



Aug 16,  
2019

## Sequencing Protocols for the One Thousand Plant Transcriptomes Initiative

Eric J. Carpenter<sup>1</sup>, Naim Matasci<sup>2,3</sup>, Shuangxiu Wu<sup>4</sup>, Jing Sun<sup>4</sup>, Jun Yu<sup>4</sup>, Fabio Rocha Jimenez Vieira<sup>5</sup>, Chris Bowler<sup>5</sup>, Richard G. Dorrell<sup>5</sup>, Matt Gitzendanner<sup>6</sup>, Ling Li<sup>7</sup>, Wensi Du<sup>7</sup>, Kristian Ullrich<sup>8</sup>, Michael S. Barker<sup>9</sup>, James H. Leebens-Mack<sup>10</sup>, Gane Ka-Shu Wong<sup>11</sup>

<sup>1</sup>Department of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada.,

<sup>2</sup>CyVerse, University of Arizona, Arizona, U.S.A., <sup>3</sup>Current address: Lawrence J. Ellison Institute for Transformative Medicine, University of Southern California, Los Angeles, CA 90033, U.S.A., <sup>4</sup>CAS Key Laboratory of Genome Sciences and Information, Beijing, Institute of Genomics, Chinese Academy of Sciences, Beijing 100101, People's Republic of China., <sup>5</sup>École Normale Supérieure, Paris., <sup>6</sup>Department of Biology, University of Florida, Gainesville, Florida 32611, USA., <sup>7</sup>BGI-Shenzhen, Beishan Industrial Zone, Yantian District, Shenzhen 518083, People's Republic of China., <sup>8</sup>Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Biology, Plön, Germany., <sup>9</sup>Department of Ecology & Evolutionary Biology, University of Arizona, Tucson, AZ 85721 USA., <sup>10</sup>Department of Plant Biology, University of Georgia, Athens, GA 30602, USA., <sup>11</sup>Department of Biological Sciences, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada.BGI-Shenzhen, Beishan Industrial Zone, Yantian District, Shenzhen 518083, People's Republic of China.Department of Medicine, University of Alberta, Edmonton, Alberta, T6G 2E1, Canada.

**2** Works for me dx.doi.org/10.17504/protocols.io.38jgrun



### ABSTRACT

The 1000 Plants (1KP) initiative explored the genetic diversity of green plants (Viridiplantae) by sequencing RNA from 1,342 samples representing 1,173 species. All of the analyses done for the 1KP capstone, and previous studies on subsets of these data, are based on a series of de novo transcriptome assemblies and related outputs that will be described in this publication. We expect that these data will also be useful to other researchers with interests in specific gene families, either across the green plant tree of life or in more focused lineages. These protocols provide additional details on the sample and sequence processing, hopefully providing insight for reproducibility and tools for other researchers working on plant transcriptomics and evolution.

### Collection protocols



This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited