Figure S1. Analysis of scRNA-seq dataset of E11.5 to E14.5 female germ cells. (A) Uniform Manifold Approximation and Projection (UMAP) of oocytes colored by embryonic time point. (B) UMAP of oocytes colored by pseudotime analysis. (C) Expression of *Pou5f1*, *Stra8*, *Taf4b*, and *Taf4a* plotted in terms of pseudotime and colored based on embryonic time point. (D) Table of top 10 genes (in addition to *Taf4b*) that are expressed significantly higher in *Taf4b*-expressing oocytes. Colors indicate association with gene ontology (GO) term synaptonemal complex assembly (yellow) and meiosis I/meiotic cell cycle (red).