Supplemental Materials for

A single domain antibody inhibits SFTSV and mitigates virus-induced pathogenesis in vivo

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Conflict of interest statement: The authors have declared no conflict of interest. A patent application on SNB02 was submitted by Y-Clone Medical science Co. Ltd., under PCT/CN2019/097350.

Supplemental Figure 1. Camel anti-sera inhibit SFTSV to infect Vero cells. 4th anti-sera represents camel anti-sera after the 4th immunization o sGn (green line), pre-bleed is the sera from the camel before the immunization of sGn.

Supplemental Figure 2. The construction and verification of VHH phage library. (A) RNA extraction. Lane M: Ladder DL5000, Lane 1, RNA extraction from camel PBMC after final sGn immunization. (B) 1st PCR product， M: Marker DL2000 Lane 1~12: Primer 1 pairs (12 tubes); (C) 2nd PCR product, M: Marker DL5000 depicted as (A), Lane 1~8: Primer pairs (1 ~ 8); (D) Phage library characterization. Lane M: Marker DL2000 depicted as (B), the left lanes are single bacterial clones randomly picked up from bacterial phage library.

Supplemental Figure 3. Analysis of sGn-VHH antibody phage library. The alignment of VHH sequences. 50 clones were randomly selected from phage library for sequencing and their sequences were converted into VHH amino acid sequences and aligned.

Supplemental Figure 4. Sequence analysis of positive VHHs. (A) Evolutionary relationships of 142 VHHs was analyzed using the Neighbor-Joining method. The optimal tree with the sum of branch length = 6.61901583 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The analysis involved 142 amino acid sequences of VHH. All positions containing gaps and missing data were eliminated. There were a total of 93

positions in the final dataset. Evolutionary analyses were conducted in MEGA6. The reliability values indicated at the branch nodes were determined using 1,000 bootstrap replications. Bootstrap value was labeled at nodes. **(B)** Clonal lineage analysis. Each slice represents one clonal lineage; the size of the slice is proportional to the number of clones in the lineage. The total number of clones is shown in the center of the pie. Lineage numbering can be found in Data file S1. Clonal lineages were assigned based on the identical amino acids. **(C**) CDRH1, CDR H2 and CDRH3 length distribution.

Supplemental Figure 5. The SPR affinity profiles of SNB binding to sGn protein. (**A**) Summary of affinity constants of SNBs binding with sGn as determined by SPR. Ka, associate constant; kd, dissociate constant; KD, affinity constant; Rmax, the maximum response unit. Kinetic binding curve of SNBs with sGn. Different color curves represent different concentrations, sGn protein was bound by SNB02 (**B**), SNB07 (**C**) and SNB112 (**D**).

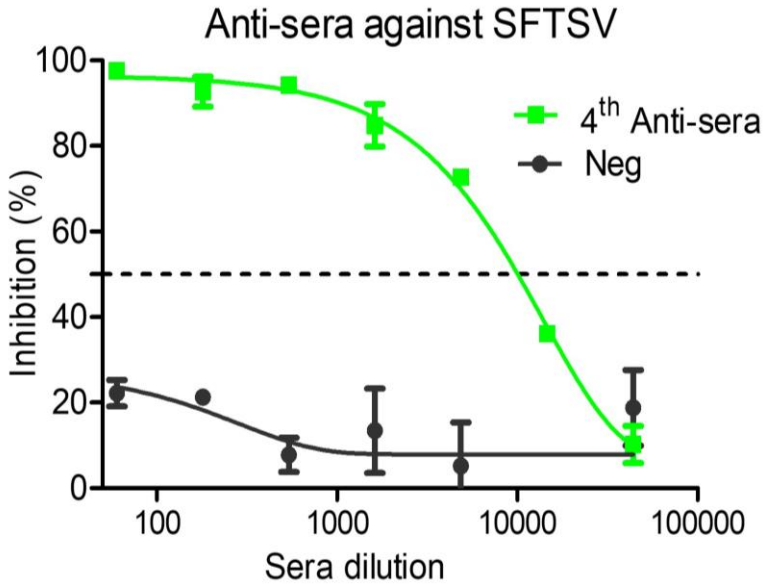
Supplemental Figure 6. Characterization of SNB02 binding with various subtypes of sGn. (**A)** ELISA analysis of the reactivity of SNB02 with various subtypes of sGn. sGn-A-E indicate the sGn protein from subtypes A-E, respectively. BSA binding with SNB02 was taken as antibody negative control (Negative). Data represent mean ± SEM. (**B)** Western-blot analysis of the reactivity of 0.5 μg/ml SNB02 with various subtypes of 2 μg sGN. Lane M: Maker, lane1: sGn-A, lane 2: sGn-B, lane 3: sGn-C, lane 4: sGn-D, lane 5: sGn-E, lane 6: BSA protein taken as negative control.

Supplemental Figure 7. Characterization of humanized SNB02. (**A**) ELISA analysis of the reactivity of SNB02 and humanized SNB02 (Hu-SNB02) with sGn. PBS binding with sGn was served as Blank control (Blank). (**B**) Neutralization activity of SNB against live SFTSV infection of Vero E6 cell. SNB-ctl, One VHH-huFc antibody without binding with sGn, was taken as antibody negative control. All experiments were repeated twice.

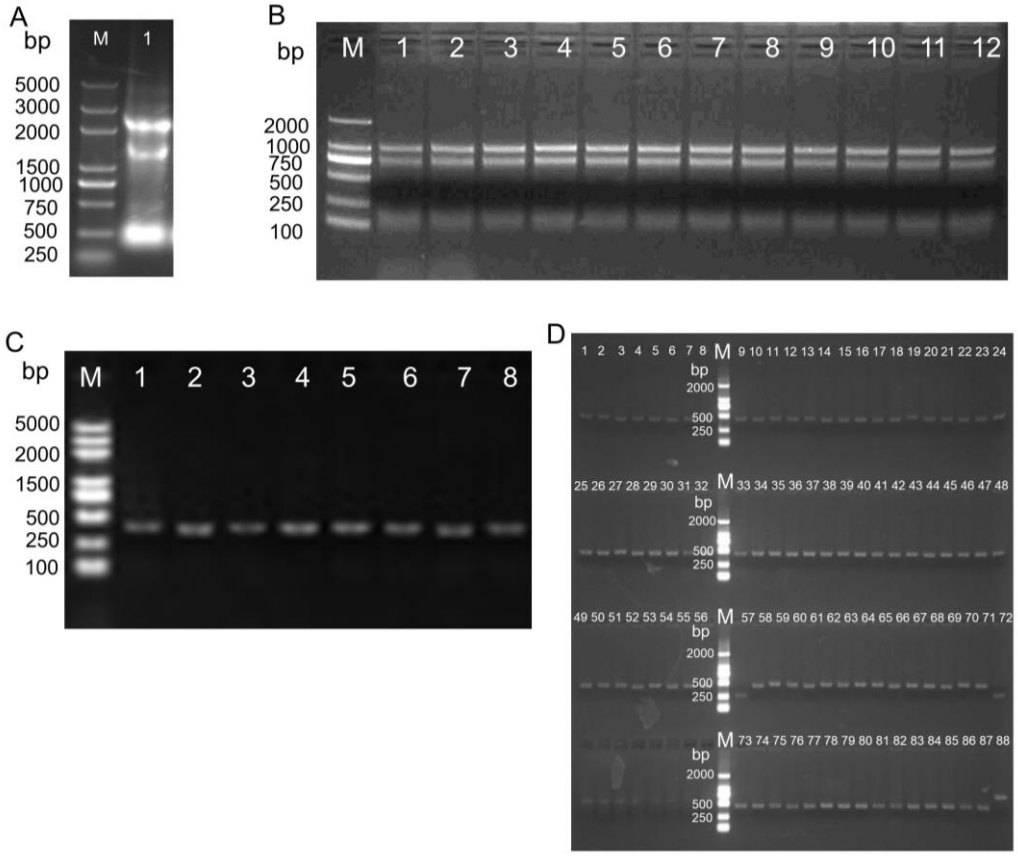
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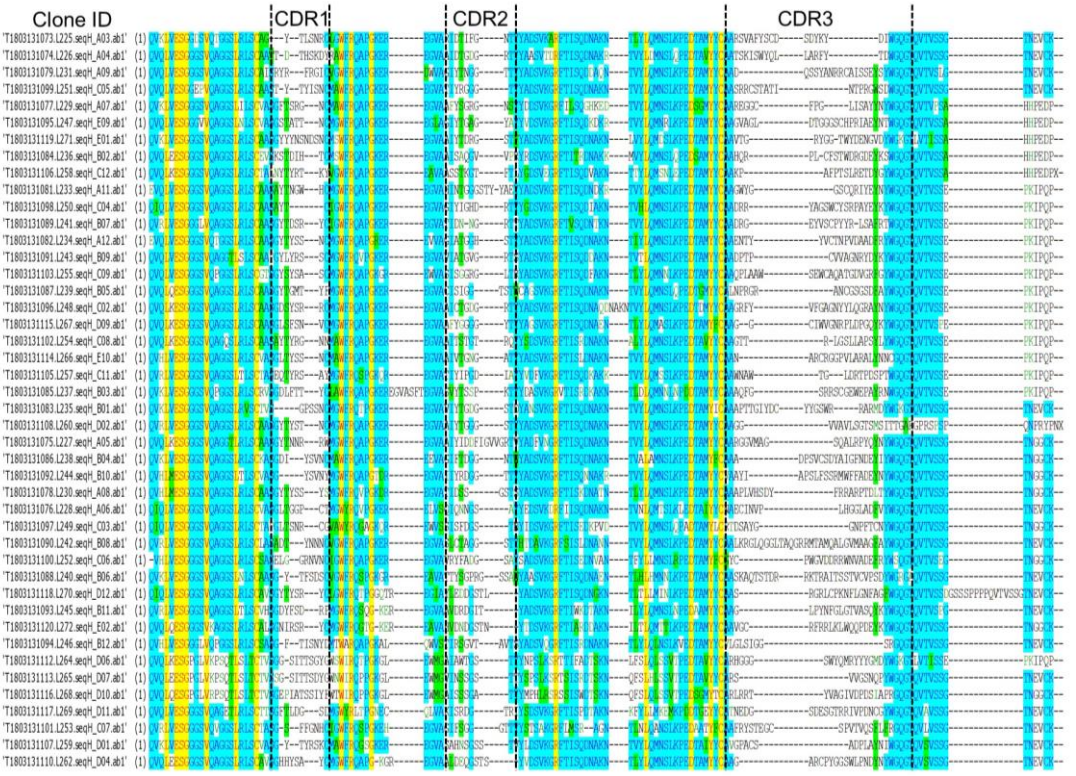
Supplemental Table 3. Summary of CDR sequences of 142 positive VHH clones



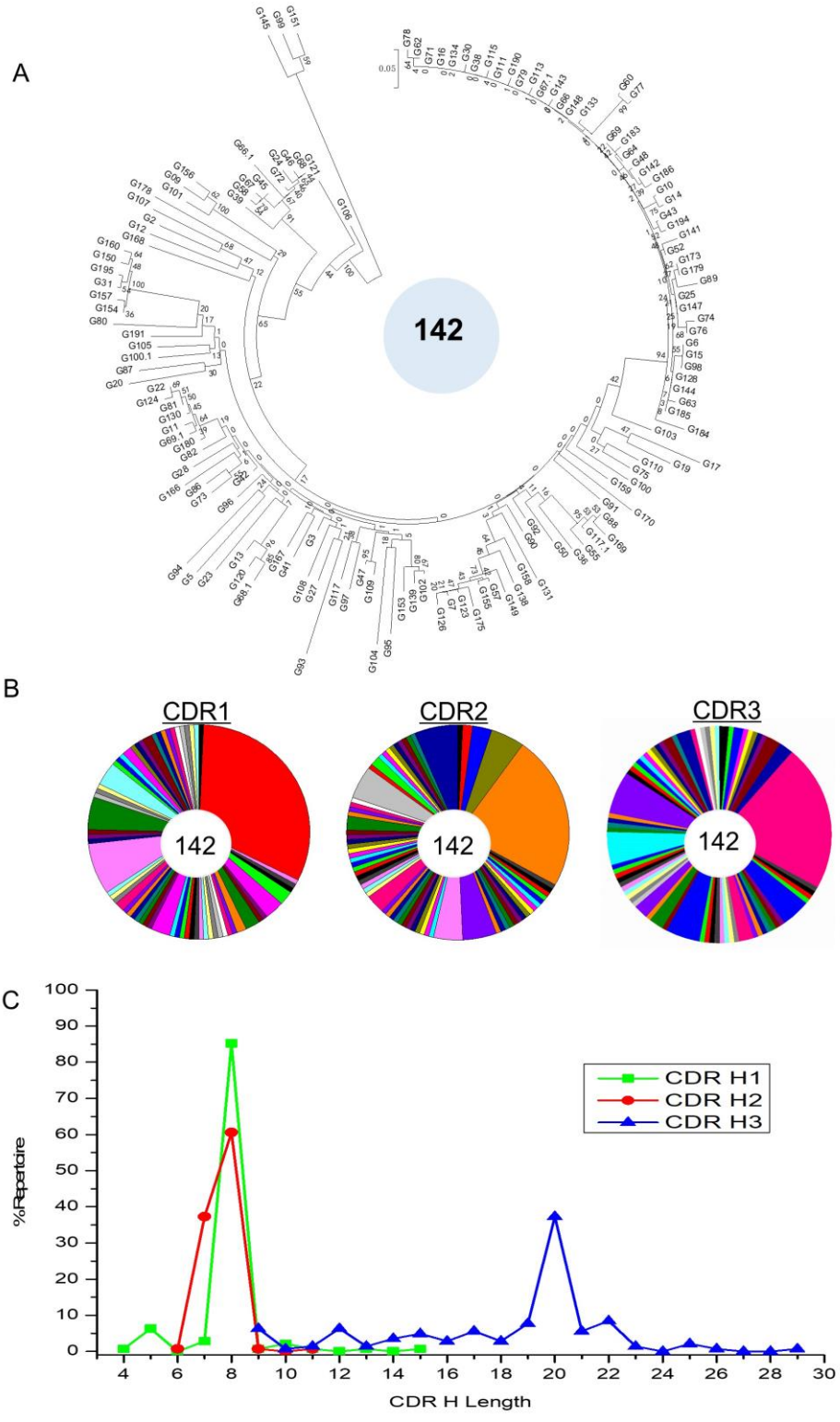
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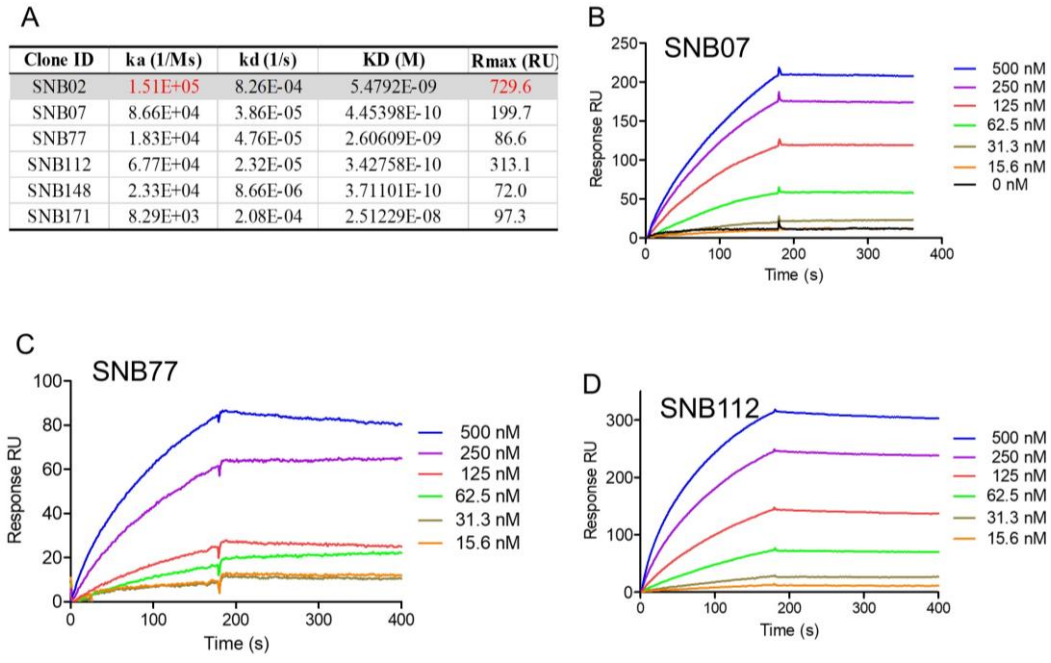


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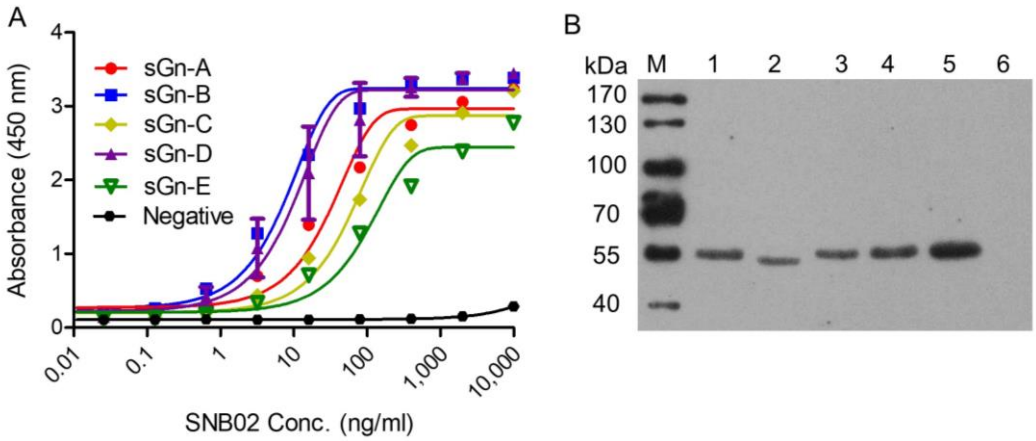
used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The analysis involved 142 amino acid sequences of VHH. All positions containing gaps and missing data were eliminated. There were a total of 93 positions in the final dataset. Evolutionary analyses were conducted in MEGA6. The reliability values indicated at the branch nodes were determined using 1,000 bootstrap replications. Bootstrap value was labeled at nodes. **(B)** Clonal lineage analysis. Each slice represents one clonal lineage; the size of the slice is proportional to the number of clones in the lineage. The total number of clones is shown in the center of the pie. Lineage numbering can be found in Data file S1. Clonal lineages were assigned based on the identical amino acids. **(C**) CDRH1, CDR H2 and CDRH3 length distribution.

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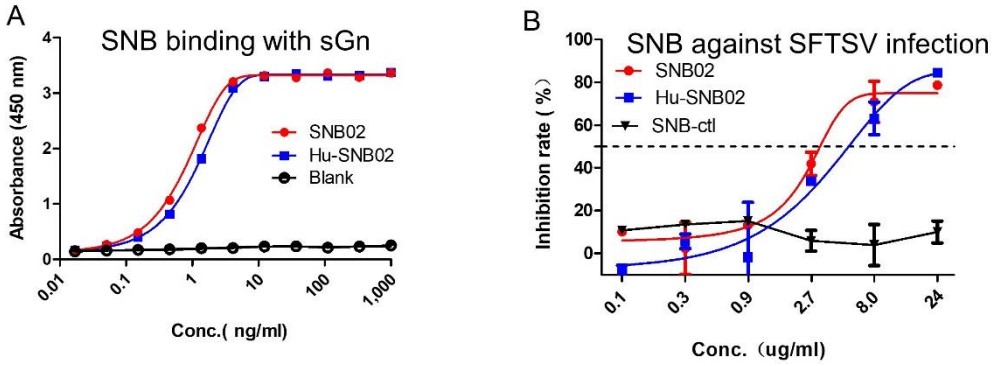
Clone ID	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)
SNB02	1.51E+05	8.26E-04	5.4792E-09	729.6
SNB07	8.66E+04	3.86E-05	4.45398E-10	199.7
SNB77	1.83E+04	4.76E-05	2.60609E-09	86.6
SNB112	6.77E+04	2.32E-05	3.42758E-10	313.1
SNB148	2.33E+04	8.66E-06	3.71101E-10	72.0
SNB171	8.29E+03	2.08E-04	2.51229E-08	97.3



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Supplemental Table 1. Summary of sGn-VHH library panning against sGn protein.

Project	Ag	Round	Input(pfu)	Output (pfu)	Enrichment	Positive rate(%)
sGn-VHH library	sGn protein 20ug/ml; 150ul/well;	1st	1x10^12	1.38x10^6	1	/
	sGn protein 100ug/ml; 150ul/well;	2nd	2x10^12 (1st amplified phage 3.2x10^13)	2.7x10^7	3.75	24.5%
	sGn protein 50ug/ml; 150ul/well;	3rd	1.2x10^12 (2nd amplified phage 1.21x10^13)	1.44x10^8	8.89	67%

Supplemental Table 2. The representative bacterial supernatant binding with sGn as determined by ELISA.

	◇	1	2	3	4	5	6	7	8	9	10	11	12
sGn	A	0.300	0.231	0.161	0.126	0.126	0.100	0.360	0.203	0.068	3.027	3.034	0.115
	B	0.384	0.163	0.182	0.175	0.109	0.335	0.804	0.094	0.153	0.188	0.219	0.076
	C	0.303	0.279	0.255	0.217	1.619	0.370	0.057	0.259	0.078	0.105	0.179	0.062
	D	0.091	0.315	0.055	0.102	0.094	0.914	0.157	0.094	0.142	0.065	0.078	0.120
	E	0.422	0.085	3.383	0.545	0.060	0.268	0.096	0.191	1.876	0.090	0.258	0.106
	F	0.212	2.312	0.478	3.607	0.180	0.574	0.168	0.159	0.072	0.066	0.186	0.096
	G	0.174	0.073	0.129	3.282	0.185	0.198	0.229	0.203	0.220	0.246	0.078	0.589
	H	0.145	0.206	0.075	0.102	0.532	0.301	0.141	0.965	0.148	2.982	0.243	0.205
	◇	1	2	3	4	5	6	7	8	9	10	11	12
Blank	A	0.088	0.079	0.068	0.076	0.071	0.075	0.090	0.077	0.059	0.090	0.121	0.068
	B	0.096	0.062	0.065	0.090	0.058	0.082	0.131	0.060	0.065	0.070	0.109	0.055
	C	0.123	0.076	0.080	0.073	0.104	0.097	0.053	0.083	0.063	0.060	0.069	0.051
	D	0.057	0.087	0.050	0.058	0.064	0.170	0.070	0.060	0.072	0.059	0.060	0.066
	E	0.098	0.055	0.096	0.097	0.057	0.078	0.065	0.099	0.110	0.058	0.076	0.065
	F	0.100	0.121	0.091	0.091	0.083	0.115	0.067	0.081	0.054	0.054	0.066	0.062
	G	0.070	0.059	0.094	0.088	0.104	0.092	0.101	0.076	0.090	0.074	0.060	0.172
	H	0.069	0.102	0.059	0.064	0.138	0.137	0.082	0.244	0.084	0.111	0.153	0.084
	◇	1	2	3	4	5	6	7	8	9	10	11	12
sGn/Blank	A	3.428	2.927	2.370	1.663	1.789	1.318	4.021	2.643	1.152	33.637	24.993	1.682
	B	3.988	2.607	2.797	1.940	1.866	4.083	6.127	1.566	2.364	2.687	2.005	1.395
	C	2.457	3.664	3.184	2.962	15.552	3.829	1.073	3.136	1.246	1.764	2.579	1.224
	D	1.592	3.628	1.097	1.768	1.487	5.392	2.249	1.580	1.981	1.095	1.287	1.810
	E	4.314	1.560	35.347	5.646	1.060	3.422	1.481	1.935	17.105	1.537	3.404	1.620
	F	2.127	19.172	5.252	39.589	2.164	4.979	2.513	1.962	1.340	1.237	2.807	1.561
	G	2.476	1.247	1.375	37.460	1.784	2.157	2.272	2.660	2.447	3.310	1.318	3.422
	H	2.096	2.008	1.287	1.605	3.844	2.188	1.736	3.957	1.764	26.987	1.593	2.440

Note: Each readout represents bacterial supernatant binding with sGn protein (upper table) and blank control (middle table). The lower table is the readout of sGn binding/the readout of blank binding from the same bacterial supernatant.

Supplemental Table 3. Summary of CDR sequences of 142 positive VHH clones

ID	Clone ID	SNBID	CDR1	CDR2	CDR3
P01	G02		GFTFDDS-------N	IK----SDGSTS	AA-------AWRPPCVP----------
P02	G03		GHTLSSN-------C	I---YTGGGHTY	AADLSPYDCYTGS----LDMASR------FT
P03	G05		GPFY-------NTHC	VY---P--HLTY	AA----VLCTDDYKMAPAN----------Y
P04	G06		GDTS-------TAYY	IY---RGGRATV	AAGLAGGSGYLPLNWAGF----------RY
P05	G07		GDTY-------SSSC	IC---SDG-SAA	AARR--------TWHAGF----------PY
P06	G10		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P07	G11		GFT---S--------C	IYT---RDGRPY	AANRRAY-PYGGDCRLRHAEFD--------Y
P08	G12		G-------VTLDDFL	ID----SEGRID	AADVPGRREVRGLGPCDRMY---------DY
P09	G13		GFSF-------NAYC	ID----S-GGSSS	AAKVPFGRGSCAYSTAHWFP----------Y
P10	G14		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P11	G15		GDTS-------TAYY	IY---RGGRATV	AAGLDGGSGYLPLNWAGF----------RY
P12	G16		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWDGF----------RY
P13	G17		GYTF-------SNTC	ID----R-SGSAS	VADLSAWCRAVRPG-VIT----Y-------NY
P14	G19		GRTY-------RTYC	IT----ALSATS	AADPRDPNGSSRTDCTVLTSKDLY--------NS
P15	G20		EDAHSTTEYIVSTTC	TY----RHGGTTV	AAGPG--------CSWSSF----------AY
P16	G22		GFT---S--------C	IYT---RDGRPY	AANRRAY-PYGGDCRLRHAEFD--------Y
P17	G23		GVTY-------GSYC	LE----S-DGSTS	VAMTWDGTCHITSEFYY----------
P18	G24		GFTLS-------MYD	IY---TSGRRPW	AAVIGVDIR----------
P19	G25		GDTS-------TAYY	IF---RGGRSTV	AAGLDGGSGYLPLNWDGF----------RY
P20	G27		EYTGSRN-------C	ISILYSGITVSY	AIRWGDCDSASWS------RRTWY-------AV
P21	G28		GYTYNNY-------R	IS--AGGD-HTY	ARSRASLW---SGNWYRSLSEDEY------NS
P22	G30		GDTS-------TAYY	IY---RGGRSTV	AAGHDGGSGYLPLNWDGF----------RY
P23	G31		GLYY-------PPLC	ID----R-DGSTS	AAA--DAQRGRTCFFGA----------
P24	G36		RYDY-------SRTC	IC---SDG-STS	AVRW--------YWDAGF----------KY
P25	G38		GDTS-------TAYY	IY---RGGRSTV	AAGHDGRSGYLPLNWAGF----------RY
P26	G39		GFTVS-------RYD	IF---VSGRSPW	AAVIGYDIR----------
P27	G41		GSAYSTN-------C	I---YRDDGTTY	AADSRTPSDCYSGSWLEKYPSEY--------SY
P28	G42		GYTYSSN-------C	I---YTGGGSTY	AADVVSYYSDYVC----TDAADF--------GY
P29	G43	SNB43	GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P30	G45		GFTFN-------AYD	IF-RSGRTSW	AAVIGVDIR----------
P31	G46		GFTLS-------MYD	IF---TSGRRPW	AAVIGVDIR----------
P32	G47		VYTYRGN-------N	IT--STGT-RQY	AAGTTRLG---------SLLAPTY----------RY
P33	G48		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P34	G50		RYTP-------TITR	IY---TRGDRTF	AAGFMYGETRSP-NWV----------NY
P35	G52		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P36	G55		VYTSSTM-------W	I---YRGNGATG	AKKR-TYDCYSGT----------CS
P37	G57		GDTY-------SSSC	IC---SDG-SAA	AARR--------TWHAGF----------PY
P38	G58		GFTFN-------AYD	IF-RSGRTSW	AAVIGVDIR----------
P39	G60		GYTS-------TAYY	IW---RGGHSTL	AAGLYGGSPYFPLNWTGF----------RY
P40	G62		GGTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P41	G63		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P42	G64		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P43	G66		GDTS-------TAYY	IY---RGGRSTV	AAGLRGGSGYLPLNWAGF----------RY
P44	G66.1		GFTSS-------AYD	IF-SSGRRPW	AAVIGVDIR----------
P45	G67		GDTS-------TAYY	IY---RGGRSTV	AAGHDGGSGYLPLNWAGF----------RY
P46	G67.1		GFTFN-------AYD	IF---RSGRTSW	AAVIGVDIR----------
P47	G68	SNB109	GFSF-------NAYC	ID----S-GGSSS	AAKVPFGRGSCAYSTAHWFP----------Y
P48	G68.1		GFTLS-------MYD	IF---TSGRRPW	AAVIGVDIR----------
P49	G69	SNB07	GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P50	G69.1		GFT---S--------C	IYT---RDGRPY	AANRRAY-PYGGDCRLRHAEFD--------Y
P51	G71		GDTS-------TAYY	IF---RGGRSTV	AAGLDGGSGYLPLNWDGF----------RY
P52	G71.1		GFTS-------SSCG	LH----TDGLTS	KTVKDPTSPPGCSR----------GY
P53	G72		GFTLS-------MYD	IF---TSGRRSW	AAVIGVDIR----------
P54	G73		GYTYSSV-------C	I---YTATGRTY	AADL-LIGACSQM-----RRTNF-------DY
P55	G74	SNB74	GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P56	G75		GYTYNTA-------Y	ID--SDGS--TS	AANPYSPG-------AGRELLSYPY------TD
P57	G76		GDTS-------TAYY	IF---RGGRSTV	AAGLDGGSGYLPLNWDGF----------RY
P58	G77	SNB77	GYTS-------TAYY	IW---RGGHSTL	AAGLYGGSPYFPLNWTGF----------RY
P59	G78	SNB78	GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P60	G79	SNB79	GGTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P61	G80	SNB87	GYAY-------STYC	ID----S-DGVTD	AAN--QGS-GDYC-YMAMLIYGM------FY
P62	G81	SNB95	GFT---S--------C	IYT---RDGRPY	AANRRAY-PYGGDCRLRHAEFD--------Y
P63	G82		GYTYNEY-------S	IN--SVG--RTR	AAR---------DGSWFLSLVPATY------GY
P64	G86		GYNFNNV-------C	I---YTSIGRTY	AADL-QIGSCSQM-----RRYNY-------AY
P65	G87		EYTR-------SSRC	IE----H-DGKII	GAD--PGE-GSYCAYEAPEVGAL-------DI
P66	G88		VYTSSTM-------W	I---YRGNGATG	AAGR-TYDCYPGT----------CS
P67	G89		GDTS-------TAYY	IY---RGGRNTV	AAGLAGGSGYLPLNWAGF----------RY
P68	G90		GSTDSRR-------C	I---YRGSGTTH	AASLRARWVQRGA---PLLPSFY------GY
P69	G91		GYPYSSKTY--TNNC	I---YLANGATY	AAG-PWVA--------TPEIANEY-----NY
P70	G92		RYSSSRR-------C	I---YHGDGTTY	VAG-IWTCG-------RSALTDPN-----NY
P71	G93		GYIYN-------DYF	IG-----SDGTTK	AATFGLFWESWEWYKNWH----------Y
P72	G94		TYNY-------ESSQ	VS---PRGESIY	AADP-GVLCGRSW-VGRFP----------Y
P73	G95		TTTN----------Y	IF---SSRDYTD	AAH----GAFAARNDPR----------QWRY
P74	G96		GYTY-------NYYC	ID----T-GGSTY	AADW---GTCQGLLLSRYFA----------Y
P75	G97		GYTYYN----SNC	IY---TRDSRTY	AAAHEPGSWTD-IEARGKISDDP------FGY
P76	G98	SNB171	GDTS-------TAYY	IY---RGGRATV	AAGLAGGSGYLPLNWAGF----------RY
P77	G99		GGSVTTG-----NYY	IT----ASGSTY	ARASFR----GSWFFEG----------
P78	G100	SNB112	GYTFNTR-------C	ISA---GGISID	AAARR---WYYENSCLKVLRSPGD-------Y
P79	G100.1		LYTYSYN-------C	WG---SVGSSTTY	AAGPPSGPL-------RACHESVF------GY
P80	G101	SNB29	GFTS-------NSCG	IF----SDGETA	KTVRDPASPPSCSG----------GY
P81	G102	SNB35	G-MMSNA-------C	I---YTGIGTTY	AADR-VLGRCSRR-----LLSDF-------GY
P82	G103		GYTH-------SSDS	IY---TGDGSTH	AAGTTYLG-SDYDPPRY-EY----------KY
P83	G104		RSVNR-------DTC	IS----AQGVIPG	AAKERPLCGSFWERGD----------EYAS
P84	G105		AFIS-------NNHC	ID----S-AGSTR	AAVSWACWRLSGTG--------F-------NY
P85	G106		GFTFS-------SYD	IR---SGGGNTY	AADLGVDDYS----DYLDHPFGY----------
P86	G107		GFTFDDS-------D	ISR---IDNSTY	AADIG---GSWPRKPHPDPNFGGECGGYGMAF
P87	G108		GY----R--------C	FVT---GAGSTY	AADSSSLPCYPRAAQFPRLR----------Y
P88	G109	SNB02	AYTYRGN-------N	IT--VTGT-RQY	AAGTTRLG---------SLLAPTY----------RY
P89	G110		GATYNIN-------F	ID--NNGVLST	AARPAPDPTSGITRFRLNRSLLPNEY------NS
P90	G111	SNB111	GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P91	G112	SNB113	GDTS-------TAYY	IF---RGGRSTV	AAGLDGGSGYLPLNWDGF----------RY
P92	G113		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWANF----------RY
P93	G117	SNB117	GYTY-------SNY	ID---TNGS-TS	AAE---GGWRDYVRSWGRN----------FGY
P94	G117.1		VYTSSTM-------W	I---YRGNGATG	AAGR-TYDCYPGT----------CS
P95	G120		GFSF-------NAYC	ID----S-GGSSS	AAKVPFGRGSCAYSTAHWFP----------Y
P96	G121		GFTFS-------SYY	IY---RDGSAPY	AADLWRGPPFGGYWSPTKSEFAY----------
P97	G122		GDTY-------SSSC	IC---SDG-SAA	AARR--------TWHAGF----------PY
P98	G123		GFT---S--------C	IYT---RDGRPY	AANRRAY-PYGGDCRVRHAEFD--------Y
P99	G126		GDTY-------SSSC	IC---SDG-SAA	AARR--------TWHAGF----------PY
P100	G128		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P101	G130	SNB130	GFT---S--------C	IYT---RDGRPY	AANRRAY-PYGGDCRLRHAEFD--------Y
P102	G131		GSIYS-------SNA	IY---TGGSATS	AAR-----FRAHDGYWNWQNAGN------YNY
P103	G133		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P104	G134		GDTS-------TAYY	IF---RGGRSTV	AAGLDGGSGYLPLNWDGF----------RY
P105	G138		GDTY-------SSAC	IC---SDG-SSA	AARH--------YWSAGF----------PY
P106	G139		G-MYSNT-------C	I---YTGIGSTY	AADR-VLGRCSRR-----ILSDF-------GY
P107	G141		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P108	G142		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P109	G143		GDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P110	G144		GDTS-------TAYY	IY---RGGRSTV	AAGHDGGSGYLPLNWAGF----------RY
P111	G145		GGSITTN-----YYG	IG----YSGSTY	ARSSPR----TVVAGFG----------D
P112	G147		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P113	G148	SNB148	GDSS-------TAYY	IY---RGGRSTV	AAGLDGGNGYLPLNWAGF----------RY
P114	G149		GNTY-------TSSC	IC---SDG-STA	AARR--------TWHAGF----------PY
P115	G150		GLYY-------PPLC	ID----R-DGSTS	AAA--DAQRGRTCFFGA----------
P116	G151		GGSITTA-----GYG	IT----FTGRTL	ARGPFGCYSVSGCYRKGGVD----------NY
P117	G153		G-MYSNT-------C	I---YTNVGTTY	AADR-VLGRCSRR-----LLSDF-------GY
P118	G154		GLYY-------LPLC	ID----R-DGRTS	AAA--DAQRGRTCFFGA----------
P119	G155		GDTY-------SSSC	IC---SDG-SAA	AARR--------TWHAGF----------PY
P120	G156	SNB176	GFTS-------NSCG	IH----TDGSTS	KTVRDPTSPRSCSG----------GY
P121	G157		GLWH-------PPLC	ID----R-DGSTS	AAA--DAQRGRTCFFGA----------
P122	G158		GDTY-------SSSC	IC---SDG-SAA	AAGLDGGSGYLPLNWAGF----------RY
P123	G159		GYTY-------GSYC	SN----TNGGSTY	AAYHSGSWCYLP-HLGSY----------GY
P124	G160		GLYY-------SPLC	ID----R-DGSTS	AAA--DAQRGRTCFFGA----------
P125	G166	SNB166	RYT---S--------S	TN----RDGMSY	AAGWR--------LSLRVSDFN---------Y
P126	G167		GYTYSSN-------C	V---YNDGGHTY	AASFRPTWFCRG-------LAPYKY-------NL
P127	G168	SNB168	GYRYN-------ACS	IF----TRGTTK	TSAS-LTWDGGNWYCPTHG----------Y
P128	G169		VYTSSTM-------W	I---YRGNGATG	AAGR-TYDCYSGT----------CS
P129	G170	SNB170	GNPS-------GRKF	LY---LGGSITY	AAGAYRAS---------F----------TY
P130	G173		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P131	G175		GDTY-------SSSC	IC---SDG-SAA	AARR--------TWHAGF----------PY
P132	G178		GSSG----LIFSGSA	ID----TIGEID	NT-MWGARQNK-----D----------
P133	G179		GDTS-------TAYY	IF---RGGRSTV	AAGHDGGSGYLPLNWAGF----------RY
P134	G180		GFT---S--------C	IYT---RDGRPY	AANRRPY-PYGGDCRLRHAEFD--------Y
P135	G183		EDTS-------TAYY	IY---RGGHSTV	AAGLDGGSGYLPLNWAGF----------RY
P136	G184		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLAWAGF----------RY
P137	G185		GDTS-------TAYY	IF---RGGRSTV	AAGLDGGSGYLPLNWDGF----------RY
P138	G186		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWARF----------RY
P139	G190		GDTS-------TAYY	IY---RGGRSTV	AAGVAGGSGYLPLNWAGF----------RY
P140	G191		GYTY-------SSHC	LD---G-DGRVR	AAG--FAGCYGSSWYGSADFG----------Y
P141	G194		GDTS-------TAYY	IY---RGGRSTV	AAGLDGGSGYLPLNWAGF----------RY
P142	G195		GLYY-------PPLC	ID----R-DGSTS	AAA--DAQRGRTCFFGA----------