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MPAPASS Software Collection

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1 Works for me dx.doi.org/10.17504/protocols.io.bm3gk8jw

Translational Nanobiology Section

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ABSTRACT

This is collection contains the protocols required for each step in the mpapass software pipeline for performing stitched multiplex analysis. This is one of a number of protocols in the pipeline for using the mpapass software package and is applicable to the latest release of the software.

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BEFORE START

MPAPASS software can be found at https://nano.ccr.cancer.gov/mpapass.

DISCLAIMER:

This protocol summarizes key steps for a specific type of method, which is one of a collection of methods and assays used for EV analysis in the NCI Translational Nanobiology Section at the time of submission of this protocol. Appropriate use of this protocol requires careful, cohesive integration with other methods for EV production, isolation, and characterization.

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This is collection contains the protocols required for each step in the mpapass software pipeline for performing stitched multiplex analysis. This is one of a number of protocols in the pipeline for using the mpapass software package and is applicable to the latest release of the software.

FILES

MPAPASS - Gating flow cytometry multiplex data

Version 1

by Joshua Welsh, Translataional Nanobiology Section, Laboratory of Pathology, Center for Cancer Research, National Cancer Institute, National Institutes of Health

MPAPASS - Creating an MPAPASS database

Version 1

by Joshua Welsh, Translataional Nanobiology Section, Laboratory of Pathology, Center for Cancer Research, National Cancer Institute, National Institutes of Health

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