

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:54:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173855.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_SRR10173855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173855_1.fastq.gz SRR10173855_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:54:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,846,802
Mapped reads	9,571,475 / 97.2%
Unmapped reads	275,327 / 2.8%
Mapped paired reads	9,571,475 / 97.2%
Mapped reads, first in pair	4,796,792 / 48.71%
Mapped reads, second in pair	4,774,683 / 48.49%
Mapped reads, both in pair	9,379,702 / 95.26%
Mapped reads, singletons	191,773 / 1.95%
Secondary alignments	0
Supplementary alignments	992,581 / 10.08%
Read min/max/mean length	30 / 133 / 128.22
Duplicated reads (estimated)	7,279,684 / 73.93%
Duplication rate	64.1%
Clipped reads	3,969,246 / 40.31%

2.2. ACGT Content

Number/percentage of A's	334,373,786 / 29.63%
Number/percentage of C's	225,456,040 / 19.98%
Number/percentage of T's	334,321,867 / 29.63%
Number/percentage of G's	234,243,474 / 20.76%
Number/percentage of N's	13,048 / 0%

GC Percentage	40.74%
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2.3. Coverage

Mean	0.3647
Standard Deviation	4.9756

2.4. Mapping Quality

Mean Mapping Quality	52.72
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2.5. Insert size

Mean	929,089.57
Standard Deviation	8,944,553.02
P25/Median/P75	145 / 204 / 293

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	11,694,443
Insertions	113,738
Mapped reads with at least one insertion	1.15%
Deletions	274,933
Mapped reads with at least one deletion	2.8%
Homopolymer indels	42.67%

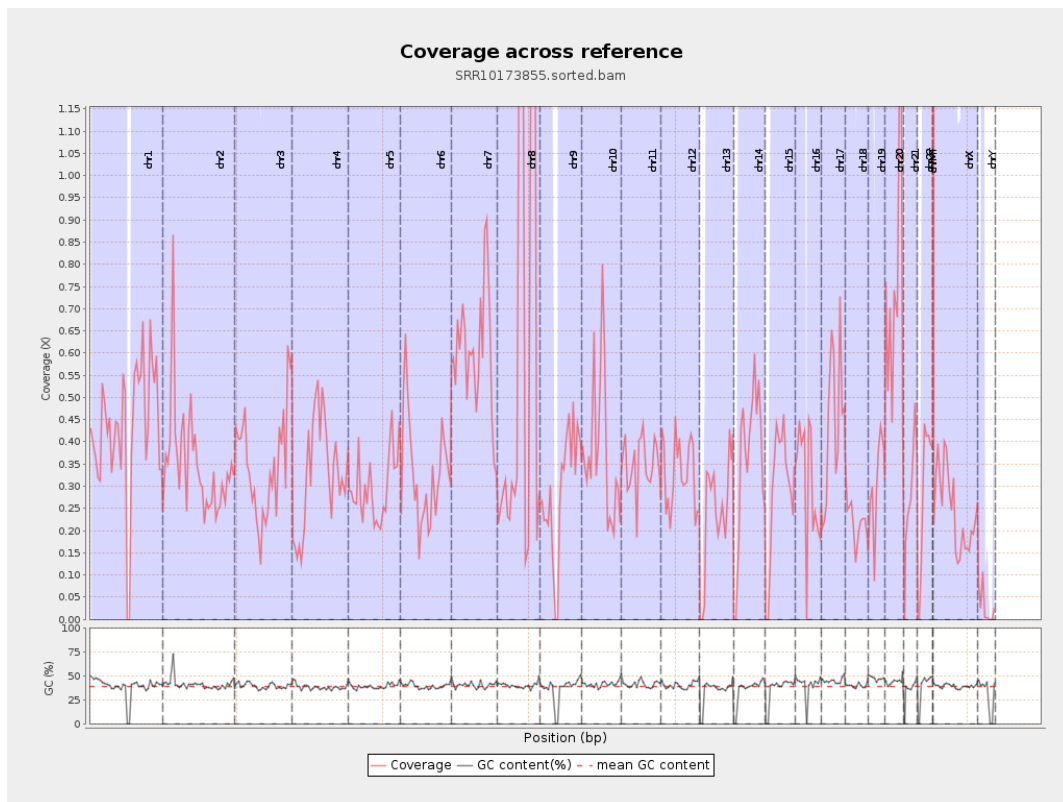
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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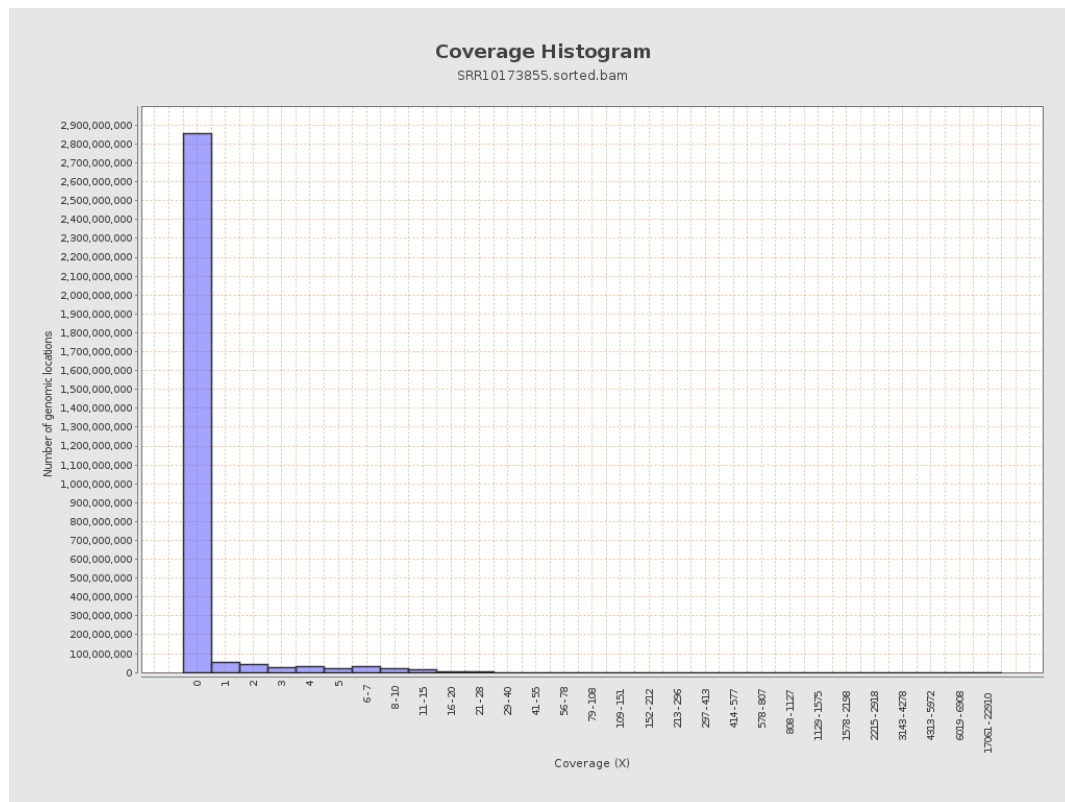
		bases	coverage	deviation
chr1	249250621	107395185	0.4309	2.4753
chr2	243199373	84666587	0.3481	15.9045
chr3	198022430	68830013	0.3476	1.6523
chr4	191154276	63192510	0.3306	2.0273
chr5	180915260	54295120	0.3001	1.515
chr6	171115067	56634740	0.331	1.6613
chr7	159138663	95268287	0.5986	4.1506
chr8	146364022	102278117	0.6988	2.9592
chr9	141213431	40665767	0.288	1.9328
chr10	135534747	51160528	0.3775	4.2151
chr11	135006516	47214920	0.3497	1.6955
chr12	133851895	44261987	0.3307	1.613
chr13	115169878	27654261	0.2401	1.3535
chr14	107349540	39302923	0.3661	1.7148
chr15	102531392	29426220	0.287	1.4834
chr16	90354753	27707462	0.3067	2.0275
chr17	81195210	35403601	0.436	2.0396
chr18	78077248	17506872	0.2242	2.3142
chr19	59128983	17736022	0.3	1.9232
chr20	63025520	48149318	0.764	2.5056
chr21	48129895	13624851	0.2831	1.5901
chr22	51304566	14630598	0.2852	1.4384
chrMT	16571	2449085	147.7934	104.6075
chrX	155270560	37904158	0.2441	1.3781

chrY	59373566	1708218	0.0288	1.1266
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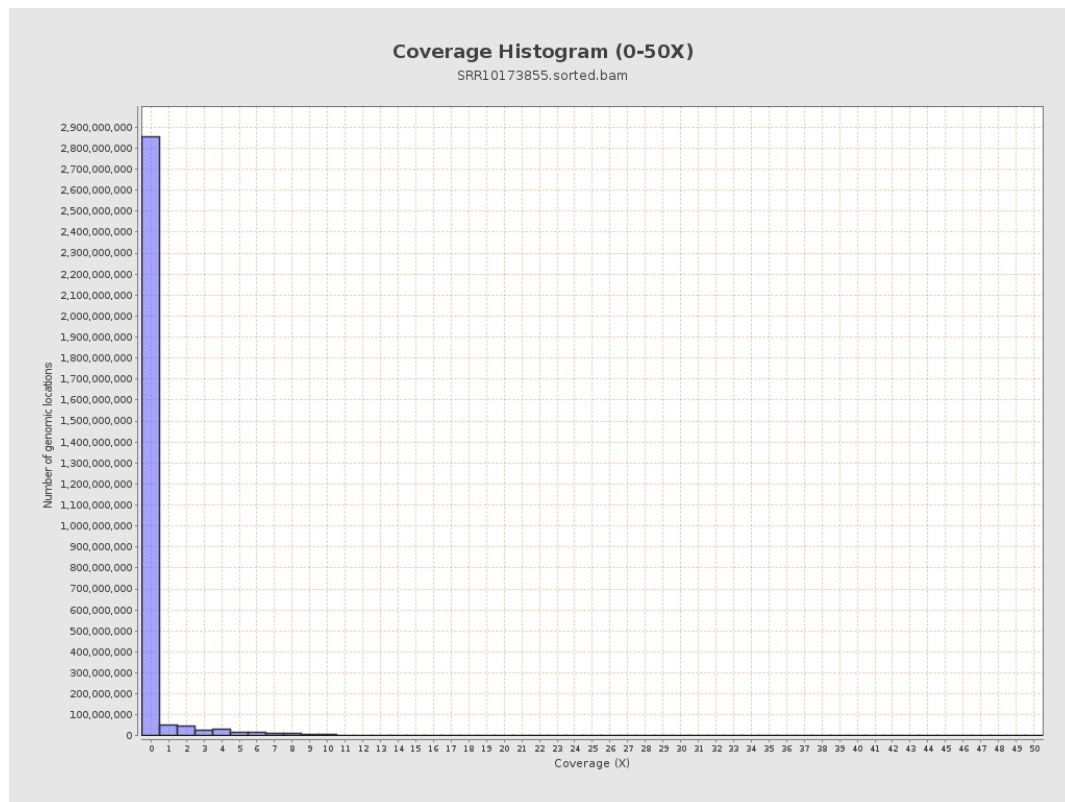
3. Results : Coverage across reference



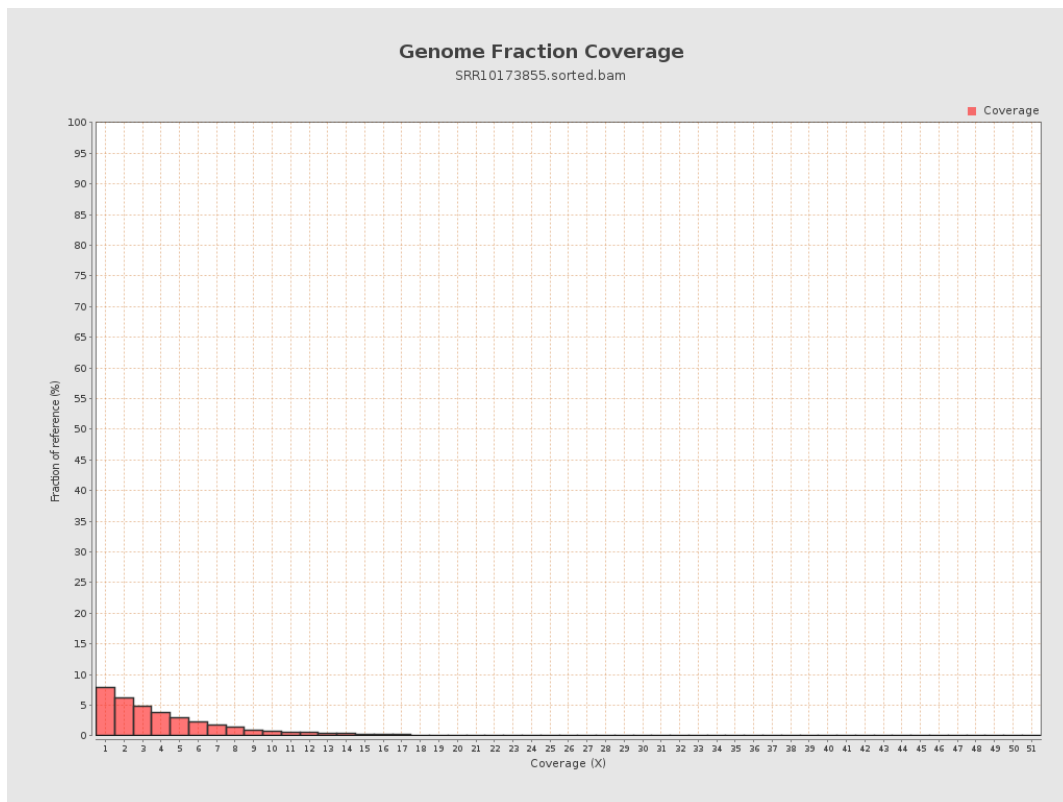
4. Results : Coverage Histogram



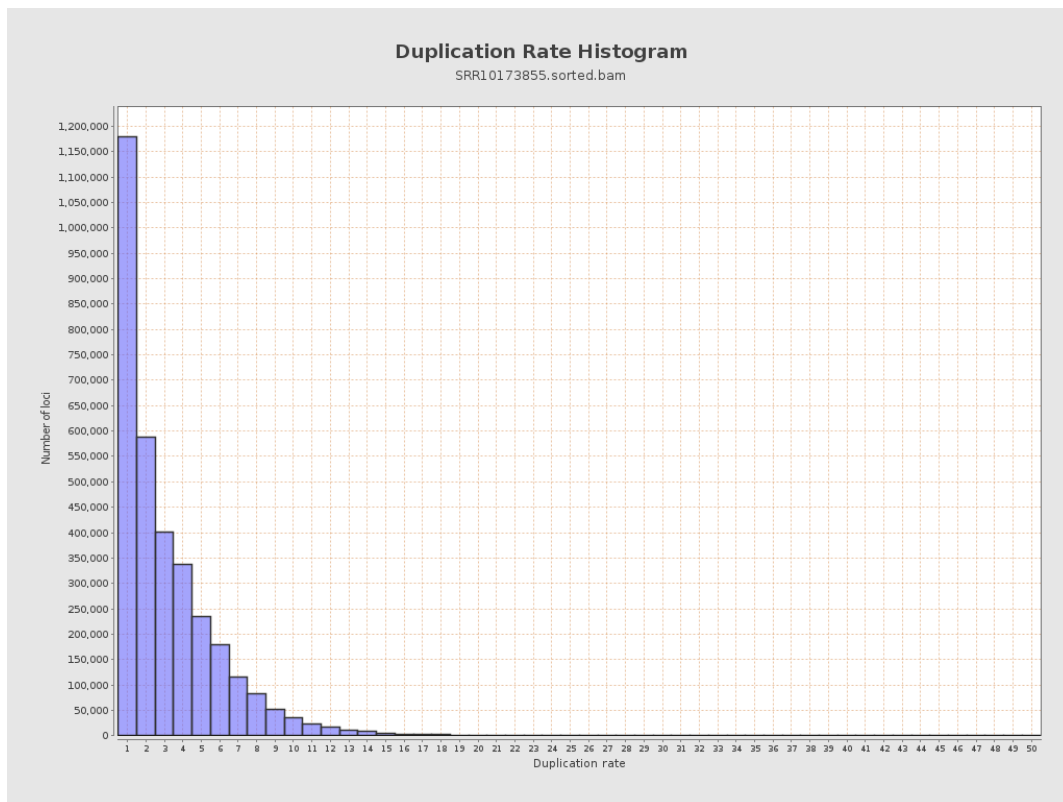
5. Results : Coverage Histogram (0-50X)



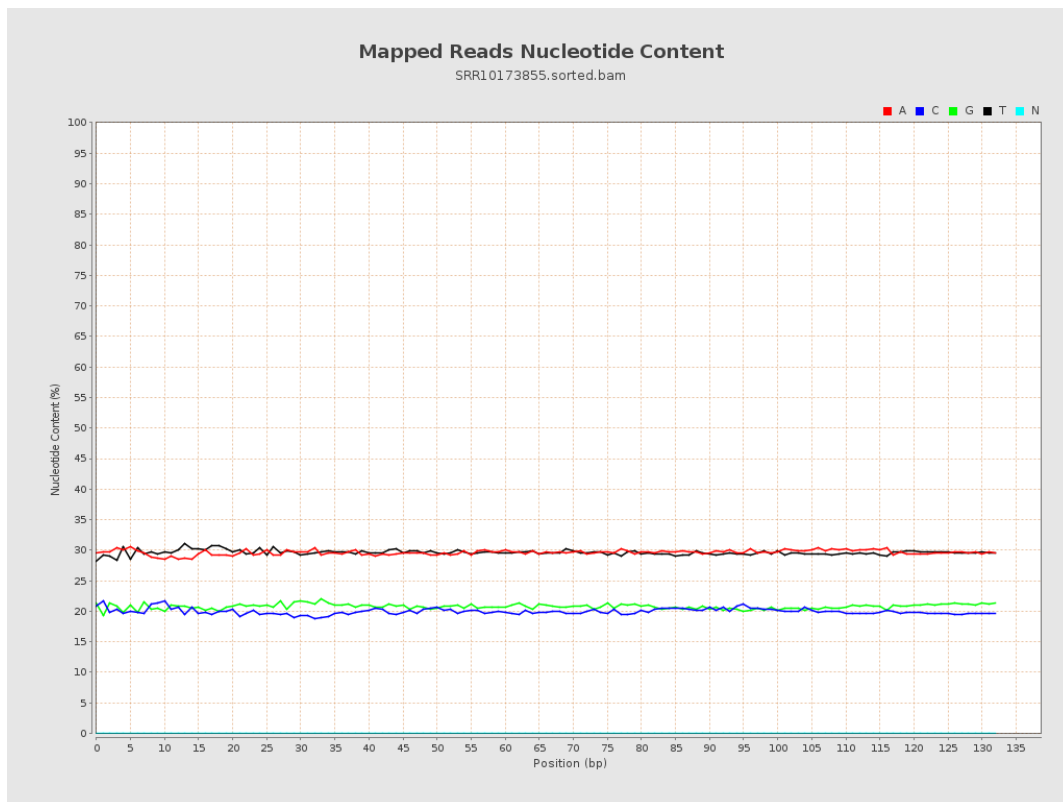
6. Results : Genome Fraction Coverage



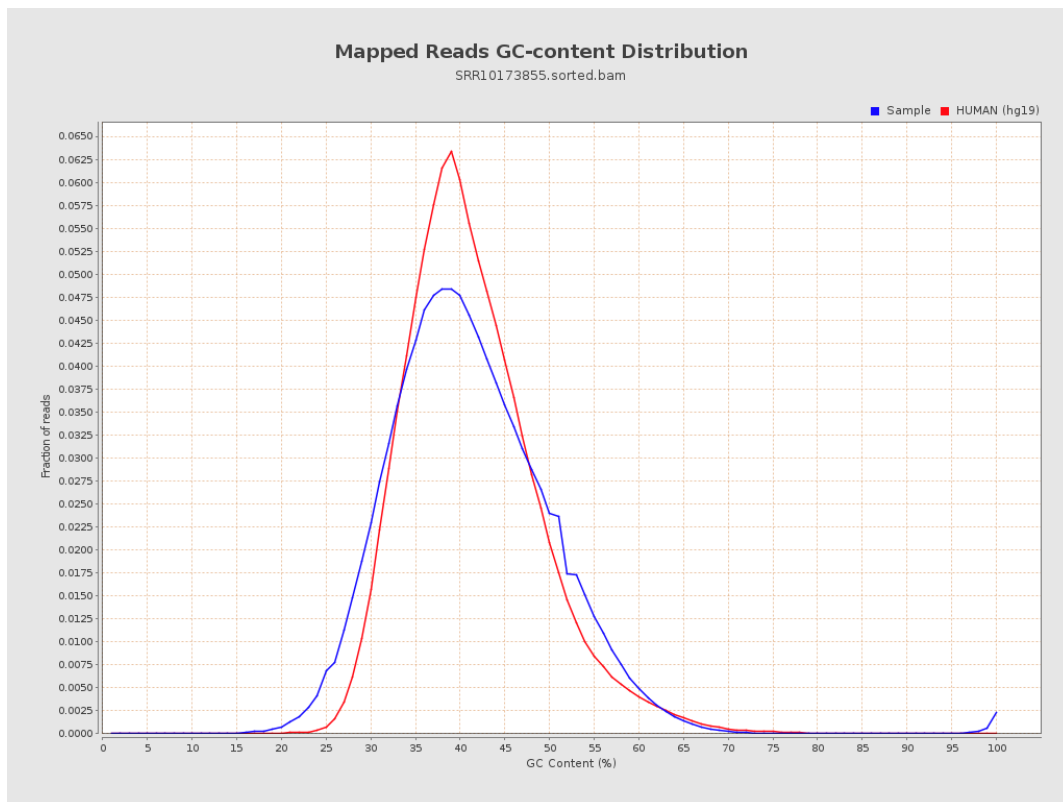
7. Results : Duplication Rate Histogram



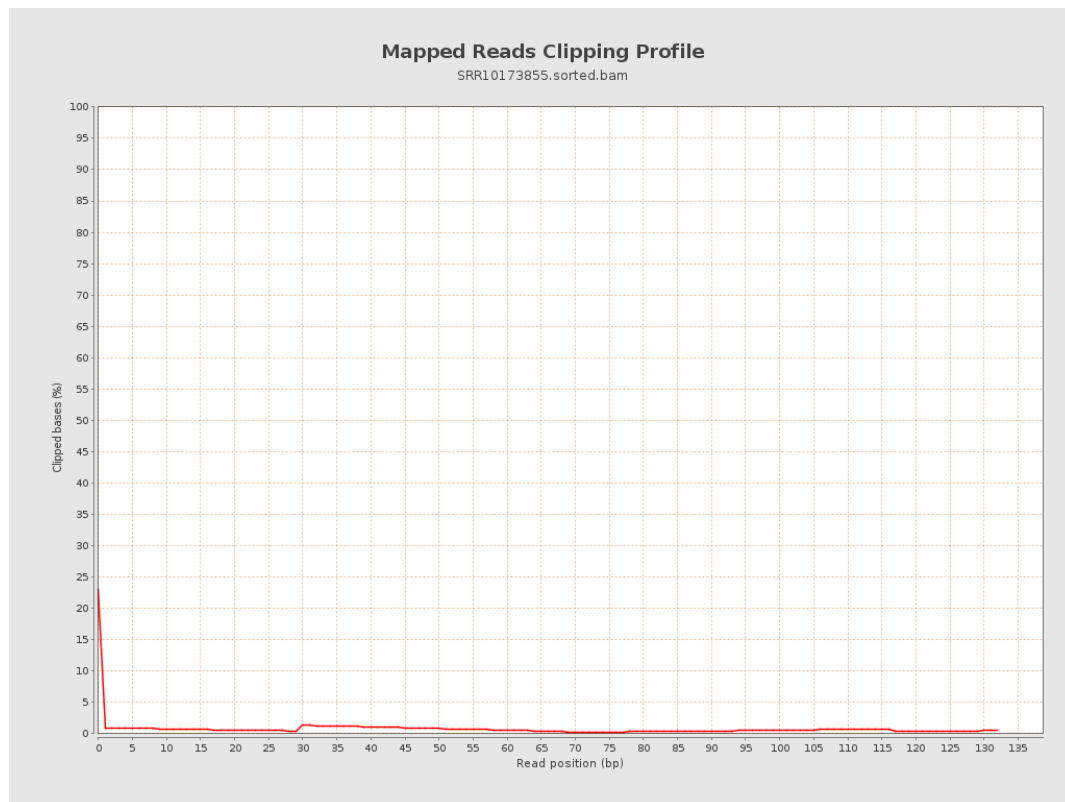
8. Results : Mapped Reads Nucleotide Content



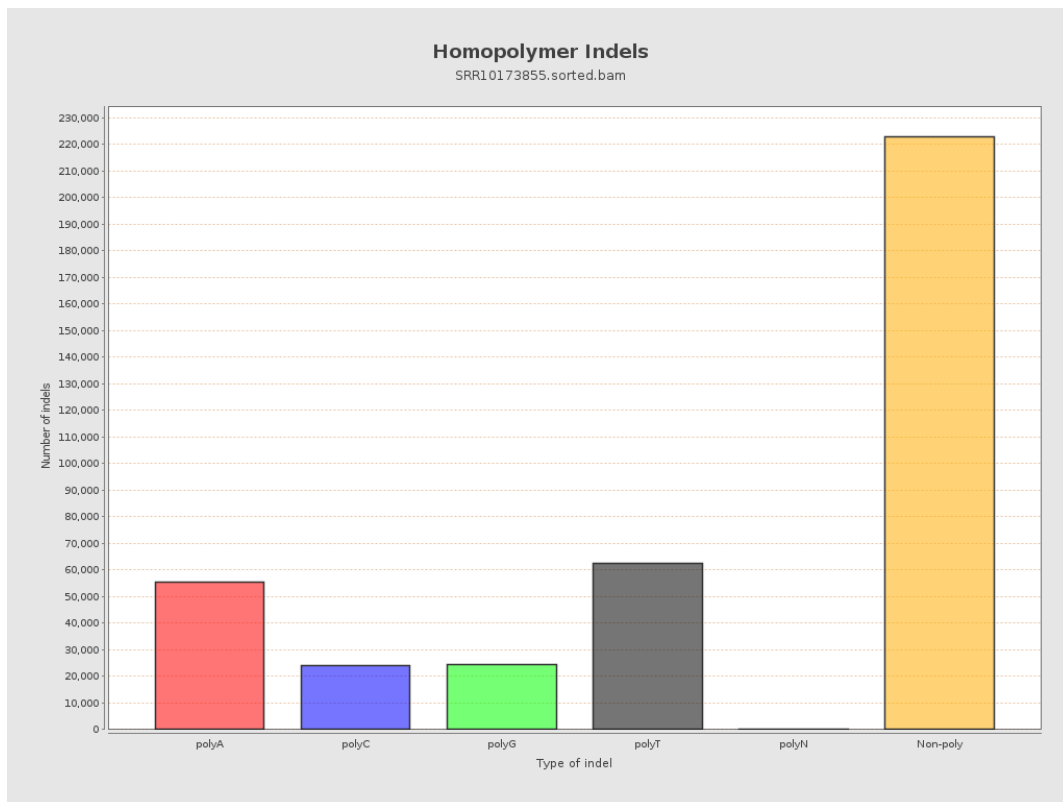
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



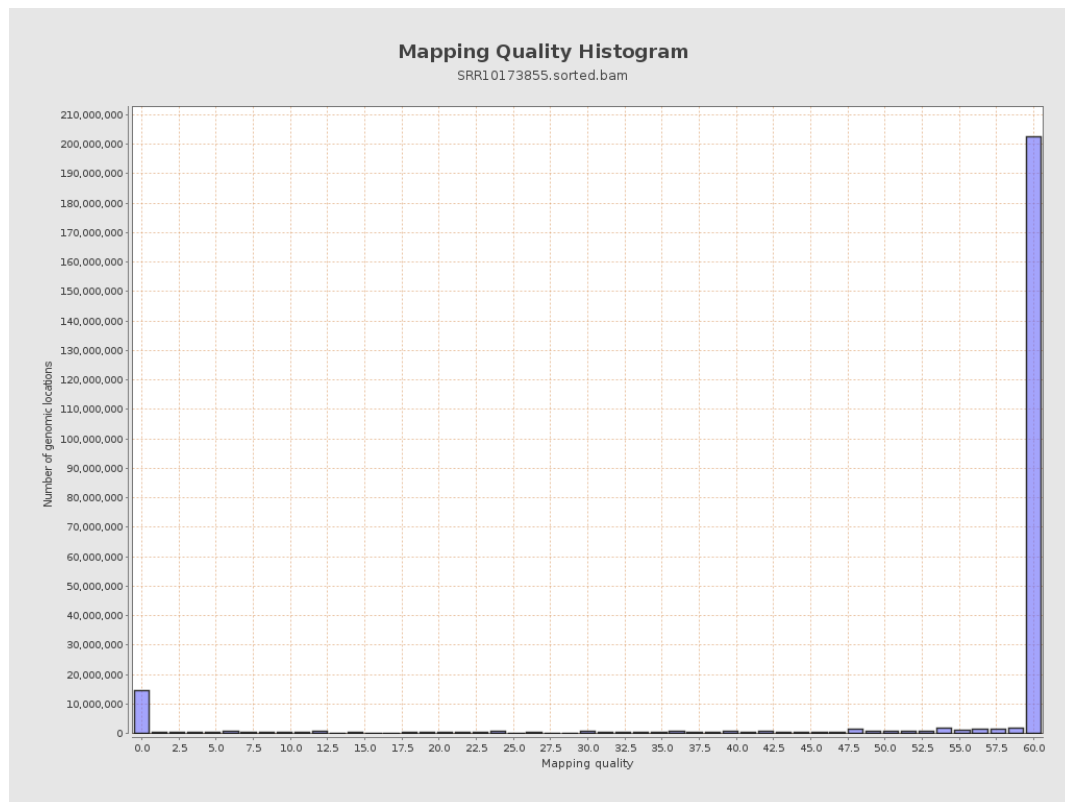
11. Results : Homopolymer Indels



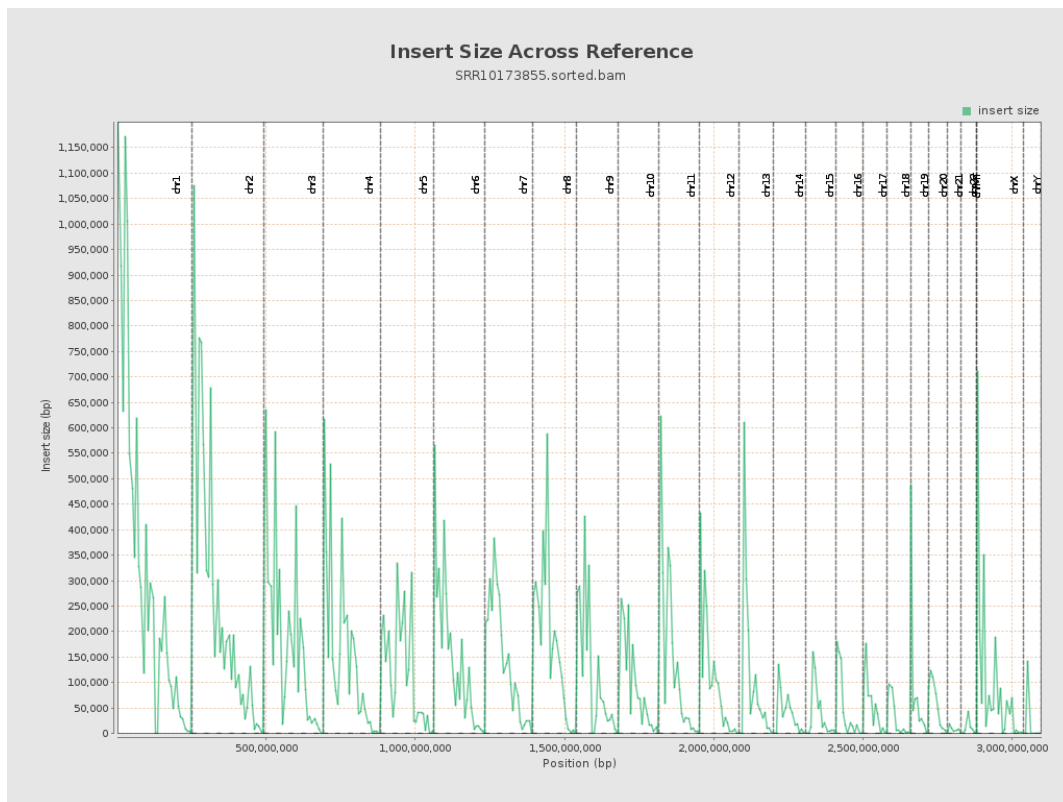
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

