

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:11:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716170.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_SRR9716170 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716170.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:11:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716170.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	448,158
Mapped reads	418,574 / 93.4%
Unmapped reads	29,584 / 6.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,008 / 1.79%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	6,866 / 1.53%
Duplication rate	1.19%
Clipped reads	425,499 / 94.94%

2.2. ACGT Content

Number/percentage of A's	8,806,488 / 26.35%
Number/percentage of C's	6,553,545 / 19.61%
Number/percentage of T's	9,888,563 / 29.59%
Number/percentage of G's	8,166,298 / 24.44%
Number/percentage of N's	2,356 / 0.01%
GC Percentage	44.05%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1293
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2.4. Mapping Quality

Mean Mapping Quality	47.91
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2.5. Mismatches and indels

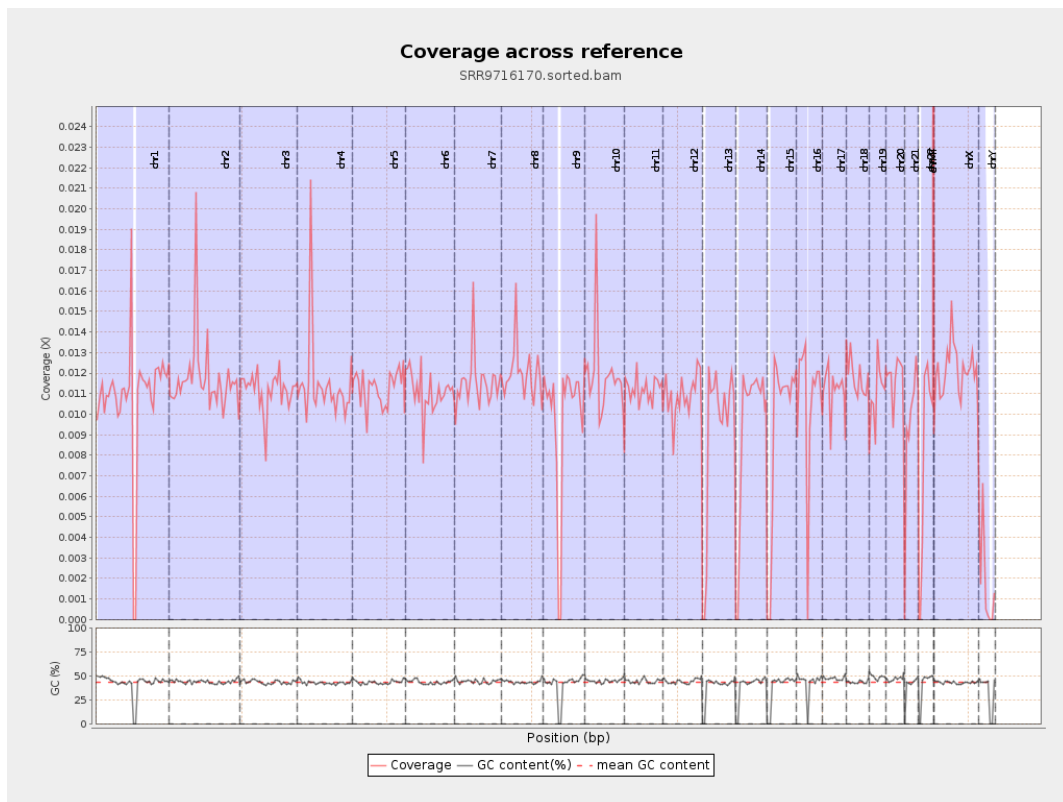
General error rate	0.66%
Mismatches	212,480
Insertions	2,927
Mapped reads with at least one insertion	0.69%
Deletions	8,126
Mapped reads with at least one deletion	1.91%
Homopolymer indels	42.83%

2.6. Chromosome stats

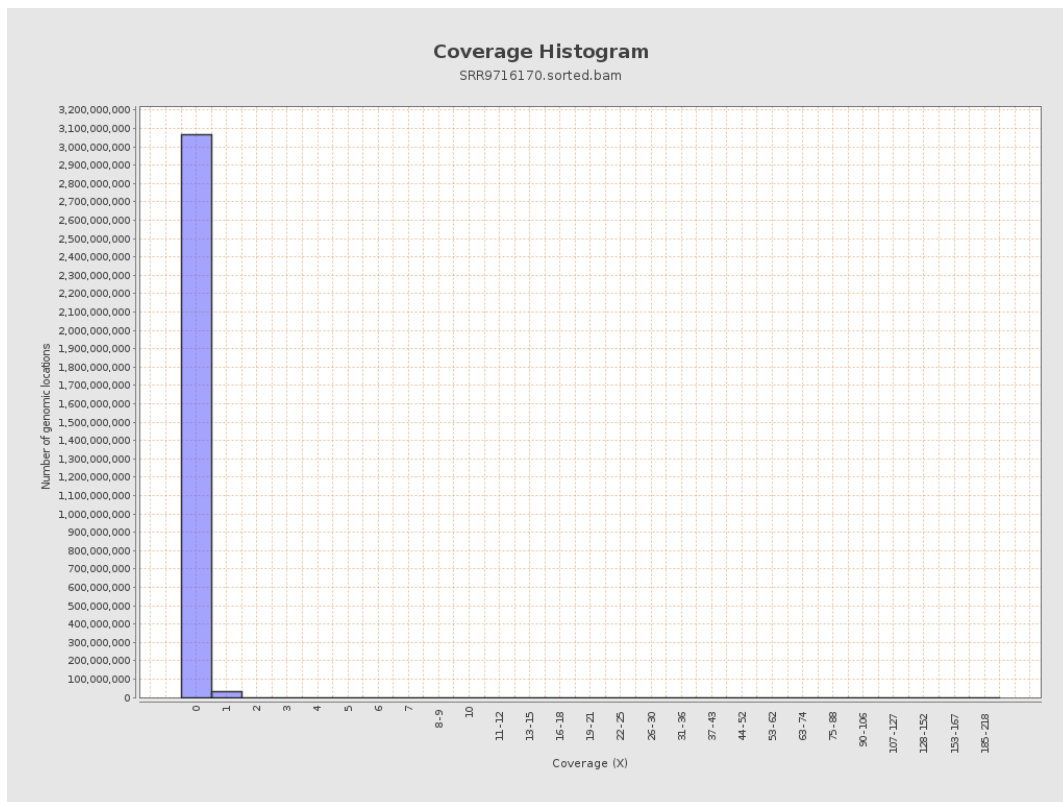
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2685106	0.0108	0.1997
chr2	243199373	2850108	0.0117	0.1387
chr3	198022430	2205343	0.0111	0.1087
chr4	191154276	2176517	0.0114	0.1198
chr5	180915260	2039029	0.0113	0.1099
chr6	171115067	1896068	0.0111	0.1122
chr7	159138663	1842106	0.0116	0.1495

chr8	146364022	1748490	0.0119	0.1427
chr9	141213431	1366463	0.0097	0.1197
chr10	135534747	1606678	0.0119	0.1351
chr11	135006516	1506786	0.0112	0.1218
chr12	133851895	1456085	0.0109	0.1078
chr13	115169878	1048662	0.0091	0.0983
chr14	107349540	1007879	0.0094	0.1016
chr15	102531392	968877	0.0094	0.1003
chr16	90354753	967605	0.0107	0.1101
chr17	81195210	900523	0.0111	0.1138
chr18	78077248	921847	0.0118	0.1642
chr19	59128983	653124	0.011	0.154
chr20	63025520	734942	0.0117	0.1126
chr21	48129895	460013	0.0096	0.105
chr22	51304566	406515	0.0079	0.0928
chrMT	16571	2003	0.1209	0.3545
chrX	155270560	1881683	0.0121	0.1184
chrY	59373566	100354	0.0017	0.0657

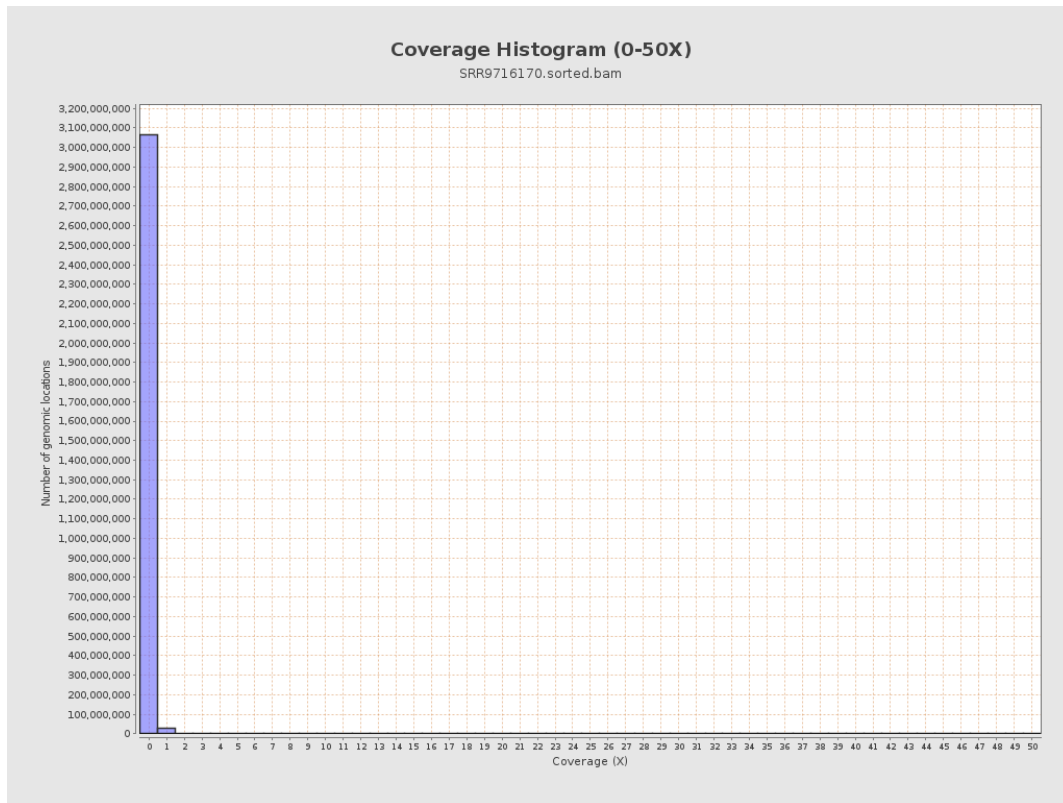
3. Results : Coverage across reference



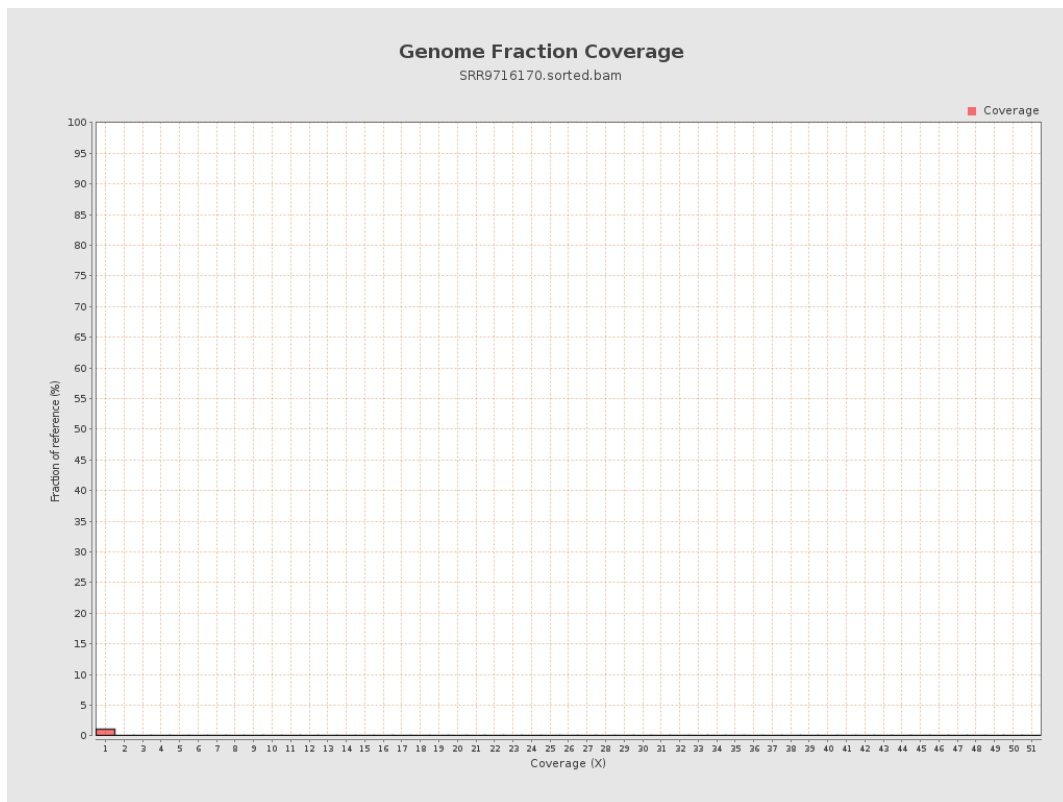
4. Results : Coverage Histogram



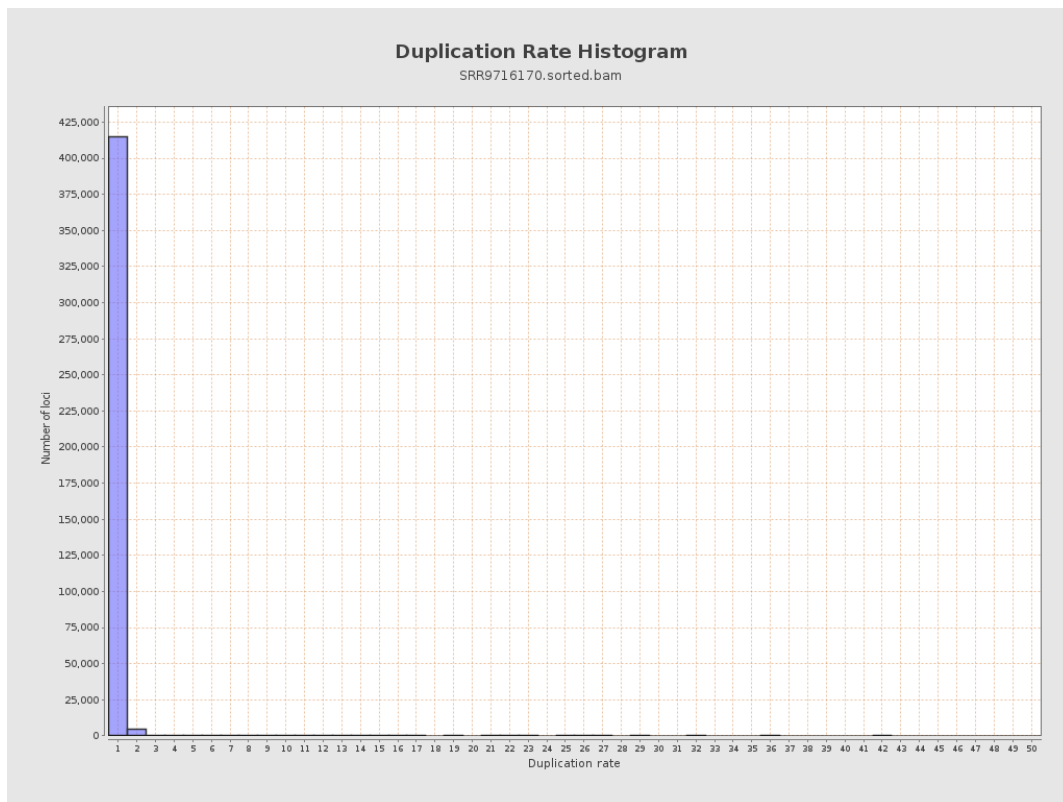
5. Results : Coverage Histogram (0-50X)



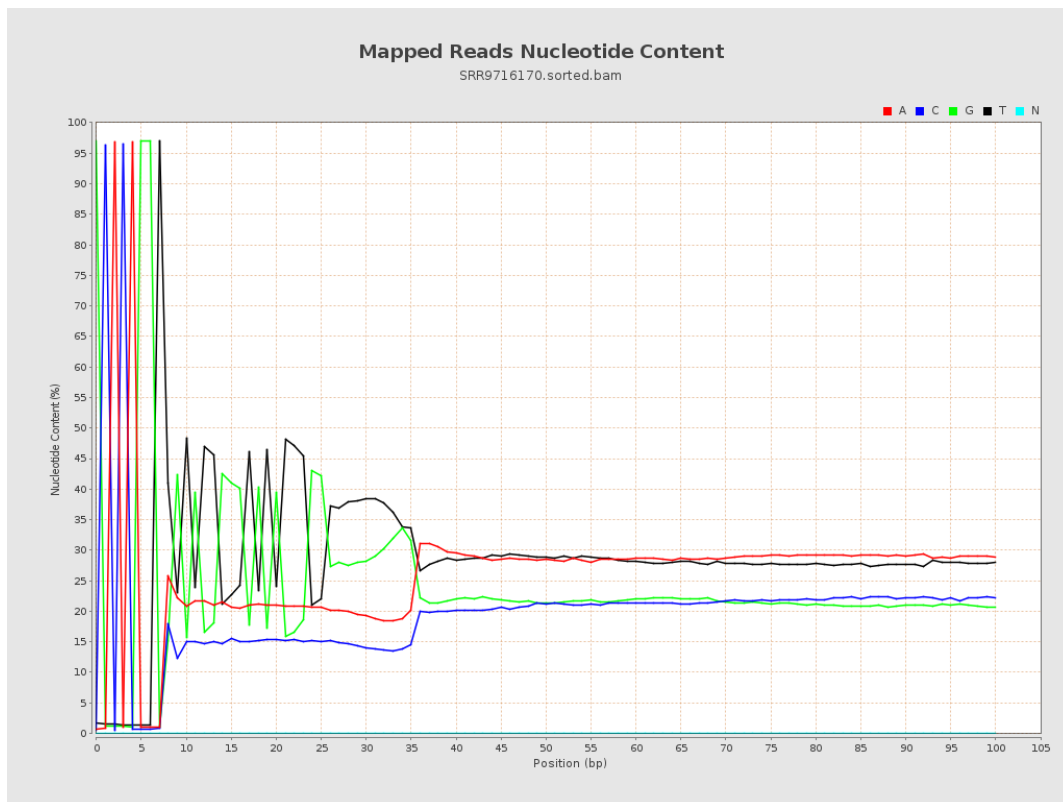
6. Results : Genome Fraction Coverage



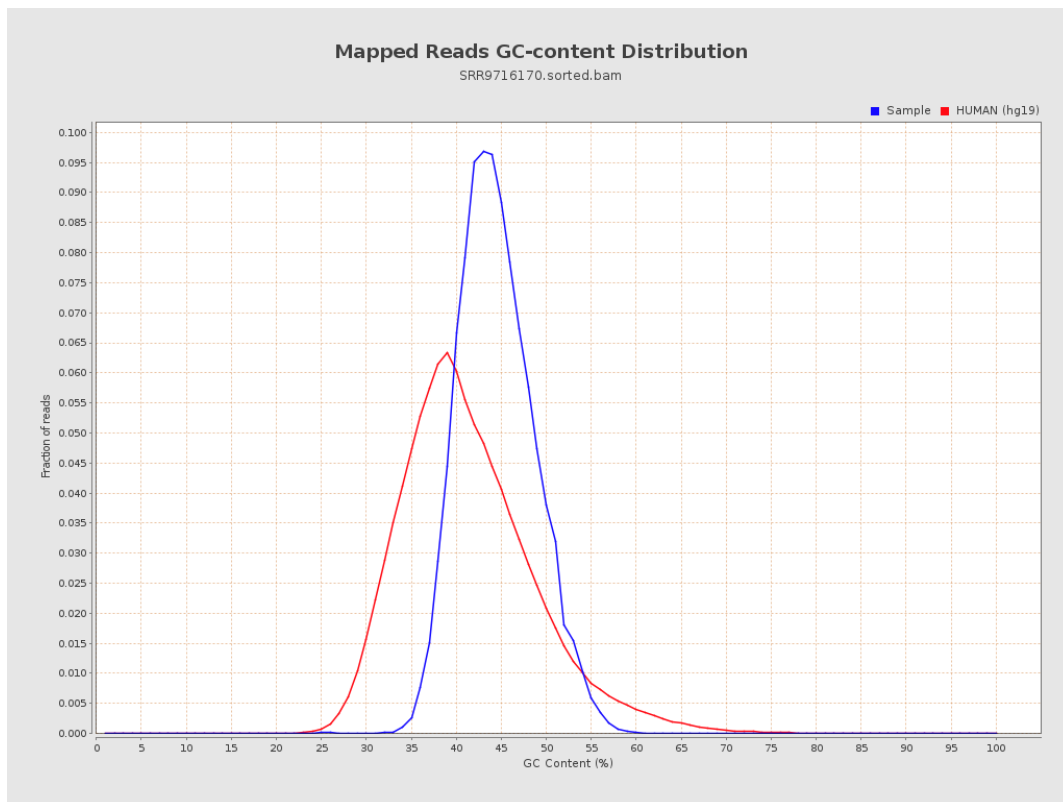
7. Results : Duplication Rate Histogram



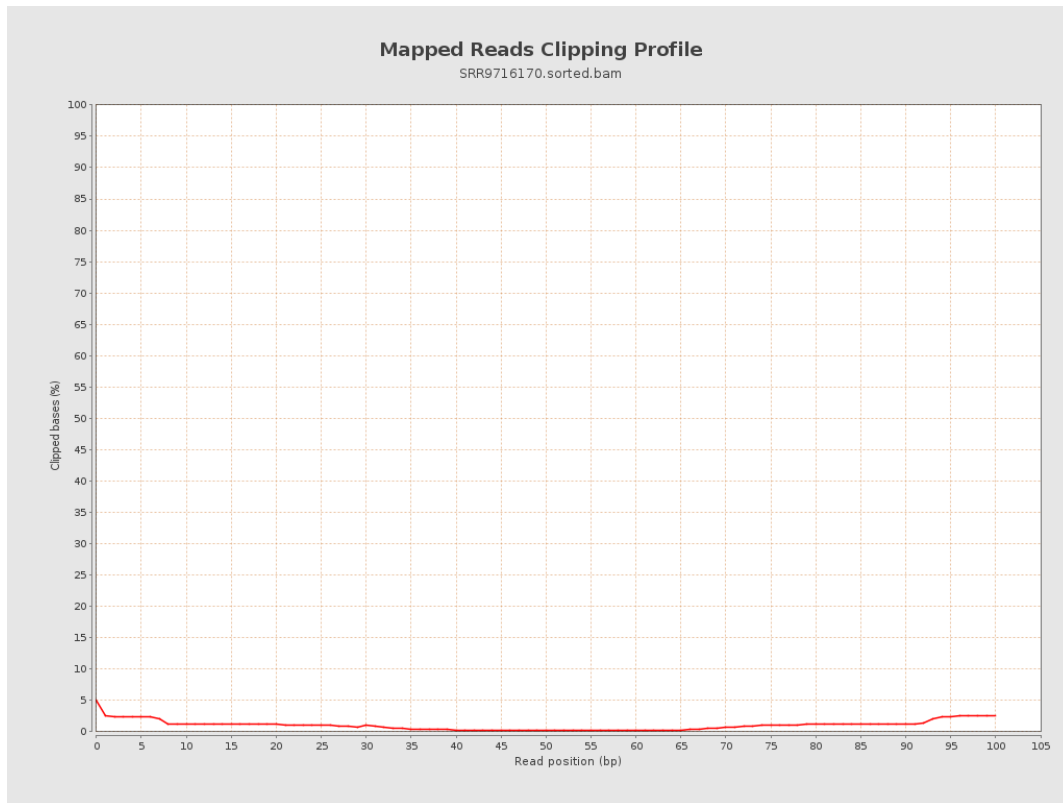
8. Results : Mapped Reads Nucleotide Content



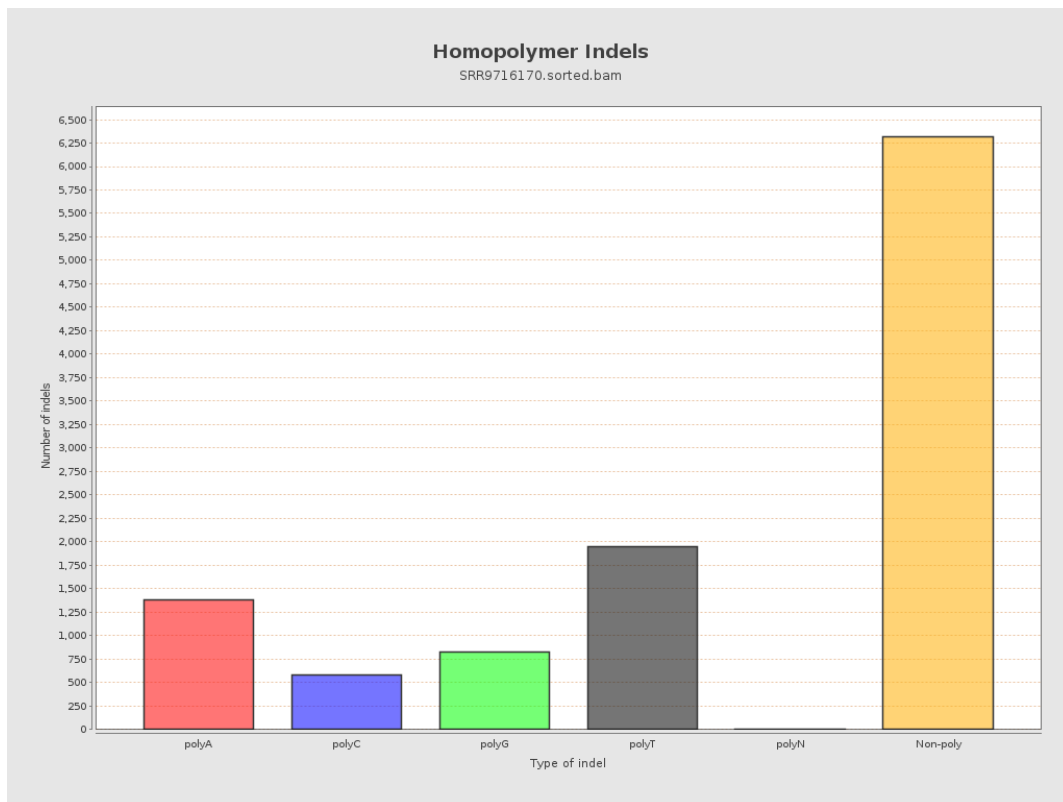
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

