

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 06:40:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504753.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_SRR504753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 06:40:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,946,538
Mapped reads	1,736,260 / 89.2%
Unmapped reads	210,278 / 10.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	32 / 32 / 32
Duplicated reads (estimated)	204,614 / 10.51%
Duplication rate	8.36%
Clipped reads	2,536 / 0.13%

2.2. ACGT Content

Number/percentage of A's	16,117,660 / 29.01%
Number/percentage of C's	11,130,075 / 20.03%
Number/percentage of T's	17,159,280 / 30.89%
Number/percentage of G's	11,147,927 / 20.07%
Number/percentage of N's	306 / 0%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0179
Standard Deviation	0.4536

2.4. Mapping Quality

Mean Mapping Quality	7.85
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2.5. Mismatches and indels

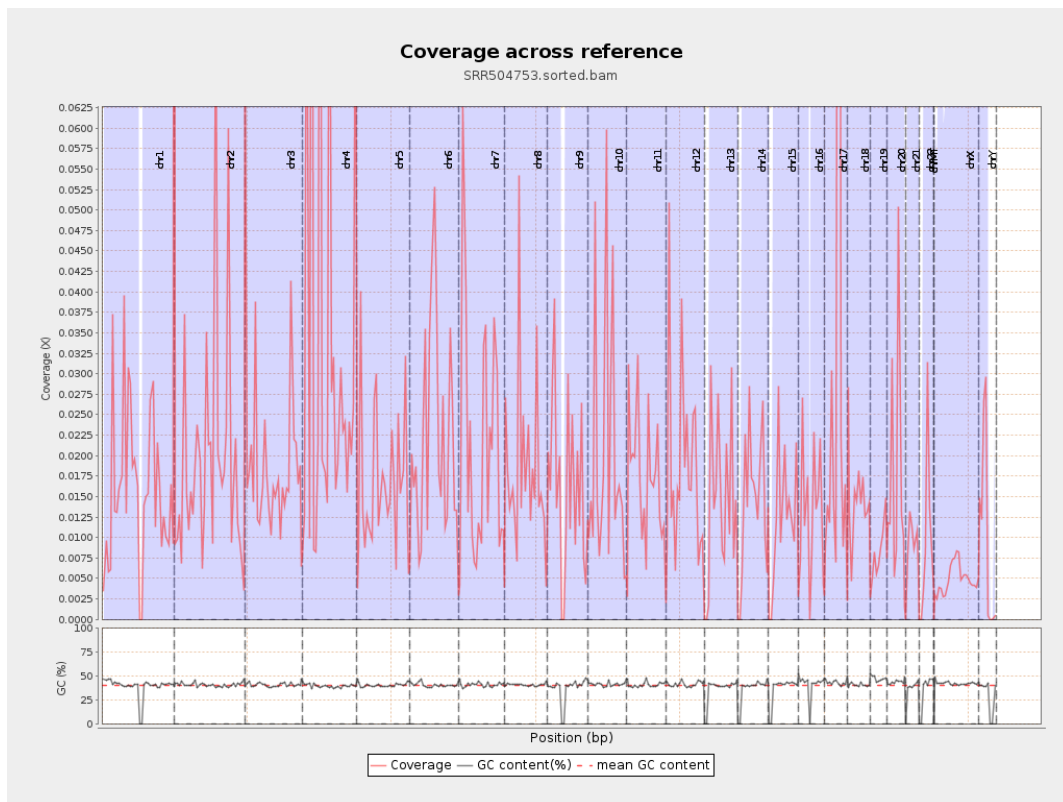
General error rate	0.04%
Mismatches	21,972

2.6. Chromosome stats

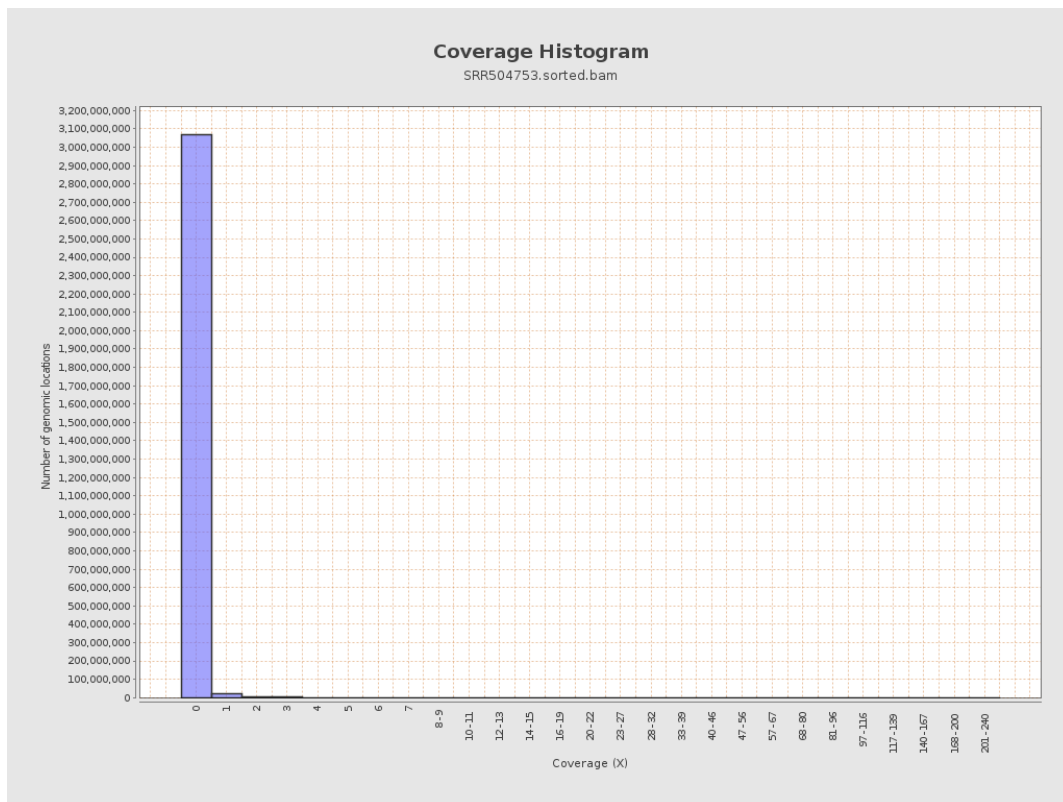
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4243238	0.017	0.3265
chr2	243199373	4718572	0.0194	0.416
chr3	198022430	3726948	0.0188	0.3099
chr4	191154276	7007178	0.0367	1.0783
chr5	180915260	3089562	0.0171	0.2514
chr6	171115067	3768678	0.022	0.381
chr7	159138663	3305046	0.0208	0.3965
chr8	146364022	2727934	0.0186	0.4432
chr9	141213431	2297222	0.0163	0.2528
chr10	135534747	2663330	0.0197	0.4064
chr11	135006516	2377692	0.0176	0.2383
chr12	133851895	2450374	0.0183	0.3044
chr13	115169878	1628398	0.0141	0.2561
chr14	107349540	1528442	0.0142	0.2174
chr15	102531392	1288026	0.0126	0.1963

chr16	90354753	1169900	0.0129	0.2287
chr17	81195210	2560128	0.0315	1.3326
chr18	78077248	1123042	0.0144	0.1859
chr19	59128983	485118	0.0082	0.1434
chr20	63025520	1081096	0.0172	0.3219
chr21	48129895	434976	0.009	0.1232
chr22	51304566	492872	0.0096	0.2794
chrMT	16571	0	0	0
chrX	155270560	771946	0.005	0.084
chrY	59373566	615530	0.0104	0.2482

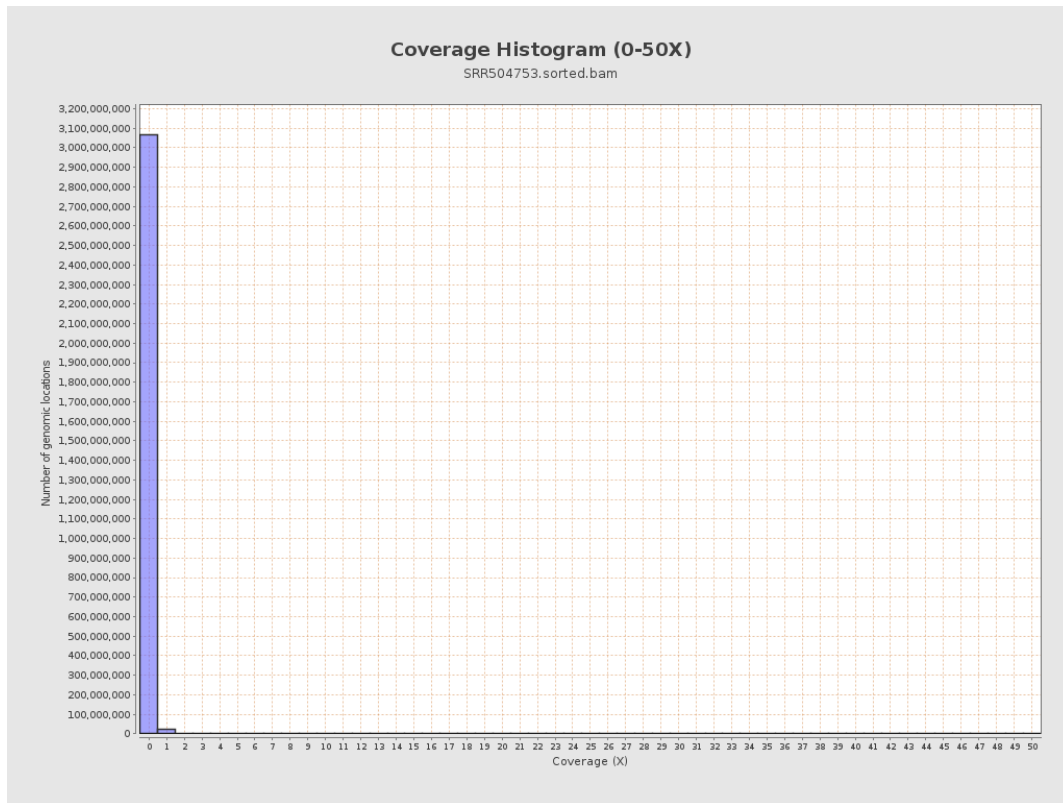
3. Results : Coverage across reference



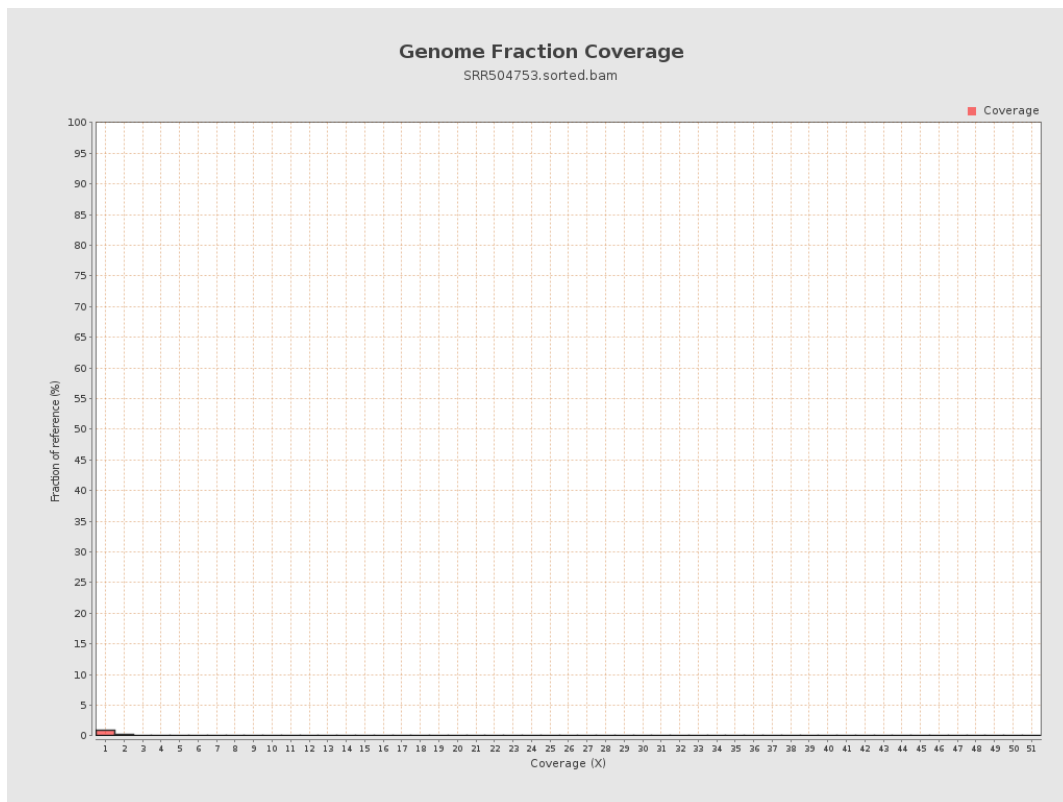
4. Results : Coverage Histogram



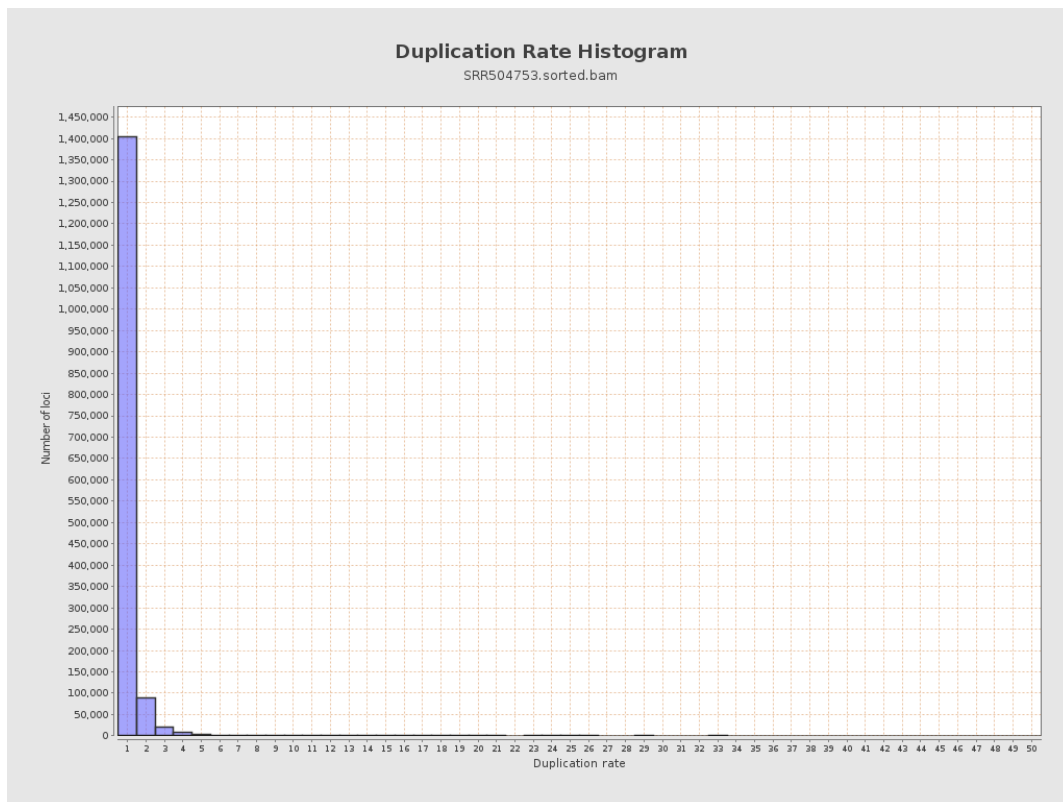
5. Results : Coverage Histogram (0-50X)



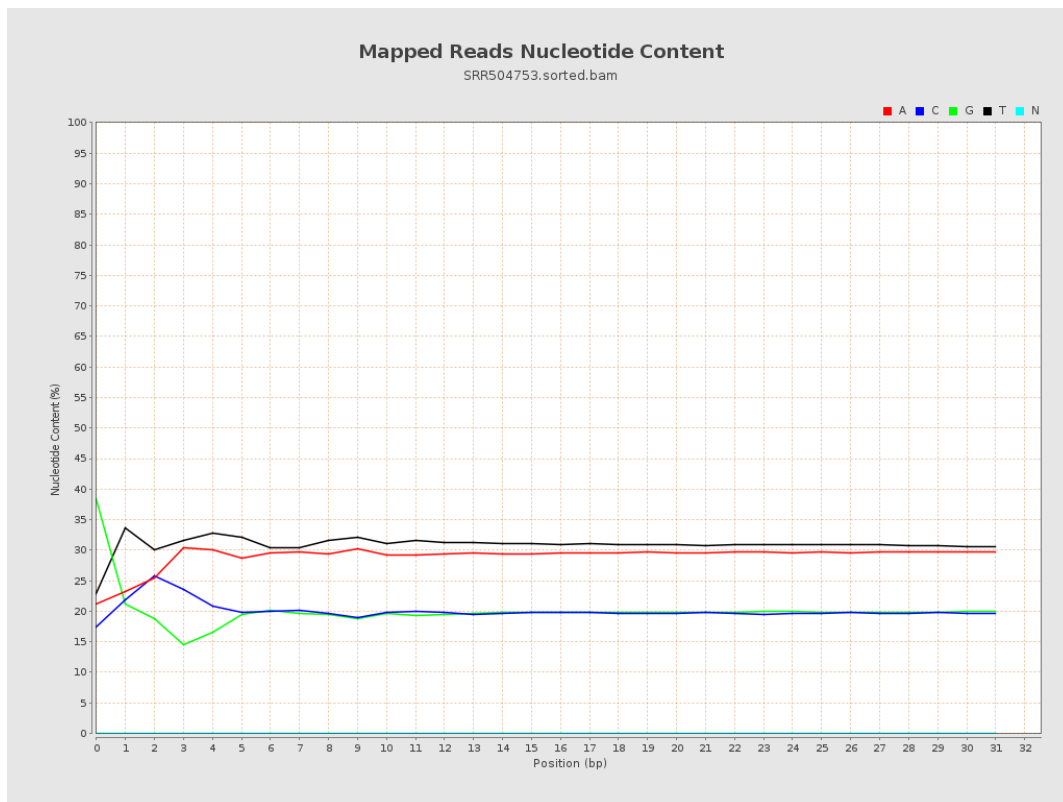
6. Results : Genome Fraction Coverage



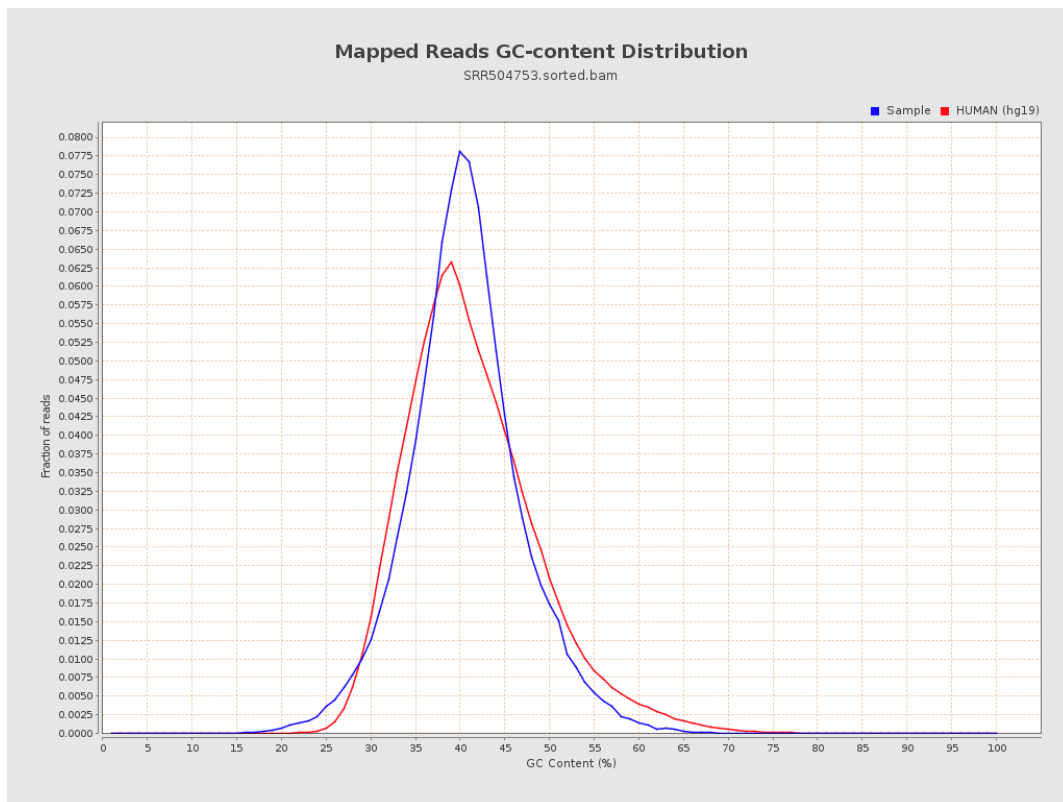
7. Results : Duplication Rate Histogram



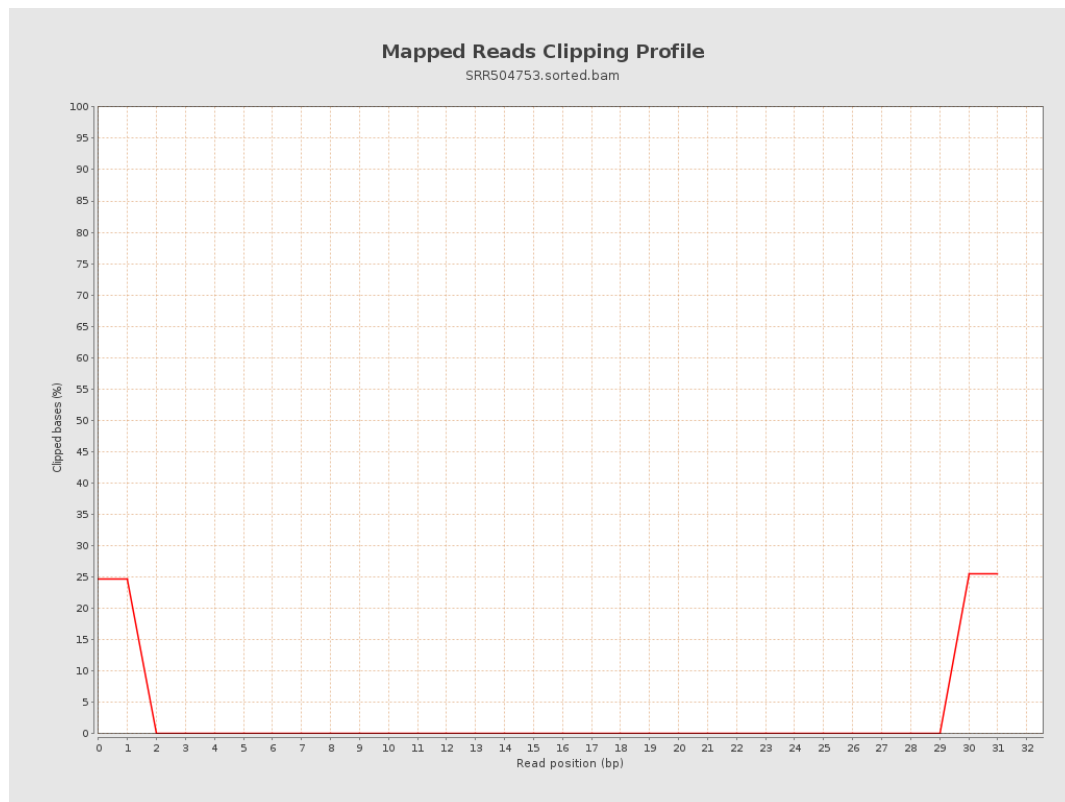
8. Results : Mapped Reads Nucleotide Content



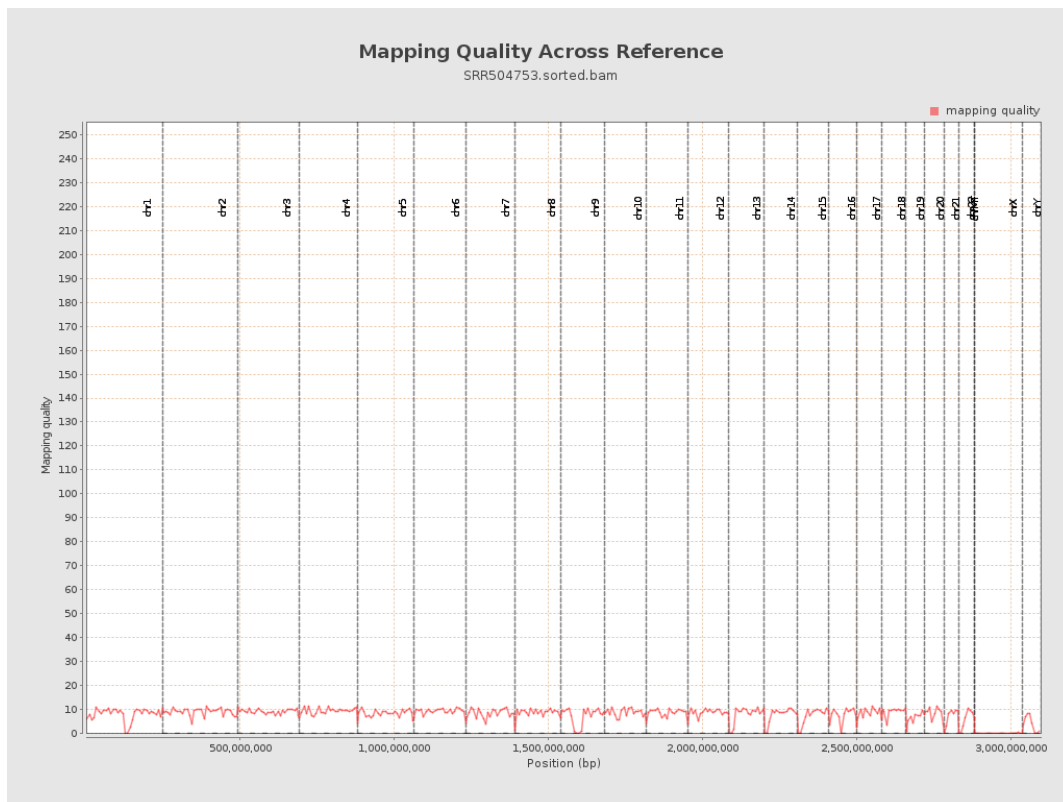
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

