Bioinformatics Analysis To Identify Potential Transcription Factors That Enhance Reprogramming of Somatic Cells Into Induced Pluripotent Stem Cells

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Induced pluripotent stem cells (iPSCs) are becoming a research trend nowadays as they overcome the limitations associated with embryonic stem cells (ESCs) usage and demonstrate a promising tool for disease modeling and treatment. The generation of iPSCs is dependent on reprogramming of somatic cells by forced introduction of the reprogramming factors into the cell. Although many reprogramming factors had been identified, the process remains inefficient and only small number of cells can undergo complete reprogramming process. Therefore, it is crucial to identify robust reprogramming factors that increase the efficiency of generating iPSCs, improve the quality of reprogramming and fasten the reprogramming time. In fact, we had previously tested whether there is a difference in reprogramming efficiency and iPSCs generation from different fibroblast samples, in a trial to eventually identify the key factors in somatic cell reprogramming. Using Sendai virus reprogramming protocol, we were able to successfully generate different phenotypes of human iPSCs from four dermal fibroblast samples. One of the samples generated under such reprogramming conditions showed a significant increase in the number of iPSC colonies produced. Based on this indication, we have investigated the transcriptomic analysis on those phenotypes and identified the genes expressed in human iPSCs with high number of colonies. These results are benchmarked against other phenotypes that have produced lower numbers of colonies.

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