Protocol
Targeted LC-MS/MS-based metabolomics and lipidomics on limited hematopoietic stem cell numbers

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Publisher’s note: Undertaking any experimental protocol requires adherence to local institutional guidelines for laboratory safety and ethics.
Protocol

Targeted LC-MS/MS-based metabolomics and lipidomics on limited hematopoietic stem cell numbers

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SUMMARY

Metabolism is important for the regulation of hematopoietic stem cells (HSCs) and drives cellular fate. Due to the scarcity of HSCs, it has been technically challenging to perform metabolome analyses gaining insight into HSC metabolic regulatory networks. Here, we present two targeted liquid chromatography–mass spectrometry approaches that enable the detection of metabolites after fluorescence-activated cell sorting when sample amounts are limited. One protocol covers signaling lipids and retinoids, while the second detects tricarboxylic acid cycle metabolites and amino acids. For complete details on the use and execution of this protocol, please refer to Schönberger et al. (2022).

BEFORE YOU BEGIN

The protocol below describes the specific steps for the extraction of metabolites in hematopoietic stem and progenitor populations after fluorescence-activated cell sorting (FACS). However, this protocol is also applicable to other rare cell types that require FACS purification for isolation.

Note that it is critical to perform all steps as quickly and as cold as possible. Before you begin, pre-cool all reagents and centrifuges used in steps 1–9 to 4°C, and after metabolite extraction pre-cool centrifuges to −9°C. It is important to highlight that some of the reagents used are hazardous. When applicable, we have added P Codes and H Codes of Globally Harmonized System (GHS) Precautionary Statements. Moreover, all types of materials used throughout the protocol can influence metabolite recovery. It is highly recommended to use the same materials for all repeating experiments (for recommended materials, see key resources table).

The establishment of the method, analysis, and interpretation of results for this liquid chromatography–mass spectrometry (LC-MS/MS) protocol require a skilled mass spectrometrist.
Institutional permissions

All mice were bred in-house in the animal facility at the MP-IE in individually ventilated cages (IVCs). Mice were euthanized by cervical dislocation according to German guidelines. Animal procedures were performed according to protocols approved by the German authorities and the Regierungsspräsidium Freiburg (the sacrificing of animals for scientific purposes according to §4 (3) of the German Animal Protection Act). Please remember that permissions from your local authorities will be required to conduct animal experiments.

**KEY RESOURCES TABLE**

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|---------------------|--------|------------|
| Antibodies          |        |            |
| CD8a-PE/Cy7 (1:1000) | BioLegend | Cat#100722; RRID: AB_312761 |
| CD11b-PE/Cy7 (1:1000) | BioLegend | Cat#101216; RRID: AB_312799 |
| Gr1-PE/Cy7 (1:1000) | BioLegend | Cat#108416; RRID: AB_313381 |
| TER119-PE/Cy7 (1:500) | BioLegend | Cat#116221; RRID: AB_2137789 |
| B220-PE/Cy7 (1:1000) | BioLegend | Cat#103222; RRID: AB_313005 |
| CD4-PE/Cy7 (1:1000) | BioLegend | Cat#100422; RRID: AB_2660860 |
| cKit-PE (1:1000) | BioLegend | Cat#105808; RRID: AB_313217 |
| Sca1-APC/Cy7 (1:500) | BioLegend | Cat#108126; RRID: AB_10645327 |
| CD150-BV605 (1:300) | BioLegend | Cat#115927; RRID: AB_11204248 |
| CD48-BV421 (1:1000) | BioLegend | Cat#103428; RRID: AB_2650894 |
| CD8a-Biotin (1:500) | BioLegend | Cat#100704; RRID: AB_312743 |
| CD11b-Biotin (1:500) | BioLegend | Cat#101204; RRID: AB_312787 |
| Gr1-Biotin (1:500) | BioLegend | Cat#108404; RRID: AB_313369 |
| TER119-Biotin (1:500) | BioLegend | Cat#116204; RRID: AB_313705 |
| B220-Biotin (1:500) | BioLegend | Cat#103204; RRID: AB_312989 |
| CD4-Biotin (1:500) | BioLegend | Cat#100404; RRID: AB_312689 |
| Chemicals, peptides, and recombinant proteins |        |            |
| PBS | Sigma | Cat#D8537 |
| Methanol LC-MS/MS grade | Carl Roth | Cat#HN41.2 |
| Acetonitrile LC-MS/MS grade | VWR Chemicals | Cat#83640.320 |
| 2-Propanol LC-MS/MS grade | Carl Roth | Cat#AE73.1 |
| Water (for preparing extraction solutions and LC buffers) | Milli-Q | n/a |
| 13C yeast standard | ISOTopic solutions | Cat#ISO-1 |
| Dynabeads Untouched Mouse CD4 Kit | Life Technologies | Cat#11415D |
| OneComp eBeads | eBioscience | Cat#01-1111-41 |
| ACK Lysing Buffer | Lonza | Cat#10-548E |
| Ammonium Carbonate | Fisher Chemical | Cat#A/3686/50 |
| Ammonium Hydroxide 25% Solution | Millipore | Cat#30501-1L-M |
| Ammonium Formate | Sigma-Aldrich | Cat#S16961-100G |
| Glycerol | Carl Roth | Cat#3783.1 |
| Experimental models: Organisms/strains |        |            |
| CS7BL/6J (CD45.2), females, 8–24 weeks old | MPI-IE | RRID: IMSR_JAX:002014 |
| Software and algorithms |        |            |
| FACSdiva | BD | RRID: SCR_001456 |
| MassHunter8 | Agilent | |
| Other |        |            |
| Biosphere® SafeSeal Tube 1.5 mL | Sarstedt | Cat#72.706.200 |
| Filter-cap FACS tube | Coming | Cat#352235 |
| Cell strainer 40 μm Nylon | Coming | Cat#352340 |
| twintec PCRPlate 96LoBind skirted | Eppendorf | Cat#0030129512 |
| Hot seal foil “Seal&Pierce” | neoLab | Cat#7-5218 |

(Continued on next page)
### MATERIALS AND EQUIPMENT

#### 50% glycerol (v/v)

| Component                  | Volume    |
|----------------------------|-----------|
| Glycerol                   | 25 mL     |
| milliQ H₂O                 | 25 mL     |
| **Total**                  | **50 mL** |

**Note:** Glycerol is highly viscous. Pour the respective amounts of glycerol and water into a graduated cylinder and mix. This mix can be kept at 4°C for several years.

#### ¹³C internal standard stock solution

| Component                                | Volume   |
|------------------------------------------|----------|
| milliQ H₂O                               | 7.5 mL   |
| Methanol                                 | 2.5 mL   |
| ¹³C labeled extract of 2 billion yeast cells | Dry pellet |
| **Total**                                | **10 mL** |

**Note:** It is helpful to aliquot this solution in smaller quantities to avoid repeated thawing/freezing. This solution can be stored at −80°C for up to 1 month.

⚠ CRITICAL: Methanol is volatile, flammable, and toxic (H255, H301, H331, H311, H370). Keep away from heat, hot surfaces, sparks, open flames, and other ignition sources. Wear protective gloves and protective clothing (P210, P280, P301, P302, P304, P310, P311, P312, P330, P340, P352). Use under a fume hood.

#### Wash buffer

| Component                  | Volume    |
|----------------------------|-----------|
| 50% glycerol               | 5.6 mL    |
| milliQ H₂O                 | 94.4 mL   |
| **Total**                  | **100 mL** |

| REAGENT or RESOURCE         | SOURCE                | IDENTIFIER |
|----------------------------|-----------------------|------------|
| Sample vials with micro glass insert | Carl Roth             | Cat#TY82.1 |
| Snap caps for sample vials  | Fisherbrand           | Cat#11864910 |
| Luna propylamine column (50 x 2 mm, 3 μm) | Phenomenex          | Cat#008-4377-80 |
| microLC column 100 x 0.3 mm packed with Zorbax Eclipse Plus RP C18 1.8 μm | Dr. Maisch       | Cat#x.s100.3 |
| trap column 10 x 1 mm packed with Zorbax Eclipse Plus RP C18 1.8 μm | Dr. Maisch       | Cat#x.t0101 |
| MicroLC Pump Zirconium Ultra | Prolab               | 410F       |
| MicroLC ESI Source          | Prolab               | AX150      |
| UHPLC Pump                  | Agilent              | G7120A     |
| UHPLC Autosampler           | Agilent              | G7157B     |
| UHPLC Sample Thermostat     | Agilent              | G4761A     |
| UHPLC Column Thermostat     | Agilent              | G7116B     |
| Triple Quadrupole Mass Spectrometer | Agilent        | 6495B     |
| JetStream ESI Source        | Agilent              | G1958B     |
| Speedvac EZ-2 Elite         | SP Scientific        | EZ3T-23050-HN0 |
| Sample Holder for 1.5 mL tubs in Speedvac | SP Scientific  | 10-5043        |
| Table Top Centrifuge        | Eppendorf            | 5417R     |
**Note:** This wash buffer can be stored for several months at 4°C when handled under sterile conditions.

### 80% methanol extraction solution

| Component | Volume |
|-----------|--------|
| methanol  | 79.75 mL |
| milliQ H₂O | 24.25 mL |
| ¹³C internal standard stock solution | 1 mL |
| **Total** | 100 mL |

**Note:** This extraction solution should be pre-cooled to –20°C before use and can be stored at –20°C for up to 2 weeks.

### Buffer HILIC A

Ammonium hydroxide 25% solution 0.75 mL

milliQ H₂O 999.25 mL

Total 1 L

**Note:** Buffer A can be used for up to 2 days at 20°C.

▲ **CRITICAL:** Ammonium hydroxide is toxic, can cause severe skin and eye irritation, and poses an aquatic hazard (H314, H318, H335, H400, H410, H411). Wear protective gloves and protective clothing (P261, P271, P273, P280, P303, P305, P338, P351, P353, P361). Use under a fume hood.

### Buffer HILIC B

| Component | Amount |
|-----------|--------|
| Ammonium carbonate | 480 mg |
| milliQ H₂O | 100 mL |
| Acetonitrile | 900 mL |
| **Total** | 1 L |

**Note:** First dissolve ammonium carbonate in water, then add acetonitrile. Buffer B can be kept up to 1 week at 20°C.

▲ **CRITICAL:** Ammonium carbonate is harmful when swallowed (H302). Wear protective gloves and protective clothing (H301, P312, P330). Keep refrigerated to minimize unpleasant smell.

▲ **CRITICAL:** Acetonitrile is volatile, flammable, toxic, and can lead to severe eye irritation (H225, H302, H312, H319, H332). Wear protective gloves and protective clothing (P210, P280, P301, P303, P304, P305, P312, P338, P351, P353, P361). Use under a fume hood.

### Buffer microLC A1

| Component | Amount |
|-----------|--------|
| Ammonium formate | 630 mg |
| milliQ H₂O | 900 mL |
| Acetonitrile | 100 mL |
| **Total** | 1 L |

▲ **CRITICAL:** Ammonium formate can lead to severe eye irritation (H319). Wear protective gloves and protective clothing (P264, P280, P305, P313, P337, P338, P351).
Note: The buffer can be kept up to 1 week at 20°C.

| Buffer microLC A2                  | Amount |
|-----------------------------------|--------|
| Ammonium formate                  | 630 mg |
| milliQ H2O                        | 900 mL |
| Methanol                          | 100 mL |
| Total                             | 1 L    |

Note: The buffer can be kept up to 1 week at 20°C.

| Buffer microLC B1                  | Amount |
|-----------------------------------|--------|
| Ammonium formate                  | 630 mg |
| 2-Propanol                        | 900 mL |
| Acetonitrile                      | 100 mL |
| Total                             | 1 L    |

Note: Stir or sonicate buffer microLC B1 for several hours in a closed bottle to dissolve ammonium formate. The buffer can be kept up to 1 month at 20°C.

△ CRITICAL: 2-propanol is volatile, flammable, toxic, and can lead to severe eye irritation (H225, H319, H336). Wear protective gloves and protective clothing (P210, P233, P240, P241, P242, P305, P338, P351). Use under a fume hood.

Alternatives: The key resources table provides information on material and equipment that we have validated for this protocol. In some cases, alternative products may be used; although we have not tested them for this protocol:

- Reagents:
  - Organic solvents: LC-MS/MS grade solvents from other suppliers.
  - Ammonium salts and ammonium hydroxide: p.a. quality or better from other suppliers.
  - Glycerol: > 99% purity from other suppliers.

- Materials:
  - Sample vials/caps: vials with micro glass insert with matching caps from other suppliers.
  - Twintec PCR plate: other clear PCR plate that the LC autosampler will accept.

- Equipment:
  - Speedvac: rotary evaporator that can tolerate organic solvents.
  - Table top centrifuge: refrigerated centrifuge that can be used with 1.5 mL tubes.
  - UHPLC: HPLC or UHPLC that allows for at least 400 bar back pressure, sample cooling and column heating from another supplier.
  - Mass spectrometer: triple quadrupole mass spectrometer with heated ESI source that is sufficiently sensitive.

- Analysis tools:
  - MassHunter®: for data pre-processing, raw data in .d format can be converted to open .mzML format and subsequently be processed in free software such as skyline or R.

STEP-BY-STEP METHOD DETAILS

Isolation of murine bone marrow cells

© Timing: 30–45 min
Hematopoietic stem and progenitor cells reside in the bone marrow (BM) niche. In order to recover the maximum cellular output per mouse, pool the BM within mouse femurs, tibias, ilia, and vertebrae.

1. Preparation of mouse femurs, tibias, ilia and vertebrae.
   a. Mice must be handled and euthanized according to the guidelines and protocols approved by the country’s authorities.
   b. Place the mouse on its belly, if needed, secure animal onto dissecting tray by pinning front palms so that they are raised diagonally from its body, and disinfect with 70% ethanol.
   c. Isolation of mouse femurs, tibias, ilia, and vertebrae can be achieved by competent dissection of the mouse legs and spine using forceps and scissors. Isolated tissue should be kept in PBS-filled 6-well plates on ice until all bones are collected.
   d. Remove the surrounding tissue from the bones and the spinal cord from vertebrae using a scalpel. This step will avoid possible contamination as well as potential blockage during the filtration step.

2. Preparation of a BM single-cell suspension.
   a. Use a mortar and pestle to gently crush the bones with 5 mL ice-cold PBS.
   b. Filter cell suspension through a 40 μm sterile filter into a 50 mL falcon tube. Keep the tubes on ice.
   c. Repeat steps 2a and 2b until the bones appear to be completely white.

3. Lysis of erythrocytes.
   a. Centrifuge the cell suspension at 400 × g for 5 min at 4°C and remove supernatant.
   b. Re-suspend in 2 mL ice-cold ACK lysis buffer and incubate on ice for 5 min. Increase incubation time to up to 10 min dependent on the size of the pellet.
   c. Stop the reaction by adding 1 mL ice-cold PBS.
   d. Centrifuge the cell suspension at 400 × g for 5 min at 4°C and remove supernatant.

   Note: For further details on how to isolate BM cells, see protocol by (Zhang and Cabezas-Wallscheid, 2019).

   CRITICAL: Cells must be kept on ice from the moment the bones are isolated from the mouse. It is recommended to perform the entire preparation process on ice or in a cold room at 4°C.

Enrichment for hematopoietic stem and progenitor cells

Timing: 75 min

To enrich for lineage negative (Lin−) cells, we use the Dynabeads Untouched Mouse CD4 Cells Kit (Invitrogen). Note that this kit does not contain CD4 and thus does not deplete CD4 positive cells. A biotinylated CD4 antibody can be added if desired or, alternatively, a home-made lineage cocktail of biotinylated lineage antibodies can be used.

4. Incubation of cells using the lineage cocktail.
   a. Re-suspend cells in 500 μL lineage cocktail (100 μL of the cocktail provided in the kit added to 400 μL PBS per mouse BM) and transfer the supernatant into a 2 mL tube.
   b. Incubate 35 min on a rotating wheel at 4°C.

   CRITICAL: The incubation time of cells with the lineage cocktail should not exceed 45 min since this will cause lower cell recovery.
Optional: Instead of using the lineage cocktail included in the Dynabeads Untouched Mouse CD4 Cells Kit (Invitrogen), a home-made lineage cocktail can be used ([CD4/CD8a/CD11b/GR-1/B220/Ter-119]-all biotinylated). To obtain a good depletion efficiency, however, the incubation time should be adjusted to at least 45 min.

c. Meanwhile prepare the Dynabeads®.
   i. Vortex the beads for 30 s to make sure that they are well re-suspended.
   ii. Add 400 µL of the Dynabeads® into a 2 mL tube and incubate for 30 s on a depletion magnet until the solution clears.
   iii. Remove the supernatant without disturbing the beads and wash with 1 mL ice-cold PBS.
   iv. Repeat step iii for a total of two washing steps.
   v. Re-suspend in 500 µL PBS and keep on ice until use.

d. Wash the cells with 12 mL ice-cold PBS in a 15 mL falcon tube.
e. Centrifuge the cell suspension at 400 × g for 5 min at 4°C and remove supernatant.

5. Depletion of lineage positive cells.
   a. Re-suspend cell pellet in 1 mL ice-cold PBS and transfer them to the tube containing the Dynabeads®.
   b. Incubate for 20 min on a rotating wheel at 4°C.

△ CRITICAL: The incubation time of cells with the Dynabeads® should not exceed 25 min since this will lead to reduced cell recovery.

c. Incubate cells for 5 min on ice on the depletion magnet until the solution clears.
d. Transfer the entire supernatant into a new FACS tube and keep cells on ice.
e. Add 1 mL ice-cold PBS and repeat steps 5c and 5d, then combine the two supernatants.

△ CRITICAL: Shorter incubation time will reduce efficiency of the depletion process.

6. Surface staining of lineage depleted cells for sorting.
   a. Centrifuge the cell suspension at 400 × g for 5 min at 4°C and remove supernatant.
   b. Re-suspend in ice-cold PBS containing the surface antibody cocktail ([CD4/CD8a/CD11b/GR-1/B220/Ter-119]-all PeCy7, c-Kit/CD117-PE, Sca-1-APC-Cy7, CD150-BV605, CD48-BV421) and incubate for 30 min at 4°C in the dark.

Note: Other suitable combinations of fluorescent dyes can be used and will not influence the results.

Fluorescence-activated cell sorting of purified hematopoietic stem cells

© Timing: 1–3 h

Note: Depending on the abundance of the desired cell population, the number of mice, and the event rate of the sorting process, the time required for this step may differ. However, it is recommended to not exceed a sorting time of more than 4 h since this will negatively impact the metabolome and lead to a starvation phenotype of the cells.

7. Preparation of cells for FACS.
   a. Add 1 mL ice-cold PBS.
   b. Centrifuge the cell suspension at 400 × g for 5 min at 4°C and remove supernatant.
   c. Re-suspend pellet in an appropriate volume of PBS dependent on the size of the pellet (usually between 500 µL and 2 mL).
   d. Filter cells through a filter-cap FACS tube.
e. Prepare 1.5 mL RNase/DNase/ATP-free tubes containing A) 100 µL StemPro®-34 SFM (Life Technologies) without cytokines for measuring TCA-cycle metabolites and amino acids or B) 100 µL 100% acetonitrile for measuring signaling lipids and retinoids.

8. Sort A) 10,000 HSCs (Lineage− cKit+ Sca1+ CD150− CD48−) using the 100 µm nozzle of a FACS Aria II, FACS Aria III, or FACS Symphony (Becton Dickinson) or B) 40,000 HSCs using the 70 µm nozzle while constantly cooling the samples.

△ CRITICAL: Cells must not hit the side of the tube but only the surface of the liquid. Also, prepare at least two tubes as negative controls. It is crucial to treat these samples identically to those containing cells.

△ CRITICAL: Retinoids are light-sensitive metabolites. It is therefore essential to keep the samples for B) in the dark during and after the sorting process.

Note: FACS is a very stressful process for most cells.

Depending on the cell type you are interested in, a short recovery step of 20 min in the incubator (37°C; 5% CO2) might increase the number and amount of detected metabolites. However, even a short incubation period will lead to activation of metabolic pathways and, in the case of quiescent populations (such as HSCs), may not reflect the actual in vivo phenotype. Thus, it is highly recommended to adjust the experimental setup according to the biological question being asked.

### Targeted polar metabolomics: A) TCA cycle metabolites and amino acids

© Timing: 45 min–1 h

9. Wash the cells.
   a. Add 1 mL 2.8% glycerol solution per 1.5 mL tube.
   b. Centrifuge the cell suspension at 400 × g for 5 min at 4°C and remove supernatant.

△ CRITICAL: PBS contamination of the flow cytometry sorting process will interfere with the measurement and thus reduce metabolite recovery. Cells must therefore be washed with a glycerol solution. It is important to remove as much supernatant as possible without losing cells. Removing too little supernatant will lead to high background levels for all metabolites contained in the media. To estimate the background levels of the measured metabolites, the two negative controls should be processed in the exact same way (including washing process).

10. Metabolite extraction.
   a. Add 100 µL of the pre-cooled 80% MeOH extraction buffer containing 1 µL 13C yeast extract to the washed cell pellet.
   b. Ensure complete re-suspension of the cell pellet by repeated pipetting.
   c. Centrifuge 3 min at 20,000 × g and 4°C to pellet cell debris.
   d. Transfer 95 µL of clear supernatant to a fresh Eppendorf tube.

11. Vacuum concentration of the samples.
   a. Vacuum concentrate (EZ2 elite, Genevac) the samples for 35 min using the aqueous program, lamp off.

△ CRITICAL: Do not over-dry the samples, as this will lead to decreased metabolite recovery.

★★ Pause point: Samples can be stored at this point for up to 2 weeks at −80°C.
LC-MS/MS analysis of TCA cycle metabolites and amino acids

Timing: 2 h plus 10 min for every sample

12. Calibrate the mass spectrometer following the manufacturer’s recommendations. Ensure that the check tune is passed.
13. Install fresh mobile phase buffers HILIC A and HILIC B in sufficient amounts for the expected number of samples.
14. Purge liquid chromatography (LC) system with mobile phase. Purge 5 min with 3 mL/min with a 50:50 mix of both mobile phase buffers.
15. Install the Luna aminopropyl chromatography column.
16. Equilibrate the LC system with mobile phase buffers in starting conditions.
17. Check LC performance by running a blank sample. Ensure that the backpressure is below 170 bar under starting conditions and remains below 300 bar throughout the gradient run. If backpressure is too high, check for restrictions in the mobile phase flow path.
18. Equilibrate the column by running 4 blank samples.
19. It is highly recommended to use quality control samples such as pool samples, mixtures of standards, or reference material to check if the LC-MS/MS performs as expected.

| HILIC LC gradient Profile | Time (min) | % B | Flow rate (µL/min) |
|---------------------------|------------|-----|--------------------|
| Initial                   | 100        | 1000| 1000               |
| 0.5                       | 100        | 1000|                    |
| 4.7                       | 30         | 750 |                    |
| 5.1                       | 10         | 750 |                    |
| 7.5                       | 10         | 750 |                    |
| 7.8                       | 100        | 750 |                    |
| 8.4                       | 100        | 1000|                    |
| 9.5                       | 100        | 1000|                    |

| LC parameter settings     |             |
|---------------------------|-------------|
| Injection volume          | 3 µL        |
| Column temperature        | 30°C        |
| Autosampler temperature   | 5°C         |
| Max pressure limit        | 400 bar     |

Note: An Agilent 6495 Triple Quadrupole mass spectrometer coupled to an Agilent 1290 Infinity II ultra-high-performance liquid chromatography (UHPLC) system is used for quantification of metabolites in this protocol. The MS parameters are detailed in Table 1. Other LC-MS/MS systems with similar capabilities can be used. For other LC-MS/MS systems, LC and MS parameters may have to be adapted.

Note: Compound-specific MS settings were optimized separately for all compound using pure standards. These settings are machine-specific and optimization must be repeated on a different machine. Settings used for this protocol are listed in Table 2.

⚠ CRITICAL: LC systems operate under high pressure. Refer to manufacturer’s instructions to avoid leakage of mobile phase buffers.

⚠ CRITICAL: Mass spectrometers apply high temperatures to evaporate the stream of mobile phase buffer coming from the LC. Refer to manufacturer’s instructions and do not
touch hot surfaces to avoid burn wounds. Ensure sufficient ventilation to avoid accumulation of harmful or dangerous vapors. Mass spectrometers apply high voltages to ionize metabolites. Refer to manufacturer’s instructions to avoid electric shock.

**Targeted metabolomics: B) Signaling lipids and retinoids**

© Timing: 40 min

△ CRITICAL: Remember that retinoids are light-sensitive metabolites and it is essential to keep the samples protected from light during processing.

Note: Metabolites are already extracted when reaching the extraction solution. The contaminant fluid due to the droplets is roughly 1 nL/droplet when using the 70 μm nozzle and will lead to a final ACN concentration of 60%–80%, depending on the number of cells and the FACS setup.

Of note, steps 1–8 are shared for both protocols (A and B). After step 8 of protocol A, you should continue with this step (20) if assessing protocol B:

20. Vacuum concentration of the samples.
   a. Vacuum concentrate (EZ2 elite, Genevac) the samples for 35 min using the aqueous program, lamp off.

△ CRITICAL: Do not over-dry the samples, as this will lead to decreased metabolite recovery.

|| Pause point: Samples can be stored at this point for up to 2 weeks at −80 °C.

**MicroLC-MS/MS analysis of signaling lipids and retinoids**

© Timing: 3 h plus 1 h for every sample

21. Calibrate the mass spectrometer following the manufacturer’s recommendations. Ensure that the check tune is passed.

22. Install fresh mobile phase buffer microLC A2 and microLC B1 in sufficient amounts for the expected number of samples on UHPLC System (see Figure 1).
| Compound name               | Precursor ion | Product ion | Collision energy | Polarity | Expected RT (min) |
|----------------------------|---------------|-------------|------------------|----------|------------------|
| 4-OH-Proline quantifier    | 132.1         | 86          | 12               | +        | 1.7              |
| 4-OH-Proline qualifier     | 132.1         | 68          | 26               | +        |                  |
| 4-OH-Proline qualifier     | 132.1         | 58          | 30               | +        |                  |
| Acetyl-CoA quantifier      | 810.1         | 303.1       | 38               | +        | 4.2              |
| Acetyl-CoA qualifier       | 810.1         | 136         | 78               | +        |                  |
| Acetyl-CoA_13C qualifier   | 833.1         | 316.1       | 38               | +        |                  |
| Aconitic acid quantifier   | 173           | 129         | 10               |          | 3.9              |
| Aconitic acid qualifier    | 173           | 85          | 25               |          |                  |
| Aconitic acid_13C qualifier| 179           | 89          | 25               |          |                  |
| Adenosine quantifier       | 268.1         | 136         | 22               | +        | 0.5              |
| Adenosine qualifier        | 268.1         | 119         | 62               | +        |                  |
| Adenosine_13C qualifier    | 278.1         | 141         | 22               | +        |                  |
| ADP quantifier             | 426           | 328         | 22               |          | 4.1              |
| ADP qualifier              | 426           | 79          | 66               |          |                  |
| ADP_13C qualifier          | 436           | 338         | 22               |          |                  |
| AMP quantifier             | 348.1         | 136         | 22               | +        | 3.0              |
| AMP qualifier              | 348.1         | 119         | 74               | +        |                  |
| AMP_13C qualifier          | 358.1         | 141         | 22               | +        |                  |
| Arginine quantifier        | 175.1         | 116         | 18               | +        | 2.8              |
| Arginine qualifier         | 175.1         | 60          | 14               | +        |                  |
| Arginine_13C qualifier     | 181.1         | 61          | 18               | +        |                  |
| Asparagine quantifier      | 131           | 113         | 8                |          | 1.8              |
| Asparagine qualifier       | 131           | 42          | 22               |          |                  |
| Asparagine_13C qualifier   | 135           | 43          | 8                |          |                  |
| Aspartic acid quantifier   | 132           | 115         | 10               |          | 2.3              |
| Aspartic acid qualifier    | 132           | 88          | 14               |          |                  |
| Aspartic acid_13C qualifier| 136           | 91          | 14               |          |                  |
| ATP quantifier             | 506           | 408         | 22               |          | 5.2              |
| ATP qualifier              | 506           | 159         | 46               |          |                  |
| ATP_13C qualifier          | 516           | 418         | 22               |          |                  |
| cAMP quantifier            | 328           | 134         | 24               |          | 1.7              |
| cAMP qualifier             | 328           | 107         | 64               |          |                  |
| cAMP_13C qualifier         | 338           | 139         | 24               |          |                  |
| Citric acid quantifier     | 191           | 111         | 10               |          | 3.6              |
| Citric acid qualifier      | 191           | 87          | 18               |          |                  |
| Citric acid_13C qualifier  | 197           | 90          | 18               |          |                  |
| Cystine quantifier         | 241.03        | 74          | 34               | +        | 2.7              |
| Cystine qualifier          | 239.01        | 120         | 10               |          |                  |
| Cystine_13C qualifier      | 245.01        | 123         | 10               |          |                  |
| Fumaric Acid quantifier    | 115           | 71          | 6                |          | 2.4              |
| Fumaric_13C quantifier     | 119           | 74          | 6                |          |                  |
| Glutamic acid quantifier   | 146           | 128         | 6                |          | 2.3              |
| Glutamic acid qualifier    | 146           | 102         | 14               |          |                  |
| Glutamic acid_13C quantifier| 151          | 106         | 14               |          |                  |
| Glutamine quantifier       | 145.1         | 127         | 10               |          | 1.8              |
| Glutamine qualifier        | 145.1         | 109         | 10               |          |                  |
| Glutamine_13C              | 150.1         | 132         | 10               |          |                  |
| GSH quantifier             | 306.1         | 272.1       | 10               |          | 2.4              |
| GSH qualifier              | 306.1         | 143         | 22               |          |                  |
| GSH_13C quantifier         | 316.1         | 282.1       | 10               |          |                  |
| Histidine quantifier       | 156.1         | 110         | 14               | +        | 2.0              |

(Continued on next page)
| Compound name                                | Precursor ion | Product ion | Collision energy | Polarity | Expected RT (min) |
|----------------------------------------------|---------------|-------------|------------------|----------|------------------|
| Histidine qualifier                          | 156.1         | 83          | 30               | +        |                  |
| Histidine_13C qualifier                      | 162.1         | 115         | 14               | +        |                  |
| IMP quantifier                               | 349           | 137         | 22               | +        | 3.0              |
| IMP qualifier                                | 347           | 79          | 74               | –        |                  |
| IMP_13C qualifier                            | 359           | 142         | 22               | +        |                  |
| Isocitric acid quantifier                    | 191           | 73          | 25               | –        | 3.6              |
| Isocitric acid_13C qualifier                 | 197           | 75          | 25               | –        |                  |
| Isoleucine quantifier                        | 132.1         | 86          | 10               | +        | 1.0              |
| Isoleucine qualifier                         | 132.1         | 69          | 18               | +        |                  |
| Isoleucine_13C qualifier                     | 138.1         | 74          | 18               | +        |                  |
| Itaconic acid quantifier                     | 129           | 85          | 8                | –        | 2.7              |
| Itaconic acid qualifier                      | 129           | 41          | 12               | –        |                  |
| Itaconic acid_13C qualifier                  | 134           | 89          | 8                | –        |                  |
| Lactate acid quantifier                      | 89            | 45          | 10               | –        | 1.2              |
| Lactate acid qualifier                       | 89            | 43          | 10               | –        |                  |
| Leucine quantifier                           | 132.1         | 86          | 10               | +        | 0.9              |
| Leucine qualifier                            | 132.1         | 43          | 26               | +        |                  |
| Leucine_13C qualifier                        | 138.1         | 46          | 26               | +        |                  |
| Lysine quantifier                            | 147.1         | 130         | 6                | +        | 2.8              |
| Lysine qualifier                             | 147.1         | 84          | 18               | +        |                  |
| Lysine_13C qualifier                         | 153.1         | 89          | 18               | +        |                  |
| Malic acid quantifier                        | 133           | 115         | 14               | –        | 2.7              |
| Malic acid qualifier                         | 133           | 71          | 10               | –        |                  |
| Malic acid_13C qualifier                     | 137           | 119         | 10               | –        |                  |
| Methionine quantifier                        | 150.1         | 104         | 10               | +        | 1.1              |
| Methionine quantifier                        | 150.1         | 56          | 14               | +        |                  |
| Methionine_13C quantifier                    | 155.1         | 108         | 10               | +        |                  |
| N-Acetylaspartic acid quantifier             | 174           | 130         | 14               | –        | 2.5              |
| N-Acetylaspartic acid qualifier              | 174           | 88          | 18               | –        |                  |
| Niacinamide quantifier                       | 123.1         | 80          | 24               | +        | 0.3              |
| Niacinamide qualifier                        | 123.1         | 53          | 40               | +        |                  |
| Niacinamide_13C quantifier                   | 129           | 85          | 24               | +        |                  |
| Phenol Red quantifier                        | 353           | 273.1       | 28               | –        | 2.0              |
| Phenol Red qualifier                         | 353           | 195.1       | 48               | –        |                  |
| Phenylalanine quantifier                     | 166.1         | 120         | 10               | +        | 1.1              |
| Phenylalanine quantifier                     | 166.1         | 103         | 30               | +        |                  |
| Phenylalanine_13C quantifier                 | 175.1         | 128         | 10               | +        |                  |
| Proline quantifier                           | 116.1         | 43          | 30               | +        | 1.5              |
| Proline quantifier                           | 116.1         | 30          | 30               | +        |                  |
| Proline_13C quantifier                       | 121.1         | 45          | 30               | +        |                  |
| Pyruvic acid quantifier                      | 87            | 43          | 36               | –        | 1.0              |
| Pyruvic acid quantifier                      | 87            | 41          | 4                | –        |                  |
| Pyruvic acid_13C quantifier                  | 90            | 45          | 4                | –        |                  |
| Riboflavin quantifier                        | 377.2         | 243         | 28               | +        | 0.4              |
| Riboflavin quantifier                        | 377.2         | 172         | 40               | +        |                  |
| Riboflavin_13C quantifier                    | 394.2         | 184         | 28               | +        |                  |
| Serine quantifier                            | 104           | 104         | 10               | –        | 1.9              |
| Serine quantifier                            | 104           | 74          | 10               | –        |                  |
| Serine_13C quantifier                        | 107           | 76          | 10               | –        |                  |
| Succinic acid quantifier                     | 117           | 73          | 10               | –        | 2.7              |

(Continued on next page)
23. Purge UHPLC system with mobile phase. Purge 5 min with 3 mL/min with a 50:50 mix of both mobile phase buffers.

24. Equilibrate the UHPLC system with mobile phase buffers in starting conditions.

### Table 2. Continued

| Compound name                  | Precursor ion | Product ion | Collision energy | Polarity | Expected RT (min) |
|--------------------------------|---------------|-------------|------------------|----------|-------------------|
| Succinic Acid_13C qualifier    | 121           | 76          | 10               | -        |                   |
| Taurine quantifier             | 124           | 80          | 22               | -        | 1.3               |
| Taurine qualifier              | 124           | 64          | 66               | -        |                   |
| Thiamine quantifier qualifier  | 266.1         | 123         | 14               | +        | 1.5               |
| Thiamine qualifier             | 266.1         | 122         | 18               | +        |                   |
| Tyrosine quantifier qualifier  | 180.1         | 163         | 18               | -        | 1.5               |
| Tyrosine qualifier             | 180.1         | 119         | 14               | -        |                   |
| Tyrosine_13C qualifier         | 189.1         | 172.1       | 18               | -        |                   |
| Valine quantifier qualifier    | 118.1         | 72          | 10               | +        | 1.2               |
| Valine qualifier               | 118.1         | 55          | 22               | +        |                   |
| Valine_13C qualifier           | 123.1         | 76          | 10               | +        |                   |

### Valve switching time table

| Time (min) | Valve state          |
|------------|----------------------|
| initial    | load (dashed lines)  |
| 2          | elute (dotted lines) |

### UHPLC gradient Profile

| Time (min) | % B | Flow rate (µL/min) |
|------------|-----|--------------------|
| initial    | 0   | 100                |
| 5          | 0   | 100                |
| 10         | 100 | 100                |
| 25         | 100 | 100                |
| 60         | 0   | 100                |

### UHPLC parameter settings

- Injection volume: 8 µL
- Autosampler temperature: 5°C

25. Install fresh mobile phase buffer microLC A1 and microLC B1 in sufficient amounts for the expected number of samples on microLC pump.

26. Purge microLC system with mobile phase with 6 full strokes on each channel.
27. Equilibrate complete system in starting conditions.

28. Check system performance by running a blank sample. Ensure that the UHPLC backpressure is below 120 bar under starting conditions and remains below 250 bar throughout the gradient run. Ensure that the microLC backpressure remains below 900 bar throughout the gradient run. If backpressure is too high, check for restrictions in the mobile phase flow path.

**Note:** An Agilent 6495 QQQ mass spectrometer coupled to an Agilent 1290 Infinity II UHPLC system and a Prolab Zirconium Ultra is used for quantification of metabolites in this protocol. Other LC-MS/MS systems with similar capabilities can be used. In any case, the MS parameters detailed in Table 3 may need to be adapted.

**Note:** Compound-specific MS settings were optimized separately for all compounds using pure standards. These settings are machine-specific and optimization must be repeated on a different machine. Settings used for this protocol are listed in Table 4.

### LC-QQQ-MS data pre-processing

Raw liquid chromatography triple quadrupole mass spectrometry (LC-QQQ-MS) data require pre-processing to extract peak area or peak height as alternative measures of signal intensity. Signal intensity can then be used as a proxy for the concentration of metabolites in a sample. Alternative software solutions exist for LC-QQQ-MS data pre-processing, including fully automatic solutions such as MRMprobs (Tsugawa et al., 2014) and automRm (Eilertz et al., 2022), as well as solutions that facilitate manual peak review, such as skyline (MacLean et al., 2010), and vendor-specific solutions such as MassHunter.

Low-input metabolomics experiments often suffer from low signal intensity. In addition, both hydrophilic interaction liquid chromatography (HILIC) and microLC are notorious for suboptimal retention.
time reproducibility. Consequently, manual peak review is required to maximize the number of quantified metabolites. We opted to use MassHunter8 because it does not require conversion of our original data to an open format. During manual peak review, it is important to follow a set of guidelines to obtain reliable results:

Signal intensity in cell extract must be higher than in the blank sample.

Chromatographic peaks of quantifier and qualifier must align well.

The ratio in signal intensity between quantifier and qualifier must be similar across all samples. This does not apply to $^{13}$C qualifiers.

If shifts in retention time occur, they should typically be in the same direction for all metabolites and might increase in the order of measurement. Moreover, retention times could continue to shift in the same direction from sample to sample.

The location of the start and end of a chromatographic peak relative to the top of the peak should be as similar as possible for all peaks.

The choice of baseline relative to a chromatographic peak and the surrounding background signal should be as similar as possible for all peaks.

If chromatographically separated isotopes are observed, their elution order must always remain the same, even if their retention time shifts.

Signals that do not meet these criteria should be disregarded in subsequent analyses.

Some additional considerations that aid data interpretation:

The signal intensity of phenol red can be used as a proxy for the amount of medium carry over. Lower signal intensity indicates less carry over.

Some peaks can show persistent background signals (e.g., cholic acid in the microLC analysis of polar lipids or citric acid in the analysis of polar metabolites). In these cases, subtraction of background signal intensity from the signal intensities recorded for cell extracts may be advisable.

| Table 3. MS parameter settings for analysis of polar lipids |
|----------------------------------------------------------|
| Parameter                              | Value          |
| ESI source                             | ESI            |
| Gas temperature                        | 200°C          |
| Gas flow                               | 16 L/min N₂    |
| Nebulizer pressure                     | 20 psi N₂      |
| Capillary voltage positive             | 3,700 V        |
| Capillary voltage negative             | 2,800 V        |
| iFunnel high pressure RF positive      | 110 V          |
| iFunnel high pressure RF negative      | 90 V           |
| iFunnel low pressure RF positive       | 80 V           |
| iFunnel low pressure RF negative       | 60 V           |
| MS1 resolution                         | unit           |
| MS2 resolution                         | unit           |
| Fragmentor                             | 380            |
| Cell accelerator voltage               | 4 V            |
| Dwell time                             | 5 ms           |
Table 4. Compound-specific settings for analysis of polar lipids

| Compound name                     | Precursor ion | Product ion | Collision energy | Polarity | Expected RT (min) |
|-----------------------------------|---------------|-------------|------------------|----------|------------------|
| Cholic acid quantifier            | 453.3         | 407.3       | 16               | –        | 13.1             |
| Cholic acid qualifier             | 426.3         | 355.3       | 20               | +        |                  |
| Muricholic acid quantifier        | 453.3         | 407.3       | 16               | –        | 11.9             |
| Muricholic acid qualifier         | 426.3         | 355.3       | 20               | +        |                  |
| 7,25 dihydroxy cholesterol quantifier | 383.3      | 91.1        | 80               | +        | 18.1             |
| 7,25 dihydroxy cholesterol qualifier | 383.3      | 81.1        | 44               | +        |                  |
| 4-oxo-(9-cis,13-cis)Retinoic acid quantifier | 315.2 | 297.1 | 8 | + | 23.2 |
| 4-oxo-(9-cis,13-cis)Retinoic acid qualifier | 315.2 | 269.3 | 16 | – | |
| carnitine-C02 quantifier         | 204.1         | 85          | 20               | +        | 9.8              |
| carnitine-C02 qualifier          | 204.1         | 43          | 72               | +        |                  |
| carnitine-C04 quantifier         | 232.2         | 85          | 20               | +        | 10.2             |
| carnitine-C04 qualifier          | 232.2         | 43          | 48               | +        |                  |
| carnitine-C06 quantifier         | 260.2         | 85          | 28               | +        | 11.9             |
| carnitine-C06 qualifier          | 260.2         | 43          | 56               | +        |                  |
| carnitine-C08 quantifier         | 288.2         | 85          | 24               | +        | 13.6             |
| carnitine-C08 qualifier          | 288.2         | 57          | 48               | +        |                  |
| carnitine-C10 quantifier         | 316.2         | 85          | 32               | +        | 14.2             |
| carnitine-C10 qualifier          | 316.2         | 43          | 76               | +        |                  |
| carnitine-C12 quantifier         | 344.3         | 85          | 32               | +        | 15.1             |
| carnitine-C12 qualifier          | 344.3         | 43          | 76               | +        |                  |
| carnitine-C14 quantifier         | 372.3         | 85          | 28               | +        | 17.2             |
| carnitine-C14 qualifier          | 372.3         | 57          | 72               | +        |                  |
| carnitine-C16 quantifier         | 400.3         | 85          | 36               | +        | 19.9             |
| carnitine-C16 qualifier          | 400.3         | 57          | 62               | +        |                  |
| carnitine-C18 quantifier         | 428.4         | 85          | 44               | +        | 22.7             |
| carnitine-C18 qualifier          | 428.4         | 57          | 52               | +        |                  |
| carnitine-C20 quantifier         | 456.4         | 85          | 44               | +        | 24.2             |
| carnitine-C20 qualifier          | 456.4         | 57          | 52               | +        |                  |
| Chenodeoxycholic acid quantifier  | 437.3         | 391.2       | 16               | –        | 16.0             |
| Chenodeoxycholic acid qualifier   | 357.3         | 91.1        | 80               | +        |                  |
| Cholesterol quantifier           | 369.4         | 91.1        | 76               | +        | 32.4             |
| Cholesterol qualifier            | 369.4         | 81          | 56               | +        |                  |
| Glycochenodeoxycholic acid quantifier | 450.32     | 414.2       | 16               | +        | 12.4             |
| Glycochenodeoxycholic acid qualifier | 448.3      | 74.1        | 52               | –        |                  |
| Glycocholic acid quantifier       | 466.4         | 412.4       | 16               | +        | 11.1             |
| Glycocholic acid qualifier        | 466.4         | 337.3       | 24               | +        |                  |
| LPC 14-0 quantifier              | 468.3         | 184         | 28               | +        | 18.3             |
| LPC 14-0 qualifier               | 468.3         | 104.1       | 32               | +        |                  |
| LPC 16-0 quantifier              | 496.3         | 184         | 28               | +        | 21.0             |
| LPC 16-0 qualifier               | 496.3         | 104.1       | 32               | +        |                  |
| LPC 18-0 quantifier              | 524.4         | 184         | 28               | +        | 24.0             |
| LPC 18-0 qualifier               | 524.4         | 104.1       | 32               | +        |                  |
| LPC 18-1 quantifier              | 522.3         | 184         | 28               | +        | 21.9             |
| LPC 18-1 qualifier               | 522.3         | 104.1       | 32               | +        |                  |
| LPC 20-4 quantifier              | 544.4         | 184         | 28               | +        | 20.2             |
| LPC 20-4 qualifier               | 544.4         | 104.1       | 32               | +        |                  |
| LPE 16-0 quantifier              | 452.2         | 255.1       | 24               | –        | 21.4             |
| LPE 16-0 qualifier               | 452.2         | 195.9       | 24               | –        |                  |
| LPE 18-0 quantifier              | 480.2         | 283         | 24               | –        | 24.2             |
| LPE 18-0 qualifier               | 480.2         | 195.9       | 24               | –        |                  |
| LPE 18-1 quantifier              | 478.2         | 281         | 24               | –        | 22.0             |
| LPE 18-1 qualifier               | 478.2         | 195.9       | 24               | –        |                  |
| 7-hydroxy cholesterol quantifier  | 367.3         | 81          | 52               | +        | 22.2             |

(Continued on next page)
Normalization of signal intensity values can improve the quality of the results:

Normalization to cell number (determined by FACS during sample preparation) can be used to compensate for differences in the amount of input material. Differences greater than 3-fold should not be compensated in this way because non-linear effects can occur.

Normalization to total protein or total DNA in the cell pellet after extraction of metabolites can be used to compensate for differences in the amount of input material. Differences greater than 3-fold should not be compensated in this way because non-linear effects can occur.

Normalization to the signal intensity of a $^{13}$C qualifier can be used to compensate for degradation of compounds prior to analysis and differences in ionization efficiency during MS analysis. This is only reliable if a matching $^{13}$C qualifier has been recorded with sufficient signal intensity. Note that for some polar metabolites no $^{13}$C quantifier was recorded.

We advise against using quantile normalization or normalization to the sum of all metabolite signals for the data generated with the methods described in this protocol because the limited number of metabolites covered by these LC-QQQ-MS methods can introduce a bias in the data.

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### Table 4. Continued

| Compound name                      | Precursor ion | Product ion | Collision energy | Polarity | Expected RT (min) |
|------------------------------------|---------------|-------------|------------------|----------|-------------------|
| 7-hydroxy cholesterol qualifier    | 367.3         | 55.3        | 72               | +        |                   |
| 25-hydroxy cholesterol quantifier  | 367.3         | 81          | 52               | +        | 27.3              |
| 25-hydroxy cholesterol qualifier   | 367.3         | 55.3        | 72               | +        |                   |
| PC 32-0 quantifier                 | 734.5         | 184.1       | 32               | +        | 33.9              |
| PC 32-0 quantifier                 | 734.5         | 86.2        | 76               | +        |                   |
| PC 34-0 quantifier                 | 762.6         | 184.1       | 32               | +        | 34.3              |
| PC 34-0 quantifier                 | 762.6         | 86.2        | 76               | +        |                   |
| PC 34-1 quantifier                 | 760.6         | 184.1       | 32               | +        | 34.0              |
| PC 34-1 quantifier                 | 760.6         | 86.2        | 76               | +        |                   |
| PC 34-2 quantifier                 | 758.6         | 184.1       | 32               | +        | 33.3              |
| PC 34-2 quantifier                 | 758.6         | 86.2        | 76               | +        |                   |
| PC 36-2 quantifier                 | 786.6         | 86.2        | 76               | +        | 34.5              |
| PC 36-2 quantifier                 | 786.6         | 184.1       | 32               | +        |                   |
| PC 36-4 quantifier                 | 782.6         | 184.1       | 32               | +        | 33.0              |
| PC 36-4 quantifier                 | 782.6         | 86.2        | 76               | +        |                   |
| PE 32-0 quantifier                 | 692.5         | 551.5       | 24               | +        | 32.4              |
| PE 32-0 quantifier                 | 690.5         | 195.9       | 52               | –        |                   |
| PE 34-1 quantifier                 | 718.5         | 577.4       | 24               | +        | 33.4              |
| PE 34-1 quantifier                 | 716.5         | 195.9       | 52               | –        |                   |
| PE 36-2 quantifier                 | 742.5         | 281.1       | 40               | –        | 33.5              |
| PE 36-2 quantifier                 | 742.5         | 195.9       | 52               | –        |                   |
| PE 36-4 quantifier                 | 738.5         | 281.1       | 40               | –        | 33.0              |
| PE 36-4 quantifier                 | 738.5         | 195.9       | 52               | –        |                   |
| Retinal quantifier                 | 285.2         | 91.2        | 56               | +        | 22.2              |
| Retinal qualifier                  | 285.2         | 41.2        | 64               | +        |                   |
| Retinoic acid quantifier           | 301.2         | 41.2        | 72               | +        | 20.8              |
| Retinoic acid quantifier           | 299.2         | 255.2       | 20               | –        |                   |
| Retinol quantifier                 | 287.2         | 41.2        | 76               | +        | 22.3              |
| Retinol qualifier                  | 269.2         | 93.3        | 24               | +        |                   |
| Taurocholateoxycholic acid quantifier | 517.3   | 464.3       | 20               | +        | 12.4              |
| Taurocholateoxycholic acid quantifier | 498.3   | 80          | 80               | –        |                   |
| Taurocholic acid quantifier        | 533.32        | 337.2       | 36               | +        | 11.1              |
| Taurocholic acid quantifier        | 533.3         | 462.3       | 28               | +        |                   |
EXPECTED OUTCOMES

(A) TCA cycle metabolites and amino acids
Some representative chromatographic peaks of polar metabolites are plotted in Figure 2 and additional examples are given in Data S1. Note that the width of chromatographic peaks can vary between metabolites but is consistent between quantifiers and qualifiers.

(B) Signaling lipids and retinoids
Some representative chromatographic peaks of polar metabolites are plotted in Figure 3 and additional examples are given in Data S2. Note that the width of chromatographic peaks can vary between metabolites but is consistent between quantifiers and qualifiers.

LIMITATIONS
Hematopoietic stem and progenitor cells are small compared to many other cell types and popular cancer cell lines (Shariatmadar et al., 2008). Therefore, an equivalent number of hematopoietic stem and progenitor cells will contain smaller amounts of metabolites. Moreover, hematopoietic stem and progenitor cells are quiescent, which leads to lower amounts of metabolites compared to metabolically active cells. Consequently, metabolomics analysis is limited to those metabolites that exhibit a relatively high intracellular abundance.

The detection of a metabolite in a given sample depends on its concentration in the cell extract. However, additional factors are also important: I) The ionization efficiency during electro spray ionization; II) The formation of adducts or in-source fragments during electro spray ionization; III) The number of fragments formed in the collision cell; IV) The presence of other substances in the sample that have the same retention time, and thus, can cause ion suppression; V) The presence of other
substances in the sample that can cause background signals. The first three points are likely to differ among different mass spectrometers, whereas the latter two factors depend on the sample composition. Consequently, the suitability of the described workflow has to be tested for every metabolite and every type of sample.

During the isolation of primary cells from tissues and during flow cytometry-based sorting, cells are largely deprived of nutrients and encounter suboptimal conditions with respect to temperature, osmolarity, and oxygen tension. These conditions are known to impact the metabolome (Llufrio et al., 2018; Ryan et al., 2021). However, exposure of hematopoietic stem and progenitor cells to rich culture media and growth stimuli can induce activation and differentiation and thus skew the metabolic composition. To alleviate these issues, we minimize the time from isolation of mouse tissue to extraction of metabolites by reducing the number of samples that are handled in parallel. In addition, the isolated cells are kept as cool as possible to slow down metabolite interconversion.

The use of rich medium as sheath fluid during cell sorting has been described (Ryan et al., 2021), however, this approach is susceptible to contaminations in the cell sorter. Although we have tested an additional short cultivation of the sorted cells prior to metabolite extraction, we have opted to not include this step in the protocol to avoid undesired activation or differentiation of stem cells.

For data interpretation, it has to be taken into account that sample processing is expected to induce a starvation-like phenotype. Of note, we do not drive any conclusions on high-turnover metabolites such as glycolytic intermediates or adenosine triphosphate (ATP).

Figure 3. Representative chromatograms of polar lipids in biological samples, standards, and blank samples
Black and blue lines represent quantifier and qualifier, respectively. Dashed blue lines indicate that the qualifier only gives a very weak signal and can be disregarded. Integrated regions are highlighted in gray and the top of peaks are indicated by vertical dotted lines.
TROUBLESHOOTING

Problem 1
FACS staining pattern looks unusual (step: fluorescence-activated cell sorting of purified hematopoietic stem cells).

Potential solution 1

- Fluorescent dyes can degrade, and thus, lead to unusual staining patterns. Especially, coupled dyes (e.g., PeCy7) might degrade into the respective single dyes (PE and Cy7) and cause off-channel signals. Make sure to store the fluorophore-coupled antibodies according to the manufacturer’s recommendations and prepare a single staining for each antibody to assure good quality before starting the sort.
- Dead cells can cause auto-fluorescence (specifically in the FITC channel). In some cases, the quality of the metabolomics data might benefit from a live/dead staining during the sort, especially when handling cell types sensitive to tissue processing (e.g., endothelial cells). This can further improve the quantity of metabolites detected and the overall quality of the data.

Problem 2
Low internal diameters used in microLC are prone to block. This can cause excessive high backpressure in analysis of polar lipids (step: microLC-MS/MS analysis of signaling lipids and retinoids).

Potential solution 2
We routinely use in-line filters in the autosampler, at the entry to the trap column, and at the entry to the analytical column to minimize the problem. In addition, rigorous sample cleanup by centrifugation and transfer of clean supernatant is very important.

Problem 3
In microLC early eluting compounds are missing (step: microLC-MS/MS analysis of signaling lipids and retinoids).

Potential solution 3
Possibly, the trap column has not been sufficiently equilibrated. Use the loading pump to equilibrate the loading pump for longer with buffer A2.

Problem 4
Some organic acids (in particular malic acid and citric acid), as well as some organo-phosphates, are known to interact with metal surfaces such as the capillaries, column housing, and frits that are routinely used in UHPLC systems. This can cause background levels increasing in the sequence of measurement (step: LC-QQQ-MS data pre-processing).

Potential solution 4
Modification of mobile phase buffers, changes in LC hardware, and organization of LC-MS/MS measurements can help mitigate this problem:

- Use high-pH mobile phase buffers to reduce the interaction of acids and phosphates with metal surfaces.
- Consider suitable mobile phase additives such as medronic acid (Hsiao et al., 2018).
- Use fused silica capillaries or PEEK capillaries if possible. Note that there are limitations in the use of PEEK in combination with some organic solvents and the use of fused silica in combination with very high pH.
- Avoid mixing regular samples and low-input samples within one batch.
- Remove residual acids and phosphates by a sequence of blank runs prior to analysis of low-input samples.
Problem 5
Background metabolite levels within negative controls are as high as within samples (step: LC-QQQ-MS data pre-processing).

Potential solution 5
- Make sure flow stream of the fluorescence cell sorter is adjusted properly and cells do not hit the tube wall, causing cell death.
- Media contamination (method A) causes high background levels in the negative control but also the actual samples. Ensure removal of the entire supernatant after washing the cell with wash buffer.

Problem 6
Retinoids cannot be detected (step: LC-QQQ-MS data pre-processing).

Potential solution 6
Light exposure can lead to degradation of retinoids after metabolite extraction. Protect samples from light during further sample preparation and measurement.

RESOURCE AVAILABILITY
Lead contact
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Materials availability
This study did not generate new materials.

Data and code availability
The published article Schönberger et al. Cell Stem Cell (2022) includes all datasets analyzed during this study. No new datasets were generated.

SUPPLEMENTAL INFORMATION
Supplemental information can be found online at https://doi.org/10.1016/j.xpro.2022.101408.

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AUTHOR CONTRIBUTIONS
Conceptualization: K.S. and J.M.B.; methodology: K.S., M.M., N.C.-W., and J.M.B.; investigation: K.S., M.M., and J.M.B.; writing and editing: K.S. and J.M.B.; supervision: N.C.-W. and J.M.B.

DECLARATION OF INTERESTS
The authors declare no competing interests.
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