Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173891.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_SRR10173891 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173891_1.fastq.gz SRR10173891_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:26:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173891.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,377,240
Mapped reads	4,263,886 / 97.41%
Unmapped reads	113,354 / 2.59%
Mapped paired reads	4,263,886 / 97.41%
Mapped reads, first in pair	2,133,856 / 48.75%
Mapped reads, second in pair	2,130,030 / 48.66%
Mapped reads, both in pair	4,185,920 / 95.63%
Mapped reads, singletons	77,966 / 1.78%
Secondary alignments	0
Supplementary alignments	459,742 / 10.5%
Read min/max/mean length	30 / 133 / 128.56
Duplicated reads (estimated)	3,477,136 / 79.44%
Duplication rate	66.54%
Clipped reads	1,781,420 / 40.7%

2.2. ACGT Content

Number/percentage of A's	150,816,037 / 29.92%
Number/percentage of C's	99,389,298 / 19.72%
Number/percentage of T's	150,559,380 / 29.87%
Number/percentage of G's	103,263,154 / 20.49%
Number/percentage of N's	6,508 / 0%

GC Percentage	40.21%

2.3. Coverage

Mean	0.1629
Standard Deviation	2.4393

2.4. Mapping Quality

Mean Mapping Quality	52.68

2.5. Insert size

Mean	1,130,540.06
Standard Deviation	10,216,734.03
P25/Median/P75	145 / 202 / 292

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	5,145,953
Insertions	51,023
Mapped reads with at least one insertion	1.16%
Deletions	124,712
Mapped reads with at least one deletion	2.86%
Homopolymer indels	42.15%

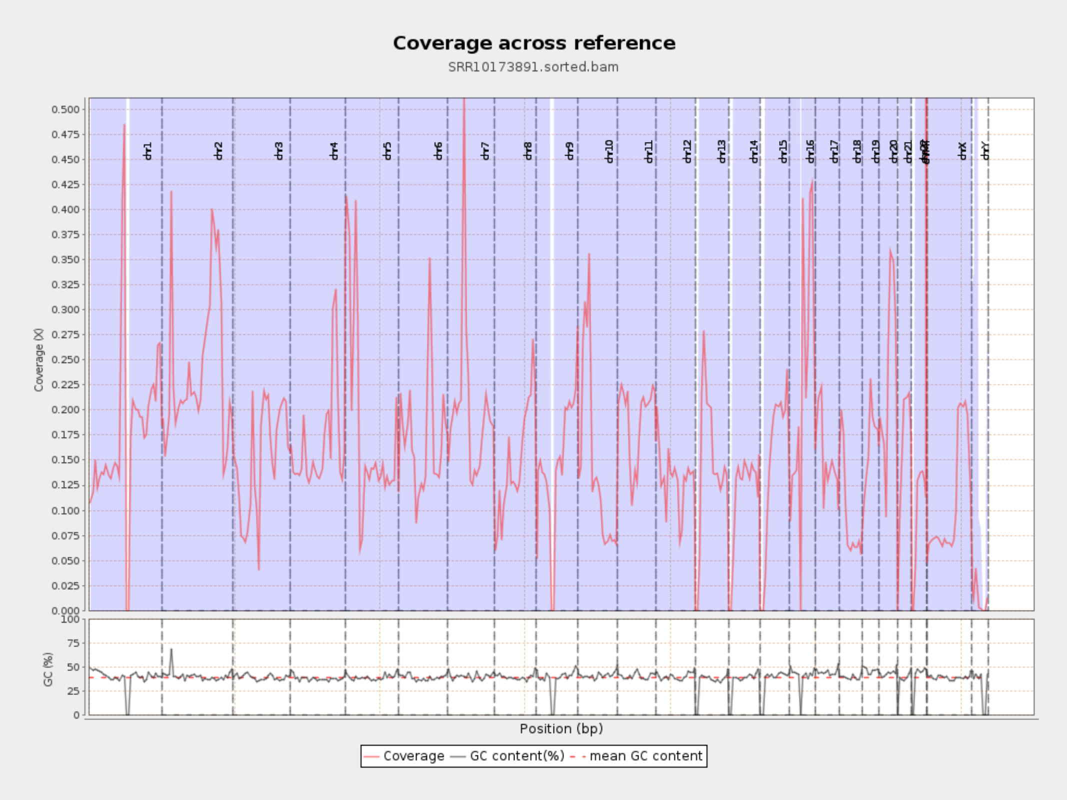
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	44302910	0.1777	2.1327
chr2	243199373	58619349	0.241	7.0397
chr3	198022430	29713715	0.1501	1.1965
chr4	191154276	31499259	0.1648	1.4169
chr5	180915260	33295345	0.184	1.3195
chr6	171115067	29751596	0.1739	1.3215
chr7	159138663	32067230	0.2015	2.113
chr8	146364022	21851586	0.1493	1.292
chr9	141213431	20556604	0.1456	1.2774
chr10	135534747	19808756	0.1462	2.0095
chr11	135006516	25632409	0.1899	1.3498
chr12	133851895	17653410	0.1319	1.1048
chr13	115169878	16478661	0.1431	1.1722
chr14	107349540	12121844	0.1129	1.0279
chr15	102531392	15046109	0.1467	1.1588
chr16	90354753	20511582	0.227	1.932
chr17	81195210	12355272	0.1522	1.2597
chr18	78077248	7580328	0.0971	1.5479
chr19	59128983	9762812	0.1651	1.8661
chr20	63025520	14953266	0.2373	1.4896
chr21	48129895	7659695	0.1591	1.2354
chr22	51304566	4682706	0.0913	0.8848
chrMT	16571	1051615	63.4612	51.7167
chrX	155270560	16724855	0.1077	1.0041

chrY	59373566	649410	0.0109	0.5257

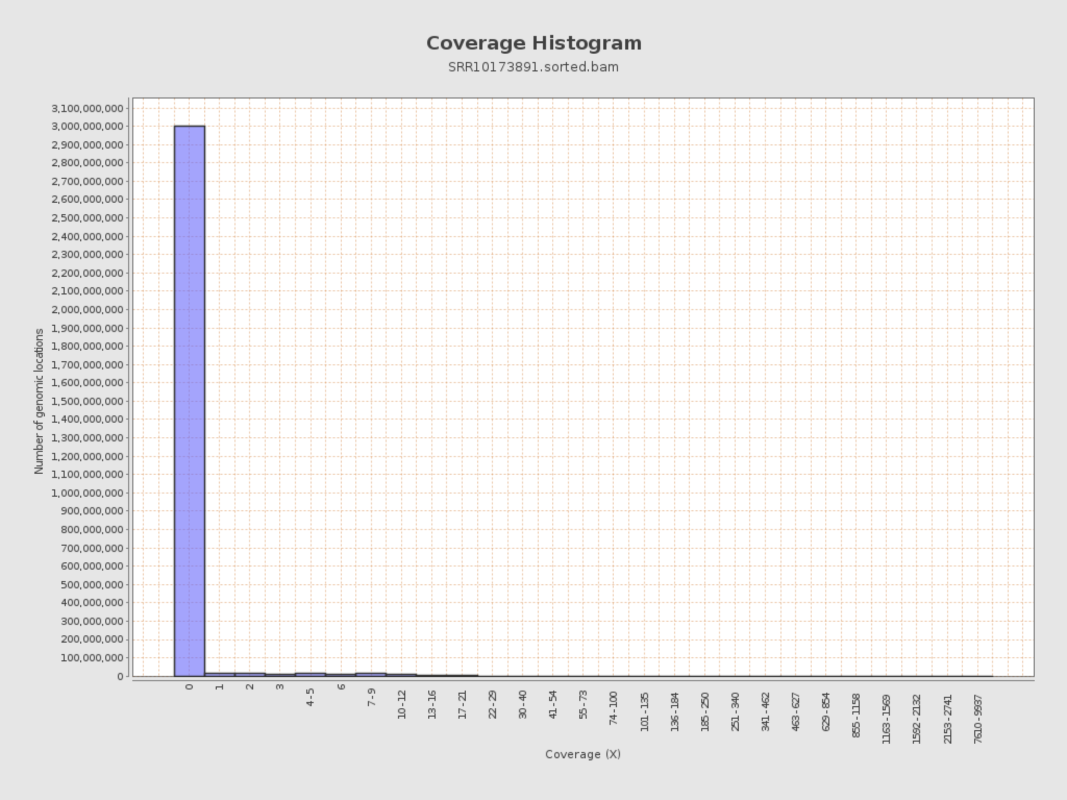
3. Results : Coverage across reference



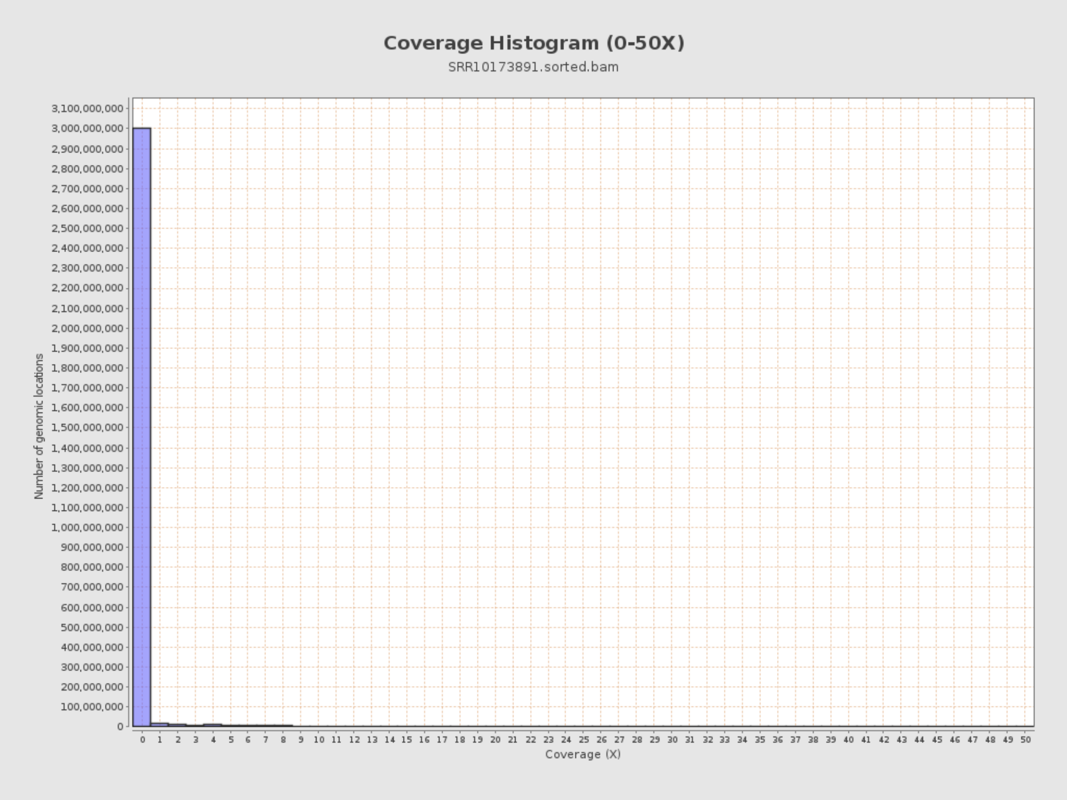
Coverage across reference

SRR10173891.sorted.bam

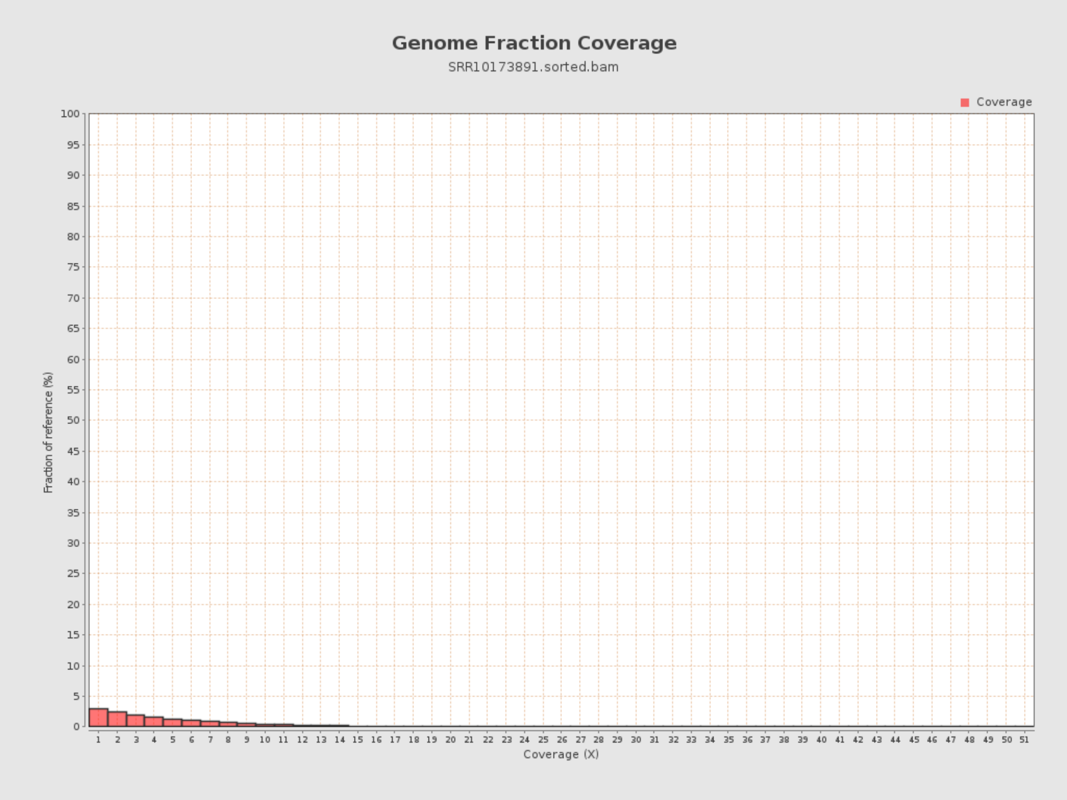
4. Results : Coverage Histogram



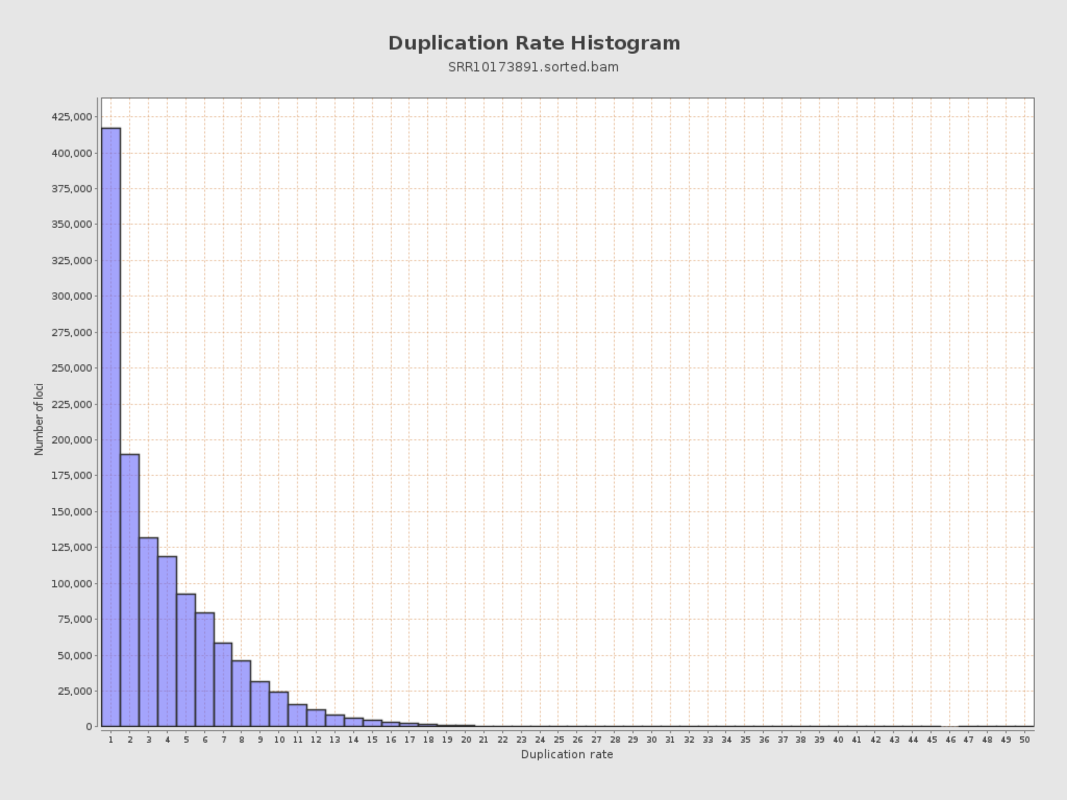
5. Results : Coverage Histogram (0-50X)



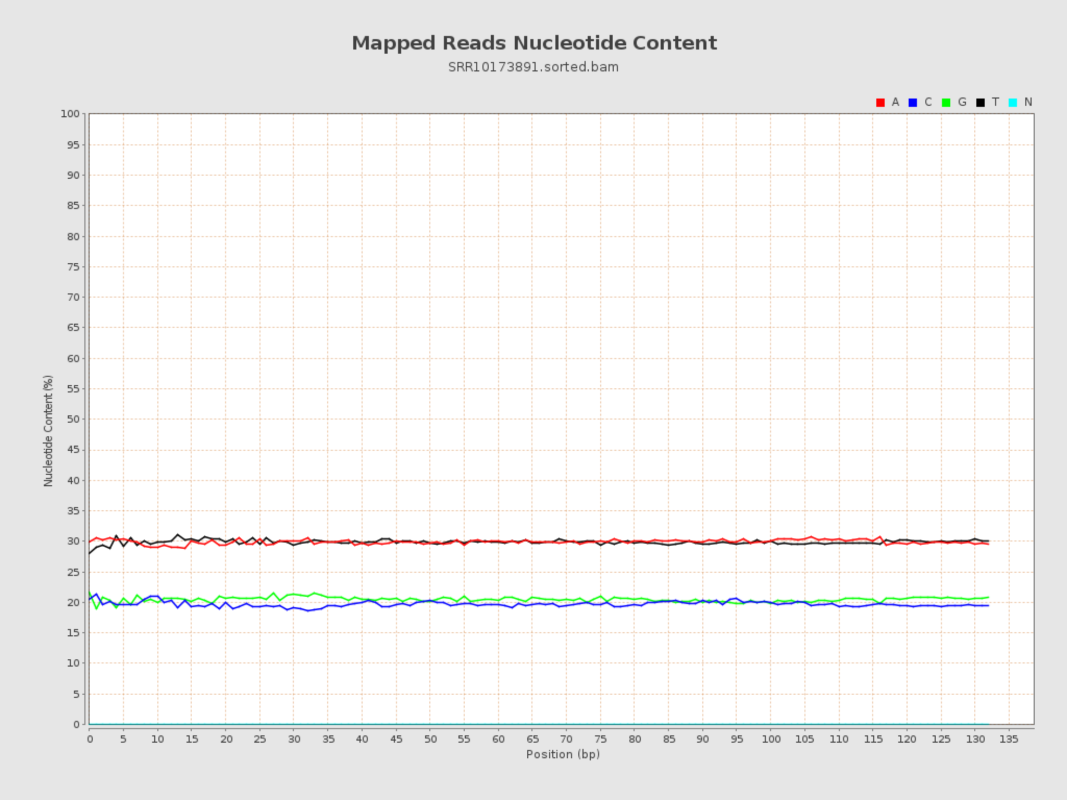
6. Results : Genome Fraction Coverage



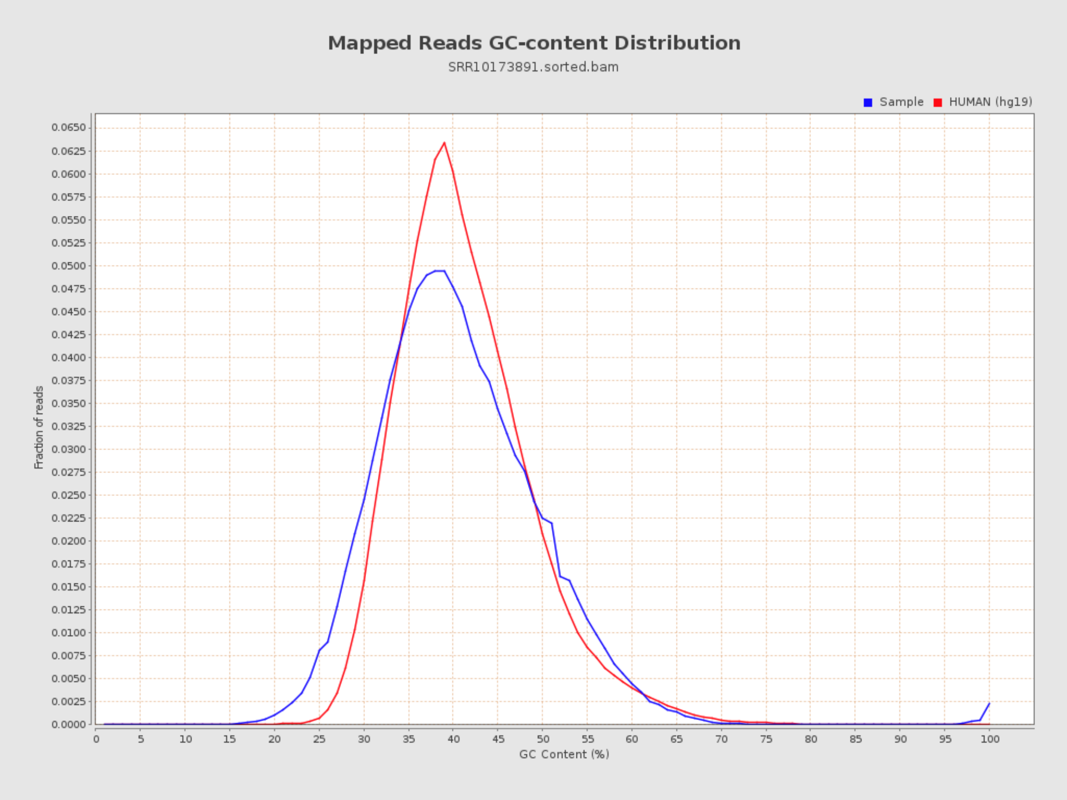
7. Results : Duplication Rate Histogram



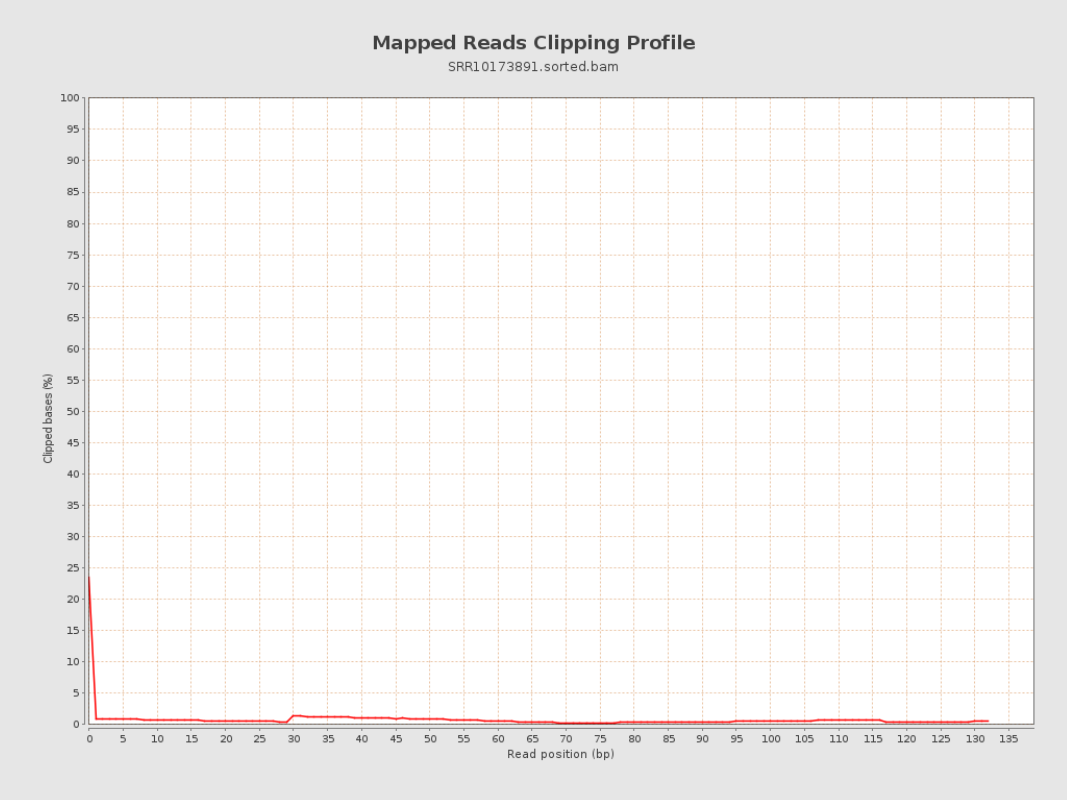
8. Results : Mapped Reads Nucleotide Content



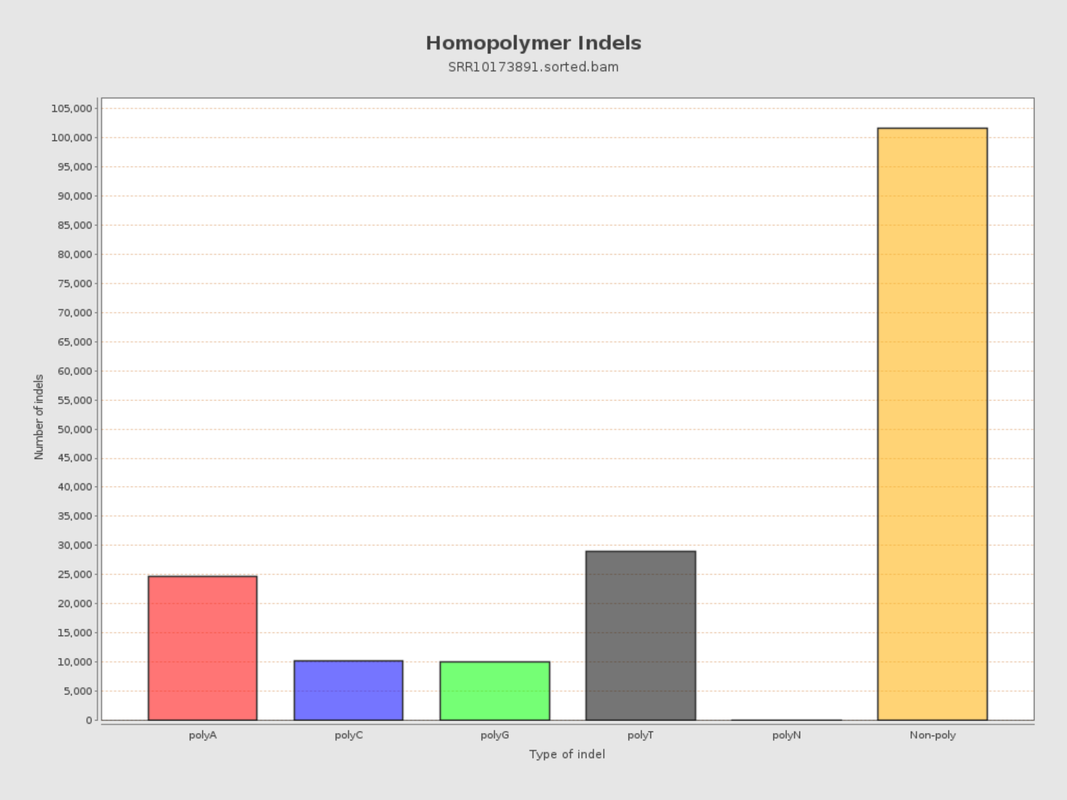
9. Results : Mapped Reads GC-content Distribution



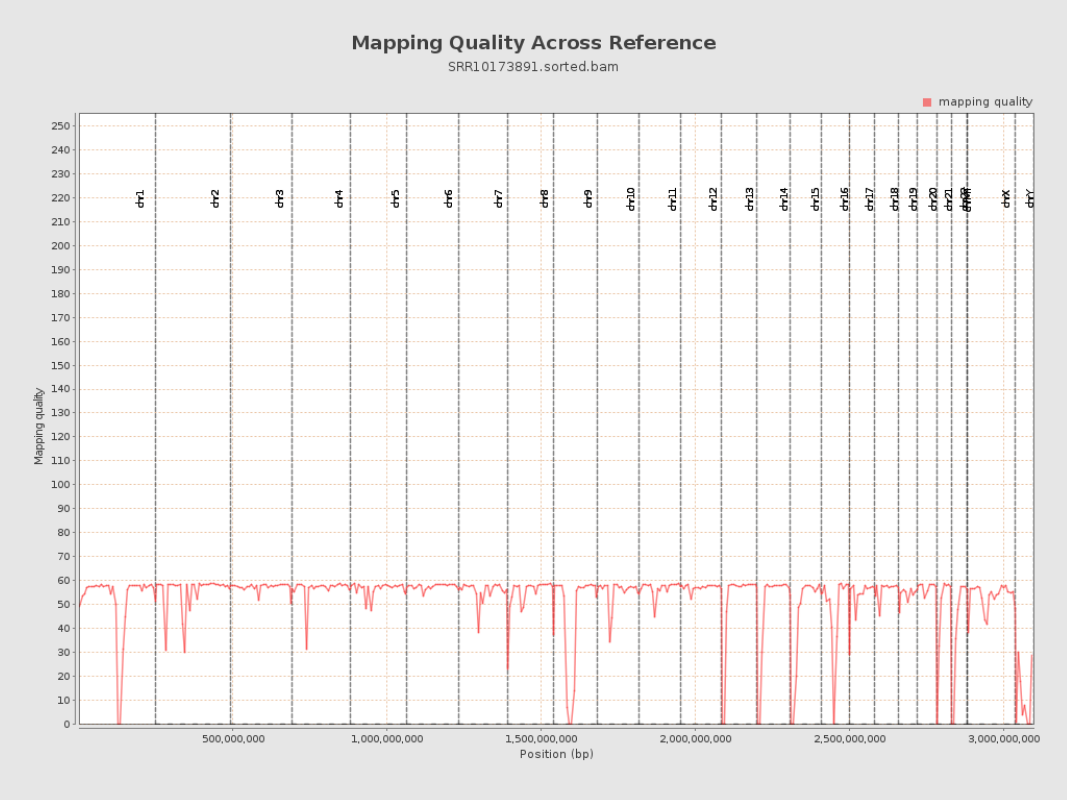
10. Results : Mapped Reads Clipping Profile



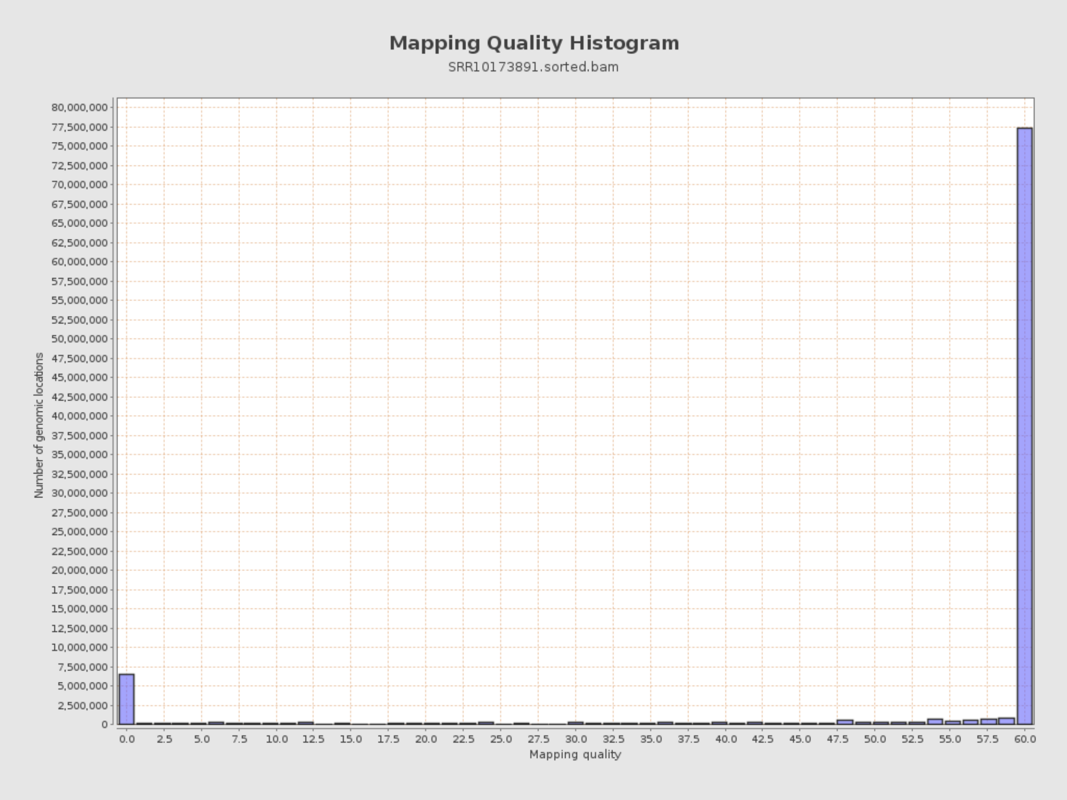
11. Results : Homopolymer Indels



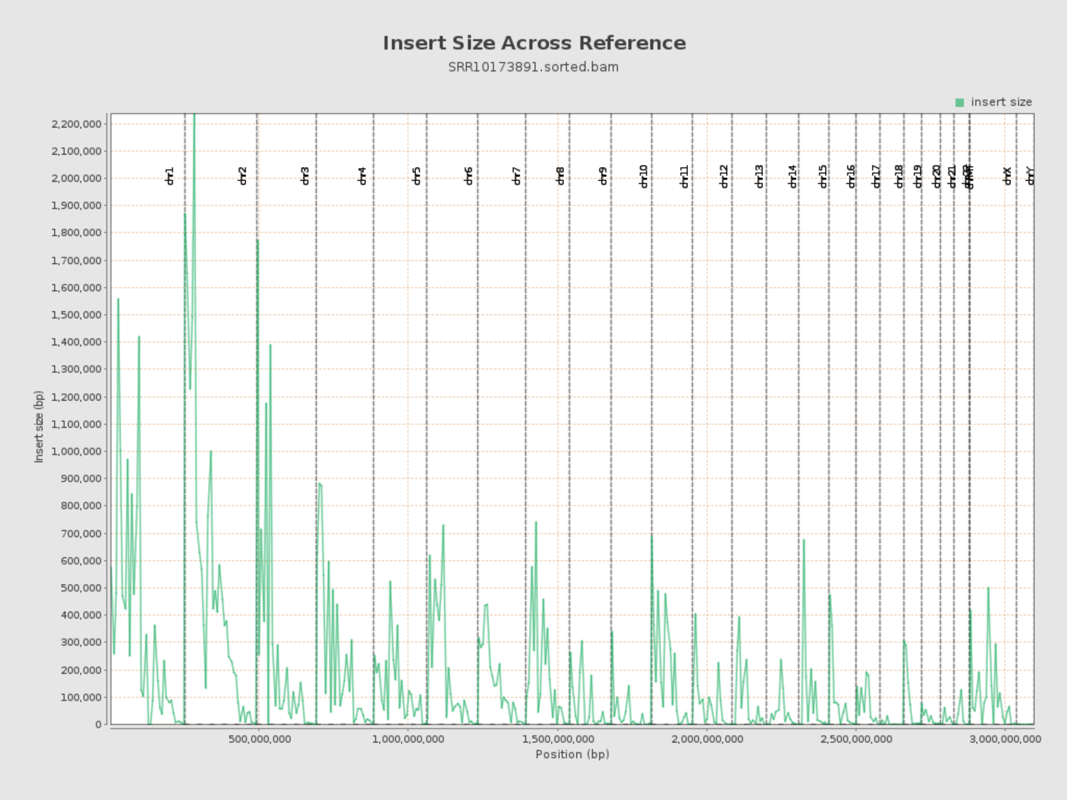
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram