

A

	FR1	HCDR1	FR2	HCDR2	FR3	HCDR3	FR4
<b>T927 lineage 1</b>							
HV4-79*02	QVQLQESGPGLVKPSSETLSLTCAVSGASISSYVWWSWIRQPPKGLKEWIGELINGNSGSTYINPNSLKSRTVTSKDKASKNQFSLKLSVTAADTAVYYCAR						
HD3-15*01						YYEDDYGYIYT	
HJ6-6*01							YYGLDSWGQGVVVTVSS
W32_P2D12	.....R.....	.....N.Y.....	.....T.A.S...Q...F.....H.....N.....I.....			H.K.F.D...E...LEGAR.....A...	
<b>T927 lineage 2</b>							
HV5-15*01	EVQLVQSGAEVKKRQPKGSEKLSCKTSKTSYSPYFVSWISWVRQMPKGLKEWMAIDPSDSDTFRYSYSPFQGVVTSADKSIKSTAYLQWSSKASDSATYYCAR						
HD6-34*01						CYSSWS	
HJ1*02							AEYFFFWGQGLVTVSS
w24_P1D08	...V.....F.....T.SD.....D.....						N.F.VGPH.G.P...D.YSVFEL.N
w24_P2D06	.....R.....D.....D.....A.....I..V..PT..F.....R.....						GPH.TS.PS...D.YSVFEL.S
w24_P1D09	.....D.T.....E.....A.....H.....T.N.....						GPH.G.PS...D.YSVFEL.S
<b>T927 lineage 3</b>							
HV4-149*01	QVQLQESGPGLVKPSSETLSLTCAVSGGFSYVWWSWIRQPPKGLKEWIGELINGNSGSTYINPNSLKSRTVTSKDKASKNQFSLKLSVTAADTAVYYCAR						
HD3_15*01						YYEDDYGYIYT	
HJ5-5*01							NSLDWGGRVLTVSS
W62_P1C05	.....TT...A.....Y.S.N..FS.....						SERSLLD...D...SSQFSHF.....I.....
W62_P1C01	.....NT...A.....Y.S...F.....R.N.....						SERSLLD...D...SSQFSQF.....I.....
<b>T927 lineage 4</b>							
HV4-149*01	QVQLQESGPGLVKPSSETLSLTCAVSGGFSYVWWSWIRQPPKGLKEWIGELINGNSGSTYINPNSLKSRTVTSKDKASKNQFSLKLSVTAADTAVYYCAR						
HD3_15*01						YYEDDYGYIYT	
HJ4-3*01							YFDYWGQGLVTVSS
W62_P1B01	.....R.....T.....T.....S.....T.S.T...A.TG...E.S.I...VT.....						TRPRLLD...D...S.YSVFEL.N
W62_P1B10	.....T.....S.H.....R.....D.VT.PR.T...A.I..Q.....VT.....						TRPRLLD...D...D.YSVFEL.S
W62_P3E08	.....E.....A.....G.....D.VT.PR.T...G.Q...L.D.V.....						TRPRLLD...D...FD.YSVFEL.S
W62_P1H10	.....D.S.H.T.....S.....N.....RVA.....						TRPRLLD...D...D.YSVFEL.S
W62_P1F05	.....H.T.....VT.PR.T...Q.T...RVT.....						TRPRLLD...D...D.YSVFEL.F
W62_P3C02	.....G.....A.R.....D.Q.L.R.T.....F.....						TRPRLLD...D...FD.YSVFEL.S
W62_P1C07	.....V.....S.H.T...S.R.....VT.PR.T...S.N...R.T.....						TRPRLLD...D...D.YSVFEL.S
W62_P3A11	.....H.T.V.....VT.PR.T...Q.V.NK...RMT.....						TRPRLLD...D...D.YSVFEL.F...LP
<b>T927 lineage 5</b>							
HV3-50*01	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPKGLKEWVAISYDGGSKKYADSVKDRFTISRDNKNMLYLQMNLLKLEDTAVYYCAR						
HD3-15*01						YYEDDYGYIYT	
HJ5-4*03							NRFDWGQGLVTVSS
w24_P2B12	.....N.I.....A.S...I.....G.....T.K.....						DRVN...S...Q.WG.L...P
w24_P1C02	.....I.S.I.....A.S...I...EP.A.K.T.IVF...S.....						DRVN...S...Q.WG.L...
w24_P1D03	.....F.....A.H.I.....D.A.S...I...F.E.L.G.L.T.IV.....						DRIN...S...F.Q.WG.L...
w24_P1A11	.....D.....K.....I.N.I.....G.S...YI.....G.....T.MV.F.K.A.F.....						DRVN...S...F.Q.WG.L...
w24_P1B05	.....L.....K.....F.PM..F.F.....D.G.SN.RYI...RG...T.RSSV...DT.R...I.F...DRIN.NYS.DG.Q.WG.L...P						DRIN.NYS.DG.Q.WG.L...P
w24_P3G11	.....F.....D.H.A.....R.D.A.SN.K.I...EFAMA...T.TIV...H.....						DRIN..ASADQ.WG.L...
<b>T925 lineage 1</b>							
HV4-117*01	QVQLQESGPGLVKPSSETLSLTCAVSGGSISSYVWWSWIRQPPKGLKEWIGELIYSGGGSTYINPNSLKSRTVTSKDKASKNQFSLKLSVTAADTAVYYCAR						
HD3-15*01						YYEDDYGYIYT	
HJ4-3*01							YFDYWGQGLVTVSS
w24_P1E09	.....N.N.....VF.RD...SL.....N.R.....						SPS...F...LG...D
w24_P1D09	.....R.....F.RD...N.N.....H.....						SPS...F...LG...D
w24_P2B11	.....G.N.....F.RD...N.N.....F.....						SPN...F...LG...D
w24_P1A12	.....M.....F.RD...N.N.....T.....						SPN...F...LG...D
w24_P1C08	.....F.D...S.N..L.....						SPN...E.H.LG...C...P
<b>T925 lineage 2</b>							
HV4-NL_33*01	QVQLQESGPGLVKPSSETLSLTCAVSGGSISSYVWWSWIRQPPKGLKEWIGELIYSGGGSTYINPNSLKSRTVTSKDKASKNQFSLKLSVTAADTAVYYCAR						
HD3-18*01						YYGSGYIYT	
HJ6-6*01							YYGLDSWGQGVVVTVSS
w24_P1F12	.....SD...A.....L...G.N.H.....R...V.....M..V.VKWG...NM.F.....						V.VKWG...NM.F.....
w24_P1F01	.....D..P.....S.....G.A...R...F...LL.....F.V.VKWG...NM.F.....						V.VKWG...NM.F.....
w24_P2C12	.....V..P.....S.I.A.D...H.Y.....G.GE.....P.....S.....						MKWG...D..NY.....
w24_P1G03	.....VG.P...T...T.....F.A.T...R...AV.A.N.E.....						MKWG...D..NY.....
w24_P1E11	.....R.....V...V...S...N...R...S...H.R.....						MKWG...D..KYA.....G...

B

	FR1	LCDR1	FR2	LCDR2	FR3	LCDR3	FR4
<b>T927 lineage 1</b>							
LV3-40*01	SYELLQPSRSVSPGQTARITCGDNIQSKSVQWYQKPPQAPVLVIYADSERPSGIPERFSGNSGNTATLITISGVEAGDEADYICQWDSDDH						
LJ2A*01						QVFGGGTRL	
W32_P2D12	.....R.....S.I.....I.....						GTDHP.....
<b>T927 lineage 2</b>							
LV2S9*01	QAALTQPPSVKSLGQSVTISCTGTSNDVGGYNDVSWYQHPGTAPRLLIYDVKSRPSGVDRFSGSKSGNTASLTISGLQAEADYICQSYRSGST						
LJ1*01						FIFGAGTRLTV	
w24_P1D08	.....L.....S...I.A.D...H.Y.....G.GE.....P.....S.....						
w24_P2D06	.....SV.....S.I.A...V.....S.T.....I.....G.....						
w24_P1D09	.....S.I.A...V.....S.T.....I.....G.....						
<b>T927 lineage 3</b>							
LV1-85*01	QSVLTQPPSVGAPGQVITISCTGSSNIIGYVQWYQQLPGTAPKLLIYENKRPSPGVDRFSGSKSGTASLTITGLQSEADYICQSYDSSLSA						
LJ2A*01						QVFGGGTRL	
W62_P1C05	.....L.....N.....V.....D...A.....R.....						H...FS.....
W62_P1C01	.....L.....N.....A.....R.A.....E.....						H...FS.....
<b>T927 lineage 4</b>							
LV1-67*2	QSVLTQPPSVSAAPGQVITISCTGSSNIIGYVQWYQQLPGTAPKLLIYQDNKRPSPGVDRFSGSKSGTASLAITGLQSEADYICQAWDSSLSA						
LJ3*01						VLFGGGTRL	
W62_P1B01	.....F.....V.....T.....A.....V...S.L.....A.S...T.H...I.....						T.T.VL.....
W62_P1B10	.....F.....V.....T.....A.....V...S.L.....A.S...T.H...I.....						T.T.VL.....
W62_P3E08	.....F.....V.....T.....A.....V...S.L.....A.S...T.H...I.....						T.T.VL.....
W62_P1H10	.....F.....V.....T.....A.....V...S.L.....A.S...T.H...I.....						T.T.VL.....
W62_P1F05	.....F.....T.....T.....H.A.A...V...S.L.....A.S...T.H...I.....						T.T.VL.....
W62_P3C02	.....F.....T.....T.....H.A.A...V...S.L.....A.S...T.H...I.....						T.T.VL.....
W62_P1C07	.....F.....T.....T.....H.A.A...V...S.L.....A.S...T.H...I.....						T.T.VL.....
W62_P3A11	.....F.....Y...KN.....A.....V...S.L.....A.S...T.H...I.....						T.T.VL.....
<b>T927 lineage 5</b>							
KV2-104*02	DIVMTQTFLSLPVTGPEPASISCRSSQLLDSDEGNTYLDWYKLPQSPQLLIYEVSNRASGVPDRFSGSGSDTDFTLKISRVEADYICQALEFF						
KJ1*01						WTFGGQTKVEIK	
w24_P2B12	.....T.....A.....G...R.....						
w24_P1C02	.....T.....A.....G...D...R.....						
w24_P1D03	.....T.....A.....G...R.....						
w24_P1A11	.....T.....A.....G...R.....						
w24_P1B05	.....G.....T.....I.....T.....A.....G...H...R.....						
w24_P3G11	.....R.....F.....T.....A.....G...H...R.....						
<b>T925 lineage 1</b>							
KV1-94*01	DIQMTQSPSSLSASVGRVTVTCRASQGINKELSWYQKPKGKAPTELLIYAASSLQTVSSSRFSGSGSDTFTLTISSLQPEDVATYYCQQDYTTPT						
KJ4*01						ITFGGQTKVEIK	
w24_P1E09	.....L.....S.....R.....						
w24_P1D09	.....D.....H.T.....N.....S.....						
w24_P2B11	.....D.....S.R.....A.....R.....						
w24_P1A12	.....E.R.....A.H.....F.....S.....R.....						
w24_P1C08	.....D.....S.....						
<b>T925 lineage 2</b>							
LV2_23*02	QAALTQPPSMGSPGQVITISCTGTSNDVGGYNDVSWYQHPGKAPKLLIYEVSNRASGVPDRFSGSKSGTASLTISGLQAEADYICSSYAGSNTF						
LJ3*01						VLFGGGTRL	
w24_P1F12	.....S.....F.....T.....L...N.....S.....I.F.....						
w24_P1F01	.....S.....G.A...N.....H.....						
w24_P2C12	.....S.....H.....K...T.....L...R.....						
w24_P1G03	.....S.....G...R.....T.....KSL.....						
w24_P1E11	.....S.....G.....N.....T.....L...V.....						

**FIG. S8 Heavy and light chain variable region sequences of antibody lineages isolated from SCIV-infected RMs.** (A, B) Heavy (H, panel A) and light (lambda [L] and kappa [K], panel B) chain variable region sequences of mature lineage members isolated from RMs T927 and T925 (listed on the left) are aligned to the deduced amino acid sequences of their respective germline variable (V), diversity (D), and joining (J) genes (indicated on the top). Framework (FR) and complementary determining regions (CDR) are color coded, with HCDR1 and LCDR1, HCDR2 and LCDR2, and HCDR3 and LCDR3 highlighted in blue, pink and red, respectively. Predicted sulfated tyrosines in the HCDR3 region (using the GPS-TSP 1.0 software at a high threshold setting) are highlighted in yellow (98). Expanded lineages (listed on the left) were identified using SONAR's automated "unseeded" lineage assignment tool, followed by manual inspection of gene assignments, HCDR3 regions, and non-templated nucleotides to confirm membership (Genbank accession numbers are listed in Table S2E at <https://doi.org/10.6084/m9.figshare.21644675>).