



August 30, 2017

Food and Drug Administration
10903 New Hampshire Avenue
Document Control Center – WO66-G609
Silver Spring, MD 20993-0002

Janssen Pharmaceutica NV
Sarah Parsons
Director, Global Regulatory Affairs
920 US Highway 202
Raritan, NJ 08869

Re: K163628
Trade/Device Name: Idylla Respiratory (IFV-RSV) Panel
Regulation Number: 21 CFR 866.3980
Regulation Name: Respiratory viral panel multiplex nucleic acid assay
Regulatory Class: II
Product Code: OCC
Dated: July 26, 2017
Received: July 28, 2017

Dear Ms. Parsons:

We have reviewed your Section 510(k) premarket notification of intent to market the device referenced above and have determined the device is substantially equivalent (for the indications for use stated in the enclosure) to legally marketed predicate devices marketed in interstate commerce prior to May 28, 1976, the enactment date of the Medical Device Amendments, or to devices that have been reclassified in accordance with the provisions of the Federal Food, Drug, and Cosmetic Act (Act) that do not require approval of a premarket approval application (PMA). You may, therefore, market the device, subject to the general controls provisions of the Act. The general controls provisions of the Act include requirements for annual registration, listing of devices, good manufacturing practice, labeling, and prohibitions against misbranding and adulteration. Please note: CDRH does not evaluate information related to contract liability warranties. We remind you, however, that device labeling must be truthful and not misleading.

If your device is classified (see above) into either class II (Special Controls) or class III (PMA), it may be subject to additional controls. Existing major regulations affecting your device can be found in the Code of Federal Regulations, Title 21, Parts 800 to 898. In addition, FDA may publish further announcements concerning your device in the Federal Register.

Please be advised that FDA's issuance of a substantial equivalence determination does not mean that FDA has made a determination that your device complies with other requirements of the Act or any Federal statutes and regulations administered by other Federal agencies. You must comply with all the Act's requirements, including, but not limited to: registration and listing (21 CFR Part 807); labeling (21 CFR Parts 801 and 809); medical device reporting (reporting of medical device-related adverse events) (21 CFR 803); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820); and if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR 1000-1050.

If you desire specific advice for your device on our labeling regulations (21 CFR Parts 801 and 809), please contact the Division of Industry and Consumer Education at its toll-free number (800) 638 2041 or (301) 796-7100 or at its Internet address <http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm>. Also, please note the regulation entitled, “Misbranding by reference to premarket notification” (21 CFR Part 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to <http://www.fda.gov/MedicalDevices/Safety/ReportaProblem/default.htm> for the CDRH’s Office of Surveillance and Biometrics/Division of Postmarket Surveillance.

You may obtain other general information on your responsibilities under the Act from the Division of Industry and Consumer Education at its toll-free number (800) 638-2041 or (301) 796-7100 or at its Internet address <http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm>.

Sincerely yours,

 Steven R. Gitterman -S for

Uwe Scherf
Director
Division of Microbiology Devices
Office of In Vitro Diagnostics
and Radiological Health
Center for Devices and Radiological Health

Enclosure

Indications for Use

510(k) Number (if known)
K163628

Device Name
Idylla Respiratory (IFV-RSV) Panel

Indications for Use (Describe)

The Idylla Respiratory (IFV-RSV) Panel is an in vitro assay intended for the qualitative detection of nucleic acids for Influenza A, Influenza A subtype H1, Influenza A subtype H3, Influenza A subtype 2009 H1, H275Y mutation of Influenza A subtype 2009 H1, Influenza B and Respiratory Syncytial Virus (A and B) from nasopharyngeal swabs in viral transport media of adult and pediatric patients. The test uses the Idylla system to aid in the diagnosis of respiratory viral infection when used in conjunction with other clinical and laboratory findings.

Negative results do not preclude respiratory virus infection or co-infection with other viruses and should not be used as the sole basis for diagnosis, treatment or other patient management decisions.

Performance characteristics for Influenza A were established when influenza A/2009 H1 and H3 were the predominant influenza A viruses in circulation. When other Influenza A viruses are emerging, performance characteristics may vary. If infection with a novel Influenza A virus is suspected based on current clinical and epidemiological screening criteria recommended by public health authorities, specimens should be collected with appropriate infection control precautions for novel virulent influenza viruses and sent to state or local health departments for testing. Viral culture should not be attempted in these cases unless a BSL3+ facility is available to receive and culture specimens.

Type of Use (Select one or both, as applicable)

Prescription Use (Part 21 CFR 801 Subpart D)

Over-The-Counter Use (21 CFR 801 Subpart C)

CONTINUE ON A SEPARATE PAGE IF NEEDED.

This section applies only to requirements of the Paperwork Reduction Act of 1995.

DO NOT SEND YOUR COMPLETED FORM TO THE PRA STAFF EMAIL ADDRESS BELOW.

The burden time for this collection of information is estimated to average 79 hours per response, including the time to review instructions, search existing data sources, gather and maintain the data needed and complete and review the collection of information. Send comments regarding this burden estimate or any other aspect of this information collection, including suggestions for reducing this burden, to:

Department of Health and Human Services
Food and Drug Administration
Office of Chief Information Officer
Paperwork Reduction Act (PRA) Staff
PRASStaff@fda.hhs.gov

"An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a currently valid OMB number."

The 510(k) summary is being provided per condition of 21CFR807.92.



-
- **Submitter:** Janssen Diagnostics, a division of Janssen Pharmaceutica NV
- Turnhoutseweg 30
- 2340 Beerse
- Belgium
-
- **US Contact:** Sarah Parsons, Director Regulatory Affairs, Janssen R&D
- **Address:** 920 US Highway 202 South, Raritan NJ 08869
- **Phone:** 585-455-4925
- **Date Summary was prepared:** July 10, 2017
-

Company name	Janssen Diagnostics NV
Device name	Idylla™ Respiratory (IFV-RSV) Panel
Common name	Qualitative nucleic acid amplification based in vitro diagnostic test for the detection of respiratory viruses
Regulatory Section	21 CFR §866.3980 - Respiratory Viral Panel Multiplex Nucleic Acid Assay
Classification	II
Product Code	OCC - Respiratory virus panel nucleic acid assay system
Review Division	Microbiology (83)
Proposed Intended Use	<p>The Idylla™ Respiratory (IFV-RSV) Panel is an in vitro assay intended for the qualitative detection of nucleic acids for Influenza A, Influenza A subtype H1, Influenza A subtype H3, Influenza A subtype 2009 H1, H275Y mutation of Influenza A subtype 2009 H1, Influenza B and Respiratory Syncytial Virus (A and B) from nasopharyngeal swabs in viral transport media of adult and pediatric patients. The test uses the Idylla™ system to aid in the diagnosis of respiratory viral infection when used in conjunction with other clinical and laboratory findings.</p> <p>Negative results do not preclude respiratory virus infection or co-infection with other viruses and should not be used as the sole basis for diagnosis, treatment or other patient management decisions.</p>

	<p>Performance characteristics for Influenza A were established when influenza A/2009 H1 and H3 were the predominant influenza A viruses in circulation. When other Influenza A viruses are emerging, performance characteristics may vary.</p> <p>If infection with a novel Influenza A virus is suspected based on current clinical and epidemiological screening criteria recommended by public health authorities, specimens should be collected with appropriate infection control precautions for novel virulent influenza viruses and sent to state or local health departments for testing. Viral culture should not be attempted in these cases unless a BSL3+ facility is available to receive and culture specimens.</p>
Indications for Use	Same as intended use.
Special Instrument Requirements	Idylla™ System manufactured by Biocartis, NV
Proposed Predicate Device	Nanosphere Verigene® Respiratory Virus Plus Nucleic Acid Test (RV+) on the Nanosphere Verigene® System (K103209)

Device Description

The Idylla™ Respiratory (IFV-RSV) Panel is a self-contained molecular diagnostic test designed to work with the Idylla™ System. The assay is performed using a single-use, disposable, multi-chambered fluidic cartridge. This includes hands-off sample preparation/purification, reverse transcription and real-time, multiplex Polymerase Chain Reaction (PCR) for the detection of viral RNA. All steps in this process are fully automated and completely integrated and results are available in less than 50 minutes.

The Idylla™ Respiratory (IFV-RSV) Panel identifies virus-specific nucleic acids for Influenza (IFV) A virus, Influenza B virus, and Respiratory Syncytial Virus (RSV). The IFV-RSV Panel targets the following genes within the viruses: matrix gene (Influenza A and Influenza B); hemagglutinin gene (Influenza A subtypes H1 and H3, Influenza A subtype 2009 H1); neuraminidase gene (H275Y mutation of 2009 H1); fusion protein gene RSV (A and B). The System amplifies a targeted region of interest generating a change in fluorescent signal, which is measured and applied against predetermined criteria to provide a qualitative result. The automated process steps in the panel are:

Sample processing: Utilizing the automated process of Idylla™ fluidics, sample and Sample Processing Control (SPC) comes in contact with the lysis buffer to release the RNA and solubilize proteins, creating a lysate. Binding buffer is mixed with the lysate to aid in the binding of nucleic acids. Purified RNA is subsequently subject to a RT-PCR reaction within the Cartridge.

RT-PCR: Reverse Transcription, amplification and fluorescent detection of viral targets occur during the RT-PCR cycling. RT-PCR reagents are present in a stable formulation in five PCR chambers located within the Cartridge. The Test contains reagents for the simultaneous detection of a sample processing control and detection of various IFV and RSV targets. Detection of these specific targets is performed using fluorescent labeled probes. All amplification, detection of fluorescence, and the interpretation of the signals are done automatically by the Idylla™ instrument system.

Comparison to Predicate Device

Feature	Subject Device:Idylla™ Respiratory (IFV-RSV) Panel	Predicate: Verigene® RV+ (K103209)
Similarities		
Regulation	866.3980	866.3980
Product Codes	OCC -Respiratory virus panel nucleic acid assay system	OCC
Device Class	Class II	Class II
Intended Use	<p>The Idylla Respiratory (IFV-RSV) Panel is an in vitro assay intended for the qualitative detection of nucleic acids for Influenza A, Influenza A subtype H1, Influenza A subtype H3, Influenza A subtype 2009 H1, H275Y mutation of Influenza A subtype 2009 H1, Influenza B and Respiratory Syncytial Virus (A and B) from nasopharyngeal swabs in viral transport media of adult and pediatric patients. The test uses the Idylla system to aid in the diagnosis of respiratory viral infection when used in conjunction with other clinical and laboratory findings.</p> <p>Negative results do not preclude respiratory virus infection or co-infection</p>	<p>The Verigene® Respiratory Virus Plus Nucleic Acid Test (RV+) on the Verigene system is a qualitative nucleic acid multiplex test intended to simultaneously detect and identify multiple respiratory virus nucleic acids in nasopharyngeal (NP) swab specimens from individuals with signs and symptoms of respiratory infection. The following virus types and subtypes are identified using the RV+: Influenza A, Influenza A subtype H1, Influenza A subtype H3, 2009H1N1, Influenza B, Respiratory Syncytial Virus (RSV) subtype A and RSV subtype B. The test is not intended to detect Influenza C virus. Detecting and identifying specific viral nucleic acids from individuals exhibiting signs and symptoms of respiratory infection aids in the diagnosis of respiratory viral infection, if used in conjunction with other clinical and laboratory findings. The use of this test aids in the diagnosis of respiratory viral infection when used in conjunction with other clinical and laboratory findings.</p>

Feature	Subject Device:Idylla™ Respiratory (IFV-RSV) Panel	Predicate: Verigene® RV+ (K103209)
	<p>with other viruses and should not be used as the sole basis for diagnosis, treatment or other patient management decisions.</p> <p>Performance characteristics for Influenza A were established when influenza A/2009 H1 and H3 were the predominant influenza A viruses in circulation. When other Influenza A viruses are emerging, performance characteristics may vary. If infection with a novel Influenza A virus is suspected based on current clinical and epidemiological screening criteria recommended by public health authorities, specimens should be collected with appropriate infection control precautions for novel virulent influenza viruses and sent to state or local health departments for testing. Viral culture should not be attempted in these cases unless a BSL3+ facility is available to receive and culture specimens.</p>	<p>Negative results do not preclude respiratory virus infection or co-infection with other viruses and should not be used as the sole basis for diagnosis, treatment or other management decisions. Positive results do not rule out bacterial infection, and the agent detected may not be the definite cause of disease.</p> <p>Performance characteristics for Influenza A were established when Influenza A/H1 and H3 were the predominant influenza A viruses in circulation. When other Influenza A viruses are emerging, performance characteristics may vary.</p> <p>If infection with a novel Influenza A virus is suspected based on current clinical and epidemiological screening criteria recommended by public health authorities, specimens should be collected with appropriate infection control precautions for novel virulent influenza viruses and sent to state or local health departments for testing. Viral culture should not be attempted in these cases unless a BSL 3+ facility is available to receive and culture specimens.</p>
Targets	<p>Influenza A</p> <p>Influenza A/H1</p> <p>Influenza A/H3</p> <p>Influenza A/2009 H1</p> <p>Influenza B</p> <p>RSV (A and B)</p>	<p>Influenza A</p> <p>Influenza A/H1</p> <p>Influenza A/H3</p> <p>Influenza A/2009 H1N1</p> <p>Influenza B</p> <p>RSV A</p> <p>RSV B</p>

Feature	Subject Device:Idylla™ Respiratory (IFV-RSV) Panel	Predicate: Verigene® RV+ (K103209)
Specimen	Nasopharyngeal Swabs in Viral Transport Media	Nasopharyngeal swabs in sample matrix
Detection Method	PCR amplification	same
Nucleic Acid Isolation	Automated internal extraction of nucleic acids isolated onto silica membrane.	Automated internal extraction of nucleic acids performed on the Processor SP using silica coated magnetic beads and chaotropic salts.
Results	Positive or negative results	Same
LoD for target analytes (200 µL)	0.09-5 TCID ₅₀ /mL	0.1 -10 TCID ₅₀ /mL
Reactivity across viral strains	Test reacts to multiple strains within analyte parameters	Same
Specificity	Test does not give false results in the presence of non-influenza and RSV viruses, interferents or bacterial cultures tested in the analytical studies	Same
Differences		
Targets	Influenza A H275Y mutation in 2009 H1 RSV A and B combined as RSV	No Influenza A H275Y mutation determination Differentiation of RSV A and RSV B
Detection Method	The Idylla™ Respiratory (IFV-RSV) Panel: Amplified nucleic acid target sequences are identified by a unique type of fluorophore attached to their respective probe that is cleaved by the exonuclease activity of the Taq polymerase enzyme and allows for the identification and differentiation of the target viruses and subtypes. Each gene marker is detected using fluorescent molecules with different excitation and emission wavelengths.	Verigene Test amplicons are hybridized to gold nanoparticles probes through a mediator oligonucleotide and target specific capture oligonucleotides on a microarray-based chip in a disposable test cartridge.
Quality control	Each cartridge contains a single Sample Process Control (SPC) in the sample chamber for monitoring adequate sample processing and downstream amplification. The SPC is co-	Multiple internal procedural quality controls: PC1 (IC1) – inhibition control; PC2 (IC2) – process control; internal positive and negative controls; external positive

Feature	Subject Device:Idylla™ Respiratory (IFV-RSV) Panel	Predicate: Verigene® RV+ (K103209)
	amplified in each chamber to monitor that proper detection has occurred and that no PCR inhibitors were present in the sample.	controls

Performance Data

Analytical Performance

The analytical performance of the Idylla™ Respiratory (IFV-RSV) Panel was established following the recommendation found in FDA guidance document class II special controls specific for respiratory viral panels and nucleic acids (Guidance for Industry and FDA Staff-Class II Special Controls Guidance Document: Respiratory Viral Panel Multiplex Nucleic Acid Assay, October 9, 2009 and Class II Special Controls Guidance Document: Testing for Detection and Differentiation of Influenza A Virus Subtypes Using Multiplex Assays, October 9, 2009). These studies included analytical sensitivity, specificity (exclusivity), reactivity (inclusivity), interfering substances, competitive inhibition, and freeze/thaw studies. The results from these studies support claims that the product is substantially equivalent to the predicate device.

Clinical Performance

The clinical performance was measured in a multi-site prospective study using samples collected during the 2015-2016 IFV-RSV season plus stored samples from the 2012-2013 and 2013-2014 IFV and RSV seasons prospectively collected under a separate protocol. The samples were distributed across four external sites and tested with the Idylla™ Respiratory (IFV-RSV) Panel at the site or sent to a reference lab for testing with an FDA cleared molecular respiratory test. A total of 1014 subjects (214 fresh and 800 archived samples) were collected with nasopharyngeal swabs in viral transport media and were available for testing during this study. An additional 40 contrived H275Y mutation samples were processed, sent blinded to the sites and tested due to a low incidence of this mutational variant circulating in the last Flu seasons. The 40 samples were not included in the agreement measures of the other targets that were evaluated using prospectively collected clinical samples. Fifteen subjects were excluded due to protocol deviation, eligibility criteria, or missing comparator data. Eighty-eight samples were excluded due to failure to pass daily quality control (QC). The daily QC was an inadvertent error in the lab protocol that continued to run patient samples after 5 instances where the daily QC did not pass but was not repeated. A study performed in-house of Nasopharyngeal swab specimens from archived banked retrospective clinical collections were tested on the Idylla™ Respiratory (IFV-RSV) Panel and comparator Assays (Culture/NAAT/Sequencing). Testing of the Idylla™ IFV-RSV Panel was conducted by three operators on three Idylla™ Systems at both 200 µL and 500 µL. A total of 419 patient samples were tested at 200 µL with 408 reported results, and a total of 449 patient samples were tested at 500 µL with 418 reported results. The results of the

prospectively collected samples testing for each target, including Positive and Negative Agreement, are presented in [Table 1](#) through [Table 6](#). The results of the retrospective collected samples testing for each target, including Positive and Negative Agreement, are presented in [Table 7](#) through Table 12. The IFV-RSV Panel performance was compared to a FDA-cleared Nucleic Acid Amplification Test (NAAT). H275Y genotype determination and discordant results between the IFV-RSV Panel and the reference method were confirmed and/or analyzed respectively by using bi-directional sequencing at an independent reference laboratory (described in the table footnotes).

Table 1: Prospective Sample Positive Percent, Negative Percent Agreement, and Sanger Sequencing for INFLUENZA A

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	142	3 ^a	145
Negative	12 ^b	803	815
Total	154	806	960
		Point Estimate	95% CI
Positive Percent Agreement		92.2%	86.9% - 95.5%
Negative Percent Agreement		99.6%	98.9% – 99.9%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	139	5 ^c	144
Negative	10 ^d	775	785
Total	149	780	929
		Point Estimate	95% CI
Positive Percent Agreement		93.3%	88.1% - 96.3%
Negative Percent Agreement		99.4%	98.5% - 99.7%

^a: Three samples were FluA positive by Idylla™ @ 200 µl but negative by the comparator. Sequencing result confirmed one of three samples as FluA positive and the two samples were FluA negative.

^b: 12 samples were FluA negative by Idylla™ @ 200 µl but FluA positive by the comparator. Sequencing result confirmed ten samples as FluA negative and two samples as FluA positive..

^c: Five samples were FluA positive by Idylla™ @ 500 µl but negative by the comparator. Sequencing result confirmed four samples as FluA negative and one sample as FluA positive.

^d: 10 samples were FluA negative by Idylla™ @ 500 µl but positive by the comparator. Sequencing result confirmed nine samples as FluA negative and one sample as FluA positive.

Table 2: Prospective Sample Positive Percent, Negative Percent Agreement, and Sanger Sequencing for INFLUENZA A H3

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	73	0	73
Negative	5 ^a	882	887
Total	78	882	960
		Point Estimate	95% CI
Positive Percent Agreement		93.6%	85.9 – 97.2%
Negative Percent Agreement		100%	99.6% – 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	71	1 ^c	72
Negative	4 ^b	853	857
Total	75	854	929
		Point Estimate	95% CI
Positive Percent Agreement		94.7%	87.1% - 97.9%
Negative Percent Agreement		99.9%	99.3% - 100%

^a Five samples were AH3 negative by Idylla™ 200 µL but positive by the comparator. Sequencing confirmed all samples AH3 negative.

^b Four samples were AH3 negative by Idylla™ 500 µL but positive by the comparator. Sequencing result confirmed all samples as AH3 negative.

^c One sample was AH3 positive by Idylla™ but negative by the comparator. Sequencing result confirmed AH3 positive.

Table 3: Prospective Sample Positive Percent, Negative Percent Agreement, and Sanger Sequencing for INFLUENZA A/2009 H1

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	66	2 ^a	68
Negative	10 ^b	882	892
Total	76	884	960
		Point Estimate	95% CI
Positive Percent Agreement		86.8%	77.4% - 92.7%
Negative Percent Agreement		99.8%	99.2% - 99.9%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	65	2 ^c	67
Negative	8 ^d	854	862
Total	73	856	929
		Point Estimate	95% CI
Positive Percent Agreement		89.0%	79.8% - 94.3%
Negative Percent Agreement		99.8%	99.2% - 99.9%

^a: Two samples were 2009H1 positive by Idylla™ and negative by the comparator. Sequencing results confirmed one sample as 2009H1 positive and one as negative.

^b: 10 samples were 2009H1 negative by Idylla™ @ 200 µl and positive by the comparator. Nine samples were confirmed negative and one sample was confirmed positive by sequencing.

^c: Two samples were 2009H1 positive by Idylla™ @ 500 µl and negative by the comparator. Sequencing results confirmed one sample as 2009H1 positive and one sample as negative.

^d: Eight samples were 2009H1 negative by Idylla™ @ 500 µl but positive by the comparator. Sequencing results confirmed seven samples as 2009H1 negative and one sample positive.

Table 4: Prospective Sample Positive Percent, Negative Percent Agreement, and Sanger Sequencing for H275Y Mutation of Influenza A Subtype 2009 H1

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive¹	Comparator Negative	Total
Positive	39	0	39
Negative	0	960	960
Total	39	960	999
	Point Estimate		95% CI
Positive Percent Agreement	100%		91.0% - 100%
Negative Percent Agreement	100%		99.6% - 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	40	0	40
Negative	0	929	929
Total	40	929	969
	Point Estimate		95% CI
Positive Percent Agreement	100%		91.2% - 100%
Negative Percent Agreement	100%		99.6% - 100%

Table 5: Prospective Sample Positive Percent, Negative Percent Agreement, and Sanger Sequencing for INFLUENZA B

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	113	2 ^a	115
Negative	19 ^b	826	845
Total	132	828	960
		Point Estimate	95% CI
Positive Percent Agreement		85.6%	78.6% - 90.6%
Negative Percent Agreement		99.8%	99.1% – 99.9%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	111	2 ^c	113
Negative	19 ^d	797	816
Total	130	799	929
		Point Estimate	95% CI
Positive Percent Agreement		85.4%	78.3% - 90.4%
Negative Percent Agreement		99.7%	99.1% – 99.9%

a: Two samples were FluB positive by Idylla but negative by the comparator @ 200 µl. Sequencing result confirmed two samples FluB negative.

b: 19 samples were FluB negative by Idylla but positive by the comparator @ 200 µl. Two samples were confirmed positive by sequencing and 17 samples were confirmed negative by sequencing.

c: Two samples were FluB positive by Idylla but negative by the comparator @ 500 µl. DNA sequencing confirmed both samples as FluB negative.

d: 19 samples were FluB negative by Idylla but positive by the comparator @ 200 µl. DNA sequencing confirmed three samples as FluB positive and 16 samples as FluB negative.

Table 6: Prospective Sample Positive Percent, Negative Percent Agreement, and Sanger Sequencing for RSV (A or B)

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	96	3 ^a	99
Negative	14 ^b	847	861
Total	110	850	960
		Point Estimate	95% CI
Positive Percent Agreement		90.2%	85.0% - 94.0%
Negative Percent Agreement		99.7%	99.1% – 99.9%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	90	3 ^c	93
Negative	13 ^d	823	836
Total	103	826	929
		Point Estimate	95% CI
Positive Percent Agreement		87.4%	79.6% - 92.4%
Negative Percent Agreement		99.6%	98.9% – 99.9%

a: Three samples were RSV positive by Idylla @ 200 µl but RSV negative by the comparator. Two samples were confirmed negative and one sample was confirmed positive by sequencing.

b: 14 samples were RSV negative by Idylla @ 200 µl but RSV positive by the comparator. Four samples were confirmed RSV negative by sequencing. 10 samples were confirmed RSV positive by sequencing.

c: Three samples were RSV positive by Idylla but negative by the comparator @ 500 µl. Sequencing results confirmed one RSV positive and two RSV negative samples.

d: 13 samples were RSV negative @ 500 µl by Idylla and RSV positive by the comparator. Sequencing results confirmed four samples as RSV negative and nine samples as RSV positive.

Table 7: Retrospective Sample Positive Percent and Negative Percent Agreement for INFLUENZA A

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	80	0	80
Negative	4 ^b	324	328
Total	84	324	408
		Point Estimate	95% CI
Positive Percent Agreement		95.2%	88.4% - 98.1%
Negative Percent Agreement		100%	98.9% – 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	82	0	82
Negative	3 ^a	333	336
Total	85	333	418
		Point Estimate	95% CI
Positive Percent Agreement		96.5%	90.1% - 98.8%
Negative Percent Agreement		100%	98.9% – 100%

b: four samples were FluA negative by Idylla @ 200ul but positive by the comparator. One sample was negative at 200ul by Idylla but detected at 500ul by Idylla, therefore sample was not tested in sequencing. Two samples were confirmed FluA negative by sequencing. one of the sample had insufficient volume remained to complete sequencing.

a: Three samples were FluA negative by Idylla @ 500ul but positive by the comparator. Two of the three samples were confirmed FluA negative by sequencing. One sample had insufficient volume to complete DNA sequencing.

Table 8: Retrospective Sample Positive Percent and Negative Percent Agreement for INFLUENZA A H3

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	27	0	27
Negative	1 ^a	380	381
Total	28	380	408
		Point Estimate	95% CI
Positive Percent Agreement		96.4%	82.3% - 99.4%
Negative Percent Agreement		100%	99.0% – 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	28	0	28
Negative	1 ^a	389	390
Total	29	389	418
		Point Estimate	95% CI
Positive Percent Agreement		96.6%	82.8% - 99.4%
Negative Percent Agreement		100%	99.0% - 100%

a: One sample was negative for AH3 by Idylla @ 200ul and 500ul but the comparator result was AH3 positive. Insufficient material remained for DNA Sequencing

Table 9: Retrospective Sample Positive Percent and Negative Percent Agreement for INFLUENZA AH1

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	25	0	25
Negative	1 ^a	382	383
Total	26	382	408
		Point Estimate	95% CI
Positive Percent Agreement		96.2%	81.1% - 99.3%
Negative Percent Agreement		100%	99.0% – 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	25	0	25
Negative	0	393	393
Total	25	393	418
		Point Estimate	95% CI
Positive Percent Agreement		100%	86.7% - 100%
Negative Percent Agreement		100%	99.0% - 100%

a: one sample was Idylla negative for AH1 at 200uL but detected by Idylla at 500uL, therefore not tested in sequencing.

Table 10: Retrospective Sample Positive Percent and Negative Percent Agreement for INFLUENZA A 2009H1

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	28	0	28
Negative	1 ^a	379	380
Total	29	379	408
		Point Estimate	95% CI
Positive Percent Agreement		96.6%	82.8% - 99.4%
Negative Percent Agreement		100%	99.0% - 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	29	0	29
Negative	1 ^a	388	389
Total	30	388	418
		Point Estimate	95% CI
Positive Percent Agreement		96.7%	83.3% - 99.4%
Negative Percent Agreement		100%	99.0% - 100%

a: One sample was 2009H1 negative at 200uL and 500uL by Idylla, but detected by the comparator. DNA sequencing confirmed the absence of H1N1 2009 and Influenza A.

Table 11: Retrospective Sample Positive Percent and Negative Percent Agreement for INFLUENZA B

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	102	1 ^a	103
Negative	5 ^b	300	305
Total	107	301	408
		Point Estimate	95% CI
Positive Percent Agreement		95.3%	89.5% - 98.0%
Negative Percent Agreement		99.7%	98.1% – 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	106	1 ^c	107
Negative	6 ^d	305	311
Total	112	306	418
		Point Estimate	95% CI
Positive Percent Agreement		94.6%	88.8% - 97.5%
Negative Percent Agreement		99.7%	98.2% – 99.9%

a: One sample was FluB positive by Idylla @ 200ul but negative by the comparator. This sample was confirmed FluB positive by DNA sequencing.

b: Five samples were FluB negative by Idylla @ 200ul and positive by the comparator. All five samples were confirmed FluB positive by sequencing.

c: One sample was FluB positive by Idylla but negative by the comparator @ 500ul. DNA sequencing confirmed this sample as FluB positive.

d: Six samples were FluB negative by Idylla @ 500 but positive by the comparator. All six samples were confirmed FluB positive by DNA sequencing.

Table 12: Retrospective Sample Positive Percent and Negative Percent Agreement for RSV (A or B)

200 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	69	1 ^a	70
Negative	4 ^b	334	338
Total	73	335	408
		Point Estimate	95% CI
Positive Percent Agreement		94.5%	86.7% - 97.9%
Negative Percent Agreement		99.7%	98.3% – 100%
500 µL VTM			
IFV-RSV Panel Result	Comparator Positive	Comparator Negative	Total
Positive	81	1 ^c	82
Negative	7 ^d	329	336
Total	88	330	418
		Point Estimate	95% CI
Positive Percent Agreement		92.1%	84.5% - 96.1%
Negative Percent Agreement		99.7%	98.3% – 100%

a: One sample was RSV positive by Idylla @ 200ul but negative by the comparator. Insufficient sample remained for DNA sequencing.

b: Four samples were RSV negative by Idylla @ 200ul but positive by the comparator. All four samples were confirmed negative by sequencing.

c: One RSV sample was positive by Idylla but negative by the comparator.@500ul. Sequencing result confirmed this sample as RSV positive.

d: Seven samples were RSV negative by Idylla @ 500ul but the comparator. Six samples were confirmed RSV negative and one sample confirmed RSV positive by sequencing.

Conclusion:

In the multisite clinical study, nasopharyngeal swabs in VTM tested at 200 μ L or 500 μ L demonstrated at least 90% positive percent agreement (PPA) with a lower bound of the two-sided 95% CI greater than 80% for Influenza A, Influenza A H3, Influenza A H275Y 2009 H1. From the multisite study, results for Influenza A 2009/H1N1, for influenza B, and for RSV in nasopharyngeal swabs did not meet acceptance criteria in this study. However, the RSV call came very close to meeting the acceptance criteria with a point estimate of 87.4 and CI of 79.6-92.5% for nasopharyngeal swabs. Bidirectional sequencing results agreed most often with the Idylla™ results. When the discordant results were re-evaluated following sequencing of the samples, ALL targets (including the combined RSV call) demonstrated at least 90% PPA with a lower bound of the two-sided 95% CI greater than 80%.

When the results of the multisite prospective clinical study are combined with the retrospective testing, nasopharyngeal swabs tested in 200 μ L or 500 μ L VTM demonstrated at least 90% positive percent agreement (PPA) with a lower bound of the two-sided 95% CI greater than 80% for Influenza A, Influenza A H1, Influenza A H275Y 2009/H1 and Influenza A H3. From the combined testing, results for Influenza A 2009 H1 (200 μ L), Influenza B (500 μ L), and RSV (500 μ L) in nasopharyngeal swabs met acceptance criteria when rounding of the PPA is applied. Bidirectional sequencing results agreed most often with the Idylla™ results. When the discordant results were re-evaluated following sequencing of the samples, ALL targets (including the RSV call) demonstrated at least 90% PPA with a lower bound of the two-sided 95% CI greater than 80%.

In the multisite clinical study, nasopharyngeal swab specimens in 200 μ L or 500 μ L VTM demonstrated negative percent agreement (NPA) exceeding 99% with a lower bound of 95% (two-sided) confidence interval exceeding 90% for all targets meeting and exceeding acceptance criteria.

A comparison of the Intended Use, device features, non-clinical and clinical data support the Idylla™ Respiratory (IFV-RSV) Panel is substantially equivalent to the predicate device.