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Please use this identifier to cite or link to this item: http://hdl.handle.net/123456789/3444 Title: Labeling and Sorting of Arabidopsis SAM Cell Populations to Capture Their Transcriptome Profile Authors: Mahajan, M. (/jspui/browse?type=author&value=Mahajan%2C+M.) Yadav, R.K. (/jspui/browse?type=author&value=Yadav%2C+R.K.) Kevwords: GFP Stem cells Sorting **FACS** Issue Date: 2020 Publisher: Springer Link Citation: Methods in Molecular Biology 2094, pp. 39-47 Abstract: In higher plants, the cells that form aboveground tissues and organs are derived from the shoot apical meristem (SAM). SAM is dynamic in nature and divided into central zone (CZ), peripheral zone (PZ), and rib meristem (RM). Stem cells reside in the CZ, and their progenitors differentiate to form lateral organs in PZ and stem tissue in RM. Besides zones, the SAM is also divided into distinct clonal cell layers that show patterned cell division. Here, we describe methods to tag and isolate cell types from both cell layers and zones of SAM in high purity using cell sorter. This method enable plant biologist in rapid isolation of desired cell types from SAM to record their transcriptome, epigenome, proteome, and metabolome. The information generated by this approach will elucidate the mechanism of stem cell self-renewal, differentiation, and organogenesis in SAM. URI: https://link.springer.com/protocol/10.1007%2F978-1-0716-0183-9_5 (https://link.springer.com/protocol/10.1007%2F978-1-0716-0183-9_5) http://hdl.handle.net/123456789/3444 (http://hdl.handle.net/123456789/3444) Appears in Research Articles (/jspui/handle/123456789/9)

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