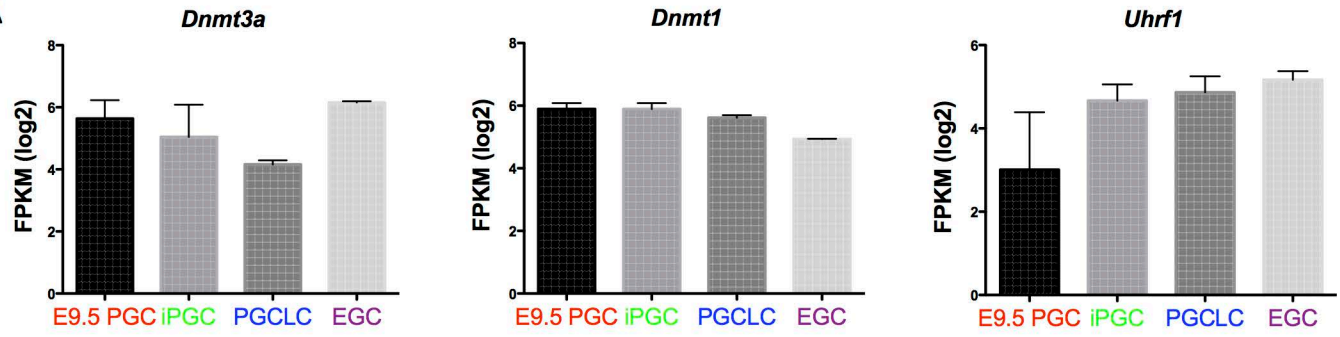
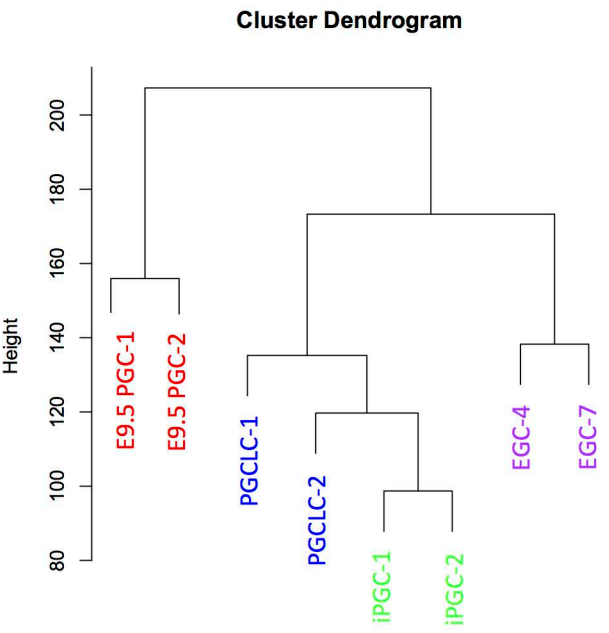
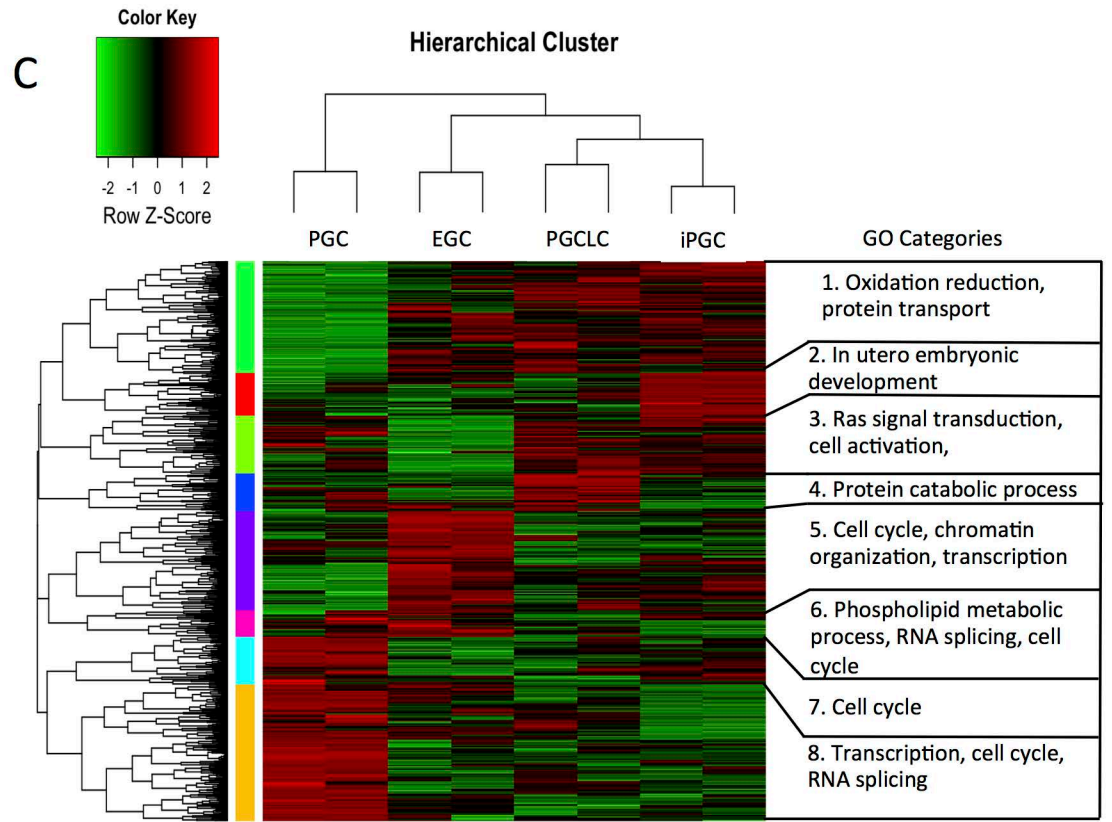


Stem Cell Reports

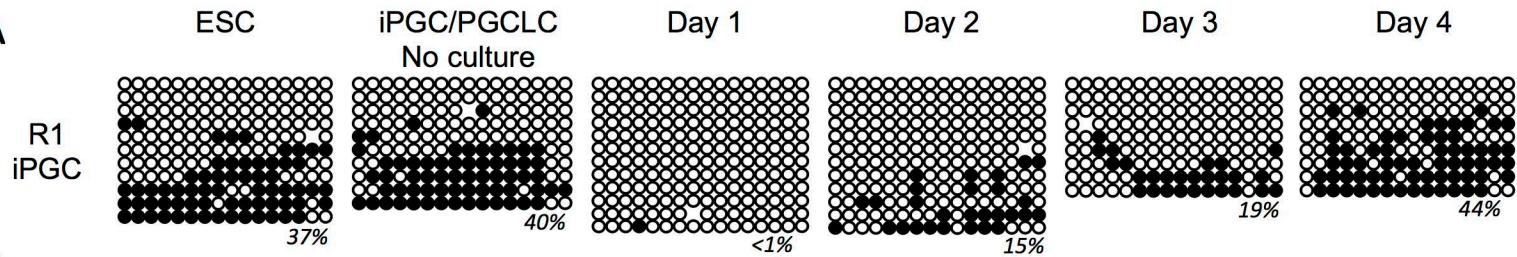
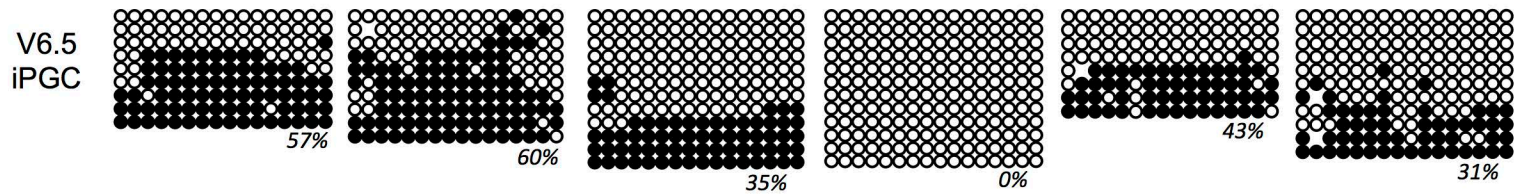
Supplemental Information

**PGC Reversion to Pluripotency Involves Erasure  
of DNA Methylation from Imprinting Control Centers  
followed by Locus-Specific Re-methylation**

Marisabel Oliveros-Etter, Ziwei Li, Kevin Nee, Linzi Hosohama, Joseph Hargan-Calvopina, Serena A. Lee, Prakash Joti, Juehua Yu, and Amander T. Clark

**A****B****C**

P&lt;=0.01

**A****B**

**Supplemental Figure 1: Characterization of PGCs generated from ESCs. Related to Figure 5.**

Average gene expression of DNA methyltransferases from the RNA-Seq. (A) Unsupervised Hierarchical clustering of all RNA-Seq samples (n=2 biological replicates in technical duplicate). (B) EGC-4 and EGC-7 refer to the independent EGC line name. The numbers 1 or 2 after the PGC, iPGC and PGCLC RNA-Seq samples indicate the biological replicate number. Heat map showing differentially expressed genes and corresponding major clusters. (C) Major gene ontology groups are shown for each cluster. Green is repressed and red is enriched.

**Supplemental Figure 2: *Snrpn* ICC is erased in iPGCs derived from ESCs. Related to Figure 6.**

Shown are BS-PCR results for *Snrpn* ICC in iPGCs differentiated from V6.5 ESCs and R1 ESCs and with four days of culture in 7F medium. Open circles indicate unmethylated CpGs and closed circles indicate methylated CpGs (n = 1 biological series with  $\geq 8$  independent clones per time point).