

NOV 02, 2023

OPEN BACCESS



DOI:

dx.doi.org/10.17504/protocol s.io.36wgqjb5ovk5/v1

Collection Citation: Sean M Cook, Vera A Tang, Joanne Lannigan, Jennifer C. Jones, Joshua A Welsh 2023. Quantitative Flow Cytometry (qFCM) protocols for end-to-end optimization of cross-platform extracellular vesicle studies. protocols.io https://dx.doi.org/10.17504/protocols.io.36wgqjb5ovk5/v1

License: This is an open access collection distributed under the terms of the Creative Commons
Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working We use this collection and it's working

Quantitative Flow Cytometry (qFCM) protocols for end-toend optimization of cross-platform extracellular vesicle studies

Sean M Jennifer C. $Cook^1$, Vera A Tang 2 , Joanne Lannigan 3 , Jones 1 , Joshua A Welsh 1

¹Laboratory of Pathology, Translational Nanobiology Section, Centre for Cancer Research, National Institute of Health, National Institutes of Health:

²aculty of Medicine, Department of Biochemistry, Microbiology, and Immunology, University of Ottawa, Flow Cytometry and Virometry Core Facility;

³Flow Cytometry Support Services

Translational Nanobiology Section



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.

Created: Jan 30, 2023

Last Modified: Nov 02,

2023

COLLECTION integer ID:

76090

Funders Acknowledgement:

NIH

Grant ID: ZIA BC011502

NIH

Grant ID: ZIA BC011503

NIH

Grant ID: 4UH3TR002881-03

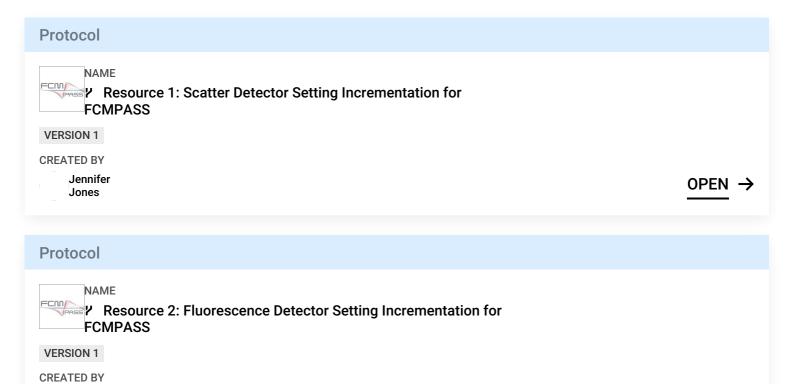
ABSTRACT

Flow cytometry (FCM) is a common extracellular particles (EPs), including viruses and extracellular vesicles (EVs), characterization method. Frameworks such as MIFlowCyt-EV exist to provide reporting guidelines for metadata, controls, and data reporting. However, tools to optimize FCM for EP analysis in a systematic and quantitative way are lacking. Here, we demonstrate a cohesive set of methods and software tools that optimize FCM settings and facilitate cross-platform comparisons for EP studies. We introduce an automated small particle optimization (SPOT) pipeline to optimize FCM fluorescence and light scatter detector settings for EP analysis and leverage quantitative FCM (qFCM) as a tool to further enable FCM optimization of fluorophore panel selection, laser power, pulse statistics, and window extensions. Finally, we demonstrate the value of qFCM to facilitate standardized cross-platform comparisons, irrespective of instrument configuration, settings, and sensitivity in a cross-platform standardization study utilizing a commercially available EV reference material.

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.

FILES



Jennifer

OPEN \rightarrow

Protocol

NAME

Resource 3: SSC Collection Optics and

Calibration

VERSION 1

CREATED BY

Jennifer Jones

 $OPEN \rightarrow$

Protocol

NAME

Resource 4: rEV Serial

Dilution

VERSION 1

CREATED BY

Jennifer Jones

 $OPEN \rightarrow$

Protocol

Resource 5: rEV Scatter Detector Setting

Incrementation

VERSION 1

CREATED BY

Jennifer Jones

OPEN →

Protocol

Resource 6: rEV Fluorescent Detector Setting Incrementation

VERSION 1

CREATED BY

Jennifer Jones

OPEN →

Protocol

Oct 2 2023



Jennifer

Jones

OPEN →