Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:32:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524931.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_SRR10524931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524931.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:32:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524931.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,347,726
Mapped reads	2,168,408 / 92.36%
Unmapped reads	179,318 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,600 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	141,501 / 6.03%
Duplication rate	5.04%
Clipped reads	2,172,053 / 92.52%

2.2. ACGT Content

Number/percentage of A's	32,045,157 / 25.43%
Number/percentage of C's	23,630,380 / 18.75%
Number/percentage of T's	40,585,161 / 32.21%
Number/percentage of G's	29,739,682 / 23.6%
Number/percentage of N's	1,018 / 0%
GC Percentage	42.36%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.3528

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

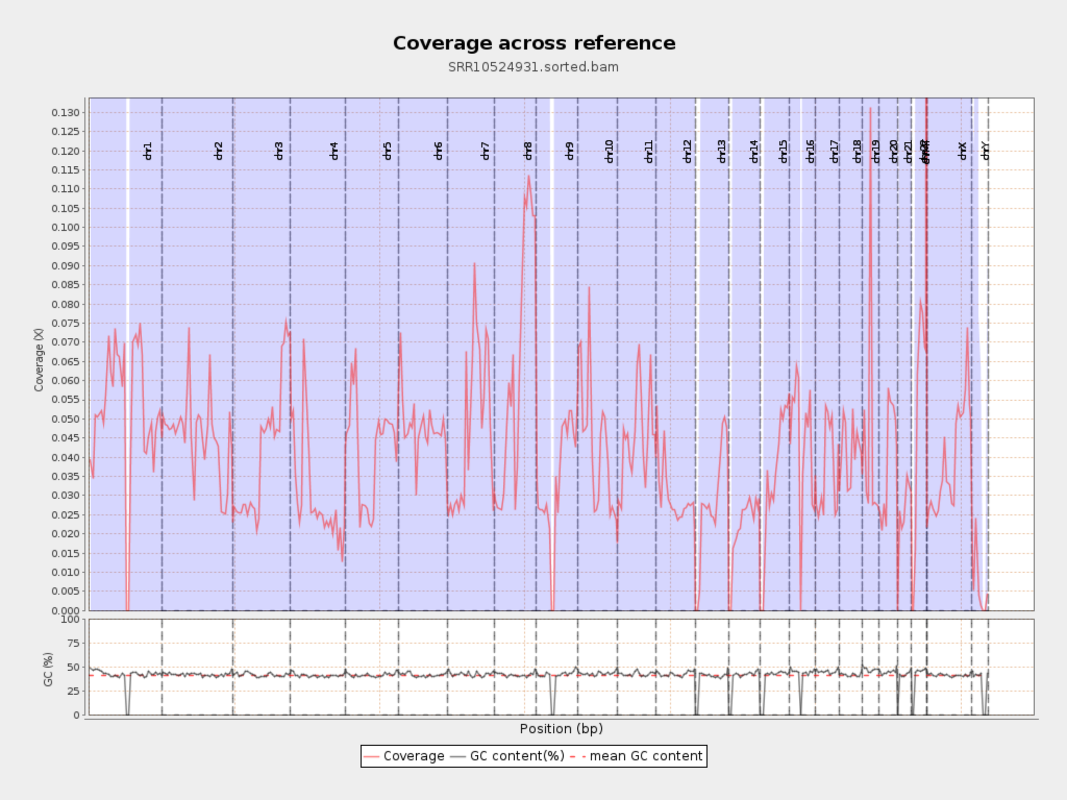
General error rate	0.52%
Mismatches	637,841
Insertions	8,330
Mapped reads with at least one insertion	0.38%
Deletions	24,006
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.5%

2.6. Chromosome stats

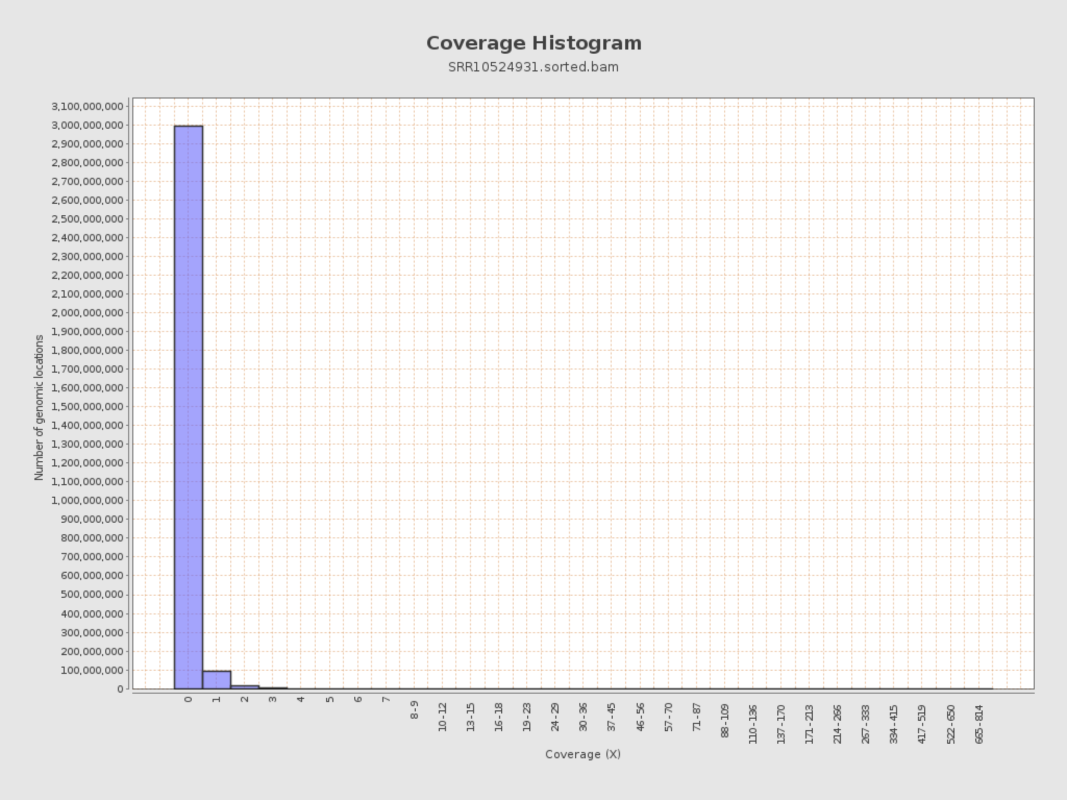
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12973873	0.0521	0.6423
chr2	243199373	11137583	0.0458	0.4453
chr3	198022430	8149676	0.0412	0.239
chr4	191154276	5670483	0.0297	0.2582
chr5	180915260	7655460	0.0423	0.241
chr6	171115067	8240729	0.0482	0.2727
chr7	159138663	7618162	0.0479	0.4432

chr8	146364022	9386001	0.0641	0.4218
chr9	141213431	4646843	0.0329	0.2879
chr10	135534747	5864704	0.0433	0.4002
chr11	135006516	6101553	0.0452	0.3069
chr12	133851895	4014492	0.03	0.2127
chr13	115169878	3215194	0.0279	0.1949
chr14	107349540	2295825	0.0214	0.1835
chr15	102531392	3489038	0.034	0.2169
chr16	90354753	3951254	0.0437	0.2642
chr17	81195210	2970136	0.0366	0.2339
chr18	78077248	3304175	0.0423	0.4895
chr19	59128983	2676985	0.0453	0.4548
chr20	63025520	2508097	0.0398	0.2423
chr21	48129895	1224222	0.0254	0.2267
chr22	51304566	2493116	0.0486	0.2597
chrMT	16571	7957	0.4802	0.7593
chrX	155270560	6086004	0.0392	0.2579
chrY	59373566	360002	0.0061	0.2116

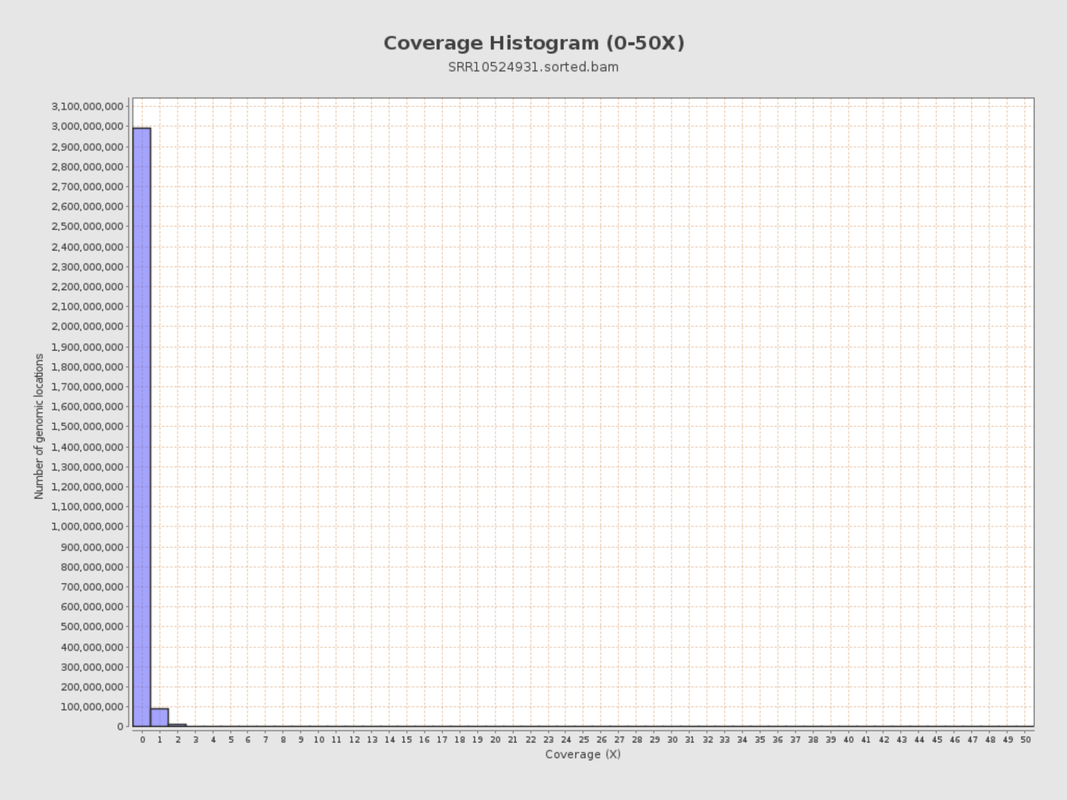
3. Results : Coverage across reference



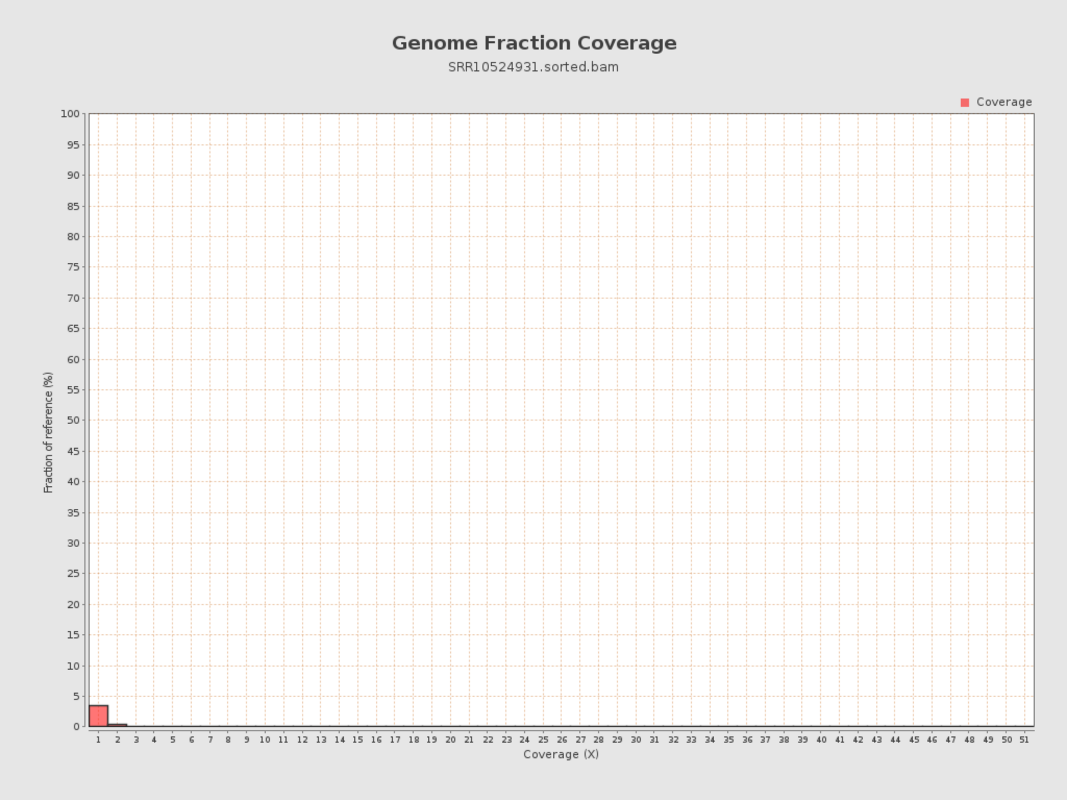
4. Results : Coverage Histogram



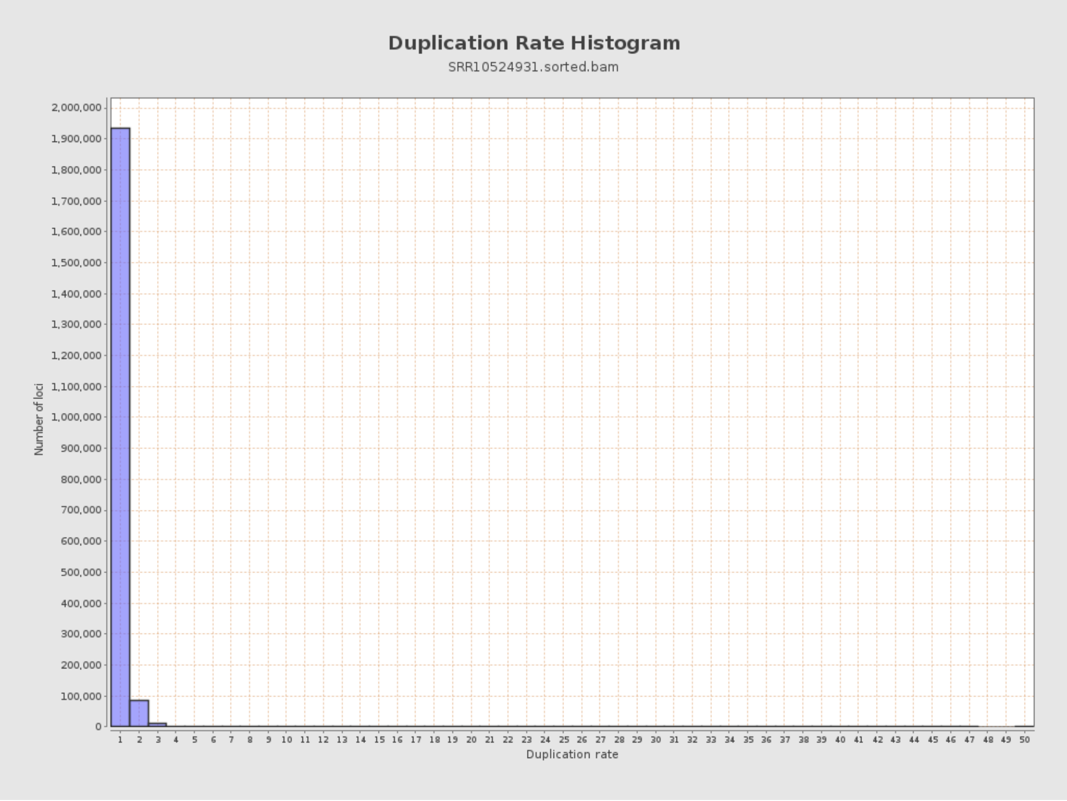
5. Results : Coverage Histogram (0-50X)



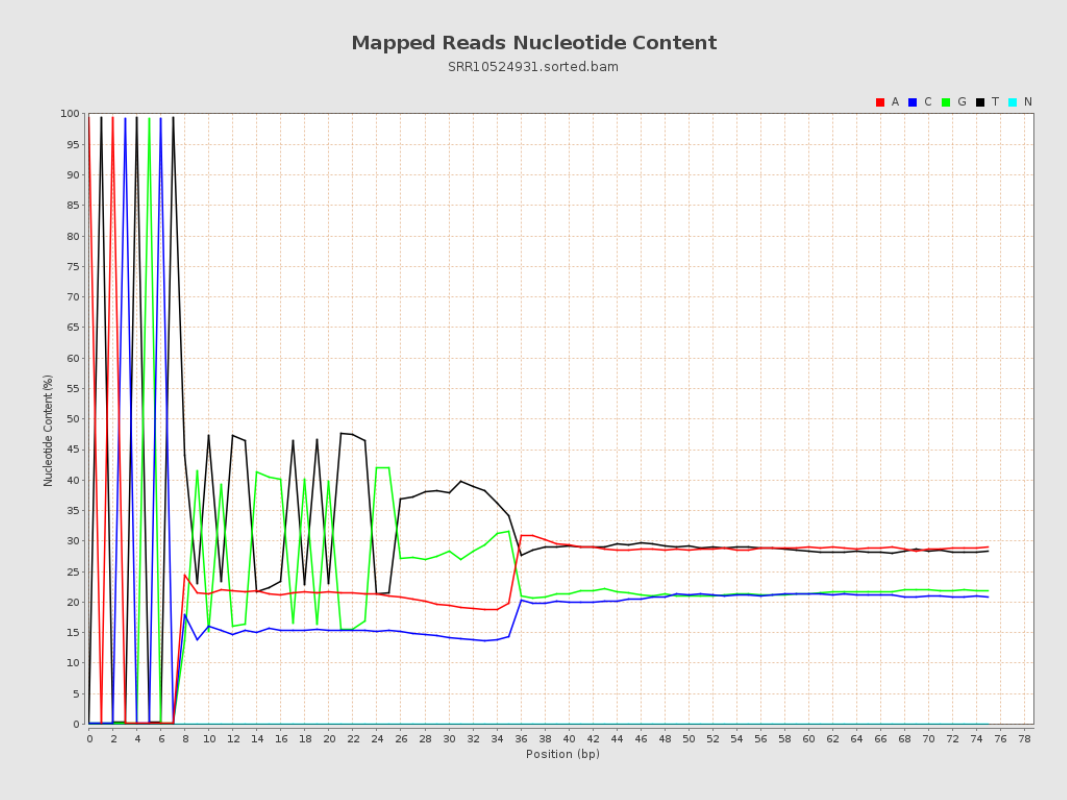
6. Results : Genome Fraction Coverage



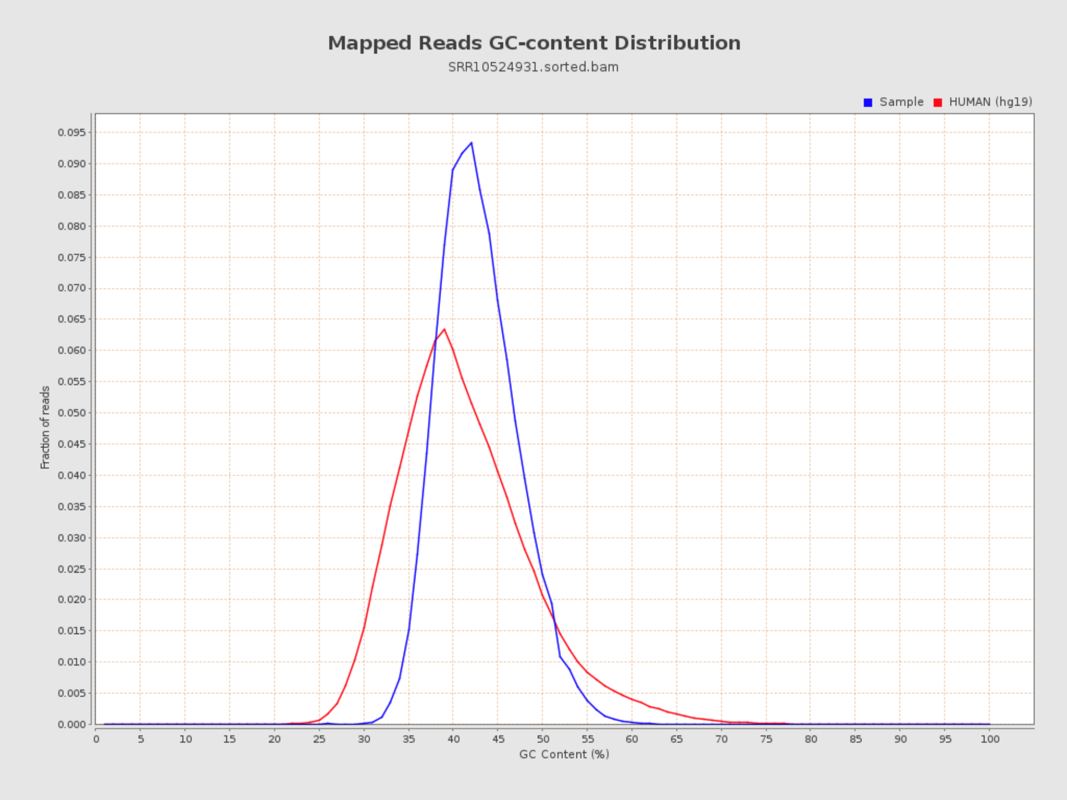
7. Results : Duplication Rate Histogram



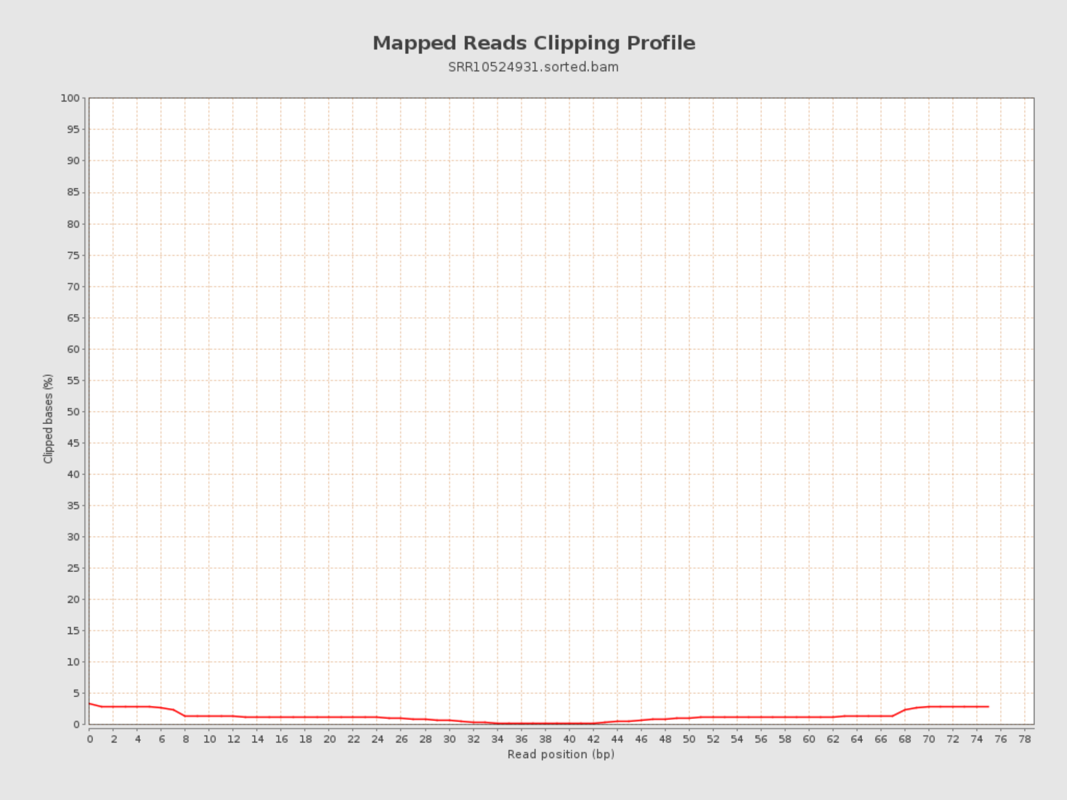
8. Results : Mapped Reads Nucleotide Content



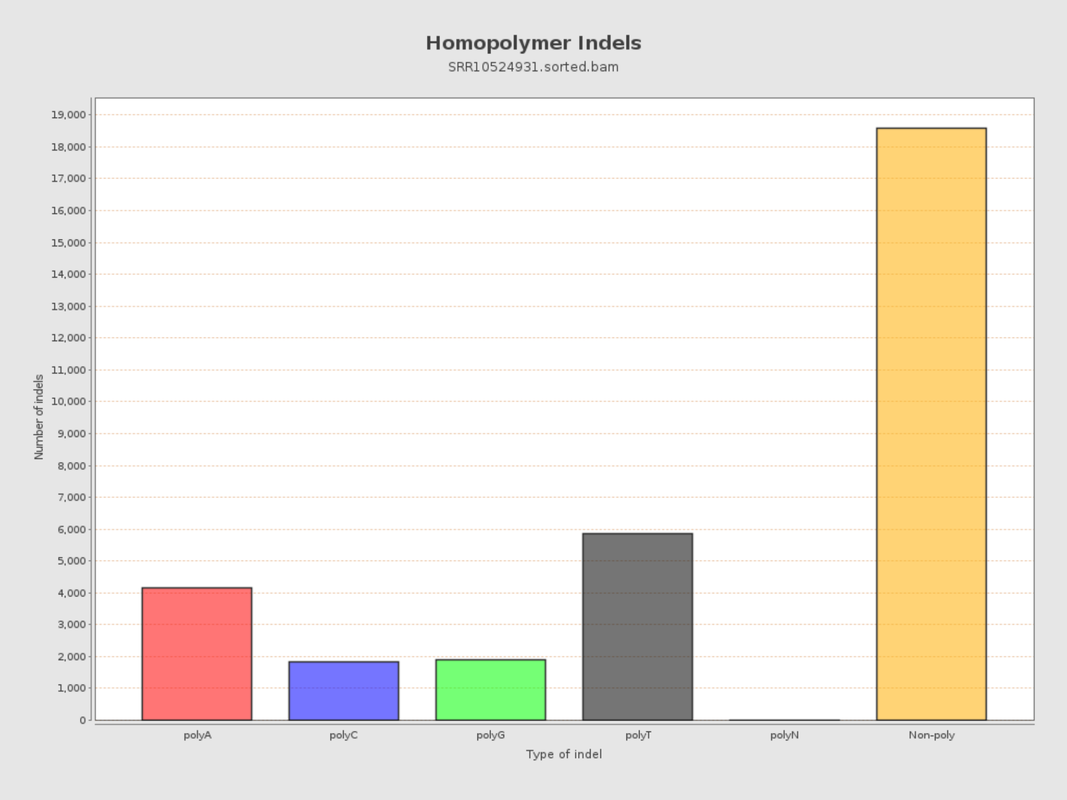
9. Results : Mapped Reads GC-content Distribution



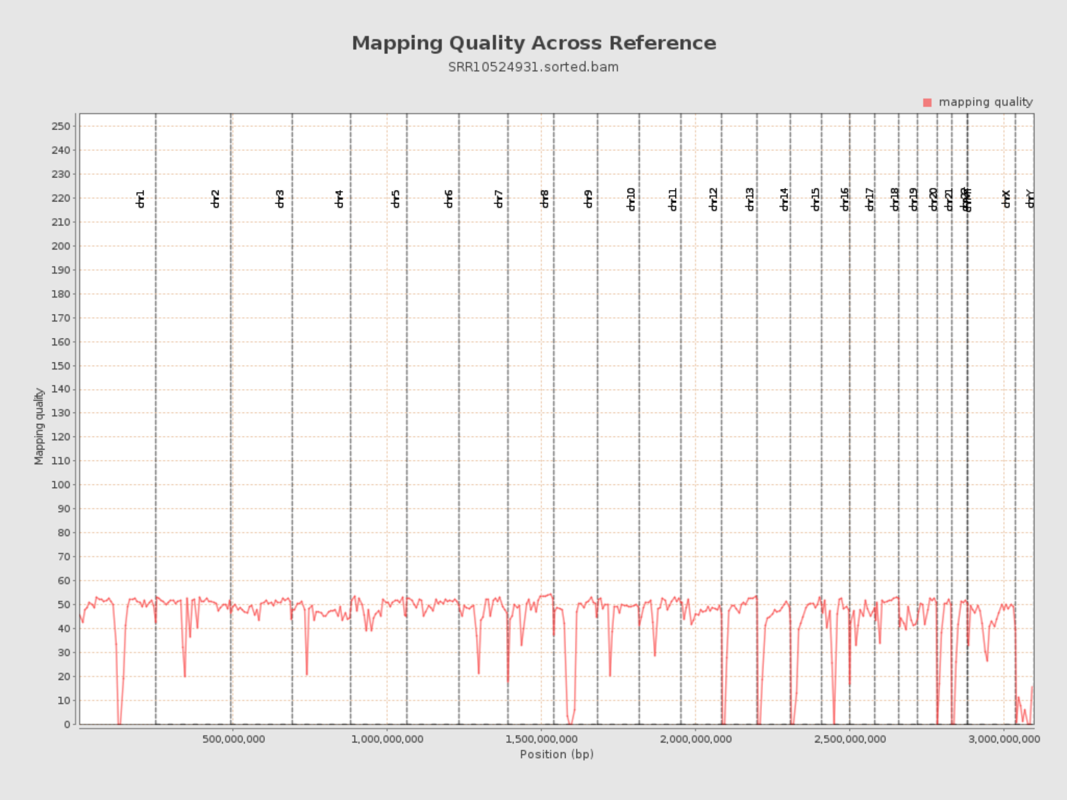
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram