NGS Target Capture Kit for Flowering Plant Phylogenetics

OVERVIEW

The new myBaits® Angiosperms-353 Expert Panel enriches hundreds of putatively single-copy genes that are orthologous across all flowering plants. Combining the flexible power of in-solution target capture with an expertly selected set of orthologous loci, this new probe set has been demonstrated to enrich hundreds of genes across a broad taxonomic range of angiosperms. Probes were designed from 5-15 representative angiosperm species’ sequences from 353 loci, selected using a novel k-medoids clustering approach to maximize taxonomic breadth. This panel provides a user-friendly solution for phylogenetic research across the entire angiosperm clade.

The Angiosperms-353 panel is provided as a complete in-solution target capture kit, including buffers, blockers, and baits, along with an easy-to-use protocol. Alternatively, the myReads® NGS service team at Arbor Biosciences is available to perform library preparation, target capture, and sequencing for your entire project.

FEATURES & BENEFITS

- **Ready-To-Go Panel** – Designed by expert plant geneticists, ready for immediate shipment
- **Proven Results** – Demonstrated utility across a broad taxonomic range
- **Open Platform** – Compatible with any NGS library preparation system
- **Simple Protocol** – Perfect for new or expert NGS users
- **Complete Solution** – Convenient kits include hybridization & wash reagents

APPLICATIONS

- Plant Genetics
- Phylogenetics
- Variant Discovery
- Exon Sequencing
- Herbarium Sequencing
myBaits kits can greatly enhance the efficiency and cost-effectiveness of any NGS research project. If a complete solution is needed, from sample preparation to data delivery, our myReads® services team is available to handle projects of any size. Contact our scientists today regarding your next project, and join a community of researchers in adopting one of the most versatile and fastest-growing technologies in genetics research.

Fig 1. Gene Recovery Heatmap of Angiosperms-353 Panel. Rows = samples, columns = genes. Colored according to recovered percentage of total intended target length (average of all k-medoid transcript sequences). Figure 3 from Johnson et al. (2018), Systematic Biology, with permission.

Fig 2. Total Recovered Per-Locus Sequence Length for Exon and Flanking Regions. For each of the 353 loci targeted by the Angiosperms-353 panel, the total amount of sequence recovered when mapped to exons alone (in orange) or exons + flanking non-coding/intron regions (in blue). Total targeted length of the panel (exons only) was 261Kb; median sequence recovered was 137Kb total for exons and 217Kb for flanking regions. Modified from figure 4, Johnson et al. (2018), Systematic Biology, with permission.

**PRODUCT TABLE**

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*All prices in USD.