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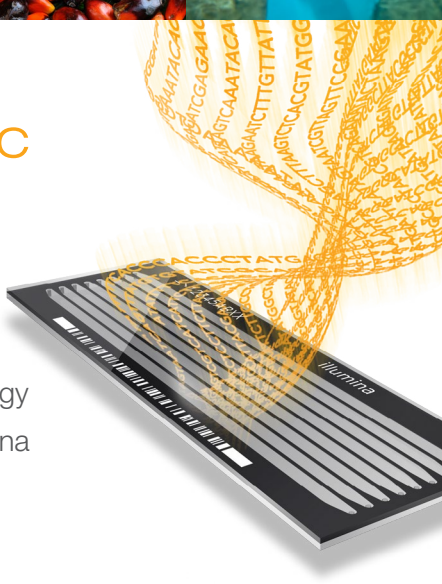
Accelerate agrigenomic breakthroughs

New long-read solution. Unprecedented accuracy. Push-button analysis.

TruSeq® Synthetic Long-Read DNA Library Prep

Combines new library prep method with the leading sequencing technology and informatics tools—all on an Illumina sequencing platform.



WHAT ARE SYNTHETIC LONG READS?

Long sequence reads can be used to complement shorter, paired-end reads for genomic analysis. With TruSeq Synthetic Long-Read technology, a genomic DNA sample is first fragmented to approximately 10 kilobases. Next, these fragments are clonally amplified, sheared, and marked with a unique barcode. They are then sequenced using Illumina technology. The TruSeq Long-Read Assembly App, offered in the BaseSpace® cloud computing environment, uses the barcodes to assemble short sequencing reads into synthetic long fragments accurately.

HOW CAN LONG READS HELP ME?

Longer sequence reads can facilitate alignment and improve the accuracy of genome assembly by providing insight into traditionally challenging regions, such as stretches of repetitive elements.

WHICH APPLICATIONS CAN BENEFIT FROM LONG READS?

Genome finishing, metagenomics, *de novo* assembly, and hybrid assembly with long and short reads are the most common applications that can benefit from long-read technology.

HOW MUCH STARTING DNA DO I NEED?

Libraries can be created from as little as 500 ng of starting DNA.

WHAT IS BASESPACE AND HOW DO I CONNECT TO IT?

BaseSpace is the Illumina genomics computing environment for next-generation sequencing data analysis. BaseSpace Core Apps provide push-button bioinformatics solutions for life science researchers, for the most common Illumina sequencing workflows. To create a free account, visit basespace.illumina.com.

HOW DOES THE BASESPACE APP WORK?

Designed for use with the TruSeq Synthetic Long-Read DNA Library Prep Kit, the TruSeq Long-Read Assembly App constructs long sequences from shorter sequencing reads. The intuitive user interface simplifies the informatics so that researchers can analyze data simply by selecting the sample and destination. The app then performs pre-processing of the shorter reads, assembles contigs, and performs contig scaffolding. The assembled reads are exported in industry-standard FASTQ format, which can be imported directly into various downstream assembly tools. The TruSeq Long-Read Assembly App enables one-click long-read assembly without requiring bioinformatics expertise or additional infrastructure.

To learn more about Illumina technology for long reads, visit
www.illumina.com/aglongreads

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Long-read *de novo* sequencing and genome finishing

Longer read lengths for improved assemblies.

OIL PALM

Elaeis guineensis | 1.83 Gb | 16 Chromosomes

Generate longer contigs and better scaffolds for genomes with highly repetitive regions such as oil palm.

CORN

Zea mays | 2.3 Gb | 10 Chromosomes

Combine short-read sequencing with long reads to compare and contrast the progenitors of today's commercial maize germplasm.

RICE

Oryza sativa | 420 Mb | 12 Chromosomes

Compare genome structure organization between strains and other cereal grass species to pinpoint highly conserved or rapidly evolving regions.

CALIFORNIA CONDOR

Gymnogyps californianus | ~1.2 Gb | 40 Chromosomes

Obtain unique information on a model system for avian conservation genomics.