

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 21:47:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174018.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_SRR10174018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174018_1.fastq.gz SRR10174018_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 21:47:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,621,564
Mapped reads	5,471,287 / 97.33%
Unmapped reads	150,277 / 2.67%
Mapped paired reads	5,471,287 / 97.33%
Mapped reads, first in pair	2,737,336 / 48.69%
Mapped reads, second in pair	2,733,951 / 48.63%
Mapped reads, both in pair	5,370,962 / 95.54%
Mapped reads, singletons	100,325 / 1.78%
Secondary alignments	0
Supplementary alignments	543,406 / 9.67%
Read min/max/mean length	30 / 133 / 128.21
Duplicated reads (estimated)	4,279,605 / 76.13%
Duplication rate	65.01%
Clipped reads	2,182,413 / 38.82%

2.2. ACGT Content

Number/percentage of A's	194,882,313 / 30.12%
Number/percentage of C's	126,628,403 / 19.57%
Number/percentage of T's	194,517,539 / 30.07%
Number/percentage of G's	130,886,902 / 20.23%
Number/percentage of N's	8,325 / 0%

GC Percentage	39.81%
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2.3. Coverage

Mean	0.2091
Standard Deviation	3.0554

2.4. Mapping Quality

Mean Mapping Quality	52.72
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2.5. Insert size

Mean	917,503.64
Standard Deviation	8,524,602.41
P25/Median/P75	146 / 204 / 294

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	6,528,993
Insertions	67,873
Mapped reads with at least one insertion	1.19%
Deletions	140,423
Mapped reads with at least one deletion	2.5%
Homopolymer indels	43.09%

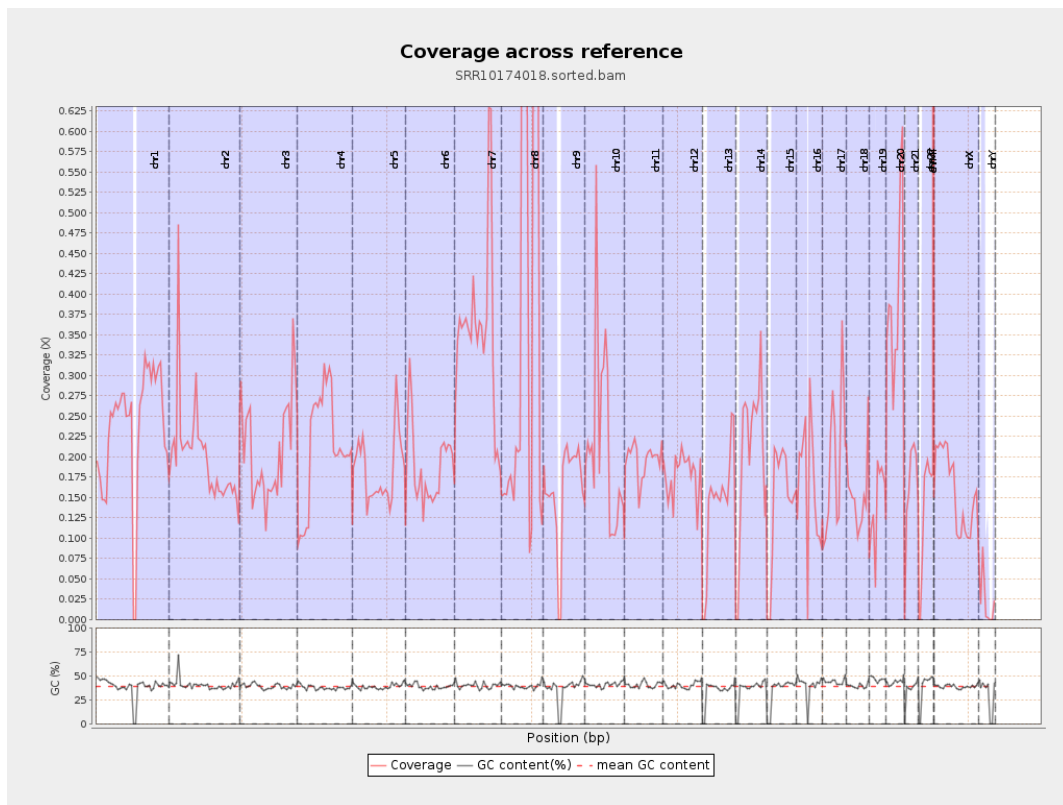
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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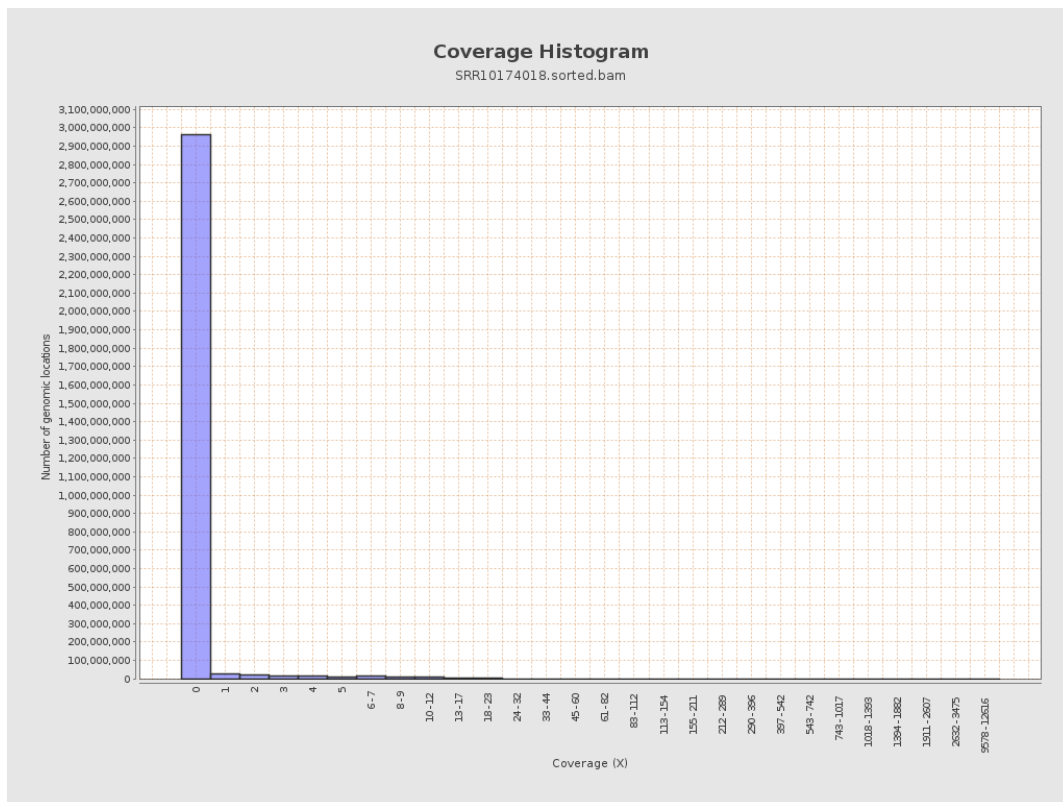
		bases	coverage	deviation
chr1	249250621	58646793	0.2353	1.7346
chr2	243199373	48683363	0.2002	8.8466
chr3	198022430	41248943	0.2083	1.335
chr4	191154276	40320598	0.2109	1.7219
chr5	180915260	33144965	0.1832	1.2389
chr6	171115067	31833628	0.186	1.3071
chr7	159138663	56984885	0.3581	3.4052
chr8	146364022	63539516	0.4341	2.4387
chr9	141213431	22323960	0.1581	1.4955
chr10	135534747	29435610	0.2172	3.8463
chr11	135006516	26404803	0.1956	1.3056
chr12	133851895	23792888	0.1778	1.231
chr13	115169878	16511741	0.1434	1.102
chr14	107349540	21900686	0.204	1.3343
chr15	102531392	15054540	0.1468	1.0985
chr16	90354753	14719966	0.1629	1.6245
chr17	81195210	15928068	0.1962	1.4239
chr18	78077248	11747974	0.1505	1.826
chr19	59128983	8294679	0.1403	1.3746
chr20	63025520	24777381	0.3931	1.8649
chr21	48129895	7781923	0.1617	1.3019
chr22	51304566	6599865	0.1286	1.0037
chrMT	16571	1714760	103.4796	83.9591
chrX	155270560	24588245	0.1584	1.1619

chrY	59373566	1302360	0.0219	0.9453
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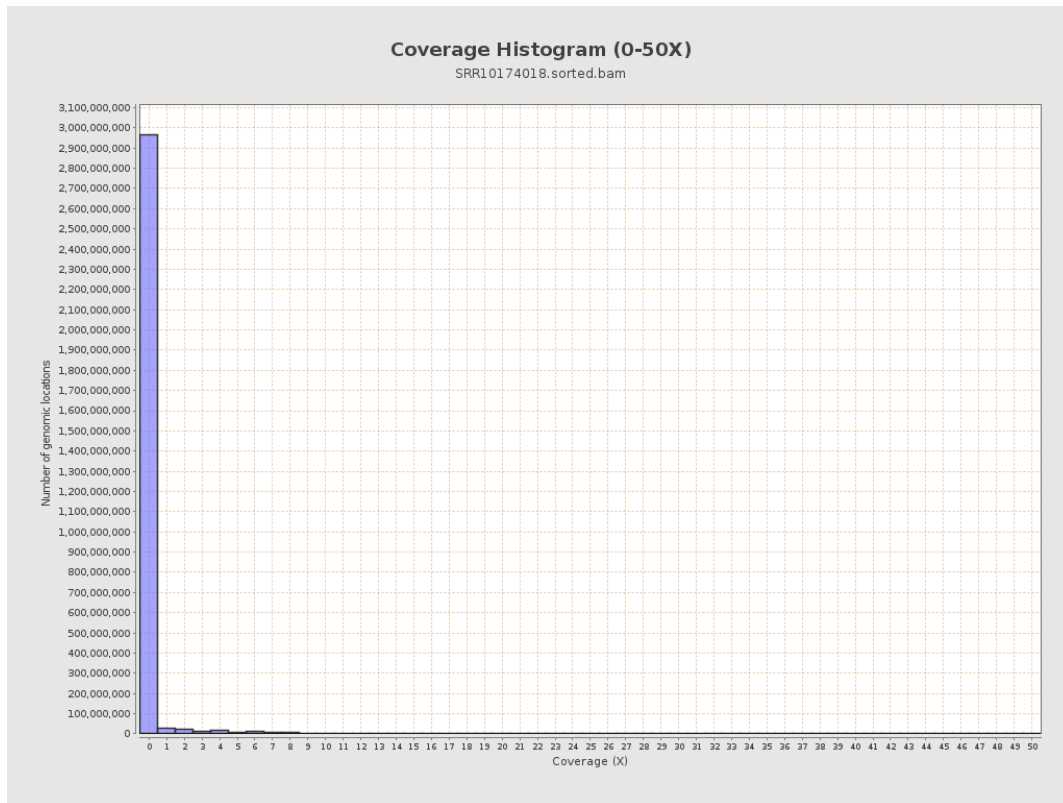
3. Results : Coverage across reference



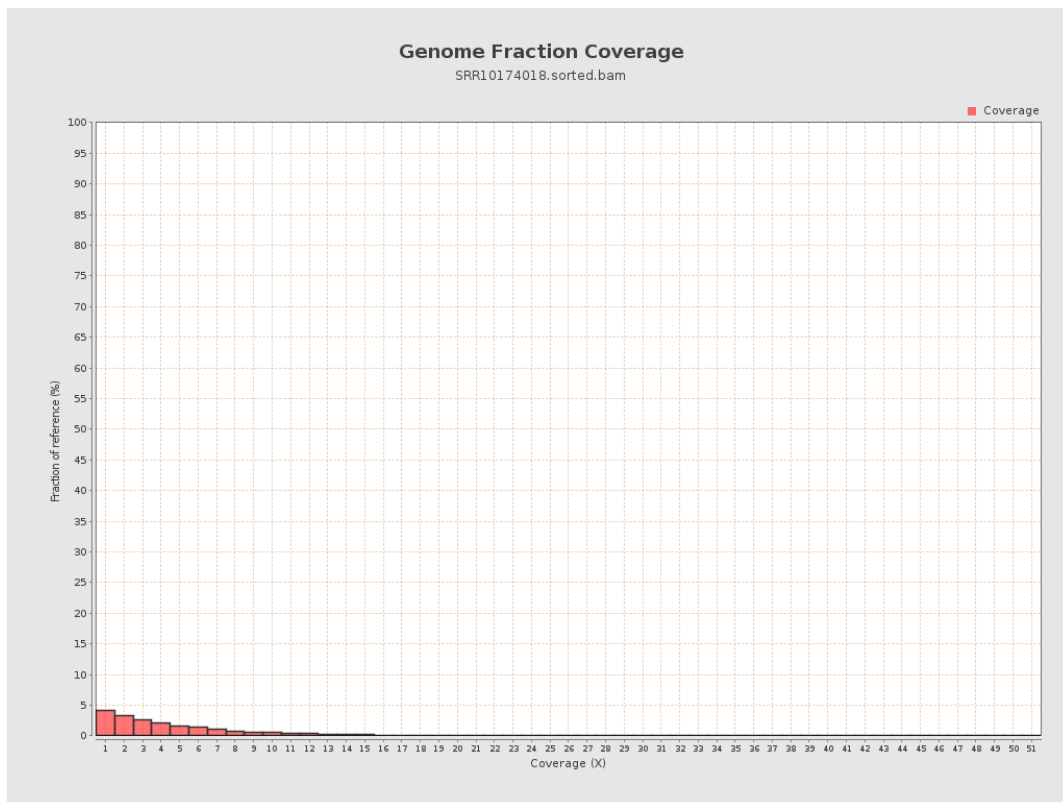
4. Results : Coverage Histogram



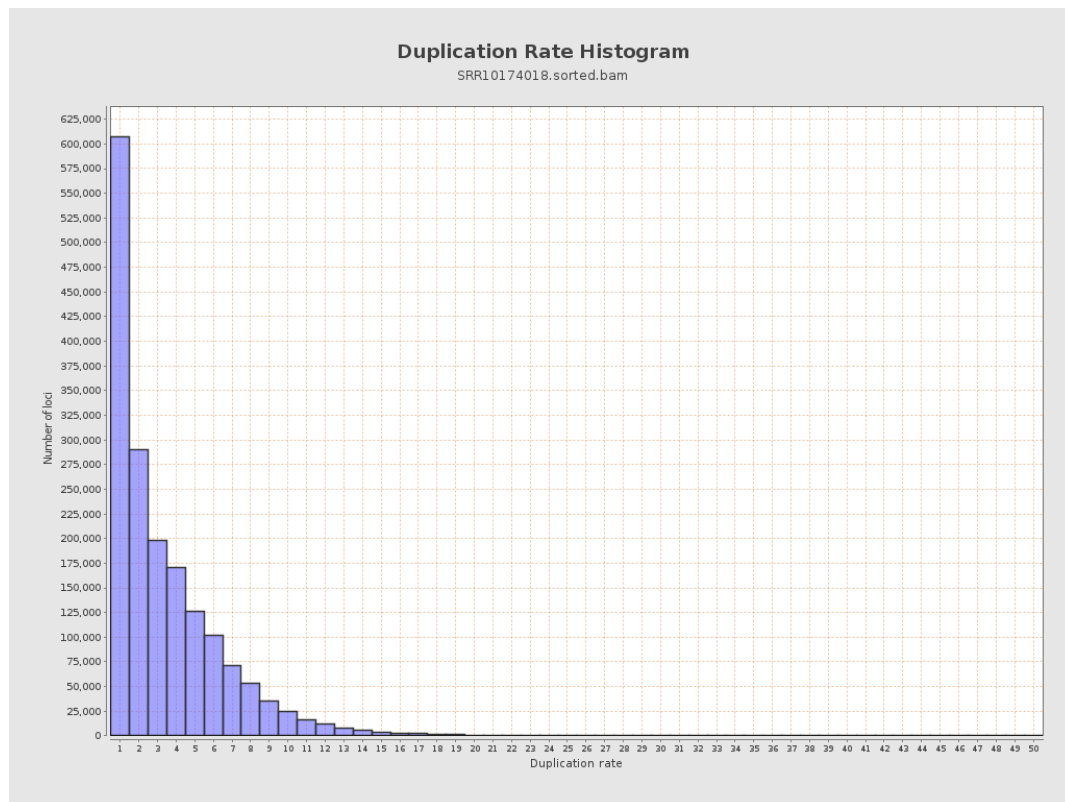
5. Results : Coverage Histogram (0-50X)



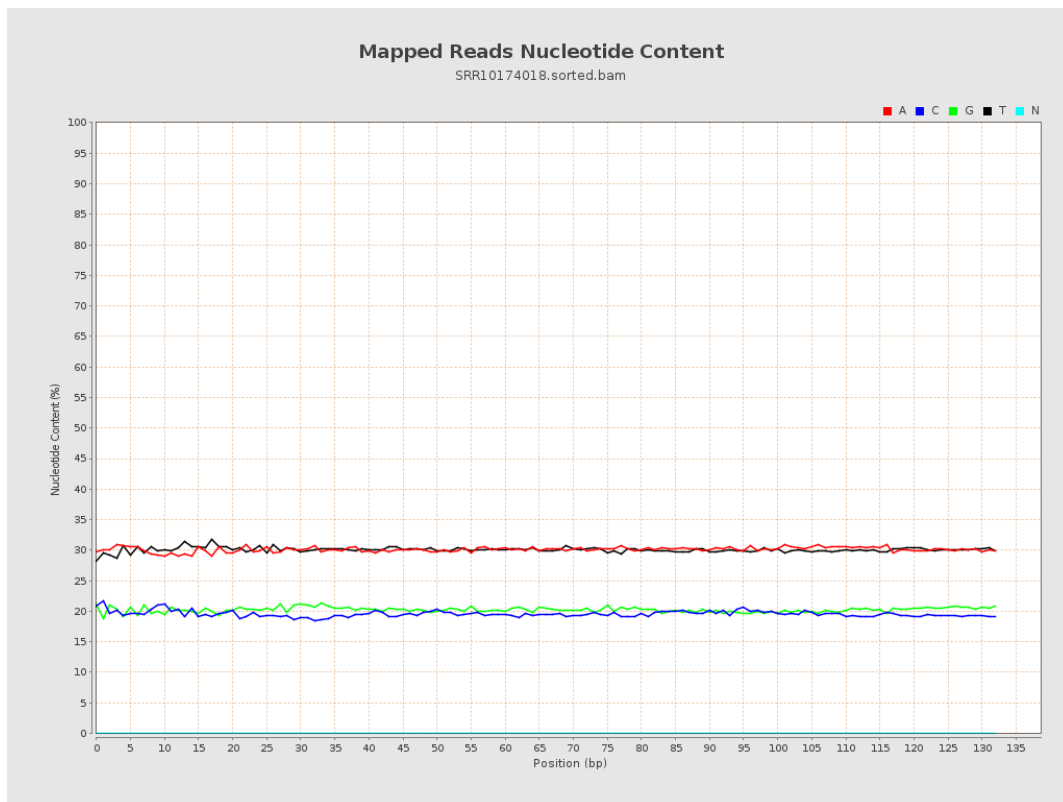
6. Results : Genome Fraction Coverage



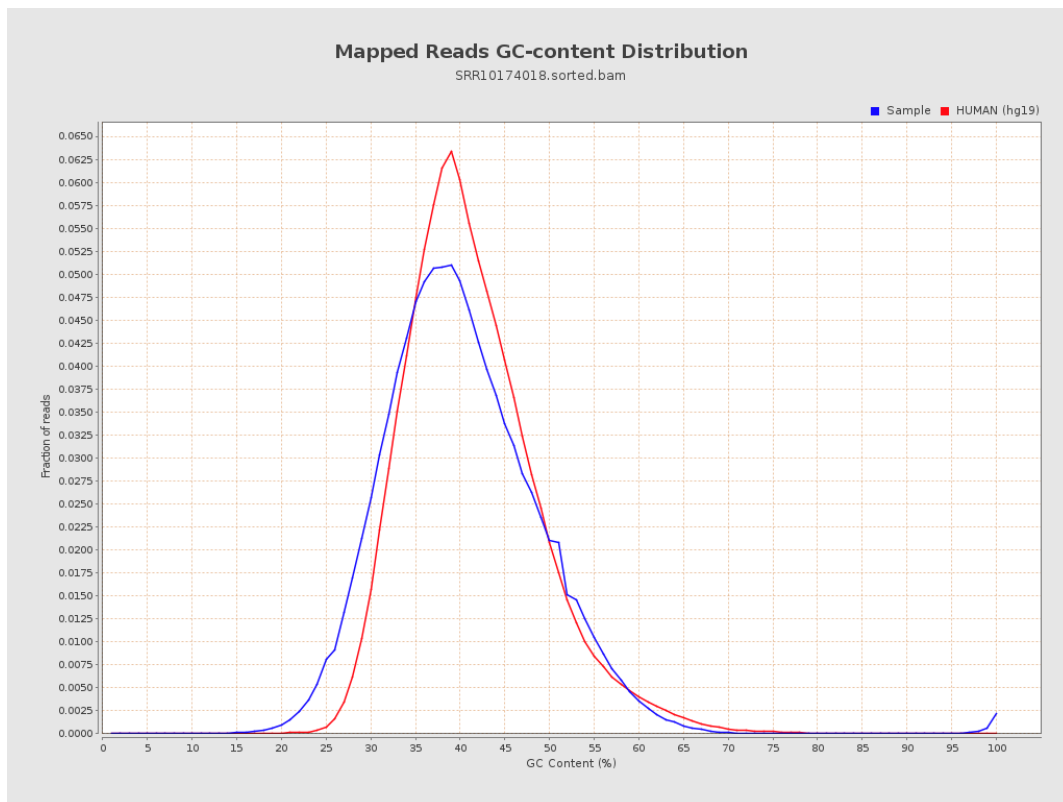
7. Results : Duplication Rate Histogram



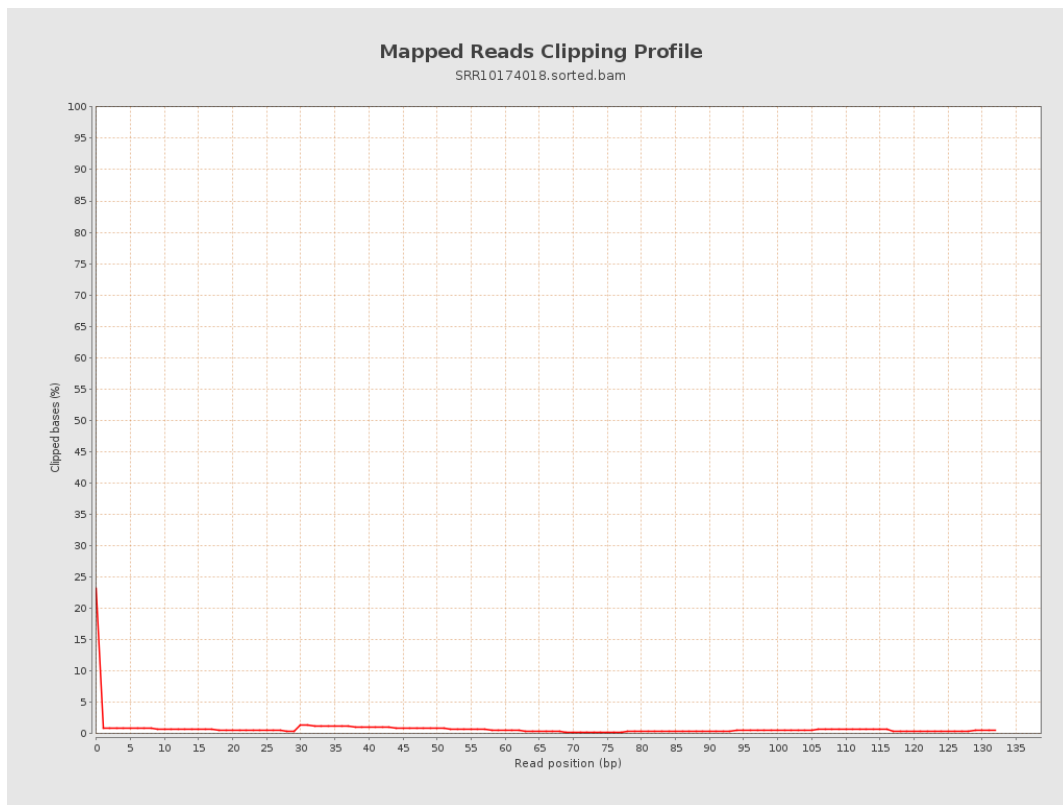
8. Results : Mapped Reads Nucleotide Content



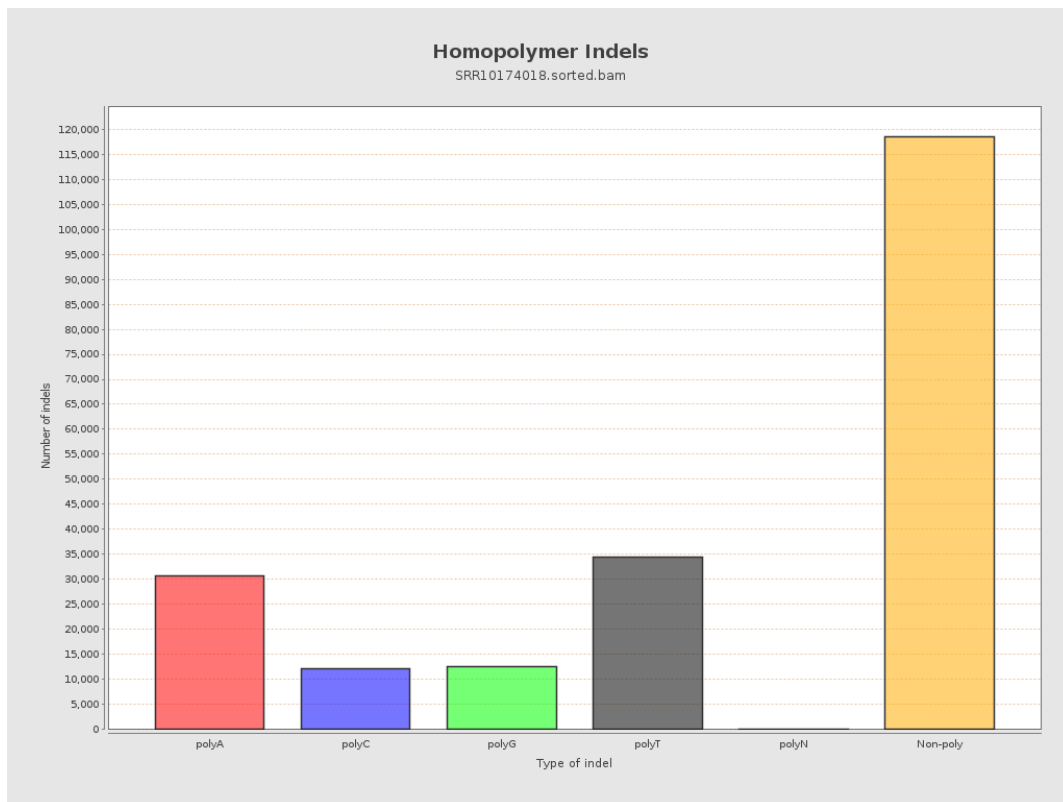
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



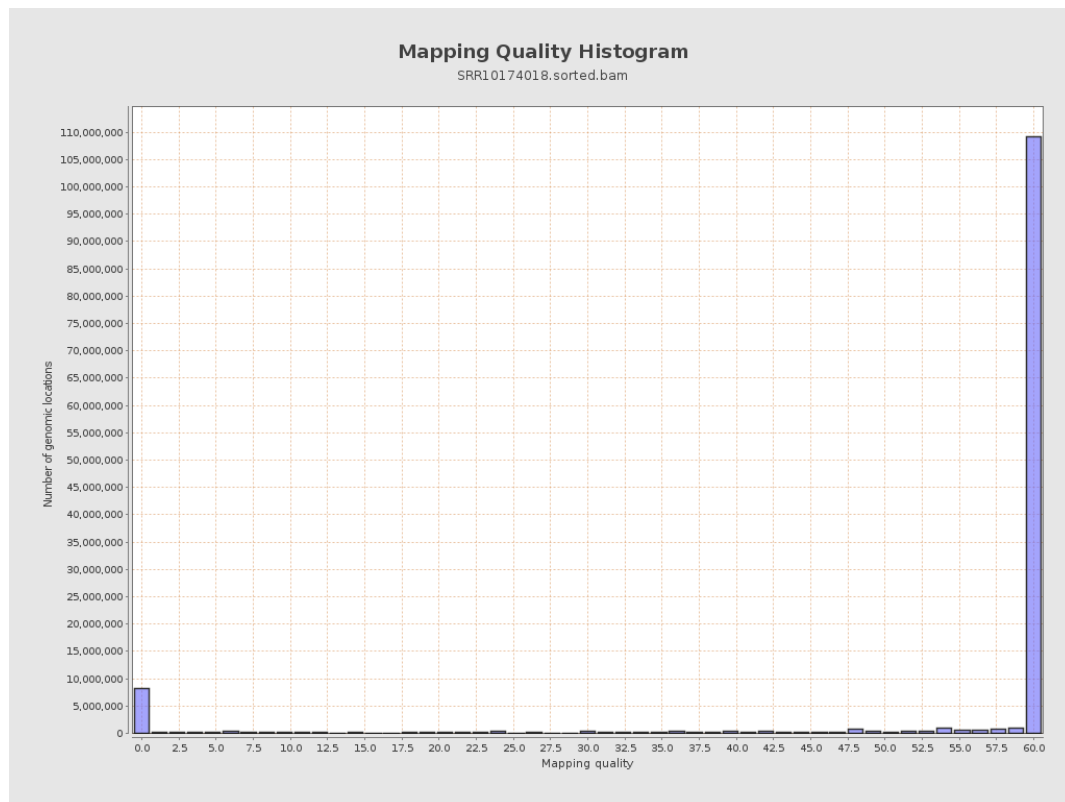
11. Results : Homopolymer Indels



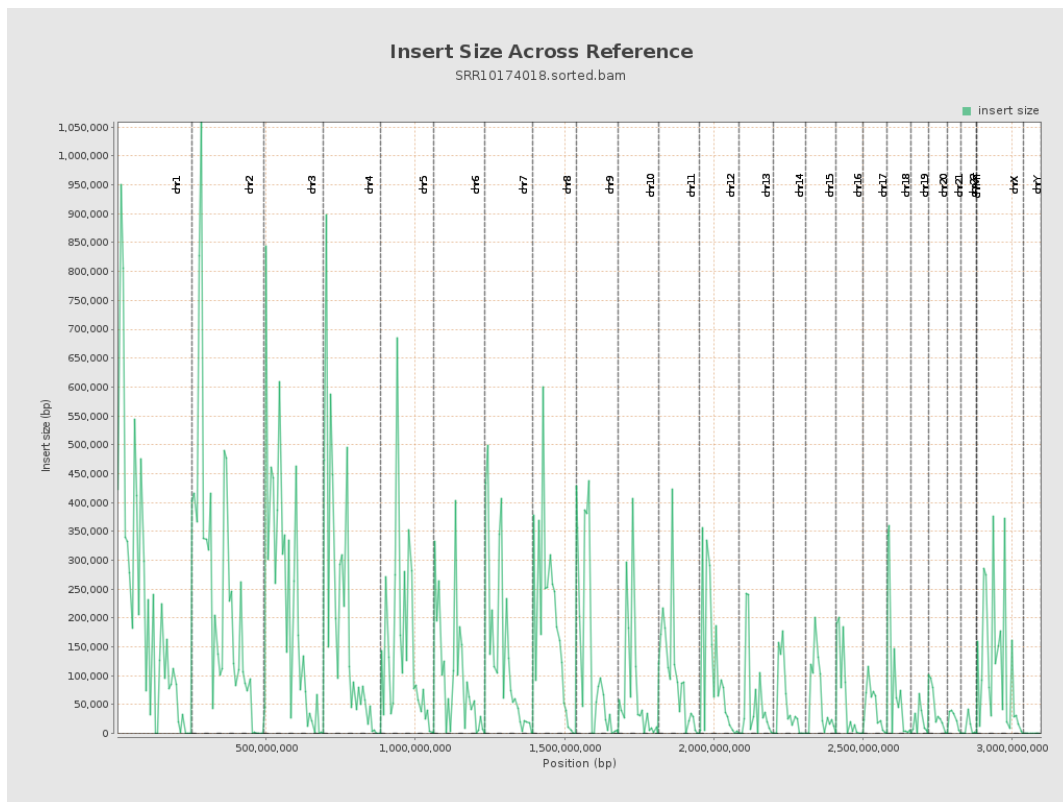
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

