

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:33:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472463.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_SRR3472463 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472463_1.fastq.gz SRR3472463_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:33:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472463.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,370,364
Mapped reads	17,242,538 / 99.26%
Unmapped reads	127,826 / 0.74%
Mapped paired reads	17,242,538 / 99.26%
Mapped reads, first in pair	8,640,101 / 49.74%
Mapped reads, second in pair	8,602,437 / 49.52%
Mapped reads, both in pair	17,164,626 / 98.82%
Mapped reads, singletons	77,912 / 0.45%
Secondary alignments	0
Supplementary alignments	57,659 / 0.33%
Read min/max/mean length	30 / 100 / 99.42
Duplicated reads (estimated)	10,915,922 / 62.84%
Duplication rate	48.19%
Clipped reads	1,109,210 / 6.39%

2.2. ACGT Content

Number/percentage of A's	468,507,692 / 27.66%
Number/percentage of C's	378,998,023 / 22.38%
Number/percentage of T's	469,762,864 / 27.74%
Number/percentage of G's	376,061,473 / 22.21%
Number/percentage of N's	211,316 / 0.01%

GC Percentage	44.58%
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2.3. Coverage

Mean	0.5471
Standard Deviation	17.2017

2.4. Mapping Quality

Mean Mapping Quality	55.17
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2.5. Insert size

Mean	16,520.94
Standard Deviation	1,285,877.72
P25/Median/P75	154 / 211 / 280

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	8,859,617
Insertions	93,515
Mapped reads with at least one insertion	0.54%
Deletions	86,918
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.57%

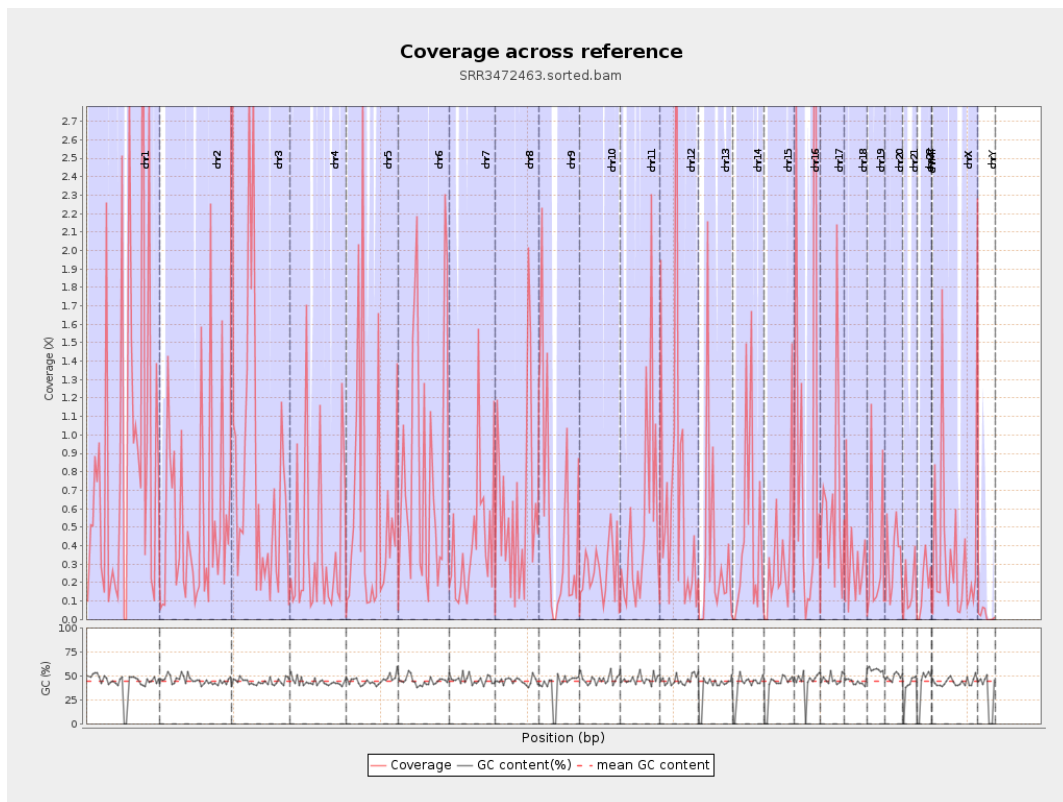
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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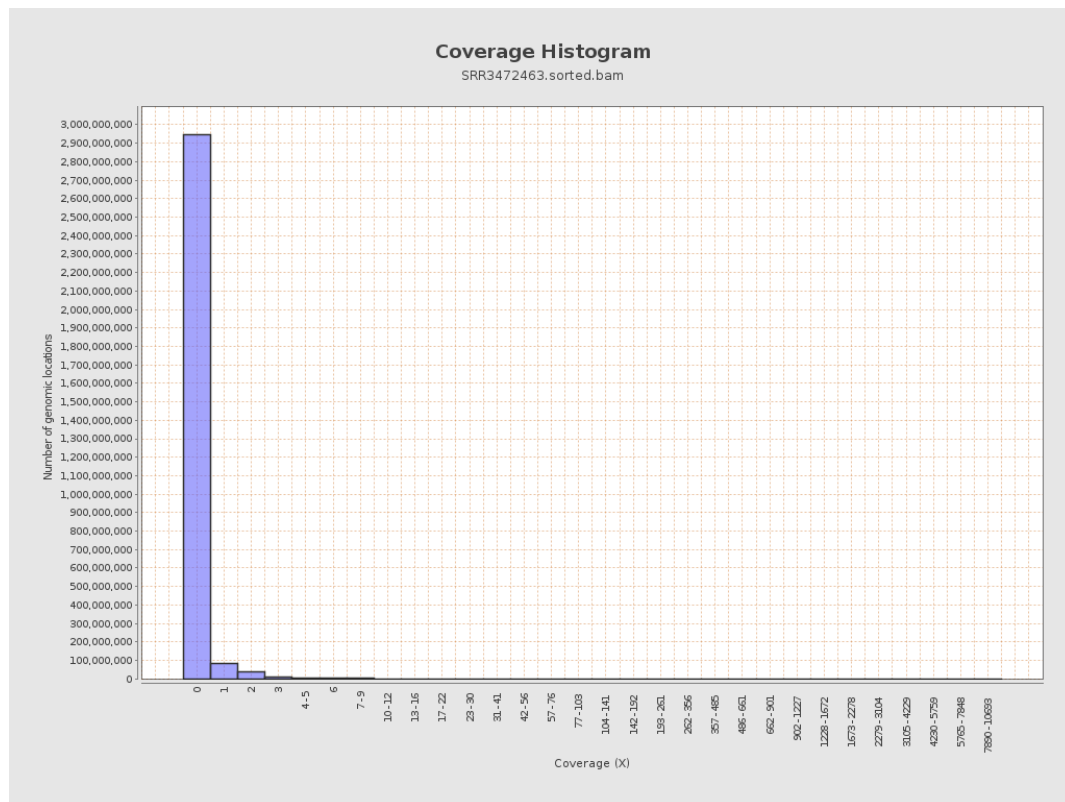
		bases	coverage	deviation
chr1	249250621	228278065	0.9159	26.2617
chr2	243199373	129301318	0.5317	16.1775
chr3	198022430	168261093	0.8497	16.7588
chr4	191154276	71199795	0.3725	13.513
chr5	180915260	108742134	0.6011	18.9813
chr6	171115067	142669391	0.8338	23.831
chr7	159138663	68439059	0.4301	11.8224
chr8	146364022	93001026	0.6354	16.8145
chr9	141213431	76675319	0.543	13.2261
chr10	135534747	35883689	0.2648	8.4107
chr11	135006516	70196400	0.5199	18.0648
chr12	133851895	96143871	0.7183	24.4327
chr13	115169878	40057196	0.3478	11.3993
chr14	107349540	46168085	0.4301	14.4679
chr15	102531392	34410319	0.3356	11.9011
chr16	90354753	92708194	1.026	31.8998
chr17	81195210	49949090	0.6152	14.8617
chr18	78077248	25297032	0.324	9.3316
chr19	59128983	22157394	0.3747	11.1682
chr20	63025520	21156804	0.3357	13.002
chr21	48129895	8249618	0.1714	8.1814
chr22	51304566	9422805	0.1837	4.6172
chrMT	16571	3461	0.2089	0.5745
chrX	155270560	54001776	0.3478	9.6761

chrY	59373566	1372466	0.0231	0.5633
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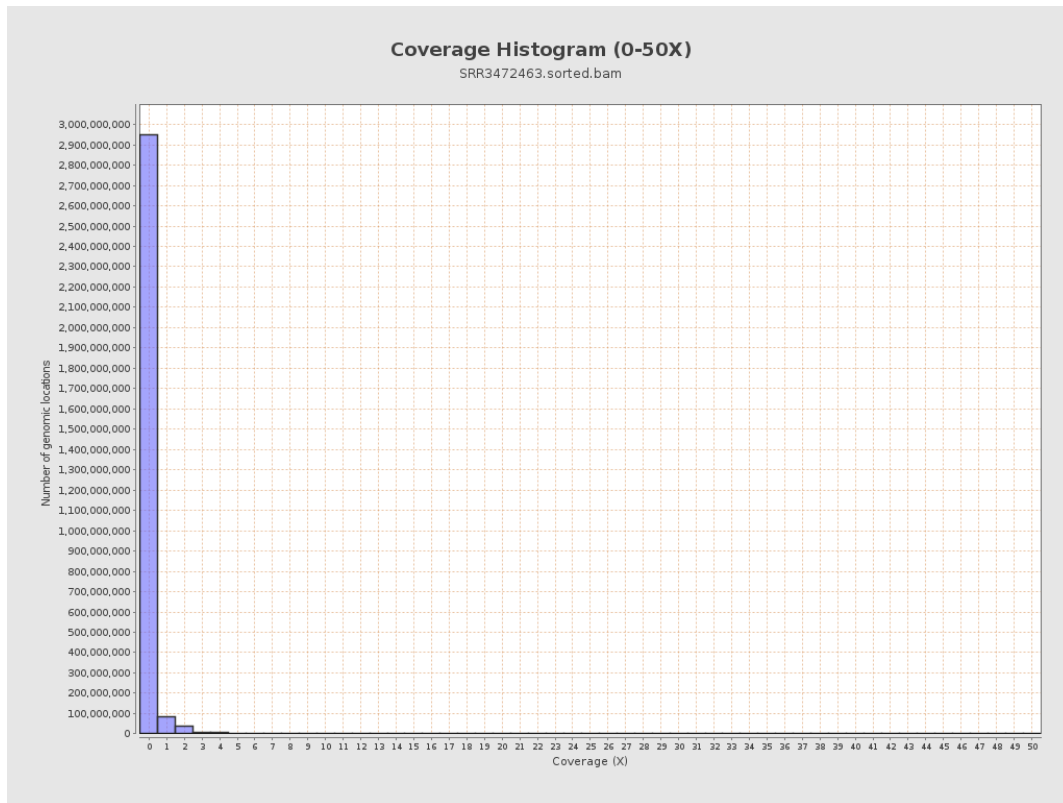
3. Results : Coverage across reference



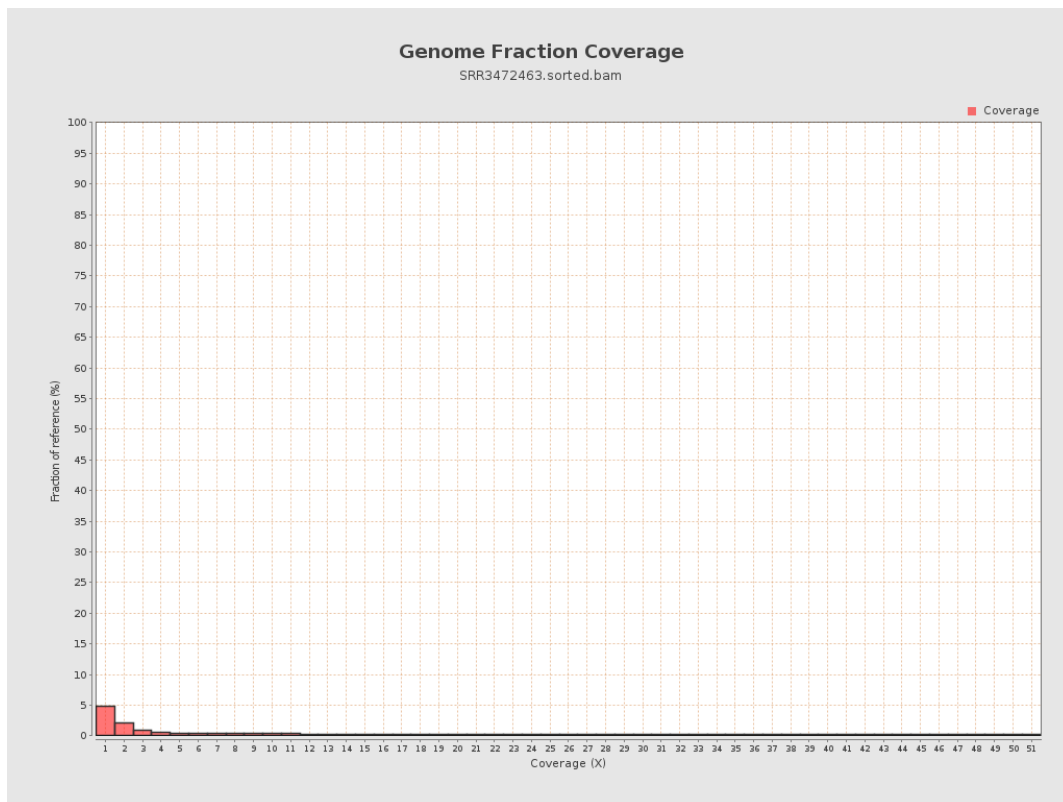
4. Results : Coverage Histogram



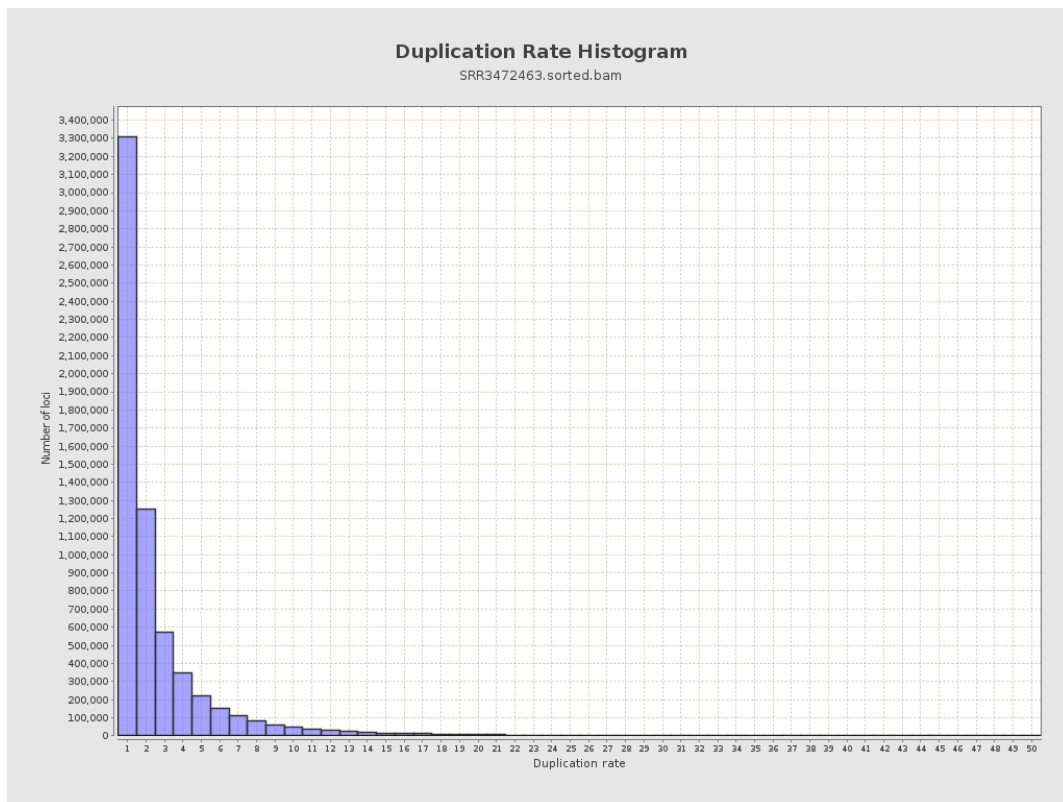
5. Results : Coverage Histogram (0-50X)



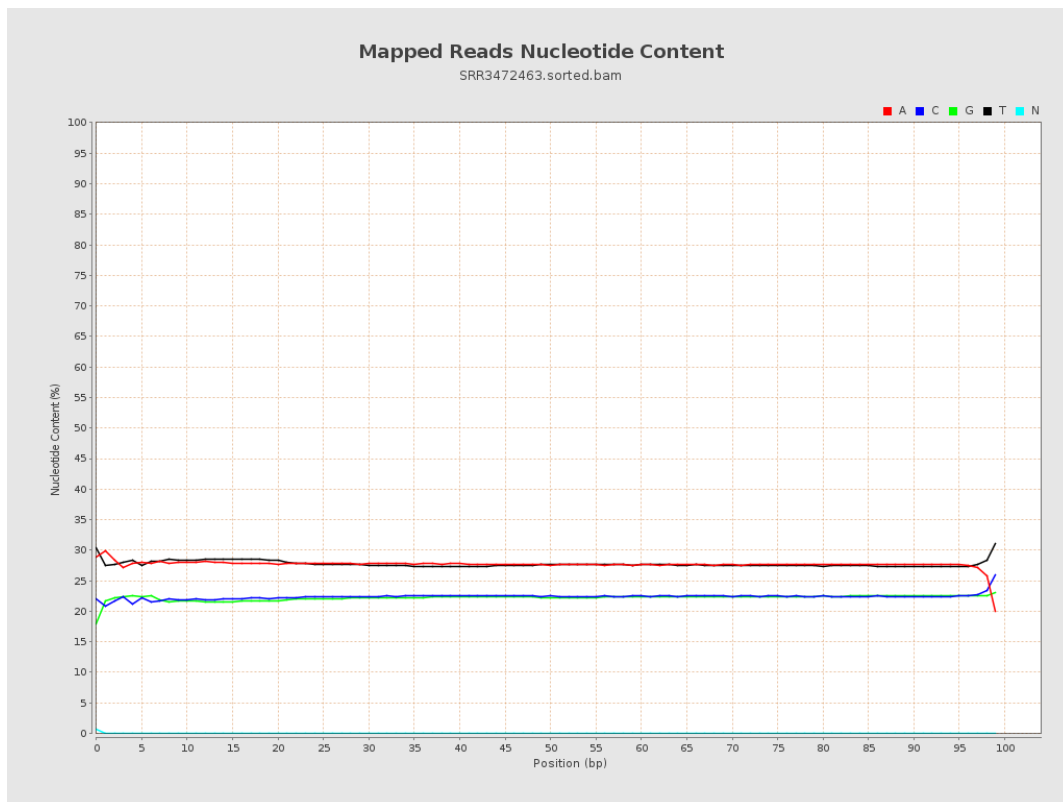
6. Results : Genome Fraction Coverage



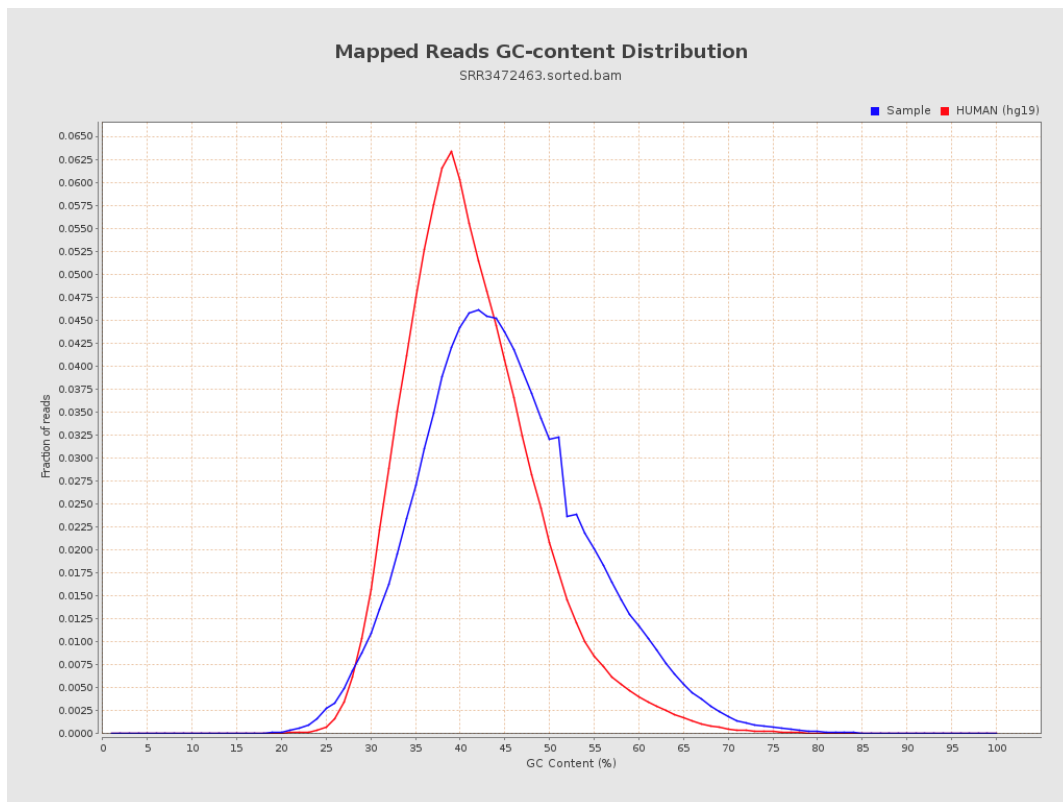
7. Results : Duplication Rate Histogram



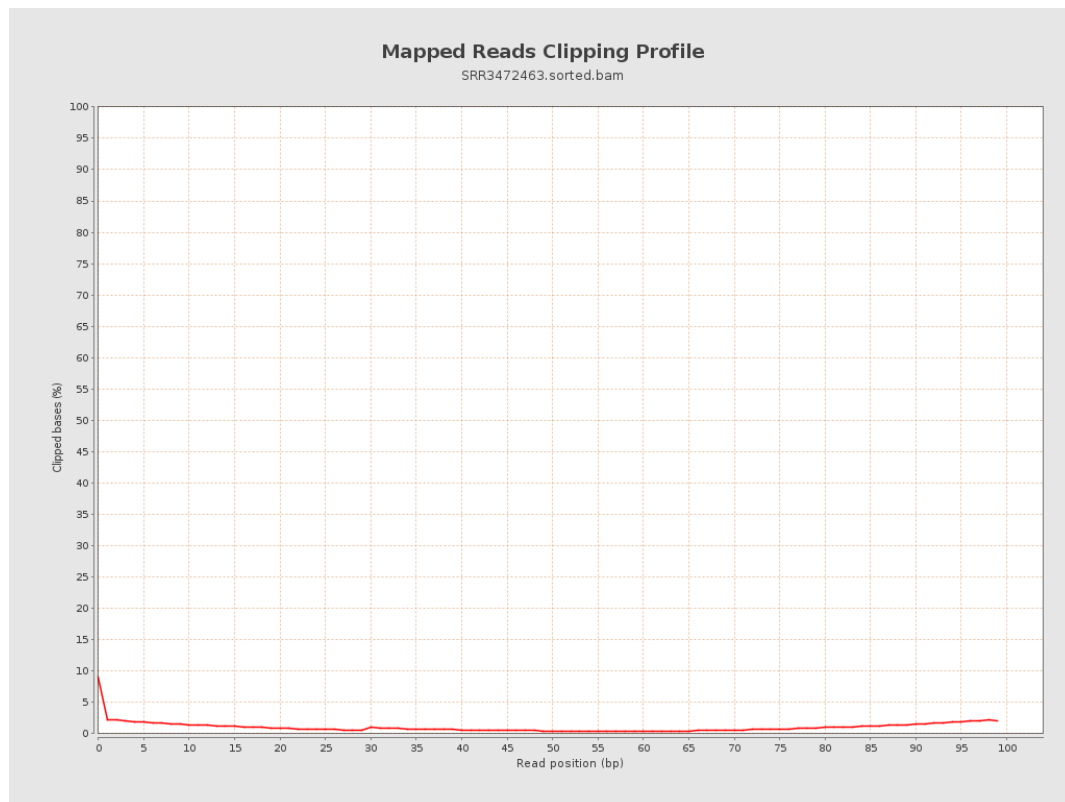
8. Results : Mapped Reads Nucleotide Content



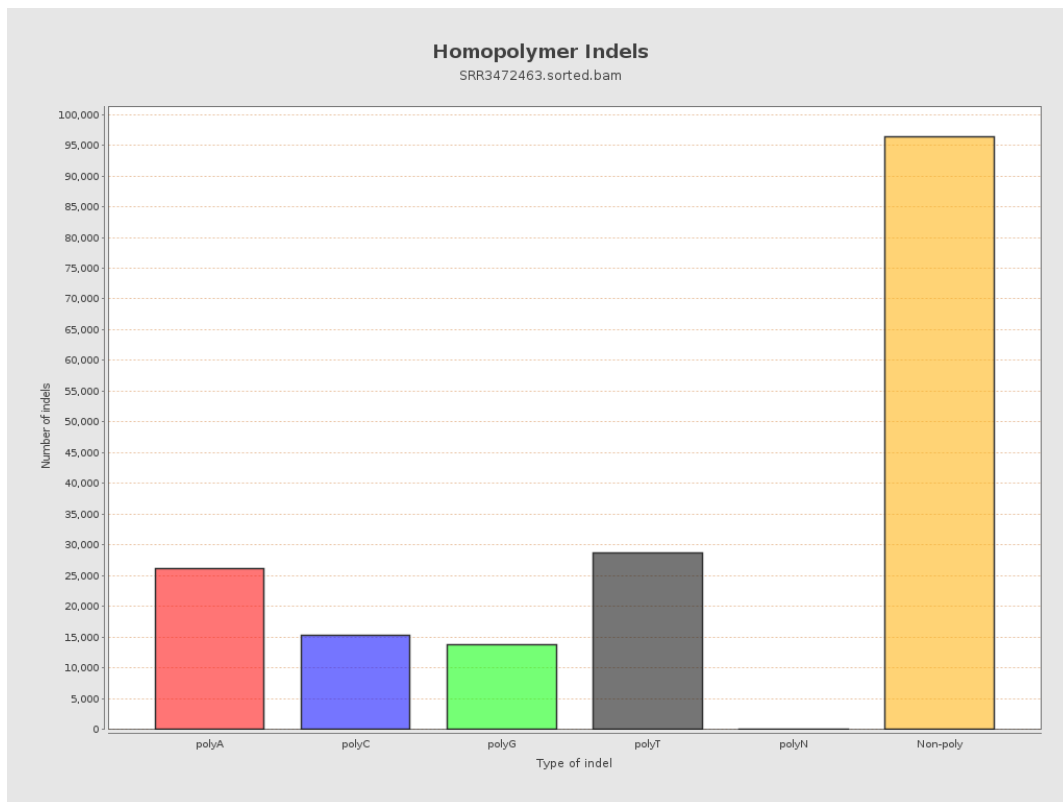
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



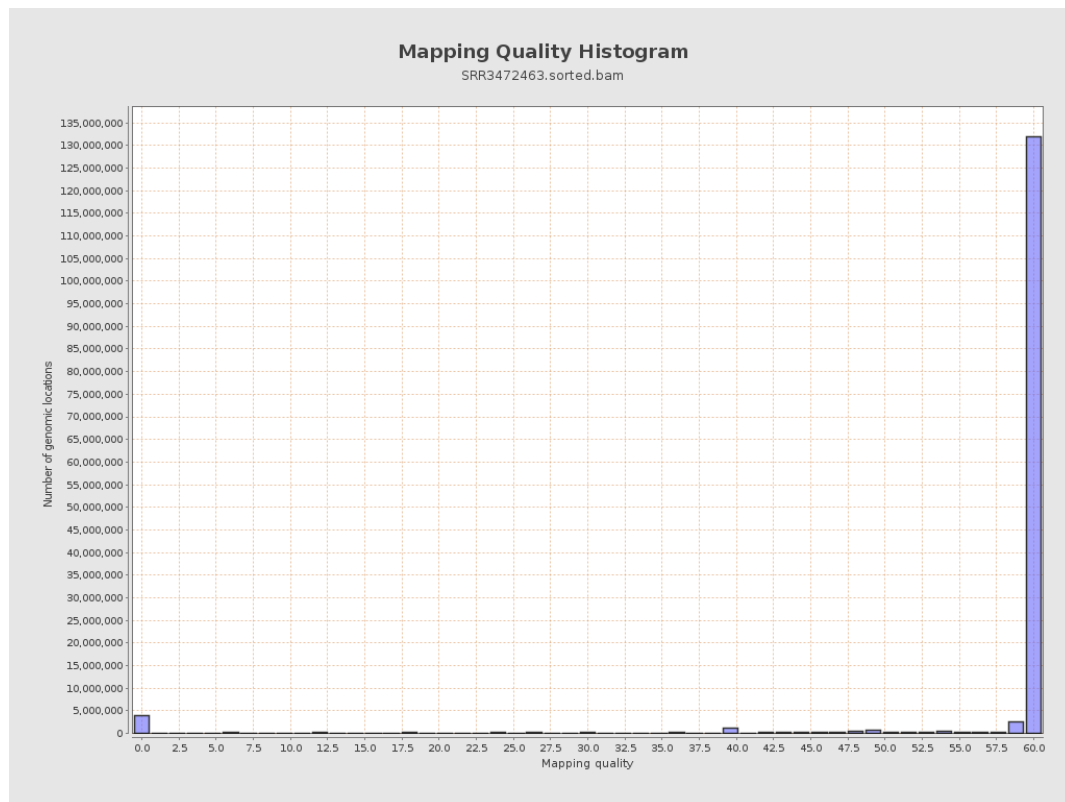
11. Results : Homopolymer Indels



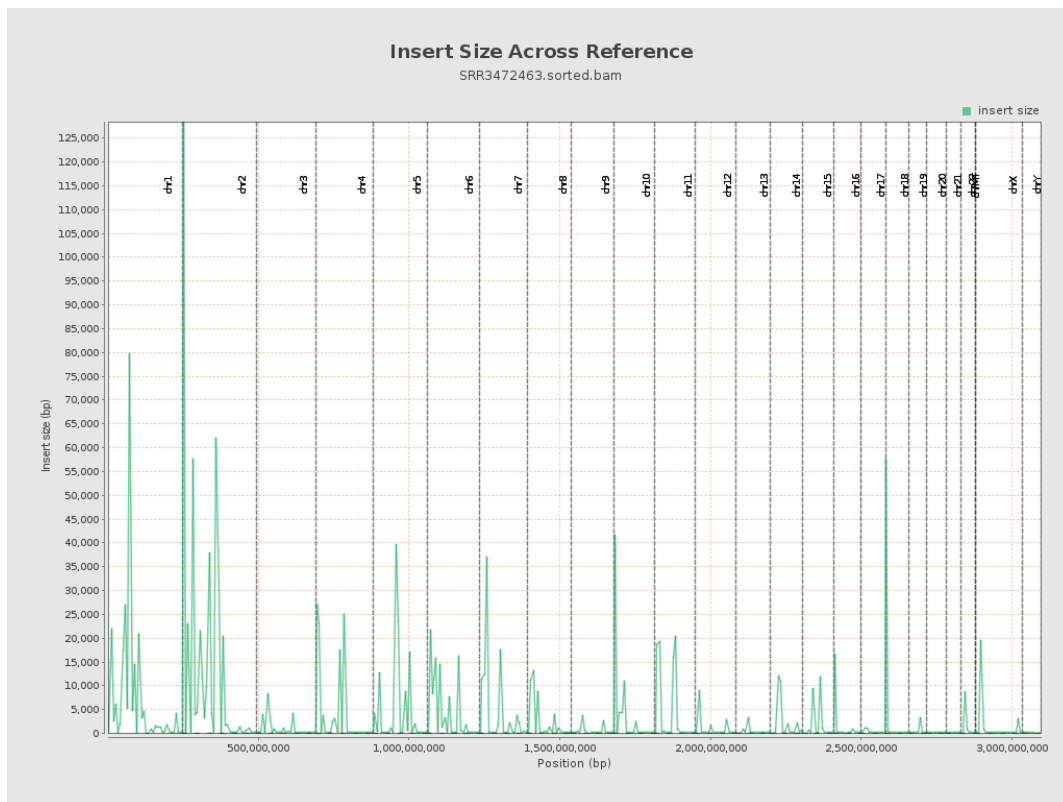
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

