

CORRIGENDUM

Corrigendum to “Dysregulated glucuronic acid metabolism exacerbates hepatocellular carcinoma progression and metastasis through the TGF β signalling pathway”

Gao Q, Cheng B, Chen C, et al. Dysregulated glucuronic acid metabolism exacerbates hepatocellular carcinoma progression and metastasis through the tumour growth factor beta signalling pathway. *Clin Transl Med.* 2022;12:e995. <https://doi.org/10.1002/ctm2.995>

In this article, Figure 6G were inadvertently assembled by errors. We have now updated the staining image for Snail in the “*Gstz1*^{-/-}; *sgUgdh*” group in Figure 6G. The corrected Figure 6G is as follows.

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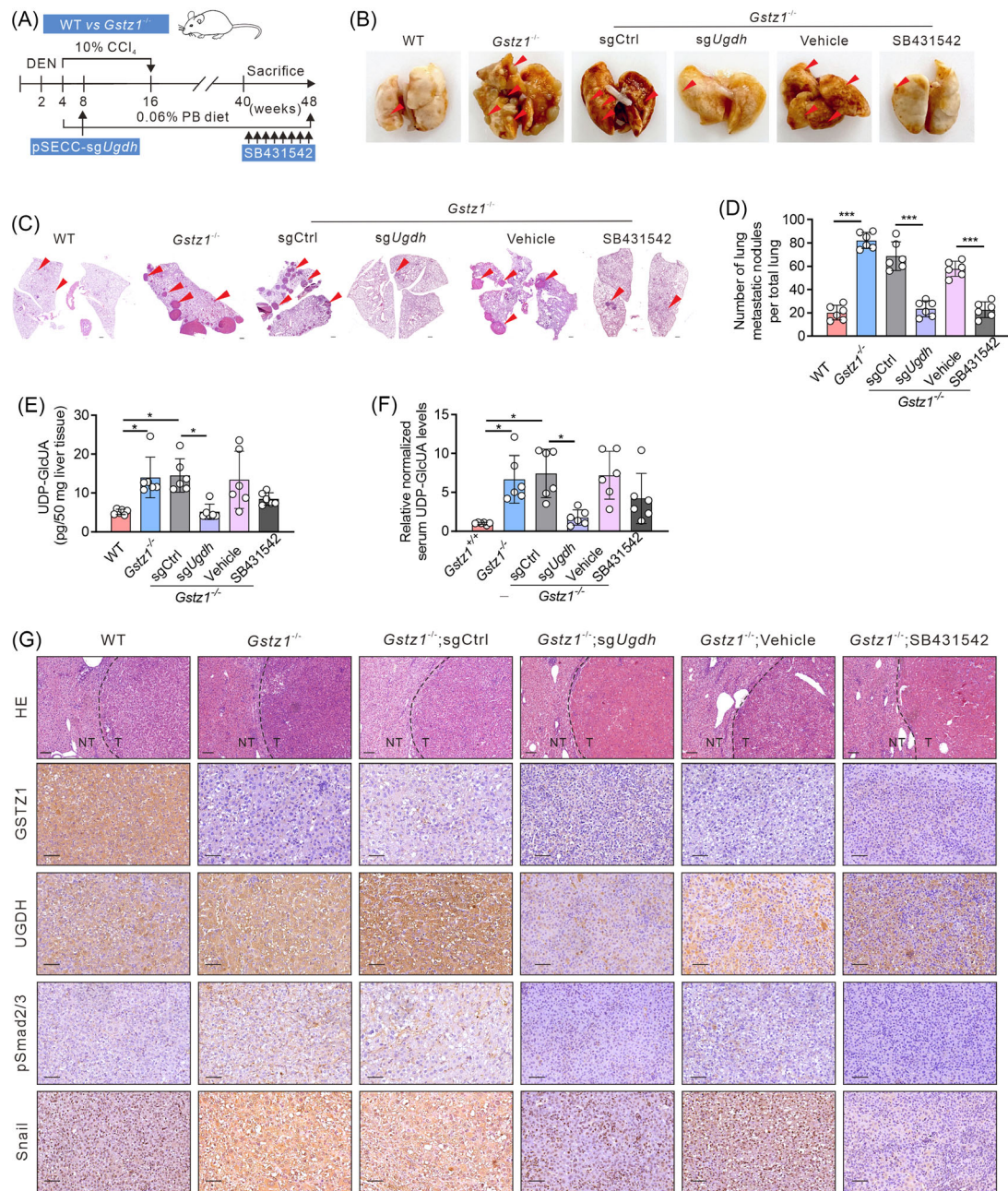


FIGURE 6 Blockage of the glucuronic pathway or tumour growth factor beta (TGF β) signalling blunts hepatocellular carcinoma (HCC) metastasis driven by *Gstz1* loss. (A) Schematic representation of diethylnitrosamine (DEN) and CCl₄-induced mouse model of HCC. PB, phenobarbital. (B) Representative images of lung metastasis. (C) Hematoxylin-and-eosin (H&E) staining of occult metastases in lung tissue sections. Scale bar, 500 μ m. (D) Number of lung metastases. Data represent mean \pm SD of the relative number of nodules per mouse for six mice. (E) UDP-GlcUA levels in mouse liver tissues. $n = 6$. (F) The relative content of UDP-GlcUA normalized to the average UDP-GlcUA level in serum samples obtained from *Gstz1*^{+/+} mice. $n = 6$. (G) Hematoxylin-and-eosin (H&E) and Immunohistochemistry (IHC) staining for GSTZ1, UGDH, pSmad2/3 and Snail in WT and *Gstz1*^{-/-} mouse liver sections. NT, non-tumour; T, tumour. Scale bar: 50 μ m. Data are mean \pm SD. p -Values were derived from a one-way analysis of variance (ANOVA) followed by the Tukey test (D–F) (* $p < .05$, *** $p < .001$).

The author apologizes for this error move this after the artwork and figure caption.