

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 05:44:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504707.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_SRR504707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504707.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 05:44:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,223,752
Mapped reads	2,007,040 / 90.25%
Unmapped reads	216,712 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	374,376 / 16.84%
Duplication rate	11.08%
Clipped reads	3,218 / 0.14%

2.2. ACGT Content

Number/percentage of A's	18,621,589 / 29%
Number/percentage of C's	12,832,169 / 19.98%
Number/percentage of T's	19,914,548 / 31.01%
Number/percentage of G's	12,850,458 / 20.01%
Number/percentage of N's	80 / 0%
GC Percentage	39.99%

2.3. Coverage

Mean	0.0207
Standard Deviation	0.7252

2.4. Mapping Quality

Mean Mapping Quality	7.51
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2.5. Mismatches and indels

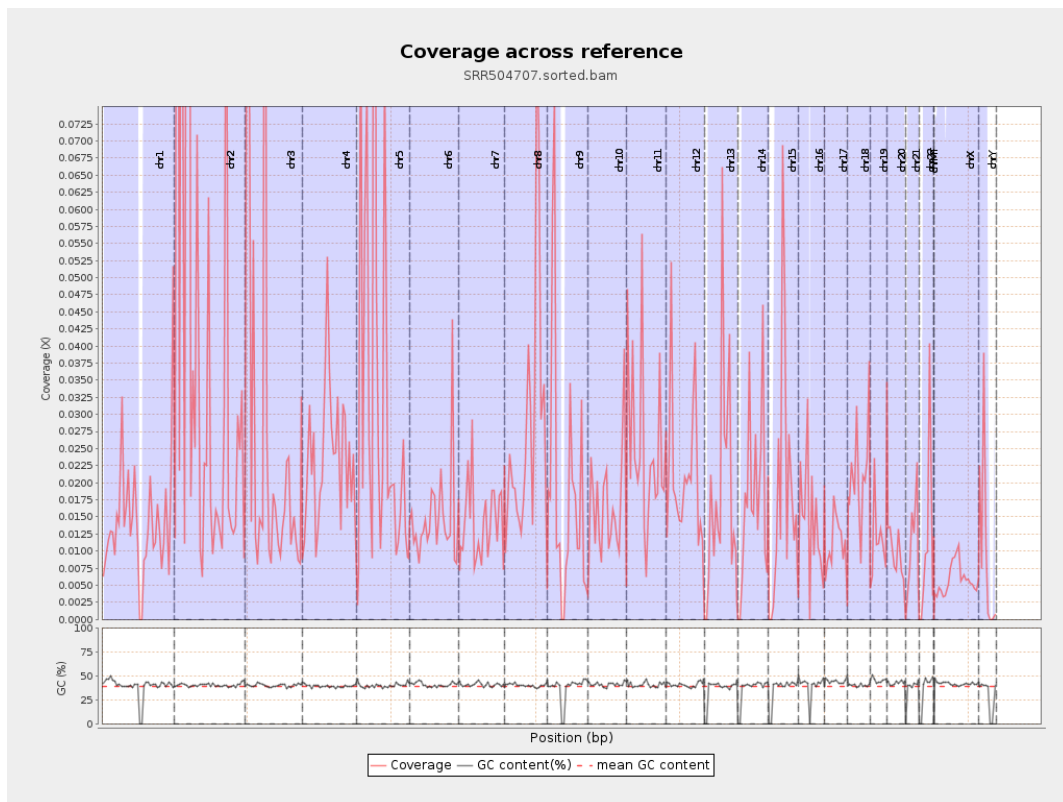
General error rate	0.04%
Mismatches	28,043

2.6. Chromosome stats

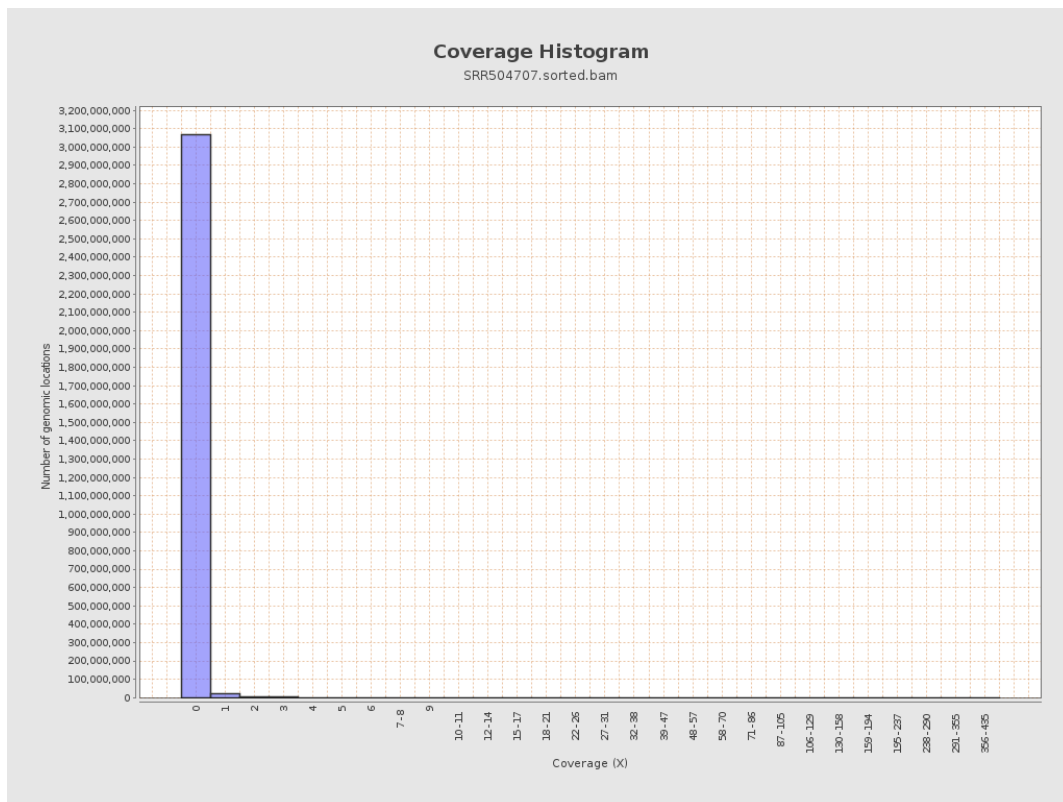
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3602710	0.0145	0.3172
chr2	243199373	10776390	0.0443	1.8352
chr3	198022430	5496198	0.0278	0.9458
chr4	191154276	4509322	0.0236	0.3806
chr5	180915260	6350410	0.0351	1.3554
chr6	171115067	2532140	0.0148	0.2548
chr7	159138663	2257796	0.0142	0.2094
chr8	146364022	4051062	0.0277	0.5747
chr9	141213431	2704018	0.0191	0.4353
chr10	135534747	2213638	0.0163	0.3042
chr11	135006516	3380616	0.025	0.4804
chr12	133851895	2807640	0.021	0.3274
chr13	115169878	2084894	0.0181	0.4205
chr14	107349540	1865728	0.0174	0.3046
chr15	102531392	1940746	0.0189	0.5535

chr16	90354753	1245968	0.0138	0.2294
chr17	81195210	876116	0.0108	0.186
chr18	78077248	1640906	0.021	0.3536
chr19	59128983	735948	0.0124	0.2185
chr20	63025520	590410	0.0094	0.134
chr21	48129895	512876	0.0107	0.1783
chr22	51304566	547504	0.0107	0.2432
chrMT	16571	0	0	0
chrX	155270560	917114	0.0059	0.1016
chrY	59373566	578694	0.0097	0.3206

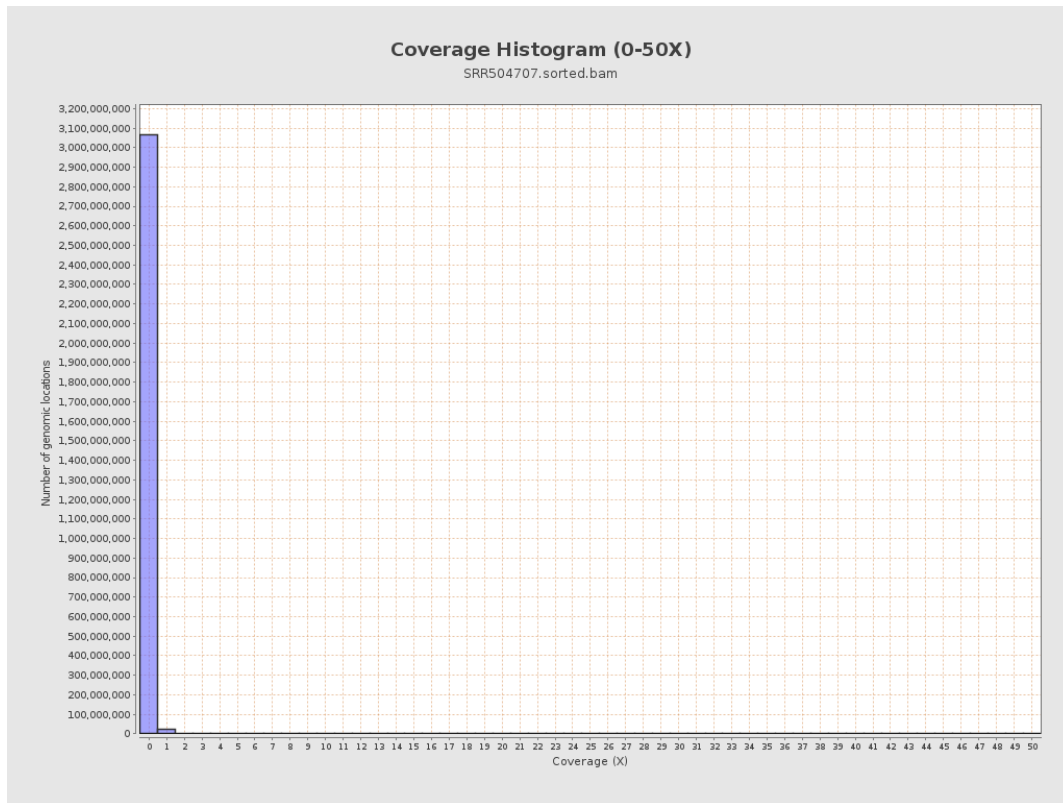
3. Results : Coverage across reference



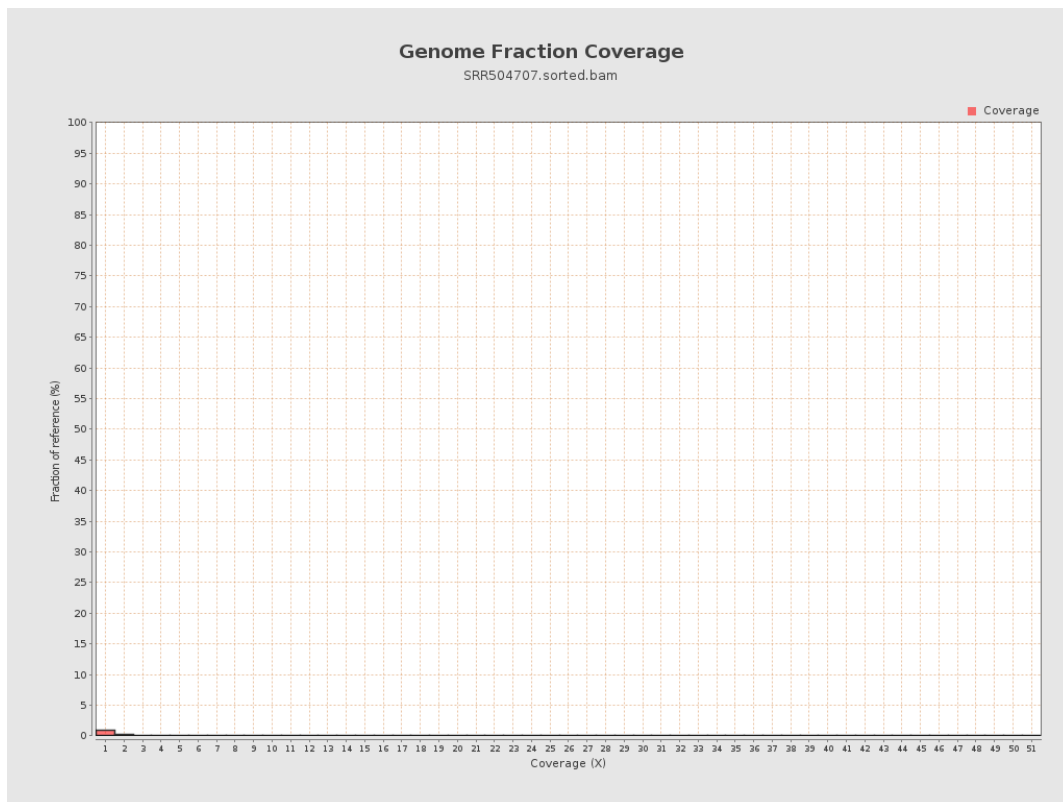
4. Results : Coverage Histogram



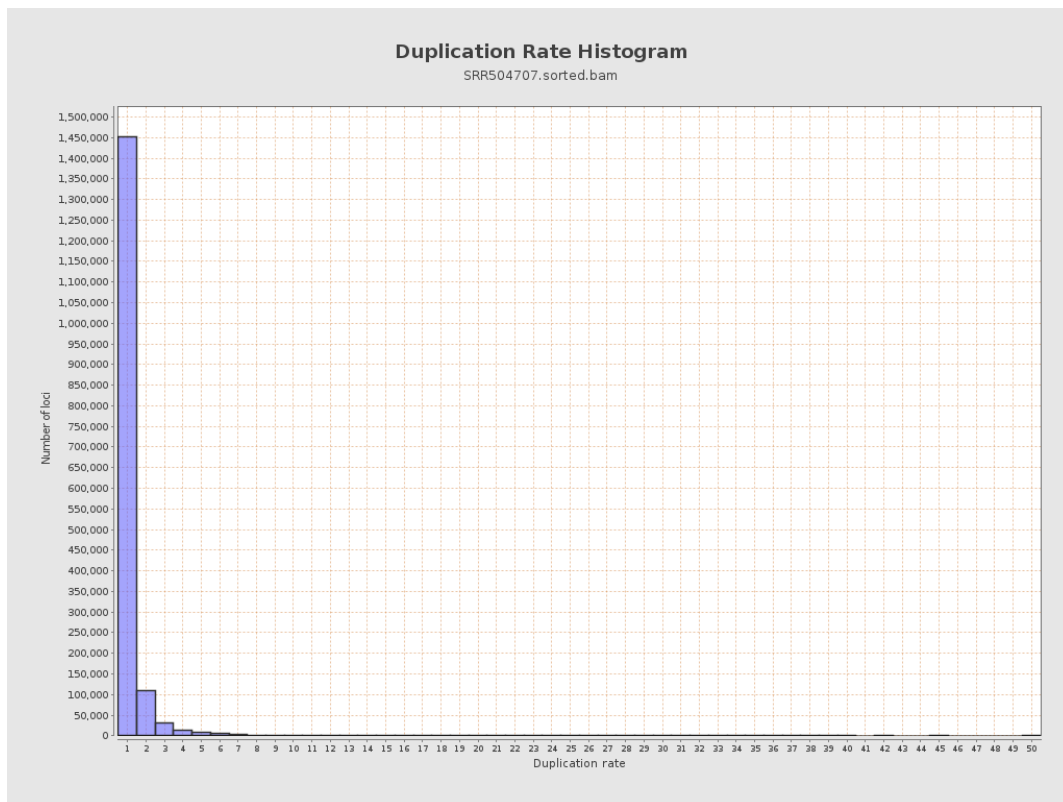
5. Results : Coverage Histogram (0-50X)



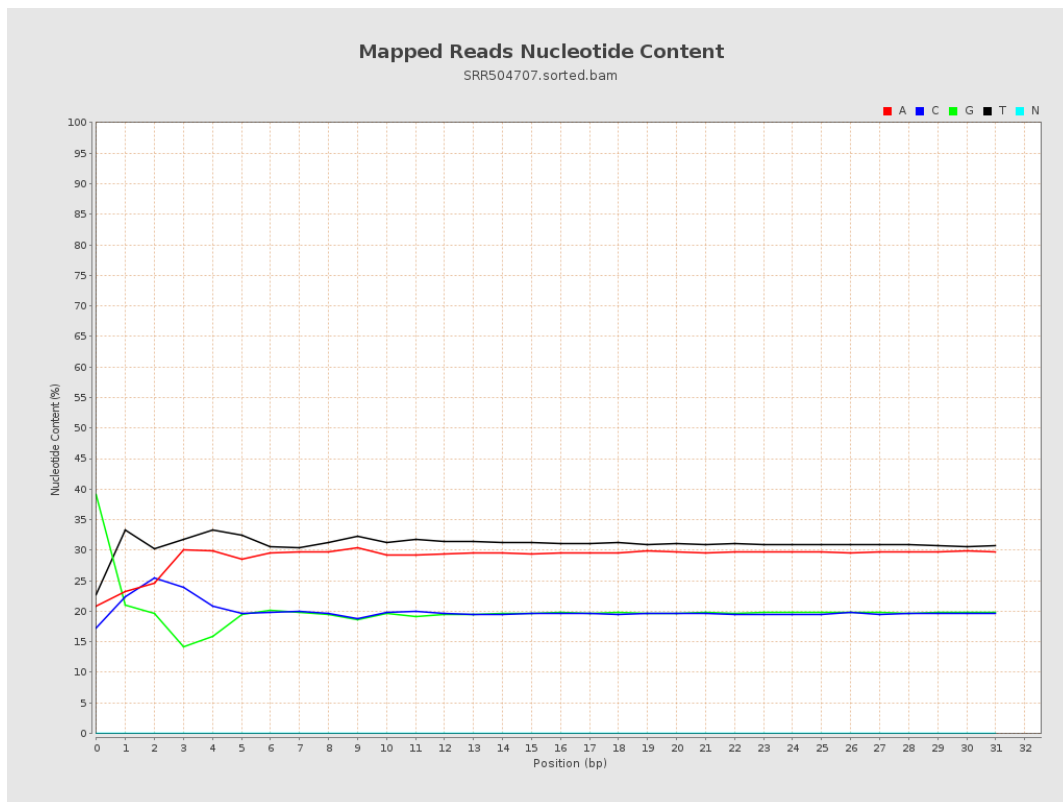
6. Results : Genome Fraction Coverage



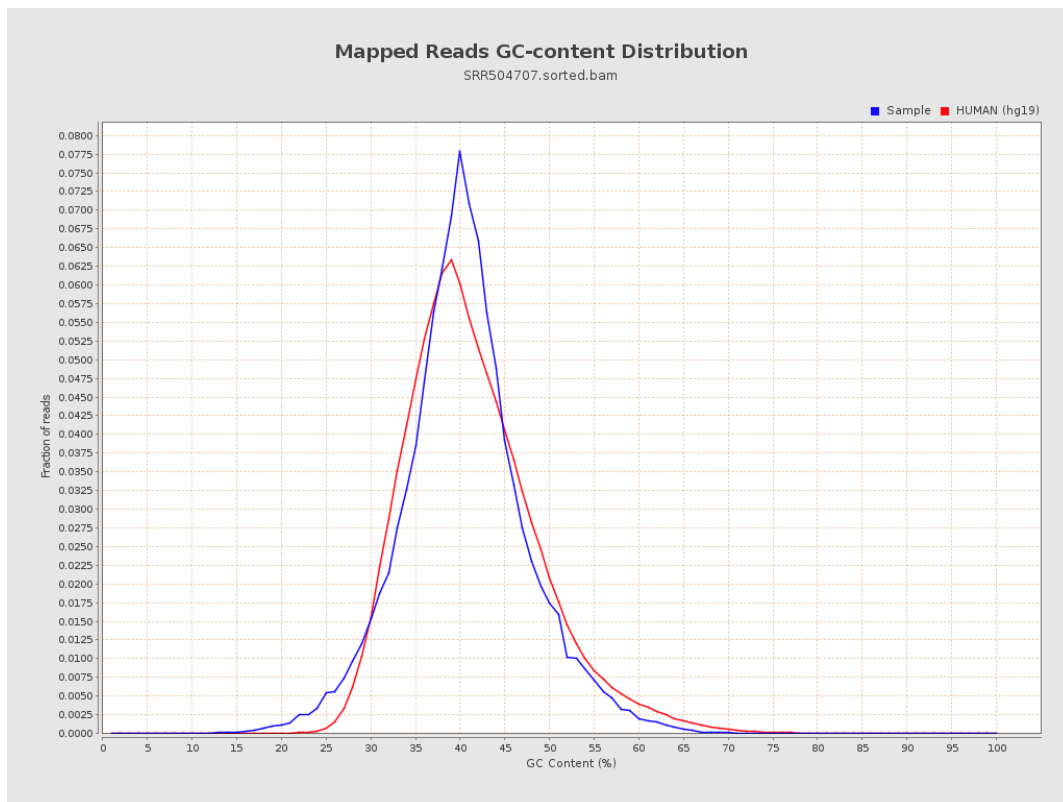
7. Results : Duplication Rate Histogram



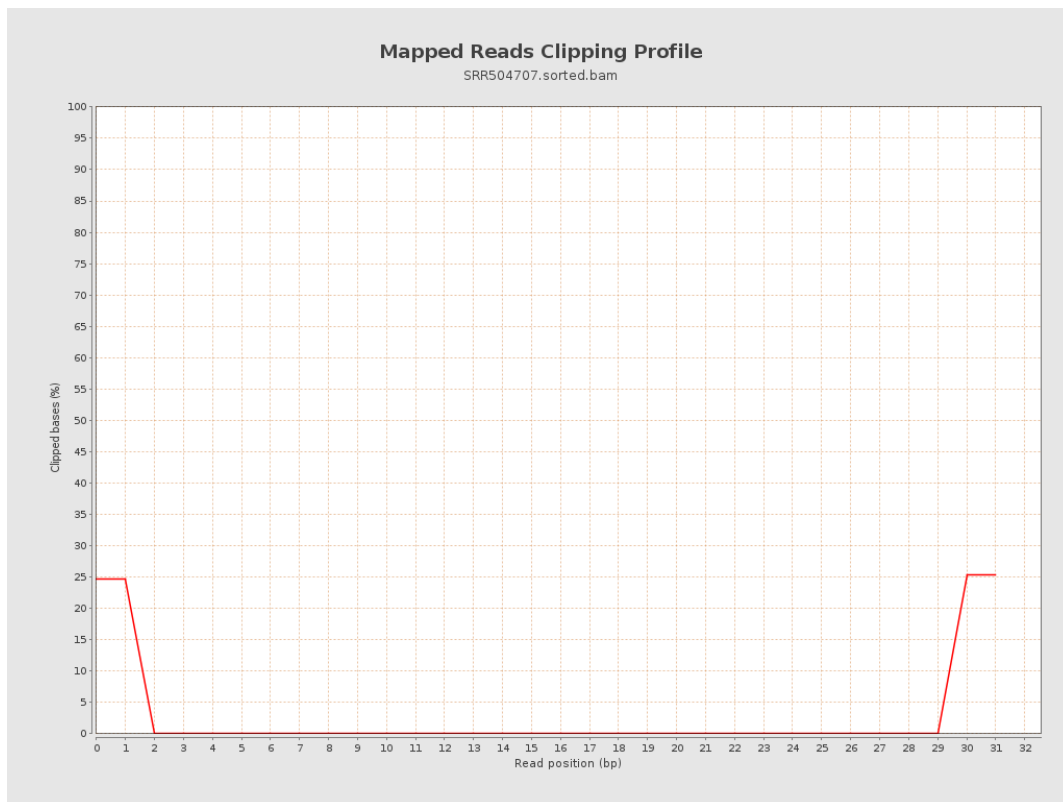
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

