Aim: To identify the tissue-specific methylation markers

Aim: Paired samples to investigate the non-hematopoietic tissue-of-origin of plasma

Aim: To investigate the non-hematopoietic tissue-of-origin of plasma cfDNA.
Figure S3

A

Liver
Lung
Stomach
Colon
Kidney
Pancreas
Muscle
Skin

0 2 4 8 16
Known fraction(%)

0 2 4 8 16
Predicted fraction(%)

R²=0.891
p-value<0.001

R²=0.944
p-value<0.001

R²=0.978
p-value<0.001

R²=0.984
p-value<0.001

R²=0.939
p-value<0.001

R²=0.979
p-value<0.001

Figure A showing scatter plots for different organs (Liver, Lung, Stomach, Colon, Kidney, Pancreas, Muscle, Skin) with predicted and known fractions. Each plot includes correlation coefficients (R²) and p-values.
Figure S4

A

B

Liver-derived DNA (GE/mL)

Female

Male

n.d.

cor = -0.25

Age

Liver-derived DNA (GE/mL)
Figure S5

A

![Graph A showing cfDNA Concentration (ng/ml) across different patient groups: Healthy individuals, Cholelithiasis patients, Cirrhosis patients, HCC(≤3cm) patients, HCC(3-5cm) patients, HCC(>5cm) patients.]

B

![Graph B showing a positive correlation between ALT (U/L) and Liver-derived DNA fraction concentration (%). Correlation coefficient (cor) = 0.69.]

**Notes:**
- *** indicates statistical significance.
- n.d. stands for not determined.
Figure S6