

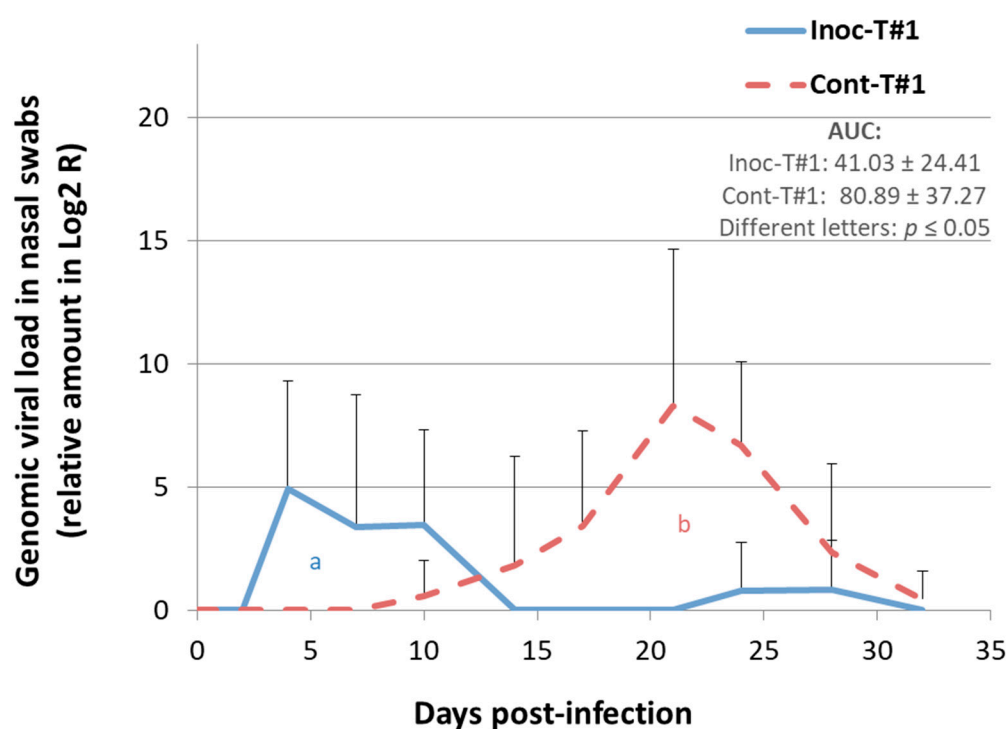
# Supplementary Materials:

**Table S1:** Presentation of the vaccine strains isolated from vaccinated and contact pigs from Trial#1 and Trial#2.

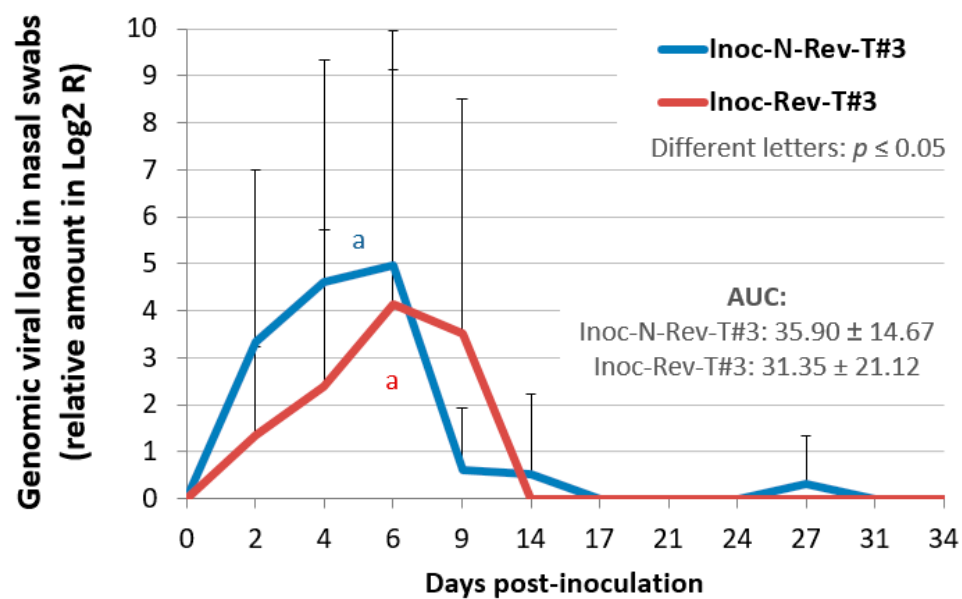
Trial	Inoculated or Contact pig	Pen	Pig No.	Dpi selected for DV strain isolation
#1	Inoc	1	2012_1	14
	Inoc	1	2012_2	10
	Inoc	1	2012_3	7
	Cont	1	2012_4	14
	Cont	1	2012_5	21
	Cont	1	2012_6 **	21
	Inoc	2	2012_7 *	14
	Inoc	2	2012_8	10
	Inoc	2	2012_9	10
	Cont	2	2012_10	17
	Cont	2	2012_11	24
#2	Inoc	1	2017_12	10
	Inoc	1	2017_13	14
	Inoc	1	2017_14	14
	Cont	1	2017_15	21
	Cont	1	2017_16	17
	Cont	1	2017_17	24
	Inoc	2	2017_18	14
	Inoc	2	2017_19	17
	Inoc	2	2017_20	17

Cont	2	2017_21	24
Cont	2	2017_22	21
Cont	2	2017_23	24

The days post-infection (dpi) chosen for the DV strain isolation was selected at viremia peak for each pig. Dpi, days post-infection; inoc, inoculated; cont, contact. \* Isolate from the pig No. 2012\_7 was used as inoculum in Inoc-N-Rev-T#3 inoculated pigs from Trial#3. \*\* Isolate from the pig No. 2012\_6 was used as inoculum in Inoc-Rev-T#3 inoculated pigs from Trial#3.



**Figure S1:** Evolution of the mean genomic viral loads (relative amount expressed in Log2 R) in inoculated Inoc-T#1 and contact Cont-T#1 pigs in nasal swab supernatants after inoculation (day 0) during Trial#1. Different letters ("a" and "b") indicate that the groups are significantly different from each other after comparison of Area Under the Curve (AUC) values with  $p \leq 0.05$ .



**Figure S2:** Evolution of the mean genomic viral loads (relative amount expressed in Log2 R) in Inoc-N-Rev-T#3 and Inoc-Rev-T#3 inoculated pigs in nasal swab supernatants after inoculation (day 0) during Trial#3. Different letters indicate that the groups are significantly different from each other after comparison of of Area Under the Curve (AUC) values with  $p \leq 0.05$ .

P1-I-2012											
2012_1		2012_2		2012_3		2012_7 *		2012_8		2012_9	
nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa
				T>G	L>W			T>G	L>W	T>G	L>W
				1066	282			1066	282	1066	282
		T>C	S>P					T>C	S>P		
		2472	751					2472	751		
A>G	N>D			A>G	N>D						
2505	762			2505	762						
				G>T	R>I						
				2572	784						
		C>T	T>M					C>T	T>M		
		2644	808					2644	808		
C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S		
2895	892	2895	892	2895	892	2895	892	2895	892		
C>T	P>S									C>T	P>S
2928	903									2928	903
C>T	P>L	C>T	P>L			C>T	P>L	C>T	P>L		
3325	1035	3325	1035			3325	1035	3325	1035		
		C>T	S>L					C>T	S>L		
		11836	14					11836	14		
				A>G	N>S						
				11995	67					A>G	N>S
T>C	Y>H										
12234	147										
		G>A	A>T					G>A	A>T		
		12470	23					12470	23		
										T>C	S>P
										12575	58
T>C	S>P	T>C	S>P	T>C	S>P			T>C	S>P		
12689	96	12689	96	12689	96			12689	96		
						G>A	R>Q				
						13029	266				
T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L
13571	25	13571	25	13571	25	13571	25	13571	25	13571	25
		A>G	N>S					A>G	N>S		
		14014	174					14014	174		

P2-C-2012											
2012_4		2012_5		2012_6 **		2012_10		2012_11			
nt	aa	nt	aa	nt	aa	nt	aa	nt	aa		
T>G	L>W					T>G	L>W	T>G	L>W		
1066	282					1066	282	1066	282		
								A>G	T>A		
								1484	425		
T>C	S>P	T>C	S>P	T>C	S>P	T>C	S>P				
2472	751	2472	751	2472	751	2472	751				
								A>G	N>D		
								2505	762		
								G>T	R>I		
								2572	784		
C>T	T>M	C>T	T>M	C>T	T>M	C>T	T>M				
2644	808	2644	808	2644	808	2644	808				
C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S		
2895	892	2895	892	2895	892	2895	892	2895	892		
										C>T	P>S
										2928	903
C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L		
3325	1035	3325	1035	3325	1035	3325	1035	3325	1035		
C>T	R>C	C>T	R>C	C>T	R>C	C>T	R>C				
3879	1220	3879	1220	3879	1220	3879	1220				
C>T	S>L	C>T	S>L	C>T	S>L	C>T	S>L	C>T	S>L		
11836	14	11836	14	11836	14	11836	14	11836	14		
										A>G	N>S
										11995	67
G>A	A>T	G>A	A>T	G>A	A>T	G>A	A>T	G>A	A>T		
12470	23	12470	23	12470	23	12470	23	12470	23		
										T>C	S>P
										12575	58
T>C	S>P	T>C	S>P	T>C	S>P	T>C	S>P	T>C	S>P		
12689	96	12689	96	12689	96	12689	96	12689	96		
										G>A	R>Q
										13029	266
T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L
13571	25	13571	25	13571	25	13571	25	13571	25	13571	25
		A>G	N>S					A>G	N>S		
		14014	174					14014	174		

**Figure S3:** Identification of non-conservative mutations in P1-I-2012 and P2-C-2012 sequences from inoculated and contact pigs from Trial#1 using the P0-2012 sequence as reference. Mutation location were indicated in nucleotide (nt) and amino acid (aa) sequences position, starting from the first nt of the 5' nontranslated region (5'NTR) on the KF991509.2 full-length sequence and the start codon of each open reading frame (ORF), respectively. \* Isolate from the pig No. 2012\_7 was used as inoculum in Inoc-N-Rev-T#3 inoculated pigs from Trial#3. \*\* Isolate from the pig No. 2012\_6 was used as inoculum in Inoc-Rev-T#3 inoculated pigs from Trial#3.

P1-I-2017												P2-C-2017											
2017_12		2017_13		2017_14		2017_18		2017_19		2017_20		2017_15		2017_16		2017_17		2017_21		2017_22		2017_23	
nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa	nt	aa
								G>A	G>S	G>A	G>N												
								1041	274	1041	274												
T>G	L>W							T>G	L>W	T>G	L>W												
1066	282							1066	282	1066	282												
A>G	T>A	A>G	T>A			A>G	T>A					A>G	T>A	A>G	T>A			A>G	T>A	A>G	T>A	A>G	T>A
1484	425	1484	425			1484	425					1484	425	1484	425			1484	425	1484	425	1484	425
A>G	N>D	A>G	N>D	A>G	N>D	A>G	N>D			A>G	N>D	A>G	N>D	A>G	N>D	A>G	N>D	A>G	N>D	A>G	N>D		
2505	762	2505	762	2505	762	2505	762			2505	762	2505	762	2505	762	2505	762	2505	762	2505	762		
				G>T	R>I							G>T	R>I										
				2572	784							2572	784										
C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S
2895	892	2895	892	2895	892	2895	892	2895	892	2895	892	2895	892	2895	892	2895	892	2895	892	2895	892	2895	892
C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S	C>T	P>S		
2928	903	2928	903	2928	903	2928	903			2928	903	2928	903	2928	903	2928	903	2928	903	2928	903		
C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L	C>T	P>L		
3325	1035	3325	1035	3325	1035	3325	1035	3325	1035	3325	1035	3325	1035	3325	1035	3325	1035	3325	1035	3325	1035		
C>A	P>Q											C>A	P>Q					C>A	P>Q				
3463	1081											3463	1081					3463	1081				
T>C	L>P											T>C	L>P					T>C	L>P				
6862	2214											6862	2214					6862	2214				
		C>T	S>L					C>T	S>L			C>T	S>L										
		11836	14					11836	14			11836	14										
				A>G	N>S	A>G	N>S							A>G	N>S	A>G	N>S						
				11995	67	11995	67							11995	67	11995	67						
										T>A	Y>N							T>C	Y>H				
										12234	147							12234	147				
				T>C	S>P									T>C	S>P								
				12575	58									12575	58								
		T>C	S>P					T>C	S>P	T>C	S>P					T>C	S>P						
		12689	96					12689	96	12689	96					12689	96						
				G>A	R>Q									G>A	R>Q								
				13029	266									13029	266								
C>T	H>Y											C>T	H>Y					C>T	H>Y				
13270	109											13270	109					13270	109				
T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L	T>C	F>L		
13571	25	13571	25	13571	25	13571	25	13571	25	13571	25	13571	25	13571	25	13571	25	13571	25	13571	25		

**Figure S4:** Identification of non-conservative mutations in P1-I-2017 and P2-C-2017 sequences from inoculated and contact pigs from Trial#2 using the P0-2017 sequence as reference. Mutation location were indicated in nucleotide (nt) and amino acid (aa) sequences position, starting from the first nt of the 5' nontranslated region (5'NTR) on the KF991509.2 full-length sequence and the start codon of each open reading frame (ORF), respectively.