Text S1..... Supplemental Discussion

Table S1..... Complete inventory of Mia with storage locations

Table S2..... Barcoded amplicon concentration for QC and pooling

Table S3..... Sample information and sequencing results

Table S4..... Amino acid differences between Mia nanopore results and the nearest CVV (A/Ohio/35/2017)

Table S5..... Actual timeline of the Mia deployment from opening the cases in the barn to sending the sequences for vaccine synthesis

Table S6..... Accessioned Data

Table S7..... Primers used in this study

Figure S1 ..... Albacore results summary screenshot

Figure S2 ..... BC01 coverage screenshot

Figure S3 ..... BC05 coverage screenshot

Figure S4 ..... BC06 coverage screenshot

Figure S5 ..... BC07 coverage screenshot

Figure S6 ..... BC08 coverage screenshot

Figure S7 ..... BC09 coverage screenshot

Figure S8 ..... BC10 coverage screenshot

Figure S9 ..... BC11 coverage screenshot

Figure S10 ..... BC13 coverage screenshot

Figure S11 ..... BC14 coverage screenshot

Figure S12 ..... BC15 coverage screenshot

Figure S13 ..... BC16 coverage screenshot

Figure S14 ..... BC17 coverage screenshot

Figure S15 ..... BC18 coverage screenshot

Figure S16 ..... BC19 coverage screenshot

Figure S17 ..... BC20 coverage screenshot

Figure S18 ..... BC21 coverage screenshot

Figure S19 ..... BC22 coverage screenshot

Figure S20 ..... BC23 coverage screenshot

Figure S21 ..... BC24 coverage screenshot

Figure S22 ..... HA tree screenshot. Heatmap indicates the top Blast hit for a given sample's segment, over a user-defined minimum identity. Annotations are those used by the Zoonotic Virus Team at CDC and include: Avian North American Lineage (AvNAL), Avian North American 2009 H1N1 Pandemic Lineage (AvNAL_H1N1Pdm09), Classical Swine North American Lineage (CSNAL), Classical Swine North American 2009 H1N1 Pandemic Lineage (CSNAL_H1N1Pdm09), European Swine Lineage (ESL), European Swine 2009 H1N1 Pandemic Lineage (ESL_H1N1Pdm09), Human Seasonal Lineage (HSL), Human Seasonal 2009 H1N1 Pandemic Lineage (HSL_H1N1Pdm09) and Human Seasonal-Like Lineage (HSLL). Further HA annotations are viewed by the coloring of strain names and include: alpha, beta, gamma and H1N1pdm09 subclades of Classical Swine North American Lineages, delta-1 and delta-like (more contemporaneously referred to as delta-2) subclades of Human Seasonal H1 Lineage and IVA and IVB subclades of Human Seasonal H3 Lineage.

Figure S23 ..... NA tree screenshot. Annotations are described in Figure S22.

Figure S24 ..... PB2 tree screenshot. Annotations are described in Figure S22.

Figure S25 ..... PB1 tree screenshot. Annotations are described in Figure S22.

Figure S26 ..... PA tree screenshot. Annotations are described in Figure S22.

Figure S27 ..... NP tree screenshot. Annotations are described in Figure S22.

Figure S28 ..... M tree screenshot. Annotations are described in Figure S22.

Figure S29 ..... NS tree screenshot. Annotations are described in Figure S22.

Figure S30 ..... CVV Variants tab screenshot details numerous amino acid differences to current WHO Candidate Vaccine Viruses, including changes in known antigenic sites.

Figure S31 ..... MinION vs MiSeq coverages are highly concordant, albeit on different scales.

Figure S32 ..... MinION coverage vs identity to MiSeq. MinION derived sequences achieve maximum consensus identity at 10-fold coverage.

Figure S33 ..... Post-field maximum-likelihood phylogenetic analysis: HA H1 gamma. In-field PCR amplicons sequenced by MiSeq are in green and additional swine IAV samples collected around the fair and laboratory-processed are in red. Mia references are in light blue. Diverse swine IAV sequenced from up-to-date USDA surveillance are in dark gray. Scale bar indicates average nucleotide substitutions per site.

Figure S34 ..... Post-field phylogenetic analysis: HA H3 2010 human-like. Annotations are described in Figure S33.

Figure S35 ..... Post-field phylogenetic analysis: NA N1. Annotations are described in Figure S33.

Figure S36 ..... Post-field phylogenetic analysis: NA N2. Annotations are described in Figure S33.

Figure S37 ..... Post-field phylogenetic analysis: PB2. Annotations are described in Figure S33.

Figure S38 ..... Post-field phylogenetic analysis: PB1. Annotations are described in Figure S33.

Figure S39 ..... Post-field phylogenetic analysis: PA. Annotations are described in Figure S33.

Figure S40 ..... Post-field phylogenetic analysis: NP. Annotations are described in Figure S33.

Figure S41 ..... Post-field phylogenetic analysis: M. Annotations are described in Figure S33.

Figure S42 ..... Post-field phylogenetic analysis: NS. Annotations are described in Figure S33.

Figure S43 ..... The assembled Mia pipeline occupies two suitcases and a cooler. The contents are listed in Table S1.

Figure S44 ..... A photograph of the Mia setup mid workflow. We worked overnight in a vacant horse stall near the swine pins. From left to right: high performance laptop, minION, mini8 thermocyclers, Malania Wilson, power strips, tube racks and working space, pipette tips, centrifuge, vortex, paper towels, Matthew Keller, plastic consumables, pipettes hanging on a chair.