

# Pan-Plant riboPOOL

## Universal, Efficient Ribosomal RNA Depletion For Flowering Plants (Angiosperms)

- ✓ Efficient rRNA depletion tool
- ✓ Broad coverage of flowering plants
- ✓ For leaf, seed & root tissue
- ✓ Targets 28S, 18S, 5.8S & 5S rRNA
- ✓ Targets mitochondrial rRNA
- ✓ Targets plastid rRNA

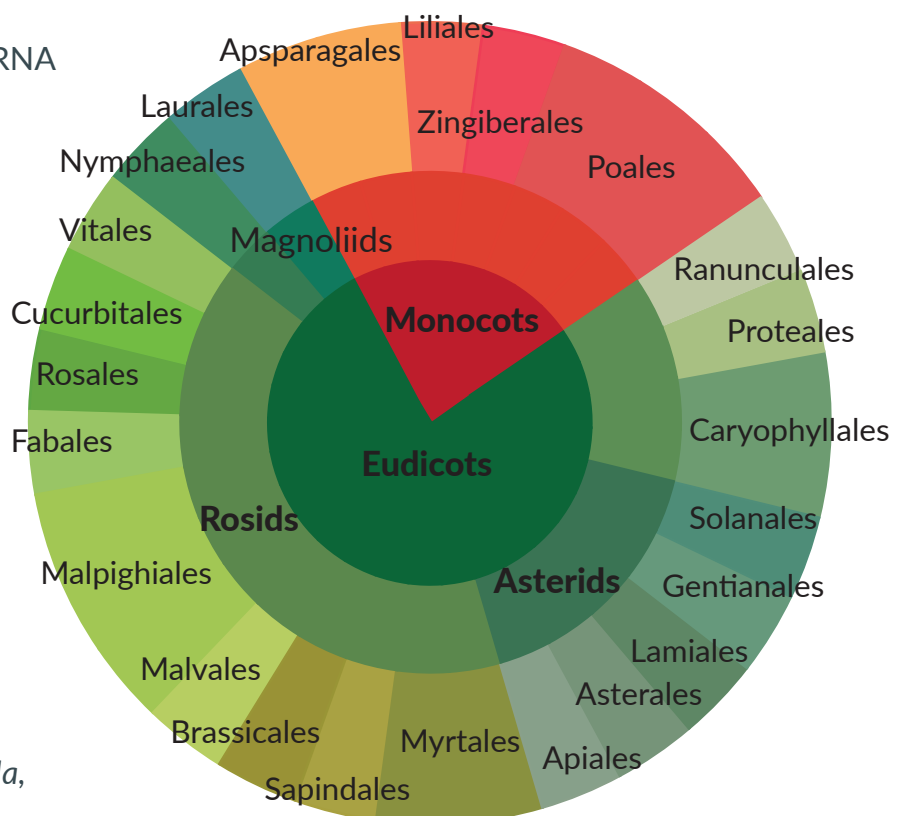
The high abundance of ribosomal RNA (rRNA) limits detection efficiency of relevant RNAs of the transcriptome by RNA-Seq. The **Pan-Plant riboPOOL** offers a universal solution to selectively deplete cytoplasmic (28S, 18S, 5.8S & 5S), plastid and mitochondrial rRNA of flowering plants in leaf, seed and root tissue.

### Wide Species Coverage of Pan-Plant riboPOOL

The Pan-Plant riboPOOL consists of a highly complex mixture of biotinylated oligos, designed to optimally cover major phyla of flowering plants.

The Pan-Plant riboPOOL depletes rRNA for more than 30 orders:

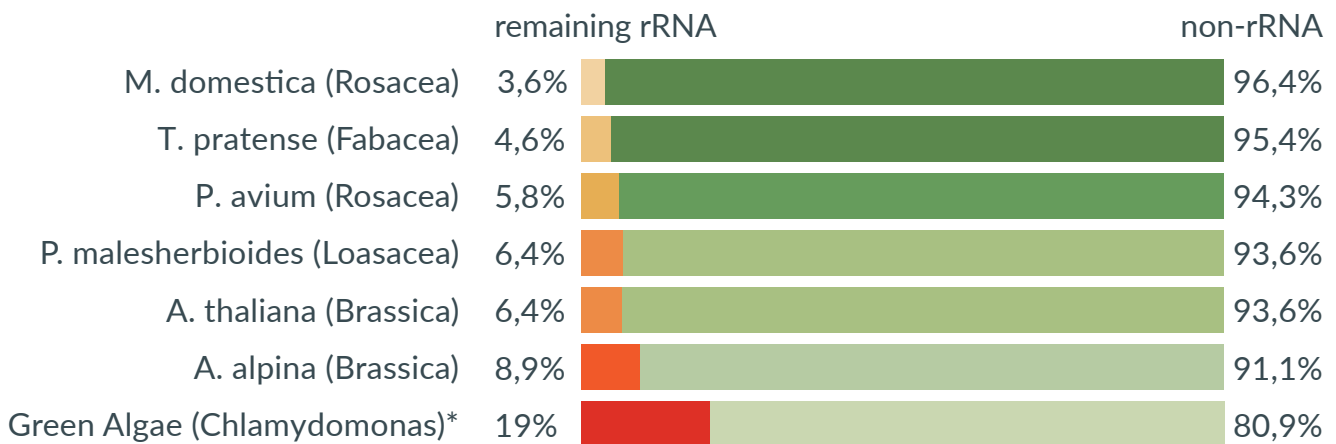
- Rice • Jatropha • Soy Bean
- Potato • Cotton • Coffee
- Carrot • Artichoke • Olive
- Arabidopsis • Corn • Aster
- Wheat • Apple • Orange
- Buckwheat • and more



*\*If your species is not within these phyla, please enquire about our **custom riboPOOLS**.*

## Data with Pan-Plant riboPOOL – Efficient Across Phyla

The Pan-Plant riboPOOL efficiently depleted rRNA (> 91%) when tested on six species of Angiosperms from genera Fabacea, Loasacea, Brassicae and Rosaceae. Remarkably, a species from the primitive Green Algae phyla when tested showed > 80% rRNA depletion efficiency, suggesting that the Pan-Plant riboPOOL may be successfully applied to other phyla aside from Angiosperms.



\*Green Algae is a primitive Algae, very distantly related to Angiosperms. The Pan-Plant riboPOOL was designed for Angiosperms.

Data kindly provided by Dr. Bruno Huettel and Dr. Christian Wöhle, Max Planck Genome Centre Cologne. RNA (1 µg, RIN ~8) was isolated with QIAgen RNeasy and subject to rRNA depletion with Pan-Plant riboPOOL, followed by clean-up with RNA XPClean (Beckman Coulter). Library preparation and sequencing was performed with NEB kit (modified) and Illumina HiSeq3000 respectively.

### Further information:

- Enzyme-free depletion
- No Poly-A selection
- Completed in 70 mins
- Suitable for RNA input amounts from 100 ng - 3 µg
- Compatible with various RNA clean-up methods & RNA-Seq library preparation kits
- Can be used as Combination riboPOOL with other riboPOOLS to study mixed species samples. E.g. plant microbiota

### Available formats:

1. Probes alone with nuclease-free water	2 nmol (20 rx)	5 nmol (50 rx)	10 nmol (100 rx)	
2. Complete riboPOOL kits (includes buffers, streptavidin-magnetic beads, reaction tubes and ethanol precipitation reagents)	6 rx Trial (one-time purchase)	12 rx	24 rx	96 rx

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