Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:59:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524895.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_SRR10524895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524895.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:59:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,921,635
Mapped reads	1,774,406 / 92.34%
Unmapped reads	147,229 / 7.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,022 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	79,953 / 4.16%
Duplication rate	3.39%
Clipped reads	1,776,851 / 92.47%

2.2. ACGT Content

Number/percentage of A's	25,836,829 / 24.96%
Number/percentage of C's	18,278,876 / 17.66%
Number/percentage of T's	32,562,965 / 31.45%
Number/percentage of G's	26,833,969 / 25.92%
Number/percentage of N's	13,106 / 0.01%
GC Percentage	43.58%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.3227

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

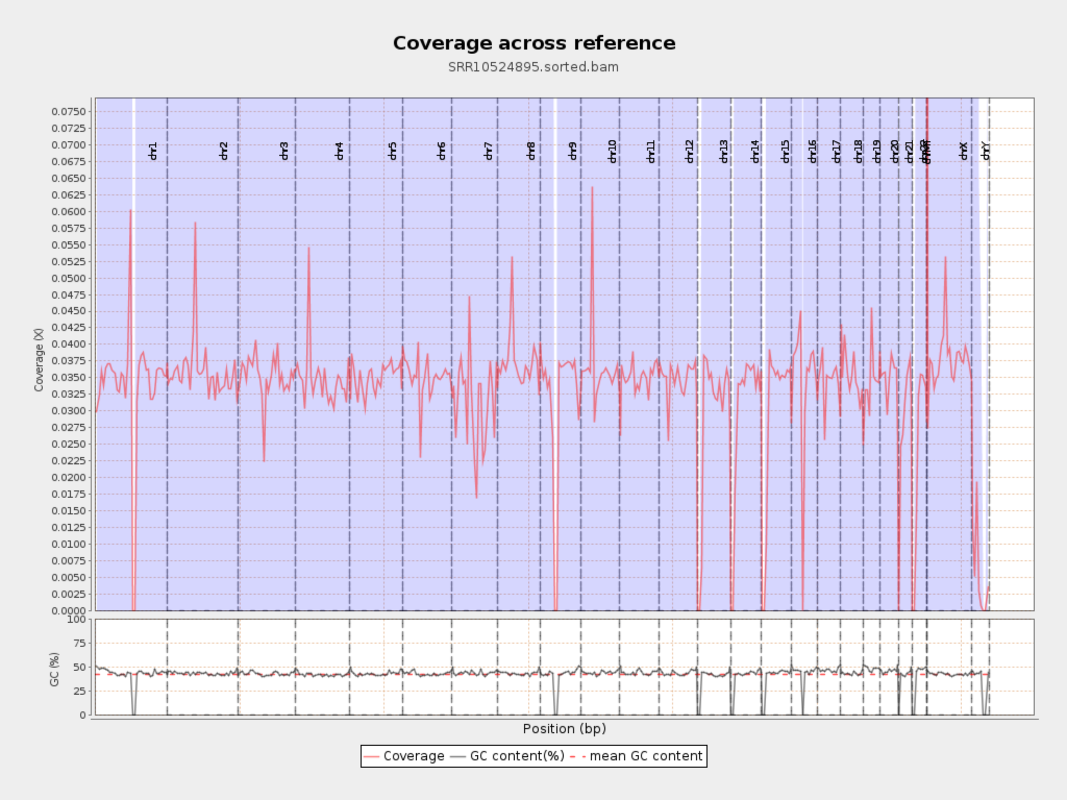
General error rate	0.5%
Mismatches	506,304
Insertions	6,941
Mapped reads with at least one insertion	0.39%
Deletions	19,407
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.52%

2.6. Chromosome stats

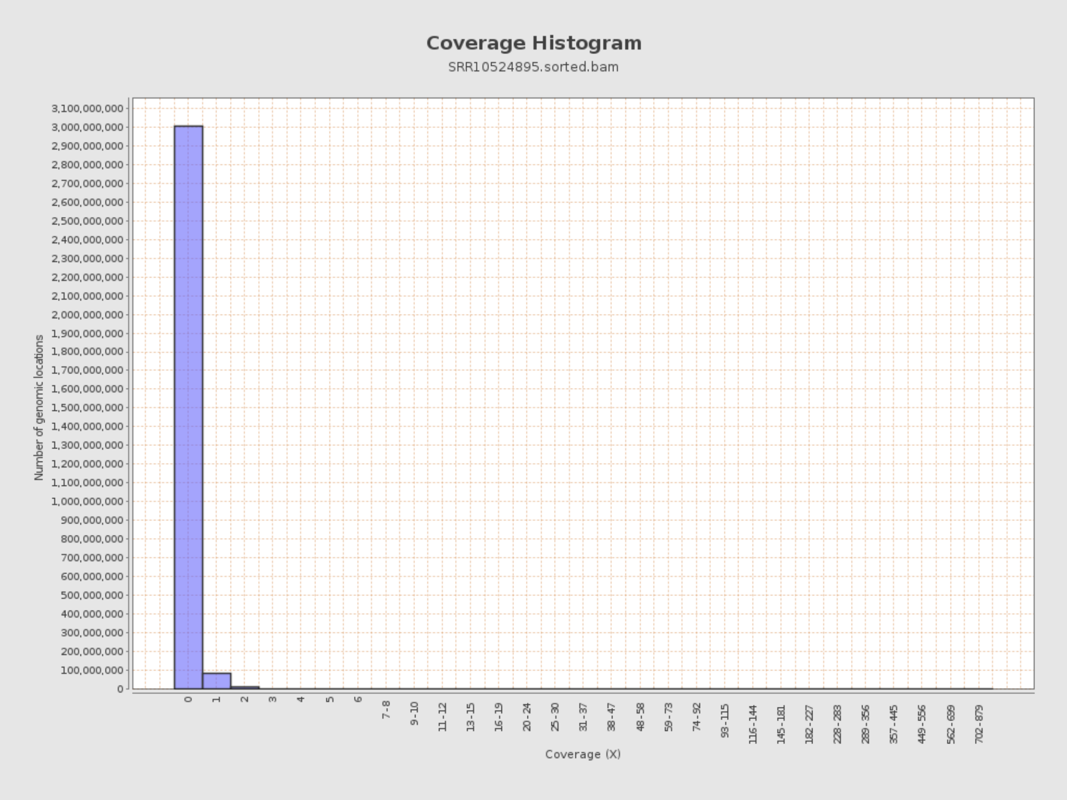
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8375228	0.0336	0.6499
chr2	243199373	8760709	0.036	0.345
chr3	198022430	6967873	0.0352	0.206
chr4	191154276	6671897	0.0349	0.2305
chr5	180915260	6376366	0.0352	0.2079
chr6	171115067	5999699	0.0351	0.2254
chr7	159138663	4975461	0.0313	0.3849

chr8	146364022	5489292	0.0375	0.3214
chr9	141213431	4420792	0.0313	0.2772
chr10	135534747	4966089	0.0366	0.3097
chr11	135006516	4742239	0.0351	0.2946
chr12	133851895	4662147	0.0348	0.2117
chr13	115169878	3293650	0.0286	0.1858
chr14	107349540	3167831	0.0295	0.1972
chr15	102531392	2977855	0.029	0.1869
chr16	90354753	3061328	0.0339	0.2194
chr17	81195210	2805448	0.0346	0.2226
chr18	78077248	2769654	0.0355	0.5536
chr19	59128983	2049510	0.0347	0.4396
chr20	63025520	2194487	0.0348	0.2122
chr21	48129895	1364564	0.0284	0.2072
chr22	51304566	1221124	0.0238	0.1691
chrMT	16571	48709	2.9394	2.3115
chrX	155270560	5882698	0.0379	0.2483
chrY	59373566	311856	0.0053	0.1425

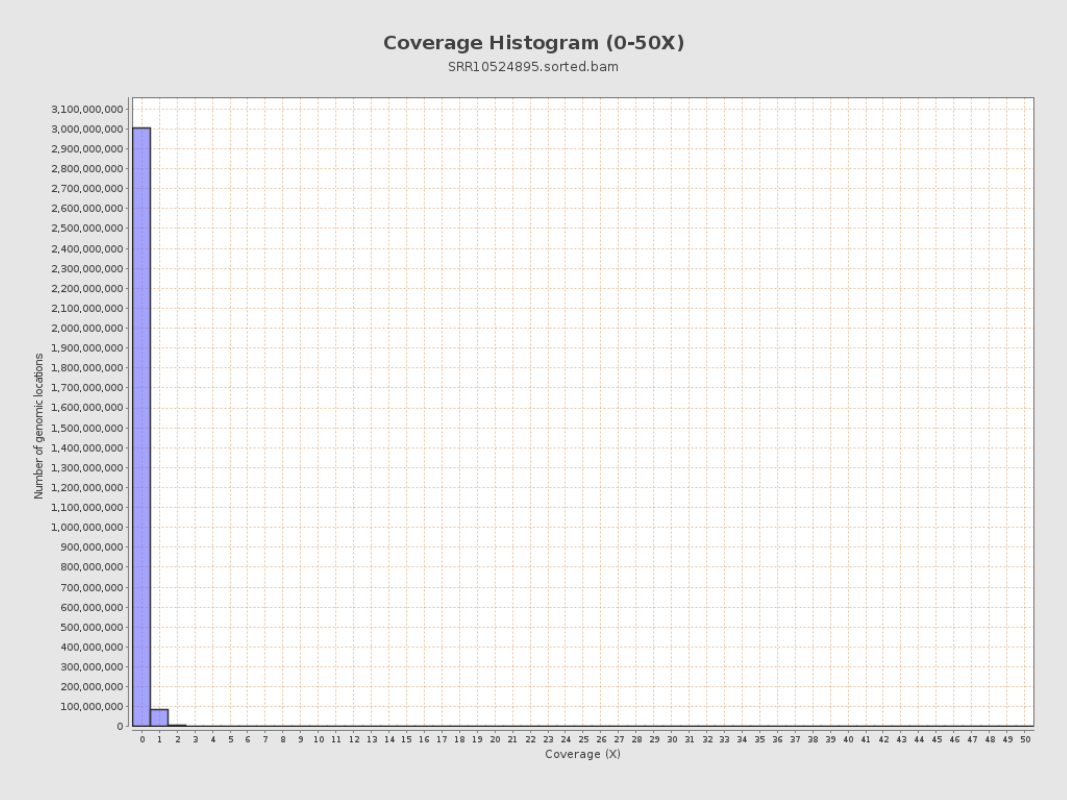
3. Results : Coverage across reference



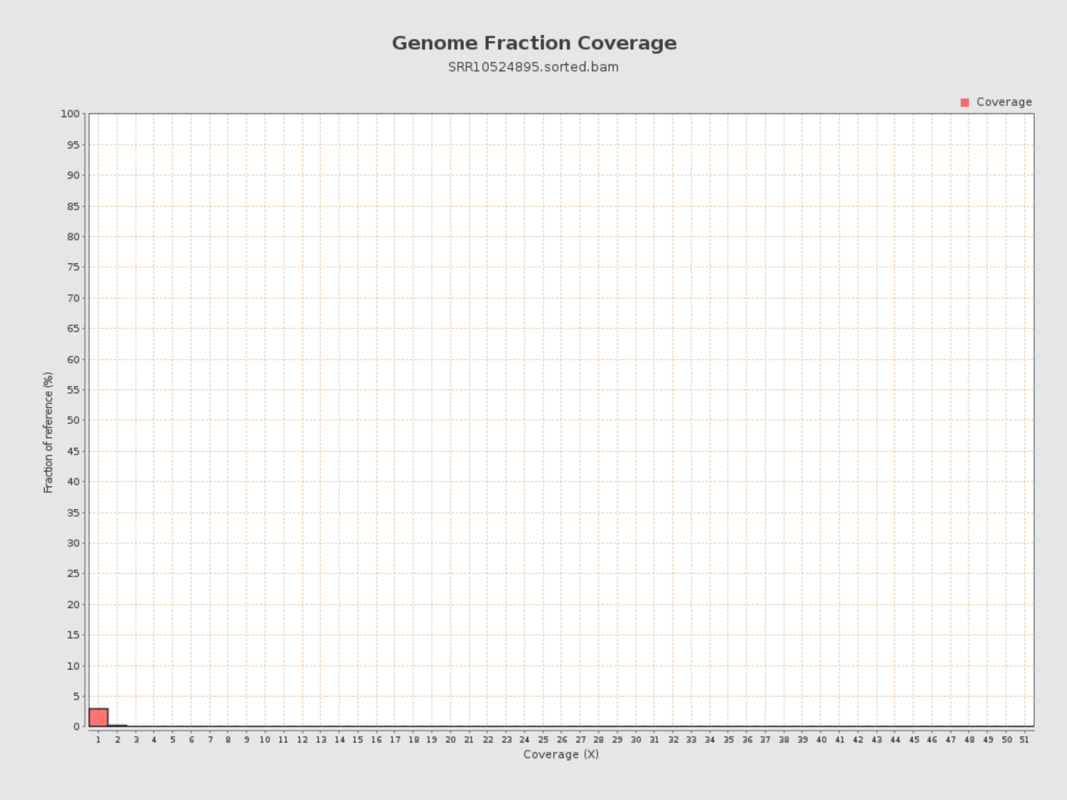
4. Results : Coverage Histogram



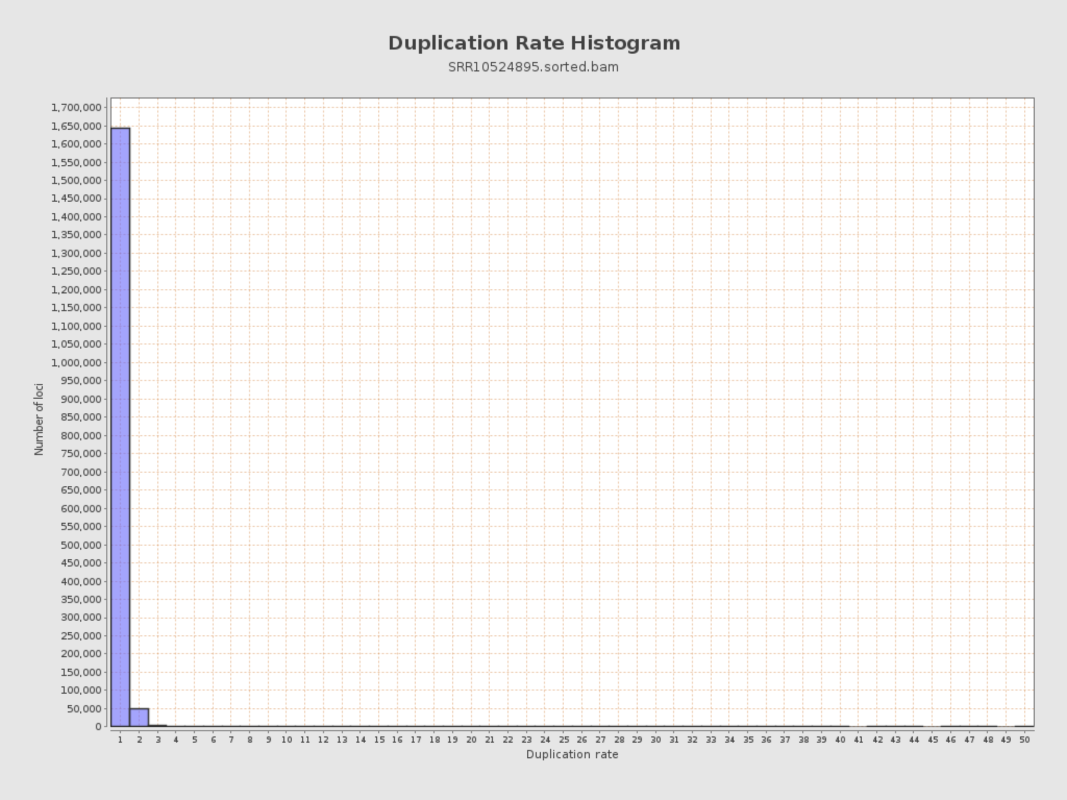
5. Results : Coverage Histogram (0-50X)



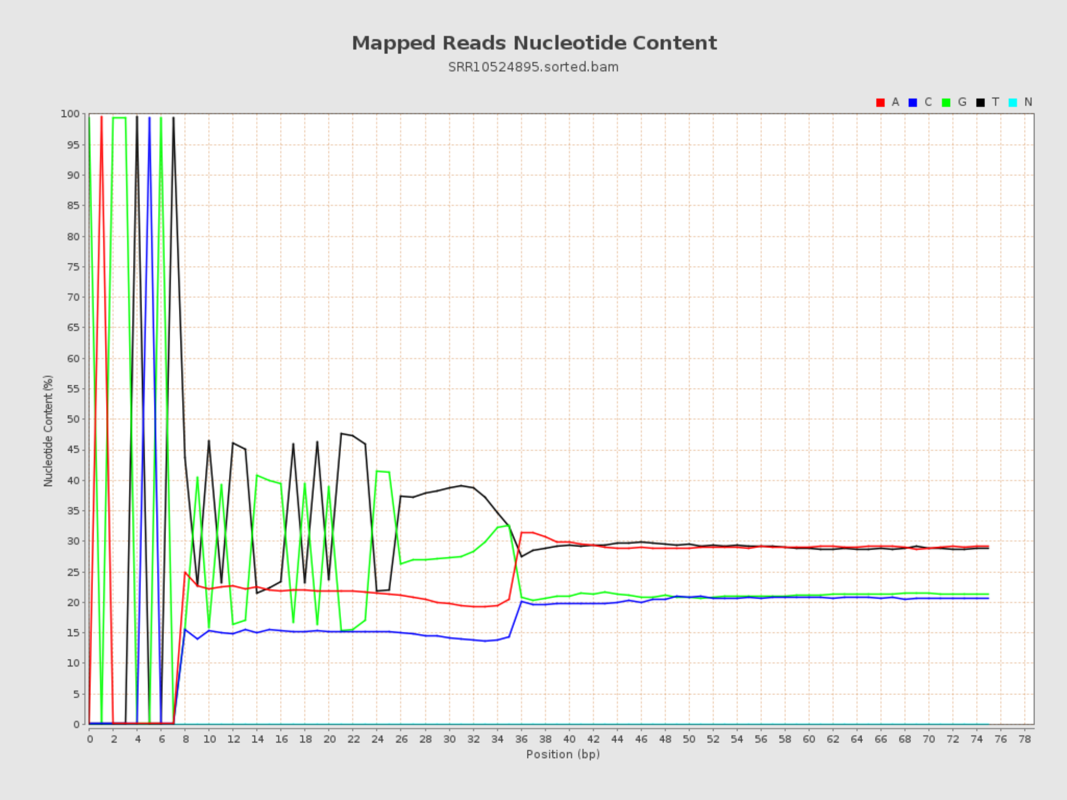
6. Results : Genome Fraction Coverage



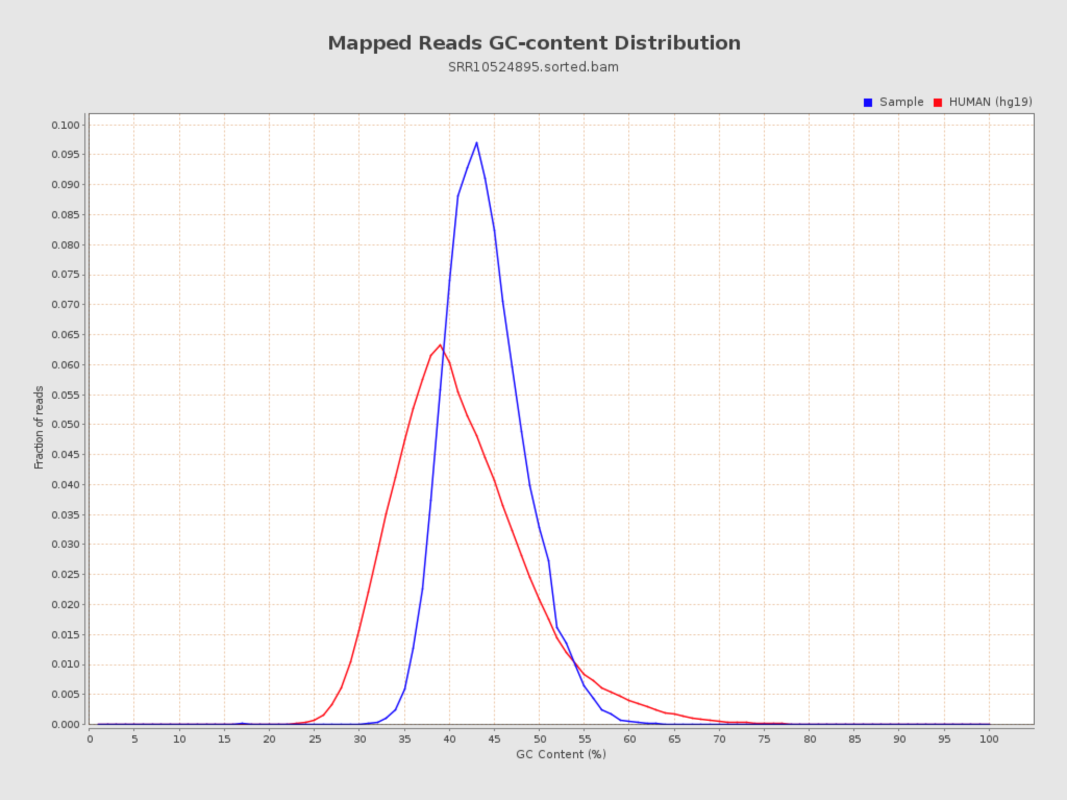
7. Results : Duplication Rate Histogram



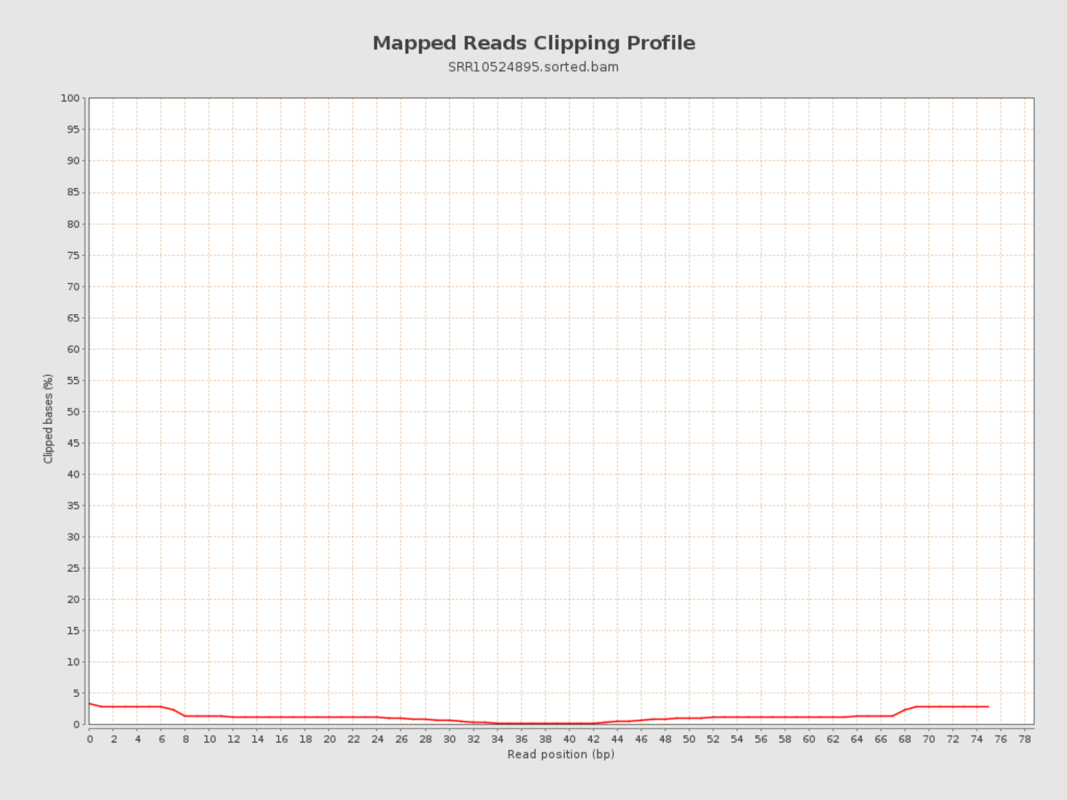
8. Results : Mapped Reads Nucleotide Content



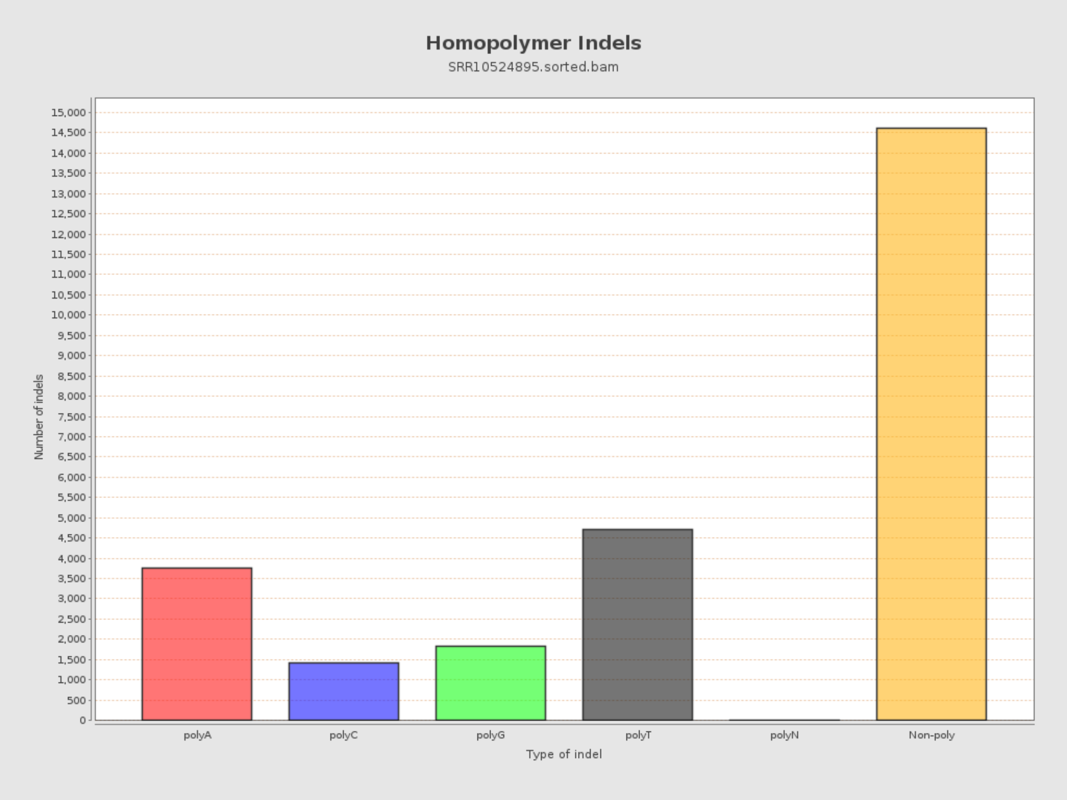
9. Results : Mapped Reads GC-content Distribution



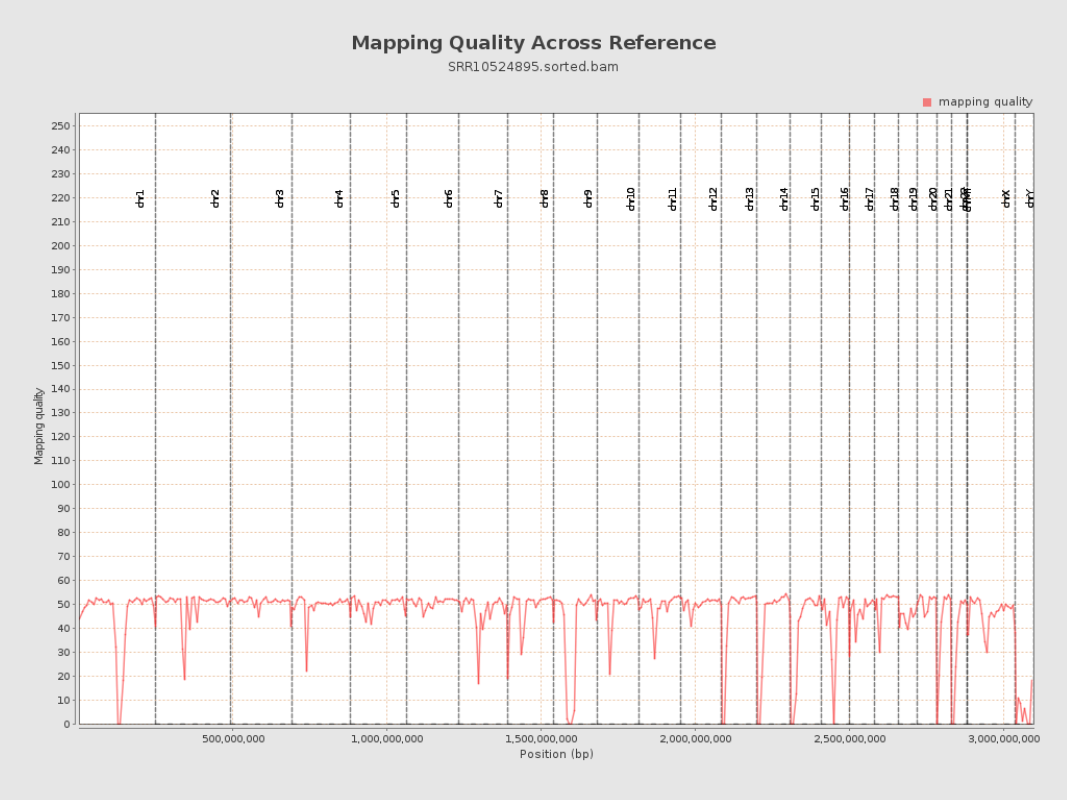
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram