

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:22:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173899.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_SRR10173899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173899_1.fastq.gz SRR10173899_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:22:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,056,336
Mapped reads	9,791,787 / 97.37%
Unmapped reads	264,549 / 2.63%
Mapped paired reads	9,791,787 / 97.37%
Mapped reads, first in pair	4,896,344 / 48.69%
Mapped reads, second in pair	4,895,443 / 48.68%
Mapped reads, both in pair	9,616,942 / 95.63%
Mapped reads, singletons	174,845 / 1.74%
Secondary alignments	0
Supplementary alignments	1,014,495 / 10.09%
Read min/max/mean length	30 / 133 / 128.36
Duplicated reads (estimated)	7,829,893 / 77.86%
Duplication rate	66.14%
Clipped reads	3,994,700 / 39.72%

2.2. ACGT Content

Number/percentage of A's	350,403,493 / 30.27%
Number/percentage of C's	224,456,749 / 19.39%
Number/percentage of T's	349,347,122 / 30.18%
Number/percentage of G's	233,215,399 / 20.15%
Number/percentage of N's	13,316 / 0%

GC Percentage	39.54%
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2.3. Coverage

Mean	0.3741
Standard Deviation	5.4679

2.4. Mapping Quality

Mean Mapping Quality	52.57
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2.5. Insert size

Mean	806,328.04
Standard Deviation	7,971,417.3
P25/Median/P75	144 / 201 / 288

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	11,757,885
Insertions	122,825
Mapped reads with at least one insertion	1.21%
Deletions	287,632
Mapped reads with at least one deletion	2.87%
Homopolymer indels	42.71%

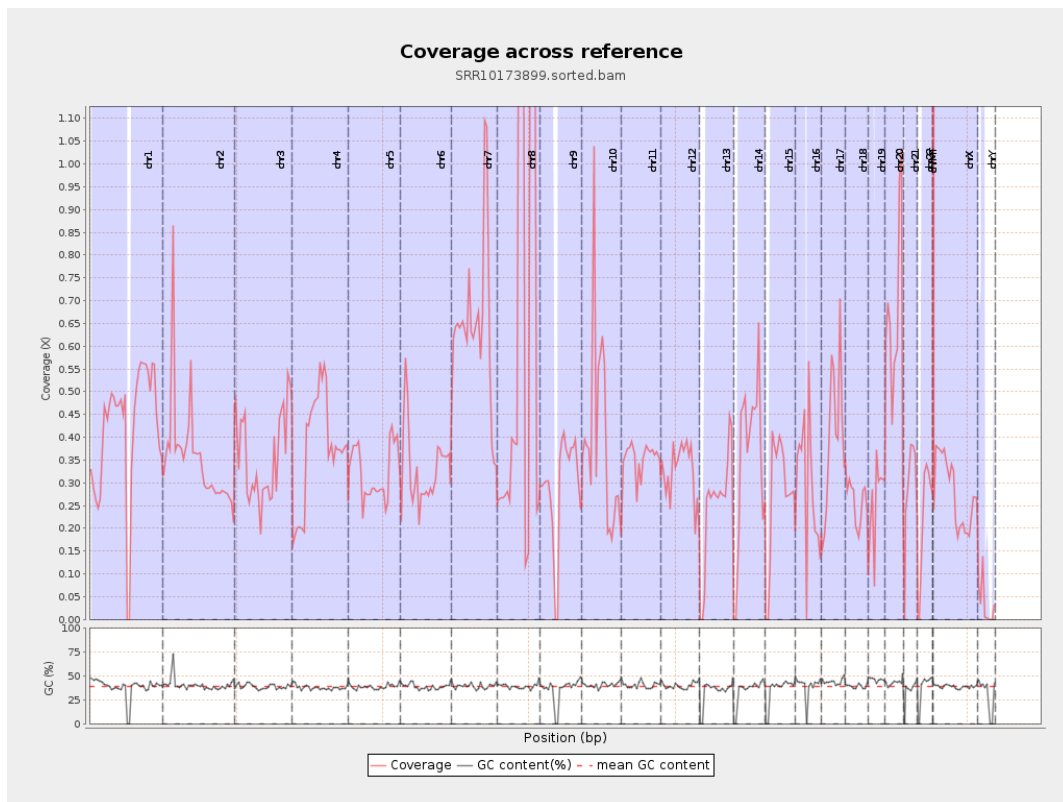
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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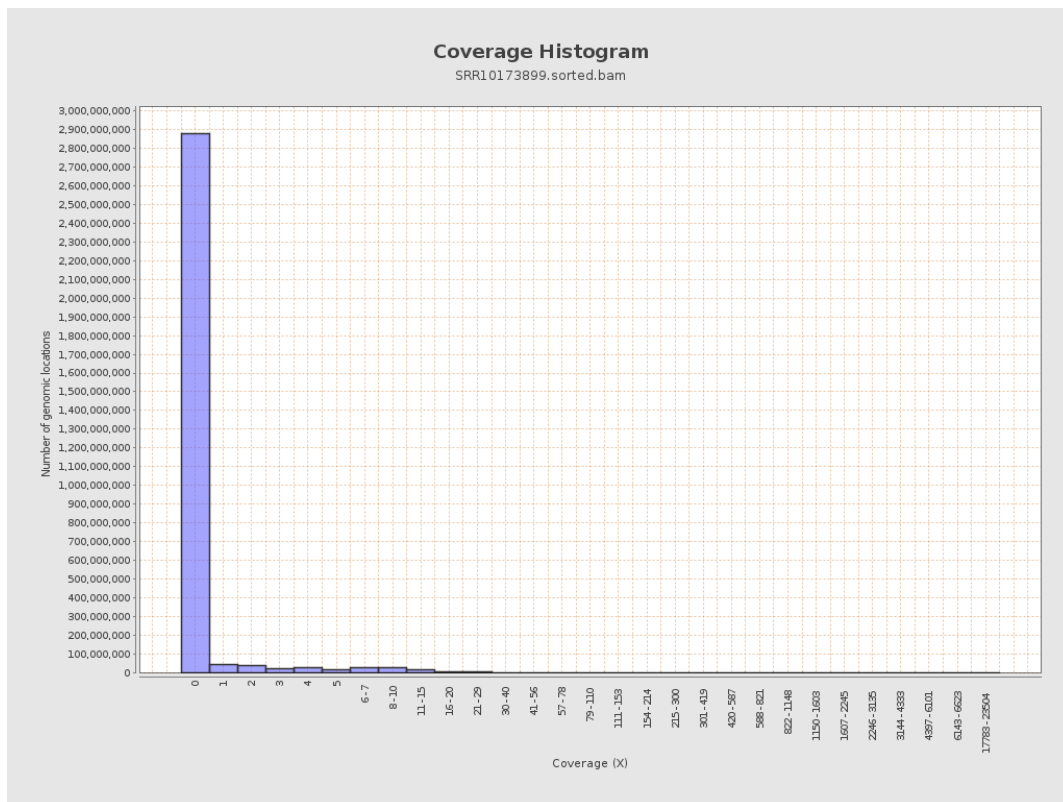
		bases	coverage	deviation
chr1	249250621	104010179	0.4173	2.939
chr2	243199373	85450275	0.3514	16.4135
chr3	198022430	71036100	0.3587	1.8234
chr4	191154276	72297100	0.3782	2.6042
chr5	180915260	58104244	0.3212	1.6831
chr6	171115067	56715779	0.3314	1.8823
chr7	159138663	101198899	0.6359	5.8347
chr8	146364022	116173856	0.7937	3.6622
chr9	141213431	41373176	0.293	2.4318
chr10	135534747	53285202	0.3931	7.3508
chr11	135006516	47440459	0.3514	1.8752
chr12	133851895	43726671	0.3267	1.7456
chr13	115169878	29215814	0.2537	1.5213
chr14	107349540	39027789	0.3636	1.8494
chr15	102531392	28045154	0.2735	1.5643
chr16	90354753	26404544	0.2922	2.8077
chr17	81195210	32400406	0.399	2.2533
chr18	78077248	20567609	0.2634	3.266
chr19	59128983	15279397	0.2584	2.2522
chr20	63025520	42662274	0.6769	2.5796
chr21	48129895	13925337	0.2893	1.8145
chr22	51304566	11417410	0.2225	1.3595
chrMT	16571	3236251	195.2961	147.9678
chrX	155270560	43075158	0.2774	1.6097

chrY	59373566	2058436	0.0347	1.4195
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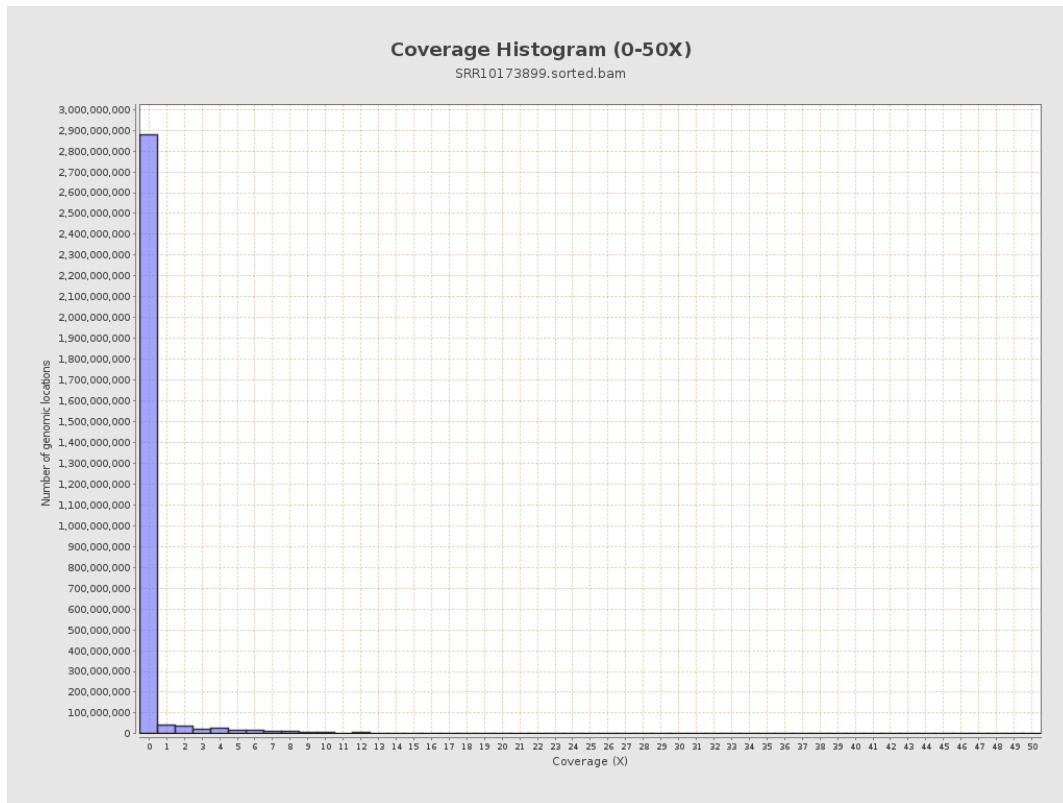
3. Results : Coverage across reference



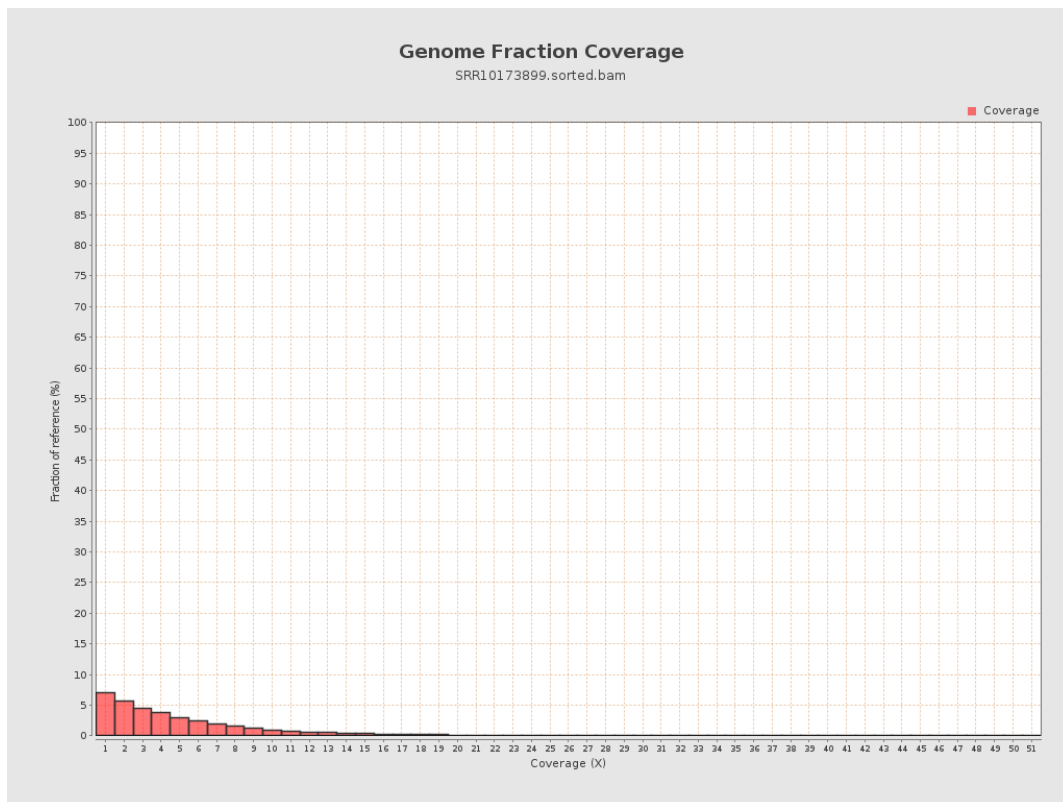
4. Results : Coverage Histogram



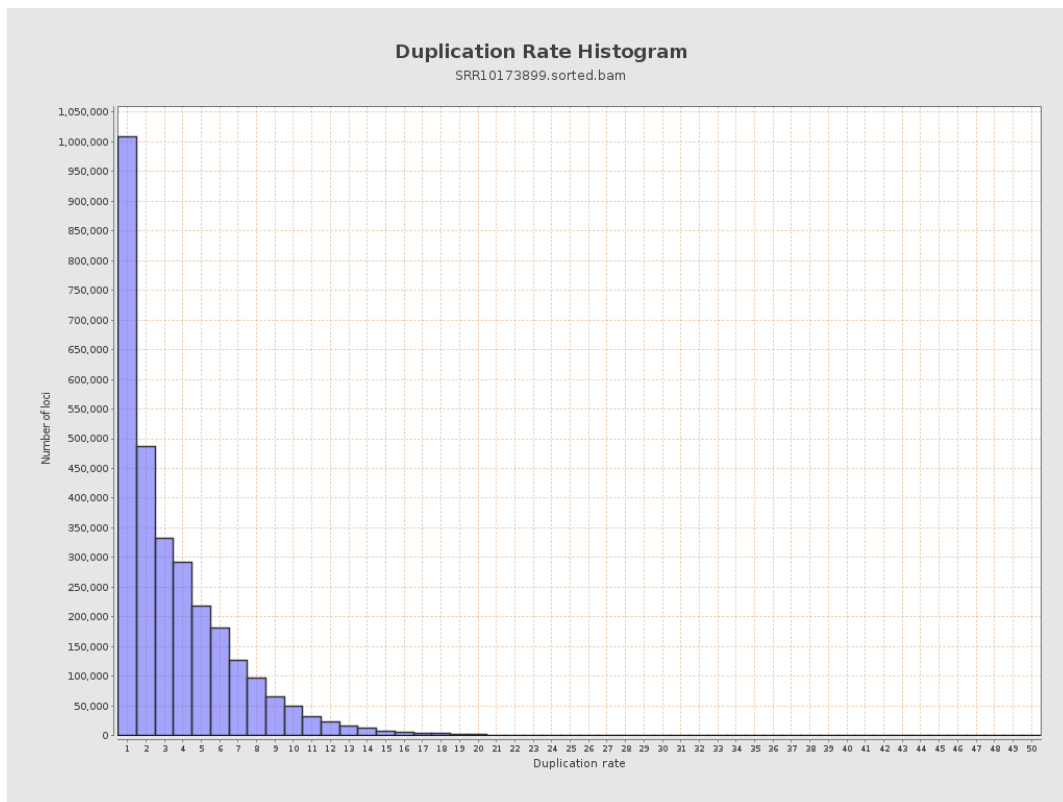
5. Results : Coverage Histogram (0-50X)



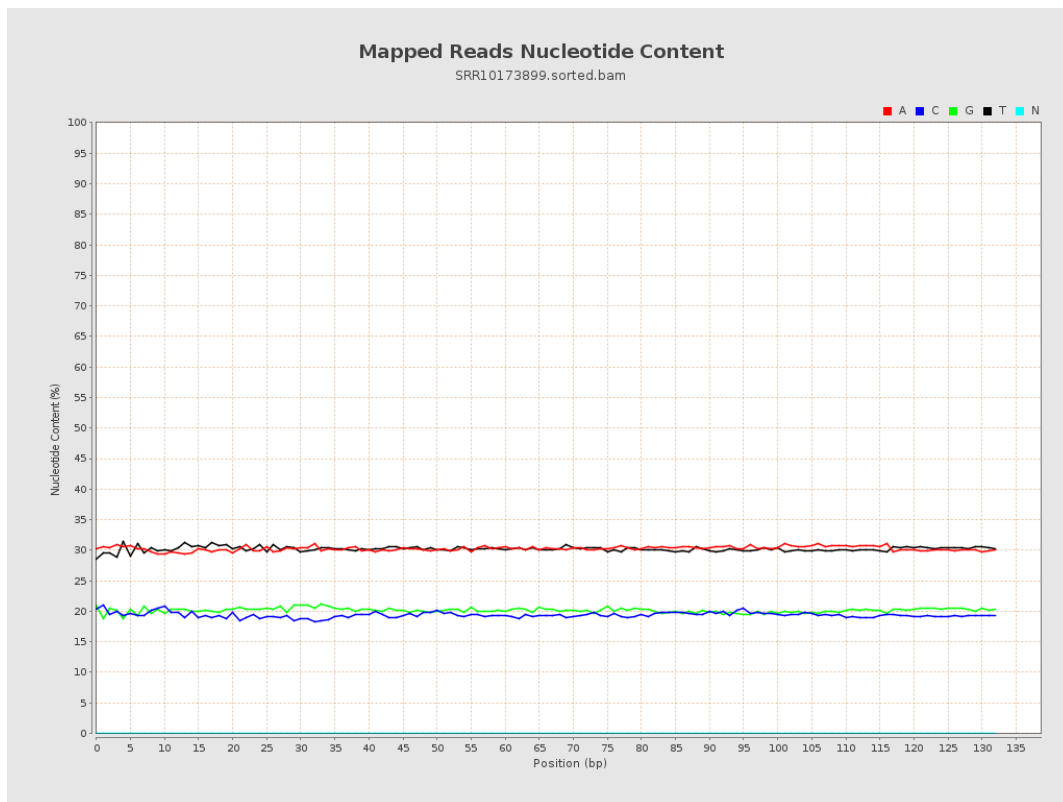
6. Results : Genome Fraction Coverage



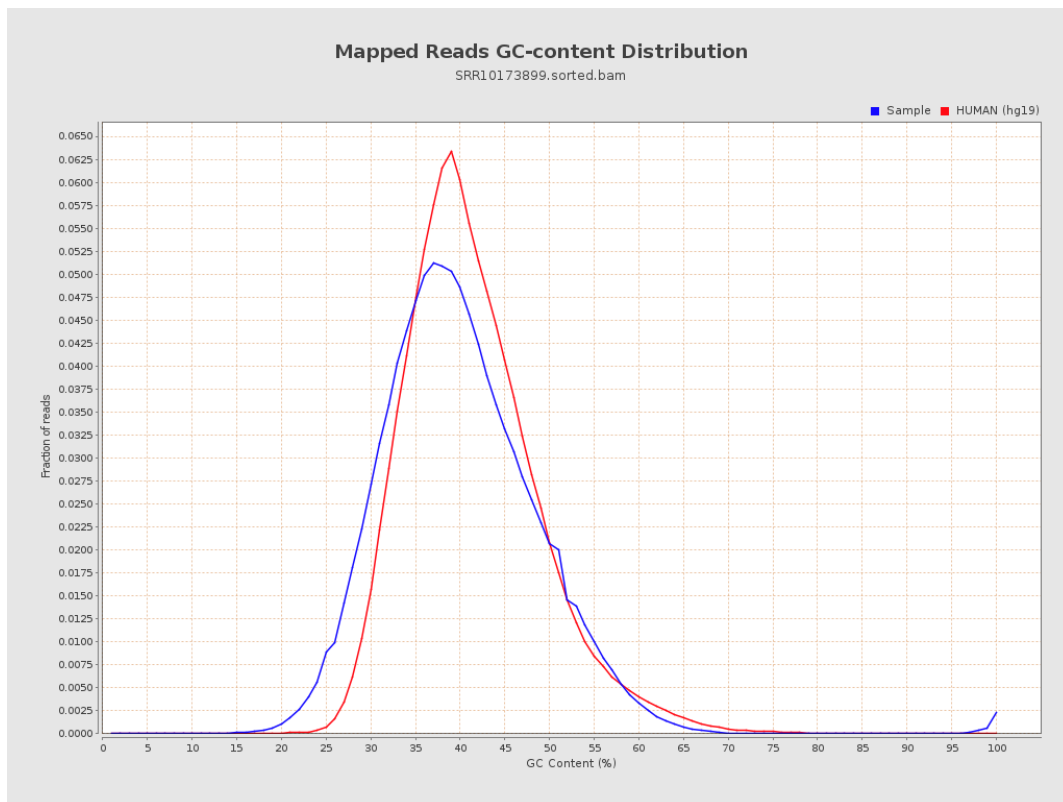
7. Results : Duplication Rate Histogram



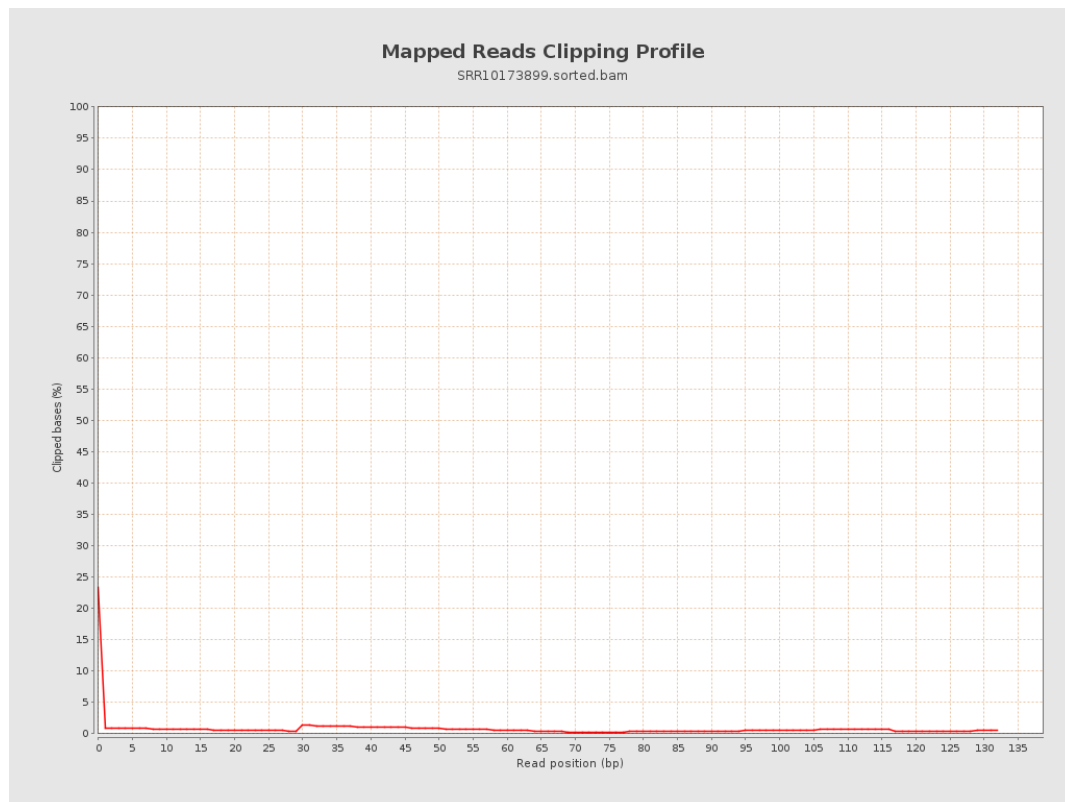
8. Results : Mapped Reads Nucleotide Content



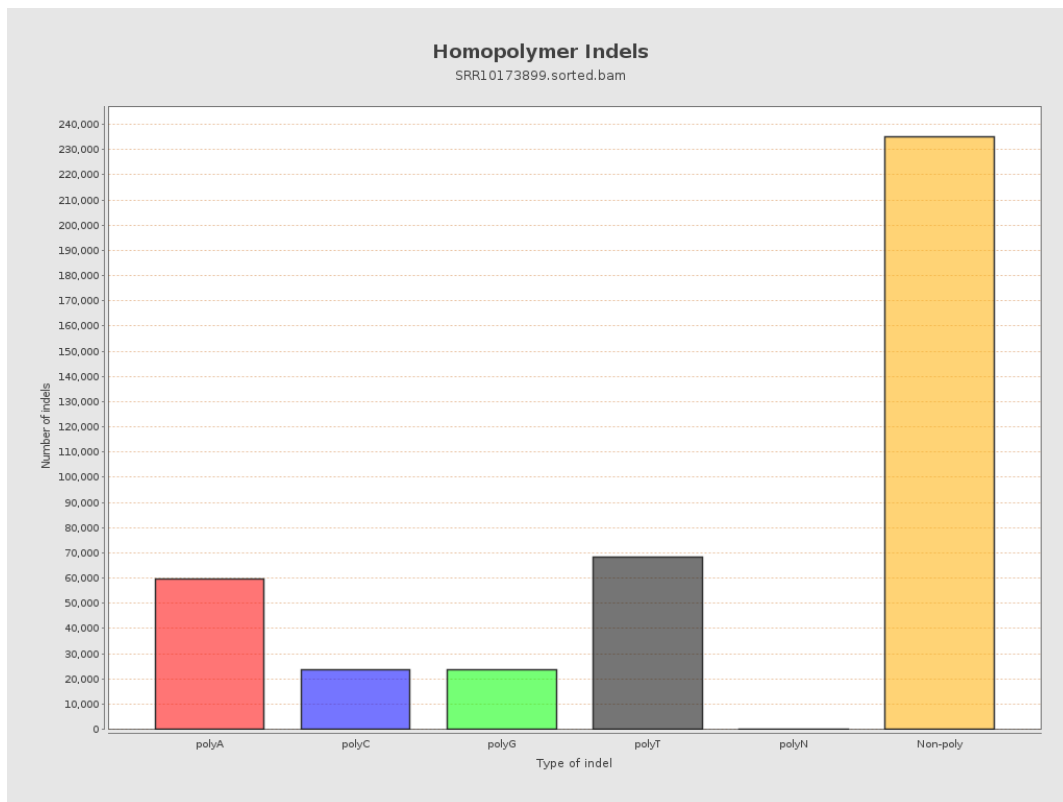
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



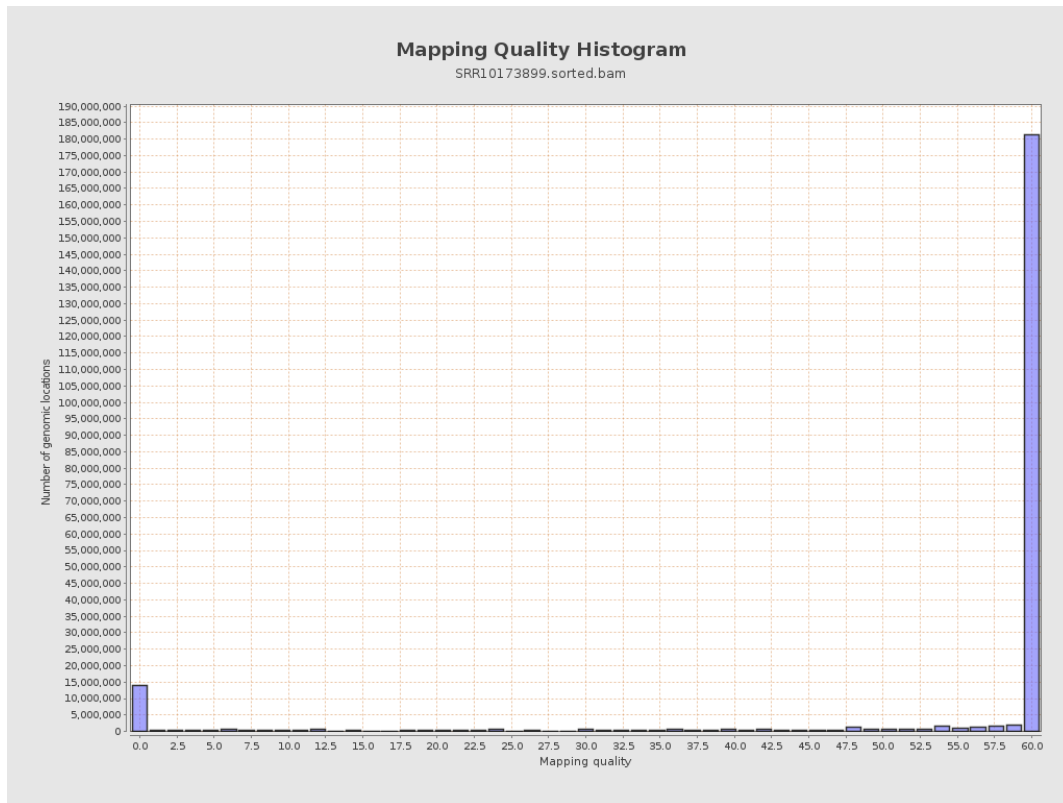
11. Results : Homopolymer Indels



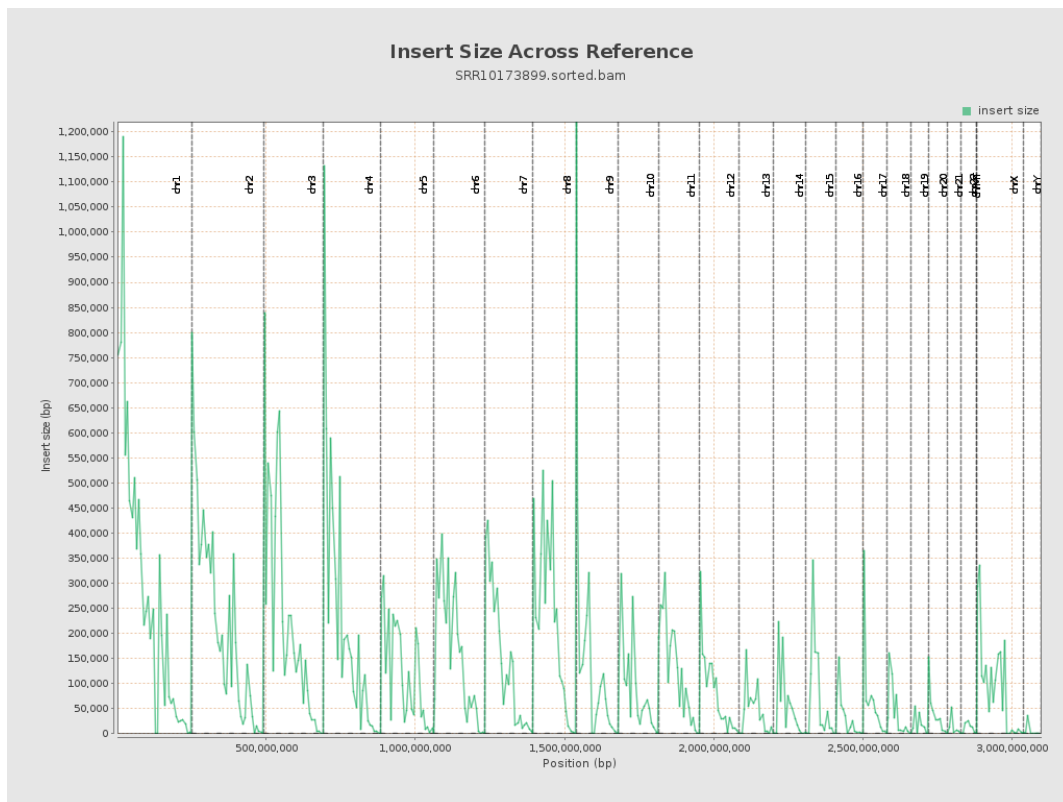
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

