

An Overview of NimbleGen Expression Scientific Publications

Expression microarrays have become an important tool for pinpointing differentially expressed genes and mapping transcription activity within genomes. NimbleGen's high-density, long-oligo arrays incorporate multiple probes/gene for performing demanding gene expression studies, providing increased statistical confidence in experiment results. An increasing number of scientists are taking advantage of the improved sensitivity and discrimination provided by NimbleGen's technology, as evidenced by the peer-reviewed publications citing this platform. These publications as of May 2007 include:

References	Description
Eukaryotic Publications	
Batista F, et al. (2007) Potential targets of FOXL2, a transcription factor involved in craniofacial and follicular development, identified by transcriptomics. <i>Proc Natl Acad Sci USA</i> , 104:3330.	Identification by microarray analysis of genes that are over- or under-expressed in response to FOXL2 facilitated bioinformatic analysis of potential FOXL2-regulated genes.
Bertone P, et al. (2005) Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. <i>Science</i> , 306:2242.	Tiling microarray study designed to catalog the global gene expression in the human genome.
Gurova K, et al. (2005) Small molecules that reactivate p53 in renal cell carcinoma reveal a NF- B-dependent mechanism of p53 suppression in tumors. <i>Proc Natl Acad Sci USA</i> , 102:17448.	Gene expression profiling confirms the specificity of 9-aminoacridine effects on p53- and NF-κB-regulated genes.
Kaushik N, et al. (2005) Gene expression in peripheral blood mononuclear cells from patients with chronic fatigue syndrome. <i>J Clin Pathol</i> , 58:826.	Identification of altered gene expression profiles in patients with Chronic fatigue syndrome.
Li L, et al. (2005) Tiling microarray analysis of rice chromosome 10 to identify the transcriptome and relate its expression to chromosomal architecture. <i>Genome Biol</i> , 6:R52.	Tiling microarray study designed to catalog the gene expression in rice.
Li R and Li C (2006) Identification of estrogen-responsive genes in the parenchyma and fat pad of the bovine mammary gland by microarray analysis. <i>Physiol Genomics</i> , 27:42.	Gene expression analysis identified 124 estrogen-responsive genes in bovine parenchyma and fat pad, accelerating progress in the study of genes responsible for ruminant mammary gland development.
Li RW, et al. (2006) Butyrate induces profound changes in gene expression related to multiple signal pathways in bovine kidney epithelial cells. <i>BMC Genomics</i> , 7:234.	Gene expression analysis identified 450 butyrate-responsive genes in bovine kidney epithelial cells, suggesting a wide-ranging role of butyrate in cattle energy metabolism.
Maeda A, et al. (2006) Effects of Potent Inhibitors of the Retinoid Cycle on Visual Function and Photoreceptor Protection from Light Damage in Mice. <i>Mol Pharm</i> , 70:1220.	Microarray analysis was used to assess potential side effects of a visual cycle inhibitor.
Pischke M, et al. (2006) A Transcriptome-Based Characterization of Habituation in Plant Tissue Culture. <i>Plant Physiol</i> , 140:1255.	Expression study identifying factors involved in plant tissue differentiation.
Rinaldi C, et al. (2007) Transcript Profiling of Poplar Leaves upon Infection with Compatible and Incompatible Strains of the Foliar Rust <i>Melampsora larici-populina</i> . <i>Plant Physiol</i> , 144:347.	A gene with a previously unknown function is the most highly upregulated gene identified by expression profiling of infected poplar leaves.
Rinn J, et al. (2007) Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Non-coding RNAs. <i>Cell</i> , 129:1311.	Tiling microarray of four clustered HOX gene identified novel non-coding RNAs that are involved in gene regulation.
Stolc V, et al. (2005) A pilot study of transcription unit analysis in rice using oligonucleotide tiling-path microarray. <i>Plant Mol Biol</i> , 59:137.	Tiling array study designed to identify novel transcripts in the rice genome.
Stolc V, et al. (2005) Identification of transcribed sequences in <i>Arabidopsis thaliana</i> by using high-resolution genome tiling arrays. <i>Proc Natl Acad Sci USA</i> , 102:4453.	Tiling microarray study designed to catalog the global gene expression in <i>Arabidopsis thaliana</i> .
Stolc V, et al. (2004) A Gene Expression Map for the Euchromatic Genome of <i>Drosophila melanogaster</i> . <i>Science</i> , 306:655.	Tiling microarray study designed to catalog the global gene expression in <i>Drosophila melanogaster</i> .
The Honeybee Genome Sequencing Consortium (2006) Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 443:931.	Whole-genome tiling microarray was used to validate gene assignment in the honeybee genome.
Tuskan G, et al. (2006) The genome of black cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 313:1596	Expression profiling provides empirical confirmation of bioinformatically identified genes.
Udall J, et al. (2006) A Novel Approach for Characterizing Expression Levels of Genes Duplicated by Polyploidy. <i>Genetics</i> , 173:1.	Researchers at Iowa State University used a NimbleGen array to study allele specific expression of genes in the cotton genome.

References	Description
Prokaryotic Publications	
Beller H, <i>et al.</i> (2006) Whole-Genome Transcriptional Analysis of Chemolithoautotrophic Thiosulfate Oxidation by <i>Thiobacillus denitrificans</i> under Aerobic versus Denitrifying Conditions. J Bacteriology , 188:7005.	Gene expression analysis identified almost 300 genes in <i>T. denitrificans</i> that are differentially expressed under aerobic or denitrifying conditions.
Ganesan B, <i>et al.</i> (2006) Identification of the Leucine-to-2-Methylbutyric Acid Catabolic Pathway of <i>Lactococcus lactis</i> . Appl Environ Microbiol , 72:4264.	Gene expression analysis showed that lactococci contained redundant genes for branched-chain fatty acid production that were regulated by an unknown mechanism linked to carbon metabolism.
Ganesan B, <i>et al.</i> (2007) Carbohydrate Starvation Causes a Metabolically Active but Nonculturable State in <i>Lactococcus lactis</i> . Appl Environ Microbiol , 73:2498.	Gene expression profiling facilitated efficient characterization of gene regulation as cells enter nonculturability state.
Haugen B, <i>et al.</i> (2007) <i>In Vivo</i> Gene Expression Analysis Identifies Genes Required for Enhanced Colonization of the Mouse Urinary Tract by Uropathogenic <i>Escherichia coli</i> Strain CFT073 dsdA. Infection and Immunity , 75:278.	Gene expression analysis identified a gene responsible for increased colonization of mouse urinary tract.
Holzer T, <i>et al.</i> (2006) Expression profiling by whole-genome interspecies microarray hybridization reveals differential gene expression in procyclic promastigotes, lesion-derived amastigotes, and axenic amastigotes in <i>Leishmania Mexicana</i> . Mol Biochem Parasitol , 146:198.	Demonstration that different closely related protozoan parasites can be studied using a single expression microarray design.
Li L, <i>et al.</i> (2006) Genome-wide transcription analyses in rice using tiling microarrays. Nat Genet , 38:124.	Tiling microarray study designed to catalog the global gene expression in rice.
Motegi M, <i>et al.</i> (2006) Assessment of Genes Associated with <i>Streptococcus mutans</i> Biofilm Morphology. Appl Environ Microbiol , 72:6277.	Microarray analysis of two <i>S. mutans</i> strain identified a gene responsible for biofilm formation.
Nie L, <i>et al.</i> (2006) Correlation of mRNA Expression and Protein Abundance Affected by Multiple Sequence Features Related to Translational Efficiency in <i>Desulfovibrio vulgaris</i> : A Quantitative Analysis. Genetics , 174:2229.	Microarray analysis was used to study the correlation between mRNA and protein expression.
Nuwaysir E, <i>et al.</i> (2002) Gene expression analysis using oligonucleotide arrays produced by maskless photolithography. Genome Res , 12:1749.	The first report describing the use of NimbleGen Maskless Array Synthesis Technology for gene expression analysis.
Samanta M, <i>et al.</i> (2006) Global identification of noncoding RNAs in <i>Saccharomyces cerevisiae</i> by modulating an essential RNA processing pathway. Proc Natl Acad Sci USA , 103:4192.	Expression tiling microarray study designed to catalog the non-coding RNAs in yeast.
Smeianov V <i>et al.</i> (2007) Comparative High-Density Microarray Analysis of Gene Expression during Growth of <i>Lactobacillus helveticus</i> in Milk versus Rich Culture Medium. Appl Environ Microbiol , 73:2661.	Expression tiling microarray identified genes that are responsible for growth in various culture conditions.
Snyder J, <i>et al.</i> (2004) Transcriptome of Uropathogenic <i>Escherichia coli</i> during Urinary Tract Infection. Infection and Immunity , 72:6373.	Expression analysis identified multiple genes that may be responsible for urinary tract pathogenesis of <i>E. coli</i> .
Snyder J, <i>et al.</i> (2005) Coordinate Expression of Fimbriae in Uropathogenic <i>Escherichia coli</i> . Infection and Immunity , 73:7588.	Expression analysis identified the inverse coregulation of two <i>E. coli</i> fimbrial genes during urinary tract infection.
Stolc V, <i>et al.</i> (2005) Genome-wide transcriptional analysis of flagellar regeneration on <i>Chlamydomonas reinhardtii</i> identifies orthologs of ciliary disease genes. Proc Natl Acad Sci USA , 102:3703.	Tiling microarray study designed to catalog the global gene expression in <i>Chlamydomonas reinhardtii</i> .
Ulijasz A, <i>et al.</i> (2004) Regulation of Iron Transport in <i>Streptococcus pneumoniae</i> by RitR, an Orphan Response Regulator. J Bacteriol , 186:8123.	Identification of regulatory targets for an orphan two-component signal regulator and virulence factor in <i>Streptococcus pneumoniae</i> .
Whitby P, <i>et al.</i> (2006) Transcriptional Profile of <i>Haemophilus influenzae</i> : Effects of Iron and Heme. J Bacteriol , 188:5640.	Microarray analysis identified 162 genes that are differentially expressed under iron/heme replete or restricted growth conditions.
Brown D, <i>et al.</i> (2007) The <i>Fusarium verticillioides</i> FUM gene cluster encodes a Zn(II)2Cys6 protein that affects FUM gene expression and fumonisin production, Eukaryotic Cell , 6:1210.	Microarray analysis reveals differential expression of spliced forms of a newly identified gene involved in the regulation of fumonisin production.
Ochiai A, <i>et al.</i> (2007), Plant Cell Wall Degradation by <i>Saprophytic Bacillus subtilis</i> : Gene Clusters Responsible for Rhamnogalacturonan Depolymerization, Appl Environ Microbiol , 73:3803.	Gene expression analysis facilitated identification of three gene clusters involved in degradation of plant cell wall component during infection.