Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:58:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716405.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_SRR9716405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716405.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:58:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716405.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,331,331
Mapped reads	994,119 / 74.67%
Unmapped reads	337,212 / 25.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,485 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	23,728 / 1.78%
Duplication rate	1.76%
Clipped reads	996,759 / 74.87%

2.2. ACGT Content

Number/percentage of A's	14,040,422 / 25.1%
Number/percentage of C's	11,320,811 / 20.24%
Number/percentage of T's	17,083,141 / 30.54%
Number/percentage of G's	13,493,907 / 24.12%
Number/percentage of N's	718 / 0%
GC Percentage	44.36%

2.3. Coverage

Mean	0.0181

Standard Deviation	0.1743

2.4. Mapping Quality

Mean Mapping Quality	42.2

2.5. Mismatches and indels

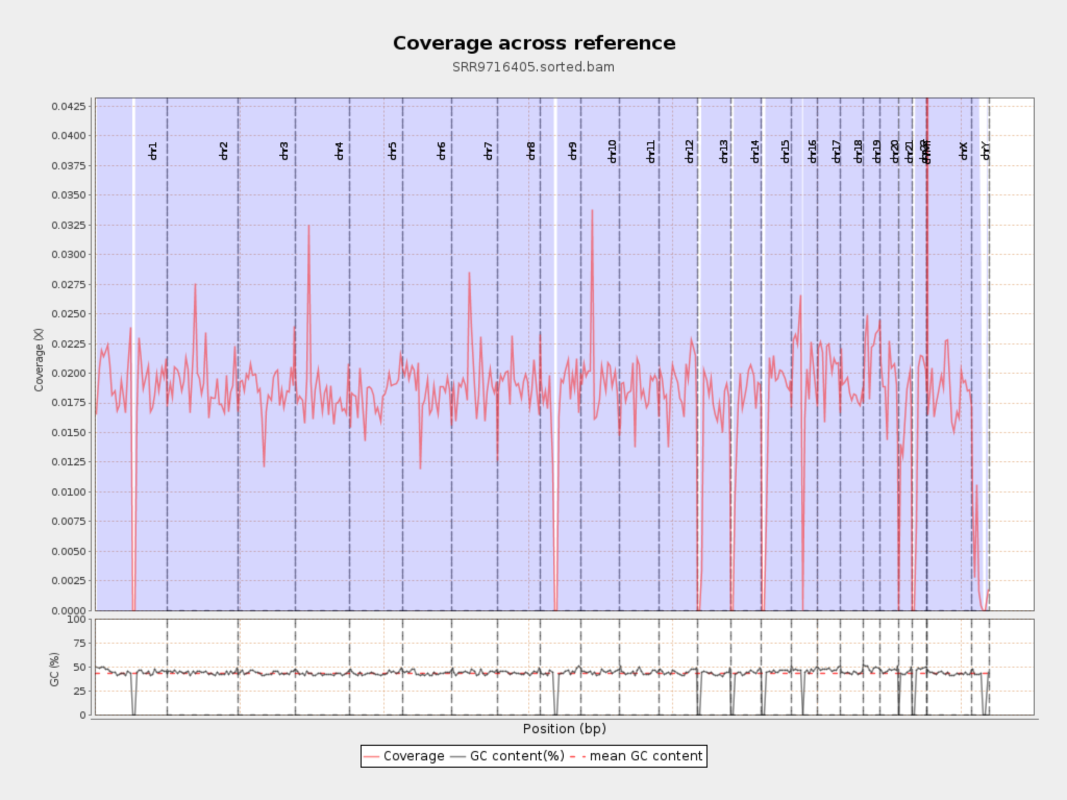
General error rate	0.54%
Mismatches	293,674
Insertions	3,538
Mapped reads with at least one insertion	0.35%
Deletions	10,254
Mapped reads with at least one deletion	1.02%
Homopolymer indels	40.73%

2.6. Chromosome stats

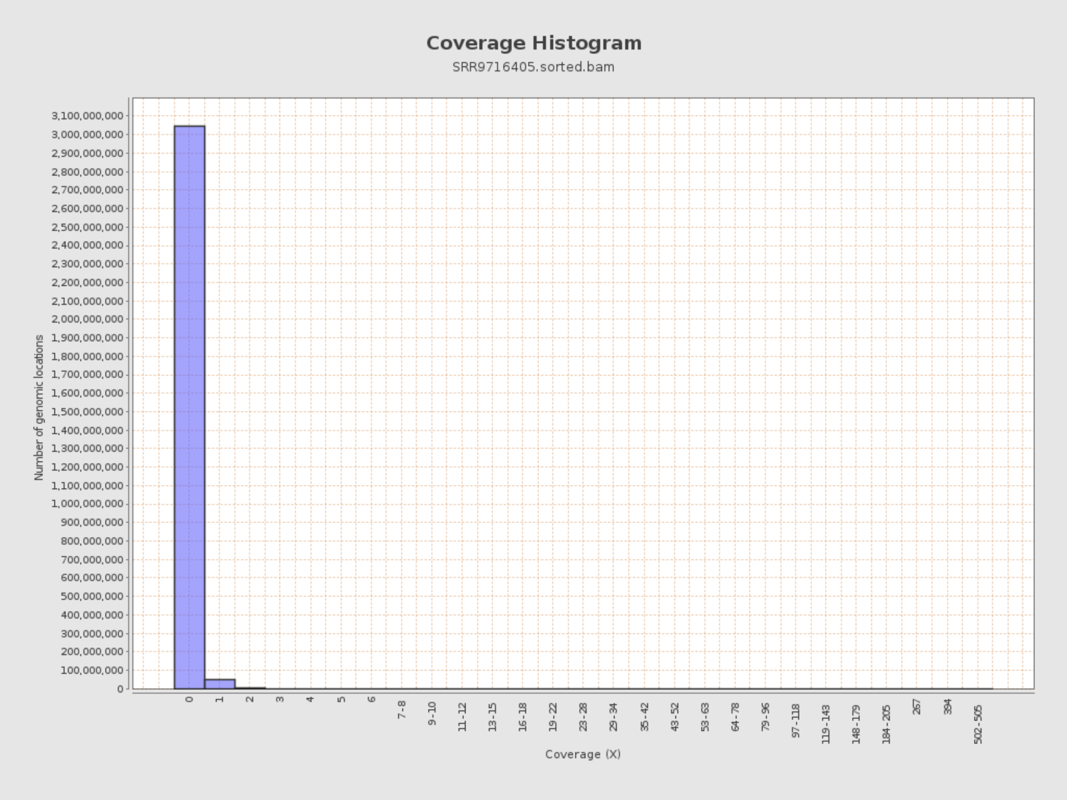
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4562582	0.0183	0.2057
chr2	243199373	4694528	0.0193	0.2608
chr3	198022430	3684400	0.0186	0.146
chr4	191154276	3536680	0.0185	0.1586
chr5	180915260	3318012	0.0183	0.1447
chr6	171115067	3161943	0.0185	0.1568
chr7	159138663	3088607	0.0194	0.2165

chr8	146364022	2806741	0.0192	0.1662
chr9	141213431	2325471	0.0165	0.1553
chr10	135534747	2697539	0.0199	0.1944
chr11	135006516	2524465	0.0187	0.1611
chr12	133851895	2567938	0.0192	0.1492
chr13	115169878	1720215	0.0149	0.1305
chr14	107349540	1696236	0.0158	0.1381
chr15	102531392	1653816	0.0161	0.1375
chr16	90354753	1723145	0.0191	0.1574
chr17	81195210	1687414	0.0208	0.1612
chr18	78077248	1445383	0.0185	0.2081
chr19	59128983	1318526	0.0223	0.1983
chr20	63025520	1209542	0.0192	0.1504
chr21	48129895	718117	0.0149	0.1418
chr22	51304566	737770	0.0144	0.1297
chrMT	16571	14441	0.8715	1.0334
chrX	155270560	2881425	0.0186	0.1539
chrY	59373566	180813	0.003	0.0899

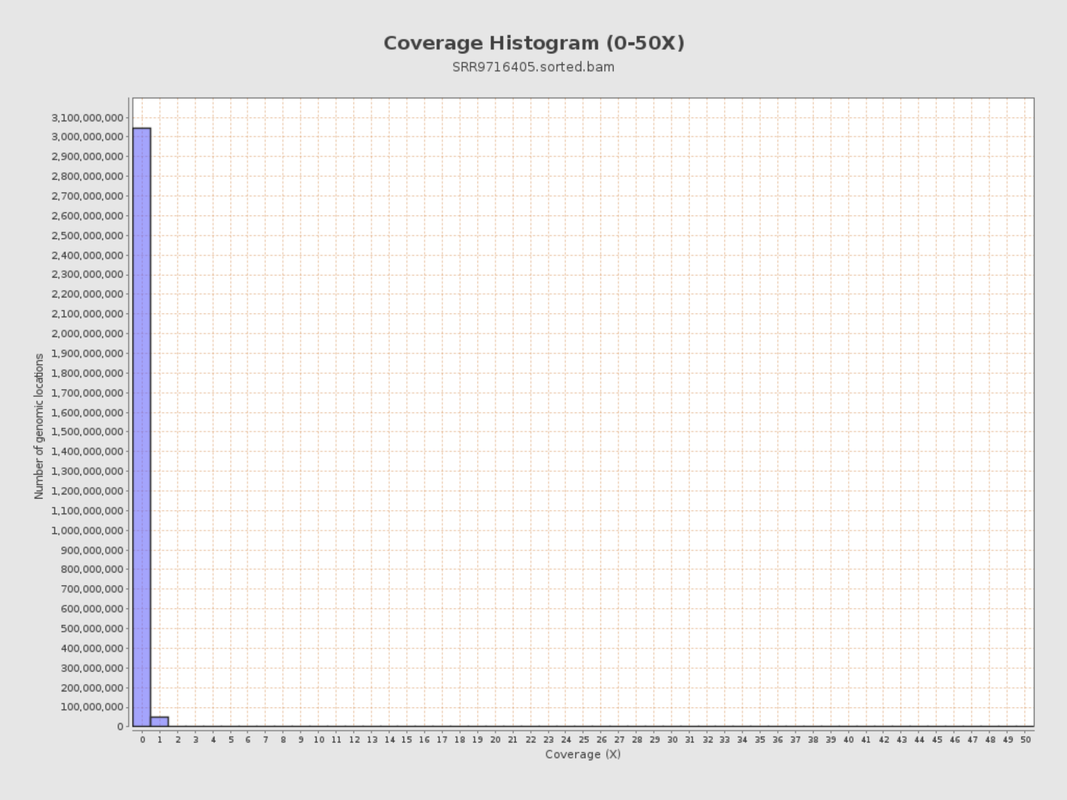
3. Results : Coverage across reference



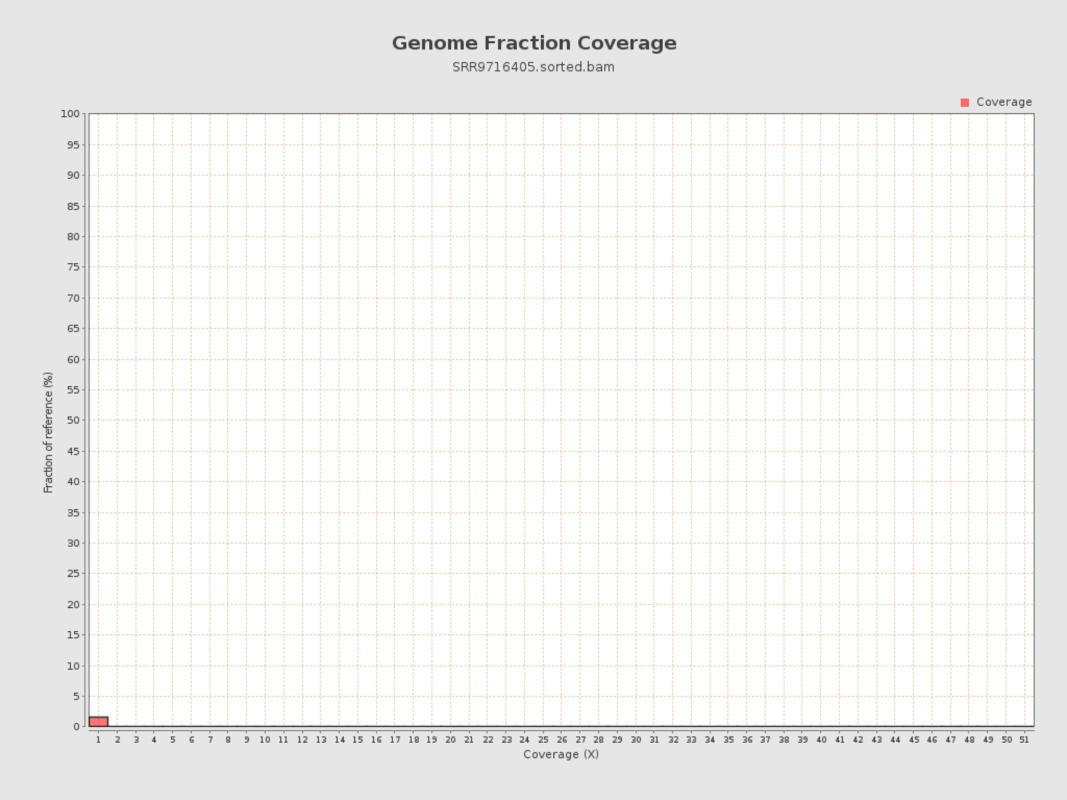
4. Results : Coverage Histogram



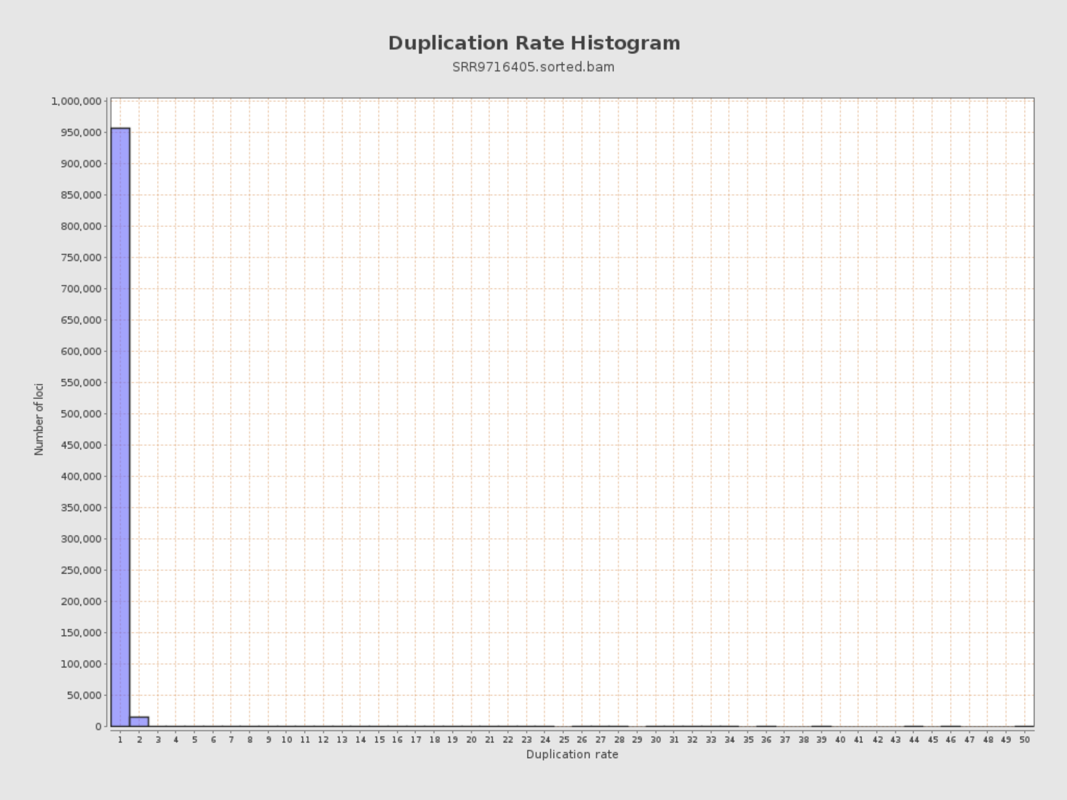
5. Results : Coverage Histogram (0-50X)



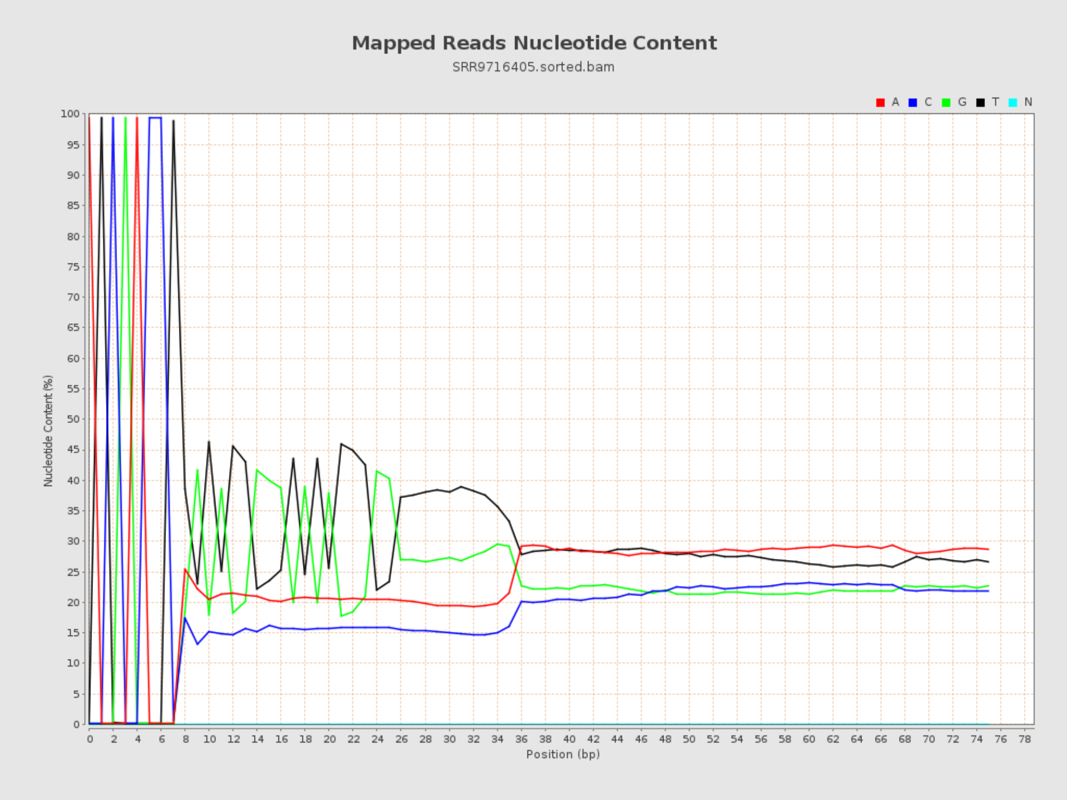
6. Results : Genome Fraction Coverage



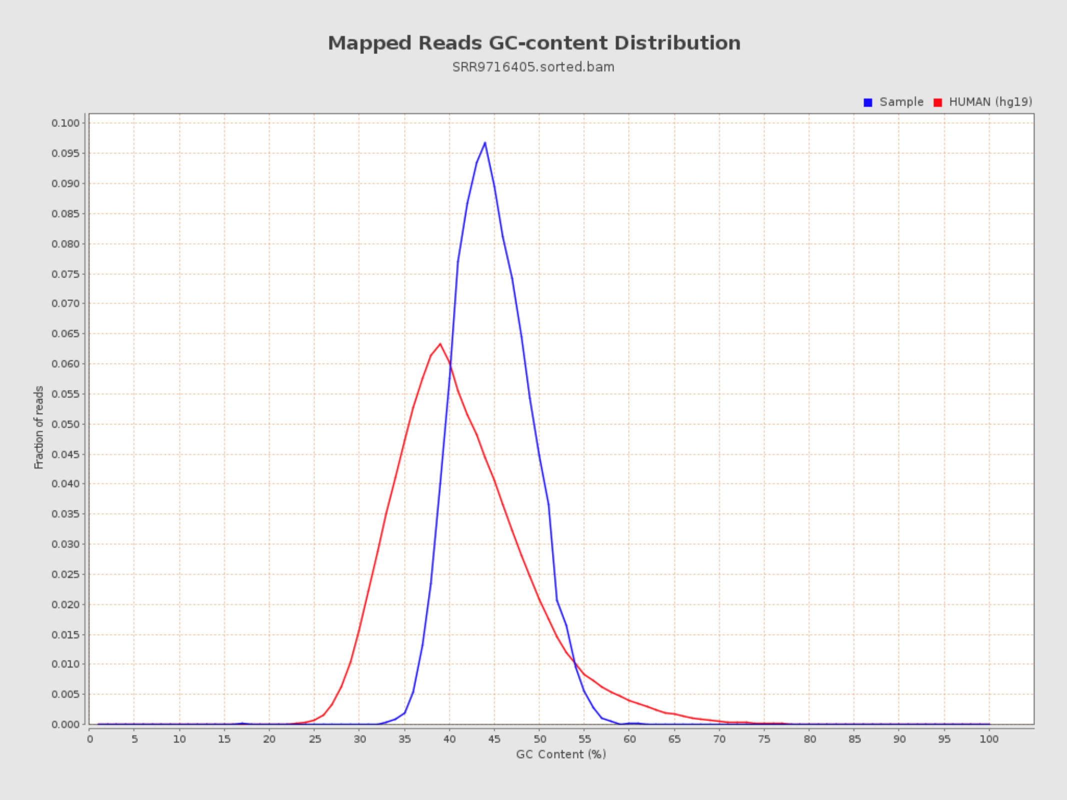
7. Results : Duplication Rate Histogram



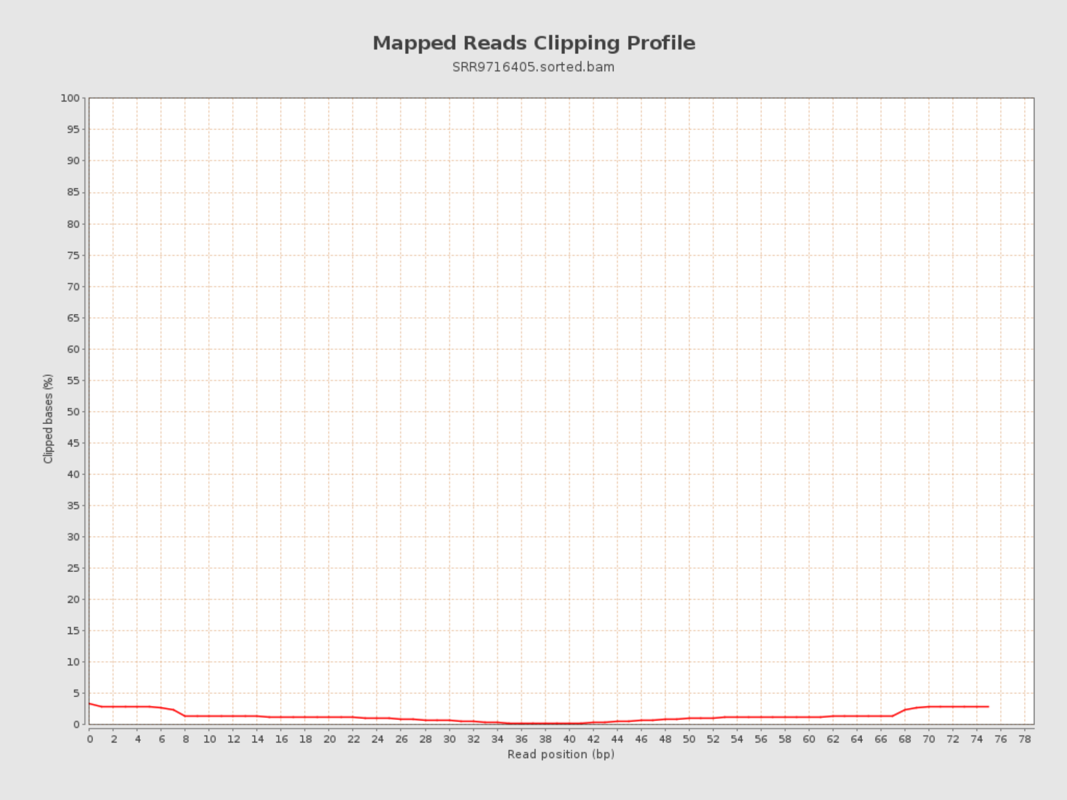
8. Results : Mapped Reads Nucleotide Content



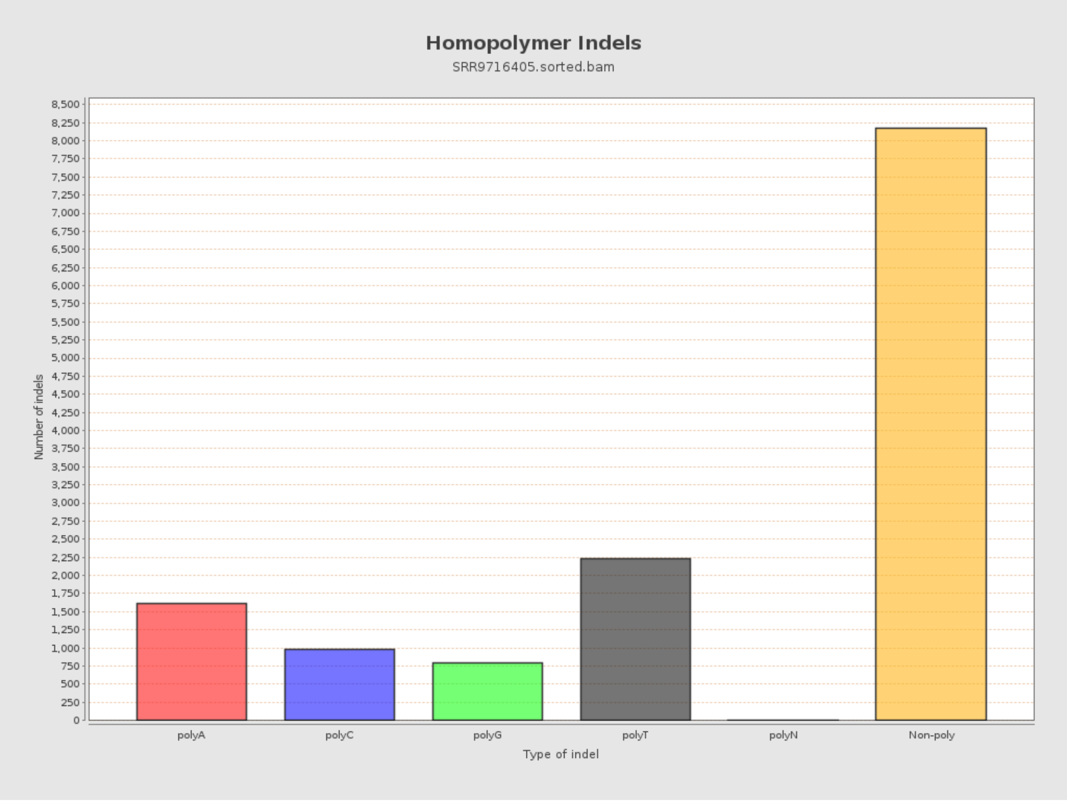
9. Results : Mapped Reads GC-content Distribution



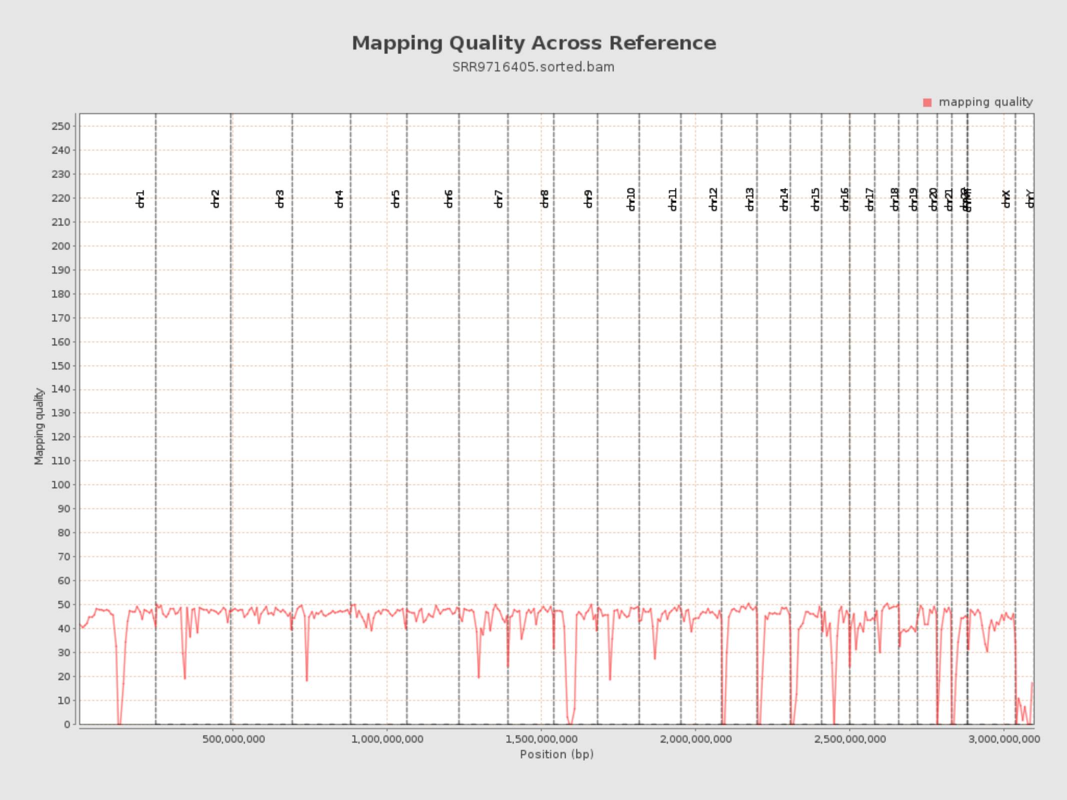
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram