

Supplementary information

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Supplementary Table S1: Purity of the cell populations isolated from 11 SFV-infected individuals

PBMC populations from the 11 SFV-infected individuals (sampled at two time points for BAD348, BAD468 and BAK74) were purified and stained with anti-CD3-FITC, anti-CD14-PE, anti-CD16-V450, anti-CD56-PC7, anti-CD8-APC, anti-CD4-APC-H7, and anti-CD20-PC5. LIVE/DEAD® Fixable Dead Cell Stain Kit was used to identify viable cells. Cells were gated by forward scatter and side scatter, and viable cells were selected based on live/dead labeling. CD4+ and CD8+ cells were defined in the CD3+ population. CD20+, CD14+, CD16+, and CD56+ cells were defined in the CD3- population. The purity of the isolated subset is indicated in red.

Individual	Cell subset	CD3+ CD4+ (% among live cells)	CD3+ CD8+ (% among live cells)	CD20+ (% among live cells)	CD14+ (% among live cells)	CD16+ or CD56+ (% among live cells)
AKO394	CD4+	94.7	2.6	0.0	0.1	2.1
	CD8+	1.1	81.3	0.0	0.1	18.1
	CD19+	3.9	3.6	76.2	0.7	4.3
	CD14+	4.5	5.3	0.2	58.5	21.0
	CD56+	0.7	4.7	0.2	0.5	91.2
BAD348 14/03/2013	CD4+	90.0	1.4	0.1	0.1	3.5
	CD8+	3.2	88.5	0.1	0.9	4.8
	CD19+	2.6	1.9	70.6	1.3	2.1
	CD14+	2.6	1.4	2.2	71.1	16.3
	CD56+	4.2	30.3	0.4	3.2	51.7
BAD348 19/11/2013	CD4+	96.7	1.2	0.0	1.6	0.6
	CD8+	2.2	94.1	0.3	1.6	1.7
	CD19+	0.8	0.9	88.3	5.7	2.2
	CD14+	5.8	2.6	0.6	87.8	4.4
	CD56+	3.1	30.6	2.5	9.8	47.1
BAD447	CD4+	93.2	2.2	0.0	0.0	2.3
	CD8+	1.5	96.8	0.6	0.3	0.9
	CD19+	2.2	4.6	85.4	1.0	0.8
	CD14+	5.6	8.0	1.1	50.9	28.3
	CD56+	2.5	7.3	2.1	22.9	59.7
BAD456	CD4+	90.8	2.5	0.0	0.0	5.0
	CD8+	2.6	77.6	1.5	1.1	18.6
	CD19+	1.8	9.1	77.1	1.3	3.1
	CD14+	5.4	4.9	1.2	60.5	25.9
	CD56+	2.6	17.2	0.9	4.4	71.3
BAD463	CD4+	96.5	1.0	0.0	1.7	0.8
	CD8+	5.9	91.3	1.0	2.3	3.6
	CD19+	2.8	4.8	80.4	7.9	1.9
	CD14+	8.7	2.9	0.5	82.1	4.4
	CD56+	3.6	16.2	0.4	21.8	50.5
BAD468 04/09/2012	CD4+	96.4	0.4	0.1	0.2	1.3
	CD8+	1.1	84.1	0.3	0.5	11.5
	CD19+	3.1	2.6	94.9	0.9	0.9
	CD14+	2.0	0.7	2.1	78.5	9.5
	CD56+	2.6	8.2	1.3	18.7	62.6

BAD468	CD4+	95.0	1.0	0.0	0.0	2.4
15/11/2013	CD8+	2.2	87.0	0.8	0.2	9.7
	CD19+	2.6	3.6	80.9	2.6	9.5
	CD14+	6.8	3.4	1.2	54.4	28.3
	CD56+	2.2	6.1	8.6	11.2	68.7
	BAK177	CD4+	87.9	1.2	0.3	0.7
	CD8+	0.6	67.4	0.4	1.0	26.8
	CD19+	0.8	0.7	75.3	0.9	2.1
	CD14+	1.0	0.9	3.7	54.9	32.7
	CD56+	0.2	5.3	0.4	1.0	88.9
	BAK232	CD4+	94.9	1.6	0.0	2.8
	CD8+	2.1	91.0	1.8	2.1	3.1
	CD19+	2.1	8.2	71.0	11.2	1.8
	CD14+	6.5	3.9	0.3	90.2	2.2
	CD56+	2.0	13.5	1.4	17.2	63.3
	BAK55	CD4+	93.0	1.1	0.0	2.2
	CD8+	1.7	93.3	0.5	0.6	4.6
	CD19+	2.8	9.4	72.8	7.6	2.8
	CD14+	10.2	2.2	0.2	84.2	2.8
	CD56+	1.1	16.9	0.7	3.2	75.6
	BAK74	CD4+	97.4	0.6	0.0	0.1
04/09/2012	CD8+	2.0	92.5	0.3	0.4	4.6
	CD19+	1.8	2.5	90.6	0.5	0.9
	CD14+	3.0	0.6	0.6	87.7	3.6
	CD56+	2.4	44.1	0.1	1.0	40.6
	BAK74	CD4+	98.2	0.6	0.0	0.7
15/11/2013	CD8+	1.4	96.3	0.7	0.3	1.5
	CD19+	1.2	4.3	80.8	2.2	3.4
	CD14+	3.5	0.7	0.3	94.8	0.6
	CD56+	2.2	43.0	0.6	3.6	38.1
	LOBAK2	CD4+	90.7	5.1	0.0	0.1
	CD8+	5.0	89.0	1.0	0.6	4.5
	CD19+	2.9	7.3	74.5	1.0	1.4
	CD14+	2.6	4.8	0.6	69.0	21.6
	CD56+	3.8	34.2	0.5	9.3	50.6
	Mean (all individuals)	CD4+	94.0	1.6	0.1	0.7
	CD8+	2.3	87.9	0.7	0.8	8.1
	CD19+	2.2	4.5	79.9	3.2	2.7
	CD14+	4.9	3.0	1.1	73.2	14.4
	CD56+	2.4	19.8	1.4	9.1	61.4
	Standard deviation (all individuals)	CD4+	3.1	1.2	0.1	1.0
	CD8+	1.5	8.1	0.5	0.7	7.9
	CD19+	0.9	2.9	7.5	3.5	2.2
	CD14+	2.6	2.2	1.0	15.2	11.7
	CD56+	1.1	14.0	2.2	8.0	16.4

AKO394	1051	ATA	GAA	GCT	TAT	GGA	CCT	CAG	AGA	GGA	AGT	AGC	GAG	GAG	AGG	GTG	TGG	TGG	AAA	ACC	ACT	AGT	ACC	CTA	GGG	AAG
BAD348									G																	
BAD447																										
BAD456																										
BAD463																							G			
BAD468																										
BAK177																										
BAK232																										
BAK55																										
BAK74																										
LOBAK2																										

AKO394	1125	GAT	GAA	GAA	TAT	TAT	AGA	AGT	GAG	GGA	GAA	GAA	GAA	TGT	TTC	CCC	AAC	AGT	CCT	GCT	CCT	CAT	CGC	CGT	ACT	TGG
BAD348			G			C	C	G			G			G												
BAD447			G																							
BAD456			G																							
BAD463			G																							
BAD468			G			C	C	G			G			G												
BAK177			G																						T	
BAK232			G																							
BAK55			G			C	C	G			G			G												
BAK74			G																							
LOBAK2			G			C	C	G			G			G												

AKO394	1201	ACA	GAG	AGG	CAT	AAA	GTC	CTT	GCC	TTG	TCA	CCA	TTC	GCT	ACT	CCC	TCT	GAT	ATC	CAA	AAG	TGG	GTT	ACA	AGG	GCA
BAD348				A					T																	
BAD447																										
BAD456							A																			
BAD463									T								T									
BAD468				A					T																	
BAK177																										
BAK232							A																			
BAK55				A					T																	
BAK74																										
LOBAK2				A																						

AKO394	1276	CTA	CCT	TAT	AAG	TGG	AAA	GTA	ATC	ACT	TCA	GAT	GGG	GAT	GAT	TAT	GTT	AGT	ATG	AGA	ACA	GTT	AAA	ACC	TTG	AAA
BAD348				C									A													
BAD447																										
BAD456																										
BAD463																										
BAD468				C																						
BAK177																										
BAK232																										
BAK55					C																					
BAK74																										
LOBAK2				GC										A												

AKO394	1351	GAA	CTA	ACT	CAA	GAT	GAA	ATT	AAA	TGC	CGA	TGG	GAA	AAA	GGC	AAC	TCT	AAC	CCT	TTC	TAT	GAT	TCA	GGC	AGT	GAC
BAD348								C												G						
BAD447																										
BAD456																										
BAD463		G							C													T				
BAD468									C														G			
BAK177																										
BAK232																										
BAK55									C														G			
BAK74																										
LOBAK2									C														G			

AKO394	1426	TCA	GAT	GGC	CCC	TTT	TAA
BAD348				A			
BAD447							
BAD456							
BAD463				A			
BAD468				A			
BAK177				A			
BAK232							
BAK55				A			
BAK74							
LOBAK2				A			

Supplementary Figure S2: Alignment of SFV Bet amino-acid sequences from 11 SFV-infected hunters. Uncultured PBMC samples from 11 SFV-infected hunters accidentally infected by a *Gorilla gorilla* SFV strain were analyzed for the presence of SFV sequences. *bet* ORF-1 and ORF-2 were sequenced and translated. Dots represent identical residues.

AKO394 **1** MDTYQEEES VAS TS GVQDLQTLSELVGP GAAGEGEDT L S DTEEVS KRS RKNTKRGAKMI TFHAYKEI EDKNPQNLKLNWI PTPEEMI NKKVQNQDLGTI LS
 BAD348 E R E
 BAD447 E D
 BAD456 E
 BAD463 E R
 BAD468 E R E
 BAK177 . . . E E R
 BAK232 E D
 BAK55 E R E
 BAK74 E R
 LOBAK2 E R E

AKO394 **102** FGVKHLKGI T S LGRNDPGRDPS AMS P VLP VVTP WPFS QDHYAPTLYGI LLQYYKYS QNNEKI PRVWQFTCLEDP S GKRYMGTRI WVPPLGQVTI QFYKNFVV
 BAD348 . D I
 BAD447
 BAD456
 BAD463 . D . R K
 BAD468 . D I
 BAK177
 BAK232
 BAK55 . D I
 BAK74
 LOBAK2 . D I

AKO394 **205** L T V C Q A V D P W A N W F H G S E E E M Y D I E S E P D V W C S A A L C F K V I Y E G N I N Q K Q E M K S W L C R L G H G H K D G V S E F K R V D L F A M R K R K V N P Y K D K G D P W L Q Y A Y Q V K R
 BAD348 . . I . . L G
 BAD447 G
 BAD456 G
 BAD463 G
 BAD468 . . I . . L G
 BAK177 G
 BAK232 G
 BAK55 . . I . . L G
 BAK74 G
 LOBAK2 . . I . . L G

AKO394 **307** E T K A A N L S D Q A L R W K A L N F H R A L M C D L T N A R I G E G H V A N G Y H M A I E A Y G P Q R G S S E E R V W W K T T S T L G K D E E Y Y R S E G E E E C F P N S P A P H R R T W T E R H K V L A
 BAD348 G
 BAD447 G I
 BAD456 G
 BAD463 G K A
 BAD468 G
 BAK177 G
 BAK232 G I
 BAK55 G
 BAK74 G
 LOBAK2 G

AKO394 **409** L S P F A T P S D I Q K W T R A L P Y K W K V I T S D G D D Y V S M R T V K T L K E L T Q D E I K C R W E K G N S N P F Y D S G S D S D G P F *
 BAD348
 BAD447
 BAD456
 BAD463
 BAD468
 BAK177
 BAK232
 BAK55
 BAK74
 LOBAK2 C