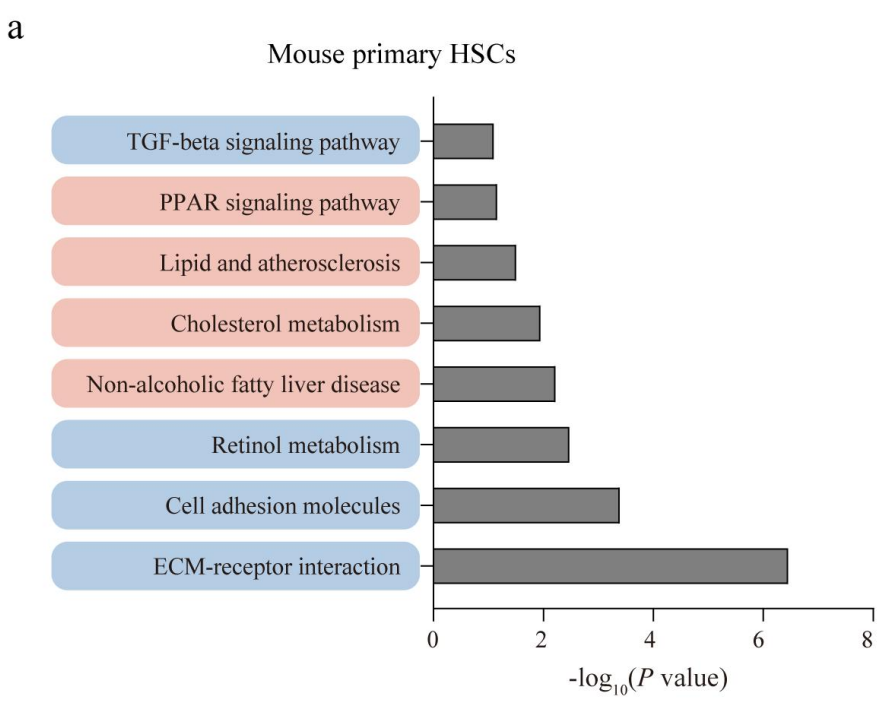
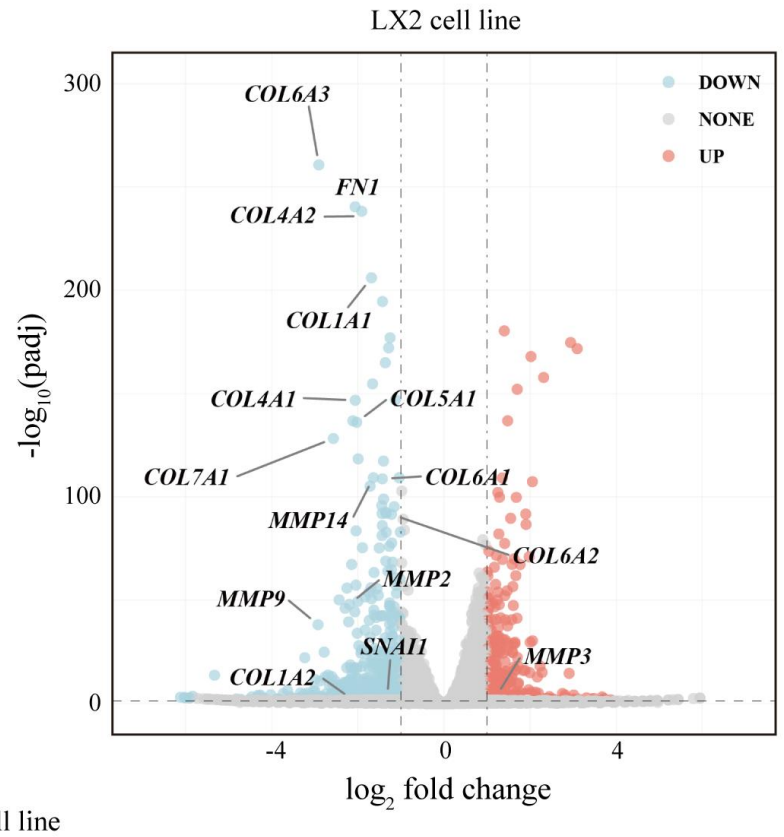
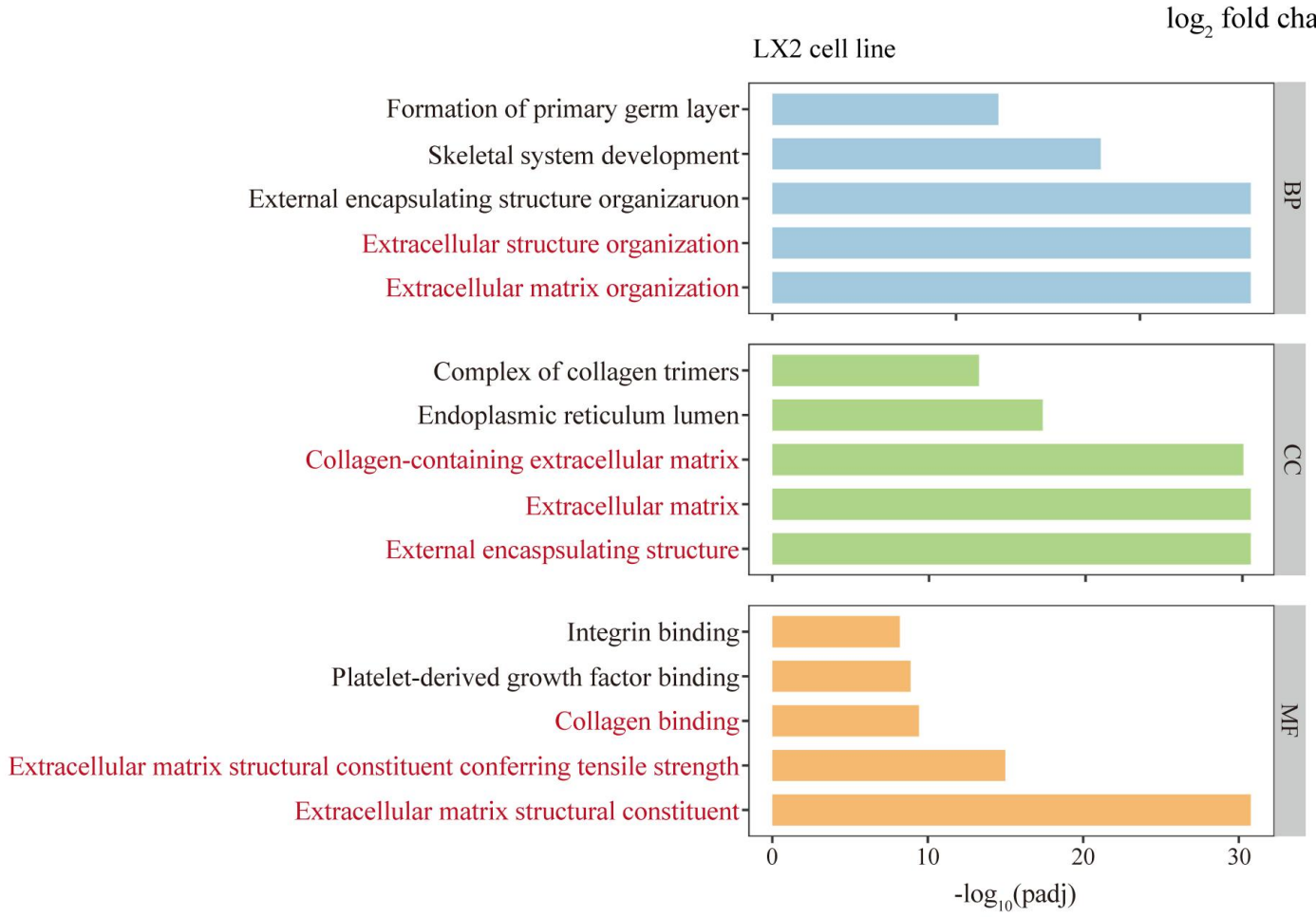
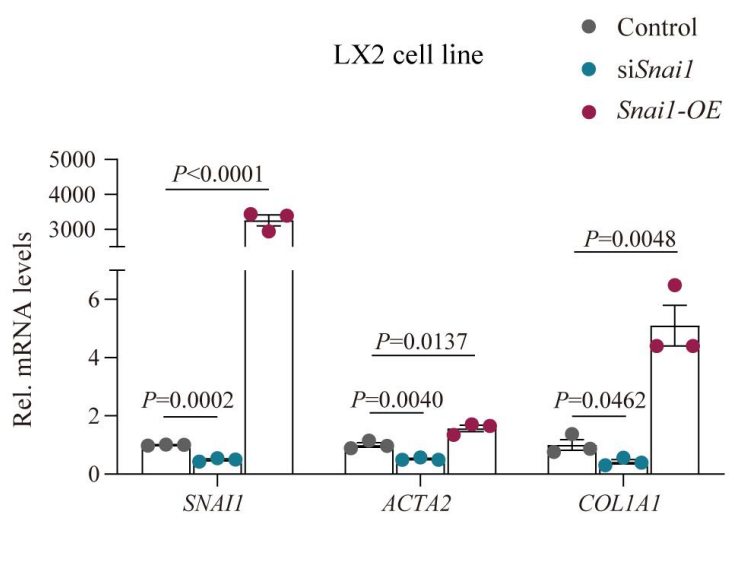
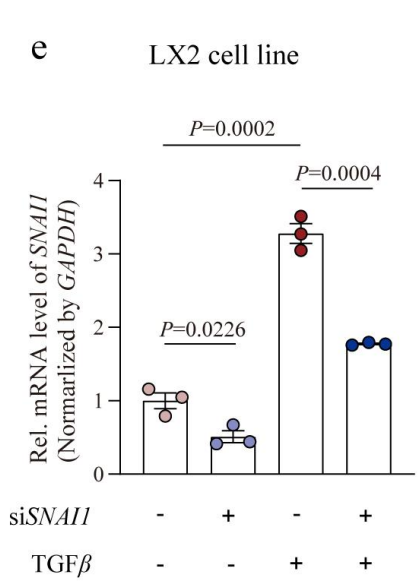
Fig. S3











Supplementary Fig. S3. The modulation of fibrotic gene expression by *Snai1* under basal condition.

(a) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis in primary HSCs. Cells were isolated from *Snai1*$^{flox/flox}$ and *Snai1*$^{\Delta HSC}$ mice liver and activated *in vitro*. (b and c) TGFβ treated LX2 cells were transfected with siScramble or si*SNAI1* for 48 h. (b) volcano plot of differentially expressed genes (log2FC > 1 and padj < 0.05). (c) Downregulated Gene Ontology (GO) pathway enrichment analysis. (d) The expression of *SNAI1*, *ACTA2* and *COL1A1* in LX2 cells with *SNAI1* overexpression or knockdown *SNAI1*. (e) *SNAI1* expression in LX2 cells. Cells were transfected with siRNA (siScramble and si*SNAI1*) and treated with 10 μM TGFβ for 48 h. Data are presented as mean ± SEM and analyzed by two-tailed Student's t test. $p < 0.05$ indicates significant difference.