Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:47:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716969.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_SRR9716969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716969.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:47:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,888,705
Mapped reads	1,579,567 / 83.63%
Unmapped reads	309,138 / 16.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,856 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	38,792 / 2.05%
Duplication rate	1.82%
Clipped reads	1,582,136 / 83.77%

2.2. ACGT Content

Number/percentage of A's	19,893,673 / 23.01%
Number/percentage of C's	19,694,895 / 22.78%
Number/percentage of T's	25,399,259 / 29.38%
Number/percentage of G's	21,468,135 / 24.83%
Number/percentage of N's	2,226 / 0%
GC Percentage	47.61%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.2127

2.4. Mapping Quality

Mean Mapping Quality	40.09

2.5. Mismatches and indels

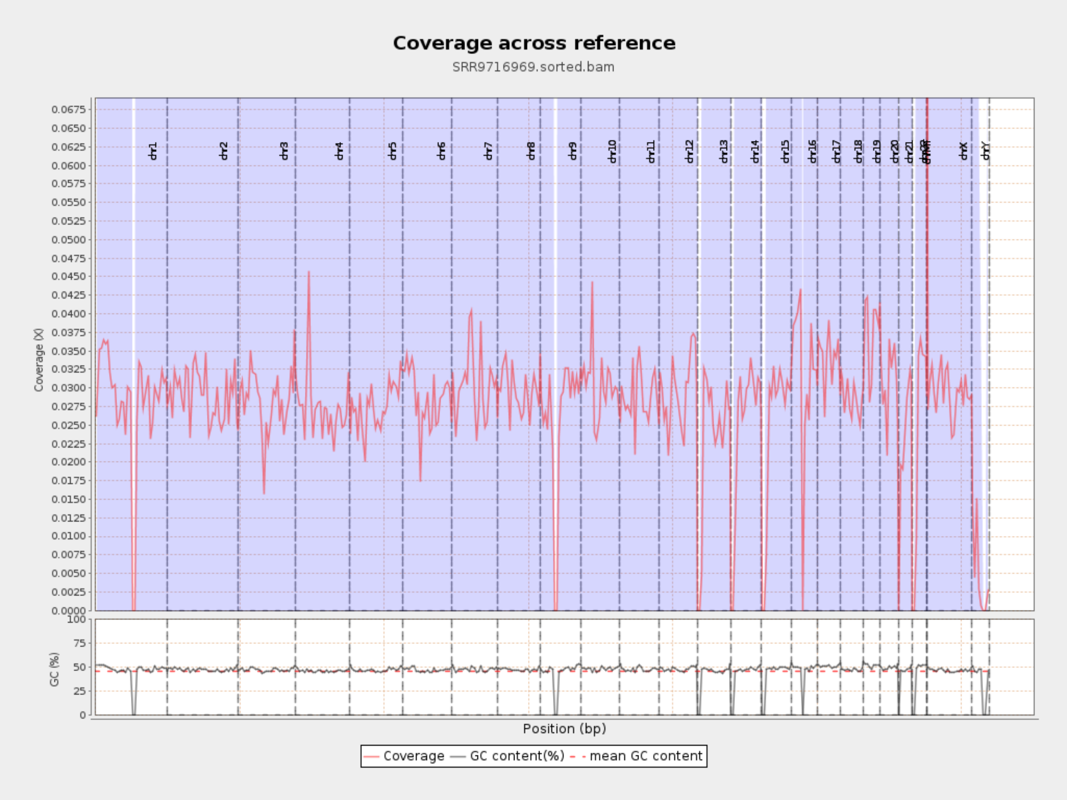
General error rate	0.52%
Mismatches	441,933
Insertions	5,696
Mapped reads with at least one insertion	0.36%
Deletions	13,107
Mapped reads with at least one deletion	0.82%
Homopolymer indels	36.97%

2.6. Chromosome stats

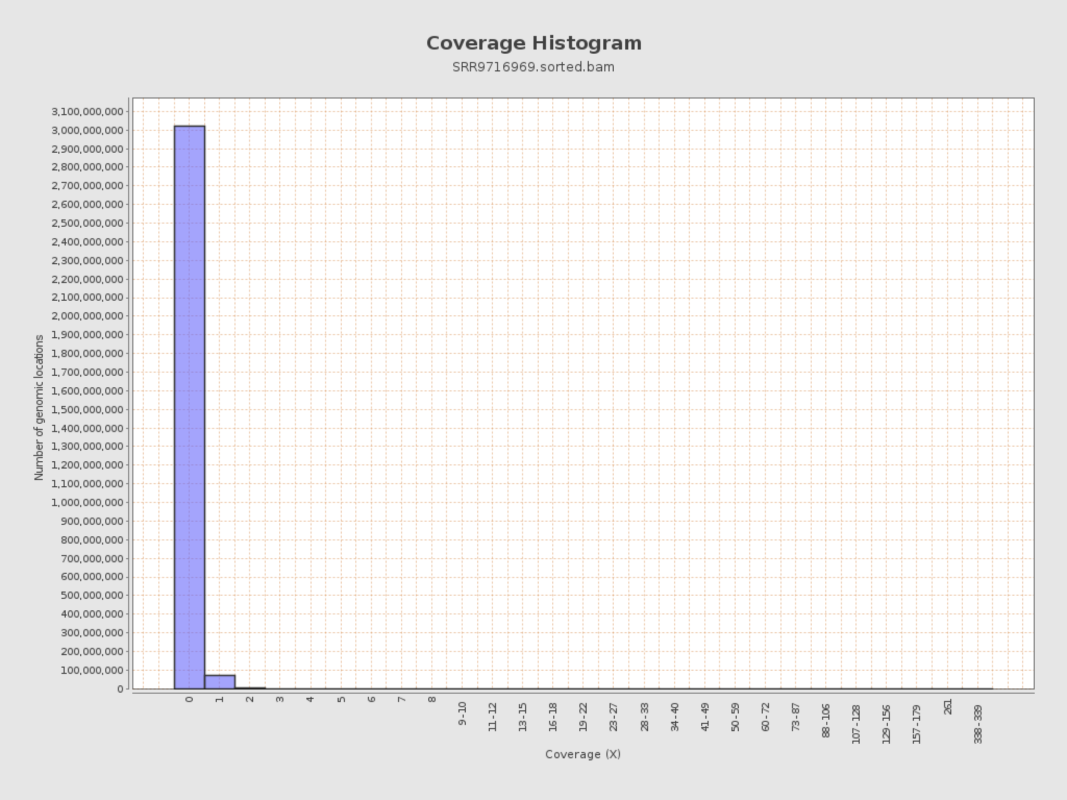
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7009638	0.0281	0.2278
chr2	243199373	7089342	0.0292	0.2601
chr3	198022430	5565778	0.0281	0.1911
chr4	191154276	5281527	0.0276	0.2031
chr5	180915260	4994435	0.0276	0.1837
chr6	171115067	4900705	0.0286	0.1925
chr7	159138663	4848452	0.0305	0.2633

chr8	146364022	4313603	0.0295	0.2015
chr9	141213431	3602191	0.0255	0.1957
chr10	135534747	4125757	0.0304	0.2512
chr11	135006516	3926561	0.0291	0.2348
chr12	133851895	3951346	0.0295	0.1923
chr13	115169878	2609483	0.0227	0.1676
chr14	107349540	2642930	0.0246	0.1803
chr15	102531392	2487365	0.0243	0.1779
chr16	90354753	2839310	0.0314	0.2105
chr17	81195210	2761585	0.034	0.212
chr18	78077248	2214349	0.0284	0.2592
chr19	59128983	2201363	0.0372	0.2447
chr20	63025520	1934134	0.0307	0.2001
chr21	48129895	1110662	0.0231	0.1865
chr22	51304566	1215207	0.0237	0.1761
chrMT	16571	8074	0.4872	0.7892
chrX	155270560	4573333	0.0295	0.2064
chrY	59373566	272024	0.0046	0.1229

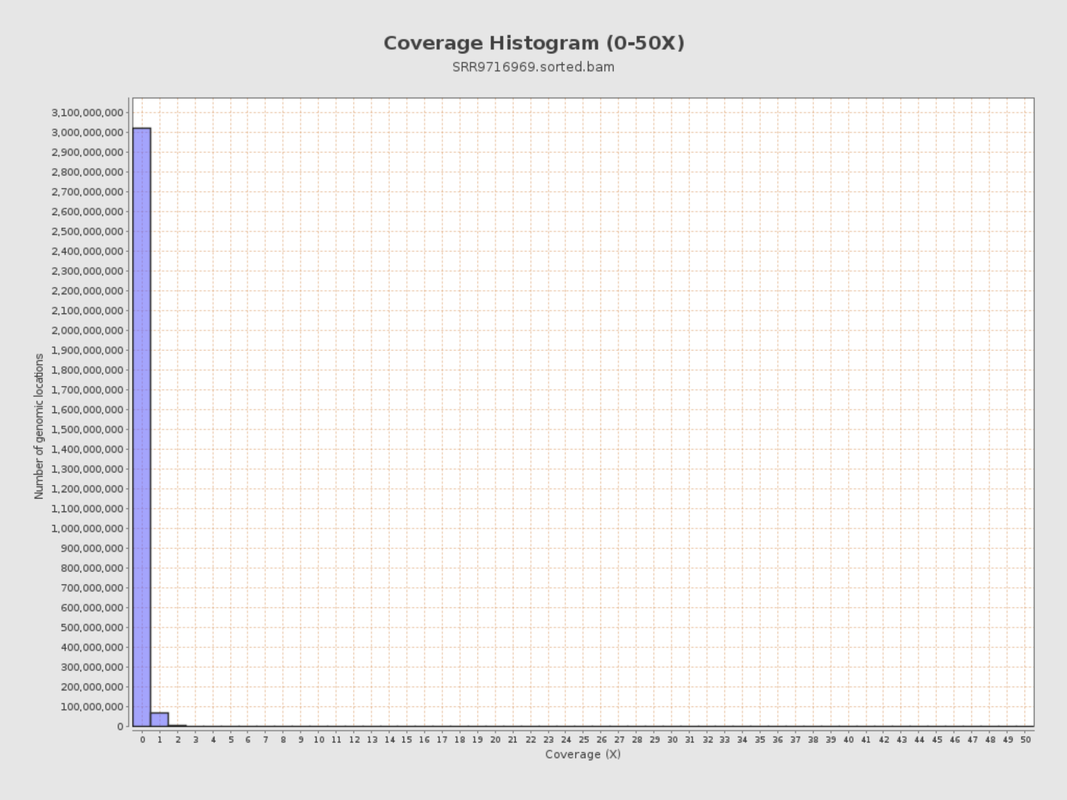
3. Results : Coverage across reference



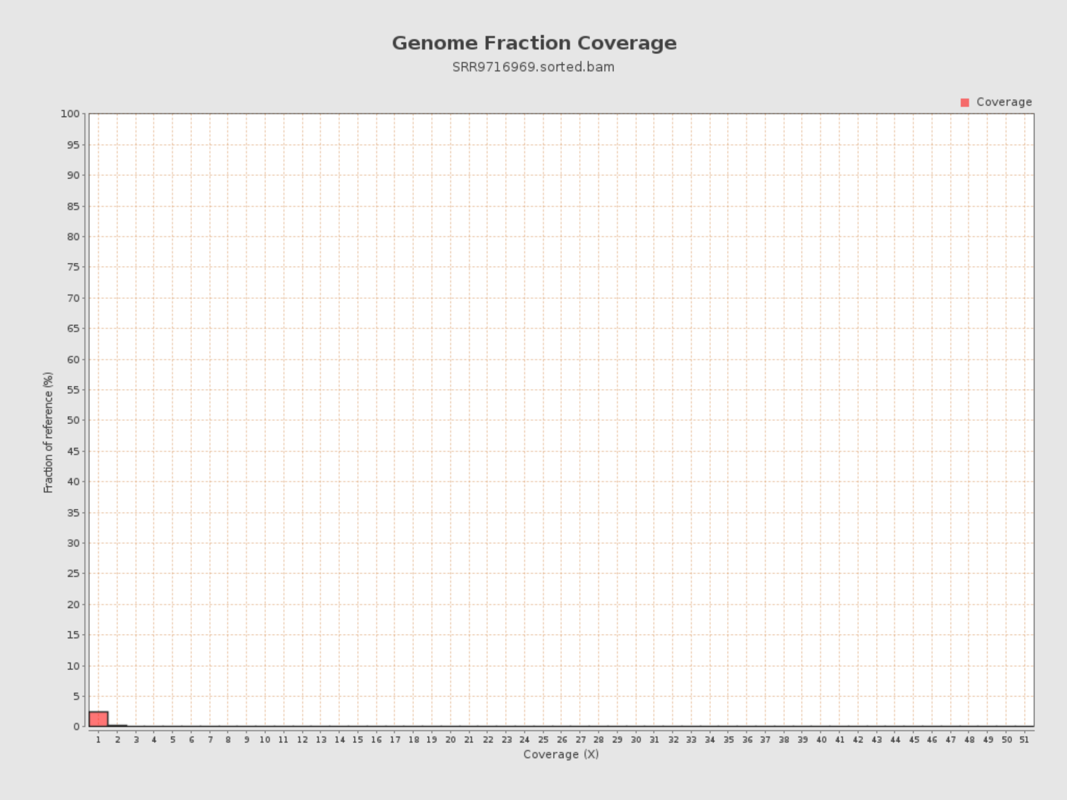
4. Results : Coverage Histogram



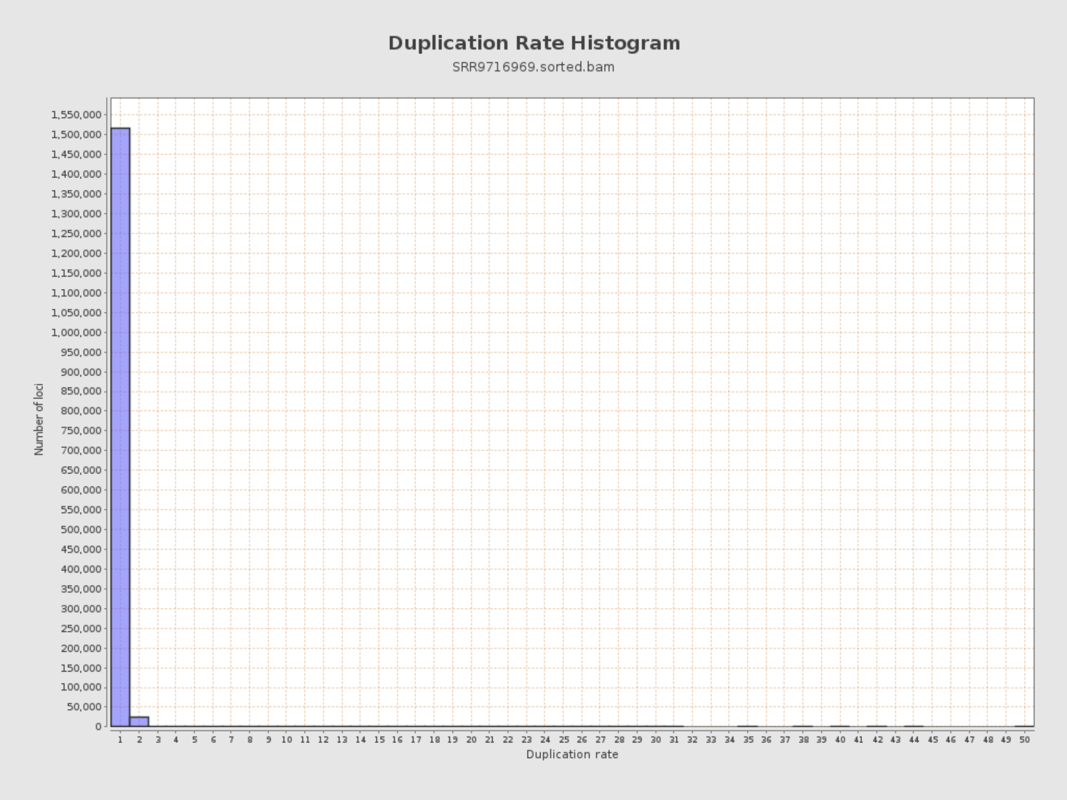
5. Results : Coverage Histogram (0-50X)



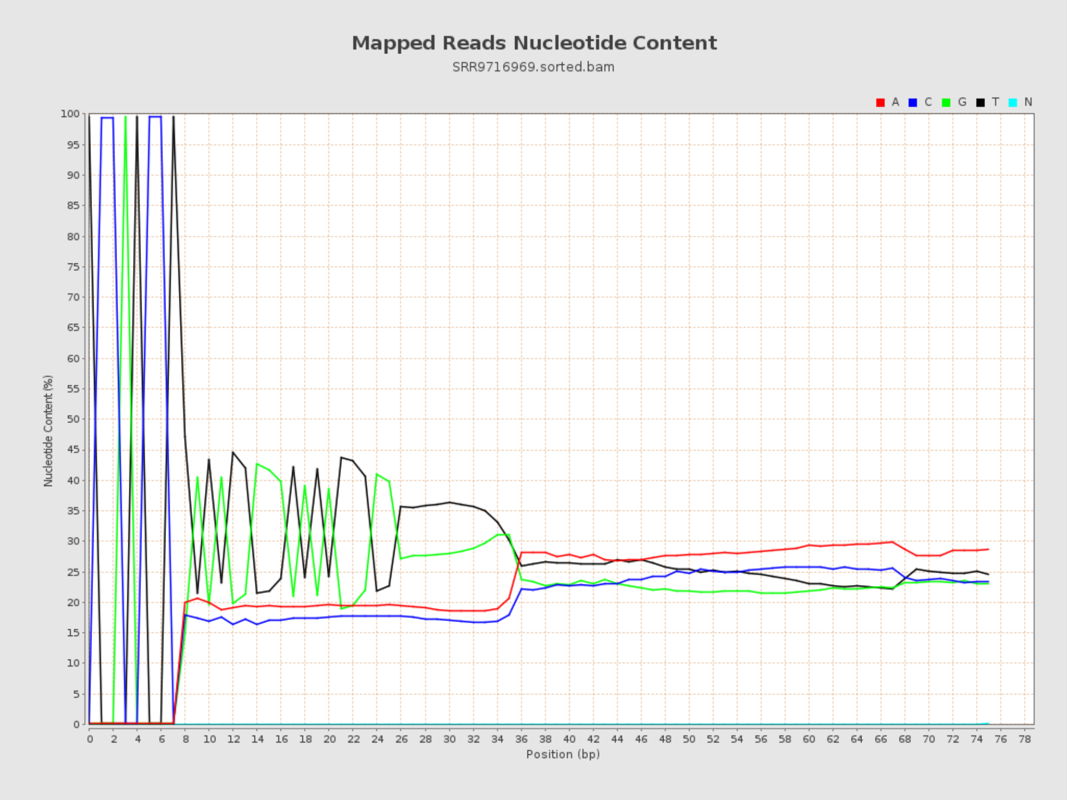
6. Results : Genome Fraction Coverage



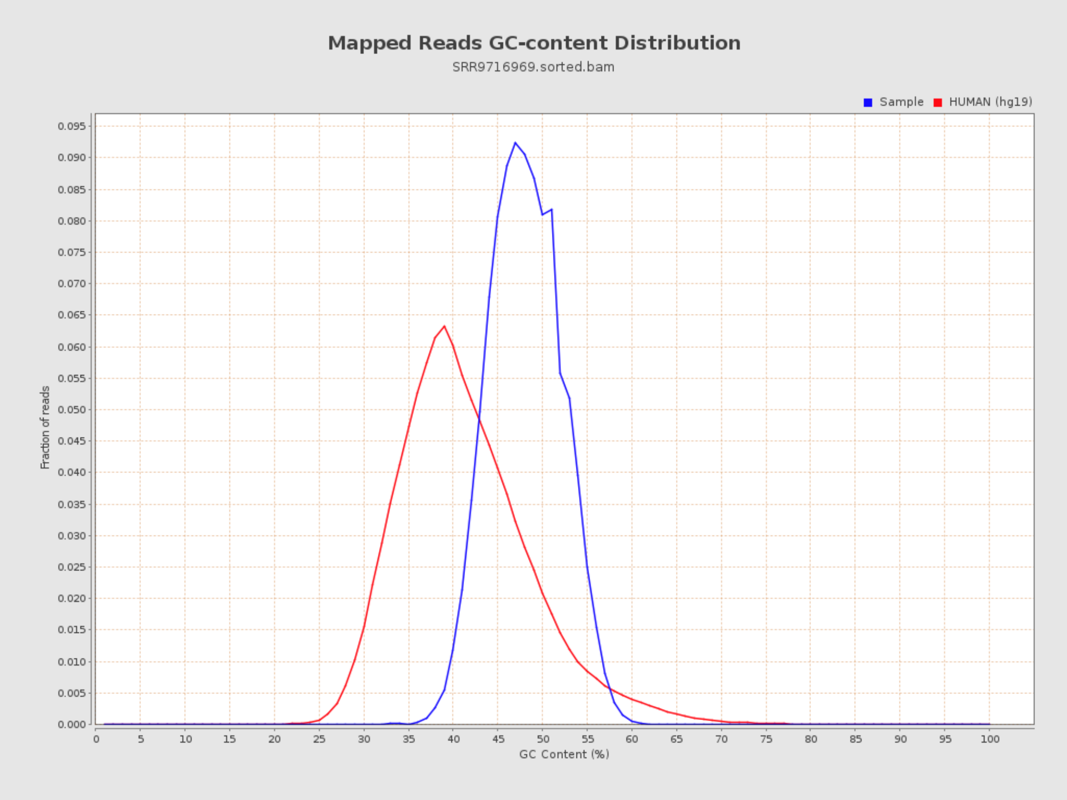
7. Results : Duplication Rate Histogram



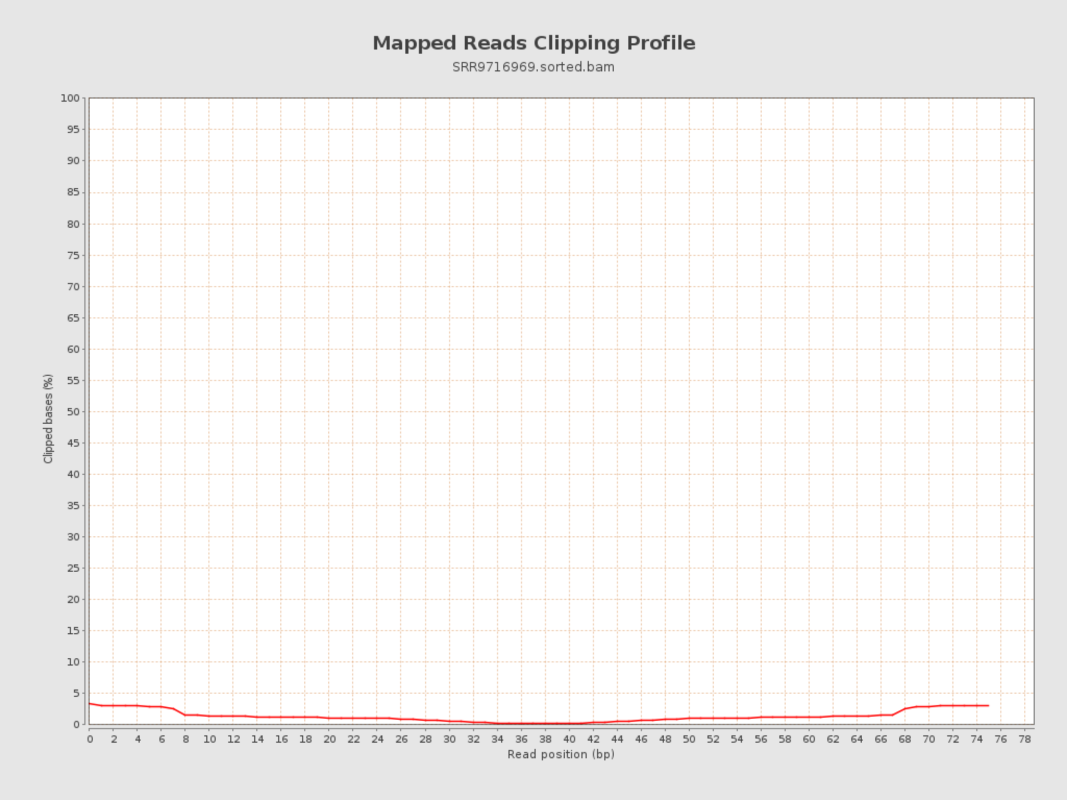
8. Results : Mapped Reads Nucleotide Content



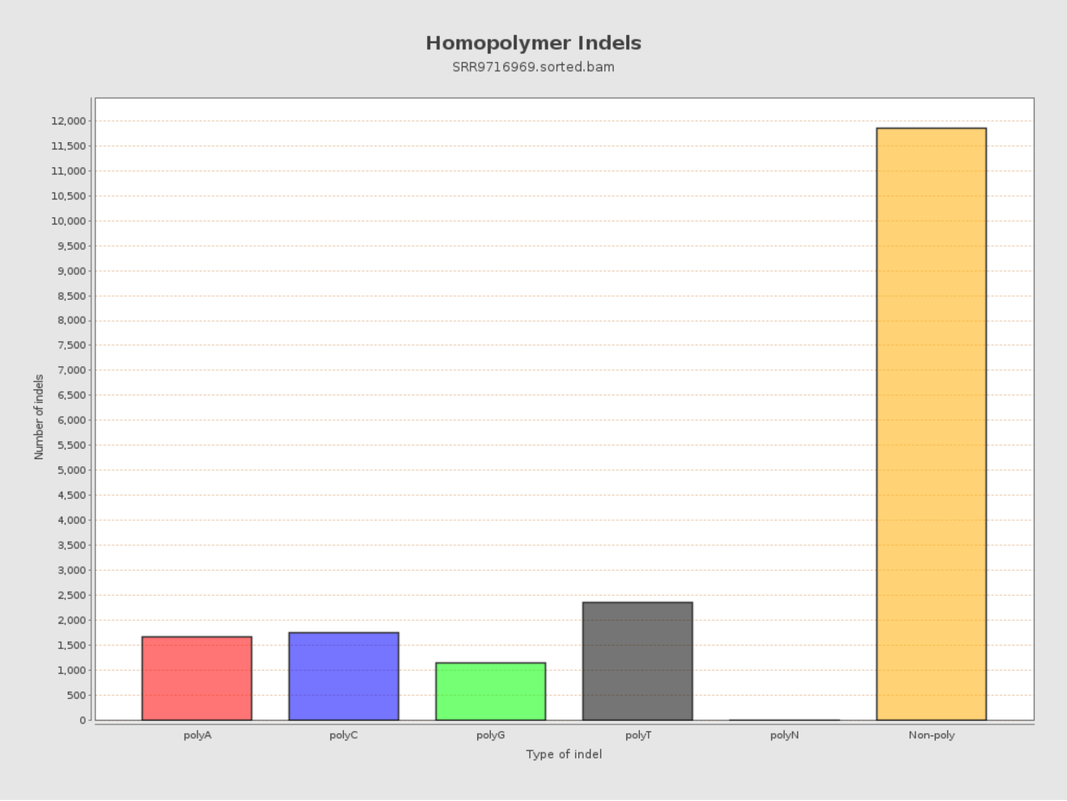
9. Results : Mapped Reads GC-content Distribution



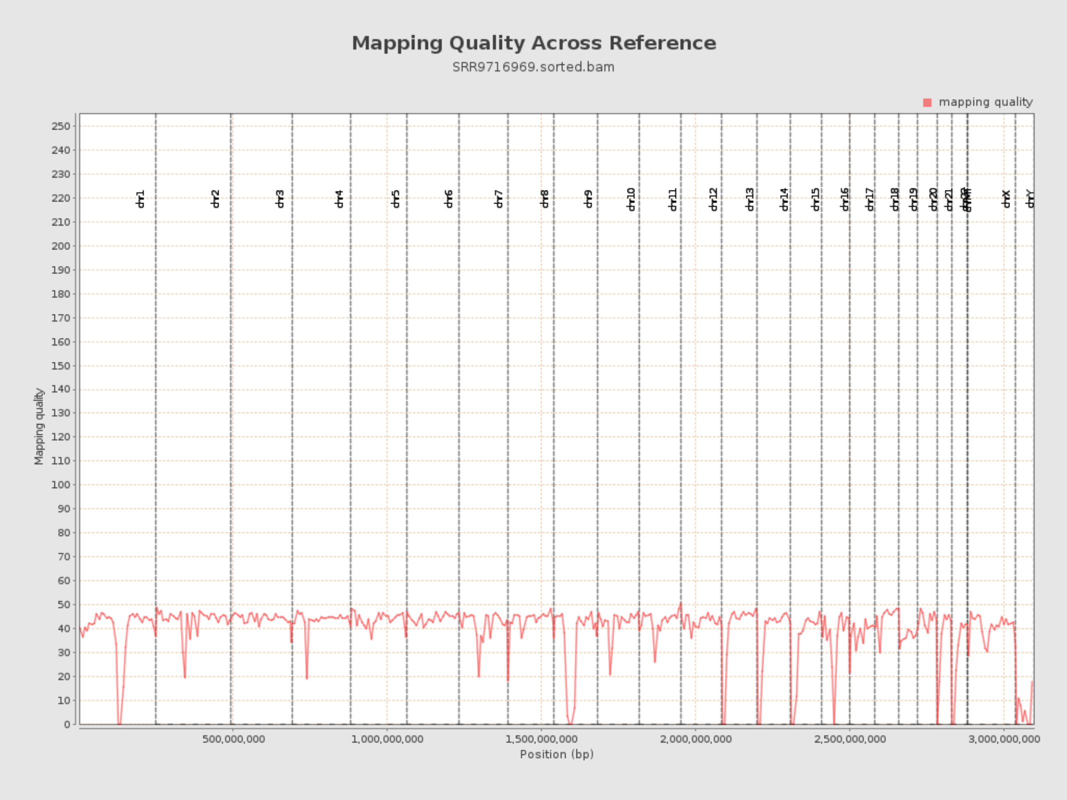
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram