

# Wuhan-coronavirus homologue map

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## Background and Objective

**Background:** At the beginning of 2020, global risk of infection of a new 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 influences the accuracy greatly. **Objective:** Therefor, I provide a "map" of homological regions of coronavirus genome to other virus and animal genomes 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\_seqids  
Query: megablast -d <<DB name>> -i <<query sequence>> -W 10

### Self-BLAST

Fragmentation: fragment bf=<<input file>> S=25 G=25 cs=1  
DB: same as above.  
Query: same as above.

### Window-fourier

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

### Selection of frequent homologues

Vertebrates: base-hit count >= 5; seq-length >= 5  
Viruses: base-hit count >= 18; seq-length >= 5

## Result

### The homologues

Vertebrates						Viruses					
No.	homologue	start	end	count	in CDS	No.	homologue	start	end	count	in CDS
1	AATTTTA	1787	1793	6	Yes	15	CAAGATCTCAATGGTAACTGGTATGATTTCGGTGATT	14 068	14 104	21	Yes
2	GATGAGGATGAAGAAGAAGGT	3047	3067	6	Yes	16	TGGTAATGCTGC	14 775	14 786	18	Yes
3	CTACAAAGAAAACAGTTAC	5866	5884	5	Yes	17	ACAAAACGTAATGTCATCCCTACTATAACTCAAATGAATCTTAAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCCTAGCTGGTGTCTCTAT	15 031	15 125	32	Yes
4	ATAAATATTATAATTG	6944	6960	7	Yes	18	CTTATGGGTTGGGATTATCCTAAATGTGATAGAGCCATGCCTAA	15 280	15 323	37	Yes
5	TTGCAT	7425	7430	5	Yes	19	GATGCCACAACCTGCTTATGCTAATAGTGTTTTTAACAT	15 490	15 527	19	Yes
6	CCATCCATCTTTACTTTGATAAA	7764	7786	7	Yes	20	CAAAACAATGTTTTATGCTGAAGCAAAATGTTGGACTGAGACTGACCTTACTAAAGGACCTCATGAATTTTGCTCTCAACATACA	15 805	15 891	26	Yes
7	TTTTTGTGTGCTATTTTCTATTTA	8607	8632	9	Yes	21	GGTTGTGATGGTGGCAGTTTGATGTAATAAACATGCATTCCACACACC	19 276	19 325	27	Yes
8	ATTTCTCTGTTTGTITTTGT	11 167	11 186	7	Yes	22	TATGAGAGTTATACATTTTGGTGTGGTTCTGATAAAGGAGTTGCACCAGGTAC	20 850	20 903	21	Yes
9	AAAAGT	12 198	12 203	5	Yes	23	CCGAGGCCACGCGGAGTACGATCGAGTGTACAG	29 732	29 764	32	No
10	ATAAAATAGAAGAA	19 121	19 134	6	Yes						
11	TGTTTGTTTTTCTTGTTTATTGC	21 564	21 587	14	Yes						
12	TATTAAAATATAATGAA	22 389	22 405	5	Yes						
13	TTTTCT	26 495	26 500	5	No						
14	CCTAA	29 375	29 379	5	Yes						

### The map

