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## DNA-based Mutation Assays

This is a template for use in outlining the known status of an assay that is to be used in a trial. The Clinical Laboratory Scientists who will be performing the tests should fill out this form. Not all parameters will be known a priori. Please enter as much information as you can. Enter N/A for not available or applicable where appropriate. **This template is intended only for DNA-based somatic mutations and not for RNA-based mutations.** It is also primarily intended for assays for markers that are integral for a trial. The information provided will be useful for an FDA pre-IDE review.

It is recommended that Jennings et. al. Recommended Principles and Practices for Validating Clinical Molecular Pathology Tests. Arch Pathol Lab Med 133:743-755, 2009 be read as a reference before completing this template.

Section	Heading
1	Assay, Patient and Specimen Parameters
2	Design of Mutation Assay
3	Assay Performance
4	Laboratory that is performing this assay



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**1 Assay, Patient and Specimen Parameters**

**A. Name of the Mutated gene(s) Gene ID that are measured, please follow nomenclature for mutation as supported by the Association of Molecular Pathology and the NCI EVS – example below:**

**Gene 1**

**Gene 2**

**Gene 3**

**Gene 4**

**Gene 5**

**Gene 6**

**Gene 7**

**Please Use HUGO nomenclature for Gene ID (<http://www.genenames.org> )**

**Then please use the following format to identify the specific mutation:**

**Gene ID RefSeq#.Version c. nt # reference nt>altered nt (p. ref AA>mut AA)**

**Example: BRAF NM\_004333.4 c. 1799 T>A (p.Val600Glu)**

**N.B.: version number for refseq reference is critical because allows traceability**

**If performing a panel of more than 7 mutations, please provide in spreadsheet as an appendix,**

**B How will the assay and its marker(s) be used in the clinical trial?**

Integral

Integrated

Research

**C Assay Purpose in Study**

**D Tissue Collection Consent Method under which samples are (were) obtained**



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**E Pre-Analytic Variables**

**E1 ischemic Time From Collection to Specimen Processing or Fixation**

Maximum Warm ischemia time (=time from cutting blood supply to removal from body) allowed in minutes if known:

Maximum Cold ischemia time (=time until specimen fixed/frozen or processed after removal from body) allowed in minutes if known:

(If not known enter 99; If considered not important for assay - enter 98 for answers to previous 2 questions)

**E2 Type of Specimen**



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**F3 If sample is fluid (blood, ascites, pleural, cyst or other fluid), how was sample initially stabilized?**

**F4 Type of Stabilization of specimen**

F4a If fixed, was 10% Neutral Buffered Formalin Used?

F4b If other fixatives are acceptable, what are they?

F4c How long was the sample fixed?

F4d If frozen, how was specimen frozen?



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F4e If frozen, at what temperature do you store the specimen?

**G. Specimen Characteristics**

G1 What type of specimen do you analyze (check all that apply)?

G1a Please specify if other type of specimen

G2 Do you record the size/mass of specimen or number of cells that you use for analysis?

G2a Please indicate which characteristic is most important for specimen:

G2b Please give the minimum value (as appropriate): Size (Diameter in cm), Mass (mg), or Cells (Number)



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- G3 Is an adjacent tissue section stained and examined by H&E?
  - G3a If yes, was it used to assess cellularity and tumor content?
  - G3b Do you keep reference images of the H&E section?
  
- G4 Tumor content of specimen
  - G4a How is tumor content reported?
    - G4ai. What is other method for reporting tumor content?
  - G4b How is tumor content determined?
    - G4bi. Other method of determining tumor content?
  - G4c What is the minimum acceptable % tumor content/cellularity?



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G5 Do you enrich the sample for tumor cells?

G5a If so, what method did you use?

G5ai. Other method for tumor cell enrichment?

**2 Design of Mutation Assay**

A Describe the assay platform (please attach the complete SOP as an Appendix if you have one (including reagent details (lab manufactured protocols and commercial product/kit numbers & vendor))

A1 If other method is used for mutation assay, please specify

A2 Does the assay use molecular methods to enhance detection of mutations in a heterogeneous specimen?



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A2a If so, what are the methods?

A3 Is assay instrument (sequencer or PCR machine) tested for calibration or performance?

SOP

A3a If so, please provide the protocols as an Appendix if not included in the

A3b If not, how is confidence obtained that assay performs as intended?

B DNA quality

B1 Does your lab use an automated or semi-automated method to extract DNA?

B1a If yes, which instrument do you use?





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B1b If your lab uses a manual method, does it use a commercially available kit?

B1c If yes, which reagents do you use?

B1ci. If another kit or reagents, what is (are) they?

B1d if not, please check all reagents included in your DNA extraction:

B1e If another reagent, what is it?

C Do you assess DNA Concentration?

C1 If you do, how is DNA concentration assessed?



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C1a If other method is used to assess DNA concentration, what is it?

**D Assay Quality Assessment**

D1 Do you assess DNA purity?

D2 How is DNA purity assessed?

D2a If you assess purity by another technique, what is that method?

D3 Do you assess DNA integrity?

D3a How is DNA integrity assessed?

D4. If second/next generation sequencing is used, is there a library preparation step?

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E Data analysis

E1 How are raw data normalized, filtered, analyzed and reported?

E1a Provide detailed SOP's for data analysis.

E1b What software and version is used?

E1c Are there limits set for reportable signal (e.g. maximum allowable Ct, parameters for somatic mutation calling by sequencing)

E2 If limits of reportable signal have been set, describe how these were determined.

E3 How is assay result reported (e.g. positive for mutation or negative for mutation)?  
OR, "report as low or high level"

E4 Are there instructions for reasons why a sample should be repeated?

E4a If so, what are the instructions?

**3 Assay Performance**

A Accuracy (Closeness to "true")

A1 was accuracy established using reference material?



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A2 if yes, what reference material was used?

A3 was accuracy established by comparison to a reference method(s)?

A4 if yes, which method(s)?

A5 how many true positives were there (known positive samples that tested positive)?

A6 how many true negatives were there (known negative samples that tested negative)?

A7 how many false positives were there (known negative samples that tested positive)?

A8 how many false negatives were there (known positive samples that tested negative)?

A9 Total number of samples

B Repeatability of a qualitative assay

B1 were replicates of control or reference samples performed (within-run repeats)?

B2 how many replicates of control or reference samples were performed?

B3 what is the percent concordance for within-run repeats?



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B4 were samples tested repeatedly between runs?

B5 how many between-run repeats were performed?

B6 What is the percent concordance for between-run repeats?

B7 Do you run multiple positive controls?

B8 How often are positive controls run if there is just one mutation being assayed?

B8a If Other, please specify frequency

B9 How often are positive controls run if several mutations are being assayed?

B9a If other, please specify frequency

B10 If positive controls are rotated when several mutations are assayed, how are they rotated?

B10a

B11 How often are negative controls run?

B11a If other, please specify frequency

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C Limit of detection (lowest amount of analyte that gives an informative result)

C1 What is the lowest % of mutant or variant allele that can be reliably detected in a wild type background.

D Interfering substances (substances that, at a given concentration may lead to erroneous results)

D1 were interfering substances assessed?

D2 What biological matrix materials have been tested for interference?

D2i. At what concentrations

E Please attach as part of your SOP a description of the bioinformatics methods/program that are used to analyze the assay's data

E1 Is the bioinformatics methods/program attached?

**FOR QUANTITATIVE ASSAYS only**

F Repeatability of a quantitative assay

F1. how many repeats were performed to establish precision?

F2. what is the coefficient of variation at or near the lower limit of quantification?



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F3. what is the coefficient of variation at or near the middle of the analytical measurement range?

F4. what is the coefficient of variation at or near the upper limit of quantification?

G Limit of detection (lowest amount of analyte that can reliably be distinguished from background)

G1 What is the lowest amount of analyte that can be distinguished from background with 95% confidence?

H Limits of quantification (lowest and highest concentrations of analyte that can be determined with acceptable total error)

H1. What is the lowest amount of analyte that can be distinguished from background with acceptable total error?

H2. What is the highest amount of analyte that can be quantified with acceptable total error?

H3. Units of concentration

I reference range

I1 How many samples were used to establish the normal reference range?

I2 What are the selection criteria for these normal controls?

I3 what is the normal reference range for this assay ~~ZIM XQW~~ ?



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J Reportable range (range of all possible results that are shown to be analytically valid, i.e. with acceptable error)

J1 what is the reportable range of this assay?

J1a. Units of reportable range

**4 Laboratory that is performing this assay**

A which type of lab will perform the assay?

B Does the lab meet GLP standards?

C What is the training and experience of the operator?

D Is the lab CLIA certified or accredited? (Only necessary if assay is to used for medical decision-making)

**E Ongoing quality control measures**

E1 Is there a program for proficiency testing (PT)?

E1a If yes, how many challenges is PT done?

E1b If yes, how frequently is PT done per year?





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E2 Is there ongoing assessment of technician competency?

E3 Is data kept on control samples?