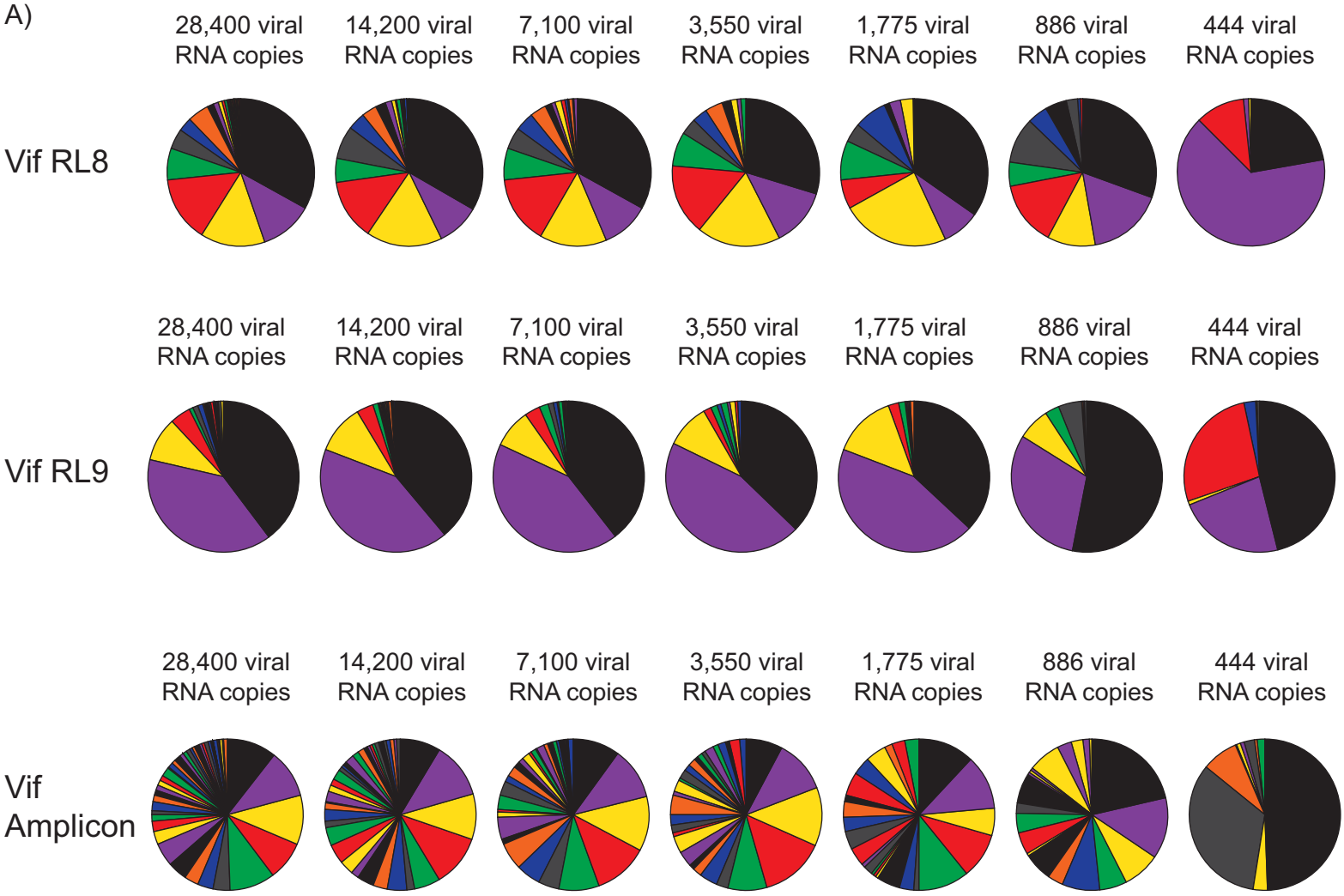
Supplementary Figure 1

A)

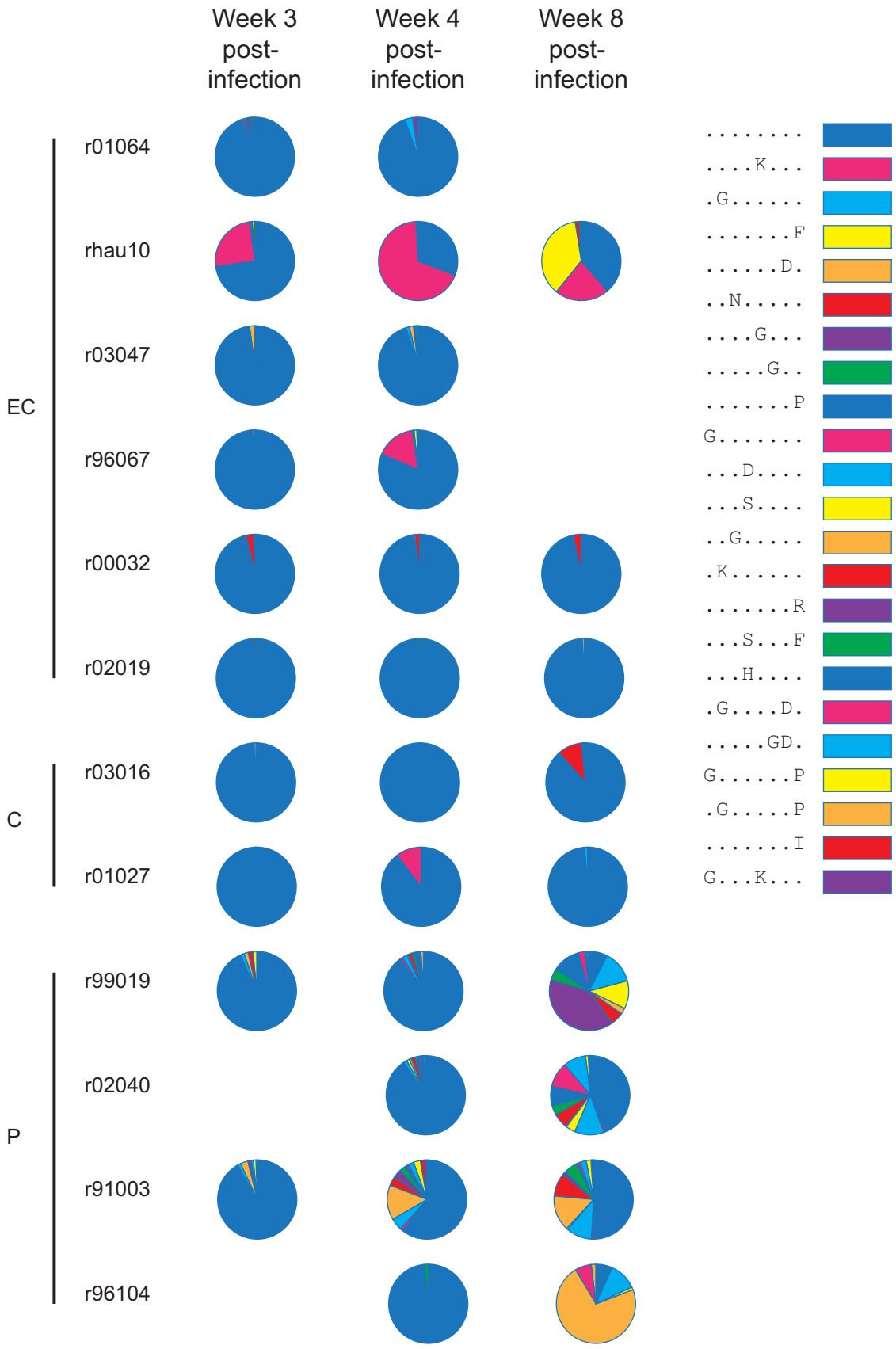


B)

Animal	Input viral RNA copies		
	Week 3	Week 4	Week 8
r01064	30,500	4,740	
rhau10	38,400	4,770	1,643
r03047	22,500	3,170	
r96067	24,880	17,400	3,555
r00032	23,560	8,680	4,035
r02019	33,520	9,090	2,305
r03016	98,000	104,500	2,993
r01027	30,800	13,300	5,750
r99019	58,400	43,750	238,500
r02040	22,600	11,800	24,500
r91003	222,000	25,150	77,500
r96104		44,000	30,500

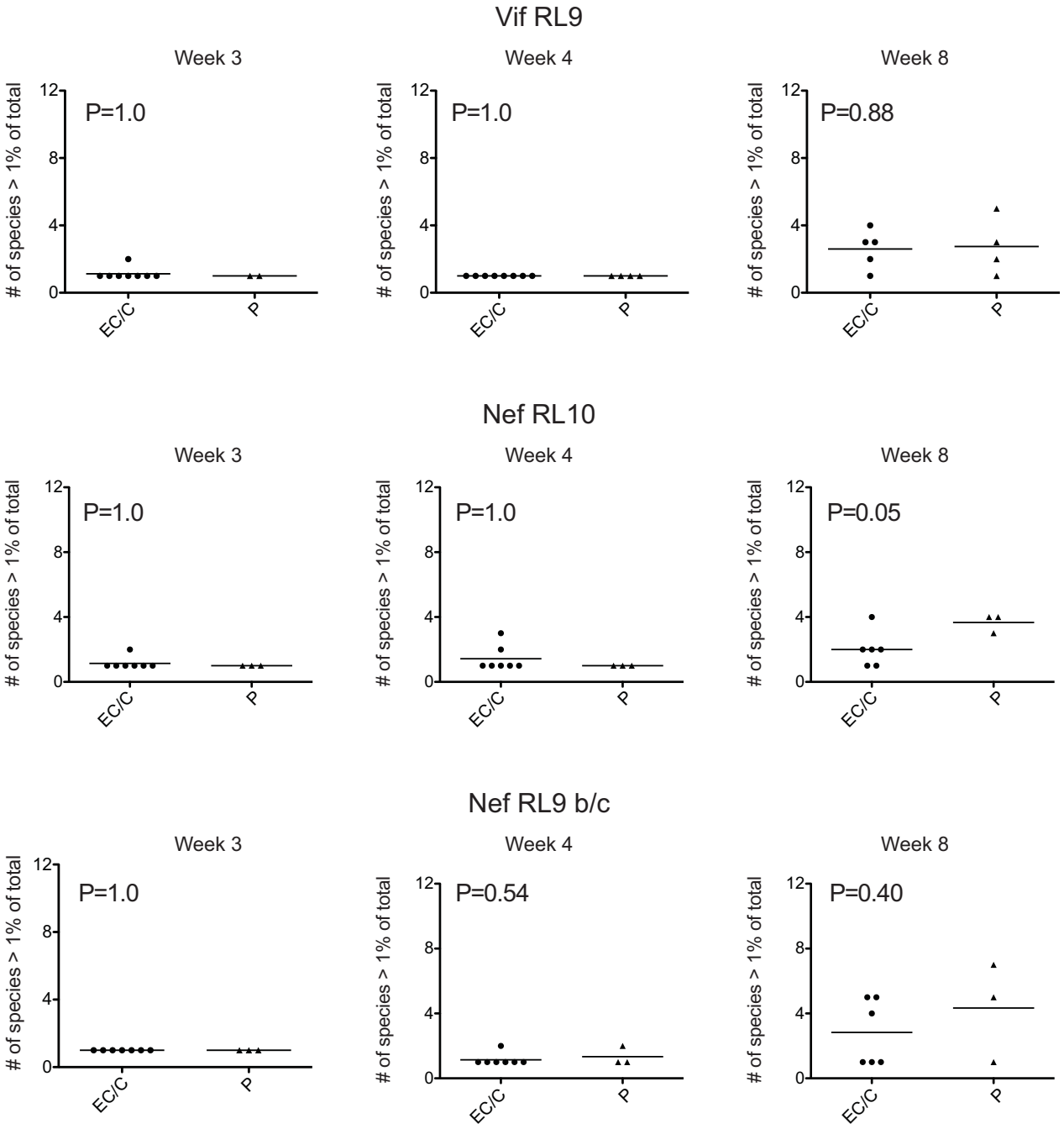
Supplementary Figure 1. PCR re-sequencing bias does not affect the experimental design when input viral RNA quantities greater than or equal to 1,775 viral RNA copies per reaction are used. In panel A), viral RNA prepared from progressor animal r99019 at week 8 post-infection was diluted so that the indicated number of input viral RNA copies were amplified in individual RT-PCR reactions prior to sequencing. Values for input viral RNA copies per reaction were calculated from the quantitative viral load performed on the same sample used for sequencing. Each unique variant present within the viral quasispecies is indicated by a separate color. Vif RL8 (Vif172-179), Vif RL9 (Vif123-131) and the entire amplified region of Vif (Vif Amplicon; Vif123-179) are each analyzed separately. Re-sequencing of specific variants, as indicated by variation in the proportions of the pie graphs, is detected at 886 and 444 viral RNA copies per reaction. In panel B), the input viral RNA copy number is given for each sample sequenced in our study. All samples were sequenced using more than 1,775 viral RNA copies per reaction except for the week 8 sample from rhau10, which contained 1,643 viral RNA copies in each sequenced reaction.

Supplementary Figure 2



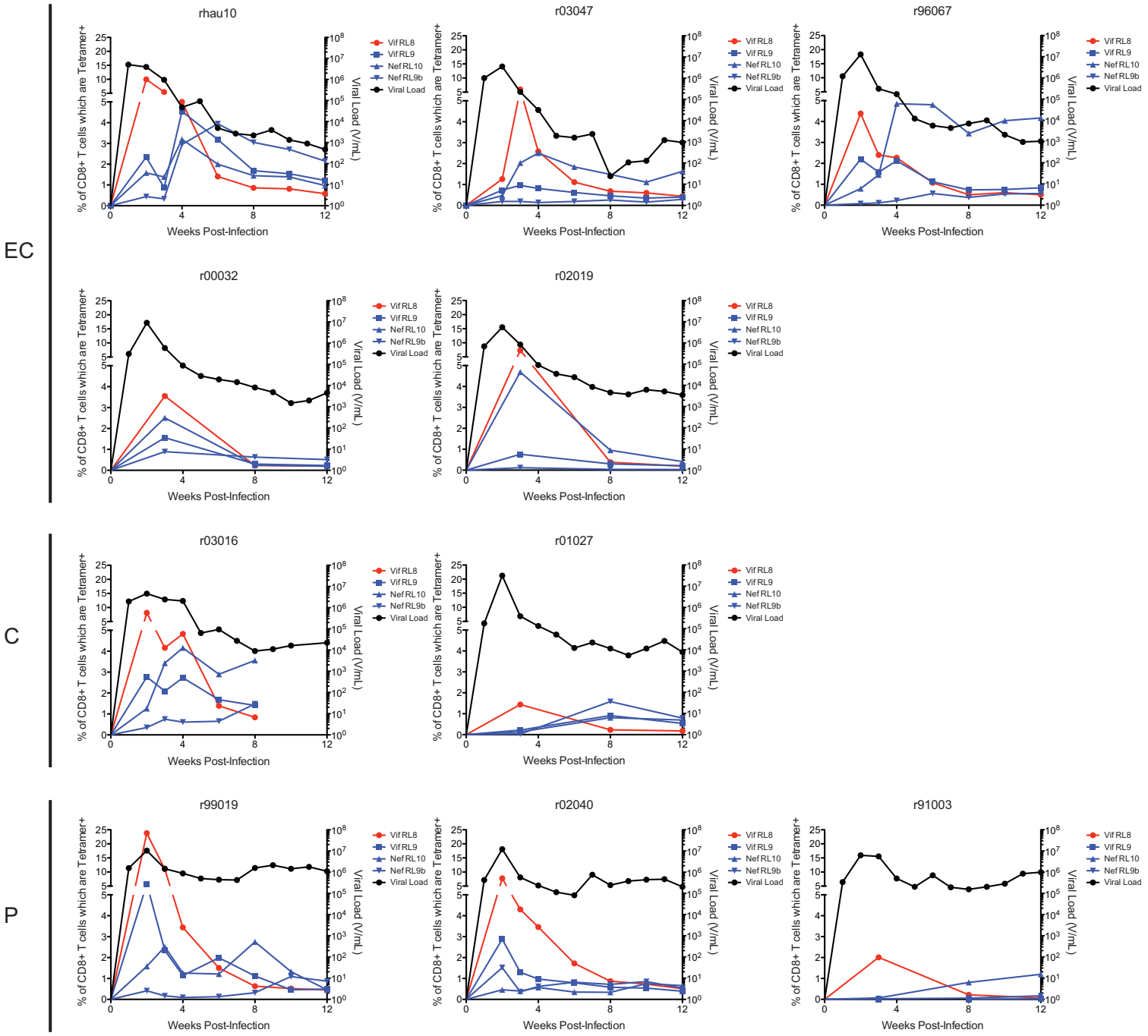
Supplementary Figure 2. Individual viral variants within the Vif RL8 epitope are distinct in progressor animals when compared with animals that control virus. P animals display more sequence diversity when compared with EC and C animals.

Supplementary Figure 3



Supplementary Figure 3. No difference in the diversity of viral quasispecies can be detected during acute infection for the other Mamu-B*00801-restricted immunodominant epitopes comparing EC/C and P animals. The number of viral quasispecies increases at 8 weeks post-infection for all of the immunodominant epitopes, suggesting CD8+ T lymphocyte escape, however, this difference only borders on significance for the Nef RL10 epitope. No significant differences are seen in the other immunodomiant epitopes.

Supplementary Figure 4



Supplementary Figure 4. Viral load and individual MHC class I tetramer responses over time for a subset of SIV-infected Mamu-B*00801+ macaques. Vif RL8 and Vif RL9 T cell responses arise early, detected as soon as 2 weeks post-infection, whereas Nef RL10 and Nef RL9b T cell responses increase gradually, peaking around 4 weeks post-infection.