

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:13:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504719.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_SRR504719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:13:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,026,636
Mapped reads	1,788,219 / 88.24%
Unmapped reads	238,417 / 11.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	215,584 / 10.64%
Duplication rate	3.55%
Clipped reads	2,845 / 0.14%

2.2. ACGT Content

Number/percentage of A's	16,597,982 / 29.01%
Number/percentage of C's	11,534,738 / 20.16%
Number/percentage of T's	17,494,864 / 30.58%
Number/percentage of G's	11,589,654 / 20.26%
Number/percentage of N's	80 / 0%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0185
Standard Deviation	0.9776

2.4. Mapping Quality

Mean Mapping Quality	8.33
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2.5. Mismatches and indels

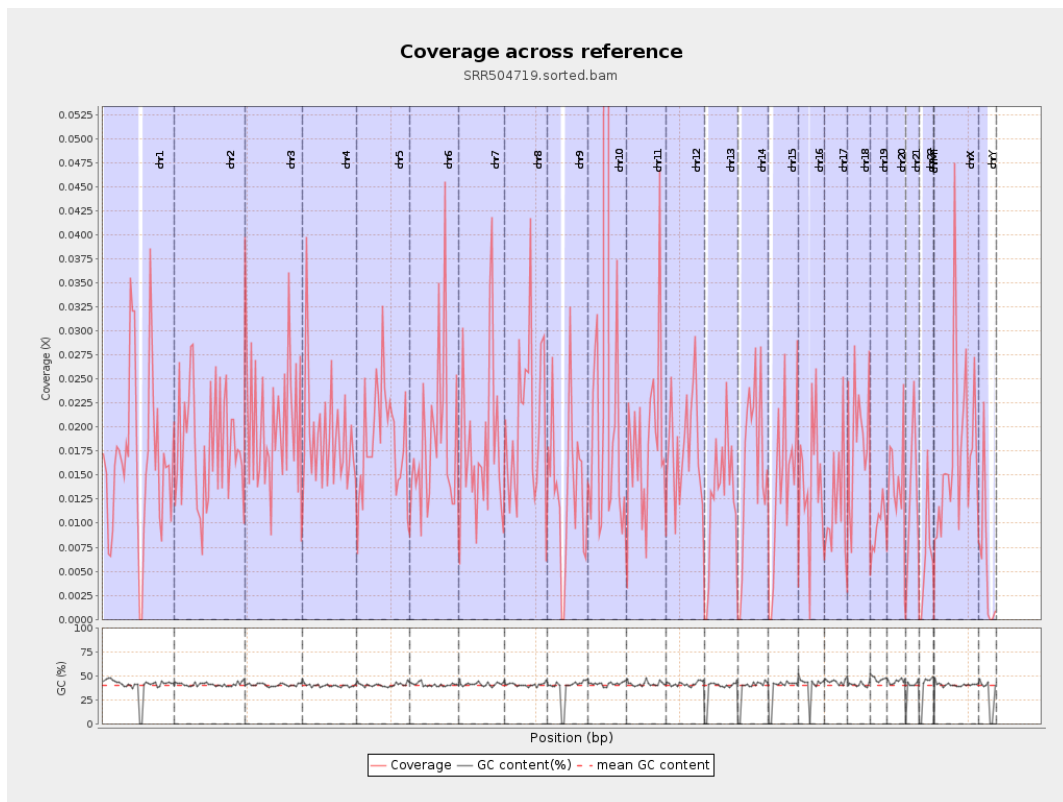
General error rate	0.06%
Mismatches	32,667

2.6. Chromosome stats

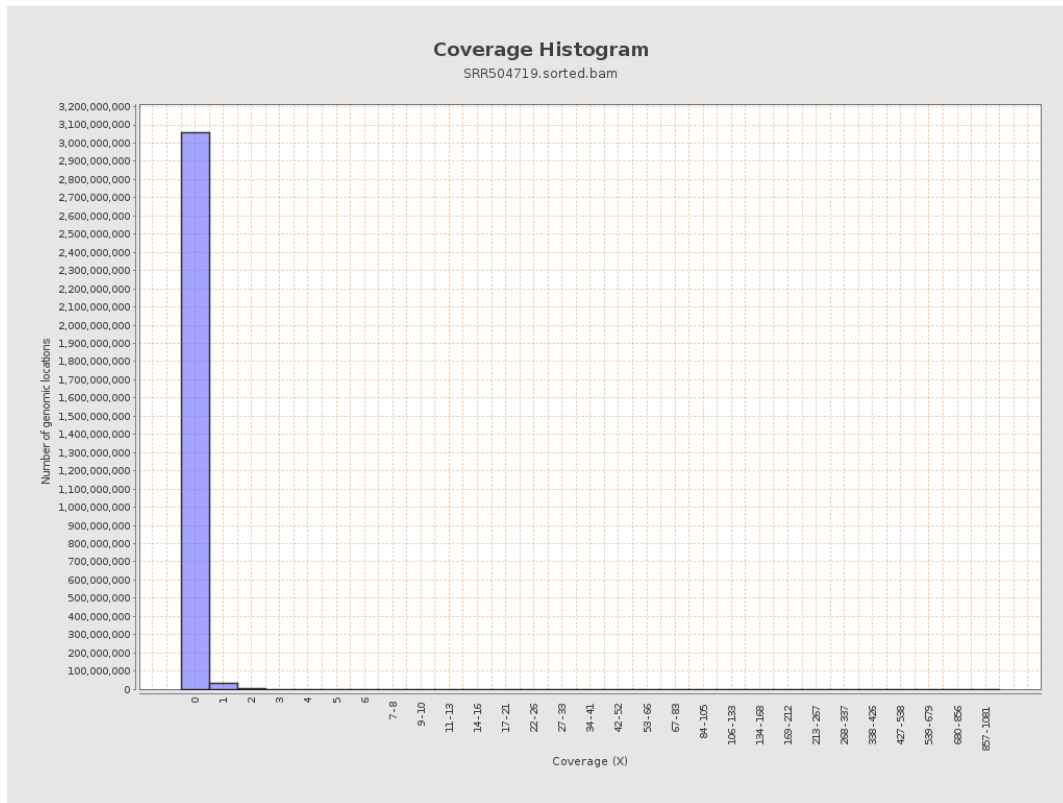
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4064562	0.0163	0.2157
chr2	243199373	4398550	0.0181	0.1959
chr3	198022430	4043418	0.0204	0.2279
chr4	191154276	3558788	0.0186	0.2052
chr5	180915260	3416154	0.0189	0.1955
chr6	171115067	3123626	0.0183	0.2294
chr7	159138663	2810846	0.0177	0.2239
chr8	146364022	2966218	0.0203	0.2283
chr9	141213431	1941032	0.0137	0.1831
chr10	135534747	8157638	0.0602	4.5741
chr11	135006516	2531730	0.0188	0.2302
chr12	133851895	2387732	0.0178	0.1981
chr13	115169878	1452554	0.0126	0.1573
chr14	107349540	1724690	0.0161	0.2073
chr15	102531392	1423180	0.0139	0.1699

chr16	90354753	1282792	0.0142	0.2048
chr17	81195210	944878	0.0116	0.1779
chr18	78077248	1481220	0.019	0.2086
chr19	59128983	562308	0.0095	0.1221
chr20	63025520	923666	0.0147	0.1693
chr21	48129895	610930	0.0127	0.1628
chr22	51304566	326102	0.0064	0.1257
chrMT	16571	0	0	0
chrX	155270560	2735282	0.0176	0.2418
chrY	59373566	349422	0.0059	0.1203

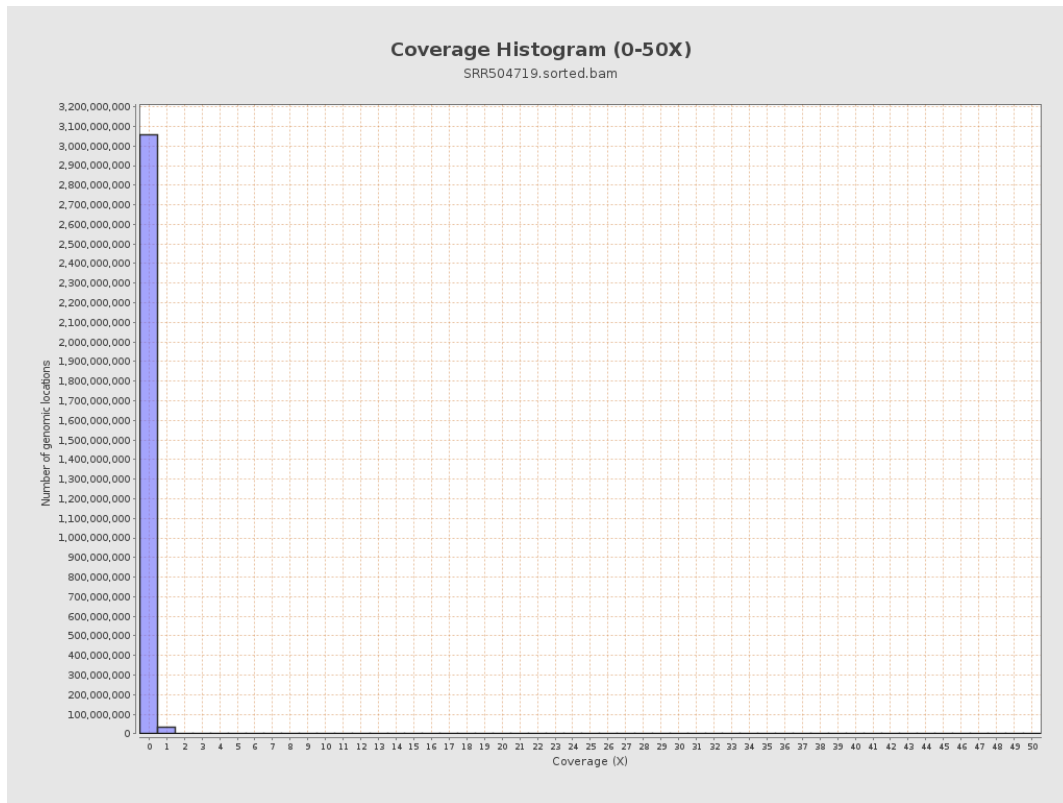
3. Results : Coverage across reference



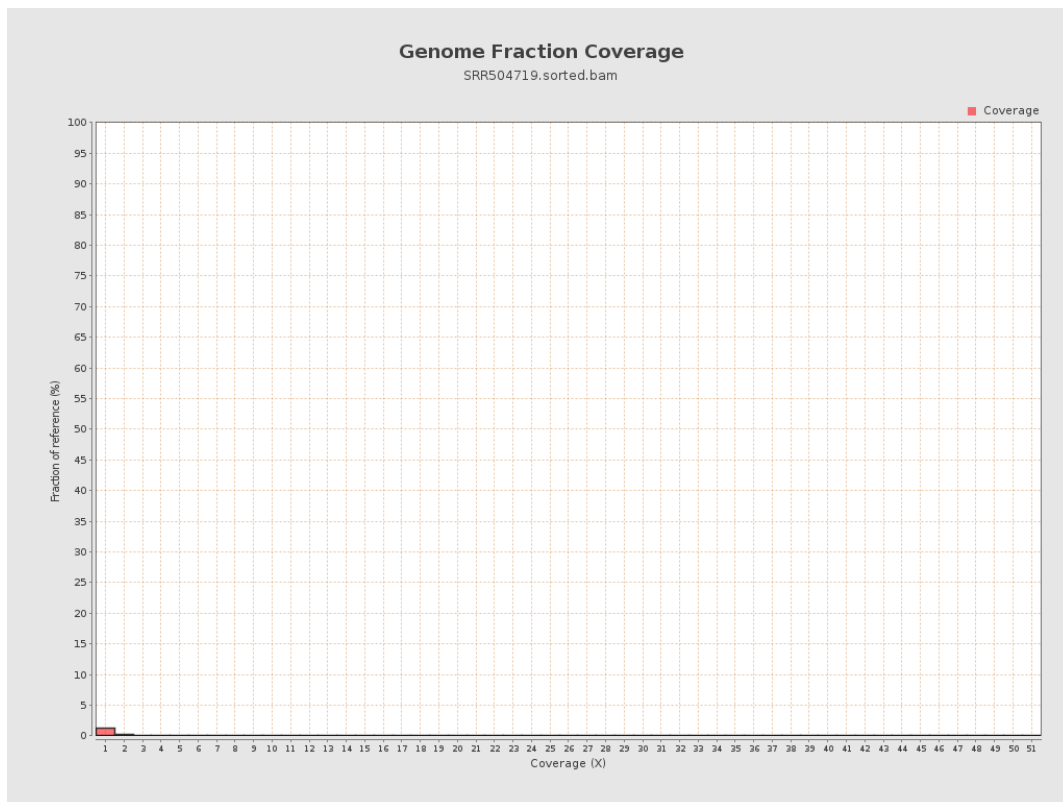
4. Results : Coverage Histogram



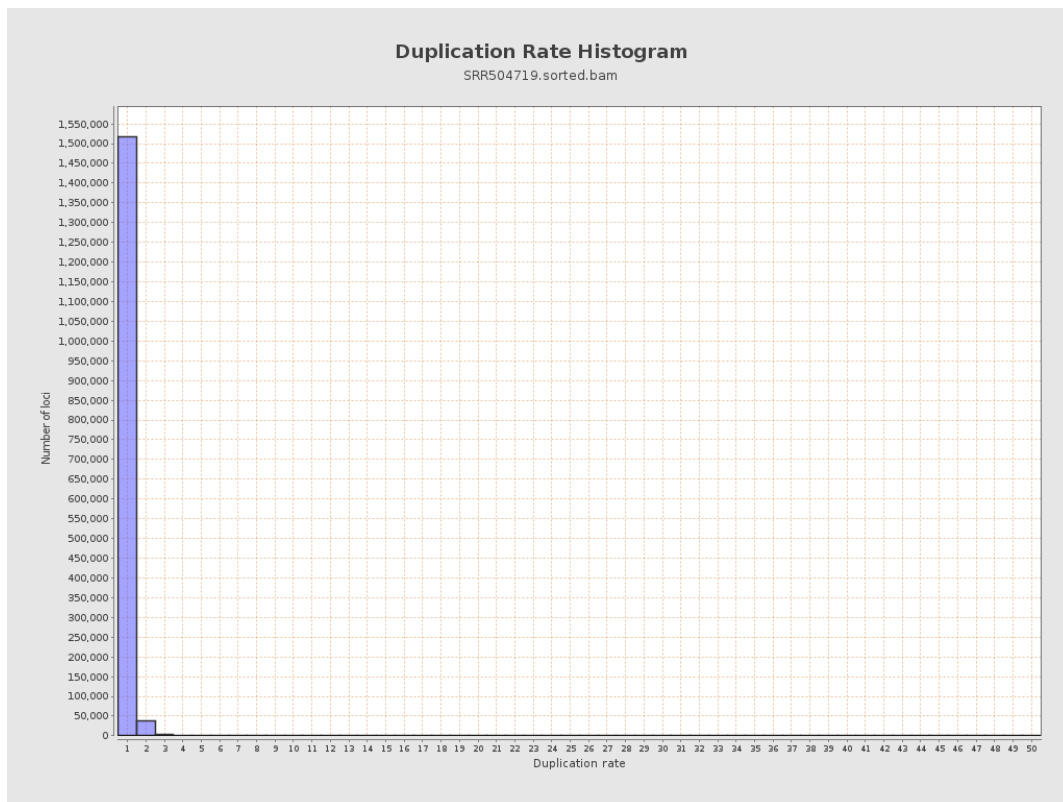
5. Results : Coverage Histogram (0-50X)



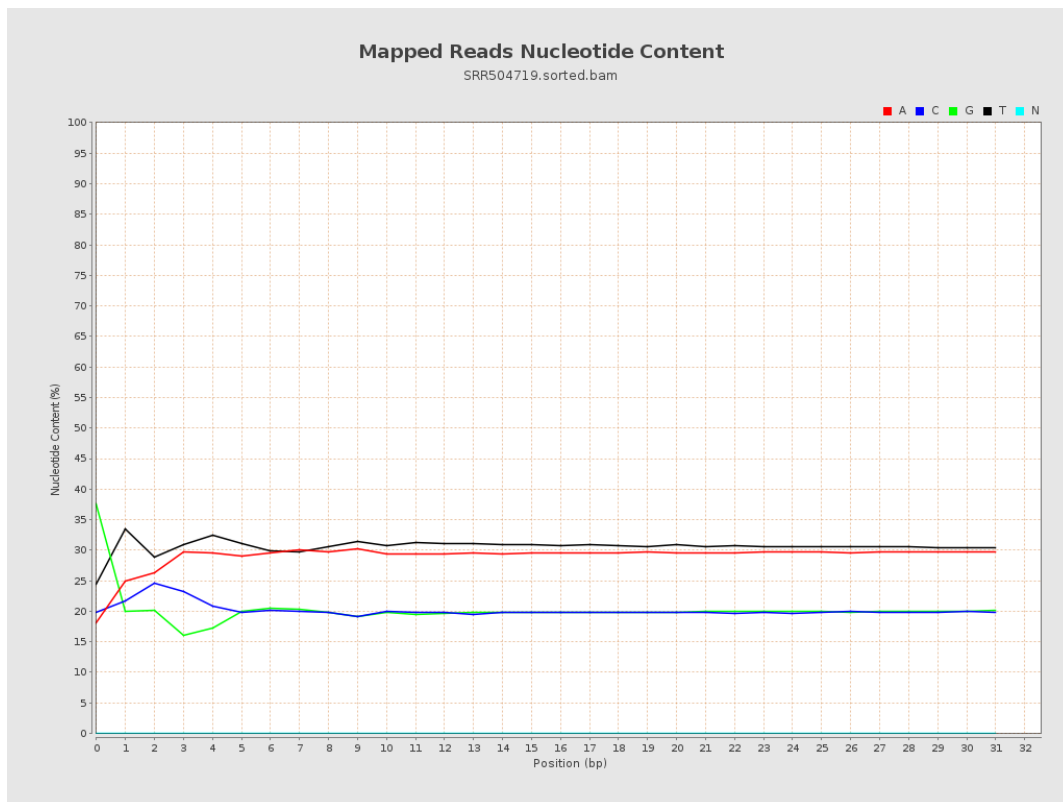
6. Results : Genome Fraction Coverage



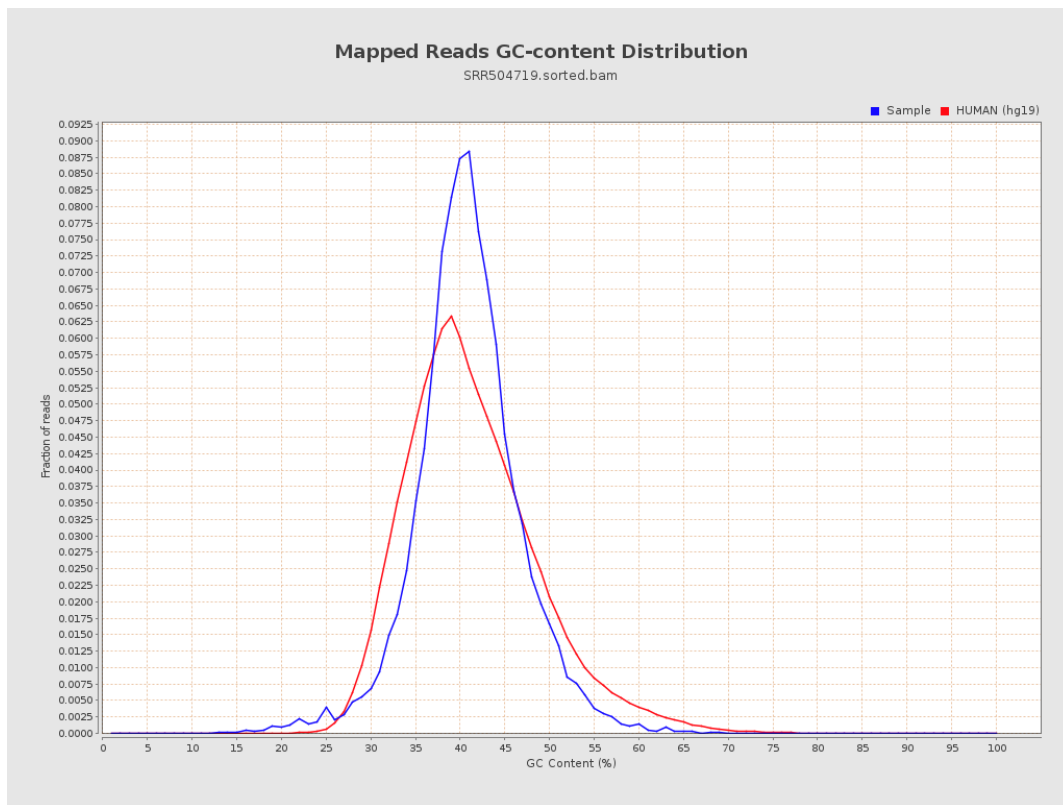
7. Results : Duplication Rate Histogram



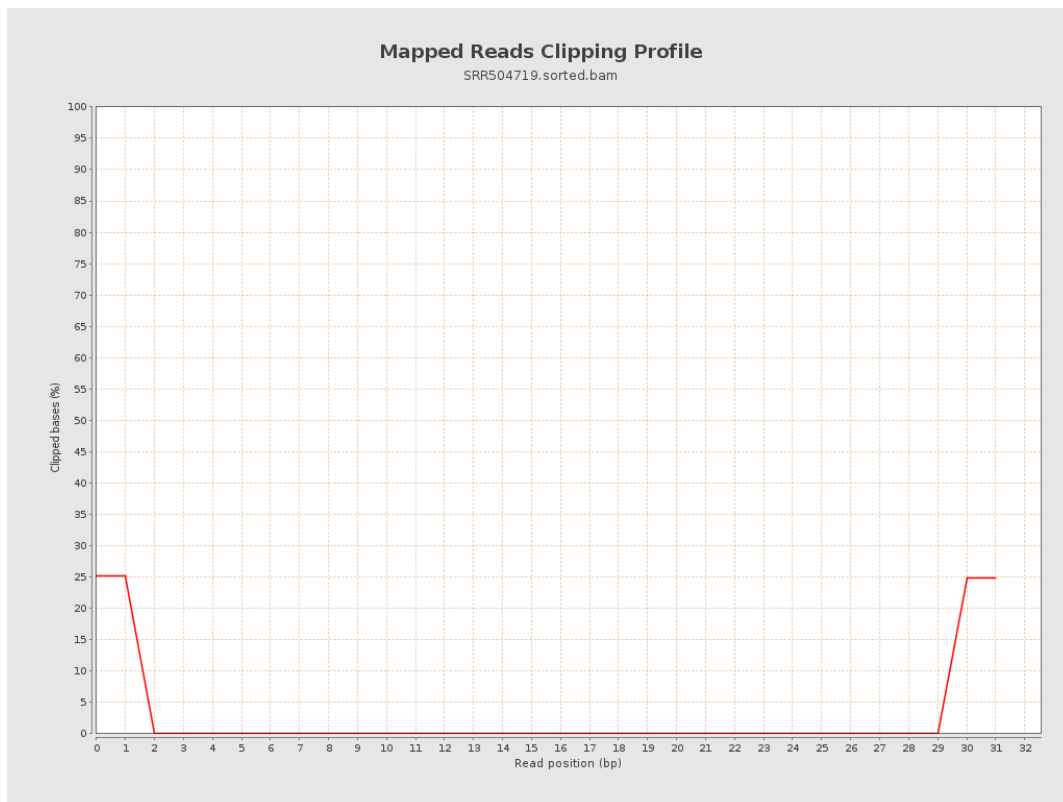
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

