TruSeq® Genotype N_e Kit

A cost-effective, flexible solution for targeted genotyping by sequencing for any plant or animal species.

Highlights

- **Customizable Panel**
  Achieve consistent genotyping performance from content designed by Illumina Concierge services
- **Flexible Solution**
  Identify novel variants and easily update your panel content with new genotyping information
- **Integrated Workflow**
  Access streamlined library prep, reliable sequencing, and user-friendly data analysis

Introduction

The TruSeq Genotype N_e Kit is a flexible, cost-effective solution for targeted genotyping by sequencing (GBS) for parentage, purity studies, and breeding decisions for any plant and nonhuman animal species (Table 1). The TruSeq Genotype N_e Kit is designed and optimized to work with up to 5000 markers and is easily scalable from hundreds to tens of thousands of samples.

All-Inclusive Solution

The integrated Illumina workflow for amplicon sequencing enables labs to access a fully supported solution, from design through analysis (Figure 1). The TruSeq Genotype N_e Kit is designed and optimized for use on the MiniSeq™, MiSeq®, and NextSeq® Series of Sequencing Systems, without requiring additional instrumentation. A single source of technical and field specialists for design, library preparation, sequencing, and data analysis, and the combined expertise of the Illumina support team, ensure rapid resolution and minimize potential laboratory downtime.

Confident Assay Design

The TruSeq Genotype N_e Kit is a fully customizable sequencing assay. Illumina Concierge Service offers design support for all oligonucleotide probes for the TruSeq Genotype N_e Kit to ensure consistent performance. Illumina Concierge Service enables customers to:

- Include multiple marker types such as single nucleotide polymorphisms (SNPs), insertions/deletions (indels), etc, in a single panel
- Update existing panels without large sample commitment
- Design panels even in the absence of a complete reference sequence

Contact an Illumina representative for access to Illumina Concierge Service.

Streamlined Workflow

A key element of Illumina NGS is high-quality library preparation. Illumina library prep protocols can accommodate a range of throughput needs, from lower-throughput protocols for small laboratories to fully automated library preparation workstations for large laboratories or genome centers. Different methods are employed to capture regions of interest from input DNA and prepare sequencing libraries.

The TruSeq Genotype N_e assay uses an amplicon generation approach. Amplicon generation employs a hybridization followed by extension-ligation approach, creating a single-stranded template from a double-stranded genomic DNA (gDNA) population that is later amplified via PCR (Figure 2). The library preparation protocol can be completed with less than 2.5 hours of hands-on time (Figure 3).

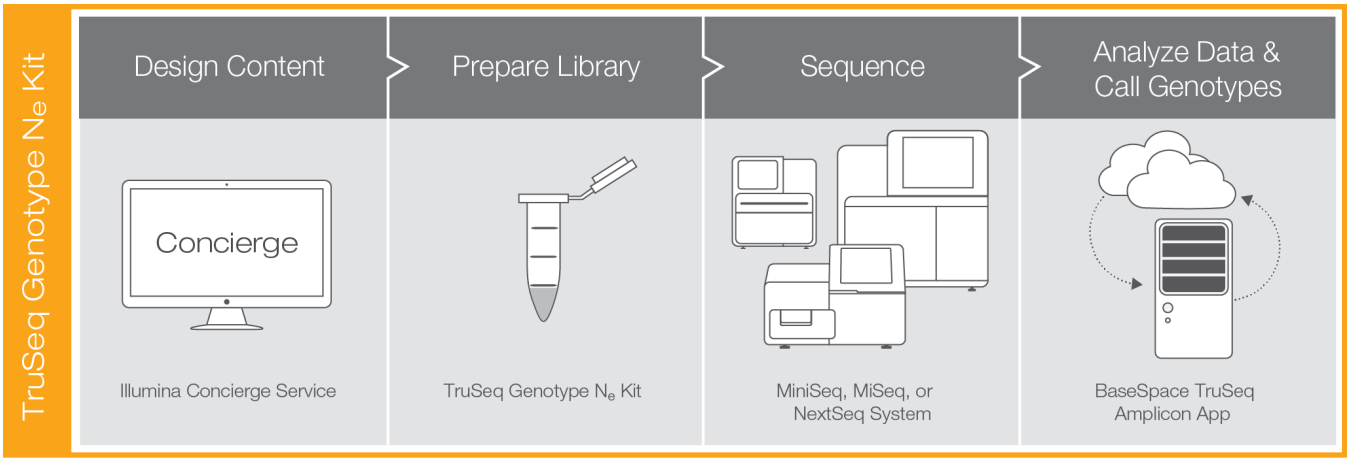

Figure 1: TruSeq Genotyping N_e Workflow— The TruSeq Genotyping N_e Kit provides a fully supported, comprehensive solution for genotyping by sequencing from probe design with Illumina Concierge Service through library preparation, sequencing, and data analysis.

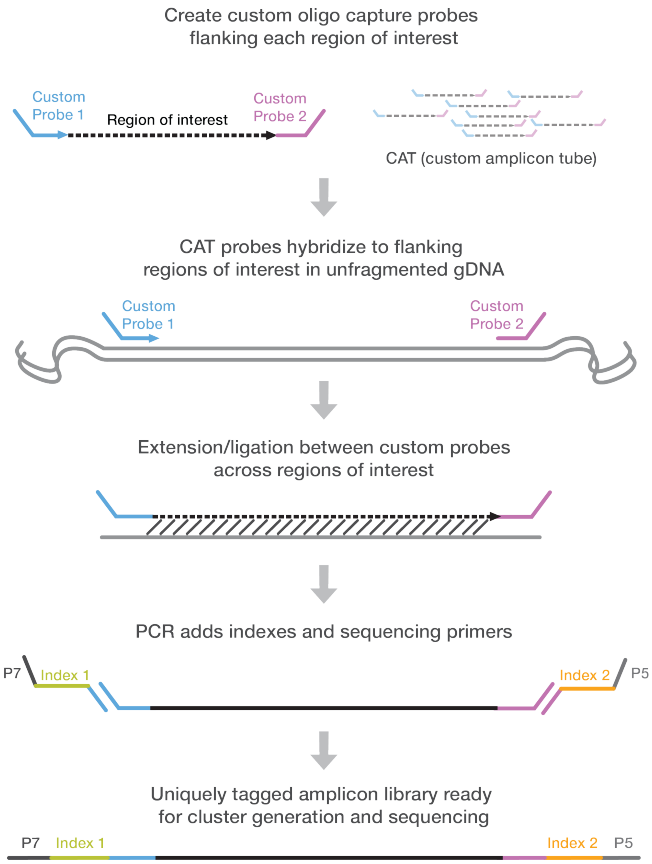

Figure 2: Amplicon Chemistry— The TruSeq Genotype N$_e$ Kit uses an extension/ligation-based method to prepare custom, sequencing-ready libraries.

Industry-Leading Data Quality

The TruSeq Genotype N$_e$ Kit is compatible with the MiniSeq, MiSeq, and NextSeq Systems, which use proven Illumina sequencing by synthesis (SBS) chemistry. More than 90% of the world's sequencing data are generated by Illumina SBS chemistry.* Illumina systems deliver the highest percentage of sequenced bases over Q30 in the industry.[1–5] With consistent high-quality results, researchers can be confident in the accuracy of their data, even with challenging targets of interest (eg, repetitive regions, GC-rich content).[6]

Simplified Data Analysis

Data can be seamlessly streamed from Illumina sequencing systems to BaseSpace® Sequence Hub, a user-friendly genomics cloud computing platform that offers simplified data management, analytical sequencing tools, and data storage. The TruSeq Genotype N$_e$ Kit uses the TruSeq Amplicon App to streamline analysis of custom panels.

Figure 3: Library Prep Workflow— The TruSeq Genotype N$_e$ Kit enables simplified library preparation with less than three hours of hands-on time.

* Data calculations on file. Illumina, Inc., 2015.

Table 1: TruSeq Genotype N_e Kit Specifications

Feature	Specification
Species	Any Nonhuman Species
Input Requirement	50 ng Genomic DNA
Target Multiplexing	16–5000 in a single panel
Sample Multiplexing	Up to 384

Summary

The TruSeq Genotype N_e Kit is a flexible, cost-effective solution for targeted GBS for parentage, purity studies, and breeding decisions. With content designed through Illumina Concierge services, the TruSeq Genotype N_e Kit provides a fully customizable panel for GBS for any plant and nonhuman animal species. With an integrated workflow that includes library preparation through sequencing and data analysis, customers have a single source of support.

Learn More

To learn more about the TruSeq Genotype N_e Kit and other plant and animal sequencing and genotyping options, visit www.illumina.com/agrigenomics.

Ordering Information

Product	No. of Samples	Catalog No.
TruSeq Genotype N_e Kit(includes all necessary reagents)	96 samples, up to 384 indexes	20018978

References

1. Perkins TT, Tay CY, Thirriot F, Marshall B. Choosing a benchtop sequencing machine to characterize Helicobacter pylori genomes. *PLoS One*. 2013;8:e67539.
2. Quail MA, Smith M, Coupland P, et al. A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. *BMC Genomics*. 2012;13:341.
3. Ross MG, Russ C, Costello M, et al. Characterizing and measuring bias in sequence data. *Genome Biol*. 2013;14:R51.
4. Jünemann S, Sedlazeck FJ, Prior K, et al. Updating benchtop sequencing performance comparison. *Nat Biotechnol*. 2013;31:294–296.
5. Loman NJ, Misra RV, Dallman TJ, et al. Performance comparison of benchtop high-throughput sequencing platforms. *Nat Biotechnol*. 2012;30:434–439.
6. Wong SQ, Fellowes A, Doig K, et al. Assessing the clinical value of targeted massively parallel sequencing in a longitudinal, prospective population-based study of cancer patients. *Br J Cancer*. 2015;112:1411–1420.

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