

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:15:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504720.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_SRR504720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504720.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:15:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504720.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,975,987
Mapped reads	1,757,870 / 88.96%
Unmapped reads	218,117 / 11.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	171,525 / 8.68%
Duplication rate	7.67%
Clipped reads	2,822 / 0.14%

2.2. ACGT Content

Number/percentage of A's	16,254,414 / 28.9%
Number/percentage of C's	11,226,865 / 19.96%
Number/percentage of T's	17,784,946 / 31.62%
Number/percentage of G's	10,979,898 / 19.52%
Number/percentage of N's	73 / 0%
GC Percentage	39.48%

2.3. Coverage

Mean	0.0182
Standard Deviation	0.3886

2.4. Mapping Quality

Mean Mapping Quality	8.24
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2.5. Mismatches and indels

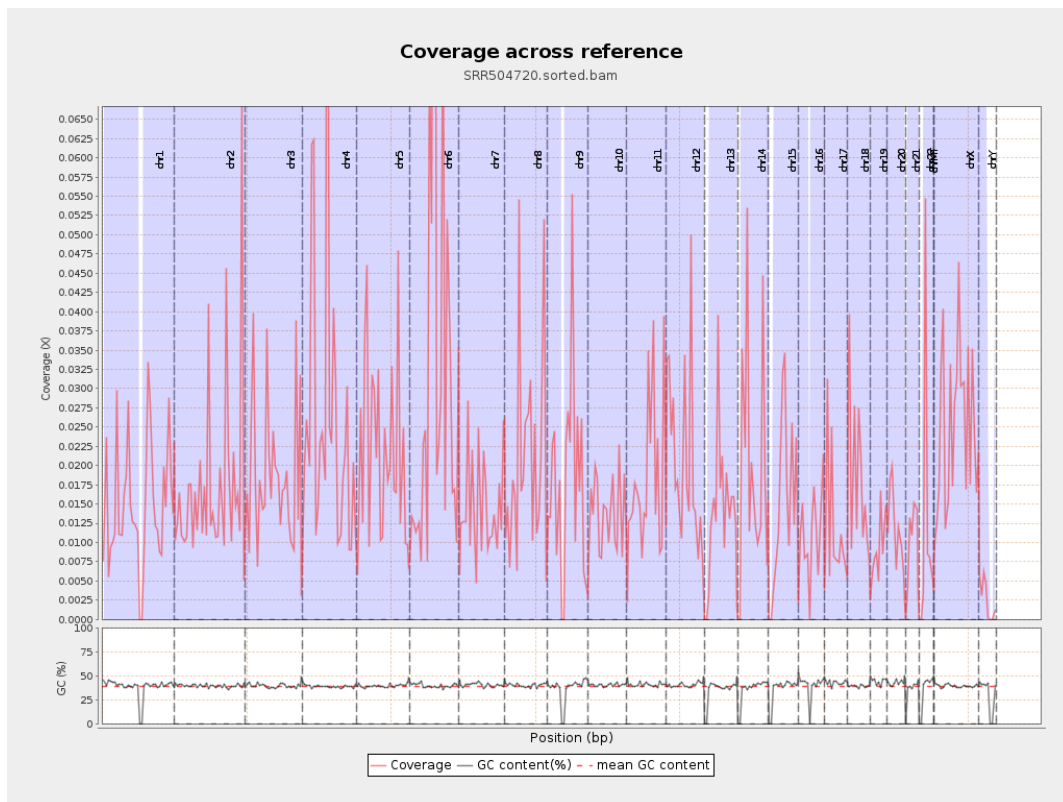
General error rate	0.06%
Mismatches	33,649

2.6. Chromosome stats

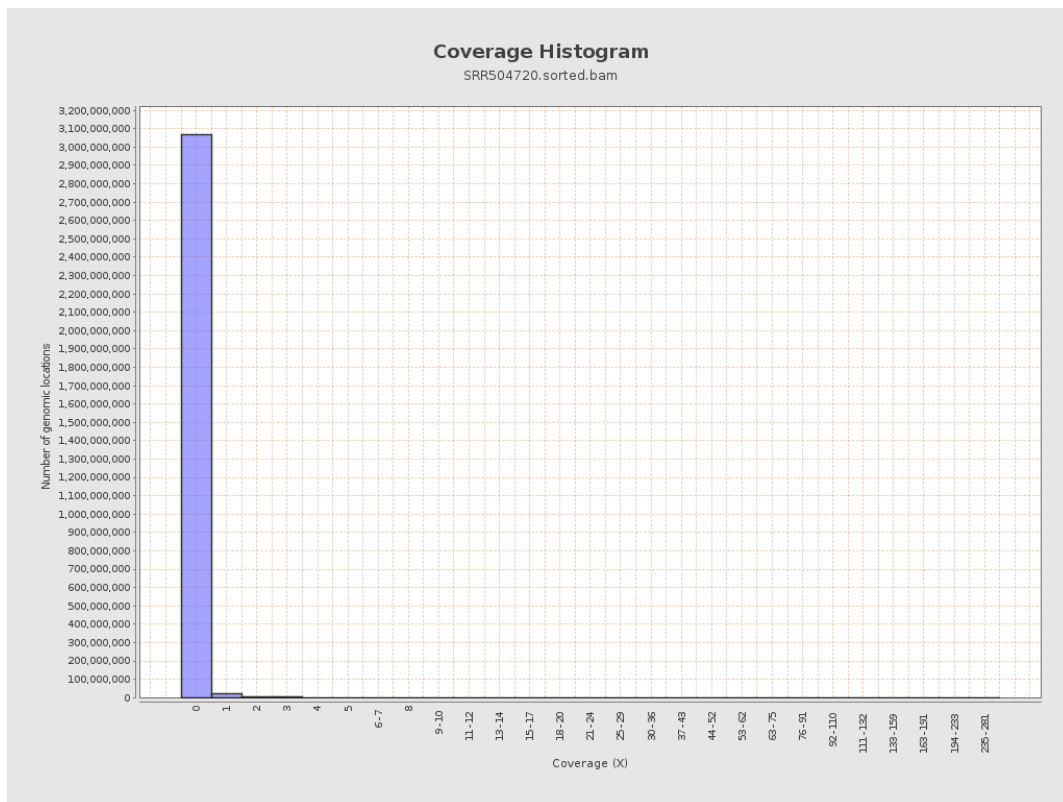
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3710628	0.0149	0.2389
chr2	243199373	4239178	0.0174	0.3519
chr3	198022430	3765416	0.019	0.3016
chr4	191154276	5142808	0.0269	0.6658
chr5	180915260	4005288	0.0221	0.4035
chr6	171115067	5439944	0.0318	0.806
chr7	159138663	2318176	0.0146	0.2446
chr8	146364022	2971564	0.0203	0.3805
chr9	141213431	2482180	0.0176	0.3393
chr10	135534747	1871624	0.0138	0.1894
chr11	135006516	2450322	0.0181	0.3249
chr12	133851895	2725832	0.0204	0.3338
chr13	115169878	1606684	0.014	0.211
chr14	107349540	2051220	0.0191	0.4736
chr15	102531392	1589156	0.0155	0.3274

chr16	90354753	973332	0.0108	0.2558
chr17	81195210	948816	0.0117	0.2611
chr18	78077248	1492044	0.0191	0.3937
chr19	59128983	558422	0.0094	0.1812
chr20	63025520	733362	0.0116	0.191
chr21	48129895	465962	0.0097	0.1436
chr22	51304566	626398	0.0122	0.484
chrMT	16571	128	0.0077	0.0875
chrX	155270560	3930018	0.0253	0.3352
chrY	59373566	147694	0.0025	0.0573

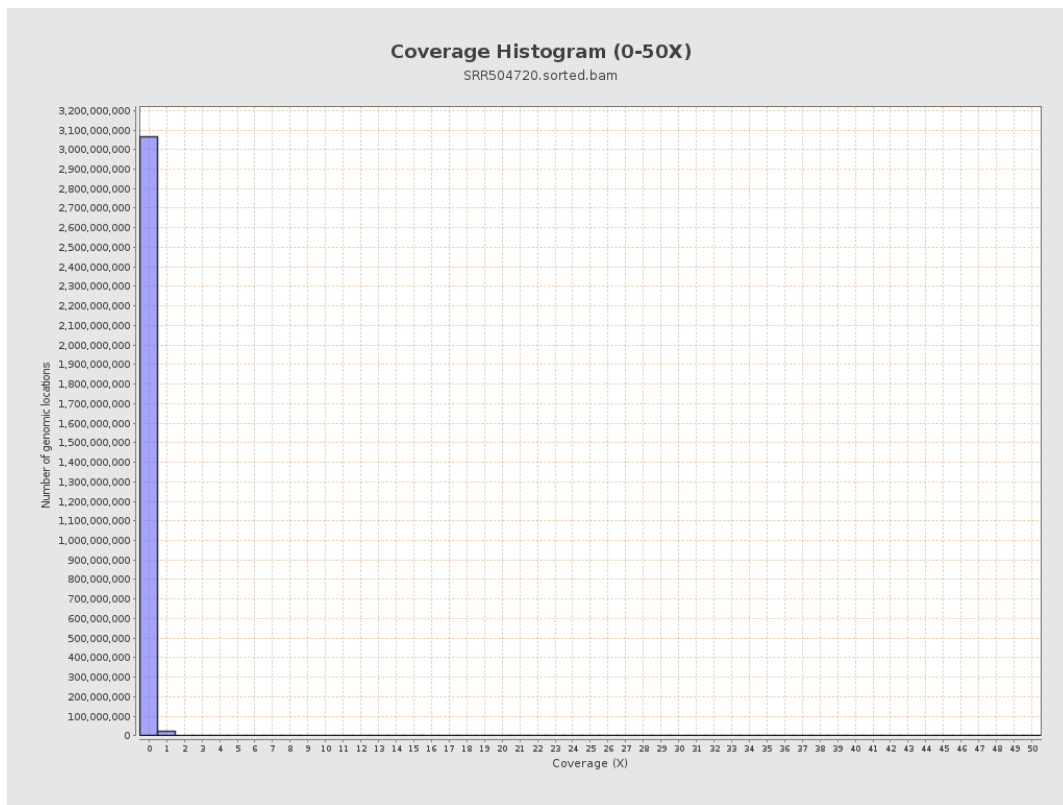
3. Results : Coverage across reference



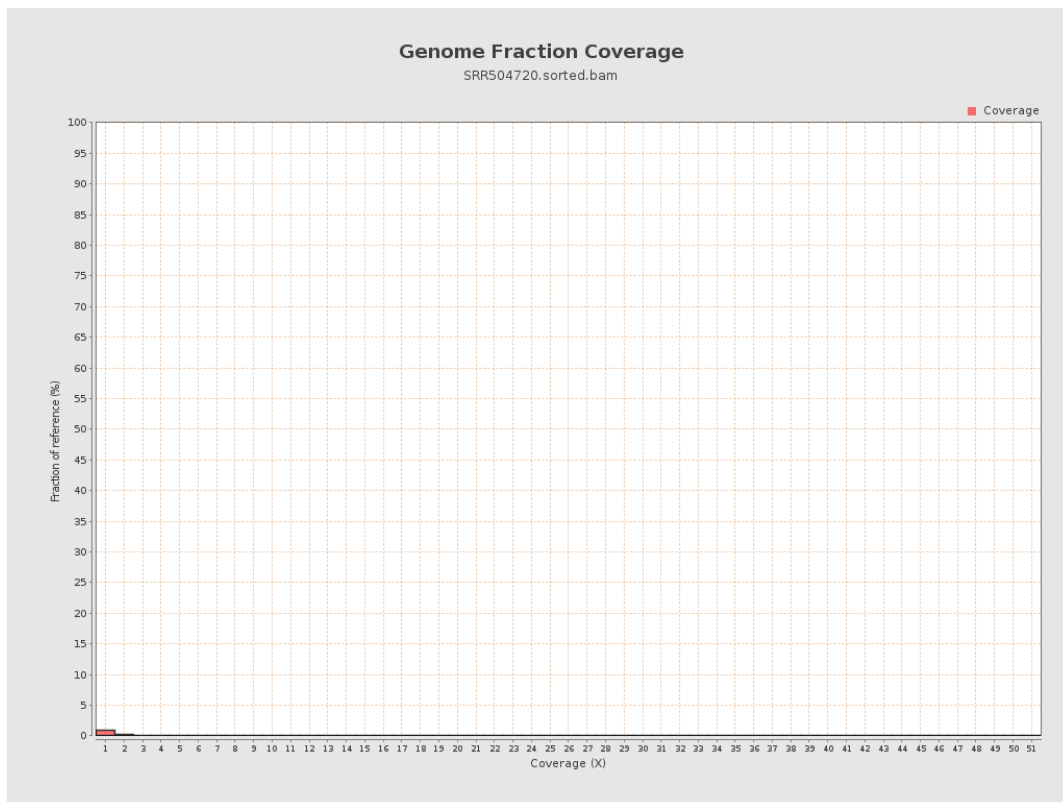
4. Results : Coverage Histogram



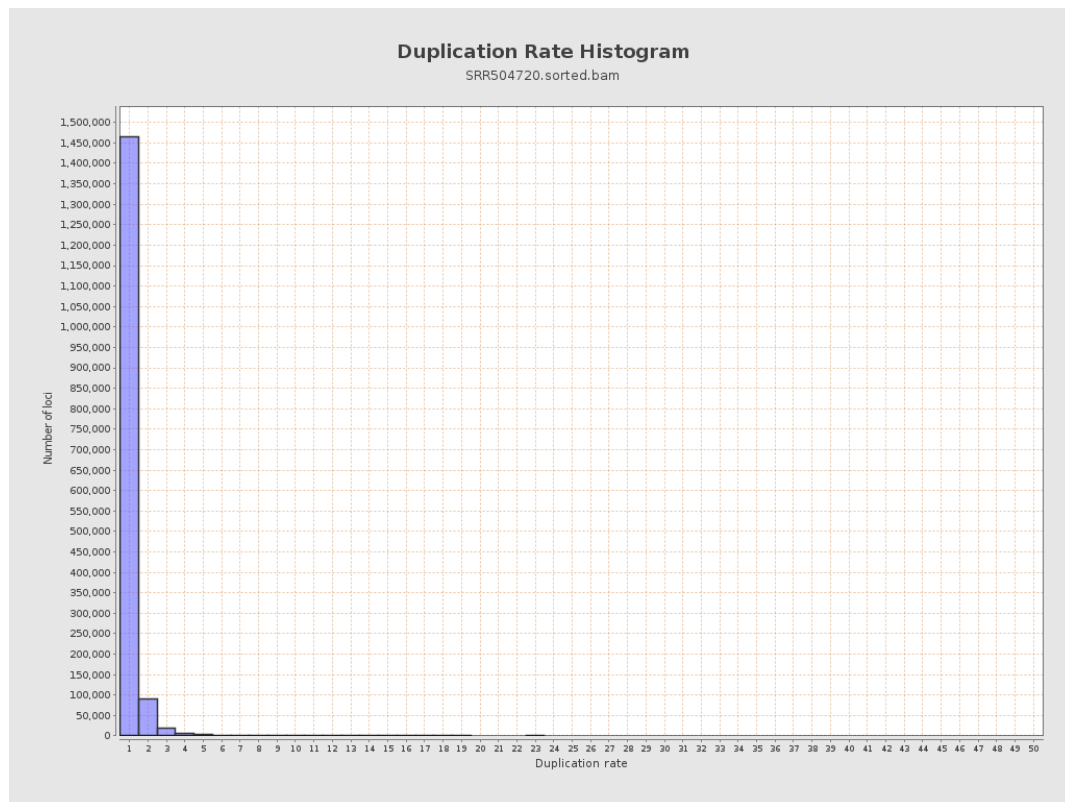
5. Results : Coverage Histogram (0-50X)



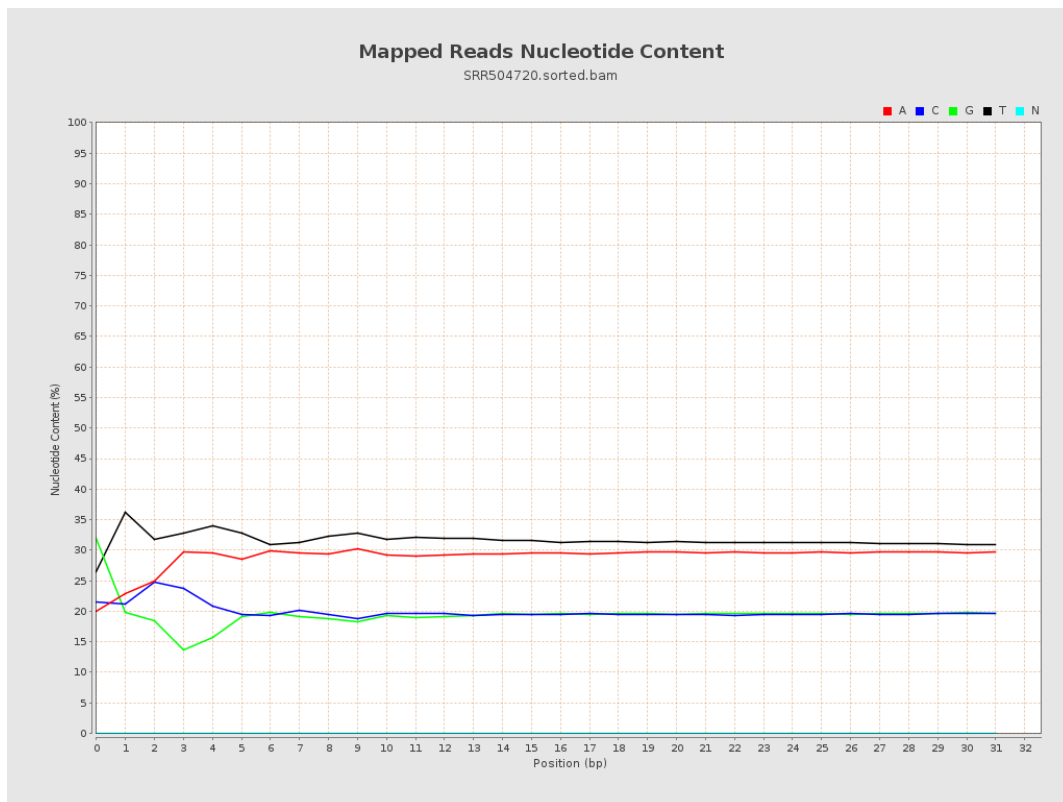
6. Results : Genome Fraction Coverage



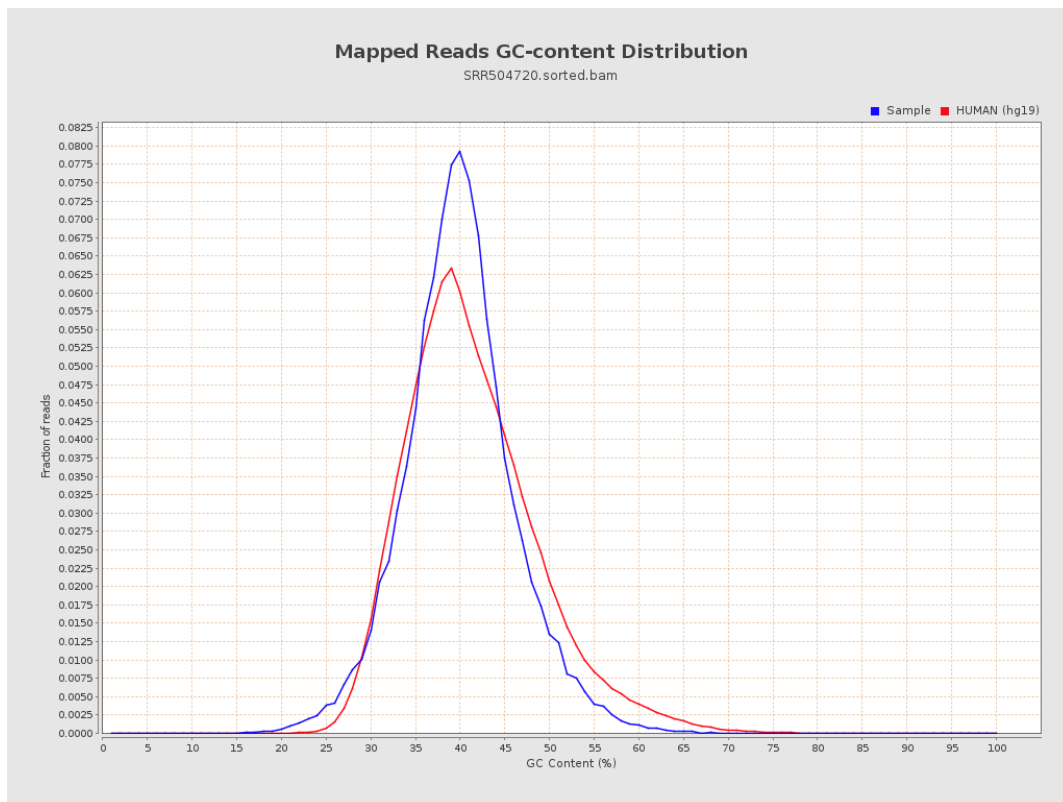
7. Results : Duplication Rate Histogram



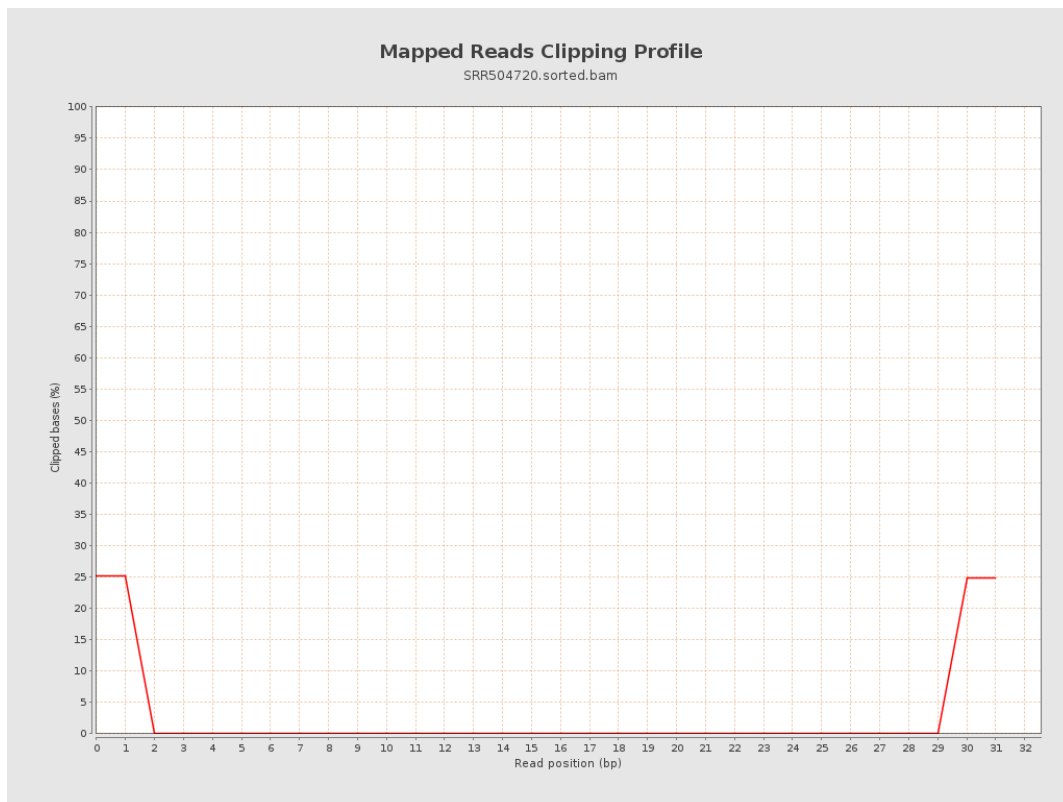
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

