

# RayPlex<sup>®</sup> Human Receptor-27 Magnetic Bead Array

Quantitative Measurement of 27 Human  
Receptors by Flow Cytometry

Catalog numbers:

**FAHM-RC-27-48 (48 tests)**

**FAHM-RC-27-96 (96 tests)**

**FAHM-RC-27-192 (192 tests)**

**FAHM-RC-27-480 (480 tests)**

User Manual Version 1.0  
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## I. Overview

|                                |                                                                                                                                                                                                                                                                     |
|--------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Format</b>                  | Bead-based                                                                                                                                                                                                                                                          |
| <b>Proteins Detected (27)</b>  | <u>Receptors</u> : TRAIL R3, DR6, CD14, CEACAM-1, IL-1 R1, PECAM-1, E-Selectin, Endoglin (CD105), Trappin-2, ErbB3, CD30, IL-2 R $\gamma$ , CD80, Contactin-2, uPAR, Dtk, ALCAM, LIMP2, MICA, TIM-1, IL-17 RA, XEDAR, Fas, IL-21 R, CD40 ligand, Flt-3 ligand, GITR |
| <b>Detection Method</b>        | Flow Cytometry using a Flow Cytometer equipped with a blue (or green) laser (PE channel) and red laser (Alexa Fluor 700 and Alexa Fluor 647/APC channel) OR Luminex instrument                                                                                      |
| <b>Minimal Sample Volume</b>   | 25 $\mu$ L per test after dilution. <i>The optimal dilution must be determined empirically by the researcher</i>                                                                                                                                                    |
| <b>Compatible Sample Types</b> | Serum, Plasma, Cell Culture Supernatant                                                                                                                                                                                                                             |
| <b>Number of Replicates</b>    | At least 2 replicates. Each replicate is considered a test                                                                                                                                                                                                          |
| <b>Reproducibility</b>         | See Section VII (page 24) for Inter-CV and Intra-CV percentages for each protein                                                                                                                                                                                    |
| <b>Assay Duration</b>          | 4 hours                                                                                                                                                                                                                                                             |

## II. Introduction

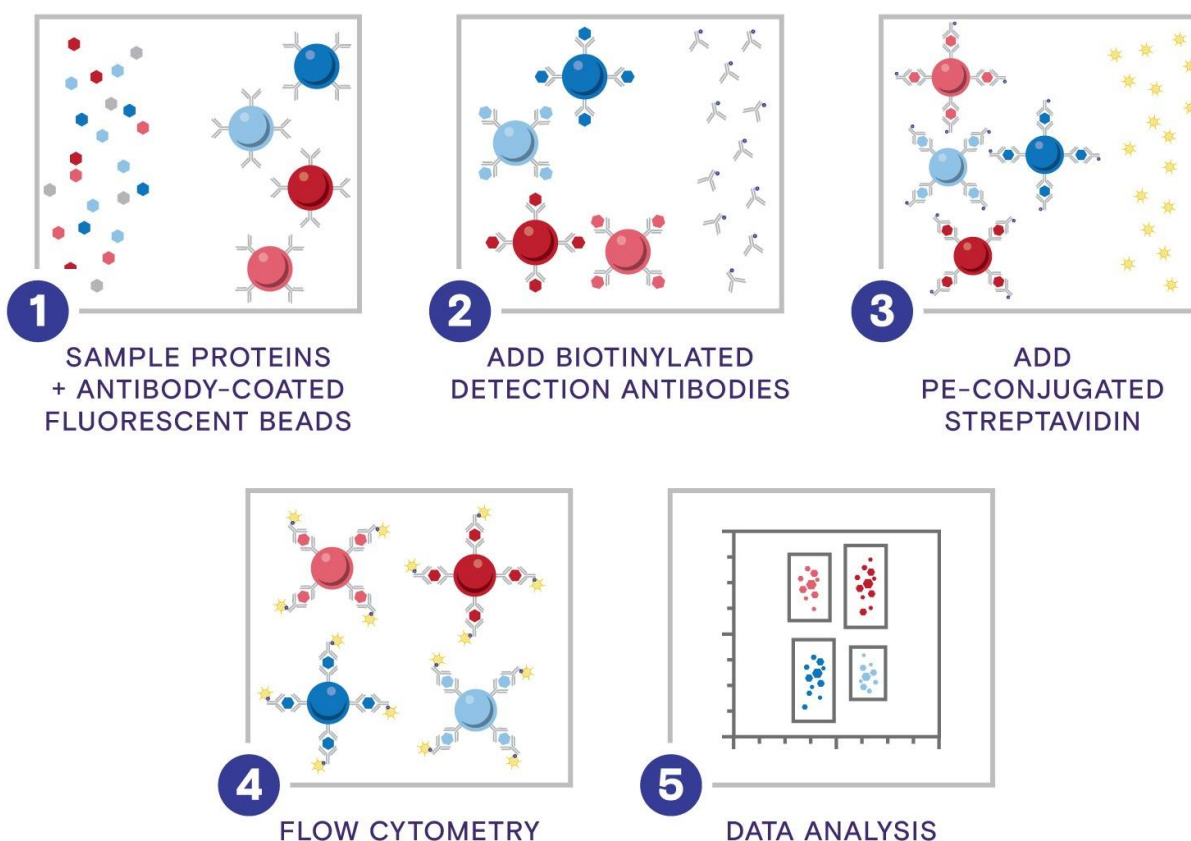
Soluble proteins play vital roles in homeostasis and disease development, including innate immunity, apoptosis, angiogenesis, cell growth, and differentiation. Thus, protein profiling has research and clinical applications, such as disease biomarker discovery and drug development. The traditional technique for detecting and quantifying soluble proteins is the enzyme-linked immunosorbent assay (ELISA), which only allows detection of one analyte each time. However, using this method to detect multiple proteins – particularly for precious samples with small quantities – becomes challenging as the processing time and required sample volume increase.

RayPlex® is a multiplexed sandwich- and bead-based quantitative antibody array for the simultaneous detection of multiple proteins using small sample volumes. It couples the versatility of RayBiotech's vast antibody pair library with familiar, reliable flow cytometry methodology. Together this creates a multiplex bead-based array requiring no dedicated instrumentation, only common flow cytometers equipped with blue (or green) and red lasers. This kit can also be used with Luminex systems.

The RayPlex® Human Receptor-27 Magnetic Bead Array Kit is designed to assay 27 common human inflammatory receptors simultaneously. The kit uses magnetic beads that allow the use of an automatic plate washing system with magnetic separation ability during washing steps. For data in this manual, a BioTek 405 TS Washer and LifeSep™ 96F magnetic separator unit were used. Further details are included in Section VI.

### III. How it Works

RayPlex® arrays are first prepared by immobilizing capture antibodies onto same size beads with dual fluorochromes and different fluorescence intensity; there is only one target's capture antibody per fluorochrome/intensity combination. The capture antibodies bind to their specific protein targets during sample incubation, and unbound proteins are removed with washing. Biotinylated detection antibodies and PE-conjugated streptavidin molecules are added, thus enabling protein detection via the PE- streptavidin-biotin-antibody complex. Individual proteins are identified by their specific bead-fluorochrome combination, while the level of PE fluorescence reflects the amount of protein that has been captured onto the beads. The protein amount can be determined (i.e., quantified) by comparing the PE signal to a standard curve generated from purified protein standards at known concentrations.

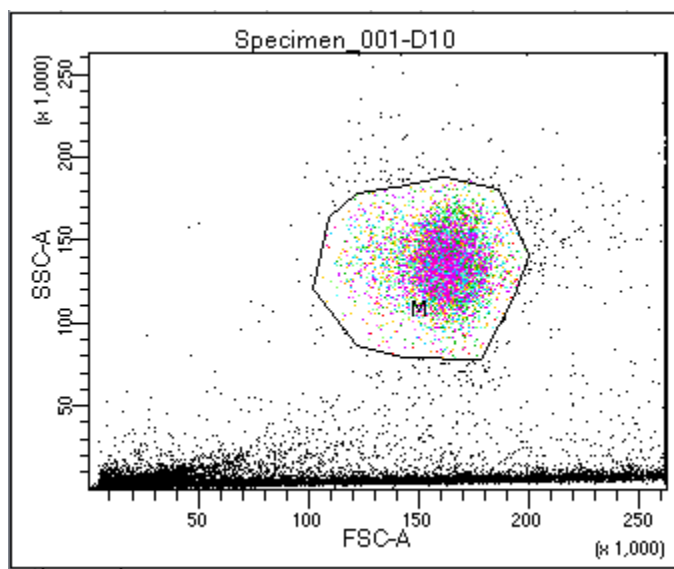


**A schematic showing how RayPlex® enables multiplex protein detection with flow cytometry.**

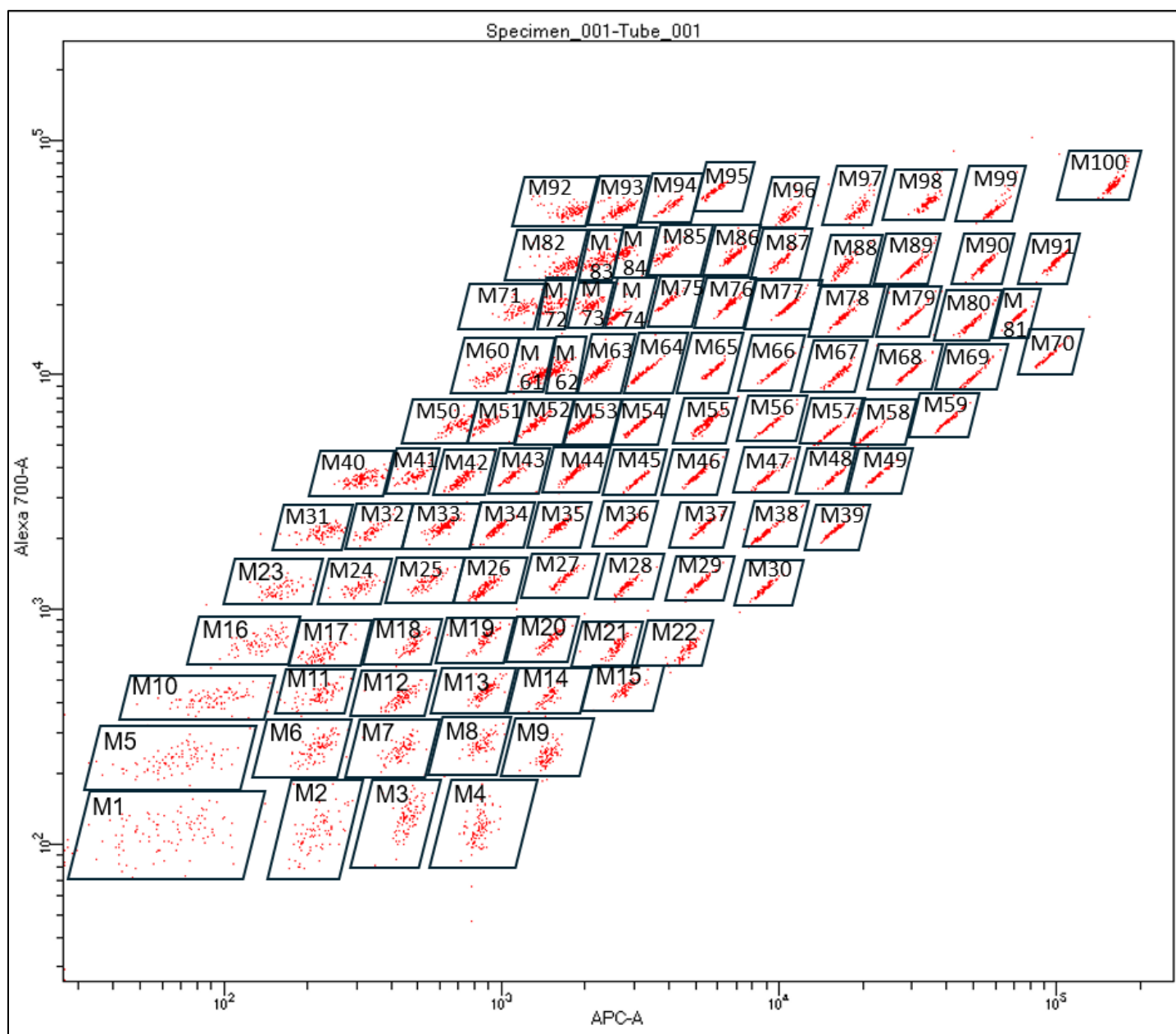
## IV. Bead ID and Distribution

### A. General View of RayPlex® Magnetic Multiplex Beads

RayPlex® Human Receptor-27 Magnetic Bead Array Kit uses M-100 series magnetic multiplex beads which have 100 populations based on the barcode determined by the incorporated dual fluorochrome with different intensities. All the M-100 beads are equal in size. This kit uses 27 populations out of 100. (Figures 1 and 2).



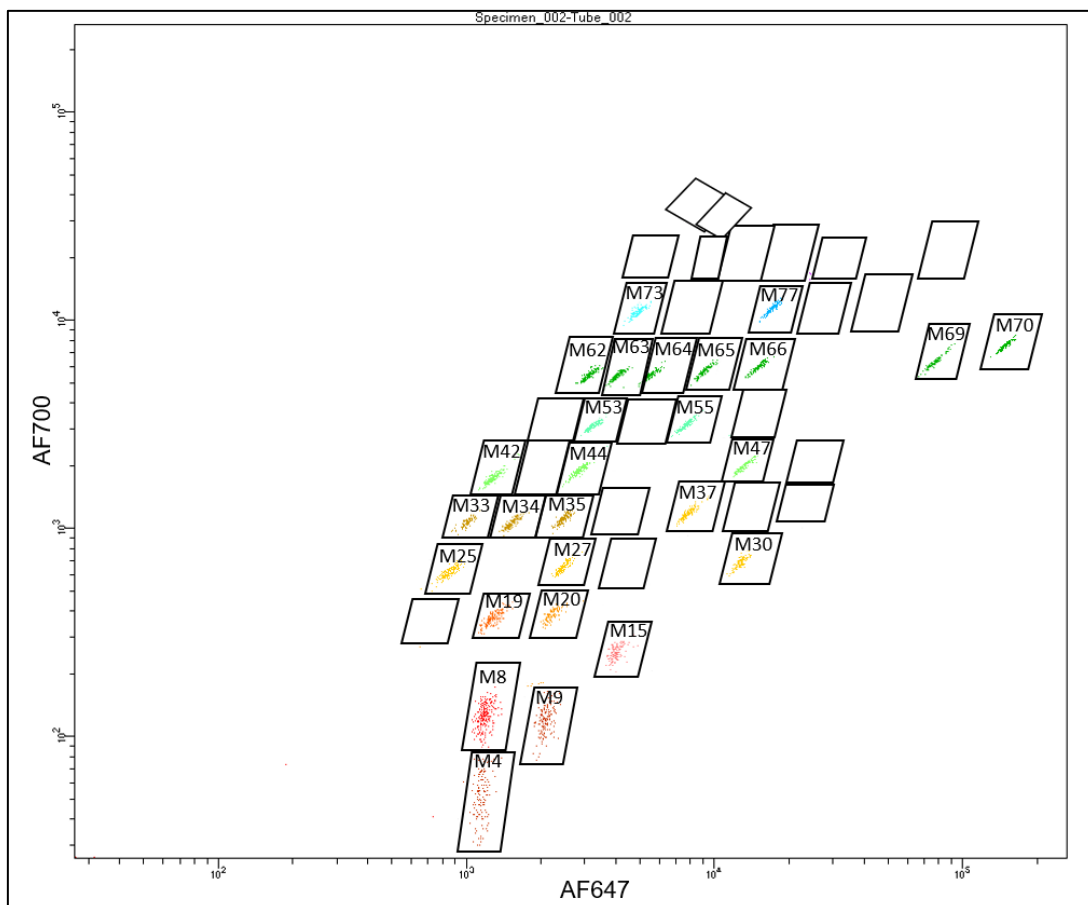
**Figure 1. RayPlex® M100 beads are the same size.**



**Figure 2. Different populations of beads with dual fluorescence combinations (“M#”) enable multiplex protein detection with RayPlex® arrays.**

## B. Target Proteins and Associated Bead IDs in This Kit

| Bead ID | Target       |
|---------|--------------|
| M4      | TRAIL R3     |
| M8      | DR6          |
| M9      | CD14         |
| M15     | CEACAM-1     |
| M19     | IL-1 R1      |
| M20     | PECAM-1      |
| M25     | E-Selectin   |
| M27     | CD105        |
| M30     | Trappin-2    |
| M33     | ErbB3        |
| M34     | CD30         |
| M35     | IL-2 Ry      |
| M37     | CD80         |
| M42     | Contactin-2  |
| M44     | uPAR         |
| M47     | Dtk          |
| M53     | ALCAM        |
| M55     | LIMP2        |
| M62     | MICA         |
| M63     | TIM-1        |
| M64     | IL-17 RA     |
| M65     | XEDAR        |
| M66     | Fas          |
| M69     | IL-21 R      |
| M70     | CD40 ligand  |
| M73     | Flt-3 ligand |
| M77     | GITR         |



## V. Materials Provided

Upon receipt, the Lyophilized Protein Standard Mix (Item 5) should be stored at -20°C or below. Other components should be stored at 4°C. Use reagents immediately after preparation. Additional vials of the Lyophilized Protein Standard Mix can be purchased separately (Catalog # FAHM-RC-27-Item5). If stored at the proper temperature, the kit will retain complete activity for at least 6 months.

| Catalog #        | Description                                 | Per 48 Tests     | Per 96 Tests      |
|------------------|---------------------------------------------|------------------|-------------------|
| FAHM-RC-27-Item1 | RayPlex® Magnetic Multiplex Bead Cocktail   | 1.25 mL x 1 vial | 1.25 mL x 2 vials |
| FAX-AD-1-Item2   | 1X Assay Diluent                            | 25 mL x 1 vial   | 25 mL x 2 vials   |
| FAX-WB-Item3     | 20X Wash Buffer                             | 5 mL x 1 vial    | 5 mL x 2 vials    |
| 137-00022-Item4  | RayBio® Human Serum/Plasma Diluent          | 2.5 mL x 1 vial  | 2.5 mL x 2 vials  |
| FAHM-RC-27-Item5 | Lyophilized Protein Standard Mix            | 1                | 2                 |
| FAHM-RC-27-Item6 | 1X Biotinylated Detection Antibody Cocktail | 1.25 mL x 1 vial | 1.25 mL x 2 vials |
| FAX-PE-Item7     | 10X Streptavidin-PE                         | 250 µL x 1 vial  | 250 µL x 2 vials  |
| FAHM-RC-27-Item8 | Flow Cytometer Setup Bead Cocktail**        | 100 µL x 1 vial  | 100 µL x 1 vial   |
| FAX-FB-Item9     | Flat-Bottom 96-well Microplate              | 1                | 1                 |
| FAX-VB-Item10    | V-Bottom 96-well Microplate                 | 1                | 1                 |

### Notes:

1. \*\*Flow Cytometer Setup Bead Cocktail (Item 8) is an additional aliquot of all beads used in this kit that is provided to assist in the setup of the flow cytometer. It can also be used to test for bead loss during washing prior to performing the assay. A detailed procedure for bead loss prevention is outlined in Section VI.F.
2. RayBio® Human Serum/Plasma Diluent (Item 4) is a solution that contains similar concentrations of proteins and other components shared by human serum and plasma to mimic the matrix. The diluent included in this kit is a 1:1 PBS-diluted version of the original product (Catalog #137-00022). Larger lots of the original product can be purchased here: <https://www.raybiotech.com/human-serum-plasma-diluent-137-00022>
3. RayBiotech recommends using a **Flat-Bottom 96-well Microplate (Item 10)** in conjunction with an **automated plate washing system** that uses magnetic separation.

## Additional Materials Required

- Orbital 96-well plate shaker (with ability to reach 1000 rpm)
- Flow Cytometer with blue (or green) and red lasers capable of measuring phycoerythrin (PE), Alexa Fluor 700 (AF700), and Alexa Fluor 647 (AF647)/APC channels OR Luminex instrument
- Aluminum foil or 96-well Plate Aluminum Sealers
- Deionized (DI) water
- PBS
- 1.5 mL polypropylene microcentrifuge tubes or similar
- Microcentrifuge
- **Recommended**: Automated plate washing system with magnetic separation
- Optional: 96-well round bottom plate (to prepare samples)
- Optional: High Throughput Sampler (HTS) for 96-well plate reading
- Optional: Vacuum manifold compatible with a 96-well microplate if using a Filter 96-Well Microplate

## VI. Assay Protocol

### A. Preparation of Samples

- We recommend the following parameters for your samples: 25 µL of diluted serum, plasma, cell culture media or other fluids. Actual sample dilutions may need to be empirically determined.
- It's recommended to use a 96-well round bottom plate to prepare samples before transferring the samples to the test plate or test tubes.
- We recommend analyzing samples at least in duplicate.
- **Serum or Plasma Samples**
  - **Dilute samples 2-fold with PBS** (e.g., dilute 30 µL of serum/plasma with 30 µL of PBS), **which is equal to 4-fold total dilution after mixed with beads.**
  - If further dilution is needed, RayBio® Human Serum/Plasma Diluent (Item 4) should be used.
- **Cell Culture Supernatant**
  - **Samples: No extra dilution needed, total dilution will be equal to 2-fold after mixed with beads.**
  - The use of serum (e.g., fetal bovine serum; FBS) in cell culture media can result in high background. To learn how to prepare samples, see our **Tips on Sample Preparation here:** <https://www.raybiotech.com/tips-on-sample-preparation/>
  - If cell culture supernatant from serum-containing media is tested, it is highly recommended that complete medium be used as diluent to reconstitute the protein standard since many types of serum contain proteins that may cross-react with the antibodies.
  - For serum-free media, 1X Assay Diluent (Item 2) should be used to dilute samples.
- A preliminary assay before testing your precious samples is recommended.

**Note:** Levels of target protein(s) may vary between different samples. Optimal dilution factors for each sample must be determined empirically by the investigator.

**Note:** Matrix effects are a common cause of non-linear dilution responses. This can occur when proteins or other components within the sample affect the immunoreactivity

*of the target molecule. These matrix components can also affect the ability of the antibody to recognize its target within the sample. Auto-antibodies, binding proteins, hemolysis, or certain disease states can contribute to this phenomenon. If matrix effects are suspected, centrifuge the sample(s), and dilute further such that matrix effects become negligible.*

**Note:** *If you experience high background or the readings exceed the detection range, further dilution of your sample is recommended.*

**Note:** *If you are using an automatic plate washing system that is not the same as defined in this manual, it is recommended to perform a bead loss prevention check as outlined in Section VI.F.*

## **B. Preparation of Reagents**

- Keep all reagents on ice
  - Protect fluorescent multiplex beads from light
1. Dilute and prepare only what is needed to perform the tests for each experiment.
  2. Vortex RayPlex® Magnetic Multiplex Bead Cocktail (Item 1) for 30 seconds before use. Use 25 µL beads per test.
  3. Dilute the 20X Wash Buffer (Item 3) 20-fold with DI H<sub>2</sub>O to prepare 1X Wash Buffer (see example note below).  
**Example:** A 20-fold dilution would be 1-part 20X Wash Buffer and 19 parts DI H<sub>2</sub>O
  4. Dilute the 10X Streptavidin-PE (Item 7) 10-fold in 1X Assay Diluent (Item 2) to prepare a 1X Streptavidin-PE working stock. Use 50 µL per test.

## **C. Preparation of Protein Standards**

**NOTE:** *Use the Lyophilized Protein Standard Mix (Item 5) within 1 hour of preparation.*

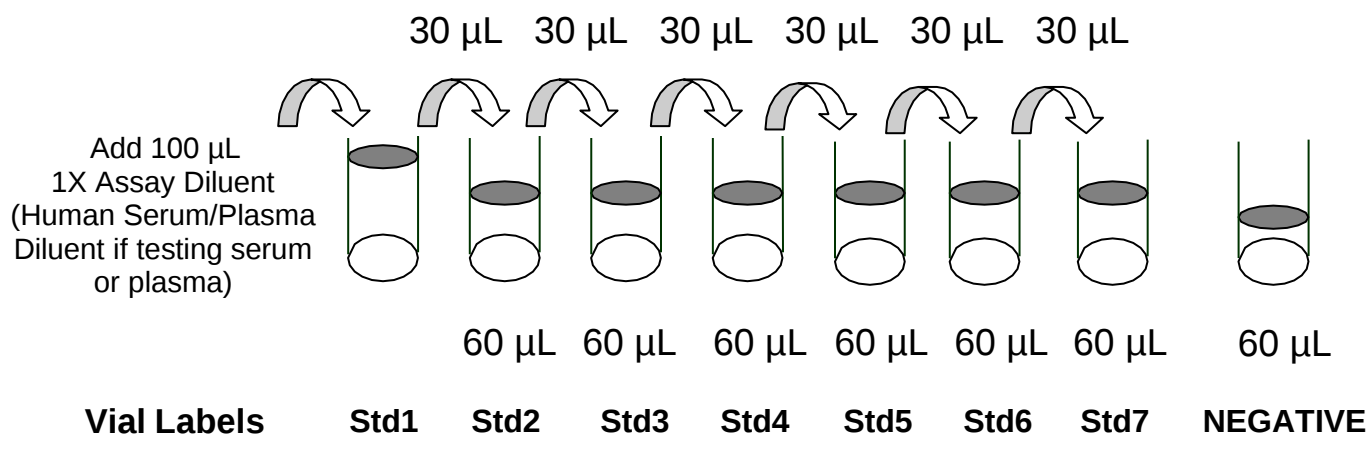
**NOTE:** *When testing serum or plasma, RayBio® Human Serum/Plasma Diluent (Item 4) should be used to reconstitute and serially dilute the standard mixture.*

1. Centrifuge the Lyophilized Protein Standard Mix (Item 5) briefly (1-3 seconds) to collect contents to the bottom of the vial.
2. Reconstitute the Lyophilized Protein Standard Mix (Item 5):
  - For **serum or plasma** samples, add 100 µL RayBio® Human Serum/Plasma Diluent (Item 4) to the tube. Dissolve the powder thoroughly and gently by pipetting up and

down 5-10 times. Label this tube as Std1. Further dilution of the standards should use the same RayBio® Human Serum/Plasma Diluent.

- For **serum-free media or non-serum fluids** add 100  $\mu$ L 1X Assay Diluent (Item 2) or serum-free media to the tube.
  - For **media containing bovine serum**, such as cell culture media, complete media should be used to reconstitute the protein standard with the same procedures as above.
3. Obtain six clean 1.5 mL microcentrifuge tubes (or use a 96-well round-bottom plate). Label the tubes/wells as Std2 to Std7. Add 60  $\mu$ L 1X Assay Diluent (Item 2) or RayBio® Human Serum/Plasma Diluent (Item 4) as applicable to each tube.
  4. Pipette 30  $\mu$ L Std1 into tube Std2 and mix gently. Perform five more serial dilutions by adding 30  $\mu$ L of Std2 to tube Std3, mix, and so on. (See also image below).

### Prepare Serial Dilutions of Protein Standards



5. Add 60  $\mu$ L 1X Assay Diluent (Item 2) or RayBio® Human Serum/Plasma Diluent (Item 4) to another tube labeled as NEGATIVE. Do not add standard or samples to the NEGATIVE tube. This tube will be used as the negative control.

**NOTE:** The exact concentrations of each standard protein for the Std1 to Std7 serial dilutions in this kit can be found in Section VII.

## **D. Assay Procedure**

1. Prepare a Flat-Bottom 96-well Microplate (Item 9), V-Bottom Microplate (Item 10) or 1.2

µm filter plate (not supplied) and mark positions for the standards and samples. Duplicate tests are recommended for all standards and samples.

**NOTE:** We recommend using a Flat-Bottom 96-well Microplate (Item 9) in conjunction with a magnetic plate washing system. Data in this manual were obtained using a **LifeSep™ magnetic separator unit** and **BioTek 405 TS Washer**. Please note that if alternative systems are used, unforeseen bead loss may occur. It is highly recommended for investigators to follow the procedure outlined in Section VI.F to check for bead loss prior to beginning the assay.

**NOTE:** A Filter 96-well plate can be used for the washing steps if desired. The filter plate requires a vacuum manifold compatible with a standard 96-well microplate. Alternatively, a V-Bottom 96-well microplate can be used along with a centrifuge.

2. Add 25 µL of RayPlex® Multiplex Bead Cocktail (Item 1) to each well that will contain the NEGATIVE, Standard, or Sample.
3. Add 25 µL of the NEGATIVE, Standard, or Sample to the appropriate well. The total volume in each well is now 50 µL (**serum or plasma sample is diluted 4-fold totally with beads in 50 µL reaction system, cell culture supernatant / serum-free media is diluted 2-fold totally with beads**). Place plate on an orbital plate shaker. Shake at 1000 rpm at room temperature for 2 hours.

**NOTE:** Data collected for this kit used the above procedure for incubation; however, the incubation step can also be performed overnight at 4°C, which may increase the signal-to-noise ratio, particularly for proteins with low concentrations. The optimal incubation length (i.e. room temperature for 2 hours or overnight at 4°C) for the experiment must be determined empirically by the investigator.

4. Wash the beads using 1X Wash Buffer (*diluted* Item 3; See Section B).
  - **Automated Washing System:** Place the **Flat-Bottom 96-well Microplate (Item 9)** on the magnetic separator unit for 5 minutes to allow the magnetic beads to migrate to the bottom. Place the Flat-Bottom 96-well Microplate and Magnetic Separator Unit on the platform of an automated plate washer and perform one wash cycle. One wash cycle should include two rounds of dispensing 200 µL of 1X Wash Buffer (*diluted* Item 3) and aspiration. It is recommended to adjust the settings such that the first aspiration leaves approximately 2 mm of 1X Wash

Buffer, and the final aspiration removes all liquid. It is pivotal that all liquid is removed at the end of washing. Remove the plate from the magnetic separator unit once washing is complete. Exact washing procedures may vary depending on the automated system used.

- **V-Bottom 96-well Microplate:** Add 200 µL 1X Wash Buffer (*diluted* Item 3) to each well. Spin the V-Bottom Microplate (Item 10) down at 1000 g for 5 minutes at room temperature and remove the supernatant using a multichannel pipette. Repeat once more.
  - **Filter 96-well Microplate:** Add 200 µL 1X Wash Buffer (*diluted* Item 3) to each well. Turn on the vacuum, open the valve, and place the filter plate on the vacuum. Do not allow pressure to exceed 10 inches Hg (254 mm Hg). Close the valve and remove the plate when the wells have drained. Repeat once more.
5. Add 25 µL of Biotinylated Detection Antibody Cocktail (Item 6) to each well. Resuspend the beads by gently pipetting and incubate on an orbital shaker at 1000 rpm at room temperature for 1 hour.
  6. Wash plate as outlined in Step 4.
  7. Add 50 µL of 1X Streptavidin-PE (*diluted* Item 7; See Section B) to each well, incubate on an orbital shaker at 1000 rpm at room temperature for 30 minutes.
  8. Wash plate as outlined in Step 4.
  9. Resuspend in 150 µL of 1X Wash Buffer (*diluted* Item 3).
  10. Prepare samples for analysis on a flow cytometer:
    - Automated High Throughput Sampler (HTS): if using a Flat-Bottom or V-bottom plate, directly read samples from the plate. If using a Filter-plate, transfer samples to a V-Bottom Microplate (Item 10).
    - Manual reading: transfer samples to compatible tubes.
  11. Analyze samples on a flow cytometer (see Section E).

## **E. Flow Cytometer Set-up and Data Acquisition**

**NOTE:** The RayPlex® Human Receptor-27 Magnetic Bead Array Kit requires a flow

*cytometer that is equipped with blue (or green) and red lasers capable of detecting fluorescence in the PE, AF700, and AF647/APC channels or a Luminex instrument. The instructions below describe the set up for a flow cytometer. For Luminex instrument set up, please refer to the instrument manual.*

**NOTE:** *Perform standard QC and optimization steps to prepare the flow cytometer, then set up the flow cytometer as you would for normal use. Manual adjustment of the PE, AF700, and AF647/APC compensation may be necessary to decrease the spill-over of AF647/APC signal into PE channel.*

**NOTE:** *These instructions are general for all RayPlex® assays. The target count, and bead populations may differ from the assay above. Please see your assay's specific manual Section IV and VII for the bead populations present in your array.*

1. Depending on the brand of the flow cytometer, you may need to start the acquisition software and run Quality Control beads before proceeding further.

**Note:** *The Quality Controls beads are fluorescent particles that are used for flow cytometer setup, e.g., CS&T beads for a BD flow cytometer.*

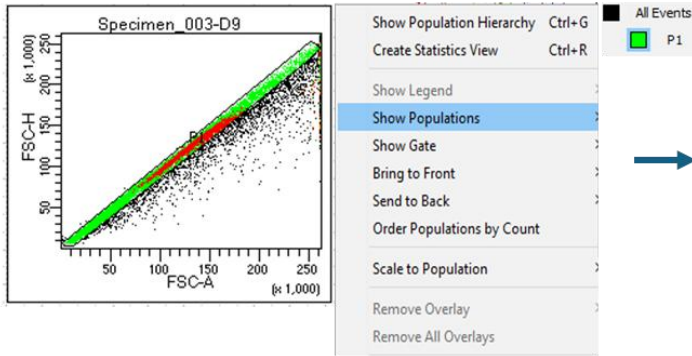
2. Start a new experiment with PE, AF700, and AF647/APC channels.
3. Resuspend 100 µL of the provided Flow Cytometer Setup Bead Cocktail (Item 8) in 200 µL 1X Wash Buffer (*diluted* Item 3) and run them on the flow cytometer.
4. Create an FSC-H/FSC-A daughter population for “Single beads” selection to remove and limit doublets or higher complexes (Figure 3A).
5. Create a new dot plot from the “Single beads” parent gate P1, adjust voltage for FSC (forward scatter, linear mode) and SSC (side scatter, linear mode) so that the bead population is clearly defined. Then create a gate around the beads (Figure 3B).
6. Create a new dot plot from the beads parent gate M. Create gates for all bead populations for the assay based on AF700 (log mode) and AF647/APC (log mode). Adjust PMT voltage of AF700 and AF647/APC channels so that all populations are well separated throughout in a prominent area (Figure 3C).
7. Create a statistical view to show the PE MFI for each population (Figure 3D-E).
8. Run a small amount of beads from the NEGATIVE control. Adjust the PE voltage so that

the PE median fluorescent intensity (MFI) is around  $10^{2-3}$  for each bead population.

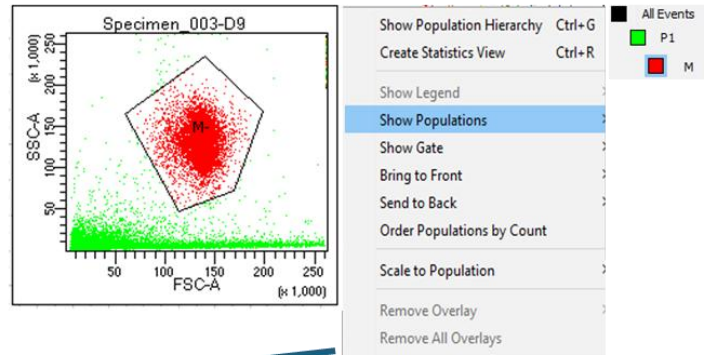
**Note:** *To keep the testing consistent for each assay, we recommend the use of Rainbow Particles, Rainbow Beads, or a similar product to standardize the assay if they are run prior to every analysis. The optimized MFI for both the AF647/APC and PE channels for the Rainbow Particles allow the experiment to be consistent from time to time and machine to machine.*

9. Set the number of bead events to be acquired to at least 200 per target population for best results. More beads will improve data accuracy.
10. Following setup, run the standards and samples. The MFI of all analytes and samples can be exported in Excel format by “Batch Analysis” of a whole specimen in FACSDiva. Researchers can also export raw data as “FCS” files and analyze in FlowJo software.

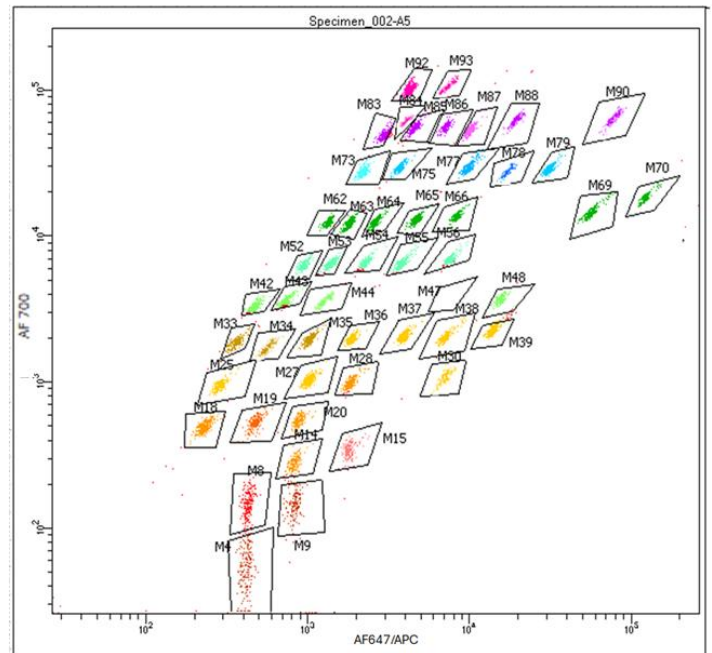
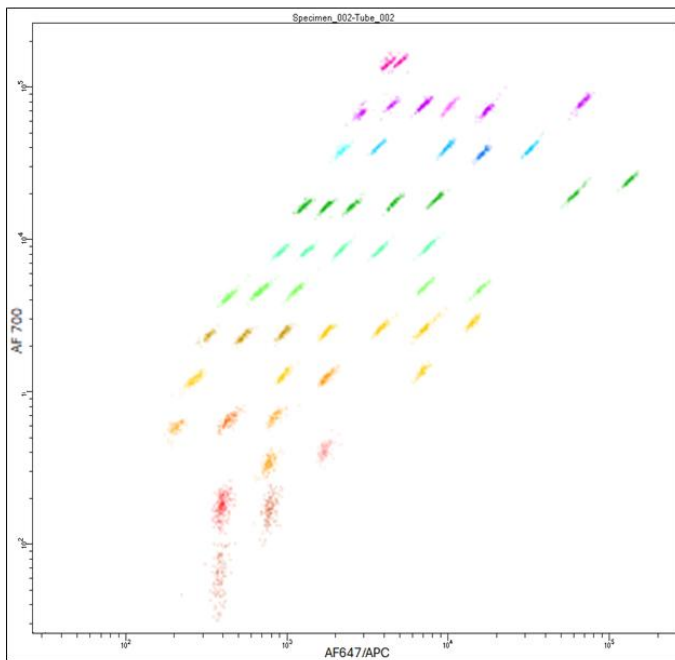
A.



B.



C. Gate



D. Create Statistics View

Well: A5

| Population | #Events | %Parent | %Total |
|------------|---------|---------|--------|
| All Events | 21,325  | ####    | 100.0  |
| M          | 1,723   | 8.1     | 8.1    |
| M4         | 0       | 0.0     | 0.0    |
| M8         | 0       | 0.0     | 0.0    |
| M9         | 75      | 4.4     | 0.4    |
| M14        | 86      | 5.0     | 0.4    |
| M15        | 0       | 0.0     | 0.0    |
| M18        | 0       | 0.0     | 0.0    |
| M19        | 66      | 3.8     | 0.3    |
| M20        | 0       | 0.0     | 0.0    |
| M25        | 0       | 0.0     | 0.0    |
| M27        | 0       | 0.0     | 0.0    |
| M28        | 1       | 0.1     | 0.0    |
| M30        | 0       | 0.0     | 0.0    |
| M33        | 92      | 5.3     | 0.4    |
| M34        | 0       | 0.0     | 0.0    |
| M35        | 95      | 5.5     | 0.4    |
| M36        | 80      | 4.6     | 0.4    |
| M37        | 69      | 4.0     | 0.3    |
| M38        | 70      | 4.1     | 0.3    |

Menu options:

- Show Population Hierarchy Ctrl+G
- Create Statistics View Ctrl+R (selected)
- Show Legend
- Show Populations
- Show Gate
- Bring to Front
- Send to Back
- Order Populations by Count
- Scale to Population
- Remove Overlay
- Remove All Overlays
- Duplicate Ctrl+D
- Paste Gate Ctrl+V
- Cut Ctrl+X
- Copy Ctrl+C
- Delete

E. Show PE-A MFI reading

Well Na... A5

| Population | PE-A Median |
|------------|-------------|
| M          | 11,009      |
| M4         | ####        |
| M8         | ####        |
| M9         | 7,638       |
| M14        | 4,723       |
| M15        | ####        |
| M18        | ####        |
| M19        | 10,892      |
| M20        | ####        |
| M25        | ####        |
| M27        | ####        |
| M28        | 20,005      |
| M30        | ####        |
| M33        | 13,871      |
| M34        | ####        |
| M35        | 1,843       |
| M36        | 29,854      |
| M37        | 40,390      |
| M38        | 62,576      |

Menu options:

- Edit Statistics View
- Export Statistics
- Cut Ctrl+X
- Copy Ctrl+C
- Delete

Edit Statistics View

| Parameters          | All                      | Min                      | Max                      | Geo M.                   | Mean                     | Median                   | SD                       |
|---------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| FSC-A               | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| SSC-A               | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| Time                | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| PE-A                | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| Raybright Red 647-A | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| Raybright Red 700-A | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| Decimal Places      | 0                        | 0                        | 0                        | 0                        | 0                        | 0                        | 0                        |

Sort by Parameter (selected) or Sort by Formula

Display Range: Linear Scale (0-10,000)

**Figure 3. Representative Images of Gated Flow Cytometry Scatter Plots Using RayPlex® Arrays with M-100 series beads.** (A) Single beads are used to (B) create the parent bead gate M. (C) Bead populations are separated with dual fluorescence and gated. (D, E) Statistics view is created and edited to show PE-A MFI reading. All PE-A Median values should be selected and exported based on gates of (C).

**NOTE:** The above figures are for demonstration purposes only.

## F. Bead Loss Prevention Check (Optional)

**NOTE:** Due to differences in automated plate washing systems, it is recommended to perform a bead loss prevention check prior to starting the assay to prevent loss of beads if an automated washing machine is being used.

1. Resuspend the contents of **the Flow Cytometer Setup Bead Cocktail (Item 8)** and add 25 µL to one well of a 96-well plate.
2. Add 25 µL of 1X Wash Buffer (*diluted* Item 3) to the same well to mimic the assay protocol.
3. Perform one wash cycle using the automated plate washing system.
  - One wash cycle should always consist of two rounds of 200 µL 1X Wash Buffer being added then removed.
4. Repeat steps 2 and 3 two more times for a total of 3 wash cycles.
5. Resuspend the beads in 150 µL of 1X Wash Buffer (*diluted* Item 3). In normal conditions, 50 µL should have more than 100 events for each bead ID.
6. Run the sample either by transferring to tubes and running in “Tube Mode” or directly from the plate with HTS mode. Optional: Run a sample of unwashed beads to compare beads with and without washing.

**Note:** If the bead count is less than 100 bead events for any bead IDs, it is recommended to reconsider the washing procedure used for the assay. Bead events should ideally be more than 200 for each bead ID. Using a filter-plate for washing will prevent bead loss most effectively.

## G. Data Analysis

1. The MFI of all analytes and samples can be exported in Excel format by “Batch Analysis” of a whole specimen in FACSDiva (See **Appendix: RayPlex® Data Analysis Using BD FACS Diva Batch Analysis**).
2. MFI data of each analyte for all samples can also be acquired by exporting the entire dataset as FCS files. Analyze data in FlowJo or equivalent software and export the PE MFI into an Excel (or similar) format.

## VII. Assay Information

### A. 8-Point Standard Protein Concentrations (pg/mL)

The concentrations of target proteins corresponding to standard (Std) 1-7 serial dilutions are displayed below in pg/mL. These concentrations are used to produce the standard curves.

| Target       | STD1     | STD2    | STD3    | STD4   | STD5   | STD6  | STD7  | CTRL |
|--------------|----------|---------|---------|--------|--------|-------|-------|------|
| TRAIL R3     | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| DR6          | 85000.0  | 28333.3 | 9444.4  | 3148.1 | 1049.4 | 349.8 | 116.6 | 0.0  |
| CD14         | 90000.0  | 30000.0 | 10000.0 | 3333.3 | 1111.1 | 370.4 | 123.5 | 0.0  |
| CEACAM-1     | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| IL-1 R1      | 80000.0  | 26666.7 | 8888.9  | 2963.0 | 987.7  | 329.2 | 109.7 | 0.0  |
| PECAM-1      | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| E-Selectin   | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| CD105        | 33300.0  | 11100.0 | 3700.0  | 1233.3 | 411.1  | 137.0 | 45.7  | 0.0  |
| Trappin-2    | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| ErbB3        | 80000.0  | 26666.7 | 8888.9  | 2963.0 | 987.7  | 329.2 | 109.7 | 0.0  |
| CD30         | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| IL-2 Ry      | 30000.0  | 10000.0 | 3333.3  | 1111.1 | 370.4  | 123.5 | 41.2  | 0.0  |
| CD80         | 60000.0  | 20000.0 | 6666.7  | 2222.2 | 740.7  | 246.9 | 82.3  | 0.0  |
| Contactin-2  | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| uPAR         | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| Dtk          | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| ALCAM        | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| LIMP2        | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| MICA         | 90000.0  | 30000.0 | 10000.0 | 3333.3 | 1111.1 | 370.4 | 123.5 | 0.0  |
| TIM-1        | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| IL-17 RA     | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| XEDAR        | 150000.0 | 50000.0 | 16666.7 | 5555.6 | 1851.9 | 617.3 | 205.8 | 0.0  |
| Fas          | 50000.0  | 16666.7 | 5555.6  | 1851.9 | 617.3  | 205.8 | 68.6  | 0.0  |
| IL-21 R      | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |
| CD40 ligand  | 10000.0  | 3333.3  | 1111.1  | 370.4  | 123.5  | 41.2  | 13.7  | 0.0  |
| Flt-3 ligand | 50000.0  | 16666.7 | 5555.6  | 1851.9 | 617.3  | 205.8 | 68.6  | 0.0  |
| GITR         | 100000.0 | 33333.3 | 11111.1 | 3703.7 | 1234.6 | 411.5 | 137.2 | 0.0  |

**Note:** It is recommended that the researcher dilute their samples so that the reading falls into the standard range.

## B. Representation of Standard Curve MFI Values

The values in the tables below are an example of MFI values that can be used to generate a standard curve. These values are for demonstration purposes only. A standard curve must be run with each assay since the MFI values will vary from experiment to experiment.

|                | TRAIL R3 | DR6     | CD14    | CEACAM-1 | IL-1 R1 | PECAM-1  | E-Selectin | CD105   |
|----------------|----------|---------|---------|----------|---------|----------|------------|---------|
| Std 1 (pg/ml)  | 100000.0 | 85000.0 | 90000.0 | 100000.0 | 80000.0 | 100000.0 | 100000.0   | 33300.0 |
| Standard 1 MFI | 18814.3  | 28881.3 | 14453.7 | 10227.3  | 17817.3 | 23933.3  | 19241.3    | 27467.3 |
| Standard 2 MFI | 13788.3  | 16729.7 | 5621.7  | 3777.7   | 13406.3 | 17757.7  | 9699.7     | 19653.7 |
| Standard 3 MFI | 9884.0   | 8151.0  | 2809.7  | 1508.0   | 8733.7  | 12764.0  | 4179.7     | 12583.0 |
| Standard 4 MFI | 5823.7   | 3661.3  | 1412.3  | 1032.0   | 4382.0  | 7155.3   | 1776.7     | 6677.7  |
| Standard 5 MFI | 3483.7   | 1965.0  | 856.7   | 588.3    | 1878.7  | 3308.0   | 1073.0     | 3351.0  |
| Standard 6 MFI | 2221.7   | 1197.7  | 682.3   | 653.7    | 785.3   | 1493.0   | 859.3      | 1770.3  |
| Standard 7 MFI | 1815.7   | 1011.3  | 657.0   | 546.3    | 415.7   | 817.0    | 801.7      | 1164.7  |
| Negative MFI   | 1524.3   | 799.0   | 581.0   | 533.3    | 148.0   | 430.3    | 677.7      | 801.3   |

|                | Trappin-2 | ErbB3   | CD30     | IL-2 Ry  | CD80    | Contactin-2 | uPAR     | Dtk      |
|----------------|-----------|---------|----------|----------|---------|-------------|----------|----------|
| Std 1 (pg/ml)  | 100000.0  | 80000.0 | 100000.0 | 30000.0  | 60000.0 | 100000.0    | 100000.0 | 100000.0 |
| Standard 1 MFI | 16045.7   | 42796.7 | 30263.3  | 128193.0 | 12167.3 | 16744.0     | 17813.0  | 13473.0  |
| Standard 2 MFI | 17089.0   | 26639.0 | 20415.0  | 27735.3  | 16192.3 | 7214.3      | 7593.3   | 7387.0   |
| Standard 3 MFI | 17935.3   | 15030.3 | 12202.3  | 8156.0   | 11934.7 | 2227.3      | 3378.7   | 3396.7   |
| Standard 4 MFI | 15563.3   | 6786.0  | 6442.3   | 2985.7   | 5909.3  | 672.7       | 1479.3   | 1483.7   |
| Standard 5 MFI | 9739.7    | 2999.3  | 2913.3   | 1642.3   | 2756.3  | 339.7       | 654.7    | 775.0    |
| Standard 6 MFI | 5228.0    | 1608.3  | 1665.0   | 1184.0   | 1271.7  | 240.3       | 434.3    | 535.0    |
| Standard 7 MFI | 2719.3    | 1212.3  | 1131.7   | 1052.7   | 1082.7  | 241.3       | 374.0    | 425.0    |
| Negative MFI   | 906.3     | 838.7   | 634.7    | 864.7    | 585.3   | 170.7       | 267.0    | 327.3    |

|                | ALCAM    | LIMP2    | MICA    | TIM-1    | IL-17 RA | XEDAR    | Fas      | IL-21 R  |
|----------------|----------|----------|---------|----------|----------|----------|----------|----------|
| Std 1 (pg/ml)  | 100000.0 | 100000.0 | 90000.0 | 100000.0 | 100000.0 | 150000.0 | 50000.0  | 100000.0 |
| Standard 1 MFI | 23726.7  | 50792.0  | 32682.0 | 19691.0  | 19300.7  | 73795.7  | 184211.7 | 11149.7  |
| Standard 2 MFI | 18480.7  | 17973.7  | 17337.3 | 13568.3  | 13077.0  | 39932.0  | 59792.3  | 3970.0   |
| Standard 3 MFI | 12449.0  | 7199.0   | 8761.7  | 9943.7   | 8267.0   | 24817.7  | 17203.3  | 1472.3   |
| Standard 4 MFI | 5698.7   | 2689.0   | 3809.7  | 5887.3   | 4039.7   | 11385.3  | 5262.7   | 616.3    |
| Standard 5 MFI | 2731.3   | 1035.7   | 1674.3  | 2925.3   | 1831.0   | 5045.0   | 2104.7   | 354.7    |
| Standard 6 MFI | 1611.0   | 448.7    | 707.3   | 1274.0   | 770.7    | 2390.7   | 1050.3   | 249.7    |
| Standard 7 MFI | 1299.7   | 278.0    | 418.7   | 674.0    | 500.3    | 1517.0   | 749.3    | 226.3    |
| Negative MFI   | 1015.3   | 148.0    | 207.7   | 290.0    | 267.7    | 754.3    | 529.7    | 175.0    |

|                | CD40 ligand | Flt-3 ligand | GITR     |
|----------------|-------------|--------------|----------|
| Std 1 (pg/ml)  | 10000.0     | 50000.0      | 100000.0 |
| Standard 1 MFI | 163724.3    | 11440.7      | 7874.7   |
| Standard 2 MFI | 68268.0     | 8734.3       | 3903.7   |
| Standard 3 MFI | 32980.0     | 7407.0       | 2035.0   |
| Standard 4 MFI | 9971.0      | 5718.0       | 1076.0   |
| Standard 5 MFI | 3499.7      | 3578.7       | 688.7    |
| Standard 6 MFI | 1312.3      | 1807.3       | 558.0    |
| Standard 7 MFI | 803.3       | 889.7        | 524.7    |
| Negative MFI   | 353.7       | 293.0        | 455.7    |

## C. Lower Limit of Detection (LOD) of Target Proteins

The LOD is the minimum detectable concentration (i.e., sensitivity) of the assay. It was determined by spiking each purified protein standard into RayBio® Human Serum/Plasma Diluent (Item 4).

| Target       | LOD (pg/mL) |
|--------------|-------------|
| TRAIL R3     | 186.29      |
| DR6          | 181.06      |
| CD14         | 278.24      |
| CEACAM-1     | 510.16      |
| IL-1 R1      | 13.49       |
| PECAM-1      | 13.76       |
| E-Selectin   | 203.26      |
| CD105        | 15.02       |
| Trappin-2    | 8.62        |
| ErbB3        | 68.52       |
| CD30         | 62.97       |
| IL-2 Ry      | 196.05      |
| CD80         | 54.75       |
| Contactin-2  | 821.92      |
| uPAR         | 733.72      |
| Dtk          | 394.52      |
| ALCAM        | 188.69      |
| LIMP2        | 197.20      |
| MICA         | 21.86       |
| TIM-1        | 26.99       |
| IL-17 RA     | 41.84       |
| XEDAR        | 126.77      |
| Fas          | 194.08      |
| IL-21 R      | 491.66      |
| CD40 ligand  | 25.32       |
| Flt-3 ligand | 17.76       |
| GITR         | 391.13      |

**NOTE:** The LOD may vary from run-to-run and batch-to-batch.

## D. Cross Reactivity

No detectable or significant cross reactivity was detected between antibodies or targets.

## E. Percent (%) Recovery of Spiked Standards

For spike recovery of standards, target proteins with concentrations corresponding to standard 2 (Std2) were spiked into RayBio® Human Serum/Plasma Diluent (Item 4) across 9 replicates. The spiked proteins were assayed and the measured concentrations were compared to the expected concentrations.

| Target          | Percent Recovery |
|-----------------|------------------|
| TRAIL R3        | 104.1%           |
| DR6             | 100.0%           |
| CD14            | 100.3%           |
| CEACAM-1        | 96.1%            |
| IL-1 R1         | 105.4%           |
| PECAM-1         | 103.1%           |
| E-Selectin      | 100.3%           |
| CD105           | 103.2%           |
| Trappin-2       | 99.6%            |
| ErbB3           | 104.5%           |
| CD30            | 109.7%           |
| IL-2 R $\gamma$ | 98.9%            |
| CD80            | 84.3%            |
| Contactin-2     | 99.0%            |
| uPAR            | 100.1%           |
| Dtk             | 100.2%           |
| ALCAM           | 101.4%           |
| LIMP2           | 100.6%           |
| MICA            | 100.4%           |
| TIM-1           | 103.3%           |
| IL-17 RA        | 109.3%           |
| XEDAR           | 99.0%            |
| Fas             | 100.5%           |
| IL-21 R         | 100.0%           |
| CD40 ligand     | 100.2%           |
| Flt-3 ligand    | 93.3%            |
| GITR            | 100.4%           |

## F. Linearity of Dilution

To test the linearity of dilution, samples (n = 12) were serially diluted in RayBio® Human Serum/Plasma Diluent (Item 4) 1:3, 1:9, and 1:27. The measured concentrations of serially diluted samples were compared to that of the undiluted samples and averaged. See data below.

| Target       | Linearity of Dilution |
|--------------|-----------------------|
| TRAIL R3     | 100.5%                |
| DR6          | 93.3%                 |
| CD14         | 102.2%                |
| CEACAM-1     | 104.9%                |
| IL-1 R1      | 99.6%                 |
| PECAM-1      | 104.9%                |
| E-Selectin   | 99.7%                 |
| CD105        | 100.8%                |
| Trappin-2    | 108.5%                |
| ErbB3        | 100.5%                |
| CD30         | 105.5%                |
| IL-2 Ry      | 108.9%                |
| CD80         | 111.9%                |
| Contactin-2  | 100.3%                |
| uPAR         | 102.8%                |
| Dtk          | 101.0%                |
| ALCAM        | 88.4%                 |
| LIMP2        | 104.1%                |
| MICA         | 101.2%                |
| TIM-1        | 102.7%                |
| IL-17 RA     | 102.0%                |
| XEDAR        | 94.0%                 |
| Fas          | 102.7%                |
| IL-21 R      | 101.3%                |
| CD40 ligand  | 99.3%                 |
| Flt-3 ligand | 100.1%                |
| GITR         | 99.4%                 |

## G. Intra- and Inter-Assay Precision

### 1) Intra-Assay Precision

Spiked standard protein in RayBio® Human Serum/Plasma Diluent (Item 4) was analyzed in triplicate. Data was chosen from one of three replicates for each target as indicated at the concentrations of protein standard 2 (Sample #1) and 3 (Sample #2) respectively. The intra-assay precision, or coefficient of variation (CV), of the samples is provided below.

| Target          | Sample # | Mean (pg/mL) | Standard Deviation | CV %  |
|-----------------|----------|--------------|--------------------|-------|
| TRAIL R3        | 1        | 33268.7      | 1405.0             | 4.2%  |
|                 | 2        | 11333.3      | 516.5              | 4.6%  |
| DR6             | 1        | 28605.3      | 264.9              | 0.9%  |
|                 | 2        | 9225.2       | 275.2              | 3.0%  |
| CD14            | 1        | 29472.0      | 769.5              | 2.6%  |
|                 | 2        | 10594.3      | 662.5              | 6.3%  |
| CEACAM-1        | 1        | 33488.2      | 12.9               | 0.0%  |
|                 | 2        | 10539.0      | 338.2              | 3.2%  |
| IL-1 R1         | 1        | 27218.4      | 646.0              | 2.4%  |
|                 | 2        | 8774.0       | 354.0              | 4.0%  |
| PECAM-1         | 1        | 33706.7      | 7505.1             | 22.3% |
|                 | 2        | 11039.4      | 1524.9             | 13.8% |
| E-Selectin      | 1        | 33427.2      | 122.0              | 0.4%  |
|                 | 2        | 11038.5      | 307.3              | 2.8%  |
| CD105           | 1        | 10827.6      | 837.8              | 7.7%  |
|                 | 2        | 3882.2       | 294.0              | 7.6%  |
| Trappin-2       | 1        | 11109.3      | 2111.6             | 19.0% |
|                 | 2        | 3503.2       | 347.8              | 9.9%  |
| ErbB3           | 1        | 26609.8      | 562.8              | 2.1%  |
|                 | 2        | 9015.2       | 269.0              | 3.0%  |
| CD30            | 1        | 30981.0      | 3009.6             | 9.7%  |
|                 | 2        | 13756.0      | 2669.3             | 19.4% |
| IL-2 R $\gamma$ | 1        | 9957.5       | 135.3              | 1.4%  |
|                 | 2        | 3460.3       | 351.3              | 10.2% |
| CD80            | 1        | 15854.0      | 137.4              | 0.9%  |
|                 | 2        | 13174.6      | 935.6              | 7.1%  |
| Contactin-2     | 1        | 33355.7      | 23.8               | 0.1%  |
|                 | 2        | 11052.4      | 68.0               | 0.6%  |
| uPAR            | 1        | 33418.3      | 422.7              | 1.3%  |
|                 | 2        | 11012.6      | 719.9              | 6.5%  |
| Dtk             | 1        | 33594.3      | 215.2              | 0.6%  |
|                 | 2        | 10894.5      | 362.4              | 3.3%  |
| ALCAM           | 1        | 27459.3      | 6217.2             | 22.6% |
|                 | 2        | 11037.3      | 596.7              | 5.4%  |
| LIMP2           | 1        | 33197.9      | 616.2              | 1.9%  |
|                 | 2        | 11125.1      | 767.8              | 6.9%  |
| MICA            | 1        | 30056.9      | 441.1              | 1.5%  |
|                 | 2        | 9948.0       | 504.3              | 5.1%  |
| TIM-1           | 1        | 33747.1      | 4589.4             | 13.6% |
|                 | 2        | 11243.7      | 921.8              | 8.2%  |

| Target       | Sample # | Mean (pg/mL) | Standard Deviation | CV %  |
|--------------|----------|--------------|--------------------|-------|
| IL-17 RA     | 1        | 33252.0      | 1467.1             | 4.4%  |
|              | 2        | 11102.8      | 957.5              | 8.6%  |
| XEDAR        | 1        | 32224.5      | 5080.5             | 15.8% |
|              | 2        | 11718.3      | 872.3              | 7.4%  |
| Fas          | 1        | 16737.7      | 64.9               | 0.4%  |
|              | 2        | 5452.8       | 41.4               | 0.8%  |
| IL-21 R      | 1        | 33380.9      | 99.9               | 0.3%  |
|              | 2        | 10871.9      | 234.2              | 2.2%  |
| CD40 ligand  | 1        | 3363.5       | 122.6              | 3.6%  |
|              | 2        | 1179.7       | 101.2              | 8.6%  |
| Flt-3 ligand | 1        | 14119.5      | 1505.1             | 10.7% |
|              | 2        | 5575.4       | 209.7              | 3.8%  |
| GITR         | 1        | 33194.5      | 186.2              | 0.6%  |
|              | 2        | 11462.0      | 183.8              | 1.6%  |

## 2) Inter-Assay Precision

Spiked standard protein in RayBio® Human Serum/Plasma Diluent (Item 4) was analyzed in triplicate across three independent assays. Samples were spiked in with the concentrations of protein standard 2 (Sample #1) and 3 (Sample #2). The inter-assay precision in CV of the samples is provided below.

| Target      | Sample # | Mean (pg/mL) | Standard Deviation | CV %  |
|-------------|----------|--------------|--------------------|-------|
| TRAIL R3    | 1        | 31709.7      | 4487.4             | 14.2% |
|             | 2        | 11924.5      | 719.3              | 6.0%  |
| DR6         | 1        | 28328.2      | 1175.4             | 4.1%  |
|             | 2        | 9527.9       | 810.9              | 8.5%  |
| CD14        | 1        | 28585.7      | 1768.7             | 6.2%  |
|             | 2        | 11348.8      | 1192.7             | 10.5% |
| CEACAM-1    | 1        | 33476.9      | 3026.2             | 9.0%  |
|             | 2        | 12008.8      | 2115.7             | 17.6% |
| IL-1 R1     | 1        | 26472.5      | 3168.4             | 12.0% |
|             | 2        | 9110.4       | 1039.3             | 11.4% |
| PECAM-1     | 1        | 31662.2      | 4798.6             | 15.2% |
|             | 2        | 11915.0      | 565.6              | 4.7%  |
| E-Selectin  | 1        | 33348.8      | 2306.5             | 6.9%  |
|             | 2        | 11209.4      | 1469.9             | 13.1% |
| CD105       | 1        | 11004.7      | 454.8              | 4.1%  |
|             | 2        | 3772.5       | 136.8              | 3.6%  |
| Trappin-2   | 1        | 3144.6       | 797.8              | 25.4% |
|             | 2        | 3708.4       | 682.8              | 18.4% |
| ErbB3       | 1        | 26036.3      | 673.9              | 2.6%  |
|             | 2        | 9289.1       | 203.6              | 2.2%  |
| CD30        | 1        | 34245.0      | 11544.2            | 33.7% |
|             | 2        | 11235.1      | 1905.2             | 17.0% |
| IL-2 Ry     | 1        | 9802.0       | 265.7              | 2.7%  |
|             | 2        | 3865.5       | 115.4              | 3.0%  |
| CD80        | 1        | 15854.0      | 137.4              | 0.9%  |
|             | 2        | 13174.6      | 935.6              | 7.1%  |
| Contactin-2 | 1        | 33374.4      | 2552.6             | 7.6%  |
|             | 2        | 11052.5      | 477.7              | 4.3%  |
| uPAR        | 1        | 33138.4      | 2187.1             | 6.6%  |
|             | 2        | 11442.8      | 706.9              | 6.2%  |
| Dtk         | 1        | 33710.9      | 7511.2             | 22.3% |
|             | 2        | 11115.1      | 1212.9             | 10.9% |
| ALCAM       | 1        | 32925.5      | 7984.8             | 24.3% |
|             | 2        | 11712.6      | 687.2              | 5.9%  |
| LIMP2       | 1        | 32489.1      | 1058.9             | 3.3%  |
|             | 2        | 11982.2      | 955.1              | 8.0%  |
| MICA        | 1        | 29608.7      | 1288.6             | 4.4%  |
|             | 2        | 10462.2      | 960.9              | 9.2%  |
| TIM-1       | 1        | 28630.8      | 2377.2             | 8.3%  |
|             | 2        | 12236.2      | 1095.6             | 9.0%  |

| Target       | Sample # | Mean (pg/mL) | Standard Deviation | CV %  |
|--------------|----------|--------------|--------------------|-------|
| IL-17 RA     | 1        | 32224.5      | 5080.5             | 15.8% |
|              | 2        | 11718.3      | 872.3              | 7.4%  |
| XEDAR        | 1        | 46906.2      | 8641.2             | 18.4% |
|              | 2        | 20040.5      | 3058.0             | 15.3% |
| Fas          | 1        | 16676.8      | 1905.8             | 11.4% |
|              | 2        | 5498.2       | 270.3              | 4.9%  |
| IL-21 R      | 1        | 33276.0      | 1892.6             | 5.7%  |
|              | 2        | 11048.8      | 840.3              | 7.6%  |
| CD40 ligand  | 1        | 3249.2       | 263.7              | 8.1%  |
|              | 2        | 1296.6       | 239.5              | 18.5% |
| Flt-3 ligand | 1        | 12381.8      | 895.4              | 7.2%  |
|              | 2        | 5793.4       | 986.5              | 17.0% |
| GITR         | 1        | 33118.0      | 895.4              | 2.7%  |
|              | 2        | 11568.9      | 986.5              | 8.5%  |

**NOTE:** All data in Section VII were obtained using a Flat-Bottom plate. Five-parameter logistic curve fitting was used for generation of standard curve and calculation of concentrations.

## VIII. Troubleshooting Guide

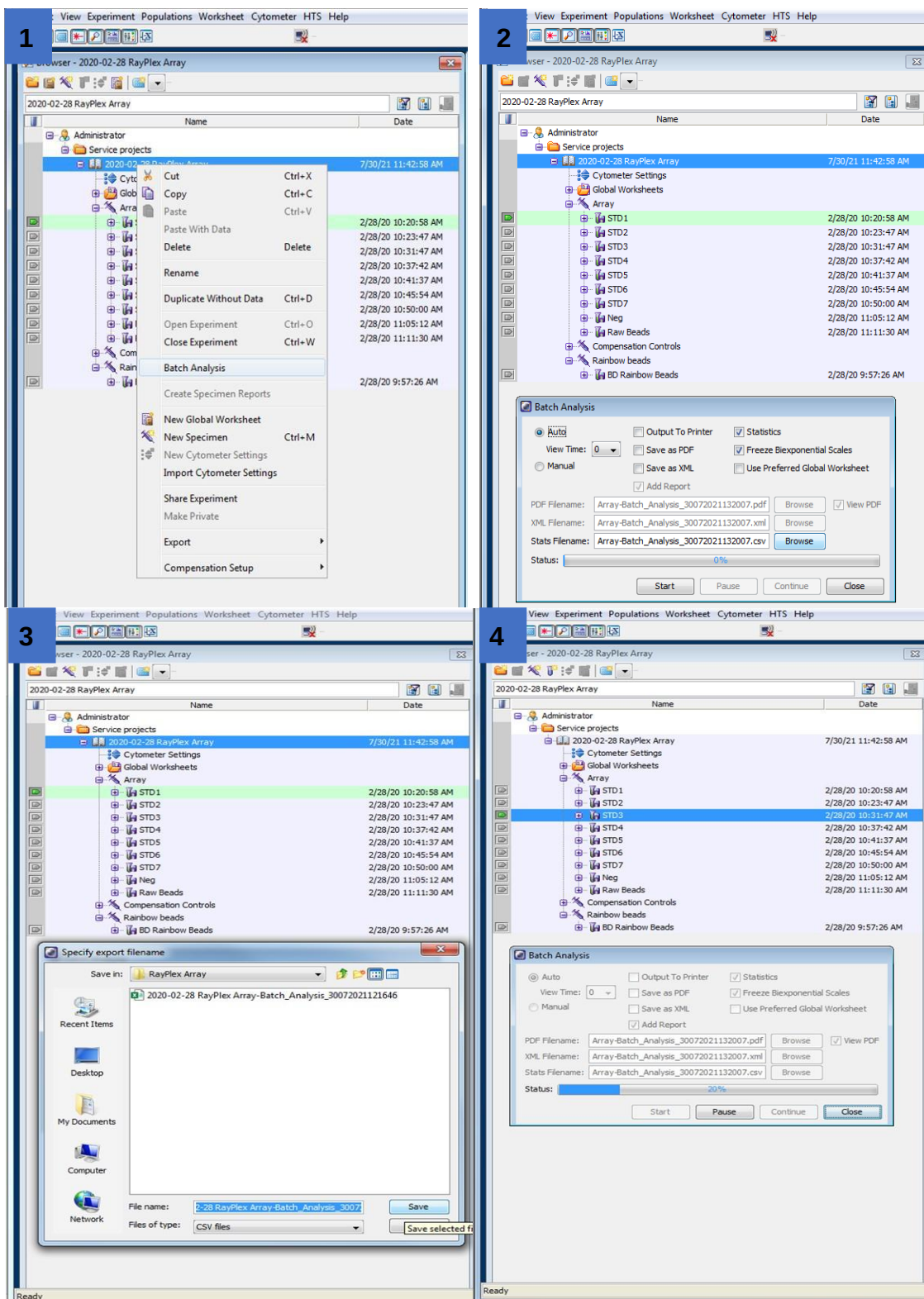
| Issue                      | Possible Causes                                                            | Recommendations                                                                                                                                                                                                                                                                                            |
|----------------------------|----------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Weak Signal</b>         | Low protein content in sample                                              | <p>Increase the length of the sample-bead incubation to overnight at 4°C (see Section VI.D “Assay Procedure”, step 3)</p> <p>Decrease sample dilution</p> <p>Note that even if the incubation is increased or the sample dilution is decreased, it is not guaranteed that the protein will be detected</p> |
|                            | Sample matrix effect                                                       | <p>Optimize sample dilution</p> <p>For serum or plasma samples, prepare the standards in the provided RayBio® Human Serum/Plasma Diluent (Item 4)</p> <p>Adjust the PE MFI using a small amount of beads from the negative control to around <math>10^{2-3}</math></p>                                     |
|                            | Improper storage of kit                                                    | Store kit at suggested temperature and use within 6 months of receipt                                                                                                                                                                                                                                      |
| <b>Poor Standard Curve</b> | Cross-contamination from neighboring wells                                 | Avoid overflowing wells during wash steps                                                                                                                                                                                                                                                                  |
|                            | Lyophilized Protein Standard Mix (Item 5) not properly prepared            | Serially dilute the Lyophilized Protein Standard Mix (Item 5) according to this manual                                                                                                                                                                                                                     |
|                            | Lyophilized Protein Standard Mix (Item 5) degraded or not properly diluted | Store Lyophilized Protein Standard at -20°C or lower. Reconstitute the Lyophilized Protein Standard Mix (Item 5) on ice before making serial dilutions                                                                                                                                                     |
| <b>High Background</b>     | Improper flow cytometer setup and optimization                             | Run Flow Cytometer Setup Bead Cocktail (Item 8) before assay. Make sure the top standard signal is not out of the linear range                                                                                                                                                                             |
|                            | PE voltage PMT voltage is not set up correctly                             | Set PE voltage using a small amount of beads from the negative control so that the PE MFI is around $10^{2-3}$                                                                                                                                                                                             |
|                            | Insufficient washing                                                       | <p>Increase wash time</p> <p>Use more wash buffer</p>                                                                                                                                                                                                                                                      |
| <b>Bead Loss</b>           | Magnetic separator unit not strong enough to hold beads                    | Try a different magnetic separator unit or leave the 96-well plate with beads on the unit for longer before washing and in-between dispensing/aspirating wash buffer                                                                                                                                       |
|                            | Aspiration/Dispensing not optimized                                        | Edit the rate of aspiration and/or dispensing wash buffer using the plate washing machine's programming                                                                                                                                                                                                    |
|                            | Washing system is not compatible with magnetic beads                       | Switch to using a Filter Plate to avoid any bead loss                                                                                                                                                                                                                                                      |

## IX. Appendix

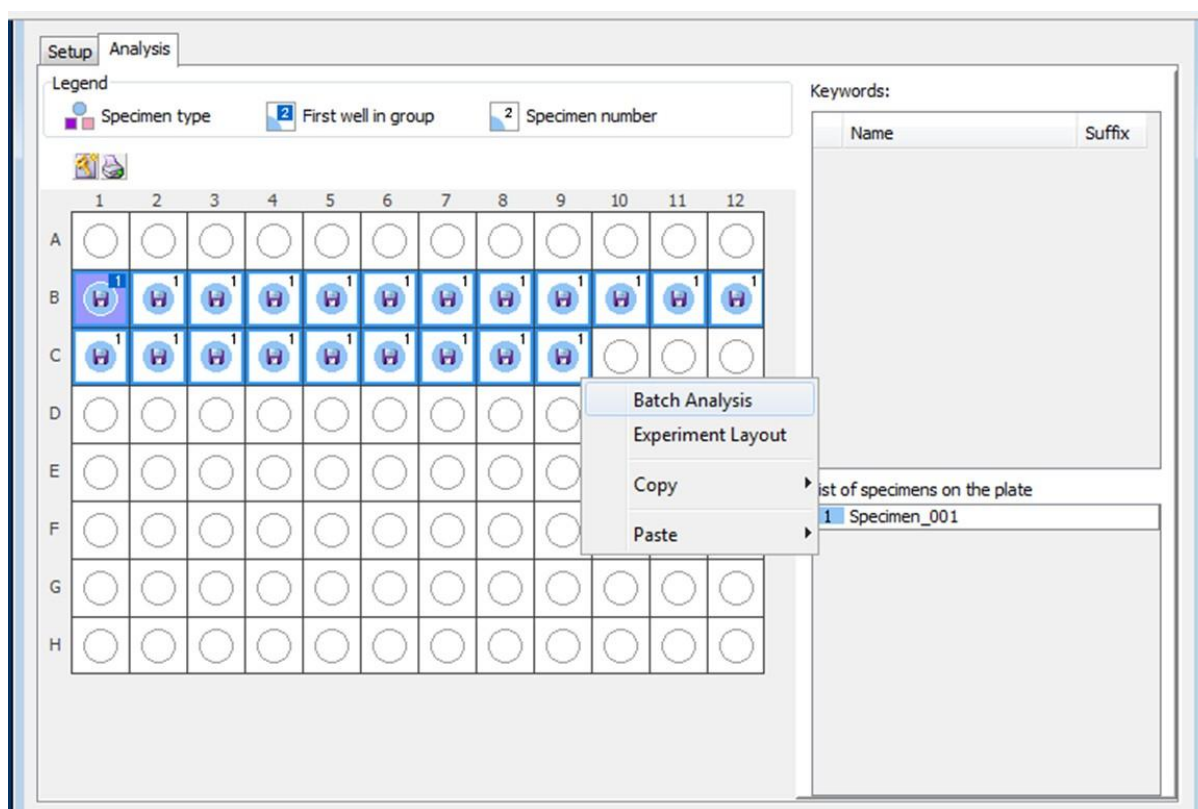
### Data Analysis using Batch Analysis

Batch analysis allows exporting PE MFI data of each bead population directly from FACS Diva software. Before batch analysis, it is important to create statistics view from the dot plot of gated beads population and choose “PE-A Median” to be shown (Figure 3D-E). Batch analysis can be done in either manual tube mode or HTS mode. Both methods for batch analysis are described below (Figure 4 and 5).

1. Create a dot plot to show all beads populations and make a gate for each population (see Figure 3 in Section VI.E). Right click on the dot plot to “Create Statistics View”, then edit the statistics view so that “PE-A Median” of gated beads populations are shown (Figure 3E).
2. **Batch Analysis from Manual Tube Mode:** Right click on the open folder containing your experiment data and select ‘Batch Analysis.’ When the pop-up appears, select the desired destination folder, and then hit start.
3. **Batch Analysis from HTS Mode:** When the HTS is done running samples, click on the ‘Analysis’ tab and highlight all the samples. Right click and select ‘Batch Analysis.’ After selecting Batch Analysis through the HTS mode, the steps from Manual mode are the same.
4. Open the CSV file in the destination folder and select ‘Save As’ to save the data as an Excel workbook (Figure 6).



**Figure 4. Screen shot showing how to begin the batch analysis through manual tube mode.**



**Figure 5. Screen shot showing how to begin HTS batch analysis.**

|    | A         | B              | C              | D              | E              | F              | G              | H              | I              | J               | K               | L               | M               | N |
|----|-----------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|-----------------|-----------------|-----------------|-----------------|---|
| 1  | Tube Name | R1 PE-A Median | R2 PE-A Median | R4 PE-A Median | R5 PE-A Median | R6 PE-A Median | R7 PE-A Median | R8 PE-A Median | R9 PE-A Median | R10 PE-A Median | R12 PE-A Median | R13 PE-A Median | R14 PE-A Median |   |
| 2  | STD1      | 42203          | 35160          | 38647          | 48464          | 34527          | 28324          | 17515          | 15124          | 16826           | 14729           | 15436           | 16014           |   |
| 3  | STD2      | 24909          | 20453          | 22914          | 27861          | 20279          | 15538          | 10087          | 8766           | 10267           | 8787            | 9270            | 9982            |   |
| 4  | STD3      | 14359          | 11430          | 12524          | 16493          | 11076          | 7942           | 5942           | 4757           | 5882            | 5029            | 5248            | 5735            |   |
| 5  | STD4      | 7268           | 5314           | 5760           | 8796           | 5327           | 3730           | 3017           | 2098           | 2580            | 2201            | 2248            | 2607            |   |
| 6  | STD5      | 4158           | 2565           | 2781           | 4726           | 2554           | 1904           | 1461           | 963            | 1230            | 1027            | 1035            | 1226            |   |
| 7  | STD6      | 2639           | 1333           | 1437           | 3354           | 1327           | 1074           | 712            | 503            | 612             | 522             | 532             | 646             |   |
| 8  | STD7      | 1928           | 749            | 823            | 2339           | 835            | 682            | 393            | 286            | 360             | 305             | 318             | 392             |   |
| 9  | Neg       | 457            | 378            | 430            | 1676           | 456            | 377            | 182            | 134            | 174             | 140             | 143             | 206             |   |
| 10 | Raw Beads | 4              | 2              | 2              | 6              | 15             | 43             | 1              | 0              | 1               | 2               | 6               | 10              |   |
| 11 |           |                |                |                |                |                |                |                |                |                 |                 |                 |                 |   |
| 12 |           |                |                |                |                |                |                |                |                |                 |                 |                 |                 |   |
| 13 |           |                |                |                |                |                |                |                |                |                 |                 |                 |                 |   |
| 14 |           |                |                |                |                |                |                |                |                |                 |                 |                 |                 |   |
| 15 |           |                |                |                |                |                |                |                |                |                 |                 |                 |                 |   |

**Figure 6. Representative raw data obtained from batch analysis.** Rows = data from samples. Left-most column = standard or sample name. (The names of beads are variable for different assays.

## X. Notes

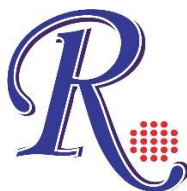
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