

Supplementary information Fig. S11 SCENIC analysis reveals the gene regulatory network of Hyper-organoids

**a**, Enrichment of the gene network analyzed by SCENIC in all single cells from Hyperorganoids compared with ENR-organoids (top) and Hyper-organoids without VPA/EPZ6438 (bottom).

- b, Gene expression heatmap of 500 differentially expressed genes between two branches in a pseudo-temporal order. Successful and failed regenerative trajectories (including pre-branch) are shown on the left and right, respectively. Representative genes of *Tead2* regulon are shown on the right.
- c, ForceAtlas embedding plot displaying *Tead2*, *Sp5* and *Myc* regulons (red dots, active; blue dots, inactive) as well as their intensity distributions from Hyper-organoids with and without VPA/EPZ6438 shown in Fig. 3f.
- **d**, Box plots displaying *Tead2* regulon activity measured by area under the curve (AUC) of Lgr5<sup>+</sup> cell in –VE and Hyper organoids.
- e, Representative images and quantification of total organoid number cultured under the indicated conditions after the knockdowns with the indicated shRNA. –VEorganoids (left) or Hyper-organoids (right) were cultured in the 8C condition for 10 days. Scale bars, 100 μm.