

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:18:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504735.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_SRR504735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:18:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,158,225
Mapped reads	1,899,900 / 88.03%
Unmapped reads	258,325 / 11.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	408,402 / 18.92%
Duplication rate	8.79%
Clipped reads	3,376 / 0.16%

2.2. ACGT Content

Number/percentage of A's	17,754,611 / 29.21%
Number/percentage of C's	11,956,850 / 19.67%
Number/percentage of T's	18,962,864 / 31.19%
Number/percentage of G's	12,115,622 / 19.93%
Number/percentage of N's	101 / 0%
GC Percentage	39.6%

2.3. Coverage

Mean	0.0196
Standard Deviation	1.6493

2.4. Mapping Quality

Mean Mapping Quality	7.6
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2.5. Mismatches and indels

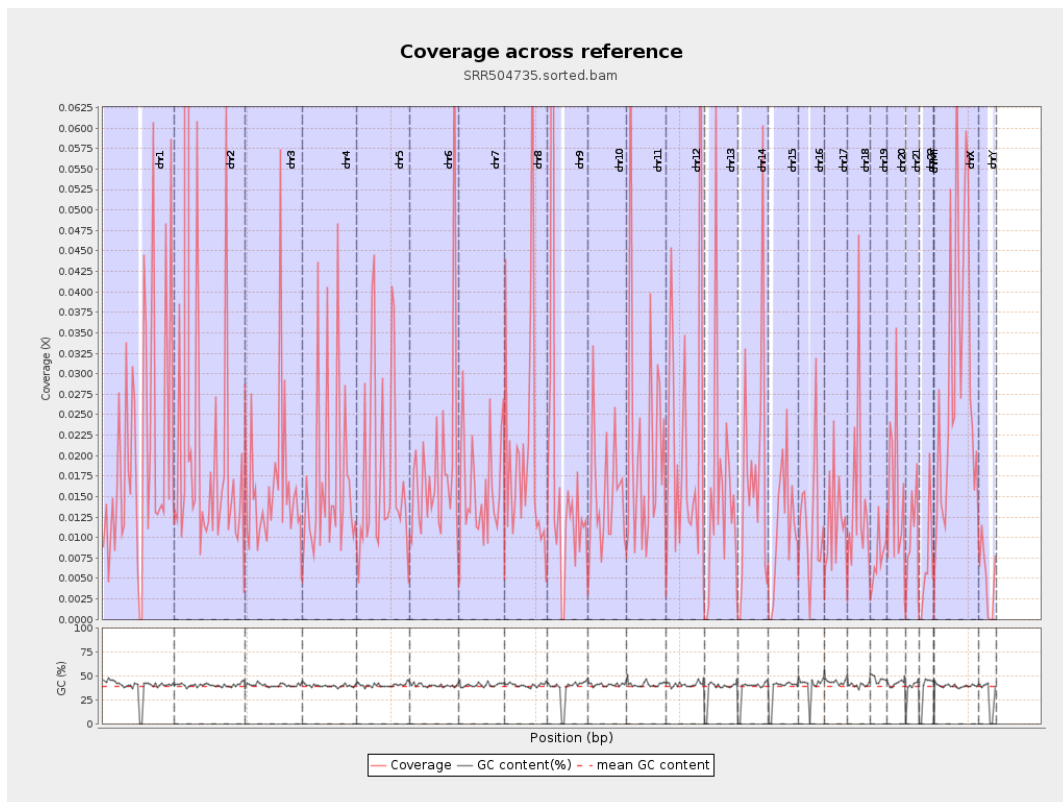
General error rate	0.05%
Mismatches	30,606

2.6. Chromosome stats

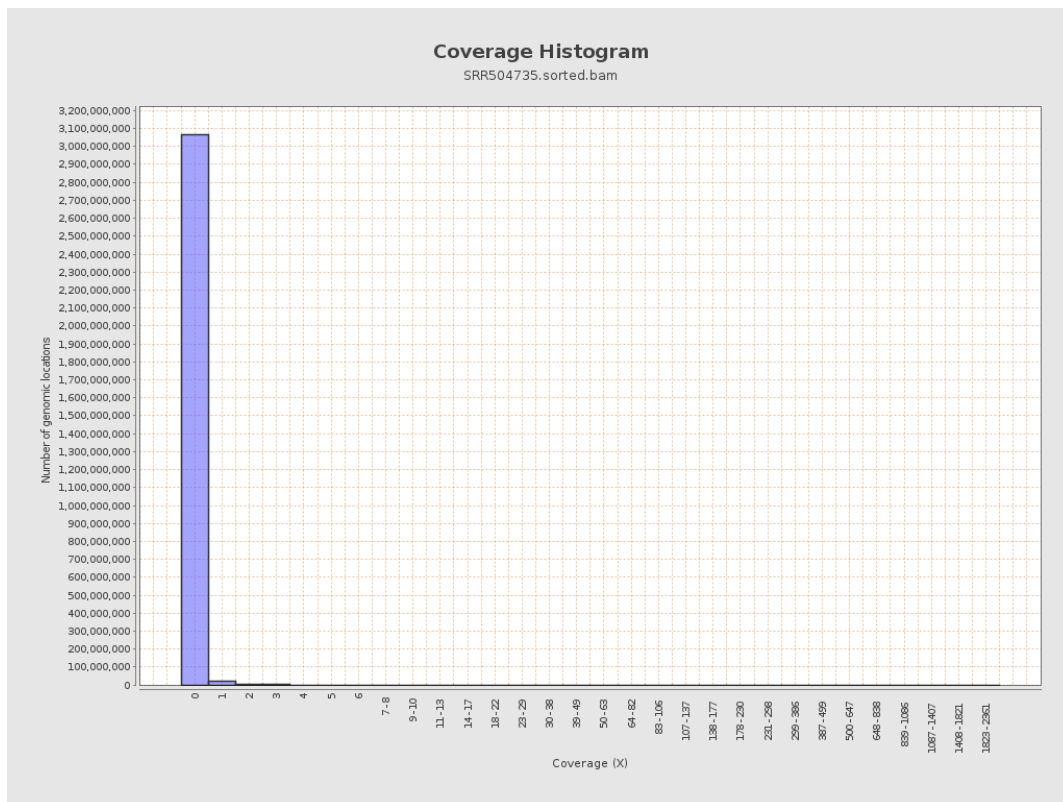
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4907278	0.0197	0.4092
chr2	243199373	11546356	0.0475	5.7038
chr3	198022430	3233318	0.0163	0.3192
chr4	191154276	3172184	0.0166	0.3165
chr5	180915260	3284744	0.0182	0.366
chr6	171115067	3189514	0.0186	0.4563
chr7	159138663	2587672	0.0163	0.2543
chr8	146364022	3010662	0.0206	0.5419
chr9	141213431	2672392	0.0189	0.8268
chr10	135534747	2039644	0.015	0.282
chr11	135006516	2907952	0.0215	0.4548
chr12	133851895	3036862	0.0227	0.7102
chr13	115169878	1750632	0.0152	0.4322
chr14	107349540	1812042	0.0169	0.377
chr15	102531392	1179808	0.0115	0.194

chr16	90354753	1083130	0.012	0.2224
chr17	81195210	962080	0.0118	0.1932
chr18	78077248	1185140	0.0152	0.3687
chr19	59128983	450608	0.0076	0.1221
chr20	63025520	1010976	0.016	0.313
chr21	48129895	491352	0.0102	0.1944
chr22	51304566	323994	0.0063	0.1595
chrMT	16571	0	0	0
chrX	155270560	4659400	0.03	0.5149
chrY	59373566	292308	0.0049	0.1627

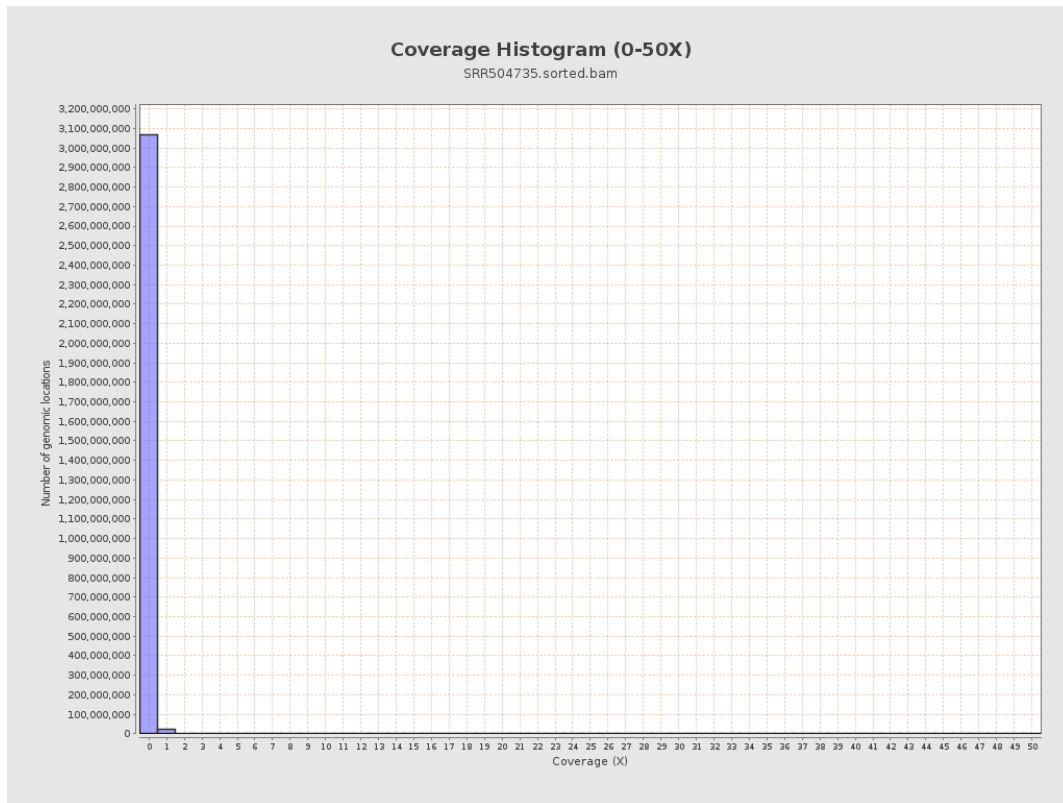
3. Results : Coverage across reference



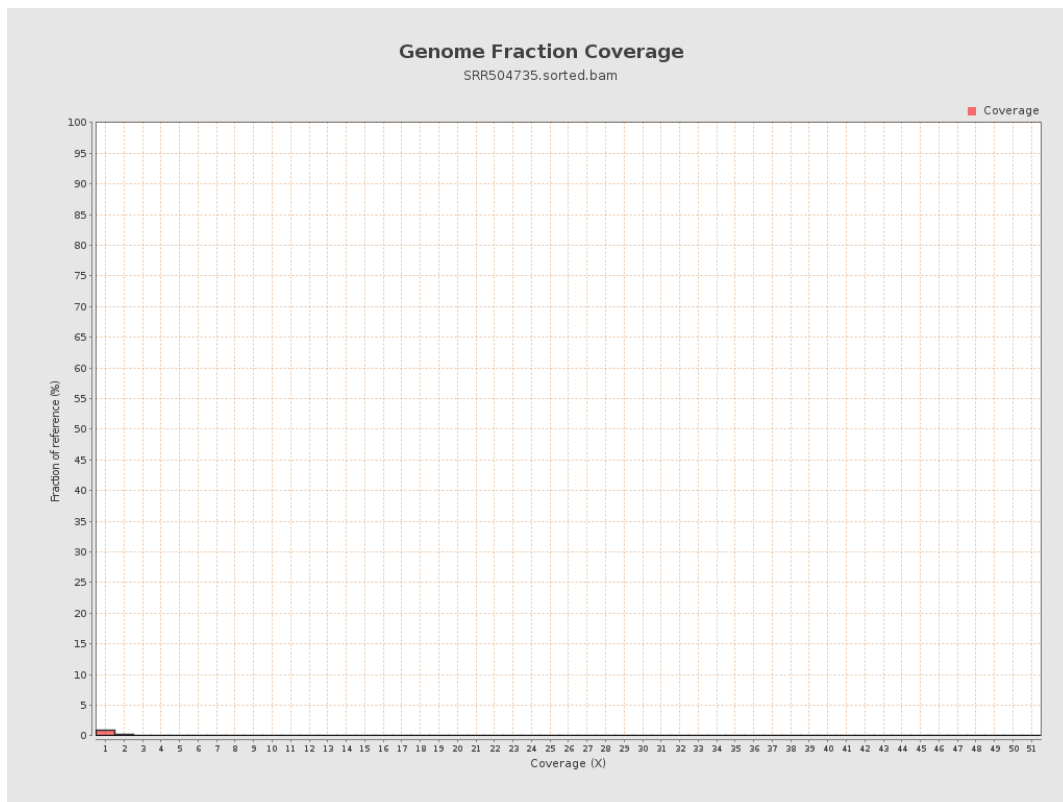
4. Results : Coverage Histogram



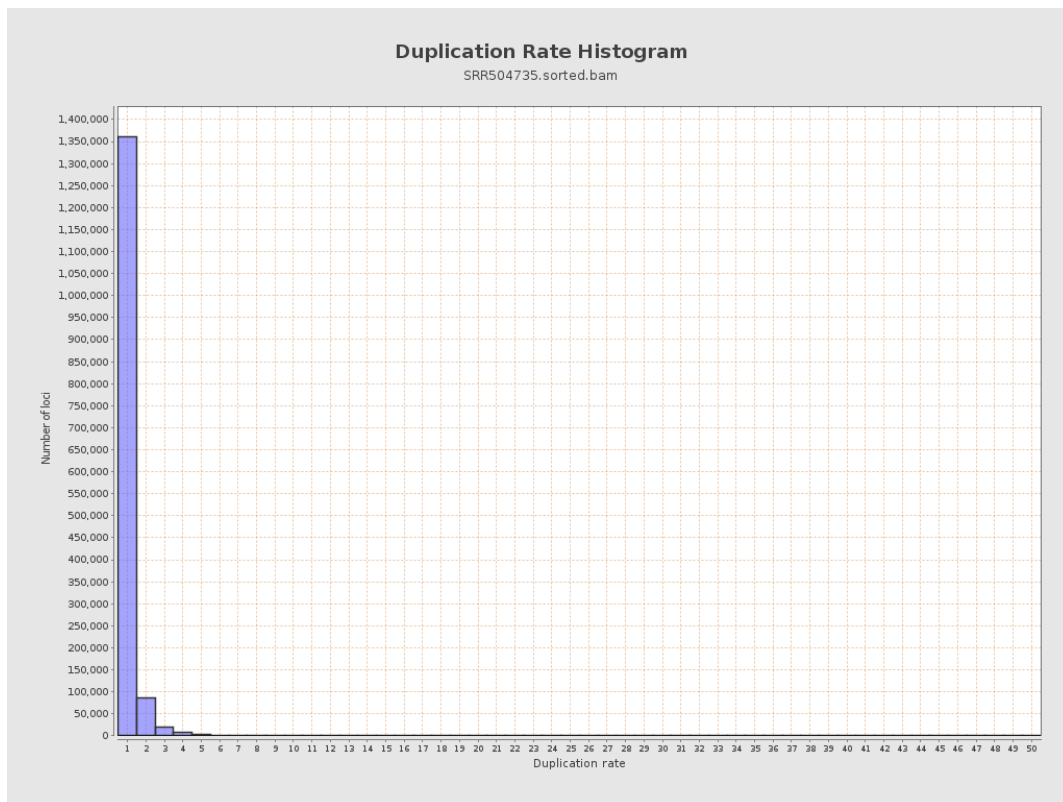
5. Results : Coverage Histogram (0-50X)



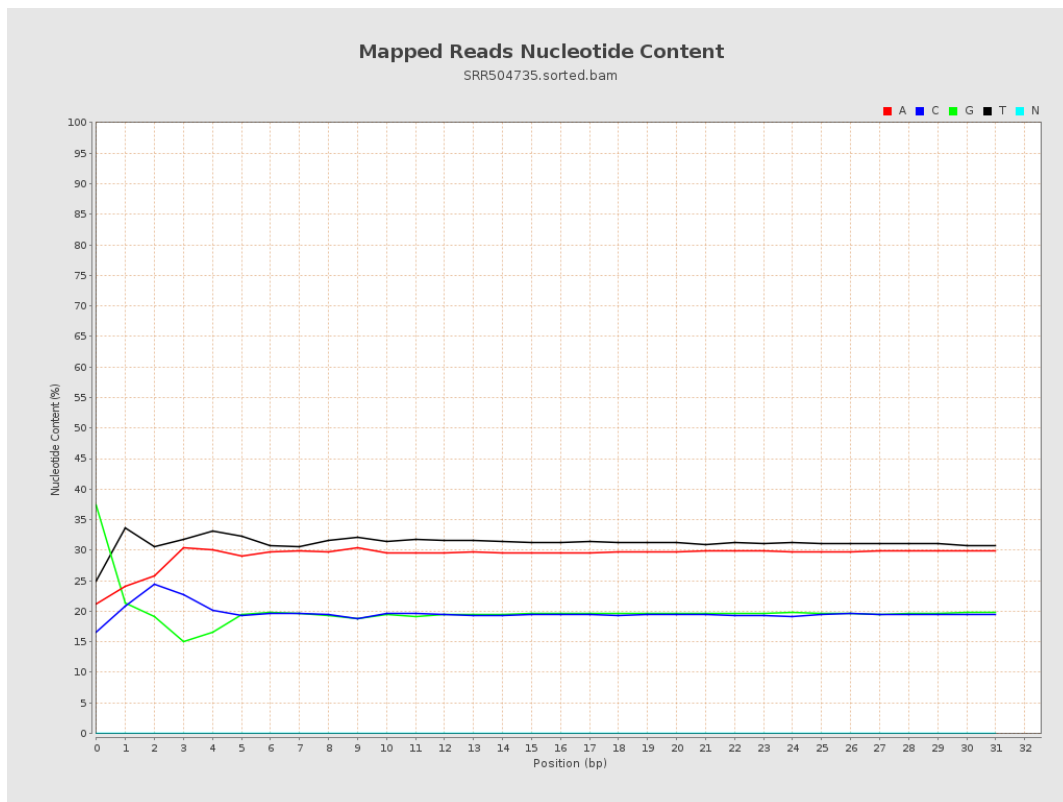
6. Results : Genome Fraction Coverage



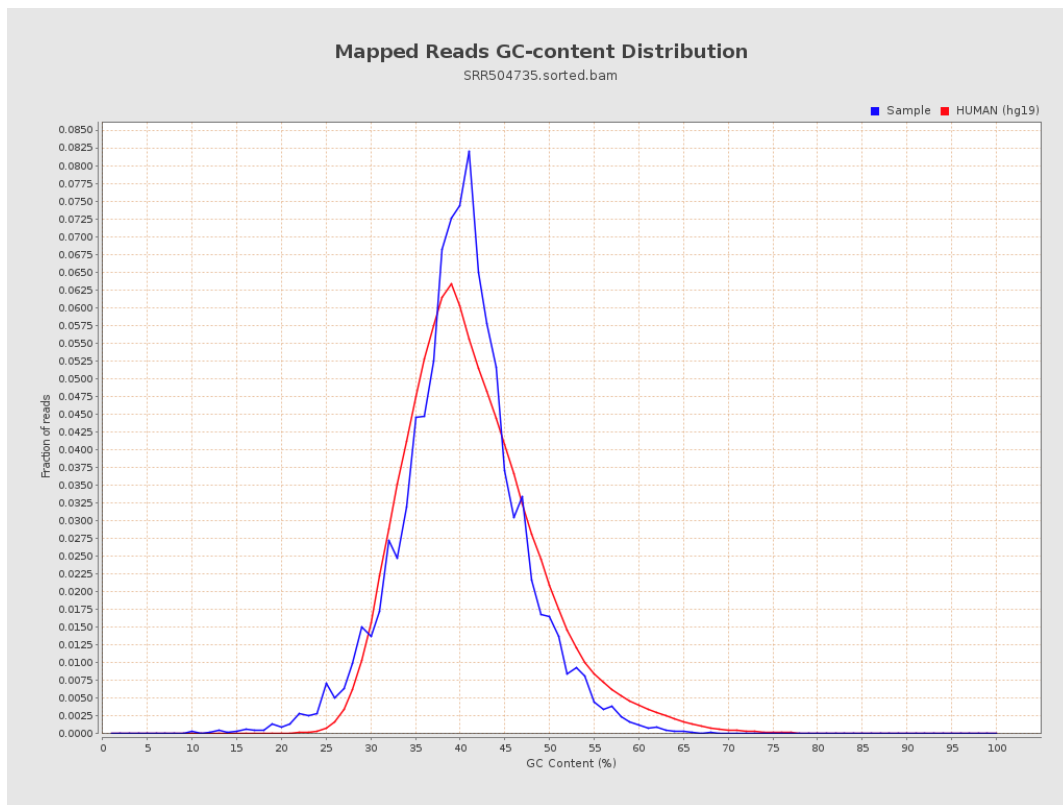
7. Results : Duplication Rate Histogram



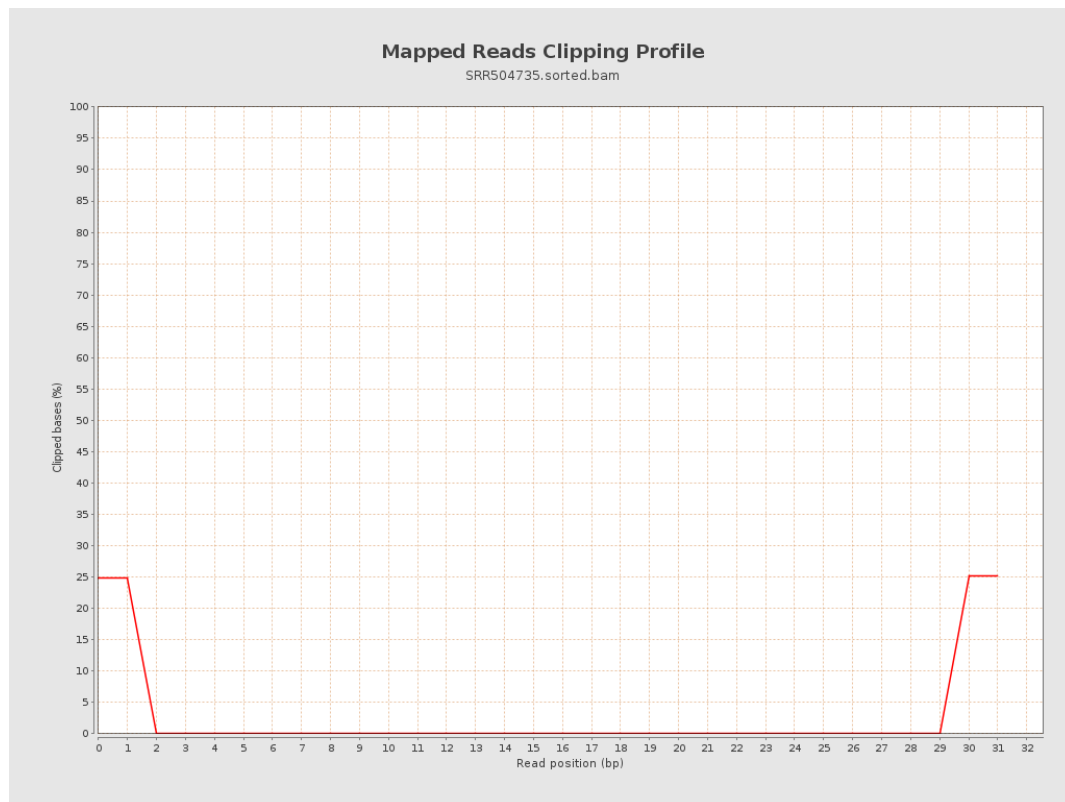
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

