

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:44:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716492.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_SRR9716492 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716492.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:44:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716492.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	849,151
Mapped reads	730,232 / 86%
Unmapped reads	118,919 / 14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,816 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	18,747 / 2.21%
Duplication rate	1.98%
Clipped reads	731,929 / 86.2%

2.2. ACGT Content

Number/percentage of A's	10,438,377 / 24.99%
Number/percentage of C's	8,663,838 / 20.74%
Number/percentage of T's	13,146,971 / 31.47%
Number/percentage of G's	9,524,168 / 22.8%
Number/percentage of N's	569 / 0%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0135

Standard Deviation	0.152
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2.4. Mapping Quality

Mean Mapping Quality	44.44
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2.5. Mismatches and indels

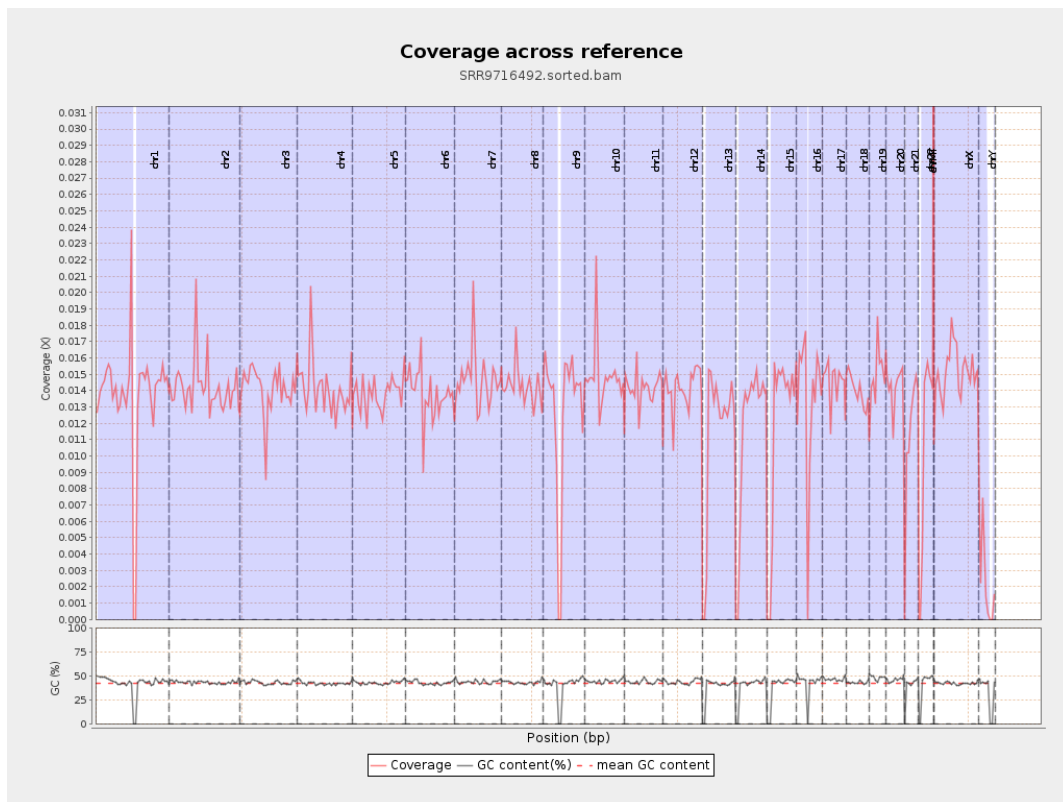
General error rate	0.53%
Mismatches	215,990
Insertions	2,703
Mapped reads with at least one insertion	0.37%
Deletions	7,831
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.01%

2.6. Chromosome stats

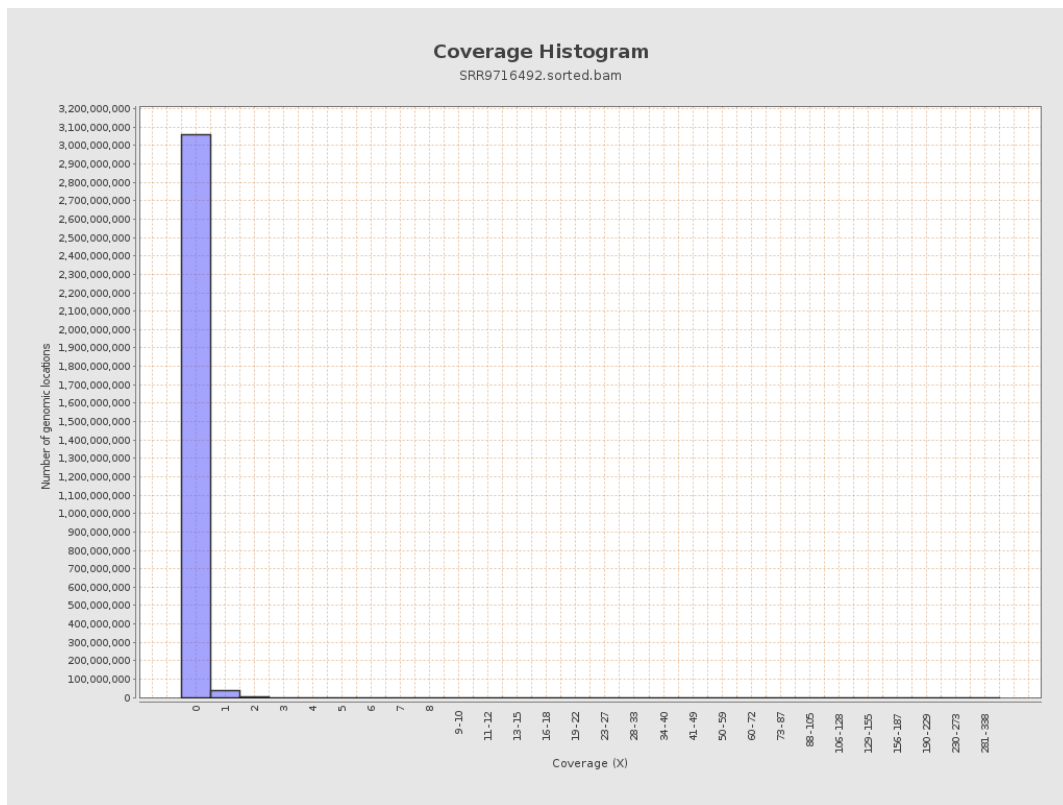
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3400994	0.0136	0.2479
chr2	243199373	3462320	0.0142	0.1914
chr3	198022430	2788932	0.0141	0.1255
chr4	191154276	2694268	0.0141	0.1298
chr5	180915260	2493530	0.0138	0.1236
chr6	171115067	2358078	0.0138	0.1318
chr7	159138663	2341161	0.0147	0.1707

chr8	146364022	2086599	0.0143	0.1457
chr9	141213431	1786356	0.0127	0.1317
chr10	135534747	2005320	0.0148	0.1479
chr11	135006516	1908084	0.0141	0.1416
chr12	133851895	1895212	0.0142	0.1259
chr13	115169878	1299263	0.0113	0.112
chr14	107349540	1241173	0.0116	0.1181
chr15	102531392	1213388	0.0118	0.1171
chr16	90354753	1219104	0.0135	0.1256
chr17	81195210	1173302	0.0145	0.1297
chr18	78077248	1093480	0.014	0.1872
chr19	59128983	890440	0.0151	0.1798
chr20	63025520	886954	0.0141	0.1253
chr21	48129895	548286	0.0114	0.1166
chr22	51304566	523750	0.0102	0.1072
chrMT	16571	1089	0.0657	0.2672
chrX	155270560	2344861	0.0151	0.1362
chrY	59373566	129982	0.0022	0.0695

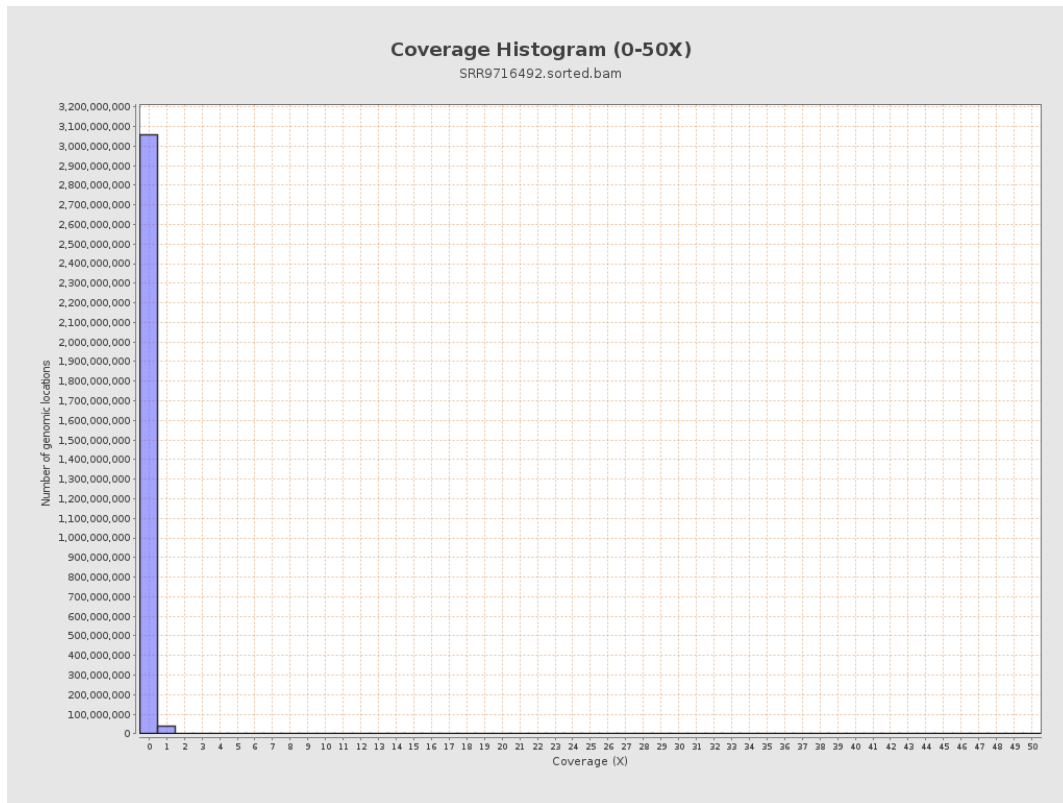
3. Results : Coverage across reference



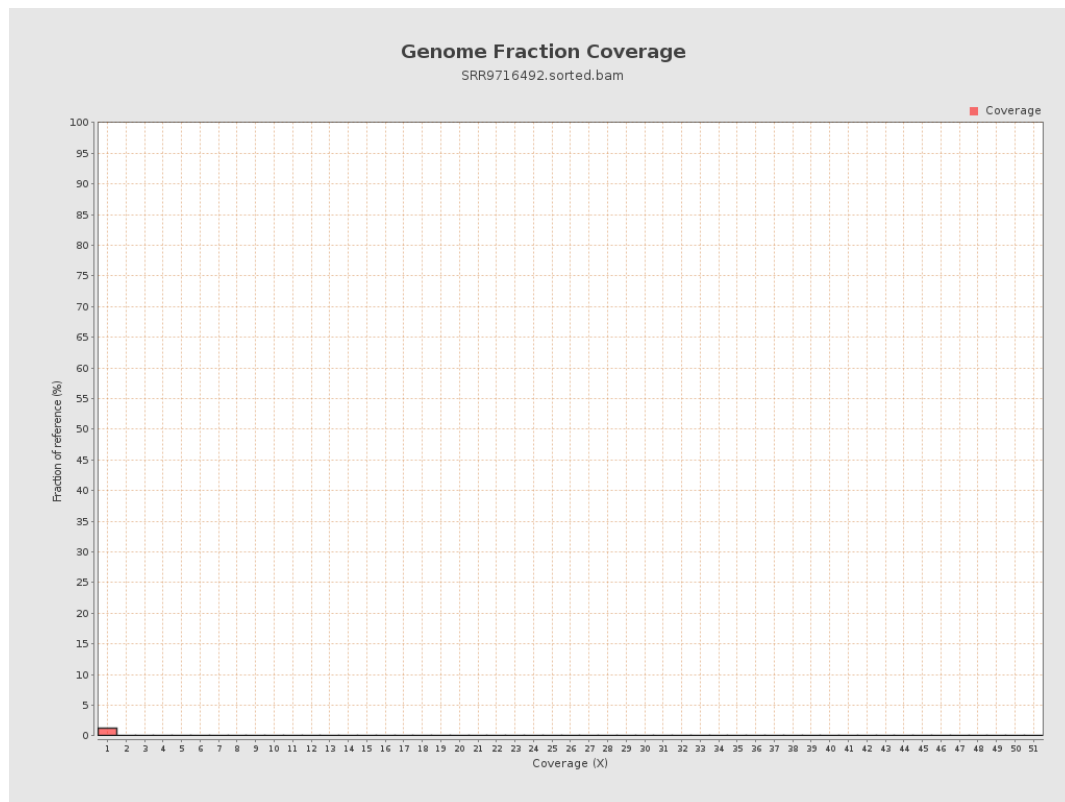
4. Results : Coverage Histogram



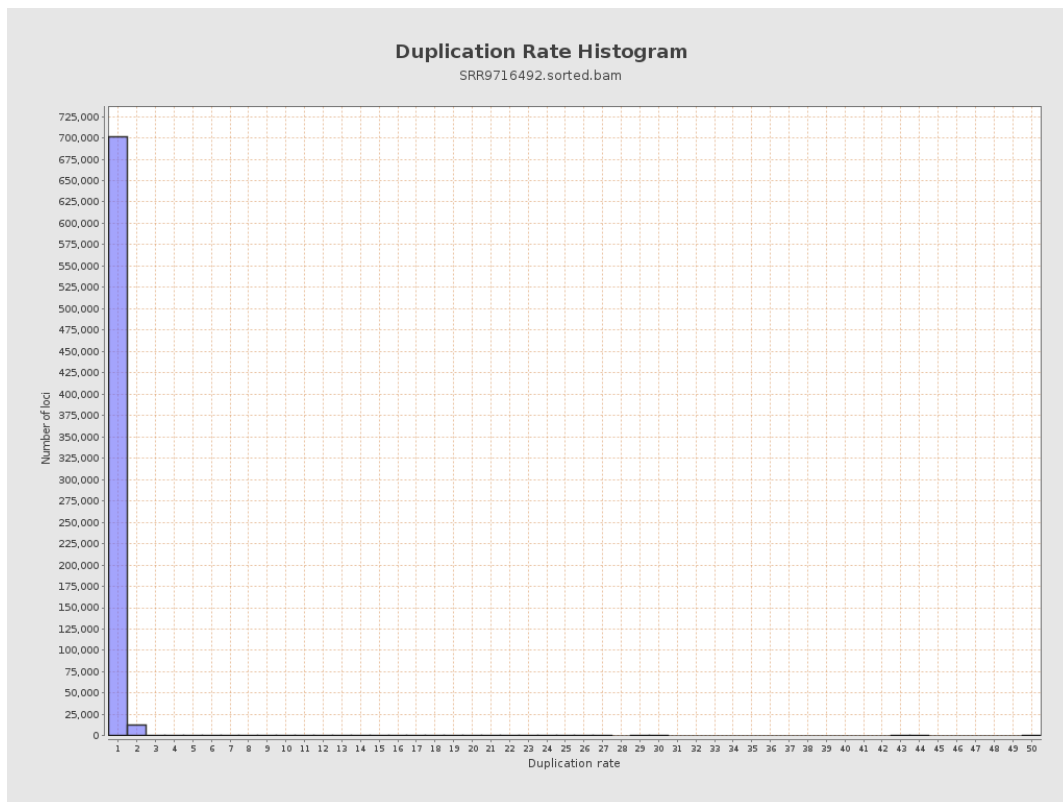
5. Results : Coverage Histogram (0-50X)



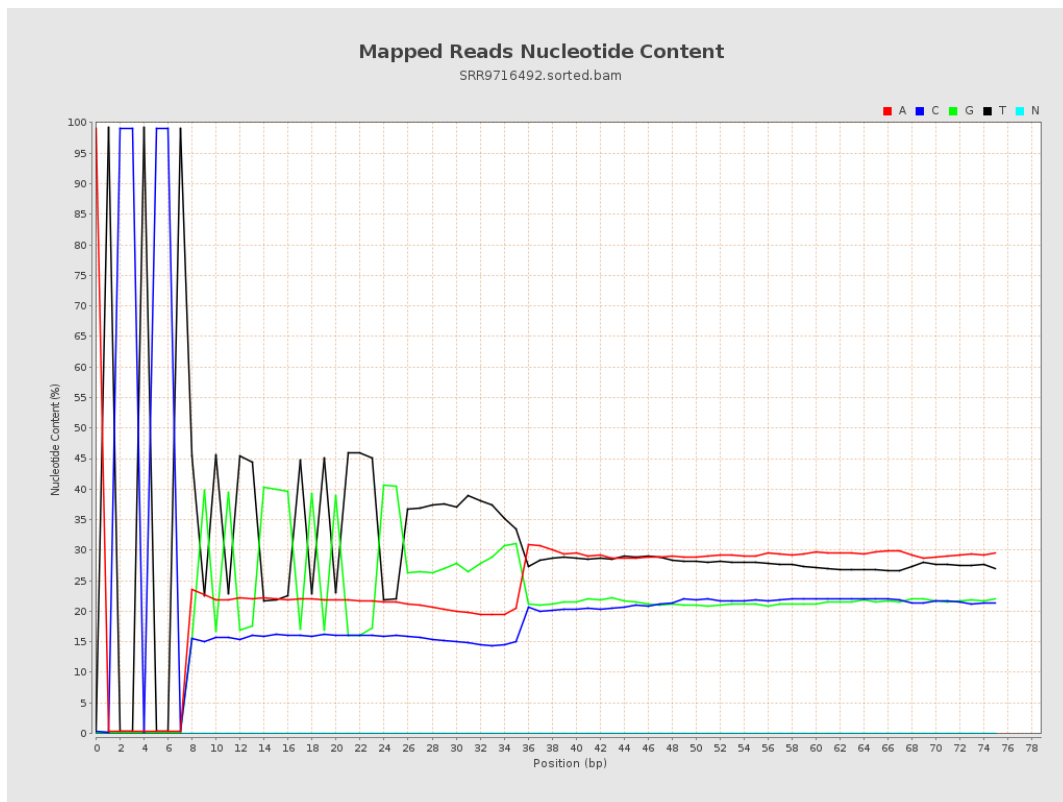
6. Results : Genome Fraction Coverage



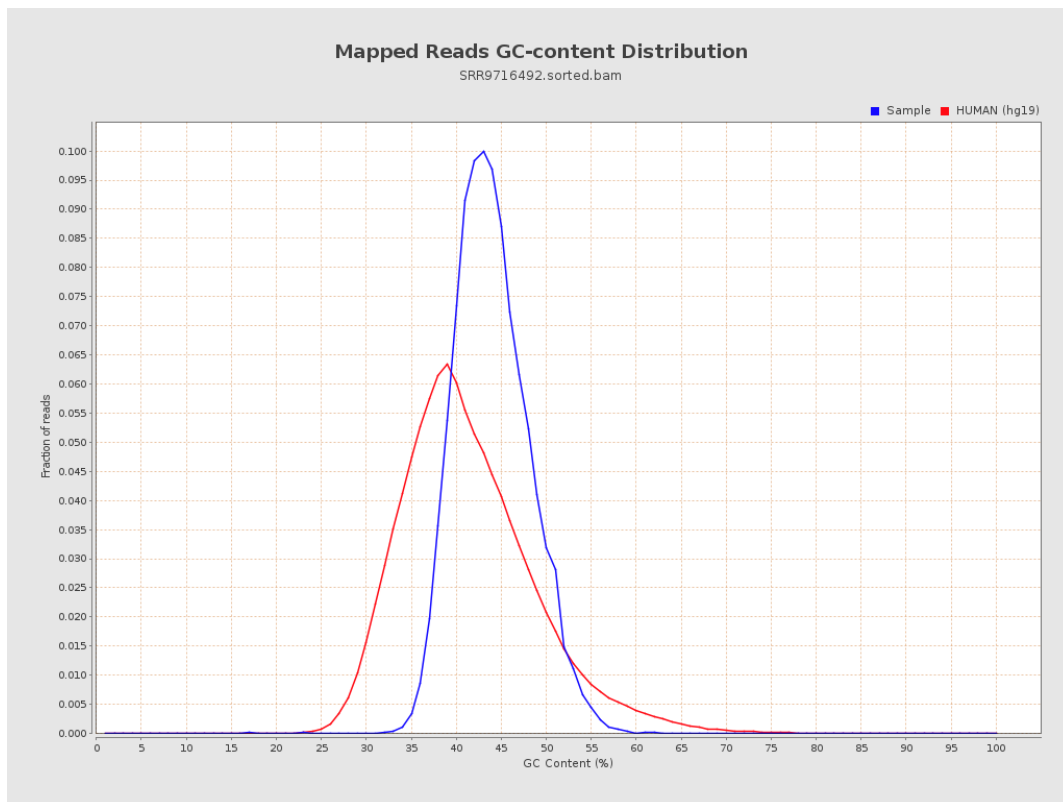
7. Results : Duplication Rate Histogram



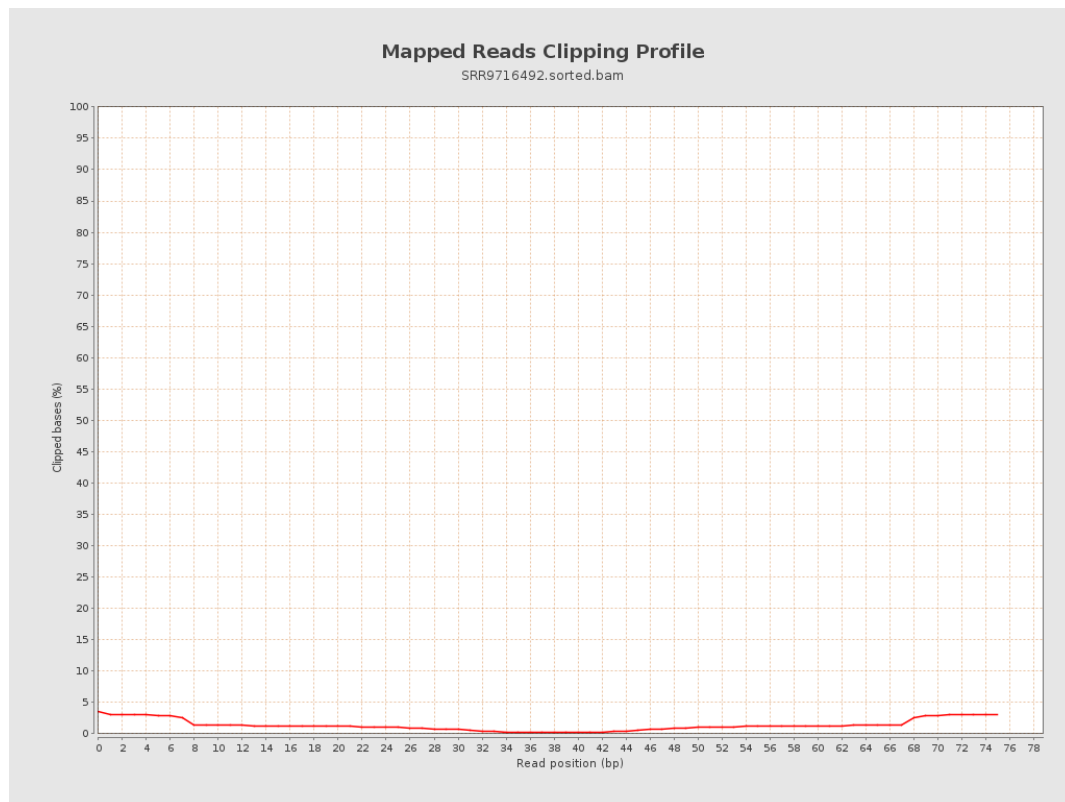
8. Results : Mapped Reads Nucleotide Content



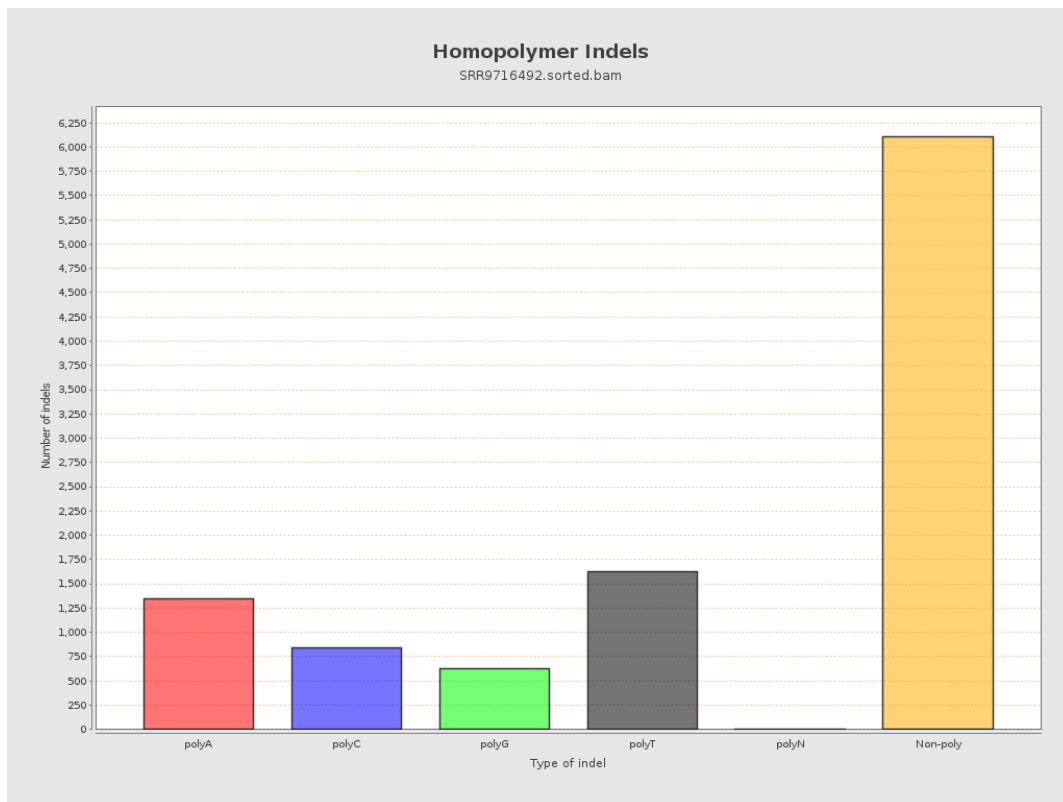
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

