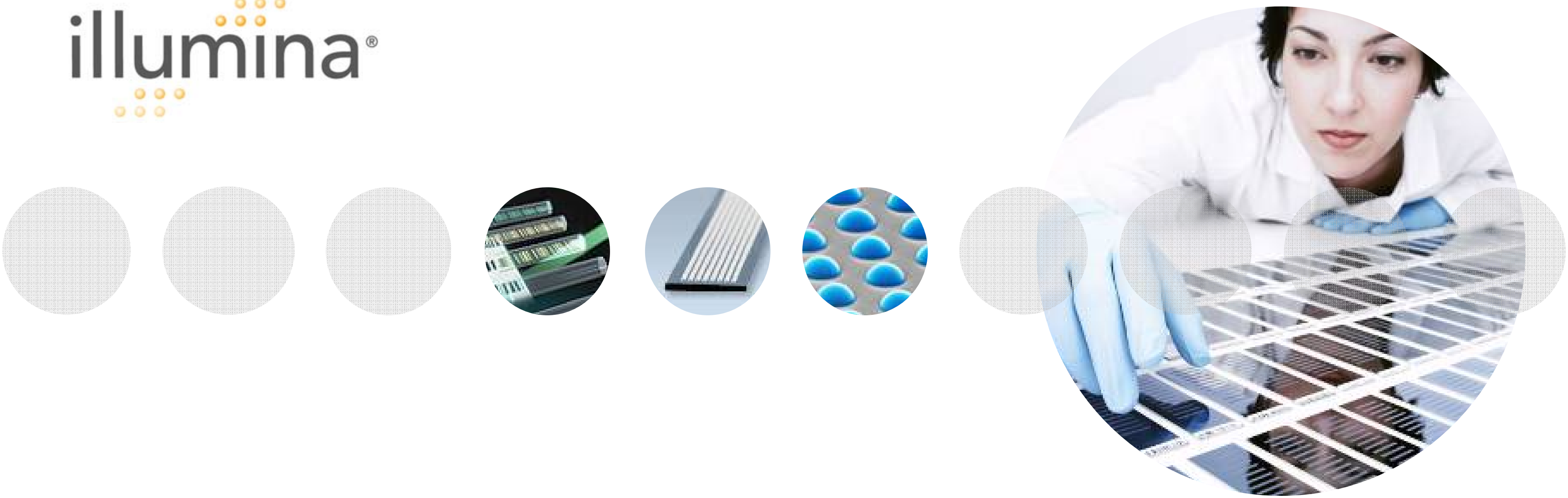
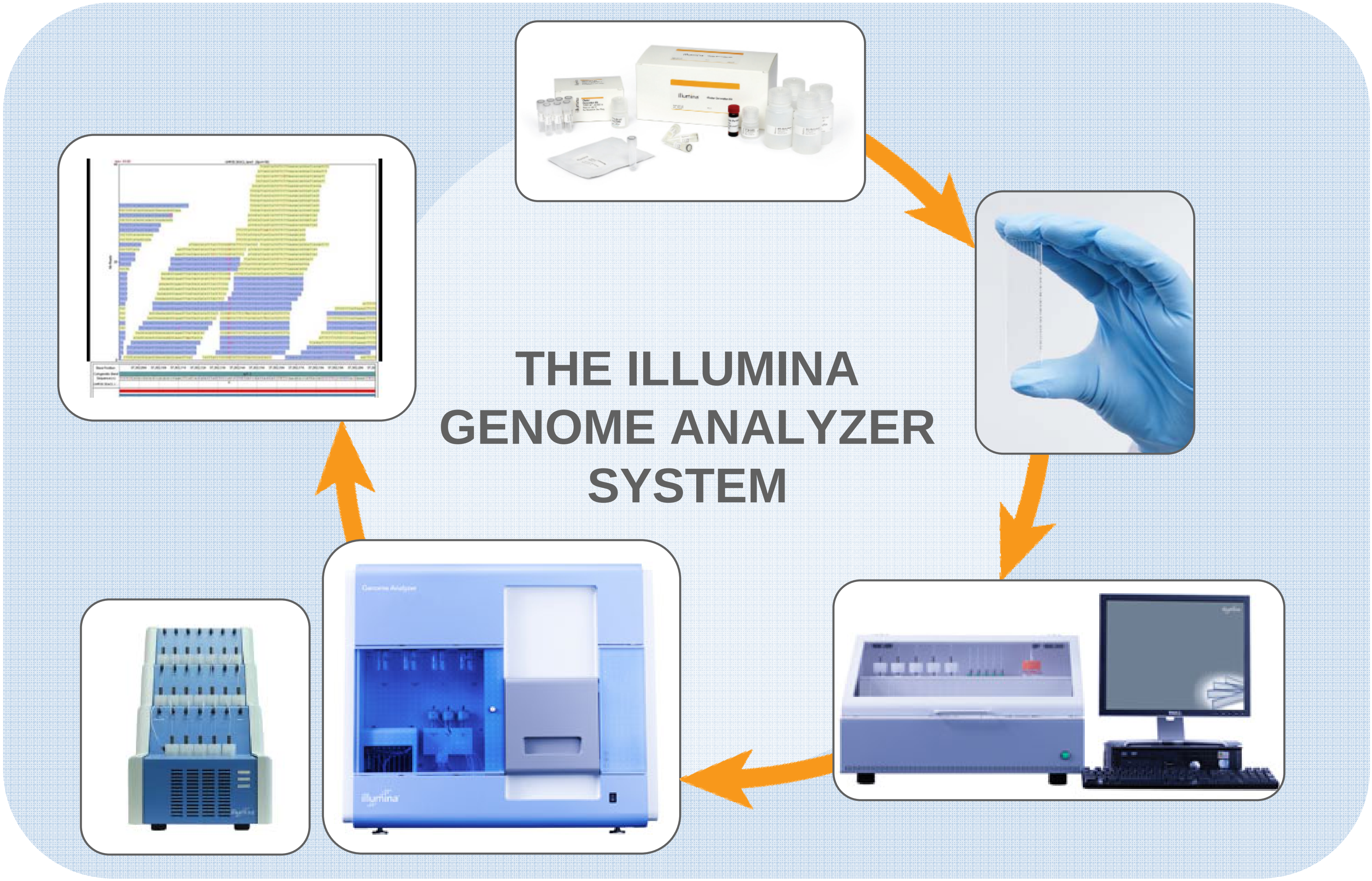


New Genome Analyzer$_{IIx}$ and Software Advancements

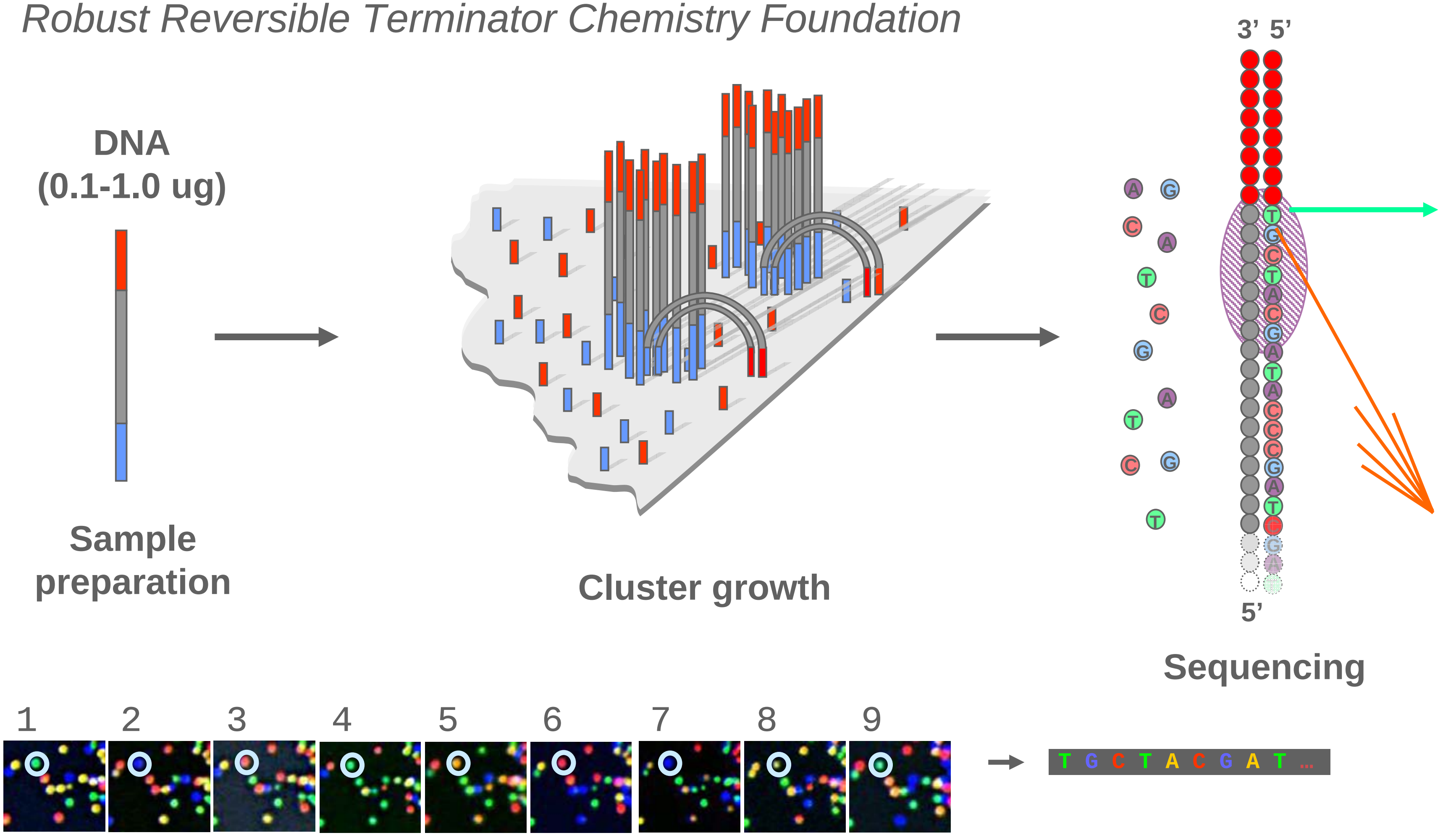
More data, better data, easier-to-use



THE ILLUMINA GENOME ANALYZER SYSTEM

Illumina Sequencing Technology

Robust Reversible Terminator Chemistry Foundation



DNA
(0.1-1.0 ug)

Sample preparation

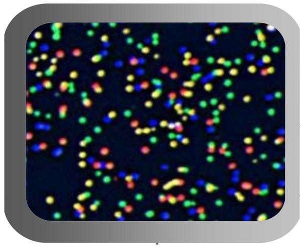
Cluster growth

Sequencing

Image acquisition

Base calling

Broad Range of Customer Demonstrated Applications



Human Genome Resequencing

Bacterial Sequencing
Targeted Resequencing

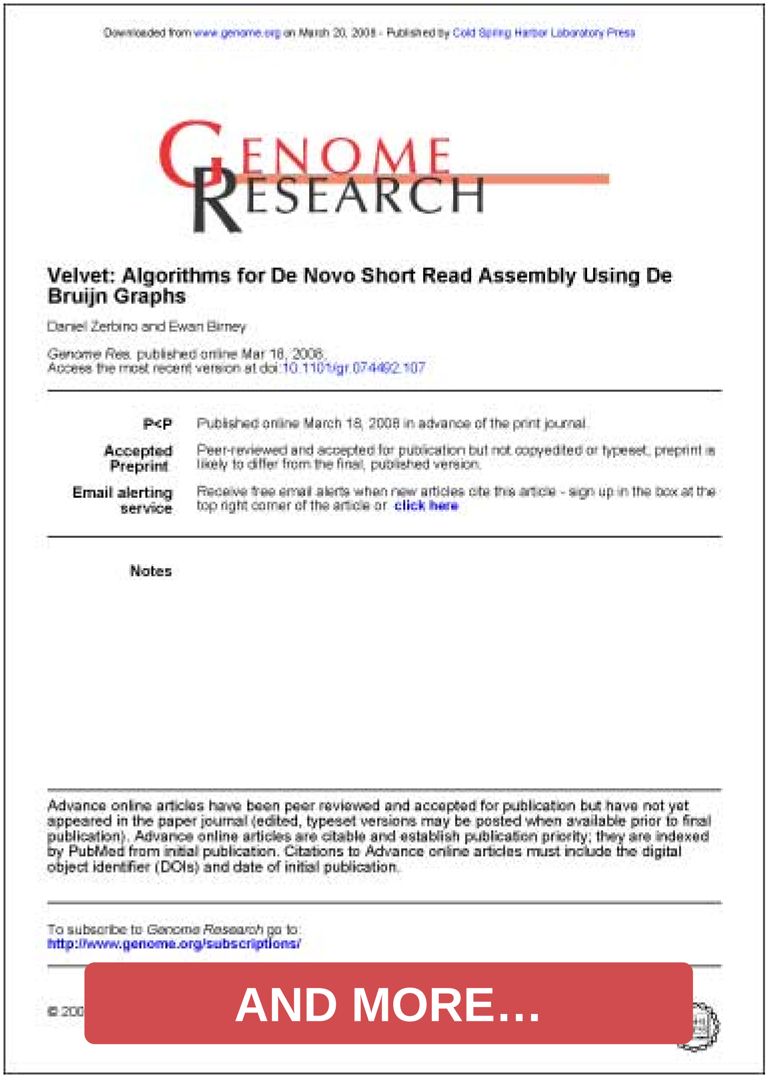
De novo Sequencing
ChIP-Seq
Small RNA Discovery

Structural Variant Detection
mRNA-Seq
DNase I Hypersensitivity
Methylation

Molecular Cytogenetics
AFLP
Ribosome Profiling
CNV
Nucleosome Mapping

Unprecedented Rate of Peer-Reviewed Publications

324 Peer-Reviewed Publications Since 2007 Launch (as of July, 2009)



GENOME RESEARCH

Velvet: Algorithms for De Novo Short Read Assembly Using De Bruijn Graphs

Daniel Zerbino and Ewan Birney

Genome Res. published online Mar 18, 2008;
Access the most recent version at doi:10.1101/gr.074492.107

P<P	Published online March 18, 2008 in advance of the print journal.
Accepted Preprint	Peer-reviewed and accepted for publication but not copyedited or typeset; preprint is likely to differ from the final, published version.
Email alerting service	Receive free email alerts when new articles cite this article - sign up in the box at the top right corner of the article or **click here**

Notes

Advance online articles have been peer reviewed and accepted for publication but have not yet appeared in the paper journal (edited, typeset versions may be posted when available prior to final publication). Advance online articles are citable and establish publication priority; they are indexed by PubMed from initial publication. Citations to Advance online articles must include the digital object identifier (DOIs) and date of initial publication.

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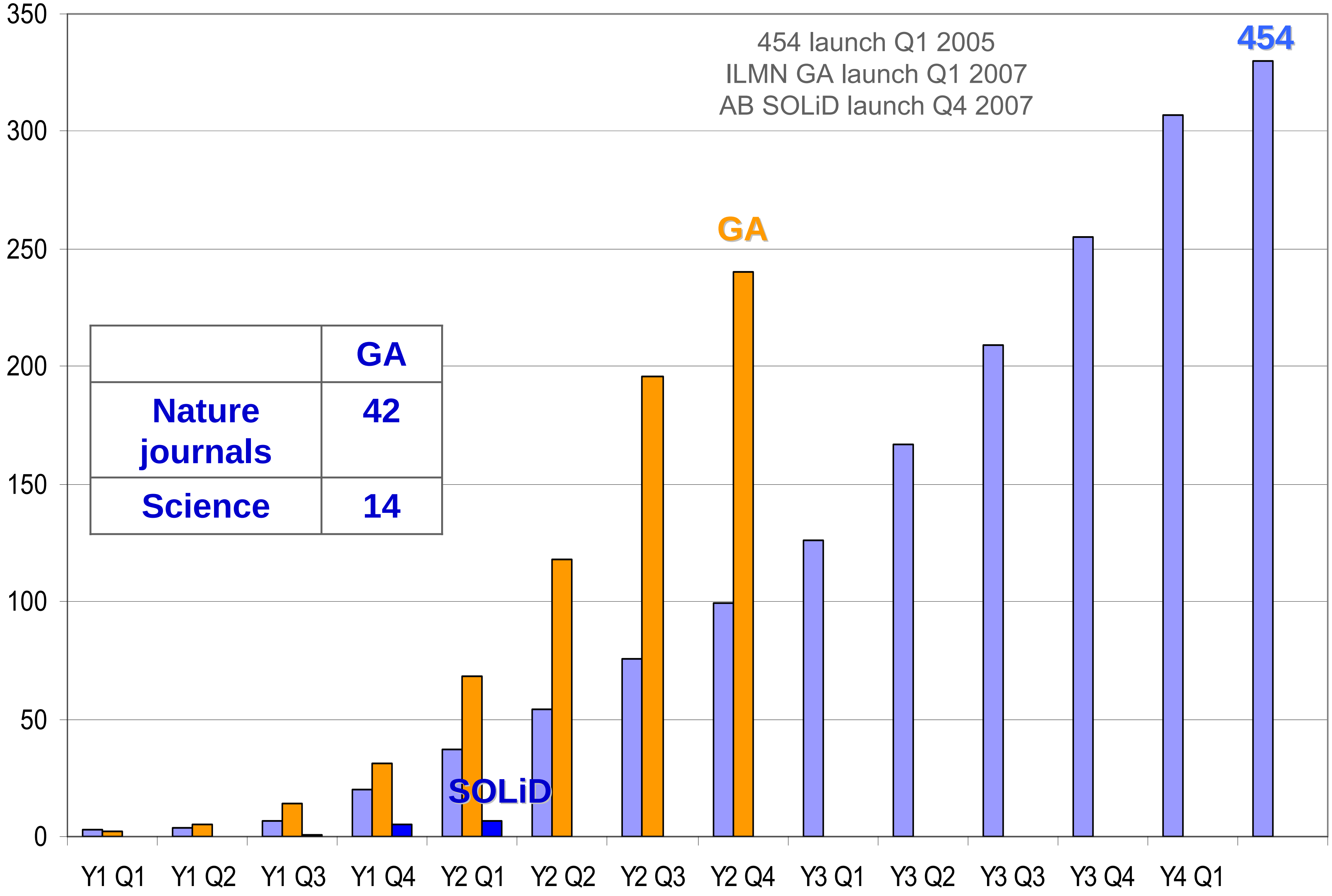
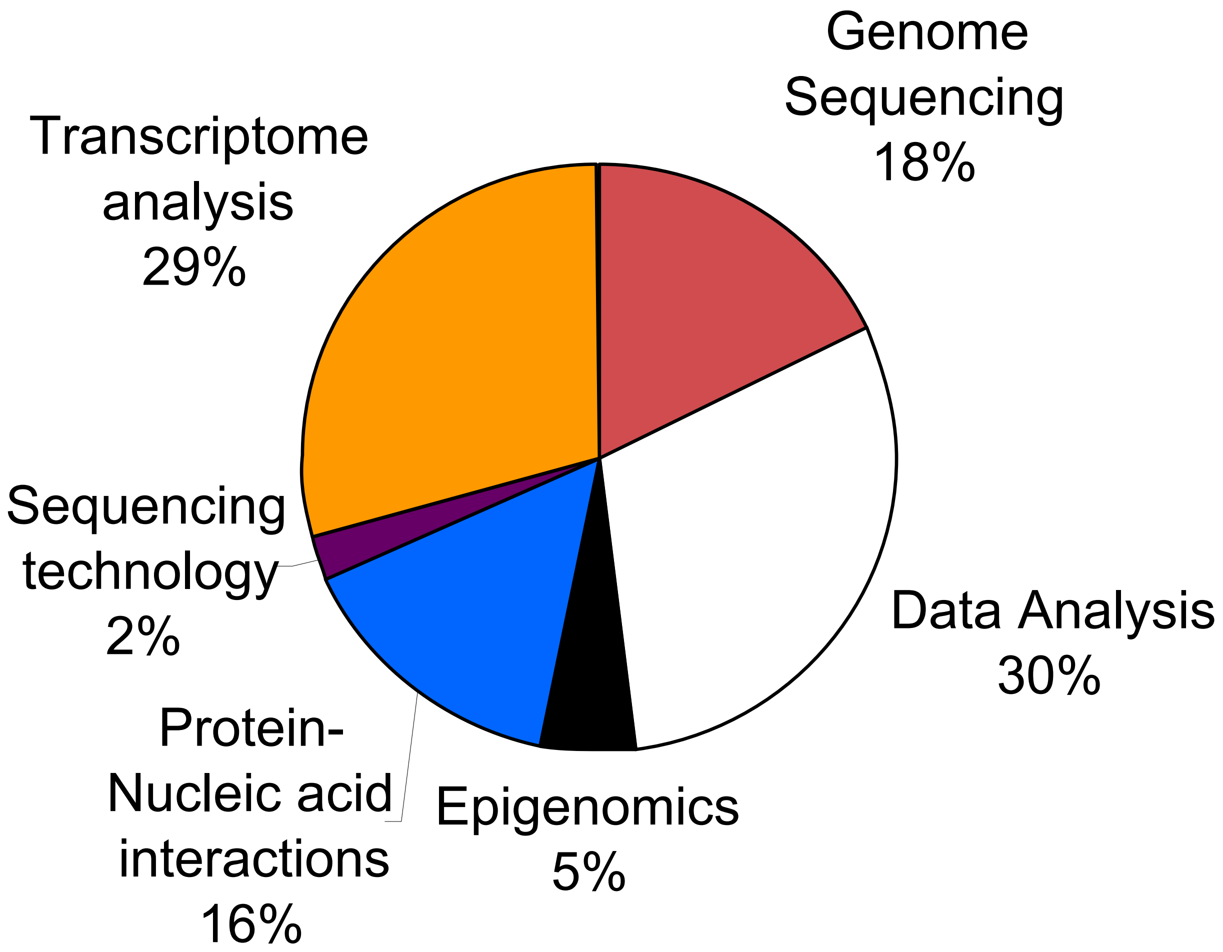
AND MORE…



454 launch Q1 2005
ILMN GA launch Q1 2007
AB SOLiD launch Q4 2007

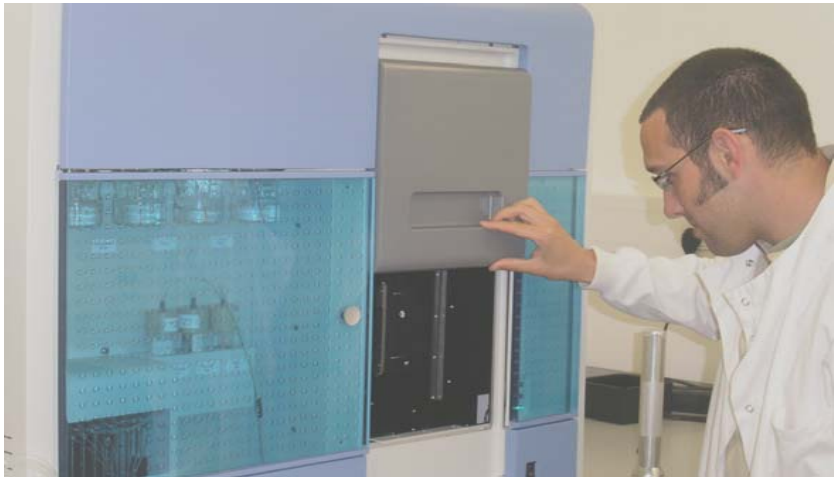
	GA
Nature journals	**42**
Science	**14**

GA Original publications



Illumina Genome Analyzer: a Paradigm Shift

- Rooms of sample prep robots to fragment, clone, grow, preps, sequence, clean-up
- ≈ 100 sequencers
- Dozens lab staff
- 96 lanes x 600 bp → 60,000 bp/run
- 1.2M bases/day/instrument
- $1-2M for 1Gb raw data



- 1 Lab Bench
- 1 Sequencer
- 1 Guy (with sideburns)
- 170 M spots x 150 b → 25 Gb/run
- ~2.5 Gb/day per instrument
- ~$350 - 450 for 1Gb raw data

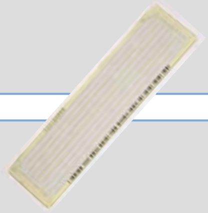
Sequencing Process

1 *Library prep (~ 6 hrs)*

Fragment DNA
↓
Repair ends / Add A overhang
↓
Ligate adapters
↓
Select ligated DNA

2 *Automated Cluster Generation (~ 5 hrs)*

1-96 samples



Hybridize to flow cell
↓
Extend hybridized oligos
↓
Perform bridge amplification

3 *Sequencing (2+ days*)*

1-96 samples

Perform sequencing on forward strand
↓
Re-generate reverse strand
↓
Perform sequencing on reverse strand

* 2 days for 36 cycles

illumina®

Genome Analyzer IIx - Benefits to User

More data, better data, easier-to-use

- New supported read length of 2 x 75bp ✓
- More data and higher quality data ✓
- Real time data processing and base calling on instrument workstation ✓
- Reduced computing infrastructure required ✓
- Easier to use ✓

~150% increase in data output over GA_{II} based on supported read length

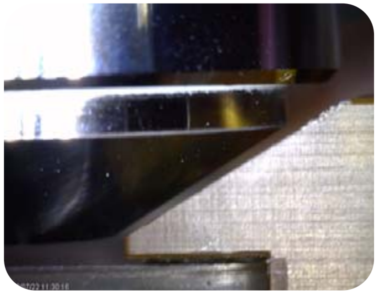
~65% increase in data output based on same read length

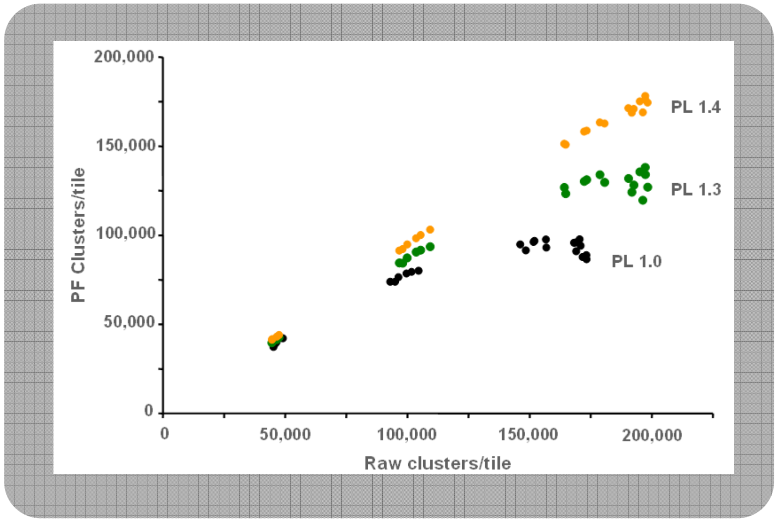
New Genome Analyzer$_{IIx}$ and Software Advancements

More data, reduced computing infrastructure

GA$_{IIx}$ and Upgrade

- Hardware
  - Higher output and ease-of-use for long reads
    - Larger reagent cooler
    - Manifold
- Software
  - Higher output, data quality and ease-of-use
  - Real-time base calling
  - Reduced computing infrastructure
    - Pipeline 1.4
    - System Control Software 2.4



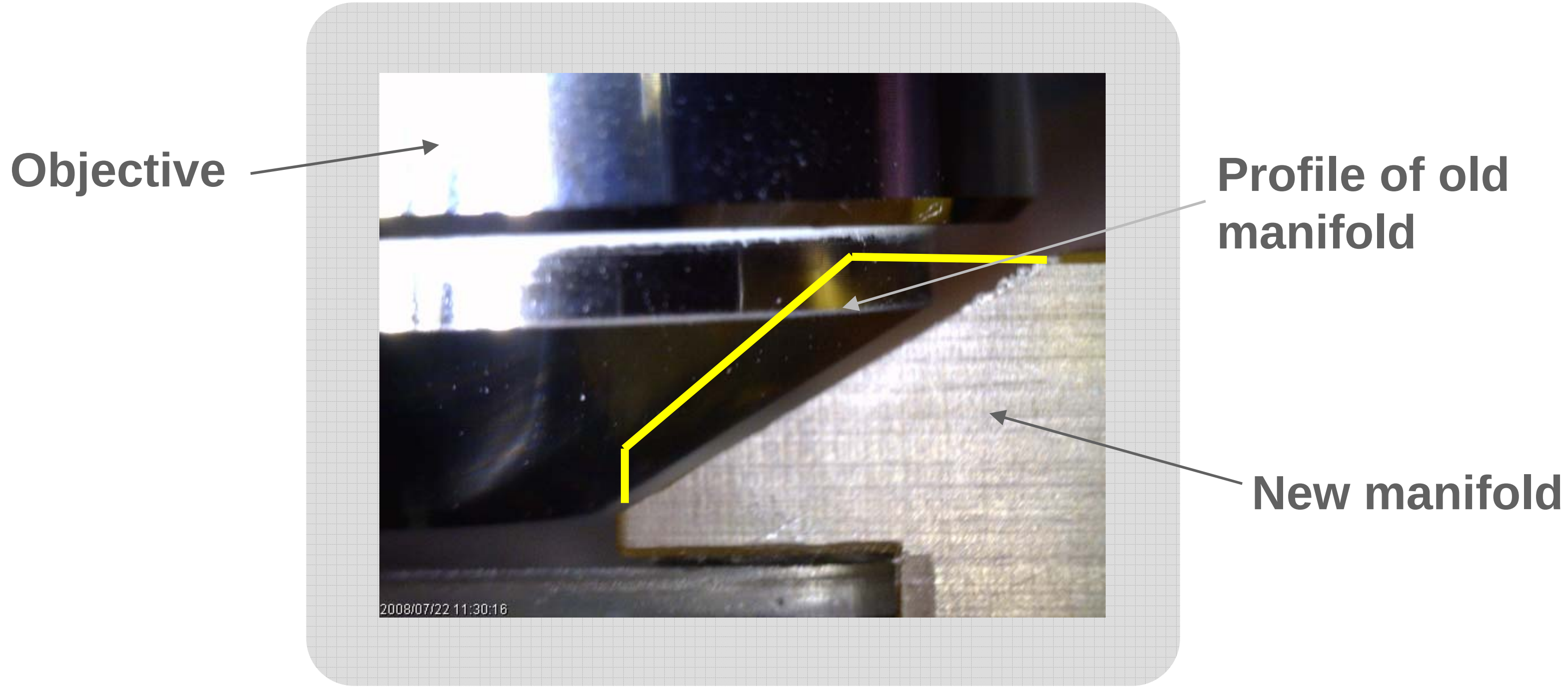


Larger Reagent Cooler

Enables unattended long read sequencing

- Unattended operation of 108 cycles
  - 150 ml tubes hold 3x36 cycle kits
- Maintains pre-cooled reagents @ 4C

New Manifold Increases Yield per Flowcell



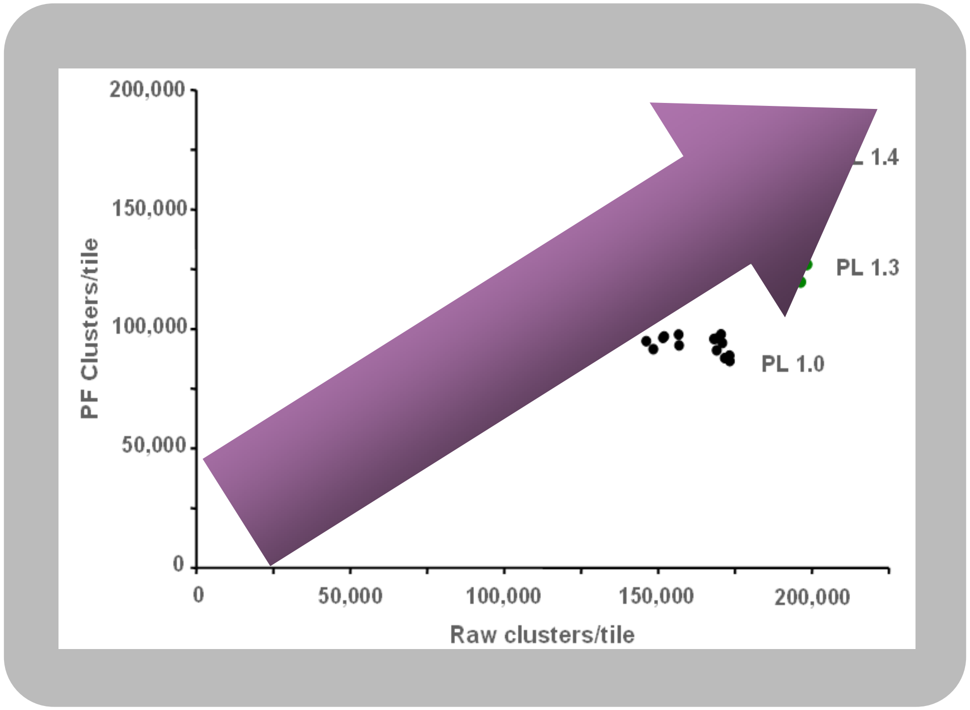
- Objective can travel further along the flowcell
- 20% gain in imaging area

New Software Delivers Up to 40% More Data Per Run

Pipeline 1.4 and SCS 2.4

- Enhanced analysis algorithm increases yield and improves accuracy
  - More clusters pass filter
  - Improved cluster delineation
    - Lower error rates
  - Load denser flowcells!

More clusters passing filter

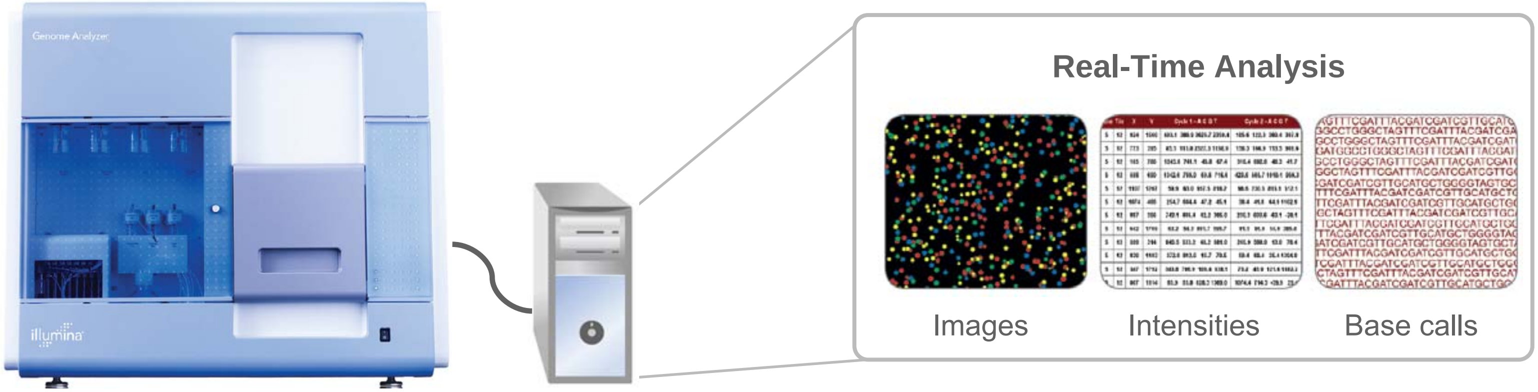


Increased output with reduced computing infrastructure

More gigabases of data for fewer gigabytes of computing power!

System Control Software v2.4

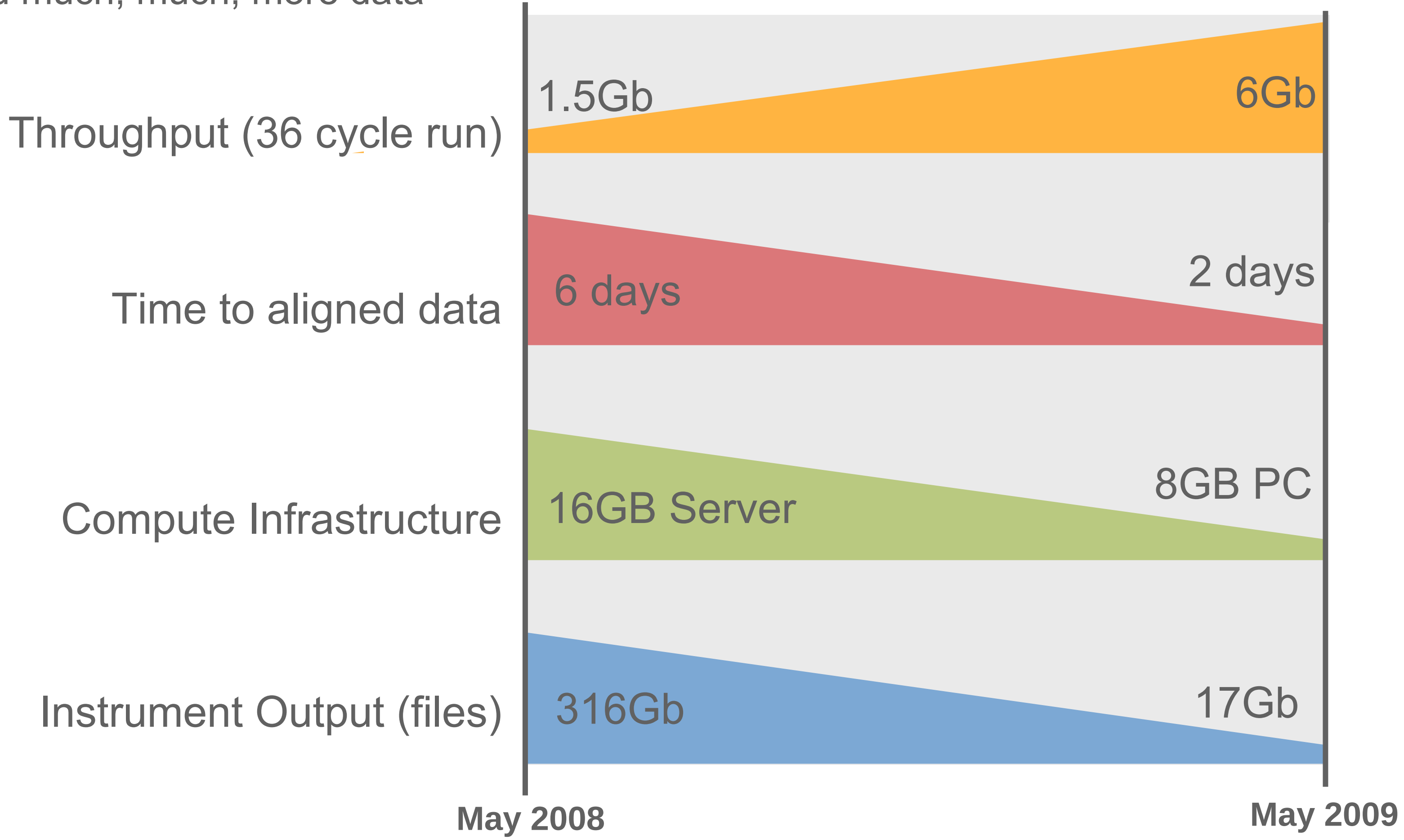
- Includes new Real Time Analysis (RTA) feature
- Real time base calling and image extraction on instrument computer
- Shorter time to results
  - Performed simultaneously with sequencing
  - Eliminates need to transfer images and intensities across network
  - Base calls and quality scores within hours of end of run



Reversing the Trend

Simplified computing, Smaller storage needs, Faster analysis

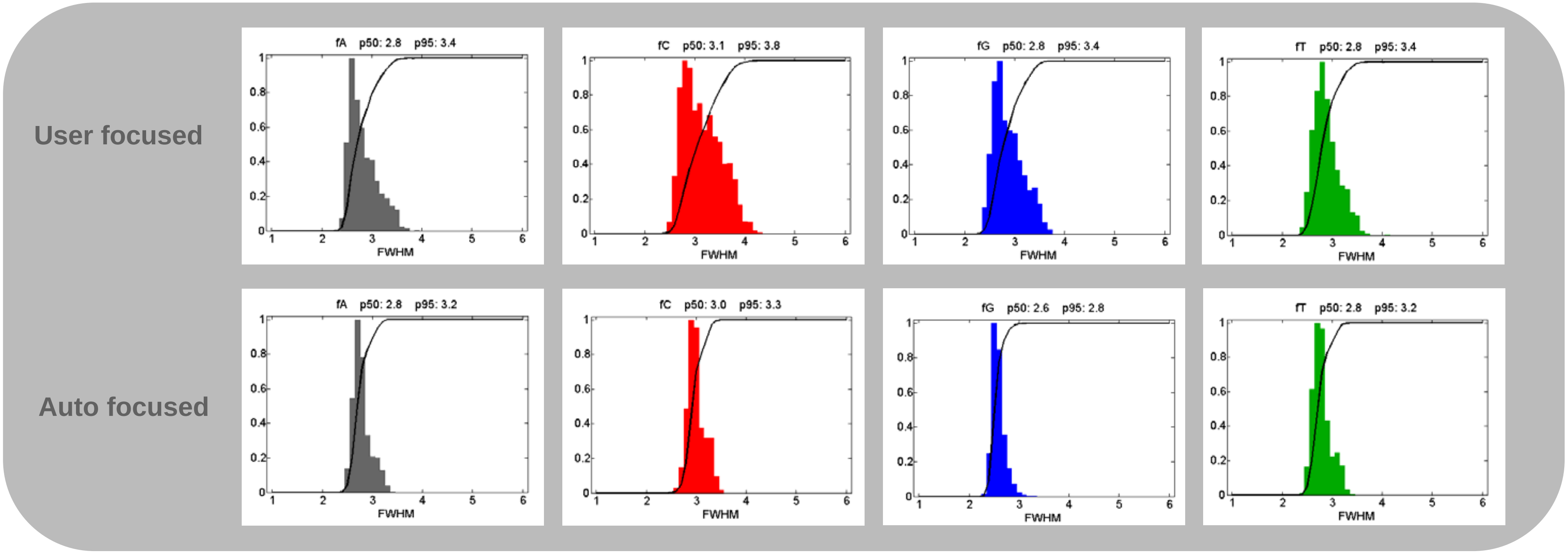
…and much, much, more data



New Integrated focal assist

Easier to use, reduces user error

- Superior performance over manual focus
- Results in less variability in focus quality
- Maximizes number of successful runs



Genome Analyzer$_{IIx}$ Performance Specifications

*65% increase in data output**

- 20-25 GB per run
- 2-2.5 GB per day
- 138-168M reads
- Run Time:
  - 2.5 day 35 bp run
  - 6.5 day 2 x 50 bp run
- Supported Read Length: 75bp
- Raw Accuracy: ≥ 98.5% (2x75)

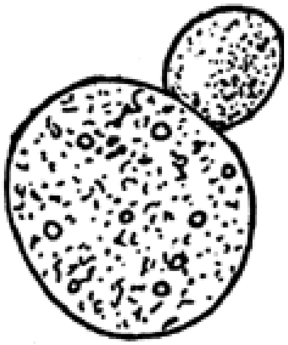
*vs GAII w/PL 1.3 (2x75), 150% increase based on supported read length.

What can you do with just *one lane* of GA data?

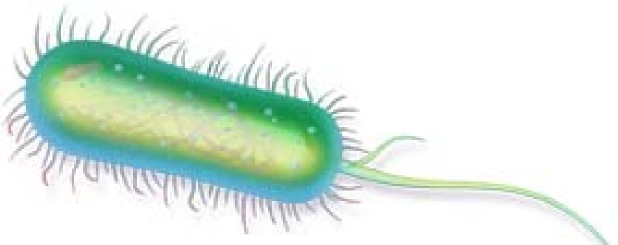
1X Human Genome

30X Arabidopsis

25X Drosophila

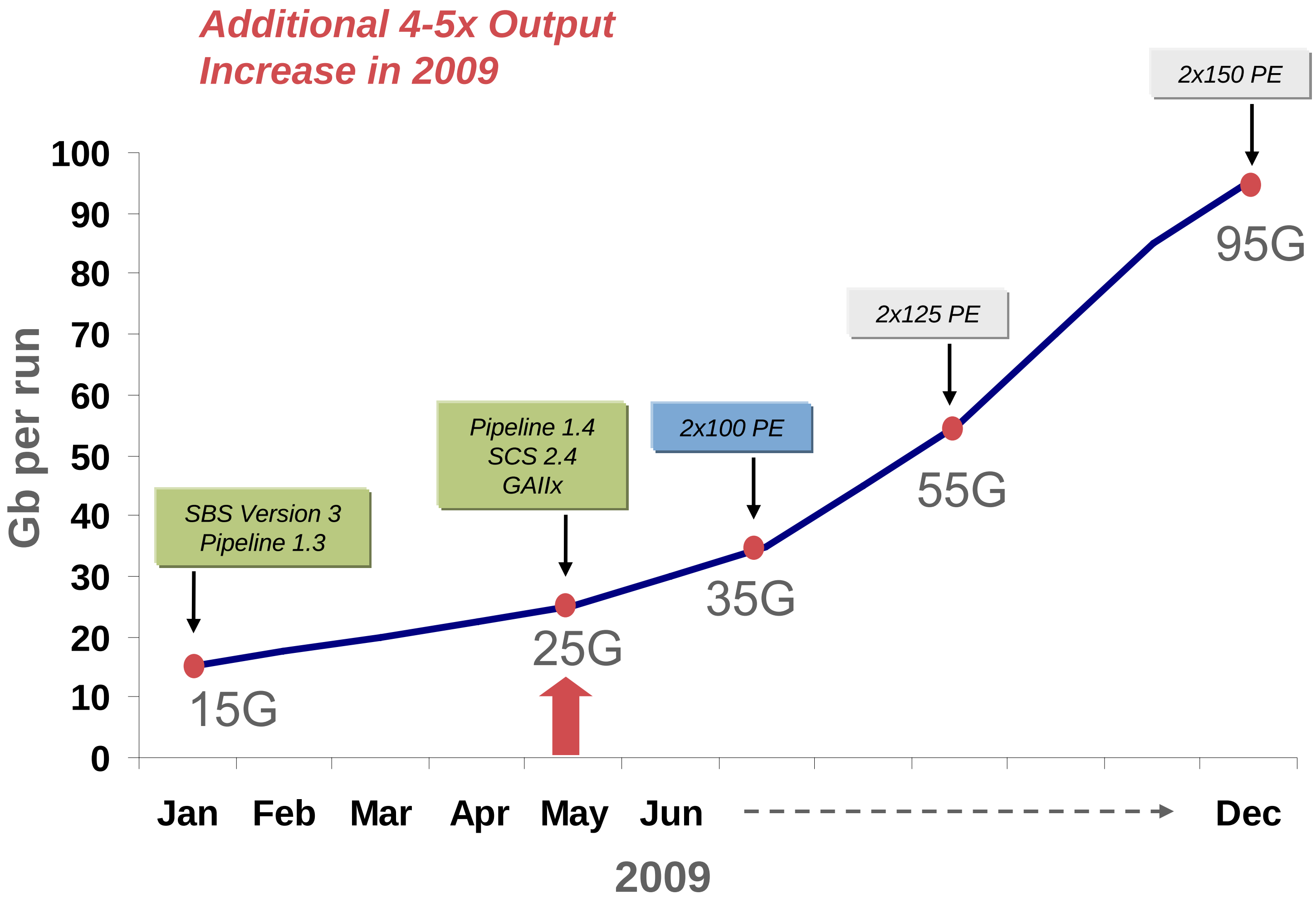


200X Yeast Genome



650X *E. coli*

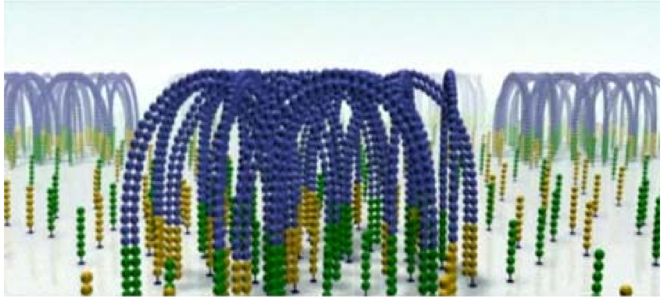
Delivering on Roadmap Milestones



Reagent enhancements – soon to come!

Longer reads, better data, faster

- New Cluster Generation Kit (v4)
  - High fidelity enzyme



- New SBS Kit (v4)
  - Enables 2 x 100 bp reads - supported
  - Faster sequencing polymerase
  - Reduces time per cycle
  - Higher output per day