

**Table S3. Estimates of the overall *dn* and *ds* distance and the *dn/ds* ratios**

|            | <i>dn</i>   | <i>ds</i>   | <i>dn/ds</i> |
|------------|-------------|-------------|--------------|
| <i>gag</i> | 0.003±0.001 | 0.013±0.003 | 0,23         |
| <i>pol</i> | 0.002±0.001 | 0.005±0.002 | 0,4          |
| <i>env</i> | 0.003±0.001 | 0.004±0.002 | 0,75         |

\*To include the polymorphisms in all phases the analysis involved 16 KoRV sequences.  
 Codon positions included were 1st+2nd+3rd.  
 All positions containing gaps or missing data were eliminated.  
 There were 521 codon positions for *gag*, 1126 for *pol*, and 657 for *env* in the final dataset.