

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:42:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504754.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_SRR504754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:42:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,820,418
Mapped reads	1,654,735 / 90.9%
Unmapped reads	165,683 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	198,605 / 10.91%
Duplication rate	7.54%
Clipped reads	2,628 / 0.14%

2.2. ACGT Content

Number/percentage of A's	15,184,691 / 28.68%
Number/percentage of C's	10,783,893 / 20.37%
Number/percentage of T's	16,084,431 / 30.38%
Number/percentage of G's	10,892,918 / 20.57%
Number/percentage of N's	331 / 0%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0171
Standard Deviation	0.4761

2.4. Mapping Quality

Mean Mapping Quality	8.09
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2.5. Mismatches and indels

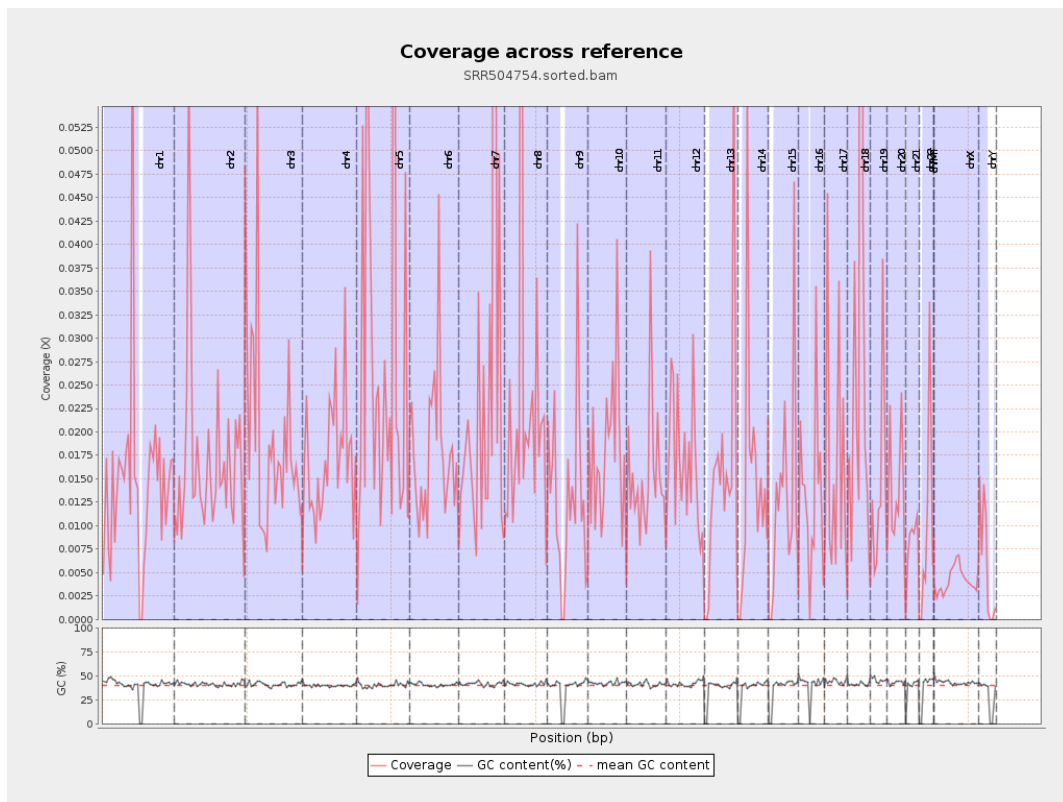
General error rate	0.05%
Mismatches	24,702

2.6. Chromosome stats

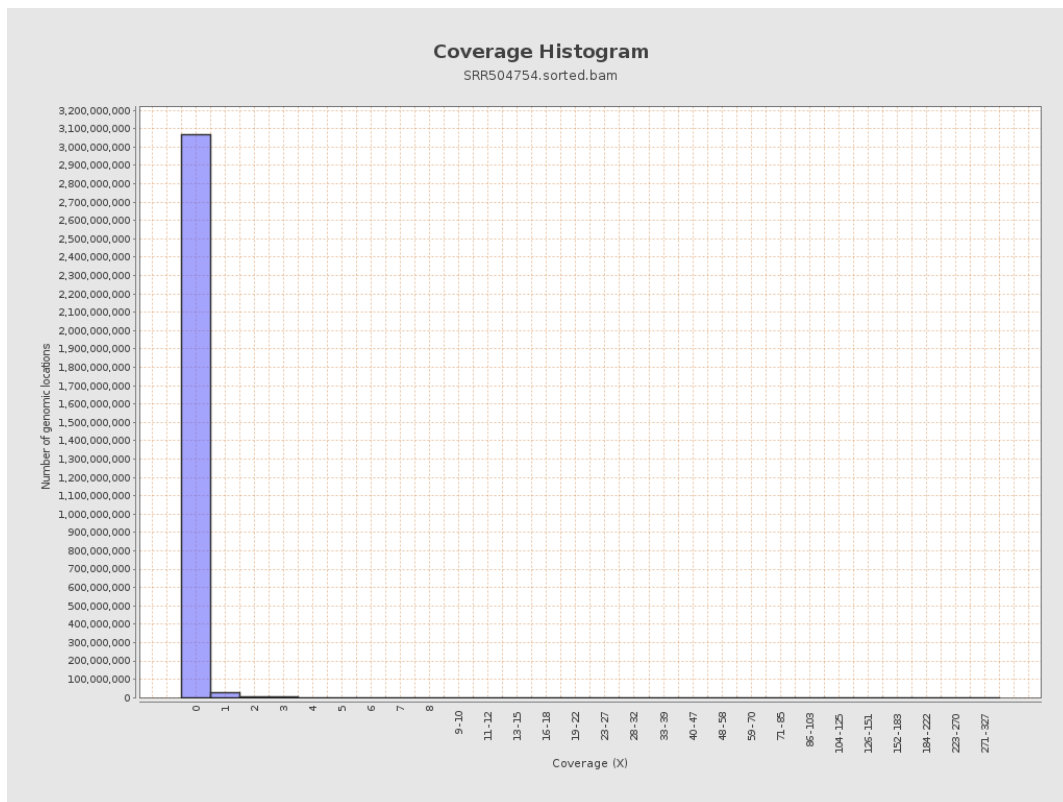
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3704710	0.0149	0.2872
chr2	243199373	4151626	0.0171	0.2837
chr3	198022430	3820978	0.0193	0.377
chr4	191154276	3235774	0.0169	0.2015
chr5	180915260	5123692	0.0283	0.8489
chr6	171115067	3033384	0.0177	0.2142
chr7	159138663	3869804	0.0243	0.7395
chr8	146364022	3558960	0.0243	0.796
chr9	141213431	1883342	0.0133	0.2098
chr10	135534747	2412420	0.0178	0.2909
chr11	135006516	2072630	0.0154	0.2289
chr12	133851895	2233710	0.0167	0.2192
chr13	115169878	1825274	0.0158	0.3832
chr14	107349540	1559912	0.0145	0.294
chr15	102531392	1329866	0.013	0.3236

chr16	90354753	1158412	0.0128	0.2191
chr17	81195210	1294276	0.0159	0.42
chr18	78077248	3144256	0.0403	1.5698
chr19	59128983	779170	0.0132	0.2313
chr20	63025520	868092	0.0138	0.2294
chr21	48129895	392398	0.0082	0.1148
chr22	51304566	494454	0.0096	0.6235
chrMT	16571	32	0.0019	0.0439
chrX	155270560	651040	0.0042	0.0746
chrY	59373566	348052	0.0059	0.0936

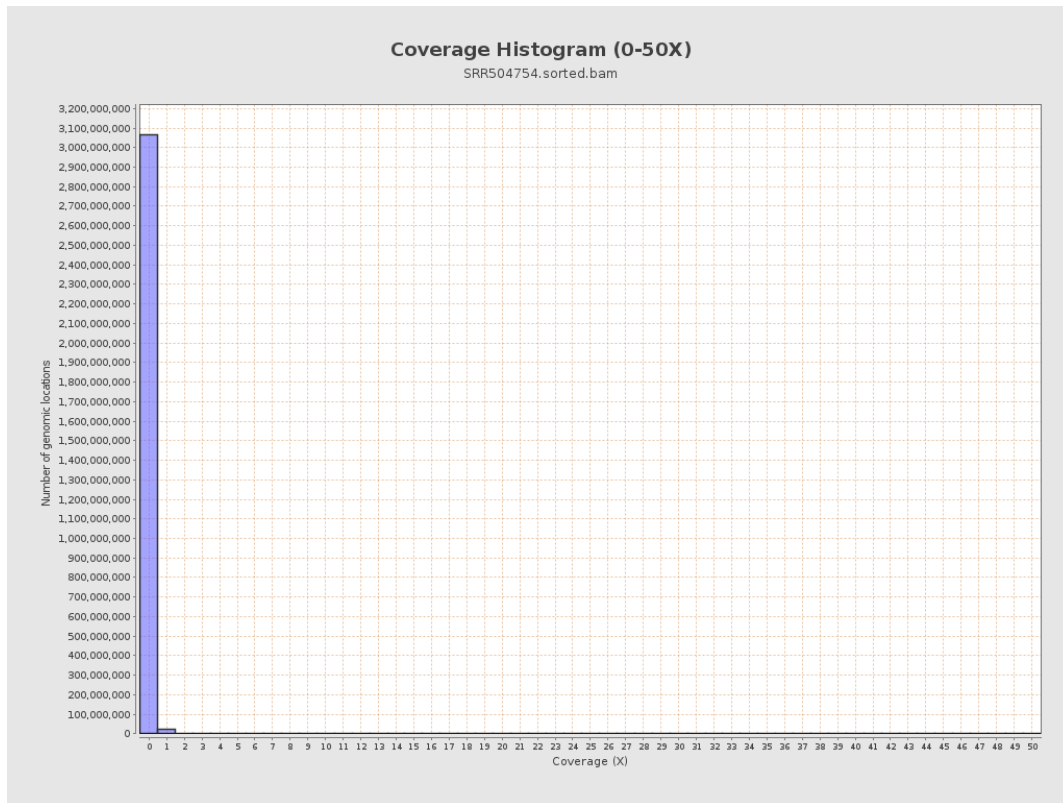
3. Results : Coverage across reference



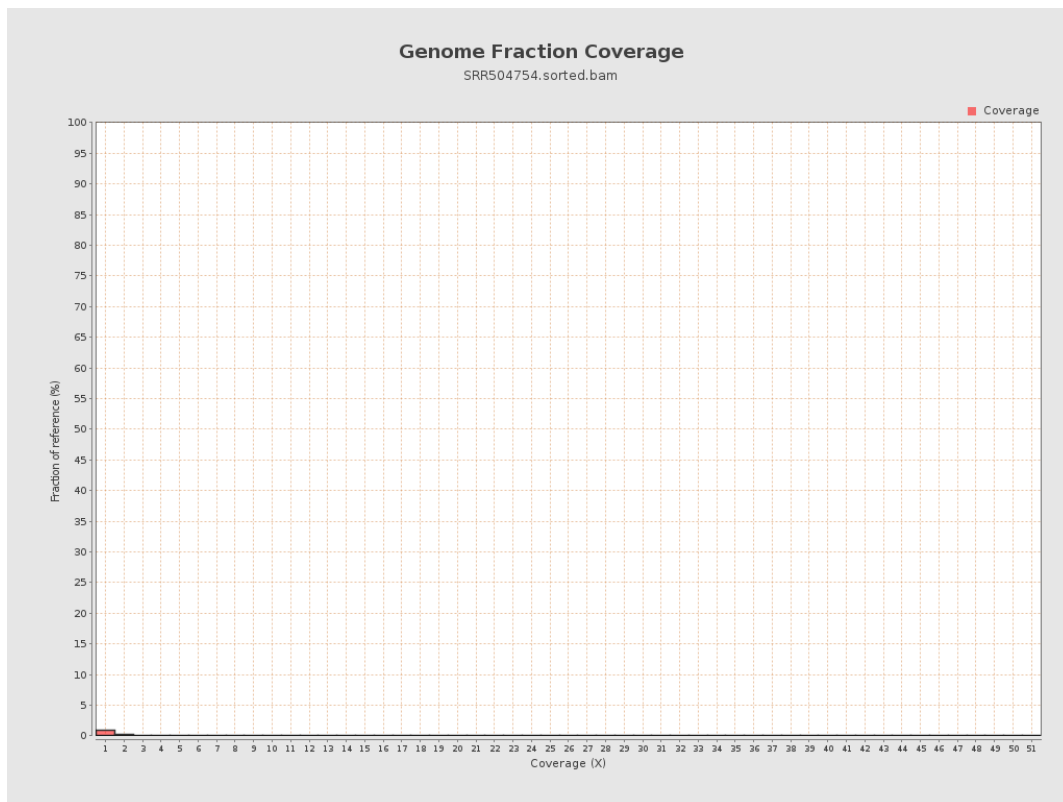
4. Results : Coverage Histogram



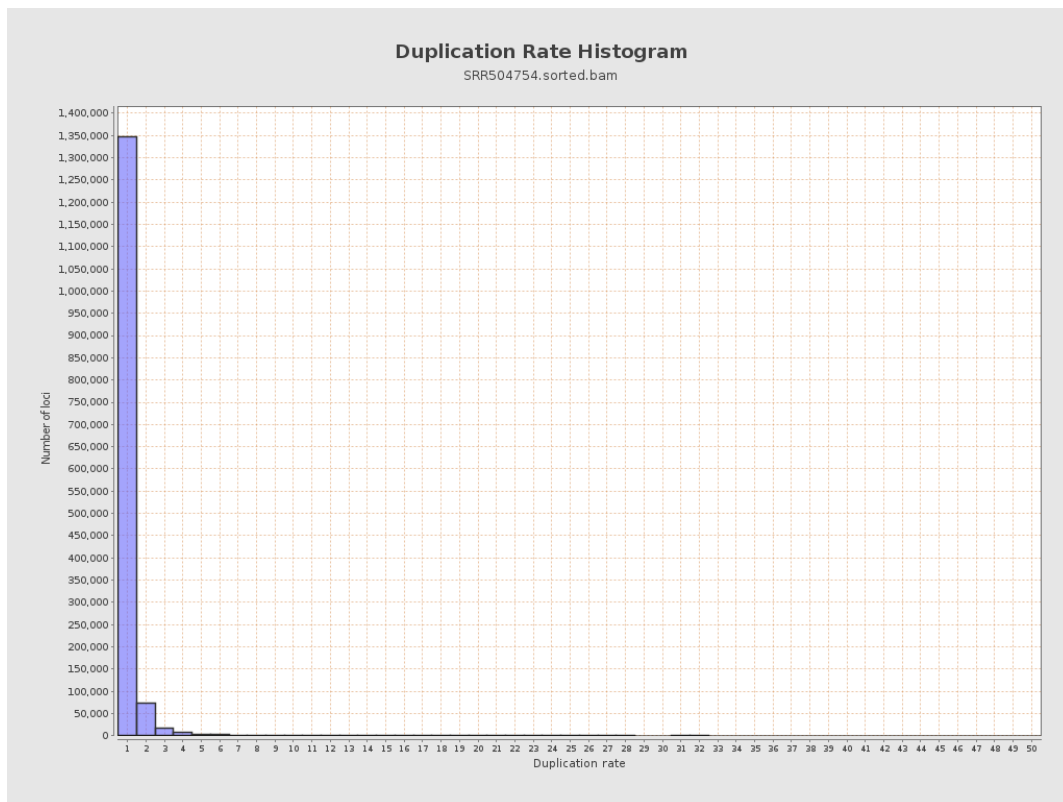
5. Results : Coverage Histogram (0-50X)



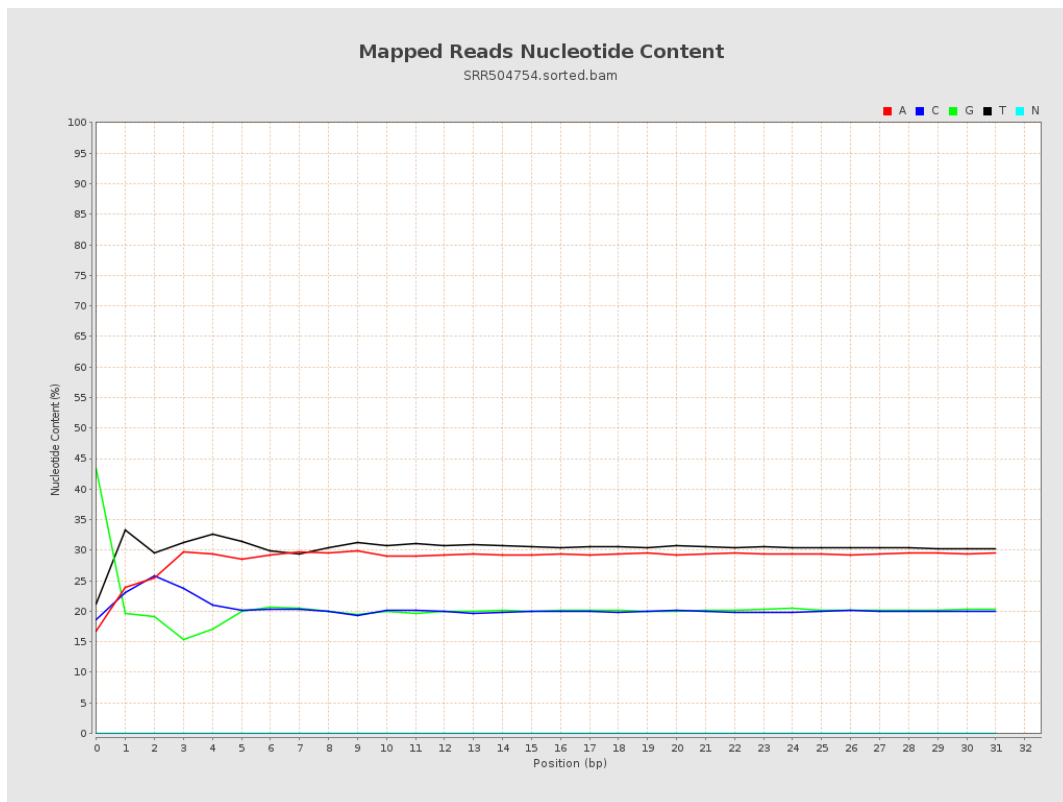
6. Results : Genome Fraction Coverage



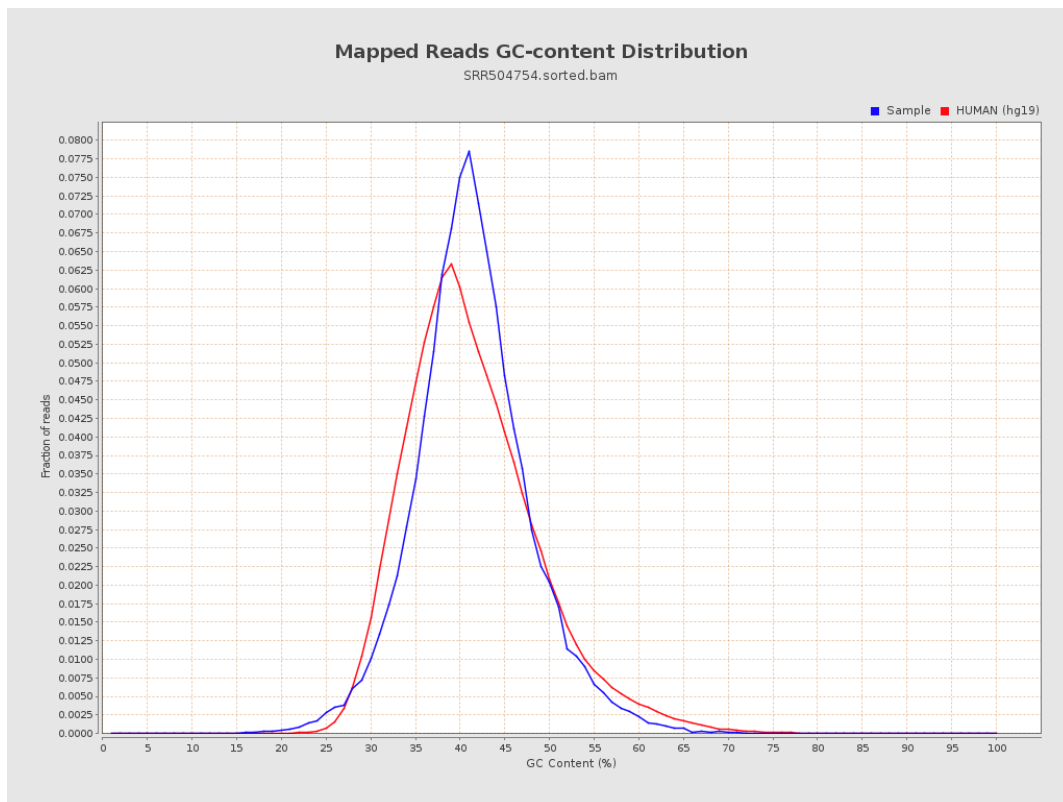
7. Results : Duplication Rate Histogram



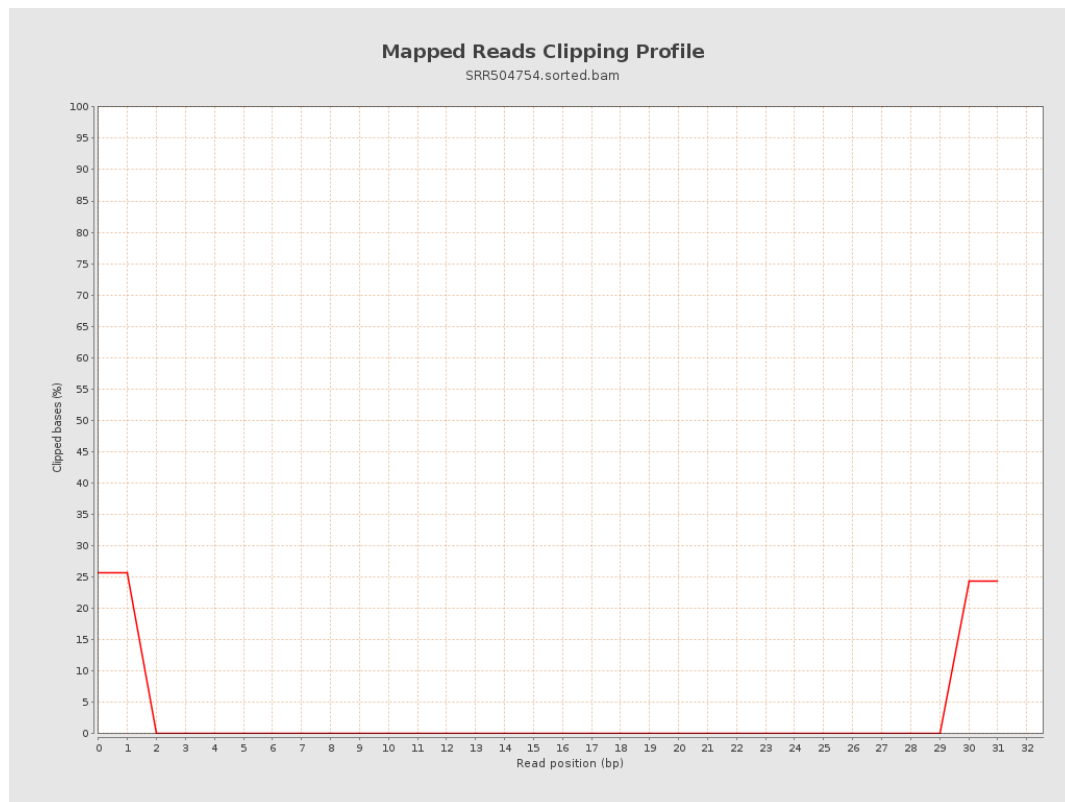
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

