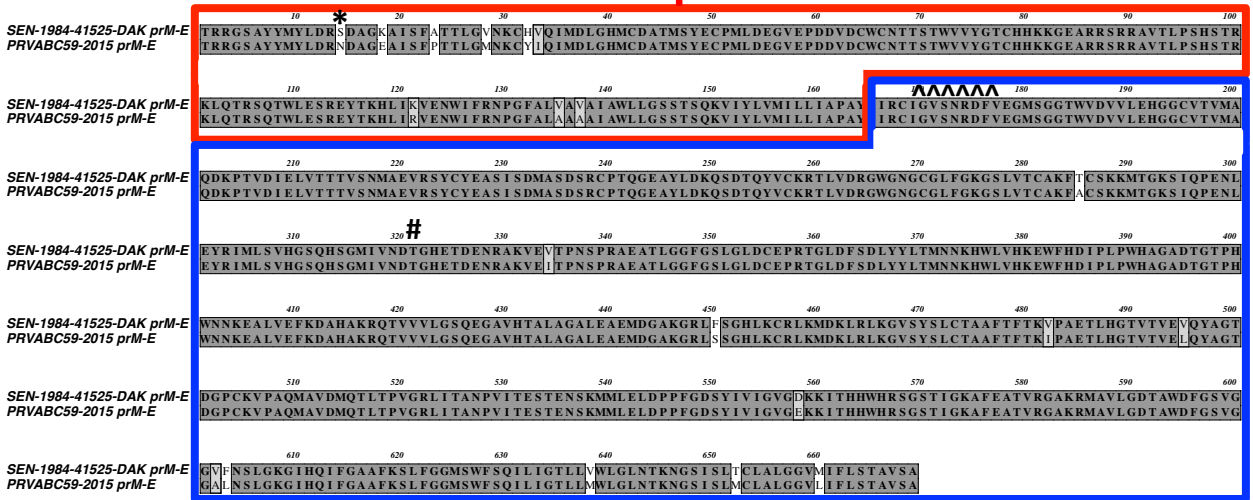


Efficacy of a T Cell-Biased Adenovirus Vector as a Zika Virus Vaccine

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Supplementary Figure 1

prM



Envelope

Supplementary Figure 1

Alignment of the African strain ZIKV Dakar 41525 to the Asian strain ZIKV PRVABC59.

A ClustalW alignment of the prM-E region from the African ZIKV Dakar 41525 strain used in the challenge studies and the Asian ZIKV PRVABC59 strain used in the construction of the vectored vaccine. The CD8⁺ T cell epitope E₄₋₁₂ is indicated by a ^ symbol(37). The * symbol indicates a S139N mutation that is associated with increased virulence in neural progenitor cells (54). The # symbol indicates a motif associate with increased virulence (55).

Supplementary Table 1

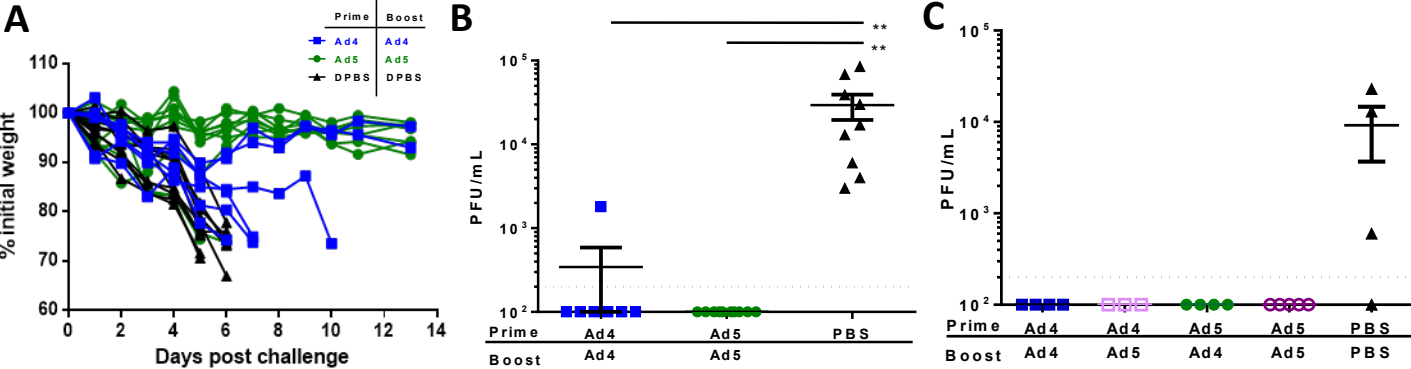
Peptide #	Sequence	Position (E#1-504)
1	IRCIGVSNRDFVEGM	1-15
2	IGVSNRDFVEGMSGG	4-18
3	SNRDFVEGMSGGTWV	7-21
6	SGGTWVDVLEHGGC	16-30
8	DVLEHGGCVTMAQ	22-36
19	EVRSYCYEASISDMA	55-69
21	YEASISDMASDSRCP	61-75
24	SDSRCPTQGEAYLDK	70-84
25	RCPTQGEAYLDKQSD	73-87
102	SYSLCTAAFTFKIP	304-318
103	LCTAAFTFKIPAET	307-321
104	AAFTFKIPAETLHG	310-324
119	VGRLITANPVITEST	355-369
120	LITANPVITESTENS	358-372
123	ESTENSKMMLELDPP	367-381
124	ENSKMMLELDPPFGD	370-384

Supplementary Table 1

The positive peptides in T-cell mapping of the E region of ZIKV.

The peptides determined to be positive during the T-cell mapping of the Envelope region of ZIKV as indicated in Fig. 3. Peptides were positive if the response was 4 times that of the PBS sham vaccinated mice. Amino acid sequence and position number on the E protein are indicated.

Supplementary Figure 2



Supplementary Figure 2

Individual mice weight loss during the *lfnar1*^{-/-} mice challenge and viremia on day 4 post infection based on plaque assay.

The individual mouse weights during the challenge of the *lfnar1*^{-/-} mice in Fig. 5 are plotted in (A). The plaque forming units per mL (PFU/mL) in the sera at day 4 post infection in the *lfnar1*^{-/-} challenge model (B) (p<0.01; one-way ANOVA) and anti-*lfnar1* challenge model (C). Data are expressed as the mean with standard error (SEM).

500 vp/cell

1 MOI

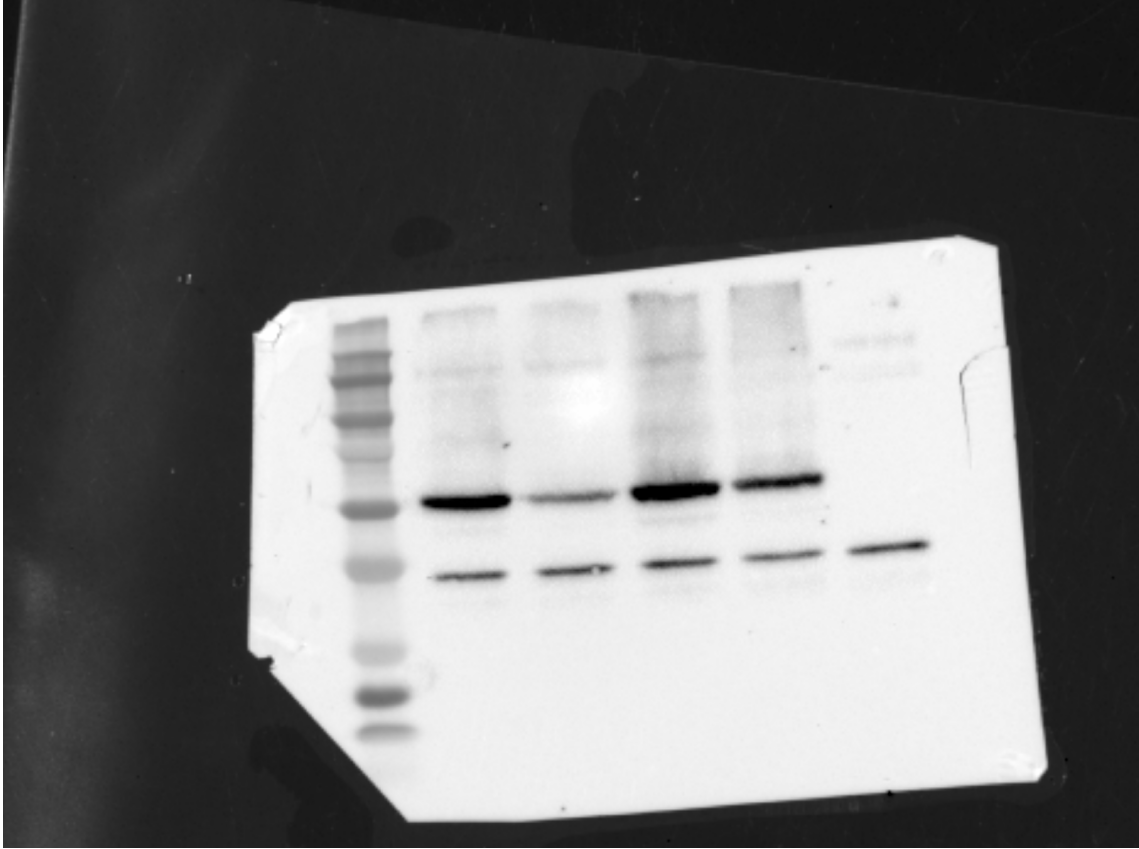
Ad5-
prME

Ad4-
prME

Ad5-
prME

Ad4-
prME

Uninfected



ZIKV-E
GAPDH