

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 22:07:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174021.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_SRR10174021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174021_1.fastq.gz SRR10174021_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 22:07:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,983,720
Mapped reads	1,937,523 / 97.67%
Unmapped reads	46,197 / 2.33%
Mapped paired reads	1,937,523 / 97.67%
Mapped reads, first in pair	966,750 / 48.73%
Mapped reads, second in pair	970,773 / 48.94%
Mapped reads, both in pair	1,907,822 / 96.17%
Mapped reads, singletons	29,701 / 1.5%
Secondary alignments	0
Supplementary alignments	179,810 / 9.06%
Read min/max/mean length	30 / 133 / 127.69
Duplicated reads (estimated)	1,495,160 / 75.37%
Duplication rate	65.52%
Clipped reads	702,504 / 35.41%

2.2. ACGT Content

Number/percentage of A's	69,408,525 / 30.14%
Number/percentage of C's	45,306,812 / 19.67%
Number/percentage of T's	69,101,953 / 30.01%
Number/percentage of G's	46,467,071 / 20.18%
Number/percentage of N's	2,986 / 0%

GC Percentage	39.85%
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2.3. Coverage

Mean	0.0744
Standard Deviation	1.2228

2.4. Mapping Quality

Mean Mapping Quality	52.87
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2.5. Insert size

Mean	732,817.15
Standard Deviation	8,010,926.77
P25/Median/P75	144 / 199 / 280

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	2,285,786
Insertions	23,467
Mapped reads with at least one insertion	1.17%
Deletions	40,441
Mapped reads with at least one deletion	2.03%
Homopolymer indels	44.77%

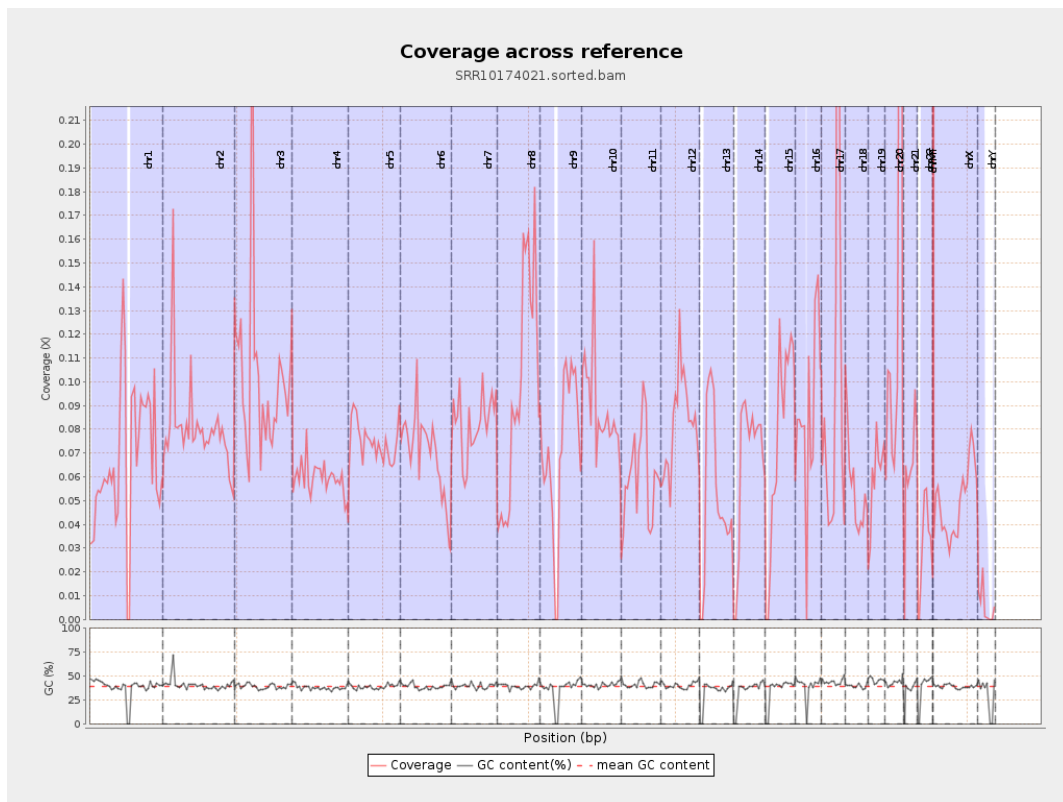
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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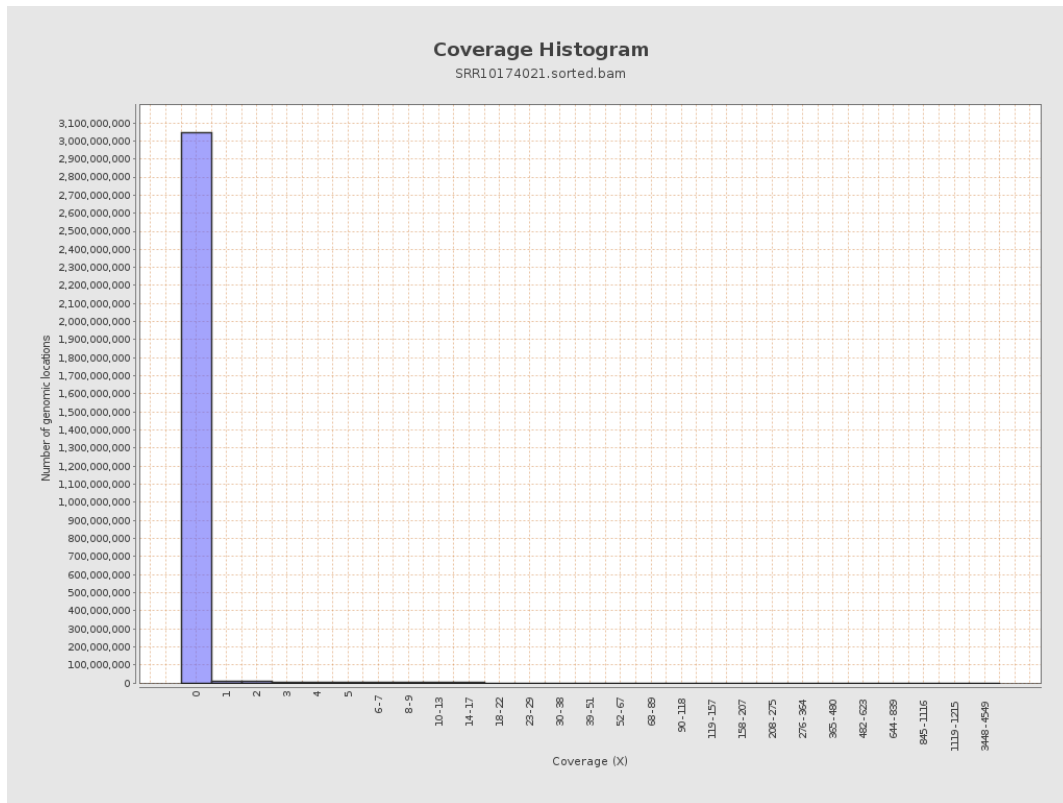
		bases	coverage	deviation
chr1	249250621	16748945	0.0672	0.8492
chr2	243199373	19451873	0.08	3.2515
chr3	198022430	20079443	0.1014	0.9205
chr4	191154276	11382441	0.0595	0.7462
chr5	180915260	13509642	0.0747	0.7835
chr6	171115067	11922935	0.0697	0.8081
chr7	159138663	13129083	0.0825	0.9341
chr8	146364022	14080774	0.0962	1.0202
chr9	141213431	10088446	0.0714	0.828
chr10	135534747	12051885	0.0889	1.1596
chr11	135006516	8079916	0.0598	0.7005
chr12	133851895	11056517	0.0826	0.8286
chr13	115169878	5891275	0.0512	0.6584
chr14	107349540	7251776	0.0676	0.745
chr15	102531392	7650620	0.0746	0.7794
chr16	90354753	7750375	0.0858	0.9014
chr17	81195210	9210337	0.1134	0.9858
chr18	78077248	4352084	0.0557	0.8811
chr19	59128983	3569703	0.0604	0.7654
chr20	63025520	9929829	0.1576	1.1697
chr21	48129895	3061391	0.0636	0.7363
chr22	51304566	1602332	0.0312	0.4828
chrMT	16571	579032	34.9425	36.0124
chrX	155270560	7622933	0.0491	0.6274

chrY	59373566	342696	0.0058	0.283
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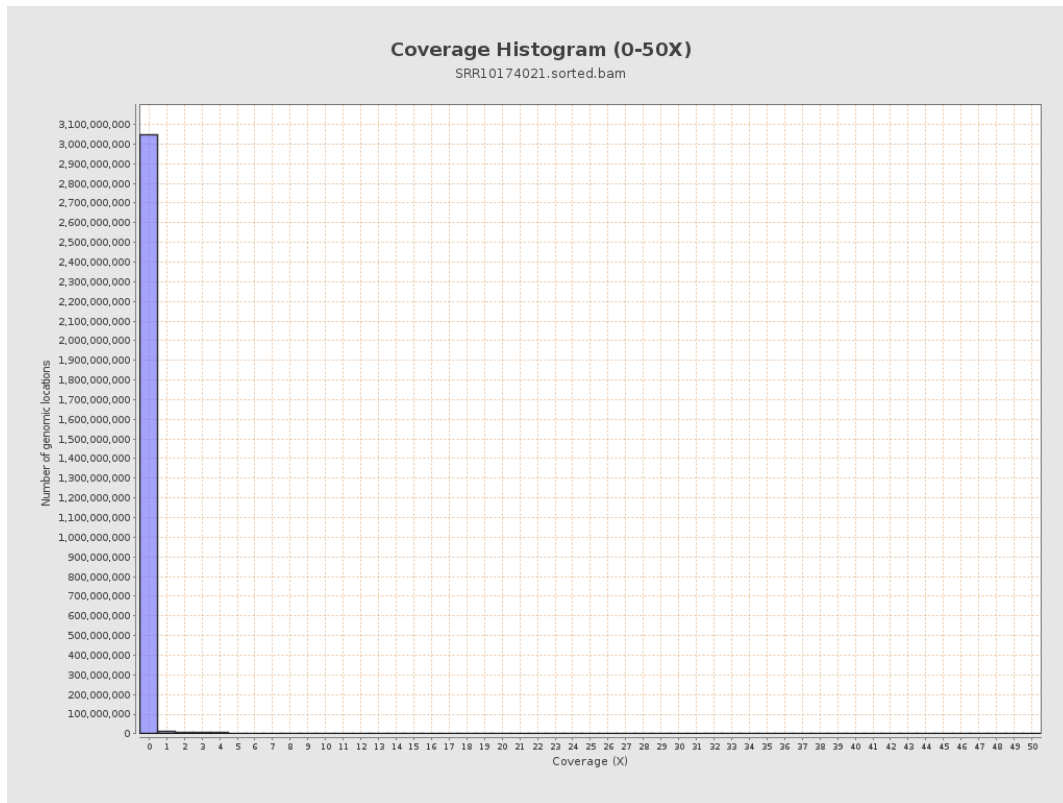
3. Results : Coverage across reference



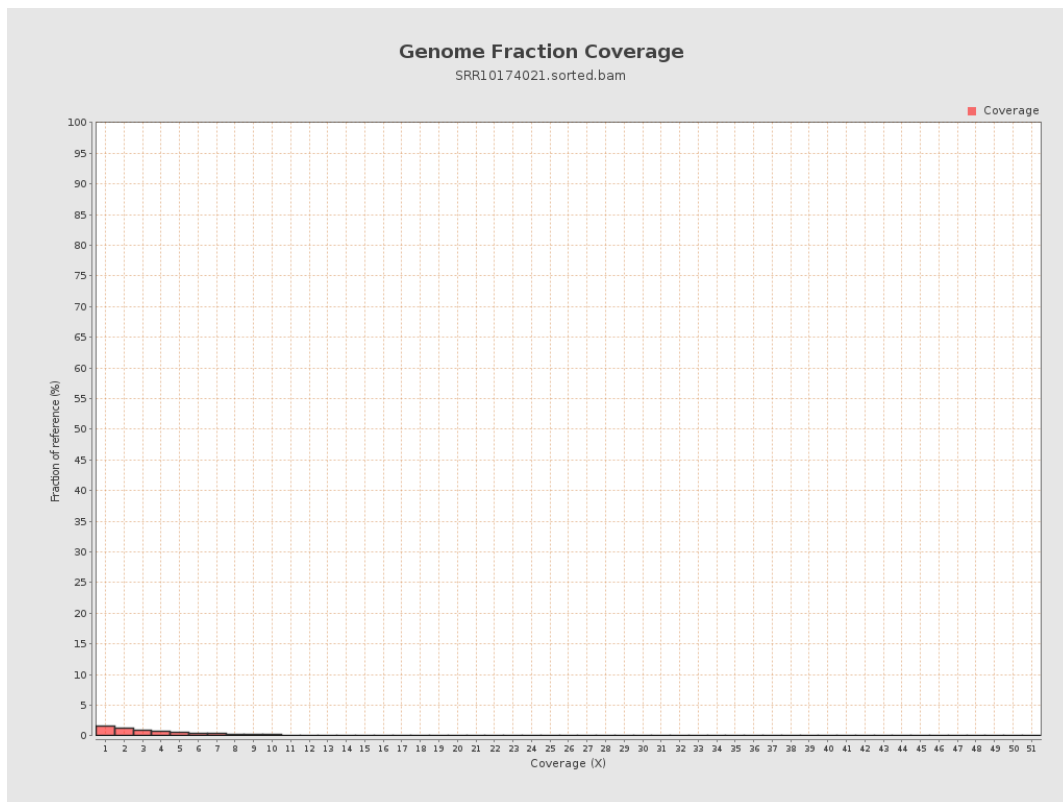
4. Results : Coverage Histogram



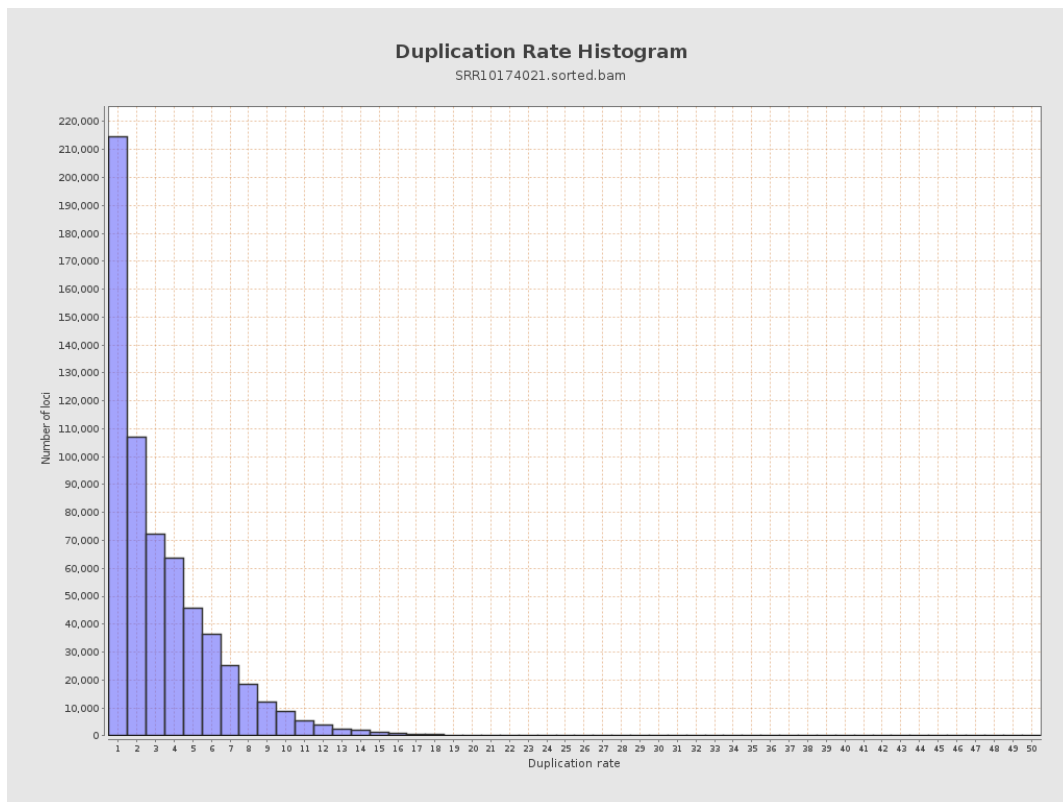
5. Results : Coverage Histogram (0-50X)



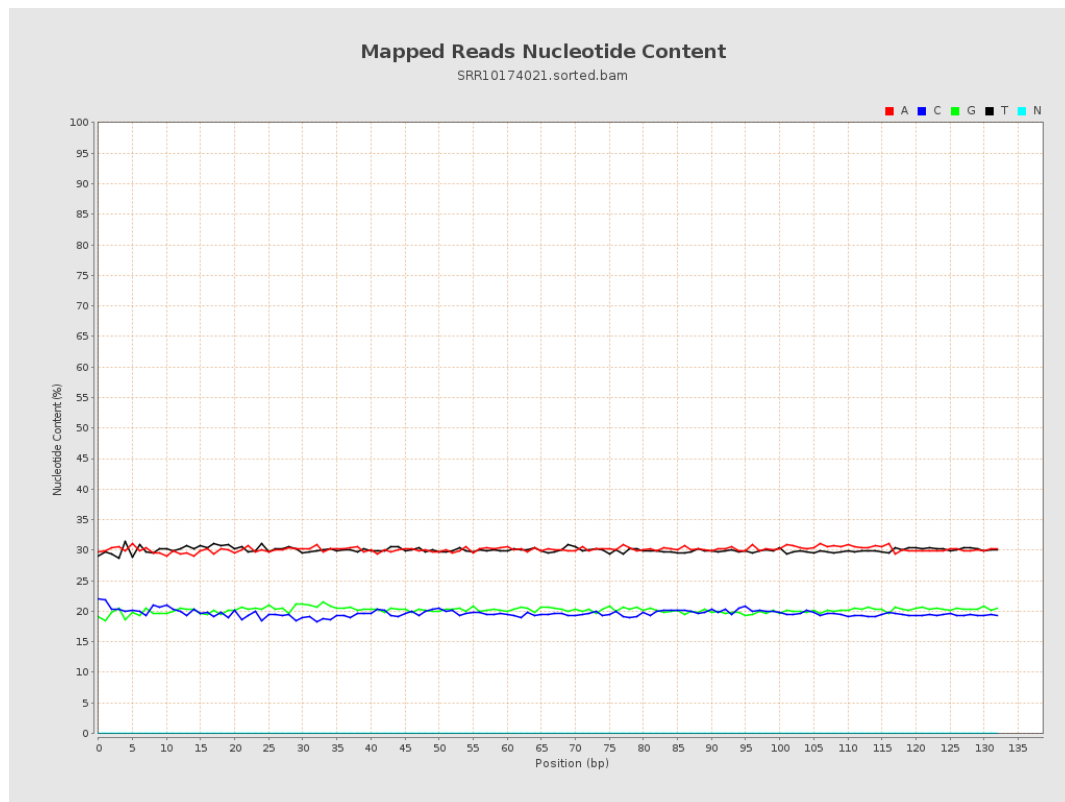
6. Results : Genome Fraction Coverage



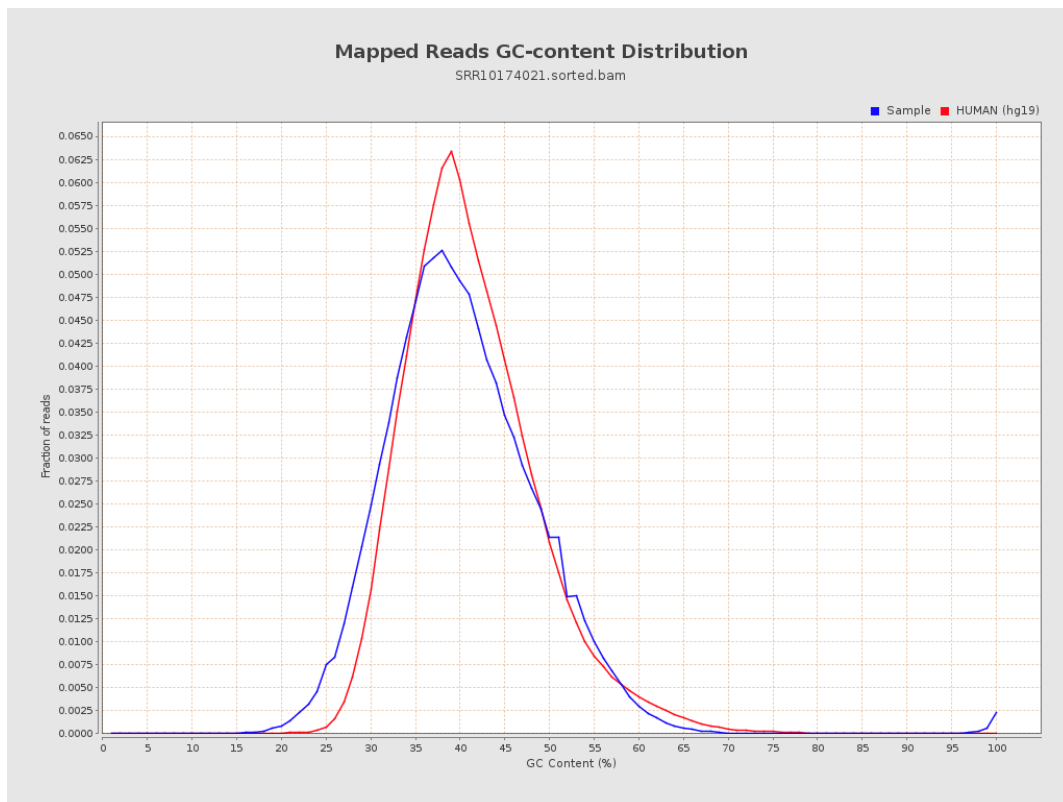
7. Results : Duplication Rate Histogram



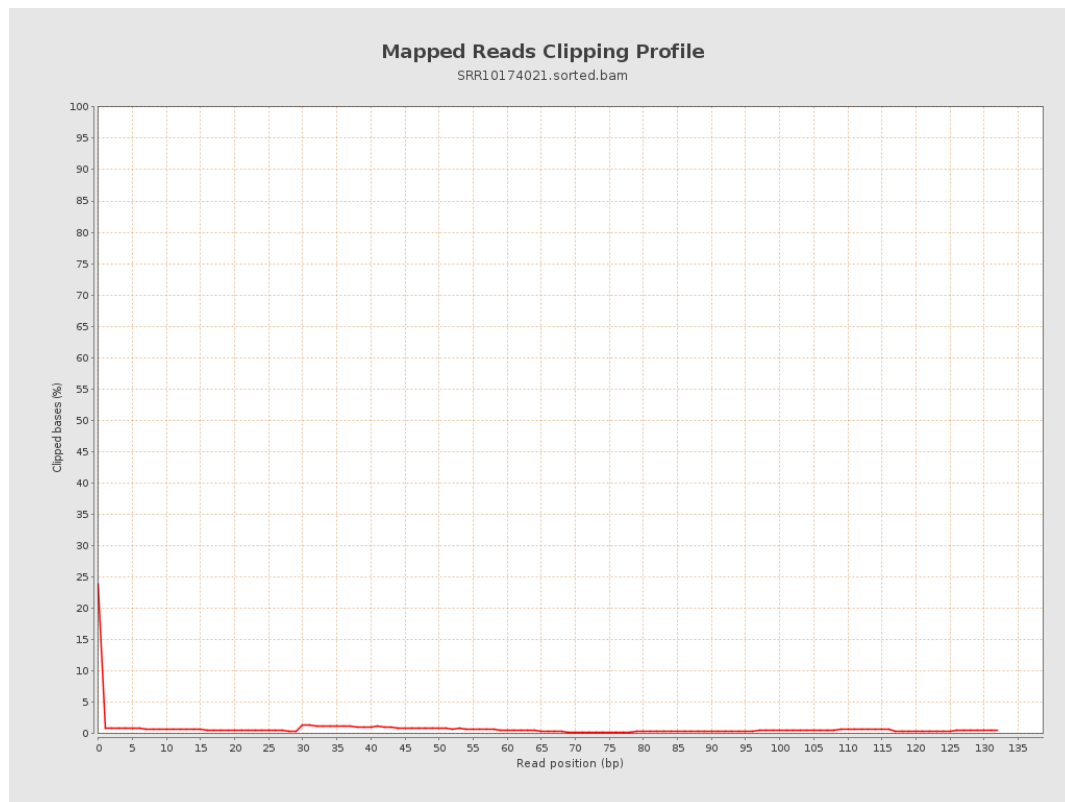
8. Results : Mapped Reads Nucleotide Content



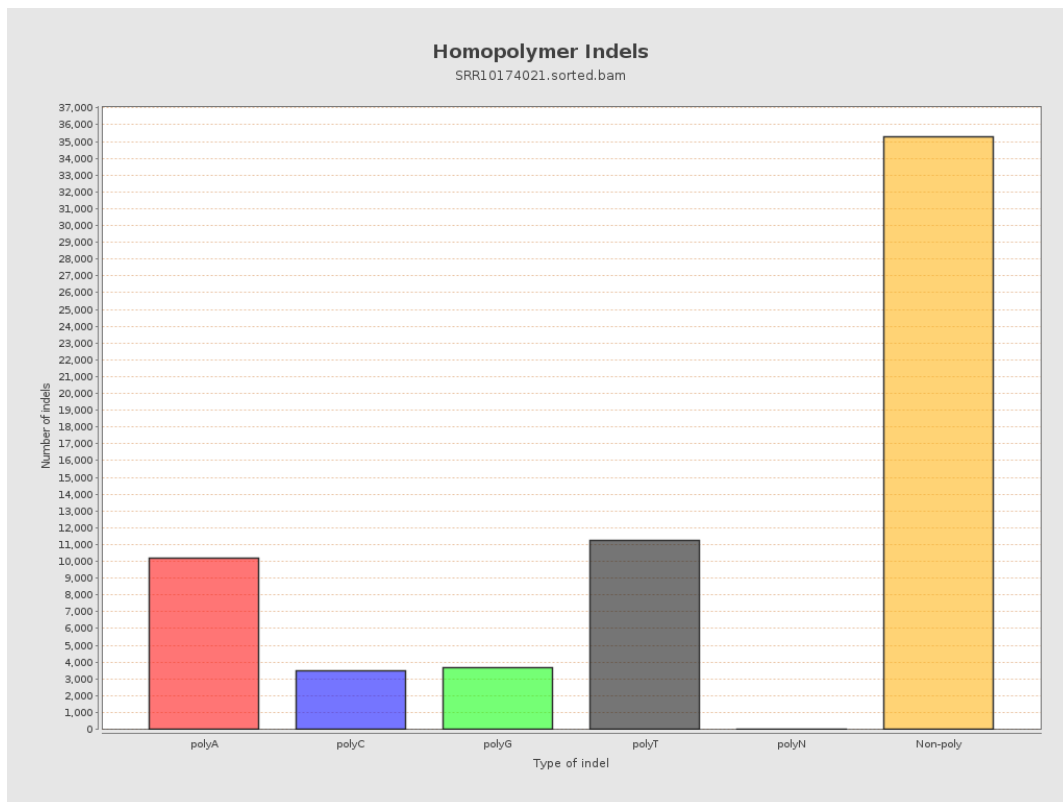
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



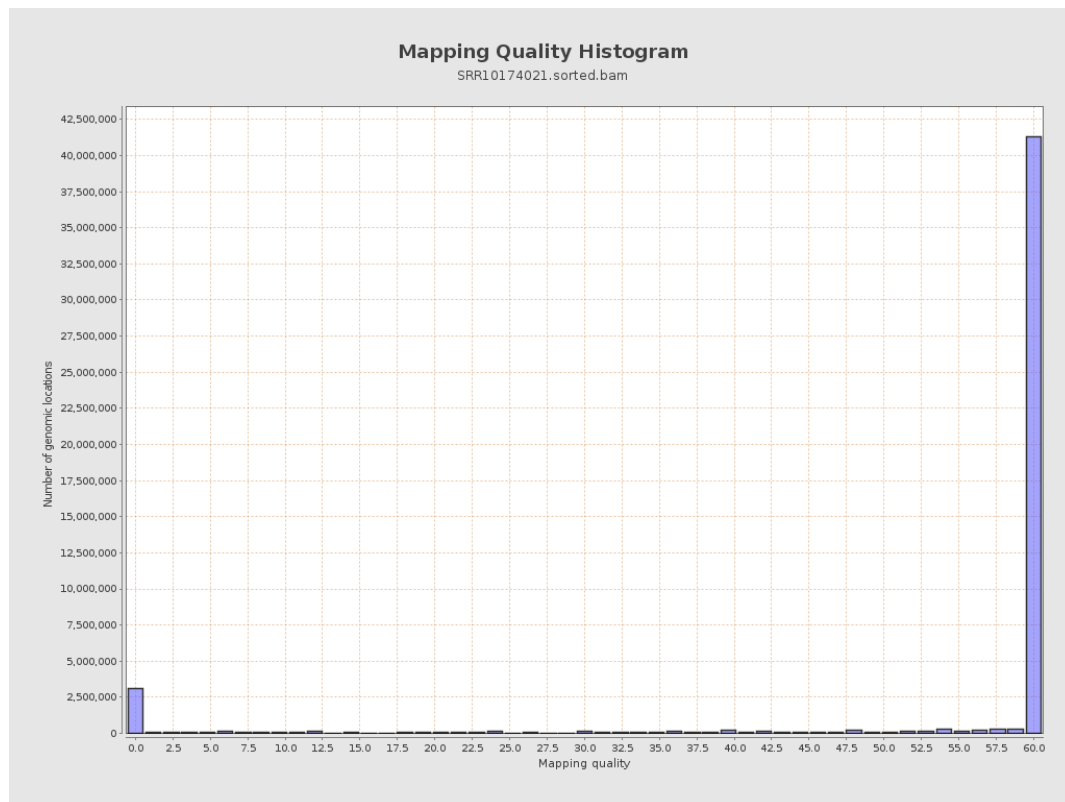
11. Results : Homopolymer Indels



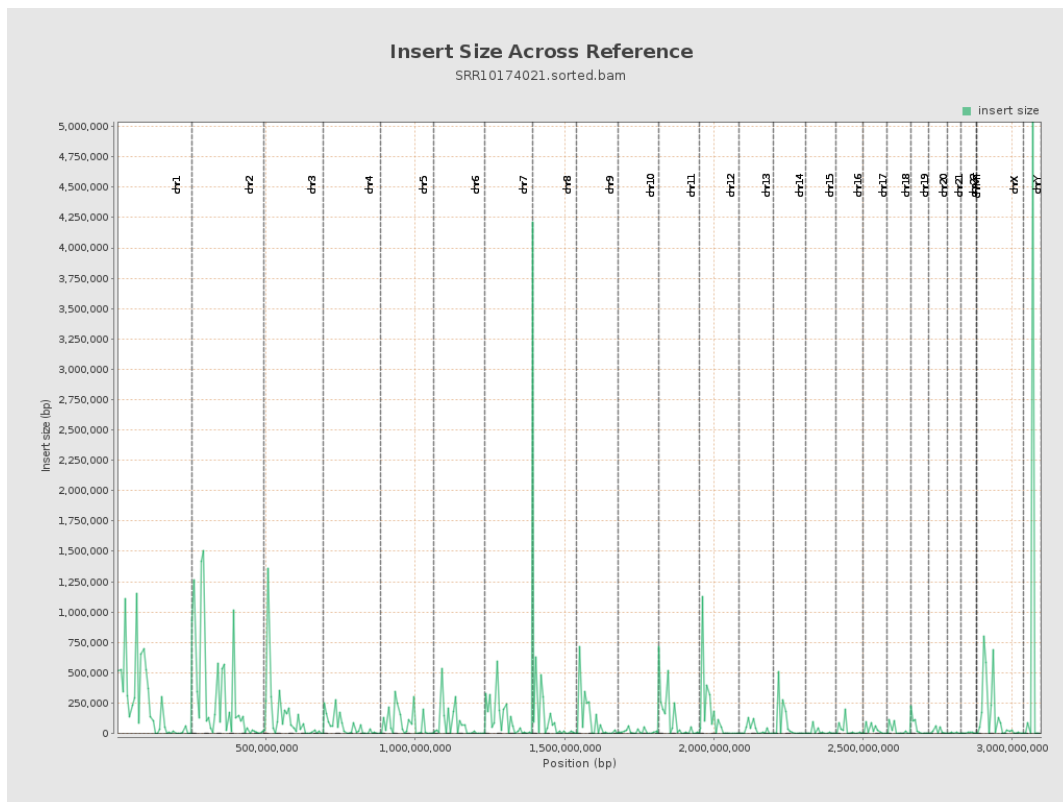
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

