Figure S1. Schematic representation of the strategy used to reconstruct human and mouse networks of genes that are either up-regulated or down-regulated in reprogramming

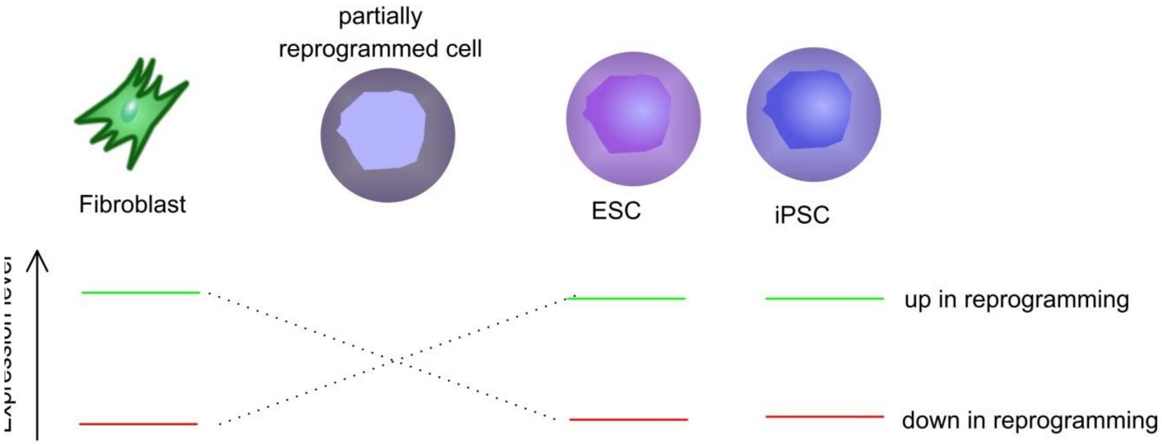
Strategy for network building

1 Collect published transcriptional profiling of starting cell population, iPSC and control ESC

2 Calculate percentrank and weighted percentrank for all probesets

3 . Summarize at Unigene cluster level by keeping the highest expressed probe in ESC

4. Pairwise comparisons for each dataset of iPS vs. starting cell and ESC vs. starting cell



5. Overlap top 1000 changes (up and down, judged by difference in weighted percentrank) for all human datasets on one side and mouse datasets on the other side

6. Keep changes present in at least 44% of all comparisons (separately for each species)

7. Build network (String, Medusa) separating up and downregulated genes

8. Literature analysis of the members of the network

9. Overlap with transcription factor binding sites, chromatin marks...