

Phylogenetic tree showing relationships between various influenza virus strains. The tree is rooted at the bottom left and branches out to the right. Bootstrap values are indicated at the nodes. The strains are listed on the right side of the tree.

Strains and their corresponding bootstrap values (from top to bottom):

- China CD (100)
- USA IN05 (100)
- ChinaWHNRH (76)
- USA IA00 (100)
- JXChina97 (100)
- USA NY01 (100)
- USA UT01 (100)
- Bahrain (100)
- Italy BS89 (100)
- France SD (100)
- Spain AST89 (85)
- Saudi Arabia (62)
- Korea 90 (100)
- Mexico 89 (100)
- Czech V351 (99)
- Germany FRG (99)
- Italy 90 (100)

Phylogenetic tree showing relationships between various countries and their corresponding SARS-CoV-2 sequences. The tree is rooted at the bottom with Italy 90. Bootstrap values are indicated at the nodes. A box highlights a cluster of sequences from JXChina97, USA IA00, USA NY01, USA UT01, China CD, USA IN05, and ChinaWHNRH.

Country/Sequence	Bootstrap Value
Italy 90	-
Czech V351	92
Germany FRG	100
Mexico 89	100
Saudi Arabia	86
Korea 90	65
France SD	100
Spain AST89	100
Italy BS89	100
Bahrain	100
ChinaWHNRH	100
USA IN05	100
China CD	100
USA UT01	80
USA NY01	99
USA IA00	100
JXChina97	100