



# Learning Objectives

After completing this lesson, you will be able to:

- ▶ List the HiSeq reagents
- ▶ Identify key characteristics of the HiSeq flow cell
- ▶ Describe how the HiSeq performs dual surface imaging



# HiSeq 2000/1000 System



	HiSeq 2000	HiSeq 1000
<b>Output (2 × 100 bp)</b>	600 Gb	300 Gb
<b>Run Time (2 × 100 bp)</b>	~11 days	~8.5 days
<b>Cluster Generation</b>	cBot	cBot
<b>Paired-end Reads</b>	6 Billion	3 Billion
<b>Single Reads</b>	3 Billion	1.5 Billion
<b>Maximum Read Length**</b>	2 × 100 bp	2 × 100 bp
<b>Quality Scores***</b>	> 85% (2 x 50 bp) > 80% (2 x 100 bp)	

\*\*\*Based on an Illumina PhiX library at supported cluster densities.

# HiSeq 2500/1500 System



	HiSeq 2500		HiSeq 1500	
<b>Run Mode</b>	High Output	Rapid Run*	High Output	Rapid Run*
<b>Output (2 × 100 bp)</b>	600 Gb	120 Gb	300 Gb	60 Gb
<b>Run Time (2 × 100 bp)</b>	~11 days	~27 hours	~8.5 days	~27 hours
<b>Cluster Generation</b>	cBot	On board	cBot	On board
<b>Paired-end Reads</b>	6 Billion	1.2 Billion	3 Billion	600 Million
<b>Single Reads</b>	3 Billion	600 Million	1.5 Billion	300 Million
<b>Maximum Read Length**</b>	2 × 100 bp	2 × 150 bp	2 × 100 bp	2 × 150 bp
<b>Quality Scores***</b>	> 85% (2 × 50 bp) > 80% (2 × 100 bp)			

\*\*\*Based on an Illumina PhiX library at supported cluster densities.





# HiSeq Reagents

# HiSeq Reagent kits

Reagent Kits	
200 cycles	209 cycles of sequencing
50 cycles	58 cycles of sequencing



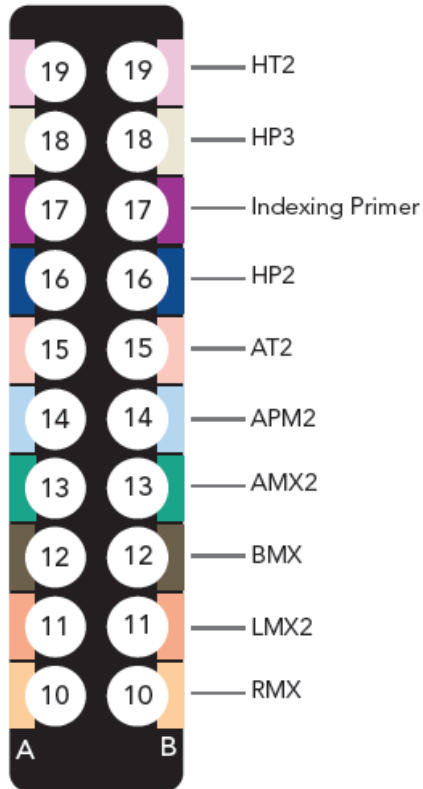
TruSeq SBS Kit v3 – HS (200-cycle)



TruSeq SBS Kit v3 – HS (50-cycle)

# Reagents Layout HiSeq 2000

## Rear of Fridge



Paired-End Rack



Flow Cell A Rack



Flow Cell B Rack

## Front of Fridge





# Gasket Maintenance and Best Practices

Gasket placement



Replace before every maintenance wash





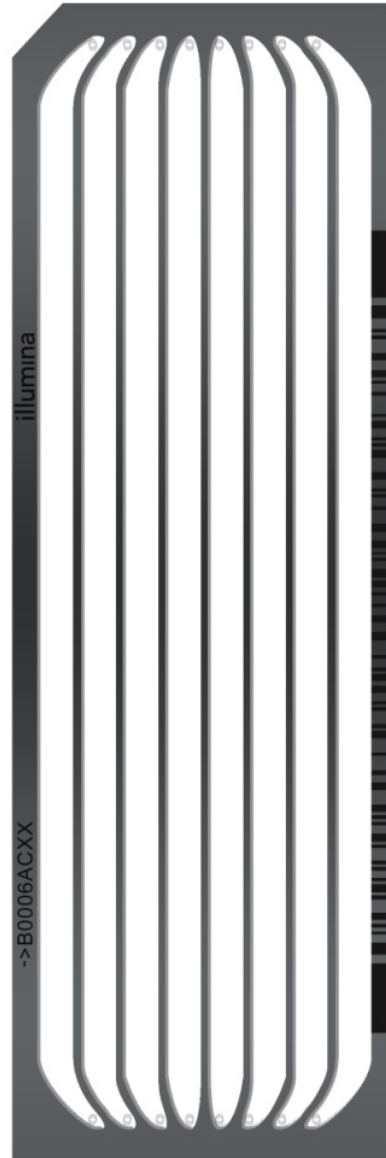
# HiSeq System Hardware



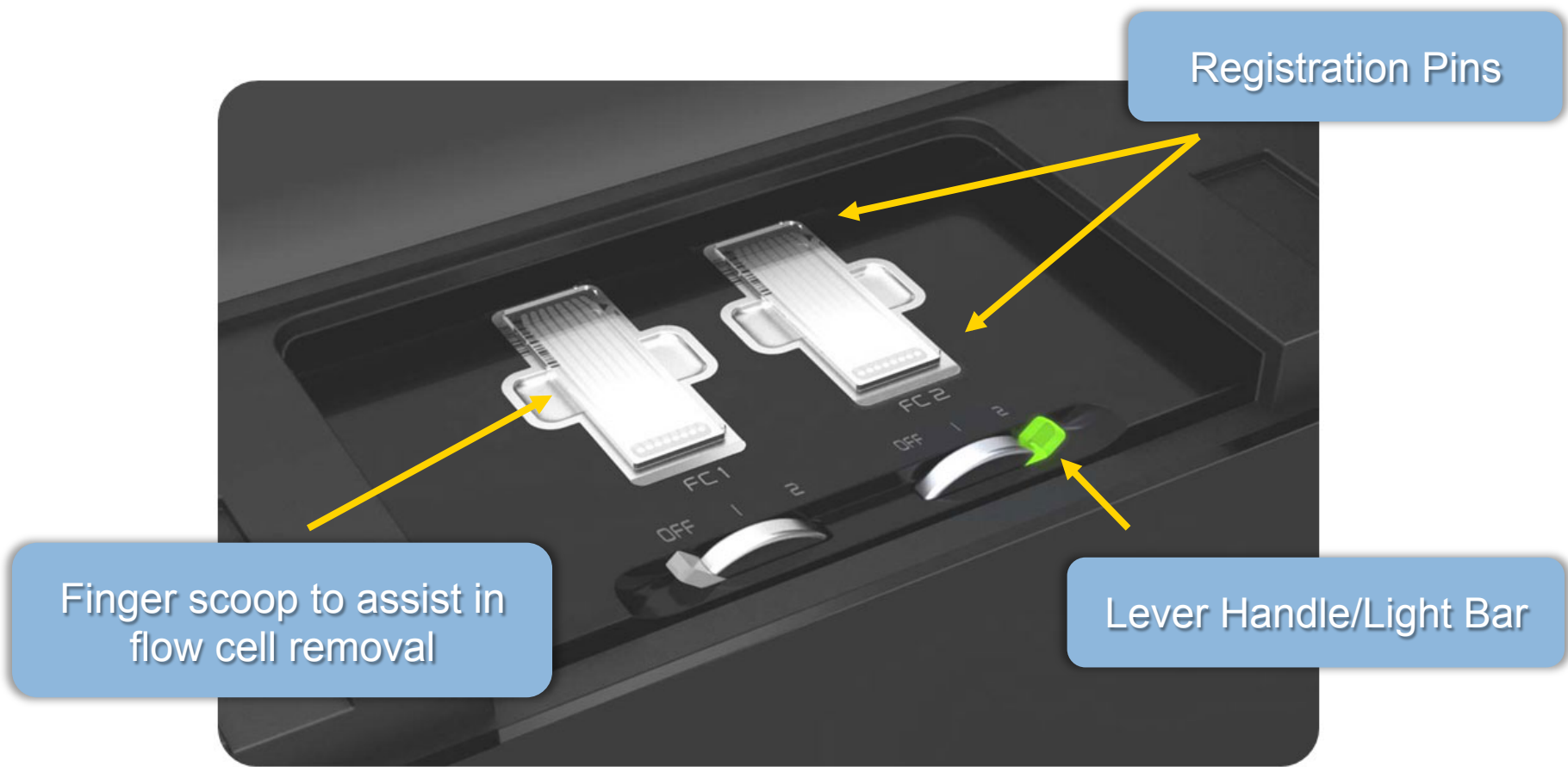
# Flow Cell Design

Dual-surface enabled

- 8 lane format
- 25mm wide x 75mm long
- 1.7mm-wide lanes
- Only compatible with cBot



# Flow Cell Stage



Registration Pins

Finger scoop to assist in flow cell removal

Lever Handle/Light Bar



# Flow Cell Loading



cBot

- Ensure the notched position is on the upper-right corner of the flow cell, relative to the instrument operator



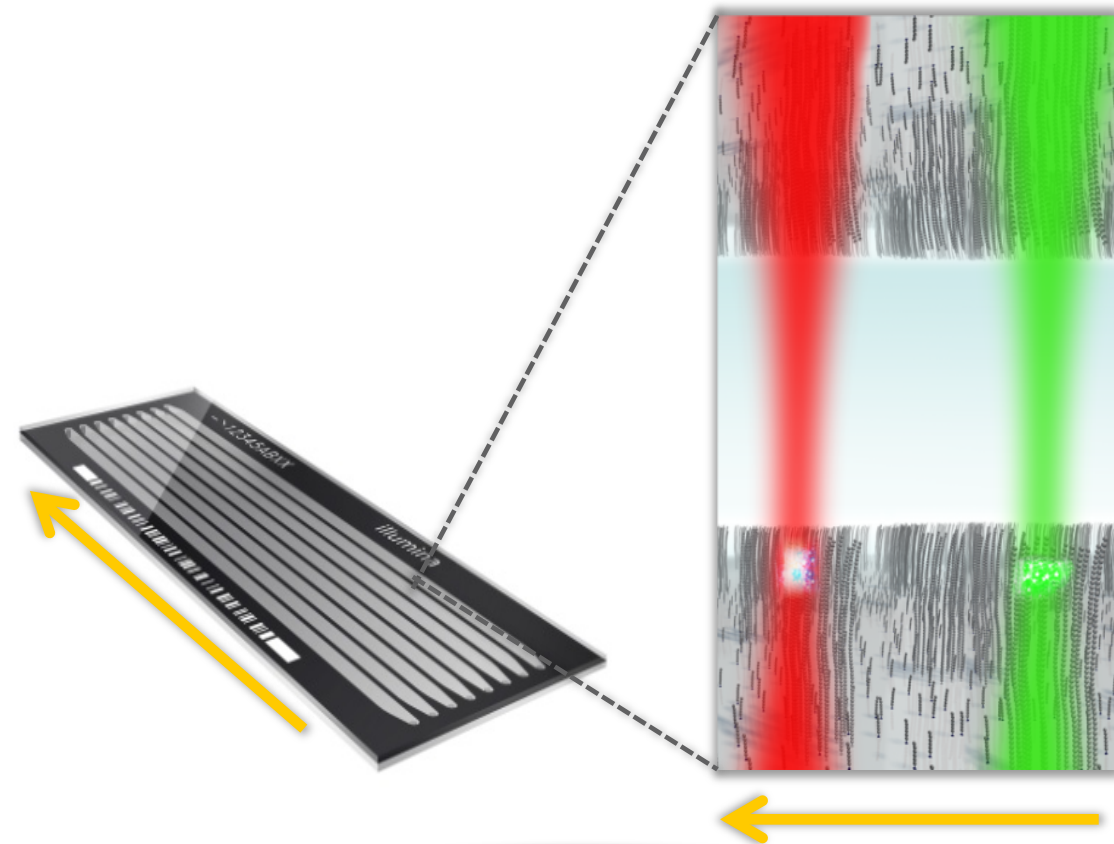
HiSeq

- Ensure the notched position is on the upper-left corner of the flow cell, relative to the instrument operator



Performing this simple check will ensure correct sample orientation

# HiSeq System Imaging



## Operates in epi-illumination mode

- Fluorescence and emission from the same side of the sample

## Continuous Scanning

- Cameras operate in time delay integration (TDI)
- Fluorescence image continually read

## Dual Surface Scanning

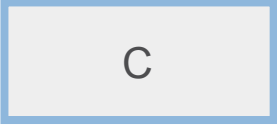
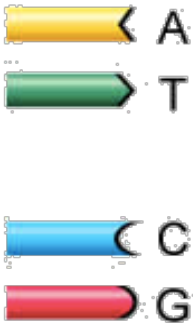
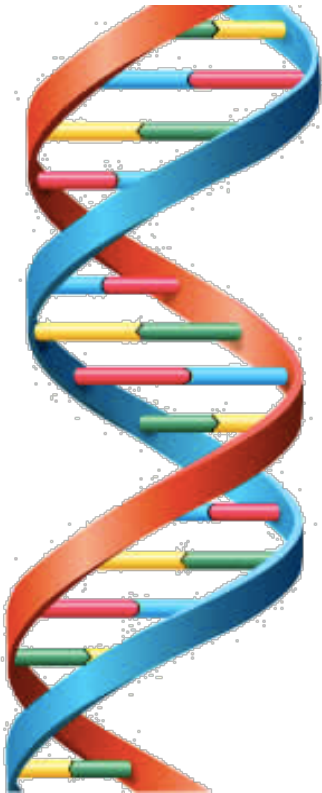
- First: Top of flow cell, all lanes
- Second: Bottom of flow cell, all lanes

3 swaths/lane + 2 surfaces/lane =  
6 scanning events/lane

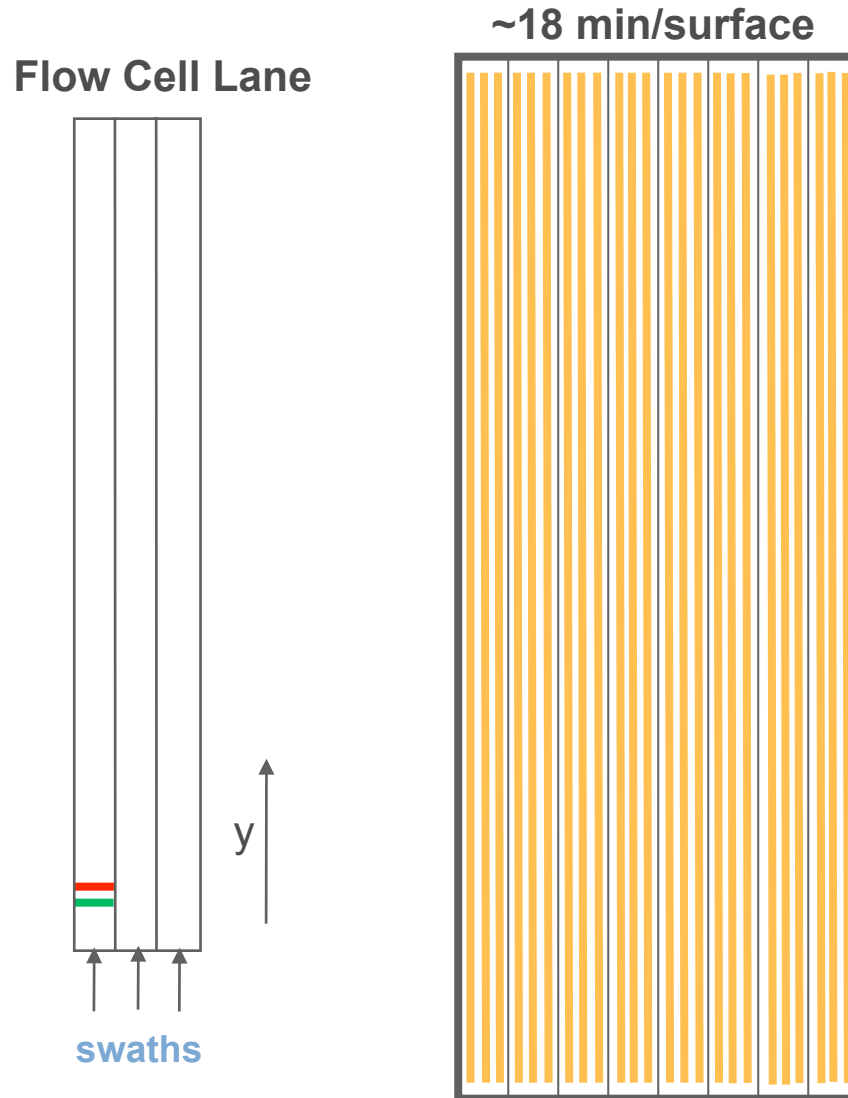
# Emission Capture

Capture image for each swath simultaneously

4 cameras—1 per base



# Excitation and Scanning on HiSeq System

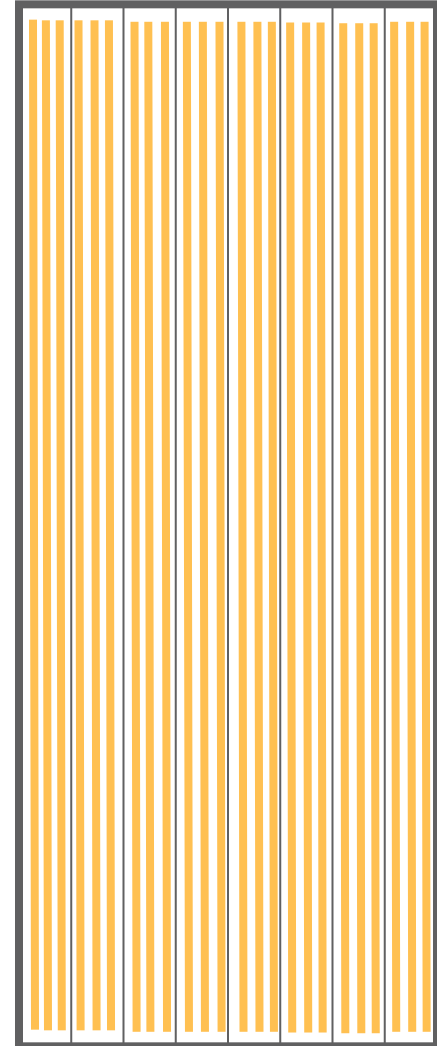


# Flow Cell Swath/Tile

Tile

Swath

Flow Cell



HiSeq Control Software (HCS) divides 1 swath into 16 tiles for image analysis



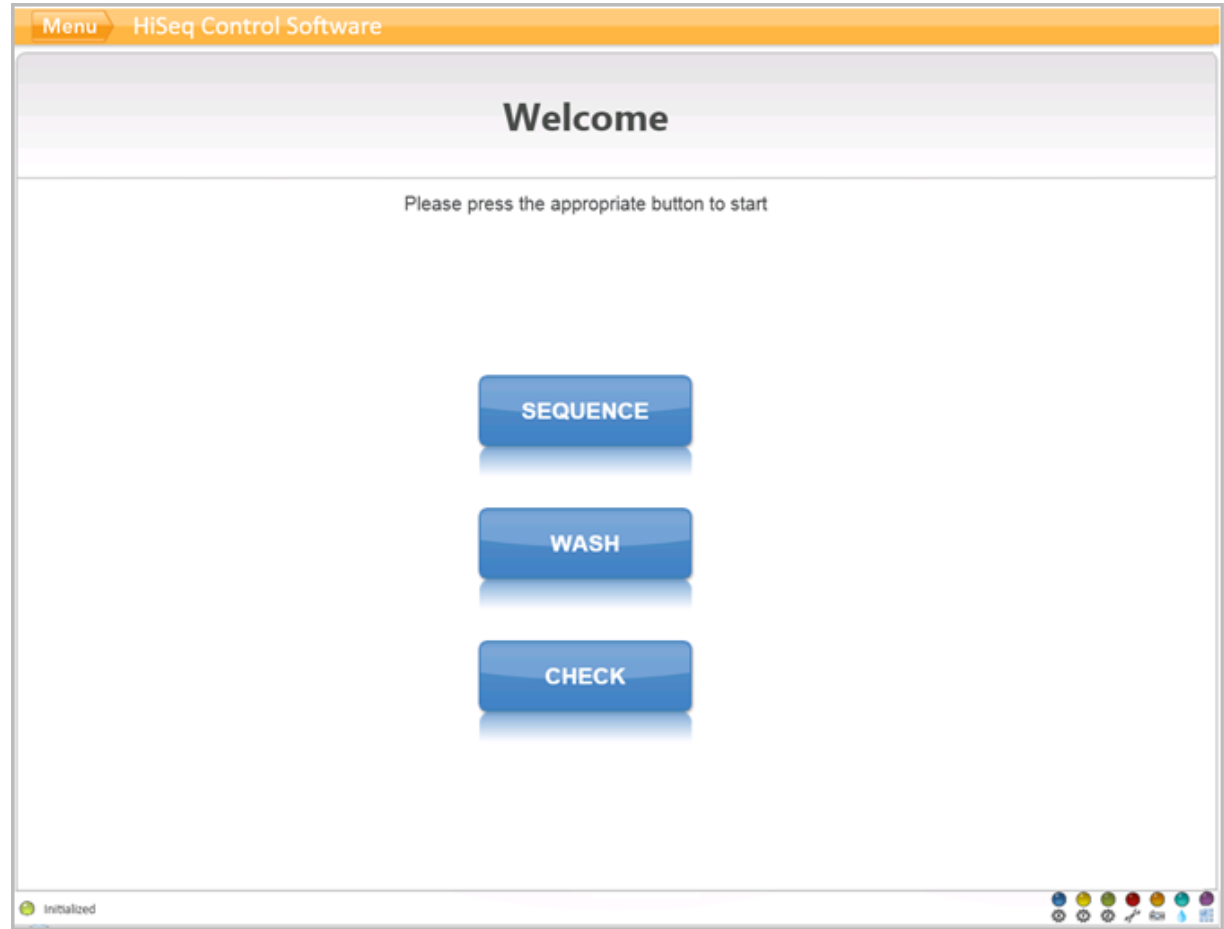


# HiSeq Control Software

# HiSeq Control Software (HCS)

## Simple Operation

- Step-by-step run setup
- Enter read length: single, paired-read, indexing
- Real-time run monitoring
- Reagents usage tracking
- Remote monitoring from Web browser
- Multimedia help menu





# Starting a Run Using the HiSeq System

# How to Start a Run

## Workflow

Cluster a Flow cell  
using cBot

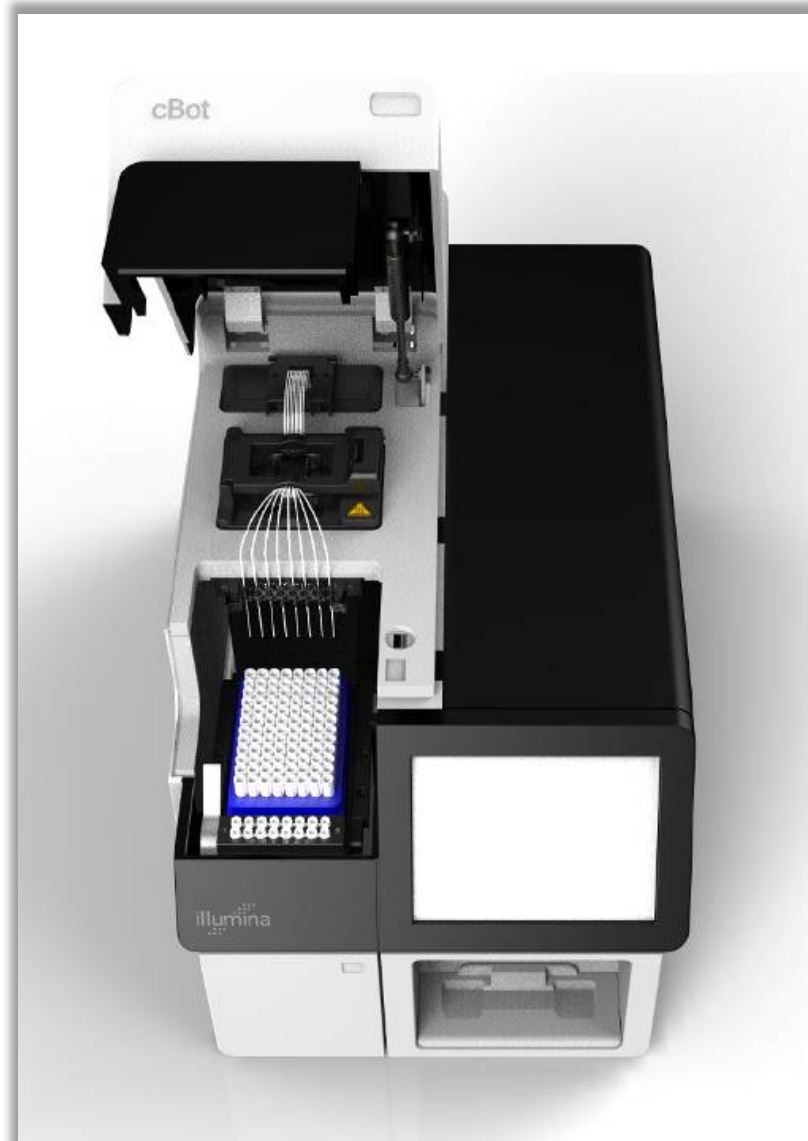
Prepare HiSeq  
reagents

Setting up a  
sequencing Run

# Clustering a Flow cell using cBot

Automates the formation of amplified clonal clusters from the DNA single molecules

- Aspirates DNA samples into flow cell
- Delivers fluidics and controls temperature
- Clustering takes 4.5 hr
- Single manifold per run





# Cluster a Flow cell using cBot workflow

## Thaw reagents

- In RT water bath, 1 hour
- Keep on ice or 4 CC after they are thawed

## Prepare Samples

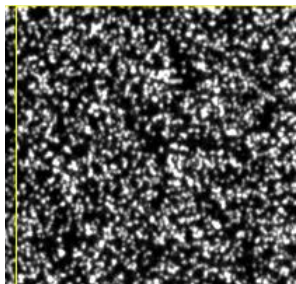
- Denature
- Dilute
- Spike in PhiX if possible

## Set up clustering process

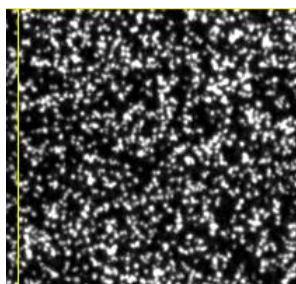
- Load FC
- Load Reagents
- Load Template/Custom Primers

# Maximize data quality and quantity

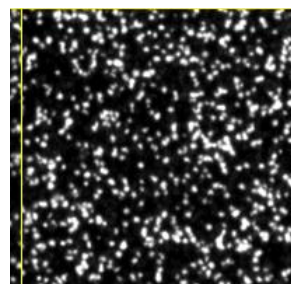
*Optimized flow cell clustering determines data quality and overall data yield*



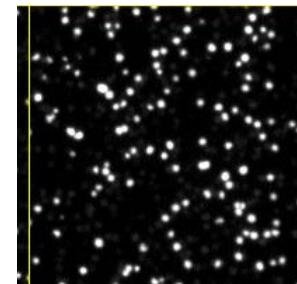
20pM



10pM



5pM



1pM

**Overclustering can result in:**

- Loss of data quality and data output
- Loss of focus
- Reduced base calls and Q30 scores
- Complete run failure

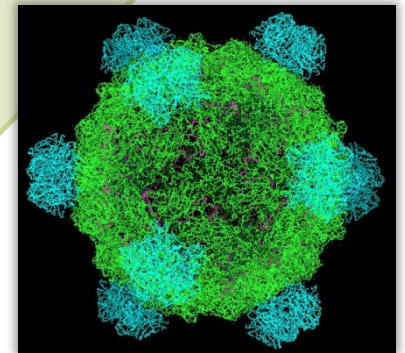
**Underclustering can result in:**

- Loss of time and money

# Using a PhiX Control for HiSeq Sequencing Runs

## What are PhiX Control Libraries?

- **Small:** PhiX is a small genome, which enables quick alignment and estimation of error rates
- **Diverse:** PhiX genome contains ~45% GC and 55% AT
- **Well-defined:** PhiX has a well-defined genome sequence



Structure of phage phiX 174 capsid

## How to use a PhiX Control

- Low-concentration spike-in of 1%
- Dedicated control lane
- High-concentration spike-in of 40% or higher

# How to Start a Run

## Workflow

Cluster a Flow cell  
using cBot

Prepare HiSeq  
reagents

Setting up a  
sequencing Run

# Prepare HiSeq Reagents Workflow

## Thaw reagents

- Leave EDP in -15-25 CC storage until you are ready to prepare ICB
- Thaw SRE and in a RT water bath for ~90 min
- Thaw the LFN in a RT water bath for 20 min.

## Prepare ICB

- Prepare ICB for Read 1 and Read 2 separate
- Prepare ICB for Read 1 and Read 2 (Alternative Workflow)

Keep reagents on 2-8 CC storage until you are ready to load



# How to Start a Run

## Workflow

Cluster a Flow cell  
using cBot

Prepare HiSeq  
reagents

Setting up a  
sequencing Run

# Setting up a sequencing run workflow

## Prerequisites

- You have recently performed an instrument wash
- You have prepared sequencing reagents
- You have a clustered HiSeq FC

## Enter Run parameters

- Provide a Sample Sheet for indexed runs

## Load Reagents

- Load SBS Reagents
- Load Indexing Reagents
- Prime Reagents, collect and measure priming waste

## Load the clustered FC, start the run

- Confirm Proper Flow



Questions?