

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/03 06:27:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365342.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_SRR5365342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365342_1.fastq.gz SRR5365342_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Nov 03 06:27:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	472,923,614
Mapped reads	436,182,504 / 92.23%
Unmapped reads	36,741,110 / 7.77%
Mapped paired reads	436,182,504 / 92.23%
Mapped reads, first in pair	218,705,325 / 46.25%
Mapped reads, second in pair	217,477,179 / 45.99%
Mapped reads, both in pair	433,222,310 / 91.61%
Mapped reads, singletons	2,960,194 / 0.63%
Secondary alignments	0
Supplementary alignments	1,769,479 / 0.37%
Read min/max/mean length	30 / 125 / 125.15
Duplicated reads (estimated)	312,588,658 / 66.1%
Duplication rate	41.63%
Clipped reads	308,949,938 / 65.33%

2.2. ACGT Content

Number/percentage of A's	13,293,320,051 / 29.84%
Number/percentage of C's	8,761,572,040 / 19.66%
Number/percentage of T's	12,906,032,396 / 28.97%
Number/percentage of G's	9,575,428,652 / 21.49%
Number/percentage of N's	18,200,515 / 0.04%

GC Percentage	41.16%
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2.3. Coverage

Mean	14.3971
Standard Deviation	122.4247

2.4. Mapping Quality

Mean Mapping Quality	53.79
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2.5. Insert size

Mean	70,722.37
Standard Deviation	2,596,600.61
P25/Median/P75	125 / 198 / 312

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	261,962,608
Insertions	13,276,812
Mapped reads with at least one insertion	2.98%
Deletions	6,947,627
Mapped reads with at least one deletion	1.55%
Homopolymer indels	50.11%

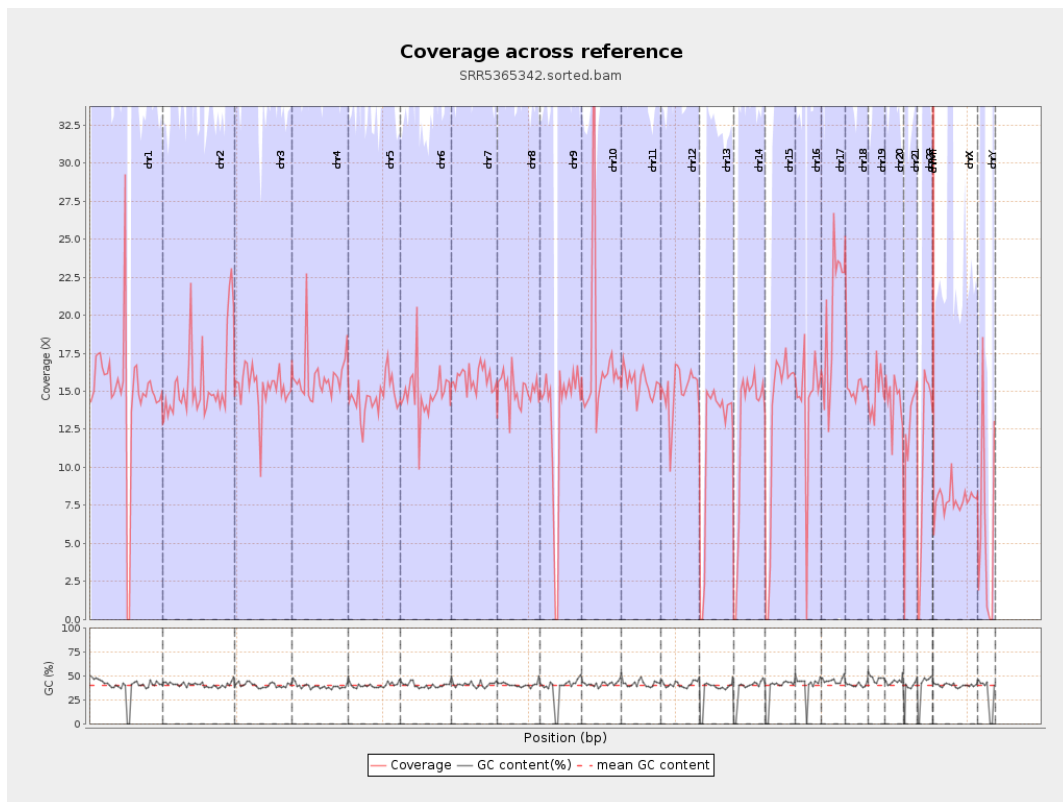
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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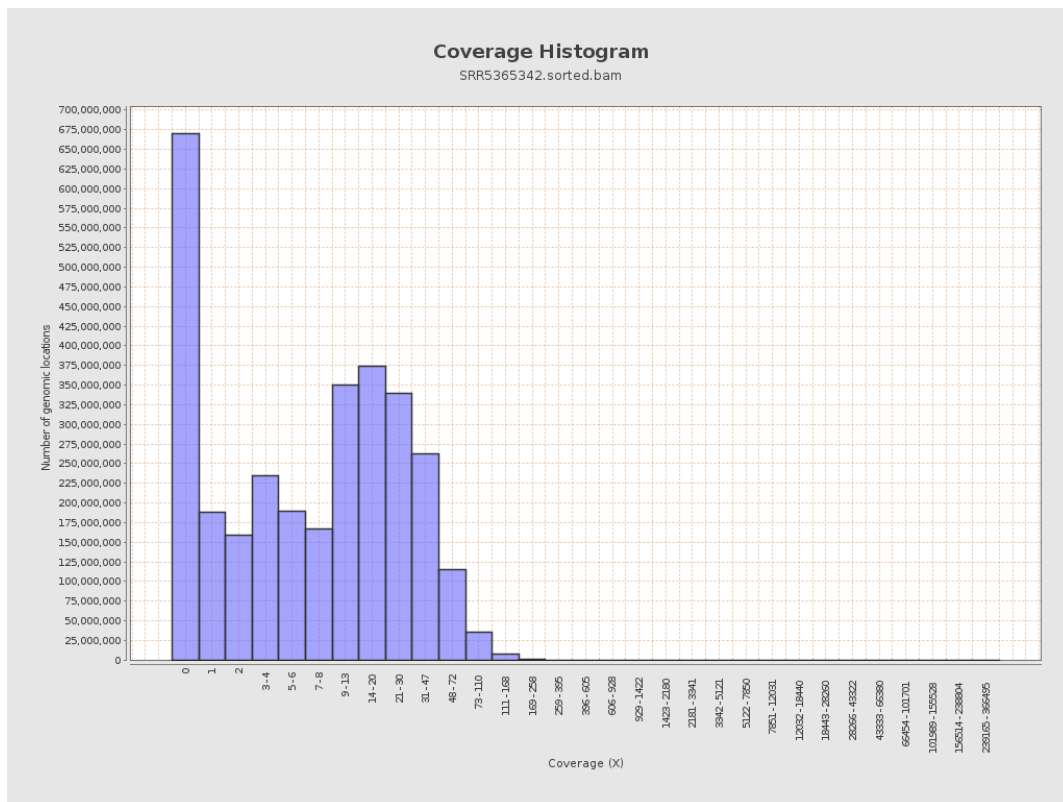
		bases	coverage	deviation
chr1	249250621	3717349044	14.9141	338.5265
chr2	243199373	3803483956	15.6394	67.9508
chr3	198022430	3016529400	15.2333	22.9591
chr4	191154276	3051017225	15.961	74.2505
chr5	180915260	2643432790	14.6114	19.9927
chr6	171115067	2543259423	14.8629	66.4316
chr7	159138663	2521469276	15.8445	76.0086
chr8	146364022	2205232090	15.0668	45.5506
chr9	141213431	1885433677	13.3517	91.6375
chr10	135534747	2277052581	16.8005	207.356
chr11	135006516	2094716048	15.5157	72.1315
chr12	133851895	2023804192	15.1197	33.7946
chr13	115169878	1371466573	11.9082	17.0183
chr14	107349540	1355817028	12.6299	18.9923
chr15	102531392	1325058715	12.9234	22.3431
chr16	90354753	1286326321	14.2364	42.3689
chr17	81195210	1633248058	20.1151	75.7676
chr18	78077248	1216369341	15.579	120.2135
chr19	59128983	876210072	14.8186	168.9235
chr20	63025520	905078595	14.3605	25.966
chr21	48129895	588874556	12.2351	43.8308
chr22	51304566	549996815	10.7202	34.8388
chrMT	16571	102131940	6,163.2937	1,158.1633
chrX	155270560	1220347002	7.8595	29.304

chrY	59373566	355293966	5.984	134.1389
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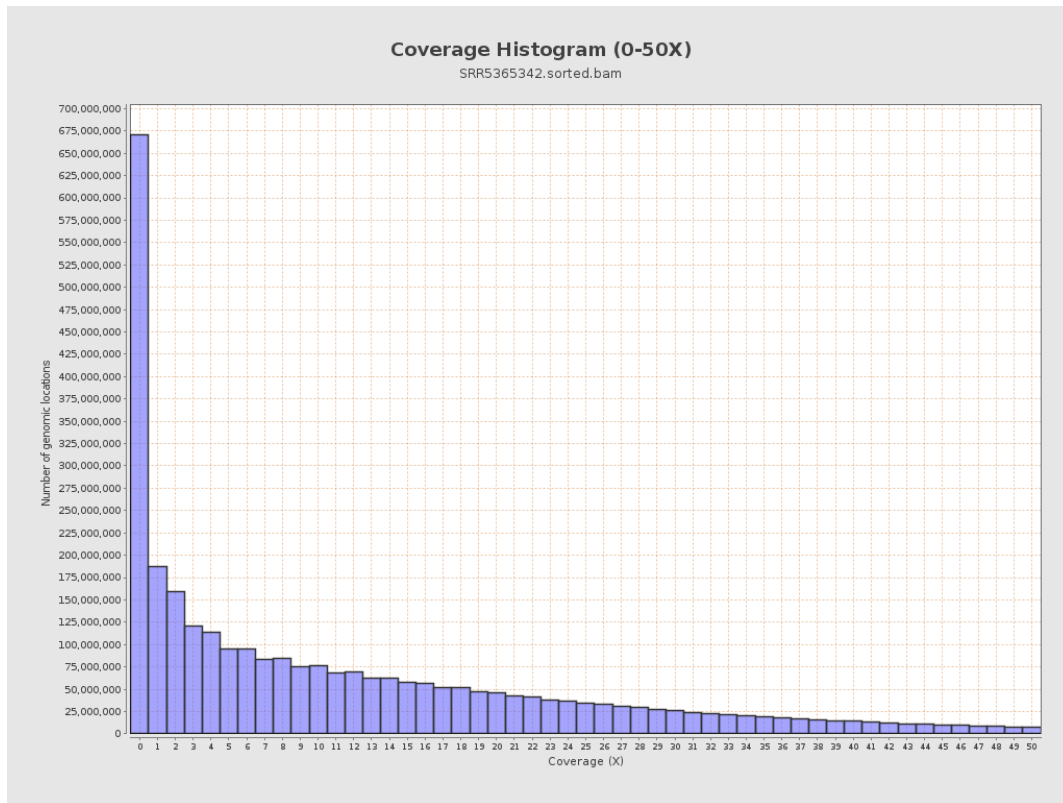
3. Results : Coverage across reference



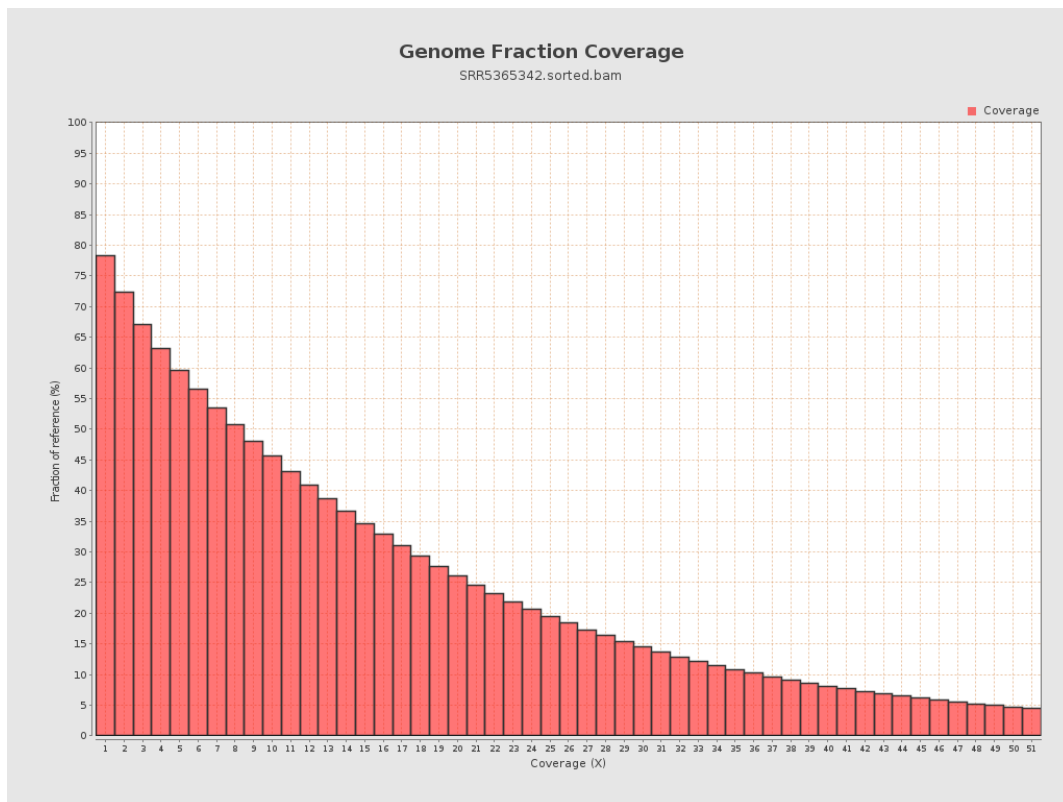
4. Results : Coverage Histogram



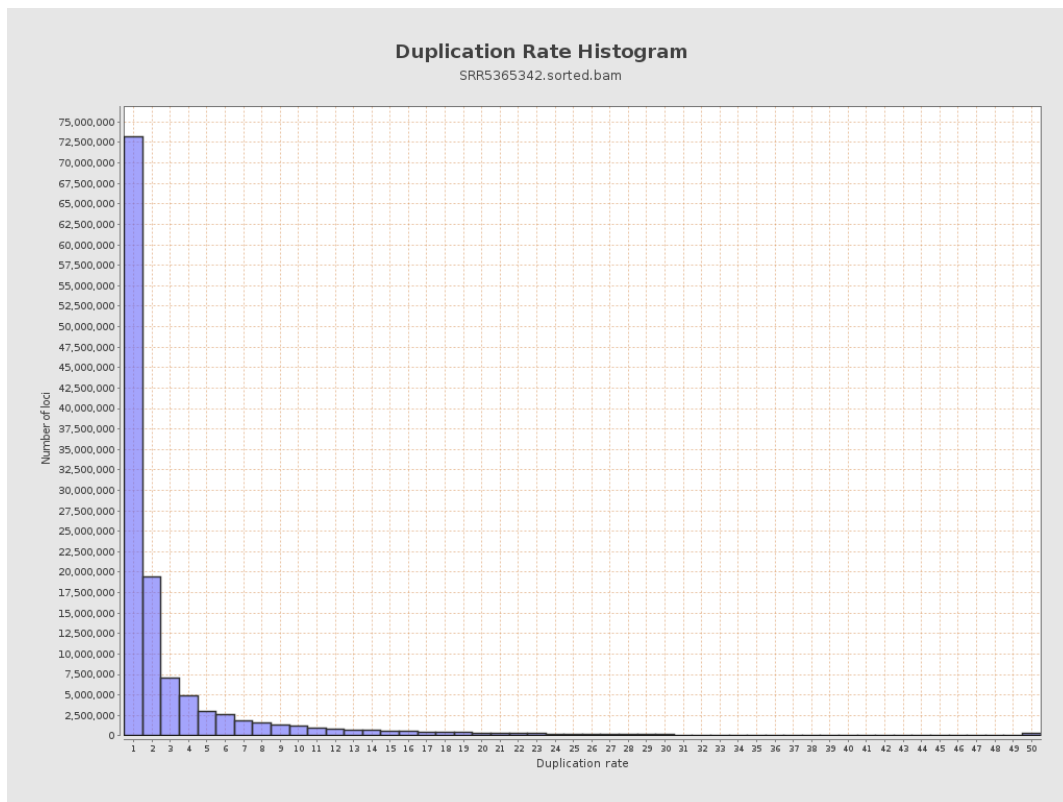
5. Results : Coverage Histogram (0-50X)



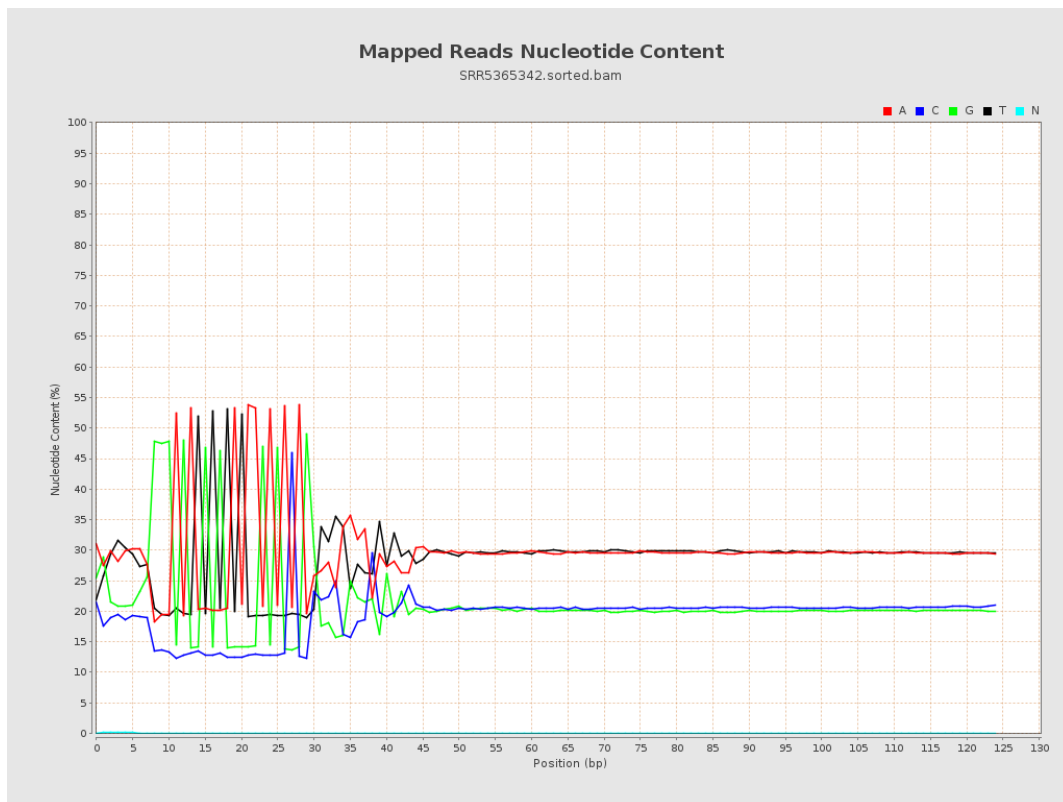
6. Results : Genome Fraction Coverage



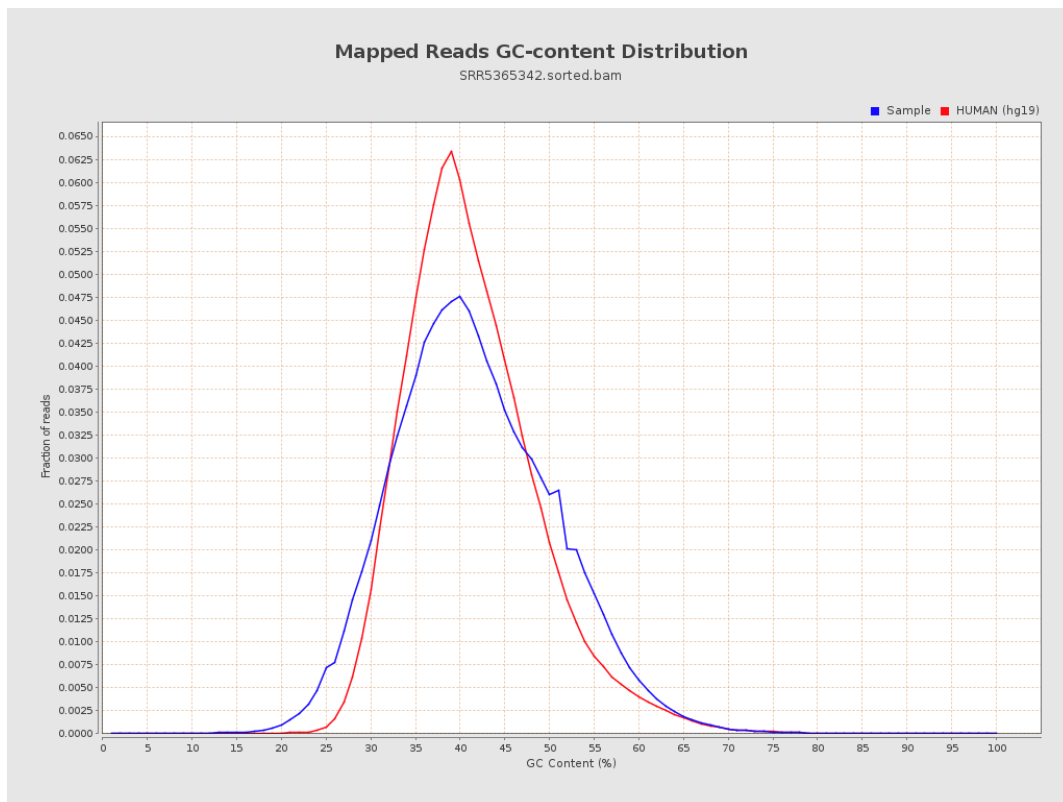
7. Results : Duplication Rate Histogram



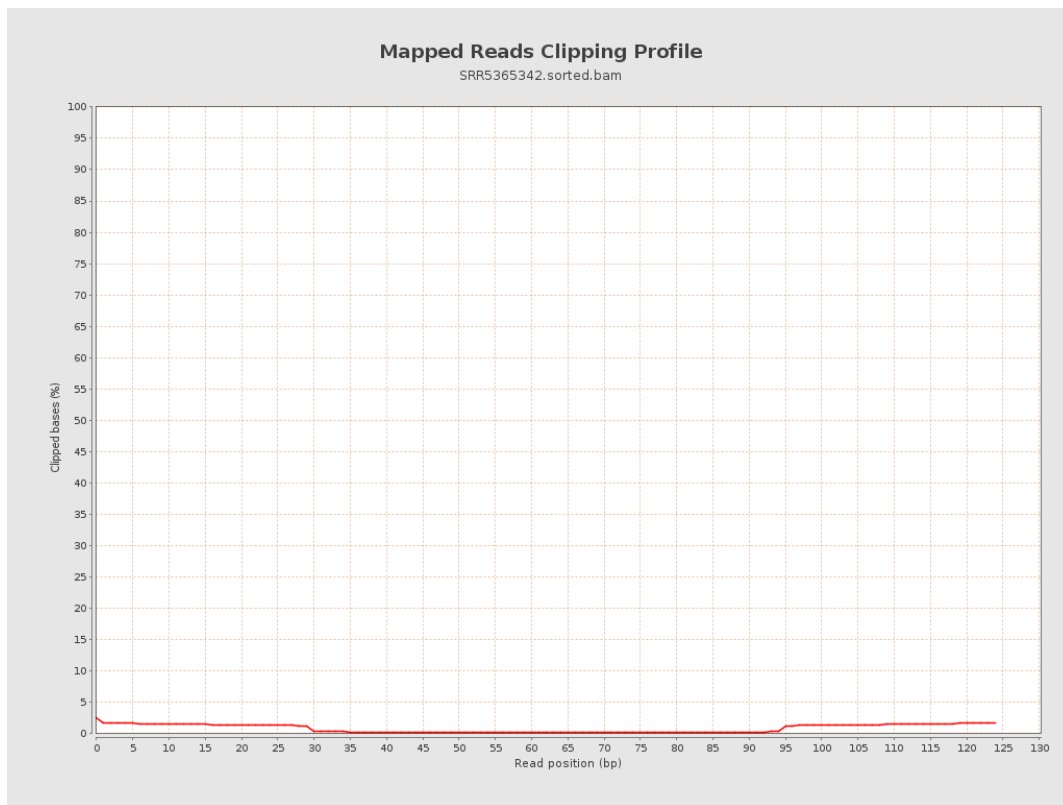
8. Results : Mapped Reads Nucleotide Content



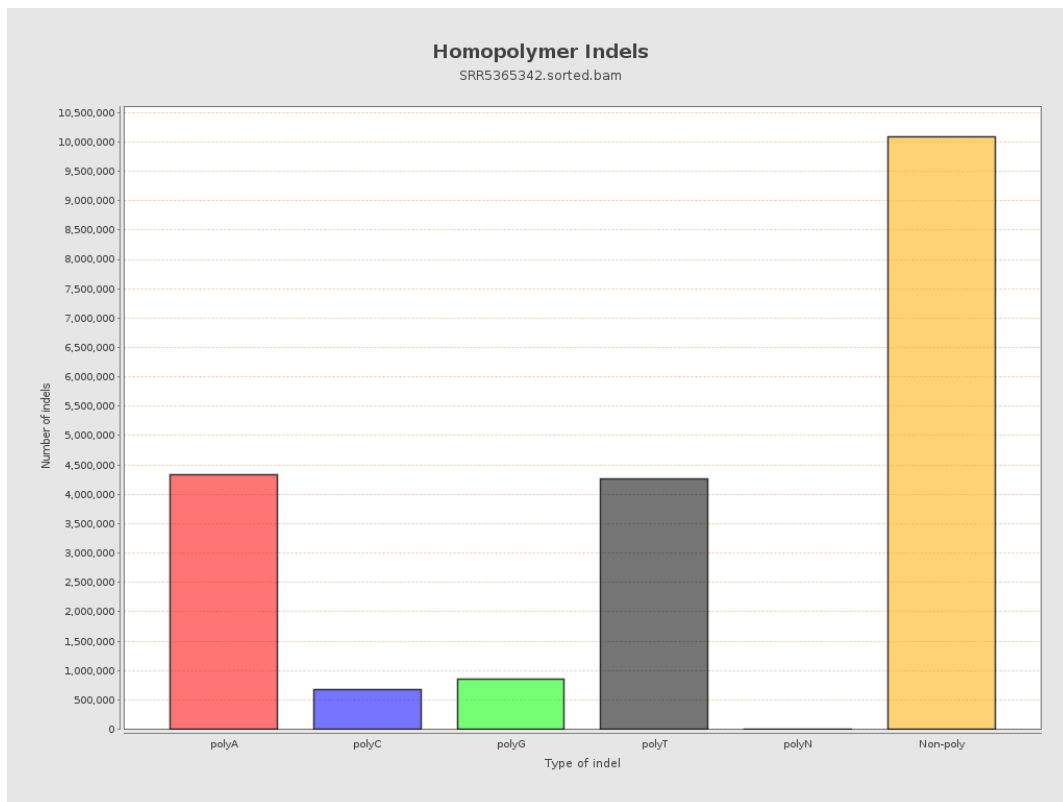
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



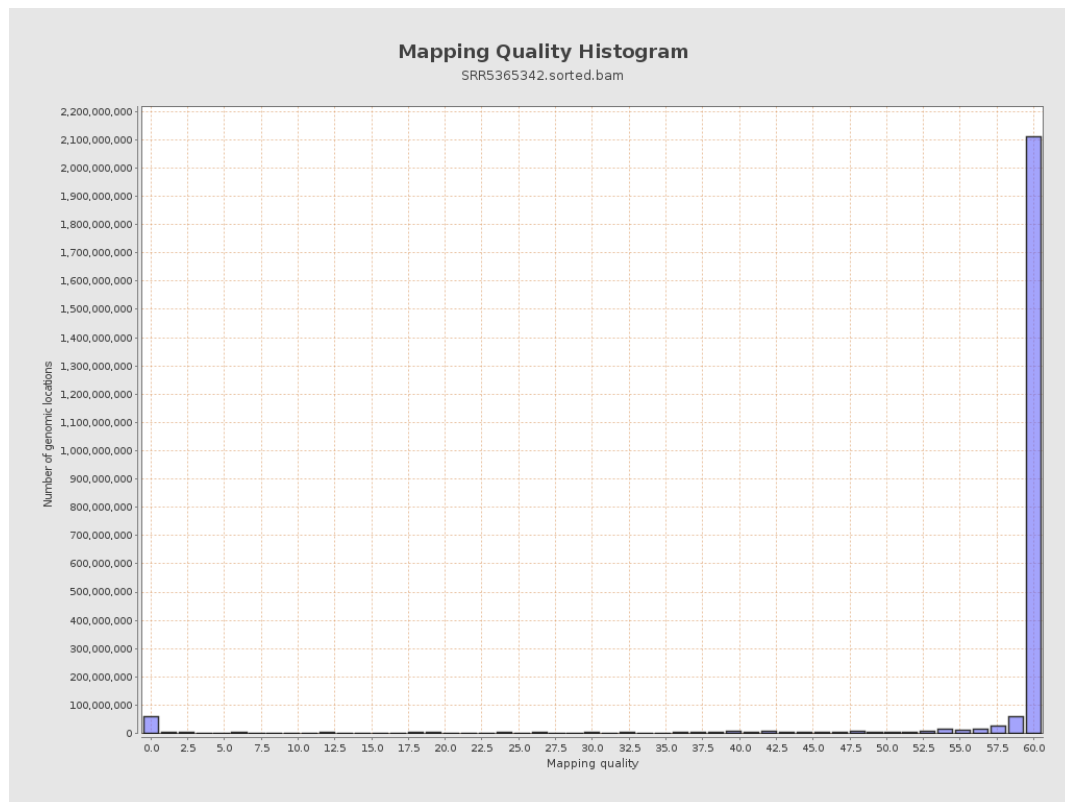
11. Results : Homopolymer Indels



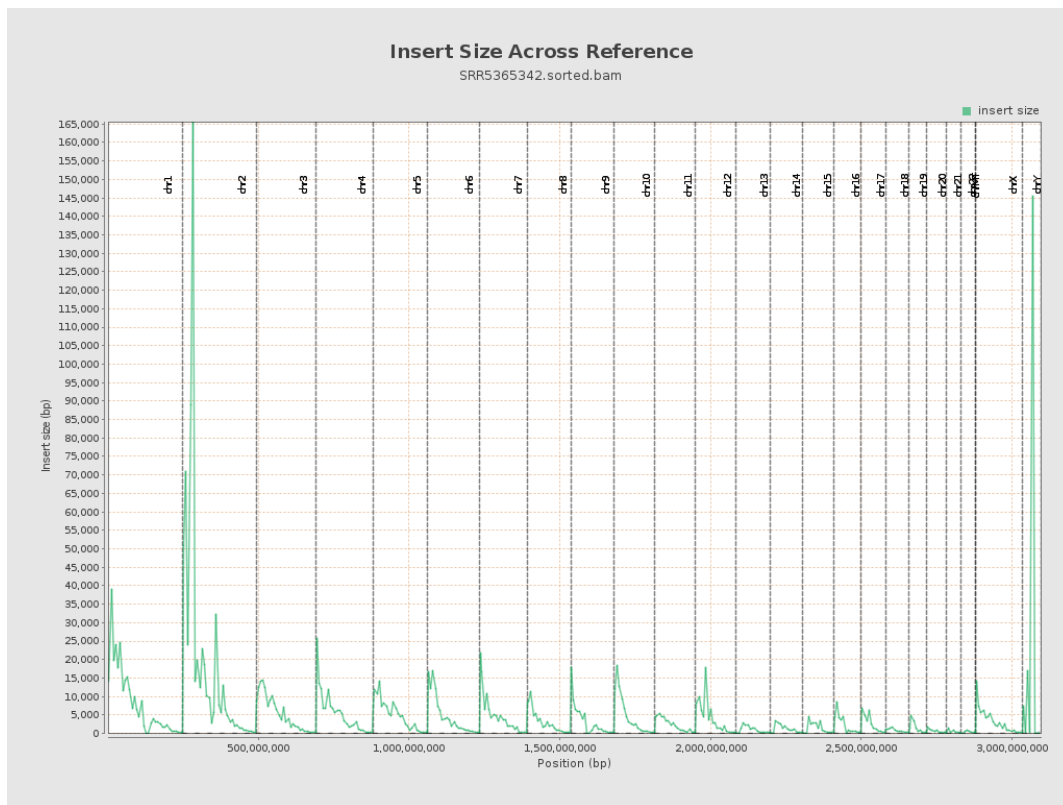
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

