

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:49:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716234.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_SRR9716234 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716234.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:49:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,206,944
Mapped reads	981,139 / 81.29%
Unmapped reads	225,805 / 18.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,794 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	20,396 / 1.69%
Duplication rate	1.48%
Clipped reads	982,868 / 81.43%

2.2. ACGT Content

Number/percentage of A's	12,976,490 / 23.68%
Number/percentage of C's	10,984,040 / 20.04%
Number/percentage of T's	16,720,594 / 30.51%
Number/percentage of G's	14,125,827 / 25.77%
Number/percentage of N's	1,631 / 0%
GC Percentage	45.81%

2.3. Coverage

Mean	0.0177

Standard Deviation	0.168
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2.4. Mapping Quality

Mean Mapping Quality	39.64
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2.5. Mismatches and indels

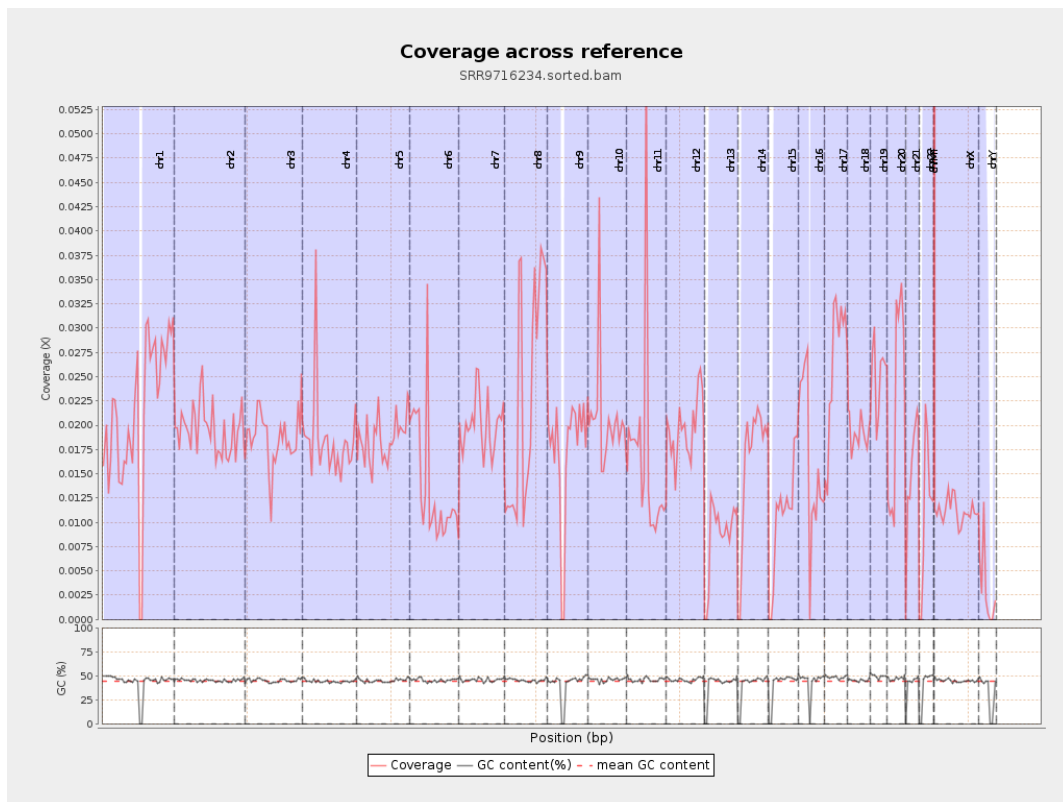
General error rate	0.55%
Mismatches	289,872
Insertions	4,670
Mapped reads with at least one insertion	0.47%
Deletions	9,250
Mapped reads with at least one deletion	0.93%
Homopolymer indels	33.74%

2.6. Chromosome stats

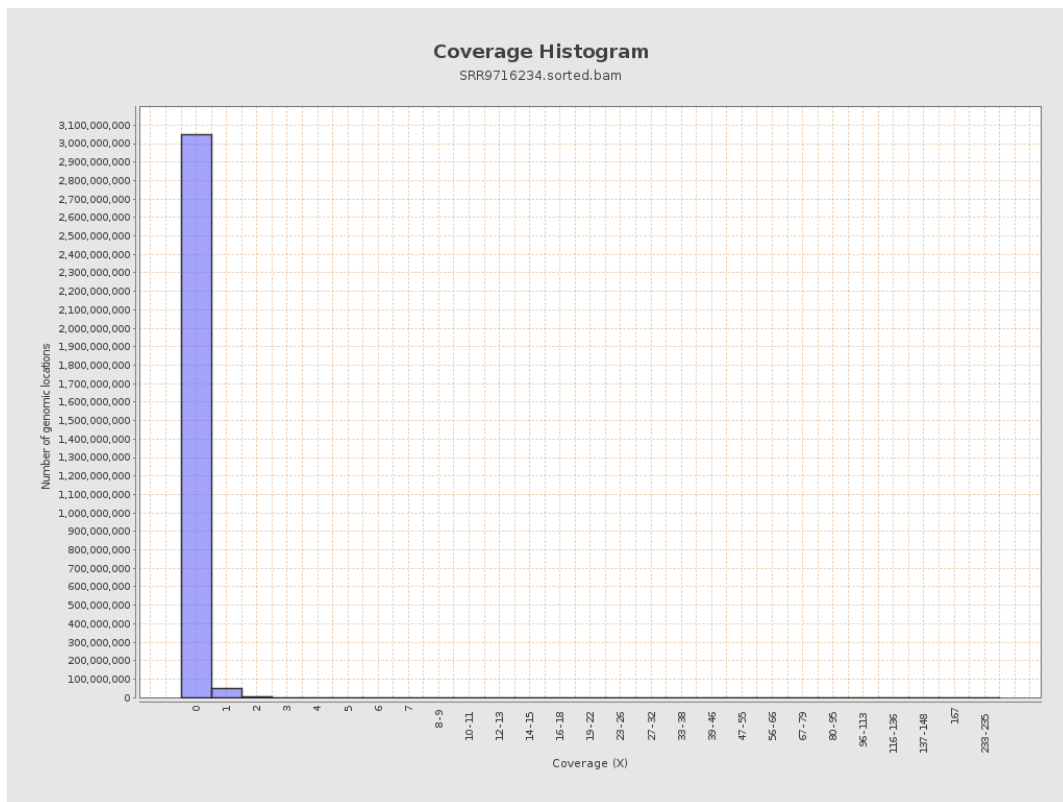
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5325375	0.0214	0.196
chr2	243199373	4748492	0.0195	0.2032
chr3	198022430	3676951	0.0186	0.1524
chr4	191154276	3542192	0.0185	0.1696
chr5	180915260	3392934	0.0188	0.1476
chr6	171115067	2357213	0.0138	0.1294
chr7	159138663	3189304	0.02	0.1927

chr8	146364022	3357880	0.0229	0.1756
chr9	141213431	2428258	0.0172	0.1502
chr10	135534747	2803286	0.0207	0.2526
chr11	135006516	2268927	0.0168	0.1647
chr12	133851895	2634085	0.0197	0.1519
chr13	115169878	982418	0.0085	0.1024
chr14	107349540	1737963	0.0162	0.1395
chr15	102531392	1087765	0.0106	0.113
chr16	90354753	1474625	0.0163	0.1474
chr17	81195210	2134003	0.0263	0.1864
chr18	78077248	1498492	0.0192	0.1846
chr19	59128983	1483199	0.0251	0.204
chr20	63025520	1385272	0.022	0.1673
chr21	48129895	738076	0.0153	0.1543
chr22	51304566	588800	0.0115	0.1186
chrMT	16571	71753	4.33	3.8507
chrX	155270560	1734901	0.0112	0.1229
chrY	59373566	182658	0.0031	0.1079

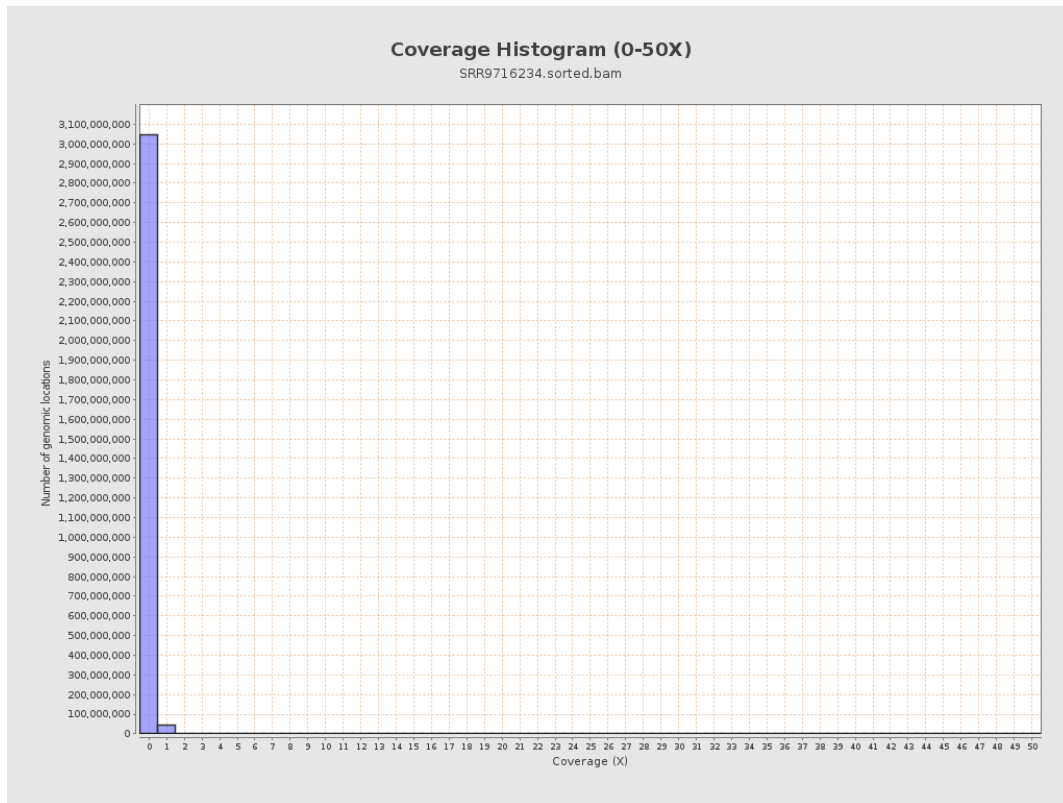
3. Results : Coverage across reference



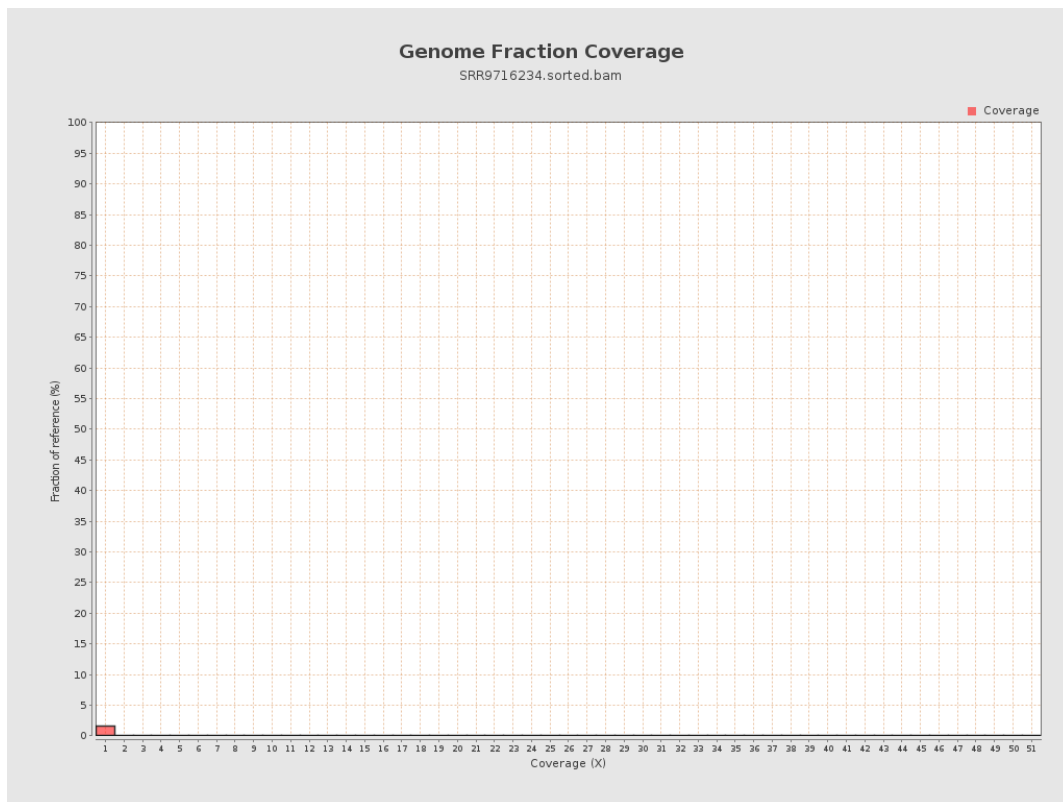
4. Results : Coverage Histogram



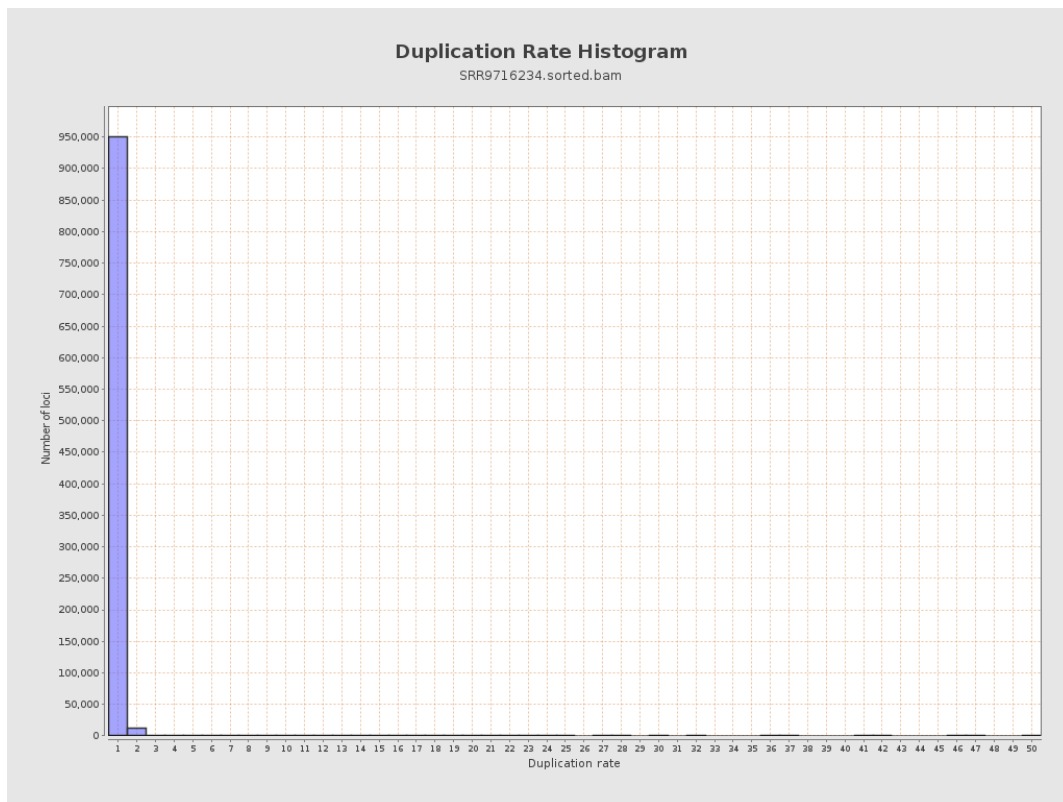
5. Results : Coverage Histogram (0-50X)



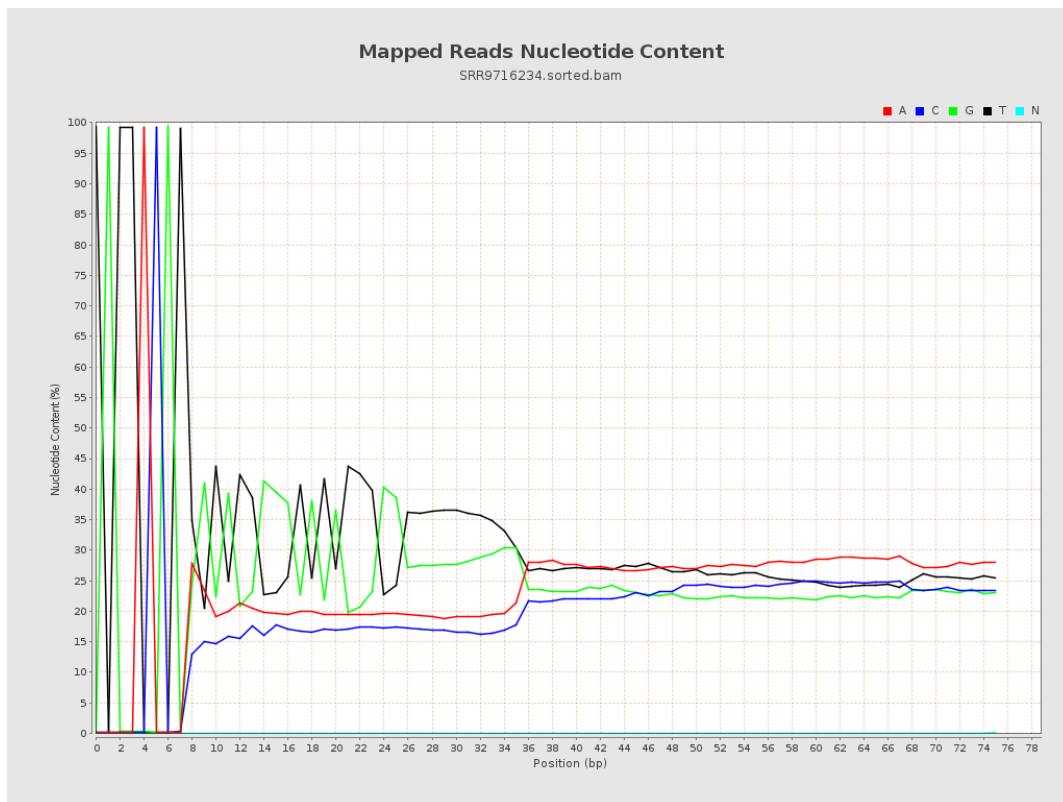
6. Results : Genome Fraction Coverage



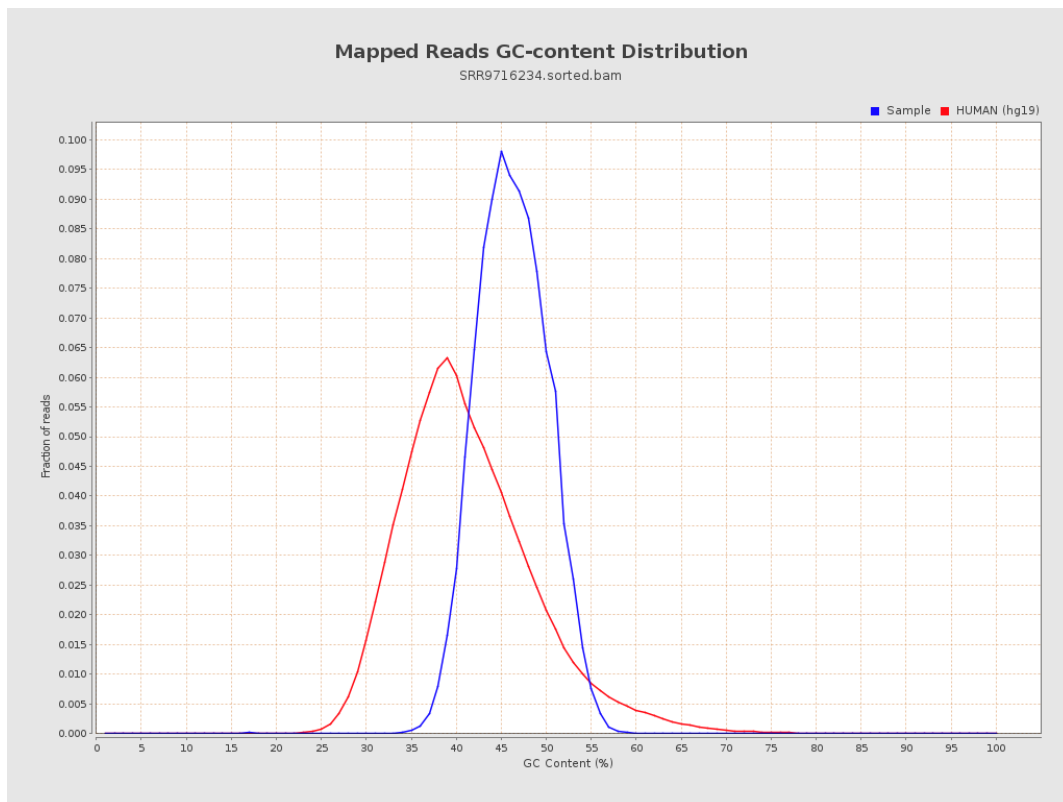
7. Results : Duplication Rate Histogram



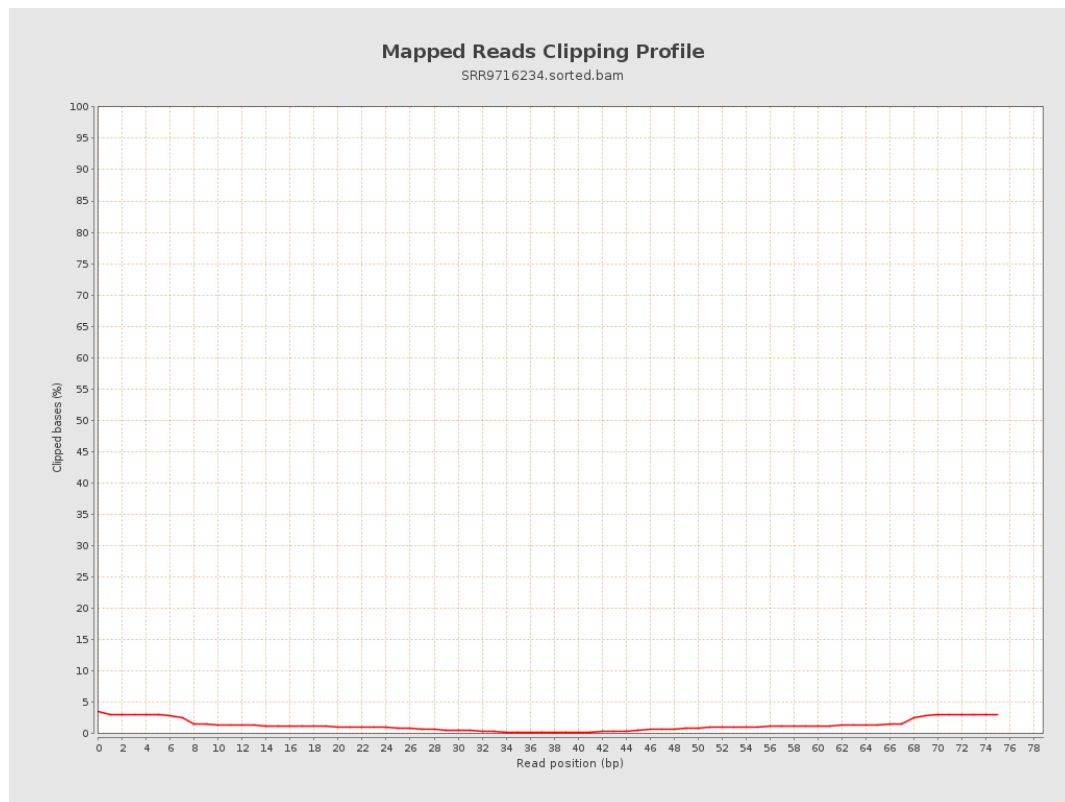
8. Results : Mapped Reads Nucleotide Content



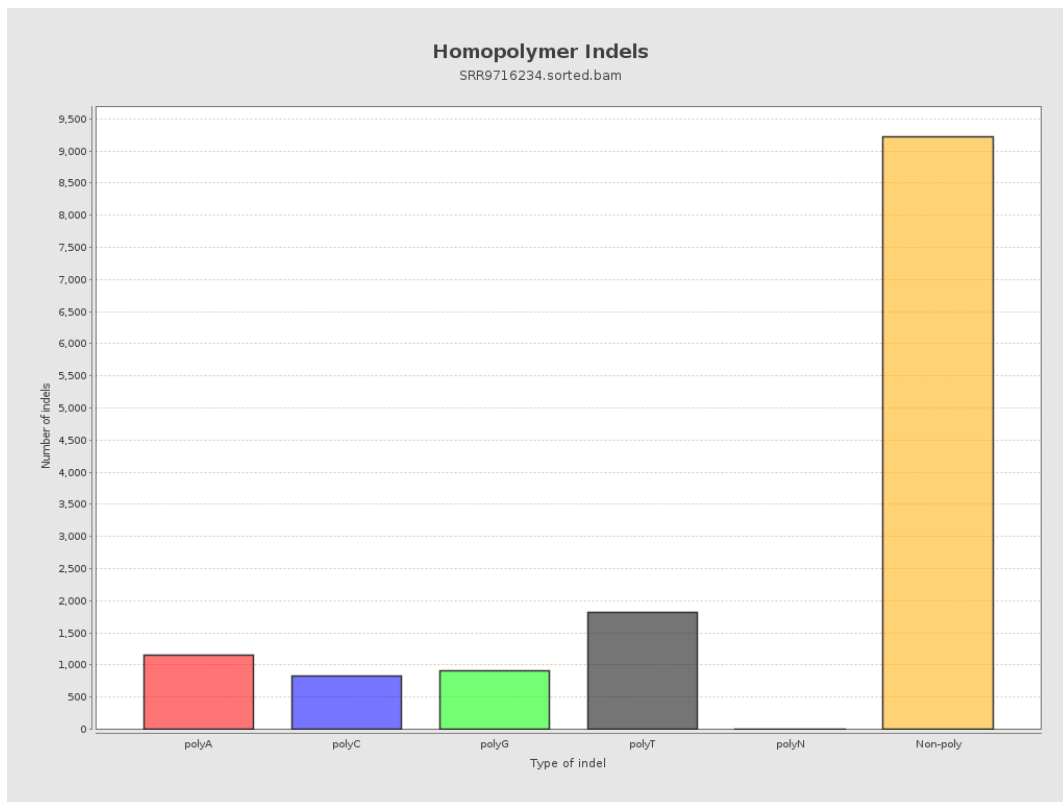
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

