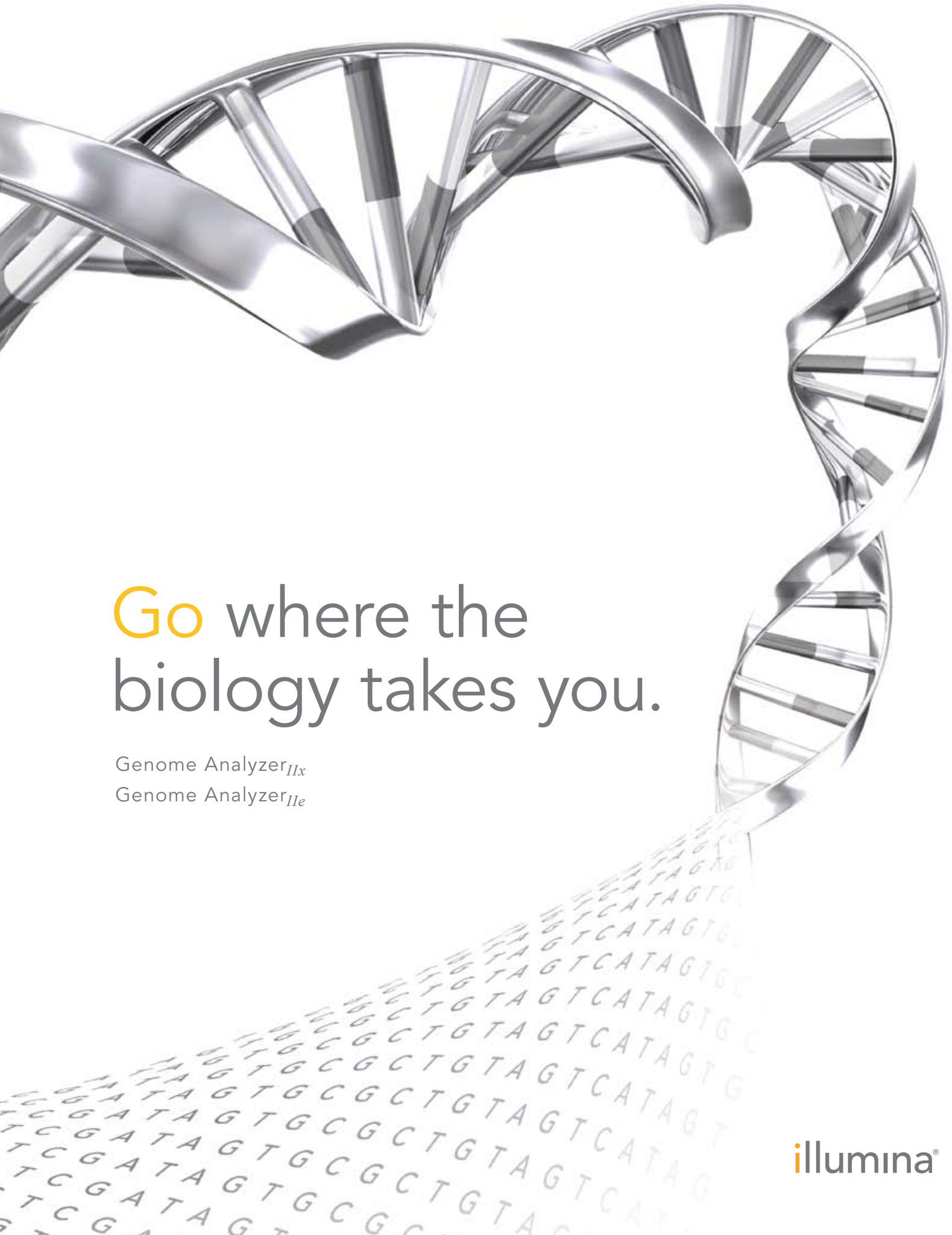


Go where the biology takes you.

Genome Analyzer$_{IIx}$
Genome Analyzer$_{IIe}$

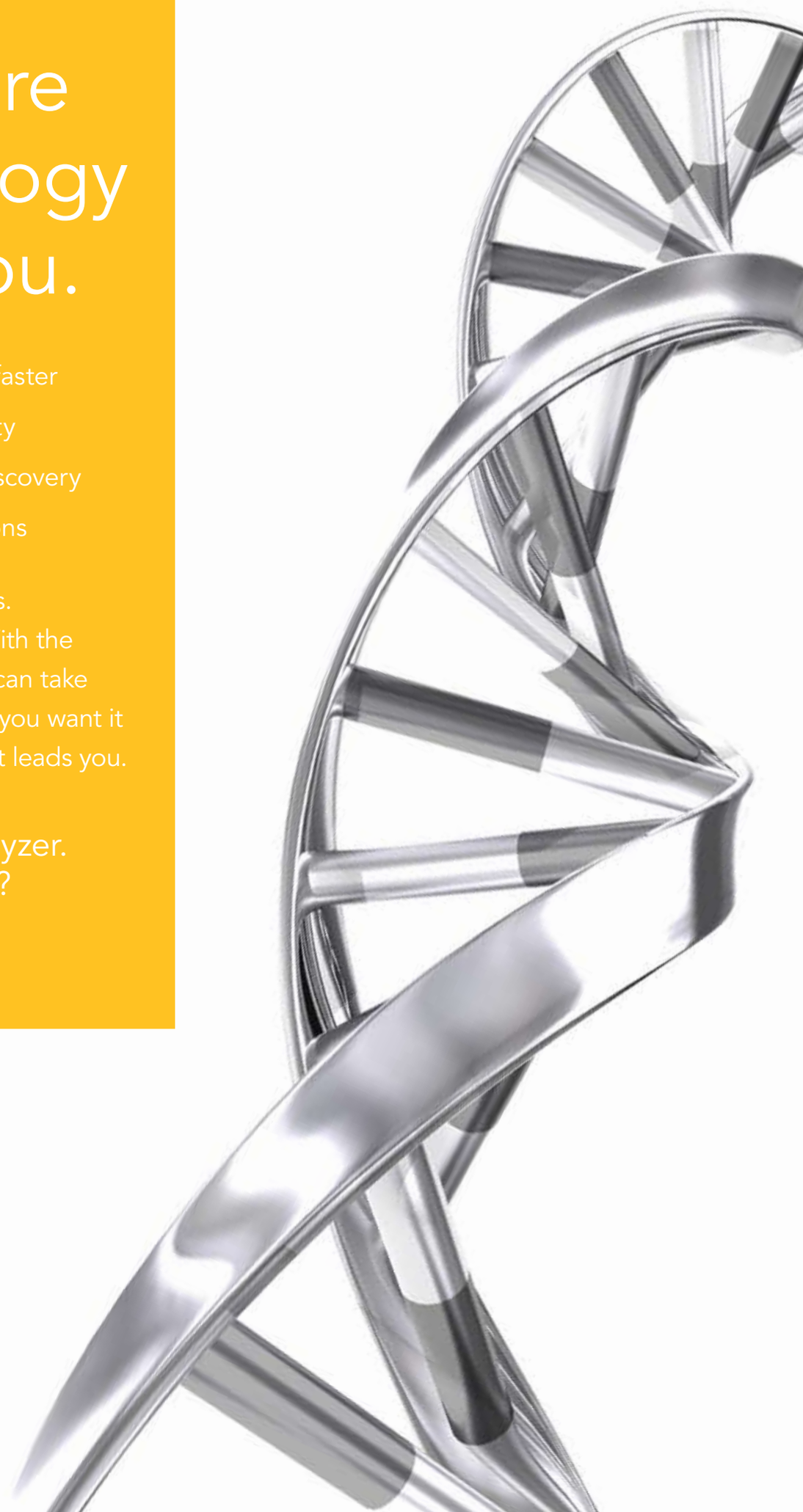
illumina®

Go where the biology takes you.

- To published results faster
- With proven scalability
- To the forefront of discovery
- To limitless applications

Unprecedented answers. Unexpected insights. With the Genome Analyzer, you can take your research wherever you want it to go. Then see where it leads you.

The Genome Analyzer.
Where will you go?



Genome Analyzer$_{IIx}$

Genome Analyzer$_{IIe}$

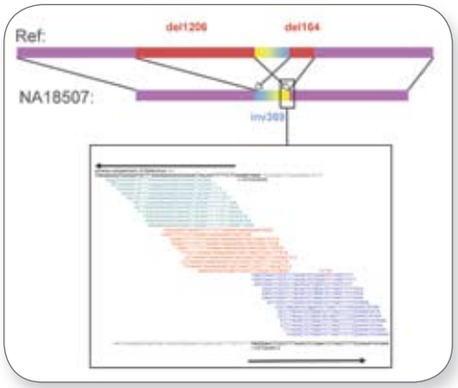
Two models. Which will you choose?

The Genome Analyzer$_{IIx}$ is the most widely adopted next-generation sequencing platform. Proven and published across the broadest range of research applications.

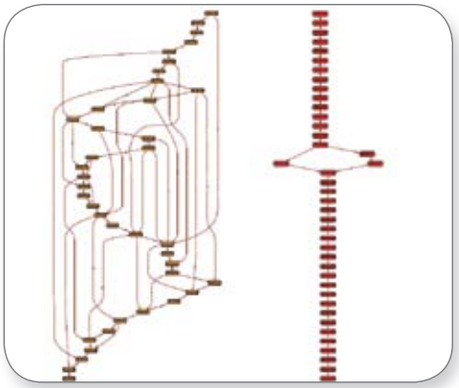
The Genome Analyzer$_{IIe}$ makes industry-leading next-generation sequencing technology accessible to more laboratories.

Learn more about Illumina's portfolio of sequencing solutions, visit www.illumina.com/systems

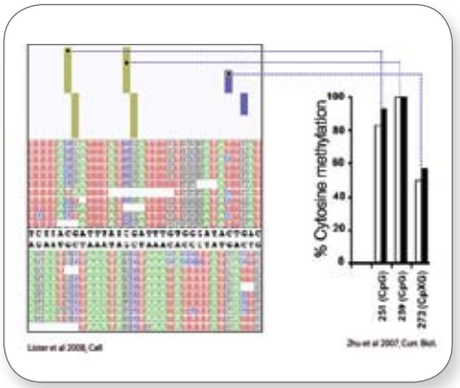
Powerful applications. Unlimited discovery.



Complex human genome rearrangements are identified using a combination of alignment and *de novo* assembly.



Human transcript profiling reveals a vastly more complex picture (left) than previously observed in Ensembl (right).



Genome-wide methylation status in arabidopsis is revealed and quantified with single-base resolution.

DNA Sequencing

Any genome. Every genetic variant. The Genome Analyzer gives you the power to comprehensively characterize the genome with both short-insert paired-end and long-insert mate pair libraries. Go from DNA to data in under a week with less than four hours of hands-on time. Applications flexibility. Superior raw-read accuracy. It's sequencing power for every researcher.

Transcriptome Analysis

Unmatched sensitivity. Complete transcripts. A combination of long reads, millions of counts, uniform coverage and strand specificity allows you to annotate coding SNPs, discover transcript isoforms, and determine the relative abundance of transcripts. All in one experiment. Evidenced by a large, rapidly growing list of peer-reviewed publications, the Genome Analyzer allows you to see the transcriptome like you've never seen it before. Long reads. Deep coverage. The right combination for your study.

Gene Regulation and Control

The complete picture. With the Genome Analyzer, you can assess a wide range of epigenetic and gene control events with single-base resolution. Take advantage of chemistry that's uniquely suited to give you visibility into epigenetic change at any base in the genome. Uncompromised experimental design. Comprehensive results. Find out what you have been missing in the epigenome.

Open architecture. Streamlined analysis.

Powerful software. Easy-to-use interface. Our suite of integrated applications is built to take you quickly from image capture to interactive analysis. Quickly and easily assess the success of your run. Customize your workflow with our flexible architecture. It's massive-scale data analysis, simplified.

SCS and RTA

The Illumina Sequence Control Software (SCS) with Real Time Analysis (RTA) provides a complete set of software tools for managing and executing Genome Analyzer experiments runs, from sample tracking and initial run set up through completion of primary analysis. SCS enables completely flexible yet unattended instrument operation, while its real-time reports and graphs give continuous run feedback. Image analysis, base calling, and base call quality calibration are accomplished automatically during the run with the Real Time Analysis module - when the run completes, the data is ready.

CASAVA

CASAVA is a complete secondary analysis package for processing sequence from the Genome Analyzer. Align reads, detect single nucleotide variations, identify small insertions and deletions, and perform RNA counting analysis. Cover more of the genome with new gapped, multi-seed alignment. Rapidly transform data into biologically relevant information.

GenomeStudio® Software

GenomeStudio Software is a graphical data analysis package that allows you to explore data from multiple genetic analysis applications in the same genome browser. Conveniently compare and correlate data from all Illumina platforms to obtain a complete picture of the genome and elucidate disease mechanisms. All on your laptop.

Enabling Innovation

Optimize. Analyze. Collaborate. Your research will take you down many analysis paths. That's why we distribute our CASAVA software source code to each customer, making algorithmic modifications and integration with third-party applications easy. From advanced analysis applications to integrated data management, you can take advantage of a growing number of third party software tools. Our collaborative environment allows you to tap into the power of the Illumina software development community.

CLC Bio

CLC Bio's Genomic Workbench software is a high performance solution for reference-assisted and *de novo* assembly of next-generation sequencing data. It integrates seamlessly with the Genome Analyzer to identify variations in sequence data derived from a variety of genomic applications.

GenoLogics

Geneus lab and data management software from GenoLogics simplifies end-to-end sample and data management, ensures sample traceability, and improves lab operation efficiency. Geneus accommodates workflows on the Genome Analyzer and helps manage data across a multitude of people, projects, and platforms.

For a full list of recommended third-party applications, visit www.illumina.com/iconnect

Genome Analyzer Analysis Workflow

1.800.809.4566 toll-free 1.858.202.4566 tel

DE NOVO SEQUENCING

- **Paired Reads –** Generate long scaffolds and highly accurate contigs using multiple insert lengths with high library diversity.
- **Read Length –** Use paired-end reads in excess of 2 x 100 bases for mammalian-scale *de novo* assembly.
- **Raw-Read Accuracy –** Access the highest yield of perfect reads and Q30 data to generate long, error-free contigs.
- **Assembly Tools –** Leverage a rapidly growing number of assemblers optimized for Genome Analyzer reads, such as Velvet, SOAPdenovo, ABySS and Forge.

RESEQUENCING

- **Single Nucleotide Polymorphisms (SNPs) –** Maximize accuracy through direct base interrogation of SNPs without the need for complex data conversion.
- **Insertions and Deletions (indels) –** Precisely detect indels of varying size using both short-insert paired-end and long-insert mate pair libraries.
- **Copy Number Variations (CNVs) –** Enable genome-wide characterization of copy number variation with comprehensive, uniform coverage.
- **Structural Variation –** Catalog and characterize a broad range of complex structural variants with flexible insert lengths and the ability to perform local *de novo* assembly.

TRANSCRIPT PROFILING

- **High Throughput –** Generate transcript profiles in a single day.
- **Unmatched Sensitivity –** Identify and quantify both rare and common transcripts, with six orders of magnitude of dynamic range.
- **Protocol Flexibility –** Answer any question using mRNA-Seq or Small RNA Analysis.

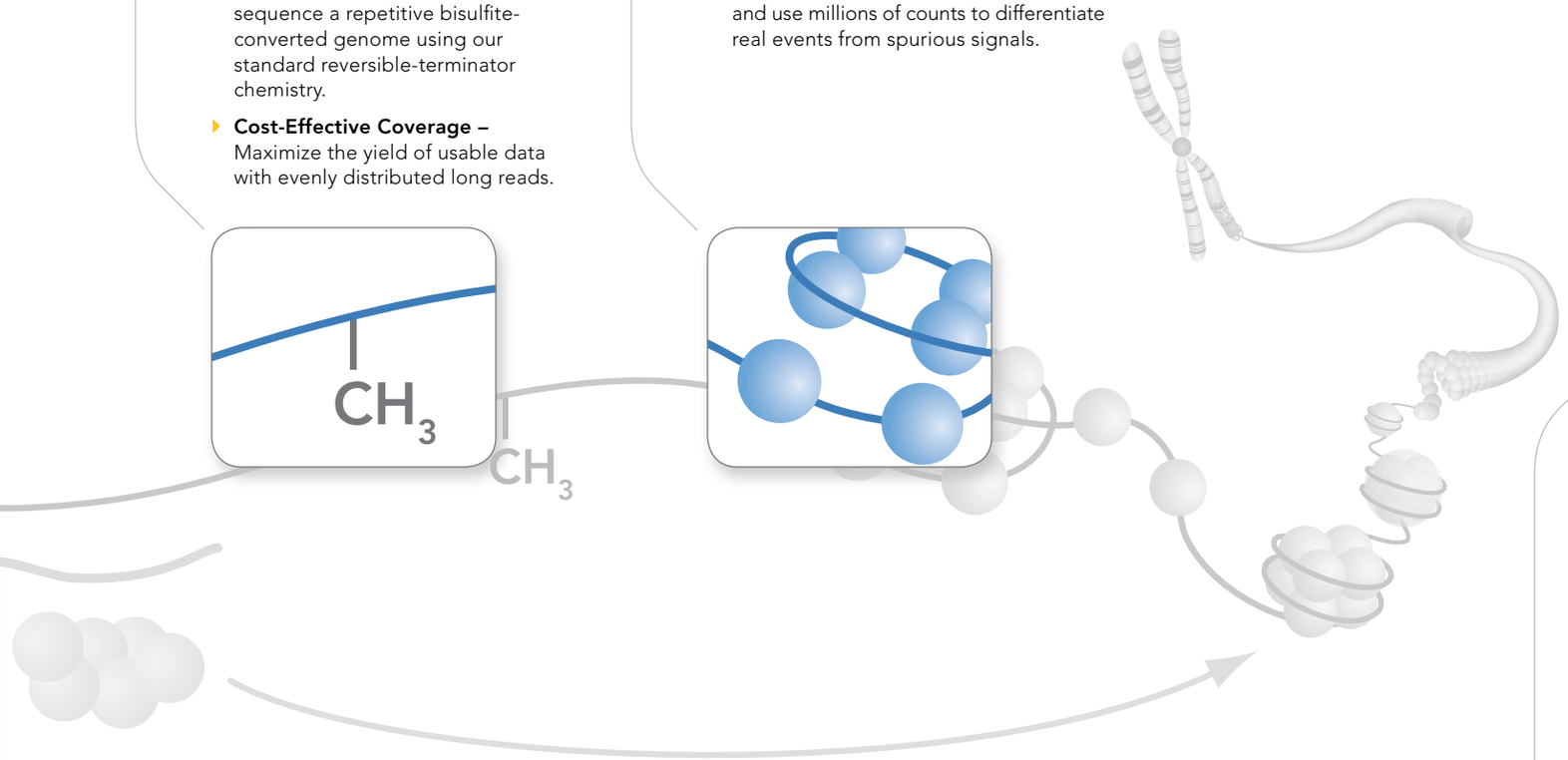
DNA Sequencing | Transcriptome Analysis | Gene Regulation and Control

BISULFITE SEQUENCING

- **Mapping Accuracy –** Correctly map more reads to the epigenome using accurate 100 base paired-end reads.
- **Library Preparation –** Easily prepare the highly diverse libraries needed for comprehensive epigenome characterization.
- **Universal Protocol –** Evenly sequence a repetitive bisulfite-converted genome using our standard reversible-terminator chemistry.
- **Cost-Effective Coverage –** Maximize the yield of usable data with evenly distributed long reads.

ChIP SEQUENCING

- **Low Sample Input –** Generate accurate, precise DNA-protein interaction maps using as little as 10 ng of sample from a single immunoprecipitation.
- **Precision Mapping –** Pinpoint rare binding events to within 50 bases of the actual binding site.
- **High Sensitivity –** Identify a broad range of interactions with confidence, and use millions of counts to differentiate real events from spurious signals.



TRANSCRIPT DISCOVERY

- **Comprehensive Characterization –** Characterize splice variants, coding SNPs, and relative expression of alleles in one experiment.
- **Low Sample Input –** Use 1–10 µg of sample to create paired-end libraries to better characterize alternate isoforms.
- **Read Length –** Span multiple exons with single or paired reads of 100 bases or longer.
- **Unbiased Coverage –** Identify rare transcripts reliably with reproducible, unbiased coverage.
- **Strand Specificity –** Differentiate between plus and minus strand, allowing discovery and profiling of overlapping transcripts.

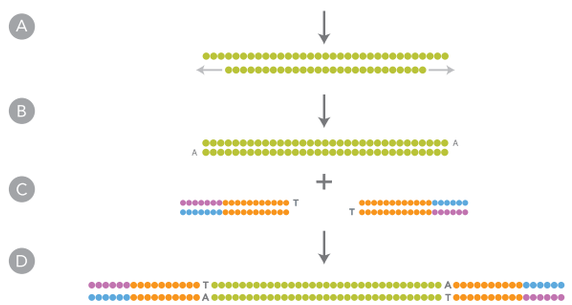
Simple workflow.
Single-user operation.

System automation. Turnkey operation. The simple Genome Analyzer workflow enables even small labs to have sequencing capabilities rivaling those of genome centers. With the fastest and least labor-intensive workflow of any sequencing technology, your lab can generate highly accurate results in less than a week. Automation frees you to complete groundbreaking studies in minimal time. Workflow optimization. Faster publication. It's genomic power for everyone.

Automated Workflow

1 LIBRARY PREPARATION

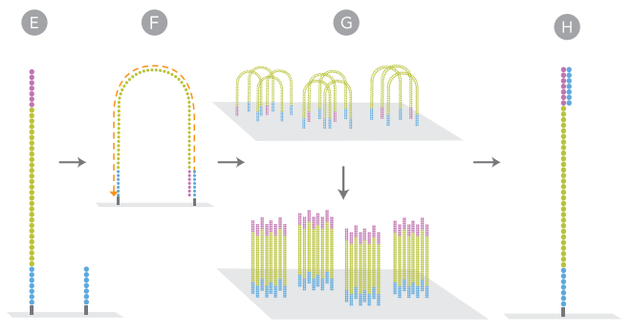
6 hours
3 hours hands-on time



- A Fragment DNA
- B Repair ends
  Add A overhang
- C Ligate adapters
- D Select ligated DNA

2 CLUSTER GENERATION

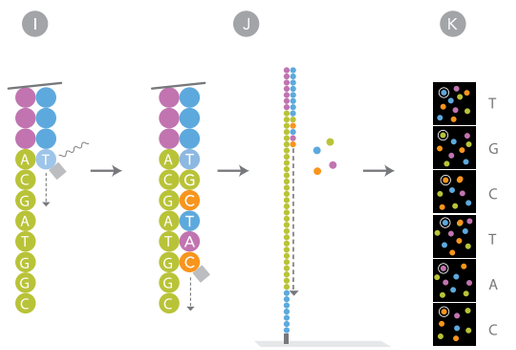
4 hours
< 10 minutes hands-on time
1–96 samples



- E Attach DNA to
  flow cell
- F Perform bridge
  amplification
- G Generate clusters
- H Anneal sequencing
  primer

3 SEQUENCING

1–3 days single-read run
3–9 days paired-end run
30 minutes hands-on time
8 lanes, up to 96 samples
per flow cell (run)



- I Extend first base,
  read, and deblock
- J Repeat step above
  to extend strand
- K Generate base calls

Worldwide coverage.
Personalized service.

Dedicated installation. Ongoing support. Our Field Service Engineers travel to your lab to install and certify each Genome Analyzer, followed by Field Application Scientists who conduct on-site training. This personalized support continues long after your initial training. One call to our Technical Support Group puts you in touch with a team of Ph.D. scientists who are experts on Illumina systems, assays, and software. Our dedicated service and support teams give you peace of mind to focus on that next breakthrough study.

To learn more, visit www.illumina.com/support

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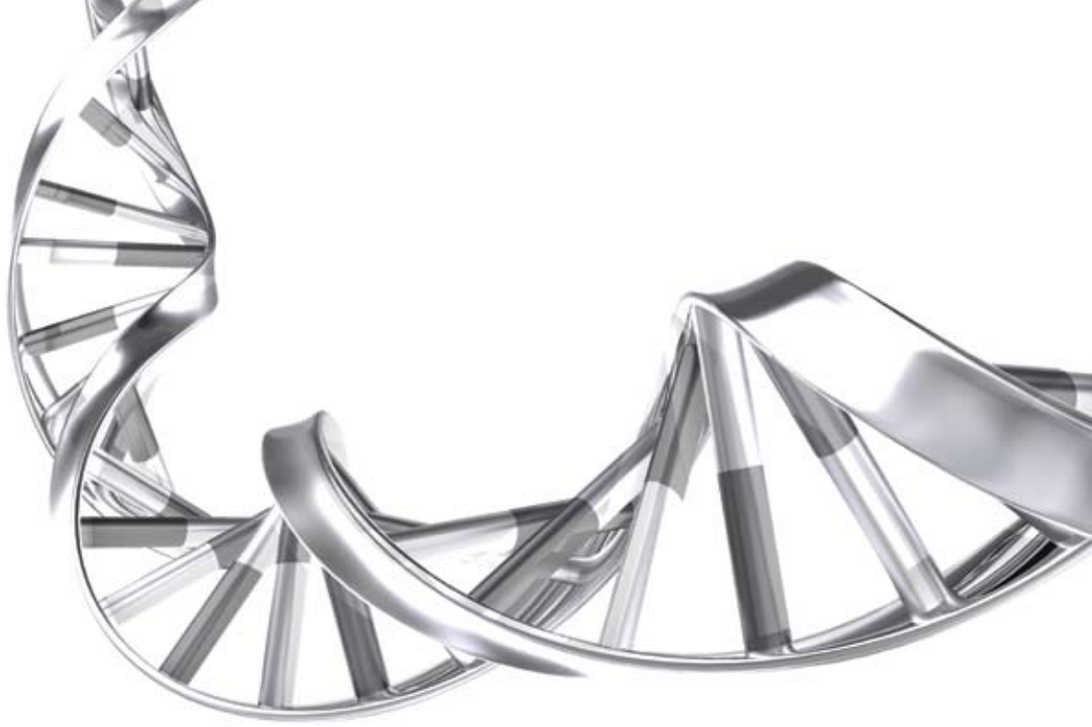

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