

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:35:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716267.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_SRR9716267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716267.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:35:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,321,804
Mapped reads	1,656,783 / 71.36%
Unmapped reads	665,021 / 28.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,917 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	186,808 / 8.05%
Duplication rate	9.61%
Clipped reads	1,655,475 / 71.3%

2.2. ACGT Content

Number/percentage of A's	18,685,413 / 21.78%
Number/percentage of C's	13,794,807 / 16.08%
Number/percentage of T's	28,360,290 / 33.06%
Number/percentage of G's	24,939,079 / 29.07%
Number/percentage of N's	1,512 / 0%
GC Percentage	45.15%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2442
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2.4. Mapping Quality

Mean Mapping Quality	42.66
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2.5. Mismatches and indels

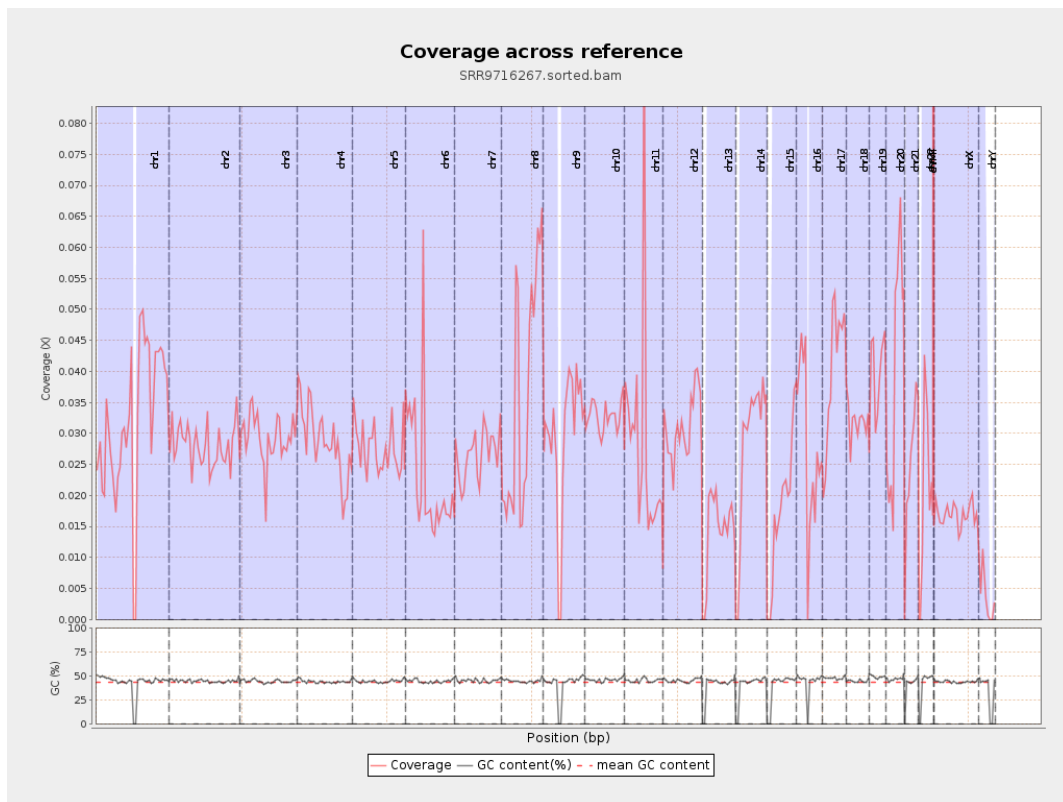
General error rate	0.68%
Mismatches	571,042
Insertions	5,184
Mapped reads with at least one insertion	0.31%
Deletions	11,616
Mapped reads with at least one deletion	0.7%
Homopolymer indels	40.76%

2.6. Chromosome stats

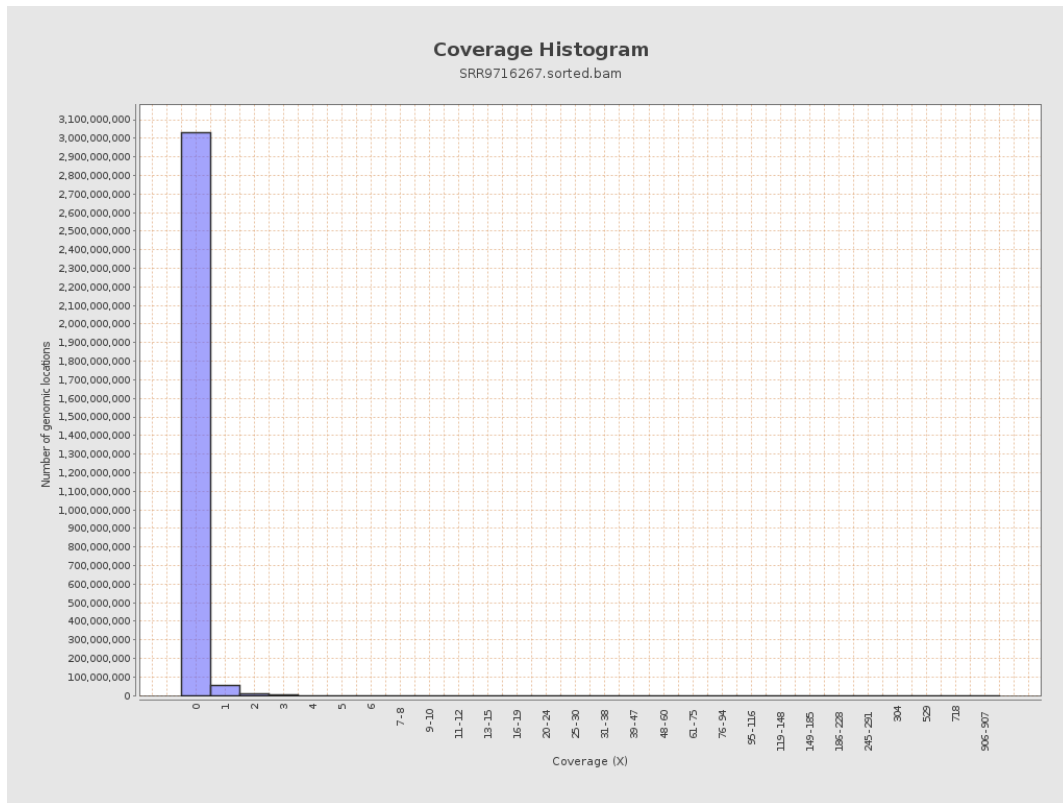
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7956955	0.0319	0.2611
chr2	243199373	6843192	0.0281	0.4076
chr3	198022430	5788972	0.0292	0.2153
chr4	191154276	5477926	0.0287	0.2173
chr5	180915260	5004278	0.0277	0.2059
chr6	171115067	3907784	0.0228	0.2345
chr7	159138663	4221899	0.0265	0.2256

chr8	146364022	5306267	0.0363	0.2485
chr9	141213431	4160155	0.0295	0.2324
chr10	135534747	4436196	0.0327	0.2449
chr11	135006516	3827557	0.0284	0.2358
chr12	133851895	4161730	0.0311	0.2218
chr13	115169878	1641442	0.0143	0.151
chr14	107349540	3016870	0.0281	0.2122
chr15	102531392	1810071	0.0177	0.169
chr16	90354753	2528357	0.028	0.2212
chr17	81195210	3307693	0.0407	0.2667
chr18	78077248	2487769	0.0319	0.2463
chr19	59128983	2342326	0.0396	0.3244
chr20	63025520	2492804	0.0396	0.2644
chr21	48129895	1227511	0.0255	0.2089
chr22	51304566	1011167	0.0197	0.185
chrMT	16571	6566	0.3962	0.7545
chrX	155270560	2621706	0.0169	0.1696
chrY	59373566	213420	0.0036	0.0886

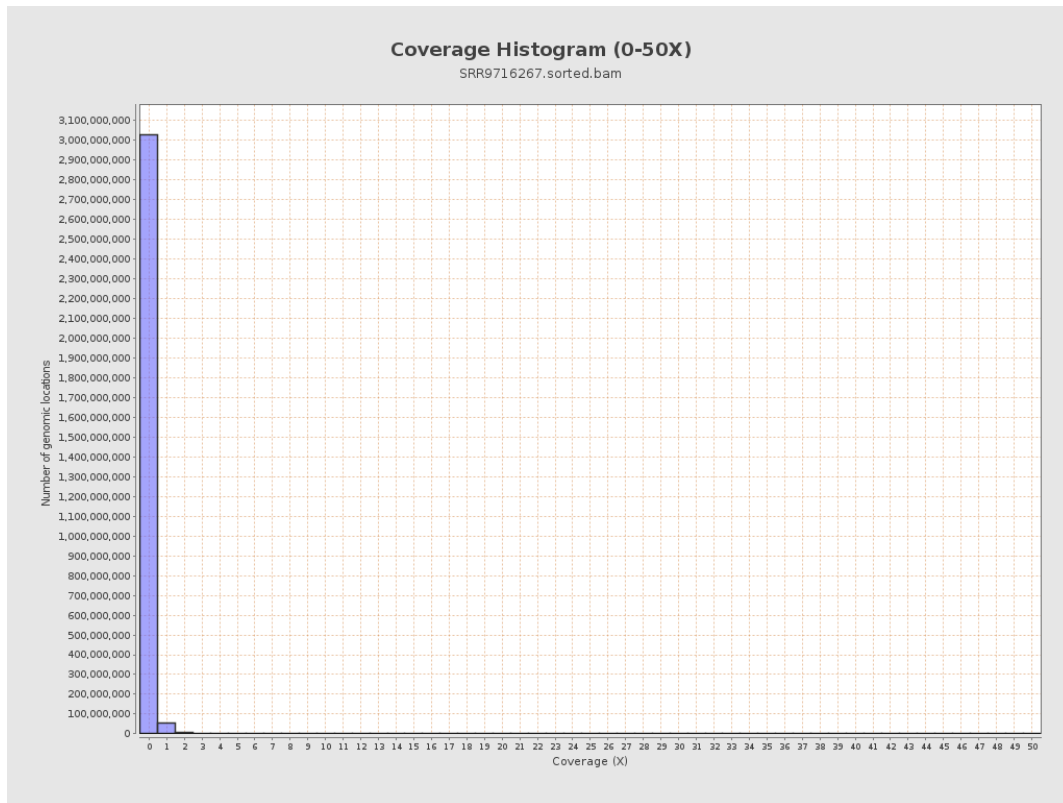
3. Results : Coverage across reference



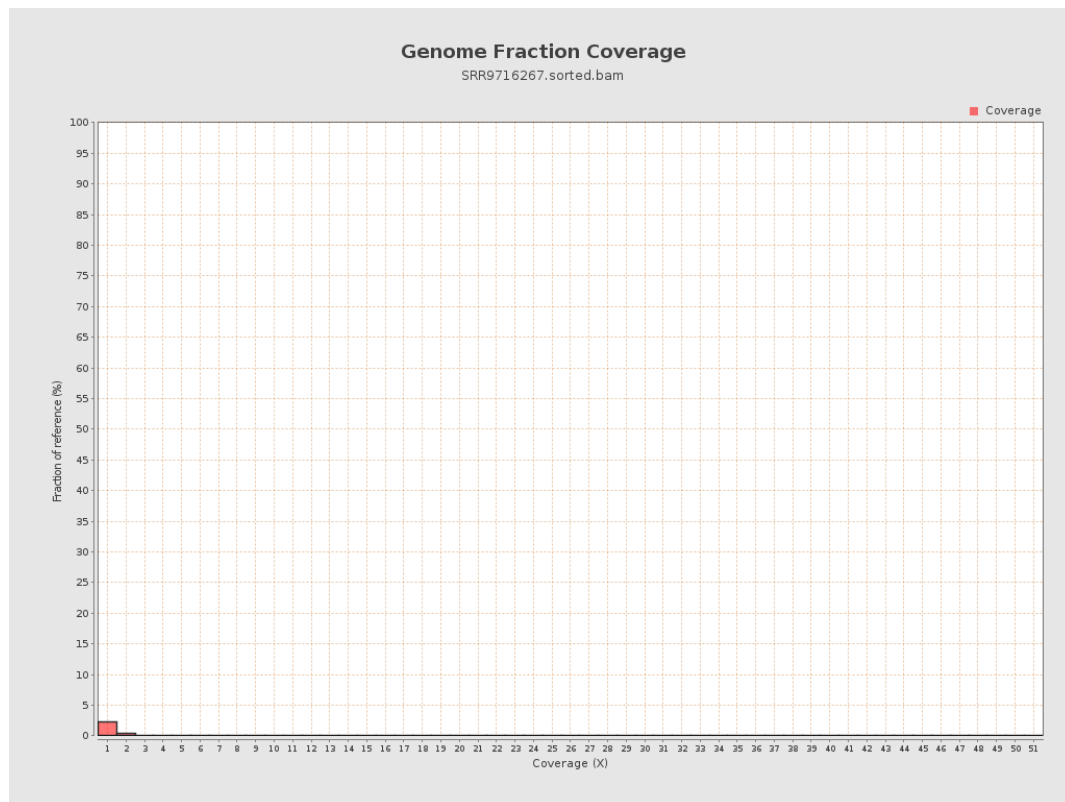
4. Results : Coverage Histogram



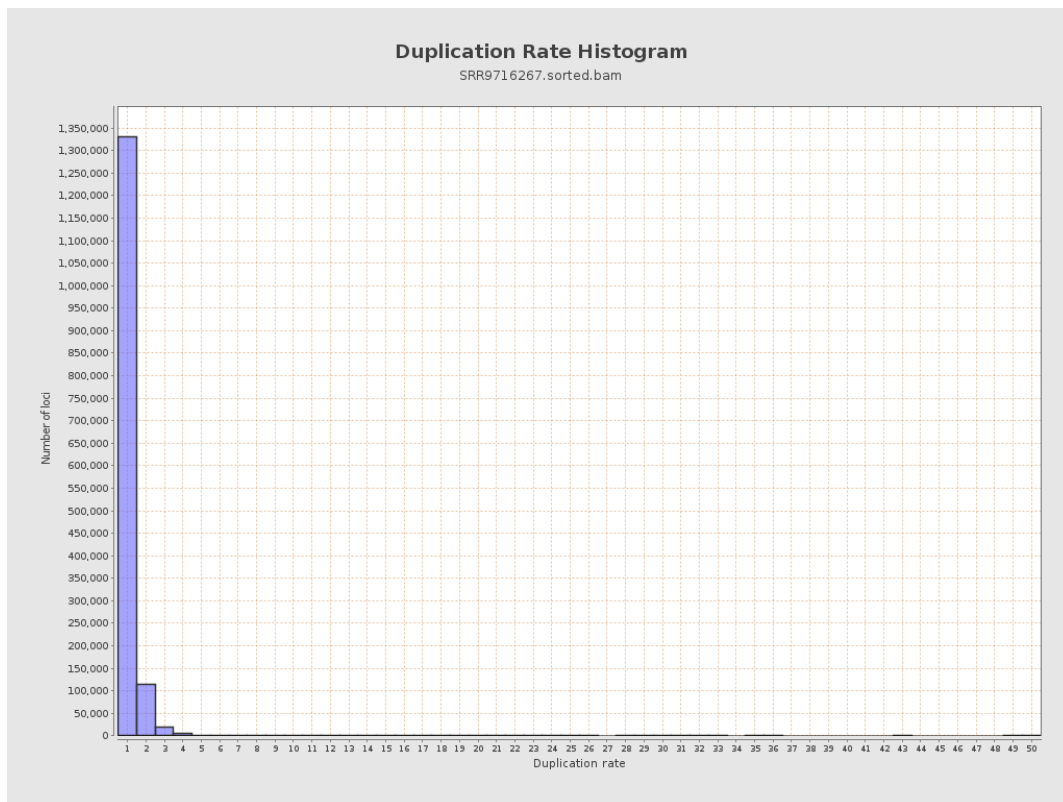
5. Results : Coverage Histogram (0-50X)



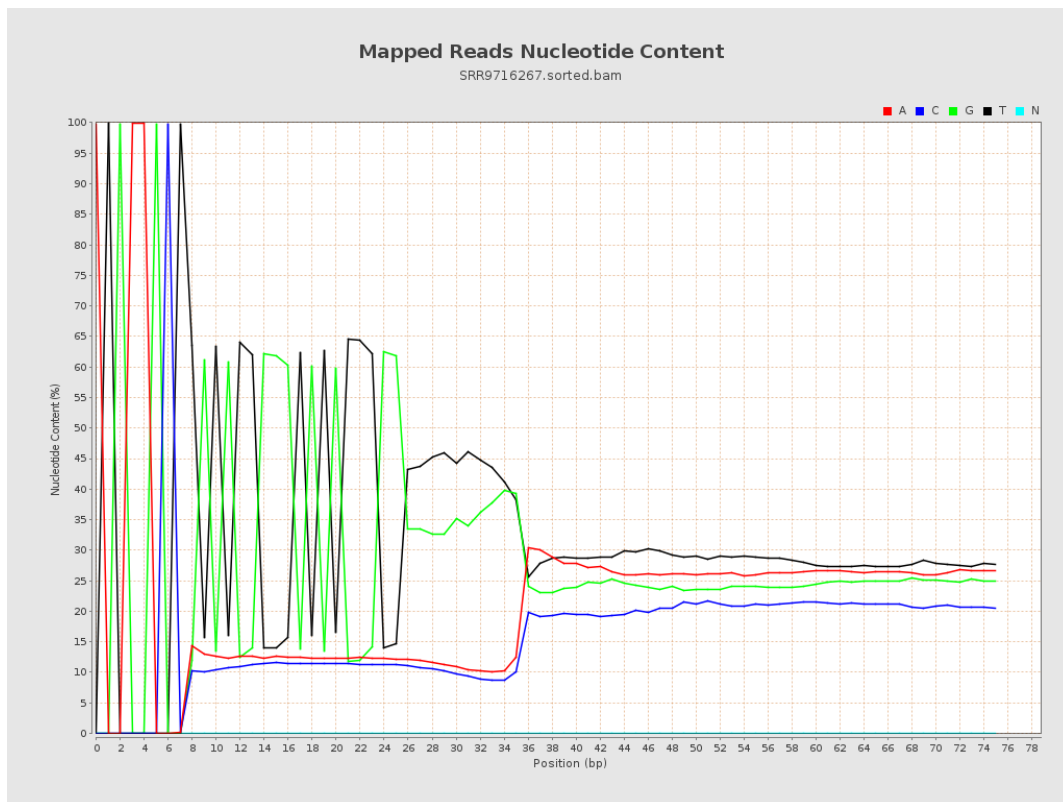
6. Results : Genome Fraction Coverage



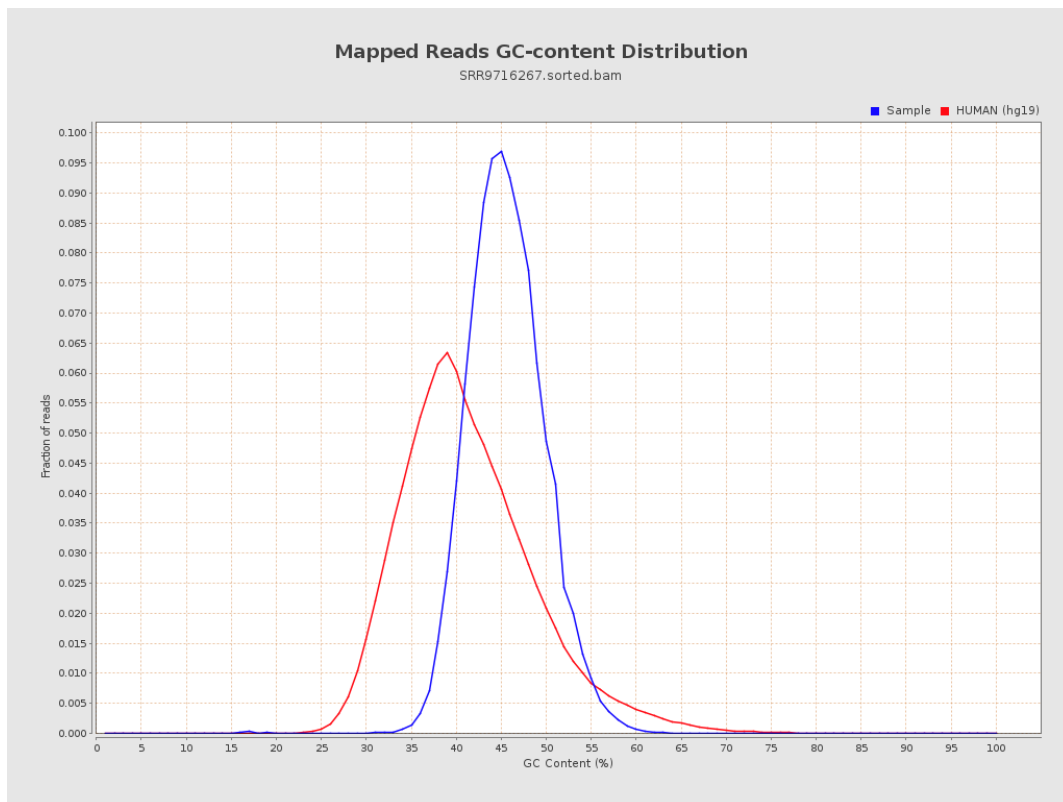
7. Results : Duplication Rate Histogram



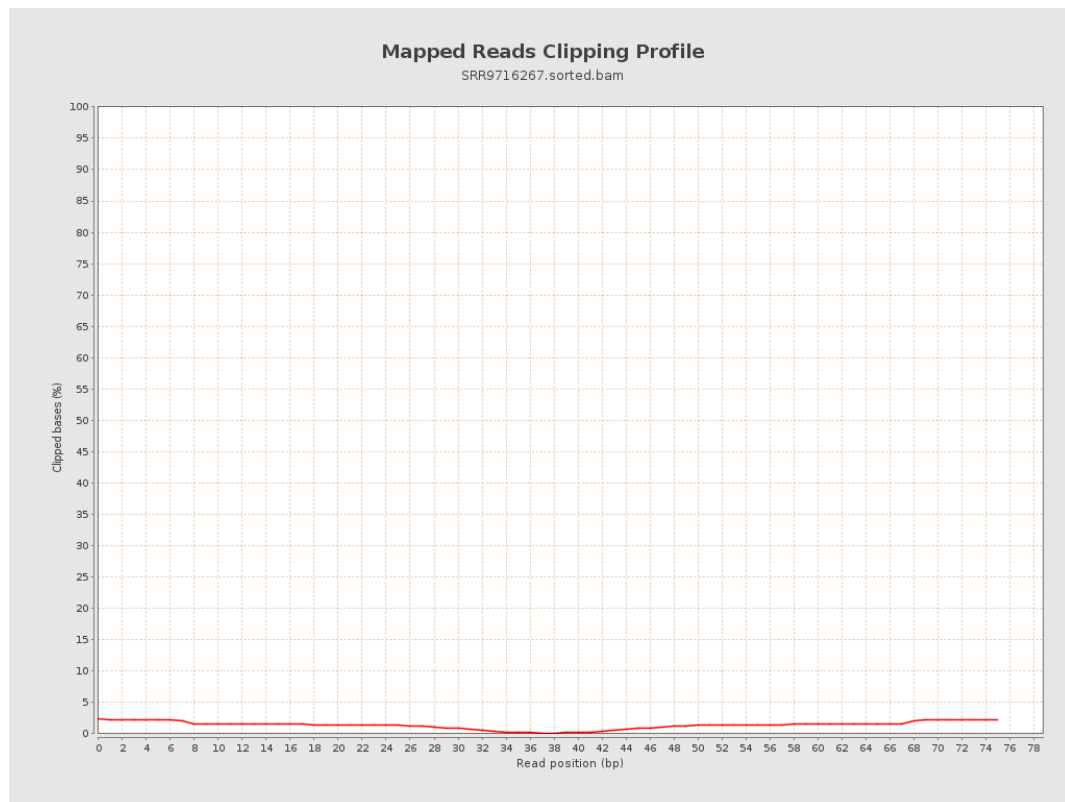
8. Results : Mapped Reads Nucleotide Content



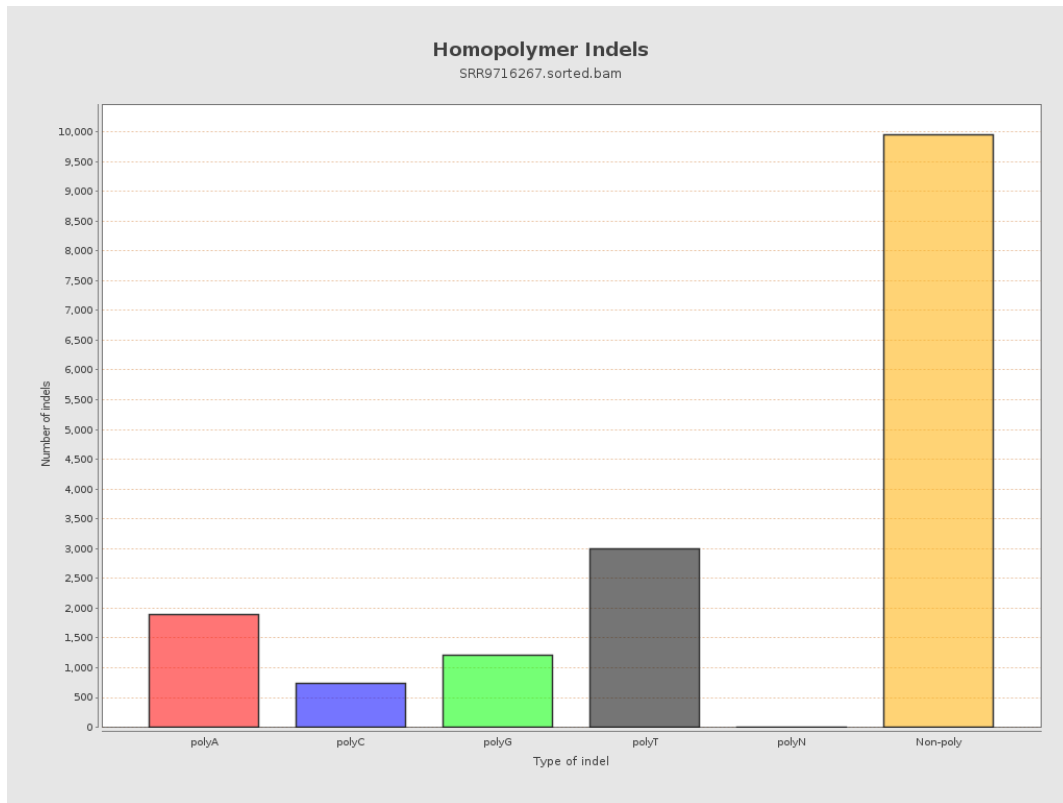
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

