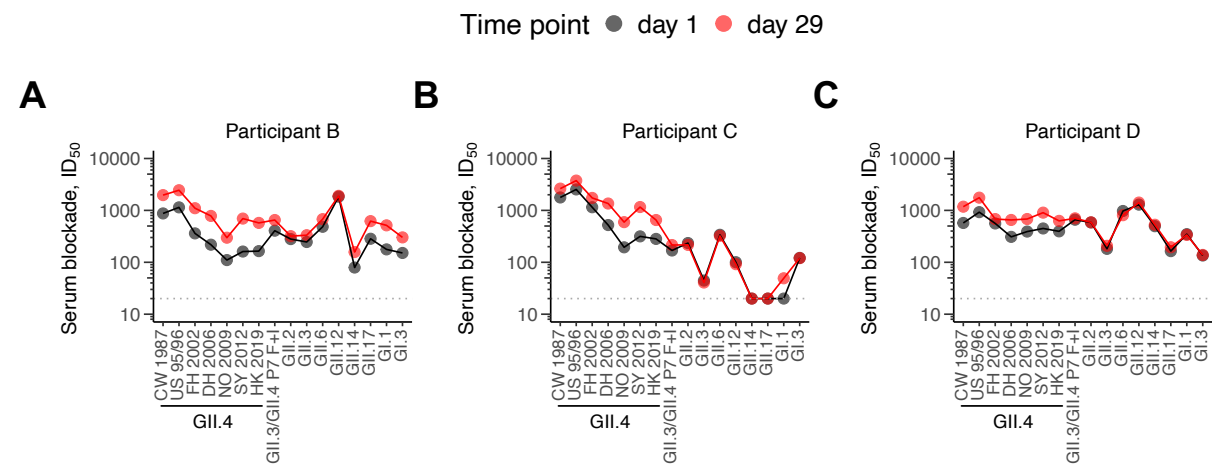
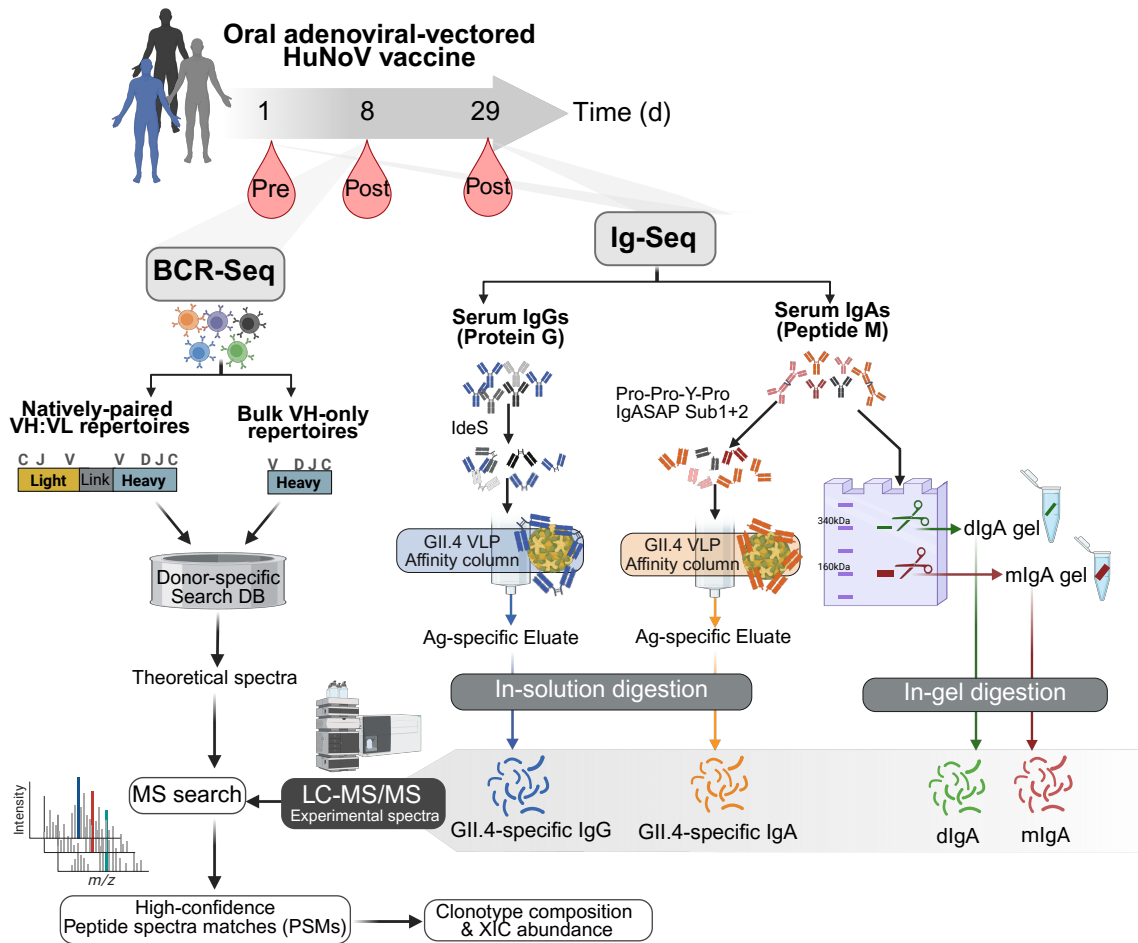


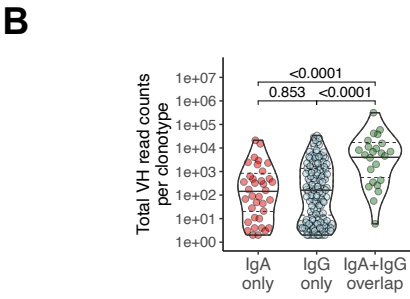
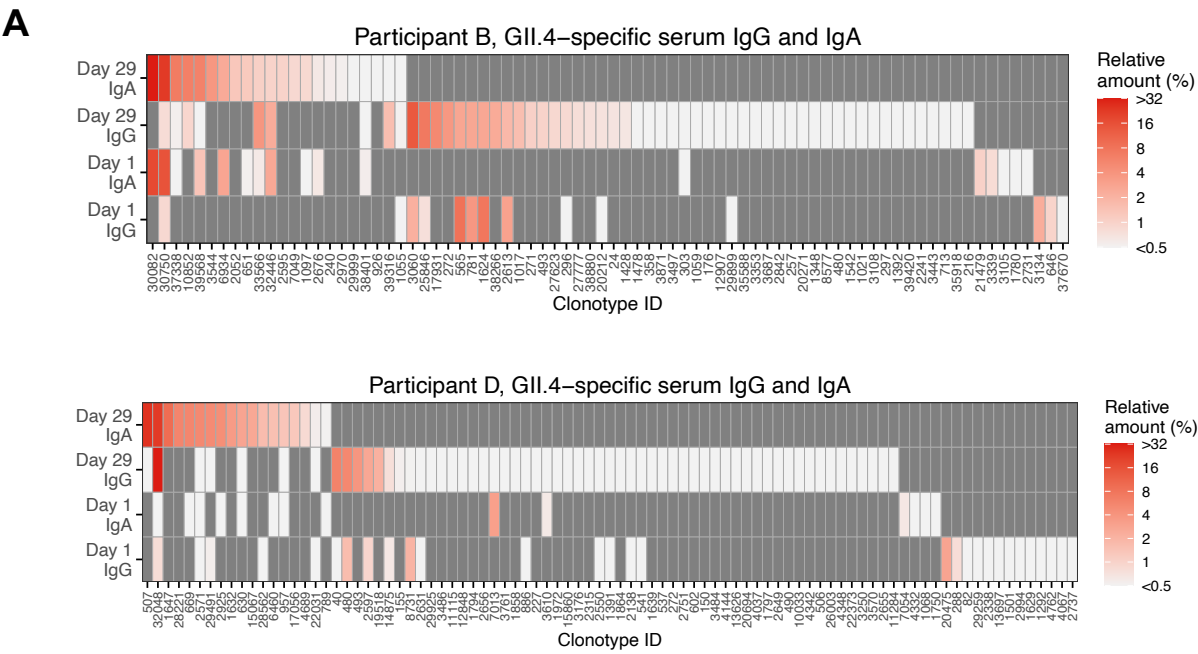
SUPPLEMENTARY FIGURE 1.



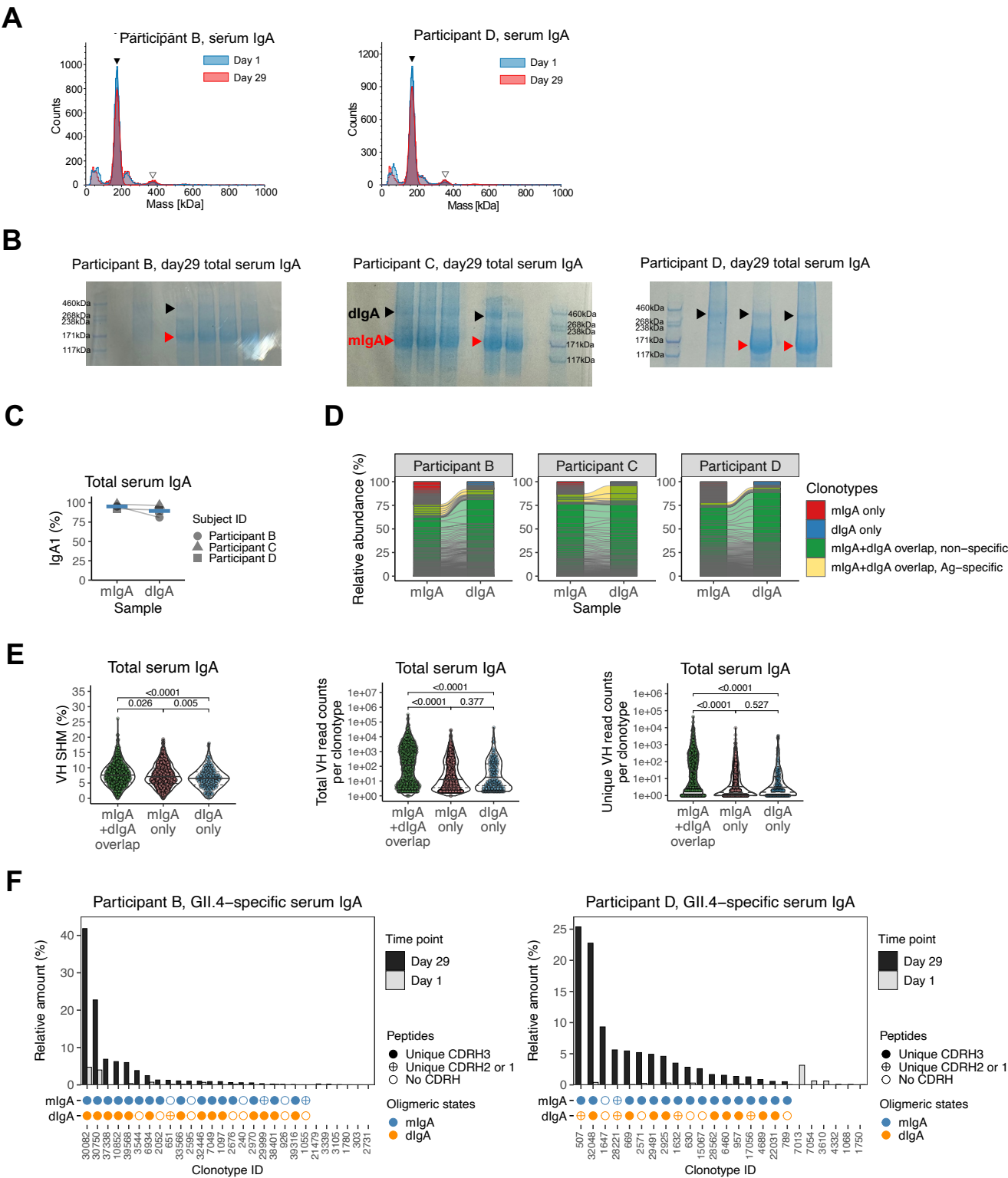
SUPPLEMENTARY FIGURE 2.



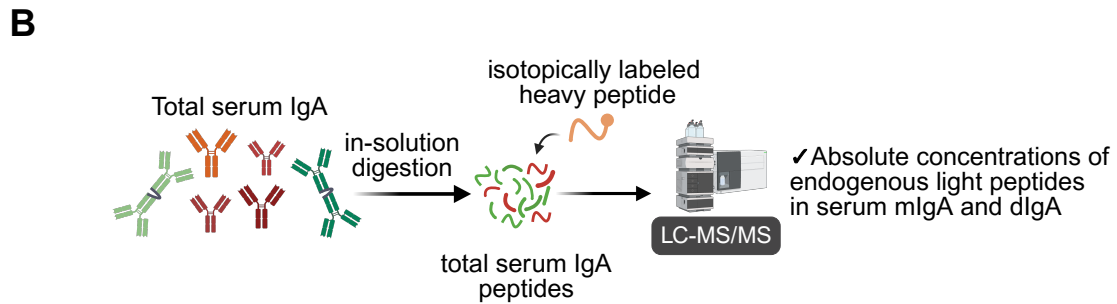
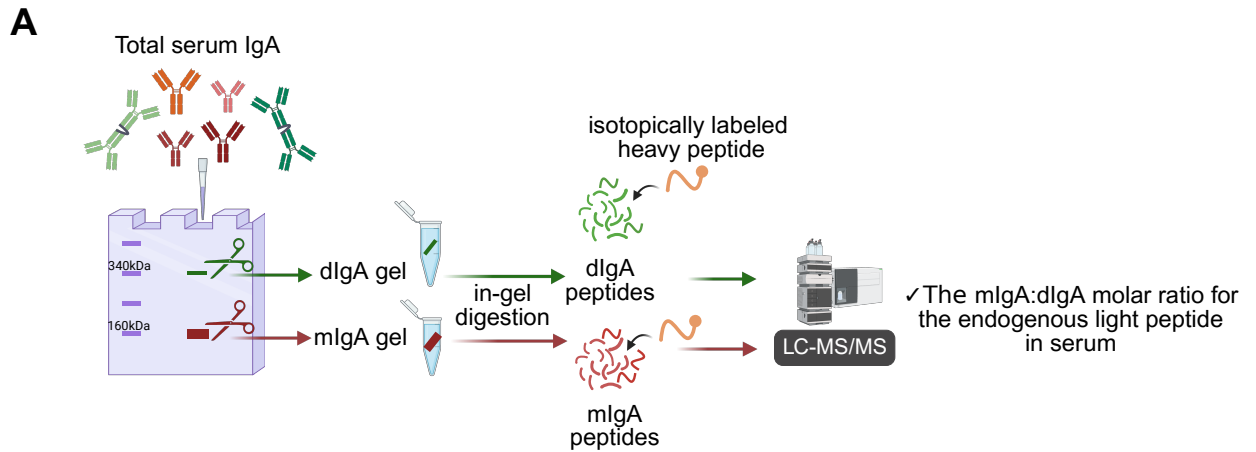
SUPPLEMENTARY FIGURE 3.



SUPPLEMENTARY FIGURE 4.

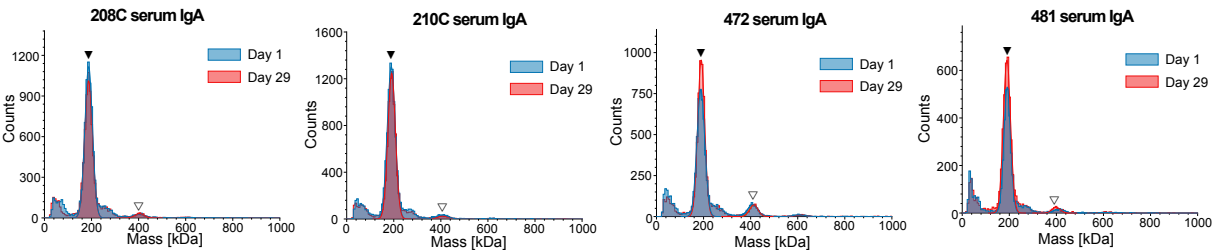


SUPPLEMENTARY FIGURE 5.

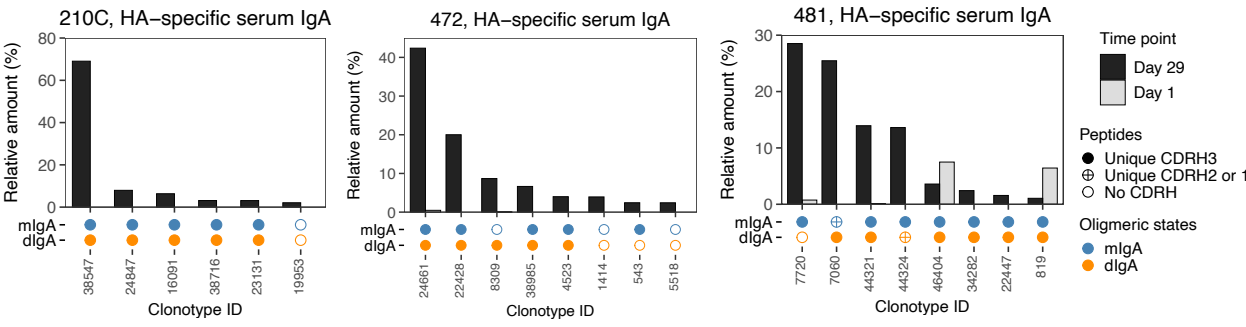


SUPPLEMENTARY FIGURE 6.

A



B



SUPPLEMENTARY FIGURE 7.

A

Site	A					C	D	E			F	G	NE RK	Undefined											
Capsid Residue	294	296	297	298	372	340	391	393	407	412	413	327	404	356	357	234	17	98	268	348	382	425	426	456	459
P3.D1	A	T	Q	E	S	R	D	G	N	D	G	V	V	V	H	V	N	S	T	K	R	S	F	E	Q
P3.D156	A	T	Q	V	S	R	D	S	D	D	V	V	V	A	D	V	N	S	T	K	R	S	F	E	Q
P3.D262	E	T	Q	V	S	R	D	S	D	G	V	V	V	A	E	V	S	S	I	K	R	T	Y	D	Q
P3.D581	E	S	Q	V	N	S	N	S	D	G	I	K	E	A	E	I	S	G	I	K	K	T	Y	D	Q
P3.D683	E	S	K	V	N	S	N	S	D	G	I	K	E	A	E	I	S	G	I	T	K	T	Y	D	R
581.D1	A	T	Q	E	S	R	D	G	N	D	G	V	V	V	H	V	N	S	T	K	R	S	F	E	Q
581.F1	E	S	Q	E	N	S	N	G	N	G	G	K	E	V	H	I	S	G	I	K	K	T	Y	D	Q
581.F2	E	T	Q	V	S	R	D	S	D	G	G	V	V	A	E	V	S	S	I	K	R	S	F	E	Q
581.F3	A	S	Q	V	N	S	D	S	D	G	G	V	V	A	E	V	N	G	T	K	K	T	F	E	Q
581.F4	E	S	Q	V	N	R	N	S	D	G	G	V	V	A	E	V	S	S	I	K	R	T	Y	D	Q
581.F5	E	S	Q	V	N	S	N	S	S	T	G	V	V	A	E	I	S	G	I	K	K	T	Y	D	Q
581.A4A	E	S	Q	E	N	S	N	S	D	G	I	K	E	V	H	I	S	G	I	K	K	T	Y	D	Q
GII.4 FH 2002	A	T	H	N	N	G	D	N	S	T	G	V	V	V	H	V	N	G	T	K	K	T	F	E	Q

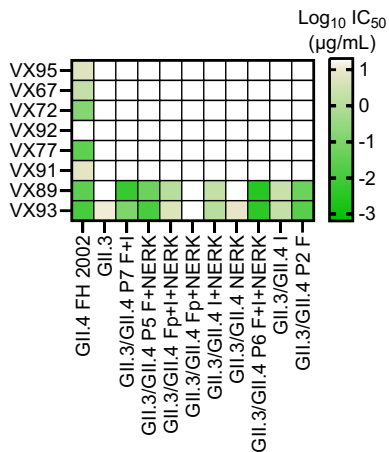
B

Site GII.4 Capsid Residue	NERK					F					I					
	234	310	316	484	493	254	256	257	327	404	402	403	504	505	506	
GII.3	I	P	D	R	K	T	E	N	I	R	S	Q	W	D	S	P
GII.3/GII.4 Fp	I	P	D	R	K	T	E	N	I	V	V	Q	W	D	S	P
GII.3/GII.4 I	I	P	D	R	K	T	E	N	I	R	S	Q	W	Q	H	D
GII.3/GII.4 Fp+I	I	P	D	R	K	T	E	N	I	V	V	Q	W	Q	H	D
GII.3/GII.4 NERK	V	N	E	R	K	T	E	N	I	R	S	Q	W	D	S	P
GII.3/GII.4 Fp+NERK	V	N	E	R	K	T	E	N	I	V	V	Q	W	D	S	P
GII.3/GII.4 I+NERK	V	N	E	R	K	T	E	N	I	R	S	Q	W	Q	H	D
GII.3/GII.4 Fp+I+NERK	V	N	E	R	K	T	E	N	I	V	V	Q	W	Q	H	D
GII.3/GII.4 P2 F	I	P	D	R	K	S	G	A	F	V	V	Q	W	D	S	P
GII.3/GII.4 P5 F+NERK	V	N	E	R	K	S	G	A	F	V	V	Q	W	D	S	P
GII.3/GII.4 P6 F+I+NERK	V	N	E	R	K	S	G	A	F	V	V	Q	W	Q	H	D
GII.3/GII.4 P7 F+I	V	P	D	R	K	S	G	A	F	V	V	Q	W	Q	H	D
GII.4 FH 2002	V	N	E	R	K	S	G	A	F	V	V	Q	W	Q	H	D

C

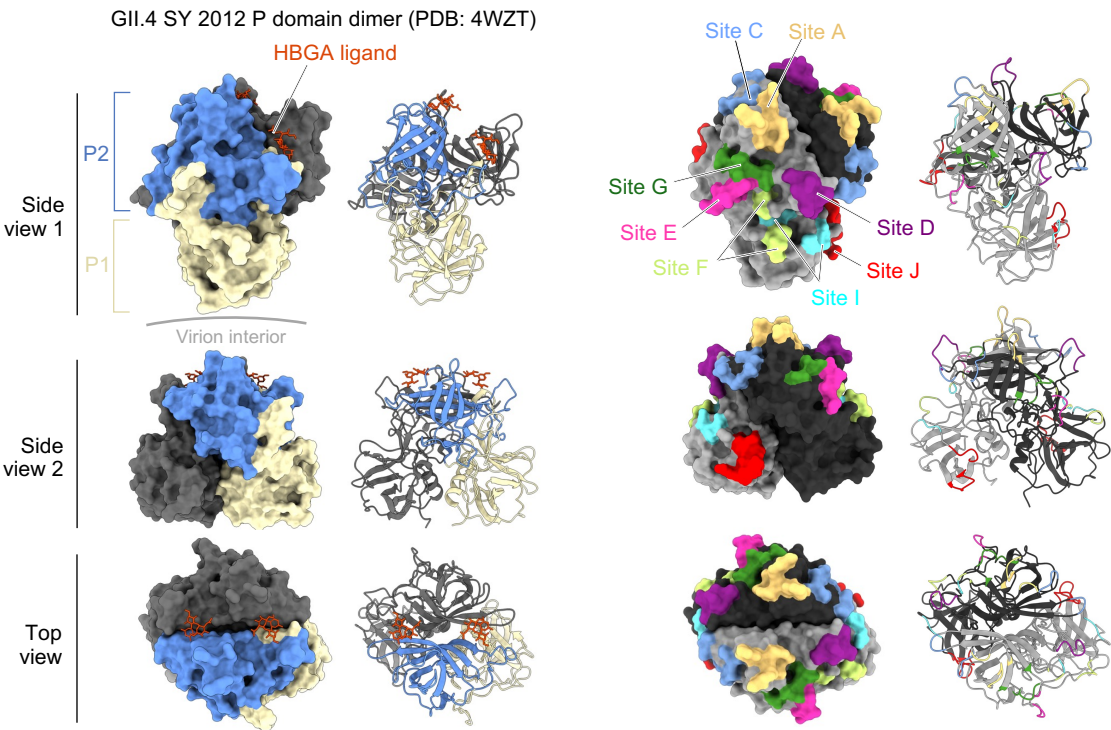
IC ₅₀ (μg/ml)	P3.D1	P3.D156	P3.D262	P3.D581	P3.D683	581.F1	581.F2	581.F3	581.F4	581.F5	581.A4A
VX95	3.136	10.821	>16	>16	>16	7.471	>16	>16	>16	>16	4.090
VX67	0.020	0.123	0.235	4.923	7.885	0.480	0.527	2.679	11.523	>16	0.087
VX72	>16	>16	>16	>16	>16	14.061	>16	ND	ND	>16	7.493
VX92	>16	>16	>16	>16	>16	>16	>16	ND	>16	>16	>16
VX77	0.007	>16	>16	>16	>16	0.009	>16	>16	>16	>16	0.004
VX91	1.508	>16	>16	>16	>16	0.917	>16	>16	>16	>16	2.649

D

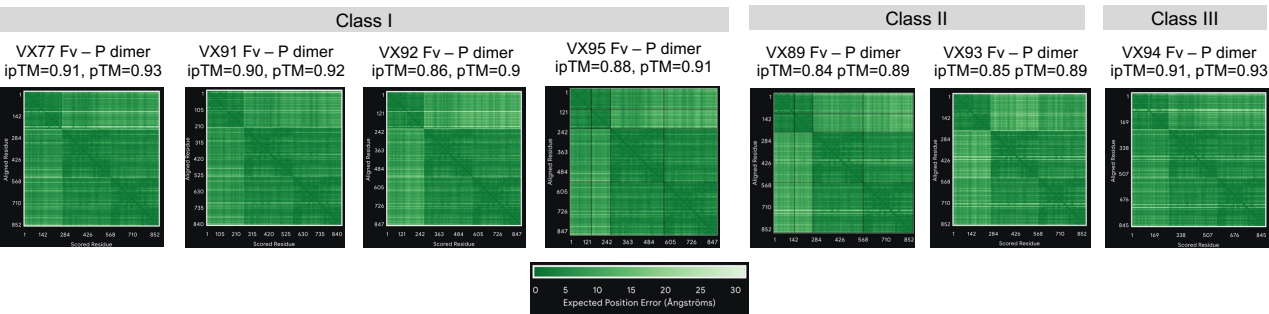


SUPPLEMENTARY FIGURE 8.

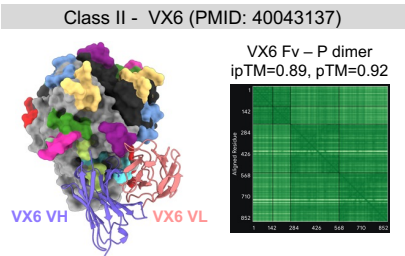
A



B



C

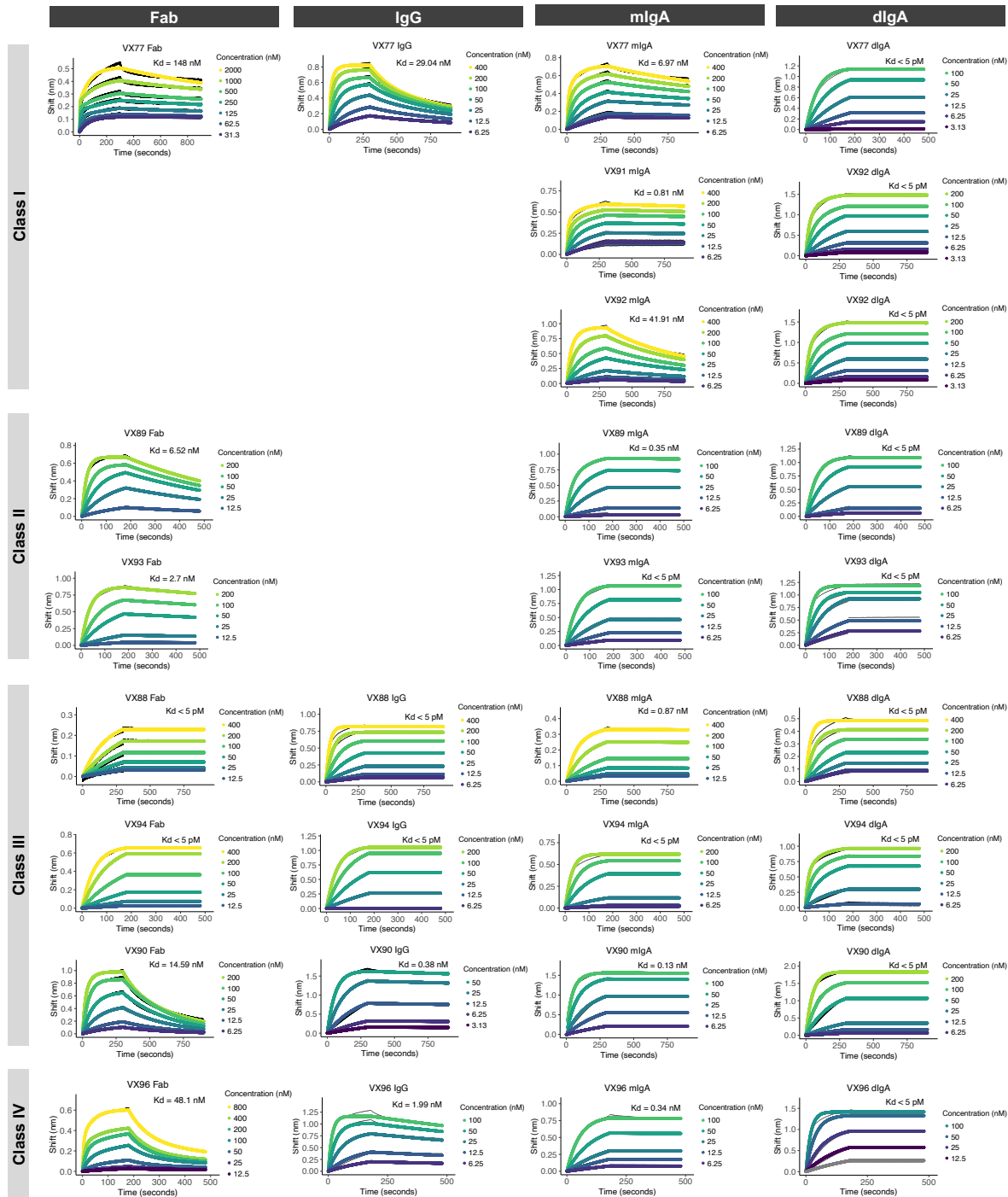


D

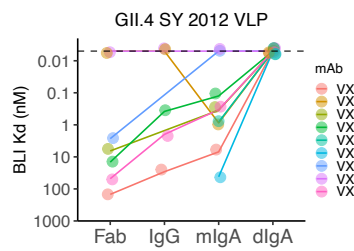
VX92_VH_original QVQLVESGGG LVKPGGSLRL SCTVSGFSFS EYMSWIRQA PGKGLEWISY ISPIMSSSTNY ADSVKGRFTI SRDSAKNSVY LQMNSLRAED TAVYYCARD S
VX92_VH_AF3Q.T... ..AA...T.. D..... ..G...Y... ..K.N.....
110 120
VX92_VH_original ASGATSYNA NWGQGLTVTV SS
VX92_VH_AF3 .Y.SR.....
10 20 30 40 50 60 70 80 90 100
VX92_VL_original QSVLTQPPSV SGAPGQRTVI SCTGSSANIG AGYDVHWYQQ LPTGTAPKLLI HGNNNRPSGV PDRFSGSKSG TSASLAITGL QAEDADYYC QSYDTGLSGS
VX92_VL_AF3 .T.V..... ..S..... ..D-S..... Y..... ..SS....
110
VX92_VL_original HYVFGTGTRV TVL
VX92_VL_AF3 R-...S.K. ...

SUPPLEMENTARY FIGURE 9.

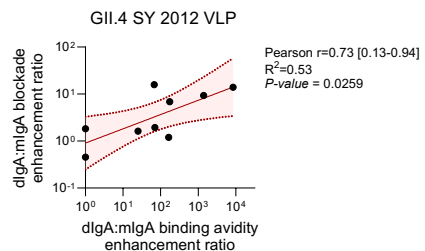
A



B

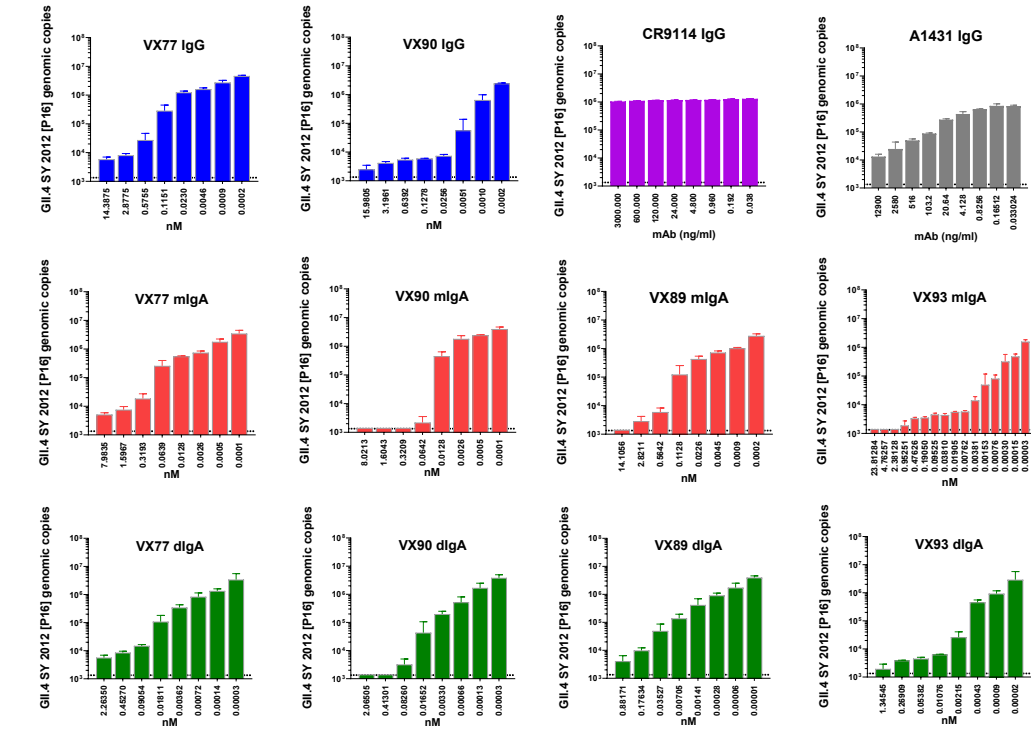


C

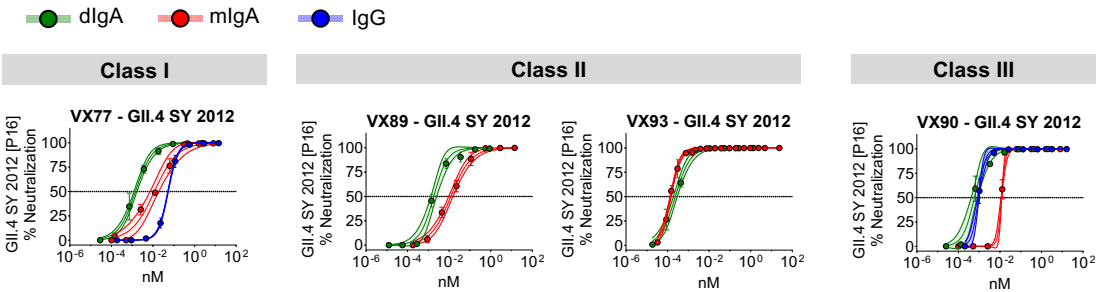


SUPPLEMENTARY FIGURE 10.

A

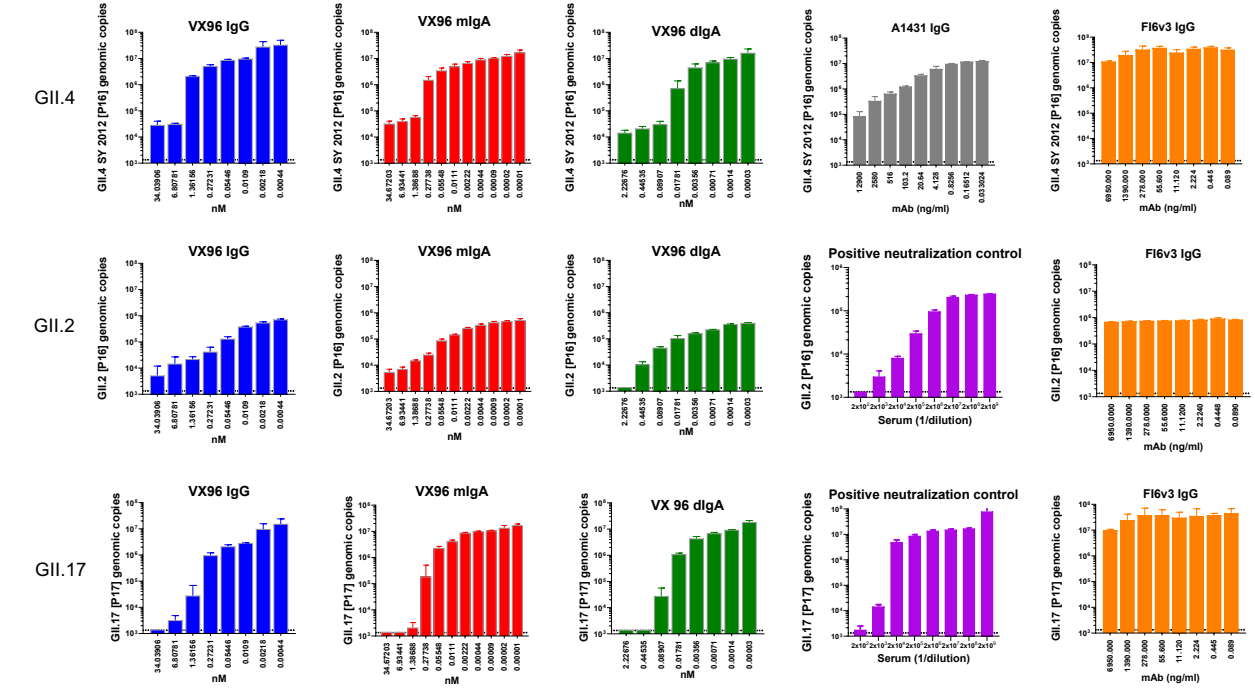


B

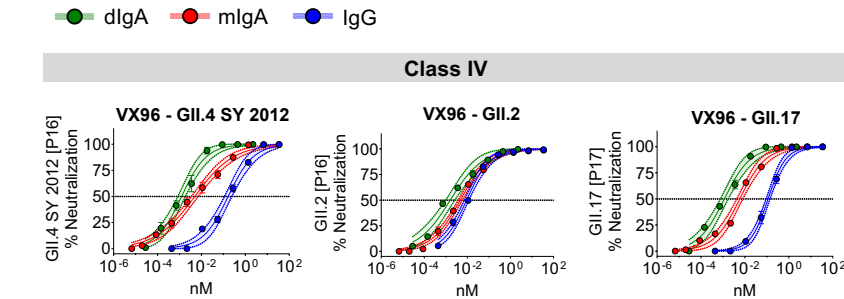


SUPPLEMENTARY FIGURE 11.

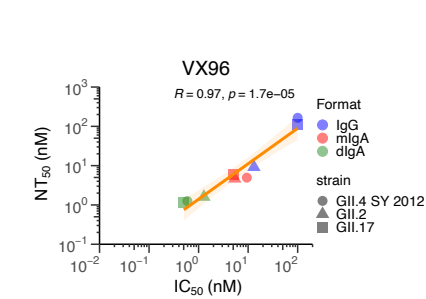
A



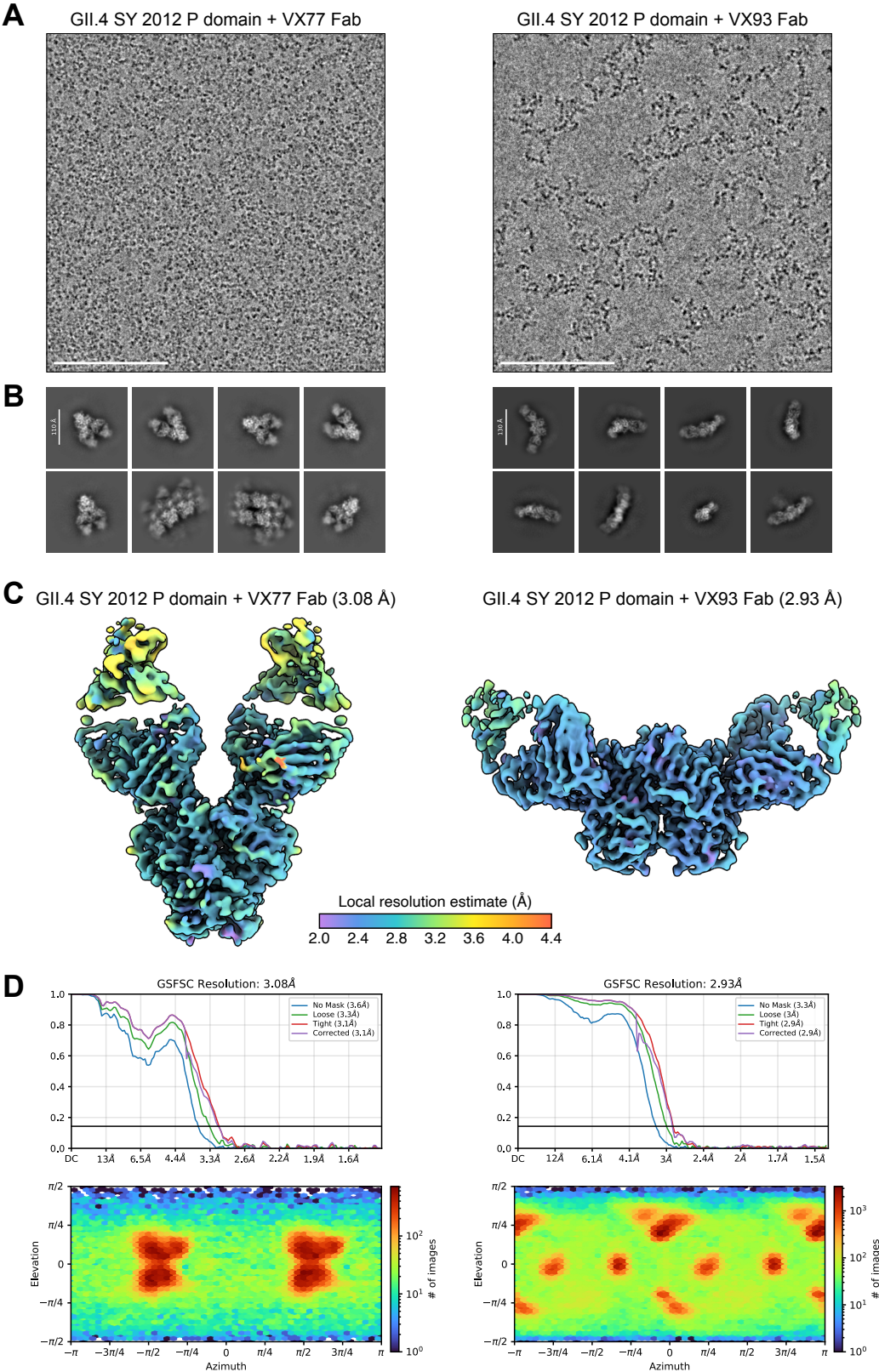
B



C



SUPPLEMENTARY FIGURE 12.



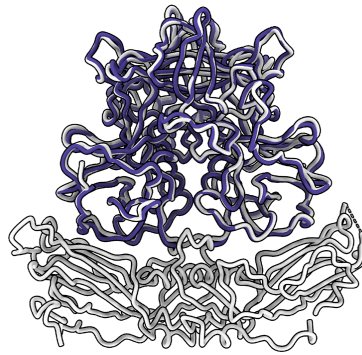
SUPPLEMENTARY FIGURE 13.

A



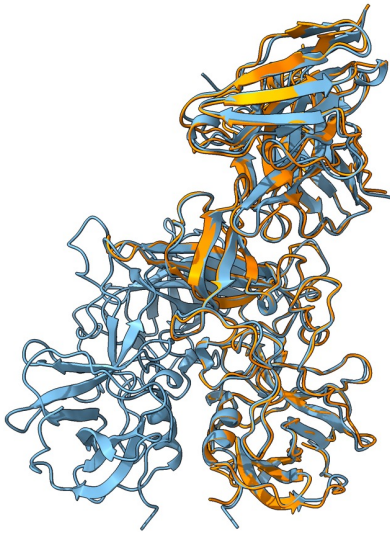
VX77 Fab-bound GII.4 SY 2012 P domain dimer (This study)
VP1 dimer extracted from GII.4 HOV 2002 VLP (PDB 7K6V)
RMSD across all 306 pairs: 0.828 Å

B



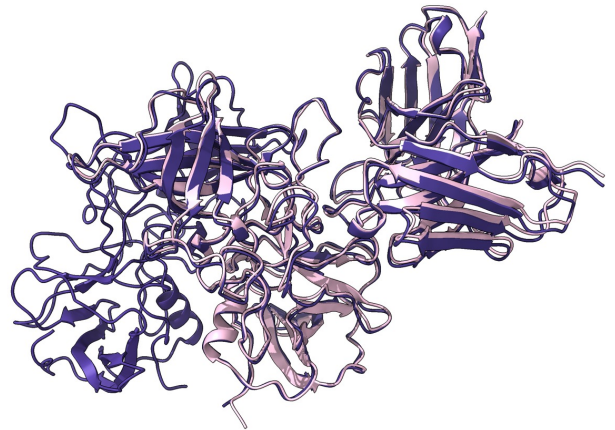
VX93 Fab-bound GII.4 SY 2012 P domain dimer (This study)
VP1 dimer extracted from GII.4 HOV 2002 VLP (PDB 7K6V)
RMSD across all 306 pairs: 0.824 Å

C



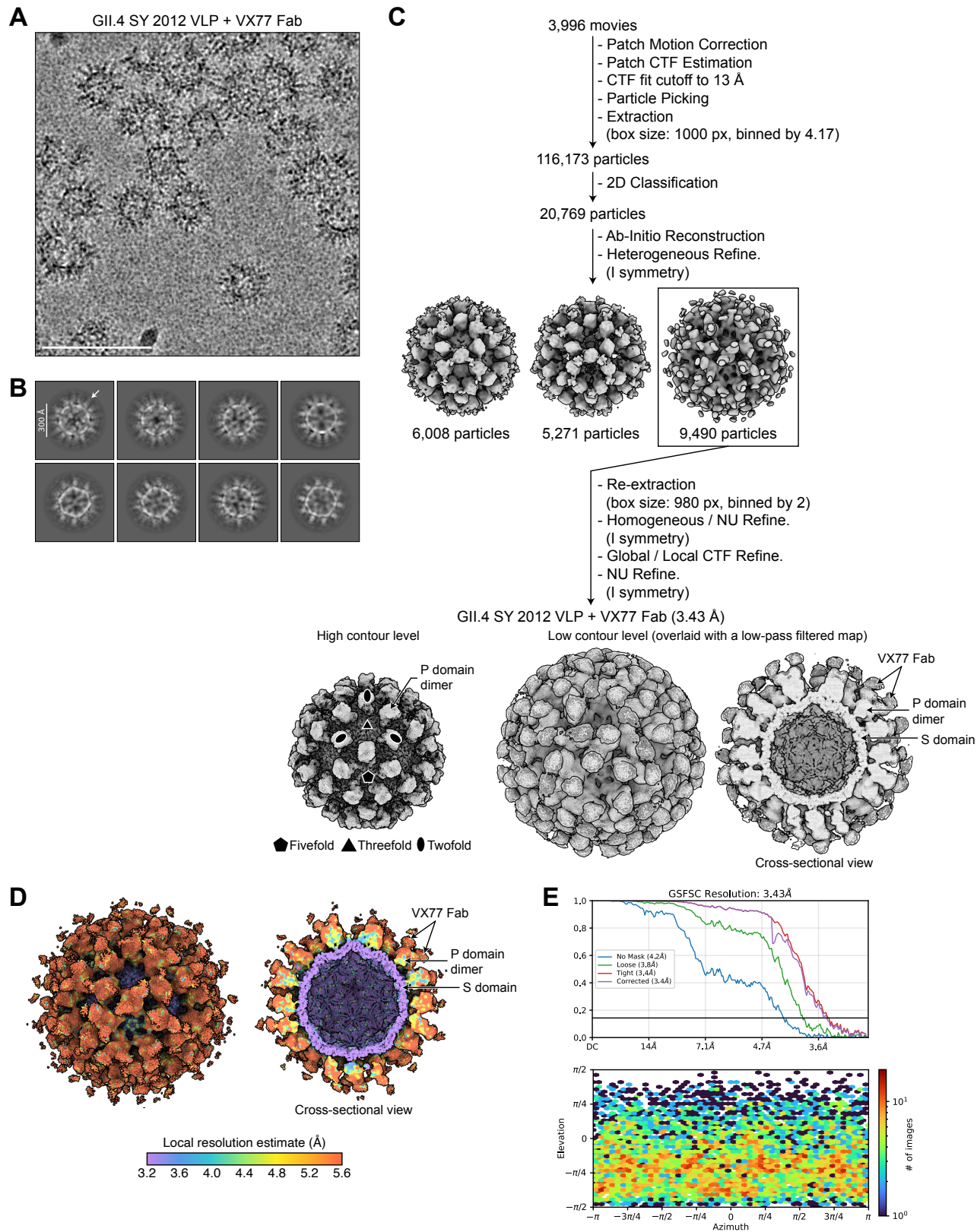
Cryo-EM model of VX77 Fab bound to GII.4 SY 2012 P dimer (This study)
AlphaFold3 model of VX77 Fab in complex with P domain
RMSD across all 306 pairs: 0.710 Å

D

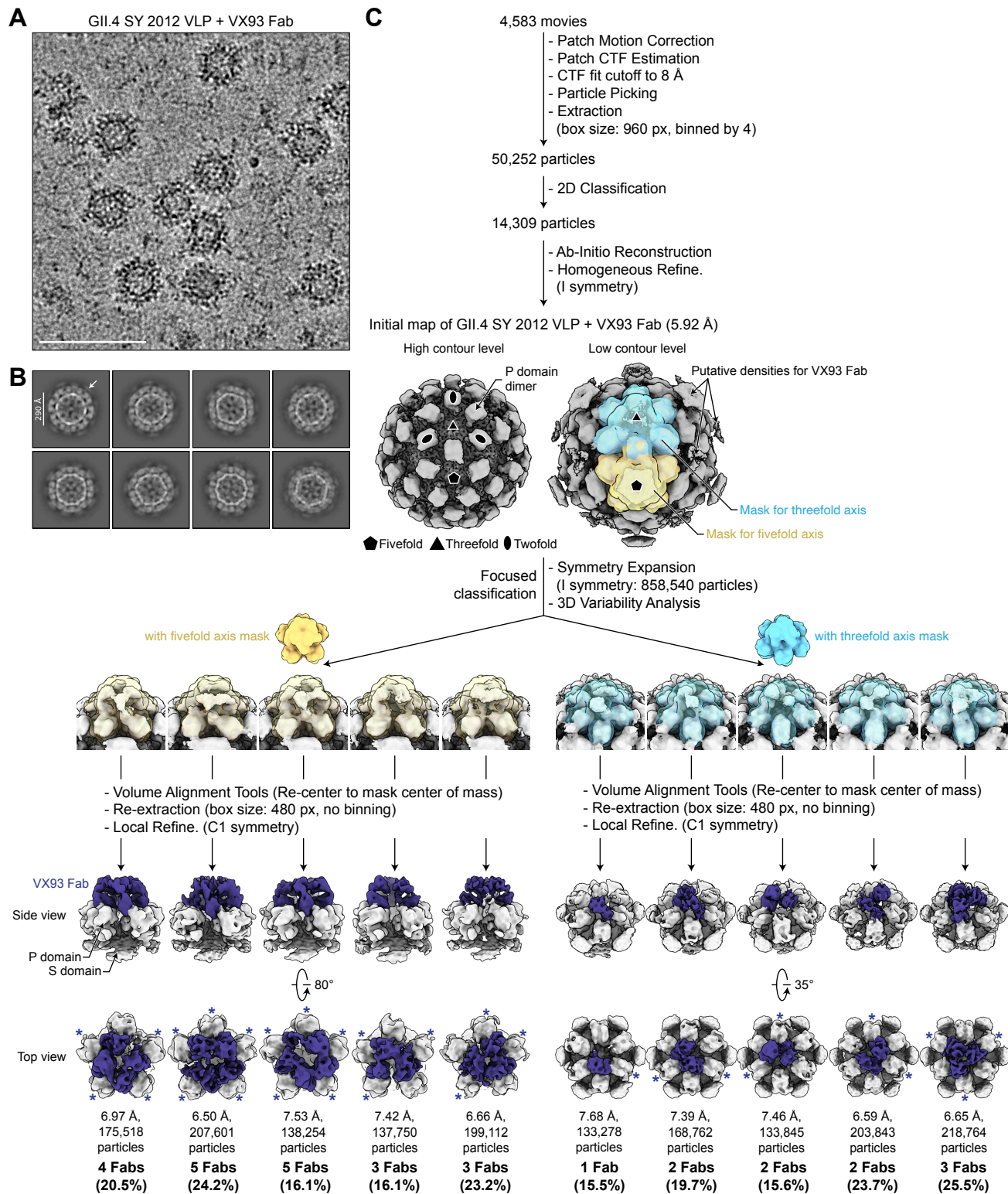


Cryo-EM model of VX93 Fab bound to GII.4 SY 2012 P dimer (This study)
AlphaFold3 model of VX93 Fab in complex with P domain
RMSD across all 306 pairs: 0.554 Å

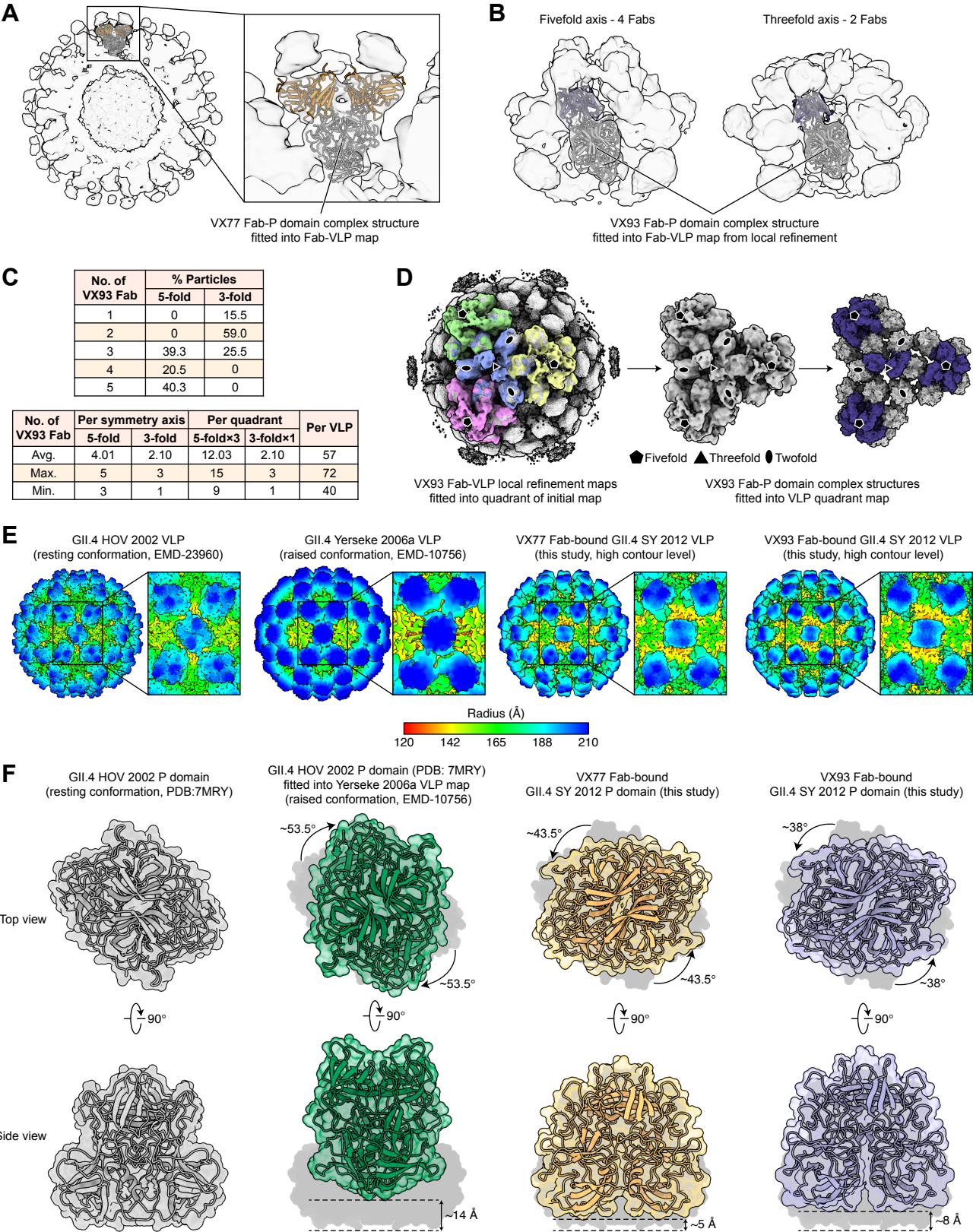
SUPPLEMENTARY FIGURE 14.



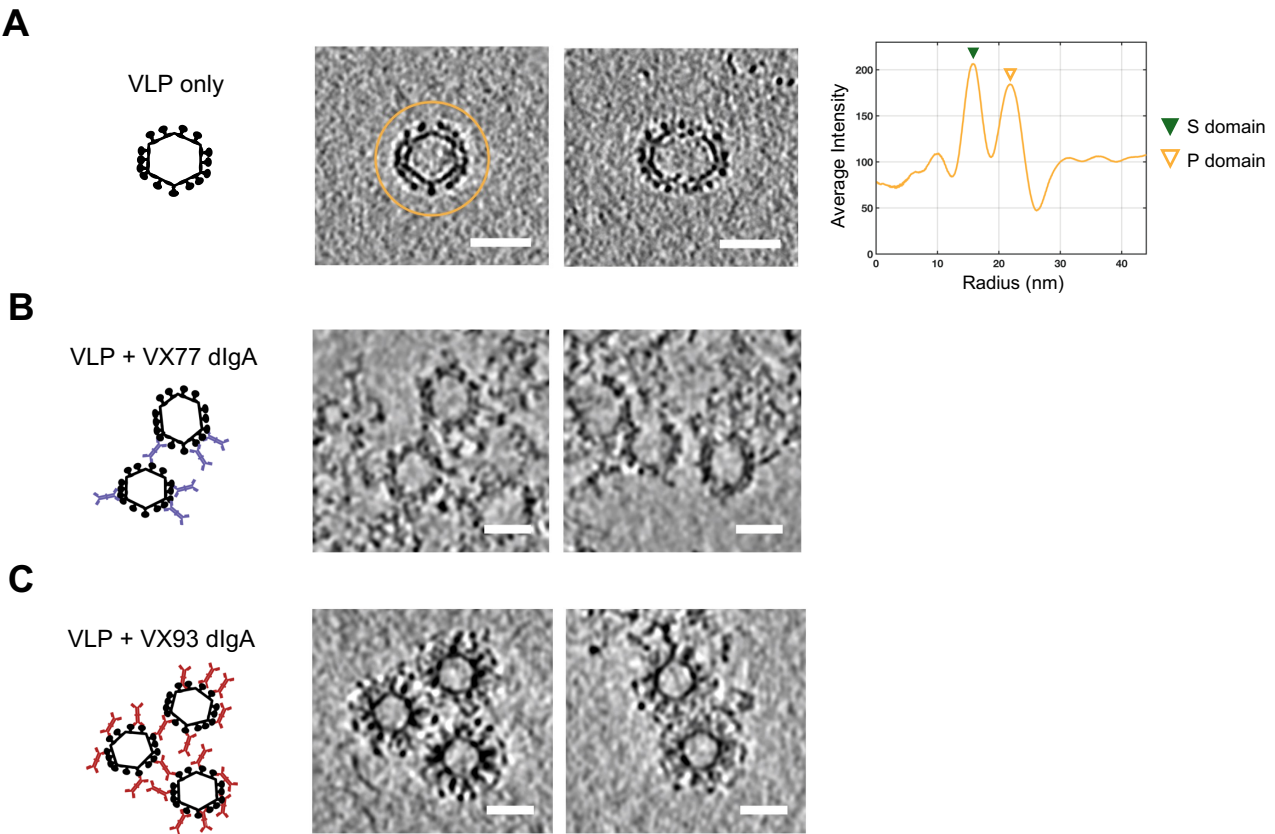
SUPPLEMENTARY FIGURE 15.



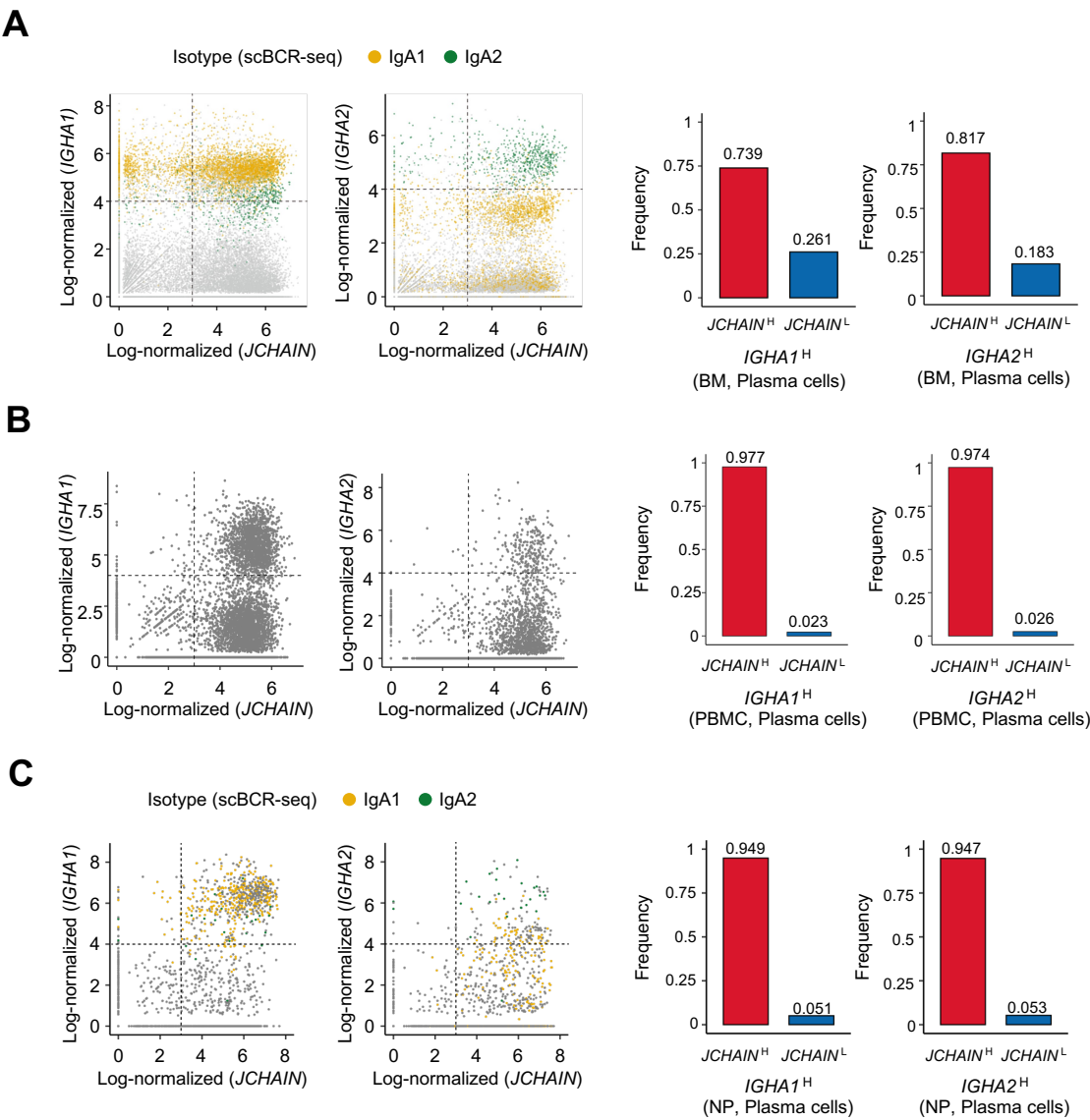
SUPPLEMENTARY FIGURE 16.



SUPPLEMENTARY FIGURE 17.



SUPPLEMENTARY FIGURE 18.



SUPPLEMENTARY TABLE 1.

Baseline characteristics							
Subject ID	Participant B§	Participant C	Participant D	208C	210C	472	481
Vaccination type	Vaxart monovalent norovirus GII.4	Vaxart bivalent norovirus GII.4/GI.1	Vaxart bivalent norovirus GII.4/GI.1	Fluzone quadrivalent standard dose 2019-2020 flu season	Fluzone quadrivalent standard dose 2019-2020 flu season	Fluzone quadrivalent standard dose 2019-2020 flu season	Fluzone quadrivalent standard dose 2019-2020 flu season
Vaccination route	oral	oral	oral	intramuscular	intramuscular	intramuscular	intramuscular
Vaccination year (mm/dd/yyyy)	03/20/2019	05/23/2019	05/29/2019	12/11/2019	01/25/2020	01/13/2020	01/07/2020
Age (years)	37	40	36	12	11	67	67
Sex	Female	Female	Male	Male	Female	Female	Female
Body mass index (kg/m ²)	23	28	29	15	31	26	N/A
Race	White	White	Asian	White	White	White	Black
Ethnicity	Caucasian	Caucasian	Not Hispanic or Latino	Caucasian	Caucasian	Caucasian	African American
Blood group	A	O	O	N/A	N/A	N/A	N/A

SUPPLEMENTARY TABLE 2.

GII.4 SY 2012 VLP-specific															
Subject ID	Clonotype ID	mAb ID	Day1, IgA\$	Day1, IgG\$	Day29, IgA\$	Day29, IgG\$	VH	DH	JH	CDRH3	Avg VH SHM (%)	VL*	JL*	CDRL3*	Avg VL SHM (%)*
Participant C	50337	VX89	1.89	0.90	43.39	0.04	IGHV4-31	IGHD6-13	IGHJ3	CAGGRVSSSWYREDADFDMW	10.0	IGKV4-1	IGKJ3	CQQYFSAPFTF	4.4
	50996	VX93	20.66		22.11		IGHV4-31	IGHD3-22	IGHJ4	CVRGWVSSSYRLDYFDYW	8.6	IGKV4-1	IGKJ3	CQQYYSIPLTF	9.2
	43333	VX77	0.71	3.72	10.94	5.81	IGHV3-11	IGHD2-2	IGHJ5	CARSAQYSSAINCYLVDPW	6.0	IGLV1-40	IGLJ1	CQSYDRSLSGSHYVF	3.8
	48426	VX91			5.49		IGHV5-51	IGHD3-10	IGHJ4	CARSQTRYGSGAYYNSNW	7.9	IGKV3-11	IGKJ4	CQQRSTGVTF	4.3
	26954	VX96		0.12	4.38	1.84	IGHV6-1	IGHD6-19	IGHJ5	CARDLGNSGWVFTVTRKNSFPDW	6.6				
	38050			2.93	2.43	2.37	IGHV4-31	IGHD6-13	IGHJ4	CVRAPFSSNNWYREESFDYW	10.3				
	1954		2.22		1.74		IGHV3-30	IGHD2-8	IGHJ4	CVRGQFRPGNYNNIIRDYFDYW	16.7				
	1166		0.76		1.70		IGHV4-31	IGHD6-13	IGHJ5	CAREIADSAWYRGNWIDSW	10.2				
	50686	VX90	3.07		1.46	0.08	IGHV2-26	IGHD5-12	IGHJ4	CARIWGNSGYDFHAQRAFDYW	7.5	IGLV1-40	IGLJ3	CQSYDNSLRGWVF	4.9
	49926	VX92		0.60	1.18	0.91	IGHV3-11	IGHD3-10	IGHJ4	CARDSAYGSRSYNNANW	6.2	IGLV1-40	IGLJ1	CQSYDSSLSGSRVVF	1.1
	16180				1.07		IGHV3-11	IGHD5-12	IGHJ5	CARDKVAPPSAYSDHW	12.0				
	11194				0.90		IGHV3-11	IGHD2-15	IGHJ4	CARISVASNPVHYDYW	11.0				
	46625	VX94			0.69		IGHV4-34	IGHD2-15	IGHJ4	CARFRKALWTSADRLVDIWI	13.5	IGKV1-17	IGKJ3	CLQHNSYPFTF	8.5
	34207	VX88	11.46	2.21	0.57	6.69	IGHV3-23	IGHD6-13	IGHJ4	CSKGVAAGTSGRPFYFDSW	5.8	IGKV4-1	IGKJ3	CQQYSSPTF	2.1
	15712				0.50		IGHV3-11	IGHD3-16	IGHJ4	CARDWWGGPKTVGGPKTSVAYS DYW	7.2				
	14390				0.36	0.53	IGHV3-11	IGHD4-23	IGHJ4	CSRDTTGGTIMGPENW	9.6				
	5183				0.35		IGHV3-11	IGHD2-15	IGHJ3	CARPLSGGRTLDADFWD	7.0	IGLV1-51	IGLJ2	CGTWDFSLTTWVF	2.2
	544		0.34		0.32		IGHV1-3	IGHD2-15	IGHJ6	CATRSTNPRVASFKDFYYYMDVW	12.8				
	351				0.25		IGHV4-31	IGHD3-10	IGHJ6	CASNERVLAKPGLGTPYYMDVW	13.3				
	27485				0.18		IGHV3-11	IGHD6-19	IGHJ4	CARDSSFGSDSGSTMGPDYW	8.3	IGLV3-27	IGLJ3	CYSAADKRMF	5.0
	291	VX67		1.09		15.56	IGHV4-61	IGHD1-1	IGHJ3	CASRRRHNNNDNPFDIW	22.9	IGKV1-5	IGKJ2	CQQYFSYSF	6.9
	50547	VX95		2.45		6.89	IGHV3-11	IGHD5-18	IGHJ4	CVRQNQMDKAMVPDYW	9.4	IGLV1-40	IGLJ2	CQSFDTSLSGSIVF	5.5
	37059			1.72		5.63	IGHV4-61	IGHD2-2	IGHJ5	CARGGGYCSSFACYGPFDPW	17.2	IGLV1-47	IGLJ2	CAAWDDSLSGGVF	3.2
	46954			5.75		4.70	IGHV4-31	IGHD6-13	IGHJ4	CARGVSSSWYRHDFYFDSW	7.6	IGKV4-1	IGKJ2	CQQYFSPPLTF	6.1
	214			0.06		3.46	IGHV3-11	IGHD2-2	IGHJ4	CVRQVVGICRVNCTFDSW	10.7				
	828			0.08		1.59	IGHV4-34	IGHD3-16	IGHJ3	CARGRSFMATFGVIRSPFDAFDMW	12.2				
	12227				1.17		IGHV4-59	IGHD2-2	IGHJ4	CARASIVAPAAFYDYW	6.3	IGLV1-36	IGLJ3	CAAWDDSLNAWVF	5.5
	39705			0.44		0.96	IGHV4-31	IGHD6-19	IGHJ4	CARRHISGYFDSW	10.6	IGLV2-23	IGLJ2	CCSYAGYTVVF	8.9
	915			1.34		0.87	IGHV4-28	IGHD3-10	IGHJ6	CARDCTSTQIYYGLDFW	11.4				
	48639	VX72			0.81		IGHV4-59	IGHD4-23	IGHJ4	CARAAIQPAAFYFDHW	9.1	IGLV1-36	IGLJ3	CAAWDDSLNAWVF	5.5
	18026				0.72		IGHV1-69	IGHD3-16	IGHJ3	CARDQRQLLDRAFPDFTW	10.2	IGKV3-15	IGKJ4	CQQYHNWPLTF	8.3
	50969			1.29		0.70	IGHV3-11	IGHD2-21	IGHJ3	CARAINLNDRSSGDFW	6.3	IGLV1-40	IGLJ7	CQSYDRSLSGHAVF	2.5
	45402			0.79		0.67	IGHV3-30	IGHD3-16	IGHJ4	CVRAFGYW	7.5	IGKV1-16	IGKJ4	CQQYHTYPLTF	4.7
						0.52	IGHV3-30	IGHD3-3	IGHJ3	CTQTARPYRDFLASTSYGPPGH DAY DVW	19.5				
	273				0.47		IGHV1-3	IGHD3-3	IGHJ6	CARDIAVATFLGLTSPRMDVW	5.2				
	1521		0.79		0.46		IGHV3-30	IGHD3-10	IGHJ5	CAATIIRGVMYGWFPDW	10.5				
	2408		0.19		0.41		IGHV3-11	IGHD2-2	IGHJ5	CVRQIVAPAAFPDPW	7.3	IGKV1-39	IGKJ5	CQASYSTRISF	4.7
	50545		1.96		0.41		IGHV3-11	IGHD1-26	IGHJ3	CARARGSGSLDAFDIWI	8.9				
	786		0.60		0.37		IGHV3-11	IGHD1-7	IGHJ4	CARAFNLPGTTSNVFDFW	8.0				
	313				0.34		IGHV3-11	IGHD2-2	IGHJ4	CARDMVLPSAYSQDW	9.3				
	521									CAGPTRSPRPLTKFERIVKKMKPD LA VEGKNDYVFDIWI	16.7				
	349				0.32		IGHV1-69	IGHD2-21	IGHJ3	CATDRPCSSSSPVCYSVPHYMGVW	6.2				
	758			0.25	0.28		IGHV3-7	IGHD2-2	IGHJ6	CVRLHVVAGAIHFDSW	4.9	IGKV1-39	IGKJ4	CQQSYSTPQALTF	6.8
	47287				0.21		IGHV3-7	IGHD6-19	IGHJ4	CARYVLLPPAARIDSW	11.4				
	206				0.20		IGHV3-11	IGHD2-2	IGHJ4	CAKESGMRTMPFDDW	9.8				
	1423			0.10	0.09		IGHV3-30	IGHD1-26	IGHJ4	CATSTRHTYAQGRQHYYGLDWW	8.3	IGLV1-47	IGLJ3	CEAWDDSLNGRVF	5.3
	29286				0.09		IGHV4-34	IGHD3-22	IGHJ6	CARDRVEPIAFMEYW	8.6				
	799				0.08		IGHV3-11	IGHD1-26	IGHJ4	CARERQNYDYTDNDRTKLESTAYW	8.4				
	1609				0.07		IGHV3-30	IGHD3-22	IGHJ4	CAHMTKKFYPGSGTHSWFDPW	6.7	IGKV1-5	IGKJ1	CQQYISFWTF	5.4
	48227			0.08	0.06		IGHV2-5	IGHD3-10	IGHJ5	CAKPRNDFWGSIDSW	3.4	IGLV1-36	IGLJ2	CAAWDDSLNVVVS	3.0
	1446				0.05		IGHV3-30	IGHD3-3	IGHJ4	CARSNYMGFFDLW	10.7				
	595			0.05	0.04		IGHV4-34	IGHD3-10	IGHJ2	CARVSGIDYW	7.6				
	1284			0.06	0.04		IGHV4-59	IGHD1-14	IGHJ4	CAKDASYGDYVFAYW	4.5				
	1065				0.03		IGHV3-30	IGHD4-17	IGHJ4	CARDEGMDYGDHRDWFYDLW	4.2				
	718			0.02	0.02		IGHV4-59	IGHD4-17	IGHJ2	CAKDDATYCSGGSCLFETW	8.2				
	304				0.02		IGHV3-30	IGHD2-15	IGHJ5	CARDFTTGAPWGYLDYW	8.3	IGLV1-40	IGLJ1	CQSYDSSLVYVVF	6.3
	48931			0.29	<0.01		IGHV3-30	IGHD2-2	IGHJ4	CARTTCSNSCFRRNSYDIW	10.4	IGKV1-12	IGKJ4	CQQGNSLPLTF	7.6
	25773		1.71				IGHV4-59	IGHD2-2	IGHJ3	CARAIAPVADCTDGSCYAFGYW	9.7	IGKV3-20	IGKJ1	CQQYVGAPWTF	4.0
	25		1.46	0.37			IGHV3-11	IGHD2-15	IGHJ4	CARGIKIRIVWMRTGAALSYW	7.5				
	672		0.36				IGHV4-34	IGHD3-3	IGHJ4	CARDHLGSAVAFPDFW	6.1				
	14294		0.26				IGHV3-11	IGHD2-15	IGHJ4	CTTVHGDYVFRYDYSW	6.1				
	1920		0.19	0.23			IGHV1-69	IGHD4-17	IGHJ4	CARSQTRYGSESLYFSDW	11.9				
	186		0.18				IGHV5-51	IGHD3-10	IGHJ4	CVRRIGYDLWGLRRGYHYMDVW	7.6				
	1049			0.04			IGHV4-34	IGHD3-3	IGHJ6	CAKHVFGQSRWSWYFINYGM DVW	7.4	IGLV1-40	IGLJ2	CQSYDSSLSSSVF	5.9
	8050			0.05			IGHV3-23	IGHD2-2	IGHJ6	CARVPMVRGVDFWDPW	3.7				
	1806			0.06			IGHV1-2	IGHD3-10	IGHJ5	CTRQEYRDFWSAHDYW	6.4	IGKV4-1	IGKJ4	CQQYYSPLNF	4.4
	35434			0.10			IGHV3-73	IGHD3-3	IGHJ4	CAREKDGDISPAFDYW	4.6				
	1600			0.10			IGHV1-69	IGHD4-17	IGHJ4	CARDRRHYDFWGSYSGRDYW	9.0	IGLV6-57	IGLJ3	CQSYDSANWVF	1.5
	15112			0.13			IGHV4-28	IGHD3-3	IGHJ4	CARSQTRYGSGAYYNSNW	7.9	IGKV3-11	IGKJ4	CQQRSTGVTF	4.3
	48426			0.15			IGHV5-51	IGHD3-10	IGHJ4	CARDRSGSYDYW	5.1	IGKV3-20	IGKJ2	CQQYGSSPRTF	0.6
	1562			0.19			IGHV4-55	IGHD3-3	IGHJ4	CAKDTLIDSW	9.6	IGLV4-69	IGLJ3	CQTWGTGFRVF	2.0
	47184			0.20			IGHV3-53	IGHD5-12	IGHJ4						

SUPPLEMENTARY TABLE 3.

Subject ID	Clonotype ID	GII.4 SY 2012 VLP-specific				VH	DH	JH	CDRH3	Avg VH SHM (%)	VL*	JL*	CDRL3*	Avg VL SHM (%)
		Day1, IgA§	Day1, IgG§	Day29, IgA§	Day29, IgG§									
Participant B	30082	4.72		41.83		IGHV1-69	IGHD6-6	IGHJ6	CAINAIPARRGSSSYLYRMDVW	13.9	IGKV2-28	IGKJ4	CMQGLQTPPTF	4.0
	30750	4.00	0.28	22.74	0.56	IGHV3-11	IGHD2-8	IGHJ6	CTRELMGARYYMDVW	9	IGLV4-69	IGLJ3	CQTWGTDIRVF	5.9
	37338	0.02		6.88	0.37	IGHV4-59	IGHD5-24	IGHJ5	CARTIESWRVGNWFDPW	7	IGKV1-39	IGKJ4	CQQSYRTPFTFGGGTTF	4.4
	10852			6.25	0.64	IGHV4-59	IGHD3-16	IGHJ1	CARFEINKVGDRAEYFQHW	1	IGKV1-39	IGKJ3	CQQSYTPTFTF	5.7
	39568	0.37		5.99	0.02	IGHV4-55	IGHD4-11	IGHJ6	CARGPDYSNYYHSYMDVW	8.7	IGLV3-19	IGLJ2	CASRDVSANHLIF	7.3
	3544			3.84		IGHV1-2	IGHD3-10	IGHJ4	CARGGSSGYWRPPDYW	1.2				
	6934	0.73		2.49		IGHV3-9	IGHD1-1	IGHJ4	CAKADSTVSGTHYFDQW	10	IGLV3-19	IGLJ3	CNSRDNTGNPNWVF	7.2
	2052			1.32		IGHV3-11	IGHD6-19	IGHJ5	CASQWRVGGGWFDPW	7.8				
	651	0.14		1.24		IGHV3-30	IGHD3-22	IGHJ3	CARDYSPSTVVRWASEFW	5.7	IGLV2-11	IGLJ3	CCSYVPSFTLVF	4.4
	33566	0.16		1.07	2.68	IGHV4-59	IGHD3-22	IGHJ4	CARYDDNRSIDSW	4	IGLV2-8	IGLJ1	CTSYAGNFNTVF	4.1
	32446	0.69		1.00	1.63	IGHV3-11	IGHD2-2	IGHJ4	CARERFGSWYYFDYW	7.7	IGLV4-69	IGLJ3	CQTWGTGIRVF	3.2
	2595			1.00		IGHV4-34	IGHD2-2	IGHJ4	CARGRGGFSTNWWYFDYW	10.8				
	7049			0.90		IGHV3-23	IGHD3-3	IGHJ6	CAKDSSTDFWSRYYSFYNGMDVW	4.1	IGLV2-14	IGLJ3	CSSYTSSSTWWF	1.7
	1097	0.05		0.88		IGHV3-23	IGHD1-26	IGHJ4	CAKDPRWEQLDLRDSW	4.9				
	2676	0.17		0.62		IGHV3-23	IGHD3-16	IGHJ6	CATGRWGAGHFYGLDW	6.6	IGKV2-28	IGKJ4	CMHGRQTLTF	
	240			0.58		IGHV4-28	IGHD6-13	IGHJ4	CARDIFPTSGDLGPTFPKYW	15	IGKV1-5	IGKJ1	CQQKYSYTPLTF	12.6
	2970			0.54		IGHV3-48	IGHD1-26	IGHJ4	CARMGQEDYW	6.1				
	29999			0.33		IGHV3-23	IGHD3-10	IGHJ4	CSRDLYNLFGWRRGDDYW	7.1	IGLV2-14	IGLJ3	CSSYTSTNTRVF	5.6
	38401	0.15		0.24	0.03	IGHV3-11	IGHD3-16	IGHJ6	CARYARLGDVMPGDVW	11	IGLV1-36	IGLJ3	CAAWDDSLKWWVF	8.3
	926			0.17		IGHV4-59	IGHD3-22	IGHJ4	CATYYDSRNSYSPGFAYW	6.4				
	39316			0.12	1.11	IGHV3-74	IGHD2-21	IGHJ4	CARDPCGGDCMDFW	7.5	IGKV1-39	IGKJ4	CLQSDSSPLTF	9.3
	1055		0.05	0.03	0.36	IGHV3-49	IGHD4-17	IGHJ4	CSRVGKDFDGLFDSW	7	IGLV2-23	IGLJ3	CCLYAGRSLWWF	5.5
	3060		0.70		9.41	IGHV3-48	IGHD1-14	IGHJ6	CATNNGYGGRRSGRGGYYHYGMDFW	8.6	IGKV1-39	IGKJ2	CQQYSAPPTF	9.4
	25846		0.24		4.94	IGHV4-59	IGHD2-8	IGHJ1	CATFVVISGSTRSEFRHW	7.7	IGKV1-39	IGKJ3	CQOQSHSTPFTF	7.9
	17931			3.55		IGHV3-11	IGHD3-9	IGHJ4	CARGLNFDWPKDGGYYFDYW	11.1	IGKV4-1	IGKJ1	CQQYYSTPPTF	4.3
	272			2.58		IGHV4-59	IGHD5-18	IGHJ4	CARYADDKGFONW	6.1	IGLV2-14	IGLJ3	WCSHTTAALSFL	6.0
	565		2.68		1.90	IGHV4-61	IGHD1-1	IGHJ6	CARES/GRPPYYGIDVW	12.6				
	781		1.20		1.86	IGHV4-59	IGHD3-3	IGHJ6	CARYYENGNNRACGLDW	9.7	IGKV4-1	IGKJ3	CQQYYRTPFTF	4.0
	1624		2.42		1.85	IGHV4-59	IGHD3-10	IGHJ3	CSSQIRIGGGV/GAFDLW	6.7				
	38266			1.69		IGHV4-59	IGHD6-19	IGHJ5	CARTLEVPRRGGLAGNWFDPW	4.3	IGKV1-39	IGKJ4	CQQSYSTPFTF	5.8
	2613		0.96		1.25	IGHV5-51	IGHD1-7	IGHJ5	CARLPNNWHFFAPW	11.4				
	1017			1.11		IGHV3-30	IGHD1-14	IGHJ4	CAKDLGGTWSFDSW	7.5	IGLV2-14	IGLJ3	CNSYTSSSTWWF	2.7
	271			0.73		IGHV4-34	IGHD6-19	IGHJ4	CATVELRAAAGKAVAGSKDHYW	1.8				
	493			0.69		IGHV1-69	IGHD5-12	IGHJ4	CARGGEGGYDRFGNW	8	IGKV1-9	IGKJ3	CQTLNSYPRVTF	6.4
	27623			0.62		IGHV3-33	IGHD1-1	IGHJ5	CVRTSDPFFSNARNWFGPW	8.1				
	296		0.11	0.60		IGHV3-30	IGHD3-9	IGHJ6	CAKNLFSYFARSGDWGMDVW	10.1	IGLV1-47	IGLJ3	CAAGDDSLSGWVF	4.9
	27777			0.54		IGHV4-59	IGHD2-2	IGHJ4	CAKYVDTSAFGDW	8.1	IGKV4-1	IGKJ3	CQQYYRTPFAF	5.4
	38880			0.51		IGHV3-53	IGHD7-27	IGHJ5	CARGLSGAPPGGFDSW	9.9	IGLV9-49	IGLJ3	CGADHASGTFNVYVF	5.1
	20212		0.10	0.50		IGHV3-30	IGHD4-11	IGHJ4	CARNKGPKYYNSNLQYFQYW	3.6	IGLV1-51	IGLJ2	CGTWDDSLNAGVF	2.4
	24			0.48		IGHV4-59	IGHD3-10	IGHJ6	CVGARDYYYGSGRPNRQQTDSGMDVW	7.8	IGKV4-1	IGKJ4	CQQYYSTPLTF	4.8
	1428			0.45		IGHV3-15	IGHD5-24	IGHJ4	CVKDPYSYGNWGHNFYEY	16.7				
	1478			0.30		IGHV3-23	IGHD1-1	IGHJ6	CAKLGGRSYYFYSIDVW	3.1				
	358			0.29		IGHV4-59	IGHD2-2	IGHJ4	CARYTEHRLGPAALDYW	1.1	IGLV2-14	IGLJ3	CSSYTSSSTWWF	1.7
	3871			0.22		IGHV4-34	IGHD6-6	IGHJ5	CATKKGRIARVGSWFDPW	8.4				
	3497			0.21		IGHV1-3	IGHD6-6	IGHJ5	CARFRIARRRFPDW	2				
	303	0.03		0.18		IGHV1-18	IGHD5-18	IGHJ4	CVRSAYNSGLDYW	9.8				
	1059			0.17		IGHV4-39	IGHD4-17	IGHJ4	CVSSPQDFFRYW	10.3	IGLV3-21	IGLJ3	CQVWDTDSHRIVF	9.7
	176			0.16		IGHV4-59	IGHD2-15	IGHJ5	CARAEAVVAAMVGDSGWWWFDPW	0.3	IGLV3-1	IGLJ2	CQAWDSSVWF	0.9
	12907			0.15		IGHV3-11	IGHD1-1	IGHJ6	CARDORQAPVYGMGVW	14.2	IGLV2-8	IGLJ2	CSSYAGGNLWWF	7.7
	29899		0.07	0.12		IGHV3-49	IGHD1-20	IGHJ4	CVRDSTWNADAYW	5	IGLV1-47	IGLJ5	CAAWDDSLSGRVF	4.0
35588			0.11		IGHV4-59	IGHD3-22	IGHJ4	CATYDRSGLNYW	5.3	IGKV4-1	IGKJ4	CQQYHTTPFTF	6.0	
3353			0.09		IGHV1-46	IGHD4-23	IGHJ5	CARDLTRTAVITPAFDSW	4.9					
3687			0.09		IGHV2-70	IGHD3-10	IGHJ3	CARMPNLIGQVKDDAFDW	5.9					
2842			0.09		IGHV3-48	IGHD6-6	IGHJ6	CARDQRGVTPRPPYYFYMDVW	8.4					
257			0.08		IGHV4-59	IGHD2-2	IGHJ6	CARLVDCSTPRCQLGASAMDVW	8.5					
20271			0.07		IGHV4-59	IGHD6-6	IGHJ3	CARNLVSRRDDAFDVW	5.8	IGKV1-39	IGKJ3	CQQSYRTPFTF	6.4	
1348			0.07		IGHV4-55	0	IGHJ4	CAGRQSFQYW	10.7					
8577			0.07		IGHV6-1	IGHD4-17	IGHJ4	CARNRPNDYADYLLDYW	5.3					
480			0.07		IGHV1-2	IGHD3-16	IGHJ3	CVRDGGORAFDIW	0.7					
1542			0.07		IGHV3-74	IGHD2-15	IGHJ6	CARDTKASPDYYMAVW	9.4					
1021			0.06		IGHV3-30	IGHD6-19	IGHJ3	CARDGGFLNSGWPSHLGEYW	5.5					
3108			0.06		IGHV3-74	IGHD6-6	IGHJ4	CVRDDEGLDYW	7.4					
297			0.05		IGHV4-55	IGHD5-12	IGHJ4	CARAPSGYRCYGLDYW	11.1					
1392			0.05		IGHV3-74	IGHD1-14	IGHJ6	CAGSRLDYNNAMDVW	6.1	IGLV3-19	IGLJ1	CCSRDTNENHYVF	5.0	
39420			0.05		IGHV4-39	IGHD3-10	IGHJ5	YARGVWGSGSRVWWFDPW	6.7	IGLV1-44	IGLJ2	CAAWDDSLNGVPV	3.4	
2241			0.04		IGHV3-53	IGHD5-18	IGHJ4	CARGMGYSAYLMDFW	13.8	IGKV1-39	IGKJ1	CLQTYNTPLAF	6.2	
3443			0.04		IGHV4-59	IGHD6-13	IGHJ5	CAREEITPGYVDHW	5.6					
713			0.04		IGHV3-49	IGHD6-6	IGHJ4	CIRGGLTEWQRFDSW	6.7					
35918			0.03		IGHV3-30	IGHD2-21	IGHJ4	CVKDDMSNWWYFDYW	8.5	IGKV1-5	IGKJ4	CQQYTYLPLTF	6.9	
216			0.03		IGHV4-39	IGHD2-15	IGHJ4	CARGPLRLRGVWVSPHGDW	8.9	IGLV2-14	IGLJ3	CSSFTATSTLEMF	6.9	
21479	0.27				IGHV4-59	IGHD3-9	IGHJ4	CARSKTRDSDWPHFDSW	8.1	IGLV2-8	IGLJ2	CSSYSSYAGSKNLFV	5.9	
3339	0.21				IGHV3-21	IGHD6-13	IGHJ4	CARDKYSSSWYYFDYW	2.5					
3105	0.08				IGHV3-64	IGHD4-17	IGHJ4	CVKQMTTVTTTRGQSFQYW	7.5					
1780	0.03				IGHV1-8	IGHD3-10	IGHJ5	CARGRGGLSYWFDSW	12.1	IGLV1-40	IGLJ1	CQSYDYMLSGSYVF	7.8	
2731	0.03				IGHV3-53	0	IGHJ4	CAGRADYW	13.7					
3134		0.76			IGHV4-55	IGHD5-18	IGHJ4	CAGARGYIGYAYW	7.1					
646		0.31			IGHV4-59	IGHD7-27	IGHJ3	CAGDVWGLTAKDRDAFNWV	1.3	IGKV3-20	IGKJ2	CQQHGGSSPPYTF	5.1	
37670		0.14			IGHV3-11	IGHD2-15	IGHJ6	CATYPKLGNAMPGVW	15.8	IGLV1-44	IGLJ3	CAVWDDSLKWWVF	10.6	

SUPPLEMENTARY TABLE 4.

GII.4 SY 2012 VLP-specific														
Subject ID	Clonotype ID	Day1, IgA\$	Day1, IgG\$	Day29, IgA\$	Day29, IgG\$	VH	DH	JH	CDRH3	Avg VH SHM (%)	VL*	JL*	CDRL3*	Avg VL SHM (%)
Participant D	507			25.38	0.01	IGHV3-33	IGHD4-23	IGHJ6	CVKDRAALATPPFYGLDAW	11.8	IGKV2-28	IGKJ4	CMQALQTPPTTF	5.5
	32048	0.40	0.81	22.76	41.65	IGHV3-11	IGHD3-16	IGHJ6	CARYARLGDVMPGDVW	10.9	IGLV1-44	IGLJ3	CAAWDESLKWWF	12.2
	1647			9.31		IGHV3-53	IGHD4-11	IGHJ6	CAKVPGYIDCSDGIRCHIRHYGLEVV	17.6				
	28221			5.62		IGHV3-33	IGHD4-23	IGHJ3	CAKDRAGLVTPPFYGIDGW	13.6				
	669	0.05		5.46		IGHV3-23	IGHD5-24	IGHJ4	CAQAKRLGEGWPIDYW	13				
	2571	0.26	0.04	5.19	0.03	IGHV3-30	IGHD1-26	IGHJ4	CAKDRRAWERNFDSW	10.3				
	29491		0.56	4.92	0.32	IGHV3-11	IGHD6-25	IGHJ6	CAAPRFSPDTGGDLVW	14.6	IGKV3-20	IGKJ5	CQWYGYSSSGTF	10.1
	2925	0.30		4.59		IGHV4-59	IGHD1-26	IGHJ4	CARYRESLTVGATKGFEYW	5.3	IGKV1-17	IGKJ3	CLQHNSHPPTTF	7.9
	1632			3.50		IGHV3-21	IGHD3-9	IGHJ6	CVRERYDILGDDPPVW	8.6	IGKV1-5	IGKJ1	CQQYYSMKGSF	4
	630	0.30		2.84	0.23	IGHV3-23	IGHD3-10	IGHJ5	CARVTSYYYGSAIRWFGPW	12.6	IGKV1-5	IGKJ2	CQQYSSRYTTF	3.9
	15067			2.61		IGHV3-11	IGHD5-12	IGHJ4	CARGTMTGKSLPHYW	10	IGLV1-40	IGLJ3	CQTYDSSRRTHWWF	5.1
	28562		0.07	1.67		IGHV1-8	IGHD4-17	IGHJ4	CARGGPYDFW	7.2	IGKV3-20	IGKJ2	CQQYSSSPETF	5.4
	6460	0.10		1.55		IGHV3-7	IGHD6-19	IGHJ4	CARSIVSVSGTDRDFQW	8.2				
	957	0.17		1.36	0.04	IGHV3-74	IGHD1-14	IGHJ4	CVRDSVTNRDFW	10.8				
	17056			1.29		IGHV5-51	IGHD2-15	IGHJ4	CARSSFSFKFYFDAW	14.9	IGKV1-39	IGKJ2	CQQGYKTPYTF	12.5
	4689			0.86		IGHV4-31	IGHD6-13	IGHJ4	CASSPSYSSRSDYW	6.1	IGLV2-14	IGLJ1	CSSYTSTSGQIVF	4.4
	22031		0.09	0.57	0.03	IGHV4-31	IGHD3-9	IGHJ5	CGGDRSGYYQIKSW	11.5				
	789	0.04		0.51		IGHV3-30	IGHD2-21	IGHJ3	CAKGFPLSCGRNCRNDAFDVW	10.9				
	40		0.50	5.92		IGHV1-18	IGHD3-10	IGHJ4	CARDPRGDMVRGVNPFDPYW	1.5				
	480		1.66	5.33		IGHV3-23	IGHD3-10	IGHJ5	CVRVSERYYYGSQTRSLDPW	14.3	IGKV3-20	IGKJ2	CQQYGRSVYTF	5.8
	493			3.91		IGHV3-38	IGHD6-6	IGHJ6	CTKVPGLDCTGDCRCQTRYGMEWW	11.6				
	2597		0.95	2.67		IGHV3-53	IGHD5-18	IGHJ6	CAKVPGYDICTGDCRCQTRYGMEWW	18.2				
	19518			2.16		IGHV3-11	IGHD2-8	IGHJ6	CARDERAQAPVYAMGVW	16.6	IGLV2-8	IGLJ3	CSSFAGGNPWVWF	13.1
	14875		0.64	0.77		IGHV7-81	IGHD6-19	IGHJ6	CARDRPGIAVAGLNGMDVW	11.6				
	155			0.54		IGHV4-28	IGHD1-14	IGHJ3	CARRPISINFLEVPPTKIQNGYDWW	13.8	IGLV1-36	IGLJ3	CATWDDSLNAWWF	6.5
	8731		1.99	0.51		IGHV3-30	IGHD3-10	IGHJ4	CAKSIDTYKYGAGSPGLAYW	5.3				
	2631		0.02	0.38		IGHV3-74	IGHD1-1	IGHJ6	CARDEKLSTPDYGYMDVW	12.1	IGKV1-39	IGKJ3	CQQSYSLYGSPPHFH	11.3
	29925			0.38		IGHV1-2	IGHD3-9	IGHJ6	CARYYDILTGERDGMVW	5.6				
	3486			0.31		IGHV4-34	IGHD3-10	IGHJ6	CARRFGELFGRGGGMDVW	7.2				
	11115			0.26		IGHV1-18	IGHD3-9	IGHJ6	CARDIVRPENIPRGGMVW	9.2	IGKV3-11	IGKJ1	CQQRSSWPWTF	6.1
	12848			0.22		IGHV1-69	IGHD4-17	IGHJ6	CARELDQDYGDPDYGDKESGLDWW	12	IGLV1-47	IGLJ3	CATWDDSLTGPWWL	6.1
	1794			0.21		IGHV3-23	IGHD5-24	IGHJ4	CAKEGGWEDGYKRIDLDSW	14.9	IGLV1-51	IGLJ3	CGTWESYLNPPWWF	4.7
	2656			0.17		IGHV3-11	IGHD1-1	IGHJ6	CARDKRRQAPIYAMDVW	14.9				
	7013	3.15		0.17		IGHV4-34	IGHD3-22	IGHJ3	CARGRTMIRIW	1.1				
	3761			0.11		IGHV3-33	IGHD6-13	IGHJ4	CAKDEQLVHGIDYW	3				
	1858			0.11		IGHV3-11	IGHD5-12	IGHJ4	CARFRDIVAADHFDHW	14.8	IGLV3-1	IGLJ2	CQWDRSTVWF	8.3
	886		0.17	0.10		IGHV3-7	IGHD6-6	IGHJ4	CARSRTAFFW	3.1	IGLV2-14	IGLJ3	CSSYTSSSTLVF	1.8
	227			0.08		IGHV4-31	IGHD6-13	IGHJ1	CARAAAVIGIRASIEYFQHW	2.6	IGKV1-39	IGKJ1	CQQSYSIYWTF	0.8
	3610		0.62	0.07		IGHV3-53	IGHD6-19	IGHJ3	CASRHHYVSGFDIW	8.5	IGKV3-11	IGKJ1	CQQRNNWPWTF	5.8
	1972			0.07		IGHV1-18	IGHD1-1	IGHJ4	CVRDRGELEDRDFDFW	15.1				
	15860			0.06		IGHV2-5	IGHD6-25	IGHJ4	CARLDSGAANHFAFW	9.2				
	3176			0.06		IGHV1-18	IGHD6-13	IGHJ4	CARDGGRGYSSSW	2.7				
	2315			0.05		IGHV3-30	IGHD5-12	IGHJ4	CARDRWLRGLTDSW	3.2				
	2550		0.12	0.05		IGHV4-59	IGHD5-24	IGHJ4	CAGGRDGYTYW	1.3				
	1391		0.14	0.05		IGHV3-48	IGHD3-3	IGHJ5	CARENHGLAIFGVPYARKNYFDPW	7.6	IGLV1-40	IGLJ3	CQSHDSSLSGSVF	2.8
	1864			0.05		IGHV4-31	IGHD2-2	IGHJ5	CARGFCDTSSCYRSPDPW	10.3				
	2138		0.21	0.05		IGHV3-30	IGHD5-18	IGHJ4	CARVPFASMATQYHFDW	12.3				
	541		0.08	0.05		IGHV3-30	IGHD1-1	IGHJ4	CVRDSRDSRRITYCERLCLYSDSW	11.9				
	1639			0.05		IGHV3-30	IGHD5-12	IGHJ4	CAKDAFMYSHGWHKFDW	11.5	IGLV1-51	IGLJ3	CGTWDTNLGAWWF	4.8
	537			0.04		IGHV1-18	IGHD2-2	IGHJ5	CARDVVVPAPMRGGCDPW	6.8				
272			0.04		IGHV3-11	IGHD2-2	IGHJ4	CARKWQAEFFG	11.5					
2751			0.04		IGHV4-59	IGHD3-16	IGHJ4	CARGEKGVLMDYFDYW	2.1					
602			0.04		IGHV5-51	IGHD6-19	IGHJ3	CARPRGLGWRDFTDWW	6.8					
150			0.04		IGHV4-4	IGHD6-6	IGHJ4	CARDELDFYDIDW	9.4	IGKV1-5	IGKJ2	CQQYKSHSPPTTF	8.9	
3484			0.03		IGHV4-39	IGHD5-24	IGHJ4	CARREGYKSEAFDYW	1.7					
4144			0.03		IGHV3-7	IGHD2-15	IGHJ4	CARDRGWKSFDYW	7	IGLV2-8	IGLJ1	CSSYAVSGVVF	1.2	
13626			0.03		IGHV4-55	IGHD3-3	IGHJ5	CARGADWSGYTLNWFDPW	7.7	IGLV1-40	IGLJ3	CQSYESSLSGWVW	3.2	
20694			0.02		IGHV1-46	IGHD4-17	IGHJ6	CATPRDGNLNYGMDVW	5.3	IGKV1-39	IGKJ1	CQQTYRFLQTF	7.8	
4037			0.02		IGHV1-18	IGHD3-10	IGHJ5	CARDGPRTFLRGGDFPW	9.8					
1797			0.02		IGHV4-59	IGHD2-8	IGHJ4	CAKEYSHW	3.7	IGLV7-43	IGLJ3	CLLYYGAWWF	1.6	
2649			0.02		IGHV1-18	IGHD1-20	IGHJ4	CARDHASNNARQVDYW	6.2					
490			0.02		IGHV1-46	IGHD3-22	IGHJ4	CARDYYDTRVPDYW	8.6					
10033			0.02		IGHV1-69	IGHD2-21	IGHJ6	CARASIPFDMVW	10.5					
4342			0.02		IGHV3-30	IGHD3-22	IGHJ4	CARGPEGLVVITGEVDYW	2.5					
506			0.02		IGHV3-53	IGHD7-27	IGHJ3	CARVGTNNGSMPLDWW	12					
26003			0.01		IGHV4-28	IGHD2-2	IGHJ6	CARDCTSTCQIYYGMDFW	10.8	IGKV1-39	IGKJ2	CQQSHSTPRTF	4.6	
4348			0.01		IGHV6-1	IGHD2-2	IGHJ4	CARGPLGTAAGDYW	3.9					
22373			0.01		IGHV4-4	IGHD2-15	IGHJ4	CGREHYSGKYIDSW	8.4					
3250			0.01		IGHV3-30	IGHD6-19	IGHJ5	CARDRVGYSSGWCDHW	6.7					
3570			0.01		IGHV1-2	IGHD3-22	IGHJ6	CARVRHYDTSAYKSYGMDVW	4.6					
2655			0.01		IGHV1-3	IGHD3-22	IGHJ4	CARDKIMIGLLDYW	5.1					
11284			<0.01		IGHV3-30	IGHD5-18	IGHJ4	CARDLLDTAVDYW	5.4	IGLV2-14	IGLJ3	CCSYTTSSTWWF	6.9	
7054	0.64				IGHV1-69	IGHD6-6	IGHJ6	CARNMGSAARRGSTYYYMDVW	10.2	IGKV2-28	IGKJ4	CMQGLQTPLSF	4.6	
4332	0.09				IGHV3-30	IGHD5-24	IGHJ4	CARGLKMAPASDW	3.2					
1068	0.08				IGHV3-15	IGHD2-15	IGHJ4	CTTDRGGRGGYASFFDQW	8.7	IGKV1-5	IGKJ1	CQQYNSYWTF	9.6	
1750	0.05				IGHV4-39	IGHD1-26	IGHJ3	CASRSVTYNVDAFDLW	8.8	IGLV1-51	IGLJ3	CGAWDRSLTAWWF	9.1	
20475		2.85			IGHV4-59	IGHD2-8	IGHJ1	CATFVMSGRTSEYFRHW	7.7	IGKV1-39	IGKJ3	CQQSHSTPPTF	6.2	
288		0.80			IGHV4-55	IGHD1-26	IGHJ4	CARRAVGVNFDYW	9.4	IGKV1-13	IGKJ3	CQQFDSYPLTF	1.9	
82		0.36			IGHV3-30	IGHD2-2	IGHJ3	CVRDLGAYYNGRRFGTEAFDLW	9.2	IGKV1-9	IGKJ4	CQQLNSYPSF	2.2	
29259		0.22			IGHV3-30	IGHD2-15	IGHJ6	CVRDRSTSTPIYGLAWW	8.5	IGLV1-40	IGLJ3	CQSYNRSLSVMF	6.6	
2338		0.21			IGHV4-59	IGHD6-19	IGHJ4	CAREPYSSGWNHLDYW	5.8					
13697		0.16			IGHV4-39	IGHD4-17	IGHJ5	CARGPTVTRRRGYFDPW	16	IGLV1-51	IGLJ3	CGAWDSSLSLMMF	8	
1501		0.12			IGHV3-11	IGHD3-9	IGHJ5	CARSTSTYQRLIGYSNWFDLW	9.6					
2994		0.05			IGHV3-33	IGHD3-10	IGHJ5	CVKGPSFGELPFDYW	5.7					
1629		0.04			IGHV3-13	IGHD2-2	IGHJ2	CVRASGDIGLLPARWNFDLW	3.7	IGLV1-40	IGLJ3	CQSYDTSLRWWF	5.2	
1292		0.03			IGHV3-30	IGHD6-13	IGHJ6	CARYPAAAGTTFSDGMDVW	1.6					
4762		0.03			IGHV1-69	IGHD3-10	IGHJ5	CARAKVRGVGYSIDPW	7.3					
4067		0.03			IGHV3-30	IGHD6-19	IGHJ4	CARDLGGSSDFW	3					
2737		0.02			IGHV1-46	IGHD5-24	IGHJ3	CARERYLQFFKGRDAFDVW	5.2					

SUPPLEMENTARY TABLE 5.

Subject ID	Clonotype ID	mAb ID	IGHV	IGHD	IGHJ	CDRH3	VH SHM (%)	VL	JL	CDRL3	VL SHM (%)	Isotypes/format used to express recombinant mAbs
Participant C	50337	VX89	IGHV4-31	IGHD6-13	IGHJ3	CAGGRVSSSWYREDAFDMW	10	IGKV4-1	IGKJ3	CQQYFSAPFTF	5.4	mlgA, dlgA
	50996	VX93	IGHV4-31	IGHD2-15	IGHJ4	CVRGWFFSSYYRLDYFDSW	10.3	IGKV4-1	IGKJ3	CQQYYSIPLTF	7.3	mlgA, dlgA
	43333	VX77	IGHV3-11	IGHD3-22	IGHJ5	CARSAQYICITRSRCYLVFDPW	8.6	IGLV1-40	IGLJ1	CQSYDTGLSGSHYVF	3.5	IgG, mlgA, dlgA
	48426	VX91	IGHV5-51	IGHD3-10	IGHJ4	CAKSLTHLGSGTFYNDSW	10	IGKV3-11	IGKJ4	CQQRSTGVTF	4.3	mlgA, dlgA
	26954	VX96	IGHV6-1	IGHD6-19	IGHJ5	CARDLGNSGWFFVTRKNSFAPW	6.5	IGLV1-51	IGLJ3	CGTWDGSLSAGVF	5.4	IgG, mlgA, dlgA
	50686	VX90	IGHV2-26	IGHD5-12	IGHJ4	CARIWGNSGYDFHAQRAFDYW	7.5	IGLV1-40	IGLJ3	CQSYDNSLRGWVF	4.9	IgG, mlgA, dlgA
	49926	VX92	IGHV3-11	IGHD3-10	IGHJ4	CARDSASGATSYNNANW	9.2	IGLV1-40	IGLJ1	CQSYDTGLSGSHYVF	3.5	mlgA, dlgA
	46625	VX94	IGHV4-34	IGHD3-3	IGHJ4	CARFRKALWSADSREMVDW	9.2	IGKV1-17	IGKJ3	CLQHNSYPFTF	7.3	IgG, mlgA, dlgA
	34207	VX88	IGHV3-23	IGHD6-13	IGHJ4	CSKGVSAAGTTGIPYFFDSW	7.2	IGKV4-1	IGKJ3	CQQYYSTPTF	5.6	IgG, mlgA, dlgA
	291	VX67	IGHV4-61	IGHD1-1	IGHJ3	CASRRRRHNWNDNPFDIW	22.9	IGKV1-5	IGKJ1	CQQYFSYSF	6.9	IgG
	50547	VX95	IGHV3-11	IGHD5-18	IGHJ4	CVRQNMMDKAVVPDYW	9.4	IGLV1-40	IGLJ2	CQSFDTSLSGSIVF	6.1	IgG
	48639	VX72	IGHV4-59	IGHD4-23	IGHJ4	CARAAIQPPAAAYFDHW	9.1	IGLV1-44	IGLJ3	CAAWDDSLNAWVF	5.5	IgG

SUPPLEMENTARY TABLE 6.

Map	VX77 Fab + GII.4 SY 2012 P domain	VX93 Fab + GII.4 SY 2012 P domain	VX77 Fab + GII.4 SY 2012 VLP	VX93 Fab + GII.4 SY 2012 VLP											
				Global reconstruction	5-fold axis local map	5-fold axis local map	5-fold axis local map	5-fold axis local map	5-fold axis local map	3-fold axis local map	3-fold axis local map	3-fold axis local map	3-fold axis local map	3-fold axis local map	3-fold axis local map
				(4 Fabs)	(5 Fabs-1)	(5 Fabs-2)	(3 Fabs-1)	(3 Fabs-2)	(1 Fab)	(2 Fabs)	(2 Fabs)	(2 Fabs)	(2 Fabs)	(3 Fabs)	
EMDB	EMD-71602	EMD-71603	EMD-72540	EMD-72541	EMD-72542	EMD-72543	EMD-72544	EMD-72545	EMD-72546	EMD-72547	EMD-72548	EMD-72549	EMD-72550	EMD-72551	
Data collection															
Microscope	TFS Glacios		TFS Glacios	TFS Glacios											
Voltage (kV)	200	200	200	200											
Detector	Falcon 4	Falcon 4	Falcon 4	Falcon 4											
Recording mode	Counting	Counting	Counting	Counting											
Nominal magnification	190,000x	190,000x	190,000x	190,000x											
Movie micrograph pixel size (Å)	0.725	0.725	0.725	0.725											
Dose rate (e ⁻ /[(camera pixel)*s])	6.107	6.092	7.807	6.801											
EER number of fractions	40	40	40	40											
Movie micrograph exposure time (s)	3.88	3.88	3.03	3.47											
Total dose (e ⁻ /Å ²)	45	45	45	45											
Defocus range (µm)	-0.7 to -1.5	-0.7 to -1.7	-0.8 to -2.0	-0.8 to -1.8											
EM data processing															
Number of movie micrographs	3,965	3,620	3,089	3,750											
Number of particle images in map	128,751	332,242	9,381	14,309	175,518	207,601	138,254	137,750	199,112	133,278	168,762	133,845	203,843	218,764	
Symmetry	C2	C2	I	I	C1	C1	C1	C1	C1	C1	C1	C1	C1	C1	
Map resolution (FSC 0.143; Å)	3.08	2.93	3.43 (binned by 2)	3.34 (binned by 2)	6.97	6.5	7.53	7.42	6.66	7.68	7.39	7.46	6.59	6.65	
Map sharpening B-factor (Å ²)	-92.3	-109.6	-66.3	-108	-108	-478.9	-544.2	-588.7	-473.5	-565	-548.7	-590.1	-450.4	-466.1	
Structure building and validation															
Number of atoms in deposited model															
P domain	4,790	4,790													
Fab Fv	3,588	3,776													
MolProbity score	1.44	1.14													
Clashscore	1.52	1.79													
Map correlation coefficient, CC (Mask)	0.7	0.77													
EMRinger score	1.6	3.32													
d FSC model (0.5; Å)	3.7	3.5													
RMSD Bonds															
Bond length [Å]	0.006	0.006													
Bond angles [°]	1.128	0.998													
Ramachandran plot															
Favored (%)	93.87	97.77													
Allowed (%)	6.13	2.23													
Outliers (%)	0	0													
Side chain rotamer outliers (%)	1.52	1.59													
Cβ outliers (%)	0	0													
PDB	9PFJ	9PFK													

SUPPLEMENTARY TABLE 7.

GII.4 SY 2012 P domain Chain	Amino Name 1	Amino number 1	Atom	Epitope site (defined previously)	VX77 Chain	Amino Name 2	Amino number 2	Distance (Å)	Predicted interaction
A	THR	291	OG1-O		H	SER	100C	2.84	Hydro-Bond
A	ILE	293	CB-O		H	CYS	100E	3.23	Van-der-Waals
A	ILE	293	CD1-OE1		H	GLN	97	3.29	Van-der-Waals
A	THR	294	N-O	A	H	CYS	100E	3.31	Hydro-Bond
A	THR	294	O-CA	A	H	TYR	100F	3.84	Van-der-Waals
A	THR	294	O-CD1	A	H	LEU	100G	3.24	Van-der-Waals
A	GLY	295	C-CD1	A	H	LEU	100G	3.68	Van-der-Waals
A	SER	296	CB-CD1	A	H	LEU	100G	3.43	Van-der-Waals
A	SER	296	OG-CZ	A	H	TYR	33	3.21	Van-der-Waals
A	SER	296	OG-OH	A	H	TYR	33	3.35	Hydro-Bond
A	ARG	297	NE-OH	A	H	TYR	50	2.98	Hydro-Bond
A	ARG	297	NH2-OG	A	H	SER	56	2.85	Hydro-Bond
A	ARG	297	NH2-O	A	H	THR	57	2.71	Hydro-Bond
A	ARG	297	NH2-N	A	H	ASP	58	3.74	Van-der-Waals
A	ASN	298	OD1-OH	A	H	TYR	33	2.99	Hydro-Bond
A	ASN	302	OD1-NH2		H	ARG	100B	2.35	Hydro-Bond
A	LYS	329	CE-CG1		H	VAL	53	3.62	Van-der-Waals
A	THR	350	OG1-SD		H	MET	54	3	Van-der-Waals
A	TYR	352	CD2-OD2	G	H	ASP	31	3.24	Van-der-Waals
A	GLY	363	C-NH1		H	ARG	100B	3.84	Van-der-Waals
A	ARG	364	CG-NH1	G	H	ARG	100B	3.17	Van-der-Waals
A	GLU	368	OE2-OD1	A	H	ASP	31	3.91	Van-der-Waals
A	GLU	368	OE1-CG2	A	H	VAL	53	2.92	Van-der-Waals
A	GLU	368	OE1-CG	A	H	MET	54	3.31	Van-der-Waals
A	THR	369	O-CE		H	MET	54	3.82	Van-der-Waals
A	ASP	391	OD2-ND2	D	H	ASN	73	3.34	Hydro-Bond
A	THR	294	CG2-CD2	A	L	TYR	31	3.42	Van-der-Waals
A	THR	294	CB-CD2	A	L	TYR	91	3.78	Van-der-Waals
A	GLY	295	CA-CE1	A	L	TYR	91	3.69	Hydr-Phbc
A	GLY	295	CA-CD1	A	L	TYR	91	3.79	Hydr-Phbc
A	GLY	295	O-OH	A	L	TYR	96	2.49	Hydro-Bond
A	ASP	372	OD2-CD2	A	L	HIS	95D	3.08	Van-der-Waals
A	ARG	373	NH1-N	A	L	GLY	94	3.22	Van-der-Waals
A	ARG	373	NH2-NE2	A	L	HIS	95D	3.01	Van-der-Waals

SUPPLEMENTARY TABLE 8.

GII.4 SY 2012 P domain Chain	Amino Name 1	Amino number 1	Atom	Epitope site (defined previously)	VX93 Chain	Amino Name 2	Amino number 2	Distance (Å)	Predicted interaction
A	PHE	250	CE2-O		H	SER	100	3.97	Van-der-Waals
A	PHE	250	CZ-CD1		H	TYR	100A	3.62	Hydr-Phbc
A	PHE	250	CE1-CD1		H	TYR	100A	3.98	Hydr-Phbc
A	PHE	250	CE2-CD1		H	TYR	100B	3.57	Hydr-Phbc
A	PHE	250	CD2-CE1		H	TYR	100B	3.73	Hydr-Phbc
A	PHE	250	CE2-CE1		H	TYR	100B	3.75	Hydr-Phbc
A	GLY	252	CA-CD1		H	TYR	100B	3.87	Hydr-Phbc
A	GLY	252	CA-CG		H	TYR	100B	3.89	Hydr-Phbc
A	PRO	253	O-CD2		H	TYR	100B	2.93	Van-der-Waals
A	PRO	253	CD-CB		H	TYR	100B	3.97	Hydr-Phbc
A	SER	255	OG-CE2	F	H	TYR	52	3.49	Van-der-Waals
A	SER	255	O-CE1	F	H	TYR	53	3.73	Van-der-Waals
A	SER	255	O-ND2	F	H	ASN	54	2.86	Hydro-Bond
A	ALA	256	O-CA	F	H	GLY	32	3.92	Van-der-Waals
A	ALA	256	O-N	F	H	GLY	33	3.14	Hydro-Bond
A	ALA	256	CA-CD2	F	H	TYR	52	3.45	Hydr-Phbc
A	ALA	256	CB-CD2	F	H	TYR	52	3.61	Hydr-Phbc
A	ALA	256	CB-CE2	F	H	TYR	52	3.69	Hydr-Phbc
A	ALA	256	CA-CE2	F	H	TYR	52	3.96	Hydr-Phbc
A	ALA	256	CA-CG	F	H	TYR	52	3.98	Hydr-Phbc
A	ALA	256	O-CE1	F	H	TYR	53	3.4	Van-der-Waals
A	ALA	256	CB-CD2	F	H	PHE	97	3.33	Hydr-Phbc
A	ALA	256	CB-CE2	F	H	PHE	97	3.42	Hydr-Phbc
A	PHE	257	CE2-CD2	F	H	TYR	100B	3.75	Hydr-Phbc
A	PHE	257	CD1-CA	F	H	GLY	33	3.65	Hydr-Phbc
A	PHE	257	CE1-CA	F	H	GLY	33	3.72	Hydr-Phbc
A	PHE	257	O-OH	F	H	TYR	53	2.83	Hydro-Bond
A	PHE	257	CZ-CD2	F	H	PHE	97	3.46	Hydr-Phbc
A	PHE	257	CE2-CD2	F	H	PHE	97	3.47	Hydr-Phbc
A	PHE	257	CE2-CE2	F	H	PHE	97	3.89	Hydr-Phbc
A	PHE	257	CZ-O	F	H	SER	98	3.93	Van-der-Waals
A	PHE	257	CE1-OG	F	H	SER	99	3.4	Van-der-Waals
A	VAL	258	CG2-O		H	ARG	30	3.56	Van-der-Waals
A	VAL	258	CG2-O		H	THR	31	3.12	Van-der-Waals
A	VAL	258	CG2-OH		H	TYR	53	3.4	Van-der-Waals
A	VAL	258	CG2-CZ		H	TYR	53	3.52	Hydr-Phbc
A	VAL	258	CG2-CE2		H	TYR	53	3.74	Hydr-Phbc
A	THR	395	CG2-CE2	D	H	TYR	100F	3.37	Van-der-Waals
A	HIS	396	O-OH	D	H	TYR	100F	3.08	Hydro-Bond
A	ASN	398	O-CZ2		H	TRP	96	3.06	Van-der-Waals
A	GLN	401	NE2-OH		H	TYR	34	3.34	Hydro-Bond
A	GLN	402	OE1-CB	I	H	SER	99	3.73	Van-der-Waals
A	TRP	403	CZ2-OH	I	H	TYR	100B	3.65	Van-der-Waals
A	TRP	403	CD1-OG	I	H	SER	99	3.59	Van-der-Waals
A	PHE	433	CD2-OH		H	TYR	100B	3.02	Van-der-Waals
A	PHE	433	CE2-CZ		H	TYR	100B	3.69	Hydr-Phbc
A	PHE	433	CD2-CZ		H	TYR	100B	3.78	Hydr-Phbc
A	ARG	435	NH2-O		H	SER	100	2.4	Hydro-Bond
A	ARG	435	NH1-O		H	SER	100	3.41	Hydro-Bond
A	ARG	435	NH1-CE1		H	TYR	100A	3.71	Van-der-Waals
A	ASN	446	OD1-OG		H	SER	100	2.09	Hydro-Bond
A	ASN	446	ND2-OG		H	SER	100	3.24	Hydro-Bond
A	ASP	448	OD2-CA		H	SER	100	3.11	Van-der-Waals
A	ASP	448	OD2-OG		H	SER	100	3.27	Hydro-Bond
A	ASP	450	OD2-OH		H	TYR	100B	2.61	Hydro-Bond
A	ASP	450	OD2-O		H	SER	99	3.61	Van-der-Waals
A	GLN	504	OE1-CB	I	H	TYR	100A	3.47	Van-der-Waals
A	GLN	504	NE2-N	I	H	TYR	100B	3.81	Van-der-Waals
A	GLN	504	NE2-CG	I	H	ARG	100C	3.5	Van-der-Waals
A	ARG	397	NH2-NZ	D	L	LYS	30	3.6	Van-der-Waals
A	GLN	504	OE1-OH	I	L	TYR	27D	2.44	Hydro-Bond
A	GLY	393	O-OG	D	L	SER	56	2.73	Hydro-Bond

SUPPLEMENTARY TABLE 9.

Sample	dlgA-GII.4 SY 2012 VLPs
Microscope	Talos Glacios
Voltage (keV)	200
Detector	Falcon 4
Recording Mode	Counting
Pixel size (Å)	2.01
Defocus range (µm)	-4 to -6
Acquisition scheme	-60/60°, 3°
Total Dose (electrons/Å ²)	~120

SUPPLEMENTARY TABLE 10.

VLP	GenBank Accession number
GI.1	AFJ38516.1
GI.3	AFK75851.1
GI.5	KJ402295.1
GII.4 CW 1987	AAK50355.1
GII.4 US 95/96	AFJ04707.1
GII.4 FH 2002	AFJ04708.1
GII.4 DH 2006	AFU92665.1
GII.4 NO 2009	ADQ43781.1
GII.4 SY 2012	AGJ52172.1
GII.4 SF 2017	WKD81245.1
GII.4 HK 2019	QEL43936.1
GII.2	QLI46383.1
GII.3	AFK75854.1
GII.3/GII.4 I	PP581626
GII.3/GII.4 Fp+I	PP581627
GII.3/GII.4 NERK	PP581628
GII.3/GII.4 Fp+NERK	PP581629
GII.3/GII.4 I+NERK	PP581630
GII.3/GII.4 Fp+I+NERK	PP581631
GII.3/GII.4 P2	PP581632
GII.3/GII.4 P5	PP581633
GII.3/GII.4 P6	PP581634
GII.3/GII.4 P7	PP581635
GII.6	CRL46967.1
GII.12	AJP13623.1
GII.14	AAN05735.1
GII.17	KP698930.1
GII.4 2006a.581	QCG74409.1
GII.4 2006a.Day1	ACT68309.1
GII.4 2006a.Day156	WYV93084.1
GII.4 2006a.Day262	WYV93085.1
GII.4 2006a.Day683	ACT68310.1
GII.4 2006a.581.F1	PP405051
GII.4 2006a.581.F2	PP405052
GII.4 2006a.581.F3	PP405053
GII.4 2006a.581.F4	PP405054
GII.4 2006a.581.F5	PP405055
GII.4 2006a.581.A4A	MK614085

SUPPLEMENTARY TABLE 11.

Compound	m/z	z	Compound	m/z	z
IgA mass exclusion list			IgG mass exclusion list		
YLTWASR	448.7349	2	AGVETTKPSK	339.86	3
TPLTATLSK	466.2766	2	GPRPFHCR	342.84	3
WLQGSQELPREK	490.9282	3	DTLMISR	418.22	2
QIQVSWLR	515.2956	2	VTVLGQPK	421.26	2
SYScQVTHEGSTVEK	571.2579	3	VATVSLPR	421.76	2
FTcTVHTDLPSPLK	572.959	3	DTLMISR	426.22	2
KGDTFScmVGHEALPLAFTQK	589.0383	4	WYVDGVEVHNAK	472.9	3
GVALHRPDVYLLPPAR	592.0089	3	FMETVAEK	485.73	2
VSVFVPPRDGFFGNPR	597.6494	3	AGVETTTPSK	495.76	2
WLQGSQELPR	607.3198	2	HITSLEVIK	520.31	2
QEPSQGTTFFAVTSILR	612.6548	3	KYWNDCEPPDSR	522.89	3
EPQVYTLPPSRDELTK	624.9949	3	HKVYACEVTHQGLSSPVTK	536.03	4
LlcQATGFSPR	625.3215	2	FNWYVDGVEVHNAK	559.94	3
EPQVYTLPPSREEMTK	635.6523	3	WQQGNVFCScVMHEALHNHYTQK	561.06	5
EPQVYTLPPSR	643.8406	2	THTCPPCPAPELLGGPSVFLFPPKPK	569.7	5
ANPTVTLFPPSSEELQANK	681.6846	3	SYScQVTHEGSTVEK	571.26	3
TFTcTAAYPESK	688.3136	2	NQVSLTCLVK	581.32	2
NVPLPVIAELPPK	693.9214	2	DHHHPHKPHEHGPPPPDER	588.28	4
YAATSQVLLPSKDVmQGTDEHVcK	698.8453	4	SCDTPPPCPR	593.75	2
HYTNPSQDVTVPcPVPPPPcCHPR	728.0875	4	GPSVFPLAPSSK	593.83	2
TPEVTcVVVDVSHEDPEVKFNWYVDGVEVHNAK	760.3681	5	SGTASVCLLNIFYPR	599.97	3
TFTcTAAYPESKTLPLTATLSK	763.3875	3	VVSVLTVLHQDWLNGK	603.34	3
DASGVTFTWTPSSGK	770.8675	2	TTPPVLDSDGSFFLYSK	625.31	3
QSNNKYAASSYLSLTPEQWK	772.3816	3	VYACEVTHQGLSSPVTK	625.98	3
KGDTFScmVGHEALPLAFTQK	779.7171	3	EPQVYTLPPSREEMTK	635.65	3
KGDTFScmVGHEALPLAFTQK	785.0487	3	EPQVYTLPPSREEMTK	640.98	3
NFPPSQDASGDLYTTSSQLTLPATQcLAGK	792.8843	4	EPQVYTLPPSR	643.84	2
NFPPSQDASGDLYTTSSQLTLPATQcPDGK	799.8739	4	GPSVFPLAPCSR	644.33	2
YVTSAPMPEPQAPGR	800.893	2	TVAAPSVFIFPPSDEQLK	649.35	3
YVTSAPMPEPQAPGR	808.8905	2	STSGGTAALGCLVK	661.34	2
QVGSGVTDDQVQAEAK	809.4076	2	AAPSVTLFPPSSEELQANK	662.68	3
GQPLSPEKYVTSAPmPEPQAPGR	818.4092	3	SCDKTHTCPPCPAPELLGGPSVFLFPPKPK	667.73	5
VFAIPPSFASIFLTK	819.4687	2	ANPTVTLFPPSSEELQANK	681.68	3
cYTAVVPLVYGGETK	828.9187	2	TFTCTAAYPESK	688.31	2
ESDWLSQSmFTcR	831.848	2	WQQGNVFCScVMHEALHNHYTQK	701.07	4
DLcGcYSVSSVLPgCgAEPWNHGK	865.0471	3	RTVAAPSVFIFPPSDEQLK	701.38	3
YAASSYLSLTPEQWK	872.433	2	WQQGNVFCScVMHEALHNHYTQK	705.07	4
SAVQGPPERDLcGcYSVSSVLPgCgAEPWNHGK	879.4039	4	WYVDGVEVHNAK	708.85	2
FSScGGGGGSGFAGGGFGSR	883.371	2	THTCPPCPAPELLGGPSVFLFPPKPK	711.87	4
QEPSQGTTFFAVTSILR	918.4785	2	STSESTAALGCLVK	712.36	2
EGVQKEDIADLSQDVPDTESETR	919.1017	3	VDNALQSGNSQESVTEQDSK	712.66	3
EVQLVESGGGLVQPGGSLR	941.5051	2	TPEVTCVVVDVSHEDPEVK	713.68	3
EIVLTQSPGTLSLSPGER	942.5073	2	HKVYACEVTHQGLSSPVTK	714.37	3
ANPTVTLFPPSSEELQANK	1022.0233	2	CPAPELLGGPSVFLFPPKPK	717.73	3
NFPPSQDASGDLYTTSSQLTLPATQcLAGK	1056.8433	3	CCVECPCCAPPVAGPSVFLFPPKPK	727.86	4
NFPPSQDASGDLYTTSSQLTLPATQcPDGK	1066.1628	3	DSTYLSSTLTLSK	751.88	2
KcDPTEVELDNQIVTATQSNicDEDSATETcYTYDRNK	1121.7416	4	KCCVECPCCAPPVAGPSVFLFPPKPK	759.88	4
NFPPSQDASGDLYTTSSQLTLPATQcLAGK	1584.7613	2	TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK	760.37	5

SUPPLEMENTARY TABLE 12.

GII.4 Amino number	Epitope site
254	F
255	F
256	F
257	F
294	A
295	A
296	A
297	A
298	A
327	F
339	C
340	C
341	C
343	ligand
344	ligand
345	ligand
347	ligand
352	G
355	G
356	G
357	G
359	G
364	G
368	A
372	A
373	A
374	ligand
375	C
376	C
377	C
378	C
391	D
392	D
393	D
394	D
395	D
396	D
397	D
402	I
403	I
404	F
407	E
411	E
412	E
413	E
414	E
442	ligand
443	ligand
444	ligand
479	J
480	J
481	J
482	J
483	J
484	J
504	I
505	I
506	I
509	J
510	J
511	J
512	J
513	J