

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:48:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472391.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_SRR3472391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472391_1.fastq.gz SRR3472391_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:48:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,484,628
Mapped reads	18,282,857 / 98.91%
Unmapped reads	201,771 / 1.09%
Mapped paired reads	18,282,857 / 98.91%
Mapped reads, first in pair	9,173,942 / 49.63%
Mapped reads, second in pair	9,108,915 / 49.28%
Mapped reads, both in pair	18,162,302 / 98.26%
Mapped reads, singletons	120,555 / 0.65%
Secondary alignments	0
Supplementary alignments	75,049 / 0.41%
Read min/max/mean length	30 / 100 / 99.5
Duplicated reads (estimated)	11,078,942 / 59.94%
Duplication rate	46.84%
Clipped reads	1,236,428 / 6.69%

2.2. ACGT Content

Number/percentage of A's	489,272,762 / 27.25%
Number/percentage of C's	410,249,064 / 22.84%
Number/percentage of T's	489,394,786 / 27.25%
Number/percentage of G's	406,671,627 / 22.65%
Number/percentage of N's	220,120 / 0.01%

GC Percentage	45.49%
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2.3. Coverage

Mean	0.5802
Standard Deviation	16.4748

2.4. Mapping Quality

Mean Mapping Quality	54.81
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2.5. Insert size

Mean	23,959.9
Standard Deviation	1,505,999.94
P25/Median/P75	167 / 232 / 313

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	10,591,523
Insertions	107,477
Mapped reads with at least one insertion	0.58%
Deletions	90,015
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.93%

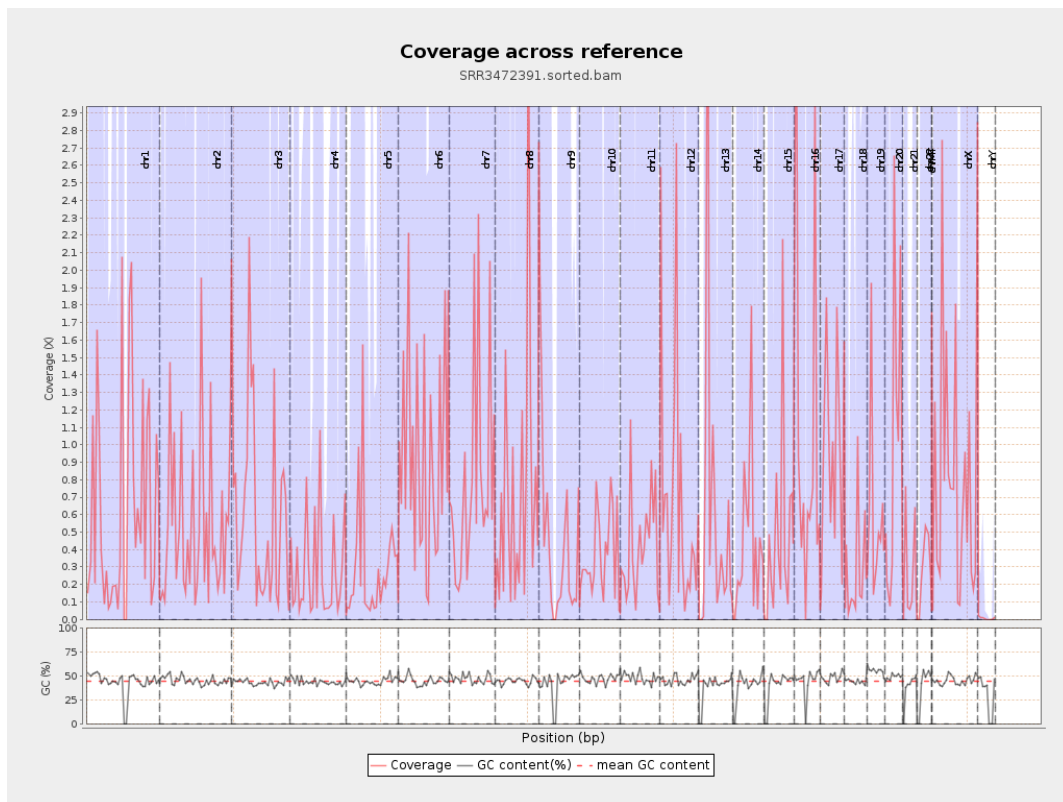
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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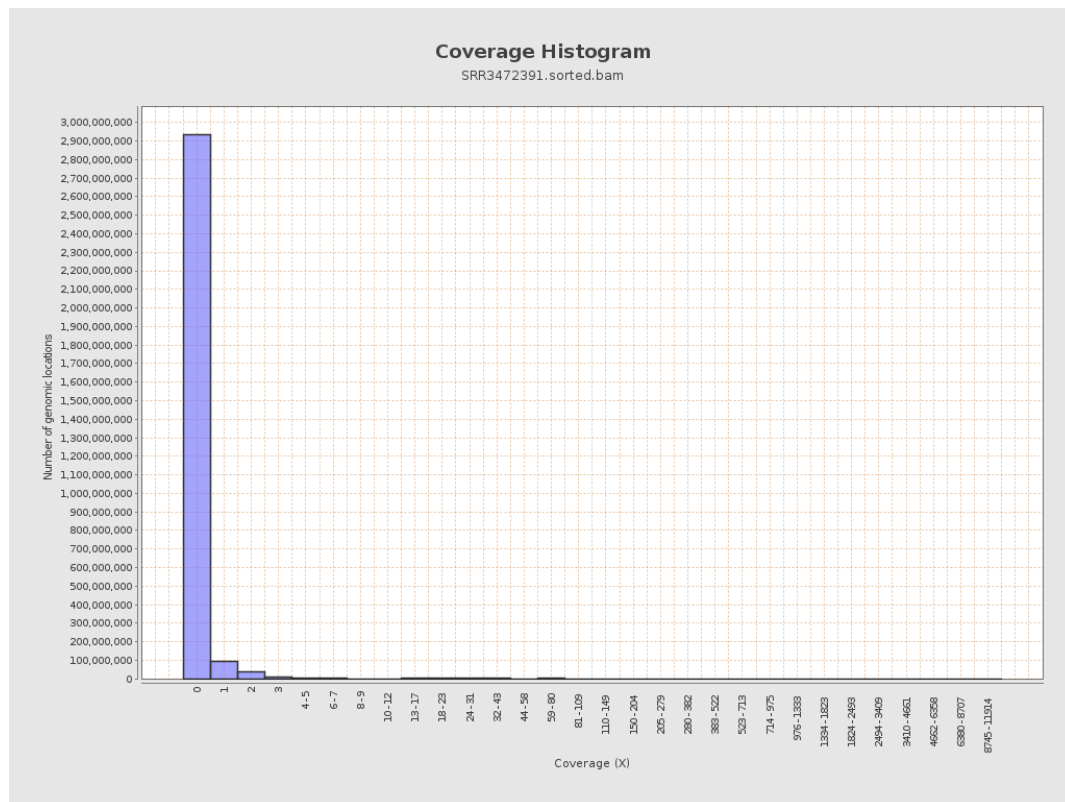
		bases	coverage	deviation
chr1	249250621	160865087	0.6454	18.9451
chr2	243199373	131116871	0.5391	14.8707
chr3	198022430	123237548	0.6223	13.0779
chr4	191154276	52132708	0.2727	9.8429
chr5	180915260	53329002	0.2948	7.9468
chr6	171115067	157282920	0.9192	20.9651
chr7	159138663	127828331	0.8033	19.5844
chr8	146364022	107345676	0.7334	20.3045
chr9	141213431	63723764	0.4513	10.5363
chr10	135534747	50195159	0.3703	10.7868
chr11	135006516	57939712	0.4292	12.0845
chr12	133851895	92337587	0.6898	17.3519
chr13	115169878	71995164	0.6251	22.7517
chr14	107349540	46232138	0.4307	11.7406
chr15	102531392	48872707	0.4767	28.1812
chr16	90354753	99555786	1.1018	24.038
chr17	81195210	76461302	0.9417	20.0076
chr18	78077248	22167654	0.2839	9.9464
chr19	59128983	37044596	0.6265	10.7747
chr20	63025520	63403708	1.006	23.2803
chr21	48129895	13323261	0.2768	12.0395
chr22	51304566	14580868	0.2842	7.6368
chrMT	16571	29179	1.7608	1.9361
chrX	155270560	124654963	0.8028	17.1515

chrY	59373566	365565	0.0062	0.3391
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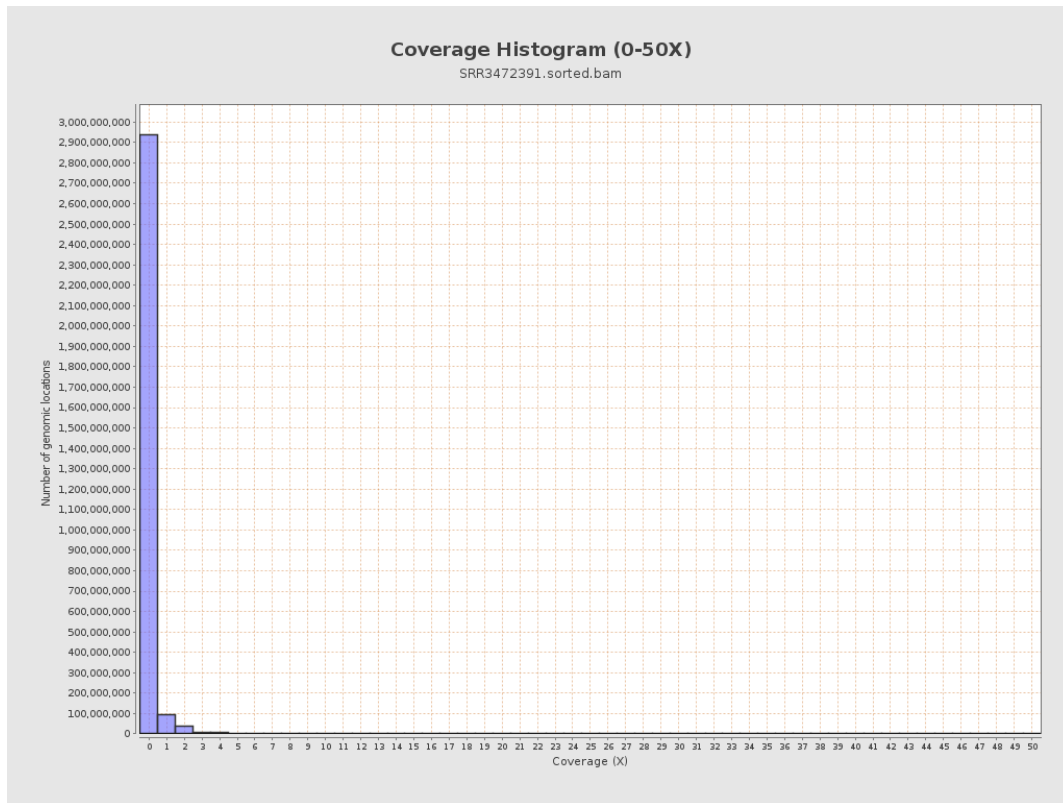
3. Results : Coverage across reference



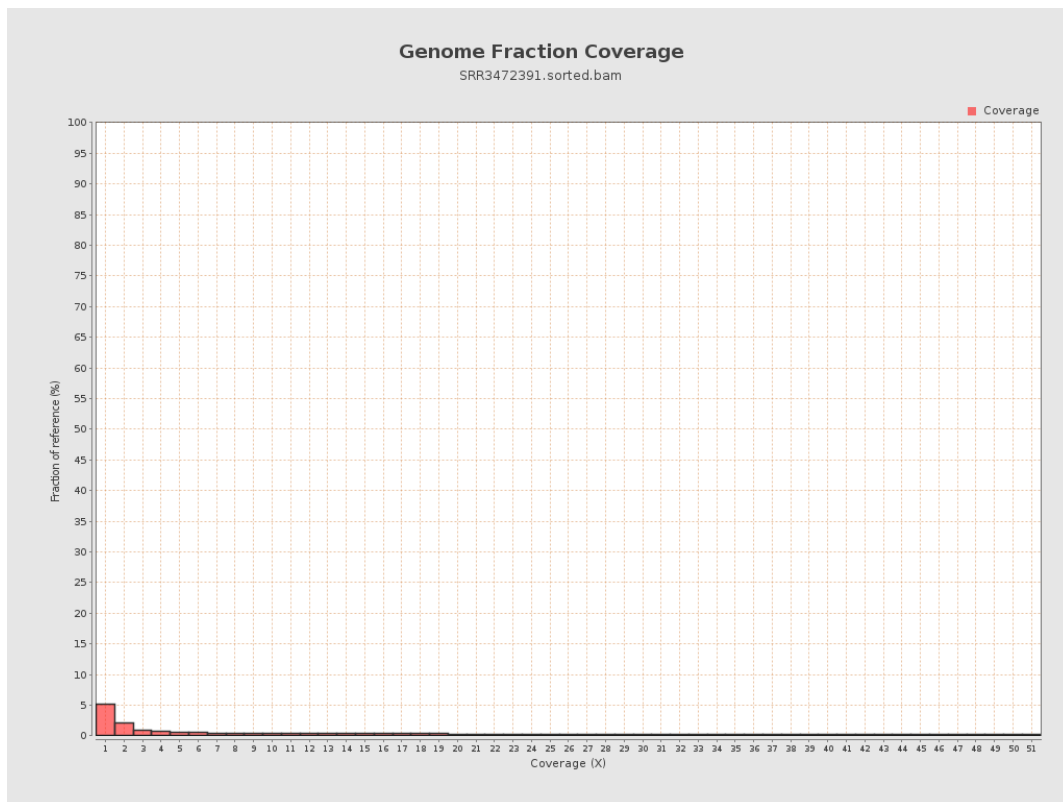
4. Results : Coverage Histogram



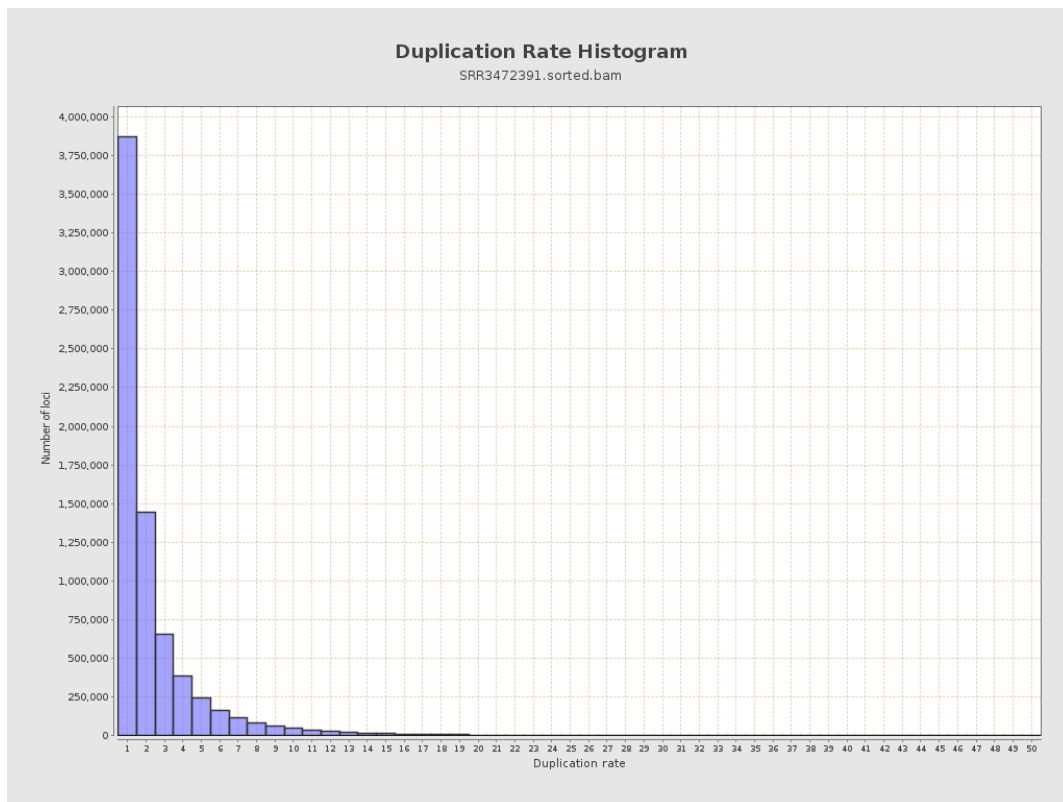
5. Results : Coverage Histogram (0-50X)



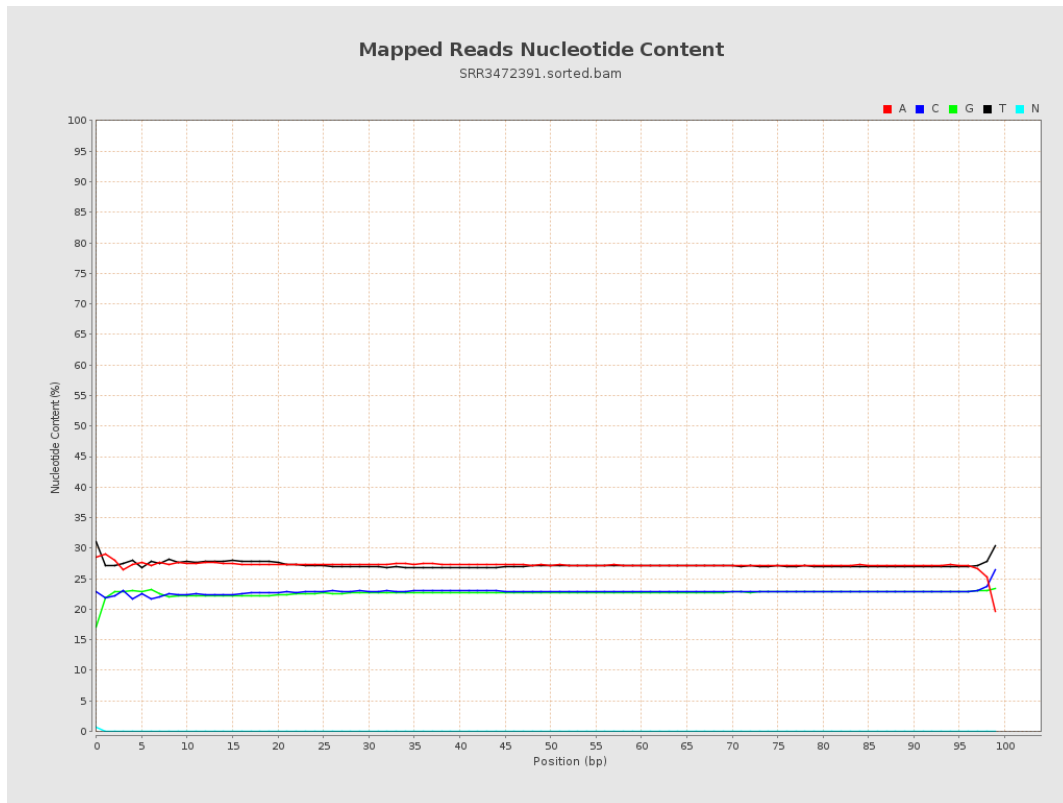
6. Results : Genome Fraction Coverage



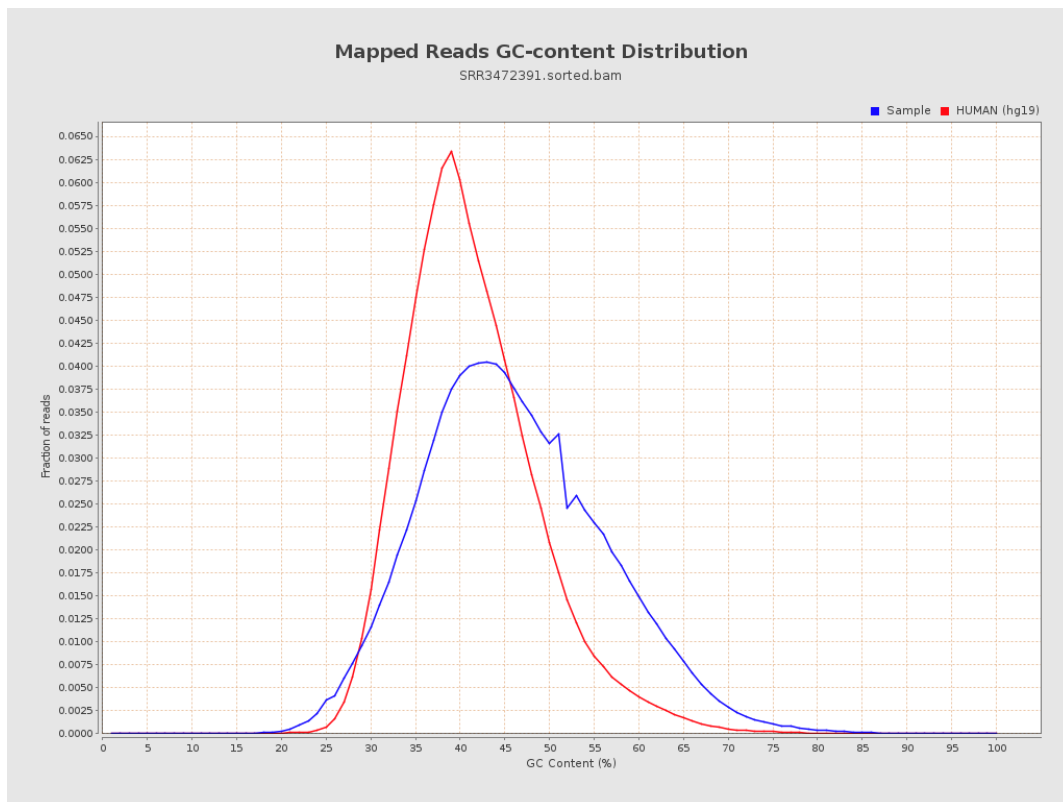
7. Results : Duplication Rate Histogram



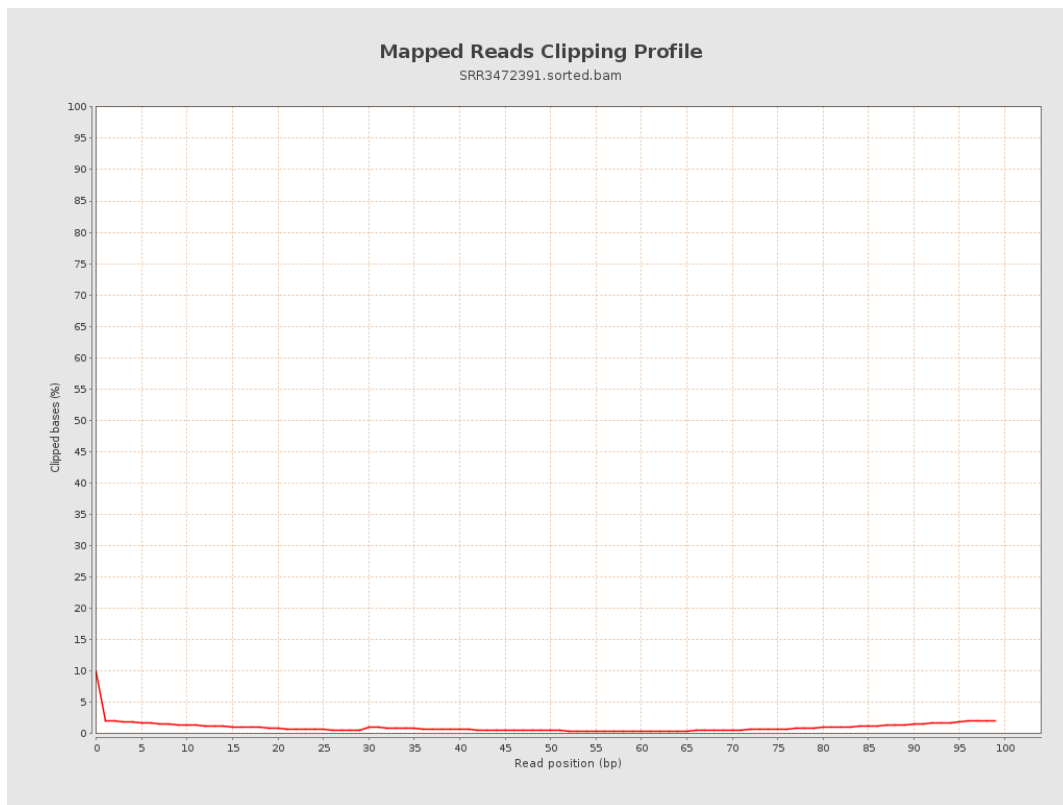
8. Results : Mapped Reads Nucleotide Content



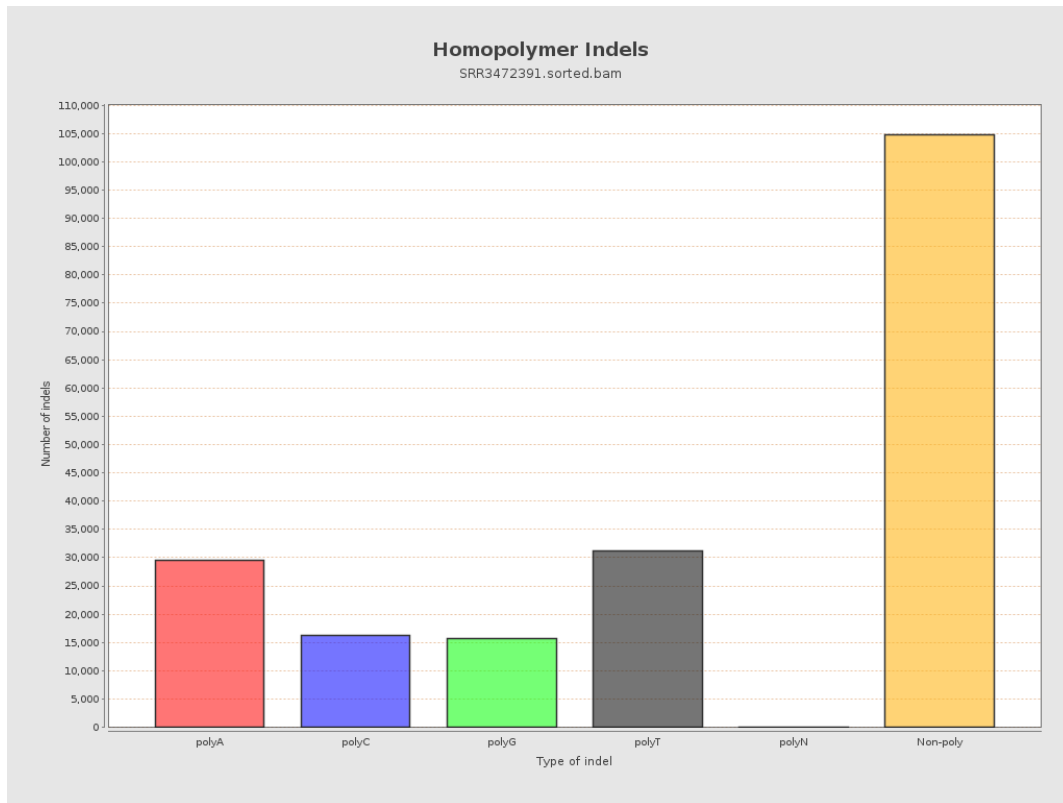
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



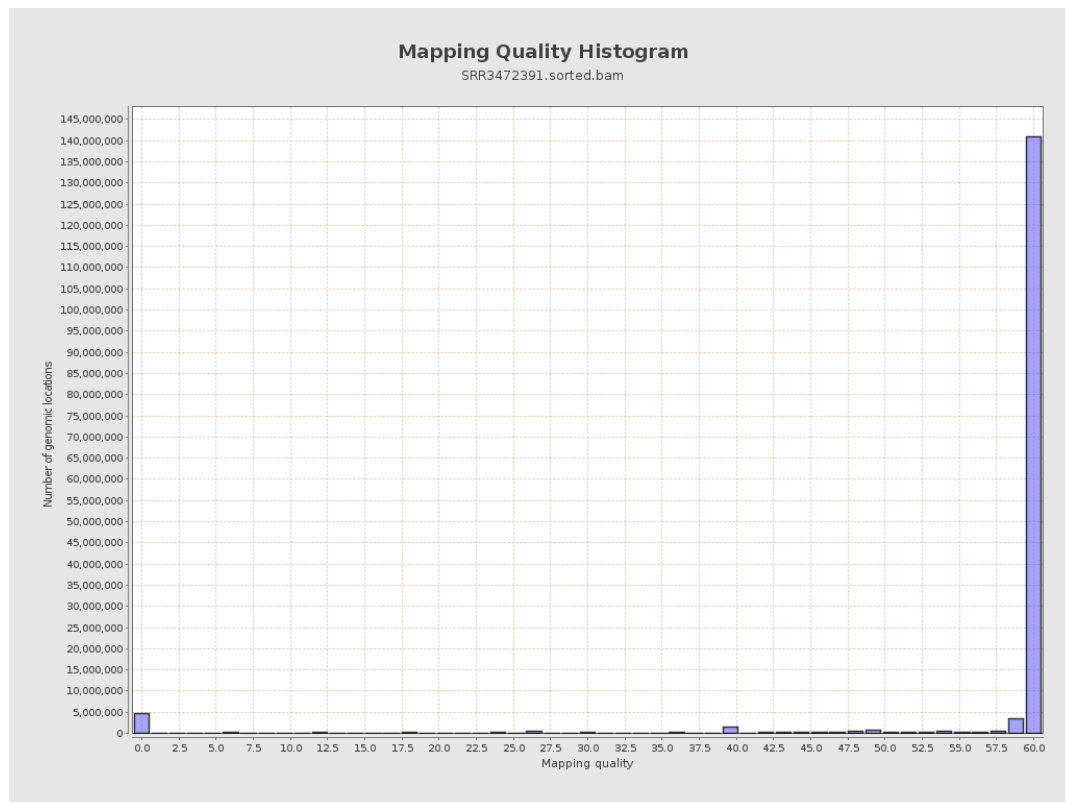
11. Results : Homopolymer Indels



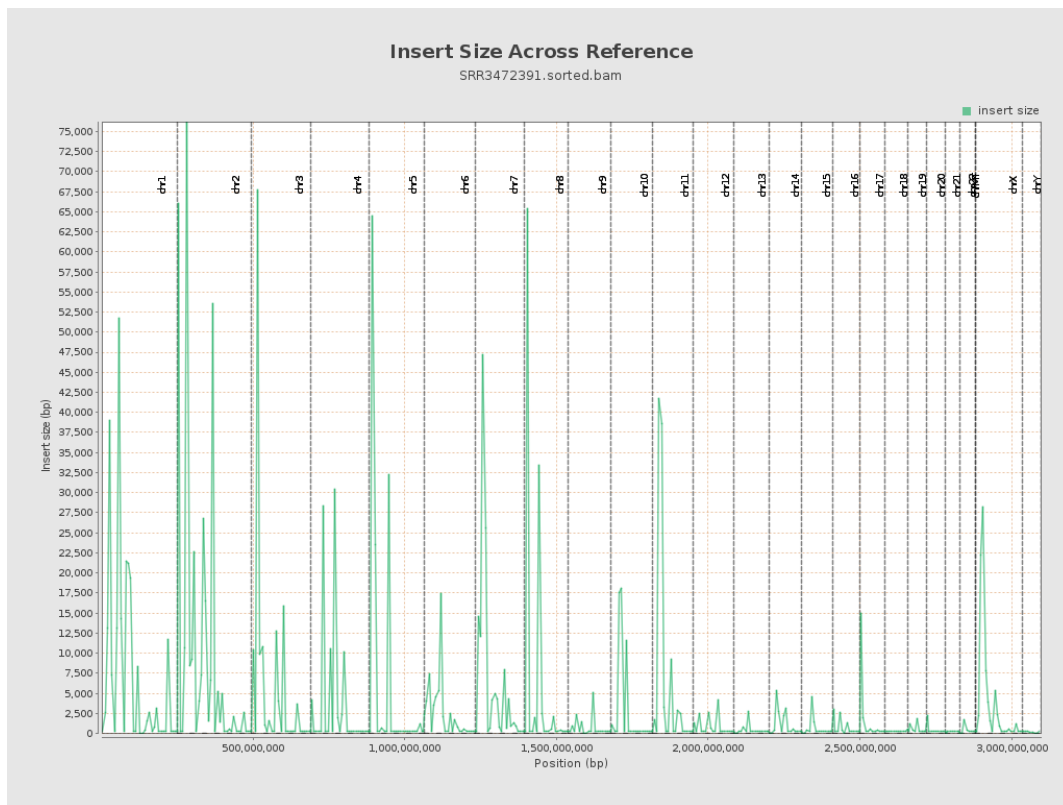
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

