

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/01 22:46:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365331.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_SRR5365331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365331_1.fastq.gz SRR5365331_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Nov 01 22:46:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	160,488,970
Mapped reads	157,080,523 / 97.88%
Unmapped reads	3,408,447 / 2.12%
Mapped paired reads	157,080,523 / 97.88%
Mapped reads, first in pair	78,876,693 / 49.15%
Mapped reads, second in pair	78,203,830 / 48.73%
Mapped reads, both in pair	156,192,754 / 97.32%
Mapped reads, singletons	887,769 / 0.55%
Secondary alignments	0
Supplementary alignments	1,235,900 / 0.77%
Read min/max/mean length	30 / 151 / 151.34
Duplicated reads (estimated)	72,721,542 / 45.31%
Duplication rate	33.93%
Clipped reads	93,860,354 / 58.48%

2.2. ACGT Content

Number/percentage of A's	6,149,225,971 / 29.75%
Number/percentage of C's	4,119,621,801 / 19.93%
Number/percentage of T's	6,066,228,405 / 29.35%
Number/percentage of G's	4,333,077,440 / 20.96%
Number/percentage of N's	1,214,857 / 0.01%

GC Percentage	40.89%
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2.3. Coverage

Mean	6.6792
Standard Deviation	55.1542

2.4. Mapping Quality

Mean Mapping Quality	54.28
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2.5. Insert size

Mean	76,949.57
Standard Deviation	2,749,736.91
P25/Median/P75	149 / 202 / 275

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	142,310,443
Insertions	6,315,413
Mapped reads with at least one insertion	3.9%
Deletions	3,094,849
Mapped reads with at least one deletion	1.91%
Homopolymer indels	50.72%

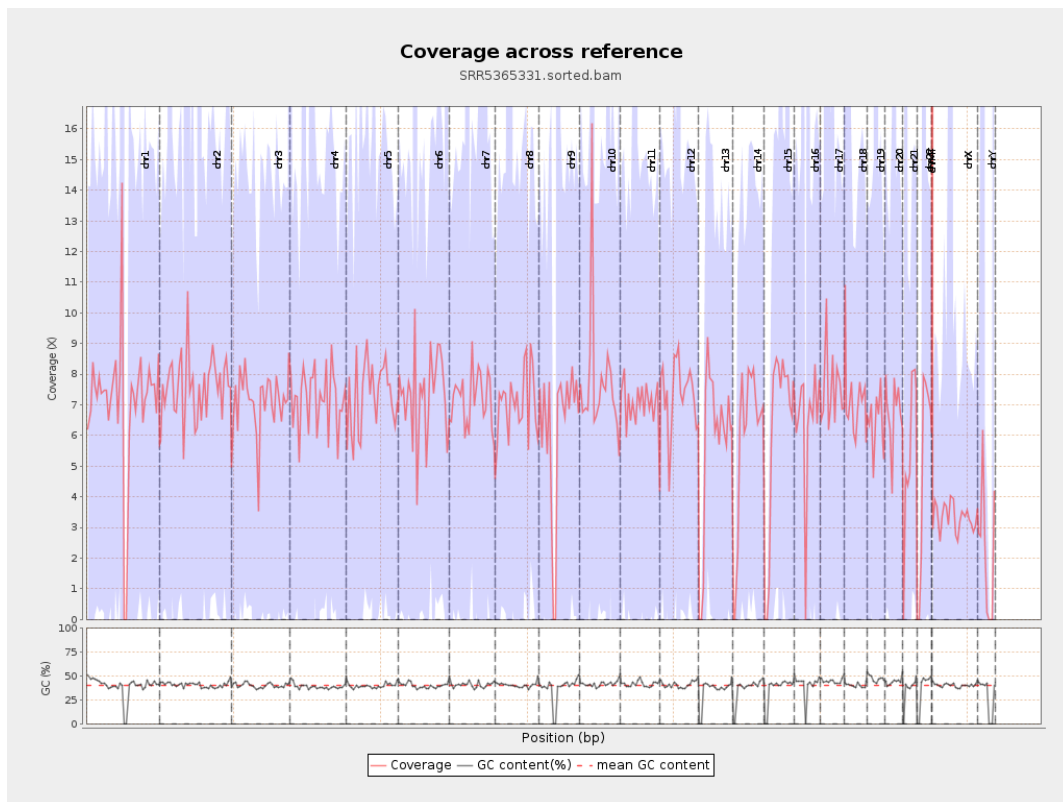
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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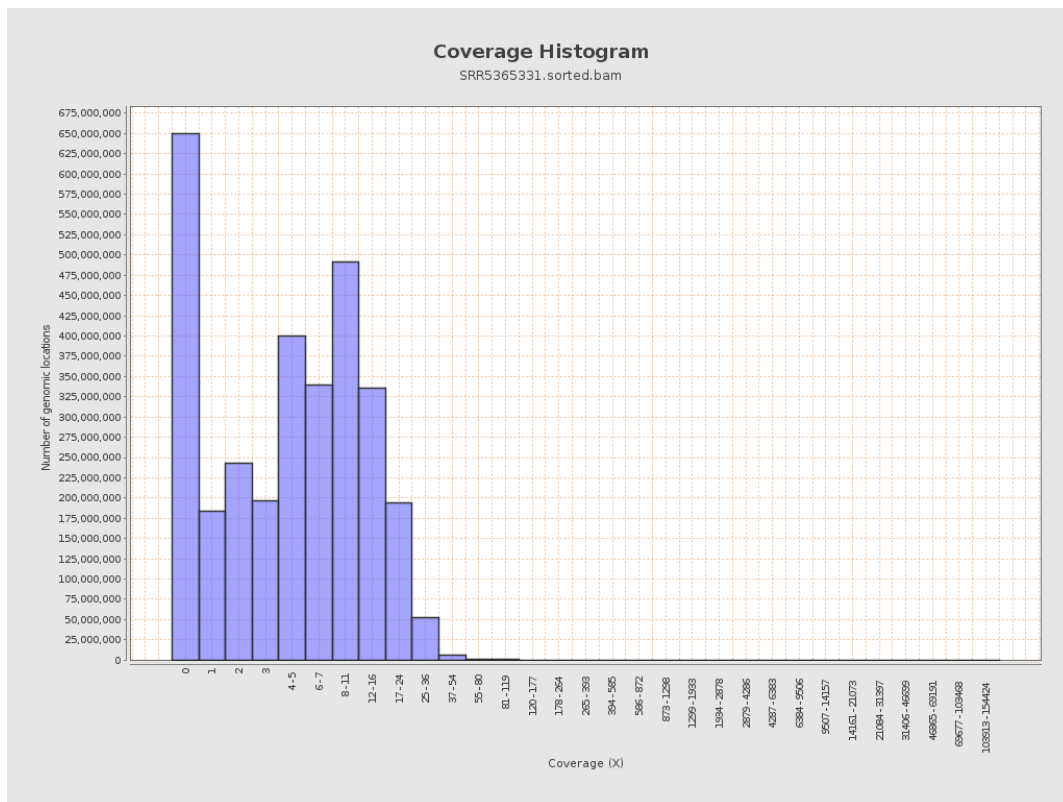
		bases	coverage	deviation
chr1	249250621	1780913161	7.1451	153.4794
chr2	243199373	1848234068	7.5997	36.1705
chr3	198022430	1403496748	7.0876	7.5652
chr4	191154276	1374382311	7.1899	25.4212
chr5	180915260	1318829766	7.2898	7.8386
chr6	171115067	1251858686	7.3159	33.4624
chr7	159138663	1142030828	7.1763	26.2048
chr8	146364022	1046045543	7.1469	19.2513
chr9	141213431	868828721	6.1526	49.0242
chr10	135534747	1050340914	7.7496	84.5352
chr11	135006516	955321427	7.0761	44.3887
chr12	133851895	987656497	7.3787	39.0744
chr13	115169878	663165436	5.7582	6.5371
chr14	107349540	629418043	5.8633	7.0036
chr15	102531392	619468556	6.0417	18.5289
chr16	90354753	583724740	6.4604	15.339
chr17	81195210	605317807	7.4551	36.3681
chr18	78077248	547341165	7.0103	48.6259
chr19	59128983	383040190	6.478	79.04
chr20	63025520	424683566	6.7383	11.5035
chr21	48129895	269680898	5.6032	19.924
chr22	51304566	258733200	5.0431	17.2974
chrMT	16571	11995093	723.8605	170.6741
chrX	155270560	515008693	3.3168	14.0208

chrY	59373566	137337247	2.3131	47.4277
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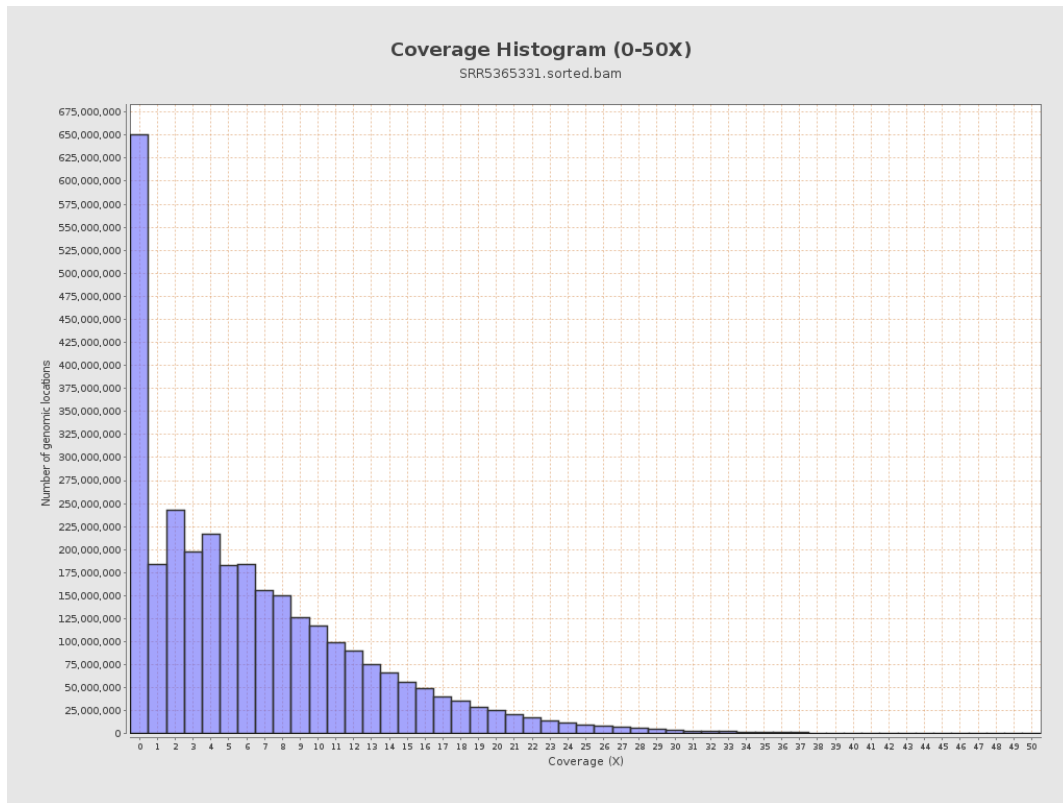
3. Results : Coverage across reference



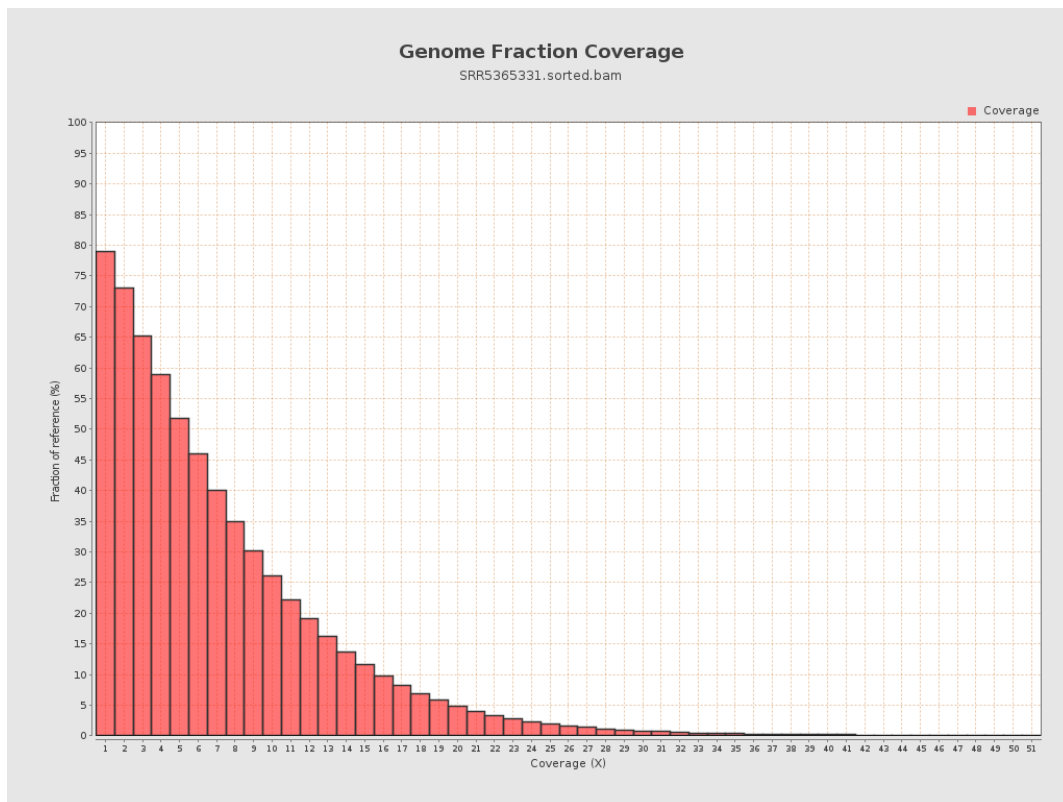
4. Results : Coverage Histogram



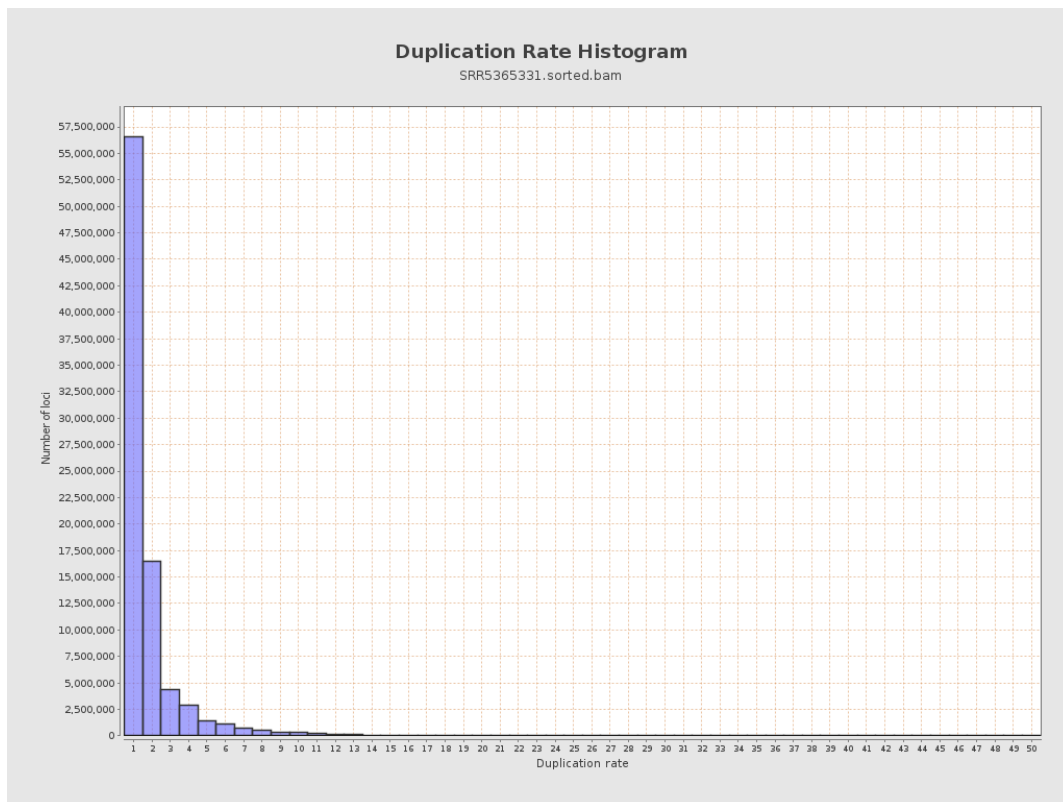
5. Results : Coverage Histogram (0-50X)



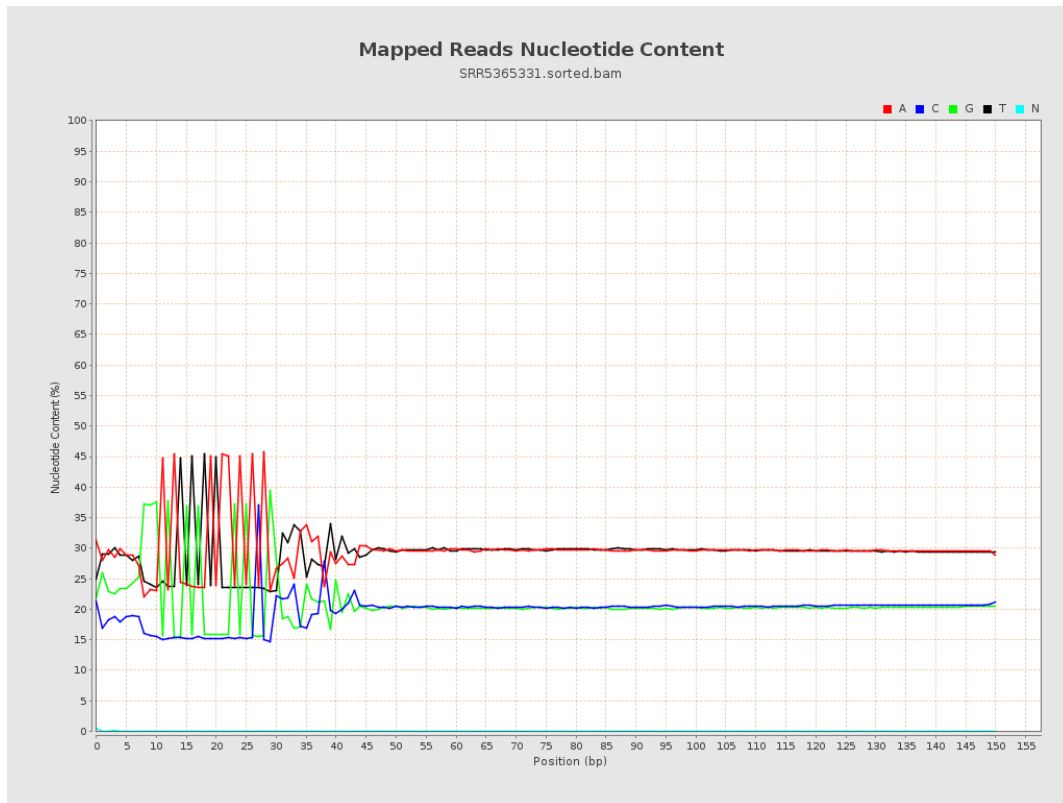
6. Results : Genome Fraction Coverage



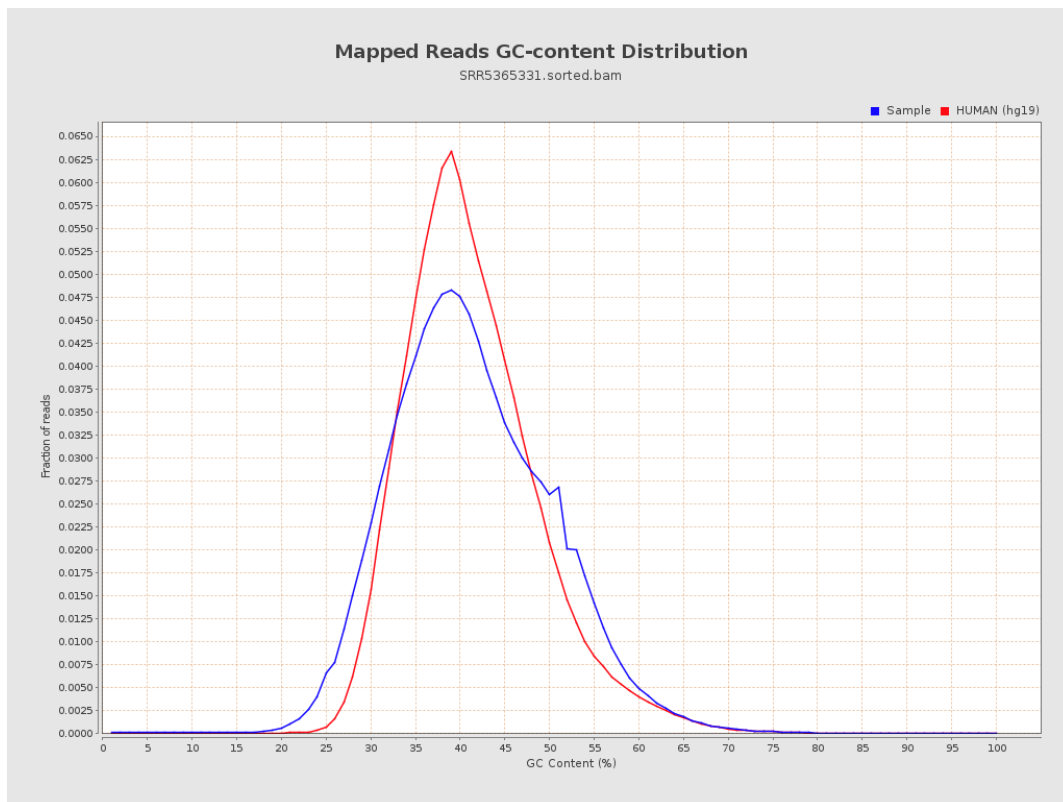
7. Results : Duplication Rate Histogram



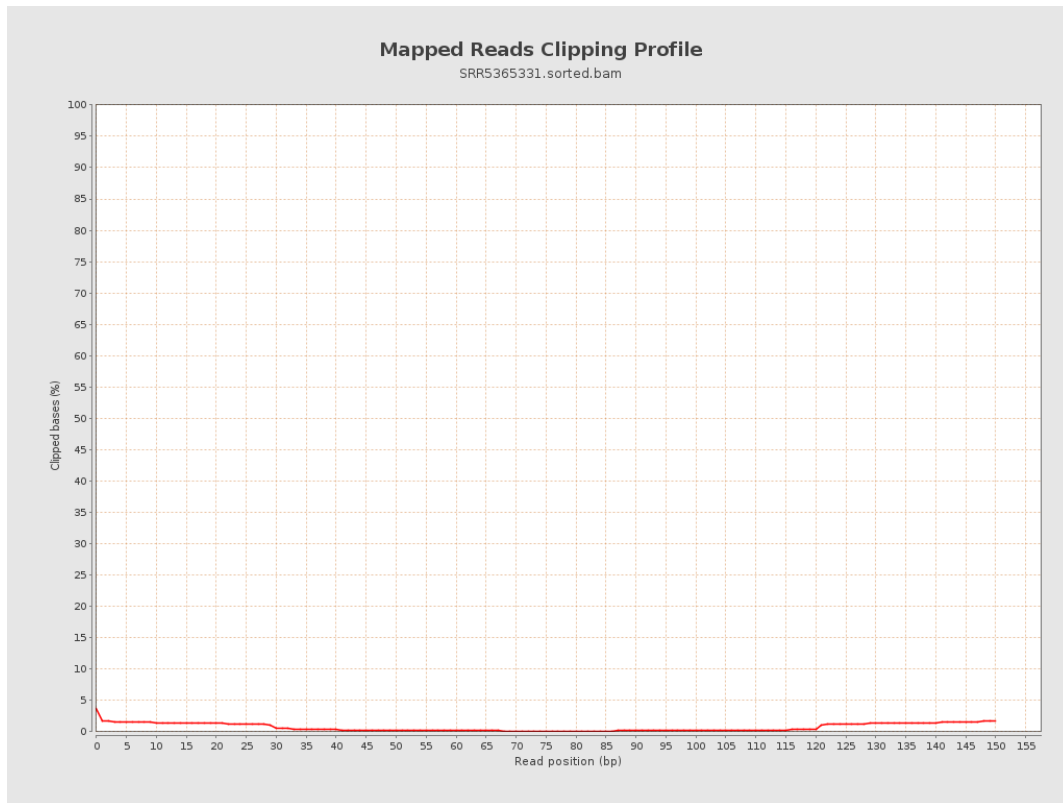
8. Results : Mapped Reads Nucleotide Content



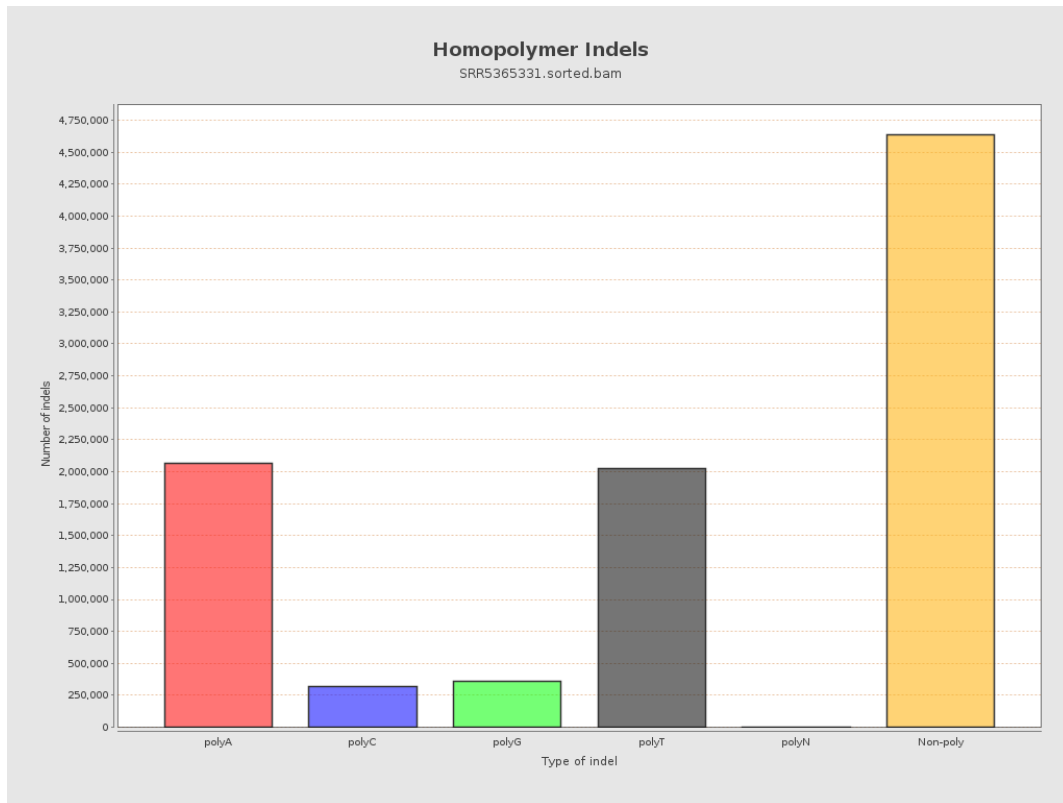
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



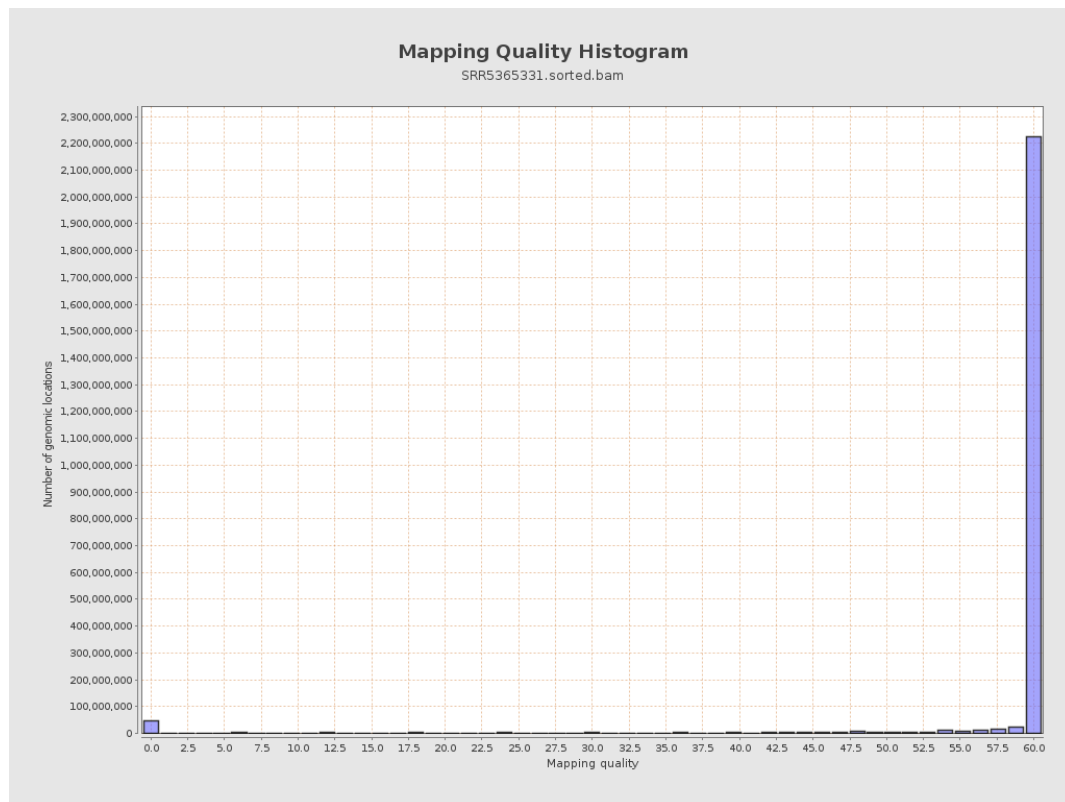
11. Results : Homopolymer Indels



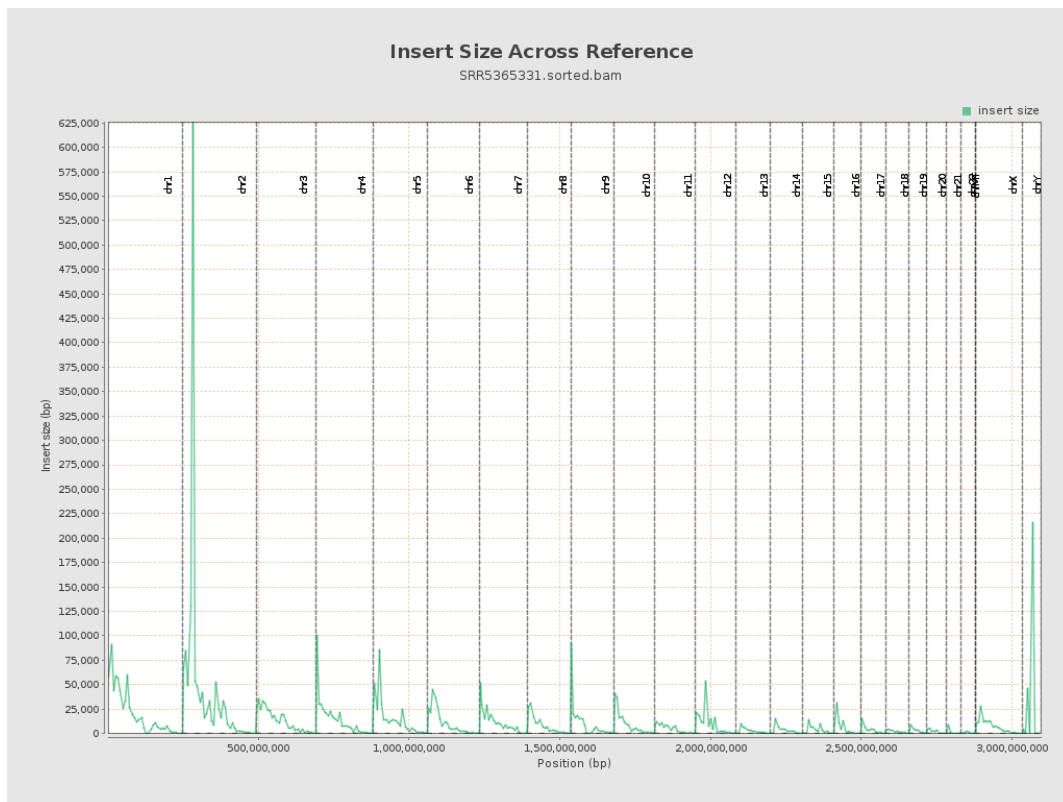
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

