

■ Bibliography of Affymetrix Tiling Array Publications

CHROMATIN IMMUNOPRECIPITATION

1. Isogai Y., *et al.* Novel TRF1/BRF target genes revealed by genome-wide analysis of Drosophila Pol III Transcription. *EMBO Journal* 26:76-89 (2007).
2. Kiyofumi K., *et al.* An integrated map of p53-binding sites and histone modification in the human ENCODE regions. *Genomics* 89(2):178-88 (2006).
3. Carroll J., *et al.* Genome-wide analysis of estrogen receptor binding sites. *Nature Genetics* 38(11):1289-97 (2006).
4. Carroll J., *et al.* Chromosome-Wide Mapping of Estrogen Receptor Binding Reveals Long-Range Regulation Requiring the Forkhead Protein FoxA1. *Cell* 122:33-43 (2005).
5. Swinburne I., *et al.* Genomic localization of RNA binding proteins reveals links between pre-mRNA processing and transcription. *Genome Research* 16(7):912-21 (2006).
6. Brodsky A., *et al.* Genomic mapping of RNA polymerase II reveals sites of co-transcriptional regulation in human cells. *Genome Biology* 6(8):R64 (2005).
7. Cawley S., *et al.* Unbiased mapping of transcription factor binding sites along human chromosomes 21 and 22 points to widespread regulation of noncoding RNAs. *Cell* 116(4):499-509 (2004).
8. Bernstein B., *et al.* Genomic Maps and Comparative Analysis of Histone Modification in Human and Mouse. *Cell* 120:169-181 (2005).
9. Reidel C., *et al.* Protein phosphatase 2A protects centromeric sister chromatid cohesion during meiosis I. *Nature* 441(7089):53-61 (2006).
10. Bernstein B., *et al.* A bivalent chromatin structure marks key developmental genes in embryonic stem cells. *Cell* 125(2):315-26 (2006).
11. Schwartz Y., *et al.* Genome-wide analysis of Polycomb targets in Drosophila melanogaster. *Nature Genetics* 38(6):700-5 (2006).
12. Yang, *et al.* Relationships between p63 Binding, DNA Sequence, Transcription Activity, and Biological Function in Human Cells. *Molecular Cell* 24:1-10 (2006).
13. Kahn T., *et al.* Polycomb complexes and the propagation of the methylation mark at the Drosophila *ubx* gene. *J Biol Chem* 281(39):29064-75 (2006).
14. Huebert D., *et al.* Genome-wide analysis of histone modifications by ChIP-on-chip. *Methods* 40(4):365-9 (2006).

TRANSCRIPT MAPPING

15. Kapranov P., *et al.* RNA maps reveal new RNA classes and a possible function for Pervasive Transcription. *Science* 10:1126 (2007).
16. Manak J., *et al.* Biological function of unannotated transcription during the early development of Drosophila melanogaster. *Nature Genetics* 38(10):1151-8 (2006).
17. Cheng J., *et al.* Transcriptional Maps of 10 Human Chromosomes at 5-Nucleotide Resolution. *Science* 308(5725):1149-54.

- 18. Kampa D., *et al.* Novel RNAs identified from an in-depth analysis of the transcriptome of human chromosomes 21 and 22. *Genome Research* 14(3):331-42 (2004).
- 19. Kapranov P., *et al.* Large-scale transcriptional activity in chromosomes 21 and 22. *Science* 296(5569):916-9 (2002).
- 20. Kapranov P., *et al.* Examples of the complex architecture of the human transcriptome revealed by RACE and high-density tiling arrays. *Genome Research* 15:987-997 (2005).
- 21. Yamada K., *et al.* Empirical analysis of transcriptional activity in the Arabidopsis genome. *Science* 302(5646):842-6 (2003).
- 22. David L., *et al.* A high-resolution map of transcription in the yeast genome. *PNAS* 103(14):5320-5 (2006).
- 23. Liu W., *et al.* CD127 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T reg cells. *J Exp Med* 203(7):1701-11 (2006).
- 24. Biemar F., *et al.* Comprehensive identification of Drosophila dorsal-ventral patterning genes using a whole-genome tiling array. *PNAS* 103(34):12763-8 (2006).
- 25. Biemar F., *et al.* Spatial regulation of microRNA gene expression in the Drosophila embryo. *PNAS* 102(44):15907-11 (2005).
- 26. Hasegawa Y., *et al.* A RecA-mediated exon profiling method. *Nucleic Acids Research* 34(13) (2006).

OTHER APPLICATIONS

- 27. ENCODE Consortium. The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science* 306(5956):636-640 (2004).
- 28. Gresham, *et al.* Genome-wide Detection of Polymorphisms at Nucleotide Resolution with a Single DNA Microarray. *Science* 311(5769):1932-6 (2006).
- 29. Jeon Y., *et al.* Temporal profile of replication of human chromosomes. *PNAS* 102(18):6419-6424 (2005).

DNA REPLICATION

- 30. Katis V., *et al.* Spo13 facilitates monopolin recruitment to kinetochores and regulates maintenance of centromeric cohesion during yeast meiosis. *Current Biology* 14(24):2183-96 (2004).
- 31. Strom L., *et al.* Postreplicative recruitment of cohesin to double-strand breaks is required for DNA repair. *Molecular Cell* 16(6):1003-15 (2004).
- 32. Lengronne A., *et al.* Cohesin relocation from sites of chromosomal loading to places of convergent transcription. *Nature* 430(6999):573-8 (2004).
- 33. Katou Y., *et al.* S-phase checkpoint proteins Tof1 and Mrc1 form a stable replication-pausing complex. *Nature* 424(6952):1078-83 (2003).
- 34. Riedel C., *et al.* Protein phosphatase 2A protects centromeric sister chromatid cohesion during meiosis I. *Nature* 441(7089):53-61 (2006).
- 35. Jeon Y., *et al.* Temporal profile of replication of human chromosomes. *PNAS* 102(18):6419-24 (2005).

METHYLATION

- 36. Zhang X., *et al.* Genome-wide High-Resolution Mapping and Functional Analysis of DNA Methylation in Arabidopsis. *Cell* 126(6):1189-201 (2006).

- 37. Schumacher A., *et al.* Microarray-based DNA methylation profiling: technology and applications. *Nucleic Acids Research* 34(2):528-42 (2006).*
- 38. Hayashi H., *et al.* High-resolution mapping of DNA methylation in human genome using oligonucleotide tiling array. *Human Genetics* 120(5):701-11 (2007).

DATA ANALYSIS METHODS

- 39. Moses A., *et al.* Large-Scale Turnover of Functional Transcription Factor Binding Sites in Drosophila. *PLoS Comput Biology* 2(10):e130 (2006).
- 40. Ghosh S., *et al.* Rank-statistics based enrichment-site prediction algorithm developed for chromatin immunoprecipitation on chip experiments. *BMC Bioinformatics* 7:434 (2006).
- 41. Li W., *et al.* A hidden Markov model for analyzing ChIP-chip experiments on genome tiling arrays and its application to p53 binding sequences. *Bioinformatics* 21(1):274-282 (2005).
- 42. Ji H., *et al.* TileMap: create chromosomal map of tiling array hybridizations. *Bioinformatics* 21(18):3629-36 (2005).
- 43. Toyoda T., *et al.* Tiling array-driven elucidation of transcriptional structures based on maximum-likelihood and Markov models. *Plant Journal* 43(4):611-21 (2005).
- 44. Royce T. Issues in the analysis of oligonucleotide tiling microarrays for transcript mapping. *Trends in Genetics* 21(8):466-75 (2005).
- 45. Munch K., *et al.* A hidden Markov model approach for determining expression from genomic tiling micro arrays. *BMC Bioinformatics* 7(1):239 (2006).
- 46. Johnson W., *et al.* Model-based analysis of tiling-arrays for ChIP-chip. *PNAS* 103(33):12457-62 (2006).

REVIEWS AND BACKGROUND INFORMATION

- 47. Duttagupta R., *et al.* Applications of high density tiling microarrays: Interrogation of genomic sequences of functional elements. *Cell Technology* 25(10):1139-1147 (2006).
- 48. Emanuelsson O., *et al.* Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome. *Genome Research* (Epub Nov 2006)
- 49. Mattick J. The functional genomics of noncoding RNA. *Science* 309(5740):1527-8 (2005).
- 50. Guigo R., *et al.* EGASP: the human ENCODE Genome Annotation Assessment Project. *Genome Biology* 7(1):S2.1-31 (2006).
- 51. Mockler T., *et al.* Applications of DNA tiling arrays for whole-genome analysis. *Genomics* 85(1):1-15 (2005).
- 52. Johnson J., *et al.* Dark matter in the genome: evidence of widespread transcription detected by microarray tiling experiments. *Trends in Genetics* 21(2):93-102 (2005).
- 53. Willingham A. *et al.* TUF Love for “Junk” DNA. *Cell* 125(7):1215-20 (2006).
- 54. Gingeras T., *et al.* The multitasking genome. *Nature Genetics* 38(6):608-9 (2006).

*This paper does not use GeneChip® Tiling Arrays, but is included as an example of using DNA methylation assays with tiling arrays.