Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:24:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716225.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_SRR9716225 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716225.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:24:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,301,741
Mapped reads	1,164,243 / 89.44%
Unmapped reads	137,498 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,876 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	37,337 / 2.87%
Duplication rate	2.42%
Clipped reads	1,167,864 / 89.72%

2.2. ACGT Content

Number/percentage of A's	16,202,389 / 24.41%
Number/percentage of C's	11,724,626 / 17.66%
Number/percentage of T's	21,769,718 / 32.8%
Number/percentage of G's	16,674,516 / 25.12%
Number/percentage of N's	1,063 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0214

Standard Deviation	0.2144

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

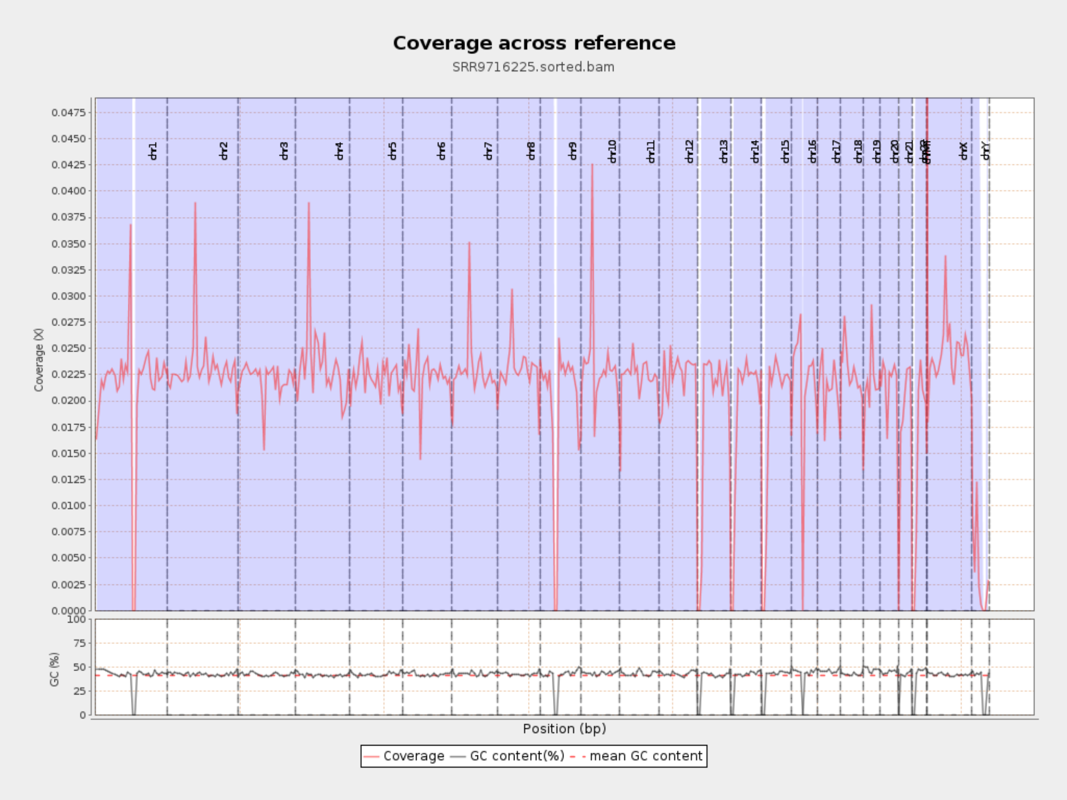
General error rate	0.58%
Mismatches	374,904
Insertions	3,796
Mapped reads with at least one insertion	0.32%
Deletions	11,432
Mapped reads with at least one deletion	0.97%
Homopolymer indels	45.65%

2.6. Chromosome stats

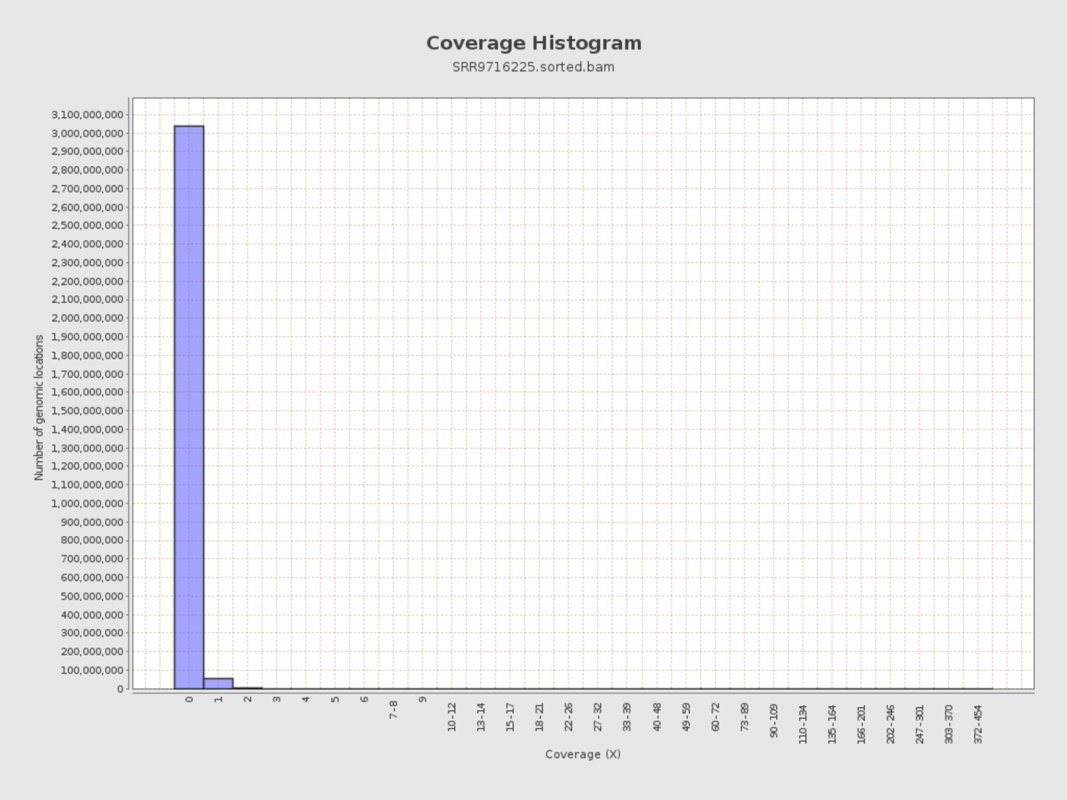
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5302149	0.0213	0.3569
chr2	243199373	5654435	0.0233	0.2295
chr3	198022430	4369428	0.0221	0.1578
chr4	191154276	4466145	0.0234	0.1783
chr5	180915260	4048318	0.0224	0.1608
chr6	171115067	3815396	0.0223	0.173
chr7	159138663	3662909	0.023	0.2471

chr8	146364022	3376753	0.0231	0.2402
chr9	141213431	2763261	0.0196	0.2135
chr10	135534747	3182561	0.0235	0.2281
chr11	135006516	3026666	0.0224	0.2017
chr12	133851895	2987391	0.0223	0.1638
chr13	115169878	2138861	0.0186	0.1441
chr14	107349540	2013639	0.0188	0.155
chr15	102531392	1865736	0.0182	0.1431
chr16	90354753	1907449	0.0211	0.1647
chr17	81195210	1723829	0.0212	0.1641
chr18	78077248	1786375	0.0229	0.3596
chr19	59128983	1292972	0.0219	0.2762
chr20	63025520	1353099	0.0215	0.1617
chr21	48129895	878643	0.0183	0.1605
chr22	51304566	751182	0.0146	0.1291
chrMT	16571	1853	0.1118	0.3484
chrX	155270560	3810323	0.0245	0.1901
chrY	59373566	212133	0.0036	0.0938

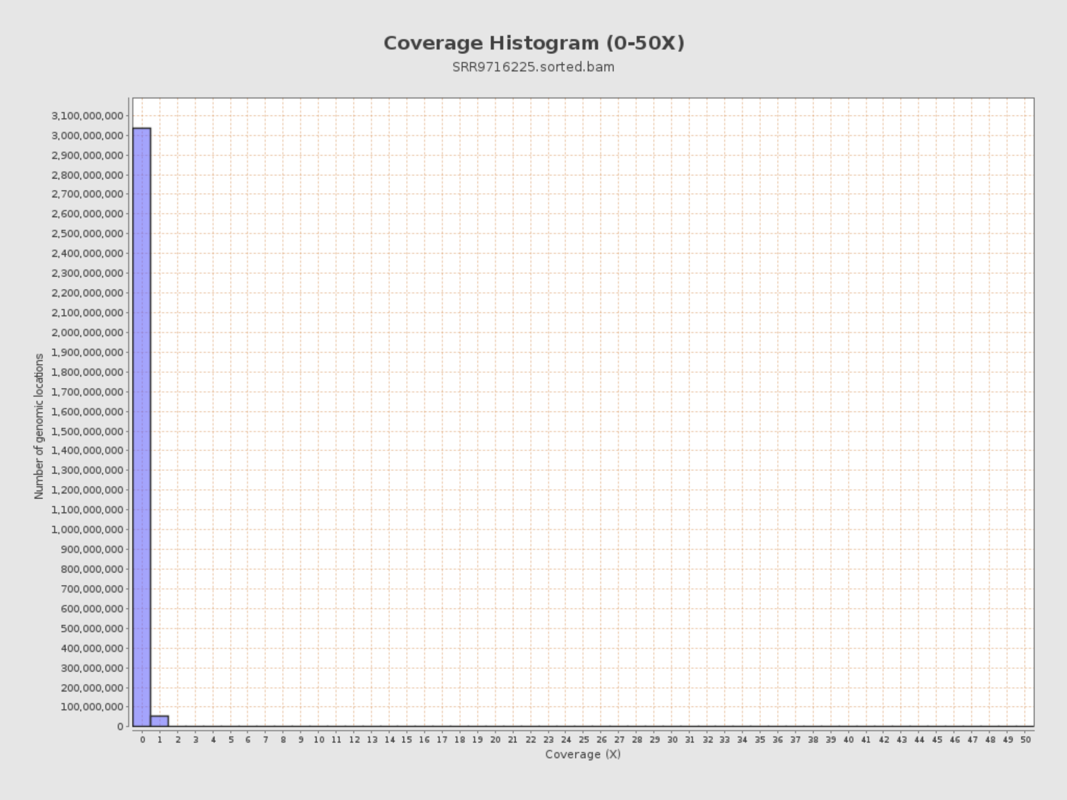
3. Results : Coverage across reference



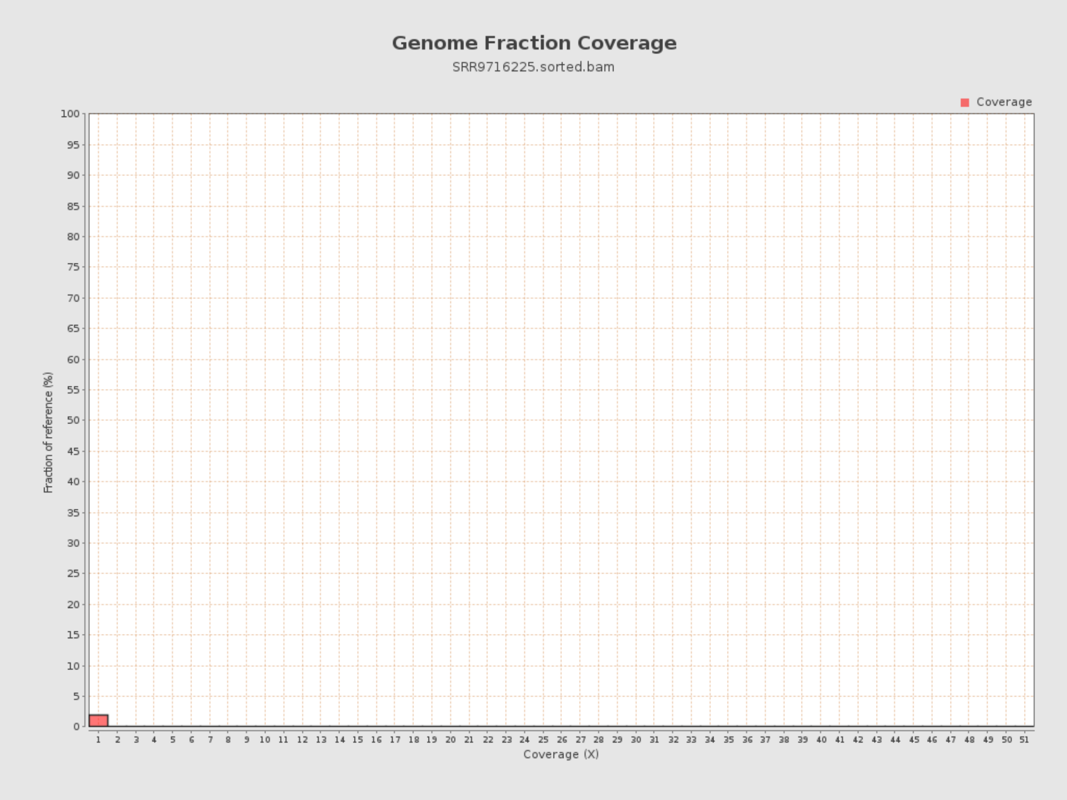
4. Results : Coverage Histogram



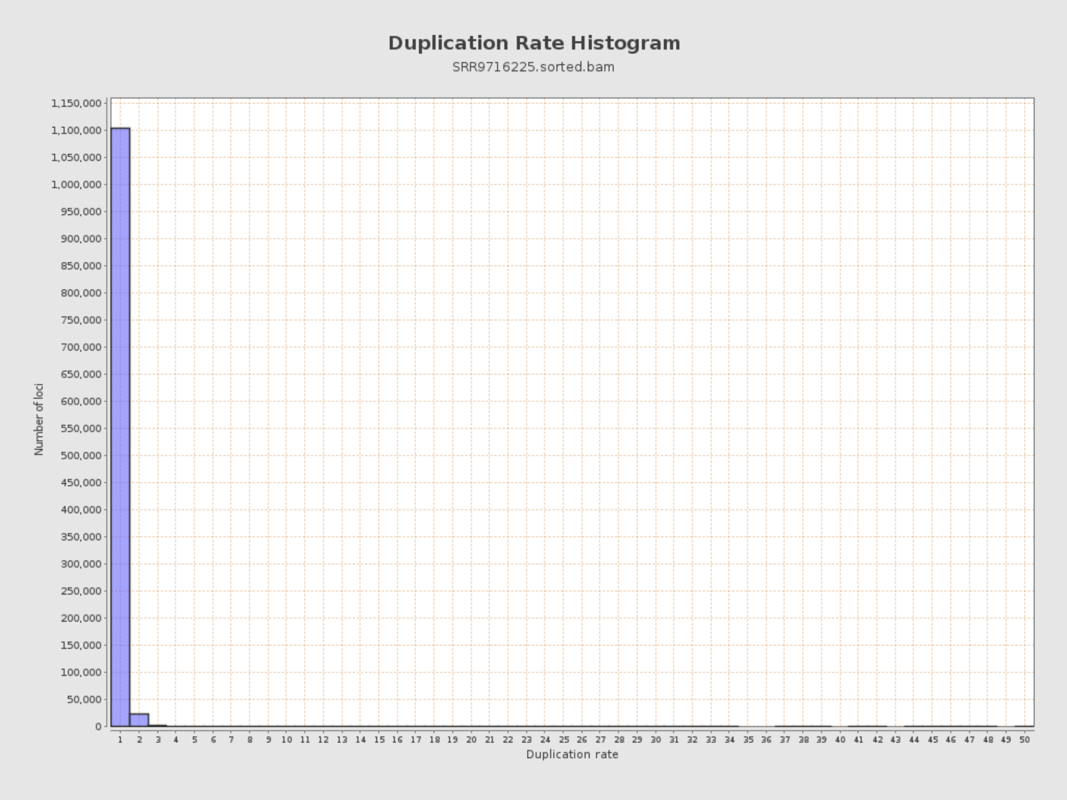
5. Results : Coverage Histogram (0-50X)



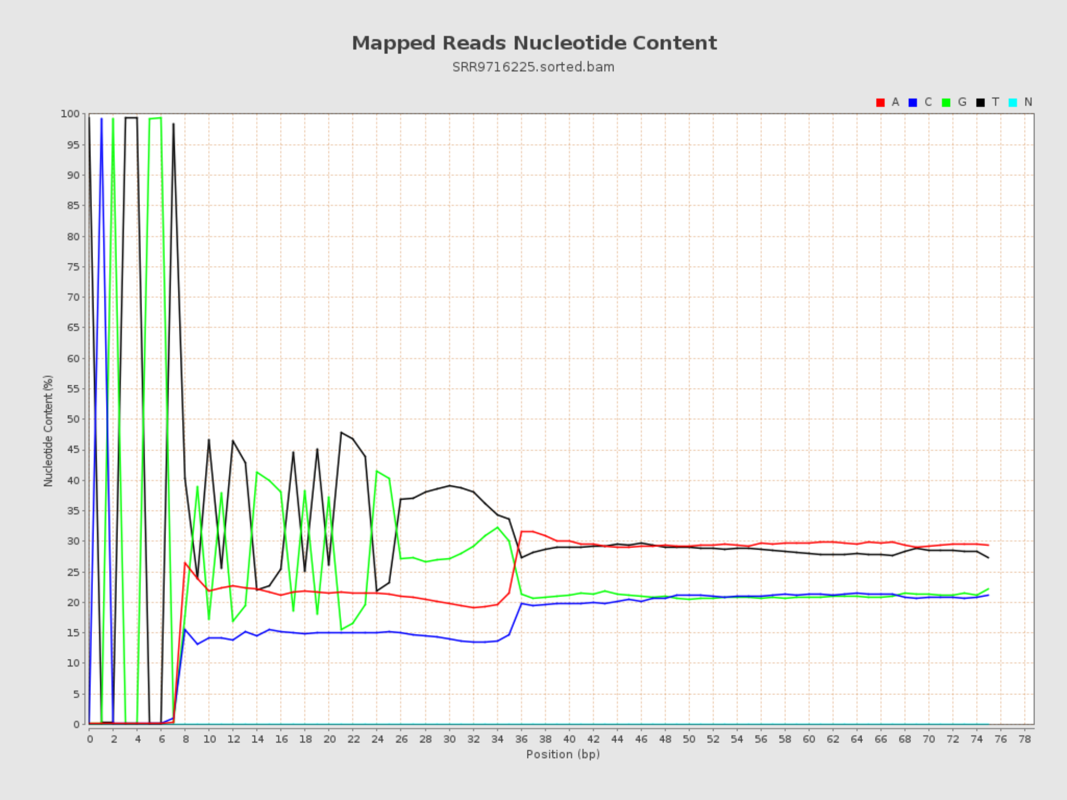
6. Results : Genome Fraction Coverage



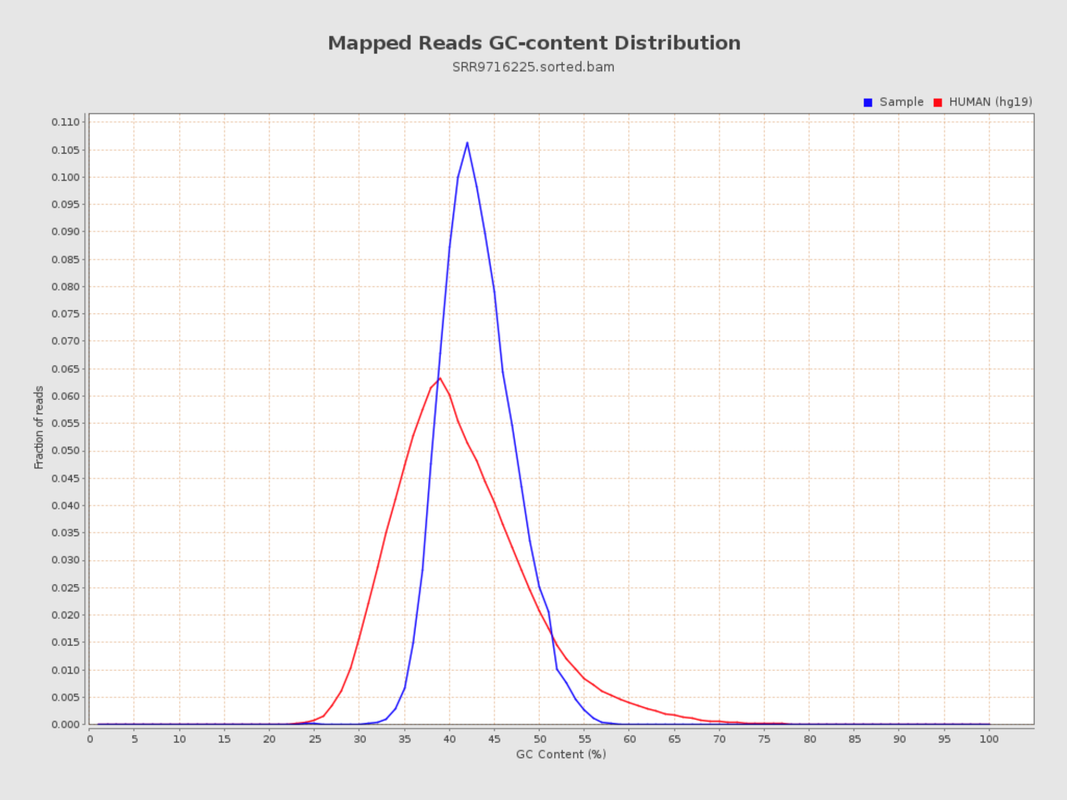
7. Results : Duplication Rate Histogram



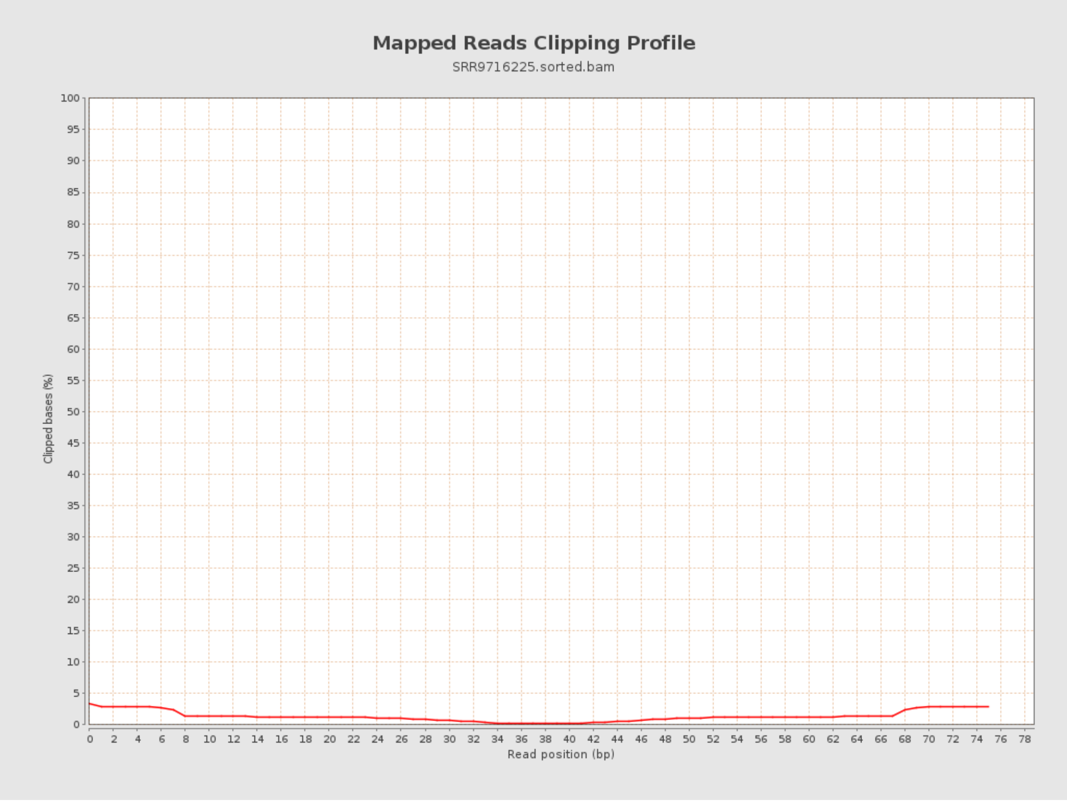
8. Results : Mapped Reads Nucleotide Content



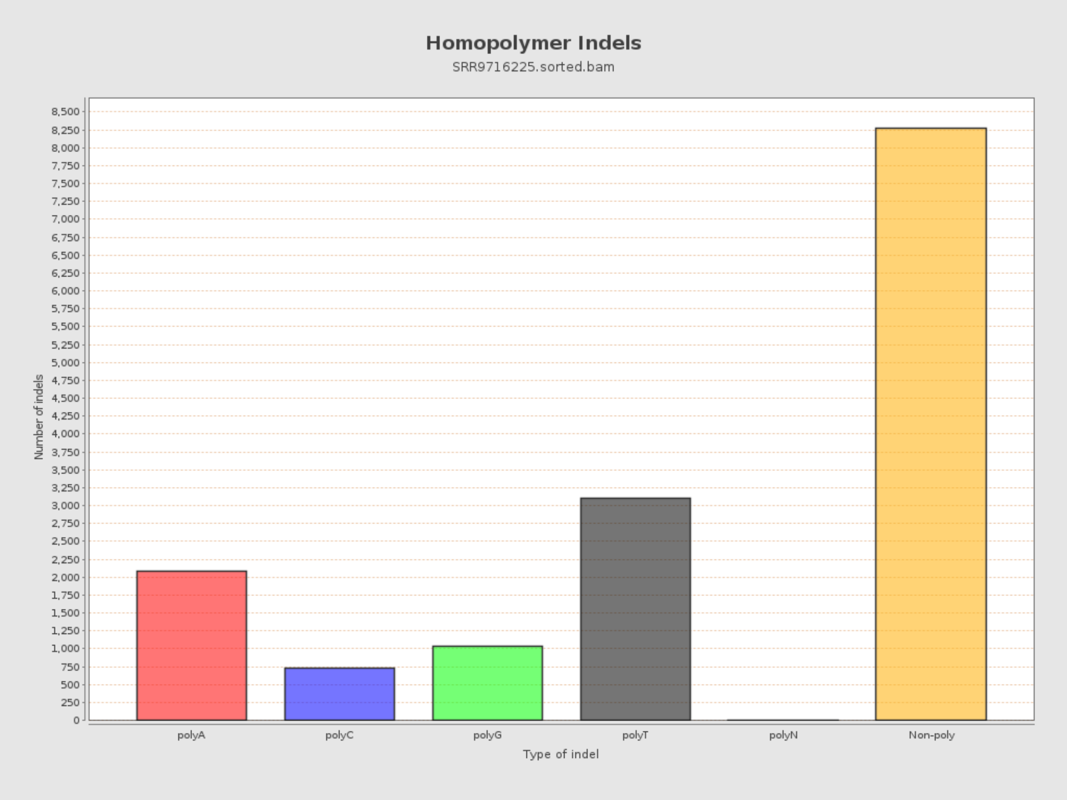
9. Results : Mapped Reads GC-content Distribution



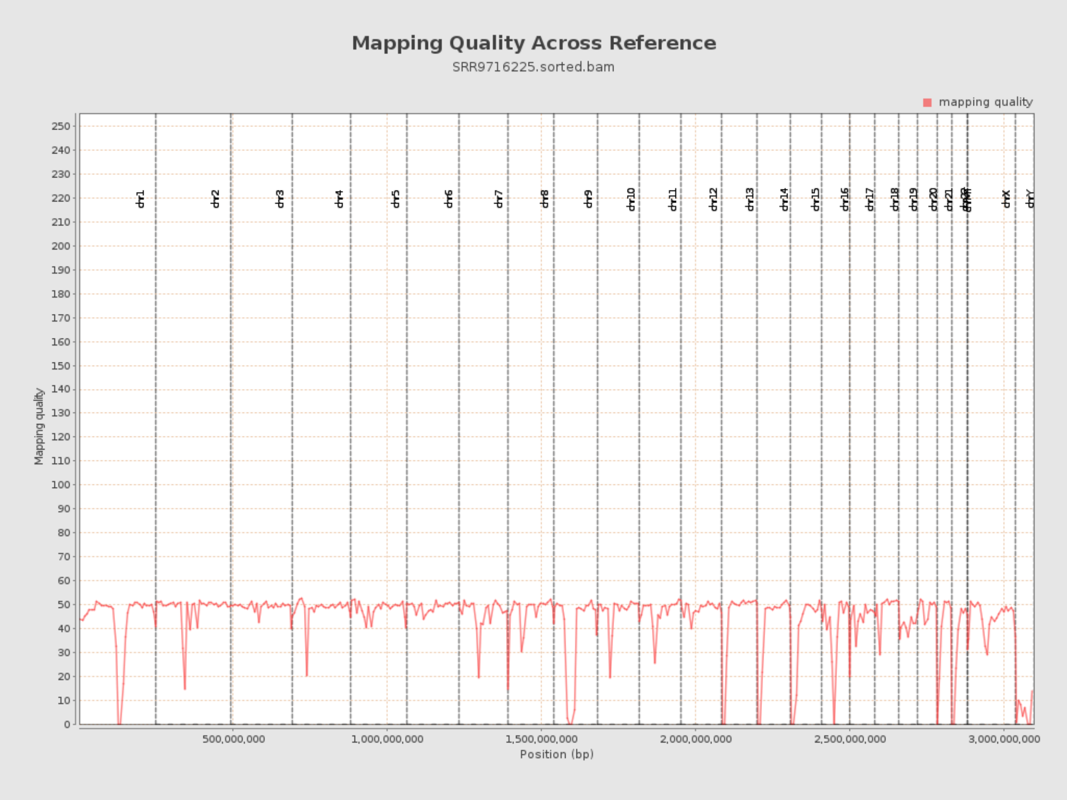
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram