SI Figures

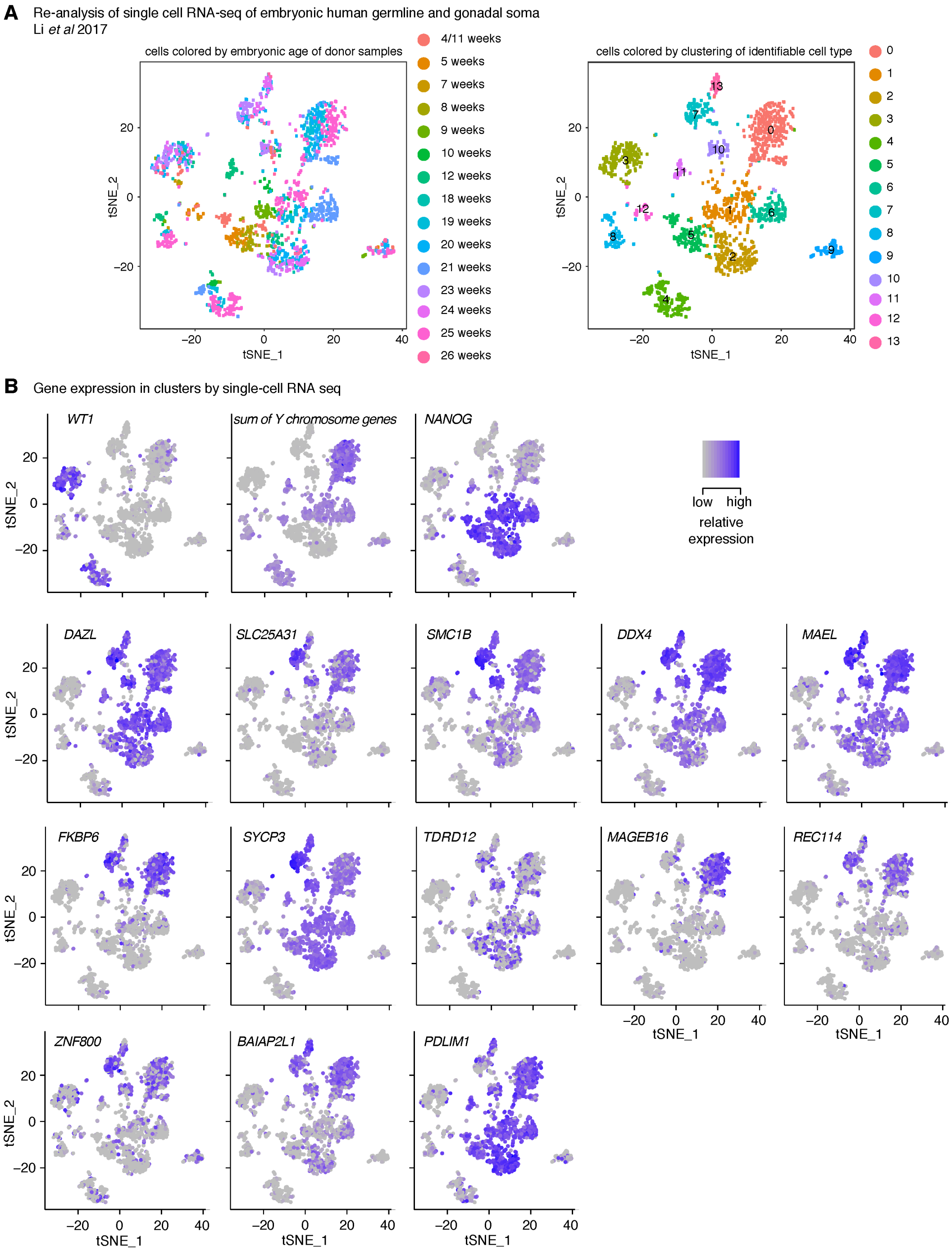

Fig. S1. Re-analysis of single cell RNA-seq from human embryos.

(*A*) tSNE plots of all cells collected from human embryos. Left: cells colored according to embryonic origin. Right: cells colored according to un-supervised clustering. Migratory germline cells are found in cluster 5 (green). Male gonadal germline cells correspond to clusters 1, 11, and 6; and female gonadal germline cells to clusters 5 and 2. (*B*) Expression of cell type-specific marker genes (top panels, *n* = 3), and commonly induced genes (lower panels, *n* = 13), in human single-cell RNA-seq, according to clustering. Somatic cells visualized by *WT1* expression, male cells by summed expression of all Y-chromosome genes, and the pluripotency network expressed by migratory and newly gonadal germline cells illustrated by expression of *NANOG*.