

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:47:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504758.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_SRR504758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:47:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,935,094
Mapped reads	1,720,640 / 88.92%
Unmapped reads	214,454 / 11.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	388,905 / 20.1%
Duplication rate	12.65%
Clipped reads	2,769 / 0.14%

2.2. ACGT Content

Number/percentage of A's	15,802,766 / 28.7%
Number/percentage of C's	11,212,799 / 20.37%
Number/percentage of T's	16,682,194 / 30.3%
Number/percentage of G's	11,356,812 / 20.63%
Number/percentage of N's	371 / 0%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0178
Standard Deviation	0.8305

2.4. Mapping Quality

Mean Mapping Quality	7.19
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2.5. Mismatches and indels

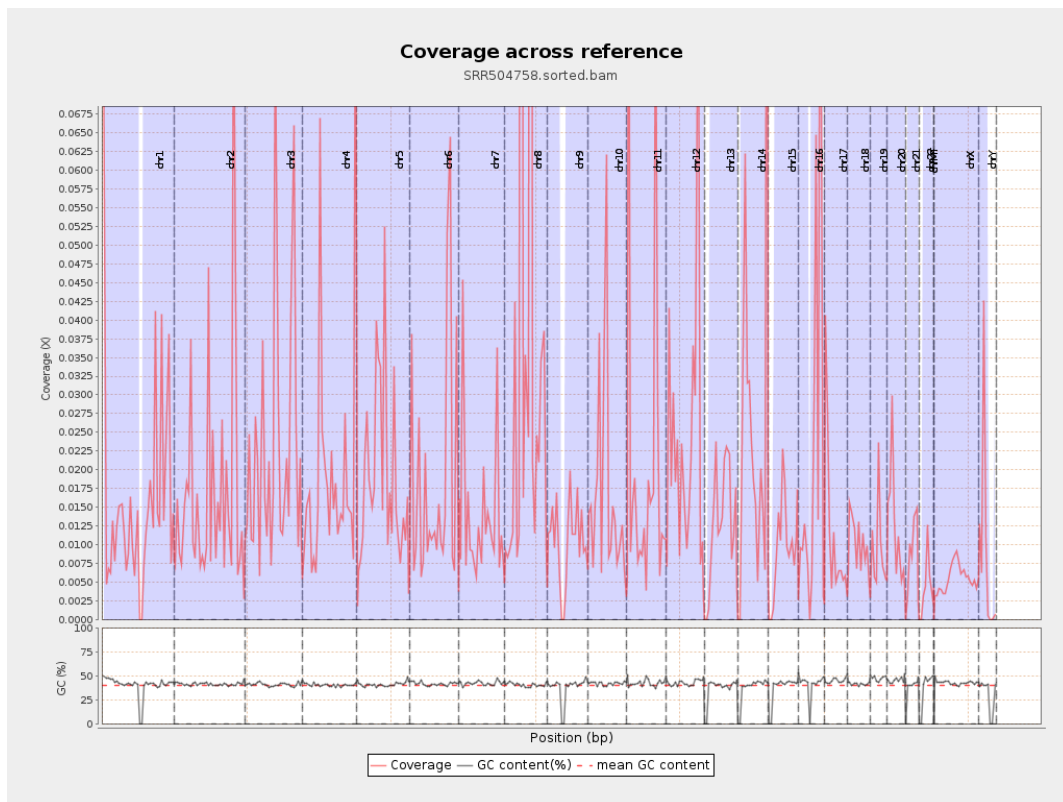
General error rate	0.04%
Mismatches	24,013

2.6. Chromosome stats

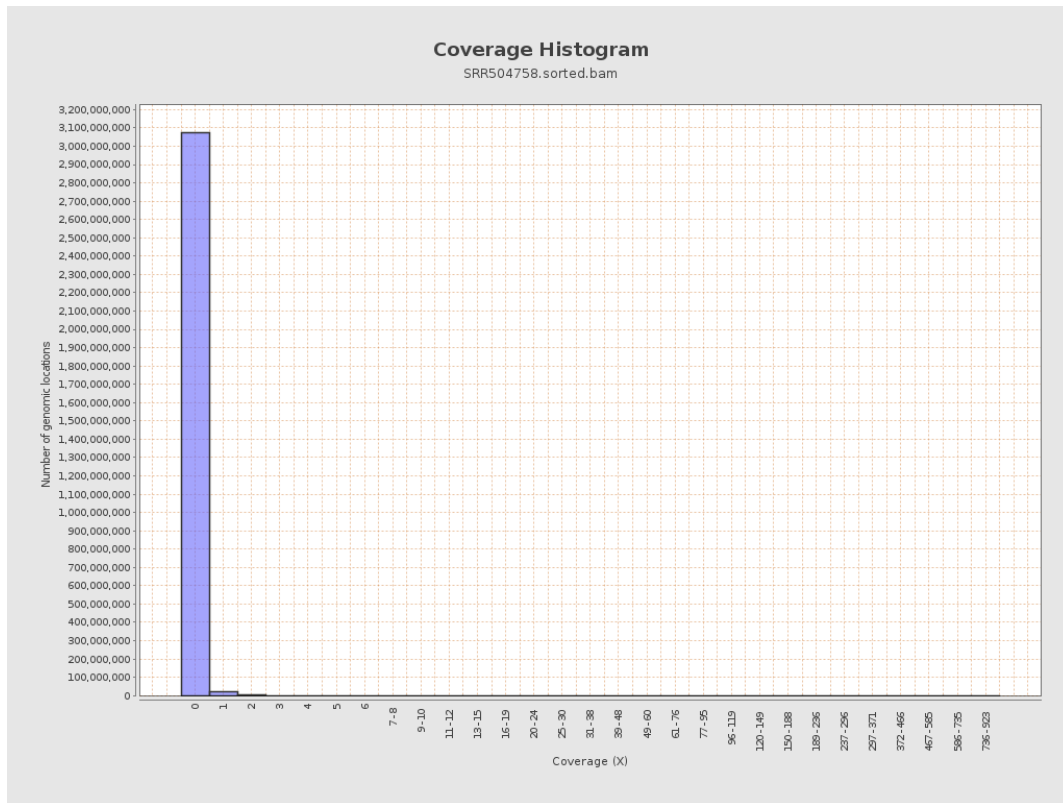
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3927410	0.0158	0.5742
chr2	243199373	4216862	0.0173	0.5322
chr3	198022430	4459862	0.0225	0.4968
chr4	191154276	3705370	0.0194	0.6787
chr5	180915260	3477738	0.0192	0.3884
chr6	171115067	3055628	0.0179	0.537
chr7	159138663	2158254	0.0136	0.3073
chr8	146364022	7345696	0.0502	2.9468
chr9	141213431	1479784	0.0105	0.1869
chr10	135534747	2230416	0.0165	0.3702
chr11	135006516	3116690	0.0231	1.0481
chr12	133851895	3143158	0.0235	0.58
chr13	115169878	1470466	0.0128	0.2028
chr14	107349540	3085706	0.0287	1.193
chr15	102531392	1003114	0.0098	0.1711

chr16	90354753	2027834	0.0224	0.9481
chr17	81195210	967914	0.0119	0.3035
chr18	78077248	803890	0.0103	0.1668
chr19	59128983	554260	0.0094	0.2511
chr20	63025520	796228	0.0126	0.2512
chr21	48129895	400634	0.0083	0.1878
chr22	51304566	233140	0.0045	0.1214
chrMT	16571	0	0	0
chrX	155270560	857998	0.0055	0.1215
chrY	59373566	536890	0.009	0.2388

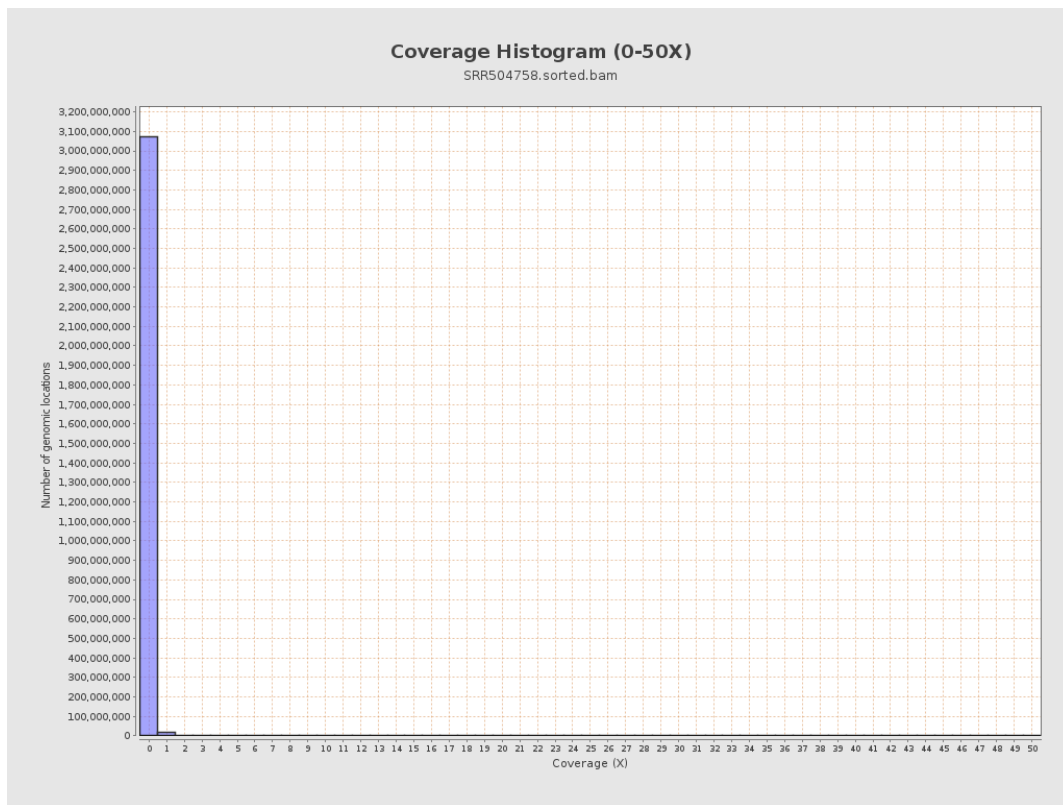
3. Results : Coverage across reference



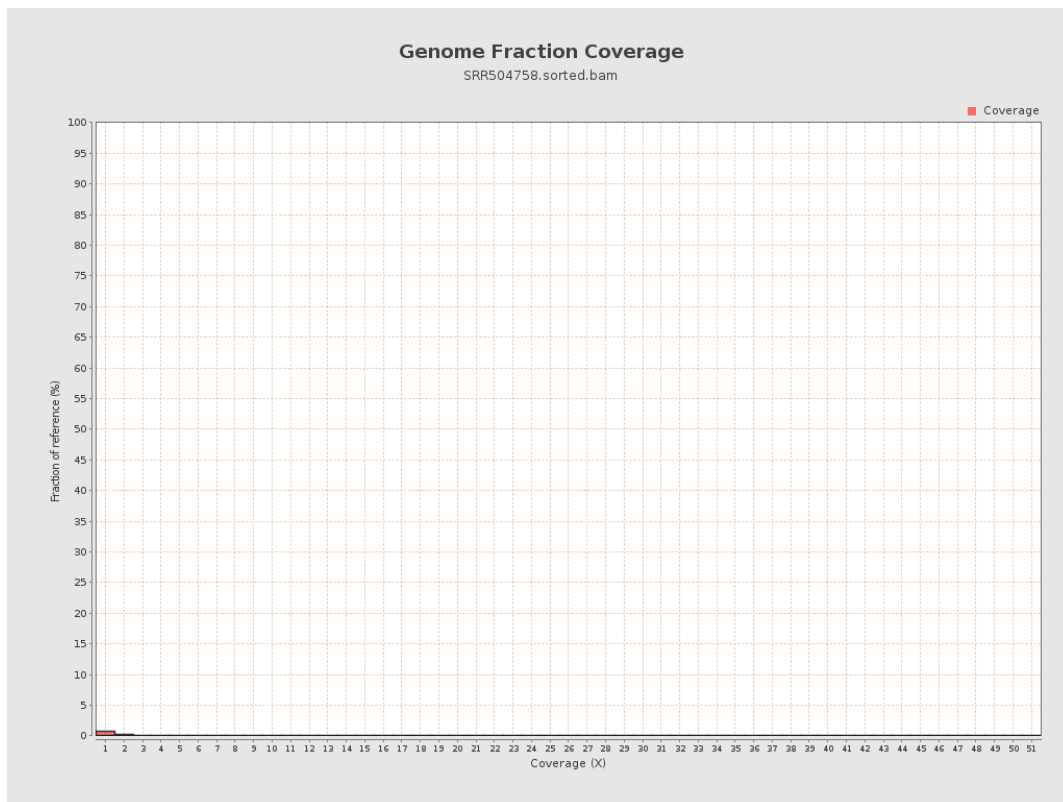
4. Results : Coverage Histogram



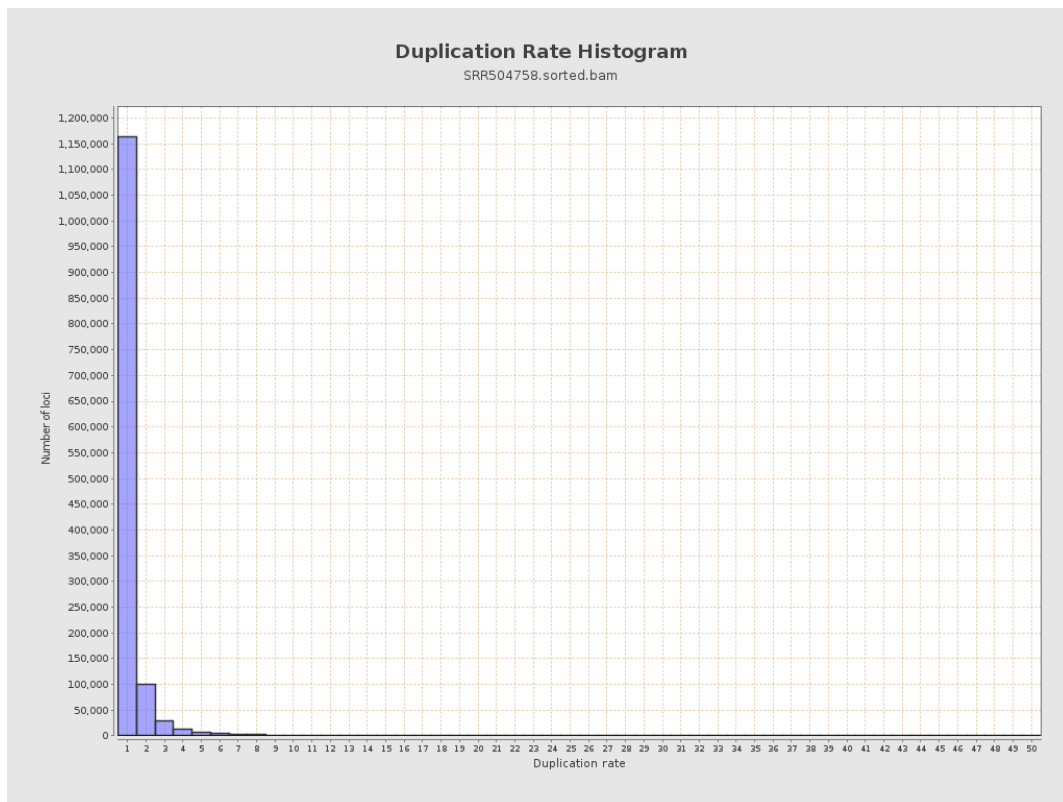
5. Results : Coverage Histogram (0-50X)



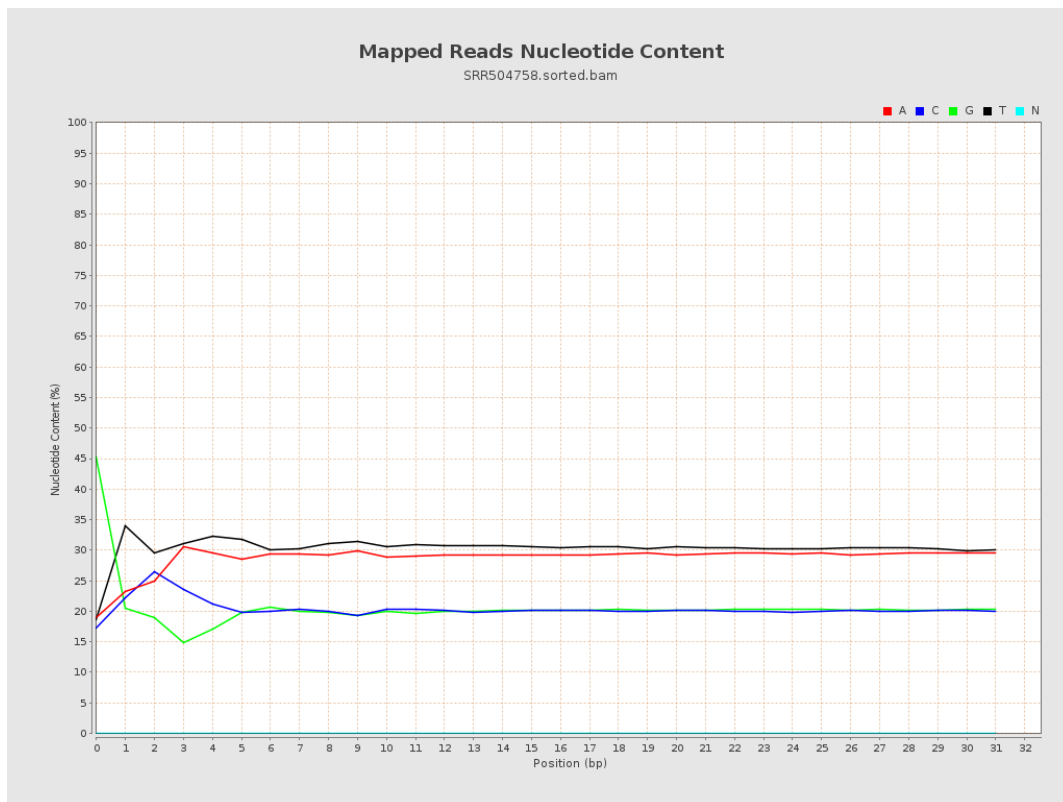
6. Results : Genome Fraction Coverage



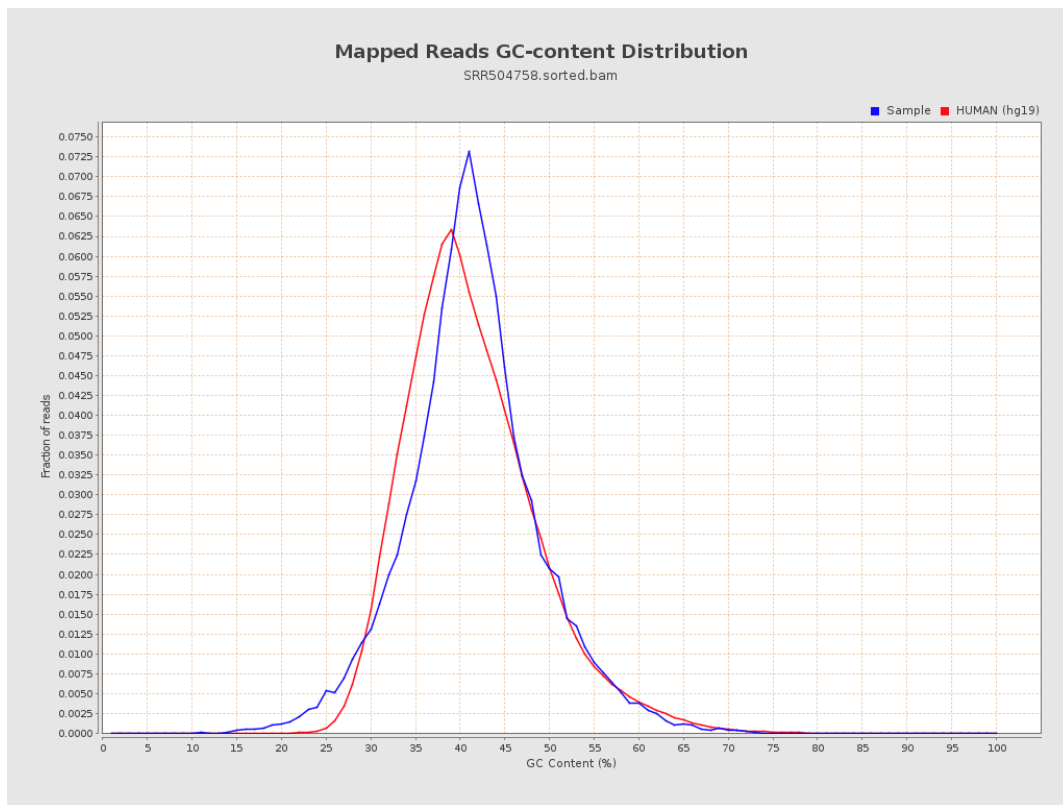
7. Results : Duplication Rate Histogram



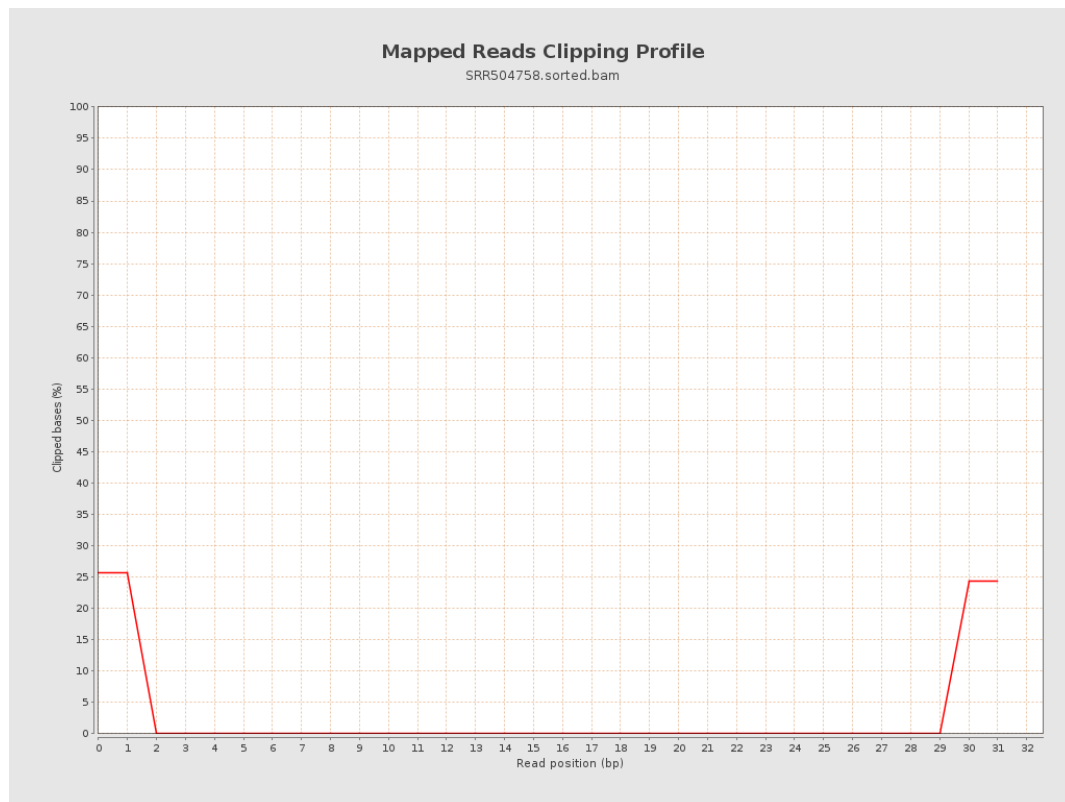
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

