Supplementary Table 1: Embryos (separate file)

List of embryos, stage, sex, number of cells, mean number of genes and UMIs (per cell) sequenced.

Supplementary Table 2: Single-cell barcodes and embryo IDs (separate file)

List assigning single-cell barcodes to embryo IDs.

Supplementary Table 3: Marker genes (separate file)

List of all marker genes and their expression profiles used for cell to cell state assignment. Data is presented as processed with Cell Ranger v2 (n = 712) and v3 (n = 706) and includes which genes are designated as top 30 marker genes for each state.

Supplementary Table 4: Percent of positive cells (separate file)

Expression profile per state in percent of positive cells per gene.

Supplementary Table 5: Embryo proportions (separate file)

List of embryos, stage, number of cells and fraction per cell state.

Supplementary Table 6: Differentially expressed genes (separate file)

Differentially expressed genes per cell state based on binary (percent positive cells) expression measurement. Percent of cells per cell state in WT and KO expressing these genes, their difference and $\log_2$ fold-change.

Supplementary Table 7: Gene Ontology for recurrently up- and downregulated genes (separate file)

Associated q values for all ontologies with $Q < 0.05$ in at least one gene set. Columns include the Q values for recurrently deregulated gene sets, either differentially up- or downregulated in ≥2 states of any given KO within either the embryonic or extraembryonic lineage. Here, extraembryonic includes both the Xecto and Xendo states and Xmeso is part of the embryonic lineage as it is specified within the posterior-proximal most region of the epiblast.

Supplementary Table 8: DNA methylation valleys (separate file)

DNA methylation valley (DMV) information, including the epiblast methylation of non-CpG island CpGs across relevant PRC KOs and WT, cluster assignment as shown in **Extended Data Fig. 5g**, associated gene names, and enrichment for H3K27me3.

Supplementary Table 9: Hox gene expression (separate file)

List of all detected *Hox* genes and the percent of positive cells per cell state in WT and KO.

Supplementary Table 10: sgRNA sequences (separate file)

Supplementary Table 11: mESC Nanostring expression data (separate file)

Supplementary Figure 1: Western blot for H3K27me3 and H4 in WT and Eed^{KO} mESCs

Images of the two membrane parts that were separately immunoblotted for H3K27 methylation and for histone H4 which served as a loading control.