

Supplementary figure/tables titles and legends

Figure S1. Complementary information for main figures.

- (a) Morphological analysis of wild-type (WT) and *Commd10^{Null}* (Null) embryos at E9.5. White scale bar is 0.1 mm. The *Commd10^{Null}* embryo is shown at higher magnification to visualize the degrading structure of the failed embryo.
- (b) List of RNA samples from WT and *Commd10^{Null}* mouse embryos used in RNA-seq analysis presented in Figure 2.
- (c) Full legend for Figure 2d annotating cell clusters by different colors, and a schematic single-cell molecular map of mouse gastrulation and early organogenesis up to day E8.5 of embryogenesis [22]. Presented legend picture is from a single-cell molecular map of mouse gastrulation and early organogenesis (cam.ac.uk) website.
- (d) mRNA expression analysis of Sox10 in WT and *Commd10^{Null}* embryos at E8.5, E9.5, and E10.5. Total RNA was purified from whole mouse embryos and mRNA was amplified by RT-qPCR using GAPDH as internal control. Data are presented as relative quantity (RQ) Mean \pm SE.

Supplementary Tables. GO:Biological Process of the top 15 genes upregulated in *Commd10^{Null}* embryos and the GO:Biological Process of the top 20 genes downregulated in *Commd10^{Null}* embryos. Gene functional enrichment analysis for the top 15-20 upregulated or downregulated DEGs was performed using ToppGene Suite (<https://toppgene.cchmc.org>) [54]. Both tables contain Hyperlinks to webpages with more detailed information about the analyses in both spreadsheet and graphical forms online.