약 력

1. 인적사항

	성 명	Thomas Albert
	소속기관	NimbleGen Systems, Inc.
	직 위	Director of Molecular Research
	전자메일	

2. 학력/경력

연 도	학교 / 기관	전공 / 직위	학위 / 비고
	University of Michigan	Chemistry	BS
	University of Wisconsin-Madison	Molecular Toxicology	PhD.

3. 주요연구실적(개조식, 간단하게)

4. 발표시 사용 기자재

* LCD projector의 사용을 원칙으로 합니다.
* LCD 사용을 위해 CD나, 저장 매체에 담아 오시는 것을 권장하며, Zip드라이브는 학회에서 준비하지 않습니다.

High-Resolution Microarrays for Mapping Promoter Binding sites and Copy Number Variation in the Human Genome

Thomas Albert

NimbleGen Systems, Inc.

NimbleGen has developed strategies to use its high-density oligonucleotide microarray platform (385,000 probes per array) to map both promoter binding sites and copy number variation at very high-resolution in the human genome. Here we describe a genome-wide map of active promoters determined by experimentally locating the sites of transcription imitation complex binding throughout the human genome using microarrays combined with chromatin immunoprecipitation. This map defines 10,567 active promoters corresponding to 6,763 known genes and at least 1,196 un-annotated transcriptional units. Microarray-based comparative genomic hybridisation (CGH) is animportant research tool for investigating chromosomal aberrations frequently associated with complex diseases such as cancer, neuropsychiatric disorders, and congenital developmental disorders. NimbleGen array CGH is an ultra-high resolution (0.5 - 50 Kb) oligo array platform that can be used to detect amplifications and deletions and map the associated breakpoints on the whole-genome level or with custom fine-tiling arrays. For whole-genome array CGH, probes are tiled through genic and intergenic regions with a median probe spacing of 6 Kb, which provides a comprehensive, unbiased analysis of the genome.