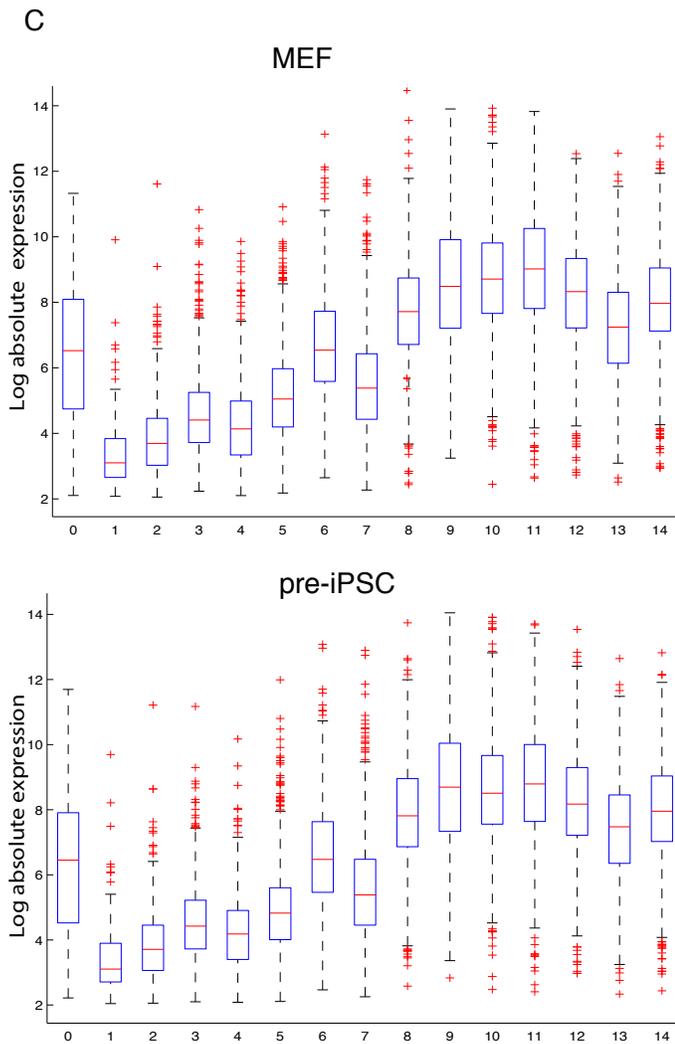
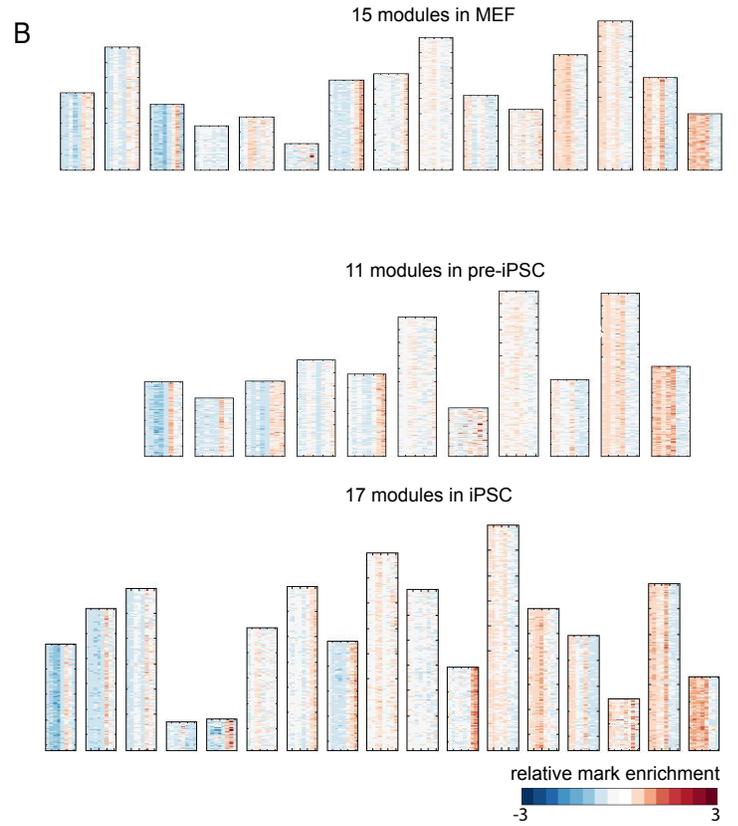
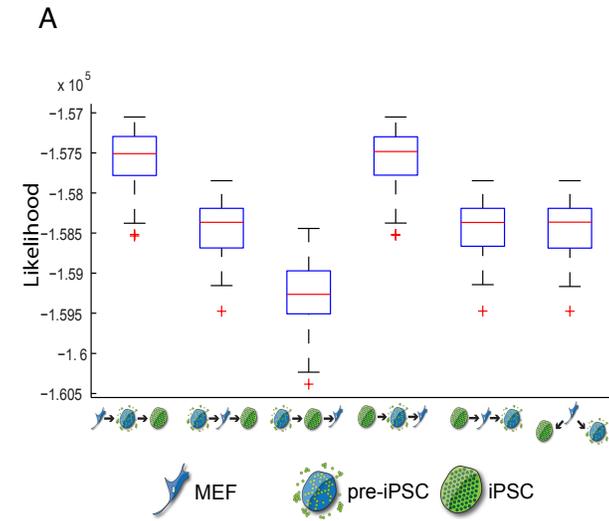


Supp Fig S4: Using CMINT for further analysis of reprogramming cell types. **A.** Possible trajectories for the three the cell types. Data log likelihood value of CMINT models using different types of topologies. **B.** Modules obtained at optimal k values for each of the cell types. **C.** Box plots of gene expression of the chromatin modules in MEF (top) and pre-iPSC (bottom) for the modules shown in **Fig 3A**. **D.** Gene ontology enrichment for each of the modules in iPSC. The top two categories are listed along with the $-\log(\text{p-value})$ of enrichment as scores.

Supp Fig S4



D

Module #	Ontology	Score
0	Cation binding	6.02
1	Sensory transduction Taste transduction	23.47 7.38
2	Receptor activity Inflammatory response	38.33 9.96
3	Serine hydroxylase activity Response to wounding	11.67 10.3
4	Transmembrane receptor activity Cell-cell adhesion	20.53 16.18
5	Transcription - morphogenesis Organ development	43.96 35.87
6	Regulation of cell communication Regulation of developmental process	6.94 6.78
7	Regulation of intracellular process Cell differentiation	4.32 3.5
8	Mitochondrion related Transcription factor activity	4.67 3.63
9	Chromatin assembly Organ development	9.22 4.25
10	Protein metabolism- ubiquitination Transcription	10.22 9.81
11	Translation Gene expression	28.48 14.8
12	Protein Vesicle transport Dna repair	11.32 9.65
13	Mitochondrion related Metal binding	8.98 7.42
14	Biopolymer modification Kinase activity	13.79 5.55