Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:58:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524372.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_SRR10524372 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524372.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:58:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524372.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	537,245
Mapped reads	490,279 / 91.26%
Unmapped reads	46,966 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,502 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	12,401 / 2.31%
Duplication rate	1.91%
Clipped reads	490,958 / 91.38%

2.2. ACGT Content

Number/percentage of A's	7,299,598 / 25.41%
Number/percentage of C's	5,479,681 / 19.08%
Number/percentage of T's	9,157,418 / 31.88%
Number/percentage of G's	6,781,566 / 23.61%
Number/percentage of N's	4,209 / 0.01%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1245

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

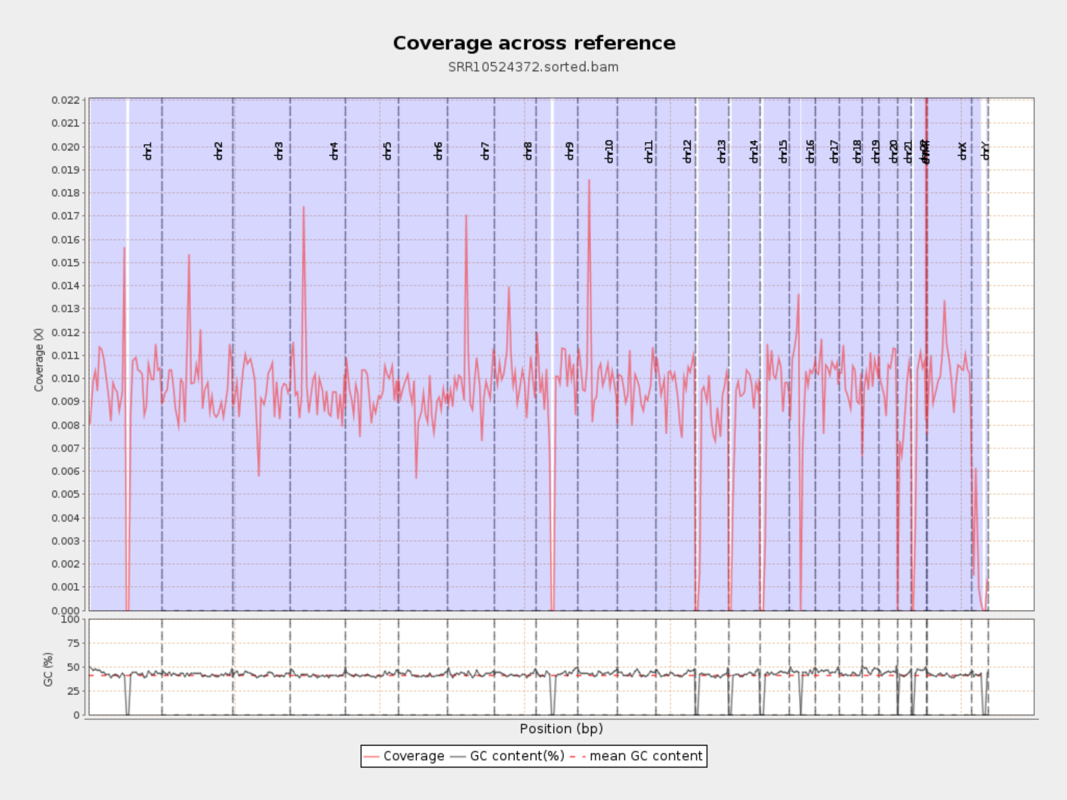
General error rate	0.54%
Mismatches	148,956
Insertions	2,490
Mapped reads with at least one insertion	0.51%
Deletions	5,258
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.25%

2.6. Chromosome stats

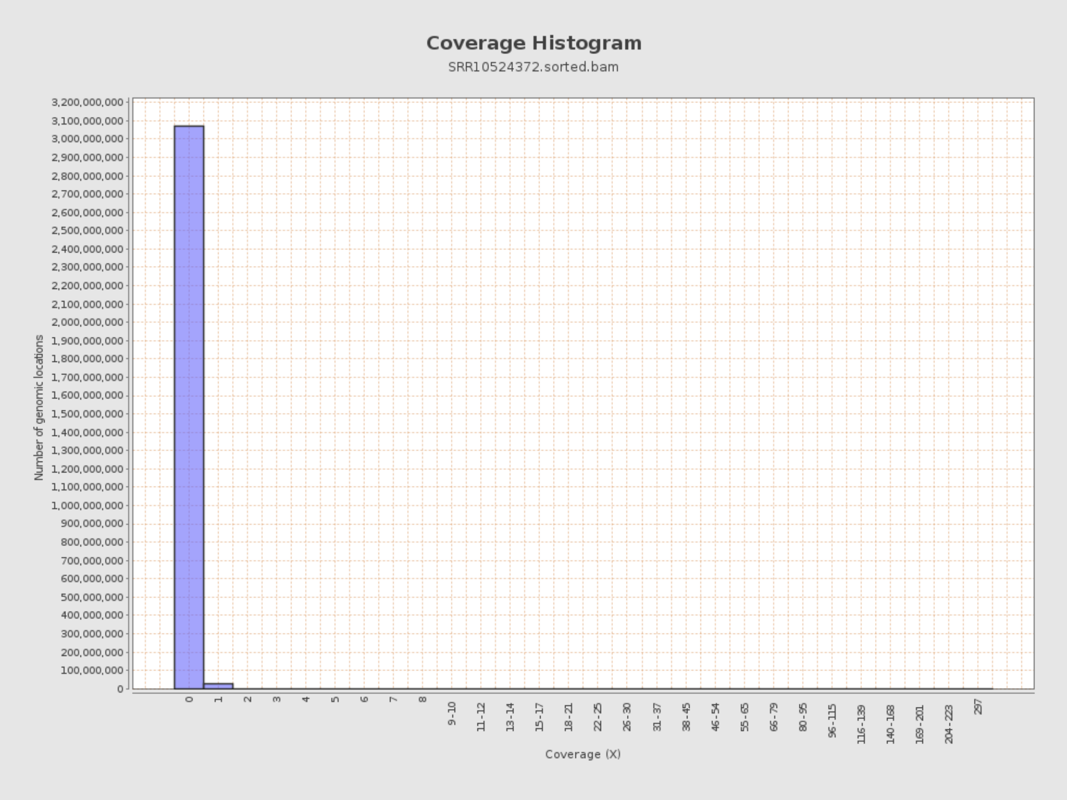
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2354387	0.0094	0.1886
chr2	243199373	2360522	0.0097	0.1605
chr3	198022430	1878618	0.0095	0.1016
chr4	191154276	1841842	0.0096	0.1113
chr5	180915260	1714600	0.0095	0.1015
chr6	171115067	1531464	0.0089	0.1016
chr7	159138663	1582360	0.0099	0.1496

chr8	146364022	1492468	0.0102	0.1218
chr9	141213431	1252110	0.0089	0.1099
chr10	135534747	1407552	0.0104	0.1273
chr11	135006516	1302264	0.0096	0.1157
chr12	133851895	1300029	0.0097	0.104
chr13	115169878	860164	0.0075	0.0902
chr14	107349540	863501	0.008	0.0954
chr15	102531392	842067	0.0082	0.0946
chr16	90354753	865158	0.0096	0.105
chr17	81195210	832359	0.0103	0.1083
chr18	78077248	767569	0.0098	0.1691
chr19	59128983	592337	0.01	0.1414
chr20	63025520	633522	0.0101	0.1063
chr21	48129895	374736	0.0078	0.0964
chr22	51304566	374398	0.0073	0.0894
chrMT	16571	16566	0.9997	1.2013
chrX	155270560	1590755	0.0102	0.1096
chrY	59373566	99285	0.0017	0.0613

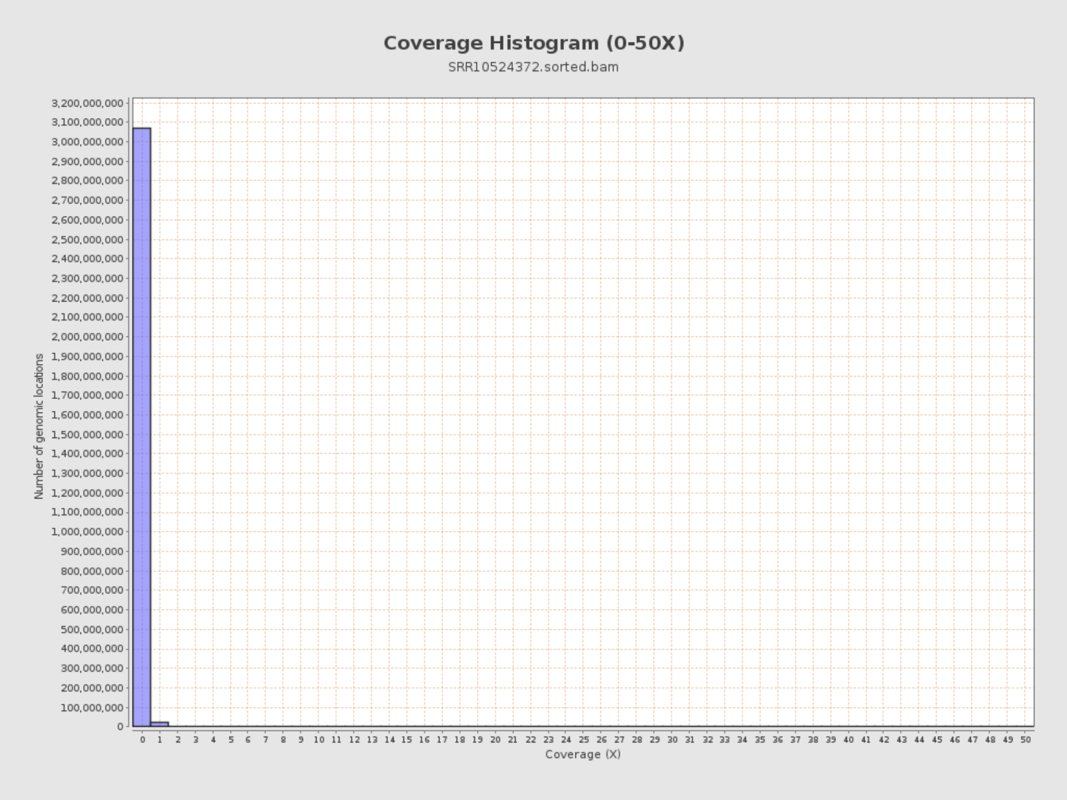
3. Results : Coverage across reference



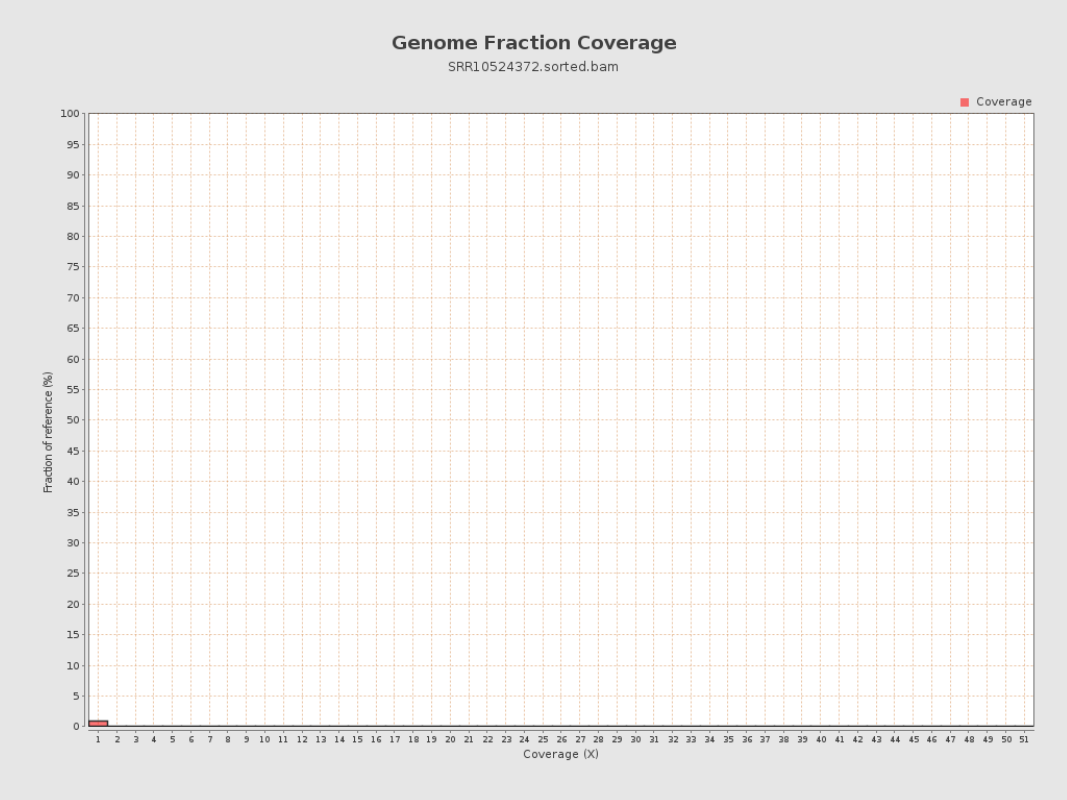
4. Results : Coverage Histogram



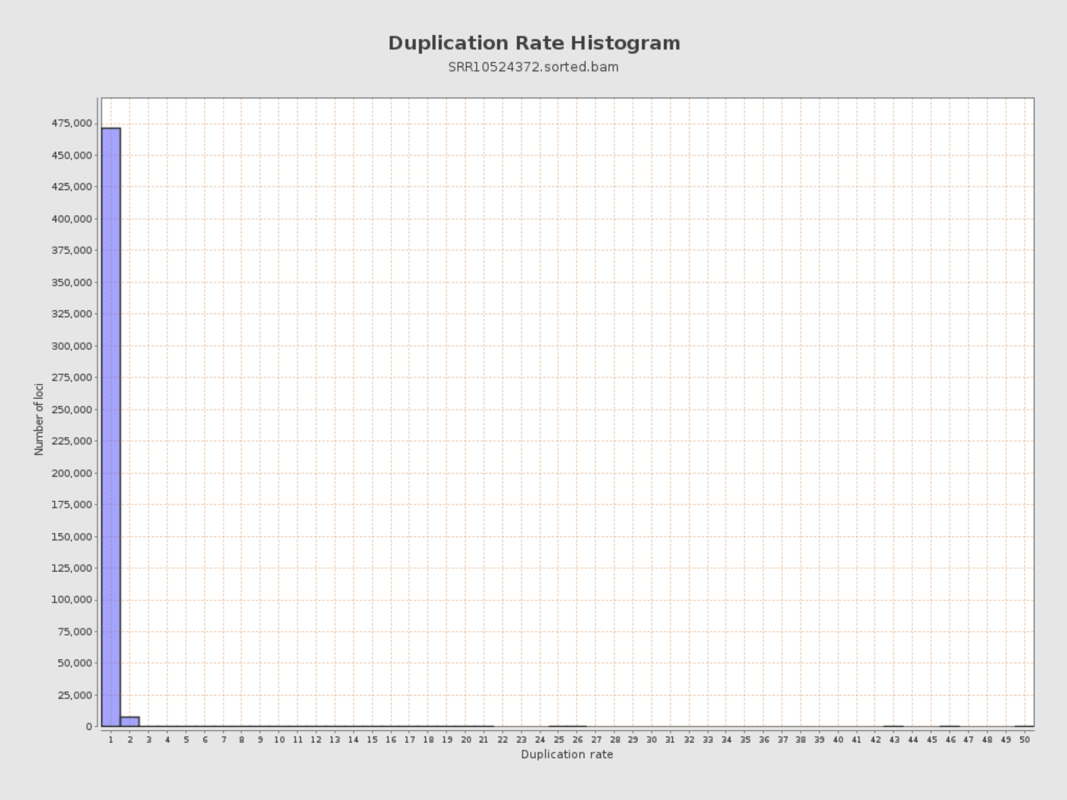
5. Results : Coverage Histogram (0-50X)



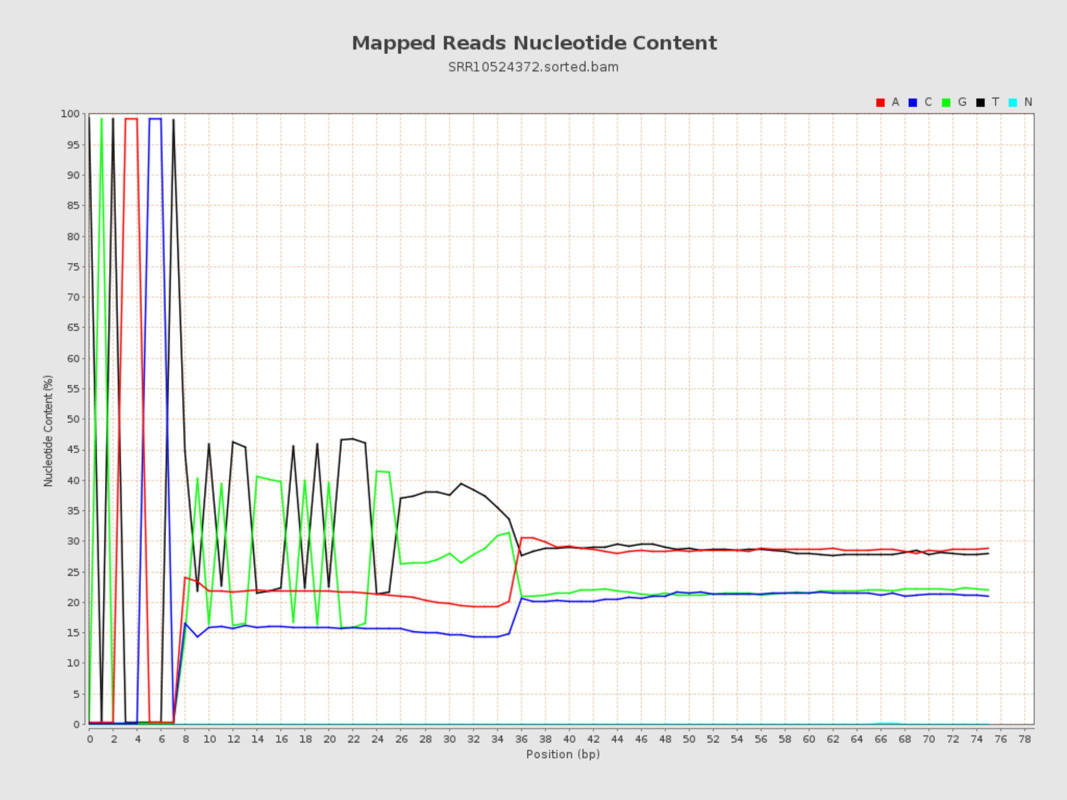
6. Results : Genome Fraction Coverage



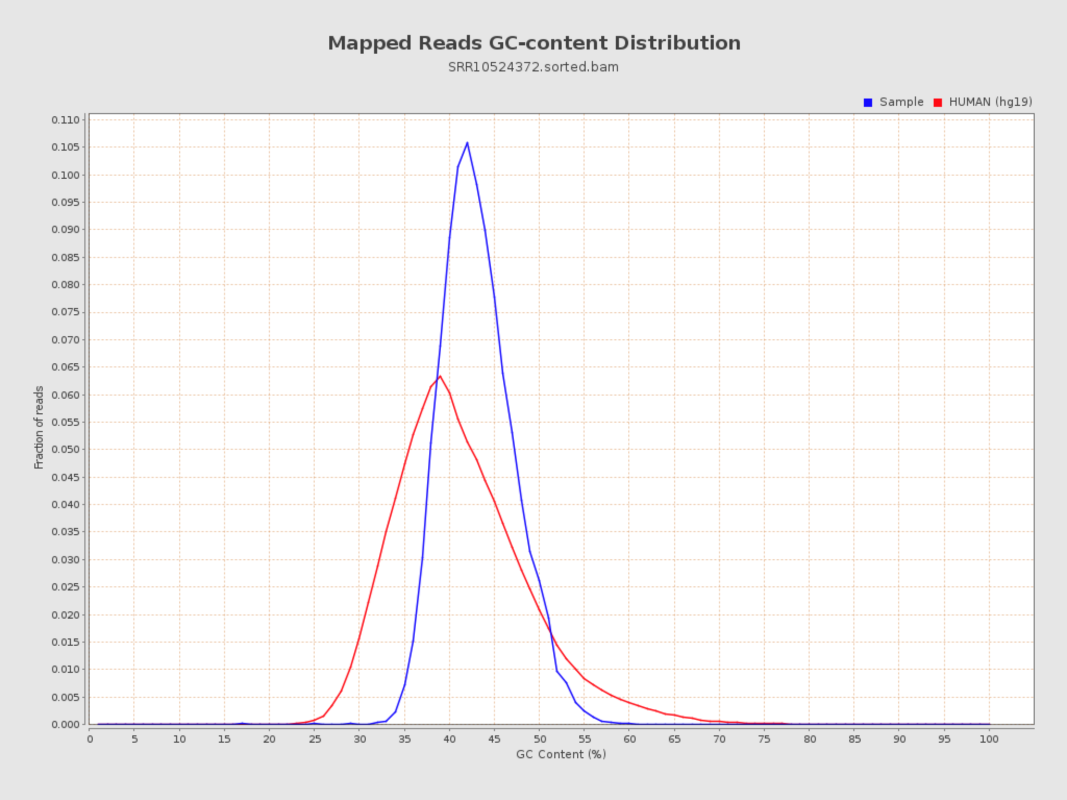
7. Results : Duplication Rate Histogram



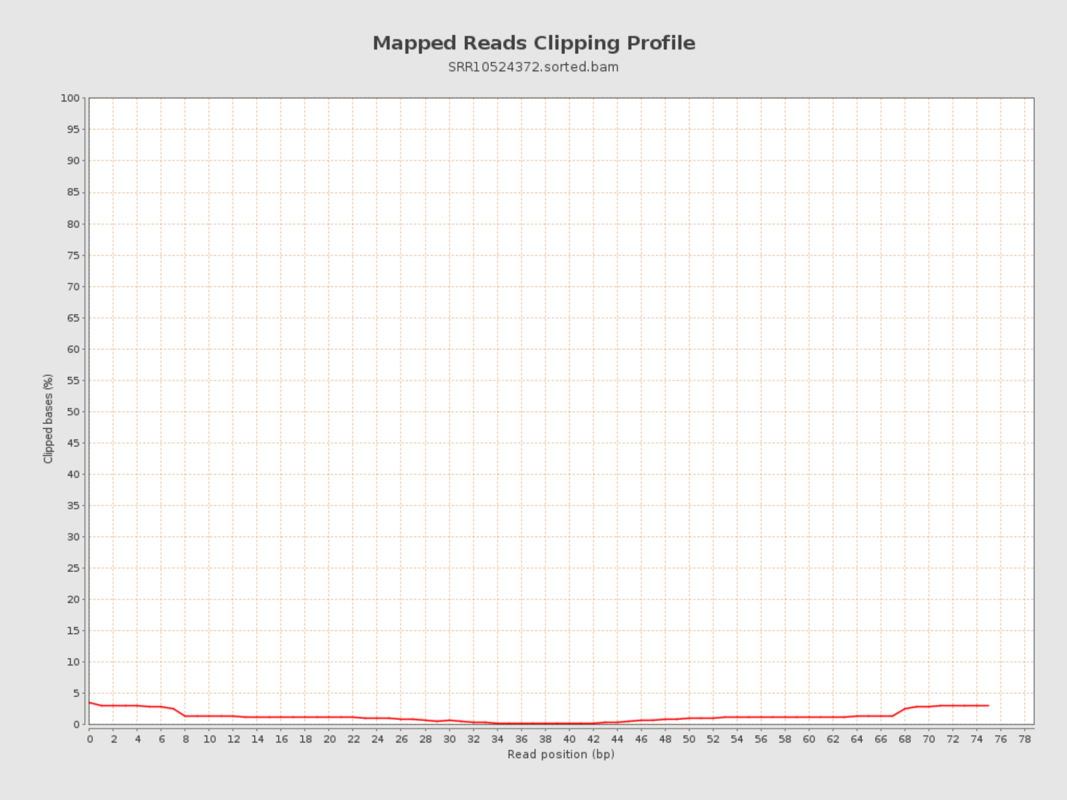
8. Results : Mapped Reads Nucleotide Content



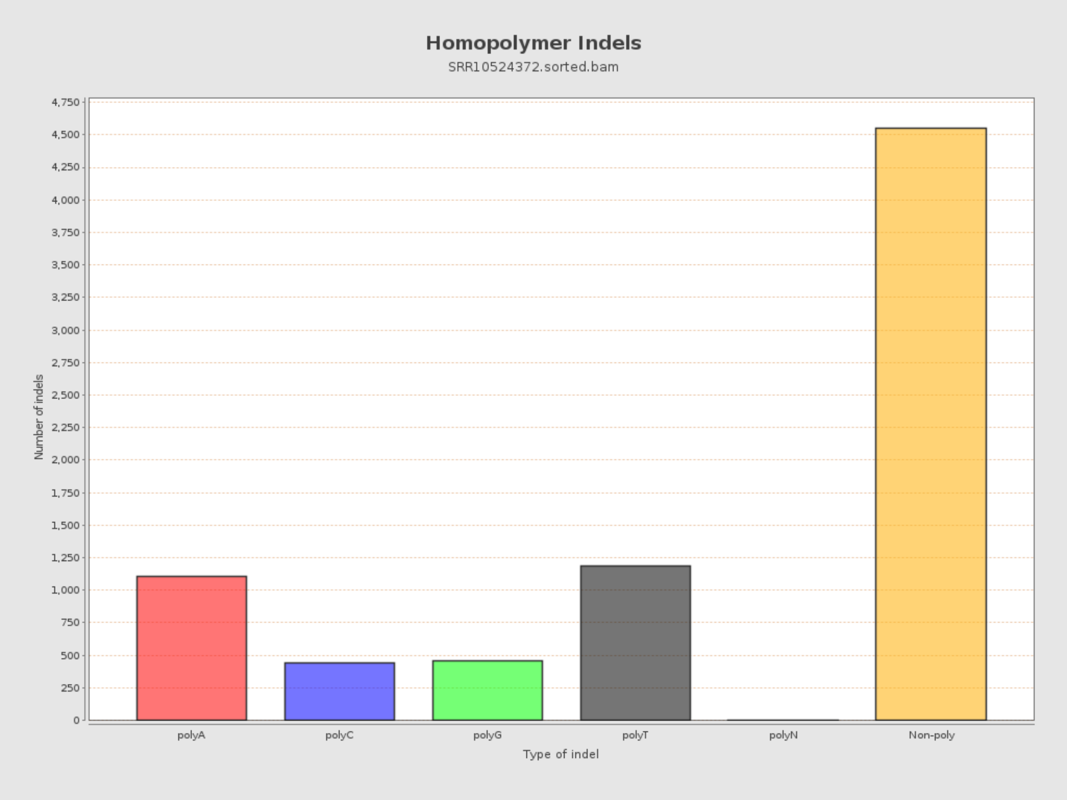
9. Results : Mapped Reads GC-content Distribution



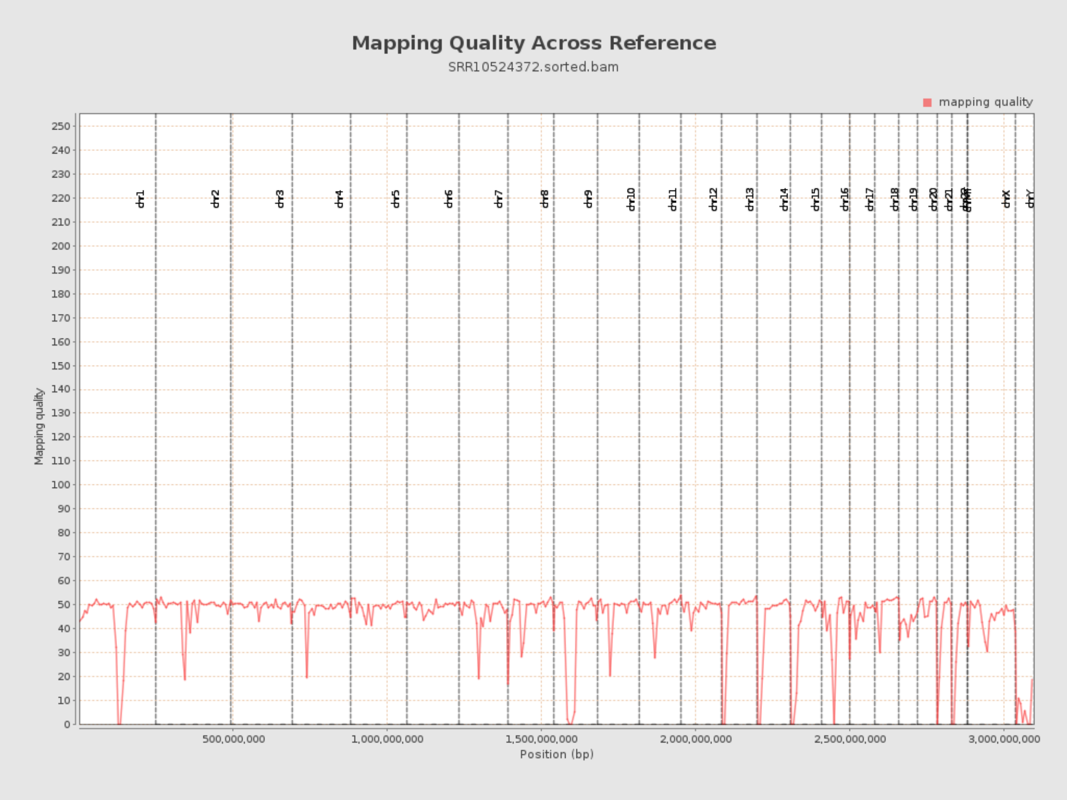
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram