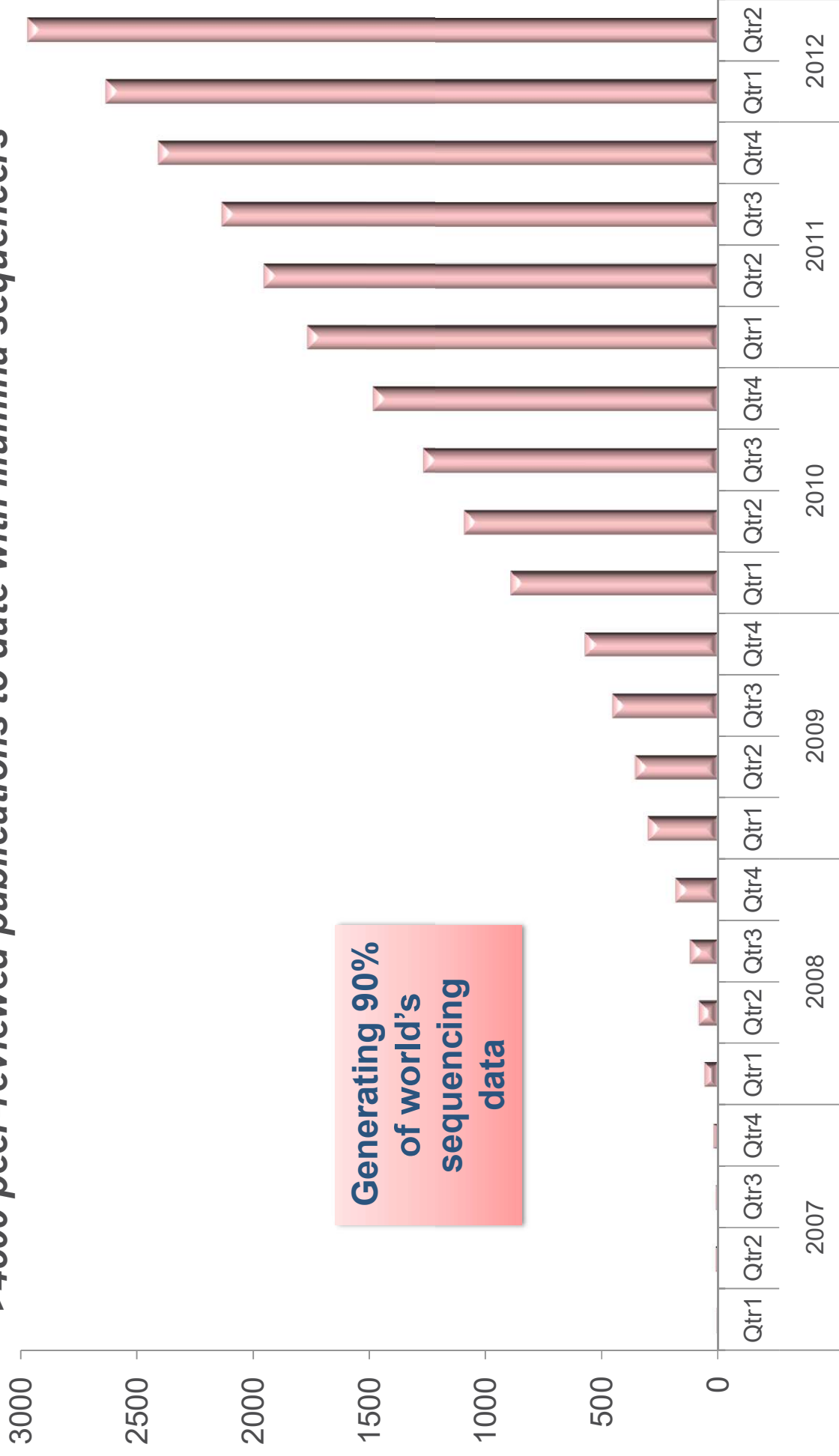
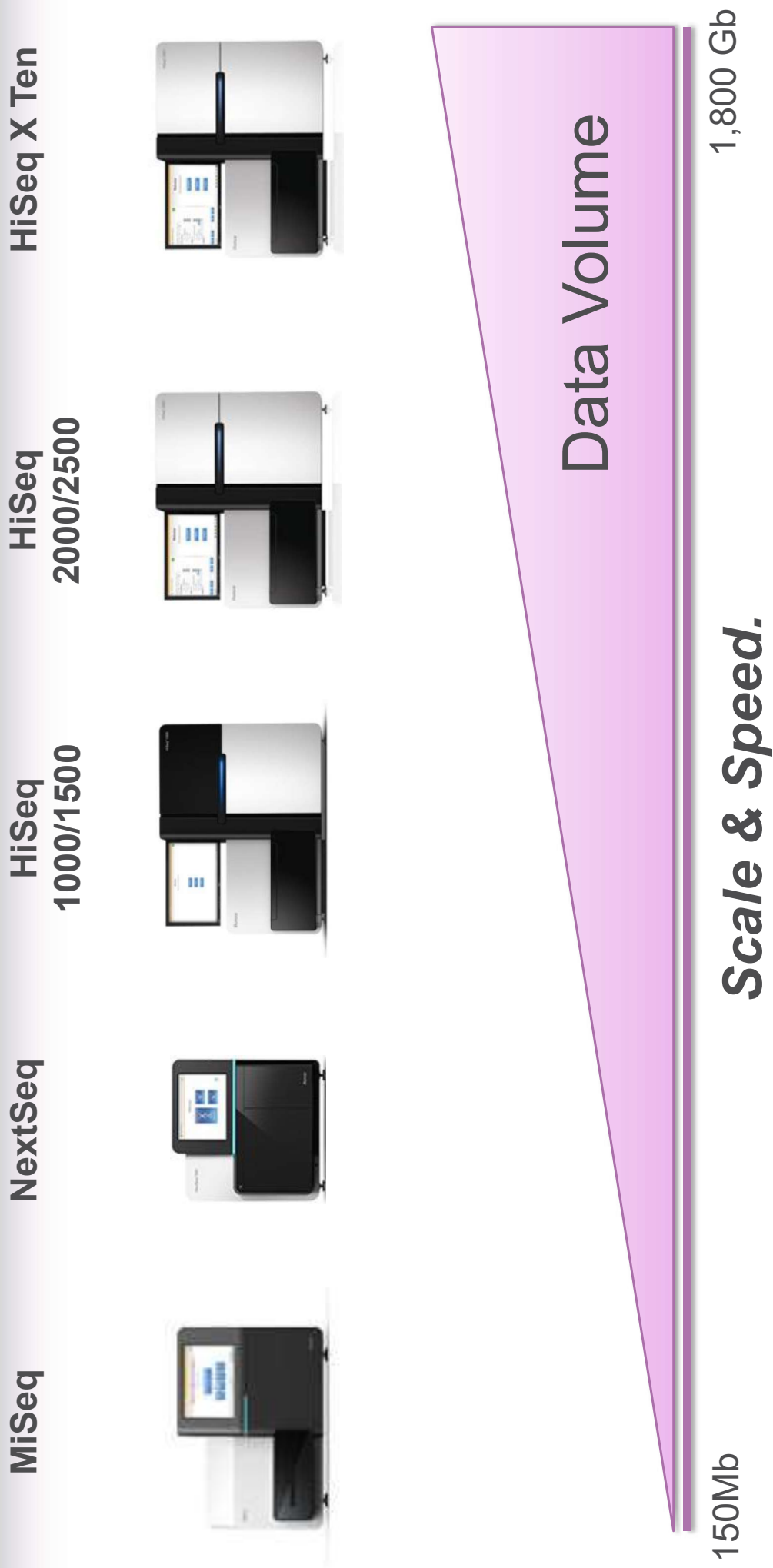


Fastest Publication Rate

>4500 peer-reviewed publications to date with Illumina sequencers



Illumina Sequencing Instruments

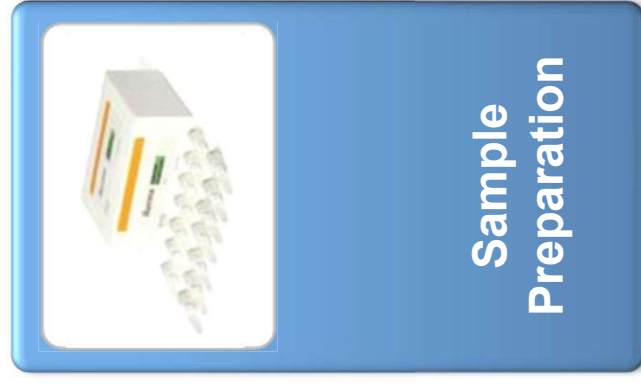


Illumina Sequencing Workflow

How stuff works...



It's all in the workflow!



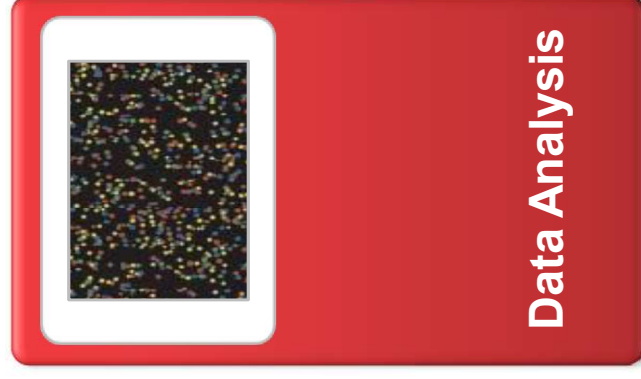
**Sample
Preparation**



**Cluster
Generation**



Sequencing

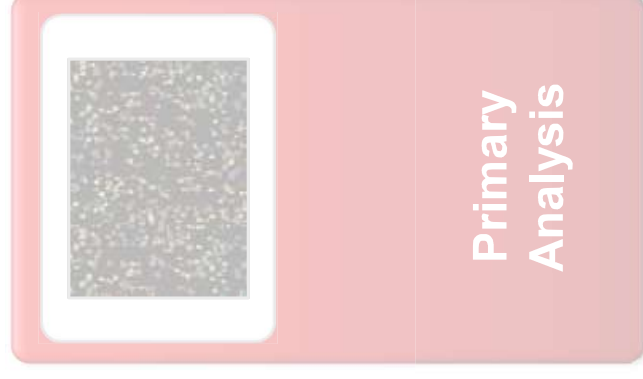
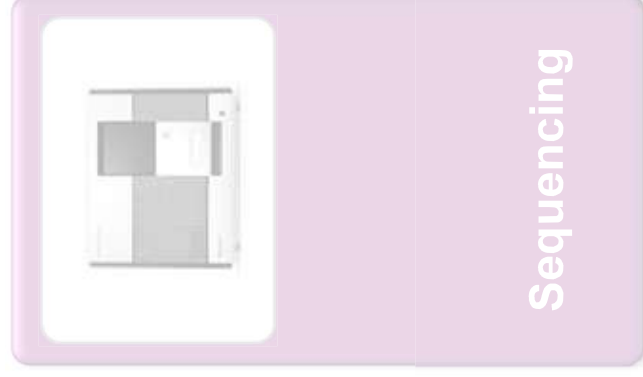
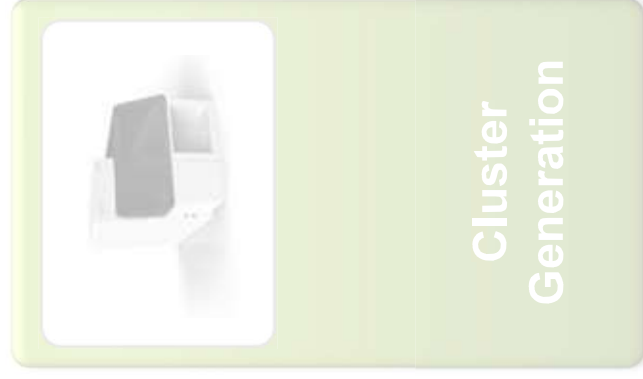
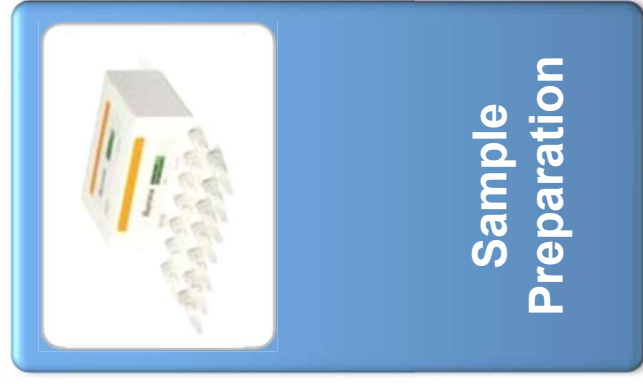


Data Analysis

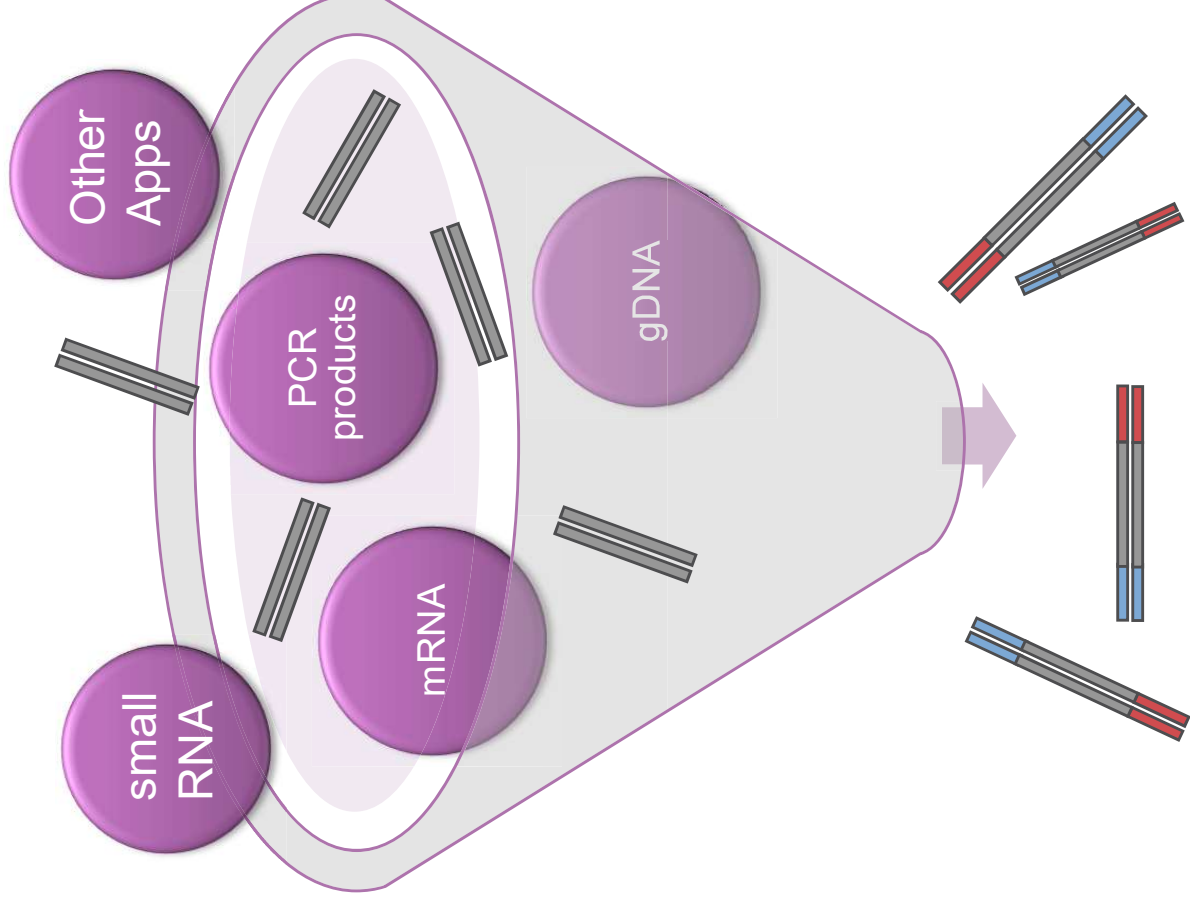


“The simplest, fastest, and most automated workflow.”

Sequencing Workflow: Sample Preparation



Library Preparation

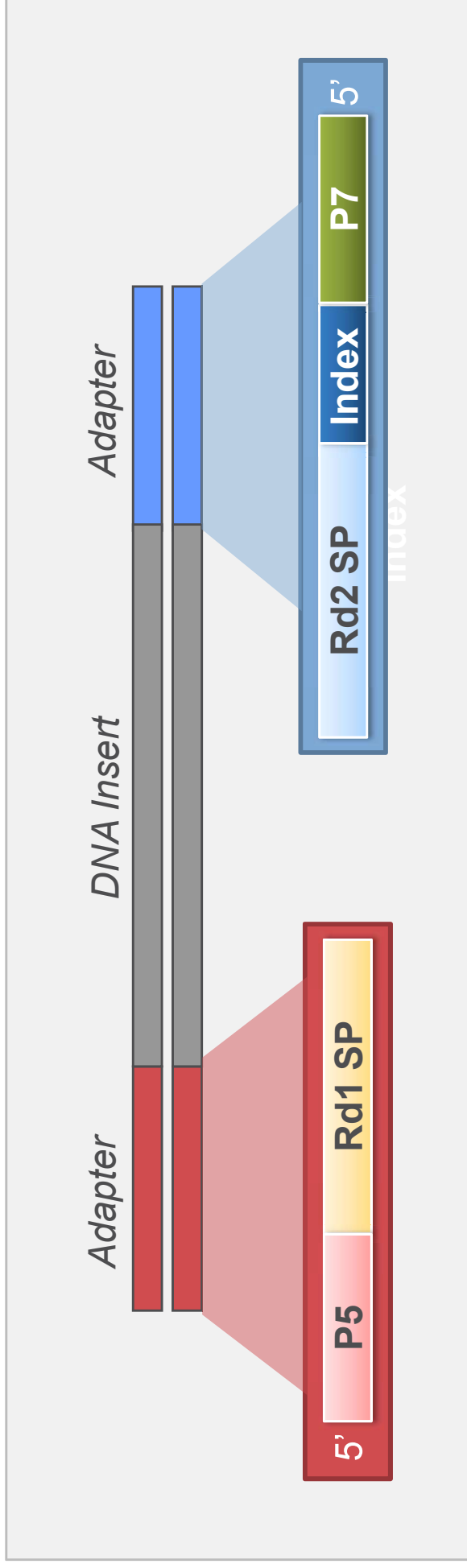


Library Preparation

Ligate adapters on both ends of fragmented nucleic acid

Library Preparation: Anatomy of Illumina Library

- ▶ Library – DNA insert plus full adapter
- ▶ Read 1 Sequencing Primer (Rd1 SP)
- ▶ Read 2 Sequencing Primer (Rd2 SP)

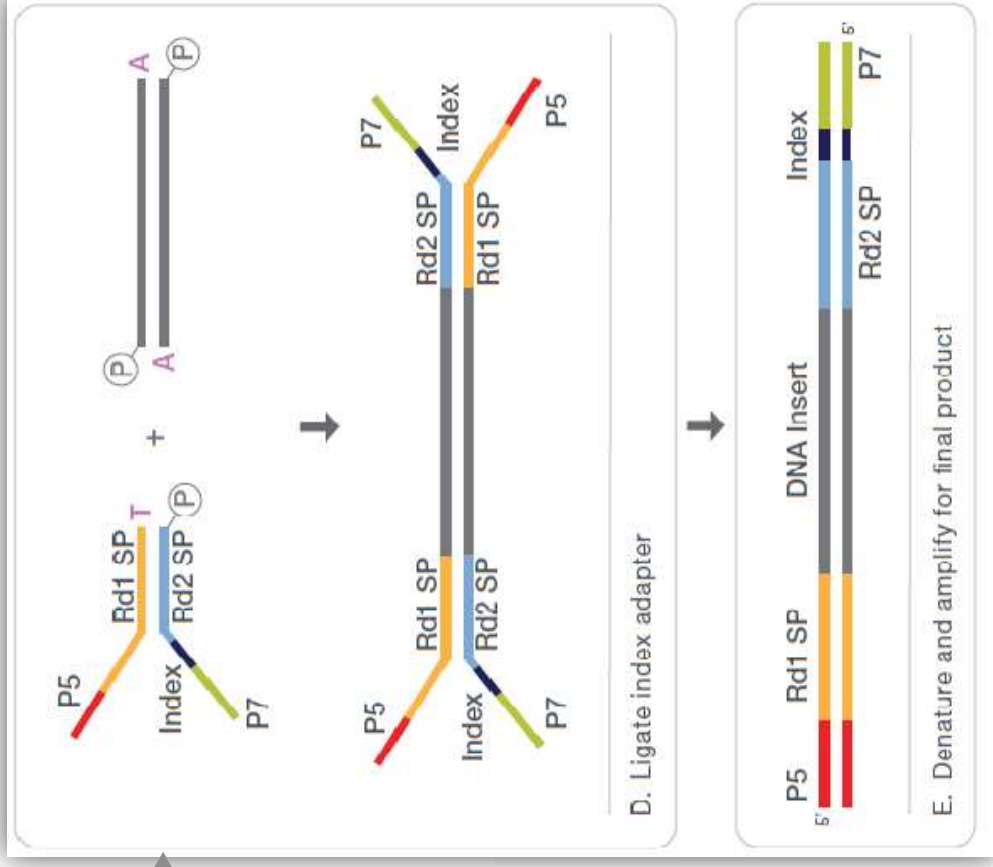
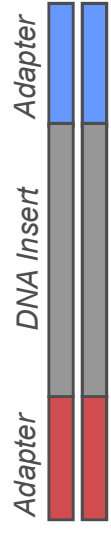
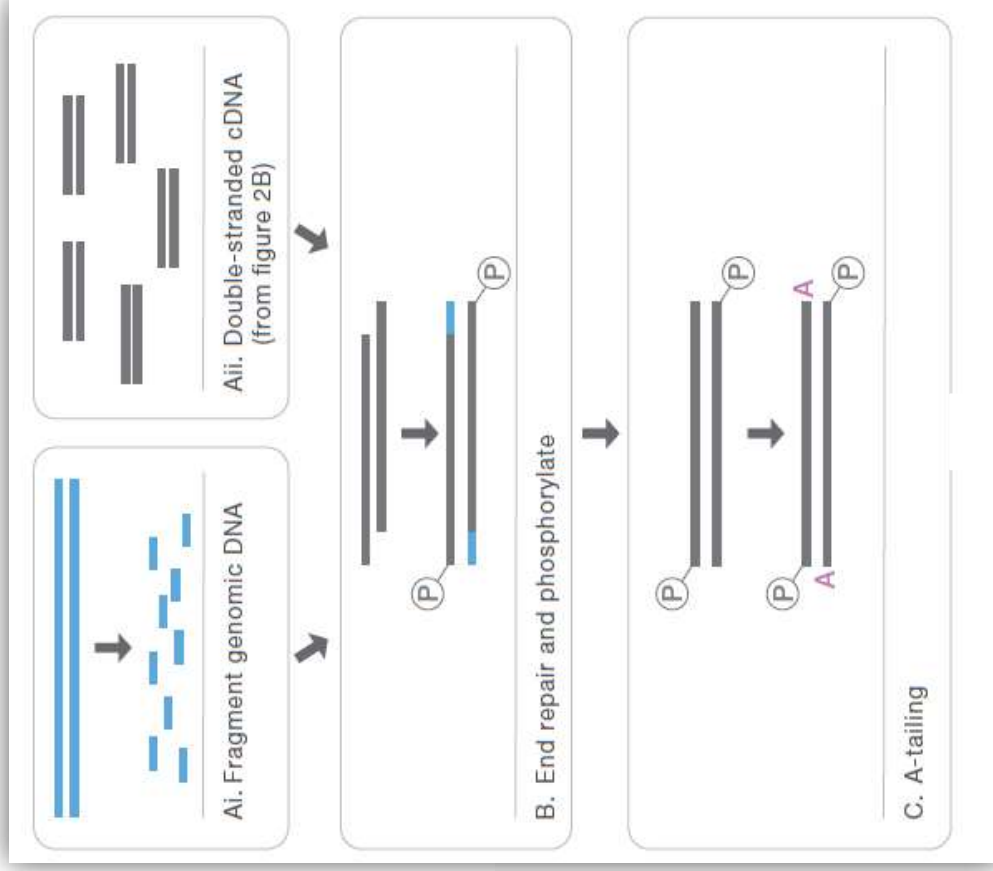


TruSeq Library Prep Kits for RNA & DNA

Simple, scalable, cost-effective

DNA

RNA

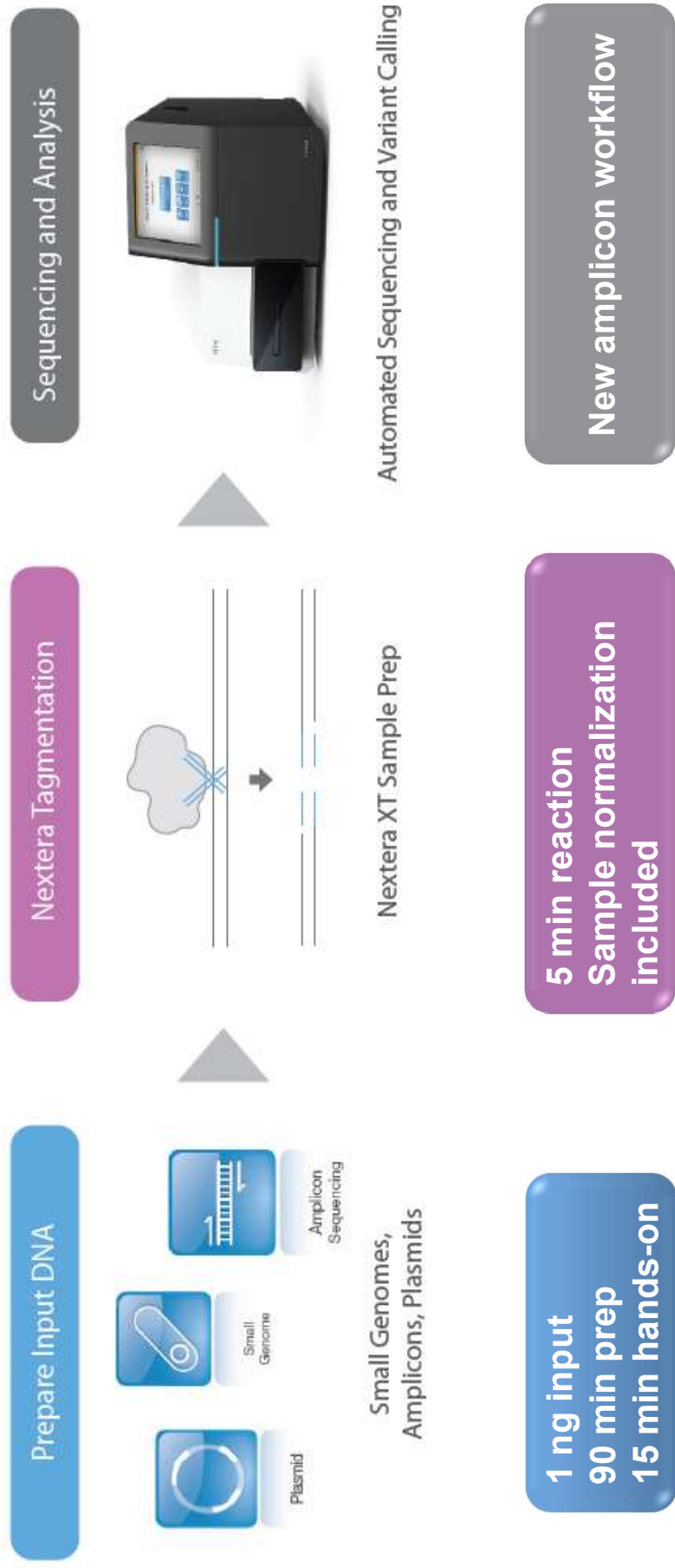


Nextera XT Library Prep

Complete DNA to data in only 8 hr with MiSeq

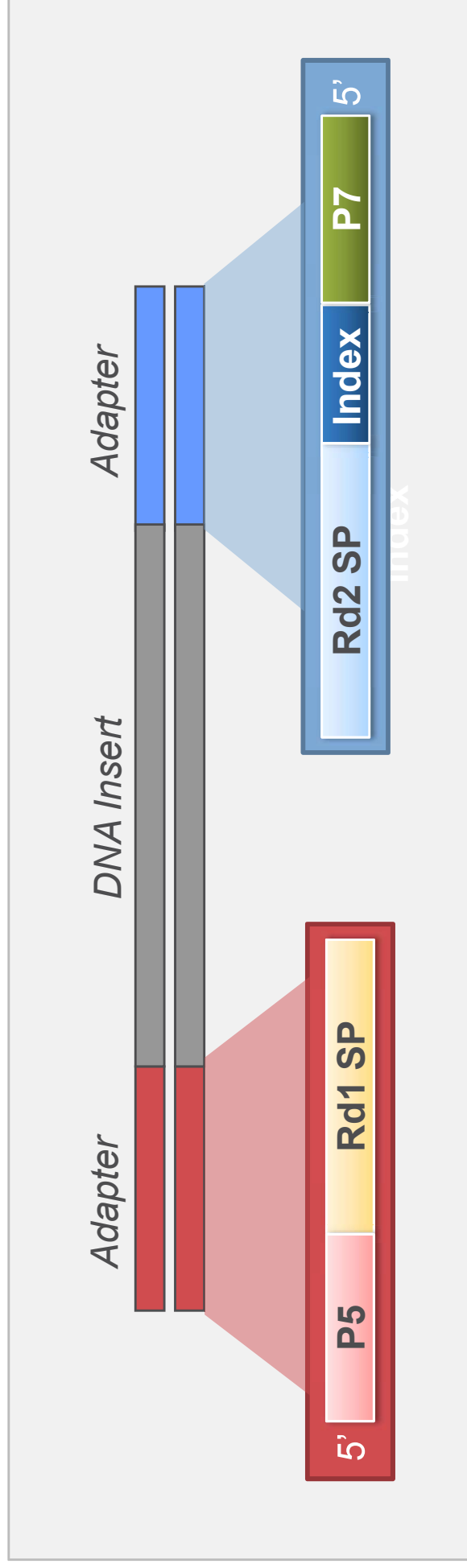
XTra easy. XTremely fast.

Introducing **Nextera XT** DNA Sample Preparation Kit. Specially designed for:



Library Preparation: Anatomy of Illumina Library

- ▶ Library – DNA insert plus full adapter
- ▶ Read 1 Sequencing Primer (Rd1 SP)
- ▶ Read 2 Sequencing Primer (Rd2 SP)



Sequencing Workflow: Cluster Generation




Sample Preparation

This step is represented by a blue rounded rectangle containing an image of a white box and a blister pack of pills.



Cluster Generation

This step is represented by a green rounded rectangle containing an image of a white sequencing instrument.



Sequencing

This step is represented by a purple rounded rectangle containing an image of a sequencing instrument.



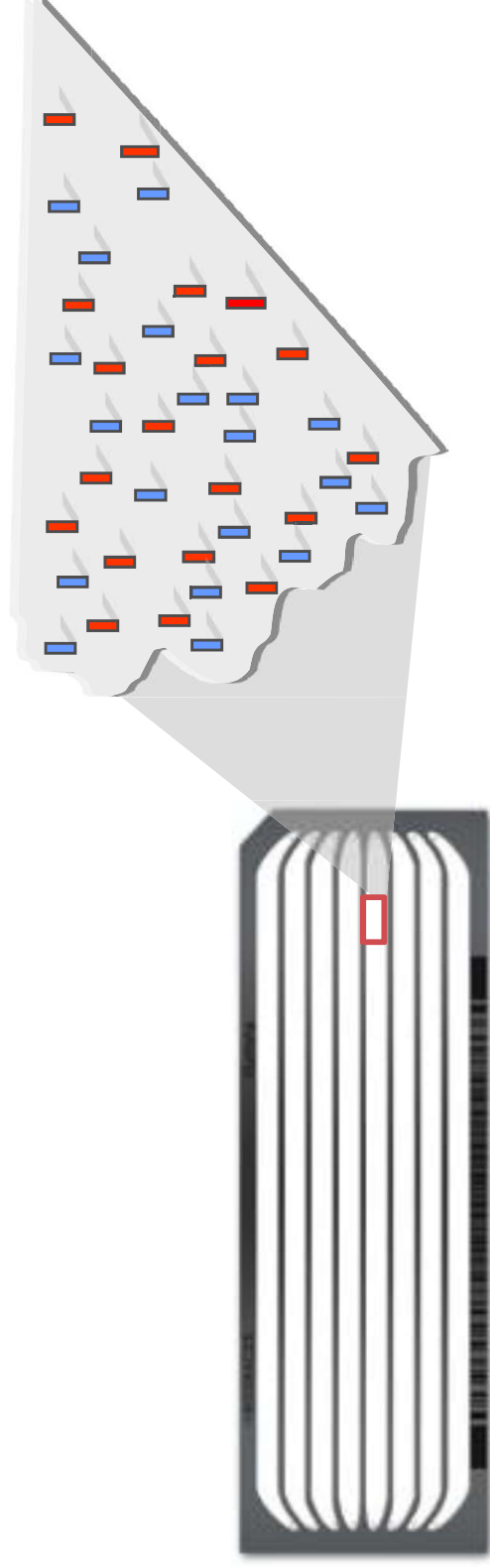
Primary Analysis

This step is represented by a red rounded rectangle containing an image of a microarray or sequencing data visualization.



Introducing the Flow Cell

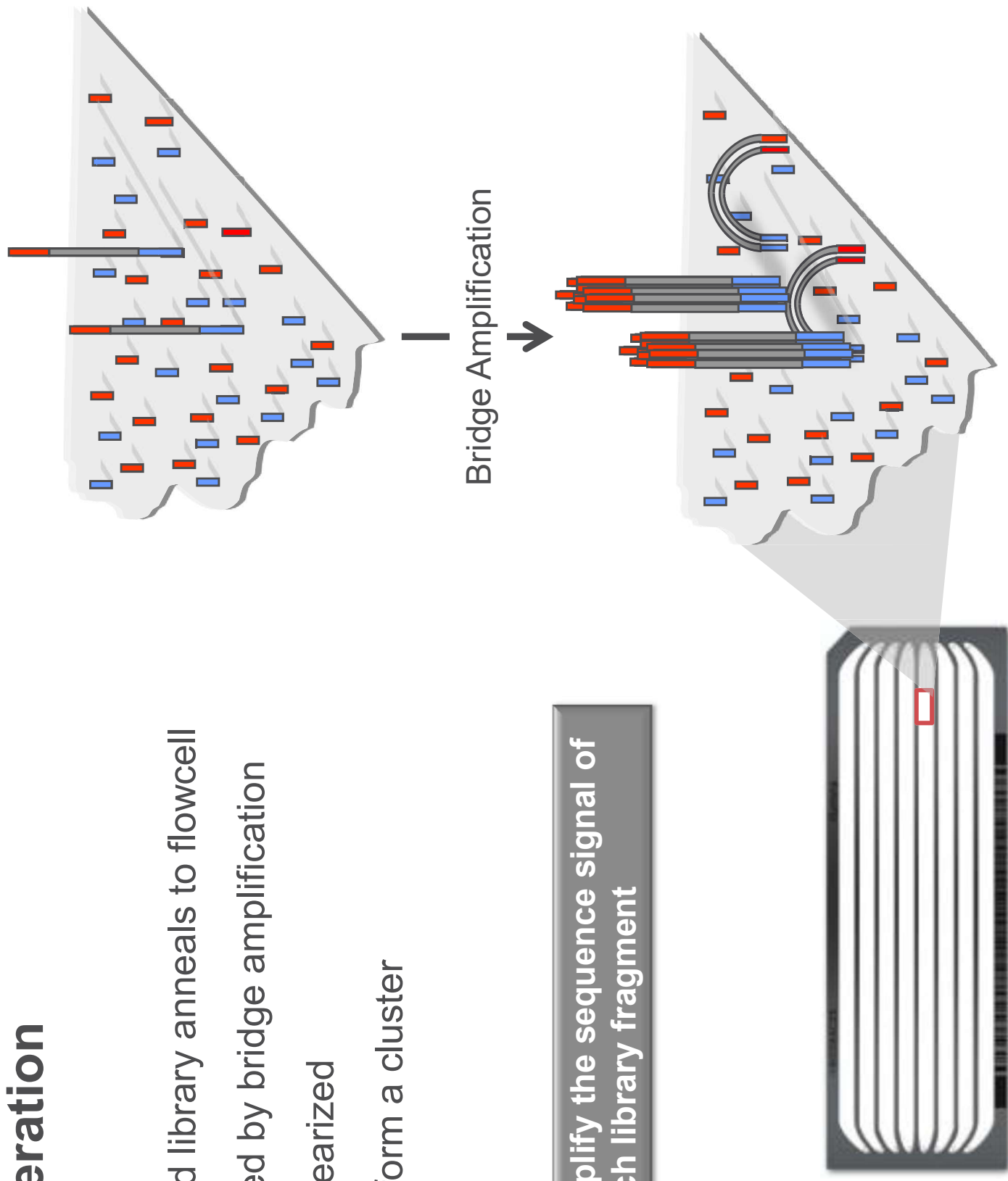
- ▶ The flow cell is covered by an oligo lawn; sequences complementary to the library adapters
- ▶ Reagents flow through to generate clusters and sequence the library



Cluster Generation

1. Single stranded library anneals to flowcell
2. Library is copied by bridge amplification
3. Strands are linearized
4. ~1000 copies form a cluster

Clusters amplify the sequence signal of each library fragment



Sequencing Workflow: Sequencing



Sample Preparation

This step is represented by a blue rounded rectangle. On the left, there is an image of a white box and a blister pack containing several white capsules. On the right, the text "Sample Preparation" is written in white.



Cluster Generation

This step is represented by a light green rounded rectangle. On the left, there is an image of a white laboratory instrument with a grey tray. On the right, the text "Cluster Generation" is written in white.



Sequencing

This step is represented by a purple rounded rectangle. On the left, there is an image of a black and white laboratory instrument with a monitor displaying data. On the right, the text "Sequencing" is written in white.

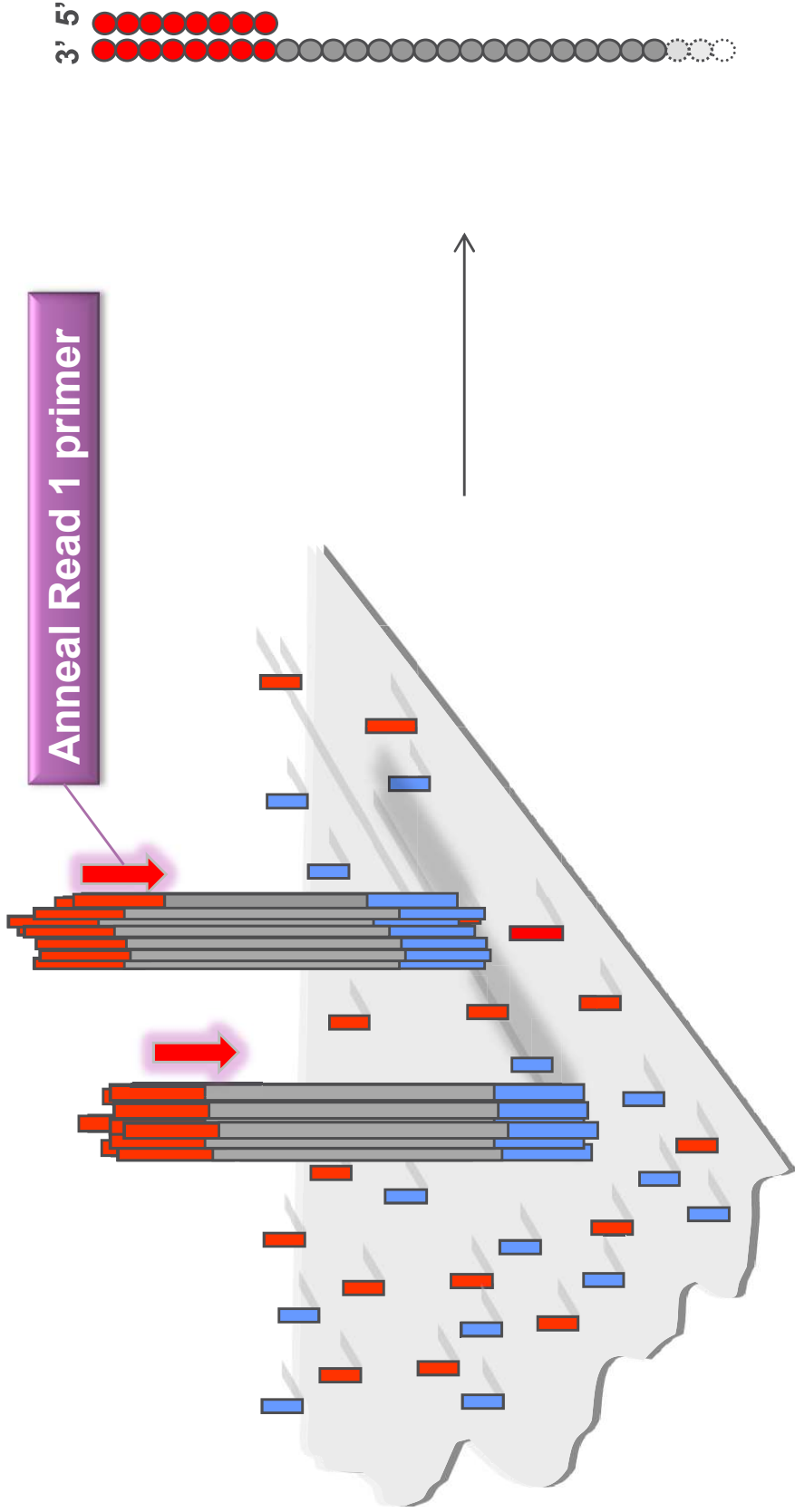


Primary Analysis

This step is represented by a red rounded rectangle. On the left, there is an image of a white microarray slide with a grid of small spots. On the right, the text "Primary Analysis" is written in white.



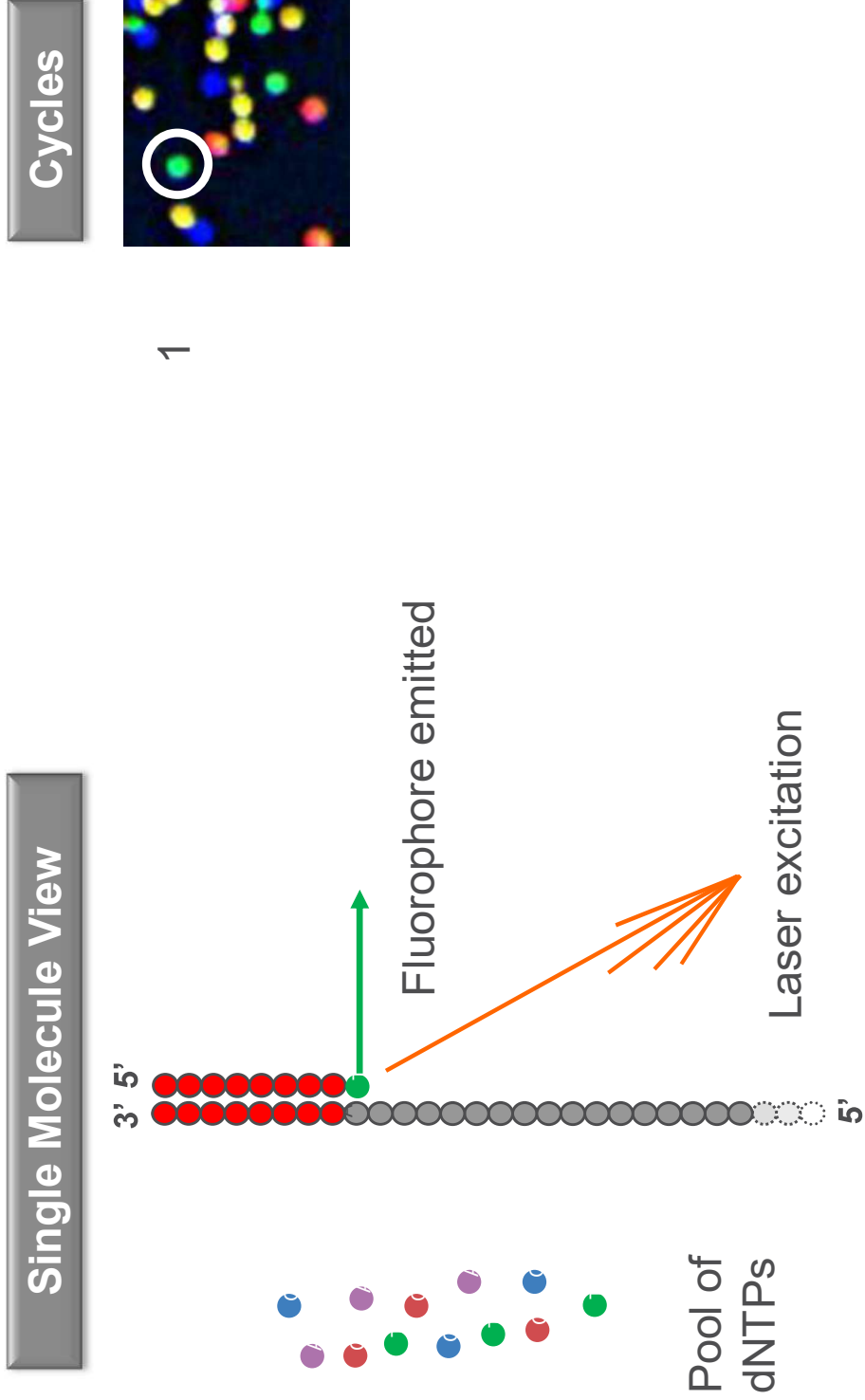
Illumina Sequencing By Synthesis



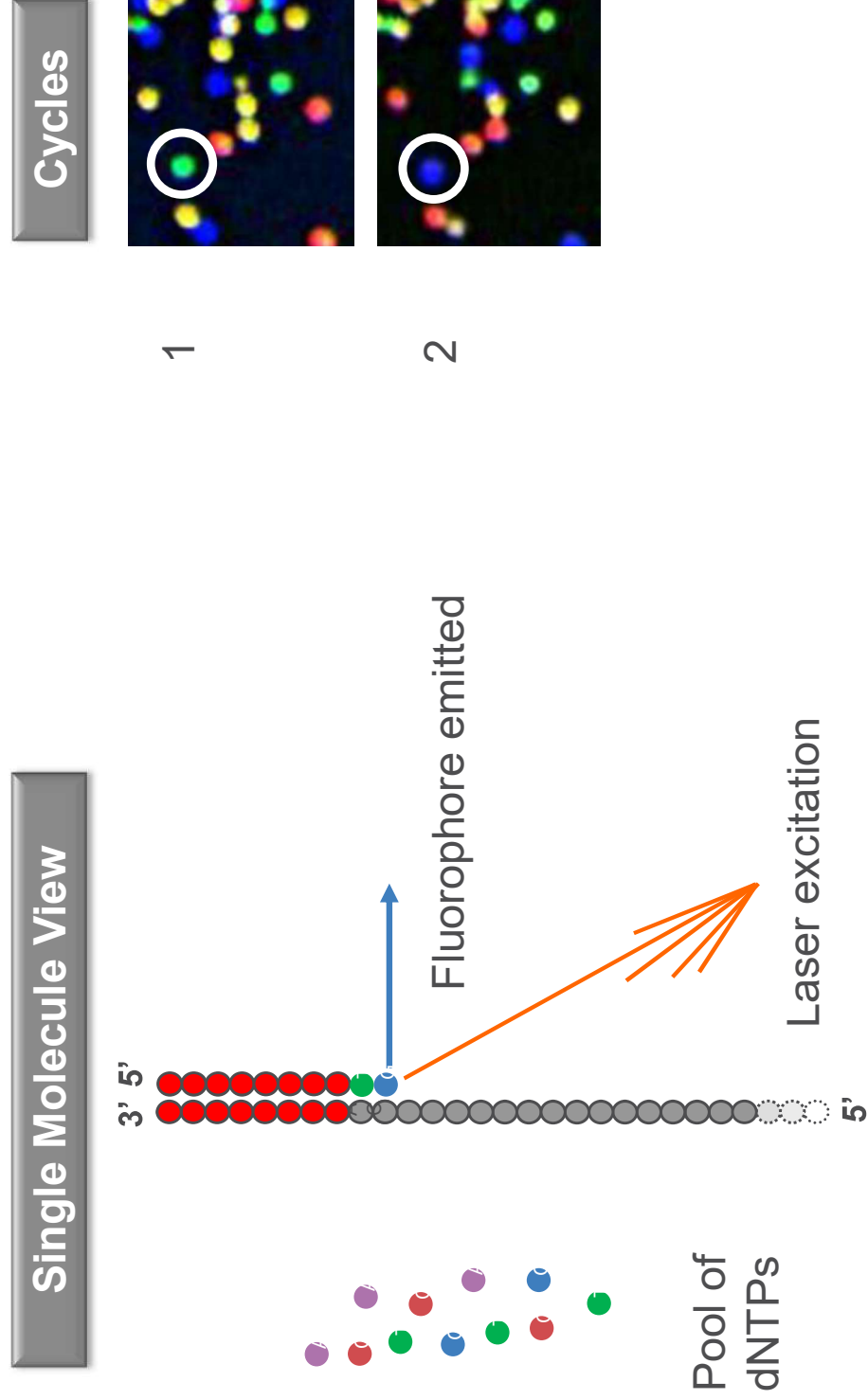
Clusters on Flow Cell Surface

Single Molecule View

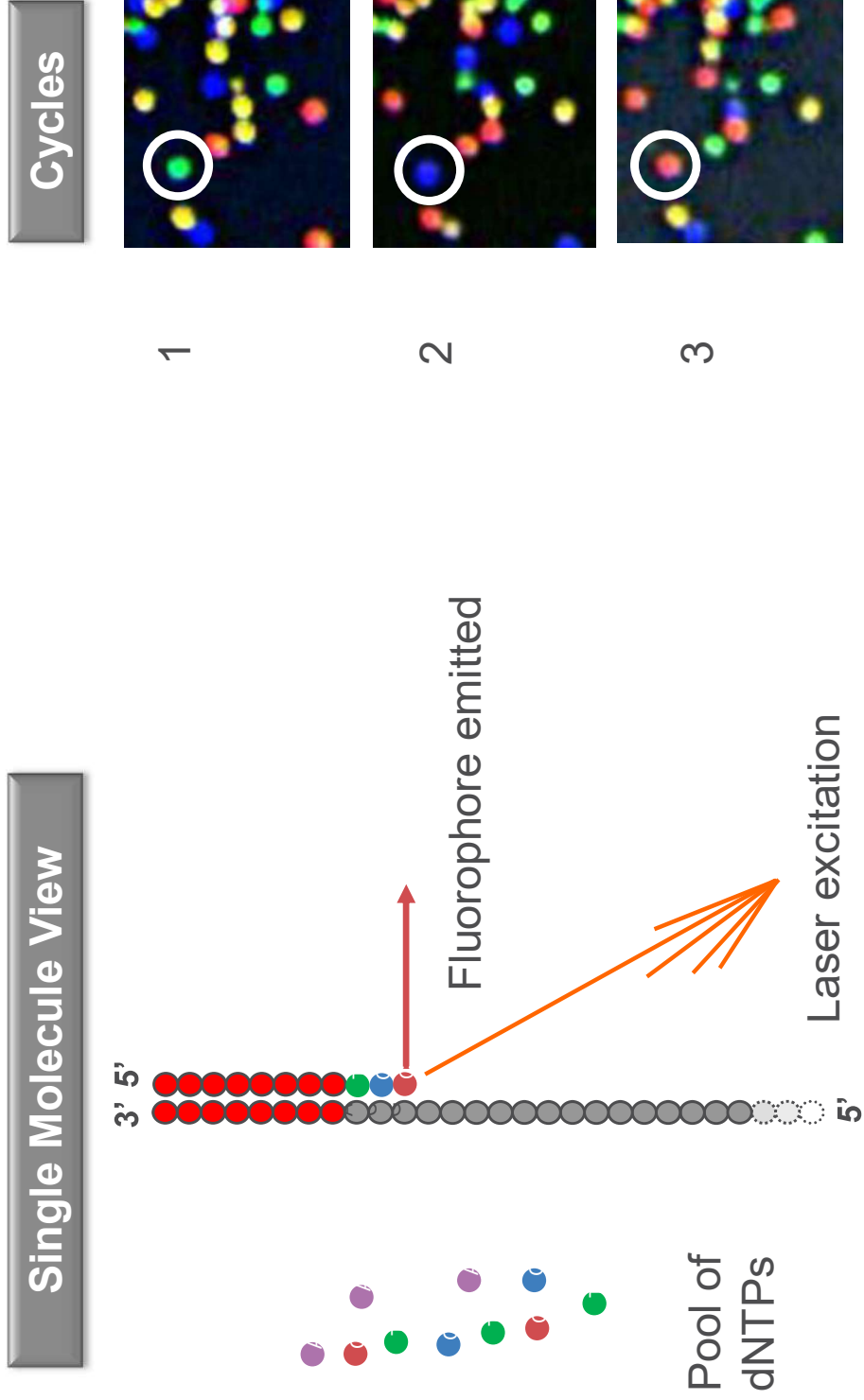
Illumina Sequencing By Synthesis: Imaging



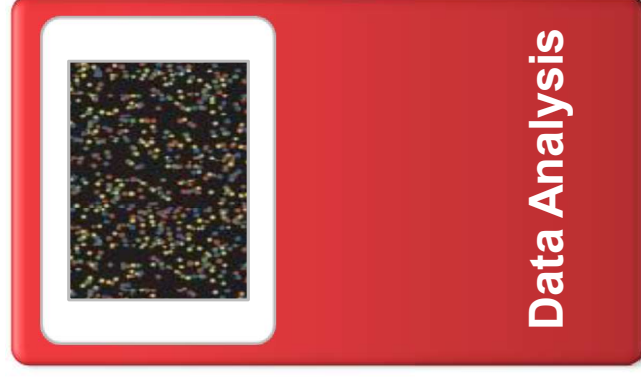
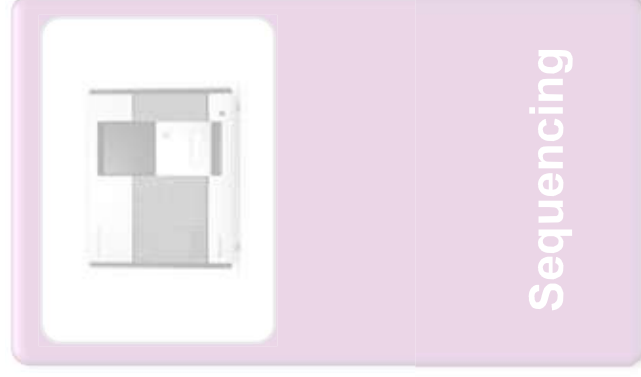
Illumina Sequencing By Synthesis: Imaging



Illumina Sequencing By Synthesis: Imaging

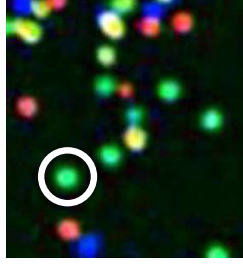
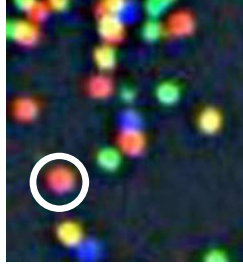
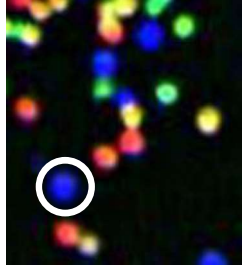
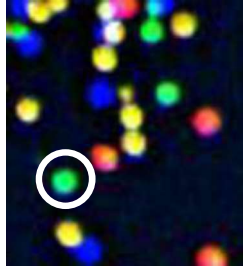


Sequencing Workflow: Primary Analysis



Data Analysis

- ▶ Bases are called
- ▶ Quality scores (Q Scores) are assigned for all base calls

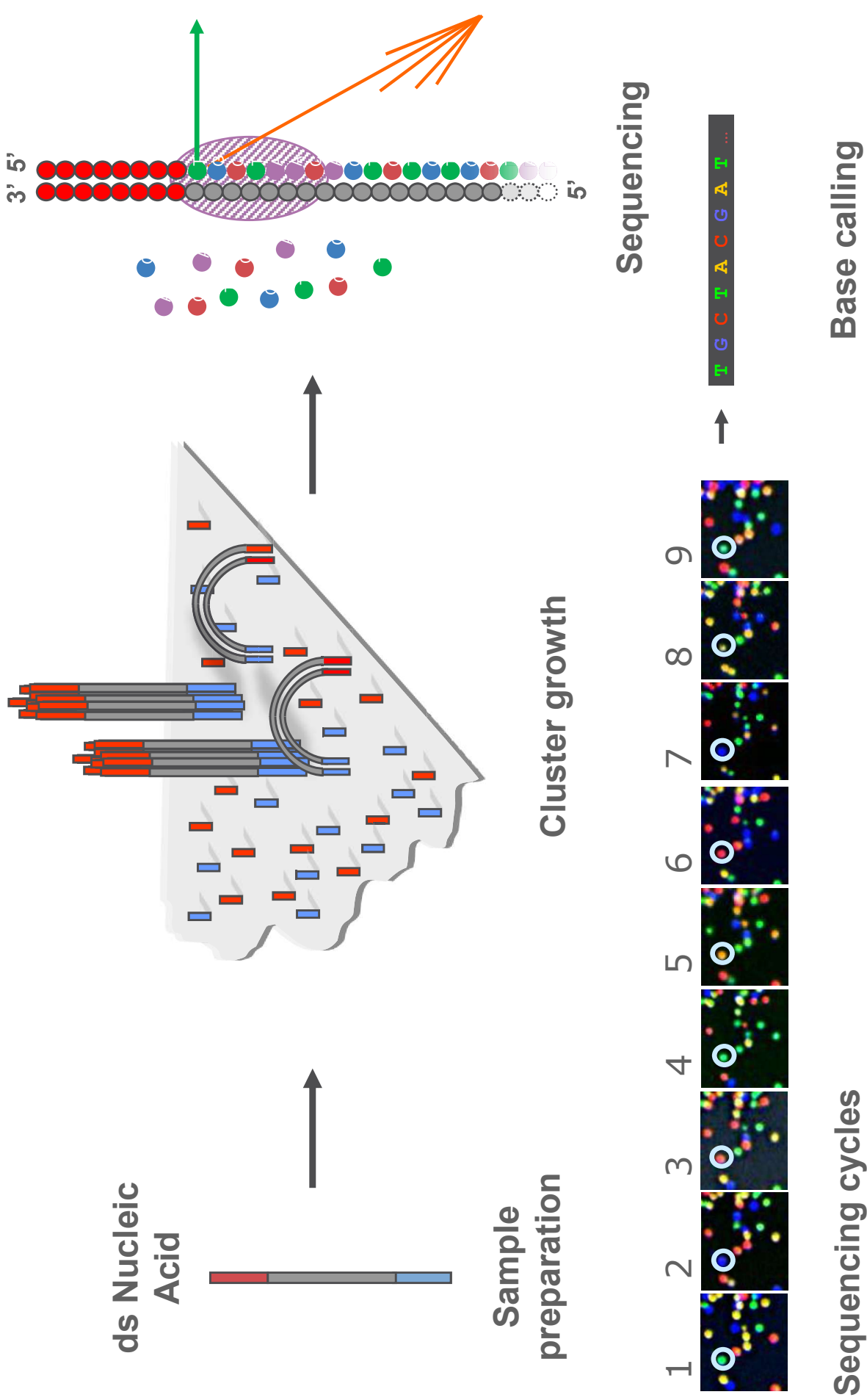


= **TGCT**

- ▶ Q scores reflect probability of an incorrect base call

Q Score	Probability of error
Q30	1 in 1000
Q20	1 in 100

Illumina Sequencing



Illumina Sequencing Platforms

Our menu, something for every NGS customer...



Our Sequencing Platforms

Sequencing



MISeq

Focused power. Speed and simplicity for targeted and small genome sequencing.

[REQUEST PRICING](#)



MISeqDx

Focused Dx power. The first FDA-cleared IVD next-generation sequencing system.

[REQUEST PRICING](#)



NextSeq 500

Flexible power. Speed and simplicity for everyday genomics.

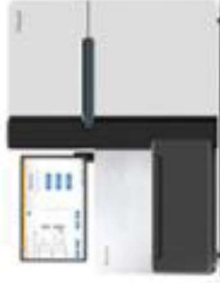
[REQUEST PRICING](#)



HiSeq 2500

Production power. Power and efficiency for large-scale genomics.

[REQUEST PRICING](#)



HiSeq X Ten

Population power. Maximum throughput and lowest cost for population-scale sequencing.

[REQUEST PRICING](#)

Diversity of research applications



Different application has different output requirements



And many more...

Something for every NGS customer

Different outputs, different read lengths for different applications....

Specifications	MiSeq		NextSeq		HighSeq 2500		
	v2 kit	v3 kit	Mid Output	High Output	Rapid Run	v3 kit	v4 kit
Output (Gb)	8.5	15	39	120	180	300	1000
Read Length (bp)	2 x 250	2 x 300	2 x 150	2 x 150	2 x 150	2 x 100	2 x 125
Estimated run time	39 hr	55 hr	26 hr	29 hr	40 hr	11 days	6 days

Advantages of MiSeq



- ▶ **Positioned as the personal NGS system**
 - 610 Mb to 15 Gb (depending on flowcell, run parameters and mode)
- ▶ **Speed:**
 - System that can produce data in the shortest time
 - 1 x 36 bp run in 8hr
- ▶ **Flexibility:**
 - Wide range of flowcells and kits to meet different output requirements
- ▶ **MiSeq Dx:**
 - First FDA approved NGS system

Advantages of HiSeq



- ▶ **Positioned as high output system**
 - 47 Gb to 1000 Gb (depending on flowcell, run parameters and mode)
- ▶ **Production Powerhouse**
 - High output mode offers the lowest \$/Gb for most apps, as well as the highest throughput and largest sample batches
- ▶ **Longer reads** (Launched in Nov 2014)
 - Rapid Run read length increase from 2 x 125 bp to 2 x 250 bp
- ▶ **HiSeq X Ten** (Launched in Jan 2014)
 - Highest output at 1800 Gb
 - Human genome sequencing

Advantages of NextSeq (Launched in Jan 2014)



- ▶ **Positioned as mid to high output system**
 - 19.5 Gb to 120 Gb (depending on flowcell, run parameters and mode)
- ▶ **Speed:**
 - 25% faster run times relative to HiSeq Rapid Run
 - 2 x 150 bp in 29 hours vs. 40 hours
- ▶ **Flexibility:**
 - Mid output FC offers additional flexibility
 - High volume, high depth targeted studies
- ▶ **Cost-effectiveness:**
 - 30% lower price per data point relative to Rapid Run
 - \$51/Gb vs. \$33/Gb

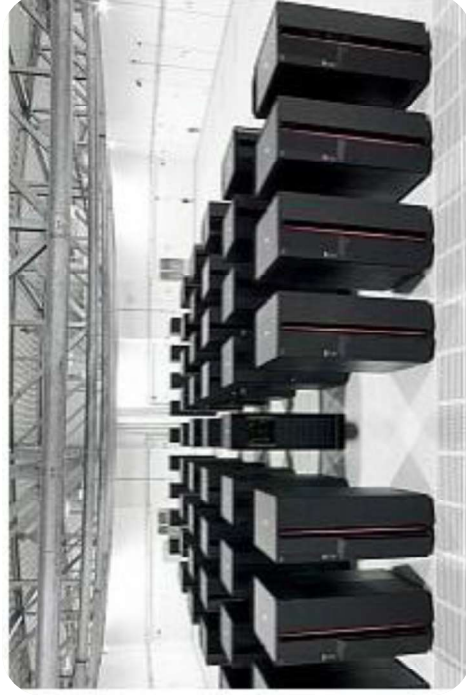
BaseSpace

Understanding the NGS data...



NGS Informatics Challenges

A Costly Endeavor For Labs



Build infrastructure

Requires IT staff to maintain

Multiple vendors to coordinate for
troubleshooting

A Painful Process For Researchers



Different software for each part of the
workflow

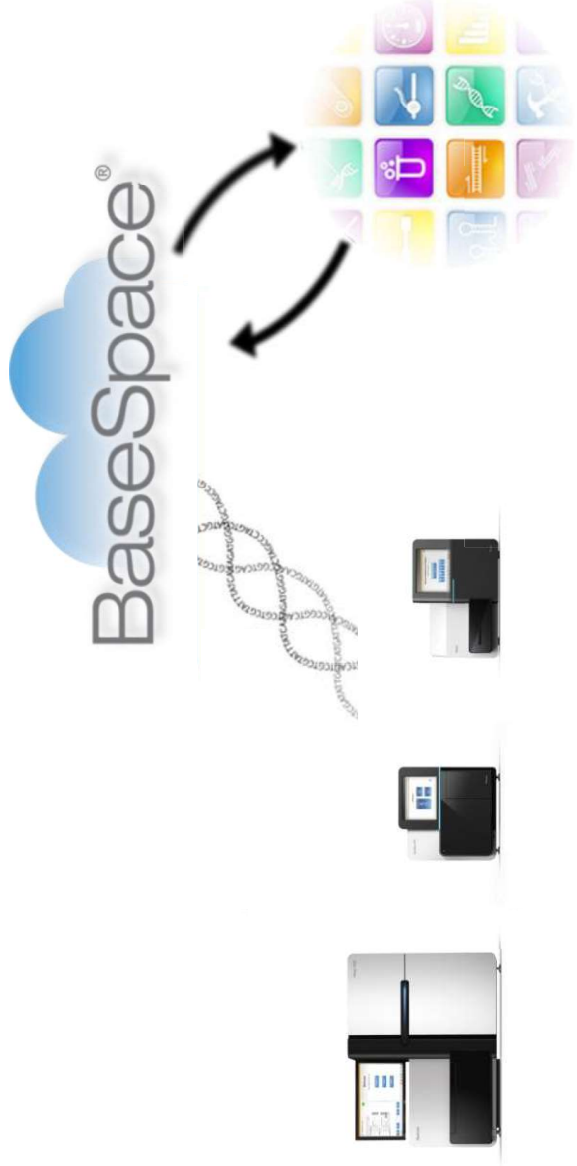
Bioinformatics team is required to write
analysis programs to manage data

Illumina Sequencing

Streamlined NGS infrastructure, optimized for speed

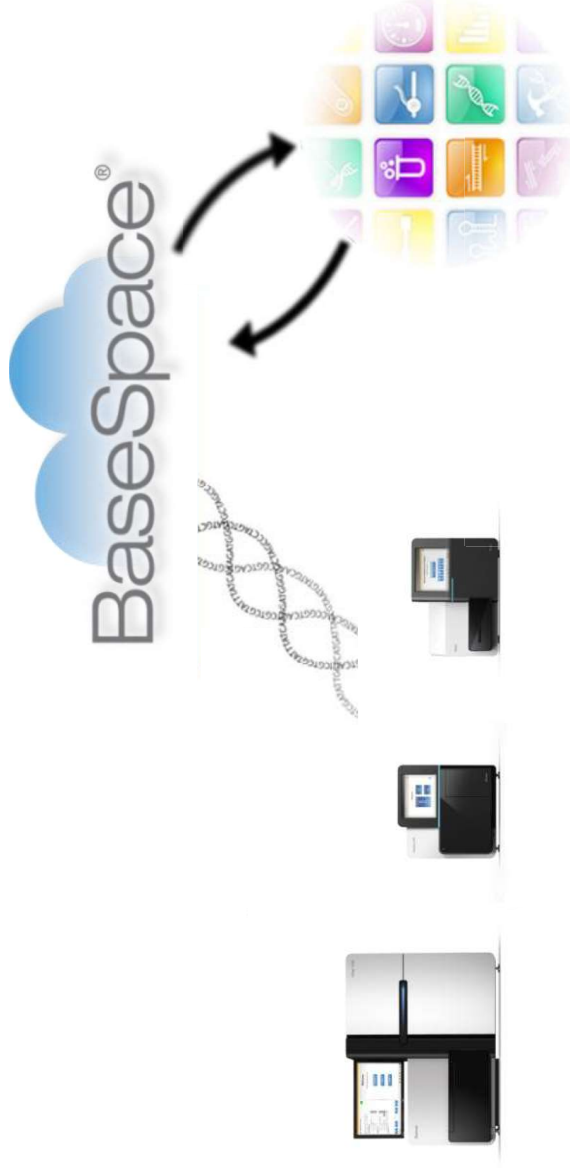


NGS infrastructure for data management



BaseSpace

For easy data storage, analysis and collaboration



- ▶ Sample to Answer
 - ▶ Designed by biologists, for biologists
 - ▶ Zero configuration, install or management
 - ▶ High security during transfer and storage
-
- ▶ Monitor runs from any location
 - ▶ Analysis with Illumina and 3rd party Apps
 - ▶ Share data for scientific collaboration
 - ▶ Transfer data ownership from a core lab to a customer

BaseSpace OnSite

For Those Who Want to Keep All Data On Site



BaseSpace Dashboard

BaseSpace®
Dashboard

Prep
Runs
Projects
Apps
Public Data
Help

illumina®

0 BaseSpace iCredits

[Add More](#)

TIP OF THE DAY

Did you know you can now transfer the ownership of a run or a project? [Learn more](#) »

[contact us](#)

NOTIFICATIONS

BaseSpace Updates: NextSeq 500 and More

Jan 16, 2014

It's barely midway through the first month of 2014, and we already have breaking news to share...

Wishing you Happy Holidays with a Festive Competition!

Dec 21, 2013

As we near the end of the year, we'd like to share a fun competition put together by James H...

karthik prabu accepted your invitation to the Run training181213

Dec 19, 2013

RUNS

Paused training181213

Complete HISeq RR Training 17th Dec

Uploading ER

PROJECTS

00- Core Apps Demo

BaseSpace Tumor Normal WGS Demo

Demo2

HISeq 2500: TruSeq Stranded mRNA LT (SEQC: U...

ANALYSES

00- Core... BWA Whole Genome Sequencin...

00- Core... BWA Enrichment 01/16/2014 4...

00- Core... APP NOT RELEASED YET! TopHa...

00- Core... Tumor Normal 01/09/2014 8:29...

Help
FAQ
Developers
Terms
Blog

BaseSpace Applications Portfolio

A wide array of applications, no install required

Library QC

Clone checking

Amplicon Sequencing

Custom Amplicon

ChIP-Seq

Reresequencing

Targeted Resequencing

Custom Enrichment

RNA-Seq

Small RNA sequencing

Regulation

Plasmid

Small genome

16S Metagenomics

De novo sequencing

ChIP-Seq

Amplicon Sequencing

Clone checking

Targeted Resequencing

Custom Enrichment

RNA-Seq

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Custom Enrichment

RNA-Seq

Small RNA sequencing

Regulation

Plasmid

Small genome

16S Metagenomics

De novo sequencing

Push Button Exome Analysis in BaseSpace

Statistics in aggregated reports highlighted in intuitive and graphical format

BaseSpace illumina

Navigation icons: Home, Search, Help, Refresh, Print, Share, Download, Upload, Run, Stop, Start, Pause, Play, Stop, Start, Pause, Play

Project: BWA Enrichment (12plex, Manifest v1.2) 01/16/2014 9:15:22

Analysis Info

Inputs

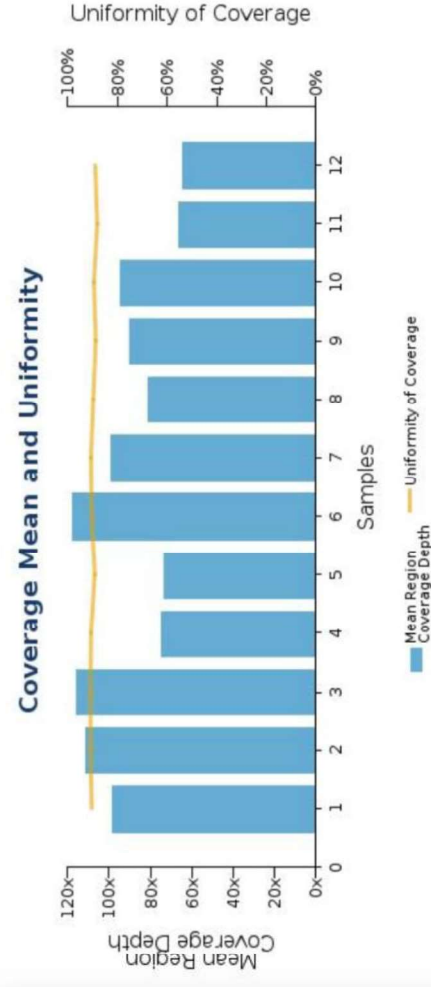
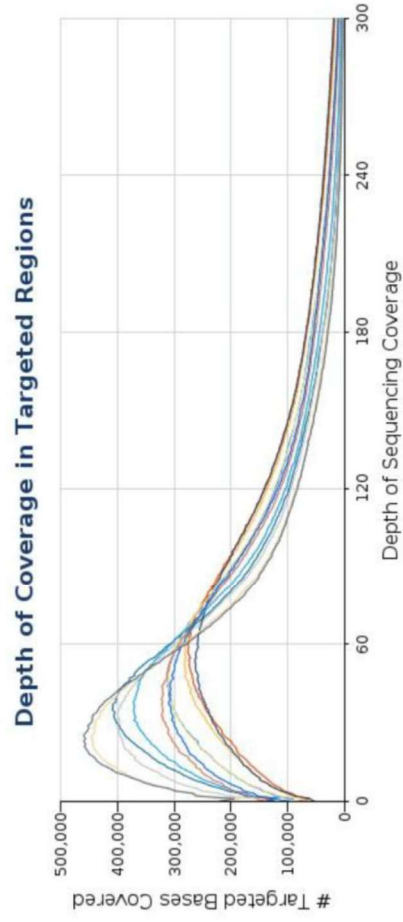
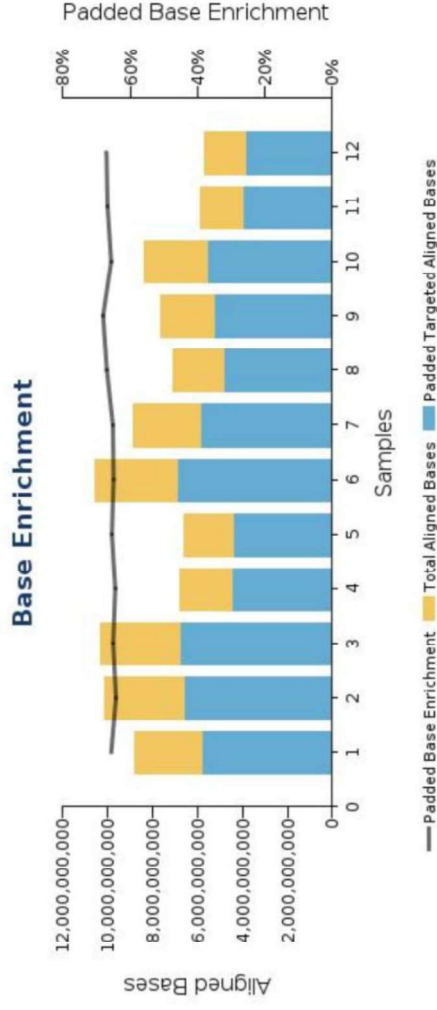
Output Files

Analysis Reports

Aggregates Summary

Sample	Sample Name	Mean Coverage	Target Coverage at 1X	Target Coverage at 10X	Target Coverage at 20X	Target Coverage at 50X
1	FCL_NA12878_01	101.6 X	99.3%	95.5%	90.0%	68.6%
2	FCL_NA12878_04	115.1 X	99.5%	96.5%	91.9%	73.6%
3	FCL_NA12878_07	119.2 X	99.5%	96.5%	92.3%	75.0%
4	FCL_NA12878_10	77.1 X	99.2%	94.0%	86.0%	57.0%
5	FCL_NA12891_02	76.2 X	99.3%	93.2%	84.4%	55.5%
6	FCL_NA12891_05	121.7 X	99.6%	96.6%	92.1%	74.8%
7	FCL_NA12891_08	102.2 X	99.6%	95.9%	90.4%	68.8%
8	FCL_NA12891_11	83.9 X	99.4%	94.5%	87.1%	60.4%

contact us



BaseSpace Applications Portfolio

True Push-Button Bioinformatics



Analysis Platform with Unlimited Potential

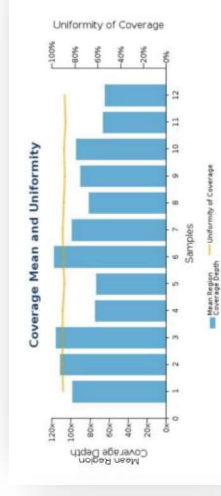
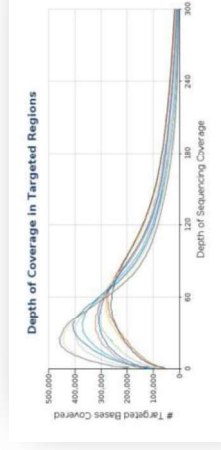
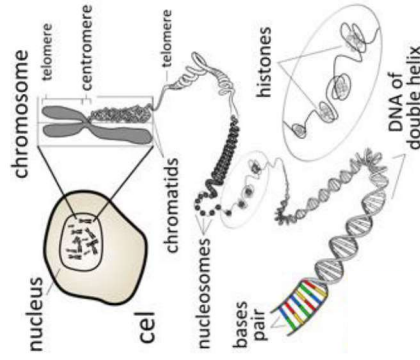
- ▶ Apps store will allow you to select a huge choice of analysis options.
 - Illumina (iSAAC, SAV, Strelka, Grouper, ...)
 - Open Source (GATK, BWA, Tophat+Cufflinks, ...)
 - Individuals (professors, grad students)
 - Commercial partners



Summary

illumina

BaseSpace®



Sample

Answer