

## **INNOVATIVE APPROACHES FOR RNASEQ LIBRARY PREPARATION REPRESENT VALUABLE TOOLS TO IMPROVE PLANT POPULATION STUDIES**

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Large scale mRNA profiling technologies constitute a powerful tool for genome-wide eQTL mapping in plants, allowing thousands of eQTLs to be detected in a single experiment and potentially providing functional insights on genotypic differences. However, despite sequencing costs have progressively decreased in the last years, those of RNAseq library preparation remained stable and can currently account for up 2/3 of total costs, thus limiting the application of this technology for large population studies. New library preparation methods, enabling high levels of sample multiplexing, have recently been released to overcome this issue. However the technical features of these protocols has not been investigated yet in relation to traditional RNAseq libraries and their performances for population studies has to be proven. In this work we tested and compared with a standard approach, two new RNAseq kits by Lexogen and Alithea, respectively, that allow to process up to 96 samples simultaneously, thus strongly reducing library prep costs and hand-on-time. The methods have been compared in terms of technical performances, number of detected genes and functional pathways identified. Results demonstrated that the transcriptome quantification obtained with the new approaches was highly correlated with that achieved with the traditional method. In addition, the large majority of detected genes was shared across technologies. Finally, the transcriptome analysis of a population of 417 common bean (*P. vulgaris*) RNA samples using one multiplexing kit allowed to appropriately cluster samples according to growth location conditions and genotypes, demonstrating the suitability of the method for studying large cohorts. The identification of technologies that enable efficient and cost-effective

RNAseq analysis is important to facilitate and expand plant population studies, in order to provide a better understanding on the underlying phenotypic and genotypic variations, ultimately improving biodiversity conservation and the identification of resilience traits to climate changes.