

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:29:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354857.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_SRR22354857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354857_1.fastq.gz SRR22354857_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:29:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,927,626
Mapped reads	17,632,380 / 98.35%
Unmapped reads	295,246 / 1.65%
Mapped paired reads	17,632,380 / 98.35%
Mapped reads, first in pair	8,848,986 / 49.36%
Mapped reads, second in pair	8,783,394 / 48.99%
Mapped reads, both in pair	17,533,912 / 97.8%
Mapped reads, singletons	98,468 / 0.55%
Secondary alignments	0
Supplementary alignments	209,151 / 1.17%
Read min/max/mean length	30 / 150 / 150.54
Duplicated reads (estimated)	12,392,331 / 69.12%
Duplication rate	66.48%
Clipped reads	2,512,346 / 14.01%

2.2. ACGT Content

Number/percentage of A's	731,036,449 / 28.72%
Number/percentage of C's	534,666,940 / 21.01%
Number/percentage of T's	738,903,496 / 29.03%
Number/percentage of G's	540,707,493 / 21.24%
Number/percentage of N's	13,442 / 0%

GC Percentage	42.25%
---------------	--------

2.3. Coverage

Mean	0.8226
Standard Deviation	14.7763

2.4. Mapping Quality

Mean Mapping Quality	54.12
----------------------	-------

2.5. Insert size

Mean	66,154.18
Standard Deviation	2,711,056.61
P25/Median/P75	314 / 450 / 587

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	23,572,352
Insertions	446,997
Mapped reads with at least one insertion	2.34%
Deletions	425,176
Mapped reads with at least one deletion	2.29%
Homopolymer indels	41.9%

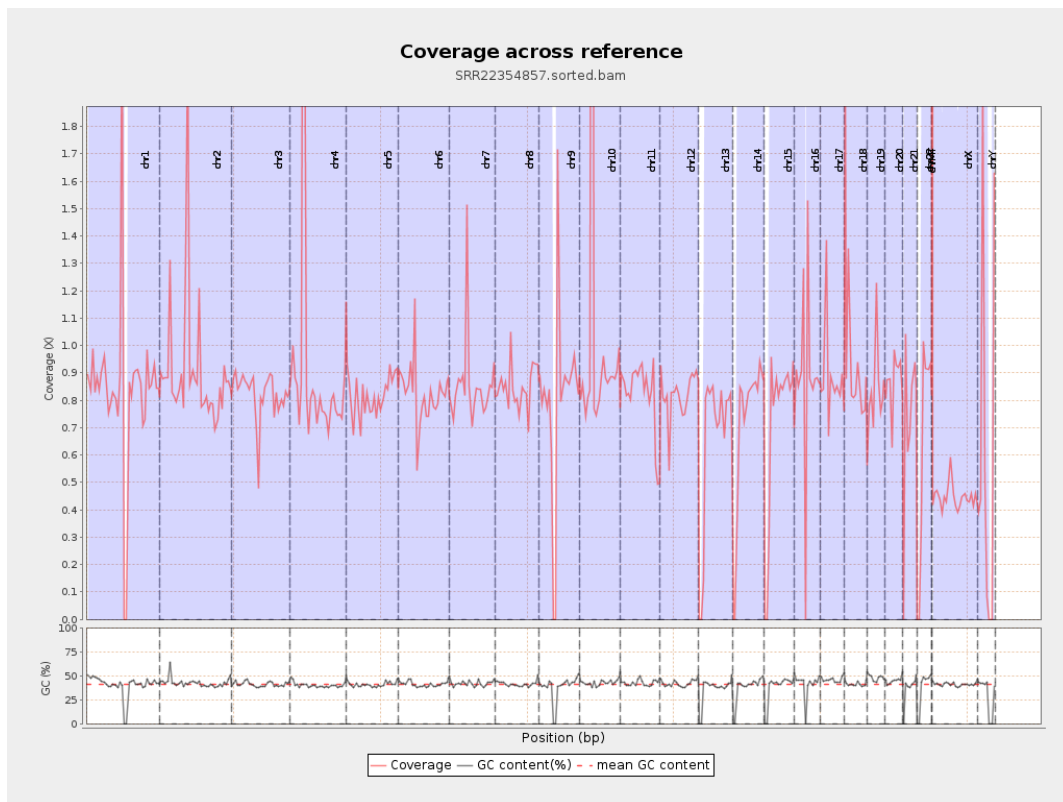
2.7. Chromosome stats

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

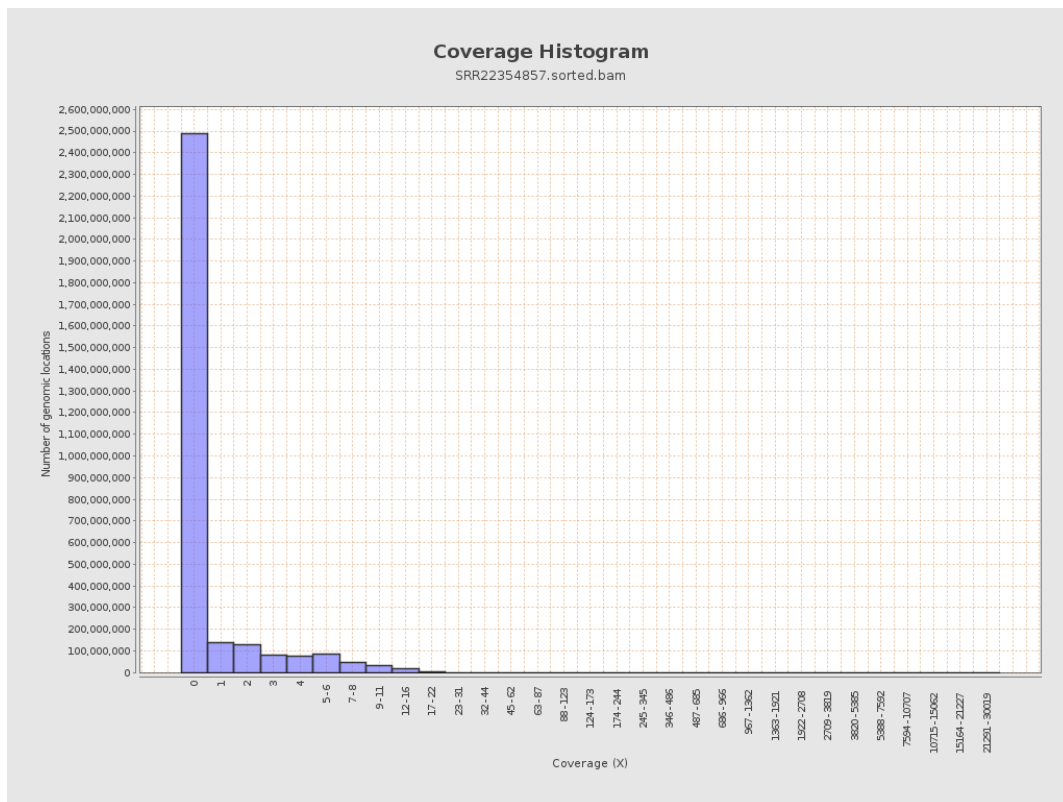
		bases	coverage	deviation
chr1	249250621	210927750	0.8462	29.3698
chr2	243199373	222201072	0.9137	17.2891
chr3	198022430	162797768	0.8221	2.3319
chr4	191154276	172043519	0.9	19.6785
chr5	180915260	147924209	0.8176	2.1864
chr6	171115067	141481015	0.8268	4.3096
chr7	159138663	136194944	0.8558	14.0122
chr8	146364022	124256555	0.849	4.6268
chr9	141213431	112405272	0.796	18.8084
chr10	135534747	149256016	1.1012	31.3185
chr11	135006516	111831667	0.8283	5.007
chr12	133851895	109626527	0.819	2.1616
chr13	115169878	75498648	0.6555	1.898
chr14	107349540	76066608	0.7086	2.084
chr15	102531392	71895804	0.7012	2.0176
chr16	90354753	79746431	0.8826	5.9214
chr17	81195210	71568750	0.8814	6.1658
chr18	78077248	73671474	0.9436	16.531
chr19	59128983	49658727	0.8398	14.6823
chr20	63025520	54805668	0.8696	6.1468
chr21	48129895	36108185	0.7502	9.1437
chr22	51304566	33618534	0.6553	2.8912
chrMT	16571	15772079	951.788	211.1077
chrX	155270560	69307289	0.4464	2.0432

chrY	59373566	37922549	0.6387	19.6411
------	----------	----------	--------	---------

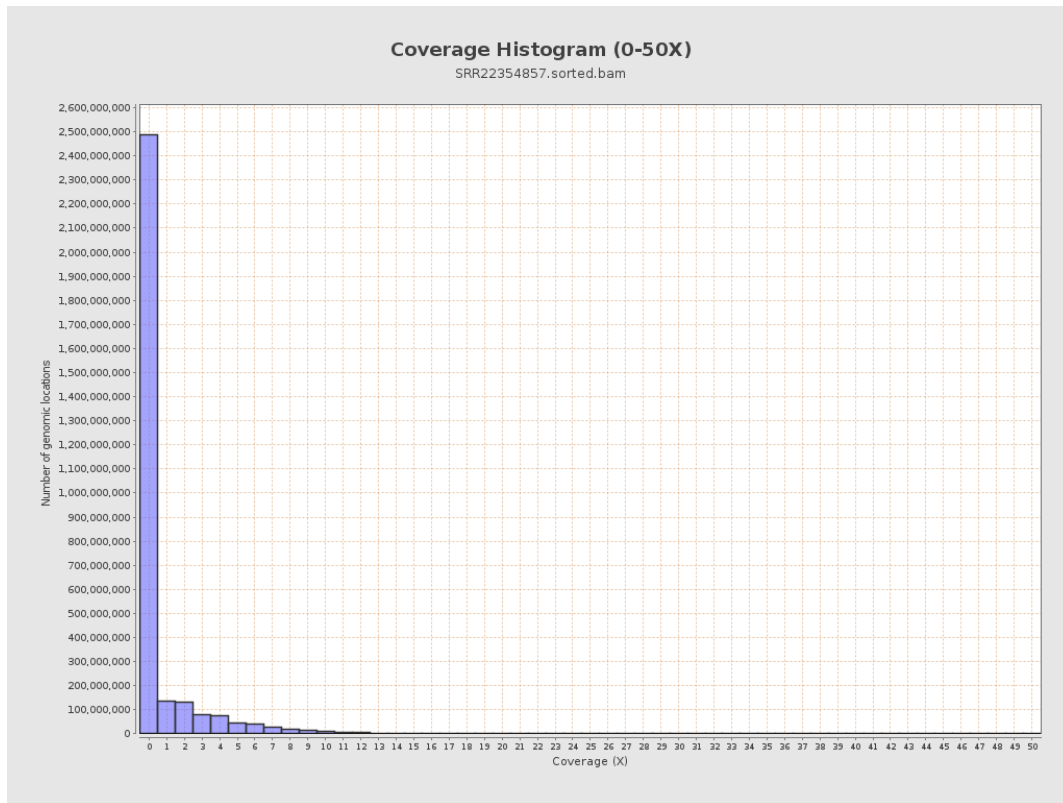
3. Results : Coverage across reference



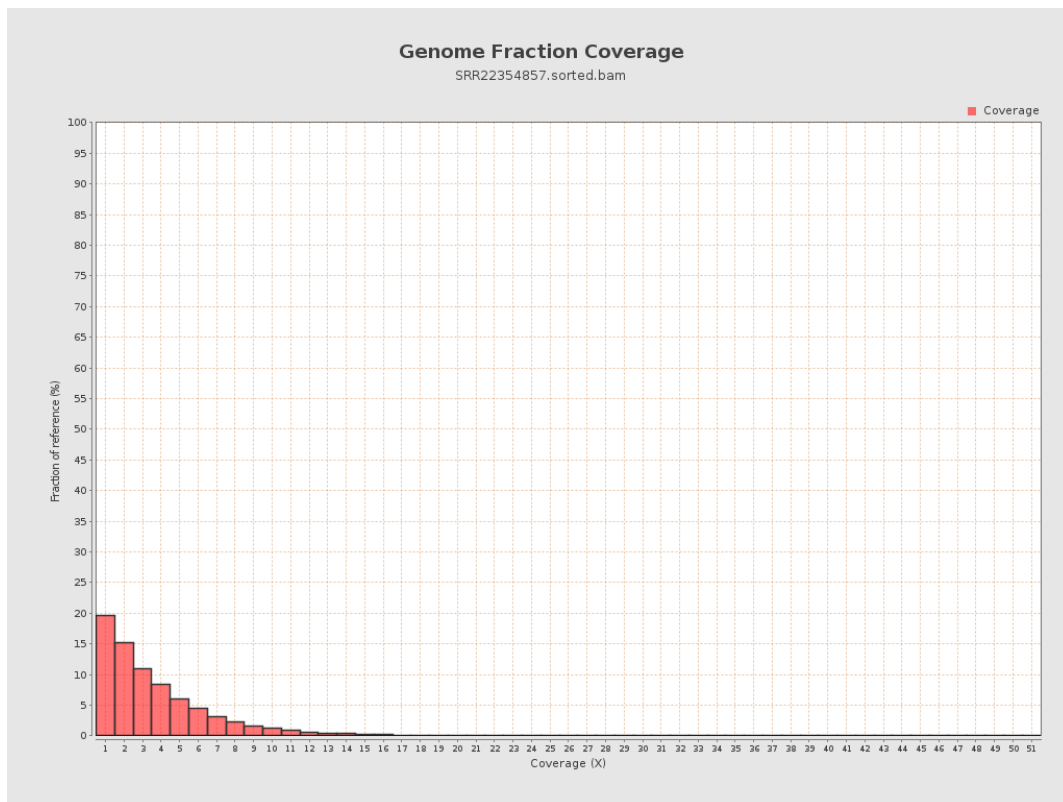
4. Results : Coverage Histogram



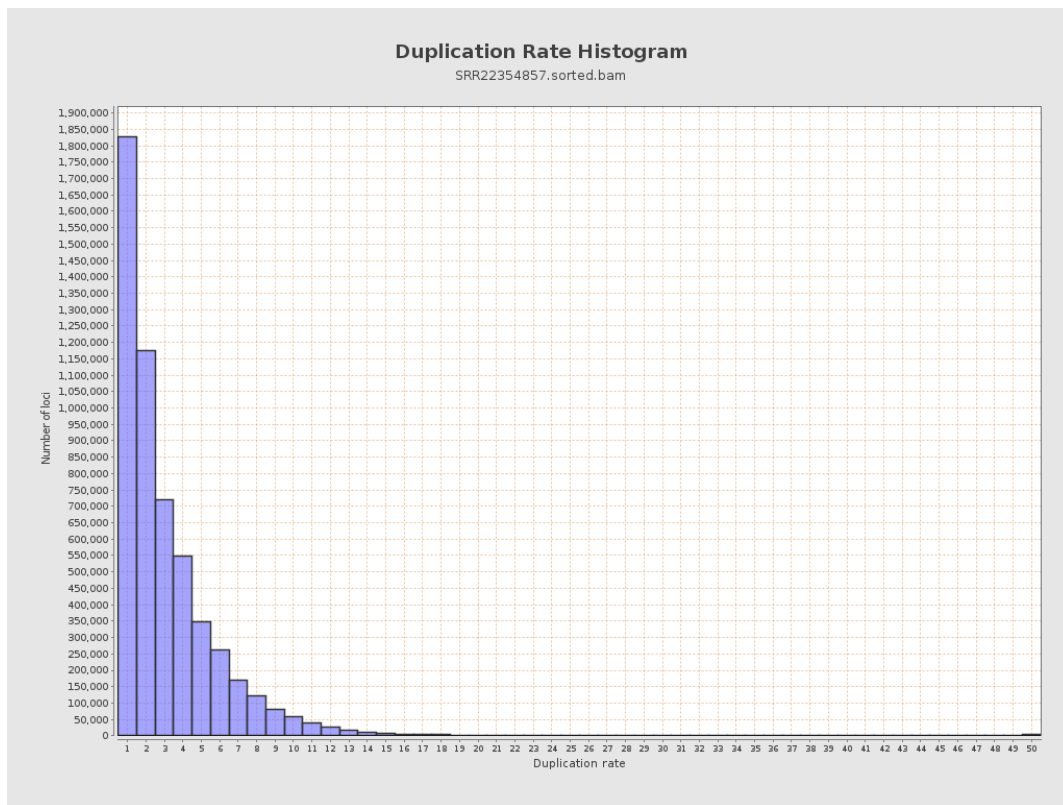
5. Results : Coverage Histogram (0-50X)



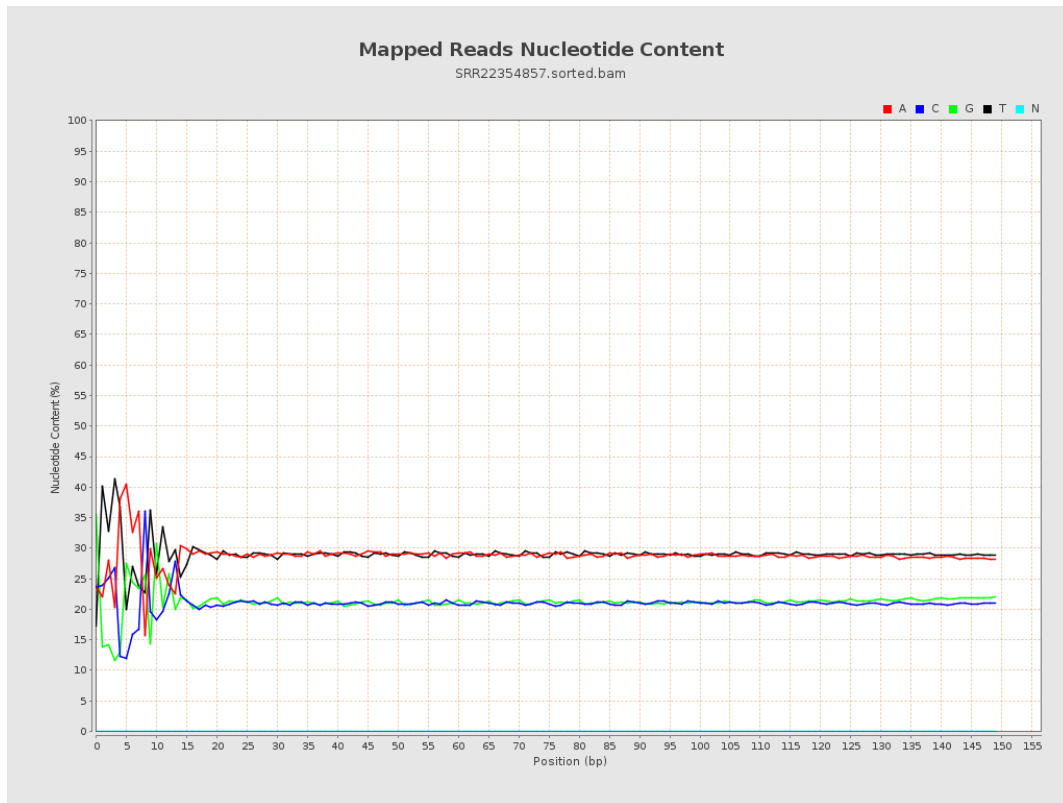
6. Results : Genome Fraction Coverage



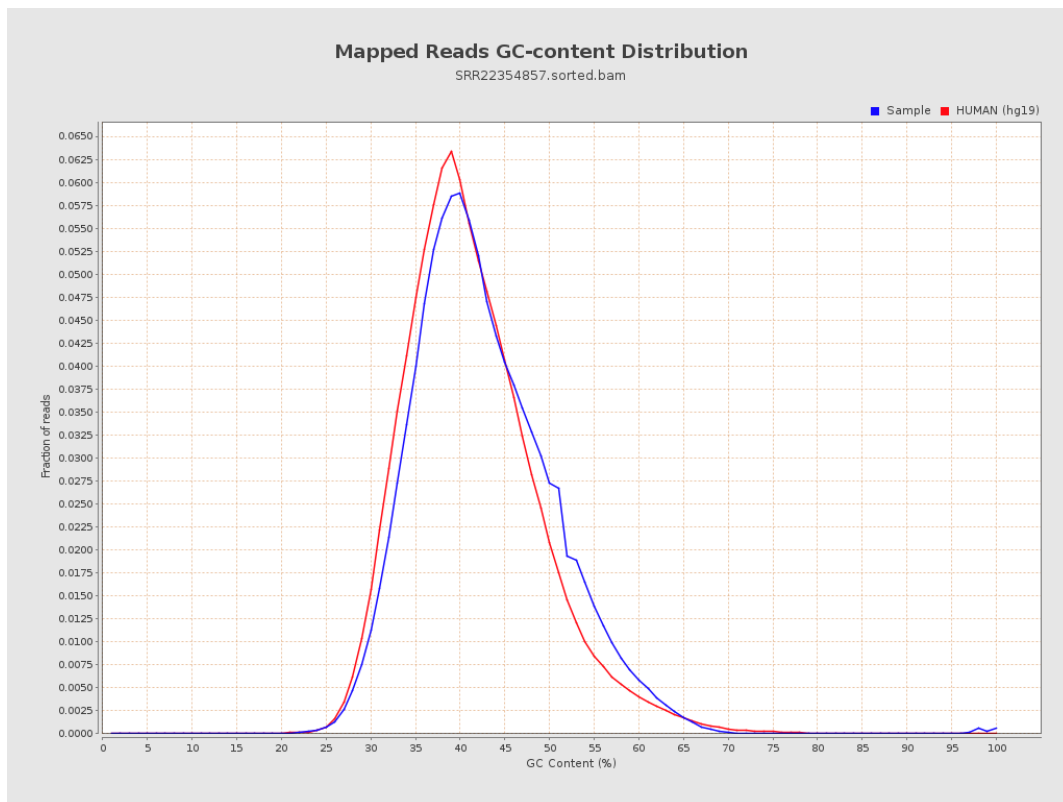
7. Results : Duplication Rate Histogram



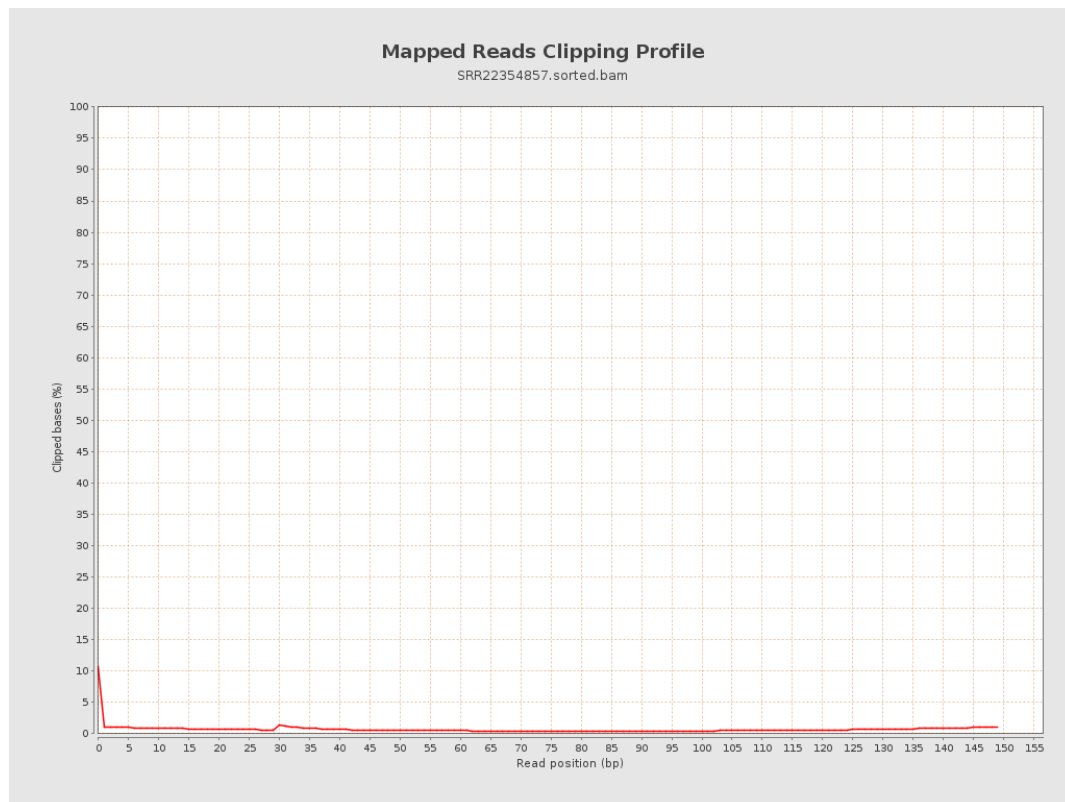
8. Results : Mapped Reads Nucleotide Content



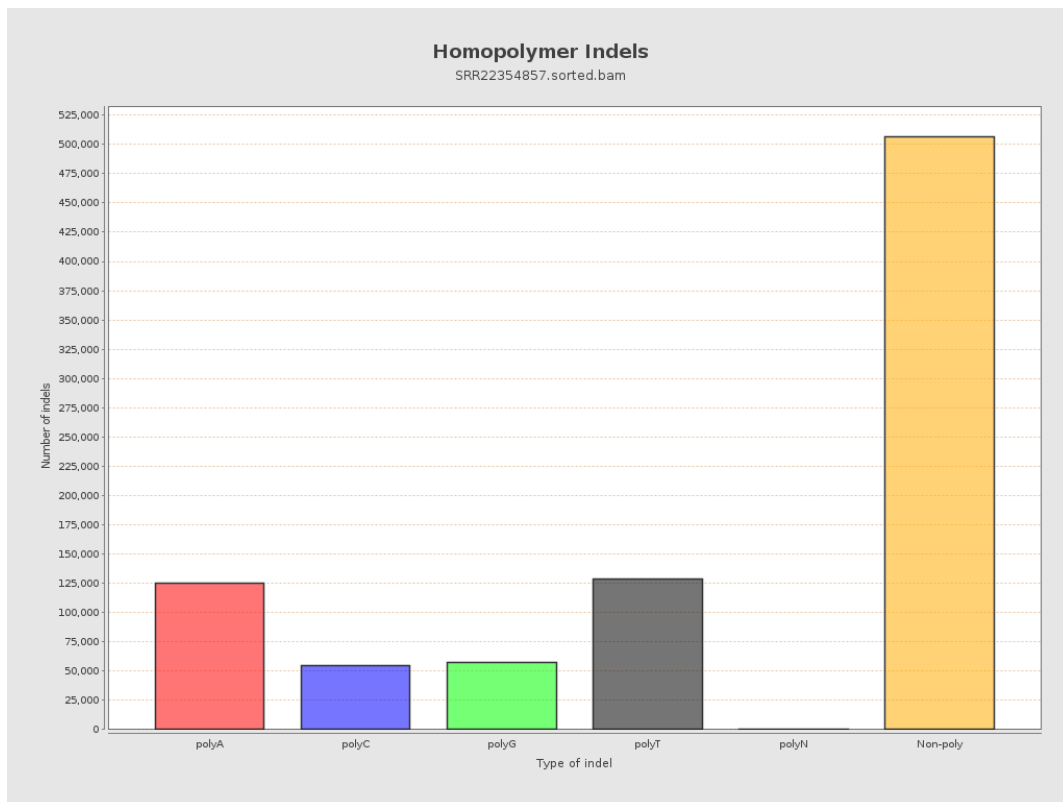
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



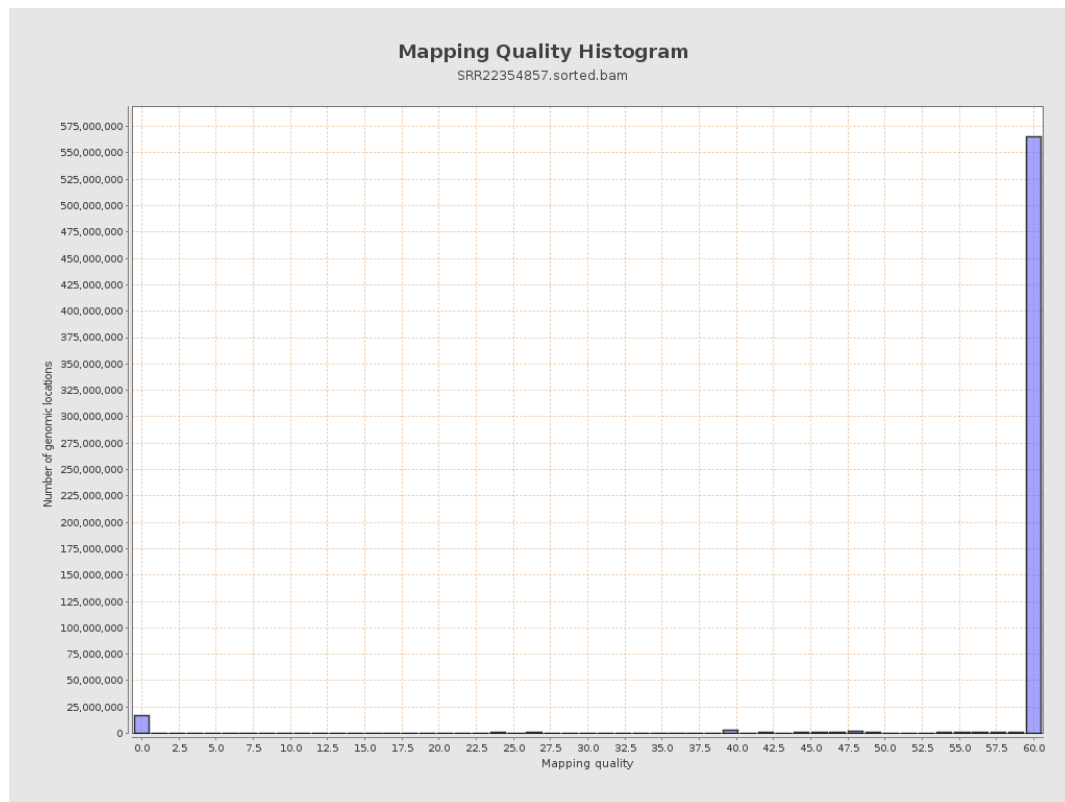
11. Results : Homopolymer Indels



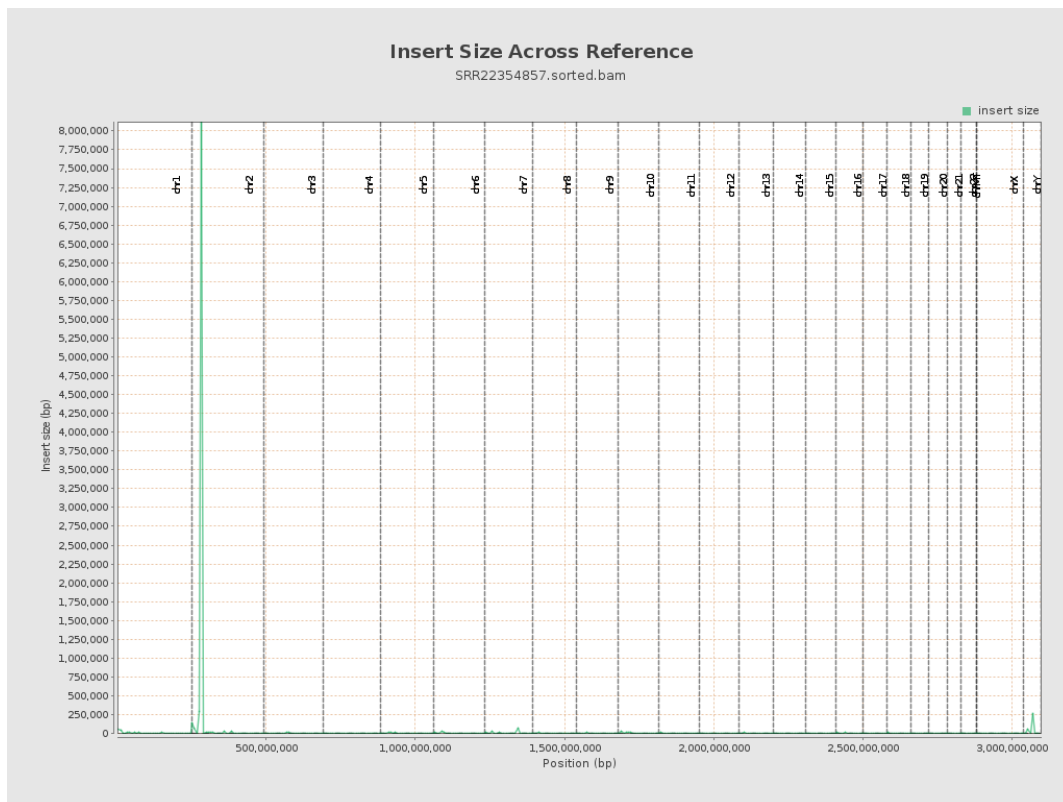
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

