

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:38:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472511.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_SRR3472511 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472511_1.fastq.gz SRR3472511_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:38:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472511.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,596,680
Mapped reads	14,406,540 / 98.7%
Unmapped reads	190,140 / 1.3%
Mapped paired reads	14,406,540 / 98.7%
Mapped reads, first in pair	7,229,795 / 49.53%
Mapped reads, second in pair	7,176,745 / 49.17%
Mapped reads, both in pair	14,306,598 / 98.01%
Mapped reads, singletons	99,942 / 0.68%
Secondary alignments	0
Supplementary alignments	49,316 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	8,845,507 / 60.6%
Duplication rate	44.91%
Clipped reads	1,181,407 / 8.09%

2.2. ACGT Content

Number/percentage of A's	396,412,052 / 27.97%
Number/percentage of C's	313,942,793 / 22.15%
Number/percentage of T's	394,231,969 / 27.82%
Number/percentage of G's	312,370,037 / 22.04%
Number/percentage of N's	216,906 / 0.02%

GC Percentage	44.19%
---------------	--------

2.3. Coverage

Mean	0.4578
Standard Deviation	17.3246

2.4. Mapping Quality

Mean Mapping Quality	54.97
----------------------	-------

2.5. Insert size

Mean	28,072.24
Standard Deviation	1,642,041.53
P25/Median/P75	171 / 241 / 330

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	8,737,820
Insertions	76,856
Mapped reads with at least one insertion	0.53%
Deletions	74,235
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.99%

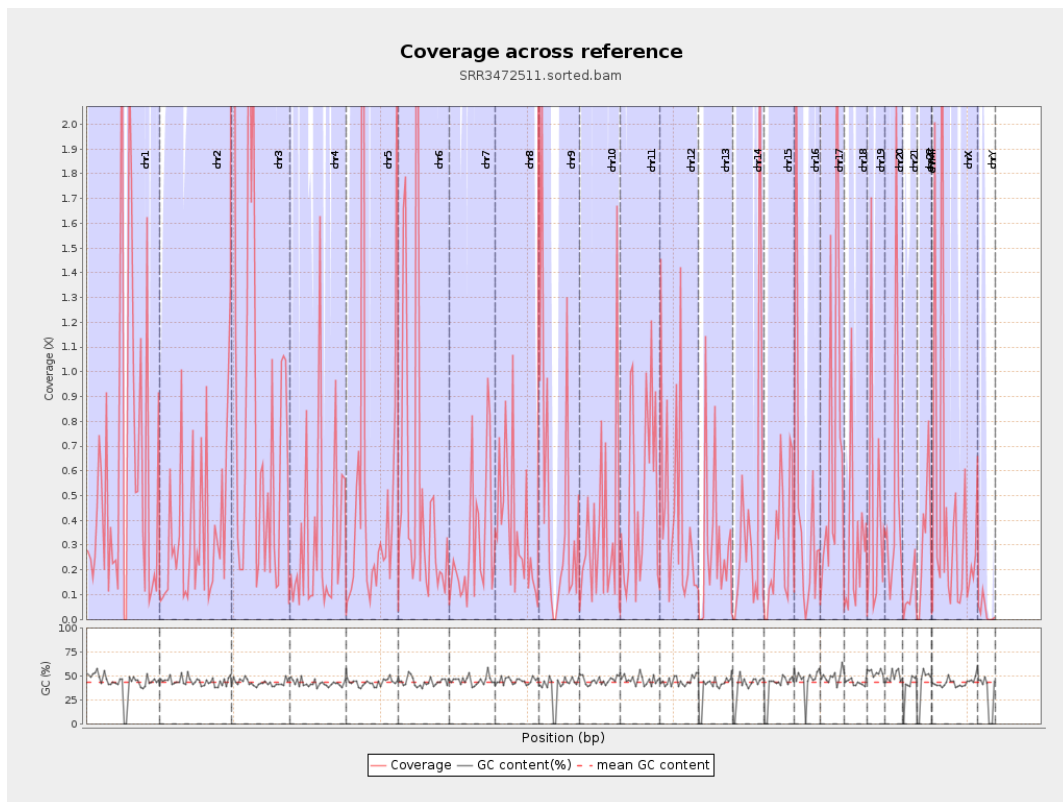
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

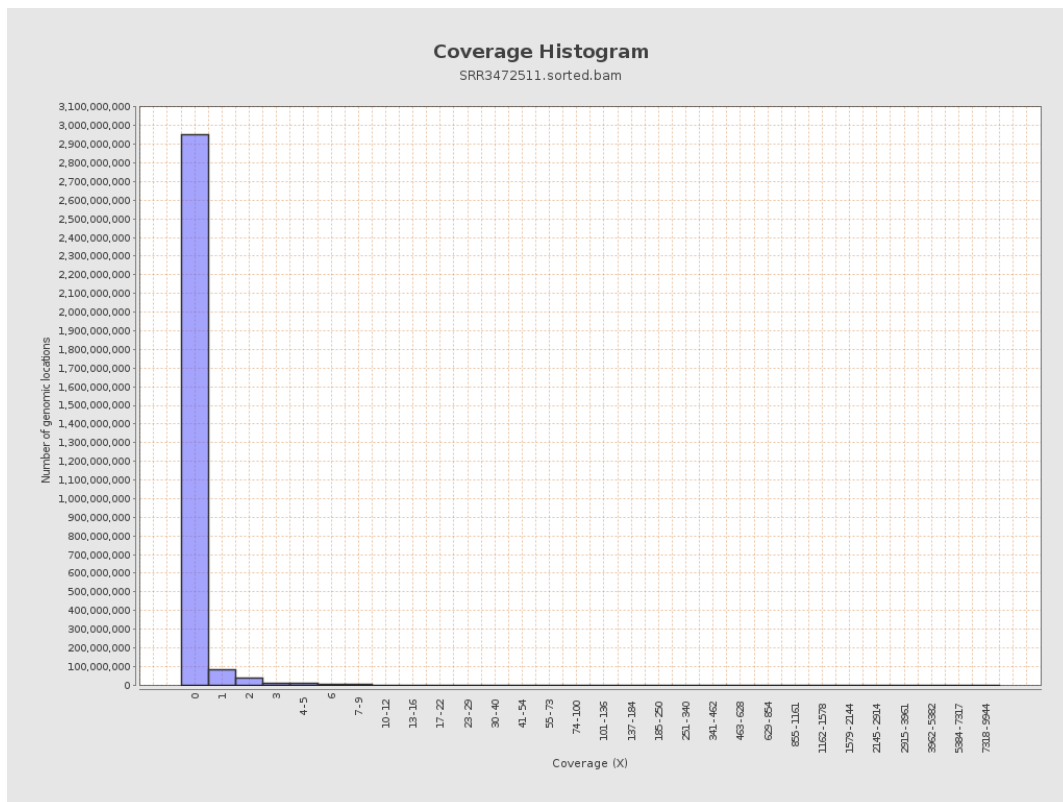
		bases	coverage	deviation
chr1	249250621	151277357	0.6069	19.6717
chr2	243199373	88016065	0.3619	13.4849
chr3	198022430	195228992	0.9859	25.3679
chr4	191154276	61577610	0.3221	12.6199
chr5	180915260	101679320	0.562	25.6889
chr6	171115067	94054412	0.5497	18.3068
chr7	159138663	48400598	0.3041	11.2087
chr8	146364022	53113293	0.3629	11.8524
chr9	141213431	68144252	0.4826	11.1542
chr10	135534747	49337639	0.364	16.5212
chr11	135006516	68018959	0.5038	17.7294
chr12	133851895	60022716	0.4484	12.2268
chr13	115169878	35160421	0.3053	11.475
chr14	107349540	40351499	0.3759	24.3733
chr15	102531392	32229227	0.3143	11.7317
chr16	90354753	38537376	0.4265	12.6937
chr17	81195210	55867838	0.6881	28.7406
chr18	78077248	23121454	0.2961	16.3751
chr19	59128983	26811655	0.4534	14.0226
chr20	63025520	32387076	0.5139	23.5304
chr21	48129895	4997763	0.1038	2.8337
chr22	51304566	16238451	0.3165	12.6031
chrMT	16571	1245	0.0751	0.306
chrX	155270560	70836355	0.4562	17.1

chrY	59373566	1947229	0.0328	1.3938
------	----------	---------	--------	--------

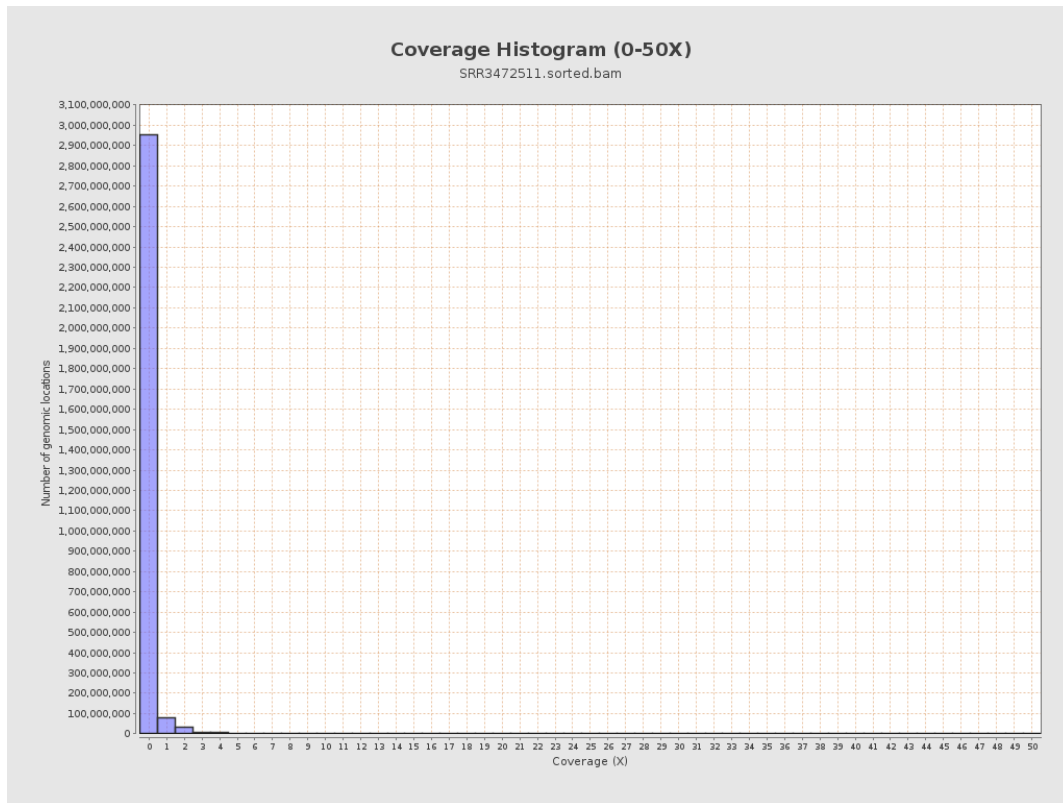
3. Results : Coverage across reference



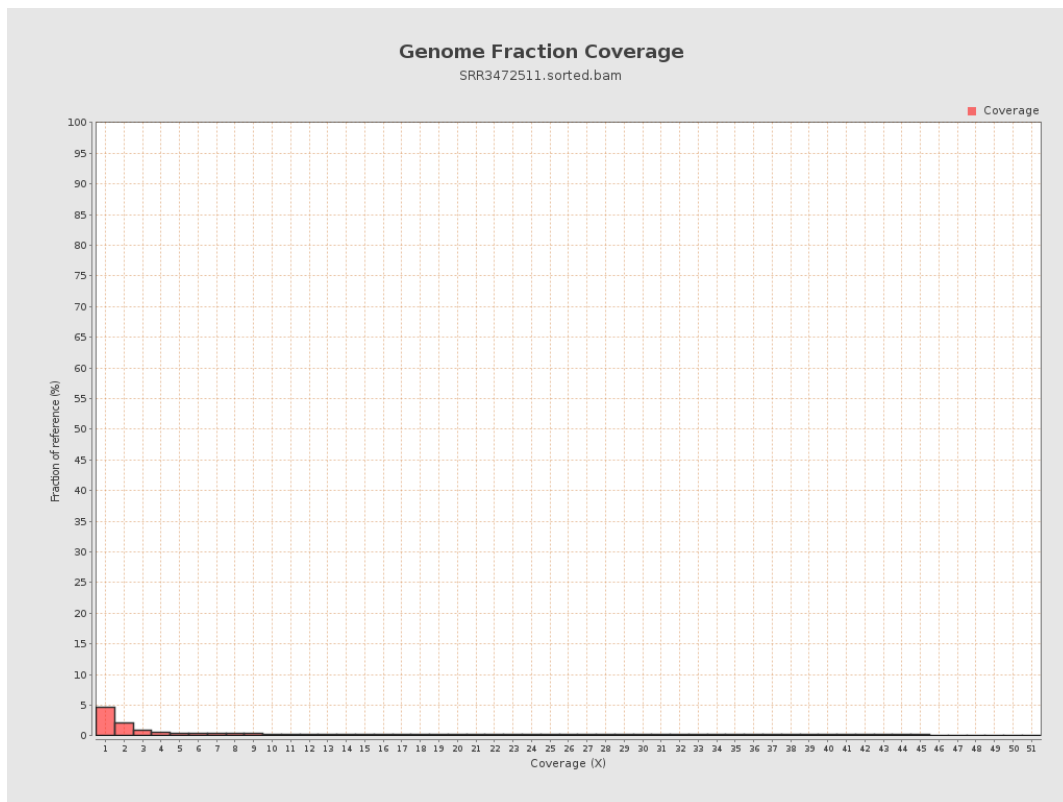
4. Results : Coverage Histogram



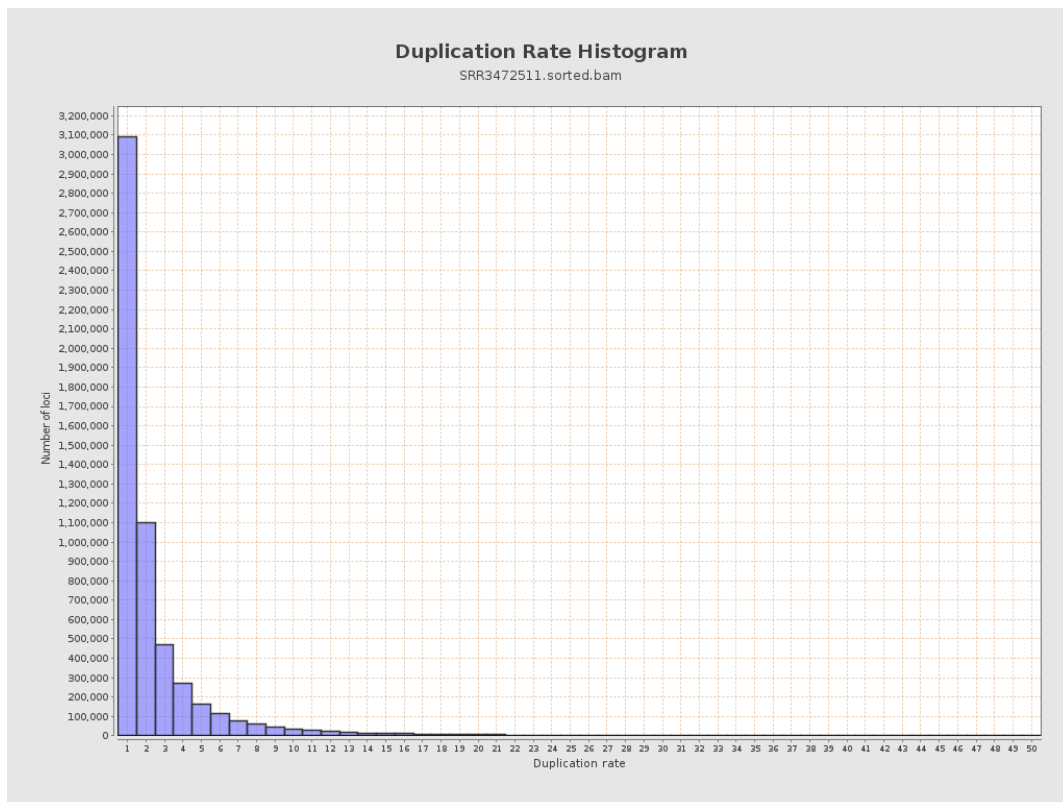
5. Results : Coverage Histogram (0-50X)



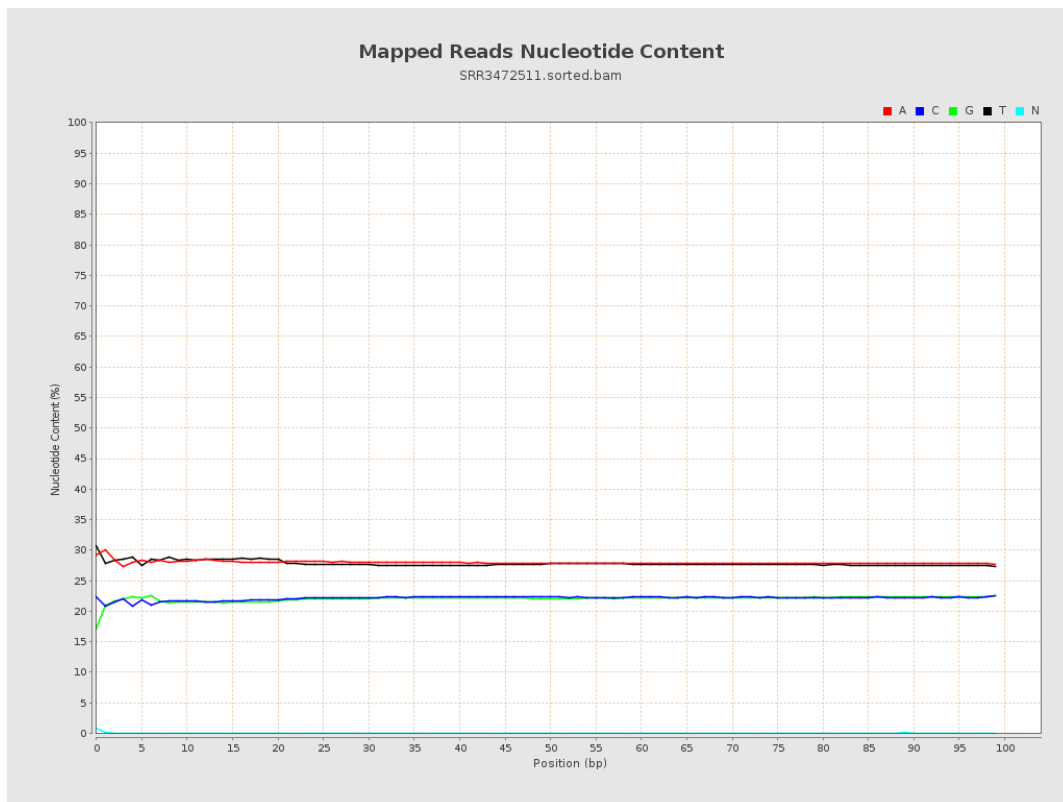
6. Results : Genome Fraction Coverage



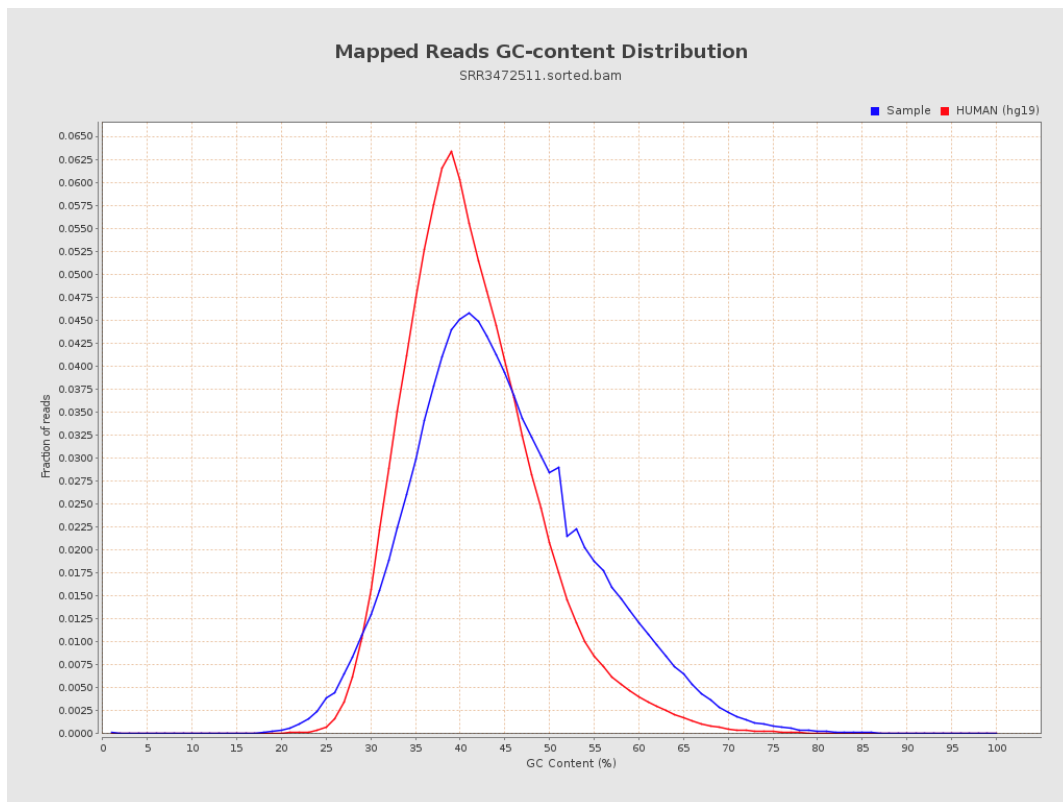
7. Results : Duplication Rate Histogram



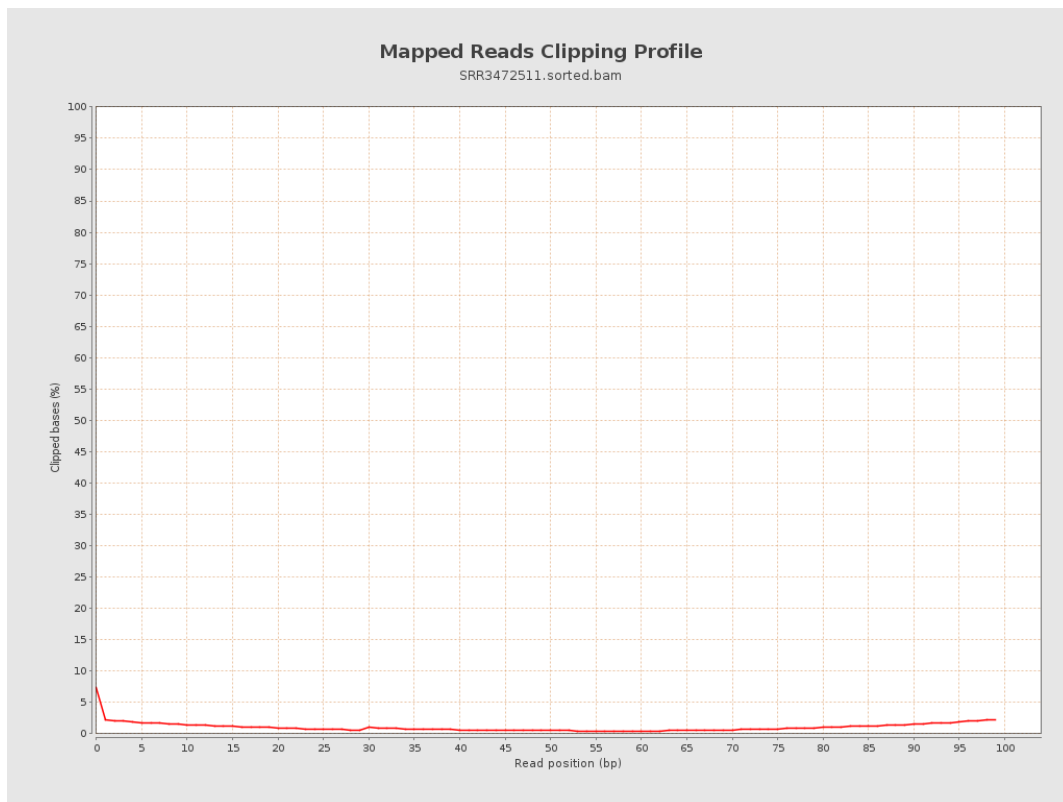
8. Results : Mapped Reads Nucleotide Content



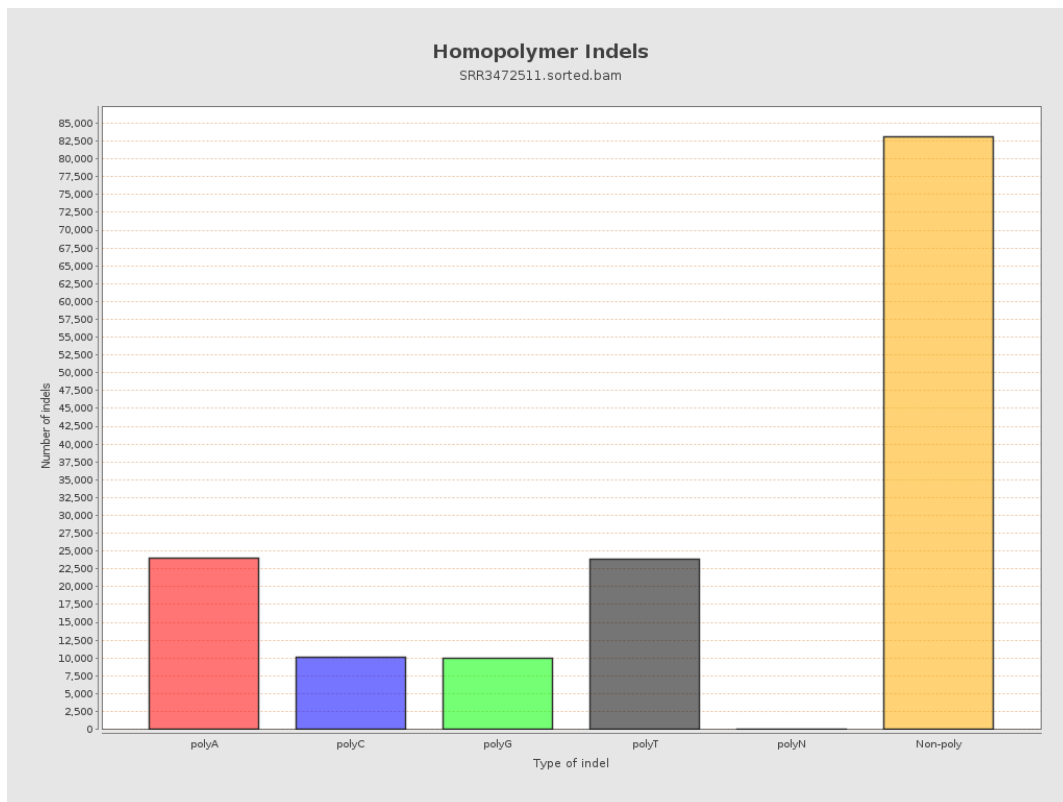
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



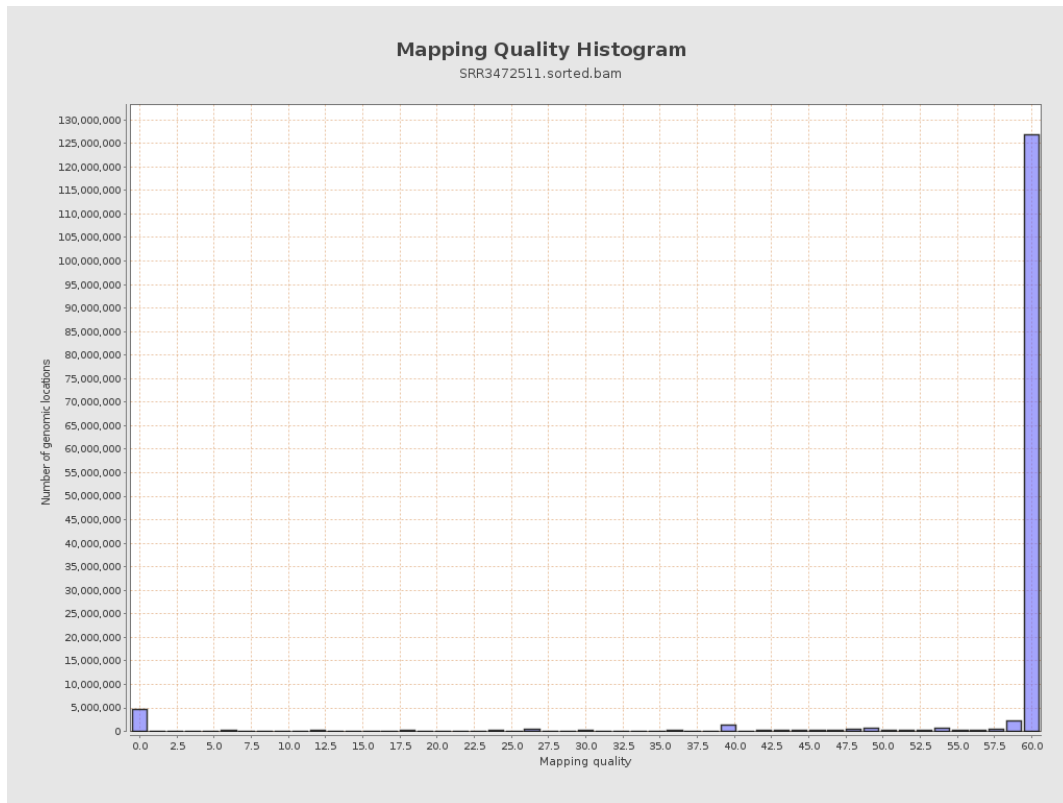
11. Results : Homopolymer Indels



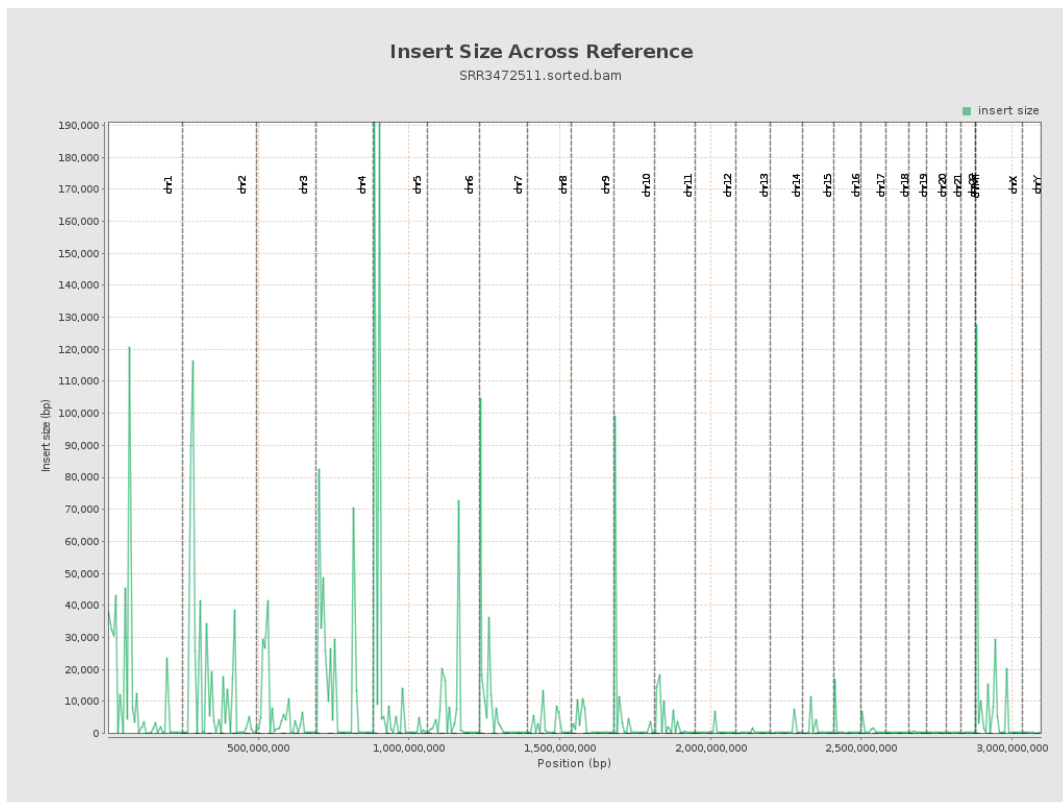
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

