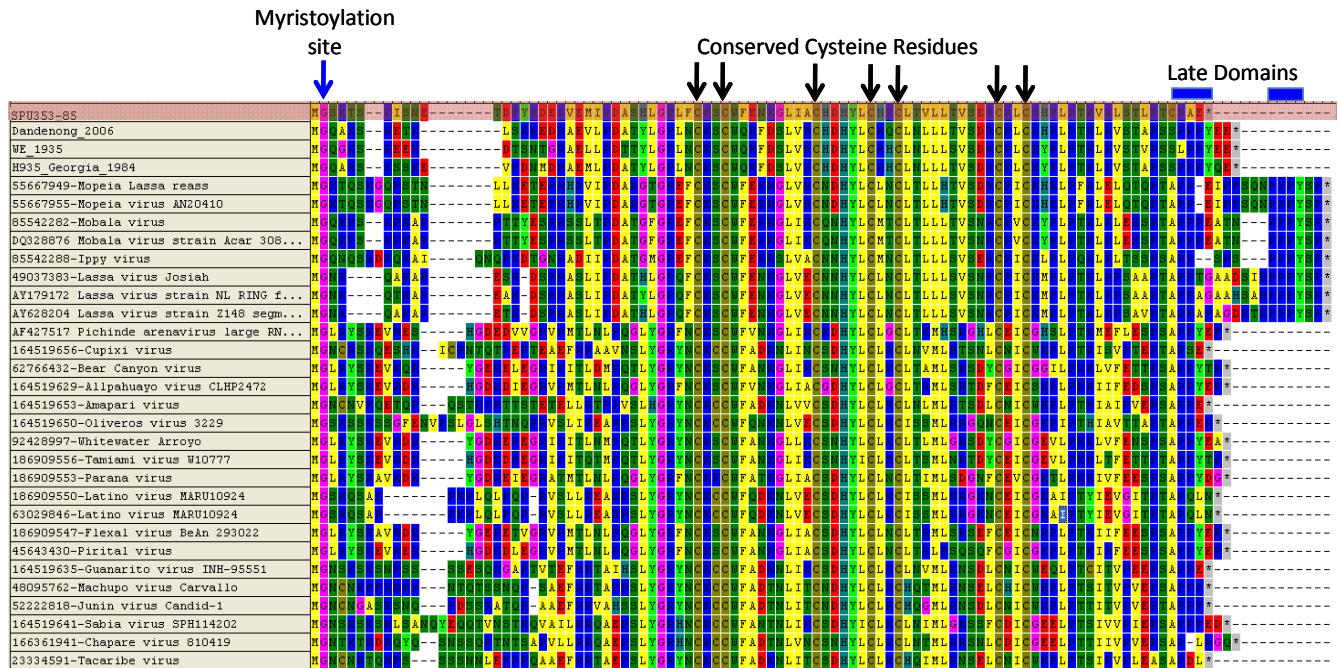
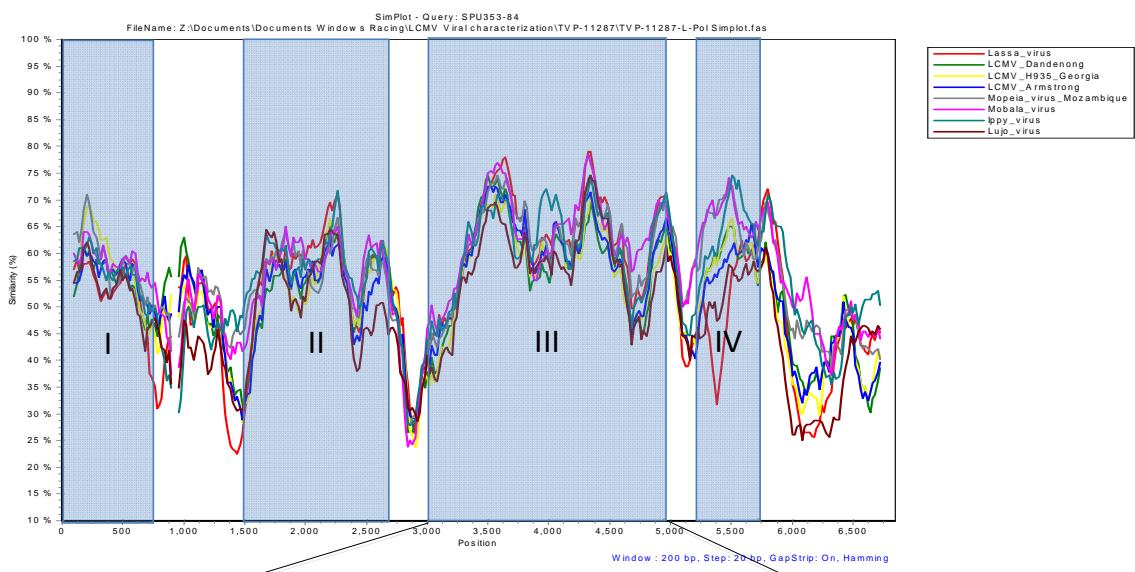


**Supplementary Fig. S1.** Bayesian analyses of Merino Walk virus (MWV), inferred based on the NP nucleotide sequence.

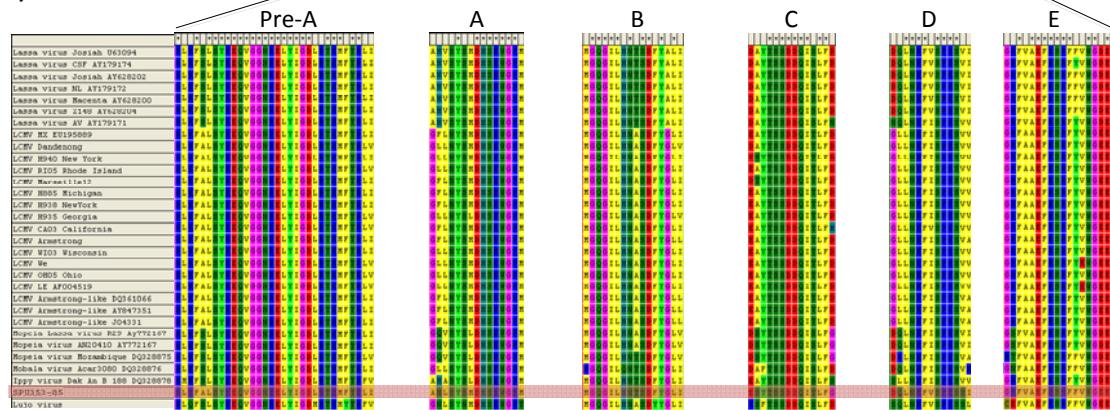


**Supplementary Fig. S2.** Motifs in the Z protein of MWV conserved with other Arenaviruses. The shortened Z protein of MWV contains neither conserved late domain.

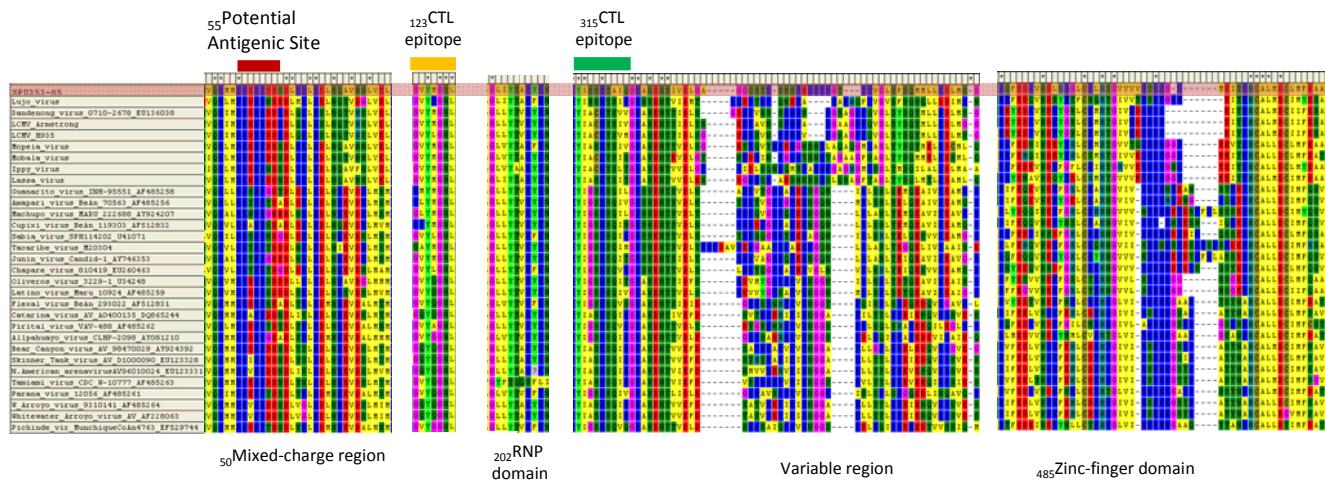
(a)



(b)

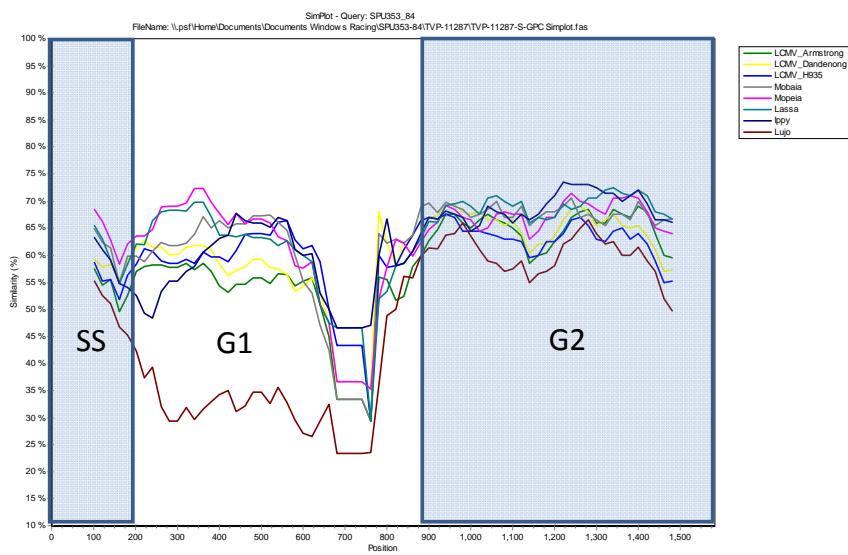


**Supplementary Fig. S3.** Simplot of L segment (a) and motifs (b) in region III (pre-A, A, B, C, D, E) of MWV conserved with other Old World arenaviruses.

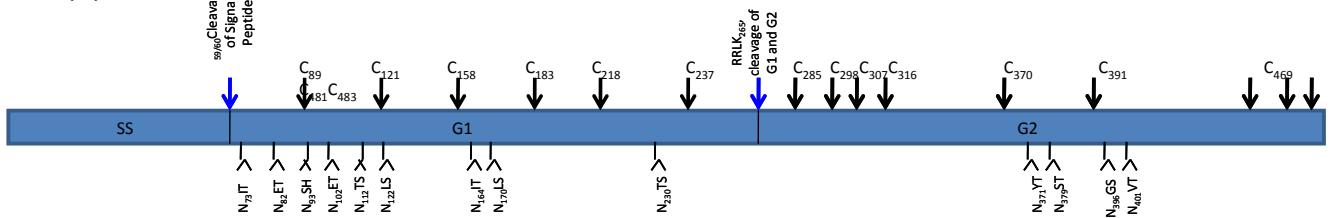


**Supplementary Fig. S4.** Motifs, variable region and zinc-finger domain in the nucleocapsid protein of MWV conserved with other arenaviruses.

(a)



(b)



**Supplementary Fig. S5.** Simplot of the M segment (a) with other Old World arenaviruses and conserved motifs (b) among the signal sequence, G1 and G2 proteins.