Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:32:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173892.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_SRR10173892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173892_1.fastq.gz SRR10173892_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:32:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,355,070
Mapped reads	2,296,145 / 97.5%
Unmapped reads	58,925 / 2.5%
Mapped paired reads	2,296,145 / 97.5%
Mapped reads, first in pair	1,149,278 / 48.8%
Mapped reads, second in pair	1,146,867 / 48.7%
Mapped reads, both in pair	2,255,212 / 95.76%
Mapped reads, singletons	40,933 / 1.74%
Secondary alignments	0
Supplementary alignments	236,894 / 10.06%
Read min/max/mean length	30 / 133 / 128.58
Duplicated reads (estimated)	1,795,565 / 76.24%
Duplication rate	64.17%
Clipped reads	915,395 / 38.87%

2.2. ACGT Content

Number/percentage of A's	82,098,370 / 30.13%
Number/percentage of C's	53,189,089 / 19.52%
Number/percentage of T's	81,945,935 / 30.07%
Number/percentage of G's	55,242,360 / 20.27%
Number/percentage of N's	2,870 / 0%

GC Percentage	39.79%

2.3. Coverage

Mean	0.0881
Standard Deviation	1.4309

2.4. Mapping Quality

Mean Mapping Quality	52.67

2.5. Insert size

Mean	1,261,038.33
Standard Deviation	10,634,607.26
P25/Median/P75	149 / 207 / 292

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	2,798,925
Insertions	28,455
Mapped reads with at least one insertion	1.2%
Deletions	59,388
Mapped reads with at least one deletion	2.53%
Homopolymer indels	42.63%

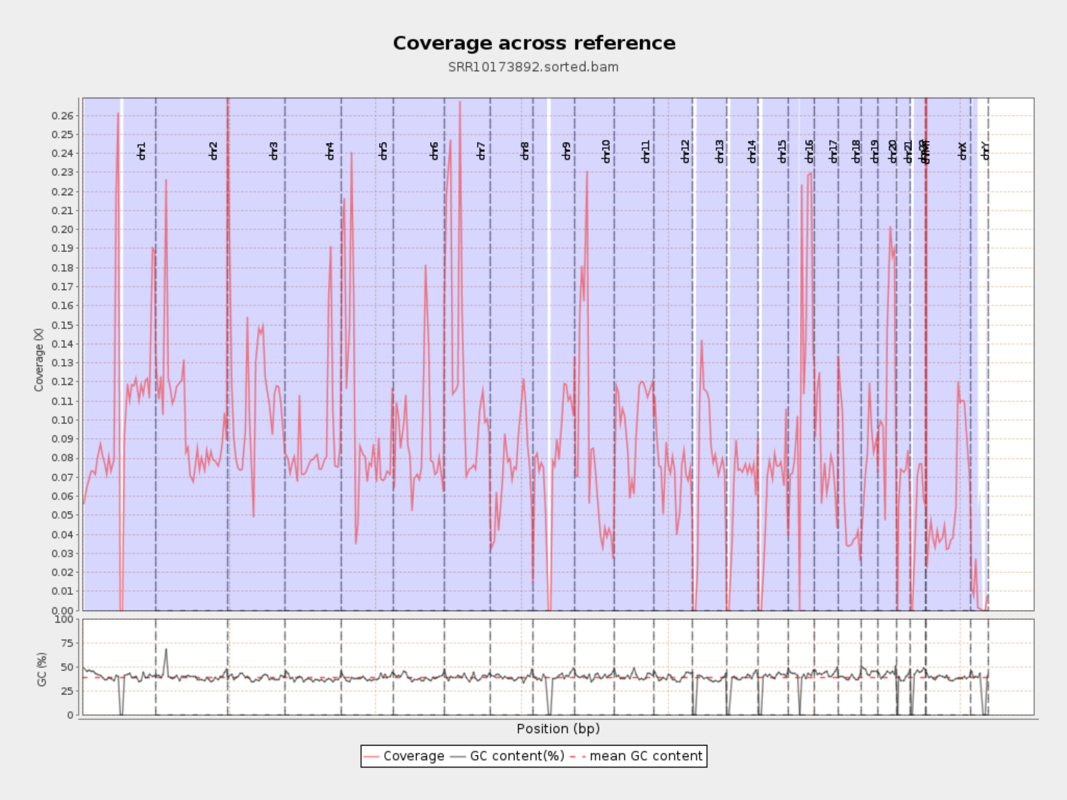
2.7. Chromosome stats

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

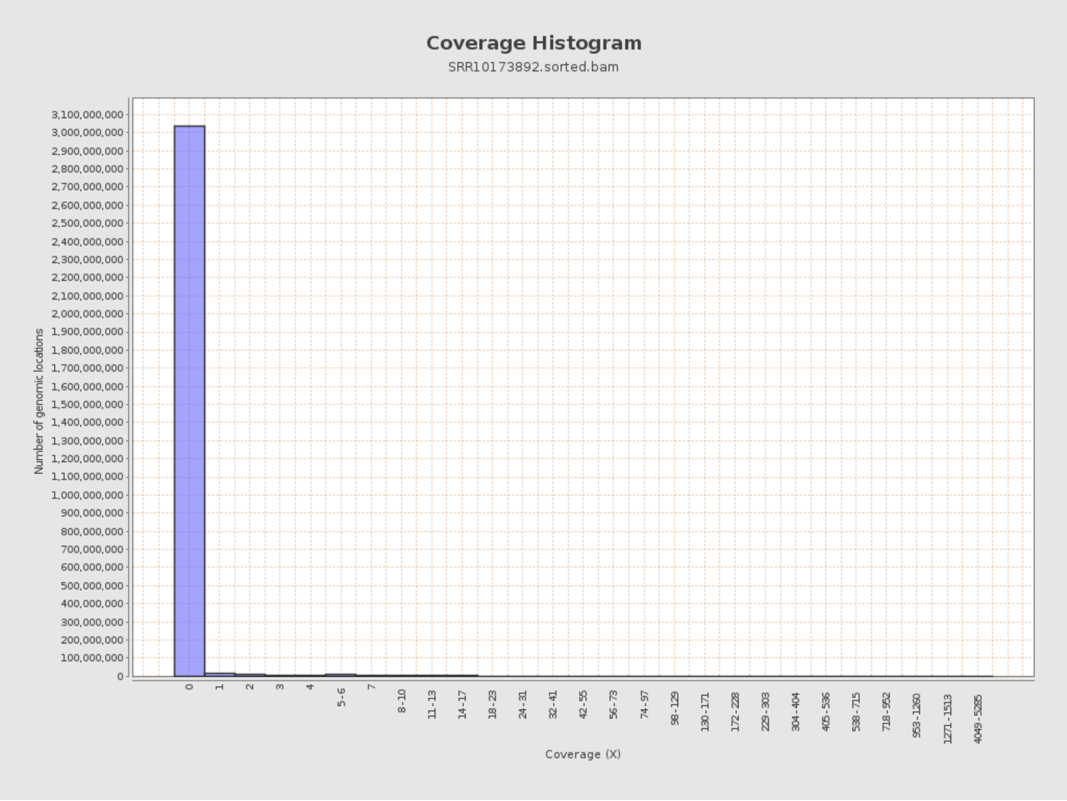
		bases	coverage	deviation
chr1	249250621	25578611	0.1026	1.3467
chr2	243199373	24102603	0.0991	3.799
chr3	198022430	22363930	0.1129	0.9807
chr4	191154276	16773777	0.0877	0.9327
chr5	180915260	18496558	0.1022	0.9322
chr6	171115067	15257650	0.0892	0.8814
chr7	159138663	20497246	0.1288	1.241
chr8	146364022	10893974	0.0744	0.8555
chr9	141213431	11214538	0.0794	0.8926
chr10	135534747	11419607	0.0843	1.4111
chr11	135006516	13562395	0.1005	0.9272
chr12	133851895	9836711	0.0735	0.7878
chr13	115169878	9061953	0.0787	0.8189
chr14	107349540	6664618	0.0621	0.7271
chr15	102531392	6059745	0.0591	0.6914
chr16	90354753	11047537	0.1223	1.2533
chr17	81195210	6476458	0.0798	0.8465
chr18	78077248	4459837	0.0571	1.0361
chr19	59128983	4870942	0.0824	1.2195
chr20	63025520	8365144	0.1327	1.0397
chr21	48129895	3076294	0.0639	0.7496
chr22	51304566	2499124	0.0487	0.6059
chrMT	16571	664851	40.1214	33.7607
chrX	155270560	8971334	0.0578	0.689

chrY	59373566	408623	0.0069	0.3195

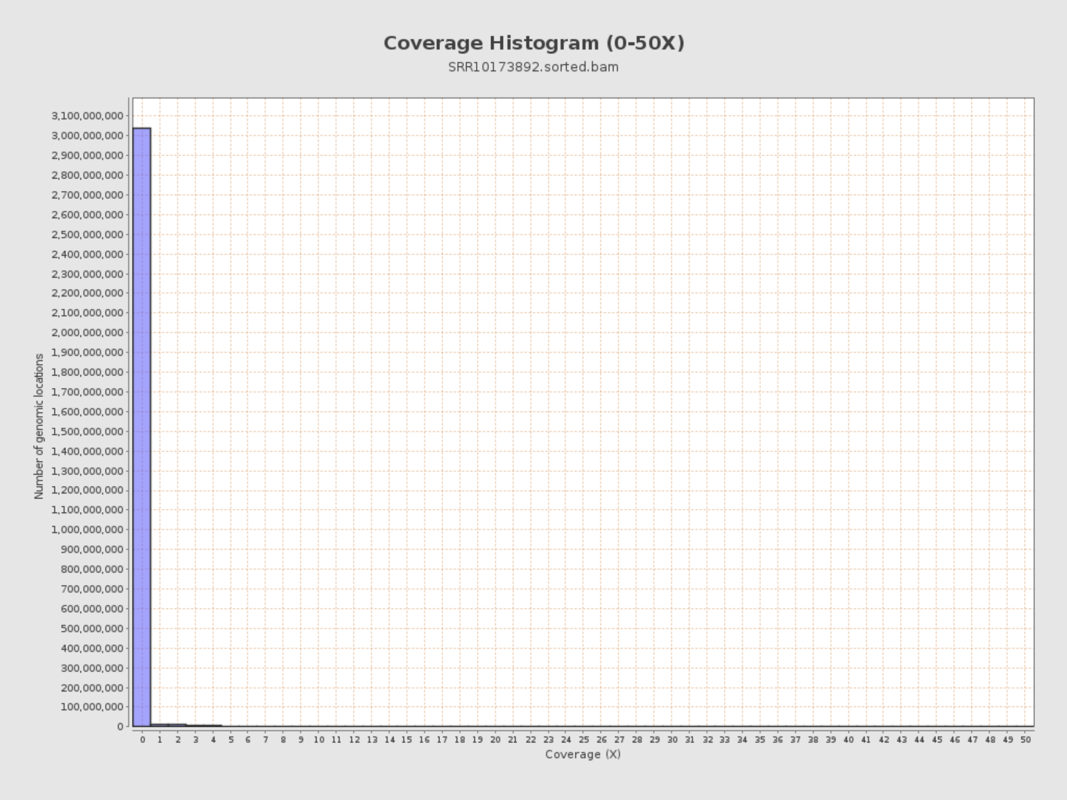
3. Results : Coverage across reference



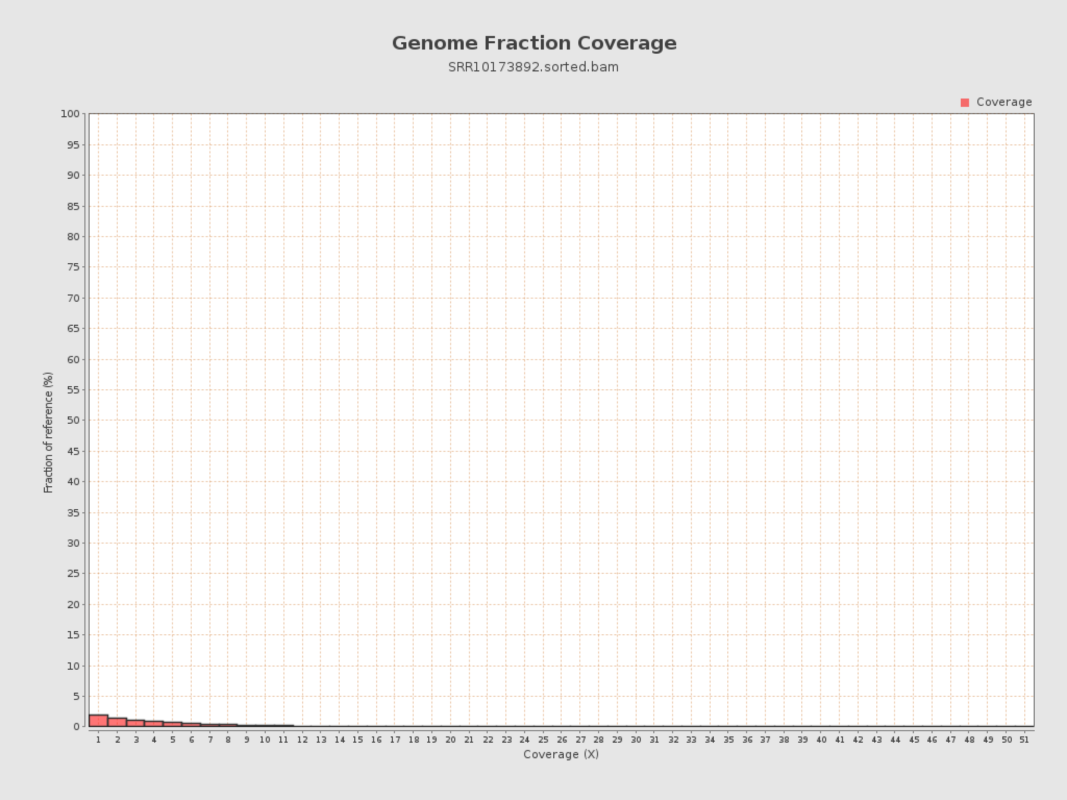
4. Results : Coverage Histogram



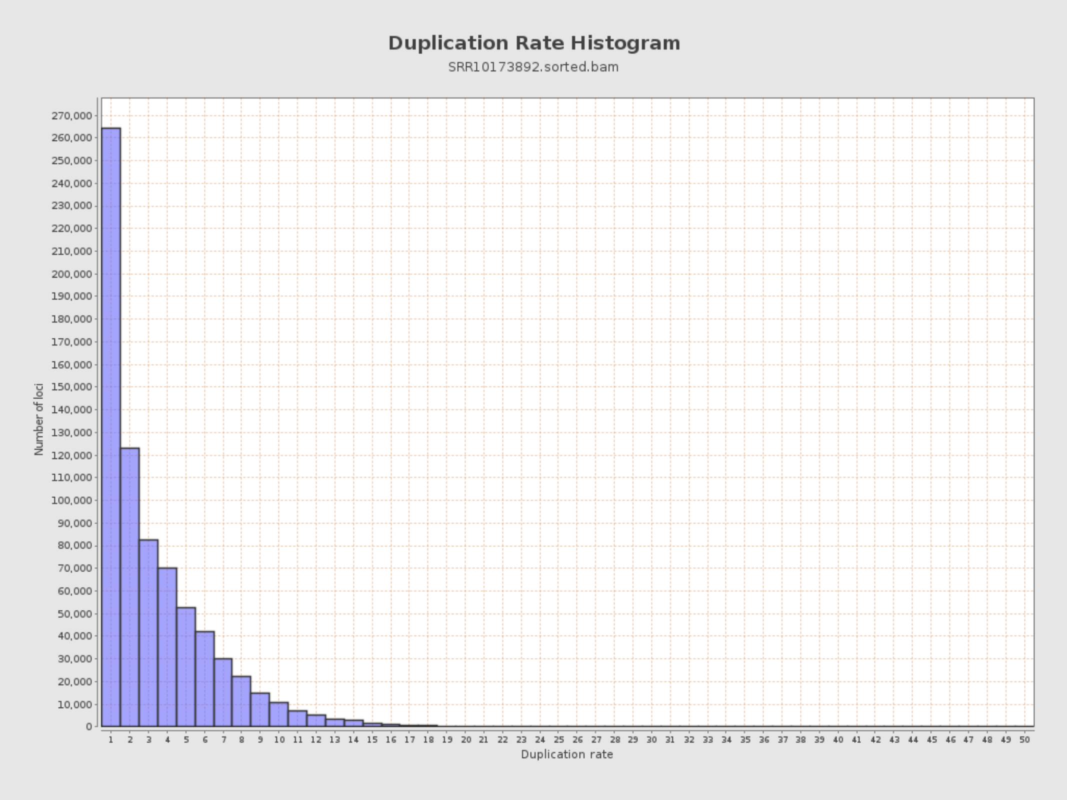
5. Results : Coverage Histogram (0-50X)



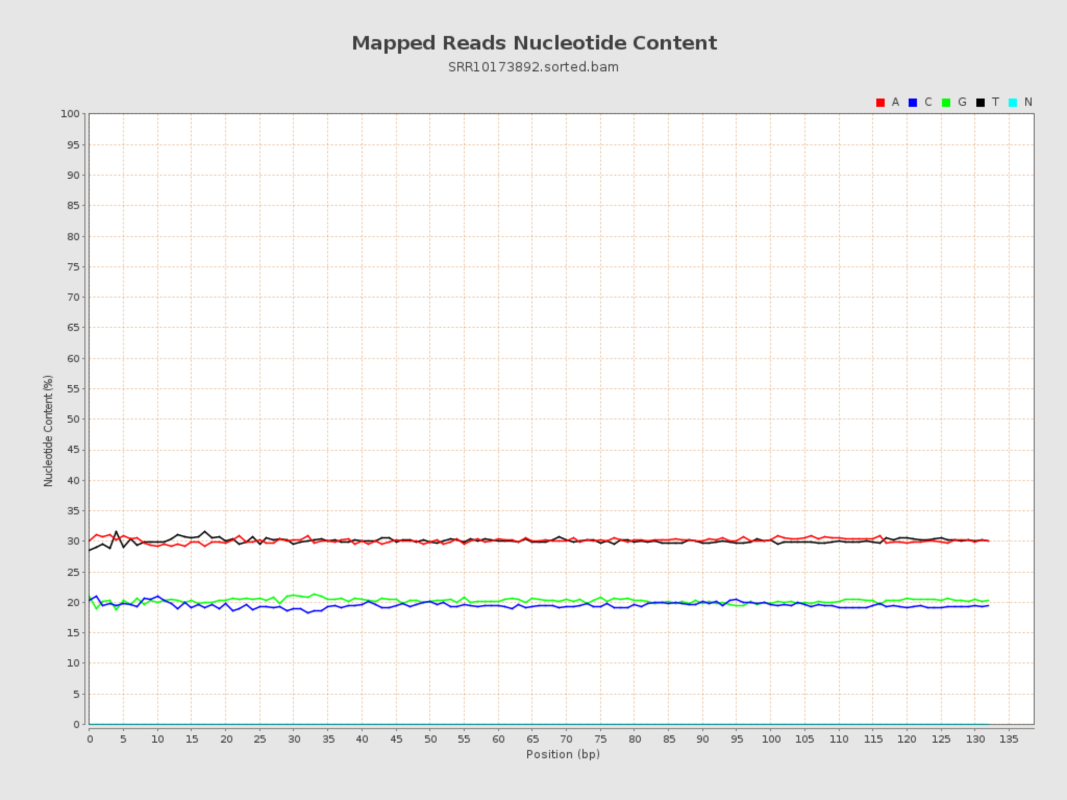
6. Results : Genome Fraction Coverage



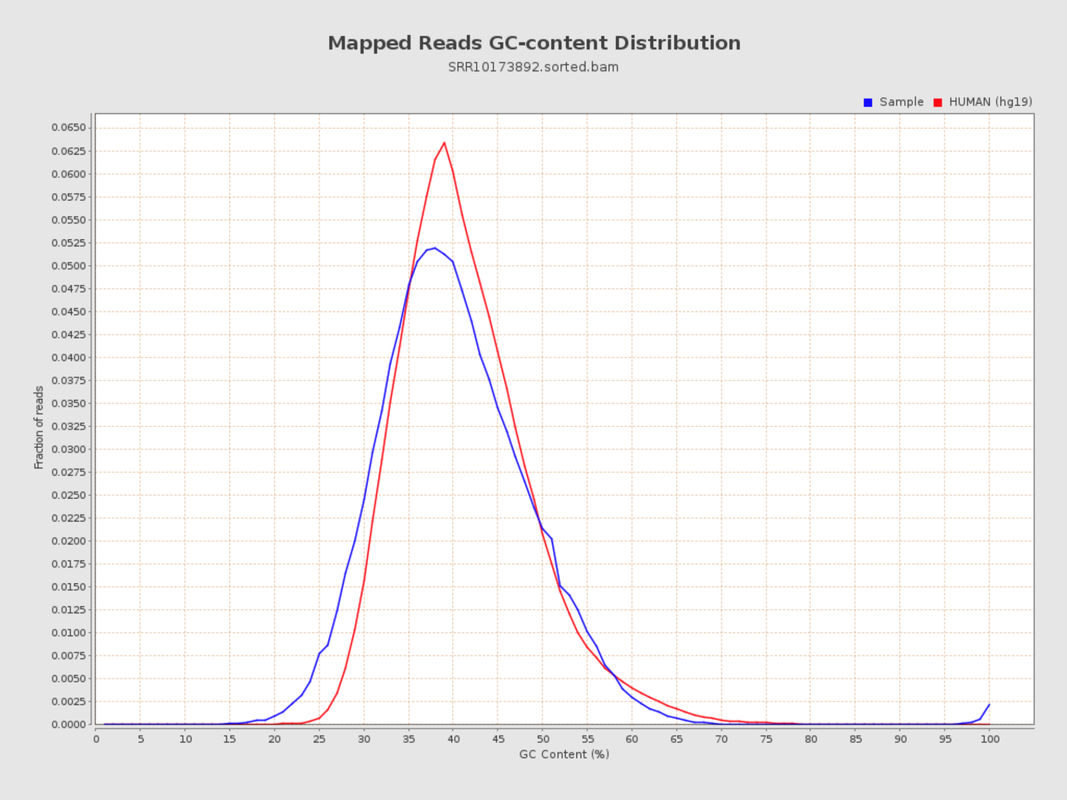
7. Results : Duplication Rate Histogram



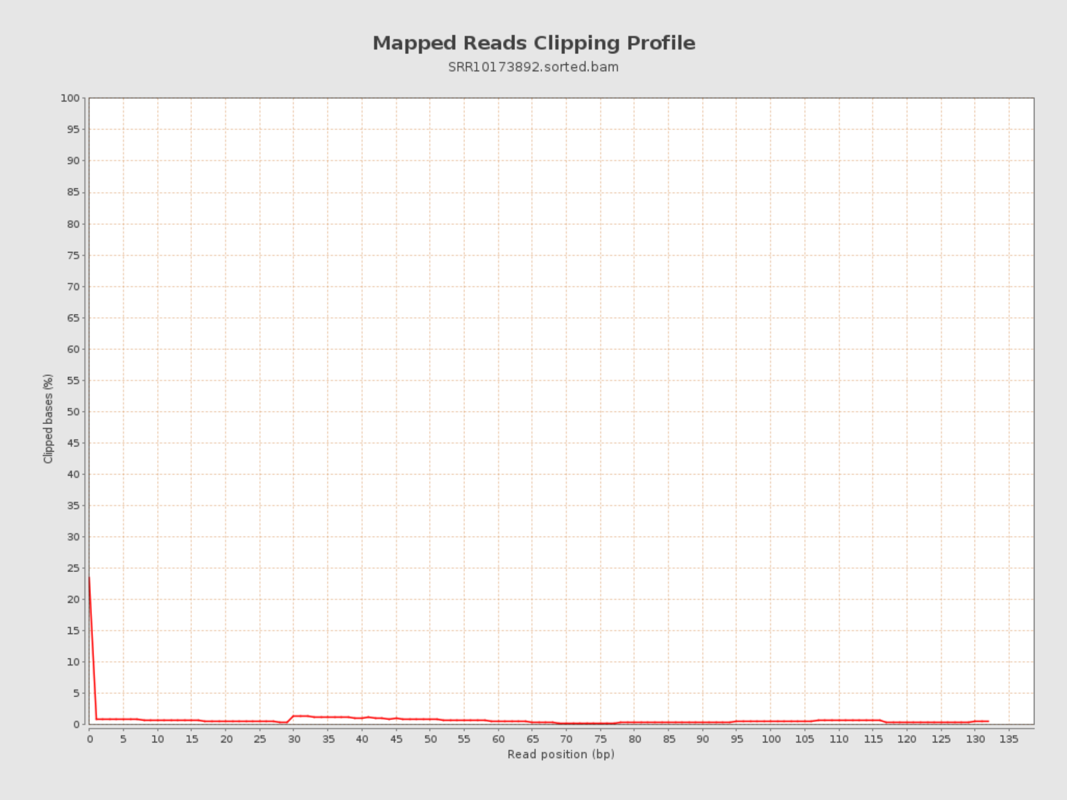
8. Results : Mapped Reads Nucleotide Content



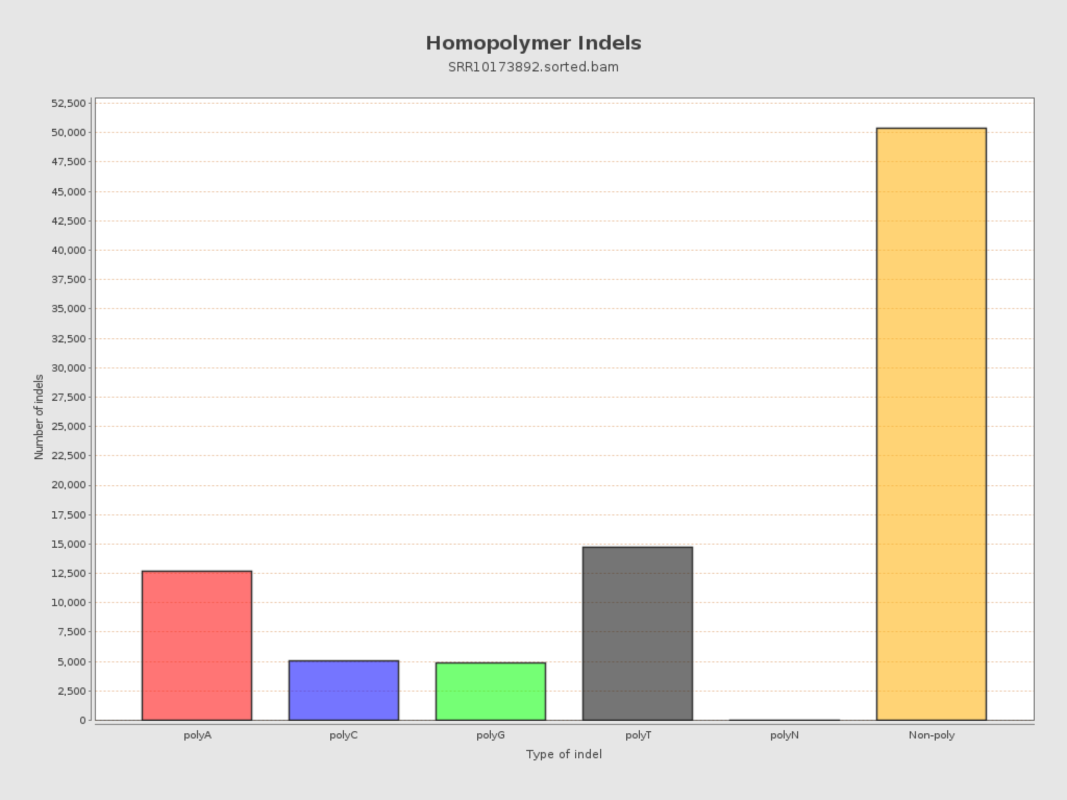
9. Results : Mapped Reads GC-content Distribution



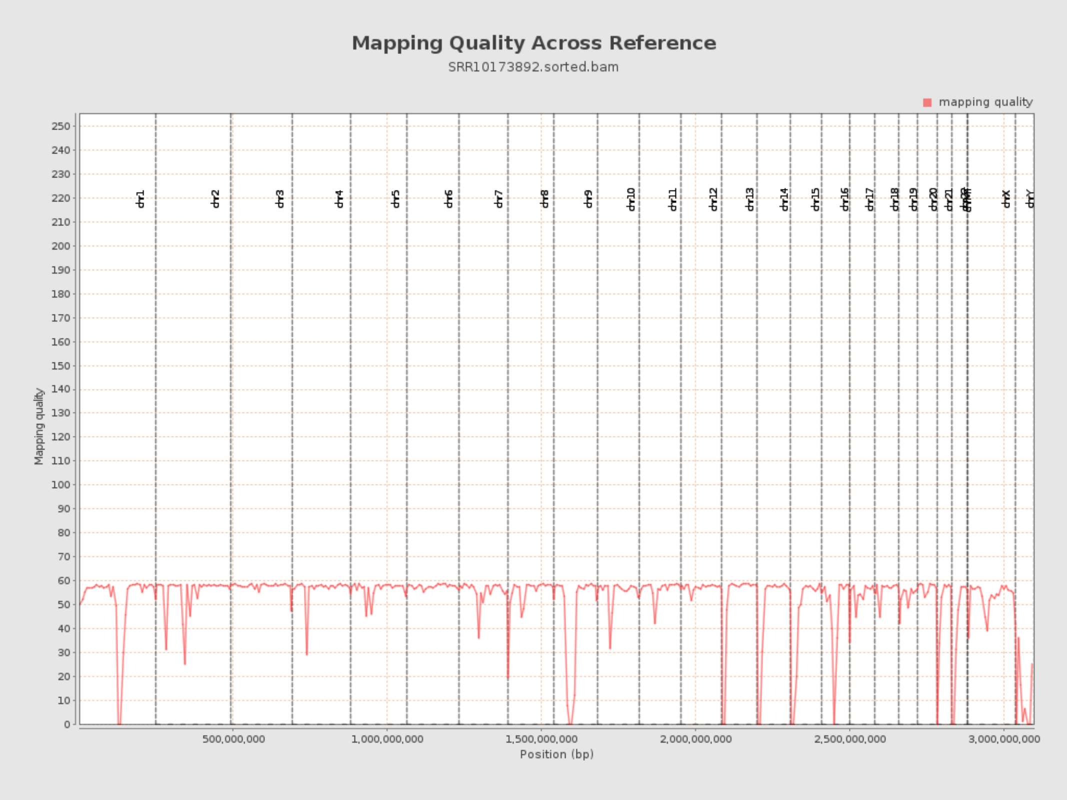
10. Results : Mapped Reads Clipping Profile



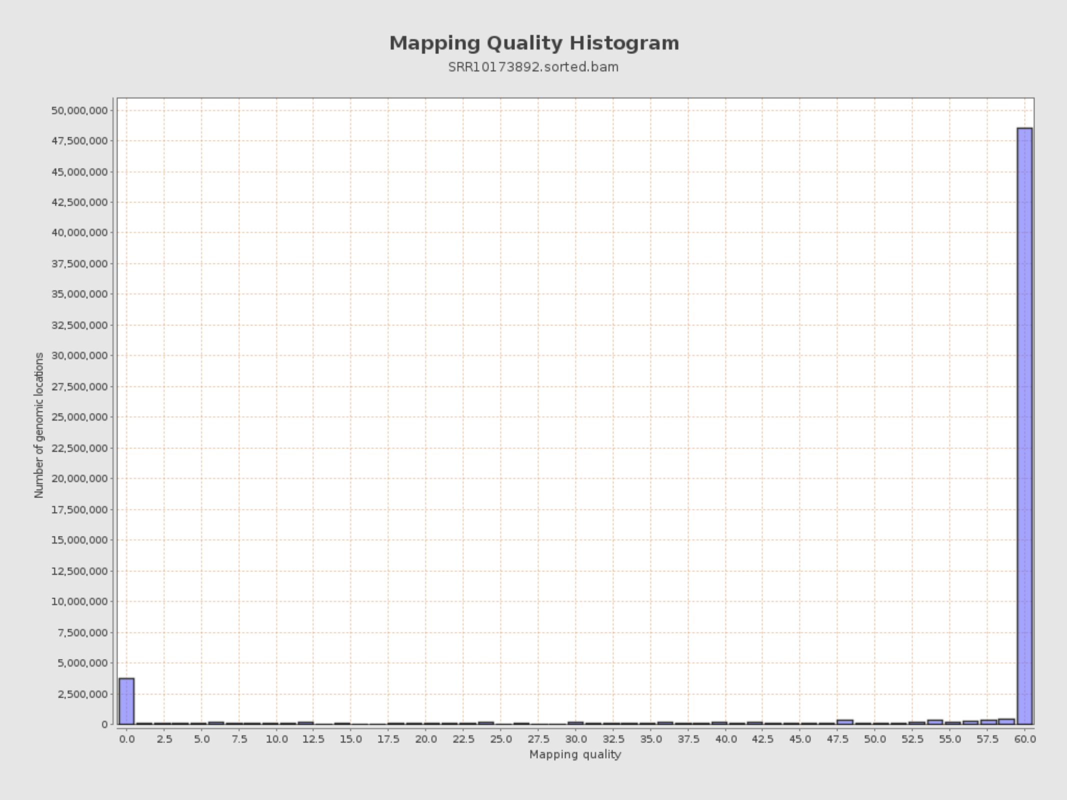
11. Results : Homopolymer Indels



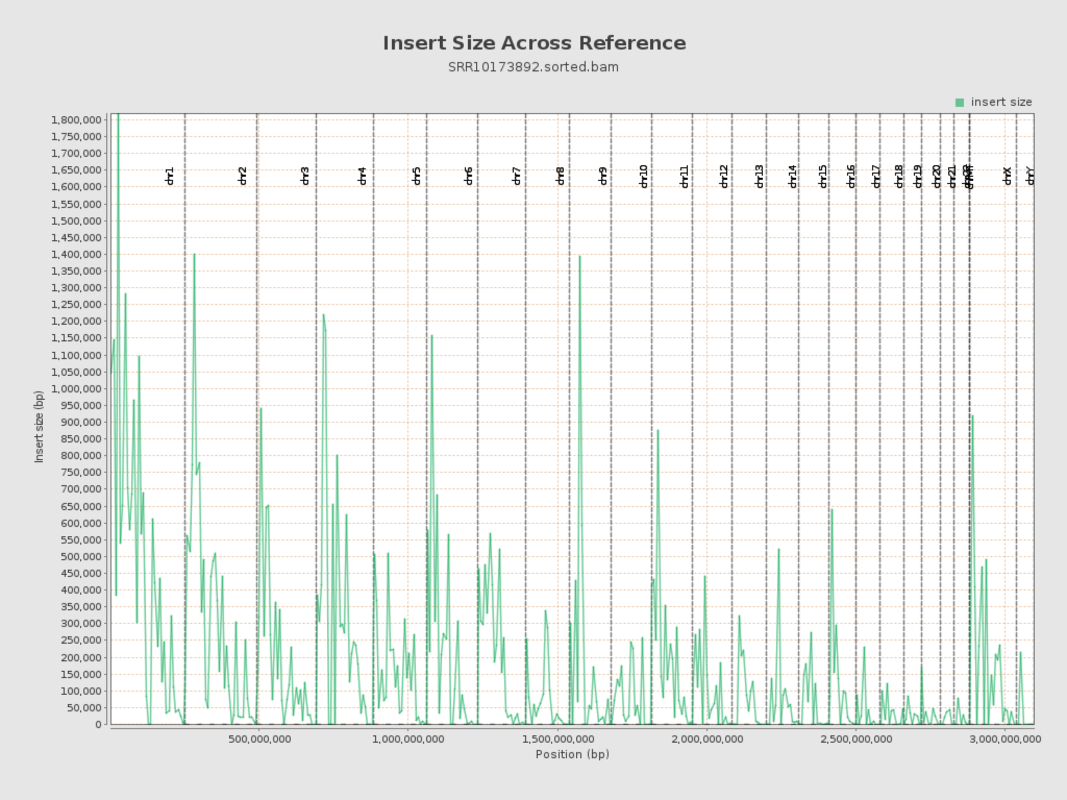
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram