UHN Microarray Centre

Publications using UHNMAC Services

A number of researchers have published data obtained through experiments carried out by the UHNMAC Service Team, using the Affymetrix, Agilent, or in-house array platform.

Affymetrix Platform

References	Summary
Jones RA, *et al*. Characterization of a Novel Primary Mammary Tumor Cell Line Reveals that Cyclin D1 Is Regulated by the Type I Insulin-Like Growth Factor Receptor. Mol Cancer Res, 2008, 6:819	This study used the Affymetrix GeneChip Mouse Genome 430 2.0 to characterise the first primary murine mammary tumour cell line with inducible insulin-like growth factor receptor (IGF-IR) expression. These cells provide a powerful model to examine the function of IGF-IR in mammary tumourigenesis.
Tone AA, *et al*. Gene expression profiles of luteal phase fallopian tube epithelium from BRCA mutation carriers resemble high-grade serous carcinoma. Clin Cancer Res, 2008, 14(13):4067	Using the Affymetrix platform to profile the gene expression of histologically normal fallopian tube epithelial from *BCRA1/2* mutation carriers, this study found that the increased expression of SKIL, combined with decreased expression of DAB2, could represent some of the earliest initiating or predisposing events of serous carcinoma.
Lovegrove FE, *et al*. Expression Microarray Analysis Implicates Apoptosis and Interferon-Responsive Mechanisms in Susceptibility to Experimental Cerebral Malaria. Am J Pathol 2007, 171(6):1	Using Affymetrix mouse whole genome expression arrays and computational biology tools, researchers assessed whole-brain transcriptional responses of cerebral malaria by comparing genetically resistant and susceptible inbred mouse strains infected with a strain of *Plasmodium berghei*. By examining the disease progression in cerebral malaria, novel therapeutic targets may be identified.

Agilent Platform

References	Summary
Kovalenko A,*et al*. Caspase-8 deficiency in epidermal keratinocytes triggers an inflammatory skin disease**.** J Exp Med 2009, 206(10):2161	Using the Agilent gene expression platform, this study investigated mice with chronic skin inflammation triggered by caspase-8 - deficient basal epidermal keratinocytes. This study found that the inflammatory response was not dependent on TNF, IL-1, dermal macrophage function, or expression of toll-like receptor adaptor proteins MyD88 or TRIF, and that alterations in gene expression resulting from caspase-8-deficiency are initiated before birth, around the same time as cornification.
Xuan W, *et al*. Interleukin-24 Induces Expression of β4 Integrin but Suppresses Anchorage-Independent Growth of Rat Mammary Tumor Cells by a Mechanism That Is Independent of β4. Mol Cancer Res 2009, 7:433	Some cell lines from tumours induced in resistant Copenhagen x Wistar-Furth F1 rats were able to grow in soft agar but a significant number displayed anchorage-dependent growth. This study used microarrays to identify the genes that are differentially expressed in these cell lines. The data shows that IL-24 suppresses the growth of rat mammary tumours and that β4 integrin, a downstream target of IL-24, does not play a direct role in regulating the proliferative capacity of mammary tumours.
Ponzielli R, *et al*. Optimization of experimental design parameters for high-throughput chromatin immunoprecipitation studies**.** Nucleic Acids Res 2008, 36(21):e144	This study is the first to provide a comprehensive evaluation of experimental ChIP-chip design parameters. Parameters specific to ChIP-chip, such as antibody purity, amplification method for enriched DNA, and the array hybridisation control were evaluated, in addition to parameters previously evaluated for gene expression studies.
Zippo A, *et al*. PIM1-dependent phosphorylation of histone H3 at serine 10 is required for MYC-dependent transcriptional activation and oncogenic transformation. Nature Cell Biol, 2007, 9(8):932	Expression profiling in this study revealed that PIM1 contributes to the regulation of 20% of the c-MYC-regulated genes. This study also establishes serine/threonine kinase PIM1 as a MYC cofactor that phosphorylates the chromatin at MYC-target loci and suggests that nucleosome phosphorylation contributes to MYC-dependent transcriptional activation and cellular transformation.

In-house(UHNMAC) arrays

References	Summary
Goranov AI, *et al*. The rate of cell growth is governed by cell cycle stage. Genes Dev 2009, 23(12):1408	Using custom printed yeast arrays and the UHNMAC gene expression service, this study uses budding yeast to show that cells grow differently during the various stages of the cell cycle. This study found that cell growth is faster in cells arrested in anaphase and G1, and the establishment of a polarised actin cytoskeleton attenuates protein synthesis and growth.
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.
Hauck TS, *et al*. Assessing the Effect of Surface Chemistry on Gold Nanorod Uptake, Toxicity, and Gene Expression in Mammalian Cells. Small, 2008, 4(1):153	UHNMAC H10K cDNA arrays were used to examine the molecular changes of cells exposed to gold nanorods coated with polydiallyldimethylammonium chloride (PDADMAC). The finding that these nanorods have negligible impact on cell function suggests the nanorods are well suited for therapeutic applications, such as thermal cancer therapy, due to their tunable cell uptake and low toxicity.
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, and differential methylation hybridisation, this study found a candidate gene, leucine zipper tumor suppressor-1 (LZTS1), located in chromosome region 8p12-22, strongly linked to rapid metastasis.