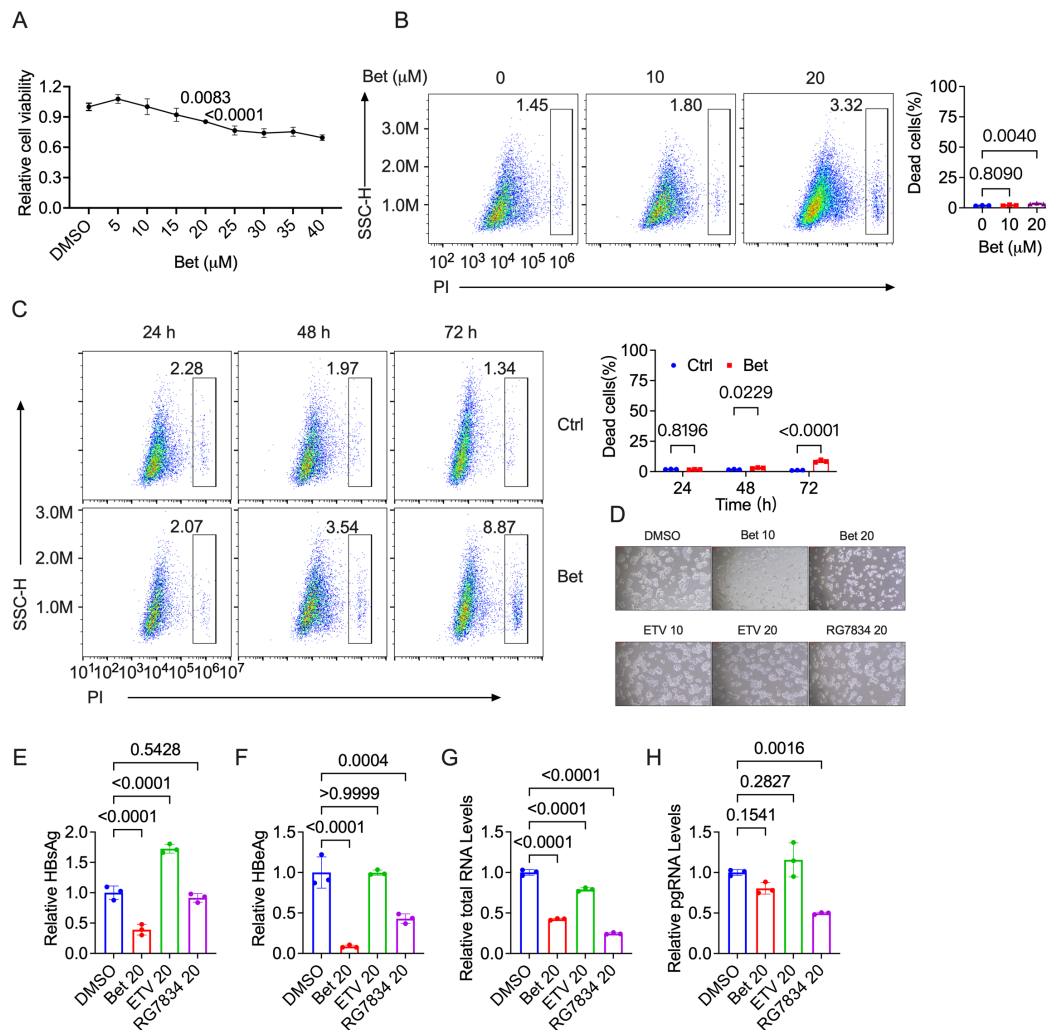


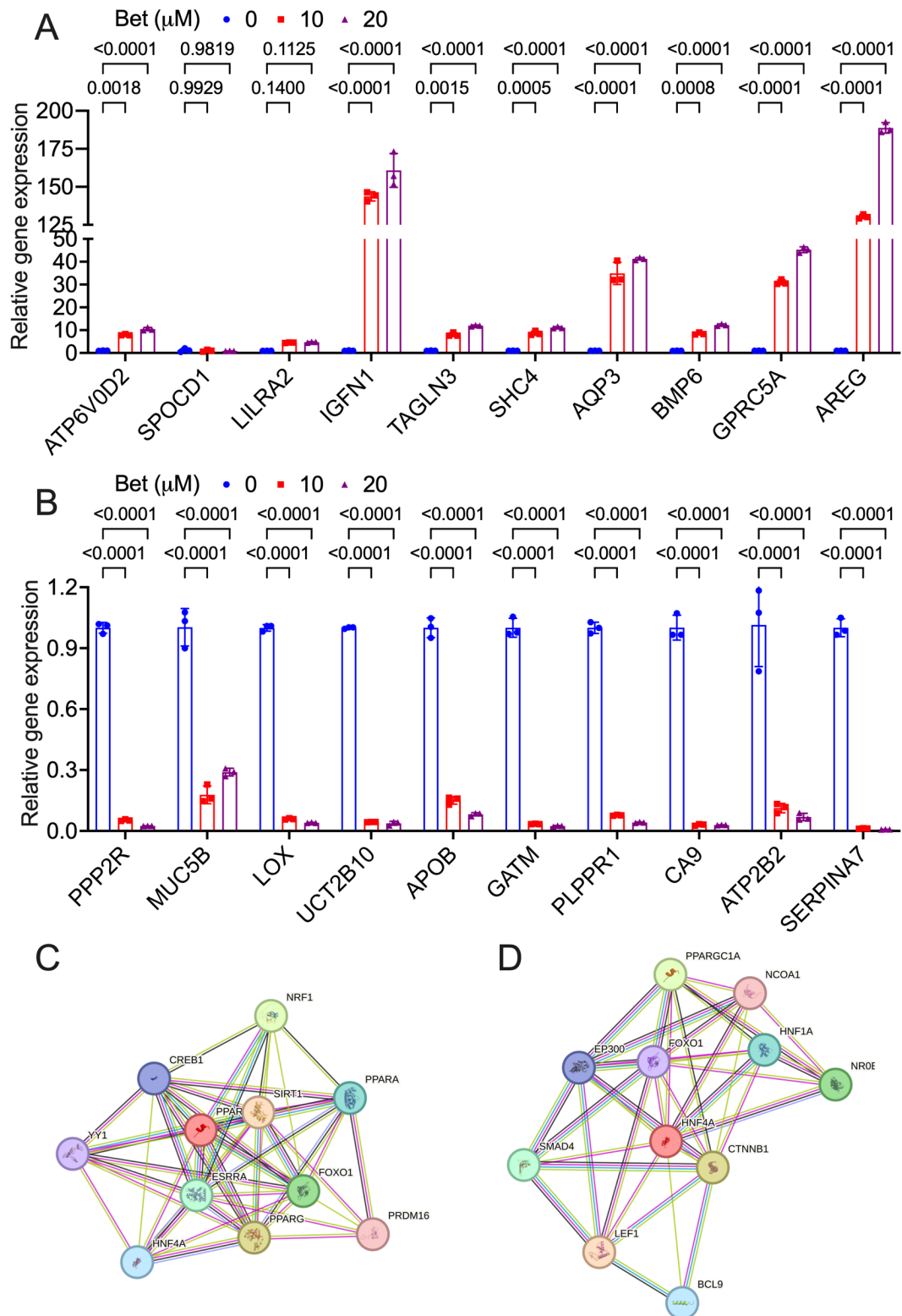
## Supplementary Figure. 1



### Supplementary Fig. 1

(A) Cytotoxicity assessment of Bet using CCK-8 assay after 48-hour treatment. (B&C) Cell death rates were monitored by PI staining coupled with flow cytometry. (D) Cell morphology after drug treatment for 48 h, (scale bar: 50.000  $\mu\text{m}$ ). (E&F) Secretion levels of HBsAg and HBeAg in the supernatant of HepG2.2.15 cells following a 48 h culture in medium containing DMSO, Bet (20  $\mu\text{M}$ ), ETV (20  $\mu\text{M}$ ), or RG7834 (20  $\mu\text{M}$ ). (G&H) HepG2.2.15 cells were cultured in medium containing DMSO, Bet (20  $\mu\text{M}$ ), ETV (20  $\mu\text{M}$ ), or RG7834 (20  $\mu\text{M}$ ) for 48 h, after which RT-qPCR quantified intracellular HBV RNA expression.

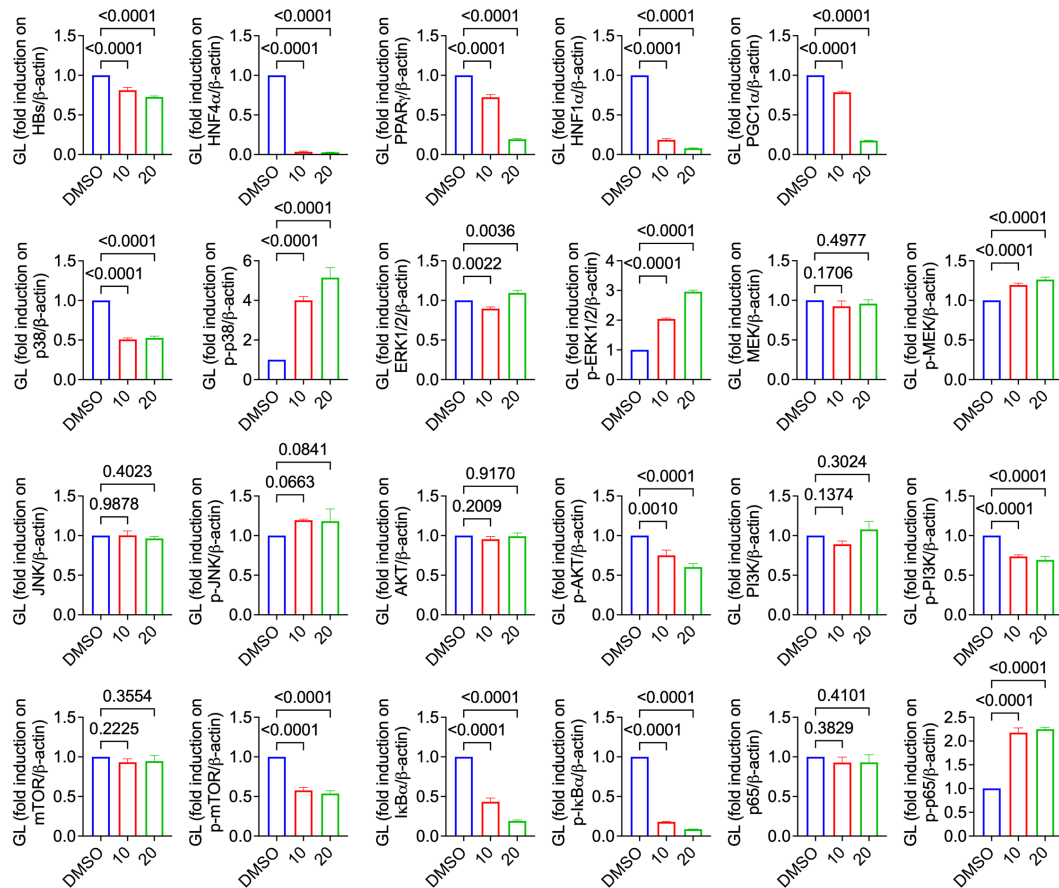
## Supplementary Figure. 2



**Supplementary Fig. 2**

(A&B) The expression levels of Twenty DEGs in RNA-seq data. (C&D) Protein interaction network of HNF4 $\alpha$  and PGC1 $\alpha$ .

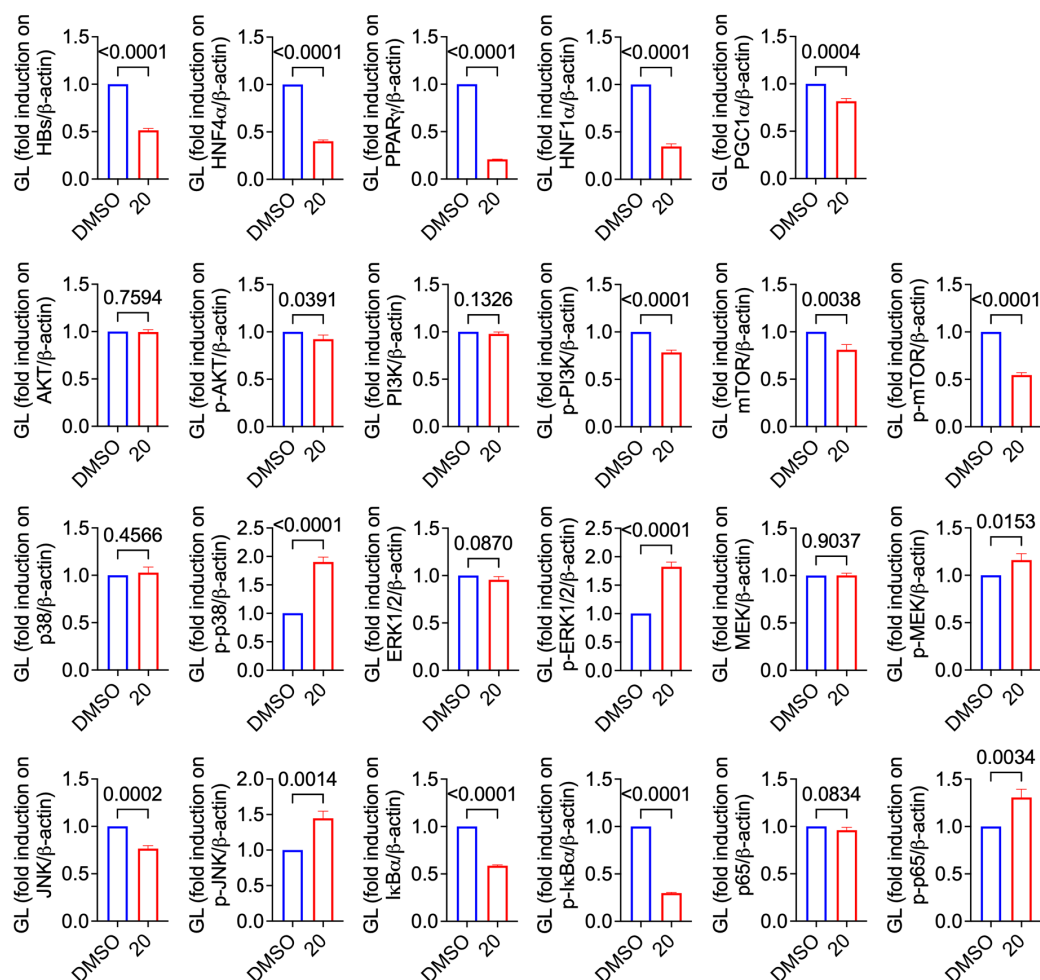
## Supplementary Figure. 3



### Supplementary Fig. 3

Densitometric analysis of Western blot bands presented in Figure 3A-D was conducted with ImageJ software. The relative expression levels of the target proteins were quantitatively determined by normalization.

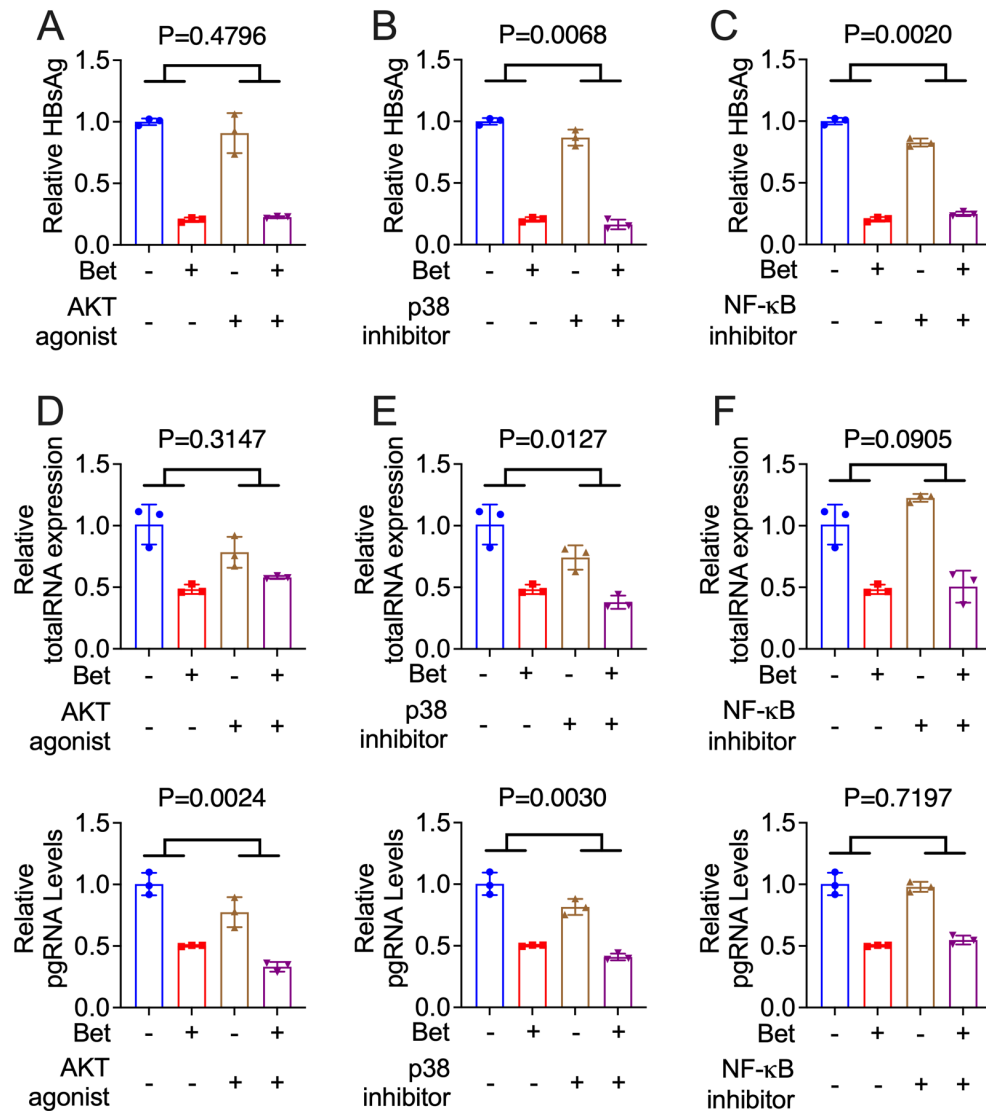
## Supplementary Figure. 4



### Supplementary Fig. 4

Densitometric analysis of Western blot bands presented in Figure 4F-I was conducted with ImageJ software. The relative expression levels of the target proteins were quantitatively determined by normalization.

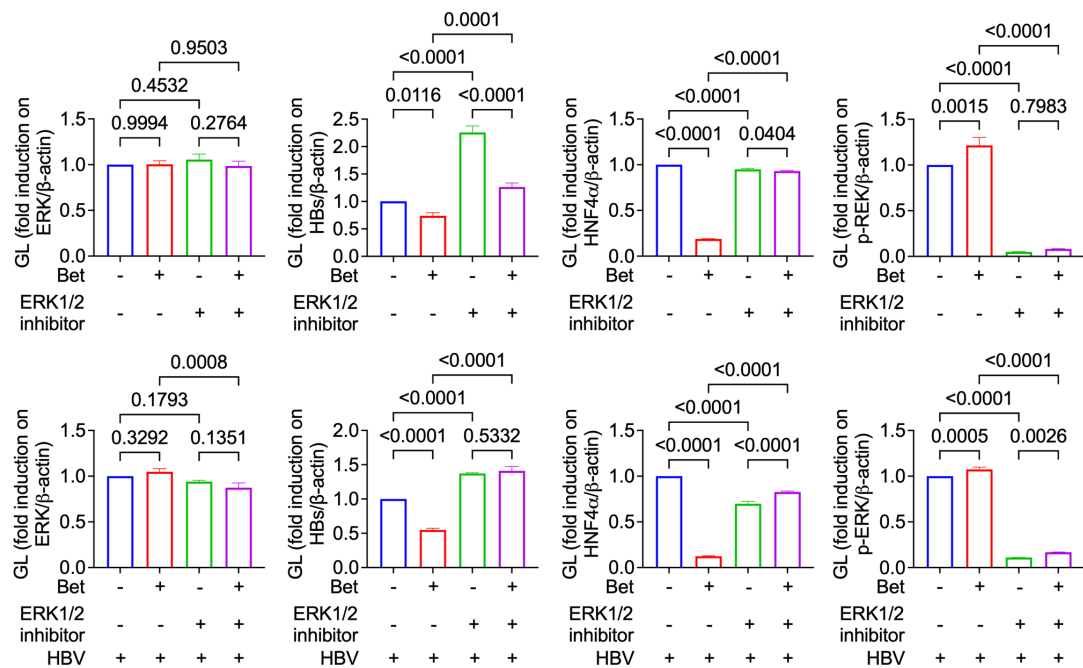
## Supplementary Figure. 5



### Supplementary Fig. 5

(A-C) The inhibitory effect of Bet on HBsAg, whether administered alone or in combination with inhibitors or agonists, was assessed using enzyme-linked immunosorbent assay (ELISA). (D-F) The rescue effect of inhibitors or agonists on Bet-induced suppression at the RNA level was evaluated by RT-qPCR.

## Supplementary Figure. 6



### Supplementary Fig. 6

Densitometric analysis of Western blot bands presented in Figure 5H-I was conducted with ImageJ software. The relative expression levels of the target proteins were quantitatively determined by normalization.