

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 21:36:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046541.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_SRR2046541 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046541_1.fastq.gz SRR2046541_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 21:36:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046541.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	176
Mapped reads	89 / 50.57%
Unmapped reads	87 / 49.43%
Mapped paired reads	89 / 50.57%
Mapped reads, first in pair	64 / 36.36%
Mapped reads, second in pair	25 / 14.2%
Mapped reads, both in pair	50 / 28.41%
Mapped reads, singletons	39 / 22.16%
Secondary alignments	0
Supplementary alignments	1 / 0.57%
Read min/max/mean length	40 / 100 / 100.23
Duplicated reads (estimated)	5 / 2.84%
Duplication rate	5.88%
Clipped reads	28 / 15.91%

2.2. ACGT Content

Number/percentage of A's	2,307 / 27.69%
Number/percentage of C's	1,833 / 22%
Number/percentage of T's	2,530 / 30.36%
Number/percentage of G's	1,662 / 19.95%
Number/percentage of N's	0 / 0%

GC Percentage	41.95%
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2.3. Coverage

Mean	0
Standard Deviation	0.0018

2.4. Mapping Quality

Mean Mapping Quality	6.9
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2.5. Insert size

Mean	25,909.61
Standard Deviation	120,731.46
P25/Median/P75	86 / 140 / 174

2.6. Mismatches and indels

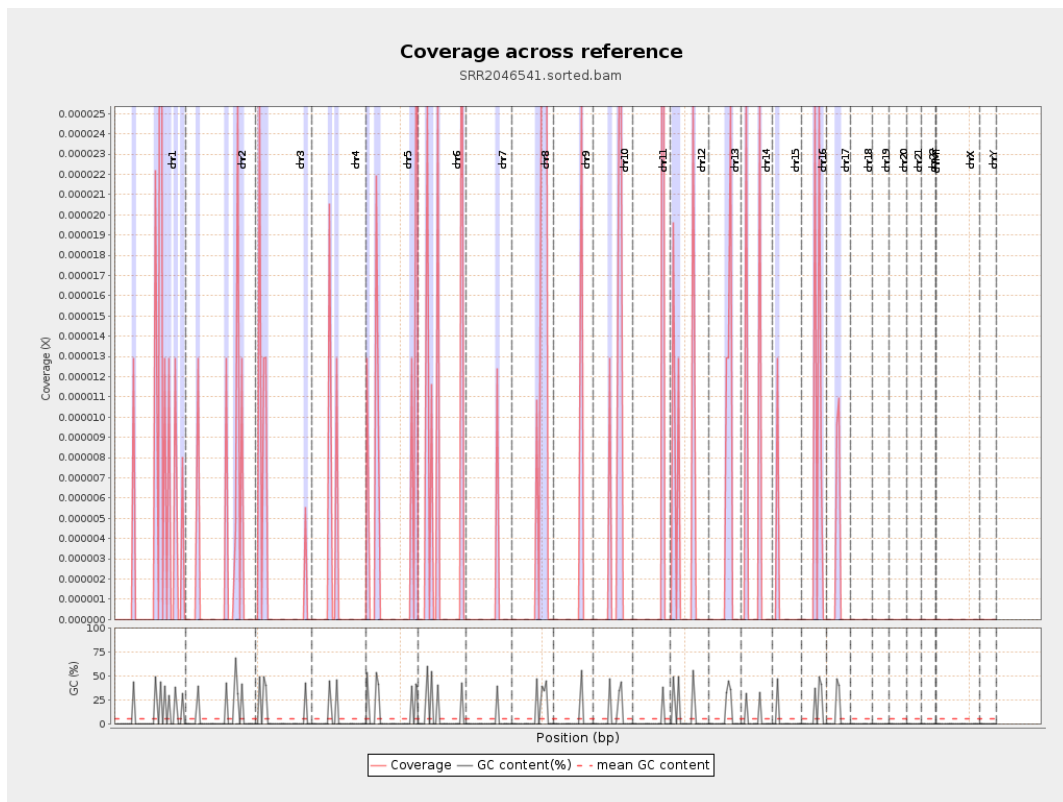
General error rate	0.53%
Mismatches	44

2.7. Chromosome stats

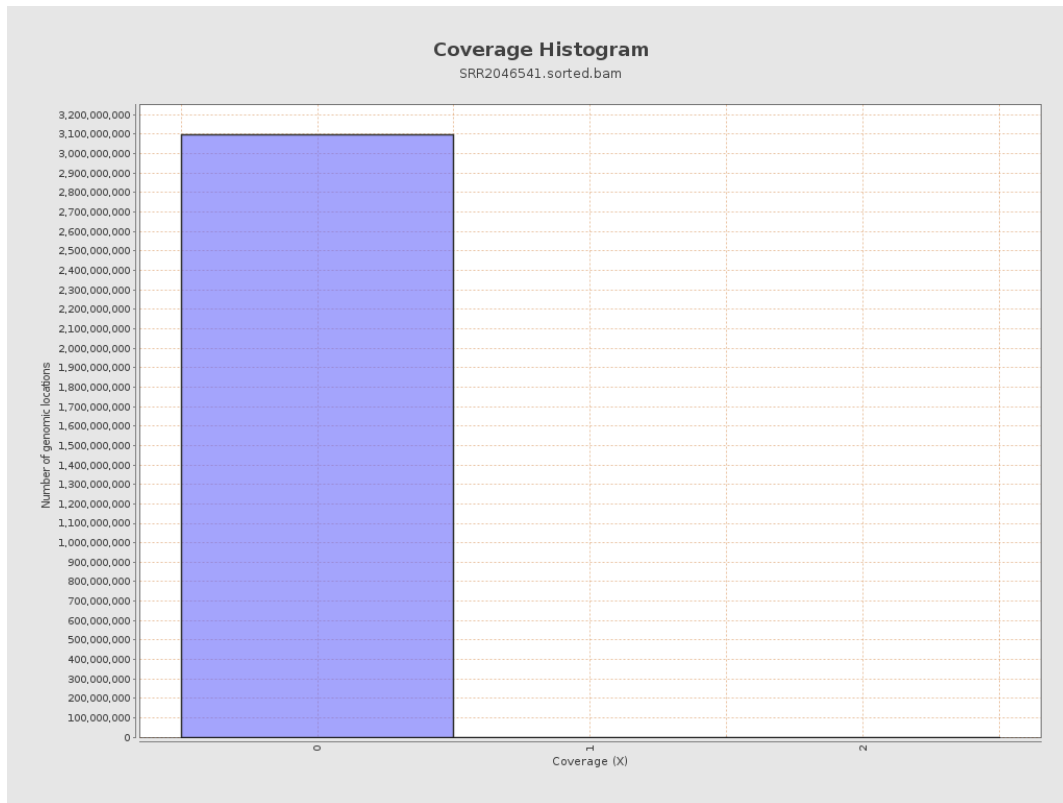
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1155	0	0.0024
chr2	243199373	535	0	0.0016
chr3	198022430	443	0	0.0015
chr4	191154276	259	0	0.0015
chr5	180915260	744	0	0.0024

chr6	171115067	790	0	0.0024
chr7	159138663	96	0	0.0008
chr8	146364022	1241	0	0.0034
chr9	141213431	200	0	0.0016
chr10	135534747	497	0	0.0019
chr11	135006516	400	0	0.0017
chr12	133851895	452	0	0.0021
chr13	115169878	397	0	0.0019
chr14	107349540	406	0	0.0022
chr15	102531392	100	0	0.001
chr16	90354753	457	0	0.0029
chr17	81195210	160	0	0.0014
chr18	78077248	0	0	0
chr19	59128983	0	0	0
chr20	63025520	0	0	0
chr21	48129895	0	0	0
chr22	51304566	0	0	0
chrMT	16571	0	0	0
chrX	155270560	0	0	0
chrY	59373566	0	0	0

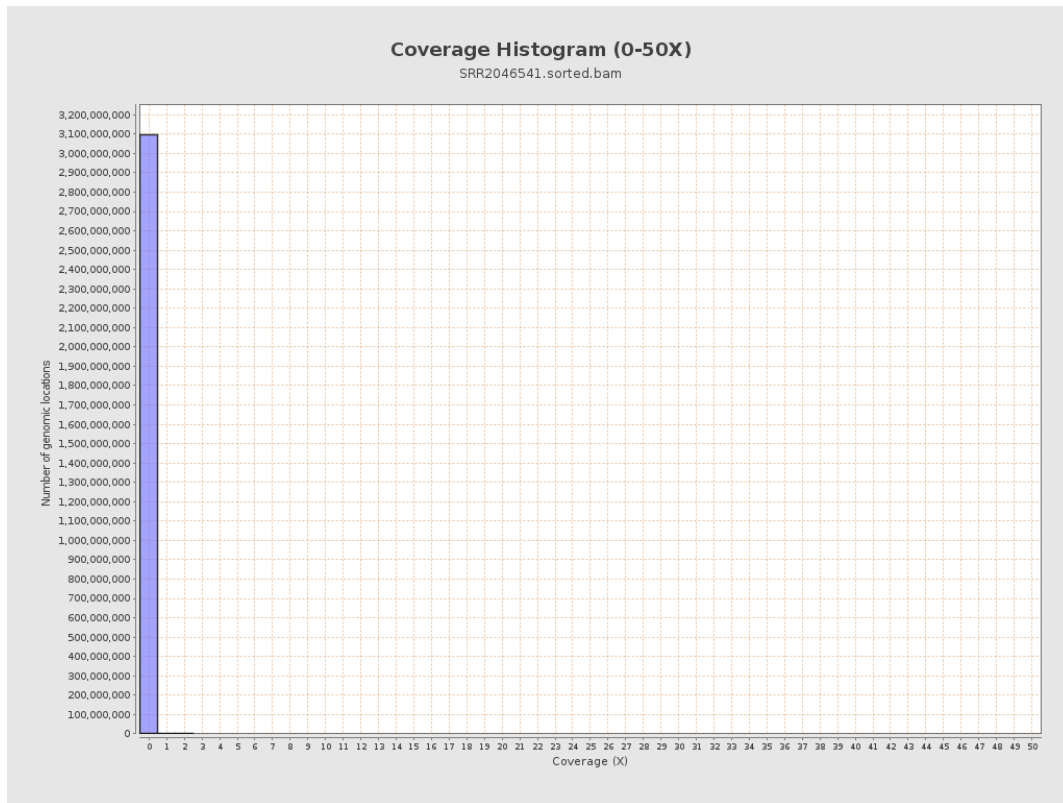
3. Results : Coverage across reference



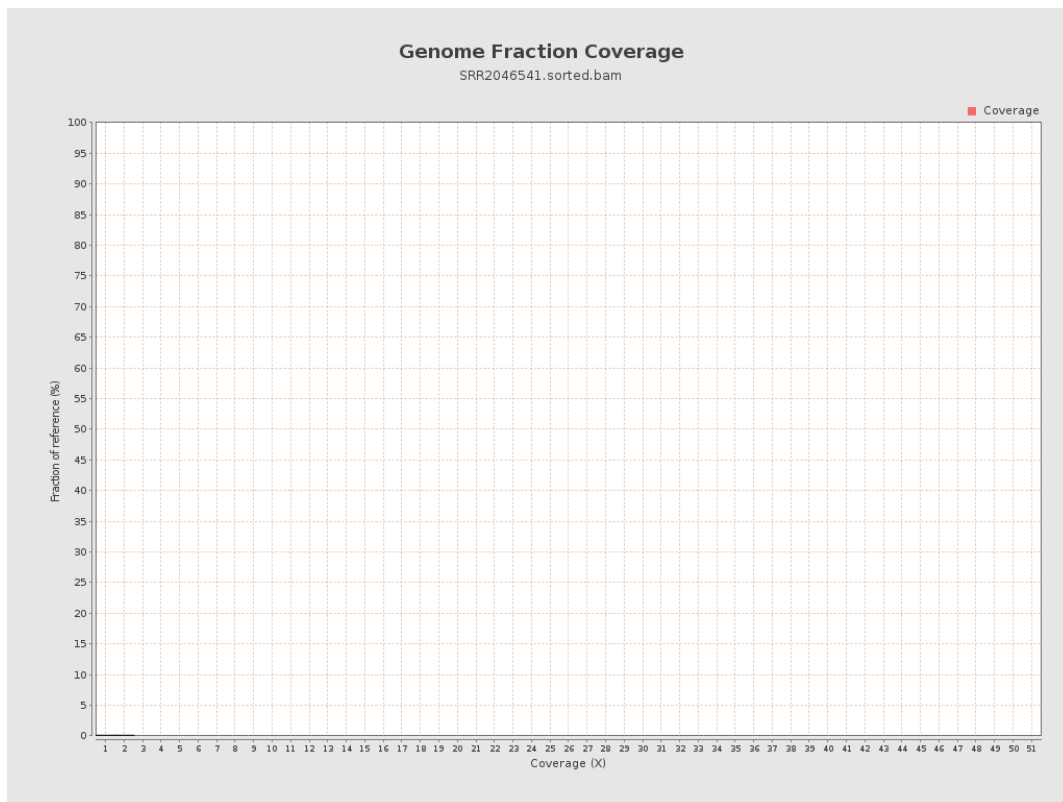
4. Results : Coverage Histogram



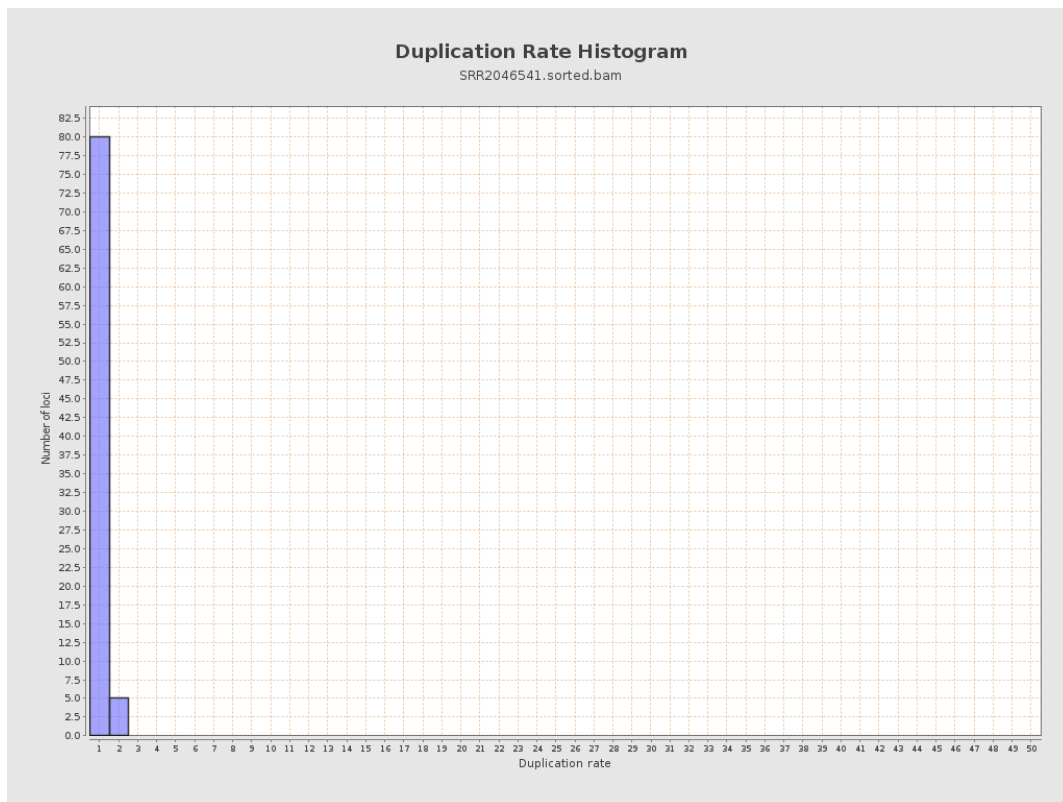
5. Results : Coverage Histogram (0-50X)



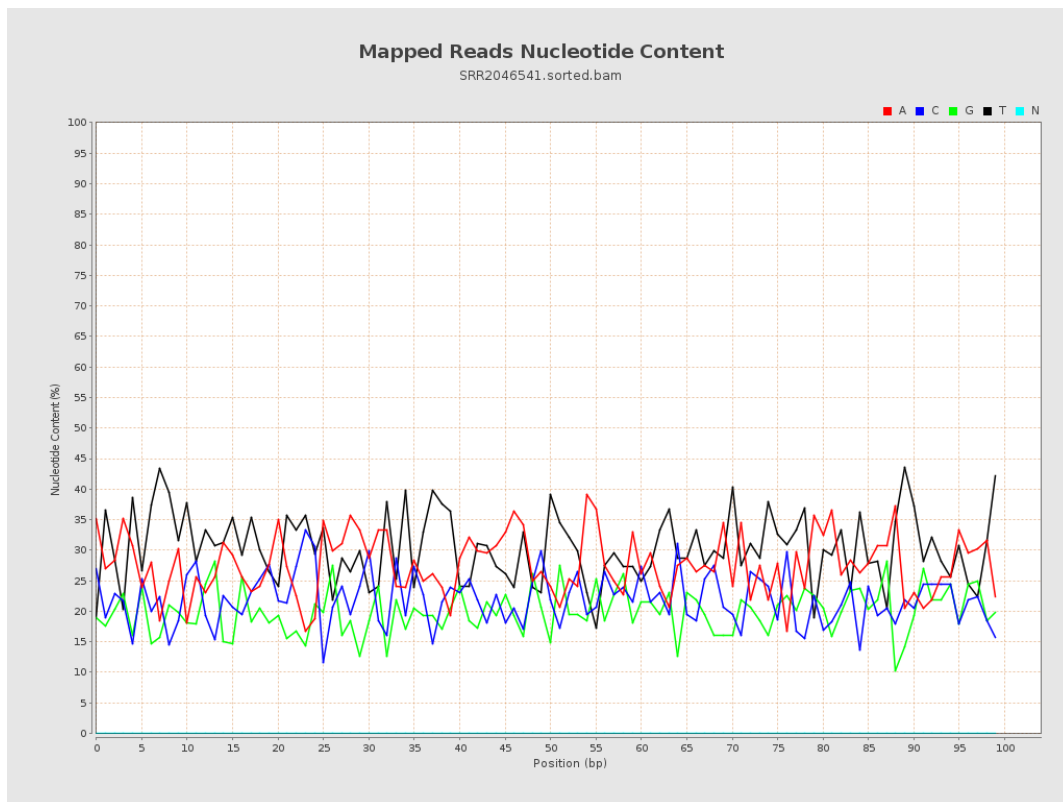
6. Results : Genome Fraction Coverage



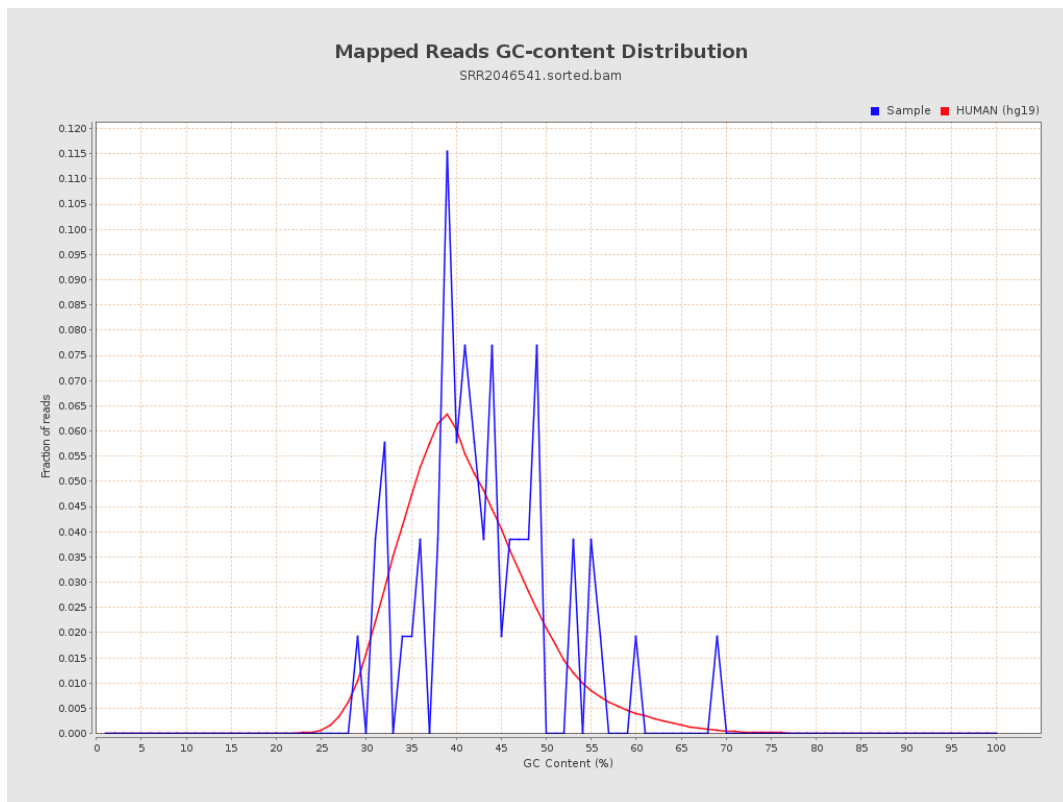
7. Results : Duplication Rate Histogram



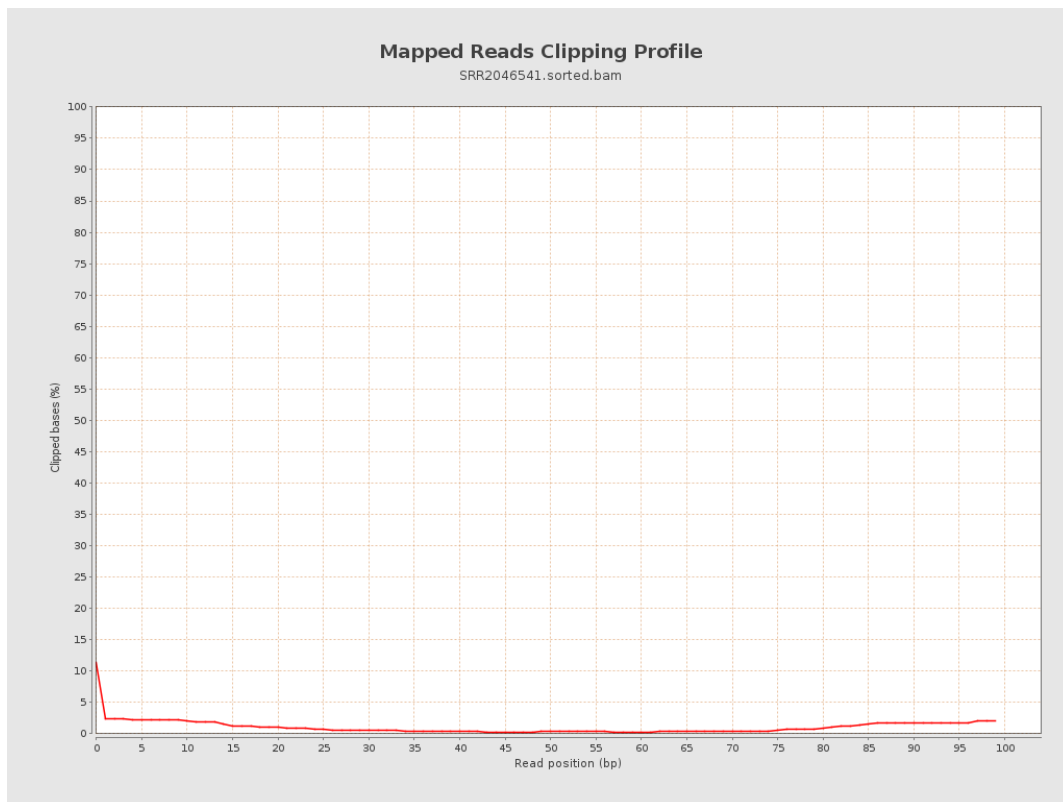
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



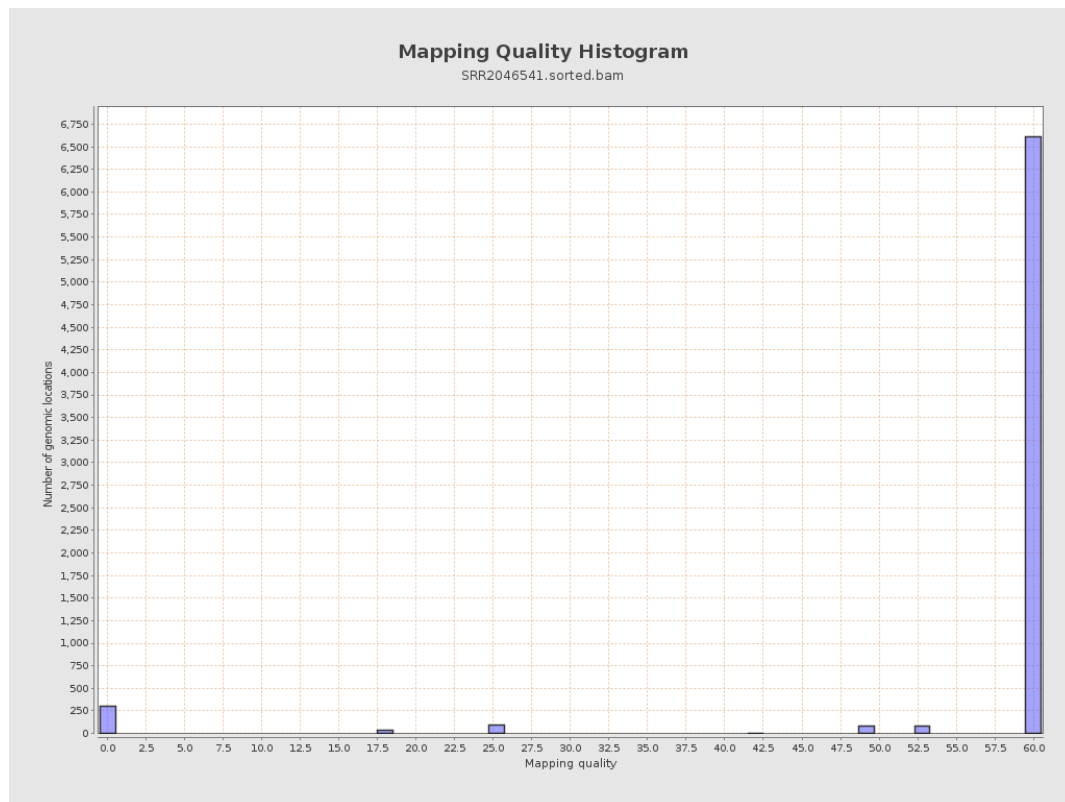
10. Results : Mapped Reads Clipping Profile



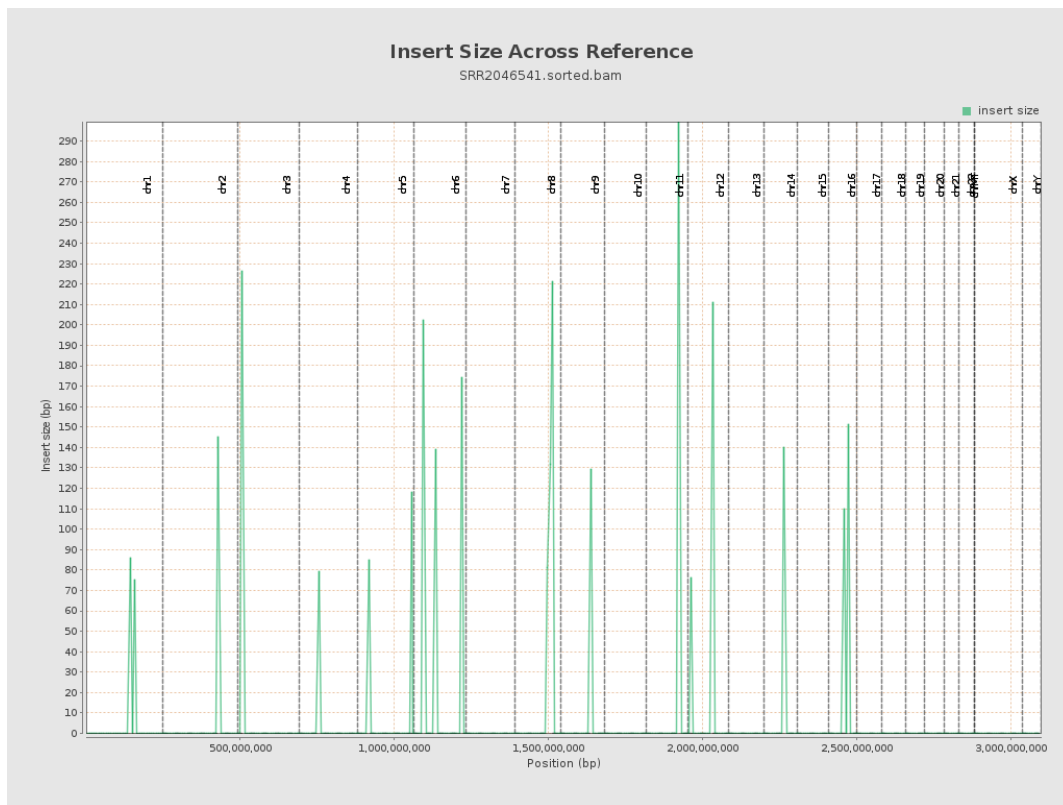
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

