

## **Description of Additional Supplementary Files**

### **Supplementary Data Legends:**

**Supplementary Data 1:** Normalized transcriptome sequencing reads. This file contains transcript counts of  $n = 2$  undifferentiated iPSC12 cells and  $n = 2$  of each iPSC12 cells differentiated into endoderm, ectoderm, and mesoderm. The counts have been normalized to counts per million by edgeR.

**Supplementary Data 2:** Differentially expressed transcripts. This file contains differentially expressed transcripts between germ layer-differentiated samples and undifferentiated iPSC12 cells. They were determined by using the edgeR function glmTreat with Benjamini Hochberg false discovery post-hoc correction at a p-value threshold of 0.05.

**Supplementary Data 3:** Identified potential cell fate markers. This file contains genes which may serve as marker genes to discriminate between early human induced pluripotent stem cells differentiation states. They were obtained by filtering for high log2 fold changes unique for individual early germ layer differentiation states and the undifferentiated state.