

Fig. S3. Expression of genes activated on PGC colonization, and of general and naïve pluripotency factors in the mammalian germline.

max TPM

E13.5 XX E13.5 XY

gonadal

late

E11.5

early | gonadal

0 0.5 1 proportion of maximum TPM

(A, B) Heatmap; expression of factors commonly induced on PGC colonization (upper panel) and species-specific naïve and general pluripotency factors (lower panel) in migratory, early and late gonadal germline cells, derived from single-cell RNA-seq of human embryos (left, A) and RNAseq of mouse embryos (right, B). Each gene's expression is shown as a proportion of its maximum expression. Gene order in upper panel as displayed in Fig. 1D, and in lower panel by hierarchical clustering for each species. TPM, transcripts per million.