

A Potent, Broadly Protective Vaccine Against SARS-CoV-2 Variants of Concern

SUPPLEMENTARY INFORMATION

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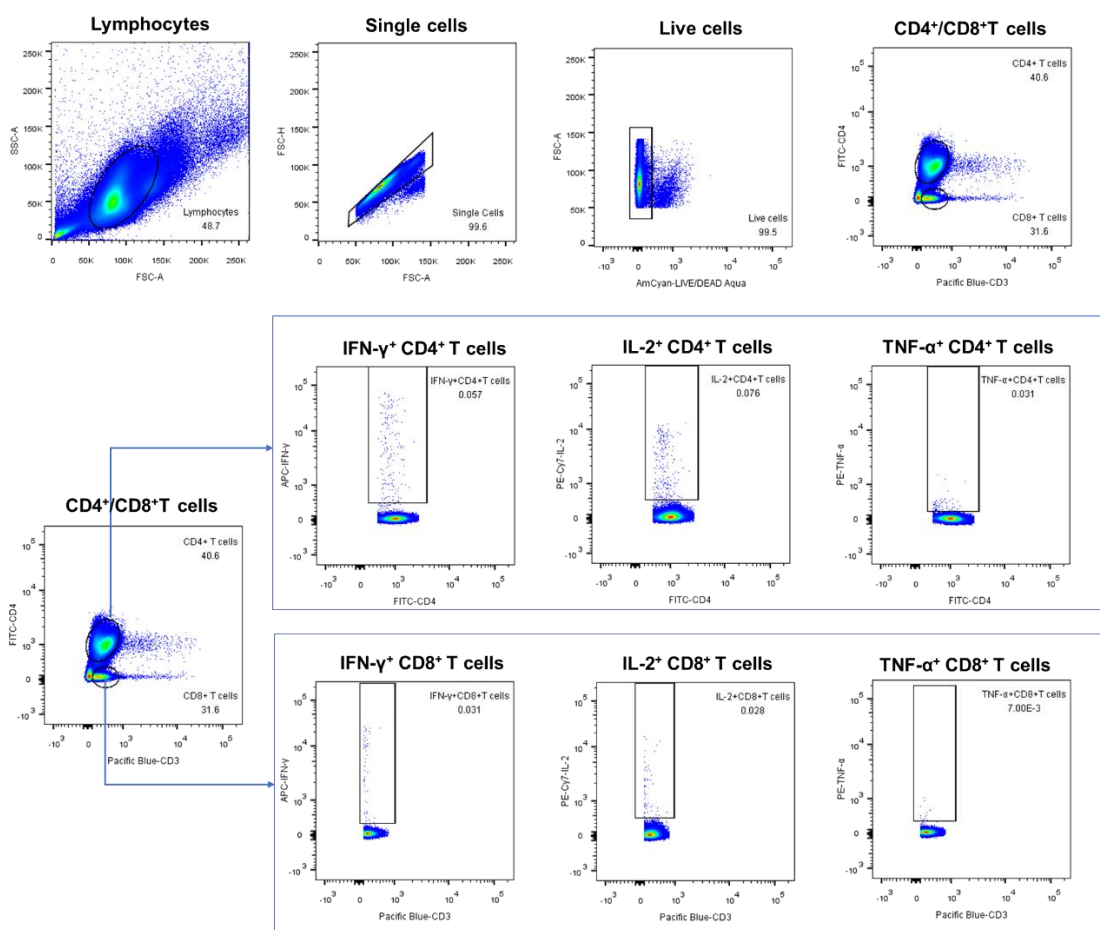
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Supplementary Figure 1. Gating strategy for detection of IFN- γ^+ /IL-2 $^+$ /TNF- α^+ Cells within CD4 $^+$ and CD8 $^+$ T cell populations.



Supplementary Table 1. S spike peptide pool from Wuhan-Hu-1 strain. Each peptide is 18 amino acids in length with 7 amino acids offset and 11 amino acids overlapped.

Index	Peptide Sequence	Index	Peptide Sequence
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1	QCVNLTTRTQLPPAYTNS	86	AVLYQDVNCTEVPVAIHA
2	RTQLPPAYTNSFTRGVYY	87	NCTEVPVAIHADQLTPTW
3	YTNSFTRGVYYPDKVFRS	88	AIHADQLTPTWRVYSTGS
4	GVYYPDKVFRSSVLHSTQ	89	TPTWRVYSTGSNVFQTRA
5	VFRSSVLHSTQDLFLPFF	90	STGSNVFQTRAGCLIGAE
6	HSTQDLFLPFFSNVTWFH	91	QTRAGCLIGAEHVNNSYE
7	LPFFSNVTWFHAIHVSGT	92	IGAEHVNNSYECDIPIGA
8	TWFHAIHVSGTNGTKRFD	93	NSYECDIPIGAGICASYQ
9	VSGTNGTKRFDNPVLPFN	94	PIGAGICASYQTQTNSPG
10	KRFDNPVLPFNDGVYFAS	95	ASYQTQTNSPGGSGSVAS
11	LPFNDGVYFASTEKSNI I	96	NSPGGSGSVASQSIIAYT
12	YFASTEKSNIIRGWIFGT	97	SVASQSIIAYTMSLGAEN
13	SNIIRGWIFGTTLDSKTQ	98	IAYTMSLGAENSVAYSNN
14	IFGTTLDSKTQSLIVNN	99	GAENSVAYSNNNSIAIPTN
15	SKTQSLIVNNATNVVIK	100	YSNNNSIAIPTNFTISVTT
16	IVNNATNVVIKVCEFQFC	101	IPTNFTISVTTEILPVSM
17	VVIKVCEFQFCNDPFLGV	102	SVTTEILPVSMTKTSVDC
18	FQFCNDPFLGVYYHKNNK	103	PVSMTKTSVDCTMYICGD
19	FLGVYYHKNNKSWMESEF	104	SVDCTMYICGDSTECSNL
20	KNNKSWMESEFRVYSSAN	105	ICGDSTECSNLLQYGSF
21	ESEFRVYSSANNCTFEYV	106	CSNLLQYGSFCTQLNRA
22	SSANNCTFEYVSQPFLMD	107	YGSFCTQLNRALTGIAVE
23	FEYVSQPFLMDLEGKQGN	108	LNRRALTGIAVEQDKNTQE
24	FLMDLEGKQGNFKNLREF	109	IAVEQDKNTQEVFAQVKQ
25	KQGNFKNLREFVFKNIDG	110	NTQEVFAQVKQIYKTPPI
26	LREFVFKNIDGYFKIYSK	111	QVKQIYKTPPIKDFGGFN
27	NIDGYFKIYSKHTPINLV	112	TPPIKDFGGFNFSQILPD
28	IYSKHTPINLVRDLPQGF	113	GGFNFSQILPDPSKPSKR
29	INLVRDLPQGFSALEPLV	114	ILPDPSKPSKRSFIEDLL
30	PQGFSALEPLVDLPIGIN	115	PSKRSFIEDLLFNKVTLA
31	EPLVDLPIGINITRFQTL	116	EDLLFNKVTLADAGFIKQ
32	IGINITRFQTLALHRSY	117	VTLADAGFIKQYGDCLGD
33	FQTLALHRSYLTPGDSS	118	FIKQYGDCLGDIAARDLI
34	HRSYLTPGDSSSGWTAGA	119	CLGDIAARDLICAQKFNG
35	GDSSSGWTAGAAAYVGY	120	RDLICAQKFNGLTVLPPL
36	TAGAAAYVGYLQPRTFL	121	KFNGLTVLPPLLTDEMIA
37	YVGYLQPRTFLLKYNENG	122	LPPLLTDEMIAQYTSALL
38	RTFLLKYNENGTITDAVD	123	EMIAQYTSALLAGTITSG
39	NENGTITDAVDCALDPLS	124	SALLAGTITSGWTFGAGA
40	DAVDCALDPLSETKCTLK	125	ITSGWTFGAGAALQIPFA
41	DPLSETKCTLKSFVEKG	126	GAGAALQIPFAMQMAYRF
42	CTLKSFTVEKGIYQTSNF	127	IPFAMQMAYRFNGIGVTQ
43	VEKGIYQTSNFRVQPTES	128	AYRFNGIGVTQNVLYENQ
44	TSNFRVQPTESIVRFPNI	129	GVTQNVLYENQKLIANQF

45	PTESIVRFPNITNLCPFG	130	YENQKLIANQFNSAIGKI
46	FPNITNLCPFGEVFNATR	131	ANQFNSAIGKIQDSLST
47	CPFGEVFNATRFASVYAW	132	IGKIQDSLSTASALGKL
48	NATRFASVYAWNRKRISN	133	LSSTASALGKLQDVVNQN
49	VYAWNRKRISNCVADYSV	134	LGKLQDVVNQNAQALNTL
50	RISNCVADYSVLYNSASF	135	VNQNAQALNTLVKQLSSN
51	DYSVLYNSASFSTFKCYG	136	LNTLVKQLSSNFGAISSV
52	SASFSTFKCYGVSPTKLN	137	LSSNFGAISSVLNDILSR
53	KCYGVSPTKLNLDLCFTNV	138	ISSVLNDILSRLDPPEAE
54	TKLNLDLCFTNVYADSFVI	139	ILSRLDPPEAEVQIDRLI
55	FTNVYADSFVIRGDEVQR	140	PEAEVQIDRLITGRLQSL
56	SFVIRGDEVQRQIAPGQTG	141	DRLITGRLQSLQTYVTQQ
57	EVQRQIAPGQTGKIADYNY	142	LQSLQTYVTQQLRAAEI
58	GQTGKIADYNYKLPDDFT	143	VTQQLRAAEIRASANLA
59	DYNYKLPDDFTGCVIAWN	144	AAEIRASANLAATKMSEC
60	DDFTGCVIAWNSNNLDSK	145	ANLAATKMSECVLGQSKR
61	IAWNSNNLDSKVGGNYY	146	MSECVLGQSKRVDFCGKG
62	LDSKVGGNYYLYRFLFRK	147	QSKRVDFCGKGYHLMSFP
63	NYYLYRFLFRKSNLKPFE	148	CGKGYHLMSFPQSAPHGV
64	LFRKSNLKPFERDISTEI	149	MSFPQSAPHGVVFLHVTY
65	KPFERDISTEIQAGSTP	150	PHGVVFLHVTYVPAQEK
66	STEIQAGSTPCNGVEGF	151	HVTYVPAQEKNF'TTAPAI
67	GSTPCNGVEGFNCYFPLQ	152	QEKNF'TTAPAI CHDGKAH
68	VEGFNCYFPLQSYGFQPT	153	APAICHDGKAHF'PREGVF
69	FPLQSYGFQPTNGVGYQP	154	GKAHF'PREGV'FVSN'GTHW
70	FQPTNGVGYQPYRVVLS	155	EGVFVSN'GTHWFV'TQRNF
71	GYQPYRVVLSFELLHAP	156	GTHWFV'TQRNFYEP'QIIT
72	VVLSFELLHAPATVCGPK	157	QRNFYEP'QIIT'DNTFVS
73	LHAPATVCGPKKSTNLVK	158	QIIT'DNTFVSGNCDVVI
74	CGPKKSTNLVKNKCVNFN	159	TFVSGNCDV'VIGIVNNTV
75	NLVKNKCVNFN'FNGLTGT	160	DV'VIGIVNNTVYDPLQPE
76	VNFN'FNGLTGTGVLTESN	161	NNTVYDPLQPELDSFKEE
77	LTGTGVLTESNKKFLPFQ	162	LQPELDSFKEELD'KYFKN
78	TESNKKFLPFQQFGRDIA	163	FKEELD'KYFKNHTSPD'VD
79	LPFQQFGRDIADTTDAVR	164	YFKNHTSPD'VDLGDISGI
80	RDIADTTDAVRDPQ'TLEI	165	PD'VDLGDISGINASV'VNI
81	DAVRDPQ'TLEILDITPCS	166	ISGINASV'VNIQKEIDRL
82	TLEILDITPCSFGGVS'VI	167	VVNIQKEIDRLNEVAKNL
83	TPCSFGGVS'VITPGTNTS	168	IDRLNEVAKNLNESLIDL
84	VSVITPGTNTSNQVAVLY	169	AKNLNESLIDLQELGKYE
85	TNTSNQVAVLYQDVNCTE	170	SLIDLQELGKYEQYIKWP *

Note: * End of sequence, overlap 12 AA