Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:05:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716191.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_SRR9716191 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716191.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:05:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	849,649
Mapped reads	803,056 / 94.52%
Unmapped reads	46,593 / 5.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,166 / 2.02%
Read min/max/mean length	30 / 101 / 101.74
Duplicated reads (estimated)	26,319 / 3.1%
Duplication rate	2.64%
Clipped reads	819,489 / 96.45%

2.2. ACGT Content

Number/percentage of A's	15,719,577 / 25.08%
Number/percentage of C's	13,432,994 / 21.43%
Number/percentage of T's	18,132,920 / 28.93%
Number/percentage of G's	15,401,399 / 24.57%
Number/percentage of N's	2,282 / 0%
GC Percentage	46%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.1951

2.4. Mapping Quality

Mean Mapping Quality	46.79

2.5. Mismatches and indels

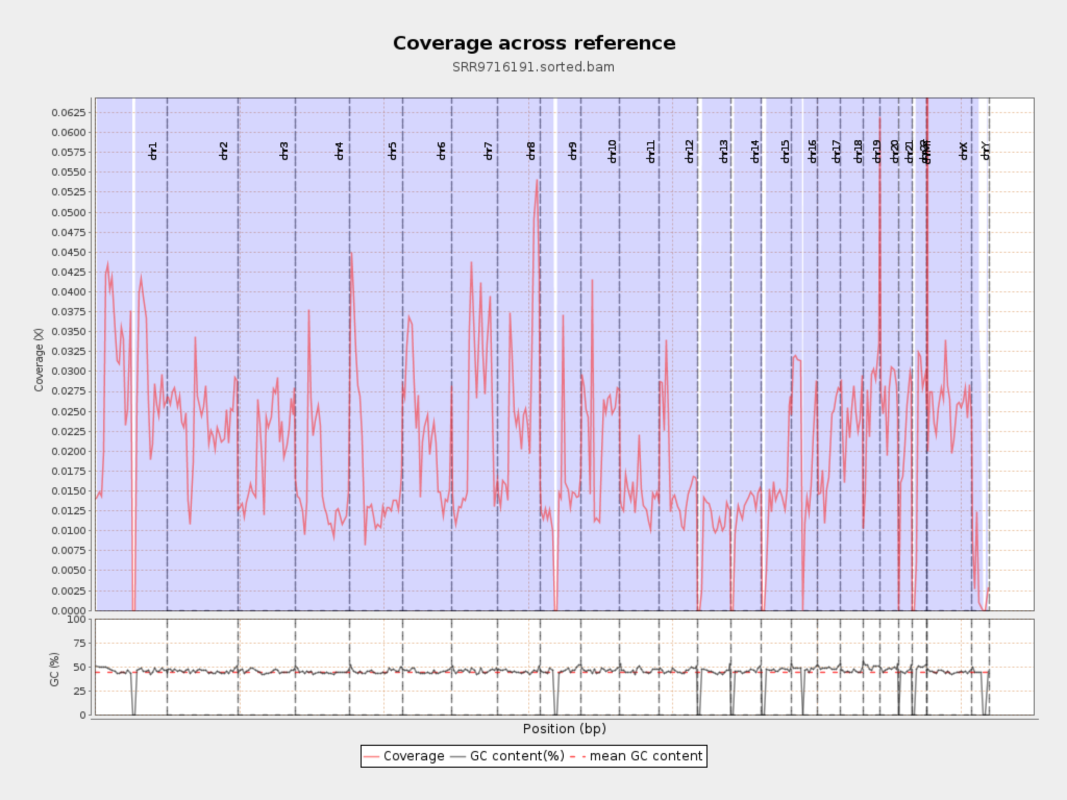
General error rate	0.66%
Mismatches	399,607
Insertions	4,883
Mapped reads with at least one insertion	0.6%
Deletions	11,950
Mapped reads with at least one deletion	1.46%
Homopolymer indels	39.26%

2.6. Chromosome stats

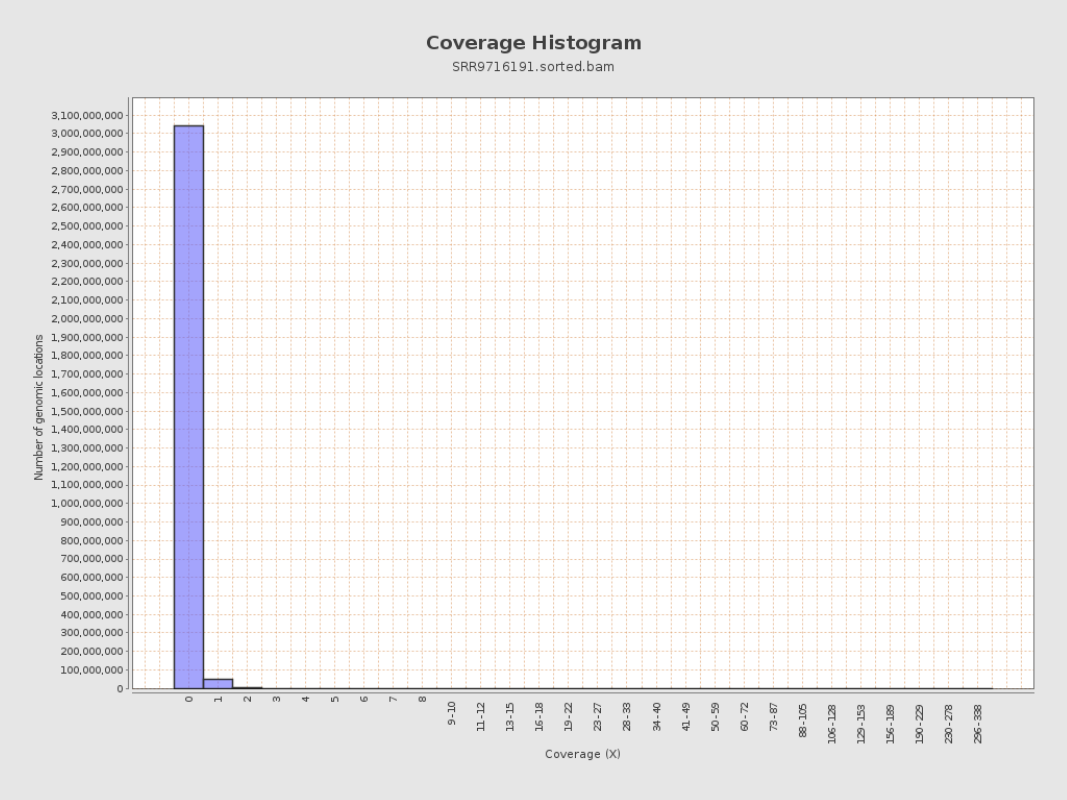
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6966231	0.0279	0.3366
chr2	243199373	5823921	0.0239	0.2088
chr3	198022430	4007806	0.0202	0.1553
chr4	191154276	3031540	0.0159	0.1703
chr5	180915260	3189932	0.0176	0.1454
chr6	171115067	3843512	0.0225	0.1685
chr7	159138663	3880036	0.0244	0.239

chr8	146364022	3889451	0.0266	0.2122
chr9	141213431	1882121	0.0133	0.1435
chr10	135534747	3201262	0.0236	0.2393
chr11	135006516	1939817	0.0144	0.1545
chr12	133851895	2375701	0.0177	0.1461
chr13	115169878	1150797	0.01	0.1078
chr14	107349540	1250895	0.0117	0.1202
chr15	102531392	1320412	0.0129	0.1229
chr16	90354753	1910587	0.0211	0.1634
chr17	81195210	1616869	0.0199	0.1625
chr18	78077248	1879747	0.0241	0.2111
chr19	59128983	1604766	0.0271	0.2659
chr20	63025520	1698012	0.0269	0.1843
chr21	48129895	986939	0.0205	0.1748
chr22	51304566	1042124	0.0203	0.1602
chrMT	16571	22216	1.3407	1.5787
chrX	155270560	4003417	0.0258	0.1804
chrY	59373566	195733	0.0033	0.1166

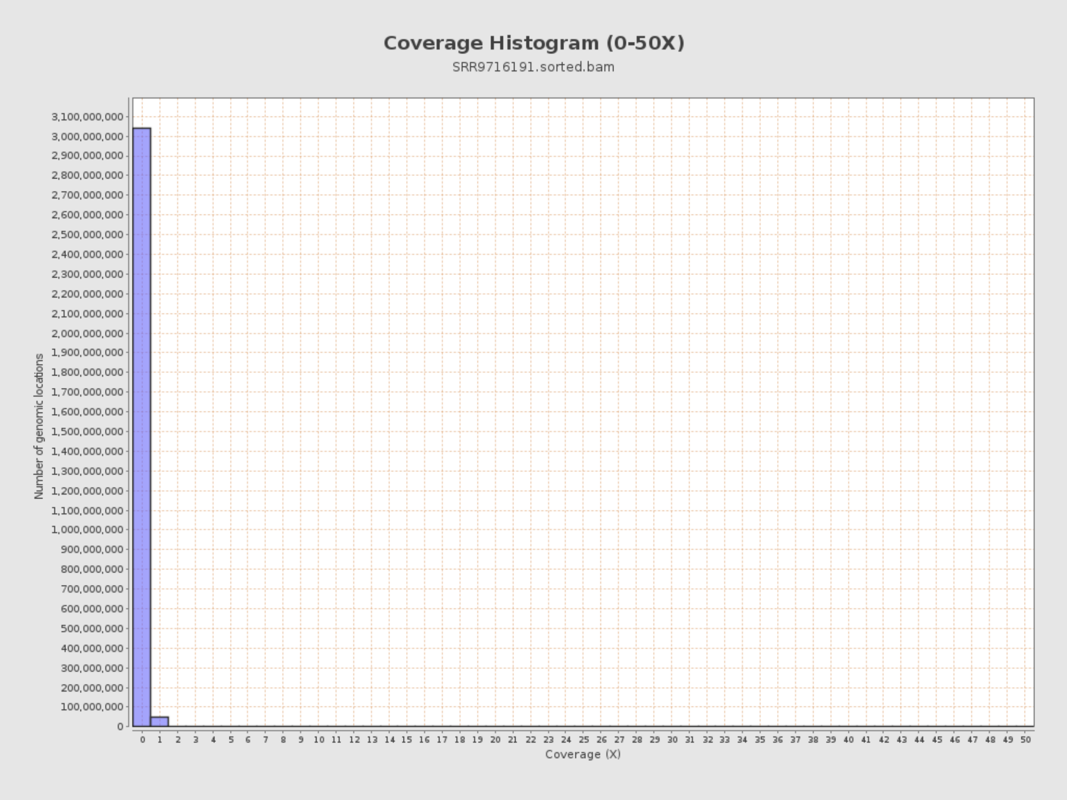
3. Results : Coverage across reference



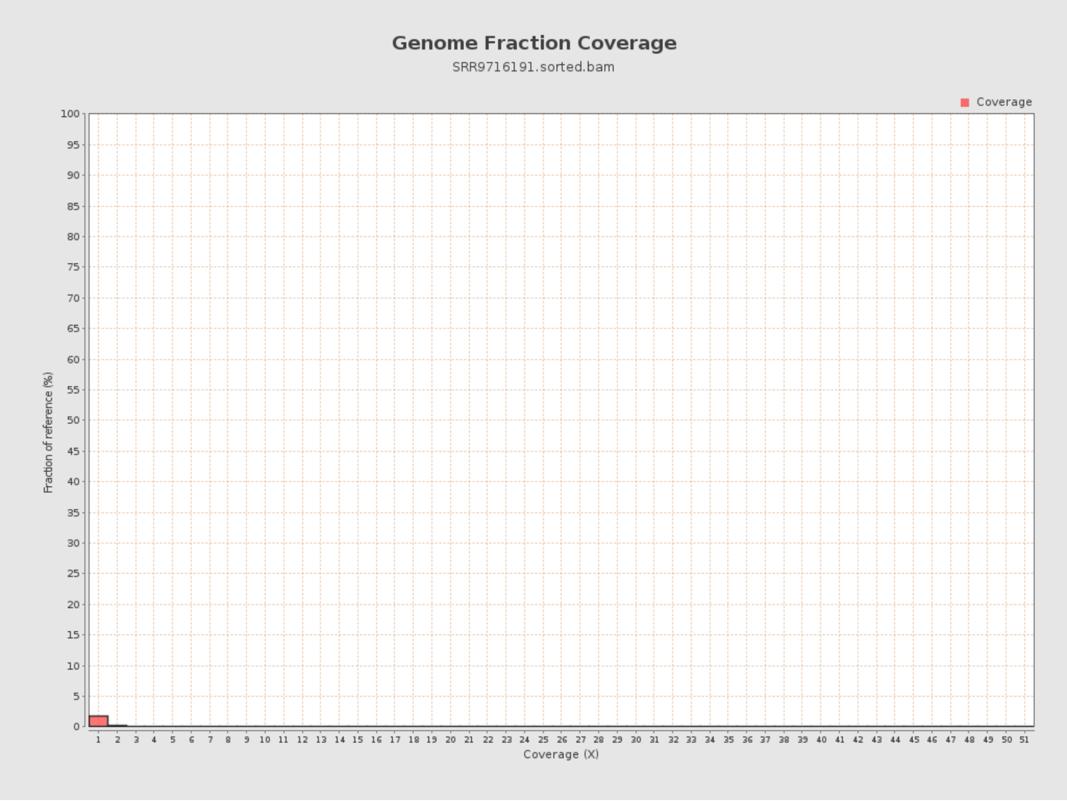
4. Results : Coverage Histogram



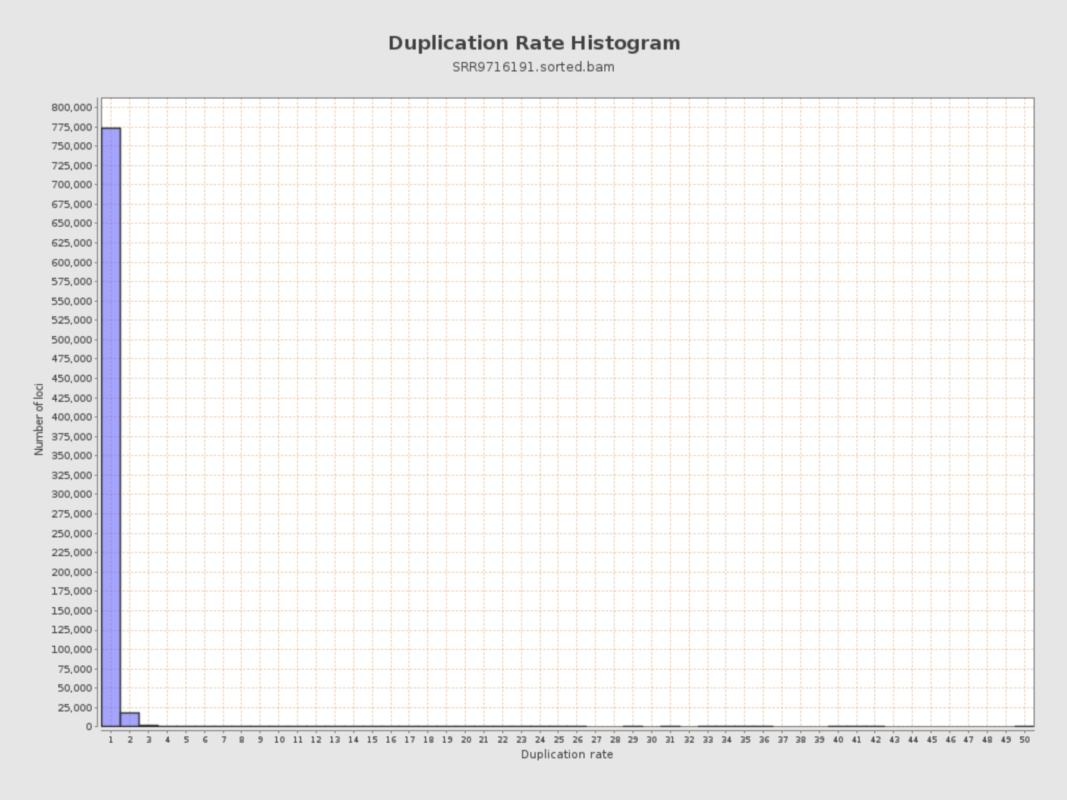
5. Results : Coverage Histogram (0-50X)



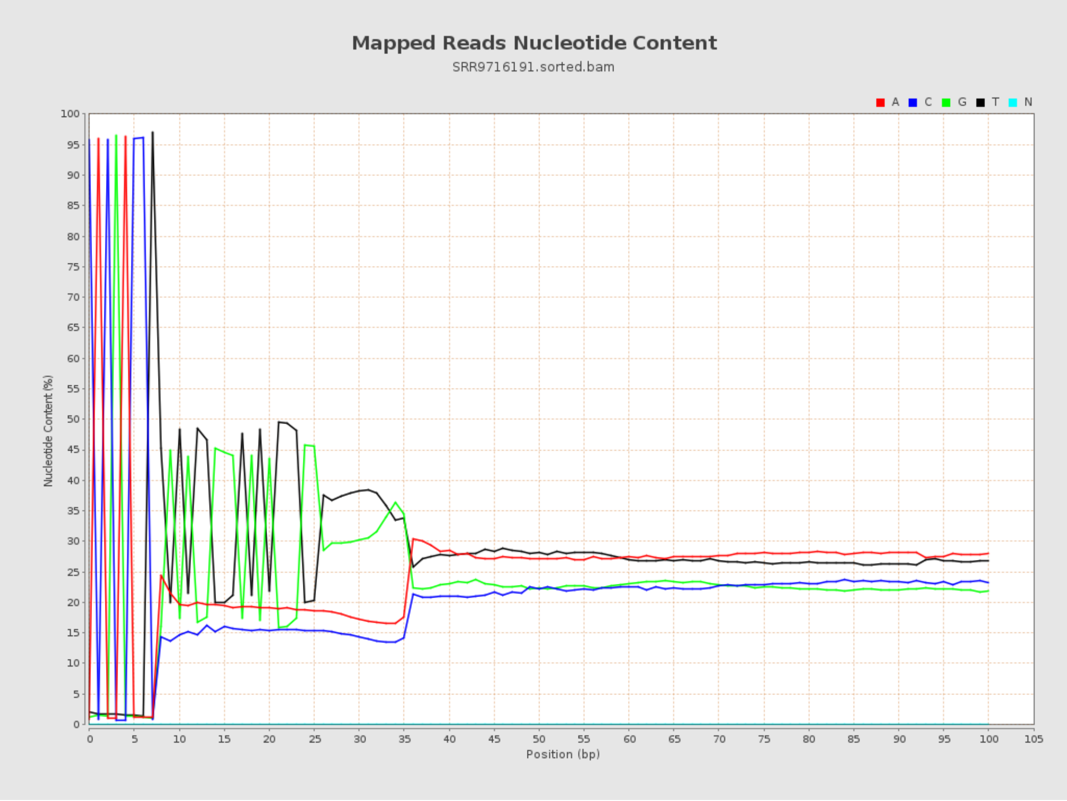
6. Results : Genome Fraction Coverage



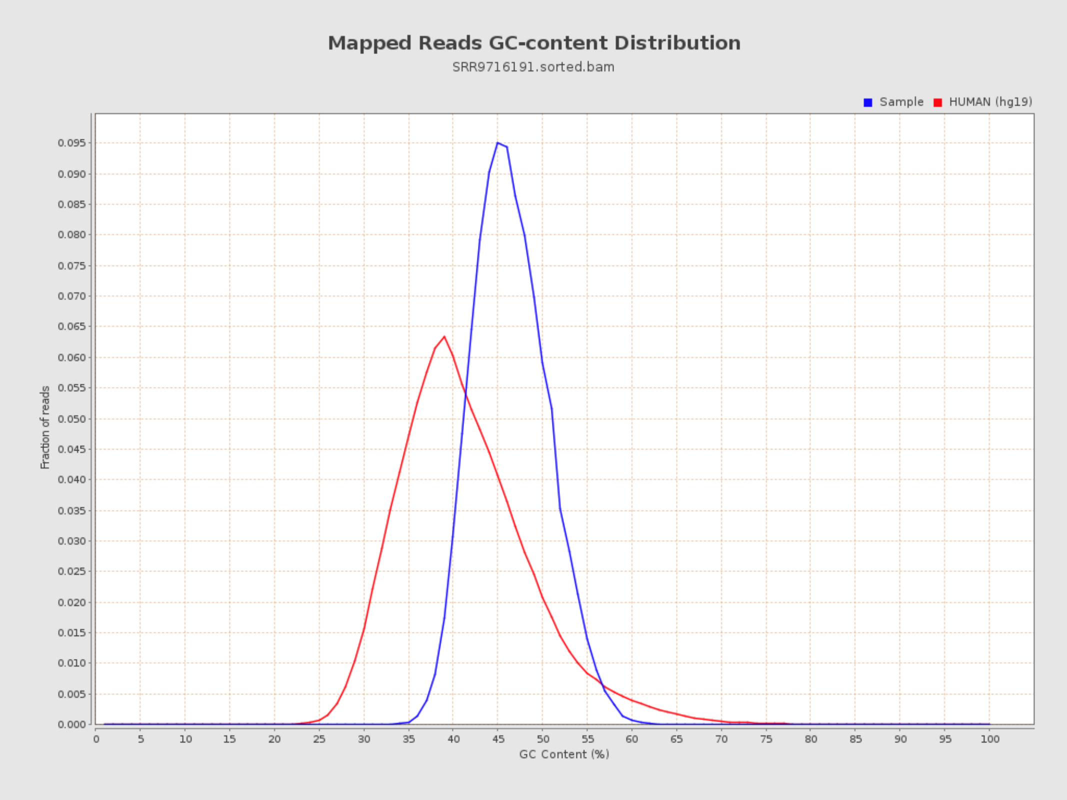
7. Results : Duplication Rate Histogram



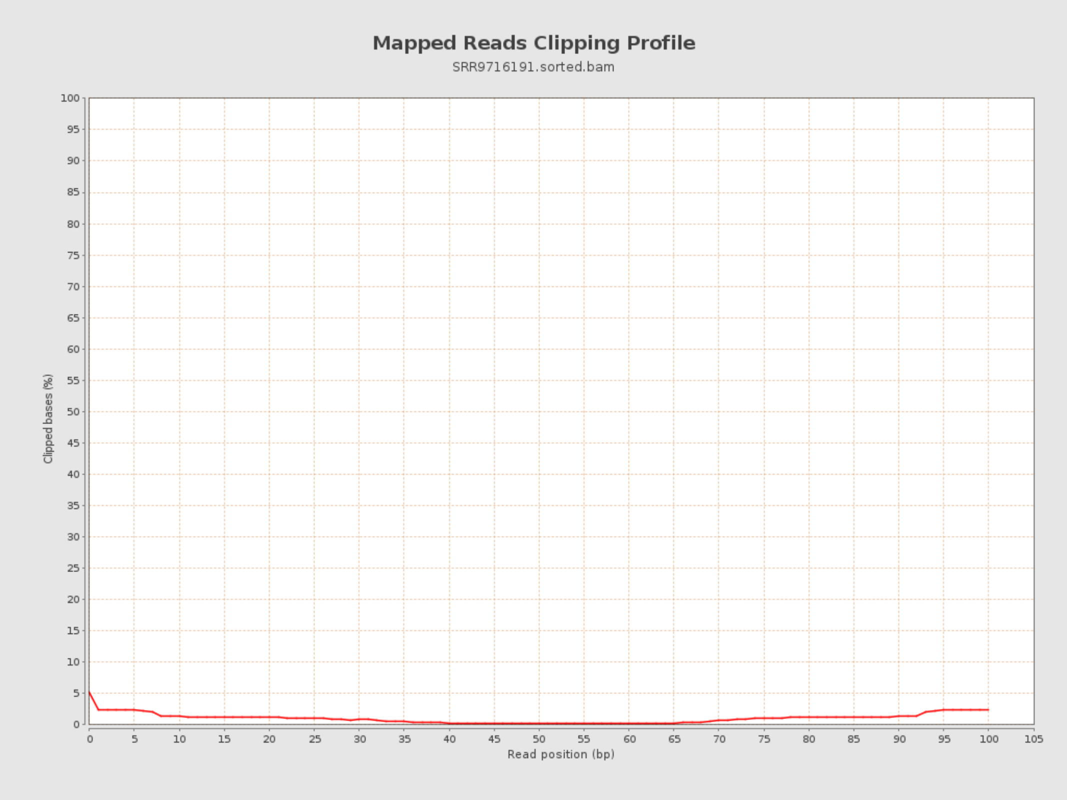
8. Results : Mapped Reads Nucleotide Content



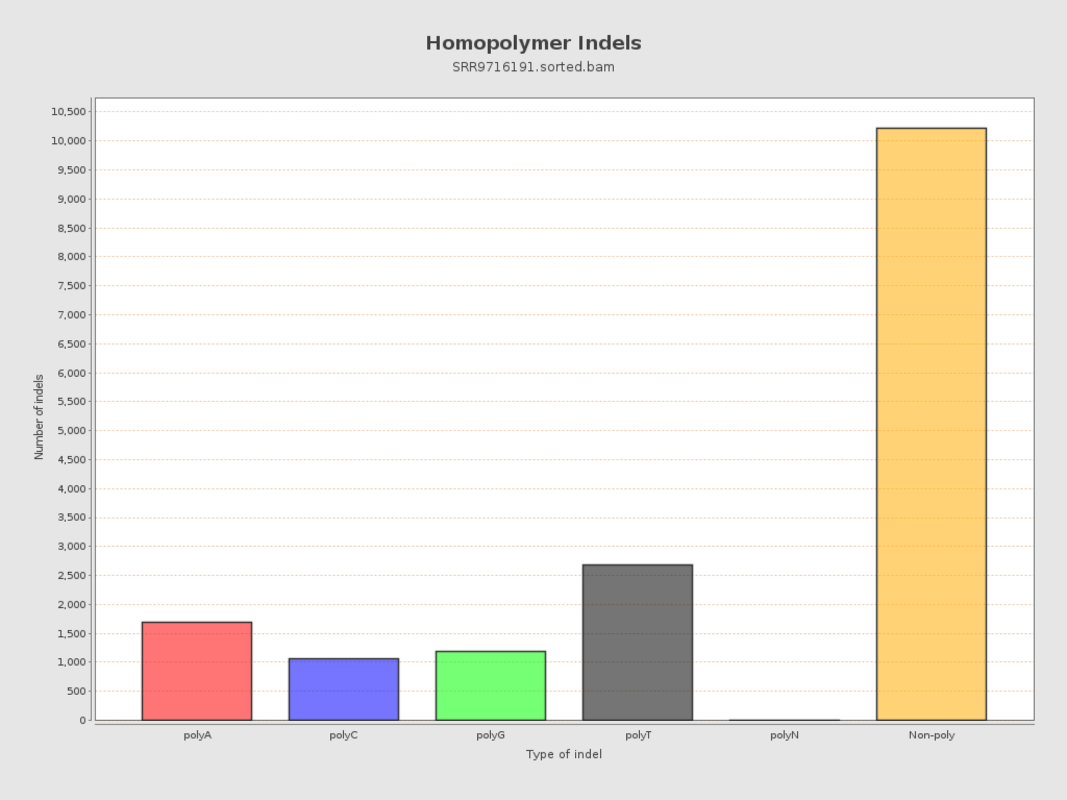
9. Results : Mapped Reads GC-content Distribution



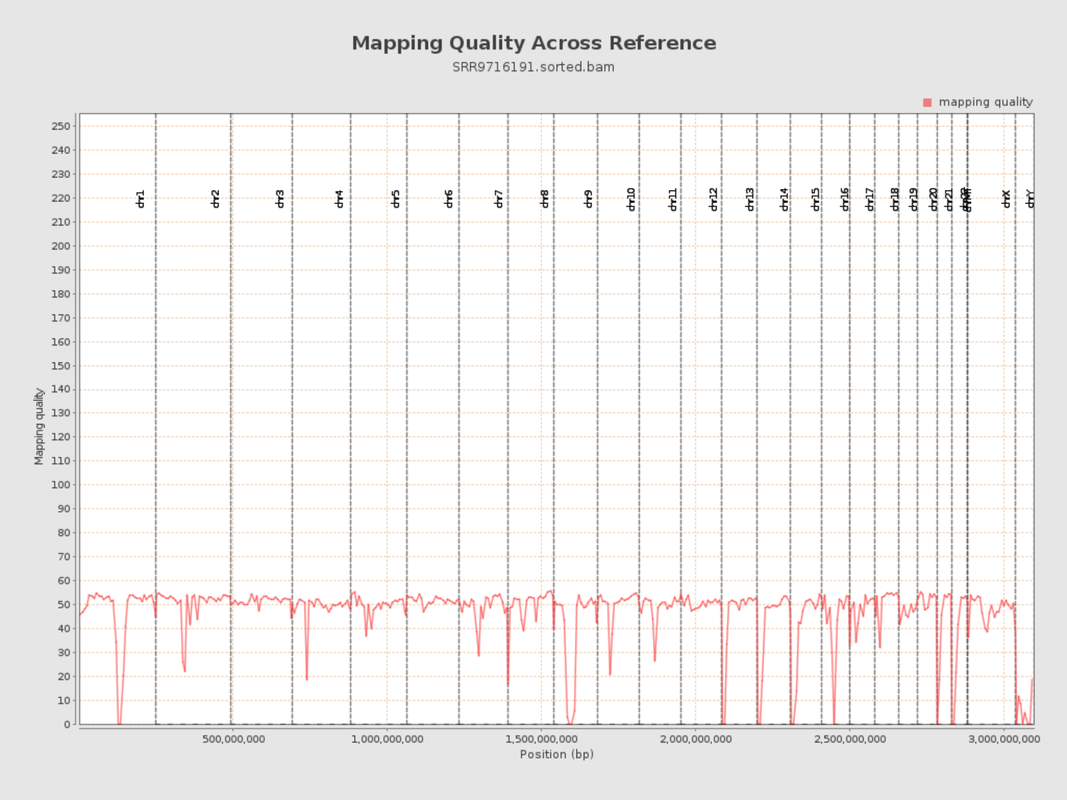
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram