

# 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 primers influence the accuracy greatly. **Objective:** Therefor, I provide a "map" of homological region of coronavirus to other viruses and animals 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**  
Fragmentation: fragment bf=<<input file>> S=25 G=25 cs=1 > <<output file>>  
DB: same as above.  
Query: same as above.

**Window-fourrier**  
Fragmentation: 30 fragments; 1000 bases / fragment  
Conversion: "A" -> 1, "T" -> -1, "G" -> I, "C" -> -I  
Fourier transform:  $Ft$ (<<each fragment>>)

**Selection of frequent homologues**  
Vertebrate: base-hit count >= 5; seq-lenght >= 5  
Viruses: base-hit count >= 18; seq-lenght >= 5

## Result

