Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:52:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524934.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_SRR10524934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524934.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:52:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,719,796
Mapped reads	2,516,346 / 92.52%
Unmapped reads	203,450 / 7.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,828 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	172,548 / 6.34%
Duplication rate	5.22%
Clipped reads	2,518,684 / 92.61%

2.2. ACGT Content

Number/percentage of A's	36,406,375 / 24.77%
Number/percentage of C's	27,694,103 / 18.85%
Number/percentage of T's	47,139,839 / 32.08%
Number/percentage of G's	35,714,344 / 24.3%
Number/percentage of N's	1,104 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0475

Standard Deviation	0.4145

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

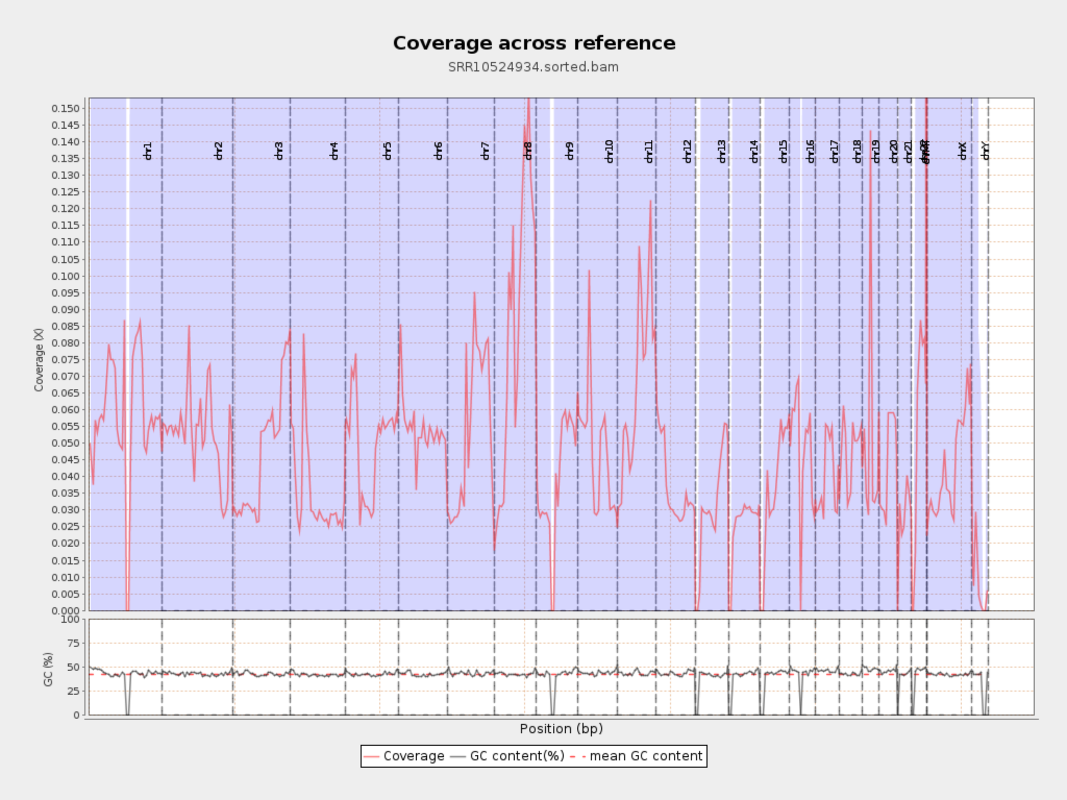
General error rate	0.52%
Mismatches	739,172
Insertions	10,109
Mapped reads with at least one insertion	0.4%
Deletions	28,743
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.18%

2.6. Chromosome stats

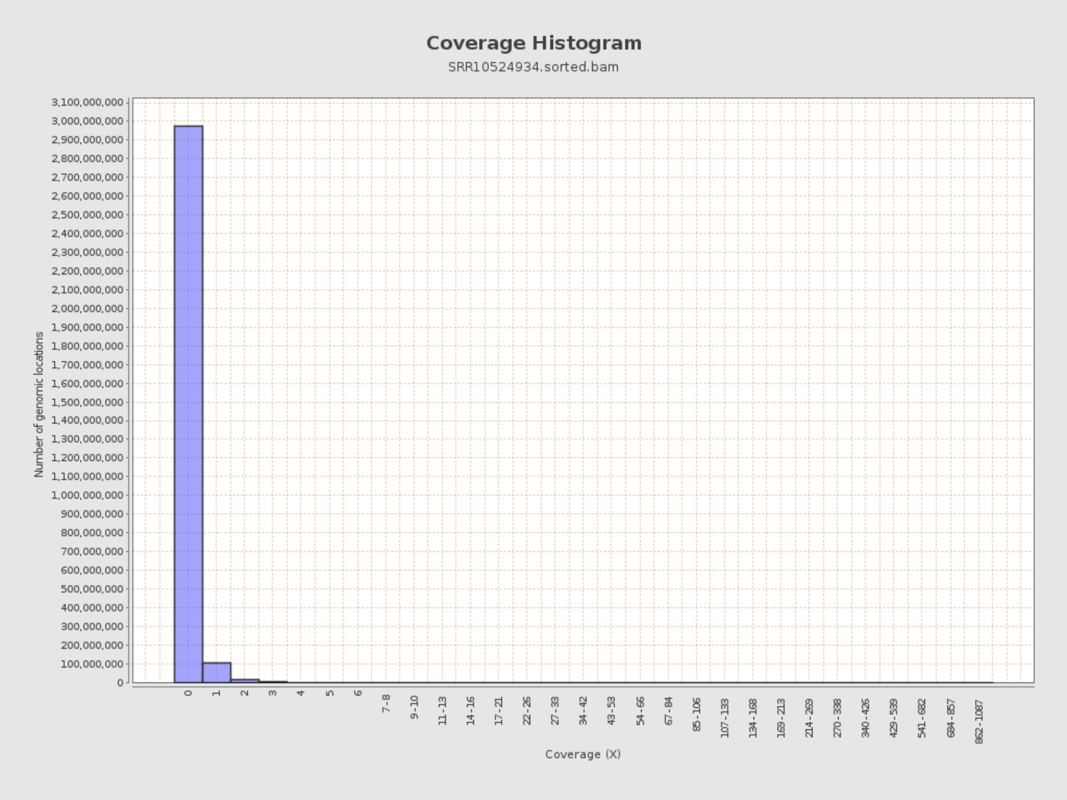
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14490515	0.0581	0.8196
chr2	243199373	12914004	0.0531	0.4871
chr3	198022430	9209817	0.0465	0.2555
chr4	191154276	6556537	0.0343	0.2889
chr5	180915260	9005892	0.0498	0.2614
chr6	171115067	9323311	0.0545	0.2954
chr7	159138663	8669895	0.0545	0.519

chr8	146364022	12711825	0.0869	0.5469
chr9	141213431	5369666	0.038	0.319
chr10	135534747	6423170	0.0474	0.461
chr11	135006516	9234316	0.0684	0.368
chr12	133851895	4879158	0.0365	0.2315
chr13	115169878	3542977	0.0308	0.2065
chr14	107349540	2702699	0.0252	0.2016
chr15	102531392	3679905	0.0359	0.2236
chr16	90354753	4306522	0.0477	0.2808
chr17	81195210	3238018	0.0399	0.2466
chr18	78077248	3774201	0.0483	0.5542
chr19	59128983	3044852	0.0515	0.5442
chr20	63025520	2809047	0.0446	0.2608
chr21	48129895	1338341	0.0278	0.2578
chr22	51304566	2700232	0.0526	0.2731
chrMT	16571	20072	1.2113	1.3852
chrX	155270560	6619881	0.0426	0.271
chrY	59373566	438695	0.0074	0.2589

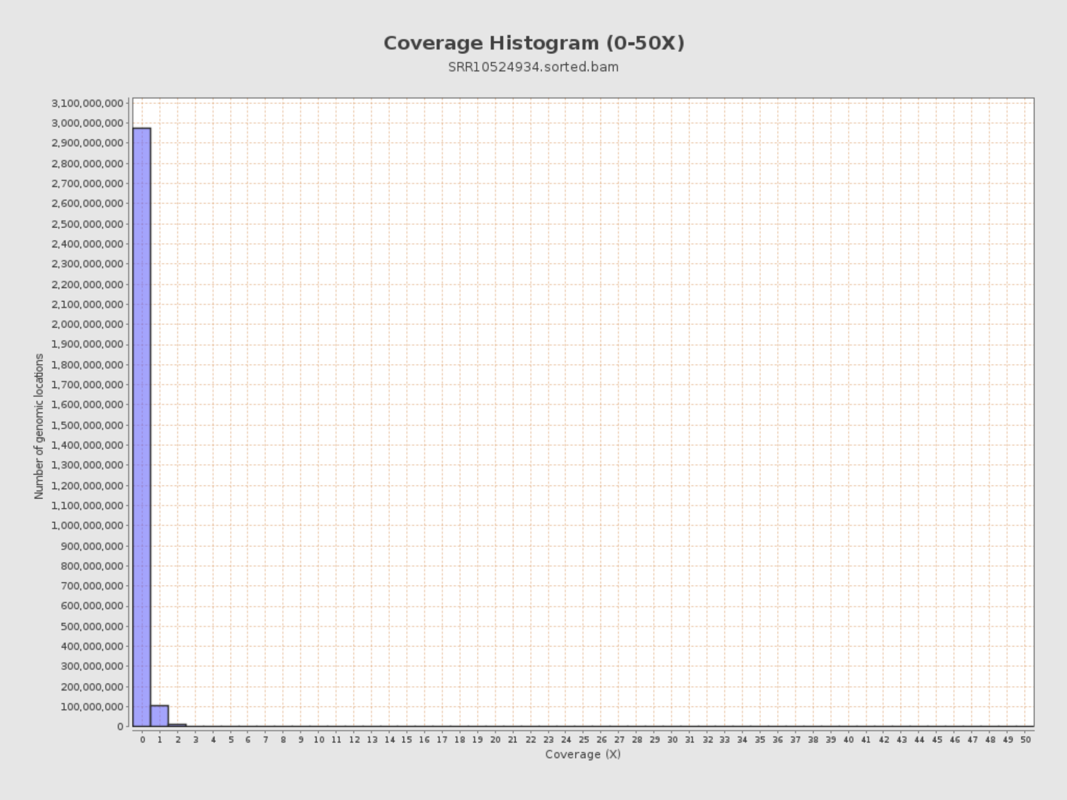
3. Results : Coverage across reference



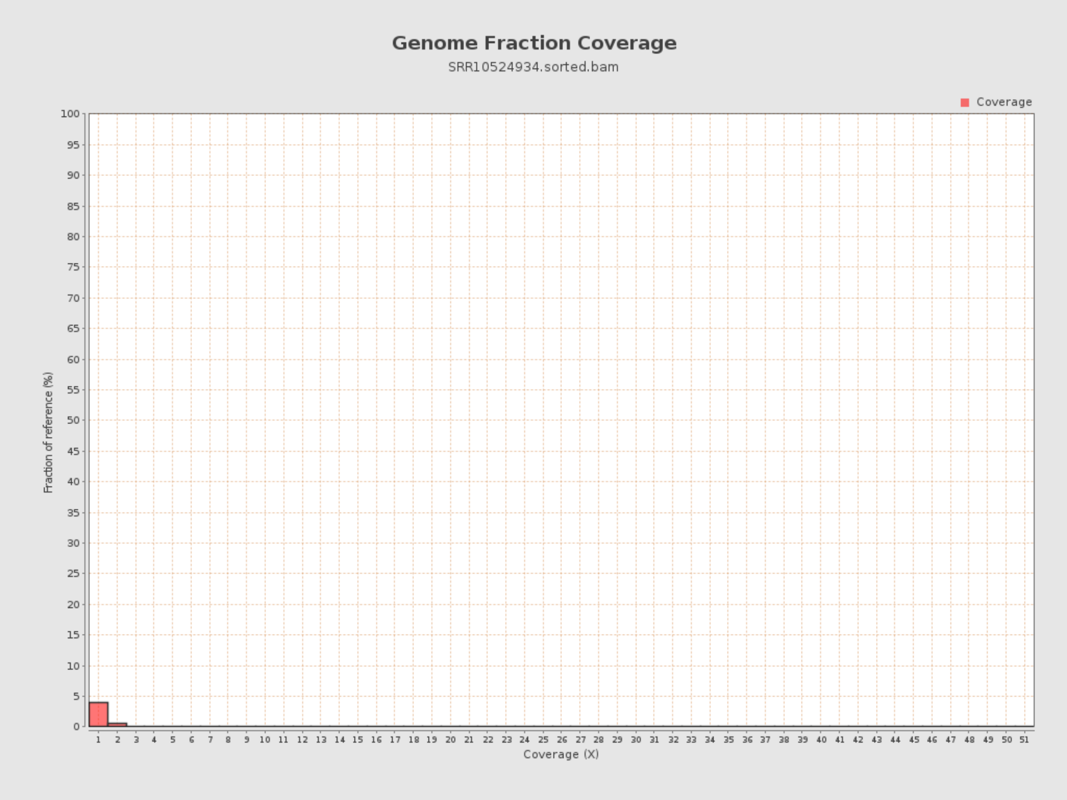
4. Results : Coverage Histogram



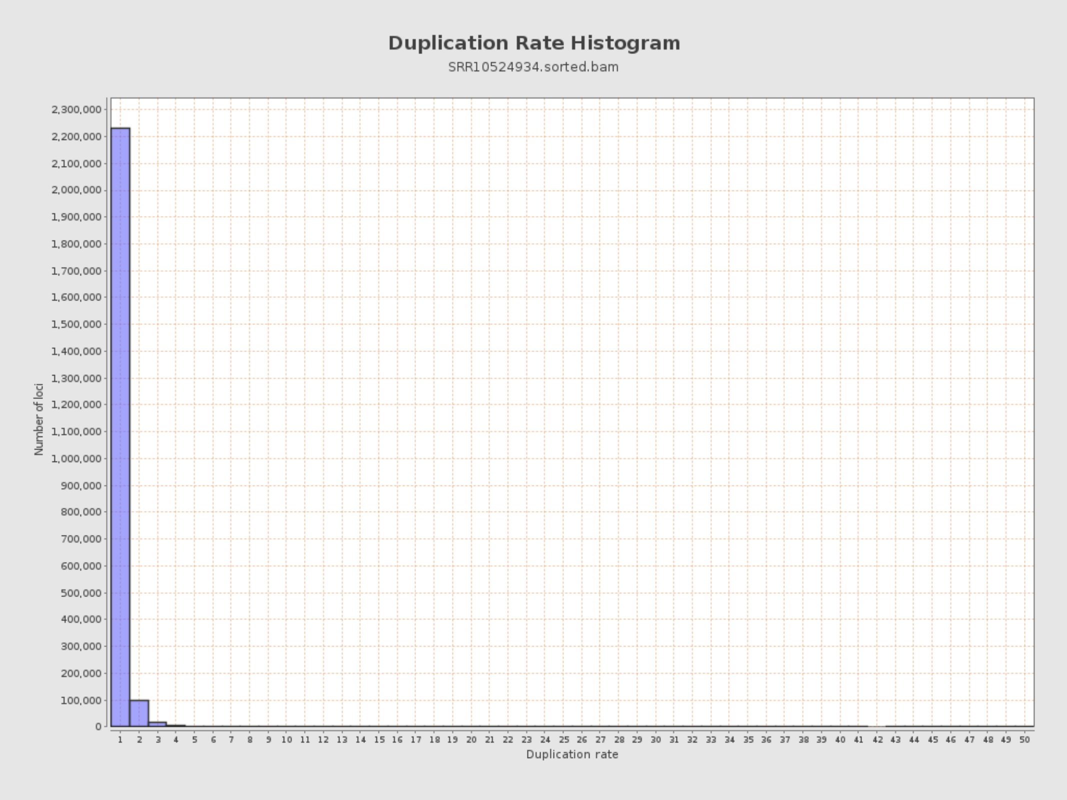
5. Results : Coverage Histogram (0-50X)



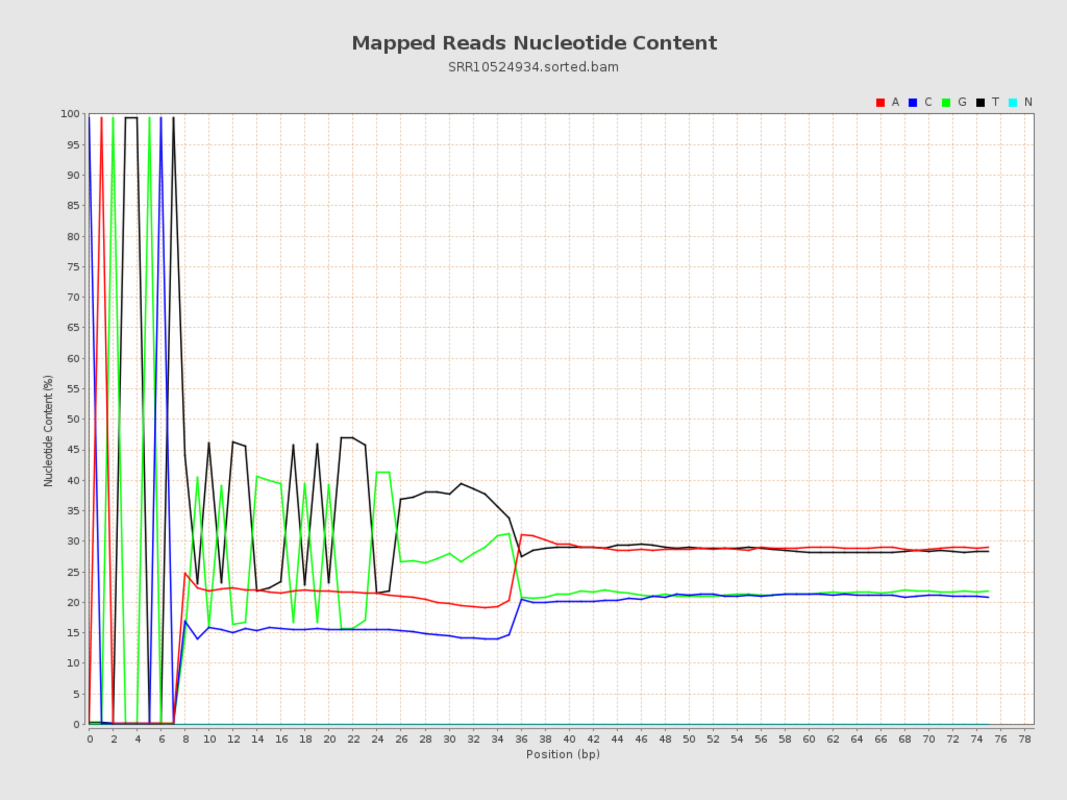
6. Results : Genome Fraction Coverage



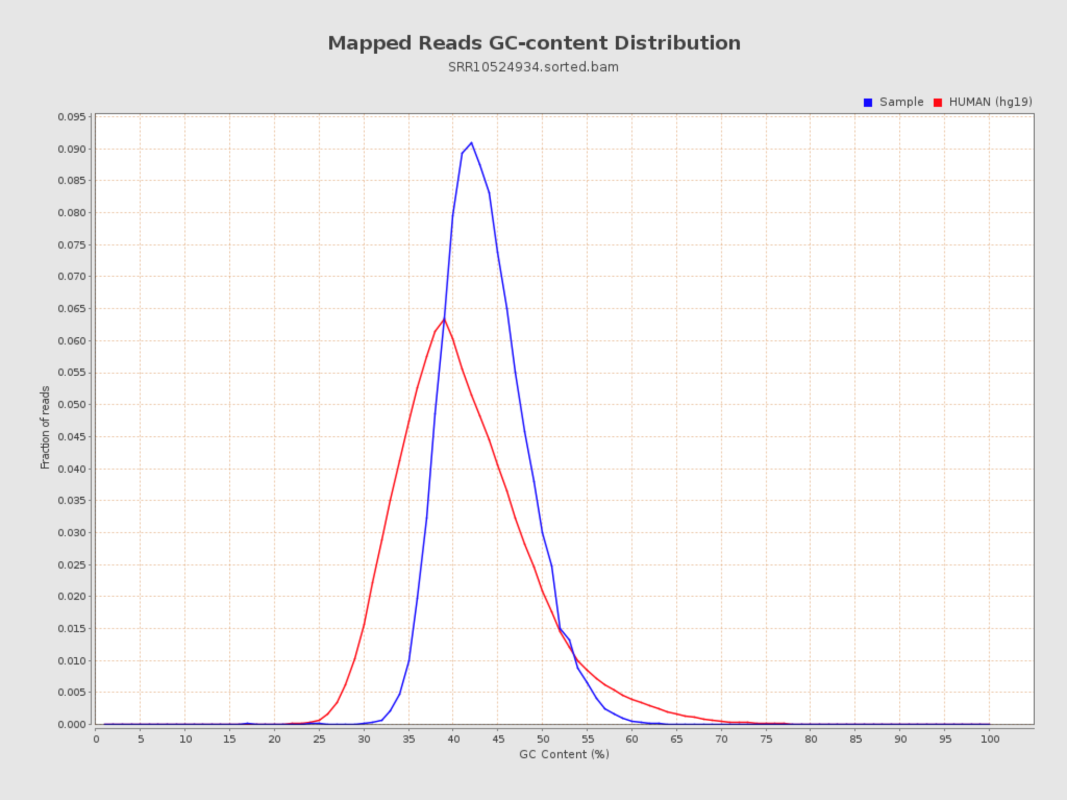
7. Results : Duplication Rate Histogram



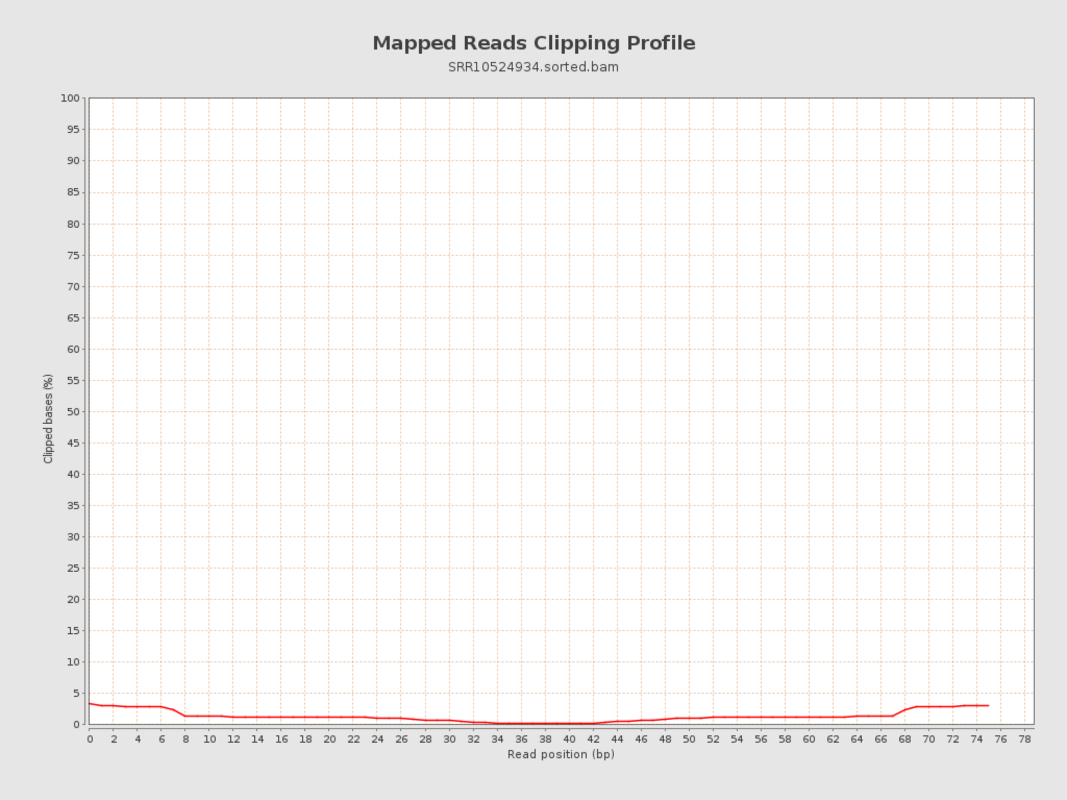
8. Results : Mapped Reads Nucleotide Content



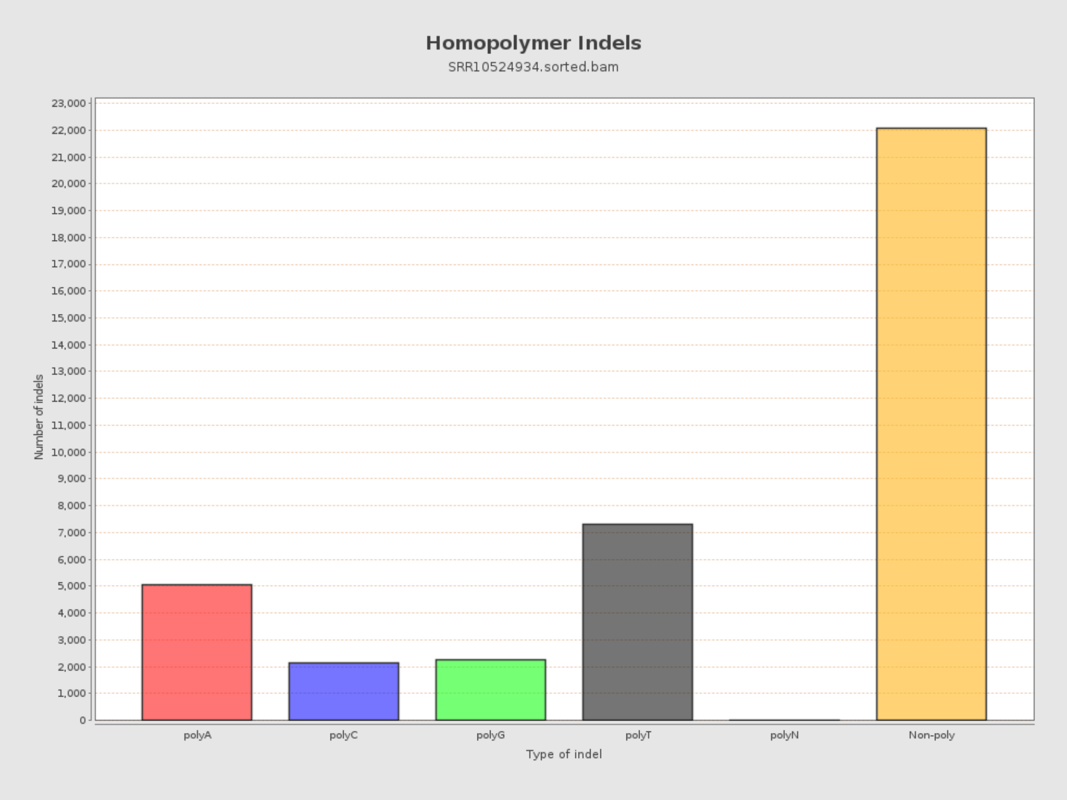
9. Results : Mapped Reads GC-content Distribution



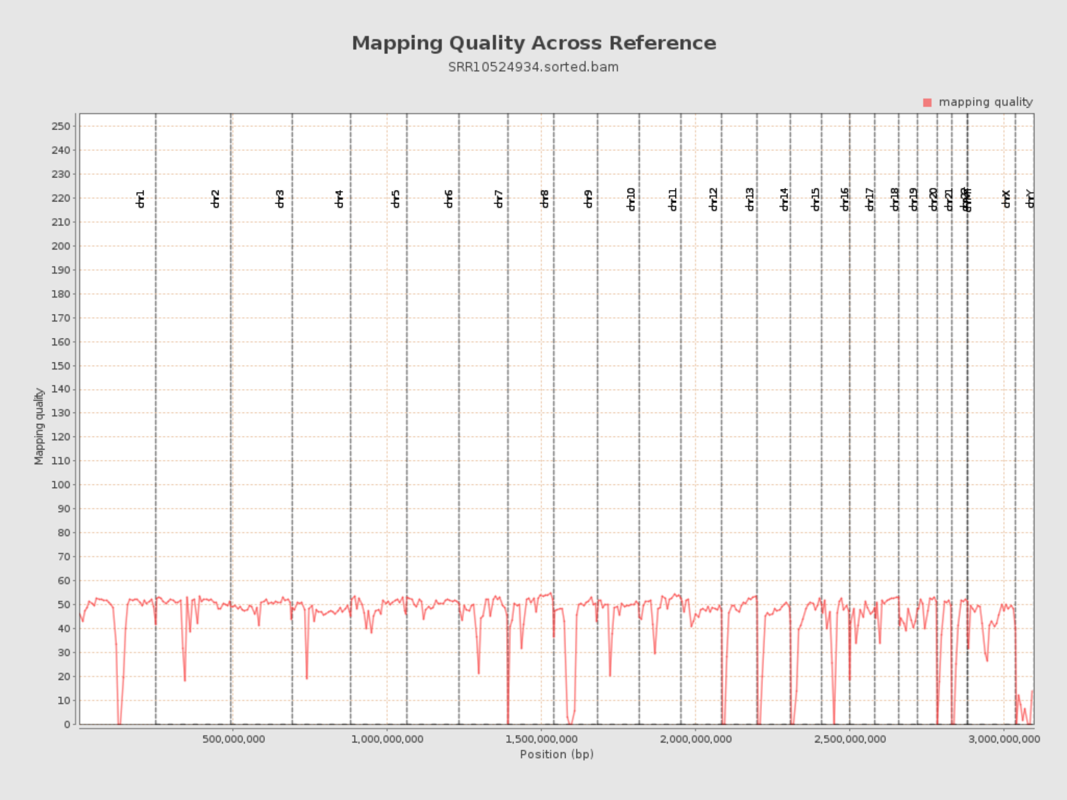
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram