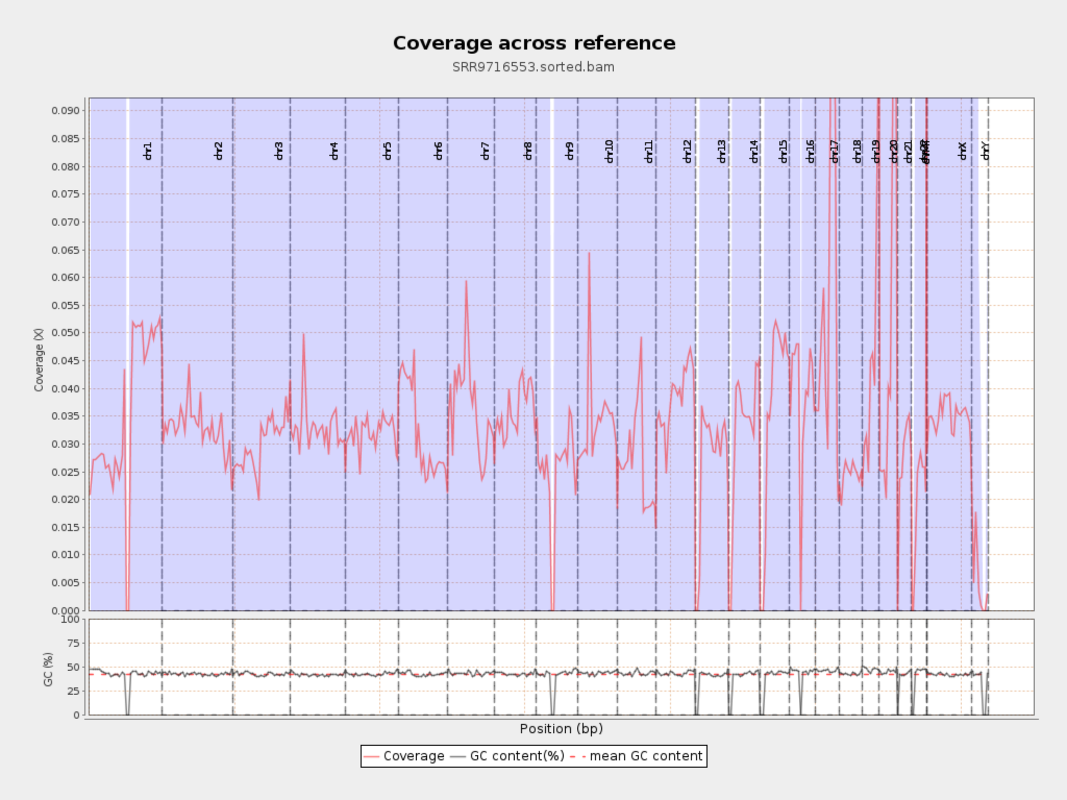
General error rate	0.54%
Mismatches	542,131
Insertions	6,596
Mapped reads with at least one insertion	0.36%
Deletions	18,749
Mapped reads with at least one deletion	1.03%
Homopolymer indels	39.6%

2.6. Chromosome stats

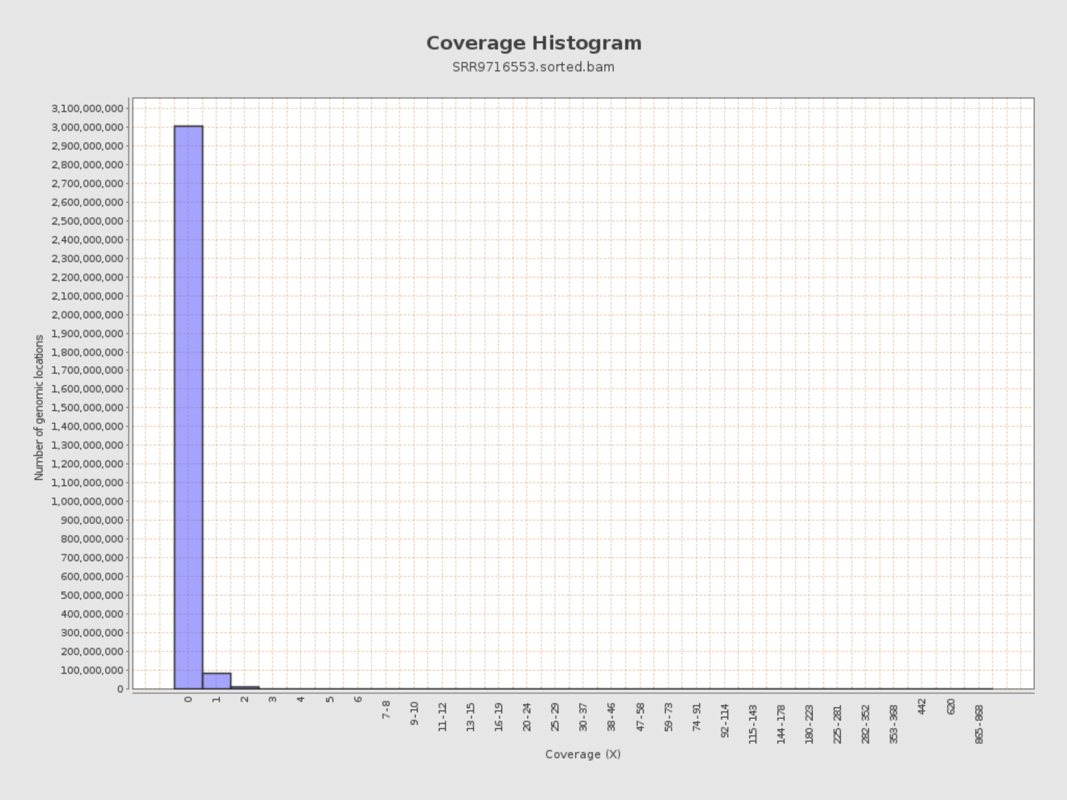
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8739870	0.0351	0.3516
chr2	243199373	8006711	0.0329	0.4026
chr3	198022430	5927331	0.0299	0.1957
chr4	191154276	6274390	0.0328	0.217
chr5	180915260	5802545	0.0321	0.1953
chr6	171115067	5493585	0.0321	0.2344
chr7	159138663	5891993	0.037	0.3938

chr8	146364022	5281703	0.0361	0.2642
chr9	141213431	3452460	0.0244	0.203
chr10	135534747	4619105	0.0341	0.335
chr11	135006516	3671457	0.0272	0.2217
chr12	133851895	5132255	0.0383	0.2173
chr13	115169878	3064213	0.0266	0.1781
chr14	107349540	3389004	0.0316	0.2032
chr15	102531392	3705104	0.0361	0.2139
chr16	90354753	3473264	0.0384	0.2303
chr17	81195210	4561560	0.0562	0.2764
chr18	78077248	1915319	0.0245	0.3143
chr19	59128983	2762375	0.0467	0.3356
chr20	63025520	3313287	0.0526	0.2665
chr21	48129895	1279560	0.0266	0.1935
chr22	51304566	940186	0.0183	0.1479
chrMT	16571	2511	0.1515	0.5332
chrX	155270560	5453696	0.0351	0.2207
chrY	59373566	305972	0.0052	0.1432

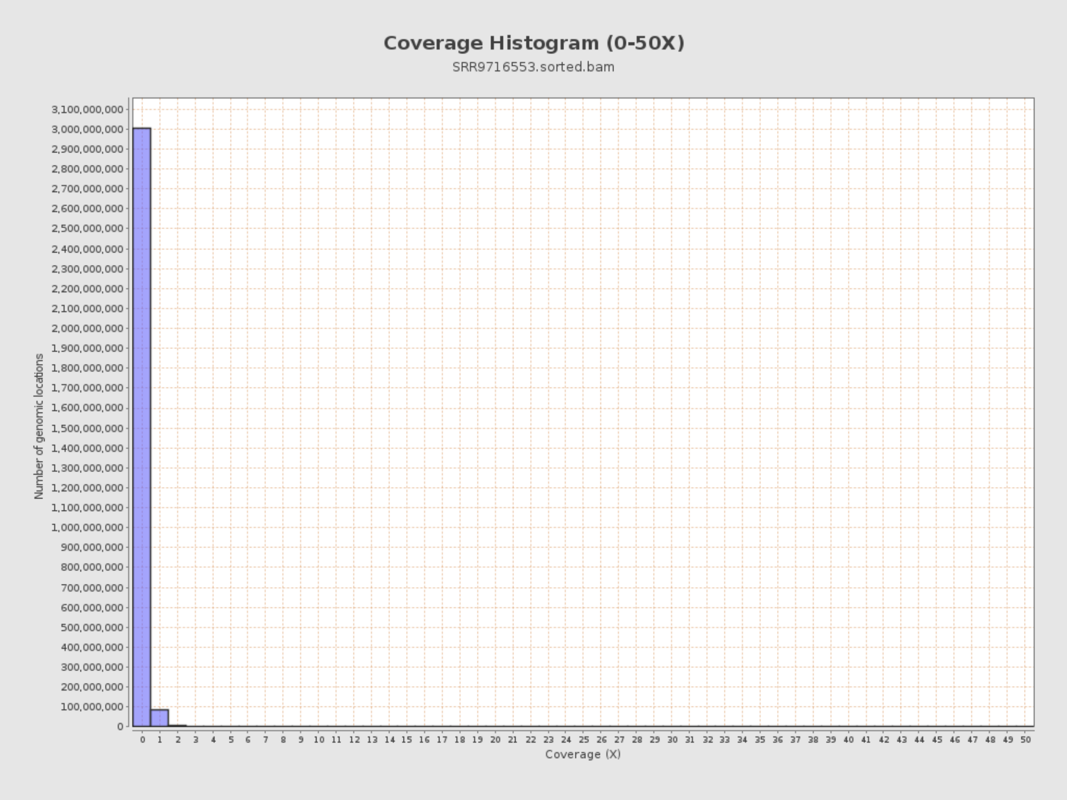
3. Results : Coverage across reference



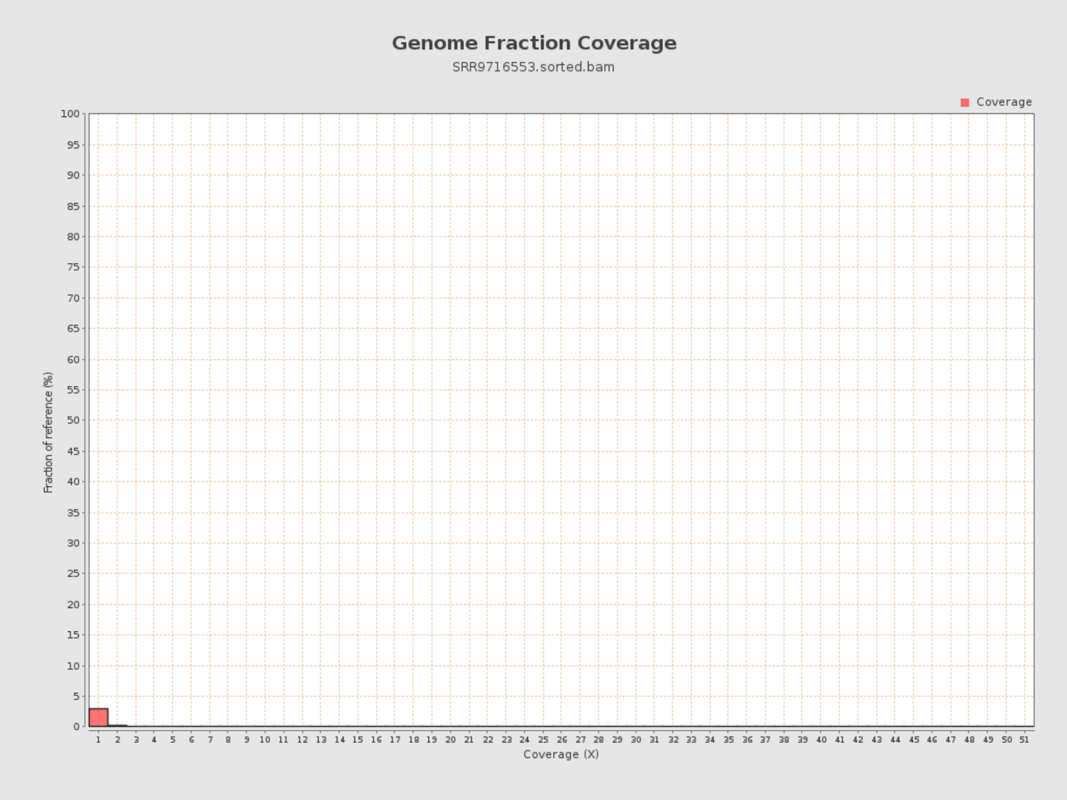
4. Results : Coverage Histogram



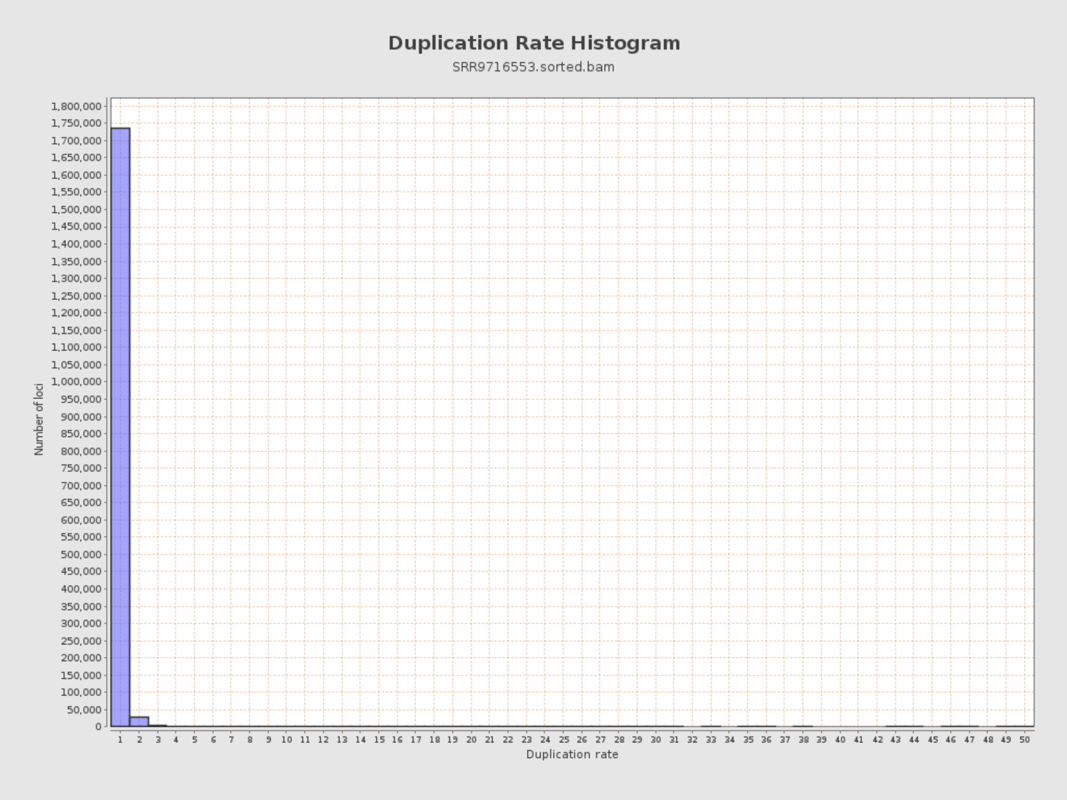
5. Results : Coverage Histogram (0-50X)



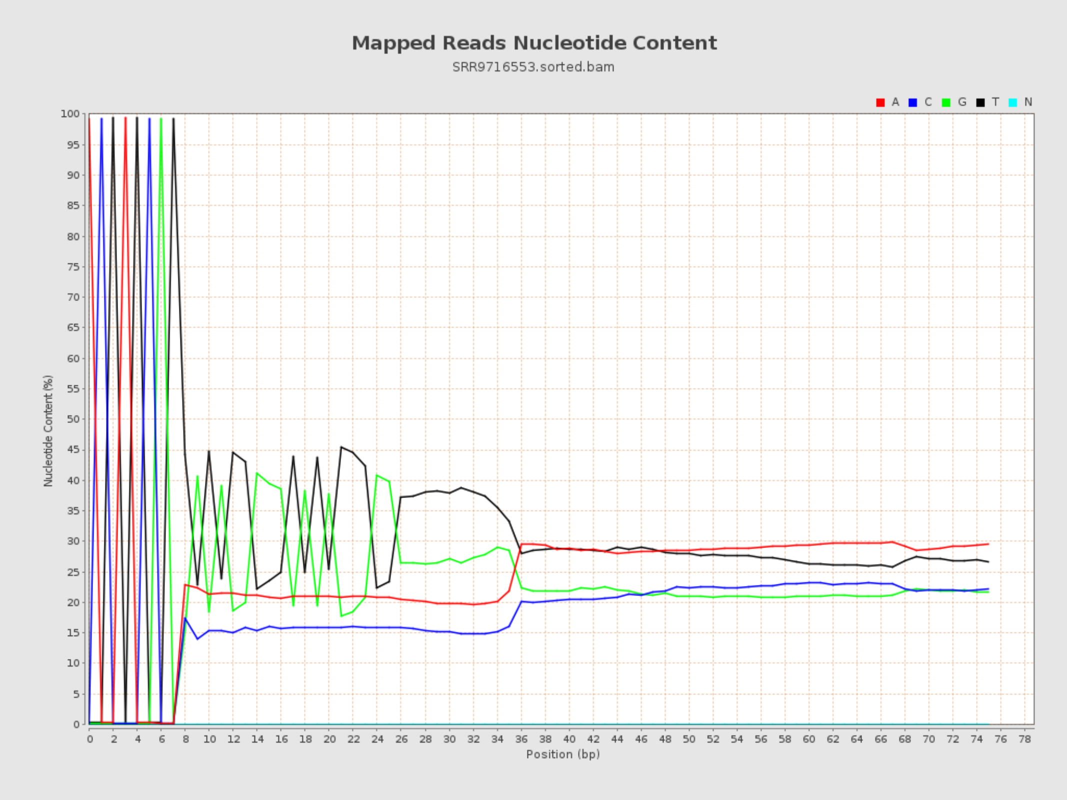
6. Results : Genome Fraction Coverage



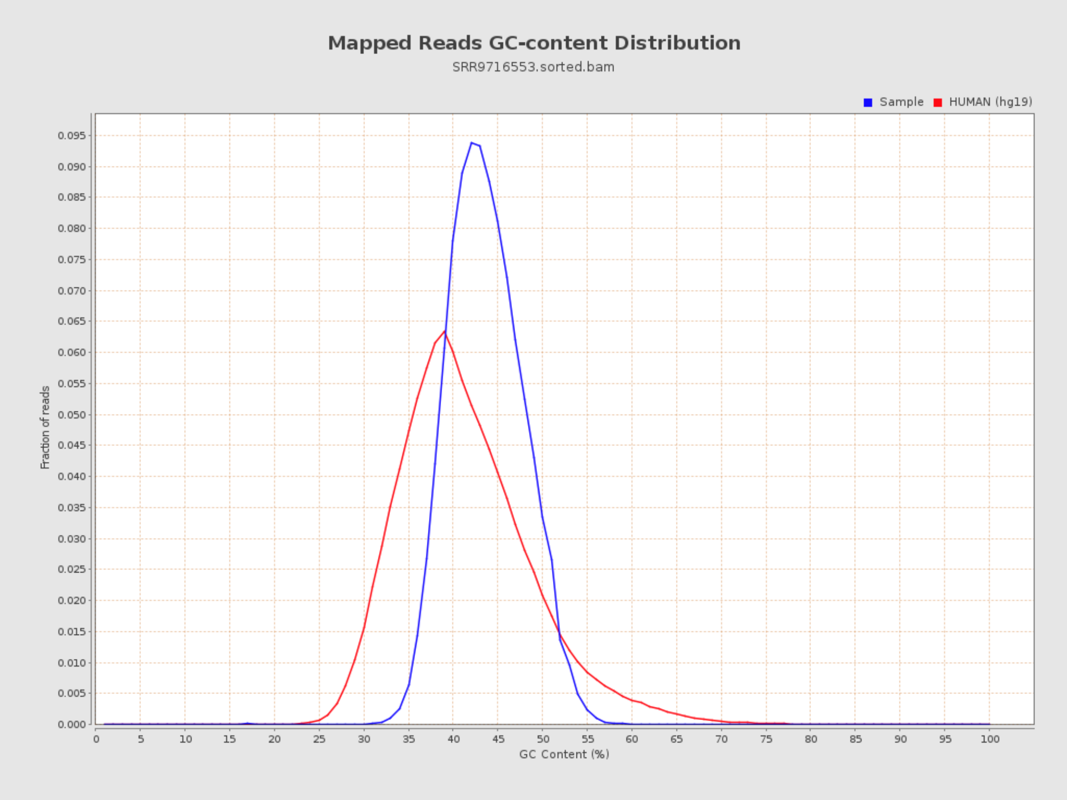
7. Results : Duplication Rate Histogram



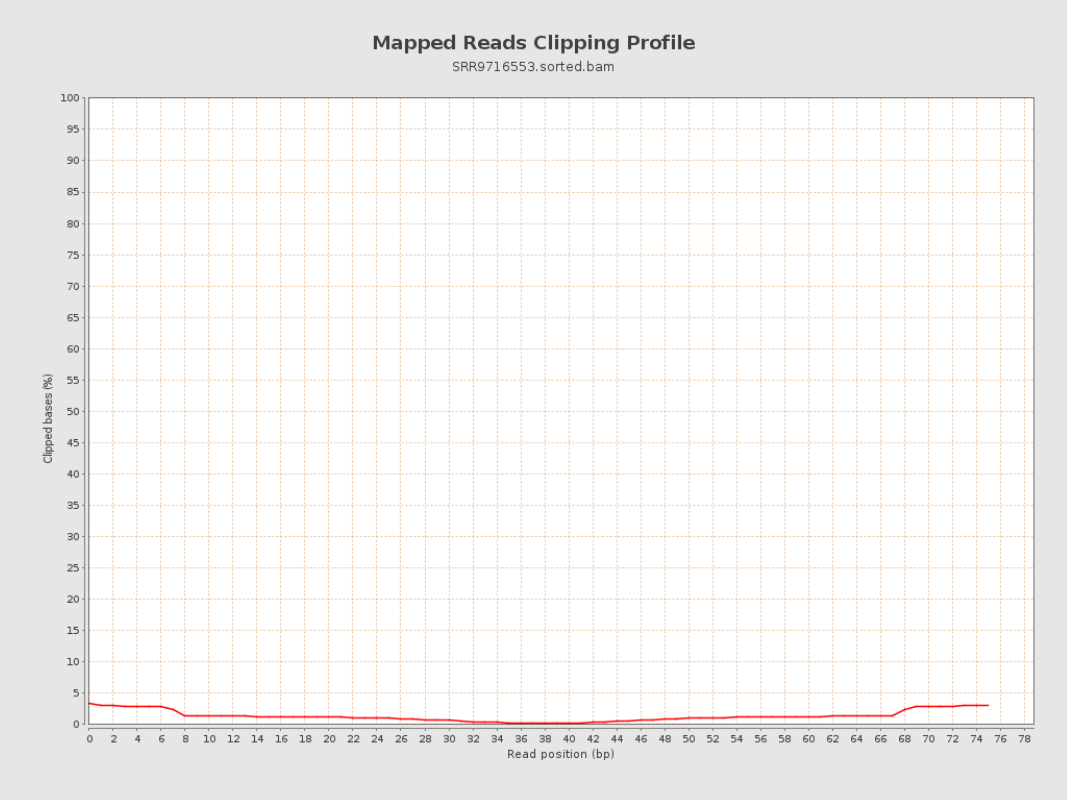
8. Results : Mapped Reads Nucleotide Content



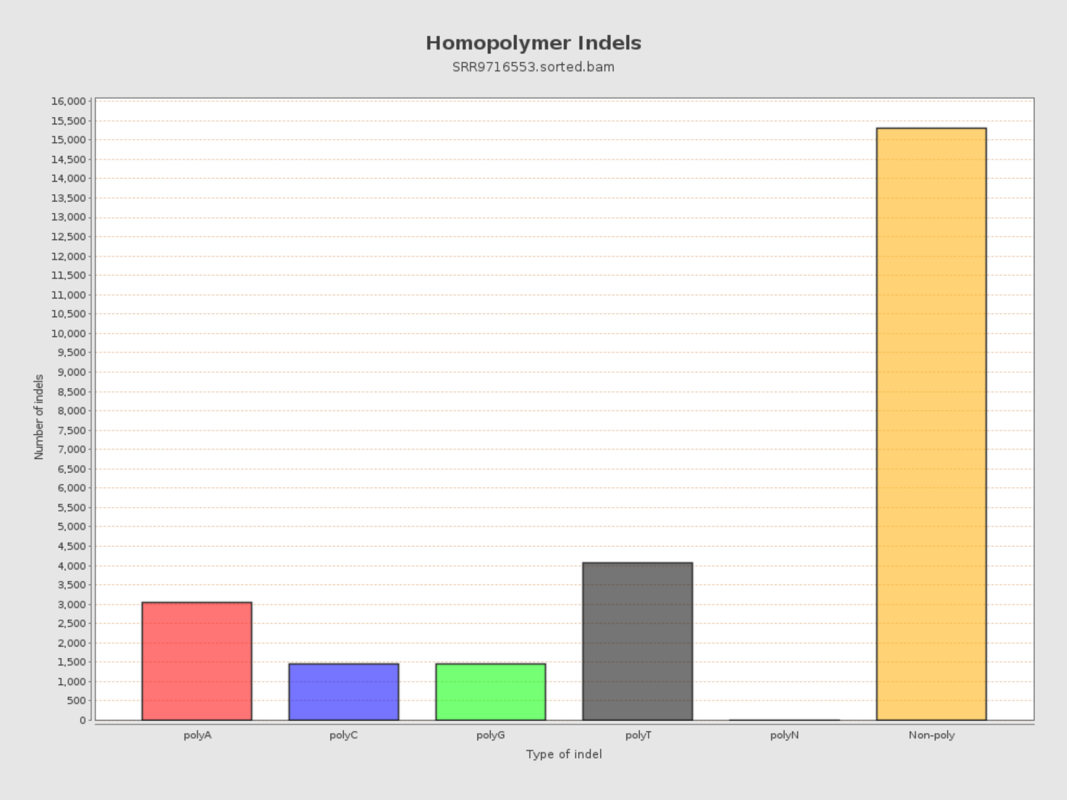
9. Results : Mapped Reads GC-content Distribution



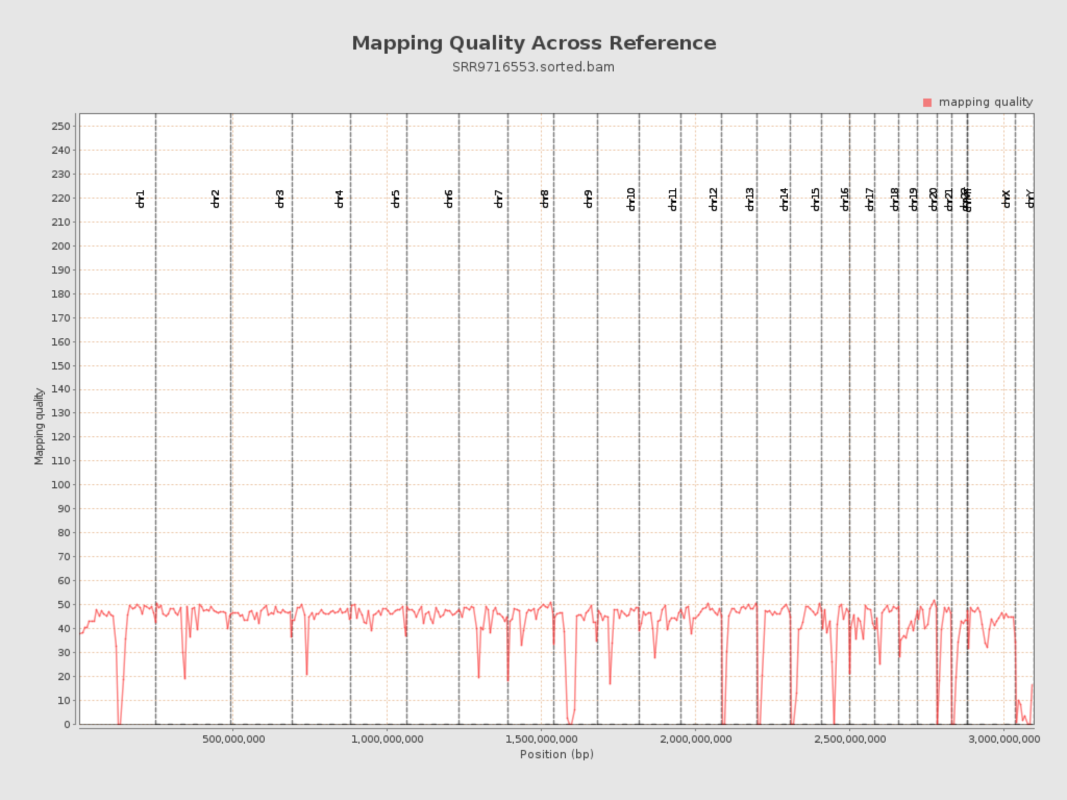
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram