Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:53:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524369.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_SRR10524369 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524369.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:53:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524369.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,803,777
Mapped reads	2,576,694 / 91.9%
Unmapped reads	227,083 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,115 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	207,771 / 7.41%
Duplication rate	5.92%
Clipped reads	2,581,680 / 92.08%

2.2. ACGT Content

Number/percentage of A's	37,411,604 / 24.62%
Number/percentage of C's	30,419,107 / 20.02%
Number/percentage of T's	46,911,834 / 30.87%
Number/percentage of G's	37,190,625 / 24.47%
Number/percentage of N's	21,390 / 0.01%
GC Percentage	44.49%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.4737

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

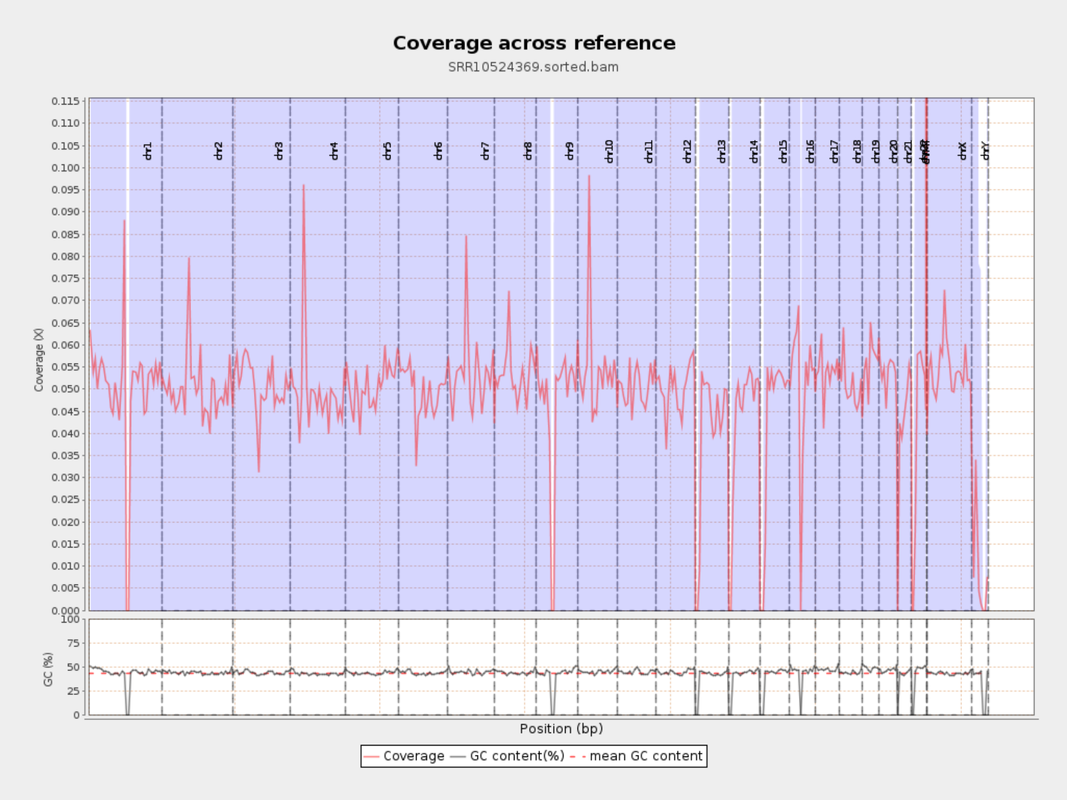
General error rate	0.54%
Mismatches	787,488
Insertions	12,542
Mapped reads with at least one insertion	0.48%
Deletions	27,546
Mapped reads with at least one deletion	1.06%
Homopolymer indels	39.78%

2.6. Chromosome stats

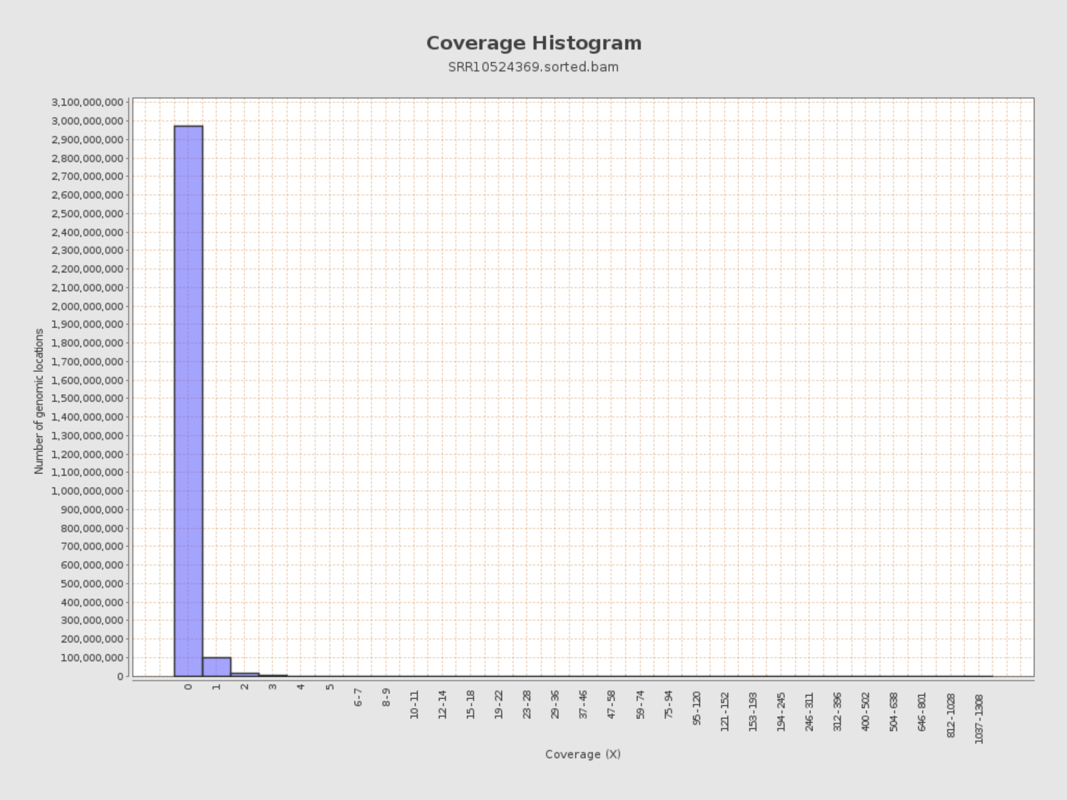
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12468172	0.05	0.93
chr2	243199373	12238434	0.0503	0.6259
chr3	198022430	10039037	0.0507	0.27
chr4	191154276	9438930	0.0494	0.3545
chr5	180915260	9162452	0.0506	0.2743
chr6	171115067	8524232	0.0498	0.3004
chr7	159138663	8530592	0.0536	0.5811

chr8	146364022	7841908	0.0536	0.4329
chr9	141213431	6449254	0.0457	0.3688
chr10	135534747	7348576	0.0542	0.4713
chr11	135006516	6820295	0.0505	0.3937
chr12	133851895	6712468	0.0501	0.277
chr13	115169878	4529037	0.0393	0.2399
chr14	107349540	4523440	0.0421	0.2689
chr15	102531392	4326953	0.0422	0.2462
chr16	90354753	4619139	0.0511	0.3035
chr17	81195210	4359886	0.0537	0.3153
chr18	78077248	3983225	0.051	0.7823
chr19	59128983	3326860	0.0563	0.6045
chr20	63025520	3358756	0.0533	0.2919
chr21	48129895	2027931	0.0421	0.3262
chr22	51304566	1977076	0.0385	0.2407
chrMT	16571	408385	24.6446	14.9753
chrX	155270560	8445528	0.0544	0.3224
chrY	59373566	537950	0.0091	0.2809

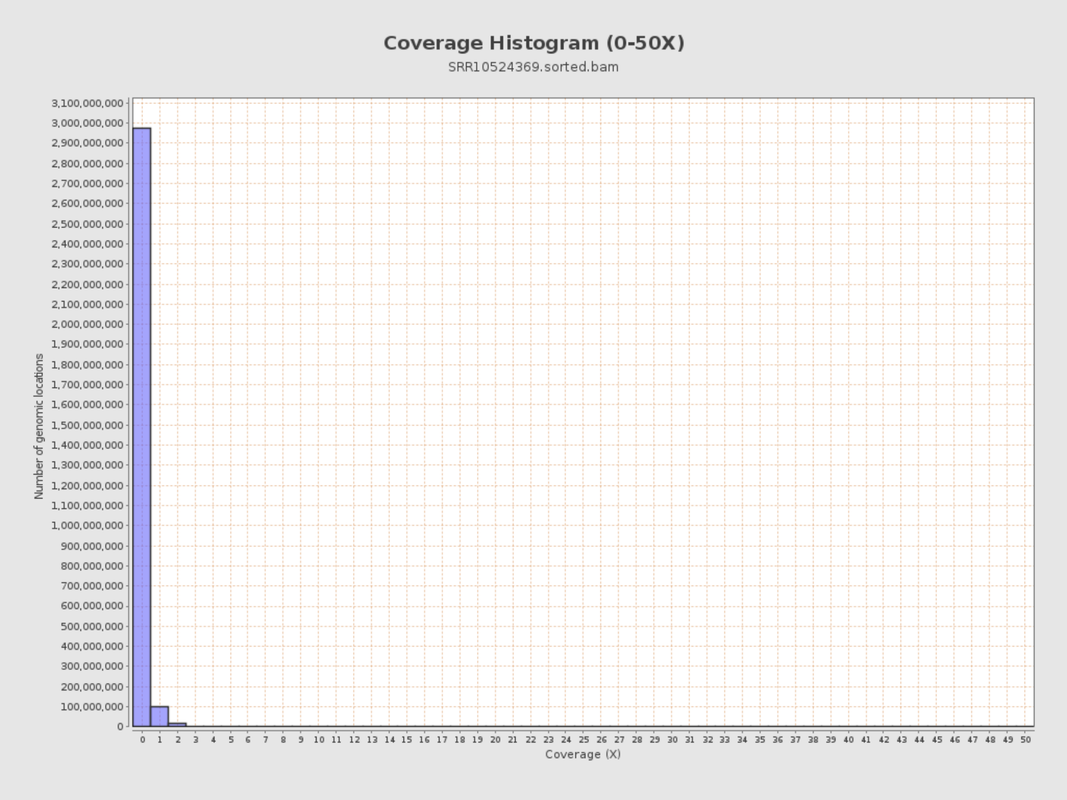
3. Results : Coverage across reference



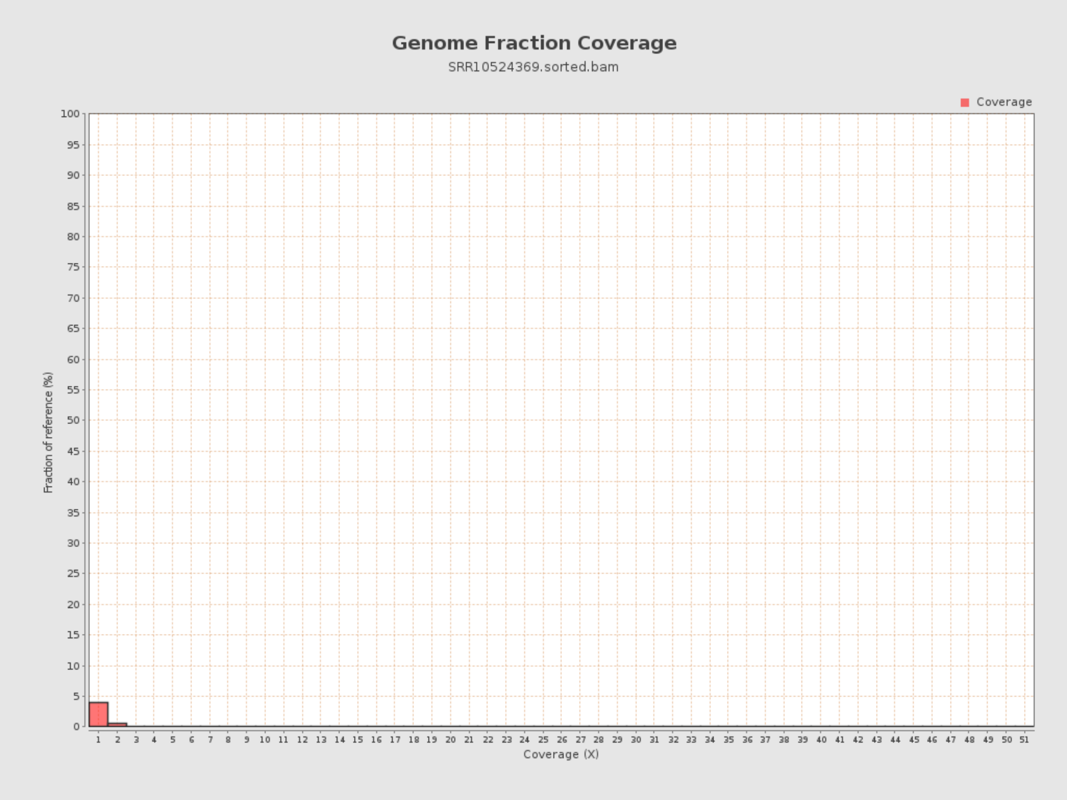
4. Results : Coverage Histogram



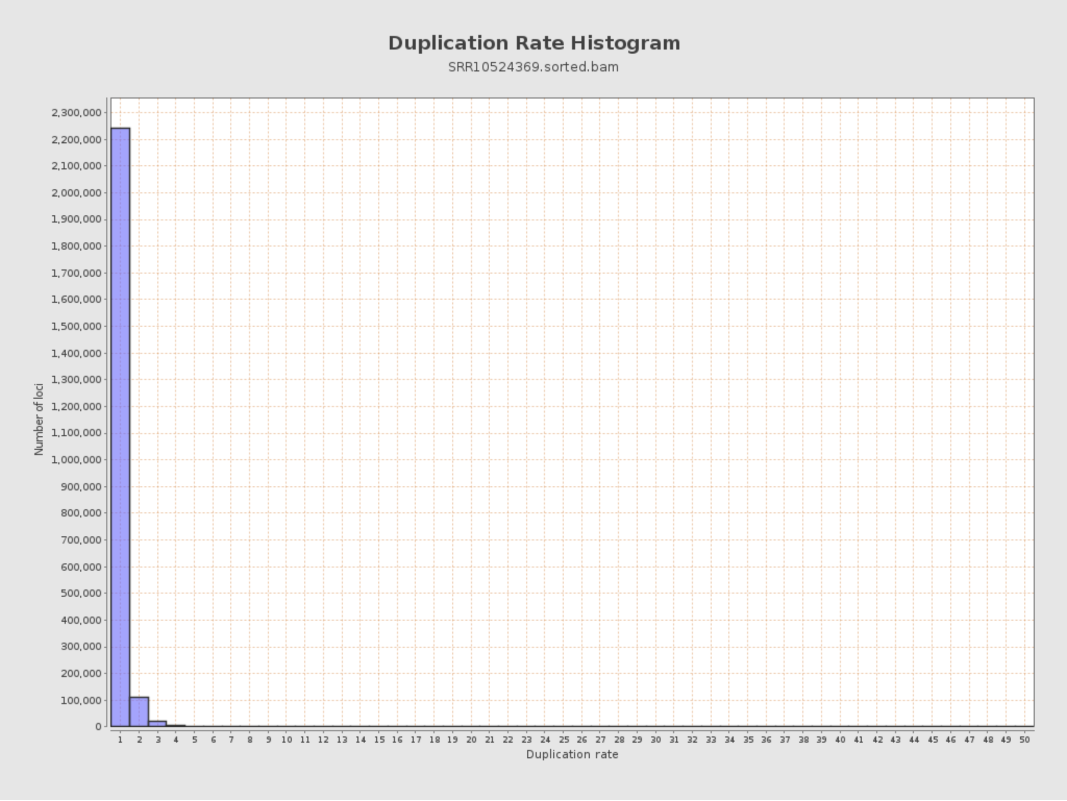
5. Results : Coverage Histogram (0-50X)



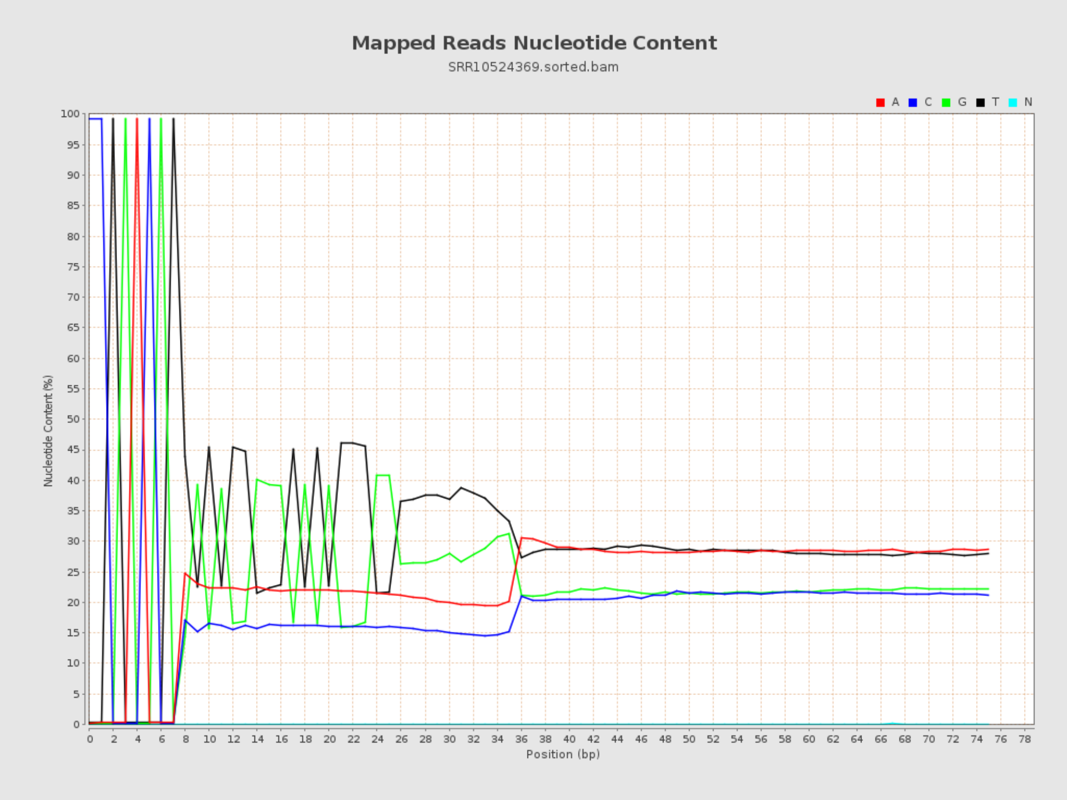
6. Results : Genome Fraction Coverage



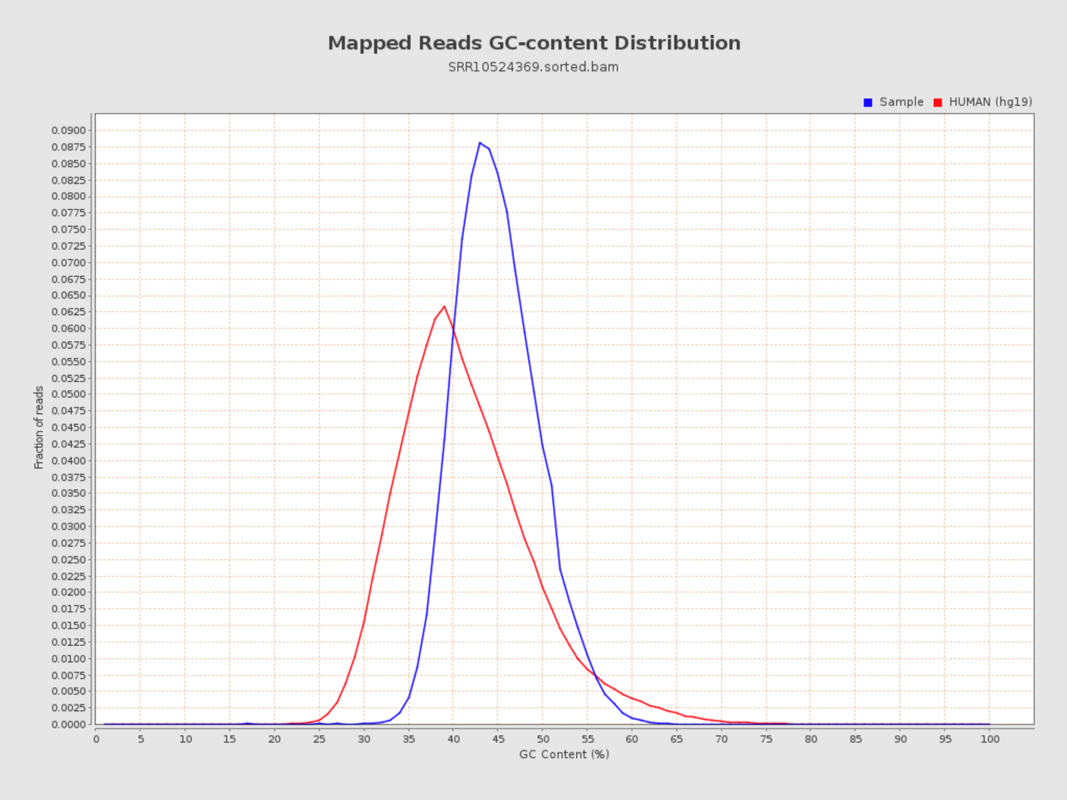
7. Results : Duplication Rate Histogram



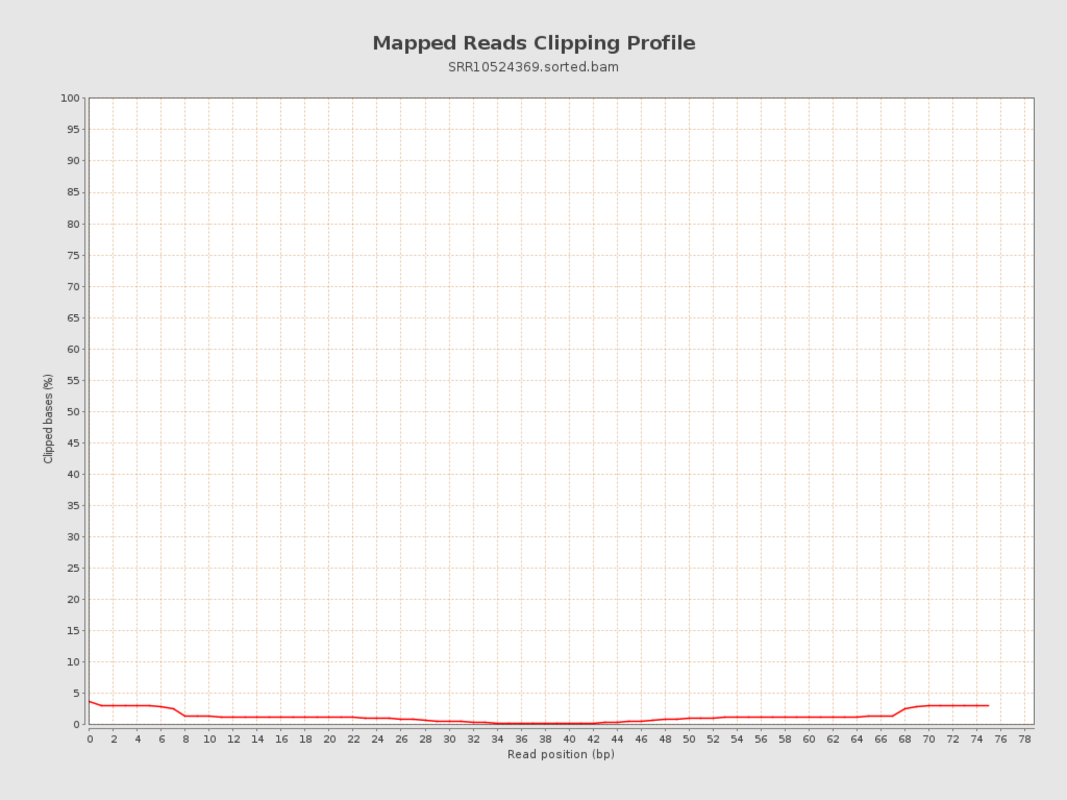
8. Results : Mapped Reads Nucleotide Content



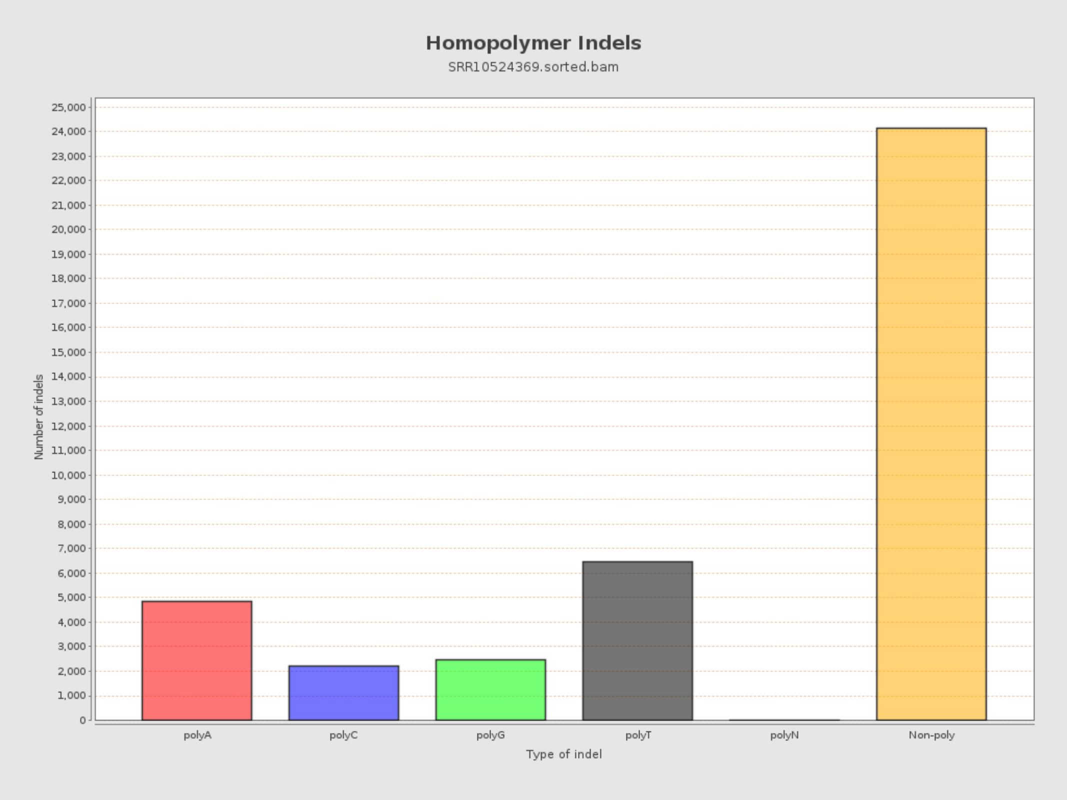
9. Results : Mapped Reads GC-content Distribution



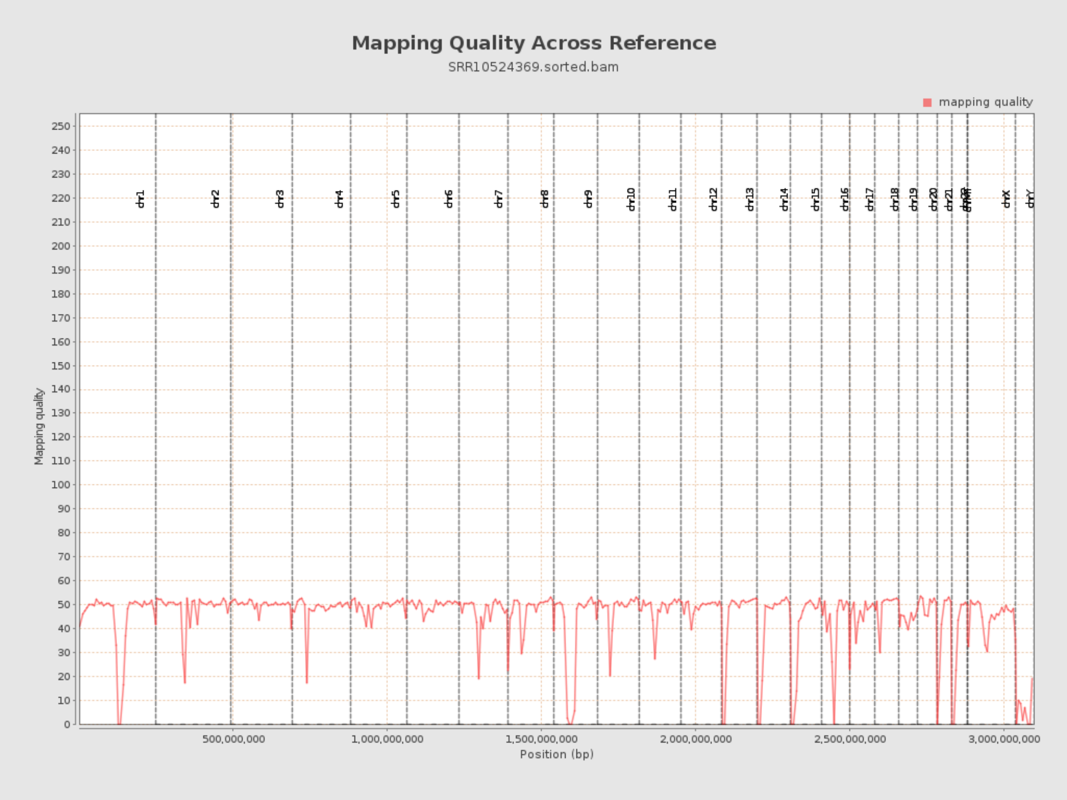
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram