Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 16:31:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617373.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_SRR617373 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617373_1.fastq.gz SRR617373_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 16:31:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617373.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,678,552
Mapped reads	1,473,369 / 87.78%
Unmapped reads	205,183 / 12.22%
Mapped paired reads	1,473,369 / 87.78%
Mapped reads, first in pair	751,382 / 44.76%
Mapped reads, second in pair	721,987 / 43.01%
Mapped reads, both in pair	1,425,374 / 84.92%
Mapped reads, singletons	47,995 / 2.86%
Secondary alignments	0
Supplementary alignments	3,953 / 0.24%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	30,118 / 1.79%
Duplication rate	0.96%
Clipped reads	154,890 / 9.23%

2.2. ACGT Content

Number/percentage of A's	43,703,842 / 30.41%
Number/percentage of C's	28,398,751 / 19.76%
Number/percentage of T's	42,932,101 / 29.87%
Number/percentage of G's	28,638,734 / 19.93%
Number/percentage of N's	40,884 / 0.03%

GC Percentage	39.69%

2.3. Coverage

Mean	0.0464
Standard Deviation	0.5281

2.4. Mapping Quality

Mean Mapping Quality	53.2

2.5. Insert size

Mean	43,118.96
Standard Deviation	1,958,603.97
P25/Median/P75	168 / 204 / 260

2.6. Mismatches and indels

General error rate	1.71%
Mismatches	2,422,176
Insertions	14,409
Mapped reads with at least one insertion	0.95%
Deletions	17,245
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.1%

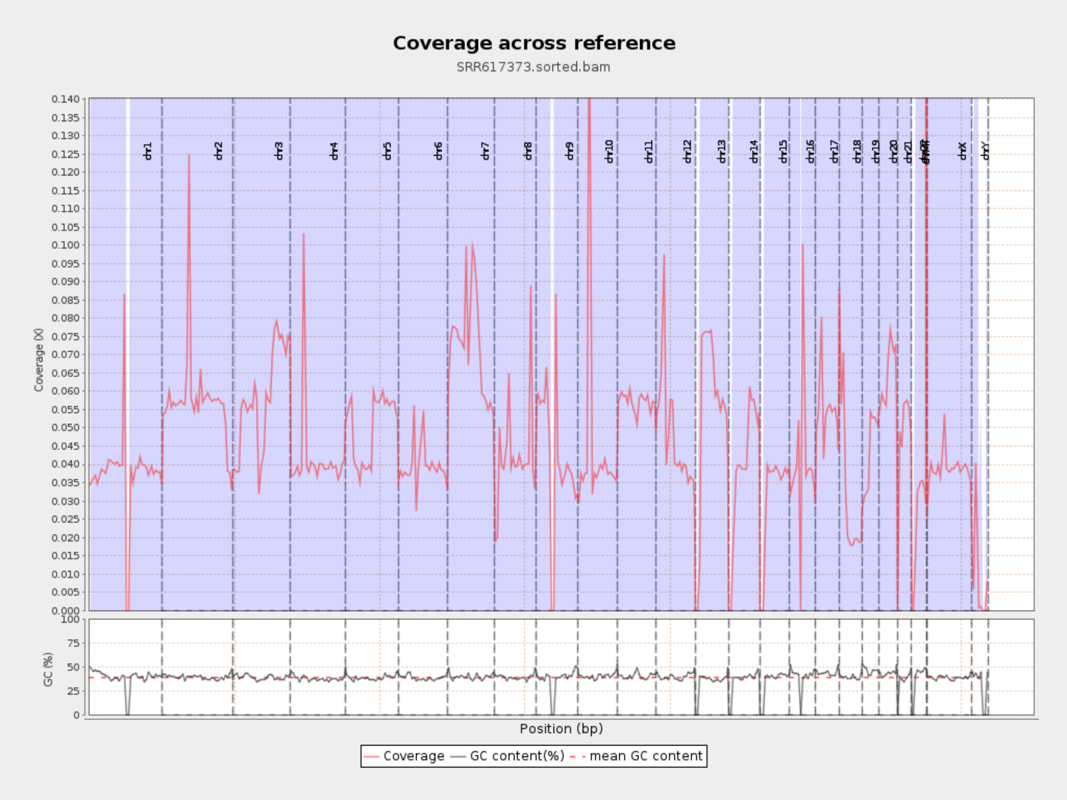
2.7. Chromosome stats

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

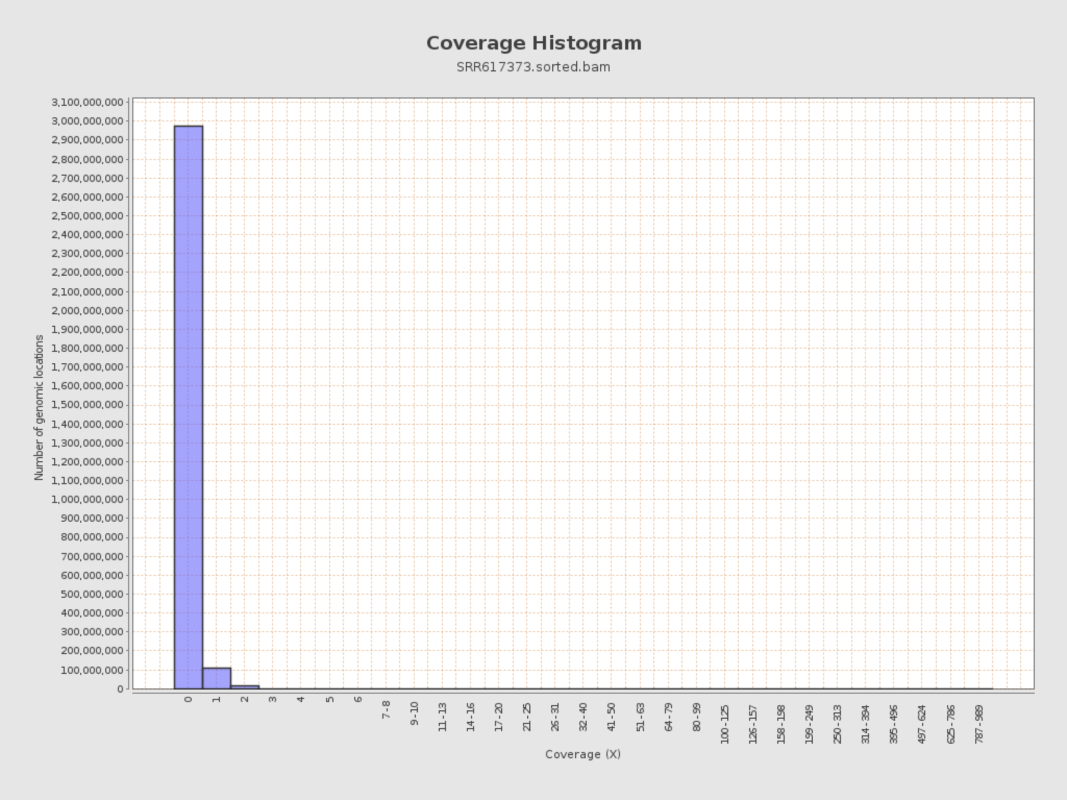
		bases	coverage	deviation
chr1	249250621	9388282	0.0377	1.0188
chr2	243199373	14069048	0.0578	0.4822
chr3	198022430	11492034	0.058	0.2633
chr4	191154276	7913682	0.0414	0.4864
chr5	180915260	9054850	0.0501	0.2454
chr6	171115067	6809209	0.0398	0.2748
chr7	159138663	11673043	0.0734	0.6153
chr8	146364022	6172511	0.0422	0.4203
chr9	141213431	5988852	0.0424	0.7135
chr10	135534747	6046046	0.0446	1.0341
chr11	135006516	7684704	0.0569	0.3501
chr12	133851895	6409649	0.0479	0.2394
chr13	115169878	6296351	0.0547	0.2537
chr14	107349540	4174089	0.0389	0.2167
chr15	102531392	3227416	0.0315	0.193
chr16	90354753	3638679	0.0403	0.4728
chr17	81195210	4433148	0.0546	0.4387
chr18	78077248	2529717	0.0324	0.7365
chr19	59128983	2573123	0.0435	0.4832
chr20	63025520	4071181	0.0646	0.2901
chr21	48129895	2272926	0.0472	0.277
chr22	51304566	1221614	0.0238	0.1673
chrMT	16571	87889	5.3038	2.5268
chrX	155270560	6046631	0.0389	0.2557

chrY	59373566	480267	0.0081	0.3776

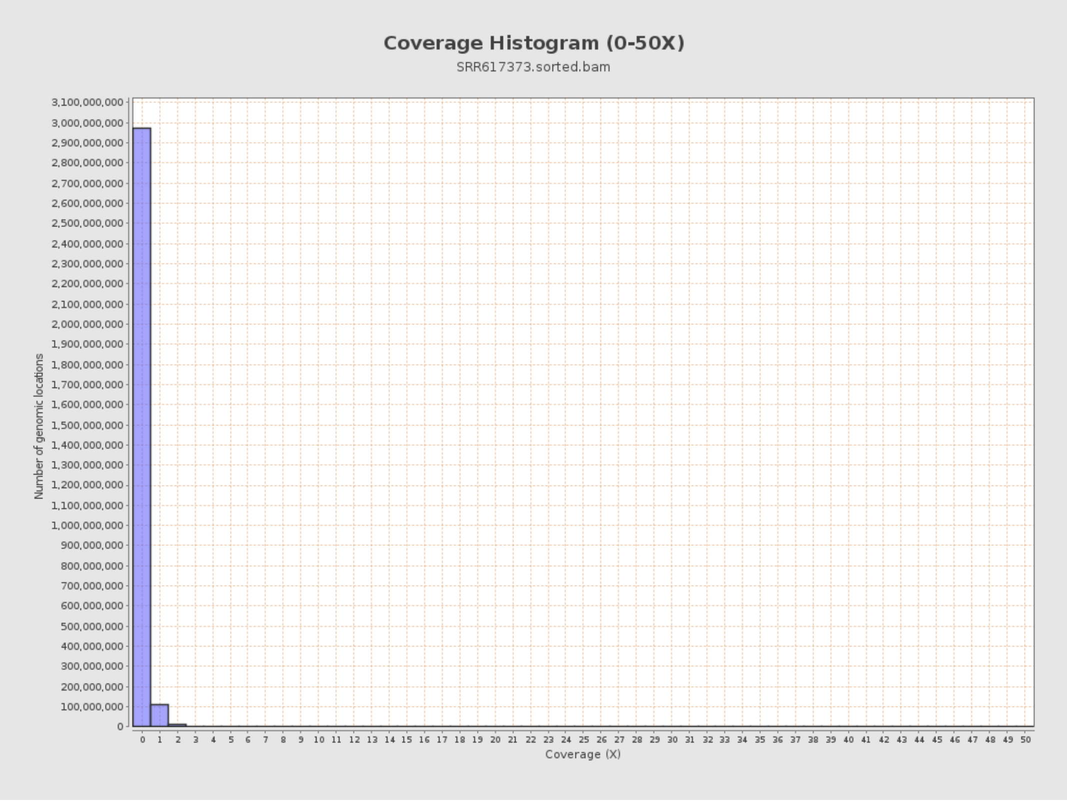
3. Results : Coverage across reference



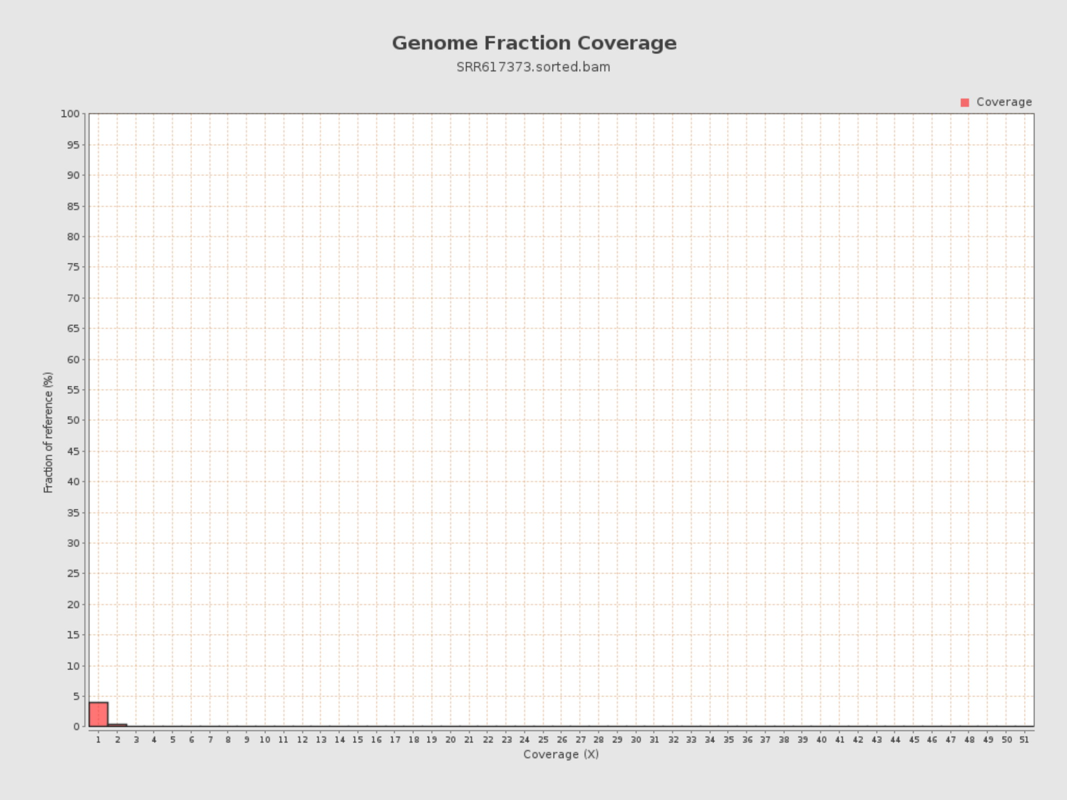
4. Results : Coverage Histogram



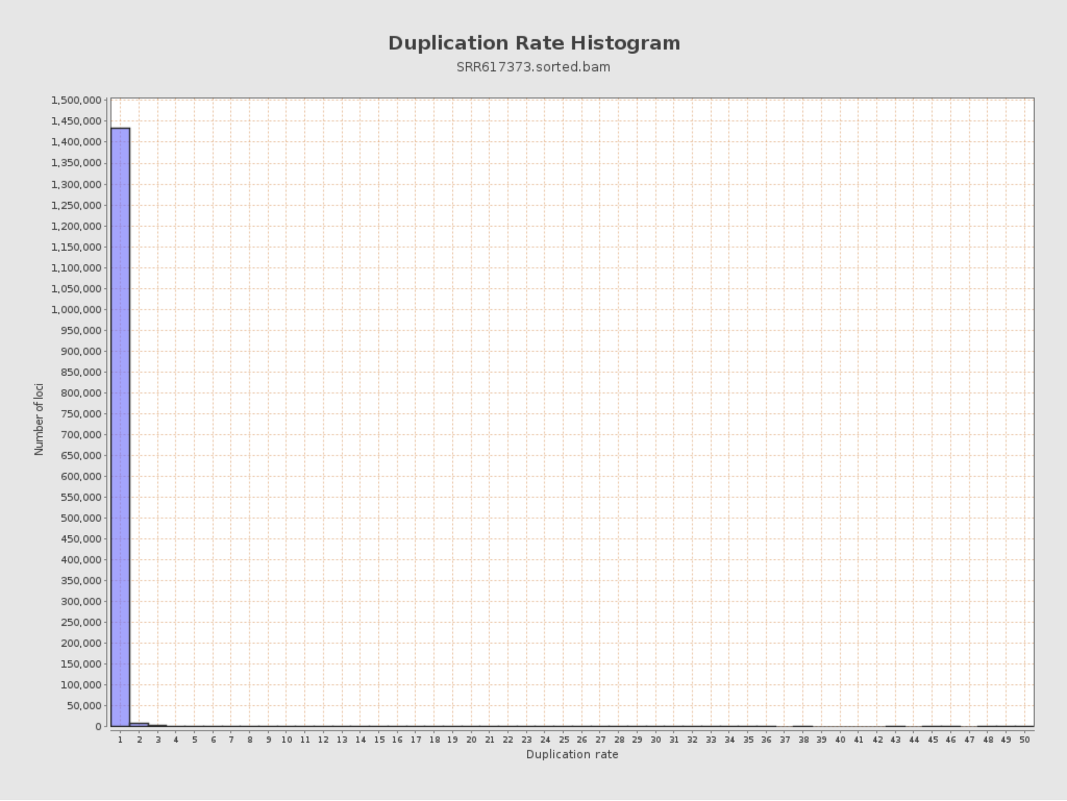
5. Results : Coverage Histogram (0-50X)



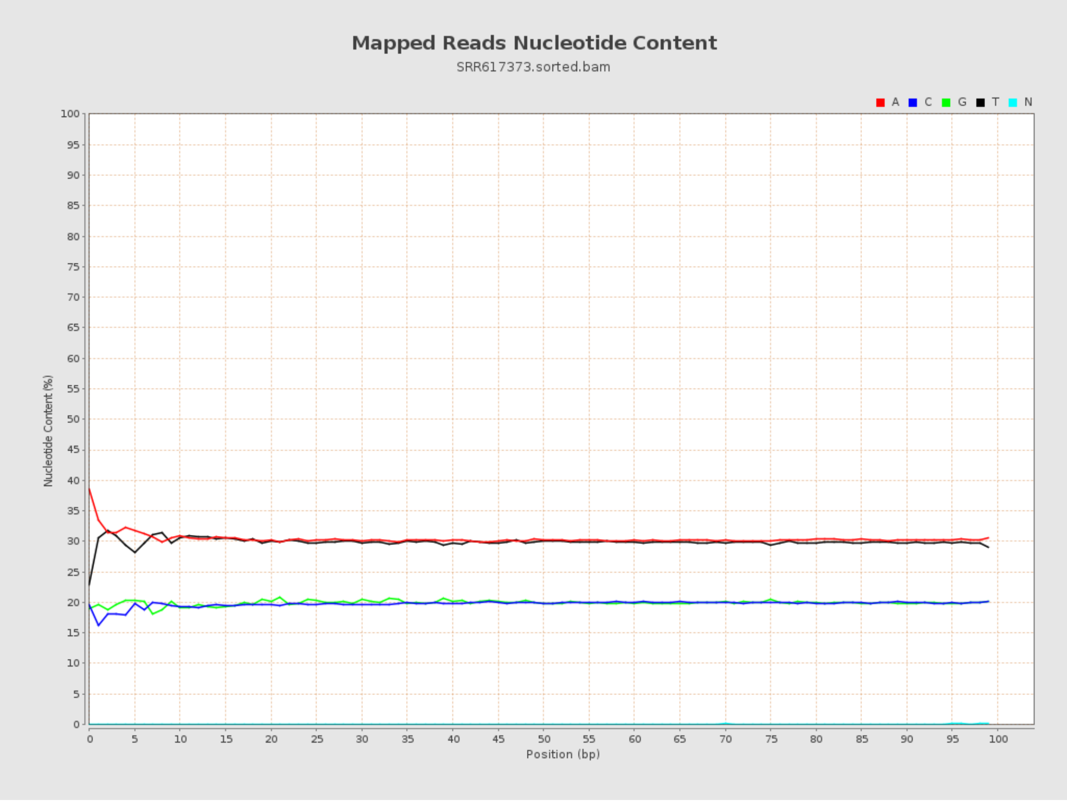
6. Results : Genome Fraction Coverage



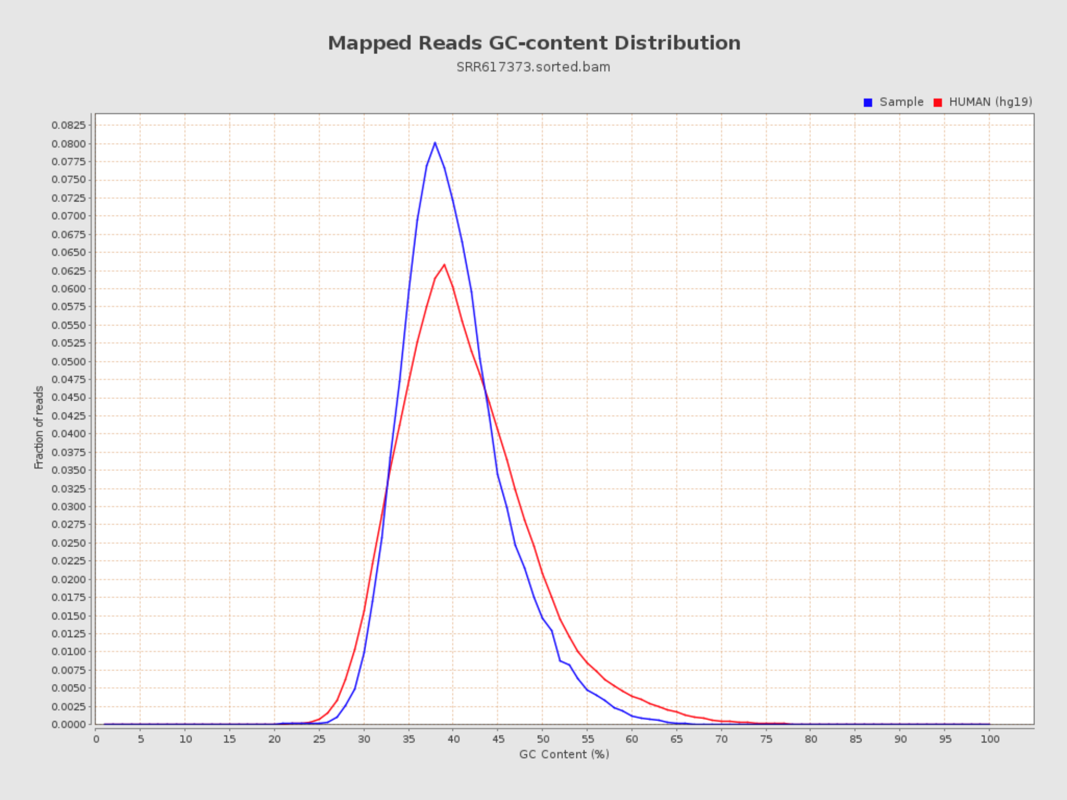
7. Results : Duplication Rate Histogram



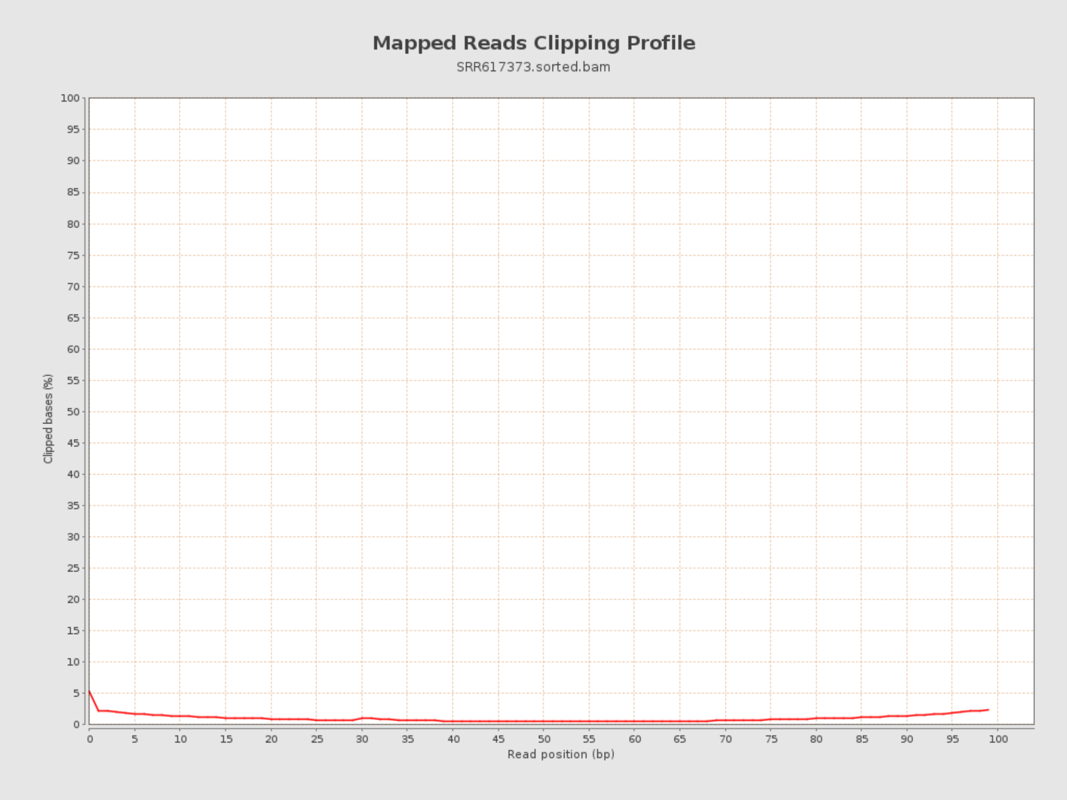
8. Results : Mapped Reads Nucleotide Content



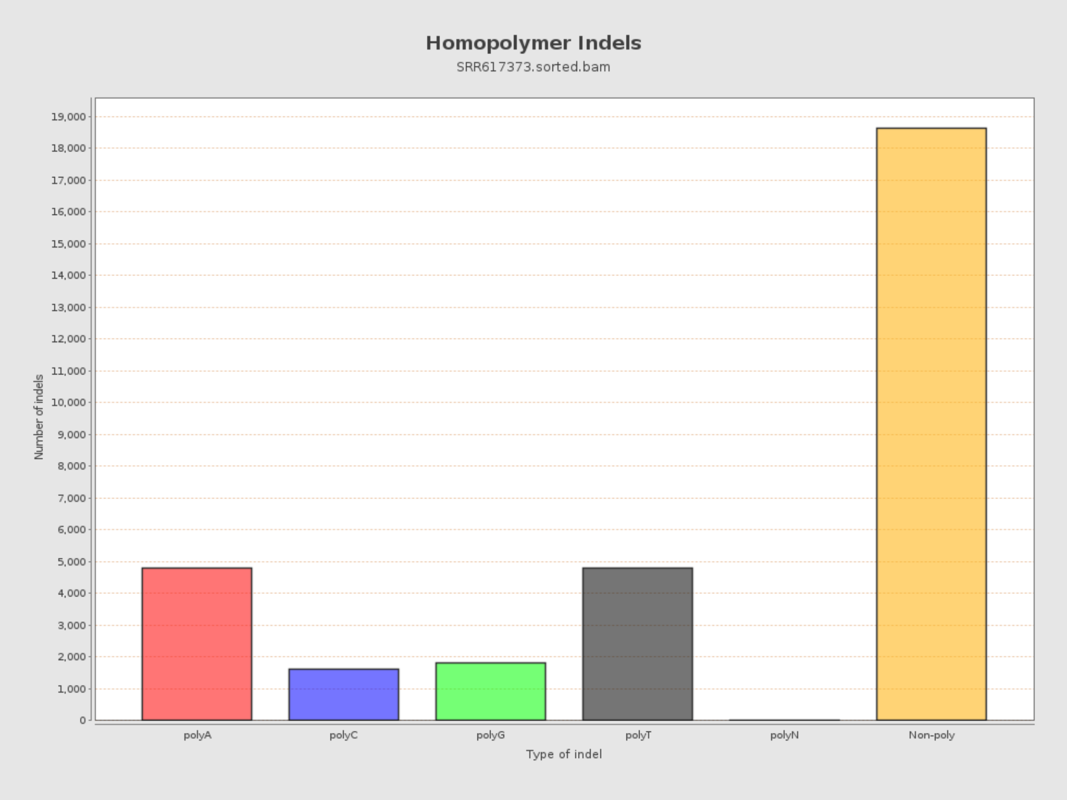
9. Results : Mapped Reads GC-content Distribution



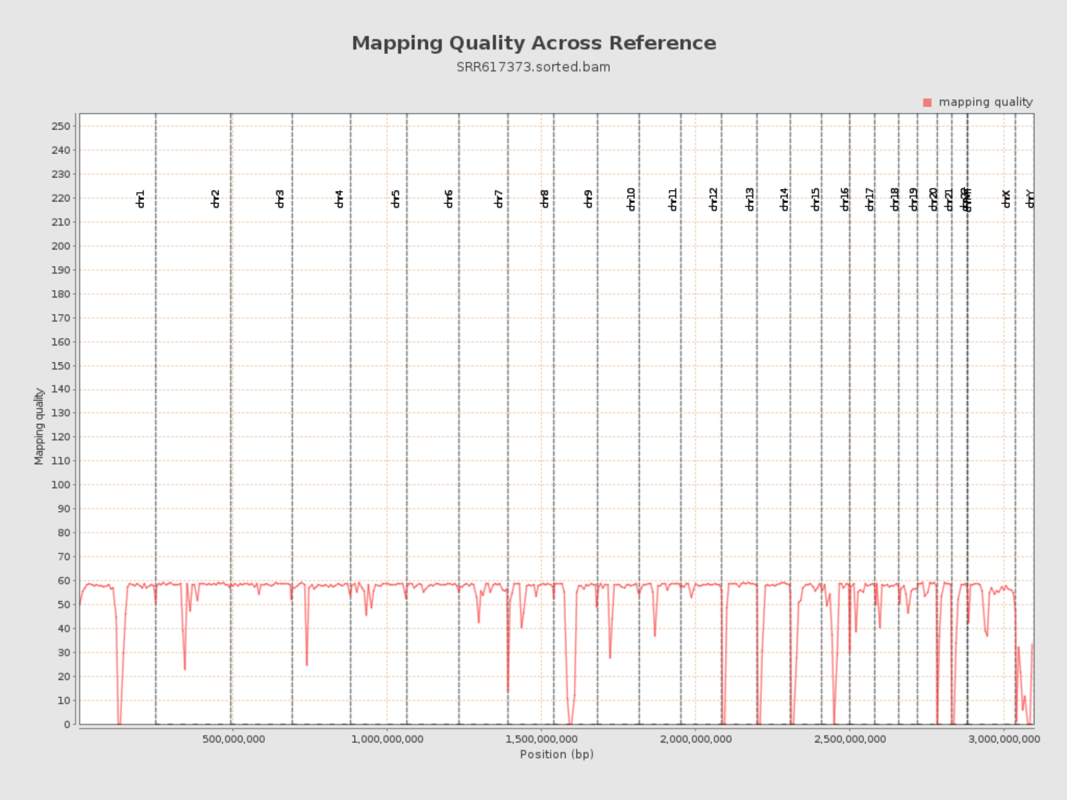
10. Results : Mapped Reads Clipping Profile



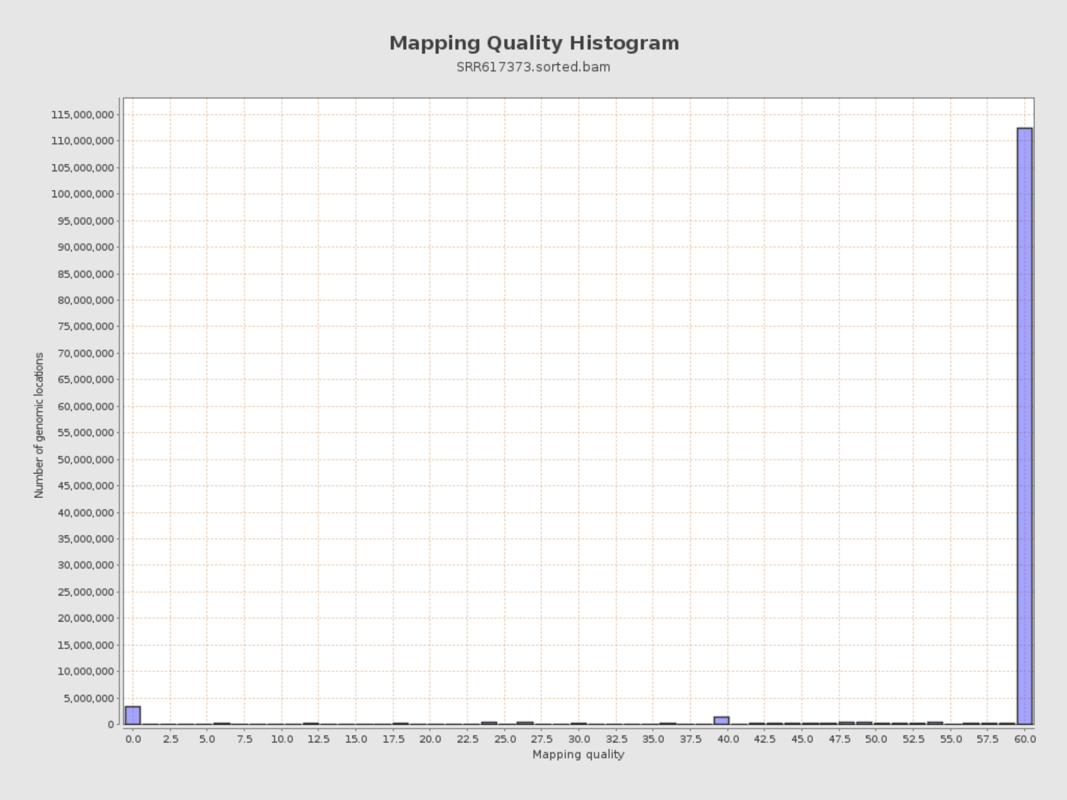
11. Results : Homopolymer Indels



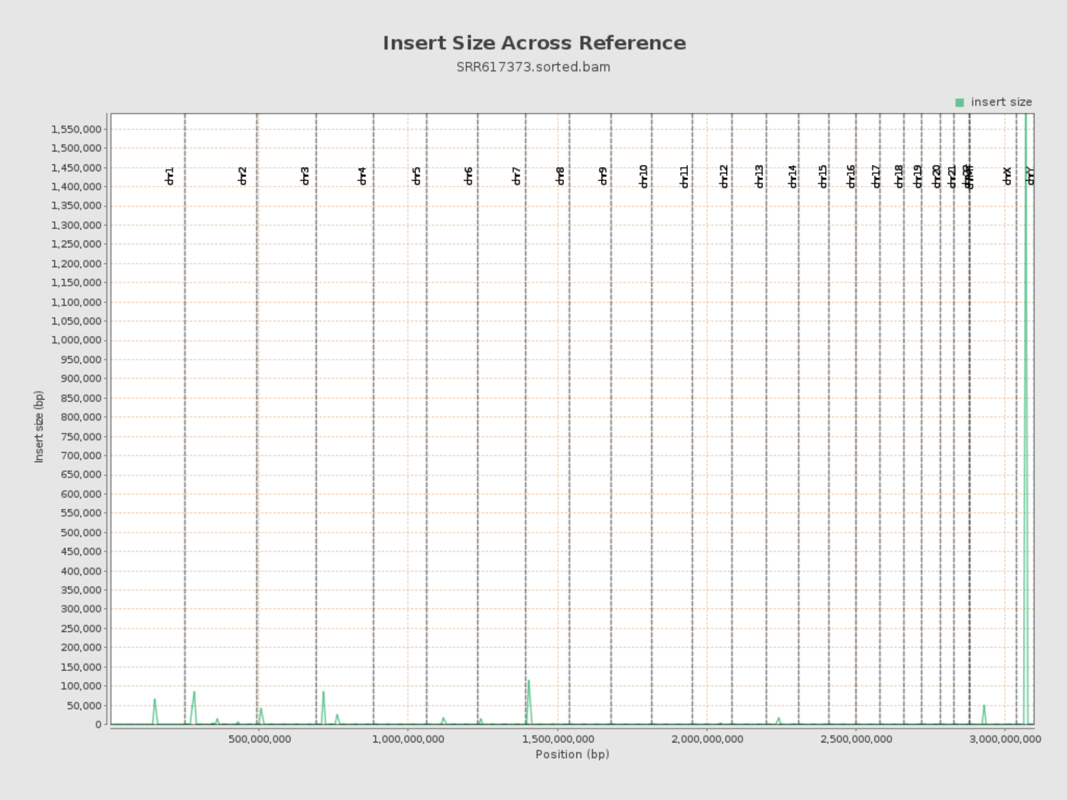
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram