Result name: 20220329\_Yoshikawa\_B\_Nakamura\_Celegans\_MSAmanda\_limma\_trial2

Result file: D:\PD25\_data\Yoshikawa\20220328\_Yoshikawa\_B\_Nakamura\_Celegans\20220329\_Yoshikawa\_B\_Nakamura\_Celegans\_MSAmanda\_limma\_trial2.pdResult

Description: -

Workflow based on template: LFQ\_limma\_Celegans

Creation date: 3/30/2022 9:26:04 AM

Created with Discoverer version: 2.5.0.400

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

The workflow tree:

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

 |-(0) MSF Files

 |-(1) PSM Grouper

 |-(2) Peptide Validator

 |-(3) Peptide and Protein Filter

 |-(4) Protein Scorer

 |-(5) Protein FDR Validator

 |-(6) IMP-NormalisationPlus

 |-(7) limma

 |-(8) Protein Grouping

 |-(9) Peptide in Protein Annotation

 |-(10) Modification Sites

 |-(18) IMP-apQuant Peptide and Protein Quantifier

 |-(6) IMP-NormalisationPlus

 |-(7) limma

 |-(12) Protein Marker

 |-(14) Peptide Isoform Grouper

 |-(13) Protein Annotation

Post-processing nodes:

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

 |-(15) Data Distributions

 |-(17) Display Settings

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

Processing node 0: MSF Files

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

1. Storage Settings:

- Spectra to Store: Identified or Quantified

- Feature Traces to Store: All

2. Merging of Identified Peptide and Proteins:

- Merge Mode: Globally by Search Engine Type

3. FASTA Title Line Display:

- Reported FASTA Title Lines: All

- Title Line Rule: standard

4. PSM Filters:

- Maximum Delta Cn: 0.1

- Maximum Rank: 1

- Maximum Delta Mass: 0 ppm

- 1. Score: MS Amanda 2.0: Amanda Score

- 1. Threshold: 100

Hidden Parameters:

- MSF File(s): D:\PD25\_data\Yoshikawa\20220328\_Yoshikawa\_B\_Nakamura\_Celegans\20220329\_Yoshikawa\_B\_Nakamura\_Celegans\_MSAmanda\_limma\_trial2.msf

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

Processing node 1: PSM Grouper

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

1. Peptide Group Modifications:

- Site Probability Threshold: 75

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

Processing node 2: Peptide Validator

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

1. General Validation Settings:

- Validation Mode: Automatic (Control peptide level error rate if possible)

- Target FDR (Strict) for PSMs: 0.01

- Target FDR (Relaxed) for PSMs: 0.05

- Target FDR (Strict) for Peptides: 0.01

- Target FDR (Relaxed) for Peptides: 0.05

2. Specific Validation Settings:

- Validation Based on: q-Value

- Target/Decoy Selection for PSM Level FDR Calculation Based on Score: Automatic

- Reset Confidences for Nodes without Decoy Search (Fixed score thresholds): False

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

Processing node 3: Peptide and Protein Filter

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

1. Peptide Filters:

- Peptide Confidence At Least: High

- Keep Lower Confident PSMs: False

- Minimum Peptide Length: 7

- Remove Peptides Without Protein Reference: False

2. Protein Filters:

- Minimum Number of Peptide Sequences: 1

- Count Only Rank 1 Peptides: False

- Count Peptides Only for Top Scored Protein: False

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

Processing node 4: Protein Scorer

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

No parameters

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

Processing node 5: Protein FDR Validator

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

1. Confidence Thresholds:

- Target FDR (Strict): 0.01

- Target FDR (Relaxed): 0.05

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

Processing node 6: IMP-NormalisationPlus

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

- Normalisation Method: sum

- Imputation Method: 5 percentile

- Filter fraction: 0.65

Protein Filter:

- Master only: True

- Minimum confidence: High

- Exclude contaminants: False

Sample Filter:

- Exclude Washes: False

- Wash Pattern: Wash

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

Processing node 7: limma

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

No parameters

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

Processing node 8: Protein Grouping

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

1. Protein Grouping:

- Apply strict parsimony principle: True

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

Processing node 9: Peptide in Protein Annotation

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

1. Flanking Residues:

- Annotate Flanking Residues of the Peptide: False

- Number Flanking Residues in Connection Tables: 1

2. Modifications in Peptide:

- Protein Modifications Reported: Only for Master Proteins

3. Modifications in Protein:

- Modification Sites Reported: All And Specific

- Minimum PSM Confidence: High

- Report Only PTMs: True

4. Positions in Protein:

- Protein Positions for Peptides: Only for Master Proteins

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

Processing node 10: Modification Sites

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

1. General:

- Report Only PTMs: True

- Only Master Proteins: True

- Motif Radius: 6

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

Processing node 18: IMP-apQuant Peptide and Protein Quantifier

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

1. Confidence Parameters:

- Scoring Method: sum

- apQuant Confidence High Cutoff: 0.01

- apQuant Confidence Medium Cutoff: 0.05

- Set Arealess to Low: False

- Score Components to use: DeltaT1; DeltaT2; DeltaM1; F1; F2; F3; distF

- Replacement Value: 5

- Use Robust Methods: True

2. Protein Area:

- ID Confidence Level: Medium

- MBR Confidence Level: Medium

- Peptides to Use: Unique + Razor

- Grouping Method: sum

- Peptides to use for Protein Area:: iBAQ

3. Peptide Area:

- Minimum Area: 50000

- Confidence to use: mode(lowest)

- Confidence check: accross runs

- test: True

- Check for overlaps: True

- Check for overlaps C13: True

4. Modifications to use:

- Use all modifications for Quantification: True

5. iBAQ Parameters:

- Enzyme Name: Trypsin (Full)

- Min peptide length: 7

6. Top X Parameters:

- Usage of peptides: average

- # peps for protein area: 3

7. Other:

- Summary Confidence Level: Unknown

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

Processing node 12: Protein Marker

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

1. Contaminant Database:

- Protein Database: MaxQuant\_contaminants.fasta

5. Annotate Species:

- As Species Map: False

- As Species Names: False

6. Mark Additional Entities:

- Annotation Groups: False

- Pathway Groups: False

- Modification Sites: True

- Peptide Isoform Groups: True

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

Processing node 14: Peptide Isoform Grouper

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

No parameters

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

Processing node 13: Protein Annotation

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

1. Annotation Aspects:

- 1. Aspect: Biological Process

- 2. Aspect: Cellular Component

- 3. Aspect: Molecular Function

- 4. Aspect: None

- 5. Aspect: None

- 6. Aspect: None

2. Annotation/Pathway Groups:

- Protein Database: C.elegans\_tr\_sp[6239].fasta

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

Processing node 15: Data Distributions

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

1. ID Distributions (Bottom-up):

- Peptides to Use: All PSMs

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

Processing node 17: Display Settings

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

1. General:

- Filter Set:

 ###

 ### This file contains the following filters:

 ###

 ### Row Filter for PSMs:

 ### ------------------------------------

 ### AND

 ### |

 ### +--Confidence is at least High

 ### |

 ### +--Amanda Score is greater than 150.00

 ### ------------------------------------

 ###

 ###

 ### Row Filter for Proteins:

 ### ------------------------------------

 ### AND

 ### |

 ### +--Master is equal to Master

 ### |

 ### +--in category

 ### | |

 ### | +--Protein FDR Confidence

 ### | |

 ### | +--1

 ### |

 ### +--MaxPeptides is greater than or equal to 3

 ### ------------------------------------

 ###

 ###

 ### Row Filter for Input Files:

 ### ------------------------------------

 ### FileName does not end with msf

 ### ------------------------------------

 ###

 'magellan filter set' 1 'PROTmasterConfHigh3peps\_PSM150confHigh.filterset' FiltersetProperties 1 'LastFileName' '\\storage.imp.ac.at\groups\massspec\User\Gerhard\\_WFs\202104\_LFQ\PROTmasterConfHigh3peps\_PSM150confHigh.filterset' Filter 'TargetPeptideSpectrumMatch' FilterProperties 1 'Filter/DisplayPropertyHint' 'PSMs' 1 NARY\_AND 2 BETTEREQUAL FilterConditionProperties 1 'NamedComparableFilterCondition/DisplayPropertyHint' 'Confidence' property 'Thermo.Magellan.Proteomics.MatchConfidence, Thermo.Magellan.Proteomics' 'MatchConfidence' constant 'Thermo.Magellan.Proteomics.MatchConfidence, Thermo.Magellan.Proteomics' 'High' > FilterConditionProperties 1 'NamedComparableFilterCondition/DisplayPropertyHint' 'Amanda Score' property 'System.Nullable`1[[System.Double, mscorlib]], mscorlib' 'AmandaScore' constant 'System.Nullable`1[[System.Double, mscorlib]], mscorlib' '150.00' Filter 'TargetProtein' FilterProperties 2 'Filter/DisplayPropertyHint' 'Proteins' 'FilterConditionProperties/FilterScope' 'FilterConditionProperties/FilterScopeValueMainGrid' 1 NARY\_AND 3 = FilterConditionProperties 1 'NamedComparableFilterCondition/DisplayPropertyHint' 'Master' property 'Thermo.PD.EntityDataFramework.MasterProteinAssessment, Thermo.Magellan.EntityDataFramework' 'IsMasterProtein' constant 'Thermo.PD.EntityDataFramework.MasterProteinAssessment, Thermo.Magellan.EntityDataFramework' 'IsMasterProtein' datadistribution\_particular FilterConditionProperties 1 'NamedComparableFilterCondition/DisplayPropertyHint' 'Protein FDR Confidence' property 'Thermo.Magellan.EntityDataFramework.DataDistributionValue, Thermo.Magellan.EntityDataFramework' 'ProteinFDRConfidence' constant 'Thermo.Magellan.EntityDataFramework.DataDistributionValue, Thermo.Magellan.EntityDataFramework' 'position\_id\_1' Filter '7899A5F8-6954-4E95-8C2D-BB0C83221B21' 1 datadistribution\_level\_equals property 'System.Nullable`1[[System.Int32, mscorlib]], mscorlib' '6AED4774-1ECD-4202-B746-B79D936A3D77' constant 'System.Nullable`1[[System.Int32, mscorlib]], mscorlib' '4' >= FilterConditionProperties 1 'NamedComparableFilterCondition/DisplayPropertyHint' 'MaxPeptides' property 'System.Int32, mscorlib' 'MaxPeptides' constant 'System.Int32, mscorlib' '3' Filter 'WorkflowInputFile' FilterProperties 1 'Filter/DisplayPropertyHint' 'Input Files' 1 NARY\_AND 1 endsnotwith property 'System.String, mscorlib' 'FileName' constant 'System.String, mscorlib' 'msf'

- Layout Definition: No summary generated for layout.

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

Workflow messages:

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

03/30/2022 04:41 PM Job Execution: Processing D:\PD25\_data\Yoshikawa\20220328\_Yoshikawa\_B\_Nakamura\_Celegans\20220329\_Yoshikawa\_B\_Nakamura\_Celegans\_MSAmanda\_limma\_trial2.pdResult

03/30/2022 04:41 PM (0) MSF Files: D:\PD25\_data\Yoshikawa\20220328\_Yoshikawa\_B\_Nakamura\_Celegans\20220329\_Yoshikawa\_B\_Nakamura\_Celegans\_MSAmanda\_limma\_trial2.msf

03/30/2022 04:41 PM (0) MSF Files: All 1 files are ready for processing.

03/30/2022 04:41 PM (0) MSF Files: Start transferring results of 1 msf files...

03/30/2022 04:45 PM (0) MSF Files: Transferred 27205 Proteins to result file in 3 min 47 s.

03/30/2022 04:50 PM (0) MSF Files: Transferred 26975 Decoy Proteins to result file in 5 min 8 s.

03/30/2022 05:03 PM (0) MSF Files: Added 735348 Mass Spectra to result file.

03/30/2022 05:03 PM (0) MSF Files: Added 24 traces to result file.

03/30/2022 05:03 PM (0) MSF Files: Added 12 Input Files to result file.

03/30/2022 05:04 PM (0) MSF Files: Added 485243 PSMs to result file.

03/30/2022 05:04 PM (0) MSF Files: Added 250105 Decoy PSMs to result file.

03/30/2022 05:05 PM (0) MSF Files: Added 1076054 MS/MS Spectrum Info to result file.

03/30/2022 05:05 PM (0) MSF Files: Added 1076054 Precursors to result file.

03/30/2022 05:05 PM (0) MSF Files: Added 12 Mass Recalibrations to result file.

03/30/2022 05:05 PM (0) MSF Files: Added 78866 Correction Landmarks to result file.

03/30/2022 05:05 PM (0) MSF Files: Added 24 Specialized Traces to result file.

03/30/2022 05:06 PM (0) MSF Files: Added 165264 apQuant Features to result file.

03/30/2022 05:06 PM (0) MSF Files: Added 132 apQuant Alignment to result file.

03/30/2022 05:06 PM (0) MSF Files: Added 165264 apQuant Decoy Features to result file.

03/30/2022 05:06 PM (0) MSF Files: Added 2 KeyValueEntity to result file.

03/30/2022 05:08 PM (0) MSF Files: Copying data took 27 min 4 s.

03/30/2022 05:10 PM (0) MSF Files: Finding unique sequences took 36.1 s.

03/30/2022 05:10 PM (0) MSF Files: Filtering PSMs took 27.7 s.

03/30/2022 05:10 PM (0) MSF Files: Filter 0/23485 Proteins (23485 excluded) took: 9.8 s

03/30/2022 05:10 PM (0) MSF Files: Filter 0/26971 Decoy Proteins (26971 excluded) took: 4.4 s

03/30/2022 05:10 PM (0) MSF Files: Filtering proteins took 14.3 s.

03/30/2022 05:12 PM (0) MSF Files: -- Total execution of MSF Files (0) took 30 min 21 s --

03/30/2022 05:12 PM (1) PSM Grouper: Grouping 'PSMs'

03/30/2022 05:13 PM (1) PSM Grouper: Found 10814 Peptide Groups.

03/30/2022 05:13 PM (1) PSM Grouper: Grouping 'Decoy PSMs'

03/30/2022 05:14 PM (1) PSM Grouper: Found 3 Decoy Peptide Groups.

03/30/2022 05:14 PM (1) PSM Grouper: -- Total execution of PSM Grouper (1) took 2 min 23 s --

03/30/2022 05:14 PM (2) Peptide Validator: Start PSM and Peptide validation in 'Automatic (Control peptide level error rate if possible)' mode...

03/30/2022 05:14 PM (2) Peptide Validator: Updated PSM confidences in 7.9 s.

03/30/2022 05:14 PM (2) Peptide Validator: Use svm score for 'peptide' qvality run.

03/30/2022 05:15 PM (2) Peptide Validator: Updated peptide confidences using qvality in 49.3 s.

03/30/2022 05:15 PM (2) Peptide Validator: Calculating Mascot thresholds.

03/30/2022 05:15 PM (2) Peptide Validator: -- Total execution of Peptide Validator (2) took 57.7 s --

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filter Peptide Groups

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filter 10806/10814 Peptide Groups (8 excluded) and 66948/66958 PSMs (10 excluded) took 3.9 s

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filtering Proteins

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filter 3713/3720 Proteins (7 excluded) took 9.6 s

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filter Decoy Peptide Groups

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filter 0/3 Decoy Peptide Groups (3 excluded) and 0/3 Decoy PSMs (3 excluded) took 830.5 ms

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filtering Decoy Proteins

03/30/2022 05:15 PM (3) Peptide and Protein Filter: Filter 0/4 Decoy Proteins (4 excluded) took 4.2 s

03/30/2022 05:16 PM (3) Peptide and Protein Filter: Updating counts took 51.8 s.

03/30/2022 05:16 PM (3) Peptide and Protein Filter: -- Total execution of Peptide and Protein Filter (3) took 1 min 11 s --

03/30/2022 05:16 PM (4) Protein Scorer: Calculating Coverage and Counts

03/30/2022 05:16 PM (4) Protein Scorer: Calculated counts and coverages in 7.4 s.

03/30/2022 05:16 PM (4) Protein Scorer: Scoring target proteins

03/30/2022 05:16 PM (4) Protein Scorer: Scored 3713 proteins in 14.3 s.

03/30/2022 05:16 PM (4) Protein Scorer: Scoring decoy proteins

03/30/2022 05:16 PM (4) Protein Scorer: Scored 0 decoy proteins in 102.5 ms.

03/30/2022 05:16 PM (4) Protein Scorer: -- Total execution of Protein Scorer (4) took 22 s --

03/30/2022 05:16 PM (5) Protein FDR Validator: Apply confidences based on protein scores of 3713 proteins.

03/30/2022 05:16 PM (5) Protein FDR Validator: Cannot validate proteins because all decoy proteins were filtered out.

03/30/2022 05:16 PM (5) Protein FDR Validator: -- Total execution of Protein FDR Validator (5) took 43.5 ms --

03/30/2022 05:17 PM (8) Protein Grouping: Retrieving 2254 protein groups took 254.9 ms.

03/30/2022 05:17 PM (8) Protein Grouping: Storing, updating and connecting protein groups, PSMs and peptides took 35.1 s.

03/30/2022 05:17 PM (8) Protein Grouping: Check 2254 protein groups.

03/30/2022 05:18 PM (8) Protein Grouping: Applying strict parsimony took 21.4 s.

03/30/2022 05:18 PM (8) Protein Grouping: Found 2248 protein groups.

03/30/2022 05:18 PM (8) Protein Grouping: Storing, updating and connecting protein groups, PSMs and peptides took 789.3 ms.

03/30/2022 05:18 PM (8) Protein Grouping: Found 0 decoy protein groups.

03/30/2022 05:18 PM (8) Protein Grouping: -- Total execution of Protein Grouping (8) took 1 min 16 s --

03/30/2022 05:18 PM (14) Peptide Isoform Grouper: Grouping PSMs by modification isoform

03/30/2022 05:18 PM (14) Peptide Isoform Grouper: Grouping 'PSMs'

03/30/2022 05:22 PM (14) Peptide Isoform Grouper: Found 10845 Peptide Isoforms.

03/30/2022 05:22 PM (14) Peptide Isoform Grouper: Grouping 'Decoy PSMs'

03/30/2022 05:24 PM (14) Peptide Isoform Grouper: Found 0 Decoy Peptide Isoforms.

03/30/2022 05:24 PM (14) Peptide Isoform Grouper: -- Total execution of Peptide Isoform Grouper (14) took 6 min 31 s --

03/30/2022 05:24 PM (9) Peptide in Protein Annotation: Start retrieving flanking residues and positions...

03/30/2022 05:26 PM (9) Peptide in Protein Annotation: Annotated PSMs/peptides for 3713 proteins.

03/30/2022 05:26 PM (9) Peptide in Protein Annotation: Start annotating peptide groups with flanking residues and positions...

03/30/2022 05:26 PM (9) Peptide in Protein Annotation: Annotate Peptide Groups items

03/30/2022 05:26 PM (9) Peptide in Protein Annotation: Start retrieving flanking residues and positions...

03/30/2022 05:27 PM (9) Peptide in Protein Annotation: Annotated PSMs/peptides for 3713 proteins.

03/30/2022 05:27 PM (9) Peptide in Protein Annotation: Start annotating peptide groups with flanking residues and positions...

03/30/2022 05:27 PM (9) Peptide in Protein Annotation: Annotate Peptide Isoforms items

03/30/2022 05:27 PM (9) Peptide in Protein Annotation: Start calculating protein coverage...

03/30/2022 05:27 PM (9) Peptide in Protein Annotation: -- Total execution of Peptide in Protein Annotation (9) took 2 min 47 s --

03/30/2022 05:27 PM (10) Modification Sites: Start extracting Modification Sites.

03/30/2022 05:27 PM (10) Modification Sites: Extracting Modification Sites

03/30/2022 05:28 PM (10) Modification Sites: Annotated PSMs/peptides for 3713 proteins.

03/30/2022 05:28 PM (10) Modification Sites: Start connecting Modification Sites with PSMs.

03/30/2022 05:28 PM (10) Modification Sites: Connecting Modification Sites

03/30/2022 05:28 PM (10) Modification Sites: Connected Modification sites with PSMs and Peptide Groups for 3713 proteins.

03/30/2022 05:28 PM (10) Modification Sites: Connected Modification sites with PTM Peptide Groups for 3713 proteins.

03/30/2022 05:28 PM (10) Modification Sites: -- Total execution of Modification Sites (10) took 57.7 s --

03/30/2022 05:28 PM (18) IMP-apQuant Peptide and Protein Quantifier: Starting IMP-apQuant Quantifier version: 3.2.14.19291

03/30/2022 05:28 PM (18) IMP-apQuant Peptide and Protein Quantifier: Calculating Areas

03/30/2022 05:28 PM (18) IMP-apQuant Peptide and Protein Quantifier: Calculating Scores

03/30/2022 05:29 PM (18) IMP-apQuant Peptide and Protein Quantifier: Calculating q-Values

03/30/2022 05:29 PM (18) IMP-apQuant Peptide and Protein Quantifier: Connecting tables

03/30/2022 05:30 PM (18) IMP-apQuant Peptide and Protein Quantifier: Calculating overlaps

03/30/2022 05:30 PM (18) IMP-apQuant Peptide and Protein Quantifier: Add overlaps to QuanResults

03/30/2022 05:30 PM (18) IMP-apQuant Peptide and Protein Quantifier: Finished calculating overlaps

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Quantifying peptides

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Write data to TargetPeptideIsoformGroup table

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Write data to TargetPeptideGroup table

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Quantifying Proteins

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Combining peptide areas

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Write quantifying peptides to file

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Write areas to file

03/30/2022 05:31 PM (18) IMP-apQuant Peptide and Protein Quantifier: Write id column to file

03/30/2022 05:32 PM (18) IMP-apQuant Peptide and Protein Quantifier: Finished writing

03/30/2022 05:32 PM (18) IMP-apQuant Peptide and Protein Quantifier: Add feature buttons

03/30/2022 05:33 PM (18) IMP-apQuant Peptide and Protein Quantifier: Add decoy buttons

03/30/2022 05:33 PM (18) IMP-apQuant Peptide and Protein Quantifier: Add quanresult buttons

03/30/2022 05:33 PM (18) IMP-apQuant Peptide and Protein Quantifier: Add Alignment buttons

03/30/2022 05:33 PM (18) IMP-apQuant Peptide and Protein Quantifier: IMP-apQuant Quantifier finished in 00:05:24

03/30/2022 05:33 PM (6) IMP-NormalisationPlus: Node v1.10, Assembly v1.16.8102.18927

03/30/2022 05:33 PM (6) IMP-NormalisationPlus: Proteins: Found quantification property 'apQuant Areas'

03/30/2022 05:33 PM (6) IMP-NormalisationPlus: Proteins: Using normalisation method 'sum'.

03/30/2022 05:33 PM (6) IMP-NormalisationPlus: Proteins: Using imputation method '5 percentile'.

03/30/2022 05:34 PM (6) IMP-NormalisationPlus: Proteins: Calculating ratios finished.

03/30/2022 05:34 PM (6) IMP-NormalisationPlus: Peptide Groups: Found quantification property 'apQuant Areas'

03/30/2022 05:34 PM (6) IMP-NormalisationPlus: Peptide Groups: Calculating ratios finished.

03/30/2022 05:34 PM (6) IMP-NormalisationPlus: PSMs: No quantification property found, skipping further processing for this entity.

03/30/2022 05:34 PM (6) IMP-NormalisationPlus: Peptide Isoforms: Found quantification property 'apQuant Areas'

03/30/2022 05:34 PM (6) IMP-NormalisationPlus: Peptide Isoforms: Calculating ratios finished.

03/30/2022 05:34 PM (7) limma: Node v1.15, Assembly v1.20.8102.18845

03/30/2022 05:34 PM (7) limma: Processing ratio '(daf-2 hlh-30) / (daf-2)'.

03/30/2022 05:34 PM (7) limma: 1646 proteins written to file "C:\ProgramData\Thermo\Proteome Discoverer 2.5\Scratch\Job195\limma(7)\NormalisedapQuantAreas\_(daf-2 hlh-30) - (daf-2)\_source.txt".

03/30/2022 05:34 PM (7) limma: Loading required package: XML

03/30/2022 05:34 PM (7) limma: Warning in install.packages("XML", repos = "https://cran.wu.ac.at") :

03/30/2022 05:34 PM (7) limma: 'lib = "C:/Program Files/R/R-4.1.3/library"' is not writable

03/30/2022 05:34 PM (7) limma: Error in install.packages("XML", repos = "https://cran.wu.ac.at") :

03/30/2022 05:34 PM (7) limma: unable to install packages

03/30/2022 05:34 PM (7) limma: In addition: Warning message:

03/30/2022 05:34 PM (7) limma: In library(package, lib.loc = lib.loc, character.only = TRUE, logical.return = TRUE, :

03/30/2022 05:34 PM (7) limma: there is no package called 'XML'

03/30/2022 05:34 PM (7) limma: Execution halted

03/30/2022 05:34 PM (7) limma: System.IO.IOException: The pipe has been ended.

 at System.IO.\_\_Error.WinIOError(Int32 errorCode, String maybeFullPath)

 at System.IO.FileStream.WriteCore(Byte[] buffer, Int32 offset, Int32 count)

 at System.IO.StreamWriter.Flush(Boolean flushStream, Boolean flushEncoder)

 at System.IO.StreamWriter.Write(Char[] buffer, Int32 index, Int32 count)

 at IMP.LimmaNode.LimmaNode.ProcessLimma(String areaGuid, String ratioGuid, PropertyDescription pValueDescription, PropertyDescription minPValueDescription, PropertyDescription pAdjustedDescription, PropertyDescription significanceDescription)

 at IMP.LimmaNode.LimmaNode.Process()

 at IMP.LimmaNode.LimmaNode.OnParentNodeFinished(IProcessingNode sender, ResultsArguments eventArgs)

03/30/2022 05:34 PM Job Execution: ----- Job execution until failure took: 52 min 37 s. -----