Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:16:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524972.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_SRR10524972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524972.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:16:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	971,774
Mapped reads	901,713 / 92.79%
Unmapped reads	70,061 / 7.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,010 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	25,308 / 2.6%
Duplication rate	2.14%
Clipped reads	902,705 / 92.89%

2.2. ACGT Content

Number/percentage of A's	12,629,710 / 24.13%
Number/percentage of C's	9,174,535 / 17.53%
Number/percentage of T's	17,271,648 / 33%
Number/percentage of G's	13,256,364 / 25.33%
Number/percentage of N's	548 / 0%
GC Percentage	42.86%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.1719

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

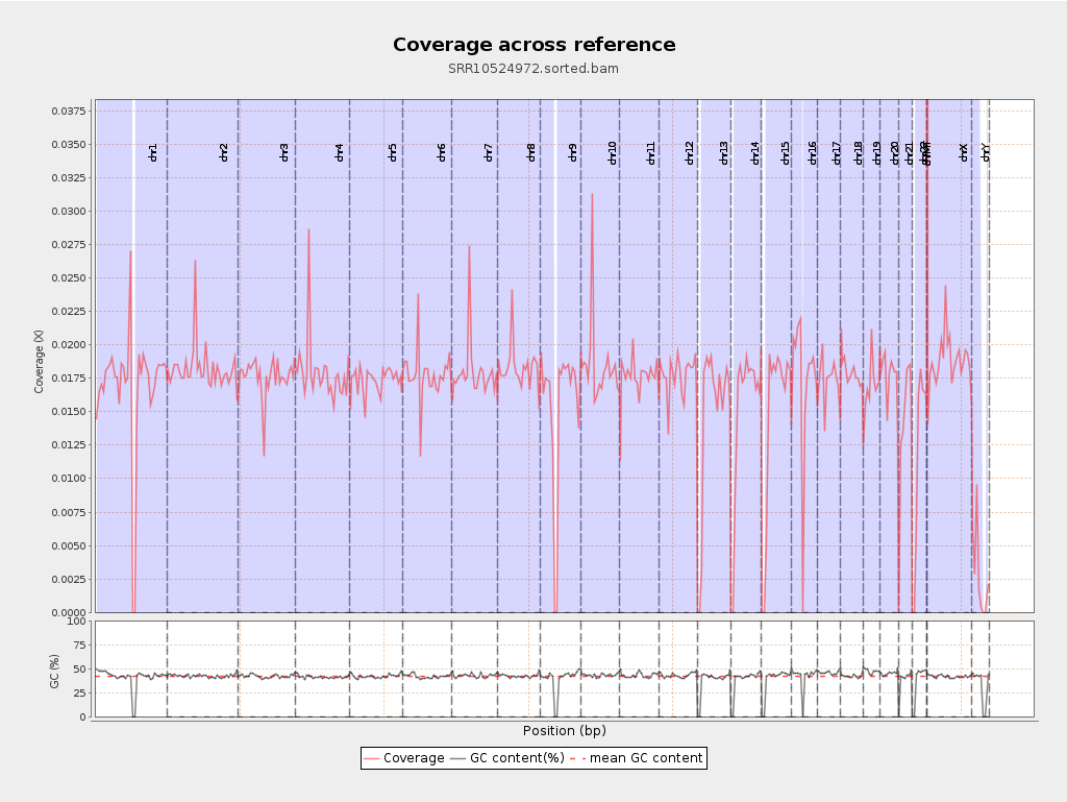
General error rate	0.49%
Mismatches	250,529
Insertions	2,811
Mapped reads with at least one insertion	0.31%
Deletions	9,493
Mapped reads with at least one deletion	1.05%
Homopolymer indels	45.76%

2.6. Chromosome stats

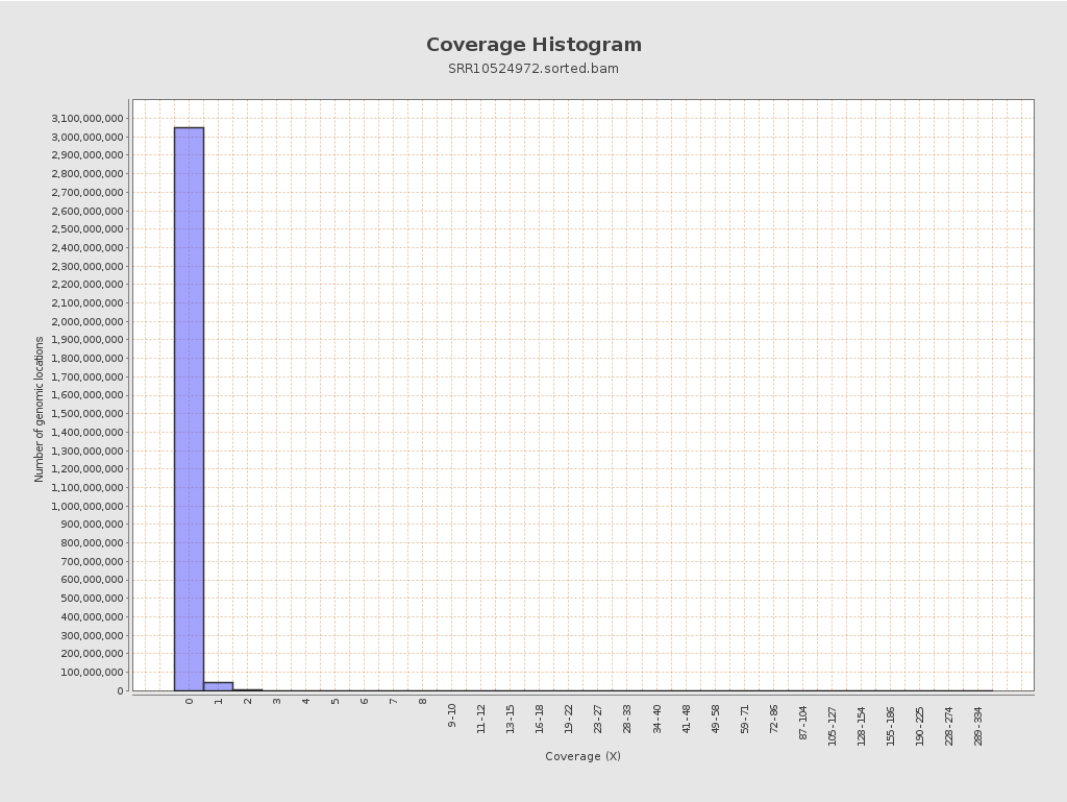
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4181144	0.0168	0.2634
chr2	243199373	4434174	0.0182	0.1914
chr3	198022430	3480510	0.0176	0.141
chr4	191154276	3429223	0.0179	0.1558
chr5	180915260	3159570	0.0175	0.1403
chr6	171115067	3034662	0.0177	0.1589
chr7	159138663	2864815	0.018	0.2046

chr8	146364022	2686102	0.0184	0.1832
chr9	141213431	2167025	0.0153	0.1549
chr10	135534747	2510019	0.0185	0.1859
chr11	135006516	2401681	0.0178	0.1696
chr12	133851895	2371063	0.0177	0.1418
chr13	115169878	1675273	0.0145	0.1279
chr14	107349540	1591349	0.0148	0.1334
chr15	102531392	1506787	0.0147	0.1304
chr16	90354753	1538342	0.017	0.1427
chr17	81195210	1407440	0.0173	0.149
chr18	78077248	1403354	0.018	0.2231
chr19	59128983	1011067	0.0171	0.2055
chr20	63025520	1115368	0.0177	0.1427
chr21	48129895	685522	0.0142	0.1345
chr22	51304566	602358	0.0117	0.1144
chrMT	16571	7607	0.4591	0.7311
chrX	155270560	2924017	0.0188	0.1548
chrY	59373566	160902	0.0027	0.0848

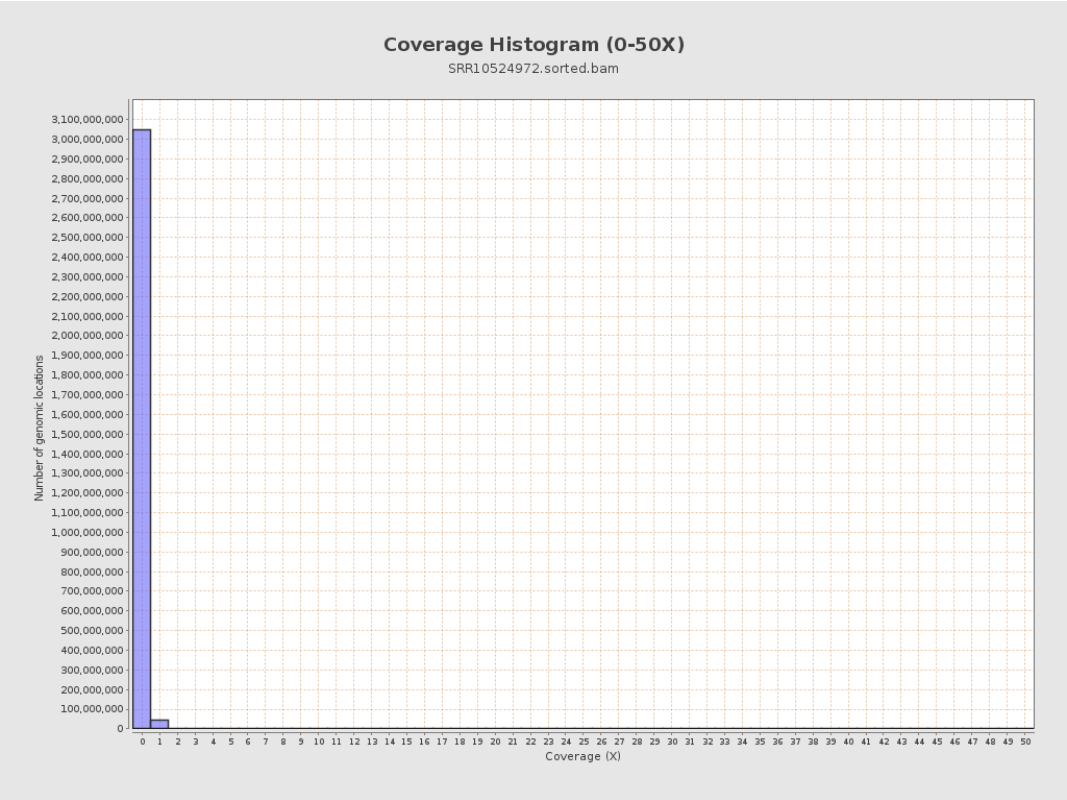
3. Results : Coverage across reference



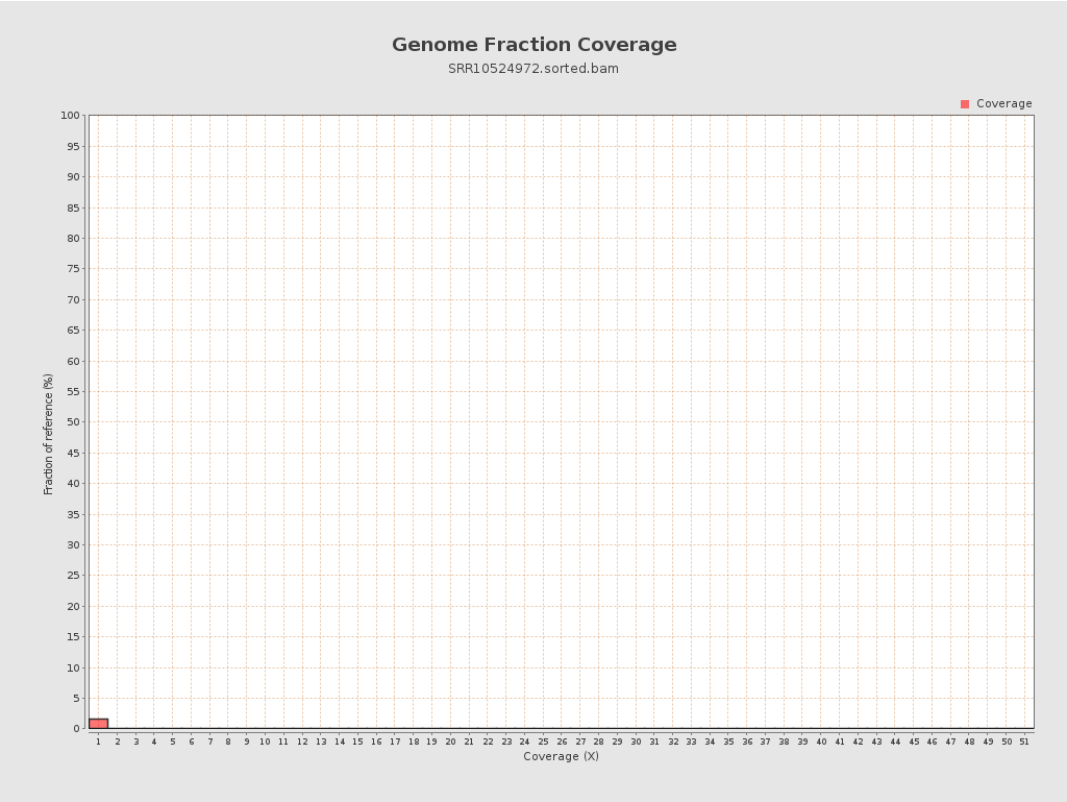
4. Results : Coverage Histogram



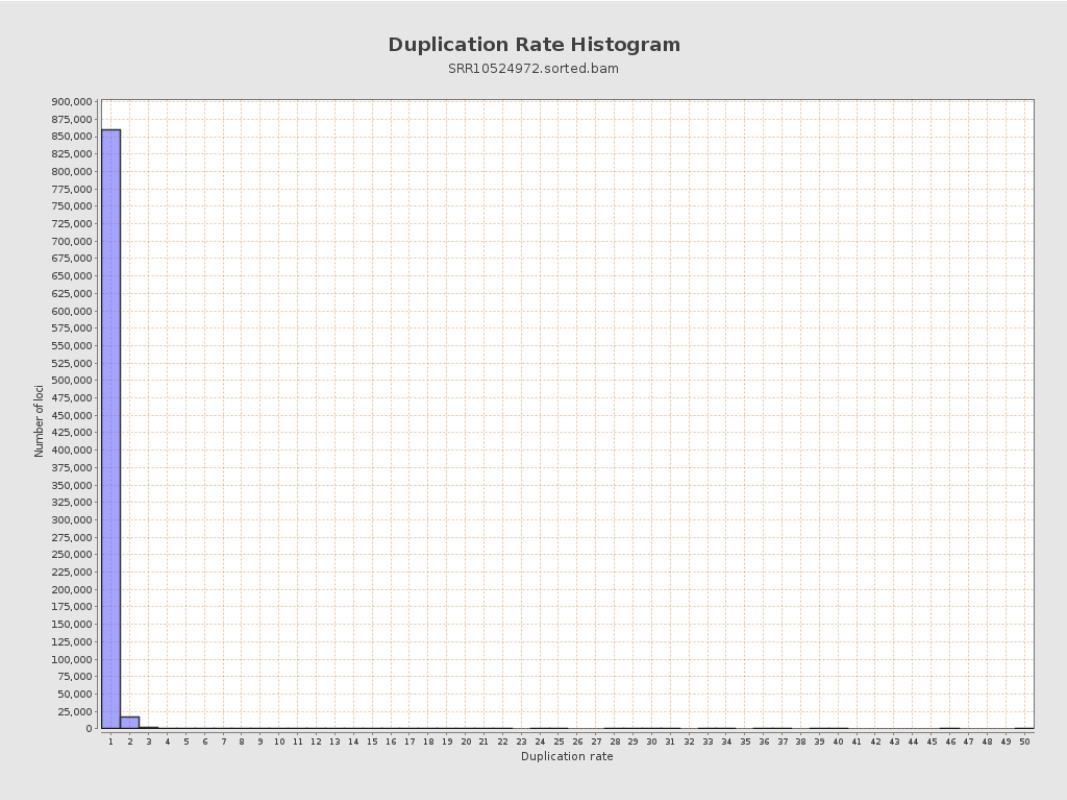
5. Results : Coverage Histogram (0-50X)



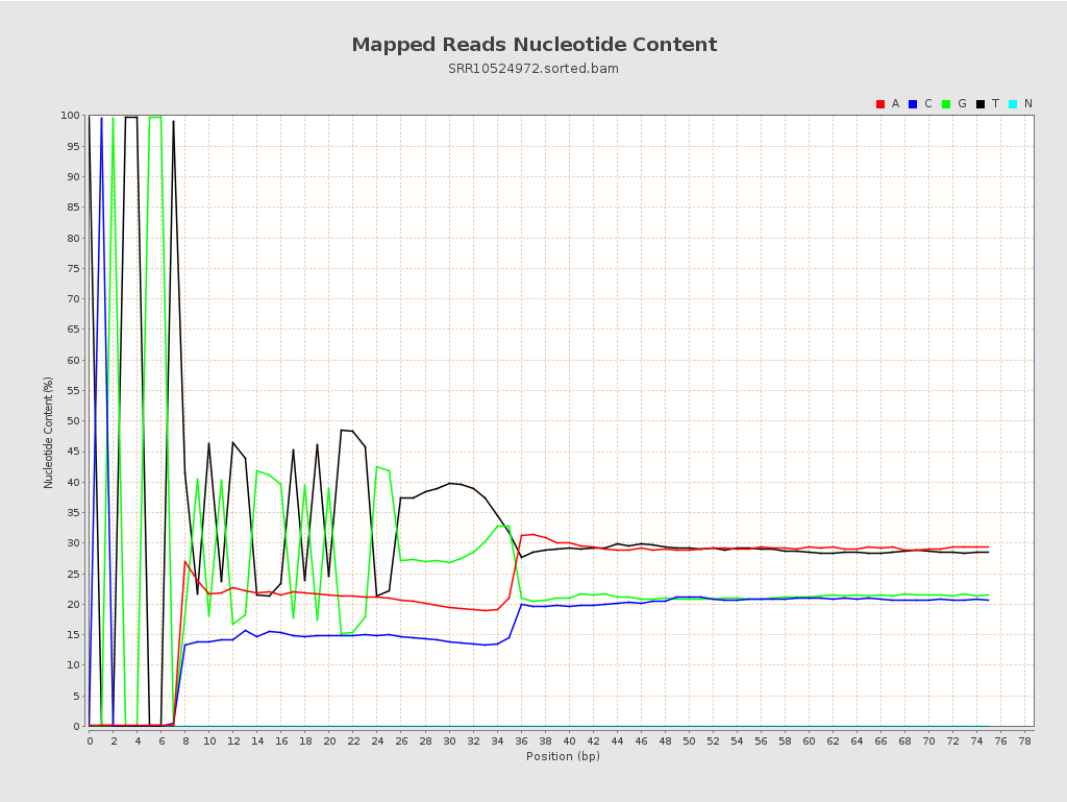
6. Results : Genome Fraction Coverage



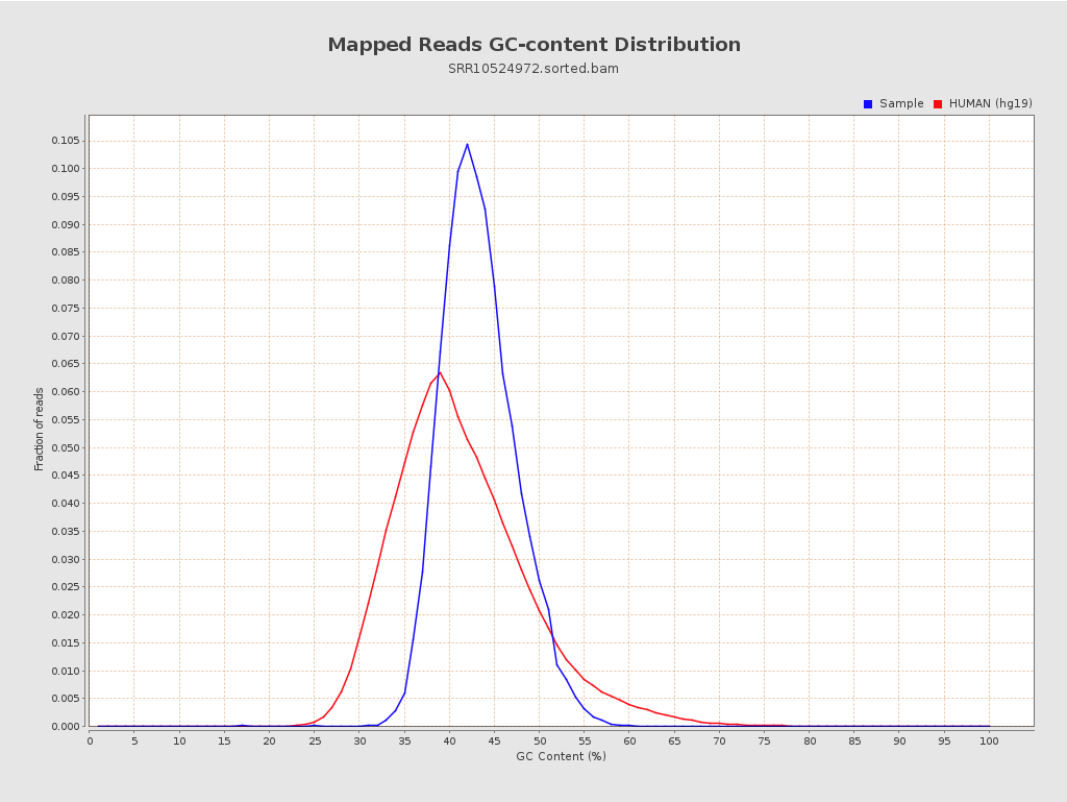
7. Results : Duplication Rate Histogram



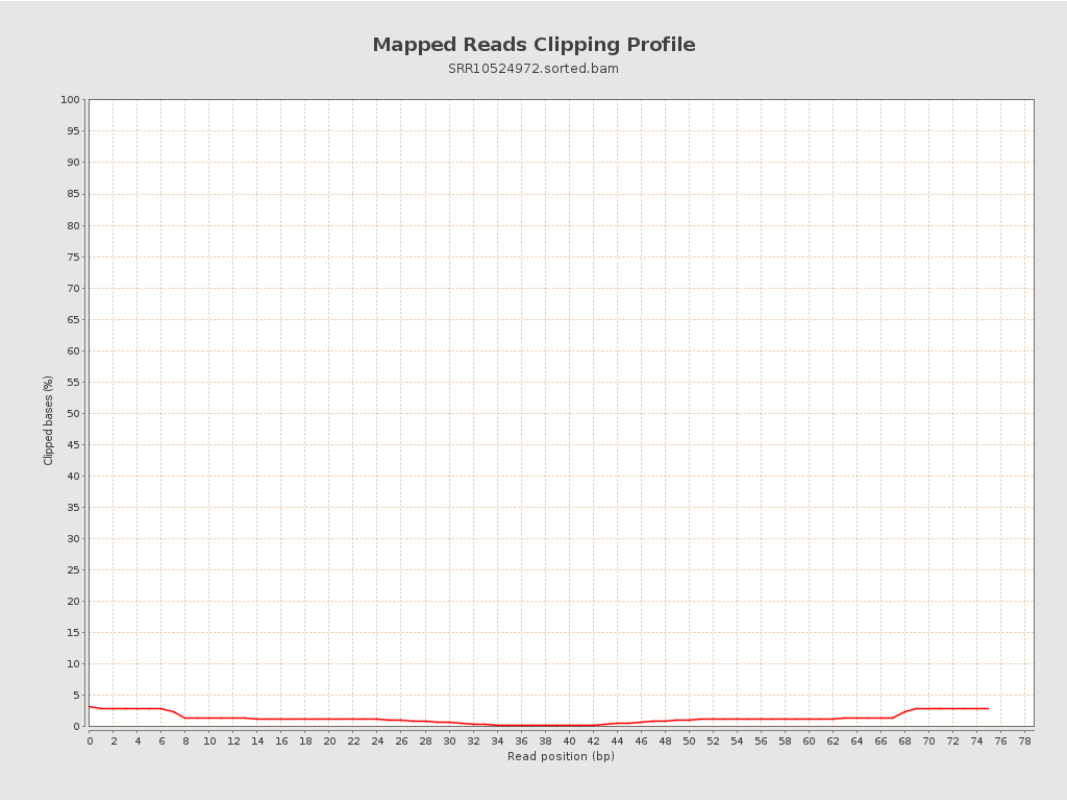
8. Results : Mapped Reads Nucleotide Content



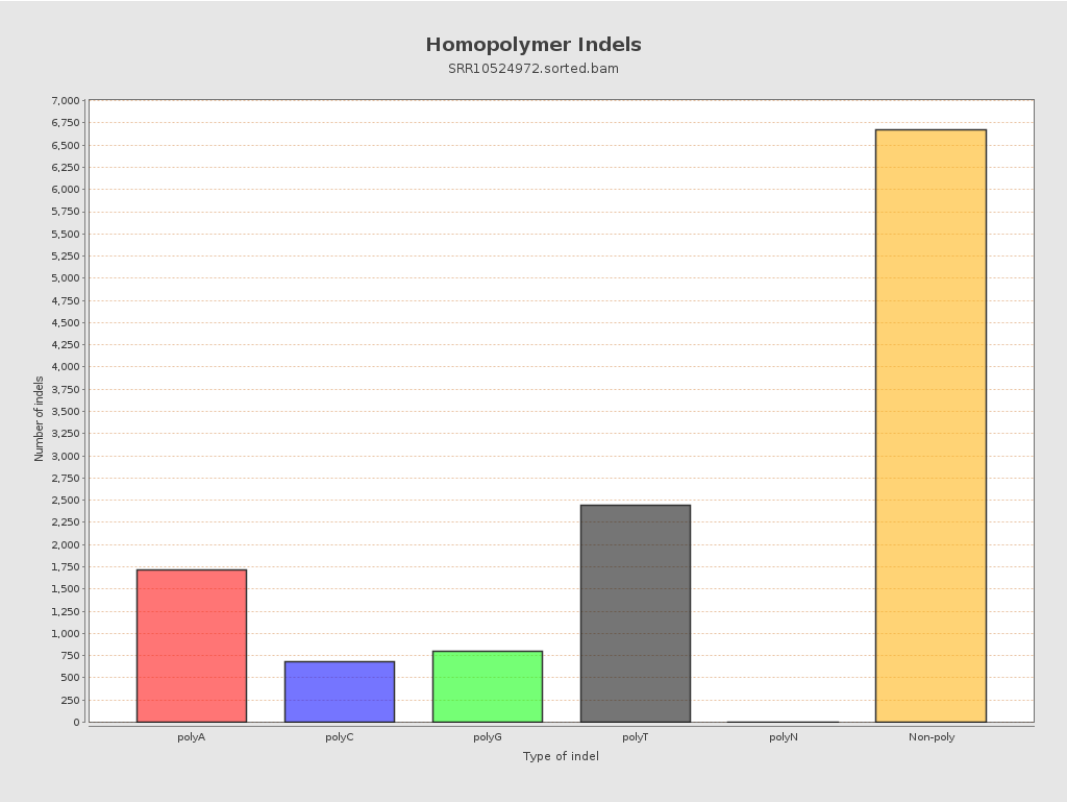
9. Results : Mapped Reads GC-content Distribution



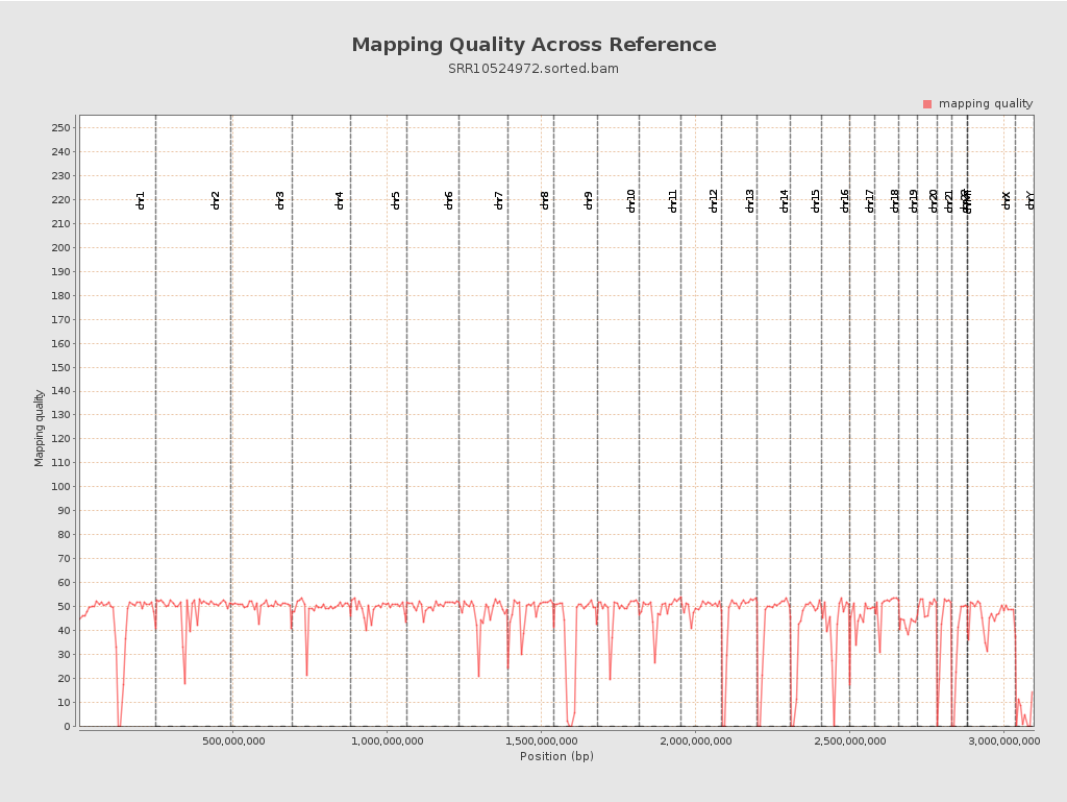
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram