

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 22:02:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365340.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_SRR5365340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365340_1.fastq.gz SRR5365340_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 22:02:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	103,631,074
Mapped reads	101,178,839 / 97.63%
Unmapped reads	2,452,235 / 2.37%
Mapped paired reads	101,178,839 / 97.63%
Mapped reads, first in pair	50,852,092 / 49.07%
Mapped reads, second in pair	50,326,747 / 48.56%
Mapped reads, both in pair	100,472,974 / 96.95%
Mapped reads, singletons	705,865 / 0.68%
Secondary alignments	0
Supplementary alignments	834,347 / 0.81%
Read min/max/mean length	30 / 151 / 151.36
Duplicated reads (estimated)	44,882,016 / 43.31%
Duplication rate	30%
Clipped reads	62,050,586 / 59.88%

2.2. ACGT Content

Number/percentage of A's	3,955,033,383 / 29.86%
Number/percentage of C's	2,625,235,119 / 19.82%
Number/percentage of T's	3,900,726,923 / 29.45%
Number/percentage of G's	2,764,142,365 / 20.87%
Number/percentage of N's	474,465 / 0%

GC Percentage	40.69%
---------------	--------

2.3. Coverage

Mean	4.2804
Standard Deviation	49.7979

2.4. Mapping Quality

Mean Mapping Quality	54.15
----------------------	-------

2.5. Insert size

Mean	84,714.57
Standard Deviation	2,843,086.96
P25/Median/P75	146 / 199 / 273

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	100,033,711
Insertions	3,944,014
Mapped reads with at least one insertion	3.78%
Deletions	2,096,432
Mapped reads with at least one deletion	2%
Homopolymer indels	49.6%

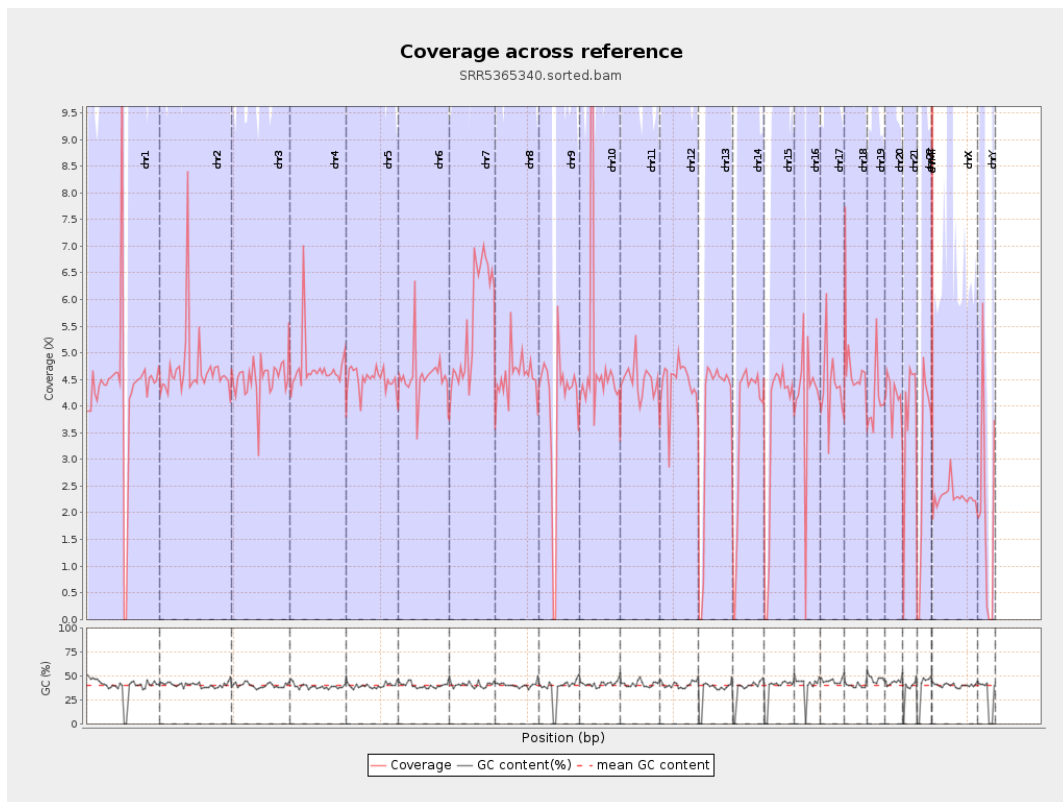
2.7. Chromosome stats

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

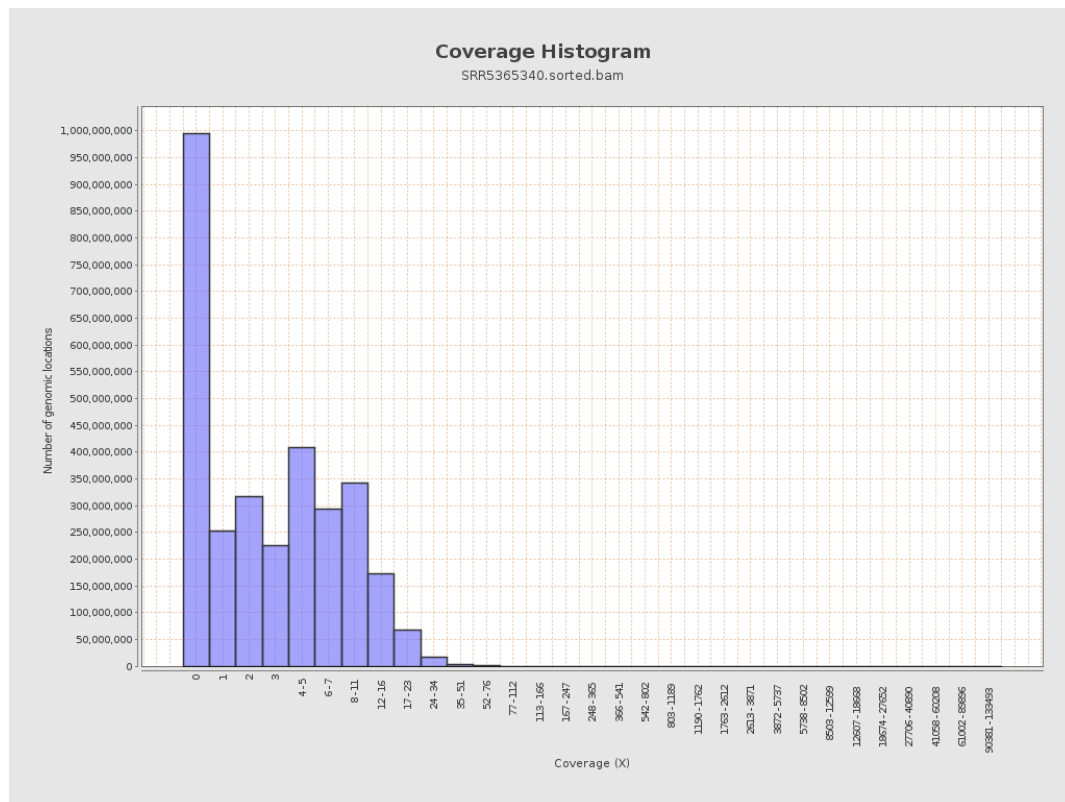
		bases	coverage	deviation
chr1	249250621	1083707013	4.3479	132.7009
chr2	243199373	1142174852	4.6965	28.723
chr3	198022430	891219015	4.5006	6.8795
chr4	191154276	899538971	4.7058	25.1231
chr5	180915260	812647336	4.4919	6.1495
chr6	171115067	783327916	4.5778	21.5159
chr7	159138663	891513493	5.6021	34.0072
chr8	146364022	671206343	4.5859	15.9863
chr9	141213431	555201945	3.9317	44.6441
chr10	135534747	684663344	5.0516	101.0204
chr11	135006516	602137547	4.4601	32.6549
chr12	133851895	592861918	4.4292	22.0208
chr13	115169878	435521264	3.7816	4.9021
chr14	107349540	398469709	3.7119	5.3642
chr15	102531392	363229525	3.5426	11.4796
chr16	90354753	374487855	4.1446	16.737
chr17	81195210	353916726	4.3588	26.9327
chr18	78077248	366406469	4.6929	48.6554
chr19	59128983	242264323	4.0972	68.1066
chr20	63025520	262414395	4.1636	10.0386
chr21	48129895	187356638	3.8927	17.6432
chr22	51304566	154036970	3.0024	15.3267
chrMT	16571	25693874	1,550.5325	320.7286
chrX	155270560	357074075	2.2997	11.1835

chrY	59373566	119700202	2.0161	44.4878
------	----------	-----------	--------	---------

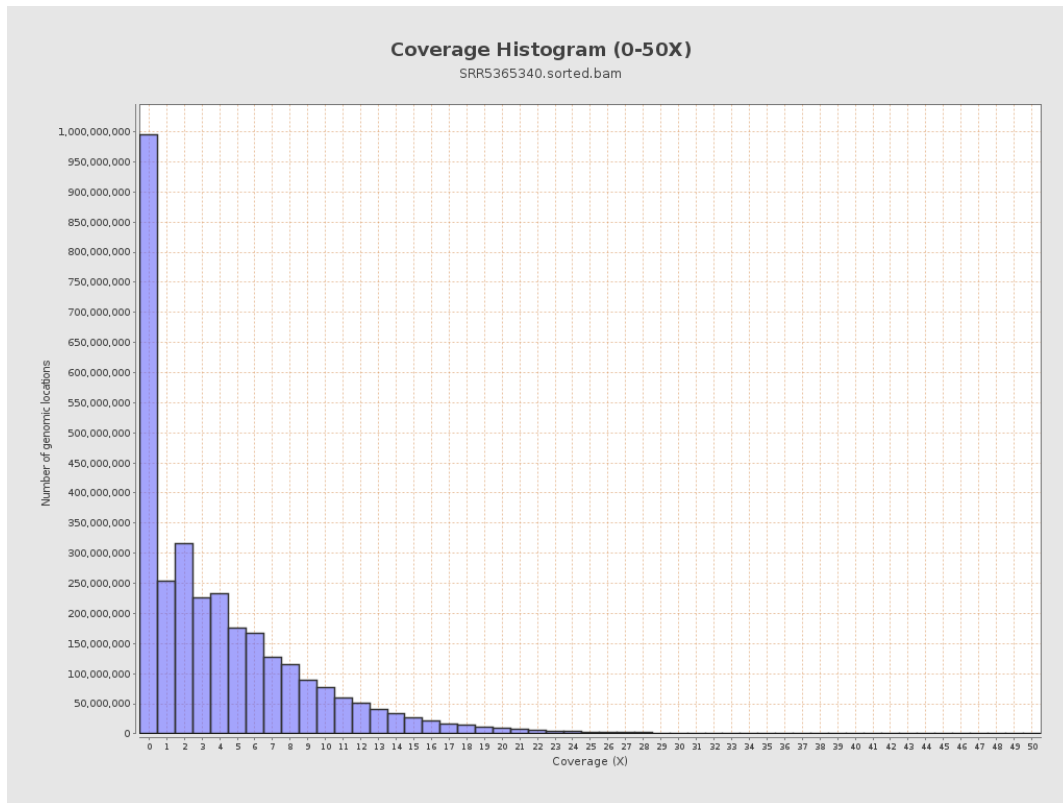
3. Results : Coverage across reference



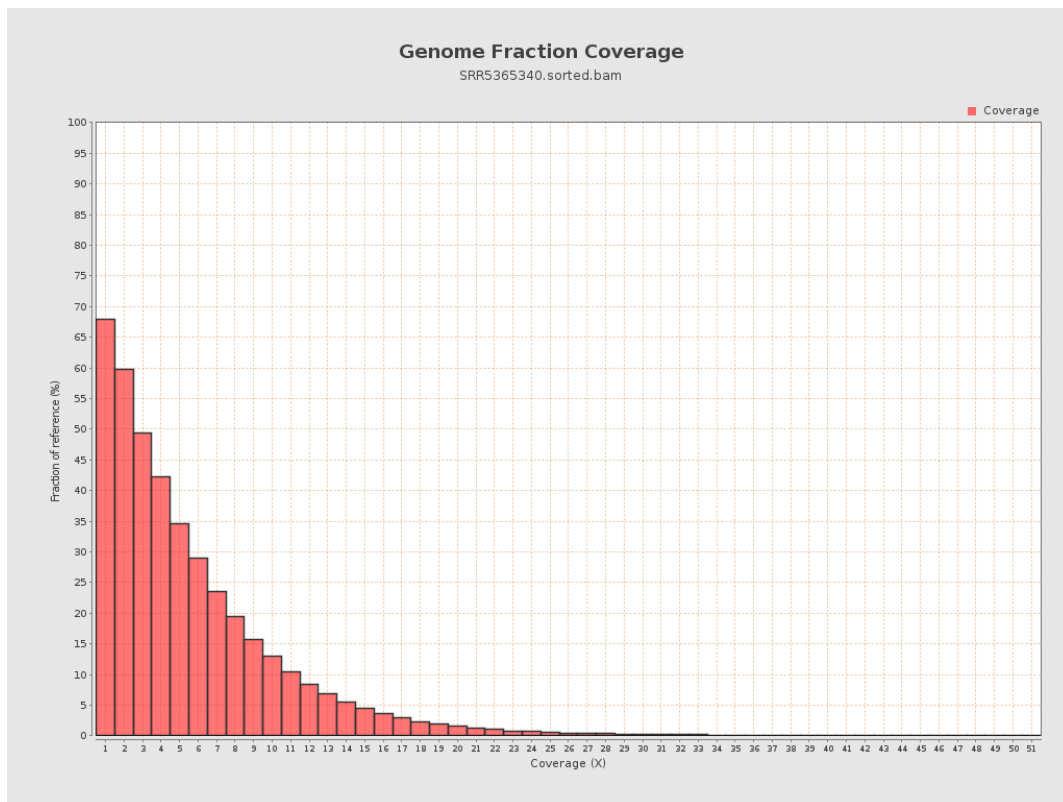
4. Results : Coverage Histogram



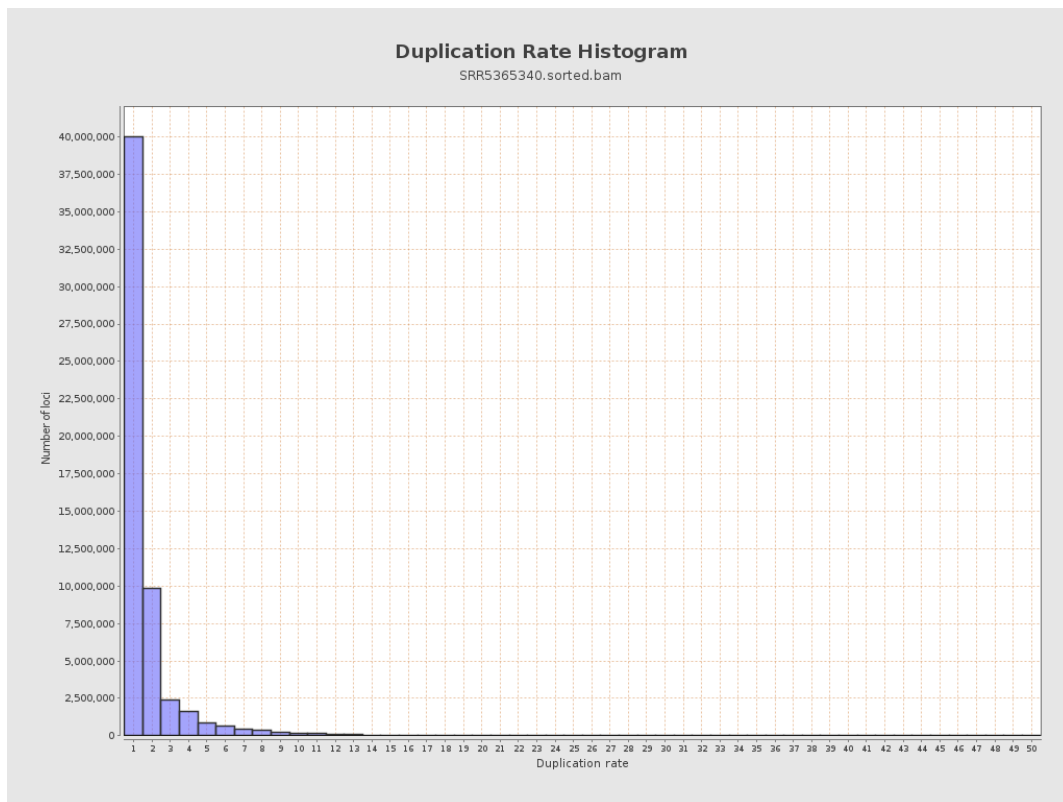
5. Results : Coverage Histogram (0-50X)



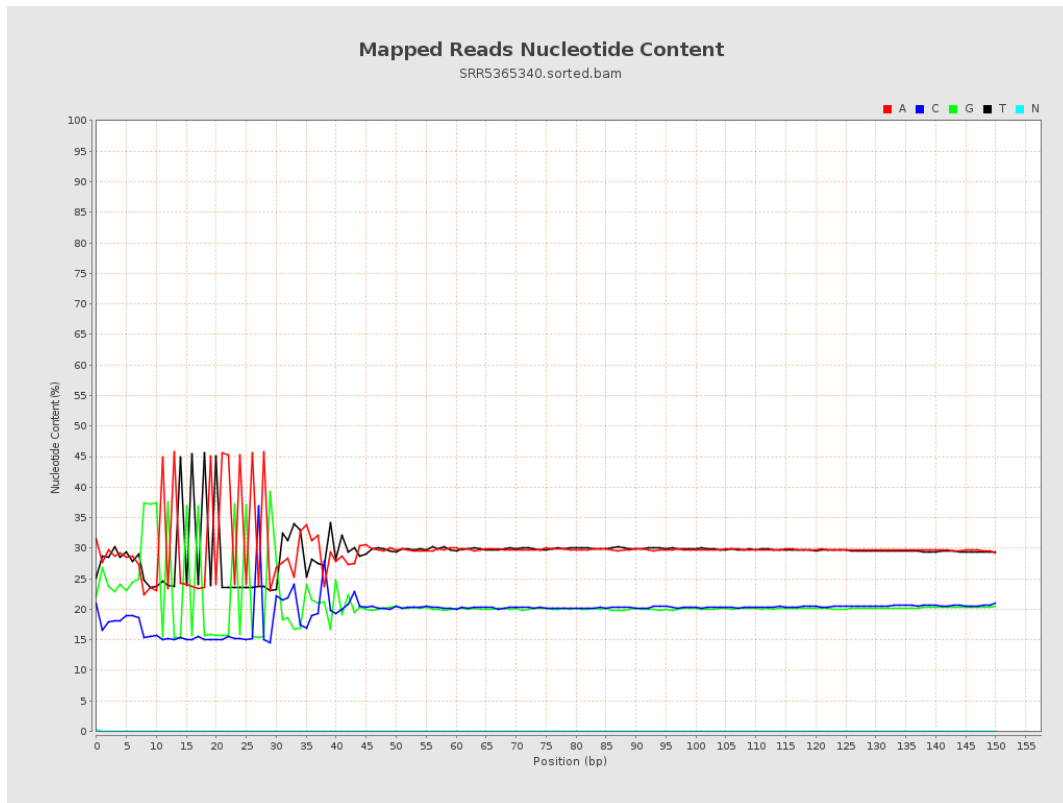
6. Results : Genome Fraction Coverage



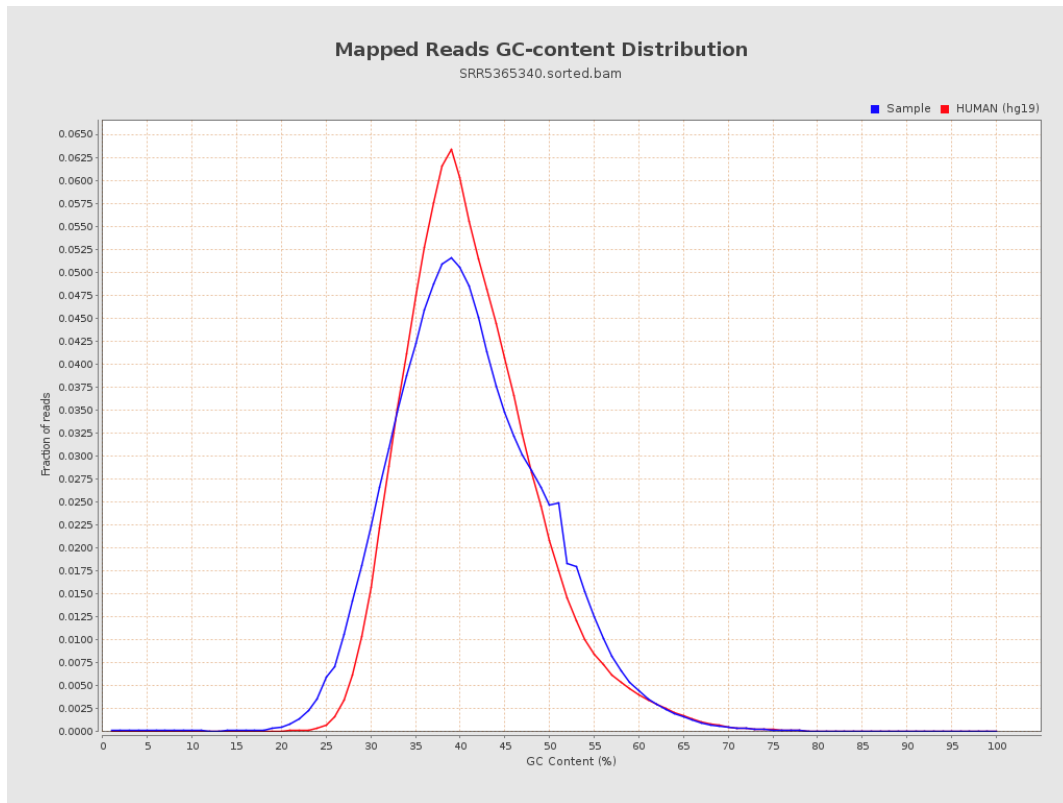
7. Results : Duplication Rate Histogram



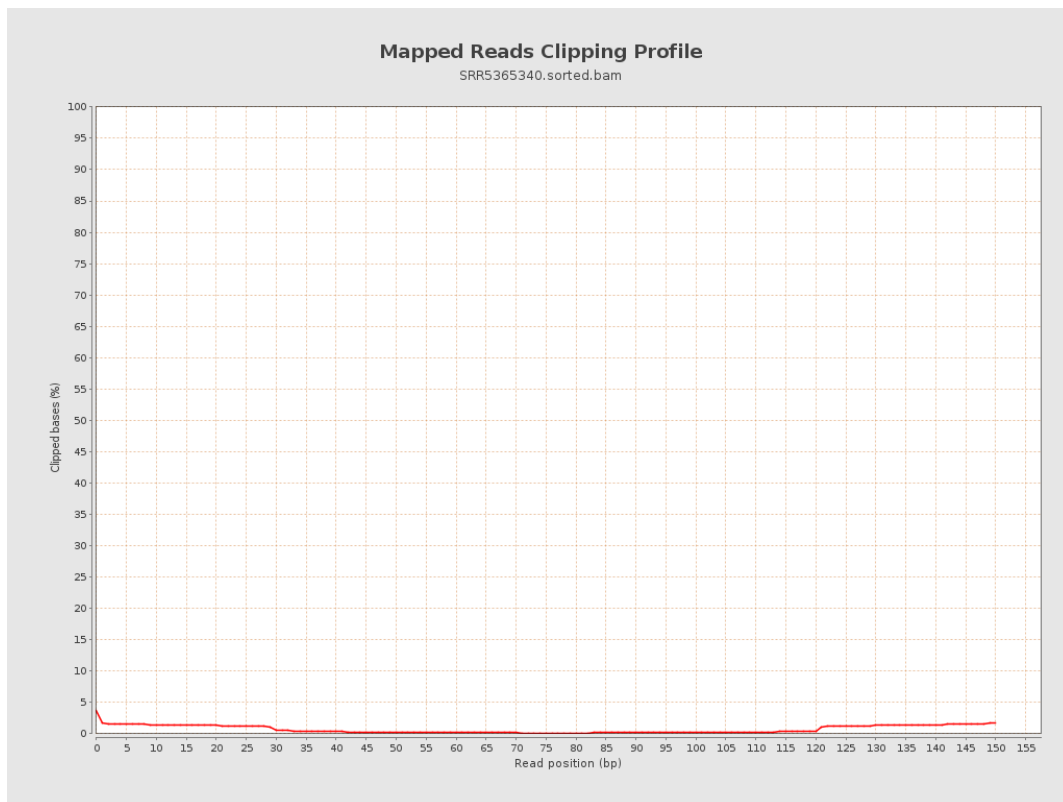
8. Results : Mapped Reads Nucleotide Content



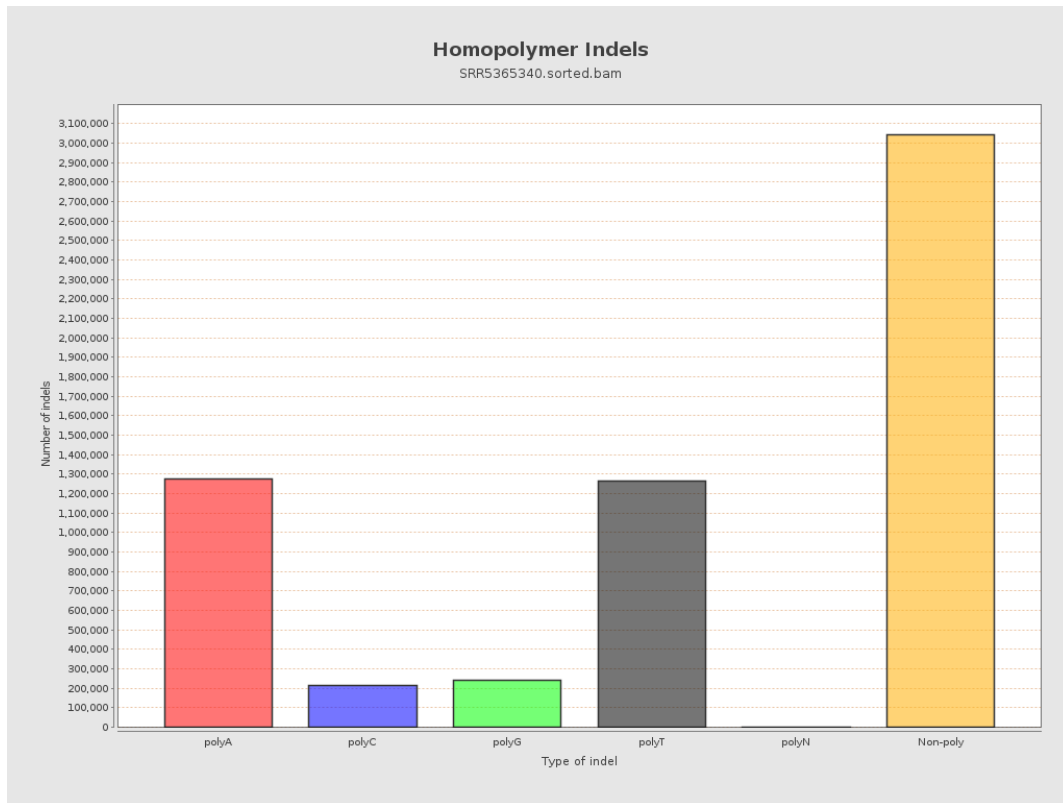
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



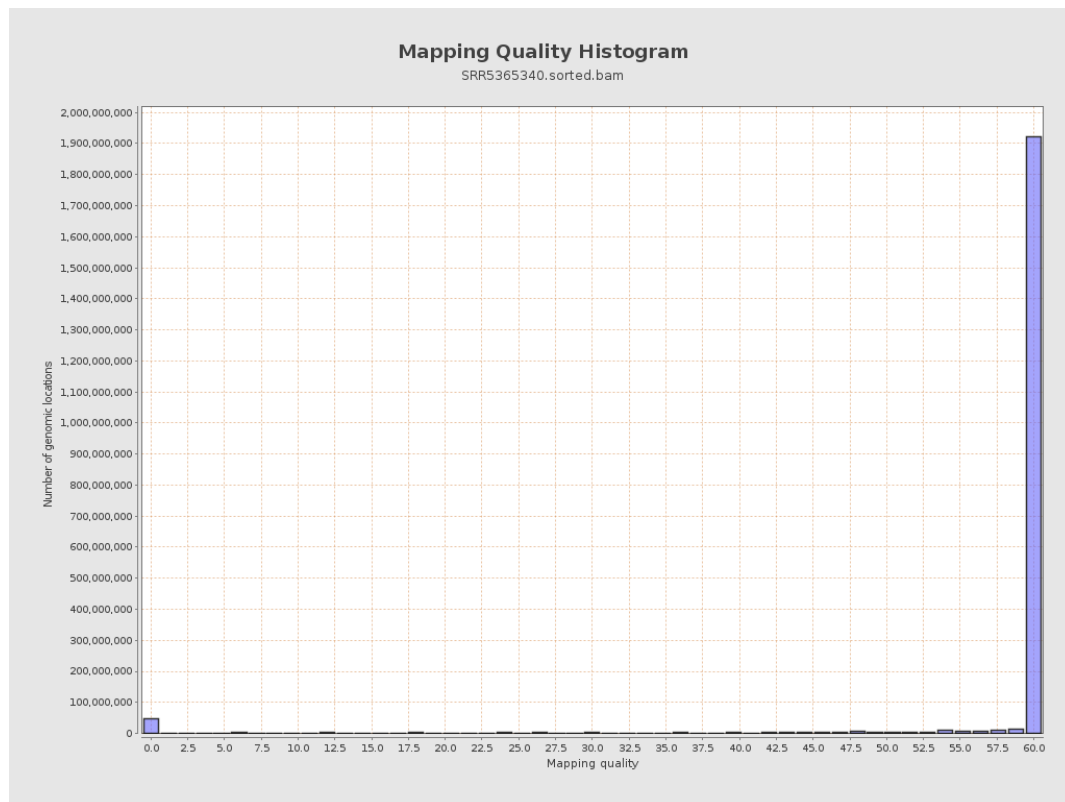
11. Results : Homopolymer Indels



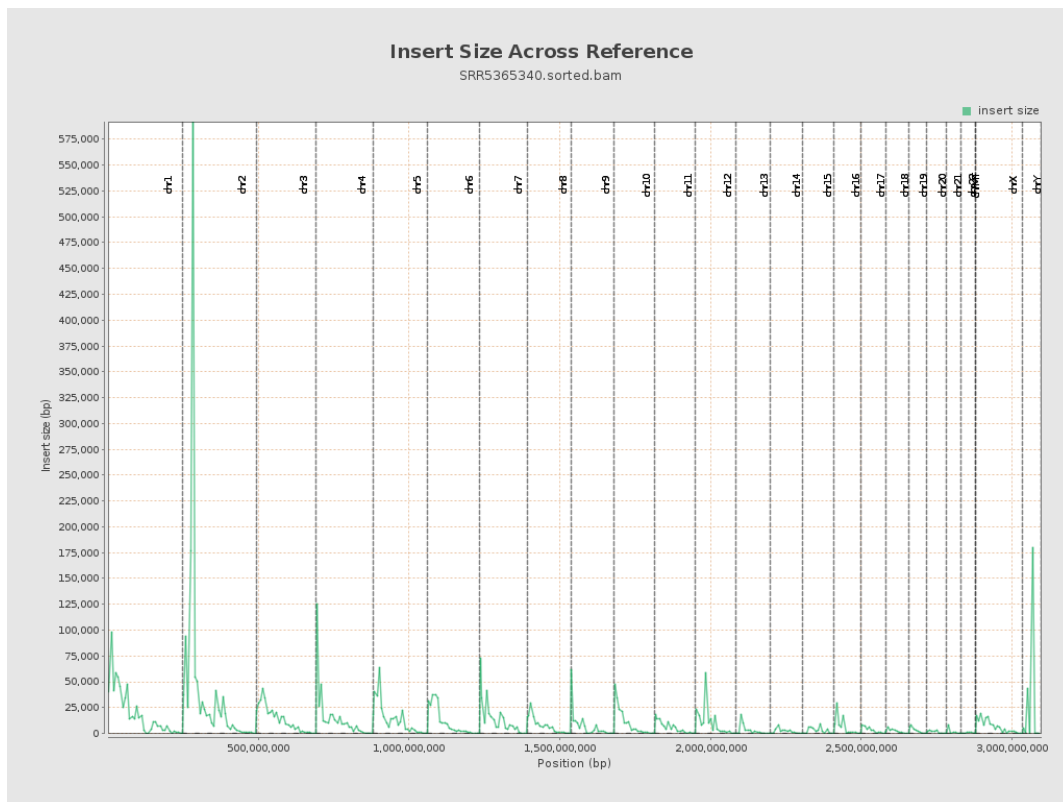
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

