================================================================================

Consensus Step Workflow

================================================================================

Result name: PDAC\_Control\_samples

Result file: D:\Jana\Creatics\cr01\_001\_1\PDAC\_Control\_samples.pdResult

Description: Export results - PDAC Control by Sample

Workflow based on template: 120315 LFQProfiler\_consensus\_export

Creation date: 1/27/2016 12:09:21 PM

Created with Discoverer version: 2.1.0.81

------------------------------------------------------------------

The pipeline tree:

------------------------------------------------------------------

|-(0) MSF Files

|-(1) LFQProfiler

Post-processing nodes:

--------------------------------

|-(2) Result Exporter

------------------------------------------------------------------

Processing node 0: MSF Files

------------------------------------------------------------------

1. Spectrum Storage Settings:

- Spectra to Store: Identified or Quantified

2. Merging of Identified Peptide and Proteins:

- Merge Mode: Globally by Search Engine Type

- File Limit for Automatic Merge.: 10

3. FASTA Title Line Display:

- Reported FASTA Title Lines: Best match

- Title Line Rule: standard

4. PSM Filters:

- Maximum Delta Cn: 0.05

- Maximum Rank: 0

- Maximum Delta Mass: 0 ppm

------------------------------------------------------------------

Processing node 1: LFQProfiler

------------------------------------------------------------------

1. Feature linking:

- Perform map alignment: True

- Max. RT difference [min]: 1

- Max. m/z difference: 10 ppm

2. ID mapping:

- Max. RT difference [min]: 1

- Max. m/z difference: 10 ppm

- q-Value threshold: 0.05

- Protein database: RefNCBInr\_human\_120814\_base.fasta

- Enzyme: Trypsin

3. Protein quantification:

- Use peptides: greedy

- top: 0

- Averaging: mean

- Include all: False

- Filter charge: True

- Fix peptides: True

4. General:

- CPU Cores: 1

------------------------------------------------------------------

Processing node 2: Result Exporter

------------------------------------------------------------------

1. Output Data:

- R-friendly Headers: True