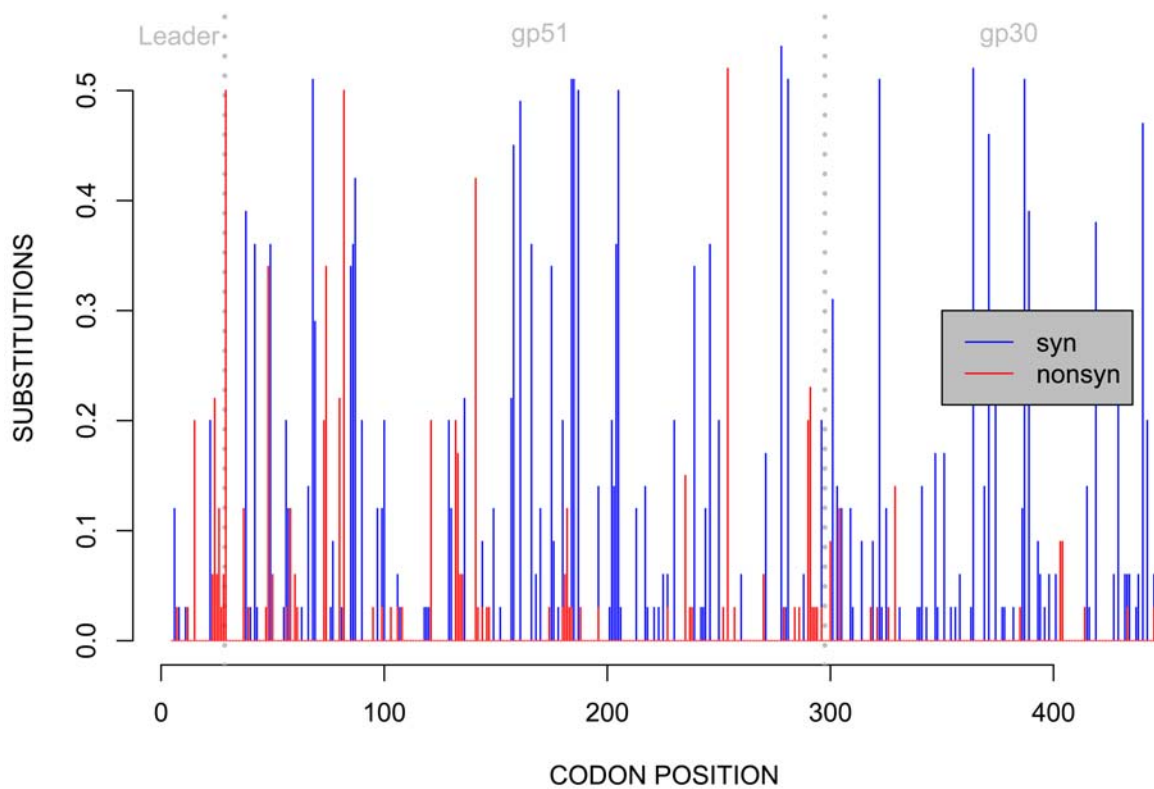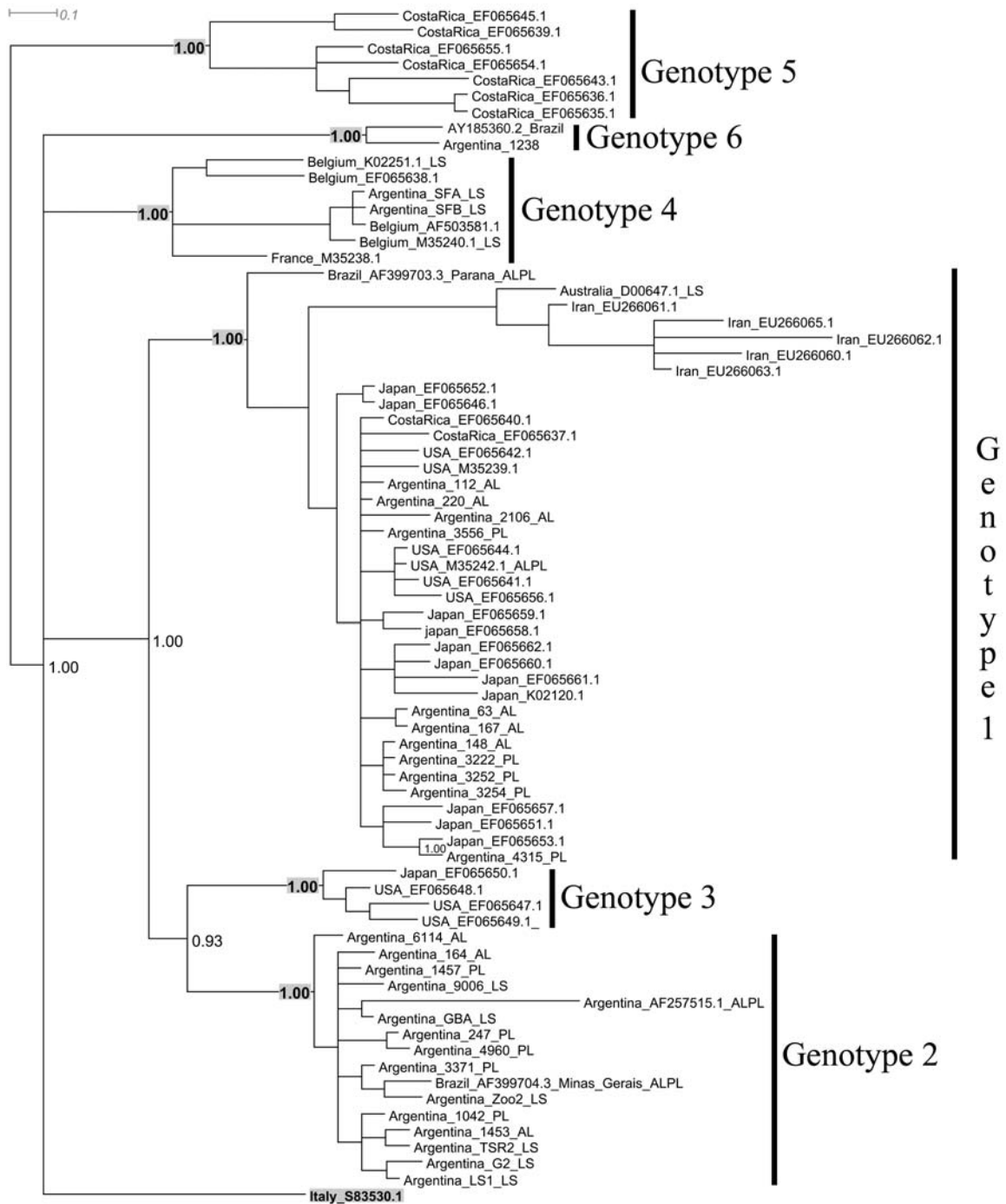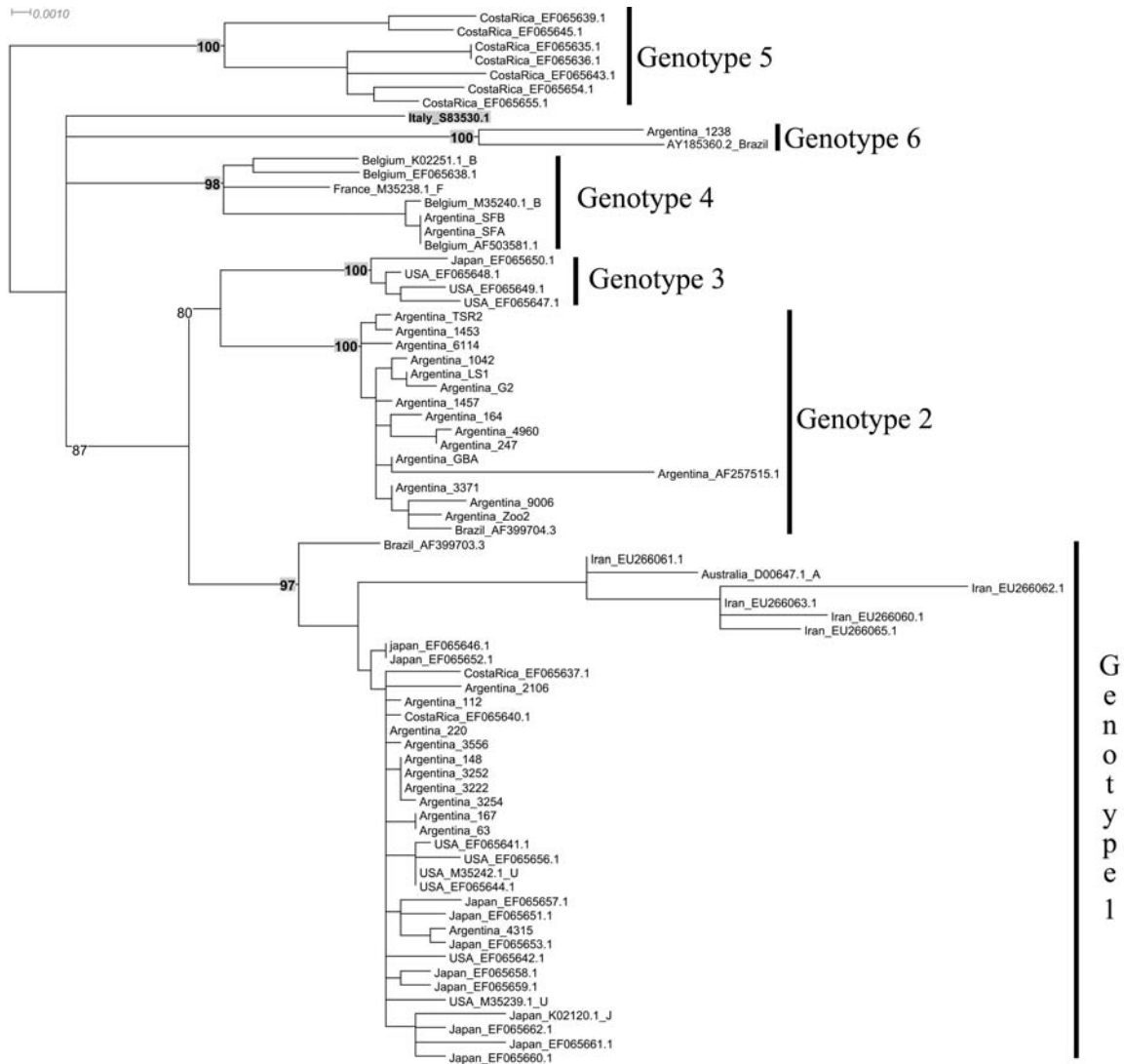**Supplementary Fig. S1.** Distribution of informative (red) and uninformative (blue) substitutions along the 74 *env* sequences analysed. The *x*-axis corresponds to sequence positions relative to the reference sequence K02120.1. The *y*-axis corresponds to the number of nucleotide substitutions given in the phylogenetic tree, which was obtained with TNT.

Rodriguez, S. M., Golemba, M. D., Campos, R. H., Trono, K. & Jones, L. R. (2009). Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two new clades. *J Gen Virol* **90**, 2788–2797.

Supplementary Fig. S2. Distribution of synonymous (blue) and non-synonymous (red) substitutions along the 74 *env* sequences analysed. The *x*-axis corresponds to sequence positions relative to the reference sequence K02120.1. The *y*-axis corresponds to the mean number of substitutions in pair-wise sequence comparisons.

Rodriguez, S. M., Golemba, M. D., Campos, R. H., Trono, K. & Jones, L. R. (2009). Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two new clades. *J Gen Virol* **90**, 2788–2797.

Supplementary Fig. S3. Maximum-likelihood phylogenetic tree of 74 *env* sequences from different geographical locations worldwide (Supplementary Table S1). Genotypes 1 to 6, which were identified here, are indicated with vertical lines. The tree is rooted on genotype 5 for improved display. Numbers on nodes indicate bootstrap support (*n*=100). The strain from Italy that does not cluster in any of the six genotypes is indicated with a grey background.

Rodriguez, S. M., Golemba, M. D., Campos, R. H., Trono, K. & Jones, L. R. (2009). Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two new clades. *J Gen Virol* **90**, 2788–2797.

Supplementary Fig. S4. Bayesian phylogenetic tree of 74 *env* sequences from different geographical locations worldwide (Supplementary Table S1). Genotypes 1 to 6, which were identified here, are indicated with vertical lines. The tree is rooted on genotype 5 for improved display. Numbers on nodes indicate posterior probabilities. The strain from Italy that does not cluster in any of the six genotypes is indicated with a grey background.

Rodriguez, S. M., Golemba, M. D., Campos, R. H., Trono, K. & Jones, L. R. (2009). Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two new clades. *J Gen Virol* **90**, 2788–2797.

Supplementary Fig. S5. Neighbour-joining phylogenetic tree of 74 *env* sequences from different geographical locations worldwide (Supplementary Table S1). Genotypes 1 to 6, which were identified here, are indicated with vertical lines. The tree is rooted on the genotype 5 for improved display. Numbers on nodes indicate bootstrap support (*n*=100). The strain from Italy that does not cluster in any of the six genotypes is indicated with a grey background.

Rodriguez, S. M., Golemba, M. D., Campos, R. H., Trono, K. & Jones, L. R. (2009). Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two new clades. *J Gen Virol* **90**, 2788–2797.