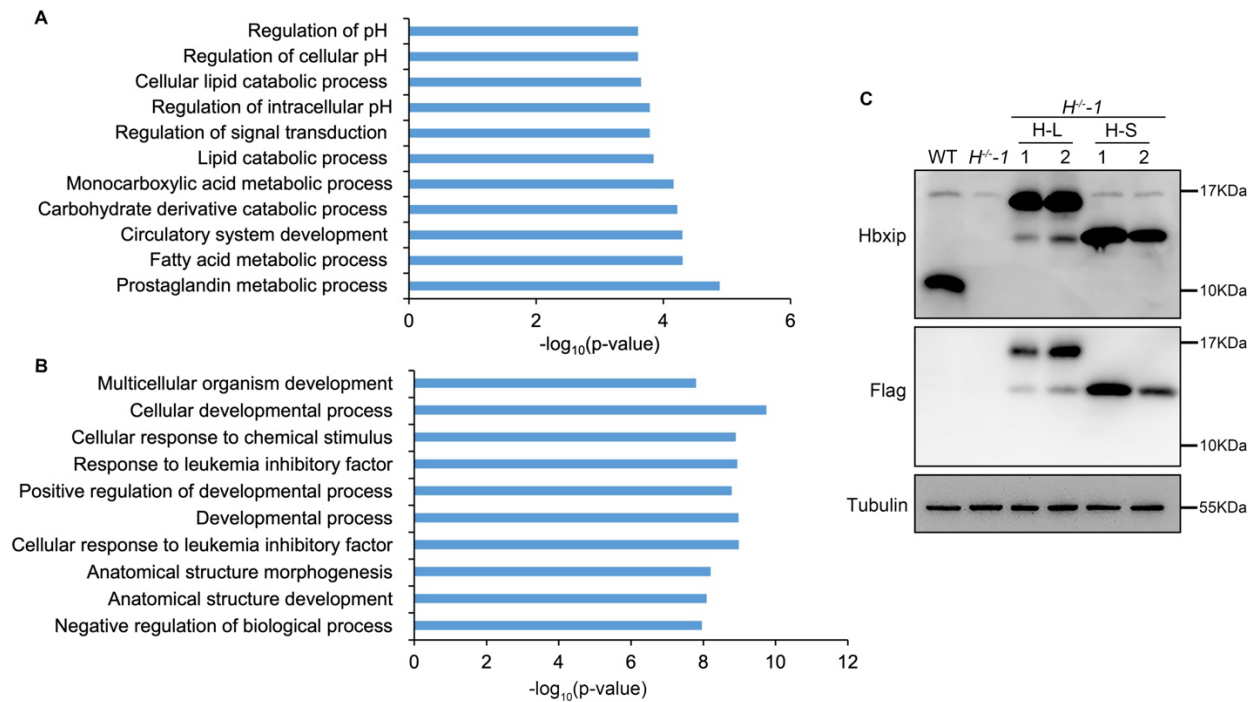


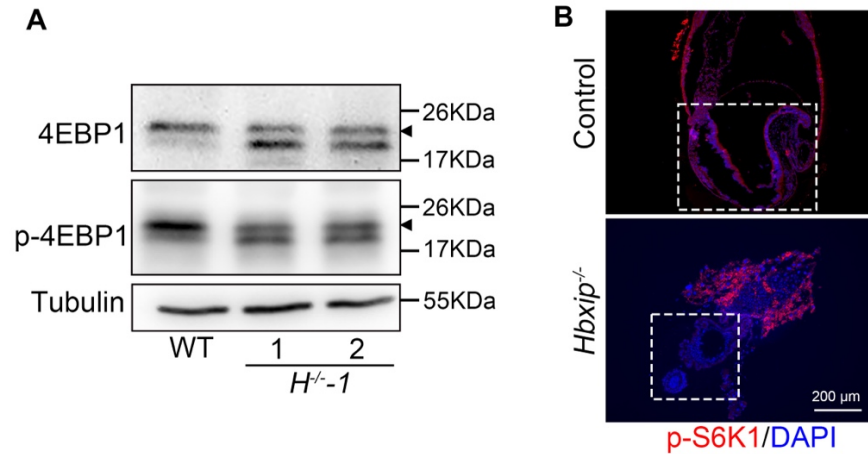
**Fig. S1. Related to Fig. 2. Validation of *Hbxip*<sup>-/-</sup> ESC clones.**

(A) and (B) Sequencing chromatograph of the *Hbxip* gene around the Cas9 targeting site in *H*<sup>-/-</sup>-1 (A) and *H*<sup>-/-</sup>-2 (B) ESCs. Orange triangles mark the indel mutations introduced by Cas9 cutting. (C) Sequence alignment of the *Hbxip* gene around the Cas9 targeting site in WT, *H*<sup>-/-</sup>-1 and *H*<sup>-/-</sup>-2 ESCs. (D-F) Karyotyping (D), cell cycle (E), and apoptosis (F) analyses of WT and *Hbxip*<sup>-/-</sup> ESCs. (D) More than 30 metaphase spreads were counted for each cell line. Scale bar: 20  $\mu$ m. (E) and (F) For cell cycle and apoptosis analyses, data are shown as mean  $\pm$  SD (n=3). Statistical analysis was performed with two-way ANOVA test.  $p > 0.05$  was considered as statistical non-significance.



**Fig. S2. Related to Figs 2, 3. *Hbxip* KO affects gene expression and mTORC1 activity.**

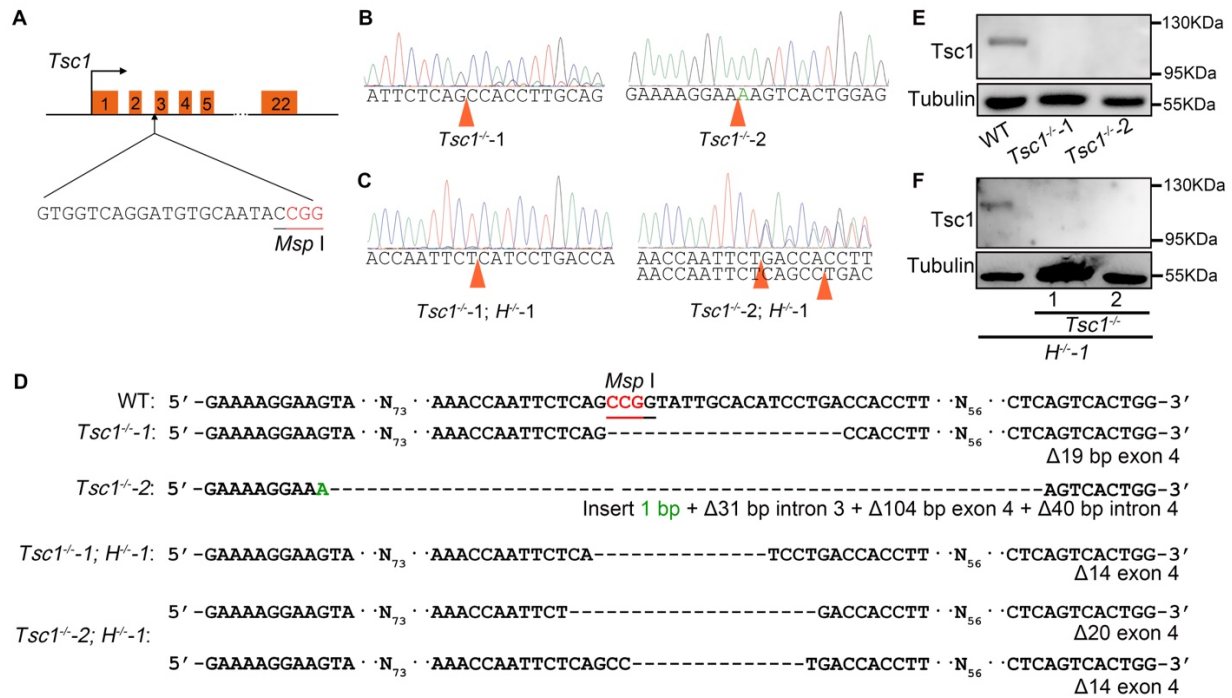
(A) GO annotation of the upregulated genes in *Hbxip*<sup>-/-</sup> ESCs (Related to Fig. 2G, H). (B) GO annotation of the commonly upregulated genes by *Hbxip* KO (Related to Fig. 3C-F). (C) Validation of the overexpression of Flag tagged Hbxip, including H-L and H-S (Related to Fig. 3G).



**Fig. S3. Related to Fig. 5. Reduced mTORC1 activity in *Hbxip*<sup>-/-</sup> ESCs and embryos.**

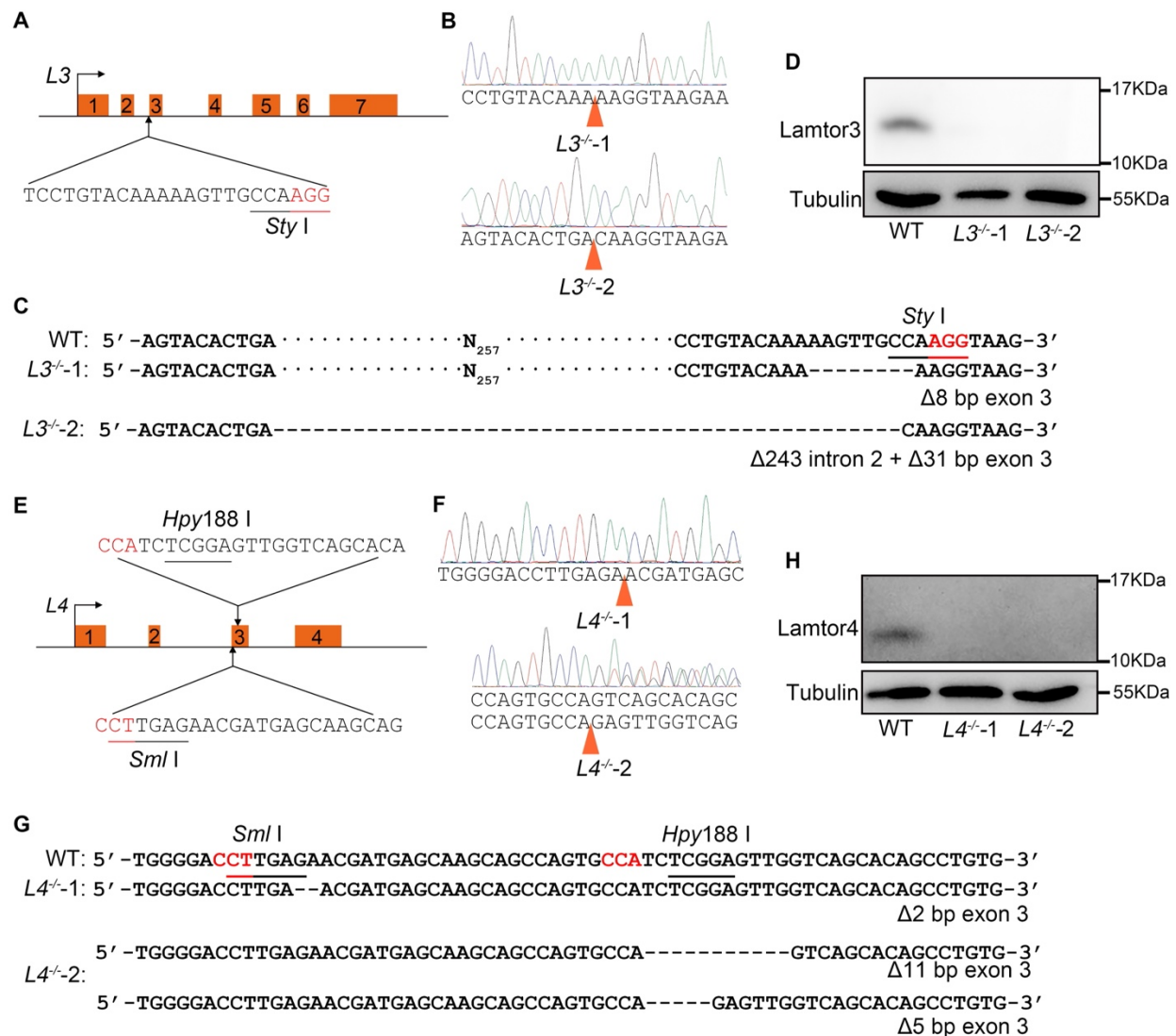
(A) Western blots of 4EBP1 and p-4EBP1 in WT and *Hbxip*<sup>-/-</sup> ESCs demonstrate the reduced mTORC1 activity in *Hbxip*<sup>-/-</sup> ESCs. Triangles mark the specific bands for 4EBP1 and p-4EBP1.

(B) Immunofluorescence staining of p-S6K1 in control and *Hbxip*<sup>-/-</sup> E8.5 embryo sections. Dashed rectangles mark the embryo part. Control (including WT and *Hbxip*<sup>+/-</sup>), n=4; *Hbxip*<sup>-/-</sup>, n=4. Scale bar: 200 μm.



**Fig. S4. Related to Fig. 5. Validation of *Tsc1*<sup>-/-</sup> ESC clones.**

(A) Schematic illustration of the strategy for knocking out *Tsc1* in ESCs. The targeting sequence of sgRNA is shown. The protospacer-adjacent motif (PAM) is highlighted in red, and the *Msp* I site is underlined. (B) and (C) Sequencing chromatograph of the *Tsc1* gene around the Cas9 targeting site in *Tsc1*<sup>-/-</sup> (B) and *Tsc1*<sup>-/-</sup>; *H*<sup>-/-</sup>-1 (C) ESCs. Orange triangles mark the indel mutations introduced by Cas9 cutting. (D) Sequence alignment of the *Tsc1* gene around the Cas9 targeting site in WT, *Tsc1*<sup>-/-</sup> and *Tsc1*<sup>-/-</sup>; *H*<sup>-/-</sup>-1 ESCs. (E) and (F) Validation of *Tsc1* knockout in *Tsc1*<sup>-/-</sup> (E) and *Tsc1*<sup>-/-</sup>; *H*<sup>-/-</sup>-1 (F) ESCs by Western blot.



**Fig. S5. Related to Fig. 6. Validation of *Lamtor3*<sup>-/-</sup> and *Lamtor4*<sup>-/-</sup> ESC clones.**

(A) and (E) Schematic illustration of the strategy for knocking out *Lamtor3* (A) and *Lamtor4* (E) in ESCs. The targeting sequences of sgRNAs (one for *Lamtor3* and two for *Lamtor4*) are shown. The protospacer-adjacent motif (PAM) is highlighted in red, and the *Sty* I, *Sml* I and *Spy*188 I sites are underlined. (B) and (F) Sequencing chromatograph of the *Lamtor3* and *Lamtor4* gene around the Cas9 targeting site in *Lamtor3*<sup>-/-</sup> (B) and *Lamtor4*<sup>-/-</sup> (F) ESC clones. Orange triangles mark the indel mutations introduced by Cas9 cutting. (C) and (G) Sequence alignment of the *Lamtor3* (C) and *Lamtor4* (G) gene around the Cas9 targeting site in WT, *Lamtor3*<sup>-/-</sup> (C) and *Lamtor4*<sup>-/-</sup> (G) ESCs. (D) and (H) Validation of *Lamtor3* (D) and *Lamtor4* (H) knockout in *Lamtor3*<sup>-/-</sup> (D) and *Lamtor4*<sup>-/-</sup> (H) ESCs by Western blot.

**Table S1. Primers for quantitative RT-PCR**

Gene	Forward	Reverse
<i>Nanog</i>	TACAAGGGTCTGCTACTGAGATGC	TTGGGACTGGTAGAAGAATCAGGG
<i>Oct4</i>	ATCAGCTTGGGCTAGAGAAGGATG	AAAGGTGTCCCTGTAGCCTCATAC
<i>Sox2</i>	GCGGAGTGGAACTTTTGTCC	CGGGAAGCGTGTACTTATCCTT
<i>Nestin</i>	CTGGATCTGGAAGTCAACAGAGGT	ATCCTCAGTTTCCACTCCTGTAGC
<i>Gata4</i>	GCTATGCATCTCCTGTCACTCAGA	CCAAGTCCGAGCAGGAATTTGAAG
<i>Gata6</i>	CTTCTCCTTCTACACAAGCGACCA	ATACTTGAGGTCACTGTTCTCGGG
<i>T</i>	CATCGGAACAGCTCTCCAACCTAT	TACCATTGCTCACAGACCAGAGAC
<i>Celsr2</i>	CACGATGGCCTGAGGGTTT	CCTTGTGGAGAAAGGTGTCCT
<i>Dlx3</i>	CACTGACCTGGGCTATTACAGC	GAGATTGAACTGGTGGTGGTAG
<i><math>\beta</math>-Actin</i>	CAGAAGGAGATTACTGCTCTGGCT	TACTCCTGCTTGCTGATCCACATC

**Table S2. Differentially expressed genes (DEGs) identified in *Hbxip*<sup>-/-</sup> ESCs, compared to WT ESCs.**

[Click here to download Table S2](#)

**Table S3. DEGs identified in differentiated *Hbxip*<sup>-/-</sup> ESCs, compared to differentiated WT ESCs.**

WT, *H*<sup>-/-</sup>-1, and *H*<sup>-/-</sup>-2 ESCs were differentiated for 4 days by two methods, LIF withdrawal and EB. RNA purified from these differentiated cells were subjected to RNA-seq analysis.

[Click here to download Table S3](#)

**Table S4. Hbxip interacting proteins identified by co-IP and mass spectrometry.**

[Click here to download Table S4](#)