Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:17:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524494.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_SRR10524494 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524494.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:17:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524494.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,753,321
Mapped reads	1,597,061 / 91.09%
Unmapped reads	156,260 / 8.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,662 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	73,612 / 4.2%
Duplication rate	3.57%
Clipped reads	1,596,571 / 91.06%

2.2. ACGT Content

Number/percentage of A's	23,785,733 / 25.53%
Number/percentage of C's	17,343,419 / 18.61%
Number/percentage of T's	29,823,121 / 32.01%
Number/percentage of G's	22,215,977 / 23.84%
Number/percentage of N's	1,814 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2738

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

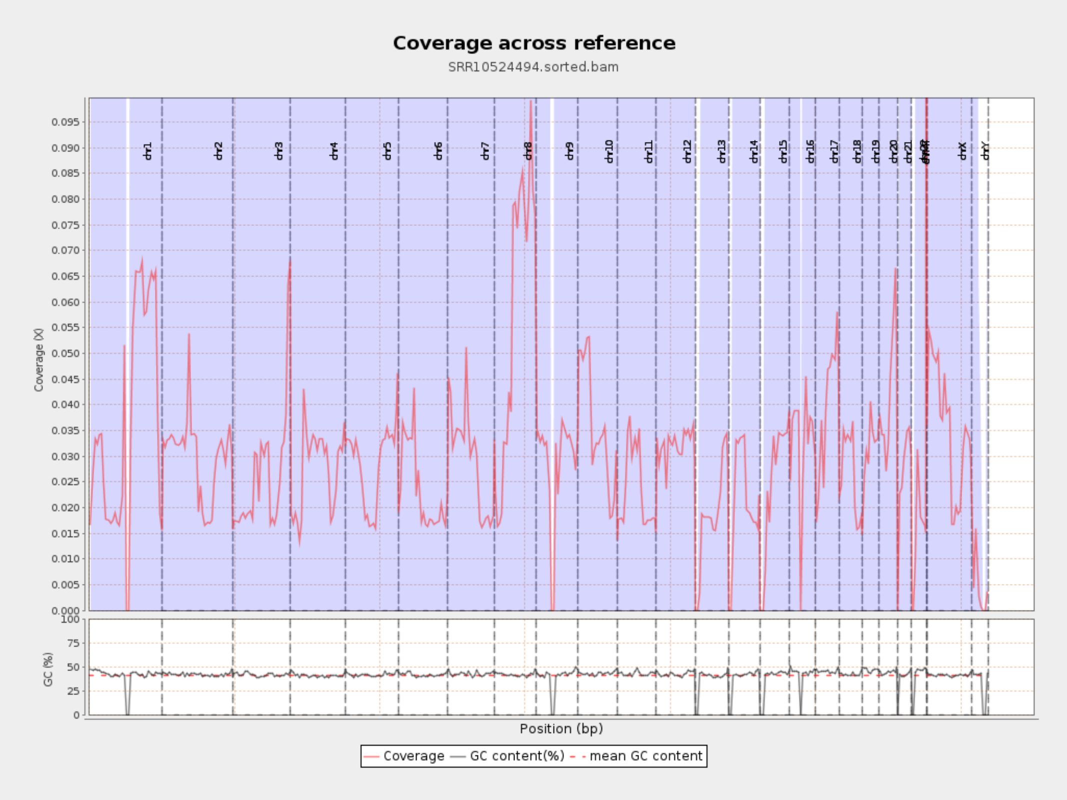
General error rate	0.48%
Mismatches	436,231
Insertions	5,895
Mapped reads with at least one insertion	0.37%
Deletions	17,166
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.66%

2.6. Chromosome stats

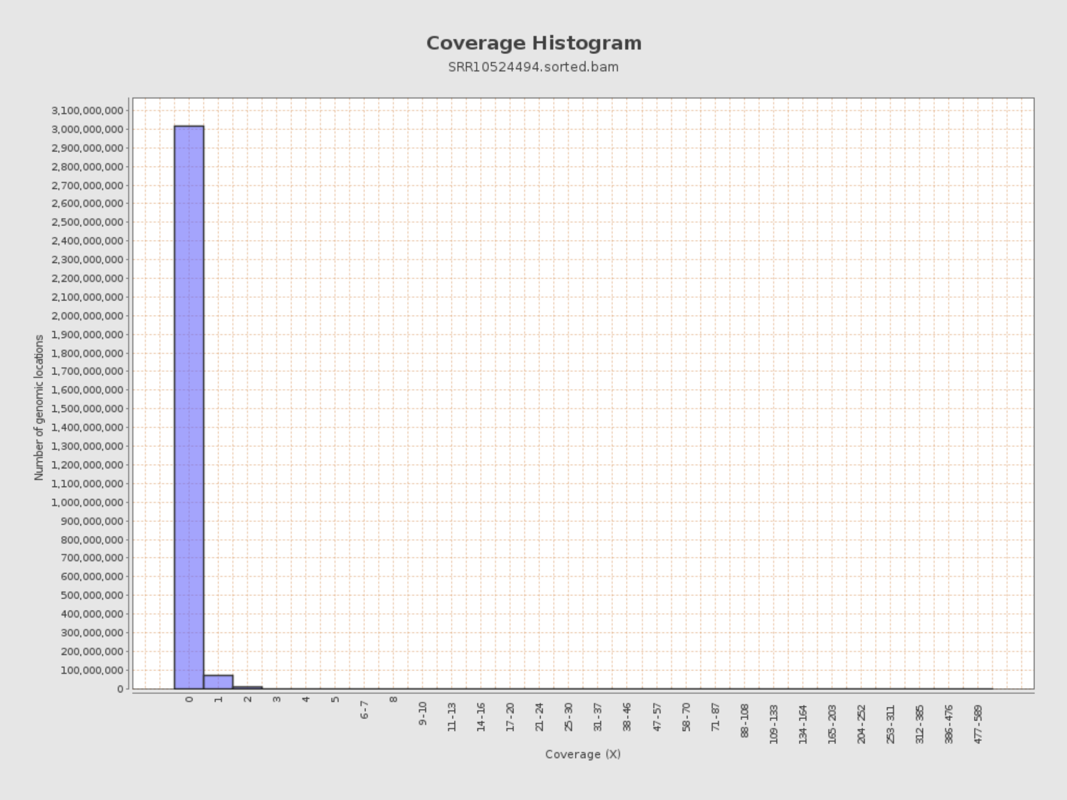
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9184239	0.0368	0.477
chr2	243199373	7317918	0.0301	0.3135
chr3	198022430	5068654	0.0256	0.1796
chr4	191154276	5248878	0.0275	0.2086
chr5	180915260	5161486	0.0285	0.1887
chr6	171115067	4037401	0.0236	0.2154
chr7	159138663	4701519	0.0295	0.3724

chr8	146364022	8516613	0.0582	0.308
chr9	141213431	3978780	0.0282	0.2441
chr10	135534747	4883717	0.036	0.2732
chr11	135006516	3203164	0.0237	0.2672
chr12	133851895	4312985	0.0322	0.2
chr13	115169878	2122882	0.0184	0.1532
chr14	107349540	2246217	0.0209	0.1661
chr15	102531392	2506167	0.0244	0.1791
chr16	90354753	2946317	0.0326	0.2134
chr17	81195210	3218575	0.0396	0.235
chr18	78077248	2091479	0.0268	0.4047
chr19	59128983	1880835	0.0318	0.3438
chr20	63025520	2676787	0.0425	0.2327
chr21	48129895	1283057	0.0267	0.194
chr22	51304566	754136	0.0147	0.1346
chrMT	16571	8173	0.4932	0.8613
chrX	155270560	5564092	0.0358	0.2316
chrY	59373566	285474	0.0048	0.1225

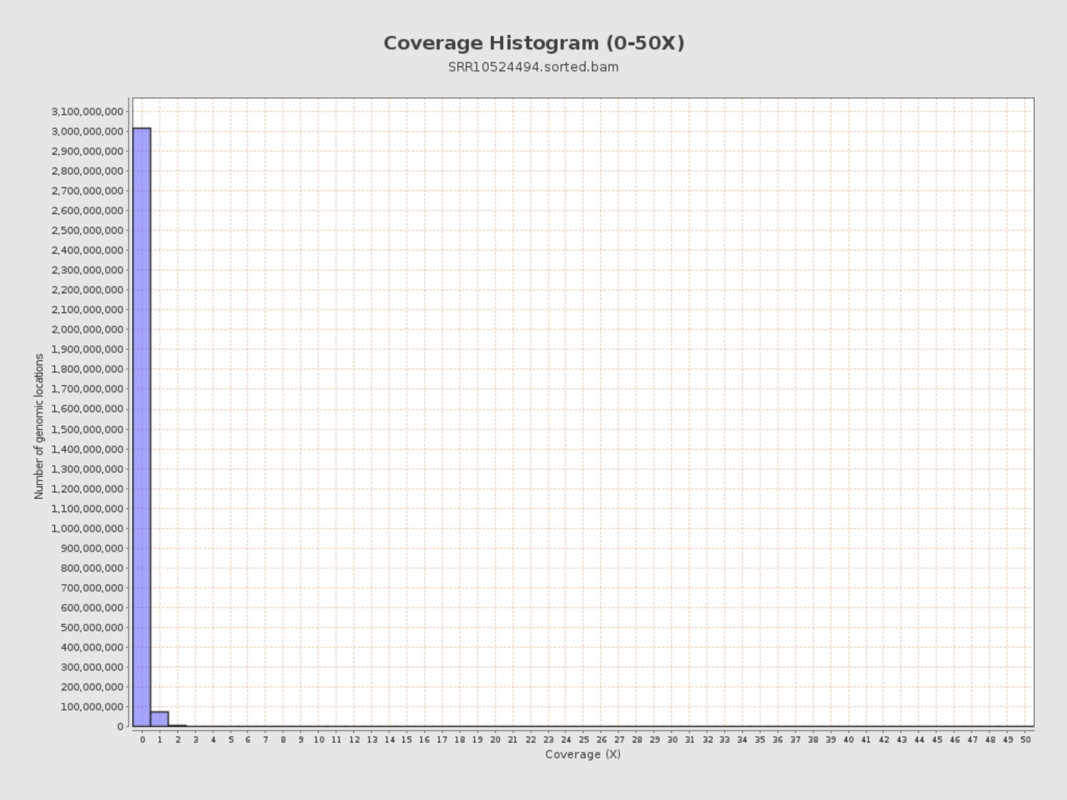
3. Results : Coverage across reference



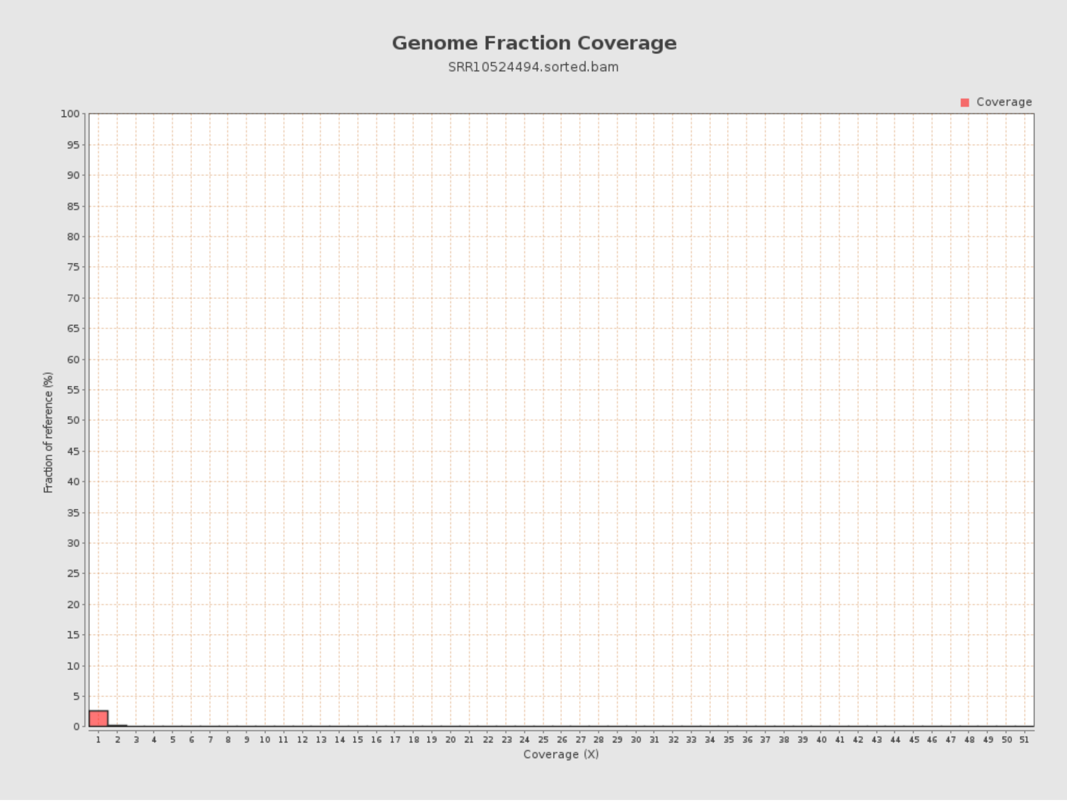
4. Results : Coverage Histogram



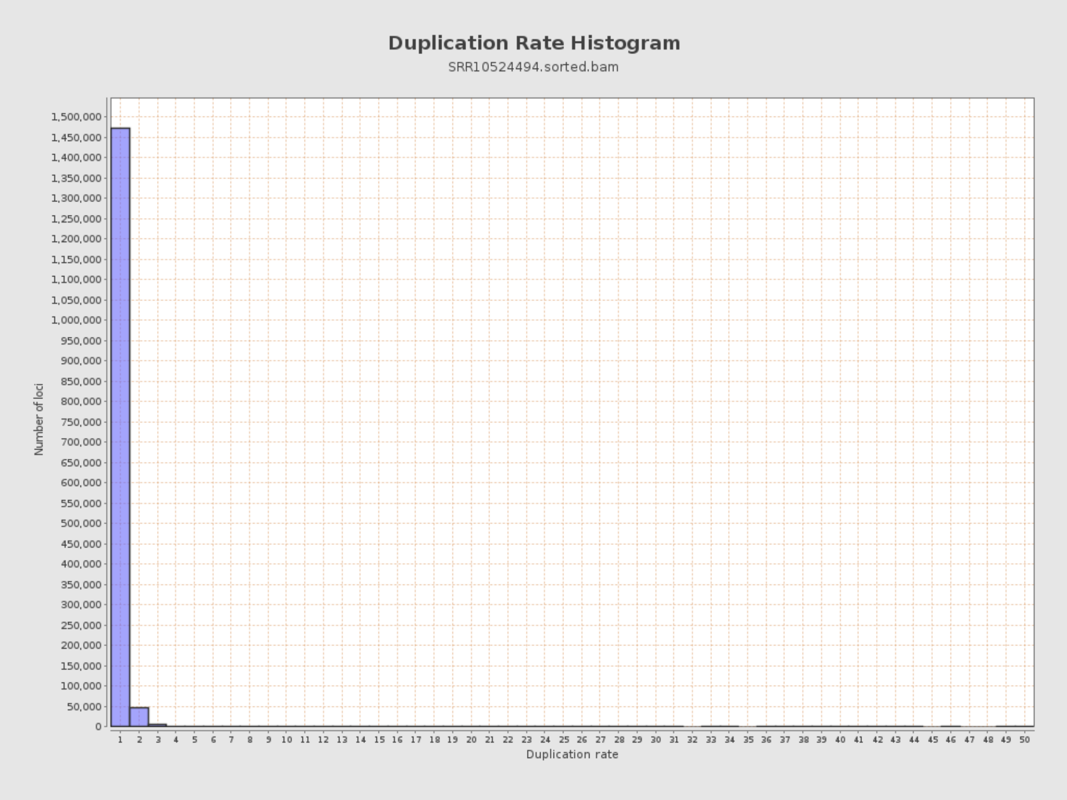
5. Results : Coverage Histogram (0-50X)



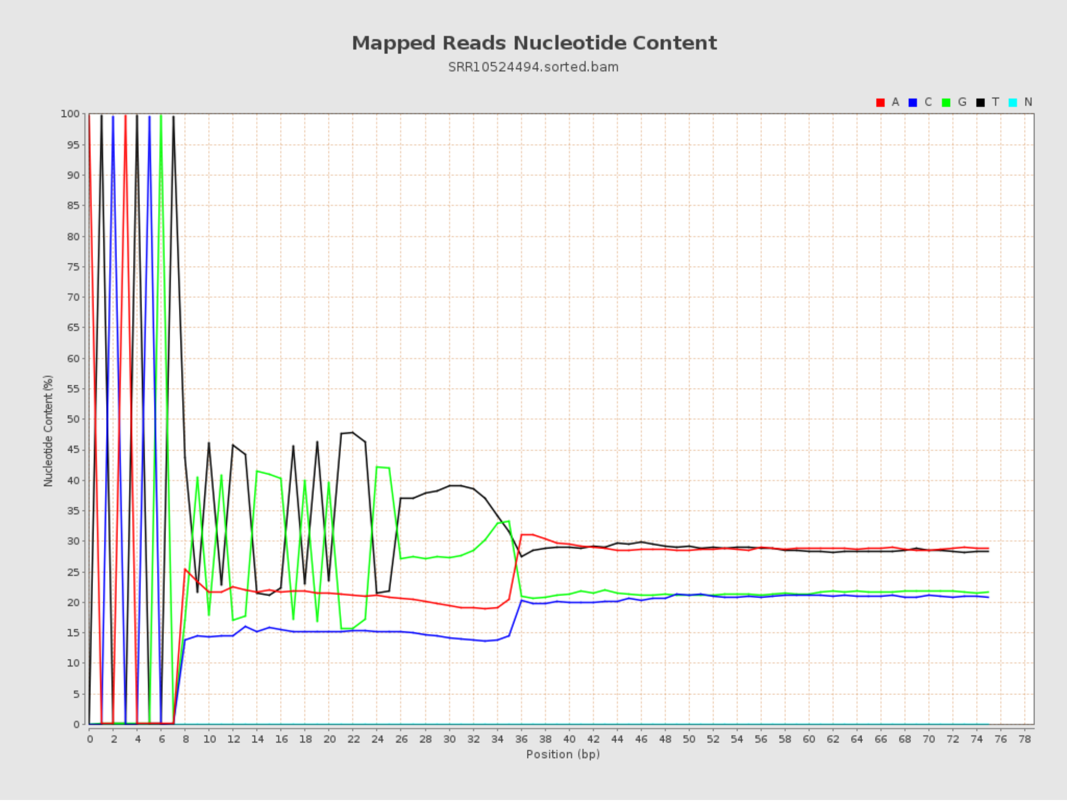
6. Results : Genome Fraction Coverage



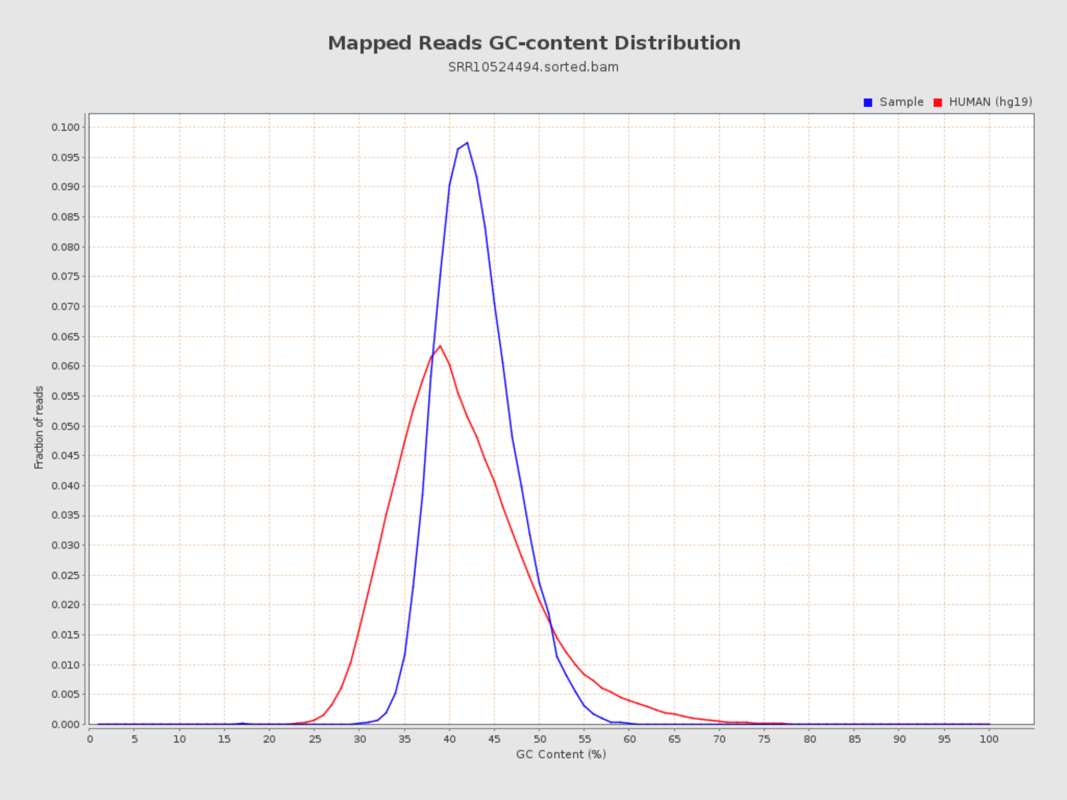
7. Results : Duplication Rate Histogram



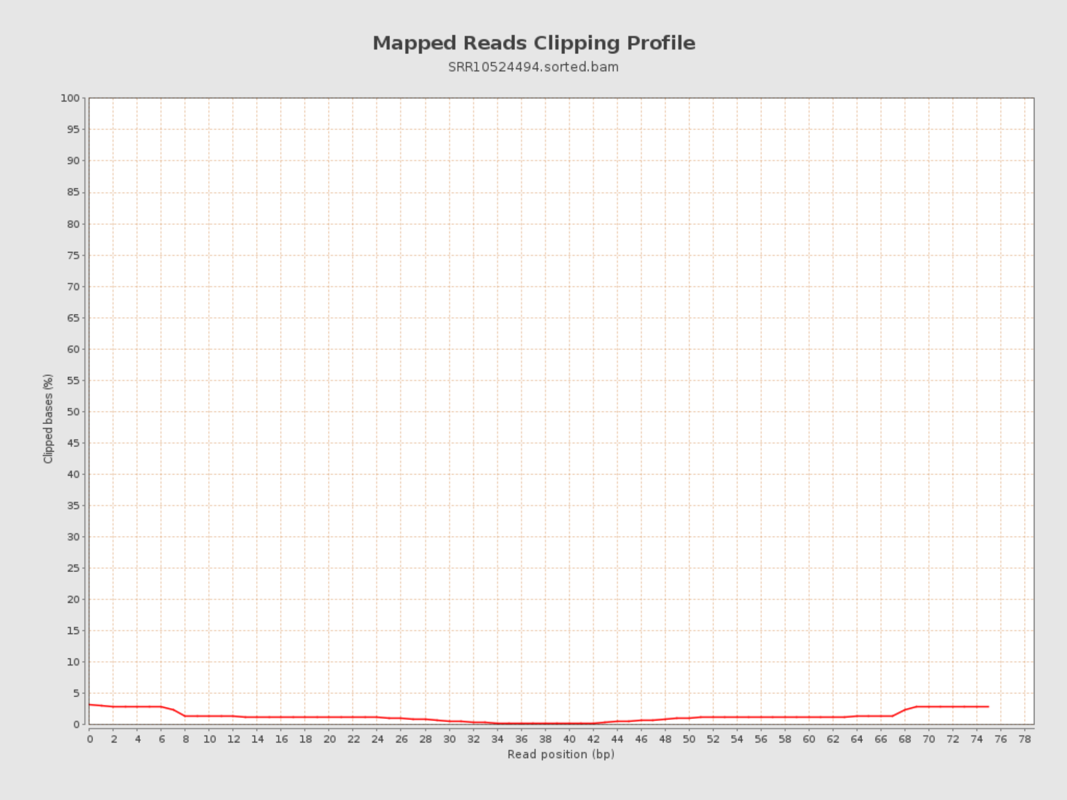
8. Results : Mapped Reads Nucleotide Content



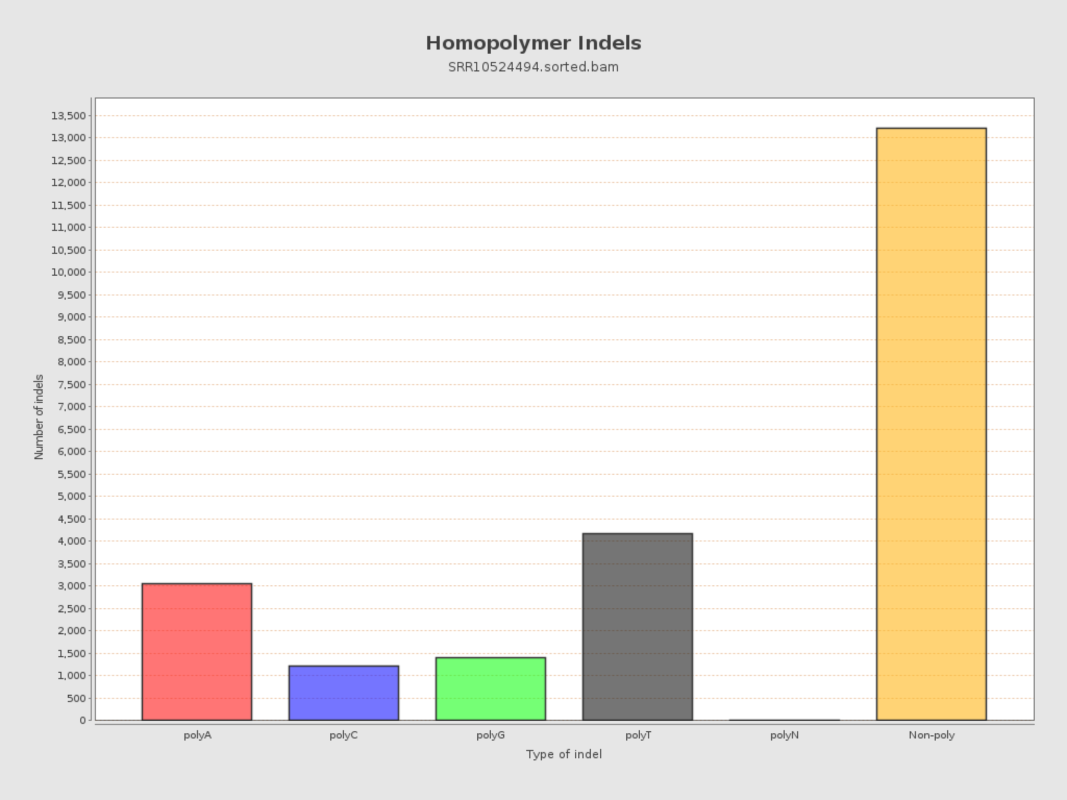
9. Results : Mapped Reads GC-content Distribution



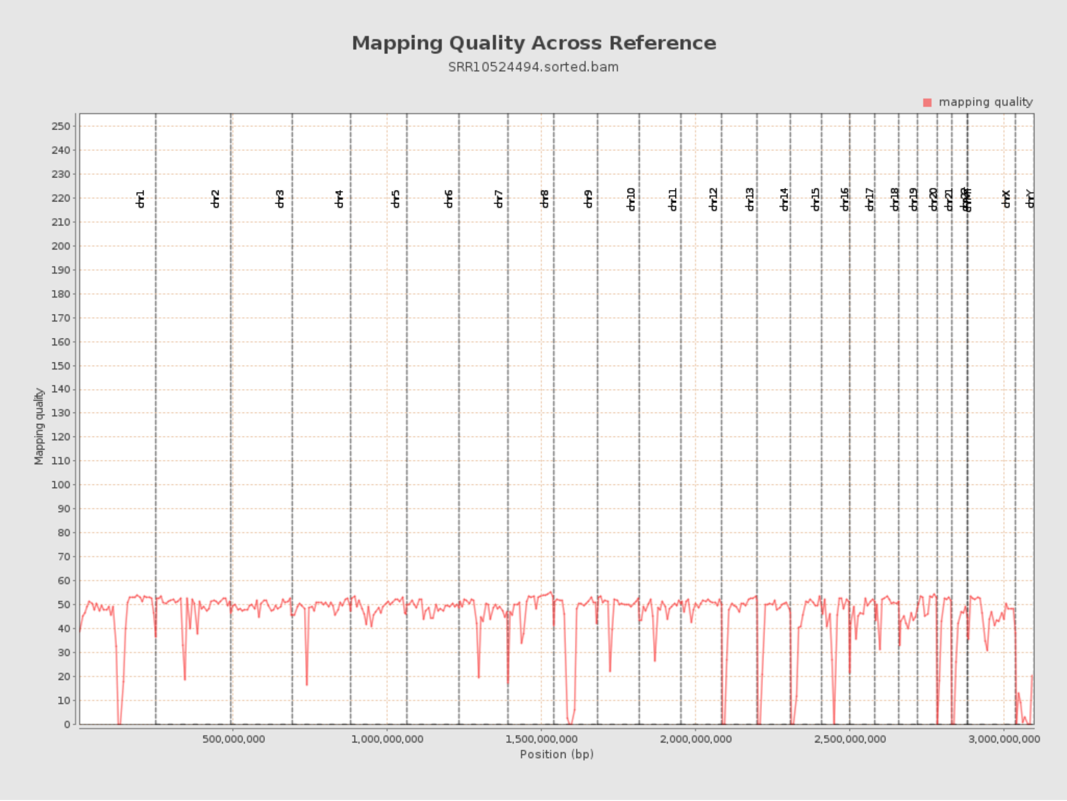
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram