Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:50:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716800.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_SRR9716800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:50:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,336,943
Mapped reads	1,219,115 / 91.19%
Unmapped reads	117,828 / 8.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,283 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	42,627 / 3.19%
Duplication rate	2.78%
Clipped reads	1,222,072 / 91.41%

2.2. ACGT Content

Number/percentage of A's	17,511,068 / 24.59%
Number/percentage of C's	13,784,579 / 19.36%
Number/percentage of T's	22,426,091 / 31.49%
Number/percentage of G's	17,483,417 / 24.55%
Number/percentage of N's	1,039 / 0%
GC Percentage	43.91%

2.3. Coverage

Mean	0.023

Standard Deviation	0.209

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

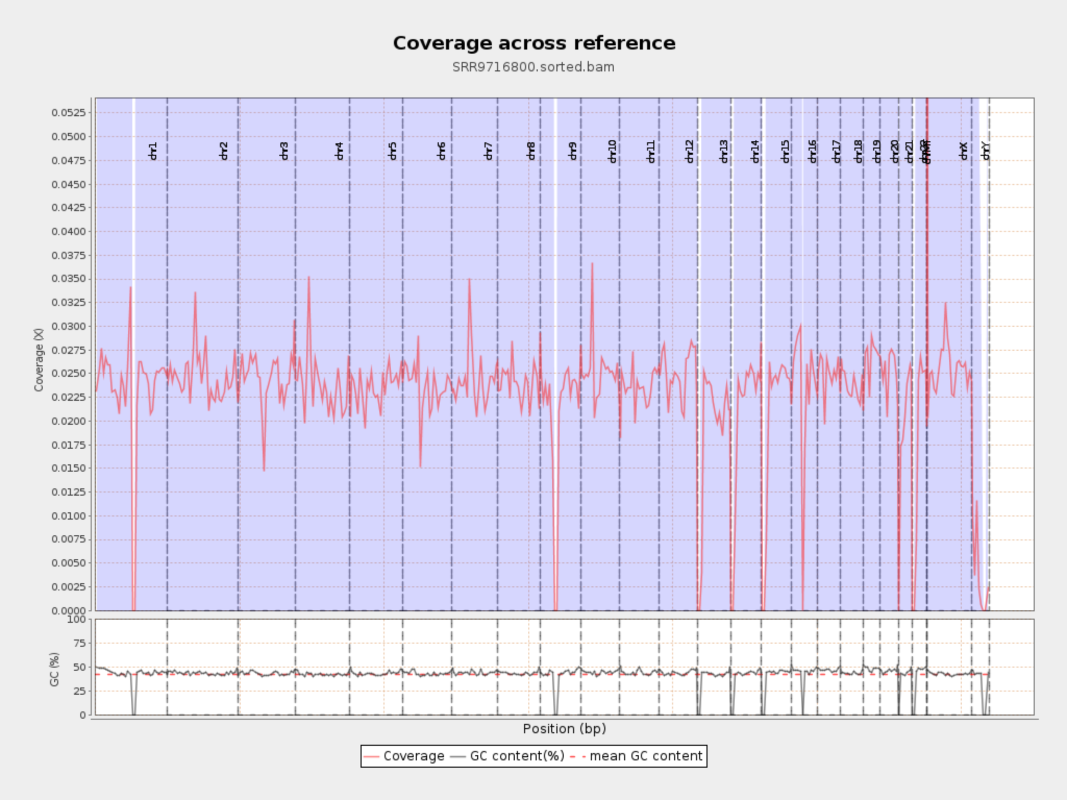
General error rate	0.51%
Mismatches	350,715
Insertions	5,384
Mapped reads with at least one insertion	0.44%
Deletions	13,010
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.93%

2.6. Chromosome stats

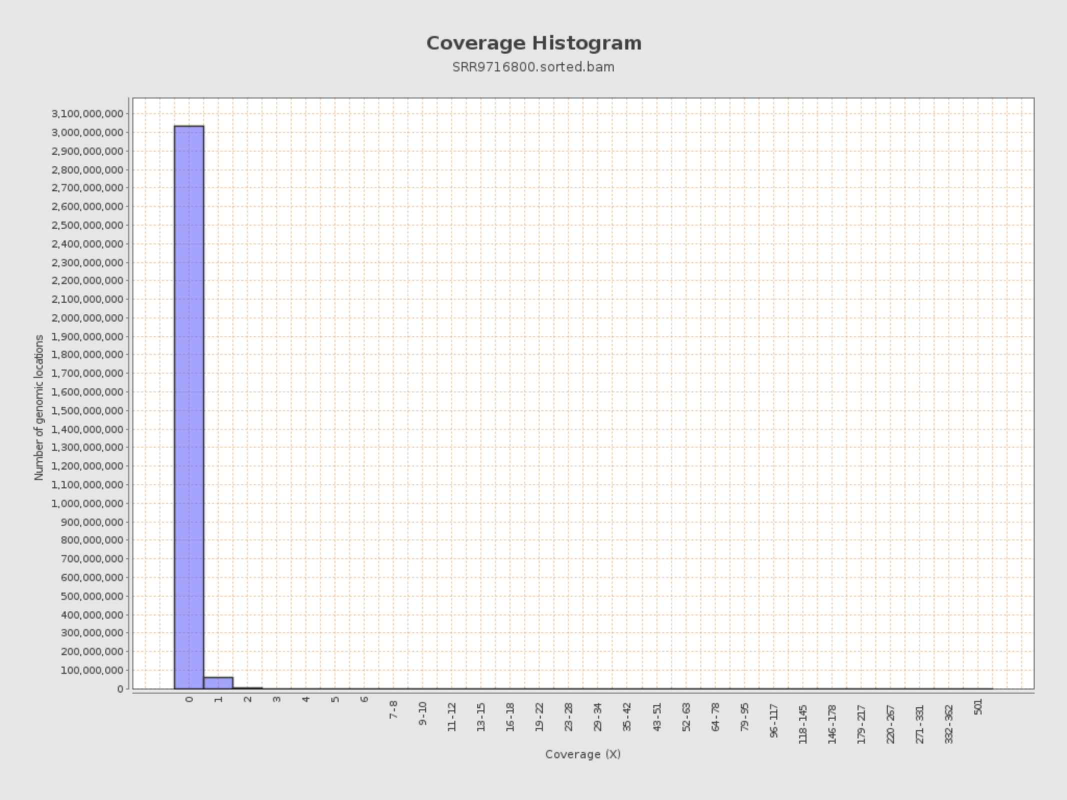
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5770917	0.0232	0.3156
chr2	243199373	6010001	0.0247	0.2752
chr3	198022430	4836585	0.0244	0.1714
chr4	191154276	4562413	0.0239	0.1792
chr5	180915260	4284697	0.0237	0.1688
chr6	171115067	4038637	0.0236	0.1915
chr7	159138663	3879659	0.0244	0.2461

chr8	146364022	3497467	0.0239	0.1915
chr9	141213431	2895660	0.0205	0.1803
chr10	135534747	3426159	0.0253	0.2098
chr11	135006516	3185876	0.0236	0.1963
chr12	133851895	3357591	0.0251	0.1746
chr13	115169878	2130535	0.0185	0.1484
chr14	107349540	2156944	0.0201	0.1605
chr15	102531392	2055681	0.02	0.1592
chr16	90354753	2085121	0.0231	0.1742
chr17	81195210	2028212	0.025	0.1801
chr18	78077248	1853727	0.0237	0.282
chr19	59128983	1579593	0.0267	0.2584
chr20	63025520	1588305	0.0252	0.1754
chr21	48129895	941394	0.0196	0.163
chr22	51304566	882227	0.0172	0.1436
chrMT	16571	5738	0.3463	0.6894
chrX	155270560	3961520	0.0255	0.1869
chrY	59373566	212133	0.0036	0.0938

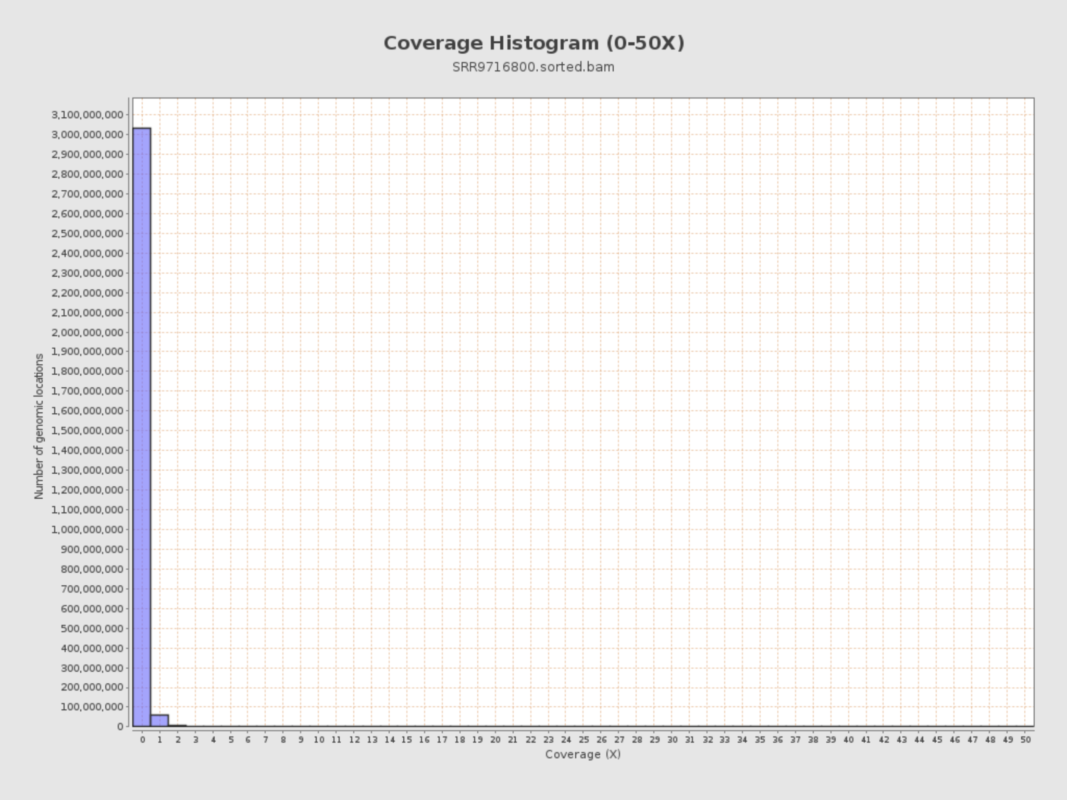
3. Results : Coverage across reference



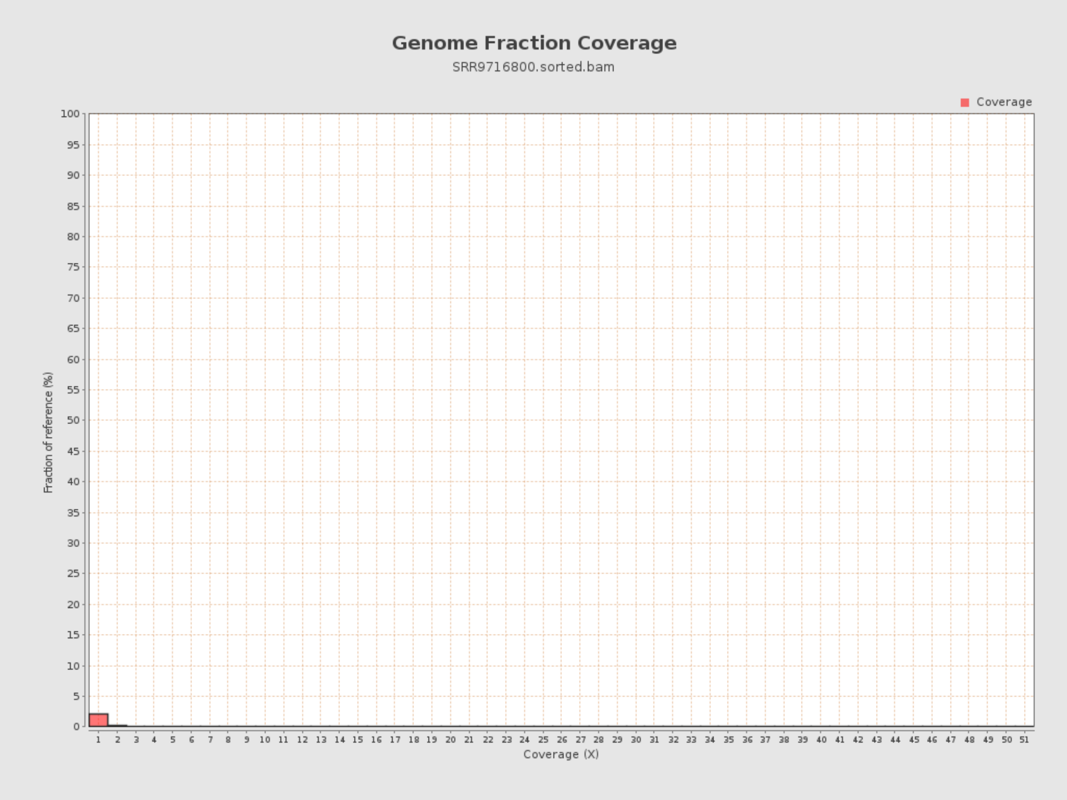
4. Results : Coverage Histogram



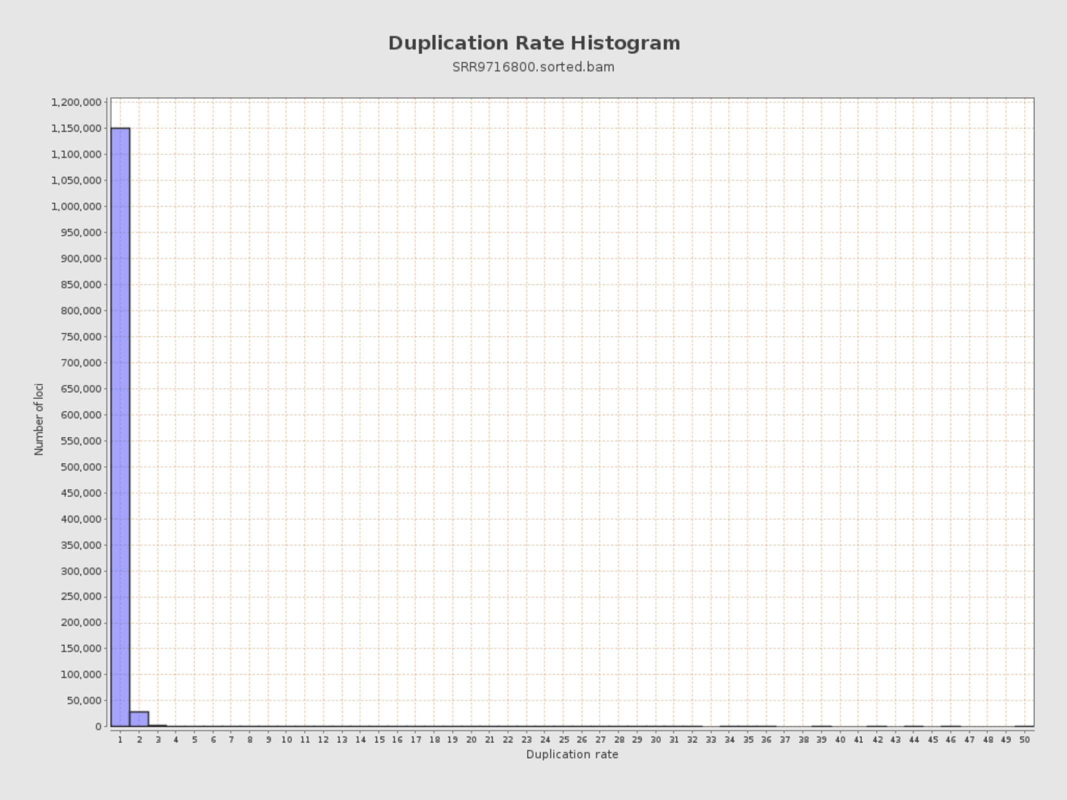
5. Results : Coverage Histogram (0-50X)



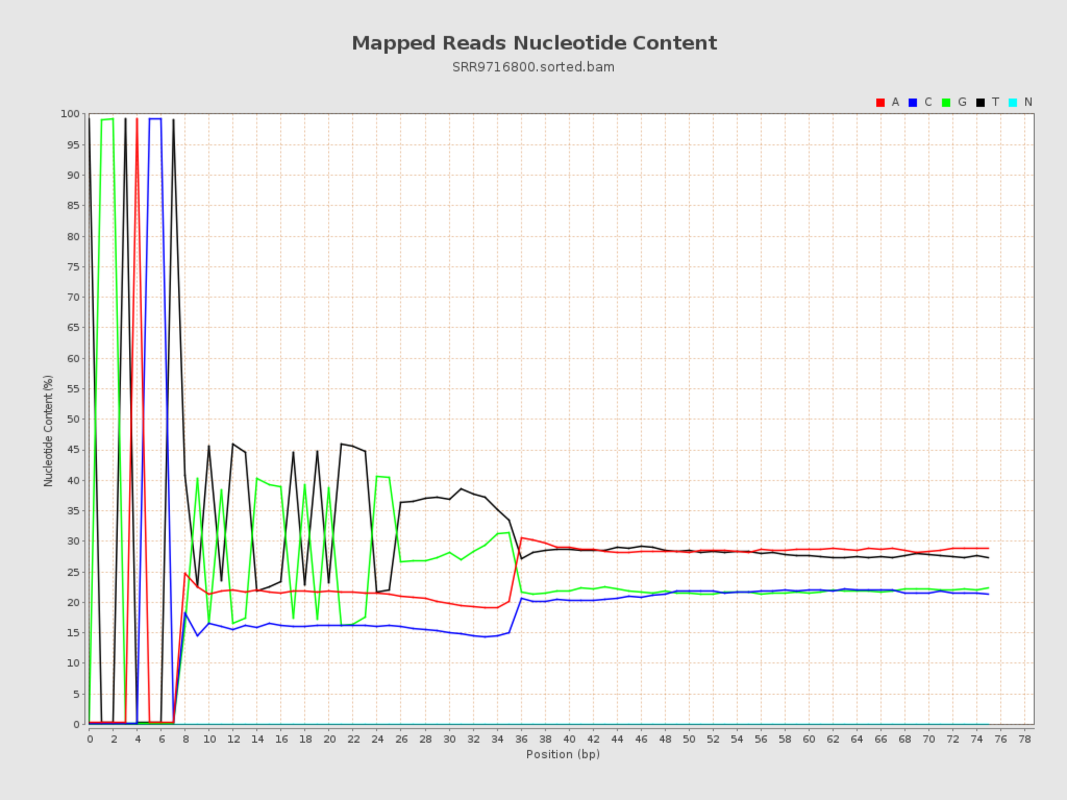
6. Results : Genome Fraction Coverage



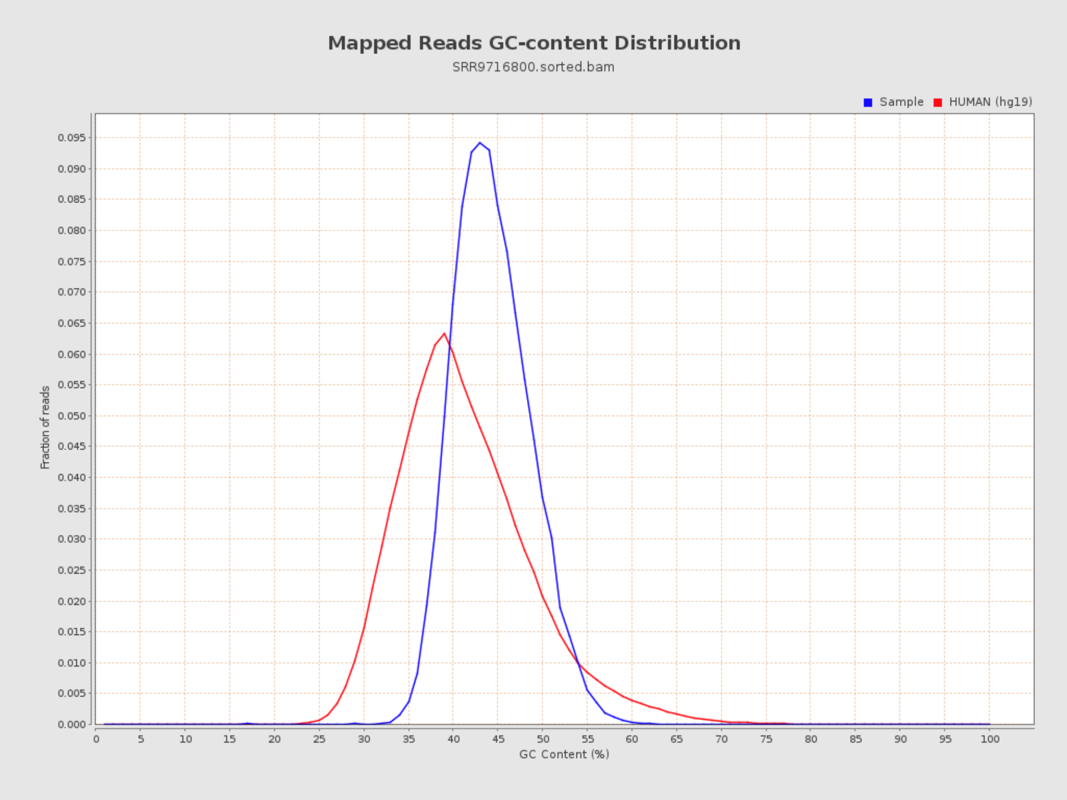
7. Results : Duplication Rate Histogram



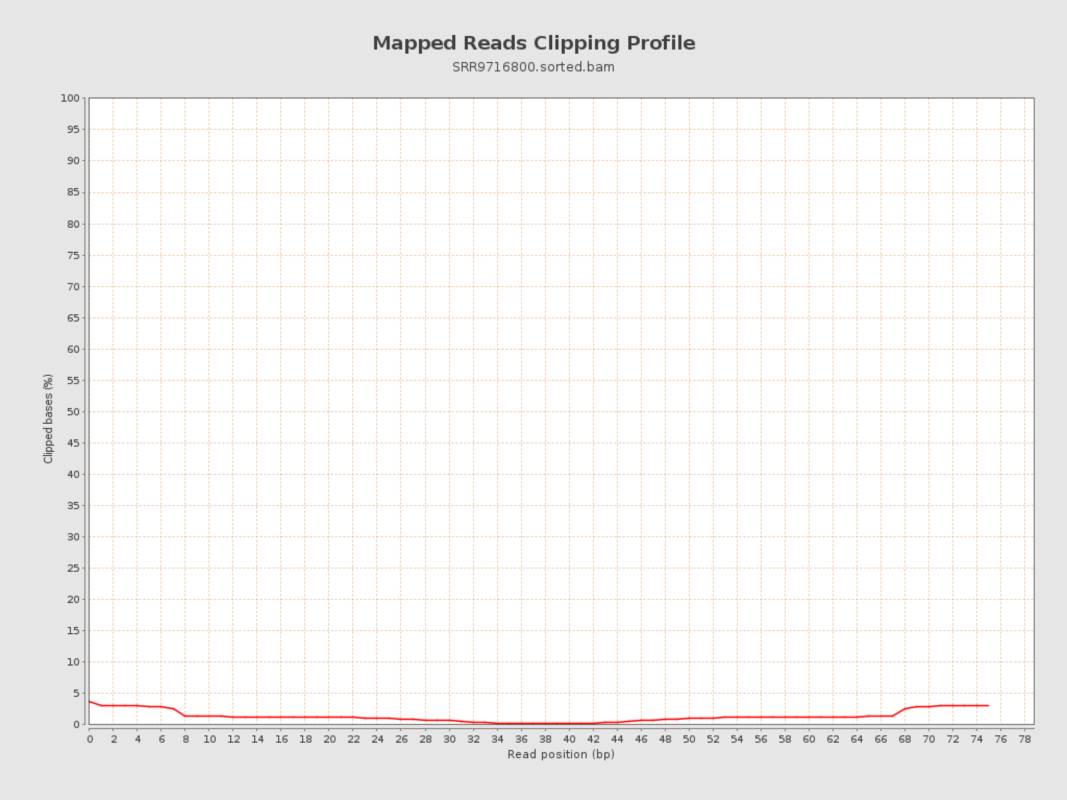
8. Results : Mapped Reads Nucleotide Content



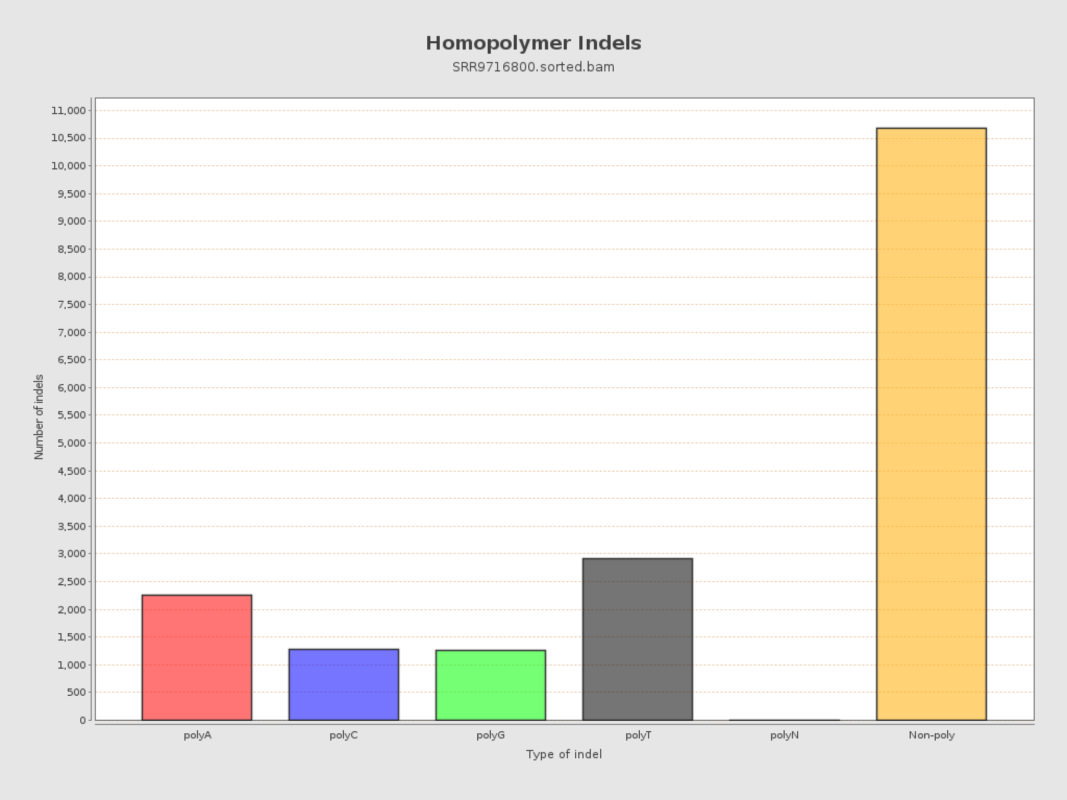
9. Results : Mapped Reads GC-content Distribution



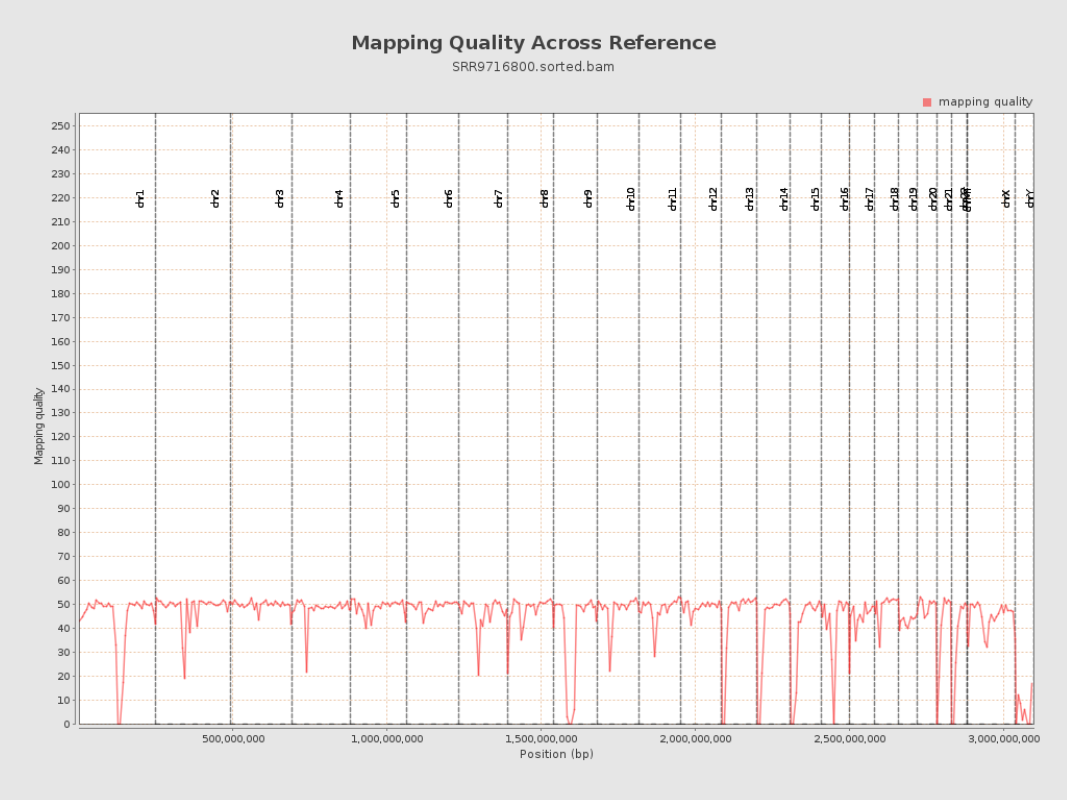
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram