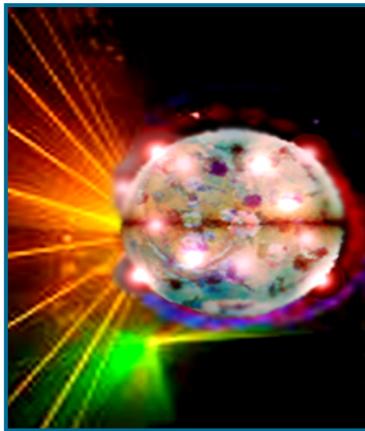


MRD Assessment in AML

Validation considerations for global clinical trial data



MetroFlow 2014

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Hematology – Flow Cytometry
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Overview

- Biomarkers defined
- Fit-for-purpose validation
 - General
 - Considerations for Flow cytometry
- AML-MRD panel development
 - as a Biomarker in Clinical Trials
 - Challenges/solutions

Definitions

- Biomarker
 - Biological marker, pharmacodynamic (PD) marker, pharmacological read-out
 - A characteristic that is measured and evaluated as an indicator of:
 - normal biologic processes
 - pathogenic processes
 - pharmacologic responses to a therapeutic intervention
- Clinical Endpoint
 - A characteristic or variable that measures how a patient feels, functions, or survives
- Surrogate Endpoint
 - A biomarker intended to substitute for a clinical endpoint
 - To predict clinical benefit or harm based on epidemiological, therapeutic, or pathophysiological scientific evidence

Biomarkers for Decision Making

- Target Validation

- Biomarkers that validate the importance of the target in humans disease

- Target/compound Interaction

- Biomarkers that define the chemical physical interaction of the compound with its target

- Pharmacodynamic Activity

- Biomarkers that define consequences of compound interaction with the target

- Patient Stratification

- Biomarkers that define likelihood of patients to response or not to the compound

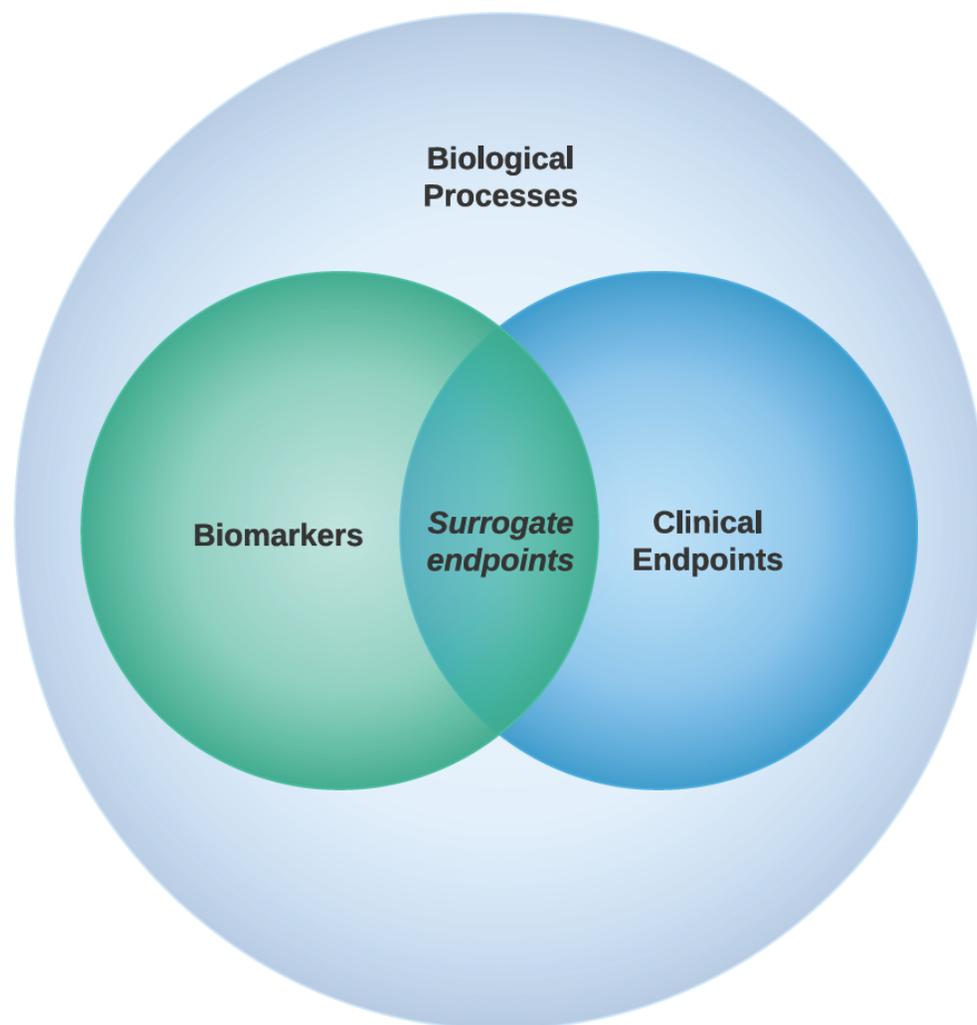
- Adaptive Design

- Biomarkers that facilitate decision making during early clinical development via repeated measures that adjust study parameters

•Adapted from Feuerstein G et al. Translational Medicine Perspectives. Am Drug Discovery 3(2), 2008

•Slide courtesy of Ole Vesterqvist

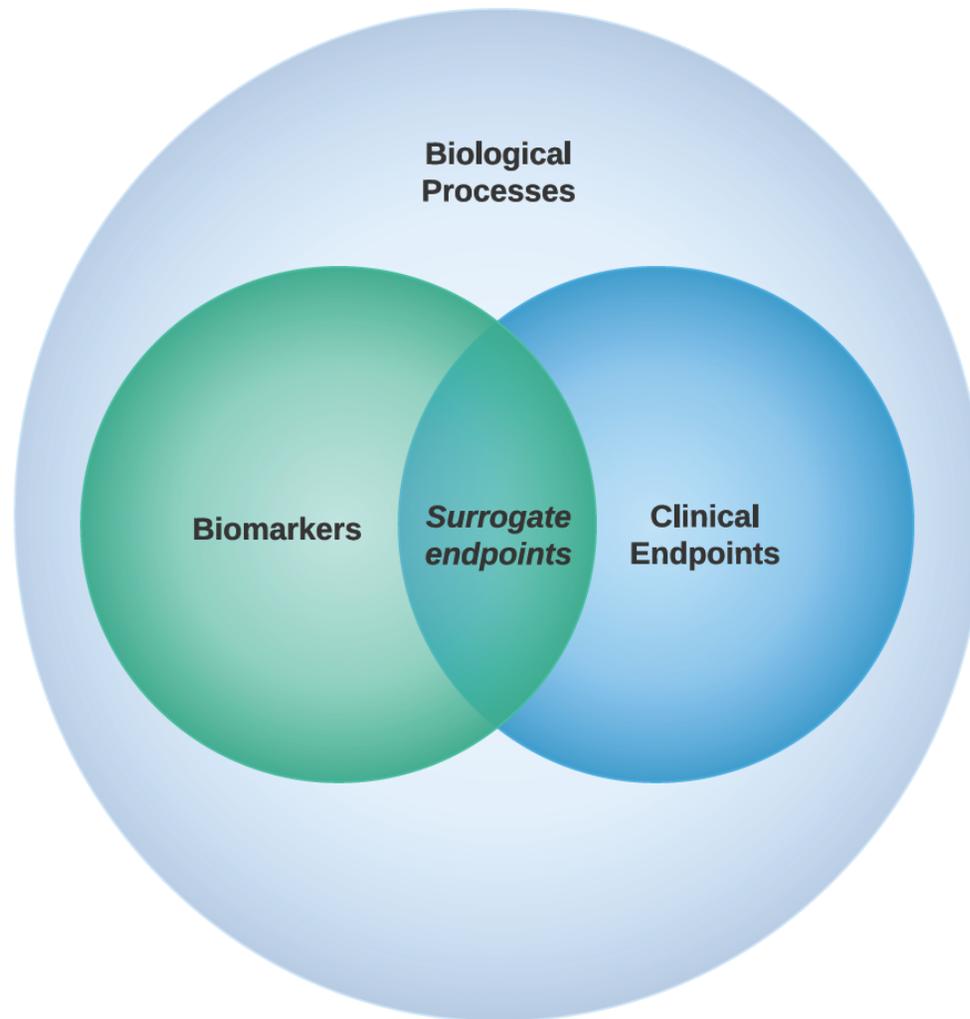
Biomarkers vs. Surrogate Endpoints in Clinical Trials



A biomarker is

- measurable indications of a biological process or state
- must be *objective, quantifiable, reproducible*
- may or may not be clinically relevant
- may include physiological, biochemical, molecular interactions

Biomarkers vs. Surrogate Endpoints in Clinical Trials

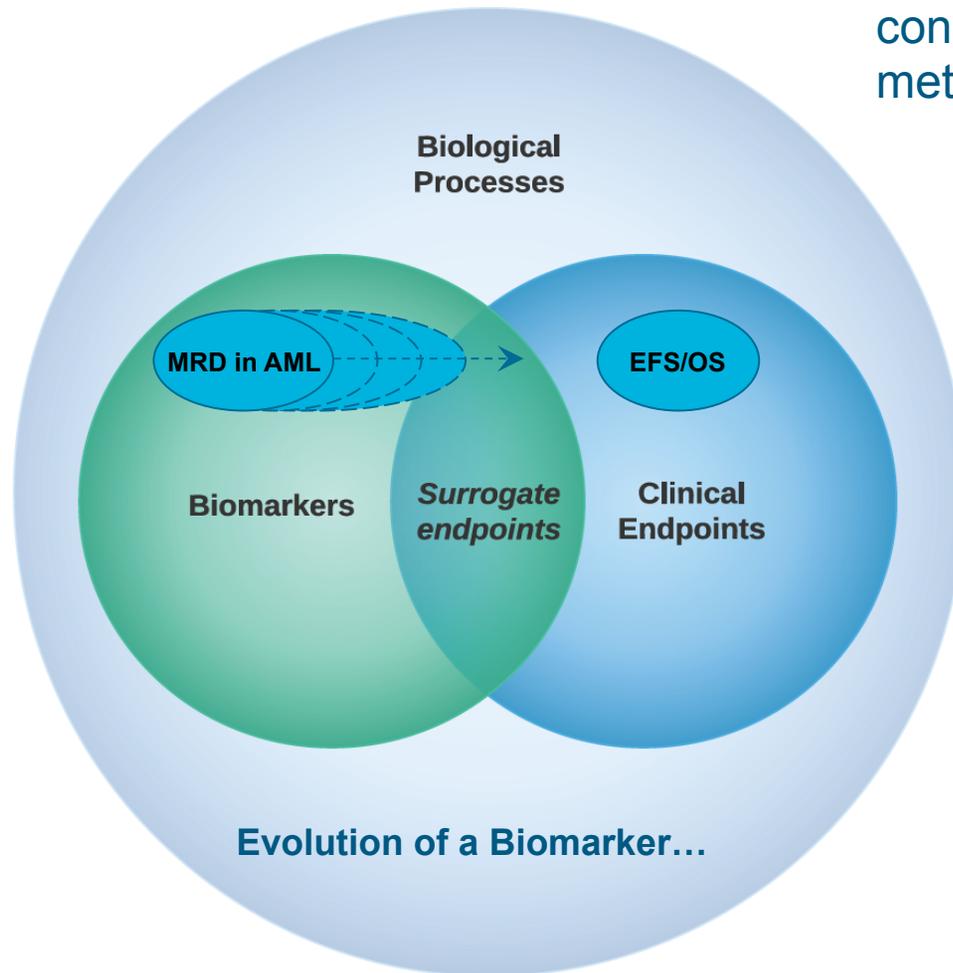


A surrogate endpoint is:

- biomarker subset with clinical relevance
- may stand-in for a clinical endpoint
- do not necessarily inform MoA or causation
- larger burden of proof is required, empirical data critical
- need to show *relevance* and *validity* or *ongoing evaluation* required (e.g. iterative approach)

Defining Biomarker validation “space”

“When is a laboratory-developed test (LDT) considered a pharmacodynamic biomarker method?”



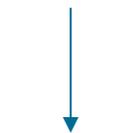
What is our validation space?

or

What is the purpose of our data?

for patient care
and treatment

indicate response
to a drug



LDT



PD Biomarker

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Flow Cytometry Validation

- The flexibility of flow cytometry allows for numerous potential applications but also adds to the complexity of assay development and validation.
 - Flow cytometric methods are challenging to develop and validate.
 - These challenges are related to:
 - Cellular analytes
 - Complex instrumentation
 - Reagents—light sensitive fluorochromes, mAb
 - Lack of cellular reference material
- 

Fit-For-Purpose

Pharmaceutical Research, Vol. 22, No. 4, April 2005 (© 2005)
10.1007/s11095-005-2495-9

Conference Report

Method Validation and Measurement of Biomarkers in Nonclinical and Clinical Samples in Drug Development: A Conference Report

Jean W. Lee,^{1,17} Russ S. Weiner,² Jeff M. Sailstad,³ Ronald R. Bowsher,⁴ Dean W. Knuth,⁵ Peter J. O'Brien,⁶ Jean L. Fourcroy,⁷ Rakesh Dixit,⁸ Lini Pandite,⁹ Robert G. Pietrusko,¹⁰ Holly D. Soares,¹¹ Valerie Quarmby,¹² Ole L. Vesterqvist,² David M. Potter,¹¹ James L. Witliff,¹³ Herbert A. Fritche,¹⁴ Timothy O'Leary,¹⁵

Pharmaceutical Research, Volume 23, No. 2, February 2006 (© 2006)
DOI: 10.1007/s11095-005-9045-3

Research Paper

Fit-for-Purpose Method Development and Validation for Successful Biomarker Measurement

Jean W. Lee,^{1,16,17} Viswanath Devanarayan,² Yu Chen Barrett,³ Russell Weiner,³ John Allinson,⁴ Scott Fountain,⁵ Stephen Keller,⁶ Ira Weinryb,⁷ Marie Green,⁸ Larry Duan,⁹ James A. Rogers,¹⁰ Robert Millham,¹⁰ Peter J. O'Brien,¹¹ Jeff Sailstad,¹² Masood Khan,¹³ Chad Ray,¹⁴ and John A. Wagner¹⁵

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Fit-for-Purpose Approach in Flow Cytometry



Research paper

Recommendations for the validation of flow cytometric testing during drug development: I instrumentation

Cherie L. Green^{a}, Lynette Brown^b, Jennifer J. Stewart^b, Yuanxin Xu^c, Virginia Litwin^d, Thomas W. McCloskey^e*

Recommendations for the validation of flow cytometric testing during drug development: II assays

Denise M. O'Hara^a, Yuanxin Xu^b, Zhiyan Liang^c, Manjula P. Reddy^d, Dianna Y. Wu^e, Virginia Litwin^{f,}*

JIM, 363:104-119, 2011

JIM, 363:120-134, 2011

The Role of Biomarkers in Clinical Trials and The Fit-for-Purpose Method Validation Approach, V. Litwin and C. Green
<http://www.fda.gov/MedicalDevices/NewsEvents/WorkshopsConferences/ucm334772.htm>

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Biomarker Validation Concerns

Limited experience interpreting biomarker data and an unclear regulatory climate

Recommendations might adhere too strictly to existing guidelines

GLP

- FDA guidelines for bioanalytical drug assays and safety monitoring

CAP/CLIA

- Diagnostic Assays

May not be suitable for many biomarker assays

Validation criteria could stifle creative biomarker solutions

Biomarker Validation Questions

What experiments should be performed?

What data are necessary?

What acceptance criteria are appropriate?

Fit-For-Purpose Validation

Fit

- Biomarker data must be reliable and accurate data

Purpose

- Decision making during drug development

Fit-for-Purpose

- Analytical requirements should be stage-specific
- the intended use of the biomarker data
- the regulatory requirements associated with that use
- Practical, iterative approach

Conclusions Fit-for-Purpose

“It is impossible to apply one set of rules to all assay platforms.”

Unlike drug assays, novel biomarker assays are accompanied by unique analytical issues, in many cases ruling out the use of universal, strict validation guidelines

These issues include the common absence of suitable reference standards, the employment of unique analytical reagents and assay platforms, the presence of endogenous biomarkers in a sample, analyte heterogeneity, and a variety of disease-specific effects

Fit-for-Purpose Approach in Flow Cytometry

Compared to other methodologies commonly used in drug development, such as plate-based ligand binding assays and mass spectrometry, flow cytometric methods can be more challenging to validate.

These challenges are related to the combination of cells, reagents, lack of cellular reference material and complex instrumentation.

Flow Cytometry Validation

- The flexibility of flow cytometry allows for numerous potential applications but also adds to the complexity of assay development and validation.
 - Flow cytometric methods are challenging to develop and validate.
 - These challenges are related to:
 - Cellular analytes
 - Complex instrumentation
 - Reagents—light sensitive fluorochromes, mAb
 - Lack of cellular reference material
- 

Getting Started with Validation

Prior to assay validation

- Assay Development Phase
- Panel Design
 - Antigen selection and fluorochrome pairing
 - Gating strategy and reportable results
- Instrument Setup and Compensation

Establish the validation pathway

- Type of Validation
 - IVD
 - RUO
 - LDT
 - Technology transfer
 - Level of stringency
 - Assay requirements
 - Assay limitations
- 

Validation Considerations

1. Assay Complexity

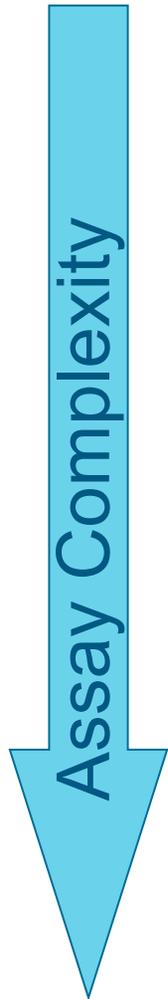


2. Validation Stringency & Regulatory Requirements



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Validation Considerations



Surface phenotyping

- Simple/complex (IVD/RUO)
- Quantitative antigen expression (MESF/ABC)

• Intracellular

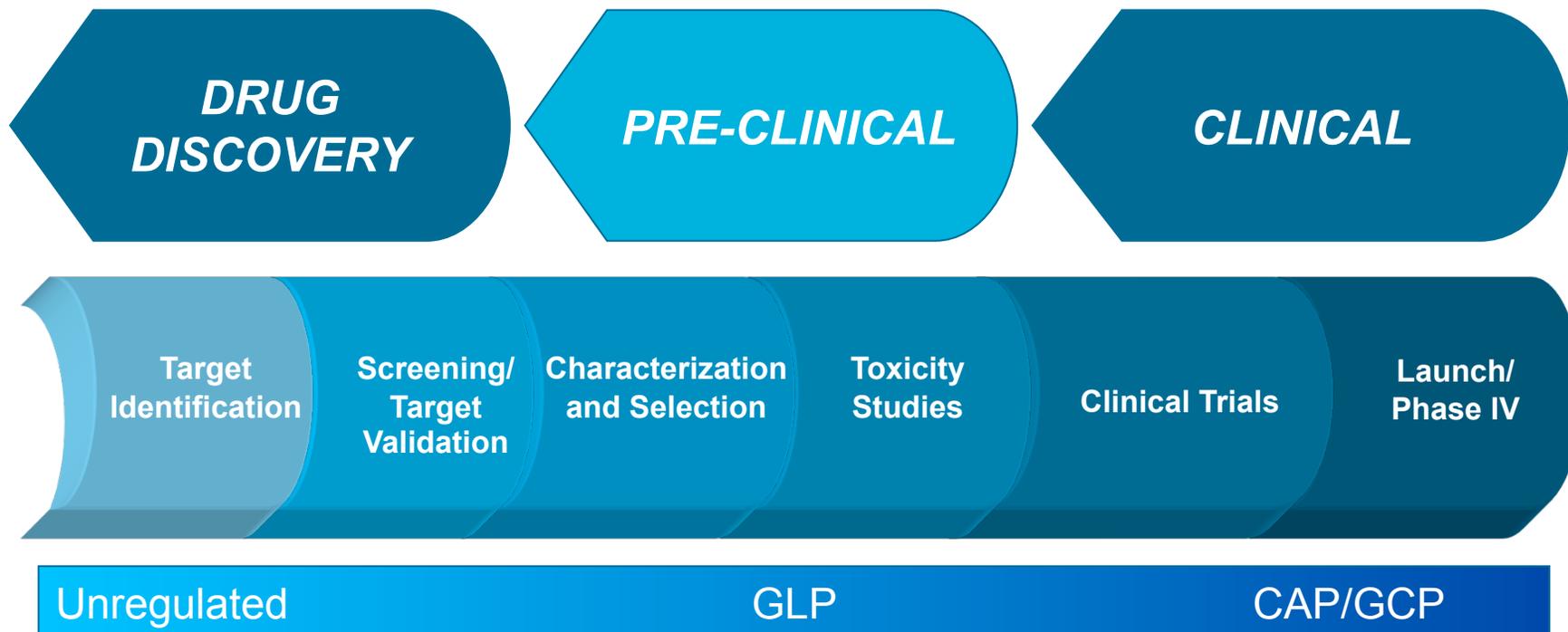
- Cytokines
- Nuclear proteins
- Phosphorylated antigen detection (Phosflow)

• Neutralizing antibody (NAb), Anti-drug Antibody (ADA)

• Receptor Occupancy



Validation Considerations



- Stage of Drug Development
- Sample Type

- Methodology
- Data Type
- Intended Use

Validation Considerations

2. Validation Stringency & Regulatory Requirements

- GLP, CLIA, GMP
- Establish what the method needs to do
 - ❑ Companion Diagnostic
 - ❑ Safety
 - ❑ Enrollment biomarker
 - ❑ PD biomarker
 - ❑ Exploratory biomarker



Lot release



Certificate of Analysis



Toxicity



Potency



PD Biomarker



Dosing

Iterative Approach

Assay development

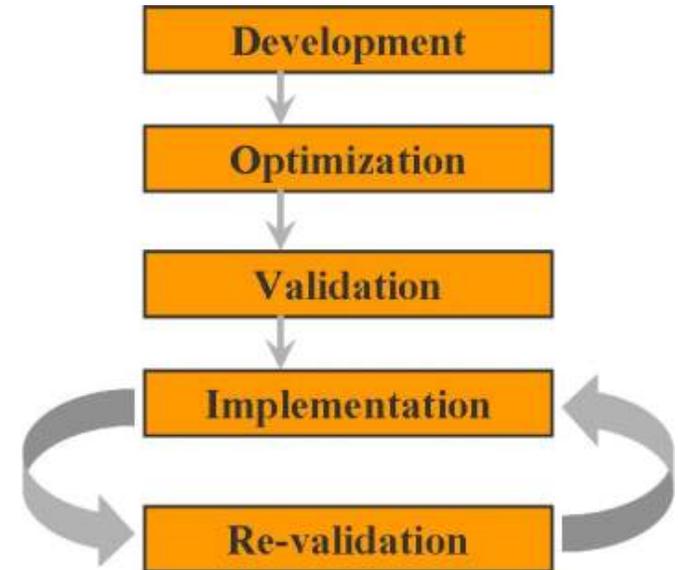
- ✓ State-of-the-art
- ✓ Fully optimized prior to validation

Assess performance

- ✓ Additional validation, as needed

Initial validation/record keeping

- ✓ Quality: Data must be able to be used if stringency requirements increase

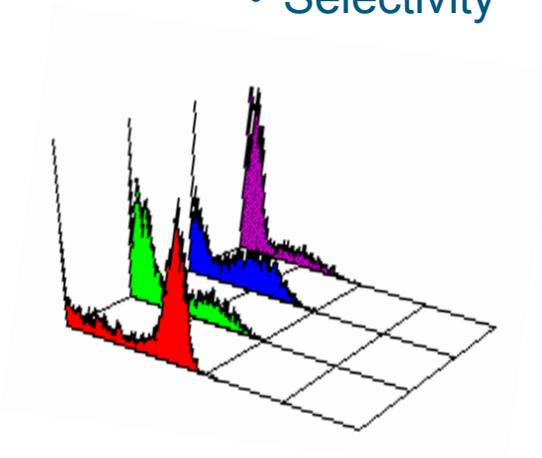


Validation of Flow Biomarker Methods

Validation Objective for Research-Use-Only (RUO), Lab Developed Test (LDT)

Establish method performance

- Accuracy
- Precision/Robustness
- Sensitivity/Limit of Detection
- Specificity
- Reference Intervals
- Stability
- Selectivity
- Standard Calibrators
- Range of Quantification
- Dilutional linearity
- Incurred Sample Reanalysis
- Interference (Matrix, Drug)
- Normal signal distribution
- Prozone effect

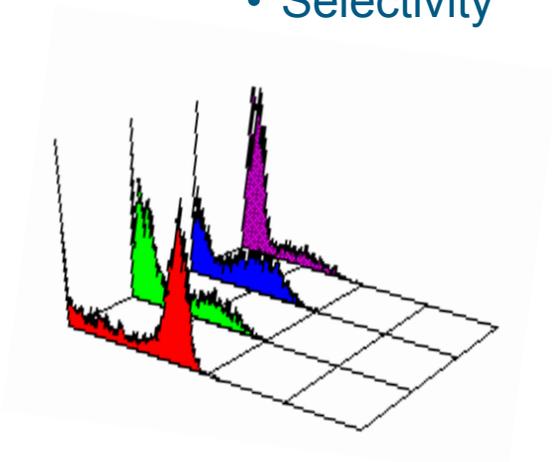


Validation of Flow Biomarker Methods

Validation Objective for Research-Use-Only (RUO), Lab Developed Test (LDT)

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- *Reference Intervals*
- Stability
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- Range of Quantification
- Dilutional linearity
- Incurred Sample Reanalysis
- Interference (Matrix, Drug)
- Normal signal distribution
- Prozone effect



Specificity for Flow Biomarker Assays

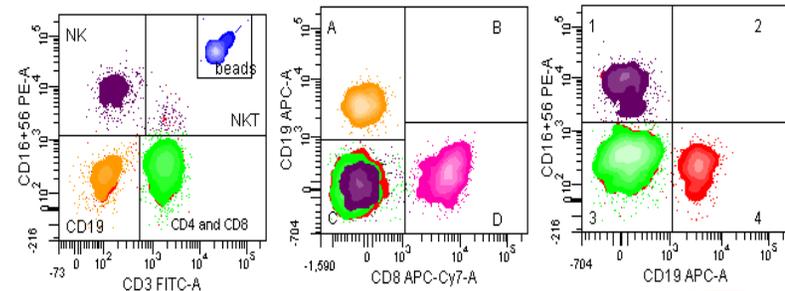
NON-REG

GLP

CLIA

Immunophenotyping

- CD markers used to define the cellular population or antigens of interest must be justified from the literature
- Monoclonal antibody specificity should be verified by the Leucocyte Differentiation Antigens Workshops or peer reviewed publication
- Novel/custom mAb specificity must be well documented internally
- Gating strategies must be verified to establish the cell subset of interest is included while other cell subsets and non-specific events are excluded



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Accuracy

Standard Definition

- closeness of the result compared to the true value of the analyte

GLP

- Determined by the mean bias determined in spiked recovery experiments

CAP/CLIA

- comparison to “gold standard” method
 - measured concentrations in an official reference sample
 - measuring a concentration in comparison to an official standard

Accuracy for Flow

Flow IVD

- CAP Proficiency Testing Surveys are available
- QC material with target values are available

Novel/Advanced Immunophenotyping

- Lack of proficiency testing programs
- Lack of cellular reference/QC material with target values for the populations of interest
- For novel or proprietary methods, sample exchange is not possible

Specificity for Flow

CD markers used to define the cellular population or antigens of interest must be justified or recent published data sought

Monoclonal antibody specificity should be verified by the **Leucocyte Differentiation Antigens Workshops** or peer-reviewed publication

Gating strategies must be verified to establish:

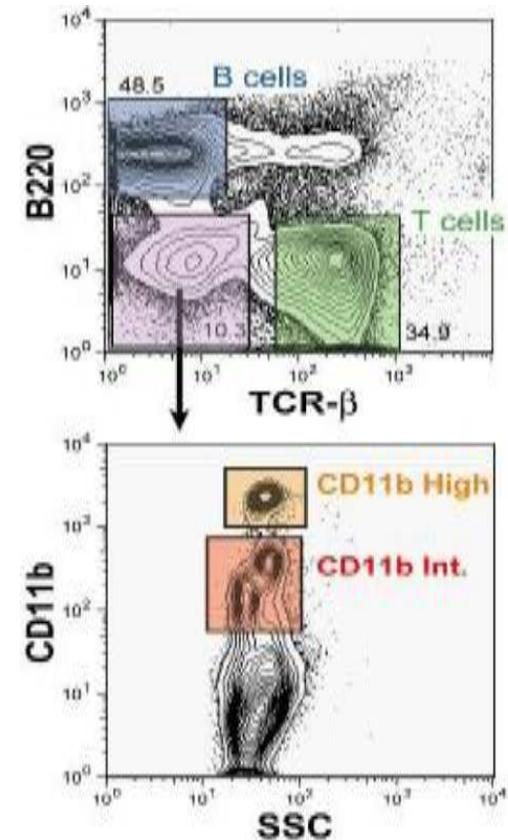
- cell subset of interest is included
- other cell subsets and non-specific events are excluded

Precision for Flow

Precision

- Difficult to find samples with varying levels of each reportable result
 - Use different donors or QC material
- <10 %CV desirable for all methods
- <20-25 %CV acceptable for immunoassays per Fit-for-Purpose paper
- <30 %CV may be acceptable for rare event detection use as exploratory biomarkers
 - With poor precision, more replicates and samples are required

↓
“Iteration in validation”



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Sensitivity

Sensitivity

- the lowest reportable result

CAP/CLIA

- response above the limit of detection (LOD)

GLP

- lower limit of quantification (LLOQ) as the lowest concentration that can be measured with acceptable accuracy and precision (e.g., $\pm 20\%$ CV)

Sensitivity for Flow

Lower Limit of Detection (LOD)

- FMO controls +3 SD

Lower Limit of Quantitation (LLOQ)

- Difficult to find samples
- Mix stained and unstained samples
- Targeted cell depletion followed by re-spiking

Weighted importance for biomarker data

Need to know at what point are the results are imprecise

Reference Intervals for Biomarkers

Reference Intervals

- Not required for first usage exploratory biomarkers
- Required for disease biomarkers or companion diagnostics (e.g. iterative approach)

Stability

- Acceptance criteria vs. precision

Costs

Not applicable for AML-MRD assessment in our case

Validation Acceptance Criteria

CAP/CLIA

- criteria are established depending on the intended clinical use of an assay
- ATE

GLP

- Mean bias (% relative error) and % coefficient of variation should be less than 15% (20% at the LLOQ)

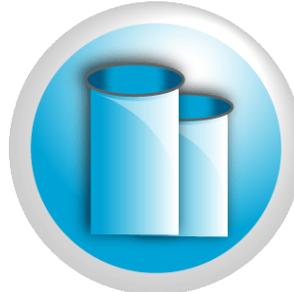
Fit for Purpose

- accuracy (mean bias) and imprecision (%CV) should be within 25% (30% for the LLOQ)
- Should meet the predefined needs of the study rather than simply reflecting the performance capabilities of the assay
- The nature of the assay methodology and the data generated using that assay
- The biological variability of the biomarker within and between the study populations

Challenges of flow cytometry in global clinical trials



Advanced, High-Complexity Technology
Requires highly skilled staff



Limited Specimen Stability
Requires regional sample processing



Global Standardization
Necessary for site-to-site and longitudinal data combinability



Lead Time for Assay Development and Validation



Validation Approach
Fit-for-purpose



Expense

(Final) Validation Considerations

...that are critical in global clinical trials:

Reduce variability

- site-to-site
- longitudinally over time

Standardize

- instrumentation
- processes
- analysis (centralized gating)

Monitor performance

- via Standardization criteria
- QC variability (baseline for true response)



Standardization, QC, and Biomarker Data in Clinical Trials

“The Goal in Quality Control is to ensure reduced instrument variation so biological variation can be measured.”

From the Clinical Flow Cytometry in Hematological Malignancies Workshop, *“Standards and Controls in High-Dimensional Flow Cytometry”*, Stephen P. Perfetto, Staff Scientist and Director of the Flow Cytometry Core, NIAID, VRC

AML-MRD assay

Potential Reportable Results (abridged)

| Description of Potential Sub-classification and Phenotypes | | | | |
|--|--|--|-------------------------|---|
| Population | Phenotype | Reportable Result | Derived from Assay Tube | Comments |
| M1-M2 Neutrophil lineage | CD45 ^{low} , CD34 (75%), CD33 (75%), CD117 (75%), CD13 (75%), HLA-DR (75%), CD15 (75%), | % of total CD45 ⁺ leucocytes and a free text description of the phenotype | 2 | HLA-DR ⁺ , CD4, and CD14 ⁻ |
| M3 | CD45 ^{low} , CD34 (<10%), CD33 (>80%), CD117 (30%), CD13 (>80%), HLA-DR (<10%), CD15 (75%), | % of total CD45 ⁺ leucocytes and a free text description of the phenotype | 2 | HLA-DR ⁻ , CD4, and CD14 ⁻ |
| for erythroid lineage | CD71 ⁺ , CD34 ^{-/+} , CD117 ^{-/+} , HLA-DR ^{-/+} , CD13 ⁺ | % of total CD45 ⁺ leucocytes and a free text description of the phenotype | 2 | |
| M4 | CD45 ^{low} , CD34 (<10%), CD117 (30-75%), HLA-DR (>80%), CD13(75%), CD64(>80%), CD123 ⁻ , CD4 or CD14 ⁺ | % of total CD45 ⁺ leucocytes and a free text description of the phenotype | 3 | CD13 ⁺ CD33 ⁺ MPO ⁻ , CD4 or CD14 ⁺ AML5 CD13 ⁺ CD33 ⁺ MPO ⁺ HLA-DR ⁺ , CD4 or CD14 ⁺ |
| AML5 | CD45 ^{low} , CD34 (<10%), CD117 (30-75%), HLA-DR (>80%), CD13(75%), CD64(>80%), CD123 ⁻ , CD4, or CD14 ⁺ | % of total CD45 ⁺ leucocytes and a free text description of the phenotype | 3 | CD13 ⁺ CD33 ⁺ MPO ⁻ , CD4 or CD14 ⁺ AML5 CD13 ⁺ CD33 ⁺ MPO ⁺ HLA-DR ⁺ , CD4 or CD14 ⁺ |

AML-MRD Assay

AML Configuration

- 5-tube, 8-color assay based on:

EuroFlow recommendations

[van Dongen et al., Leukemia (2012), 1908-1975.]

Work by Brent Woods and colleagues

[Wood et al., J Clin Oncol (2001), 29:1190-1197.]

| Detector | FL1 | FL2 | FL3 | FL4 | FL5 | FL6 | FL7 | FL8 |
|---------------|--------|-------|------|------|-------------|--------|-------|--------|
| Fluor Tube | BV421 | BV510 | FITC | PE | PerCP-Cy5.5 | PE-Cy7 | APC | APC-H7 |
| FMO | HLA-DR | CD34 | | CD13 | | | | CD45 |
| Exp1 | HLA-DR | CD34 | CD15 | CD13 | CD117 | CD33 | CD71 | CD45 |
| Exp2 | HLA-DR | CD34 | CD64 | CD13 | CD4 | CD14 | CD123 | CD45 |
| Exp3 | HLA-DR | CD34 | CD38 | CD13 | CD117 | CD19 | CD56 | CD45 |
| Exp4 | HLA-DR | CD34 | CD2 | CD13 | CD117 | CD11b | CD7 | CD45 |

Acute myeloid leukemia (AML)

- clonal hematopoietic disorder
- derived from an HSC or lineage-specific progenitor cell
- ~20% blast population in bone marrow is expected at diagnosis (<20% for some genetic variants)
- Characterized by clonal heterogeneity, antigenic drift over course of disease
 - Phenotypic changes
 - Emergence of subclones
- Current standard for minimal residual disease (MRD) is 0.01% for AML and ALL.

Acute myeloid leukemia (AML)

How do we define abnormalities?

- aberrant lineage expression (e.g. CD19, CD7, CD56) on myeloid blasts
- Blasts lacking lineage markers entirely
- Asynchrony of marker expression
 - early/progenitor markers (e.g. CD34, CD117) being co-expressed with more mature markers (e.g. CD33, CD13)
- Aberrant up- or down-modulation of Ag expression

AML-MRD Assay

AML strategy for MRD detection

AML is clonally heterogeneous and can exhibit frequent antigenic changes

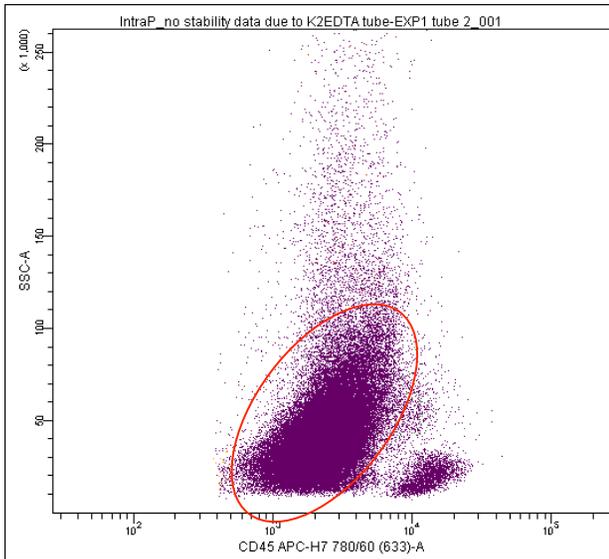
- take advantage of longitudinality
 - use baseline to establish clonal phenotypes of interest
 - create individualized patient templates
 - monitor possible antigenic drift to ensure MRD detection is robust
 - follow multiple abnormal phenotypes to increase tracking specificity

Populations at MRD level can be lost in the noise of normal bone marrow

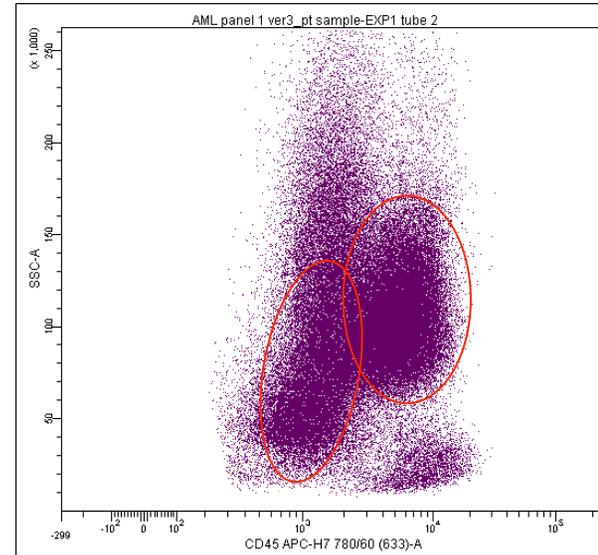
- Focus on blast population (“Les Bermudes”) which lacks mature cell types
- Look for “empty spaces” to mitigate confounding effects of normal bone marrow populations
- Design a spiking technique to more closely mimic MRD during LLOQ experiments

Variability in AML-MRD

Gross heterogeneity of AML samples

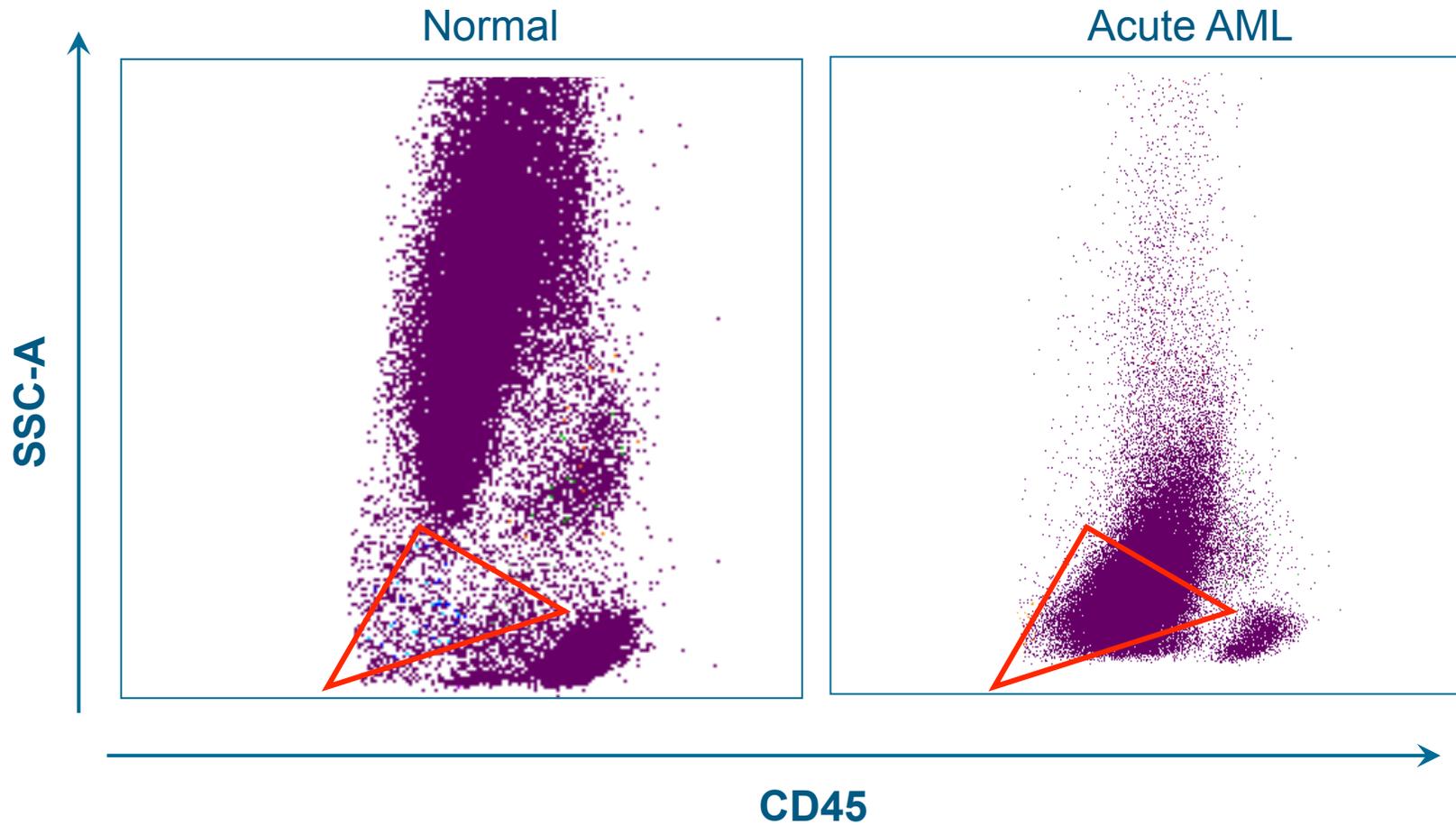


Defined blast population



Defined blast population with extensive myelomonocytic expansion

Normal vs. Acute Blasts in AML-MRD



red triangle; blast region/les "Bermudes"

Immunophenotype heterogeneity in AML blasts

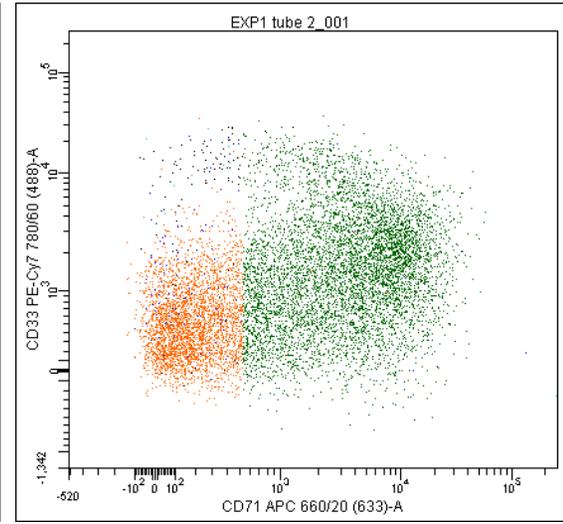
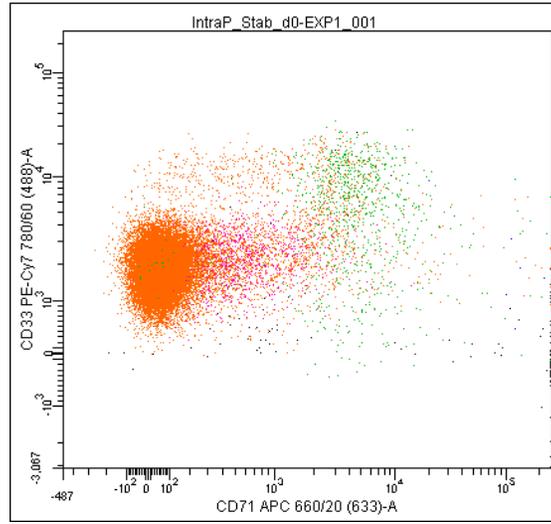
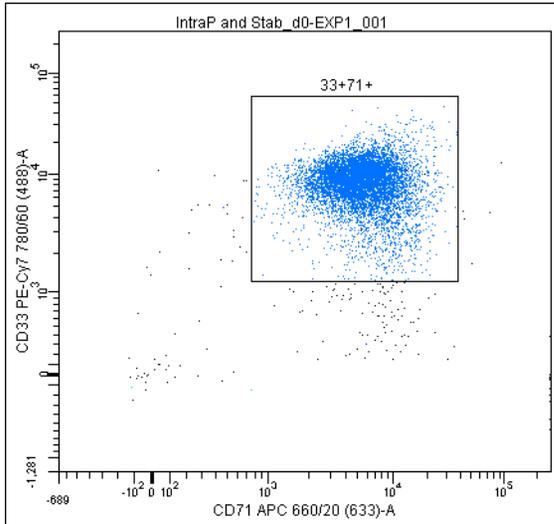
Patient:

A

B

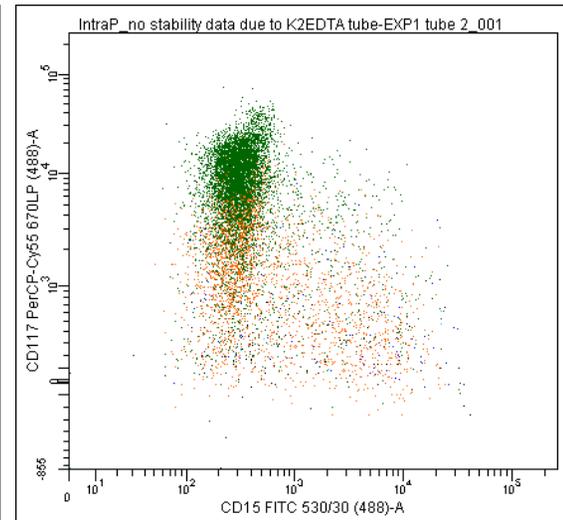
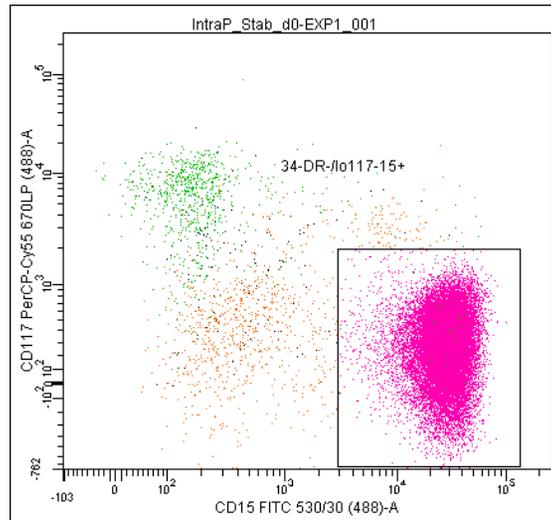
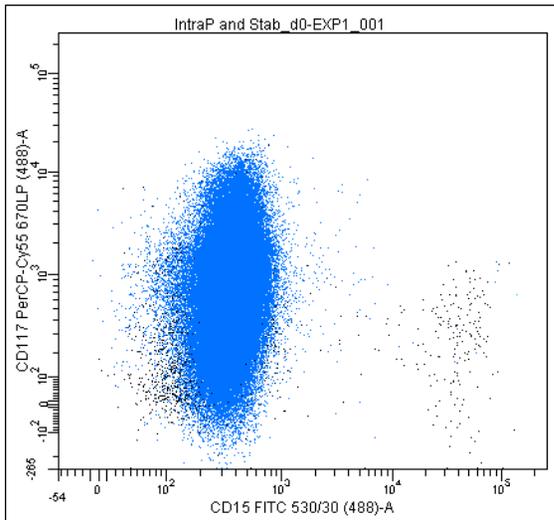
C

CD33



CD71

CD117



CD15

AML-MRD

Assay Performance Summary

Intra-assay imprecision (Intra-precision)

- 29 total phenotypically-distinct populations from 6 individual AML patients were assessed for (im)precision.
 - Imprecision ranged from 0.11% to 11.25%.
- 12 total phenotypically-distinct populations from 3 normal bone marrows were assessed for (im)precision.
 - Imprecision ranged from 0.71% to 8.81%.

AML-MRD

Assay Performance Summary

Normal Bone Marrow

Table 6.4. Intra-assay Precision Summary – Normal Bone Marrow Samples

| Relative Percentage (%) | Mean %CV* | | | Grand Mean %CV |
|---------------------------------------|-----------|------|------|----------------|
| | NBM1 | NBM2 | NBM3 | |
| CD2 ⁺ | 2.42 | 4.13 | 3.62 | 3.39 |
| CD4 ⁺ , CD123 ⁺ | 2.61 | 5.69 | 6.67 | 4.99 |
| CD7 ⁺ | 3.57 | 3.75 | 3.90 | 3.74 |
| CD11b ⁺ | 1.46 | 0.07 | 0.61 | 0.71 |
| CD14 ⁺ , CD64 ⁺ | 2.17 | 0.32 | 2.04 | 1.51 |
| CD19 ⁺ , CD38 ⁺ | 5.89 | 4.79 | 2.54 | 4.41 |
| CD33 ⁺ , CD13 ⁺ | 1.67 | 0.98 | 2.87 | 1.84 |
| CD33 ⁺ , CD15 ⁺ | 5.89 | 1.44 | 0.78 | 2.70 |
| CD33 ⁺ , CD71 ⁺ | 1.55 | 1.95 | 2.78 | 2.09 |
| CD34 ⁺ , CD19 ⁺ | 16.90 | 4.76 | 4.76 | 8.81 |
| CD56 ⁺ | 1.65 | 3.96 | 2.08 | 2.56 |
| CD117 ⁺ | 4.50 | 4.51 | 3.28 | 4.10 |

AML-MRD

Assay Performance Summary

LLOQ

- 8 total phenotypically-distinct populations from 3 individual patients were assessed for LLOQ
- 1 population was excluded due to extensive overlap with unspiked bone marrow (i.e. normal)
- LLOQ = 0.0027% (Assay limit set at LOD = 0.0037%)
- Equivalent to < 20 events in a background of 750,000-1,000,000 total events.

AML-MRD

Assay Performance Summary

Table 6.1. Analytical Sensitivity / LOD

| Relative Percentage (%) | Un-spiked Rep1 | Un-spiked Rep 2 | Un-spiked Rep 3 | Mean | SD | %CV | Mean +3SD |
|--|----------------|-----------------|-----------------|---------|---------|---------|-----------|
| CD13 ^{lo} , CD15 ⁺ , CD117 ⁻ | 0.01150 | 0.01782 | 0.01957 | 0.0163 | 0.0042 | 25.767 | 0.02890 |
| CD13 ⁻ , CD15 ⁺ | 0.00068 | 0.00000 | 0.00059 | 0.0004 | 0.00037 | 92.500 | 0.00151 |
| CD13 ^{hi} , CD64 ^{-/lo} | 0.00086 | 0.00084 | 0.00088 | 0.0009 | 0.0000 | 2.3256 | 0.0009 |
| CD34 ⁻ , HLA-DR ^{hi} , CD13 ^{hi} , CD11b ⁺ | 0.00078 | 0.00065 | 0.00058 | 0.0007 | 0.0001 | 14.9254 | 0.0010 |
| CD34 ⁺ , CD13 ⁺ | 0.00260 | 0.00229 | 0.00170 | 0.0022 | 0.0005 | 22.7273 | 0.0037 |
| CD34 ^{hi} , CD123 ⁺ | 0.00140 | 0.00093 | 0.00121 | 0.0012 | 0.0002 | 16.6667 | 0.0018 |
| CD34 ⁺ , CD13 ^{hi} , CD38 ^{dim} | 0.00104 | 0.00066 | 0.00086 | 0.0009 | 0.0002 | 22.2222 | 0.0015 |
| CD34 ⁺ , CD13 ^{hi} , CD7 ⁺ | 0.00008 | 0.00014 | 0.00015 | 0.00012 | 0.00004 | 33.333 | 0.00024 |
| Number of Events | Un-spiked Rep1 | Un-spiked Rep 2 | Un-spiked Rep 3 | Mean | SD | %CV | Mean +3SD |
| CD13 ^{lo} , CD15 ⁺ , CD117 ⁻ | 17 | 24 | 33 | 24.667 | 8.021 | 32.517 | 48.730 |
| CD13 ⁻ , CD15 ⁺ | 1 | 0 | 1 | 0.6667 | 0.577 | 86.546 | 2.398 |
| CD13 ^{hi} , CD64 ^{-/lo} | 9 | 8 | 9 | 8.6700 | 0.5770 | 6.6551 | 10.4010 |
| CD34 ⁻ , HLA-DR ^{hi} , CD13 ^{hi} , CD11b ⁺ | 8 | 7 | 6 | 7.0000 | 1.0000 | 14.2857 | 10.0000 |
| CD34 ⁺ , CD13 ⁺ | 26 | 23 | 17 | 22.0000 | 4.5830 | 20.8318 | 35.7490 |
| CD34 ^{hi} , CD123 ⁺ | 15 | 10 | 13 | 12.6700 | 2.5170 | 19.8658 | 20.2210 |
| CD34 ⁺ , CD13 ^{hi} , CD38 ^{dim} | 11 | 7 | 9 | 9.0000 | 2.0000 | 22.2222 | 15.0000 |
| CD34 ⁺ , CD13 ^{hi} , CD7 ⁺ | 1 | 2 | 2 | 1.67 | 0.577 | 34.551 | 3.401 |

AML-MRD

Assay Performance Summary

Table 6.2.e. CD13^{hi},CD64^{-/lo} LLOQ2 - Relative Percentage (%)

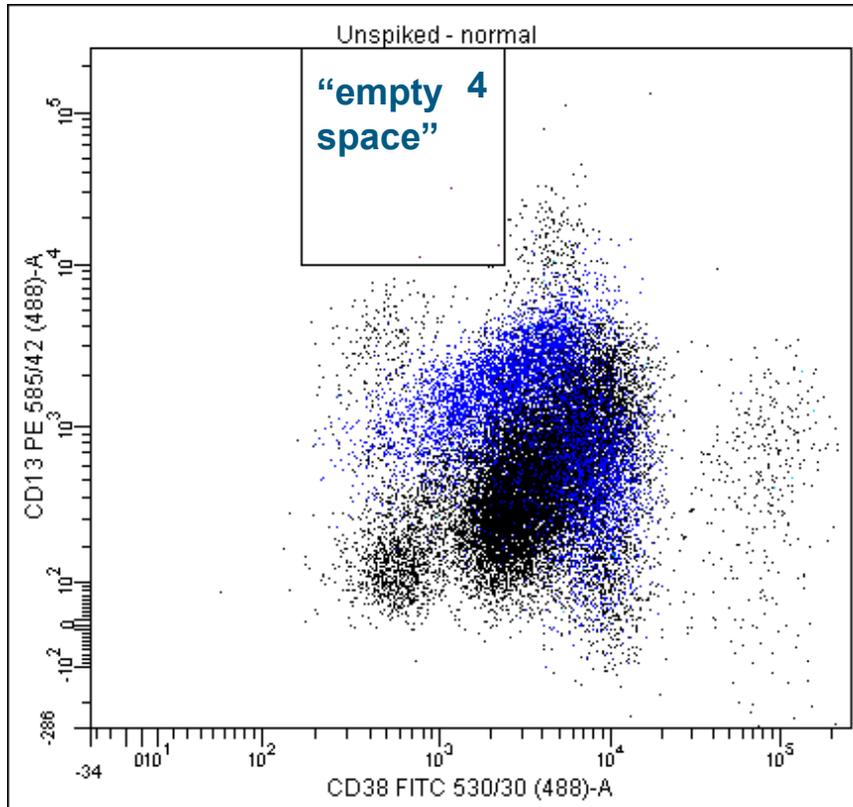
| Dilution level | LLOQ2 | | | | | |
|----------------|---------|---------|---------|---------|---------|-------|
| | Rep1 | Rep2 | Rep3 | Mean | SD | %CV |
| 1 | 0.00059 | 0.00054 | 0.00024 | 0.00046 | 0.00019 | 41.30 |
| 2 | 0.00031 | 0.00060 | 0.00108 | 0.00066 | 0.00039 | 59.09 |
| 3 | 0.00323 | 0.00224 | 0.00268 | 0.0027 | 0.0005 | 18.52 |

Table 6.2.f. CD13^{hi},CD64^{-/lo} LLOQ2 - Events

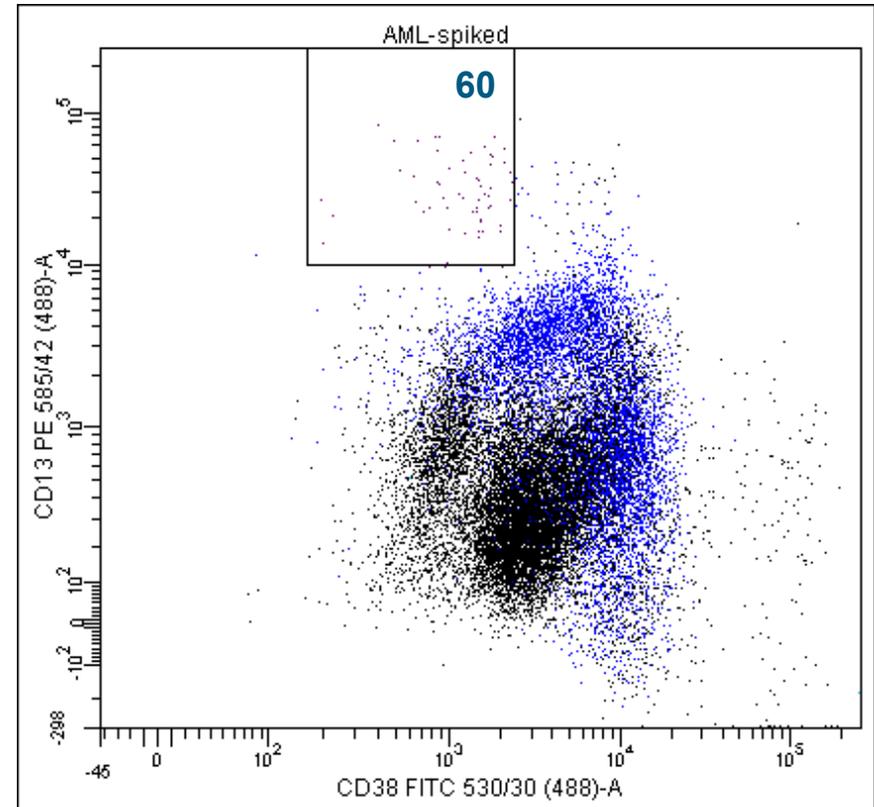
| Dilution Factor | LLOQ2 | | | | | |
|-----------------|-------|------|------|--------|-------|-------|
| | Rep1 | Rep2 | Rep3 | Mean | SD | %CV |
| 1 | 5 | 5 | 2 | 4.000 | 1.732 | 43.30 |
| 2 | 2 | 4 | 7 | 4.333 | 2.517 | 58.09 |
| 3 | 23 | 16 | 19 | 19.333 | 3.512 | 18.17 |

Detection of AML cells in normal bone marrow

Normal, unspiked



AML-spiked



AML-MRD

Assay Performance Summary

QC material

Table 6.5. Inter-assay Precision Summary

| Relative Percentage (%) | %CV | | Grand Mean %CV |
|--|-------|-------|----------------|
| | CDSS1 | CDSS2 | |
| CD2 ⁺ | 8.56 | 13.21 | 10.89 |
| CD4 ⁺ | 13.31 | 15.21 | 14.26 |
| CD7 ⁺ | 12.52 | 12.52 | 12.52 |
| CD11b ⁺ , CD13 ⁺ | 1.41 | 5.64 | 3.53 |
| CD13 ⁺ , CD33 ⁺ | 11.36 | 9.58 | 10.47 |
| CD14 ⁺ , CD64 ⁺ | 7.64 | 2.71 | 5.18 |
| CD15 ⁺ | 1.07 | 3.07 | 2.07 |
| C19 ⁺ | 0.93 | 1.12 | 1.03 |
| CD38 ⁺ | 10.88 | 11.73 | 11.31 |
| CD56 ⁺ | 13.51 | 16.02 | 14.77 |
| CD71 ⁺ , CD117 ⁺ | 16.74 | 8.23 | 12.49 |
| CD123 ⁺ | 3.95 | 7.84 | 5.90 |

AML-MRD

Assay Performance Summary

Table 6.8. Specimen Stability Summary – Abnormal Bone Marrow

| Relative Percentage (%) | Day 1 | | Day 2 | |
|-------------------------|----------|-------|----------|-------|
| | % Change | %CV | % Change | %CV |
| ABM1 | 23.60 | 21.77 | 16.91 | 13.94 |
| ABM2 | 9.82 | 6.83 | 9.24 | 6.94 |
| ABM3 | 18.67 | 11.78 | 45.82 | 24.72 |
| ABM6 | 16.43 | 13.07 | 23.71 | 19.44 |

AML-MRD as a Flow Biomarker Assay

| Population | #Events | %Parent | %Total |
|--------------------|---------|---------|--------|
| ■ All Events | 537,487 | #### | 100.0 |
| ☒ Time | 537,487 | 100.0 | 100.0 |
| ■ SSC singlet | 527,468 | 98.1 | 98.1 |
| ■ FSC singlet | 524,788 | 99.5 | 97.6 |
| ■ excluding debris | 497,570 | 94.8 | 92.6 |
| ■ CD45+ Leukocytes | 480,249 | 96.5 | 89.4 |
| ■ Lymphs | 27,904 | 5.8 | 5.2 |
| ■ Grans | 72,074 | 15.0 | 13.4 |
| ■ Blasts | 61,393 | 12.8 | 11.4 |
| ■ CD34+ | 9,313 | 15.2 | 1.7 |
| ■ P3-1 blasts | 34,437 | 56.1 | 6.4 |
| ■ P3-4 (117+) | 20,185 | 32.9 | 3.8 |
| ■ P3-5 | 674 | 1.1 | 0.1 |
| ■ Monocytes | 315,692 | 65.7 | 58.7 |
| ■ P3-1 mono | 51,032 | 16.2 | 9.5 |
| ■ P3-2 | 73,981 | 23.4 | 13.8 |
| ■ P3-3 | 794 | 0.3 | 0.1 |
| ■ CD34+-1-1 | 380 | 0.1 | 0.1 |
| ■ P3-5-1 | 1,898 | 0.4 | 0.4 |
| ■ CD34+CD38dim | 4,666 | 1.0 | 0.9 |
| ■ CD34+CD38int | 3,196 | 0.7 | 0.6 |

AML-MRD as a Flow Biomarker Assay

| Reportable Results | |
|--------------------|--|
| Population | Phenotype |
| % MRD | Patient-specific |
| Phenotype | Free text (consulting hematopathologist) |

Acknowledgments

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Questions?