

LABORATORY SEQUENCE ANALYSIS REPORT

Report number: ST-000001
Report date: 03/01/2020

SUBMITTER INFORMATION

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SEQUENCE SUBMISSION INFORMATION

Number of sequences submitted: 4
Date of submission: 02/27/2020
Sequencer (make/model): Illumina MiSeq
Suspected microorganism: SARS-CoV-2
Submission comments:

Sequence table

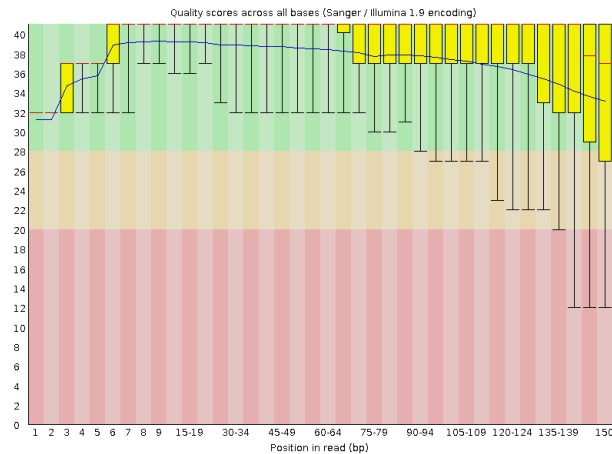
#	SEQUENCE ACCESSION/TAXA LABEL	SIZE (bp)
1	AA00001/State/Date1/Human	29,308
2	AA00002/State/Date1/Human	28,991
3	AA00003/State/Date1/Human	29,991
4	AA00004/State/Date1/Human	30,172

Sequence Quality

MEASURE	VALUE
Sequences flagged as poor quality	0
Number of identical sequences	2

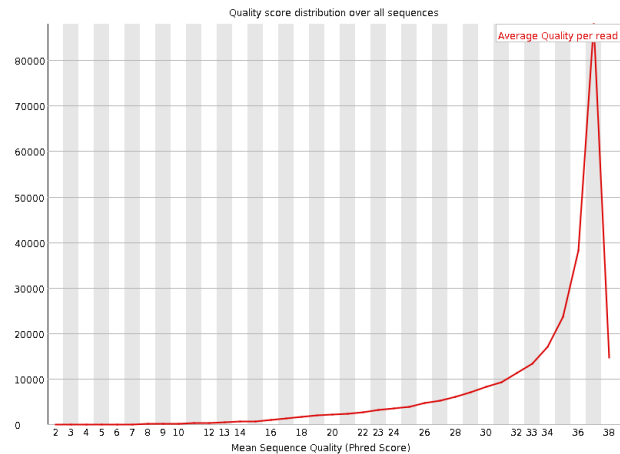
Per base sequence quality

Plot of aggregated quality score statistics at each position along all reads.



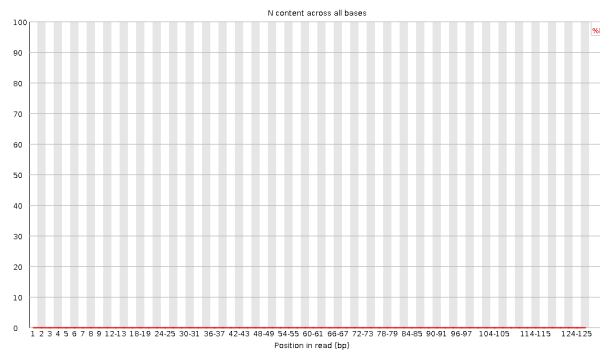
Quality Scores per Sequence

Total number of reads vs the average quality score over full length of that read.



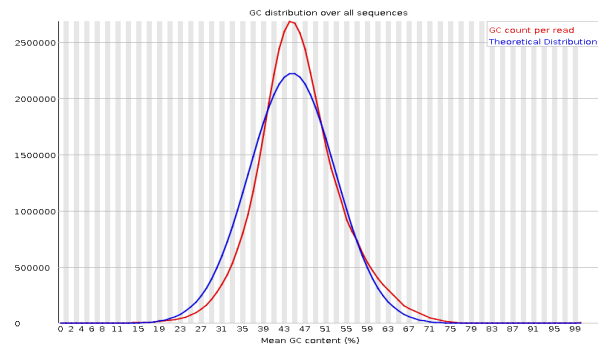
Per Base N Content

Percent of bases at each position or bin with no base call (i.e. 'N').



Sequence GC Content

Plot of the number of reads vs. GC% per read. Theoretical Distribution plot assumes a uniform GC content for all reads.



Sequence Phylogenetics

Reference Genomes:

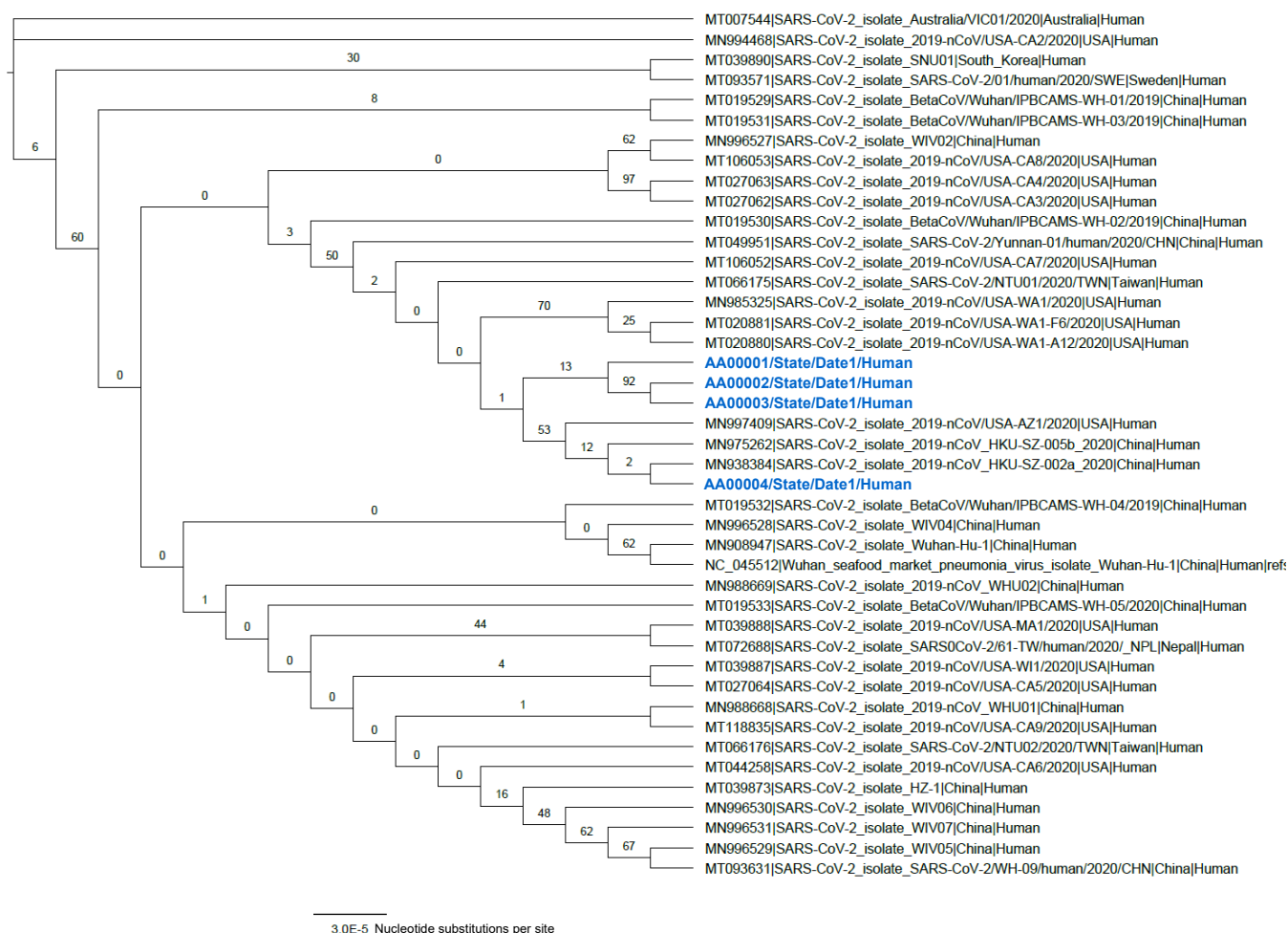
Human SARS-CoV-2

Phylogenetic Method:

Maximum-likelihood (ML) estimation

Branch Confidence Estimation:

Bootstrap



Interpretation:

Phylogenetic analyses of submitted sequences were estimated with a dataset of SARS-CoV-2 reference genomes. The estimated phylogeny suggests that the following submitted sequences:

AA000001/State/Date1/Human
 AA000002/State/Date1/Human
 AA000003/State/Date1/Human
 AA000004/State/Date1/Human

fall within the human SARS-CoV-2 clade.

2 sequences were found to be identical:

AA000002/State/Date1/Human
 AA000003/State/Date1/Human

*Note: Bootstrap values <50 on phylogeny branches should be interpreted with caution.

Report comments: