

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:09:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173851.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_SRR10173851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173851_1.fastq.gz SRR10173851_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:09:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,394,898
Mapped reads	1,359,232 / 97.44%
Unmapped reads	35,666 / 2.56%
Mapped paired reads	1,359,232 / 97.44%
Mapped reads, first in pair	679,512 / 48.71%
Mapped reads, second in pair	679,720 / 48.73%
Mapped reads, both in pair	1,337,020 / 95.85%
Mapped reads, singletons	22,212 / 1.59%
Secondary alignments	0
Supplementary alignments	127,668 / 9.15%
Read min/max/mean length	30 / 133 / 127.69
Duplicated reads (estimated)	1,030,378 / 73.87%
Duplication rate	63.96%
Clipped reads	522,409 / 37.45%

2.2. ACGT Content

Number/percentage of A's	48,542,048 / 30.22%
Number/percentage of C's	31,381,322 / 19.54%
Number/percentage of T's	48,306,021 / 30.08%
Number/percentage of G's	32,385,935 / 20.16%
Number/percentage of N's	2,030 / 0%

GC Percentage	39.7%
---------------	-------

2.3. Coverage

Mean	0.0519
Standard Deviation	0.935

2.4. Mapping Quality

Mean Mapping Quality	52.99
----------------------	-------

2.5. Insert size

Mean	820,616.85
Standard Deviation	8,578,228.43
P25/Median/P75	143 / 200 / 280

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	1,642,145
Insertions	18,439
Mapped reads with at least one insertion	1.3%
Deletions	33,398
Mapped reads with at least one deletion	2.4%
Homopolymer indels	43.1%

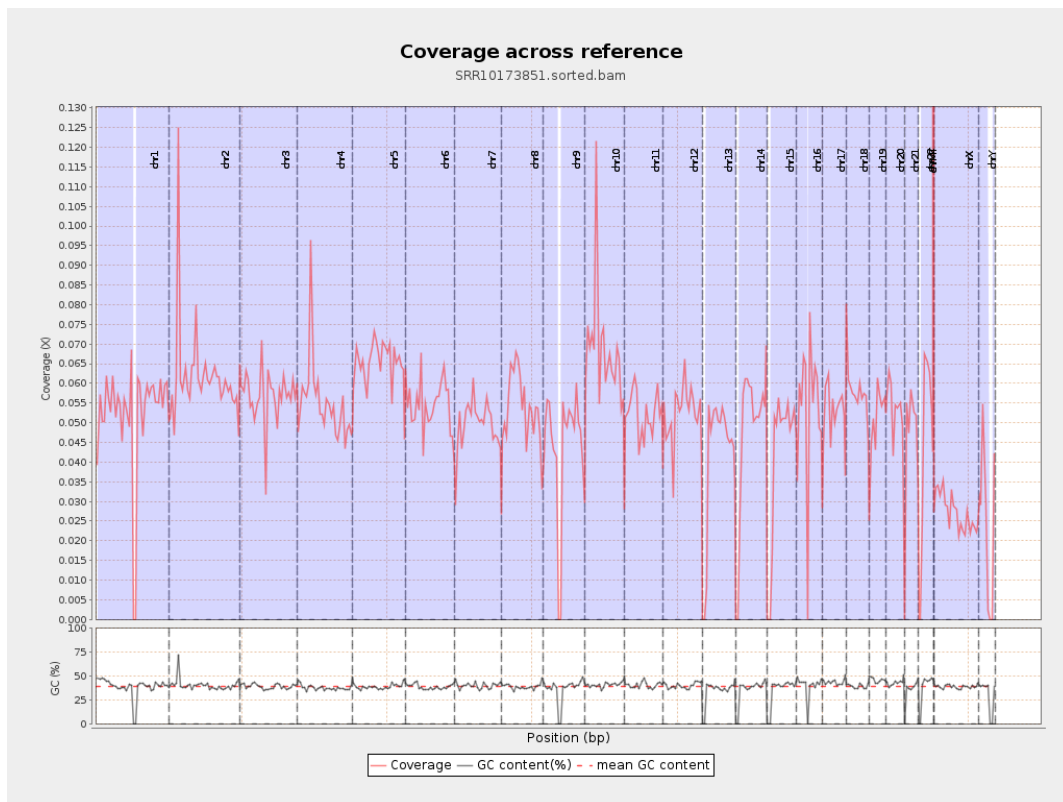
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

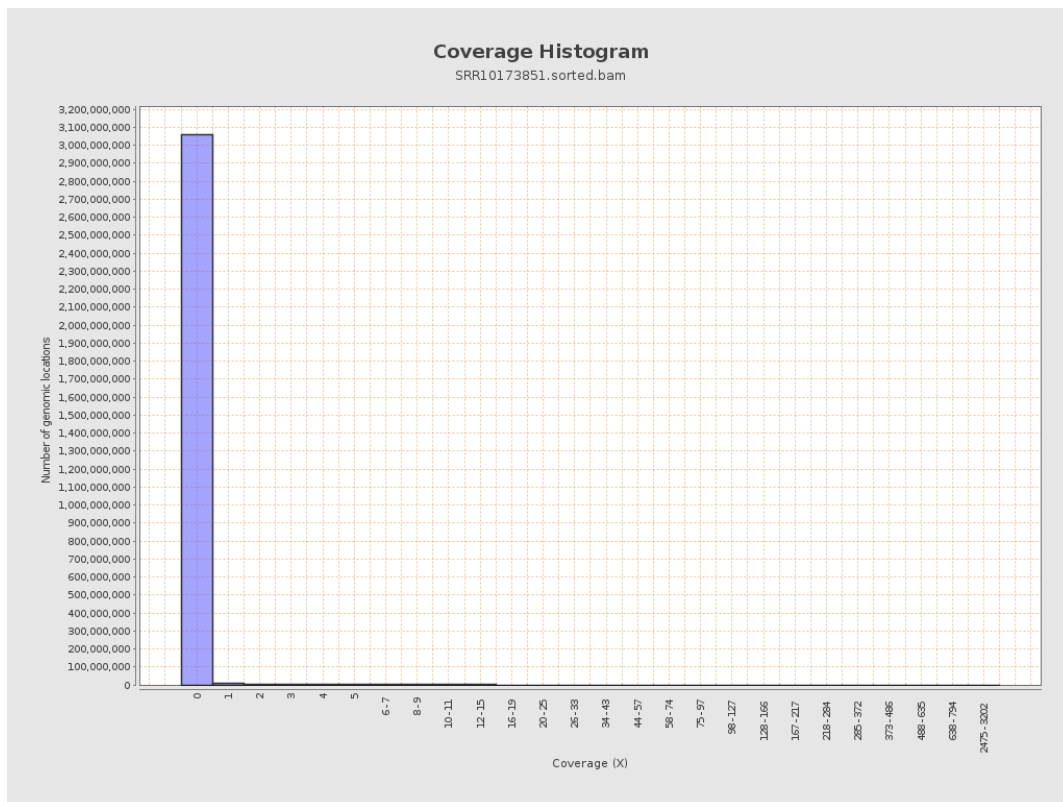
		bases	coverage	deviation
chr1	249250621	13006849	0.0522	0.7532
chr2	243199373	15028581	0.0618	2.3285
chr3	198022430	11267270	0.0569	0.668
chr4	191154276	10462447	0.0547	0.7278
chr5	180915260	11843990	0.0655	0.7183
chr6	171115067	9331689	0.0545	0.6924
chr7	159138663	7938886	0.0499	0.706
chr8	146364022	7888563	0.0539	0.8823
chr9	141213431	6246502	0.0442	0.6549
chr10	135534747	9295506	0.0686	0.9088
chr11	135006516	7023677	0.052	0.6455
chr12	133851895	7041306	0.0526	0.6417
chr13	115169878	4752702	0.0413	0.5721
chr14	107349540	5053968	0.0471	0.6071
chr15	102531392	4272513	0.0417	0.5602
chr16	90354753	4837733	0.0535	0.6847
chr17	81195210	4260360	0.0525	0.6404
chr18	78077248	4531675	0.058	0.9357
chr19	59128983	3029231	0.0512	0.6994
chr20	63025520	3334108	0.0529	0.649
chr21	48129895	2218850	0.0461	0.6809
chr22	51304566	2212322	0.0431	0.5996
chrMT	16571	247626	14.9433	15.1449
chrX	155270560	4195690	0.027	0.4582

chrY	59373566	1381745	0.0233	0.489
------	----------	---------	--------	-------

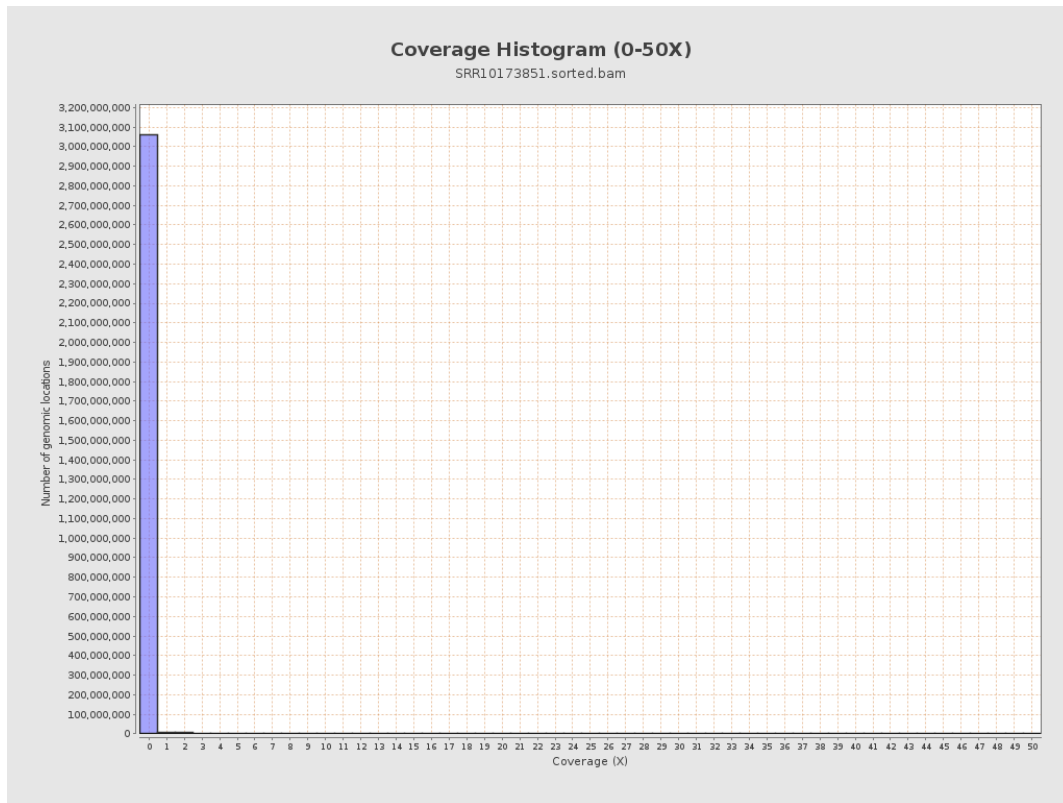
3. Results : Coverage across reference



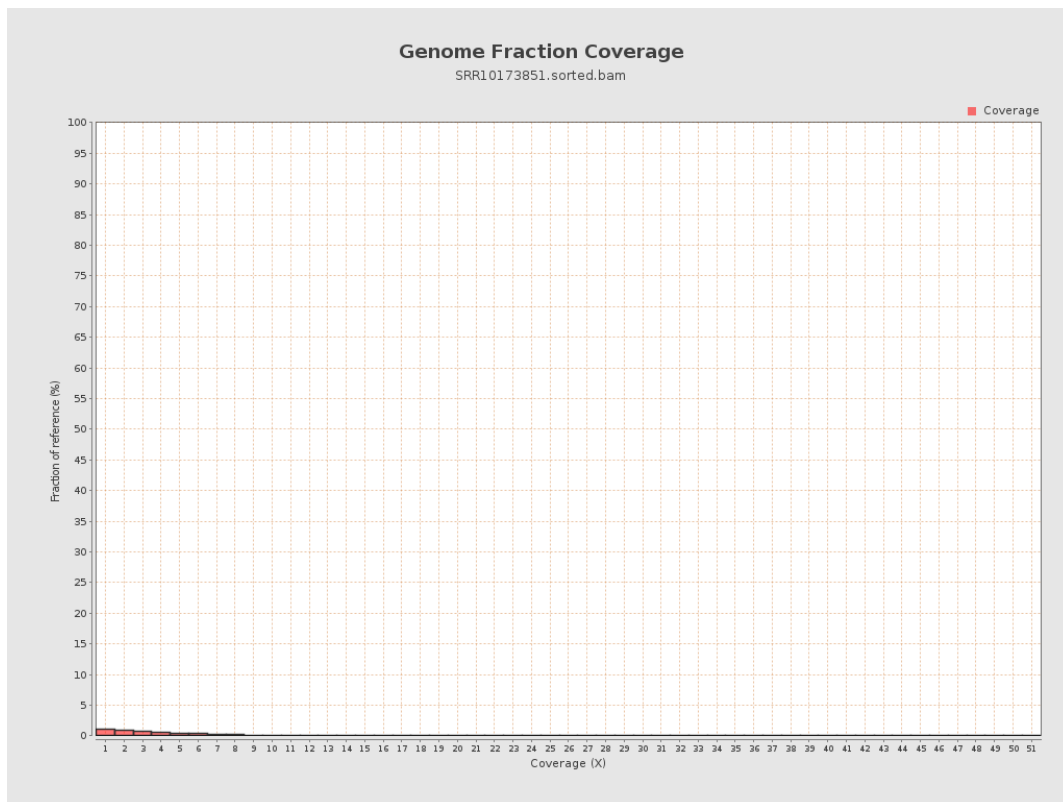
4. Results : Coverage Histogram



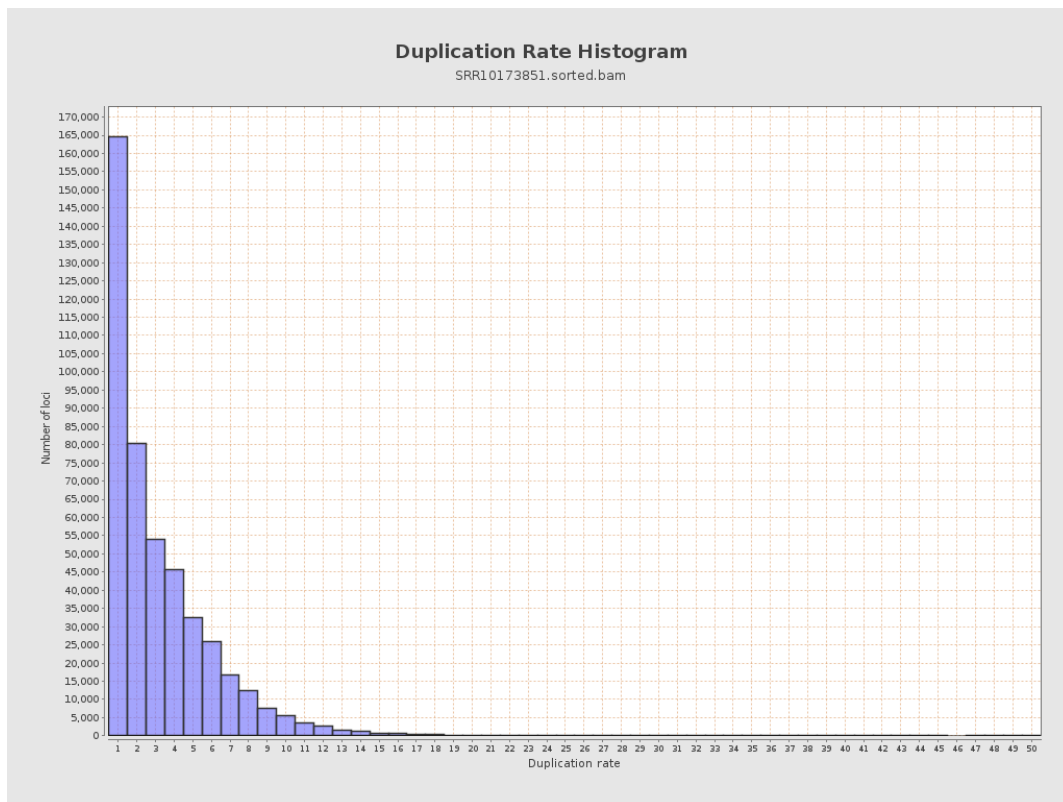
5. Results : Coverage Histogram (0-50X)



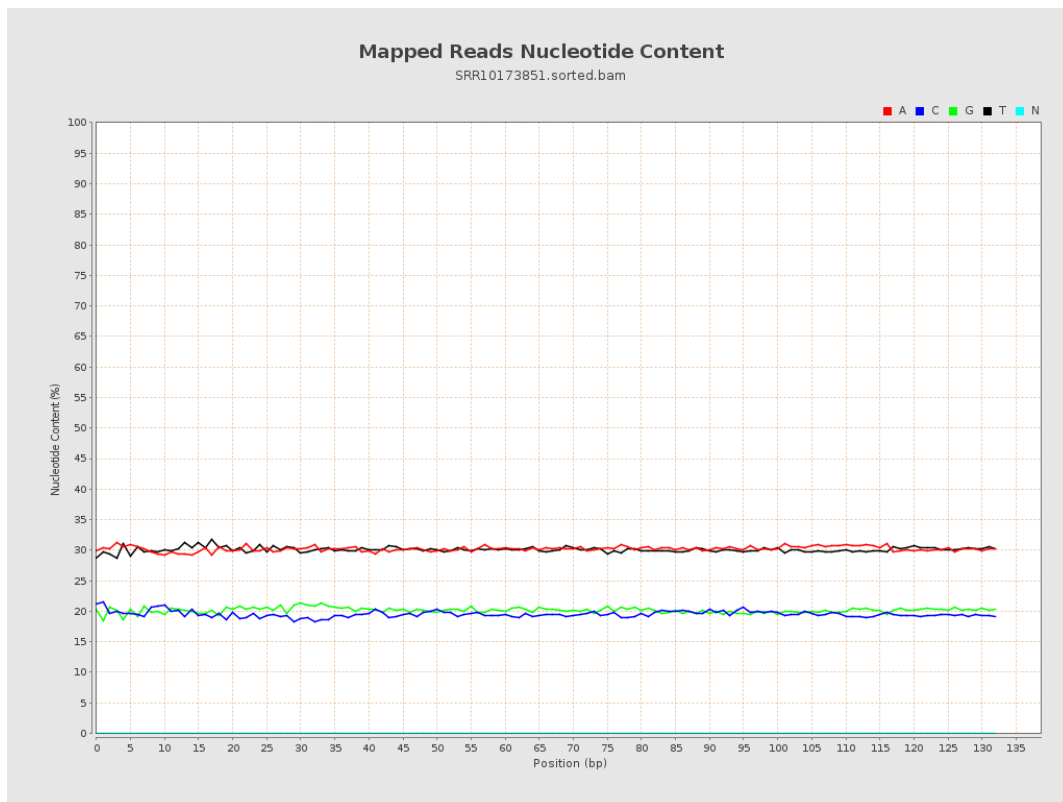
6. Results : Genome Fraction Coverage



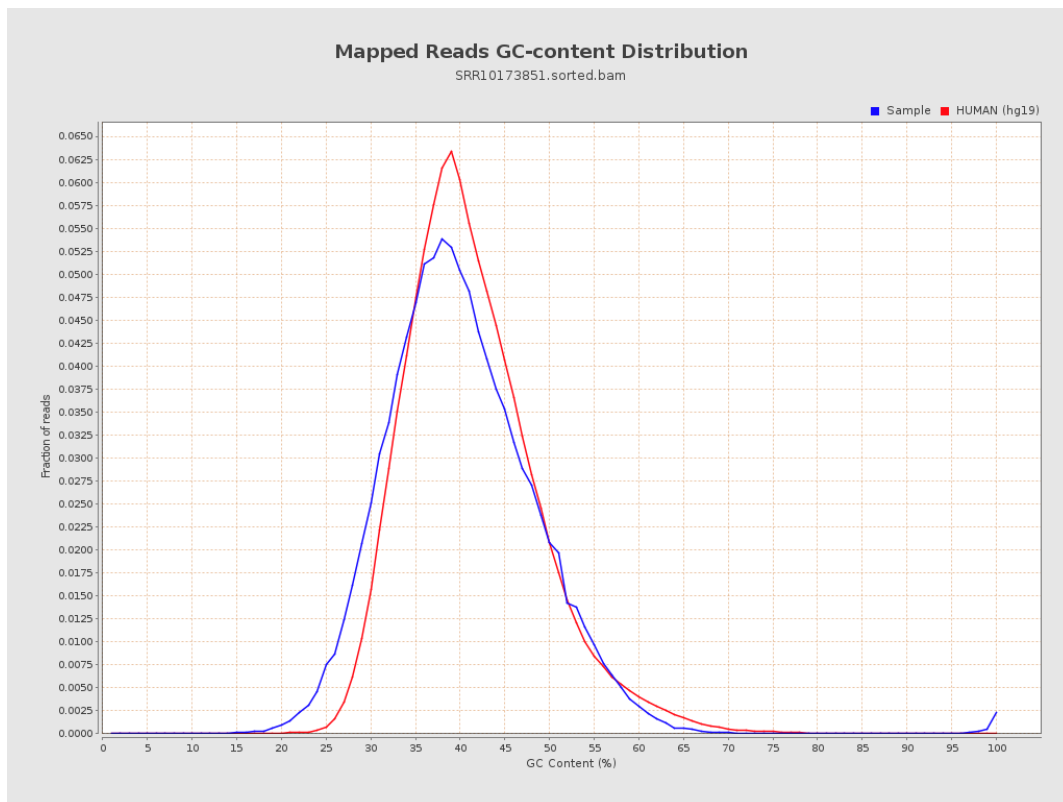
7. Results : Duplication Rate Histogram



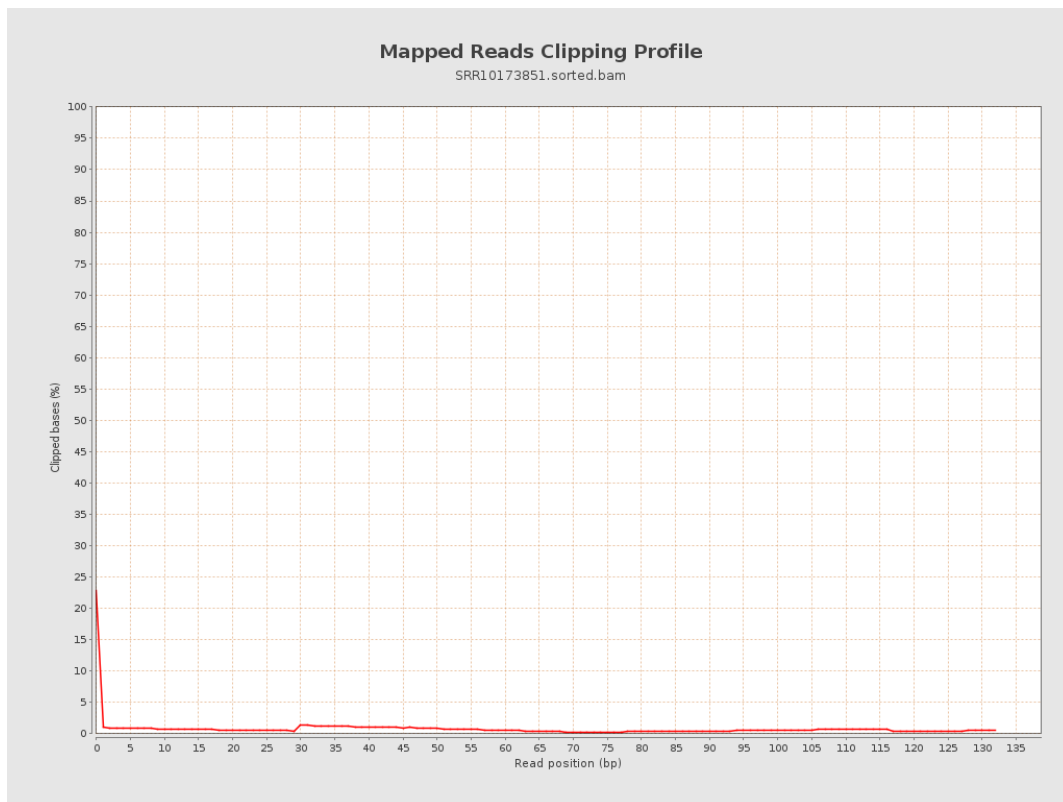
8. Results : Mapped Reads Nucleotide Content



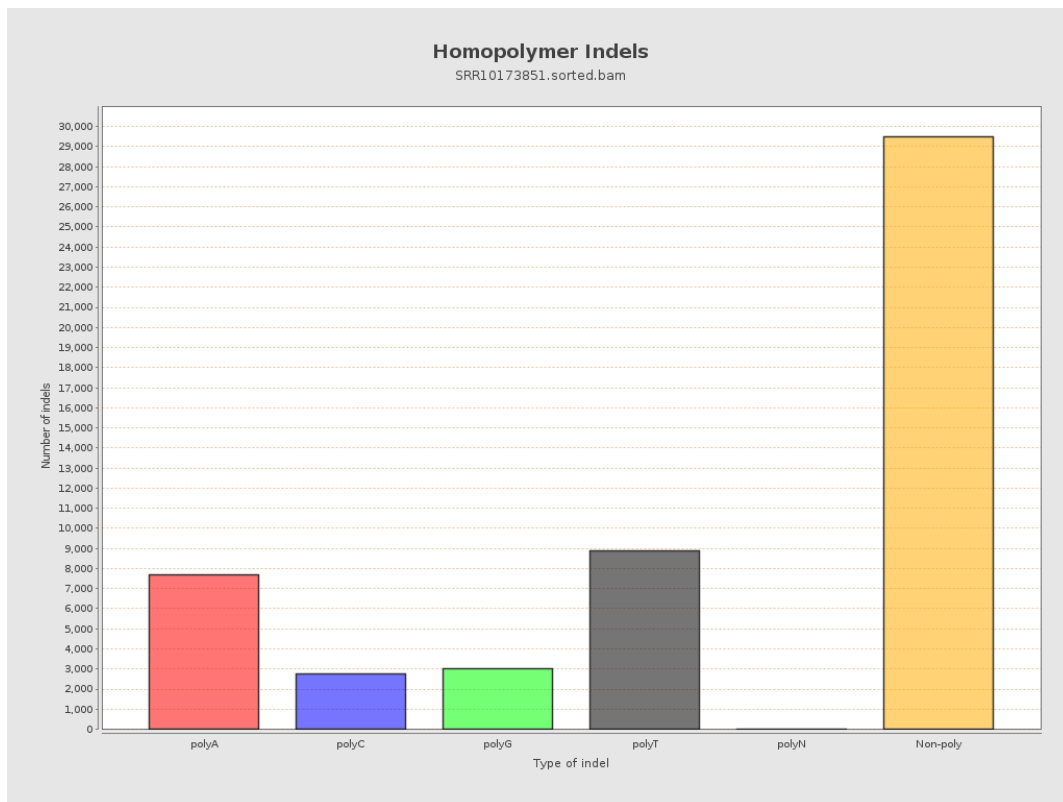
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



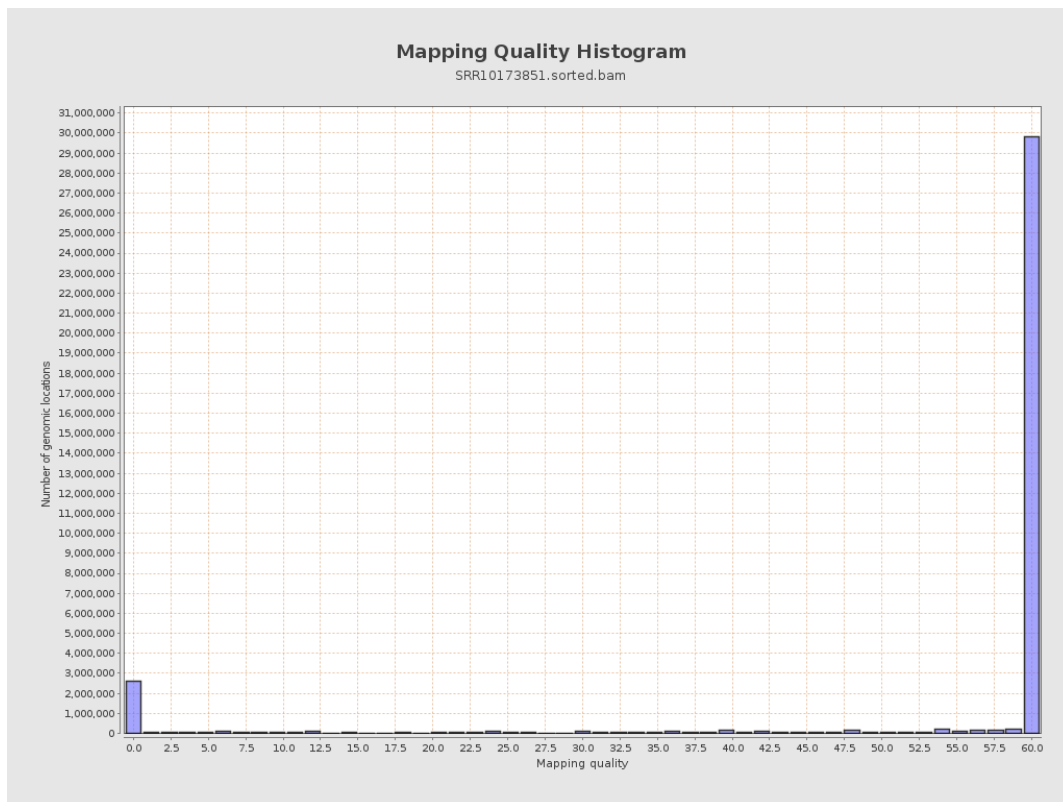
11. Results : Homopolymer Indels



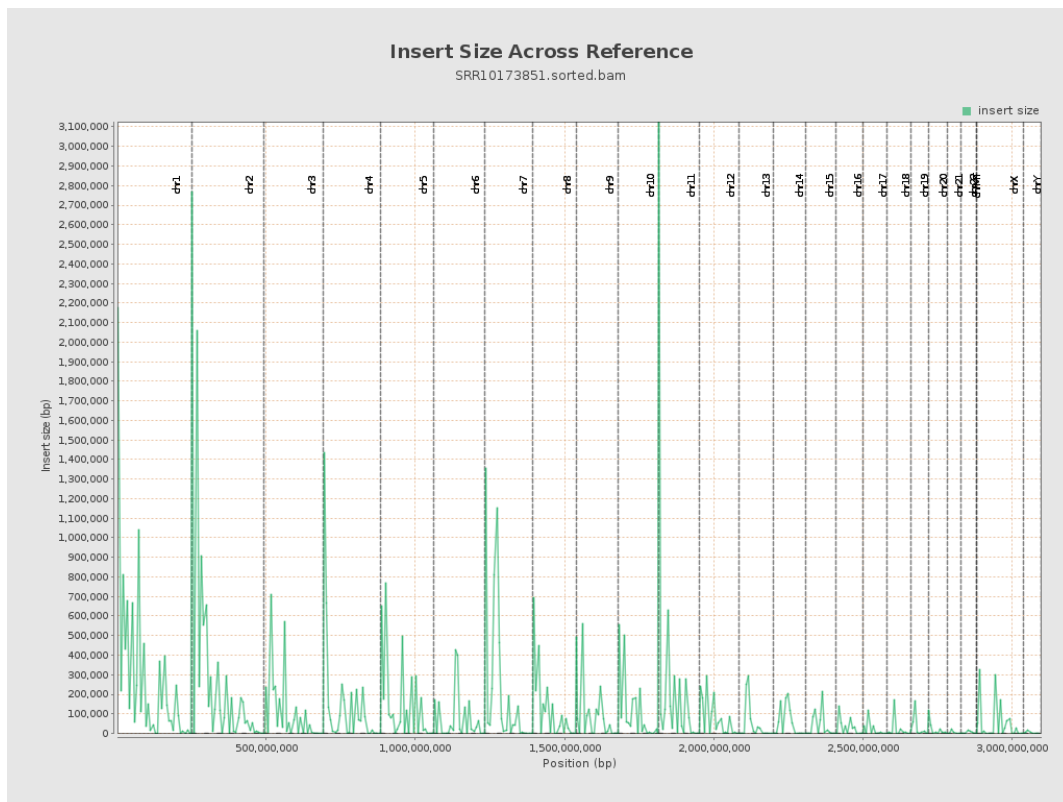
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

