

Table S1. Number of sequences obtained for each participant, time point, and tissue ^a

	PID 1774						PID 1727						PID 1679								
Tissue	PL	PB			LN			PL	PB			LN			PL	PB			LN		
Time point	0	0	3	6	0	3	6	0	0	3	6	0	3	6	0	0	3	6	0	3	6
Step in Pipeline:	Number of gag Sequences:																				
Align sequences from within each sample	32	36	59	37	44	15	39	11	45	19	43	15	46	16	37	23	0	17	16	32	24
Collapse identical sequences that likely result from clonal expansion or PCR resampling (Number of unique gag sequences)	5	7	6	5	9	4	5	4	37	1	4	2	5	3	5	4	0	6	4	13	7
Translate alignments, omit sequences that have stop codons	5	7	5	5	9	4	5	4	37	0	0	2	5	1	5	3	0	2	4	5	0

^a The *gag* sequences from Lorenzo-Redondo *et al.* were downloaded from GenBank (Accession Numbers KT829617–KT831260) and processed as indicated above, using an in-house program to collapse identical sequences and remove sequences with stop codons.