

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:47:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173873.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_SRR10173873 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173873_1.fastq.gz SRR10173873_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:47:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173873.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,504,024
Mapped reads	2,434,281 / 97.21%
Unmapped reads	69,743 / 2.79%
Mapped paired reads	2,434,281 / 97.21%
Mapped reads, first in pair	1,218,502 / 48.66%
Mapped reads, second in pair	1,215,779 / 48.55%
Mapped reads, both in pair	2,390,442 / 95.46%
Mapped reads, singletons	43,839 / 1.75%
Secondary alignments	0
Supplementary alignments	249,252 / 9.95%
Read min/max/mean length	30 / 133 / 128.04
Duplicated reads (estimated)	1,903,590 / 76.02%
Duplication rate	64.94%
Clipped reads	987,811 / 39.45%

2.2. ACGT Content

Number/percentage of A's	86,741,715 / 30.22%
Number/percentage of C's	55,904,107 / 19.48%
Number/percentage of T's	86,515,636 / 30.14%
Number/percentage of G's	57,835,475 / 20.15%
Number/percentage of N's	3,630 / 0%

GC Percentage	39.63%
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2.3. Coverage

Mean	0.0928
Standard Deviation	1.5011

2.4. Mapping Quality

Mean Mapping Quality	52.89
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2.5. Insert size

Mean	992,075.91
Standard Deviation	9,268,426.25
P25/Median/P75	142 / 200 / 288

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	3,010,395
Insertions	31,435
Mapped reads with at least one insertion	1.25%
Deletions	63,092
Mapped reads with at least one deletion	2.53%
Homopolymer indels	42.86%

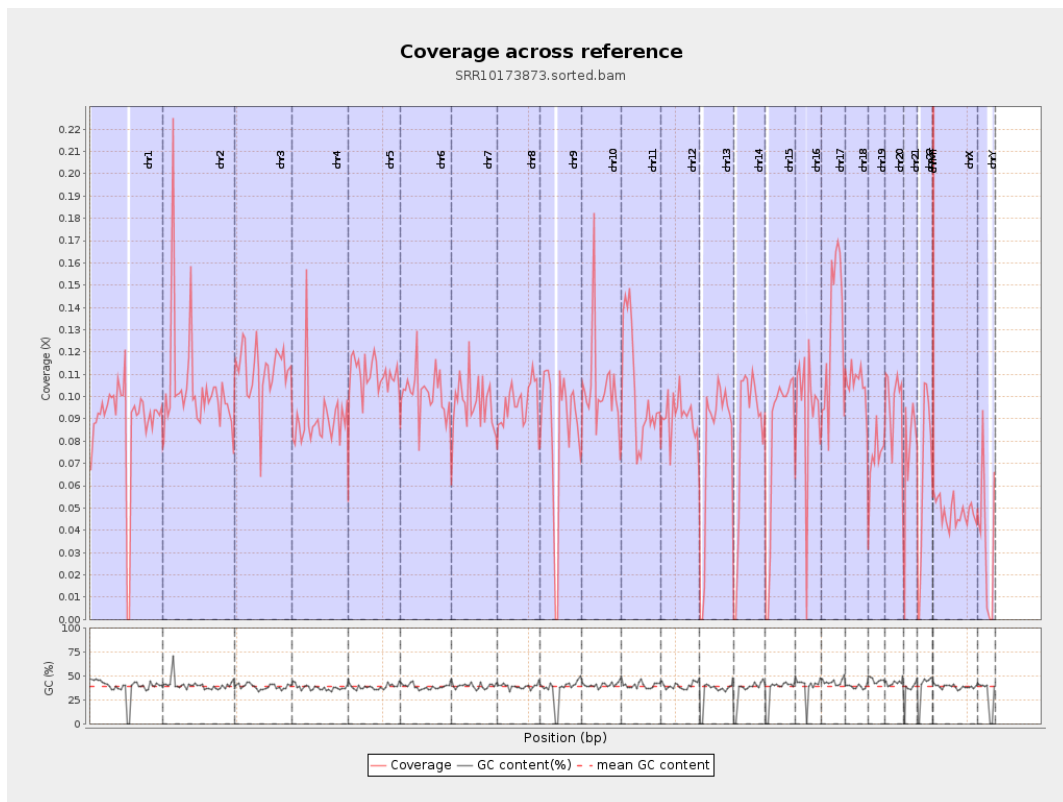
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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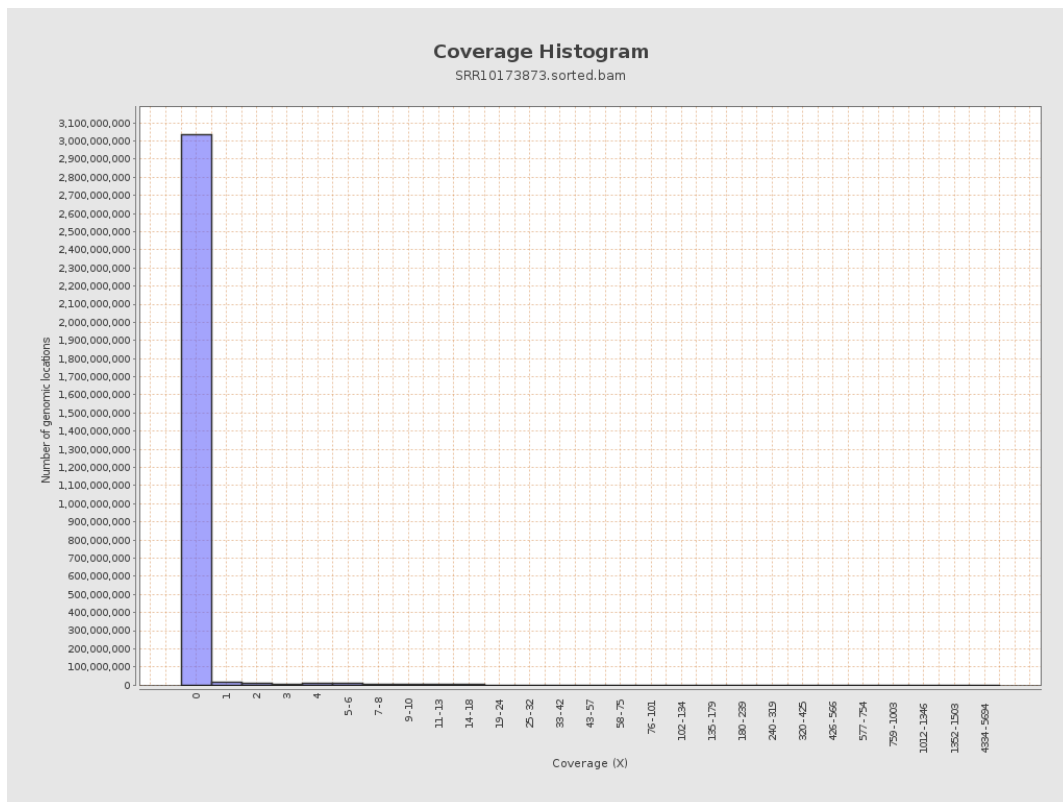
		bases	coverage	deviation
chr1	249250621	22048682	0.0885	1.0865
chr2	243199373	25192858	0.1036	4.054
chr3	198022430	22104369	0.1116	0.9694
chr4	191154276	17279702	0.0904	1.0276
chr5	180915260	19801446	0.1095	0.9703
chr6	171115067	17390566	0.1016	1.0013
chr7	159138663	15305132	0.0962	1.1565
chr8	146364022	14210795	0.0971	1.4212
chr9	141213431	12232267	0.0866	1.0578
chr10	135534747	14039528	0.1036	1.2637
chr11	135006516	13822945	0.1024	0.9354
chr12	133851895	12174050	0.091	0.881
chr13	115169878	9164498	0.0796	0.8214
chr14	107349540	8984420	0.0837	0.8368
chr15	102531392	8320165	0.0811	0.8153
chr16	90354753	8358346	0.0925	0.991
chr17	81195210	10668338	0.1314	1.0899
chr18	78077248	8307711	0.1064	1.4136
chr19	59128983	4326058	0.0732	0.8884
chr20	63025520	6136158	0.0974	0.9095
chr21	48129895	3696062	0.0768	0.9006
chr22	51304566	3390231	0.0661	0.7469
chrMT	16571	535768	32.3317	28.3448
chrX	155270560	7495680	0.0483	0.6362

chrY	59373566	2171295	0.0366	0.6706
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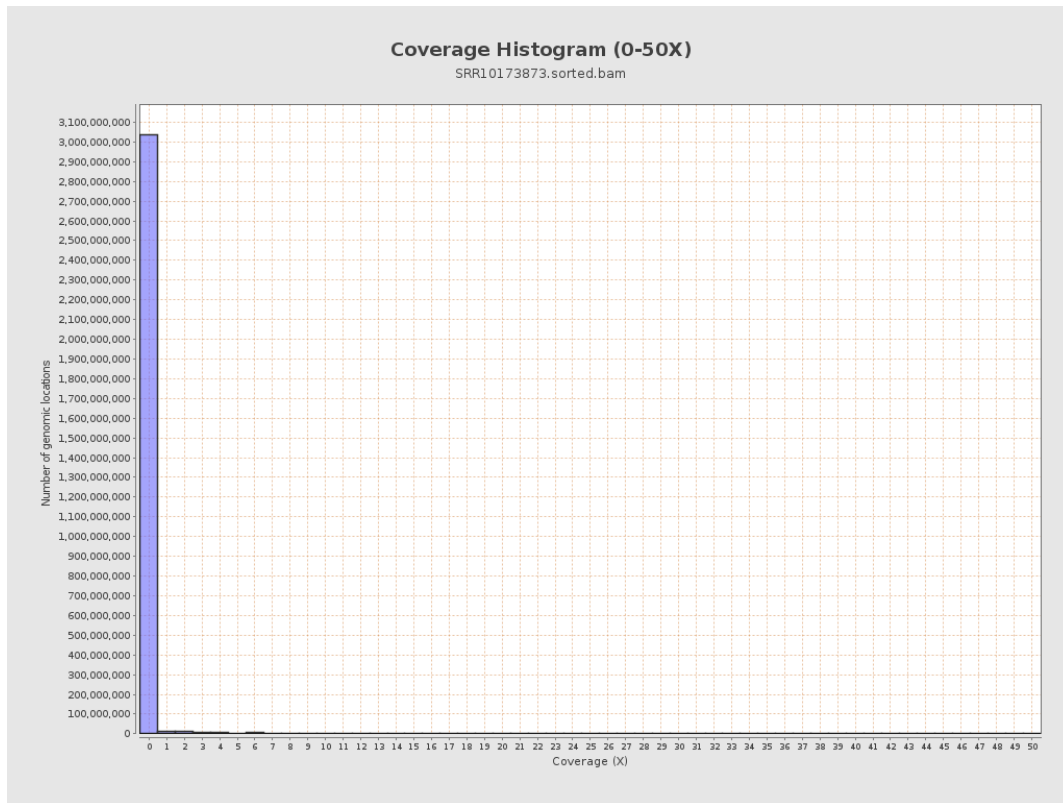
3. Results : Coverage across reference



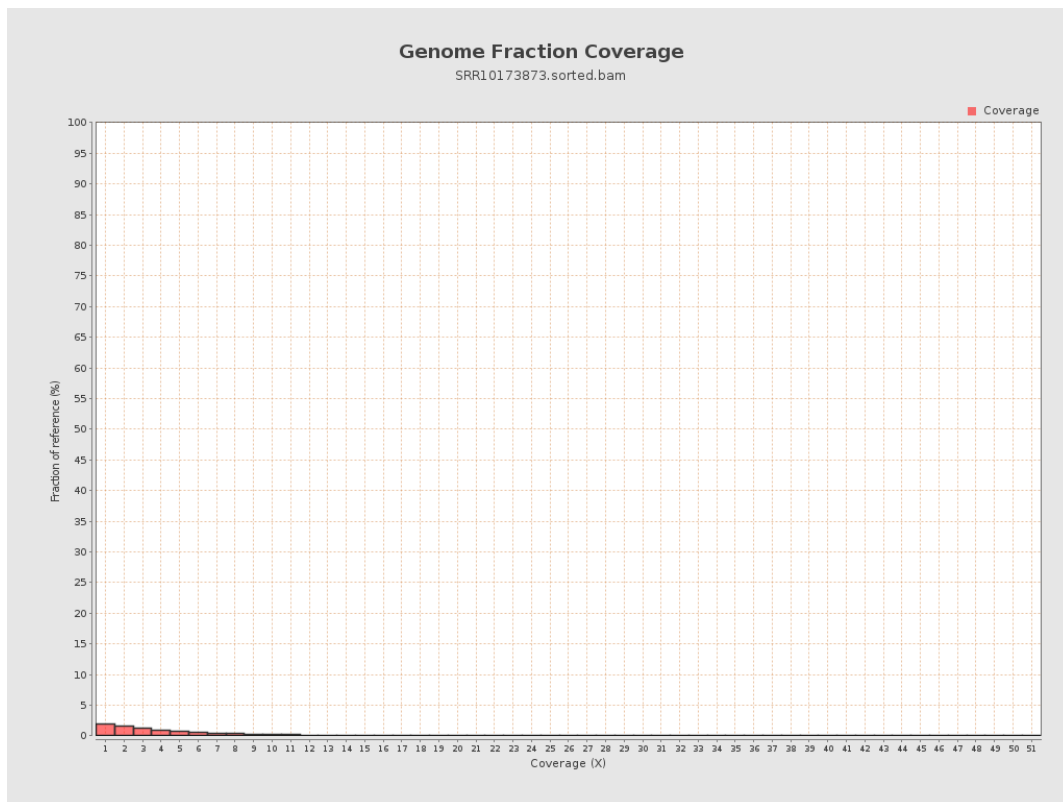
4. Results : Coverage Histogram



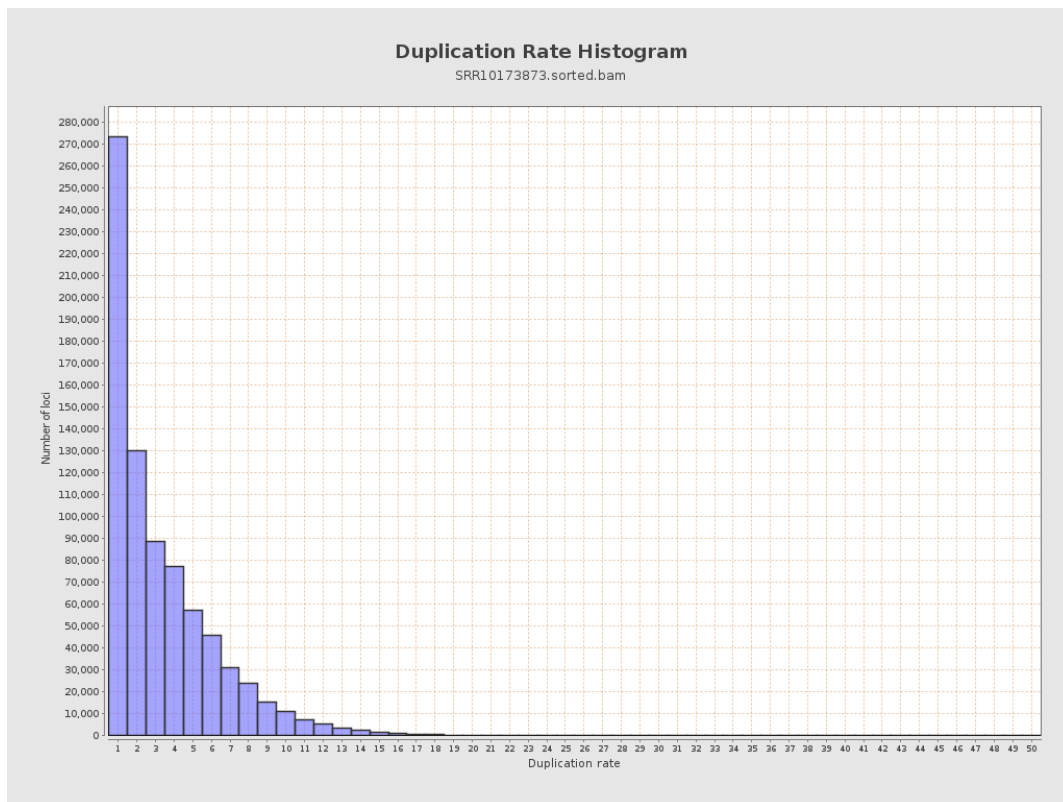
5. Results : Coverage Histogram (0-50X)



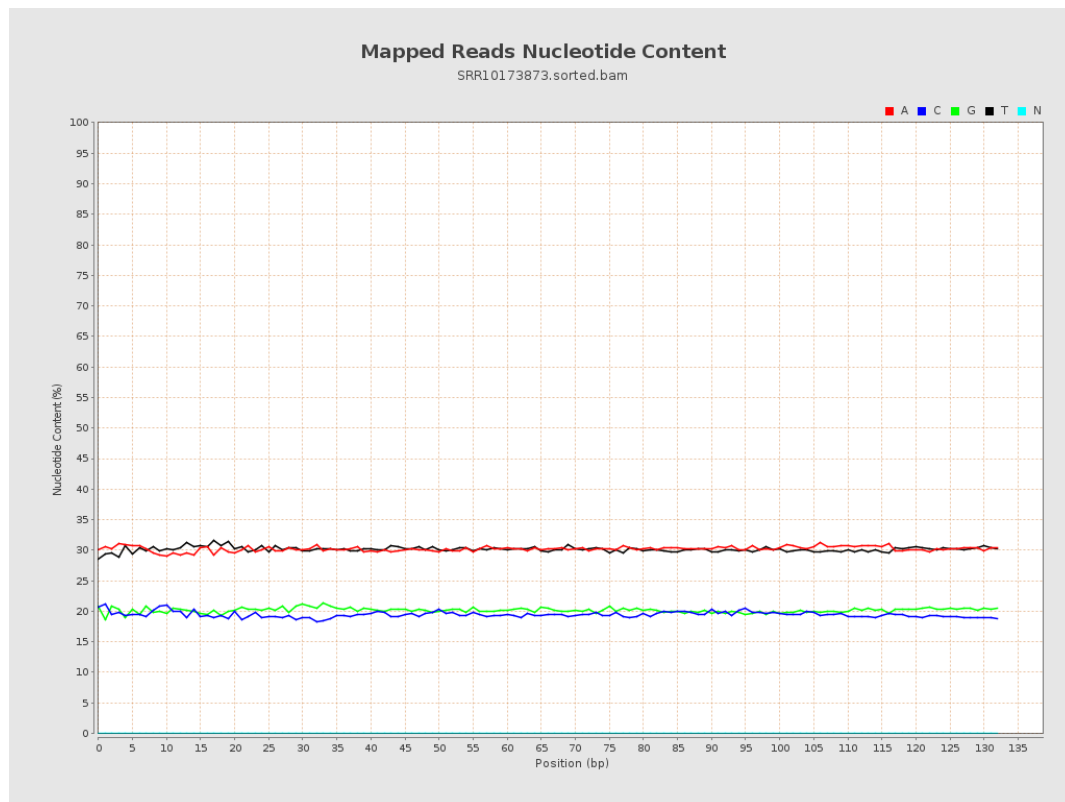
6. Results : Genome Fraction Coverage



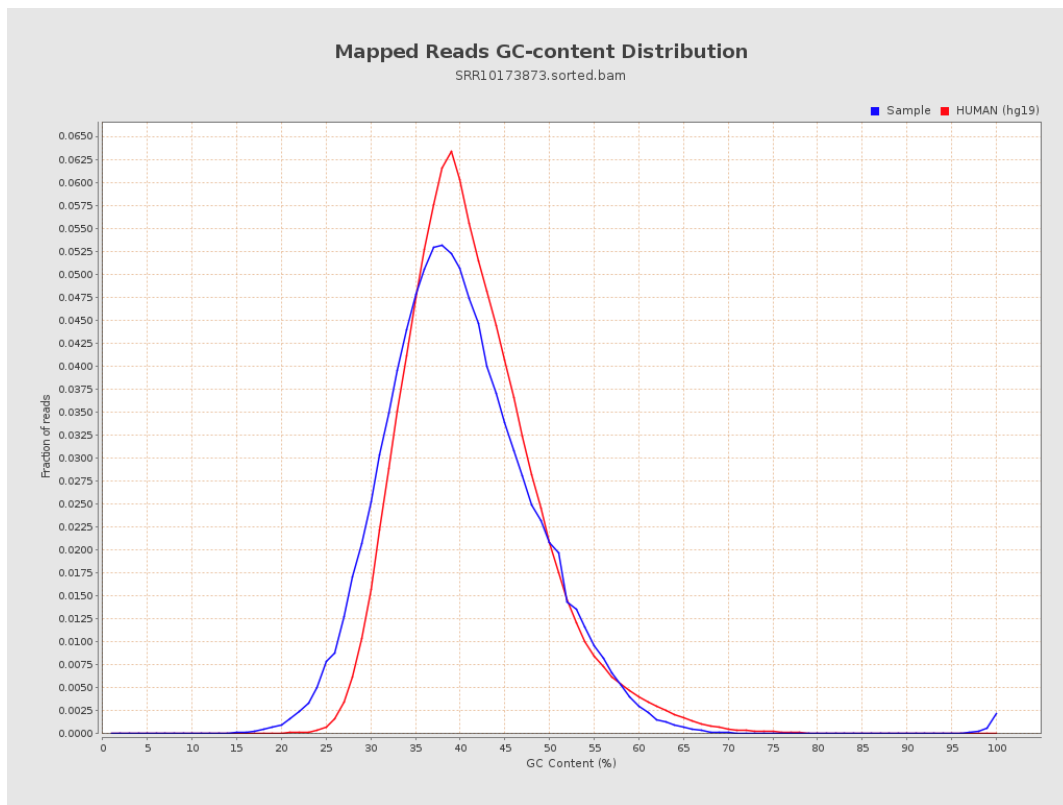
7. Results : Duplication Rate Histogram



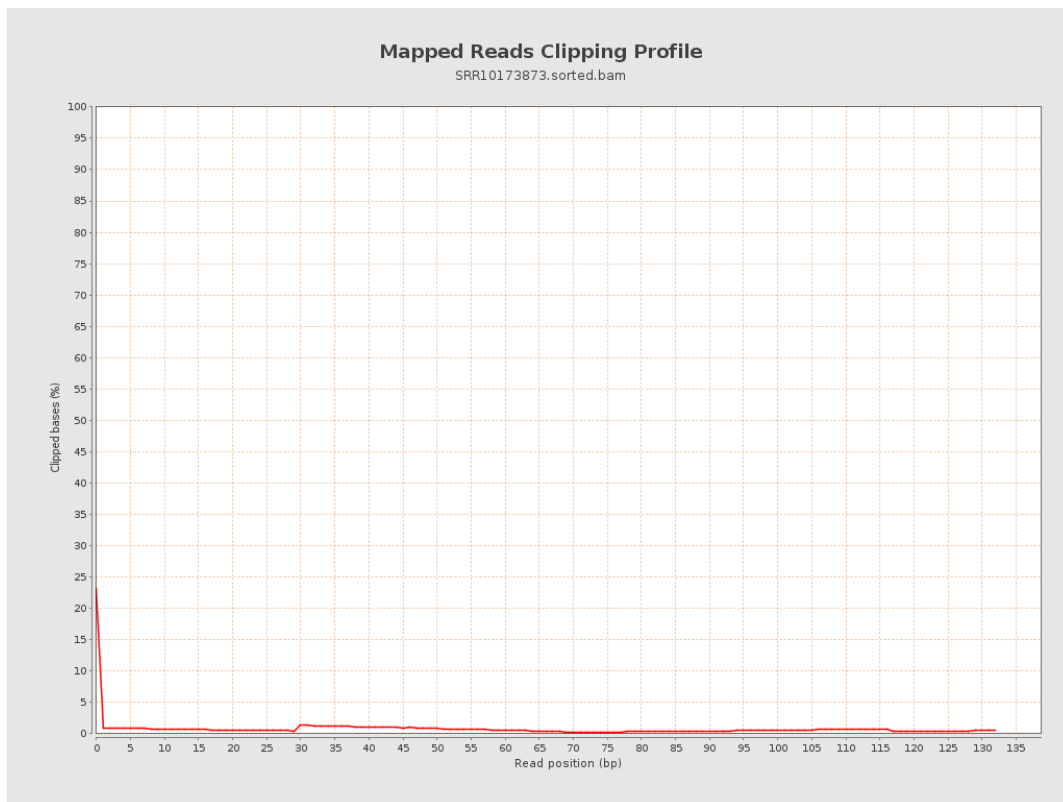
8. Results : Mapped Reads Nucleotide Content



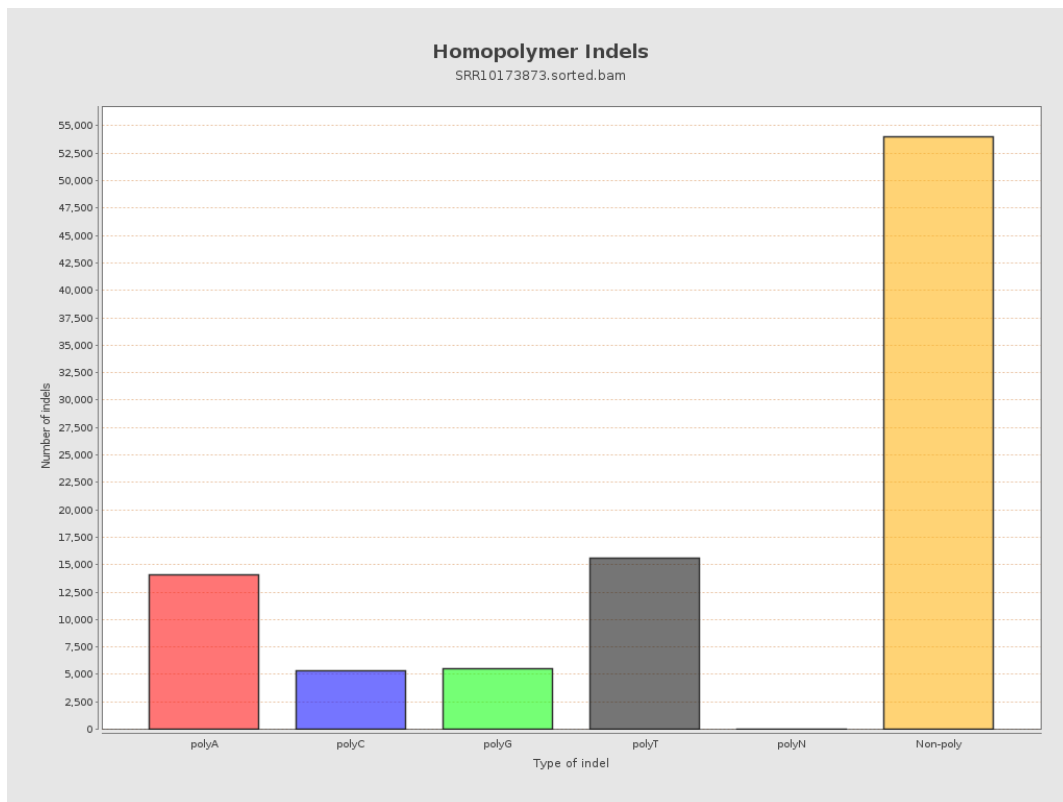
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



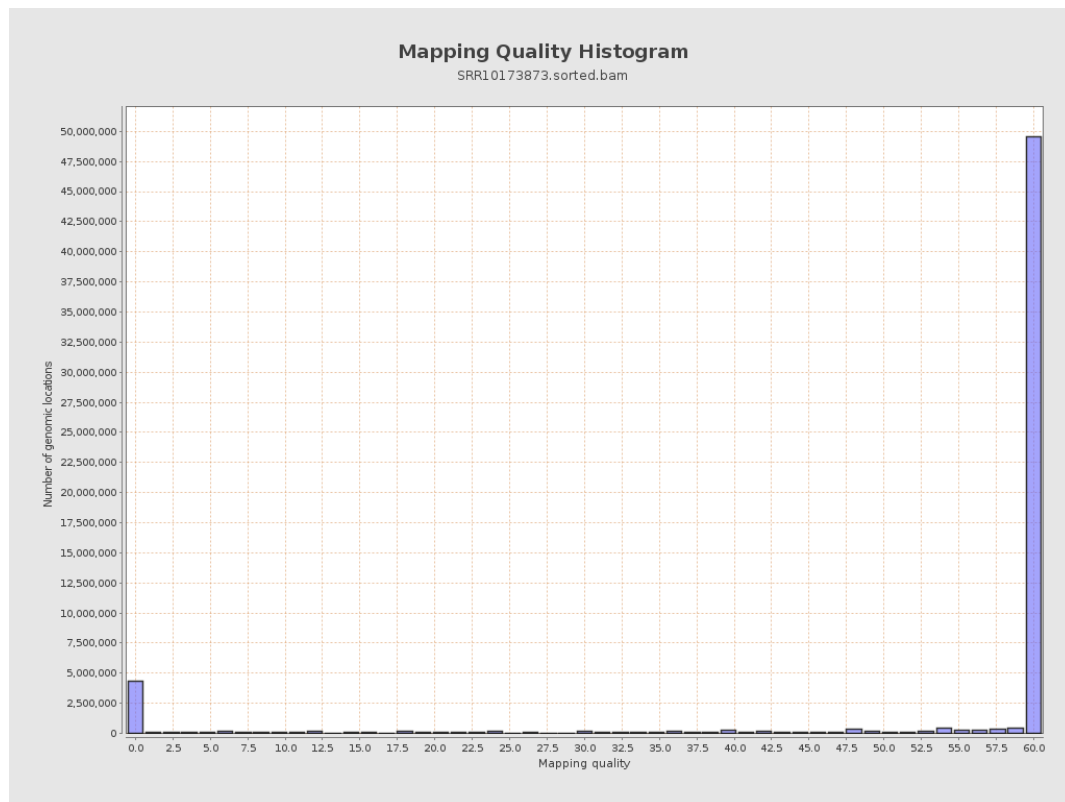
11. Results : Homopolymer Indels



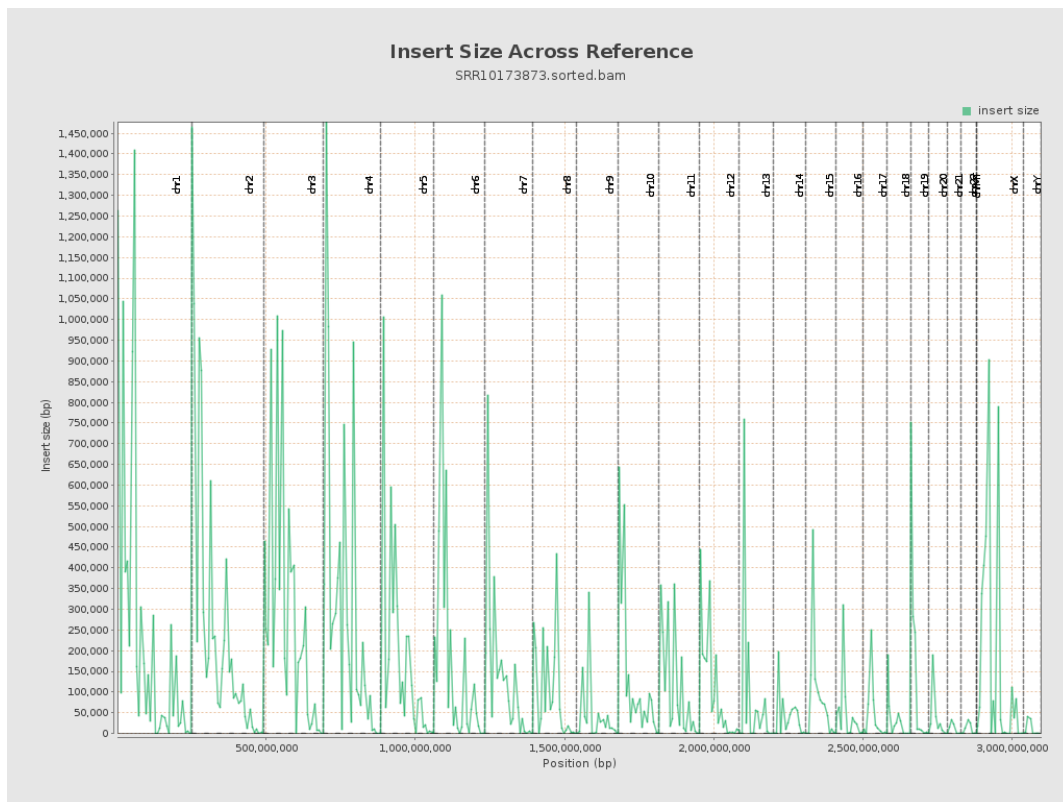
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

