## West Nile Virus Lineage 2 in Horses and Other Animals with Neurologic Disease, South Africa, 2008–2015

## **Technical Appendix**

**Technical Appendix Table.** Association of clinical signs with West Nile virus positivity among 1,069 horses, South Africa, 2008–2015\*

	Adjusted odds ratio (95% CI)	
iable	Model 1	Model 2
d or euthanized	1.48 (0.90–2.43)	1.42 (0.84–2.39)
/er	1.25 (0.75-2.06)	0.87 (0.52-1.47)
urologic signs		
ny†	4.12 (1.59–10.70)	
taxia		0.96 (0.54-1.72)
Paralysis		1.82 (0.78-4.24)
Paresis		2.74 (1.30–5.79)
Recumbent		0.32 (0.11-0.88)
Seizure		1.47 (0.47-4.58)
ongue paralysis		7.73 (1.27–47.18)
er signs		
norexia		0.40 (0.15–1.04)
cterus		1.55 (0.63–3.77)
Rectal prolapse		5.93 (0.94-37.26)
d or euthanized ver urologic signs ny† taxia Paralysis Parasis Recumbent seizure ongue paralysis ter signs norexia cterus Rectal prolapse	1.48 (0.90–2.43) 1.25 (0.75–2.06) 4.12 (1.59–10.70)	1.42 (0.84–2.39 0.87 (0.52–1.47 1.82 (0.78–4.24 2.74 (1.30–5.79 0.32 (0.11–0.88 1.47 (0.47–4.58 7.73 (1.27–47.18 0.40 (0.15–1.04 1.55 (0.63–3.77 5.93 (0.94–37.26

\*For model 1, death, fever, and the presence of any neurologic sign were used as covariates. For model 2, death, fever, and a specific neurologic and nonneurologic sign were used as covariates.

†Defined as the presence of any specific neurologic sign or the clinician indicated that it was a neurologic case without indicating specific neurologic signs.



**Technical Appendix Figure.** Maximum likelihood analysis of West Nile virus (WNV) nonstructural protein 5 (NSP5) region sequences used to determine the lineage of WNV isolates from South Africa, 2008–2015. GenBank accession numbers of study isolates are indicated in parentheses. Maximum likelihood phylogram was recovered from a RAxML analysis excluding invariable sites on the NSP5 region of WNV. Bootstrap support (850 replicates using the autoMRE bootstopping criterion in RAxML) with values ≥70 are indicated on branches. JEV, Japanese encephalitis; KUN, Kunjin virus.