Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:31:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716611.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_SRR9716611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716611.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:31:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	798,444
Mapped reads	660,664 / 82.74%
Unmapped reads	137,780 / 17.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,759 / 2.35%
Read min/max/mean length	30 / 101 / 101.85
Duplicated reads (estimated)	10,310 / 1.29%
Duplication rate	1.01%
Clipped reads	678,194 / 84.94%

2.2. ACGT Content

Number/percentage of A's	13,224,075 / 26.14%
Number/percentage of C's	10,075,385 / 19.92%
Number/percentage of T's	14,991,654 / 29.64%
Number/percentage of G's	12,282,542 / 24.28%
Number/percentage of N's	6,648 / 0.01%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0163

Standard Deviation	0.1685

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

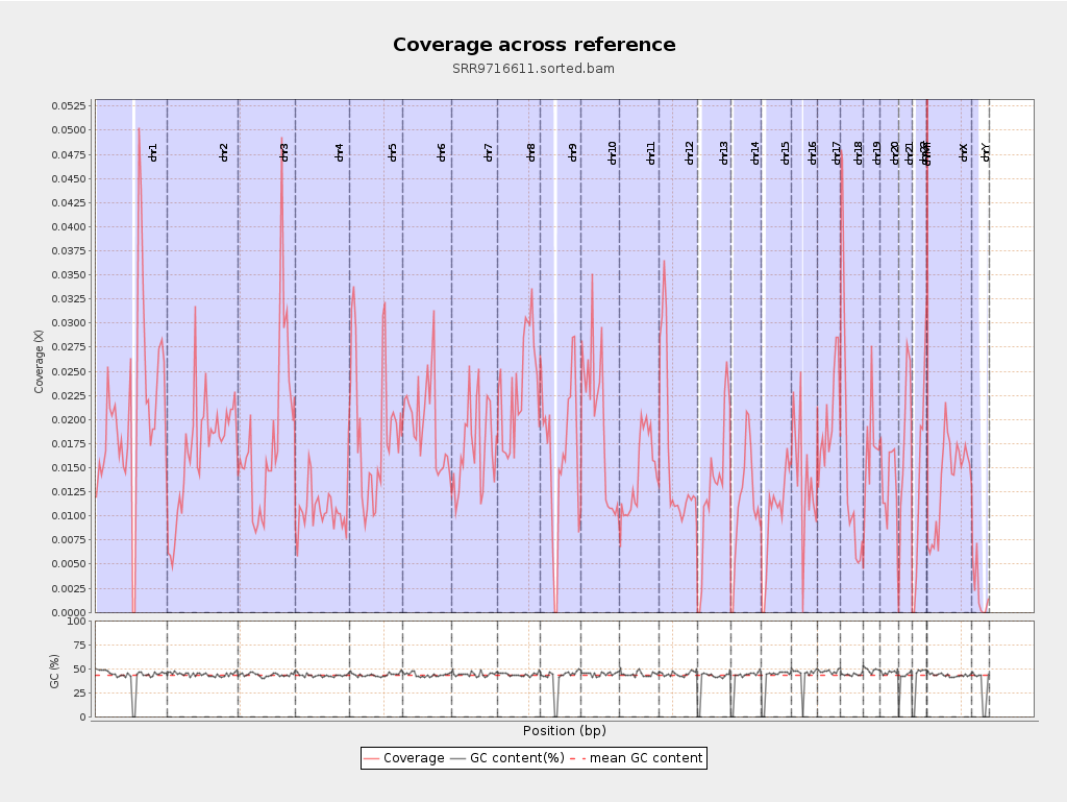
General error rate	0.75%
Mismatches	370,456
Insertions	4,253
Mapped reads with at least one insertion	0.64%
Deletions	10,696
Mapped reads with at least one deletion	1.6%
Homopolymer indels	40.85%

2.6. Chromosome stats

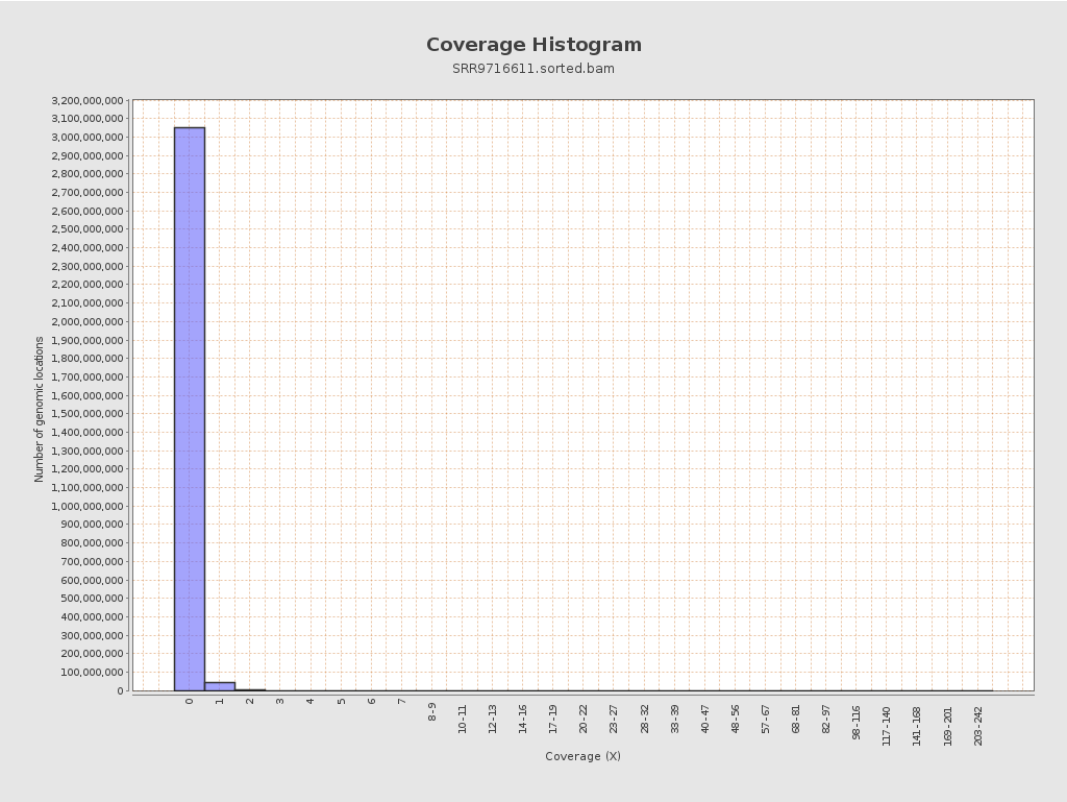
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5111598	0.0205	0.2428
chr2	243199373	4095424	0.0168	0.2178
chr3	198022430	3630193	0.0183	0.1438
chr4	191154276	2057437	0.0108	0.1119
chr5	180915260	3429161	0.019	0.144
chr6	171115067	3357439	0.0196	0.1558
chr7	159138663	2751365	0.0173	0.2127

chr8	146364022	3431352	0.0234	0.2007
chr9	141213431	2354937	0.0167	0.16
chr10	135534747	2644385	0.0195	0.2049
chr11	135006516	1944907	0.0144	0.1477
chr12	133851895	2166010	0.0162	0.1336
chr13	115169878	1529271	0.0133	0.1199
chr14	107349540	1215846	0.0113	0.118
chr15	102531392	1040444	0.0101	0.105
chr16	90354753	1255233	0.0139	0.1282
chr17	81195210	1635513	0.0201	0.1594
chr18	78077248	1243581	0.0159	0.2151
chr19	59128983	1014927	0.0172	0.2009
chr20	63025520	837536	0.0133	0.122
chr21	48129895	869107	0.0181	0.1423
chr22	51304566	708323	0.0138	0.1243
chrMT	16571	3836	0.2315	0.5183
chrX	155270560	2150247	0.0138	0.1304
chrY	59373566	121361	0.002	0.0772

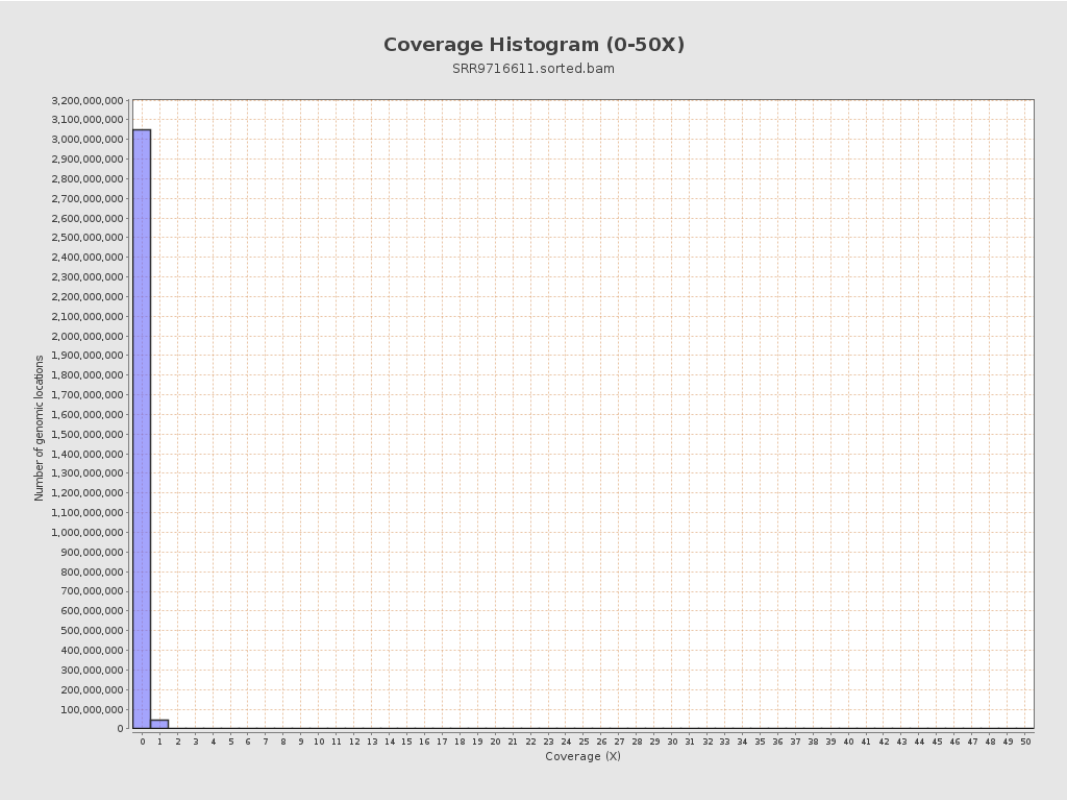
3. Results : Coverage across reference



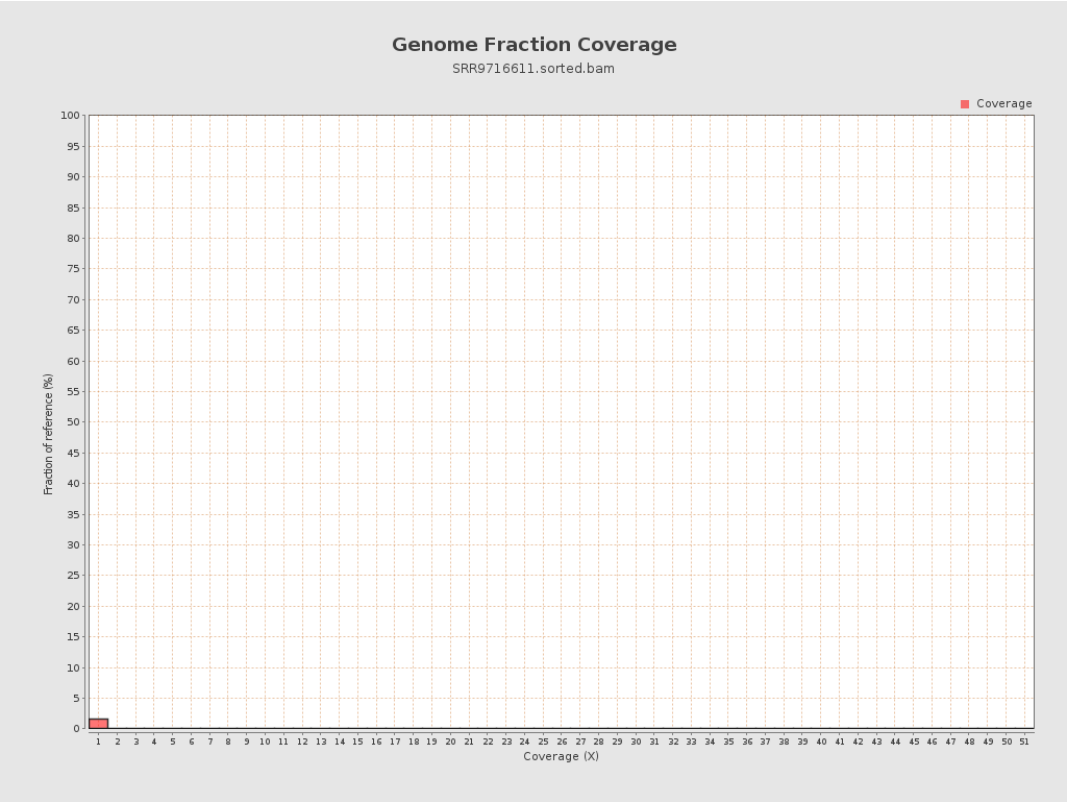
4. Results : Coverage Histogram



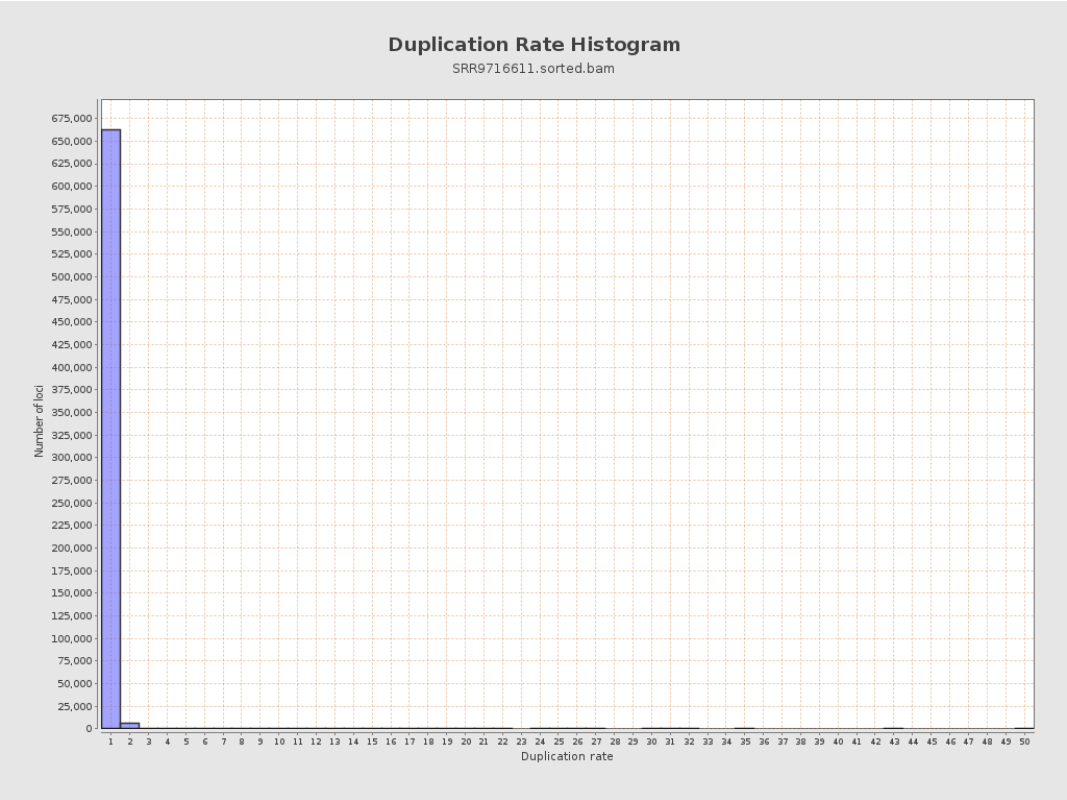
5. Results : Coverage Histogram (0-50X)



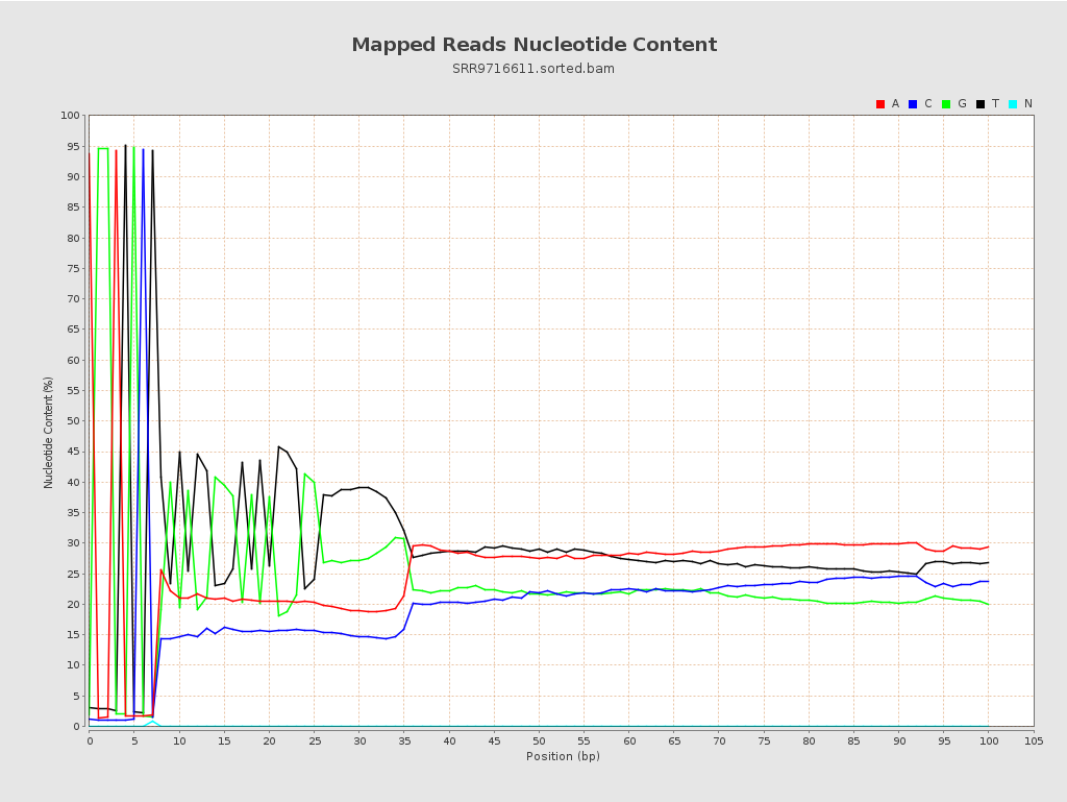
6. Results : Genome Fraction Coverage



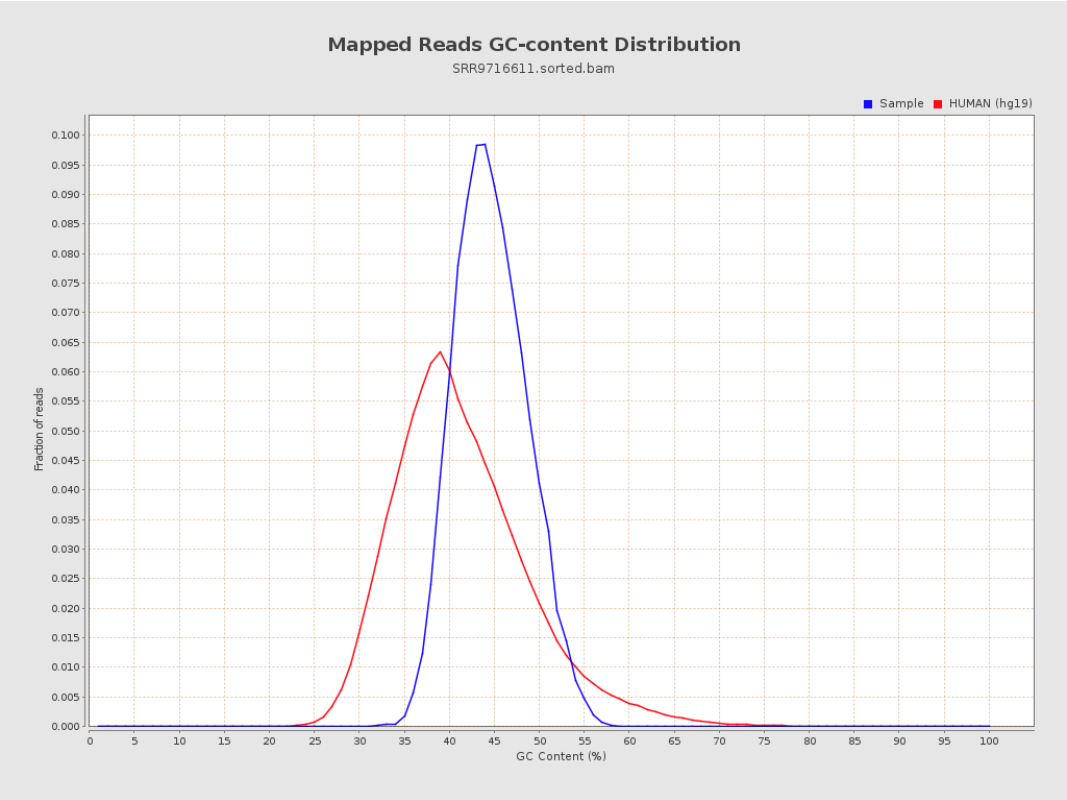
7. Results : Duplication Rate Histogram



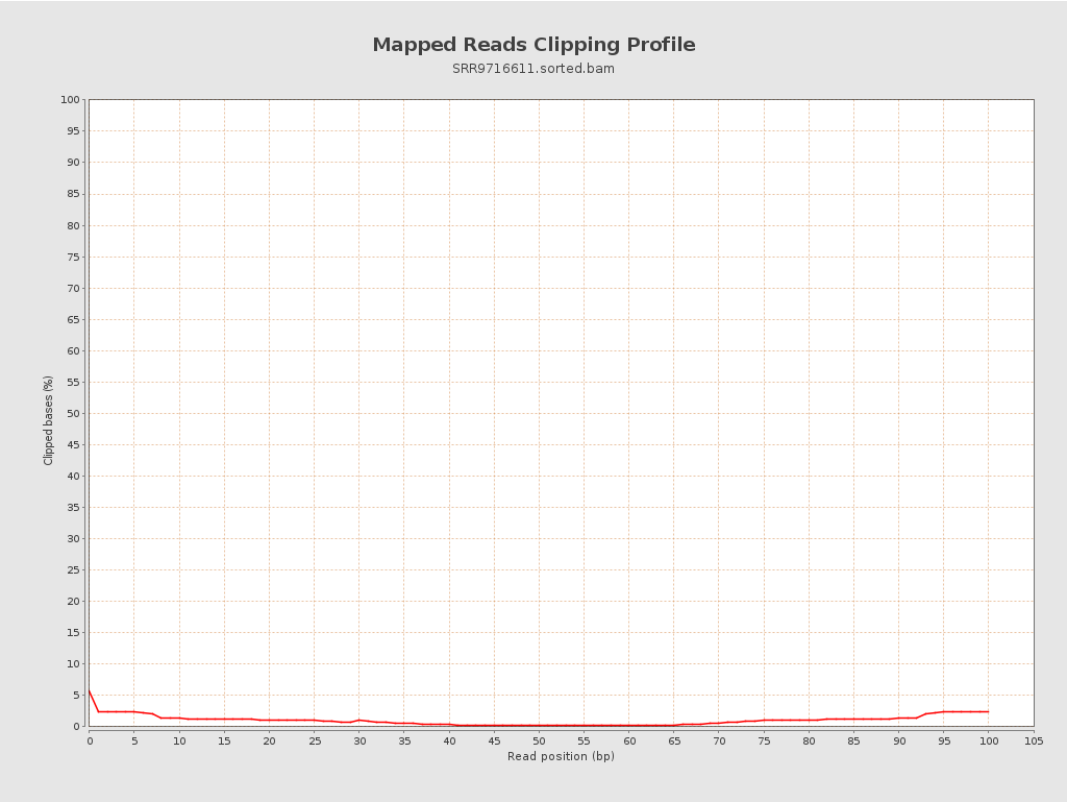
8. Results : Mapped Reads Nucleotide Content



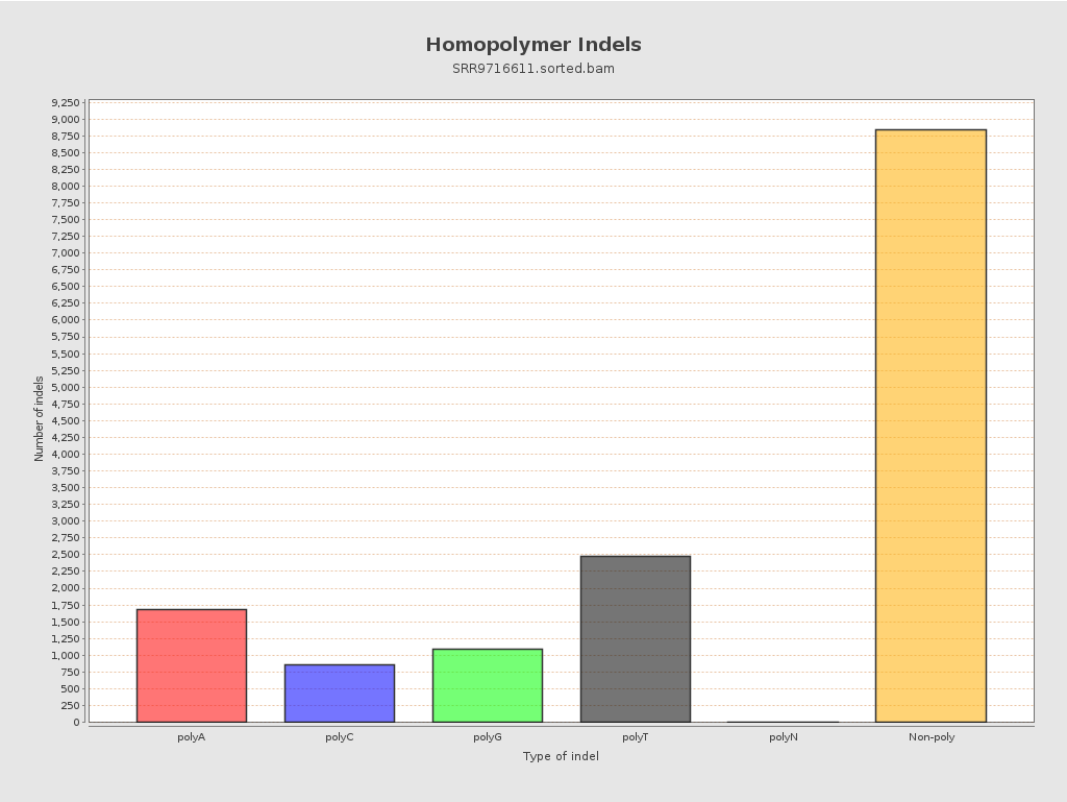
9. Results : Mapped Reads GC-content Distribution



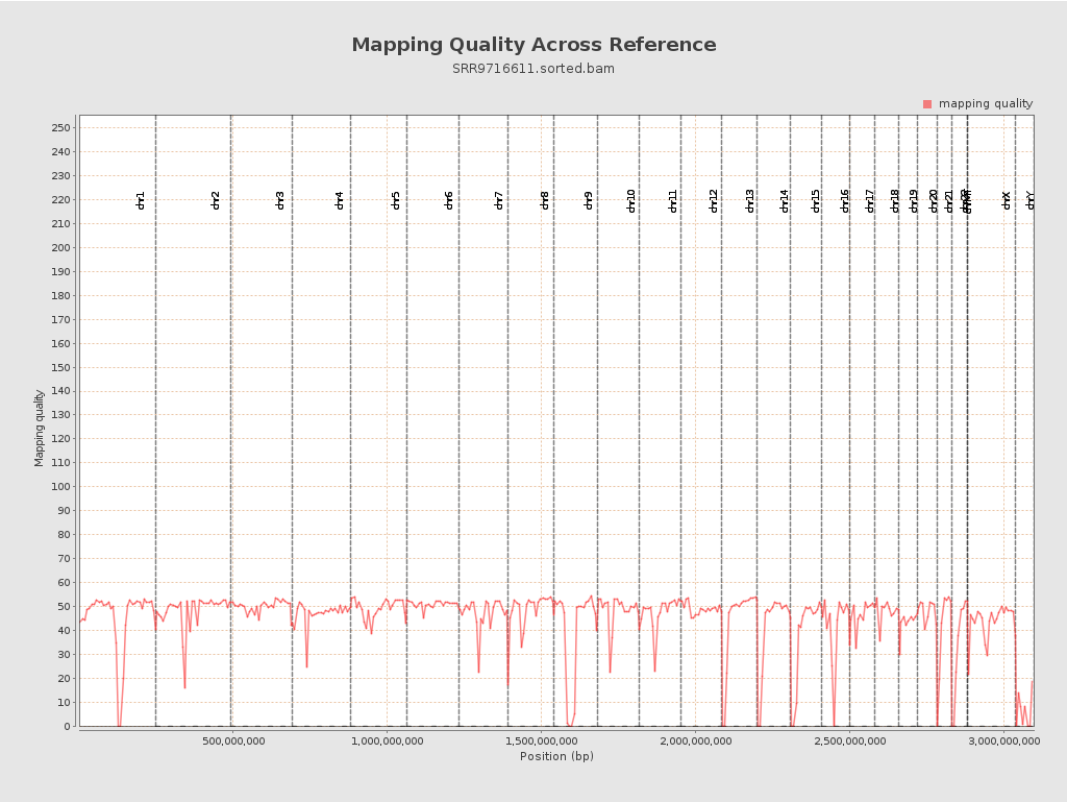
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram