

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/17 14:41:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365364.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_SRR5365364 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365364_1.fastq.gz SRR5365364_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Nov 17 14:41:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365364.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	638,624,950
Mapped reads	582,686,126 / 91.24%
Unmapped reads	55,938,824 / 8.76%
Mapped paired reads	582,686,126 / 91.24%
Mapped reads, first in pair	290,927,682 / 45.56%
Mapped reads, second in pair	291,758,444 / 45.69%
Mapped reads, both in pair	577,414,572 / 90.42%
Mapped reads, singletons	5,271,554 / 0.83%
Secondary alignments	0
Supplementary alignments	46,405,961 / 7.27%
Read min/max/mean length	30 / 150 / 153.73
Duplicated reads (estimated)	314,454,052 / 49.24%
Duplication rate	37.75%
Clipped reads	320,293,922 / 50.15%

2.2. ACGT Content

Number/percentage of A's	21,797,627,212 / 27.65%
Number/percentage of C's	17,699,868,171 / 22.45%
Number/percentage of T's	21,239,925,858 / 26.94%
Number/percentage of G's	18,106,195,903 / 22.96%
Number/percentage of N's	4,588,111 / 0.01%

GC Percentage	45.41%
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2.3. Coverage

Mean	25.4918
Standard Deviation	455.0059

2.4. Mapping Quality

Mean Mapping Quality	53.36
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2.5. Insert size

Mean	113,696.12
Standard Deviation	2,909,996.23
P25/Median/P75	130 / 166 / 217

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	796,994,435
Insertions	18,397,128
Mapped reads with at least one insertion	2.87%
Deletions	16,811,961
Mapped reads with at least one deletion	2.64%
Homopolymer indels	36.6%

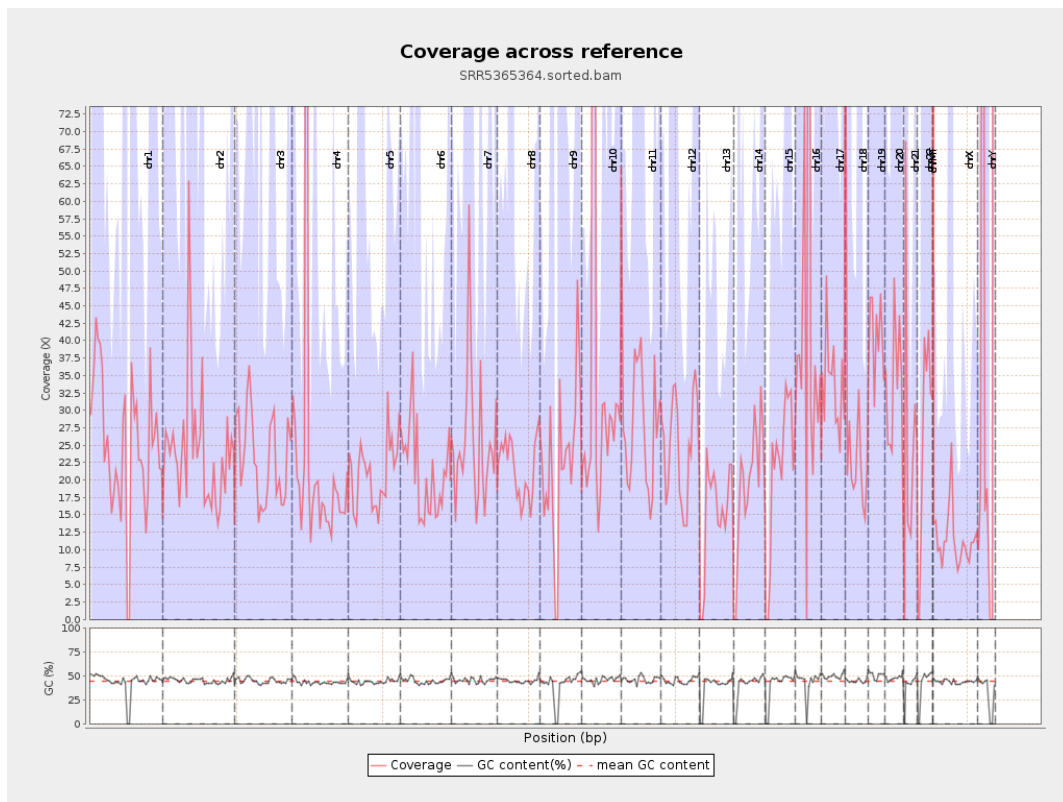
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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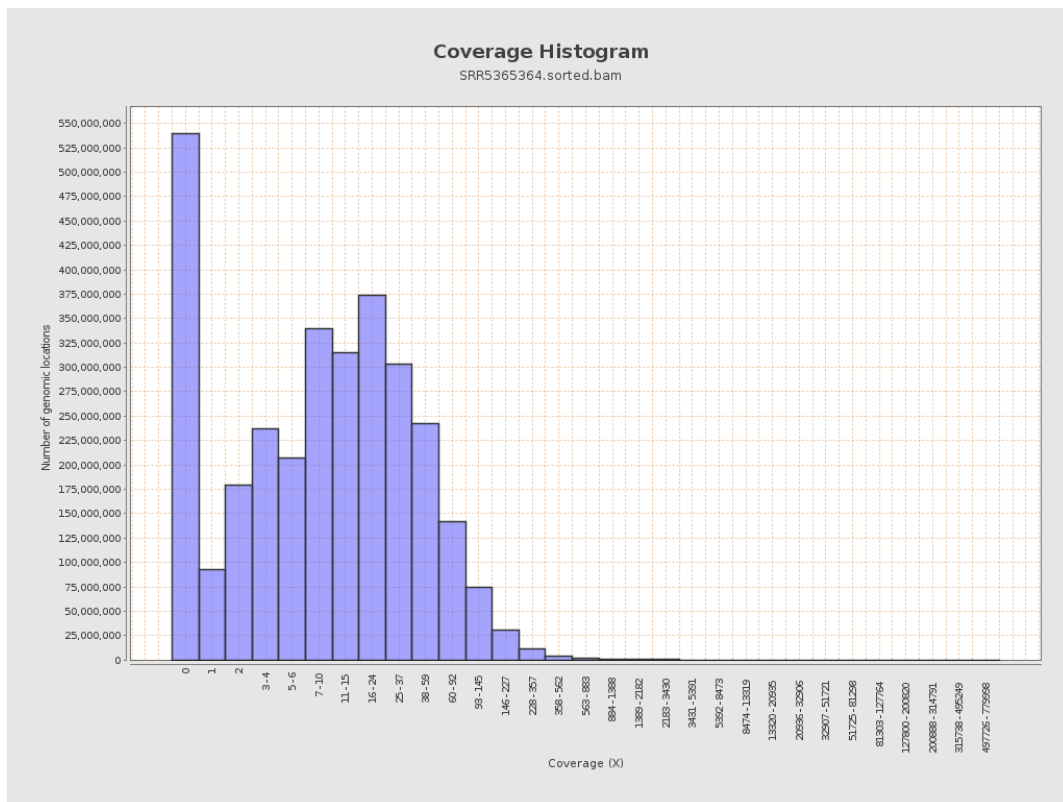
		bases	coverage	deviation
chr1	249250621	6239232791	25.032	221.1764
chr2	243199373	5935987930	24.4079	281.4177
chr3	198022430	4569046165	23.0734	106.533
chr4	191154276	4537971495	23.7398	753.9185
chr5	180915260	3825518268	21.1454	63.3025
chr6	171115067	3613271446	21.116	126.3914
chr7	159138663	4094305296	25.7279	107.7533
chr8	146364022	3171074139	21.6657	74.3115
chr9	141213431	3148396867	22.2953	197.215
chr10	135534747	4865856831	35.9012	1,190.0505
chr11	135006516	3793943469	28.1019	108.762
chr12	133851895	3327866356	24.8623	58.9067
chr13	115169878	1764972458	15.3249	29.4028
chr14	107349540	2113655611	19.6895	48.478
chr15	102531392	2151325510	20.9821	41.0456
chr16	90354753	4153722123	45.9713	882.472
chr17	81195210	2749961402	33.8685	377.3927
chr18	78077248	1990963658	25.4999	787.8495
chr19	59128983	2389187153	40.4064	161.5996
chr20	63025520	2086377523	33.1037	297.7228
chr21	48129895	1273365843	26.4569	465.2096
chr22	51304566	1332728193	25.9768	71.735
chrMT	16571	32974872	1,989.9144	1,040.2289
chrX	155270560	1782363609	11.4791	82.4836

chrY	59373566	3970751269	66.8774	1,551.0226
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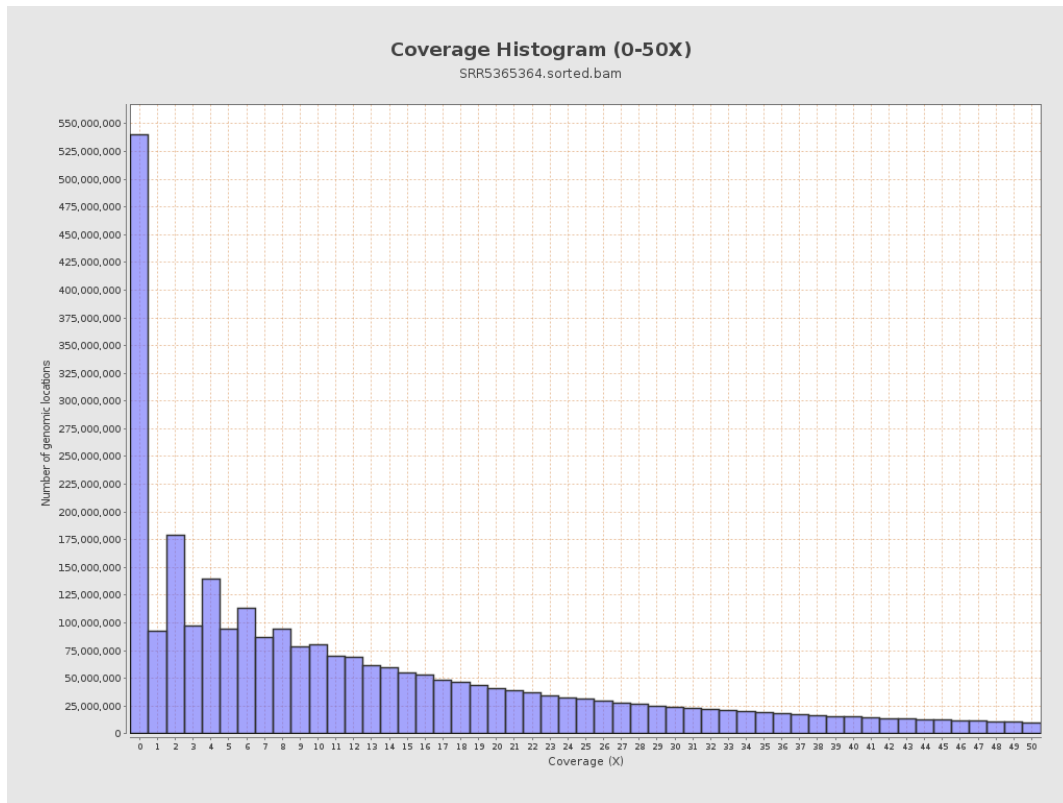
3. Results : Coverage across reference



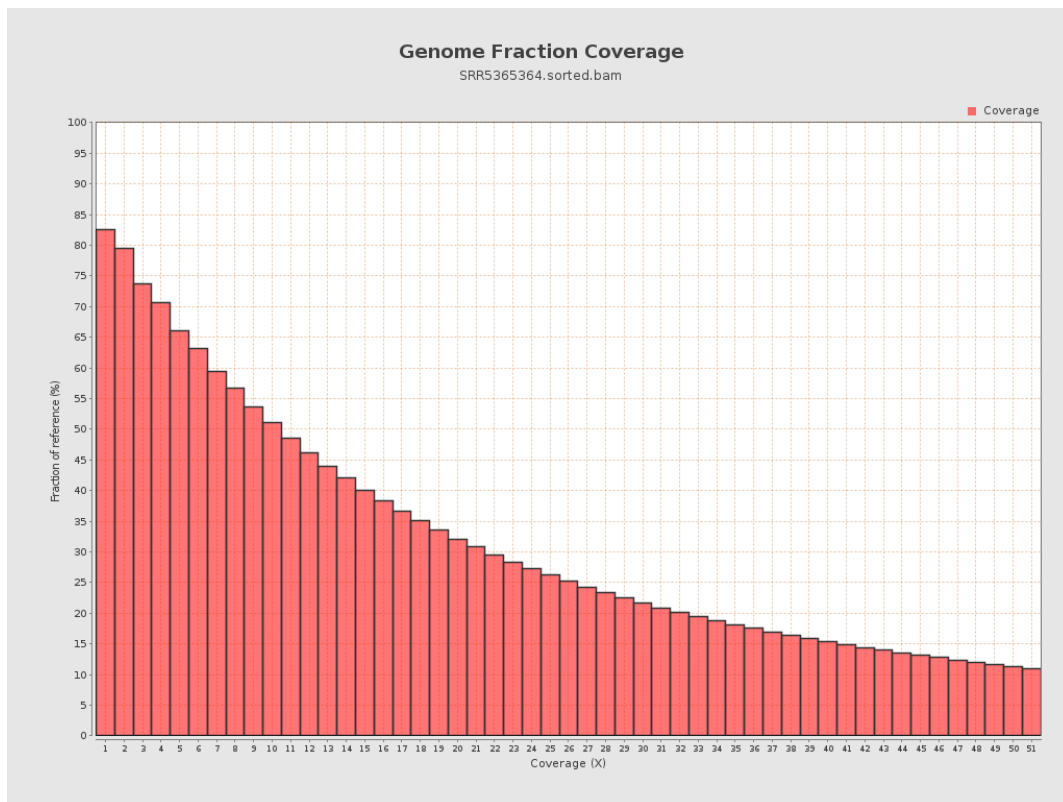
4. Results : Coverage Histogram



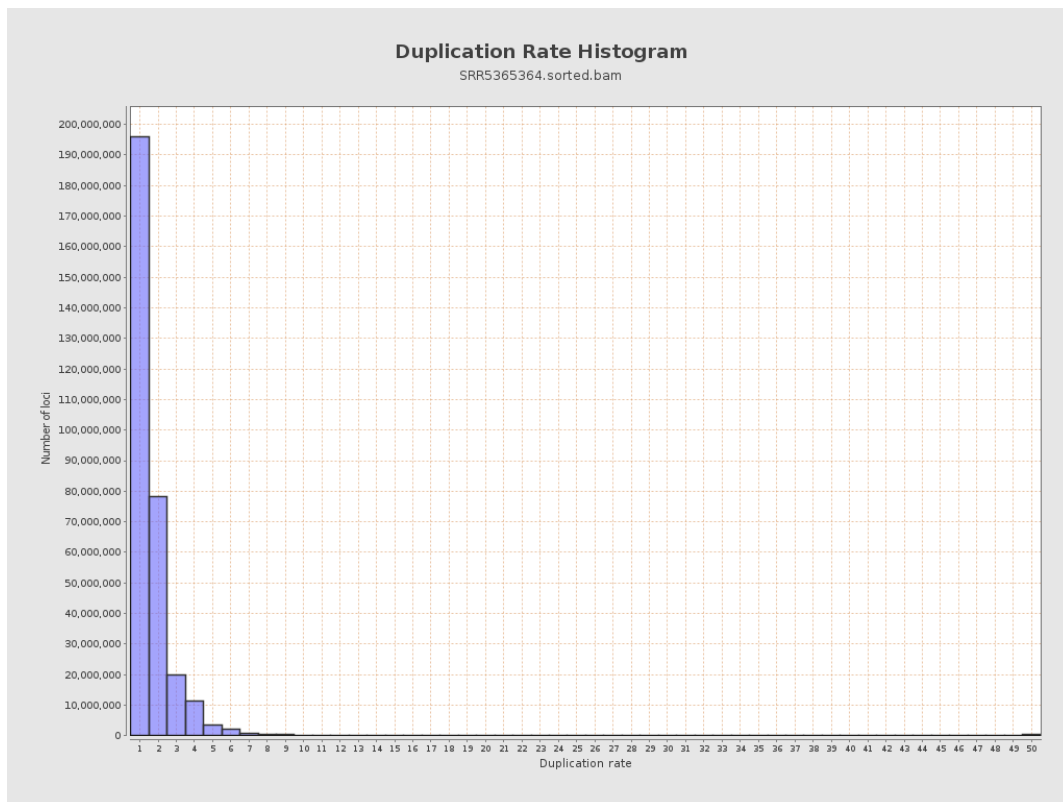
5. Results : Coverage Histogram (0-50X)



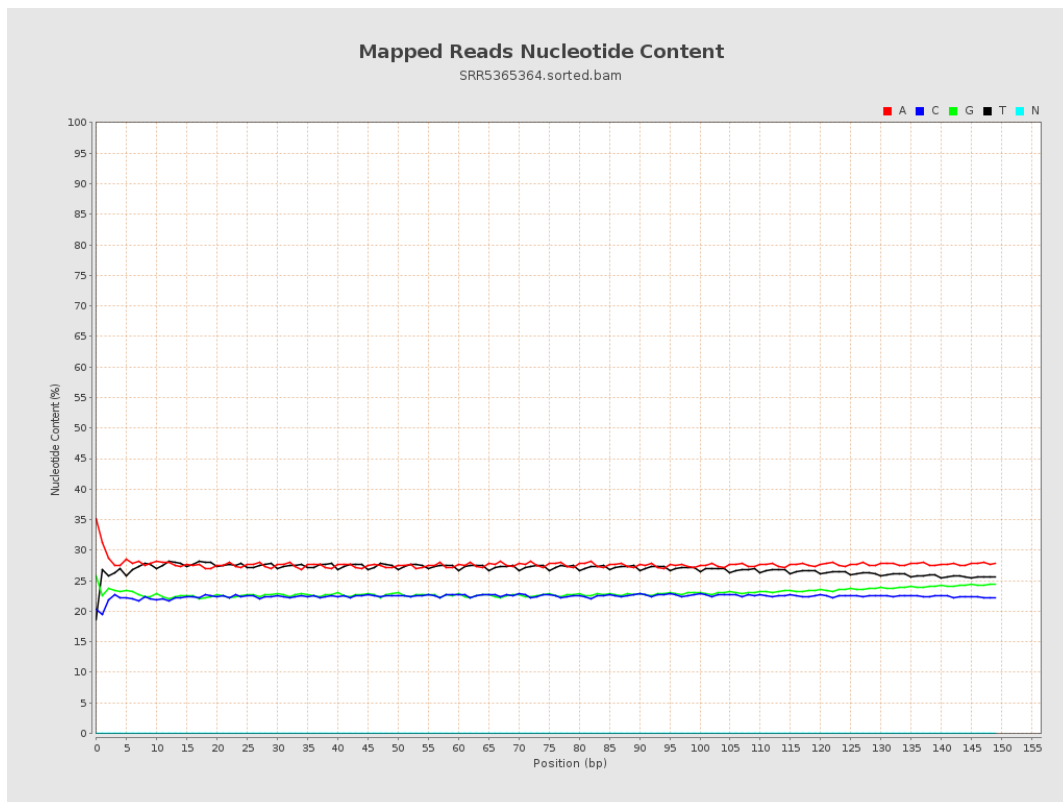
6. Results : Genome Fraction Coverage



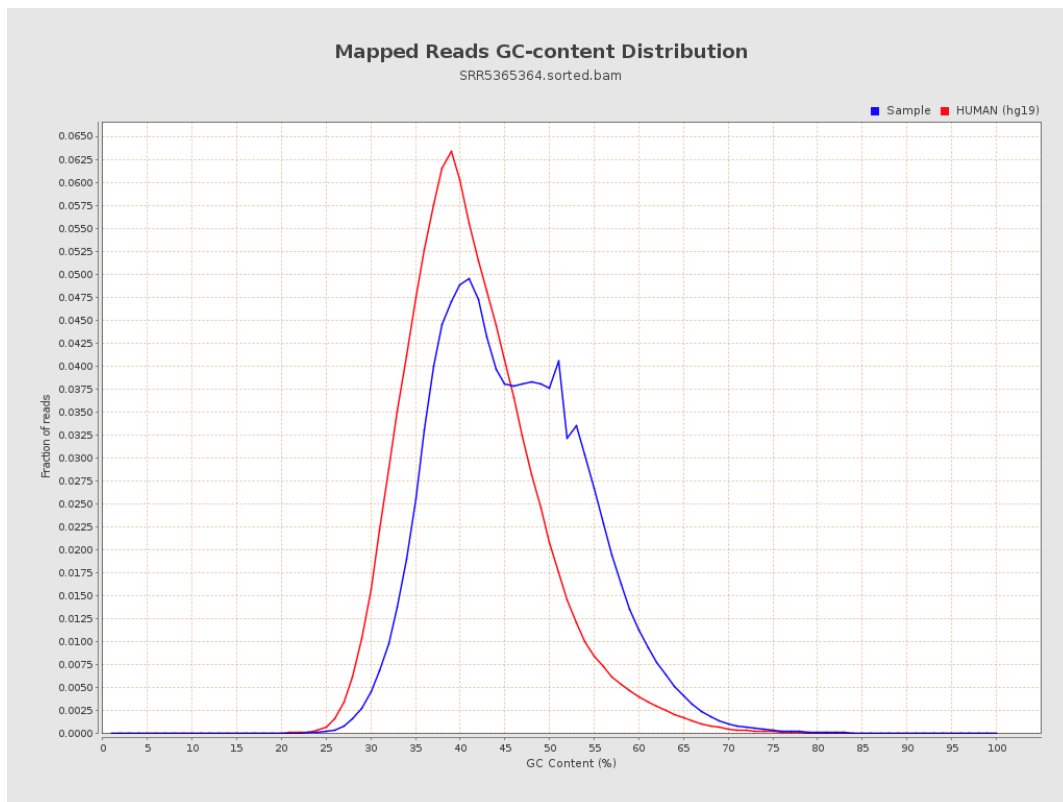
7. Results : Duplication Rate Histogram



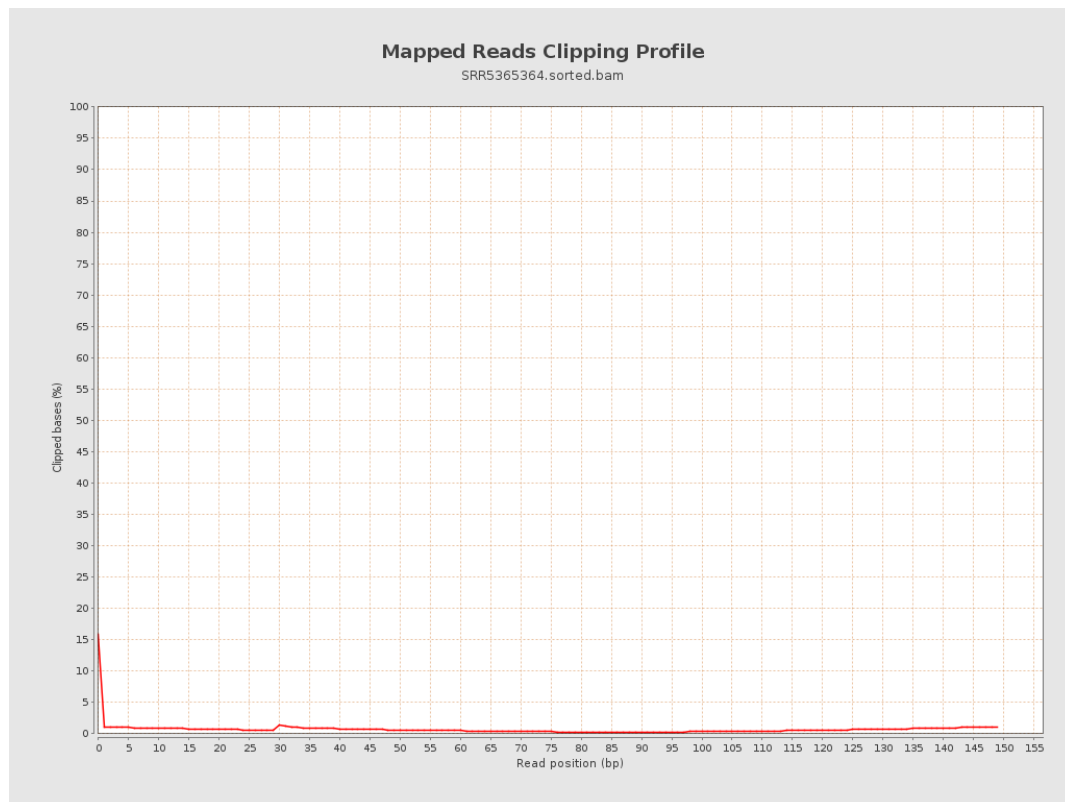
8. Results : Mapped Reads Nucleotide Content



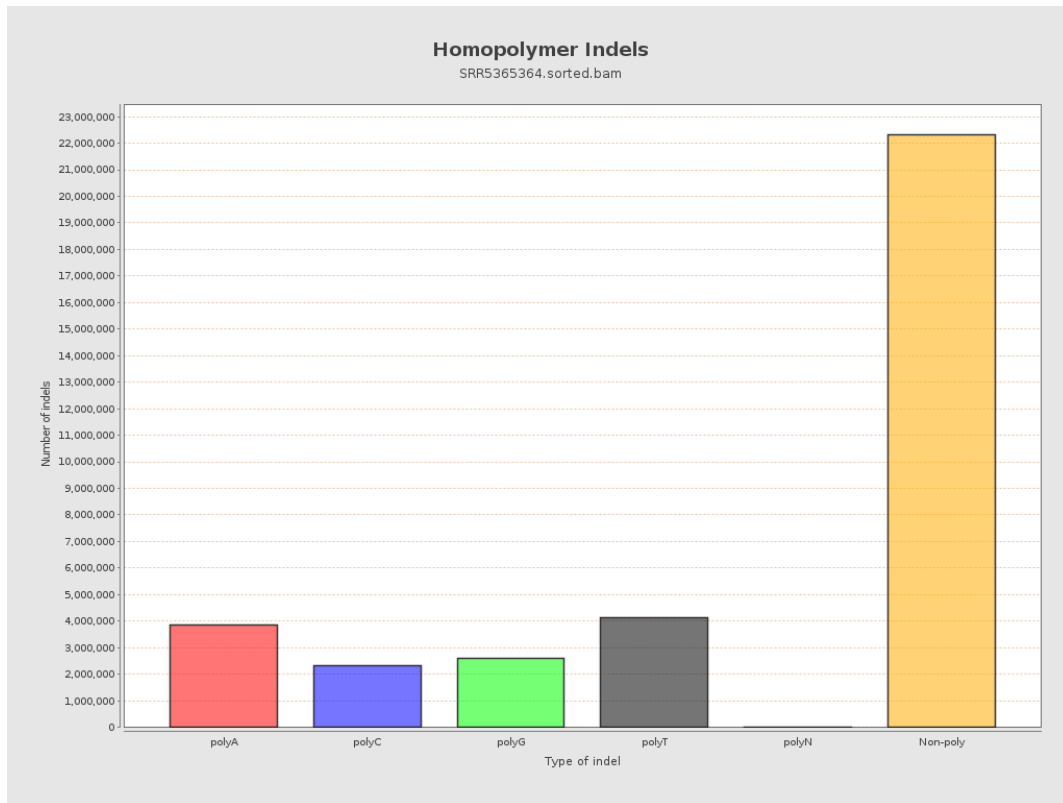
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



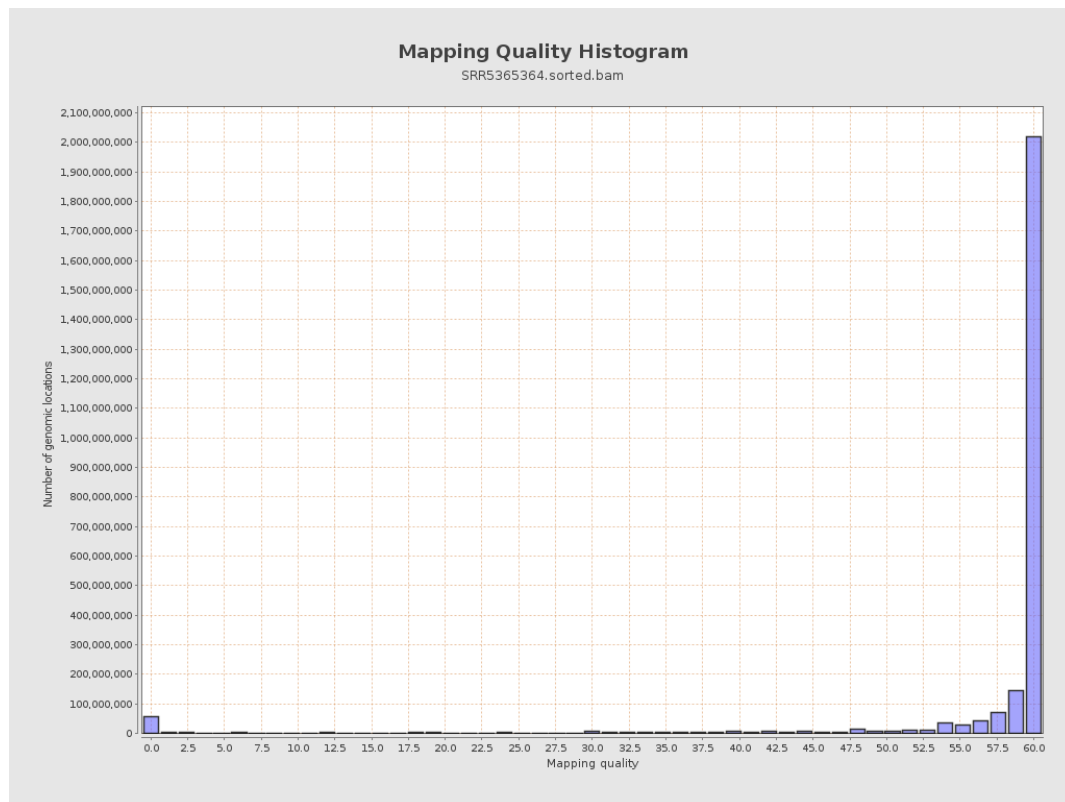
11. Results : Homopolymer Indels



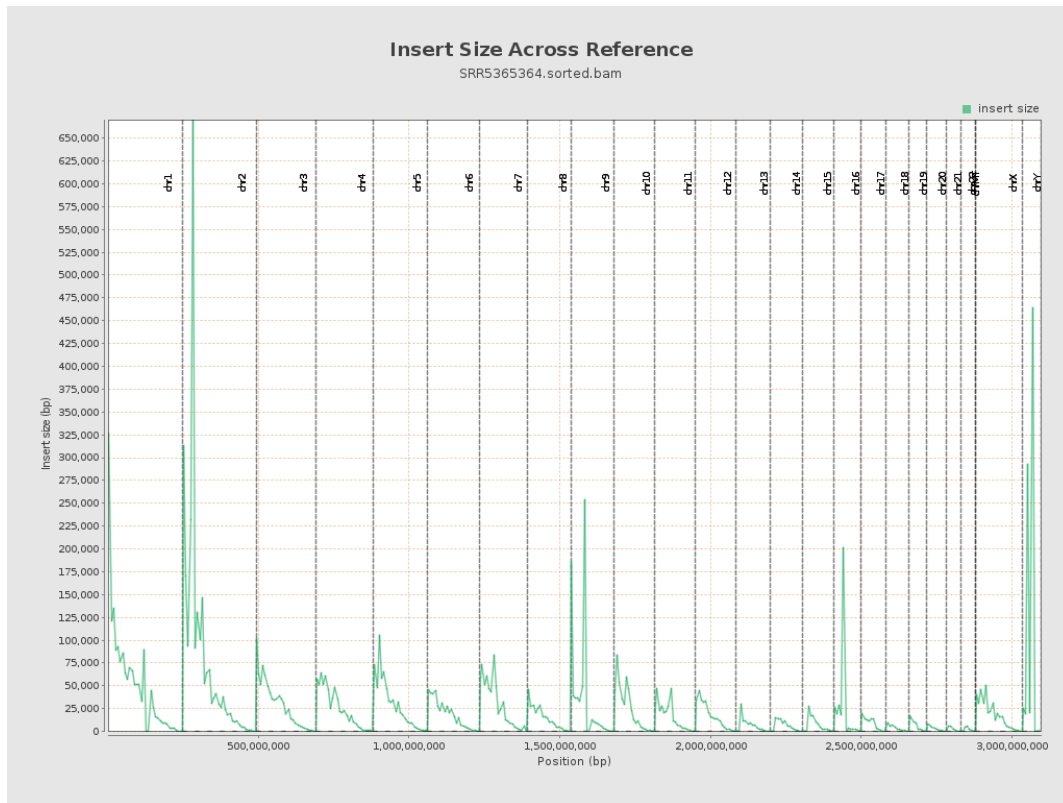
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

