Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:39:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716349.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_SRR9716349 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716349.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:39:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716349.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	628,803
Mapped reads	589,642 / 93.77%
Unmapped reads	39,161 / 6.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,745 / 1.87%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	12,074 / 1.92%
Duplication rate	1.47%
Clipped reads	600,536 / 95.5%

2.2. ACGT Content

Number/percentage of A's	11,991,076 / 25.59%
Number/percentage of C's	8,945,167 / 19.09%
Number/percentage of T's	14,094,550 / 30.08%
Number/percentage of G's	11,820,196 / 25.23%
Number/percentage of N's	3,231 / 0.01%
GC Percentage	44.32%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1627

2.4. Mapping Quality

Mean Mapping Quality	47.76

2.5. Mismatches and indels

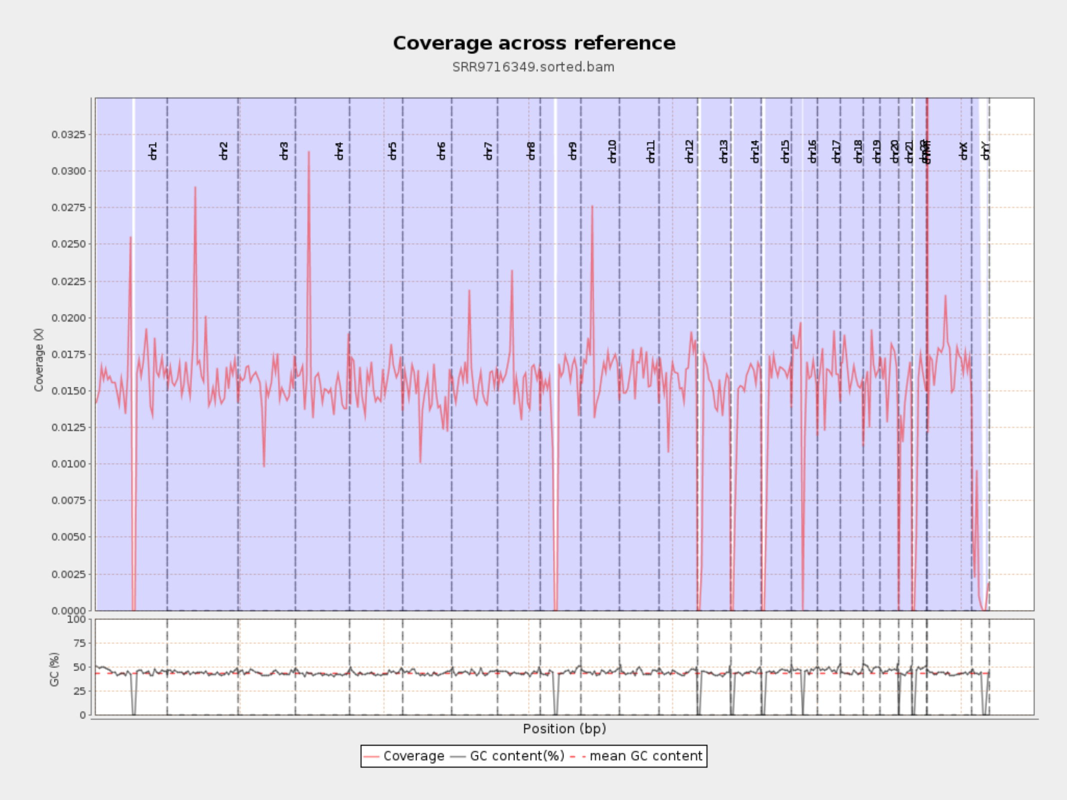
General error rate	0.66%
Mismatches	299,844
Insertions	3,954
Mapped reads with at least one insertion	0.66%
Deletions	11,793
Mapped reads with at least one deletion	1.97%
Homopolymer indels	42.81%

2.6. Chromosome stats

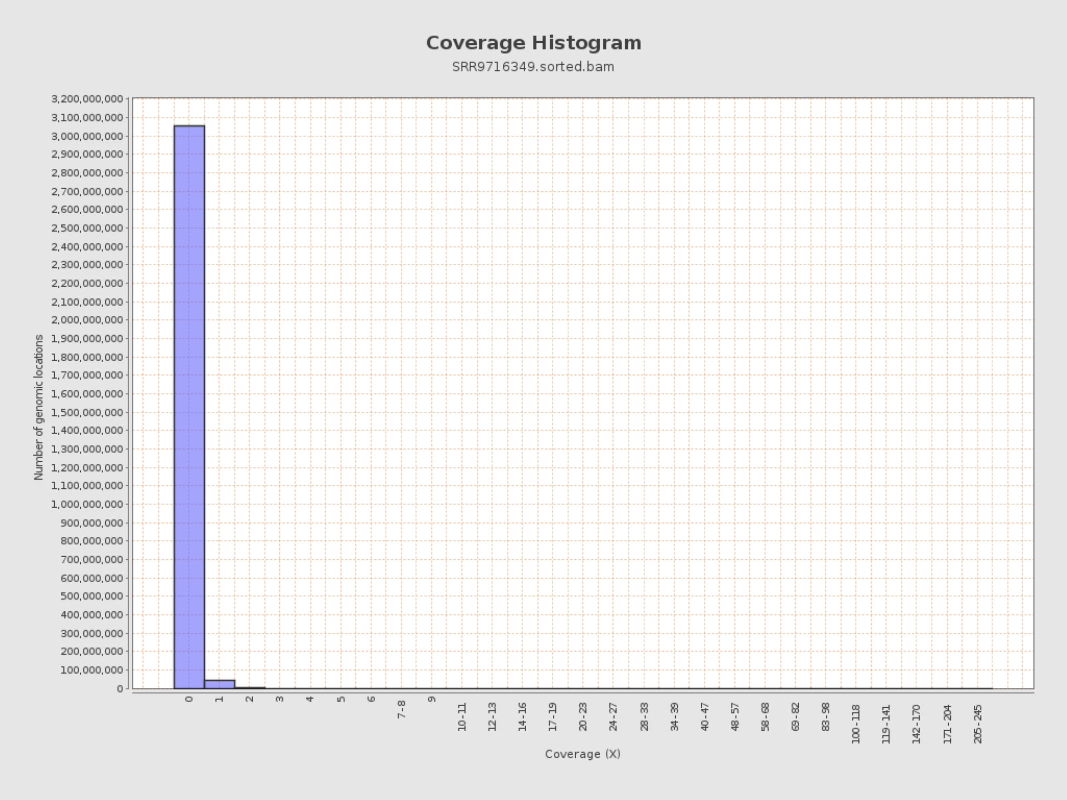
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3788396	0.0152	0.2498
chr2	243199373	3966116	0.0163	0.1823
chr3	198022430	3051747	0.0154	0.1291
chr4	191154276	3039292	0.0159	0.1481
chr5	180915260	2851460	0.0158	0.1314
chr6	171115067	2511264	0.0147	0.1306
chr7	159138663	2516008	0.0158	0.1938

chr8	146364022	2346359	0.016	0.1929
chr9	141213431	1977639	0.014	0.1517
chr10	135534747	2302104	0.017	0.1734
chr11	135006516	2192559	0.0162	0.1584
chr12	133851895	2145754	0.016	0.1324
chr13	115169878	1474794	0.0128	0.1178
chr14	107349540	1427379	0.0133	0.1242
chr15	102531392	1379007	0.0134	0.1211
chr16	90354753	1368148	0.0151	0.1323
chr17	81195210	1312255	0.0162	0.1409
chr18	78077248	1267856	0.0162	0.2221
chr19	59128983	940477	0.0159	0.185
chr20	63025520	1026561	0.0163	0.1368
chr21	48129895	627337	0.013	0.1298
chr22	51304566	571592	0.0111	0.1105
chrMT	16571	3557	0.2147	0.4601
chrX	155270560	2644870	0.017	0.1452
chrY	59373566	144391	0.0024	0.0954

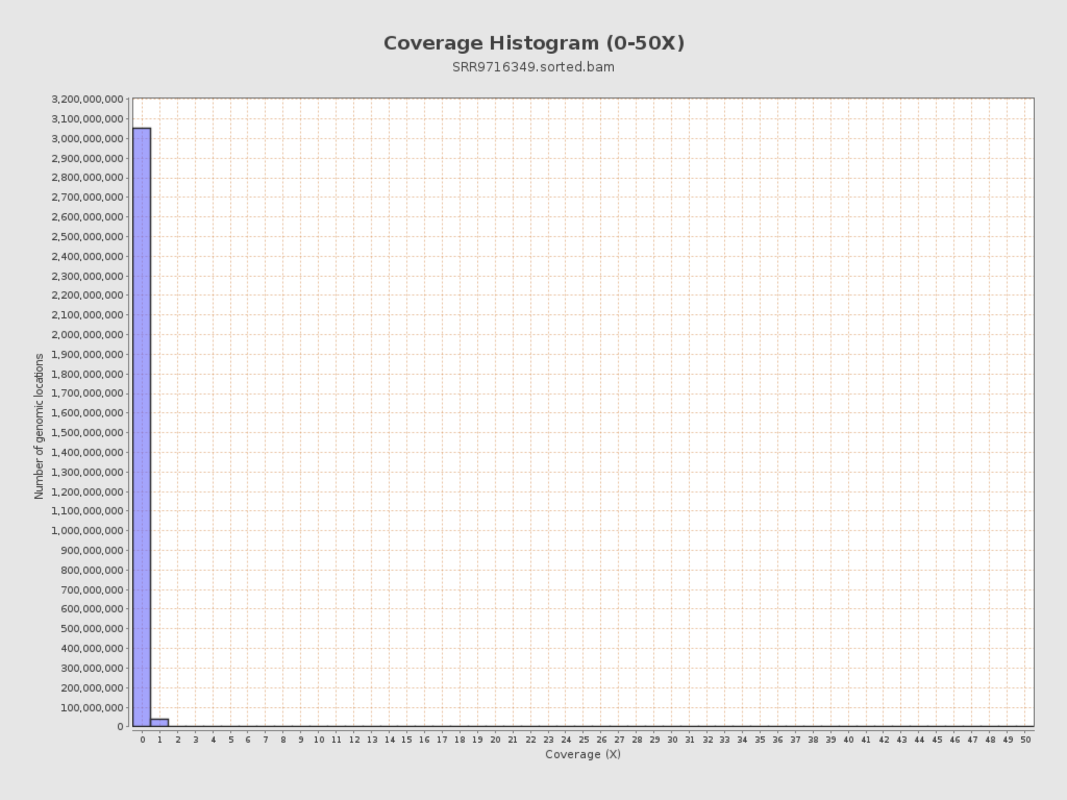
3. Results : Coverage across reference



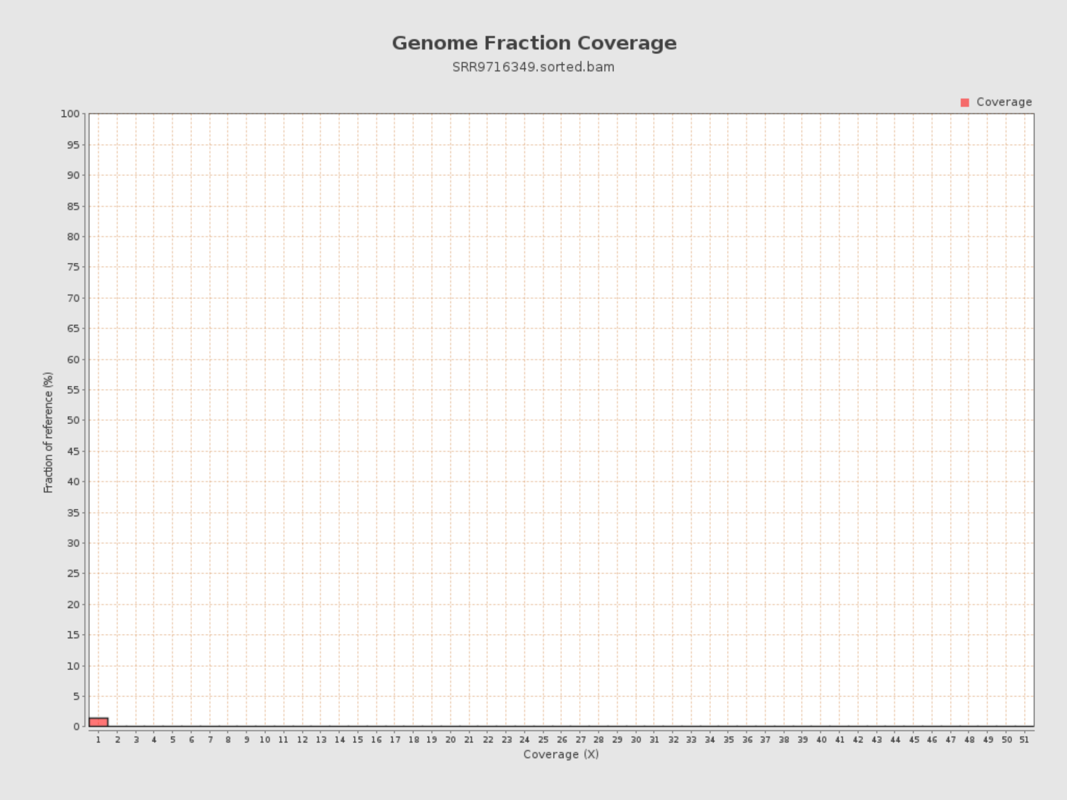
4. Results : Coverage Histogram



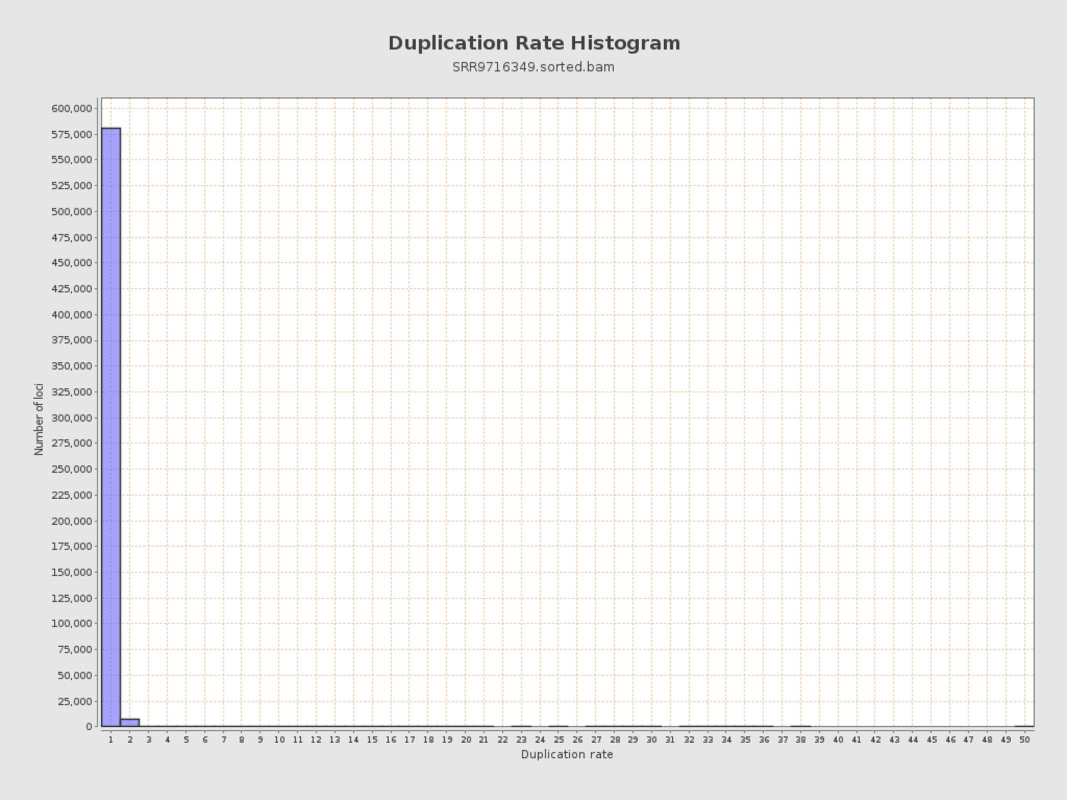
5. Results : Coverage Histogram (0-50X)



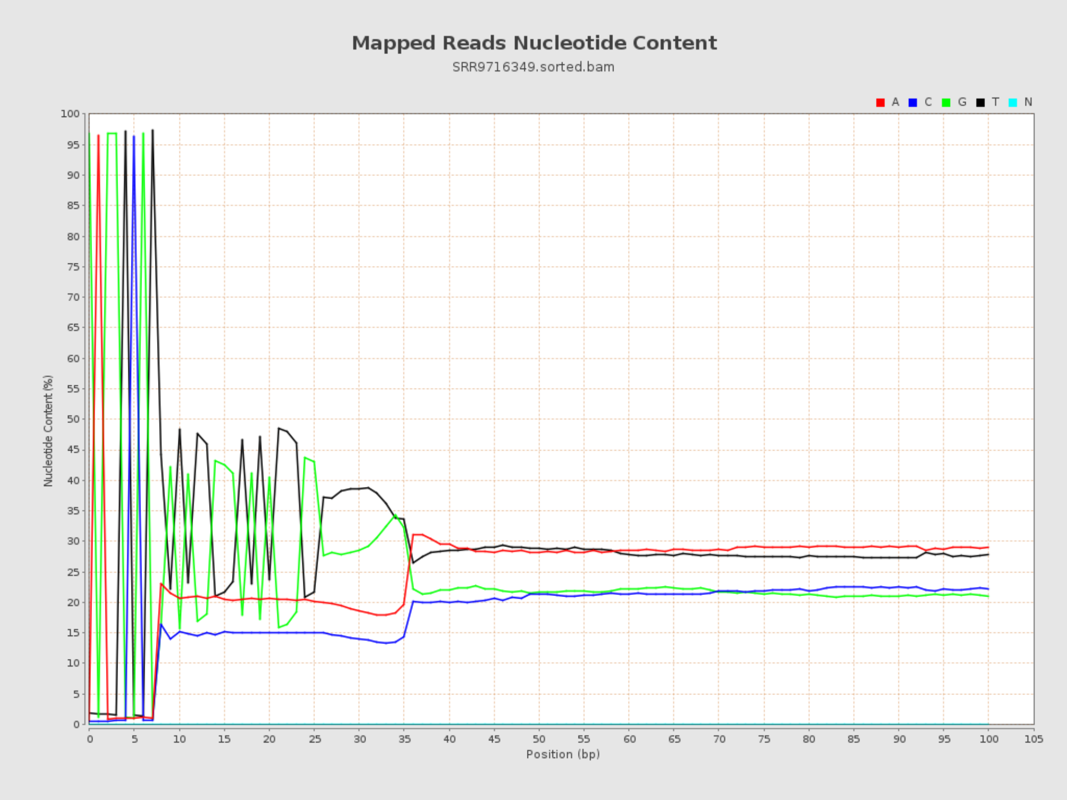
6. Results : Genome Fraction Coverage



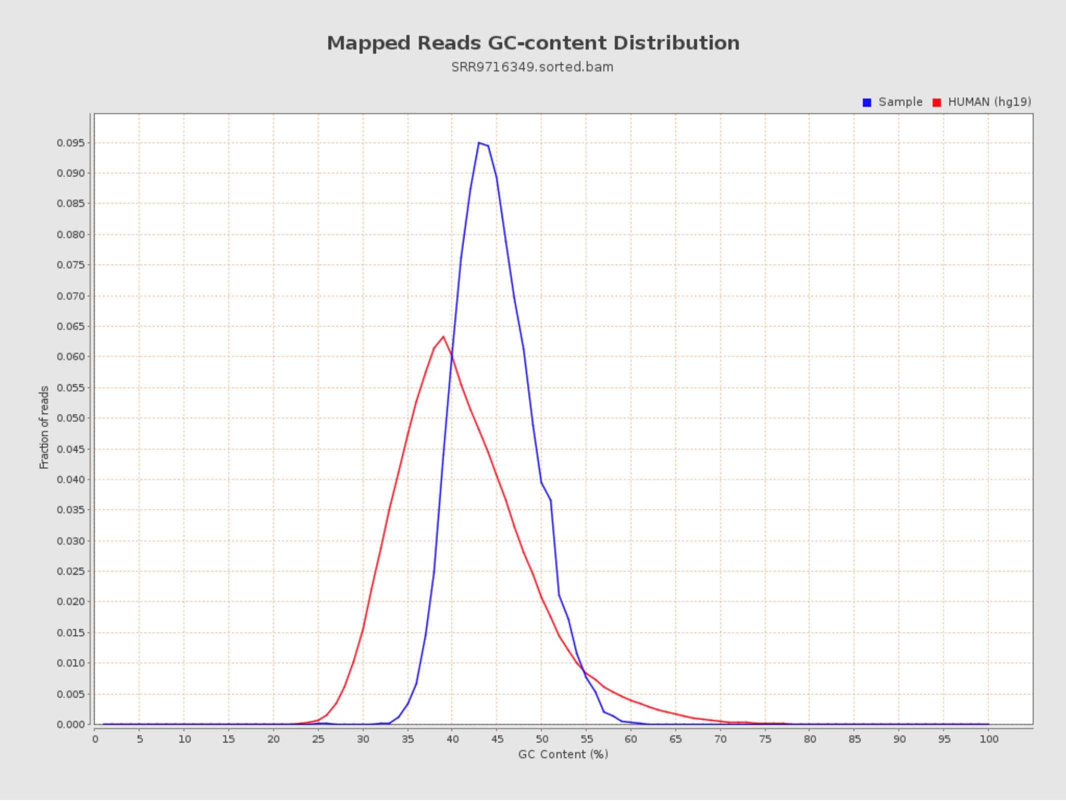
7. Results : Duplication Rate Histogram



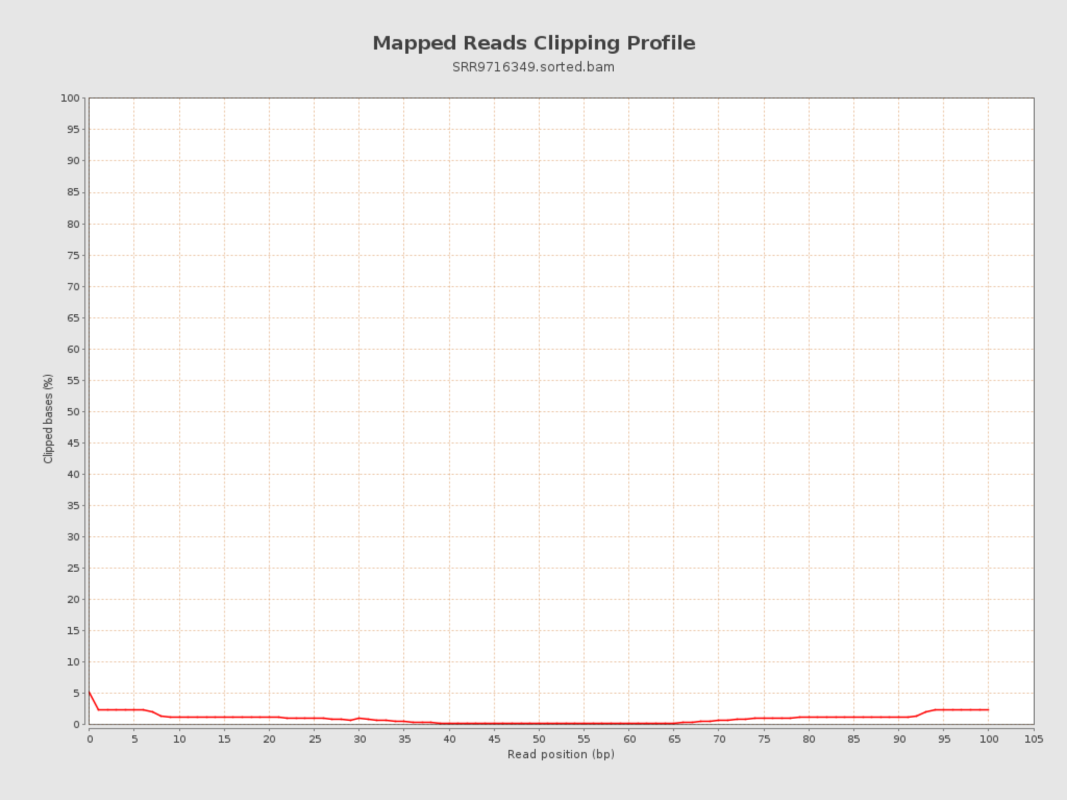
8. Results : Mapped Reads Nucleotide Content



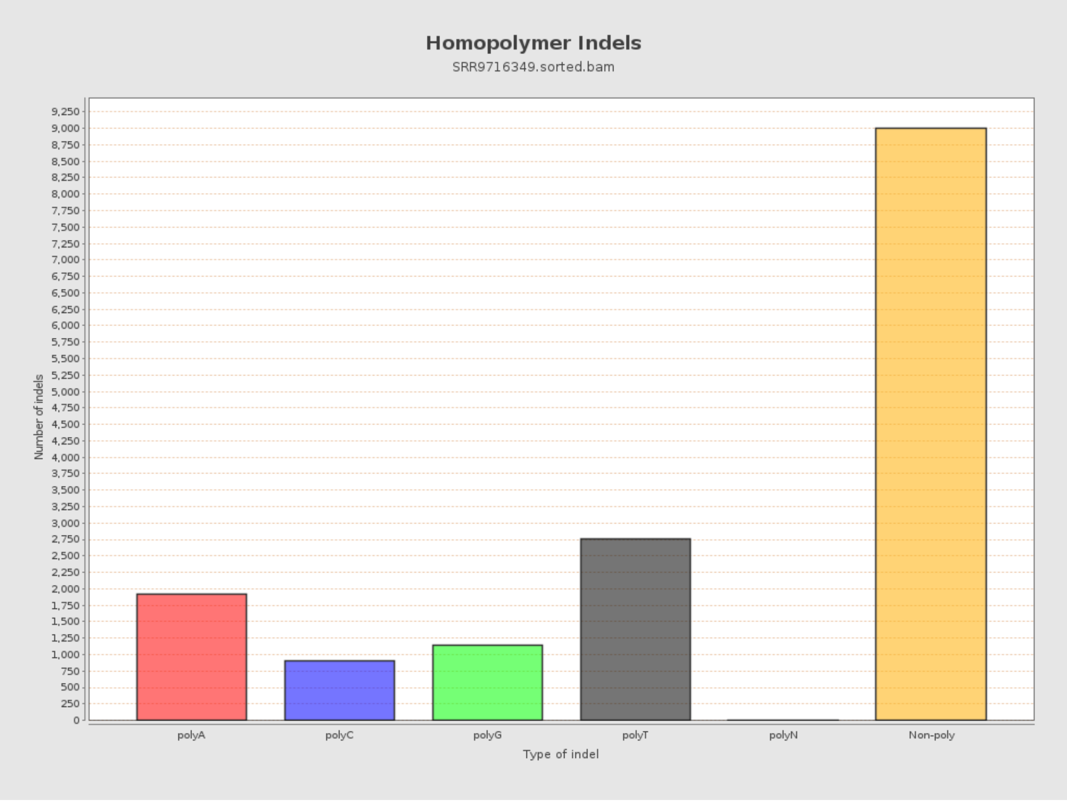
9. Results : Mapped Reads GC-content Distribution



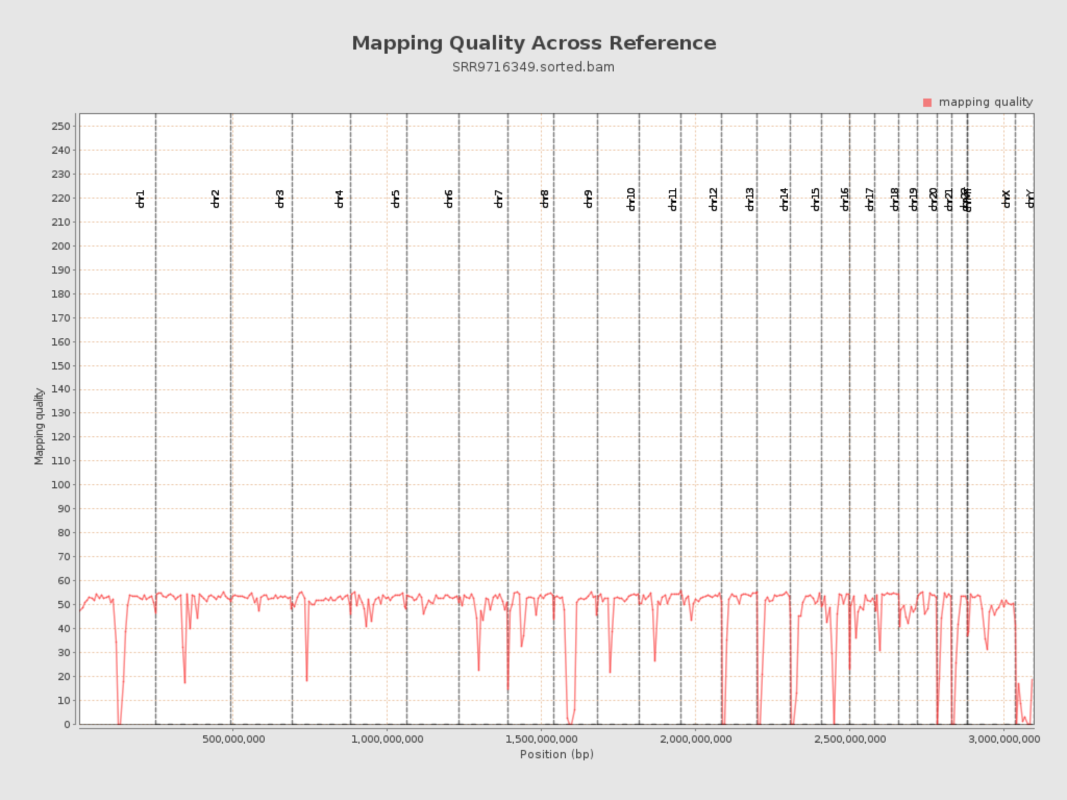
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram