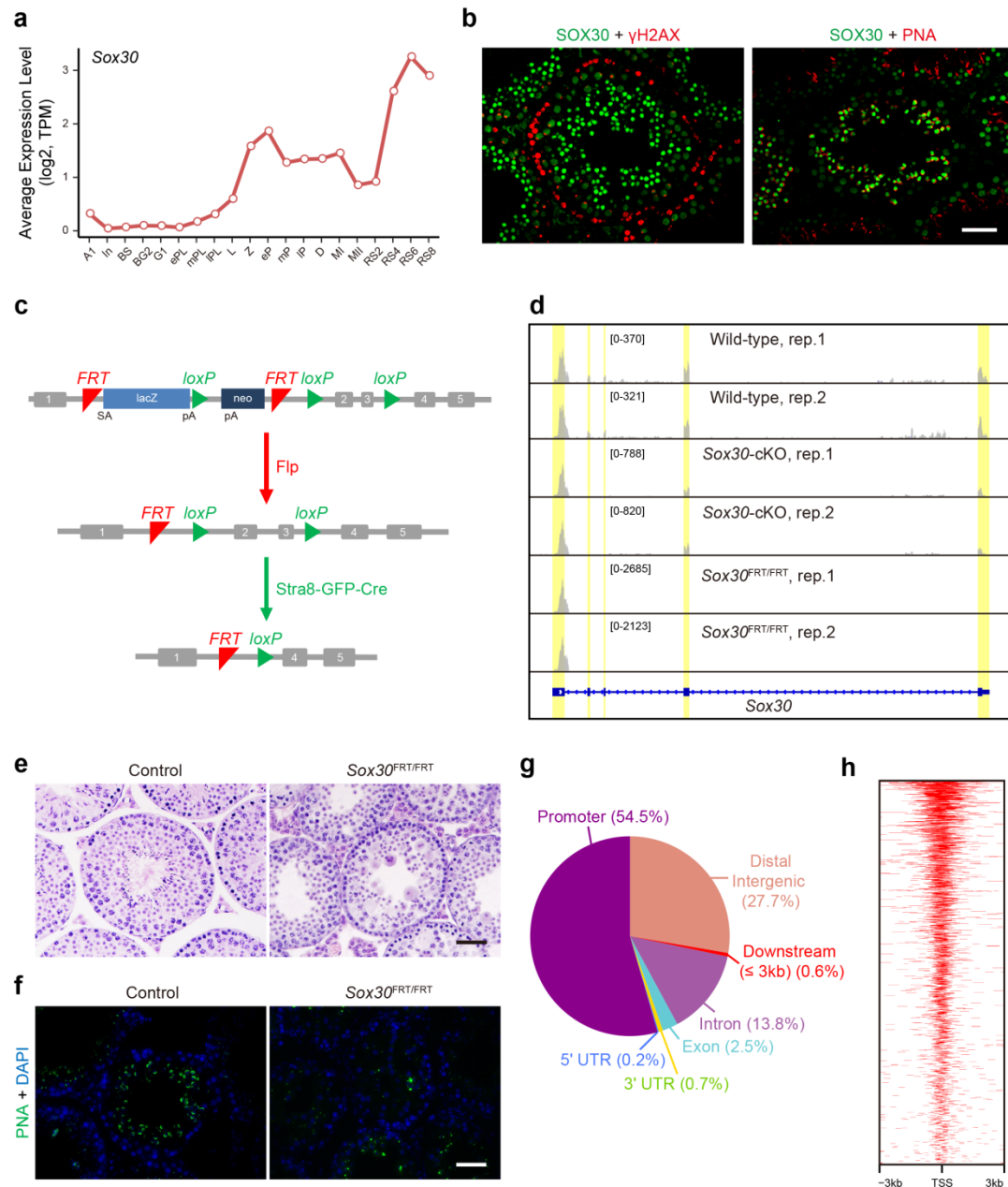


**Figure S22 *Sox30* is an essential transcriptional factor for spermiogenesis. a** Line graph showing the average expression level of *Sox30* across all stages in wild-type mice. The circle represents the mean of the expression level, which is calculated by  $\log_2(\text{TPM}/10 + 1)$ . **b** Immunohistochemical staining for SOX30 (green),  $\gamma$ H2AX (red,



left panel), PNA (red, right panel) and DAPI (blue) in sections from adult wild-type mice. Scale bar, 50  $\mu$ m. **c** Schematic diagram for the “Knockout-first” conditional allele of *Sox30*<sup>tm1a(KOMP)Wtsi</sup> mice. **d** Snapshots showing the enrichment of RNA-seq reads of *Sox30* in wild-type, *Sox30*-cKO and *Sox30*<sup>FRT/FRT</sup> by bulk RNA-seq. Each group has two replicates. **e** H&E staining of wild-type control and *Sox30*<sup>FRT/FRT</sup> testes sections at 8-weeks old. Scale bar, 50  $\mu$ m. **f** Testes sections from adult wild-type control and *Sox30*<sup>FRT/FRT</sup> mice were immunostained with PNA (green) and DAPI (blue). Scale bar, 50  $\mu$ m. **g**. Pie chart showing the distribution of peaks in genomic elements called from *Sox30* wild-type mice by bulk ChIP-seq. The total number of peaks is 2,959. The number in the parentheses indicates the percentages of peaks belonging to different genomic regions. **h** Heatmap showing the peak enrichment of *Sox30* wild-type mice in promoter regions by bulk ChIP-seq. The promoter is defined as transcription start site (TSS)  $\pm$  3 kb. Each row represents a promoter region of a gene. The intensity from red to white stands for the relative enrichment from high to low.