

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:53:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716801.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_SRR9716801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:53:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	865,518
Mapped reads	780,210 / 90.14%
Unmapped reads	85,308 / 9.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,835 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	18,656 / 2.16%
Duplication rate	1.87%
Clipped reads	781,552 / 90.3%

2.2. ACGT Content

Number/percentage of A's	11,788,959 / 25.76%
Number/percentage of C's	8,898,378 / 19.44%
Number/percentage of T's	13,638,984 / 29.8%
Number/percentage of G's	11,438,493 / 24.99%
Number/percentage of N's	596 / 0%
GC Percentage	44.44%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1567
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2.4. Mapping Quality

Mean Mapping Quality	45.07
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2.5. Mismatches and indels

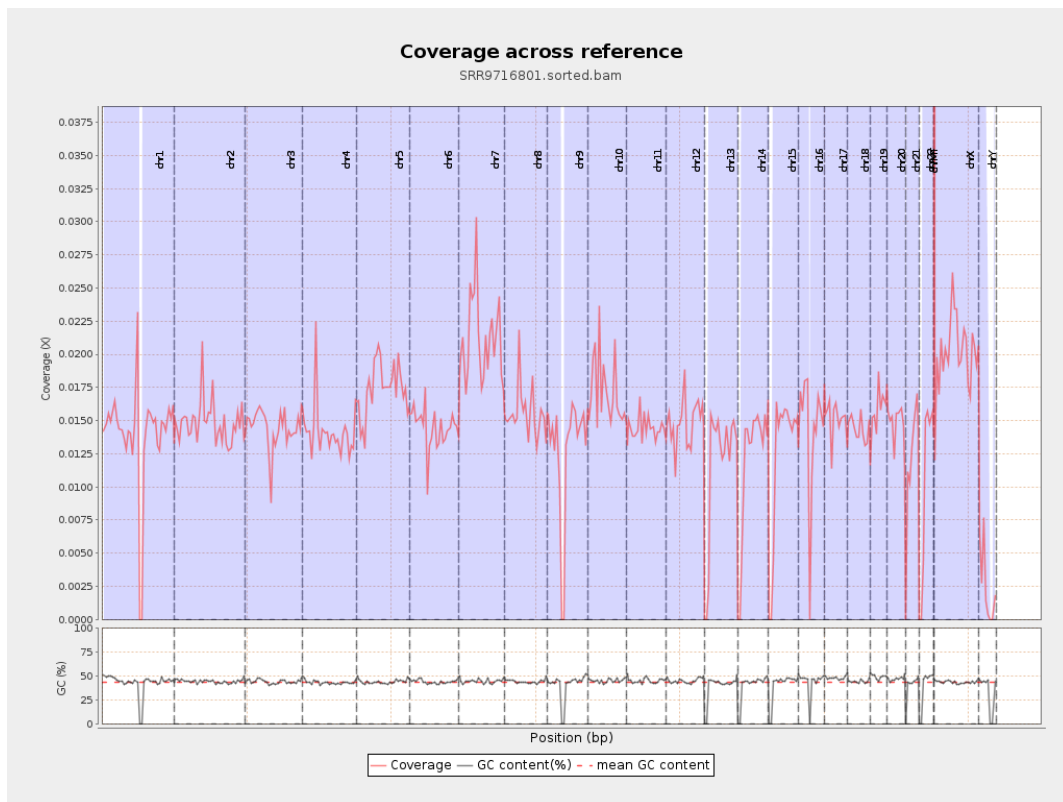
General error rate	0.51%
Mismatches	225,292
Insertions	3,264
Mapped reads with at least one insertion	0.42%
Deletions	8,243
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.37%

2.6. Chromosome stats

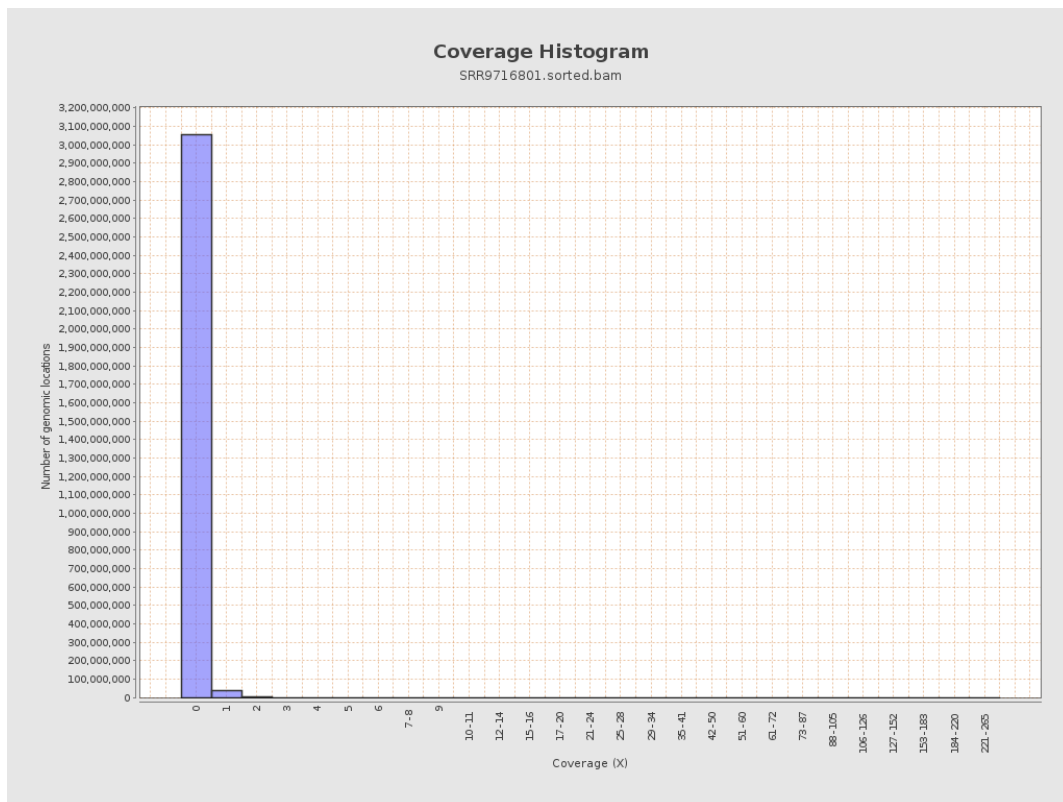
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3476350	0.0139	0.243
chr2	243199373	3613129	0.0149	0.174
chr3	198022430	2855337	0.0144	0.1263
chr4	191154276	2715504	0.0142	0.1313
chr5	180915260	3161664	0.0175	0.1397
chr6	171115067	2475894	0.0145	0.1368
chr7	159138663	3379532	0.0212	0.2254

chr8	146364022	2277545	0.0156	0.1486
chr9	141213431	1787243	0.0127	0.1335
chr10	135534747	2326665	0.0172	0.1581
chr11	135006516	1953535	0.0145	0.1434
chr12	133851895	1977468	0.0148	0.1289
chr13	115169878	1338919	0.0116	0.1134
chr14	107349540	1278328	0.0119	0.1166
chr15	102531392	1259126	0.0123	0.1175
chr16	90354753	1278871	0.0142	0.1285
chr17	81195210	1224509	0.0151	0.1329
chr18	78077248	1122214	0.0144	0.1906
chr19	59128983	939330	0.0159	0.1823
chr20	63025520	930903	0.0148	0.1298
chr21	48129895	583697	0.0121	0.121
chr22	51304566	537295	0.0105	0.1076
chrMT	16571	7387	0.4458	0.8151
chrX	155270560	3135946	0.0202	0.1556
chrY	59373566	142124	0.0024	0.0731

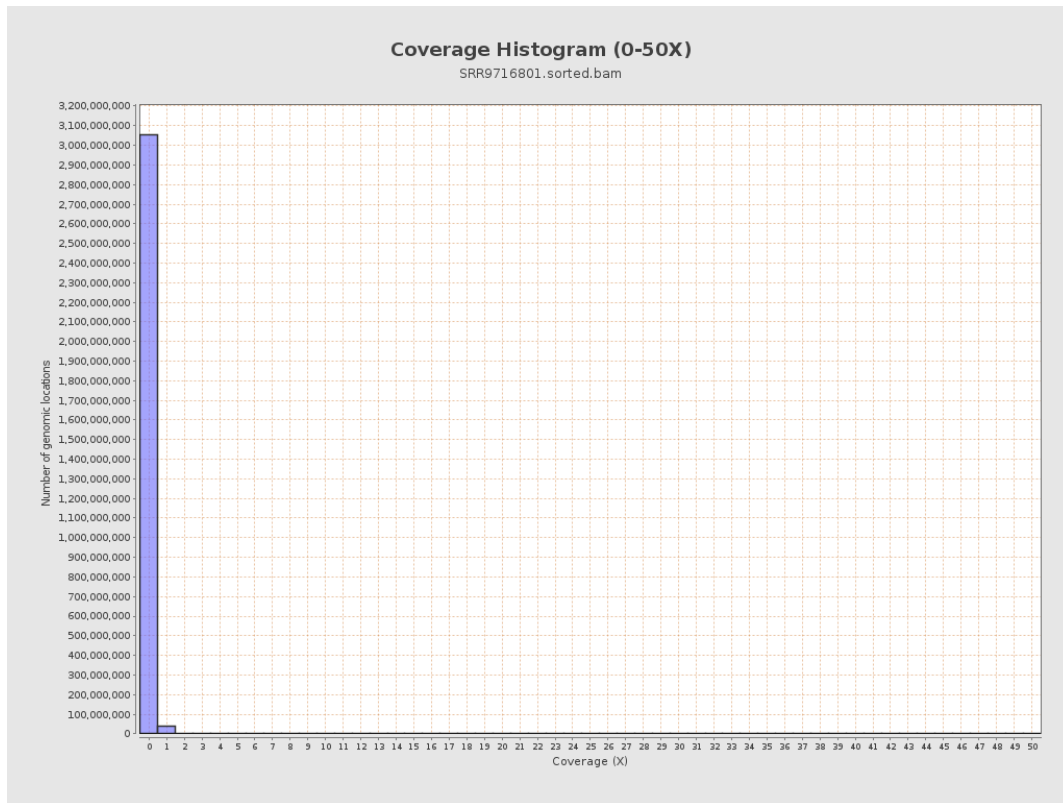
3. Results : Coverage across reference



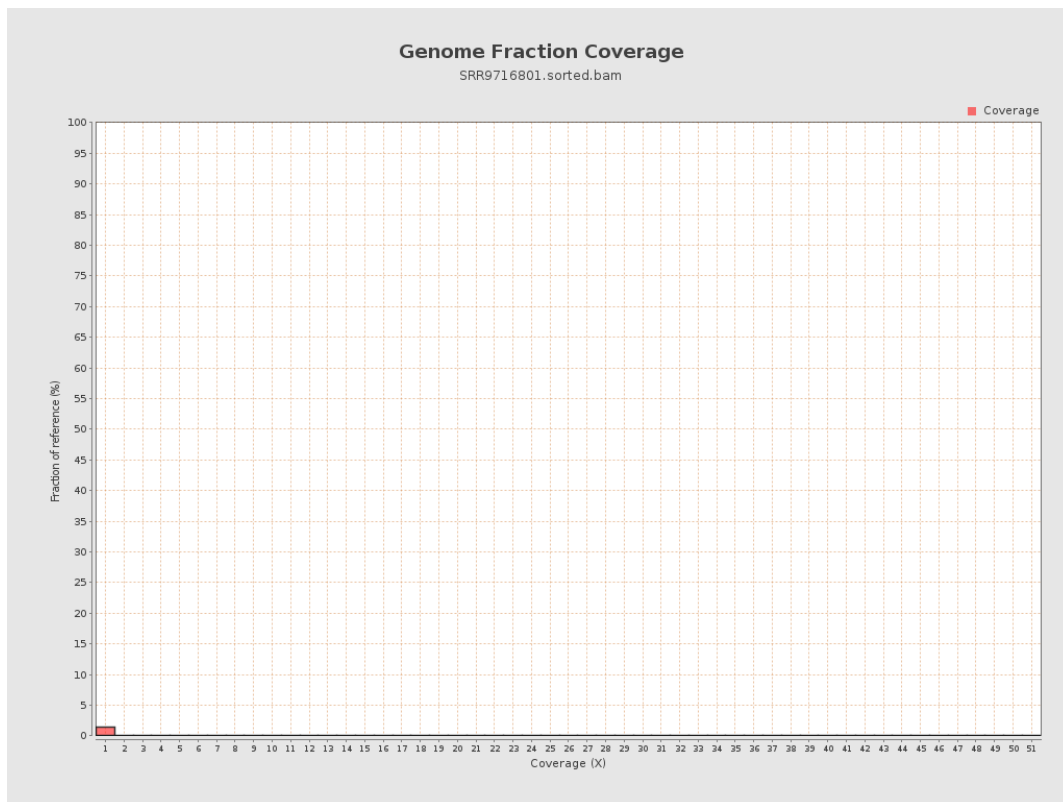
4. Results : Coverage Histogram



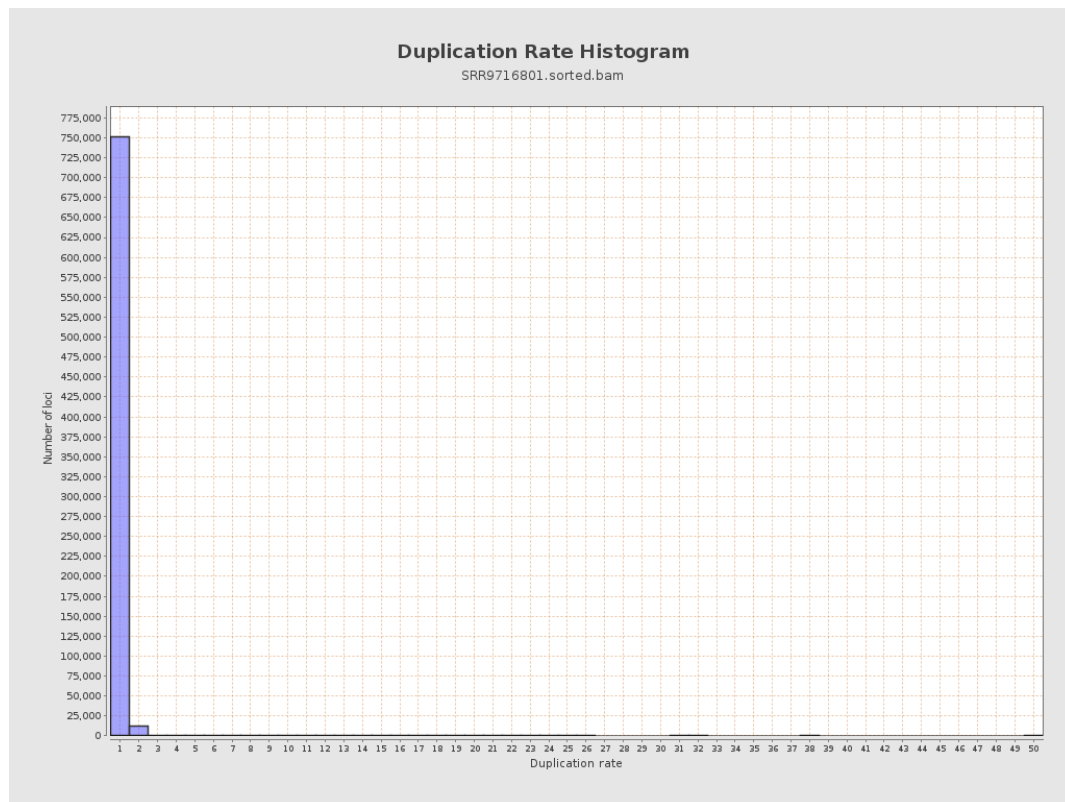
5. Results : Coverage Histogram (0-50X)



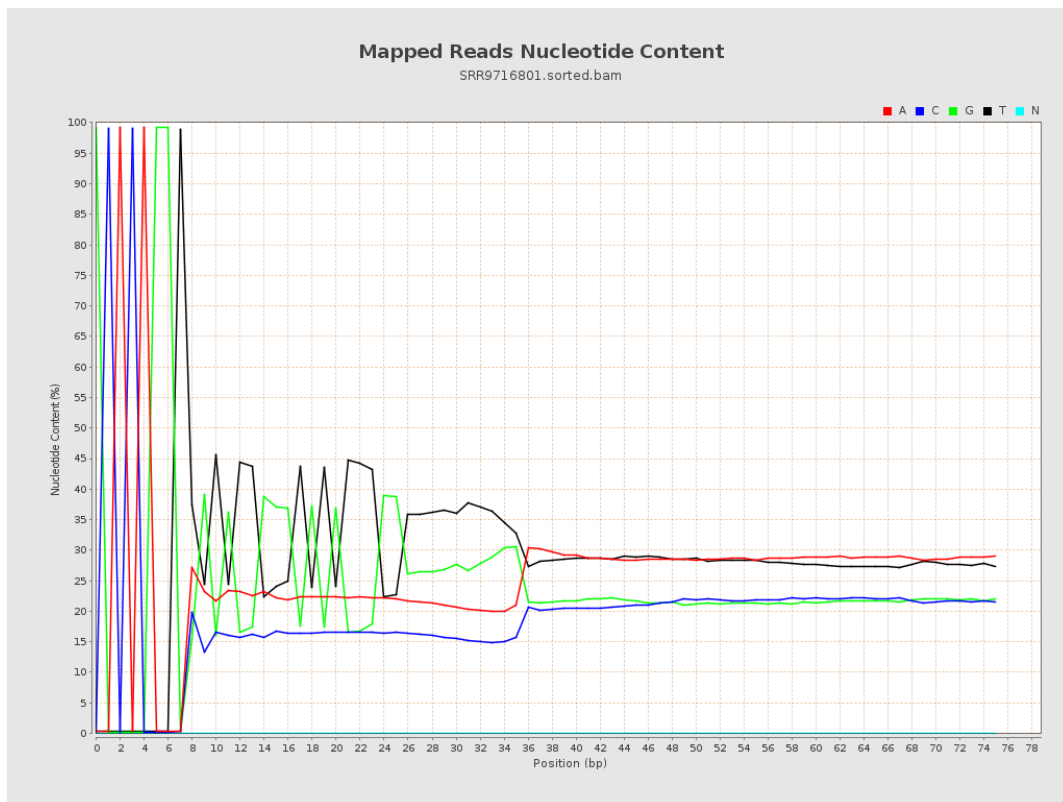
6. Results : Genome Fraction Coverage



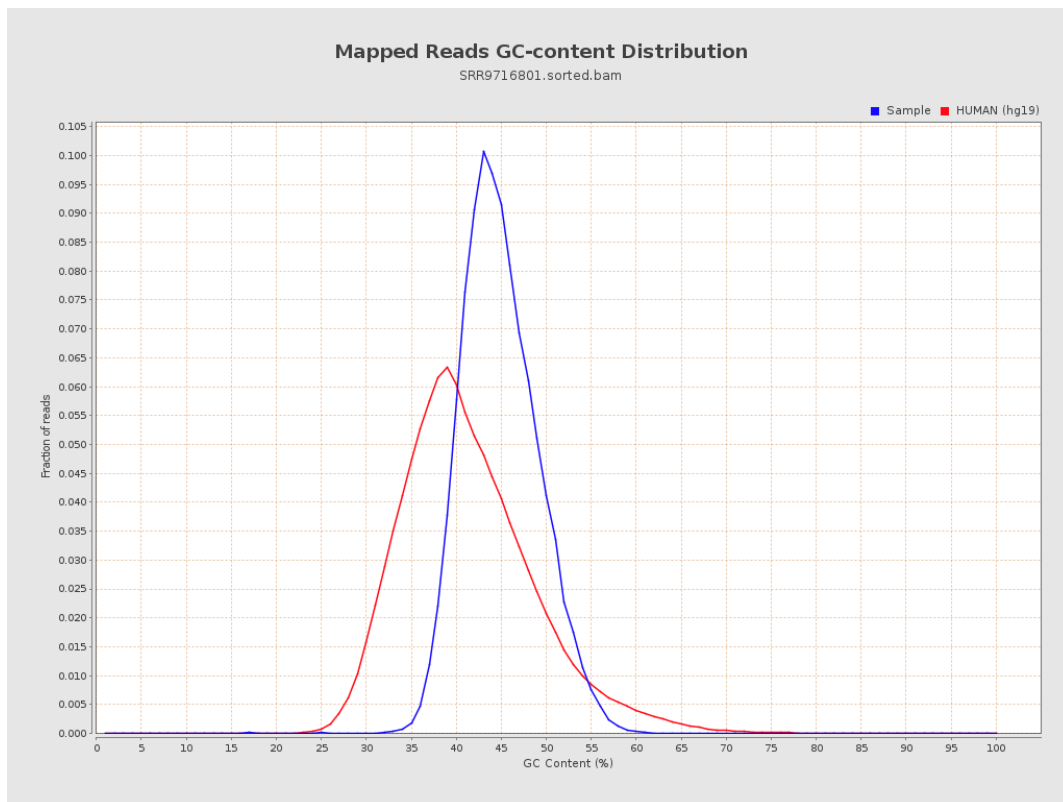
7. Results : Duplication Rate Histogram



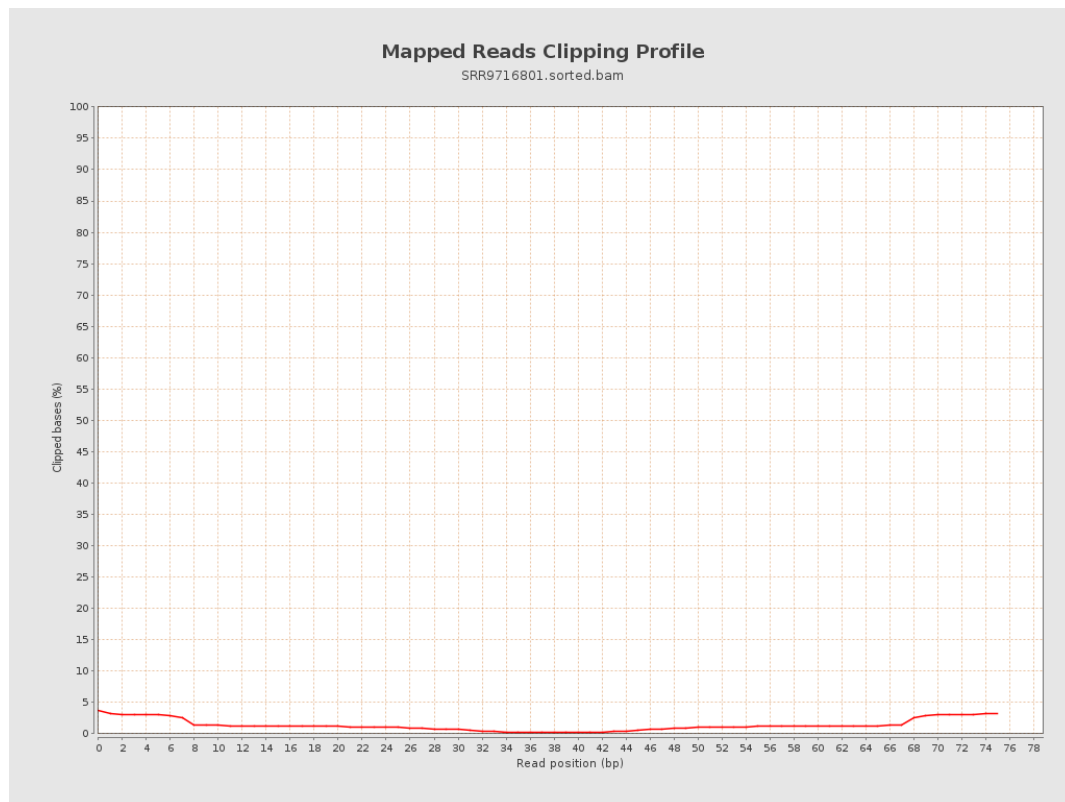
8. Results : Mapped Reads Nucleotide Content



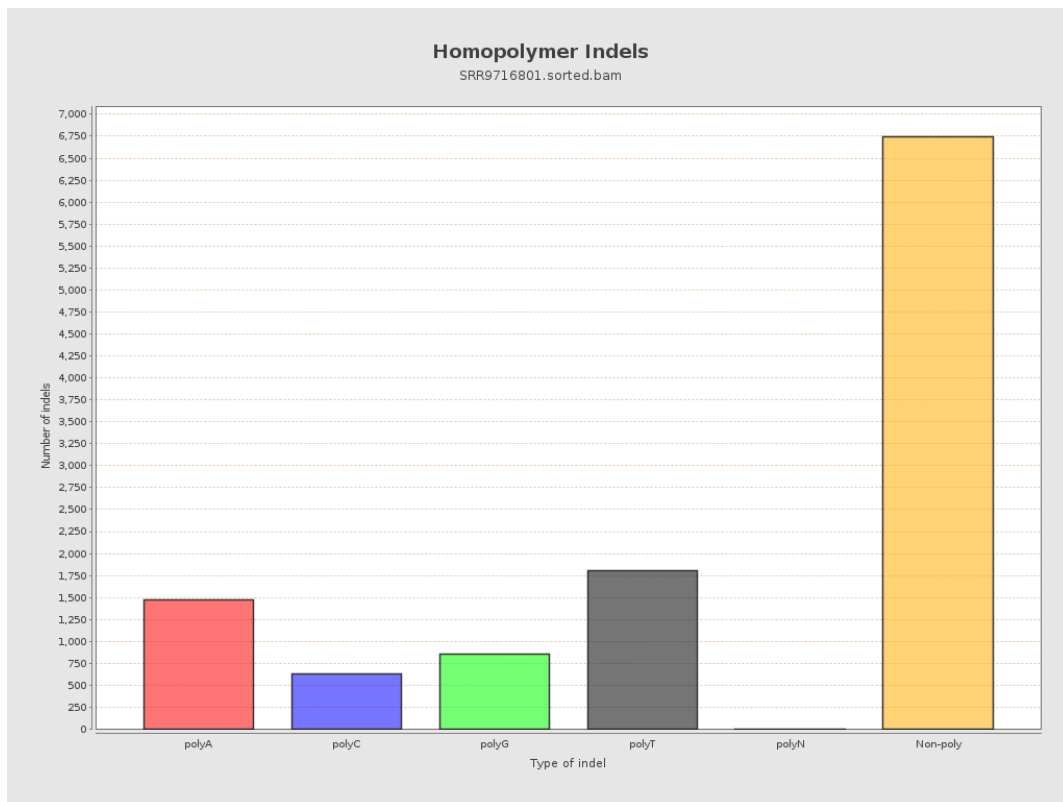
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

