

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:40:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716653.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_SRR9716653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716653.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:40:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,044,023
Mapped reads	832,361 / 79.73%
Unmapped reads	211,662 / 20.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,754 / 2.28%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	14,543 / 1.39%
Duplication rate	1.14%
Clipped reads	854,576 / 81.85%

2.2. ACGT Content

Number/percentage of A's	16,377,951 / 26.23%
Number/percentage of C's	12,787,947 / 20.48%
Number/percentage of T's	18,208,378 / 29.16%
Number/percentage of G's	15,055,246 / 24.11%
Number/percentage of N's	7,675 / 0.01%
GC Percentage	44.59%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.1899
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2.4. Mapping Quality

Mean Mapping Quality	44.78
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2.5. Mismatches and indels

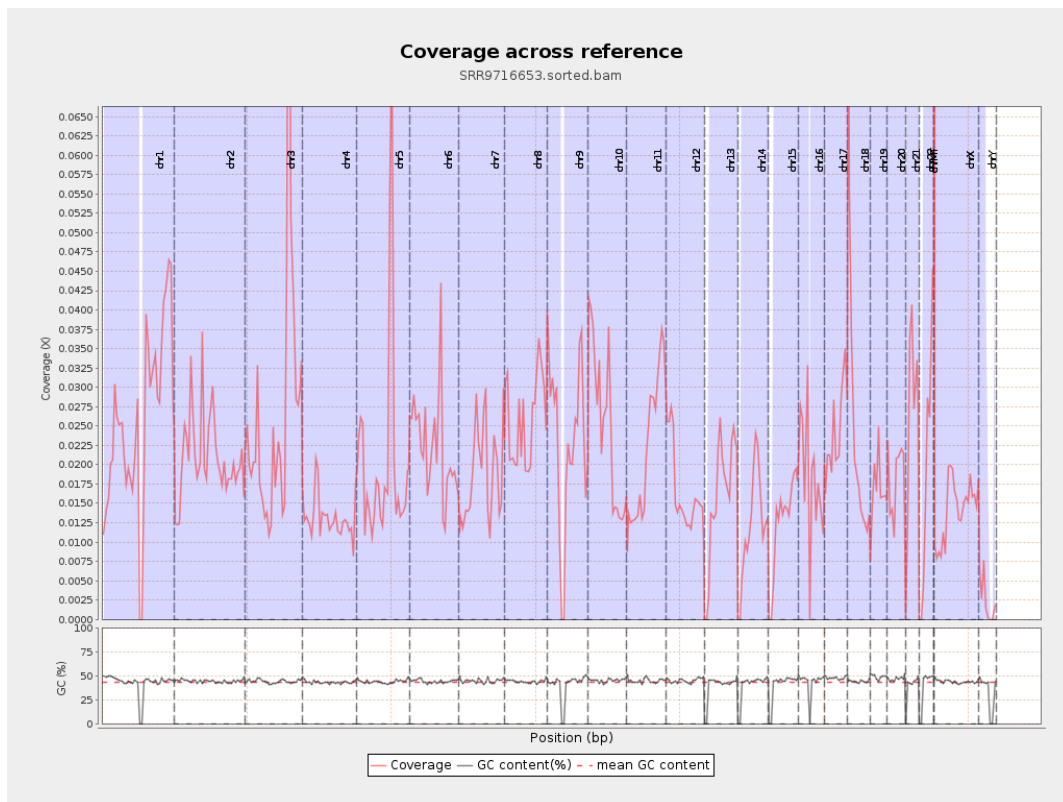
General error rate	0.79%
Mismatches	481,164
Insertions	5,628
Mapped reads with at least one insertion	0.67%
Deletions	12,650
Mapped reads with at least one deletion	1.5%
Homopolymer indels	40.26%

2.6. Chromosome stats

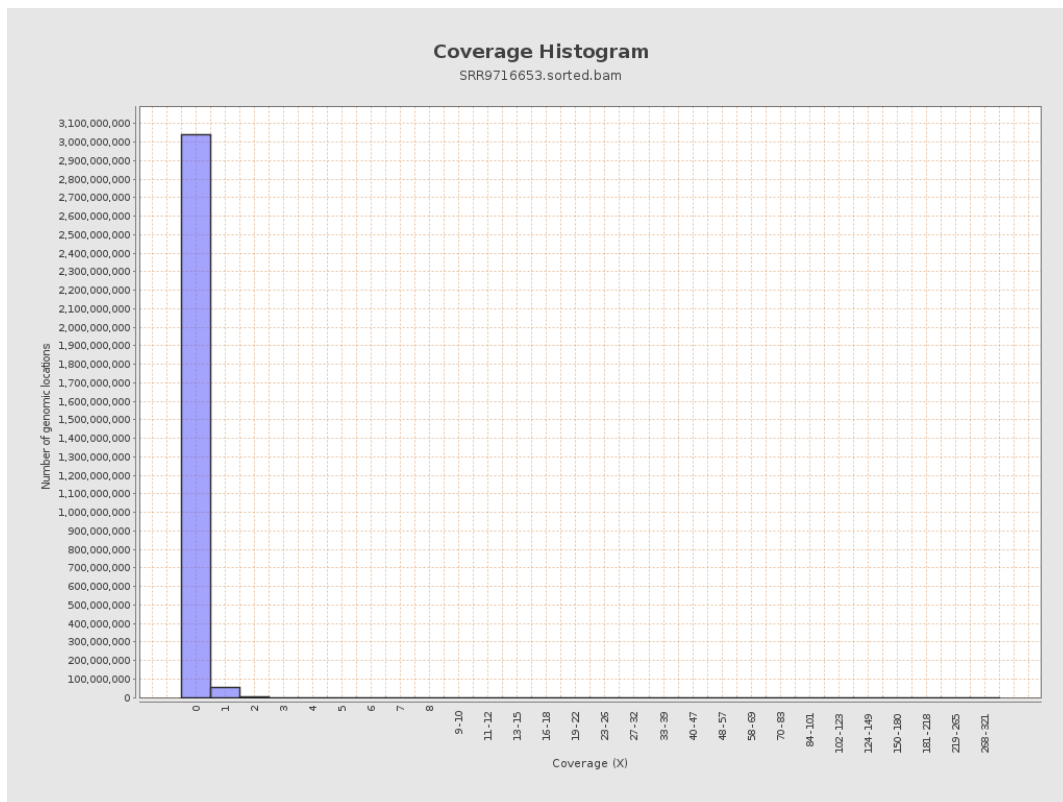
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6360145	0.0255	0.2407
chr2	243199373	5114200	0.021	0.2781
chr3	198022430	5368456	0.0271	0.1772
chr4	191154276	2527493	0.0132	0.1282
chr5	180915260	3746551	0.0207	0.1531
chr6	171115067	3827926	0.0224	0.1685
chr7	159138663	2992734	0.0188	0.2255

chr8	146364022	3800043	0.026	0.2305
chr9	141213431	3229581	0.0229	0.1922
chr10	135534747	3402941	0.0251	0.2038
chr11	135006516	2968093	0.022	0.1747
chr12	133851895	2220442	0.0166	0.1358
chr13	115169878	1858427	0.0161	0.1335
chr14	107349540	1302073	0.0121	0.1214
chr15	102531392	1283816	0.0125	0.1173
chr16	90354753	1643647	0.0182	0.1513
chr17	81195210	1996631	0.0246	0.1738
chr18	78077248	1927709	0.0247	0.2771
chr19	59128983	1013198	0.0171	0.2219
chr20	63025520	1130228	0.0179	0.1465
chr21	48129895	1303545	0.0271	0.1779
chr22	51304566	1004733	0.0196	0.1495
chrMT	16571	83588	5.0442	3.8056
chrX	155270560	2213129	0.0143	0.1394
chrY	59373566	139946	0.0024	0.0774

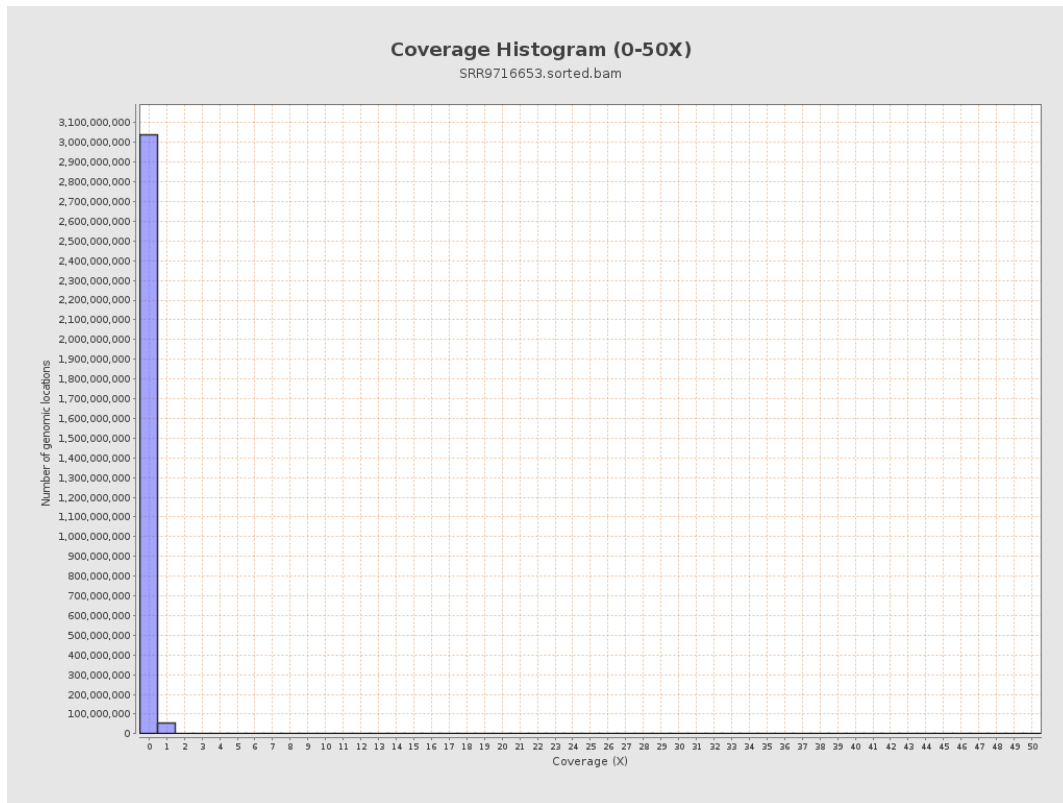
3. Results : Coverage across reference



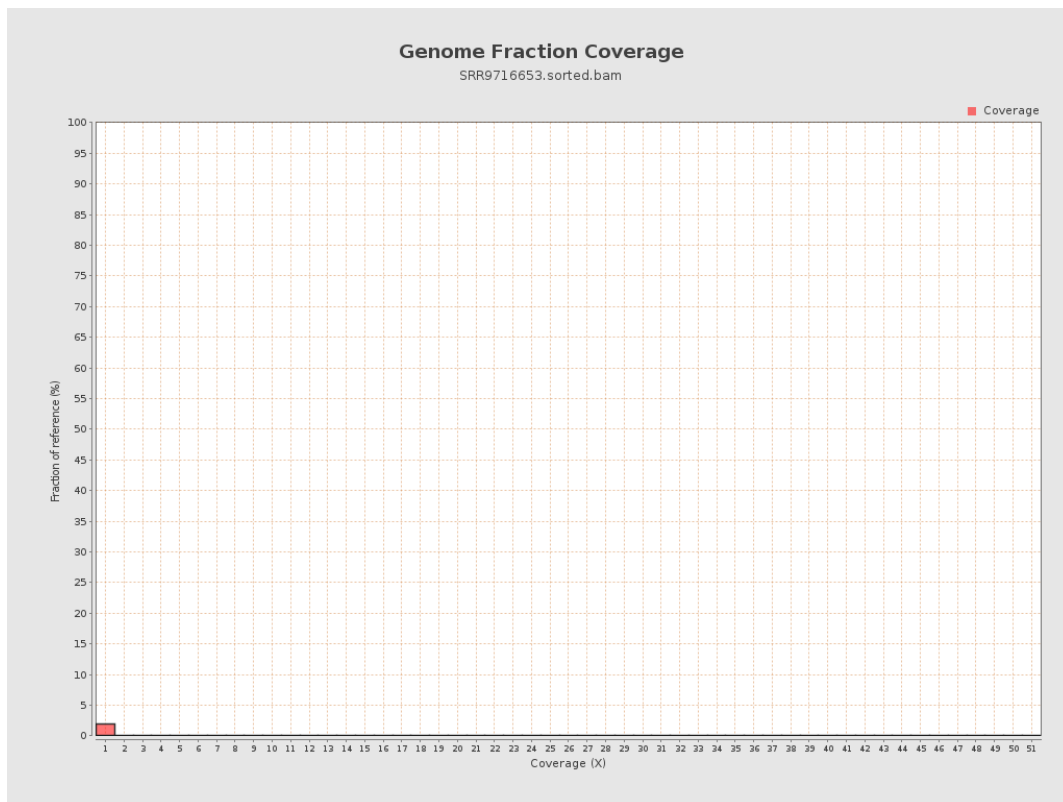
4. Results : Coverage Histogram



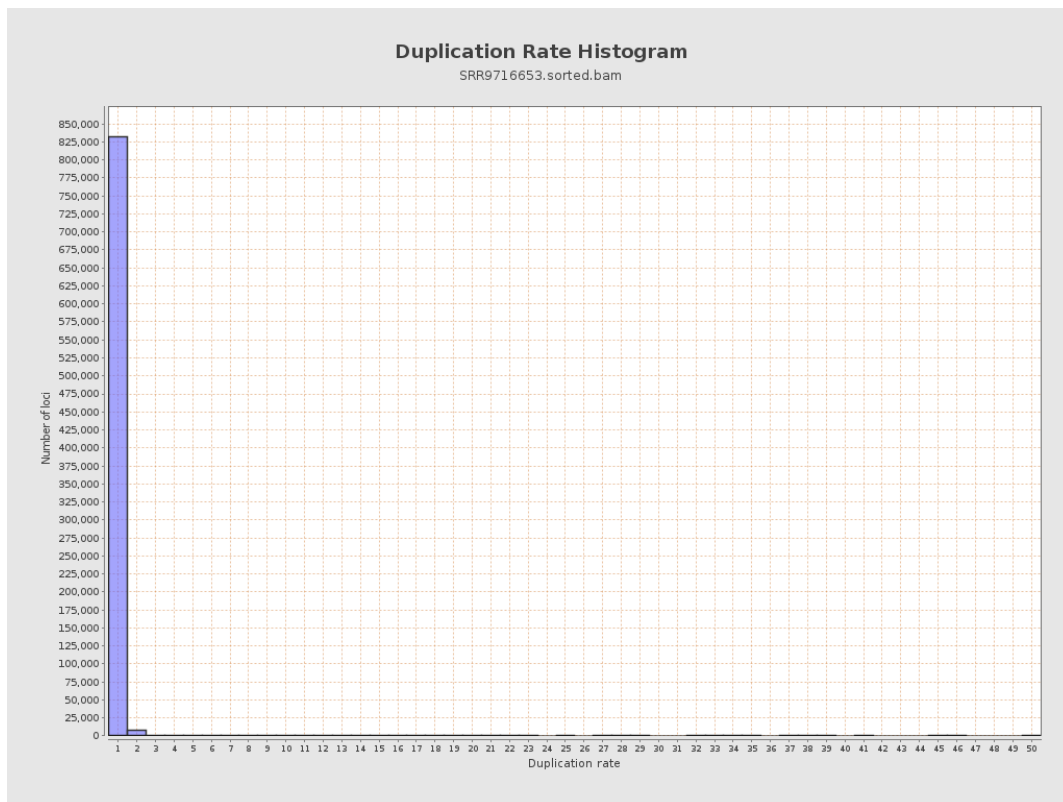
5. Results : Coverage Histogram (0-50X)



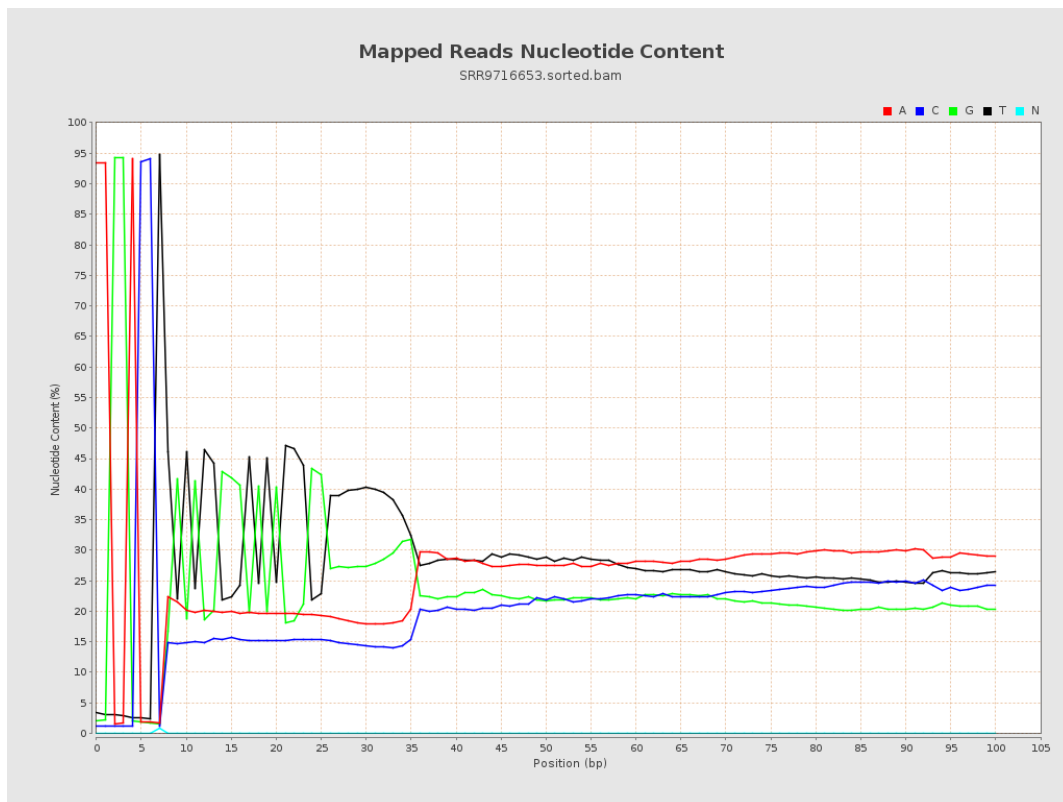
6. Results : Genome Fraction Coverage



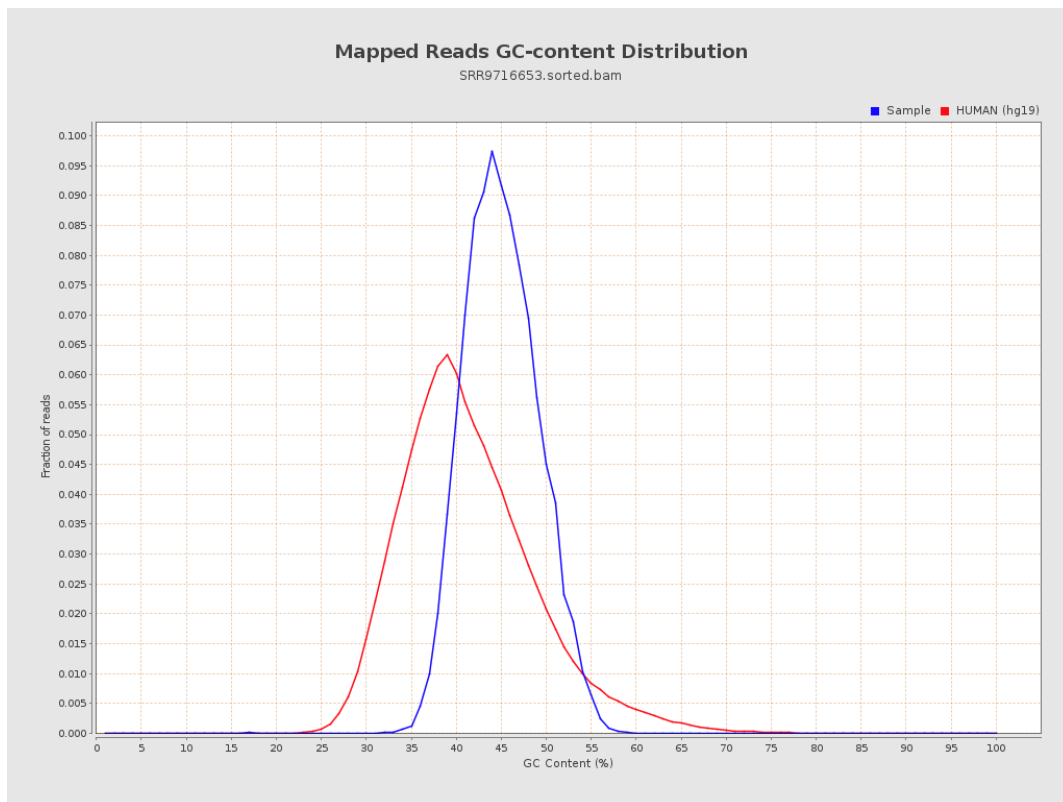
7. Results : Duplication Rate Histogram



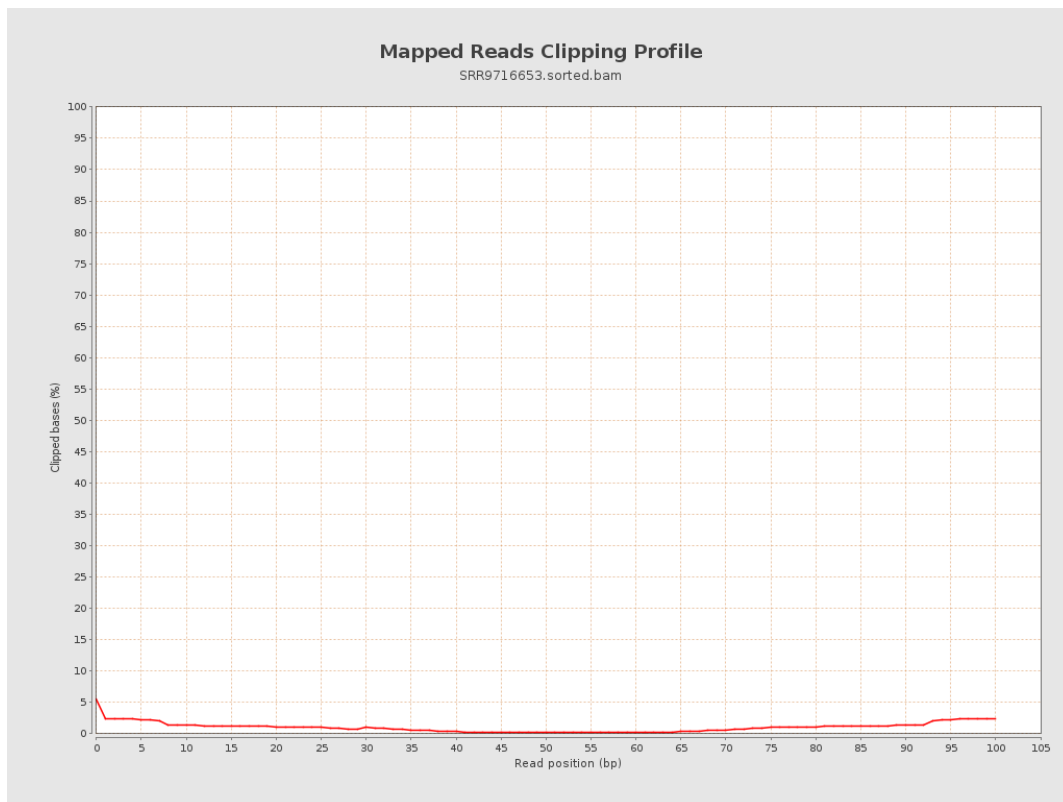
8. Results : Mapped Reads Nucleotide Content



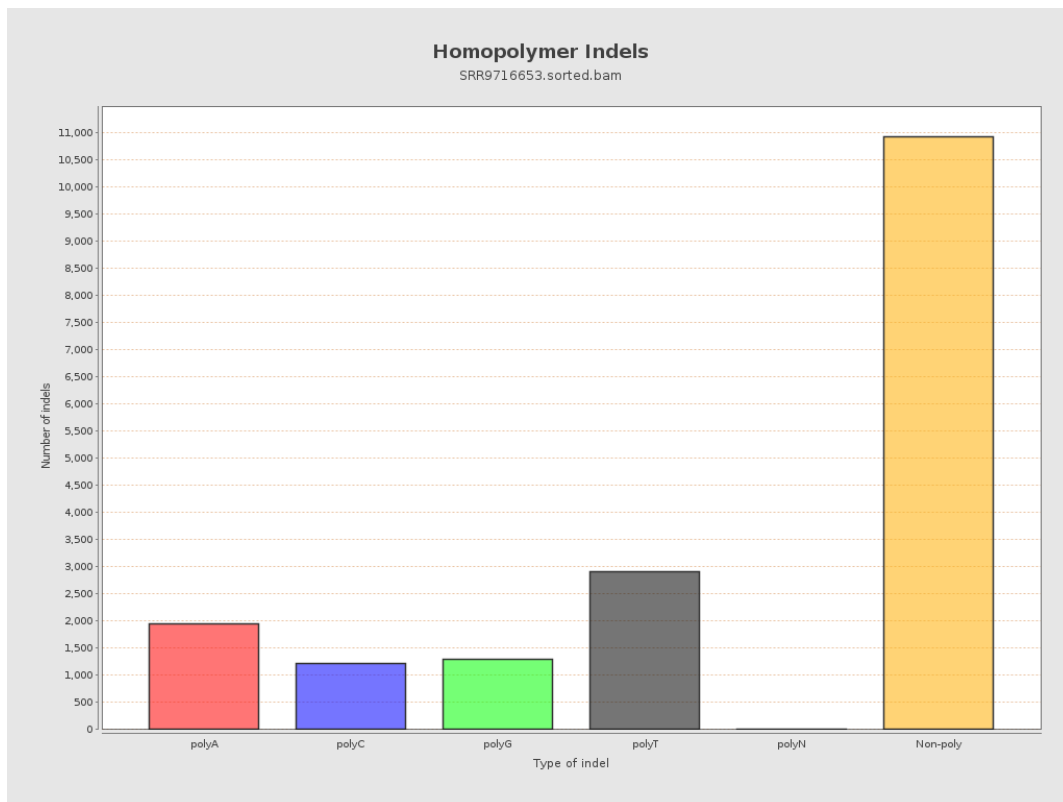
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

