



Figure 3. Early germ cell determination in the mouse. (A) Two models summarize the mode by which germ cells are determined in various organisms. The preformationist mode assumes one or more localized determinants in the oocyte or early embryo specify progeny cells becoming PGCs. In the epigenesis mode, a signal emanating from a neighboring cell(s) in the early embryo determines the future PGCs. (B) This part of the figure highlights the features that contribute to the repression of somatic gene programs during germline specification in various organisms. In *Caenorhabditis elegans*, the germline lineage (red) is specified after the first division of the zygote by expression of *Pie1*, which confers transcriptional quiescence. The other cell (blue) gives rise to somatic tissues. In *Drosophila melanogaster*, the precursors of the germ cells are the so-called pole cells contained on one side of the zygote syncytium (i.e., multinucleated); transcriptional quiescence in these cells depends on localized RNA from the gene *Pgc* and high levels of H3K9 methylation. In *Mus musculus*, the earliest precursors of the germ cells are visible by expression of *Blimp1* at the base of the allantois. *Blimp1* initiates transcriptional quiescence in these cells.