

Supplementary information, Fig S1 cGAS is localized in mitochondria in cancer cells

a, Representative LC-MS/MS spectra of a tryptic peptide of cGAS. The peptide sequence is shown on the top with the collision-induced fragmentation pattern. The b and y ions are shown in green and orange, respectively, which are generated during peptide fragmentation in LC-MS/MS. b, Representative immunofluorescence images staining for TOM20 in Hep3B cells expressing Mito-GFP. Colocalization analysis of immunofluorescence images using the colocalization plugin, which calculates Pearson's Correlation Coefficient. Scale bars, 20 µm. c, Representative immunofluorescence images staining for cGAS in PLC cells with Mito-GFP expression. The nucleus was stained with DAPI. Colocalization analysis of immunofluorescence images using the colocalization plugin, which calculates Pearson's Correlation Coefficient. Scale bars, 20 µm. d, Representative fluorescence images showing the colocalization of mitochondria (Mito-GFP) and cGAS-mCherry in Hep3B cells. Colocalization analysis of fluorescence images using the colocalization plugin, which calculates Pearson's Correlation Coefficient. The nucleus was stained with DAPI. Scale bars, 10 µm. e, Western blotting analysis of the protein levels of cGAS in subcellular fractions including nucleus, cytosol and mitochondria in cancer cell lines. Fractionation fidelity was verified by detection of Lamin B in the nuclear fraction, Tubulin in the cytosolic fraction and TOM20 in the mitochondrial fraction. f, Western blotting analysis of the protein levels of cGAS in mitochondrial fraction in paired adjacent noncancerous tissues and liver tumor tissues from YAP5SA-induced HCC bearing mice. Fractionation fidelity was verified by detection of GAPDH in the cytosolic fraction and TOM20 in the mitochondrial fraction. The diagram showed the HCC mouse model induced by YAP5SA injection.