UHN Microarray Centre

Publications using UHNMAC arrays for array Comparative Genomic Hybridisation (aCGH)

Several researchers have used UHNMAC arrays for genomic research, including aCGH using human cDNA or yeast ORF microarrays.

References	Summary
Gerstein AC, *et al*. Ploidy reduction in *Saccharomyces cerevisiae*. Biol Lett 2008, 4:91-94	Using yeast arrays for aCGH, researchers investigated the mechanisms involved in ploidy reduction for *Saccharomyces cerevisiae*. The results of this study suggest the existence of a mitotic mechanism allowing the elimination of an entire set of chromosomes, thus reducing the ploidy level.
Iakovlev VV, *et al*. Genomic Differences Between Pure Ductal Carcinoma In Situ of the Breast and that Associated with Invasive Disease: a Calibrated aCGH Study. Clin Cancer Res 2008, 14:4446	aCGH was used to compare the genomic alterations between ductal carcinoma in situ (DCIS) and DCIS with infiltrating duct carcinoma (IDC). This study found that gain on 17q22-24.2 was associated with higher histologic grade, large IDC size, lymphatic/vascular invasion, and lymph node metastasis ($P < 0.05$), and is a candidate region as a predictor of invasion in DCIS.
Ghazani AA, *et al*. Genomic Alterations in Sporadic Synchronous Primary Breast Cancer Using Array and Metaphase Comparative Genomic Hybridization. Neoplasia 2007, 9(6):511	This study used aCGH and metaphase CGH to examine the genetic alterations of 23 synchronous breast cancers from 10 patients. When compared to their matched counterparts, synchronous breast cancers frequently had chromosomal gains of 1q, 3p, 4q, and 8q, and losses of 11q, 12q, 16q, and 17p. Copy number amplification of 1p31.3-1p32.3 (which harbours *JAK1*) was present in all tumour samples.
Pandita A, *et al*. Malignant and benign ganglioglioma: A pathological and molecular study. Neuro Oncol, 2007, 9(2):124	This molecular-pathological study provides insight into the pathogenesis of gangliogliomas and associated rare malignant progression. aCGH analyses using Human 19K cDNA arrays found chromosomal losses to be predominant in the benign areas of the ganglioglioma, with gains more prevalent in the malignant component. Direct analysis demonstrated loss of p19 expression and p53 mutation in the malignant areas, highly suggestive of these alterations being involved in the malignant progression of the ganglioglioma.

aCGH using UHNMAC arrays (continued)

References	Summary
Gerstein AC, *et al*. Genomic Convergence toward Diploidy in *Saccharomyces cerevisiae*. PLoS Genet, 2006, 2(9):e145	Using Yeast 6.4K ORF arrays, researchers used aCGH to investigate genome size evolution in haploid, diploid, and tetraploid initially isogenic lines of the yeast *Saccharomyces cerevisiae*. Over the course of ~1,800 generations of mitotic division, and in both stressful and unstressful environments, convergence toward diploid DNA content in all replicate lines was observed.
Ghazani AA, *et al*. Limited tissue fixation times and whole genome amplification do not impact array CGH profiles. J Clin Pathol 2006, 59:311-315	This study investigates the suitability and integrity of the DNA extracted from formalin fixed, paraffin embedded (FFPE) MCF7 breast cancer cells for aCGH applications. Similar profiles between FFPE MCF7 cells and their fresh counterpart and between amplified and non-amplified FFPE MCF7 cells were observed. This study used Human 19K and 1.7K arrays.