

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:04:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173867.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_SRR10173867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173867_1.fastq.gz SRR10173867_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:04:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173867.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,813,198
Mapped reads	4,671,385 / 97.05%
Unmapped reads	141,813 / 2.95%
Mapped paired reads	4,671,385 / 97.05%
Mapped reads, first in pair	2,343,904 / 48.7%
Mapped reads, second in pair	2,327,481 / 48.36%
Mapped reads, both in pair	4,575,102 / 95.05%
Mapped reads, singletons	96,283 / 2%
Secondary alignments	0
Supplementary alignments	462,357 / 9.61%
Read min/max/mean length	30 / 133 / 127.81
Duplicated reads (estimated)	3,529,278 / 73.33%
Duplication rate	63.58%
Clipped reads	1,985,981 / 41.26%

2.2. ACGT Content

Number/percentage of A's	165,575,801 / 30.22%
Number/percentage of C's	106,601,705 / 19.46%
Number/percentage of T's	165,093,634 / 30.14%
Number/percentage of G's	110,559,111 / 20.18%
Number/percentage of N's	6,654 / 0%

GC Percentage	39.64%
---------------	--------

2.3. Coverage

Mean	0.1771
Standard Deviation	2.6891

2.4. Mapping Quality

Mean Mapping Quality	52.66
----------------------	-------

2.5. Insert size

Mean	857,372.21
Standard Deviation	8,429,012.31
P25/Median/P75	139 / 196 / 282

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	5,614,065
Insertions	57,976
Mapped reads with at least one insertion	1.2%
Deletions	121,519
Mapped reads with at least one deletion	2.54%
Homopolymer indels	42.95%

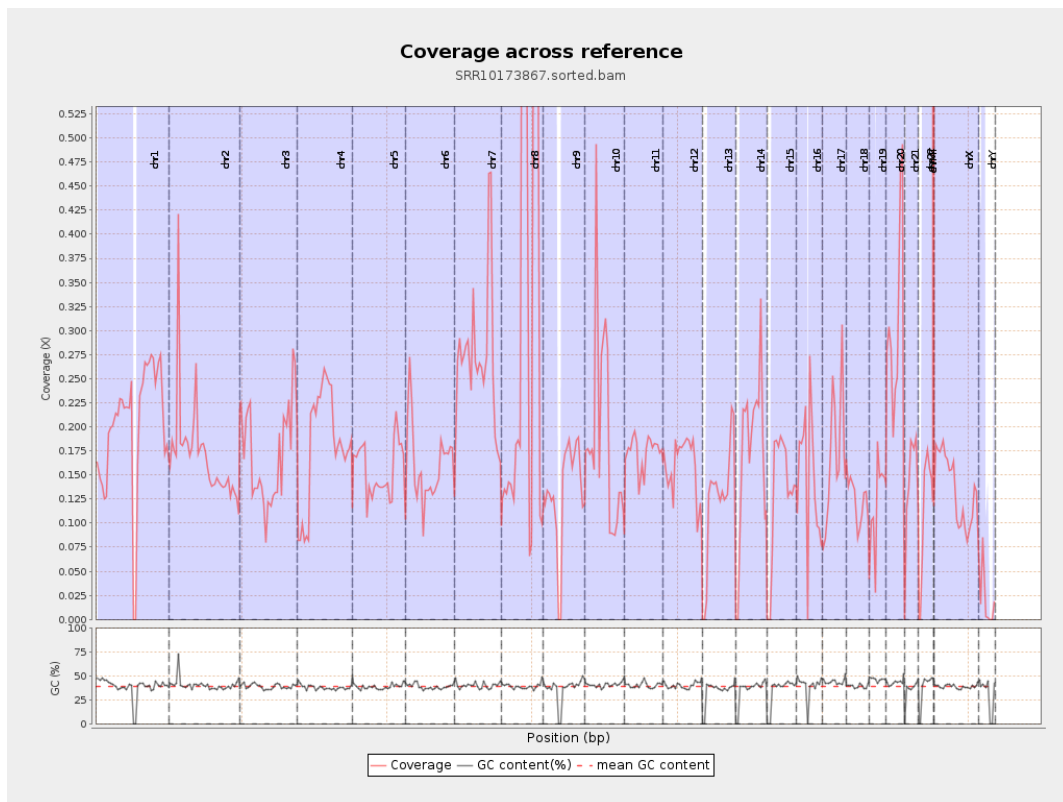
2.7. Chromosome stats

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

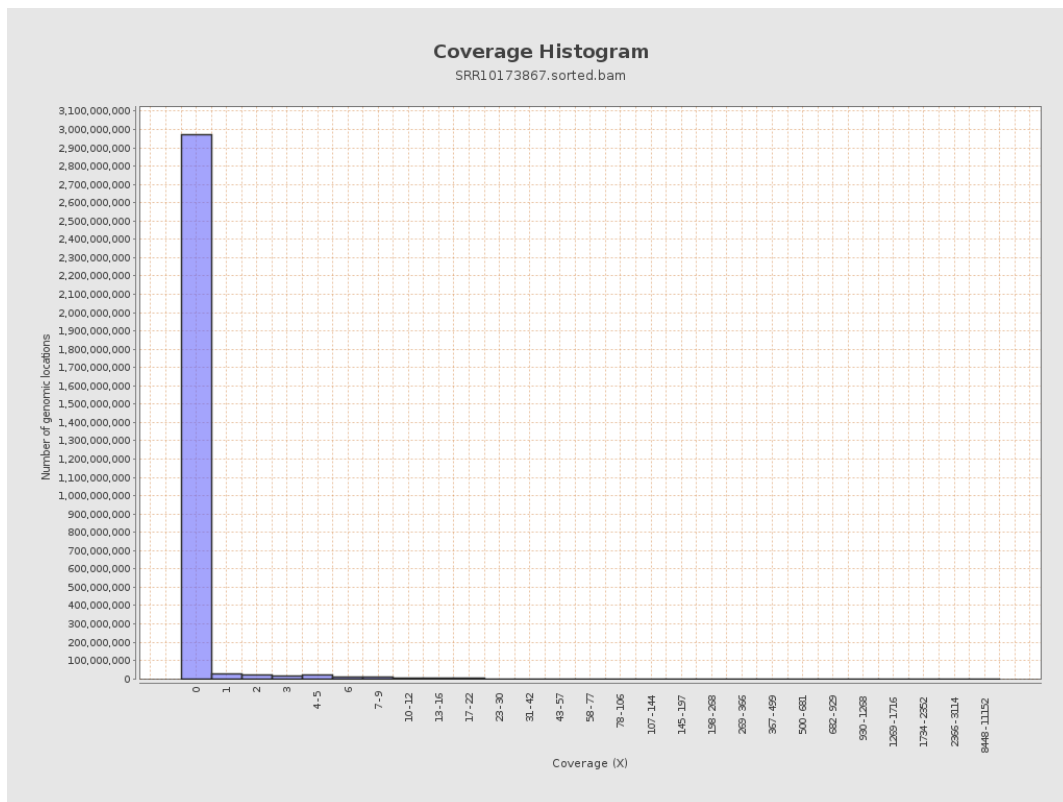
		bases	coverage	deviation
chr1	249250621	50046241	0.2008	1.6175
chr2	243199373	41602909	0.1711	7.8318
chr3	198022430	33876000	0.1711	1.1695
chr4	191154276	34414556	0.18	1.5202
chr5	180915260	28164230	0.1557	1.0958
chr6	171115067	27129639	0.1585	1.1575
chr7	159138663	43613874	0.2741	2.6807
chr8	146364022	54271298	0.3708	2.077
chr9	141213431	18722656	0.1326	1.3367
chr10	135534747	25840630	0.1907	3.4044
chr11	135006516	23312110	0.1727	1.1828
chr12	133851895	21400816	0.1599	1.1157
chr13	115169878	14374315	0.1248	0.9943
chr14	107349540	18621335	0.1735	1.1785
chr15	102531392	13586396	0.1325	1.0017
chr16	90354753	13156433	0.1456	1.473
chr17	81195210	13821812	0.1702	1.311
chr18	78077248	9732217	0.1246	1.6555
chr19	59128983	7138495	0.1207	1.1842
chr20	63025520	19187558	0.3044	1.5746
chr21	48129895	6784870	0.141	1.1399
chr22	51304566	5666719	0.1105	0.892
chrMT	16571	1563564	94.3554	68.3271
chrX	155270560	20941476	0.1349	1.021

chrY	59373566	1174500	0.0198	0.8981
------	----------	---------	--------	--------

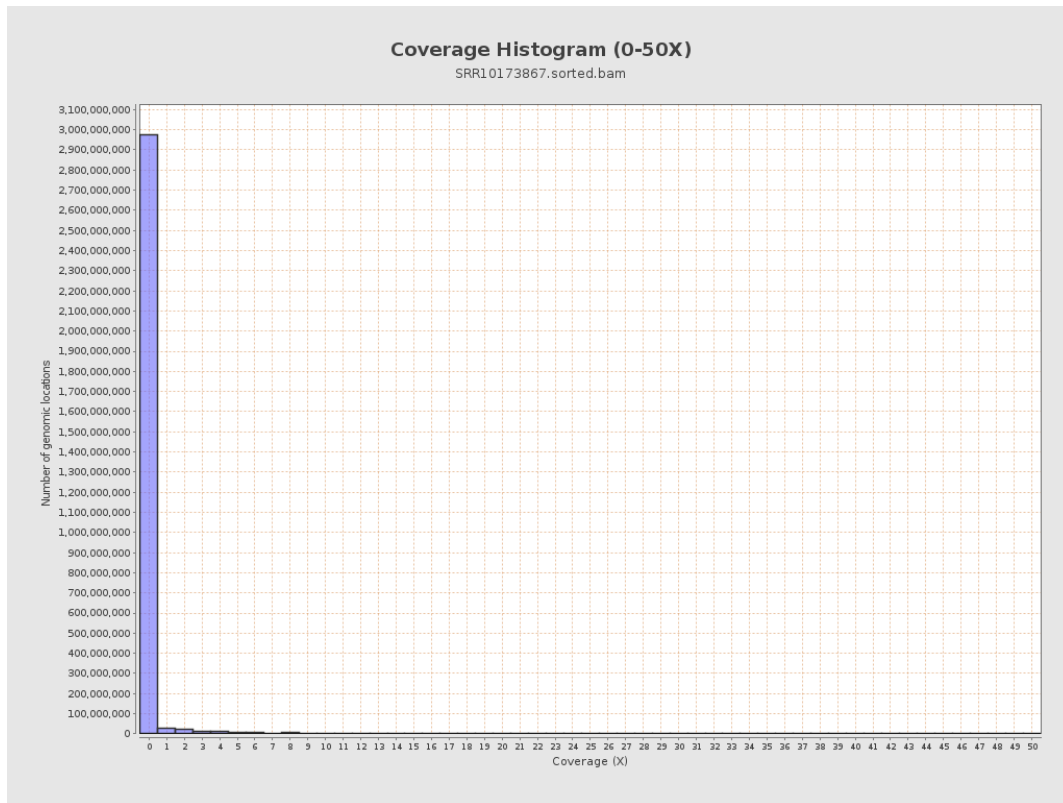
3. Results : Coverage across reference



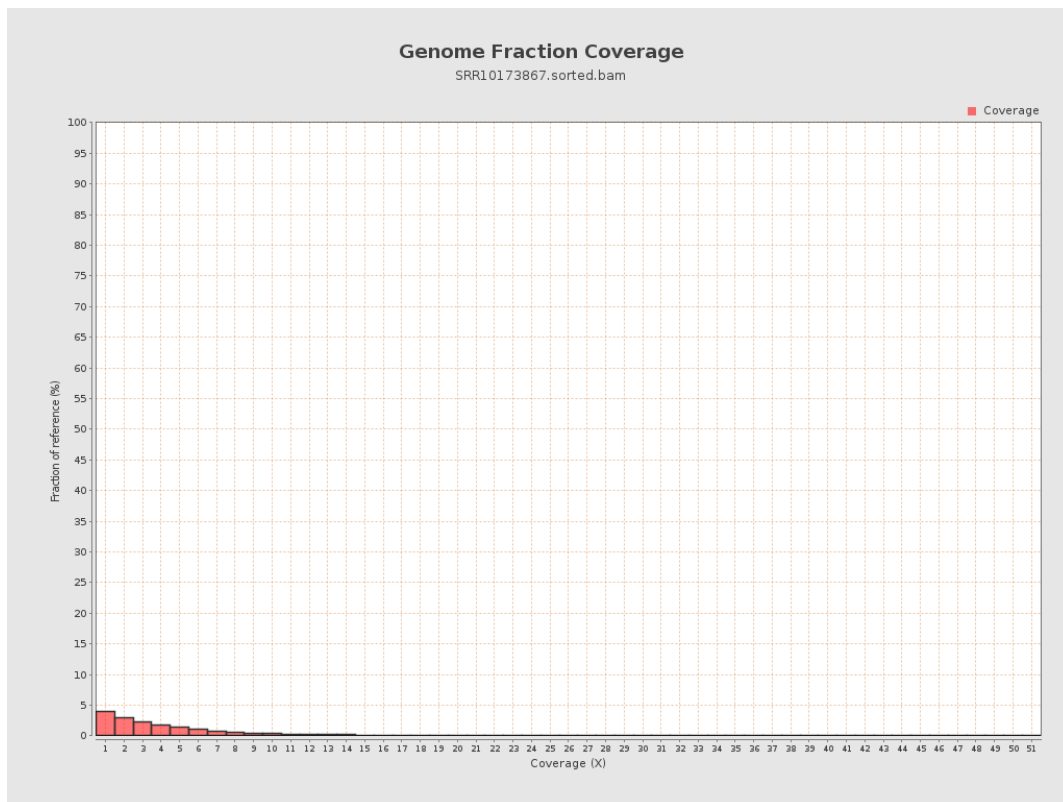
4. Results : Coverage Histogram



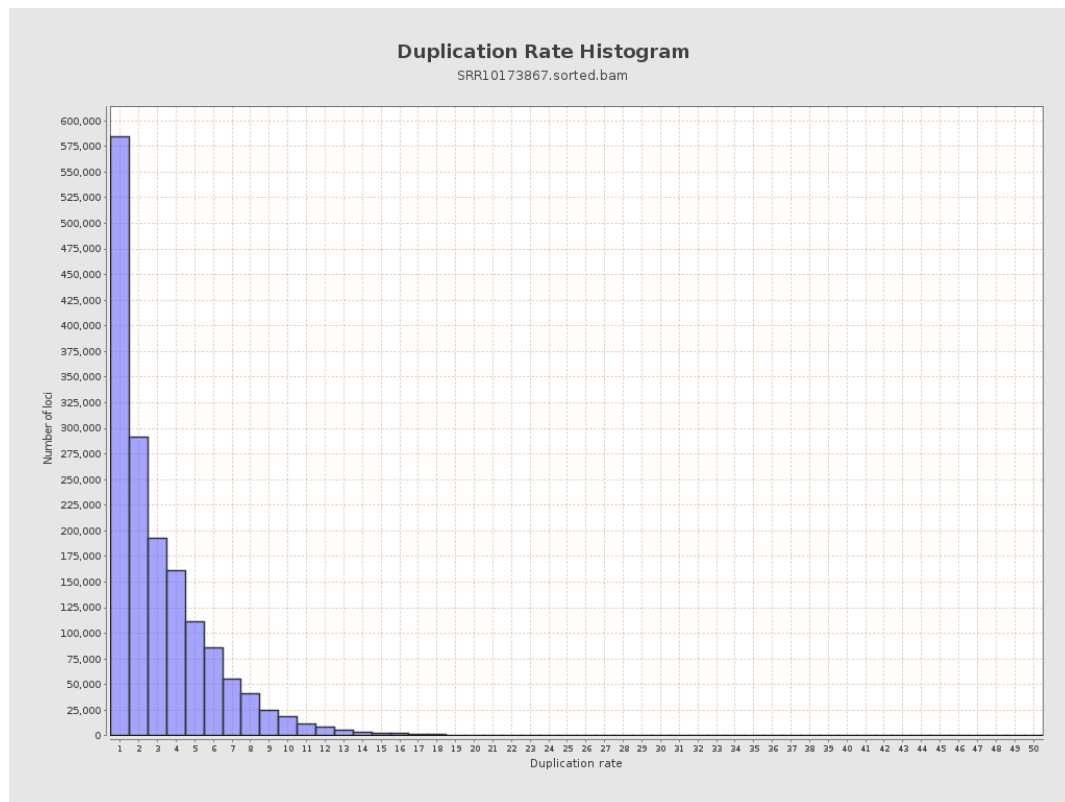
5. Results : Coverage Histogram (0-50X)



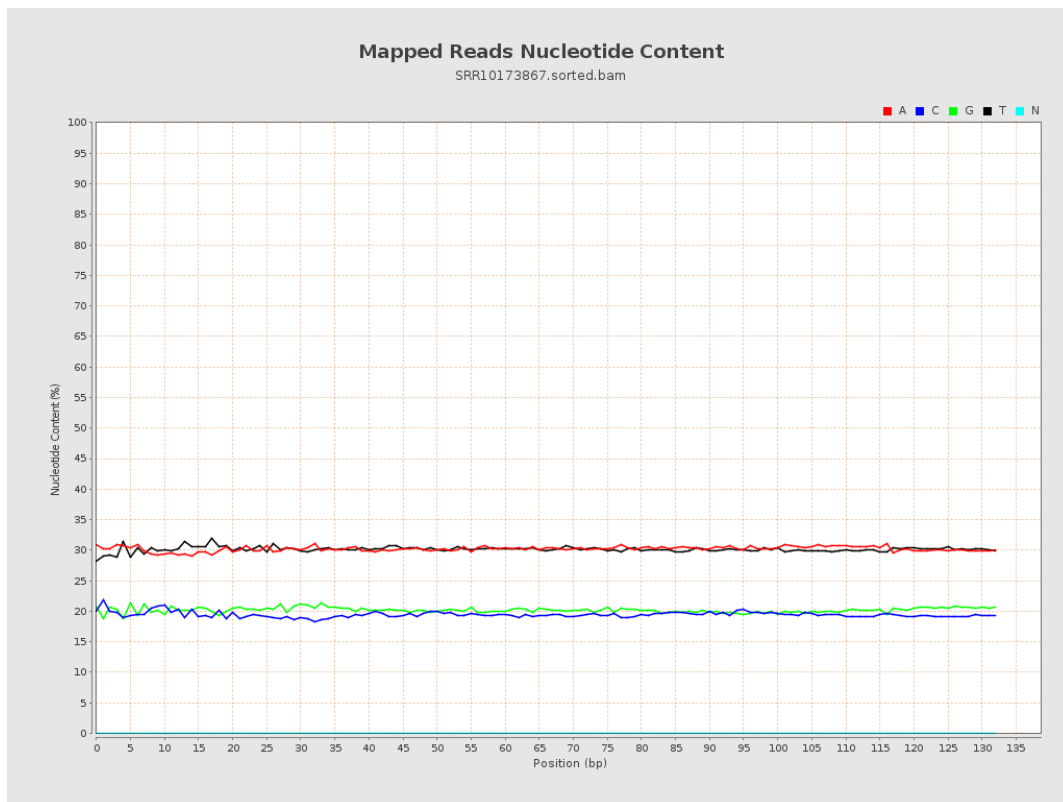
6. Results : Genome Fraction Coverage



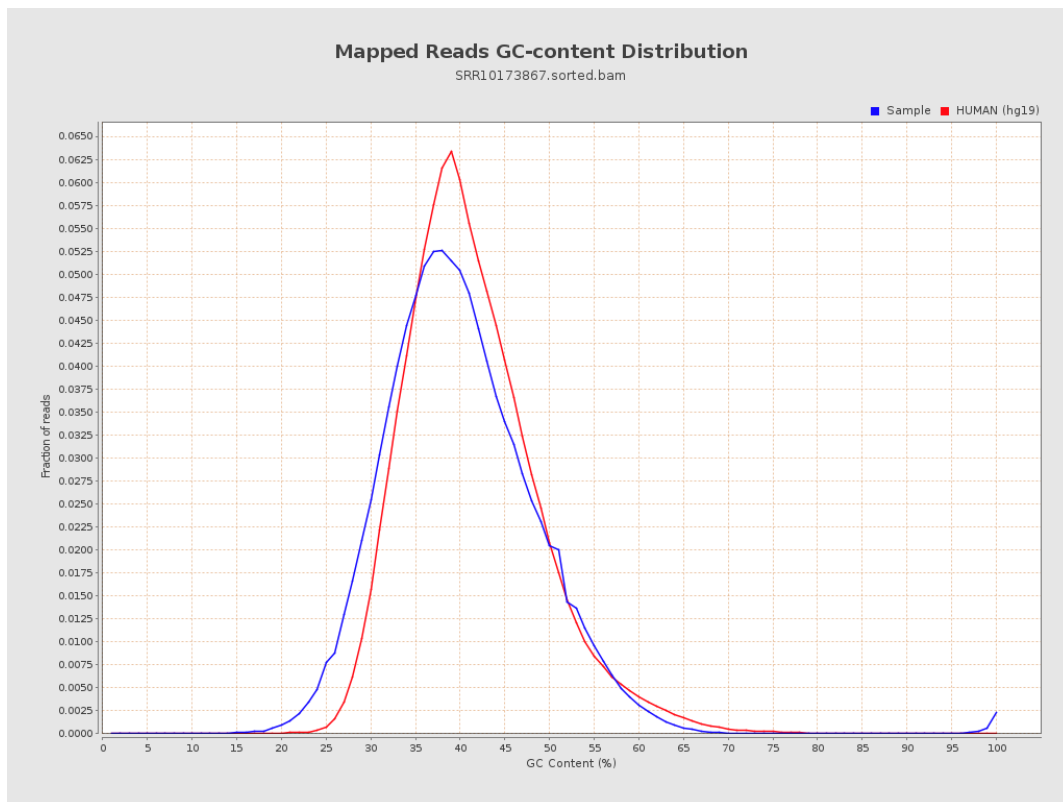
7. Results : Duplication Rate Histogram



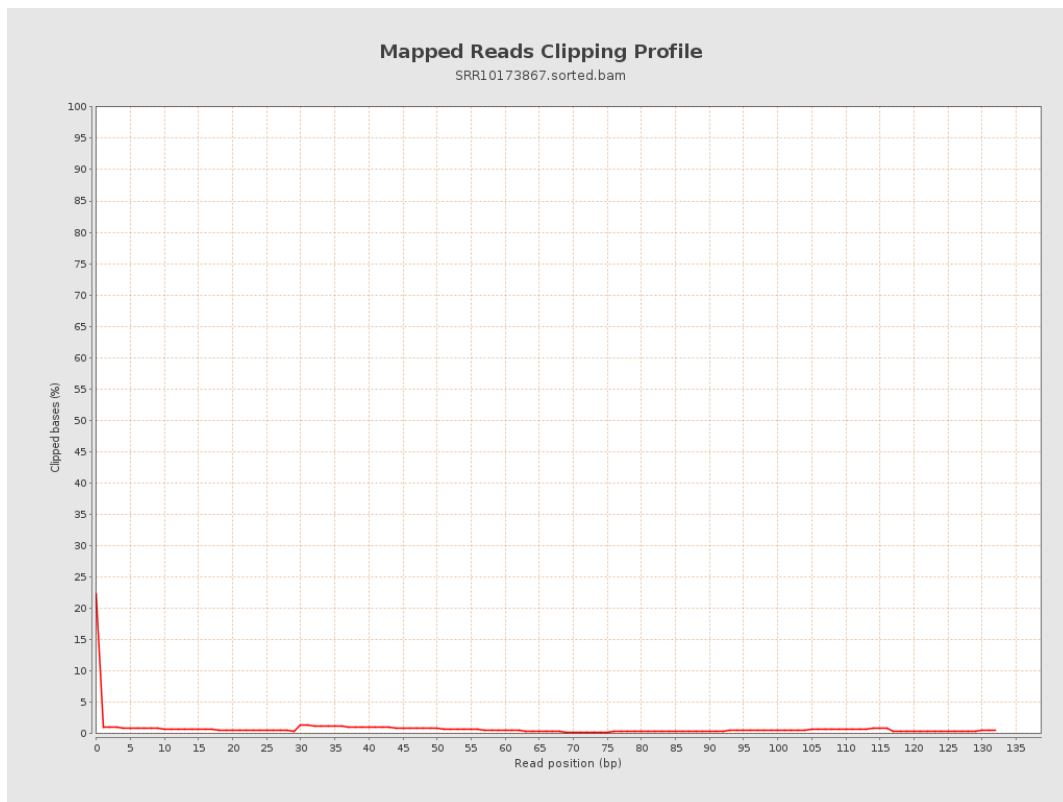
8. Results : Mapped Reads Nucleotide Content



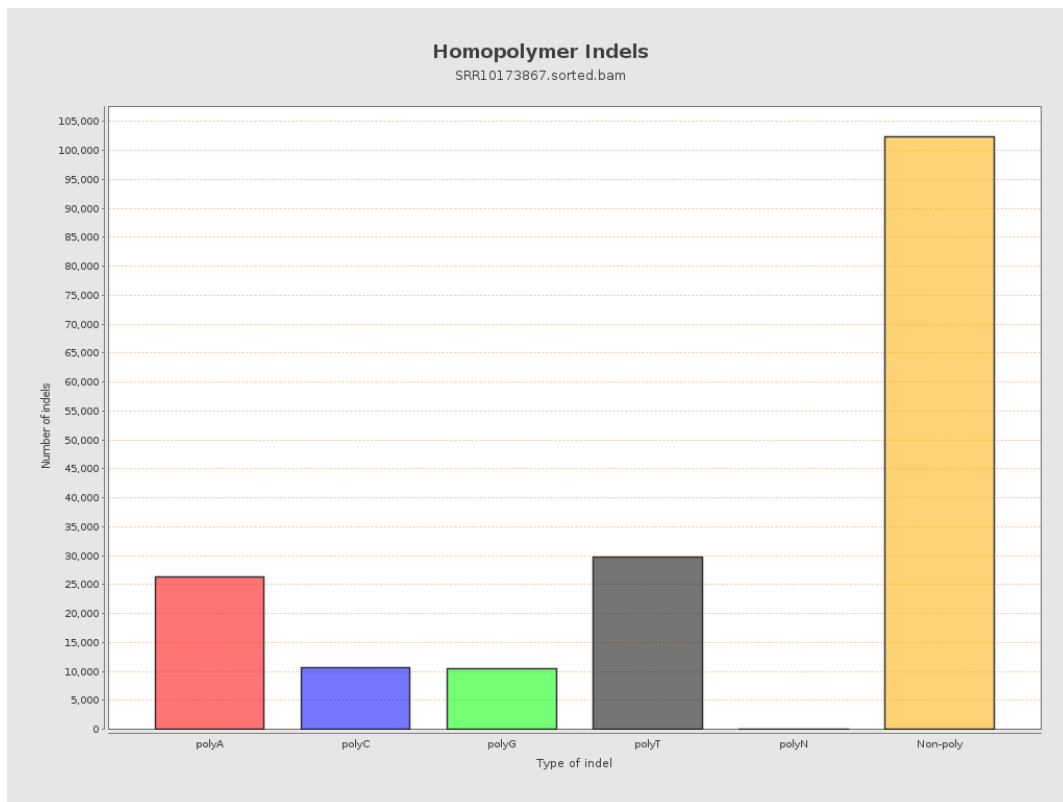
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



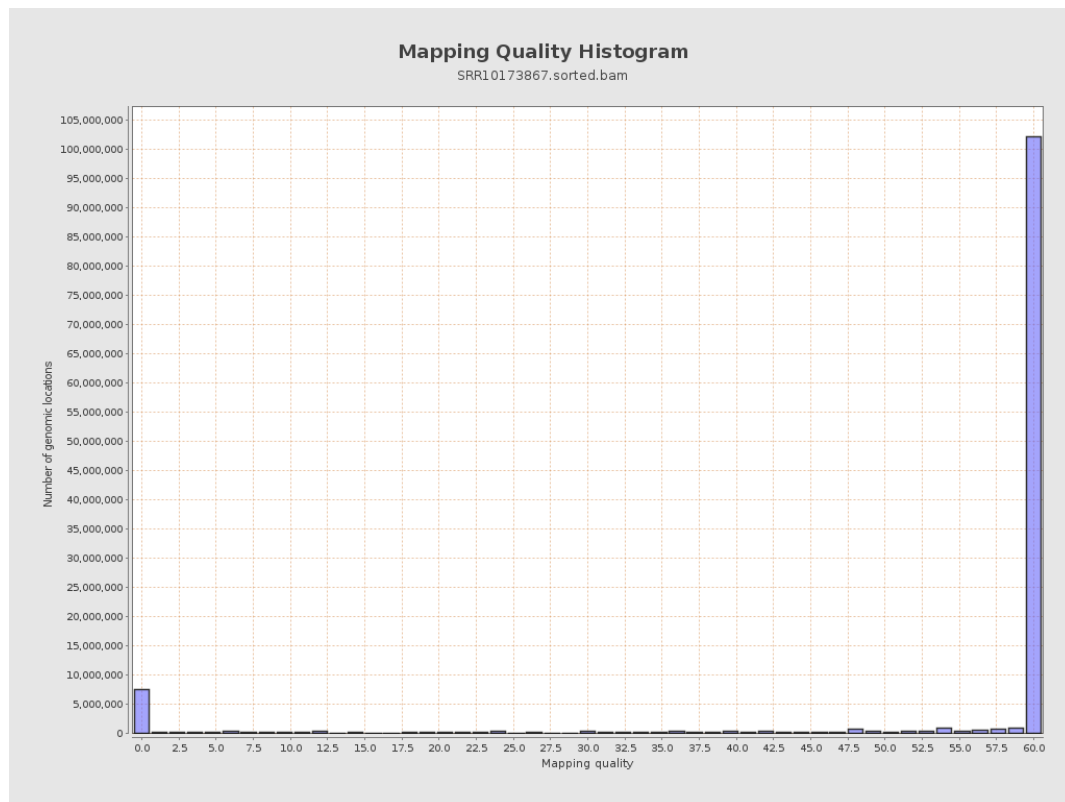
11. Results : Homopolymer Indels



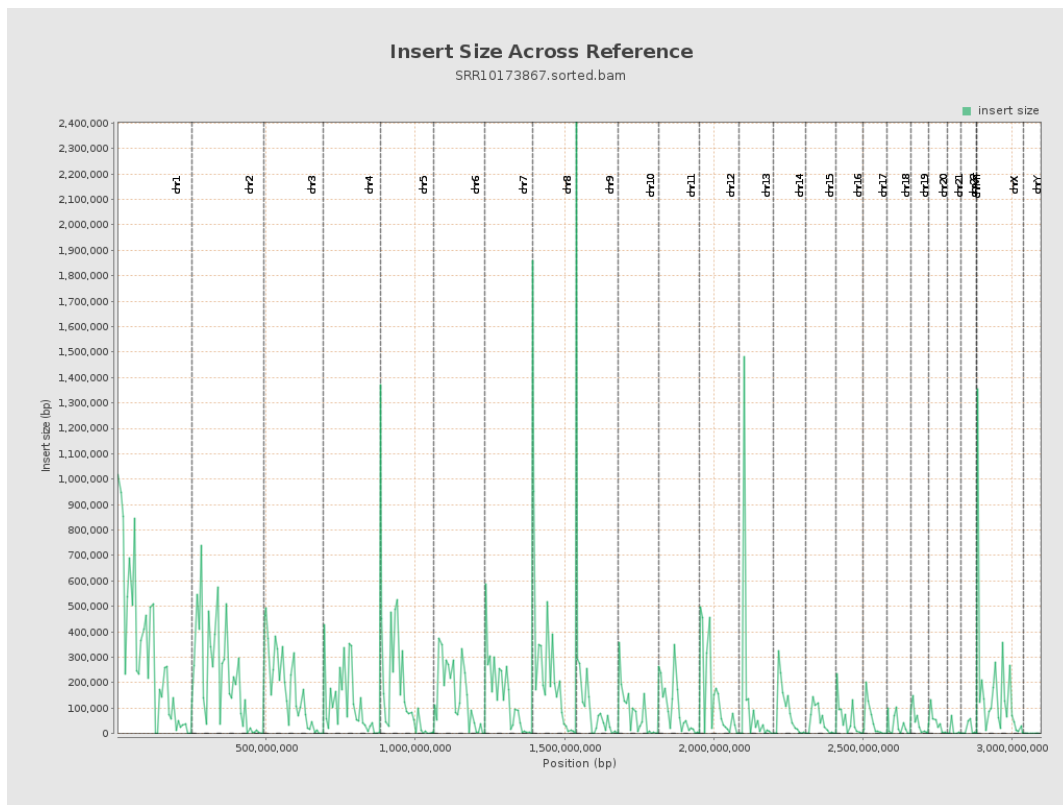
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

