## S60-1 Protein network for methylation in nuclei

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Epigenetic states of chromatin determine multi-potency and differentiated phenotypes in diverse cell systems. Methylation of DNA and nuclear proteins including histories play critical roles in epigenetic regulation. While DNA and protein methyltransferases use S-adenosylmethionine (SAM) as a methyl donor, it has been unclear how SAM is delivered to methyltransferases in nuclei. SAM can mediate DNA alkylation, positing a system to avoid mutagenic effect. We show that methionine adenosyltransferase II (MATII), which produces its S-adenosylmethionine (SAM), interact with diverse chromatin- and transcription-related proteins including methyltransferases and DNA binding transcription factors. Functions of MATII in oxidative stress response and heterochromatin silencing will be discussed.