hepatomiR®

microRNA Biomarkers of Liver Function and Disease

hepatomiR® kit

Instructions for Use v4.1

January 2025

TAmiRNA

stability for life.

CE IVD REF KT-031-HEP EN

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Further information and technical notes can be found at **www.tamirna.com/hepatomiR**

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Revision history

Date	Revision	Details about change
May 2022	1.0	Creation of the IFU
September 2023	2.0	Lab Protocol Step 14
January 2024	3.0	Updated list of "not-supplied reagents (p. 21); Improvement of the lab protocol to reduce error probability (p. 23).
November 2024	4.0	Update of Table 6 (p.22); addition of qPCR setup with ROX (p. 28); Update of sections "Data Export and Analysis" (p. 30).
January 2025	4.1	Correction of tube cap colour (p. 20).

1

Product Summary

Intended-Use

Intended use

The hepatomiR® kit is intended to be used to quantify the levels of three human miRNAs, hsa-miR-122-5p, hsa-miR-192-5p, and hsa-miR-151a-5p (Table 1) in human platelet-poor plasma samples (Table 1). The hepatomiR® software calculates and returns a score ("p-score"), that can be used as a surrogate of liver function. The hepatomiR® p-score ranges between 0 and 1. A high p-score indicates reduced liver function and higher risk of adverse outcomes (see below "other intended use").

Table 1
List of microRNAs included in the hepatomiR® kit

microRNAs measured by the hepatomiR® kit.

microRNA ID (miRbase v22)	miRbase Accession Number	microRNA Sequence
hsa-miR-122-5p	MIMAT0000421	UGGAGUGUGACAAUGGUGUUUG
hsa-miR-192-5p	MIMAT0000222	CUGCCAAUUCCAUAGGUCACAG
hsa-miR-151a-5p	MIMAT0004697	UCGAGGAGCUCACAGUCUAGU

Key publications:

- Starlinger P, Hackl H, Pereyra D, Skalicky S, Geiger E, Finsterbusch M, Tamandl D, Brostjan C, Grünberger T, Hackl M, Assinger A. (2019). Predicting Postoperative Liver Dysfunction Based on Blood Derived MicroRNA Signatures. Hepatology. 2019 Jun;69(6):2636-2651. doi: 10.1002/hep.30572. Epub 2019 Apr 10

Definition of the patient population

The population used to develop hepatomiR® included both men (69%) and women (31%). The age range was 22-90 years with a median of 65 years. Three major tumor types were represented in this cohort, specifically hepatocellular (HCC) (20%), cholangiocellular (CCC) (19%), and metastatic colorectal carcinomas (mCRC) (41%). Other tumor types (9%) and benign tumors (5.5%) were represented as well.

Other intended use

The hepatomiR® p-score has been found to be potentially useful for preoperative (pre-OP) assessment of liver function in patients undergoing hepatic surgery. Together with other clinical parameters, the hepatomiR® p-score can inform about a patient's risk of

posthepatectomy liver failure (PHLF).

Therefore, the test can be applied in patients in need of partial liver resection (for example for the treatment of mCRC, CCC, or HCC cancers) who are eligible for liver resection based on tumor size and localization, general health status and liver function status according to traditional liver function parameters for the following reasons:

- To identify patients with high risk of PHLF, who may likely not benefit from hepatectomy.
- To identify patients with low risk of PHLF, who can be operated without delay.
- To identify patients with intermediate risk of PHLF, who are eligible of preoperative intervention with the aim of improving liver function.
- To monitor of liver function before, during, and after intervention with the aim of improving liver function.

Additional use cases for hepatomiR® are: the assessment of liver function in the context of acute or chronic liver diseases.

Diagnostic performance for the prognosis of post-hepatectomy liver failure (PHLF)

Starlinger et al. (Hepatology, Vol. 69, No. 6, 2019) retrospectively analyzed the utility of hepatomiR® p-score for the prognosis of PHLF in 146 oncological patients suffering from HCC, CCC, or mCRC, respectively. Table 2 summarizes the observed prognostic performance for PHLF for two cut-offs.

Table 2

Prognostic performance characteristics of the hepatomiR® p-score for PHLF.

Cut-off	Odds Ratio	PPV	NPV	Sensitivity	Specificity
p> 0.59	18.7	0.70	0.89	0.55	0.94
p> 0.68	19.7	0.83	0.85	0.34	0.98

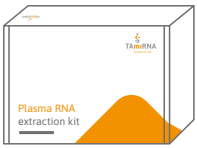
The hepatomiR® test could therefore satisfy the urgent clinical need for an easily assessable preoperative test to assess the liver function in patients with liver cancer, specifically HCC, CCC, and mCRC, and predict liver function recovery after partial liver resection. This is critical to identify patients with high risk of PHLF, and to plan according risk reduction measures.

Workflow Components

The following components are required for the measurement of 3 heptomiRs and 5 quality controls in human platelet poor plasma samples:

- Plasma RNA extraction kit
- hepatomiR® chemistry, including spike-ins, RT chemistry and miGreen Mix
- primer coated hepatomiR® 96- or 384-well qPCR plates

Figure 1
Overview of required components



Plasma RNA extraction kit

hepatomiR® chemistry, including spike-ins, RT chemistry and miGreen Mix

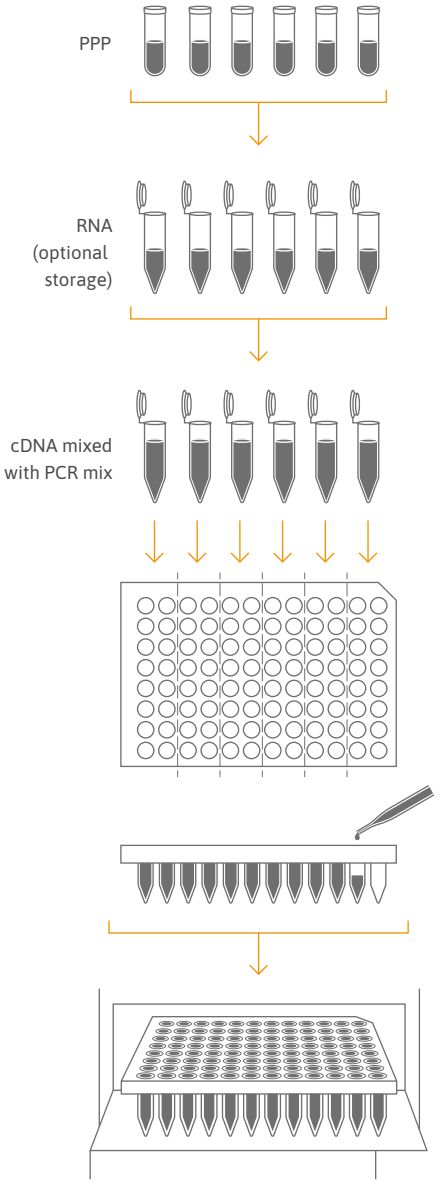
primer coated hepatomiR® 96- or 384-well qPCR plates

This combination of kits enables the measurement of microRNAs in platelet poor plasma in a single day.

The entire workflow consists of five main steps shown in Figure 2:

1. RNA extraction
2. cDNA synthesis
3. Preparation of PCR Mastermix
4. Real-time PCR amplification
5. Data analysis

Figure 2
Workflow summary



1 RNA extraction (1.5h)

Extract RNA using the Plasma RNA extraction kit

2 cDNA synthesis (1.5h)

Prepare cDNA using the hepatomiR® chemistry kit reagents

3 Preparation of PCR Mastermix

Mix cDNA with miGreen Mix and nuclease free water

4 Real-time PCR amplification (2.5h)

Distribute PCR mix into wells on the ready-to-use hepatomiR® plate and start qPCR run

5 Data analysis

Export data for further analysis, data pre-processing, normalization and statistical analysis

Kit Technology

RNA Extraction

The Plasma RNA extraction kit enables the isolation of microRNA, from a maximum of 200 µl of sample. The phenol-free protocol uses spin column technology without the need for a vacuum pump. It allows analysis of extracellular vesicle RNA through lysis of the vesicles. The kit is designed to isolate high quality microRNA in amounts sufficient for qPCR analysis using the hepatomiR® chemistry kit.

The workflow consists of 5 simple steps:

1. Lysis of biofluid components
2. Precipitation and removal of proteins
3. Precipitation of RNA using isopropanol and column loading
4. Washing
5. Elution

In the first part of the RNA isolation process, membranized particles/cells are lysed using the provided lysis solution. Proteins are precipitated using the precipitation solution and the supernatant (including RNA) is mixed with isopropanol for precipitation. This solution is loaded onto a spin-column, where a resin binds RNA in a manner that depends on ionic concentrations. Thus, microRNA will bind to the column, while the residual proteins will be removed in the flow-through or retained on the top of the resin. The bound microRNA is then washed with the provided wash solutions in order to remove any remaining impurities, and the purified microRNA is eluted with RNase free water.

Reverse Transcription Quantitative PCR Detection

A universal reverse transcription (RT) reaction is performed, as shown in Figure 3 (Step 1–2), which means that all microRNA species are converted into complementary DNA (cDNA) at the same time. This enables parallel quantitative PCR (qPCR) detection of different microRNA sequences in one cDNA sample using the hepatomiR® test plate.

Universal RT is achieved by first adding a poly-A tail to the mature microRNA template (Step 1). Complementary cDNA is synthesized using a poly-T-primer with a 3' degenerate anchor and a 5' universal tag.
During qPCR, the cDNA is then amplified using microRNA-specific and LNA™-enhanced forward and reverse primers using miGreen for detection of double-stranded DNA (Step 2).

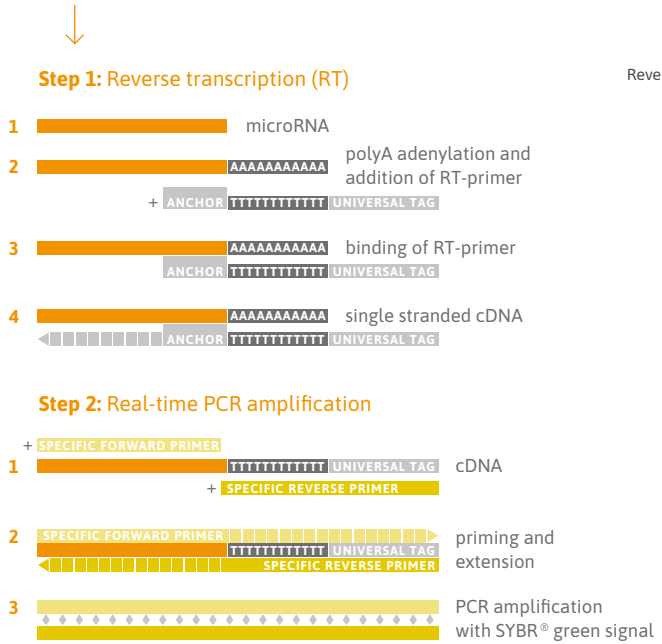


Figure 3
Reverse transcription and PCR amplification

LNA™ Technology

Locked Nucleic Acids (LNA™) are chemically modified nucleotides, which offer substantially increased affinity for its complementary strand, compared to traditional DNA or RNA oligonucleotides. This results in unprecedented sensitivity and specificity and makes LNA™ oligonucleotides ideal for the detection of microRNAs, due to their short length and varying content of G-C and A-T bases. Without LNA™, the heterogeneous hybridization properties could result in unspecific and low efficient primer binding and compromise data quality.

Storage and Stability of Kit Components

The hepatomiR® chemistry kit will be shipped on dry ice and **must be stored at -20°C.** The hepatomiR® qPCR plates will be shipped at room temperature and **must be stored at -20°C.** The Plasma RNA extraction kit is shipped at room temperature. Store the spin columns immediately at 2-8°C. Under these conditions, all components are stable until the expiration date, which is provided on the package or vial. Please note that each product component (Plasma RNA extraction kit, hepatomiR® chemistry kit, hepatomiR® qPCR plates) has an individual shelf-life with potentially differing expiration dates.

Warnings and precautions

The hepatomiR® Kit workflow should be performed by qualified and trained staff to avoid the risk of erroneous results. Use separate areas for the preparation of patient samples, RNA, cDNA and qPCR to avoid contamination.

- This product is intended for in-vitro diagnostic use only.
- Blood specimens should always be treated as if infectious and/or biohazardous in accordance with safe laboratory procedures.
- Follow necessary precautions when handling blood specimens. Use personal protective equipment (PPE) consistent with current guidelines for the handling of potentially infectious samples.
- Always use pipette tips with aerosol barriers. Tips that are used must be sterile and free from DNases and RNases.
- Do not eat, drink, smoke, or apply cosmetic products in the work areas.
- Do not use the kit after the expiry date.
- Do not use the kit when components are damaged after delivery.
- Dispose of waste in compliance with the local regulations.
- The reagents must be stored in the correct storage conditions before and after use.
- Try to only use LOTs for components 1, 2, and 3 that have been delivered together. Do not mix LOTs of components that have not been delivered together.
- The hepatomiR® components might have different expiration dates. We recommend to check and record the dates of each component (Plasma extraction kit, hepatomiR® chemistry kit, hepatomiR® qPCR plates upon arrival.
- Wash Buffer 1 and Lysis Buffer contain guanidine thiocyanate, which can form highly reactive compounds when combined with bleach. If liquid containing these solutions is spilt, clean with suitable laboratory detergent and water. If the spilt liquid contains potentially infectious agents, clean the affected area first with laboratory detergent and water, and then with 1% (v/v) sodium hypochlorite.

Material Safety Data Sheets (MSDS) are available online in convenient and compact PDF format at https://www.tamirna.com/hepatomir-kit-ce-ivd/ where you can find, view and print the MSDS.

- Any serious incident that has occurred in relation to the device must be reported to the manufacturer and the competent authority of the Member State in which the user and/or patient is established.

2

Important Pre-Analytical Considerations

Choice of Biofluid

Sample type: The hepatomiR® test requires the use of double-centrifuged plasma in order to obtain reliable results. Please refer to page 22 of this manual for the specific collection protocol. **Important**: Heparin as an anticoagulant is not compatible with RT-qPCR analysis and must be avoided. CTAD (Citrate, Theophyllin, Adenosin and Dipyridamol) has been exclusively used during the development of the hepatomiR® kit. Citrate has been shown to yield comparative results.
Table 3 summarizes the type of anti-coagulants and tube manufacturers, which have been tested and shown comparable results:

Table 3
Compatible collection tubes

Compatible collection tubes

Manufacturer	Catalog number	Anti-coagulant	Volume mL
Greiner, VACUETTE®	454387	Citrate	3.5 mL
Greiner, VACUETTE®	454064	CTAD	3.5 mL

Pre-analytical Standardization

Conditions during plasma processing can affect the detection of microRNAs mainly because of hemolysis, platelet activation or platelet and other blood cell contamination. In order to minimize pre-analytical variability and improve data quality, all protocols for collection and processing of platelet-poor-plasma (PPP) need to be standardized.
We recommend to incorporate the following points in the pre-analytical study protocols:

- Patient variation: if possible standardize the time for blood collection. Circadian rhythm, activity and diet are known to influence the levels of circulating microRNA content in patients.
- Use standardized needles and only plasma collection tubes that have been specified in table 3. We recommend to use 21 gauge needles for blood collection. Ensure that only the specified blood collection materials are used during the entire study.

- Blood collection must be performed by a person that is trained and familiar with the study protocol. Gloves must be worn at all times when handling specimens. This includes amongst others removal of the rubber stopper from the blood tubes, centrifugation, pipetting, disposal of contaminated tubes, and clean-up of any spills. Tubes, needles, and pipets must be properly disposed of in biohazard containers, in accordance with institutional requirements.
- Universal precautions and OSHA (Occupational Safety and Health Administration) and institutional requirements (http://www.osha.gov/SLTC/biologicalagents/index.html) should be followed, including gloves, eye protection or working in a biosafety cabinet for blood processing.
- Incubation and centrifugation protocols for obtaining plasma from whole blood must be standardized and followed strictly (see “Plasma Collection” on page 22 for exact protocols).
- Hemolysis (visible as red-colored biofluid) must be recorded for all samples used (see “Quality Control” on page 17 for more details on how to detect hemolysis in your samples).
- Plasma samples can contain substances that inhibit the RT-qPCR reaction. A prominent inhibitor is heparin. Hence, the use of lithium-heparin as an anticoagulant must be avoided.
- After thawing of collected plasma samples at room temperature, ensure that samples are kept cool (on ice or 4°C) at all times and avoid frequent freeze-thaw cycles. Low temperature is essential for RNA stability and sample matrix.
- For handling of plasma as well as RNA/DNA RNase-free filter tips and nuclease-free microcentrifuge tubes with optimized surface properties to prevent adsorption of nucleic acids (“low binding”), must be used.

Storage and Stability of PPP, RNA and DNA

Following the blood collection, PPP should be used for analysis (RNA isolation) within 120 minutes. If immediate analysis is not feasible, PPP can be stored at -80°C for up to 1 year.

All samples should be stored in nuclease-free plastic tubes with minimized absorption rates for nucleic-acids "low binding". To avoid freeze-thaw cycles the generation of aliquots of PPP is recommended. We recommend aliquot volumes of 225 µL PPP.

PPP, and RNA samples must be stored at -80°C for long term storage and kept on ice at all times during working procedures.

Total RNA samples should be stored in nuclease-free low-binding tubes at -80°C for not more than 6 months prior to analysis.

Undiluted cDNA must be stored at -20°C and can be used for up to 5 weeks after initial storage. Avoid more than 5 freeze/thaw cycles of frozen RNA and undiluted cDNA samples.

Working with RNA

RNases are very stable and robust enzymes that degrade RNA. Before working with RNA, it is recommended to create an RNase-free environment following the precautions below:

- The RNase-free working environment should be located away from microbiological work stations.
- Clean, disposable gloves should be worn at all times when handling reagents, samples, pipettes, disposable tubes, etc.
- It is recommended that gloves are changed frequently to avoid contamination.
- Designated solutions, tips, tubes, lab coats, pipettes, etc. should be prepared for RNA work only.
- All solutions that will be used should be prepared using molecular biology grade nuclease-free water.
- Clean all surfaces with commercially available RNase decontamination solutions.
- When working with purified RNA samples, ensure that they remain on ice.
- Spin down all reaction and sample tubes before opening.
- Use filter barrier pipette tips to avoid aerosol-mediated contamination.

It is recommended to establish and maintain designated areas for PCR setup, PCR amplification, and DNA detection of PCR products, due to the risk of contaminating reagents and mastermixes with amplified DNA.

The isolation of RNA and the reaction steps preceeding real-time PCR should be performed in rooms or areas, which are separated from areas where PCR experiments are performed in order to avoid contamination with amplified DNA. Use separate clean lab coats for RNA sample preparation, cDNA synthesis and when setting up PCR reactions or handling PCR products. Avoid bringing and opening tubes with amplified PCR products into the PCR setup area.

Quality Control

Synthetic spike-in Controls

In general, spike-in controls are used to monitor the efficiency and correct result of every workstep in the experiment. They can be used to identify outliers due to the presence of inhibiting factors or incorrect handling.

Uniform Cq-values obtained for the spike-ins demonstrate successful and homogenous RNA isolation, reverse transcription and qPCR for the samples. Synthetic spike-ins do not reveal the RNA content and quality in the biological sample.

RNA spike-in – The synthetic RNA spike-in is added to the sample during RNA extraction. It is used to monitor RNA extraction efficiency. The sequence has been designed to not match eukaryotic genomes and can therefore be applied across all species.

cDNA spike-in – The synthetic cDNA spike-in is added to the extracted RNA during reverse transcription into cDNA. It is used as a control for reverse transcription efficiency. It shares the natural microRNA sequence from C. elegans, which is not found in mammalian species. Reverse transcription efficiency is known to introduce the highest technical variance to RT-qPCR data.

PCR spike-in – This synthetic DNA template together with primers is spotted at a fixed position on every hepatomiR® test plate. The PCR spike-in is used to monitor PCR efficiency and to detect the presence of PCR inhibitors in samples.

The results obtained from all three spike-ins are analyzed by the hepatomiR analysis toolkit and used for quality control purposes. Only samples where spike-in values are found within range will be used for computation of the hepatomiR® p-score.

Hemolysis

Hemolysis can be a major cause of variation in serum/plasma microRNA levels due to contamination with cellular RNA.

The presence of hemolysis should be assessed visually for each sample. In addition, hemolysis can be assessed using the Hemolysis Index, which is based on the relative expression of miR-451a-5p compared to miR 23a-3p. An increase in miR-451a-5p relative to miR-23a-3p indicates the presence of hemolysis in human serum or plasma samples. The hepatomiR® analysis toolkit will automatically calculate and check the Hemolysis Index. Only samples with a Hemolysis Index < 7 will pass quality control and be used for computation of the hepatomiR® p-score.

Another option to determine hemolysis is the measurement of the absorbance peak of free haemoglobin by assessing free haemoglobin using a spectrophotometer such as NanoDrop™. Human serum or plasma samples are classified as being hemolyzed if the absorption at 414 nm is exceeding 0.2. However, the presence of small amounts of cellular contamination in serum or plasma samples is not readily detectable by visual or spectrophotometric means.

RNA Yield

Determination of RNA yield from 200 µL PPP is not possible by optical spectrophotometry or NanoDrop™ due to the lack in sensitivity of the method. We therefors use a RNA spike-in control to monitor RNA extraction efficiency. In addition, the entire analytical protocol precisely specifies to fluid volumes throughout the entire workflow (see “Lab Protocol” on page 23). The hepatomiR® kit uses 200 µL PPP for RNA extraction and 4 µL RNA for reverse transcription into cDNA. This is the optimum sample input in order to avoid inhibition of the reverse transcription reaction due to inhibitors that are co-extracted with total RNA.

3

Lab Protocol

Essential components

Table 4
Essential components

1 Plasma RNA extraction kit (Component 1/3)

This box contains enough reagents to extract RNA from 50 PPP samples.

1x	Lysis Buffer	20 mL
1x	Protein Precipitation Buffer	8 mL
1x	Wash Buffer 1	15 mL*
1x	Wash Buffer 2	11 mL**
1x	RNase-free water	10 mL
1x	Spin columns with 2 mL collection tube (no lid)	50
1x	Collection tube 1.5 mL (with lid)	50
1x	Collection tube 2 mL (no lid)	50

* Add 30 mL of 96%-100% Ethanol
** Add 44 mL of 96%-100% Ethanol

2 hepatomiR® chemistry (Component 2/3)

This box contains spike-in controls, all reagents for cDNA synthesis, as well as the miGreen Mix . Each reagent is labelled with expiration date.

1x	RNA spike-in Mix (blue cap)	dried
1x	cDNA spike-in Mix (yellow cap)	dried
1x	5x RT Buffer (brown cap)	0.1 mL
1x	10x RT Enzyme Mix (red cap)	0.05 mL
1x	ROX Reference Dye	1 mL
4x	RNase-free water (transparent cap)	1.5 mL
5x	2x miGreen Mix (green cap)	1 mL
1x	Glycogen (5 mg/mL) (transparent cap)	0.125 mL

3 Primer coated hepatomiR® qPCR plates (Component 3/3)

Plate format depends on the qPCR instrument. Format type, LOT, and expiration date are provided on the plate label.

8x	Primer coated 96 well qPCR plates	
2x	Primer coated 384 well qPCR plates	

Consumables and Equipment not supplied by TAmiRNA

Check to ensure that you have all the necessary user supplied consumables and equipment before proceeding.

Table 5
List of not-supplied reagents

Check	Reagent	Purpose	Suggested Supplier
☐	Ethanol absolute for analysis	• RNA Isolation: dilution of Buffers 1 and 2 (Step 1)	Merck-Millipore Cat: 1.00983.1011
☐	Isopropanol for analysis	• RNA Isolation: Step 8.	Merck-Millipore Cat: 1.09634.1011
☐	Nuclease Free Water	• Preparation of 80% EtOH for washing (Step 10c).	Qiagen Cat: 129115

Check	Materials and Equipment	Purpose	Suggested Supplier
☐	Nuclease-free PCR tubes (0.1 mL)	• Performance of reverse transcription reaction	General lab supplier
☐	Nuclease-free, low nucleic acid binding tubes (1.5 mL)	• Elution and storage of extracted total RNA.	e.g. Starlab Cat: E1415-2600 e.g. Eppendorf Cat: 0030108418
☐	Nuclease-free, filter pipette tips	• All pipetting steps.	General lab supplier
☐	Calibrated pipettes that cover 0.2–2 µL, 0.5–10 µL, 2–20 µL, 20–200 µL, 10–100 µL, 100–1000 µL	• All pipetting steps.	General lab supplier
☐	Centrifuge for 1.5-2.0 mL microtubes with cooling (4°C) and 12,000 rcf.	• Pre-analytical preparation of platelet-poor plasma (PPP). • RNA isolation (steps 3, 5, 8-10)	• Eppendorf models 5418R, 5425R, or 5427R • Hettich Mikro 200 R • iFuge M24PR
☐	Centrifuge for multiwell plates	• Preparation of qPCR plates (steps 19-20)	General lab supplier
☐	PCR- or thermocycler with ability to incubate 10 µl reactions in 0.1 mL PCR tubes	• cDNA synthesis (step 15)	Eppendorf Mastercycler
☐	Vortex Mixer	• All sample mixing steps.	General lab supplier
☐	Quantitative PCR (qPCR) machine with SYBR® green channel	• qPCR (step 20)	See table 5 below for all supported instruments.
☐	Sealing foils for PCR plates, transparent, suitable for qPCR	• qPCR (step 19)	e.g. Starlab, Cat: E2796-9795

Table 6
Plate format and PCR cycler

Plate format and PCR cycler

Plate Format 96-well	Cycler
A	QuantStudio 5 / 5 Dx (96-well Standard Block)
D	Bio-Rad CFX96™
F	Roche® LightCycler® 480 (96-well block)
Plate Format 384-well	**Cycler**
G	Roche® Light Cycler® 480 (384-well)

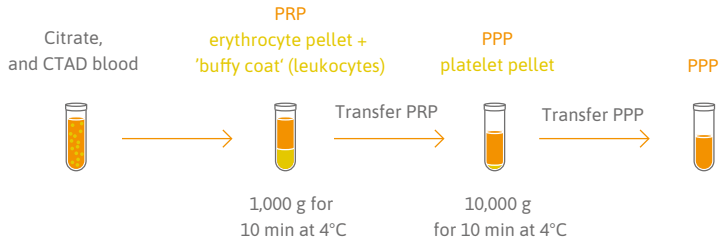
Plasma Collection

The hepatomiR® Workflow requires 200 µL platelet-poor plasma (PPP).

For blood collection we recommend to use 21 gauge needles and collection tubes specified in table 3 on page 13, which have so far been successfully tested.

Filled plasma collection tubes should be immediately inverted 8–10 times after blood collection. Plasma tubes can be incubated in an upright position at room temperature for **up to 2 hours before centrifugation.**

Figure 4
Workflow for the preparation of PPP



Centrifuge the blood sample at 1,000 g for 10 minutes at 4°C in a horizontal rotor (swing-out head). After centrifugation the supernatant (plasma) must be transferred to a new RNase-free tube of sufficient volume.

Centrifuge the plasma sample at 10,000 g for 10 minutes at 4°C in a horizontal rotor to obtain platelet-poor-plasma (PPP). Use a clean pipette and nuclease-free filter tips to

carefully transfer PPP into a pre-labeled/barcoded nuclease-free (1.5 mL) tube. Aliquot volume is recommended to be 225 µL, so that 200 µL can be safely used for RNA extraction. Close the caps on the vials tightly.

Note: Never pour off plasma; pouring off plasma directly from the draw tube will introduce excess cells to the specimen. To remove plasma, start from the top, gently draw specimen into pipette as you go further down tube. Leaving approximately 0.5 mL of plasma will insure that you do not disturb the buffy coat and cell layer.
Check that all aliquot vial caps are secure and that all vials are labeled. Place all aliquots upright in a specimen box or rack in an -80°C or colder freezer. All specimens should remain at -80°C or colder prior to analysis or shipping. The sample aliquots should not be thawed prior to analysis or shipping.

Lab Protocol

The RNA extraction has been **standardized to a volume of 200 µL PPP** as starting material to ensure high RNA yield and prevent inhibition of downstream PCR applications.

RNA Extraction

Important points before starting

- **Lysis Buffer and Wash Buffer 1 may form a precipitate upon storage. If necessary, redissolve by warming and then place at room temperature.**
- **Equilibrate buffers at room temperature before starting the protocol.**
- **Prepare 80% ethanol for Step 10c.**
- **All steps should be performed at room temperature. Work quickly!**

Important Note:
In case your are performing the hepatomiR® analysis for the first time, we highly recommend to start with a pilot analysis. Use only a small subset of your samples for this pilot analysis and analyze your data using the hepatomiR® data analysis application, see page 29. Once you have confirmed that sample quality and data quality are OK, proceed to the full analysis.

Caution **CAUTION: DO NOT add bleach or acidic solutions directly to waste containing Lysis Buffer and Wash Buffer 1**

This protocol is designed for human PPP.

First time use only

Notes

Step 1
Preparation of Wash Buffer 1 and Wash Buffer 2

Add 30 mL of >99 % ethanol to Wash Buffer 1. Add 44 mL of >99 % ethanol to Wash Buffer 2.
Note: The label on the bottle has a box that should be checked to indicate that the ethanol has been added.

Step 2
Reconstitution of lyophilized spike-in controls (RNA spike-in and cDNA spike-in)

- Spin down vials before use by centrifugation at 3,000 g for 2 min at room temperature.
- Resuspend the spike-ins (provided with hepatomiR® chemistry kit) by adding 80 µL nuclease-free water.
- Mix by vortexing and spin down. Store on ice for 20 min.
- Mix by vortexing again and aliquot in low bind tubes (not provided).
  (20 µL aliquots are recommended)
- Store at -20°C.

Step 3
Prepare 80% EtOH

Mix 10 mL nuclease free water with 40 mL Ethanol (see Table 5) to obtain 50 mL 80% Ethanol (required for step 10c).

RNA Isolation

Step 4
Thaw PPP samples and glycogen

After thawing on room temperature, centrifuge the PPP samples at 12,000 g for 5 min at 4°C to pellet any debris and insoluble components and to reduce effect of inhibitors/nucleases. Transfer exactly 200 µL PPP to a new 1.5 mL tube (not provided). Thaw glycogen on room temperature and store on ice.

Step 5
PPP lysis

Prepare lysis mix: For one sample add 1 µL RNA spike-in to 60 µL Lysis Buffer. For multiple samples prepare a mastermix including 2 extra reactions.
Add 61 µL Lysis mix to the 200 µL PPP. Vortex for 5 sec and incubate for 3 min at room temperature.

Important note: The RNA spike-in must be mixed with the Lysis Buffer before mixing with the PPP sample – if added directly to the sample it will be rapidly degraded.

Notes

Step 6 **Protein precipitation**	Add 20 µL of Protein Precipitation Buffer. Vortex for >10 sec and incubate for 3 min at room temperature. When processing multiple samples vortex immediately after addition of Protein Precipitation Buffer. The solution should become a milky suspension. Centrifuge for 3 min at 12,000 g at room temperature.
Step 7 **Transfer supernatant**	Transfer exactly 200 µL of the clear supernatant (aqueous phase) into a new 1.5 mL tube with lid (provided with the kit) and add 2 µL glycogen (5 mg / mL). Vortex and spin down.
Step 8 **Adjust binding conditions**	Add 200 µL Isopropanol. Vortex for 5 sec and spin down.
Step 9 **Load column**	Take a Spin Column with collection tube and load the entire sample onto the column. Centrifuge for 30 sec at 8,000 g at room temperature. Discard flow-through and place column back into the collection tube.
Step 10a **Wash and dry**	Add 700 µL Wash Buffer 1 to the spin column. Centrifuge for 30 sec at 8,000 g at room temperature. Discard flow-through and place column back into the collection tube.
Step 10b **Wash and dry**	Add 500 µL Wash Buffer 2 to the spin column. Centrifuge for 30 sec at 8,000 g at room temperature. Discard flow-through and place column back into the collection tube.
Step 10c **Wash and dry**	Add 500 µL 80% ethanol to the spin column. Centrifuge for 2 min at 8,000 g at room temperature. Place the spin column in a new 2 mL collection tube without lid (provided with the kit). Centrifuge column for 5 min at 12,000 g at room temperature. After centrifugation leave column open for 1 min to dry the membrane completely.
Step 11 **Elute**	Place the spin column in a clean 1.5 mL collection tube with lid (not provided, preferentially low-bind, see Table 5). Add 30 µL RNase free water directly onto the membrane of the spin column. Incubate for 1 min at room temperature. Close the lid and centrifuge for 1 min at 12,000 g at room temperature.
Step 12 **Storage**	Store the RNA sample immediately at -80°C or proceed to cDNA synthesis (Step 13).

cDNA Synthesis

Keep samples, reagents and reactions on ice (or at 4°C) at all time.

Notes

Step 13
Thaw total RNA

Thaw total RNA (from step 12) and cDNA spike-in on ice.

Step 14
Prepare reagents

Thaw 5x RT reaction buffer and nuclease free water and put on ice. Immediately before use, remove the enzyme mix from the freezer, mix by flicking the tube and place on ice. Spin down all reagents.

Step 15
Prepare cDNA synthesis mix

If performing cDNA synthesis on multiple RNA samples, prepare a mastermix including 1 extra reaction.

Reagent (Volumes in µL)	10 µL Rxn
5x Buffer	2
cDNA spike-in	1
Nuclease-free water	2
Enzyme mix	1
Total Volume Mix	6

Pipet 4 µL RNA template in each tube and add 6 µL cDNA mastermix. Mix by pipetting and spin down.

Step 16
Incubate and heat inactivate

Incubate the reaction at 42°C for 60 min.
Heat-inactivate the reverse transcriptase at 95°C for 5 min. Immediately cool to 12°C.

Step 17
Storage

Transfer the undiluted cDNA into nuclease-free low bind tubes (not provided) and freeze at -20°C for up to 5 weeks.

Important Note:

For qPCR Mastermix Setup without ROX (Roche Light Cycler/BioRad CFX) follow instructions on page 27 (Step 18a-21a).
For qPCR Mastermix Setup with ROX (ThermoFisher Quantstudio 5) follow instructions on page 28 (Step 18b-21b).

qPCR Mastermix Setup without ROX (Roche LightCycler/Biorad CFX)

Notes

Step 18a
Thaw reagents

Thaw cDNA (from step 17) and miGreen master mix on ice for 15–20 minutes. Keep reagents on ice all the time. Before use mix the Master mix by pipetting up and down. 6 samples can be measured in duplicates on a 96-well plate. 24 samples can be measured in duplicates on a 384-well plate

Step 19a
Mix cDNA with water and qPCR Master mix

Mix 3.6 µL cDNA with 86.4 µL nuclease free water, then add 90 µL miGreen Master mix (in total 180 µL). Mix by pipetting up and down, spin down to collect the liquid at the bottom. Repeat this step for all samples.
Caution: miGreen Master mix is light sensitive and should not be exposed to light for extended time periods.

Step 20a
Prepare hepatomiR® plate

Add 10 µL reaction mixture (from step 19a) (cDNA, NFW, Master mix) according to figure 5 and 6 to each of the 16 wells. Seal the plate with the appropriate optical sealing. Spin plate at 1,000 g for 90 sec. and incubate at 4°C for a minimum of 1 hour.

Note: The plate can be stored up to 24 hours at 4°C protected from light.

Step 21a
Perform qPCR

Before running the qPCR, spin plate at 1,000 g for 90 sec. Perform qPCR and melting curve analysis as shown below.

Step	Setting
Polymerase activation/ denaturation	95°C , 2 min, ramp-rate 4.4°C/sec
Amplification – 45 cycles	Analysis mode: Quantification 95°C, 10 sec, ramp 4.4°C/sec 56°C, 60 sec, ramp 2.2°C/sec Acquisition mode: single
Melting curve	Analysis mode: Melting curve 95°C, 10 sec, ramp 4.4°C/sec 55°C, 60 sec, ramp 2.2°C/sec 99°C, acquisition mode: Continuous, ramp 0.11°C/sec, acquisition per °C: 5

When the qPCR run is finished discard plates without opening the sealing foil (to avoid cross contamination).

qPCR Mastermix Setup with ROX (ThermoFisher Quantstudio 5)

Notes

Step 18b
Thaw reagents

Thaw cDNA (from step 17), ROX dye and miGreen master mix on ice for 15–20 minutes. Keep reagents on ice all the time. Before use mix the Master mix by pipetting up and down. 6 samples can be measured in duplicates on a 96-well plate.

Step 19b
Mix cDNA with water and qPCR Master mix

Add 10 µL ROX dye to 1mL of miGreen qPCR Mix. Label the tube to record that ROX has been added. Mixture can be stored at -20°C for repeated use.
Mix 3.6 µL cDNA with 86.4 µL nuclease free water, then add 90 µL miGreen Master mix (in total 180 µL). Mix by pipetting up and down, spin down to collect the liquid at the bottom. Repeat this step for all samples.
Caution: miGreen Master mix is light sensitive and should not be exposed to light for extended time periods.

Step 20b
Prepare hepatomiR® plate

Add 10 µL reaction mixture (from step 19b) (cDNA, NFW, Master mix including ROX) according to figure 5 and 6 to each of the 16 wells. Seal the plate with the appropriate optical sealing. Spin plate at 1,000 g for 90 sec. and incubate at 4°C for a minimum of 1 hour.

Note: The plate can be stored up to 24 hours at 4°C protected from light.

Step 21b
Perform qPCR

Before running the qPCR, spin plate again at 1,000 g for 90 sec.

Perform qPCR and melting curve analysis as shown below.

Step	Setting
Polymerase activation/ denaturation	Hold Stage: 95°C, 2 min, ramp-rate 3.66°C/sec
Amplification – 45 cycles	PCR Stage: 95°C, 10 sec, ramp 3.66°C/sec 56°C, 60 sec, ramp 2.2°C/sec + Acquisition
Melting curve	Melt Curve Stage: 95°C, 10 sec, ramp 3.66°C/sec 55°C, 60 sec, ramp 2.2°C/sec Continuous until 99°C, ramp 0.11°C/sec, acquisition per °C: 5

When the qPCR run is finished discard the plates without opening the sealing foil (to avoid cross-contaminations).

qPCR Amplification

The hepatomiR® test plate contains 8 different microRNA or QC primer sets.

Figure 5
96-well plate layout
and pipetting scheme

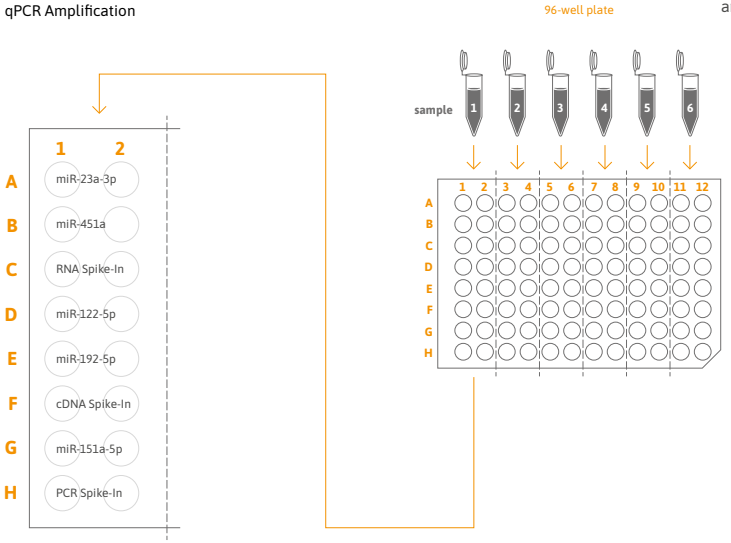
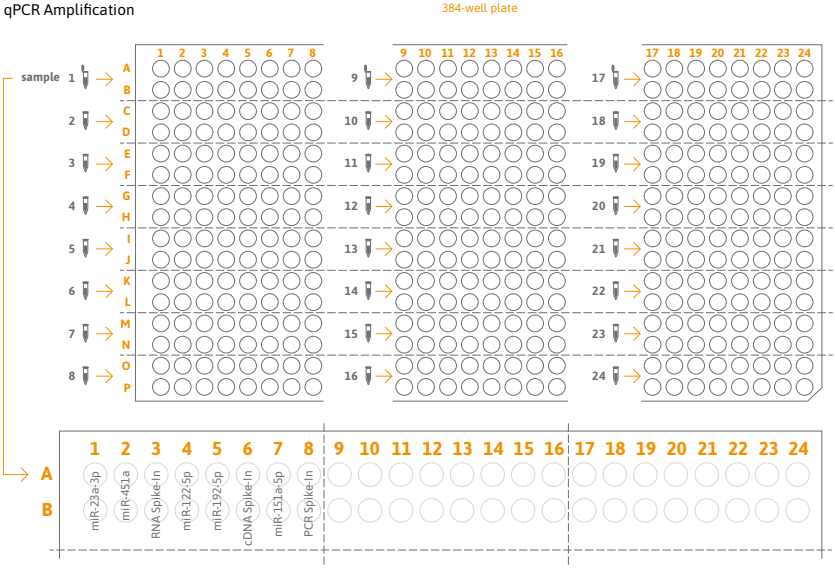


Figure 6
384-well plate layout
and pipetting scheme



Data Export and Analysis

Exporting qPCR Raw Data for hepatomiR® Software

The hepatomiR® software requires raw fluorescence data from qPCR experiments for analysis. **Manual calculation of Ct or Cq values on the instrument is not necessary.**

To ensure proper data analysis, please export your raw qPCR data in the correct file format based on the instrument used:

Roche Light Cycler: Export the data as a text file (.txt).
Bio-Rad CFX: Export the data as a comma-separated values file (.csv).
Thermo Fisher QuantStudio: Export the data as a Excel file (.xls or .xlsx)

Once the raw data has been exported in the appropriate format, you can proceed with the data analysis as described in the next section.

Accessing the software and analysing data

The most recent version of the software can be accessed under the URL: https://hepatomir.tamirna.com using a functional browser (e.g. Google Chrome) with an internet connected computer. After the login, using the provided username and password, a tab structured application will lead the user through the process of data analysis.

The **Main** tab provides general information and download links for the most recent version of the instructions for use of the kit and software.

In order to analyse data, the user has to navigate to the tab **Analyse**. The applied plate layout (96-well vs 384-well) is selected by the user via a checkbox. Raw fluorescence data can be uploaded from all supported qPCR instruments (see list on page 22 of this manual). After the confirmation of all input parameters (qPCR device, plate layout and uploaded filename) the application will automatically call Cq-values using the second-derivative maximum method. Based on Cq-values from spike-in controls (please read information on page 17), hemolysis controls, and the endogenous microRNAs hsa-miR-122-5p, hsa-miR-192-5p, hsa-miR-151a-5p a quality check (QC) will be performed. All samples that have passed the QC will be used to compute the hepatomiR® p-score from the PCR duplicates. After a final check of the PCR duplicates, a report is generated

that contains information on the QC status (valid or invalid) for all samples as well as the estimated p-score for all samples that have passed the QC. For samples that have not passed the QC the respective reason is displayed in the report. The report also gives interpretation support in case specific quality controls have failed. The Troubleshooting section (pages 31-32) in this manual can be used in case of experimental issues.

Important: the software application does not process any information about sample IDs that might have been assigned in the PCR software. Therefore, the user must record the information about sample IDs and sample position.

During analysis sample names to be used in the generated report can be entered in the hepatomiR software.

The tab **Instruction for use** provides detailed information about the usage of the current software version and how to interpret error messages and a step-by-step guide for data analysis.
Information about the software version, the software developer, a support address, the company imprint and a disclaimer can be found under the tab **About**.

Troubleshooting

RNA Isolation

Notes

Poor RNA Recovery

Column has become clogged	In most cases this can happen when recommended amounts of starting materials were exceeded. For plasma samples this is unlikely to occur. See also "Clogged Column" below
An alternative elution solution was used	For maximum RNA recovery it is recommended to elute the RNA with the RNase-free water supplied with this kit.
RNA content	The RNA content in plasma is low therefore the concentration measurement of the purified RNA (e.g. spectrophotometric or with fluorescent dyes) is not accurately possible. The protocol is optimized using fixed volumes.

Clogged Column

Temperature too low	Ensure that the centrifuge and solutions remain at room temperature (18 - 25°C) throughout the procedure. Temperatures below 15°C may result in salt precipitates that may clog the columns. If salt precipitation is present, heat the solution to 30°C until completely redissolved and let the solutions cool to room temperature before use.

Degraded RNA

RNase contamination	RNases may be introduced when working with the samples. Ensure that proper procedures are followed when working with RNA. Please refer to "Working with RNA" at the beginning of this manual
Procedure not performed quickly enough	In order to maintain the integrity of the RNA, it is important that the procedure be performed quickly.

		Notes
Improper storage of the purified RNA	For short term storage RNA samples may be stored at -20°C for a few days. It is recommended that samples be stored at -70°C for longer term storage **Avoid repeated freeze/thaw-cycles by freezing aliquots of your RNA.**	

RNA does not perform well in downstream applications

Salt or Ethanol carryover	Traces of salt and ethanol from the binding step can interfere with downstream applications. Therefore, Step 6 Of the Protocol (Wash) is important for the quality of your RNA sample To avoid remaining salts please make sure that the RNA bound to the column is washed 3 times with the provided Wash Solution and ensure that the dry spin is performed, in order to remove traces of ethanol prior to elution.	
Inhibitors	Some individual plasma samples can contain inhibitors. Using spike-ins that control every step of the protocol inhibitors can be easily detected. Samples that contain inhibitors must be excluded from the analysis.	

cDNA and qPCR Amplification

Problem	Suggestion	Notes
No fluorescent signal is detected during the PCR	Confirm that the PCR setup was correct by checking the signal obtained for the PCR spike-in control.	
No fluorescent signal detected during the PCR, but the PCR spike-in gives a valid signal.	Check that the filter in the qPCR cycler was set to SYBR Green. Check that the optical read is at the correct step of the qPCR cycles.	

Related Services

TAmiRNA offers a broad range of high quality RNA services performed by experts according to GLP standards, including RNA isolation, next generation sequencing and qPCR analysis. Read more about there services at
www.tamirna.com/small-rna-sequencing-services/

Related Products

TAmiRNA also offers research-use kits for novel microRNA biomarkers in cardiovascular disease and in bone quality. Read more about these products at www.tamirna.com.

Further reading on quality controls for circulating microRNA experiments

1. TAmiRNA TechNote TN-05. Quality controls and best practices for analyzing microRNAs in cell-free biofluids by RT-qPCR. April 2019

2. Mussbacher M, Krammer TL, Heber S, Schrottmaier WC, Zeibig S, Holthoff HP, et al. Impact of Anticoagulation and Sample Processing on the Quantification of Human Blood-Derived microRNA Signatures. Cells. 2020 Aug 18;9(8):1915.

3. Blondal T, Jensby Nielsen S, Baker A, Andreasen D, Mouritzen P, Wrang Teilum M, et al. Assessing sample and miRNA profile quality in serum and plasma or other biofluids. Methods 2013;59:S1–6.

4. Shah JS, Soon PS, Marsh DJ. Comparison of methodologies to detect low levels of hemolysis in serum for accurate assessment of serum microRNAs. PLoS One 2016;11:1–12.

5. Mestdagh P, Hartmann N, Baeriswyl L, Andreasen D, Bernard N, Chen C, et al. Evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study. Nat Methods 2014;11.

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Patents for the in-vitro diagnostic application of microRNAs for the prediction of liver dysfunction are granted in the EU (EP3814533B1) and US (US 17278624), Japan (JP7045527), South Korea (KR102339206), Canada (CA3110668C), and China (CN112867802B).

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Explanation of the used symbols

IVD	In-vitro-diagnostic
REF	Catalogue number
LOT	Batch number
	Manufacturer
	Do not re-use
	Use by
	Do not use if package is damaged
	Consult instructions for use or consult electronic instructions for use
	Store at 2°C-30°C
	Store at -31°C- -15°C

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