

Description of Additional Supplementary Files

Supplementary data 1 – Statistics for the comparison of the glial and random trajectories

Results of two-sided Wilcoxon signed-rank test comparing mean spherical distances for 1000 paths sampled from the glial trajectory in comparison to 1000 random trajectories.

Supplementary data 2 – Statistics for the comparison of the neuronal and random trajectories.

Results of two-sided Wilcoxon signed-rank test comparing mean spherical distances for 1000 paths sampled from the neuronal trajectory in comparison to 1000 random trajectories.

Supplementary data 3 – Statistics for the comparison of the neuronal and glial trajectories

Results of two-sided Mann-Whitney U test comparing mean spherical distances for 1000 paths sampled from the neuronal trajectory in comparison to 1000 paths sampled from the glial trajectory.

Supplementary data 4 – Gene modules

Gene modules identified using the Antler algorithm (<https://github.com/juliendelile/Antler>).

Supplementary data 5 – Csde1 binding sites

Csde1 binding sites identified using a script published by Moore et al., 2018.

Supplementary data 6 – Csde1 binding site statistics

Results of one-sided permutation testing to assess the enrichment of gene modules in Csde1 binding sites.

Supplementary data 7 – Csde1 knockdown statistics

Results of two-sided Fisher exact test to determine whether gene modules are biased towards genes which are up- or down-regulated upon Csde1 knockdown. Data on CSDE1 knockdown in hESCs taken from Ju Lee et al., 2017.

Supplementary data 8 – Csde1 iCLIP statistics

Results of one-sided hypergeometric test to determine whether gene modules are enriched in RNA targets of Csde1. Data on Csde1 targets taken from Wurth et al., 2016 (iCLIP-seq data in human melanoma).

Supplementary data 9 – ANCC motifs

Motifs enriched in peaks more accessible ($\log_{2}FC \geq 1$, $p_{adj} \leq 0.01$) in ANCCs (one-sided hypergeometric test).

Supplementary data 10 – EGC motifs

Motifs enriched in peaks more accessible ($\log_{2}FC \geq 1$, $p_{adj} \leq 0.01$) in EGCs (one-sided hypergeometric test).

Supplementary data 11 – Contingency table

Contingency table used for testing whether gene modules are biased towards genes which are up- or down-regulated upon Csde1 knockdown (Fisher exact test).