A

CBS

CSE

Normal
Cancer

B

Ser | Gly

Cth | GSH

Cys | γ-Glu-Cys

C

Ser | Gly

Cth | GSH

Cys | γ-Glu-Cys

M+0   M+1   M+2

Supplementary Figure S5.

Total levels of cysteine and glutathione intermediates in liver and pancreas cancer models (related to Fig. 4). **A,** Log scaled gene expression profile for CBS and CSE based on LIHC (liver hepatocellular carcinoma) and PAAD (pancreatic adenocarcinoma) datasets in TCGA and GTEx. |Log_2FC| cutoff, 1; p-value cutoff, 0.01; log-scale, $log_2(TPM+1)$. **B,** Analysis of the total signal of serine, glycine, cystathionine, glutathione, cysteine and γ-glutamylcysteine in liver tissues (N=8) compared to HCC tumors (N=8) and their matched serum normal (N=8) and HCC (N=5) following infusion with 1-[$^{13}C_3$]-serine. **C,** Analysis of the total signal of serine, glycine, cystathionine, glutathione, cysteine and γ-glutamylcysteine in pancreas tissues (N=5) compared to PDAC tumors (N=5), and their matched serum from normal (N=5) and PDAC (N=5) following infusion with 1-[$^{13}C_3$]-serine. For **B** and **C**, data are presented as mean ± SD. N.D., not detected. The total signal is the sum of all isotopologue signals. The peak intensities of isotopologues were measured as AreaTop (mean of three top points in the peak). Ser, serine; Cth, cystathionine; Cys, cysteine; Gly, glycine; GSH, glutathione; γ-Glu-Cys, γ-glutamylcysteine. *$p < 0.05$.