

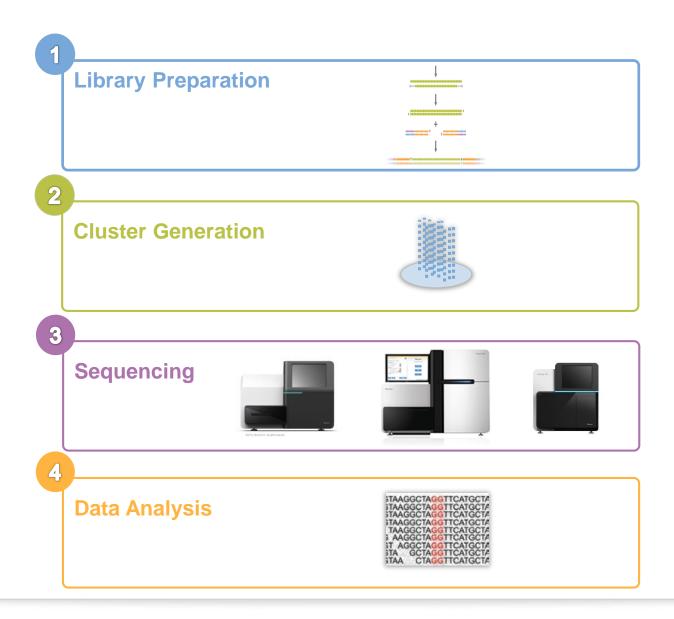
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Session Objectives

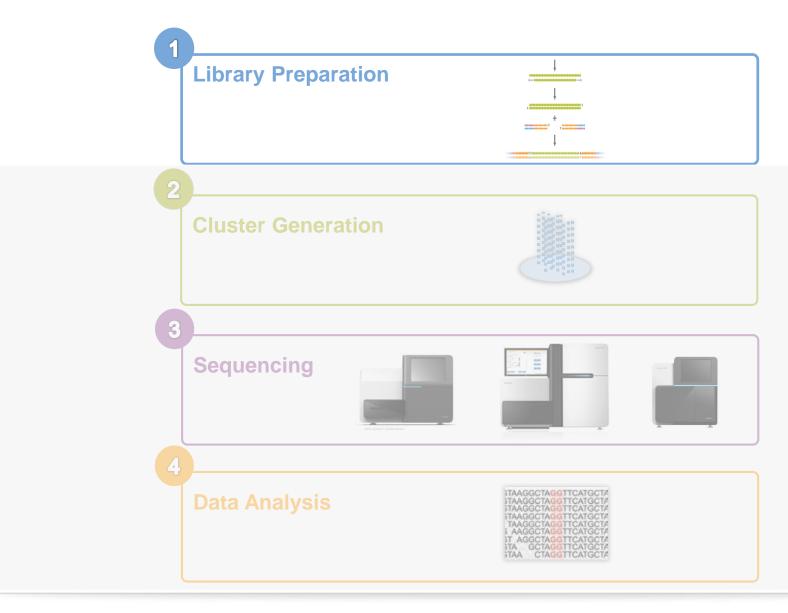
- By the end of this training, you will be able to:
 - List the major steps in the Illumina sequencing workflow
 - Describe cluster generation
 - Discuss the sequencing by synthesis process

Illumina Sequencing Workflow

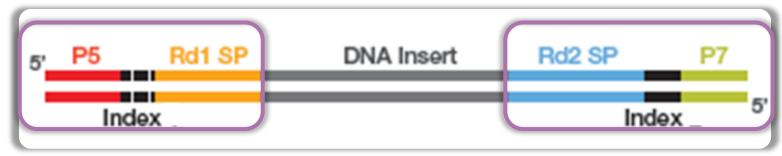




Illumina Sequencing Workflow



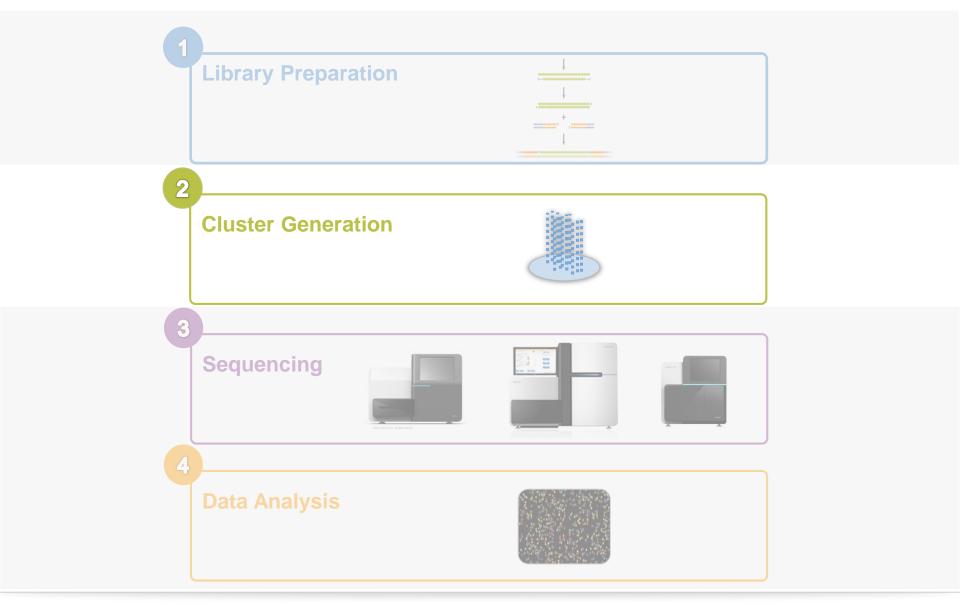
Library Prep is Critical for Successful Sequencing



Dual Index Library shown

The aim of library prep is to obtain nucleic acid fragments with adapters attached on both ends

Illumina Sequencing Workflow

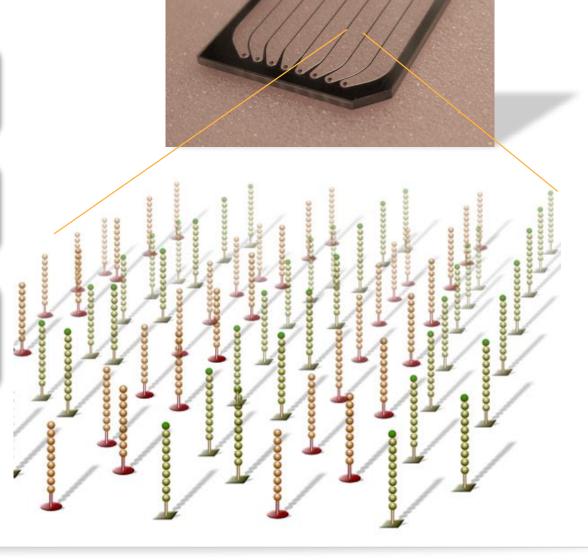


What is a Flow Cell?

Cluster generation occurs on a flow cell

A flow cell is a thick glass slide with channels or lanes

Each lane is randomly coated with a lawn of oligos that are complementary to library adapters

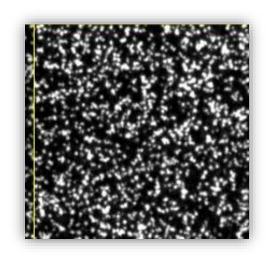




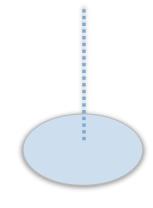
What is a Cluster?

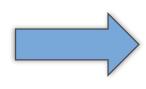
Clusters are bright spots on an image

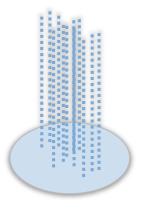
Each cluster represents thousands of copies of the same DNA strand in a 1–2 micron spot



Single DNA Library



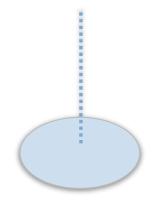


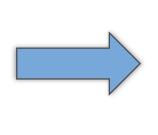


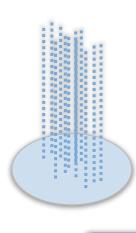
Amplified Clonal Cluster

Instrumentation

Single DNA Library

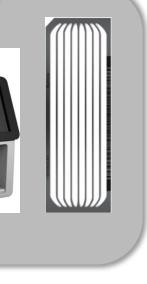






Amplified Clonal Cluster







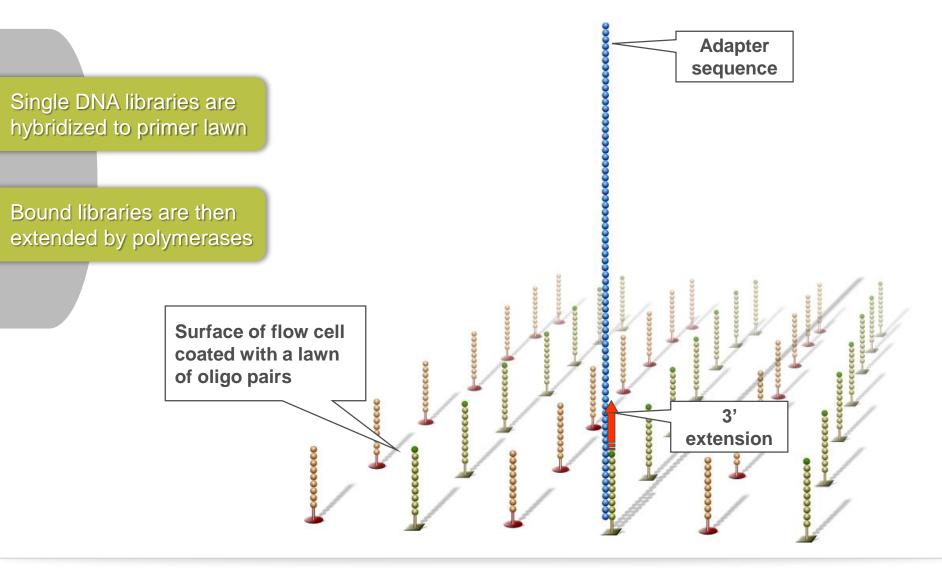




Sequencer



Hybridize Fragment & Extend

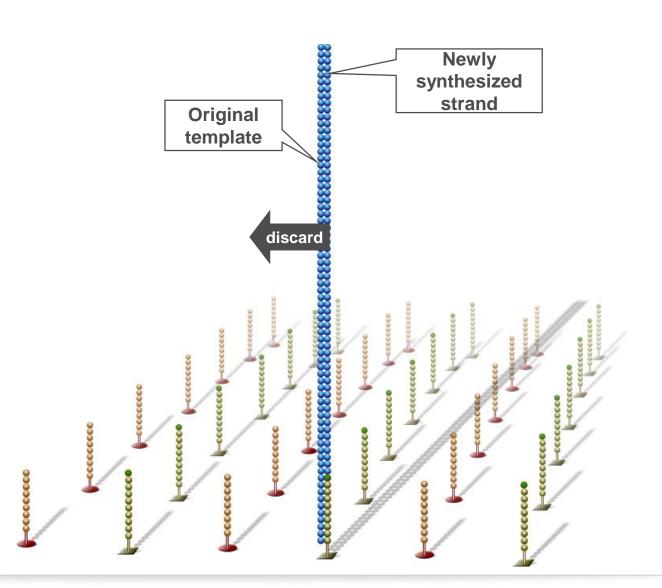


Denature Double-Stranded DNA

Double-stranded molecule is denatured

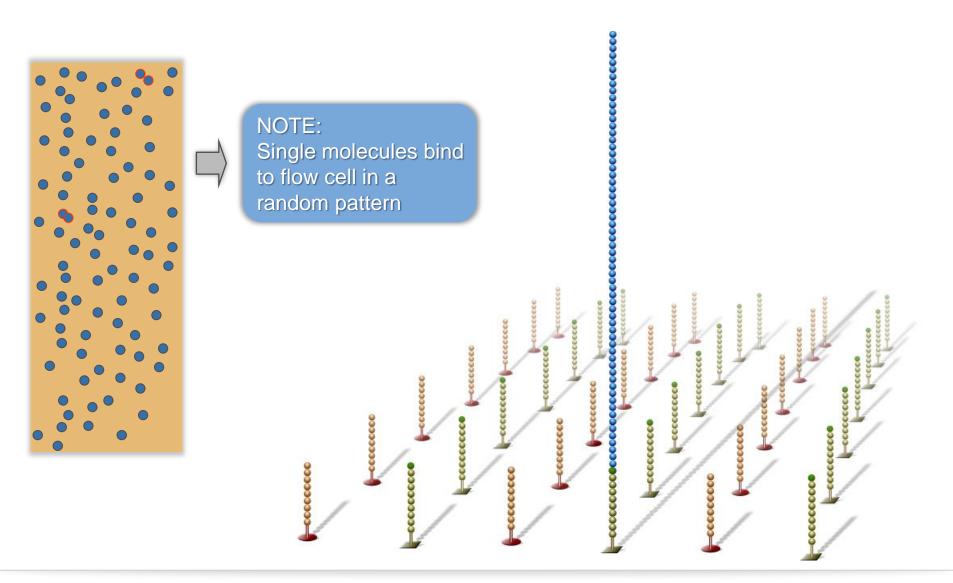
Original template washed away

Newly synthesized strand is covalently attached to flow cell surface





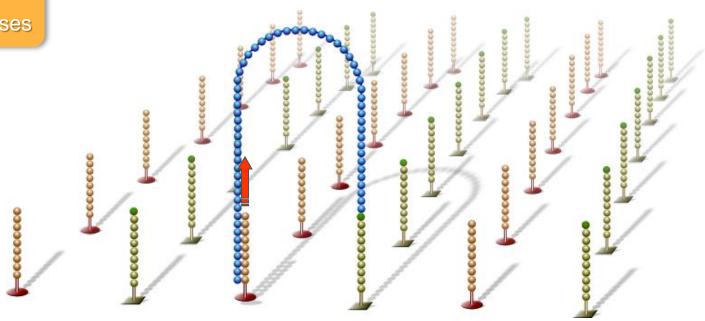
Single-Stranded DNA



Bridge Amplification

Single-stranded molecule flips over and forms a bridge by hybridizing to adjacent, complementary primer

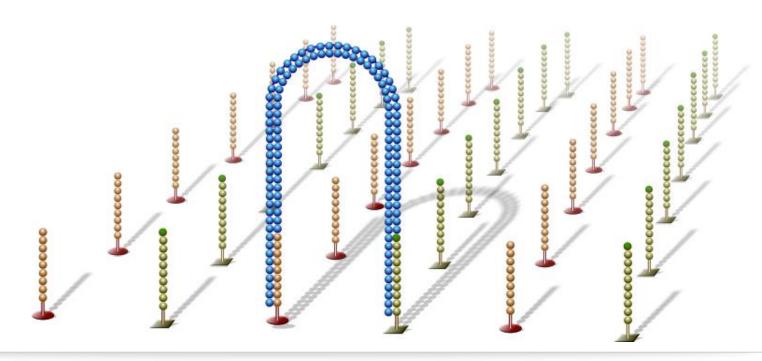
Hybridized primer is extended by polymerases





Bridge Amplification

Double-stranded bridge is formed



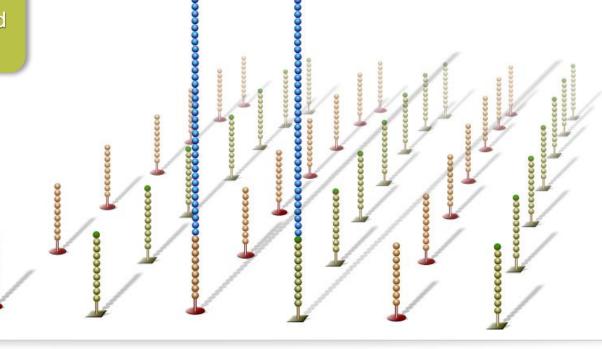


Denature Double-Stranded Bridge

Double-stranded bridge is denatured

Result:

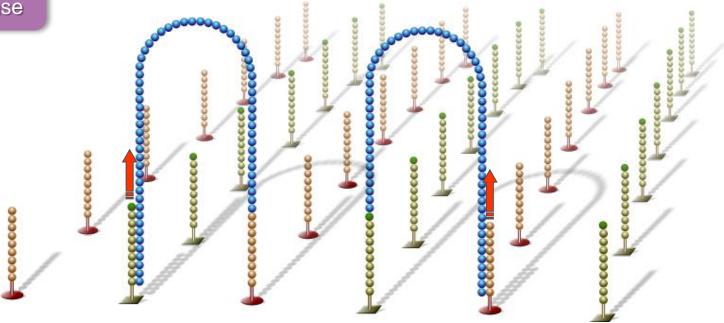
Two copies of covalently bound single-stranded templates



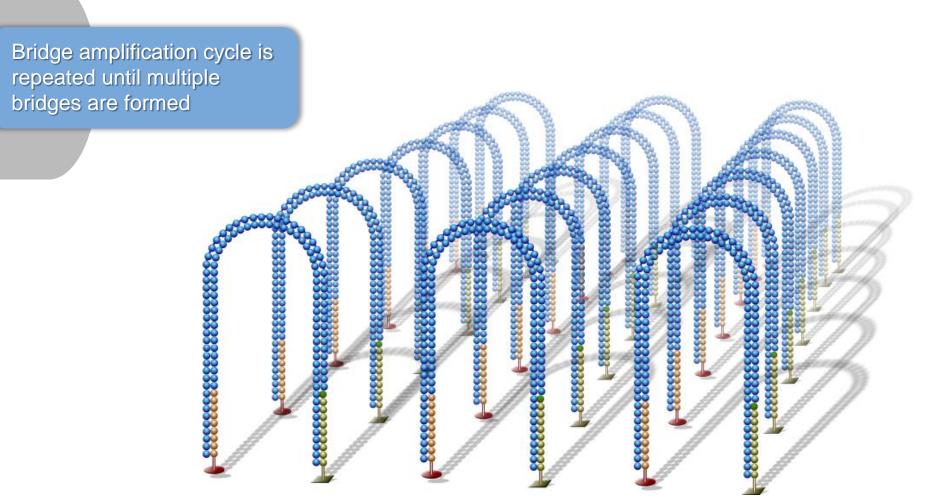
Bridge Amplification

Single-stranded molecules flip over to hybridize to adjacent primers

Hybridized primer is extended by polymerase

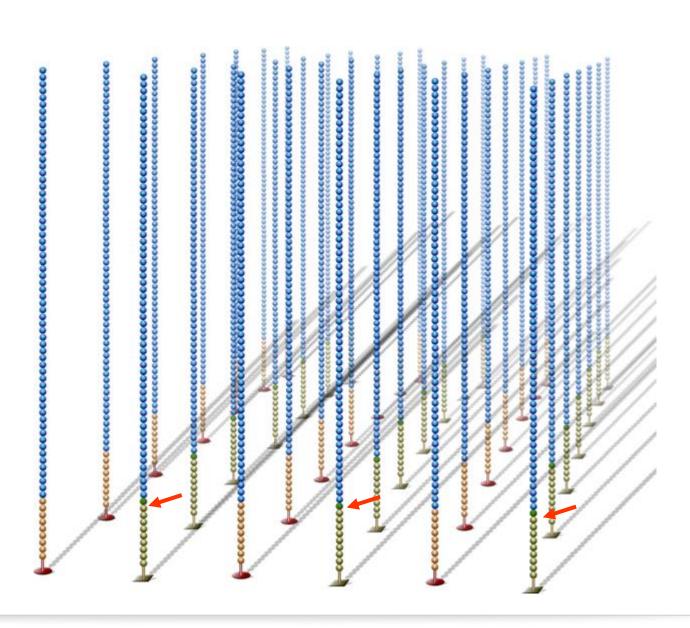


Bridge Amplification



Linearization

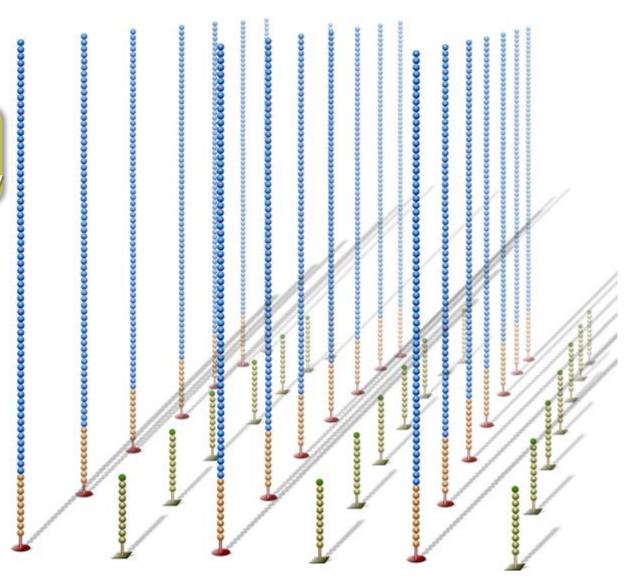
dsDNA bridges are denatured





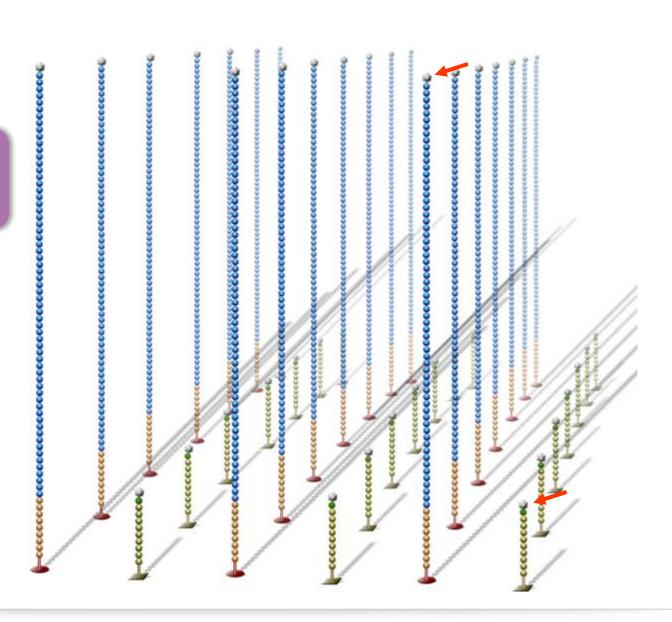
Reverse Strand Cleavage

Reverse strands are cleaved and washed away, leaving a cluster with forward strands only



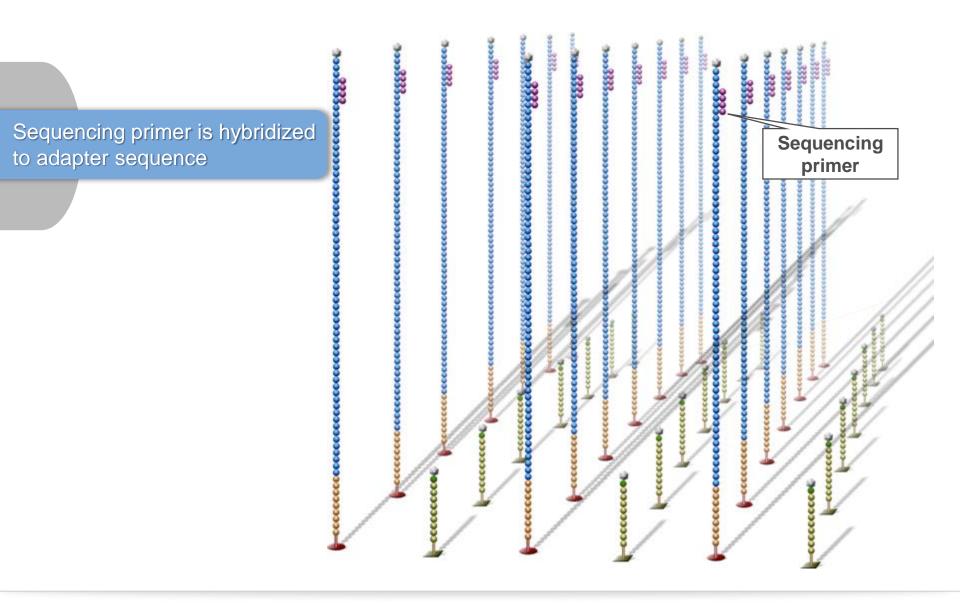
Blocking

Free 3' ends are blocked to prevent unwanted DNA priming

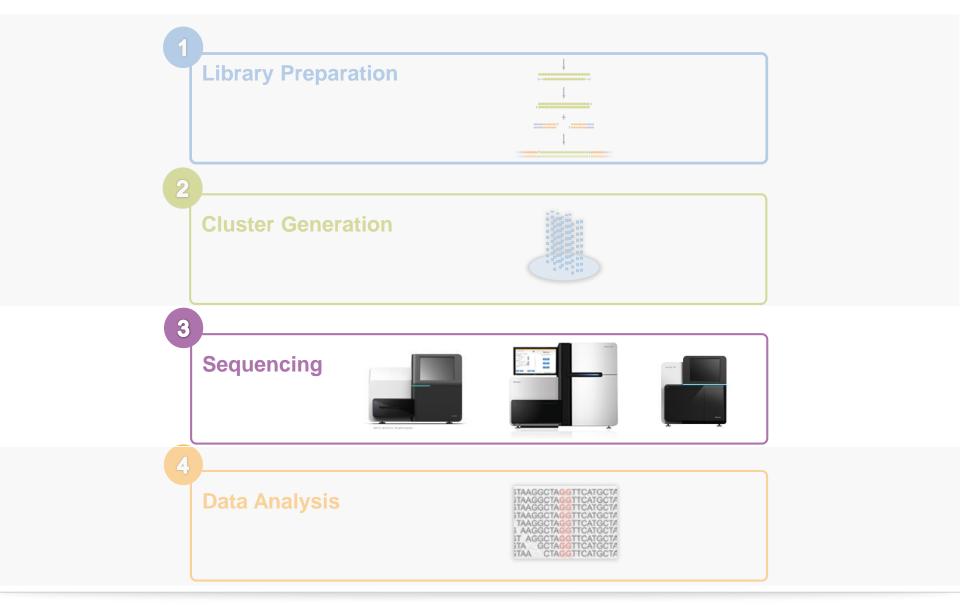




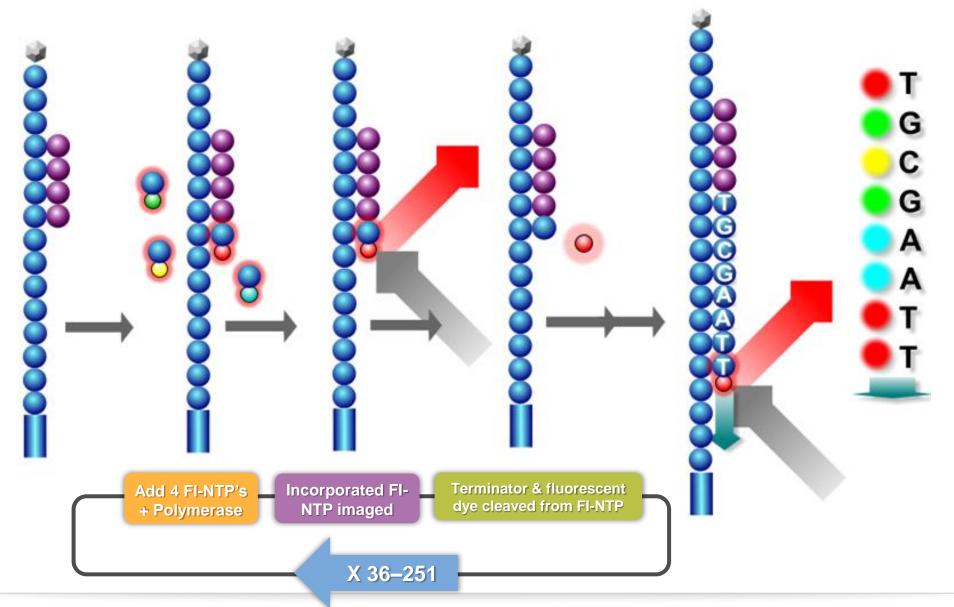
Read 1 Primer Hybridization



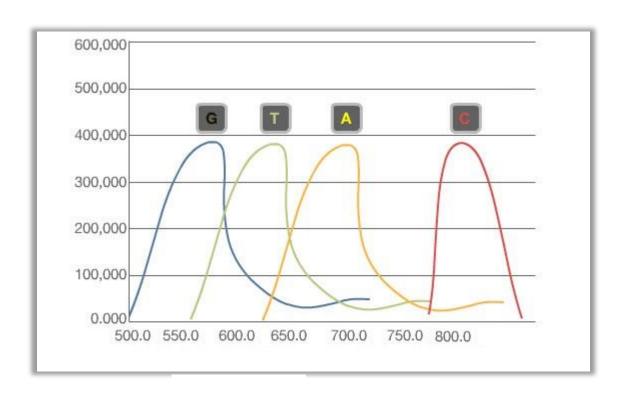
Illumina Sequencing Workflow



Sequencing By Synthesis (SBS)



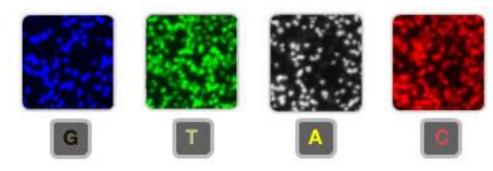
Four Channel SBS Chemistry: GA, HiSeq, MiSeq



Each of the four DNA bases emit an intensity of a unique wavelength

Collects four images:

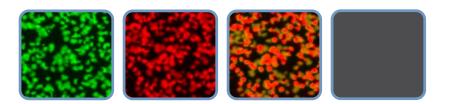
 During each cycle, each cluster appears in only one of four images

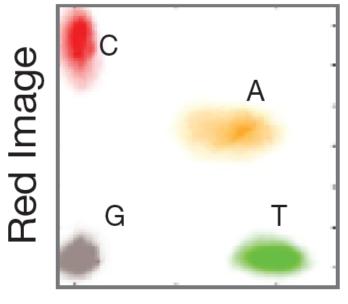




Two Channel SBS – NextSeq 500

- Two channel SBS uses two images
- Clusters appearing in green only are T
- Clusters appearing in red only are C
- Clusters appearing in both images are A
- Clusters not present in either green nor red are G
- Cluster intensities are plotted and bases are called accordingly

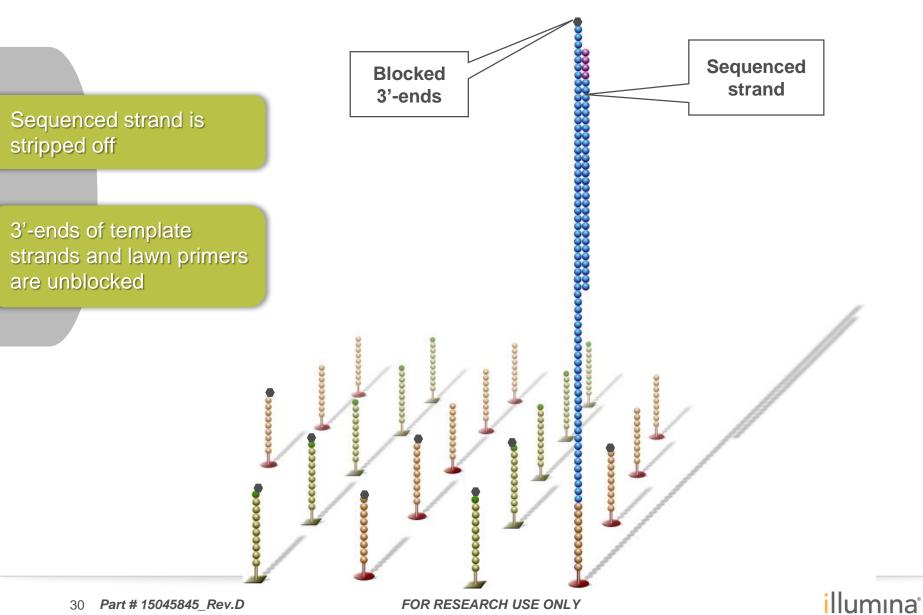




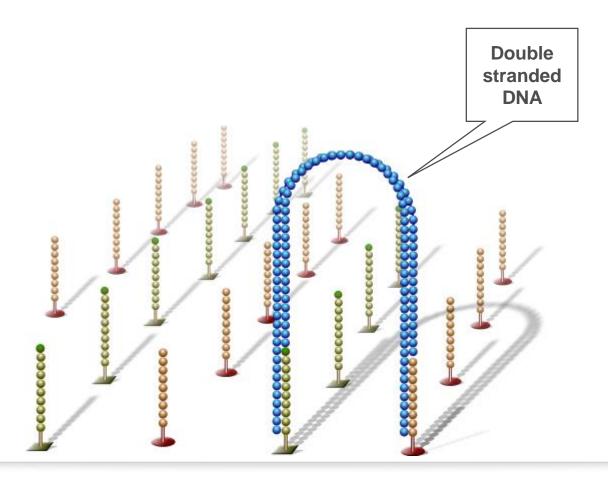
Green Image

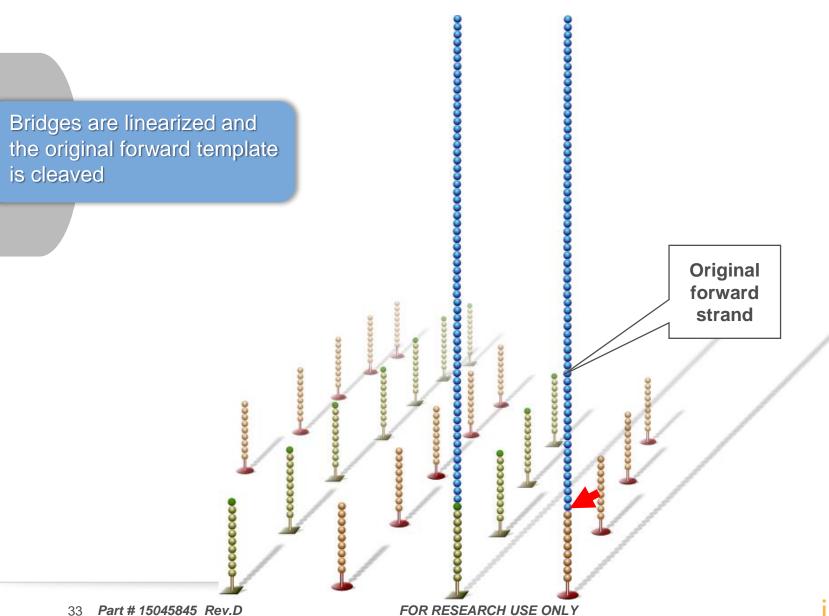


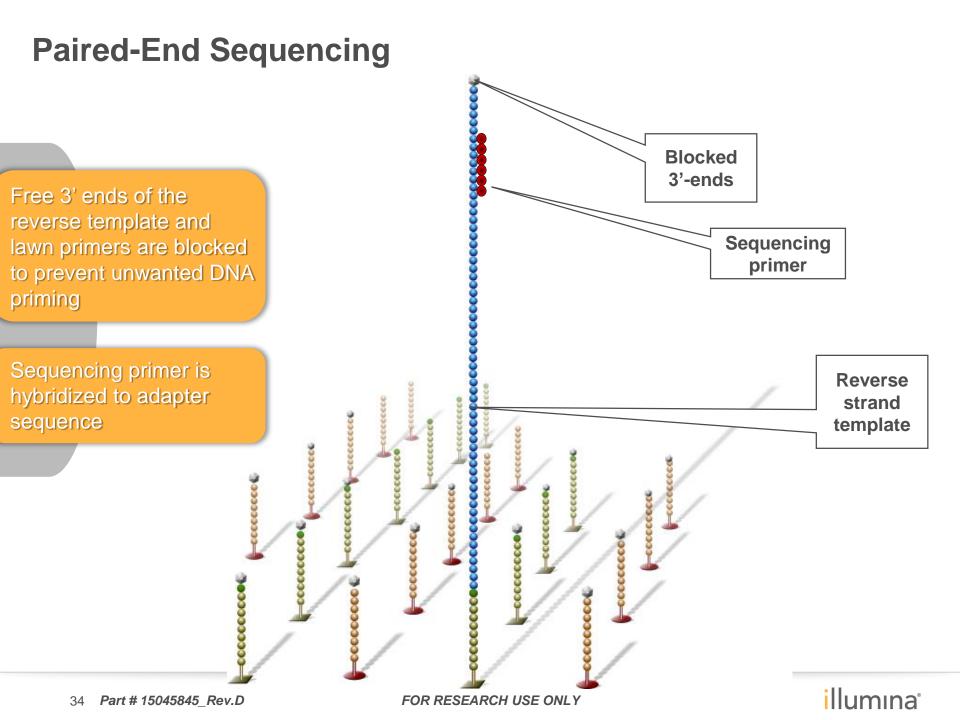




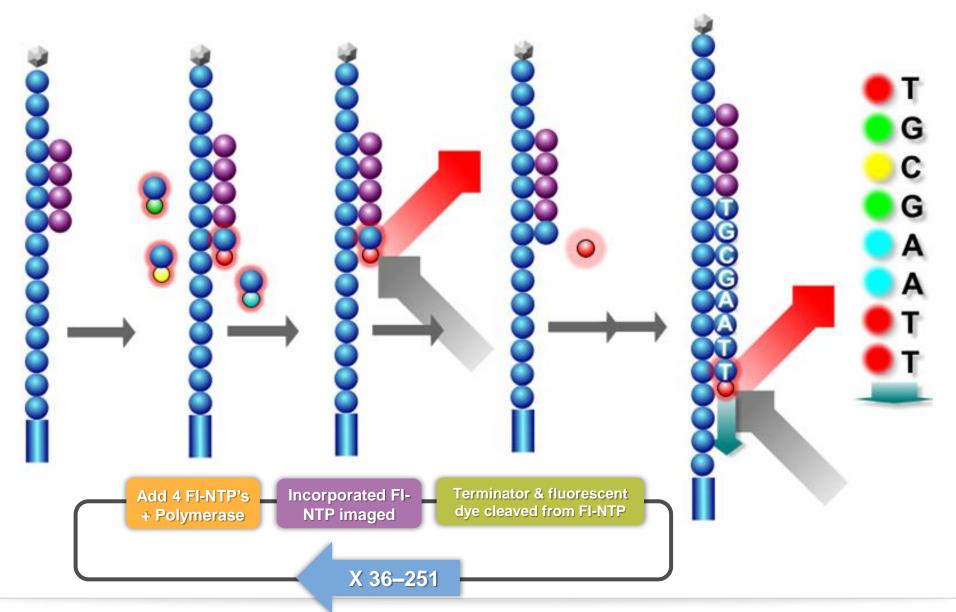
Single-stranded template loops over to form a bridge by hybridizing with a lawn primer Bridge formation 3'-ends of lawn primer are extended 3' extension



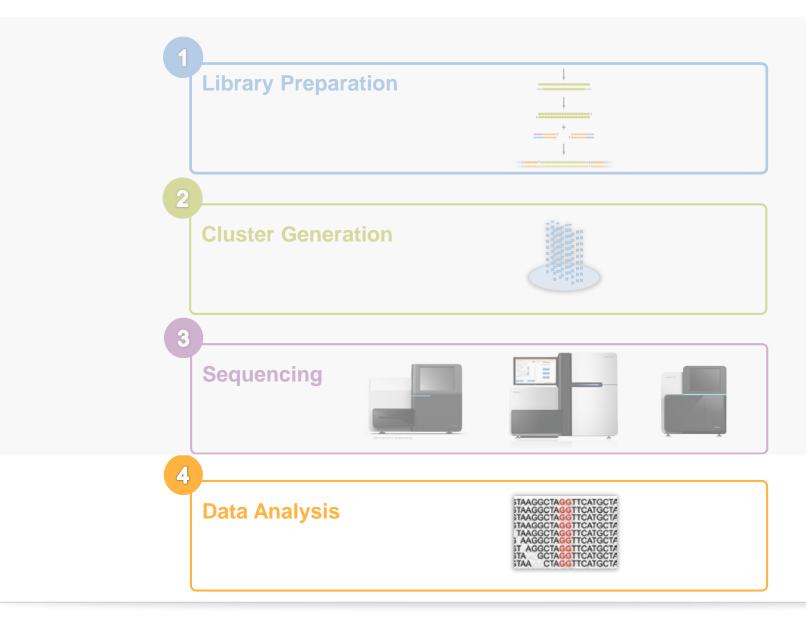




Sequencing By Synthesis 2nd Read



Illumina Sequencing Workflow





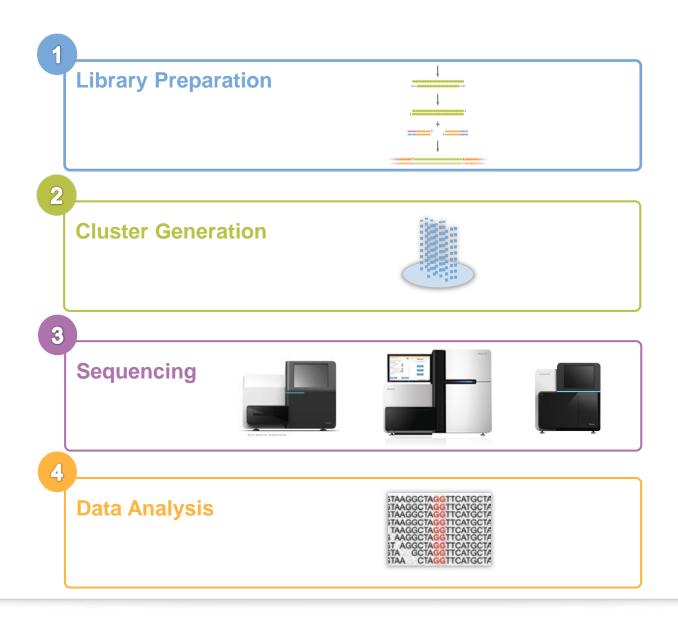
Data Analysis Overview



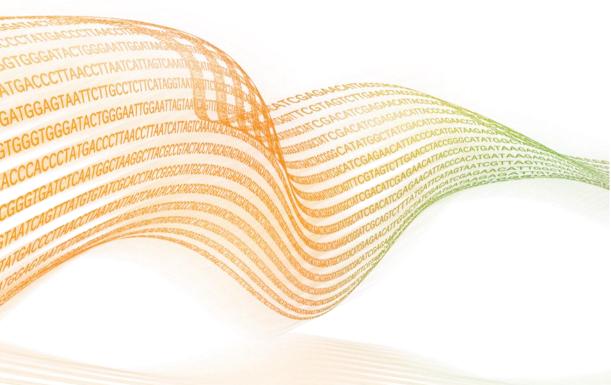
Analysis Overview

Analysis Type Software Outputs Control Software Images, Intensities and Base Calls ICS/MCS/RTA **CASAVA HiSeq Analysis Analysis Software Software MiSeq Reporter Alignments, Variant Detection** Visualization **Software** Annotation, Filtering, Reports

Summary



Questions?



AGTCAGGTCAGTCAAGCTTACTG GGTCAGTCAAGCTTACTGCATCG TCAGGTCAGTSAAGCTTACTGAA **AAGTT AGTG** CAGTCACTGT AGTCAAGCTG CTTAAGTCA GGTCAGTAG AAGCTTACTG AGTCAGGTC GGTCAGTCA GCTTACTGAA AAGCTTACTG AAGTT AGTCA GCAGTCACTGT AGTCAGGTCAGTCAAGCTTACTG CTTAAGTCAGGTCAGTCAAGCTG **GGTCAGTAGTCA CAAGCTTACTG** AGTCAGGTCAGTCAAGCTTACTG