



NATIONAL GENOMICS CORE CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

is proud to submit 34 whole genome sequences of SARS-CoV-2 from Indian Samples under DBT'S PAN-INDIA-1000 GENOME CONSORTIUM

Our tireless endeavours will continue to bring more!



National Genomics Core

Centre for DNA Fingerprinting and Diagnostics Inner Ring Road, Uppal, Hyderabad - 500 039, Telangana, INDIA

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Virus detail

Virus name: hCoV-19/India/NGC-CDFD-34/2020

Accession ID: EPI_ISL_466872

Type: betacoronavirus

Lineage (GISAID Clade): B.1.1.8 (GR)

Passage details/history: Original

Sample information

Collection date: 2020-05-30

Location: Asia / India / Telangana

Host: Human

Additional location information:

Gender: Female
Patient age: 70
Patient status: unknown

Specimen source: Naso-pharyngeal swab

Additional host information:

Outbreak:

Last vaccinated:

Treatment:

Sequencing technology: Illumina MiSeq
Assembly method: BWA-MEM
Coverage: 3334.0

Comment:

Institute information

Originating lab: National Genomics Core-Center for DNA Fingerprinting and Diagnostics

Address: Uppal, Hyderabad, Telangana, India

Sample ID given by the sample

provider:

Authors:

Submitting lab: National Genomics Core- Center for DNA Fingerprinting and Diagnostics (NGC-CDFD)- DBT's

PAN-INDIA-1000 Genome consortium

Address: Uppal, Hyderabad, Telangana, India

C1124

Sample ID given by the

submitting laboratory:

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BASHYAM, DEBASHIS MITRA, DIVYA VASHISHT, ASHWIN DALAL

Submitter information

Submitter: Vashisht, Divya **Submission Date:** 2020-06-12

Address: Inner Ring Rd, Survey Colony 500039 Hyderabad

Important note: In the GISAID EpiFluTM 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 EpiFluTM Database Access Agreement in respect of such data in the same manner as if they were data relating to influenza viruses.