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| STANDARD OPERATING PROCEDURE |
| |  |  | | --- | --- | | **Title: Mini-validation of Samples (Repeatability)** | | |  |  | | **Version #: 3** | **Author: PNNL Lab** | | **Date: 07/01/2016** |  | |

# Purpose

The purpose of this document is to describe the characterization of a set of assays according to its repeatability of measurement over 5 days. This is to estimate the performance of the assay measured in a complex sample over multiple days.

# Scope

This procedure covers overall preparation and running of samples for generating the validation samples with regards to CPTAC Assay Characterization Guidance experiment #2.

# Responsibilities

It is the responsibility of person(s) performing this procedure to be familiar with laboratory safety procedures. The interpretation of results must be done by a person trained in the procedure and familiar with such interpretation.

# Equipment

Microcentrifuge

Eppendoff Thermomixer

# Materials

Waters glass vial

# Solutions

Mobile phase A: 0.1% FA in H2O

Mobile phase B: 0.1% FA in ACN

# Reagents

Water, HPLC grade (H2O)

Acetonitrile, HPLC grade (ACN) (Fisher Scientific, A955-4)

Formic Acid (0.1%)/Acetonitrile (EMD, FX0437P-1)

Formic Acid (FA) (Agilent Technologies, G2453-85060)

**Peptide Standards:**

Both pure heavy stable isotope-labeled peptides and sequence matched pure light versions were synthesized. Heavy peptides incorporated a fully atom labeled 13C and 15N isotope at the C-terminal lysine (K) or arginine (R) position of each (tryptic) peptide, resulting in a mass shift of +8 or +10 Da, respectively. Those pure peptides were purified to >95% purity by HPLC from the vendor. They were quantified by amino acid analysis and aliquots were stored in 5% acetonitrile/0.1% formic acid at -80°C until use. Pure light peptides are spiked in as internal standards (IS). The stock of light internal standard was stored in -80 ºC freezer. Pure heavy peptides were mixed together at three different concentrations, including low, median, and high and further stored in -80 ºC until use.

**Matrix:**

A background matrix consisting of ovarian cancer tumor tissue digest was used for experiment 2. Tissue sample was processed as described in SOP TP-1 (Tissue sample Preparation). Digestion was performed according to SOP TD-1 (Trypsin Digestion of tissue sample). The tissue digest was aliquoted and independent digestions were performed for each replicate of repeatability validation to make complete process replicates for each sample. Following digestion, tissue digest was first diluted to a concentration of 0.1 µg/µl and prepared for future use.

# Procedure

**Determination of spike levels and preparation of samples**

1. Peptides were multiplexed according to the LLOQ and linear range determined from the response curves (experiment 1) in order to prepare validation samples at an appropriate concentration. Pure heavy peptides were spiked into tissue digest matrix with the following spike levels:

Low: 3 LOQ

Med: 50-100 LOQ

High: >100 LOQ

1. The stock heavy peptide mix is serially diluted with tissue digest matrix (0.1 µg/µl) to create the required concentration above.
2. 2 µl of each concentration point of heavy peptide mix is added to different aliquots of tissue digest matrix to create low, med and high concentrations of heavy peptide for each day.
3. 1 µl of light peptide IS mix (40 fmol/µL) is added to make a highest concentration of a sample, and the final volume of each sample is 40 µl, while both heavy and light peptide mix account for 5% of final volume. The final light peptide concentration is 10 fmol/µg.
4. Store sample in the LC autosampler (4 ºC) and get ready for MRM analysis (See SOP LC-1 for Liquid Chromatography and SOP PM-1 for Peptide MRM on TSQ Vantage).
5. Analyze different samples in triplicates in randomized order on 5 consecutive days.

# Referenced Documents

SOP TD-1 for Trypsin Digestion of tissue sample.pdf

SOP TP-1 for Tissue Sample Preparation.pdf

SOP LC-1 for Liquid Chromatography.pdf  
SOP PM-1 for Peptide MRM on TSQ Vantage.pdf