



savyonDIAGNOSTICS

member of the gamida diagnostics division

 **NanoCHIP® GIP- Gastrointestinal Panel
Combi II**

REF: 899057

Test kit for 96 determinations

Store at -20°C

For use with the NanoCHIP® 400 Instrument

For Professional Use Only  



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I. INTRODUCTION

Intended Use

The NanoCHIP® GIP Combi II assay performed on the NanoCHIP® system is an automated qualitative in vitro diagnostic test for the direct detection and differentiation of NanoCHIP® human diarrheal bacteria and parasites in stool specimens from symptomatic patients. The bacteria in the panel are: *Salmonella* spp., *Shigella* spp and *Campylobacter* spp. The parasites in the panel include *Entamoeba histolytica*, *Entamoeba dispar*, *Giardia lamblia*, *Cryptosporidium* spp., *Dientamoeba fragilis* and *Blastocystis hominis*. The test is performed directly on extracted DNA from stool specimens and detects DNA genes specifically characterizing the organisms in the panel. The test is intended to be used in the clinical laboratory in healthcare settings.

For *in-vitro* professional diagnostic use.

Background and Explanation of the Procedure

Infectious gastroenteritis is one of the most common diseases worldwide². Estimation has been made in which about 3.5 billion people are affected, and that 450 million are ill as a result of these infections, the majority being children. Transmission of intestinal parasites and enteropathogenic bacteria is characterized as fecal-oral human-to-human transmission¹⁵.

Diarrhea diseases are widely common in developed as well as developing countries and are major causes of morbidity and mortality, affecting millions of individuals each year. The etiologies of diarrhea include viruses (e.g., Norwalk-like viruses, rotaviruses, and enteric adenoviruses), bacteria (e.g., *Campylobacter*, *Shigella*, *Salmonella*, and cytotoxigenic *Clostridium difficile*), and parasites (e.g., *Entamoeba histolytica*, *Giardia lamblia*, *Dientamoeba fragilis*, *Blastocystis hominis* and *Cryptosporidium* spp.)².

1. **Parasites.** In developing countries diarrheal diseases are ranked by the World Health Organization (WHO) as the second most common cause of morbidity and mortality in children⁶:
 - A. ***Entamoeba histolytica* and *dispar*.** It has been reported that 10% of the world's population are infected with *Entamoeba* species, in which pathogenic *E. histolytica* constitute 10% of these infections and the remaining 90% are infected by non-pathogenic *E. dispar*. *E. histolytica* infection can result in colitis, dysentery and abscess in organs, most often the liver, with an estimated 40.000 – 100.000 deaths annually^{9,14}. Specific detection of *E. histolytica* cannot be achieved with microscopy alone as cysts and (small) trophozoites of *E. histolytica* and *E. dispar* are morphologically indistinguishable.
 - B. ***Giardia lamblia*.** Within the genus *Giardia*, *Giardia duodenalis* (syn. *Giardia intestinalis* and *Giardia lamblia*) is the only species that infects humans, although it is also found in other mammals, including pets and livestock¹. Clinical presentation ranges from asymptomatic carriage to acute and chronic gastrointestinal infections¹².
 - C. ***Dientamoeba fragilis*.** *D. fragilis* is a pathogenic parasite that has been shown to cause acute gastrointestinal disease and chronic infections. Recurrent clinical symptoms associated with *D. fragilis* are diarrhea and abdominal pain¹².
 - D. ***Cryptosporidium* spp.** *Cryptosporidium* species are distributed worldwide and have the ability to infect a wide range of vertebrate hosts. *Cryptosporidium parvum* and *Cryptosporidium hominis* are usually associated with human cryptosporidiosis^{2,12}.
 - E. ***Blastocystis hominis*.** *B. hominis* is the most frequently isolated parasite worldwide. It is now evident that patients with *B. hominis* have to be diagnosed and may require treatment^{10, 11}.

2. **Bacteria.** There is a large diversity of bacteria in the human gastrointestinal tract, some are unculturable by conventional microbiological methods.
- A. ***Campylobacter spp.*** Thermophilic *Campylobacter* species, primarily *Campylobacter jejuni* and *C. coli*, are curved, Gram-negative organisms, belonging to the ϵ -*Proteobacteria*, and are most commonly recognized as a major cause of acute bacterial diarrhea in the Western world⁷.
- B. ***Shigella spp.*** *Shigella* species are Gram negative, non-sporulating, facultative anaerobes that cause bacillary Dysentery⁸. *Shigella* is one of the most common bacterial agents causing acute diarrhea. It has been estimated that 165 million cases of shigellosis occur annually worldwide, resulting in 1.1 million deaths, mainly in the Third World¹³. *Shigella* is a human-restricted pathogen that is highly contagious⁵.
- C. ***Salmonella enterica.*** *Salmonella* species are main causes of enteritis throughout the world. *Salmonella enterica* Typhi and Paratyphi serotypes are important causes of enteric fever⁴. Most infections are zoonotic and are transmitted from animals to humans through the ingestion of contaminated food³.

The NanoCHIP® Gastrointestinal Panel Combi II assay offers a convenient methodology for identification and differentiation of enteric parasites and bacterial pathogens from stool specimens. The test detects simultaneously pathogens responsible for gastroenteritis, due to *Salmonella spp.*, *Campylobacter spp. (jejuni and coli)*, *Shigella spp.*, *Entamoeba histolytica*, *Entamoeba dispar*, *Giardia lamblia*, *Cryptosporidium spp.*, *Blastocystis hominis* and *Dientamoeba fragilis*. Please refer to Table 1 for the pathogens list and their respective target gene.

The NanoCHIP® GIP test is based on detecting genes that specifically mark the presence of each of the pathogens in the panel. Following a multiplex Polymerase Chain Reaction (PCR) in a single tube, the resulted amplicons are hybridized to complementary capture oligonucleotides, which are embedded in a hydrogel layer that covers the microarray. The capture oligonucleotides are biotinylated at the 5' or 3' end, and are bound to streptavidin which has been previously incorporated in the hydrogel. The capture oligonucleotides as well as the amplicons are electronically addressed to specific loci upon their applications. Reporting is made possible by fluorescent discriminator oligonucleotides that passively hybridize to complementary sequences on the amplicons. Sequential cycles of hybridization-imaging-thermal stripping of the fluorescent reporters allow the high multiplex capabilities of the system.

Table 1: Target genes used for identification of the bacteria and parasites in the GIP Combi II assay

Bacteria	Target gene
<i>Campylobacter spp.</i>	<i>mapA and asp</i>
<i>Shigella spp.</i>	<i>ipah</i>
<i>Salmonella enterica</i>	<i>invA</i>
Parasites	Target gene
<i>Entamoeba histolytica</i>	<i>18S</i>
<i>Entamoeba dispar</i>	<i>18S</i>
<i>Giardia lamblia</i>	<i>16S</i>
<i>Dientamoeba fragilis</i>	<i>16S</i>
<i>Cryptosporidium spp.</i>	<i>cowp</i>
<i>Blastocystis hominis</i>	<i>18S</i>

Principles of the Procedure

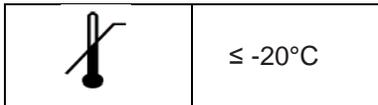
Stool specimens are collected from patients and transported to the laboratory unpreserved in a clean container or preserved in Cary-Blair transport media. A 10 µL loop is inserted to the specimen container to obtain the appropriate amount of sample required for the DNA extraction process (extraction may be carried out manually or automatically utilizing available instrumentation for this purpose). Once DNA is extracted, 2.5 µl of each sample is loaded into the PCR plate along with the PCR mix reagents for multiplex amplification in a thermo-cycler. As soon as the amplification process is completed, the PCR plate is loaded onto the NanoCHIP® 400 instrument along with the NanoCHIP® cartridge and the NanoCHIP® GIP kits reagents, the run is started and no further operator intervention is required.

The assay also includes an internal control, a bacterial endogenous gene, and a positive control to indicate that the whole process from DNA extraction throughout the NanoCHIP® reactions functions properly.

Kit Contents

The GIP Combi II kit contains amplification buffers and primer mix for 96 samples/controls and detection reagents for 3 runs. One to 96 samples/controls can be analyzed in a single detection run.

Kit Box Storage



Using NanoCHIP® Cartridge

The NanoCHIP® GIP Combi II Kit is designed to analyze 96 samples on a NanoCHIP® 400 Cartridge. A cartridge may be used up to 6 times for the GIP Combi II, or until the available test sites on the chip are utilized. Store either brand new or used cartridges at 2-8°C. The used cartridge may be reused up to 2 months if stored properly.

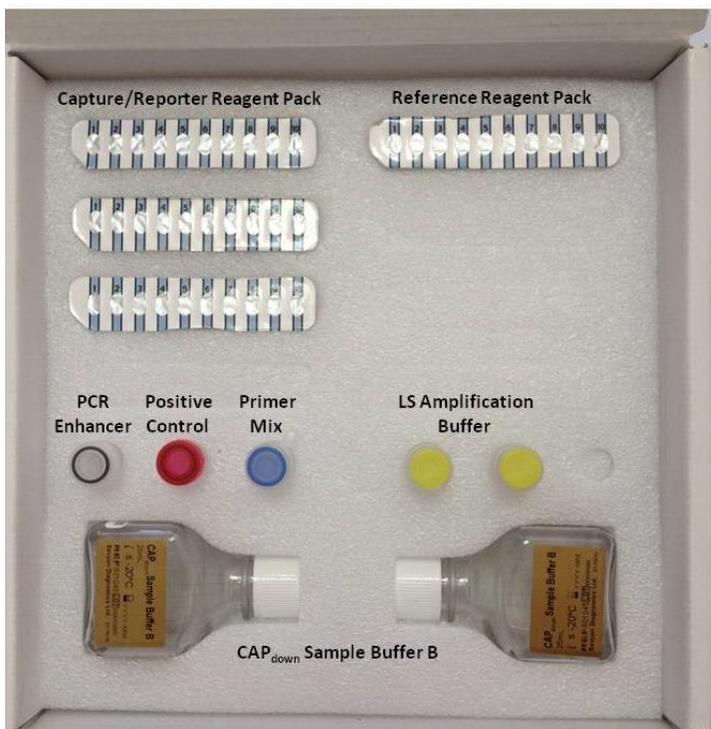
NanoCHIP® Cartridge Handling

Handle the cartridge by holding the outer black covering only; do not touch the clear plastic or electrical contact area. Exposure to static electricity may damage the cartridge and may affect results. Ensure that the flowcell window (clear plastic on the underside of the cartridge) is clear of any debris. If debris is present, always use a new (not previously opened) Bausch & Lomb Pre-Moistened Tissue to clean the window. Do not use excessive force when wiping the flowcell window. Clean the flowcell window only if debris is present.

II. MATERIALS AND EQUIPMENT

Kit Reagents Contents

Product Description	Contents
Gastrointestinal Panel Combi II Kit; 96 Samples; Cat.# 899057 	3 x GIP II Capture/Reporter Reagent Pack 1 x GIP II Reference Reagent Pack 1 x vial (150 µL) PCR Enhancer 1 x vial (30 µL) Positive Control (red cap) 1 x vial (210 µL) GIP II Primer Mix (blue cap) 2 x vial (850 µL) LS Amplification Buffer (yellow cap) 2 x CAP _{down} Sample Buffer B (25 ml)



Materials Available from Savyon

Ref.	Description	Contents
800160	NanoCHIP® 400 Cartridge	1 cartridge
800161	NanoCHIP® 400 Fluidics Cartridges	4 x fluidics cartridges
800154	NC400 Low Salt Buffer	6 x bottles (25 mL each)
800155	NC400 High Salt Buffer	6 x bottles (25 mL each)
800156	NC400 Target Prep Buffer	6 x bottles (25 mL each)
800061	NanoCHIP® Microplate Seals	100 x 96-well plate seals

Equipment and Materials Required But Not Provided

Plasticware and Consumables

- Sample Plates
 - 96-well ABI PCR plates (ABI N801-0560)
 - 96-well Thermo-Fast PCR plates (AB-1100)
- MicroAmp™ Compression Pads (ABI 4312639)
- 0.2 µm filters (Nalgene 5660020)

Reagents

- FastStart Taq DNA polymerase (Roche) Cat# 04 738 420 001
- Reagents to run NanoCHIP® 400 system:
 - L-histidine (Sigma H-8000)
 - Triton® X-100 (Sigma X-100)
 - Water, deionized

Required Equipment

- NanoCHIP® 400 System
- Thermal Cycler¹

¹ *The following models are recommended:*
GeneAmp® Thermal Cycler 2700, 2720, or 9700
MJ Research Peltier Thermal Cycler PTC200
Biometra T Gradient Thermocycler

III. PRECAUTIONS

Amplification technologies can amplify target nucleic acid sequences over a billion-fold and provide a means of detecting very low concentrations of target. Care must be taken to avoid contamination of samples with target molecules from other samples, or amplicons from previous amplifications. Follow these recommendations to help control contamination.

1. Separate pre-amplification steps from post-amplification steps. Use separate locations for pre- and post-amplification. Use dedicated lab equipment for each stage. Prepare samples in a laminar flow hood using dedicated equipment to minimize contamination. Set up the post-amplification area in a low-traffic area with dedicated equipment.
2. Use disposable containers, disposable barrier pipette tips, disposable bench pads, and disposable gloves. Avoid washable lab wear.
3. Use a diluted bleach solution (0.2% sodium hypochlorite) to treat waste from the post-amplification and detection areas, as the waste contains amplicon. Use the bleach solution to wipe down equipment and bench areas, and to treat drains used to dispose of liquid waste.
4. Monitor contamination with regular swabbing. Use a wet cotton swab to wipe areas of the bench or equipment, and rinse the swab with 500 μL of water. Test a few microliters of the rinse solution in the amplification assay to detect possible contamination. If contamination is detected, follow internal de-contamination procedures.
5. Use negative controls to monitor for possible contamination during reaction setup. If reagent contamination is detected, dispose of the suspect reagents.

References for Contamination Control

- Kwok, S. and Higuchi, R. (1989). Avoiding false positives with PCR. *Nature (London)* 339, 237.
- Victor, T. et al. (1993). Laboratory experience and guidelines for avoiding false positive polymerase chain reaction results. *Eur. J. Clin. Chem. Clin. Biochem.* 31, 531.
- Yap, E.P.H. et al. (1994). False-positives and contamination in PCR. In: *PCR Technology: Current Innovations*. Griffin, H.G. and Griffin, A.M., eds., CRC Press, Boca Raton, FL.

IV. INSTRUCTIONS FOR USE

Sample Collection/Transport

In order to obtain an adequate sample, the procedure for sample collection must be followed closely. Using a dry, clean container, liquid or soft stool samples are collected according to the following procedure:

1. Unpreserved samples: Transfer liquid or soft stool samples to a dry, clean container. Avoid contamination with water or urine. Label the container and transport to the laboratory according to institutional standard operating procedures (Refer to the Sample Storage and Stability section). Avoid mixing toilet paper, water or soap with the sample.
2. Cary-Blair preserved samples: Transfer liquid or soft stool samples to the 15 mL transport device according to the manufacturer's instructions. Avoid contamination with water or urine. Label the container and transport to the laboratory according to institutional standard operating procedures (Refer to the Sample Storage and Stability section).

Collected samples, either unpreserved stool or stool stored in modified Cary-Blair transport media should be kept between 2°C to 25°C during transport. Protect against freezing or exposure to excessive heat.

Sample Storage and Stability

Specimens received in the laboratory should be processed upon arrival. In case of delay, store specimens refrigerated (2-8°C) for up to 48 hours or at -20°C for a longer period. Store purified nucleic acids at $\leq -20^{\circ}\text{C}$.

Sample Preparation for PCR

Extraction

Genomic DNA should be extracted from stool sample using an appropriate DNA extraction kit. Extraction may be carried out manually or automatically utilizing available instrumentation. Several DNA extraction systems were validated for the NanoCHIP system: QIAamp (Qiagen), EasyMag (BioMerieux), Liaison IXT/Arrow (DiaSorin) MagNA Pure 96 (Roche) and Bullet Pro (DiaSorin). An internal control, which is imbedded in the GIP Primer Mix, indicates proper extraction of high quality genomic DNA from the sample (B16 gene).

Amplification

The following should be performed in an amplicon-free area.

1. Take out the LS Amplification Buffer and the GIP II Primer Mix from the $\leq -20^{\circ}\text{C}$ freezer. Thaw at room temperature and vortex.
Note: The LS Amplification Buffer and the GIP II Primer Mix may be frozen two additional times. Reagents can be stored at 2-8° for one week.
2. Prepare PCR Master Mix using the following guidelines per sample (see Table 2). To ensure an adequate volume of Master Mix, add 2 reaction volumes to the required number of reactions. Multiply the sum by the volume of each component shown in Table 2.
Note: Take out the FastStart Taq DNA Polymerase from the freezer just before its usage, and return it back to the freezer promptly.

Table 2: PCR¹ Guidelines for preparing the Master Mix

Component	Volume per one reaction (µl)
LS Amplification Buffer	6.25
PCR Enhancer	1.35
GIP Combi II Primer Mix	1.9
FastStart Taq DNA Polymerase	0.5
Total Master Mix	10

- Add 10 µl of the PCR Master Mix to reaction wells in the PCR plate.
 - Add 2.5 µl of the **Positive Control** into the first well (position well A1) in the PCR plate.
 - Add 2.5 µl of each sample's nucleic acid to individual reaction wells containing the Master Mix.
 - Add 2.5 µl of ultra-pure water for the Negative Control to the last well containing the Master Mix.
- Notes:** Do not scale up an amplification reaction; always use 12.5 µl reaction volumes. The concentration of the template DNA should be at least 10 ng/µl.
- Seal the PCR plate with a microplate seal and place it into a thermal cycler.
- Notes:** Place the ABI MicroAmp Compression Pad over the sealed PCR 96-well plate and close the lid of the thermal cycler.
- Program the thermal cycler using the parameters described in Table 3.

Table 3: GIP Assay, Thermal Cycler Parameters

Temperature (°C)	Time	Number of Cycles
95	4 minutes	1
95	30 seconds	43
60	1 min	
72	45 seconds	
72	5 minutes	1
4	Hold	

- Once cycling is completed, remove the PCR plate from the thermal cycler. The prepared plate may be stored at 2-8°C for up to one week, or at ≤ -20°C for up to six months.

To optimize workflow, you can begin other activities during sample amplification. For example, you can prepare the system and thaw reagents. During cartridge initialization, you can write the protocol and prepare the sample plate.

¹ Refer to Appendix B: Legal Notices, for PCR information.

Sample Plate Preparation

Sample dilution for the NanoCHIP® GIP assay can be performed automatically by the NanoCHIP instrument (the template default) or alternatively by manual procedure for additional use of the DNA sample. Please choose the **Onboard Sample Dilution** option (mark with arrow in Figure 1) or alternatively by performing a **Manual Sample Dilution** setting is unchecked.

Onboard Sample Dilution

Remove the ABI MicroAmp™ Compression Pad from the ABI PCR plate covered with Microplate Seal, attach the sample plate to the PCR Plate base and insert into plate position 2 of the NanoCHIP® 400 instrument. Please see more information of this procedure at the Running the assay section.

Note: The Onboard Dilution Option can only be used with the ABI 96 well plate (ABI N801-0560) or the Thermo-Fast 96-well PCR plates (AB-1100) attached to the PCR Base Plate. Use of other plate types may cause damage to the instrument.

Manual Sample Dilution

1. Take out CAP_{down} Sample Buffer B from the freezer. Upon thawing, vortex the solution thoroughly until all precipitates are dissolved.
Note: Once thawed, CAP_{down} Sample Buffer B can be stored at 2-8°C for up to one week. Do not refreeze.
2. For each individual amplification reaction, pipette 60 µL of CAP_{down} Sample Buffer B into one well of a 96-well plate.
3. Add 8 µL of each amplification reaction into a well containing CAP_{down} Sample Buffer B. Carefully pipette up and down to mix.
4. Cover plate with a Microplate Seal.

Avoid opening PCR plate to prevent contamination with Positive Amplicons in the laboratory

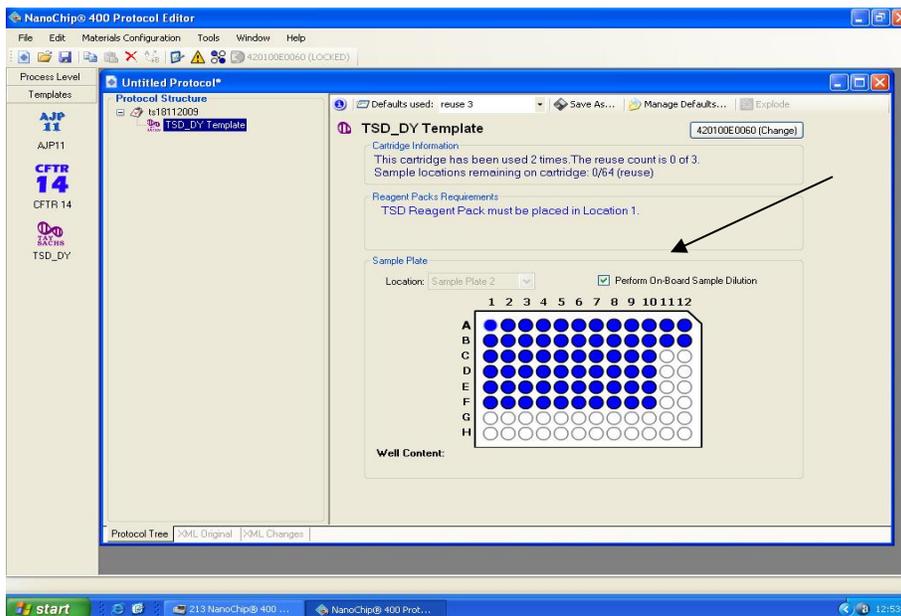


Figure 1. Protocol Editor Screen.

V. OPERATING THE NANOCHIP® 400 SYSTEM

Refer to the *NanoCHIP® 400 User's Guide (REF 140530)* for detailed instructions on the basic operation of the system, including system maintenance and cartridge handling.

Preparing Solutions for Use in the NanoCHIP® 400 Instrument

Preparing Wash Solution

It is required to prepare fresh Wash Solution (50 mM histidine, 0.1% Triton X-100) prior to daily run. Leftover of the solution should be disposed at the end of the day.

1. Add 500 mL of the 50 mM histidine solution to a 1L buffer bottle.
2. Add 2.5 mL of the 20% Triton X-100 solution and mix thoroughly.

50 mM histidine solution: In a bottle/beaker, add 7.8 g of L-histidine to a final volume of 1 L of dH₂O for 50 mM histidine. Mix until histidine powder is dissolved completely. Filter the solution using a 0.2 µm filter.

Note: This solution is stable for up to two weeks at 2–8°C.

20% Triton X-100 solution: Add 4 mL or 4.24 g of Triton X-100 to approximately 15 mL of dH₂O for a final volume of 20 mL. Mix solution thoroughly (approximately 10 minutes).

Note: This solution is stable for up to three months at 2-8°C.

Additional Solutions Required for the Run (Provided by Savvyon)

The following table describes the required solutions, and their assigned locations within the instrument.

Table 4: Location of Bottles in the NanoCHIP® 400 Instrument

Solution	Bottle	Location	Minimum Volume*
Water	1 L	H ₂ O position	500 mL
Wash Solution	1 L	BUF position	500 mL
High Salt Buffer	30 mL	Position 1	25 mL
Low Salt Buffer	30 mL	Position 2	25 mL
Target Prep Buffer	30 mL	Position 3	25 mL
**CAP _{down} Sample Buffer B	30 mL	Position 4	25 mL

* The minimum volume of liquid that should be in the listed bottle before starting the assay run.

CAP_{down} Sample Buffer B is only required when performing **OnBoard dilution.

Preparing the NanoCHIP® Cartridge and Instrument

1. Take the following reagent packs out from the freezer and place them at room temperature to thaw.
 - GIP II Capture/Reporter Reagent Pack
 - GIP II Reference Reagent Pack

The GIP II Reference Reagent Pack is only required for the **first use** of a cartridge.

Notes: These reagent packs must be used within 8 hours of thawing. All items listed above are single use only, discard after use.

2. Take a NanoCHIP® Cartridge out from 2-8°C storage. Keep at room temperature for at least 15 minutes before using.

Note: Bringing the cartridge to room temperature before insertion into the instrument avoids the formation of condensation in the cartridge window, which could cause the cartridge to fail initialization.

3. Initialize and prime the NanoCHIP® 400 Instrument following the guidelines listed in the *NanoCHIP® 400 User's Guide*.

4. From the Dock Bar, select the instrument icon to start the NanoCHIP® 400 Instrument Manager 

5. Ensure that the flowcell window (clear plastic on the underside of the cartridge) is clear of any debris. If debris is present, use a new (not previously opened) Bausch & Lomb Pre-Moistened Tissue to clean the window.

Note: Do not use excessive force when wiping the flowcell window. Clean the flowcell only when debris is present.

6. Scan the barcode of the NanoCHIP® Cartridge using the attached barcode scanner.

Note: The barcode will not be displayed in the Instrument Manager until step 8 has been completed.

7. Insert the cartridge into the instrument, ensuring that it is properly seated.

8. Close the cartridge door by pressing the button located below the cartridge slot on the instrument.

9. When the Cartridge Initialization window appears, select **Initialize Cartridge with Hydration** (see figure 2).

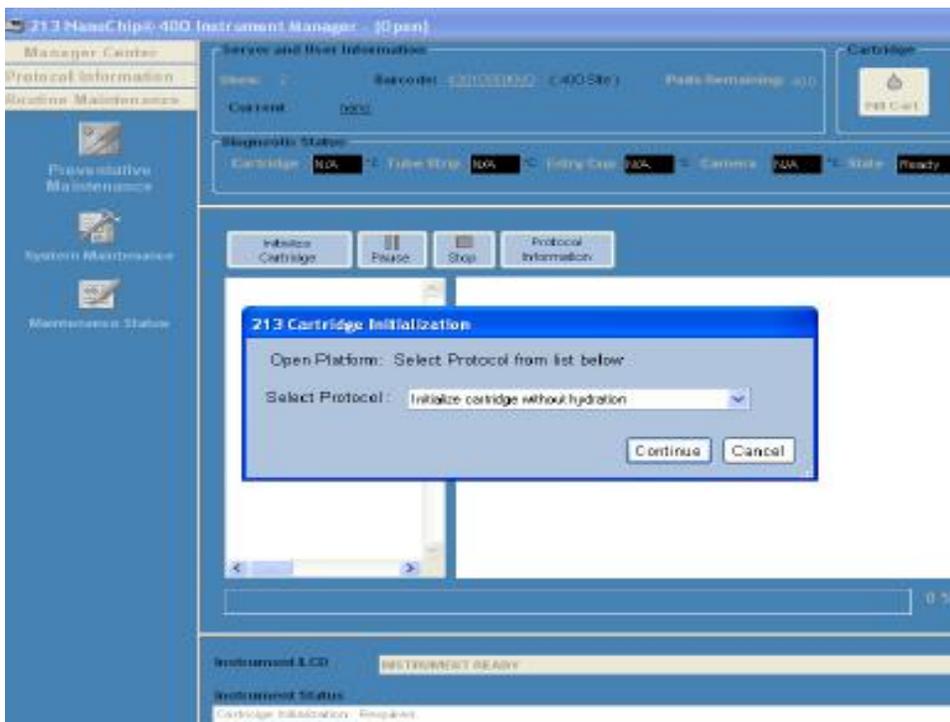


Figure 2: NC instrument Manager

10. Cartridge initialization will take approximately 15 minutes. When initialization is completed, the LCD will display "Instrument Ready".
11. Write the protocol as described in the following section.
Note: The protocol can be written while the cartridge is initializing.

Creating a Protocol

Using the Protocol Editor, create the following protocol to address and report 1-96 samples/ controls. Create a new protocol for each sample run. For detailed instructions on using Protocol Editor, see the *NanoCHIP® 400 User's Guide*.

1. From the Dock Bar select **Protocol Editor**  (see figure 3).

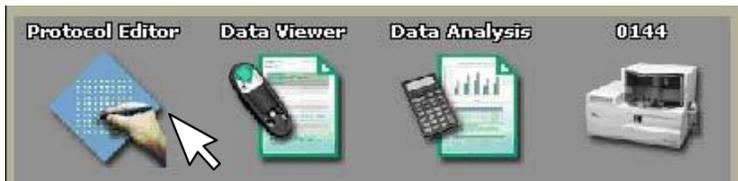


Figure 3. NanoChip 400 DockBar.

2. Select **Create A New Protocol**; select **OK**.
3. Select the **GIP II** icon from the available templates on the left column.
Note: The **GIP II** template automatically determines prior pad utilization, and maps capture and sample addressing beginning with the first unused sample position.
4. The Plate Specification Window appears; choose the correct plate type intended for the assay from the options in the pull-down menu. Select **OK**.
Note: Selecting a sample plate type other than what is placed on the NanoCHIP® 400 Instrument deck at the start of a run can cause damage to the system and fail the run. Use caution to select the appropriate plate type.
5. The Set Cartridge window appears; choose **Select The Cartridge**. From the pull-down menu, select the serial number of the cartridge that will be used in the run (or type the serial number into the window). Select **OK**.
Note: If the cartridge selected is still initializing, a cartridge presently in use window will appear. Select **Yes** to indicate that you still want to use this cartridge for the protocol you are creating.
Warning: Select **No** if the cartridge selected is in use with a GIP Protocol and wait for the protocol to complete before creating a new GIP protocol for the selected cartridge. If **Yes** is selected, the pad usage for the new protocol may not map correctly.
6. When a screen like the one shown in figure 4 appears, mark the wells with the samples on the plate drawing and select "**Perform On Board Dilution**".

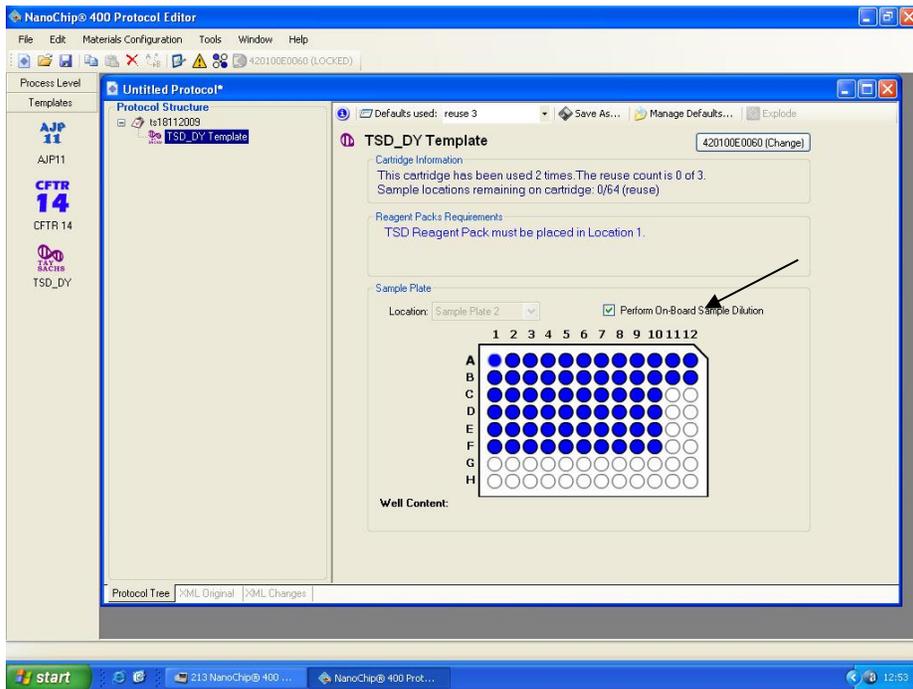


Figure 4. Protocol Editor Screen

7. Click on the run name you entered earlier (located under protocol structure), if no name was inserted it will appear as "untitled". **Scroll to 'Plate location 2'** (See figure 5). Here you can either write down your samples names or import it from an excel sheet. LIS connection is also optional. **Note:** A cartridge may be used up to 6 times for the GIP assay, or until the available test sites are utilized, whichever comes first.

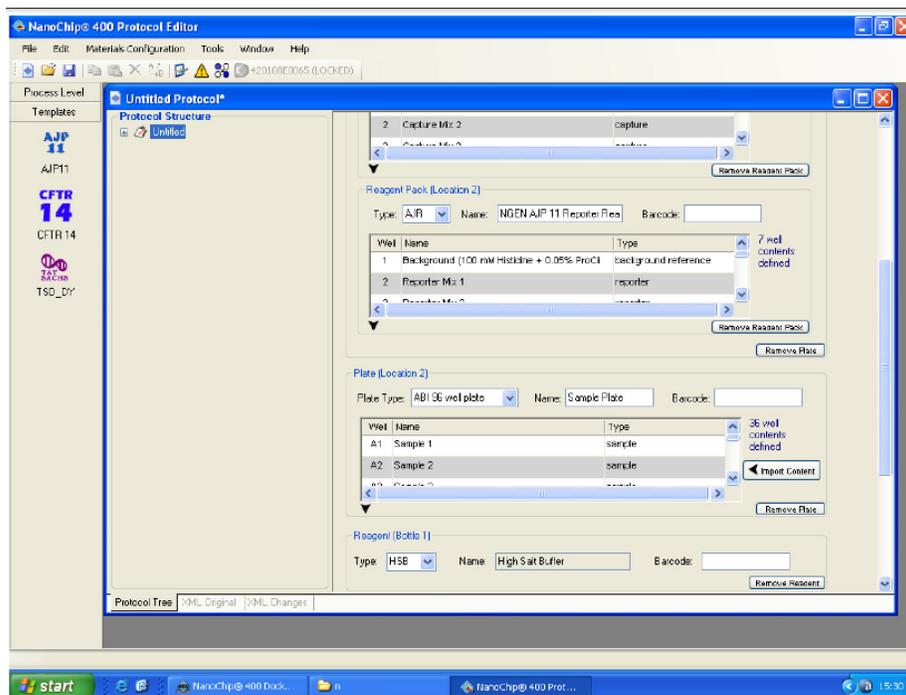


Figure 5. Protocol Editor Screen

8. **Click the template** (located on the left under protocol structure) click **'OK'** on the popup, this will make sure the template is updated with your recently added information. Make sure that on the plate drawing the wells you chose are blue with black dot in them.
9. Go to the Protocol Editor toolbar and select the Protocol Summary icon . A summary will display the materials configuration checklist that can be used when setting up the materials to run the protocol. To print out the summary, select the Print icon at the top left-hand side of the screen.
Note: that the following details can be found in the Protocol Summary.
 - Estimated protocol run time.
 - Estimated waste volume to be generated.
 - Materials Configuration Checklist, including:
 - Water and Buffer Bottle contents and approximate volume consumption;
 - Reagent bottle contents and approximate volume consumption;
 - Reagent pack location and well contents;
 - Sample plate location with well contents and volumes.
 - Specific pad use.
10. Save the protocol by going to file "save as", click ok on the pad mapping popup and save the file under the proper library. Your protocol is now ready for run. Close the protocol editor.

Running the Assay

1. Select the Instrument Manager icon from the DockBar to display an Instrument Manager screen. Selecting the **Open** button generates a browser allowing the user to select the desired protocol. When a protocol is selected the screen updates to display the details for that protocol.
2. Ensure that the correct protocol is displayed before selecting the **Run** button. A pop-up showing the calculated volume of fluid waste that the protocol will be generates. If the waste container does not have enough room to hold the waste, empty the container and return it to its position under the Instrument before selecting the **OK** button. After selecting the **OK** button, the user will be prompted to place the protocol materials in the Instrument.
3. Load reagents on the instrument deck
 - A. Place the following buffer bottles on the instrument deck as instructed by the Instrument LCD prompts.

Table 5: Location of Bottles in the NanoCHIP® 400 Instrument

Solution	Bottle Size	Location
High Salt Buffer	30 mL	Slot 1
Low Salt Buffer	30 mL	Slot 2
Target Prep Buffer	30 mL	Slot 3
CAP _{down} Sample Buffer B*	30 mL	Slot 4

*Required for Onboard Sample Dilution option only. This position is left empty when sample dilution is done manually.

- B. Place the GIP II Capture/Reporter Reagent Pack and the GIP I Reference Pack Plate in the Reference Pack Plate before they are placed in the instrument deck as follows:
 - GIP II Capture/Reporter– Position 1
 - GIP II Reference Pack– Position 2
 The GIP II Reference Reagent Pack is only required for the first use of a cartridge.
 - C. Place the Reagent Pack Plate in the instrument deck (Location 1) as instructed by the LCD prompt.
 4. Place the sample plate in Plate (Location 2) of the instrument deck as instructed by LCD prompt.

Note: When using an ABI 96-well sample plate on deck, always position the plate with well A1 in the upper left-hand corner.

5. Once the protocol materials are placed in the Instrument and the robot door is closed, the Instrument automatically runs the protocol. If the instrument needs to be stopped or paused, press the **Pause** or **Stop** buttons on the computer screen or the **Pause** button on the front of the Instrument. When the protocol has completed running, the Instrument LCD displays the message INSTRUMENT READY.
6. After the run is complete, select **Eject** from the Instrument Manager screen. When the LCD displays "Remove Cartridge", remove the cartridge from the instrument. If the cartridge has not been fully used, return the cartridge to its pouch and store at 2 - 8°C. If the cartridge has been fully used, discard it.
Note: When the eject button is selected, a window will appear asking the user to strip and/or fill the cartridge before ejecting: Select **Fill**; Scroll down and Choose **Water**.
7. Remove all buffers and replace the Wash Buffer with water. Perform routine maintenance as is appropriate.

Results

The data are analyzed in a Microsoft Office Excel based spreadsheet. Refer to section IV for a description of the GIP Combi II Data Analysis Spreadsheet features, instructions for setting preferences, and data calculations.

Export the data from a GIP NanoCHIP® 400 run as follows:

- A. Select **Data Analysis**  from the NanoCHIP® 400 DockBar
 - B. Select **Export Processed Data**. Select **Next**.
 - C. Select the appropriate cartridge and session number. The session numbers are listed by date, followed by the time the assay run started.
 - D. Select all red and green image data files; select **Finish**.
 - E. A new screen appears. In the View tab, select **Show Non-Activated Pads**.
 - F. Select **Export** on the lower right side of the NanoCHIP® 400 Data Analysis window.
 - G. A new screen will appear; be sure to check all the boxes and select **Export**.
 - H. Enter a file name (for example, the cartridge serial number and date of the run) and select **Save**. An Excel spreadsheet will automatically be generated.
 - I. Close the NanoCHIP® 400 Data Analysis software.
2. Import the GIP data into the GIP Combi II Data Analysis Spreadsheet:
 - A. Open the GIP Data Analysis Spreadsheet.
 - B. Select the **Import** button. Find the file you just saved and select **Open**.
 - C. A new message appears that prompts the user to save the Data Analysis Spreadsheet. A default name is given, but another name may be assigned.
Notes: If Show Non-Activated Pads was not selected during data export, an error message will appear when data import is attempted to the GIP Data Analysis Spreadsheet. If this occurs, repeat the data export process by selecting the Show Non-Activated Pads. To prevent data overwriting, the Import button is removed after a set of data is imported.
 - D. Select **Analyze** to view your results.
 - E. **Save** your changes to the spreadsheet

VI. GIP DATA ANALYSIS SPREADSHEET

Data Analysis Spreadsheet

Read Only

The GIP Combi II Data Analysis Spreadsheet is a Read-Only file and will prompt the user to save the file with a new name when preferences are set.

Preference Setting

1. Information Header
Open the GIP Combi II Data Analysis Spreadsheet. Enter information for the header where prompted on the Samples Worksheet. The information header will appear on every worksheet and on every printed page.
2. Save Settings
Select **File/Save As** and save your preferences with a new file name.

GIP Combi II Worksheets

After importing and analyzing the test results into the "GIP Data Analysis Spreadsheet" (as explained in the Results section) the user can move between the different fields (worksheets).

Samples Worksheet

The sample ID, cartridge number, cartridge session number, operator ID and instrument ID are imported to the Samples Worksheet. The Sample IDs and Sample ethnicities may be edited on this sheet. Boxes for the information header and comments are provided. All other cells are protected and cannot be edited. Footer with lines for "Reviewed By" and "Approved By" is on the printed sheet See figure 6.

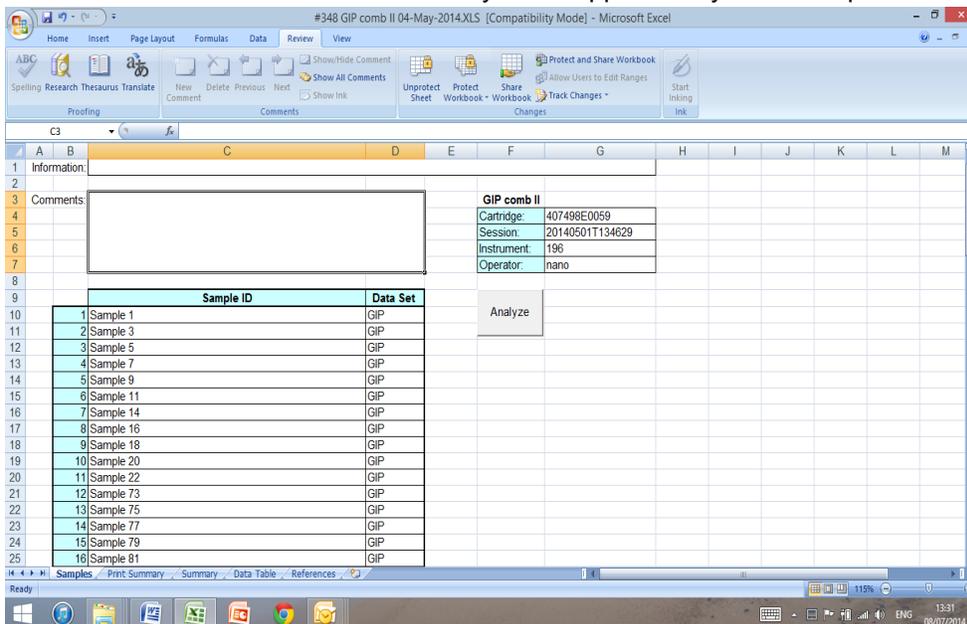


Figure 6. GIP Combi II Data Analysis Spreadsheet; Samples worksheet.

Summary Worksheet

This sheet provides an overview of the sample calls. Sample positions that were run in the current session, sample IDs, Sample ethnicities, and results are displayed in adjacent columns as indicated in Figure 7. The interpretation relies on the presence of the fragments enhanced and detected in the reaction as mentioned in Table 1 and indicated in Table 6A and, 6B.

The sample is Negative if all the markers are negative (-) and the Negative Validation Control (NVC) is positive. The sample is designated as "Invalid Sample" if all the target markers are negative (-). In this event there is a need for a new DNA extraction.

Position	Sample ID	Data Set	PARASITES					BACTERIA		
			<i>Dientamoeba fragilis</i>	<i>Cryptosporidium</i> spp.	<i>Giardia lamblia</i>	<i>Entamoeba histolytica</i>	<i>Entamoeba dispar</i>	<i>Blastocystis hominis</i>	<i>Shigella spp./EIEC</i>	<i>Campylobacter</i> spp.
1	Sample 3	GIP	-	-	-	-	-	-	POS	-
2	Sample 5	GIP	-	POS	-	-	-	-	POS	-
3	Sample 7	GIP	-	-	-	-	-	-	-	POS
4	Sample 9	GIP	-	-	-	-	-	POS	-	-
5	Sample 11	GIP	-	-	POS	-	-	-	-	-
6	Sample 14	GIP	-	POS	POS	-	-	-	-	-
7	Sample 16	GIP	-	-	-	-	POS	-	-	-
8	Sample 18	GIP	-	-	-	POS	-	-	-	-
9	Sample 20	GIP	POS	-	-	-	-	-	-	-
10	Sample 22	GIP	-	-	-	-	POS	-	-	-
11	Sample 73	GIP	-	-	POS	POS	POS	-	POS	-
12	Sample 75	GIP	-	-	POS	POS	POS	-	POS	-
13	Sample 77	GIP	-	-	-	-	-	-	-	POS
14	Sample 79	GIP	-	POS	-	-	-	-	-	-
16	Sample 83	GIP	-	POS	-	-	-	POS	-	-

Figure 7. GIP Combi II Data Analysis Spreadsheet; Summary worksheet

The Summary Worksheet also displays the information header, cartridge number, cartridge session number, and operator ID. When printed, a footer with lines for "Reviewed By" and "Approved By" will appear. The print settings for this sheet are editable. All cells in this sheet are protected and cannot be edited.

Table 6: Data Interpretation by Target Gene for bacteria panel (A) and Parasites panel (B)

A. Bacteria

NVC	<i>mapA</i>	<i>asp</i>	<i>ipaH</i>	<i>invA</i>	Interpretation
-/+	-	-	-	+	<i>Salmonella enterica</i>
-/+	-	-	+	-	<i>Shigella spp.</i>
-/+	-	+	-	-	<i>Campylobacter coli</i>
-/+	+	-	-	-	<i>Campylobacter jejuni</i>
-/+	+	+	-	-	<i>Campylobacter jejuni</i> and <i>C. coli</i>
+	-	-	-	-	Negative
-	-	-	-	-	Invalid sample

B. Parasites

NVC	BH 18S	COWP	<i>Giardia</i> 16S	ED 18S	EH 18S	DF 16S	Interpretation
-/+	-	-	-	-	-	+	<i>Dientamoeba fragilis</i>
-/+	-	-	-	-	+	-	<i>Entamoeba histolytica</i>

-/+	-	-	-	+	-	-	<i>Entamoeba dispar</i>
-/+	-	-	+	-	-	-	<i>Giardia lamblia</i>
-/+	-	+	-	-	-	-	<i>Cryptosporidium spp.</i>
-/+	+	-	-	-	-	-	<i>Blastocystis hominis</i>
+	-	-	-	-	-	-	Negative
-	-	-	-	-	-	-	Invalid sample

Data Table Worksheet

The information displayed in the Data Table sheet are sample ID, cartridge number, cartridge session number, operator ID, and the calculated data that are described below. The information displayed for each sample and mix is the Green signal.

The Data Table Worksheet also displays the information header, cartridge number, cartridge session number, and operator ID. When printed, a footer with lines for “Reviewed By” and “Approved By” will appear. The print settings for this worksheet are editable. All cells in this sheet are protected and cannot be edited.

The Positive Control sample is used for the validation of the PCR. The call designated for the Positive Control is "Pass" as appearing in position 0 of the table.

References Worksheet

The signal data for the References and average Reference Mix backgrounds are listed on this sheet (Figure 8). Additionally, it lists whether or not the references pass the signal threshold and signal-to-background criteria. In the event that a Reference fails, all samples are designated as “Reference Failure” and no calls can be made on the Summary Worksheet or Data Table Worksheet. In this case, please refer to Table 8 below for further actions.

The References Worksheet also displays the information header, cartridge number, cartridge session number, and operator ID. When printed, footer with lines for “Reviewed By” and “Approved By” will appear. The print settings for this worksheet are editable. All cells in this sheet are protected and cannot be edited.

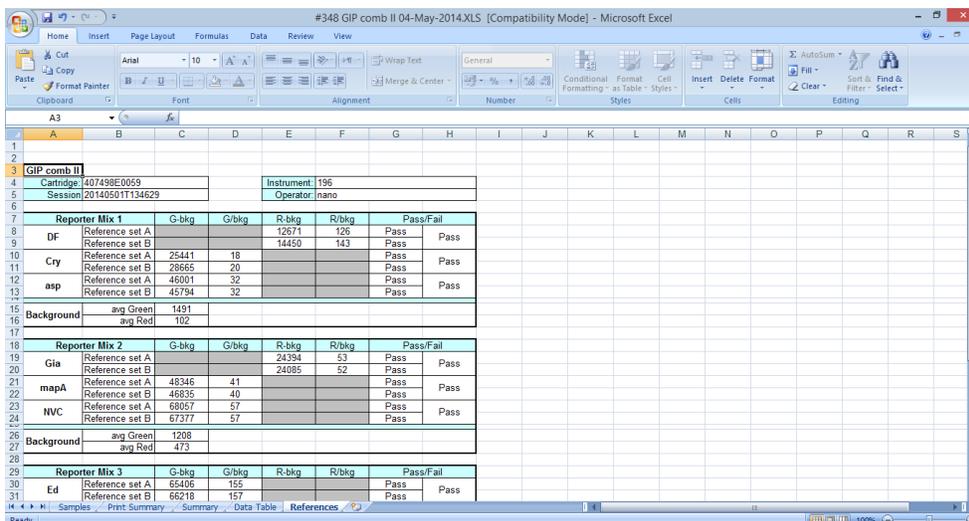


Figure 8. GIP Combi II Data Analysis Spreadsheet; References sheet

Data Calculations

Data calculation and analysis are performed automatically by the Excel software. The raw data is available for the user convenience.

In order to determine if a specific amplicon is present in the tested sample, the signal corresponding to this sample is compared to the signal from the irrelevant capture (background). The Flowchart in figure 9 describes the GIP assay application algorithm for determine if a certain sample is positive or negative.

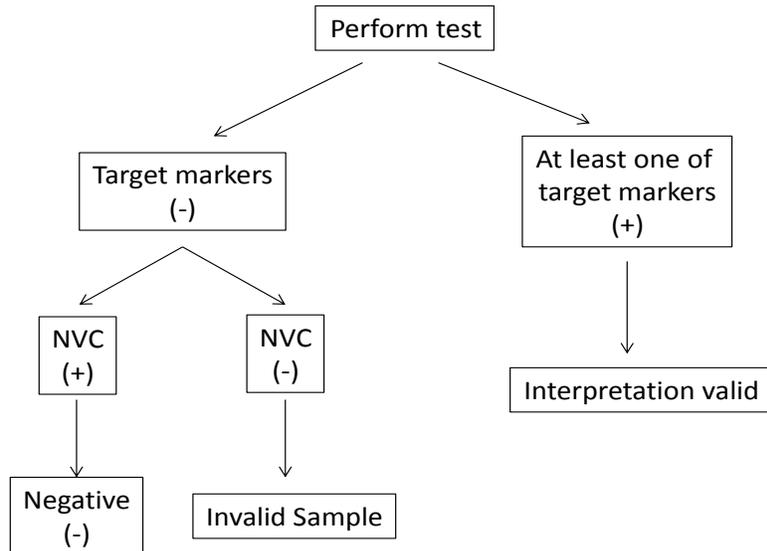


Figure 9. Data interpretation flowchart.

In viewing the Data Table Worksheet, the first column indicates the sample position on the cartridge. The sample column lists the sample ID. The marker column lists the markers present in the mix. Each row of markers for a sample corresponds to capture mixes 1 - 4 in order. The Green listed is the raw signals intensity for that pad. The Control signal is the sample specific background. The ratio listed is the value of the Green signal of the sample divided by the Control signal of the same sample. This value determines the signal requirements and ratio criteria described in Table 7.

For example, if for a certain specimen the following conditions are met: (1) Sample ratio of COWP gene reporter is >2. (2) Fluorescence signal is > 6500 and (3) other markers (reporters) are below the minimum signal criteria then the specimen is positive for COWP and the call designated as "*Cryptosporidium spp.*" as mentioned in table 6B.

Table 7: Signal level and Ratio of the various markers in the test.

Pathogen	Minimum Signal	Minimum Ratio
<i>D. fragilis</i>	4900	4
<i>Cryptosporidium spp.</i>	6500	2
<i>Giardia</i>	5500	5.5
<i>E. histolytica</i>	6000	3
<i>E. dispar</i>	3000	5
<i>Blastocystis hominis</i>	4500	3

<i>Salmonella</i>	7500	5
<i>Shigella</i>	10000	5
<i>Campylobacter coli (asp)</i>	10000	3.5
<i>Campylobacter jejuni (mapA)</i>	9000	6
NVC	2500	2

Table 8: Action for Failed Reference Criteria and Invalid Control Designations

Description	Criteria	Action
Failure reference signal	≤ 10000 above reference background	In the event of a reference failure, repeat testing of all samples on the cartridge, using previously amplified samples
Invalid Sample designation	1. Ratios for all markers are below the ratio specification listed in Table 7 2. The Positive Control sample is Valid (Pass)	In this event, the samples DNA is Invalid for testing, re-extract the sample in question
	1. Ratios for all markers are below the ratio specification listed in Table 7 2. The Positive Control sample is Invalid	In the event of Invalid Samples and Positive Control, repeat the PCR step with the extracted DNA

Limitations of the Procedure

1. The NanoCHIP® assays can only be performed only on the NanoCHIP® instruments.
2. The NanoCHIP® assay is a qualitative test and does not provide the quantitative value of detected organism present.
3. The NanoCHIP® GIP assay is intended for use only with unpreserved and Cary-Blair preserved stool samples.
4. All results should be used and interpreted in the context of a full clinical evaluation as an aid in the diagnosis of gastrointestinal infection.
5. Error results may occur from improper sample collection, handling, storage, technical error, sample mix-up, or because the number of organisms in the sample is below the analytical sensitivity of the test.
6. There is a risk of false negative values due to the presence of strain/species sequence variability in the targets of the assay, procedural errors, amplification inhibitors in specimens, or inadequate numbers of organisms for amplification.
7. As with all PCR-based in vitro diagnostic tests, extremely low levels of target below the analytical sensitivity of the assay may be detected, but results may not be reproducible.
8. If a certain sample result is Invalid then the sample should be repeated from DNA extraction.

VII. PERFORMANCE CHARACTERISTICS

Clinical Sensitivity and Specificity

Clinical performance characteristics of the NanoCHIP® GIP- Gastrointestinal assay were assessed in clinical study performed in several external sites by evaluation of clinically-obtained prospective and retrospective (frozen), specimens. Study specimens consisted of unpreserved samples (parasites testing) or Cary-Blair preserved (bacteria testing) liquid to soft stools from symptomatic patients with acute gastroenteritis for whom diagnostic procedures were indicated and ordered.

Specimens were characterized by the source site's routine laboratory methodologies and included direct culture, microscopy or immunoassay which comprised the reference method for specimens obtained from each site. Discrepant results analysis was performed by further investigation of the sample in qRT-PCR (FDA / CE approved) assay or by amplicon sequencing. Genomic DNA was extracted using NucliSENS easyMag (bioMerieux), MagNA Pure (Roche) and Arrow (DiaSorin) DNA extraction automated systems, as well as with manual stool DNA extraction kit (Qiagen). All extracts were stored at -20°C before and after use.

Table 9, presents cumulative results obtained from three **Retrospective** evaluations performed in Israel in comparison to the lab reference methods. Table 10, presents combined results of two **Prospective** evaluations performed in reference laboratory in comparison to the lab reference methods.

Table 9: Overall sensitivity and specificity of the NanoCHIP® GIP- Gastrointestinal Panel Combi II assay from three Retrospective Studies.

Pathogen	Site 1		Site 2		Site 3		ALL	
	Positive Agreement		Positive Agreement		Positive Agreement		Specificity	
	TP/ (TP+FN)	Percent	TP/ (TP+FN)	Percent	TP/ (TP+FN)	Percent	TN/ (TN+FP)	Percent
<i>Campylobacter</i>	17/17	100	27/27	100	2/2	100	257/258	100
<i>Salmonella</i>	26/29	90	14/14	100	3/3	100	238/249	96
<i>Shigella</i>	6/6	100	17/17	100	13/13	100	263/266	99
<i>Giardia lamblia</i>	18/18	100	16/16	100	26/27	96	239/241	99
<i>Cryptosporidium</i>	N/A	N/A	2/2	100	1/1	100	299/299	100
<i>E. histolytica</i>	N/A	N/A	1/1	100	3/3	100	298/298	100
<i>E. dispar</i>	16/16	100	1/1	100	N/A	N/A	301/301	100
<i>D. fragilis</i>	22/23	96	63/66	95	8/8	100	210/225	93
<i>Blastocystis</i>	21/21	100			7/7	100	245/247	99

Table 10: Overall sensitivity, specificity, PPV and NPV of the NanoCHIP® GIP- Gastrointestinal Panel Combi II assay from two Prospective Studies.

Pathogen	Laboratory reference methods							
	Positive Percent agreement		95% CI	Negative Percent agreement		95% CI	PPV	NPV
<i>Blastocystis</i>	40/40	100%	89% - 100%	204/204	100%	97.6% - 100%	100%	100%
<i>D. fragilis</i>	48/48	100%	90.9% - 100%	196/196	100%	97.5% - 100%	100%	100%
<i>Salmonella</i>	4/4	100%	39.5% - 100%	239/240	99.6%	97.3% - 99.9%	80%	100%
<i>Shigella</i>	23/23	100%	82.8% - 100%	220/221	99.5%	97.1% - 99.9%	96%	100%
<i>Campylobacter</i>	21/21	100%	80.7% - 100%	222/223	99.5%	97.1% - 99.9%	95%	100%

<i>Giardia lamblia</i>	8/8	100%	46.3% - 100%	236/236	100%	97.3% - 99.9%	83%	100%
<i>Cryptosporidium spp.</i>	2/2	100%	19.7% - 100%	242/242	100%	98% - 100%	100%	100%
<i>E. histolytica</i>	0	-	-	244/244	100%	98% - 100%	-	100%
<i>E. dispar</i>	0	-	-	244/244	100%	98% - 100%	-	100%

CI- 95% Confidence Interval (Lower limit – Upper limit)

PPV- Positive Predictive Value; NPV- Negative Predictive Value

Precision / Reproducibility (between runs)

Positive samples for the indicated parasites and bacteria were tested by different users, in 3 different runs and on different PCR and NC400 instruments (Table 11).

Table 11: Reproducibility

Pathogen	Run 1	Run2	Run 3
	Positive results		
<i>Shigella</i>	5/5 (100%)	5/5 (100%)	5/5 (100%)
<i>Salmonella</i>	3/3 (100%)	3/3 (100%)	3/3 (100%)
<i>Campylobacter jejuni</i>	7/7 (100%)	7/7 (100%)	7/7 (100%)
<i>Campylobacter coli</i>	3/3 (100%)	3/3 (100%)	3/3 (100%)
<i>Cryptosporidium spp.</i>	3/3 (100%)	3/3 (100%)	3/3 (100%)
<i>Giardia lamblia</i>	4/4 (100%)	4/4 (100%)	4/4 (100%)
<i>D. fragilis</i>	3/3 (100%)	3/3 (100%)	3/3 (100%)
<i>Blastocystis hominis</i>	7/7 (100%)	7/7 (100%)	7/7 (100%)
<i>E. histolytica</i>	2/2 (100%)	2/2 (100%)	2/2 (100%)
<i>E. dispar</i>	4/4 (100%)	4/4 (100%)	4/4 (100%)
NVC	28/28 (100%)	28/28 (100%)	28/28 (100%)

The results demonstrate complete accordance between all runs.

Precision / Repeatability (of same sample run)

A representative positive sample for each of the indicated target genes was run repeatedly 6 times. The repeatability was tested in view of the specifications, as presented in the table for each of the target genes, and the resulted interpretation (Table 12).

Table 12: Repeatability

Pathogen	Target gene	Minimum Signal	Signal/ Noise ratio per Target	Signal level reading	Signal level Median	Positive Interpretation
<i>Shigella</i>	<i>ipaH</i>	10000	5	80800 - 89400	86163	6/6 (100%)
<i>Salmonella</i>	<i>invA</i>	7500	5	81700 - 87700	83091	6/6 (100%)
<i>Campy. jejuni</i>	<i>mapA</i>	9000	6	62800 - 70900	69908	6/6 (100%)
<i>Campy. coli</i>	<i>asp</i>	10000	3.5	62800 - 77000	74776	6/6 (100%)
<i>Cryptosporidium spp.</i>	<i>cowp1</i>	6500	2	56000 - 69500	61837	6/6 (100%)
<i>Giardia lamblia</i>	16S rDNA	5500	5.5	58000 - 73500	70176	6/6 (100%)
<i>D. fragilis</i>	16S rDNA	4900	4	33000 - 72000	68356	6/6 (100%)
<i>Blastocystis</i>	18S rRNA	4500	3	55200-66100	60401	6/6 (100%)
<i>E. histolytica</i>	18S rDNA	6000	3	23300 - 56000	32836	6/6 (100%)
<i>E. dispar</i>	18S rDNA	3000	5	13200-28500	22710	6/6 (100%)
NVC	R16S	2500	2	11300 - 17600	13797	6/6 (100%)

The results show complete repeatability of all the tested samples for all the target genes.

Limit of Detection (LoD) Determination Using Viable Bacteria and Parasites with characterized Clinical Feces samples

The analytical sensitivity (LoDs) of the GIP assay was assessed by analyzing serial dilutions of simulated positive samples made from known stocks of commercial strains. All simulated specimens were prepared by spiking in negative clinical stool. The data from serial dilutions were confirmed in at least 8 replicates of the selected dilution for each target. LoD was defined as the lowest concentration at which 100% of all replicates tested gave positive results (Table 13).

Table 13: LoD determination of different pathogens

Pathogens	GIP 100% LoD	
<i>Salmonella enterica</i>	1.00E+05	cfu/ml
<i>Shigella spp./EIEC</i>	1.00E+04	cfu/ml
<i>Campylobacter spp.</i>	1.40E+04	cfu/ml
<i>Giardia lamblia</i>	5.00E+03	cells/ml
<i>Dientamoeba fragilis</i>	5.00E+03	cells/ml
<i>Entamoeba histolytica/ dispar</i>	5.00E+03	cells/ml

APPENDICES

Appendix A: GIP Assay Format

The GIP assay uses a capture down format to recognize the markers based on identified sample ethnicity. Following the single tube multiplex polymerase chain reaction, the amplicons are specifically bound to a permeation layer that covers the electronic microarray via hybridization to complementary capture oligonucleotides. These captured oligonucleotides are biotinylated at the 5' or 3' end and are bound to streptavidin that has been incorporated into the permeation layer.

The NanoCHIP® GIP Combi II Kit components include the following:

1. GIP Combi II Primer Mix: set of forward and reverse amplification primers that specifically amplify fragments (markers) that are shown to be associated to pathogenic bacteria and parasites (Table 1).
2. LS Amplification Buffer: a general purpose reagent used for the PCR amplification of DNA in an ionic environment optimized for analysis on the NanoCHIP® 400 electronic microarray.
3. GIP I Capture/Reporter Pack: a 9 well pack containing a set of 4 unique capture mixes and 5 unique reporter mixes. Each capture is a biotinylated synthetic oligonucleotides complementary to one of the amplicons generated with the GIP Primer Mix. Each capture is present in one of the 4 capture mixes. Reporter mixes contain discriminators and universal reporters. Each discriminator contains a segment that is complementary to the fragments that specifically characterize the pathogens of interest. Each GIP reporter mix contains numerous pairs of discriminators.
4. GIP I Reference Pack: a 4 well pack containing a set of 4 unique mixes of biotinylated reference oligonucleotides. The reference oligonucleotides have a segment complementary to one or more discriminator oligonucleotides. The green/red signals generated from the references indicate that the reporter mixes and reporting protocol are working properly.
5. CAP_{down} Sample Buffer B: a general purpose reagent used for the delivery of amplicons to the activated test sites on the NanoCHIP® 400 electronic microarray.

Starting with the amplified material, the GIP protocols generated as described in the “Creating a Protocol” section consist of the following five steps.

1. **Capture addressing:** the capture oligonucleotides mixes specific for the GIP Combi II assay are electronically addressed to predetermined pads across the cartridge in a sequential manner. The number of pads addressed with each mix is equal to the number of samples/controls being analyzed. Wells 1–4 of the GIP I Capture/Reporter Reagent Pack contain Capture Mixes 1–4.
2. **Reference addressing:** the reference oligonucleotides mixes specific for the GIP assay are electronically addressed to predetermined pads in the NanoCHIP® microarray. Each reference mix is addressed in two separate electronic activation events to separate pads. References are addressed in the first use of the cartridge— subsequent cartridge runs utilize references addressed in the first use. The reference mixes are in wells 1–4 of the GIP I Reference Reagent Pack.
3. **Amplicon Hybridization:** amplification reaction products diluted in CAP_{down} Sample Buffer B are simultaneously addressed to 4 pads that comprise the full set of the Capture Mixes 1-4. The amplicons are sorted across the 4 pads by hybridization to specific captures. An amplicon hybridizes only 1 of the 4 capture pads.
4. **Reporting:** sequential cycles of passive hybridization-thermal discrimination-fluorescence imaging-thermal stripping ensure for each of the 5 reporter mixes contained in the GIP I Capture/Reporter Reagent Pack in wells 5-9. The thermal stripping step removes the discriminator/universal reporters but leaves the amplicon bound to the capture oligonucleotide for the next reporter mix.
5. **Reverse Bias Washing:** each pad that was addressed with sample is subjected to a reverse bias wash to remove bound amplicon that can potentially interfere with future assays on the microarray.

After Reverse Bias Washing, the system automatically fills the cartridge with Water for storage between uses.

Table 14 presents the markers in the context of the capture/reporter mixture matrix. Each reporter mix reports markers across the 4 sample pads and has a minimum of one pad not used. The unused pad serves as the background for that reporting. Each sample has its own background pad.

Table 14: Map of Reporter Mixes 1–5 across Capture Pads 1–4

	Reporter mix 1		Reporter mix 2		Reporter mix 3	Reporter mix 4	Reporter mix 5
	RED	Green	RED	Green	Green	Green	Green
Capture mix 1	<i>D. fragilis</i>	<i>Crypto</i>					<i>Salmonella</i>
Capture mix 2					<i>E. dispar</i>		<i>Shigella</i>
Capture mix 3		<i>C. coli</i>	<i>Giardia</i>	<i>C. jejuni</i>			
Capture mix 4				<i>NVC</i>	<i>E. histolytica</i>	<i>Blasto</i>	

Appendix B: Legal Notices

Notice to Recipients about Licenses

Certain usages of the product described herein have been licensed from Beckman-Coulter Incorporated under United States Patent No. 5,653,939 and foreign counterparts thereof, and may be covered by Genetic Technologies Limited, United States Patent No. 5,612,179, applications and foreign counterparts thereof.

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