

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:47:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716353.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_SRR9716353 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716353.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:47:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716353.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,060,329
Mapped reads	987,165 / 93.1%
Unmapped reads	73,164 / 6.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,158 / 1.9%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	27,680 / 2.61%
Duplication rate	1.97%
Clipped reads	1,006,645 / 94.94%

2.2. ACGT Content

Number/percentage of A's	20,453,134 / 26.28%
Number/percentage of C's	15,643,879 / 20.1%
Number/percentage of T's	23,495,999 / 30.19%
Number/percentage of G's	18,227,601 / 23.42%
Number/percentage of N's	5,365 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0252

Standard Deviation	0.2543
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2.4. Mapping Quality

Mean Mapping Quality	47.27
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2.5. Mismatches and indels

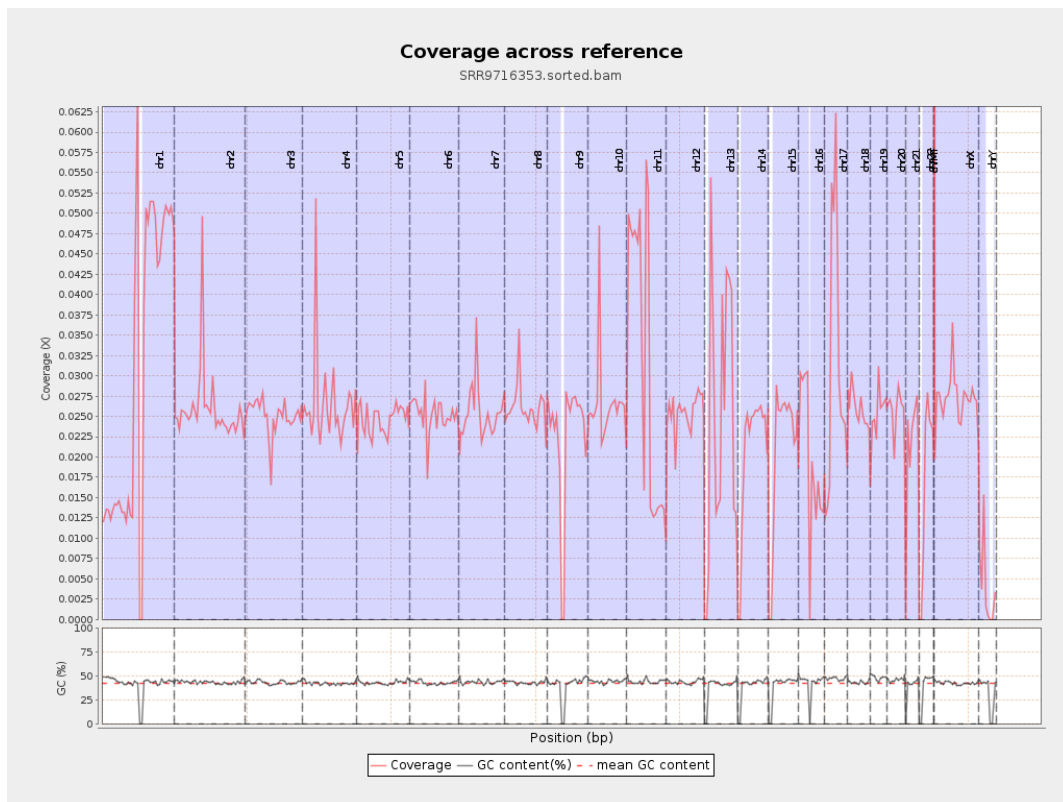
General error rate	0.66%
Mismatches	500,554
Insertions	6,084
Mapped reads with at least one insertion	0.61%
Deletions	17,861
Mapped reads with at least one deletion	1.78%
Homopolymer indels	43.83%

2.6. Chromosome stats

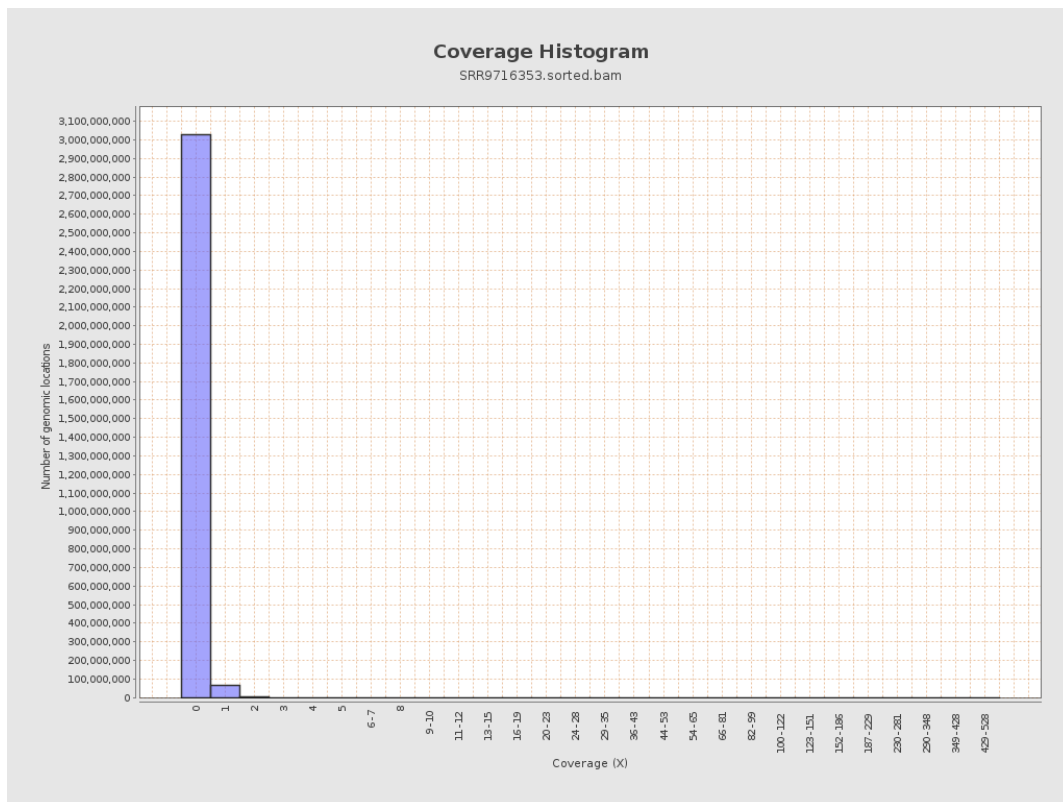
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7560641	0.0303	0.4953
chr2	243199373	6297562	0.0259	0.2713
chr3	198022430	4961032	0.0251	0.1692
chr4	191154276	5063167	0.0265	0.2101
chr5	180915260	4482678	0.0248	0.1688
chr6	171115067	4307004	0.0252	0.1811
chr7	159138663	4048576	0.0254	0.2801

chr8	146364022	3817799	0.0261	0.276
chr9	141213431	3158086	0.0224	0.2224
chr10	135534747	3603368	0.0266	0.2579
chr11	135006516	4295061	0.0318	0.2866
chr12	133851895	3417440	0.0255	0.1721
chr13	115169878	2726168	0.0237	0.1652
chr14	107349540	2207339	0.0206	0.1624
chr15	102531392	2128500	0.0208	0.154
chr16	90354753	1743689	0.0193	0.1579
chr17	81195210	2489059	0.0307	0.2171
chr18	78077248	2023420	0.0259	0.3381
chr19	59128983	1510143	0.0255	0.3256
chr20	63025520	1608046	0.0255	0.1782
chr21	48129895	1031791	0.0214	0.174
chr22	51304566	879515	0.0171	0.1416
chrMT	16571	26784	1.6163	1.5632
chrX	155270560	4240101	0.0273	0.1998
chrY	59373566	232985	0.0039	0.1371

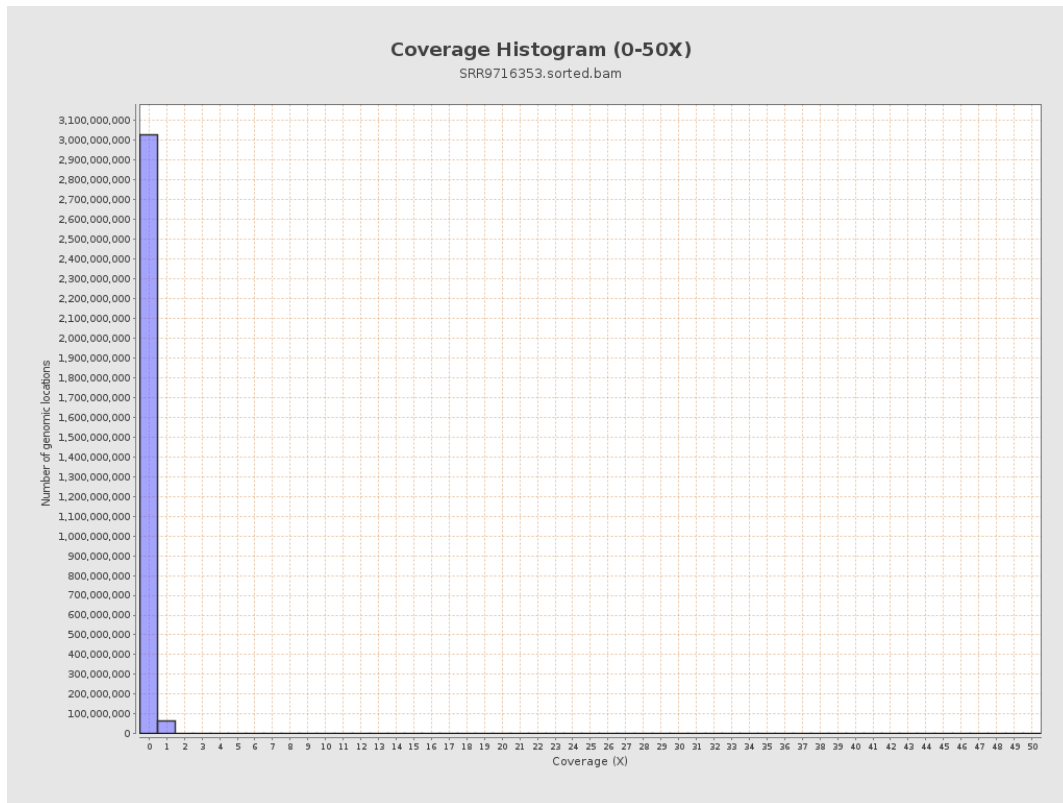
3. Results : Coverage across reference



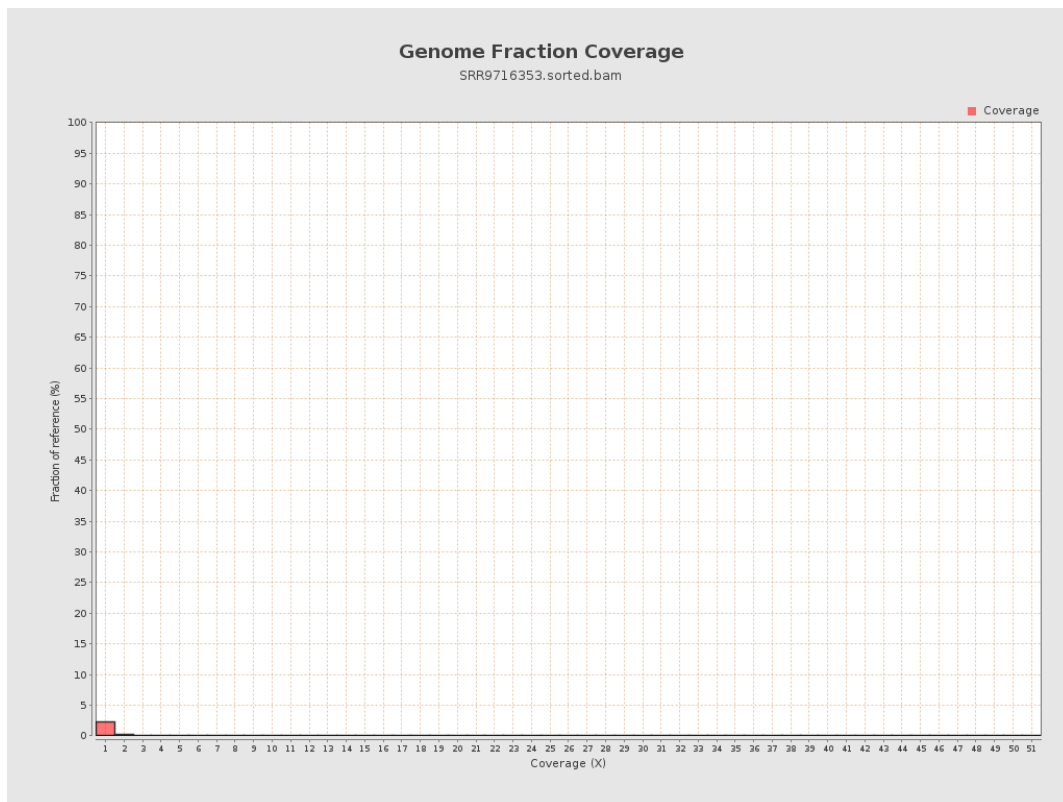
4. Results : Coverage Histogram



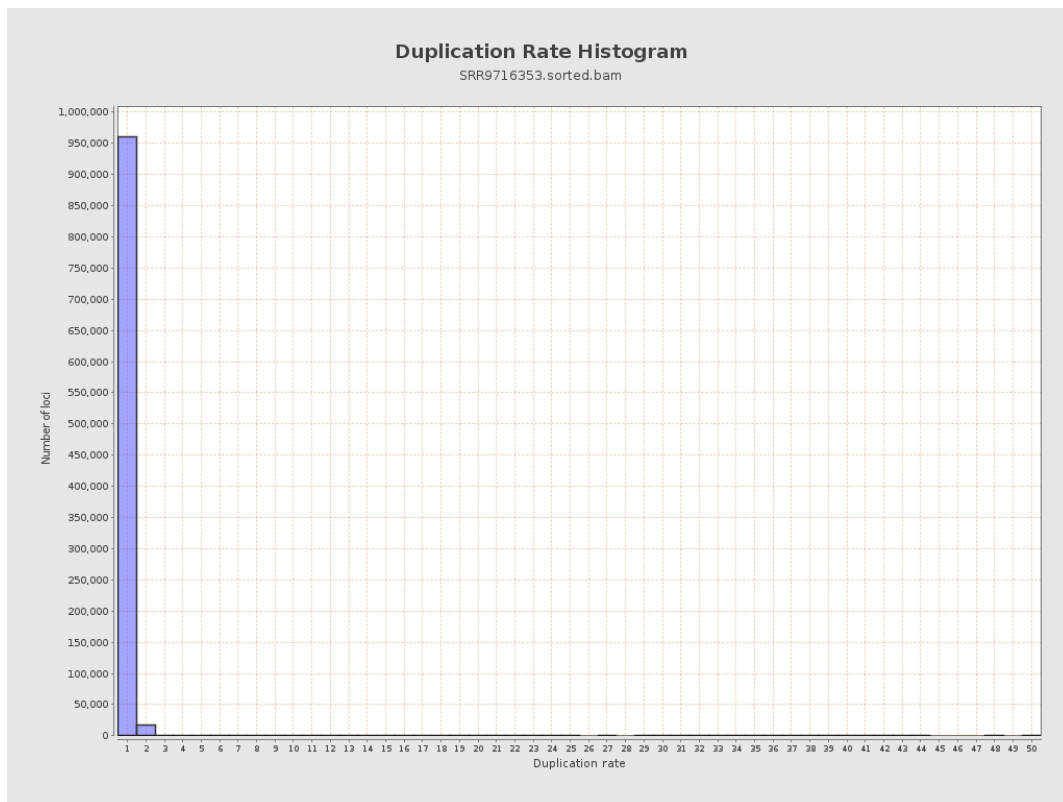
5. Results : Coverage Histogram (0-50X)



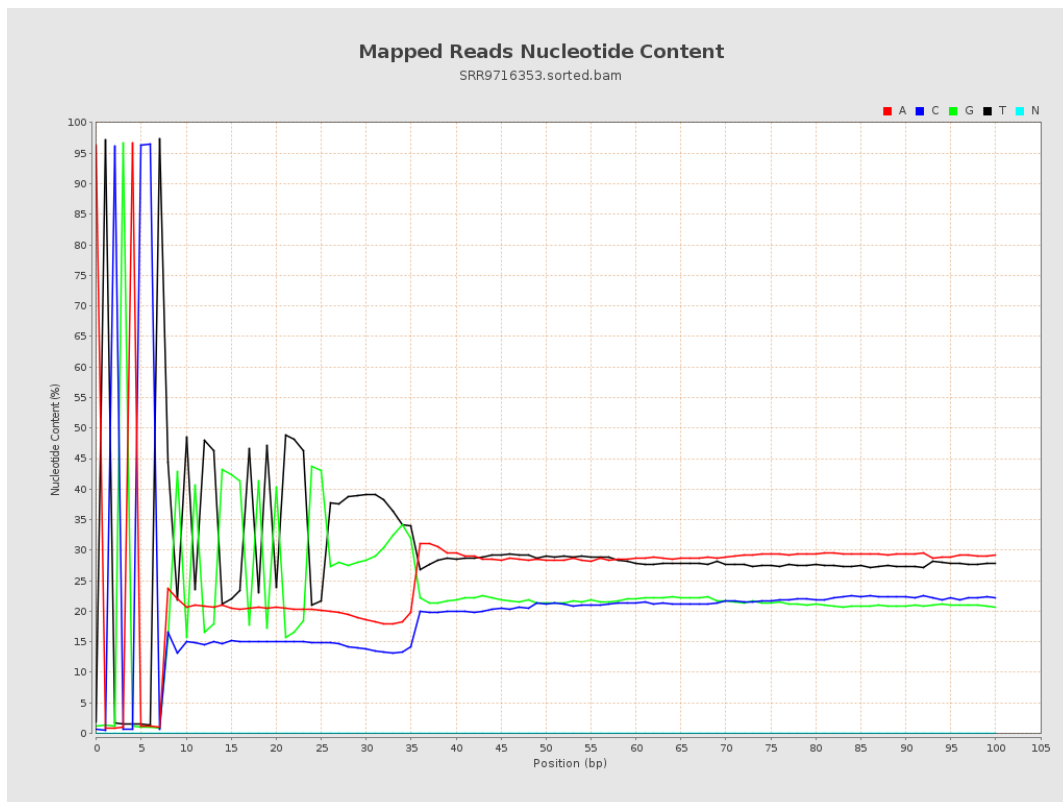
6. Results : Genome Fraction Coverage



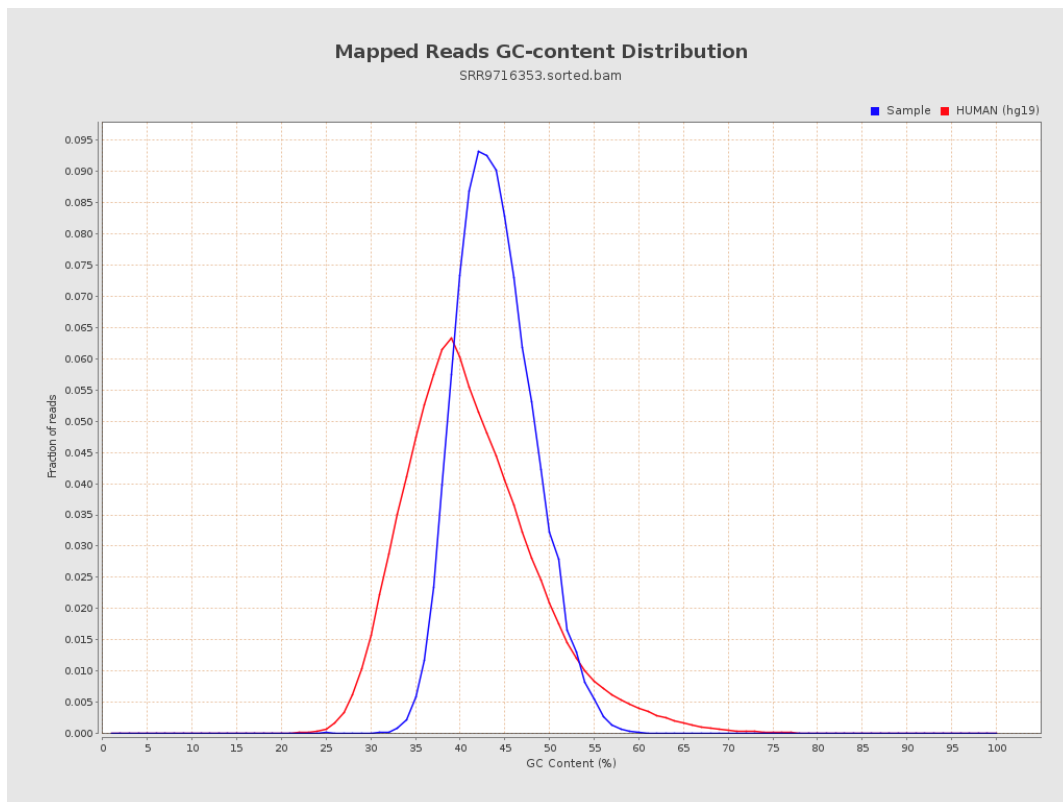
7. Results : Duplication Rate Histogram



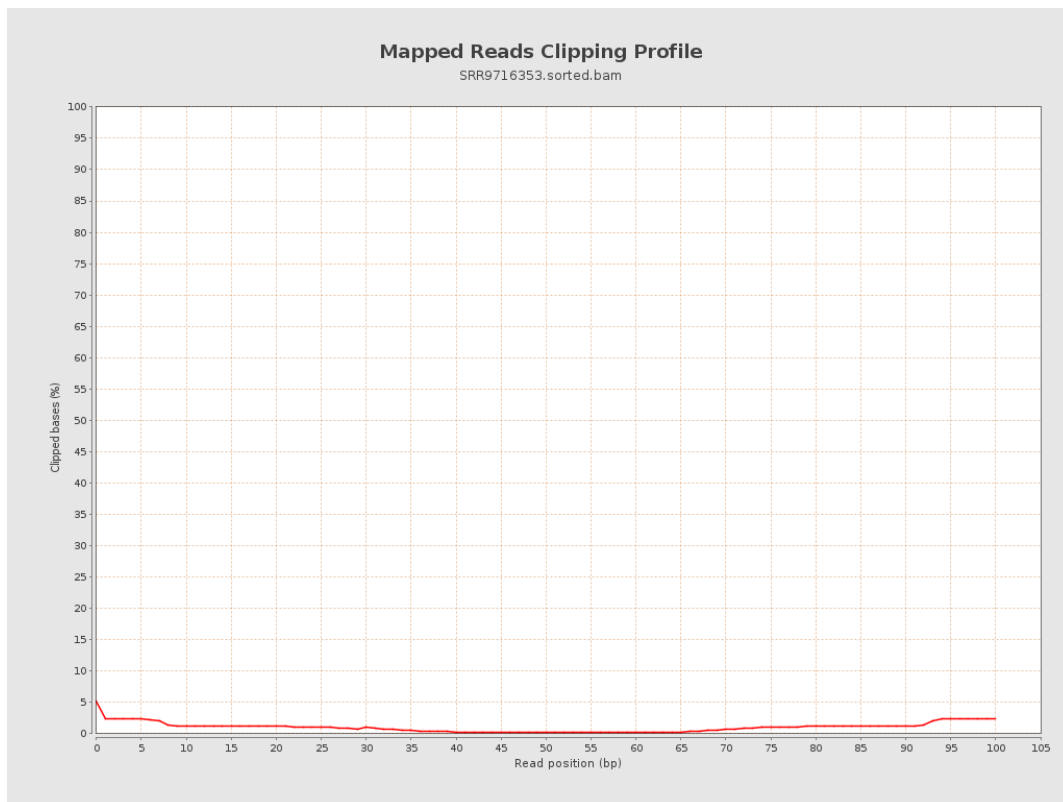
8. Results : Mapped Reads Nucleotide Content



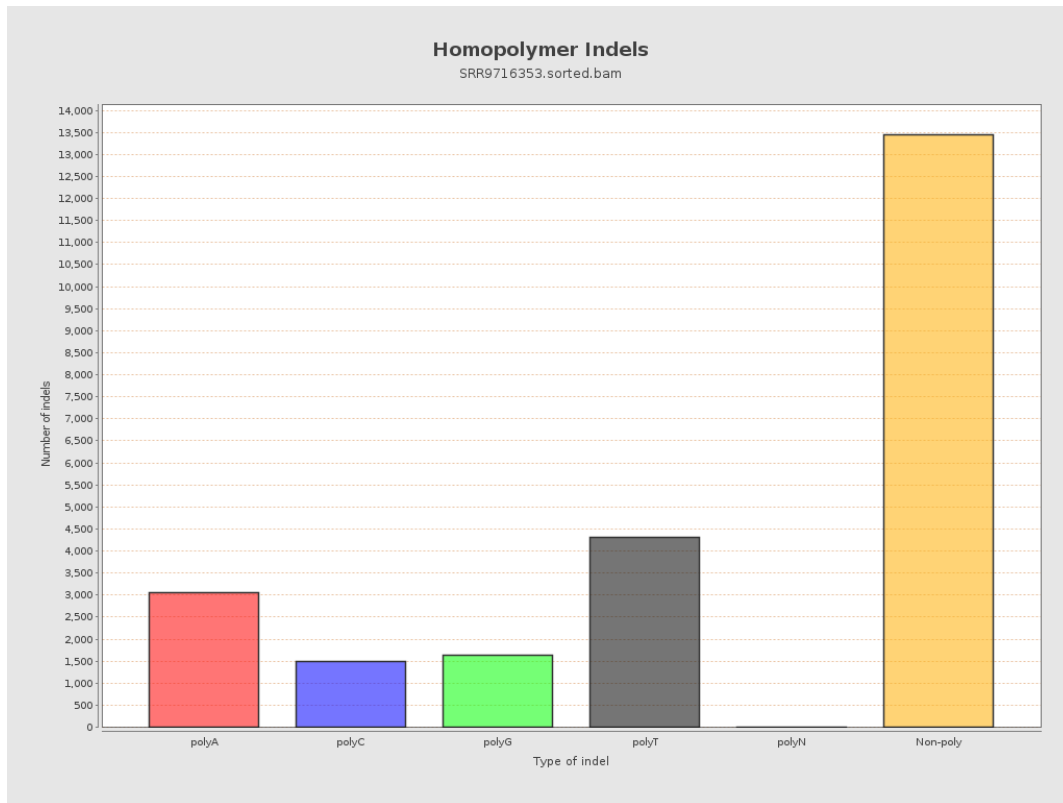
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

