



Test Kit
for Influenza A Virus Typing

Version 01

For Investigational Use Only. Not Intended for Use in
Clinical Diagnostics.

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BACKGROUND

Influenza A virus is a genus within the family Orthomyxoviridae. It infects wild birds and poultry as well as humans and other mammals, and its genome consists of a ~13.5-kb single-stranded, negative-sense RNA organized in eight segments. Influenza A viruses show a high degree of genetic and antigenic variability. A total of 16 hemagglutinin (HA) subtypes and 9 neuraminidase (NA) subtypes have been described to date. Influenza A viruses of all subtypes are found in birds, whereas populations of humans, pigs, and horses are endemically affected by certain species-adapted subtypes.

To date, Virus subtyping is routinely accomplished after virus isolation in embryonated chicken eggs and is combined with the hemagglutination inhibition assay or reverse transcription (RT)-PCR, followed by partial or complete sequencing of the HA and NA genes. Microarrays present an alternative to RT-PCR and sequencing as they can detect many target sequences in parallel. The ArrayStrip system uses low density microarrays integrated in microtiter plate strips and signal amplification by enzyme-catalyzed local precipitation staining. Hybridisation and analysis are conducted using standard laboratory equipment complemented by the CLONDIAG ArrayMate™ Reader. In addition to all N- and H-types and the new Influenza A(H1N1) virus, the assay is targeting the HA0 cleavage region of avian influenza viruses.

The FluTypeA-Hybridisation Kit contains specific chemistry to perform Influenza A genotyping using CLONDIAG's ArrayStrip™ platform in conjunction with the ArrayMate Reader.

This manual contains additional protocols for Influenza A virus typing that have been adopted from scientific laboratory protocols (fully cited at the end of the manual).

GENERAL INSTRUCTIONS FOR USE

Intended Use

The kit is intended for the identification of Influenza A, H and N types, from Biotin labelled RT-PCR products that are obtained from viral RNA preparations. It is intended for use by personnel that are well-trained in molecular biology techniques. The kit is intended for research use only. It is not intended for use in clinical diagnostics.

TEST PRINCIPLE. Viral RNA needs to be extracted, reverse transcribed into DNA, PCR amplified and Biotin-labelled prior to application of the CLONDIAG FluTypeA Hybridisation Kit. Biotin-labelled PCR primers suitable for the amplification of relevant Influenza target sequences are

delivered along with the kit. Compatible RT-PCR reagents are listed below, but not included in the kit and need to be purchased separately.

Biotin-labelled PCR product is transferred and hybridized to microarrays with 218 different DNA Influenza virus markers, represented by 535 different spots of DNA probes on the array at the bottom of the disposable ArrayStrip. Biotin labelled PCR products bind specifically to the corresponding array spots and are visualised by the Streptavidin-Horseradish-Peroxidase system. PCR primers and the corresponding DNA probes on the arrays consist of markers required for H and N typing, respectively.

Two array spots consist of Biotin-linked polymers and serve as staining controls (Streptavidin-Horseradish Peroxidase conjugate binds to and catalyses a staining of these two positions at the final protocol step).

The ArrayMate Reader automatically acquires optical raw data from the ArrayStrips and an in-built proprietary pattern recognition software assigns the raw data to the respective subtype variants.

THE RESULTING data indicates if the sample contained Influenza A and the genotype of the virus.

Specifications

Upon receipt the assay components **need to be stored at different temperatures as specified on the package insert**. The assay is to be performed at an ambient temperature of 18°C to 28°C unless otherwise specified.

Technical Support

CLONDIAG provides technical assistance. Please contact:

Tel.: +49 (0) 3641 3111 116

e-mail: dorit.lichter@clondiag.com

Safety Precautions

Virual RNA preparation must be performed under the biosafety conditions as defined by the local authorities for work with Influenza virus.

Always wear protective clothes as regulated for laboratory work by the local authorities.

Material Safety Data Sheets (MSDS)

Per OSHA 29CFR1910.1200, Commonwealth of Australia [NOHSC:1005, 1008(1999)] and the latest amendments to the European Union Directives 67/548/EC and 1999/45/EC, the enclosed reagents do not require a Material Safety Data Sheet (MSDS). They do not contain more than 1% of a component classified as hazardous and do not contain more than 0.1% of a component classified as carcinogenic. MSDS therefore are not provided. Nevertheless, the buffers may cause irritation if they come into contact with eyes or skin, and may cause harm if swallowed. The regular precautions associated with laboratory work should be obeyed (e.g.: wear protective goggles, gloves and lab coat and avoid contact with the reagents). In case buffers or solutions are spilled, clean with laboratory detergent and water. CLONDIAG assumes no liability for damage resulting from handling or contact with these products. If you have any questions please contact our Technical Support (see above).

Shipping Precautions

RID/ADR: Kein Gefahrgut/ No dangerous goods

IMDG: No dangerous goods

IATA: No dangerous goods

KIT COMPONENTS, STORAGE AND STABILITY

RNA reverse transcription, amplification and labelling

- **PrimerMix (HA and NA, 2 tubes each):** lyophilized oligonucleotides, Biotin labelled. Each tube sufficient for 60 PCR reactions. Store at <-10°C. Reactivate/dissolve primers in 120 µL of RNase free water. Store at <-10°C. **Keep RNase free!**

Hybridisation and Detection

- **ArrayStrips**, protected against light and sealed under inert gas. Store at 18°C to 28°C. After opening to be used within two weeks. Close the unused wells with caps, protect them against humidity and dust and store them at a dark place. Avoid ANY touching or scratching the microarray on the bottom of the well.
CAUTION: Do not store or handle unused wells above 60% relative humidity since this may irreversibly corrode the spots.
- **CapStrips** (12 times)
- **C1:** Hybridisation Buffer. Store at 18-28 °C, protect against sunlight. Surplus: 100%.
- **C2:** Washing Buffer 1. Store at 18 °C - 28 °C, protect against direct sunlight. Surplus: 100%.
- **C3:** HRP Conjugate 100x. Store at 2-8 °C, protect against direct sunlight. Surplus: 50%.
- **C4:** Conjugate Buffer. Store at 18°C to 28°C, protect against direct sunlight. Surplus: 100%
- **C5:** Washing Buffer 2. Store at 18°C to 28°C, protect against direct sunlight. Surplus: 200%.
- **D1:** Horseradish Peroxidase Substrate. Store at 2-8°C, protect against direct sunlight. Surplus: 25%.

Expiry date is to be found on each bottle and on the outer package

All components have been tested for stability for short term shipment (<1 week) at ambient temperature (< 37 °C).

Components required but not provided by CLONDIAG

- RNA preparation: The assay has been tested with the QIAmp viral RNA mini Kit from Qiagen.

- SuperScript™ III One-Step RT-PCR System with Platinum® Taq DNA Polymerase, Invitrogen, Cat. No. 12574

Instrumentation provided by CLONDIAG (to be ordered separately)

- ArrayMate Reader

Materials required but not provided by ClonDIAG

- Equipment needed for RNA isolation, e.g. pipettes, centrifuge, thermomixer or robot
- Thermocycler
- Thermomixer (we recommend the Thermomixer comfort from Eppendorf) equipped with a platform for the warming of Microtiter Plates.
- Pipettes: suitable for 1µL-5µL volumes, 90µL, 100µL, 200µL, 1000µL
- Multichannel Pipettes for 100-200 µL
- Reagent tubes suitable for PCR, **RNAse free!**

PROTOCOL

1. viral RNA and RT-PCR

The required specimen for the application of the CLONDIAG FluType A Hybridisation kit is Biotin labelled RT-PCR product from viral RNA preparations.

The protocol for RNA extraction and RT-PCR/ Biotin labelling has been adopted from scientific publications without validation by CLONDIAG (see comprehensive citation of the literature at the end of the manual).

RNA preparation; mind RNase-free conditions

As a starting material any source of viral RNA may be used, including field samples (swaps).

Viral RNA may be prepared with any RNA extraction method; so far, the assay has been tested with the QIAmp viral RNA mini Kit from Qiagen. Local safety precautions are to be obeyed.

RT-PCR; mind RNase-free conditions

A strict separation of pre-PCR steps and post-PCR steps according to Good Laboratory Practice is necessary in order to avoid cross contamination. We strongly recommend to include a negative control (H₂O instead of viral Specimen) into each test run.

The assay has been tested with the QIAmp viral RNA mini Kit from Qiagen. Local safety precautions are to be obeyed.

RT-PCR and labelling is performed with the SuperScript™ III One-Step RT-PCR System with Platinum® Taq DNA Polymerase, Invitrogen, Cat. No. 12574 (to be purchased separately).

Two different PCR reactions are to be set up for each specimen with primers for Haemagglutinin (HA) or Neuraminidase (NA), respectively:

number of tests (add surplus for 1 PCR!)	1	3	5	7	9
RNase-free, ultrapure water	8.5 µL	25,5 µL	42,5 µL	59,5 µL	76,5 µL
Rxn Mix (Invitrogen kit)	12.5 µL	37,5 µL	62,5 µL	87,5 µL	112,5 µL
Primer Mix (HA OR NA)	2.0 µL	6 µL	10 µL	14 µL	18 µL
SSIII RT/ PlatinumTaq Mix	1.0 µL	3 µL	5 µL	7 µL	9 µL
Specimen (RNA isolate or control)	1 x 1 µL	3 x 1 µL	5 x 1 µL	7 x 1 µL	9 x 1 µL
total	25 µL	75 µL	125 µL	175 µL	225 µL

We recommend to produce a MasterMix consisting of all reagents except RNA, mix it thoroughly, make 24 μL aliquots of this MasterMix and then to add 1 μL of RNA to each aliquot. A surplus of MasterMix for 1 PCR is recommended in order to compensate fluid loss upon pipetting. Use only RNAse-free tubings, pipette tips and water.

Perform the following thermocycler protocol (required time: approximately 2 hours)

Pre-heat cover/lid to 105°C	
Reverse transcription	30 min at 50°C
Activation of Taq Polymerase	2 min at 94°C
45 cycles with	45 sec at 50°C
	45 sec at 68°C
	30 sec at 94°C
Final elongation	5 min at 68 °C
Cool down to 4°C, hold	

2. Worklist

It is obligatory to up-load a worklist onto the ArrayMate Reader before an analysis can be performed. It may be exported from a LIMS or designed in EXCEL or any other appropriate software. The final format must be a wordpad (*.txt)-format that can be imported into the test specific ArrayMate software (see below). For setting up a worklist:

- Create a list with at least three columns.
- The columns must have headers written into the first line.
- Each header **MUST** be one word (different words may be linked by “_”).
- Don’t use special characters like : ; (/ \ etc.
- The following headers are obligatory (in this order):

position sampleID assayID

where:

- position = position in a 96 well format i.e. 1 = A1, 8=H1, 9=A2 etc.

List position numbers of wells that are to be analysed in a continuous fashion;

DO NOT leave empty lines in the worklist;

If you use EXCEL: You need to type the position numbers into column A (Note: the raw numbers of the EXCEL spread template sheet CAN NOT be used to indicate well position).

- sampleID = your sample ID as exported from your LIMS (or assigned in any different way)
- assayID = 10326 (ID number of the FluTypeA assay). DO NOT use a different assay ID since this could lead to loss of data.

- You may add further columns and headers at your convenience (Note: information from these columns will NOT appear on the result screens or the Test Report).

• Example:

position	sampleID	assayID	comment
1	12345	10326	Dr. Jones
2	12346	10326	Dr. Miller
3	12347	10326	Dr. Yale
4	12348	10326	Dr. Palmer
5	12349	10326	Dr. Jones
6	12350	10326	Dr. Jones
7	12351	10326	Dr. Chapman
8	12352	10326	Dr. Scott
9	12353	10326	control
17	12354	10326	internal test

	1	2	3	4
A	1	9	17	
B	2			
C	3			
D	4			
E	5			
F	6			
G	7			
H	8			

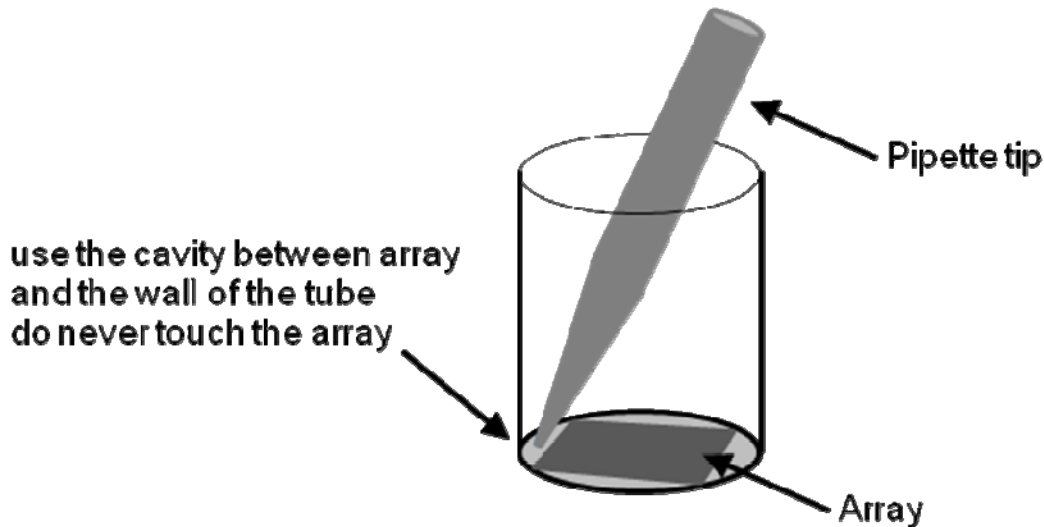
these are the corresponding positions in the 96 well format

- We recommend using a printout of the worklist as guidance for pipetting.
- Always convert your file into a wordpad (.txt) format (tabstop-delimited version!)
- Save the wordpad (*.txt) file of the worklist onto the memory stick provided along with the ArrayMate.
- To avoid confusion make sure that earlier versions of the worklist have been deleted from the memory stick.

3. Hybridisation

General Precautions

- We recommend the use of a multichannel pipette and reagent reservoirs.
- Never touch the Array surface. Remove liquid with a pipette: always place the pipette tip at the cavity between the array and the wall of the reagent well. If you touch the array surface, probes may be scratched off and this may cause an error.



- Avoid any complete drying of the array surface during processing (i.e. do not allow it to stay without liquid for more than two minutes)
- We strongly recommend that the liquid is removed by multichannel pipettes instead of inverting the wells and flicking them out.
- Always label your array strips with a laboratory marker at the recommended position. Never label them on the bottom or across the data matrix barcode! This may cause an error.



- Avoid contact of data matrix barcode with organic solvents! The ArrayMate needs the information encoded in the data matrix to perform the assay.
- Avoid touching the bottom of the microarray strip and keep it clean
- Never rinse the wells with distilled water after hybridisation

Preparation and denaturation of the hybridisation mixture

Pre-heat the thermomixer to 40 °C

- Add 2 µL of **each** PCR product (**HA** and **NA** of the **same** specimen) to 96 µL of buffer C1, mix gently (vigorous mixing results in foaming)
- heat the tubes to 95 °C for 3-5 minutes (denaturation)
- transfer tubes to ice for 1 minute (note: longer incubation on ice may result in precipitation of detergent. In this case repeat denaturation.)
- centrifuge tubes for 5 sec at > 10.000 rcf in order to collect PCR product at the bottom of the vessel

Pre-washing of the arrays (2 washing steps)

- Remove the ArrayStrip from the bag
- Insert the ArrayStrip(s) into the white frame. **Assure the correct orientation (data matrix barcode close to row A) and proper fit.**
- Close all wells that will not be used with a cap und leave it there until you use these wells. (for storage conditions after use: see section “Kit components, storage and
- Add 150 µL of ultrapure water to each well
- Mix carefully with a pipette (4x up and down) **WITHOUT TOUCHING THE ARRAY SURFACE**
- Remove and discard the water
- Add 100 µL buffer C1 to each well
- Incubate in the thermomixer at 40 °C, 550 rpm for 2 minutes (covering the wells during this step is not required)
- Remove and discard buffer C1
- Proceed promptly (hybridisation mixtures must be ready when buffer C1 is removed)

Hybridisation

- Transfer each hybridisation mixture (100 µL) to a prepared well on the ArrayStrip (avoid extensive foaming)
- Cap the wells
- Incubate for one hour at 40°C and 550 rpm on a thermomixer

4. Prepare reagents for detection and staining

Dilute Streptavidin-Horseradish-Peroxidase (C3, C4)

- Combine Reagent C3 (Streptavidin-Horseradish-Peroxidase) : Buffer C4 = 1 : 100 => C3/4
The mixture is stable for 1 day at room temperature; both reagents are delivered with a surplus of 100% each.
- Pipetting scheme:

	1 well	2-3 wells	4-6 wells	7-10 wells	11-15 wells	16-20 wells	21-30 wells	31-40 wells
C3	1.5 µL	3.5 µL	7 µL	11 µL	16 µL	21 µL	32 µL	42 µL
C4	150 µL	350 µL	700 µL	1100 µL	1600 µL	2100 µL	3200 µL	4200 µL

- put aside at room temperature until use


Pre-warm the staining reagent D1

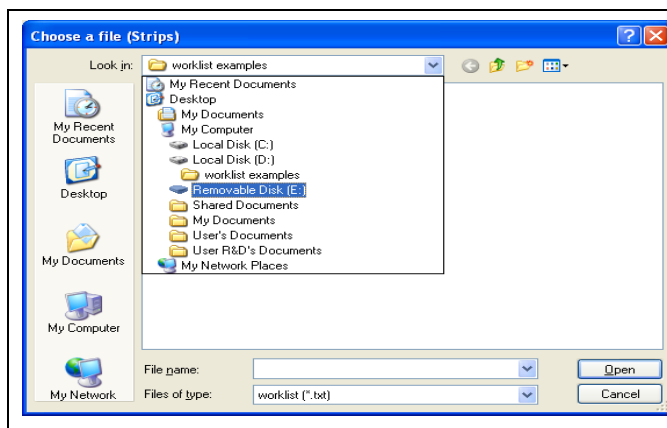
- Transfer enough reagent D1 into a separate vessel (e.g. a clean and sterile centrifuge tube), 100 µL for each well and a surplus of not more than 20%
- put aside at 20 to 25°C until use

5. Setup of the ArrayMate Reader

We recommend to set up the ArrayMate Reader after having started the hybridisation; this allows you a restart without time pressure in case of any software problems. This is a short instruction only. For more detailed information please refer to the ArrayMate User Manual.


- Switch on the ArrayMate (main switch on the rear below the electric cable plug, operating switch on the bottom/left corner of the front side).
- Switch on the screen (switch right hand below the screen).
- Login as **“User”**.
(The user interface is loaded, ArrayMate performs internal testing for < 1 minute)
- Click on the icon “New Run” (left upper edge of the screen; a suggestion for a run name for the new run appears in the top line of the screen).
- You may now modify or change the experiment name at your convenience.
- Type in your operator ID.

- If desired, you may enter a comment into the “memo” field.
- Insert your memory stick containing the worklist (use any of the USB ports down to the right side of the ArrayMate).
- Press the button:  (a folder selection dialog opens)
- Select your worklist (path: “My Computer/Removable Disk”)
- Open your selected worklist with “Enter” or the button “Open”



Caution: Make sure to select the correct worklist!

Caution: By default an example file for a worklist is selected. This file is only for training purposes! Do NOT use it for your experiments!

- Press the button:  (your imported worklist opens in a separate window). Check for correctness. If the new window is empty or the worklist is not the desired one, repeat the import.
- Press the button “ok” (worklist-window is closing).
- Leave the memory stick attached to the ArrayMate if you intend to export FluType A Test Reports afterwards.

6. Detection

Washing after hybridisation (3 washing steps)

- Remove the strips from the thermomixer
- Carefully open the wells and remove the hybridisation mixture as completely as possible (without touching the array surface)
- First and second washing step after hybridisation:
 - add 150 μ L of buffer C2
 - Incubate for 10 minutes at 40°C and 550 rpm on a thermomixer (capping of the wells is not required at this step)

- remove and discard the washing solution
- repeat this washing step.

NOTE: a carryover of more than 1% of buffer C1 to the next step will denature the HRP.

Addition of HRP-conjugate

- NOTE:**
- wells do not need to be capped any more
 - Reagent C3 contains Streptavidin-Horseradish Peroxidase (HRP) that would denature and lose its activity at 55°C. Do NOT incubate above 30°C.
- Add 100µL of C3:C4 (1:100, see above) to each well
 - Incubate for 15 minutes at 30°C and 550 rpm on a thermomixer
 - Remove and discard C3/C4
 - Washing step after binding of conjugate (2x):
 - add 150 µL of buffer C5
 - Mix carefully with a pipette (4x up and down) WITHOUT TOUCHING THE ARRAY SURFACE
 - remove and discard the washing solution
 - Repeat this step once.

Staining of bound HRP-conjugate

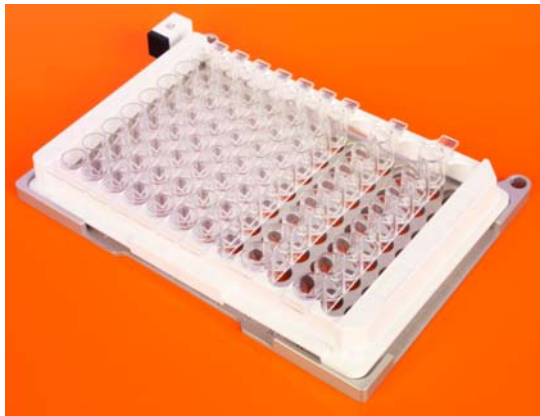
- NOTE:**
- a carryover of more than 3% of buffer C3/4 will cause higher background signals
 - wells do not need to be capped
 - do not move ArrayStrips during staining
 - Reagent D1 contains a substrate for Horseradish Peroxidase
- Add 100µL of pre-warmed reagent D1 (see above) to each well
 - Incubate at 20°C – 25°C WITHOUT agitation for 10 min
 - Remove and discard reagent D1 as completely as possible and analyse immediately (The dye precipitate is unstable and fades slowly; read out immediately but at maximum within 20 minutes).
 - **CAUTION:** the strips **MUST** be clean underneath the arrays and there **MUST NOT** be air bubbles or remains of liquid in the wells. Strips may be cleaned with lint-free wipes, bubbles may be removed by adding and removing D1 again.

7. Data Acquisition in the ArrayMate Reader

The reading process




The setup of the reader is briefly described in the section “Setup of the ArrayMate Reader”.


- Press the button “next” (bottom/right on the screen; reader is opening).
- Carefully insert the appropriate metallic adapter (if there is more than one) into the ArrayMate. Do not apply any strong force. **Assure proper fit**, otherwise the images may be out of focus.
- Carefully insert the white frame with the array strips into the metallic adapter. **Assure the correct orientation (Position A1 in the frame next to the data matrix barcode on the adapter) and proper fit**, otherwise the images may be out of focus.



ArrayStrip frame with inserted strips. Strips are inserted in accordance to the worklist.

- **CAUTION:** the strips **MUST** be clean and free from air bubbles and liquid!
- Barcodes on strips and holder must be clean.
- There must be no lids on the wells that are to be analysed (unused wells remain capped, however).
- Press the button “Next” (bottom/right on the screen; reader is closing, analysis program starts, it takes ca. 2-10 min dependent on the number of strips; reader takes images AND automatically analyses the data). The progress of the reading is indicated by the following symbols:

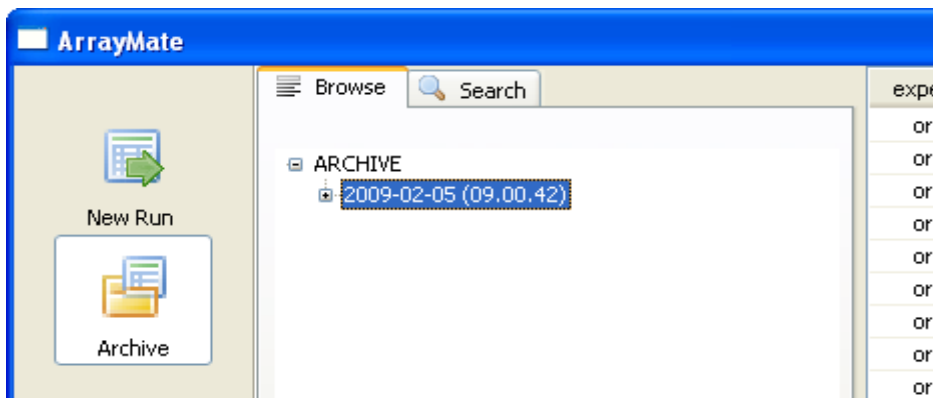
photographed:  in analysis:  ready: 

Wait until all images have been processed ( symbol for all arrays).

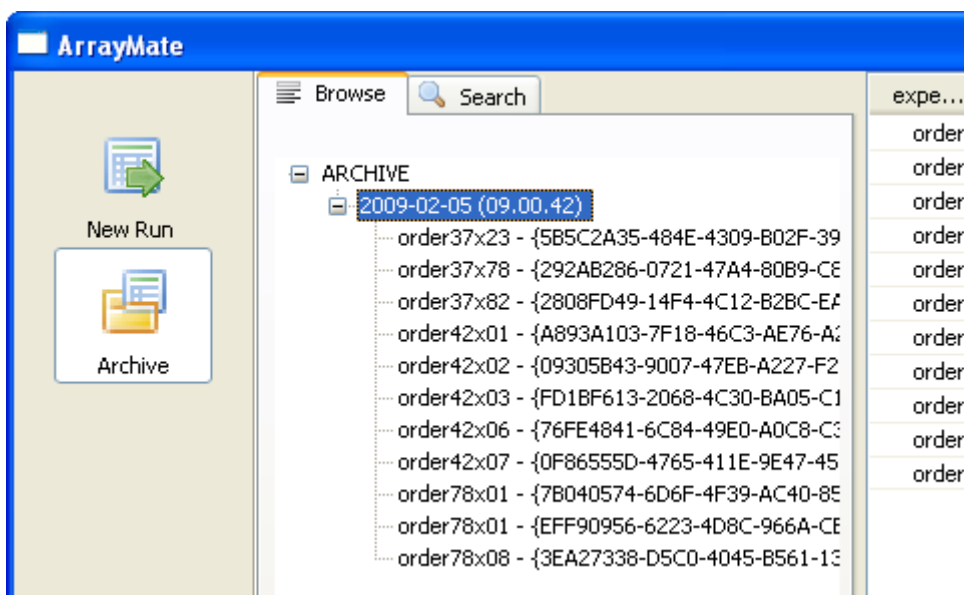
- Press the button “Next” (bottom/right on the screen; reader is opening)

- Remove the white frame with the ArrayStrip(s).
- Press the button “Next” (bottom/right on the screen; reader is closing).
- On the left hand of the screen you will see a list showing all readings stored on the ArrayMate. A reading contains the results from all arrays analysed together in one frame. If this list is not visible:
 - press the button “Archive” (left hand)
 - activate the Flag “Browse” (top left) .
- Please note:
 - the readings are organised like folders in “Windows”.

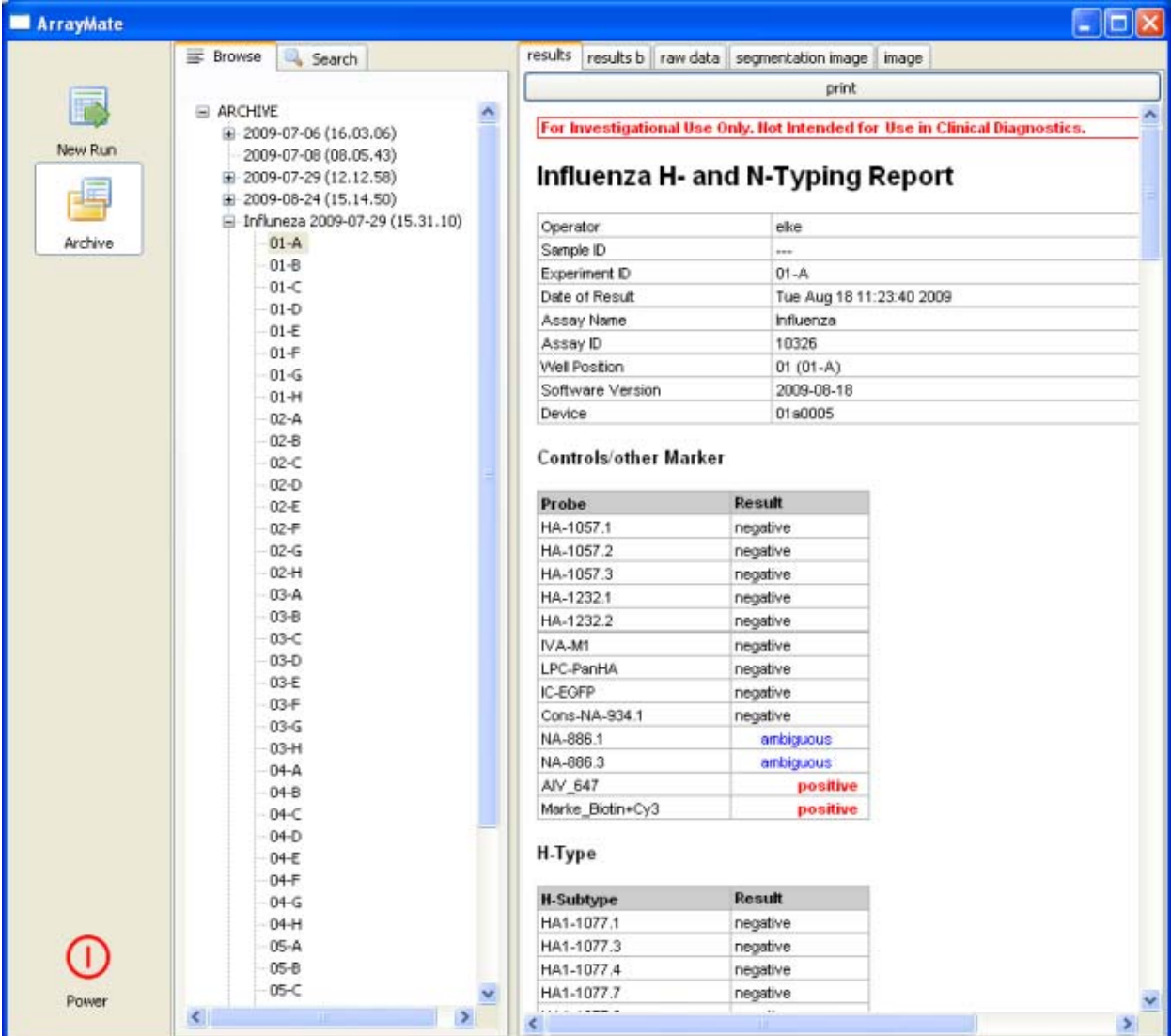
Example: there is one reading in the archive:



If you click on the plus symbol of the reading, the folder opens and you will see a list of the individual arrays (in alphabetical order according to Sample ID).



- Click on a Sample ID and the FluType Test Report for this array is shown in the window on the right:



The screenshot shows the ArrayMate software interface. On the left, there is a file browser with a tree view under 'ARCHIVE' containing several folders and a list of sample IDs (01-A to 05-C). On the right, a window titled 'Influenza H- and N-Typing Report' is displayed. The report includes a header with a warning: 'For Investigational Use Only. Not Intended for Use in Clinical Diagnostics.' Below this is a metadata table, a 'Controls/other Marker' table, and an 'H-Type' table.

Operator	elke
Sample ID	---
Experiment ID	01-A
Date of Result	Tue Aug 18 11:23:40 2009
Assay Name	Influenza
Assay ID	10326
Well Position	01 (01-A)
Software Version	2009-06-18
Device	01s0005

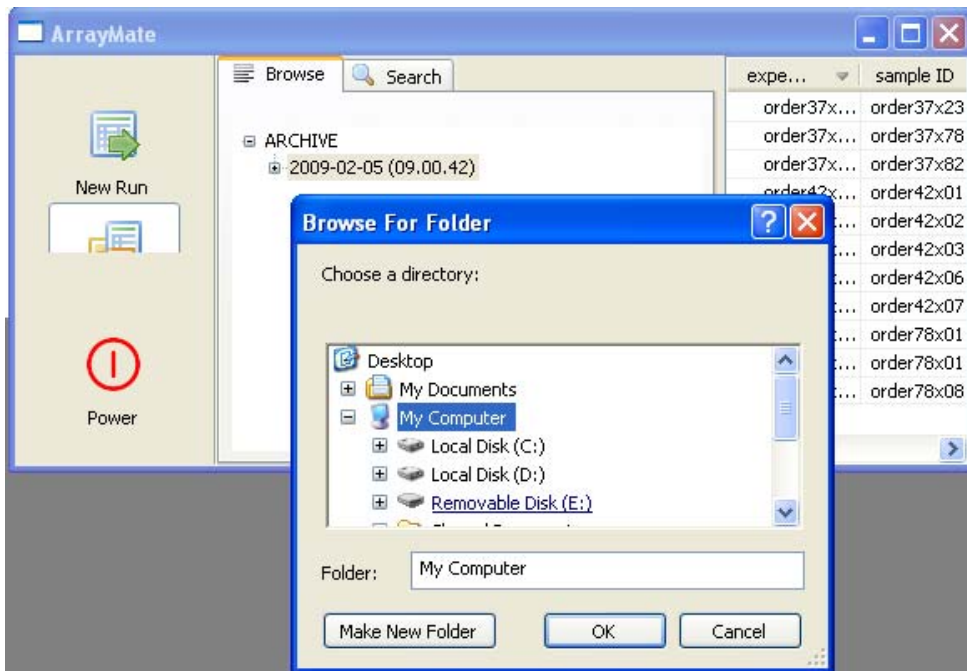
Probe	Result
HA-1057.1	negative
HA-1057.2	negative
HA-1057.3	negative
HA-1232.1	negative
HA-1232.2	negative
IVA-M1	negative
LPC-PanHA	negative
IC-EGFP	negative
Cons-NA-934.1	negative
NA-886.1	ambiguous
NA-886.3	ambiguous
AIV_647	positive
Marke_Biotin+Cy3	positive

H-Subtype	Result
HA1-1077.1	negative
HA1-1077.3	negative
HA1-1077.4	negative
HA1-1077.7	negative

Export of FluType Test Reports


- **Note: only complete readings can be exported. The export of individual FluType Test Reports is not possible**
- Right-Click on the desired reading (a menu appears with the option "Export Run Reports")

- Right-Click on “Export RunReports” (a file browser opens)



- Click on “My Computer”, then on “Removable Disk” and choose an appropriate storage place
- Click on the button “Make New Folder” (on the bottom; a new folder icon appears)
- Rename the new folder(e.g. with the experiment name)
- Click on the “Ok” button (data are exported now into the new folder on your memory stick)
- Do NOT remove the memory stick as long as the hourglass symbol is visible.

Switch off the device

Click on the “Power”-button (left/down on the screen): 

Switch off the Screen. There is no need to physically switch off the ArrayMate.

In case of any hang-up: restart the computer by pressing the on/off button (bottom/left on the ArrayMate reader face).

TROUBLESHOOTING

General

- The method relies on good-quality RNA preparations from viral specimens.

- All reagents need to be within the recommended shelf-life and stored in the appropriate way.

Staining Control

In case that Data Quality failed, the result of the Staining Control is displayed. If the Staining Control has “Passed”, viral RNA preparation and/or the RT-PCR steps may have failed. If the Staining Control has “Failed” proceed as follows:

- Horseradish Peroxidase Conjugate may have degraded during storage. Add 1µL buffer C3/4 to 9 µL D1 (substrate). If the solution turns green within 3-5 seconds, the Horseradish Peroxidase still has sufficient enzymatic activity.
- Enzymatic reaction is inhibited by carryover of buffer C1. Ensure proper washing of the wells to remove all of Buffer C1 prior to adding Horseradish Peroxidase Conjugate.

Physical damage of the array

Scratching of the array surface with a pipette tip can lead to the damage of array spots that prohibits the acquisition of a valid signal. In this case the respective marker is not assigned as “negative”, but instead the message “none” appears next to the marker name. We recommend to review Section 4 for General Precautions in array handling.

Report unavailable

If the ArrayMate Reader indicates that no report is available for an array (or multiple arrays on one strip), please check that the strip was positioned properly into the frame. If no obvious reason can be found for the fault please call the technical service of CLONDIAG.

ADDITIONAL INFORMATION

Warranty

CLONDIAG guarantees the performance as described in this manual. Usage of the Kit was successfully tested at ambient temperatures up to 37°C, a guarantee is limited to ambient temperatures in the laboratory between 18°C and 28°C. Kit components comprise the Arrays and their caps, the Lysis Enhancer, the reagents for DNA labelling and for detection of labelled DNA products on the array, the ArrayMate reader and its software. In case one of these

components fails within the expiry date due to other reason than misuse, contact CLONDIAG for replacement or refund. Terms and conditions apply (www.clondiag.com).

If you have any problem or question, please contact CLONDIAG technical service.

Quality Control

Reagents are tested for good performance with the CLONDIAG standard QC test. Arrays are stringently tested by optical inspection, there is currently no functional QC test for Influenza virus arrays, however.

LITERATURE

- Gall A. et al.: Rapid and highly sensitive neuraminidase subtyping of avian influenza viruses by a diagnostic DNA microarray. J Clin Microbiol. 2009 Jul 8. [Epub ahead of print]
- Gall A. et al.: Rapid haemagglutinin subtyping and pathotyping of avian influenza viruses by a DNA microarray. J Virol Methods. 2009 Sep;160(1-2):200-5. Epub 2009 May 15.
- Gall A. et al.: Design and validation of a microarray for detection, hemagglutinin subtyping, and pathotyping of avian influenza viruses. J Clin Microbiol. 2009 Feb;47(2):327-34.
- Gall A. et al.: Universal primer set for amplification and sequencing of HA0 cleavage sites of all influenza A viruses. J Clin Microbiol. 2008 Aug;46(8):2561-7.

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