

DNA-based In situ hybridization biomarker template (FISH, CISH)

This is a template for use in outlining the known status of a FISH or CISH assay that is to be used in a trial. It is intended to be used for assays measuring single genetic variations such as specific translocations, gene amplifications or deletions. It is not intended for array CGH or similar multiplex DNA in situ hybridization assays. Not all parameters may be known a priori. Please enter as much information as you can. Enter N/A for not available or applicable where appropriate.

It is recommended that Ventura et al., FISH analysis for the detection of lymphoma-associated chromosomal abnormalities in routine paraffin-embedded tissue. J. Mol. Diagn. 8:141-151, 2006 be read as a reference before completing this template.

**This template requires detailed information that may be known only by laboratorians, scientists who work in clinical laboratories and should be collaborating closely with clinical trialists. Please be sure to collect the appropriate responses before filling out this form. The template has the following sections with information needed from both trialists and laboratorians:**

- 6 HFVRQ + HDGLQJ**
- 1. Assay, Patient and Specimen Parameters–Trialists and Laboratorians**
  - 2 -6. Probe Characteristics – Laboratorians**
  - 7. Design of In Situ Hybridization Assay - Laboratorians**
  - 8. Assay Performance – Laboratorians**
  - 9. Laboratory Information – Trialists and Laboratorians**



Study Chair:

LOI/Concept/Protocol #

**1. Assay, Patient and Specimen Parameters**

**A. Type of DNA In Situ Hybridization Assay**

Interphase                      Metaphase

**B. Type of DNA In Situ Hybridization Probes**

Break-apart                      Dual Fusion                      Other (Please Specify)

**B1. Specify Other:**

**C. Probes**

- C1. Probe 1
- C2. Probe 2
- C3. Probe 3
- C4. Probe 4
- C5. Probe 5

**D. How will assay and its marker be used in the clinical trial (Integral, Integrated, or Research)**

Integral

,QMJUDO

,QMJDMG

5 HVHDFK

Research

**E. Assay Purpose**

**E1. Please specify ~~II~~ RWJH**

**F. Will assay be provided by a Central Reference &/ , \$ Lab, Multiple CLIA-certified Labs or Research Labs?**

&HQMDO5 H HUHGFH &/ , \$ / DE

0 XOMSOI &/ , \$ / DEV

5 HVHDFK / DEV

**G. Source and Collection of Specimens**

**G1. Specimen Type**

G1a. Please specify if other

G2. Tissue Collection supported in Trial

G3. Genetic syndromes that may impact findings, e.g Trisomy 21 or a disorder that may cause secondary aberrations (Lynch Syndrome)

G3a. Was radiation therapy given

Yes

No

G3b. If Radiation therapy was given, what biomarker(s) was used to assess the effect of radiation?

H. Pre-Analytic Variables that may affect assay results  
For Blood or bone marrow Specimens

H1. What was specimen collected in?

Heparin

EDTA

Acid-Citrate-Dextrose (ACD)

Other (please specify)

H1a. Please specify

H1b. Was specimen cultured for metaphase study?

H1bi. How long should specimen be cultured, if cultured?

H1bii. Other, specify



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If Specimen Not Cultured

H1Ci. Will erythrocytes be lysed with Ammonium Chloride

Yes	No	Unknown	Not Applicable
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H1Cii. Will cells be concentrated by density gradient centrifugation

Yes	No	Unknown	Not Applicable
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H1Ciii. Will cells be fixed before reacting with probes?

Yes	No	Unknown	Not Applicable
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H1Civ. What fixative if used?

H1Cv. Please specify

For Tissue Specimens

I1. Type of specimen stabilization

I1ai. Please specify if other

I2. If fixed, what is fixative?

I2a. If other fixative, what was it?

I2b. If fixed, what is the shortest fixation time allowed (Hours)?

I2c. If fixed, what is the longest fixation time allowed (Hours)?

I3. If frozen, how will specimen be frozen?

J. Storage of specimen

J1. How long will tissue be stored (please include unit of time, eg days, months)?

J1a. Units of time

K. Specimen Characteristics

K1. Does the specimen consist of whole nuclei or sections of nuclei, eg. Sections of formalin-fixed, paraffin-embedded tissue?

K1a. If sections of tissue, how thick are the sections (in microns)?

K2. What is the minimum number of nuclei counted?

K3. How was that minimum number of nuclei to be analyzed determined to be adequate/representative?

K4. Digestion or other steps to improve probe binding

K5. Is the marker stable when the storage time is:

2. Probe 1 Characteristics

A. Type of probe

A1. If other, please specify

B. What is the probe label (FITC, Quantum dots, etc)

B1. If other, please specify

C. Length of probe in nucleotides

D. What is the source of the probe, Commercial or synthesized in-house?

D1. If commercial, who was the manufacturer?

D1i. What is the lot number?

E. How was the probe validated?

F. How was specificity of the probe demonstrated?

F1a. If other, please specify

G. Has the proper chromosomal location of the probe target been verified by metaphase FISH?

H. Was the probe tested on cell lines that have the genetic change?

I. Have any cross-reactive or interfering substances been identified that may confound interpretation of the results with this probe?

I1. If yes, what are they?

3. Probe 2 Characteristics

A. Type of probe

A1. If other, please specify

B. What is the probe label (FITC, Quantum dots, etc)

B1. If other, please specify

C. Length of probe in nucleotides

D. What is the source of the probe, Commercial or synthesized in-house?

D1. If commercial, who was the manufacturer?

D1i. What is the lot number?

E. How was the probe validated?

F. How was specificity of the probe demonstrated?

F1a. If other, please specify

G. Has the proper chromosomal location of the probe target been verified by metaphase FISH?

H. Was the probe tested on cell lines that have the genetic change?

I. Have any cross-reactive or interfering substances been identified that may confound interpretation of the results with this probe?

I1. If yes, what are they?

4. Probe 3 Characteristics

A. Type of probe

A1. If other, please specify

B. What is the probe label (FITC, Quantum dots, etc)

B1. If other, please specify

C. Length of probe in nt

D. What is the source of the probe, Commercial or synthesized in-house?

D1. If commercial, who was the manufacturer?

D1i. What is the lot number?

E. How was the probe validated?

F. How was specificity of the probe demonstrated?

F1a. If other, please specify

G. Has the proper chromosomal location of the probe target been verified by metaphase FISH?

H. Was the probe tested on cell lines that have the genetic change?

I. Have any cross-reactive or interfering substances been identified that may confound interpretation of the results with this probe?

I1. If yes, what are they?

5. Probe 4 Characteristics

A. Type of probe

A1. If other, please specify

B. What is the probe label (FITC, Quantum dots, etc)

B1. If other, please specify

C. Length of probe in nt

D. What is the source of the probe, Commercial or synthesized in-house?

D1. If commercial, who was the manufacturer?

D1i. What is the lot number?

E. How was the probe validated?

F. How was specificity of the probe demonstrated?

F1a. If other, please specify

G. Has the proper chromosomal location of the probe target been verified by metaphase FISH?

H. Was the probe tested on cell lines that have the genetic change?

I. Have any cross-reactive or interfering substances been identified that may confound interpretation of the results with this probe?

I1. If yes, what are they?

6. Probe 5 Characteristics

A. Type of probe

A1. If other, please specify

B. What is the probe label (FITC, Quantum dots, etc)

B1. If other, please specify

C. Length of probe in nt

D. What is the source of the probe, Commercial or synthesized in-house?

D1. If commercial, who was the manufacturer?

D1i. What is the lot number?

E. How was the probe validated?

F. How was specificity of the probe demonstrated?

F1a. If other, please specify

G. Has the proper chromosomal location of the probe target been verified by metaphase FISH?

H. Was the probe tested on cell lines that have the genetic change?

Yes

No

Unknown

I. Have any cross-reactive or interfering substances been identified that may confound interpretation of the results with this probe?

Yes

No

Unknown

I1. If yes, what are they?

## 7. Design of In Situ Hybridization Assay

### A. Assay Design

A1. Describe the platform of the assay

A1a. Platform

A1b. Model Number

A1c. UDI (Unique Device Identifier - supplied on lab equipment)

<http://www.fda.gov/MedicalDevices/DeviceRegulationandGuidance/UniqueDeviceIdentifiers/default.htm>

A1d. Is the platform cleared by FDA

A2. Is there an SOP for the assay

A2a. If there is a SOP, is it attached as an appendix?

### B. Type of In Situ Hybridization

B1. If other, please specify

B2. Assay method (e.g., direct, indirect, other)

Direct

Indirect

Other

B2a. Please specify

C. Details of positive and negative controls for the assay

C1. Positive control for Probe 1

C1. Negative control for Probe 1

C2. Positive control for Probe 2

C2. Negative control for Probe 2

C3. Positive control for Probe 3

C3. Negative control for Probe 3

C4. Positive control for Probe 4

C4. Negative control for Probe 4

C5. Positive control for Probe 5

C5. Negative control for Probe 5

8. Assay Performance

A. Assistance with Interpretation

A1. Will a pathologist assist with selection of the part of the specimen to be analyzed?

A2. Will a cytogeneticist assist with the interpretation of the FISH patterns/results vs. the genetic/chromosomal mechanisms and/or artifacts of processing/cell overlaps that can confound the FISH results?

B. What statistical test(s) were used to validate the assay results?

C. How was a clinically relevant threshold selected?

C1. If Other, please define

D. Will quantitative data be collected?

E. Will data be presented qualitatively?

F. If qualitative data provided, how will thresholds be determined, eg Positive vs Negative?

G. What is the threshold or cut-off?

H. How is/was the threshold/cutoff value validated before using the assay in this trial?

I. Were assay conditions standardized to minimize variance, e.g. automated tissue processors and/or stainers?

I1. If yes, what tissue processor/stainer was used?

J. Reproducibility of assay

J1. How was hybridization quality assessed?

J2. Were replicates done?

J2a. How many replicates were done?

J3. What is the intra-lab reproducibility (%CV)

J4. What is the inter-lab reproducibility (same specimens)?

J5. Are there at least 2 readers for each sample?

J5a. If so what is the agreement between readers?

J5b. How are differences between readers resolved?

J5bi. If other, please specify

K. Assay discrimination

K1. How will staining artifacts be identified and handled (especially if image analysis is used)?

K2. If image analysis is used, describe how stacks will be analyzed to check for artifacts

K3. How will tumor heterogeneity be handled?

L. Details regarding the quantitative component of the assay

L1. What strategy will be used to select the fields to be analyzed?

L2. How many normal controls will be used to establish a false-positive cutoff for a given probe?

L2a. What will be the selection criteria for these normal controls?

L2b. How will the cells of interest be distinguished from other cells?

L2c. Was reference material used to generate this cutoff?

L2d. Has the assay been cleared by the FDA?

L2e. What is the accuracy for detecting alterations in the target?

9. Laboratory

A. Does the lab meet GLP standards?

Good Laboratory Practices (GLP) are defined by the FDA in their guidance at:  
<http://www.fda.gov/downloads/ICECI/EnforcementActions/BioresearchMonitoring/ucm133730.pdf>

B. What is the training and experience of the laboratory staff?