

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 04:15:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174067.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_SRR10174067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174067_1.fastq.gz SRR10174067_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 04:15:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,518,992
Mapped reads	8,323,014 / 97.7%
Unmapped reads	195,978 / 2.3%
Mapped paired reads	8,323,014 / 97.7%
Mapped reads, first in pair	4,155,524 / 48.78%
Mapped reads, second in pair	4,167,490 / 48.92%
Mapped reads, both in pair	8,192,346 / 96.17%
Mapped reads, singletons	130,668 / 1.53%
Secondary alignments	0
Supplementary alignments	837,459 / 9.83%
Read min/max/mean length	30 / 133 / 128.23
Duplicated reads (estimated)	6,592,779 / 77.39%
Duplication rate	66.72%
Clipped reads	3,126,038 / 36.69%

2.2. ACGT Content

Number/percentage of A's	296,570,036 / 29.95%
Number/percentage of C's	195,313,017 / 19.73%
Number/percentage of T's	296,143,475 / 29.91%
Number/percentage of G's	202,070,953 / 20.41%
Number/percentage of N's	12,304 / 0%

GC Percentage	40.14%
---------------	--------

2.3. Coverage

Mean	0.32
Standard Deviation	4.302

2.4. Mapping Quality

Mean Mapping Quality	52.83
----------------------	-------

2.5. Insert size

Mean	960,473.87
Standard Deviation	9,149,372.28
P25/Median/P75	149 / 209 / 301

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	9,990,141
Insertions	105,060
Mapped reads with at least one insertion	1.22%
Deletions	217,908
Mapped reads with at least one deletion	2.55%
Homopolymer indels	43.31%

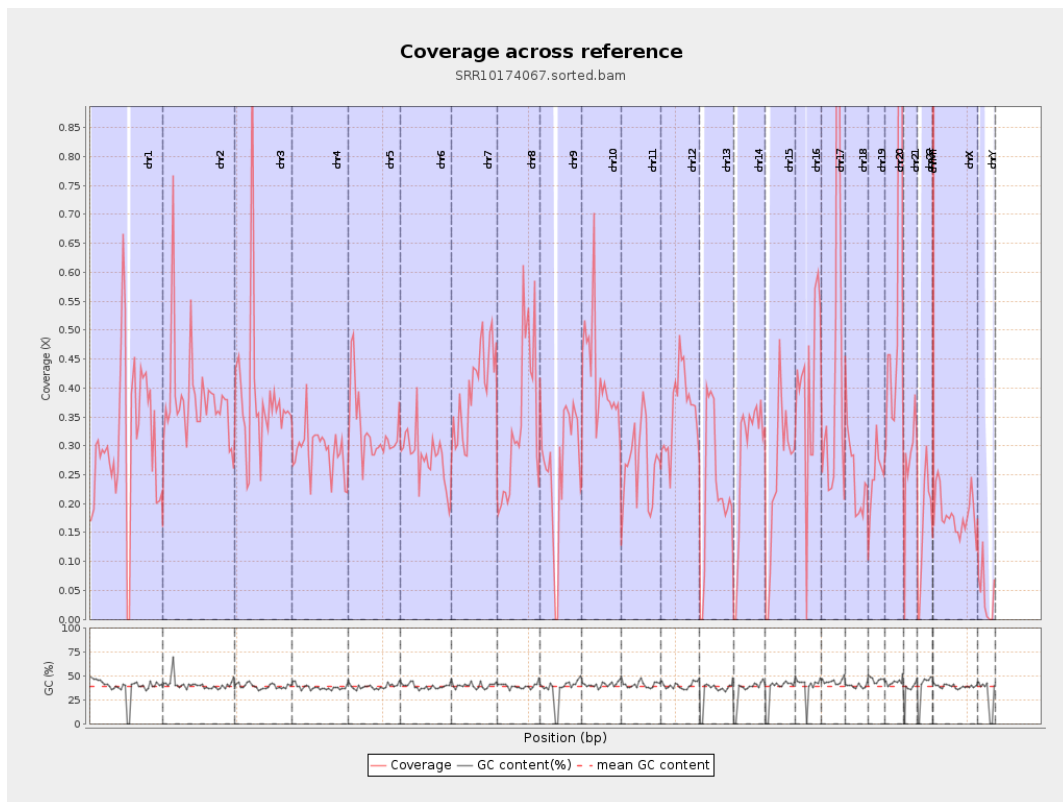
2.7. Chromosome stats

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

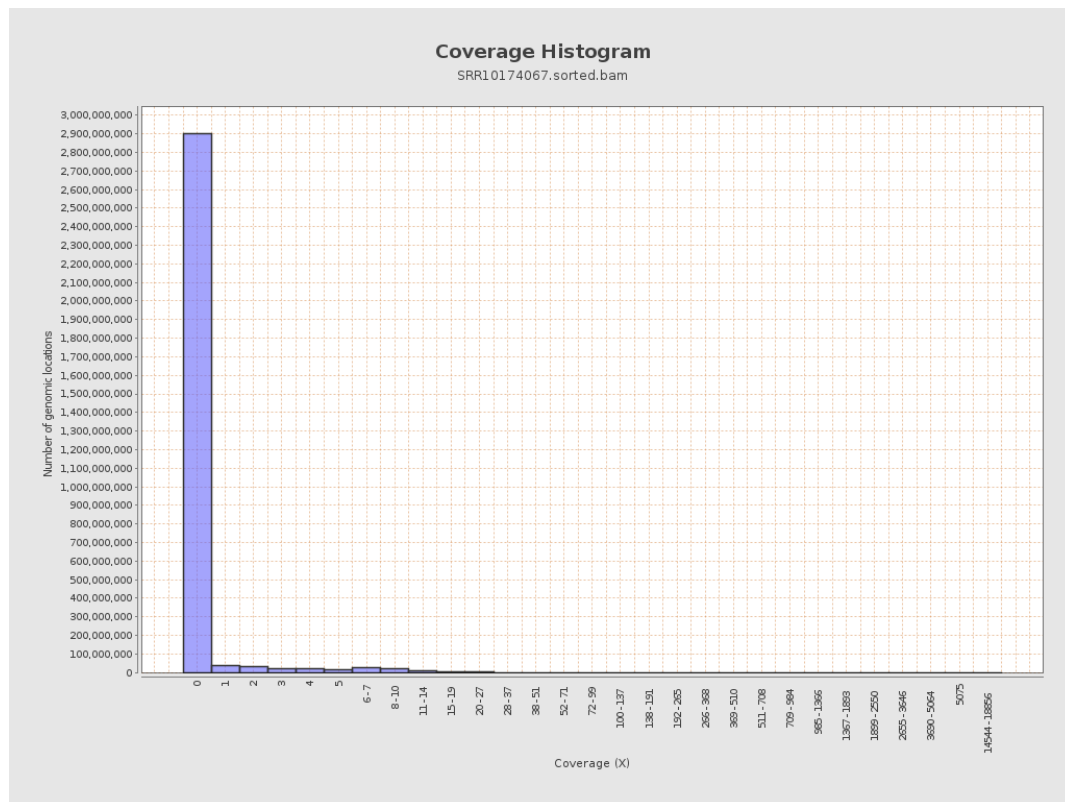
		bases	coverage	deviation
chr1	249250621	76592307	0.3073	2.618
chr2	243199373	92542010	0.3805	13.2839
chr3	198022430	75048188	0.379	1.8395
chr4	191154276	55684628	0.2913	1.9773
chr5	180915260	59108944	0.3267	1.678
chr6	171115067	48048608	0.2808	1.9574
chr7	159138663	63060840	0.3963	2.7275
chr8	146364022	49263685	0.3366	2.4705
chr9	141213431	37458313	0.2653	2.2852
chr10	135534747	56677112	0.4182	3.9115
chr11	135006516	36148840	0.2678	1.5657
chr12	133851895	48553288	0.3627	1.7737
chr13	115169878	25608805	0.2224	1.3915
chr14	107349540	30628149	0.2853	1.5698
chr15	102531392	24939916	0.2432	1.4371
chr16	90354753	36052171	0.399	2.6684
chr17	81195210	41594345	0.5123	2.5267
chr18	78077248	19592447	0.2509	3.3234
chr19	59128983	14787579	0.2501	2.2443
chr20	63025520	44842814	0.7115	2.8312
chr21	48129895	13237636	0.275	1.662
chr22	51304566	8497162	0.1656	1.1492
chrMT	16571	1823760	110.0573	99.4262
chrX	155270560	28333394	0.1825	1.2496

chrY	59373566	2521656	0.0425	1.1907
------	----------	---------	--------	--------

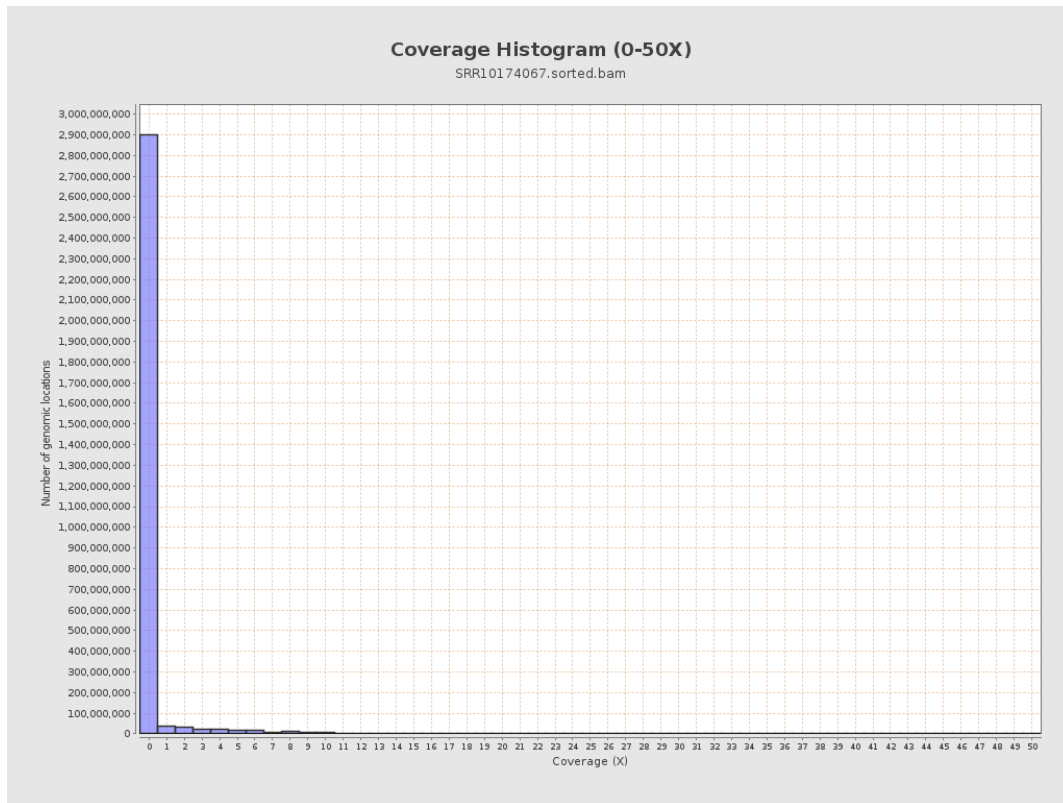
3. Results : Coverage across reference



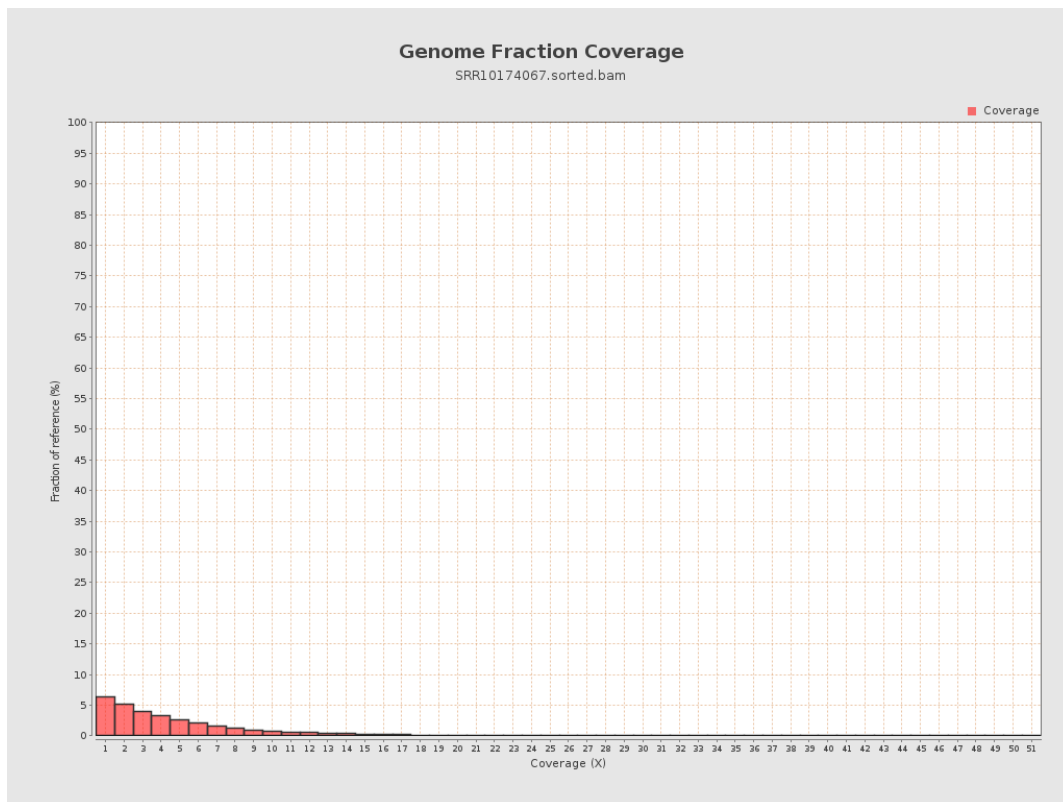
4. Results : Coverage Histogram



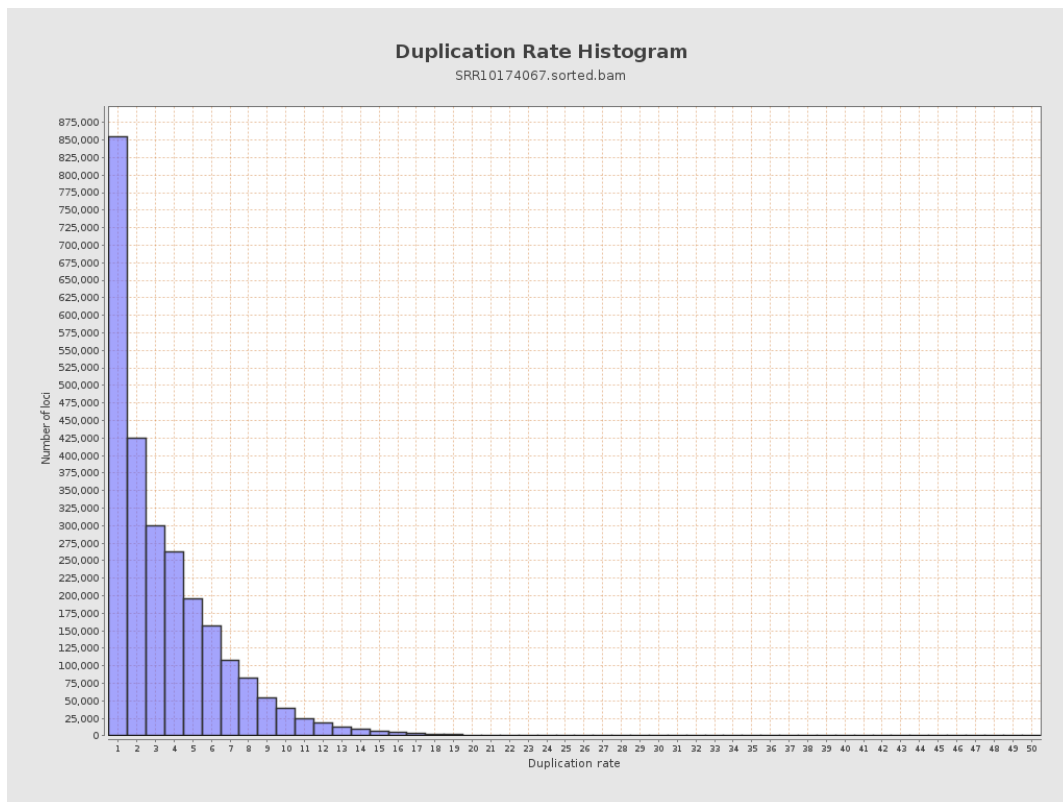
5. Results : Coverage Histogram (0-50X)



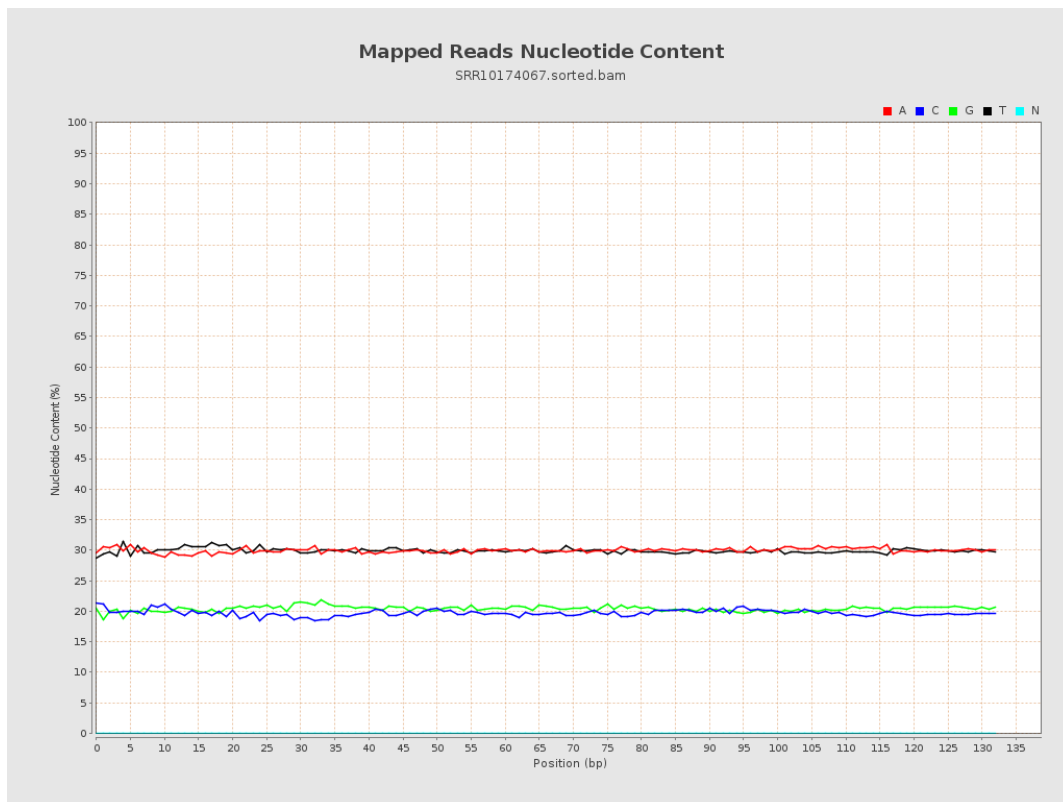
6. Results : Genome Fraction Coverage



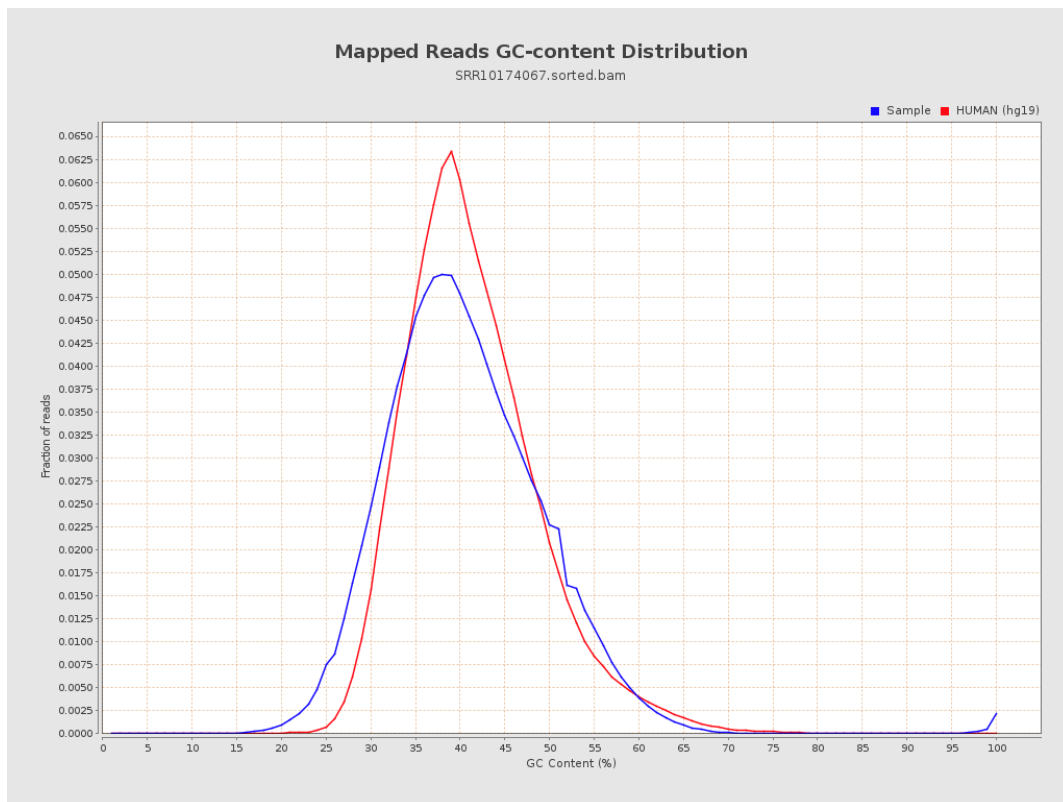
7. Results : Duplication Rate Histogram



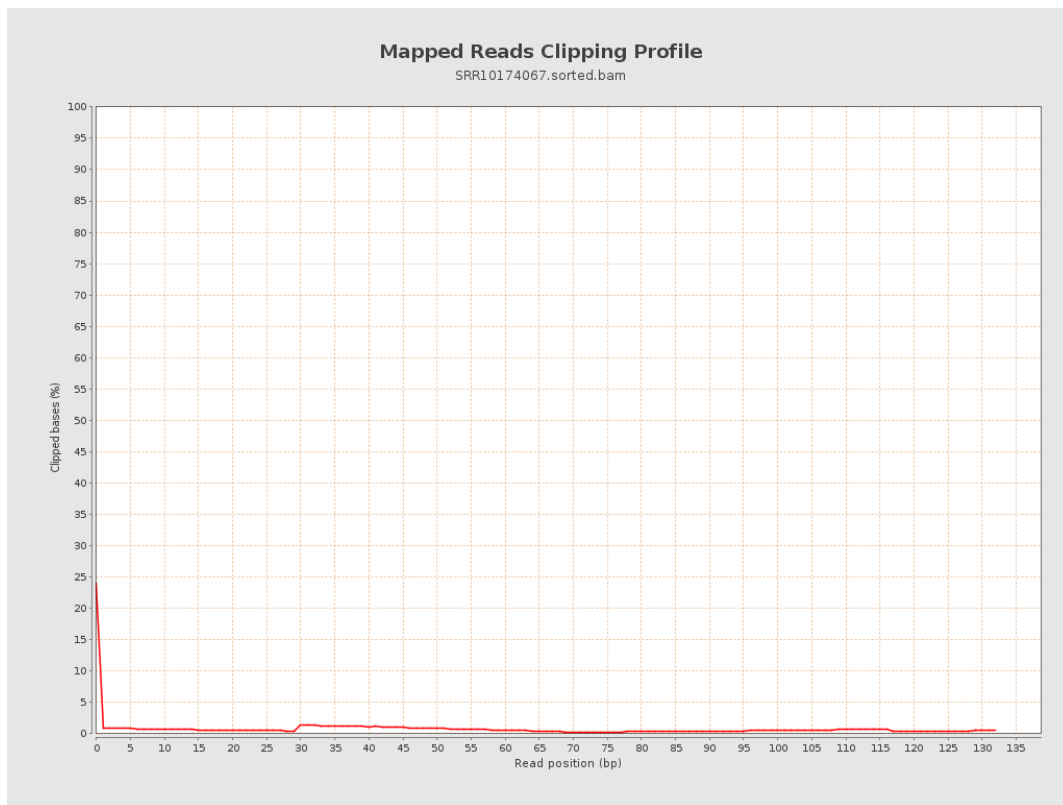
8. Results : Mapped Reads Nucleotide Content



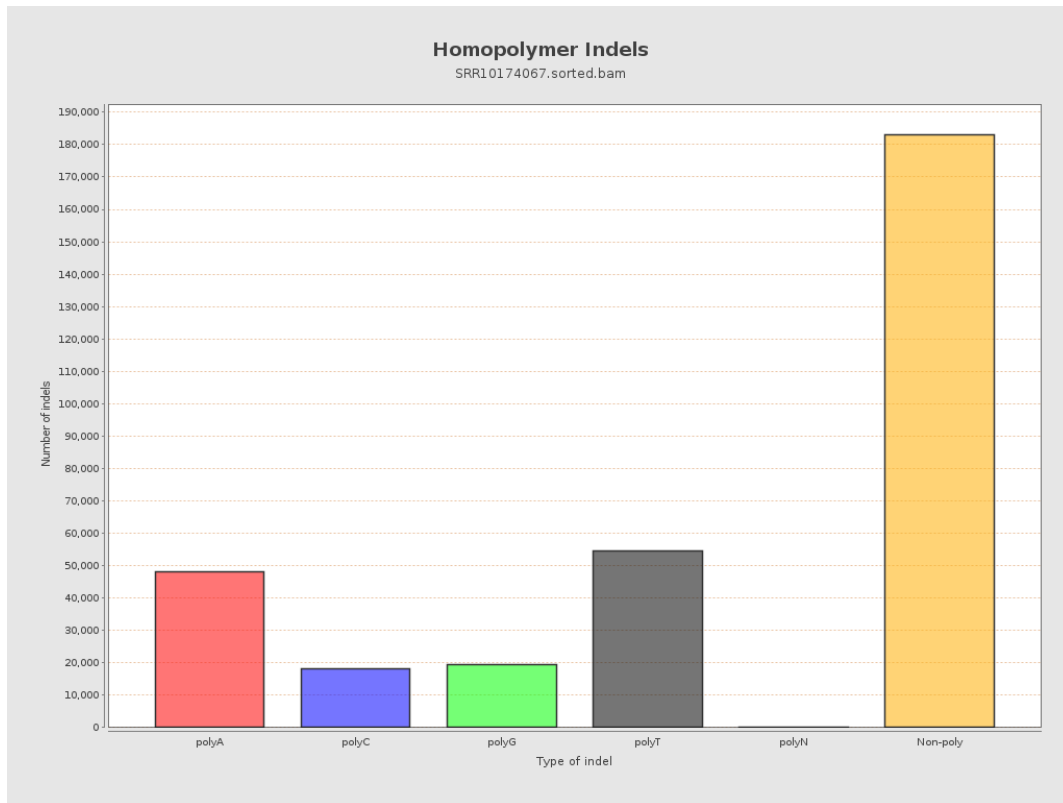
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



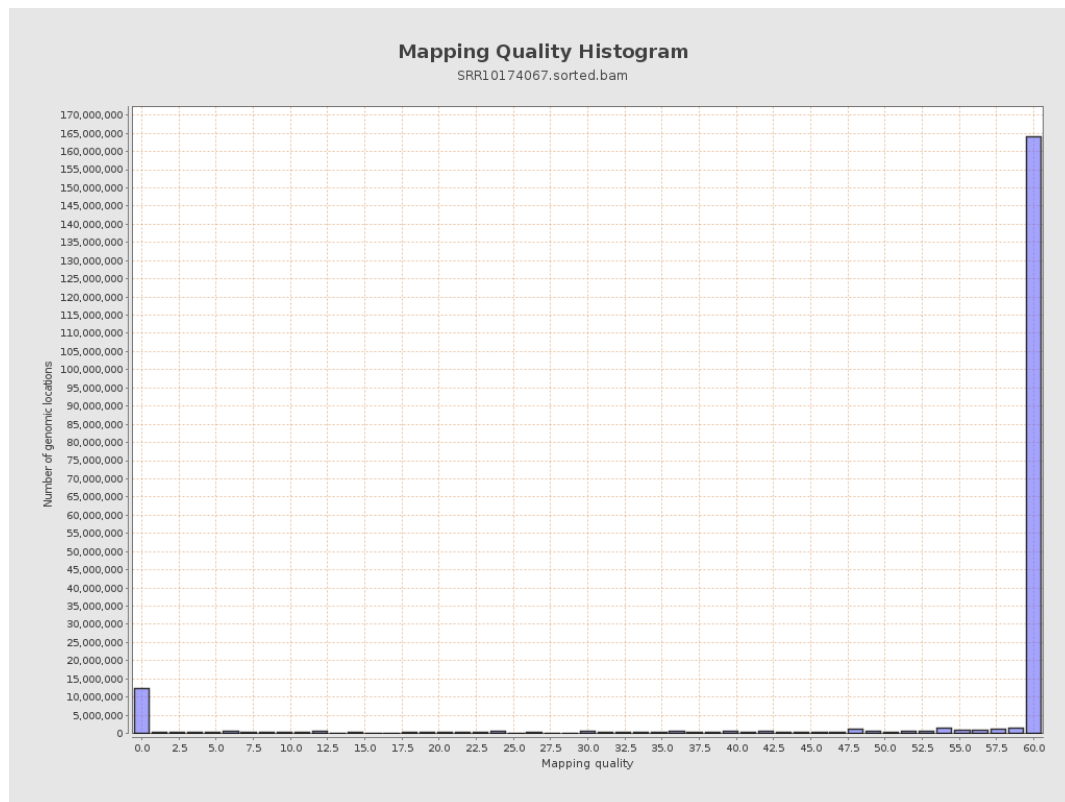
11. Results : Homopolymer Indels



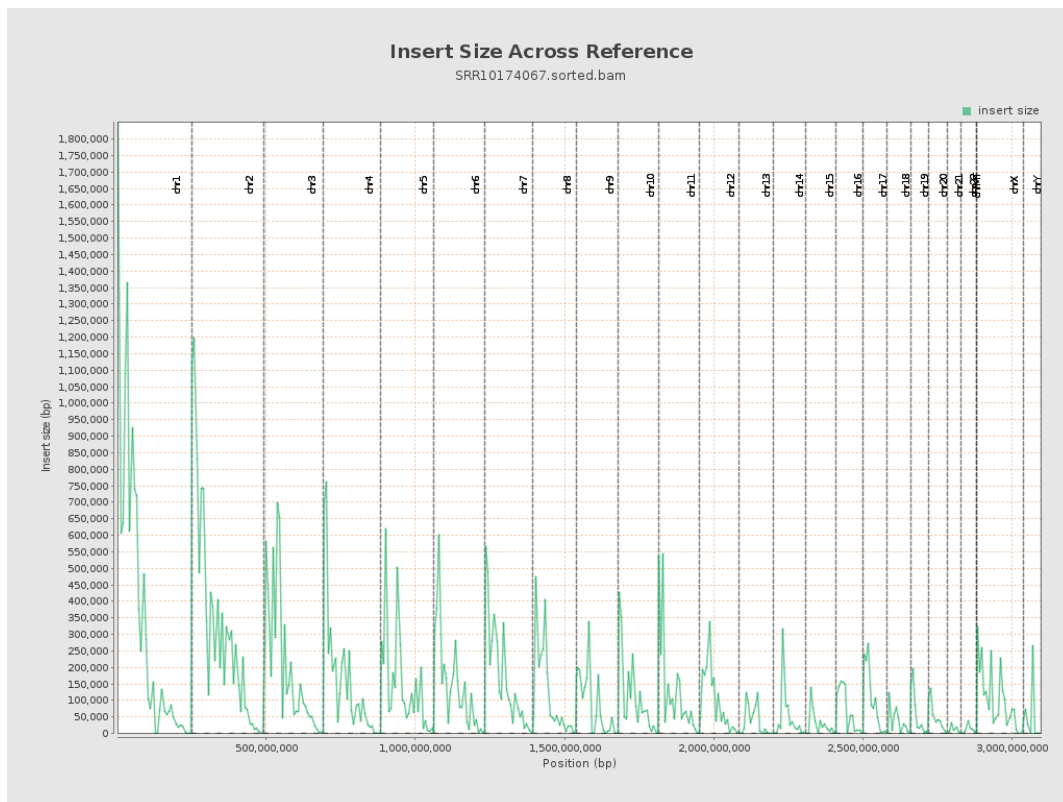
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

