

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:27:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504738.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_SRR504738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:27:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,130,902
Mapped reads	1,893,638 / 88.87%
Unmapped reads	237,264 / 11.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	313,877 / 14.73%
Duplication rate	8.28%
Clipped reads	2,905 / 0.14%

2.2. ACGT Content

Number/percentage of A's	17,510,663 / 28.9%
Number/percentage of C's	12,167,741 / 20.08%
Number/percentage of T's	18,563,262 / 30.64%
Number/percentage of G's	12,348,853 / 20.38%
Number/percentage of N's	87 / 0%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0196
Standard Deviation	0.852

2.4. Mapping Quality

Mean Mapping Quality	8.07
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2.5. Mismatches and indels

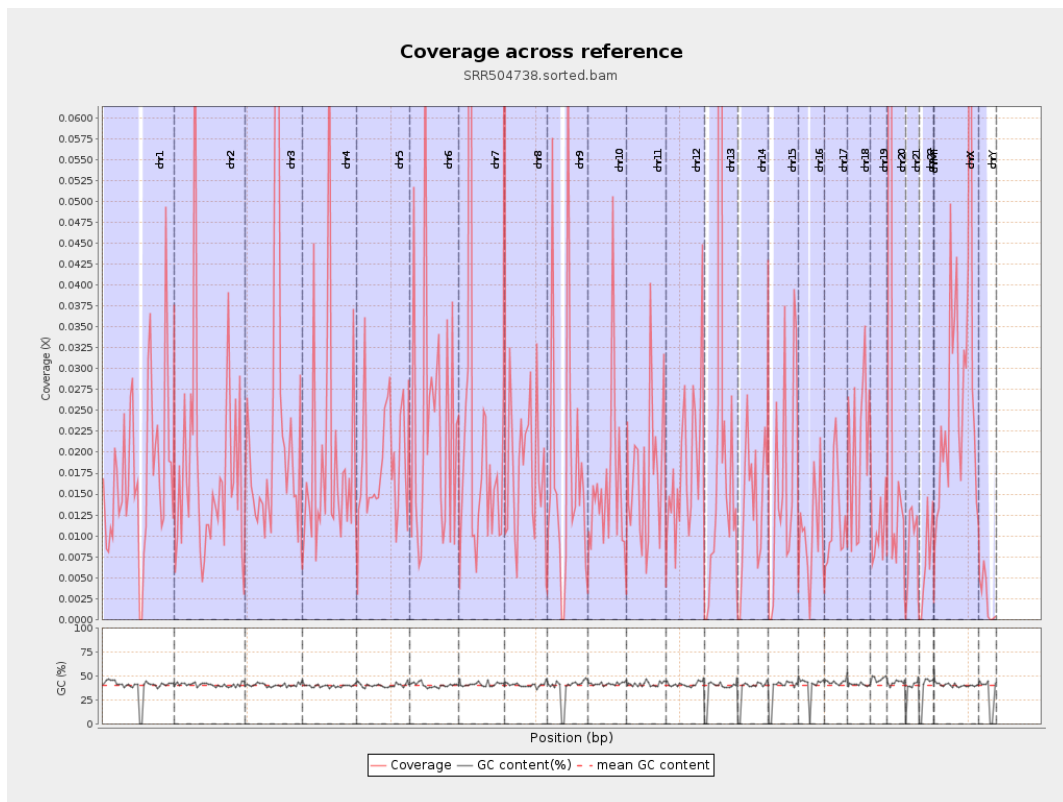
General error rate	0.05%
Mismatches	27,943

2.6. Chromosome stats

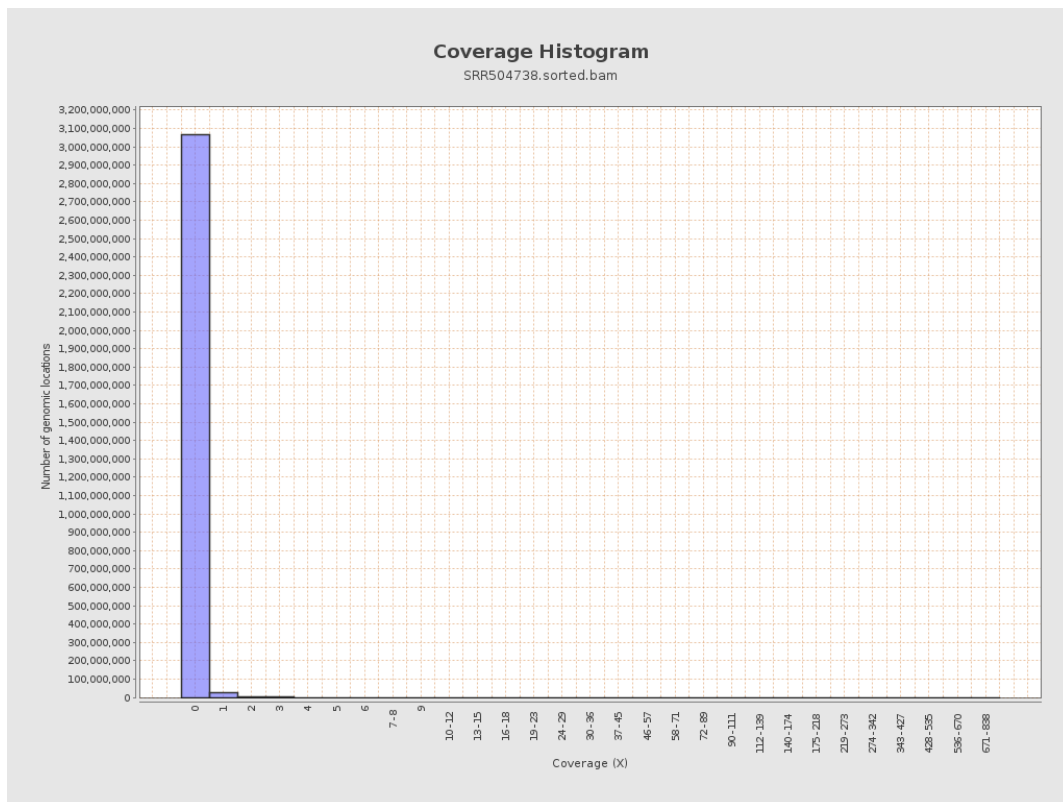
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4276460	0.0172	0.2627
chr2	243199373	4316954	0.0178	0.4253
chr3	198022430	4322518	0.0218	0.5068
chr4	191154276	3663290	0.0192	0.4644
chr5	180915260	3370554	0.0186	0.2399
chr6	171115067	4033532	0.0236	0.3993
chr7	159138663	3601410	0.0226	0.9596
chr8	146364022	2627450	0.018	0.2881
chr9	141213431	2569564	0.0182	0.5575
chr10	135534747	2149142	0.0159	0.2435
chr11	135006516	2330578	0.0173	0.2517
chr12	133851895	2477534	0.0185	0.3034
chr13	115169878	5254246	0.0456	3.5277
chr14	107349540	1530350	0.0143	0.2165
chr15	102531392	1685088	0.0164	0.3032

chr16	90354753	930684	0.0103	0.1913
chr17	81195210	966122	0.0119	0.2192
chr18	78077248	1647808	0.0211	0.4106
chr19	59128983	644138	0.0109	0.1818
chr20	63025520	2656050	0.0421	2.1813
chr21	48129895	425644	0.0088	0.1358
chr22	51304566	368438	0.0072	0.1241
chrMT	16571	32	0.0019	0.0439
chrX	155270560	4592440	0.0296	0.5825
chrY	59373566	150580	0.0025	0.0585

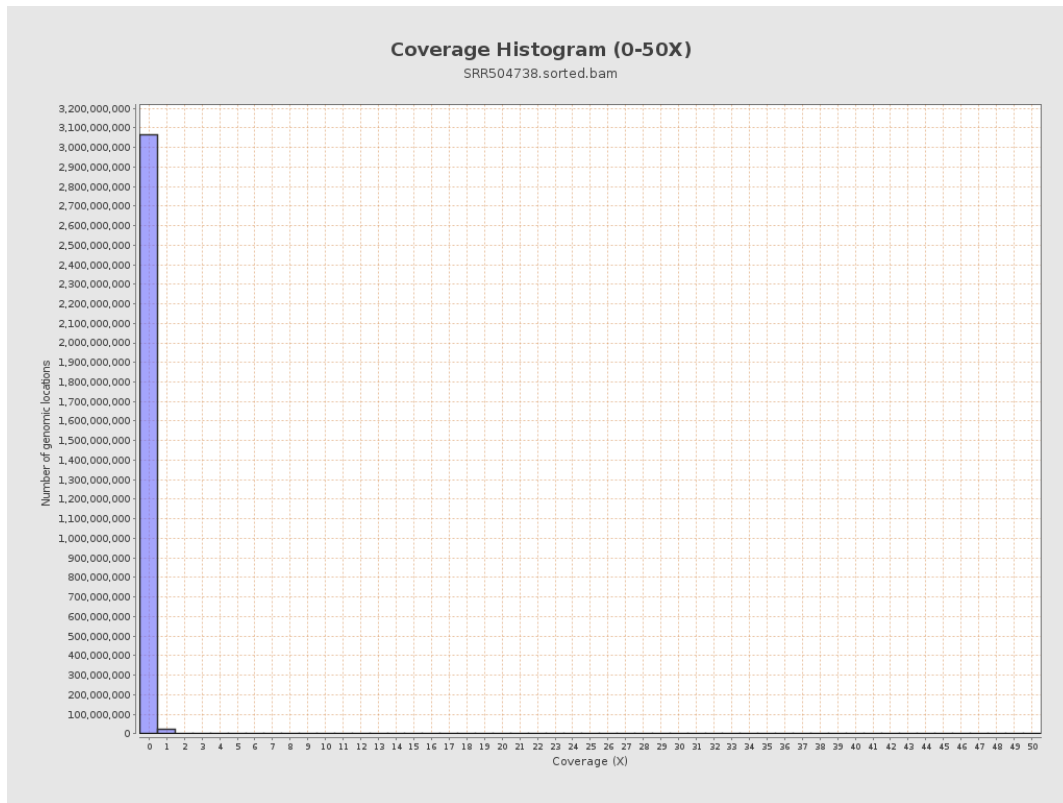
3. Results : Coverage across reference



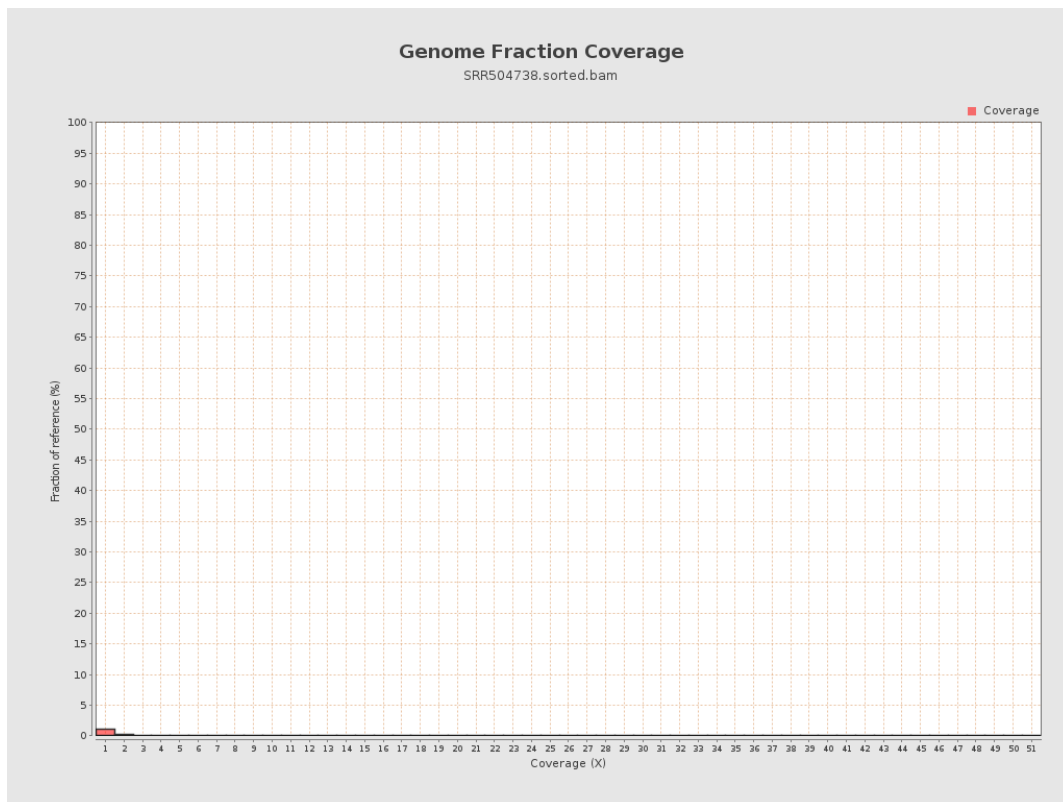
4. Results : Coverage Histogram



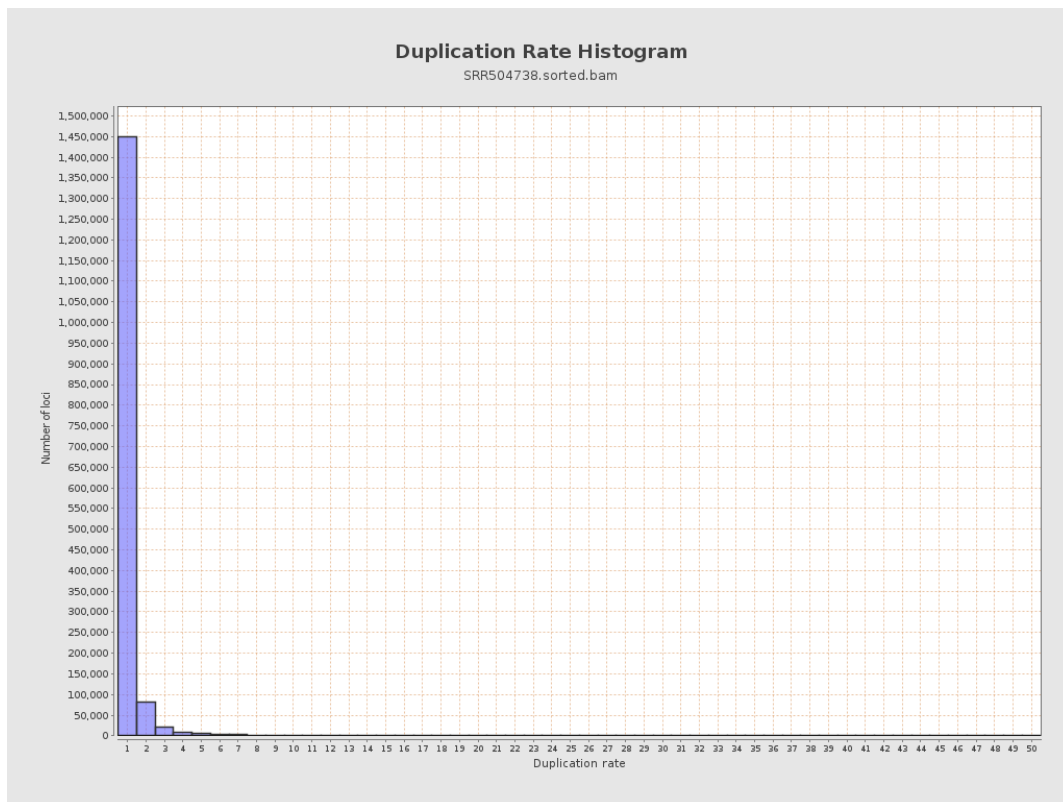
5. Results : Coverage Histogram (0-50X)



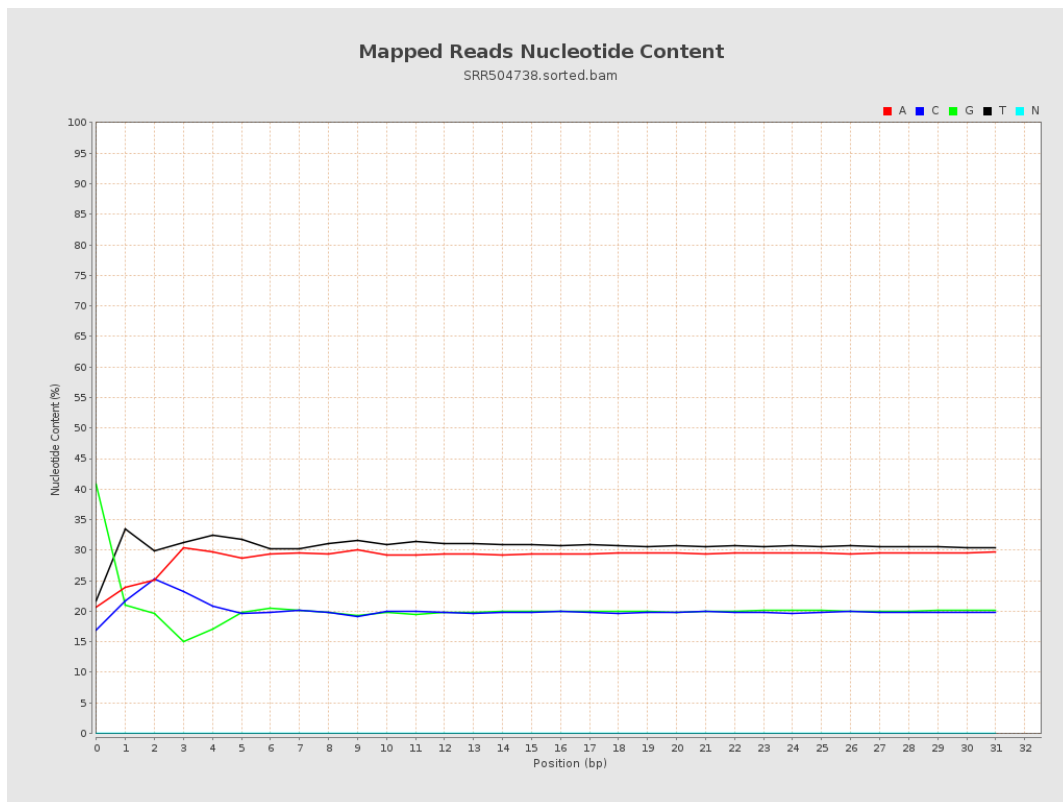
6. Results : Genome Fraction Coverage



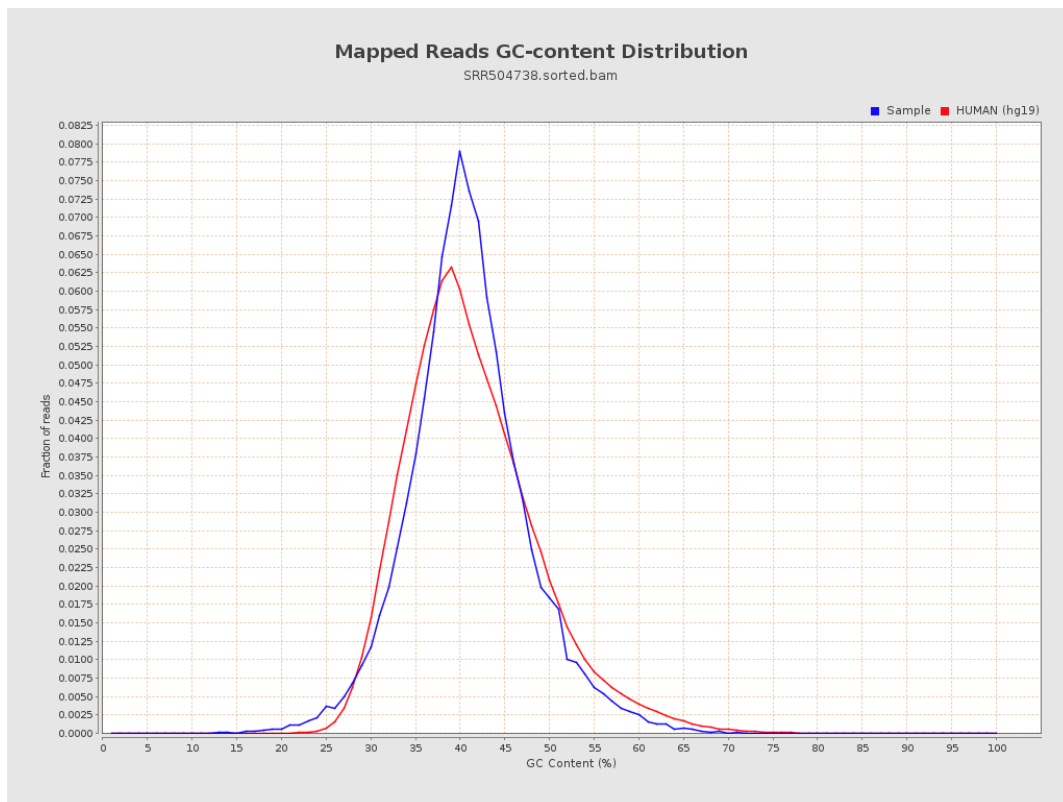
7. Results : Duplication Rate Histogram



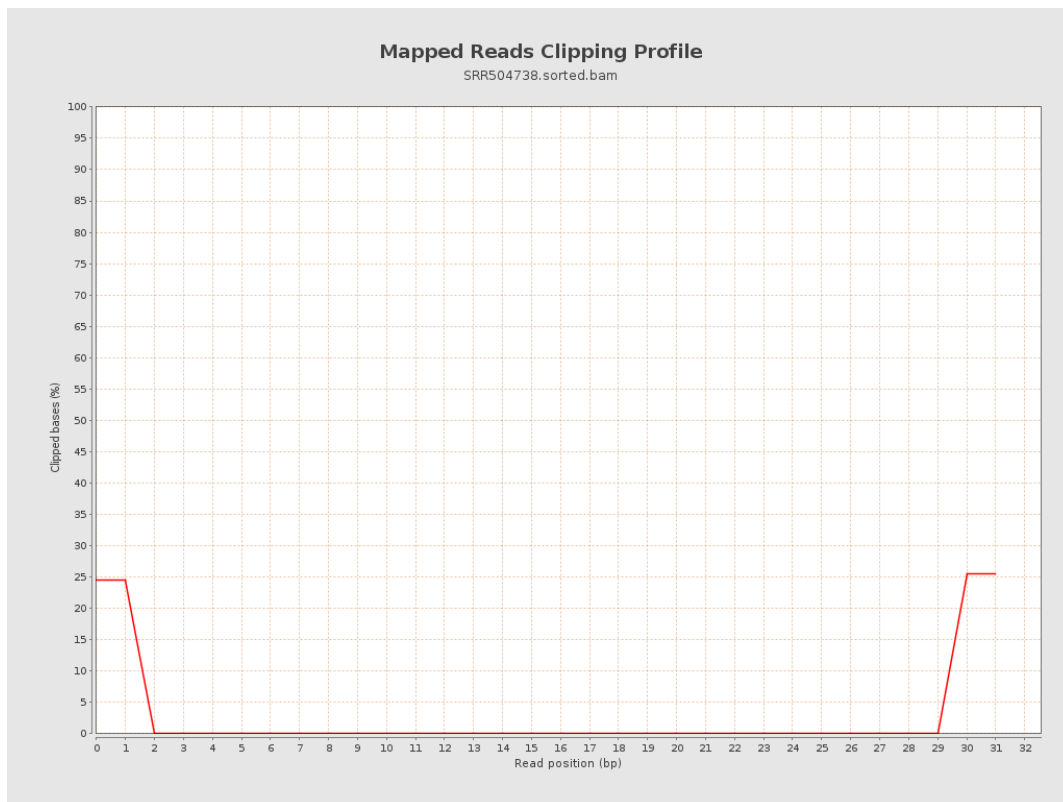
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

