

Supporting Information

Coffey et al. 10.1073/pnas.0712130105

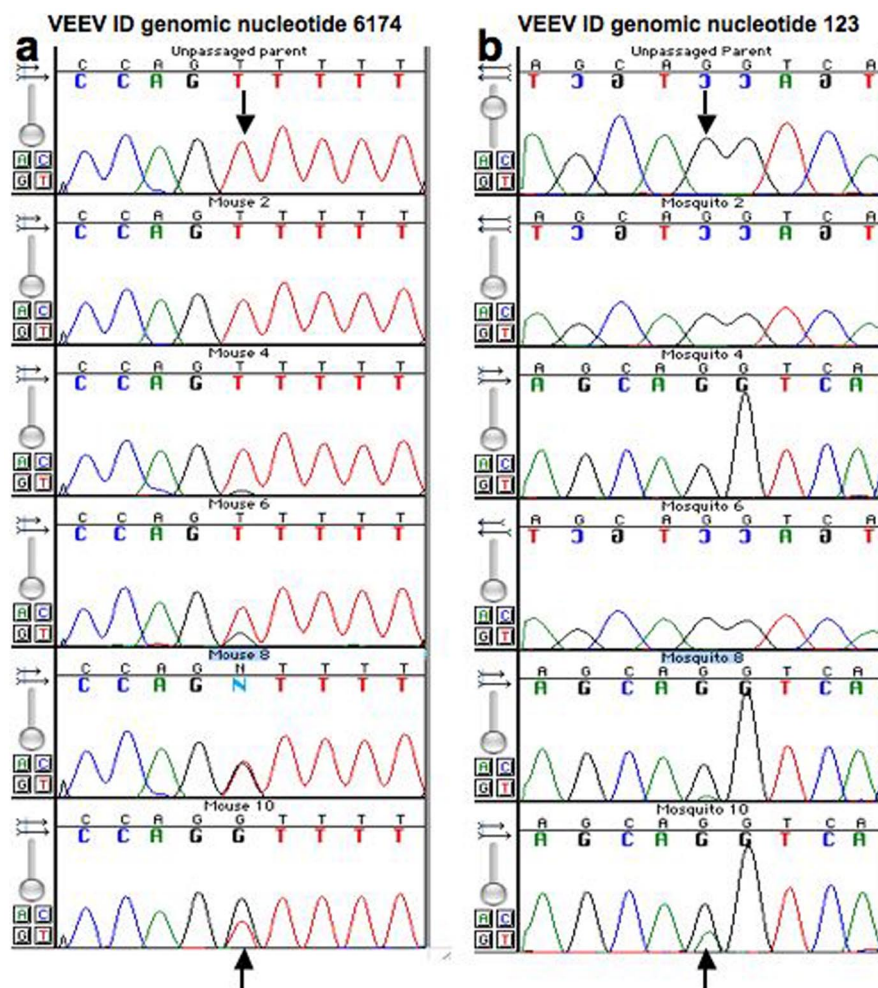








Fig. S1. Sequencing chromatograms for VEEV 8131 isolated from sera of every second mouse in the serial vertebrate passage series (a) or every second mosquito pool in the serial invertebrate passage series (b). Arrows indicate the development of mixed nucleotide populations; by the 10th mouse passage, the mutant guanine was dominant over the parental thymine (a), and the mutant nucleotide (adenine) was increasing in intensity with serial mosquito passage (b). Labels above each chromatogram correspond to the mouse/mosquito pool number.

Table S1. Genetic differences between parent, serial, and alternately *in vivo*-passaged VEE ID and IC viruses

VEEV subtype	Passage Series	Nucleotide differences vs. parent	Genome position	Gene	Amino acid change Parent->Progeny
enzootic ID		4	2889 3807 3918 6726	nsP2 nsP2 nsP3 nsP4	no no no no
		0 (1 mixture)	123 (mixture)	nsP1	no
		1	6174	nsP4	Arg » Ser
epizootic IC		3	2468 7175 8854	nsP2 nsP4 E2	no no no
		0	n.a.	n.a.	n.a.
		1	6541	nsP4	Met » Leu

n.a., not applicable.