





Figure EV1. MSOT spectra of liver, kidney, interscapular brown adipose tissue (iBAT), retroperitoneal white adipose tissue (rpWAT), aorta and Sulzer vein (SV) in vivo and main absorbers.

A-C Raw spectra of liver, kidney, iBAT, rpWAT aorta and SV in vivo. Data represent the mean from 8 animals (n = 8).

D Normalized spectra of H₂O, Hb, HbO₂ and Lipid. Data are provided as reference in ViewMSOT 3.8 software.



Figure EV2. MSOT imaging of lipid phantoms.

- A Reconstructed MSOT images (930 nm) of phantoms containing 0–100% lipid. The lipid fraction and the ROI are indicated on each image. The colour bar shows the colour coding of MSOT a.u. from 0 to 2,000 a.u. (bottom to top). Scale bar: 4 mm.
- B Absorption of lipid phantoms at 930 nm. Data represent the mean from 3 sections per phantom.
- C Linear unmixing result of lipid from the phantoms. Data represent the mean from 3 sections per phantom.



Figure EV3. MSOT imaging of liver-lipid phantoms.

A Reconstructed MSOT images (930 nm) of phantoms contains 0–60% lipid. The lipid fraction and the ROI are indicated on each image. The colour bar shows the colour coding of MSOT a.u. from 0 to 7,000 a.u. (bottom to top). Scale bar: 4mm.

B Normalized spectra of phantoms in A. Data represent the mean from 3 sections per phantom.

C Linear unmixing result of lipid in phantoms. Data represent the mean from 3 sections per phantom.



Figure EV4. Histology quantification of lipid in liver.

Each dot represents data from one animal (grade 0: n = 14; grade 1: n = 11; grade 2: n = 7; and grade 3: n = 9). Data represent the mean (\pm 95% confidence). The unpaired *t*-test was used to verify the statistical significance. Grade 0 versus grade 1: P = 6.80E-11; grade 1 versus grade 2: P = 0.0007; and grade 2 versus grade 3 P = 0.0086.



Figure EV5. Correlation analysis of different lipid detection methods.

- A Correlation between lipid linear unmixing readout and fat quantification by histology. Each dot represents data from one animal (n = 41).
- B Correlation between lipid linear unmixing readout and difference analysis readout. Each dot represents data from one animal (n = 41).