Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:38:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716795.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_SRR9716795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:38:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	866,612
Mapped reads	619,490 / 71.48%
Unmapped reads	247,122 / 28.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	608 / 0.07%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	35,869 / 4.14%
Duplication rate	5.13%
Clipped reads	619,065 / 71.44%

2.2. ACGT Content

Number/percentage of A's	6,887,878 / 21.35%
Number/percentage of C's	5,285,904 / 16.38%
Number/percentage of T's	10,593,827 / 32.83%
Number/percentage of G's	9,500,570 / 29.44%
Number/percentage of N's	458 / 0%
GC Percentage	45.82%

2.3. Coverage

Mean	0.0104

Standard Deviation	0.1244

2.4. Mapping Quality

Mean Mapping Quality	42.45

2.5. Mismatches and indels

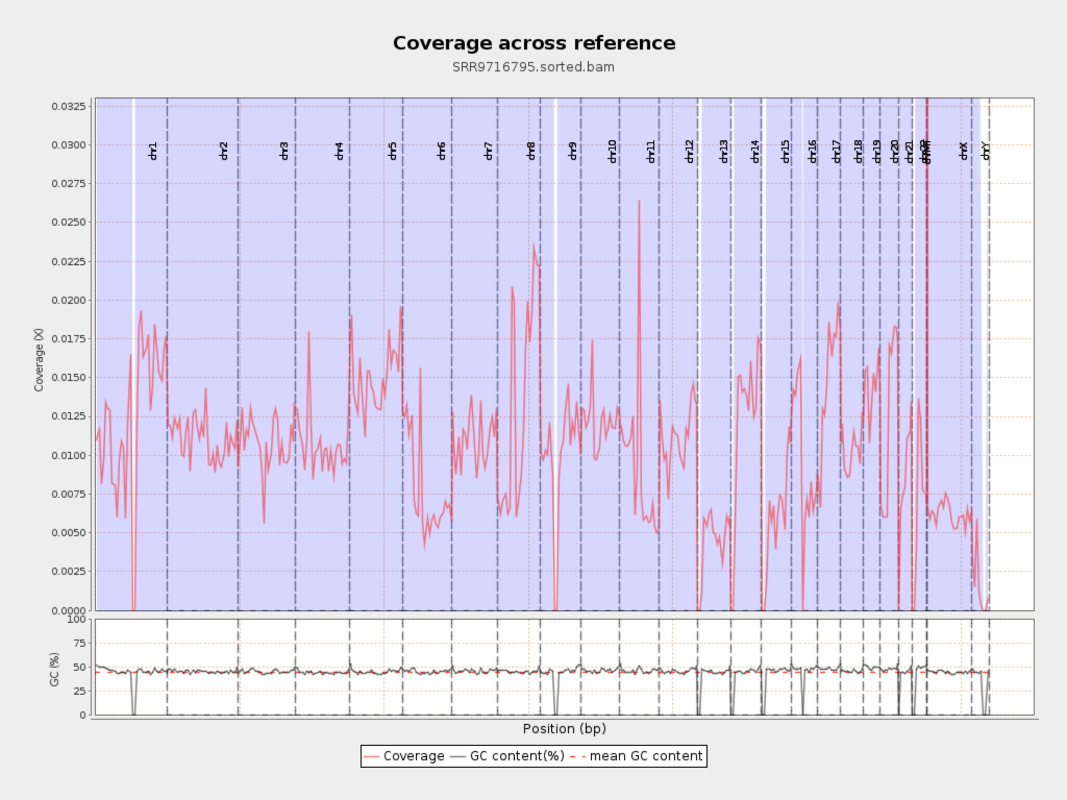
General error rate	0.71%
Mismatches	226,894
Insertions	1,827
Mapped reads with at least one insertion	0.29%
Deletions	4,913
Mapped reads with at least one deletion	0.79%
Homopolymer indels	41.74%

2.6. Chromosome stats

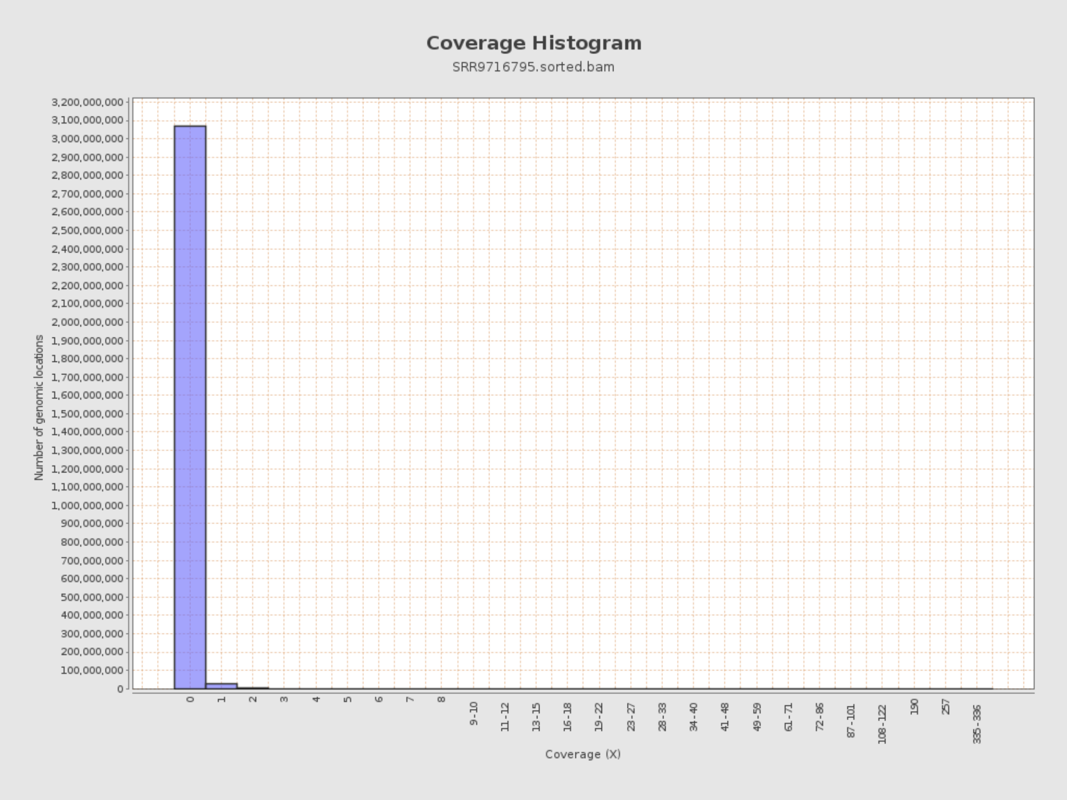
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3082483	0.0124	0.1385
chr2	243199373	2691750	0.0111	0.1783
chr3	198022430	2138003	0.0108	0.1147
chr4	191154276	2052590	0.0107	0.118
chr5	180915260	2727332	0.0151	0.135
chr6	171115067	1335820	0.0078	0.1126
chr7	159138663	1756425	0.011	0.1279

chr8	146364022	1960193	0.0134	0.1318
chr9	141213431	1393855	0.0099	0.1148
chr10	135534747	1657363	0.0122	0.1343
chr11	135006516	1252092	0.0093	0.1135
chr12	133851895	1501615	0.0112	0.1175
chr13	115169878	504253	0.0044	0.0732
chr14	107349540	1309869	0.0122	0.123
chr15	102531392	600021	0.0059	0.0851
chr16	90354753	846183	0.0094	0.115
chr17	81195210	1197872	0.0148	0.1366
chr18	78077248	802955	0.0103	0.1254
chr19	59128983	850161	0.0144	0.1496
chr20	63025520	777404	0.0123	0.1257
chr21	48129895	410326	0.0085	0.1055
chr22	51304566	362782	0.0071	0.0949
chrMT	16571	9020	0.5443	0.9205
chrX	155270560	963314	0.0062	0.0881
chrY	59373566	93188	0.0016	0.0547

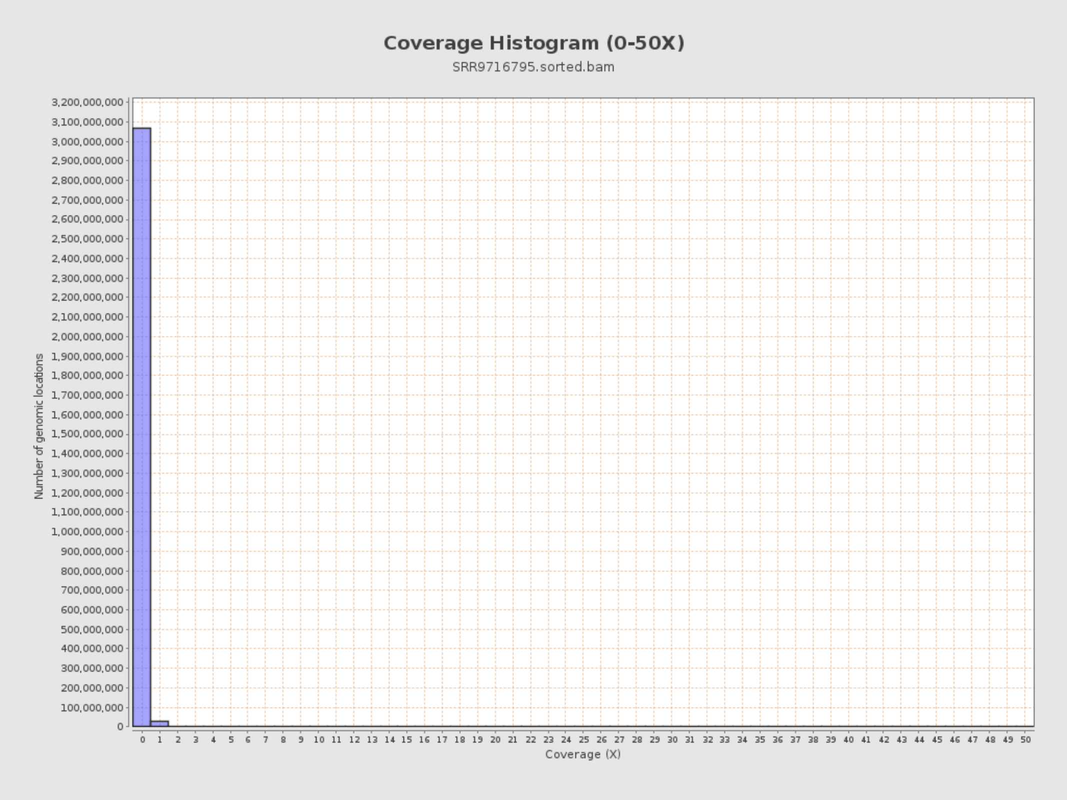
3. Results : Coverage across reference



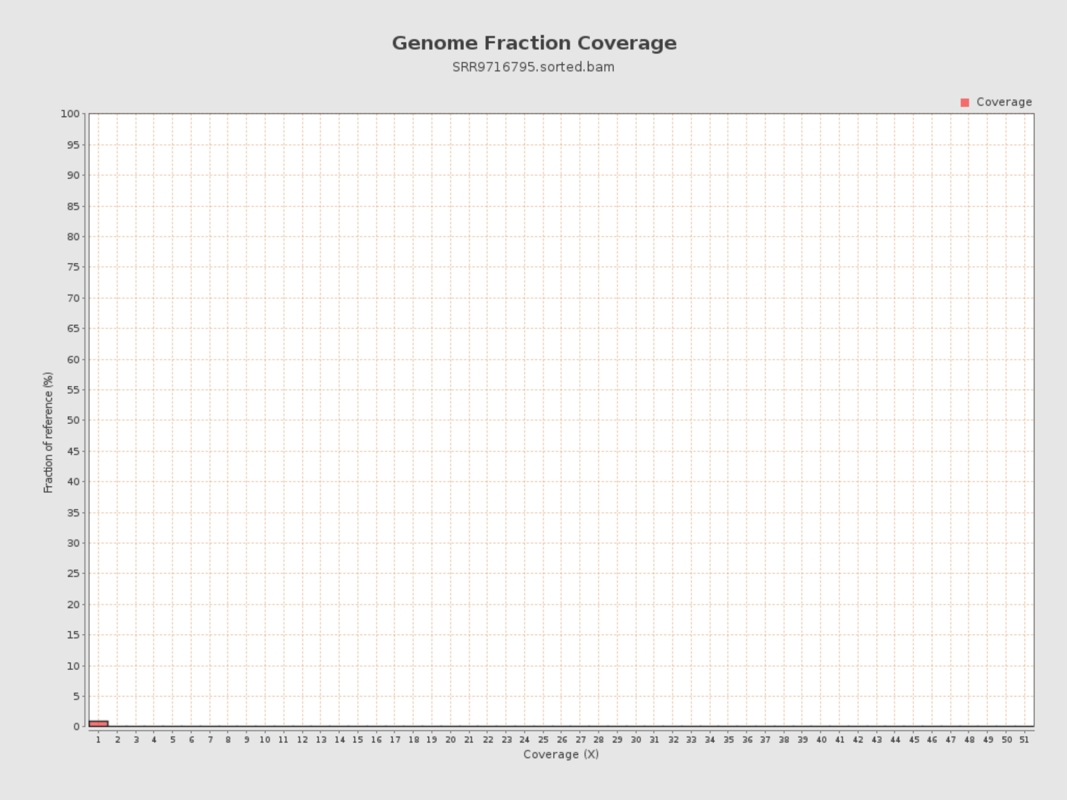
4. Results : Coverage Histogram



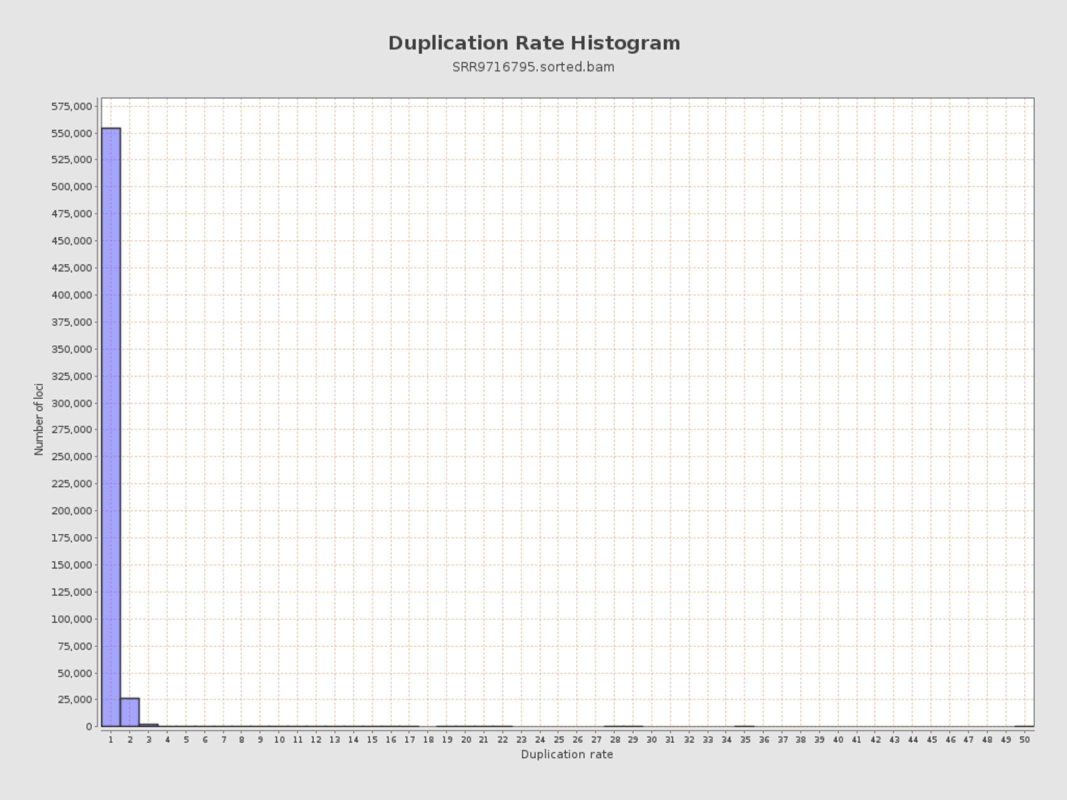
5. Results : Coverage Histogram (0-50X)



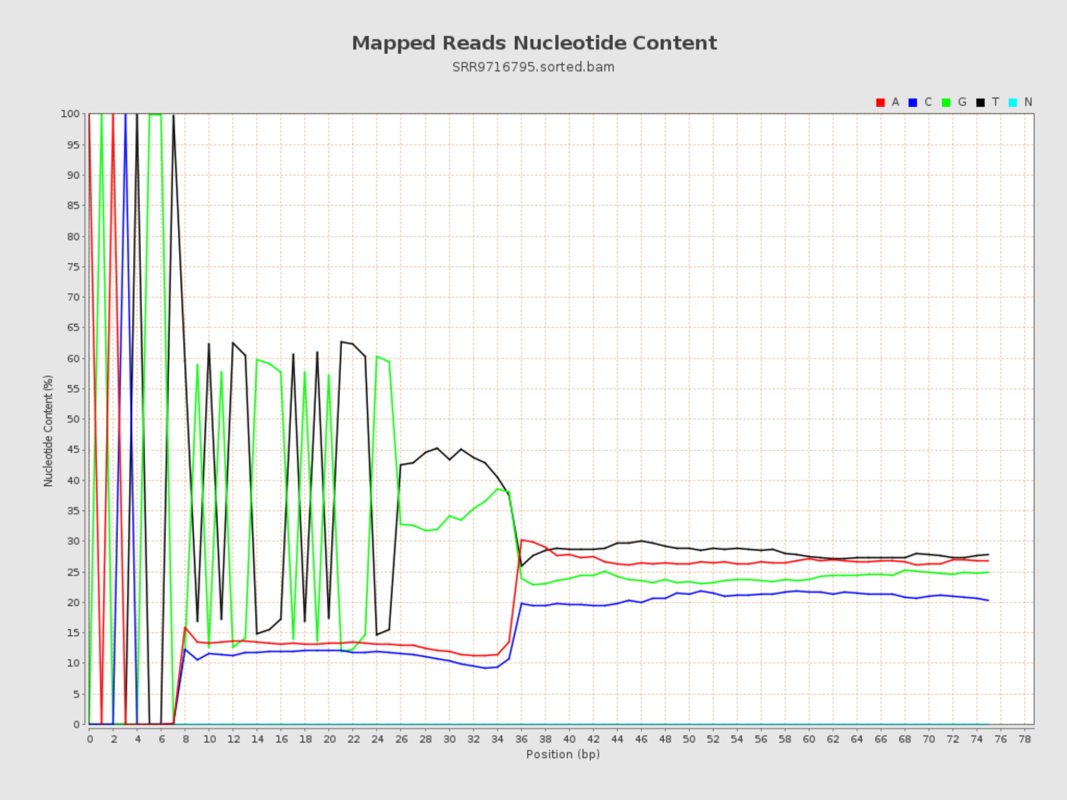
6. Results : Genome Fraction Coverage



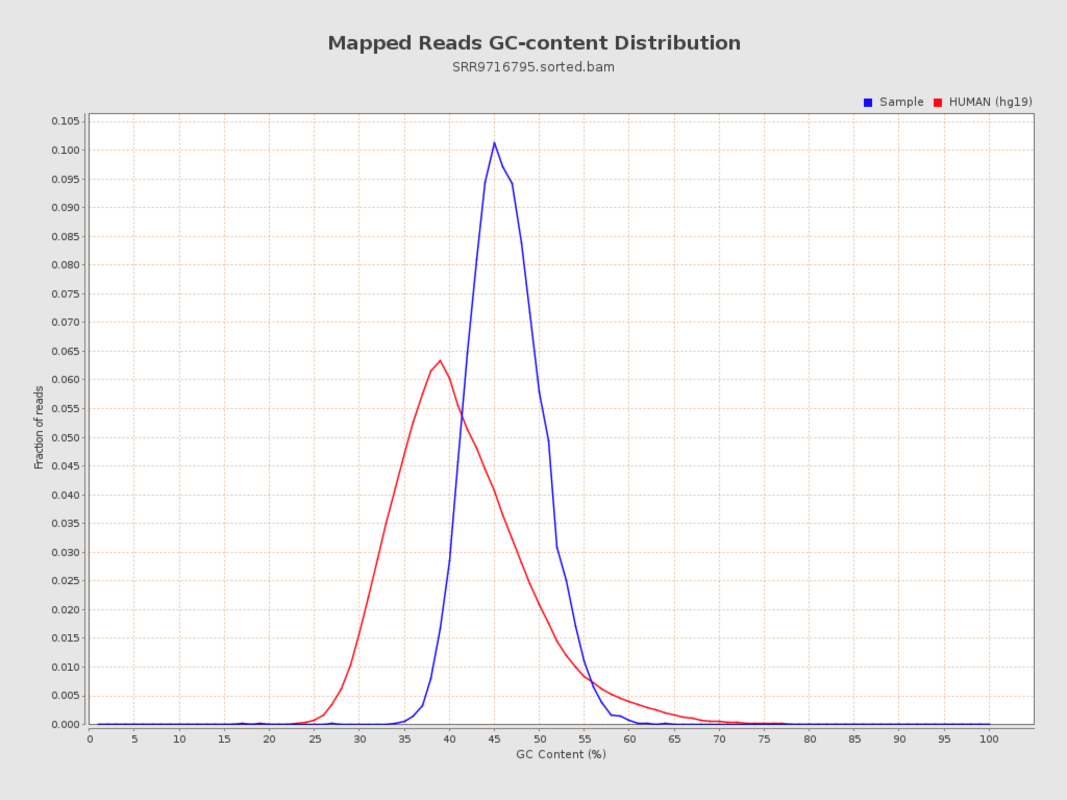
7. Results : Duplication Rate Histogram



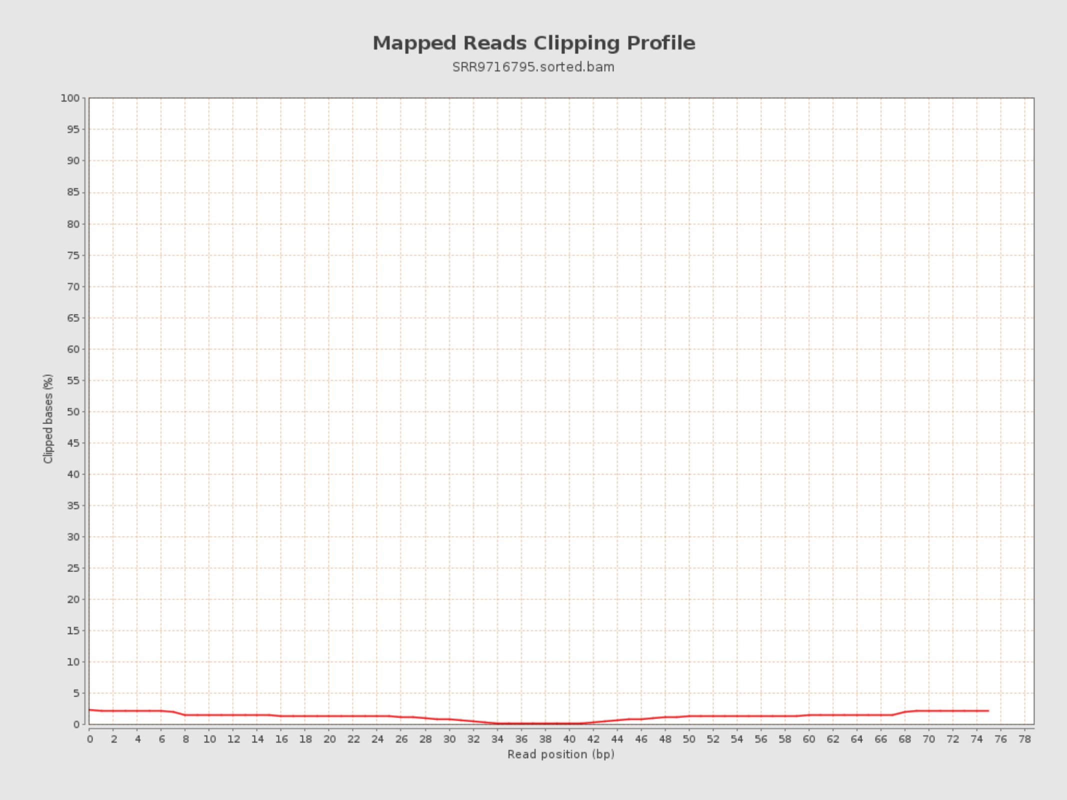
8. Results : Mapped Reads Nucleotide Content



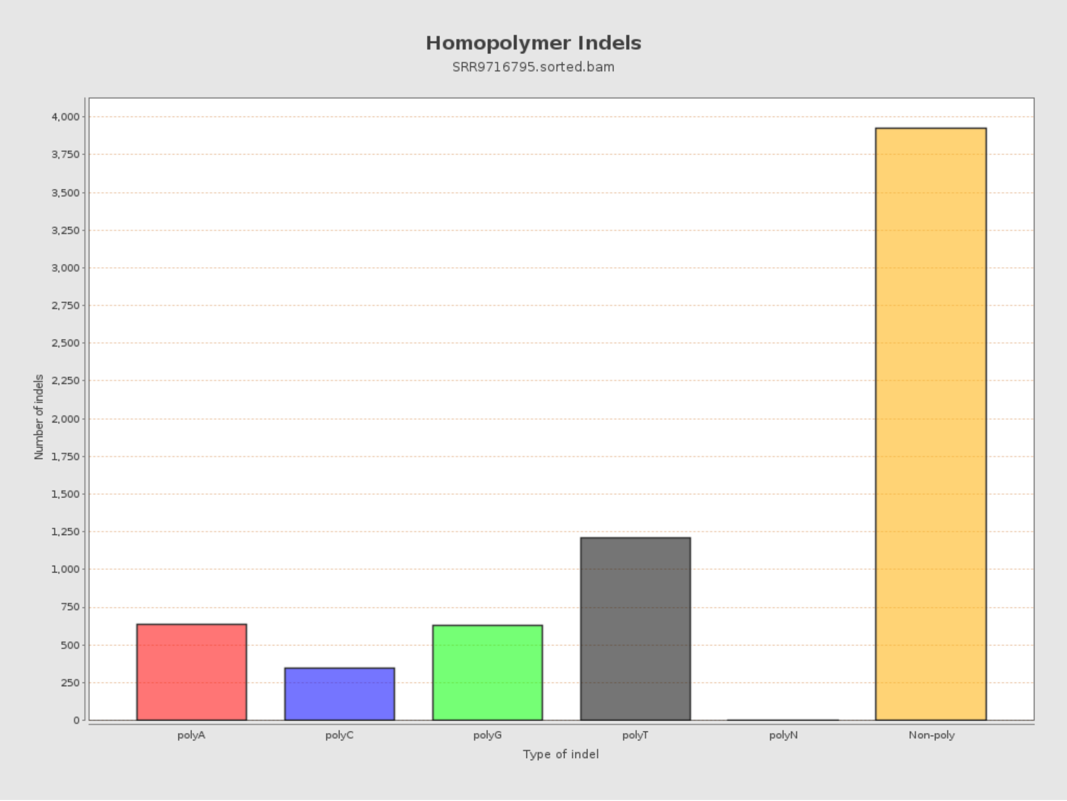
9. Results : Mapped Reads GC-content Distribution



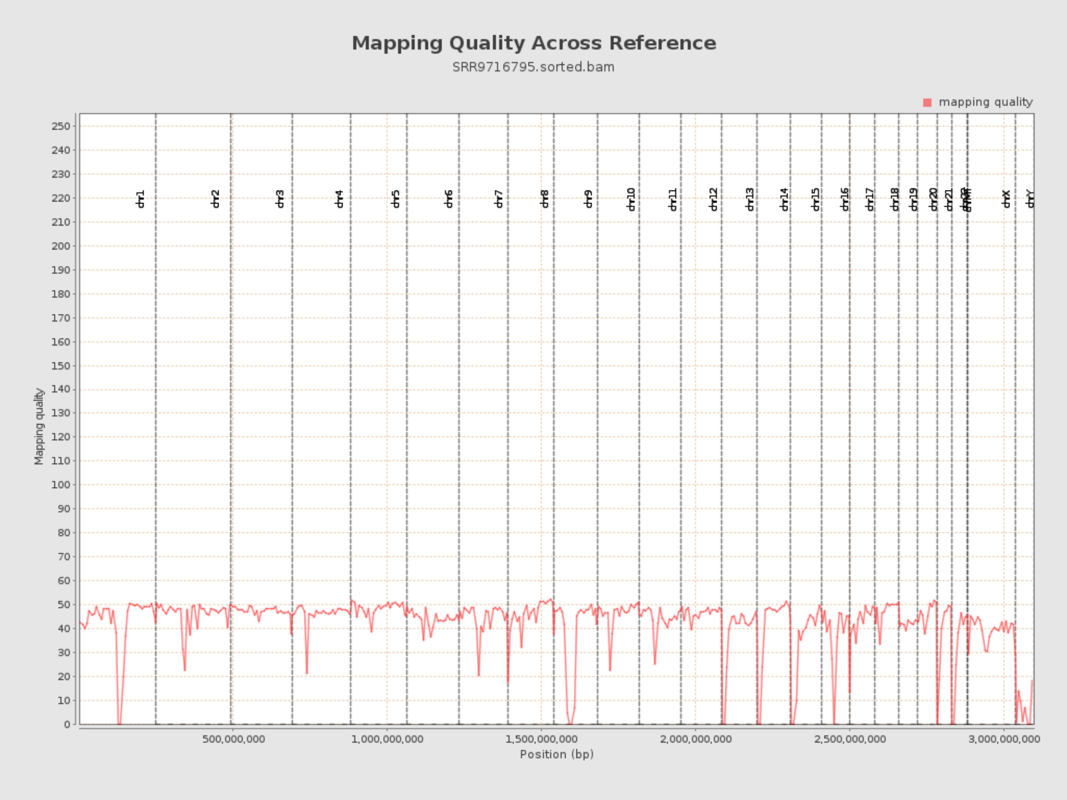
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram