

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:30:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504743.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_SRR504743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:30:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,681,635
Mapped reads	1,534,966 / 91.28%
Unmapped reads	146,669 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	5,696 / 0.34%
Duplication rate	0.37%
Clipped reads	2,592 / 0.15%

2.2. ACGT Content

Number/percentage of A's	14,238,363 / 28.99%
Number/percentage of C's	9,971,102 / 20.3%
Number/percentage of T's	14,976,123 / 30.49%
Number/percentage of G's	9,927,879 / 20.21%
Number/percentage of N's	261 / 0%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0159
Standard Deviation	0.1281

2.4. Mapping Quality

Mean Mapping Quality	9.31
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2.5. Mismatches and indels

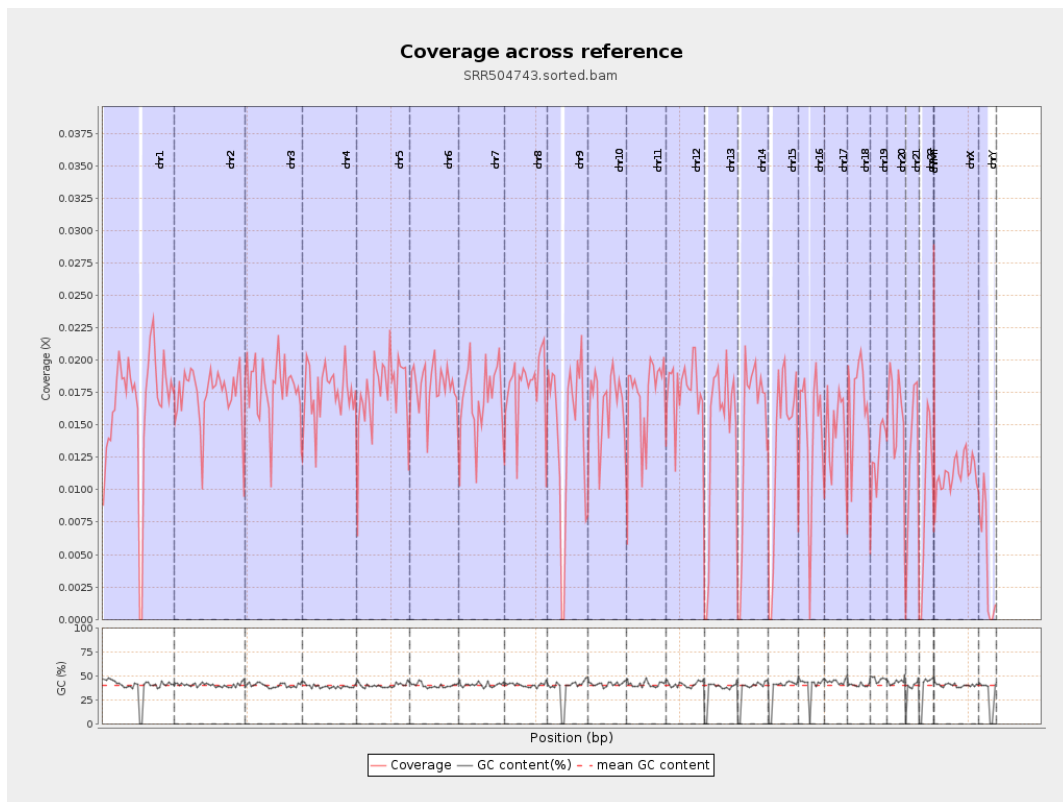
General error rate	0.06%
Mismatches	28,449

2.6. Chromosome stats

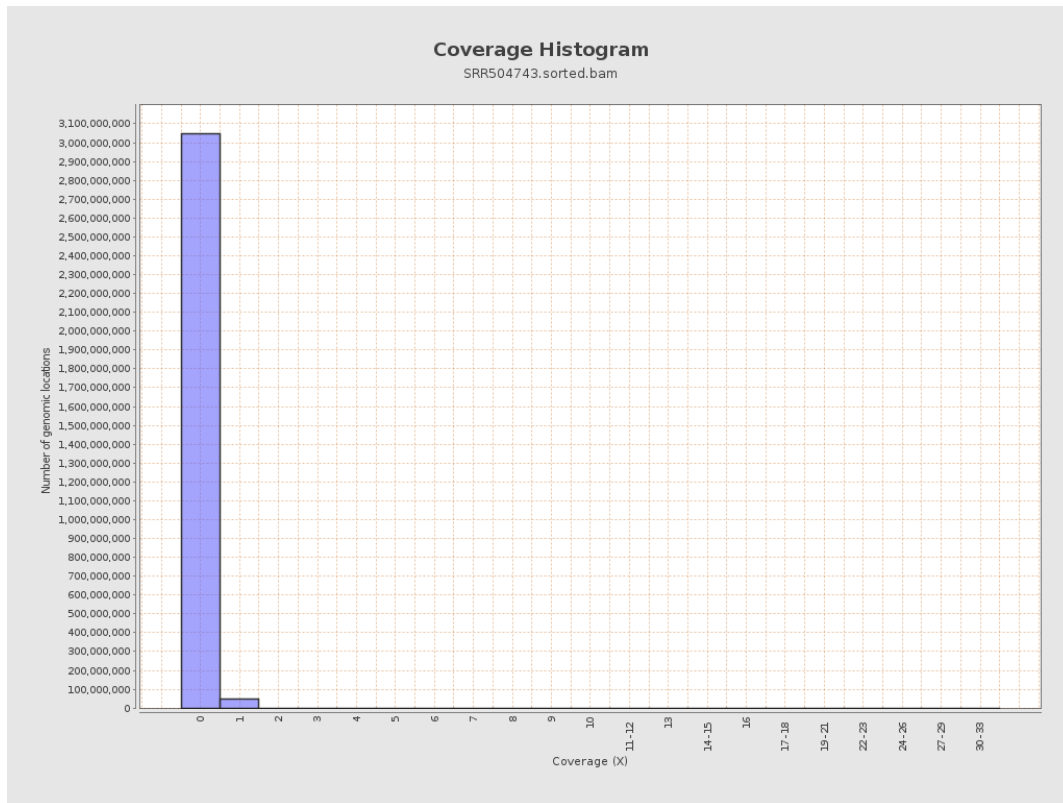
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4098162	0.0164	0.1326
chr2	243199373	4231264	0.0174	0.1335
chr3	198022430	3546668	0.0179	0.1354
chr4	191154276	3340006	0.0175	0.1339
chr5	180915260	3240626	0.0179	0.1358
chr6	171115067	3066634	0.0179	0.1362
chr7	159138663	2709172	0.017	0.1327
chr8	146364022	2627478	0.018	0.1375
chr9	141213431	2055394	0.0146	0.1221
chr10	135534747	2237368	0.0165	0.1321
chr11	135006516	2340368	0.0173	0.1331
chr12	133851895	2375166	0.0177	0.1353
chr13	115169878	1646442	0.0143	0.1214
chr14	107349540	1587606	0.0148	0.1238
chr15	102531392	1402708	0.0137	0.119

chr16	90354753	1266392	0.014	0.12
chr17	81195210	1164832	0.0143	0.1213
chr18	78077248	1351648	0.0173	0.1333
chr19	59128983	746704	0.0126	0.1151
chr20	63025520	998902	0.0158	0.1273
chr21	48129895	593422	0.0123	0.1124
chr22	51304566	474094	0.0092	0.0974
chrMT	16571	480	0.029	0.1677
chrX	155270560	1747116	0.0113	0.1071
chrY	59373566	265076	0.0045	0.0677

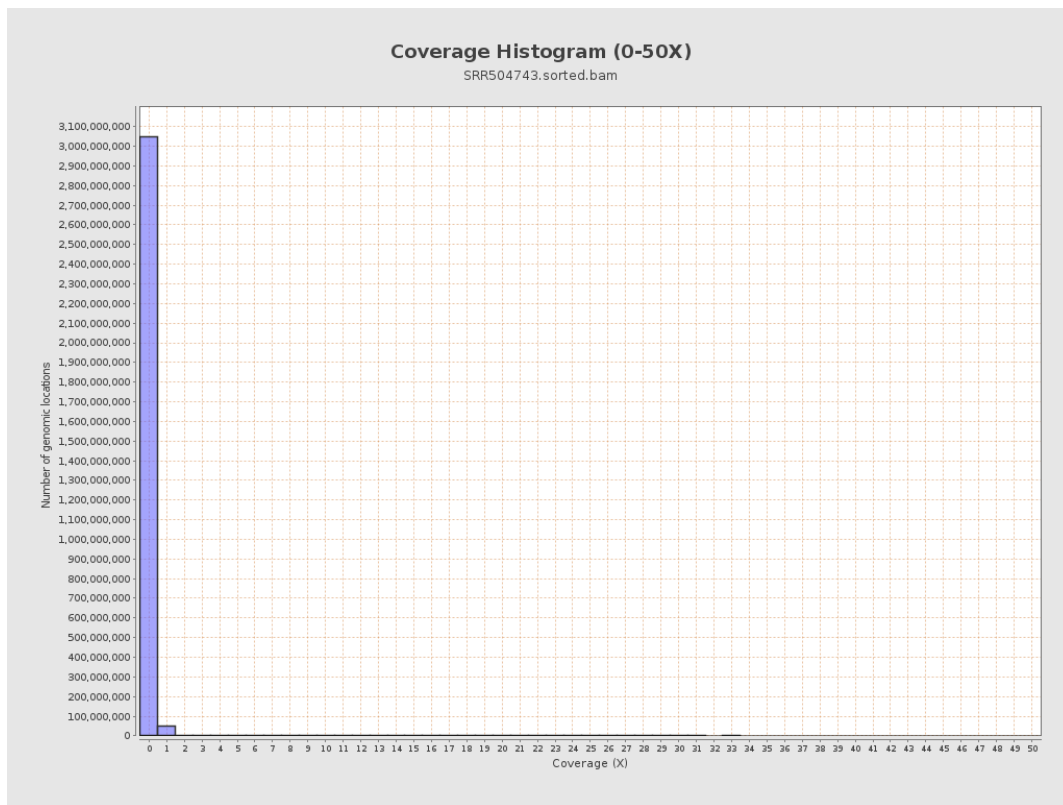
3. Results : Coverage across reference



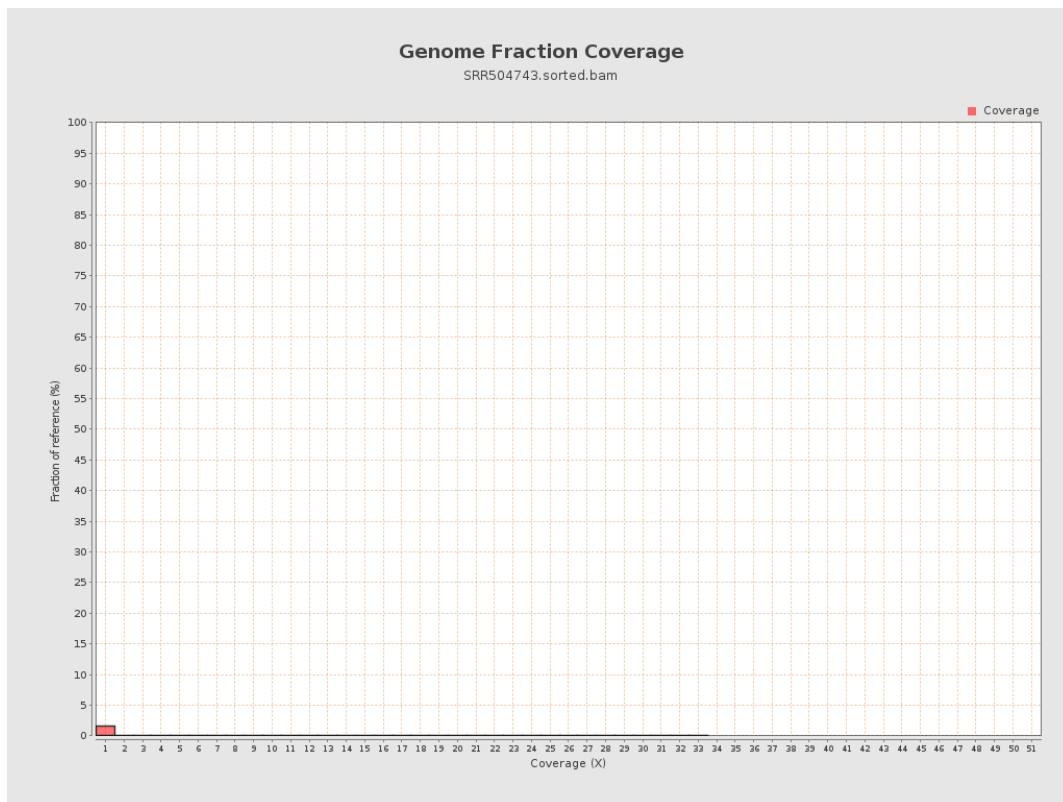
4. Results : Coverage Histogram



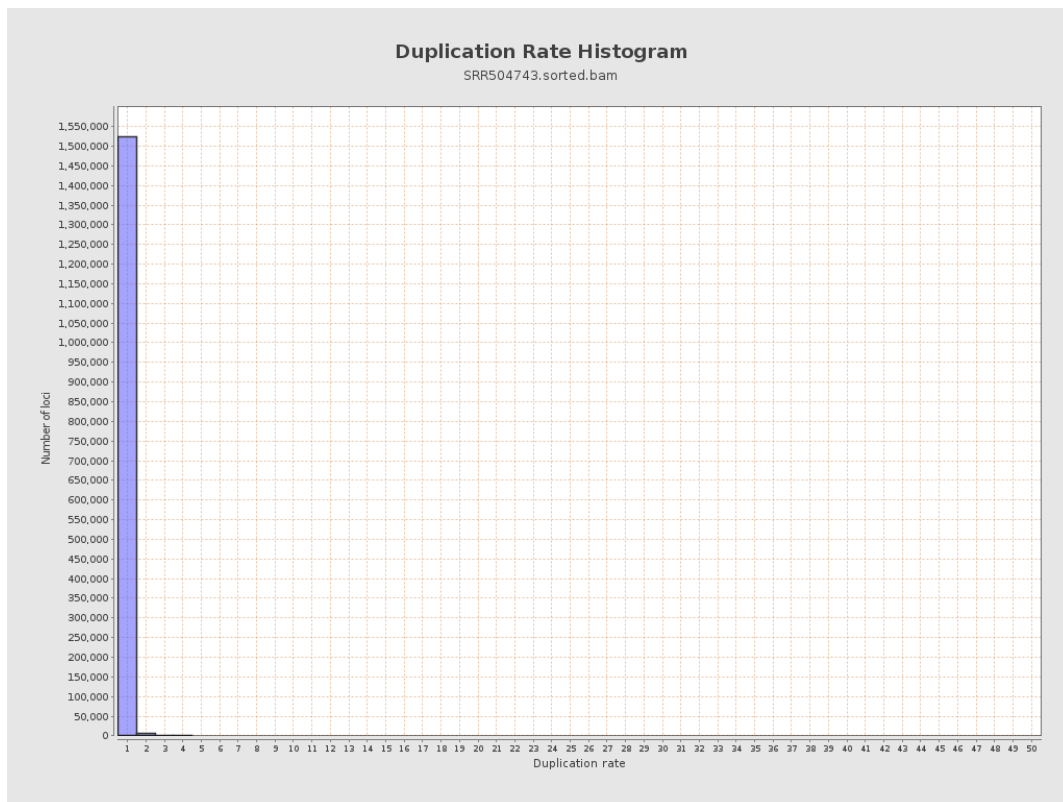
5. Results : Coverage Histogram (0-50X)



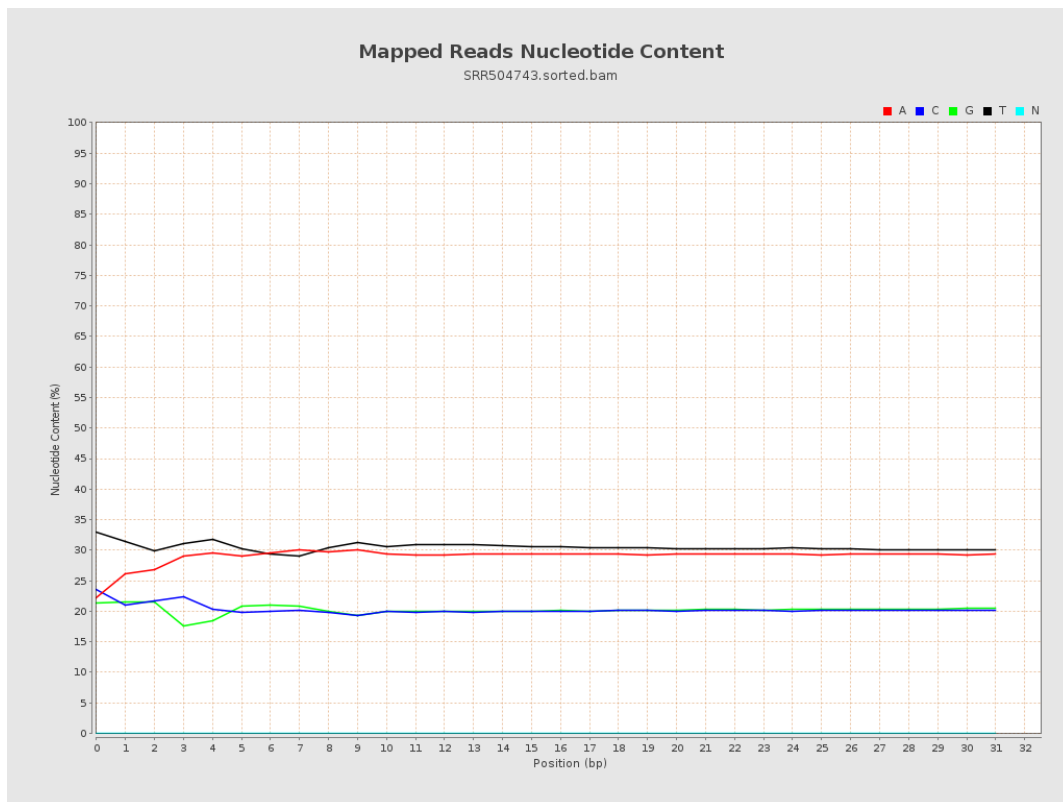
6. Results : Genome Fraction Coverage



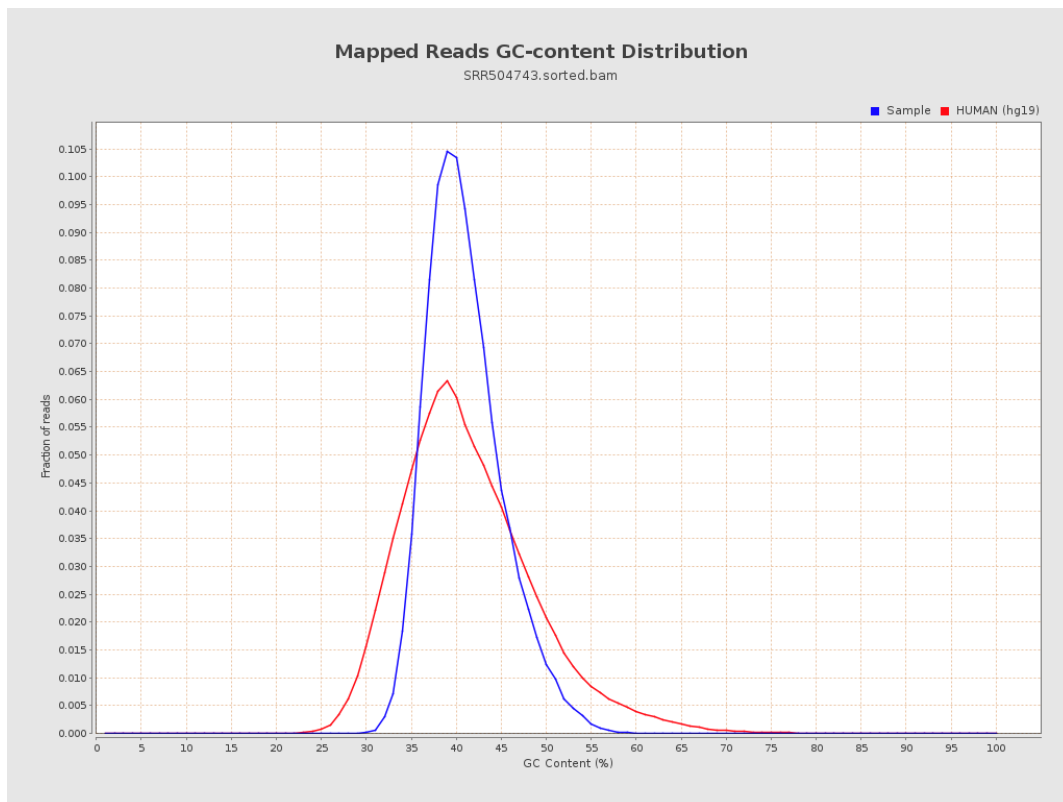
7. Results : Duplication Rate Histogram



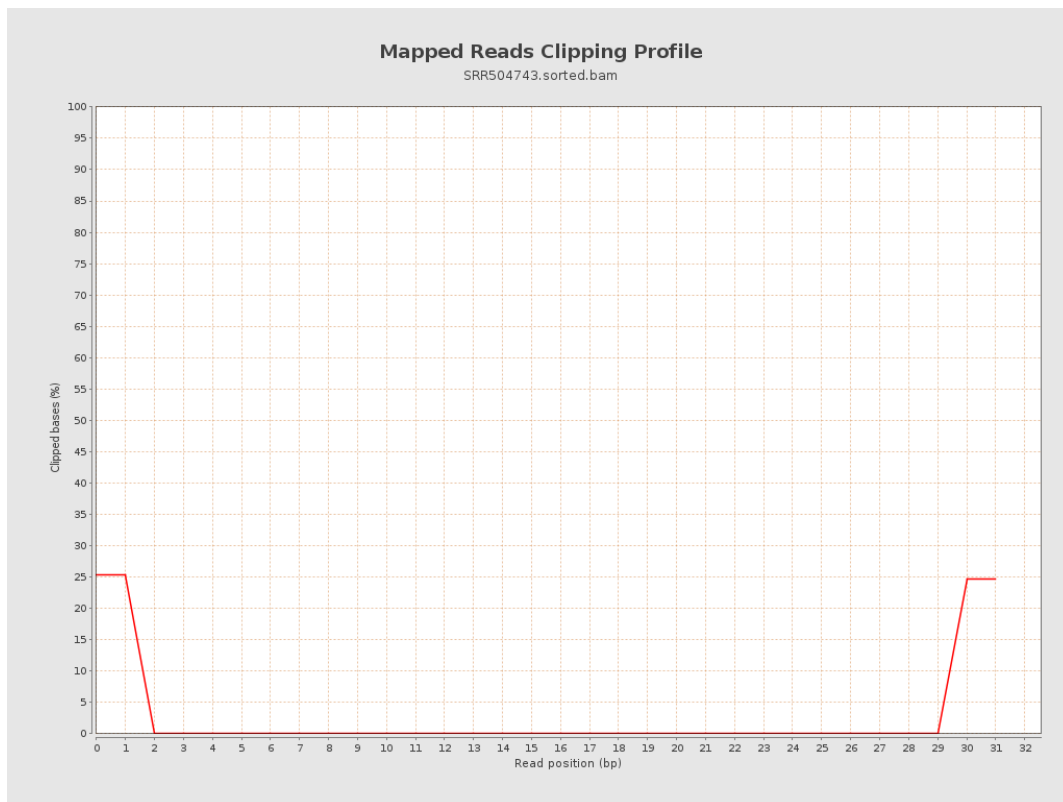
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

