

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/21 02:33:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365358.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_SRR5365358 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365358_1.fastq.gz SRR5365358_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Nov 21 02:33:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365358.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,121,462,854
Mapped reads	1,088,890,431 / 97.1%
Unmapped reads	32,572,423 / 2.9%
Mapped paired reads	1,088,890,431 / 97.1%
Mapped reads, first in pair	545,616,706 / 48.65%
Mapped reads, second in pair	543,273,725 / 48.44%
Mapped reads, both in pair	1,083,749,012 / 96.64%
Mapped reads, singletons	5,141,419 / 0.46%
Secondary alignments	0
Supplementary alignments	4,475,086 / 0.4%
Read min/max/mean length	30 / 125 / 125.17
Duplicated reads (estimated)	713,357,793 / 63.61%
Duplication rate	34.47%
Clipped reads	681,515,987 / 60.77%

2.2. ACGT Content

Number/percentage of A's	34,217,939,428 / 30.1%
Number/percentage of C's	22,290,298,620 / 19.61%
Number/percentage of T's	33,321,656,369 / 29.31%
Number/percentage of G's	23,837,321,980 / 20.97%
Number/percentage of N's	29,604,421 / 0.03%

GC Percentage	40.57%
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2.3. Coverage

Mean	36.74
Standard Deviation	469.1561

2.4. Mapping Quality

Mean Mapping Quality	53.75
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2.5. Insert size

Mean	37,039.05
Standard Deviation	1,854,651.59
P25/Median/P75	113 / 161 / 231

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	661,174,992
Insertions	34,756,428
Mapped reads with at least one insertion	3.12%
Deletions	18,555,185
Mapped reads with at least one deletion	1.66%
Homopolymer indels	49.89%

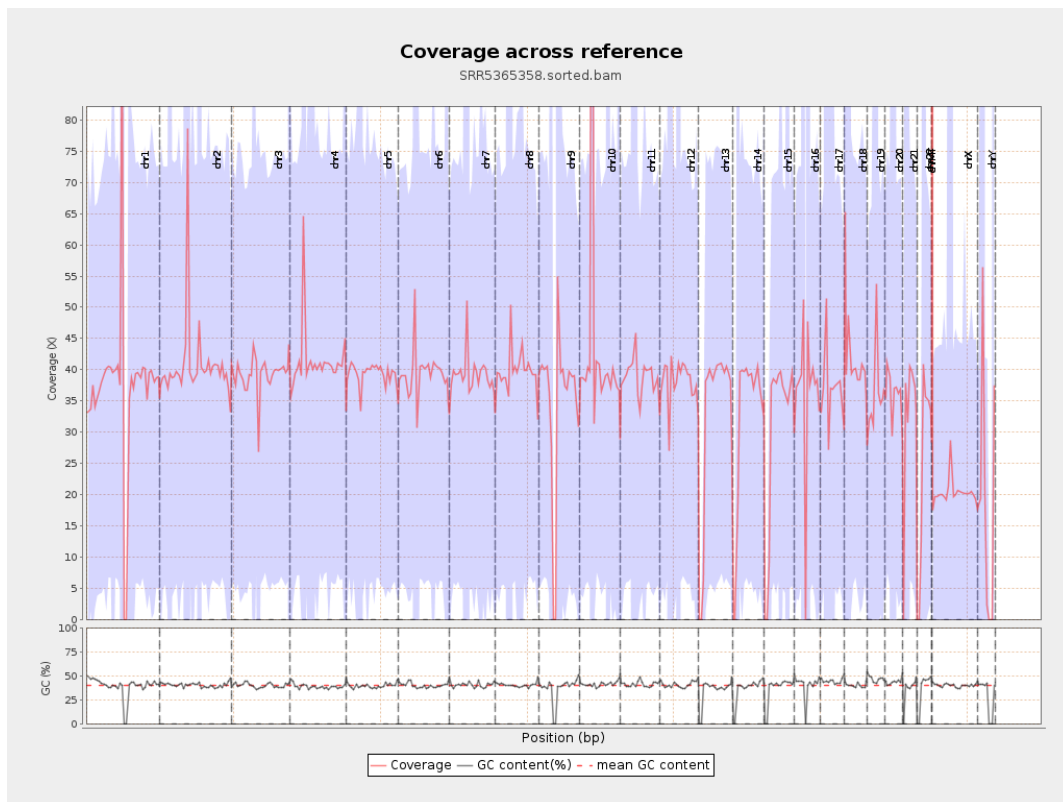
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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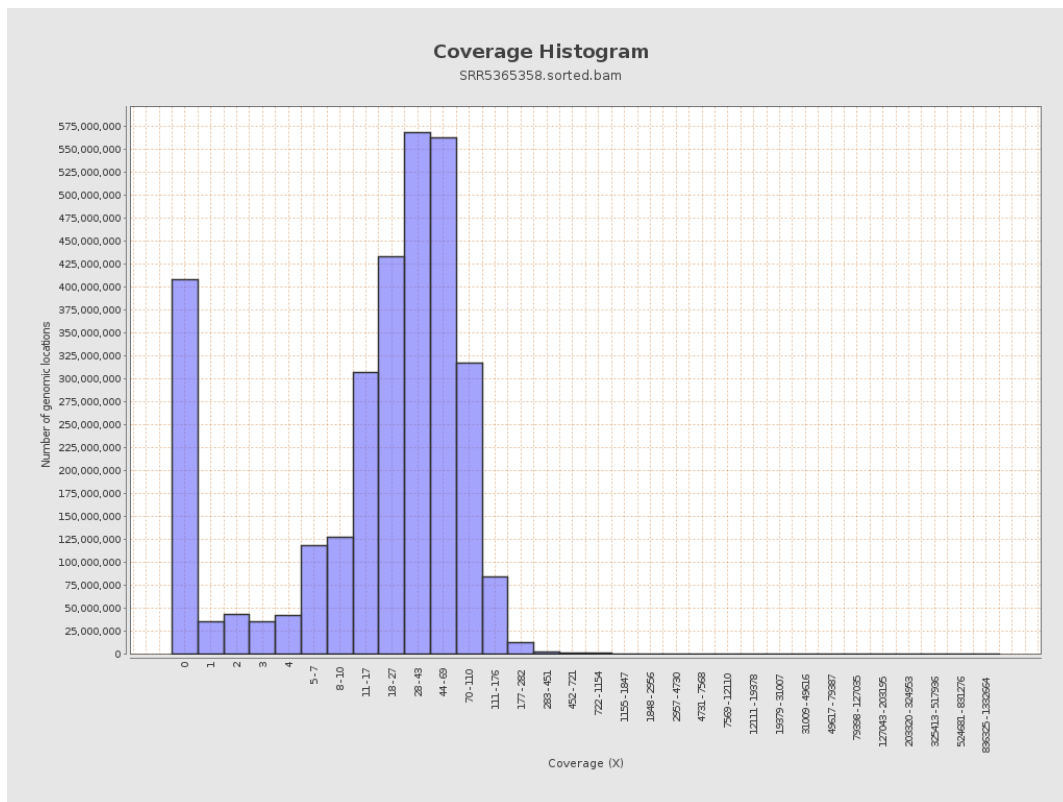
		bases	coverage	deviation
chr1	249250621	9392268050	37.682	1,272.3385
chr2	243199373	9939176144	40.8684	263.755
chr3	198022430	7747238009	39.123	75.9185
chr4	191154276	7893319721	41.2929	213.9939
chr5	180915260	7094644656	39.2153	45.0281
chr6	171115067	6766783975	39.5452	165.0917
chr7	159138663	6237053325	39.1926	265.9883
chr8	146364022	5836821514	39.8788	145.6353
chr9	141213431	4849124835	34.339	415.5164
chr10	135534747	6159652105	45.447	1,002.2836
chr11	135006516	5234465574	38.7719	257.3243
chr12	133851895	5103932085	38.1312	76.3844
chr13	115169878	3790712434	32.9141	34.1253
chr14	107349540	3469657938	32.3211	46.9971
chr15	102531392	3104433184	30.2779	45.4229
chr16	90354753	3257603569	36.0535	148.6324
chr17	81195210	2983301867	36.7423	208.2248
chr18	78077248	3230533298	41.3761	475.55
chr19	59128983	2135748958	36.1202	638.2815
chr20	63025520	2280575144	36.1849	72.4534
chr21	48129895	1611878522	33.4902	136.8537
chr22	51304566	1283326261	25.0139	113.2935
chrMT	16571	25165995	1,518.6769	291.5484
chrX	155270560	3160968425	20.3578	102.4735

chrY	59373566	1147398174	19.3251	408.6635
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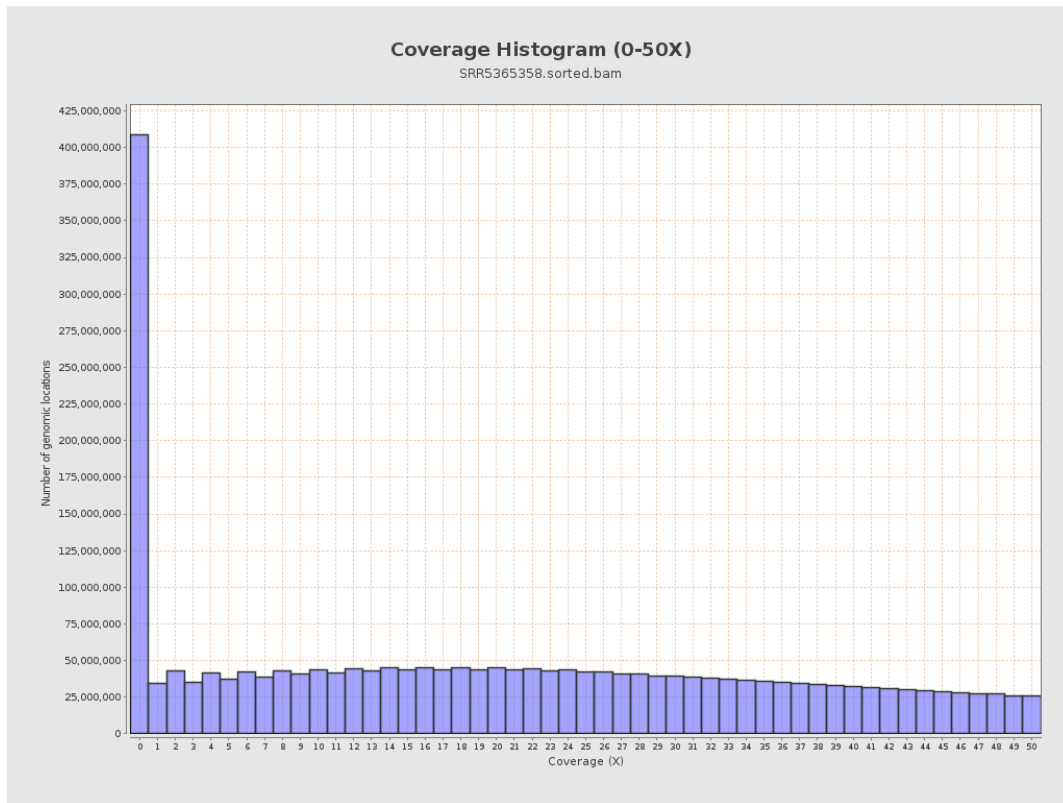
3. Results : Coverage across reference



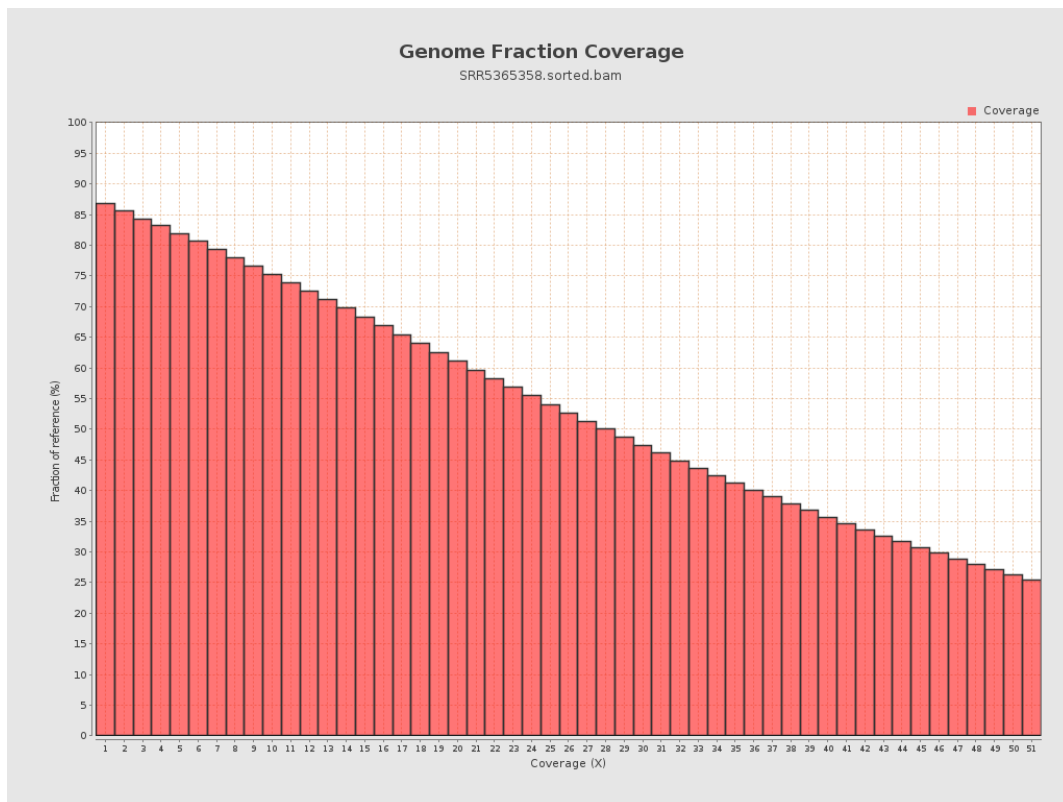
4. Results : Coverage Histogram



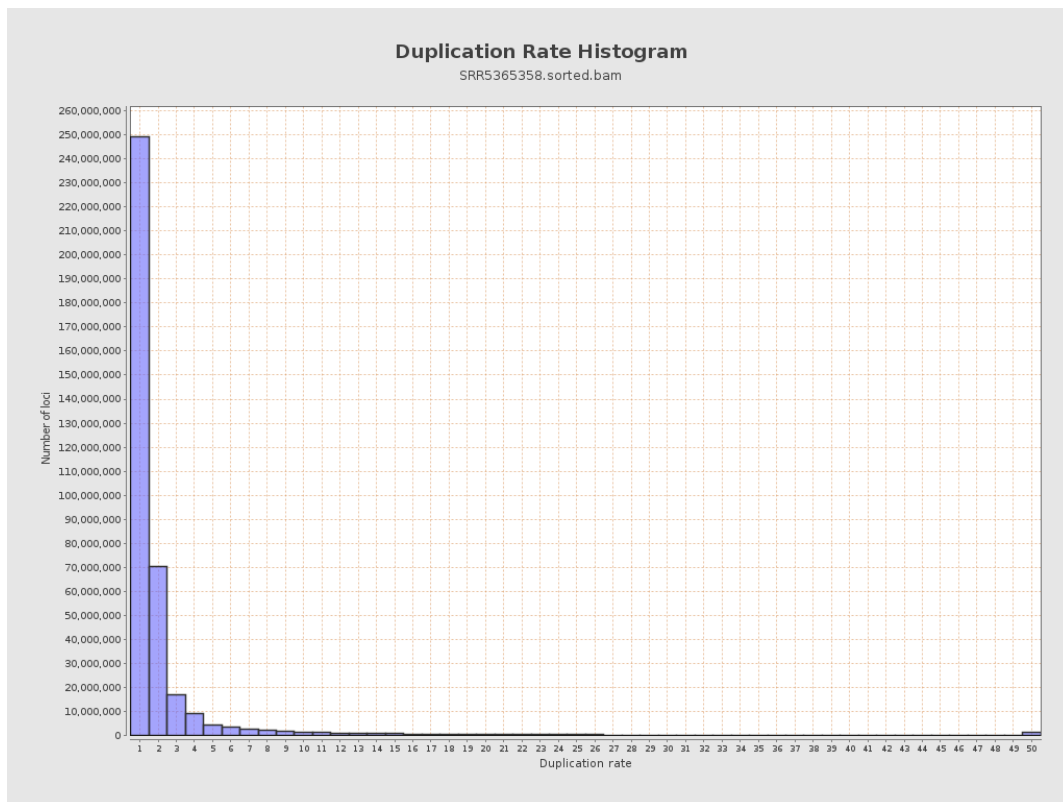
5. Results : Coverage Histogram (0-50X)



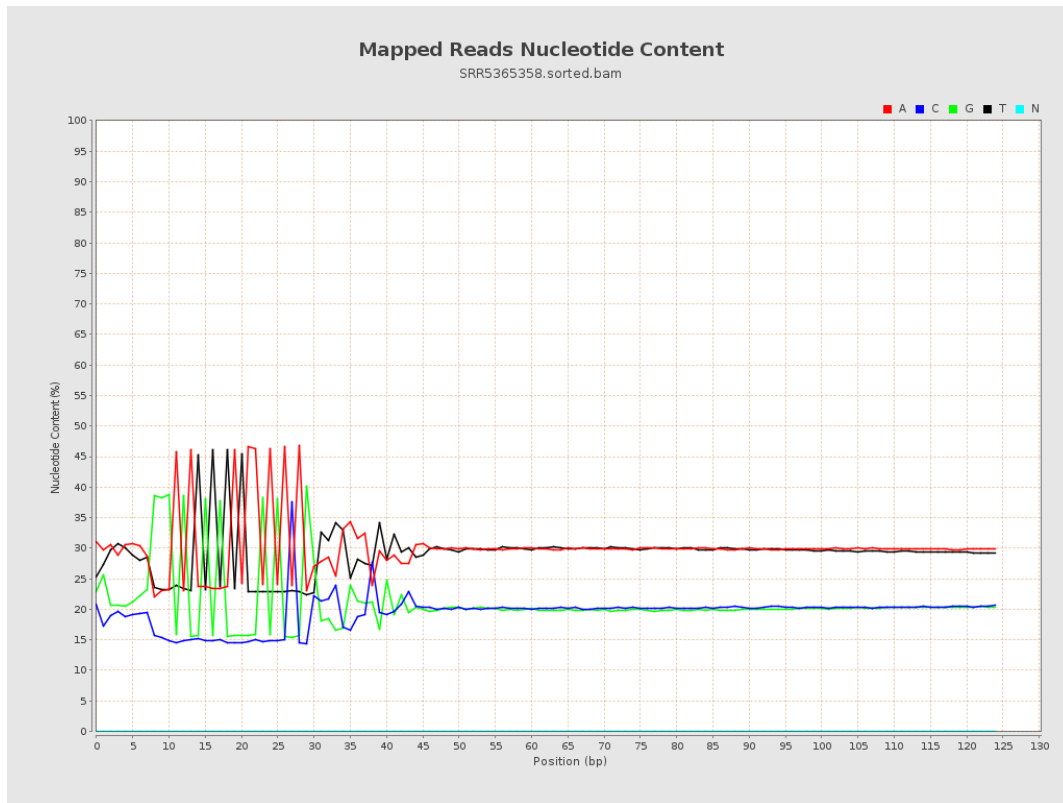
6. Results : Genome Fraction Coverage



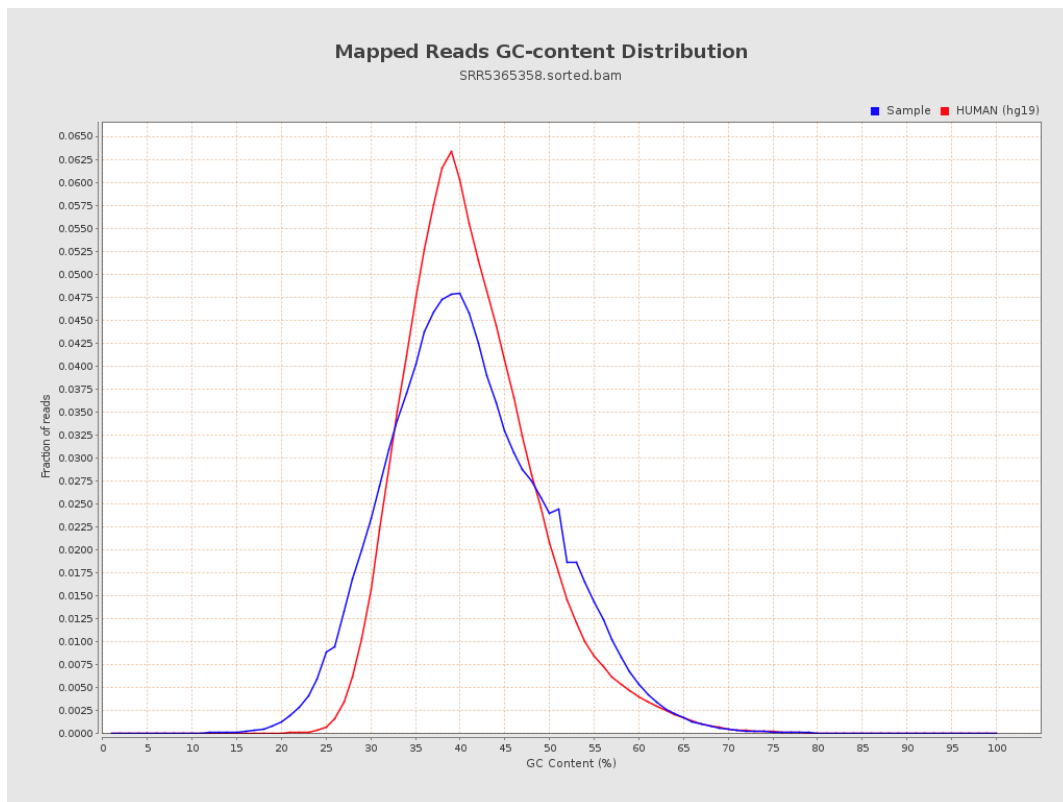
7. Results : Duplication Rate Histogram



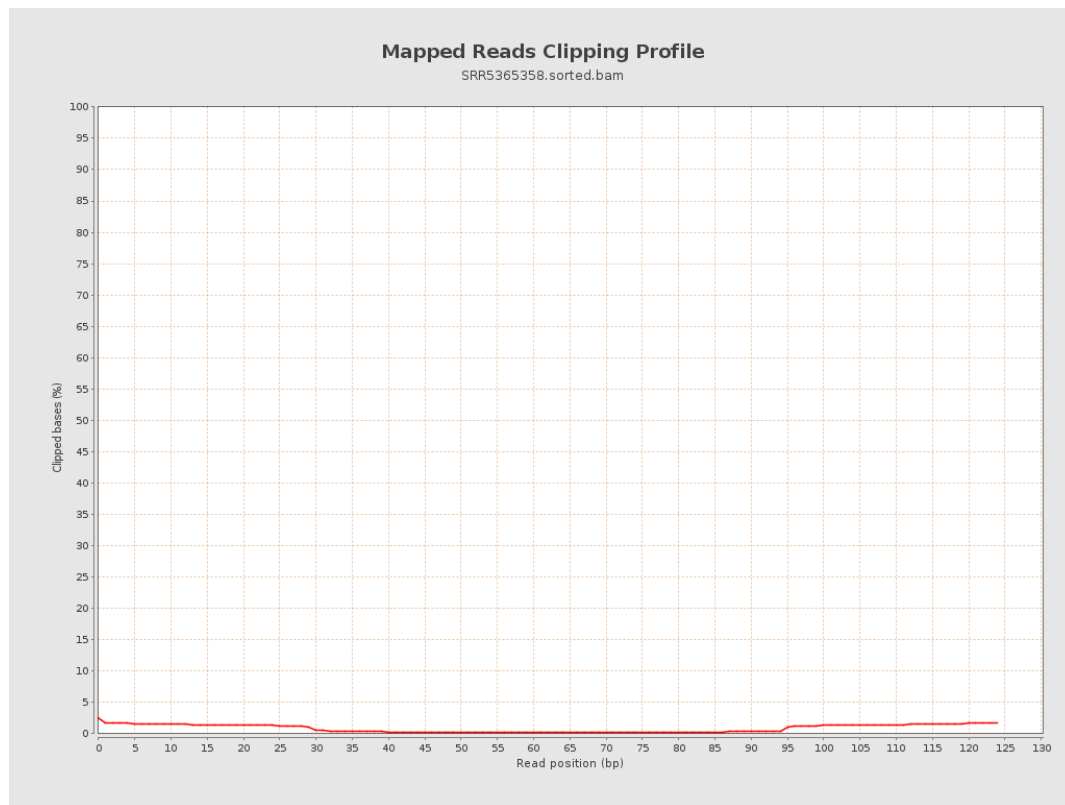
8. Results : Mapped Reads Nucleotide Content



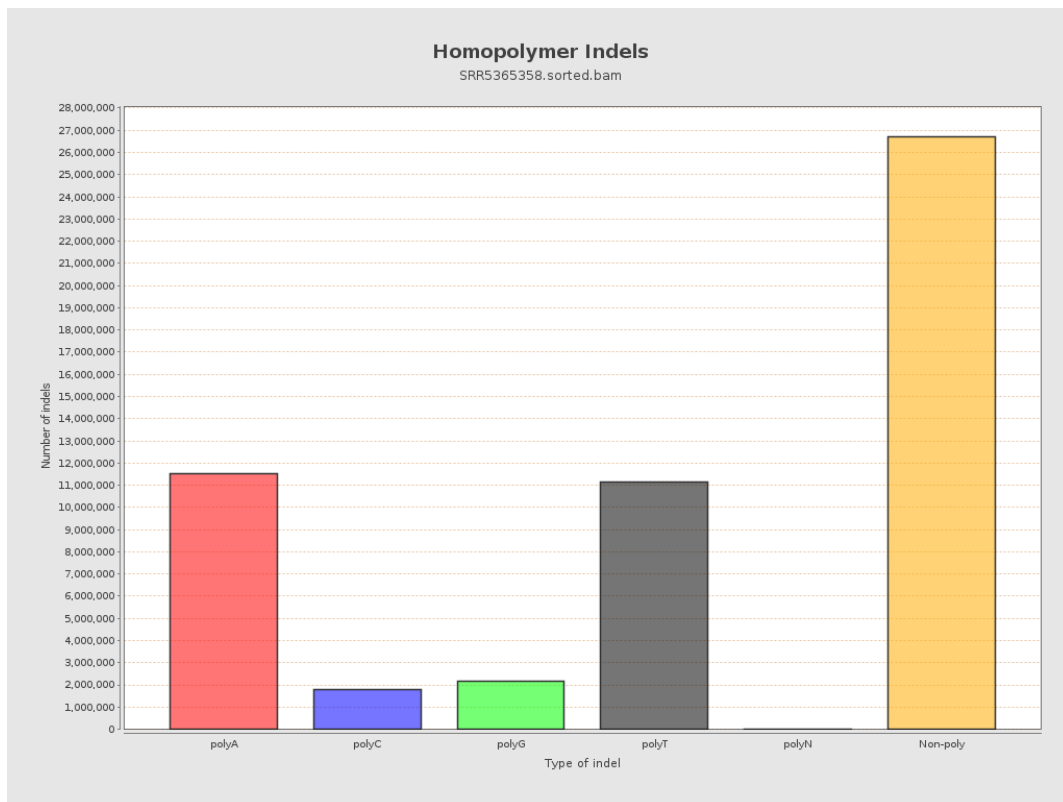
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



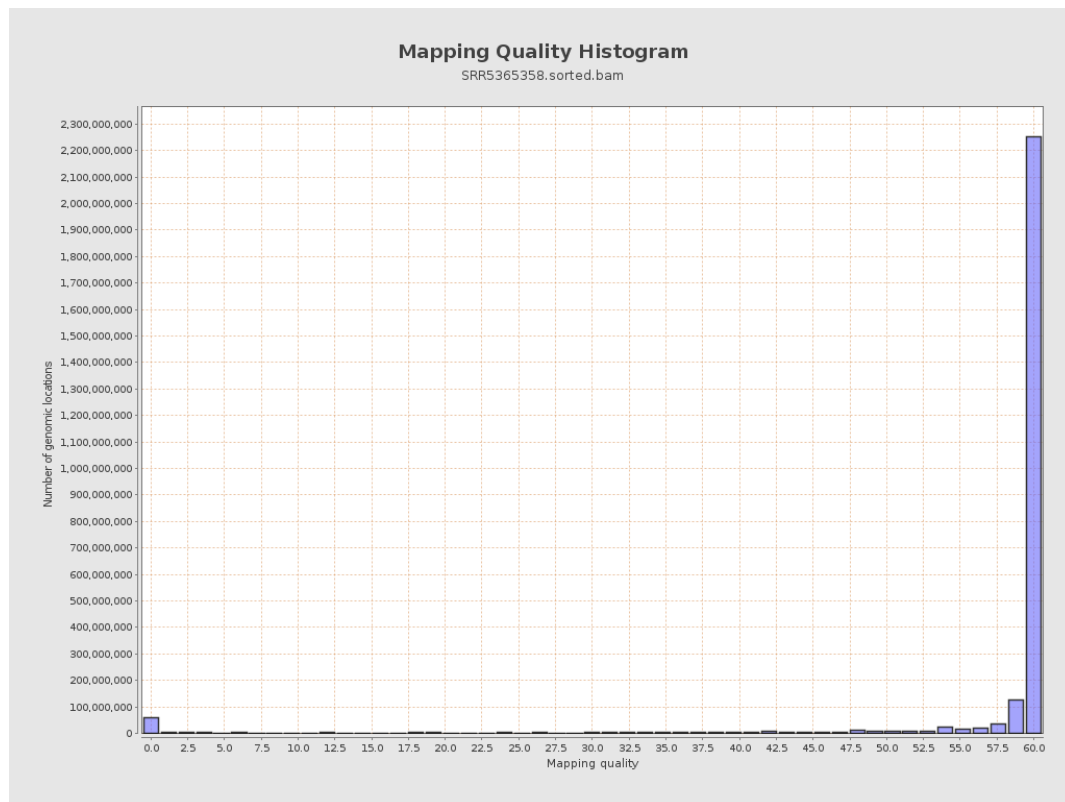
11. Results : Homopolymer Indels



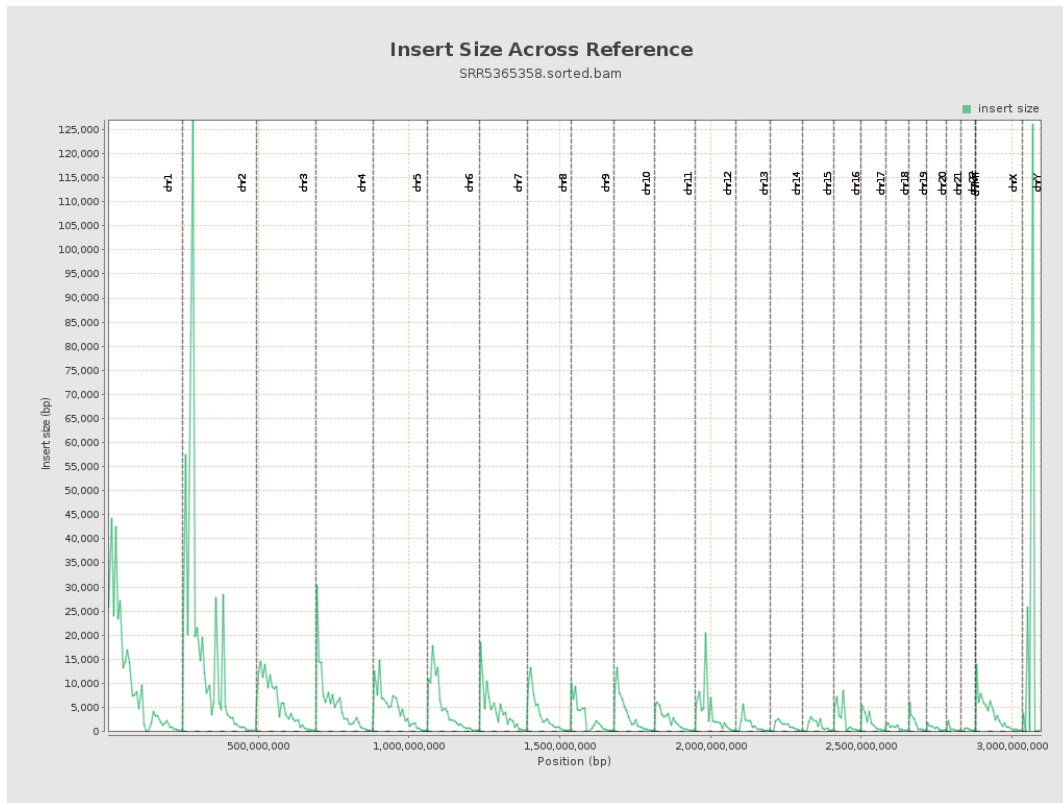
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

