Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:58:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524349.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_SRR10524349 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524349.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:58:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524349.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,890,495
Mapped reads	2,658,426 / 91.97%
Unmapped reads	232,069 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,446 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	179,020 / 6.19%
Duplication rate	4.97%
Clipped reads	2,662,089 / 92.1%

2.2. ACGT Content

Number/percentage of A's	38,667,138 / 24.96%
Number/percentage of C's	32,304,598 / 20.85%
Number/percentage of T's	46,508,240 / 30.02%
Number/percentage of G's	37,412,292 / 24.15%
Number/percentage of N's	21,067 / 0.01%
GC Percentage	45%

2.3. Coverage

Mean	0.0501

Standard Deviation	0.4544

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

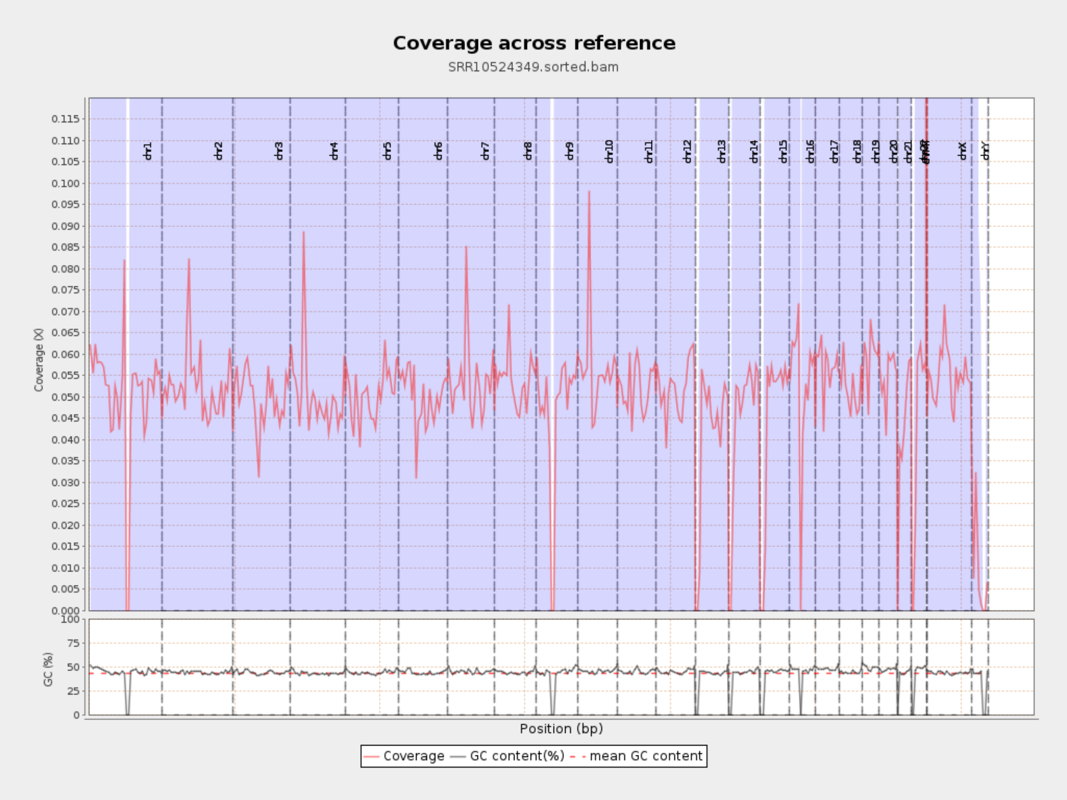
General error rate	0.53%
Mismatches	789,592
Insertions	11,639
Mapped reads with at least one insertion	0.43%
Deletions	25,871
Mapped reads with at least one deletion	0.97%
Homopolymer indels	41.24%

2.6. Chromosome stats

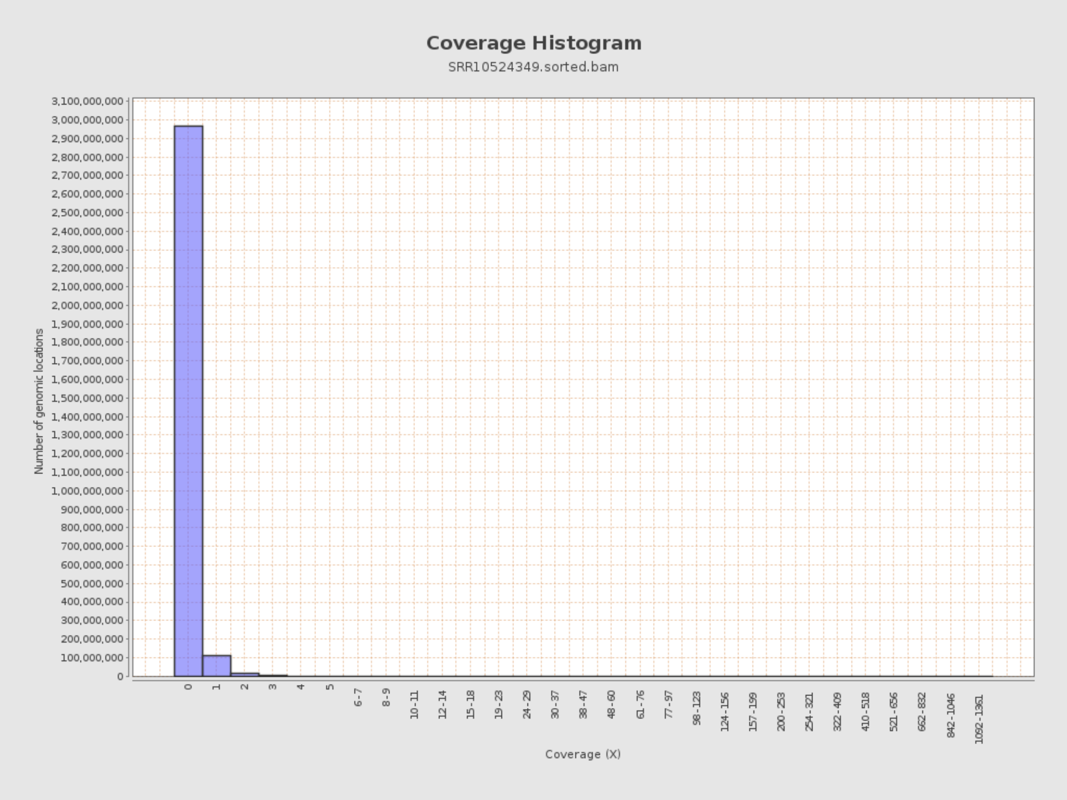
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12557572	0.0504	0.8618
chr2	243199373	12839968	0.0528	0.64
chr3	198022430	9824490	0.0496	0.2642
chr4	191154276	9623044	0.0503	0.3242
chr5	180915260	9146066	0.0506	0.2664
chr6	171115067	8549137	0.05	0.2915
chr7	159138663	8567967	0.0538	0.5882

chr8	146364022	7907699	0.054	0.37
chr9	141213431	6421377	0.0455	0.3617
chr10	135534747	7665903	0.0566	0.4438
chr11	135006516	7035594	0.0521	0.3989
chr12	133851895	6964404	0.052	0.2746
chr13	115169878	4651427	0.0404	0.2352
chr14	107349540	4715780	0.0439	0.2654
chr15	102531392	4517073	0.0441	0.2504
chr16	90354753	4790491	0.053	0.3005
chr17	81195210	4629651	0.057	0.3058
chr18	78077248	4056315	0.052	0.7528
chr19	59128983	3526557	0.0596	0.5769
chr20	63025520	3445451	0.0547	0.2891
chr21	48129895	2039210	0.0424	0.2951
chr22	51304566	2082397	0.0406	0.2406
chrMT	16571	335076	20.2206	11.7231
chrX	155270560	8536862	0.055	0.3241
chrY	59373566	525700	0.0089	0.2392

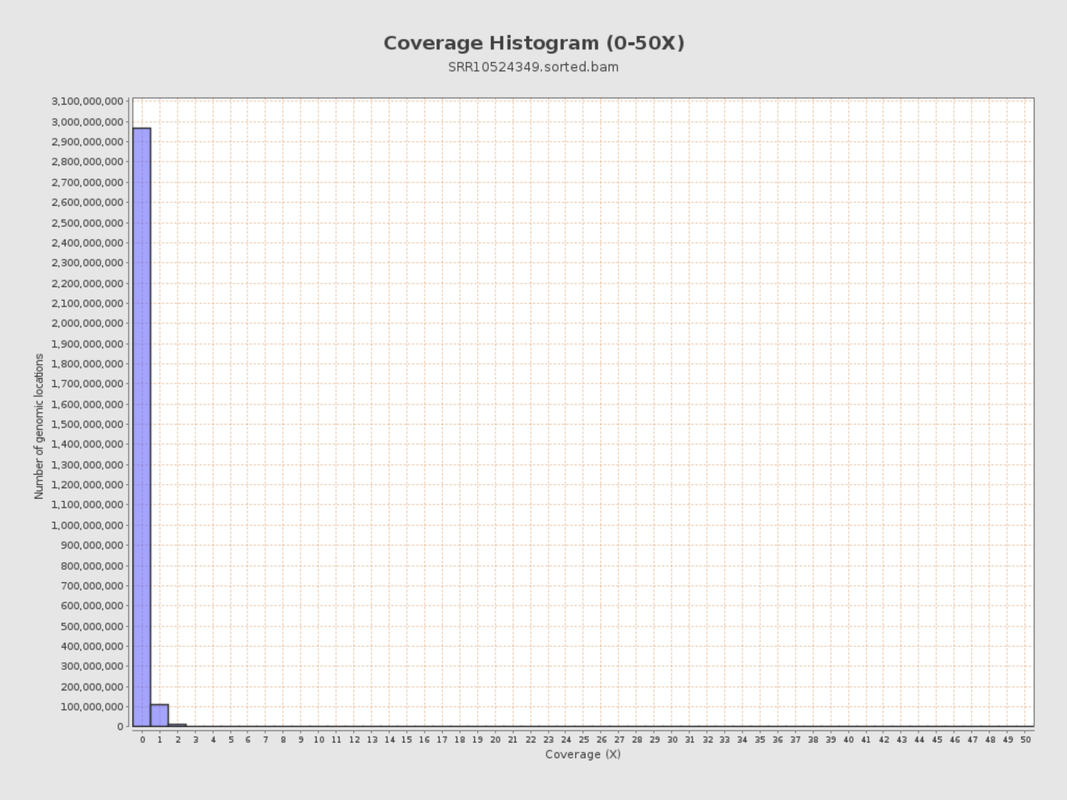
3. Results : Coverage across reference



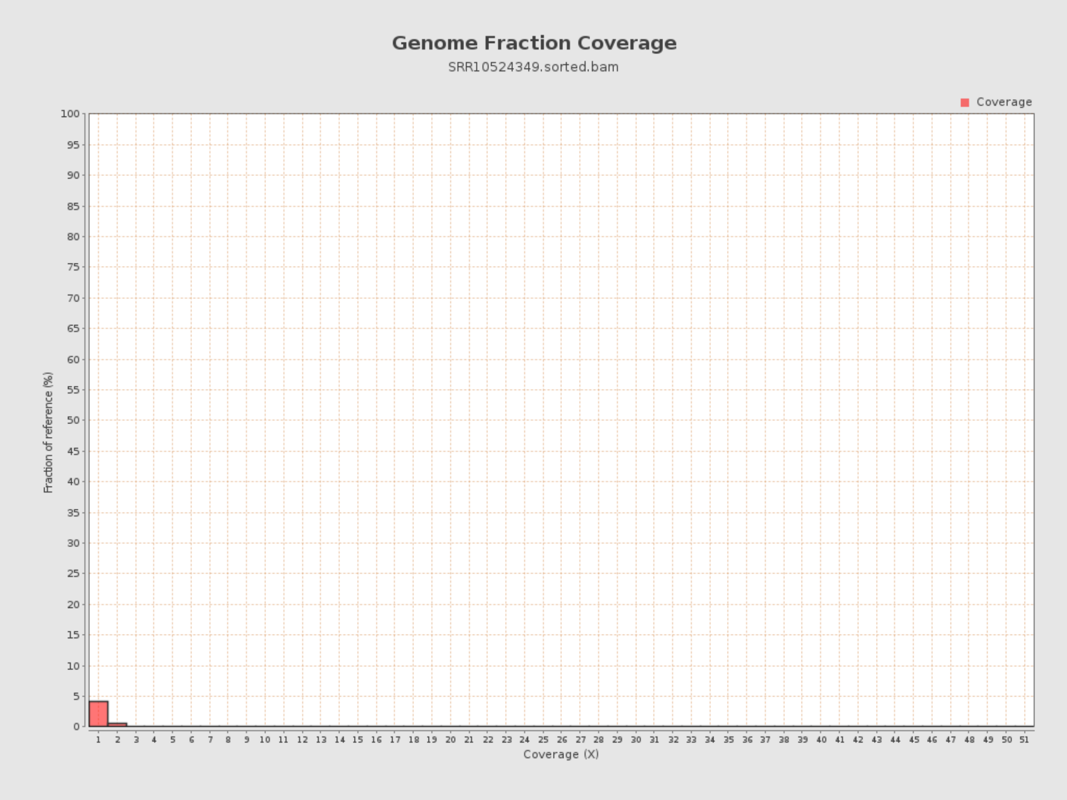
4. Results : Coverage Histogram



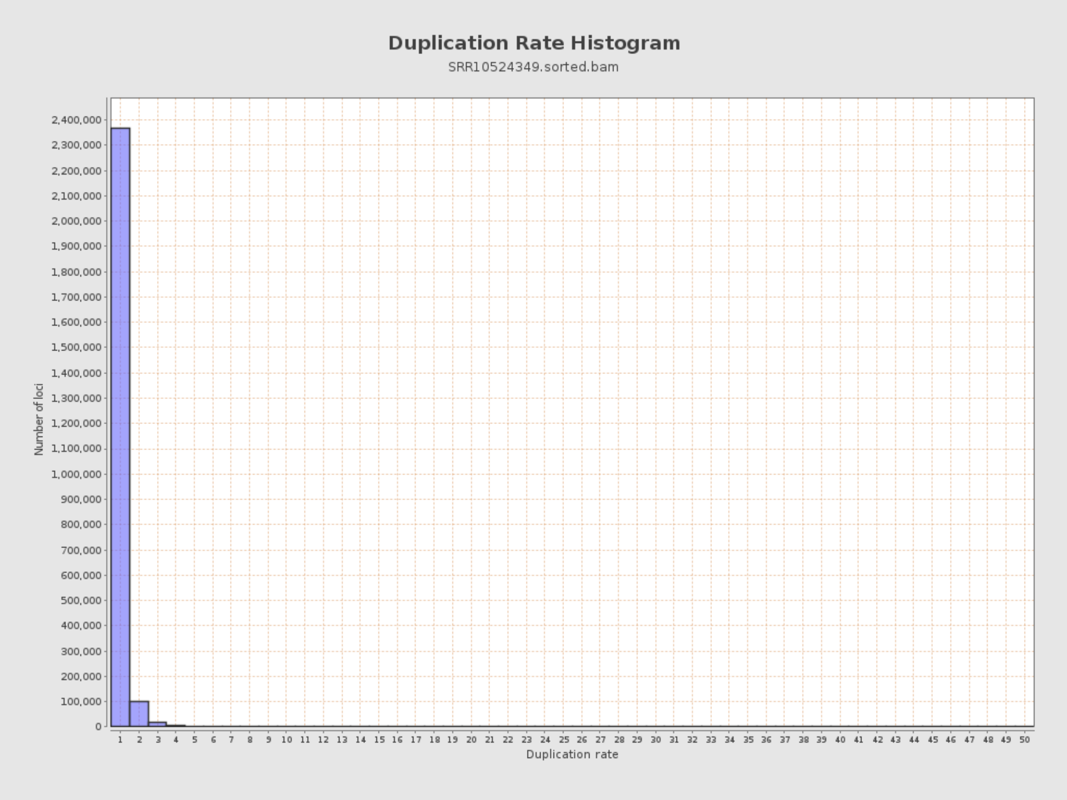
5. Results : Coverage Histogram (0-50X)



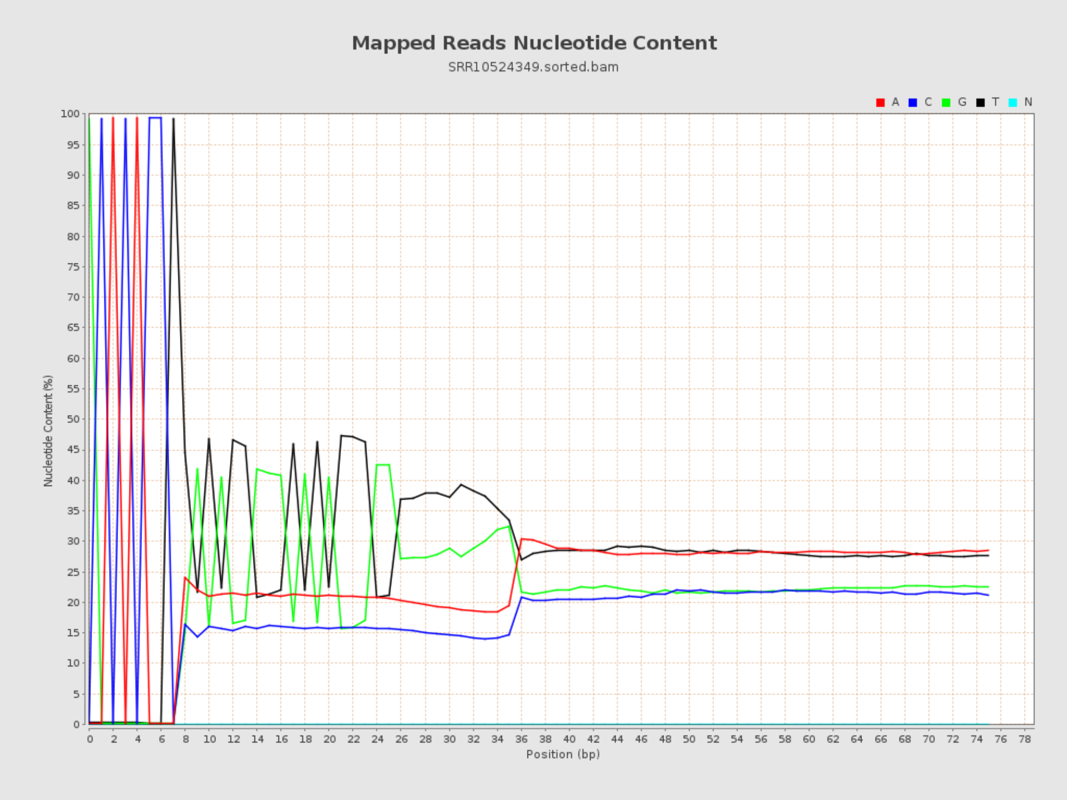
6. Results : Genome Fraction Coverage



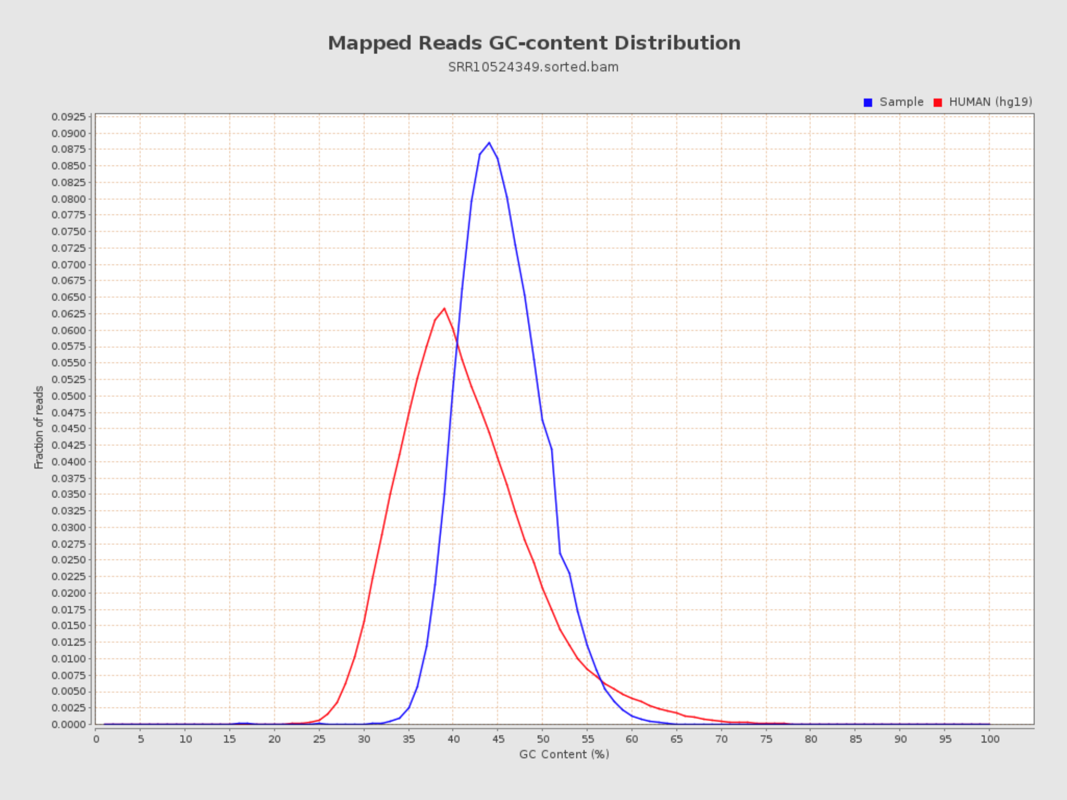
7. Results : Duplication Rate Histogram



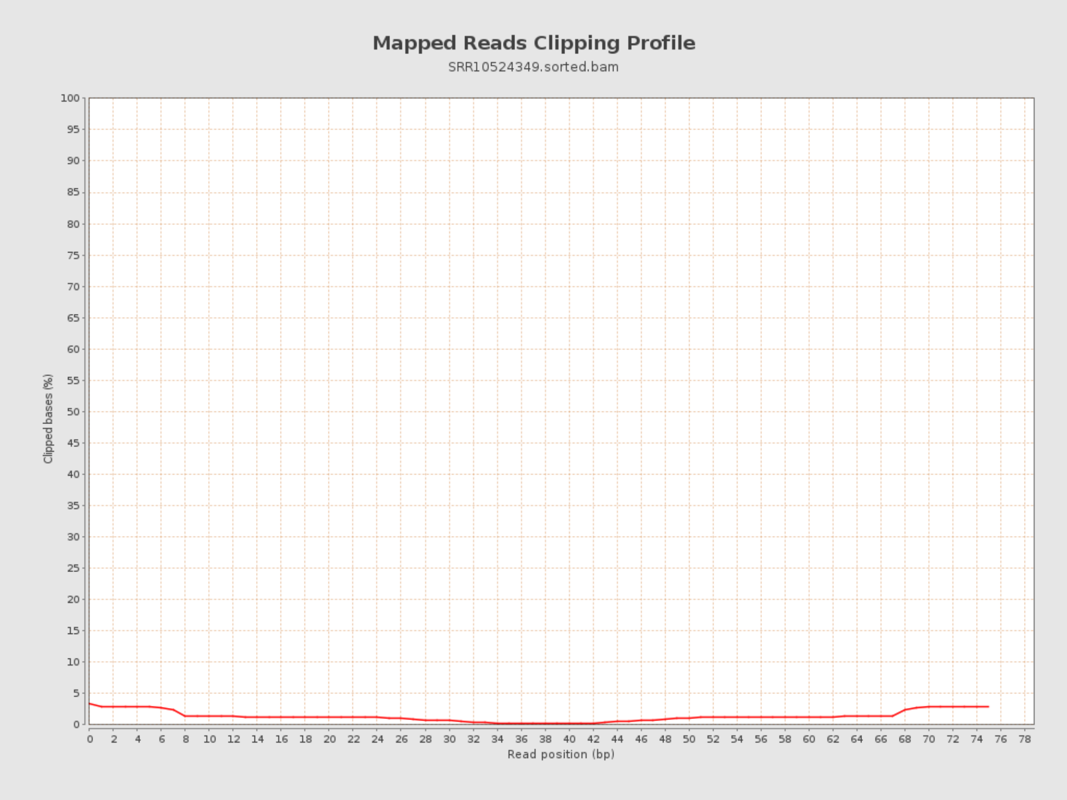
8. Results : Mapped Reads Nucleotide Content



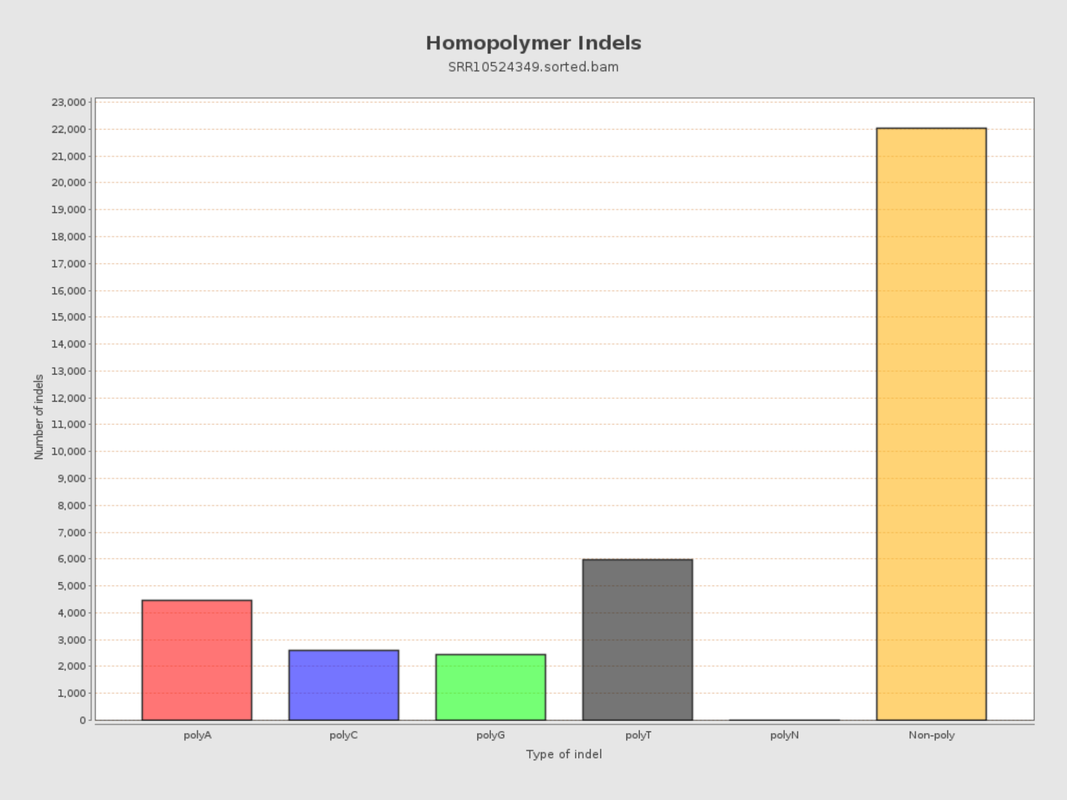
9. Results : Mapped Reads GC-content Distribution



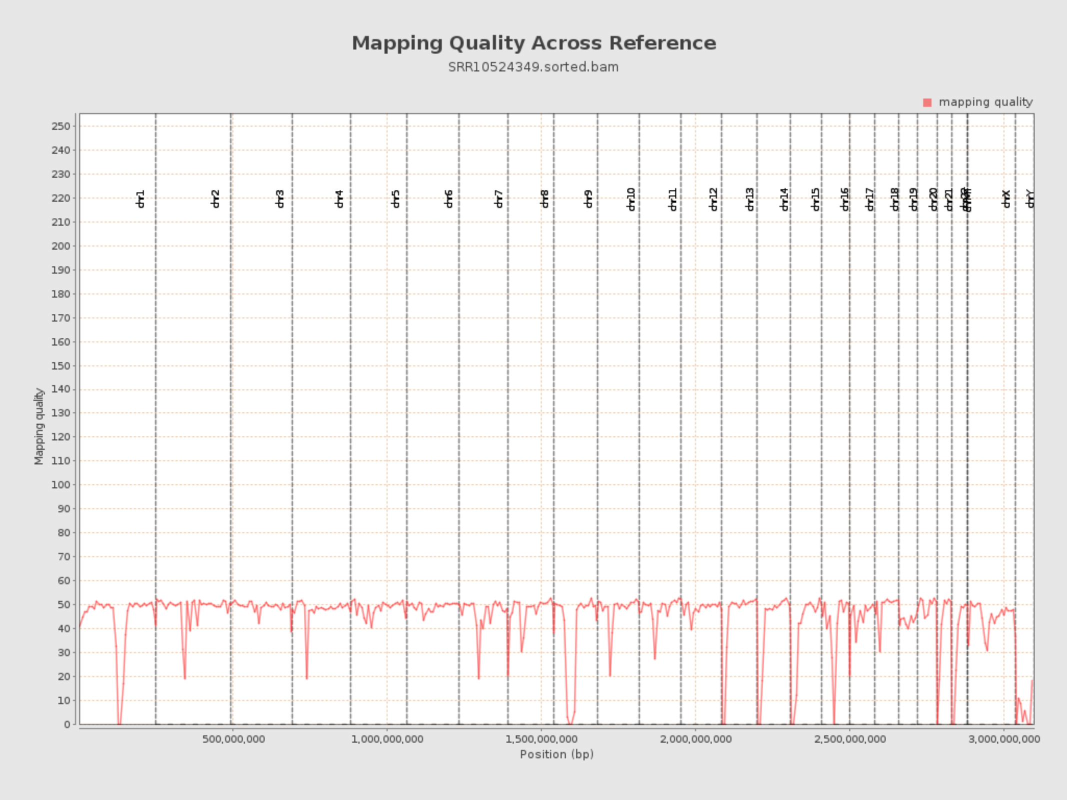
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram