### Table S4. Estimates of Tajima's D*

| | m | S | ps | Θ | π | D |
|---|---|---|---|---|---|---|
| *gag* | 16 | 34 | 0,02175 | 0,00656 | 0,00545 | -0,699737 |
| *pol* | 16 | 37 | 0,01095 | 0,0033 | 0,0031 | -0,253388 |
| *env* | 16 | 22 | 0,01116 | 0,00336 | 0,00304 | -0,390221 |

*All positions containing gaps or missing data were eliminated. There were 1563 positions for gag, 3378 for pol, and 1971 for env in the final dataset.

Abbreviations: m = number of sequences; S = Number of segregating sites; ps = S/m; Θ = ps/a1; π = nucleotide diversity

D is the Tajima test statistic