Table S3. Hemagglutinin (HA) amino acid sequence alignment of the H3.2010.1 and H3.2010.2 swine lineages used for antigenic analysis. Identity to the consensus sequences is represented by a dot (.). Antigenic motif is highlighted with red boxes.

Consensus

1. KJ941380 | A/swine/Missouri/A01410819/2014

- 2. KX981496 A/swine/Ohio/16TOSU4788/2016
- 3. MF801569.1 | A/swine/Ohio/A01354299/2017
- 4. MN931825 | Å/swine/Oklahoma/A02218157/2017 5. MN931846.1 | A/swine/Indiana/A02430356/2019

Consensus

- 1. KI941380 | A/swine/Missouri/A01410819/2014

- Xy341360 [A/swine/Ohio/A0135429/2016
 XK981569.1 [A/swine/Ohio/A0135429/2017
 MN931825 [A/swine/Oklahoma/A02218157/2017
- 5. MN931846.1 | A/swine/Indiana/A02430356/2019

Consensus

- 1. KJ941380 | A/swine/Missouri/A01410819/2014
- 2. KX981496 | A/swine/Ohio/16TOSU4788/2016
- 3. MF801569.1 | A/swine/Ohio/A01354299/2017 4. MN931825 | A/swine/Oklahoma/A02218157/2017
- 5. MN931846.1 | A/swine/Indiana/A02430356/2019

Consensus

- 1. KJ941380 | A/swine/Missouri/A01410819/2014
- 2. KX981496 | A/swine/Ohio/16TOSU4788/2016
- 2. Kr801496 JA/swine/Ohio/A01354299/2017 4. MN931825 JA/swine/Oklahoma/A02218157/2017 5. MN931846.1 JA/swine/Indiana/A02430356/2019

Consensus

- 1. KJ941380 | A/swine/Missouri/A01410819/2014
- 2. KX981496 | A/swine/Ohio/16TOSU4788/2016
- 3. MF801569.1 | A/swine/Ohio/A01354299/2017
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Consensus

- 1. KJ941380 | A/swine/Missouri/A01410819/2014
- 2. KX981496 | A/swine/Ohio/16TOSU4788/2016
- 3. MF801569.1 | A/swine/Ohio/A01354299/2017
- 4. MN931825 | A/swine/Oklahoma/A02218157/2017
- 5. MN931846.1 | A/swine/Indiana/A02430356/2019

QKLPGNDNNM		30 PNGTIVKTIT PNGTIVKTIT PNGTIVKTIT PNGTIVKTIT	NDQIEVTNAT NDQIEVTNAT NDQIEVTNAT ND R IEVTNAT	ELVQSSSXGE A F T F T N I N I		GENCTLIDAL GENCTLIDAL GENCTLIDAL GENCTLIDAL GENCTLIDAL	LGDPQCDGFQ LGDPQCDGFQ LGDPQCDGFQ LGDPQCDGFQ LGDPQCDGFQ LGDPQCDGFQ
NKNULFVER NKWOLFVER NKKULFVER NKKULFVER	SKAHSNCYPY SKAHSNCYPY SRAYSNCYPY SRAYSNCYPY	DVPDYASLRS DVPDYASLRS DVPDYASLRS DVPDYASLRS DVPDYASLRS			N S T I N K S I	R R S N K S F F S R R R S S N K S F F S R R R S S N S F F S R R R S S S S F F S R R R S S S S F F S R	LNVLTH S F LNVLTH F F
		GVHHPATCKD GVHHPATCKD GVHHPATCKD		RIIVSTKRSO RIIVSTKR N O		PRVRDIPSRİ PRVRDIPSRV PRVRDIPSR PRVRDIPSR	SIYWTIVRPG
250 DILLINSTGN DILLINSTGN	KEHFDKLYIW 260 LIAPRGYFKI LIAPRGYFK	RSGKSSIMRS	O I F L Y ARSSG 280 DAP I GK CNSÅ DAP I GK CNSÅ	CITPNGSIPN	QAVIPNIGSR 300 DKPFQNVNRI DKPFQNVNRI	PRIRDIPSR 310 TYGACPRYVK TYGACPRYVK	QNTLKLATGM
DILLINSTGN DILLINSTGN DILLINSTGN DILLINSTGN 330	L I APRGYFK I L I APRGYFK I L I APRGYFK I L I APRGYFK I 340	R S G K S S I MR S 350	360	CITPNGSIPN CITPNGSIPN 370	380	TYGACPRYVK TYGACPRYVK TYGACPRYVK TYGACPRYVK 390	ONTEKLATOM ONTEKLATOM OSTEKLATOM OSTEKLATOM 400
V	IFGALAGFIE IFGALAGFIE IFGALAGFIE IFGALAGFIE IFGALAGFIE	NGWE GMV DGW NGWE GMV DGW NGWE GMV DGW	YGFRHONSEG YGFRHONSEG YGFRHONSEG YGFRHONSEG			LNRL IGKTNE	KFHQIEKEFS
410	420	430 WSYNAELLVA WSYNAELLVA	440	DSEMNKLFEK	460	DMGNGCFKIÝ DMGNGCFKIÝ DMGNGCFKIÝ	480
D V V IRNGTYDHDV	YRDEALNNRF	WS YNAELLVA 510	LENGHTIDLT LENGHTIDLT LENGHTIDLT YKDWILWISF	AISCFLLCVÅ	TKKOLRENAE TKKOLRENAE 540 LLGFIMWACQ	550	
IRNGTYDHDV IRNGTYDHDV IRNGTYDHDV IRNETYDHNV IRNETYDHNV	YRDEALNNR F YRDEALNNR F YRDEALNNR F YXDEALNNR F YRDEALNNR F	0 K G V E L K S E 0 K G V E L K S E 0 K G V E L K S E 0 K G V E L K S G 0 K G V E L K S G				KGN I KCN I C I KGN I KCN I C I KGN I KCN I C I KGN I RCN I C I KGN I RCN I C I	