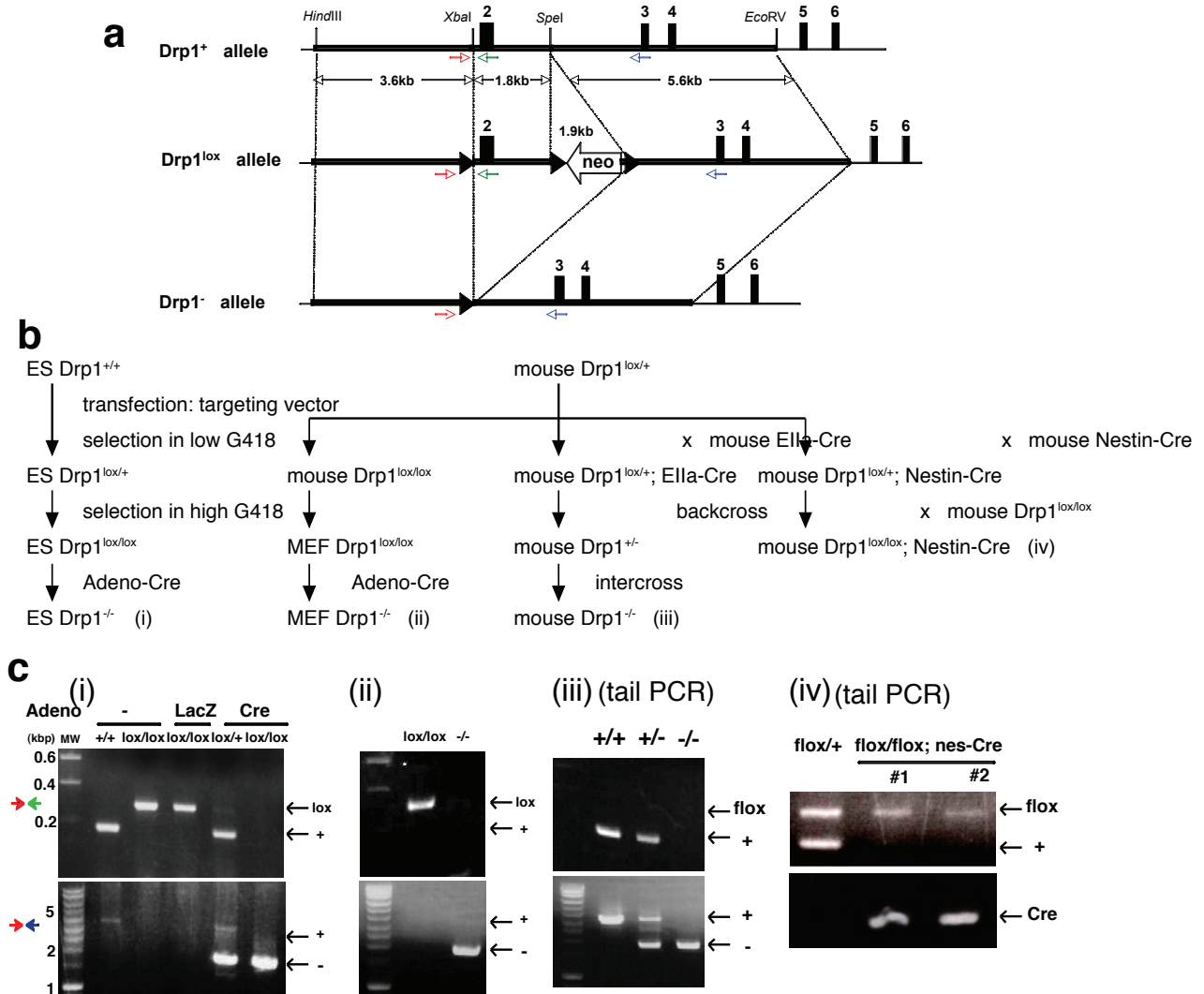
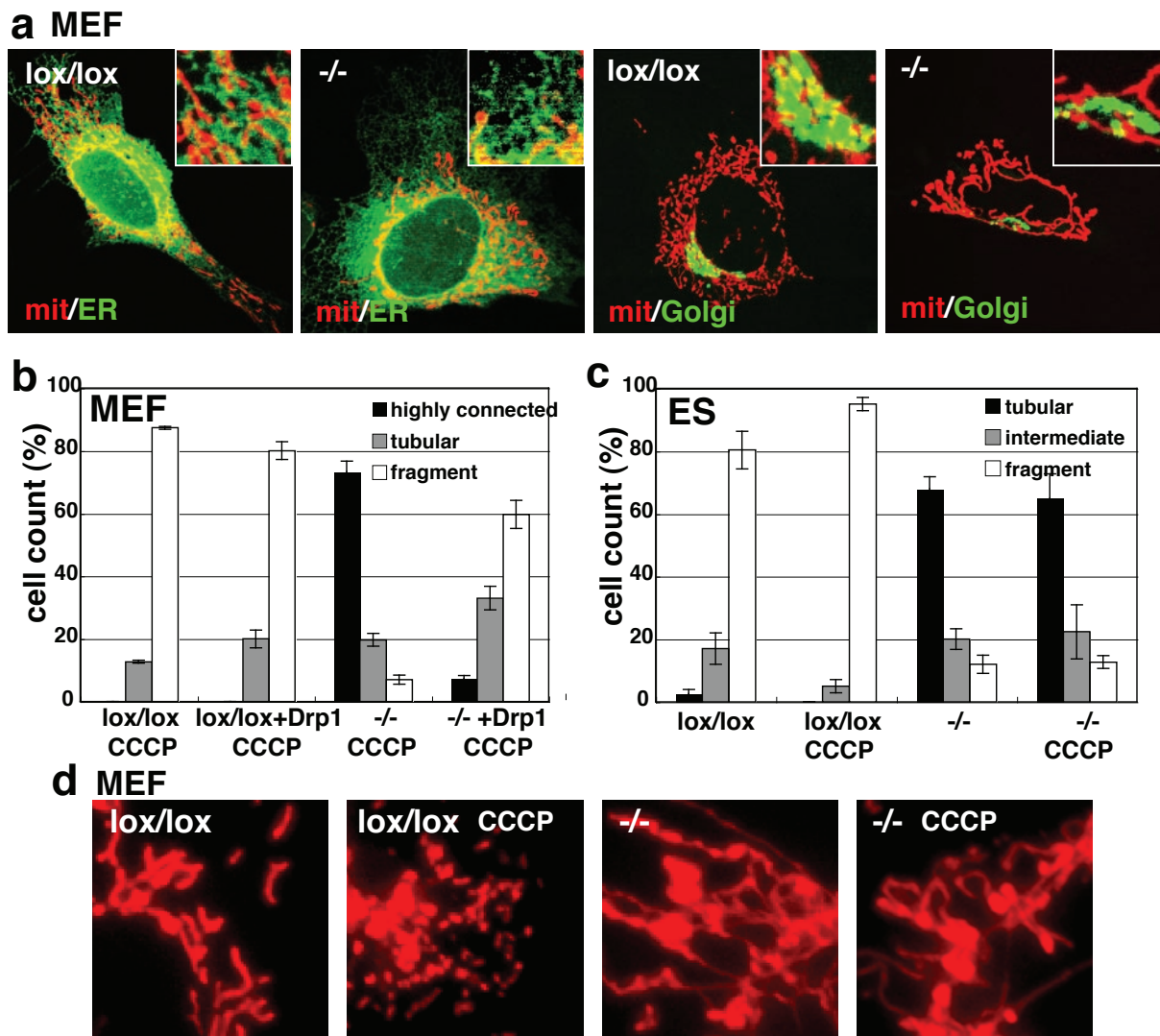


DOI: 10.1038/ncb1907



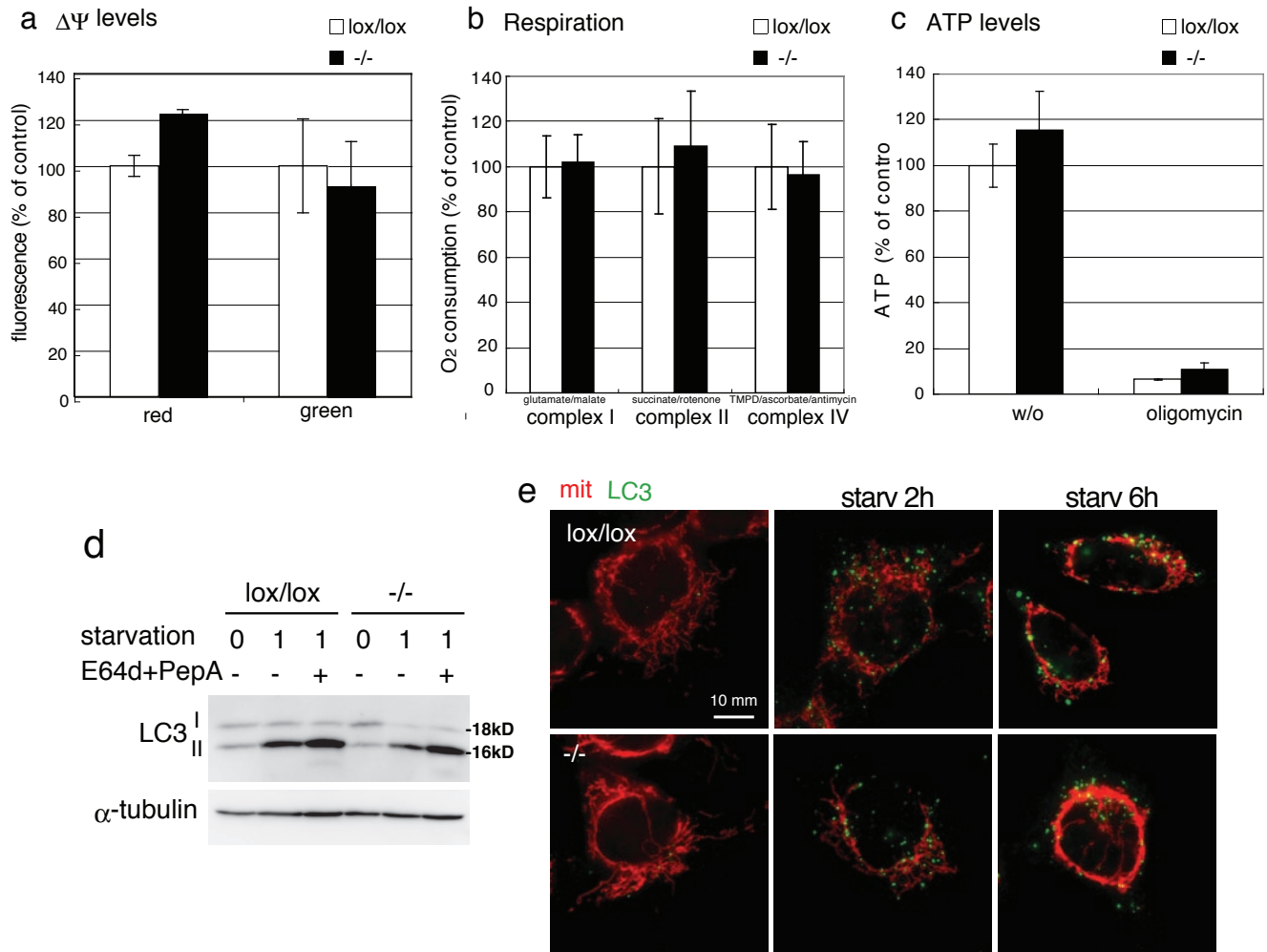
**Figure S1** Generation of  $Drp1^{-/-}$  cells and mice. **a**, Map of  $Drp1$ -targeting constructs. Wild-type  $Drp1$  locus ( $Drp1^{+}$ ), targeted  $Drp1$  locus ( $Drp1^{lox}$ ), and knockout  $Drp1$  locus ( $Drp1^{-}$ ). The arrowheads indicate the loxP sequence.

The arrows indicate primers used for genotyping by PCR. **b**, Schematic diagram of constructions. **c**, Identification of floxed, or targeted  $Drp1$  by PCR genotyping.



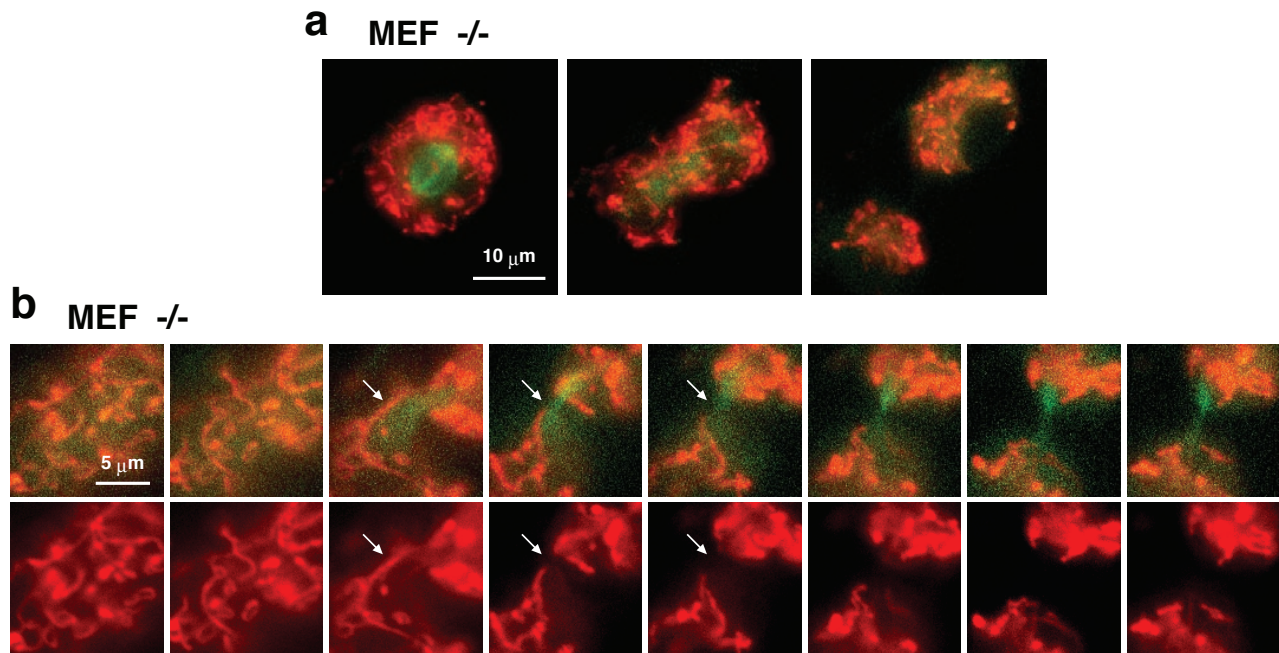
**Figure S2 a**, Morphology of the endoplasmic reticulum (GFP-cytochrome b5) and Golgi (YFP-Golgi) in controls and Drp1<sup>-/-</sup> MEFs was analyzed by fluorescence microscopy. Mitochondria (mit) were visualized by su9-RFP. **b** and **c**, MEFs and ES cells that had been transfected with or without the expression vector for rat Drp1 were treated with or without

20  $\mu$ M CCCP for 2 h, then mitochondrial morphology was analyzed as in **(a)**. Mitochondria with the indicated morphology in CCCP-treated or untreated MEFs and ES cells were quantified. At least 100 cells in 3 distinct fields were analyzed. **d**, Representative images in **(b)** are shown.

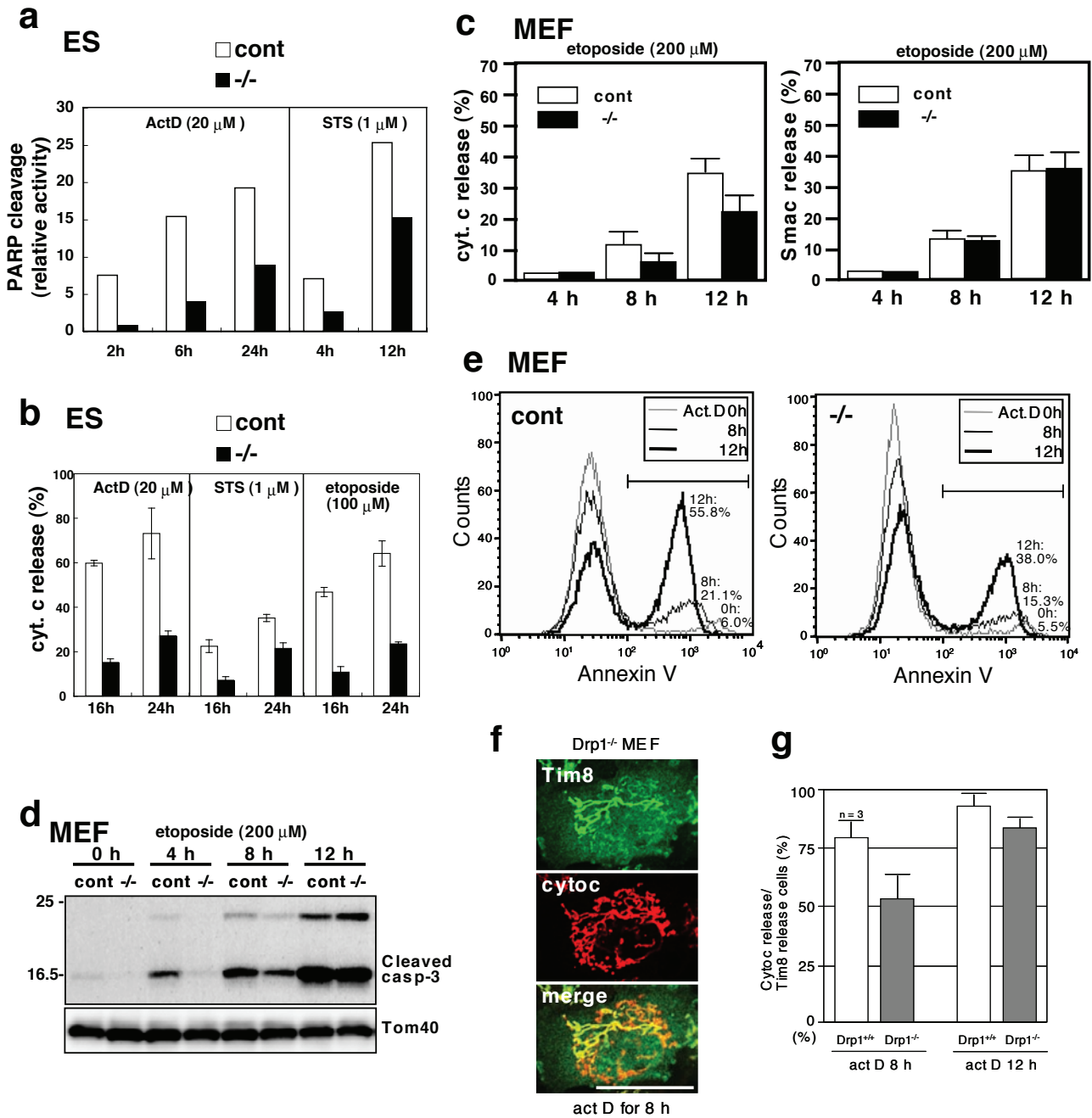


**Figure S3 a**, Analysis of the  $\Psi$  levels across the mitochondrial inner membrane. Control and Drp1<sup>-/-</sup> MEFs were cultured in the presence of 20 nM MitoTracker Red or 100 nM MitoTracker Green for 1 h. The fluorescent signal in each cell was counted for more than 100 cells in 3 distinct optical fields. **b**, Respiration of MEFs through complex I, II and IV. The harvested cells were incubated with the indicated respiratory substrates, and O<sub>2</sub> consumption was measured using oxygen electrode. **c**, MEFs were incubated with or without 10  $\mu$ M oligomycin for 10h and the cell extracts

were subjected to ATP concentration analysis using Luciferase. **d**, Wild-type and Drp1<sup>-/-</sup> MEFs were cultured in amino acids- and serum-depleted medium for 1 h in the presence or absence of lysosomal protease inhibitors (E64d + Pepstatin A). The cell lysates were subjected to SDS-PAGE and subsequent immunoblotting using the antibodies against LC3 and  $\alpha$ -tubulin. **e**, Wild-type and Drp1<sup>-/-</sup> MEFs were cultured as in (d) for the indicated time periods, incubated with the antibodies against LC3 and Tom70, and analyzed by immunofluorescence microscopy.

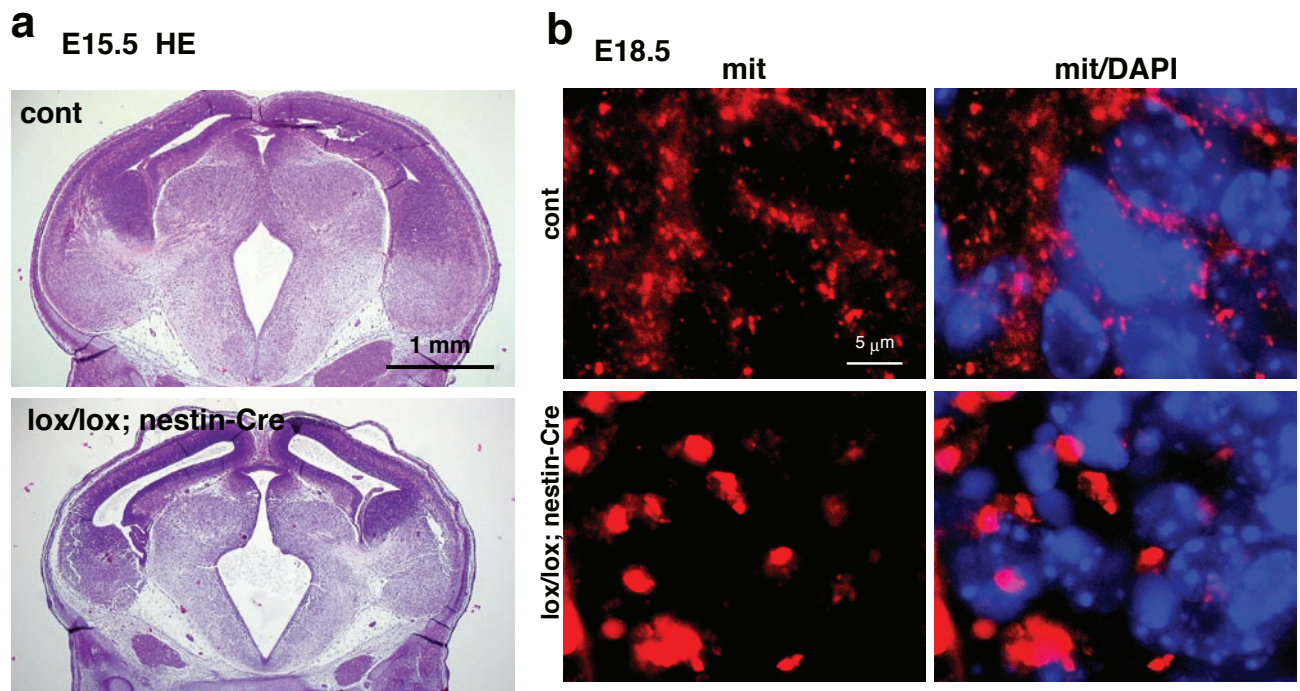


**Figure S4** Time-lapse imaging of mitotic Drp1<sup>-/-</sup> MEFs expressing su9-RFP and YFP- $\alpha$ -tubulin. **b**, Mitochondria and a mitotic spindle in living cells were observed by fluorescence video microscopy for 1 h at 37°C at 2-min intervals. **a**, Representative images from **(b)** were depicted.



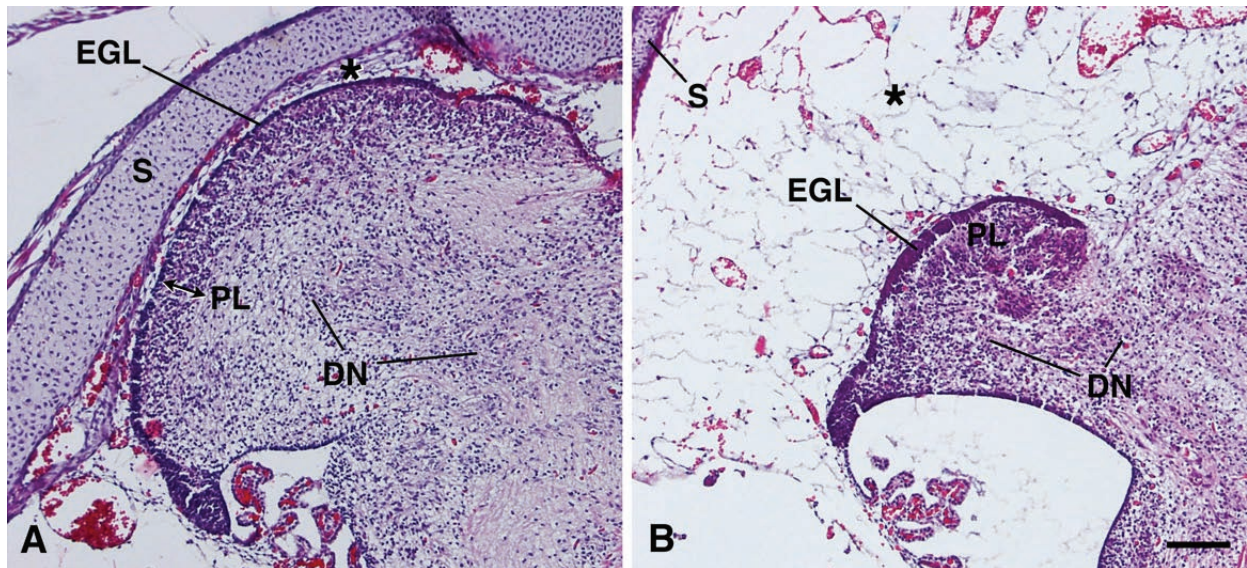
**Figure S5** Response of Drp1<sup>-/-</sup> ES cells and MEFs to proapoptotic reagents. **a**, ES cells were treated with 1  $\mu$ M staurosporine (STS) or 20  $\mu$ M actinomycin D (ActD) and the processed PARP was quantified by immunoblotting as in Fig. 3b setting the amount of unprocessed PARP at 100%. **b**, ES cells were treated with proapoptotic reagents for the indicated periods and the cells with the cytochrome c in the cytosol were quantified by immunofluorescence microscopy. At least 100 cells in more than 3 distinct fields were analyzed. **c**, Drp1<sup>-/-</sup> MEFs were treated with etoposide for the indicated periods, and the cells were analyzed by immunofluorescence microscopy. The cells with released Smac/Diablo and cytochrome c were counted. At least 100 cells in

3 independent experiments were counted. **d**, The cells obtained in (c) were analyzed by SDS-PAGE and subsequent immunoblotting using antibodies against the caspase 3 fragment and Tom40 as a loading control. **e**, MEFs were treated with actinomycin D for the indicated periods and exposure of phosphatidylserine on the outer plasma membrane was measured by flow cytometry after staining the cells with annexin V-FITC. **f** and **g**, Drp1<sup>-/-</sup> MEFs expressing Tim8-FLAG were treated with actinomycin D for the indicated periods and the number of cells that contained Tom8a-released but cytochrome c-unreleased mitochondria was counted. Thirty cells each from 3 distinct optical fields were analyzed. Scale bar, 20  $\mu$ m.



**Figure S6 a**, Coronal sections of the brain from E15.5 controls or *Drp1lox/lox; nestin-Cre* mice embryos were HE-stained. **b**, Paraffin-embedded brain sections of E18.5 *Drp1lox/lox; nestin-Cre* embryos were examined by

immunofluorescent microscopy using antibodies against the complex III core 1 protein. Forebrain regions are shown. Clustered mitochondria were observed in the *Drp1<sup>-/-</sup>* mouse brain.



**Figure S7** Parasagittal sections of cerebella from E20 control (A) and NS-Drp1<sup>-/-</sup> (B) mice. Remarkable overall size reduction of the cerebellum as well as the brainstem is noted in NS-Drp1<sup>-/-</sup> mouse. While the thickness of the forming cerebellar cortex (EGL+PL) and the formation of the DN in the NS-Drp1<sup>-/-</sup> cerebellum are comparable to those in the control, the

white matter of the former shows marked hypoplasia. Note the apparent enlargement of the subdural/subarachnoid space in the posterior fossa in NS-Drp1<sup>-/-</sup> mouse (asterisk). S; skull, EGL; external granular layer, PL; Purkinje cell layer, DN; dentate nucleus, asterisk: subdural/subarachnoid layer. Bar=100  $\mu$ m.

Fig 2h  
MEF

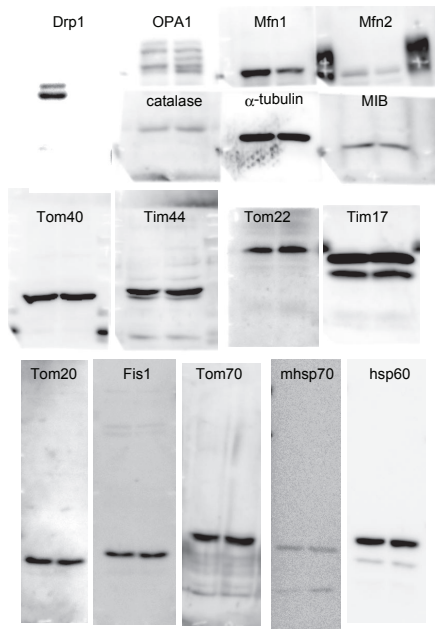


Fig 3a

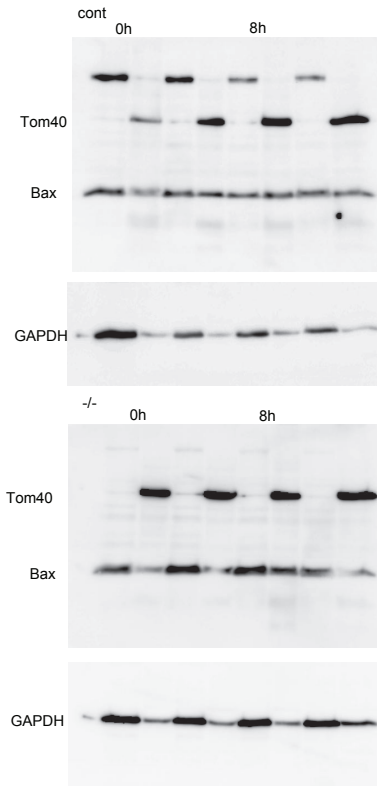


Fig 3b

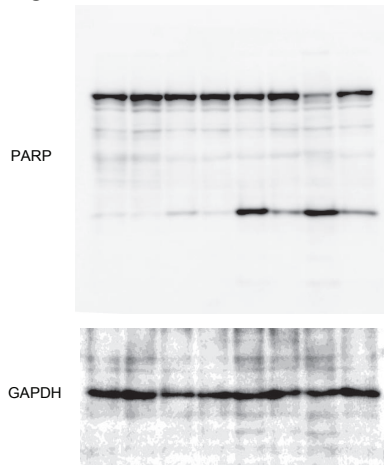


Fig 3f

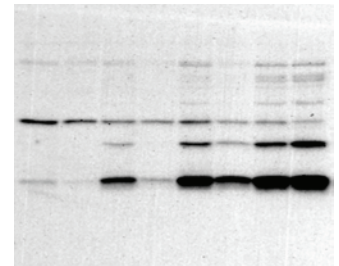


Fig S3d

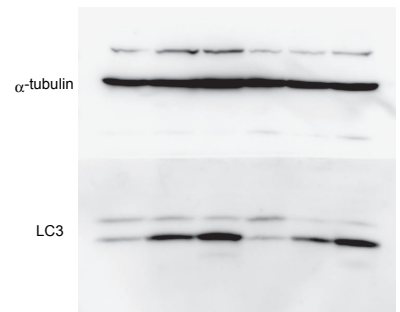


Fig S5d

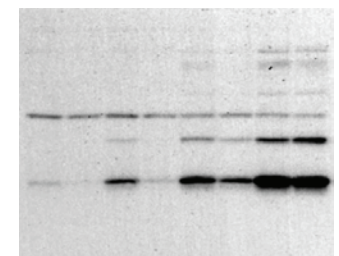


Figure S8 Full scans of the Western blots from the figures.