

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 infruence 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)
 - Beluga (NW_022097992.1 .. NW_022103895.1; 5904frgs)
 - Camel (NC_044511.1 .. NC_044547.1; 37chrs)
 - Cat (NC_018723.3 .. NC_018741.3; 19chrs)
 - Dog (NC_006583.3 .. NC_006621.3; 39chrs)
 - Ferret (NW_004569142.1 .. NW_004576923.1; 7782frgs)
 - Human (NC_000001.4 .. NC_000024.3; 24chrs)
 - Mouse (NC_000067.6 .. NC_000087.7; 21chrs)
 - Rabbit (NC_013669.1 .. NC_013690.1; 22chrs)
 - Pig (NC_010443.5 .. NC_010462.3; 20chrs)
 - Rock Pigeon (NW_004973171.1 .. NW_004988092.1; 14922frgs)
 - 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_seqs
self-blast window-fourrier selection of frequent homologues

The plot

