Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:00:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716531.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_SRR9716531 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716531.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:00:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716531.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,731,887
Mapped reads	1,578,121 / 91.12%
Unmapped reads	153,766 / 8.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,686 / 1.66%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	57,118 / 3.3%
Duplication rate	2.61%
Clipped reads	1,602,331 / 92.52%

2.2. ACGT Content

Number/percentage of A's	33,745,081 / 26.83%
Number/percentage of C's	24,657,354 / 19.6%
Number/percentage of T's	37,197,416 / 29.57%
Number/percentage of G's	30,186,522 / 24%
Number/percentage of N's	8,840 / 0.01%
GC Percentage	43.6%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.3642

2.4. Mapping Quality

Mean Mapping Quality	47.74

2.5. Mismatches and indels

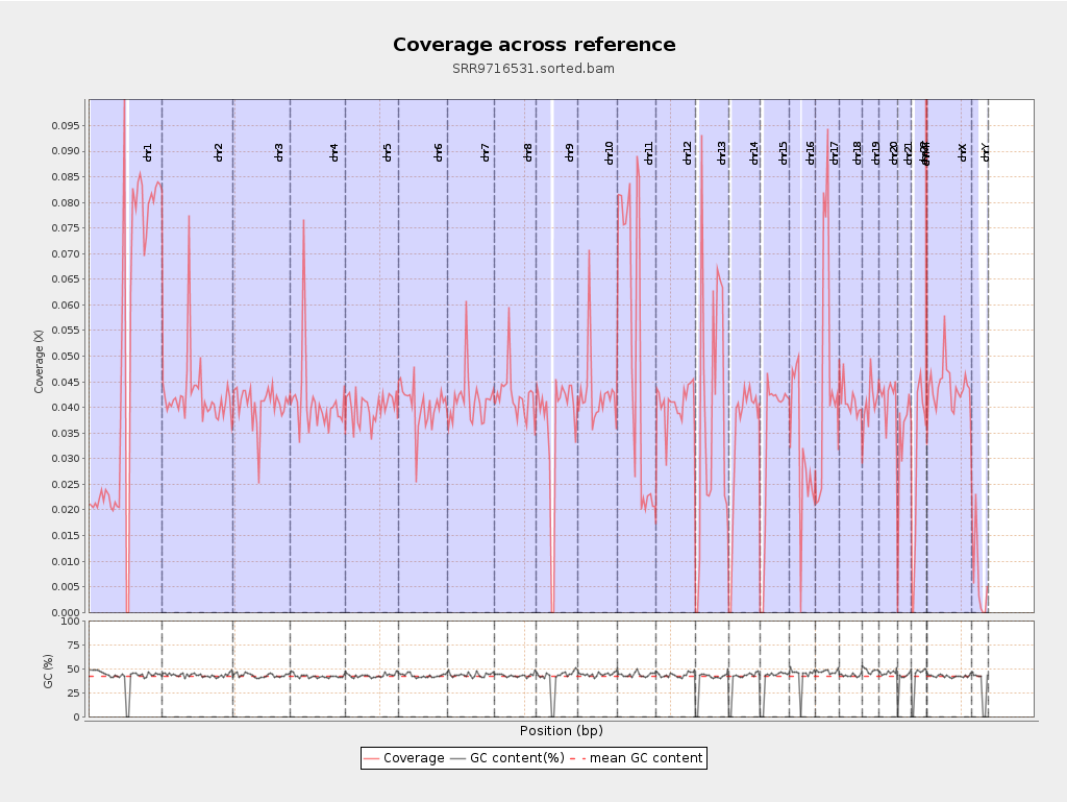
General error rate	0.67%
Mismatches	818,725
Insertions	11,590
Mapped reads with at least one insertion	0.72%
Deletions	30,723
Mapped reads with at least one deletion	1.92%
Homopolymer indels	42.23%

2.6. Chromosome stats

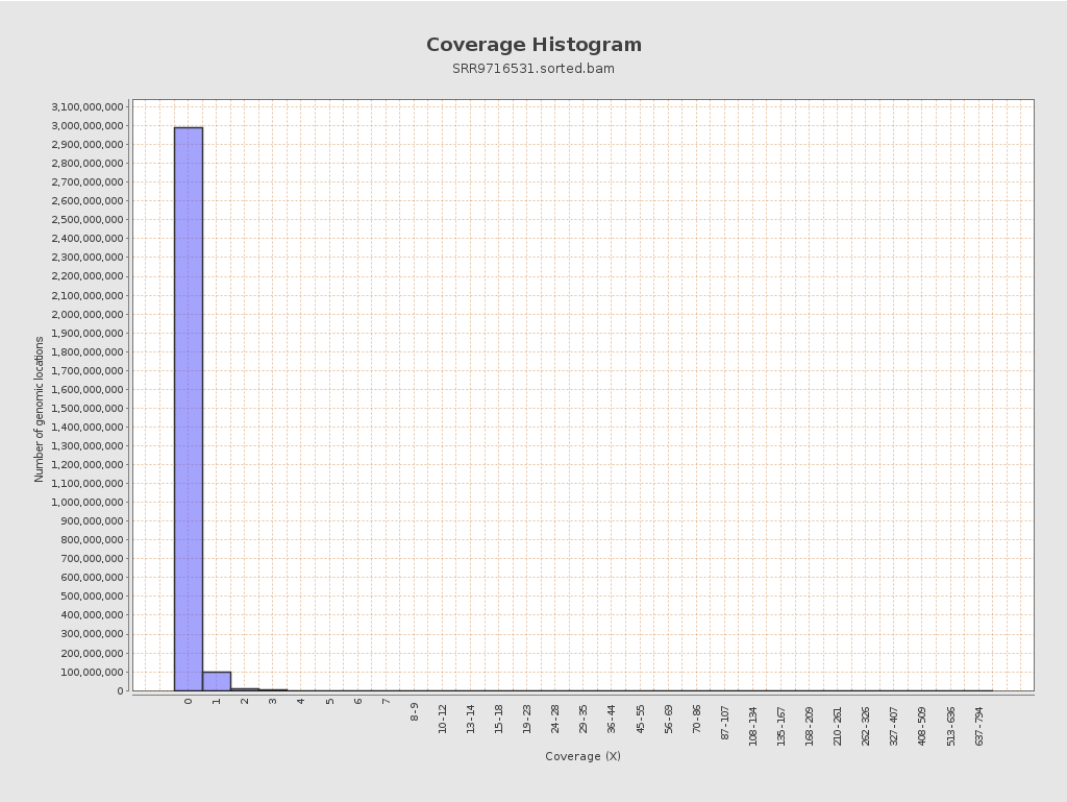
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12331501	0.0495	0.7233
chr2	243199373	10340658	0.0425	0.3999
chr3	198022430	8034340	0.0406	0.2222
chr4	191154276	7834403	0.041	0.2754
chr5	180915260	7222897	0.0399	0.2237
chr6	171115067	6907642	0.0404	0.2411
chr7	159138663	6612172	0.0415	0.4262

chr8	146364022	6182942	0.0422	0.4095
chr9	141213431	5129958	0.0363	0.3068
chr10	135534747	5766924	0.0425	0.3545
chr11	135006516	6942308	0.0514	0.4195
chr12	133851895	5468407	0.0409	0.2259
chr13	115169878	4400214	0.0382	0.2205
chr14	107349540	3663416	0.0341	0.2174
chr15	102531392	3538962	0.0345	0.206
chr16	90354753	2852170	0.0316	0.22
chr17	81195210	3894138	0.048	0.2914
chr18	78077248	3244946	0.0416	0.5148
chr19	59128983	2433003	0.0411	0.4791
chr20	63025520	2634718	0.0418	0.2383
chr21	48129895	1630649	0.0339	0.2367
chr22	51304566	1490430	0.0291	0.1909
chrMT	16571	113274	6.8357	4.4513
chrX	155270560	6819149	0.0439	0.2718
chrY	59373566	364589	0.0061	0.1945

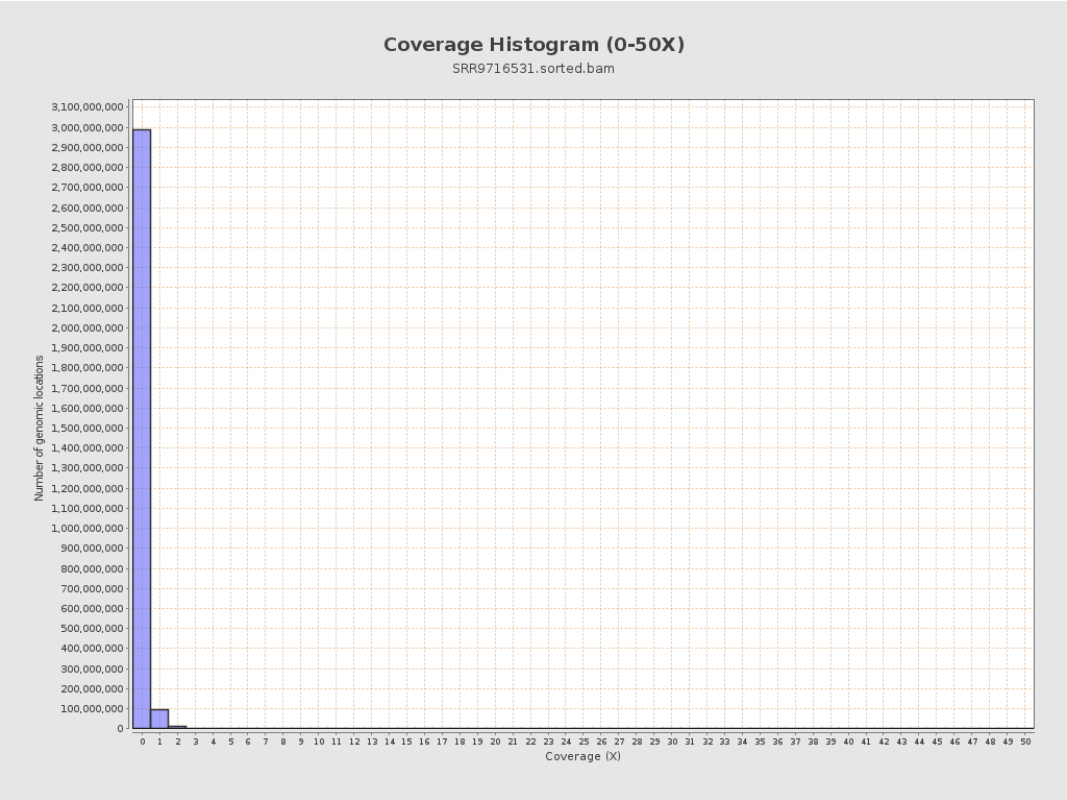
3. Results : Coverage across reference



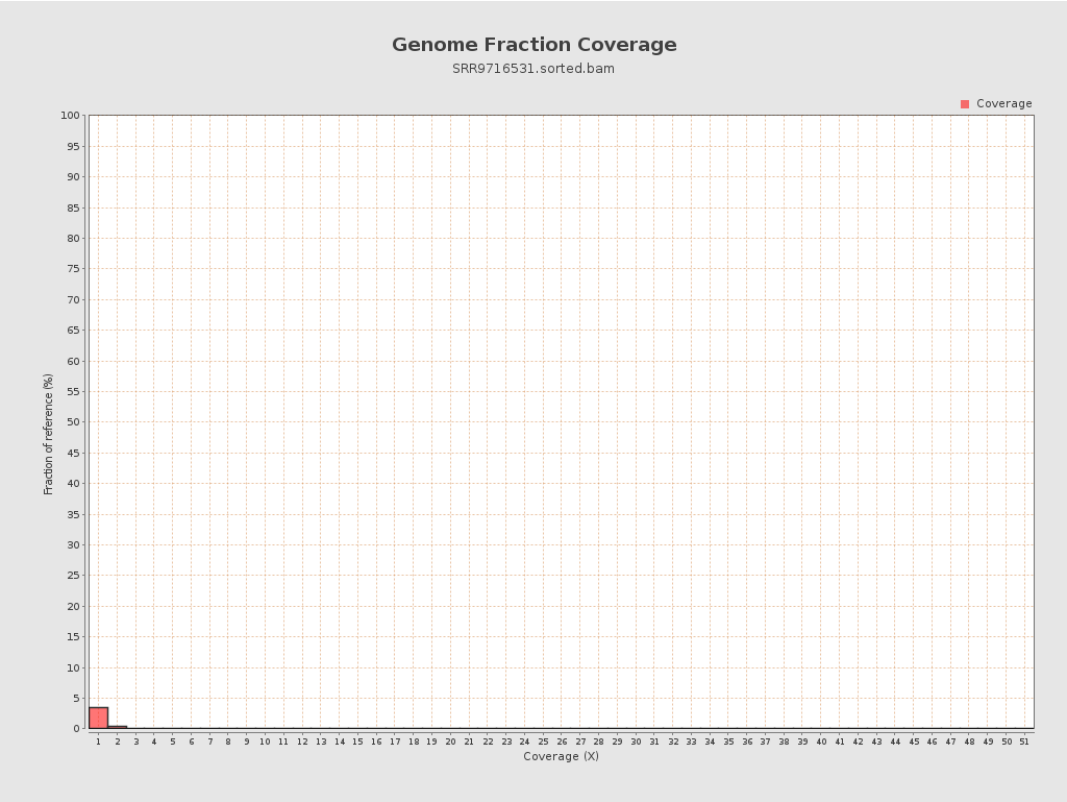
4. Results : Coverage Histogram



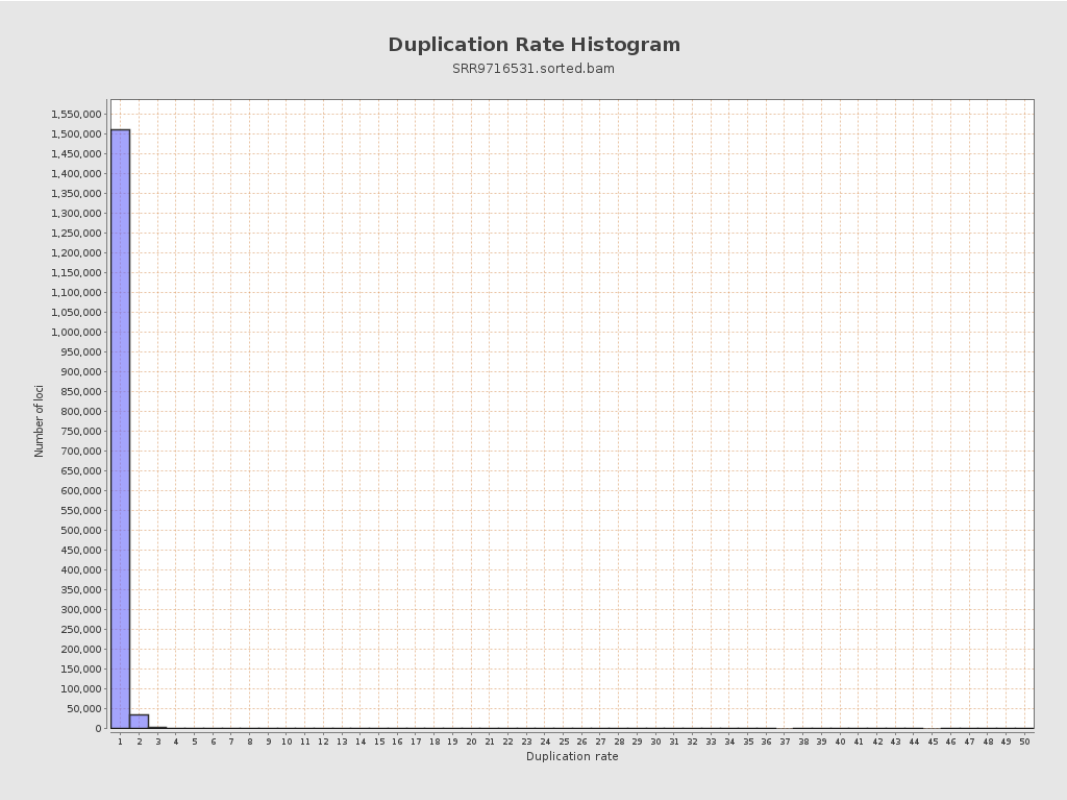
5. Results : Coverage Histogram (0-50X)



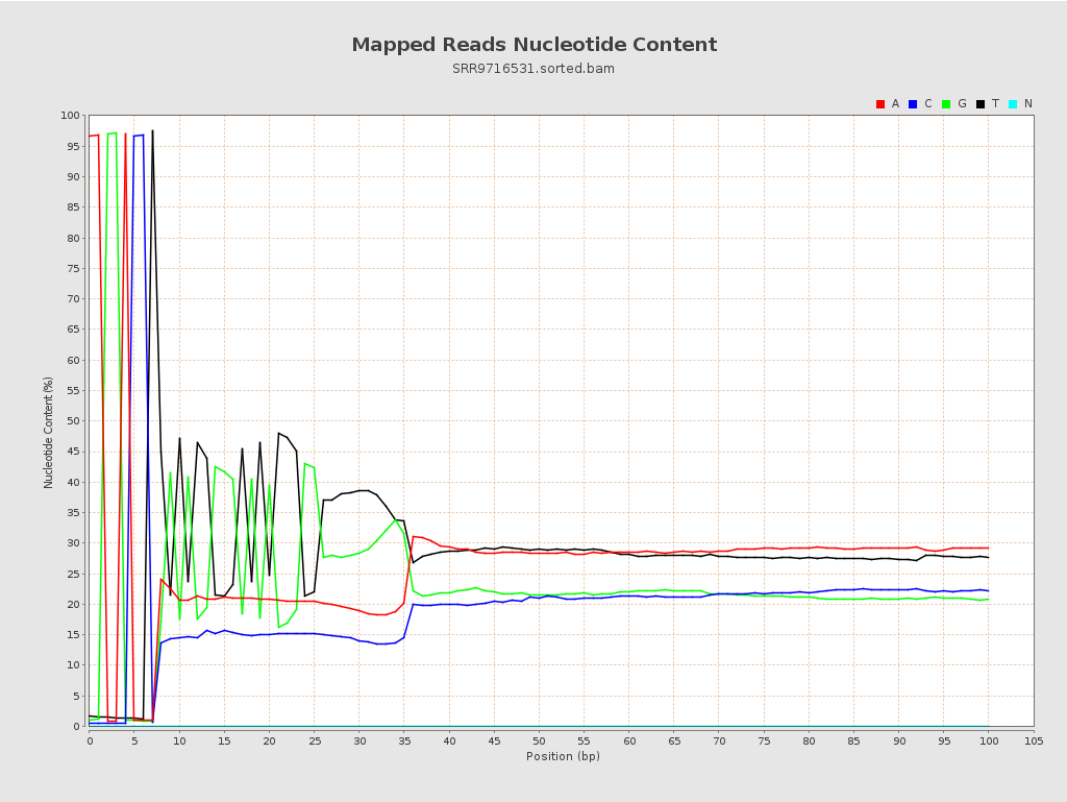
6. Results : Genome Fraction Coverage



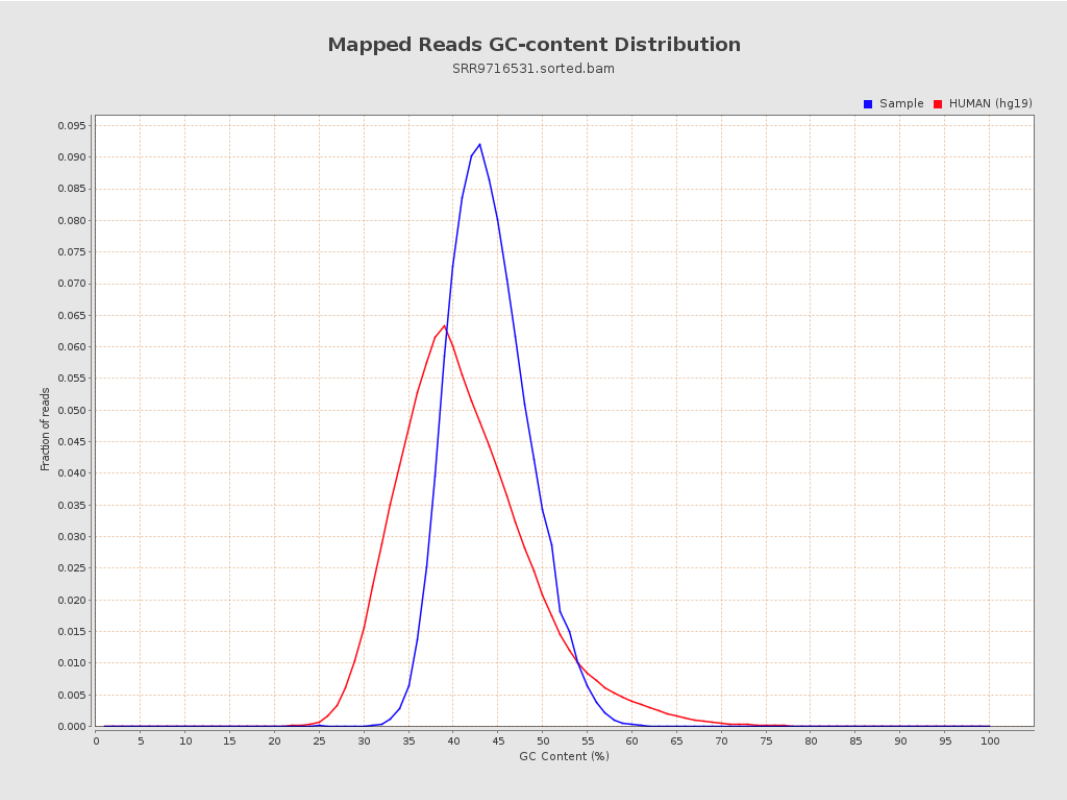
7. Results : Duplication Rate Histogram



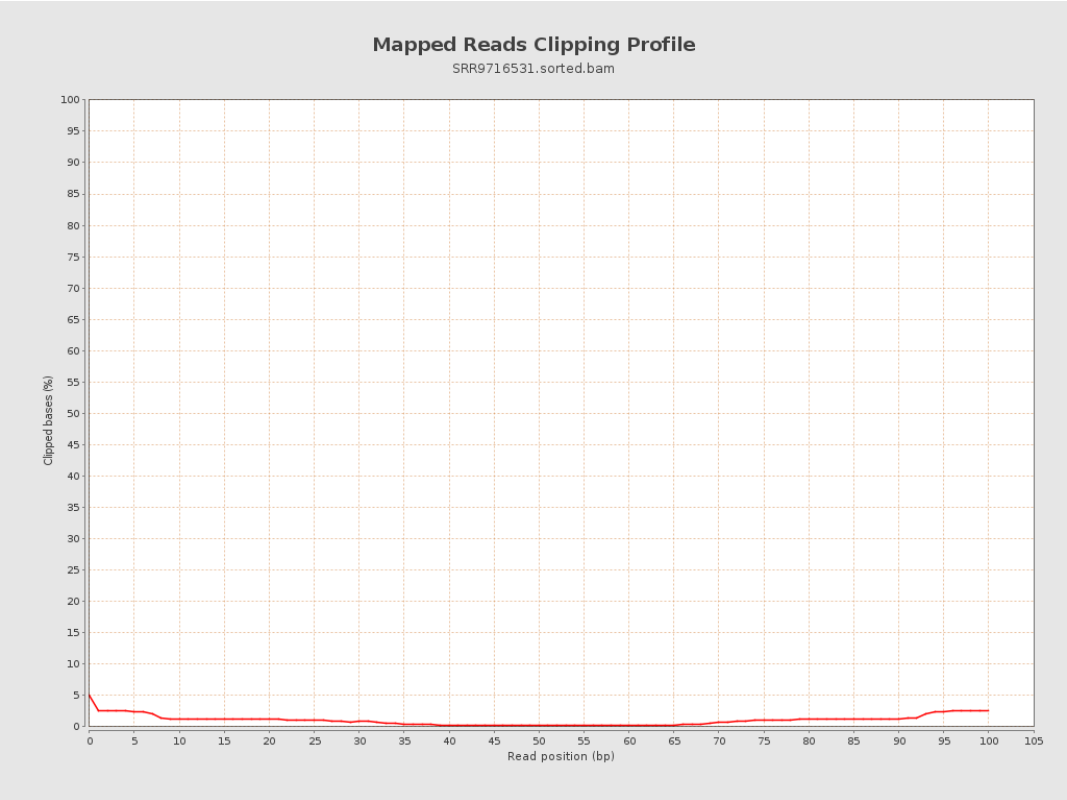
8. Results : Mapped Reads Nucleotide Content



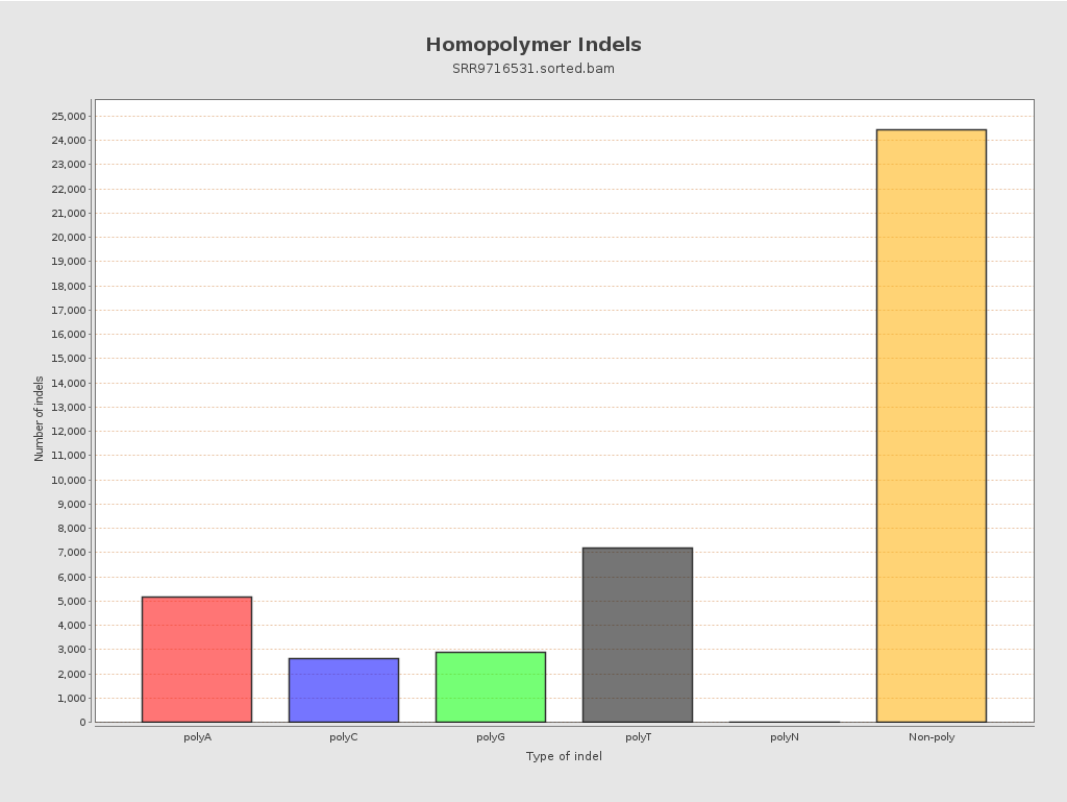
9. Results : Mapped Reads GC-content Distribution



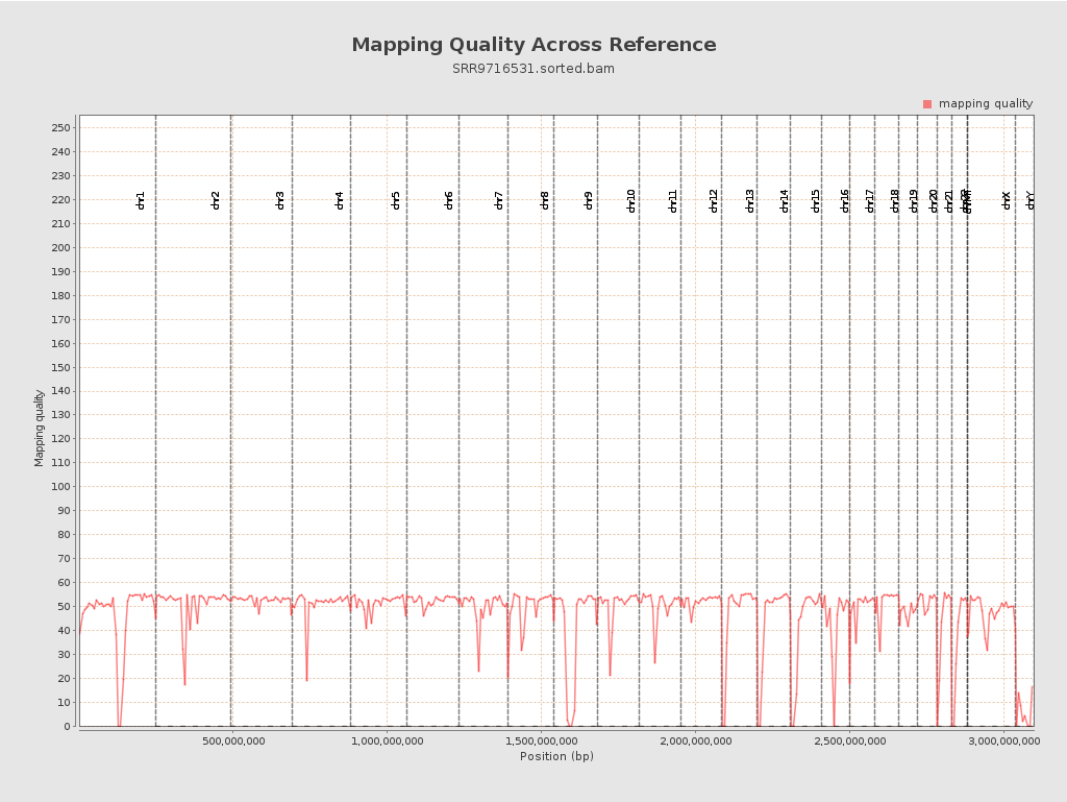
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram