Supplementary material for

Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis

Mariana G. Ferrarini^{1*}, Avantika Lal^{2*}, Rita Rebollo¹, Andreas J. Gruber³, Andrea Guarracino⁴, Itziar Martinez Gonzalez⁵, Taylor Floyd⁶, Daniel Siqueira de Oliveira⁷, Justin Shanklin⁸, Ethan Beausoleil⁸, Taneli Pusa⁹, Brett E. Pickett^{8#}, Vanessa Aguiar-Pulido^{10#}

* These authors contributed equally

Corresponding authors

¹ University of Lyon, INSA-Lyon, INRA, BF2I, Villeurbanne, France

²NVIDIA Corporation, Santa Clara, CA, USA

³Oxford Big Data Institute, Nuffield Department of Medicine, University of Oxford, Oxford, UK

⁴ Centre for Molecular Bioinformatics, Department of Biology, University Of Rome Tor Vergata, Rome, Italy

⁵ Amsterdam UMC, Amsterdam, The Netherlands

⁶Center for Neurogenetics, Weill Cornell Medicine, Cornell University, New York, NY, USA

⁷ Laboratoire de Biométrie et Biologie Evolutive, Université de Lyon; Université Lyon 1; CNRS; UMR 5558, Villeurbanne, France

⁸ Brigham Young University, Provo, UT, USA

⁹Luxembourg Centre for Systems Biomedicine, Belvaux, Luxembourg

¹⁰ Department of Computer Science, University of Miami, Coral Gables, FL, USA

Emails for correspondence: Brett E. Pickett: brett_pickett@byu.edu Vanessa Aguiar-Pulido: vxa305@miami.edu

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Supplementary Figure 1. Expression of the *ACE2* **viral receptor gene in each RNA-seq dataset**. The y-axis shows the log2 normalized counts for *ACE2* from DESeq2 results.



Supplementary Figure 2. Biological consequence enrichment analysis. A fraction of 0.5 on the x-axis (dashed line) suggests out of all significant isoforms experiencing consequence A (y-axis), 50% experience a gain in consequence A and 50% experience a loss in consequence A, indicating no global preference in the direction of consequence A for the isoform population. RSV, IAV, and HPIV3 infected samples exhibit significant global enrichment in consequences shortening the ORF, increasing sensitivity to NMD, and higher IR rates. Error bars represent 95% confidence intervals. Red error bars = significant consequence enrichment (adjusted p-value < 0.05), black error bars = non-significant consequence enrichment. ORF = open reading frame, IDR = intrinsically disordered region, NMD = nonsense-mediated decay.



Supplementary Figure 3. Enrichment analysis for alternative splicing events. RSV, IAV, and HPIV3 infected samples display global enrichment of increased IR and ATSS, alongside decreased exon skipping (MES and ES), alternative splice site usage (A5 and A3), and ATTS. Error bars represent 95% confidence intervals. Red error bars = significant consequence enrichment (p-value < 0.05), black error bars = non-significant consequence enrichment. MES = multiple exon skipping, MEE = mutually exclusive exons, IR = intron retention, ES = exon skipping, ATTS = alternative transcription termination site, ATSS = alternative transcription start site, A5 = alternative 5' splice site, A3 = alternative 3' splice site.



Top 30 Isoforms with Significant Gene Switch Usage

Supplementary Figure 4. Top 30 isoforms experiencing significant isoform usage and differential gene expression. Blue circles = isoforms experiencing significant switch in usage (dIF \ge |0.3|), gene log2 fold change \ge |1|, and adjusted p-value < 0.05; red circles = isoforms experiencing significant switch in usage (dIF \ge |0.3|) and adjusted p-value < 0.05; gray circles = non-significant isoforms. Horizontal dotted lines = dIF \ge |0.3|, vertical dotted lines = gene log2 fold change \ge |1|.



Supplementary Figure 5. Isoform usage analyses specifically with *IL6* **transcripts from IsoformSwitchAnalyzeR software.** A) Isoform fractions of the 7 detected *IL-6* isoforms within the 4 datasets of cell lines infected with SARS-CoV-2. Boxplots represent biological triplicates of each condition B) Isoform splice graphs for the detected isoforms of *IL-6*. MOI: Multiplicity of Infection.



Supplementary Figure 6. PCA plots for samples from the dataset GSE150316. A) PCA was performed based on the transformed values obtained after applying the variance stabilizing transformation ²⁸ implemented in the vst() function of DESeq2 ²⁷. Four outlier samples (Cases 4, 6, 7 and 10) were identified and discarded. B) PCA was repeated after discarding these samples. PCA: Principal Component Analysis.

Α

Comparison	Number of significant isoforms	Number of genes		
Series1 NHBE Mock vs Series1 NHBE SARS CoV 2	145	101		
Series2 A549 Mock vs Series2 A549 SARS CoV 2	82	54		
Series3 A549 Mock vs Series3 A549 RSV	1281	710		
Series4 A549 Mock vs Series4 A549 IAV	1690	956		
Series5 A549 Mock vs Series5 A549 SARS CoV 2	172	105		
Series7 Calu3 Mock vs Series7 Calu3 SARS CoV 2	133	86		
Series8 A549 Mock vs Series8 A549 HPIV3	165	109		
Series8 A549 Mock vs Series8 A549 RSV	148	101		
Series9 NHBE Mock vs Series9 NHBE IAV	48	32		
Combined	3569	1960		

Supplementary Table 1. Isoform analysis summary. Summary results for the number of significant isoforms and corresponding genes quantified. Significant isoforms were identified by exhibiting a change in usage greater than or equal to 30% in absolute value (dIF \ge |0.3|) and an adjusted p-value of 0.05.

NC_0453122 Sis 91 + TOTGGG CFLFS, RIM24 5' UTR 1778-06 0.058222711 NC_0455122 159 165 + GGACAG FMR1 5' UTR 1775-07 0.0707308752 NC_0455122 253 224 + AGGTTA ZAMB2 5' UTR 175649 0.970730851 NC_0455122 259 254 + AGGTAA ZAMB2 5' UTR 175741 0.9775120015 NC_0455122 2556 1556 + CGAACA PABC1 mtergenic 179439 0.991270639 NC_0455122 2648 + CTAAC HADRS1 intergenic 178439 0.991270639 NC_0455122 2648 + CTAAC HADRS1 intergenic 180661 0.9982320754 NC_0455122 2648 + ATATA PPIE intergenic 180601 0.99779423 NC_0455122 2648 2648 + ATATA PPIE intergenic 180601 0.99779423	ID	start	end	strand	sequence	RBP	region	Genomes	Fraction of genomes
NC 045122 154 160 + TOACAGG FMR1 5' UTR 177873 0.0970318021 NC 045122 235 240 + ASGTTT ZRANB2 5' UTR 175713 0.0970312015 NC 0455122 237 237 GGTGTGA RBM24 5' UTR 175849 0.09716132015 NC 0455122 2152 2157 + CTAAAC KHDMS1 Integenic 117449 0.0911935161 NC 0455122 21564 2157 + CTAAAC KHDRS1 Integenic 1180659 0.998099479 NC 0455122 26481 + CTAAAT KHDRS1 Integenic 1180651 0.999710868 NC 0455122 26481 * AATAT PPIE Integenic 1180601 0.99779423 NC 0455122 26481 * ATTAT PPIE Integenic 118061 0.997759423 NC 0455122 26481 * ATTAT PPIE Integenic 180656 0.997759423 NC	NC_045512.2	85	91	+	TGTGTGG	CELF5, RBM24	5' UTR	173442	0.9582272117
NC 045312 199 165 + GGACAG FMR1 Y UTR 177571 0.970779320 NC 045512 247 255 247 AGGTTA ZANB2 Y UTR 177643 0.9707395120 NC 045512 255 2157 + GGTGGA RBM24 5' UTR 177618 0.97163522 NC 045512 21557 + CGAAACA PAPC1 Intergenic 179439 0.991270629 NC 045512 2648 + CTAAAC FNDRS1 Intergenic 180688 0.99823979 NC 045512 2648 2648 + TAATA PPIE Intergenic 180688 0.99823973 NC 045512 2648 2648 + TATAT PPIE Intergenic 180601 0.99779423 NC 045512 2648 2648 + TATAT PPIE Intergenic 180601 0.99779423 NC 045512 2648 2648 + TATAT PPIE Intergenic 18061 0.99779423	NC_045512.2	154	160	+	TGACAGG	FMR1	5' UTR	175669	0.9705308752
NC 0455122 235 240 4 AGCTTT VRN82 5' UTR 17563 0.0971633202 NC 0455122 255 255 4 AGGTAA ZAN82 5' UTR 17618 0.0971031320 NC 0455122 2155 2155 4 CAAAC RAPE1 Intergenic 179423 0.098103917 NC 0455122 26479 2648 4 CAAAC RAPE1 Intergenic 130689 0.09809479 NC 0455122 26479 2648 4 CAAAT RPIE Intergenic 130683 0.998259974 NC 0455122 2648 2648 4 ATAT PPIE Intergenic 130601 0.997790423 NC 0455122 2648 2648 4 ATAT PPIE Intergenic 130601 0.997790423 NC 0455122 2648 2648 4 ATAT PPIE Intergenic 130601 0.99779423 NC 0455122 2648 2649 4 TATAT PPIE Intergen	NC_045512.2	159	165	+	GGACACG	FMR1	5' UTR	175713	0.9707739651
NC_045512.2 247 253 2 6 GTGTGA RBM24 5' UTR 17618 0.09730139292 NC_045512.2 2155 2155 F CTAAAC RMDR851 intergenic 179409 0.9911335161 NC_045512.2 2456 25469 26474 CTAAAC RMDR851 intergenic 130059 0.99302370829 NC_045512.2 26479 26481 + CTAAAT RMDR851 intergenic 130058 0.9980239794 NC_045512.2 26481 26481 + ATATA PPIE intergenic 130061 0.9997316368 NC_045512.2 26482 26481 + ATATA PPIE intergenic 130061 0.997790423 NC_045512.2 26482 26481 + ATATA PPIE intergenic 130061 0.9977970423 NC_045512.2 26482 26491 + ATATA PPIE intergenic 130058 0.9977571485 NC_045512.2 26483 26490 +	NC_045512.2	235	240	+	AGGTTT	ZRANB2	5' UTR	176643	0.9759120015
NC 0455122 Z59 Z64 + AGGTAA ZMNN2 S'UTR 17618 0.07911497 NC 0455122 Z1552 Z1557 + CTAAAC KHDRB51 intergenic 179423 0.0911305615 NC 0455122 Z6469 Ze474 + CTAAAC KHDRB51 intergenic 180683 0.098029079 NC 0455122 Z6479 Z6481 + AAATAT PPIE intergenic 180683 0.0982290735 NC 0455122 Z6481 Z6486 + AATAT PPIE intergenic 180611 0.0977790423 NC 0455122 Z6481 Z6486 + ATATA PPIE intergenic 180601 0.9977790423 NC 0455122 Z6481 Z6488 + ATATA PPIE intergenic 180601 0.997759423 NC 0455122 Z6486 Z649 + ATATA PPIE intergenic 180601 0.997564353 NC 0455122 Z6486 Z6492 + ATATA	NC_045512.2	247	253	+	GGTGTGA	RBM24	5' UTR	175869	0.9716358292
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NC_045512.2 26489 26492 + ATTA TIAL1 Intergenic 180649 0.9980442313 NC_045512.2 26493 26498 + TTAGTTT ELAVL1 intergenic 180553 0.9975138534 NC_045512.2 26493 26499 + GTTTTC TIAL, ELAVL2, CELF2 intergenic 180553 0.9972983873 NC_045512.2 26494 26499 + TTTTC TIAL, ELAVL2, TIAL1 intergenic 180551 0.9972983873 NC_045512.2 26494 26499 + TTTTC TIAL, ELAVL2, TIAL1 intergenic 180571 0.9971938323 NC_045512.2 26501 26504 + TGTTG CELF2 intergenic 180517 0.997149616 NC_045512.2 26502 26504 + TTGAGA EIF48 intergenic 180517 0.997149616 NC_045512.2 26512 26515 + TTAAT PPIE intergenic 180655 0.998021322 NC_045512.2 26513 2		26487	26492	+	ΑΤΑΤΤΑ	PPIE	intergenic	180632	0.9979503102
NC_045512.2 26490 26496 + TTAGTTT ELAVL1 intergenic 180580 0.9976630222 NC_045512.2 26493 26499 + GTTTTC TTAI, ELAVL2, CELF2 intergenic 180553 0.9975138534 NC_045512.2 26494 26499 + GTTTTC TTAI, ELAVL2, TIAL1 intergenic 180514 0.9973978323 NC_045512.2 26494 26498 + TTTTC TTAI, ELAVL2, TIAL1 intergenic 180571 0.9971393632 NC_045512.2 26500 26504 + TGTTT CELF2 intergenic 180571 0.9971413292 NC_045512.2 26501 26505 + GTTTG TIALI, TIAI intergenic 180576 0.9973149616 NC_045512.2 26502 26508 + TTTGAA EIF48 intergenic 180657 0.9973149616 NC_045512.2 26511 26515 + TTAAT PPIE intergenic 180645 0.99802132 NC_045512.2 26513		26489	26492	+	ΑΤΤΑ	TIAL1	intergenic	180649	0.9980442313
NC_045512.2 26493 26498 + GTTTT TIAI, ELAVL2, CELF2 Intergenic 180553 0.9975138534 NC_045512.2 26494 26499 + GTTTTC TIAI, ELAVL2, CILF2 intergenic 180553 0.9977378332 NC_045512.2 26494 26498 + TTTTC TIAI, ELAVL2, TIAL1 intergenic 180571 0.9976132992 NC_045512.2 26501 26504 + TTTTC CELF2 intergenic 180551 0.997134167 NC_045512.2 26502 26508 + TTTGGAA EIFAB intergenic 180517 0.9973149616 NC_045512.2 26510 26515 + TTTAA EIAVL2, TIAL1, TIA1 intergenic 180535 0.99773149616 NC_045512.2 26510 26515 + TTTAAT PPIE intergenic 180645 0.999789836 NC_045512.2 26516 + TAATT PPIE intergenic 180655 0.99973799 NC_045512.2 27384 +	 NC_045512.2	26490	26496	+	TTAGTTT	FLAVL1	intergenic	180580	0.9976630222
NC_045512.2 26499 26499 4 GTTTTC TIAL, ELAVL2, TIAL1 Intergenic 180514 0.9972983873 NC_045512.2 26494 26499 + TTTTC TIAL, ELAVL2, TIAL1 intergenic 180514 0.9973978332 NC_045512.2 26500 26504 + TGTTT CELF2 intergenic 180517 0.9976132992 NC_045512.2 26500 26505 + GTTTG CELF2 intergenic 180517 0.9977134167 NC_045512.2 26500 26508 + TTTGG TIAL1, TIA1 intergenic 180517 0.9971434616 NC_045512.2 26509 26513 + CTTTA ELAVL2, TIAL1, TIA1 intergenic 180625 0.9979184884 NC_045512.2 26510 26515 + TTTAAT PPIE intergenic 180645 0.998201322 NC_045512.2 26513 26514 + ATTTA PPIE intergenic 180677 0.998189849 NC_045512.2 27384 <	NC 045512.2	26493	26498	+	GTTTTT	TIA1. ELAVL2. CELF2	intergenic	180553	0.9975138534
NC_045512.2 26499 Zef499 Zef491 Zef499 Zef499 <thzef4189< th=""> <thzef499< th=""> <thzef49< td=""><td>NC 045512.2</td><td>26493</td><td>26499</td><td>+</td><td>GTTTTTC</td><td>TIA1. ELAVL2. TIAL1</td><td>intergenic</td><td>180514</td><td>0.9972983873</td></thzef49<></thzef499<></thzef4189<>	NC 045512.2	26493	26499	+	GTTTTTC	TIA1. ELAVL2. TIAL1	intergenic	180514	0.9972983873
NC_045512.2 26498 26498 TTTT CELF2 Intergenic 18057 0.0976132992 NC_045512.2 26500 26504 + TGTT CELF2 intergenic 180576 0.9975132992 NC_045512.2 26501 26505 + GTTG TIAL1, TIA1 intergenic 180506 0.9972541892 NC_045512.2 26502 26503 + TTTGGAA EIF48 intergenic 180517 0.9973149616 NC_045512.2 26510 26515 + TTAAT PPIE intergenic 180625 0.997988936 NC_045512.2 26511 26516 + TAATT PPIE intergenic 180655 0.998021322 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180677 0.9981989249 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180677 0.9983375804 NC_045512.2 27384 27389 + TTAAA <td< td=""><td>NC 045512.2</td><td>26494</td><td>26499</td><td>+</td><td>ттттс</td><td>TIA1. ELAVL2. TIAL1</td><td>intergenic</td><td>180532</td><td>0.9973978332</td></td<>	NC 045512.2	26494	26499	+	ттттс	TIA1. ELAVL2. TIAL1	intergenic	180532	0.9973978332
NC_045512.2 26500 26504 + TGTT CLP2 Intergenic 180495 0.0971934167 NC_045512.2 26501 26505 + GTTTG TIAL1, TIA1 intergenic 18056 0.9972541892 NC_045512.2 26502 26508 + TTTGGAA EIF4B intergenic 180517 0.9973149616 NC_045512.2 26510 26515 + TTTAA ELAVL2, TIAL1, TIA1 intergenic 180645 0.9979189868 NC_045512.2 26511 26516 + TTAAT PPIE intergenic 180645 0.998022132 NC_045512.2 26513 26518 + TAATT PPIE intergenic 180655 0.998073799 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180645 0.998073379 NC_045512.2 27384 27388 + ATTAA PPIE intergenic 179740 0.993378004 NC_045512.2 27384 27389 +	NC 045512.2	26494	26498	+	тттт	CELF2	intergenic	180571	0.9976132992
NC_045512.2 26501 26505 + GTTTG TIAL1, TIA1 intergenic 180506 0.9972541892 NC_045512.2 26502 26508 + TTTGGAA EIF4B intergenic 180517 0.9973149616 NC_045512.2 26509 26513 + CTTTA ELAVL2, TIAL1, TIA1 intergenic 180625 0.997916368 NC_045512.2 26510 26515 + TTTAAT PPIE intergenic 180645 0.998021322 NC_045512.2 26512 26517 + TAATT PPIE intergenic 180645 0.998021322 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180654 0.998021322 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180654 0.998073799 NC_045512.2 27383 27389 + ATTAA PPIE intergenic 180644 0.99822846 NC_045512.2 27384 27389 +	NC 045512.2	26500	26504	+	TGTTT	CELF2	intergenic	180495	0.9971934167
NC_045512.2 26508 + TTTGGAA EIF4B Intergenic 180517 0.9973149616 NC_045512.2 26509 26513 + CTTTA ELAVL2, TIAL1, TIA1 intergenic 180625 0.9979116368 NC_045512.2 26510 26515 + TTTAAT PPIE intergenic 180625 0.9979889836 NC_045512.2 26511 26516 + TTAATT PPIE intergenic 180645 0.9980221322 NC_045512.2 26513 26518 + ATTT<	NC 045512.2	26501	26505	+	GTTTG	TIAL1. TIA1	intergenic	180506	0.9972541892
NC_045512.2 26503 26513 + CTTA ELAVL2, TIAL1, TIA1 intergenic 180625 0.9979116368 NC_045512.2 26510 26515 + TTTAAT PPIE intergenic 180625 0.9979889836 NC_045512.2 26511 26516 + TTAATT PPIE intergenic 180645 0.9980221322 NC_045512.2 26512 26517 + TAATTT PPIE intergenic 180645 0.9980221322 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180677 0.9981989249 NC_045512.2 26514 26519 + ATTTA PPIE, TIA1, ELAVL2, TIAL1 intergenic 180677 0.9981989249 NC_045512.2 27383 27384 + ATTAAA PPIE intergenic 179742 0.993032646 NC_045512.2 27384 27384 + ACGAACA PABPC1 intergenic 179777 0.9932266316 NC_045512.2 27884 27884 <td>NC 045512.2</td> <td>26502</td> <td>26508</td> <td>+</td> <td>TTTGGAA</td> <td>EIF4B</td> <td>intergenic</td> <td>180517</td> <td>0.9973149616</td>	NC 045512.2	26502	26508	+	TTTGGAA	EIF4B	intergenic	180517	0.9973149616
NC_045512.2 26510 26515 + TTAAT PPIE Intergenic 180645 0.9979889836 NC_045512.2 26511 26515 + TTAAT PPIE intergenic 180645 0.9979889836 NC_045512.2 26512 26517 + TAATT PPIE intergenic 180645 0.998073799 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180677 0.9981989249 NC_045512.2 26514 26519 + ATTTAA PPIE intergenic 180694 0.998292846 NC_045512.2 27384 27388 + ATTAAA PPIE intergenic 179704 0.993032646 NC_045512.2 27384 27384 + ACGAACA PABPC1 intergenic 179772 0.993032646 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179777 0.9932266316 NC_045512.2 27884 27884 ACGAACA <	NC 045512.2	26509	26513	+	СТТТА	ELAVL2, TIAL1, TIA1	intergenic	180625	0.9979116368
NC_045512.2 26511 26516 + TTAATT PPIE intergenic 180645 0.998021322 NC_045512.2 26512 26517 + TAATT PPIE intergenic 180645 0.9980737399 NC_045512.2 26513 26518 + AATTT PPIE intergenic 180645 0.9980737399 NC_045512.2 26514 26519 + ATTTA PPIE intergenic 180694 0.998292846 NC_045512.2 27383 27388 + ATTAAA PPIE intergenic 179704 0.993032646 NC_045512.2 27388 27384 + ACGAACA PABPC1 intergenic 179742 0.993032646 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179777 0.9932266316 NC_045512.2 27888 27894 + ACGAACA PABPC1 intergenic 180576 0.9976409231 NC_045512.2 28260 28264 + <td< td=""><td>NC 045512.2</td><td>26510</td><td>26515</td><td>+</td><td>TTTAAT</td><td>PPIE</td><td>intergenic</td><td>180639</td><td>0.9979889836</td></td<>	NC 045512.2	26510	26515	+	TTTAAT	PPIE	intergenic	180639	0.9979889836
NC_045512.2 26512 26517 + TAATTT PPIE intergenic 180655 0.9980773799 NC_045512.2 26513 26518 + AATTTT PPIE intergenic 180657 0.9981989249 NC_045512.2 26514 26519 + ATTTA PPIE intergenic 180657 0.998292866 NC_045512.2 27383 27388 + ATTAAA PPIE intergenic 179804 0.9933758004 NC_045512.2 27384 27389 + TTAAAC KHDRBS1 intergenic 179742 0.9930326466 NC_045512.2 27384 27389 + CTAAAC KHDRBS1 intergenic 179774 0.9932266316 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179777 0.9931824334 NC_045512.2 28266 + ACGAACA PABPC1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA	NC 045512.2	26511	26516	+	TTAATT	PPIE	intergenic	180645	0.9980221322
NC_045512.2 26513 26518 + AATTT PPIE Intergenic 180677 0.9981989249 NC_045512.2 26514 26519 + ATTTA PPIE, TIA1, ELAVL2, TIAL1 intergenic 180677 0.9981989249 NC_045512.2 27383 27388 + ATTAA PPIE intergenic 179804 0.9933758004 NC_045512.2 27384 27389 + TTAAAC KHDRBS1 intergenic 179742 0.9933758004 NC_045512.2 27384 27389 + CTAAAC KHDRBS1 intergenic 179742 0.99332266316 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179779 0.9931824334 NC_045512.2 28261 + CTAAAC KHDRBS1 intergenic 180576 0.9976409231 NC_045512.2 28262 28264 + CTAAAC KHDRBS1 intergenic 180869 0.9992596808 NC_045512.2 28270 28275 +	NC 045512.2	26512	26517	+	TAATTT	PPIE	intergenic	180655	0.9980773799
NC_045512.2 26514 26519 + ATTTTA PPIE, TIA1, ELAVL2, TIAL1 intergenic 180694 0.998292846 NC_045512.2 27383 27388 + ATTAAA PPIE intergenic 179804 0.998392846 NC_045512.2 27384 27389 + TTAAAC KHDRBS1 intergenic 179742 0.993032646 NC_045512.2 27384 27389 + ACGAACA PABPC1 intergenic 180525 0.9973591598 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179777 0.9932266316 NC_045512.2 27888 27894 + ACGAACA PABPC1 intergenic 179769 0.9931824334 NC_045512.2 28266 28266 + ACGAACA PABPC1 intergenic 180576 0.9976409231 NC_045512.2 28260 28274 + CTAAAC KHDRBS1 intergenic 180869 0.998966868 NC_045512.2 28270 28275 + TAAAAT PPIE intergenic 180816 0.998966868	NC 045512.2	26513	26518	+	AATTTT	PPIE	intergenic	180677	0.9981989249
NC_045512.2 27383 27388 + ATTAAA PPIE Integranic 179804 0.9933758004 NC_045512.2 27384 27389 + TTAAAC KHDRBS1 intergenic 179804 0.9933758004 NC_045512.2 27384 27389 + TTAAAC KHDRBS1 intergenic 179742 0.993032646 NC_045512.2 27384 27389 + CTAAAC KHDRBS1 intergenic 179777 0.9932266316 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179779 0.9932266316 NC_045512.2 27888 27894 + ACGAACA PABPC1 intergenic 179769 0.9931824334 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180869 0.998966868 NC_045512.2 28270 28275 + TAAAA KHDRBS1 intergenic 180883 0.9993370276 <t< td=""><td>NC 045512.2</td><td>26514</td><td>26519</td><td>+</td><td>ΑΤΤΤΤΑ</td><td>PPIE, TIA1, ELAVL2, TIAL1</td><td>intergenic</td><td>180694</td><td>0.998292846</td></t<>	NC 045512.2	26514	26519	+	ΑΤΤΤΤΑ	PPIE, TIA1, ELAVL2, TIAL1	intergenic	180694	0.998292846
NC_045512.2 27384 27389 + TTAAAC KHDRBS1 intergenic 179742 0.9930332646 NC_045512.2 27388 27394 + ACGAACA PABPC1 intergenic 180525 0.9973591598 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179777 0.9932266316 NC_045512.2 27888 27894 + ACGAACA PABPC1 intergenic 179779 0.9931824334 NC_045512.2 28256 28261 + CTAAAC KHDRBS1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180576 0.9976409231 NC_045512.2 28260 28264 + CTAAAC KHDRBS1 intergenic 180869 0.99930370276 NC_045512.2 28270 28275 + TAAAC KHDRBS1 intergenic 18083 0.9994613349 NC_045512.2 29530 29535 <	NC 045512.2	27383	27388	+	ΑΤΤΑΑΑ	PPIE	intergenic	179804	0.9933758004
NC_045512.2 27388 27394 + ACGAACA PABPC1 intergenic 180525 0.9973591598 NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179777 0.9932266316 NC_045512.2 27888 27894 + ACGAACA PABPC1 intergenic 179769 0.9931824334 NC_045512.2 28256 28261 + CTAAAC KHDRBS1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180869 0.9992596808 NC_045512.2 28270 28275 + CTAAAA KHDRBS1 intergenic 180816 0.9989668688 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29680 29685 <	NC 045512.2	27384	27389	+	TTAAAC	KHDRBS1	intergenic	179742	0.9930332646
NC_045512.2 27884 27889 + CTAAAC KHDRBS1 intergenic 179777 0.9932266316 NC_045512.2 27888 27894 + ACGAACA PABPC1 intergenic 179769 0.9931824334 NC_045512.2 28256 28261 + CTAAAC KHDRBS1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180869 0.9992596808 NC_045512.2 28270 28275 + CTAAAC KHDRBS1 intergenic 180816 0.9989668688 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29680 29685 + TTTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + <td>NC 045512.2</td> <td>27388</td> <td>27394</td> <td>+</td> <td>ACGAACA</td> <td>PABPC1</td> <td>intergenic</td> <td>180525</td> <td>0.9973591598</td>	NC 045512.2	27388	27394	+	ACGAACA	PABPC1	intergenic	180525	0.9973591598
NC_045512.2 27888 27894 + ACGAACA PABPC1 intergenic 179769 0.9931824334 NC_045512.2 28256 28261 + CTAAAC KHDRBS1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180869 0.9992596808 NC_045512.2 28269 28274 + CTAAAA KHDRBS1 intergenic 180816 0.9993806868 NC_045512.2 28270 28275 + TAAAAT PPIE intergenic 180883 0.9993370276 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29680 29685 + TTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + TAGGGA HNRNPA1, HNRNPA12, HNRNPA2B1 3'UTR 174974 0.9666911598 <td>NC 045512.2</td> <td>27884</td> <td>27889</td> <td>+</td> <td>СТАААС</td> <td>KHDRBS1</td> <td>intergenic</td> <td>179777</td> <td>0.9932266316</td>	NC 045512.2	27884	27889	+	СТАААС	KHDRBS1	intergenic	179777	0.9932266316
NC_045512.2 28256 28261 + CTAAAC KHDRBS1 intergenic 180576 0.9976409231 NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180869 0.9992596808 NC_045512.2 28269 28274 + CTAAAA KHDRBS1 intergenic 180816 0.9992596808 NC_045512.2 28269 28274 + CTAAAA KHDRBS1 intergenic 180816 0.9993668688 NC_045512.2 28270 28275 + TAAAAT PPIE intergenic 180883 0.9993370276 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29680 29685 + TTTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + TTAGGGA HNRNPA1, HNRNPA1L2, HNRNPA2B1 3'UTR 174955 0.9665861892 NC_045512.2 29699 29704 + TAGGGA HIN28A 3'UTR 174974 0.9666911598	NC 045512.2	27888	27894	+	ACGAACA	PABPC1	intergenic	179769	0.9931824334
NC_045512.2 28260 28266 + ACGAACA PABPC1 intergenic 180869 0.9992596808 NC_045512.2 28269 28274 + CTAAAA KHDRBS1 intergenic 180869 0.9992596808 NC_045512.2 28269 28274 + CTAAAA KHDRBS1 intergenic 180816 0.9992596808 NC_045512.2 28270 28275 + TAAAAT PPIE intergenic 180883 0.9993370276 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29680 29685 + TTTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + TTAGGGA HNRNPA1, HNRNPA1L2, HNRNPA2B1 3'UTR 174955 0.9665861892 NC_045512.2 29709 29704 + TAGGGAA HNRNPA1 3'UTR 174974 0.9666911598 NC_045512.2 29701 29707	NC 045512.2	28256	28261	+	СТАААС	KHDRBS1	intergenic	180576	0.9976409231
NC_045512.2 28269 28274 + CTAAAA KHDRBS1 intergenic 180816 0.998966868 NC_045512.2 28270 28275 + TAAAAT PPIE intergenic 180883 0.9993370276 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.9994613349 NC_045512.2 29680 29685 + TTTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + TTAGGGA HNRNPA1, HNRNPA1L2, HNRNPA2B1 3'UTR 174955 0.9665861892 NC_045512.2 29699 29704 + TAGGGA HNRNPA1 3'UTR 174974 0.9666911598 NC_045512.2 29701 29707 + GGGAGGA LIN28A 3'UTR 174934 0.966470169 NC 045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	28260	28266	+	ACGAACA	PABPC1	intergenic	180869	0.9992596808
NC_045512.2 28270 28275 + TAAAAT PPIE intergenic 180833 0.9993370276 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.9993370276 NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29680 29685 + TTTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + TTAGGGA HNRNPA1L2, HNRNPA2B1 3'UTR 174955 0.9665861892 NC_045512.2 29699 29704 + TAGGGA HNRNPA1 3'UTR 174974 0.9666911598 NC_045512.2 29701 29707 + GGGAGGA LIN28A 3'UTR 174934 0.966470169 NC 045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	28269	28274	+	СТАААА	KHDRBS1	intergenic	180816	0.998966868
NC_045512.2 29530 29535 + CTAAAC KHDRBS1 intergenic 180028 0.994613349 NC_045512.2 29680 29685 + TTTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + TTAGGGA HNRNPA1, HNRNPA1L2, HNRNPA2B1 3'UTR 174955 0.9665861892 NC_045512.2 29699 29704 + TAGGGA HNRNPA1 3'UTR 174974 0.9666911598 NC_045512.2 29701 29707 + GGGAGGA LIN28A 3'UTR 174934 0.966470169 NC 045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	28270	28275	+	TAAAAT	PPIE	intergenic	180883	0.9993370276
NC_045512.2 29680 29685 + TTTAAT PPIE 3'UTR 177005 0.9779119683 NC_045512.2 29698 29704 + TTAGGGA HNRNPA1, HNRNPA1L2, HNRNPA2B1 3'UTR 174955 0.9665861892 NC_045512.2 29699 29704 + TAGGGA HNRNPA1 3'UTR 174974 0.9666911598 NC_045512.2 29701 29707 + GGGAGGA LIN28A 3'UTR 174934 0.966470169 NC_045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	29530	29535	+	CTAAAC	KHDRBS1	intergenic	180028	0.994613349
NC_045512.2 29698 29704 + TTAGGGA HNRNPA1, HNRNPA1L2, HNRNPA2B1 3'UTR 174955 0.9665861892 NC_045512.2 29699 29704 + TAGGGA HNRNPA1 3'UTR 174974 0.9666911598 NC_045512.2 29701 29707 + GGGAGGA LIN28A 3'UTR 174934 0.966470169 NC 045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	29680	29685	+	TTTAAT	PPIE	3'UTR	177005	0.9779119683
NC_045512.2 29699 29704 + TAGGGA HNRNPA1 3'UTR 174974 0.9666911598 NC_045512.2 29701 29707 + GGGAGGA LIN28A 3'UTR 174934 0.966470169 NC 045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	29698	29704	+	TTAGGGA	HNRNPA1, HNRNPA1L2. HNRNPA2B1	3'UTR	174955	0.9665861892
NC_045512.2 29701 29707 + GGGAGGA LIN28A 3'UTR 174934 0.966470169 NC_045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	29699	29704	+	TAGGGA	HNRNPA1	3'UTR	174974	0.9666911598
NC 045512.2 29743 29749 + CGGAGTA LIN28A 3'UTR 172413 0.9525422231	NC 045512.2	29701	29707	+	GGGAGGA	LIN28A	3'UTR	174934	0,966470169
	NC 045512.2	29743	29749	+	CGGAGTA	LIN28A	3'UTR	172413	0.9525422231

Supplementary Table 2. Conservation of binding motifs for human RBPs across genome sequences of SARS-CoV-2 isolates. Conserved binding sites are listed along with the number and fraction of genomes in which the sequence is conserved. RBP: RNA Binding Protein.