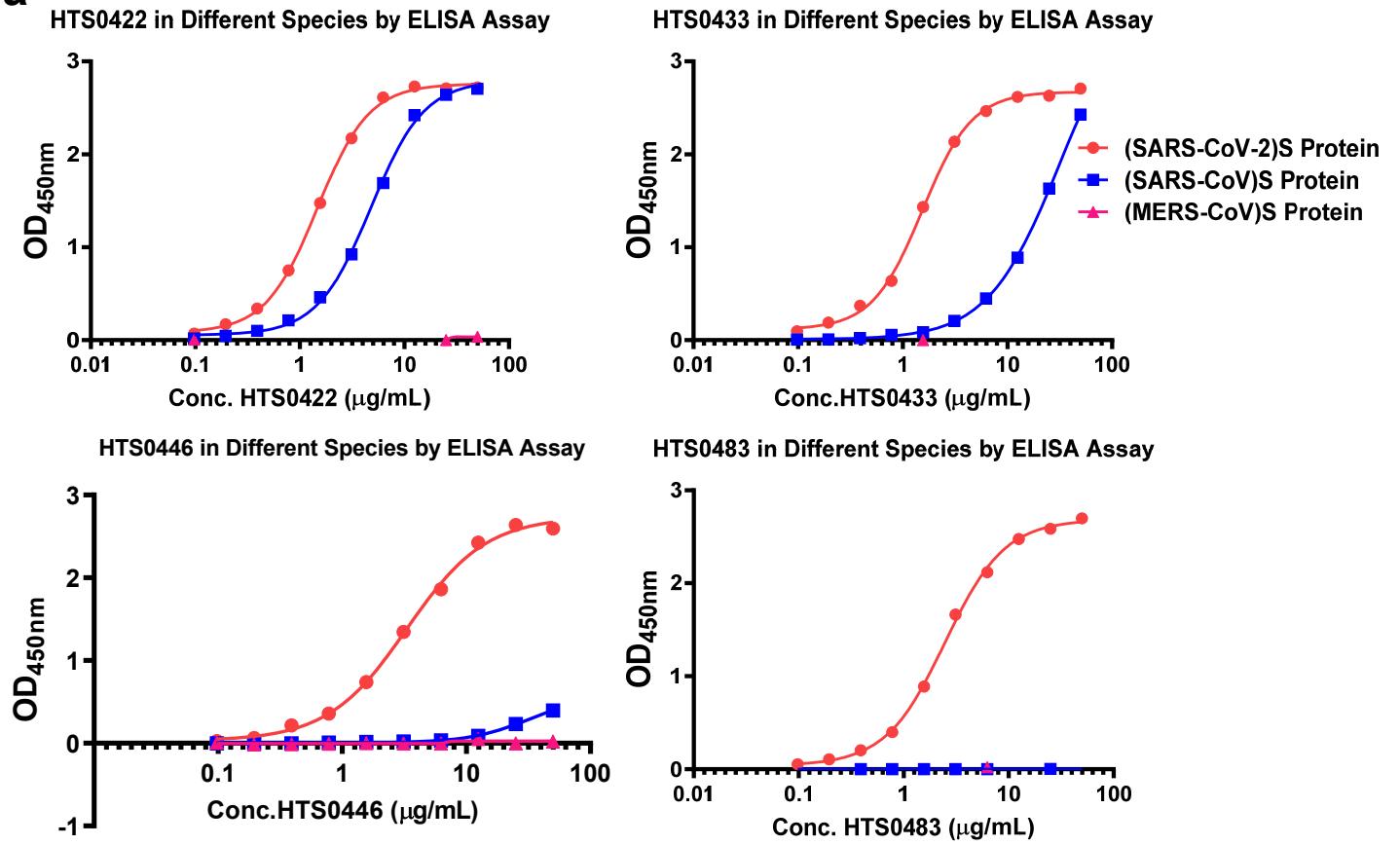
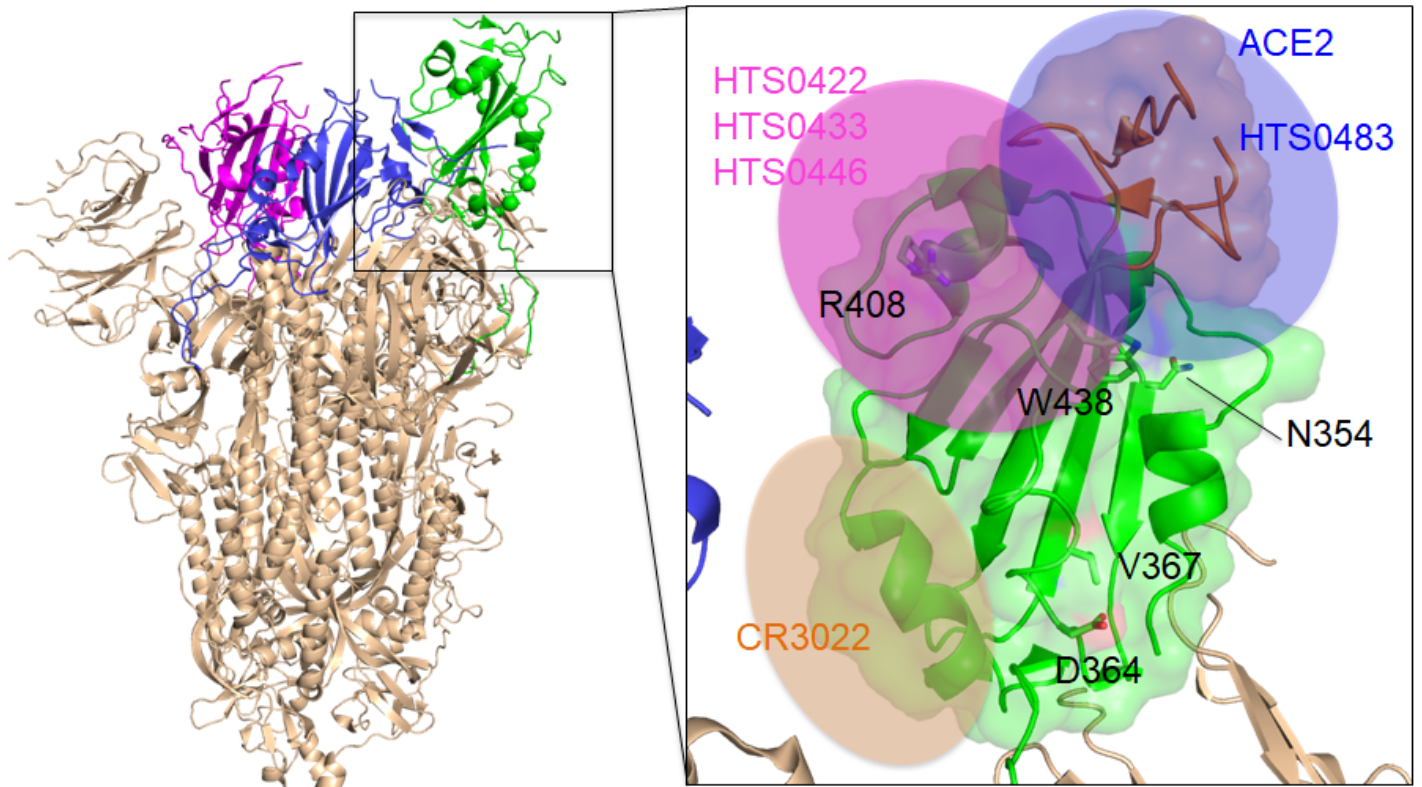


# Supplementary figure 1

**a**



**b**



Supplementary Tables 1

Clone Information			Sequence Information				AA Seq.
SN	Clone ID	Germline	CDR1	CDR2	CDR3		
1	HTS0390	VH	IGHV3-53*04	GVTVSSNY	IYSGGST	ARDLVSSGMDV	QVQLVQSGGGLVQPGGSLRLSCAASGVTVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFTISRHNKNTLYLQMNLSRAEDTAVYYCARDLVSSGMDVWVGQGTIVTVSS
		VL	IGKV1-12*01	QGISSW	AAS	QQANSFPPA	DIVMTQSPSSVSASVGDRTVITCRASQGISSWLAWEYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQANSFPPAFPGGPKTKVDIK
2	HTS0414	VH	IGHV1-18*01	GVTFTSYG	ISAYHGNT	ARGLAPSYCGGDCYPRAPFDY	EVQLVQSGAEVVKPGASVKVSCASGYFTFSYGISVWRQAPGGLEWVMSWISAYHGNTNAYAKLQGRVTMTDTSTAYMELRSLRSDDTAVYYCARGLAPSYCGGDCYPRAPFDYWGQGLTVTVSS
		VL	IGKV1-39*01	QSISSY	AAS	QQSYSTPYT	DIQLTQSPSSLSASVGDRTVITCRASQSISSYLWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQSYSTPYTFGGGKLEIK
3	HTS0422	VH	IGHV3-9*01	GFTFDDYA	ISWNSGSI	AKEDAGYYDDSSGYYPKAWHYFDL	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMHWVVRQAPGKLEWVSGISWNSGSIYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTALYYCAKEDAGYYDDSSGYYPKAWHYFDLWGRGTMVTVSS
		VL	IGKV1-39*01	QSISSY	AAS	QQSHSTPYT	AIQMTQSPSSLSASVGDRTVITCRASQSISSYLWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQSHSTPYTFGGGKTKVEIK
4	HTS0433	VH	IGHV3-9*01	GFTFDDYA	ISWNSGSI	AKEDAGYYDDSSGYYPKAWHYFDL	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMHWVVRQAPGKLEWVSGISWNSGSIYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTALYYCAKEDAGYYDDSSGYYPKAWHYFDLWGRGLTVTVSS
		VL	IGKV1-39*01	QSISSY	AAS	QQSYSTPRT	DIVMTQSPSSLSASVGDRTVITCRASQSISSYLWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQSYSTPRTFGGGKTKLEIK
5	HTS0446	VH	IGHV3-9*01	GFTFDDYA	ISWNSGSI	AKEDAGYYDDSSGYYPKAWHYFDL	QVQLVQSGGGLVQPGGSLRLSCAASGFTFDDYAMHWVVRQAPGKLEWVSGISWNSGSIYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTALYYCAKEDAGYYDDSSGYYPKAWHYFDLWGRGLTVTVSS
		VL	IGKV1-39*01	QSISSY	AAS	QQSYSTPRT	AIRMTQSPSSLSASVGDRTVITCRASQSISSYLWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQSYSTPRTFGGGKTKVEIK
6	HTS0461	VH	IGHV3-53*01	GFTVSSNY	IYSGGST	ARDLVVFGMDV	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDLVVFGMDVWVGQGTIVTVSS
		VL	IGKV1-12*01	QGISSW	AAS	QQAEA	AIRMTQSPSSVSASVGDRTVITCRASQGISSWLAWEYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQAEAFGGGKTKVEIK
7	HTS0472	VH	IGHV3-53*04	GVTVSSNY	IYSGGST	ARDLVSSGMDV	EVQLVETGGGLVQPGGSLRLSCAASGVTVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFTISRHNKNTLYLQMNLSRAEDTAVYYCARDLVSSGMDVWVGQGTIVTVSS
		VL	IGKV1-9*01	QIISY	AAS	QQLNSYPFT	EIVLTQSPSFLSASVGDRTVITCRASQIISYLWYQQEFGKAPKLLIYAESTLQGGVPSRFSGSGSDEFTLTISSLQPEDFATYYCQQLNSYPFTFGGGKTKVEIK
8	HTS0476	VH	IGHV3-53*04	GVTVSSNY	IYSGGST	ARDLVSSGMDV	EVQLVQSGGGLVQPGGSLRLSCAASGVTVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFTISRHNKNTLYLQMNLSRAEDTAVYYCARDLVSSGMDVWVGQGTIVTVSS
		VL	IGKV1-9*01	QGISSY	AAS	QQLNSYPPT	AIQLTQSPSFLSASVGDRTVITCRASQGISSYLWYQQKPGKAPKLLIYAESTLQSGVPSRFSGSGSDEFTLTISSLQPEDFATYYCQQLNSYPPTFGGGKTKVEIK
9	HTS0477	VH	IGHV1-18*01	GVTFTSYG	ISGFHGNT	ARGLAPSYCGGDCYPRAPFDY	EVQLVQSGAEVVKPGASVKVSCASGYFTFSYGISVWRQAPGGLEWVMSWISGFHGNTNAYAKLQGRVTMTDTSTAYMELRSLRSDDTAVYYCARGLAPSYCGGDCYPRAPFDYWGQGLTVTVSS
		VL	IGKV1-39*01	QSISSY	AAS	QQSYSTLLT	AIQLTQSPSSLSASVGDRTVITCRASQSISSYLWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQSYSTLLTFGGGKTKVEIK
10	HTS0478	VH	IGHV3-53*02	GFTVGSNY	IYSGGST	ARDLVVYGMV	EVQLVETGGGLIQPGGSLRLSCAASGFTVGSNYMSVWRQAPGKLEWVSLIYSGGSTYYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDLVVYGMVWVGQGTIVTVSS
		VL	IGKV1-9*01	QGISSY	AAS	QQLNSYPPT	DIVMTQSPSFLSASVGDRTVITCRASQGISSYLWYQQKPGKAPKLLIYAESTLQSGVPSRFSGSGSDEFTLTISSLQPEDFATYYCQQLNSYPPTFGGGKTKVEIK
11	HTS0483	VH	IGHV3-66*01	GITVSSNY	IYSGGST	ARDLQERGGMDV	QVQLVESGGGLVQPGGSLRLSCAASGITVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFISRDNNAKNSLYLQMNLSRAEDTAVYYCARDLQERGGMDVWVGQGTIVTVSS
		VL	IGKV3D-20*0	QSVSSSY	DAS	QQYGSPLT	EIVLTQSPATLSLSPGERATLSCGASQSVSSYLAWYQQKPGAPKLLIYDASSRATGIPDRFSGSGSDFTLTISSLQPEDFATYYCQQYGSPLTFGGGKTKVEIK
12	HTS0777	VH	IGHV3-66*01	GITVSSNY	IYSGGST	ARDLQERGGMDV	QVQLVESGGGLVQPGGSLRLSCAASGITVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFISRDNNAKNSLYLQMNLSRAEDTAVYYCARDLQERGGMDVWVGQGTIVTVSS
		VL	IGKV1-5*03	QAISNW	EAS	QQYGNWYT	DIQLTQSPSTLSASVGDRTVITCRASQAISNWLAWYQQKPGKAPKLLIYASNLESGVPSRFSGSGSDEFTLTISSLQPEDFATYYCQQYGNWYTFGGGKTKVEIK
13	HTS0778	VH	IGHV3-9*01	GFTFDDYA	ISWNSGSI	AKEDAGYYDDSSGYYPKAWHYFDL	QVQLVQSGGGLVQPGGSLRLSCAASGFTFDDYAMHWVVRQAPGKLEWVSGISWNSGSIYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTALYYCAKEDAGYYDDSSGYYPKAWHYFDLWGRGLTVTVSS
		VL	IGKV1-39*01	QSISSY	AAS	QQSYSTPLT	DIQLTQSPSSLSASVGDRTVITCRASQSISSYLWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGKTKLEIK
14	HTS0889	VH	IGHV3-30*04	GFTFSTYA	ISYDGSNK	ARVKGKRVFLGGMDV	EVQLLESGGGVVQPGGSLRLSCAASGFTFSTYAMHWVVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARVKGKRVFLGGMDVWVGQGTIVTVSS
		VL	IGKV2-28*01	QSLHNSGY	LGS	MQUALQTPYT	DIVMTQPPLSLPVTGPEPASICRSSLHNSGNYLWYDYLQKPGQSPQLLIYLSNRSASVGPDRFSGSGSDFTLTISSLQPEDFATYYCQYQYGNWYTFGGGKTKVEIK
15	HTS0896	VH	IGHV3-53*01	GFTVSRNY	IYSGGST	ARDLVVYGMV	EVQLVQSGGGLIQPGGSLRLSCAASGFTVSRNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDLVVYGMVWVGQGTIVTVSS
		VL	IGKV1-12*01	QGISSW	GAS	QQANSFPPPT	DIQMTQSPSSVSASVGDRTVITCRASQGISSWLAWEYQQKPGKAPKLLIYASLQSGVPSRFSGSGSDFTLTISSLQPEDFATYYCQQANSFPPPTFGGGKTKVEIK
16	HTS0916	VH	IGHV3-53*02	GFTVSSNY	IYSGGST	ARDLLEVGGMDV	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDLLEVGGMDVWVGQGTIVTVSS
		VL	IGKV3-20*01	ESVSSSY	GAS	QQYGSPPYT	EIVMTQSPDITLSLSPGERATLSCRASESVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSDFTLTISSLQPEDFATYYCQQYGSPPYTFGGGKTKVEIK
17	HTS0917	VH	IGHV3-15*01	EFTFSNAW	IKSKTDGGTT	TTDQPEGYGSGSVVYVYGMV	EVQLVESGGGLVQPGGSLRLSCAASEFTFSNAWMSVWRQAPGKLEWVSGRIKSKTDGGTTDYAAPVKGRFTISRDNNAKNSLYLQMNLSKTEDTAVYYCTDQPEGYGSGSVVYVYGMVWVGQGTIVTVSS
		VL	IGKV2-30*02	QSLVHSDGN	KVS	MQGTHWPPNT	DIVMTQSPSLPVTLQGPASICRSSLVHSDGNLYLWYFQQRPQSPRRLIYKVNRSRSGVDRFSGSGSDFTLTISSLQPEDFATYYCQQGTHWPPNTFGGGKTKVEIK
18	HTS0922	VH	IGHV3-15*01	EFTFSNAW	IKSKTDGGTT	TTDQPEGYGSGSVVYVYGMV	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSVWRQAPGKLEWVSGRIKSKTDGGTTDYAAPVKGRFTISRDNNAKNSLYLQMNLSKTEDTAVYYCTDQPEGYGSGSVVYVYGMVWVGQGTIVTVSS
		VL	IGKV2-30*02	QSLVHSDGN	KVS	MQGTHWPPYT	DIVMTQPPLSLPVTLQGPASICRSSLVHSDGNLYLWYFQQRPQSPRRLIYKVNRSRSGVDRFSGSGSDFTLTISSLQPEDFATYYCQQGTHWPPYTFGGGKTKVEIK
19	HTS0936	VH	IGHV3-53*01	GFTVSSNY	IYSGGST	ARDLHVVGAFDI	EVQLVQSGGGLIQPGGSLRLSCAASGFTVSSNYMSVWRQAPGKLEWVSVIYSGGSTYYADSVKGRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDLHVVGAFDIWVGQGTIVTVSS
		VL	IGKV3-20*01	QSVSSSY	GAS	QQYGSPPDT	EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYAGASSRATGIPDRFSGSGSDFTLTISSLQPEDFATYYCQQYGSPPDTFGGGKTKLEIK

**Supplementary Tables 2****Human VK Front primers with NheI**

VK1.1 Front NheI	ACTACGGCTAGCGMCATCCAGTTGACCCAG
VK1.2 Front NheI	ACTACGGCTAGCGCCATCCRGATGACCCAG
VK1.3 Front NheI	ACTACGGCTAGCRACATCCAGATGACCCAG
VK1.4 Front NheI	ACTACGGCTAGCGYCATCTGGATGACCCAG
VK2.1 Front NheI	ACTACGGCTAGCGATRTTGTGATGACTCAG
VK2.2 Front NheI	ACTACGGCTAGCGAKATTGTGATGACCCAG
VK3.1 Front NheI	ACTACGGCTAGCGAAATTGTGTTGACRCAG
VK3.2 Front NheI	ACTACGGCTAGCGAAATAGTGATGAYGCAG
VK3.3 Front NheI	ACTACGGCTAGCGAAATTGTAATGACACAG
VK4 Front NheI	ACTACGGCTAGCGACATCGTGATGACCCAG
VK5 Front NheI	ACTACGGCTAGCGAAACGACACTCACGCAG
VK6 Front NheI	ACTACGGCTAGCGAAATTGTGCTGACTCAG

**Human VK back primers with NotI**

VK1 Back NotI	CAGAATGCGGCCGCTTTGATTTCCACCTTGGTCCC
VK2 Back NotI	CAGAATGCGGCCGCTTTGATCTCCAGCTTGGTCCC
VK3 Back NotI	CAGAATGCGGCCGCTTTGATATCCACTTTGGTCCC
VK4 Back NotI	CAGAATGCGGCCGCTTTGATCTCCACCTTGGTCCC
VK5 Back NotI	CAGAATGCGGCCGCTTTAATCTCCAGTCGTGTCCC

**Human VH Front primers with SfiI**

VH1.1 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTKCAGCTGGTGCAG
VH1.2 Front SfiI	TACTCGCGGCCAGCCGGCCSAGGTCCAGCTGGTACAG
VH1.3 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTCCAGCTTGTGCAG
VH1.4 Front SfiI	TACTCGCGGCCAGCCGGCCARATGCAGCTGGTGCAG
VH1.5 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTCCAGCTGGTGCAR
VH2.1 Front SfiI	TACTCGCGGCCAGCCGGCCAGRTCACCTTGAAGGAG
VH2.2 Front SfiI	TACTCGCGGCCAGCCGGCCRRGGTACCTTGAGGGAG
VH3.1 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTGGTGGAG
VH3.2 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTGTTGGAG
VH3.3 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAWCTGGTGGAG
VH3.4 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTGTTGGAG
VH3.5 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTGGTGGAS
VH3.6 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTACAGCTGGTGGAG
VH3.7 Front SfiI	TACTCGCGGCCAGCCGGCCGAAGTGCAGCTGGTGGAG
VH3.8 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTGGTGRAG
VH4.1 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTRCAGGAG
VH4.2 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTACAGCTGCAGGAG
VH4.3 Front SfiI	TACTCGCGGCCAGCCGGCCRGCTGCAGCTGCAGGAG
VH4.4 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTGCAGGAC
VH4.5 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCGGCTGCAGGAG
VH4.6 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTACARCAG
VH5 Front SfiI	TACTCGCGGCCAGCCGGCCARGTGCAGCTGGTGCAG
VH6 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTACAGCTGCAGCAG
VH7 Front SfiI	TACTCGCGGCCAGCCGGCCAGGTGCAGCTGGTGCAA

**Human VH Back primers with XhoI**

VH1 Back XhoI	CCACCACCACTCGAGACRGTGACCAGGGTG
VH2 Back XhoI	CCACCACCACTCGAGACGGTGACCAGGGT
VH3 Back XhoI	CCACCACCACTCGAGACGGTGACCATTGT
VH4 Back XhoI	CCACCACCACTCGAGACGGTGACCGTGGT

**Supplementary Tables 3**

<b>Sample</b>	<b>Vendor</b>	<b>Cat.No.</b>	<b>AA fragment</b>	<b>Gene Accession #</b>
SARS-CoV-2 S protein RBD, His Tag	ACROBiosystems	SPD-C52H3	Arg 319 - Lys 537	QHD43416.1
SARS-CoV-2 S protein RBD(W436R), His Tag	ACROBiosystems	SPD-S52H7	Arg 319 - Phe 541	QHD43416.1
SARS-CoV-2 S protein RBD(R408I), His Tag	ACROBiosystems	SPD-S52H8	Arg 319 - Phe 541	QHD43416.1
SARS-CoV-2 S protein RBD(N354D), His Tag	ACROBiosystems	SPD-S52H5	Arg 319 - Phe 541	QHD43416.1
SARS-CoV-2 S protein RBD(V367F), His Tag	ACROBiosystems	SPD-S52H4	Arg 319 - Phe 541	QHD43416.1
SARS-CoV-2 S protein RBD(N354D, D364Y), His Tag	ACROBiosystems	SPD-S52H3	Arg 319 - Phe 541	QHD43416.1
SARS, S protein, His Tag	ACROBiosystems	SPN-S52H5	Ser 14 - Pro 1195	AAP13567.1
MERS-CoV, S Protein, His Tag	ACROBiosystems	SPD-M52H6	Glu 367 - Tyr 606	K0BRG7-1