Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:35:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173861.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_SRR10173861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173861_1.fastq.gz SRR10173861_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:35:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,553,744
Mapped reads	2,485,962 / 97.35%
Unmapped reads	67,782 / 2.65%
Mapped paired reads	2,485,962 / 97.35%
Mapped reads, first in pair	1,244,628 / 48.74%
Mapped reads, second in pair	1,241,334 / 48.61%
Mapped reads, both in pair	2,442,436 / 95.64%
Mapped reads, singletons	43,526 / 1.7%
Secondary alignments	0
Supplementary alignments	269,374 / 10.55%
Read min/max/mean length	30 / 133 / 128.41
Duplicated reads (estimated)	1,897,049 / 74.29%
Duplication rate	62.97%
Clipped reads	1,102,422 / 43.17%

2.2. ACGT Content

Number/percentage of A's	88,421,231 / 30.23%
Number/percentage of C's	56,941,242 / 19.47%
Number/percentage of T's	88,158,173 / 30.15%
Number/percentage of G's	58,922,988 / 20.15%
Number/percentage of N's	3,400 / 0%

GC Percentage	39.62%

2.3. Coverage

Mean	0.0945
Standard Deviation	1.5277

2.4. Mapping Quality

Mean Mapping Quality	52.63

2.5. Insert size

Mean	845,084.5
Standard Deviation	8,550,010.97
P25/Median/P75	139 / 194 / 279

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	2,979,882
Insertions	31,330
Mapped reads with at least one insertion	1.22%
Deletions	67,849
Mapped reads with at least one deletion	2.66%
Homopolymer indels	42.91%

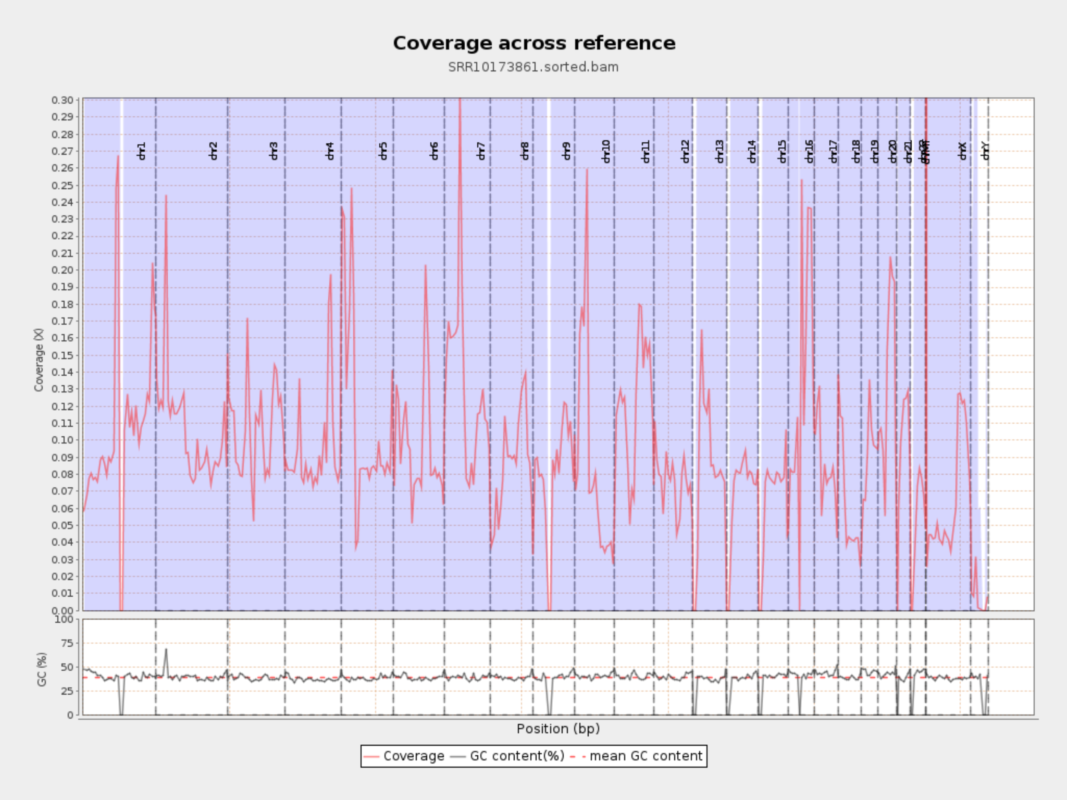
2.7. Chromosome stats

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

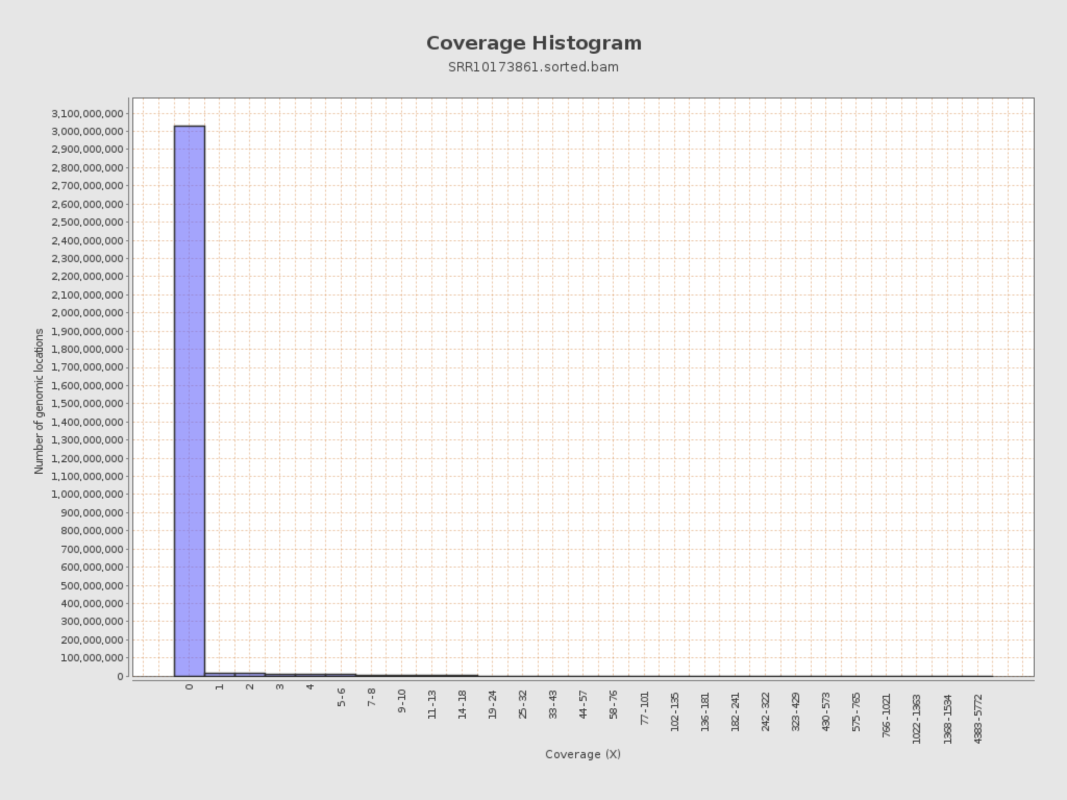
		bases	**coverage**	**deviation**
chr1	249250621	26522274	0.1064	1.3125
chr2	243199373	25704209	0.1057	4.0938
chr3	198022430	21189257	0.107	0.9334
chr4	191154276	18160857	0.095	0.9677
chr5	180915260	20517662	0.1134	0.9648
chr6	171115067	16686676	0.0975	0.9187
chr7	159138663	21270599	0.1337	1.5411
chr8	146364022	12754780	0.0871	0.9211
chr9	141213431	11410478	0.0808	0.9349
chr10	135534747	11667506	0.0861	1.5341
chr11	135006516	16413476	0.1216	0.9885
chr12	133851895	10305866	0.077	0.7854
chr13	115169878	9771596	0.0848	0.831
chr14	107349540	7388907	0.0688	0.7384
chr15	102531392	6616376	0.0645	0.7077
chr16	90354753	11757341	0.1301	1.342
chr17	81195210	6989714	0.0861	0.8946
chr18	78077248	4865102	0.0623	1.1888
chr19	59128983	5376125	0.0909	1.2651
chr20	63025520	8710391	0.1382	1.054
chr21	48129895	4567237	0.0949	0.8958
chr22	51304566	2663582	0.0519	0.61
chrMT	16571	746546	45.0514	36.97
chrX	155270560	10116221	0.0652	0.7222

chrY	59373566	442072	0.0074	0.3583

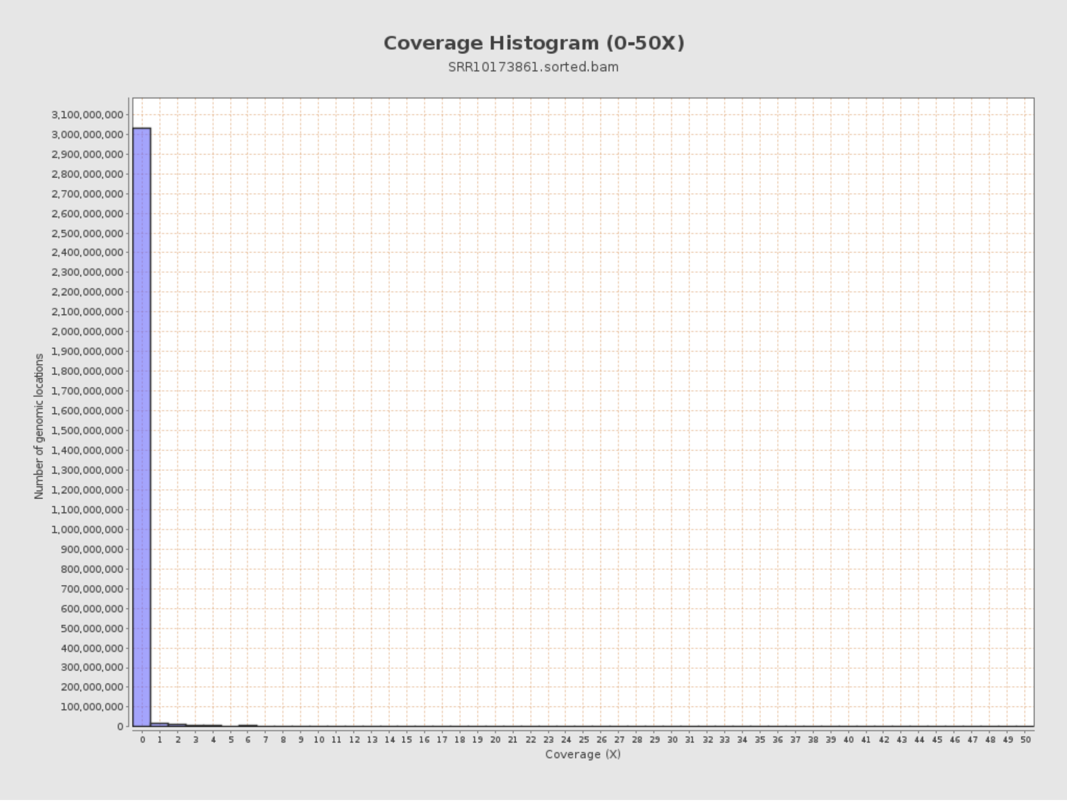
3. Results : Coverage across reference



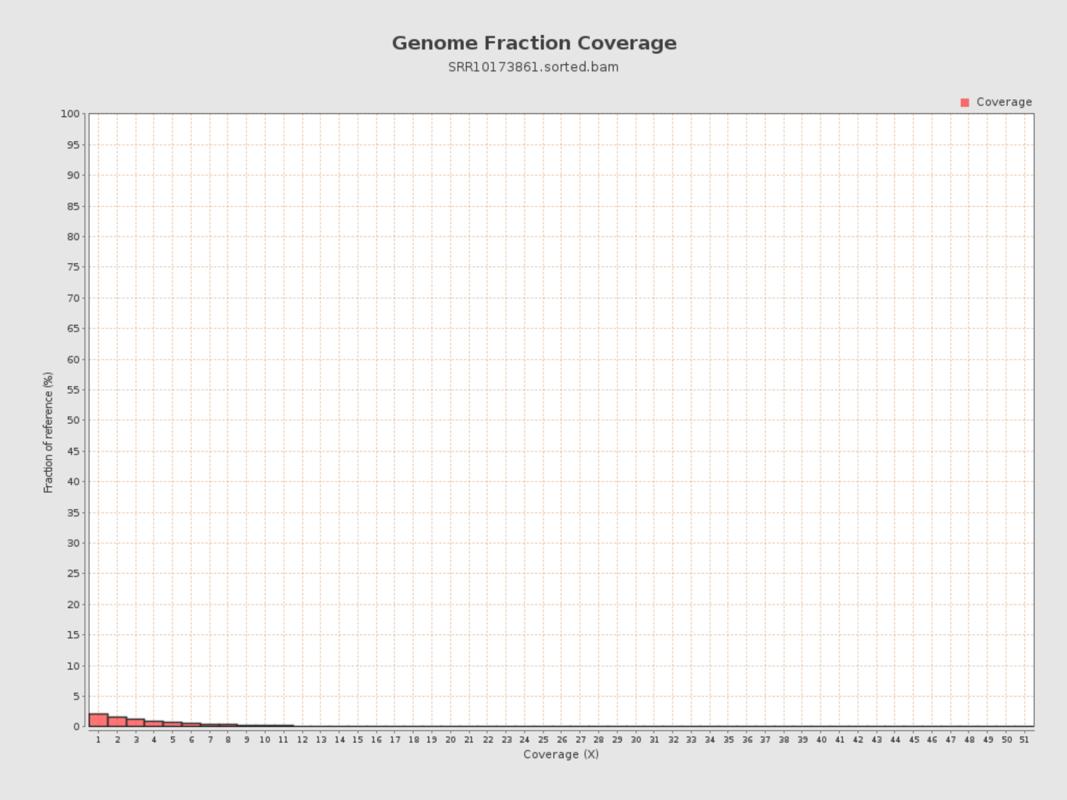
4. Results : Coverage Histogram



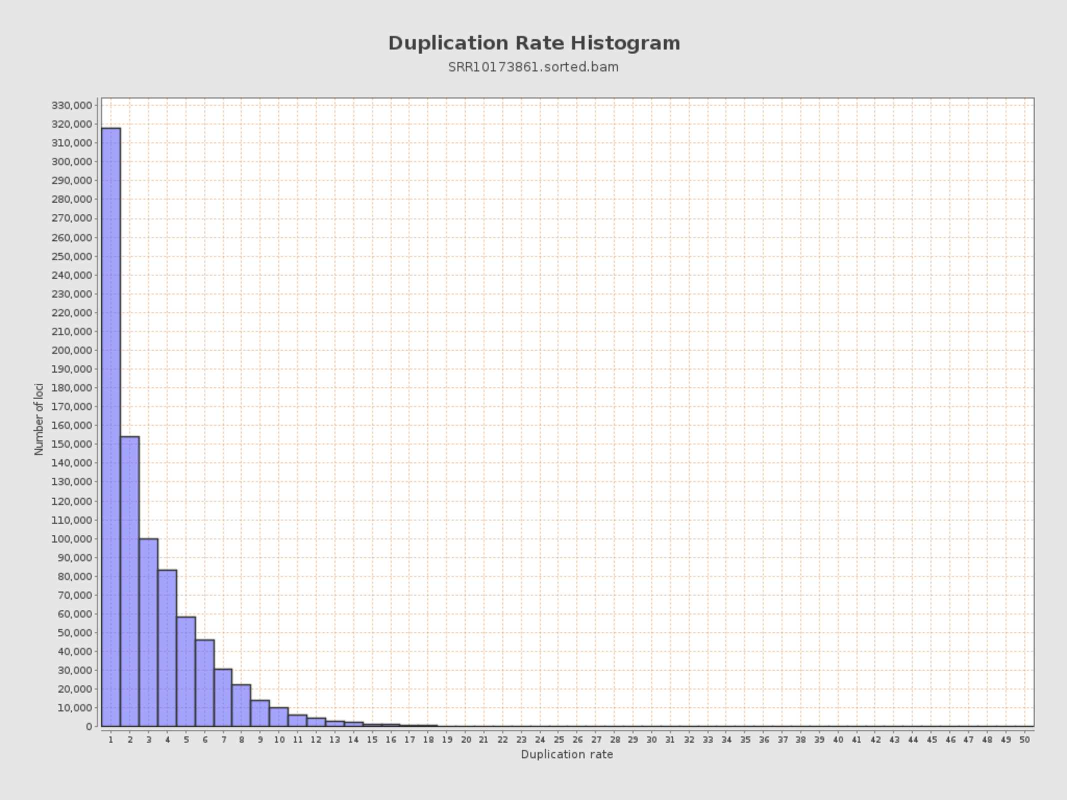
5. Results : Coverage Histogram (0-50X)



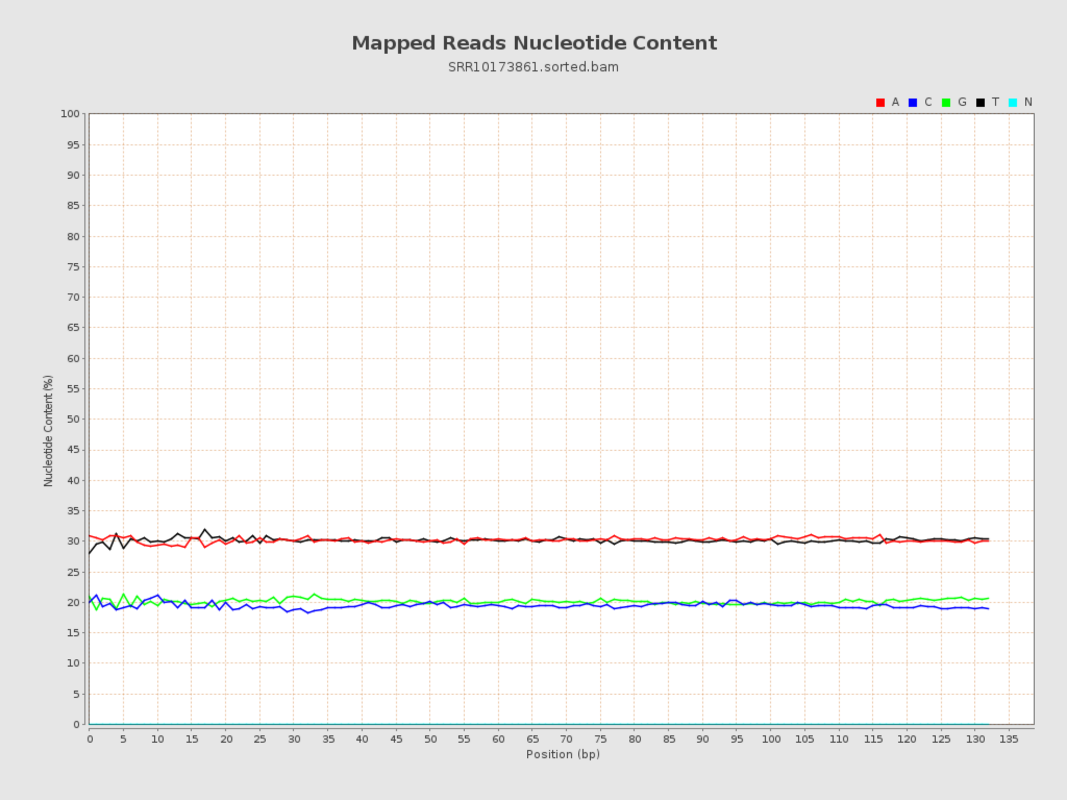
6. Results : Genome Fraction Coverage



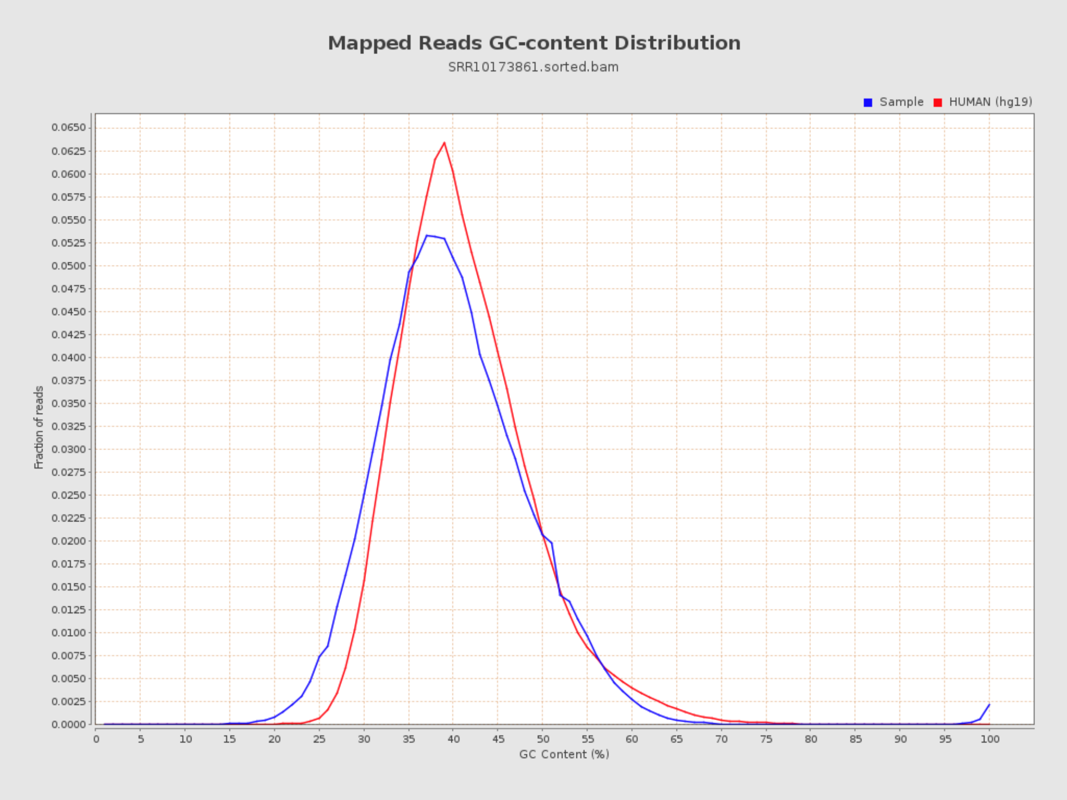
7. Results : Duplication Rate Histogram



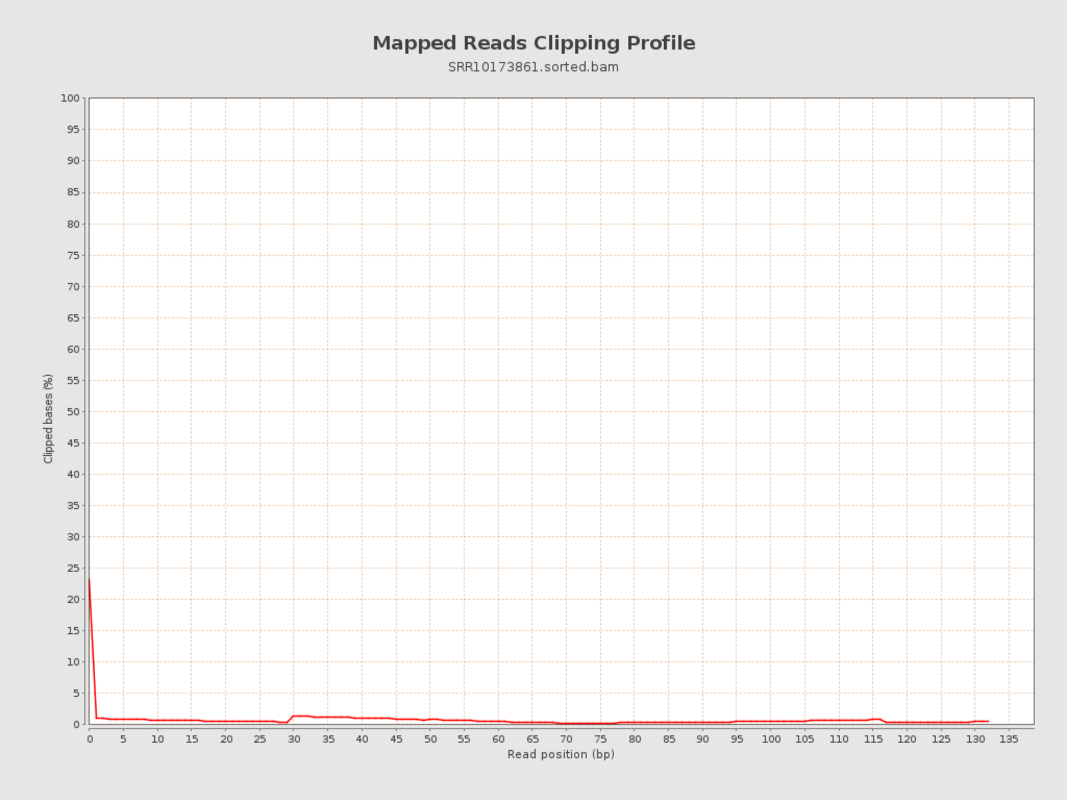
8. Results : Mapped Reads Nucleotide Content



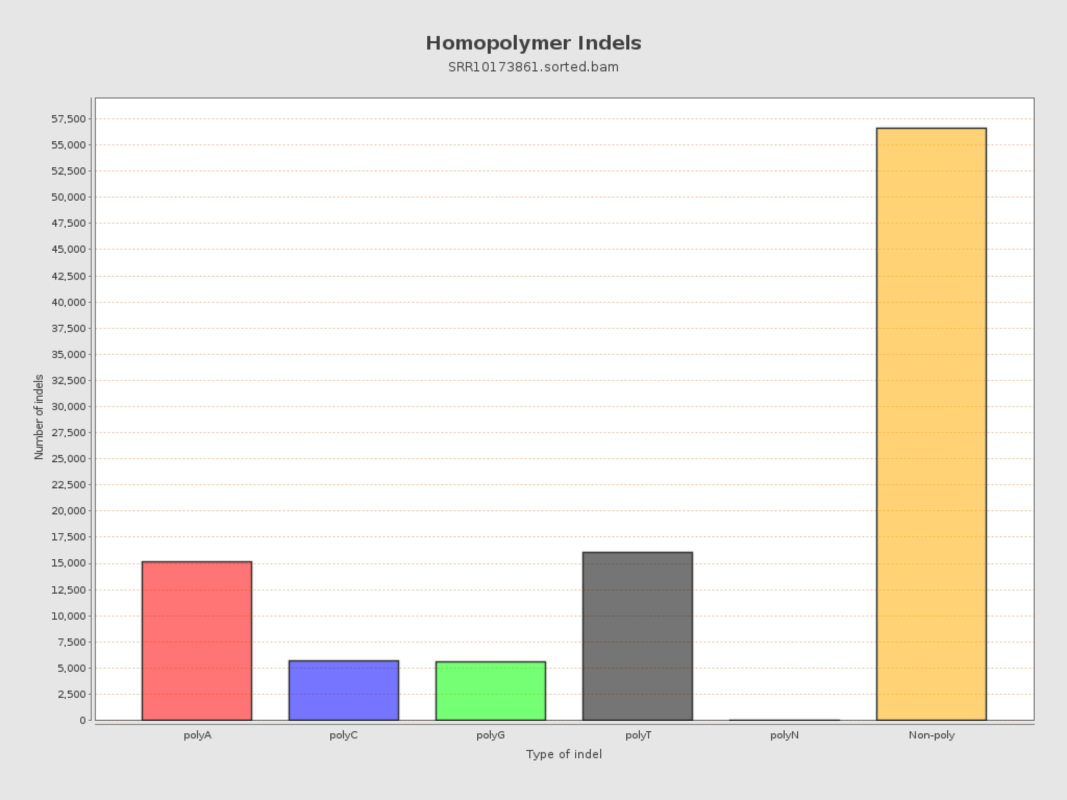
9. Results : Mapped Reads GC-content Distribution



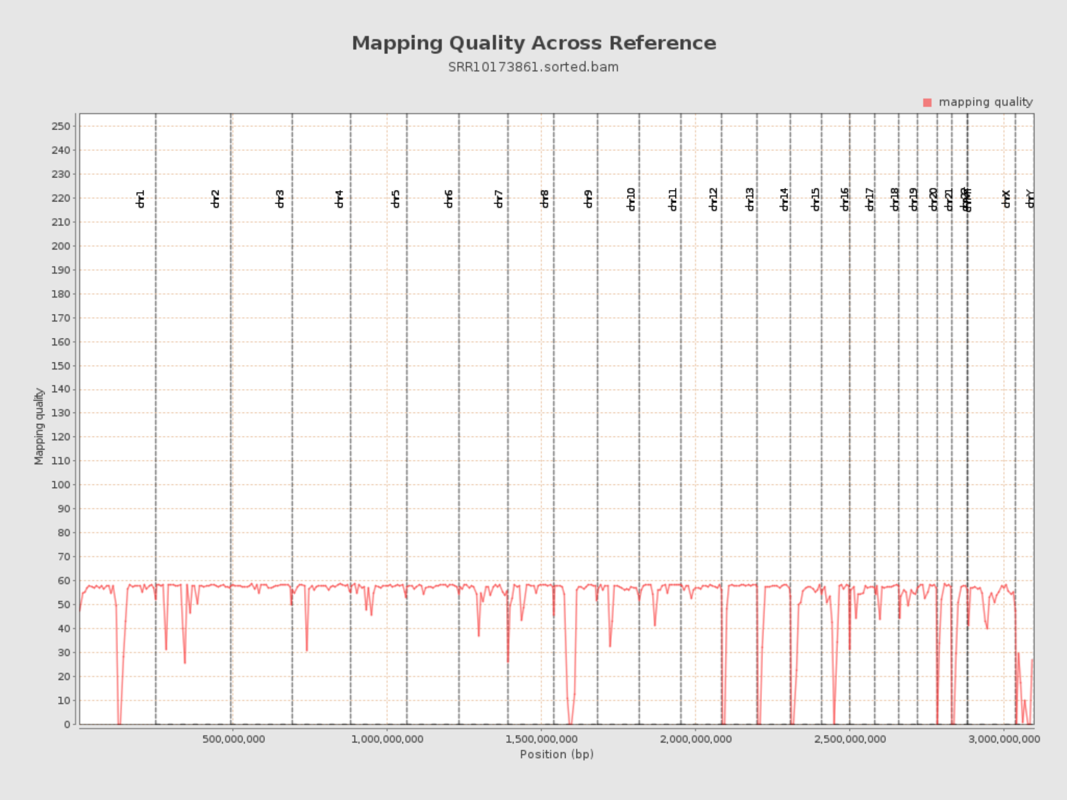
10. Results : Mapped Reads Clipping Profile



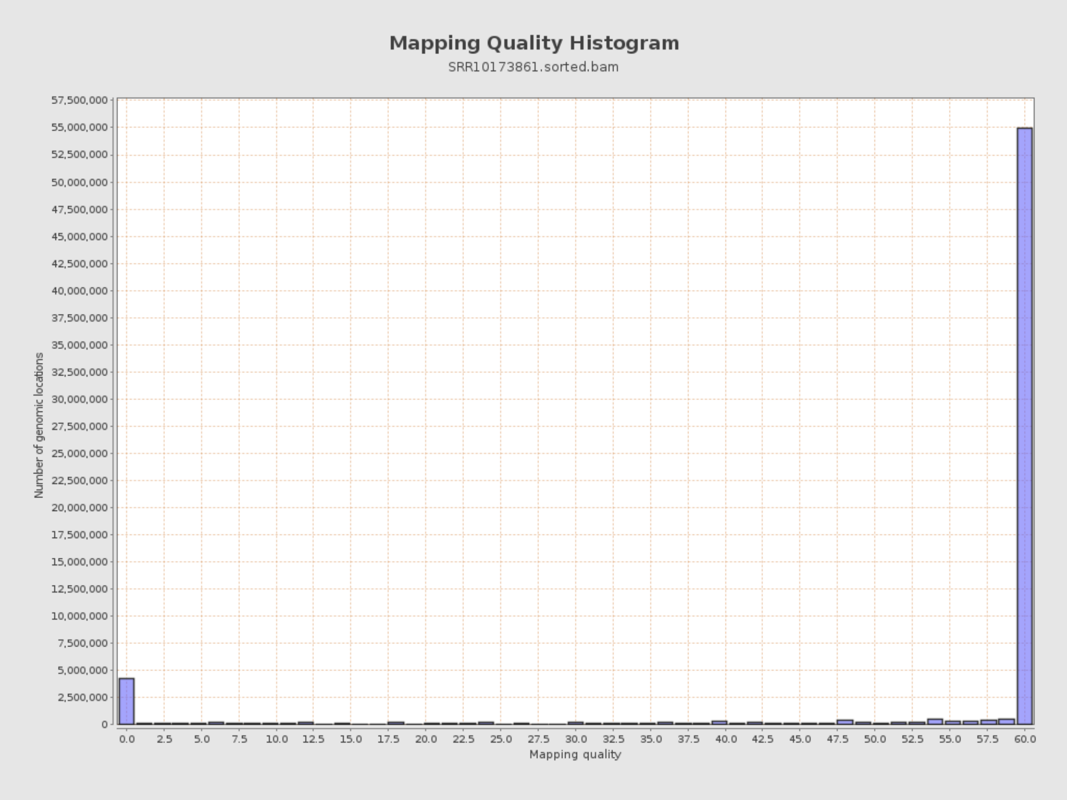
11. Results : Homopolymer Indels



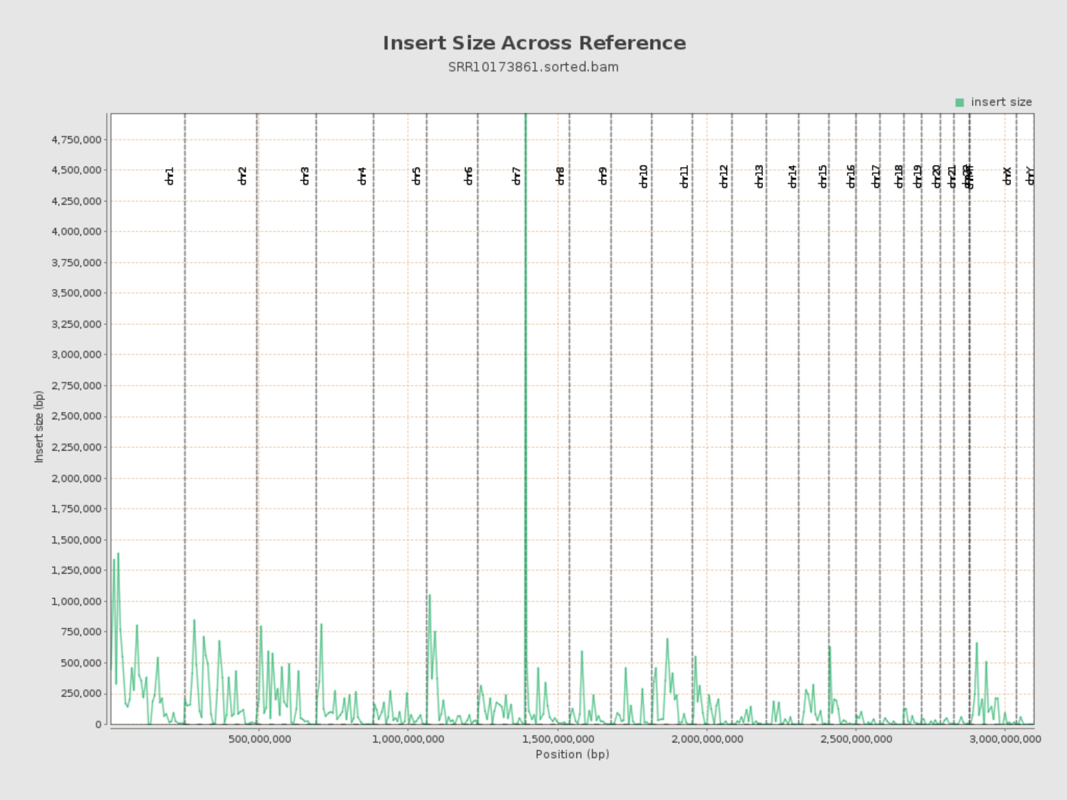
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram