

Supplemental Information

Figure S1. Each viral antigen listed in the table was coupled to a microbead population with a distinct address, e.g., R26 for SARS-CoV-2 RBD that displayed a different fluorescence intensity in the fluorescence channel, R712-APC-700 of the CytoFLEX cytometer (right plot). Because the serology assays and assays assessing cross reactivity were performed separately in different sample wells, assay performance was not affected by the overlap of the intensity addresses of R51 (spike) and R56 (SARS).

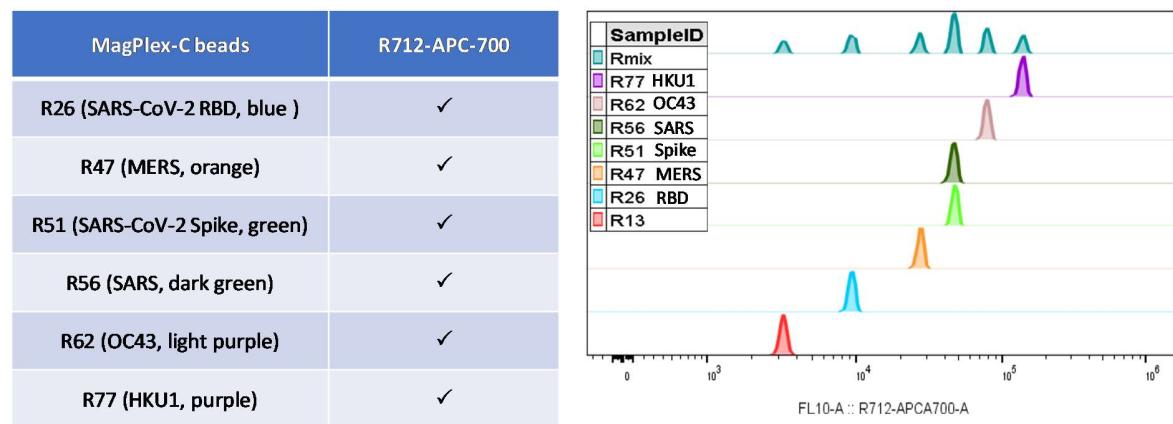
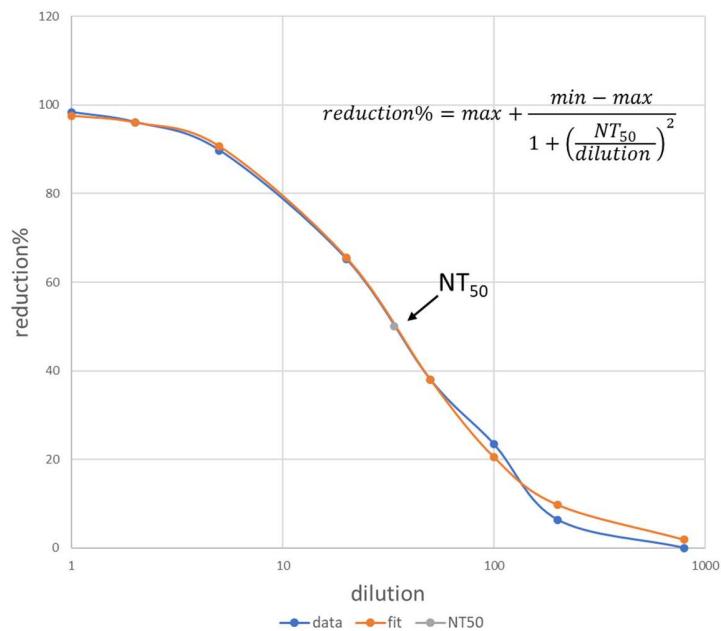
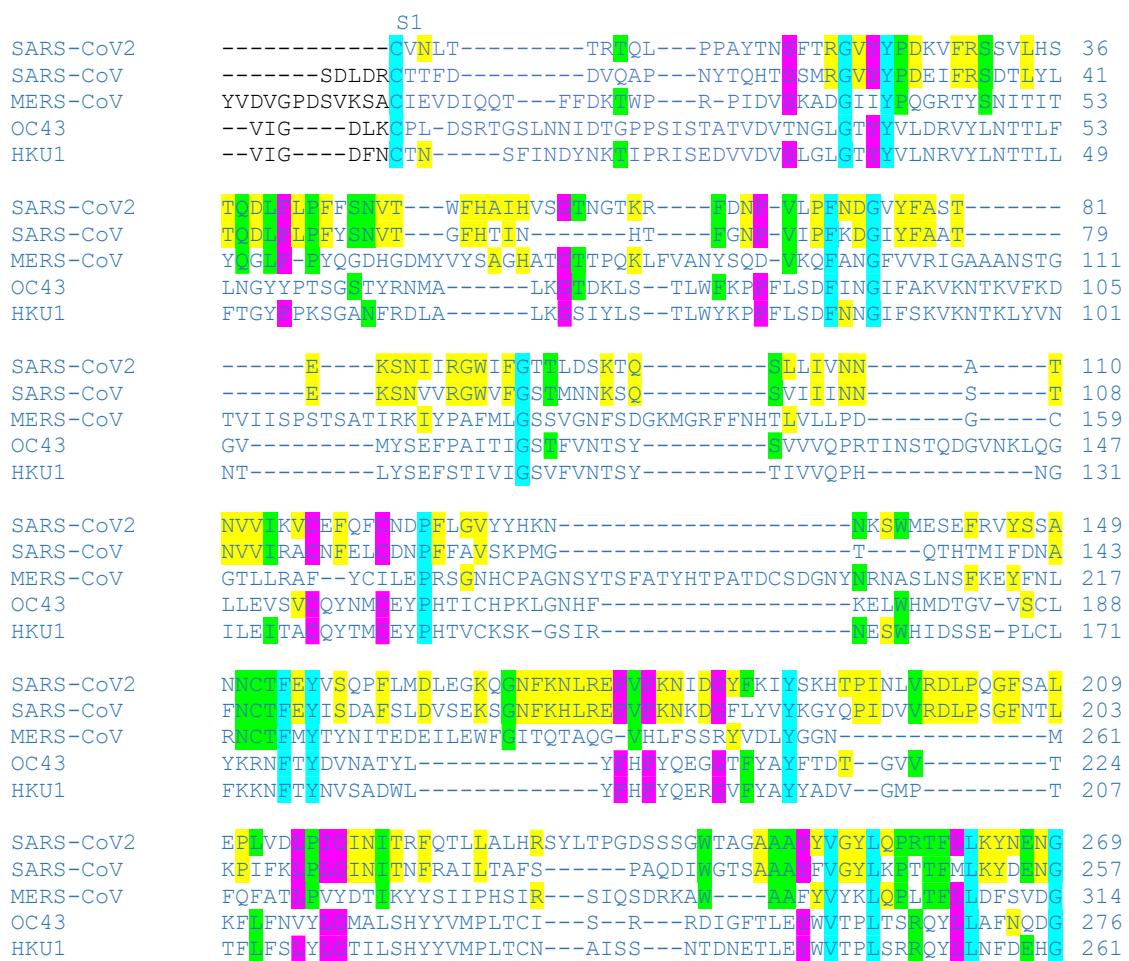


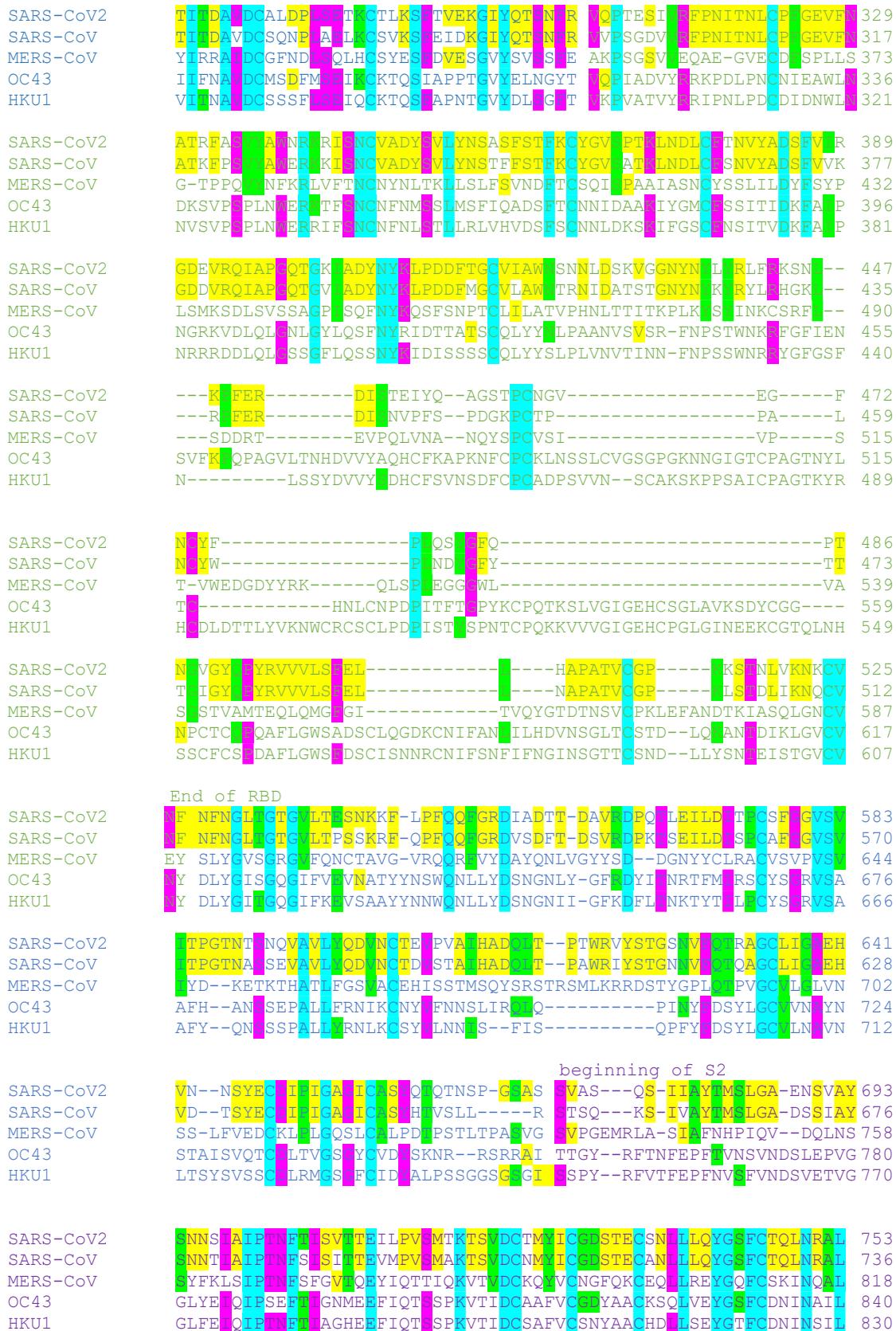
Figure S2. A plot of sample dilution vs. reduction % is shown for a positive convalescent patient sample as an example. The NT_{50} (grey dot) was determined by modeling the does-response curve shown as red line using Eq. 4 provided in the figure.



Supplemental coronaviruses spike protein sequences: Comparison of the full length spike protein sequence for R619-X16: SARS-CoV2 S-2P-3C-His8-Strep2x2 (SARS-CoV2), R619-X17: SARS-CoV S-2P-3C-His8-Strep2 (SARS-CoV), R619-X18: MERS-CoV S-2P-3C-His8-Strep2x2 (MERS-CoV), R619-X19: OC43 S-2P-3C-His8-Strep2x2 (OC43), and R619-X20: HKU1 S-2P-3C-His8-Strep2 (HKU1). The S1 section is in blue text, the RBD section green text and the S2 section purple text. The highlights indicate the homology compared with SARS-CoV2. Blue indicates all five sequences have the same the amino acid, pink indicates four of the five sequences, green for three and yellow for two sequences the same. Abbreviations: 3C, rhinovirus 3C protease cleavage site; Strep2x2, dual Strep2 epitope tag; T7, bacteriophage T7 fibritin trimerization domain; SBP, streptavidin binding peptide. The sequence alignment was carried out using Clustal Omega program (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).



RBD



SARS-CoV2	TEIAVEEDKNTQEVHQVQIYKTP----IKDFFGF-NFQIQIE-DP---SFPKRSF	803
SARS-CoV	SCIAAEEDRNTRENSQVKQMYKTST-----LKYFGGF-NFQIQIE-DP---LVPFKRSF	786
MERS-CoV	HANLRDDSVRNLTSASVYSSQSSSI-----IPGEGGDFNLTLLERVSISTGSRQARSA	872
OC43	TEVNELLDTTQLQVANSLMNGVTLSTKLKGDNVNFDINP-SVLDGLGSECYASSRSA	900
HKU1	NEVNDLLDITQLQVANALM-GVTLSSNLNTNLHSDVDNIDEKSLLGCLGSQCGS-SRSLS	889
SARS-CoV2	LEDLLFNKVILADAGFIKQYGDCL--GDIAARDLTCIAQKENGTLTVLPPLTDDEMIDQYTS	861
SARS-CoV	LEDLLFNKVILADAGEMKQYGECL--GDINARDLTCIAQKENGTLTVLPPLTDDEMIDQYTA	844
MERS-CoV	LEDLLFDKVILIDPGYMQGYDDCMQQGPASRDLTCQYVAGYKVLPPMDVNDEAYTS	932
OC43	LEDLLFDKVLSLDVGFAAAYNNCT--GGAEIRDLLCVCQSYKGIVLPPLESENQISGYTL	958
HKU1	LEDLLFNKVLSLDVGFAEAYNNCT--GGSEIRDLLCVCQSYKGIVLPPILESENQISGYTT	947
SARS-CoV2	PFLAGTITSWTFAGAAALQIPFMQMAYRFNGIGUTQNVLYENQKELIANQNSAIGKIQ	921
SARS-CoV	PVSGTATAFWTFAGAAALQIPFMQMAYRFNGIGUTQNVLYENQKQIANQFNKAISQIQ	904
MERS-CoV	SULGSIAGVWTAGLSSFAATPFAQSIFYRLNGVGITQVQLSENQKELIANKFNOALGAMQ	992
OC43	PAATSASLFPPTWIAA---AGVPFYLNQYRINGLGVTMVDVLISQNQKELIANAFNNAIDAQ	1014
HKU1	PAATVAAMFPFWSAA---AGVPFSLNVQYRINGLGVTMVDVLINKNQKELIANAFNKAISLQ	1003
SARS-CoV2	DSLSSTAALGKLOQVNVQNAQALNTLVKQLSSNFGAISSVENDIESRLDPPEAQVQIDR	981
SARS-CoV	ESLTTTISTALGKLOQVNVQNAQALNTLVKQLSSNFGAISSVENDIESRLDPPEAQVQIDR	964
MERS-CoV	TGFTTTNEAFHKVQDAVNNNAQALSKLASELSNTFGAIACIGIIIQRLDPPEQDAQIDR	1052
OC43	EGFDAATNCALVKIQAVVNANAEALNNLQQLSNRFGAISSCQEIESRLDPPEAQVQIDR	1074
HKU1	NGFTATNCALAKIQSVNVNANAQALNSLQQLFNKFGAISSCQEIESRLDPPEAQVQIDR	1063
SARS-CoV2	LITGRQLSQLQTYVTQQLIRAAEIRASANIAATKMSCEVLGQSHRVDFCGKGYHLMSHEQS	1041
SARS-CoV	LITGRQLSQLQTYVTQQLIRAAEIRASANIAATKMSCEVLGQSHRVDFCGKGYHLMSHEQA	1024
MERS-CoV	LINGRLTTLNAFVQAQQLVRSESAALSAQIAKDKVNECVKAQSPRSFCGQGQTHIVSVNVN	1112
OC43	LINGRLTALNAIVSQQLSDSTLVKFSAQAAQAMEKVNECVKSQSSRINFCCGNGNHIISLVN	1134
HKU1	LINGRLTALNAIVSQQLSDITLIKAGASRAIEKVNECVKSQSPRINFCCGNGNHILSVN	1123
SARS-CoV2	APHGVVFLHTYPAQEKNFTTAAPAIChDGKA--HFPRREGVFSN-----GTHWFVITQR	1093
SARS-CoV	APHGVVFLHTYPSQERNFTTAAPAIChDGKA--YFPRREGVFSN-----GTSWEITQR	1076
MERS-CoV	APNGLYFMHGYYPSPNHSIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTNTRIVDEWSYTGS	1172
OC43	APYGLYFIHFSYVPTKYVTAKVSPGLCIAGDR--GIAPKSGYFNVN----NNTWMYTGS	1187
HKU1	APYGLLFIHFSYKPTSFKTVLVSPLGLCLSGDR--GIAPKQGYFEIKQ----NDSWMFTGS	1176
SARS-CoV2	NPEPEPIIITDNTFJSGNCDVVIGIVNNNTVYDQLO--PELDASFKEELDKYFKNPESPQDVI	1151
SARS-CoV	NFSPQIITTDNTFJSGNCDVVIGIINNTVYDQLO--PELDASFKEELDKYFKNPESPQDVI	1134
MERS-CoV	SPEAPEPIIISLNPKYVAPQVTYQN-ISTNLPPEL LGNSTGIDFQDELEEFFKNVSTSIPN	1231
OC43	GYWYPEPIIENNVMVJMSTCAVNYTKAPYVML--NTSTEINLPDFREELDQWFKNQTSVAPL	1245
HKU1	SYWYPEPISDKNVVFMSCSUNFTKAPFIYL--NNNSIENLSDFEAEIISLWFKNQTSIAPN	1234
SARS-CoV2	EDISGINASVVNIKEIDRNLNEVAKNLNESLIDLQELGKYEQGSGYIPEAPRDGQAYVR	1211
SARS-CoV	EDISGINASVVNIKEIDRNLNEVAKNLNESLIDLQELGKYEQGSGYIPEAPRDGQAYVR	1194
MERS-CoV	FSLTQINTTLLDTYEMLSLQQVVKALNPSVYDIDKQHIGNTYGSGYIPEAPRDGQAYVR	1291
OC43	LSLD-YINVTFFLDLQEMNRQOEAIKVLN-----GSGYIPEAPRDGQAYVR	1290
HKU1	LTfnSHINATFLDLYYEMNVIQESIKSLN-----GSGYIPEAPRDGQAYVR	1280
SARS-CoV2	KDGEWVLLSTFLGRSLEVLFQGPGRHHHHHHHSAWSHPQFEKGGGGGGGGGGGGGGGGGGGG	1271
SARS-CoV	KDGEWVLLSTFLGRSLEVLFQGPGRHHHHHHHSAWSHPQFEKGGGGGGGGGGGGGGGGGG	1236
MERS-CoV	KDGEWVLLSTFLGRSLEVLFQGPGRHHHHHHHSAWSHPQFEKGGGGGGGGGGGGGGGGGG	1351
OC43	KDGEWVLLSTFLGRSLEVLFQGPGRHHHHHHHSAWSHPQFEKGGGGGGGGGGGGGGGGGG	1350
HKU1	KDGEWVLLSTFLGRSLEVLFQGPGRHHHHHHHSAWSHPQFEKGGGGGGGGGGGGGGGGGG	1322
SARS-CoV2	PER 1274	
SARS-CoV	--- 1236	
MERS-CoV	PER 1354	
OC43	PER 1353	
HKU1	--- 1322	