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Deep sequence analysis reveals epigenetic markers in fat reprogramming

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While DNA modification is adaptive to extrinsic demands, little is known about epigenetic differences and alterations associated with adipose differentiation and reprogramming. In this study we are analyzing that the comprehensive expression profiles and analyses of mRNA expressions and DNA methylations with those of several key factors, during adipose differentiation and induced pluripotent stem cell (iPSC) generation. DNA methylation analysis demonstrated that while global DNA methylation increases throughout the reprogramming transition, a few differential DNA methylated regions (DMRs) were revealed in adipose differentiation process. On the other hands, while mRNA expressions of master regulators for adipogenesis were increased strongly after initiation of adipogenesis, DNA methylations in the promoter regions were already hypo-methylated in the ADSCs and mature adipocytes, compared to iPSCs. The existence of already hypo-methylated regions without mRNA expressions reveals a novel transcriptional/promoter status of key factors in adipogenesis and raises questions as to how the transcription enables adipogenic induction without modifications of DNA methylation.