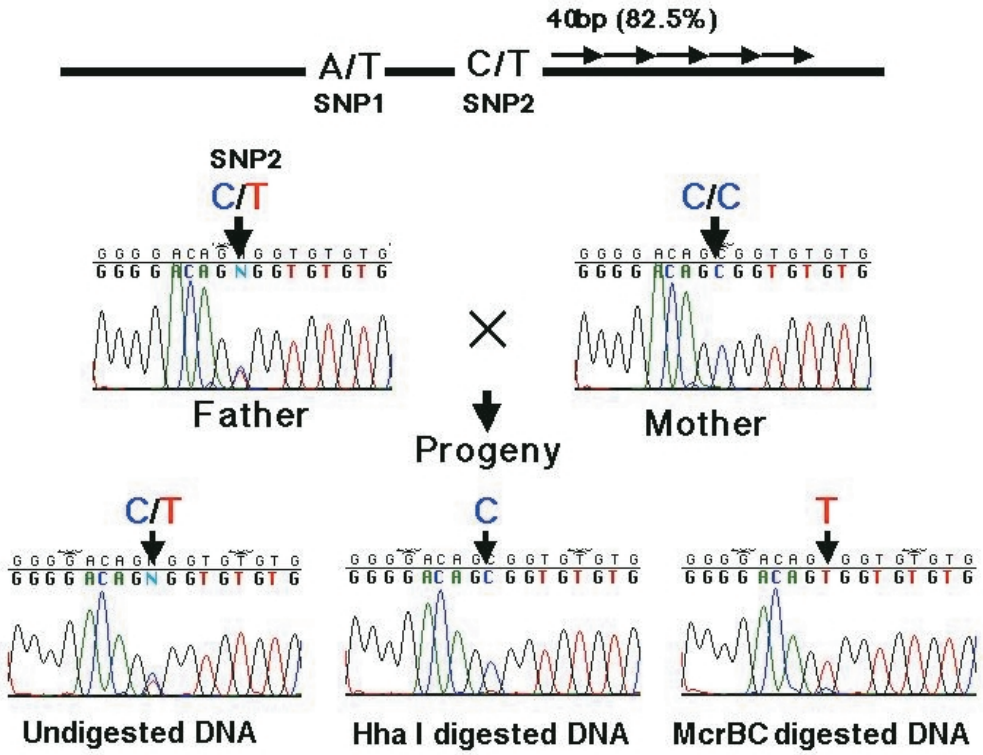
Mammalian Epigenomics

Y. Yamada, S.-Y. Feng, K. Ota & T. Ito

To draw a global picture of epigenetic modification of mammalian genome, we conducted a comprehensive methylation analysis of CpG islands on human chromosome 21. For the analysis, we developed a novel versatile screen termed HpaII-McrBC PCR, which notably allows one to evaluate allelic methylation status. Accordingly, we uncovered three regions subject to allele-specific methylation, in addition to CpG islands methylated even in normal tissues. While two of the three are subject to maternal methylation (see below), the other is methylated in an allele-specific but parental-origin-independent manner, thereby representing a novel mode of allele-specific methylation.



To address molecular mechanisms for epigenetic regulation, we develop a system for site-specific DNA methylation in the budding yeast by recruiting M.SssI DNA methylase to the vicinity of target site by means of LexA-fusion. This system may serve as a unique tool for the analysis of trans-acting factors for methylated DNAs.