



Figure S3. single cells from the embryonic development dataset were clustered using the robust clustering procedure, and the 500 most differentially expressed genes (by edgeR-QLF test adjusted P value) in any of the discovered clusters are shown in a heatmap, as well as cluster assignments and cell types. A) raw (no imputation), B) after application of *netSmooth*, C) missing values imputed using *scImpute* D) after application of *MAGIC*