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Polyclonal and convergent antibody response to Ebola virus vaccine rVSV-ZEBOV

Stefanie A. Ehrhardt^{1,16}, Matthias Zehner^{1,16}, Verena Krähling^{2,3}, Hadas Cohen-Dvashi⁴,
Christoph Kreer¹, Nadav Elad⁵, Henning Gruell^{1,6}, Meryem S. Ercanoglu¹, Philipp Schommers^{1,6,7},
Lutz Gieselmann¹, Ralf Eggeling⁸, Christine Dahlke^{9,10,11}, Timo Wolf¹², Nico Pfeifer^{8,13,14},
Marylyn M. Addo^{9,10,11}, Ron Diskin⁴, Stephan Becker^{2,3} and Florian Klein^{1,6,15} 

¹Laboratory of Experimental Immunology, Institute of Virology, Faculty of Medicine and University Hospital of Cologne, University of Cologne, Cologne, Germany. ²Institute of Virology, Faculty of Medicine, Philipps University Marburg, Marburg, Germany. ³German Center for Infection Research, Partner Site Gießen-Marburg-Langen, Marburg, Germany. ⁴Department of Structural Biology, Weizmann Institute of Science, Rehovot, Israel. ⁵Department of Chemical Research Support, Weizmann Institute of Science, Rehovot, Israel. ⁶German Center for Infection Research, Partner Site Bonn-Cologne, Cologne, Germany. ⁷Department I of Internal Medicine, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany. ⁸Methods in Medical Informatics, Department of Computer Science, University of Tübingen, Tübingen, Germany. ⁹Division of Infectious Diseases, First Department of Medicine, University Medical Center Hamburg-Eppendorf, Hamburg, Germany. ¹⁰Department of Clinical Immunology of Infectious Diseases, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany. ¹¹German Center for Infection Research, Partner Site Hamburg-Lübeck-Borstel-Riems, Hamburg, Germany. ¹²Department of Infectious Diseases, University Hospital Frankfurt, Frankfurt/Main, Germany. ¹³Faculty of Medicine, University of Tübingen, Tübingen, Germany. ¹⁴German Center for Infection Research, Partner Site Tübingen, Tübingen, Germany. ¹⁵Center for Molecular Medicine Cologne (CMMC), University Hospital of Cologne and University of Cologne, Cologne, Germany. ¹⁶These authors contributed equally: Stefanie A. Ehrhardt, Matthias Zehner. *e-mail: florian.klein@uk-koeln.de

Supplementary Table 1 rVSV-ZEBOV-vaccinated subjects (related to Fig. 1).

	EV01	EV02	EV03	EV04	EV05	EV06	Mean
Gender	female	female	male	male	male	male	67% male, 33% female
Age (years)	55	26	42	51	44	45	44
Sampling post immunization (months)	18.5	18.5	24	20.5	25	26	22
Vaccine dose (pfu)	3 x 10 ⁵	3 x 10 ⁵	3 x 10 ⁶	3 x 10 ⁵	3 x 10 ⁶	3 x 10 ⁵	n.a.

EV = rVSV-ZEBOV-vaccinated subject

n.a. = not applicable

pfu = plaque forming units

Supplementary Table 2 Information on clonal and/or produced antibody sequences (related to Fig. 2).

a EV01

Antibody	Clone #	# of clonal members	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/IGLV	IGKJ/IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
1T0114	1-26	2	yes	3-23*01	3-9*01	4*02	95.9	AKDNSYNEILTGSHGPPDY	19	κ	3-11*01	4*01	97.2	QQRSQWPPLT	10
1T0116	1-31	2	yes	3-33*01	3-22*01	4*02	96.9	ARSHNSGYRYFFDY	15	κ	3-15*01	3*01	99.3	QQYNNWPPIT	10
1T0121	1-51	2	no	4-59*08	3-3*01	6*02	92.8	ARAPRHYDFWGSYYYNGMDV	21	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0125	1-52	2	no	5-51*03	2-15*01	5*01	97.3	AKREGHCSDGLCYSVWFDS	19	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0126	1-34	2	no	3-7*01	3-10*01	4*02	97	TREVRGSAY	9	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0129	1-4	6	yes	1-2*02	1-1*01	4*02	84.9	GTGIPSDIDY	10	κ	4-1*01	2*01	84.5	QQYNTPTPT	9
1T0130	1-9	2	yes	1-46*01	3-22*01	3*02	99	ARHDSGGYDAFDI	13	λ	3-25*02	2*01	94.8	QSSDSSSTYVV	11
1T0139	1-46	3	yes	4-4*07	5-12*01	4*02	95.9	ARESYRYNAYDIHPFDY	17	λ	3-1*01	2*01	93.6	QAWASNTVV	9
1T0144	1-43	2	no	4-39*01	3-10*01	6*02	97.3	ARPIYMVRGVTSMVDV	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0148	1-44	5	no	4-4*07	6-25*01	3*02	94.9	ARGVYRWAAFSAAADNFDS	19	λ	3-1*01	2*01	95	QAWDSGTYVV	10
1T0161	1-13	2	no	1-69*04	2-2*01	6*02	97	ARDRYSAEIVVVGADYGYMDV	21	λ	2-23*02	1*01	98	YSYAGSSTYV	10
1T0162	1-8	2	no	1-3*01	6-6*01	6*02	97.2	ASAARRGYTYLDDV	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0177	1-20	2	no	3-21*01	2-15*01	5*02	93.2	ARVVCGECSGGGYCYSAWLDV	20	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0201	1-18	2	yes	3-15*01	3-3*01	6*02	95.3	TTRVDMEWKGYGTDV	15	λ	1-40*01	3*02	96.6	QSYDSRLSDSVV	12
1T0211	1-50	2	no	5-51*01	3-3*01	4*02	94.2	AKLQGFWNAYLYFDF	15	λ	1-51*01	3*02	94.3	GTWDTSLSTGLYVV	14
1T0221	1-1	7	yes	1-18*01	3-22*01	5*02	95.6	ARHVTMILDGWFDP	14	κ	3-20*01	4*01	98.6	QQYGSSPLT	9
1T0222	1-38	2	yes	3-7*01	6-13*01	4*02	98.6	AVGAAAGRY	9	κ	1-17*01	1*01	100	LQHNSYPQT	9
1T0225	1-40	2	yes	4-30-2*01	3-16*01	4*02	95	ARDPGGPTFDH	10	λ	2-14*01	2*01	95.1	SSYTSNFSVV	10
1T0227	1-15	3	yes	3-15*01	6-19*01	4*02	96.7	THVDPDYNAYYVWV	15	λ	1-40*01	1*01	96.6	QSYDIRLSDNVV	12
1T0242	1-39	5	yes	3-74*01	3-16*01	4*02	94.3	ARLDSWLVPDS	11	λ	2-8*01	1*01	93.6	CSYTRGRSPFV	10
1T0248	1-25	2	yes	3-23*01	1-26*01	4*02	93.6	AKDKGPRAFLGALLDS	16	κ	4-1*01	3*01	95	QQYFGSPFLT	9
1T0264	1-22	3	yes	3-23*01	1-26*01	4*02	93.9	AKDNVRPSSGSYVVLDY	17	λ	1-47*01	2*01	94.8	AAWDDSLSNQGV	12
1T0265	1-48	5	no	4-59*08	5-12*01	5*02	80.5	ARHPSGEGYDWNWFEP	19	λ	1-47*01	1*01	87.7	ASWDASVSAYV	11
1T0267	1-45	2	no	4-4*07	4-17*01	4*02	92.2	ASTRYPYDGYGYFAN	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0301	1-41	2	yes	4-34*12	3-10*01	6*02	95.2	ARSGVLGVYGMVDV	13	λ	1-47*01	1*01	97.3	AAWDDSLSDYV	11
1T0321	1-Single01	1	yes	1-2*02	4-17*01	6*02	94.5	ATPMTTSTRYYYHMDV	16	κ	2-28*01	1*01	98.7	MHALQTPWT	9
1T0322	1-19	2	no	3-15*01	1-26*01	2*01	90.6	TTTGGDF	7	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0325	1-23	2	yes	3-23*01	2-2*01	4*02	92.9	AKEREVAFVPGAVFNY	16	κ	4-1*01	4*01	98	QQYSLPLT	9
1T0344	1-30	2	no	3-30-3*01	2-2*01	6*02	91.2	TRGGDIVVPAADSLDYGMVDV	20	κ	1-17*01	2*01	96.9	LQCNSTPWT	9
1T0351	1-37	2	yes	3-7*01	4-11*01	4*02	96.6	ARTVRFVDY	9	κ	2-30*01	1*01	98	MQGTHWPPPT	9
1T0361	1-21	2	no	3-21*01	6-19*01	4*02	96.2	ARPGISVAGDATNFDS	16	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0371	1-12	3	yes	1-69*09	5-24*01	5*02	94.9	ATLEMATLFA	10	κ	1-16*02	4*01	98.6	QQYNSYPPT	9
1T0402	1-27	2	no	3-30*03	n.m.	6*02	98	AIGGSRSPVAMDV	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0404	1-49	2	no	4-59*01	3-22*01	4*02	95.5	ARAPRWYDRSGYSLPFDV	19	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0451	1-7	3	yes	1-3*01	3-16*01	6*02	89.1	ARGRGTSYFYAFDV	14	κ	1-39*01	2*01	93	QQTYRSPPLYT	10
1T0455	1-16	3	yes	3-15*01	3-22*01	4*02	94	TTLYH	5	λ	1-40*01	2*01	97.3	QSYDSRLSDHVV	12
1T0456	1-17	2	yes	3-15*01	3-10*01	4*02	96	IATPFLILPESG	13	λ	1-51*01	3*02	97	GTWDSLSLSTGLYVV	14
1T0473	1-14	5	yes	1-8*01	3-10*01	6*02	94.9	ARGNQWFGELSSSYGLDV	19	κ	3-20*01	3*01	95.4	QQYGSSSLIT	9
1T0474	1-29	2	no	3-30*04	2-2*01	6*02	96.3	ARDFAYGSSSYALRVGVDGMVDV	22	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0476	1-33	2	no	3-53*02	3-9*01	2*01	94.5	ARWSKDEFHDLTGPIYFDL	20	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
1T0480	1-42	7	yes	4-39*01	4-11*01	4*02	87.9	ARSWRYRRYSRNFYD	15	λ	1-40*01	2*01	89.5	QSYDTNLGDDVI	11
1T0546	1-32	2	yes	3-33*01	6-19*01	4*02	93.2	ARAGAAGAI DV	11	κ	4-1*01	4*01	96.1	QQYDSIPLT	9
1T0552	1-24	2	yes	3-23*01	3-16*01	3*02	89.5	AKFSQLFGYAFDI	13	κ	3-20*01	1*01	93.4	QQYGNSPWT	9
1T0554	1-5	2	yes	1-3*01	2-15*01	6*02	98	ASSGGRYYYVMDV	13	κ	3-20*01	4*01	100	QQYGSSPLT	9
1T0565	1-28	5	yes	3-30*03	1-14*01	6*02	90.2	AIGGSTTVPGLDV	13	κ	1D-12*01	4*01	90.9	QQAQSPFLT	9
1T0582	1-6	5	yes*	1-3*01	6-6*01	6*02	98.6	ASTSRRGYTYVMDV	14	κ	3-20*01	4*01	99.3	QQYGSSPLT	9
1T0614	1-36	3	yes	3-7*01	6-13*01	4*02	94.2	ARSLPAAAGTY	11	κ	2-30*02	1*01	97.7	MQGSHWPPPT	9
1T0623	1-11	2	yes	1-69*09	2-21*02	3*01	87.2	ATENCQGDQRPDPVDFV	19	κ	4-1*01	2*01	93.1	QQYTSPTPT	9
1T0653	1-Single02	1	yes	3-7*01	3-16*01	4*02	96.2	AKSPLISNAY	10	κ	2-30*01	1*01	97	MQGTHWPPPT	9
1T0655	1-10	2	yes	1-46*01	6-19*01	6*02	93.9	ARDRQWLPLNGYSYFNYGMDV	21	κ	1-39*01	1*01	91.6	QQSFSPTPT	9
1T0665	1-35	3	yes	3-7*01	6-13*01	6*02	98.6	ARGRQLVLV	9	λ	2-14*01	2*01	98	SSYTSRSTLV	10

b EV03

Antibody	Clone #	# of clonal members	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/IGLV	IGKJ/IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
3T0103	3-5	2	no	1-2*02	3-16*02	4*02	93.6	VRGGSLSGDRSELFFKY	16	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
3T0123	3-2	2	yes	1-18*01	6-13*01	4*02	87.1	ARGLGDSYSNANWFYVFDY	19	κ	3-15*01	2*01	88.7	QQYQSRPT	8
3T0134	3-27	3	no	3-23*01	6-6*01	4*02	91.1	ARGAAARPSPPDF	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
3T0135	3-42	2	yes	3-74*01	1-26*01	4*02	94.2	ARGNGNYLDY	10	λ	2-18*02	1*01	96.9	SSYTSSATYV	10
3T0147	3-46	2	yes	4-4*02	7-27*01	4*02	93.4	ARSLPLKRGDFD	12	λ	1-40*01	3*02	93.9	QSYDSRLRDNV	12
3T0150	3-25	7	no	3-23*01	2-2*01	4*02	90	AILGNCRSTSYARYG	16	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
3T0159	3-44	2	yes	4-34*01	3-16*01	3*02	84.9	AKSAGWAIYAFDM	13	κ	3-20*01	2*01	87.2	QLYGRSPIMYA	11
3T0166	3-31	2	no	3-23*01	6-13*01	4*01	87.5	AKGPAARPSPPDV	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
3T0182	3-37	2	no	3-49*04	3-16*01	2*01	96	SRKGEYDHWYFDL	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
3T0183	3-6	37	yes*	1-69*06	3-16*01	6*02	90.1	ARQVRLRGYMDV	13	κ	3-15*01	2*01	92.7	QQYSDWPPYT	10
3T0202	3-12	17	yes*	3-13*01	3-10*01	4*02	94.2	ARAAFGAVFFDY	12	κ	3-20*01	5*01	96.5	QQYGNSPIT	9
3T0204	3-33	2	no	3-23*01	6-19*01	4*02	90.9	AKDVFQWLALFDY	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
3T0209	3-7	12	yes*	1-8*01	3-16*02	6*02	88.2	ARGAIIGGVIALFGMDV	17	κ	1-27*01	1*01	93	QKYSSGPRT	9
3T0213	3-4	6	yes	1-2*02	2-8*02	4*02	92.9	ARGRTTAGATGPLYDN	16	λ	2-23*02	3*02	93.9	CSLAGRGNV	10
3T0215	3-35	2	yes	3-48*04	6-13*01	4*01	89.9	ARDTLEAGSWYFPFK	15	λ	3-10*01	3*02	96.6	YSTDSSTQTV	11
3T0216	3-48	2	yes	4-4*02	3-10*01	6*01	88.2	VKIPFGISGMDV	12	κ	3-20*01	2*01	91.4	QLYTRPPRYT	11
3T0245	3-22	3	yes	3-15*01	6-6*01	6*02	89	ATRVHYNGMDV	11	λ	1-40*01	3*02	95.6	QSYDSSLRDACV	12

b EV03 (continued)

Antibody	Clone #	# of clonal members	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/ IGLV	IGKJ/ IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
3T0253	3-24	3	yes	3-15*01	1-14*01	6*02	93	TTRHHRGMDV	10	λ	1-40*01	2*01	97.3	QSYDSSLSDAVV	12
3T0258	3-1	3	yes	1-18*01	6-13*01	3*01	87.6	AWRRSSWFAFDV	12	κ	3-20*01	2*01	94.1	QQYVSSPYT	9
3T0265	3-19	2	yes	3-15*01	n.m.	4*02	89.7	LTPPPRRY	8	λ	1-40*01	3*02	93.9	QSYDARLRDGEV	12
3T0303	3-10	4	yes	3-11*01	5-24*01	5*01	89.4	ASGTLKSGDCYPLFES	16	κ	1-5*03	1*01	90.7	HQYKTPWPA	9
3T0325	3-41	2	yes	3-74*01	3-3*01	6*02	93.9	ARAAYDFRSASYFGLDV	18	λ	2-18*02	1*01	97.3	SSFTTSSTYF	10
3T0331	3-26	4	yes	3-23*01	6-25*01	4*02	90.1	AKSVRLSRPSPFDL	14	κ	3-11*01	4*01	94.4	QORASWPLT	9
3T0338	3-Single02	1	yes	3-15*02	2-21*01	6*02	90.6	TTNLGGGFGPGEWSV	16	λ	1-40*01	3*02	95	QSYDSRLRDSWV	12
3T0350	3-28	3	yes	3-23*01	1-1*01	4*02	90.2	AKDLKGNWNGPFDY	15	λ	1-51*01	3*02	95.2	GTWGNLSLGPPEWV	13
3T0353	3-45	3	yes	4-34*01	3-16*01	3*02	85.1	ARTAGWGIYGFDI	13	κ	3-20*01	2*01	90.3	QLYGRSPIVYT	11
3T0368	3-49	4	yes	1-2*02	6-13*01	4*02	92.8	AAGLGH	6	λ	3-25*02	3*02	95.8	QSVDSGSAWV	10
3T0405	3-34	2	yes	3-30*03	4-17*01	4*02	95.5	AANYRDSLE	10	κ	2-30*02	1*01	96.3	MQATLWPWT	9
3T0409	3-43	4	yes	4-34*01	7-27*01	3*01	90	ARTGGWGIYAFDV	13	κ	3-20*01	2*01	93.1	QQYGRSPLIMYT	12
3T0411	3-23	2	yes	3-15*01	1-7*01	4*02	94.4	TTGHTIGTLF	10	κ	4-1*01	4*01	97.7	QQYSSMIT	9
3T0415	3-30	4	yes	3-23*01	2-8*01	6*02	92.5	AINGGV	6	κ	4-1*01	4*01	93.7	QQHYATRVY	9
3T0420	3-29	2	yes	3-23*01	3-9*01	4*02	89.5	ARDPRVATGTGVYFDS	16	λ	3-25*02	2*01	92.6	QSADTSGTLVV	11
3T0427	3-38	2	yes	3-64D*06	3-3*01	4*02	86.5	TKDHHWSGQYTDY	13	κ	3-11*01	1*01	95.1	QQRSSWRT	8
3T0442	3-32	2	yes	3-23*01	4-17*01	4*02	90.4	AMGYGIYNS	9	κ	3-15*01	1*01	94.4	QQYINWPPWT	10
3T0458	3-8	2	yes	1-8*01	3-9*01	3*01	85.8	ARGFEWRSNGNRDAFDV	17	κ	1-5*03	1*01	89.9	QHYSGYSPWT	10
3T0465	3-50	2	no	3-33*01	2-15*01	4*02	93.9	ARESCYGGSCFFDH	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
3T0478	3-47	2	yes	4-59*01	3-22*01	4*02	94.2	ARDKRYDSSGYSHFY	17	λ	1-47*01	3*02	97.6	AAWDGSLSGPV	11
3T0506	3-39	7	yes	3-72*01	3-22*01	3*02	92.7	VRVADYDFSGGYSLDAFDI	19	λ	1-51*01	3*02	94.6	ETWDTGLRGVV	11
3T0527	3-40	2	yes	3-74*03	1-26*01	1*01	90.7	AVVFLGAVR	9	κ	4-1*01	1*01	94.7	HQYDTPWT	9
3T0553	3-Single01	1	yes	3-33*01	2-8*02	6*02	94.9	ARGDDLLEVDSDYDYGLDV	20	κ	1-17*03	1*01	97.9	LQHNRYPPWT	9
3T0611	3-36	2	yes	3-48*01	4-17*01	4*02	93.1	AGILDDYRDYGYDY	14	λ	3-25*02	3*02	94.8	QSSDNNNGSYRVM	12
3T0650	3-20	2	yes	3-15*01	3-3*02	5*02	92.9	VATPHWSVA	10	λ	1-40*01	3*02	96.6	QSYDSRLRDQWV	12
3T0662	3-3	2	yes	1-2*02	5-12*01	5*02	93.5	ASPGYCSTSNCPSP	14	λ	3-25*03	2*01	92.2	QSADSGAGSLI	11
3T0673	3-21	4	yes	3-15*01	3-22*01	5*02	87.3	TTYYYDNGGYSNP	14	λ	1-40*01	2*01	94.3	QSYDSRLRDFGI	12

c EV04

Antibody	Clone #	# of clonal members	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/ IGLV	IGKJ/ IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
4T0115	4-46	2	yes	3-9*01	5-24*01	6*02	94.6	AREGRDGYNLPYYAMDV	17	κ	1-9*01	3*01	96.5	QRFNSYPIPT	10
4T0136	4-22	5	no	3-23*01	2-2*01	6*02	94.2	AKGMDCCSTTAPCFYGMVDV	20	λ	5-45*02	3*02	96.5	MIWHNLAWV	9
4T0140	4-35	2	no	3-48*01	1-26*01	4*02	92.1	AKLGSFGSFPFDS	12	λ	2-23*01	3*02	97.6	CSYAGTSAMW	10
4T0145	4-12	5	no	3-11*01	2-2*01	6*02	94.9	ARGERRHQPLFGLDV	15	κ	3-15*01	4*01	95.7	QQCNDWPLT	9
4T0149	4-13	2	no	3-11*01	2-8*01	4*02	97.3	ARDGMVYSMILLEHYFDS	18	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0154	4-10	2	yes	1-69*02	5-24*01	4*02	89.7	AVEMATPSDT	10	κ	1-16*02	2*01	95.8	LQYSTYPYPT	9
4T0159	4-49	3	yes*	4-39*01	n.m.	4*01	93.3	ARRFDS	6	κ	3-15*01	1*01	96.8	QQYNDWPPWT	9
4T0162	4-37	2	no	3-48*01	5-18*01	4*02	92.5	ARVPLRQYSLDF	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0165	4-5	2	no	1-2*02	4-11*01	5*02	93.6	ATVPTVTMTMGWFDP	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0168	4-Single01	1	yes	3-30*18	6-13*01	4*02	94.2	AKGGATAA VFDS	12	κ	4-1*01	1*01	94.4	QQYNNPPWT	9
4T0171	4-39	3	yes	3-72*01	3-22*01	3*02	91	VRVADVFDSGYSYDAFEM	19	λ	1-51*01	2*01	93.9	GTWDTSLRGLVI	11
4T0182	4-6	2	yes	1-2*02	3-10*01	6*02	95.9	AAPGETIVRGVIYHYGGMV	20	κ	2-28*01	2*01	97.7	MQALQTPT	8
4T0201	4-23	2	no	3-23*01	3-3*01	6*02	92.6	AKDLGYNFWSGPDGMVDV	17	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0202	4-45	2	no	3-74*01	3-3*01	5*02	94.9	VRDILGIYAWFDP	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0219	4-29	3	no	3-33*01	2-15*01	4*02	96.3	AREFCFGGSCYFDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0238	4-Single02	1	yes	1-3*01	3-3*02	5*02	92.9	ARDISLFPKPGFDP	14	κ	4-1*01	4*01	94.7	QQYSSPPLT	9
4T0243	4-57	3	yes	4-59*01	5-18*01	6*02	92.8	ARAPRGYSGKYNYYGLDV	19	λ	3-25*02	1*01	93.1	QSADSSGGYVV	11
4T0251	4-36	4	no	3-48*01	6-19*01	4*02	96.2	ARGQWLVEDY	10	κ	3-15*01	1*01	95.9	QQYDNWPPQT	9
4T0258	4-1	2	no	1-18*04	3-22*01	3*02	94.5	ARISIMILVGFDPDI	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0262	4-8	2	yes	1-46*01	3-10*01	5*02	91.5	ARGITMIRDGWFDH	14	κ	1-5*01	2*03	95.1	LQYSSSSPYS	10
4T0269	4-Single03	1	yes	3-30*02	3-22*01	3*01	88.8	AKLPTHYRDDNEVEFDV	17	κ	1-5*01	2*01	92.2	QQYRNIFYRT	9
4T0284	4-2	4	yes	1-18*04	3-10*01	5*02	96.3	ARGITMYRGLDWFPD	15	κ	3-15*01	4*01	97.2	QQYKNWPLT	9
4T0306	4-55	4	yes	6-1*01	3-3*01	6*02	90.5	VREYYDLWNGFYPPGAMDV	19	κ	1-33*01	2*01	93	QQYDDLPRY	9
4T0312	4-19	2	no	3-15*01	3-22*01	5*02	99.7	TTDWLRISMT	10	λ	1-40*01	3*02	97.6	QSYDSRLSLDLVW	12
4T0337	4-42	2	yes	3-74*01	5-18*01	4*02	91.5	ARGGSDRAMAHDH	13	κ	3-20*01	2*01	95.5	QQYGSAPPY	9
4T0341	4-11	2	yes	1-69*01	3-22*01	6*02	94.9	ARDYRPYYDGGSGYSSYYALDV	23	κ	1-5*03	2*01	98.2	QQYNTYST	8
4T0344	4-24	2	yes	3-23*01	4-11*01	4*02	93.6	VKGSPWPTFTVLSYFYFDV	18	κ	1-27*01	1*01	96.1	QKYNGLAPWR	9
4T0350	4-41	2	yes	3-72*01	n.m.	6*02	92	VRTMDV	6	κ	1-5*01	4*01	96.1	QHYNYSPLT	9
4T0351	4-28	2	no	3-30*02	3-22*01	2*01	82.8	AKESRQFDTSGRHTYFDL	18	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0365	4-50	2	yes	4-39*01	3-10*01	4*02	91.9	ATSSRGSVSYYSRY	14	λ	1-51*01	3*02	92.9	SVWDSLSGSRV	11
4T0369	4-34	4	no	3-48*02	3-10*01	6*02	92.5	ARAPRDLSYAMDF	13	λ	1-40*01	3*02	95.6	QTYDSSLGSGV	11
4T0412	4-Single04	1	yes	3-33*01	1-14*01	2*01	92.2	VRETFQPGGEVPLWYFDV	19	κ	1-39*01	1*01	95.1	QQSYGTPRT	9
4T0417	4-31	3	yes	3-33*01	6-13*01	4*02	93.6	ARDAHNSRLDY	11	κ	3-20*01	3*01	92.1	QQYGYSPPRIT	11
4T0418	4-56	2	no	3-23*01	2-15*01	4*02	99.7	AKRVLDY	8	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0421	4-21	2	yes	3-15*01	2-21*01	6*02	91.7	TTGDFVWRQYHQYYGMDV	18	λ	2-14*01	1*01	94.6	NSYTSGSIPFV	11
4T0423	4-47	3	yes	3-9*01	1-26*01	6*02	93.6	AKENRIELLPWGMDV	16	λ	2-23*02	3*02	95.6	CSYAGTSAPVWV	12
4T0427	4-38	3	yes	3-53*01	6-19*01	6*02	93.9	ARDEEWLFSGYGMVDV	15	λ	1-47*01	1*01	98.3	AAWDDSLSAYI	11
4T0429	4-48	3	yes	4-34*01	n.m.	6*02	89	ARHGHTGMDV	10	κ	2-28*01	4*01	96.3	MQALQTPLT	9
4T0430	4-25	3	no	3-23*01	3-3*01	2*01	93.2	AKDSTFWNGNYFDL	14	λ	1-51*01	3*02	98.3	GTWDSLSVGV	11
4T0433	4-52	2	no	4-4*02	3-16*01	4*02	94.9	ARLSHYGGD	9	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0434	4-44	2	yes	3-74*01	6-19*01	4*02	95.3	ARVDGLYNTGWIDY	14	κ	4-1*01	4*01	97.7	QQFYSPLT	9
4T0437	4-Single05	1	yes	3-23*01	2-2*01	6*02	93.8	ASGVDCSSSGRPFFYGMVDV	20	λ	5-45*02	3*02	95.2	MTWHNLVWV	9
4T0444	4-15	7	yes*	3-13*01	3-10*01	4*02	92.5	ARARFGDLALDY	12	κ	3-20*01	4*01	95.5	HQYSSSPLT	9
4T0452	4-20	3	yes	3-15*06	3-16*01	4*02	88.7	ATEPRGYDWG	10	λ	1-40*01	3*02	95.2	QSYDSRLRDNNV	12
4T0460	4-30	2	no	3-33*01	6-13*01	4*02	94.2	ARQSIASNTYFFDD	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0478	4-54	3	no	4-61*02	7-27*01	6*02	91.3	ARESRGTGQGGYNGMDV	17	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.

c EV04 (continued)

Antibody	Clone #	# of clonal members	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/ IGLV	IGKJ/ IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
4T0479	4-27	2	no	3-23*01	3-10*01	4*02	94.9	AKDVWPGPRGNLDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0484	4-43	2	no	3-74*01	6-13*01	4*02	91.5	ARGPSSNNWYGLDY	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0520	4-32	4	yes	3-33*01	5-12*01	4*02	95.2	ARQATISDFYYLDS	14	κ	1-39*01	4*01	94.4	QQYTSRPL	8
4T0525	4-Single06	1	yes	1-69*08	3-16*01	4*02	93.8	AGGGTGLFDS	10	κ	1-16*02	4*01	96.1	QQYNTLPFT	9
4T0541	4-Single10	1	yes	3-23*01	3-16*02	4*02	91.5	AKVSDYLWGSRYFDY	16	κ	1-5*01	1*01	96.2	QQYNSYSPT	9
4T0551	4-3	2	no	1-18*04	3-9*01	4*02	84	ARGIGQGTGYHY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0563	4-51	2	yes	4-39*01	6-19*01	4*02	97.7	ARRRSSSSGRFFPDY	14	κ	3-20*01	5*01	98.6	QQYGSPLT	9
4T0570	4-7	2	yes	1-46*01	2-21*02	3*02	91.5	ARALPFRVTGARDVFDI	17	κ	1-16*02	4*01	95.8	QQYYTYPLT	9
4T0577	4-9	2	no	1-69*01	2-21*01	4*02	94.9	ARSEGGDSYFDY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0635	4-16	2	no	3-13*01	3-10*02	3*02	94.5	VRAIFGSHAFDI	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0657	4-58	3	yes	3-23*01	3-3*01	4*02	92.2	AKNDDFWGGPTFDY	14	λ	1-51*01	3*02	97.3	GTWDITLSEGV	11
4T0675	4-53	2	no	4-61*02	5-18*01	6*02	93	ARDGGYTHAYAMDV	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4T0764	4-Single07	1	yes	4-59*01	3-10*01	4*02	92.8	ARGLLGSQDS	10	λ	2-14*01	2*01	96.3	SSYTRTNTHVI	11
4T0770	4-Single08	1	yes	3-74*01	3-22*01	4*02	91.2	ARGNGYNDY	10	λ	2-18*02	1*01	96.6	SSFSSNTYV	10
4T0784	4-Single09	1	yes	3-33*01	2-2*01	6*02	96.9	VRGGDLLLPDSIDYGMVDV	20	κ	1-17*01	3*01	94.7	LQHTNYFFS	9

d EV05

Antibody	Clone #	# of clonal members	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/ IGLV	IGKJ/ IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
5T0101	5-36	19	yes	3-33*01	3-16*01	4*02	92.9	ARDTLGVFDY	10	κ	2-24*01	2*01	95.7	VQSTQFPFS	9
5T0104	5-1	10	yes	1-18*01	3-22*01	6*02	91.5	ARISPSSYDRSGDFYNYQSMVDV	23	κ	4-1*01	2*01	97.7	QQYNSPYT	9
5T0106	5-20	2	no	3-15*01	3-22*01	4*02	94.9	FYMMVGA	7	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0107	5-35	2	yes	3-30*18	6-13*01	4*02	88.9	AKDRYCDAGTCSGSLDY	17	κ	2-28*01	1*01	93.4	MQSLAARPT	9
5T0119	5-38	3	no	3-33*01	1-14*01	4*02	91.9	ARDQFHHE	8	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0122	5-31	2	no	3-23*04	3-3*01	3*01	95.6	AKGVDFWSPYSFALDL	16	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0124	5-49	2	yes	4-4*07	2-8*01	6*02	90.8	ARESCNTNIECYSIHYGMVDV	20	λ	1-47*01	3*02	93.8	ASWDDRLSARL	11
5T0139	5-28	2	yes	3-23*01	3-3*01	4*02	92.9	VKKWKGFGHN	9	κ	3-20*01	2*01	96.9	QQYGGPPRT	9
5T0140	5-32	2	no	3-23*04	2-15*01	4*02	85.8	AKVLHPVGGKAAPSFDN	17	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0147	5-39	5	yes	3-49*04	5-12*01	4*02	85.4	TRGSGRYEY	9	κ	2-24*01	5*01	87	FQATEFPRT	9
5T0149	5-29	6	no	3-23*04	1-1*01	4*02	92.2	ARGSATTSYFFDF	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0160	5-2	2	no	1-18*01	3-9*01	5*02	98.6	ARDITIFSGWGPDP	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0165	5-10	2	no	3-15*01	4-11*01	4*02	94.7	ADTPTVAIVRVLTS	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0180	5-17	2	yes	3-15*01	3-22*01	4*02	94.7	VRGPFYCDTCGPNDY	15	λ	1-40*01	2*01	96.6	QTYDSRLRDQWV	12
5T0181	5-47	4	yes	3-74*01	3-10*02	4*02	93.5	TRTRYVASSADY	12	κ	2-28*01	3*01	97.7	MQALQVPL	9
5T0202	5-18	3	yes	3-15*01	3-16*02	4*02	89.7	TTSLNIGWTFYRDC	13	λ	1-40*01	3*02	94.9	QSYDSRLRDSWV	12
5T0209	5-13	3	yes	3-15*01	3-22*01	4*02	94.4	ATDYIESRGY	10	λ	1-40*01	3*02	97.3	QSYDSRLSDHWV	12
5T0223	5-16	6	yes	3-15*01	2-8*02	5*02	90.4	TKGGGGAHS	9	λ	1-40*01	3*02	93.9	QTYDSRLSDHWV	12
5T0246	5-0	1	yes	3-15*01	3-10*01	4*02	95	TTVMDFDSSG	10	λ	8-61*01	3*02	96.3	LLYMGSGISV	10
5T0256	5-24	2	no	3-15*01	3-22*01	4*02	96.7	TTDYIASRGY	10	λ	1-40*01	3*02	97.7	QSYDSRLSDSWV	12
5T0257	5-0	1	yes	3-23*01	3-3*01	4*02	98.6	AKDDDFWGGPYFDY	14	λ	1-51*02	3*02	98.6	GSWDSLSSTGV	11
5T0259	5-15	4	yes	3-15*01	3-16*01	6*02	90.5	TVVLMSPFGYGYGMGV	16	κ	2-28*01	5*01	98	MQALETSMT	9
5T0278	5-23	2	yes	3-15*01	3-9*01	5*02	91.2	YTLRFFGPGNS	11	λ	1-40*01	2*01	94.5	QSYDARLDRQV	12
5T0305	5-34	3	no	3-30*18	3-3*01	6*01	94.6	AQDGGGPTFFYFGMAV	16	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0322	5-41	10	yes	3-7*03	2-15*01	6*03	88.4	ARRSCSAAPCFEASNHCMDA	20	λ	2-11*01	2*01	92	SSITDFNKL	10
5T0337	5-25	2	yes	3-15*01	3-16*01	2*01	92.7	MTGFEHTYSYFDL	13	λ	1-40*01	3*02	95.9	QSYDSRLRDAWV	12
5T0347	5-19	4	no	3-15*01	n.m.	6*02	93.3	TTRYSGMDV	10	λ	1-40*01	2*01	97.6	QSYDSSLRDHWV	12
5T0376	5-0	1	yes	4-59*01	2-21*02	4*02	93.8	ARGLLGPGDS	10	λ	2-14*01	2*01	96.2	SSYKTGSTPVV	11
5T0377	5-60	2	yes	4-59*01	3-9*01	4*02	96.2	ARMSRYFDWLSQQWSFPLVD	21	λ	2-14*01	1*01	94.9	SSYTRTTFV	9
5T0378	5-48	2	yes	4-39*01	n.m.	4*02	98.7	ARRFDY	6	κ	3-15*01	1*01	100	QQYNNWPWT	9
5T0404	5-7	3	yes	1-69*09	2-2*01	6*03	90.1	ARLYCSSSSCSIYNYMDV	18	κ	1-33*01	2*03	95.8	QQYDSLPSY	9
5T0406	5-8	3	yes	1-69*01	3-3*01	6*02	91	ARFRFPQGGGSFYFYGLDL	19	λ	1-44*01	1*01	98	AAWDDRLNGPGV	13
5T0409	5-14	2	no	3-15*01	3-22*01	4*02	95.7	TRGPDYDSDGPHDY	14	λ	1-40*01	3*02	95.6	QSYDSRLRDQWV	12
5T0425	5-9	3	no	3-15*01	3-22*01	4*02	95.9	LYMIVGT	7	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0429	5-21	4	no	3-15*01	3-16*01	4*02	94.4	NRGPFDPHQSGPHDY	14	λ	1-40*01	3*02	94.9	QSYDSRLRDQV	12
5T0431	5-40	2	no	3-66*01	5-12*01	3*02	95.9	ARGATPDAFDI	11	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0432	5-44	2	no	3-73*02	3-10*01	4*02	96.4	SRHGV	6	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0435	5-37	2	no	3-33*01	6-19*01	4*02	99	ARDLWLVRYFDH	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0436	5-5	2	no	1-2*02	1-1*01	3*02	92.5	ARPSRYNWNDFAFEI	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0438	5-45	9	yes	3-74*01	4-17*01	4*02	89.9	VRDFTGERDF	10	λ	1-47*01	1*01	95.2	VAWDDRLSGYV	11
5T0440	5-12	2	no	3-15*05	3-22*01	5*02	94.4	TKGGSSGHS	9	λ	1-40*01	3*02	95.9	QTYDSRLSDHWV	12
5T0451	5-11	3	yes	3-15*01	3-9*01	4*02	89.7	TRGPDYDNFSGWRDY	14	λ	1-40*01	3*02	94.6	QSYDARLSDSWV	12
5T0459	5-46	2	yes	3-74*03	1-26*01	4*02	91	AQSGNYRFDY	10	λ	2-14*01	1*01	93.5	TSYTPINTFV	10
5T0464	5-6	3	yes	1-46*01	3-22*01	6*02	88.1	ARSGYPRGMDV	12	λ	2-14*01	1*01	94.2	TSFASTTSYV	10
5T0465	5-0	1	yes	4-59*01	6-19*01	6*02	95.9	ARAPRGYSSGWYNYGMVDV	19	λ	3-1*01	2*01	96.8	QAWDSSTAVV	10
5T0474	5-27	3	yes	3-23*01	1-1*01	4*02	90.8	AKTGQFDY	8	κ	2-30*01	1*01	97.7	MQGMNWPRT	9
5T0544	5-26	3	no	3-15*01	2-15*01	3*02	95.7	TTRKGGFDI	9	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0584	5-30	3	no	3-23*01	1-7*01	4*02	90.4	ARGENGNYEY	10	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
5T0623	5-33	2	no	3-23*03	3-22*01	4*02	98	ANSPYYYDSSGYGSPDY	18	λ	1-44*01	3*02	99.7	AAWDDSLNGWV	11

Shown are exemplary sequences of every identified clone.

single = non-clonal sequence that was produced as monoclonal antibody

n.m. = no match

n.d. = not determined

* = additional member/s of clone was/were produced as antibody

Supplementary Table 3 Information on sequences sharing characteristics between donors (related to Fig. 3).

Shared #	Donor	Antibody	Clone #	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/ IGLV	IGKJ/ IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
s1	EV01	1T0221	1-1	yes	1-18*01	3-22*01	5*02	95.6	ARHVTMLDGGWFD	14	κ	3-20*01	4*01	98.6	QQYSSSPLT	9
		1T0281	1-1	no	1-18*01	3-10*01	4*02	95.3	AREITMVRRGWLDY	14	κ	3-15*01	2*01	99.3	QQYNNWAT	8
		1T0465	1-1	yes	1-18*01	3-10*01	4*02	95.6	ARDITMVRGGWLDY	14	κ	3-15*01	2*01	96.1	QQYNTWAT	8
		1T0478	1-1	no	1-18*01	3-10*01	5*02	96.3	ARGITMVRGEHWLD	15	κ	4-1*01	4*01	94.9	QQFYSTPLT	9
		1T0527	1-1	no	1-18*01	3-10*01	4*02	94.3	ARDIVMVRGVGYFDY	15	κ	3-20*01	1*01	91.9	HQYSSSGPST	10
		1T0645	1-1	no	1-18*01	3-10*01	4*02	95.9	ARDITMVRGGWLDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	EV04	1T0676	1-1	no	1-18*01	3-10*01	4*02	97	AREITMVRRGWLDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		4T0173	4-2	no	1-18*04	3-10*01	5*02	91.2	ARSITMIRGGWFD	14	κ	1-5*01	1*01	96.4	QDYNGPT	7
		4T0284	4-2	yes	1-18*04	3-10*01	5*02	96.3	ARGITMVRGLDWFD	15	κ	3-15*01	4*01	97.2	QQYKNWPLT	9
		4T0510	4-2	no	1-18*01	3-10*01	5*01	96.9	ARGVTMVRRLNWFDS	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	EV05	4T0726	4-2	yes	1-18*04	3-22*01	5*02	93.5	ARTITMILLGWFD	14	κ	3-20*01	3*01	96.9	QQYGTSSPLT	9
		5T0160	5-2	no	1-18*01	3-9*01	5*02	98.6	ARDITIFSGGWFD	14	κ	3-20*01	1*01	100	QQYSSSPRT	9
		5T0605	5-2	no	1-18*01	3-9*01	5*02	98.6	ARDITIFSGGWFD	14	κ	3-20*01	1*01	100	QQYSSSPRT	9
s3	EV01	1T0241	1-0	no	3-13*01	3-10*01	4*02	97.9	ARASFGQVFFDY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0128	3-12	no	3-13*01	3-10*01	5*02	92.1	ARAAFAGVYYDL	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0158	3-12	no	3-13*01	2-8*01	4*02	90.8	ARAAFAGVYFDL	12	κ	1-39*01	4*01	99.6	QQSYSTLT	8
		3T0202	3-12	yes	3-13*01	3-10*01	4*02	94.2	ARAAFAGVFFDY	12	κ	3-20*01	5*01	96.5	QQYGNSPIT	9
		3T0226	3-12	no	3-13*01	2-8*01	4*02	92.8	ARAAFAGVYFDY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0277	3-12	no	3-13*01	3-16*01	4*02	92.1	ARAAFGHIFYDI	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0344	3-12	no	3-13*01	4-17*01	4*02	95.5	ARAAFAGVYYDN	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0351	3-12	no	3-13*01	2-8*01	4*01	90.1	VRAAFAGVYFDL	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0360	3-12	no	3-13*01	3-16*01	4*02	89	VRAAFGHVIFYDI	12	κ	3-15*01	2*01	99.3	QQYNNWAT	8
		3T0370	3-12	no	3-13*01	3-10*01	5*02	94.4	VRAAFGEIYYDL	12	κ	3-20*01	5*01	94.4	QQYSSSPIT	9
	EV03	3T0375	3-12	no	3-13*04	2-21*01	4*02	95.5	VRAAFAGVYYFD	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0460	3-12	no	3-13*01	2-15*01	4*02	89.7	VRAAFGHVFFDS	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0468	3-12	yes	3-13*01	2-21*01	4*02	91.1	ARAAFAGVYYDN	12	κ	3-20*01	5*01	92.3	QQYGRSPIT	9
		3T0517	3-12	no	3-13*01	3-10*01	4*02	90.8	VRAAFGHVFFDV	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0533	3-12	no	3-13*01	3-10*01	4*02	95.2	ARAAFAGVFFDS	12	κ	3-20*01	5*01	94.4	QQYSSSPIT	9
		3T0641	3-12	no	3-13*01	2-8*01	4*02	92.8	ARAAFAGVYFDQ	12	κ	3-20*01	5*01	96.9	QHYHNSPIT	9
		3T0674	3-12	no	3-13*01	2-8*01	4*02	89.4	VRAAFAGVYYDS	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		3T0681	3-12	no	3-13*01	4-17*01	4*02	96.6	ARAAFAGVYFDS	12	κ	3-20*01	5*01	99	QQYSSSPIT	9
		4T0134	4-15	no	3-13*01	2-21*02	4*02	95.5	ARASFGDLIFYDY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		4T0357	4-15	no	3-13*01	3-10*01	4*02	93.2	ARASFGDLFFDY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	EV04	4T0371	4-15	no	3-13*01	3-10*01	4*02	94.5	ARARFGDLALDY	12	κ	3-20*01	4*01	96.9	HQYSSSPLT	9
		4T0444	4-15	yes	3-13*01	3-10*01	4*02	92.5	ARARFGDLALDY	12	κ	3-20*01	4*01	95.5	HQYSSSPLT	9
		4T0501	4-15	no	3-13*01	3-10*01	4*02	98.3	ARARFGDLVFDY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		4T0578	4-15	yes	3-13*01	2-21*02	2*01	95.5	ARASFGDLIFYDL	12	κ	4-1*01	3*01	95.4	QQYYNSPLT	9
		4T0766	4-15	no	3-13*01	3-10*01	3*01	92.1	ARARFGDLVYDV	12	κ	3-20*01	5*01	96.5	QQYSSSPIT	9
s4	EV03	3T0155	3-22	no	3-15*01	n.m.	6*02	91.3	ATRYYYNGMDV	11	λ	1-40*01	3*02	96.3	QSYDSSLRDSTV	12
		3T0236	3-22	no	3-15*01	2-2*01	6*02	88.3	TTRYYYNGMDV	11	λ	1-40*01	2*01	93	QSYDSRLRDSAV	12
		3T0245	3-22	yes	3-15*01	6-6*01	6*02	89	ATRVHYNGMDV	11	λ	1-40*01	3*02	95.6	QSYDSSLRDACV	12
	EV05	5T0347	5-19	no	3-15*01	n.m.	6*02	93.3	TTRYYSNGMDV	10	λ	1-40*01	2*01	97.6	QSYDSSLRDHVV	12
		5T0477	5-19	no	3-15*01	3-9*01	6*02	96.7	TTRYYYNGMDV	11	λ	1-40*01	2*01	97.6	QSYDSRLRDHVV	12
		5T0604	5-19	no	3-15*01	n.m.	6*02	97	TSRYYYNGMDV	11	λ	1-40*01	2*01	97.6	QSYDSRLSDLVV	12
		5T0680	5-19	no	3-15*01	n.m.	6*02	93	TTRYSYNGMDV	11	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
s5	EV03	3T0479	3-0	no	3-23*01	3-3*01	4*02	95.6	AKDDDFWSGTGTWDY	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	EV04	4T0144	4-58	no	3-23*01	3-3*01	4*02	95.6	AKGDFWSGYFFDY	14	λ	1-47*01	1*01	98.3	AAWDDSLSGYV	11
		4T0468	4-58	no	3-23*01	3-3*01	6*02	94.5	AKGDDFWSGSPDV	13	λ	1-51*01	1*01	97.6	GTWDSLSLTFYV	12
		4T0657	4-58	yes	3-23*01	3-3*01	4*02	92.2	AKNDDFWGGPTFDY	14	λ	1-51*01	3*02	97.3	GTWDITLSEGV	11
	EV05	5T0257	5-0	yes	3-23*01	3-3*01	4*02	98.6	AKDDDFWSGYPFDY	14	λ	1-51*02	3*02	98.6	GSWDSLSLSTGV	11
s6	EV04	4T0636	4-0	no	3-23*03	3-22*01	4*02	97.6	ANSPYYYSSGNGYSFDY	18	κ	4-1*01	1*01	96.4	QQYYTTPRT	9
	EV05	5T0623	5-33	no	3-23*03	3-22*01	4*02	98	ANSPYYDSSGGYGSFDY	18	λ	1-44*01	3*02	99.7	AAWDDSLNGWV	11
		5T0693	5-33	no	3-23*03	3-22*01	4*02	97.6	ANSPYYYDSSGGYGSFDY	18	λ	1-44*01	3*02	99.7	AAWDDSLNGWV	11
s8	EV01	1T0218	1-30	no	3-30-3*01	2-2*01	6*02	95.2	ARGGDIVVPAGSLDYGMVDV	20	κ	1-17*01	2*01	99.7	LQHNYSYPT	9
		1T0344	1-30	no	3-30-3*01	2-2*01	6*02	91.2	TRGGDIVVPADSLDYGMVDV	20	κ	1-17*01	2*01	96.9	LQCNSYPT	9
	EV03	3T0131	3-0	no	3-30-3*01	2-15*01	6*02	96.6	ARGGDIVVEVGARPDYGMVDV	21	κ	1-17*03	1*01	98.9	LQHNRYPT	9
s9	EV01	1T0616	1-0	no	3-33*01	2-2*01	6*02	97.6	ARGGDLILLPDANDYYGMVDV	20	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	EV04	4T0784	4-0	yes	3-33*01	2-2*01	6*02	96.9	VRGGDLILLPDSIDYYGMVDV	20	κ	1-17*01	3*01	94.7	LQHNTPFS	9
s10	EV03	3T0465	3-50	no	3-33*01	2-15*01	4*02	93.9	ARESCYGGSCFFDH	14	λ	3-1*01	2*01	95.8	QAWDSRTTVV	9
		3T0680	3-50	no	3-33*01	2-21*02	4*02	89.9	AREFCSGGDCSLDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		4T0219	4-29	no	3-33*01	2-15*01	4*02	96.3	AREFCFGGSCYFDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	EV04	4T0611	4-29	no	3-33*01	2-15*01	4*02	98	AREYCSGGSCYFDY	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		4T0639	4-29	no	3-33*01	2-15*01	4*02	95.6	AREYCSGGTCYCDY	14	λ	3-1*01	2*01	95.8	QTWDSRTTVV	9
	EV05	5T0682	5-0	no	3-33*01	1-26*01	4*02	97.6	AREEAFGGSYIDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
s11	EV03	3T0319	3-39	no	3-72*01	3-22*01	3*02	93.4	VRVG DYWDSSGYS L DAFDI	19	λ	1-51*01	3*02	94.9	ETWDTSLRGV	11
		3T0417	3-39	no	3-72*01	3-22*01	3*02	90	VRVG DYWDSSGYS L DAFDI	19	λ	1-51*01	3*02	93.2	ETWDTSLRGV	11
		3T0454	3-39	no	3-72*01	3-22*01	3*02	90.7	VRVG DYWDSSGYS L DAFDI	19	λ	1-51*01	3*02	92.9	ETWDTSLRGV	11
		3T0506	3-39	yes	3-72*01	3-22*01	3*02	92.7	VRVADYDPSGGYS L DAFDI	19	λ	1-51*01	3*02	94.6	ETWDTSLRGV	11
		3T0557	3-39	no	3-72*01	3-22*01	3*02	90	VRVG DYWDSSGYS L DAFDI	19	λ	1-51*01	3*02	95.6	ETWDTSLRGV	11
		3T0561	3-39	no	3-72*01	3-22*01	3*02	90	VRVG DYWDSSGYS L DAFDI	19	λ	1-51*01	3*02	92.9	ETWDTSLRGV	11
		3T0652	3-39	no	3-72*01	3-22*01	3*02	92.7	VRVG DYDPSGGYS L DAFDI	19	λ	1-51*01	3*02	95.6	ETWDTSLRGV	11
	EV04	4T0171	4-39	yes	3-72*01	3-22*01	3*02	91	VRVADYDPSGGYS V DAFEM	19	λ	1-51*01	2*01	93.9	GTWDTSLRGVI	11
		4T0324	4-39	no	3-72*01	3-22*01	3*02	91	VRVADYDPSGGYS V DAFEM	19	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		4T0545	4-39	no	3-72*01	3-22*01	3*02	91	VRVADYDPSGGYS V DAFEM	19	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.

Supplementary Table 3 (continued) Information on sequences sharing characteristics between donors (related to Fig. 3).

Shared #	Donor	Antibody	Clone #	Produced	IGHV	IGHD	IGHJ	IGH	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/IGLV	IGKJ/IGLJ	IGK/IGL	V _L CDR3 (aa)	V _L CDR3 length (aa)
								Identity (%)						Identity (%)		
s12	EV03	3T0135	3-42	yes	3-74*01	1-26*01	4*02	94.2	ARGGNYLYDY	10	λ	2-18*02	1*01	96.9	SSYTSSATYV	10
		3T0273	3-42	no	3-74*01	1-26*01	4*02	94.2	ARGGNYLYDY	10	λ	2-18*02	1*01	96.3	SSYTSSATYV	10
	EV04	4T0770	4-0	yes	3-74*01	3-22*01	4*02	91.2	ARGGNYNDY	10	λ	2-18*02	1*01	96.6	SSFTSSNTYV	10
s13	EV03	3T0279	3-0	no	4-31*03	1-26*01	5*01	87.7	ARGVRDLVSFWFDS	14	λ	3-19*01	1*01	96.5	NSRDSTINHYV	11
	EV04	4T0544	4-0	no	4-31*03	3-16*01	5*02	87.2	ARGNRDIVVFWFDP	14	κ	5-2*01	4*01	100	LQHDNFLYT	9
s14	EV04	4T0133	4-49	no	4-39*01	n.m.	4*02	92.6	ARRFDL	6	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		4T0159	4-49	yes	4-39*01	n.m.	4*01	93.3	ARRFDS	6	κ	3-15*01	1*01	96.8	QQYNDWPWT	9
		4T0176	4-49	yes	4-39*02	n.m.	4*02	96.6	VRRFDY	6	κ	3-15*01	1*01	96.8	QQYNKWPWT	9
	EV05	5T0378	5-48	yes	4-39*01	n.m.	4*02	98.7	ARRFDY	6	κ	3-15*01	1*01	100	QQYNNWPWT	9
		5T0420	5-48	yes	4-39*02	n.m.	4*02	93.6	ARRFDL	6	κ	3-15*01	1*01	94.7	QQYNIWPWT	9
s15	EV04	4T0764	4-0	yes	4-59*01	3-10*01	4*02	92.8	ARGLLGSQDS	10	λ	2-14*01	2*01	96.3	SSYRTRNTHVI	11
	EV05	5T0376	5-0	yes	4-59*01	2-21*02	4*02	93.8	ARLLGPGDS	10	λ	2-14*01	2*01	96.2	SSYKTGSTPVV	11
s16	EV04	4T0243	4-57	yes	4-59*01	5-18*01	6*02	92.8	ARAPRGYSSGKYNYGLDV	19	λ	3-25*02	1*01	93.1	QSADSSGGYYV	11
		4T0511	4-57	no	4-59*01	3-10*01	6*02	96.2	ARAPRSYGRGSYYYGIDV	19	λ	3-1*01	2*01	96.8	QAWDSSTFQVV	11
		4T0571	4-57	no	4-59*01	5-18*01	6*02	95.9	ARAPRGYNNYNNYYYSHIDV	19	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
	EV05	5T0465	5-0	yes	4-59*01	6-19*01	6*02	95.9	ARAPRGYSSGWYYYGMDV	19	λ	3-1*01	2*01	96.8	QAWDSSTAVV	10

n.m. = no match

n.d. = not determined

Supplementary Table 5 Peptide sequences detected by library epitope screening (related to Fig. 4, Extended Data Fig. 6 and Supplementary Table 4).

Antibodies	Epitope	Peptide sequence
1T0130	SP GP1	LPRDRFKRTSFFLWVIL SASSGKLGLTNTIAGVA
1T0139	SP SP	LPRDRFKRTSFFLWVIL TSFFLWVILFQRTFSIP
1T0201	SP GP1 SP SP	MGVTGILQLPRDRFKRTS EPVNATEDPSSGGYYSTTI LPRDRFKRTSFFLWVIL TSFFLWVILFQRTFSIP
1T0221	GP1	EPVNATEDPSSGGYYSTTI
1T0248	SP MLD MLD	LPRDRFKRTSFFLWVIL DNSTHNTVPYKLDISEAT VYKLDISEATQVQGHRR
1T0264	SP MLD	LPRDRFKRTSFFLWVIL ATQVQGHRRADNDSTAS
1T0301	SP MLD MLD	LPRDRFKRTSFFLWVIL DNSTHNTVPYKLDISEAT ATQVQGHRRADNDSTAS
1T0325	SP SP MLD MLD	LPRDRFKRTSFFLWVIL TSFFLWVILFQRTFSIP DNSTHNTVPYKLDISEAT VYKLDISEATQVQGHRR
1T0451	MLD	VYKLDISEATQVQGHRR
1T0465	GP1 HR1/2 HR1/2	AENCYNLEIKKPDGSECL LLQRWGGTCHILGPDCCI CHILGPDCCIEPHDWTGN
1T0546	SP SP MLD MLD	MGVTGILQLPRDRFKRTS LPRDRFKRTSFFLWVIL PPTTKTGPDNSTHNTVPY DNSTHNTVPYKLDISEAT
1T0552	SP GP1	LPRDRFKRTSFFLWVIL AENCYNLEIKKPDGSECL
1T0565	MLD MLD	EDHKIMASENSSAMVQVH ENSSAMVQVHSQGRKAAV
1T0655	MPER	KNITDKIDQIHFVDKT
3T0215	Gly-cap	IDTTIGEWAFWETKKNLT
3T0258	SP GP1 GP1 GP1	LPRDRFKRTSFFLWVIL AENCYNLEIKKPDGSECL ILPQAKKDFSSHPLREP ETAGNNNTHHQDTGEESA
3T0331	IFL	VAGLITGRRTRREVIVN
3T0350	GP1 GP1	SVGLNLEGNVATDVPSA NGVATDVPSATKRWGFRS
3T0368	SP	LPRDRFKRTSFFLWVIL
3T0405	Gly-cap MLD	LTRKIRSEELSFTAVSNG ELSFTAVSNGPKNISGQS
3T0411	SP	LPRDRFKRTSFFLWVIL
3T0420	Gly-cap Gly-cap MLD MLD	TPQFLQLNETIYASGKR NETIYASGKRSNTTGKLI ENSSAMVQVHSQGRKAAV VHSQGRKAAVSHLTTLAT
3T0427	GP1 GP1 Gly-cap	GPCAGDFAFHKEGAFFLY FHKEGAFFLYDRLASTVI NETIYASGKRSNTTGKLI
3T0468	GP1 HR1/2	AENCYNLEIKKPDGSECL LLQRWGGTCHILGPDCCI
3T0611	GP1	HHQDTGEESASSGKLGLI
4m0361	SP	MGVTGILQLPRDRFKRTS
4m0368	GP1	SATKRWGFRSGVPPKVVN
4m0373	HR1/2	CIEPHDWTGNITDKIDQI
4T0159	SP SP SP GP1 GP1 GP1	MGVTGILQLPRDRFKRTS LPRDRFKRTSFFLWVIL TSFFLWVILFQRTFSIP IPLGVIHNSTLQVSDVDK STLQVSDVDKLVCRDKLS SVGLNLEGNVATDVPSA

Antibodies	Epitope	Peptide sequence
4T0168	GP1 MLD	AENCYNLEIKKPDGSECL AVSHLTTLATISTSPQPP
4T0176	SP GP1 GP1 HR1/2 HR1/2	LPRDRFKRTSFFLWVIL SVGLNLEGNVATDVPSA VNYEAGEWAENCYNLEIK LLQRWGGTCHILGPDCCI CHILGPDCCIEPHDWTGN
4T0182	IFL IFL	PNLHYWTTQDEGAAIGLA QDEGAAIGLAWIPYFGPA
4T0243	HR1/2	CHILGPDCCIEPHDWTGN
4T0284	GP1 Gly-cap GP1 GP1	IPLGVIHNSTLQVSDVDK AFWETKKNLTRKIRSEEL VNYEAGEWAENCYNLEIK FFSSHPLREPVNATEDPS
4T0350	Gly-cap Gly-cap Gly-cap Gly-cap	NETIYASGKRSNTTGKLI KRSNTTGKLIWKVNPEID LIWKVNPEIDTTIGEWAF IDTTIGEWAFWETKKNLT
4T0365	HR1/2	LLQRWGGTCHILGPDCCI
4T0423	HR1/2 HR1/2	LLQRWGGTCHILGPDCCI CHILGPDCCIEPHDWTGN
4T0429	MLD MLD	PPTTKTGPDNSTHNTVPY DNSTHNTVPYKLDISEAT
4T0520	MLD MLD	DNSTHNTVPYKLDISEAT VYKLDISEATQVQGHRR
4T0525	SP SP	LPRDRFKRTSFFLWVIL TSFFLWVILFQRTFSIP
4T0541	SP	LPRDRFKRTSFFLWVIL
4T0570	MPER MPER	KNITDKIDQIHFVDKT QIHFVDKTLPDQGDND
4T0578	SP	LPRDRFKRTSFFLWVIL
4T0764	GP1 Gly-cap HR1/2	IKKPDGSECLPAAPDGIR AFWETKKNLTRKIRSEEL TELRTFSILNRKAIDFLL
5T0107	GP1 HR1/2	AENCYNLEIKKPDGSECL TELRTFSILNRKAIDFLL
5T0257	SP	MGVTGILQLPRDRFKRTS
5T0278	GP1	VIYRGTTFAEGVVAFLIL
5T0376	GP1 Gly-cap	IKKPDGSECLPAAPDGIR AFWETKKNLTRKIRSEEL
5T0377	SP	LPRDRFKRTSFFLWVIL
5T0378	HR1/2	LLQRWGGTCHILGPDCCI
5T0420	GP1	SVGLNLEGNVATDVPSA
5T0465	SP SP GP1 Gly-cap HR1/2 HR1/2	LPRDRFKRTSFFLWVIL TSFFLWVILFQRTFSIP IPLGVIHNSTLQVSDVDK IDTTIGEWAFWETKKNLT LNRKAIDFLLQRWGGTCH CHILGPDCCIEPHDWTGN
AD115758	MPER	KNITDKIDQIHFVDKT
KZ52	SP GP1 IFL IFL	TSFFLWVILFQRTFSIP IPLGVIHNSTLQVSDVDK RRTREVIVNAQPKCNPN VNAQPKCNPNLHYWTTQD
mAb100	SP GP1 GP1 IFL HR1/2	LPRDRFKRTSFFLWVIL IPLGVIHNSTLQVSDVDK LITNTIAGVAGLITGGRR RRTREVIVNAQPKCNPN LQLFLRATTELRTFSILN
mAb114	SP Gly-cap	MGVTGILQLPRDRFKRTS AFWETKKNLTRKIRSEEL

SP: signal peptide

Supplementary Table 6 Sequence information of clonal IgG sequences obtained with alternative sorting bait EBOV GPΔTMΔMLD (related to Extended Data Fig. 4).

Antibody	Clone #	# of GPΔMLD members	# of GPΔTM members	Produced	IGHV	IGHD	IGHJ	IGH Identity (%)	V _H CDR3 (aa)	V _H CDR3 length (aa)	Light chain	IGKV/ IGLV	IGKJ/ IGLJ	IGK/IGL Identity (%)	V _L CDR3 (aa)	V _L CDR3 length (aa)
4m0302	4-44	1	2	no*	3-74*01	6-19*01	4*02	96.3	ARDVGLYNTGWIDY	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0314	4-69	2	0	yes	1-2*02	1-1*01	6*02	89.7	ASPPQNNWRLYFYGMVDV	17	λ	1-51*01	2*01	94.2	GTWDTSLRGVI	11
4m0331	4-65	2	0	no	3-21*01	3-10*01	3*02	93.6	AREGARSNYFLGDATDI	17	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0333	4-58	2	3	yes*	3-23*01	3-3*01	6*02	94.9	AKGDDFWSGSPDV	13	λ	1-51*01	1*01	97.6	GTWDSLSLTFYV	12
4m0334	4-42	2	2	no*	3-74*01	5-18*01	4*02	87.9	ARGGSDTAMAHDY	13	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0342	4-60	2	1	no	3-21*02	4-11*01	6*02	90.2	ARDNDYHDDSAGGMDV	16	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0344	4-71	1	1	no*	3-74*01	3-22*01	4*02	92.2	ARGGNYNDY	10	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0349	4-64	2	0	no	3-30*18	3-22*01	6*02	96.6	AKDRARGYYGYGMVDV	16	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0354	4-27	1	2	no*	3-23*01	3-16*01	4*02	90.2	AKDVWPGPGSLDW	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0357	4-63	2	0	yes	3-7*01	3-10*01	4*02	93.6	ARGGSGIVPAIFF	13	λ	3-10*01	3*02	97.9	YSTDSSGYHFW	12
4m0361	4-59	2	1	yes	4-39*01	4-17*01	4*02	85.8	ARVTMKNFFDS	11	λ	3-21*02	1*01	94.2	QVWDNTYV	8
4m0365	4-62	1	1	yes	3-74*01	2-21*02	5*02	100	ARAVLGVVTRYNWFDP	17	κ	1-39*01	1*01	99.7	QOSYSTPRT	9
4m0367	4-66	1	1	no	3-15*05	2-8*01	4*02	87.7	ITEMVFPTGY	10	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0368	4-52	1	2	yes	4-4*02	3-16*01	5*02	92.5	LRLSHYGA	9	κ	1-39*01	1*01	95.8	QQTYNTPRT	9
4m0373	4-12	1	5	yes	3-11*01	2-2*01	6*02	94.6	ARGERRHQVLSGMDV	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0387	4-68	1	1	yes	1-2*02	2-21*02	3*02	95.2	ARLTVVTAISAFDI	14	κ	1-5*01	1*01	95.4	QHYFDYYGA	10
4m0394	4-39	1	3	no*	3-72*01	3-22*01	3*02	91	VRVADVFDSSGYSVDAFEM	19	λ	1-51*01	2*01	93.9	GTWDTSLRGVI	11
4m0401	4-1	1	2	no	1-18*01	3-22*01	4*02	97.6	ARVISMILVGPFDP	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0407	4-2	1	4	no*	1-18*04	3-22*01	5*02	97.6	ARTITMIFLGWFDP	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0410	4-46	1	2	no*	3-9*01	5-24*01	6*02	95.6	TREGRDGNNLPYYAMDV	17	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0422	4-67	2	0	no	3-11*01	3-22*01	4*02	96.6	ARKGSIYDSPY	11	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0437	4-61	1	1	no	4-59*01	6-13*01	4*02	92.1	ARGSSNWYEGTFEY	15	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0443	4-15	1	7	no*	3-13*01	3-10*01	4*02	95.9	ARARFGDLAFDY	12	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0447	4-31	1	3	no*	3-33*01	6-13*01	4*02	92.9	ARDAHNSRLDY	11	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0450	4-70	1	1	no*	1-3*01	3-3*02	5*02	98.6	ARDISLFNPGWFDP	14	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
4m0492	4-57	1	3	no*	4-59*01	3-3*01	6*02	96.6	ARAPRGYSFWSGQYYGYGVDV	21	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.

Shown are exemplary sequences of every identified clone.

n.d. = not determined

GPΔMLD members = sequences obtained with alternative bait EBOV GPΔTMΔMLD

GPΔTM members = sequences obtained with bait EBOV GPΔTM

* = clonal member obtained with EBOV GPΔTM bait was produced as antibody

Supplementary Table 7 (related to Fig. 6).**a** Cryo-EM data collection, refinement and validation statistics

	GP/3T0331 (EMDB-EMD-4520) (PDB 6QD7)	GP/4M0368 (EMDB-EMD-4521) (PDB 6QD8)
Data collection and processing		
Magnification	96,000	96,000
Voltage (kV)	300	300
Electron exposure (e-/Å ²)	40	40
Defocus range (µm)	-0.5 – -2.3	-0.5 – -2.3
Pixel size (Å)	0.85	0.85
Symmetry imposed	C3	C3
Initial particle images (no.)	239,806	184,548
Final particle images (no.)	109,407	123,880
Map resolution (Å)	3.09	3.33
FSC threshold	0.143	0.143
Map resolution range (Å)	30-1.82	30-1.81
Refinement		
Initial model used (PDB code)	6QCU, 5JQ3	5JQ3
Model resolution (Å)	2.95	3.25
FSC threshold	0.143	0.143
Model resolution range (Å)	30-1.82	30-1.81
Map sharpening <i>B</i> factor (Å ²)	-91.52	-117.0
Model composition		
Non-hydrogen atoms	14445	14154
Protein residues	1815	1785
Ligands	45	39
<i>B</i> factors (Å ²)		
Protein	54.72	55.54
Ligand	81.49	76.16
R.m.s. deviations		
Bond lengths (Å)	0.009	0.015
Bond angles (°)	1.659	1.677
Validation		
MolProbity score	2.04	2.22
Clashscore	4.23	5.68
Poor rotamers (%)	4.53	3.96
Ramachandran plot		
Favored (%)	95.11	92.8
Allowed (%)	4.72	6.69
Disallowed (%)	0.17	0.51

b Data collection and refinement statistics (molecular replacement)

3T0331- Fab (PDB 6QCU)	
Data collection	
Space group	<i>P</i> 6 ₅ 22
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	91.1 91.1 215.4
α , β , γ (°)	90 90 120
Resolution (Å)	1.56 (1.616 - 1.56) *
<i>R</i> _{merge}	0.1322 (0.8877)
<i>I</i> / σI	10.32 (1.98)
Completeness (%)	99.99 (100.00)
Multiplicity	13.0 (13.2)
Refinement	
Resolution (Å)	1.56
No. reflections	75845
<i>R</i> _{work} / <i>R</i> _{free}	0.177/0.203
No. atoms	
Protein	3804
Ligand/ion	20
Water	506
<i>B</i> -factors	
Protein	26.6
Ligand/ion	53.2
Water	37.2
R.m.s. deviations	
Bond lengths (Å)	0.011
Bond angles (°)	1.41

*Values in parentheses are for highest-resolution shell.

A single crystal was used for data collection.