

PNAS

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Supplementary Information for

Cross-genotype protection of live-attenuated vaccine candidate for severe fever with thrombocytopenia syndrome virus in a ferret model.

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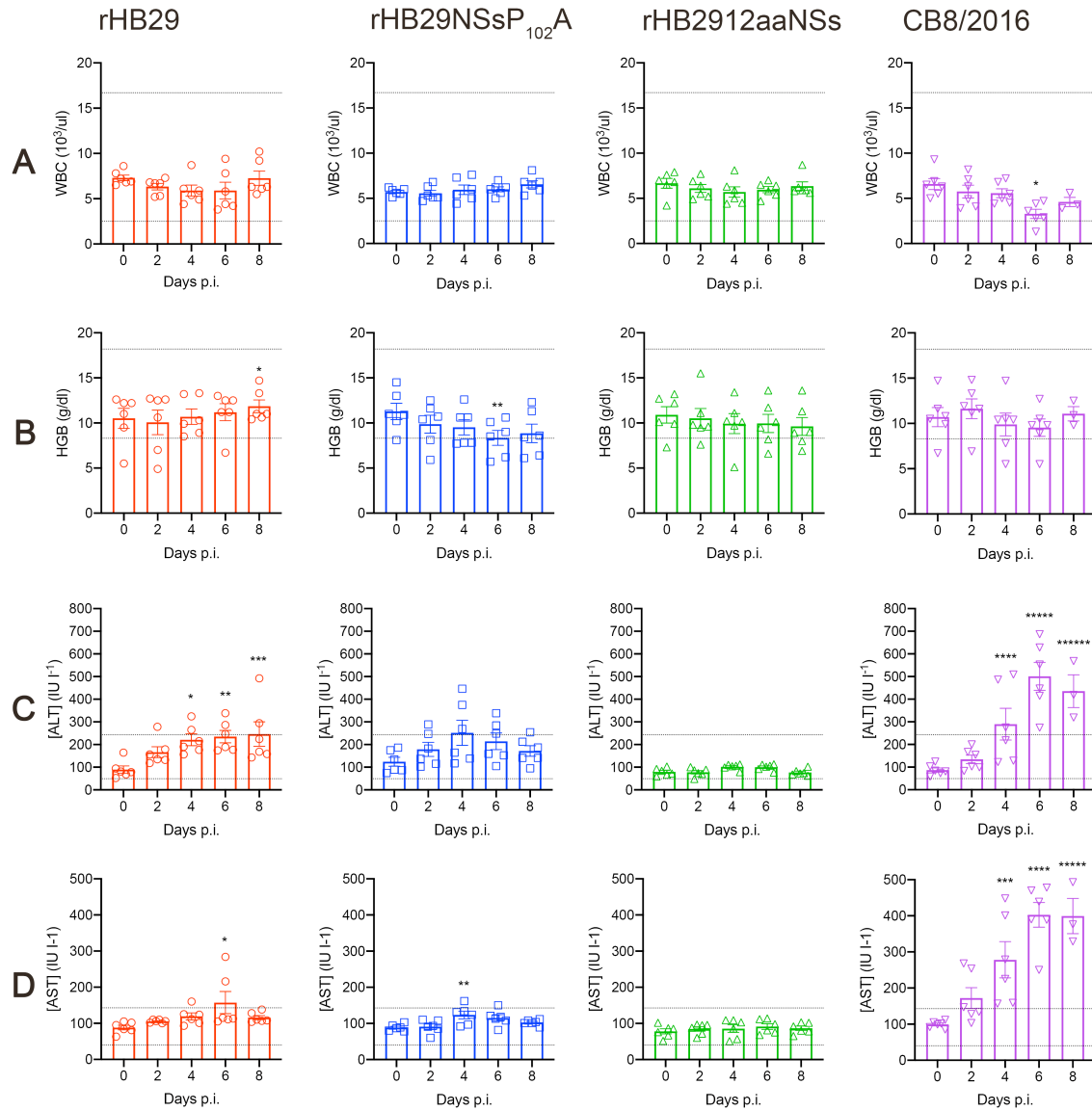


Fig S1. Hematological analysis of aged ferrets infected with recombinant or CB8/2016 SFTS viruses. (A-D) The aged ferrets in each group were inoculated with 4×10^6 PFU of rHB29 (red), 4×10^6 PFU of rHB29NSsP₁₀₂A (blue), 5×10^5 PFU of rHB2912aaNSs (green) or 5×10^5 PFU of CB8/2016 (purple) and White blood cell, WBC (A), Haemoglobin, HGB (B), Alanine transaminase, ALT (C) and Aspartate transaminase, AST (D) were analyzed until 8 days p.i. (n=6). The mean values are shown \pm standard error the mean. The asterisks indicate significance compared to each day p.i. sample by the one-way ANOVA with Dunnett's multiple comparison test. *P=0.0017 (A); *P=0.0265, **P=0.0129, ***P=0.007, ****P=0.0244, *****P<0.0001, and *****P=0.0015, (C); and *P=0.0107, **P=0.0092, ***P=0.004, ****P<0.0001, and *****P=0.0002 (D).

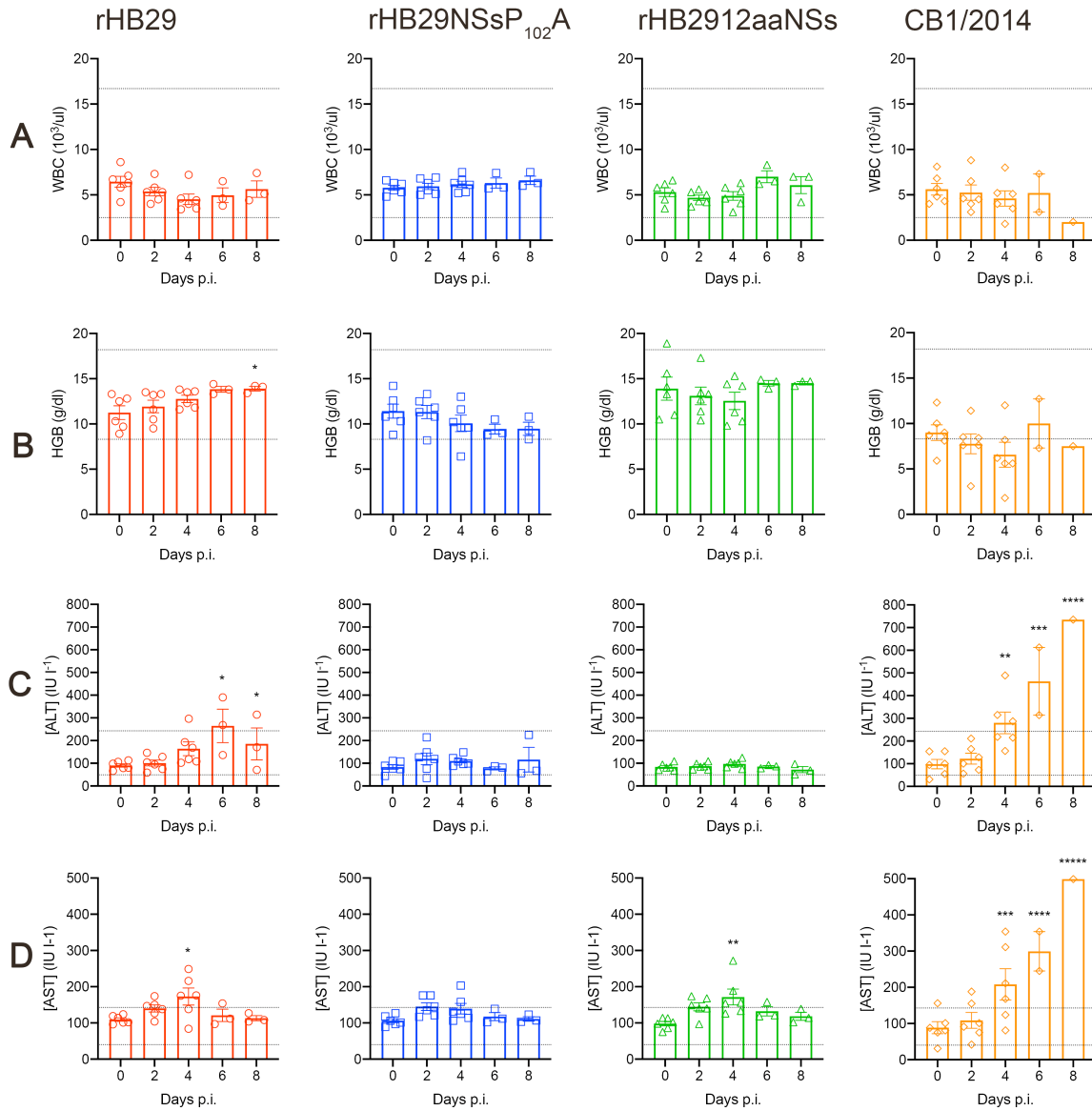


Fig S2. Hematological analysis of aged ferrets after challenged with CB1/2014 SFTS viruses. (A-D) Groups of ferrets vaccinated with rHB29 (red), rHB29NSsP₁₀₂A (blue), rHB2912aaNSs (green), respectively were challenged with CB1/2014. PBS-immunised ferrets were also infected with CB1/2014 (orange) as a control. WBC (A), HGB (B), ALT (C) and AST (D) were analyzed until 8 days p.i. (n=6). The mean values are shown \pm standard error the mean. The asterisks indicate significance compared to each day p.i. sample by the one-way ANOVA with Dunnett's multiple comparison test. *P = 0.0493 (B); *P = 0.0095, **P = 0.0154, ***P = 0.0009, and ****P < 0.0001 (C); and *P = 0.0160, **P = 0.0493, ***P = 0.0042, ****P = 0.0423, *****P = 0.0101, and *****P = 0.0003 (D).

Table S1. Identity of amino acid differences in open reading frames of SFTSV genotypes B and D. L (RNA-dependent RNA polymerase), M (M polyprotein), NSs (non-structural protein) and N (nucleocapsid protein) open reading frames.

Gene	Position	Amino acid in			
		Genotype D	Genotype D	Genotype D	Genotype B
		HB29*	CB8/2016 [#]	NSsP _{102A} *	CB1/2014 [†]
L	2	N	D	N	D
	264	D	D	D	N
	314	G	G	G	S
	566	F	Y	F	Y
	651	V	I	V	I
	719	N	S	N	S
	795	S	F	S	S
	835	K	R	K	R
	856	K	K	K	R
	1038	T	S	T	S
	1397	S	N	S	N
	1433	A	T	A	A
	1447	M	M	M	T
	1684	K	R	K	R
	1717	V	V	V	I
	1745	S	S	S	N
1903	N	N	N	S	
M	21	S	S	S	T
	37	G	G	G	N
	114	E	G	E	G
	218	G	G	G	S

272	K	K	K	E	
273	A	A	A	T	
300	E	D	E	E	
321	T	M	T	M	
371	R	K	R	K	
385	S	T	S	T	
3944	H	Q	H	Q	
404	T	T	T	A	
457	L	I	L	L	
470	T	T	T	S	
501	V	M	V	M	
506	G	G	G	R	
525	I	V	I	V	
587	P	P	P	S	
662	T	T	T	A	
737	I	T	I	T	
960	R	S	R	S	
962	D	G	D	D	
995	T	T	T	S	
1011	N	N	N	S	
1017	F	S	F	S	
1058	L	S	L	S	
1070	T	T	T	S	
NSs	102	P	P	A	P
	130	R	K	R	R
	197	L	M	L	M
	207	P	S	P	S

	223	V	V	V	I
	228	T	T	T	A
	243	V	A	V	V
	245	H	Q	H	Q
	249	H	H	H	Y
	278	I	I	I	V
	281	R	R	R	K
	291	K	K	K	E
N	51	V	V	V	M
	52	K	K	K	E

* based on accession numbers AJD86038 (L), AJD86039 (M), AJD86041 (NSs), AJD86040 (N).

based on accession numbers QDF82697 (L), QDF82698 (M), QDF82699 (NSs), QDF82700 (N).

† based on accession numbers ASW22982 (L), ASW22985 (M), ASW22988 (NSs), ASW22989 (N).