Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:26:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716790.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_SRR9716790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716790.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:26:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	999,326
Mapped reads	897,165 / 89.78%
Unmapped reads	102,161 / 10.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,389 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	26,036 / 2.61%
Duplication rate	2.26%
Clipped reads	896,718 / 89.73%

2.2. ACGT Content

Number/percentage of A's	12,320,246 / 24.09%
Number/percentage of C's	9,757,946 / 19.08%
Number/percentage of T's	17,173,116 / 33.58%
Number/percentage of G's	11,887,515 / 23.25%
Number/percentage of N's	485 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0165

Standard Deviation	0.1674

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

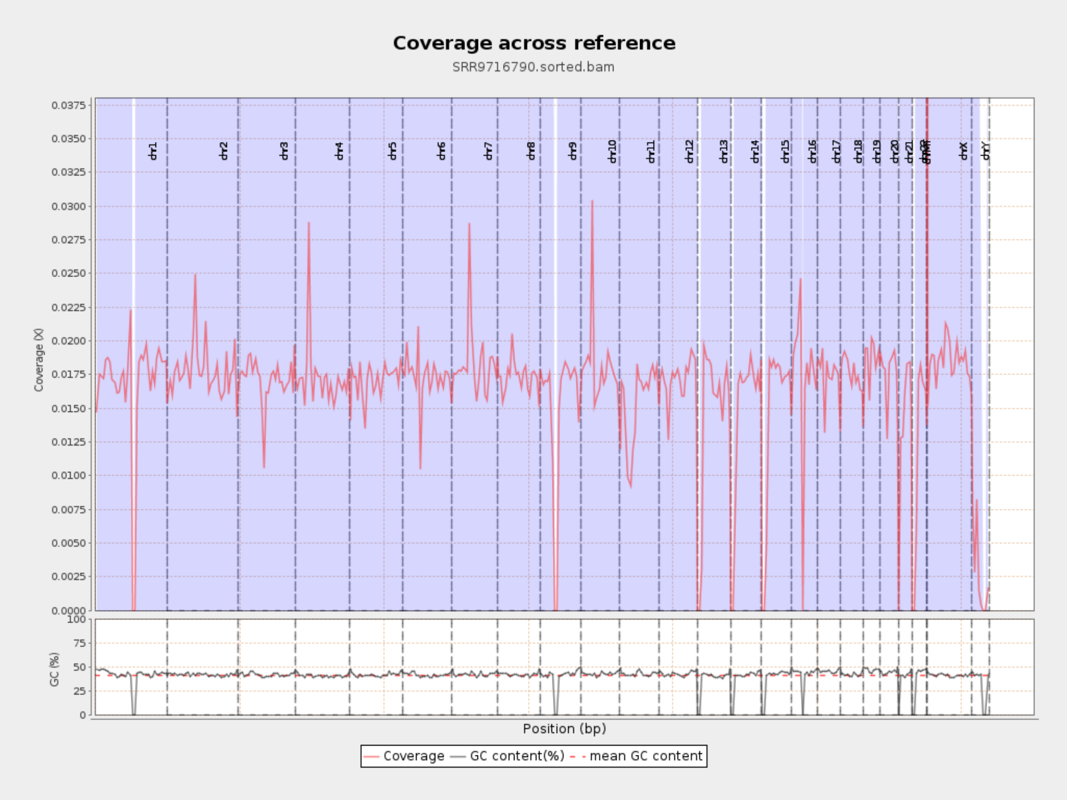
General error rate	0.52%
Mismatches	261,695
Insertions	3,411
Mapped reads with at least one insertion	0.38%
Deletions	10,737
Mapped reads with at least one deletion	1.19%
Homopolymer indels	43.17%

2.6. Chromosome stats

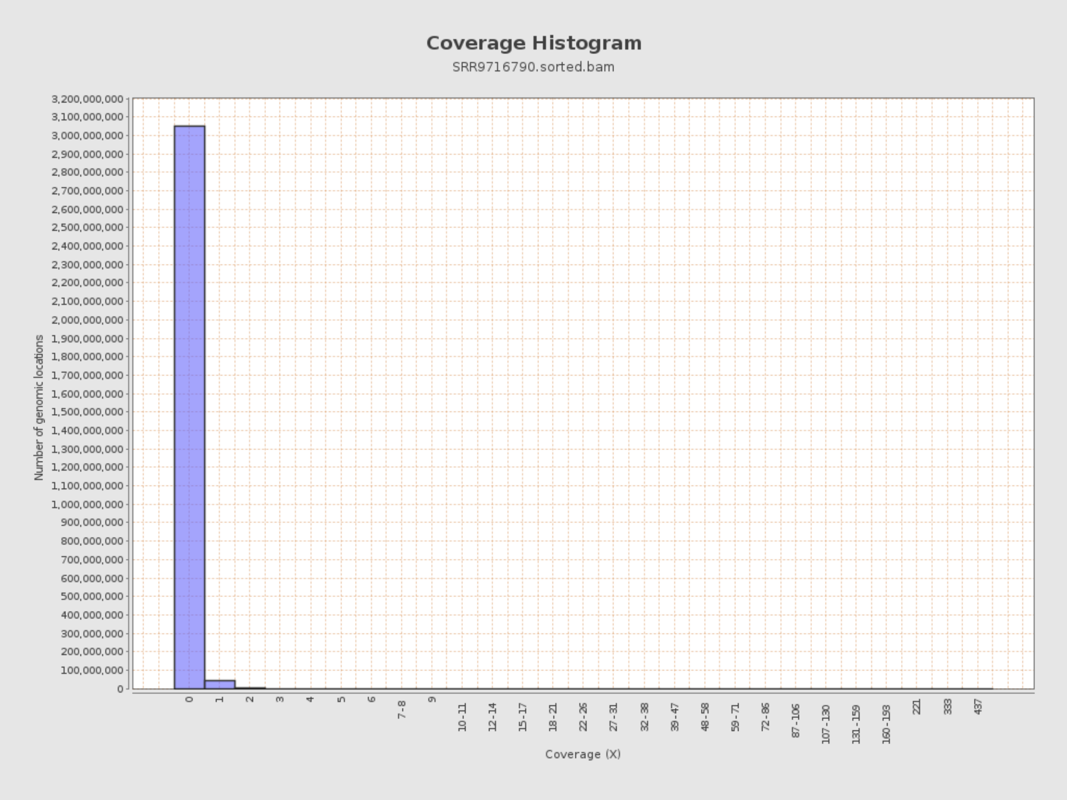
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4148623	0.0166	0.2058
chr2	243199373	4329338	0.0178	0.2363
chr3	198022430	3381064	0.0171	0.1398
chr4	191154276	3309154	0.0173	0.1497
chr5	180915260	3109591	0.0172	0.139
chr6	171115067	2956844	0.0173	0.1563
chr7	159138663	2918604	0.0183	0.2246

chr8	146364022	2535336	0.0173	0.1622
chr9	141213431	2103568	0.0149	0.1441
chr10	135534747	2461741	0.0182	0.1795
chr11	135006516	2090308	0.0155	0.1526
chr12	133851895	2294341	0.0171	0.1392
chr13	115169878	1639718	0.0142	0.1271
chr14	107349540	1538486	0.0143	0.1293
chr15	102531392	1468063	0.0143	0.128
chr16	90354753	1543582	0.0171	0.1487
chr17	81195210	1409881	0.0174	0.1456
chr18	78077248	1380087	0.0177	0.2217
chr19	59128983	1099036	0.0186	0.1818
chr20	63025520	1100044	0.0175	0.1423
chr21	48129895	683192	0.0142	0.1341
chr22	51304566	604045	0.0118	0.1155
chrMT	16571	16683	1.0068	1.1849
chrX	155270560	2880372	0.0186	0.1549
chrY	59373566	154829	0.0026	0.0779

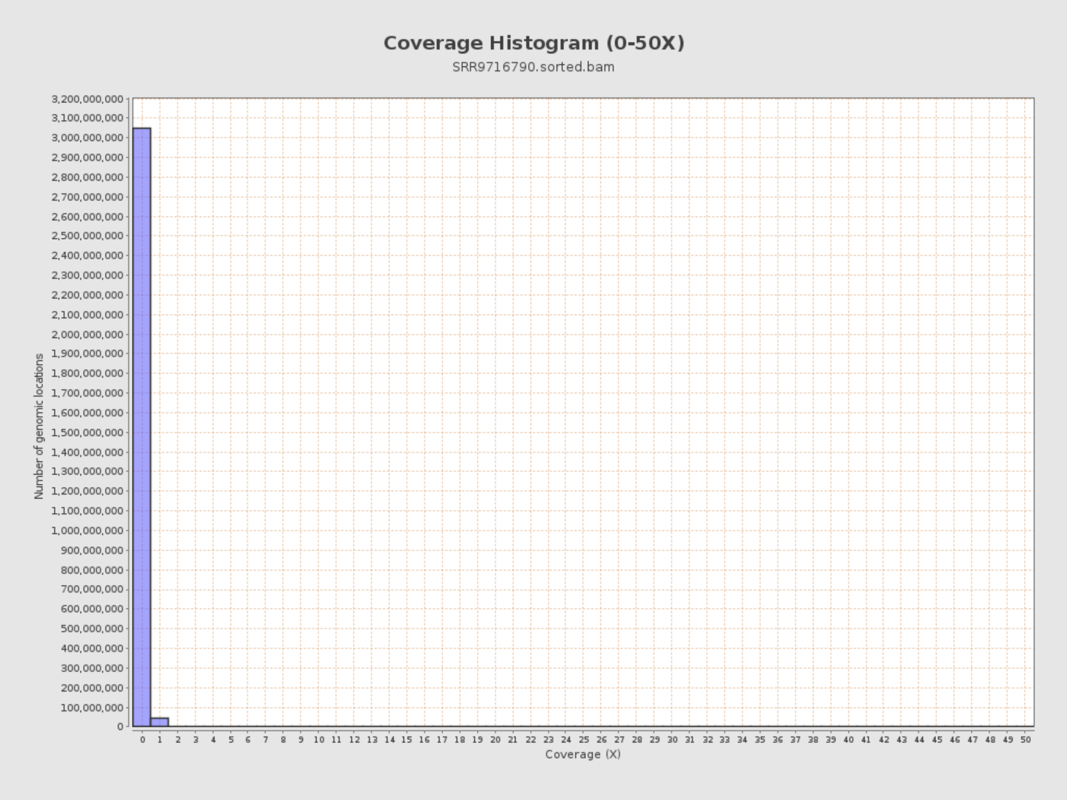
3. Results : Coverage across reference



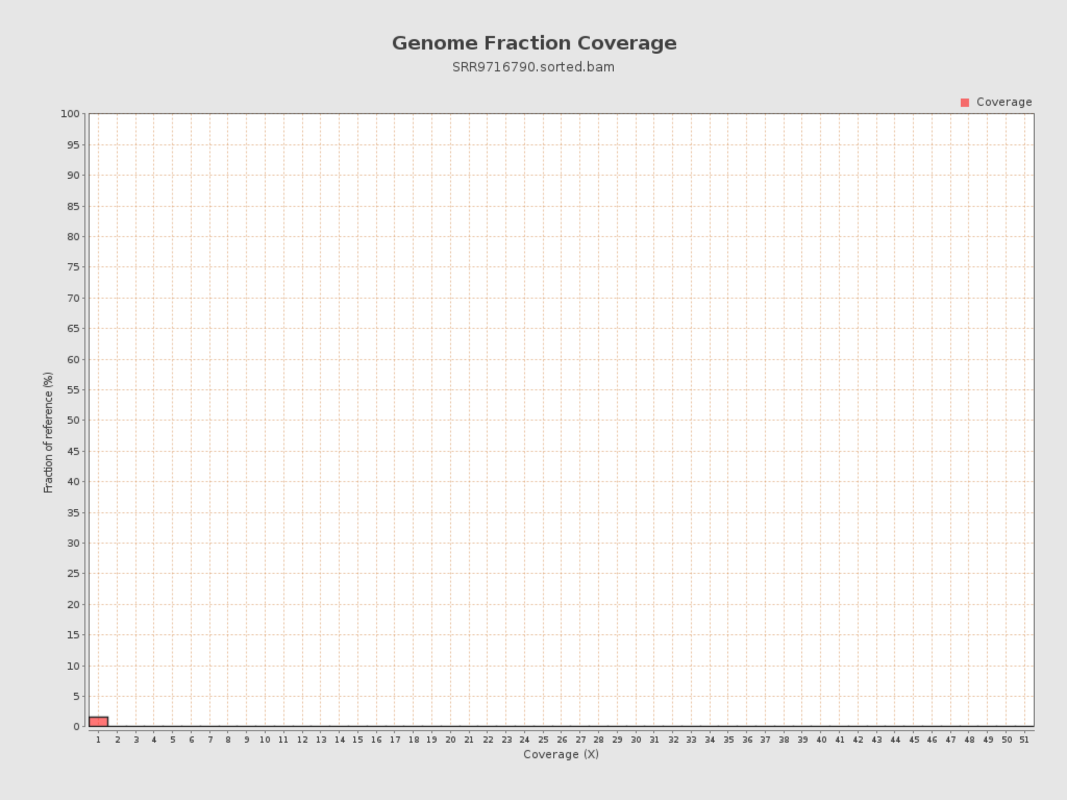
4. Results : Coverage Histogram



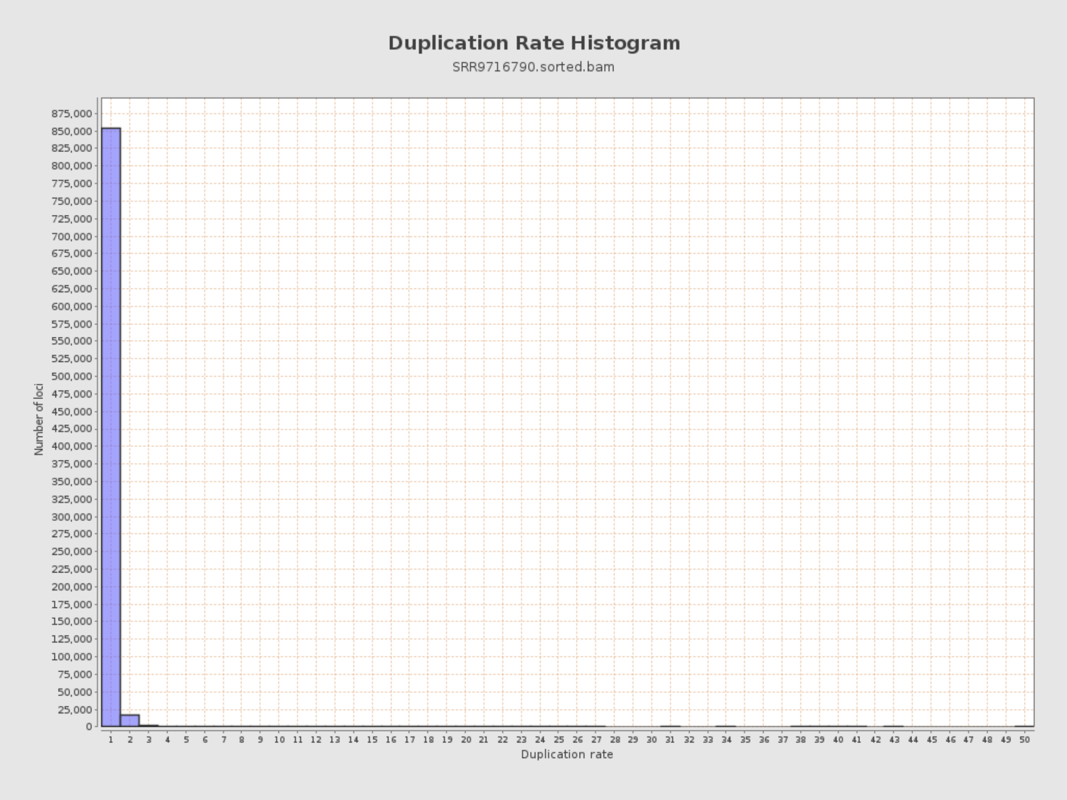
5. Results : Coverage Histogram (0-50X)



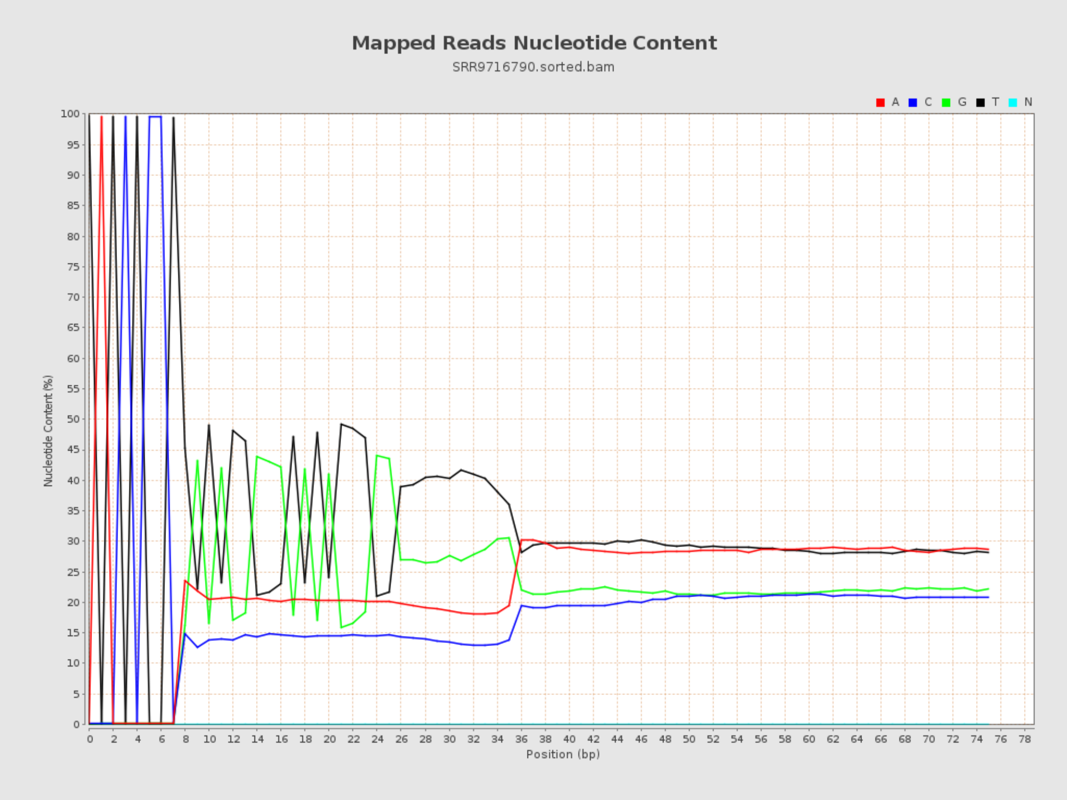
6. Results : Genome Fraction Coverage



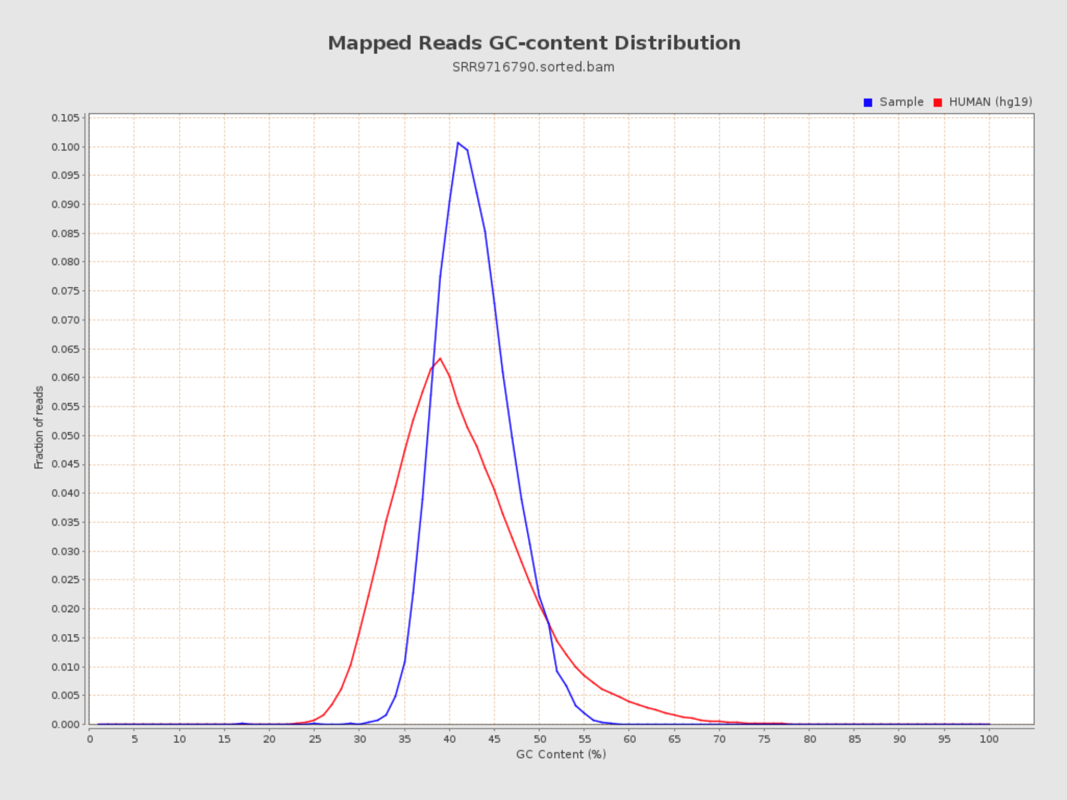
7. Results : Duplication Rate Histogram



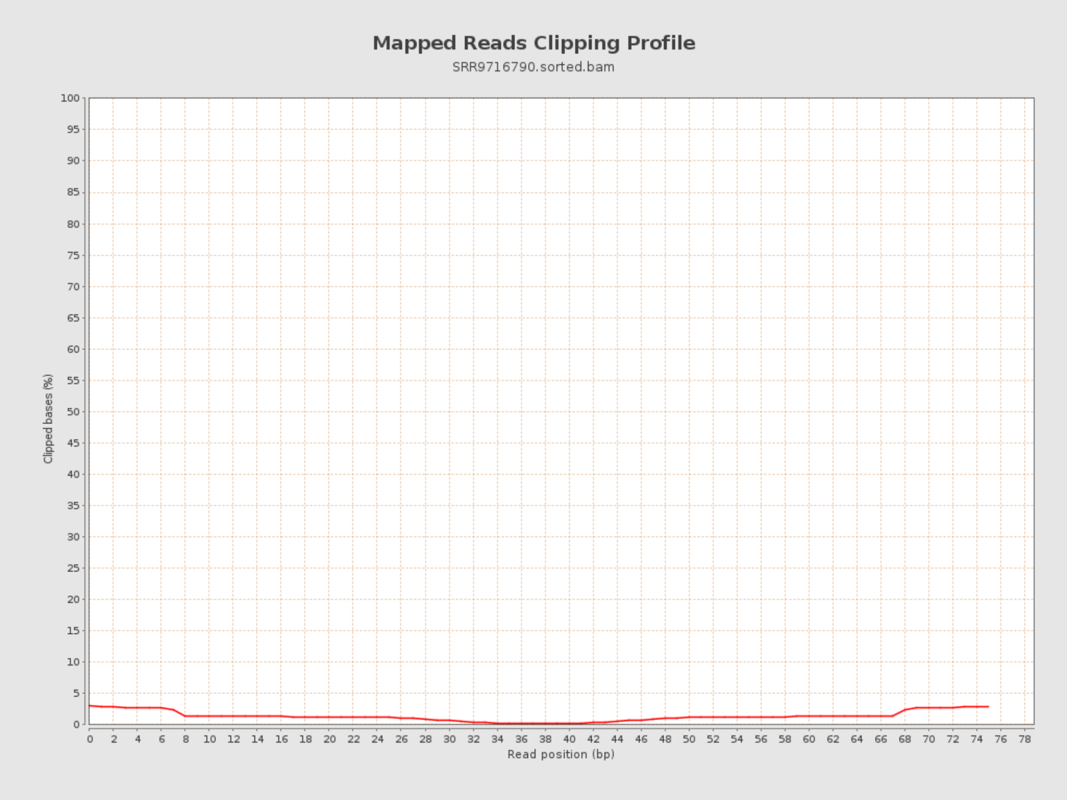
8. Results : Mapped Reads Nucleotide Content



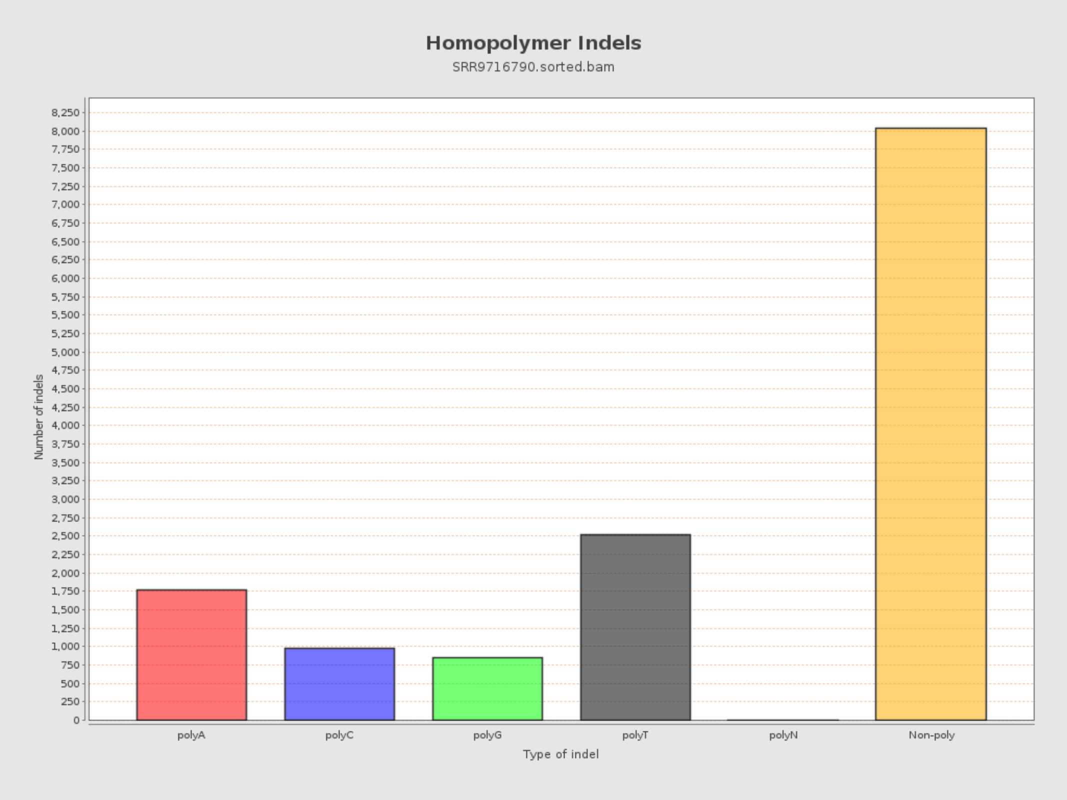
9. Results : Mapped Reads GC-content Distribution



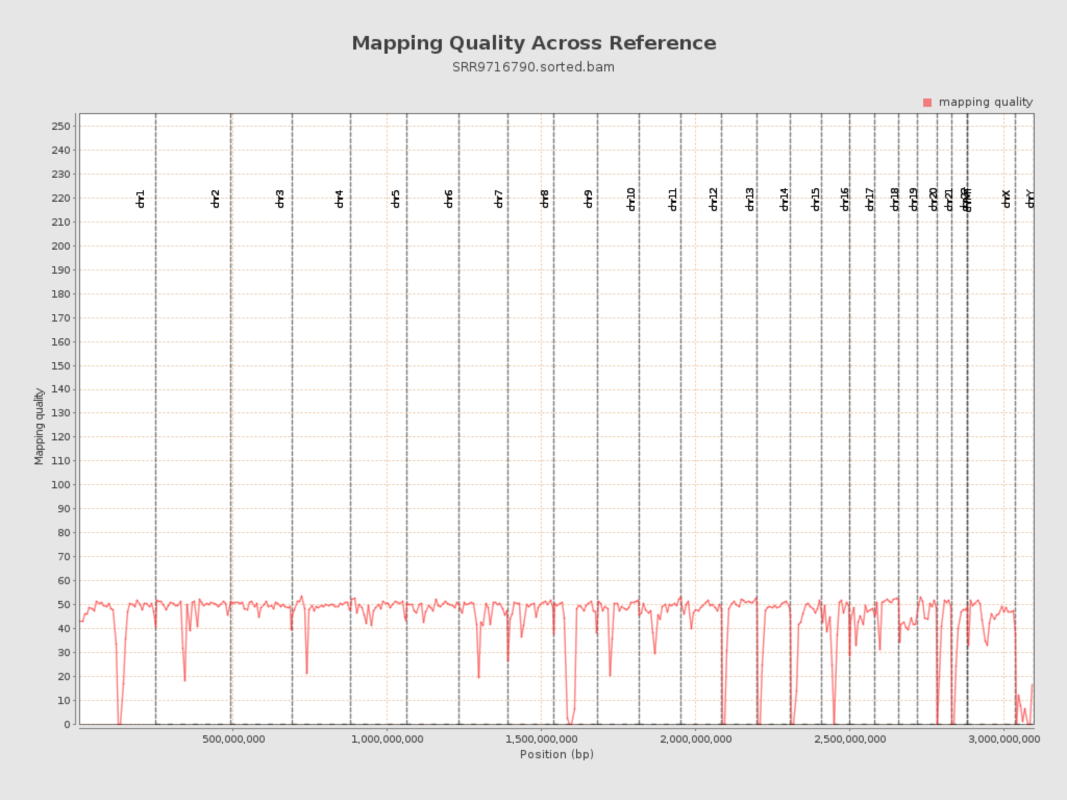
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram