

Supplementary Table S1

[illegible]

Supplementary Table S2

GeneSymbol[Uniprot]start-end	prevalence Lf	prevalence A	log odds ratio	MSigDB entry	sequence
ADAMTS17 Q8TE56 1035-1125	25.16	0.31	4.68		TITSPRALAITYKTRCDQWTVYVRCVREKLNQCDMRWYQRCCTCRDFYANKMRQPPNPS
AHI1 Q8N157 855-945	25.16	0.31	4.68		TFLFAGSGEDGIVYVWNPETGEQVAMYSLDFKSPSPIDSIYHFENMVAFCAFQGNPEILLIYDFHVAQQAEMFKRYNGTFLPGIHQS
ANKK1 Q8NF02 495-585	18.94	0.31	4.32		TLHVAAFYGVSLKVLKLTQSGAELDAQQRNLTRPLHLAVERGKVAIRQLHLKSGAVPDALQSGYGLPTAAARGYLKIMILRRYGAS
APC2 O95996 1-90	18.94	0.31	4.32		MPASSVAPEQLVRQVEALKAENSHLRQELRDNSSHLSEKLTETSGMKVEVLKHLQGLKEARVLVSGHTELEQKALQMDLTVNLNK
ARIHGA24 Q8N264 405-495	18.94	0.31	4.32		SVHLKDSRSPMLKNNKPAFNKGGSVITNFSGSSNAEGLEKQTTPNGSLQARSSSLKSVGTMKGVHSVQNGTVRGMILNSQDILGNP
BAIP3 Q94812 315-405	18.94	0.31	4.32		KGMGRYQKIVJUSARANGTAGPTEDHTDDFLGCLINPREVPVAGVDWRFLKPESSASRVWFKGHLVLEKLTQTJQRTAMSDSGRSGFLS
BTD1D Q9HC05 360-450	18.94	0.31	4.32		IVRGLSGLHSGPTDYQADNIQIEYEKKQLGQNDTGFSCDGTATFRVMFKPEIILPNVCTYCATCLGKPDSHYTGKGLKGVVHETPA
C11orf42 Q8N5U0 225-315	18.94	0.31	4.32		VYFNLISMPPLATSPADNTEAADVPPVPAPPTPTPQEGPEDEKTPRFGQPLSENWFLSPRSPPMGAQGGGPRDPDGH
LOC100128270 nan 1-90	18.94	0.31	4.32		MVTPAGCLGGRNQGREIPTGAFPRSSRAGQTQAVSVGAQVSSWRERQPCSGSRGLPHILGTGDNVDTTGLKLVPTPPRIQKETQKQAL
HMC5 Q96F22 45-135	18.94	0.31	4.32		PQSNPSLNLRLHFEEADDSERIAMPWVGLVPSVHFSPDKSPQLQNTNCRSDTVMEKRSFKVPLKGRRCVPLADGVEYVQRQCQDLM
LRAP3 Q5JTD7 135-225	56.21	0.31	6.02		LPLPDGAKSGELKTSANPIPTGKWSRLAIAVASHQVRLVNDYPLQFNGHVMGLAVASVRSLELDEGTGLNQSAQTLLDMV
CARD10 Q9BWV7 405-495	18.94	0.31	4.32		QLQYQSQIEKQYRKLQVLEAEERDELLTTLSELTALKEVLQAGQGGTCLKACASHSLSCGSLVTSWSEFSPGLGGPEATGEA
LOC100288406 nan 1-90	18.94	0.31	4.32		MPVPQSGWQHSJLTLGGTFVAGSLQTPMTNTVSSGSGKRAQRAQVAVPLVPKRTSPSTGQTKGSEKDLGVPVGLAEKGGKSELPH
DDX42 Q86Q33 90-180*	31.37	0.31	4.99	autoantigen	IPAESNTPROQKHSKPDVSDSDDDPLEAFMAEVEDQAARDMRLKEELQKERNVKGIRDDEEDQOEAFYRMAENPATGVVQVEEEDN
DMXL1 Q9Y485 675-765	31.37	0.31	4.99		LNIEESCSTQKSDTVDAFQDPSPASVYSELULWRVDPVGLSVFSGSGSELAIRNLSDVWELDITPLSGYACVNPSCAFVNAS
DUSP7 Q16829 1-90	18.94	0.31	4.32		MNKLQRLGPPARAHMSTSGAAAAGGTGAGPEGAGSGSGAGAGAGAAMPCKSAEWLQEEELRAGSALLDCRPHLFESSHIT
FAM90A3 nan 135-225	31.37	6.52	1.88		STPDSYLRVPPKMPVPHVTIKSRPRVDPVLAADGSATEMDRGSVLAISLPRKLASSSSSLGPKERTQGAADIPPTARVHRQGLEPVL
FAM29A2 A1XB55 1-185	50.00	12.73	1.92		DKADLVLNEINAYATTEPHLKLMLNFADEFKALQDYQRAEVLEAKVVEPKLTGYITVKMKRDLDAKTITARNREKATITQLERTQ
FGJ6 Q6ZV73 495-585	18.94	0.31	4.32		PKKPRHLSLPATGVLKKAASEELLEKSSYPSEKSSKSESLERNHLQHLCAQNRGSSSSDFMPPKRASEKVPVKLPHLPLFSGNPEFLKS
FL46552 nan 90-180	18.94	0.31	4.32		DFANLEDNFSTKSRFLKIQPLKRASHSPGLFVAFDEPHRSLRQ
ADGRA3 Q8IWK6 810-900	37.58	12.73	1.42		VFVGQITQRTNASKIQVGHILYHSTLTVLWVGVTARNIYKQTKAKRCQDDPEPPPPRMLRFLYGLGGIPIVCGITAAANKIN
IFT171 Q9UG01 270-360	18.94	0.31	4.32		RSRIWEAAKPEITNLTYTLALAWKRDGSLRCTLGGVEQDCLRLSKYNKFTLVYGPQVIVKNGLSGSLVPLKSHYGVEEV
KALRN1 Q60229 2430-2520	18.94	0.31	4.32		ILGNKVSYKETNSSESECDLLDPNTSMELNPNFPIQVEAPEFLVPLVDVTCLLGDVQKVGQRPKITWKGPDQNLDTNNSAT
KANK2 Q63Z33 90-180	25.16	0.31	4.68		ASGDSRHAYSVYCGRGYVQGALETGGFNPVERTLLDARRLEDQAATPTLGLSLTSAAGSTASLVGGLGPPPTPRSSGLTPTVP
KCNT2 Q6UVN3 495-585	18.94	0.31	4.32		ESTFAYEGKSFYAFHAAKHGVCILGVREDKNMILNPGRYMINTSDICFINITKPSAAGNOQDKRSNFAKVPYSGFYPSRL
KIFC2 Q96AC6 405-495	18.94	0.31	4.32		LKGNIRVLRCRPTSSLVSSVYVPGPGTVTCYGRGHRFRLLVWVPFDDASQEEVRELEPAVLSCLRGYSVCIFYGTGTGKTYSME
KRTAP5-2 Q701N4 45-135	25.16	0.31	4.68		SSSCGCGSGRYVPPCCPKVSNWPAACSCSCGSGKGCSCGSGSGKGCSCGSGSGKGCSCGSGSGKGCSCGSGSGSCGSCS
LGALS14 Q8TC9J 45-135	18.94	0.31	4.32		GSCVIITGPTLTFVKDPQLEVFNYTGMDEDSIAQFIRLHFHGPAIMNSCVFJGWRYEKKYLPFFEDGKPFELCIYVRHKEKYKVMVNG
LOC100288050 nan 1-90	18.94	0.31	4.32		MCTFLFVPSFISIHLSISISSWGRRLTSDAAASLCTGSPGVAFAHLLQGLHGLARAWKGRHVRNTQLDVKRKRQREYTVYGVK
LOC100289224 nan 1-90	18.94	0.31	4.32		MPILPRPSTQPEKPPKRLPTGHNTQAETRGADQKGRRAHNPASAGAQTCVPRRTHTQTRDRKKRREGRREGRERERLKR
LOC100289634 nan 1-90	18.94	0.31	4.32		HMSPKPRPRLQVGRGHNSQGLSPAALLEGAMLSQFCVETTGSEAGFRRPSWGGGPHVLHRMAPPSCTSAALSLDKRLPEK
LOC100294071 nan 855-945	18.94	0.31	4.32		IMPPSEYKICEEGTKFKFPWDLTNHKHRTGKPKYCECGKTTCTSSLIKHKRHTGDRPTSAKNVAKPLGDSQTLLNISKHRIK
LOC100294386 nan 1485-1575	18.94	0.31	4.32		PERHARSEWSPLRMAEVOAPVCPVFPALCAGLCVRQSIREFALGSLVRLARGPNLPVFLVGAISWPGCPLPLIAPGLAEPHG
LOC197350 nan 360-450	18.94	0.31	4.32		GYHARVDKGSQDQWTLVLEVRANPGRDLLELTLEVRNRVCEVLGPDCDELKRAKLEIRSLRRLCLQA
LOC440577 nan 90-180	18.94	0.31	4.32		TPPVVLPRFKCSGVPVHISGQHLVAVEDEADESEDEEDVLLSISGSKALLSPGSGSKVPQKVKLAIVEDDDDDDDDDDEFAEEVK
LY6G6F Q5SQ64 135-225	18.94	0.31	4.32		ADGSPCNVLLCSPVSRMDSVTVQEGKGPVGRGVQFVWGSEAAVLPV

Supplementary Figure 1

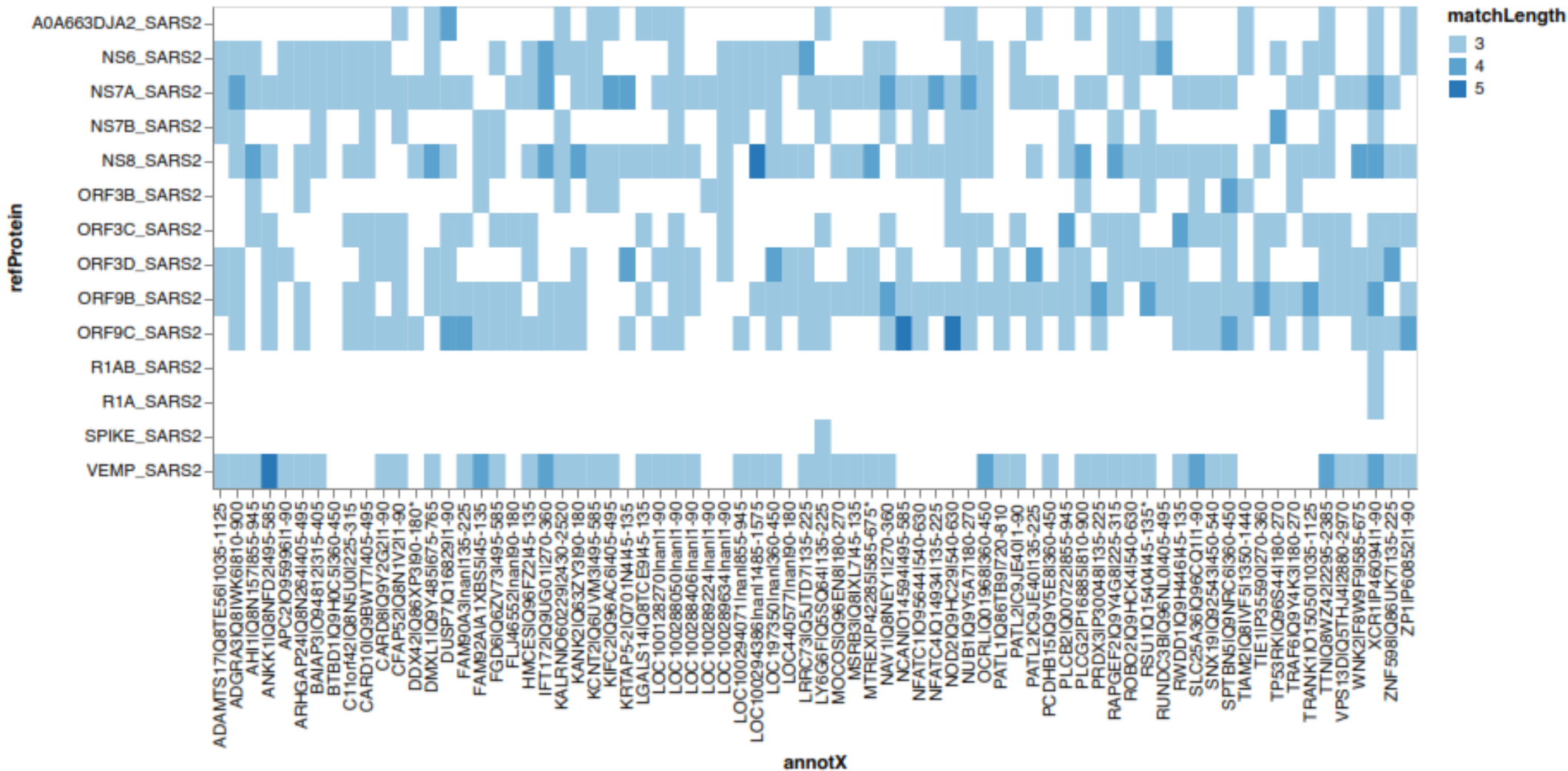


Figure S1: Sequence match (peptide length) between differentially enriched human peptides (x-axis : gene symbol | UniProtID | start position- end position: see Supplementary table S2) and reference sequence of SARS-CoV2 (<https://covid-19.uniprot.org/>) proteins. Color code indicates maximum peptide length as shown in legend.