Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:44:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716638.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_SRR9716638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716638.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:44:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,955,337
Mapped reads	1,780,068 / 91.04%
Unmapped reads	175,269 / 8.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,583 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	65,324 / 3.34%
Duplication rate	2.42%
Clipped reads	1,780,557 / 91.06%

2.2. ACGT Content

Number/percentage of A's	25,249,757 / 24.77%
Number/percentage of C's	19,668,113 / 19.3%
Number/percentage of T's	32,272,834 / 31.66%
Number/percentage of G's	24,730,014 / 24.26%
Number/percentage of N's	1,973 / 0%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.3188

2.4. Mapping Quality

Mean Mapping Quality	42.51

2.5. Mismatches and indels

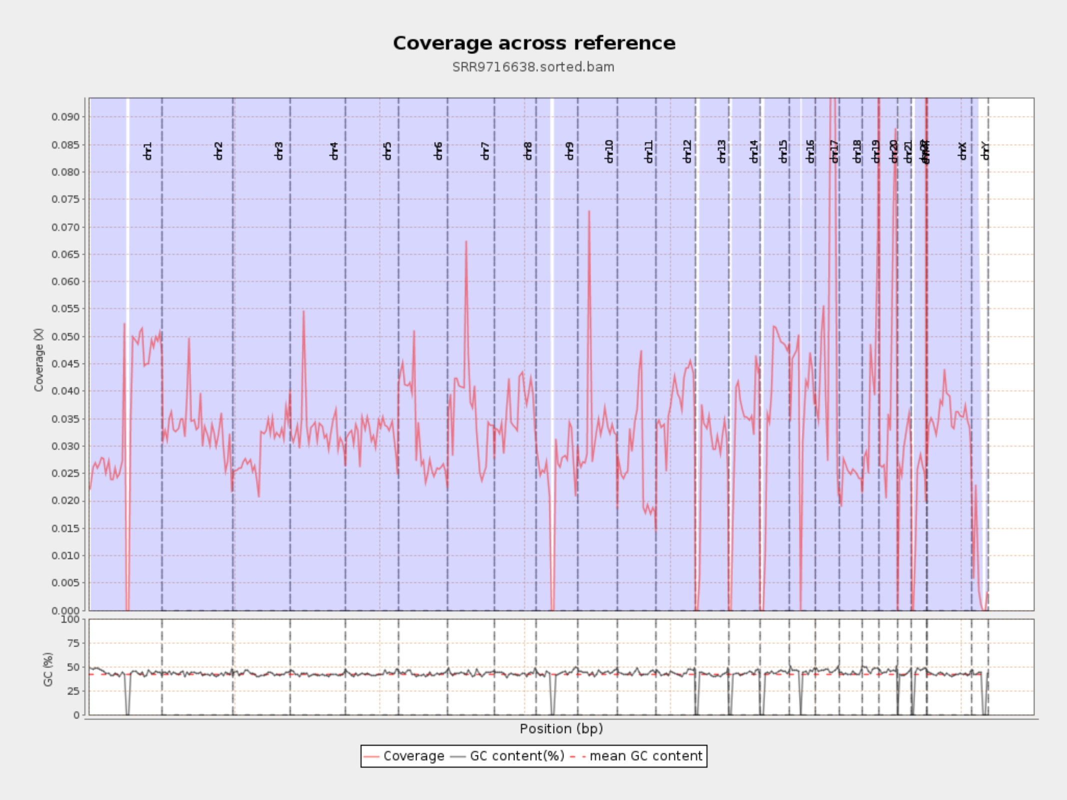
General error rate	0.54%
Mismatches	530,269
Insertions	8,190
Mapped reads with at least one insertion	0.46%
Deletions	19,598
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.92%

2.6. Chromosome stats

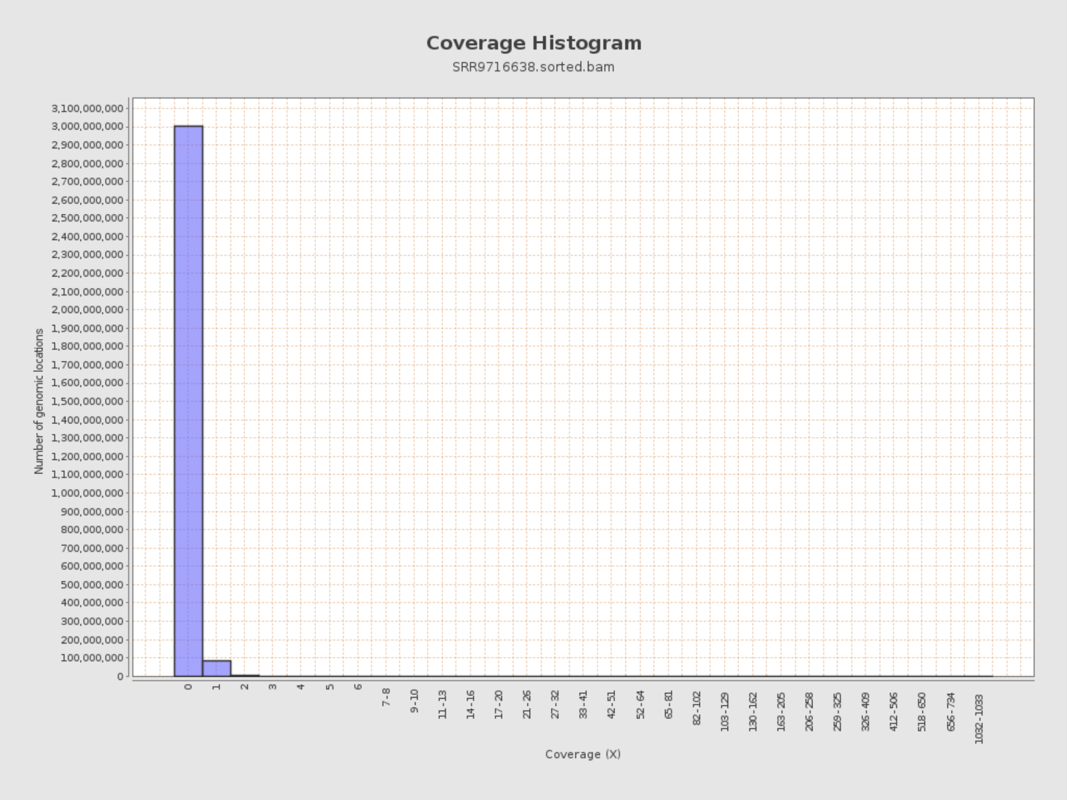
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8627985	0.0346	0.526
chr2	243199373	8073536	0.0332	0.4645
chr3	198022430	5867615	0.0296	0.1972
chr4	191154276	6339373	0.0332	0.2295
chr5	180915260	5856297	0.0324	0.1976
chr6	171115067	5517242	0.0322	0.25
chr7	159138663	5886669	0.037	0.4641

chr8	146364022	5346833	0.0365	0.3635
chr9	141213431	3417874	0.0242	0.2238
chr10	135534747	4539060	0.0335	0.3555
chr11	135006516	3641313	0.027	0.2458
chr12	133851895	5129320	0.0383	0.218
chr13	115169878	3115943	0.0271	0.1805
chr14	107349540	3438984	0.032	0.2051
chr15	102531392	3762974	0.0367	0.2166
chr16	90354753	3534130	0.0391	0.2383
chr17	81195210	4498429	0.0554	0.2711
chr18	78077248	1929429	0.0247	0.3803
chr19	59128983	2485651	0.042	0.4186
chr20	63025520	2696672	0.0428	0.2381
chr21	48129895	1310392	0.0272	0.2055
chr22	51304566	941084	0.0183	0.1494
chrMT	16571	109549	6.6109	4.726
chrX	155270560	5526658	0.0356	0.2352
chrY	59373566	360997	0.0061	0.2209

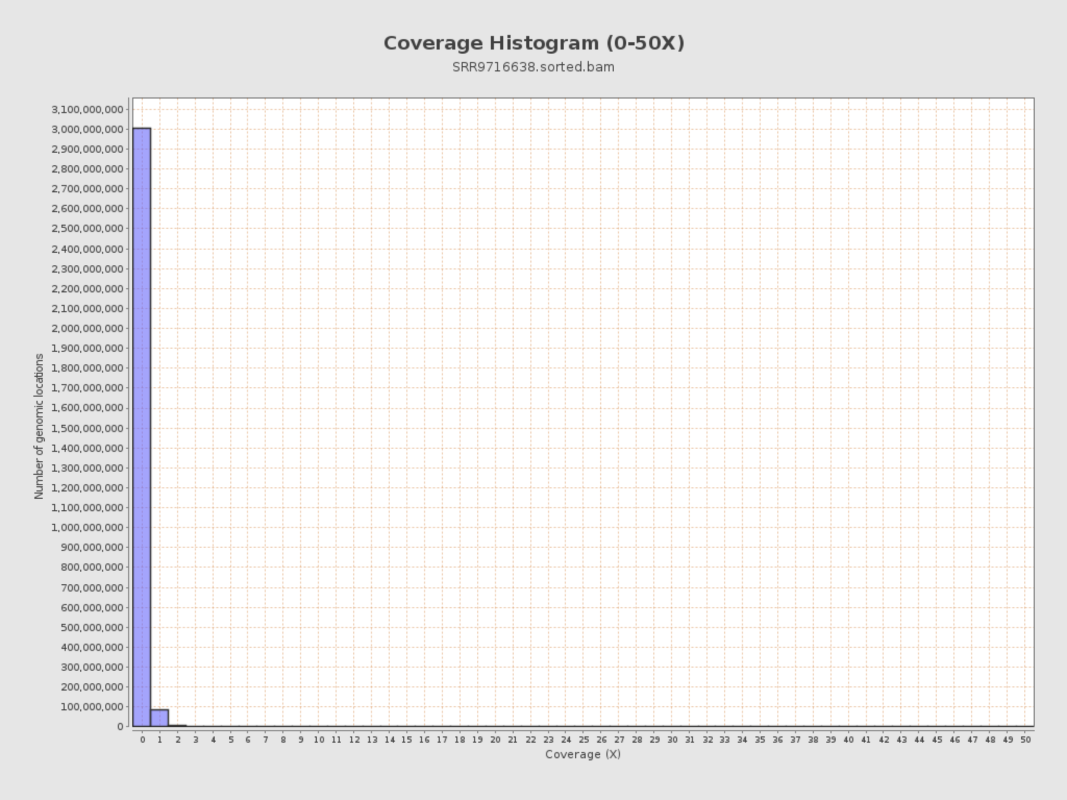
3. Results : Coverage across reference



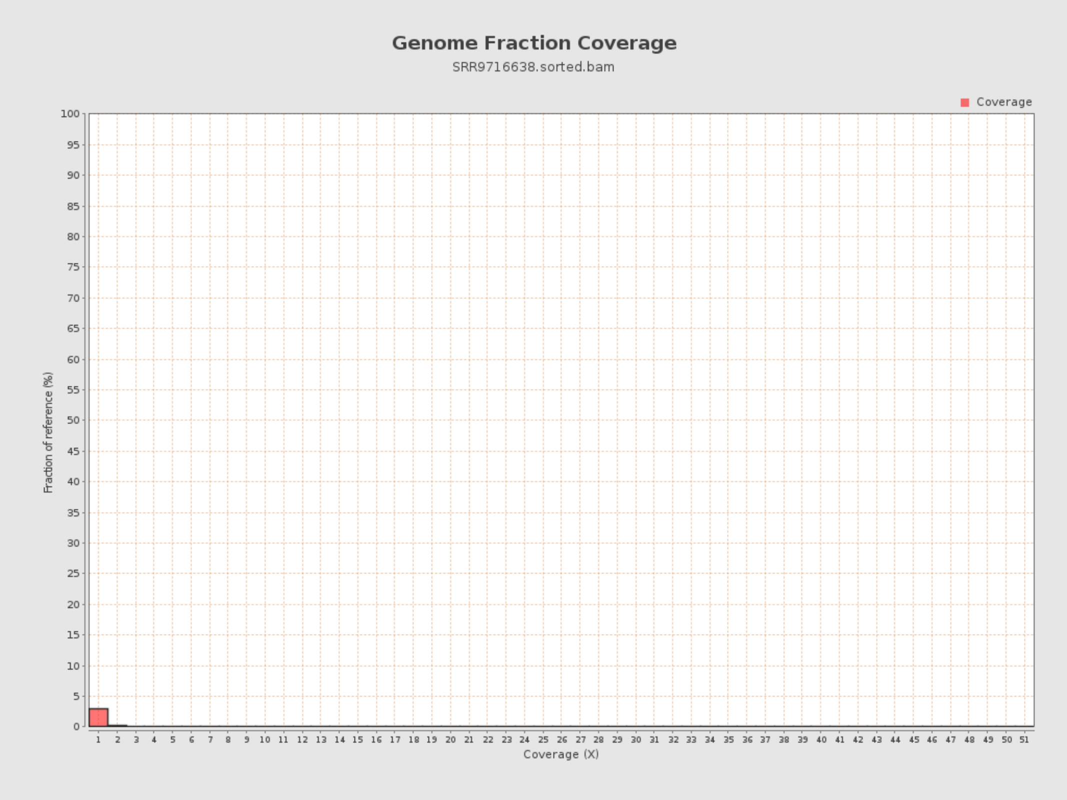
4. Results : Coverage Histogram



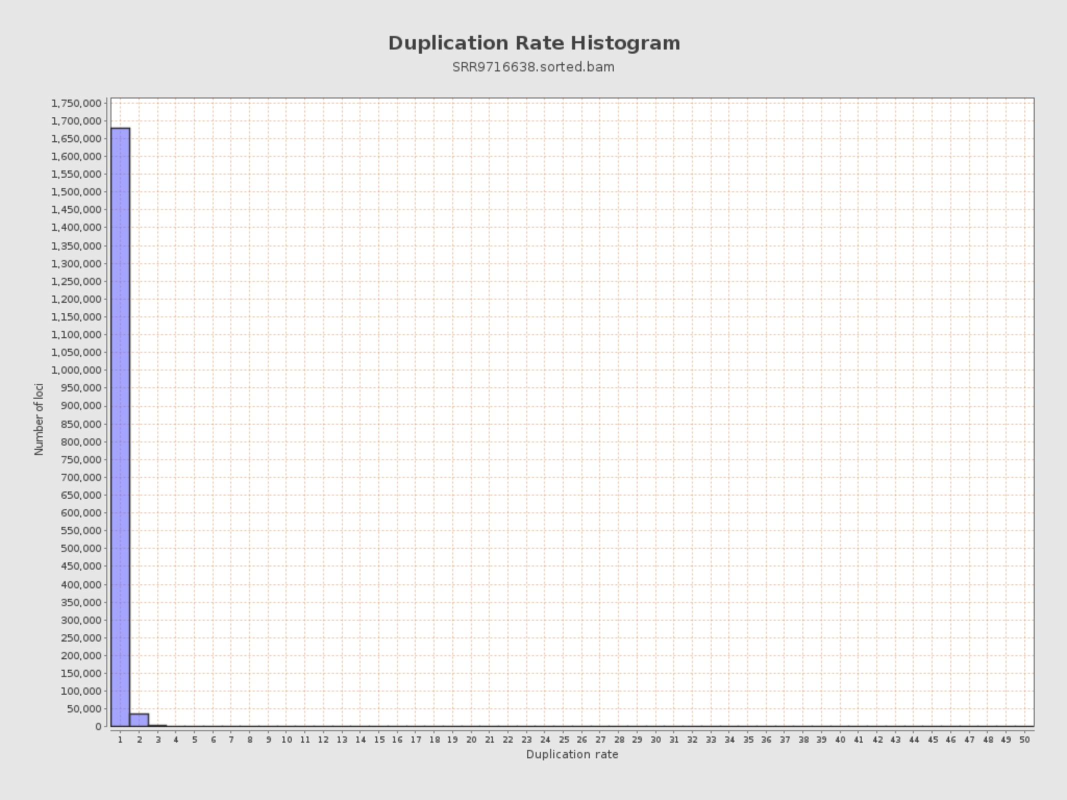
5. Results : Coverage Histogram (0-50X)



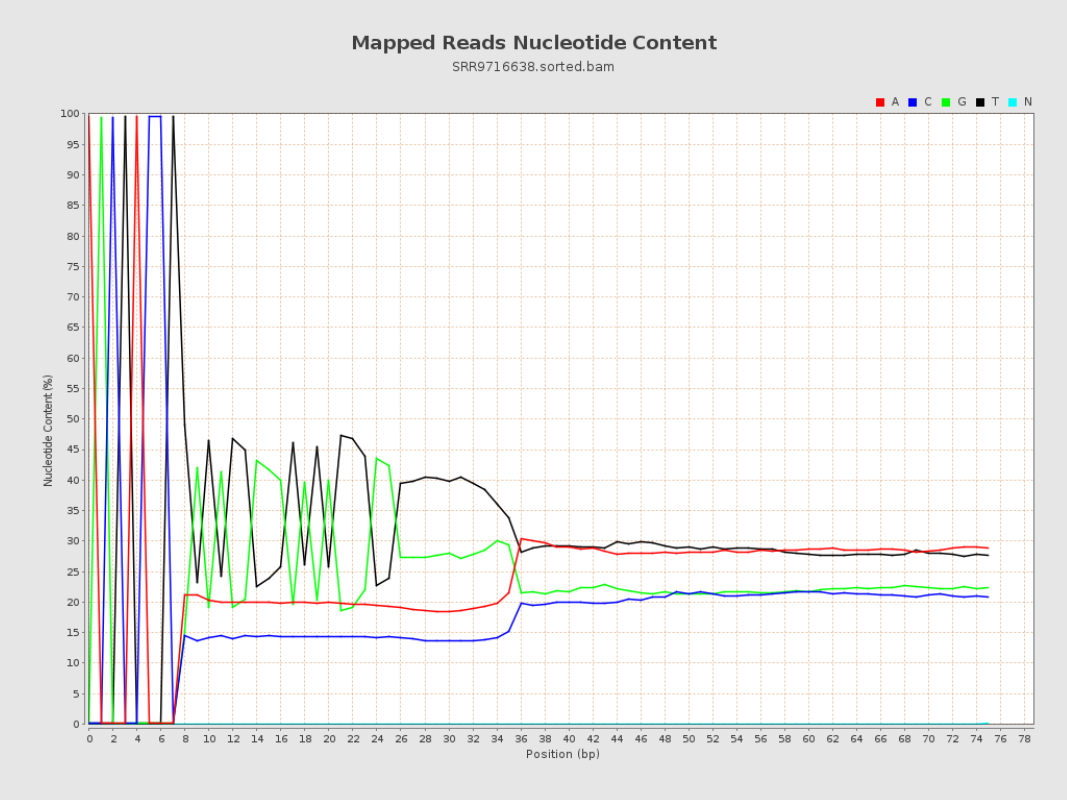
6. Results : Genome Fraction Coverage



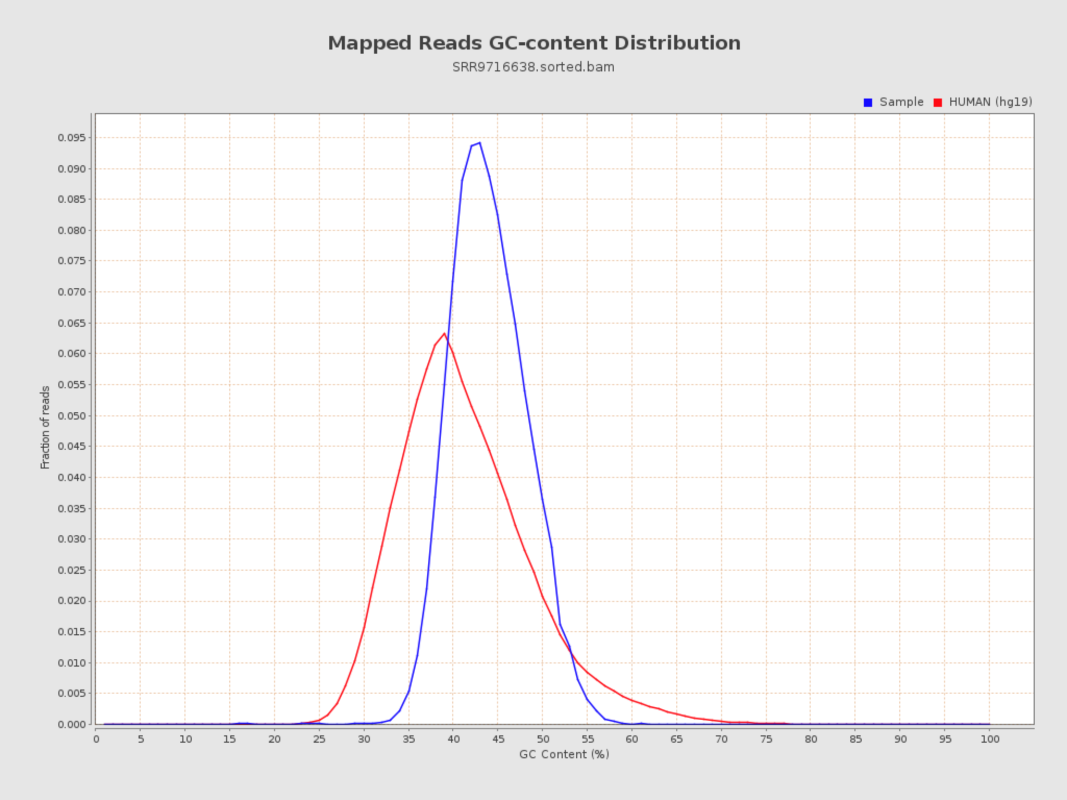
7. Results : Duplication Rate Histogram



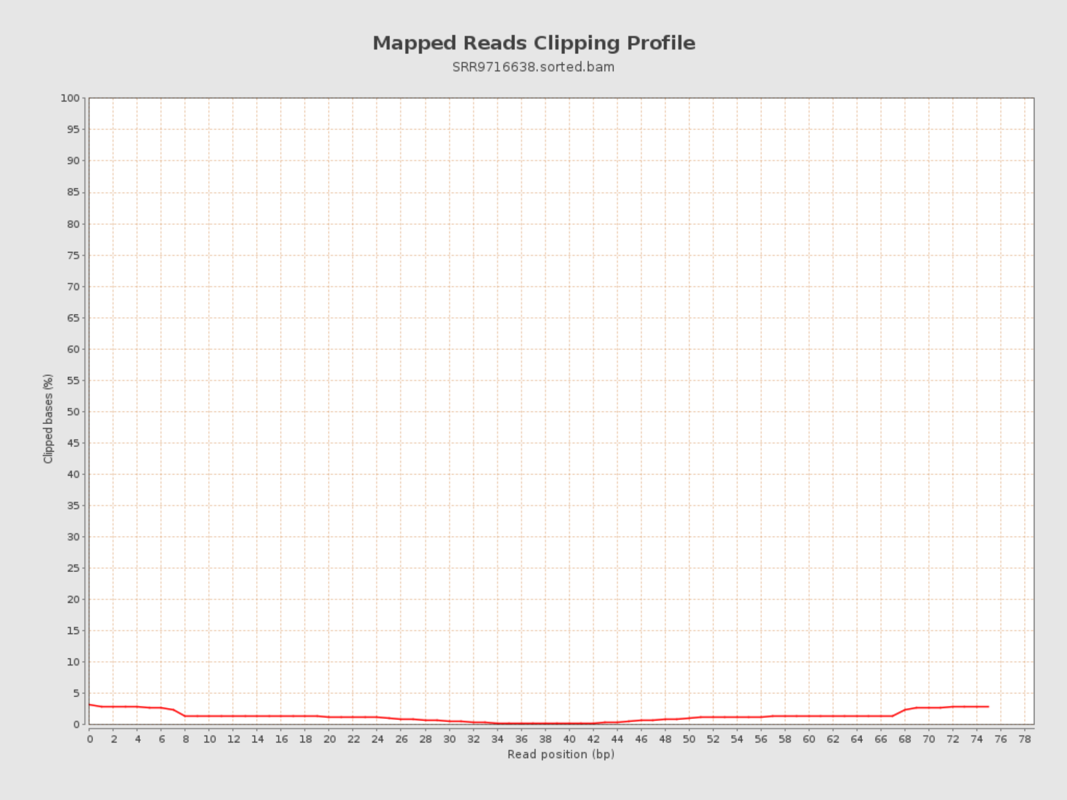
8. Results : Mapped Reads Nucleotide Content



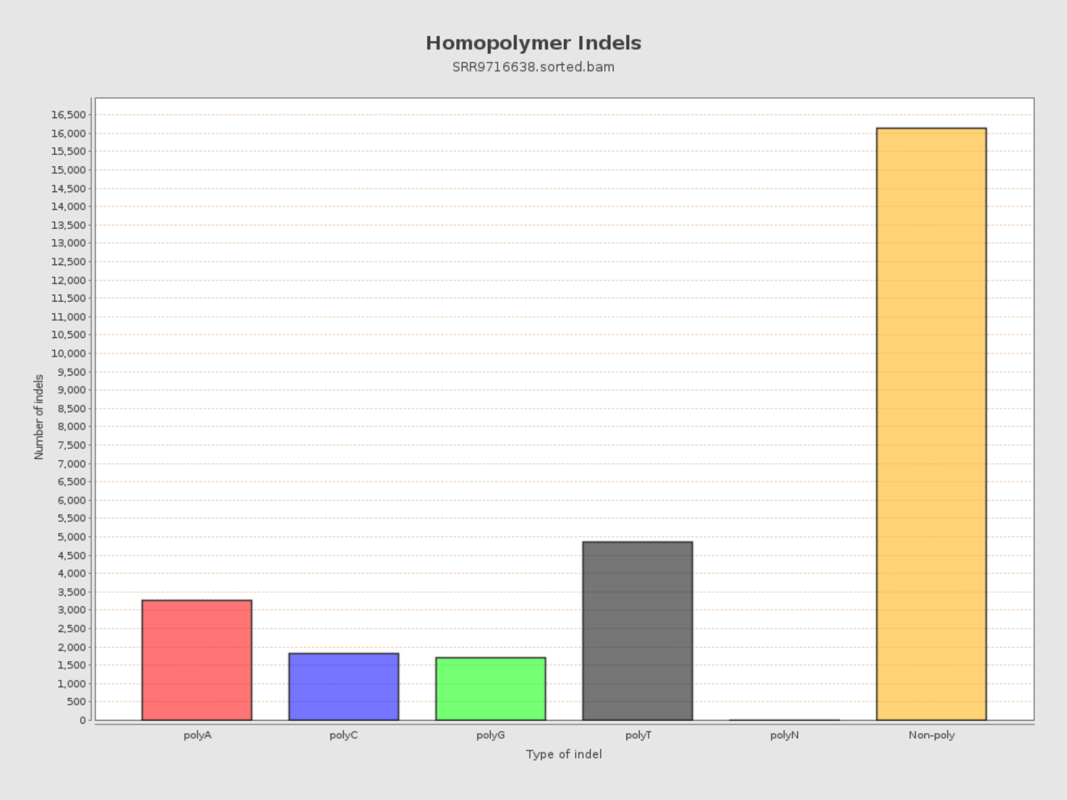
9. Results : Mapped Reads GC-content Distribution



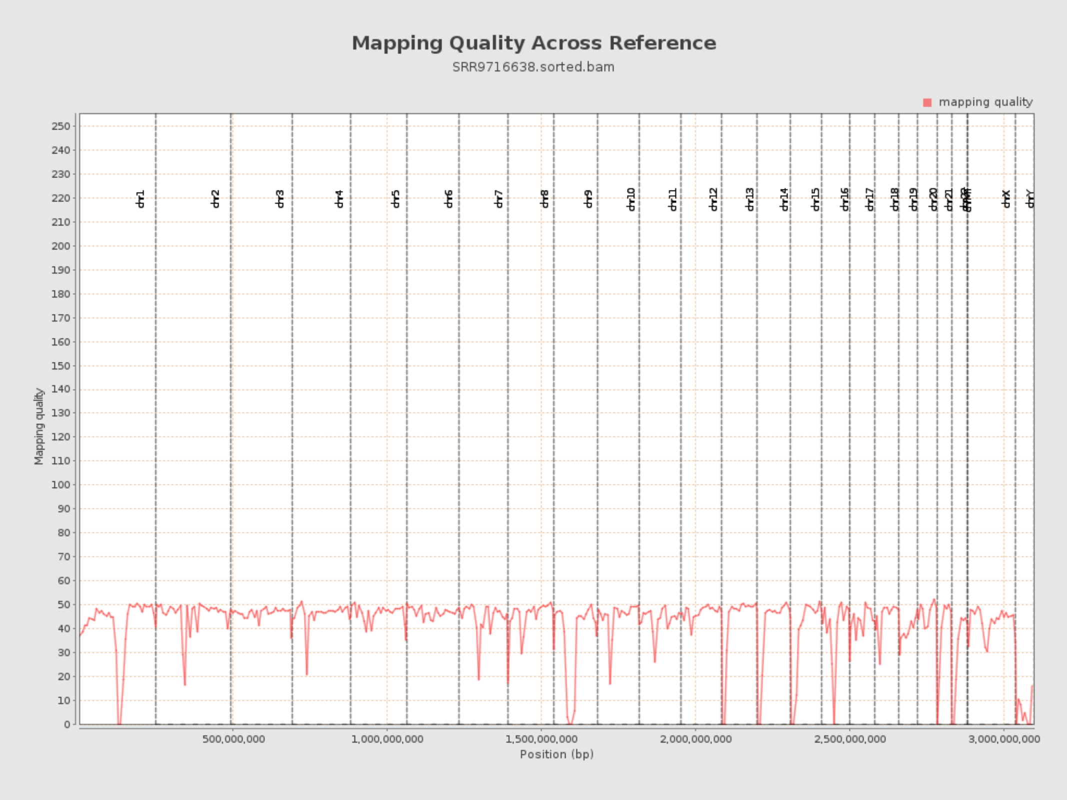
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram