Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:18:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524382.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_SRR10524382 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524382.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:18:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524382.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,382,101
Mapped reads	1,286,909 / 93.11%
Unmapped reads	95,192 / 6.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,166 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	47,007 / 3.4%
Duplication rate	2.75%
Clipped reads	1,288,301 / 93.21%

2.2. ACGT Content

Number/percentage of A's	19,479,277 / 25.71%
Number/percentage of C's	15,561,681 / 20.54%
Number/percentage of T's	22,817,245 / 30.12%
Number/percentage of G's	17,882,697 / 23.61%
Number/percentage of N's	10,222 / 0.01%
GC Percentage	44.15%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.253

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

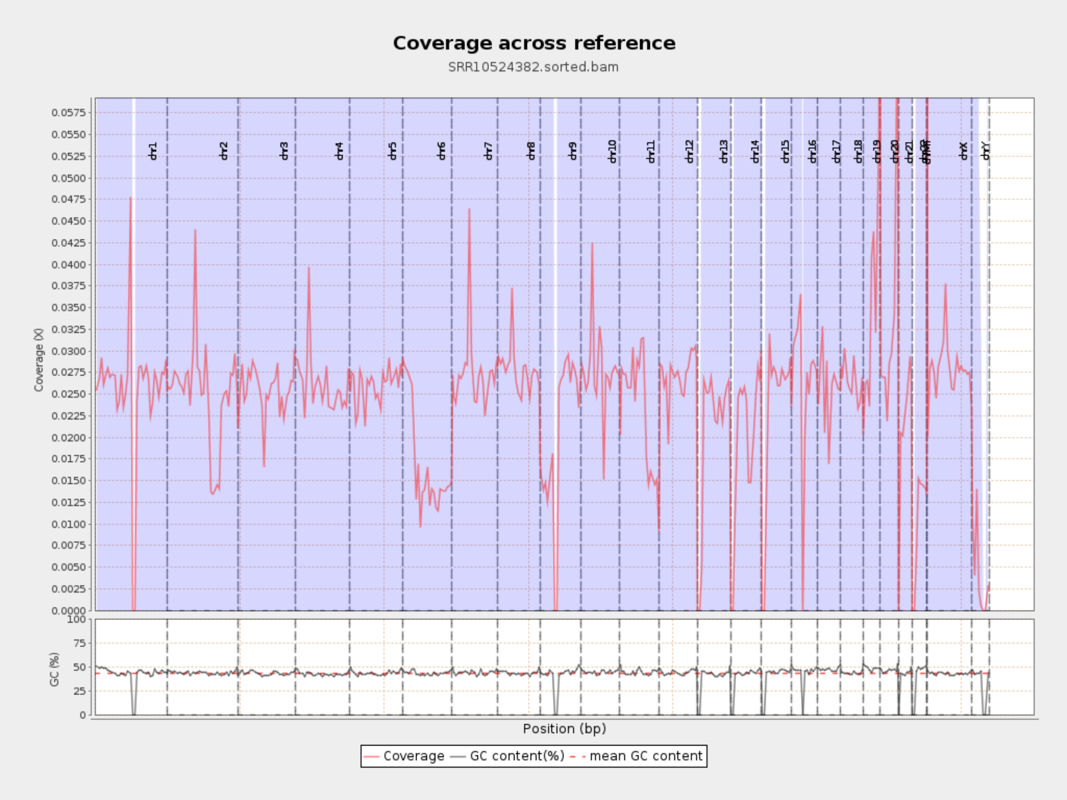
General error rate	0.5%
Mismatches	366,669
Insertions	5,686
Mapped reads with at least one insertion	0.44%
Deletions	14,049
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.81%

2.6. Chromosome stats

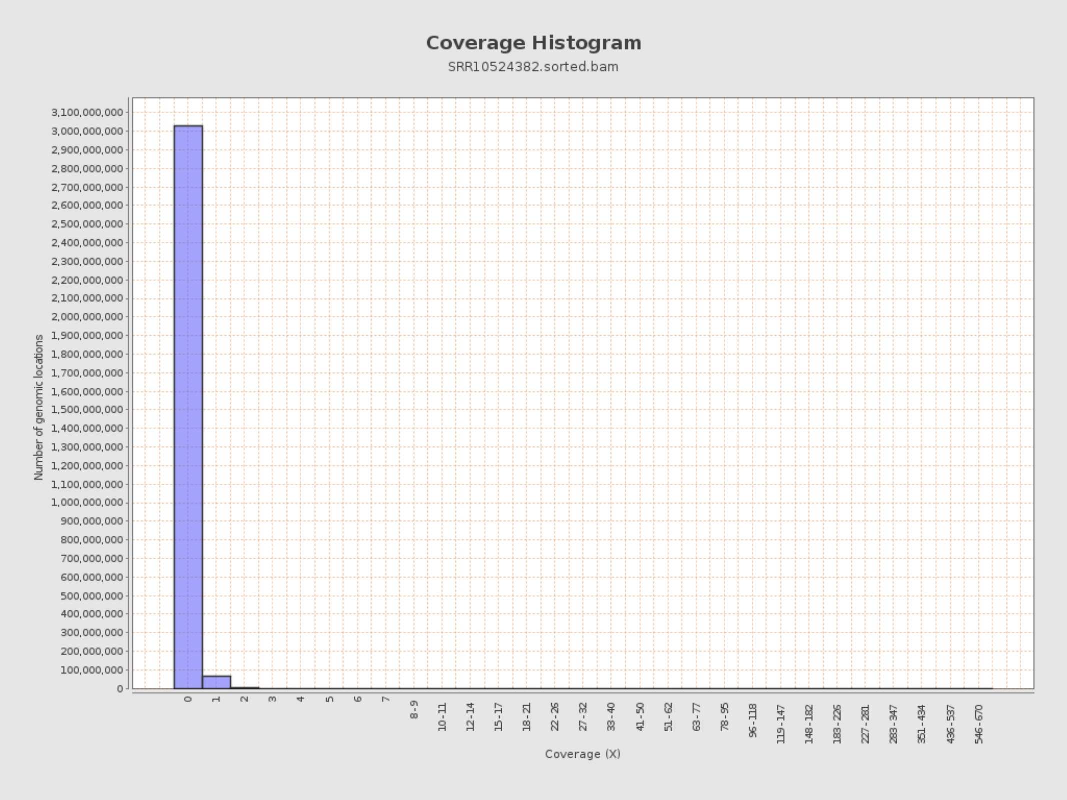
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6341234	0.0254	0.5164
chr2	243199373	6074405	0.025	0.2646
chr3	198022430	5039232	0.0254	0.1708
chr4	191154276	5009767	0.0262	0.1925
chr5	180915260	4717708	0.0261	0.1731
chr6	171115067	2889391	0.0169	0.1498
chr7	159138663	4382835	0.0275	0.3542

chr8	146364022	4091440	0.028	0.2409
chr9	141213431	2837547	0.0201	0.1942
chr10	135534747	3763061	0.0278	0.2316
chr11	135006516	3175487	0.0235	0.2039
chr12	133851895	3646260	0.0272	0.1818
chr13	115169878	2370656	0.0206	0.1539
chr14	107349540	2091671	0.0195	0.1546
chr15	102531392	2320143	0.0226	0.1608
chr16	90354753	2363377	0.0262	0.1824
chr17	81195210	2092121	0.0258	0.1872
chr18	78077248	2069956	0.0265	0.3167
chr19	59128983	2179660	0.0369	0.3756
chr20	63025520	2147827	0.0341	0.2027
chr21	48129895	1044552	0.0217	0.1776
chr22	51304566	526472	0.0103	0.1083
chrMT	16571	3178	0.1918	0.4521
chrX	155270560	4357791	0.0281	0.1955
chrY	59373566	237407	0.004	0.1181

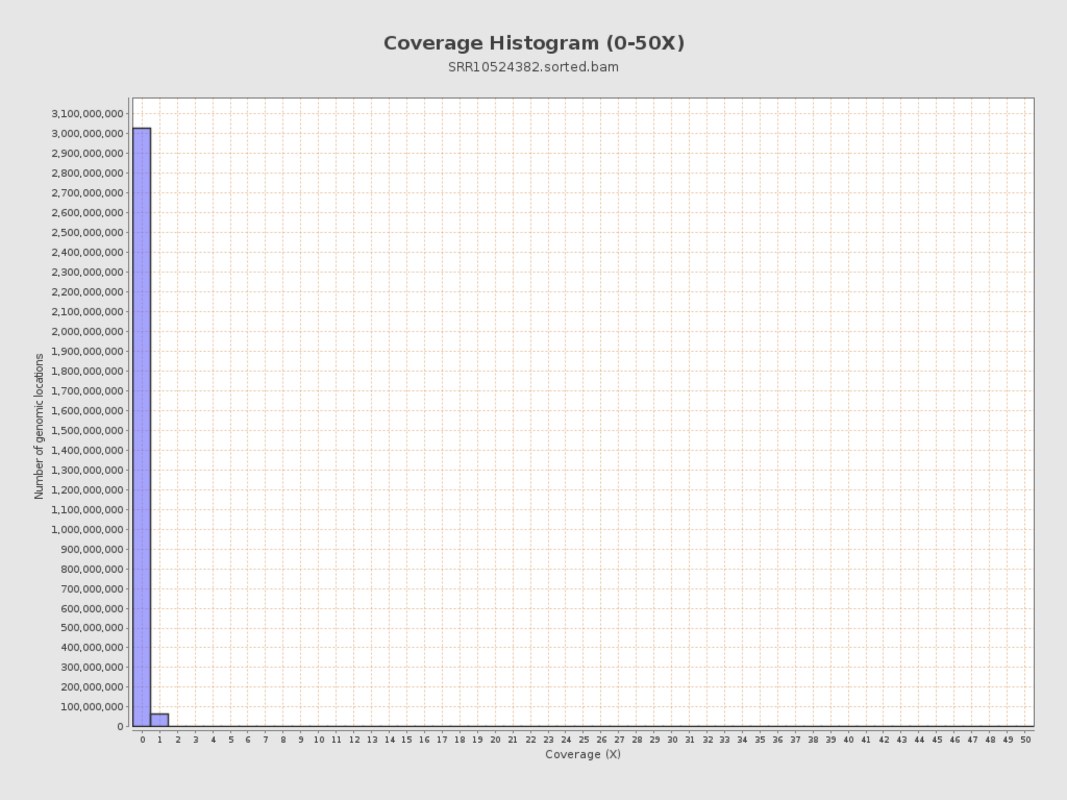
3. Results : Coverage across reference



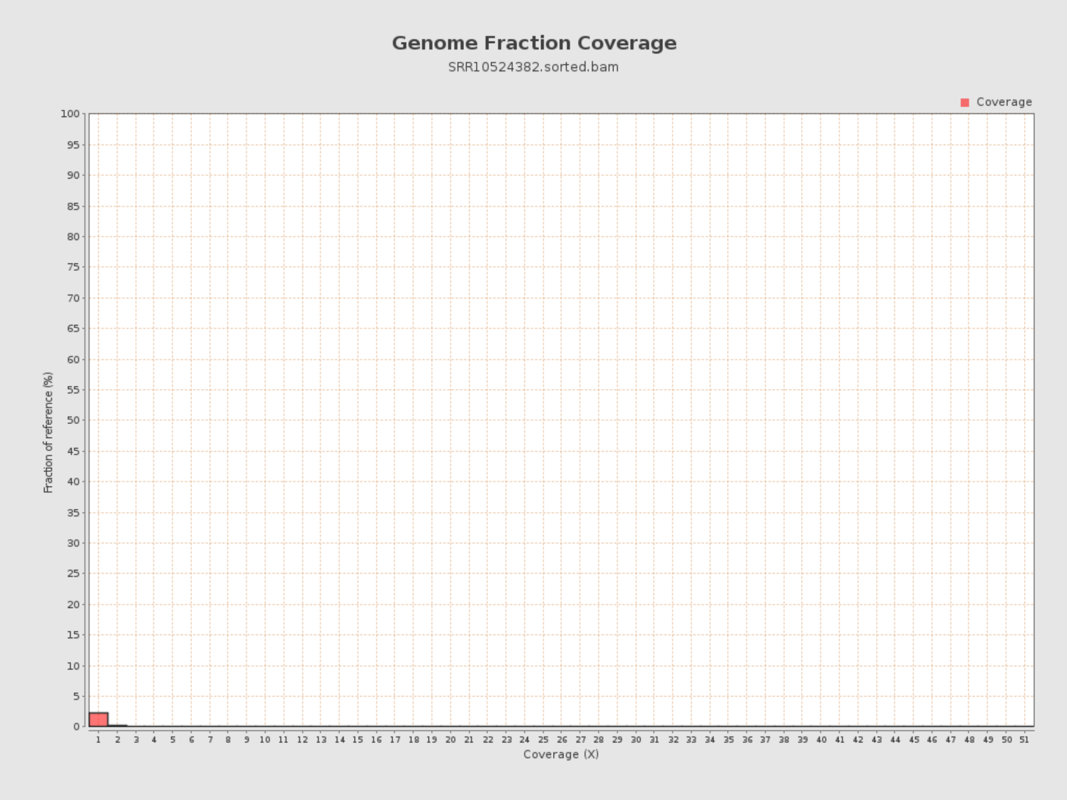
4. Results : Coverage Histogram



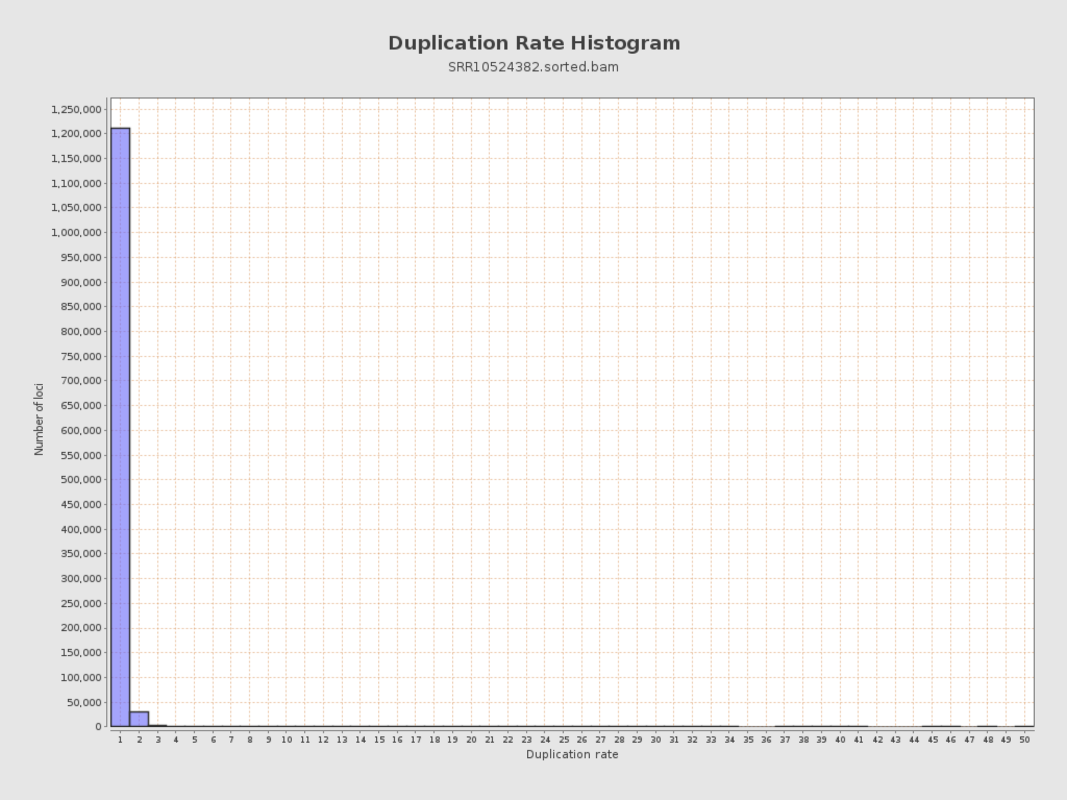
5. Results : Coverage Histogram (0-50X)



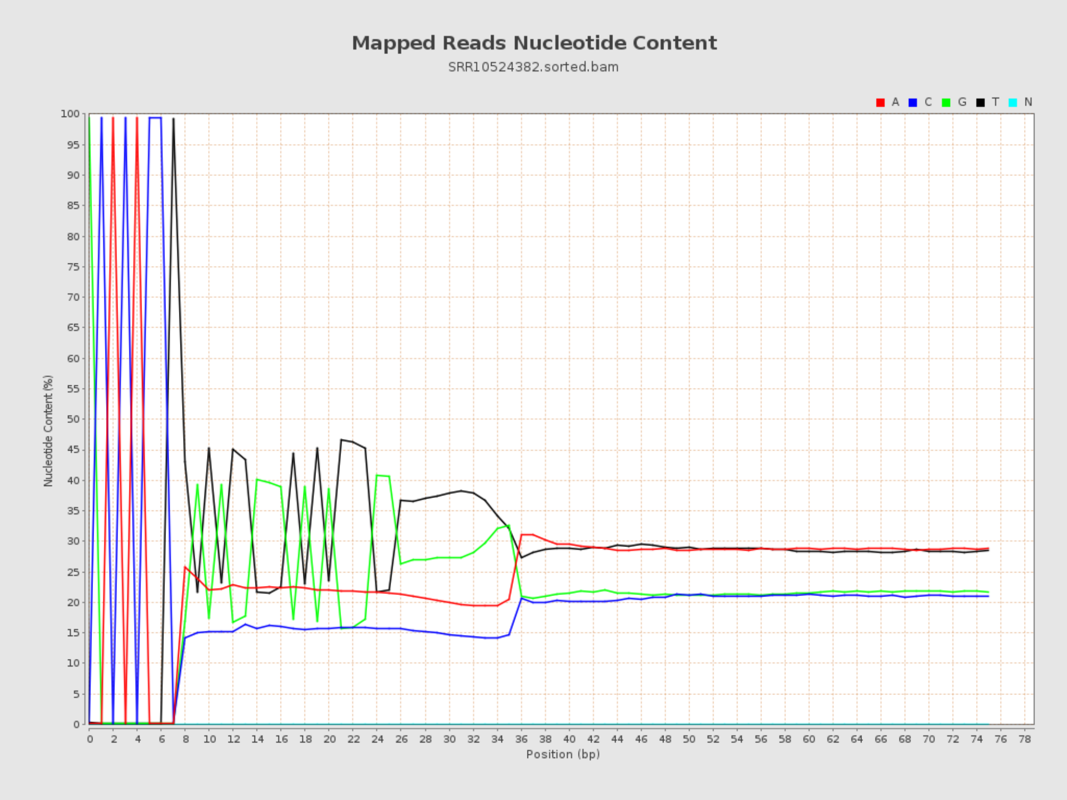
6. Results : Genome Fraction Coverage



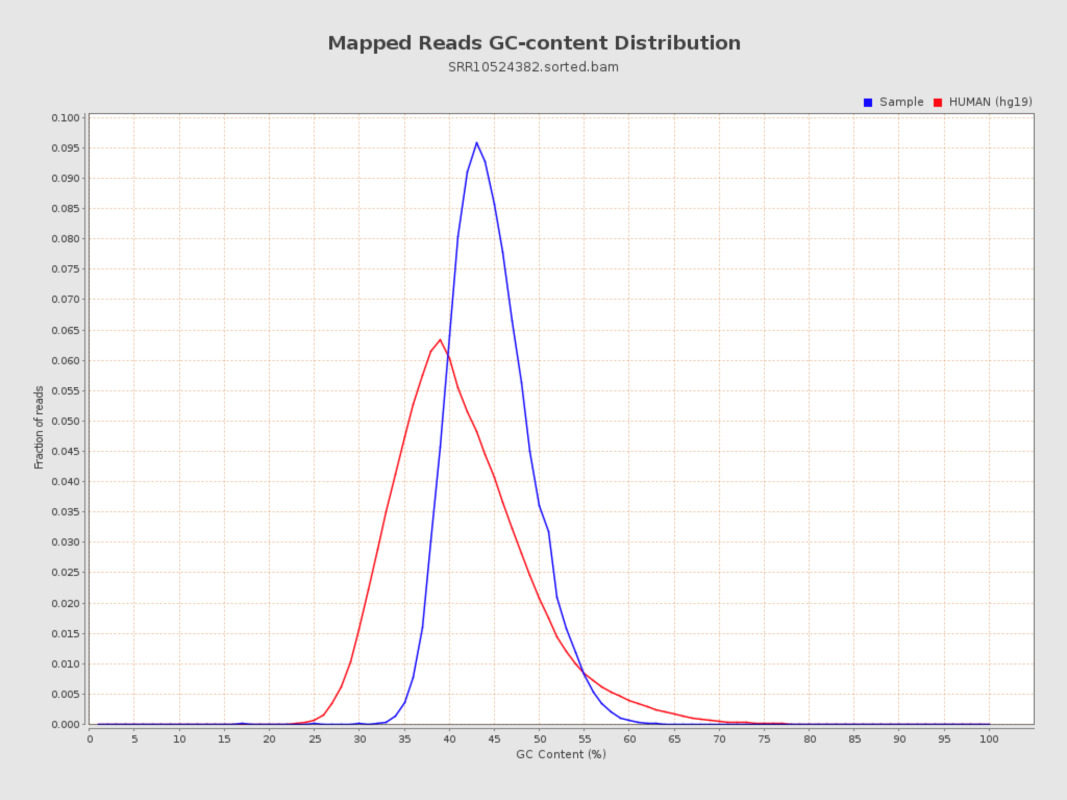
7. Results : Duplication Rate Histogram



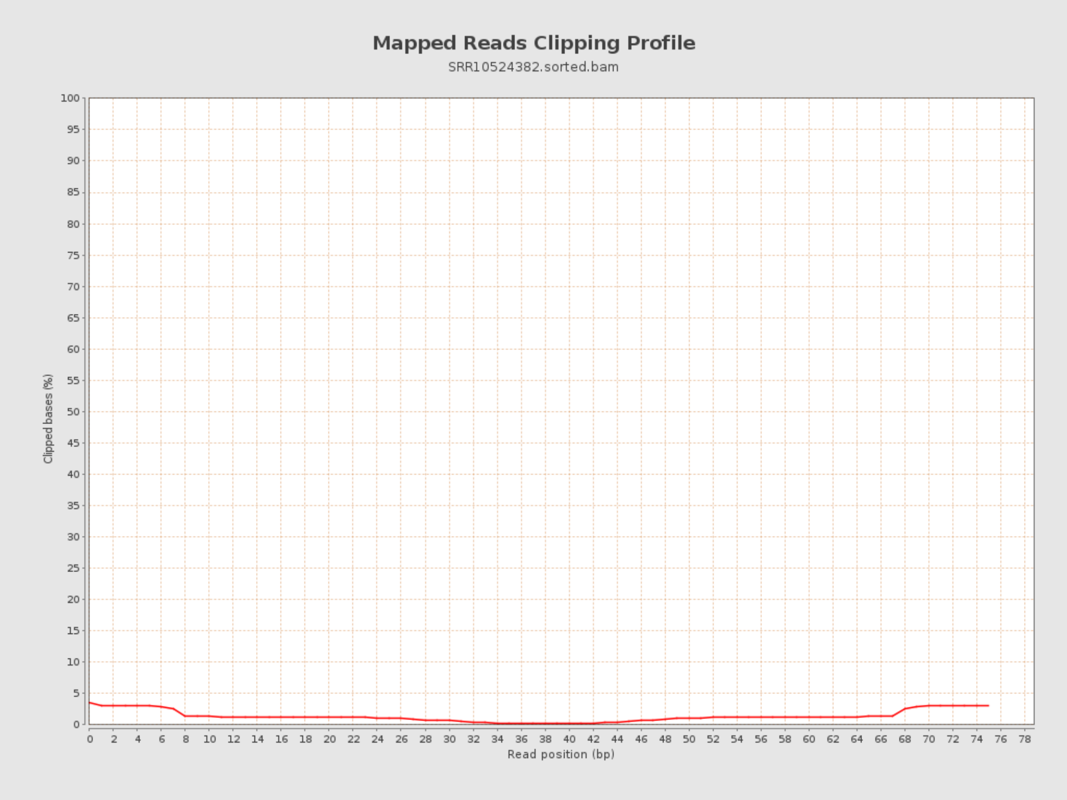
8. Results : Mapped Reads Nucleotide Content



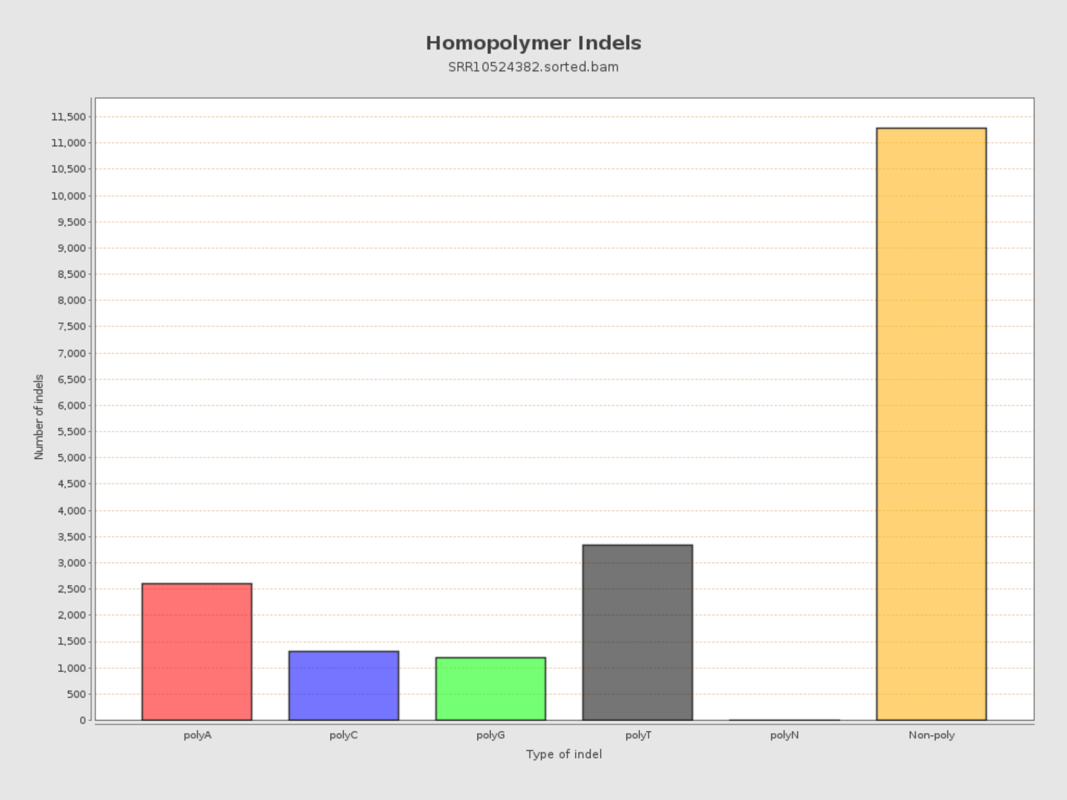
9. Results : Mapped Reads GC-content Distribution



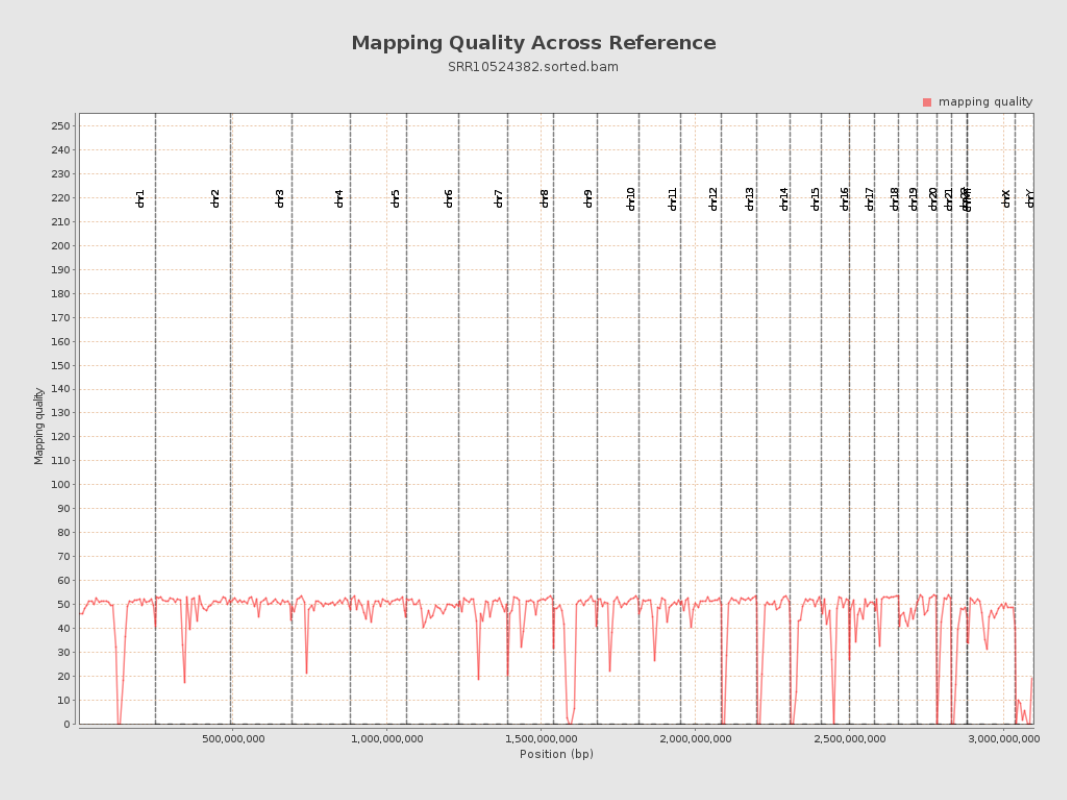
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram