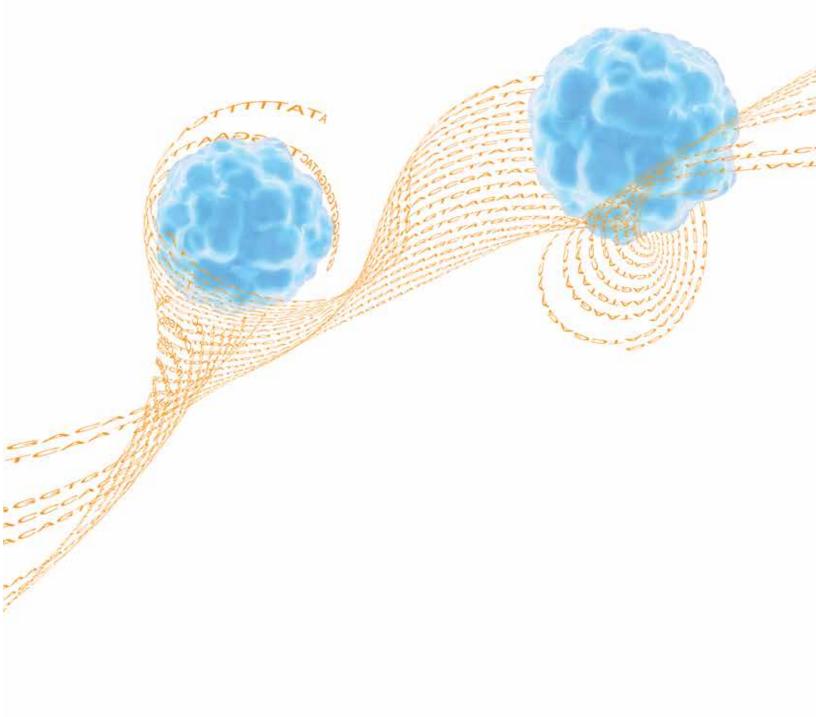
Cancer Genomics

Transforming our understanding of cancer



illumina

Accelerating translational medicine.

Technology enhances understanding. Drives discovery.



Illumina's cancer discovery initiative.

Our belief in the power of Illumina technology is so strong that we work side by side with researchers to obtain samples for our cancer discovery work. Using whole-genome sequencing, we are exploring how biomarker discovery can lead to early detection, resistance to therapy, and prognosis in ovarian, gastric, and colorectal cancer. Discovering how analyzing subtle changes in genes and chromosomes will change diagnostics forever. Ultimately leading to novel diagnostic services and products as shown in the continuum above.

Illumina's clinical services lab.

The first choice for doctor-ordered Individual Genome Sequencing services. The first to generate a complete human sequence in a clinical laboratory. Fully CLIA-certified and CAP-accredited for high-complexity molecular testing.



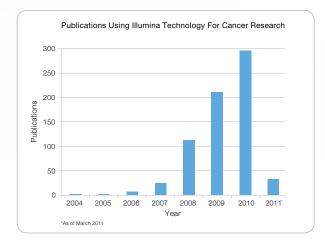
When taking a genome-wide approach to cancer, researchers can use a Circos plot¹ to visualize the extensive rearrangements and variations that are common to cancer. This plot shows variations found in a melanoma cell line, marking each chromosome on the outside ring, then showing validated indels, density of substitutions, coding substitutions, copy number variants, loss of heterozygosity, to reveal the intrachromosomal and interchromosomal structural variants in the middle of the plot

Empowering cancer research.

Sequencing. Microarrays. Real-time PCR. Technology is fueling a new era of cancer discovery and validation.

The growing Illumina community is a part of this revolution. Taking advantage of simplified workflows and streamlined platforms. Advancing research. Increasing our understanding. Publishing results.

The Illumina community is discovering more. Publishing more.



2008

- First publication describing whole-genome sequencing on human cancer²
- Accurate human whole-genome sequencing using reversible terminator chemistry³

2009

- Demonstrates the power of second-generation transcriptome sequencing for identifying rearrangements in coding genes⁴
- The largest collection of samples (24) for a single cancer type to be whole-genome sequenced, documenting large sample-to-sample variability⁵

2010

• Next-generation sequencing technology provides new insights into the mechanisms of cancer progression and a greater understanding of diagnosis and treatment options⁶⁻⁹

2011

Discovery of causative gene mutations for a rare skin cancer condition¹⁰

Transforming diagnostics.

New technologies. New discoveries. New hope. With innovation, insight, and commitment, the Illumina community is leading the way toward a brighter future in cancer diagnostics, therapy, and personalized treatment.

- New developments provide hope for earlier detection and better prognoses
- Novel biomarkers may lead to future treatments tailored to an individual's genetic disposition
- Individual Genome Sequencing services provide genetic information that will facilitate clinical decision making in cancer and medicine





Learn more about Illumina at www.illumina.com/cancer

Comprehensive cancer research portfolio.







Sequencing + Arrays

Multiplexed



Real-Time

	Sequencing	Genotyping	Sequencing + Arrays	Analysis	PCR
Find Structural Variation	5	5			
CNV Screening		+	+		•
CNV Discovery		+	+		
Detect Chromosomal Rearrangements					
Breakpoint Mapping					
Insertions, Deletions, and Translocations		+	+	+	•
Characterize Epigenetic Changes					
DNA Methylation Biomarker Panels		•	•	+	•
DNA Methylation Discovery					
ChIP-Sequencing (DNA-Protein Binding)	•		٠		
Changes in Transcription Factor and Histone Binding	•		•		
Identify Variants in Gene Regions					
Whole-Genome Genotyping		+	+		
Custom/Focused Genotyping	+	+	+	+	٠
SNP Discovery					
Whole-Genome Resequencing					
Exome Resequencing					
Custom Targeted Resequencing					
Custom Amplicon Resequencing					
Profile Gene Expression					
Whole-Genome Expression	+	+	+		
Focused Gene Expression					•
MicroRNA and Small RNA Profiling	+		+		•
MicroRNA and Small RNA Discovery	+		+		

• Illumina-supported intact samples

+ Illumina-supported intact and degraded (FFPE) samples

Customer-demonstrated intact and degraded (FFPE) samples

References:

- Heterences: I. Krzywinski M et al. (2009) Circos: an information aesthetic for comparative genomics. Genome Res. 1639–1645. 2. Ley TJ et al. (2008) DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature 456: 66–72. 3. Bentley DR et al. (2008) Accurate whole human genome sequencing using reversible terminator chemistry. Nature 456: 53–59.43. 4. Maher CA et al. (2009) Chimeric transcript discovery by paired-end transcriptome sequencing. Proc Natl Acad Sci USA 106: 12353–12358. 5. Stephens PJ et al. (2009) Complex landscapes of somatic rearrangement in human breast cancer genomes. Nature 452: 1036–1010. 6. Choi YL et al. (2010) EML-44. Kuntuations in lung cancer that confer resistance to ALK inhibitors. N Engl J Med. 363: 1734–1799. 7. Ding L et al. (2010) Analvis of next-generation enomic data in cancer: accomolishments and challenges. Hum Med Genet, 19: R188–R196

- Ung Let al. (2010) enorme removaling in a basal-like preast cancer metastass and xerografit, nature 494; 399–1005.
 Ding L et al. (2010) Analysis of next-generation genomic data in cancer: accomplishments and challenges. Hum Mol Genet. 13: R188–R196.
 Jones SJ et al. (2010) Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biol. 11: R82.
 Goude DR et al. (2011) Multiple self-healing squamous epithelioma is caused by a disease-specific spectrum of mutations in TGFBR1. Nat Genet. [Epub ahead of print].

The BeadXpress System is FDA cleared for use as an in vitro diagnostic only with FDA cleared VeraCode tests. The Illumina Eco Real-Time PCR System, Infinium HD BeadChips, HISeq Systems, and HIScan Systems are FOR RESEARCH USE ONLY.

