Illumina Two-Channel SBS Sequencing Technology

High data accuracy with faster data generation.

Introduction

Illumina sequencing platforms leverage a highly accurate and robust sequencing by synthesis (SBS) technology that has become the most successful and widely adopted next-generation sequencing platform worldwide. Illumina SBS technology supports massively parallel sequencing using a proprietary reversible terminator-based method that enables detection of single bases as they are incorporated into growing DNA strands.

Illumina SBS technology is the foundation of all Illumina sequencing systems and employs either 2-channel or 4-channel methods for the detection of individual bases. The MiniSeq® and NextSeq® 500/550 Systems employ the latest evolution in SBS technology: 2-channel SBS sequencing. The 2-channel SBS method supports reduced cycle and data processing times, enabling benchtop sequencers, such as the MiniSeq and NextSeq Series Systems, to deliver results faster than ever before.

SBS Technology

Illumina 2- and 4-channel SBS sequencing technology uses fluorescently labeled nucleotides to sequence hundreds of millions of clusters on a flow cell surface in parallel (Figure 1). During each sequencing cycle, a single labeled deoxynucleotide triphosphate (dNTP) is added to the nucleic acid chain. The nucleotide label serves as a terminator for polymerization, so after each dNTP incorporation, the fluorescent dye is imaged to identify the base and then chemically cleaved to allow incorporation of the next nucleotide. Because all 4 reversible terminator-bound dNTPs (A, C, T, G) are present as single, separate molecules, natural competition minimizes incorporation bias. Base calls are made directly from signal intensity measurements during each cycle, greatly reducing raw error rates compared to other technologies. To see an animated video of Illumina SBS technology, visit www.illumina.com/SBSvideo.

Four-Channel SBS Sequencing

In 4-channel SBS, the acquisition of 4 distinct images enables a cycle-by-cycle observation of which color dye is incorporated into an individual cluster. Cluster detection software algorithms then process the images to determine the individual base calls for each unique cluster. With 4-channel sequencing, all 4 images are required to build up the DNA sequence. The MiSeq and HiSeq Series Systems currently use 4-channel SBS.

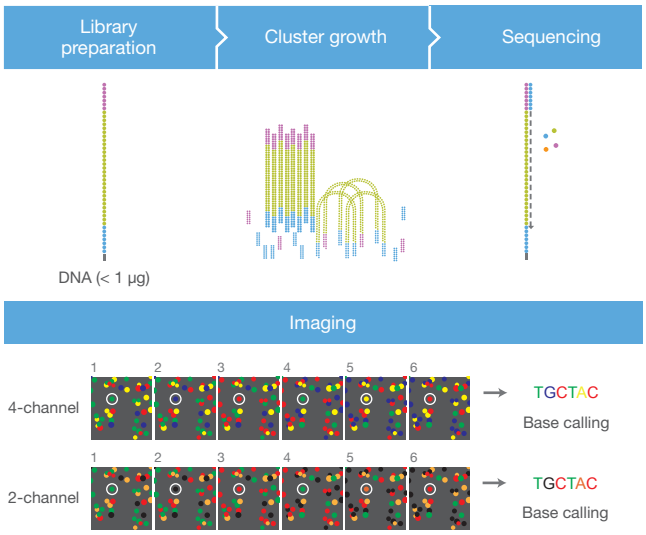

Figure 1: Four-Channel vs Two-Channel SBS Technology Image Detection and Base Calling. In 4-channel SBS, 4 images are necessary to capture the unique fluorescent dyes for each base. In contrast, 2-channel SBS requires only 2 images to determine all 4 base calls.

Two-Channel SBS Sequencing

2-channel SBS sequencing simplifies nucleotide detection, leveraging an innovative data processing approach that requires only 2 images to determine all 4 base calls. Rather than using a separate dye for each base, 2-channel sequencing uses a mix of dyes (Figure 2).

Images are taken of each cluster using red and green filter bands, with the 2-fold reduction in image acquisition, reducing sequencing time and accelerating sequence processing. Clusters seen in red or green images are interpreted as C and T bases, respectively. Clusters observed in both red and green images are flagged as A bases (appearing as yellow clusters in Figure 2), while unlabeled clusters are identified as a G base. The standard template generation process is built up over 5 cycles. In instances where clusters begin with a G base, the G base will be detected in subsequent cycles as A, C, or T bases are observed.

New v2 chemistry for the NextSeq Series Systems is optimized to improve the data quality of 2-channel SBS even further. The v2 reagents enhance signal intensities, clearly separating the clusters for more accurate base calling (Figure 2).

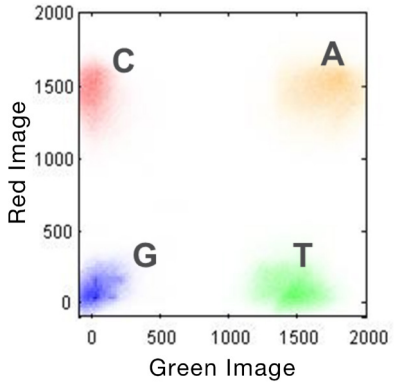

Figure 2: Two-Channel SBS Imaging. Accelerated detection of all 4 DNA bases is performed on the MiniSeq and NextSeq Series Systems using only 2 images to capture red and green filter wavelength bands. A bases will be present in both images (yellow cluster), C bases in red only, T bases in green only, and G bases in neither.

SBS Accuracy and System Compatibility

Illumina SBS-based sequencing systems deliver the most accurate sequencing data at any coverage, the highest yield of error-free reads, and the highest percentage of base calls above Q30* in the industry, even in difficult-to-sequence regions of the genome (Figure 3). This high data quality results in low false positive and false negative rates, reducing the need for extensive downstream validation and giving researchers full confidence in the data generated for their genome, exome, and transcriptome studies. Because all Illumina sequencing systems are based on the same core SBS technology, researchers can confidently transition their research from one Illumina sequencing system to another (Figure 4). Regardless of whether data are generated by a 4-channel or 2-channel SBS system, results can be seamlessly compared and analyzed in BaseSpace®, the Illumina genomics computing environment, or across a wide array of third-party analysis tools

Summary

Illumina SBS technology offers the highest NGS accuracy, enabling accurate base-by-base sequencing and robust performance across the genome. The latest evolution of this transformational technology can be found in the MiniSeq and NextSeq Series Systems, where it enables a breakthrough reduction in data generation times, enabling next-generation sequencing to become an everyday research tool.

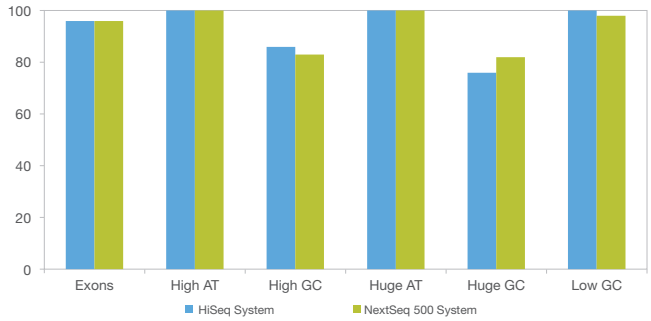

Figure 3: Coverage in Hard-to-Sequence Regions. Designed using the same fundamental sequencing chemistry technology, NextSeq, and HiSeq Systems exhibit robust performance in difficult-to-sequence regions of the genome.

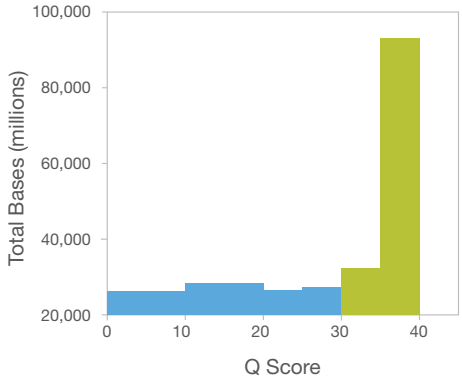

Figure 4: Base Call Accuracy and Performance. Two-channel SBS technology enables the NextSeq 500 System to deliver high-quality data, with a sequencing accuracy of > 75% of sequenced bases over Q30 at 2 × 150 bp.

References

1. www.illumina.com/systems/nextseq-sequencer/technology.html

* Q30 = 1 error in 1,000 base calls or an accuracy of 99.9%

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Pub. No. 770-2013-054 Current as of 04 January 2016

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