**CORRECTION**

# Correction to: Application of the SureSelect target enrichment system for next-generation sequencing to obtain the complete genome sequence of bovine leukemia virus

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**Correction to: Archives of Virology**
**https://doi.org/10.1007/s00705-018-3957-9**

Unfortunately, Figure 1 was incorrectly published in the original publication and the correct version is updated here.

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**Fig. 1** **a.** Maximum-likelihood phylogenetic tree constructed for the complete nucleotide sequences of four Vietnamese strains (indicated by ●), three Paraguayan strains (indicted by ■), three Chinese strains (indicated by ▲), and reference strains obtained from the GenBank database. Genotypes G1–G10 are indicated on the right of the figure. The bar at the bottom of the figure denotes evolutionary distance. **b.** Maximum-likelihood phylogenetic tree for the complete BLV *pol* gene sequences of four Vietnamese strains (indicated by ●), three Paraguayan strains (indicated by ■), three Chinese strains (indicated by ▲), and reference strains obtained from the GenBank database. Genotypes G1–G10 are indicated on the right of the figure. The bar at the bottom of the figure denotes evolutionary distance. **c.** Maximum-likelihood phylogenetic tree for the complete BLV *tax* gene sequences of four Vietnamese strains (indicated by ●), three Paraguayan strains (indicated by ■), three Chinese strains (indicated by ▲), and reference strains obtained from the GenBank database. Genotypes G1–G10 are indicated on the right of the figure. The bar at the bottom of the figure denotes evolutionary distance