

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:10:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504718.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_SRR504718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504718.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:10:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,945,643
Mapped reads	1,727,251 / 88.78%
Unmapped reads	218,392 / 11.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	126,520 / 6.5%
Duplication rate	3.57%
Clipped reads	2,797 / 0.14%

2.2. ACGT Content

Number/percentage of A's	16,161,188 / 29.24%
Number/percentage of C's	10,950,243 / 19.81%
Number/percentage of T's	17,026,016 / 30.81%
Number/percentage of G's	11,128,924 / 20.14%
Number/percentage of N's	67 / 0%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0179
Standard Deviation	0.5483

2.4. Mapping Quality

Mean Mapping Quality	8.49
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2.5. Mismatches and indels

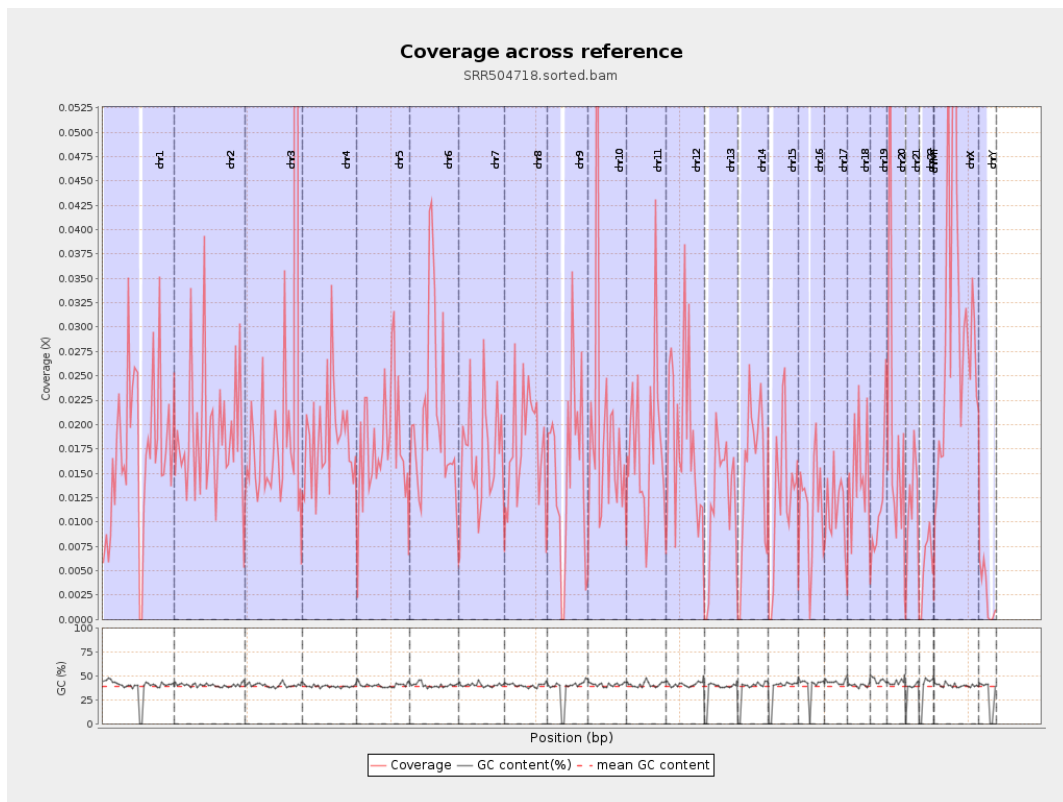
General error rate	0.06%
Mismatches	31,522

2.6. Chromosome stats

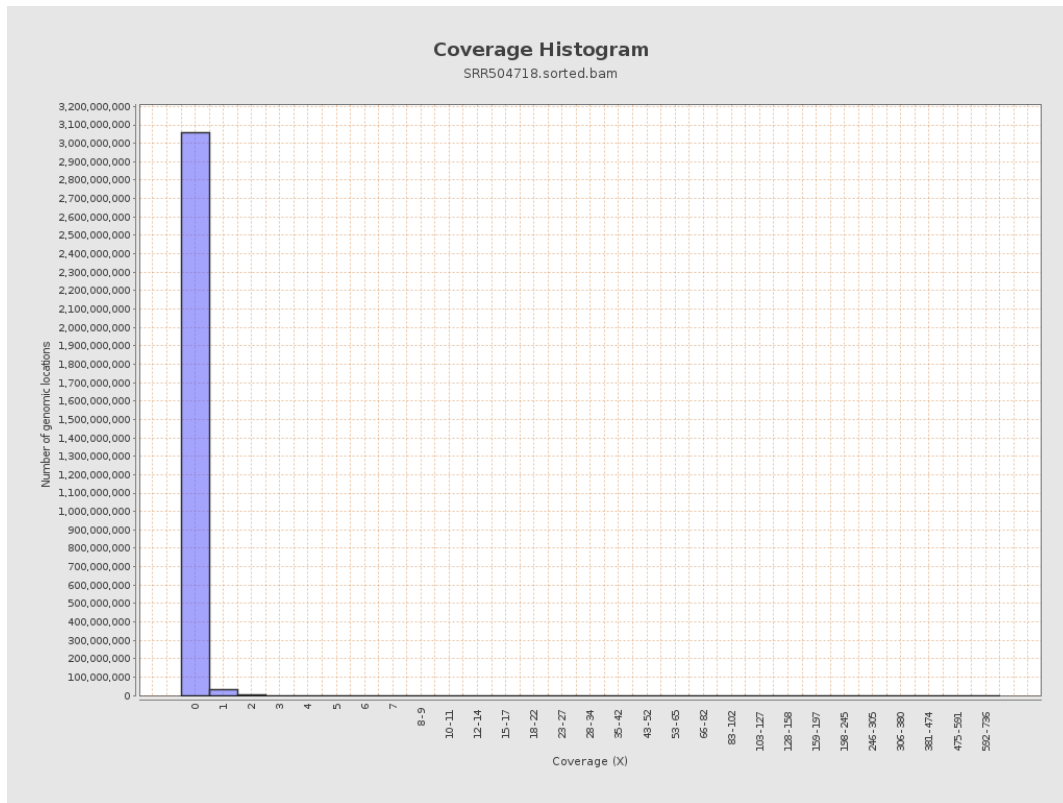
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4210460	0.0169	0.1945
chr2	243199373	4644380	0.0191	0.2313
chr3	198022430	5724972	0.0289	1.9249
chr4	191154276	3549830	0.0186	0.1801
chr5	180915260	3281750	0.0181	0.2152
chr6	171115067	3496160	0.0204	0.2409
chr7	159138663	2690234	0.0169	0.1893
chr8	146364022	2606894	0.0178	0.2058
chr9	141213431	2178486	0.0154	0.1905
chr10	135534747	2686736	0.0198	0.5763
chr11	135006516	2441814	0.0181	0.214
chr12	133851895	2482164	0.0185	0.2042
chr13	115169878	1410074	0.0122	0.1402
chr14	107349540	1579826	0.0147	0.1638
chr15	102531392	1286000	0.0125	0.1408

chr16	90354753	1022048	0.0113	0.2196
chr17	81195210	896984	0.011	0.1309
chr18	78077248	1190086	0.0152	0.1664
chr19	59128983	710376	0.012	0.194
chr20	63025520	1273324	0.0202	0.4297
chr21	48129895	549844	0.0114	0.1377
chr22	51304566	285686	0.0056	0.1069
chrMT	16571	32	0.0019	0.0439
chrX	155270560	4911428	0.0316	0.542
chrY	59373566	156850	0.0026	0.0575

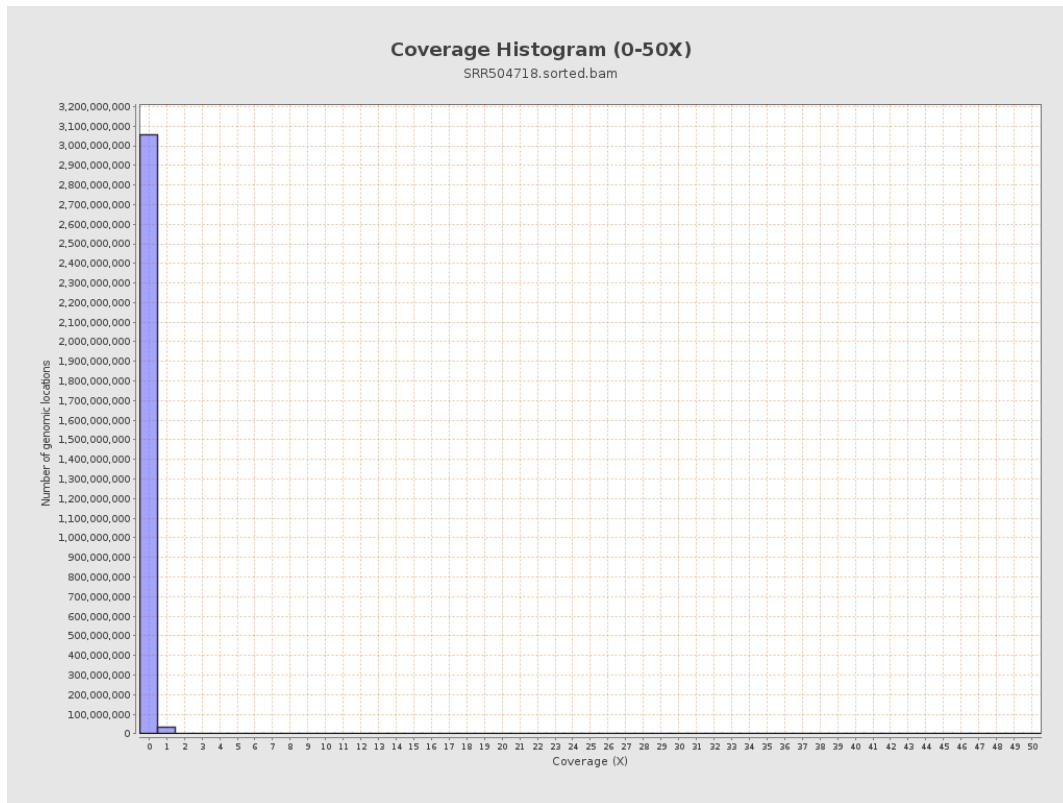
3. Results : Coverage across reference



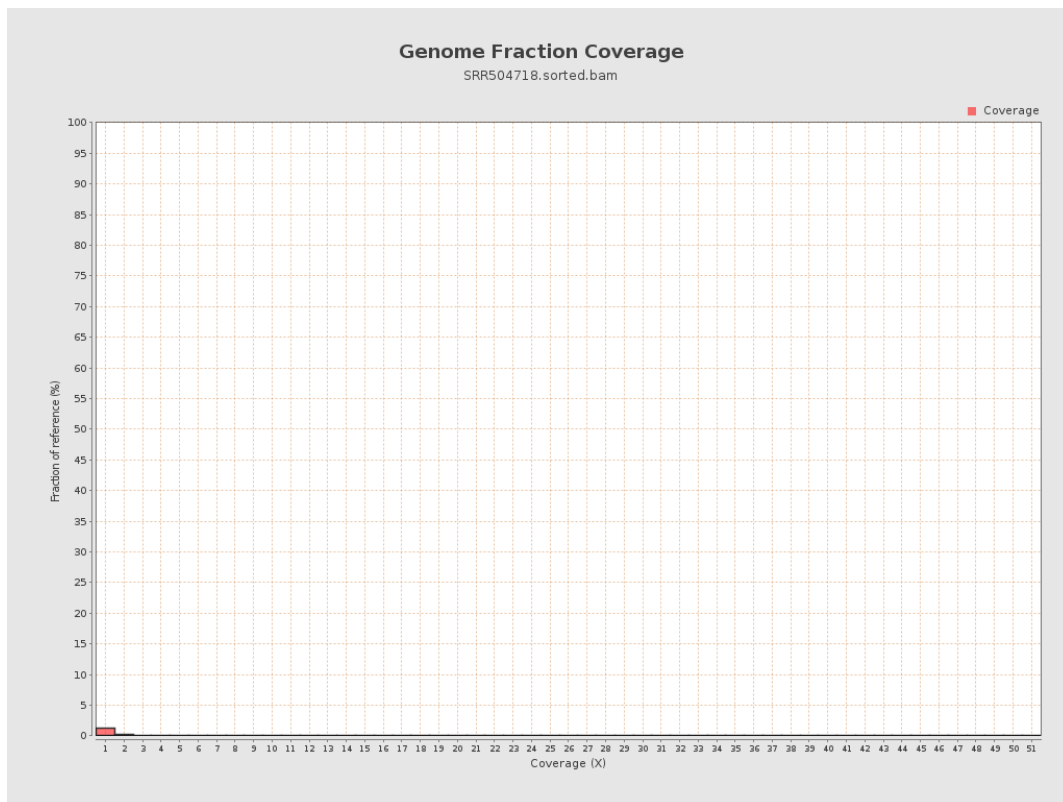
4. Results : Coverage Histogram



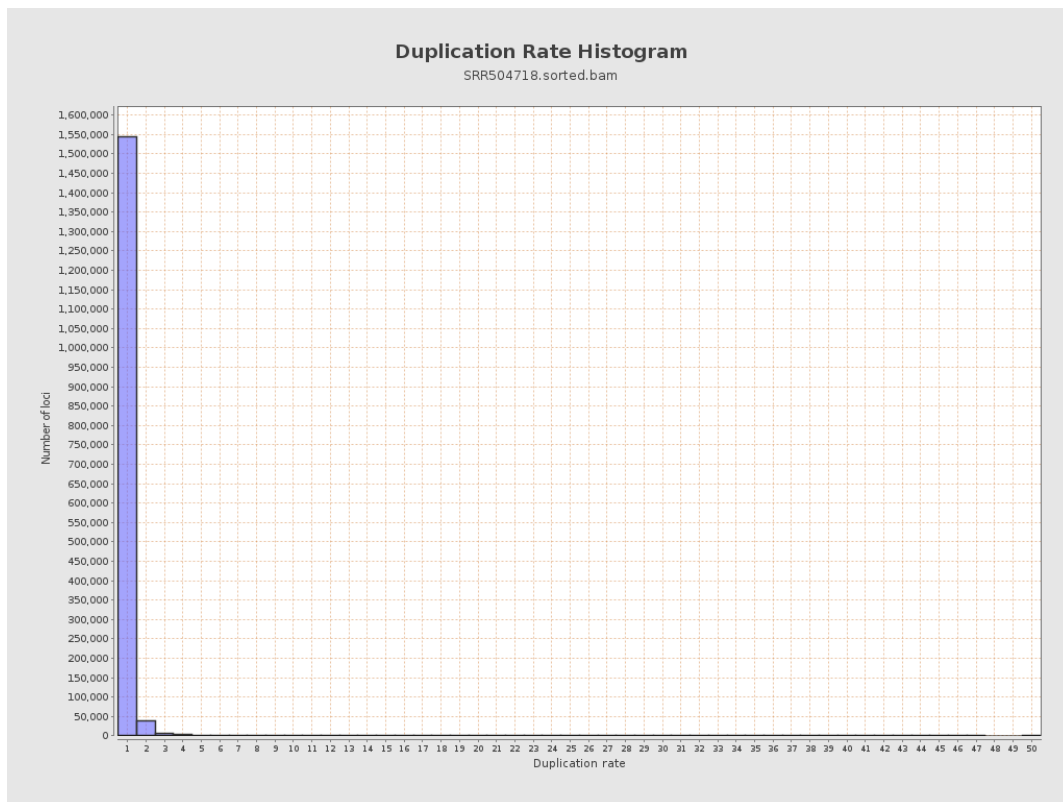
5. Results : Coverage Histogram (0-50X)



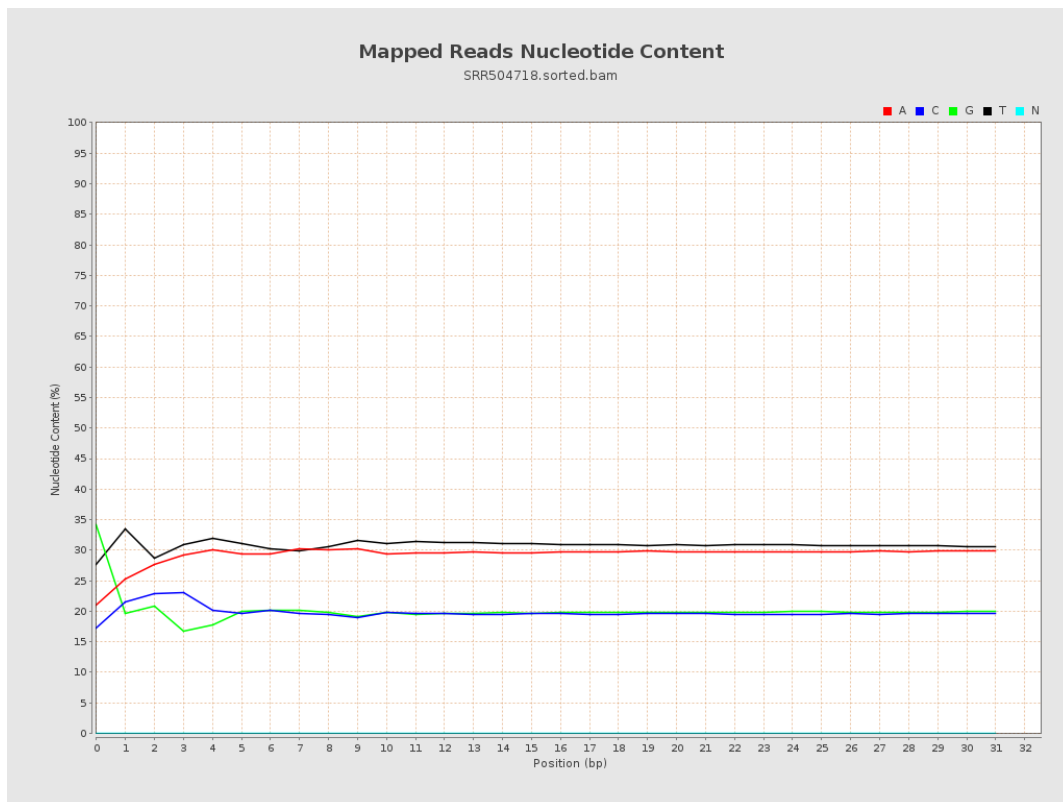
6. Results : Genome Fraction Coverage



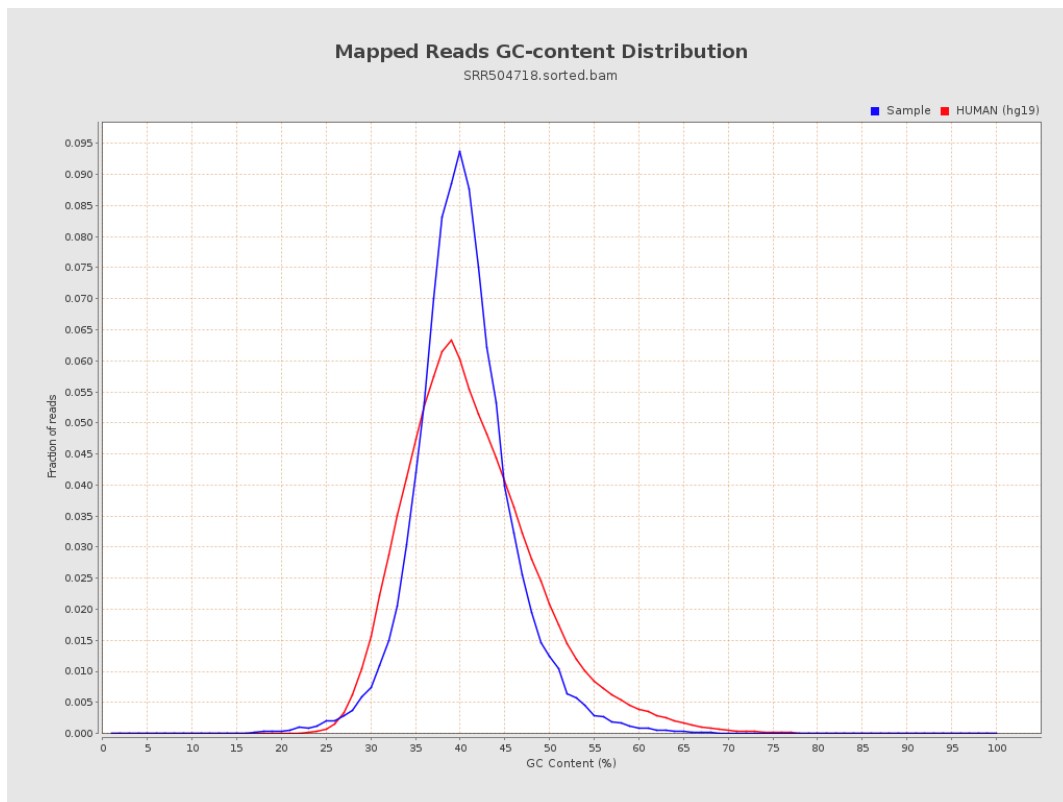
7. Results : Duplication Rate Histogram



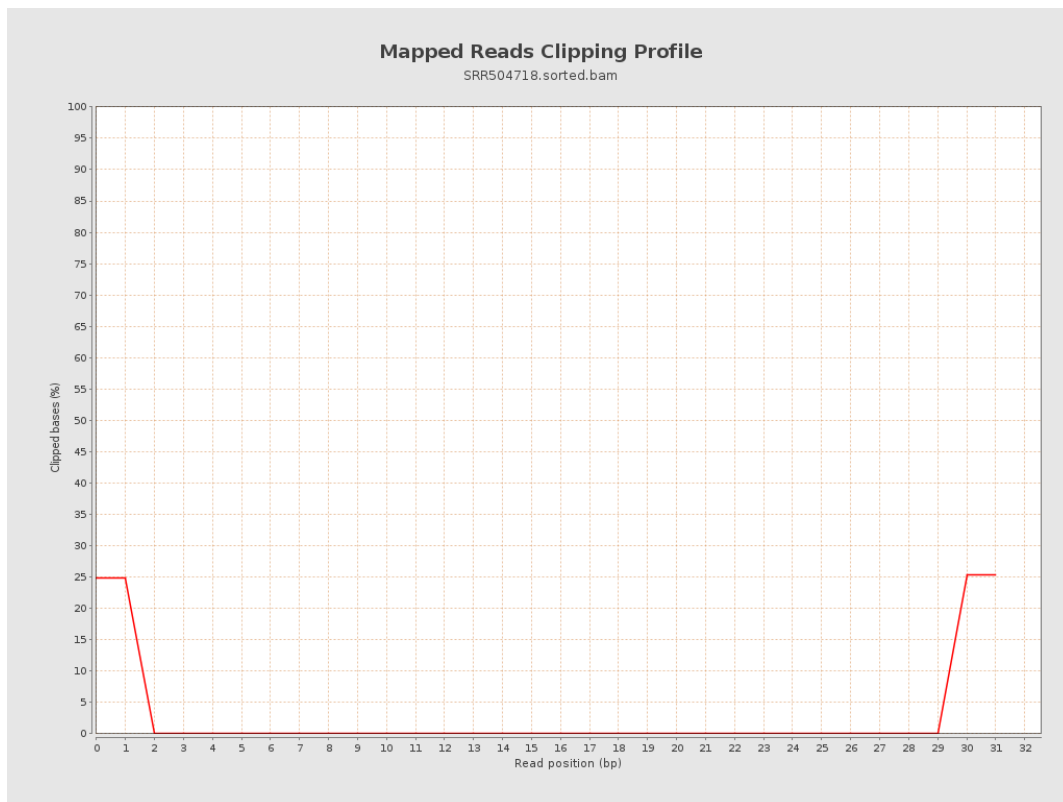
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

