Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:50:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524368.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_SRR10524368 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524368.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:50:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524368.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,515,320
Mapped reads	2,319,912 / 92.23%
Unmapped reads	195,408 / 7.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,541 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	203,236 / 8.08%
Duplication rate	6.47%
Clipped reads	2,328,412 / 92.57%

2.2. ACGT Content

Number/percentage of A's	33,411,201 / 24.46%
Number/percentage of C's	27,474,926 / 20.12%
Number/percentage of T's	42,016,961 / 30.76%
Number/percentage of G's	33,652,636 / 24.64%
Number/percentage of N's	19,513 / 0.01%
GC Percentage	44.76%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.419

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

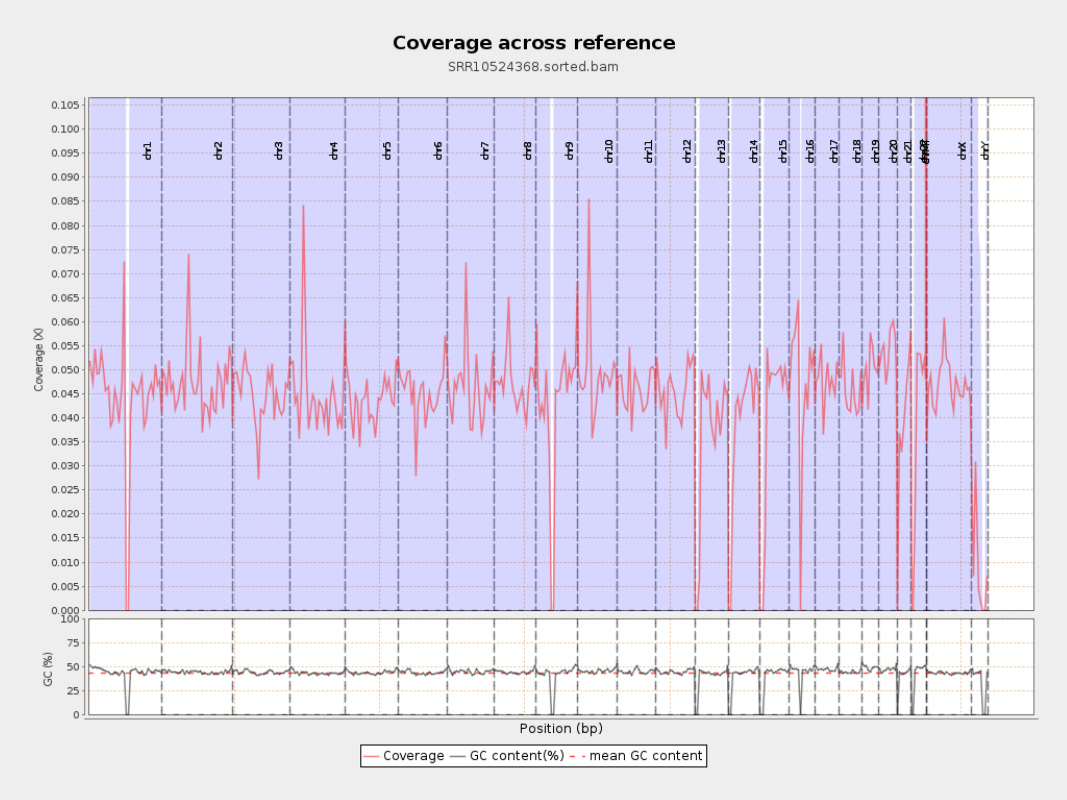
General error rate	0.52%
Mismatches	696,063
Insertions	8,535
Mapped reads with at least one insertion	0.37%
Deletions	24,389
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.98%

2.6. Chromosome stats

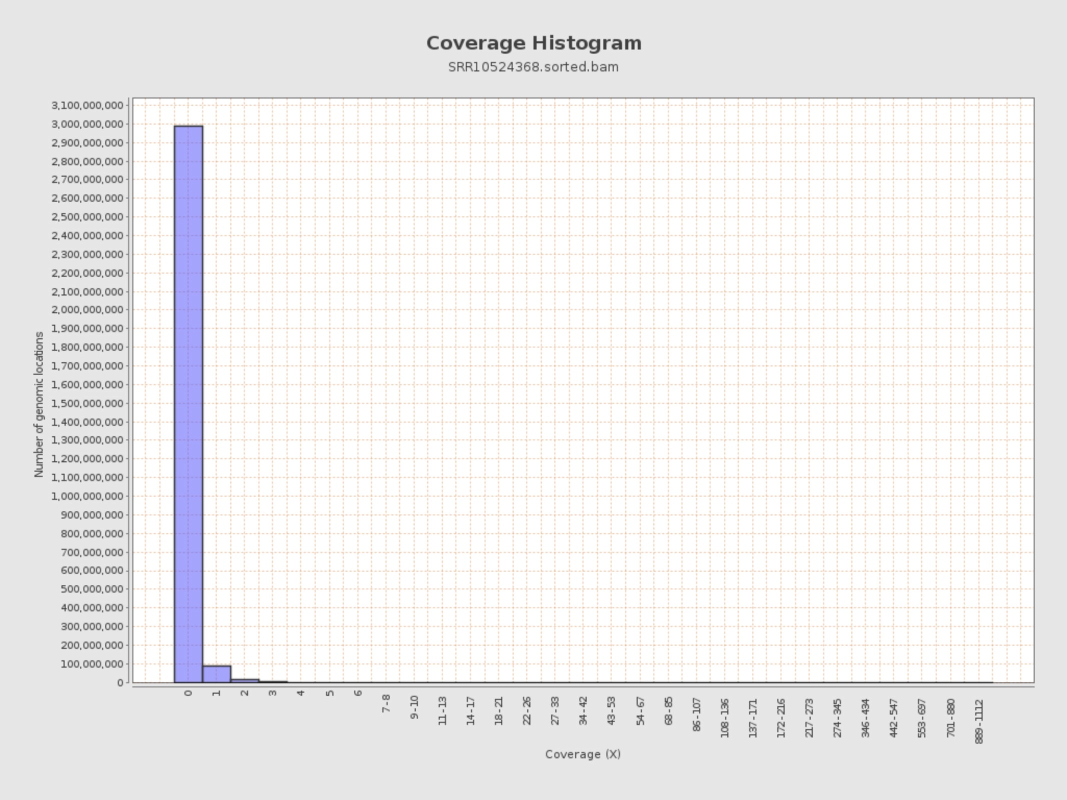
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10967259	0.044	0.7968
chr2	243199373	11562123	0.0475	0.5586
chr3	198022430	8874572	0.0448	0.2577
chr4	191154276	8529538	0.0446	0.3283
chr5	180915260	7910162	0.0437	0.2568
chr6	171115067	7763242	0.0454	0.2765
chr7	159138663	7357142	0.0462	0.5069

chr8	146364022	6925659	0.0473	0.4012
chr9	141213431	5815868	0.0412	0.3405
chr10	135534747	6632777	0.0489	0.4316
chr11	135006516	6202789	0.0459	0.3509
chr12	133851895	6122591	0.0457	0.2684
chr13	115169878	4106074	0.0357	0.2319
chr14	107349540	4116389	0.0383	0.253
chr15	102531392	4052069	0.0395	0.2415
chr16	90354753	4284320	0.0474	0.2979
chr17	81195210	3871433	0.0477	0.2916
chr18	78077248	3593329	0.046	0.6942
chr19	59128983	2969372	0.0502	0.5244
chr20	63025520	3401556	0.054	0.2981
chr21	48129895	1882976	0.0391	0.2987
chr22	51304566	1865830	0.0364	0.2398
chrMT	16571	28547	1.7227	2.0053
chrX	155270560	7283397	0.0469	0.2975
chrY	59373566	494761	0.0083	0.2483

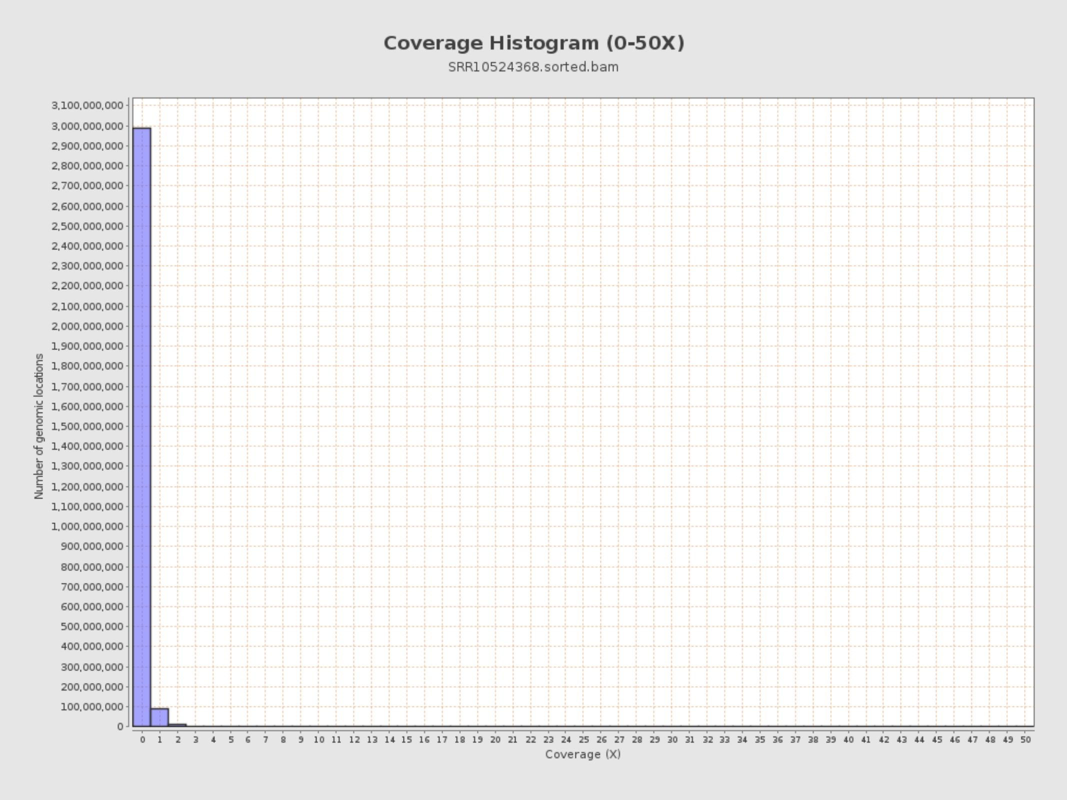
3. Results : Coverage across reference



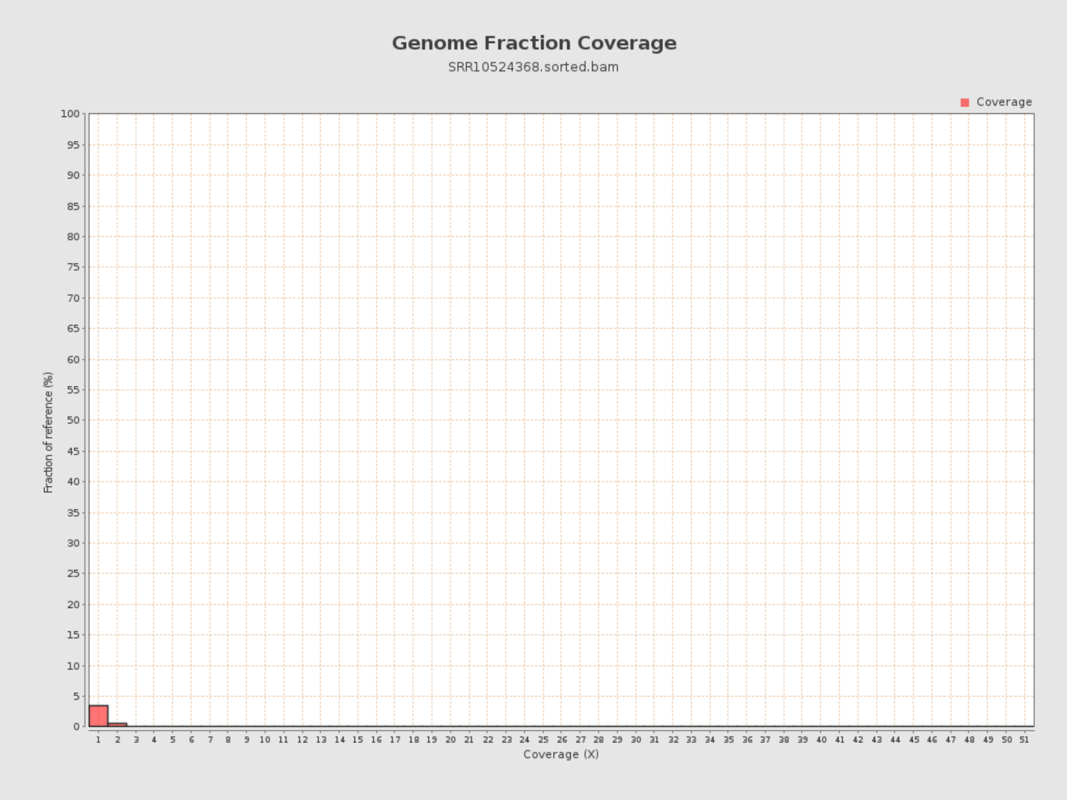
4. Results : Coverage Histogram



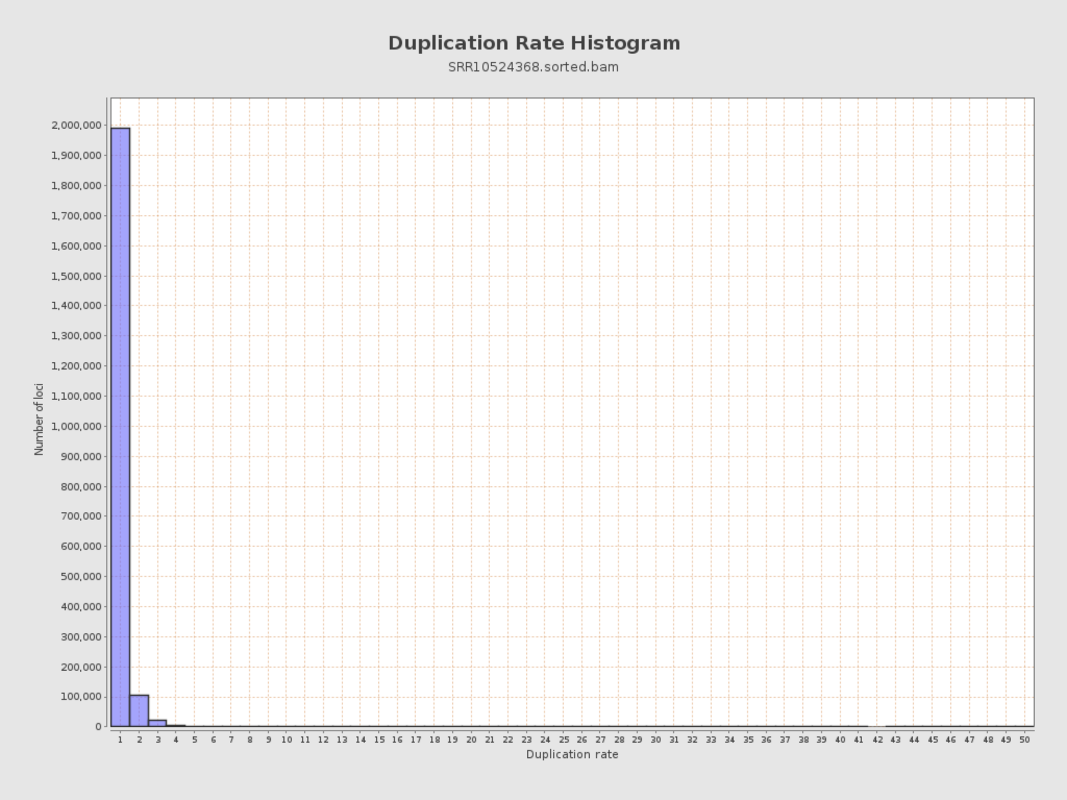
5. Results : Coverage Histogram (0-50X)



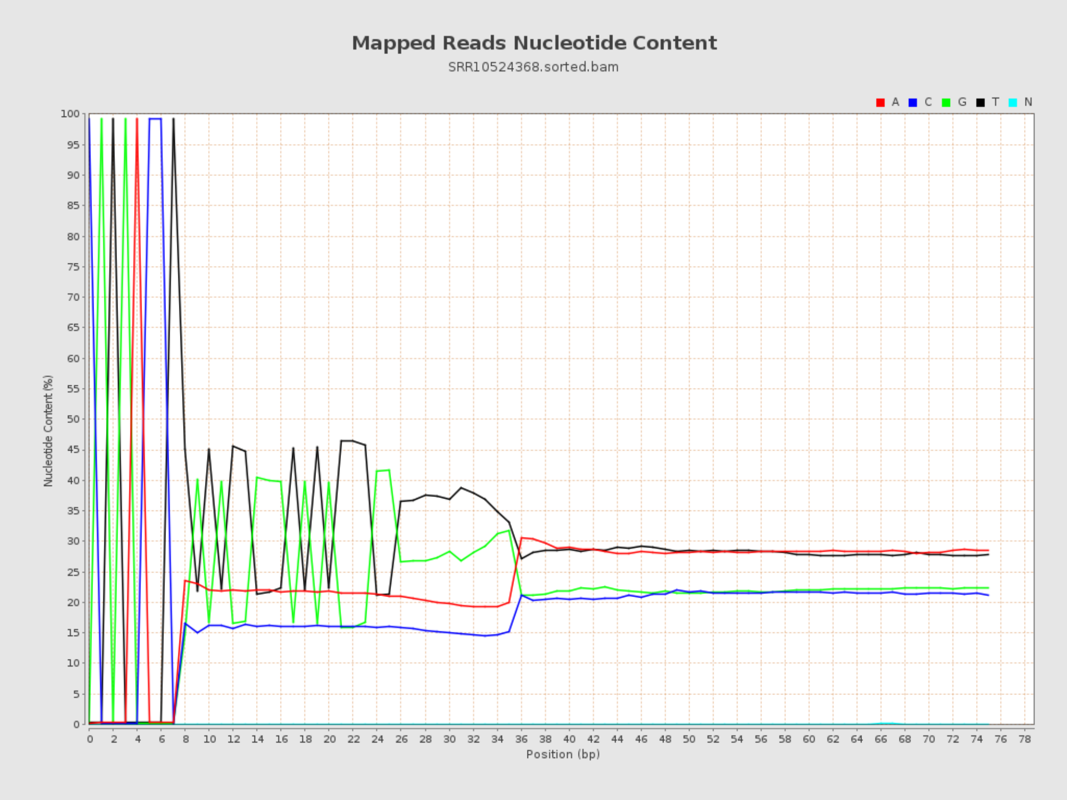
6. Results : Genome Fraction Coverage



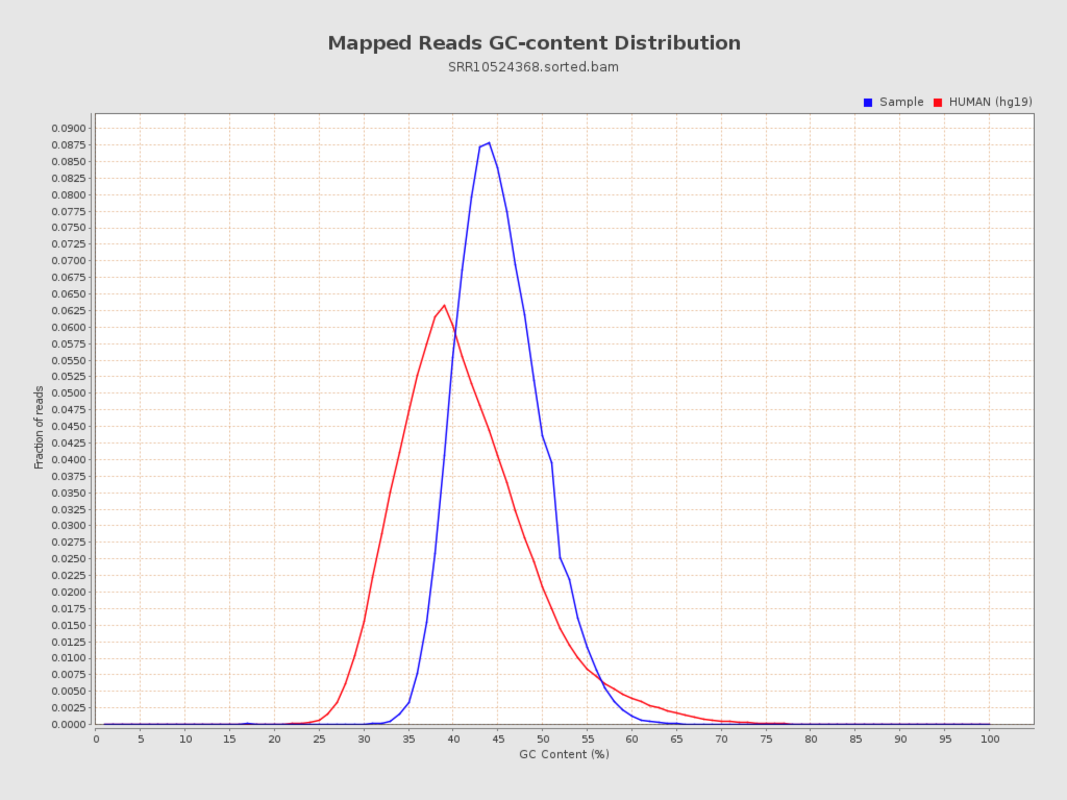
7. Results : Duplication Rate Histogram



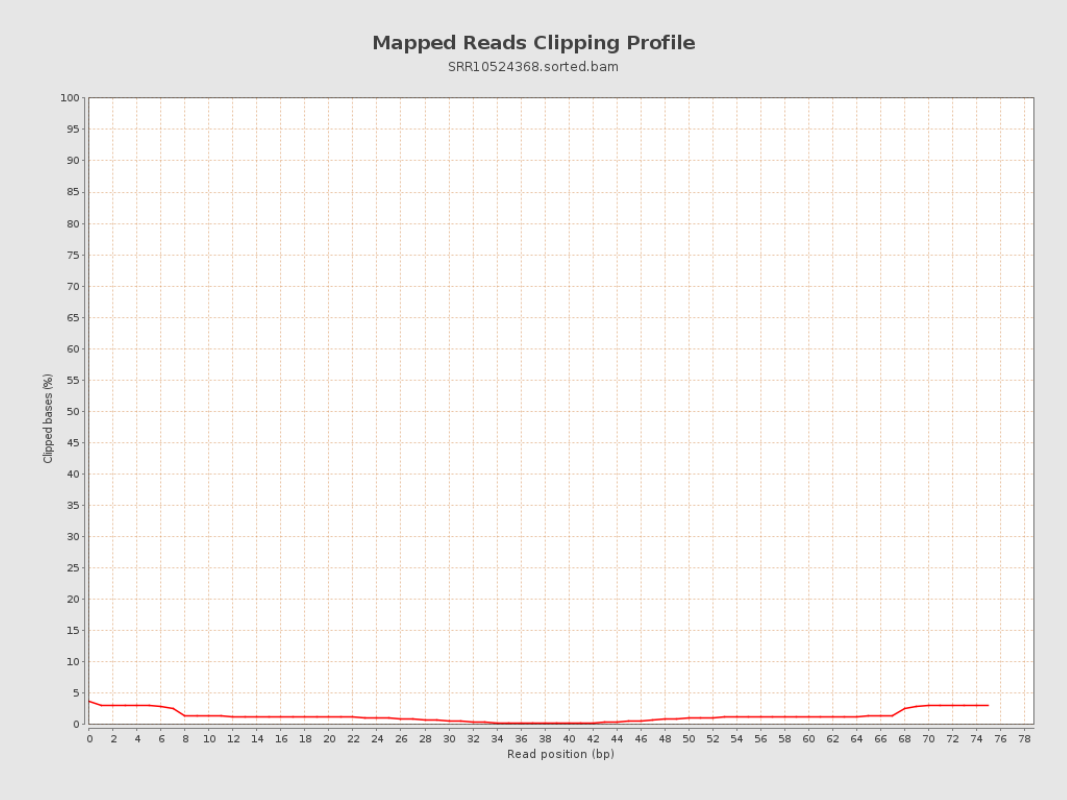
8. Results : Mapped Reads Nucleotide Content



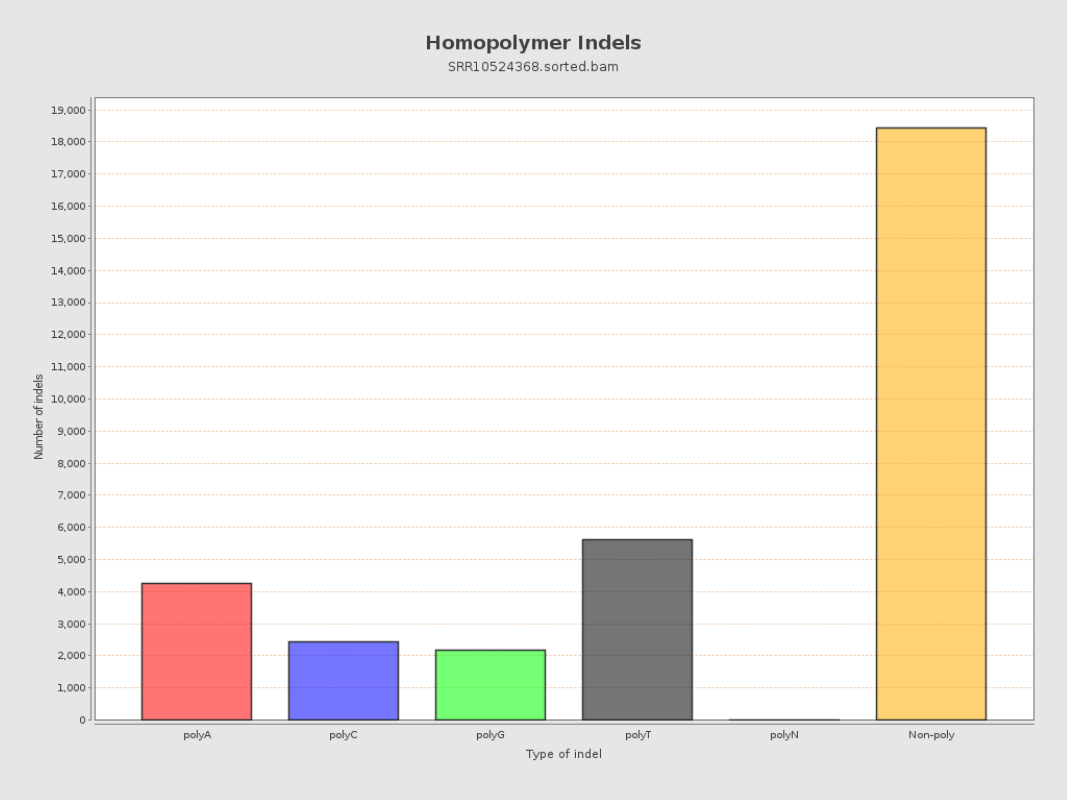
9. Results : Mapped Reads GC-content Distribution



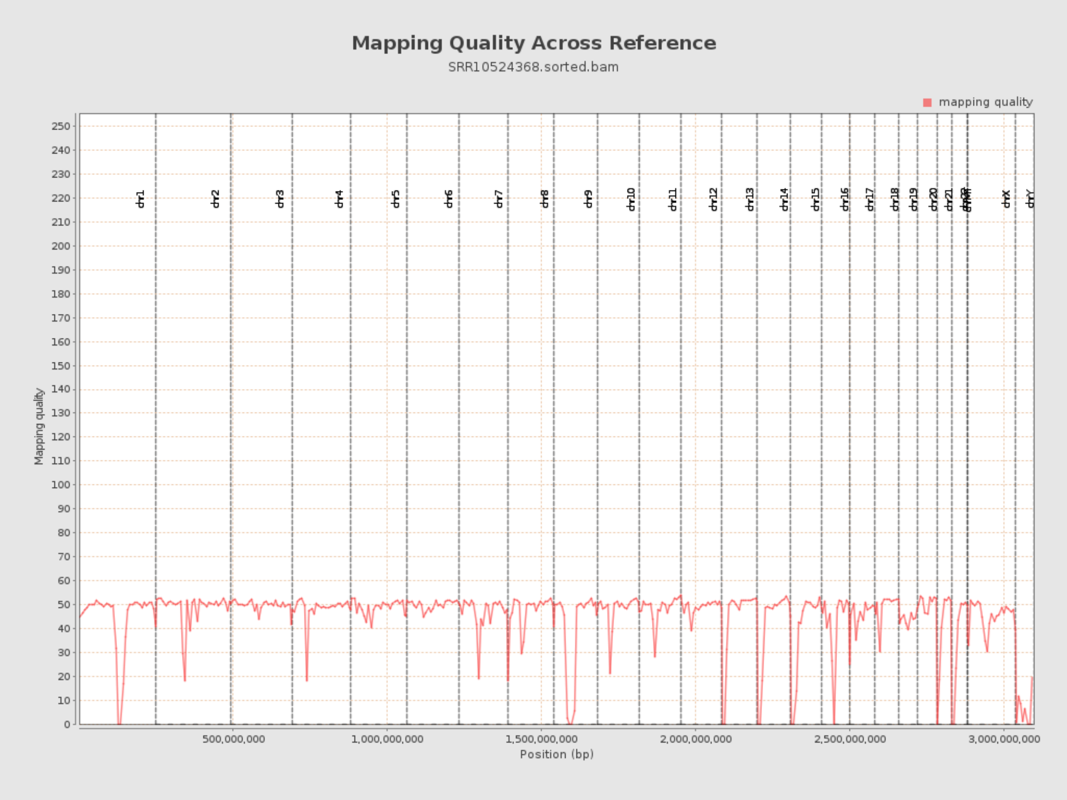
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram