

# Wuhan-coronavirus homologue map

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## Background and Objective

**Background:** At the beginning of 2020, global risk of infection of coronavirus is spreaded. The pandemic started in 2019 and governments announced a state of emergency. In Japan, the government adopted PCR as a diagnosis method of the infection. But the selection of prmers infrence the accuracy greatly.

**Objective:** Therefor, I provide a "map" of homological region of coronavirus to other viruses and annimals to help the primer design.

## Data

Vertebrates:

- |   |   |   |
|---|---|---|
| ● Bat (NW_017738920.1 .. NW_017802358.1; 63439frgs)   | ● Dog (NC_006583.3 .. NC_006621.3; 39chrs)            | ● Rabbit (NC_013669.1 .. NC_013690.1; 22chrs)               |
| ● Beluga (NW_022097992.1 .. NW_022103895.1; 5904frgs) | ● Ferret (NW_004569142.1 .. NW_004576923.1; 7782frgs) | ● Pig (NC_010443.5 .. NC_010462.3; 20chrs)                  |
| ● Camel (NC_044511.1 .. NC_044547.1; 37chrs)          | ● Human (NC_000001.4 .. NC_000024.3; 24chrs)          | ● Rock Pigeon (NW_004973171.1 .. NW_004988092.1; 14922frgs) |
| ● Cat (NC_018723.3 .. NC_018741.3; 19chrs)            | ● Mouse (NC_000067.6 .. NC_000087.7; 21chrs)          | ● Turkey (NC_015011.2 .. NC_015042.2; 32chrs)               |

Viruses:

- |                                     |  |
|-------------------------------------|--|
| ● 7554 genomes of viruses or phages | ● Wuhan-corona virus genome (MN908947.3) |
|-------------------------------------|--|

## Method

**blast**

DB: makeblastdb -in <<input file>> -out <<DB name>> -dbtype nucl -parse seqids  
Query: megablast -d <<DB name>> -i <<query sequence>> -W 10 > <<output file>>

**self-blast**

**window-fourrier**

Fragmentation: 30 fragments – 1000 bases  
Conversion: "A" -> 1, "T" -> -1, "G" -> I, "C" -> -I  
Fourier transform:  $Ft(<<each\ fragment>>)$

**selection of frequent homologues**

The plot

