

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 19:15:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504424.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_SRR504424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504424.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 19:15:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,125,260
Mapped reads	1,877,996 / 88.37%
Unmapped reads	247,264 / 11.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	110,261 / 5.19%
Duplication rate	3.74%
Clipped reads	2,946 / 0.14%

2.2. ACGT Content

Number/percentage of A's	17,467,842 / 29.07%
Number/percentage of C's	12,010,369 / 19.99%
Number/percentage of T's	18,549,962 / 30.87%
Number/percentage of G's	12,061,650 / 20.07%
Number/percentage of N's	157 / 0%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0194
Standard Deviation	0.3729

2.4. Mapping Quality

Mean Mapping Quality	8.32
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2.5. Mismatches and indels

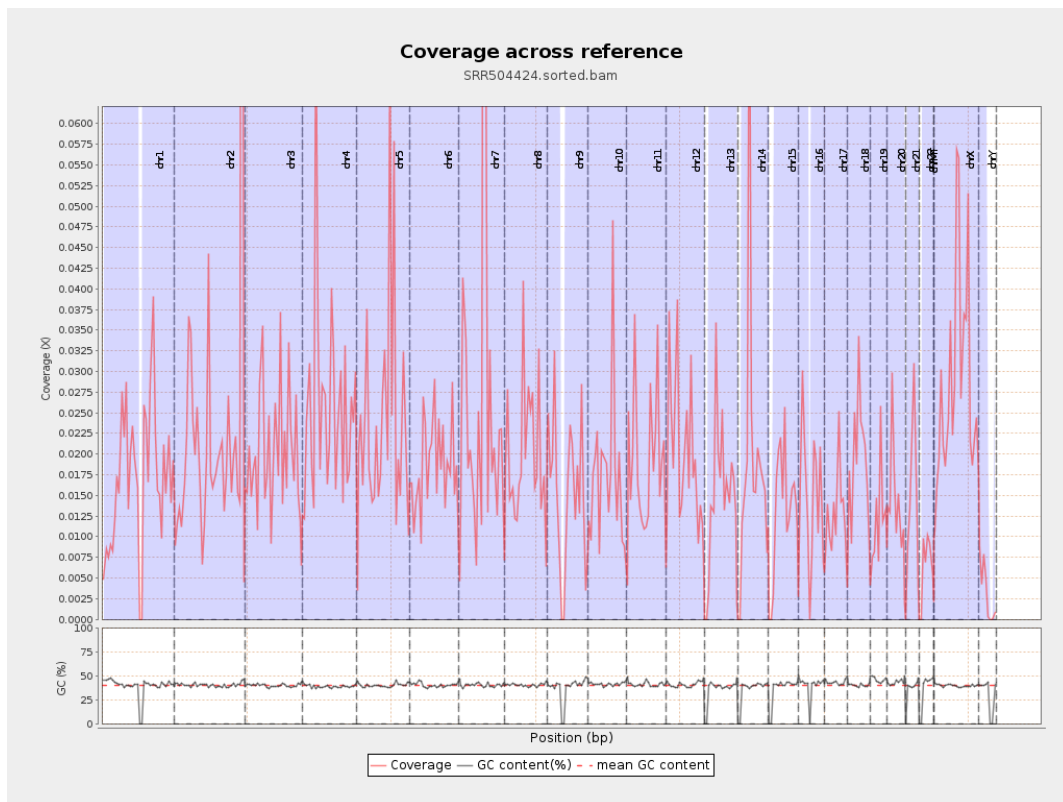
General error rate	0.06%
Mismatches	34,043

2.6. Chromosome stats

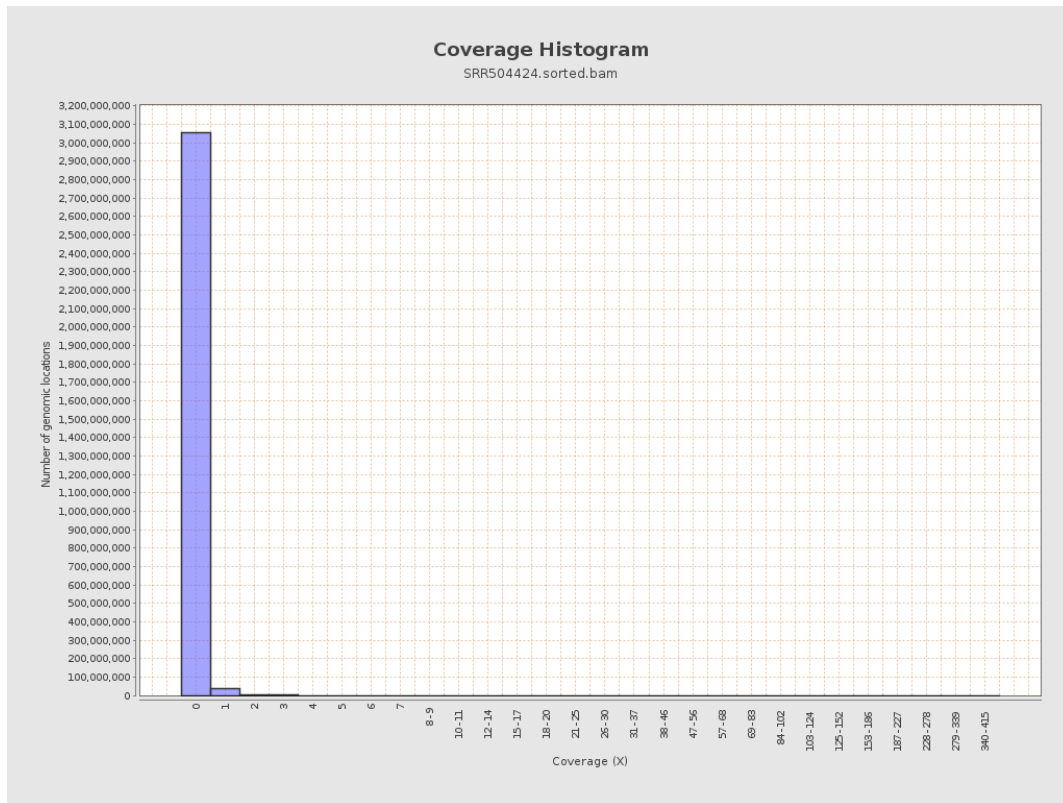
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4230896	0.017	0.2299
chr2	243199373	5830498	0.024	0.8109
chr3	198022430	3995416	0.0202	0.2145
chr4	191154276	4909762	0.0257	0.4945
chr5	180915260	4441128	0.0245	0.3523
chr6	171115067	3194468	0.0187	0.1953
chr7	159138663	4339792	0.0273	0.6711
chr8	146364022	2930160	0.02	0.1973
chr9	141213431	2182076	0.0155	0.1711
chr10	135534747	2319190	0.0171	0.2309
chr11	135006516	2594512	0.0192	0.1888
chr12	133851895	2737668	0.0205	0.2049
chr13	115169878	1723680	0.015	0.1738
chr14	107349540	2100252	0.0196	0.548
chr15	102531392	1361334	0.0133	0.1687

chr16	90354753	1314026	0.0145	0.3178
chr17	81195210	1012670	0.0125	0.1449
chr18	78077248	1553946	0.0199	0.1907
chr19	59128983	714144	0.0121	0.2893
chr20	63025520	904346	0.0143	0.1627
chr21	48129895	691190	0.0144	0.1969
chr22	51304566	327444	0.0064	0.0982
chrMT	16571	160	0.0097	0.1153
chrX	155270560	4493526	0.0289	0.2754
chrY	59373566	187696	0.0032	0.0648

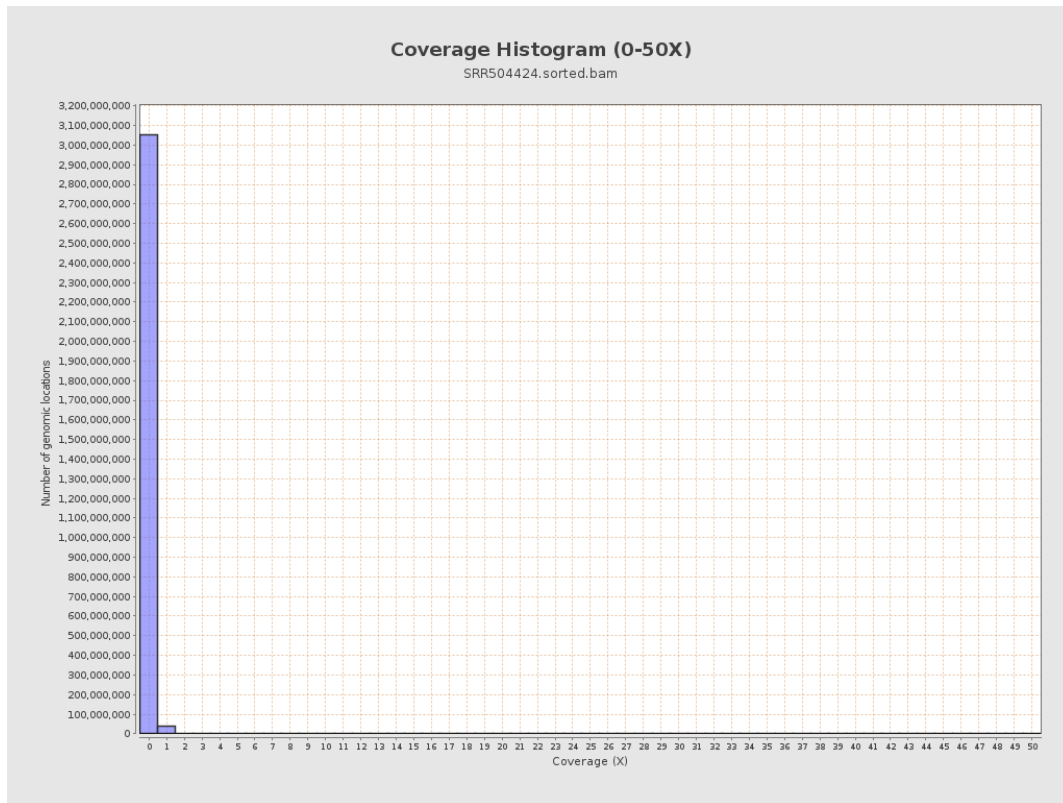
3. Results : Coverage across reference



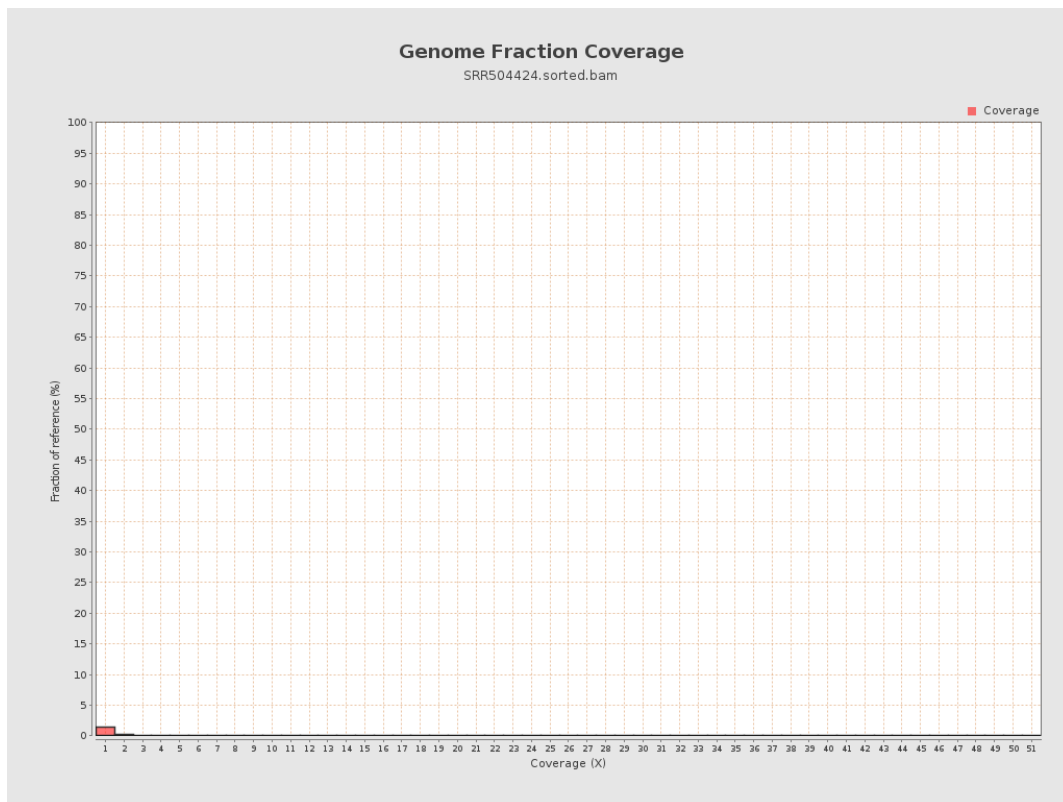
4. Results : Coverage Histogram



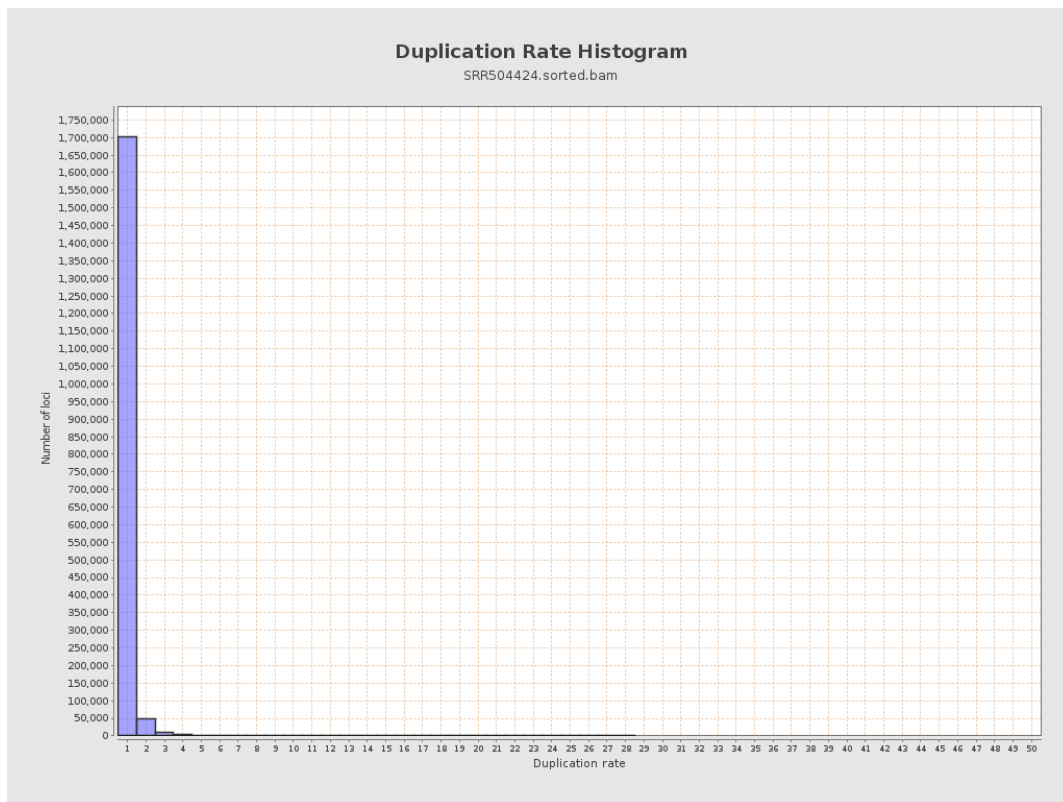
5. Results : Coverage Histogram (0-50X)



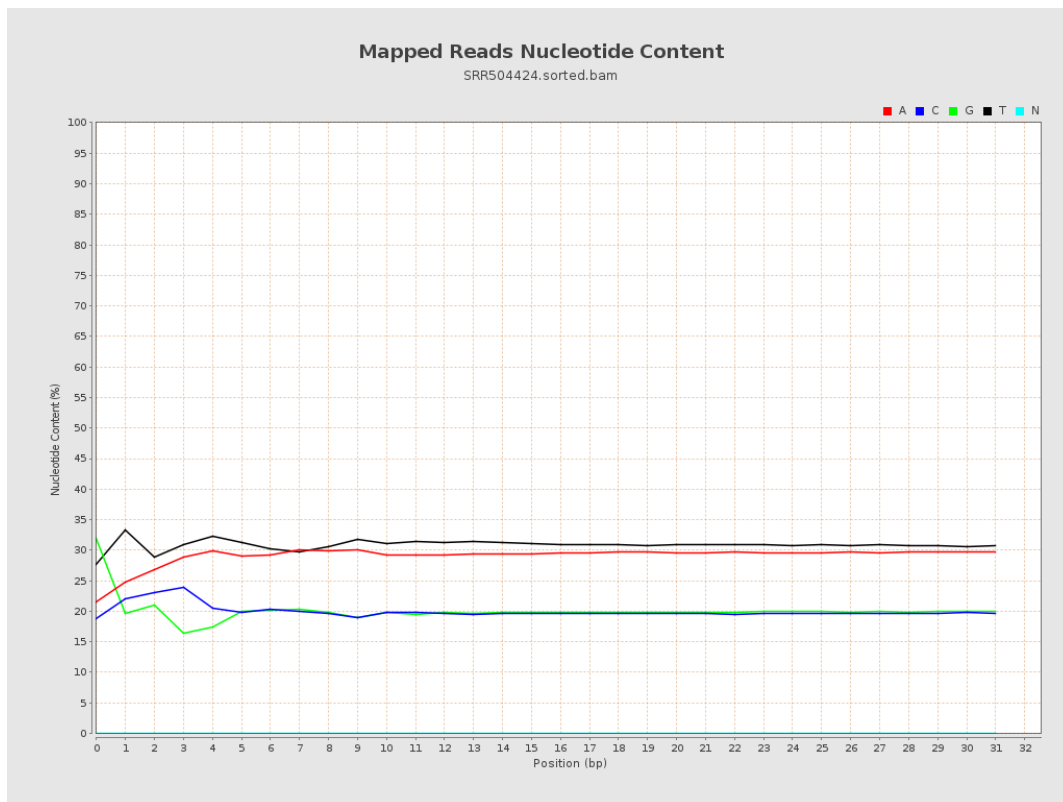
6. Results : Genome Fraction Coverage



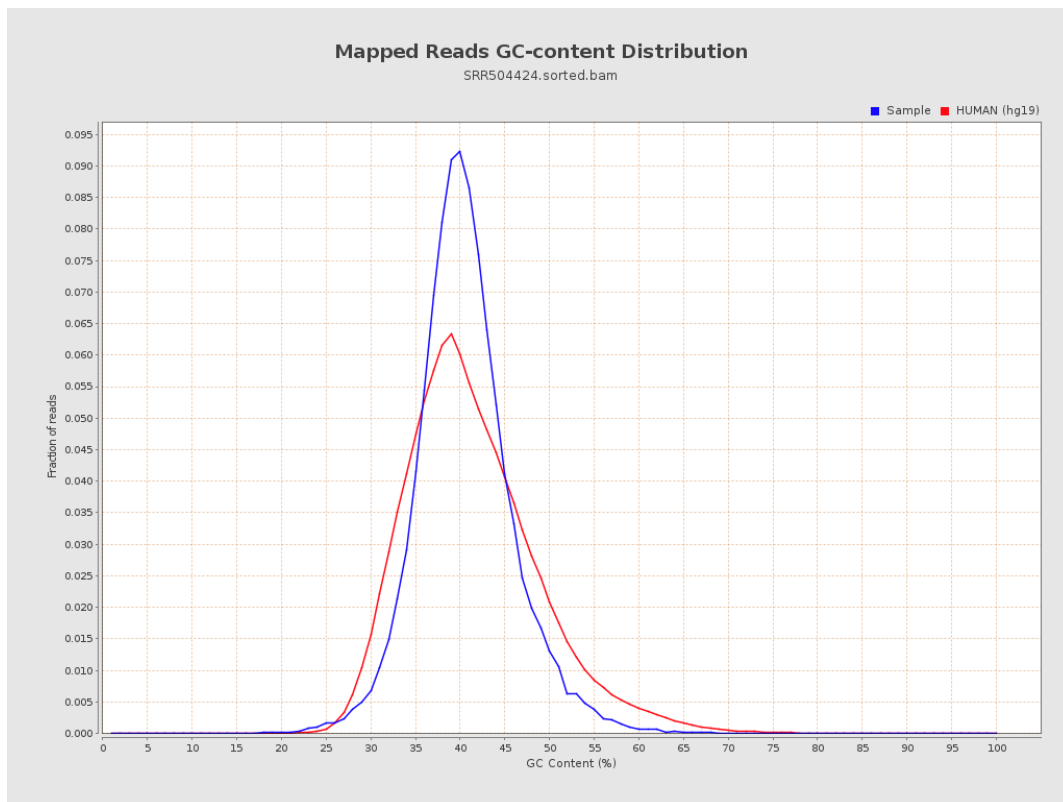
7. Results : Duplication Rate Histogram



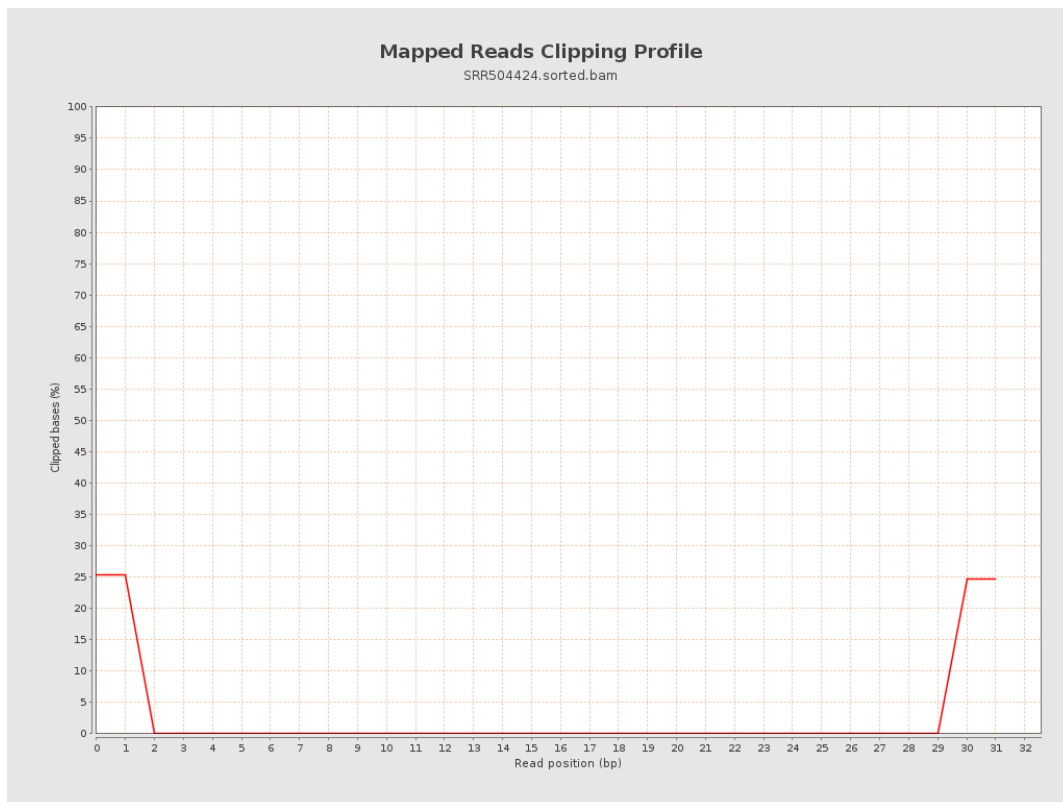
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

