

Identification of Potential Regions of SARS-CoV-2 and their Characteristics based on Human miRNAs to Unveil Comorbidities

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Genomic Regions of SARS-CoV-2	Genomic Coordinates and Sequence of SARS-CoV-2	Human miRNA	Highest number of nucleotide match with the aligned miRNA	Genomic Coverage (%)	Coded Protein
PR1	28787-5'-UACGCAGAAGGGAGCAGAGGCGGCAGUCAAGCCU-3'-28820	hsa-miR-3960, hsa-miR-10526-3p, hsa-miR-483-5p, hsa-miR-4430, hsa-miR-4787-5p, hsa-miR-6076, hsa-miR-149-3p, hsa-miR-4728-5p, hsa-miR-6778-5p, hsa-miR-135a-3p, hsa-miR-6743-5p, hsa-miR-6125, hsa-miR-6873-5p, hsa-miR-638, hsa-miR-6510-5p, hsa-miR-1249-5p	14	99.37	Nucleocapsid
PR2	13587-5'-AAAAACUAAUUGUUGUCGUCCA-3'-13610	hsa-miR-548d-5p, hsa-miR-548ay-5p, hsa-miR-548ag, hsa-miR-548ap-5p, hsa-miR-548ae-5p, hsa-miR-548ad-5p, hsa-miR-548o-5p, hsa-miR-548c-5p, hsa-miR-548aq-5p, hsa-miR-548am-5p	10	99.91	RdRp
PR3	17113-5'-AUUGGCCUAGCUCUCUACUACCCUUCUGCUCGCAUAG-3'-17149	hsa-miR-6511b-3p, hsa-miR-6511a-3p, hsa-miR-6750-3p, hsa-miR-99a-3p, hsa-miR-10398-5p, hsa-miR-4749-3p, hsa-miR-3162-3p, hsa-miR-4633-5p	8	99.26	Helicase
PR4	28029-5'-UAUAUUAGAGUAGGAGCUAGAAAAUCAGACCU'-3'-28061	hsa-miR-8084, hsa-miR-451b, hsa-miR-3914, hsa-miR-378j, hsa-miR-378i, hsa-miR-378f, hsa-miR-378b, hsa-miR-3152-3p	8	84.67	ORF8

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Genomic Regions of SARS-CoV-2	Genomic Coordinates and Sequence of SARS-CoV-2	Human miRNA	Highest number of nucleotide match with the aligned miRNA	Genomic Coverage (%)	Coded Protein
PR5	28356-5'-AGAAUGGAGAACGCAGUGGGGCGCAUCA'-3'-28384	hsa-miR-6850-5p, hsa-miR-6090, hsa-miR-6089, hsa-miR-4665-5p, hsa-miR-4655-5p, hsa-miR-4463, hsa-miR-3175, hsa-miR-197-5p	8	98.60	Nucleocapsid
PR6	28889-5'-UCUCCUGCUAGAAUGGCUGGCAUUGGCGGUGAUGCUG-3'-28925	hsa-miR-9851-5p, hsa-miR-5681a, hsa-miR-4446-3p, hsa-miR-1207-5p, hsa-miR-7705, hsa-miR-4469, hsa-miR-195-3p, hsa-miR-621	8	97.92	Nucleocapsid
PR7	29184-5'-UUGCACAAUUUGCCCCAGCGCUUCAGCGUUCUUCGGA-3'-29221	hsa-miR-4731-3p, hsa-miR-6848-3p, hsa-miR-1913, hsa-miR-2682-3p, hsa-miR-675-3p, hsa-miR-33a-3p, hsa-miR-5008-3p, hsa-miR-4707-5p, hsa-miR-10396b-3p	8	98.81	Nucleocapsid
PR8	3453-5'-UUUACCUAAACAUGGAGGAGGUGUUGCAGGAGCCUU-3'-3489	hsa-miR-4534, hsa-miR-4511, hsa-miR-877-5p, hsa-miR-4760-5p, hsa-miR-6754-5p, hsa-miR-4533, hsa-miR-7847-3p	7	99.44	NSP3
PR9	6340-5'-UGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAA-3'-6378	hsa-miR-6837-5p, hsa-miR-3198, hsa-miR-4695-5p, hsa-miR-8071, hsa-miR-12118, hsa-miR-6801-5p, hsa-miR-6789-5p	7	99.17	NSP3
PR10	11366-5'-UAUGAUGAUGGUGCUAGGAGAGUGUGGACAC-3'-11396	hsa-miR-3945, hsa-miR-1272, hsa-miR-7110-5p, hsa-miR-6849-5p, hsa-miR-2392, hsa-miR-4721, hsa-miR-12121, hsa-miR-6765-5p	7	99.63	NSP6
PR11	29436-5'-AACAGCAAACUGUGACUCUUCUCCUGCUGCAGAUUU-3'-29472	hsa-miR-548bc, hsa-miR-548ba, hsa-miR-3619-3p, hsa-miR-873-5p, hsa-miR-4279, hsa-miR-6818-3p, hsa-miR-4778-3p, hsa-miR-6823-3p	7	98.21	Nucleocapsid
PR12	350-5'-CGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGC-3'-390	hsa-miR-6831-5p, hsa-miR-3141, hsa-miR-3192-5p, hsa-miR-4281, hsa-miR-6729-5p, hsa-miR-5001-5p	6	99.06	Leader Protein
PR13	1386-5'-ACAAUUCAGAAGUAGGACCUGAGCAUAGUCUU-3'-1417	hsa-miR-10524-5p, hsa-miR-4257, hsa-miR-3193, hsa-miR-4330, hsa-miR-5000-5p, hsa-miR-6165	6	99.26	NSP2
PR14	2081-5'-GUUCAGUUGACUUCGCAGUGGCUAACUACAUCUUUGGCAC-3'-2121	hsa-miR-9985, hsa-miR-27a-3p, hsa-miR-1256, hsa-miR-199b-3p, hsa-miR-199a-3p, hsa-miR-6862-3p	6	97.48	NSP2
PR15	2720-5'-GCACCAACAAAGGUUACUUUUGGUGAU-3'-2746	hsa-miR-802, hsa-miR-548bb-3p, hsa-miR-548am-3p, hsa-miR-548ah-3p, hsa-miR-377-3p, hsa-miR-29a-5p	6	99.75	NSP3

Genomic Regions of SARS-CoV-2	Genomic Coordinates and Sequence of SARS-CoV-2	Human miRNA	Highest number of nucleotide match with the aligned miRNA	Genomic Coverage (%)	Coded Protein
PR16	4266-5'-UAAAUUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAA-3'-4305	hsa-miR-936, hsa-miR-214-3p, hsa-miR-518f-3p, hsa-miR-4269, hsa-miR-4306, hsa-miR-185-5p	6	98.85	NSP3
PR17	5537-5'-CAGCAGACAACCCUUAAGGGUGUGAGAAGCUGUUUGUA-3'-5574	hsa-miR-4509, hsa-miR-3166, hsa-miR-4764-5p, hsa-miR-521, hsa-miR-517b-3p, hsa-miR-517a-3p, hsa-miR-671-5p	6	98.88	NSP3
PR18	8165-5'-AUUUCAGCAGCUCGGCAAGGGUUUGUUGAUUC-3'-8196	hsa-miR-3529-5p, hsa-miR-4776-5p, hsa-miR-502-3p, hsa-miR-6071, hsa-miR-4750-5p, hsa-miR-6860	6	99.44	NSP3
PR19	10803-5'-UAGGACCUCUUUCUGUCUAAACUGGAAUUGCCGUUUUA-3'-10840	hsa-miR-147b-5p, hsa-miR-548au-5p, hsa-miR-548ar-5p, hsa-miR-548x-5p, hsa-miR-548g-5p, hsa-miR-548aj-5p	6	99.53	3CL-Pro
PR20	13410-5'-GUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGC-3'-13446	hsa-miR-30b-5p, hsa-miR-5587-5p, hsa-miR-6782-3p, hsa-miR-3943, hsa-miR-5691, hsa-miR-7106-3p	6	99.47	NSP10, RdRp
PR21	15090-5'-AAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUG-3'-15128	hsa-miR-4770, hsa-miR-4435, hsa-miR-6726-5p, hsa-miR-4453, hsa-miR-6789-3p, hsa-miR-4690-3p	6	98.32	RdRp
PR22	22009-5'-CAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUA-3'-22046	hsa-miR-548ah-5p, hsa-miR-3165, hsa-miR-3132, hsa-miR-320c, hsa-miR-320d, hsa-miR-320a-3p, hsa-miR-28-5p	6	98.25	endoRNase
PR23	22324-5'-UUCUUCAGGUUGGACAGCUGGUGCUGCAG-3'-22352	hsa-miR-3934-3p, hsa-miR-7158-5p, hsa-miR-6796-5p, hsa-miR-6823-5p, hsa-miR-3944-3p, hsa-miR-6861-5p	6	97.79	Spike
PR24	25329-5'-UUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUU-3'-25371	hsa-miR-891a-5p, hsa-miR-8085, hsa-miR-6781-5p, hsa-miR-650, hsa-miR-5571-5p, hsa-miR-5195-3p	6	99.31	Spike
PR25	166-5'-AGUAAUCUGUCUAUCUUCUGCAGGCU-3'-191	hsa-miR-4719, hsa-miR-6510-3p, hsa-miR-3909, hsa-miR-6842-3p, hsa-miR-6769a-3p	5	98.82	5'-UTR
PR26	825-5'-AUAACAACUUCUGUGGCCUGAUGGCUACCCUCUUGAGUG-3'-864	hsa-miR-6882-3p, hsa-miR-4456, hsa-miR-6846-3p, hsa-miR-3127-3p, hsa-miR-3940-3p, hsa-miR-4767	5	98.58	NSP2
PR27	1659-5'-GUGACUUUAAACUUAAGAAGAGAUCCGAUUAUUUUGGCAUCUUUUUCU-3'-1708	hsa-miR-548z, hsa-miR-548h-3p, hsa-miR-548ay-3p, hsa-miR-548ao-3p, hsa-miR-1282	5	98.90	NSP2
PR28	2511-5'-CAGAAGUGUUAACAGAGGAAGUUGUCUUG-3'-2539	hsa-miR-452-5p, hsa-miR-6841-5p, hsa-miR-3125, hsa-miR-106a-5p, hsa-miR-124-5p	5	99.47	NSP2
PR29	12785-5'-ACAACAAAGGGAGGUAGGUUUGUACUUG-3'-12812	hsa-miR-520d-5p, hsa-miR-30b-3p, hsa-miR-6129, hsa-miR-4747-5p, hsa-miR-658	5	99.10	NSP9

Genomic Regions of SARS-CoV-2	Genomic Coordinates and Sequence of SARS-CoV-2	Human miRNA	Highest number of nucleotide match with the aligned miRNA	Genomic Coverage (%)	Coded Protein
PR30	13385-5'-GGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUC-3'-13418	hsa-miR-147a, hsa-miR-3652, hsa-miR-548q, hsa-miR-1273h-5p, hsa-miR-548h-5p	5	99.56	NSP10
PR31	16212-5'-GUACACACCGCAUACAGUCUACAGGCUGUUGGGGCUU-3'-16249	hsa-miR-5003-3p, hsa-miR-4680-5p, hsa-miR-4666a-3p, hsa-miR-1912-3p, hsa-miR-596	5	99.58	RdRp, Helicase
PR32	17168-5'-AUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUAAAAUUAUUGC-3'-17212	hsa-miR-3681-5p, hsa-miR-4489, hsa-miR-564, hsa-miR-4711-5p, hsa-miR-128-1-5p	5	99.73	Helicase
PR33	24690-5'-GUGGAAAGGGCUAUCUUAUGUCCUCCCCUCAGUCAGCACCUCU-3'-24736	hsa-miR-6881-3p, hsa-miR-6834-3p, hsa-miR-6809-3p, hsa-miR-6759-3p, hsa-miR-6758-5p, hsa-miR-4667-3p	5	99.75	Spike
PR34	26793-5'-AUGUGGCUCAGCUACUUCUUAUUGCUUC-3'-26818	hsa-miR-6870-3p, hsa-miR-4283, hsa-miR-340-3p, hsa-miR-1184, hsa-let-7i-3p	5	85.58	Membrane
PR35	27500-5'-CUUCUGGAACAACGAGGGCAAUUCACCAUUUCAU-3'-27534	hsa-miR-539-3p, hsa-miR-494-3p, hsa-miR-4749-5p, hsa-miR-3975, hsa-miR-3616-3p	5	98.96	ORF7a
PR36	28600-5'-UUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUC-3'-28637	hsa-miR-6878-5p, hsa-miR-4744, hsa-miR-6771-5p, hsa-miR-5580-3p, hsa-miR-187-5p	5	98.63	Nucleocapsid
PR37	28915-5'-CGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAG-3'-28950	hsa-miR-1322, hsa-miR-3194-3p, hsa-miR-33b-5p, hsa-miR-3157-3p, hsa-miR-1915-5p	5	85.65	Nucleocapsid
PR38	29534-5'-ACUCAUGCAGACCACACAAGGCAGAUUGGCUAU-3'-29566	hsa-miR-3939, hsa-miR-410-3p, hsa-miR-3663-3p, hsa-miR-21-3p, hsa-miR-4789-3p	5	97.20	Nucleocapsid, ORF10

Table S1: List of 38 potential SARS-CoV-2 regions based on aligned human miRNAs along with their highest nucleotide match

Genomic Regions of SARS-CoV-2	Human miRNA	Target Human mRNA	Key Proteins in PPI Network	KEGG Pathways	FDR corrected p-value
PR1	hsa-miR-3960, hsa-miR-10526-3p, hsa-miR-483-5p, hsa-miR-4787-5p, hsa-miR-6076, hsa-miR-149-3p, hsa-miR-4728-5p, hsa-miR-6778-5p, hsa-miR-135a-3p, hsa-miR-6743-5p, hsa-miR-6125, hsa-miR-6873-5p, hsa-miR-638, hsa-miR-6510-5p, hsa-miR-1249-5p, hsa-miR-4430	POU3F3, WWP2, PCDHA11, PCDHA6, PCDHAC2, PCDHA7, PCDHA1, PCDHA9, PCDHA3, PCDHA13, INO80D, SRSF6, MYH9, MUC1L, GALNT11, RBM4B, PPP5C, SPINK8, ARID1A, TARBP1, RUSC1, CT62, IQCE, ALCAM, STK40, HR, PLA2G5, NUDT8, RNF165, CUTA, RERE, SEZ6, MNT, CCDC28A, SYT1, RPP14, ASCC2, MPI, IREB2, MYL12A, CEMIP2, LRRC3B, ARID2, ZNF385A, SPTSSA, INF2, PDLIM5, RBM41, PLK4, HMCN2, E2F3, CHD3, WDFY3, KLF6, SEMA6D, STOX2, PLS1, PIK3CA, SCN8A, POC1B, TMEM25, FOXP4, SOGA1, LENG8, C20orf96, RPH3AL, NACC1, NFIX, MPP2, SDK1, SMARCD1, FOXP4, SOGA1, RPH3AL, C20orf96, MPP2, LENG8, SMARCD1, NACC1, SYNGAP1, AR, TP53INP2, ZFHx3, RELN, TNS1, BRPF3, AP1G1, GSTM2, PAK1, PKLR, YIPF3, PAIP1, KCNMA1, FANCF, EXOC6B, GLYCTK, COA6, CHD6, PTBP3, LINC02694, SLC39A8, TULP3, TFB1M, SPRY2, CHD3, NEGR1, CDK19, DGAT2, SNW1, FUT8, GTPBP1, YTHDF2, MROH2A, KIF6, KIAA0232, EIF4EBP1, TRIM41, SLC6A12, USP35, BCORL1, FAIM2, ZDXB, DKK3, DNMT3B, SLF2, PRICKLE3, LRRC55, GABRA4, TOB2, GASK1B, USP51, ZSWIM9, SPACA7, PSMD14, SLC25A23, KDSR, HNRNP40, WDR47, NPAS4, LRRC27, CCNG2, MAFB, MRTFA, FGFR1OP2, SEPTIN4, NCDN, CDK16, KCNS1, DNAI3, MAP1A, TP53BP1, C20orf96, PACS1, SMARCD1, PDX1, PLXNA4, NPTXR, NFIX, AP1S1, ANKRD52, UBQLN4	PIK3CA, TP53BP1, CHD3, ARID1A, SNW1, E2F3, SMARCD1, ARID2, AR, RELN	Hepatocellular carcinoma Type 2 diabetes mellitus Axon guidance Maturity onset diabetes of the young ErbB signaling pathway Prostate cancer Focal adhesion Epstein-Barr virus infection Human immunodeficiency FoxO signaling pathway Glycerolipid metabolism Vascular smooth muscle contraction Insulin signaling pathway Acute myeloid leukemia	1.64E-03 4.87E-03 6.73E-01 1.59E-02 2.57E-02 3.60E-02 6.37E-02 6.46E-02 7.43E-02 7.46E-02 7.59E-02 7.73E-02 8.28E-02 8.91E-02
PR2	hsa-miR-548d-5p, hsa-miR-548ay-5p, hsa-miR-548ag-5p, hsa-miR-548ap-5p, hsa-miR-548ae-5p, hsa-miR-548ad-5p, hsa-miR-548o-5p, hsa-miR-548c-5p, hsa-miR-548aq-5p, hsa-miR-548am-5p	NFAT5, RORA, FAM135A, MINDY2, EPHA3, ZDHHC21, STXBp5, NEGR1, SACS, IGF2BP3, NFAT5, RORA, FAM135A, EPHA3, STXBp5, NEGR1, ZDHHC21, SACS, IGF2BP3, MEXD3, ZDHHC21, UBE2E3, RGL1, MOB1B, TCEG1, RIOX1, ANKRD17, CD164, PSMA8, PPP3R1	PSMB1, PSMB6, PSMC4, PSMA2, PSMA4, PSMA8, PPP3R1, UBE2E3	Th17 cell differentiation Spinocerebellar ataxia Axon guidance Prion disease Circadian rhythm Proteasome Amyotrophic lateral sclerosis Alzheimer disease VEGF signaling pathway	1.95E-01 1.95E-01 2.06E-01 2.06E-01 2.06E-01 2.06E-01 2.06E-01 2.06E-01 2.06E-01
PR3	hsa-miR-6511b-3p, hsa-miR-6511a-3p, hsa-miR-6750-3p, hsa-miR-99a-3p, hsa-miR-10398-5p, hsa-miR-4749-3p, hsa-miR-3162-3p, hsa-miR-4633-5p	ZNF229, VPS53, RTN4IP1, ZNF189, COQ10B, KHDC1, PKIB, ZNF781, ZMAT2, MAPK1, EML6, HDAC2, PKDCC, ADAMTSS, PAXBP1, UCHL3, PHAF1, MARK1, PLCL1, RPE, RSBN1L, SPRED1, RANBP6, NCKAP1L, NELFA, SOCS4, ANKRD13C, AGFG2, ZNF664, GIMAP1, SGPP1, VANG1, CENPO, SLC20A1, SMARCD2, LHFPL4, ZMIZ1, CD1E, RRM2, TEX101, GANAB, ACTN4, PLXNA1, PREP, DACT1, VPS53, CCDC140, ZBTB10, SLC36A2, EMP2, SEC14L1, CPQ, BAZ2A, KMT2D, ARHGAP28, ATP6V1C2, NOTCH4, DIO2, S1PR1, FMO5, SLC38A2, FLRT3, CAPZB, SESTD1, ZNF85, GSAP, CCNG1, ERCC6L, ZYG11B, THRFP3	MAPK1, HDAC2, KMT2D, SESTD1, ZBTB10, DACT1, ERCC6L, BAZ2A, RRM2, S1PR1	Thyroid hormone signaling pathway Sphingolipid signaling pathway Type II diabetes mellitus Notch signaling pathway MicroRNAs in cancer Prolactin signaling pathway Adherens junction p53 signaling pathway Human papillomavirus infection Chronic myeloid leukemia	1.24E-01 4.34E-01 4.34E-01 4.34E-01 4.34E-01 4.34E-01 4.34E-01 4.34E-01 4.34E-01
PR4	hsa-miR-8084, hsa-miR-451b, hsa-miR-3914, hsa-miR-378j, hsa-miR-378i, hsa-miR-378f, hsa-miR-378b, hsa-miR-3152-3p	GPM6A, SCAI, TBX18, TTF2, CFL2, ING2, ANKRD34B, SNX30, NOTCH1, RPS6KB1, NPTX1, AQP9, ZFHx3, SPTSSA, TOX3, MYCBP2, KIAA0232, TESMIN, STXBp6, SGPP2, RPS6KB1, DLG5, SLC2A1, WBP4, OSBP19, SLC25A28, NDST1, ATL1, PAX5, GTF2I, CERKL, MID1IP1, NAA25, CD164, FABP2, ZBTB41, GUCA1C, TMX4, SYTL5, USP6NL, NR2C2, KLK4, NKX3-1, KIAA1522, PHC3, ELAC1, KCNIP2, NCAPG, RAB10, JADE3, KIAA1522, TSC22D2, CD40LG, PLXNC1, FOXD4L5, CLDN11, MMP1, MUC21, SCUBE3, PLXDC2, SPTBN1	NOTCH1, PAX5, ATL1, CD40LG, CERKL, DLG5, GTF2I, NCAPG, NKX3-1, RAB10	PPAR signaling pathway Fc gamma R-mediated phagocytosis AMPK signaling pathway Breast cancer Cell adhesion molecules Pathways in cancer Phototransduction Asthma Axon guidance Allograft rejection	4.92E-01 4.92E-01 4.92E-01 4.92E-01 4.92E-01 4.92E-01 4.92E-01 4.92E-01 4.92E-01 4.92E-01
PR5	hsa-miR-6850-5p, hsa-miR-6090, hsa-miR-6089, hsa-miR-4665-5p, hsa-miR-4655-5p, hsa-miR-4463, hsa-miR-3175, hsa-miR-197-5p	MAC1R, ZNF595, RUNX1, CCDC144NL, PLEKHA1, NADK, WARS2, TUBB6, EEF2K, DUT, PIPOX, CDK14, DTX1, LOC150051, DDX6, LMX1A, ATL2, ADCY9, TSPAN2, ATP8A2, PRSS22, TMEM120B, GEMIN4, SNX27, IFT81, ABTB2, DIRAS1, AGAPI, CERS2, ARFGEF1, MECP2, GATAD2B, ACTB, CBX6, ZSWIM4, ZNF32, CASTOR2, RAB3B, NFIX, PCDHGA12, MID1, LINC02902, EIF2AK1, CAS3, AKAP7, C19orf25, ARIH1, NCOA7, ERC1, YWHAB, CLDN1, SPC25, AGO2, SLC9A4, XKR9, KLRD1, OPHN1, FGF5, ZNF207, TRIM4, SLC16A2, DAAM2, CSNK1A1, APLNR, SYNGAP1, SFTPB, PRKACA, MIEN1, ZNF609, DNAL1, ICAM5, SLC41A1, PFDN2, CD86, CHD9, ZNF124, CBX5, ULBP1, ATRNL1, BLID	ACTB, AGO2, PRKACA, CSNK1A1, MECP2, YWHAB, KLRD1, ADCY9, TUBB6, RUNX1	Gastric acid secretion Vibrio cholerae infection Oxytocin signaling pathway Tight junction Gap junction Dilated cardiomyopathy Graft-versus-host disease Thyroid hormone signaling pathway Vasopressin-regulated water reabsorption Platelet activation	3.45E-02 7.44E-02 1.49E-01 1.49E-01 1.49E-01 1.58E-01 1.87E-01 1.87E-01 1.87E-01 1.87E-01
PR6	hsa-miR-9851-5p, hsa-miR-5681a, hsa-miR-4446-3p, hsa-miR-1207-5p, hsa-miR-7705, hsa-miR-4469, hsa-miR-195-3p, hsa-miR-621	SPTY2D1, ING1, SRPK1, HIF1A, INSYN2A, GTF2A1, SLITRK3, GPD1, SLC6A6, PTPN1, PRKN, ANKS1A, SNX27, CNH, PGRMC2, TSBP1, EFNA5, ZNF609, CREBBP, C5orf24, DR1, CBX7, PHF24, BRCA1, C1orf162, FAM117A, ABCG4, ZNF99, CDK18, HAGH, SV2A, ATP11A, SOGA1, MPP2, CBX6, SH3PXD2B, DDX3X, RBBP5, SEPTIN9, CBX5, ERRF1, LIMCH1, ZC3H12B, CSMD3, RPA3, CHMP4C, BTG2, RGS17, RERE, HCN4, HTR7, GPR176, ATXN1L, MIDEAS, TMEM39A, FGF11, HOXB7, CACNA1E, CD300A, WDR43, INTU, PRKG1, CADM2, PLCXD3, KDM7A, PURA, FGL2, ABCE1, DENND1B, CHML, EBF3, NGLY1, ZFHx4, COQ2, CAPRIN1, UBQLN2, ACKR4, YPEL5, MYEF2, KLHL15	BRCA1, CREBBP, CNH, RPA3, HIF1A, GTF2A1, UBQLN2, C1orf162, CBX5, RBBP5	Homologous recombination Basal transcription factors Nucleotide excision repair Fanconi anemia pathway Notch signaling pathway Mitophagy Renal cell carcinoma Protein processing in endoplasmic reticulum Adherens junction Ubiquinone and other terpenoid-quinone biosynthesis	3.07E-01 3.07E-01 3.07E-01 3.07E-01 3.07E-01 3.07E-01 3.07E-01 3.07E-01 3.07E-01 3.62E-01
PR7	hsa-miR-4731-3p, hsa-miR-6848-3p, hsa-miR-1913, hsa-miR-2682-3p, hsa-miR-675-3p, hsa-miR-33a-3p, hsa-miR-5008-3p, hsa-miR-4707-5p, hsa-miR-10396b-3p	UBE2B, LRRTM3, HADC3, CCDC71L, NWD2, ABI1, PUM1, NOTCH2, RAB9B, PTPN4, GIPC3, SLC25A36, JADE3, SORBS3, RTP4, FBN1, MYH10, JAK2, SPTBN1, KLHL42, STIP1, TMEM104, GHITM, TPPP, THSD7B, NKIRAS2, RAB11FIP4, CRTC1, TMEM249, ANKS1A, PRKCA, SPRY2, MRC2, SLC26A7, TIA1, DMRT2, CDK14, MYRIP, CCDC115, COL12A1, ATXN1, AGPS, ADAM22, SERPINF1, CSMD3, CUL3, PPP4R3A, KCNA4, KMT5A, DDX3X, PARP8, CRISPLD1, HNRNP, PCDH17, CADM2, GUCY1A2, CACNB4, ARFGEF1, ZNF558, LSM14A, TMF1, ZNF518A, PLEKHF2, UBN2, GRIP1, SP4, TRARG1, BBIP1, EPB41L5, FAM53A	CUL3, ASB13, LSM14A, KLHL42, UBE2B, CADM2, TIA1, COPS7B, HNRNP, PRKCA	Oxytocin signaling pathway Aldosterone synthesis and secretion Vascular smooth muscle contraction Spinocerebellar ataxia Notch signaling pathway Long-term depression Hepatitis B	5.83E-01 5.83E-01 5.83E-01 5.83E-01 5.83E-01 5.83E-01 5.83E-01

Genomic Regions of SARS-CoV-2	Human miRNA	Target Human mRNA	Key Proteins in PPI Network	KEGG Pathways	FDR corrected p-value
		TGIF1, FSTL3, CWC25, GM2A, CCDC47, ZG16, COPS7B, ACOT11, CADM3, SEMA6B TAF3A, CLOCK, CERS1, ZNF319, YPEL2, ASIC1, CAMK1D, ASB13, NR4A2, RAVR2		Glioma Gastric acid secretion Gap junction	5.83E-01 5.83E-01 5.83E-01
PR8	hsa-miR-4534, hsa-miR-4511, hsa-miR-877-5p hsa-miR-4760-5p, hsa-miR-6754-5p, hsa-miR-4533 hsa-miR-7847-3p	GSG1L, ZNF213, FAM169B, ERICH3, OLA1, FOXQ1, MTCL1, FAM222B, NUMBL, TRPA1 OXR1, HMCES, EEA1, RAP2C, YWHAE, SP3, USP25, EPS8, SAMD4B, CAPS2 FGB, FOXD4L5, C5orf47, COL6A3, DDO, CEP350, ATE1, ITM2B, FXR2, CSNK1G3 UBAP1, GK5, MFSD14A, CCNT2, RSNB1, PABPC3, ABHD5, FNDC3B, FAM210B, CISD1 ZBTB4, TRIP12, NR1D2, ZDHHC9, SMG6, TOM1L2, PDE7B, HTR3C, IL17RD, PRSS16 POU2AF1, PLEKHS1, EHD2, GUCY1A2, LENG8, MPRIP, SHISA6, HTR2C, FOXJ2, SGK1 RAB1A, SYP, PSKH1, ASB12, NECAB2, NLK, CHMP1B, GSPT1, KIF1A, CALN1	TRIP12, YWHAE, FGB, RAB1A, KIF1A GSPT1, PABPC3, SMG6, SYP, TOM1L2	mRNA surveillance pathway Gap junction Inflammatory mediator regulation of TRP channels Endocytosis Serotonergic synapse Platelet activation Purine metabolism FoxO signaling pathway Alanine, aspartate and glutamate metabolism Aldosterone-regulated sodium reabsorption	2.86E-01 5.59E-01 5.59E-01 5.59E-01 5.59E-01 5.59E-01 5.59E-01 5.81E-01 5.81E-01
PR9	hsa-miR-6837-5p, hsa-miR-3198, hsa-miR-4695-5p hsa-miR-8071, hsa-miR-12118, hsa-miR-6801-5p hsa-miR-6789-5p	SYT9, PITPNM3, DEDD2, VPS39, FLRT1, SLMAP, SERF2, NHLRC3, GRB10, CSF1 FAM86B1, SMAP1, PFKP, FAM86B2, BHMT2, FAM86C1P, EMC8, MED7, KCNE5, GATA4 RIMS4, CDH15, PARP3, GFPT2, FCHSD2, UBE2Q1, R3HDM1, ZNF737, NHEJ1, OLFML1 HDAC2, SYT7, SEMA3F, RPS6KA4, CXXC4, SOGA1, NHS, GPX3, SHISA7, SSB PLEKHS1, OXSR1, PPP6C, UBE2Q1, ARID1A, CEP170, PPP1R16B, GMFB, RBIS, TMEM35B CDK8, CPPED1, AGAP9, AGAP11, AGAP5, AGAP4, AGAP6, SOX8, AZI2, LAMA3 TFB1M, PTCHD3, DCAF8, SOX10, ZBTB47, SNW1, PINK1, JPH3, RHBDD1, CASK	SNW1, GATA4, HDAC2, CDK8, CPPED1 PLEKHS1, PFKP, AGAP4, OLFML1, SOX10	Endocytosis Thyroid hormone signaling pathway Notch signaling pathway Non-homologous end-joining TNF signaling pathway Pentose phosphate pathway Galactose metabolism Base excision repair Fructose and mannose metabolism Alanine, aspartate and glutamate metabolism	1.26E-01 3.01E-01 4.19E-01 5.73E-01 5.73E-01 5.73E-01 5.73E-01 5.73E-01 5.73E-01 5.73E-01
PR10	hsa-miR-3945, hsa-miR-1272, hsa-miR-7110-5p hsa-miR-6849-5p, hsa-miR-2392, hsa-miR-4721 hsa-miR-12121, hsa-miR-6765-5p	KBTBD2, C1orf74, ZNF93, CACNB4, CLPB, MYOF, IL26, RIC8B, DTD1, RNFT2 FAM83C, ZNF28, FNIP1, TCEG1L, RIF1, TRAF5, GSG1L, SHISA7, MECP2, CISD1 ZSWIM4, DAGLA, SMARCD1, PPP6R1, NFIC, PRKACA, DNAJB5, SYNGAP1, NECTIN1, TBKBP1 SHISA7, CSDE1, CDH6, AXIN2, CCR1, CCDC68, CRACDL, TIMM23B, NDP, LRRN4CL GNG13, FAM169B, GSG1L, LPP, ISL1, RNF144A, OAZ3, BHMT, IGSF5, AFAP1L1 TSHZ3, PDYN, ARMH3, DLX3, KCNB1, CFAP77, WASF2, ASB9, BRINP2, MLLT11 ZNF99, ZNF117, ZNF468, ZNF676, ZNF208, ZNF730, ZNF107, ZNF732, LNPEP, MSRA CAPRIN2, RPS10-NUDT3, NUDT3, RAB39A, ENTDP1, C17orf97, TULP4, FBXO45, PKP4, CSTF3	GNG13, PRKACA, CCR1, PDYN, KCNB1 KBTBD2, TULP4, SYNGAP1, RNFT2, RNF144A	Herpes simplex virus 1 infection Human cytomegalovirus infection Cocaine addiction Signaling pathways regulating pluripotency of stem cells Retrograde endocannabinoid signaling Amphetamine addiction Adherens junction Alcoholism Chemokine signaling pathway Taste transduction	1.58E-02 4.24E-01 4.24E-01 4.24E-01 4.24E-01 4.24E-01 4.24E-01 4.24E-01 4.24E-01 4.24E-01
PR11	hsa-miR-548bc, hsa-miR-548ba, hsa-miR-4279 hsa-miR-3619-3p, hsa-miR-6818-3p, hsa-miR-4778-3p hsa-miR-873-5p, hsa-miR-6823-3p	ZFHx3, CDC14A, ATRNL1, PHC3, CDK13, GPC4, DGKH, FTHL17, TNPO1, SKIL ZDHHC21, UBE2E3, RGL1, MOB1B, TCEG1, RIOX1, ANKRD17, CD164, PSMA8, PPP3R1 MED13, VPS36, COL25A1, RFC5, MSI2, PSMA8, SMC2, SMC04, CYP4F3, TAOK1 PCSK5, PHF6, E2F7, EPB41L4B, ZSWIM5, MAP4K3, ARHGEF11, NKAIN3, ABCA1, CDK15 NFASC, RIMS3, INHBC, CACNA1E, PGPEP1, GLRA4, TLK2, TLL4, MYRFL, GK5 SHISA7, EIF2S1, RIMS1, OTX2, OPRM1, CREM, CGNL1, LARP7, NOTUM, RFPL4B DKC1, PINK1, RBM47, CALHM1, ITPR2, COX17, CELF4, PSMD1, CD84, ASCL1 NLK, KPNA6, SIGLEC1, STK4, C20orf203, LBH, GRIN3A, DHX58, TSPAN3, LARP1B	TNPO1, PSMD1, DKC1, GRIN3A, TAOK1 STK4, RFC5, PPP3R1, OPRM1, NOTUM	Prion disease MAPK signaling pathway Spinocerebellar ataxia Wnt signaling pathway Glutamatergic synapse Proteasome Alzheimer disease Parkinson disease Signaling pathways regulating pluripotency of stem cells Long-term potentiation	6.40E-02 6.40E-02 9.78E-02 1.25E-01 2.46E-01 2.50E-01 2.50E-01 2.50E-01 2.50E-01 3.00E-01
PR12	hsa-miR-6831-5p, hsa-miR-3192-5p, hsa-miR-4281 hsa-miR-3141, hsa-miR-6729-5p, hsa-miR-5001-5p	TMEM121B, SPRYD4, HOXB7, HOXA7, SLC9A6, LHX1, LPCAT3, NXPE3, RDH10, NAP1L1 BHLHE22, NXN, NAAA, MCM3, GPX1, ZC3H12A, PCBP3, PRR23C, CTXN1, ZNF282 AAK1, GRIP2, SHISA7, CCDC149, YBEY, RNPEPL1, MT1F, KCNQ4, SPPL2B, CALN1 DUSP1, CTTNBP2, BCL3, TGFB3R3L, PRRX1, SMIM21, CDK5R2, FAM172A, VAPB, AZIN1 MEX3C, SH3GL1, GART, AFDN, GALNS, RAB40C, PPP2R5B, PDSS1, CLPTM1, RSP04 NFIX, PACS1, GIPC3, SOGA1, KCNIP3, KCNS1, ACVRL1, PHLDB1, MDGA1, RAP1GAP2	BCL3, HOXA7, LPCAT3, SH3GL1, AAK1 AZIN1, BHLHE22, DUSP1, GART, HOXB7	Glycosaminoglycan degradation One carbon pool by folate Terpenoid backbone biosynthesis DNA replication Ferroptosis Cholesterol metabolism Glutathione metabolism Mineral absorption Arachidonic acid metabolism Retinol metabolism	5.16E-01 5.16E-01 5.16E-01 5.16E-01 5.16E-01 5.16E-01 5.16E-01 5.16E-01 5.16E-01 5.16E-01
PR13	hsa-miR-10524-5p, hsa-miR-4257, hsa-miR-4330 hsa-miR-3193, hsa-miR-5000-5p, hsa-miR-6165	YTHDF3, CALCB, ELAVL2, CLUL1, KLKB1, SERTAD2, UQCRB, STRN3, MTHFD2L, BTAf1 SFMBT1, OSBPL11, TTC9C, OCIAD2, GATM, B4GALT4, EHHADH, ZFHx4, ACER2, TUBB4A EML4, SPEN, UBXN8, MUS81, PRRC1, KCNA5, QPCTL, EEF2KMT, HTRA4, NCOR2 POGLUT3, RNGTT, RNF138, NRXN1, AGTR1, KCNK1, NPAS2, INSR, NR1D2, ABCC2 ITCH, ARGLU1, GOLT1B, VCP1P1, NOVA1, SOX2, LBH, LEPROTL1, ERCC4, SLC38A2 SEC24C, NIBAN1, MAX, P4HA1, ERN1, SIGMAR1, NUCKS1, COLQ, ANKRD34A, SNX1	ELAVL2, NOVA1, INSR, NRXN1, NR1D2 NCOR2, ANKRD34A, SPEN, SOX2, SNX1	Non-alcoholic fatty liver disease Arginine and proline metabolism Fanconi anemia pathway Protein processing in endoplasmic reticulum Diabetic cardiomyopathy Amyotrophic lateral sclerosis Alzheimer disease Parkinson disease Pathways of neurodegeneration One carbon pool by folate	1.09E-01 3.18E-01 3.18E-01 3.18E-01 3.18E-01 3.18E-01 3.18E-01 3.98E-01 3.98E-01 3.98E-01
PR14	hsa-miR-9985, hsa-miR-27a-3p, hsa-miR-1256 hsa-miR-199b-3p, hsa-miR-199a-3p, hsa-miR-6862-3p	GXYLT1, TRPV3, AFF4, GCC2, ARFGEF1, AKIRIN1, RGPDP6, NRK, PDS5B, MBTD1, PDS5B NEXMIF, SLC23A3, RHOQ, CDKN2B, RALGPS1, SMARCE1, ZNF474, ANKRD28, PDZRN4, RAB25 ITGA3, CELSR2, KATNBL1, NAA25, ETNK1, LRP2, NID2, ADAMTSL3, SERPINE2, CDNF MAFB, POGLUT1, CCNT1, SDK2, ZKSCAN2, KCNB1, ENDOV, RORA, IDS, ZNF35	AFF4, CCNT1, GCC2, GXYLT1, PDS5B PDZRN4, POGLUT1, RGPDP6	Other types of O-glycan biosynthesis Small cell lung cancer Glycosaminoglycan degradation Circadian rhythm Cholesterol metabolism Hedgehog signaling pathway Inflammatory bowel disease Thyroid hormone synthesis	1.51E-01 2.77E-01 3.90E-01 3.90E-01 3.90E-01 3.90E-01 3.90E-01 3.90E-01

Genomic Regions of SARS-CoV-2	Human miRNA	Target Human mRNA	Key Proteins in PPI Network	KEGG Pathways	FDR corrected p-value
				Arrhythmogenic right ventricular cardiomyopathy	3.90E-01
				ECM-receptor interaction	3.90E-01
PR15	hsa-miR-802, hsa-miR-377-3p, hsa-miR-29a-5p hsa-miR-548bb-3p, hsa-miR-548am-3p, hsa-miR-548ah-3p	ARPP19, ADAMTS1, NEXMIF, MTMR1, CPEB3, ERICH2, CACNA2D1, ADGRL3, CBFB, XPNPEP3 UBE2D1, CREBBP, ZCCHC14, ARFGF3, RSBN1, DYRK2, ONECUT2, DCBLD2, GRPEL2, INPP4A IKZF2, PHC3, DYRK2, CPEB4, CREBRF, GPC6, TNRC6B, B3GALT2, PRMT3, SOS2 IKZF2, PHC3, DYRK2, CPEB4, CREBRF, GPC6, TNRC6B, B3GALT2, PRMT3, SOS2 STOX2, ETS1, PUM2, CFTR, NLGN1, FBXO32, SETBP1, JAG1, DCAF12, RNMT MINDY2, B3GLCT, DENND1B, ZFX, ATP6V1C1, CEP135, ODF3, CACNA2D1, PNLDC1, GPR180	TNRC6B, CREBBP, CBFB, CPEB3, UBE2D1 CPEB4, ETS1, PUM2, PHC3, MTMR1	Renal cell carcinoma FoxO signaling pathway Vibrio cholerae infection Human papillomavirus infection Notch signaling pathway Inositol phosphate metabolism Phosphatidylinositol signaling system Prostate cancer Progesterone-mediated oocyte maturation Growth hormone synthesis, secretion and action	5.96E-02 1.73E-01 1.73E-01 1.73E-01 1.73E-01 2.17E-01 2.62E-01 2.62E-01 2.62E-01 3.14E-01
PR16	hsa-miR-936, hsa-miR-214-3p, hsa-miR-518f-3p hsa-miR-4269, hsa-miR-4306, hsa-miR-185-5p	TMEM170A, GALNT7, EVI5, ITPKC, ANKRD17, AFAP1, HS3ST5, ITGA3, CPEB3, PAWR LSM12, NAA15, ZFAND3, MFN2, MED19, RC3H1, VPS53, PIM1, SEC24C, MAPK1 ZNF281, FBXO3, TSN, TEAD3, NDUFA4, EGR1, ZNF282, SYNRG, PRICKLE2, SLC04C1 TDRP, MYORG, AHSG, ABLIM3, ESR1, EIF4H, PLXNC1, CACNA1B, RAD21, IGDC4 SLC16A2, SMG7, SOGA1, EPPK1, XYLB, ZNF704, SOX13, CDH4, RAE1, ERCC6 SLC16A2, SMG7, EPPK1, SOGA1, SOX13, XYLB, HP1BP3, RAE1, ADGRL1, CDH4	ESR1, EGR1, MAPK1, ABLIM3, AFAP1 CPEB3, HS3ST5, RAD21, RC3H1, SEC24C	AGE-RAGE signaling pathway in diabetic complications Thyroid hormone signaling pathway Prion disease Type II diabetes mellitus Retrograde endocannabinoid signaling Axon guidance Acute myeloid leukemia Prolactin signaling pathway Chemical carcinogenesis GnRH signaling pathway	2.02E-01 2.02E-01 2.02E-01 2.02E-01 2.02E-01 2.68E-01 2.68E-01 2.68E-01 3.49E-01 3.49E-01
PR17	hsa-miR-4509, hsa-miR-3166, hsa-miR-4764-5p hsa-miR-521, hsa-miR-517b-3p, hsa-miR-517a-3p hsa-miR-671-5p	LHFPL1, HIBADH, MED26, ZNF559-ZNF177, CDH8, TBL1XR1, NFIB, TGFBRAP1, GBP5, ACSL4 SMPD3, NUFIP2, KLHL23, CPEB3, PIK3CA, TTC31, FSTL5, CREBRF, ABRAXAS2, CSMD2 PLAG1, RANBP10, UBR2, NME1, POMC, KLF15, KPNA6, ZHX3, PRICKLE2, TEAD1 NEU3, PLEKHA1, NAIP, LRRC27, MC2R, DNAJC5, DST, FREM2, USP31, SLC04C1 PHF13, VSTM2B, ZNF521, HOXA5, NFIA, CBLN2, DBN1, TMCC1, PTK2B, NFIB USP46, AAK1, TBL2, C16orf72, SATB2, ST8SIA5, CFL2, KRT38, CA7, LINC02909	NFIB, TMCC1, DNAJC5, FSTL5, KLF15 MC2R, NEU3, NFIA, PLAG1, POMC	Estrogen signaling pathway Sphingolipid metabolism Cortisol synthesis and secretion Adipocytokine signaling pathway Human immunodeficiency virus 1 infection cAMP signaling pathway Fc gamma R-mediated phagocytosis Aldosterone synthesis and secretion Progesterone-mediated oocyte maturation Leukocyte transendothelial migration	4.55E-01 4.55E-01 4.55E-01 4.55E-01 4.55E-01 4.55E-01 4.55E-01 4.55E-01 4.55E-01 4.55E-01
PR18	hsa-miR-3529-5p, hsa-miR-4776-5p, hsa-miR-6071 hsa-miR-502-3p, hsa-miR-4750-5p, hsa-miR-6860	EIF4G2, ELMOD2, FZD4, SEMA3A, MTMR2, PITPNM3, TXLNG, ZBTB26, OGN, LZTS3 FOXO1, MED13, NXT2, TFPC2L1, KRT8, ASB7, PAK1, APBA1, GOLPH3, SMC2 ADAMTS3, KCTD9, FBN2, SEC63, ZFX, NAP1L5, SMIM13, DAPK1, CSDE1, SEPSECS FAM149B1, IRS1, SH3D19, SOX6, KAT6A, RBBP6, TENT5A, VGLL3, RCC1, PACSIN2 ZSCAN10, PPAN-P2RY11, BCL7C, PSME3IP1, ICAM2, MATK, C9orf116, AWAT2 DAB2IP, SIKE1, SAR1A, YTHDF1, SEC63, ARRD3C, TRABD2B, CXXC4, FMO5, SMAD6	SEMA3A, FOXO1, RBBP6, PAK1, PACSIN2 VGLL3, TXLNG, TFPC2L1, SOX6, ZFX	Longevity regulating pathway Insulin resistance Neurotrophin signaling pathway AMPK signaling pathway Thyroid hormone signaling pathway Selenocompound metabolism Natural killer cell mediated cytotoxicity FoxO signaling pathway Insulin signaling pathway Autophagy	3.91E-01 3.91E-01 3.91E-01 3.91E-01 3.91E-01 3.91E-01 3.91E-01 3.91E-01 3.91E-01 3.91E-01
PR19	h sa-miR-147b-5p, hsa-miR-548au-5p, hsa-miR-548ar-5p hsa-miR-548x-5p, hsa-miR-548g-5p, hsa-miR-548aj-5p	WAC, SEMA3A, ZNF706, LIN7A, PCDH18, MBD2, CLOCK, ARID4B, NAV3, ADAMTS5 NFAT5, RORA, FAM135A, MINDY2, EPHA3, ZDHHC21, STXBP5, NEGR1, SACS, IGF2BP3 KBTBD8, ZMAT3, SFRP2, ESR1, TAOK1, LRP6, EPS15, CREBRF, HMGA2, GPR85	CLOCK, ESR1, MBD2, ARID4B, EPHA3 HMGA2, IGF2BP3, LRP6, RORA, SEMA3A	Circadian rhythm Breast cancer Wnt signaling pathway Axon guidance Endocrine and other factor-regulated calcium reabsorption Inflammatory bowel disease Prolactin signaling pathway p53 signaling pathway Parathyroid hormone synthesis, secretion and action Th17 cell differentiation	2.66E-02 2.05E-01 2.05E-01 2.05E-01 3.11E-01 3.11E-01 3.11E-01 3.11E-01 3.11E-01 3.11E-01
PR20	hsa-miR-30b-5p, hsa-miR-5587-5p, hsa-miR-3943 hsa-miR-6782-3p, hsa-miR-5691, hsa-miR-7106-3p	CELSR3, WDR7, STOX2, ANKRA2, KLHL20, MKRN3, PPARGC1B, DCUN1D3, RORA, LIN28B COL25A1, NSF, CSNK1G3, ZHX1, TTPAL, CAND1, RC3H2, NUS1, SMAD5, TAF1 DOCK7, ONECUT2, SMC5, AXIN1, MOB1A, CCDC83, FAM199X, BRD1, MFSD4A, NR4A3 TTYH3, TRAFD1, TC2N, C1orf122, ADH1A, MTSS1, STRADB, ADH1B, MFAP2, RPS24 CYP3A5, NLRP5, RNF166, PTPRR, MAPRE1, CIPC, CREBRF, MAPK1, NR6A1, GGH PURA, PRAMEF6, PRAMEF5, ATXN10, ZDHHC11, LDB1, XPO1, USP12, DDX3X, KPNA6	XPO1, MAPK1, CAND1, DCUN1D3, KLHL20 ADH1A, ADH1B, AXIN1, DDX3X, GGH	Retinol metabolism Metabolism of xenobiotics by cytochrome P450 Drug metabolism Tyrosine metabolism Fatty acid degradation Pyruvate metabolism Signaling pathways regulating pluripotency of stem cells Endometrial cancer Influenza A Glycolysis / Gluconeogenesis	1.09E-01 1.09E-01 1.83E-01 1.83E-01 1.83E-01 1.83E-01 1.83E-01 2.32E-01 2.34E-01 2.43E-01
PR21	hsa-miR-6726-5p, hsa-miR-6789-3p, hsa-miR-4690-3p hsa-miR-4770, hsa-miR-4435, hsa-miR-4453	DENND1B, ABL2, VASH1, MS12, GXYLT1, ITM2B, EPM2AIP1, IGFBP5, PSME4, SLC16A2 SOGA1, EPHA3, SIAH1, C22orf23, PIK3R3, DCAF10, CDK6, FAM107B, CAPRIN1, PLEKHO2 ATPAF1, PLXNA4, NUCB2, GINS2, RASGRP3, SMCR8, MYCT1, HIC1, NOA1, ATP8A1 CCDC179, ARPC2, LRFN3, PRX, LRRC55, RPF2, ZNF761, AZIN1, PLPP3, SUB1 KANK2, ANO9, AOPEP, SLC7A1, OLIG1, UBE2I, PRKCQ, LRRC14, BTBD9, PLCXD3 CNTNAP2, LYSMD1, KSR2, INHBB, NMT1, UBE2D4, ARHGAP21, HNRNPR, STK32B, ZDHHC18	PIK3R3, SIAH1, UBE2I, IGFBP5, INHBB LRRC55, NOA1, OLIG1, EPHA3, PLCXD3	Fc gamma R-mediated phagocytosis Ras signaling pathway Shigellosis Autophagy Ubiquitin mediated proteolysis MicroRNAs in cancer Axon guidance Melanoma Non-small cell lung cancer	2.07E-01 2.07E-01 2.07E-01 2.07E-01 2.07E-01 2.07E-01 2.07E-01 2.07E-01 2.07E-01

Genomic Regions of SARS-CoV-2	Human miRNA	Target Human mRNA	Key Proteins in PPI Network	KEGG Pathways	FDR corrected p-value
PR22	hsa-miR-548ah-5p, hsa-miR-3165, hsa-miR-3132 hsa-miR-320c, hsa-miR-320d, hsa-miR-28-5p hsa-miR-320a-3p	ITGB8, GXYLT1, TBC1D9, ADD1, ZNFx1, PPP3CA, ATG16L1, OTUD4, RUNX1, FBXL3 HDAC2, PURA, SHISA7, C18orf54, ARMCX2, RFX5, SCN1B, PKNOX2, NCMAP, ITGA9 ICAM5, ZNF124, SLC41A1, PFDN2, CBX5, CD86, CHD9, ULBP1, TGS1, TEP1 ONECUT2, PLPPR1, KITLG, SH2B3, CDKL5, YOD1, SPOPL, GCG, HECTD2, DCP1A TNS3, GARRE1, FOXJ3, FAM126A, ASPA, IKBKB, TMEM260, NPY2R, EN2, RPTN	HDAC2, FBXL3, CBX5, RFX5, YOD1 TGS1, SPOPL, SH2B3, SCN1B, RUNX1	p53 signaling pathway	2.07E-01
				Chronic myeloid leukemia	1.09E-01
				Th17 cell differentiation	1.46E-01
				Cell adhesion molecules	1.72E-01
				Human papillomavirus infection	1.72E-01
				PI3K-Akt signaling pathway	1.72E-01
				Acute myeloid leukemia	1.72E-01
				Transcriptional misregulation in cancer	1.72E-01
				Kaposi sarcoma-associated herpesvirus infection	1.72E-01
				Amphetamine addiction	1.72E-01
				Arrhythmogenic right ventricular cardiomyopathy	1.76E-01
				Selenocompound metabolism	5.30E-01
				Terpenoid backbone biosynthesis	5.30E-01
				Butanoate metabolism	5.30E-01
PR23	hsa-miR-3934-3p, hsa-miR-7158-5p, hsa-miR-6796-5p hsa-miR-6823-5p, hsa-miR-3944-3p, hsa-miR-6861-5p	MOSMO, ANKIB1, TET3, PCYOX1, FBXO9, SDK2, KCNS1, TMEM196, CCDC9B, ZIM3 PPP6C, CNR1, RBM18, ODF3L1, DCAF10, DMXL1, RO60, IGSF1, GTF3C2, TAX1BP1 C5orf51, ERF, TMEM218, PARVA, FAM218A, FLJ44635, LIMD2, C9orf50, TXNRD1, CD1E SENP8, ATF3, EFHC1, OPRPN, CAPN15, DTNA, CYP4F11, BANK1, L2HGDH, WNT10B ICAM2, IGDCC3, VWA3B, AMIGO3, IL12RB2, WDR26, UGT3A1, ZNF704, NCS1, ATP9B ZFP3, NLK, PURB, COLEC11, RPN2, ZCCHC12, PDE3A, SLC26A3, C1orf87, S100Z	IGDCC3, NLK, SDK2, WNT10B	Wnt signaling pathway	5.30E-01
				Hepatocellular carcinoma	5.30E-01
				Various types of N-glycan biosynthesis	5.30E-01
				N-Glycan biosynthesis	5.30E-01
				Hedgehog signaling pathway	5.30E-01
				Mineral absorption	5.30E-01
				Basal cell carcinoma	5.30E-01
				Fatty acid elongation	2.52E-01
				Glycosaminoglycan biosynthesis	3.21E-01
				Cushing syndrome	3.21E-01
				Basal cell carcinoma	3.27E-01
				Inflammatory mediator regulation of TRP channels	4.74E-01
				Serotonergic synapse	4.74E-01
				Glutamatergic synapse	4.74E-01
PR24	hsa-miR-891a-5p, hsa-miR-8085, hsa-miR-6781-5p hsa-miR-5571-5p, hsa-miR-5195-3p, hsa-miR-650	HACD3, POLI, BCL11A, CCDC96, ADAMTSL1, PRKCE, UBB, CBLB, FMN2, HTR2C HIP1, HSPB6, SHANK1, CCDC97, MLLT11, ANK1, RBM20, WNT1, SNX19, HNF1B GNG13, SIX5, KMT2D, SBF1, DUSP8, MIEF2, GOLGA6L1, CNBD2, H2AB2, ST3GAL2 STRADB, AGPAT4, NCOA1, RIMS4, EBF3, THEM5, CHST2, KLF6, SYDE1, NONO TIPRL, PI15, BMP2, CD226, SH3YL1, GPR158, MIPOL1, DOCK8, SLC7A11, INTS2 ABHD17C, SRGAP1, FSCN1, FLI1, DAB2, MRTFB, KCNA4, CLCN3, ABCE1, TRIM2	UBB, HIP1, DAB2, GNG13, BMP2 CBLB, HTR2C, INTS2, POLI, PRKCE	Apelin signaling pathway	4.74E-01
				Ubiquitin mediated proteolysis	4.74E-01
				Breast cancer	4.74E-01
				Hedgehog signaling pathway	2.64E-02
				TGF-beta signaling pathway	5.96E-02
				Hippo signaling pathway	1.86E-01
				Adherens junction	2.31E-01
				Synaptic vesicle cycle	2.31E-01
				Endocytosis	2.97E-01
				Thyroid hormone signaling pathway	3.24E-01
				Cell cycle	3.24E-01
				Huntington disease	3.24E-01
				Hepatocellular carcinoma	4.54E-01
				Glycosaminoglycan biosynthesis	4.32E-01
PR25	hsa-miR-4719, hsa-miR-6510-3p, hsa-miR-3909 hsa-miR-6769a-3p, hsa-miR-6842-3p	GOLGA6L10, GOLGA6L4, USP37, ZBTB34, ZMYND8, KDM6A, SMAD2, NEXMIF, CREBBP, RC3H1 HDAC3, SMURF2, NDFIP1, TSPAN17, AEN, ARID1B, C17orf107, CTIF, SCUBE2, CLTCL1 RHBDL2, ZNF544, CHM, PBX2, KCNH5, CASKIN2, GRIA4, SLITRK4, SPICE1, TP53BP2 RERE, AGO3, CCDC28A, TEAD1, NECTIN1, ST6GALNAC6, CORO1C, DRC7, SYT1, RAPGEF5 CSNK1G2, ARGLU1, ARHGAP35, RDH12, AMPD3, PHF14, GPR107, ZNF706, CBLL1, SH3BP4	CREBBP, ARID1B, HDAC3, KDM6A, SMAD2 SMURF2, AGO3, CCDC135, CLTCL1, NDFIP1	RNA degradation	4.32E-01
				NF-kappa B signaling pathway	4.32E-01
				Ubiquitin mediated proteolysis	4.32E-01
				Protein export	4.32E-01
				JAK-STAT signaling pathway	4.32E-01
				Axon guidance	4.32E-01
				Glycine, serine and threonine metabolism	4.32E-01
				Glycosphingolipid biosynthesis	4.32E-01
				Type II diabetes mellitus	4.32E-01
				Cell cycle	1.09E-01
				Insulin resistance	3.60E-01
				Hepatitis B	3.60E-01
				Protein processing in endoplasmic reticulum	3.60E-01
				Maturity onset diabetes of the young	3.60E-01
PR26	hsa-miR-6882-3p, hsa-miR-4456, hsa-miR-6846-3p hsa-miR-3127-3p, hsa-miR-3940-3p, hsa-miR-4767	SYT9, GIGYF2, MAP1B, SLC2A6, CACNA1E, MECP2, HOXA4, GATM, AKIRIN2, ANKRD13A SOGA1, ERC1, ZNF609, ZNF131, BBX, PDGFRB, NFIA, FOXp4, ZNF711, ZNF275 VCAN, SLC26A8, GNE, SPO11, EPHA7, BTNL8, ARL4D, VPS53, C5orf15, PLS3 RCAN2, HMGXB3, EI24, RAPH1, VGLL4, CCNK, PLPPR5, SEMA4C, LSM2, ERGIC1 METTL2A, HS6ST1, CERK, EXOSC6, PITPNM3, KBTBD13, GPRIN2, GPX5, DIAPH3, SRPK1 SRP54, SOX6, CHST12, ANAPC2, KDM6B, EPN3, ZBTB22, MCF2L2, PIAS4, A4GALT	CHST12, EXOSC6, ANAPC2, CERK, EPHA7 ERC1, GNE, HS6ST1, KBTBD13, LSM2	Salmonella infection	1.48E-01
				Pantothenate and CoA biosynthesis	4.21E-01
				Protein export	4.21E-01
				Protein processing in endoplasmic reticulum	4.21E-01
				Nicotinate and nicotinamide metabolism	4.21E-01
				Ferroptosis	4.21E-01
				Vasopressin-regulated water reabsorption	4.21E-01
				Ras signaling pathway	4.21E-01
				N-Glycan biosynthesis	4.21E-01
				Cell cycle	1.09E-01
				Insulin resistance	3.60E-01
				Hepatitis B	3.60E-01
				Protein processing in endoplasmic reticulum	3.60E-01
				Maturity onset diabetes of the young	3.60E-01
PR27	hsa-miR-548h-3p, hsa-miR-548ao-3p, hsa-miR-548ay-3p hsa-miR-548z, hsa-miR-1282	UBE2D1, CREBBP, ZCCHC14, ARFGEF3, RSNB1, DYRK2, ONECUT2, DCBLD2, GRPEL2, GFPT1 CCNA2, OGT, TMEM33, SMC3, CDK17, SNRPC, MIB1, ZMAT3, SSB, BAHCC1 DNAL4, ZNF521, MAFA, PTCHD1, YBX1, DYRK1A, MFSD14A, MYCBP, SH3GLB1, XPR1 ZZEF1, TMEM263, SAR1B, TRIAP1, RNASE11, SSX7, CAVIN2, PLIN1, FBRSL1, TSPAN12	CREBBP, CCNA2, SSB, OGT, SNRPC UBE2D1, YBX1, CDK17, GFPT1, PLIN1	Other types of O-glycan biosynthesis	3.60E-01
				Salmonella infection	1.48E-01
				Pantothenate and CoA biosynthesis	4.21E-01
				Protein export	4.21E-01
				Protein processing in endoplasmic reticulum	4.21E-01
				Nicotinate and nicotinamide metabolism	4.21E-01
				Ferroptosis	4.21E-01
				Vasopressin-regulated water reabsorption	4.21E-01
				Ras signaling pathway	4.21E-01
				N-Glycan biosynthesis	4.21E-01
				Cell cycle	1.09E-01
				Insulin resistance	3.60E-01
				Hepatitis B	3.60E-01
				Protein processing in endoplasmic reticulum	3.60E-01
PR28	hsa-miR-452-5p, hsa-miR-6841-5p, hsa-miR-3125 hsa-miR-106a-5p, hsa-miR-124-5p	DACT1, CACNA2D1, SNAI2, PURA, TMOD2, FAM8A1, SNX18, AVL9, TENM1, CASD1 PRR32, GSG1, YIPF6, SMPDL3A, PUM1, NAMPT, IGBP1, TES, COPA, MPZL3 NAV3, MACO1, RALA, INO80D, RASAL2, PANK3, FSD1L, KLF8, DOCK5, GANAB ZNFx1, DYNC1L12, FYCO1, GPR137C, ENPP5, SLC40A1, PKD2, ZFYVE26, MED12L, ARHGAP12 MEF2A, AZI2, IL6ST, REV3L, PAGR1, DPP10, SEC62, RBM11, ERCC6L2, ACAD10	DOCK5, MED12L, ARHGAP12, COPA, DYNC1L12 FSD1L, MPZL3, PUM1, PURA, SEC62	Protein processing in endoplasmic reticulum	4.21E-01
				Nicotinate and nicotinamide metabolism	4.21E-01
				Ferroptosis	4.21E-01
				Vasopressin-regulated water reabsorption	4.21E-01
				Ras signaling pathway	4.21E-01
				N-Glycan biosynthesis	4.21E-01
				Cell cycle	1.09E-01
				Insulin resistance	3.60E-01
				Hepatitis B	3.60E-01
				Protein processing in endoplasmic reticulum	3.60E-01
				Maturity onset diabetes of the young	3.60E-01
				Viral carcinogenesis	3.60E-01
				Human T-cell leukemia virus 1 infection	3.60E-01
				Alanine, aspartate and glutamate metabolism	3.60E-01
				Type II diabetes mellitus	3.60E-01

Genomic Regions of SARS-CoV-2	Human miRNA	Target Human mRNA	Key Proteins in PPI Network	KEGG Pathways	FDR corrected p-value
				Fanconi anemia pathway	4.21E-01
PR29	hsa-miR-520d-5p, hsa-miR-30b-3p, hsa-miR-6129 hsa-miR-4747-5p, hsa-miR-658	PELI2, MTM1, STRBP, ELAVL2, MAPK1, TEAD1, RAP2C, HOOK3, SGIP1, ADAMTS5 IRGQ, CBX5, PHACTR4, PAPOLG, HOOK3, ARID2, RBMS2, NDST1, APOBEC3F, GNL3L KLK4, PAK3, C20orf96, MPIG6B, ATP13A3, LASP1, PRR29, GABRG2, DTX4, PSME3 PLEKHS1, MMP15, PIANP, RAP1A, POU2AF1, MECP2, FBXO11, FGF12, PACS1, FBXO41 ZEB1, NDUFA11, SORT1, FLRT1, SHC2, HOPX, CNTNAP1, YPEL4, SCARF1, KLF13	MECP2, STRBP, ELAVL2, GNL3L, MAPK1 ADAMTS5, RAP1A, PAPOLG, MTM1, MMP15	Neurotrophin signaling pathway Renal cell carcinoma ErbB signaling pathway Focal adhesion Ras signaling pathway Retrograde endocannabinoid signaling Hepatocellular carcinoma VEGF signaling pathway Chemokine signaling pathway Long-term potentiation	2.89E-02 4.56E-02 5.19E-02 5.19E-02 7.00E-02 1.34E-01 1.52E-01 1.52E-01 1.52E-01 1.52E-01
PR30	hsa-miR-147a, hsa-miR-1273b-5p, hsa-miR-548h-5p hsa-miR-3652, hsa-miR-548q	CREBRF, STPG4, LSAMP, LATS2, HDLBP, BCL2L13, SPATS2, IL13RA1, FOXP3, NFASC SEZ6, RERE, MNT, CCDC28A, SYT1, RPP14, ASCC2, MPI, IREB2, MYL12A CDR2L, VPS35, ZNF74, ZNF711, MAFA, LRRC4, KPNA4, HOXA9, ZNF773, TXNRD3 IRGQ, CBX5, PHACTR4, RBMS2, PAPOLG, HOOK3, ARID2, SOGA1, FOXP4, NDST1 NFAT5, RORA, FAM135A, MINDY2, EPHA3, ZDHHC21, STXBP5, NEGR1, SACS, IGF2BP3	FOXP3, FOXP4, HDLBP, IREB2, LATS2 LSAMP, NEGR1, NFAT5, PAPOLG, RORA	Cell adhesion molecules Axon guidance Inflammatory bowel disease Th17 cell differentiation Selenocompound metabolism Maturity onset diabetes of the young Hepatocellular carcinoma Circadian rhythm Fructose and mannose metabolism Type II diabetes mellitus	1.27E-01 1.27E-01 1.27E-01 2.43E-01 2.75E-01 2.91E-01 2.91E-01 2.91E-01 2.91E-01 3.14E-01
PR31	hsa-miR-5003-3p, hsa-miR-4680-5p, hsa-miR-4666a-3p hsa-miR-1912-3p, hsa-miR-596	ARL5A, TENM1, KLHL11, POMP, C11orf58, NRIP1, SLITRK4, RBMXL2, SP4, TMEM47 ZNF814, PHTF1, AXIN2, CYRIA, MSL1, ZNF14, RNF114, ZNF655, CWC25, ZNF492 CNOT6L, TGFBR1, RAB11FIP2, TAOK1, NR3C1, FYTDD1, DDX59, TMTC3, KIAA0408, USP25 CDYL2, RBMS1, RALA, UPF1, CMTR1, SH3BP5L, JPH3, ARID1A, GABARAPL2, KDM7A TOX3, RBFOX1, IFNK, TNNT3K, MRPS27, DPYSL2, SPTY2D1, BBS12, USP30, NFIB	NR3C1, ARID1A, CWC25, JPH3, KLHL11 NRIP1, RBFOX1, RNF114, TAOK1, USP25	Colorectal cancer Hepatocellular carcinoma Mitophagy Pancreatic cancer FoxO signaling pathway Apelin signaling pathway Gastric cancer Hippo signaling pathway Proteasome Herpes simplex virus 1 infection	7.15E-02 2.13E-01 2.13E-01 2.13E-01 4.21E-01 4.21E-01 4.21E-01 4.31E-01 4.69E-01 4.69E-01
PR32	hsa-miR-3681-5p, hsa-miR-4711-5p, hsa-miR-128-1-5p hsa-miR-4489, hsa-miR-564	SHISA7, CSDE1, AXIN2, CDH6, CCDC68, TIMM23B, CCR1, CRACDL, LRRN4CL, NOMO3 GNG13, GAS7, PRKCA, KLHL18, BET1, DAB2, PNOC, EMX2, KNO1, VSIG10 CMIP, CNBP, FAM53B, SIK3, DCANP1, NRGN, DAGLA, ZIC3, PLXNA4, TBC1D2B AGO4, MSL2, PPP2R2B, RAB11FIP2, ZDHHC17, BACH2, PDE3B, PTPRE, ZFH3, YIPF4 GNG13, CBFA2T3, IQSEC3, RHOA, TBC1D25, CDH15, NRM, EFNB3, SDK1, TMED7-TICAM2	RHOA, GNG13, PRKCA, PLXNA4, TBC1D2B CCR1, CSDE1, EFNB3, CBFA2T3, PNOC	Axon guidance Morphine addiction Human cytomegalovirus infection Sphingolipid signaling pathway Endocytosis Dopaminergic synapse Signaling pathways regulating pluripotency of stem cells Retrograde endocannabinoid signaling Wnt signaling pathway Chemokine signaling pathway	8.22E-02 8.22E-02 8.22E-02 8.22E-02 8.22E-02 8.50E-02 8.77E-02 8.77E-02 1.07E-01 1.43E-01
PR33	hsa-miR-6881-3p, hsa-miR-6834-3p, hsa-miR-6809-3p hsa-miR-6759-3p, hsa-miR-6758-5p, hsa-miR-4667-3p	SCO1, CREBBP, RBM41, HNRNPU, CYRIA, TYW1, SPAST, IGF2BP2, SLC25A33, INSIG2 CPN1, PFN2, ZFAND1, CRISPLD1, FUT11, H2BW1, ARL8B, NFYA, NKAPD1, PHAX ZNF468, ZNF99, MBNL3, PCDHA7, PCDHA1, PCDHAC1, PCDHA4, PCDHA6, PCDHA5, PCDHA10 DLG5, GOLPH3, NOL7, H2AZ1, FAM220A, CCDC83, IQGAP1, FAM71E1, NEFM, TSHZ1 CBFA2T3, NT5E, GNAQ, PEX19, RORA, SCUBE3, TMEM121B, SDK1, BASP1, MLEC NCDN, ST3GAL1, HMGXB3, ITGA10, GRAMD1B, FAM110A, TAR53, BRD2, GPR61, ZNF728	PCDHA10, PCDHA4, PCDHA7, ARL8B, CBFA2T3 CPN1, CREBBP, GOLPH3, IQGAP1, NFYA	Spinocerebellar ataxia Long-term potentiation Adherens junction Regulation of actin cytoskeleton Melanogenesis Tuberculosis Growth hormone synthesis, secretion and action Systemic lupus erythematosus Circadian rhythm Nicotinate and nicotinamide metabolism	4.79E-01 4.79E-01 4.79E-01 4.79E-01 4.79E-01 4.79E-01 4.79E-01 4.79E-01 4.79E-01 4.79E-01
PR34	hsa-miR-6870-3p, hsa-miR-340-3p, hsa-miR-1184 hsa-miR-4283, hsa-let-7i-3p	ATP1A4, TRABD2B, SLIT2, ACAA1, WAPL, MIS12, MED13L, GCDH, SMR3B, COMMD9 GNG13, BOK, FBXL16, SPRN, USP51, SMG7, NCCRP1, TAL1, FBXL12, NR5A1 TULP4, LRRC51, TAPBP, INMT, TLCOD2, CYB5R3, HUS1, ZNF850, TMEM170A, TSPYL1 DICER1, GPC6, TTYH2, CTNND1, CCDC85C, INO80D, PTCHD1, HPCAL4, TDG, DNAC6 DLX5, ADHFE1, CAMK2N1, ANKIB1, DICER1, ZC3H12B, LSM14B, SDC2, STOX1, FOXG1	FBXL16, COMMD9, TULP4, FBXL12, ACAA1 HPCAL4, TDG, SDC2, MIS12, HUS1	Tryptophan metabolism Fatty acid degradation Thyroid hormone signaling pathway Selenocompound metabolism Proximal tubule bicarbonate reclamation alpha-Linolenic acid metabolism Biosynthesis of unsaturated fatty acids Base excision repair Aldosterone-regulated sodium reabsorption Human immunodeficiency virus 1 infection	1.72E-01 1.72E-01 4.12E-01 4.12E-01 4.12E-01 4.12E-01 4.12E-01 4.12E-01 4.12E-01 4.12E-01
PR35	hsa-miR-539-3p, hsa-miR-494-3p, hsa-miR-4749-5p hsa-miR-3975, hsa-miR-3616-3p	CREBRF, PDZD2, ELAVL2, TMEM184B, SMPX, ADCYAP1, ENY2, TENM1, AKAP1, MITD1 FAM169A, ARHGAP5, SLC1A2, AGAP1, INSYN2A, AKAP8, SOCS6, STT3B, ATP8A1, KMT2A ARL15, LRATD1, PTPN22, F2R, PLGLB1, PDGFA, EEF2KMT, TMOD3, ACSL3, FOXRED2 CLDN12, CCN2, OGT, PLXNA4, SLC26A6, ANKUB1, SNX3, TDRP, SUOX, SEC24C ZSCAN32, RGS7BP, KCNB1, GALNT17, SHANK1, PRX, FAM71F2, PRR3, PTEN, SSH2	AKAP1, CTGF, ADCYAP1, AKAP8, KCNB1 PDGFA, PTPN22, PTEN, SLC1A2, SSH2	Other types of O-glycan biosynthesis Focal adhesion Melanoma Glioma Regulation of actin cytoskeleton Prostate cancer Sulfur metabolism Insulin resistance Glutamatergic synapse	2.44E-01 2.44E-01 2.44E-01 2.44E-01 2.44E-01 2.51E-01 2.51E-01 2.61E-01 2.61E-01

Genomic Regions of SARS-CoV-2	Human miRNA	Target Human mRNA	Key Proteins in PPI Network	KEGG Pathways	FDR corrected p-value
PR36	hsa-miR-6878-5p, hsa-miR-4744, hsa-miR-6771-5p hsa-miR-5580-3p, hsa-miR-187-5p	CELF3, VGLL3, MTCH2, ZNF275, AAK1, MARCKSL1, DNAAF8, SLC1A2, SF3A3, E2F2 MAP3K2, HIBADH, AFG1L, TNRC6B, SLK, RFX3, ZSCAN25, TRMT10A, EFEMP1, ANKRD50 RPL22L1, AOC3, TMEM120B, RBM5, C10orf53, NEFL, ZBED6CL, CCSER1, CYB561D1, BDKRB2 PAX4, DENR, ANO4, BTAF1, ZDHHC21, APOOL, UBR2, RASSF8, LPP, RPAP3 SLC4A4, SLITRK5, RUNX2, SEC62, EIF5A2, PPP2R2A, TEAD1, ZMYM2, HECTD2, NCKAP5	RPL22L1, SLC1A2, E2F2, EIF5A2, HECTD2 NEFL, PPP2R2A, RBM5, SF3A3, TEAD1	Fatty acid biosynthesis	3.13E-01
				Chagas disease	4.68E-01
				Sphingolipid signaling pathway	4.68E-01
				Phenylalanine metabolism	4.68E-01
				Protein export	4.68E-01
				Proximal tubule bicarbonate reclamation	4.68E-01
				Hepatitis C	4.68E-01
				Hippo signaling pathway	4.68E-01
				Maturity onset diabetes of the young	4.68E-01
				beta-Alanine metabolism	4.68E-01
				Tyrosine metabolism	4.68E-01
				Cell cycle	2.68E-01
				Cytokine-cytokine receptor interaction	2.68E-01
PR37	hsa-miR-1322 hsa-miR-3194-3p hsa-miR-33b-5p hsa-miR-3157-3p hsa-miR-1915-5p	BMPR2, CAPZA2, CD40, DACH1, CCL20, CCL18, PCDHB7, RBPM52, TBR1, XKR4 RAB30, SCN8A, CAPN7, MFHAS1, MAPRE1, BTBD9, LANCL3, ADCY1, HESX1, TFG ABCA1, CDK6, HMG2, YWHAH, CROT, RORA, HADHB, DYNC1LI2, HBS1L, CADM2 RAD21, SYTL2, ZNF644, STOX2, TMEM150A, SGK3, GID4, ADCYAP1, KCNB1, FGL2 KRT40, TCP10L, MYPN, ZNF813, TFE3, EAF1, SGIP1, ACSS3, MAP2K4, SSUH2	HADHB, DYNC1LI2, CCL20, ABCA1, CD40 RAD21, MAPRE1, CROT, ADCY1, CDK6	Transcriptional misregulation in cancer	2.68E-01
				Chemokine signaling pathway	2.68E-01
				Epstein-Barr virus infection	2.68E-01
				Lipid and atherosclerosis	2.68E-01
				Human T-cell leukemia virus 1 infection	2.68E-01
				Insulin secretion	2.68E-01
				GnRH signaling pathway	2.68E-01
				Circadian entrainment	2.68E-01
				Adrenergic signaling in cardiomyocytes	3.43E-02
				Thyroid hormone synthesis	3.43E-02
				Insulin secretion	3.43E-02
				Aldosterone synthesis and secretion	3.75E-02
				Growth hormone synthesis, secretion and action	5.24E-02
PR38	hsa-miR-3939 hsa-miR-410-3p hsa-miR-3663-3p hsa-miR-21-3p hsa-miR-4789-3p	SEMA6B, CCNL2, NACC2, TMEM170B, PLCXD1, PLCB4, L2HGDH, DGKH, INO80D, SOCS6 TENT5A, CREBZF, PRDM11, NDFIP2, STARD13, CREB5, TBX4, ZBTB44, TMEM108, NUMB ADAMTS2, CACNA2D2, SPPL2B, RGS4, TUBB2A, C1QTNF6, OSBPL11, CHSY1, FREM2, TMTC3 STK38L, PCDH19, GRIA2, ATP1B1, NAP1L5, LAMP1, UBE4B, MAP3K1, GPM6A, ZNF326 PHOSPHO-KLHL23, KLHL23, PHIP, THBS2	DGKH, GRIA2, MAP3K1, PLCB4, RGS4 ADAMTS2, ATP1B1, GPM6A, PCDH19, STARD13	Dopaminergic synapse	5.82E-02
				Huntington disease	5.82E-02
				Phagosome	5.82E-02
				Carbohydrate digestion and absorption	5.82E-02
				Cocaine addiction	5.82E-02

Table S2: List of human mRNAs associated with the human miRNAs aligned with the 38 potential SARS-CoV-2 regions along with their KEGG pathways

Genomic Regions in SARS-CoV-2	GO: Biological Pathway	FDR adjusted p-value	GO: Cellular Pathway	FDR adjusted p-value	GO: Molecular Pathway	FDR adjusted p-value
PR1	nervous system development	3.32E-02	dendrite	2.43E-02	1-phosphatidylinositol binding	4.04E-01
	nucleosome disassembly	1.07E-01	npBAF complex	1.65E-01	Notch binding	4.04E-01
	chromatin disassembly	1.07E-01	SWI/SNF complex	1.97E-01	actin binding	4.04E-01
	protein-DNA complex disassembly	1.09E-01	BAF-type complex	1.97E-01	ADP binding	4.04E-01
	chromatin-mediated maintenance of transcription	1.67E-01	dendrite membrane	1.97E-01	lipoprotein particle receptor binding	4.04E-01
PR2	calcineurin-NFAT signaling cascade	7.82E-03	nuclear transcription factor complex	3.62E-02	calcium-dependent protein serine/threonine phosphatase activity	9.13E-02
	calcineurin-mediated signaling	7.82E-03	acetylcholine-gated channel complex	1.35E-01	histone demethylase activity	9.13E-02
	inositol phosphate-mediated signaling	1.49E-02	axon	3.20E-01	histone demethylase activity	9.13E-02
	regulation of mRNA stability	1.69E-02	RNA polymerase II transcription factor complex	3.20E-01	Lys48-specific deubiquitinase activity	9.13E-02
	negative regulation of cellular component organization	6.62E-02	nucleolus	3.20E-01	transcription corepressor binding	9.13E-02
PR3	thyroid hormone generation	1.82E-01	cytoskeleton	2.53E-01	phosphatidic acid binding	1.20E-01
	regulation of receptor biosynthetic process	1.82E-01	histone methyltransferase complex	2.53E-01	protein kinase inhibitor activity	1.20E-01
	regulation of transferase activity	1.82E-01	caveola	2.53E-01	integrin binding	1.43E-01
	positive regulation of lymphocyte differentiation	1.82E-01	chromatin silencing complex	2.53E-01	nucleosomal DNA binding	1.43E-01
	positive regulation of telomere capping	1.82E-01	pseudopodium	2.53E-01	protein serine/threonine kinase inhibitor activity	1.43E-01
PR4	negative regulation of cell adhesion	2.44E-02	endoplasmic reticulum subcompartment	1.61E-02	cadherin binding involved in cell-cell adhesion	9.85E-02
	Golgi to plasma membrane transport	6.14E-02	secretory vesicle	1.61E-02	protein binding involved in cell-cell adhesion	9.85E-02
	endoplasmic reticulum tubular network organization	1.27E-01	exocytic vesicle	1.61E-02	core promoter binding	1.14E-01
	extracellular matrix disassembly	1.60E-01	endoplasmic reticulum tubular network	1.61E-02	transcription regulatory region sequence-specific DNA binding	2.41E-01
	Golgi to plasma membrane protein transport	1.60E-01	axolemma	1.45E-01	hydrogen:amino acid symporter activity	2.41E-01
PR5	regulation of cell junction assembly	2.55E-01	RISC complex	2.32E-02	protein kinase A regulatory subunit binding	6.89E-03
	regulation of bicellular tight junction assembly	2.55E-01	RNAi effector complex	2.32E-02	ubiquitin protein ligase binding	5.82E-02
	activation of protein kinase A activity	2.55E-01	Cul2-RING ubiquitin ligase complex	3.33E-02	ubiquitin-like protein ligase binding	5.82E-02
	negative regulation of translational initiation	2.55E-01	intrinsic component of the cytoplasmic side of the plasma membrane	3.33E-02	nucleosomal DNA binding	1.81E-01
	neuron differentiation	2.60E-01	small nuclear ribonucleoprotein complex	4.29E-02	myosin binding	1.81E-01
PR6	regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	1.53E-01	nucleoplasm part	9.25E-02	methylation-dependent protein binding	6.62E-03
	protein K6-linked ubiquitination	1.53E-01	ficolin-1-rich granule	1.75E-01	methyated histone binding	6.62E-03
	negative regulation of oxidative stress-induced neuron death	1.53E-01	cytoplasmic stress granule	1.75E-01	ribosomal small subunit binding	8.87E-02
	positive regulation of viral life cycle	1.53E-01	nuclear ubiquitin ligase complex	1.75E-01	ephrin receptor binding	1.21E-01
	negative regulation of reactive oxygen species metabolic process	1.93E-01	ficolin-1-rich granule lumen	1.75E-01	TBP-class protein binding	1.21E-01
PR7	regulation of osteoclast development	1.43E-01	cytoplasmic stress granule	3.28E-03	poly-purine tract binding	1.63E-02
	protein localization to cytoplasmic stress granule	1.43E-01	cytoplasmic ribonucleoprotein granule	4.93E-02	glucocorticoid receptor binding	6.07E-02
	regulation of osteoclast differentiation	1.43E-01	ribonucleoprotein granule	1.80E-01	RNA stem-loop binding	7.57E-02
	positive regulation of CREB transcription factor activity	2.71E-01	axolemma	3.32E-01	poly (A binding	7.57E-02
	positive regulation of response to biotic stimulus	2.71E-01	FACIT collagen trimer	3.32E-01	mRNA 5'-UTR binding	1.50E-01
PR8	regulation of amyloid precursor protein biosynthetic process	1.62E-01	recycling endosome membrane	4.50E-01	calcium channel regulator activity	2.22E-01
	regulation of short-term neuronal synaptic plasticity	1.62E-01	platelet alpha granule lumen	4.50E-01	serotonin receptor activity	2.22E-01
	peptidyl-serine phosphorylation	2.45E-01	nuclear transcription factor complex	4.50E-01	protein serine/threonine kinase activity	2.22E-01
	vesicle-mediated transport	2.45E-01	cyclin/CDK positive transcription elongation factor complex	4.50E-01	potassium channel regulator activity	2.22E-01
	cGMP biosynthetic process	2.45E-01	platelet alpha granule	4.99E-01	ubiquitin binding	2.22E-01
PR9	regulation of ARF protein signal transduction	2.18E-03	nuclear matrix	2.18E-01	small GTPase binding	7.62E-03
	regulation of cation channel activity	3.47E-02	early phagosome	2.18E-01	GTPase binding	7.94E-03
	regulation of Ras protein signal transduction	5.80E-02	cyclin/CDK positive transcription elongation factor complex	2.18E-01	transcription coactivator activity	1.20E-01
	vesicle-mediated transport	8.37E-02	nuclear periphery	2.18E-01	metal ion binding	1.20E-01
	positive regulation of proteolysis	8.37E-02	post-mRNA release spliceosomal complex	2.18E-01	GTPase activator activity	1.65E-01
PR10	regulation of cation channel activity	2.60E-01	centrosome	3.00E-01	zinc ion binding	2.71E-01
	cell-cell junction organization	2.60E-01	microtubule organizing center	3.00E-01	pyrophosphatase activity	2.71E-01
	cellular response to hexose stimulus	2.60E-01	cation channel complex	3.00E-01	transition metal ion binding	2.71E-01
	sulfur amino acid metabolic process	2.60E-01	cullin-RING ubiquitin ligase complex	3.00E-01	cAMP-dependent protein kinase activity	2.71E-01
	regulation of calcium ion transmembrane transporter activity	2.60E-01	npBAF complex	3.00E-01	m7G (5' pppN diphosphatase activity	2.71E-01
PR11	phosphorylation	5.33E-02	chromosome	3.41E-01	phosphotransferase activity, alcohol group as acceptor	1.07E-02
	negative regulation of mitotic cell cycle phase transition	5.33E-02	ionotropic glutamate receptor complex	3.41E-01	kinase activity	1.07E-02
	positive regulation of RIG-I signaling pathway	5.33E-02	nuclear chromosome	3.41E-01	RNA binding	1.82E-02
	regulation of MDA-5 signaling pathway	5.33E-02	cation channel complex	3.41E-01	transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding	1.85E-02
	negative regulation of Wnt signaling pathway	7.90E-02	cyclin/CDK positive transcription elongation factor complex	3.41E-01	ATP binding	1.85E-02
PR12	cell differentiation in spinal cord	9.77E-02	alpha DNA polymerase:primase complex	4.22E-01	delayed rectifier potassium channel activity	1.60E-01
	regulation of gastrulation	1.60E-01	integral component of cytoplasmic side of endoplasmic reticulum membrane	4.22E-01	potassium channel regulator activity	1.60E-01
	endoderm development	1.60E-01	lysosomal lumen	4.22E-01	transforming growth factor beta-activated receptor activity	1.60E-01
	negative regulation of gene expression	1.63E-01	nuclear replisome	4.22E-01	aspartic endopeptidase activity, intramembrane cleaving	1.60E-01
	positive regulation of embryonic development	1.63E-01	AMPA glutamate receptor complex	4.22E-01	exoribonuclease activity	1.60E-01
PR13	double-strand break repair via homologous recombination	4.71E-02	potassium channel complex	4.41E-02	endonuclease activity	1.87E-01
	interstrand cross-link repair	1.19E-01	caveola	2.16E-01	Hsp90 protein binding	1.87E-01
	recombinational repair	1.88E-01	cation channel complex	2.16E-01	deoxyribonuclease activity	1.87E-01
	regulation of lipid metabolic process	1.88E-01	protein kinase complex	2.16E-01	endodeoxyribonuclease activity	1.90E-01
	replication fork processing	1.88E-01	nuclear transcription factor complex	2.16E-01	ceramidase activity	1.90E-01
PR14	regulation of cyclin-dependent protein kinase activity	1.34E-01	extrinsic component of external side of plasma membrane	1.39E-01	xylosyltransferase activity	5.76E-03

Genomic Regions in SARS-CoV-2	GO: Biological Pathway	FDR adjusted p-value	GO: Cellular Pathway	FDR adjusted p-value	GO: Molecular Pathway	FDR adjusted p-value
	neuron projection morphogenesis	1.34E-01	cyclin/CDK positive transcription elongation factor complex	1.39E-01	UDP-xylosyltransferase activity	6.89E-03
	cellular response to nutrient levels	1.34E-01	chromosome	1.39E-01	cyclin-dependent protein serine/threonine kinase regulator activity	4.38E-02
	regulation of BMP signaling pathway	1.34E-01	pseudopodium	1.39E-01	myosin binding	9.45E-02
	regulation of nucleic acid-templated transcription	1.34E-01	N-terminal protein acetyltransferase complex	1.39E-01	UDP-glycosyltransferase activity	1.35E-01
PR15	negative regulation of cytoplasmic translation	2.98E-02	messenger ribonucleoprotein complex	5.29E-03	mRNA 3'-UTR binding	6.47E-02
	regulation of cytoplasmic translation	2.98E-02	dendrite	1.73E-01	ribosome binding	1.37E-01
	regulation of hemopoiesis	2.98E-02	L-type voltage-gated calcium channel complex	1.73E-01	mRNA binding	1.37E-01
	positive regulation of nuclear-transcribed mRNA poly (A tail shortening	2.98E-02	apical dendrite	1.73E-01	PDZ domain binding	1.37E-01
	regulation of nuclear-transcribed mRNA poly (A tail shortening	2.98E-02	filopodium tip	1.73E-01	translation factor activity, RNA binding	1.37E-01
PR16	3'-UTR-mediated mRNA destabilization	1.61E-01	cytoskeleton	2.40E-01	RNA stem-loop binding	2.56E-02
	protein localization to chromatin	1.77E-01	AP-1 adaptor complex	2.40E-01	sequence-specific DNA binding	2.56E-02
	mRNA destabilization	1.77E-01	messenger ribonucleoprotein complex	2.40E-01	ribosomal small subunit binding	2.56E-02
	positive regulation of mRNA catabolic process	1.77E-01	mitotic spindle	2.40E-01	ribosome binding	1.43E-01
	protein localization to chromosome	1.77E-01	clathrin coat of trans-Golgi network vesicle	2.40E-01	ribonuclease activity	1.60E-01
PR17	regulation of transcription from RNA polymerase II promoter	1.10E-01	apical dendrite	1.52E-02	transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	7.08E-03
	glycosphingolipid metabolic process	1.10E-01	microtubule end	6.09E-02	transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	7.08E-03
	positive regulation of transcription from RNA polymerase II promoter	1.10E-01	ruffle membrane	1.68E-01	transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	7.08E-03
	negative regulation of myeloid cell differentiation	1.60E-01	azurophil granule membrane	1.68E-01	core promoter proximal region sequence-specific DNA binding	3.87E-02
	regulation of pri-miRNA transcription from RNA polymerase II promoter	1.60E-01	messenger ribonucleoprotein complex	1.68E-01	RNA polymerase II core promoter proximal region sequence-specific DNA binding	1.61E-01
PR18	positive regulation of cellular catabolic process	6.76E-02	axon	3.99E-02	protein phosphatase 2A binding	1.04E-01
	dorsal/ventral axis specification	6.76E-02	condensed chromosome	1.59E-01	phosphatidylinositol-4-phosphate binding	1.04E-01
	regulation of vascular endothelial growth factor signaling pathway	6.76E-02	nuclear chromosome	1.59E-01	protein heterodimerization activity	1.58E-01
	positive regulation of neuron migration	6.76E-02	caveola	1.59E-01	amyloid-beta binding	1.58E-01
	negative regulation of cellular catabolic process	6.76E-02	protein kinase complex	1.61E-01	PDZ domain binding	1.58E-01
PR19	DNA damage checkpoint	3.42E-03	nuclear transcription factor complex	1.11E-01	core promoter binding	1.45E-03
	positive regulation of transcription, DNA-templated	3.42E-03	chromosome	1.11E-01	RNA polymerase II regulatory region sequence-specific DNA binding	2.22E-03
	positive regulation of transcription from RNA polymerase II promoter	3.42E-03	chromatoid body	1.11E-01	transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	2.22E-03
	negative regulation of gene expression	3.42E-03	axon	1.30E-01	C2H2 zinc finger domain binding	3.98E-03
	regulation of transcription from RNA polymerase II promoter	3.45E-03	acetylcholine-gated channel complex	1.30E-01	transcription coactivator binding	4.03E-03
PR20	embryonic eye morphogenesis	1.26E-01	ficolin-1-rich granule lumen	1.60E-01	alcohol dehydrogenase activity, zinc-dependent	1.70E-02
	positive regulation of fatty acid oxidation	1.26E-01	cytosolic small ribosomal subunit	1.60E-01	alcohol dehydrogenase (NAD activity	1.70E-02
	regulation of fatty acid oxidation	1.26E-01	small ribosomal subunit	1.60E-01	kinase binding	7.16E-02
	positive regulation of fatty acid metabolic process	1.44E-01	PML body	1.60E-01	RNA polymerase II regulatory region sequence-specific DNA binding	7.16E-02
	eye morphogenesis	1.44E-01	secretory granule lumen	1.60E-01	RNA polymerase II regulatory region DNA binding	7.16E-02
PR21	negative regulation of signal transduction	1.10E-01	axolemma	4.06E-01	ubiquitin-like protein conjugating enzyme activity	1.78E-01
	regulation of cellular catabolic process	1.39E-01	juxtaparanode region of axon	4.06E-01	phosphotyrosine residue binding	1.78E-01
	positive regulation of transferase activity	1.39E-01	synaptonemal structure	4.06E-01	protein phosphorylated amino acid binding	1.78E-01
	regulation of cellular senescence	1.76E-01	actin cytoskeleton	4.06E-01	Rab guanyl-nucleotide exchange factor activity	1.78E-01
	protein phosphorylation	1.76E-01	integral component of plasma membrane	4.06E-01	transferase activity, transferring acyl groups other than amino-acyl groups	1.78E-01
PR22	regulation of establishment of endothelial barrier	1.36E-01	main axon	1.57E-01	Lys63-specific deubiquitinase activity	3.59E-02
	regulation of bicellular tight junction assembly	1.36E-01	histone methyltransferase complex	1.57E-01	sequence-specific DNA binding	1.07E-01
	positive regulation of interleukin-2 production	1.42E-01	SCF ubiquitin ligase complex	1.57E-01	transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	1.07E-01
	protein K48-linked deubiquitination	1.42E-01	paranode region of axon	1.57E-01	RNA polymerase II regulatory region sequence-specific DNA binding	1.07E-01
	protein K63-linked deubiquitination	1.66E-01	IkappaB kinase complex	1.57E-01	repressing transcription factor binding	1.07E-01
PR23	cerebral cortex cell migration	2.55E-01	transcription factor TFIIC complex	3.80E-01	NEDD8-specific protease activity	3.42E-01
	telencephalon cell migration	2.55E-01	RNA polymerase III transcription factor complex	3.80E-01	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	3.42E-01
	5S class rRNA transcription from RNA polymerase III type 1 promoter	2.55E-01	very-low-density lipoprotein particle	4.69E-01	oligosaccharyl transferase activity	3.42E-01
	tRNA transcription from RNA polymerase III promoter	2.55E-01	intrinsic component of mitochondrial inner membrane	4.69E-01	oxalate transmembrane transporter activity	3.42E-01
	vitamin K metabolic process	2.55E-01	integral component of mitochondrial inner membrane	4.69E-01	3',5'-cyclic-GMP phosphodiesterase activity	3.42E-01
PR24	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	2.55E-01	coated vesicle	2.40E-01	endocytic adaptor activity	2.69E-02
	positive regulation of nucleic acid-templated transcription	1.30E-02	endocytic patch	2.40E-01	clathrin adaptor activity	2.69E-02
	positive regulation of gene expression	3.34E-02	actin cortical patch	2.40E-01	glutamate receptor binding	7.42E-02

Genomic Regions in SARS-CoV-2	GO: Biological Pathway	FDR adjusted p-value	GO: Cellular Pathway	FDR adjusted p-value	GO: Molecular Pathway	FDR adjusted p-value
PR25	oogenesis	7.80E-02	spectrin-associated cytoskeleton	2.40E-01	protein tyrosine/serine/threonine phosphatase activity	1.60E-01
	positive regulation of transcription, DNA-templated	8.20E-02	NMDA selective glutamate receptor complex	2.40E-01	actin binding	1.64E-01
	positive regulation of lamellipodium assembly	1.01E-01	spindle	1.49E-01	transcriptional repressor activity, RNA polymerase II transcription factor binding	2.78E-02
	negative regulation of gene expression	1.59E-01	flotillin complex	1.49E-01	transcription regulatory region sequence-specific DNA binding	3.45E-02
	regulation of cellular response to transforming growth factor beta stimulus	1.59E-01	clathrin-sculpted aminobutyric acid gamma-transport vesicle membrane	1.49E-01	RNA polymerase II transcription cofactor activity	3.45E-02
	production of miRNAs involved in gene silencing by miRNA	1.59E-01	clathrin-sculpted aminobutyric acid gamma-transport vesicle	1.49E-01	core promoter proximal region DNA binding	3.45E-02
PR26	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	1.59E-01	RISC-loading complex	1.49E-01	NF-kappaB binding	3.45E-02
	diterpenoid metabolic process	2.70E-01	integral component of Golgi membrane	2.03E-01	transmembrane receptor protein tyrosine kinase activity	1.82E-01
	dermatan sulfate biosynthetic process	1.40E-01	actin filament	2.03E-01	transmembrane receptor protein kinase activity	1.82E-01
	dermatan sulfate metabolic process	1.40E-01	signal recognition particle, endoplasmic reticulum targeting	2.03E-01	mitogen-activated protein kinase kinase binding	1.82E-01
	dermatan sulfate proteoglycan biosynthetic process	1.40E-01	lamellipodium membrane	2.03E-01	chondroitin sulfotransferase activity	1.82E-01
	chondroitin sulfate biosynthetic process	1.81E-01	U6 snRNP	2.03E-01	cation:sugar symporter activity	1.82E-01
PR27	regulation of microtubule depolymerization	1.81E-01	meiotic cohesin complex	1.88E-01	cyclin-dependent protein kinase activity	1.39E-01
	protein localization to cytoplasmic stress granule	2.86E-02	commitment complex	1.88E-01	acetylglucosaminyltransferase activity	1.39E-01
	Notch signaling pathway	3.17E-02	chromatin silencing complex	1.88E-01	microtubule motor activity	1.39E-01
	smoothened signaling pathway	1.15E-01	chromatin	1.88E-01	phosphatidic acid transporter activity	1.39E-01
	signal transduction by p53 class mediator	1.15E-01	spliceosomal complex	1.88E-01	motor activity	1.39E-01
	intrinsic apoptotic signaling pathway by p53 class mediator	1.15E-01	nuclear speck	2.43E-01	voltage-gated calcium channel activity	1.66E-01
PR28	positive regulation of muscle hypertrophy	1.02E-01	integral component of cytoplasmic side of endoplasmic reticulum membrane	2.43E-01	RNA polymerase II transcription coactivator activity	1.66E-01
	neural tube development	1.02E-01	Golgi trans cisterna	2.43E-01	transcriptional activator activity, RNA polymerase II transcription factor binding	1.66E-01
	positive regulation of cardiac muscle hypertrophy	1.02E-01	L-type voltage-gated calcium channel complex	2.43E-01	transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding	1.66E-01
	regulation of catenin import into nucleus	1.02E-01	Golgi medial cisterna	2.43E-01	ATPase binding	1.66E-01
	negative regulation of stem cell differentiation	3.15E-02	heterochromatin	1.66E-01	SH3/SH2 adaptor activity	1.60E-01
	Ras protein signal transduction	4.32E-02	late endosome	1.66E-01	SH3 domain binding	1.60E-01
PR29	endosome to lysosome transport	4.32E-02	coated vesicle	2.23E-01	metalloendopeptidase activity	1.60E-01
	Rap protein signal transduction	4.32E-02	paranode region of axon	2.23E-01	polynucleotide adenyllyltransferase activity	1.60E-01
	lysosomal transport	7.64E-02	early endosome	2.23E-01	nerve growth factor binding	1.60E-01
	neurotrophin signaling pathway	7.64E-02	nuclear transcription factor complex	1.96E-01	syntaxin-1 binding	6.43E-02
	regulation of cytokine biosynthetic process	1.58E-01	clathrin-sculpted aminobutyric acid gamma-transport vesicle membrane	1.96E-01	RNA polymerase II regulatory region DNA binding	1.72E-01
	NLS-bearing protein import into nucleus	1.71E-01	clathrin-sculpted aminobutyric acid gamma-transport vesicle	1.96E-01	polynucleotide adenyllyltransferase activity	1.72E-01
PR30	protein lipidation	1.71E-01	axon initial segment	1.96E-01	syntaxin binding	1.72E-01
	negative regulation of cellular biosynthetic process	1.71E-01	multimeric ribonuclease P complex	1.96E-01	protein transporter activity	1.72E-01
	regulation of exocytosis	1.71E-01	nuclear speck	4.05E-02	ATPase binding	3.14E-02
	regulation of transcription, DNA-templated	1.46E-01	cytoplasmic vesicle membrane	1.92E-01	ubiquitin protein ligase binding	3.14E-02
	positive regulation of filopodium assembly	1.46E-01	nuclear body	1.92E-01	ubiquitin-like protein ligase binding	3.14E-02
	negative regulation of proteasomal protein catabolic process	1.46E-01	junctional sarcoplasmic reticulum membrane	1.92E-01	RNA helicase activity	1.34E-01
PR31	activation of MAPKK activity	1.46E-01	nucleolus	1.92E-01	ATP-dependent RNA helicase activity	1.34E-01
	regulation of filopodium assembly	1.46E-01	catenin complex	1.02E-01	Rab GTPase binding	1.47E-01
	cell-cell junction assembly	1.94E-02	Cul3-RING ubiquitin ligase complex	1.56E-01	Ras GTPase binding	1.47E-01
	regulation of axonogenesis	5.06E-02	coated vesicle	1.56E-01	histone threonine kinase activity	1.47E-01
	cell junction assembly	5.06E-02	RNAi effector complex	1.56E-01	protein kinase B binding	1.47E-01
	homophilic cell adhesion via plasma membrane adhesion molecules	5.06E-02	RISC-loading complex	1.56E-01	C-C chemokine binding	1.47E-01
PR32	negative regulation of cell adhesion	5.06E-02	nuclear transcription factor complex	7.61E-02	alpha-tubulin binding	1.04E-01
	nervous system development	2.70E-02	spindle midzone	1.09E-01	beta-tubulin binding	1.04E-01
	regulation of smoothened signaling pathway	3.77E-02	RNA polymerase II transcription factor complex	1.96E-01	core promoter binding	1.04E-01
	glomerular visceral epithelial cell differentiation	9.93E-02	sex chromosome	2.37E-01	pre-mRNA binding	1.04E-01
	positive regulation of ATPase activity	2.03E-01	cytoskeleton	2.37E-01	snRNA binding	1.19E-01
	regulation of alternative mRNA splicing, via spliceosome	2.03E-01	vacuolar lumen	2.07E-01	ribonuclease activity	1.28E-01
PR33	aminoglycan metabolic process	1.45E-01	micro-ribonucleoprotein complex	2.07E-01	RNA polymerase II regulatory region DNA binding	1.28E-01
	aminoglycan catabolic process	1.45E-01	lysosomal lumen	2.07E-01	coreceptor activity involved in Wnt signaling pathway, planar cell polarity pathway	1.28E-01
	regulation of cyclin-dependent protein kinase activity	1.45E-01	RISC-loading complex	2.07E-01	cytochrome-b5 reductase activity, acting on NAD (PH	1.28E-01
	aminoglycan biosynthetic process	1.45E-01	RISC complex	2.07E-01	acetyl-CoA C-acyltransferase activity	1.28E-01
	fatty acid beta-oxidation	1.45E-01	nuclear matrix	2.53E-01	protein kinase A regulatory subunit binding	1.32E-01
	peptidyl-lysine trimethylation	5.76E-03	nuclear periphery	2.53E-01	dicarboxylic acid transmembrane transporter activity	1.43E-01
PR34	postsynaptic density assembly	2.15E-02	early phagosome	2.53E-01	protein-lysine N-methyltransferase activity	1.43E-01
	myelin maintenance	2.15E-02	NMDA selective glutamate receptor complex	2.53E-01	phospholipid transporter activity	1.43E-01
	excitatory synapse assembly	2.15E-02	neurotransmitter receptor complex	2.53E-01	PDZ domain binding	1.43E-01
	postsynaptic density organization	2.15E-02	MICOS complex	3.57E-01	anion:cation symporter activity	1.71E-01
	regulation of alternative mRNA splicing, via spliceosome	1.76E-01	spliceosomal complex	3.57E-01	transcription factor activity, RNA polymerase II distal enhancer sequence-specific binding	1.71E-01
	transcription initiation from RNA polymerase II promoter	1.76E-01	RNA polymerase II transcription factor complex	3.57E-01	primary amine oxidase activity	1.71E-01

Genomic Regions in SARS-CoV-2	GO: Biological Pathway	FDR adjusted p-value	GO: Cellular Pathway	FDR adjusted p-value	GO: Molecular Pathway	FDR adjusted p-value
	regulation of mRNA splicing, via spliceosome	1.76E-01	nuclear inner membrane	3.57E-01	AP-2 adaptor complex binding	1.71E-01
	protein targeting to membrane	1.76E-01	rough endoplasmic reticulum	3.57E-01	high-affinity glutamate transmembrane transporter activity	1.71E-01
PR37	DNA-templated transcription, initiation	1.76E-01	spanning component of plasma membrane	2.49E-01	CCR chemokine receptor binding	1.39E-01
	negative regulation of cellular senescence	7.65E-02	axon initial segment	2.49E-01	chemokine activity	1.39E-01
	action potential	7.65E-02	chromosome	2.49E-01	sterol binding	1.39E-01
	negative regulation of cell aging	7.65E-02	spanning component of membrane	2.49E-01	chemokine receptor binding	1.39E-01
	mesenchyme development	7.65E-02	CD40 receptor complex	2.49E-01	SH3 domain binding	1.39E-01
PR38	cAMP-mediated signaling	7.65E-02	integral component of cytoplasmic side of endoplasmic reticulum membrane	3.11E-01	aspartic endopeptidase activity, intramembrane cleaving	1.90E-01
	granzyme-mediated apoptotic signaling pathway	2.07E-02	lytic vacuole membrane	3.11E-01	diacylglycerol kinase activity	1.90E-01
	dendrite extension	1.95E-01	axonal growth cone	3.11E-01	protein kinase regulator activity	1.90E-01
	modulation of chemical synaptic transmission	1.95E-01	lysosomal membrane	3.11E-01	potassium-transporting ATPase activity	1.90E-01
	positive regulation of insulin-like growth factor receptor signaling pathway	1.95E-01	spindle midzone	3.09E-01	protein kinase B binding	1.90E-01

Table S3: Top 5 GO:Biological Process, GO:Molecular Function and GO:Cellular Component of the target human mRNAs for the 38 potential SARS-CoV-2 regions

Genome Regions in SARS-CoV-2	miRNA	Target Human Proteins	Drug	P-value	DrugBank ID	Treatment
PR1	hsa-miR-149-3p	SMARCD1	Trichostatin A	1.15E-04	DB04297	Antifungal Antibiotic
	hsa-miR-4728-5p					
	hsa-miR-1249-5p					
	hsa-miR-6743-5p	SNW1				
	hsa-miR-6076	E2F3				
	hsa-miR-6510-5p	TP53BP1				
	hsa-miR-10526-3p	ARID1A				
	hsa-miR-4728-5p	AR	Emodin	1.40E-04	DB07715	Breast and ovarian cancer
	hsa-miR-6076	PIK3CA				
PR2	hsa-miR-548ag	TCERG1	Resveratrol	1.46E-04	DB02709	High Cholesterol, Cancer, Heart Disease
	hsa-miR-548ag	PPP3R1				
	hsa-miR-548aq-5p	MEX3D				
	hsa-miR-548d-5p	IGF2BP3	Primaquine	1.49E-04	DB01087	Malaria
	hsa-miR-548ay-5p					
	hsa-miR-548ap-5p					
	hsa-miR-548ae-5p					
	hsa-miR-548ad-5p					
	hsa-miR-548o-5p					
	hsa-miR-548c-5p					
	hsa-miR-548aq-5p					
	hsa-miR-548am-5p					
	hsa-miR-548aq-5p	MEX3D				
	hsa-miR-548ag	RGL1				
PR3	hsa-miR-3162-3p	KMT2D	Estradiol	8.46E-06	DB00783	Estrogen
	hsa-miR-6750-3p	HDAC2				
	hsa-miR-4633-5p	ERCC6L				
	hsa-miR-10398-5p	RRM2				
	hsa-miR-4749-3p	ZBTB10				
	hsa-miR-3162-3p	S1PR1				
	hsa-miR-6511b-3p	MAPK1				
	hsa-miR-6511a-3p	MAPK1				
	hsa-miR-3162-3p	BAZ2A				
	hsa-miR-4749-3p	DACT1				
	hsa-miR-10398-5p	RRM2	Bicalutamide	3.09E-03	DB01128	Prostate Cancer
	hsa-miR-6511b-3p	MAPK1				
	hsa-miR-6511a-3p					
PR4	hsa-miR-3152-3p	CD40LG	Vinblastine	1.63E-04	DB00570	Breast, Testicular Cancer, Neuroblastoma, Hodgkin's and non-Hodgkins lymphoma, Mycosis Fungoides, Histiocytosis, and Kaposi's Sarcoma
	hsa-miR-378i	NCAPG				
	hsa-miR-378f					
	hsa-miR-378b					
	hsa-miR-3914	GTF2I				
	hsa-miR-3152-3p	CD40LG	Paclitaxel	1.57E-03	DB01229	Breast Ovarian and Non-Small Cell Lung Cancer
	hsa-miR-378i					
	hsa-miR-378f					
	hsa-miR-378b					
	hsa-miR-3914	GTF2I				

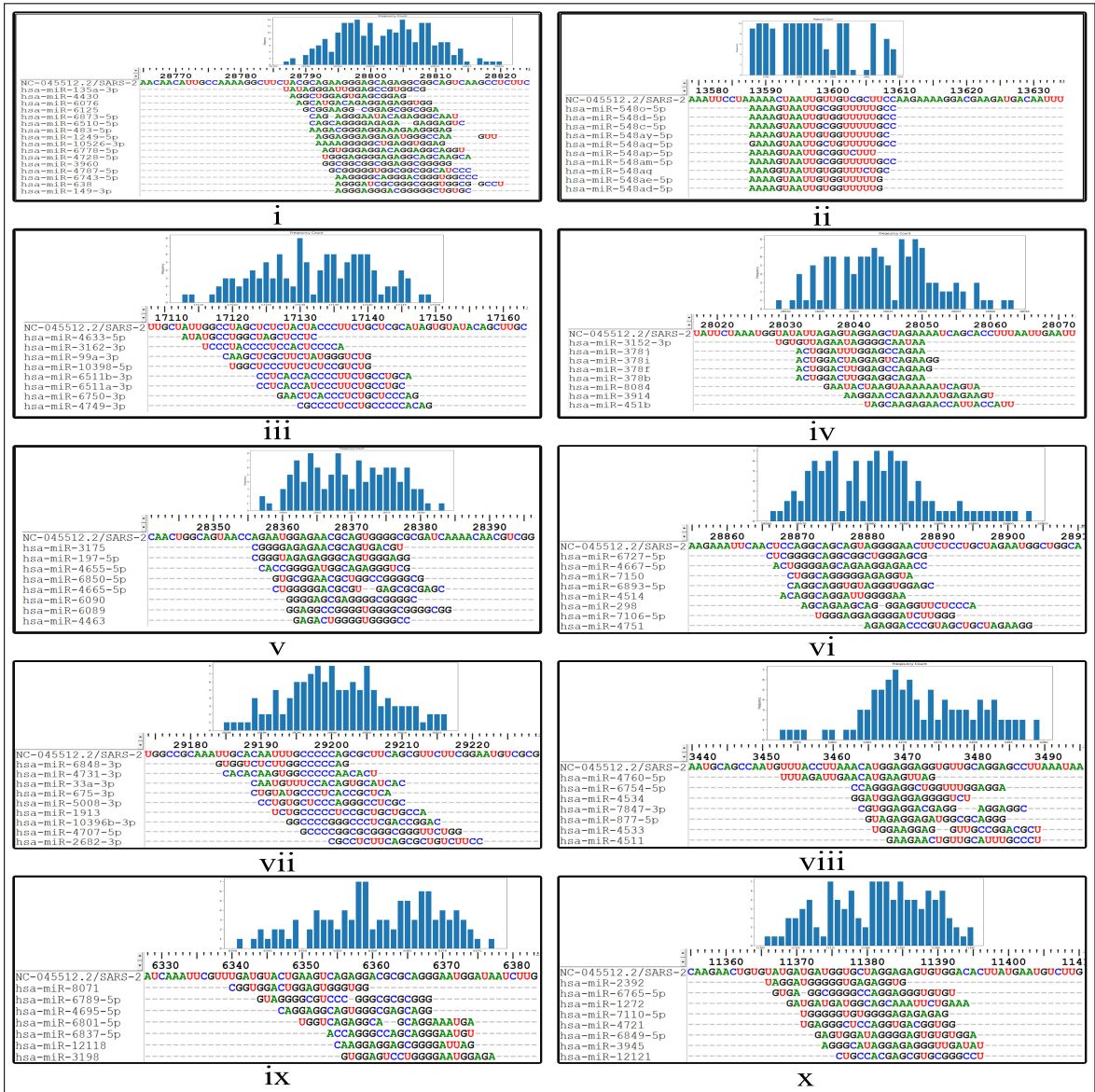
Genome Regions in SARS-CoV-2	miRNA	Target Human Proteins	Drug	P-value	DrugBank ID	Treatment
PR5	hsa-miR-3175	CSNK1A1	Mesalazine	6.62E-04	DB00244	Ulcerative Colitis
	hsa-miR-4655-5p	YWHAB				
	hsa-miR-6090	ADCY9	Diclofenac	1.04E-03	DB00586	Aches, Pains
	hsa-miR-4655-5p	YWHAB				
	hsa-miR-4463	AGO2				
PR6	hsa-miR-5681a	CREBBP	Vorinostat	3.81E-05	DB02546	Cutaneous T-cell Lymphoma
	hsa-miR-1207-5p	CBX5				
	hsa-miR-4446-3p	BRCA1				
	hsa-miR-9851-5p	HIF1A				
	hsa-miR-5681a	CREBBP	Colchicine	1.65E-04	DB01394	Inflammation and Pain
	hsa-miR-4446-3p	BRCA1				
PR7	hsa-miR-675-3p	CUL3	Emetine	4.18E-05	DB13393	Anti-protozoal and Induced Vomitting
	hsa-miR-10396b-3p	ASB13				
	hsa-miR-33a-3p	HNRNPR				
	hsa-miR-2682-3p	PRKCA				
	hsa-miR-4731-3p	UBE2B	Clopamide	5.58E-04	DB13792	Gastroparesis in pateints with diabetes
	hsa-miR-675-3p	CUL3				
	hsa-miR-33a-3p	LSM14A				
PR8	hsa-miR-7847-3p	SYP	Abacavir	8.97E-03	DB01048	Human Immunodeficiency Virus (HIV) infection
PR9	hsa-miR-8071	HDAC2	Trichostatin A	5.99E-03	DB04297	Antifungal Antibiotic
			Tanespimycin	2.72E-02	DB05134	Cancer Solid Tumors Chronic Myelogenous Leukemia
PR10	hsa-miR-6849-5p	CCR1	Tamibarotene	3.02E-02	DB04942	Recurrent APL
	hsa-miR-7110-5p	PRKACA				
	hsa-miR-7110-5p	PRKACA	Amsacrine	3.49E-02	DB00276	Remission of Tumour
PR11	hsa-miR-4281	DUSP1	Diclofenac	1.83E-02	DB00586	Aches, Pains
	hsa-miR-6729-5p	GART				
	hsa-miR-4281	DUSP1	Pyrvinium	2.02E-03	DB06816	Pinworm infestations
	hsa-miR-4281	BCL3				
PR12	hsa-miR-3193	SPEN	Sulfaguanidine	2.54E-03	DB13726	Bacillary Dysentery and other Enteric Infections
	hsa-miR-5000-5p	NOVA1				
	hsa-miR-10524-5p	ELAVL2				
	hsa-miR-3193	SPEN	Captopril	7.48E-03	DB01197	High blood pressure and Heart Failure
	hsa-miR-4330	INSR				
	hsa-miR-4330	NR1D2				
PR13	hsa-miR-6862-3p	CCNT1	Digoxin	4.50E-06	DB00390	Arrhythmias, heart failure
	hsa-miR-9985	RGPD6	Proscillaridin	8.28E-06	DB13307	congestive heart failure and cardiac arrhythmia
	hsa-miR-27a-3p					
	hsa-miR-9985	PDS5B				
	hsa-miR-27a-3p	PDS5B				
	hsa-miR-9985	AFF4				
	hsa-miR-27a-3p					
PR14	hsa-miR-802	MTMR1	Trichostatin A	5.89E-05	DB04297	Antifungal Antibiotic
	hsa-miR-548bb-3p	CREBBP	Vorinostat	6.07E-04	DB02546	T-cell lymphoma
	hsa-miR-377-3p	PUM2				
PR15	hsa-miR-518f-3p	EGR1	Artenimol	2.62E-07	DB11638	Plasmodium falciparum infection
	hsa-miR-214-3p	MAPK1	Clioquinol	7.81E-06	DB04815	Fungal Infections

Genome Regions in SARS-CoV-2	miRNA	Target Human Proteins	Drug	P-value	DrugBank ID	Treatment
	hsa-miR-4269	ESR1				
PR16	hsa-miR-4764-5p	POMC	Imipramine	2.01E-04	DB00458	Antidepressant
	hsa-miR-521	DNAJC5				
	hsa-miR-4509	NFIB	Ambroxol	3.27E-03	DB06742	Airway Secretion Clearance Therapy
	hsa-miR-517b-3p					
	hsa-miR-517a-3p					
PR17	hsa-miR-3529-5p	SEMA3A	Trichostatin A	3.58E-03	DB04297	Antifungal Antibiotic
	hsa-miR-6071	RBBP6				
	hsa-miR-4776-5p	TFCP2L1				
	hsa-miR-502-3p	ZFX				
	hsa-miR-4776-5p	FOXO1				
	hsa-miR-6071	VGLL3				
	hsa-miR-3529-5p	SEMA3A	Raloxifene	4.02E-03	DB00481	Osteoporosis and Ivasive Breast Cancer
	hsa-miR-502-3p	ZFX				
	hsa-miR-4776-5p	FOXO1				
PR21	hsa-miR-4770	IGFBP5	Menadione	1.67E-03	DB00170	Hypoprothrombinemia
	hsa-miR-6726-5p	NOA1				
	hsa-miR-4435	SIAH1				
	hsa-miR-4690-3p	INHBB	Anisomycin	9.74E-03	DB07374	Antibiotic
	hsa-miR-6789-3p	UBE2I				
	hsa-miR-4690-3p	INHBB				
PR22	hsa-miR-3165	HDAC2	Decitabine	2.23E-03	DB01262	Myelodysplastic Syndrome
	hsa-miR-548ah-5p	RUNX1				
	hsa-miR-3132	CBX5	Luteolin	2.71E-03	DB15584	Hypertension Inflammatory disorders and Cancers
	hsa-miR-320c	SH2B3				
	hsa-miR-320d					
	hsa-miR-320a-3p					
PR23	hsa-miR-6823-5p	WNT10B	Trichostatin A	1.03E-03	DB04297	Antifungal Antibiotic
	hsa-miR-3944-3p	IGDCC3				
	hsa-miR-6861-5p	NLK				
	hsa-miR-3934-3p	SDK2				
	hsa-miR-6823-5p	WNT10B	Permethrin	4.99E-03	DB04930	Scabies
PR24	hsa-miR-891a-5p	HTR2C	Clozapine	9.07E-05	DB00363	Schizophrenia
	hsa-miR-891a-5p	POLI				
	hsa-miR-891a-5p	HTR2C	Mirtazapine	5.49E-03	DB003707	Major Depression
PR25	hsa-miR-4719	SMAD2	Irinotecan	1.99E-04	DB00762	Metastatic Carcinoma of the Colon or Rectum
	hsa-miR-4719	CREBBP				
	hsa-miR-6510-3p	SMURF2				
	hsa-miR-6842-3p	AGO3	Aspirin	2.27E-03	DB00945	Pain, Fever, Inflammation, Migraines and Cardiovascular
	hsa-miR-4719	KDM6A				
	hsa-miR-4719	CREBBP				
	hsa-miR-6510-3p	HDAC3				
	hsa-miR-6510-3p	SMURF2				
PR26	hsa-miR-3940-3p	CERK	Parthenolide	3.49E-03	DB13063	Analgesic Anti-inflammatory and Antipyretic
	hsa-miR-4767	CHST12				
	hsa-miR-3940-3p	CERK	Trichostatin A	7.92E-03	DB04297	Antifungal Antibiotic

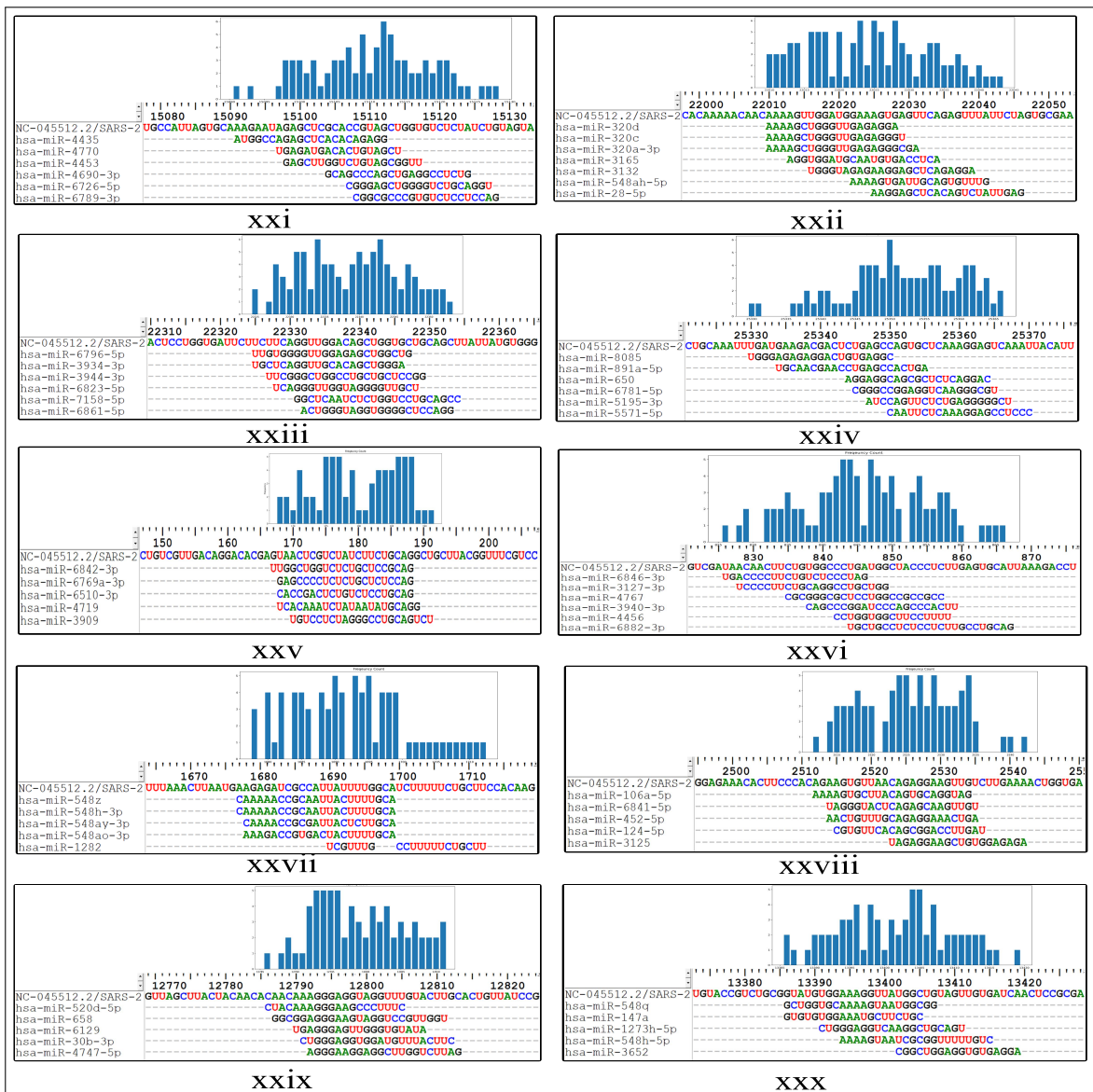
Genome Regions in SARS-CoV-2	miRNA	Target Human Proteins	Drug	P-value	DrugBank ID	Treatment
	hsa-miR-4767	CHST12				
	hsa-miR-6846-3p	GNE				
PR27	hsa-miR-548ay-3p	CCNA2	Clofibrate	2.83E-04	DB00636	Hypertriglyceridemia
	hsa-miR-548z	CREBBP				
	hsa-miR-548h-3p					
	hsa-miR-548z	GFPT1	Desipramine	5.19E-04	DB01151	Depressions and seizure
	hsa-miR-548h-3p	OGT				
	hsa-miR-548ay-3p					
PR28	hsa-miR-452-5p	PURA	Captopril	2.99E-05	DB01197	Renovascular Hypertension, Congestive Heart Failure, Left Ventricular Dysfunction, and Nephropathy
	hsa-miR-6841-5p	COPA				
	hsa-miR-106a-5p	DYNC1LI2				
	hsa-miR-6841-5p	PUM1				
	hsa-miR-124-5p	SEC62				
	hsa-miR-452-5p	PURA	Staurosporine	1.97E-04	DB02010	Anti-Tumor
	hsa-miR-6841-5p	PUM1				
	hsa-miR-124-5p	SEC62				
	hsa-miR-106a-5p	ARHGAP12				
PR29	hsa-miR-4747-5p	MECP2	Zebularine	2.51E-04	DB03068	Anti-tumor
	hsa-miR-520d-5p	MAPK1				
	hsa-miR-4747-5p	RAP1A	Fulvestrant	4.08E-04	DB00947	Breast cancer
	hsa-miR-4747-5p	MMP15				
	hsa-miR-520d-5p	MAPK1				
PR30	hsa-miR-548h-5p	NFAT5	Cyclosporin A	3.92E-03	DB00091	Immunosuppressant
	hsa-miR-147a	FOXP3				
	hsa-miR-548h-5p	RORA	Gemfibrozil	7.48E-03	DB01241	Reduction of Serum Triglyceride
PR31	hsa-miR-4666a-3p	TAOK1	Vorinostat	9.13E-04	DB02546	Cutaneous Manifestations, Recurrent Cutaneous, T-cell lymphoma
	hsa-miR-4666a-3p	NR3C1				
	hsa-miR-4680-5p	CWC25	Lanatoside C	1.21E-03	DB13467	Congestive Heart Failure, Cardiac Arrhythmia
	hsa-miR-4666a-3p	NR3C1				
	hsa-miR-1912-3p	ARID1A				
R32	hsa-miR-4489	PRKCA	Menadione	3.27E-03	DB00170	Hypoprothrombinemia
	hsa-miR-564	TBC1D2B				
	hsa-miR-128-1-5p	EFNB3	Doxorubicin	5.17E-03	DB00997	Cancers and Kaposi’s Sarcoma
	hsa-miR-4489	PRKCA				
	hsa-miR-128-1-5p	RHOA				
PR33	hsa-miR-6881-3p	CREBBP	Alsterpaullone	6.23E-06	DB04014	Anti-tumor
	hsa-miR-6759-3p	GOLPH3				
	hsa-miR-6834-3p	NFYA				
	hsa-miR-6809-3p	PCDHA4				
	hsa-miR-6809-3p	PCDHA10				
	hsa-miR-6809-3p	PCDHA7				
	hsa-miR-6834-3p	NFYA	Azacitidine	1.41E-04	DB00928	Antineoplastic
	hsa-miR-6809-3p	PCDHA4				
	hsa-miR-6809-3p	PCDHA10				
	hsa-miR-6809-3p	PCDHA7				
PR34	hsa-miR-6870-3p	MIS12	Anisomycin	2.91E-04	DB07374	Antibiotic

Genome Regions in SARS-CoV-2	miRNA	Target Human Proteins	Drug	P-value	DrugBank ID	Treatment
	hsa-miR-340-3p	HUS1	Salbutamol	1.09E-02	DB01001	Asthma Bronchitis COPD, Bronchospasms
	hsa-miR-4283	FBXL12				
	hsa-let-7i-3p	SDC2				
PR35	hsa-miR-3616-3p	KCNB1	Trichostatin A	4.26E-04	DB04297	Antifungal Antibiotic
	hsa-miR-494-3p	AKAP8				
	hsa-miR-3616-3p	PTEN				
	hsa-miR-494-3p	SLC1A2				
	hsa-miR-4749-5p	PDGFA				
	hsa-miR-539-3p	AKAP1				
	hsa-miR-3616-3p	PTEN	Lorazepam	1.80E-03	DB00186	Panic Disorders, Severe Anxiety, and Seizures
PR36	hsa-miR-6771-5p	RBM5	Metoclopramide	1.05E-02	DB01233	Gastroesophageal Reflux, Nausea and Vomiting
	hsa-miR-6878-5p	E2F2	Diclofenac	1.83E-02	DB00586	Aches, Pains
	hsa-miR-187-5p	PPP2R2A				
PR37	hsa-miR-33b-5p	ABCA1	Rimexolone	5.66E-05	DB00896	Inflammation of the eye
	hsa-miR-1322	CCL20				
	hsa-miR-33b-5p	ABCA1	Diphenylpyraline	6.69E-05	DB01146	Allergic Rhinitis Hay Fever and Allergic Skin Disorders
	hsa-miR-1322	CD40				
	hsa-miR-33b-5p	CROT				
PR38	hsa-miR-3663-3p	RGS4	Cytarabine	2.15E-04	DB00987	Leukemia
	hsa-miR-21-3p	GRIA2				
	hsa-miR-21-3p	GPM6A				
	hsa-miR-21-3p	ATP1B1				
	hsa-miR-3663-3p	RGS4	Trifluoperazine	2.57E-04	DB00831	Depression Anxiety and Agitation
	hsa-miR-21-3p	ATP1B1				

Table S4: Top 2 Drugs associated with each of the 41 potential SARS-CoV-2 regions







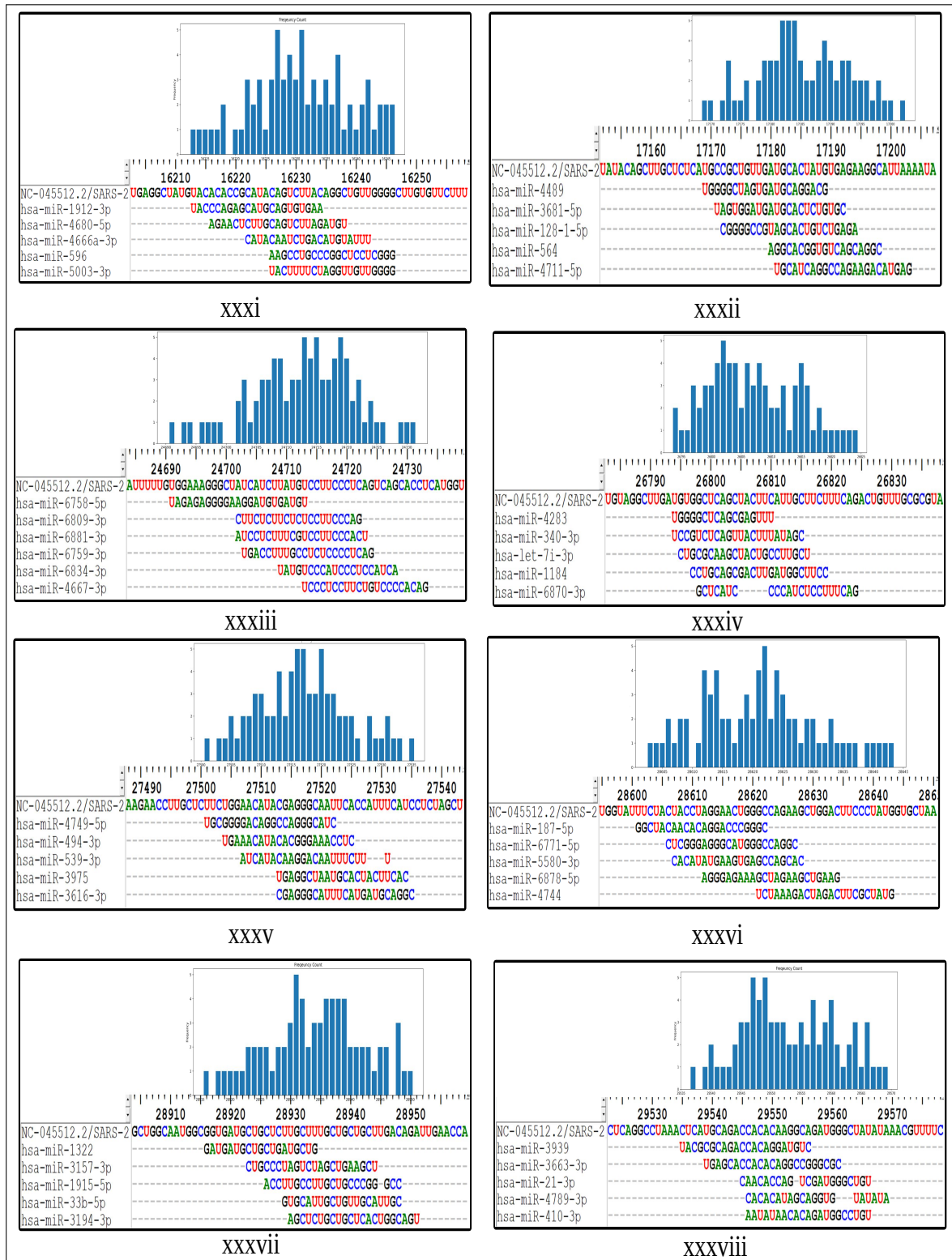
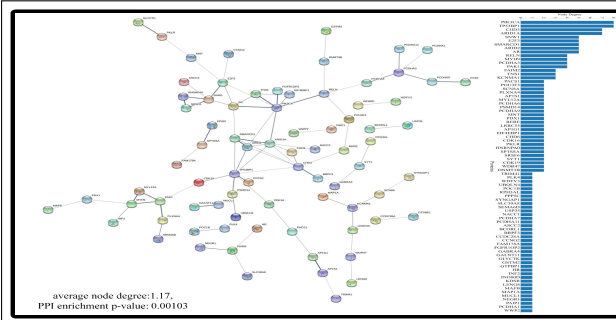
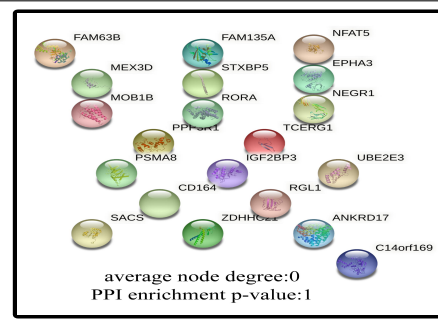


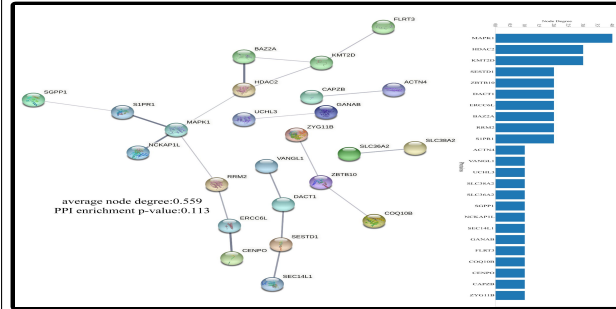
Figure S1: Alignment of the human miRNAs with the 38 potential regions of SARS-CoV-2



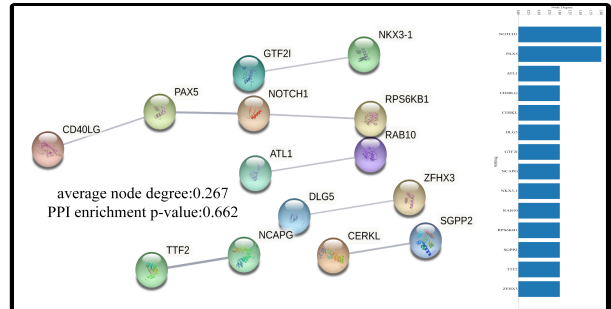
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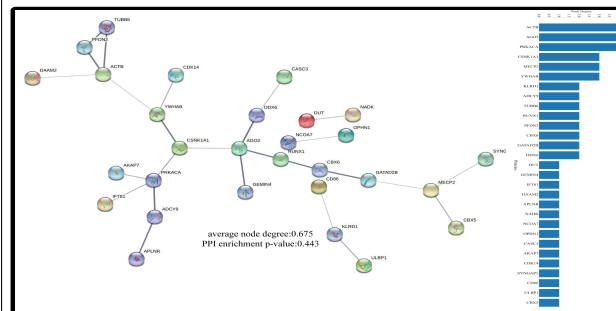
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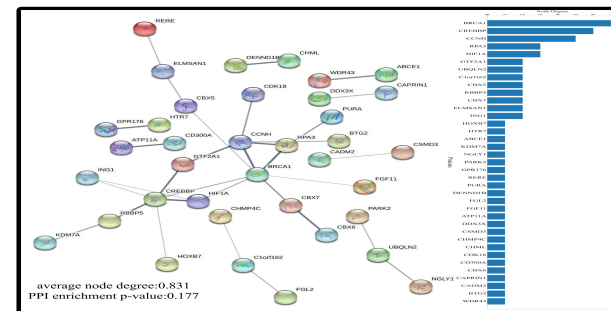
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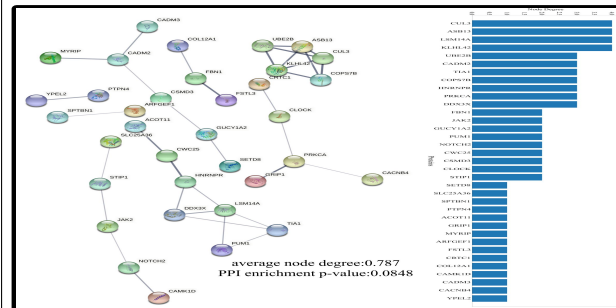
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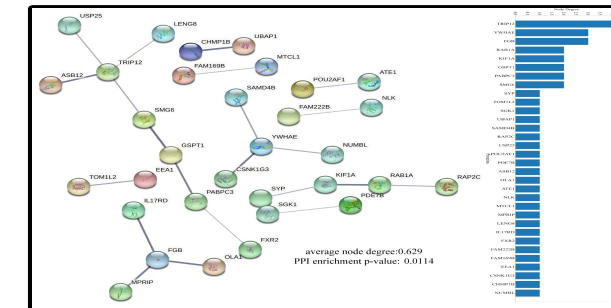
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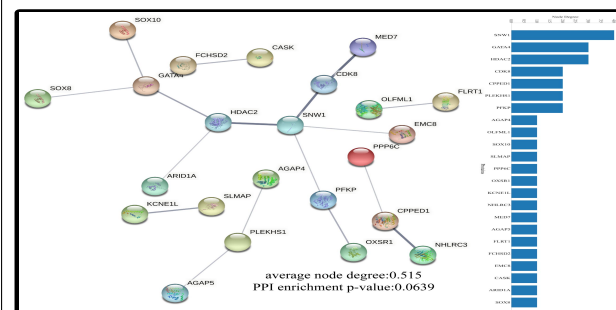
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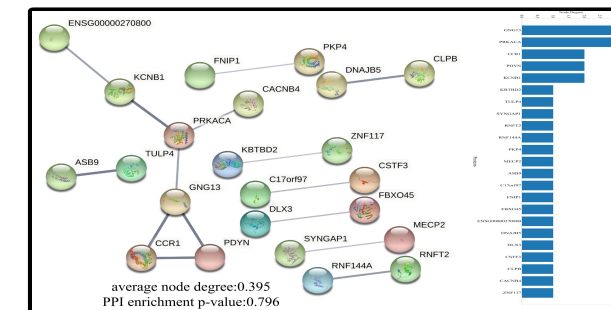
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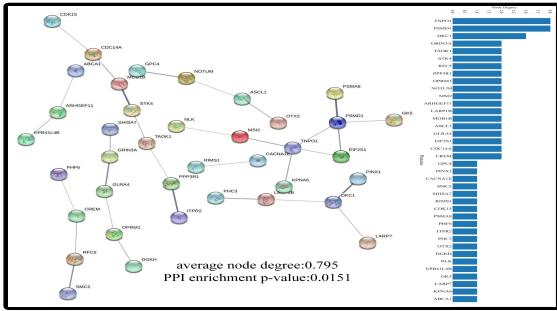
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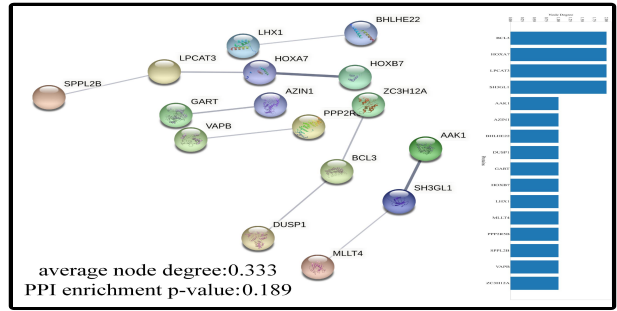
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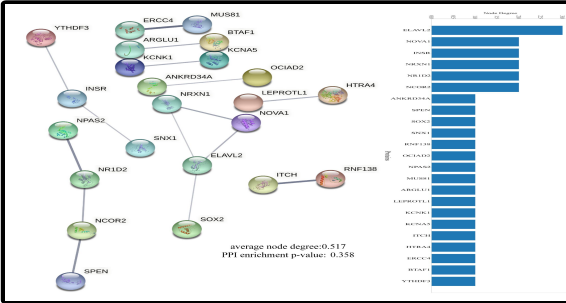
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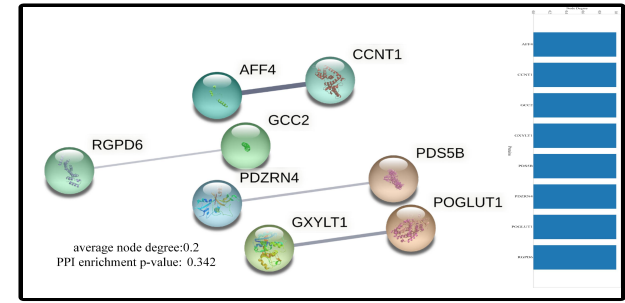
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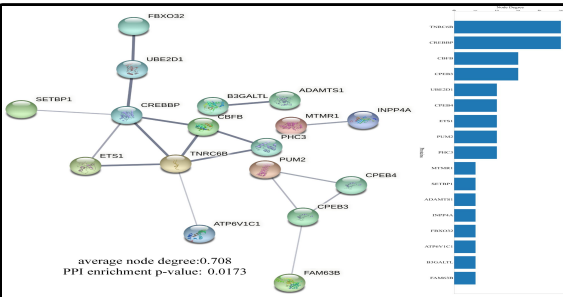
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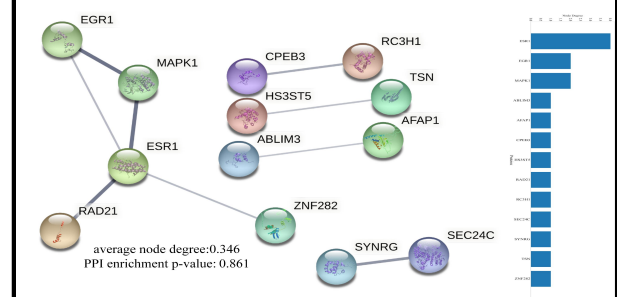
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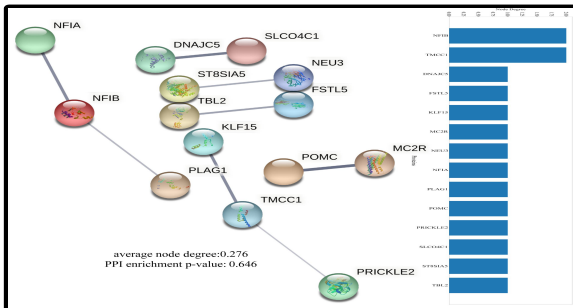
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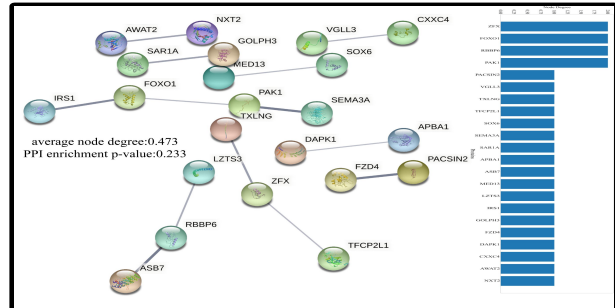
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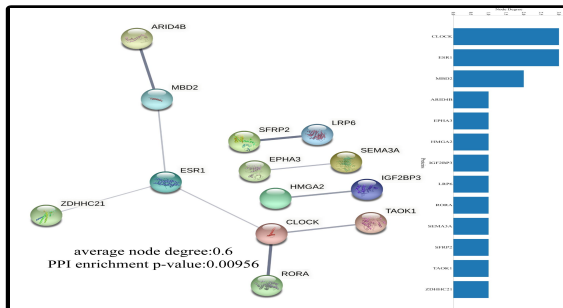
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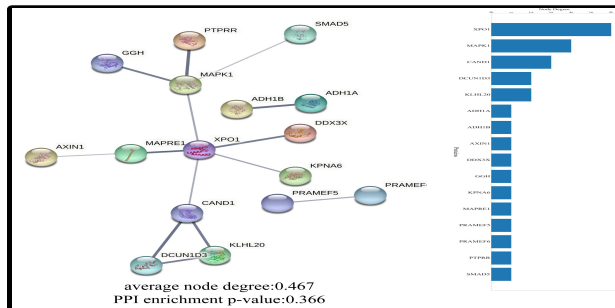
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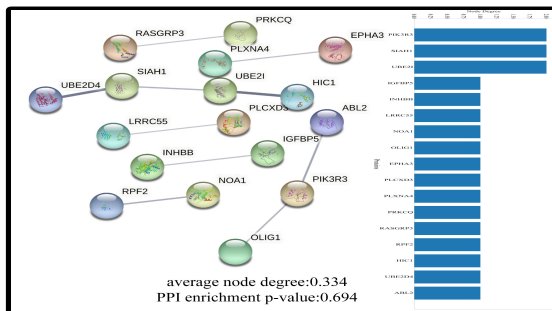
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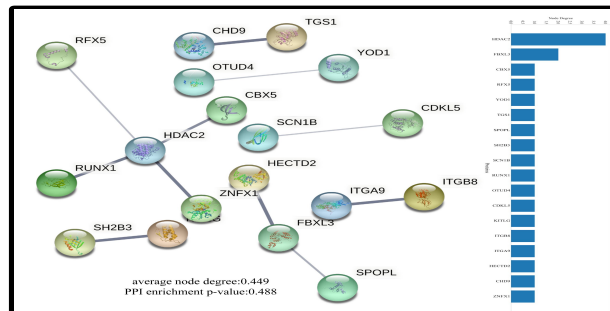
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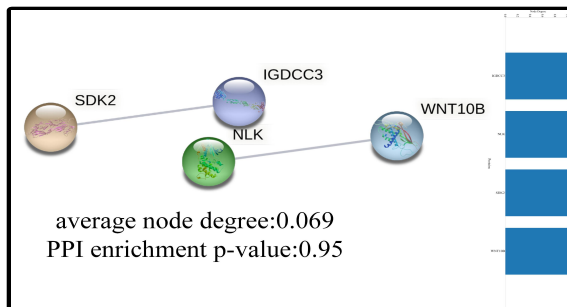
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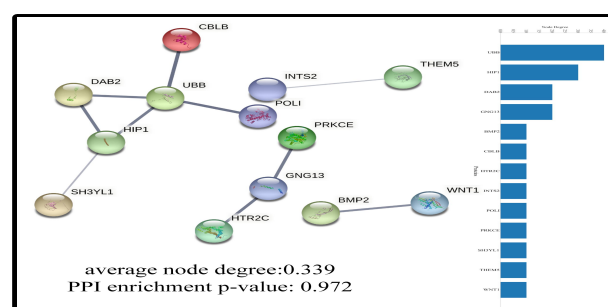
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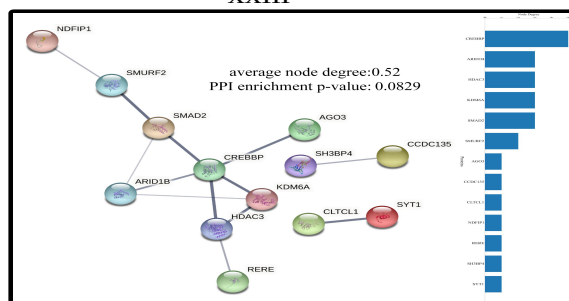
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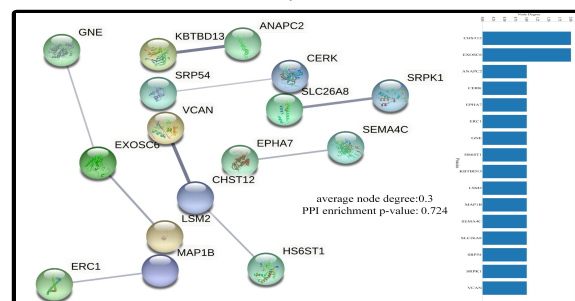
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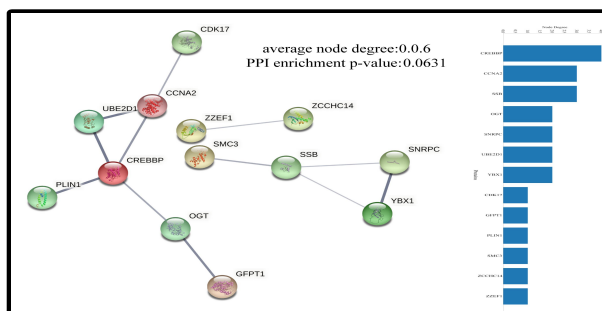
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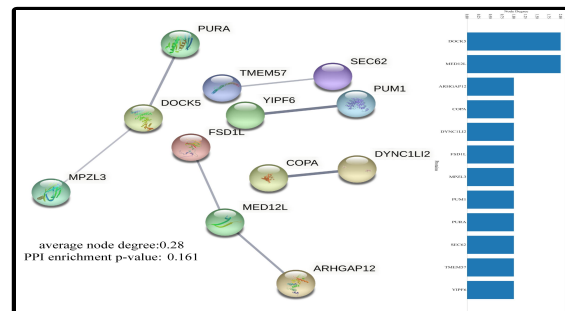
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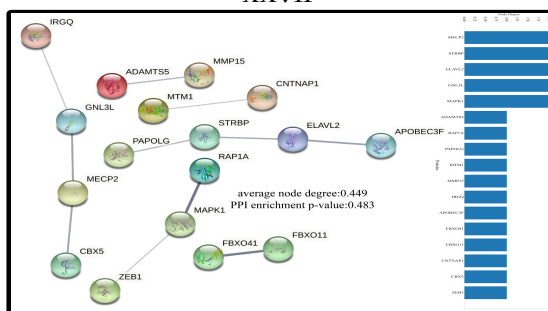
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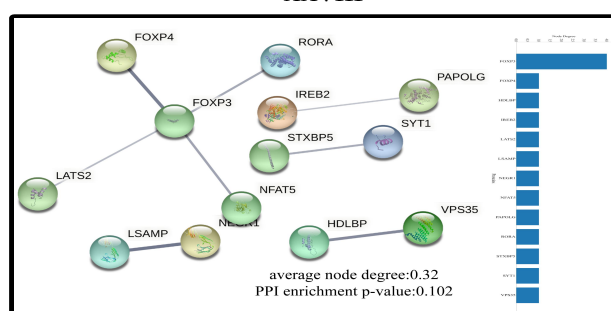
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xxviii



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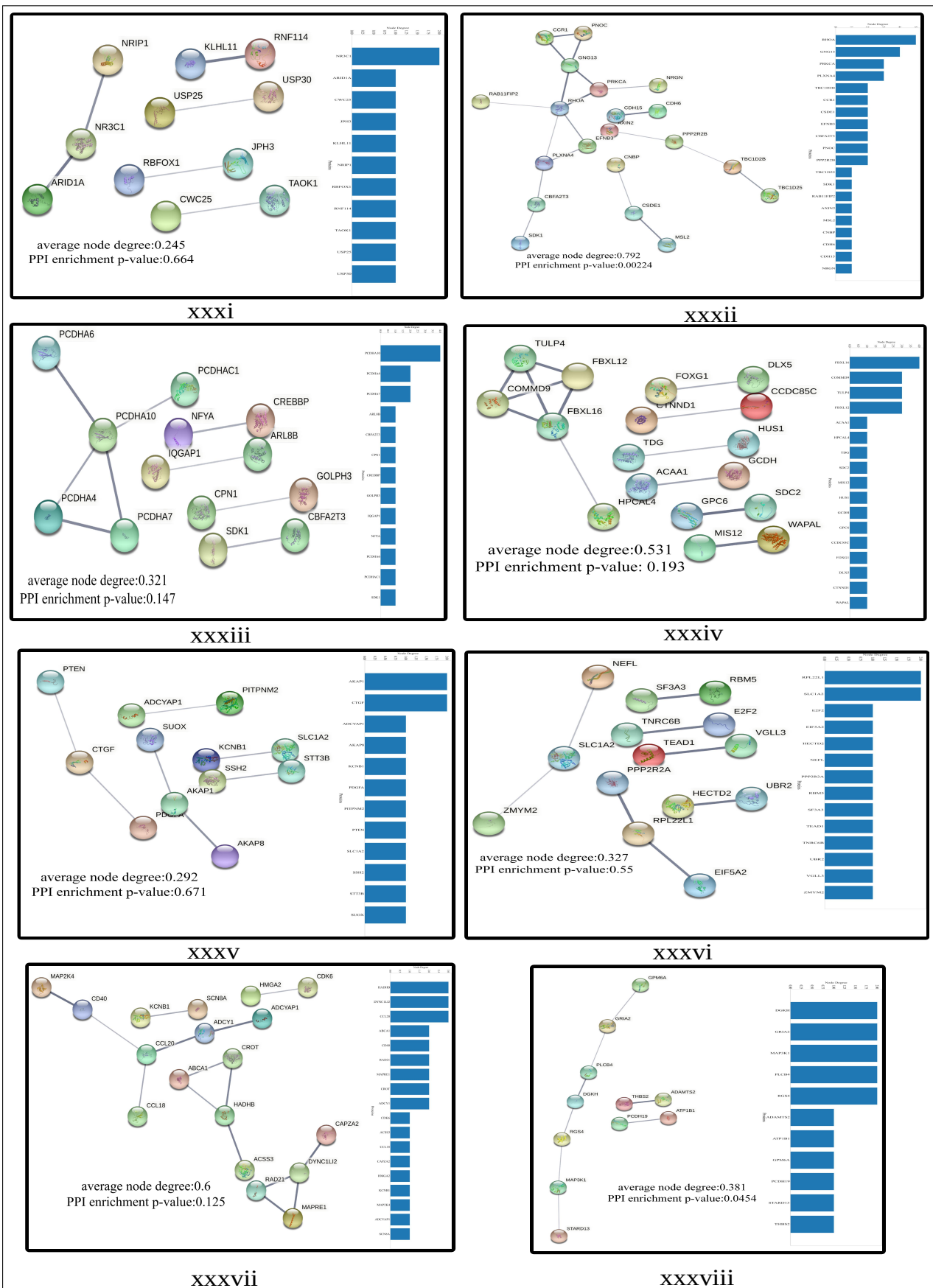


Figure S2: Protein-Protein Interactions of the 38 potential regions of SARS-CoV-2