## **Supplementary information**

## Unbiased discovery of autoantibodies associated with severe COVID-19 via genome-scale self-assembled DNAbarcoded protein libraries

In the format provided by the authors and unedited

## Contents

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pplementary Fig. 1: HaloLigand conjugation to the reverse transcription primer. a, Above he oligonucleotide reverse transcription (RT) primer sequence modified with a 5' primary ine. Below is the HaloLigand with a reactive succinimidyl ester group, separated by one ylene glycol moiety (O2). The succinimidyl ester reacts with the primary amine to form an amide-bond between the RT primer and the HaloLigand, resulting in the HaloLigand-conjugated RT primer. b, HPLC chromatogram of the RT primer without the HaloLigand modification. c, HPLC chromatogram of the RT primer with the HaloLigand modification. The conjugated product elutes later due to increased hydrophobicity conferred by the modification.



**Supplementary Fig. 2:** *Cis* versus *trans* UCI-ORF associations. Schematic of *cis* product **a**, versus *trans* side product **b**, UCI-ORF conjugation during translation of a MIPSA IVT-RNA library. **c**, Left panel: 50% *cis* conjugates ("C") composed of the correct protein-UCI associations (e.g. blue UCI with blue protein). Middle panel: unconjugated proteins then randomly associates with unconjugated UCIs in *trans* ("T"). Right panel: the ratio of correctly to incorrectly IPed UCIs in this two-species experiment is 3:1 (75%:25%), similar to experimental observations (**Fig. 2a**).



**lementary Fig. 3: Two-plex translation and IP of TRIM21 and GAPDH.** *TRIM21 APDH* (G) IVT-RNA-cDNA were translated either separately or together and then subjective.





Supplementary Fig. 5: Reproducibility and linearity of MIPSA detection of patient P2's autoantibodies. a, Mean and standard deviation of the 100 ORF fold changes for all consistently reactive monospecific UCIs (fold change > 3 in all 3 replicates). The values to the right of the error bars are the coefficients of variation. b, Numbers of overlapping reactive monospecific UCIs over three independent MIPSA analyses of P2 plasma. Areas are proportional to numbers of hits. c, Mean ORF fold changes for P2 plasma, compared to P2 plasma diluted 10-fold into a background of a healthy control plasma. Dot sizes depict the numbers of reactive UCIs corresponding to each ORF.





Supplementary Fig. 7: MIPSA analysis of interferon antibodies in serial dilution. Summary



Study Population								
G	roup	#	Age Sex		Black	White	Other	
Severe COVID-19	Died	17	67 (27,87)	F: 8, M: 9	9	4	4	
	Ventilated	13	67 (27,82)	F: 9, M: 4	4	4	5	
	Got O2	22	52 (27,82)	F: 9, M: 13	8	8	6	
	No O2	3	46 (22,49)	F: 0, M: 3	0	3	0	
COVID-19	Mild/Mod	10	35 (19,55)	F: 6, M: 4	0	8	2	
Controls	Healthy Control	10	41.5 (22,66)	F: 3, M: 7	3	5	2	
Myositis	Inclusion Body	10	53.9 (43.6,60.6)	F: 7, M: 3	1	7	2	
	Healthy Control	10	36.5 (20,60)	F: 5, M: 5	2	8	0	

**Supplementary Table 1: Severe COVID-19 patients and control study participants.** Individuals' ages were provided to investigators as intervals to protect identities of study participants.

Symbol	Gene_name	AAgAtlas	#Severe	#Controls	#Reactive_UCIs	hits_FCs	Cluster_ID
ASTL	astacin like metalloendopeptidase	no	2	1	2	5.7, (3.8,7.5)	1
BEND7	BEN domain containing 7	no	6	1	7	5.5, (3.2,16.1)	2
BLVRA	biliverdin reductase A	no	1	0	3	17.9, (17.9,17.9)	1
BMPR2	bone morphogenetic protein receptor type 2	yes	3	0	2	3.5, (3.2,4.0)	1
C1orf94	chromosome 1 open reading frame 94	no	12	0	8	5.2, (3.0,15.4)	3
C3orf18	chromosome 3 open reading frame 18	no	1	0	2	3.3, (3.3,3.3)	1
CALHM1	calcium homeostasis modulator 1	no	3	1	2	3.9, (3.3,4.4)	1
CAV2	caveolin 2	no	9	0	2	3.7, (3.1,5.0)	4
CCDC106	coiled-coil domain containing 106	no	4	0	10	4.4, (3.1,7.2)	2
CCDC146	coiled-coil domain containing 146	no	5	0	3	3.6, (3.1,4.7)	1
CD2BP2	CD2 cytoplasmic tail binding protein 2	no	2	0	3	14.9, (5.1,24.8)	5
CDC73	cell division cycle 73	no	1	0	2	4.1, (4.1,4.1)	1
CHMP7	charged multivesicular body protein 7	no	10	1	3	3.6, (3.1,4.7)	4
CTAG2	cancer/testis antigen 2	no	3	0	6	5.2, (3.0,9.4)	1
CYP2S1	cytochrome P450 family 2 subfamily S member 1	no	2	0	3	4.1, (3.2,5.0)	1
DNAJC17	DnaJ heat shock protein family (Hsp40) member C17	no	4	0	2	3.2, (3.0,3.6)	2
DOLPP1	dolichyldiphosphatase 1	no	3	0	3	4.7, (3.9,5.1)	1
EHD1	EH domain containing 1	no	2	0	14	33.4, (3.6,63.2)	1
EHD2	EH domain containing 2	no	2	0	4	4.3, (3.0,5.6)	1
ELOA2	elongin A2	no	9	0	2	3.5, (3.0,4.9)	4
EXD1	exonuclease 3'-5' domain containing 1	no	1	0	2	7.2, (7.2,7.2)	5
EXOC4	exocyst complex component 4	no	17	0	7	3.9, (3.0,4.9)	4
FAM185A	family with sequence similarity 185 member A	no	4	1	2	3.4, (3.2,3.6)	1
FAM32A	family with sequence similarity 32 member A	no	4	0	2	3.6. (3.2.4.0)	2
FBXL19	F-box and leucine rich repeat protein 19	no	2	0	3	7.0, (3.0,11.0)	1
FDFT1	farnesyl-diphosphate farnesyltransferase 1	no	1	0	2	46.8, (46.8,46.8)	1
FRG1	FSHD region gene 1	no	5	0	3	3.6, (3.2,4.3)	1
FUT9	fucosyltransferase 9	no	2	1	3	3.9, (3.5,4.3)	1
GATA2	GATA binding protein 2		5	0	2	3.6, (3.0,4.3)	4
GIMAP8	GTPase, IMAP family member 8	no	1	0	2	4.7, (4.7,4.7)	1
HNF4A	hepatocyte nuclear factor 4 alpha	no	1	0	2	11.7, (11.7,11.7)	1
HNRNPUL1	heterogeneous nuclear ribonucleoprotein U like 1	no	3	0	4	5.7, (3.6,8.6)	1
HPGD	15-hydroxyprostaglandin dehydrogenase	no	1	0	4	6.0, (6.0,6.0)	1
IFNA10	interferon alpha 10	no	2	0	5	18.8, (16.8,20.7)	2
IFNA13	interferon alpha 13	no	4	0	2	22.5, (4.6,51.4)	2
IFNA14	interferon alpha 14	no	3	0	2	19.3, (3.2,44.2)	2
IFNA2	interferon alpha 2	yes	2	0	3	42.5, (25.2,59.8)	2
IFNA21	interferon alpha 21	no	2	0	10	25.1, (14.9,35.3)	2
IFNA5	interferon alpha 5	no	2	0	3	14.6, (14.6,14.7)	2
IFNA6	interferon alpha 6	no	4	1	12	9.4, (3.3,21.8)	2
IFNA8	interferon alpha 8	no	7	0	5	9.7, (3.1,36.4)	2
IFNL3	interferon lambda 3	no	3	1	5	5.5, (4.2,7.6)	1
IFNW1	interferon omega 1	no	2	0	5	29.6, (10.6,48.5)	2
IKZF3	IKAROS family zinc finger 3	no	2	0	4	13.8, (3.3,24.2)	1
KCNJ12	potassium inwardly rectifying channel subfamily J member 12	no	1	0	2	3.1, (3.1,3.1)	1
KCNJ14	potassium inwardly rectifying channel subfamily J member 14	no	2	0	3	3.9, (3.2,4.6)	1
KLHL31	kelch like family member 31	no	1	0	2	11.3, (11.3,11.3)	2
KLHL40	kelch like family member 40	no	1	0	4	8.4, (8.4,8.4)	2
LALBA	lactalbumin alpha	no	1	0	2	3.9, (3.9,3.9)	1
LINC01547	long intergenic non-protein coding RNA 1547	no	2	0	6	19.3, (3.4,35.1)	1
MAGEE1	MAGE family member E1	no	1	0	3	17.9, (17.9,17.9)	1

**Supplementary Table 2: Proteins reactive in severe COVID-19 patients.** Symbol, gene symbol; AAgAtlas, is protein listed in AAgAtlas 1.0?; #Severe, number of severe COVID-19 patients with reactivity to at least one UCI; #Controls, number of control donors (healthy or mild-moderate COVID-19) with reactivity to at least one UCI; #Reactive\_UCIs, number of reactive UCIs associated with given ORF; Hits\_FCs, mean and range (minimum to maximum) of per-ORF maximum hits fold-change observed among the patients with the reactivity; Cluster\_ID, antigen cluster defined by Fig 4b.

MAX     MYC associated factor X     no     7     0     10     13.0, (31.20.9)     3       MBO3L1     mohawk homeobox     no     6     1     3     3.8, (31.4)     4       MKX     mohawk homeobox     no     6     1     3     3.8, (31.4)     4       MPED2     metalphosphosetrase domain containing 2     no     5     0     3     5.2, (3.1, 17, 1     1       NACG1     nucleus accumbers associated 1     no     1     0     2     6.8, (6.9, 6.9, 0)     1       NPF1F     NPFP member 15     no     1     0     2     8.3, (3.5, 1, 1     1       NVC1     nucleoptorin 62     no     1     0     2     9.0, (2.8, 9.3)     5       NVL1     nucleoptorin 62     no     1     0     2     9.0, (2.8, 9.3, (3.5, 1)     1       NVL1     nucleoptorin 62     no     1     0     2     9.0, (2.8, 9.2, (2.7, 9.2, 9.7)     1       NVL4     nucleoptorin 62     no     1     0     2	Symbol	Gene_name	AAgAtlas	#Severe	#Controls	#Reactive_UCIs	hits_FCs	Cluster_ID
MBD3L1     methyl-CpC binding domain protein 3 like 1     no     2     0     5     8, 1, 1, 1, 12, 2     1       MMPE     meallaphosphosetarase domain containing 2     no     5     0     3     3, 8, 31, 4.8     4       MPPED     meallaphosphosetarase domain containing 2     no     5     0     12     74, 17, 77, 25     5       NAPSA     napsin A sagnatic peptidase     no     3     1     0     2     6, 69, 89, 91       NAPFA     NAPF member 15     no     1     0     2     8, (3, 4, 8, 1     1       NUCOT     NOPPH oxidase organizer 1     no     3     1     2     29, (7, 29, 9)     5       NULPE     nucleoporin 62     no     1     0     7     8, (8, 4, 8, 1     1       NULPE     nucleoporin 62     no     1     0     7     8, (8, 4, 8, 1     1       NULPE     nuclear 00 file     no     1     0     2     216, (2, 6, 20, 5)     1       NULPE     nucleaporin 62     no     1 <t< td=""><td>MAX</td><td>MYC associated factor X</td><td>no</td><td>7</td><td>0</td><td>10</td><td>13.0, (3.1,30.9)</td><td>3</td></t<>	MAX	MYC associated factor X	no	7	0	10	13.0, (3.1,30.9)	3
MXX     mohawk homebox     no     6     1     3     38, (31, 48)     4       MPED2     mellaphosphosebrase domain containing 2     no     5     0     3     52, (3, 11, 7)     1       NACG1     nucleus accumbens associated 1     no     0     3     1     3     41, (3, 14, 7)     1       NBPF1     NBPF member 1     no     3     0     6     39, (3, 6, 8, 6, 8)     1       NDK0     NADPH stratege april associates organizer 1     no     3     0     6     39, (3, 4, 8, 4)     1       NUC     nuclear VCP like     no     1     0     28, (7, 25, 25)     5       NUVE     nuclear VCP like     no     1     0     216, (21, 62, 16, 21, 62, 16, 21, 62, 16, 21, 62, 16, 21, 62, 16, 21, 62, 16, 21, 62, 16, 22, 62, 17, 16, 11, 74, 72, 72, 71     1       NUVE     nuclear VCP like     no     1     0     429, (29, 72, 72, 71, 12, 72, 71     1       PLEKIF1     pleckstrin homology and FVVE domain containing 1     no     2     0     5, 74, (4, 74, 72, 22, 72, 71     1       PMMAS <td>MBD3L1</td> <td>methyl-CpG binding domain protein 3 like 1</td> <td>no</td> <td>2</td> <td>0</td> <td>5</td> <td>8.1, (4.1,12.2)</td> <td>1</td>	MBD3L1	methyl-CpG binding domain protein 3 like 1	no	2	0	5	8.1, (4.1,12.2)	1
MPPED2     metallophosphosestrase domain containing 2     no     5     0     3     5, 2, 3, 1, 1, 7, 7, 2, 7     1       NACC1     nucleus accumbers associated 1     no     2     0     12     74.9, (24, 77.52)     5       NAPSA     nappin A appric peptidase     no     1     0     2     35, (35.35, 1     1       NNPF1     NNPF member 15     no     1     0     2     35, (35.36, 1     1       NNCO1     NAPPH oxidase organizer 1     no     3     1     2     28, (21.69, 1     1       NUFPE2     nucleoporin 62     no     1     0     7     84, (8.44, 1     1       NUL     nucleoporin 62     no     1     0     2     216, (21.621.6)     1     1       NUFE4     nucleoporin 62     no     1     0     3     33, (31.3, 1     1       NUFE4     PLKHFI     plexetrin homology ond FV2 domain containing 1     no     1     0     3     33, (31.3, 1     1       PLKHFI     PLKHFI     plexetrin	MKX	mohawk homeobox	no	6	1	3	3.8, (3.1,4.8)	4
NACC1     nucleus accumbens associated 1     no     2     0     1     12     748,(74,752)     5       NAPFA     nappin A spart(peppidse     no     3     1     0     2     68,(69,69,0)     1       NBPFT     NBPF member 1     no     1     0     2     68,(69,69,0)     1       NDV0     NADPH oxidase organizer 1     no     3     0     6     39,(30,48)     1       NTSC1A     S'nucleotofas c/bosici (A     no     3     1     0     269,(72,529)     5       NUP     nucleaporin 62,000 ici (A     no     1     0     2     128,(21,62,16)     1       QLFMA     offactomedin 4     yes     5     1     3     32,9,(3,3,5)     1       PLKHF     pleckstim homology and FVE domain containing 1     no     2     0     3     3,3,(3,1,3)     1       PLKHF     pleckstim homology and FVE domain containing 1     no     2     0     3     3,3,(3,1,3,1     1       PLKHF     pleckstim homology and FVE domain containi	MPPED2	metallophosphoesterase domain containing 2	no	5	0	3	5.2, (3.1,11.7)	1
NAPSA     napsin A aspartic peptidase     no     3     1     3     4.1, (3.1, 4.7)     1       NBPFI     NBPF member 15     no     1     0     2     35, (3.5.6)     1       NNDVOI     NADPH oxidase organizer 1     no     3     0     6     39, (3.0.4.8)     1       NVCOI     NADPH oxidase organizer 1     no     3     1     2     28, (7.2.5.9.9)     5       NUP62     nuclear VCP like     no     1     0     7     84, (8.4.4.4)     1       NUL     nuclear VCP like     no     1     0     2     216, (21.6.21.6)     1       PLKHFI     plecktrin homology and FVV domain containing 1     no     2     0     3     3, (3.1.3.1     1       PLKHFI     plecktrin homology and FVV domain containing 1     no     2     0     3     3, (3.1.3.1     1       PLKHFI     plecktrin homology and FVV domain containing 1     no     1     0     3     3, (3.1.3.1     1       POLKHF     poly and hymember 5     no     <	NACC1	nucleus accumbens associated 1	no	2	0	12	74.9, (74.7,75.2)	5
NBPF1     NBPF member 1     no     1     0     2     6,6,6,8,6,9     1       NOXO1     NADPF control 15     no     1     0     2     2,6,(5,5,5)     1       NOXO1     NADPF control 15     no     3     0     6     3,9,(3,0,4,8)     1       NUFex     nucleopoint 62     no     1     0     7     8,4,(6,4,8,4)     1       NUV     nuclear VCP like     no     1     0     2     216,(21,62,1,6)     1       OLFAM     olfactomedin 4     yes     5     1     3     12,9,(4,228,1)     1       PMMEG     Plockstin homology and FVVE domain containing 1     no     2     0     3     3,(1,3,5)     1       PMA     PMMA Emily member 1     yes     1     0     3     6,4,6,4,1     2       POLDP3     DNA byenyerase deta interacting protein 3     no     5     0     3     3,2,1,3,7     4       POUDP3     DNA byenyemese deta interacting notein 3     no     1     0     3 <td< td=""><td>NAPSA</td><td>napsin A aspartic peptidase</td><td>no</td><td>3</td><td>1</td><td>3</td><td>4.1, (3.1,4.7)</td><td>1</td></td<>	NAPSA	napsin A aspartic peptidase	no	3	1	3	4.1, (3.1,4.7)	1
NBPF     member 15     no     1     0     2     3,5,3,5,3,5,1     1       NXOX01     NADPH oxidase organizer 1     no     3     1     2     26,9,(72,59,9)     5       NTFG1A     5'nucleonidase, cytosolic IA     no     1     0     7     84,(46,84,4)     1       NVE     nuclear VCP like     no     1     0     2     21,6,(21,82,18,5,1)     1       OLFMA     Offactomin 4     yes     5     1     3     3,2,3,1,3,5     1       PLEKHT     pleckstin homology and FVVE domain containing 1     no     4     1     4,8,2,7,2,9,7     1       PIMA     PMMA Mamily member 5     no     2     0     5     5,7,(40,7,4)     2       POLDP3     DNA polymerase delta intracting protein 3     no     1     0     2     3,3,3,3,1,3,5)     1       POMP     protein kinase cAMP-dependent ype 11 regulatory subunit beta     no     1     0     3     3,2,3,2,2     1       POBP1     protein kinase cAMP-dependent ype 11 regulatory subunit beta	NBPF1	NBPF member 1	no	1	0	2	6.9, (6.9,6.9)	1
NXXC1     NADPH oxidase organizer 1     no     3     0     6     39, (30, 4.8)     1       NUF62     nucleopoin 62     no     1     0     7     8.4, (64, 8.4)     1       NVL     nucleopoin 62     no     1     0     2     216, (21, 62, 16, 9)     1       NVL     nucleopoin 62     no     1     0     2     216, (21, 62, 16, 9)     1       OLFM4     Olfactomedin 4     yes     5     1     3     129, (44, 29, 8)     5       PIMERC     PICALM Interacting mitolic regulator     no     4     1     4     36, (3, 6, 4, 1     2       PIMM1     PMMA family member 1     yes     1     0     3     64, (4, 64, 4)     2       POMP     proteasom maturation protein 3     no     5     0     3     32, (3, 13, 7)     4       POUEF1     POUEf1     POUE145     no     1     0     1     20, (12, 12, 0)     1       POUEF1     potyplutamine binding protein 1     no     1     0	NBPF15	NBPF member 15	no	1	0	2	3.5, (3.5,3.5)	1
NT5C1A     5'-nucleotase, cytosolic IA     no     3     1     2     289, (72,899)     5       NUFez     nucleaportin 62     no     1     0     7     84, (84,84)     1       NUFez     nuclear VCP like     no     1     0     2     216, (21, 621, 61)     1       OLFMA     olfactomedin 4     yes     5     1     3     129, (42, 28, 35, 1)     1       PLREHFI     pleckinth monology and PTVE domain containing 1     no     2     0     3     33, (31, 35, 1)     1       PNMA     PNNA family member 1     yes     1     0     4     29, (72, 29, 72, 72, 72, 72, 72, 72, 72, 72, 72, 72	NOXO1	NADPH oxidase organizer 1	no	3	0	6	3.9, (3.0,4.8)	1
NUFE     nudeopoint 62     no     1     0     7     84, (8,48,4)     1       OLFM     oldear VCP like     no     1     0     221, (4,29,8)     5       PIMREG     PICALM interacting milotic regulator     no     4     1     4     38, (3,5,4,3)     1       PLKHF     plexktrif     plexktrif     no     2     0     3     3, (1,3,5)     1       PMA     PMNA family member 1     yes     1     0     4     297, (297, 297, 207, 1       PNMAT     PNMA family member 3     no     5     0     3     3, (1,3,7)     4       POLDIP3     DNA polymerase deta interacting protein 3     no     5     0     3     3, (1,3,7)     4       POUEF1     Polyaluamine binding protein 1     no     1     0     3     7, (3,7,3,7)     1       PCMEN     polyaluamine binding protein 17     no     1     0     3     3, (3,1,3,7)     1       PCMAR     Portein kinase ACMP-dependent type II regulatory subunit bita     no     4     <	NT5C1A	5'-nucleotidase, cytosolic IA	no	3	1	2	26.9, (7.2,59.9)	5
NVL OLFM4     Indea/VCP like     no     1     0     2     216,(21216)     1       PIMREG     PICALM Interacting mitotic regulator     no     4     1     4     38, (35,41)     1       PLEKHF1     pleckstin homology and FVVE domain containing 1     no     2     0     3     3, (3, 13, 15)     1       PLEKHF1     pleckstin homology and FVVE domain containing 1     no     2     0     3     64, (64, 64)     2       PNMA     PNMA family member 1     yes     1     0     3     64, (64, 64)     2       POLDP3     DNA polymerase delta interacting protein 3     no     5     0     3     3, (3, 13, 7)     4       POMP     proteasome maturation protein 1     no     1     0     3     12, (12,012.0)     1       POMP     proteasome maturation protein 1     no     1     0     3     23, (3, 23, 5)     1       PRAR2B     protein kinase CAMP-dependent type II regulatory subunit beta     no     1     0     3     23, (5, 3, 5, 3)     1       PR	NUP62	nucleoporin 62	no	1	0	7	8.4, (8.4,8.4)	1
OLFMA     Offactomedin 4     yes     5     1     3     12.9.(44.29.8)     5       PIMREG     PICALM interacting mitoic regulator     no     4     1     4     3.8.(35.4.1)     1       PML     PML nuclear body scafiold     no     1     0     4     29.7.(29.7.29.7)     1       PMMA     PMMA family member 1     yes     1     0     3     6.4.(6.4.6.4)     2       PNMAS     PNMA family member 5     no     2     0     5     5.7.(40.7.4)     2       POLDIP     DNA polymerase delta interacting protein 3     no     1     0     2     3.2.(31.3.7)     4       POMF1     POUG class 6 homeobox 1     no     1     0     3     12.0.(12.0.12.0)     1       POBP1     polygitatimic binding protein 1     no     1     0     3     12.3.(31.3.1)     1       PON     protein kinase cAMP-dependent type II regulatory subunit beta     no     1     0     3     5.3.(5.3.5.3)     1       RCAN anity member 3     no     1	NVL	nuclear VCP like	no	1	0	2	21.6, (21.6,21.6)	1
PIMBEG     PICALM interacting mitotic regulator     no     4     1     4     38, (3, 5, 4.1)     1       PLEKHFI     oekstrin homology and FYVE domain containing 1     no     2     0     3     33, (3, 13, 5)     1       PNIA     PMMA tamily member 1     yes     1     0     3     64, (6, 46, 4)     2       PNIAS     PNMA family member 5     no     2     0     3     33, (3, 13, 7)     4       POLDP3     DNA polymerase delta interacting protein 3     no     1     0     2     3, (2, 2, 2)     1       POLF1     POU dess 6 homeobox 1     no     1     0     3     12,0,(12,0,12,0)     1       POEP1     POU dess 6 homeobox 1     no     1     0     3     73, (73,73)     1       POER1     POUglutamine binding protein 17     no     1     0     3     2, (20, 8,2)     1       RCAN a     RCAN tamily member 3     no     1     1     5     3, (3, 1,3,9)     3       RP143 ribosomal protein 13     no     1	OLFM4	olfactomedin 4	yes	5	1	3	12.9, (4.4,29.8)	5
PLEKHF1     plecktrin     plecktrin     plecktrin     polektrin     no     2     0     3     33, (31,35)     1       PML     PML nuclear body scaffold     no     1     0     4     297, (297, 297)     1       PNMA1     PNMA family member 1     yes     1     0     3     64, (64, 64, 2     2       PNMA5     PNMA4 family member 5     no     2     0     5     57, (40,7,4)     2       POLDIP     DNA polymerase delta interacting protein 3     no     1     0     3     33, (31,37)     4       POUBF1     POUdess 6 homesbox 1     no     1     0     3     73, (73, 73, 7)     1       POUBF1     Polyglutamine binding protein 1     no     1     0     3     73, (73, 73, 7)     1       POR1     polyglutamine binding protein 17     no     1     0     3     23, (23, 62, 63)     1       RCAN3     RCAN family member 3     no     4     1     5     34, (31, 37)     1       RPL15     ribosomal	PIMREG	PICALM interacting mitotic regulator	no	4	1	4	3.8, (3.5,4.1)	1
PML     PML nuclear body scaffold     no     1     0     4     297, (29.7, 29.7)     1       PNMA1     PNMA5 family member 1     yes     1     0     3     6.4, (6.4, 6.4)     2       PNMA5     PNMA5 family member 5     no     2     0     5     5.7, (4.0, 7.4)     2       POLDP3     DNA polymerase deta interacting protein 3     no     5     0     3     3.3, (3.1, 3.7)     4       POMP     proteasome maturation protein     no     1     0     3     1.20, (12.0, 12.0)     1       POUBP1     polyglutamine binding protein 1     no     1     0     3     7.3, (7.3, 7.3)     1       PXAR2B     protein kinase cAMP-dependent type Il regulatory subunit beta     no     1     0     3     2.6, (23.6, 23.6)     1       PXAR2B     protein kinase cAMP-dependent type Il regulatory subunit beta     no     1     0     3     3.6, (3.1, 3.9)     2       REM17     RNA binding motif protein 17     no     1     0     4     4.6, (4.6, 1.0)     1     1	PLEKHF1	pleckstrin homology and FYVE domain containing 1	no	2	0	3	3.3, (3.1,3.5)	1
PNMA1     PNMA family member 1     yes     1     0     3     6.4 (6.4.6.4)     2       PNMA5     PNMA5 polymerase della interacting protein 3     no     2     0     5     5.7 (4.0,7.4)     2       POLDP3     DNA polymerase della interacting protein 3     no     1     0     2     3.2, (3.2,3.2)     1       POMP     proteasome maturation protein     no     1     0     2     3.2, (3.2,3.2)     1       POMP1     polygiutamine binding protein 1     no     1     0     3     7.2, (7.3,7.3)     1       PCBP1     polygiutamine binding protein 1     no     1     0     3     2.6, (3.3,6.23.6)     1       PKAR2B     protein kinase cAMP-dependent type II regulatory subunit beta     no     1     0     3     2.6, (3.3,6.23.6)     1       PKAN2B     protein kinase cAMP-dependent type II regulatory subunit bata     no     1     0     4     3.5, (3.1,3.9)     2       RCAN3     RCAN tamily member 3     no     1     0     4     3.4, (3.1,3.7)     1 <t< td=""><td>PML</td><td>PML nuclear body scaffold</td><td>no</td><td>1</td><td>0</td><td>4</td><td>29.7, (29.7, 29.7)</td><td>1</td></t<>	PML	PML nuclear body scaffold	no	1	0	4	29.7, (29.7, 29.7)	1
PNMA5     PNMA tamily member 5     no     2     0     5     5.7, (40.7.4)     2       POLDIP3     DNA polymerase delta interacting protein 3     no     5     0     3     3.3, (3.1, 3.7)     4       POMP     proteasome maturation protein 1     no     1     0     2     3.2, (2.3.2)     1       POUF1     POU class 6 homeobox 1     no     1     0     3     12.0, (12.0, 12.0)     1       POBP1     polyglutamine binding protein 1     no     5     0     2     3.2, (3.0.35)     5       PRKAR2B     protein kinase cAMP-dependent type II regulatory subunit beta     no     1     0     3     7.3, (7.3.7.3)     1       PXDNL     peroxidasin like     no     1     0     3     23.6, (23.6.2.8.6)     1       RCAN     RCAN tamily member 3     no     1     0     4     3.4, (3.1.3.7)     1       RP13APS     ribosomal protein L15     no     11     1     6     35.9, (35.9.35.9)     1       RP214     ribonuclease PMRP subunit p14 </td <td>PNMA1</td> <td>PNMA family member 1</td> <td>ves</td> <td>1</td> <td>0</td> <td>3</td> <td>6.4, (6.4,6.4)</td> <td>2</td>	PNMA1	PNMA family member 1	ves	1	0	3	6.4, (6.4,6.4)	2
POLDIP3     DNA polymerase delta interacting protein 3     no     5     0     3     (3, (3, 1, 3, 7))     4       POMP     proteasome maturation protein     no     1     0     2     3, (3, (1, 2, 12, 0))     1       POUGF1     POUdplans     Formeabox 1     no     1     0     3     (12, 0, (12, 0, 12, 0))     1       PQBP1     polyglutamine binding protein 1     no     1     0     3     (73, 73, 73, 1)       PXDNL     peroxidasin like     no     1     0     3     (23, (23, 62, 36), 1)       PXDNL     peroxidasin like     no     1     0     3     (23, (23, 62, 36), 1)       PXDNL     peroxidasin like     no     1     0     5     5, (3, (53, 5, 3), 1)       PXDNL     peroxidasin like     no     11     1     6     34, (31, 3, 9)     3       RP134     ribosomal protein L15     mo     11     1     6     34, (31, 3, 9)     3       RP14     ribonuclease PMRP subunit p14     no     1     0     4	PNMA5	PNMA family member 5	no	2	0	5	5.7, (4.0,7.4)	2
POMP     proteasome maturation protein     no     1     0     2     3.2, (3.2, 3.2, )     1       POUBF1     POU class 6 home obox 1     no     1     0     3     12.0, (12.0, 12.0)     1       POBP1     polyglutamine binding protein 1     no     5     0     2     3.2, (3.0, 3.5)     5       PRKAR2B     protein kinase cAMP-dependent type II regulatory subunit beta     no     1     0     3     7.3, (7.3, 7.3)     1       PXDNL     peroxidasin like     no     1     0     3     2.8, (2.3, 6.2, 6.2, 6.6, 6.1)     1       RCAN family member 3     no     1     0     5     5.3, (5.3, 5.3)     1       RPL13AP3     ribosomal protein L13 pseudogene 3     no     11     1     6     3.4, (3.1, 3.9)     3       RPP13 ribonuclease PMRP subunit p14     no     1     0     4     46.1, (46.1, 46.1, 46.1)     1       RUFY4     RUN and FYVE domain containing 4     no     1     0     4     16.3, (5.3, 5.3)     1       SNR41     Small nuclear ribonuclease P	POLDIP3	DNA polymerase delta interacting protein 3	no	5	0	3	3.3, (3.1,3.7)	4
POU6F1     POU class 6 homeobox 1     no     1     0     3     12.0, (12.0, 12.0)     1       PQBP1     polyglutamine binding protein 1     no     5     0     2     3.2, (3.0, 3.5)     5       PRKAR2B     protein kinase CAMP-dependent type II regulatory subunit beta     no     1     0     3     7.3, (7.3, 7.3)     1       PXDNL     peroxidasin like     no     1     0     3     23.6, (23.6, 23.6)     1       RCAN3     RCAN family member 3     no     1     0     3     23.6, (23.6, 23.6)     1       RPL135     ribosomal protein L13     pseudogene 3     no     1     1     6     3.4, (3.1.3)     3       RPL15     ribosomal protein L15     no     11     1     6     3.4, (3.1.3)     1       RPP30     ribonuclease PMRP subunit p14     no     1     0     4     46.1, (46.1, 46.1)     1       RUFY4     RUN and FVVE domain containing 4     no     1     0     4     7.5, (7.5, 7.5)     1       SNRP14     smal	POMP	proteasome maturation protein	no	1	0	2	3.2, (3.2,3.2)	1
POBP1     polyglutamine binding protein 1     no     5     0     2     3.2, (3.0,3.5)     5       PRRAR2B     protein kinase cAMP-dependent type II regulatory subunit beta     no     1     0     3     7.3, (7.3,7.3)     1       PXDNL     peroxidasin like     no     4     0     4     3.5, (3.1,3.9)     2       RBM17     RNA binding motif protein 17     no     1     0     3     23.6, (23.6,23.6)     1       RCAN3     RCAN family member 3     no     1     0     5     5.3, (53.5,3)     1       RPL13AP3     ribosomal protein L15     no     11     1     6     3.4, (3.1,3.7)     1       RP14     ribosomal protein L15     no     11     0     6     35.9, (35.9,35.9)     1       RP44     ribonuclease PMRP subunit p30     no     1     0     4     16.1, (146.1, 46.1)     1       SNPFA1     small nuclear irbonucleoprotein polypeptide A'     no     1     0     2     5.3, (53.5.3)     1       SNPA1     small nuclear irbonu	POU6F1	POU class 6 homeobox 1	no	1	0	3	12.0, (12.0,12.0)	1
PRKAR2B     protein kinase cAMP-dependent type II regulatory subunit beta     no     1     0     3     7.3, (7.3, 7.3)     1       PXDNL     peroxidasin like     no     4     0     4     3.5, (3.1, 3.9)     2       RBM17     RNA binding motif protein 17     no     1     0     3     2.5, (2.3, 6.2.3, 6.2.3, 6.5.3)     1       RCAN3     RCAN family member 3     no     1     0     5     5.3, (5.3, 5.3)     1       RPL135     ribosomal protein L13 a pseudogene 3     no     1     1     6     3.4, (3.1, 3.9)     3       RPP14     ribosomal protein L15     no     11     1     6     3.4, (3.1, 3.9)     3       RPP14     ribosomal protein L15     no     1     0     4     46.1, (46.1, 46.1)     1       RUFY4     RUN and FYVE domain containing 4     no     1     0     2     5.3, (5.3, 5.3)     1       SNRPA1     small proline rich protein 1B     no     1     0     4     7.5, (7.5, 7.5)     1       SYT2     spern-tail P	PQBP1	polyglutamine binding protein 1	no	5	0	2	3.2, (3.0,3.5)	5
PXDNL     peroxidasin like     no     4     0     4     35, (3, 1, 3, 9)     2       RBM17     RNA binding motif protein 17     no     1     0     3     23, 6, (23, 6, 33, 6, 1, 10, 10, 10, 10, 10, 10, 10, 10, 10,	PRKAR2B	protein kinase cAMP-dependent type II regulatory subunit beta	no	1	0	3	7.3, (7.3,7.3)	1
RBM17     RNA binding motif protein 17     no     1     0     3     23.6, (23.6, 23.6)     1       RCAN3     RCAN family member 3     no     1     0     5     5.3, (5.3, 5.3)     1       RPL13AP3     ribosomal protein L13 pseudogene 3     no     4     1     5     3.4, (3.1, 3.7)     1       RPL15     ribosomal protein L15     no     11     1     6     3.4, (3.1, 3.9)     3       RPP14     ribonuclease PMRP subunit p14     no     1     0     4     46.1, (46.1, 46.1)     1       RUFY4     RUN and FYVE domain containing 4     no     1     0     4     16.3, (16.3, 16.3)     1       SNPRA1     small nuclear ribonucleoprotein polypeptide A'     no     1     0     4     7.5, (7.5, 7.5)     1       SPRF1B     small proline rich protein 1B     no     1     0     4     7.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.6, 3.6)     1       TFAP4     transcription factor AP-4	PXDNL	peroxidasin like	no	4	0	4	3.5. (3.1.3.9)	2
RCAN3     RCAN family member 3     no     1     0     5     5,3, (5,3,5,3)     1       RPL13AP3     ribosomal protein L13a pseudogene 3     no     1     1     5     3,4, (3,1,3,7)     1       RPL15     ribosomal protein L15     no     11     1     6     3,4, (3,1,3,9)     3       RPP14     ribonuclease P/MRP subunit p14     no     1     0     6     35,9, (35,9,35,9)     1       RUF34     RUN and FYVE domain containing 4     no     1     0     4     46,1, (46,1,46,1)     1       RUF44     RUN and FYVE domain containing 4     no     1     0     2     5,3, (53,5,3)     1       SNRPA1     small nuclear ribonucleoprotein polypetide A'     no     1     0     2     5,9, (32,8,5)     1       SPRH18     small proline rich protein 1B     no     1     0     4     7,5, (7,5,7,5)     1       SYR13     Sperm-tail PG-rich repeat containing 3     no     1     0     5     3,4, (3,1,4)     1       SYT2     synaptotagmin 2 <td>RBM17</td> <td>RNA binding motif protein 17</td> <td>no</td> <td>1</td> <td>0</td> <td>3</td> <td>23.6. (23.6.23.6)</td> <td>1</td>	RBM17	RNA binding motif protein 17	no	1	0	3	23.6. (23.6.23.6)	1
RPL13AP3     ribosomal protein L13a pseudogene 3     no     4     1     5     3.4, (3.1, 3.7)     1       RPL15     ribosomal protein L15     no     11     1     6     3.4, (3.1, 3.7)     1       RP14     ribonuclease P/MRP subunit p14     no     11     0     6     35.9, (35.9, 35.9)     1       RP30     ribonuclease P/MRP subunit p30     no     1     0     4     46.1, (46.1, 46.1)     1       RUFV4     RUN and FYVE domain containing 4     no     1     0     4     16.3, (16.3, 16.3)     1       SNRPA1     small nuclear ribonucleoprotein polypeptide A'     no     1     0     2     5.3, (5.3, 5.3)     1       SPEF1     sperm flagellar 1     no     2     0     5     5.9, (3.2, 8.5)     1       SNA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-fail PC-rich repeat containing 3     no     1     0     5     3.7, (3.7, 3.7)     1       STFA2     synaptotag	RCAN3	RCAN family member 3	no	1	0	5	5.3. (5.3.5.3)	1
RPL15     ribosomal protein L15     no     11     1     6     3.4, (3.1,3.9)     3       RPP14     ribonuclease P/MRP subunit p14     no     1     0     6     35.9, (35.9, 35.9)     1       RPP30     ribonuclease P/MRP subunit p30     no     1     0     4     46.1, (46.1, 46.1)     1       RUFV4     RUN and FVVE domain containing 4     no     1     0     4     16.3, (16.3, 16.3)     1       SNRPA1     small proline rich protein 1B     no     1     0     4     7.5, (7.5, 7.5)     1       SSNA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     1     0     5     3.7, (3.7, 3.7)     1       TFAP4     transcription factor AP-4     no     1     0     2     3.7, (3.7, 3.7)     1       TMPO     thymopoietin     no	RPL13AP3	ribosomal protein L13a pseudogene 3	no	4	1	5	3.4. (3.1.3.7)	1
RPP14     ribonuclease P/MRP subunit p14     no     1     0     6     35.9, (35.9, 35.9)     1       RPP30     ribonuclease P/MRP subunit p30     no     1     0     4     46.1, (46.1, 46.1)     1       RUFY4     RUN and FYVE domain containing 4     no     1     0     4     46.3, (16.3, 16.3)     1       SNRPA1     small nuclear ribonucleoprotein polypeptide A'     no     1     0     2     5.3, (53.5.3)     1       SPRF1     sperm flagellar 1     no     1     0     4     7.5, (7.5, 7.5)     1       SSNA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.2, 4.5)     5       TBC100main family member 10B     no     3     1     2     3.4, (3.1, 4.1)     1       TFAP4     transcription factor AP-4     no	RPL15	ribosomal protein L15	no	11	1	6	3.4. (3.1.3.9)	3
RPP30     ribonuclease P/MRP subunit p30     no     1     0     4     46.1, (46.1, 46.1)     1       RUFY4     RUN and FYVE domain containing 4     no     1     0     4     16.3, (16.3, 16.3)     1       SNRPA1     small nuclear ribonucleoprotein polypeptide A'     no     1     0     2     5.3, (5.3, 5.3)     1       SPEF1     sperm flagellar 1     no     2     0     5     5.9, (3.2, 8.5)     1       SPR1B     small proline rich protein 1B     no     1     0     4     7.5, (7.5, 7.5)     1       SNRA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.2, 4.5)     5       TBC1D10B     TBC1 domain family member 10B     no     1     0     5     15.7, (3.7, 3.7)     1       TMPO     thymopoietin	RPP14	ribonuclease P/MRP subunit p14	no	1	0	6	35.9. (35.9.35.9)	1
RUFY4     RUN and FYVE domain containing 4     no     1     0     4     16.3, (16.3, 16.3)     1       SNRPA1     sperm flagellar 1     sperm flagellar 1     no     1     0     2     5.3, (5.3, 5.3)     1       SPER1     sperm flagellar 1     sperm flagellar 1     no     2     0     5     5.9, (3.2, 8.5)     1       SPER1     sperm flagellar 1     no     1     0     4     7.5, (7.5, 7.5)     1       SSNA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.2, 4.5)     5       TBC1D10B     TBC1 domain family member 10B     no     1     0     5     3.7, (3.7, 3.7)     1       TMPO     thymopoletin     no     1     0     2     3.7, (3.7, 3.7)     1       TNSF14     TNF superfamily me	RPP30	ribonuclease P/MRP subunit p30	no	1	0	4	46.1. (46.1.46.1)	1
SNRPA1     small nuclear ribonucleoprotein polypeptide A'     no     1     0     2     5.3, (5.3,5.3)     1       SPEF1     sperm flagellar 1     no     2     0     5     5.9, (3.2,8.5)     1       SPRR1B     small proline rich protein 1B     no     1     0     4     7.5, (7.5,7.5)     1       SSNA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3,6,6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3,2,4.5)     5       TBC1D10B     TBC1 domain family member 10B     no     3     1     2     3.4, (3,1,4.1)     1       TFAP4     transcription factor AP-4     no     1     0     2     3.7, (3,7,3.7)     1       TOX4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9.9)     1       TRAIP     TRAF interacting protein	RUFY4	RUN and FYVE domain containing 4	no	1	0	4	16.3. (16.3.16.3)	1
SPEF1     sperm flagellar 1     no     2     0     5     5,9,(3,2,8,5)     1       SPRR1B     small proline rich protein 1B     no     1     0     4     7,5,(7,5,7,5)     1       SNA1     SS nuclear autoantigen 1     yes     1     0     4     7,5,(7,5,7,5)     1       SNA1     SS nuclear autoantigen 1     yes     1     0     2     3,6,(3,6,3,6)     1       SYT2     synaptotagmin 2     no     6     1     4     3,6,(3,2,4,5)     5       TBC1010B     TBC1 domain family member 10B     no     3     1     2     3,4,(3,1,4,1)     1       TFAP4     transcription factor AP-4     no     1     0     5     3,7,(3,7,3,7)     1       TMPO     thympopietin     no     1     0     2     3,7,(3,7,3,7)     1       TOX4     TOX high mobility group box family member 4     no     1     0     3     9,9,9,9,9     1       TRAIP     TRAF interacting protein     no     1     0     4<	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	no	1	0	2	5.3. (5.3.5.3)	1
SPRR1B     small proline rich protein 1B     no     1     0     4     7.5, (7.5,7.5)     1       SSNA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.2, 4.5)     5       TBC1D10B     TBC1 domain family member 10B     no     3     1     2     3.4, (3.1, 4.1)     1       TFAP4     transcription factor AP-4     no     1     0     5     3.7, (3.7, 3.7)     1       TMPO     thymopotetin     no     1     0     2     3.7, (3.7, 3.7)     1       TOX4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9, 9.9)     1       TRAIP     TRAF interacting protein     no     1     0     4     10.2, (10.2, 10.2)     1       VAV1     vava guanine nucleotide exchange factor 1	SPEF1	sperm flagellar 1	no	2	0	5	5.9, (3.2,8.5)	1
SSNA1     SS nuclear autoantigen 1     yes     1     0     5     12.2, (12.2, 12.2)     2       STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.2, 4.5)     5       TBC1D10B     TBC1 domain family member 10B     no     3     1     2     3.4, (3.1, 4.1)     1       TFAP4     transcription factor AP-4     no     1     0     5     3.7, (3.7, 3.7)     1       TMPO     thymopoletin     no     1     0     2     3.7, (3.7, 3.7)     1       TNFSF14     TNF superfamily member 14     no     1     0     3     9.9, (9.9, 9.9)     1       TRAIP     TRAF interacting protein     no     1     0     4     10.2, (10.2, 10.2)     1       VAV1     vav guanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZFP2     ZFP2 zinc finger protein     no	SPRR1B	small proline rich protein 1B	no	1	0	4	7.5, (7.5,7.5)	1
STPG3     sperm-tail PG-rich repeat containing 3     no     1     0     2     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.6, 3.6)     1       SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.6, 3.6)     1       TBC1 domain family member 10B     no     3     1     2     3.4, (3.1, 4.1)     1       TFAP4     transcription factor AP-4     no     1     0     5     3.7, (3.7, 3.7)     1       TMPO     thymopoletin     no     1     0     2     3.6, (3.6, 0.0)     1       TNFSF14     TNF superfamily member 14     no     1     0     2     3.7, (3.7, 3.7)     1       TOX4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9, 9.9)     1       TRAIP     TRAF interacting protein     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     <	SSNA1	SS nuclear autoantigen 1	ves	1	0	5	12.2. (12.2.12.2)	2
SYT2     synaptotagmin 2     no     6     1     4     3.6, (3.2,4.5)     5       TBC1D10B     TBC1 domain family member 10B     no     3     1     2     3.4, (3.1,4.1)     1       TFAP4     transcription factor AP-4     no     1     0     5     3.7, (3.7,3.7)     1       TMPO     thymopoletin     no     1     0     2     3.7, (3.7,3.7)     1       TNFSF14     TNF superfamily member 14     no     1     0     2     3.7, (3.7,3.7)     1       TOX4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9,9.9)     1       TRAIP     TRAF interacting protein     no     1     0     3     4.7, (3.4,6.0)     1       VAV1     vaguanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.6, (3.1, 4.1)     2       ZNF146     zinc finger protein 146     no	STPG3	sperm-tail PG-rich repeat containing 3	no	1	0	2	3.6. (3.6.3.6)	1
TBC1D10B   TBC1 domain family member 10B   no   3   1   2   3.4, (3.1,4.1)   1     TFAP4   transcription factor AP-4   no   1   0   5   3.7, (3.7, 3.7)   1     TMPO   thymopoletin   no   1   0   5   15.7, (3.7, 2.7.)   1     TNFSF14   TNF superfamily member 14   no   1   0   2   3.9.9 (9.9.9.9)   1     TOX4   TOX high mobility group box family member 4   no   1   0   3   9.9. (9.9.9.9)   1     TRAIP   TRAF interacting protein   no   1   0   3   4.7, (3.4,6.0)   1     VAV1   var guanine nucleotide exchange factor 1   no   1   0   4   10.2, (10.2, 10.2)   1     ZBTB18   zinc finger and BTB domain containing 18   no   1   0   2   3.6, (3.3, 3.3)   1     ZPP2   ZFP2 zinc finger matrin-type 2   no   6   0   5   3.6, (3.1,4.1)   2     ZNF146   zinc finger protein 146   no   2   0   8   16.4, (3.1,29.7)   1	SYT2	synaptotagmin 2	no	6	1	4	3.6. (3.2.4.5)	5
TFAP4     transcription factor AP-4     no     1     0     5     3.7, (3.7, 3.7)     1       TMPO     thymopoietin     no     1     0     5     15.7, (3.7, 3.7)     1       TMPO     thymopoietin     no     2     0     5     15.7, (3.7, 3.7)     1       TNFSF14     TNF superfamily member 14     no     1     0     2     3.7, (3.7, 3.7)     1       TOX 4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9, 9.9)     1       TRAIP     TRAF interacting protein     no     1     0     3     4.7, (3.4, 6.0)     1       VAV1     vav guanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.3, (3.3, 3.3)     1       ZMAT2     zinc finger protein 146     no     2     0     8     16.4, (3.1, 29.7)     1       ZNF678     zinc finger protein 146     no <td>TBC1D10B</td> <td>TBC1 domain family member 10B</td> <td>no</td> <td>3</td> <td>1</td> <td>2</td> <td>3.4. (3.1.4.1)</td> <td>1</td>	TBC1D10B	TBC1 domain family member 10B	no	3	1	2	3.4. (3.1.4.1)	1
TMPO     thymopoletin     no     2     0     5     15.7, (3.7, 27.7)     1       TNFSF14     TNF superfamily member 14     no     1     0     2     3.7, (3.7, 3.7)     1       TOX 4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9, 9.9)     1       TRAIP     TRAF interacting protein     no     1     0     3     4.7, (3.4, 6.0)     1       VAV1     vav guanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.3, (3.3, 3)     1       ZFP2     ZFP2 zinc finger protein     no     6     0     5     3.6, (3.1, 4.1)     2       ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1, 29.7)     1       ZNF678     zinc finger protein 232     no     2     1     4     4.6, (3.5, 5.8)     1       ZNF678     zinc finger notein 678     <	TFAP4	transcription factor AP-4	no	1	0	5	3.7, (3.7,3.7)	1
TNFSF14     TNF superfamily member 14     no     1     0     2     3.7, (3.7, 3.7)     1       TOX4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9, 9.9)     1       TRAF interacting protein     no     1     0     3     4.7, (3.4, 6.0)     1       VAV1     vav guanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.3, (3.3, 3.3)     1       ZFP2     ZFP2 zinc finger protein     no     2     1     3     4.9, (3.1, 6.7)     1       ZMAT2     zinc finger protein     no     2     0     8     16.4, (3.1, 29.7)     1       ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1, 29.7)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4, 12.8)     1       ZSCAN54     zinc finger and SCAN domain containing 32	ТМРО	thymopoietin	no	2	0	5	15.7. (3.7.27.7)	1
TOX4     TOX high mobility group box family member 4     no     1     0     3     9.9, (9.9,9.9)     1       TRAIP     TRAF interacting protein     no     1     0     3     4.7, (3.4,6.0)     1       VAV1     vav guanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.3, (3.3, 3.3)     1       ZFP2     ZFP2 zinc finger protein     no     2     1     3     4.9, (3.1, 6.7)     1       ZMAT2     zinc finger matrin-type 2     no     6     0     5     3.6, (3.1, 4.1)     2       ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1, 29.7)     1       ZNF232     zinc finger protein 678     no     2     1     4     4.6, (3.5, 5.8)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4, 12.8)     1       ZSCAN32     zinc finger and SCAN domain	TNFSF14	TNF superfamily member 14	no	1	0	2	3.7. (3.7.3.7)	1
TRAIP     TRAF interacting protein     no     2     0     3     4.7, (3.4,6.0)     1       VAV1     vav guanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.3, (3.3, 3.3)     1       ZFP2     ZFP2 zinc finger protein     no     1     0     2     3.6, (3.1, 4.1)     2       ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1, 29.7)     1       ZNF232     zinc finger protein 678     no     2     1     4     4.6, (3.5, 5.8)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4, 12.8)     1       ZSCANS2     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1	TOX4	TOX high mobility group box family member 4	no	1	0	3	9.9. (9.9.9.9)	1
VAV1     vax guanine nucleotide exchange factor 1     no     1     0     4     10.2, (10.2, 10.2)     1       ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.3, (3.3, 3.3)     1       ZFP2     ZFP2 zinc finger protein     no     1     0     2     3.4, (3.1, 6.7)     1       ZMAT2     zinc finger matrin-type 2     no     6     0     5     3.6, (3.1, 4.1)     2       ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1, 29.7)     1       ZNF232     zinc finger protein 678     no     2     1     4     4.6, (3.5, 5.8)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4, 12.8)     1       ZSCANS2     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1       ZSCANSA     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2, 5.3)     1	TRAIP	TBAF interacting protein	no	2	0	3	4.7. (3.4.6.0)	1
ZBTB18     zinc finger and BTB domain containing 18     no     1     0     2     3.3, (3.3,3.3)     1       ZFP2     ZFP2 zinc finger protein     no     2     1     3     4.9, (3.1,6.7)     1       ZMAT2     zinc finger matrin-type 2     no     6     0     5     3.6, (3.1,4.1)     2       ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1,29.7)     1       ZNF782     zinc finger protein 232     no     2     1     4     4.6, (3.5,5.8)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4,12.8)     1       ZSCAN52     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1       ZSCAN5A     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2,5.3)     1	VAV1	vav guanine nucleotide exchange factor 1	no	1	0	4	10.2. (10.2.10.2)	1
ZFP2     ZFP2 zinc finger protein     no     2     1     3     4.9, (3.1,6.7)     1       ZMAT2     zinc finger protein     no     6     0     5     3.6, (3.1,4.1)     2       ZNF146     zinc finger protein     146     no     2     0     8     16.4, (3.1,29.7)     1       ZNF146     zinc finger protein     22     0     8     16.4, (3.1,29.7)     1       ZNF678     zinc finger protein     03     1     2     6.6, (3.4,12.8)     1       ZNF678     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1       ZSCAN5A     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2,5.3)     1	ZBTB18	zinc finger and BTB domain containing 18	no	1	0	2	3.3. (3.3.3.3)	1
ZMAT2     zinc finger matrin-type 2     no     6     0     5     3.6, (3.1,4.1)     2       ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1,29.7)     1       ZNF232     zinc finger protein 232     no     2     1     4     4.6, (3.5,5.8)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4,12.8)     1       ZSCAN32     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1       ZSCAN5A     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2, 5.3)     1	ZFP2	ZFP2 zinc finger protein	no	2	1	3	4.9. (3.1.6.7)	1
ZNF146     zinc finger protein 146     no     2     0     8     16.4, (3.1,29.7)     1       ZNF232     zinc finger protein 232     no     2     1     4     4.6, (3.5,5.8)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4,12.8)     1       ZSCAN32     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3,11.3)     1       ZSCAN5A     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2,5.3)     1	ZMAT2	zinc finger matrin-type 2	no	6	0	5	3.6. (3.1.4.1)	2
ZNF232     zinc finger protein 232     no     2     1     4     4.6, (3, 5, 8)     1       ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3, 4, 12.8)     1       ZSCAN32     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1       ZSCAN5A     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2, 5.3)     1	ZNF146	zinc finger protein 146	no	2	0	8	16.4, (3.1.29.7)	1
ZNF678     zinc finger protein 678     no     3     1     2     6.6, (3.4, 12.8)     1       ZSCAN32     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1       ZSCAN5A     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2, 5.3)     1	ZNF232	zinc finger protein 232	no	2	1	4	4.6, (3.5,5.8)	1
ZSCAN32     zinc finger and SCAN domain containing 32     no     1     0     2     11.3, (11.3, 11.3)     1       ZSCAN5A     zinc finger and SCAN domain containing 5A     no     3     0     4     4.0, (3.2, 5.3)     1	ZNF678	zinc finger protein 678	no	3	1	2	6.6, (3.4,12.8)	1
ZSCAN5A zinc finger and SCAN domain containing 5A no 3 0 4 4.0, (3.2,5.3) 1	ZSCAN32	zinc finger and SCAN domain containing 32	no	1	0	2	11.3, (11.3,11.3)	1
	ZSCAN5A	zinc finger and SCAN domain containing 5A	no	3	0	4	4.0, (3.2,5.3)	1

## **Supplementary Table 2. (continued)**

Names	Sequences
T7-Pep2_PCR1_F	5'-ATAAAGGTGAGGGTAATGTC-3'
Nextera Index 1	5'-CAAGCAGAAGACGGCATACGAGAT[i7]GTCTCGTGGGCTCGG-3'
PhIP_PCR2_F	5'-AATGATACGGCGACCACCGAGATCTACAC-[i5]-GGAGCTGTCGTATTCCAGTC-3'
P7.2	5'-CAAGCAGAAGACGGCATACGA-3'
T7-Pep2_PCR1_R+ad_min	5'-CTGGAGTTCAGACGTGTGCTCTTCCGATCAGTTACTCGAGCTTATCGT-3'
PhIP_PCR2_R	5'-CAAGCAGAAGACGGCATACGAGAT-[i7]-GTGACTGGAGTTCAGACGTGTGCTC-3'
T7-Pep2.2_SP_subA	5'-CTCGGGGATCCAGGAATTCCGCTGCGT-3'
MISEQ_MIPSA_R2	5'- ATGACGACAAGCCATGGTCGAATCAAACAAGTTTGTACAAAAAAGTTGGC-3'
MIPSA_i5_NextSeq_SP	5'-GGATCCCCGAGACTGGAATACGACAGCTCC-3'
Standard_i7_SP	5'-GATCGGAAGAGCACACGTCTGAACTCCAGTCAC-3'
HL-32_ad	HL-GACGTGTGCTCTTCCGATCAAATTATTTCTAGGTACTCGAGCTTATCG-3'
MX1_Forward	5'-ACCACAGAGGCTCTCAGCAT-3'
MX1_Reverse	5'-CTCAGCTGGTCCTGGATCTC-3'
GAPDH_Forward	5'-GAGTCAACGGATTTGGTCGT-3'
GAPDH_Reverse	5'-TTGATTTTGGAGGGATCTCG-3'
BT2_F	5'-GTCAGAGTGACACACTGT-3'
BT2_R	5'-AGAGTGACAGTCACAGTG-3'
BG4_F	5'-CACTGACTGTGTGAGTGT-3'
BG4_R	5'-TGAGACACAGTGAGTCAC-3'
NT5C1A_F	5'-CTCACAGACAGACGTCA-3'
NT5C1A_R	5'-TGTCAGTCAGTGAGTGTG-3'

Supplementary Table 3: Primer sequences used in this study.

**Supplementary Data File 1: Hits fold-change MIPSA data matrix for UCIs of reactive proteins in severe COVID-19 patients.** Proteins were included if they had at least two reactive UCIs in at least one severe patient and were not reactive in more than one control (healthy or mild/moderate convalescent plasma). Proteins were not included if they were reactive in a single severe patient and a single control. Each row corresponds to a single UCI, organized by protein in alphabetical order (gene symbol provided to left of underscore). Each column is an individual COVID-19 patient. If the UCI read counts were not significantly enriched versus the mock IPs, it is reported as "1". If the UCI read counts were significantly enriched versus mock IPs, the fold-change estimate (from EdgeR) is provided.

Source Data 1: Unprocessed western blot of Figure 1E.

Source Data 2: Unprocessed western blot of top panel in Figure 1F.

Source Data 3: Unprocessed western blot of middle panel in Figure 1F.

Source Data 4: Unprocessed western blot of bottom panel in Figure 1F.

Source Data 5: Unprocessed western blot of top panel in Figure S3.

Source Data 6: Unprocessed western blot of bottom panel in Figure S3.