

Expanded View Figures

Figure EV1. Expression of pluripotency markers in Ronin del/del ESC.

- A Quantification of Ronin signal intensity from Fig 1A normalised to the GAPDH loading control.
- B Left panel, quantification of the signal intensity of Ronin staining at day 4 (Ronin fl/del *n* cells = 56; Ronin del/del *n* cells = 45) and day 8 (Ronin fl/del *n* cells = 38; Ronin del/del *n* cells = 38). Two-tailed unpaired Student's *t* test, data represent mean $\pm$ SD; right panel quantification of the signal intensity of Oct4 staining at day 4 (Ronin fl/del *n* cells = 29; Ronin del/del *n* cells = 43) and day 8 (Ronin fl/del *n* cells = 40; Ronin del/del *n* cells = 31). Two-tailed unpaired Student's *t* test, data represent mean $\pm$ SD.
- C Ronin fl/del and Ronin del/del ESC stained for Nanog (left panel) or Sox2 (right panel). Nuclei are counterstained with DAPI. Scale bar, 10 μ m.
- D Left panel, quantification of the signal intensity of Nanog staining at day 4 (Ronin fl/del *n* cells = 41; Ronin del/del *n* cells = 20) and day 8 (Ronin fl/del *n* cells = 59; Ronin del/del *n* cells = 76). Two-tailed unpaired Student's *t* test, data represent mean $\pm$ SD; right panel quantification of the signal intensity of Sox2 staining at day 4 (Ronin fl/del *n* cells = 36; Ronin del/del *n* cells = 39) and day 8 (Ronin fl/del *n* cells = 19; Ronin del/del *n* cells = 15). Two-tailed unpaired Student's *t* test, data represent mean $\pm$ SD.

Data information: See also Fig 1.

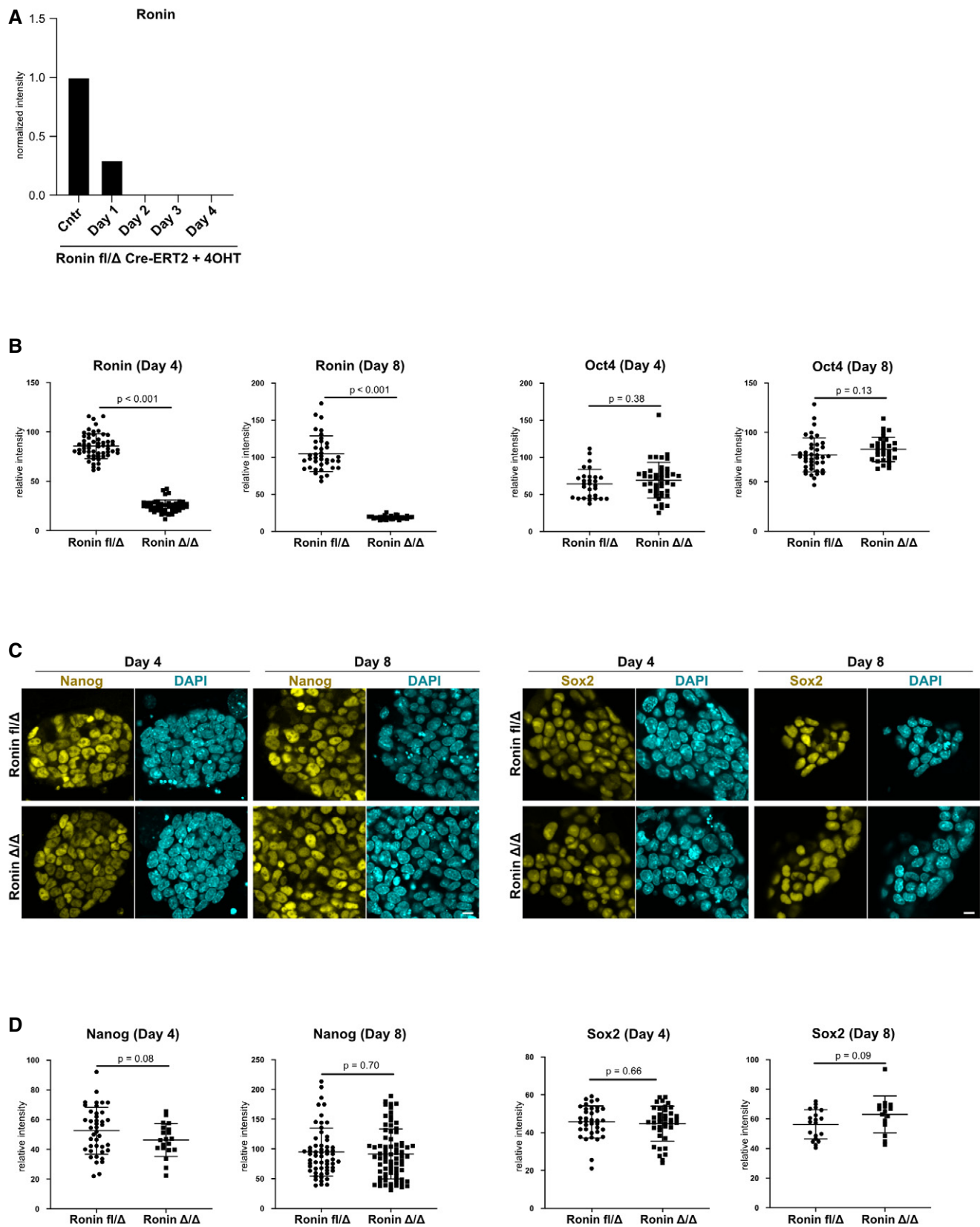
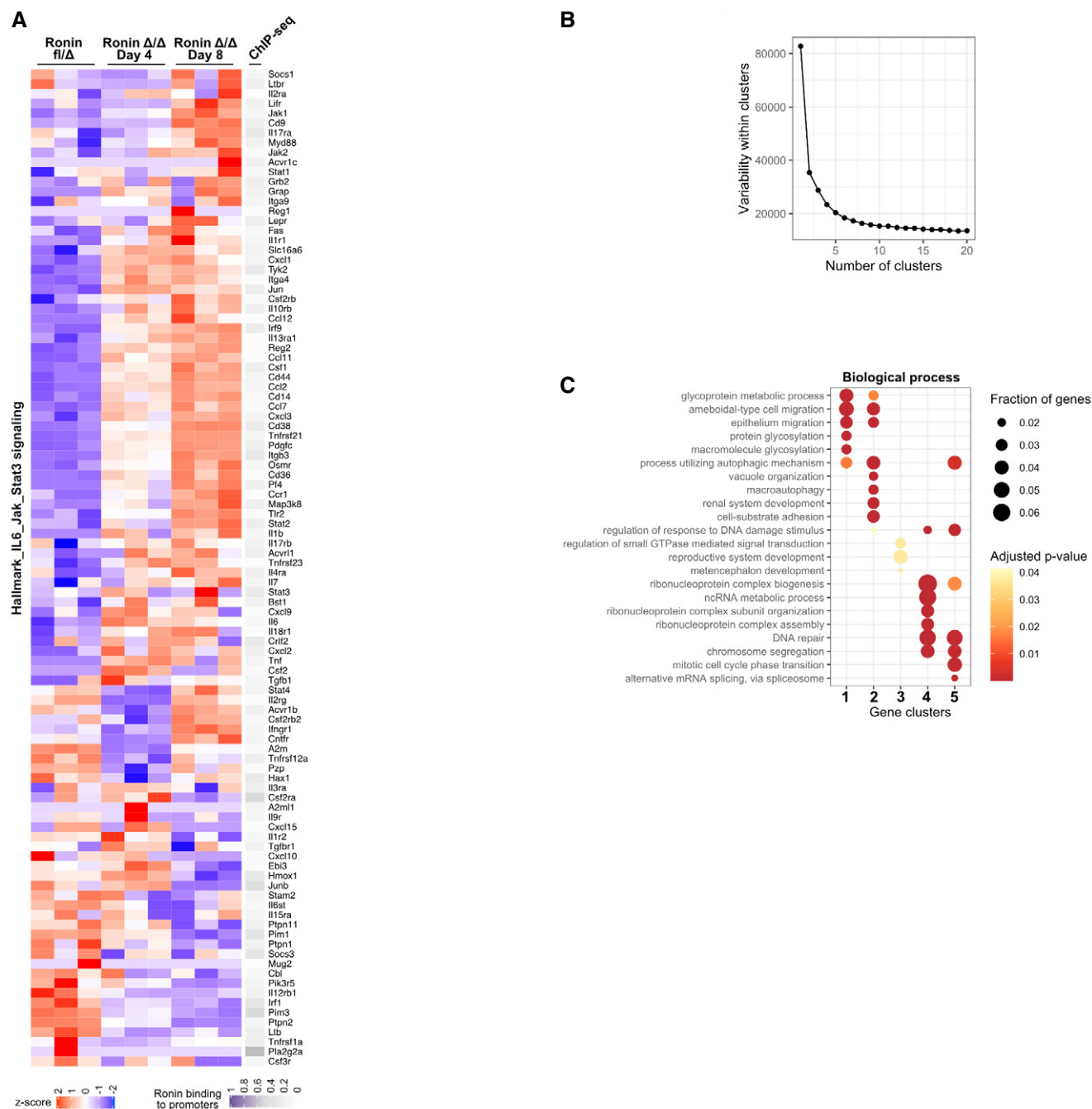


Figure EV1.



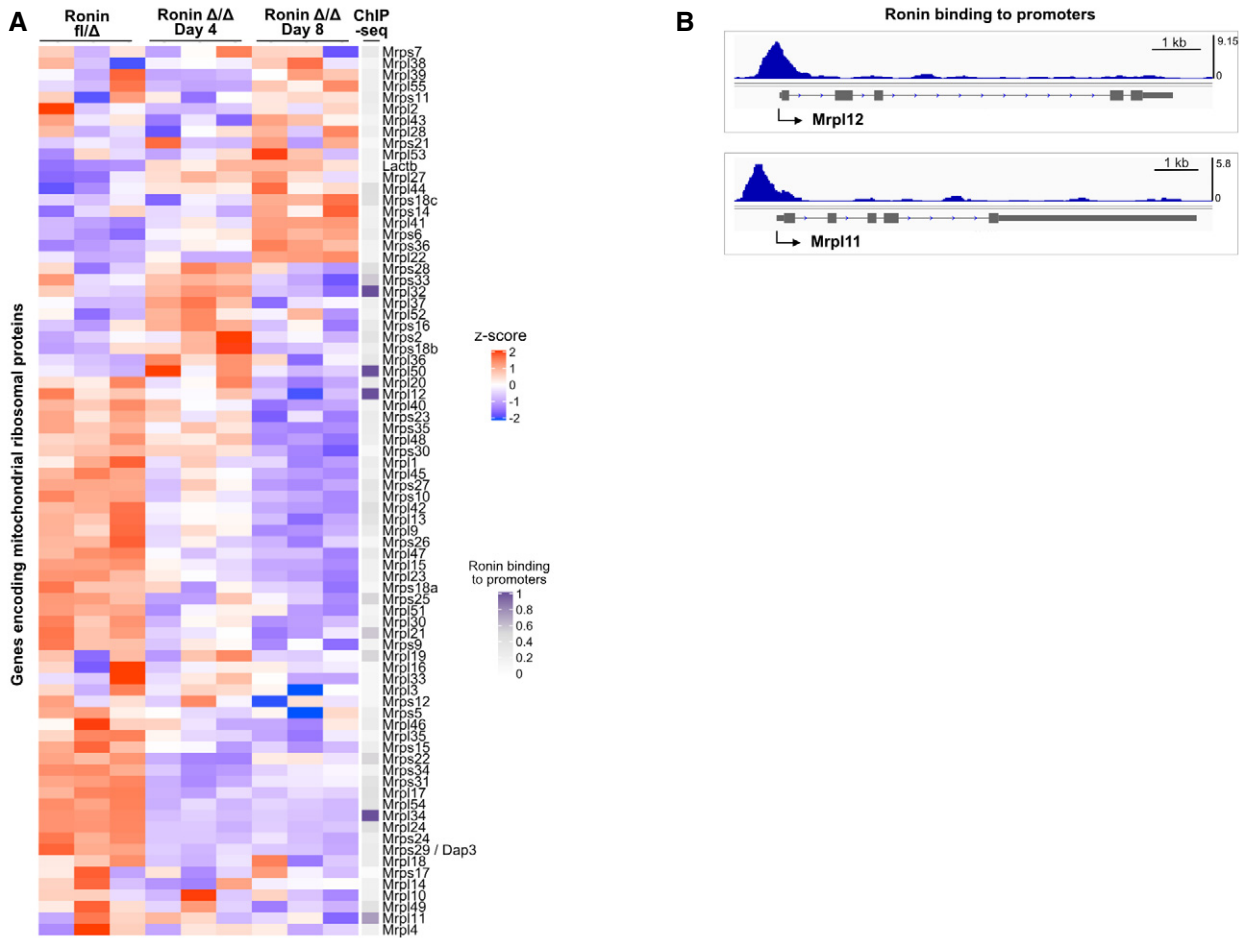


Figure EV3. Ronin tunes the expression of genes encoding mitochondrial ribosomal proteins.

A Expression and binding of Ronin to genes encoding mitochondrial ribosomal proteins.
B Binding of Ronin to the promoters of genes encoding mitochondrial ribosomal proteins.

Data information: See also Fig 4.

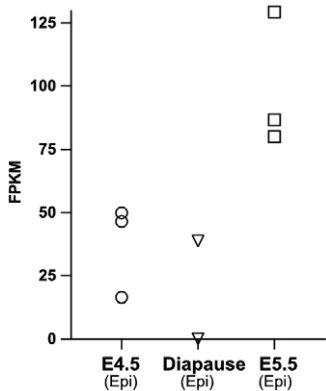


Figure EV4. Ronin expression in the epiblast.

Normalised Ronin expression (fragments per kilobase of exonic sequence per million mapped reads; FPKM) in the epiblast of E4.5, diapause and E5.5 embryos; independent RNA-seq datasets (E4.5, $n = 3$) (diapause, $n = 2$) (E5.5, $n = 3$) based on the RNA-seq dataset of Boroviak *et al* (2015).

