BioLegend®

LEGENDplex™

Multi-Analyte Flow Assay Kit

Mouse HSC Panel
Mix and Match Subpanel Manual

Please read the entire manual before running the assay.

BioLegend.com

It is highly recommended that this manual be read in its entirety before using this product. Do not use this kit beyond the expiration date.

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Chapter 1: KIT DESCRIPTION

Introduction

Stem cells are undifferentiated cells that have the ability to differentiate into specialized cell types. Hematopoietic stem cells (HSCs) are derived from mesoderm and are located in the red bone marrow. HSCs differentiate and give rise to myeloid, erythroid, and lymphoid lineages of cells, which further differentiate into specialized blood cells. Lineage development of HSCs involves interactions between cytokines, growth factors, and chemokines, which are considered as important lineage-specific markers. Lymphoid lineage-related markers such as IL-3, IL-6, IL-15, TGF-β1, SCF, LIF, and CXCL12 (SDF-1) help lymphoid progenitor cells to differentiate into B Cells, NK cells, T Cells and dendritic cells. Markers such as IL-3, IL-5, IL-34, GM-CSF, M-CSF, SCF, and CXCL12 (SDF-1) are associated with the myeloid lineage and help differentiate HSCs into monocytes, macrophages, neutrophils, eosinophils, and basophils. IL-3, IL-6, EPO, TPO, SCF, GM-CSF and CXCL12 (SDF-1) promote the differentiation of erythroid progenitor cells into erythrocytes and platelets. Dysregulation of these lineage-specific markers can lead to pathological abnormalities such as leukemias, lymphomas, myelomas, phagocyte disorders, and anemias. Quantification of these markers can help in hematopoietic stem cell research and early stage detection of various disease conditions.

The LEGENDplex™ Mouse HSC Panel (13-plex) is a bead-based multiplex assay panel, using fluorescence-encoded beads suitable for use on various flow cytometers. It allows for simultaneous quantification of 13 key targets involved in hematopoietic stem cell differentiation and lineage specification, including IL-34, IL-5, M-CSF, TPO, IL-6, GM-CSF, IL-15, TGF-β1, IL-3, LIF, SCF, EPO, and CXCL12 (SDF-1). This assay panel provides higher detection sensitivity and broader dynamic range than traditional ELISA methods. The panel has been validated for use on cell culture supernatant, serum, and plasma samples.

The Mouse HSC Panel is designed to allow flexible customization within the panel. It can also be divided into subpanels based on target type, listed below:

LEGENDplex™ Mouse HSC Panel (13-plex)
LEGENDplex™ Mouse HSC Lymphoid Panel (7-plex)
LEGENDplex™ Mouse HSC Erythroid Panel (7-plex)
LEGENDplex™ Mouse HSC Myeloid Panel (7-plex)

Please visit **www.biolegend.com/legendplex** for more information on panel design and how to mix and match within the panel.

This assay is for research use only.

Principle of the Assay

BioLegend's LEGENDplex™ assays are bead-based immunoassays using the same basic principle as sandwich immunoassays.

Beads are differentiated by size and internal fluorescence intensities. Each bead set is conjugated with a specific antibody on its surface and serves as the capture beads for that particular analyte. When a selected panel of capture beads is mixed and incubated with a sample containing target analytes, each analyte will bind to its specific capture beads. After washing, a biotinylated detection antibody cocktail is added, and each detection antibody in the cocktail will bind to its specific analyte bound on the capture beads, thus forming capture bead-analyte-detection antibody sandwiches. Streptavidin-phycoerythrin (SA-PE) is subsequently added, which will bind to the biotinylated detection antibodies, providing fluorescent signal intensities in proportion to the amount of bound analytes.

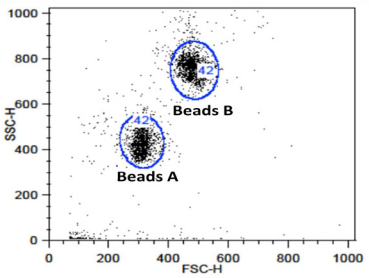
Since the beads are differentiated by size and internal fluorescence intensity on a flow cytometer, analyte-specific populations can be segregated and PE fluorescent signal quantified. The concentration of a particular analyte is determined using a standard curve generated in the same assay.

Beads Usage

The Mouse HSC Panel uses two sets of beads. Each set has a unique size that can be identified based on their forward scatter (FSC) and side scatter (SSC) profiles (Beads A and Beads B, Figure 1). Each bead set can be further resolved based on their internal fluorescence intensities. The internal dye can be detected using FL3, FL4, or APC channel, depending on the type of flow cytometer used. The smaller Beads A consists of 6 bead populations and the larger Beads B consists of 7 bead populations (Figure 2-3).

Using a total of 13 bead populations distinguished by size and internal fluorescent dye, the Mouse HSC Panel allows simultaneous detection of 13 proteins in a single sample. Each analyte is associated with a particular bead set as indicated (Figures 2-3 and Table 1).

Figure 1. Beads Differentiated by Size



Beads A = smaller beads

Beads B = larger beads

Figure 2. Beads A Classification by FL4

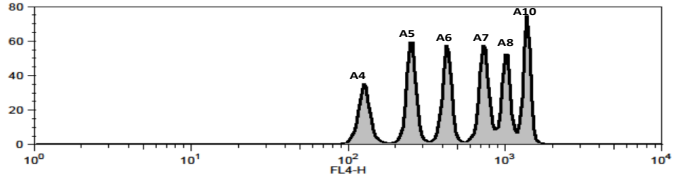
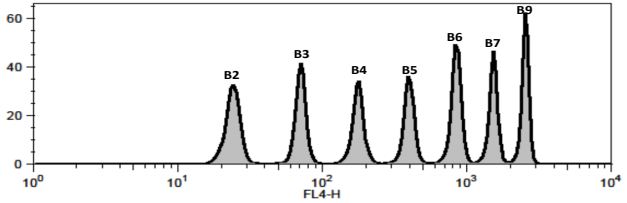


Figure 3. Beads B Classification by FL4



For Beads usage in the full panel as well as sample specific subpanels, please refer to Table 1 below.

Table 1. Panel Targets and Bead ID*

Target	Bead ID	HSC Panel (13-plex) Cat. # 740676 or 740677	HSC Lymphoid Panel (7-plex) Cat. # 740678 or 740679	HSC Erythroid Panel (7-plex) Cat. # 740680 or 740681	HSC Myeloid Panel (7-plex) Cat. # 740680 or 740683	Top Standard Concentrations
IL-34	A4	√			√	The top standard concentrations of analytes in this panel were set at various concentrations, but may be subject to change from lot to lot (please visit biolegend.com/en-us/legendplex to download a lot-specific certificate of analysis).
IL-5	A5	√			√	
M-CSF	A6	√			√	
TPO	A7	√		√		
IL-6	A8	√	√	√		
GM-CSF	A10	√		√	√	
IL-15	B2	√	√			
TGF-β1**	B3	√	√	√	√	
IL-3	B4	√	√			
LIF	B5	√	√			
SCF	B6	√	√	√	√	
EPO	B7	√		√		
CXCL12 (SDF-1)	B9	√	√	√	√	

**The mouse TGF-β1 assay detects free active TGF-β1, without sample treatment.
*Bead ID is used to associate a bead population to a particular analyte when using the LEGENDplex™ data analysis software program. For further information regarding the use of the program please visit biolegend.com/en-us/legendplex

Storage Information

Recommended storage for all original kit components is between 2°C and 8°C. DO NOT FREEZE Pre-mixed Beads, Detection Antibodies or SA-PE.

- Once the standards have been sufficiently reconstituted, immediately transfer contents into polypropylene vials. DO NOT STORE RECONSTITUTED STANDARDS IN GLASS VIALS.
- Upon reconstitution, leftover top standard should be stored at ≤-70°C for use within one month. Avoid multiple (>2) freeze-thaw cycles. Discard any leftover diluted standards.

Materials Supplied

The LEGENDplex™ kit contains reagents for 100 tests, listed in the table below. When assayed in duplicate, this is enough for an 8-point standard curve and 40 samples.

For the Mix and Match Subpanels, individual beads are provided at 13X concentration. The Buffer Set contains Setup Beads, all Buffers, Plate Sealers, Matrix, and SA-PE.

Kit Components	Quantity	Volume	Cat. #
Capture Beads (see tables below for more information)	**Varies**	**Varies**	**Varies**
Mouse HSC Panel Detection Antibodies	1 bottle	3.3 mL	740685
Mouse HSC Panel Standard	1 vial	Lyophilized	740684
LEGENDplex™ Buffer Set H1	1		741206
Filter Plate* or V-bottom Plate**	1 plate		740377* or 740379**

* For kit with filter plate. ** For kit with V-bottom plate. Only one plate is provided for each kit.

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Capture Beads for Mix and Match Subpanels*

Kit Components	Quantity	Volume	Cat.#
LEGENDplex™ Mouse IL-34 Capture Bead A4, 13X	1 vial	270 µL	740686
LEGENDplex™ Mouse IL-5 Capture Bead A5, 13X	1 vial	270 µL	741254
LEGENDplex™ Mouse M-CSF Capture Bead A6, 13X	1 vial	270 µL	740687
LEGENDplex™ Mouse TPO Capture Bead A7, 13X	1 vial	270 µL	740688
LEGENDplex™ Mouse IL-6 Capture Bead A8, 13X	1 vial	270 µL	741259
LEGENDplex™ Mouse GM-CSF Capture Bead A10, 13X	1 vial	270 µL	740689
LEGENDplex™ Mouse IL-15 Capture Bead B2, 13X	1 vial	270 µL	740690
LEGENDplex™ Mouse TGF-β1 Capture Bead B3, 13X	1 vial	270 µL	740692
LEGENDplex™ Mouse IL-3 Capture Bead B4, 13X	1 vial	270 µL	740691
LEGENDplex™ Mouse LIF Capture Bead B5, 13X	1 vial	270 µL	740693
LEGENDplex™ Mouse SCF Capture Bead B6, 13X	1 vial	270 µL	740694
LEGENDplex™ Mouse EPO Capture Bead B7, 13X	1 vial	270 µL	740695
LEGENDplex™ Mouse CXCL12 (SDF-1) Capture Bead B9, 13X	1 vial	270 µL	740696

***** Please refer to **Panel Targets and Bead ID (Table 1, page 5),** to see which capture beads are included in each panel.

LEGENDplex™ Buffer Set H1 (Cat#: 741206)

Components	Quantity	Volume	Part #
Setup Beads: PE Beads	1 vial	1 mL	77842
Setup Beads: Raw Beads	1 vial	1.8 mL	77844
LEGENDplex™ SA-PE	1 bottle	3.3 mL	77743
LEGENDplex™ Matrix A1	1 vial	Lyophilized	750000601
LEGENDplex™ Assay Buffer	1 bottle	25 mL	77562
Lyophilized Standard Reconstitution Buffer	1 vial	1 mL	75241
LEGENDplex™ Wash Buffer, 20X	1 bottle	25 mL	77564
Plate Sealers	4 sheets		78101

No plate is included in Buffer Set H1. Plate needs to be ordered separately. Please order the correct type of plate based on the preferred assay protocol (Cat# 740377 or 740378 for Filter Plate and Cat# 740379 for V-bottom Plate).

Materials to be Provided by the End-User

- A flow cytometer equipped with two lasers (e.g., a 488 nm blue laser or 532 nm green laser and a 633-635 nm red laser) capable of distinguishing 575 nm and 660 nm or a flow cytometer equipped with one laser (e.g., 488 nm blue laser) capable of distinguishing 575 nm and 670 nm.

Partial list of compatible flow cytometers:

Flow Cytometer	Reporter Channel	Channel Emission	Classification Channel	Channel Emission	Compensation needed?
BD Accuri™ C6™	FL2	585 nm	FL4	675 nm	No*
BD FACSCanto, BD FACSCanto™II	PE	575 nm	APC	660 nm	No*
BD™ LSR, LSR II BD LSRFortessa™	PE	575 nm	APC	660 nm	No*
Gallios™	PE	575 nm	APC	660 nm	No*
CytoFLEX	PE	585 nm	APC	660 nm	No*
NovoCyte	PE	572 nm	APC	660 nm	No*
Attune™ NxT	PE	574 nm	APC	670 nm	No*

***Compensation is not required for the specified flow cytometers when set up properly.**

For setting up various flow cytometers, please visit: **www.biolegend.com/legendplex** and click on the **Instrument Setup** tab.

- Multichannel pipettes capable of dispensing 5 µL to 200 µL
- Reagent reservoirs for multichannel pipette
- Polypropylene microfuge tubes (1.5 mL)
- Laboratory vortex mixer
- Sonicator bath (e.g., Branson Ultrasonic Cleaner model #B200, or equivalent)
- Aluminum foil
- Absorbent pads or paper towels
- Plate shaker (e.g., Lab-Line Instruments model #4625, or equivalent)
- Tabletop centrifuges (e.g., Eppendorf centrifuge 5415 C, or equivalent)

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If the assay is performed in a filter plate (recommended):

- A vacuum filtration unit (Millipore MultiScreen ® HTS Vacuum Manifold, cat # MSVMHTS00 or equivalent). Instructions on how to use the vacuum manifold can be found at the supplier's website.
- A vacuum source (mini vacuum pump or line vacuum, e.g., Millipore Vacuum Pump, catalog # WP6111560, or equivalent)
- If needed, additional Filter plates can be ordered from BioLegend (Cat# 740377 or 740378).

If the assay is performed in a V-bottom plate (optional):

- Centrifuge with a swinging bucket adaptor for microtiter plates (e.g., Beckman Coulter Allegra™ 6R Centrifuge with MICROPLUS CARRIER adaptor for GH3.8 and JS4.3 Rotors) .
- If needed, additional V-bottom plates can be ordered from BioLegend (Cat# 740379).

Precautions

- All blood components and biological materials should be handled as potentially hazardous. Follow universal precautions as established by the Center for Disease Control and Prevention and by the Occupational Safety and Health Administration when handling and disposing of infectious agents.
- Sodium azide has been added to some reagents as a preservative. Although the concentrations are low, sodium azide may react with lead and copper plumbing to form highly explosive metal azides. On disposal, flush with a large volume of water to prevent azide build-up.
- Do not mix or substitute reagents from different kits or lots. Reagents from different manufacturers should not be used with this kit.
- Do not use this kit beyond its expiration date.
- SA-PE and beads are light-sensitive. Minimize light exposure.

Chapter 2: ASSAY PREPARATION

Sample Collection and Handling

Preparation of Serum Samples:

- Allow the blood to clot for at least 30 minutes and centrifuge for 20 minutes at 1,000 x *g*.
- Remove serum and assay immediately or aliquot and store samples at ≤-20°C. Avoid multiple (>2) freeze/thaw cycles.
- When using frozen samples, it is recommended that samples be thawed completely, mixed and centrifuged to remove particulates prior to use.

Preparation of Plasma Samples:

- Plasma collection should be collected using an anti-coagulant (e.g., EDTA, Heparin, Citrate). Centrifuge for 20 minutes at 1,000 x *g* within 30 minutes of blood collection.
- Remove plasma and assay immediately, or aliquot and store samples at ≤-20°C. Avoid multiple (>2) freeze/thaw cycles.
- When using frozen samples, it is recommended that samples be thawed completely, mixed well and centrifuged to remove particulates.

Preparation of Cell Culture Supernatant:

- Centrifuge the sample to remove debris and assay immediately. If not possible, aliquot and store samples at ≤-20°C. Avoid multiple (>2) freeze/thaw cycles.

Reagent Preparation

Preparation of Antibody-Immobilized Beads

The individual beads (13X) should be mixed with each other and diluted to 1X final concentration with Assay Buffer prior to use. To mix the beads, follow the steps below (a 7-plex subpanel is used as an example):

1. Sonicate each bead vial for 1 minute in a sonicator bath and then vortex for 30 seconds to completely resuspend the beads.
2. Calculate the amount of mixed and diluted beads needed for the assay. Prepare extra to compensate for pipetting loss. Each reaction needs 25 µL of mixed and diluted beads. For 50 reactions, prepare 1.5 mL of mixed beads. For 100 reactions, prepare 3 mL of mixed beads.

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3. To make 1.5 mL of 7-plex 1X diluted beads, transfer 115 µL of each of the 7 individual beads (13X) to a fresh tube (total bead volume = 805 µL) and add 695 µL of Assay Buffer to make the final volume of 1.5 mL.

Preparation of Wash Buffer

- Bring the 20X Wash Buffer to room temperature and mix to bring all salts into solution.
- Dilute 25 mL of 20X Wash Buffer with 475 mL deionized water. Store unused portions between 2°C and 8°C for up to one month.

Preparation of Matrix A1 (for Serum or Plasma Samples Only)

- Add 5.0 mL LEGENDplex™ Assay Buffer to the bottle containing lyophilized Matrix A1. Allow at least 15 minutes for complete reconstitution. Vortex to mix well. Leftover reconstituted Matrix A1 should be stored at ≤-70°C for up to one month.

Standard Preparation

1. Prior to use, reconstitute the lyophilized Mouse HSC Standard with 250 µL Reconstitution Buffer.
2. Mix and allow the vial to sit at room temperature for 10 minutes, and then transfer the standard to an appropriately labeled polypropylene microcentrifuge tube. This will be used as the top standard C7.

   Note: The top standard concentrations of analytes in this panel were set at various concentrations, but may be subject to change from lot to lot (please visit biolegend.com/en-us/legendplex to download a lot-specific certificate of analysis).
3. Label 6 polypropylene microcentrifuge tubes as C6, C5, C4, C3, C2 and C1, respectively.
4. Add 75 µL of Assay Buffer to each of the six tubes. Prepare 1:4 dilution of the top standard by transferring 25 µL of the top standard C7 to the C6 tube and mix well. This will be the C6 standard.
5. In the same manner, perform serial 1:4 dilutions to obtain C5, C4, C3, C2 and C1 standards (**see the table below using the top standard at 10,000 pg/mL as an example**). Assay Buffer will be used as the 0 pg/mL standard (C0).

Tube/Standard ID	Serial Dilution	Assay Buffer to add (µL)	Standard to add	Final Conc. (pg/mL)
C7	--	--	--	10,000
C6	1:4	75	25 µL of C7	2,500

C5	1:16	75	25 µL of C6	625
C4	1:64	75	25 µL of C5	156.25
C3	1:256	75	25 µL of C4	39.01
C2	1:1024	75	25 µL of C3	9.77
C1	1:4096	75	25 µL of C2	2.44
C0	--	75	--	0

Sample Dilution

- For cell culture supernatant samples, the levels of analyte can vary greatly from sample to sample. To test cell culture supernatant samples, a preliminary experiment may be required to determine the appropriate dilution factor. If further dilution is desired, dilution should be done with corresponding fresh cell culture medium or Assay Buffer as a diluent to ensure accurate measurement.

- Serum or plasma samples must be diluted 2-fold with Assay Buffer before being tested (e.g., dilute 50 µL of sample with 50 µL of Assay Buffer). **M-CSF in serum and plasma samples might need further dilution (50-fold) for accurate measurement.** If further dilution is desired, dilution should be done with Matrix A1 to ensure accurate measurement.

  Adding serum or plasma samples without dilution will result in low assay accuracy and possibly, clogging of the filter plate.

Chapter 3: ASSAY PROCEDURE

The LEGENDplex™ assay can be performed in a filter plate, or in a V-bottom plate.

- The Filter plate assay procedure is recommended due to its good sample to sample consistency, assay robustness and ease of handling. This procedure requires a vacuum filtration unit for washing (see **Materials to be Provided by the End-User, page 8)**. If you have performed bead-based multiplex assays before, your lab may already have the vacuum filtration unit set up.
- If the Filter plate assay procedure is not possible or if you prefer, the assay can be performed in a V-bottom plate.

Performing the Assay Using a Filter Plate

- Allow all reagents to warm to room temperature (20-25°C) before use.
- Set the filter plate on an inverted plate cover at all times during assay setup and incubation steps, so that the bottom of the plate does not touch any surface. Touching a surface may cause leakage.
- Keep the plate upright during the entire assay procedure, including the washing steps, to avoid losing beads.
- The plate should be placed in the dark or wrapped with aluminum foil for all incubation steps.
- **Standards and samples should be run in duplicate and arranged on the plate in a vertical configuration convenient for data acquisition and analysis (as shown in attached PLATE MAP, page 33). Be sure to load standards in the first two columns. If an automation device is used for reading, the orientation and reading sequence should be carefully planned.**

1. Pre-wet the plate by adding 100 µL of LEGENDplex™ 1X Wash Buffer to each well and let it sit for 1 minute at room temperature. To remove the excess volume, place the plate on the vacuum manifold and apply vacuum. Do not exceed 10" Hg of vacuum. Vacuum until wells are drained (5-10 seconds). Blot excess Wash Buffer from the bottom of the plate by pressing the plate on a stack of clean paper towels. Place the plate on top of the inverted plate cover.

2. **For measuring cell culture supernatant samples,** load the plate as shown in the table below (in the order from left to right):

	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	25 µL	---
Sample wells	25 µL	---	25 µL

For measuring serum or plasma samples, load the plate as shown in the table below (in the order from left to right):

	Matrix A1	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	---	25 µL	---
Sample wells	---	25 µL	---	25 µL

*See **Sample Dilution on page 12**

3. Vortex mixed beads bottle for 30 seconds. Add 25 µL of mixed beads to each well. The volume should be 75 µL in each well after beads addition. (Note: During addition of the beads, shake mixed beads bottle intermittently to avoid bead settling).

4. Seal the plate with a plate sealer. **To avoid plate leaking, do not apply positive pressure to the sealer when sealing the plate**. Wrap the entire plate, including the inverted plate cover, with aluminum foil. Place the plate on a plate shaker, secure it with a rubber band and shake at approximate 500 rpm for 2 hours at room temperature.

5. **Do not invert the plate**! Place the plate on the vacuum manifold and apply vacuum as before in Step 1. Add 200 µL of 1X Wash Buffer to each well. Remove Wash Buffer by vacuum filtration. Blot excess Wash Buffer from the bottom of the plate with an absorbent pad or paper towels. Repeat this washing step once more.

6. Add 25 µL of Detection Antibodies to each well.

7. Seal the plate with a fresh plate sealer. Wrap the entire plate, including the inverted plate cover, with aluminum foil. Place the plate on a plate shaker and shake at approximately 500 rpm for 1 hour at room temperature.

8. **Do not vacuum!** Add 25 µL of SA-PE to each well directly.

9. Seal the plate with a fresh plate sealer. Wrap the entire plate, including the inverted plate cover, with aluminum foil. Place the plate on a plate shaker and shake at approximate 500 rpm for 30 minutes at room temperature.

10. Repeat step 5 above.

11. Add 150 µL of 1X Wash Buffer to each well. Resuspend the beads on a plate shaker for 1 minute.

12. Read samples on a flow cytometer, preferably within the same day of the assay (Note: Prolonged sample storage can lead to reduced signal).

    If the flow cytometer is equipped with an autosampler, read the plate directly using the autosampler. **Please be sure to program the autosampler to resuspend beads in the well immediately before taking samples. The probe height may need to be adjusted when using an autosampler**.

    If an autosampler is not available, the samples can be transferred from the filter plate to micro FACS (or FACS) tubes and read manually.

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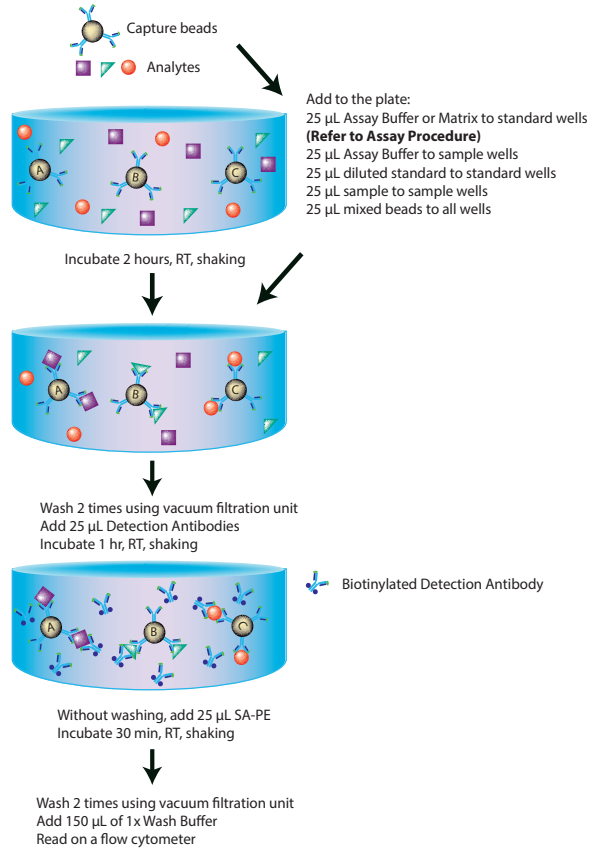
Assay Procedure Summary for Filter Plate

Add 100 µL 1X Wash Buffer to filter plate wells
Vacuum to remove excess buffer



Performing the Assay Using a V-bottom Plate

- Allow all reagents to warm to room temperature (20-25°C) before use.
- Keep the plate upright during the entire assay procedure, including the washing steps, to avoid losing beads.
- The plate should be placed in the dark or wrapped with aluminum foil for all incubation steps.
- Standards and samples should be run in duplicate and arranged on the plate in a vertical configuration convenient for data acquisition and analysis (as shown in attached PLATE MAP, page 33). Be sure to load standards in the first two columns. If an automation device is used for reading, the orientation and reading sequence should be carefully planned.

1. **For measuring cell culture supernatant samples,** load the plate as shown in the table below (in the order from left to right):

	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	25 µL	---
Sample wells	25 µL	---	25 µL

For measuring serum or plasma samples, load the plate as shown in the table below (in the order from left to right):

	Matrix A1	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	---	25 µL	---
Sample wells	---	25 µL	---	25 µL

*See **Sample Dilution on page 12**

2. Vortex mixed beads for 30 seconds. Add 25 µL of mixed beads to each well. The total volume should be 75 µL in each well after beads addition. (Note: During beads addition, shake mixed beads bottle intermittently to avoid bead settling).
3. Seal the plate with a plate sealer. Cover the entire plate with aluminum foil to protect the plate from light. Shake at 800 rpm on a plate shaker for 2 hours at room temperature **(Depending on the shaker, the speed may need to be adjusted. The optimal speed is one that is high enough to keep beads in suspension during incubation, but not too high that it may cause sample to spill from the wells)**.
4. Centrifuge the plate at 1050 rpm (~250 g) for 5 minutes, using a swinging bucket rotor (G.H 3.8) with microplate adaptor (Please refer to **Materials to be Provided by the End-User, page 8).** Do not use excessive centrifugation speed as it may make it harder to resuspend beads in later steps. **Make sure the timer of the centrifuge works properly and standby to make sure the centrifuge reaches preset speed.**

5. Immediately after centrifugation, dump the supernatant into a biohazard waste container by quickly inverting and flicking the plate **in one continuous and forceful motion**. The beads pellet may or may not be visible after dumping the supernatant. Loss of beads should not be a concern as the beads will stay in the tip of the well nicely. Blot the plate on a stack of clean paper towel and drain the remaining liquid from the well as much as possible. Be careful not to disturb the bead pellet.

   Alternatively, removal of the supernatant may be completed using a multichannel pipette set at 75 µL. Try to remove as much liquid as possible without removing any beads. Be sure to change pipette tips between each row or column.

6. Wash the plate by dispensing 200 µL of 1X Wash Buffer into each well and incubate for one minute. Repeat step 4 and 5 above. A second wash is optional, but may help reduce background.

7. Add 25 µL of Detection Antibodies to each well.

8. Seal the plate with a new plate sealer. Cover the entire plate with aluminum foil to protect the plate from light. Shake at 800 rpm on a plate shaker for 1 hour at room temperature.

9. **Do not wash the plate!** Add 25 µL of SA-PE to each well directly.

10. Seal the plate with a new plate sealer. Wrap the entire plate with aluminum foil and shake the plate on a plate shaker at approximate 800 rpm for 30 minutes at room temperature.

11. Repeat step 4, and 5.

12. (This washing step is optional but helps to reduce the background.) Wash the plate by dispensing 200 µL of 1X Wash Buffer into each well and incubate for one minute. Repeat step 4 and 5 above.

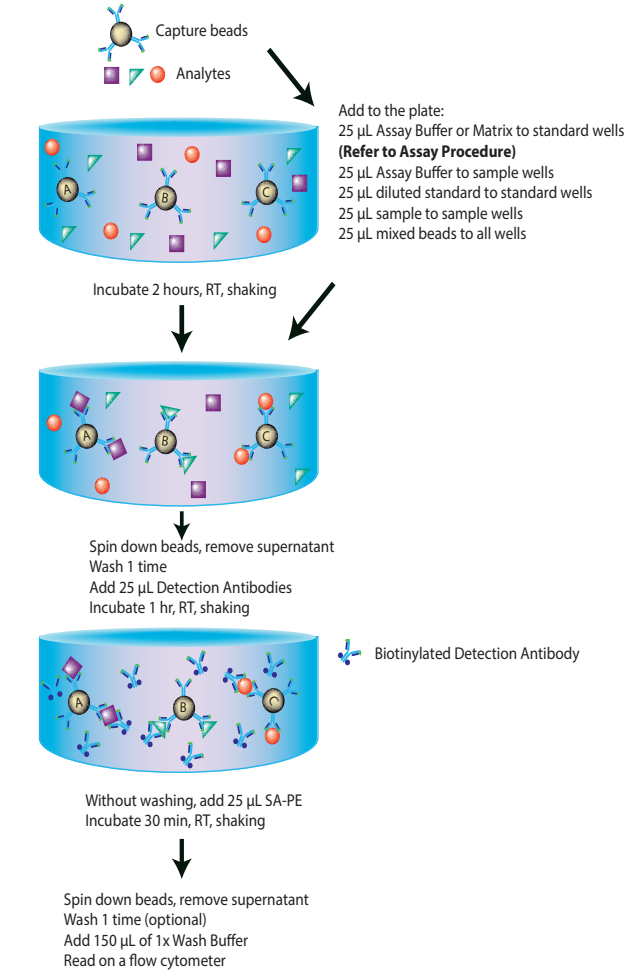
13. Add 150 µL of 1X Wash Buffer to each well. Resuspend the beads by pipetting.

14. Read samples on a flow cytometer, preferably within the same day of the assay (Note: Prolonged sample storage can lead to reduced signal).

    If the flow cytometer is equipped with an autosampler, the samples can be read directly. **Please be sure to program the autosampler to resuspend beads in the well immediately before taking samples. The probe height may need to be adjusted when using an autosampler**.

    If an autosampler is not available, the samples can be transferred from the plate to micro FACS (or FACS) tubes and read manually.

Assay Procedure Summary for V-bottom Plate



Chapter 4: FLOW CYTOMETER SETUP

In order to generate reliable data, the flow cytometer must be set up properly before data acquisition.

The setup instructions have been removed from this manual and uploaded onto our website to save paper.

To access the setup instructions, please visit: **www.biolegend.com/legendplex** and click on the **Instrument Setup** tab.

Chapter 5: DATA ACQUISITION AND ANALYSIS

Data Acquisition

1. Before reading samples, make sure that the flow cytometer is set up properly.

2. Create a new template or open an existing template (for details on how to create a cytometer-specific template, please refer to the Flow Cytometer Setup Guide).

3. Vortex each sample for 5 seconds before analysis.

4. Set the flow rate to low. Set the number of beads to be acquired to about 300 per analyte (e.g., acquire 2,100 beads for a 7-plex assay or 3,000 beads for a 13-plex assay). Do not set to acquire total events as samples may contain large amounts of debris. Instead, create a large gate to include both Beads A and Beads B (gate A+B) and set to acquire the number of events in gate A + B. This will exclude majority of the debris.

   Note: Do not acquire too few or too many beads. Too few beads acquired may result in high CVs and too many beads acquired may result in slow data analysis later.

5. Read samples.

   When reading samples, set the flow cytometer to setup mode first and wait until bead population is stabilized before recording or switching to acquisition mode.

   To simplify data analysis using the LEGENDplex™ Data Analysis Software, read samples in the same order as shown on the PLATE MAP attached at the end of the manual. For an in-plate assay, read column by column (A1, B1, C1...A2, B2, C2...).

When naming data files, try to use simple names with a consecutive numbering for easy data analysis (e.g. for standards, C0.001, C0.002, C1.003, C1.004, C2.005, C2.006, C3.007, C3.008, ... C7.015, C7.016; for samples, S1.017, S1.018, S2.019, S2.020, S3.021, S3.022…)

Store all FCS files in the same folder for each assay. If running multiple assays, create a separate folder for each assay.

6. Proceed to data analysis using LEGENDplex™ Data Analysis Software when data acquisition is completed.

Bead count for TPO is expected to be low (e.g. <50 per sample) for serum and plasma samples, but normal in cell culture supernatant samples.

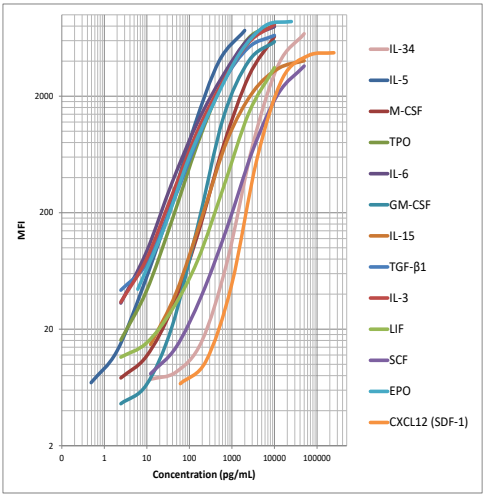
Data Analysis

- The assay FCS files should be analyzed using BioLegend's LEGENDplex™ data analysis software. The program is offered free of charge with the purchase of any LEGENDplex™ assay. For further information regarding acccess to, and use of the program please visit **biolegend.com/en-us/legendplex.**

Chapter 6: ASSAY CHARACTERIZATION

Representative Standard Curve

This standard curve was generated using the LEGENDplex™ Mouse HSC Panel for demonstration purposes only. A standard curve must be run with each assay.



Assay Sensitivity

The assay sensitivity is the theoretical limit of detection calculated using the LEGENDplex™ Data Analysis Software by applying a 5-paramater curve fitting algorithm. Assay Sensitivity presented here is ≤Mean LOD + 2x STDEV LOD.

Analyte	LOD in Assay Buffer (pg/mL)	LOD in Matrix (pg/mL)
IL-34	87.40	97.70
IL-5	1.30	1.10
M-CSF	7.30	17.70
TPO	2.30	2.20
IL-6	2.39	2.90
GM-CSF	6.40	10.60
IL-15	12.60	15.90
TGF-β1	4.90	12.80
IL-3	2.10	2.70

LIF	5.60	6.80
SCF	12.70	14.30
EPO	4.50	6.60
CXCL12 (SDF-1)	63.70	56.90

Cross-Reactivity

Mouse TGF-β1 assay detects both mouse and human free active TGF-β1. Mouse CXCL12 (SDF-1) assay detects both mouse SDF-1α and mouse SDF-1β and cross reacts with human SDF-1α and human SDF-1β. The mouse assays of SCF, EPO, and LIF have cross-reactivity with its human protein of 6.21%, 3.99%, and 0.22%, respectively.

The following recombinant proteins were tested individually at 50 ng/mL. No or negligible cross-reactivity was found.

Mouse	FLT3L, G-CSF, IFN-γ, IL-1α, IL-1β, IL-2, IL-4, IL-7, IL-10, IL-11, IL-12 (p70), TNF-α
Human	GM-CSF, IL-3, IL-5, IL-6, IL-15, IL-34, M-CSF, TNF-α, TPO

Accuracy (Spike Recovery)

For spike recovery in cell culture medium (n=2), RPMI or DMEM with 10% FCS were spiked with target proteins at three different levels within the assay range. For spike recovery in serum and plasma (n=4 each), samples were first diluted two-fold with Assay Buffer and spiked with target proteins at three different levels within the assay range.

The spiked samples were then assayed, and the measured concentrations were compared with the expected values.

Analyte	% of Spike Recovery		
	Cell Culture Supernatant	Serum	Plasma
IL-34	71%	105%	98%
IL-5	77%	81%	81%
M-CSF	68%	135%	69%
TPO	70%	72%	68%
IL-6	75%	102%	96%
GM-CSF	77%	104%	103%

IL-15	43%	77%	92%
TGF-β1	84%	120%	119%
IL-3	95%	77%	61%
*LIF	102%	90%	80%
SCF	85%	96%	100%
EPO	102%	112%	115%
CXCL12 (SDF-1)	120%	113%	144%

*Native source of LIF was spiked into diluted sample.

Linearity of Dilution

Cell culture samples (n=2) were spiked with target proteins with known concentrations in the assay range, then serially diluted 1:2, 1:4, 1:8 with Assay Buffer and assayed. Serum and plasma samples (n=4 each) were spiked with target proteins with known concentrations in the assay range, then serially diluted 1:2, 1:4, 1:8 with Matrix A1 and assayed.

The measured concentrations of serially diluted samples were then compared with the concentration of the lowest dilution based on serial dilution factor used.

Analyte	% Linearity		
	Cell Culture Supernatant	Serum	Plasma
IL-34	125%	92%	111%
IL-5	110%	109%	114%
M-CSF	118%	103%	82%
TPO	107%	117%	127%
IL-6	102%	91%	106%
GM-CSF	117%	93%	102%
IL-15	113%	118%	110%
TGF-β1	87%	112%	118%
IL-3	94%	122%	140%
*LIF	104%	114%	105%
SCF	104%	113%	112%
EPO	76%	80%	80%
CXCL12 (SDF-1)	118%	84%	80%

*Native source of LIF was spiked before serial dilution.

Intra-Assay Precision

Two samples with different concentrations of each target protein were analyzed in one assay with 16 replicates per sample. The intra-assay precision is shown below.

Analyte	Sample	Mean (pg/mL)	STDEV	%CV
IL-34	Sample 1	196.22	15.42	8%
	Sample 2	1124.51	57.83	5%
IL-5	Sample 1	9.30	0.83	9%
	Sample 2	30.61	4.03	13%
M-CSF	Sample 1	45.47	4.06	9%
	Sample 2	163.88	18.63	11%
TPO	Sample 1	42.83	4.32	10%
	Sample 2	145.52	15.89	11%
IL-6	Sample 1	45.27	4.09	9%
	Sample 2	130.84	17.84	14%
GM-CSF	Sample 1	42.10	4.23	10%
	Sample 2	156.24	12.99	8%
IL-15	Sample 1	23.31	3.25	14%
	Sample 2	82.78	4.38	5%
TGF-β1	Sample 1	45.07	3.62	8%
	Sample 2	150.61	18.30	12%
IL-3	Sample 1	47.52	3.10	7%
	Sample 2	173.53	16.40	9%
LIF	Sample 1	41.98	5.54	13%
	Sample 2	155.79	14.77	9%
SCF	Sample 1	195.96	11.53	6%
	Sample 2	616.48	54.69	9%
EPO	Sample 1	118.95	12.50	11%
	Sample 2	388.31	33.32	9%
CXCL12 (SDF-1)	Sample 1	346.17	48.32	14%
	Sample 2	1131.48	144.52	13%

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Inter-Assay Precision

Two samples with different concentrations of each target protein were analyzed in four independent assays with four replicates per sample. The inter-assay precision is shown below.

Analyte	Sample	Mean (pg/mL)	STDEV	%CV
IL-34	Sample 1	206.02	16.76	8%
	Sample 2	1184.99	32.13	3%
IL-5	Sample 1	9.40	1.36	15%
	Sample 2	38.38	4.81	13%
M-CSF	Sample 1	46.17	5.42	12%
	Sample 2	194.31	15.04	8%
TPO	Sample 1	43.90	7.90	18%
	Sample 2	182.72	28.87	16%
IL-6	Sample 1	40.53	4.12	10%
	Sample 2	160.38	21.97	14%
GM-CSF	Sample 1	44.16	5.47	12%
	Sample 2	184.50	17.19	9%
IL-15	Sample 1	26.07	3.88	15%
	Sample 2	91.61	8.14	9%
TGF-β1	Sample 1	45.56	5.13	11%
	Sample 2	176.67	26.04	15%
IL-3	Sample 1	45.35	4.42	10%
	Sample 2	194.72	22.31	11%
LIF	Sample 1	42.50	5.79	14%
	Sample 2	188.53	13.68	7%
SCF	Sample 1	197.34	22.98	12%
	Sample 2	752.63	96.42	13%
EPO	Sample 1	110.97	10.99	10%
	Sample 2	435.66	48.64	11%
CXCL12 (SDF-1)	Sample 1	377.02	61.18	16%
	Sample 2	1522.67	345.70	23%

Biological Samples

* The mouse TGF-β1 assay detects free active TGF-β1, without sample treatment.

Serum

Serum samples of the following strains were pooled from a minimum of ten mice each, and tested for the endogenous levels of the proteins. The concentrations are shown below (in pg/mL).

Analyte	C57BL/6	BALB/C	Swiss Webster	CD-1
IL-34	280.75	333.65	530.40	1295.95
IL-5	2.71	1.12	1.57	1.29
M-CSF	11799.03	12592.85	10643.42	13883.31
TPO	42.83	39.10	41.34	36.32
IL-6	29.68	171.71	12.12	17.44
GM-CSF	3.85	ND	ND	ND
IL-15	25.25	14.90	ND	ND
*TGF-β1	366.57	386.14	228.68	362.51
IL-3	ND	ND	ND	ND
LIF	14.79	13.78	9.30	11.62
SCF	59.15	41.90	37.65	30.40
EPO	673.75	269.23	39.70	67.73
CXCL12 (SDF-1)	932.50	1080.50	1468.25	1408.50

ND = Non-detectable

Plasma

Plasma samples of the following strains were pooled from a minimum of ten mice each, and tested for the endogenous levels of the proteins. The concentrations are shown below (in pg/mL).

Analyte	C57BL/6	BALB/C	Swiss Webster	CD-1
IL-34	140.27	50.98	74.25	112.88
IL-5	3.06	1.42	1.19	1.19
M-CSF	10861.68	10158.14	10721.51	18404.76
TPO	12.75	12.88	19.41	12.38
IL-6	9.73	92.10	5.94	8.09
GM-CSF	5.38	1.09	2.63	3.33
IL-15	6.83	11.38	ND	ND

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*TGF-β1	ND	ND	454.41	112.66
IL-3	ND	ND	ND	ND
LIF	10.95	11.95	10.83	13.65
SCF	38.47	31.55	33.43	33.57
EPO	447.21	228.24	110.32	60.79
CXCL12 (SDF-1)	285.67	415.50	660.67	486.08

ND = Non-detectable

Cell Culture Supernatant

Mouse bone marrow cells (2 x 10^6 cells/mL) were stimulated under various conditions (FLT3 Ligand, 5 ng/mL; GM-CSF, 20 ng/mL; 300 pg/mL, IL-4), using unstimulated cells as a control. Cell culture supernatants were collected 9 days after stimulation and assayed.

Mouse splenocyte cells (1 x 10^6 cells/mL) were stimulated with 1 µg/mL LPS, using unstimulated cells as a control. Cell culture supernatants were collected 3 days after stimulation and assayed.

The results (in pg/mL) are summarized below.

Analyte	Bone Marrow Cells			Splenocyte Cells	
	Control	FLT3L	GM-CSF + IL-4	Control	LPS
IL-34	ND	ND	ND	ND	20.75
IL-5	ND	ND	ND	0.20	0.47
M-CSF	5.37	4.85	128.16	1.37	23.49
TPO	ND	ND	7.20	ND	ND
IL-6	2.61	2.40	16.64	ND	147.77
GM-CSF	ND	ND	4024.07	ND	15.27
IL-15	ND	ND	ND	ND	ND
*TGF-β1	3.64	38.66	69.03	2.57	2.36
IL-3	ND	ND	ND	ND	9.29
LIF	ND	ND	ND	ND	6.42
SCF	ND	ND	ND	ND	9.50
EPO	ND	ND	ND	ND	ND
CXCL12 (SDF-1)	129.13	109.00	ND	ND	ND

ND = Non-detectable

TROUBLESHOOTING

Problem	Possible Cause	Solution
Bead population shifting upward or downward during acquisition	The strong PE signal from high concentration samples or standards may spill over to classification Channel (e.g., FL3/FL4/APC) and mess up the bead separation.	Optimize instrument settings using Kit Setup Beads, and make appropriate compensation between channels.
Filter plate will not vacuum or some wells clogged	Vacuum pressure is insufficient or vacuum manifold does not seal properly.	Increase vacuum pressure such that 0.2 mL buffer can be suctioned in 3-5 seconds. Clean the vacuum manifold and make sure no debris on the manifold. Press down the plate on the manifold to make a good seal.
	Samples have insoluble particles or sample is too viscous (e.g., serum and plasma samples)	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous. If some wells are still clogged during washing, try the following: 1). Add buffer to all the wells, pipette up and down the clogged wells and vacuum again. 2). Use a piece of clean wipe, wipe the under side of the clogged wells and vacuum again. 3). Take a thin needle (e.g., insulin needle), while holding the plate upward, poke the little hole under each of the clogged wells and vacuum again. Do not poke too hard or too deep as it may damage the filter and cause leaking.
	Filter plate was used without pre-wet.	Pre-wet plate with wash buffer before running the assay.

Insufficient bead count or slow reading	Beads inappropriately prepared	Sonicate bead vials and vortex just prior to addition. Agitate mixed beads intermittently in reservoir while pipetting this into the plate.
	Samples cause beads aggregation due to particulate matter or viscosity.	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous.
	Beads were lost during washing for in-tube assay	Make sure beads are spun down by visually check the pellet (beads are in light blue or blue color). Be very careful when removing supernatant during washing.
	Probe might be partially clogged.	Sample probe may need to be cleaned, or if needed, probe should be removed and sonicated.
Plate leaked	Vacuum pressure set too high	Adjust vacuum pressure such that 0.2 mL buffer can be suctioned in 3-5 seconds. Do not exceed 10” Hg of vacuum.
	Plate set directly on table or absorbent towels during incubations or reagent additions	Set plate on plate holder or raised edge so bottom of filter is not touching any surface.
	Liquid present on the under side of the plate after vacuum	After washing, press down plate firmly on a stack of clean paper towels to dry the underside of the plate.
	Pipette touching and damaged plate filter during additions.	Pipette to the side of wells.
High Background	Background wells were contaminated	Avoid cross-well contamination by changing tips between pipetting when performing the assay using a multichannel pipette.
	Insufficient washes	The background may be due to non-specific binding of SA-PE. Increase number of washes.
Debris (FSC/SSC) during sample acquisition	Debris or platelet may exist in sample solution.	Centrifuge samples before analyzing samples. Remove platelet as much as possible.

Variation between duplicate samples	Beads aggregation	Sonicate and vortex the Beads prior to use.
	Multichannel pipette may not be calibrated or inconsistent pipetting	Calibrate Pipette. Ensure good pipetting practice. Prime pipette before use may help.
	Plate washing was not uniform	Make sure all reagents are vacuumed out completely in all wash steps.
	Samples may contain particulate matters.	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous.
Low or poor standard curve signal	The standard was incorrectly reconstituted, stored or diluted	Follow the protocol to reconstitute, store and dilute standard. Double check your calculation.
	Wrong or short incubation time	Ensure the time of all incubations was appropriate.
Signals too high, standard curves saturated	PMT value for FL2/PE set too high	Make sure the PMT setting for the reporter channel is appropriate
	Plate incubation time was too long	Use shorter incubation time.
Sample readings are out of range	Samples contain no or below detectable levels of analyte	Make sure the experiment to generate the samples worked. Use proper positive controls.
	Samples concentrations higher than highest standard point.	Dilute samples and analyze again.
	Standard curve was saturated at higher end of curve.	Make sure the PMT setting for the reporter channel is appropriate. Use shorter incubation time if incubation time was too long
Missed beads populations during reading, or distribution is unequal	Sample may cause some beads to aggregate.	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous.
	Beads populations are not mixed properly	Make sure all bead populations are mixed. and in similar numbers.

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Notes

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PLATE MAP (for in-plate assay)

	1	2	3	4	5	6	7	8	9	10	11	12
A	**C0**	**C4**	Sample1	Sample5	Sample 9	Sample 13	Sample 17	Sample 21	Sample 25	Sample 29	Sample 33	Sample 37
B	**C0**	**C4**	Sample1	Sample5	Sample 9	Sample 13	Sample 17	Sample 21	Sample 25	Sample 29	Sample 33	Sample 37
C	**C1**	**C5**	Sample2	Sample6	Sample 10	Sample 14	Sample 18	Sample 22	Sample 26	Sample 30	Sample 34	Sample 38
D	**C1**	**C5**	Sample2	Sample6	Sample 10	Sample 14	Sample 18	Sample 22	Sample 26	Sample 30	Sample 34	Sample 38
E	**C2**	**C6**	Sample3	Sample7	Sample 11	Sample 15	Sample 19	Sample 23	Sample 27	Sample 31	Sample 35	Sample 39
F	**C2**	**C6**	Sample3	Sample7	Sample 11	Sample 15	Sample 19	Sample 23	Sample 27	Sample 31	Sample 35	Sample 39
G	**C3**	**C7**	Sample4	Sample8	Sample 12	Sample 16	Sample 20	Sample 24	Sample 28	Sample 32	Sample 36	Sample 40
H	**C3**	**C7**	Sample4	Sample8	Sample 12	Sample 16	Sample 20	Sample 24	Sample 28	Sample 32	Sample 36	Sample 40

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