Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:12:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524353.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_SRR10524353 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524353.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:12:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524353.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,136,432
Mapped reads	2,891,763 / 92.2%
Unmapped reads	244,669 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,803 / 0.6%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	196,323 / 6.26%
Duplication rate	4.93%
Clipped reads	2,901,570 / 92.51%

2.2. ACGT Content

Number/percentage of A's	43,789,446 / 25.61%
Number/percentage of C's	33,070,776 / 19.34%
Number/percentage of T's	54,050,916 / 31.61%
Number/percentage of G's	40,050,416 / 23.42%
Number/percentage of N's	25,070 / 0.01%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0552

Standard Deviation	0.5116

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

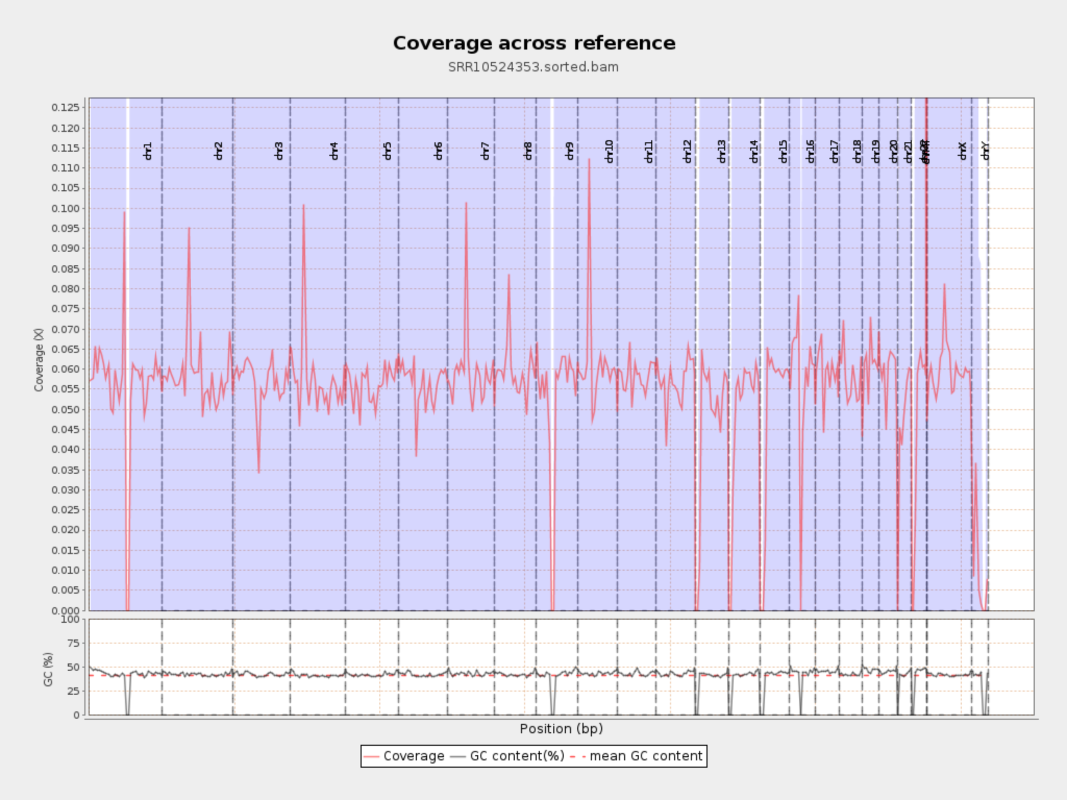
General error rate	0.54%
Mismatches	893,289
Insertions	12,187
Mapped reads with at least one insertion	0.42%
Deletions	31,144
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.23%

2.6. Chromosome stats

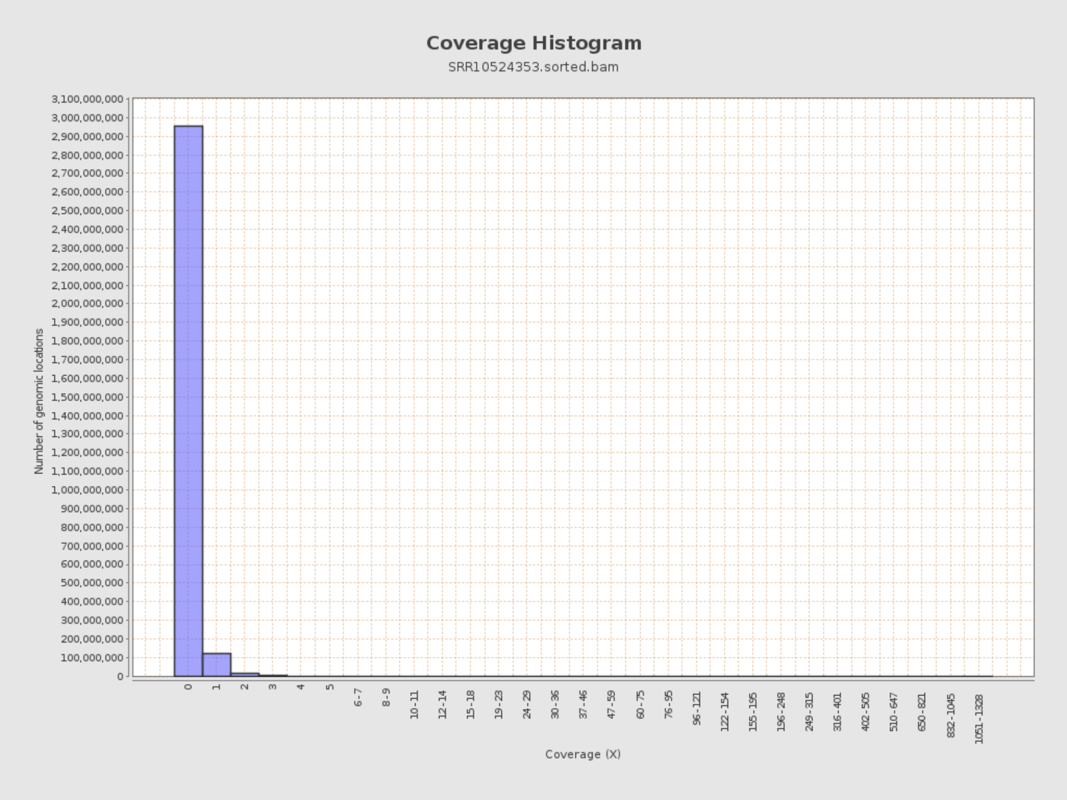
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13868586	0.0556	1.0319
chr2	243199373	14328973	0.0589	0.6328
chr3	198022430	11230572	0.0567	0.2833
chr4	191154276	10932641	0.0572	0.3612
chr5	180915260	10160803	0.0562	0.2821
chr6	171115067	9670887	0.0565	0.3119
chr7	159138663	9472647	0.0595	0.7027

chr8	146364022	8732756	0.0597	0.4592
chr9	141213431	7240451	0.0513	0.4112
chr10	135534747	8301210	0.0612	0.5042
chr11	135006516	7850468	0.0581	0.4325
chr12	133851895	7620646	0.0569	0.2925
chr13	115169878	5286743	0.0459	0.2526
chr14	107349540	5154117	0.048	0.2962
chr15	102531392	4986851	0.0486	0.2618
chr16	90354753	5159364	0.0571	0.326
chr17	81195210	4788415	0.059	0.3273
chr18	78077248	4554391	0.0583	0.903
chr19	59128983	3623079	0.0613	0.6769
chr20	63025520	3728132	0.0592	0.3045
chr21	48129895	2248551	0.0467	0.3322
chr22	51304566	2187140	0.0426	0.2462
chrMT	16571	31761	1.9167	1.7075
chrX	155270560	9290785	0.0598	0.3454
chrY	59373566	586391	0.0099	0.2982

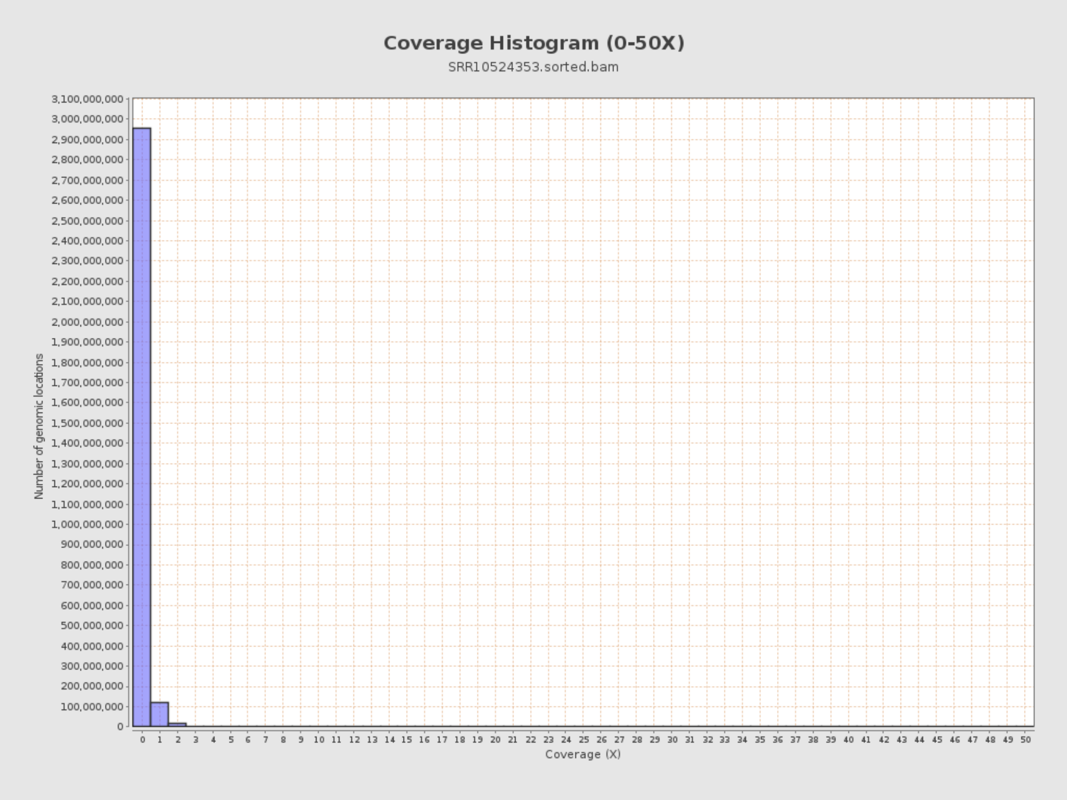
3. Results : Coverage across reference



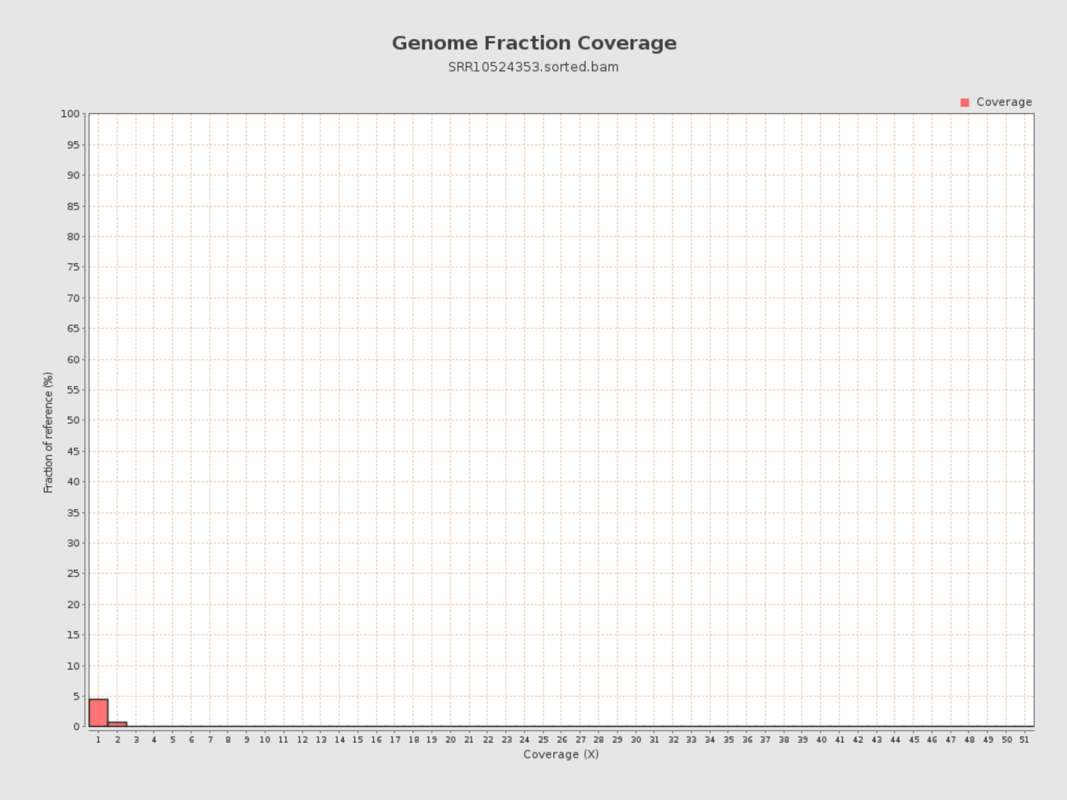
4. Results : Coverage Histogram



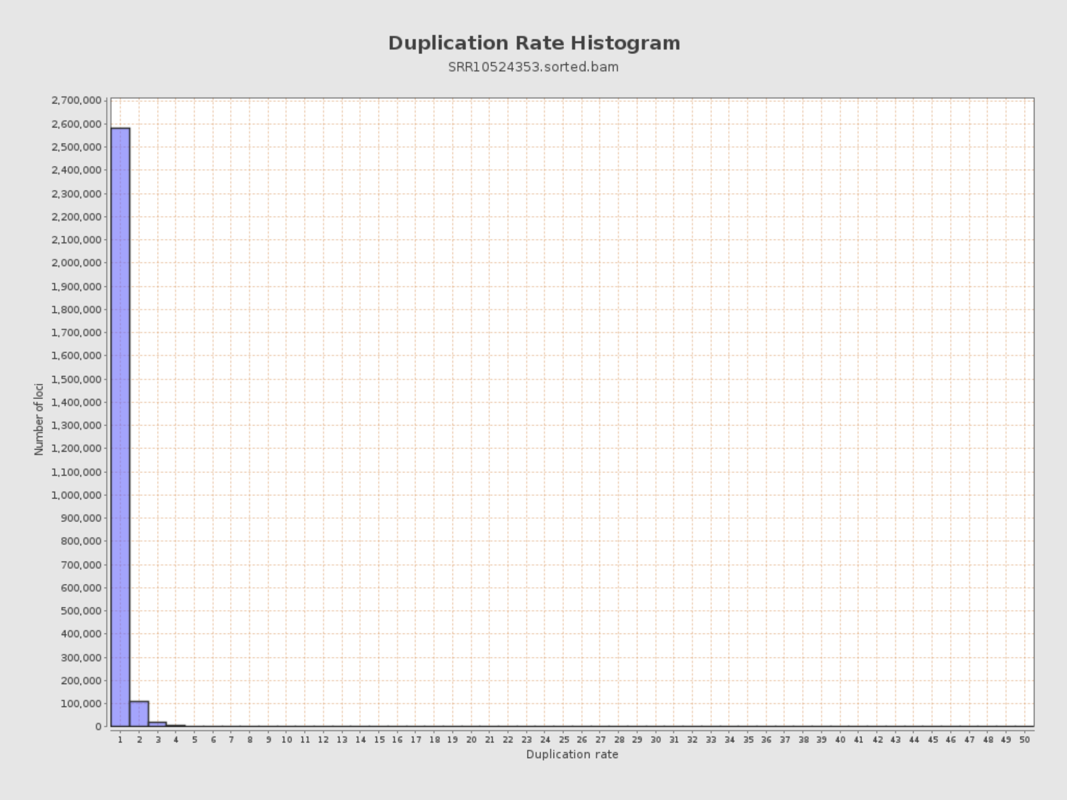
5. Results : Coverage Histogram (0-50X)



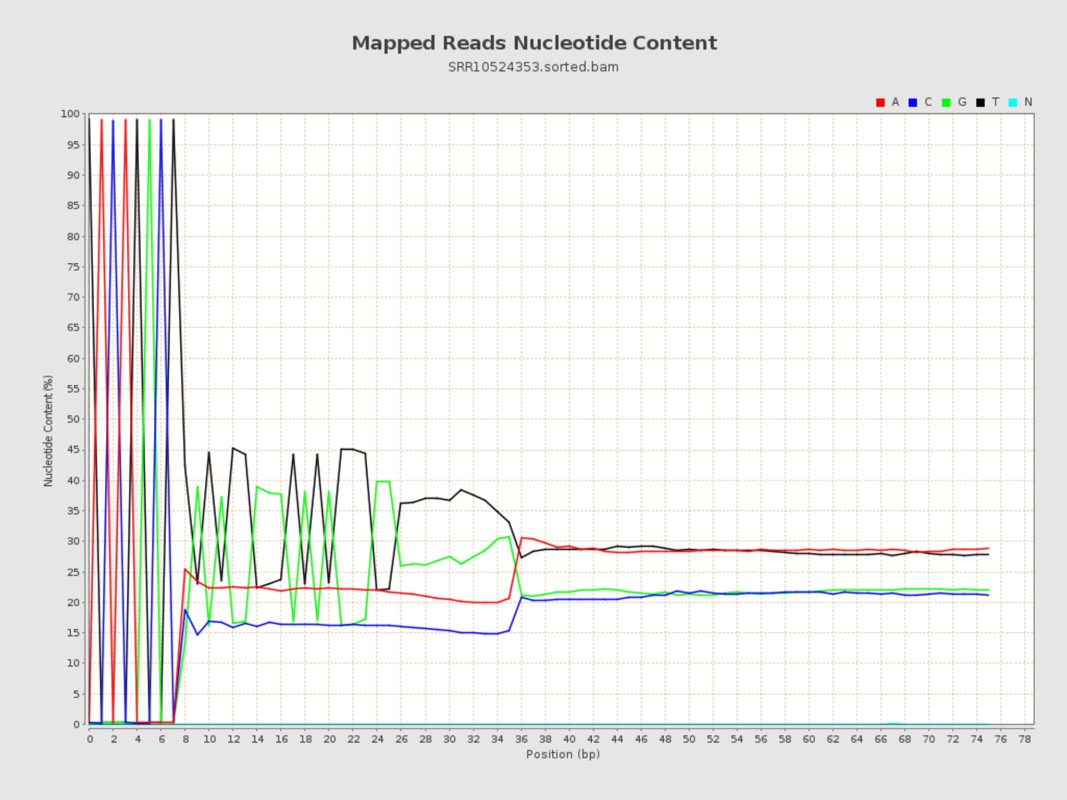
6. Results : Genome Fraction Coverage



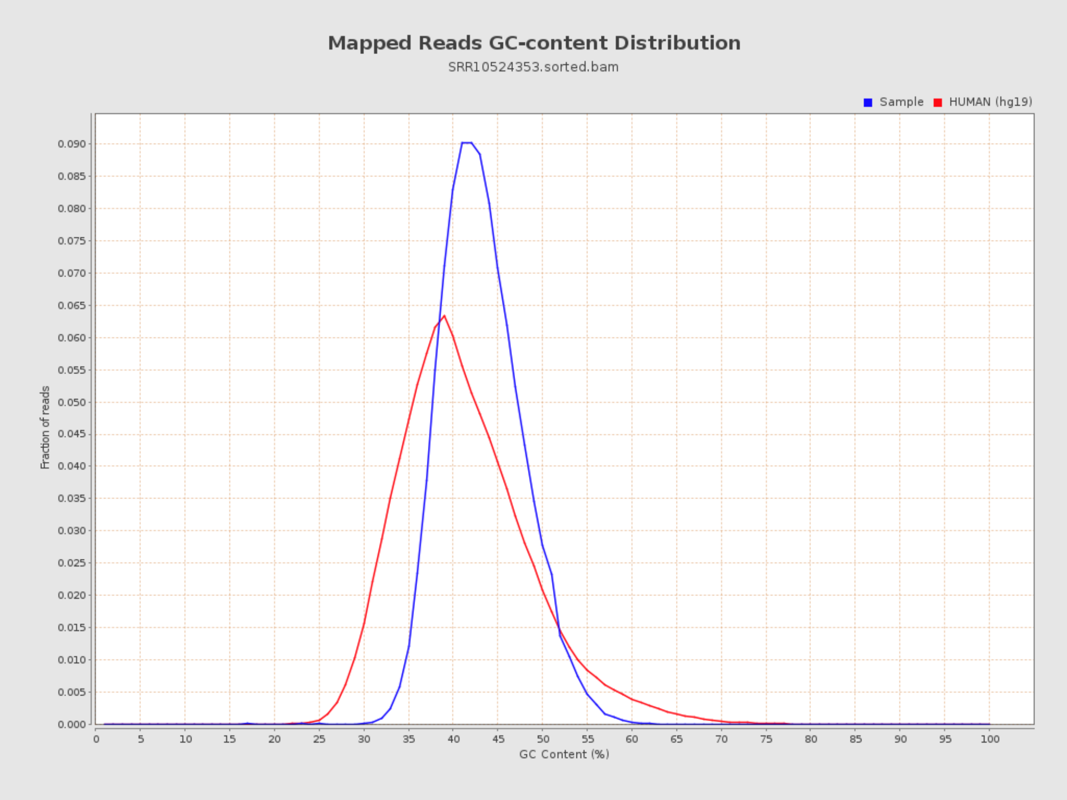
7. Results : Duplication Rate Histogram



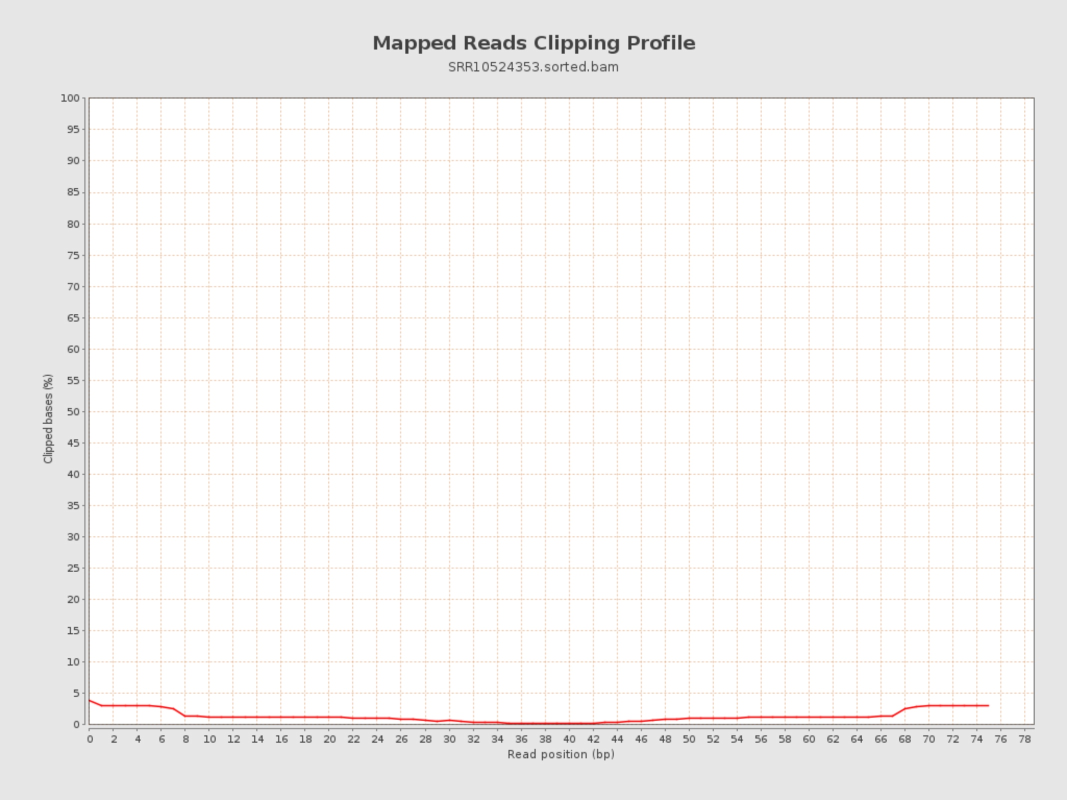
8. Results : Mapped Reads Nucleotide Content



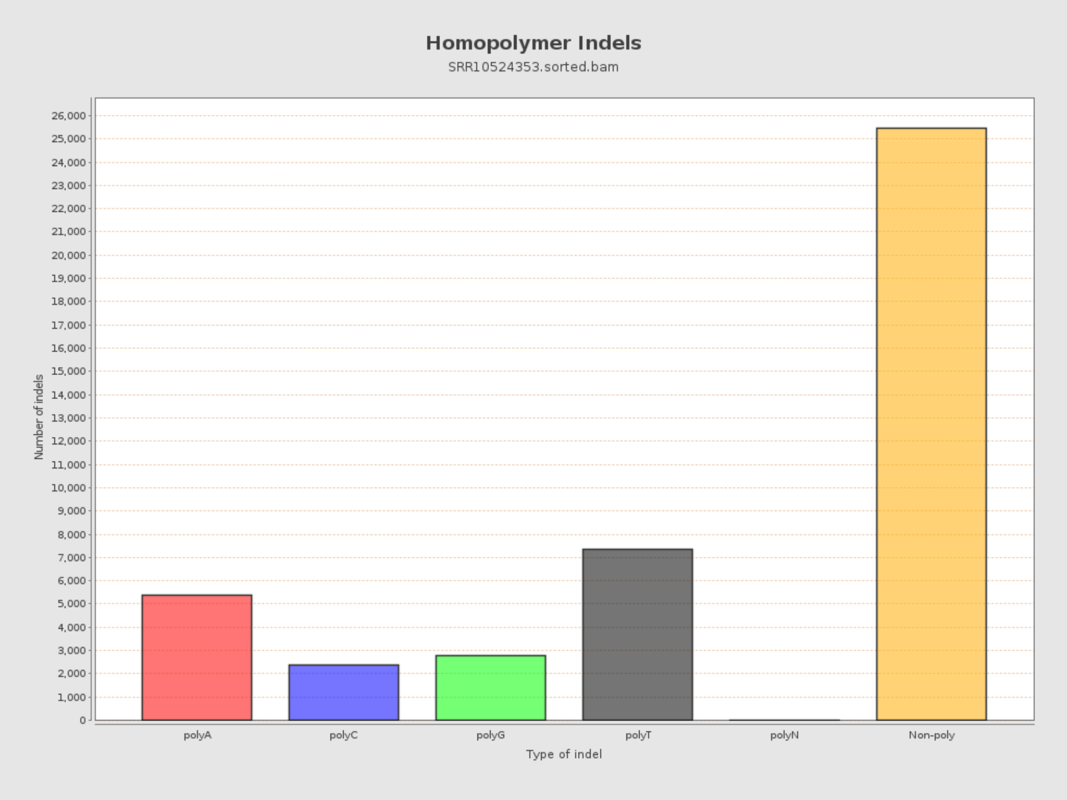
9. Results : Mapped Reads GC-content Distribution



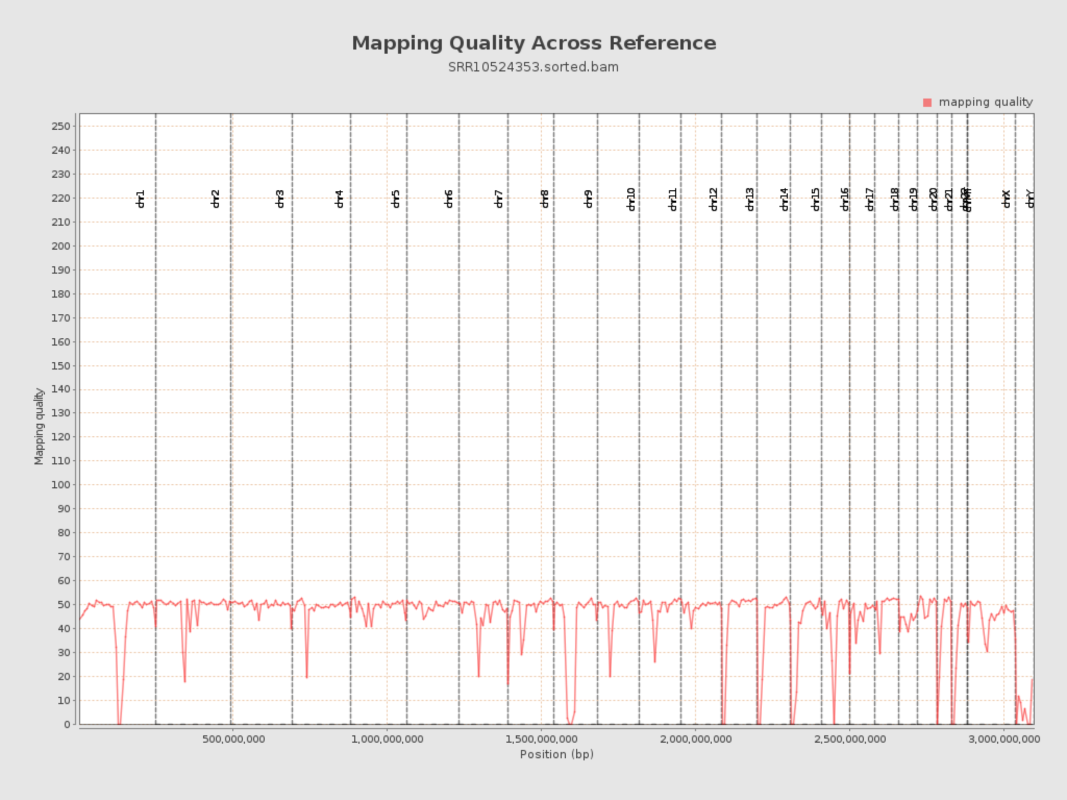
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram