Running QC & Setup on the Aurora Version: 1.01

Note: Running QC takes approximately 5 minutes and should be performed every 24 hours Windows login: username: Administrator password: BDIS#1

Prepare Cytek SpectroFlo beads:

- 1. Obtain SpectroFlo bead vial from small fridge (Check lot Number, SKU # N7-97355)
- 2. Vortex bead vial
- 3. Prepare the bead suspension by adding 1 drop of beads to ~300uL of diH2O in a FACS tube

Warm up instrument and run QC:

- 1. Ensure instrument is on (round button on left-hand side of instrument) and log into PPMS
- Open SpectroFlo and login username: Admin password: \*\*\*\*\*\*\*\*\*
- 3. Go to **QC & Setup** module
- 4. Confirm instrument has warmed up for at least 20 min.
- 5. Remove diH2O tube from sample injection port (SIP)
- 6. Vortex the bead suspension and install the tube on the instrument
- 7. The Start button in the software will become enabled
- 8. Make sure bead lot on bottle matches lot in software and hit Start
- 9. A dialog box will display when QC has completed. Possible results are:
  - a. PASSED
  - b. FAILED Run clean FLOWCELL in Cytometer menu x2 and run purge bubble filter in Cytometer menu then re-run QC.
  - c. CONTINURED FAILURE notify Flow Core staff immediately by submitting an incident report via PPMS
- 10. Click View Report or Close
- 11. Remove bead tube from instrument and perform two SIT flushes (**Cytometer** menu) to clean excess beads from the sample line
- 12. Place the tube of diH2O back on SIP
- 13. If not running samples, sign out of SpectroFlo and log out of PPMS
- 14. If running samples, proceed to experiment set up by navigating to the Acquisition module

This SOP was adapted from Cytek Biosciences Video Tutorial "System Startup and QC", found here:

https://tinyurl.com/u2rb2wm

