

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:02:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504713.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_SRR504713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504713.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:02:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,077,317
Mapped reads	1,879,426 / 90.47%
Unmapped reads	197,891 / 9.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	217,776 / 10.48%
Duplication rate	7.55%
Clipped reads	2,977 / 0.14%

2.2. ACGT Content

Number/percentage of A's	17,445,522 / 29.01%
Number/percentage of C's	12,006,323 / 19.97%
Number/percentage of T's	18,525,598 / 30.81%
Number/percentage of G's	12,158,160 / 20.22%
Number/percentage of N's	75 / 0%
GC Percentage	40.18%

2.3. Coverage

Mean	0.0194
Standard Deviation	0.5642

2.4. Mapping Quality

Mean Mapping Quality	7.86
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2.5. Mismatches and indels

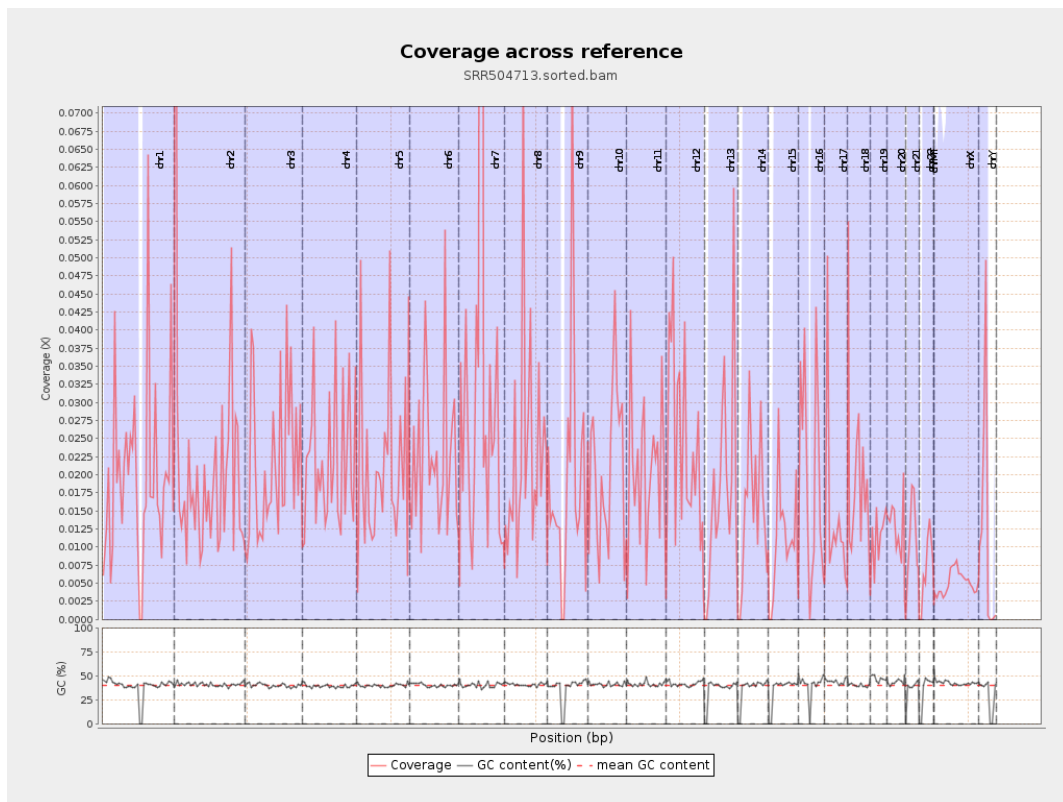
General error rate	0.05%
Mismatches	30,179

2.6. Chromosome stats

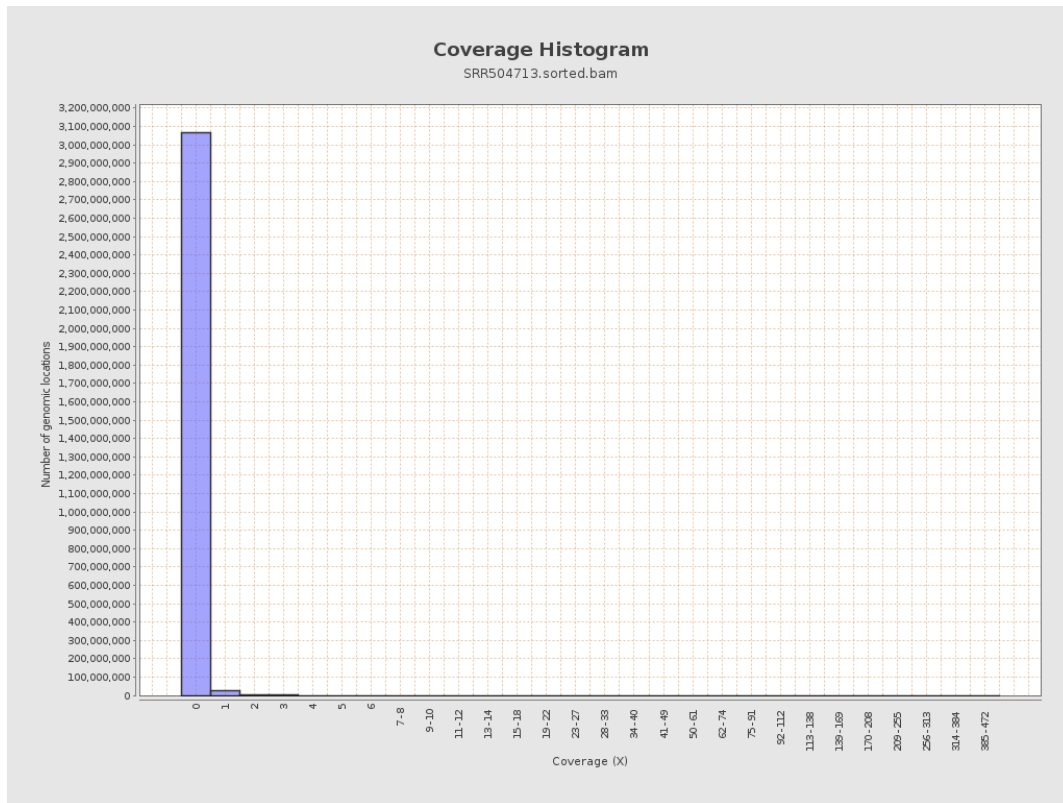
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4910538	0.0197	0.3769
chr2	243199373	5281918	0.0217	0.6097
chr3	198022430	4304498	0.0217	0.3661
chr4	191154276	4212956	0.022	0.2835
chr5	180915260	3757404	0.0208	0.3478
chr6	171115067	3926000	0.0229	0.3786
chr7	159138663	5836662	0.0367	1.9012
chr8	146364022	3386606	0.0231	0.437
chr9	141213431	2588892	0.0183	0.4017
chr10	135534747	2808720	0.0207	0.3639
chr11	135006516	2817348	0.0209	0.3465
chr12	133851895	3228962	0.0241	0.5255
chr13	115169878	2119710	0.0184	0.4448
chr14	107349540	1622472	0.0151	0.2126
chr15	102531392	1150802	0.0112	0.164

chr16	90354753	1726444	0.0191	0.4437
chr17	81195210	1093554	0.0135	0.3148
chr18	78077248	1468988	0.0188	0.2757
chr19	59128983	672438	0.0114	0.1694
chr20	63025520	813274	0.0129	0.1829
chr21	48129895	515436	0.0107	0.189
chr22	51304566	353754	0.0069	0.1181
chrMT	16571	32	0.0019	0.0439
chrX	155270560	794172	0.0051	0.0837
chrY	59373566	744098	0.0125	0.275

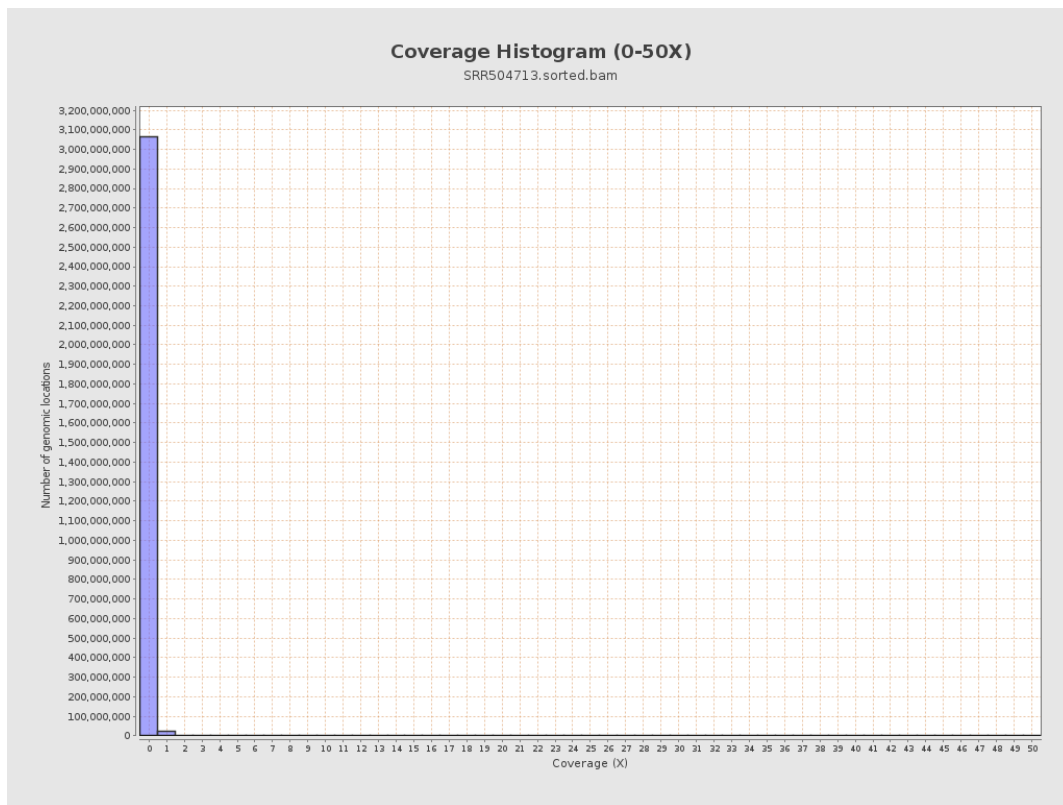
3. Results : Coverage across reference



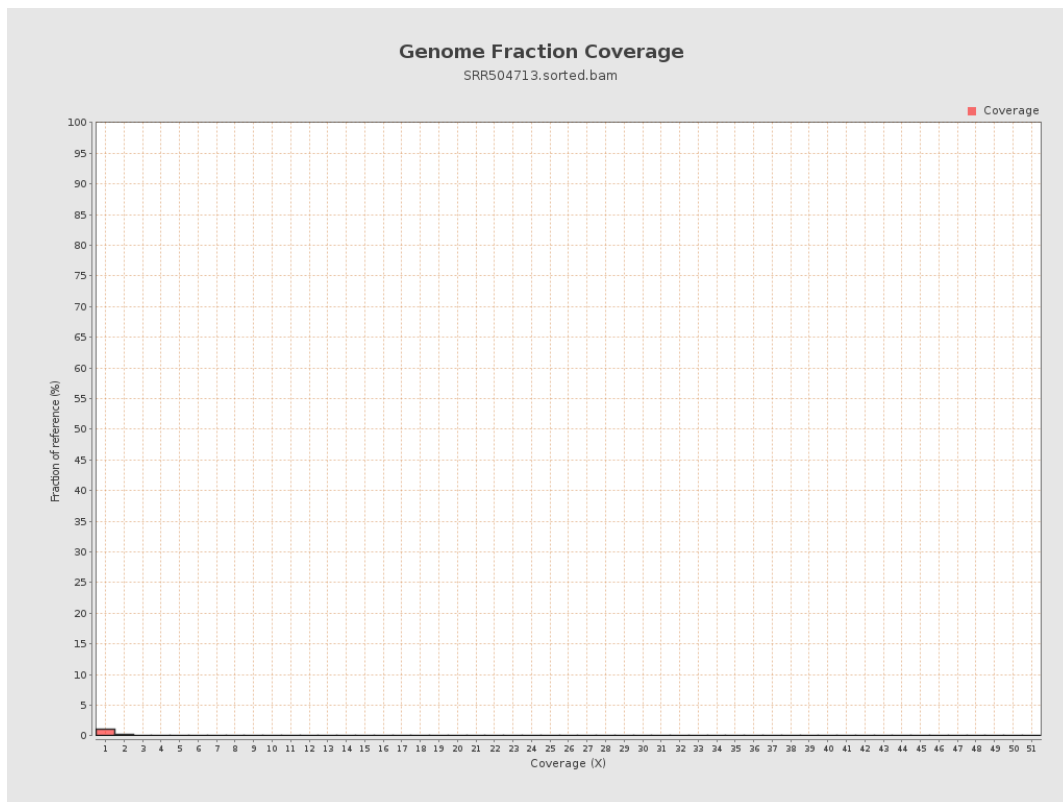
4. Results : Coverage Histogram



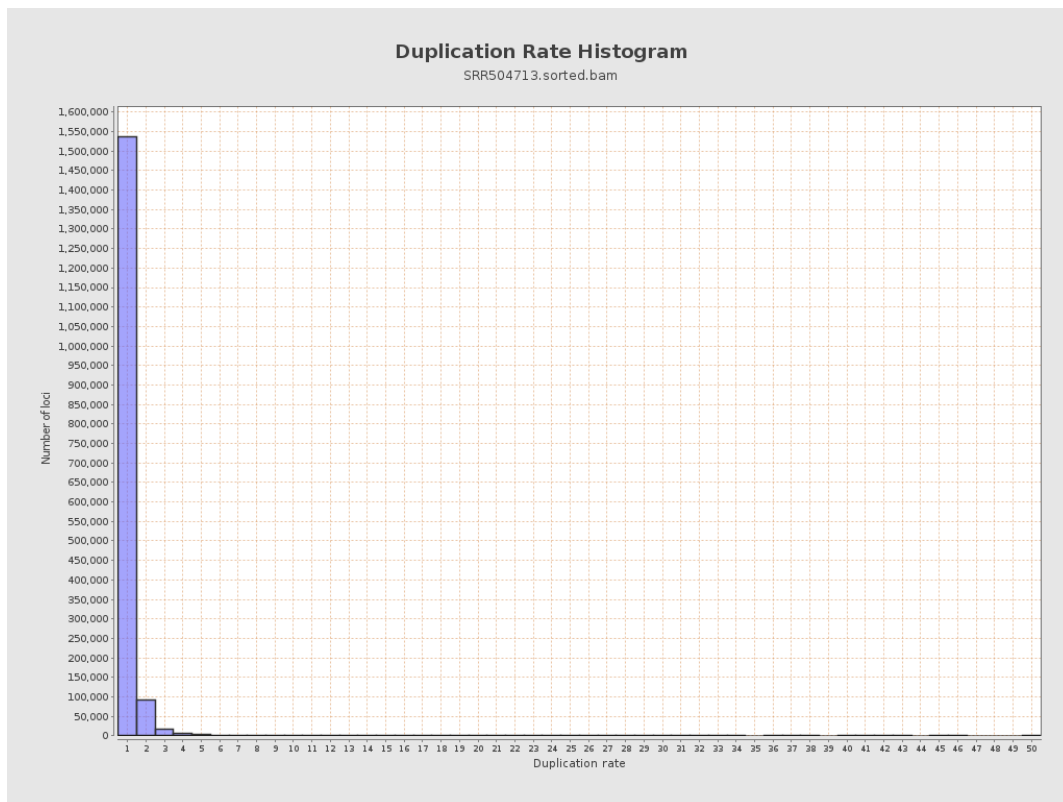
5. Results : Coverage Histogram (0-50X)



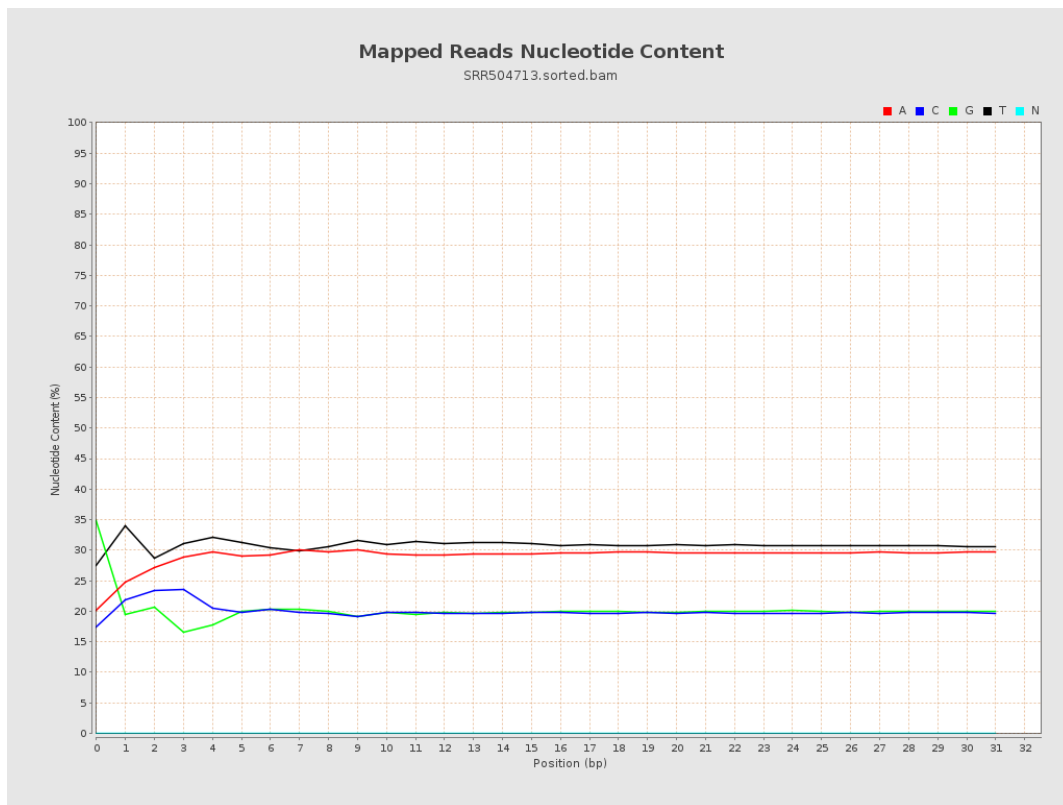
6. Results : Genome Fraction Coverage



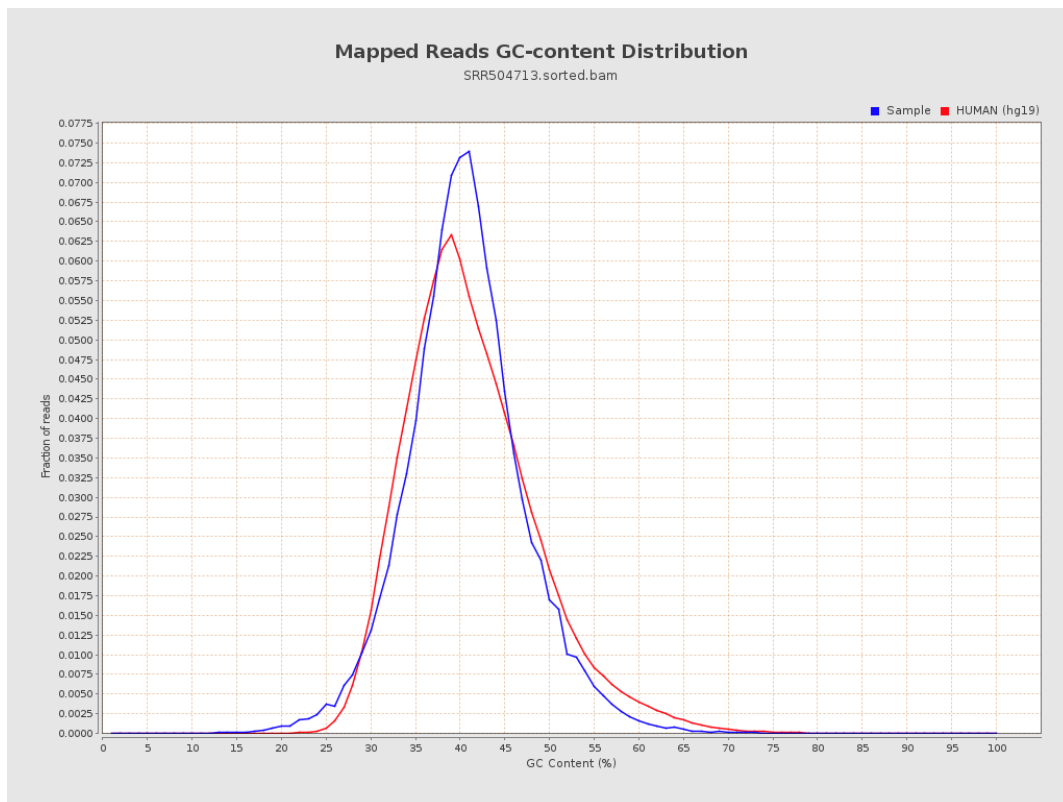
7. Results : Duplication Rate Histogram



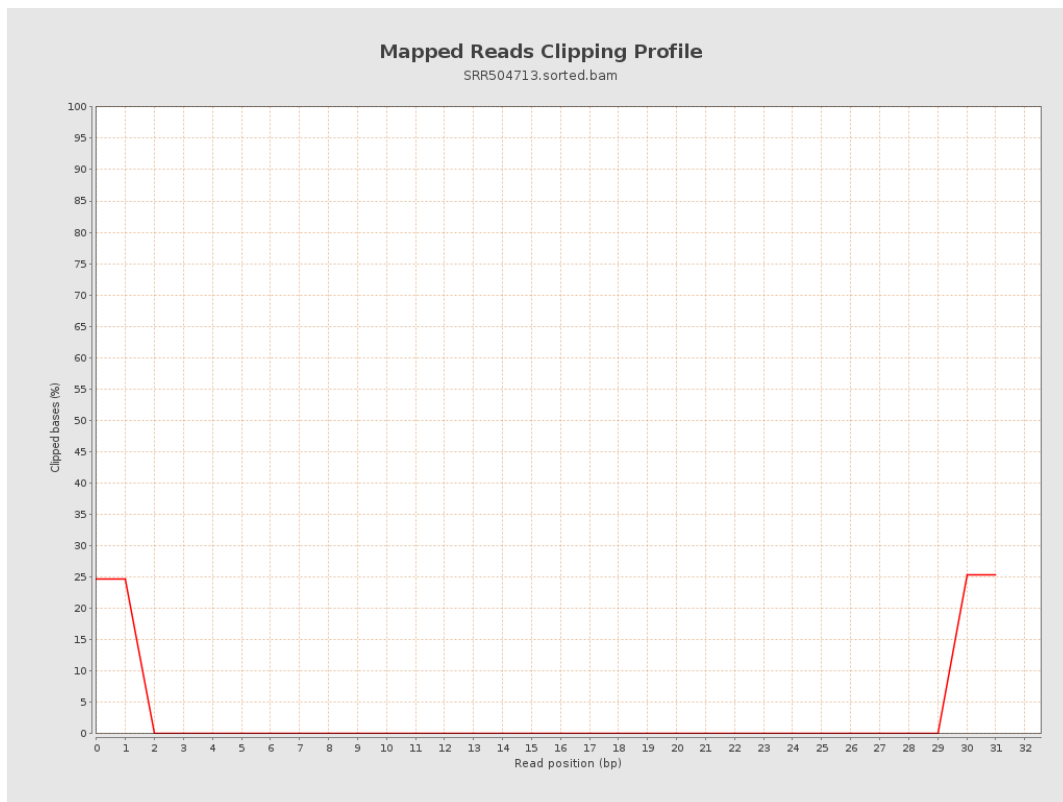
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

