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 (FTP bulk download)
- Wuhan-corona virus genome (MN908947.3)
- PCR primer (https://www.niid.go.jp/niid/images/lab-manual/2019-nCoV20200217.pdf)

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: $Abs(Ft($`<<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

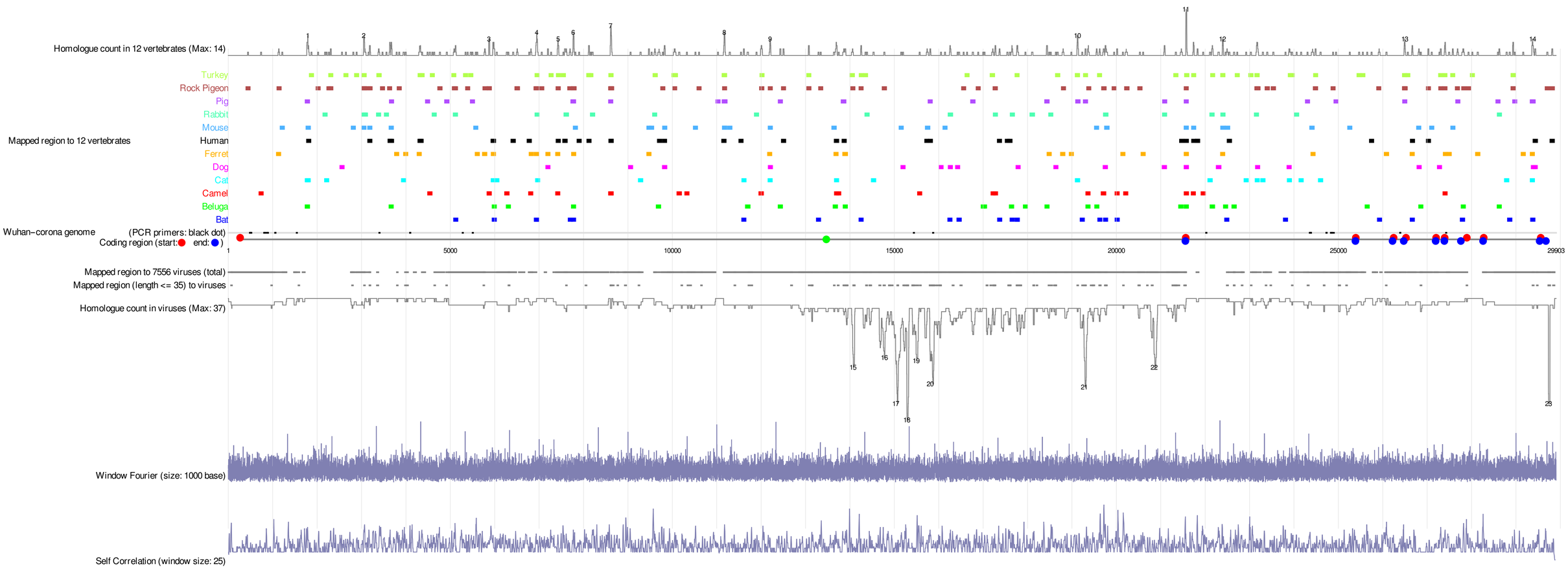
Vertebrates

No.	homologue	start	end	count	in CDS
1	AATTTTA	1787	1793	6	Yes
2	GATGAGGATGAAGAAGAAGGT	3047	3067	6	Yes
3	CTACAAAGAAAACAGTTAC	5866	5884	5	Yes
4	ATAAATATTATAATTTG	6944	6960	7	Yes
5	TTGCAT	7425	7430	5	Yes
6	CCATCCATCTTTACTTTGATAAA	7764	7786	7	Yes
7	TTTTTGTTGCTGCTATTTTCTATTTA	8607	8632	9	Yes
8	ATTTCTCTGTTTGTTTTTGT	11 167	11 186	7	Yes
9	AAAAGT	12 198	12 203	5	Yes
10	ATAAAATAGAAGAA	19 121	19 134	6	Yes
11	TGTTTGTTTTTCTTGTTTTATTGC	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

Viruses

No.	homologue	start	end	count	in CDS
15	CAAGATCTCAATGGTAACTGGTATGATTTCGGTGATT	14 068	14 104	21	Yes
16	TGGTAATGCTGC	14 775	14 786	18	Yes
17	ACAAAACGTAATGTCATCCCTACTATAACTCAAATGAATCTTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTAT	15 031	15 125	32	Yes
18	CTTATGGGTTGGGATTATCCTAAATGTGATAGAGCCATGCCTAA	15 280	15 323	37	Yes
19	GATGCCACAACTGCTTATGCTAATAGTGTTTTTAACAT	15 490	15 527	19	Yes
20	CAAAACAATGTTTTTATGTCTGAAGCAAAATGTTGGACTGAGACTGACCTTACTAAAGGACCTCATGAATTTTGCTCTCAACATACA	15 805	15 891	26	Yes
21	GGTTGTGATGGTGGCAGTTTGTATGTAAATAAACATGCATTCCACACACC	19 276	19 325	27	Yes
22	TATGAGAGTTATACATTTTGGTGCTGGTTCTGATAAAGGAGTTGCACCAGGTAC	20 850	20 903	21	Yes
23	CCGAGGCCACGCGGAGTACGATCGAGTGTACAG	29 732	29 764	32	No

The map



References are in the proceedings of the JSIMS 2020 annual meeting.
@ 2020-07-04 on JSIMS web meeting