

Virus detail	
<b>Virus name:</b>	hCoV-19/South Africa/NCV16/2020
<b>Accession ID:</b>	EPI_ISL_1363138
<b>Type:</b>	betacoronavirus
<b>Clade</b>	GH
<b>Pango Lineage</b>	B.1.351 (version: 2021-04-14)
<b>AA Substitutions</b>	Spike A701V, Spike D614G, Spike E484K, Spike K417N, Spike N501Y, E P71L, N T205I, NS3 Q57H, NS3 S171L, NS3 V55F, NSP2 G88E, NSP2 T85I, NSP4 L430stop, NSP4 Y427C, NSP5 I213M, NSP5 K90R, NSP6 F108del, NSP6 G107del, NSP6 S106del, NSP12 P323L
<b>Variant</b>	GH/501Y.v2 (B.1.351)
<b>Passage details/history:</b>	Original
Sample information	
<b>Collection date:</b>	2020-12-06
<b>Location:</b>	Africa / South Africa / Gauteng
<b>Host:</b>	Human
<b>Additional location information:</b>	
<b>Gender:</b>	Male
<b>Patient age:</b>	59
<b>Patient status:</b>	unknown
<b>Specimen source:</b>	
<b>Additional host information:</b>	
<b>Sampling strategy:</b>	Community screening
<b>Outbreak:</b>	
<b>Last vaccinated:</b>	
<b>Treatment:</b>	
<b>Sequencing technology:</b>	Illumina NextSeq
<b>Assembly method:</b>	
<b>Coverage:</b>	
<b>Comment:</b>	Stretches of NNNs (4.76% of overall sequence). NSP4_L430stop results in 14.2% truncation of the protein sequence. Gap of 9 nucleotides when compared to the reference sequence.
Institute information	
<b>Originating lab:</b>	National Health Laboratory Services
<b>Address:</b>	Charlotte Maxeke Johannesburg hospital, 7 Jubilee Road, Parktown, Johannesburg, Gauteng
<b>Sample ID given by the originating laboratory:</b>	
<b>Submitting lab:</b>	National Health Laboratory Services
<b>Address:</b>	Charlotte Maxeke Johannesburg hospital, 7 Jubilee Road, Parktown, Johannesburg, Gauteng
<b>Sample ID given by the submitting laboratory:</b>	
<b>Authors:</b>	Kathleen Subramoney, Florette Treurnicht, Arshad Ismail
Submitter information	
<b>Submitter:</b>	Subramoney, Kathleen
<b>Submission Date:</b>	2021-03-25
<b>Address:</b>	7 Parktown Road 2193 Johannesburg

Important note: In the GISAID EpiFlu™ Database Access Agreement, you have accepted certain terms and conditions for viewing and using data regarding influenza viruses. To the extent the Database contains data relating to non-influenza viruses, the viewing and use of these data is subject to the same terms and conditions, and by viewing or using such data you agree to be bound by the terms of the GISAID EpiFlu™ Database Access Agreement in respect of such data in the same manner as if they were data relating to influenza viruses.