

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 05:59:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504712.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_SRR504712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504712.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 05:59:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,279,957
Mapped reads	2,060,792 / 90.39%
Unmapped reads	219,165 / 9.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	374,742 / 16.44%
Duplication rate	8.21%
Clipped reads	3,392 / 0.15%

2.2. ACGT Content

Number/percentage of A's	18,742,684 / 28.42%
Number/percentage of C's	13,441,029 / 20.38%
Number/percentage of T's	20,110,077 / 30.5%
Number/percentage of G's	13,644,677 / 20.69%
Number/percentage of N's	93 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0213
Standard Deviation	1.0797

2.4. Mapping Quality

Mean Mapping Quality	7.99
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2.5. Mismatches and indels

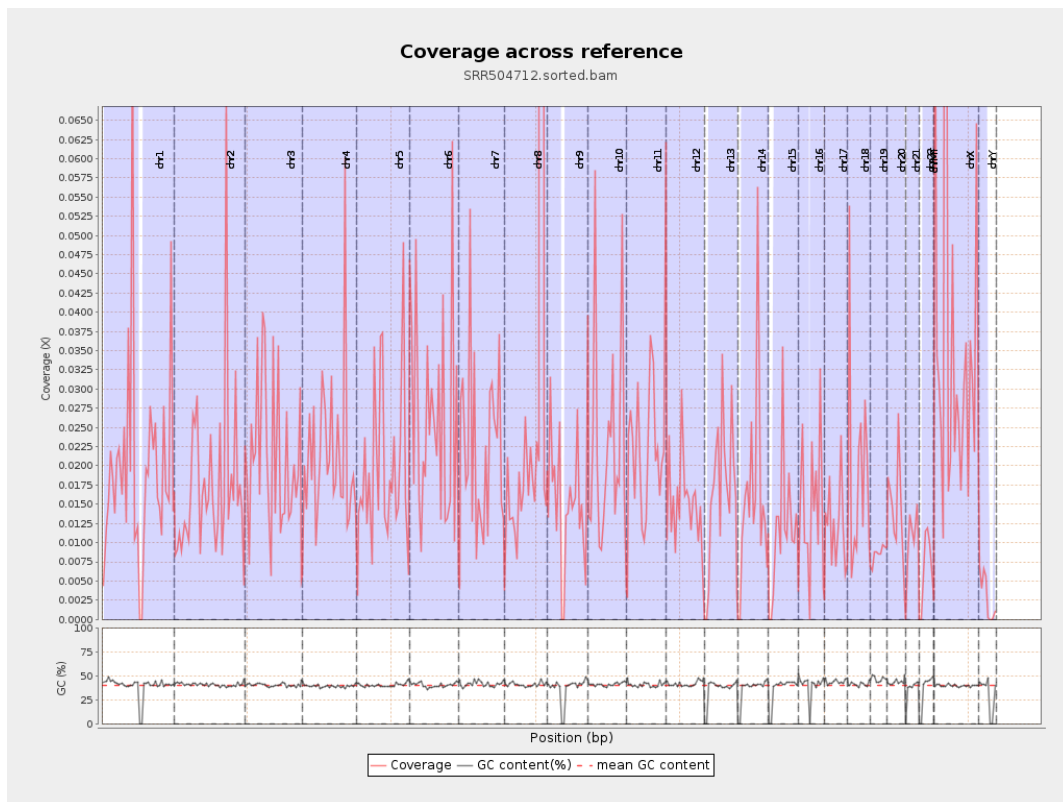
General error rate	0.05%
Mismatches	32,080

2.6. Chromosome stats

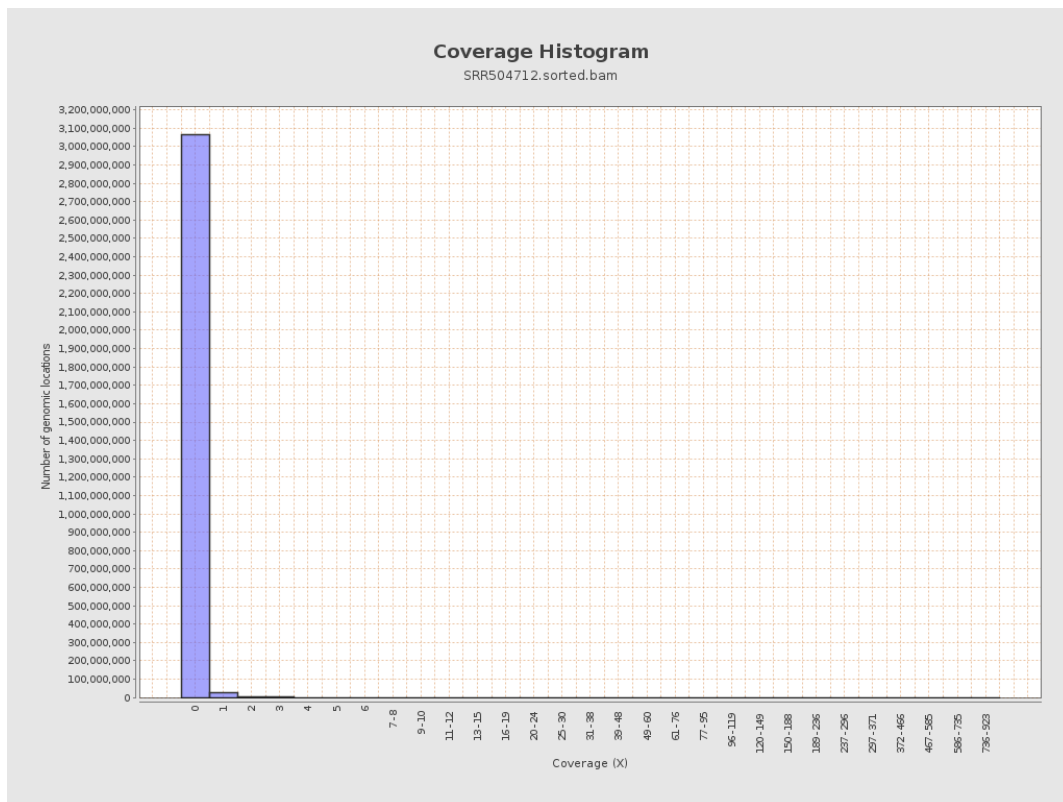
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4924514	0.0198	0.3446
chr2	243199373	4258368	0.0175	0.3605
chr3	198022430	4169488	0.0211	0.327
chr4	191154276	3994376	0.0209	0.4058
chr5	180915260	3586504	0.0198	0.2981
chr6	171115067	4456816	0.026	0.5432
chr7	159138663	3516714	0.0221	0.3679
chr8	146364022	10283642	0.0703	4.6989
chr9	141213431	2097734	0.0149	0.1986
chr10	135534747	2973866	0.0219	0.449
chr11	135006516	2937996	0.0218	0.2876
chr12	133851895	1980256	0.0148	0.2005
chr13	115169878	1940958	0.0169	0.2909
chr14	107349540	1655340	0.0154	0.2968
chr15	102531392	1191458	0.0116	0.2166

chr16	90354753	1289846	0.0143	0.2768
chr17	81195210	1007518	0.0124	0.2043
chr18	78077248	1565334	0.02	0.4073
chr19	59128983	503724	0.0085	0.1206
chr20	63025520	884858	0.014	0.233
chr21	48129895	506114	0.0105	0.166
chr22	51304566	342490	0.0067	0.1267
chrMT	16571	96	0.0058	0.0759
chrX	155270560	5698616	0.0367	0.6759
chrY	59373566	171934	0.0029	0.0687

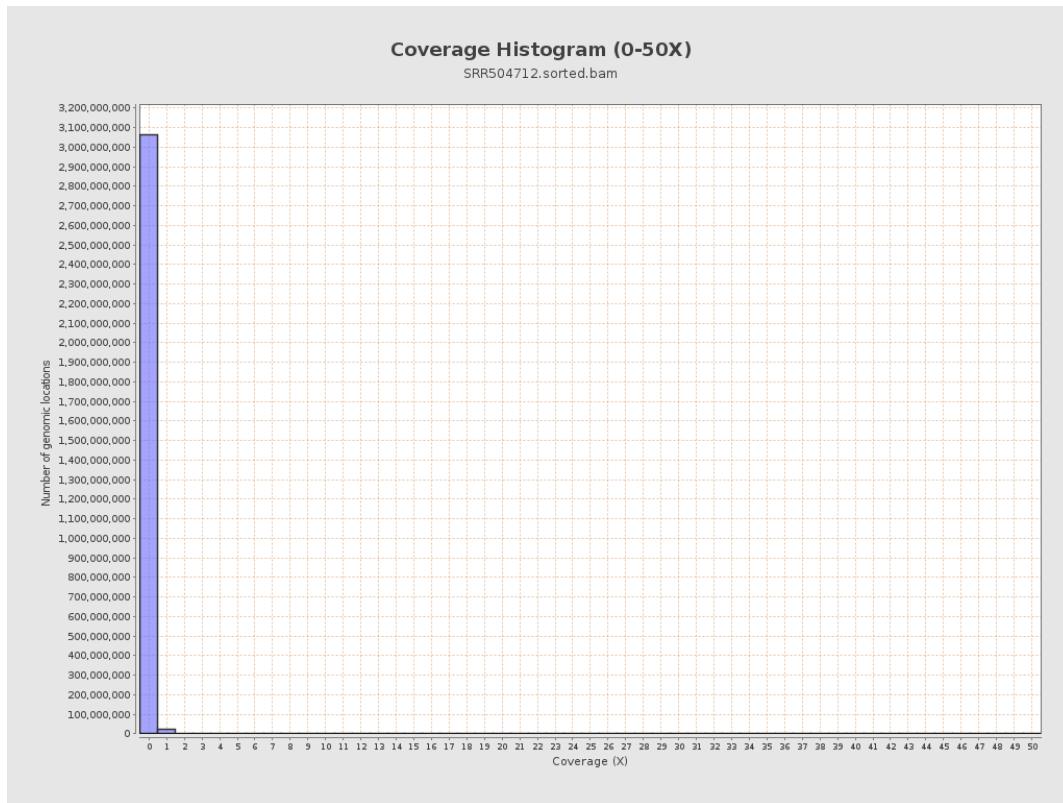
3. Results : Coverage across reference



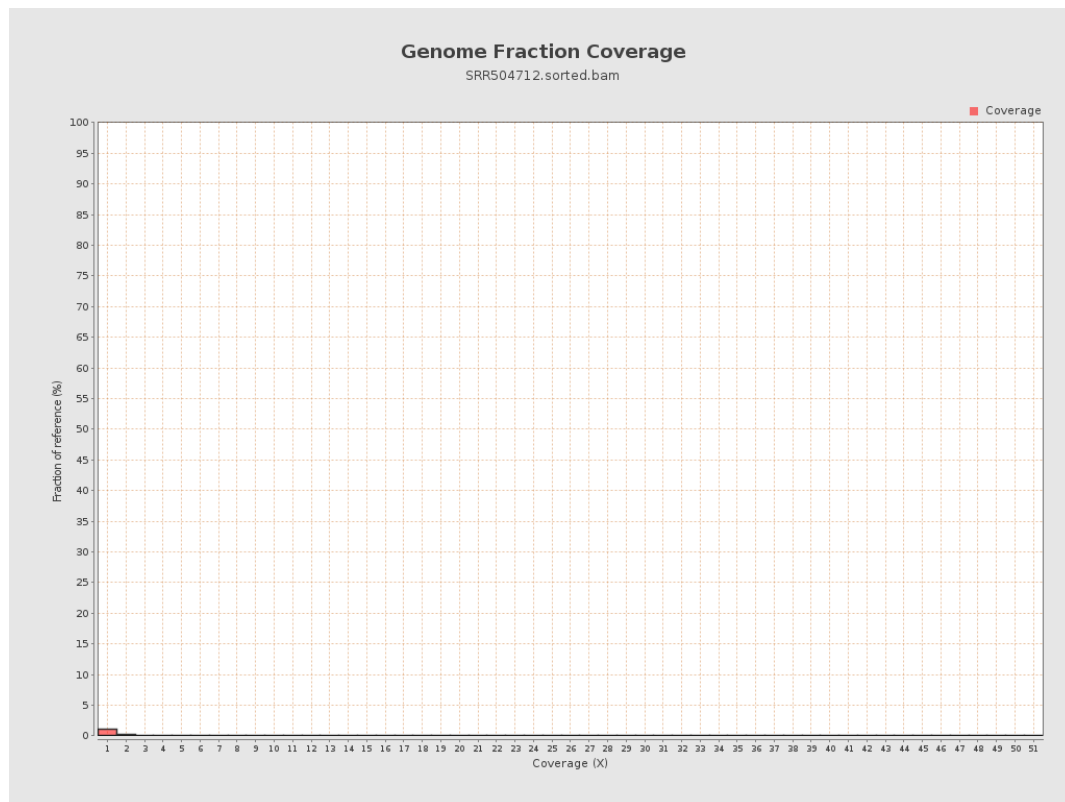
4. Results : Coverage Histogram



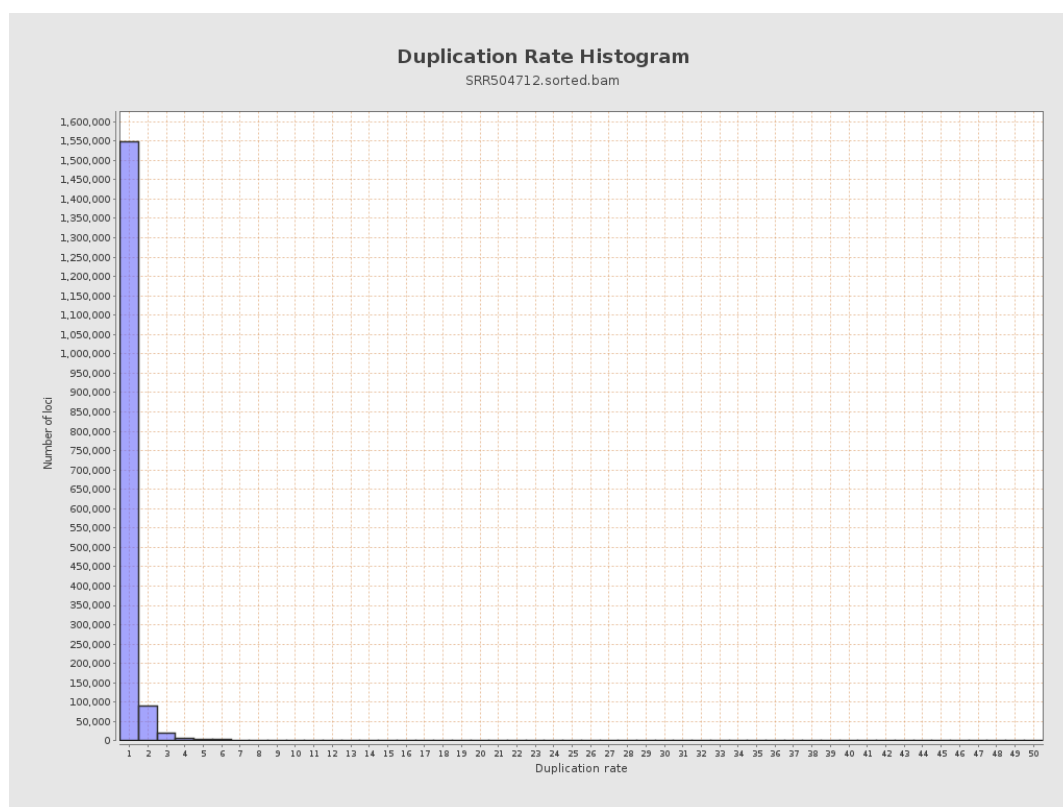
5. Results : Coverage Histogram (0-50X)



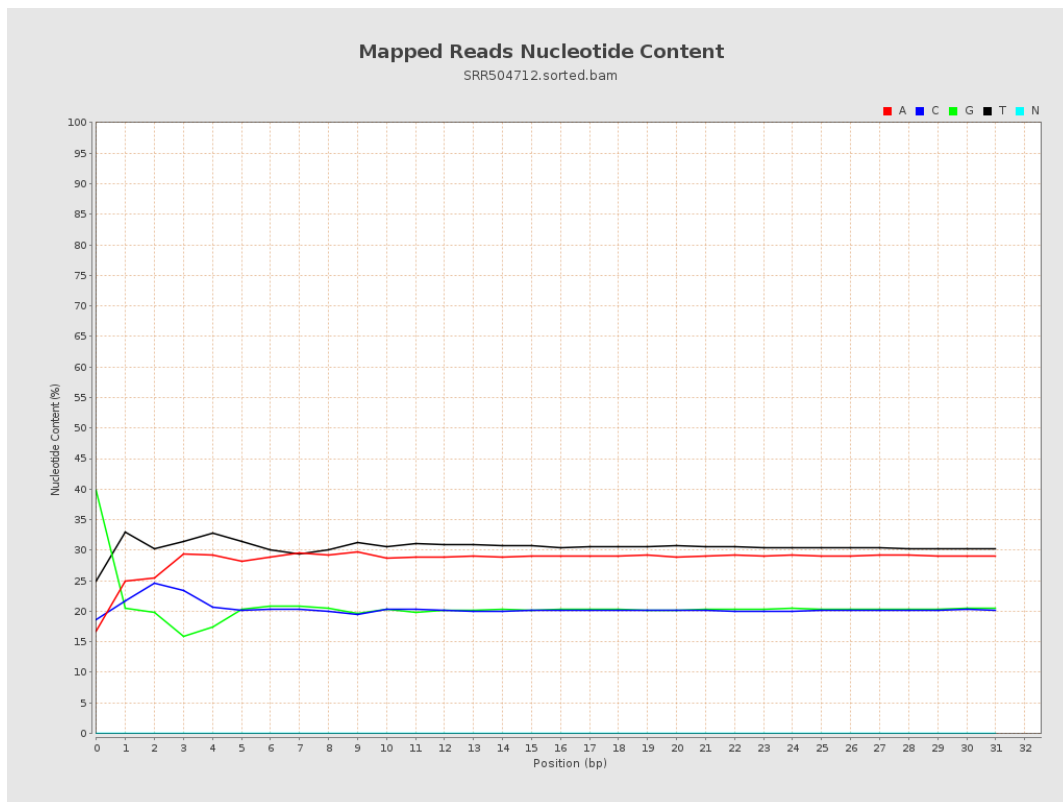
6. Results : Genome Fraction Coverage



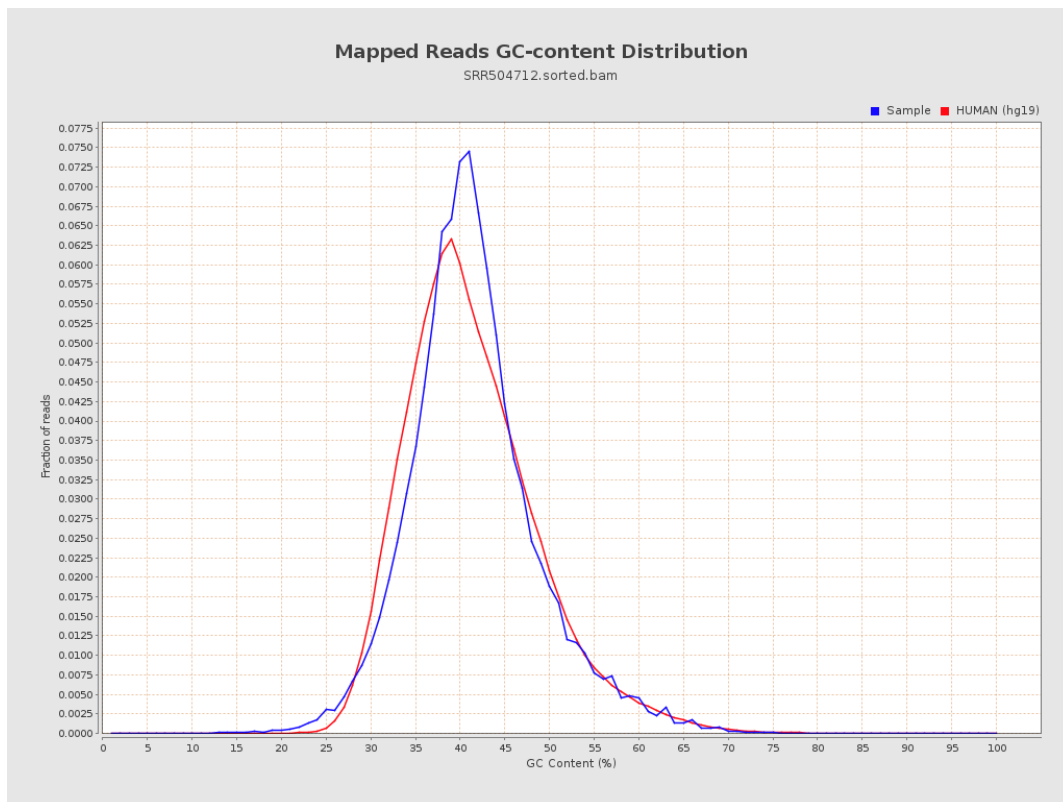
7. Results : Duplication Rate Histogram



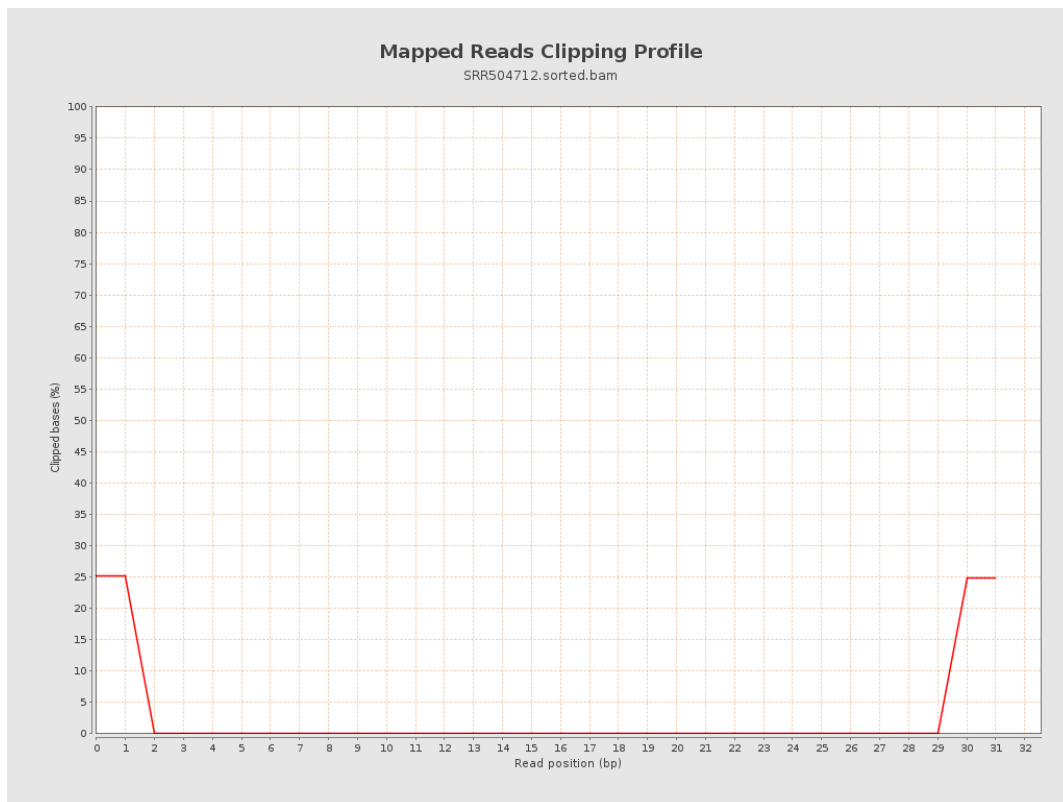
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

