UHN Microarray Centre

Publications using UHNMAC arrays for DNA Methylation Studies

A number of researchers have used UHNMAC human and mouse CpG island (CGI) microarrays for DNA methylation profiling. Publications using CpG island microarrays used for methylated DNA immunoprecipitation (MeDIP) can also be found here. This collection only includes articles published in the past several years.

Human CGI arrays

References	Summary
Kaminsky ZA, Tang T, Wang S-C, et al. DNA methylation profiles of monozygotic and dizygotic twins. Nature Genetics 2009, 41:240	Using HCGI 12K arrays for methylation profiling, this study investigated the epigenetic variation among monozygotic twins and the epigenetic similarity between monozygotic and dizygotic twins. The results indicate that the epigenetic similarity in monozygotic twins was more highly conserved in regulatory regions of the genome, suggesting a functional stratification of the epigenome.
Kaminsky Z, *et al*. Epigenetics of personality traits: an illustrative study of identical twins discordant for risk-taking behavior. Twin Res Hum Genet. 2008 11(1):1	HCGI12K arrays were used to identify DNA methylation differences between phenotypically discordant identical twins. This study found that differential methylation of CpG islands proximal to the homeobox DLX1 gene could modulate stress responses and risk taking behaviour.
Lai HC, *et al*. Identification of novel DNA methylation markers in cervical cancer. Int J Cancer. 2008, 123(1):161	The aim of this study was to identify novel genes that are methylated in cervical cancers and to test their potential in clinical applications. Using CGI arrays to uncover methylated genes in squamous cell carcinomas (SCC) of the uterine cervix, researchers reported 6 genes (*SOX1*, *PAX1*, *LMX1A*, *NKX6-1*, *WT1* and *ONECUT1*) more frequently methylated in SCC tissues than in their normal controls. These novel DNA methylations may be a promising approach for the screening of cervical cancers.
Mill J, *et al*. Epigenomic profiling reveals DNA-methylation changes associated with major psychosis. Am J Hum Genet. 2008 Mar;82(3):696	Researchers identified DNA-methylation changes in the frontal cortex and germline associated with schizophrenia and bipolar disorder. This study found evidence for psychosis-associated DNA methylation differences in numerous loci (including brain development and neurotransmission) and evidence for a strong correlation between DNA methylation in the MEK1 gene promoter region and lifetime antipsychotic use in schizophrenia patients.

Human CGI arrays (continued)

References	Summary
Onken MD, *et al*. A Metastasis Modifier Locus on Human Chromosome 8p in Uveal Melanoma Identified by Integrative Genomic Analysis. Clin Cancer Res 2008, 14(12):3737	The purpose of this study was to identify genes that modify metastatic risk in uveal melanoma, a type of cancer that has a consistent metastatic pattern. Using integrative genomic methods, including gene expression profiling, aCGH, differential hybridisation methylation, and SNP-based detection of loss of heterozygosity, this study found a candidate gene, leucine zipper tumor suppressor-1 (*LZTS1*), located in chromosome region 8p12-22, strongly linked to rapid metastasis.
Estécio MRH, *et al.* High-throughput methylation profiling by MCA coupled to CpG island microarray. Genome Res, 2007, 17:1529	Researchers present an improved method to identify methylated genes genome-wide by hybridising a CpG island microarray with amplicons obtained by the methylated CpG island amplification technique. This method was validated in three cancer cell lines and 15 primary colorectal tumours, resulting in the discovery of hundreds of new methylated genes in cancer.
Ho S, Tang W. Techniques used in studies of epigenome dysregulation due to aberrant DNA methylation: An emphasis on fetal-based adult diseases. Reprod Toxicol, 2007, 23(3):267	A review of existing and emerging technologies used in studying DNA methylation including methylation sensitive restriction fingerprinting (MSRF), restriction landmark genomic scanning (RLGS), methylation CpG island amplification-representational difference analysis (MCA-RDA), differential methylation hybridisation (DMH), and cDNA microarrays combined with treatment with demethylating agents and inhibitors of histone deacetylase.

Mouse CGI arrays

References	Summary
Gowher H, *et al.* Vezf1 regulates genomic DNA methylation through its effects on expression of DNA methyltransferase Dnmt3b. Genes Dev 2008, 22:2075	Using MCGI 4.6K arrays, Gowher *et al*. report that mouse embryonic stem cell line deletion of vascular endothelial zinc finger 1 (*Vezf1*) results in loss of DNA methylation throughout the genome due to a decrease in the abundance of the *de novo* DNA methyltransferase, Dnmt3b. This result suggests that *Vezf1* mutations may have widespread effects on the epigenetic regulation of gene expression.
Novikova SI, *et al*. Maternal Cocaine Administration in Mice Alters DNA Methylation and Gene Expression in Hippocampal Neurons of Neonatal and Prepubertal Offspring. PLoS ONE 2008, 3(4):e1919	Using MCGI 7.3K arrays, the hypothesis that maternal cocaine exposure could alter the fetal epigenetic machinery sufficiently to cause lasting neurochemical and functional changes in the offspring was tested. Following maternal cocaine exposure, global DNA methylation was profiled in offspring at 3 (P3) and 30 (P30) days postnatum. By P30, some cocaine-associated effects at P3 endured, reversed to opposite directions, or disappeared, and additional sets of abnormally methylated targets emerged at P30 that were not observed at P3.