

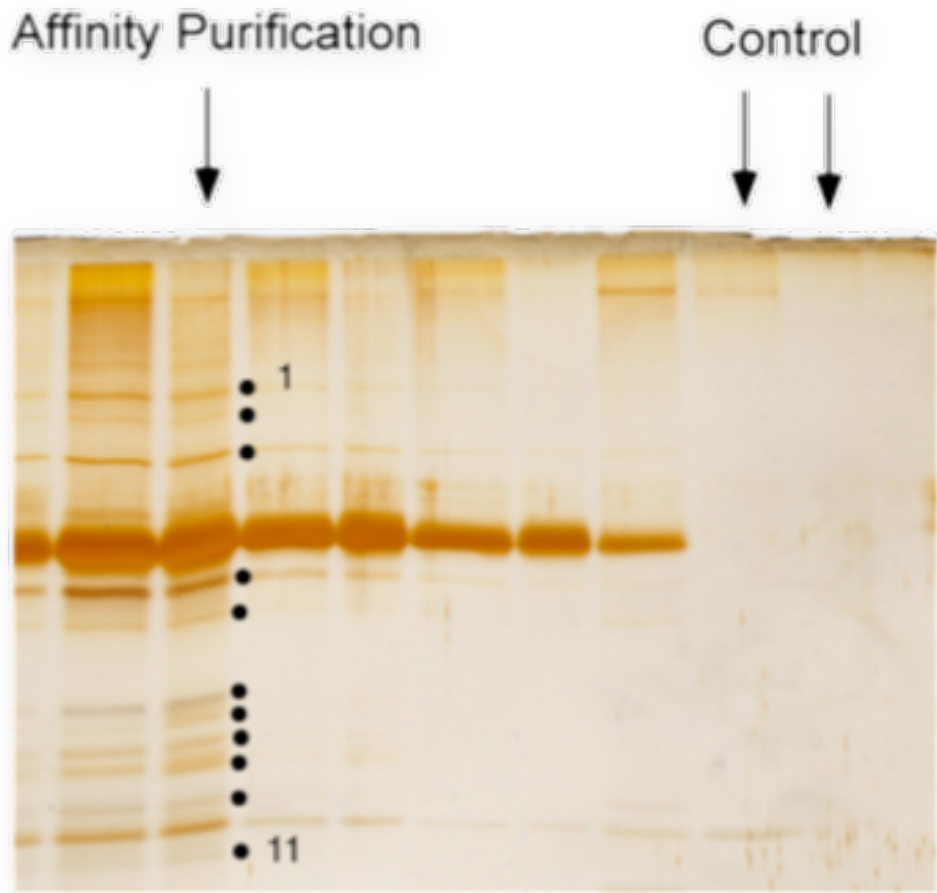
Introduction to Proteomic Data Analysis II

Analysis of Differential Protein Expression

University College Dublin, Conway Institute

Matthias Wilm, MD PhD,
Conway Institute, UCD,
Belfield, Dublin 4

Protein Analysis



Category	Item	Value	Unit	Notes
General Information	Project Name	Project A		
	Project ID	12345		
	Project Manager	John Doe		
	Project Start Date	2023-01-01		
	Project End Date	2023-12-31		
	Project Status	In Progress		
	Project Budget	\$1,000,000		
	Project Location	New York, NY		
	Project Description	Development of a new software application.		
	Project Contact	John Doe		
Financial Data	Revenue	\$500,000		
	Cost	\$300,000		
	Profit	\$200,000		
	Revenue Growth	10%		
	Cost Reduction	5%		
	Profit Margin	20%		
	Revenue per Unit	\$100		
	Cost per Unit	\$60		
	Profit per Unit	\$40		
	Revenue per Hour	\$100		
Operational Data	Production Volume	10,000		
	Production Cost	\$300,000		
	Production Time	100 hours		
	Production Efficiency	90%		
	Production Quality	95%		
	Production Defects	5%		
	Production Wastage	2%		
	Production Scrap	1%		
	Production Rework	1%		
	Production Yield	98%		
Human Resources	Number of Employees	50		
	Number of Contractors	10		
	Number of Consultants	5		
	Number of Interns	2		
	Number of Volunteers	1		
	Number of Retirees	0		
	Number of Part-timers	10		
	Number of Full-timers	40		
	Number of Seasonal Workers	5		
	Number of Temporary Workers	10		
Marketing Data	Marketing Spend	\$50,000		
	Marketing Revenue	\$100,000		
	Marketing Profit	\$50,000		
	Marketing Growth	15%		
	Marketing Cost	\$25,000		
	Marketing Efficiency	80%		
	Marketing Quality	90%		
	Marketing Defects	5%		
	Marketing Wastage	2%		
	Marketing Scrap	1%		
Sales Data	Sales Volume	10,000		
	Sales Revenue	\$1,000,000		
	Sales Profit	\$200,000		
	Sales Growth	10%		
	Sales Cost	\$800,000		
	Sales Efficiency	85%		
	Sales Quality	92%		
	Sales Defects	3%		
	Sales Wastage	1%		
	Sales Scrap	0%		

O60610-2;O60610-3;O60610	O60610-2;O60610-3;O60610	10;10;
O60613;O60613-2	O60613;O60613-2	4;2
O60645	O60645	
O60664-4;O60664;O60664-3;O60664-2	O60664-4;O60664;O60664-3	17;17;
O60684;O15131	O60684;O15131	7;4
O60701-3;O60701;O60701-2	O60701-3;O60701;O60701-2	6;6;5
O60711;O60711-2	O60711;O60711-2	11;10
O60716;O60716-17;O60716-2;O60716-4;O60716-6;O60716-3;O60716-5	O60716;O60716-17;O60716-2;O60716-4;O60716-6;O60716-3;O60716-5	8;8;8;8
O60725	O60725	
O60739	O60739	
O60749-2;O60749	O60749-2;O60749	6;6
O60762	O60762	
O60763;O60763-2	O60763;O60763-2	25;25
O60784;O60784-4;O60784-2;O60784-3	O60784;O60784-4;O60784-2	5;4;4;2
Q99880;Q99879;Q99877;Q93079;Q5QNW6;P62807;P58876;O60814;Q50826	Q99880;Q99879;Q99877;Q93079;Q5QNW6;P62807;P58876;O60814;Q50826	9;9;9;9
O60826	O60826	
O60828-2;O60828;O60828-5;O60828-4;O60828-6;O60828-3	O60828-2;O60828;O60828-5;O60828-4	3;3;2;2
O60832;O60832-2	O60832;O60832-2	8;6
O60841	O60841	

Protein Analysis

MaxQuant



- Protein Identification
- Quantification

Perseus



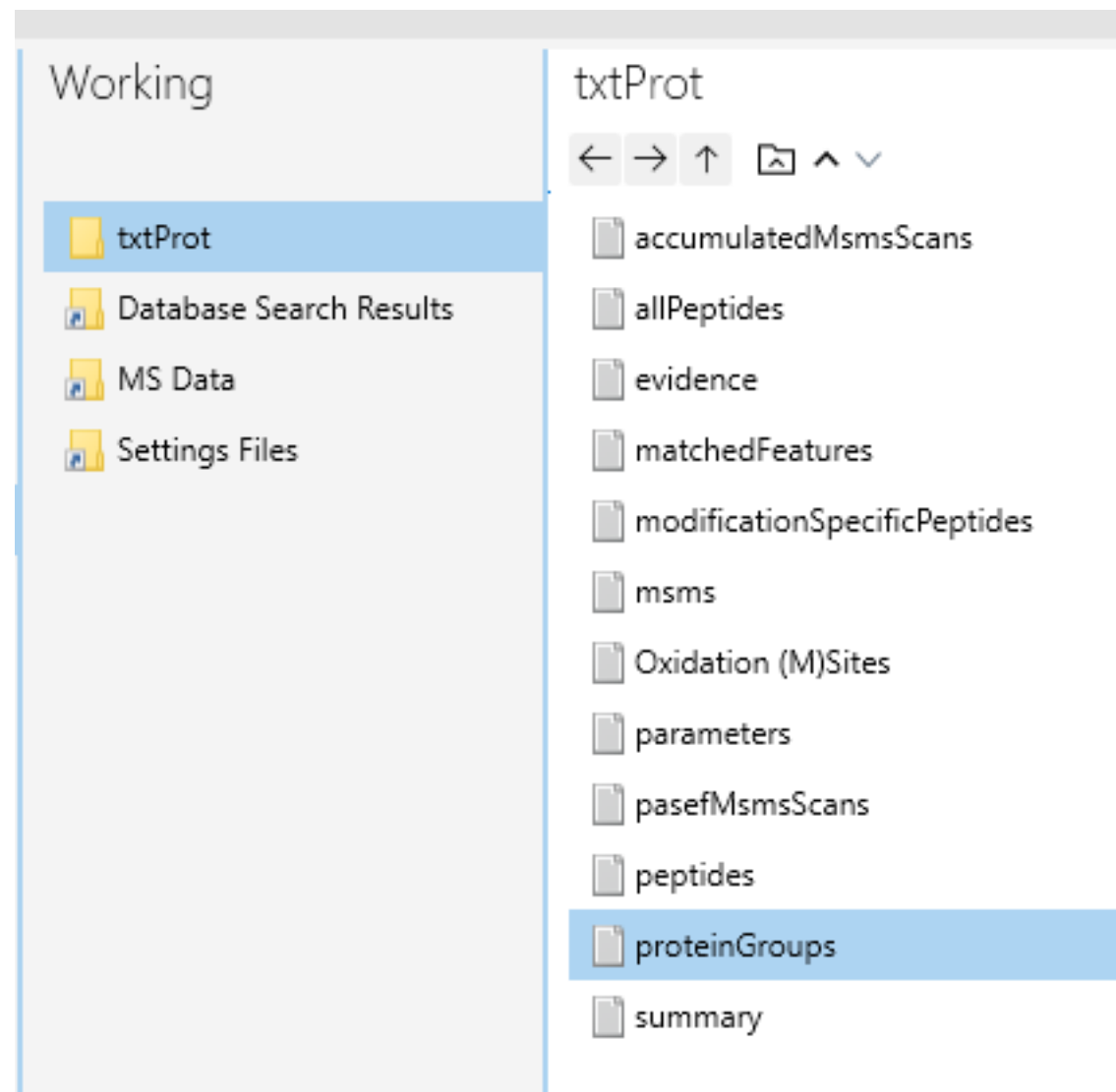
- Statistical Analysis of Quantitative Results

String

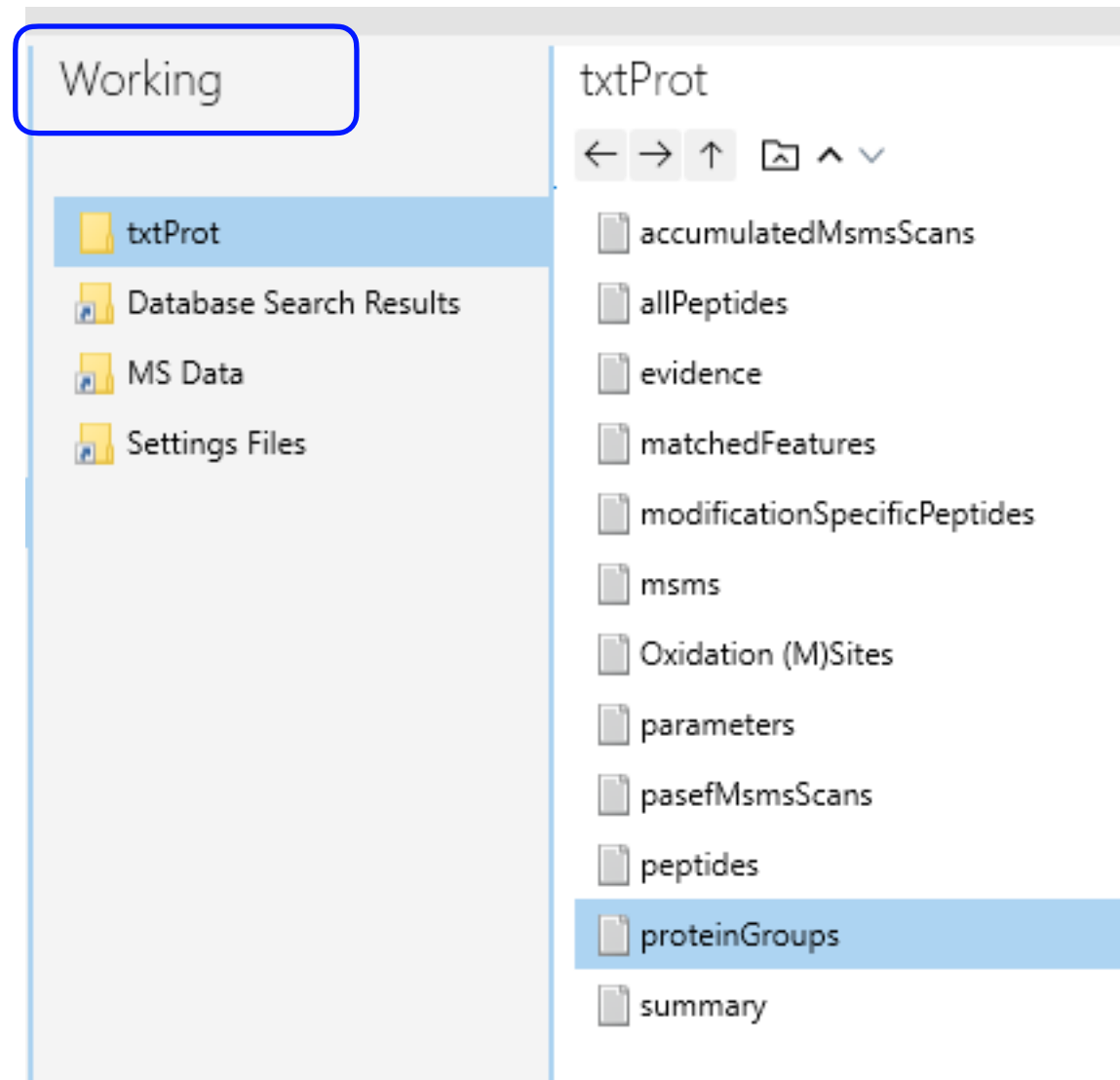


- Protein Network & Pathway Analysis

Data Organization: Move the txt folder to the Working Folder



Data Organization: Move the txt folder to the Working Folder



Data Organization: Generate Sample Meta-Data File

summary

Raw file	Experiment	Sample Type
211111kw_Simeng_Cntr_1_S1-C1_1_6427	Cntr_1_S1-C1_1_6427	S1 B1 T1
211111kw_Simeng_Cntr_1_S1-C2_1_6428	Cntr_1_S1-C2_1_6428	S1 B1 T2
211111kw_Simeng_Cntr_2_S1-C3_1_6429	Cntr_2_S1-C3_1_6429	S1 B2 T1
211111kw_Simeng_Cntr_2_S1-C4_1_6430	Cntr_2_S1-C4_1_6430	S1 B2 T2
211111kw_Simeng_Cntr_3_S1-C5_1_6431	Cntr_3_S1-C5_1_6431	S1 B3 T1
211111kw_Simeng_Cntr_3_S1-C6_1_6432	Cntr_3_S1-C6_1_6432	S1 B3 T2
211111kw_Simeng_Diff1_S1-A7_1_6409	Diff1_S1-A7_1_6409	S2 B1 T1
211111kw_Simeng_Diff1_S1-A8_1_6410	Diff1_S1-A8_1_6410	S2 B1 T2
211111kw_Simeng_Diff2_S1-A10_1_6412	Diff2_S1-A10_1_6412	S2 B2 T1
211111kw_Simeng_Diff2_S1-A9_1_6411	Diff2_S1-A9_1_6411	S2 B2 T2
211111kw_Simeng_Diff3_S1-A11_1_6413	Diff3_S1-A11_1_6413	S2 B3 T1
211111kw_Simeng_Diff3_S1-A12_1_6414	Diff3_S1-A12_1_6414	S2 B3 T2
211111kw_Simeng_DiffHyp1_S1-A1_1_6403	DiffHyp1_S1-A1_1_6403	S3 B1 T1
211111kw_Simeng_DiffHyp1_S1-A2_1_6404	DiffHyp1_S1-A2_1_6404	S3 B1 T2
211111kw_Simeng_DiffHyp2_S1-A3_1_6405	DiffHyp2_S1-A3_1_6405	S3 B2 T1
211111kw_Simeng_DiffHyp2_S1-A4_1_6406	DiffHyp2_S1-A4_1_6406	S3 B2 T2
211111kw_Simeng_DiffHyp3_S1-A5_1_6407	DiffHyp3_S1-A5_1_6407	S3 B3 T1
211111kw_Simeng_DiffHyp3_S1-A6_1_6408	DiffHyp3_S1-A6_1_6408	S3 B3 T2

What is the Aim of the Analysis ?

Which proteins are over expressed / enriched in comparison to the control in a statistically significant way ?

What is the Aim of the Analysis ?

Which proteins are over expressed / enriched in comparison to the control in a statistically significant way ?

summary

Raw file	Experiment	Sample Type
211111kw_Simeng_Cntr_1_S1-C1_1_6427	Cntr_1_S1-C1_1_6427	S1 B1 T1
211111kw_Simeng_Cntr_1_S1-C2_1_6428	Cntr_1_S1-C2_1_6428	S1 B1 T2
211111kw_Simeng_Cntr_2_S1-C3_1_6429	Cntr_2_S1-C3_1_6429	S1 B2 T1
211111kw_Simeng_Cntr_2_S1-C4_1_6430	Cntr_2_S1-C4_1_6430	S1 B2 T2
211111kw_Simeng_Cntr_3_S1-C5_1_6431	Cntr_3_S1-C5_1_6431	S1 B3 T1
211111kw_Simeng_Cntr_3_S1-C6_1_6432	Cntr_3_S1-C6_1_6432	S1 B3 T2
211111kw_Simeng_Diff1_S1-A7_1_6409	Diff1_S1-A7_1_6409	S2 B1 T1
211111kw_Simeng_Diff1_S1-A8_1_6410	Diff1_S1-A8_1_6410	S2 B1 T2
211111kw_Simeng_Diff2_S1-A10_1_6412	Diff2_S1-A10_1_6412	S2 B2 T1
211111kw_Simeng_Diff2_S1-A9_1_6411	Diff2_S1-A9_1_6411	S2 B2 T2
211111kw_Simeng_Diff3_S1-A11_1_6413	Diff3_S1-A11_1_6413	S2 B3 T1
211111kw_Simeng_Diff3_S1-A12_1_6414	Diff3_S1-A12_1_6414	S2 B3 T2
211111kw_Simeng_DiffHyp1_S1-A1_1_6403	DiffHyp1_S1-A1_1_6403	S3 B1 T1
211111kw_Simeng_DiffHyp1_S1-A2_1_6404	DiffHyp1_S1-A2_1_6404	S3 B1 T2
211111kw_Simeng_DiffHyp2_S1-A3_1_6405	DiffHyp2_S1-A3_1_6405	S3 B2 T1
211111kw_Simeng_DiffHyp2_S1-A4_1_6406	DiffHyp2_S1-A4_1_6406	S3 B2 T2
211111kw_Simeng_DiffHyp3_S1-A5_1_6407	DiffHyp3_S1-A5_1_6407	S3 B3 T1
211111kw_Simeng_DiffHyp3_S1-A6_1_6408	DiffHyp3_S1-A6_1_6408	S3 B3 T2

What is the Aim of the Analysis ?

Which proteins are over expressed / enriched in comparison to the control in a statistically significant way ?

summary

Raw file	Experiment	Sample Type
211111kw_Simeng_Cntr_1_S1-C1_1_6427	Cntr_1_S1-C1_1_6427	S1 B1 T1
211111kw_Simeng_Cntr_1_S1-C2_1_6428	Cntr_1_S1-C2_1_6428	S1 B1 T2
211111kw_Simeng_Cntr_2_S1-C3_1_6429	Cntr_2_S1-C3_1_6429	S1 B2 T1
211111kw_Simeng_Cntr_2_S1-C4_1_6430	Cntr_2_S1-C4_1_6430	S1 B2 T2
211111kw_Simeng_Cntr_3_S1-C5_1_6431	Cntr_3_S1-C5_1_6431	S1 B3 T1
211111kw_Simeng_Cntr_3_S1-C6_1_6432	Cntr_3_S1-C6_1_6432	S1 B3 T2
211111kw_Simeng_Diff1_S1-A7_1_6409	Diff1_S1-A7_1_6409	S2 B1 T1
211111kw_Simeng_Diff1_S1-A8_1_6410	Diff1_S1-A8_1_6410	S2 B1 T2
211111kw_Simeng_Diff2_S1-A10_1_6412	Diff2_S1-A10_1_6412	S2 B2 T1
211111kw_Simeng_Diff2_S1-A9_1_6411	Diff2_S1-A9_1_6411	S2 B2 T2
211111kw_Simeng_Diff3_S1-A11_1_6413	Diff3_S1-A11_1_6413	S2 B3 T1
211111kw_Simeng_Diff3_S1-A12_1_6414	Diff3_S1-A12_1_6414	S2 B3 T2
211111kw_Simeng_DiffHyp1_S1-A1_1_6403	DiffHyp1_S1-A1_1_6403	S3 B1 T1
211111kw_Simeng_DiffHyp1_S1-A2_1_6404	DiffHyp1_S1-A2_1_6404	S3 B1 T2
211111kw_Simeng_DiffHyp2_S1-A3_1_6405	DiffHyp2_S1-A3_1_6405	S3 B2 T1
211111kw_Simeng_DiffHyp2_S1-A4_1_6406	DiffHyp2_S1-A4_1_6406	S3 B2 T2
211111kw_Simeng_DiffHyp3_S1-A5_1_6407	DiffHyp3_S1-A5_1_6407	S3 B3 T1
211111kw_Simeng_DiffHyp3_S1-A6_1_6408	DiffHyp3_S1-A6_1_6408	S3 B3 T2

Comparison between two samples: **t-Test**

t-Test: Is the mean of two groups of measurement repeats the same ?

What is the Aim of the Analysis ?

Which proteins are over expressed / enriched in comparison to the control in a statistically significant way ?

summary

Raw file	Experiment	Sample Type
211111kw_Simeng_Cntr_1_S1-C1_1_6427	Cntr_1_S1-C1_1_6427	S1 B1 T1
211111kw_Simeng_Cntr_1_S1-C2_1_6428	Cntr_1_S1-C2_1_6428	S1 B1 T2
211111kw_Simeng_Cntr_2_S1-C3_1_6429	Cntr_2_S1-C3_1_6429	S1 B2 T1
211111kw_Simeng_Cntr_2_S1-C4_1_6430	Cntr_2_S1-C4_1_6430	S1 B2 T2
211111kw_Simeng_Cntr_3_S1-C5_1_6431	Cntr_3_S1-C5_1_6431	S1 B3 T1
211111kw_Simeng_Cntr_3_S1-C6_1_6432	Cntr_3_S1-C6_1_6432	S1 B3 T2
211111kw_Simeng_Diff1_S1-A7_1_6409	Diff1_S1-A7_1_6409	S2 B1 T1
211111kw_Simeng_Diff1_S1-A8_1_6410	Diff1_S1-A8_1_6410	S2 B1 T2
211111kw_Simeng_Diff2_S1-A10_1_6412	Diff2_S1-A10_1_6412	S2 B2 T1
211111kw_Simeng_Diff2_S1-A9_1_6411	Diff2_S1-A9_1_6411	S2 B2 T2
211111kw_Simeng_Diff3_S1-A11_1_6413	Diff3_S1-A11_1_6413	S2 B3 T1
211111kw_Simeng_Diff3_S1-A12_1_6414	Diff3_S1-A12_1_6414	S2 B3 T2
211111kw_Simeng_DiffHyp1_S1-A1_1_6403	DiffHyp1_S1-A1_1_6403	S3 B1 T1
211111kw_Simeng_DiffHyp1_S1-A2_1_6404	DiffHyp1_S1-A2_1_6404	S3 B1 T2
211111kw_Simeng_DiffHyp2_S1-A3_1_6405	DiffHyp2_S1-A3_1_6405	S3 B2 T1
211111kw_Simeng_DiffHyp2_S1-A4_1_6406	DiffHyp2_S1-A4_1_6406	S3 B2 T2
211111kw_Simeng_DiffHyp3_S1-A5_1_6407	DiffHyp3_S1-A5_1_6407	S3 B3 T1
211111kw_Simeng_DiffHyp3_S1-A6_1_6408	DiffHyp3_S1-A6_1_6408	S3 B3 T2

Comparison between two samples: **t-Test**

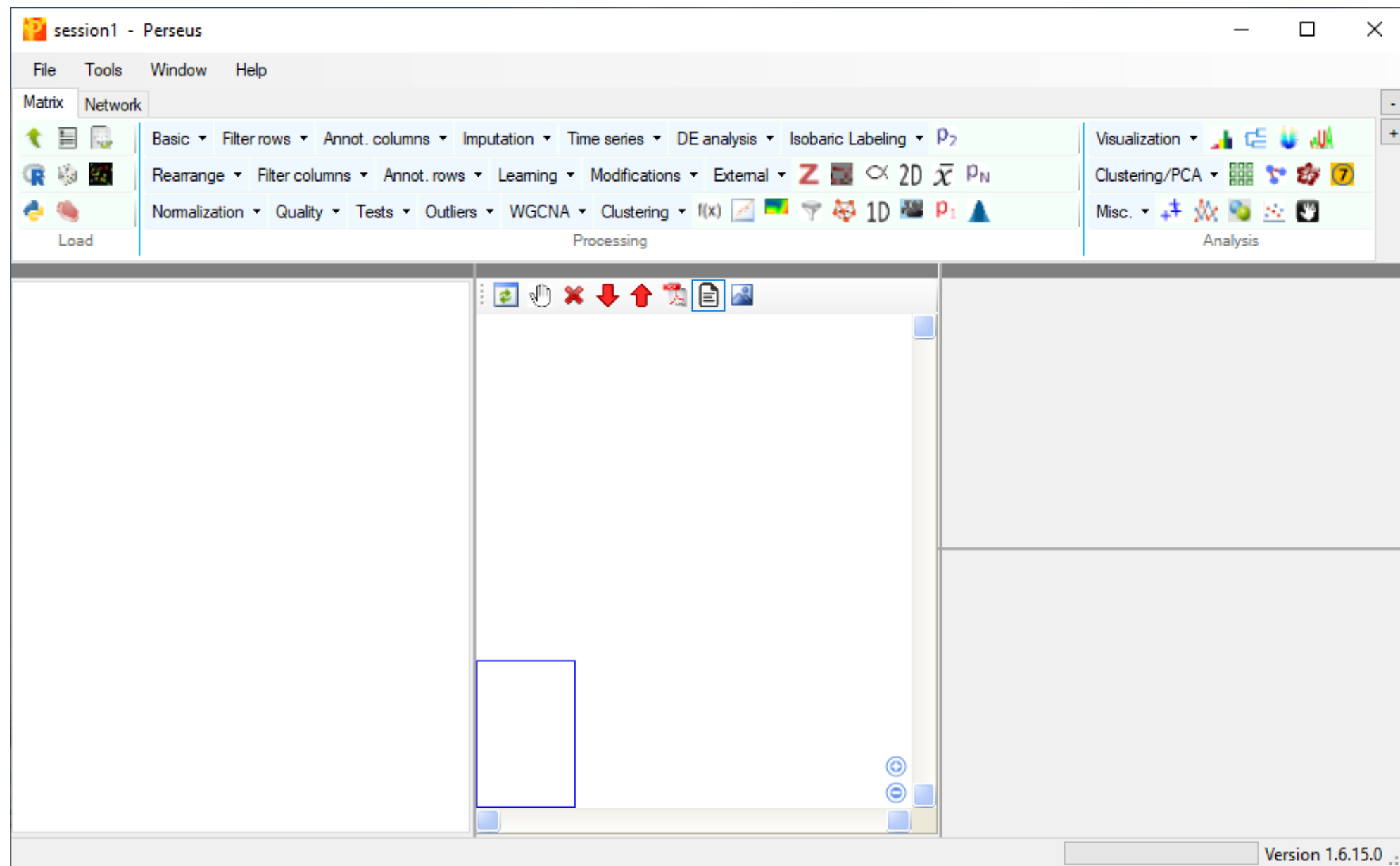
t-Test: Is the mean of two groups of measurement repeats the same ?

Comparison between several samples:

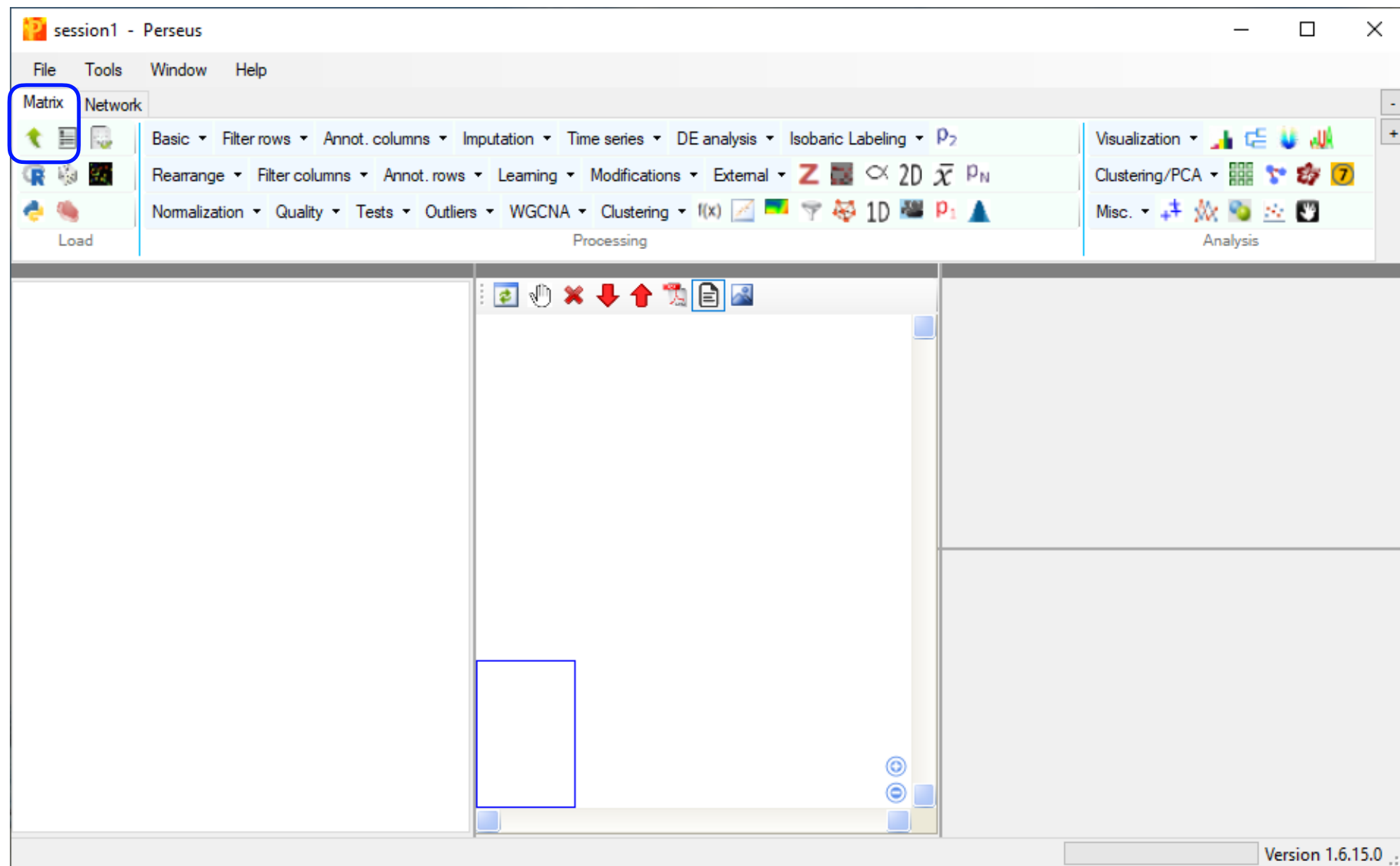
ANOVA - Test

ANOVA-Test: Are the means of several groups of measurement repeats the same ?

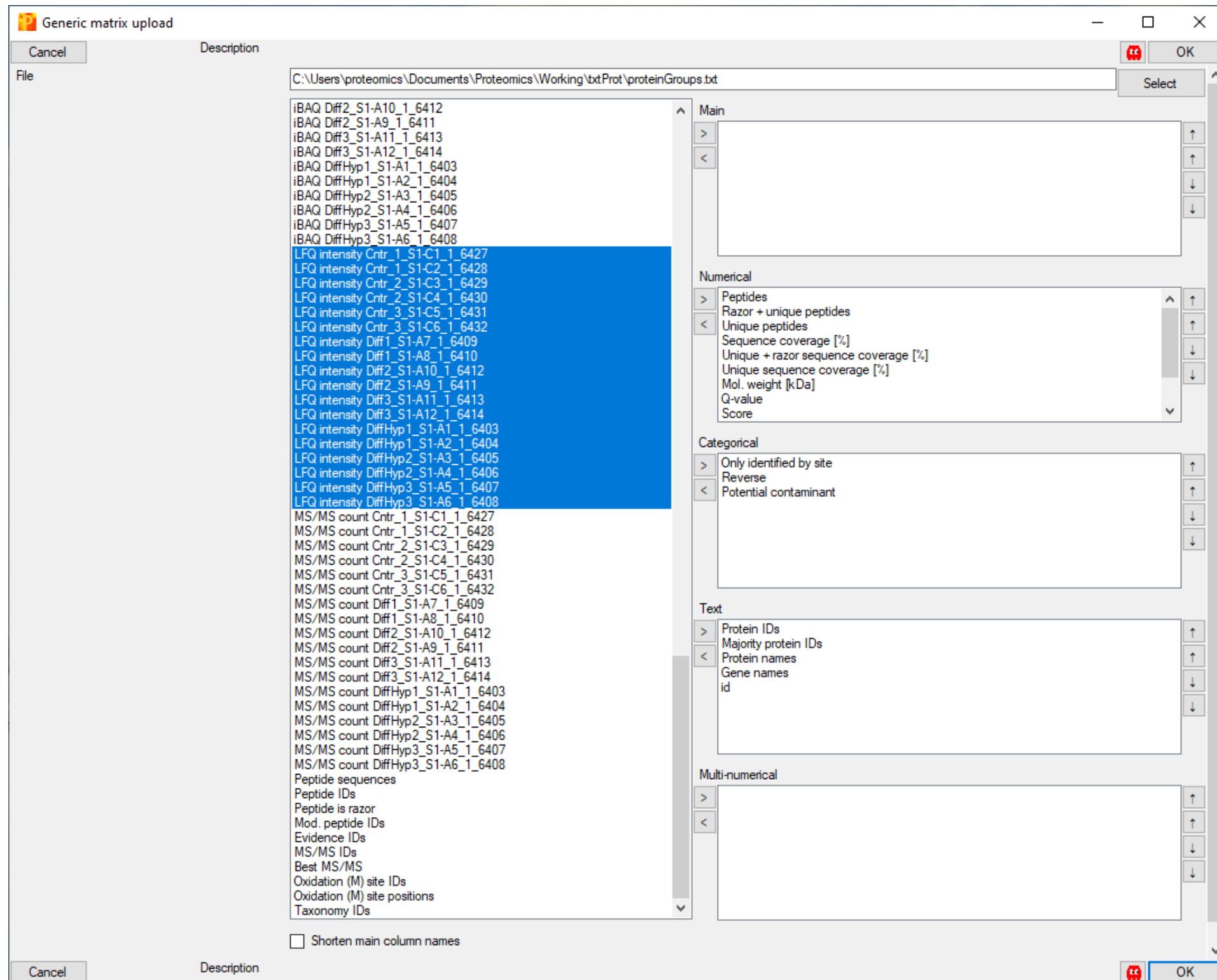
Start Perseus and Load Data: proteinGroups.txt



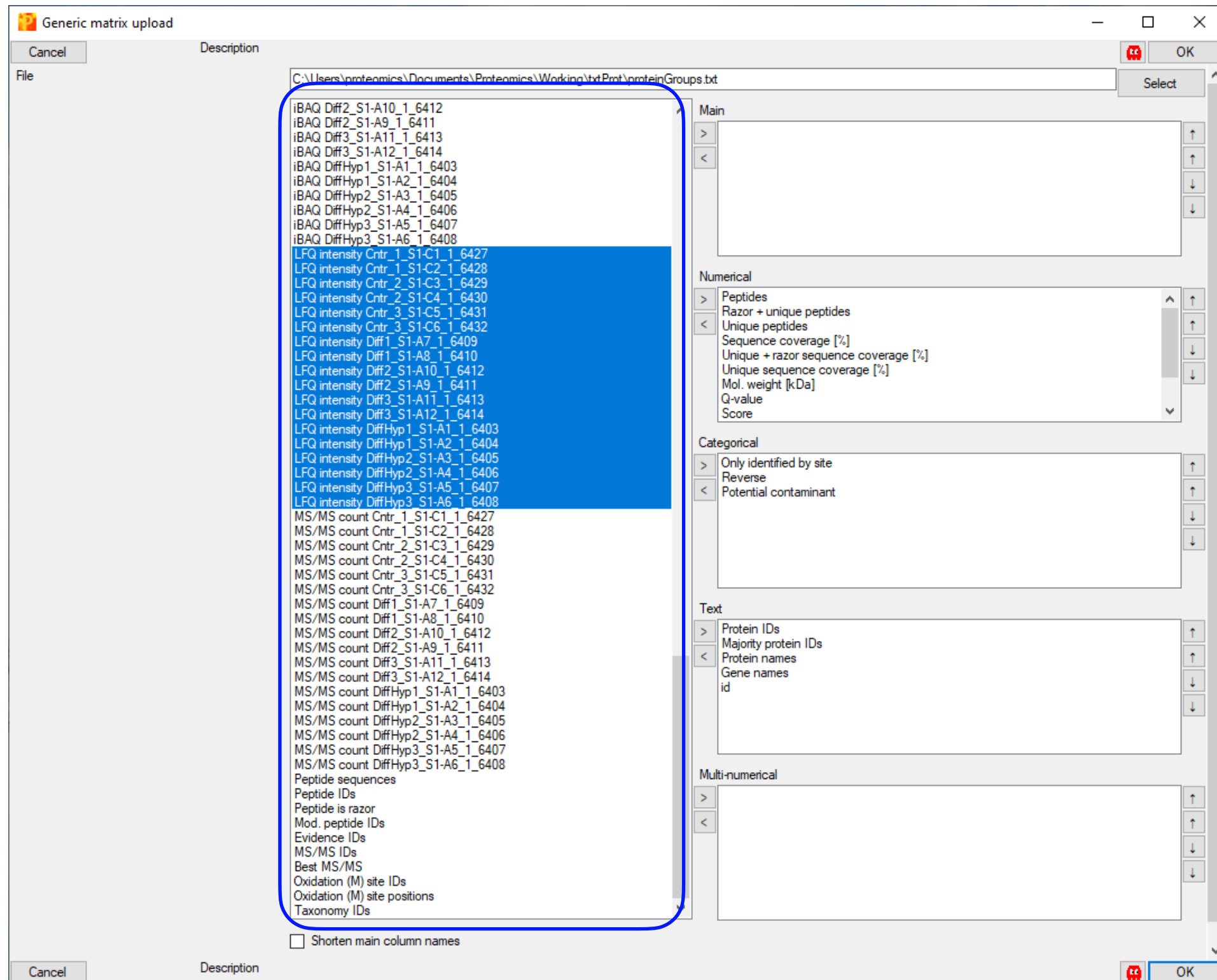
Start Perseus and Load Data: proteinGroups.txt



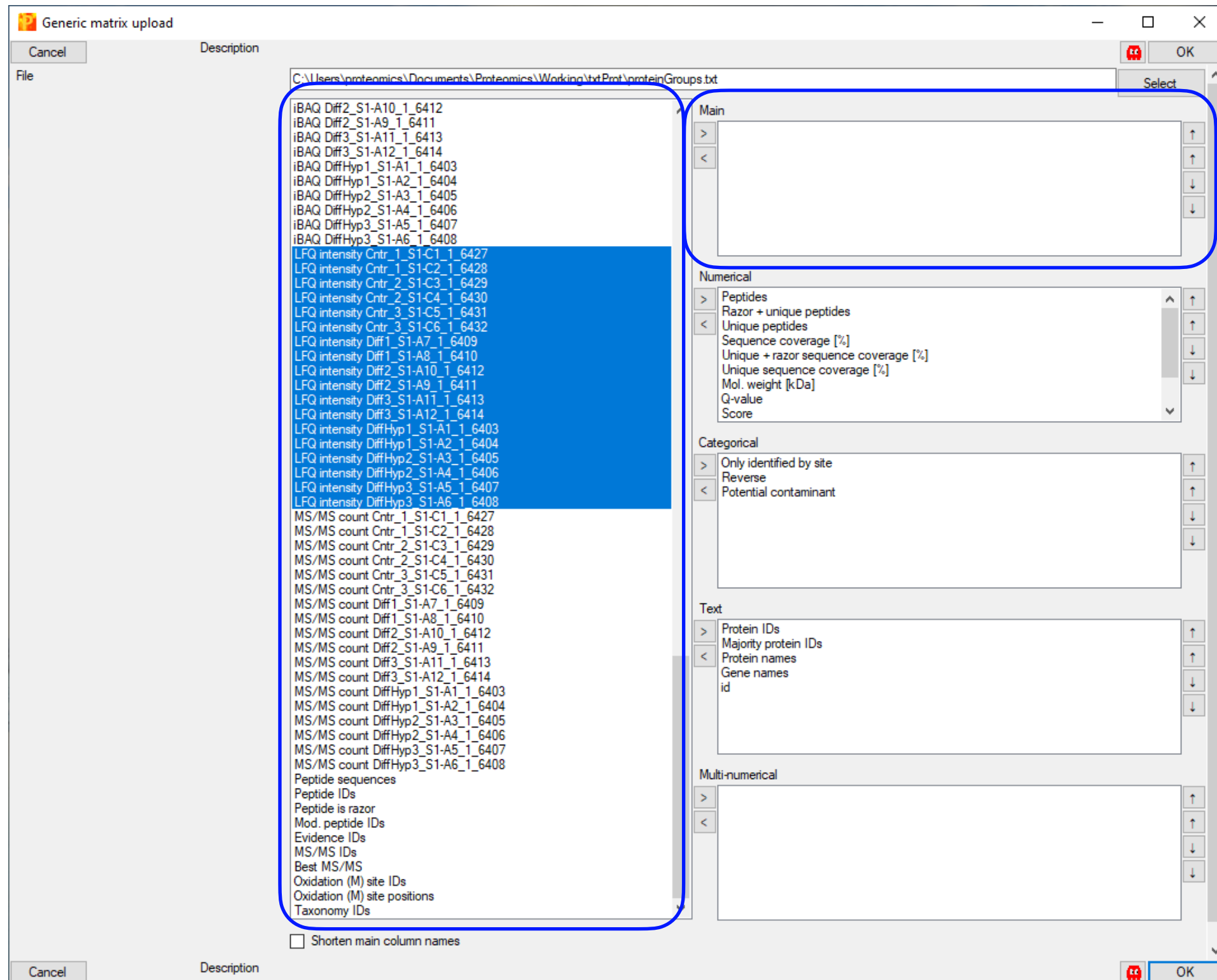
Start Perseus and Load Data: proteinGroups.txt



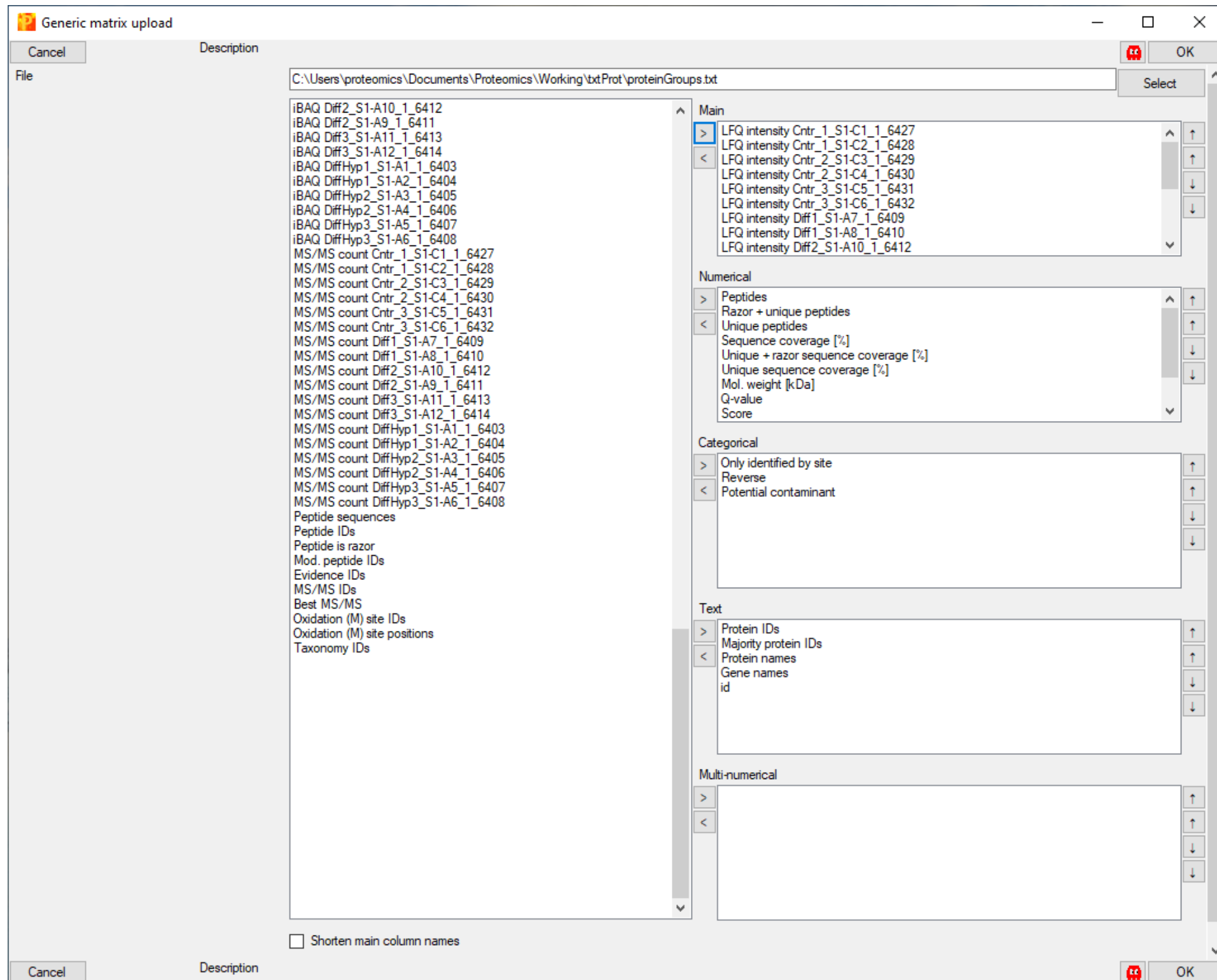
Start Perseus and Load Data: proteinGroups.txt



Start Perseus and Load Data: proteinGroups.txt



Start Perseus and Load Data: proteinGroups.txt



Start Perseus and Load Data: proteinGroups.txt

Generic matrix upload

Cancel Description

File C:\Users\proteomics\Documents\Proteomics\Working\txtProt\proteinGroups.txt Select

iBAQ Diff2_S1-A10_1_6412
 iBAQ Diff2_S1-A9_1_6411
 iBAQ Diff3_S1-A11_1_6413
 iBAQ Diff3_S1-A12_1_6414
 iBAQ DiffHyp1_S1-A1_1_6403
 iBAQ DiffHyp1_S1-A2_1_6404
 iBAQ DiffHyp2_S1-A3_1_6405
 iBAQ DiffHyp2_S1-A4_1_6406
 iBAQ DiffHyp3_S1-A5_1_6407
 iBAQ DiffHyp3_S1-A6_1_6408
 MS/MS count Cntr_1_S1-C1_1_6427
 MS/MS count Cntr_1_S1-C2_1_6428
 MS/MS count Cntr_2_S1-C3_1_6429
 MS/MS count Cntr_2_S1-C4_1_6430
 MS/MS count Cntr_3_S1-C5_1_6431
 MS/MS count Cntr_3_S1-C6_1_6432
 MS/MS count Diff1_S1-A7_1_6409
 MS/MS count Diff1_S1-A8_1_6410
 MS/MS count Diff2_S1-A10_1_6412
 MS/MS count Diff2_S1-A9_1_6411
 MS/MS count Diff3_S1-A11_1_6413
 MS/MS count Diff3_S1-A12_1_6414
 MS/MS count DiffHyp1_S1-A1_1_6403
 MS/MS count DiffHyp1_S1-A2_1_6404
 MS/MS count DiffHyp2_S1-A3_1_6405
 MS/MS count DiffHyp2_S1-A4_1_6406
 MS/MS count DiffHyp3_S1-A5_1_6407
 MS/MS count DiffHyp3_S1-A6_1_6408
 Peptide sequences
 Peptide IDs
 Peptide is razor
 Mod. peptide IDs
 Evidence IDs
 MS/MS IDs
 Best MS/MS
 Oxidation (M) site IDs
 Oxidation (M) site positions
 Taxonomy IDs

Main
 > Labeled intensity Cntr_1_S1-C1_1_6427
 < Labeled intensity Cntr_1_S1-C2_1_6428
 Labeled intensity Cntr_2_S1-C3_1_6429
 Labeled intensity Cntr_2_S1-C4_1_6430
 Labeled intensity Cntr_3_S1-C5_1_6431
 Labeled intensity Cntr_3_S1-C6_1_6432
 Labeled intensity Diff1_S1-A7_1_6409
 Labeled intensity Diff1_S1-A8_1_6410
 Labeled intensity Diff2_S1-A10_1_6412

Numerical
 > Peptides
 < Razor + unique peptides
 Unique peptides
 Sequence coverage [%]
 Unique + razor sequence coverage [%]
 Unique sequence coverage [%]
 Mol. weight [kDa]
 Q-value
 Score

Categorical
 > Only identified by site
 < Reverse
 Potential contaminant

Text
 > Protein IDs
 < Majority protein IDs
 Protein names
 Gene names
 id

Multi-numerical
 >
 <

☐ Shorten main column names

Cancel Description OK

Start Perseus and Load Data: proteinGroups.txt

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,596 items

100% ↑

matrix1

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,596)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Version 1.6.15.0

Start Perseus and Load Data: proteinGroups.txt

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,596 items

100% ↑

Generic matrix u...

matrix1

matrix1

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,596)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Version 1.6.15.0

Start Perseus and Load Data: proteinGroups.txt

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,596 items

100% ↑

matrix1

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,596)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Version 1.6.15.0

Start Perseus and Load Data: proteinGroups.txt

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,596 items

100% ↑

matrix1

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,596)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Version 1.6.15.0

Start Perseus and Load Data: proteinGroups.txt

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,596 items

100% ↑

matrix1

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,596)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Generic matrix u...

matrix1

Version 1.6.15.0

Start Perseus and Load Data: proteinGroups.txt

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,596 items

100% ↑

matrix1

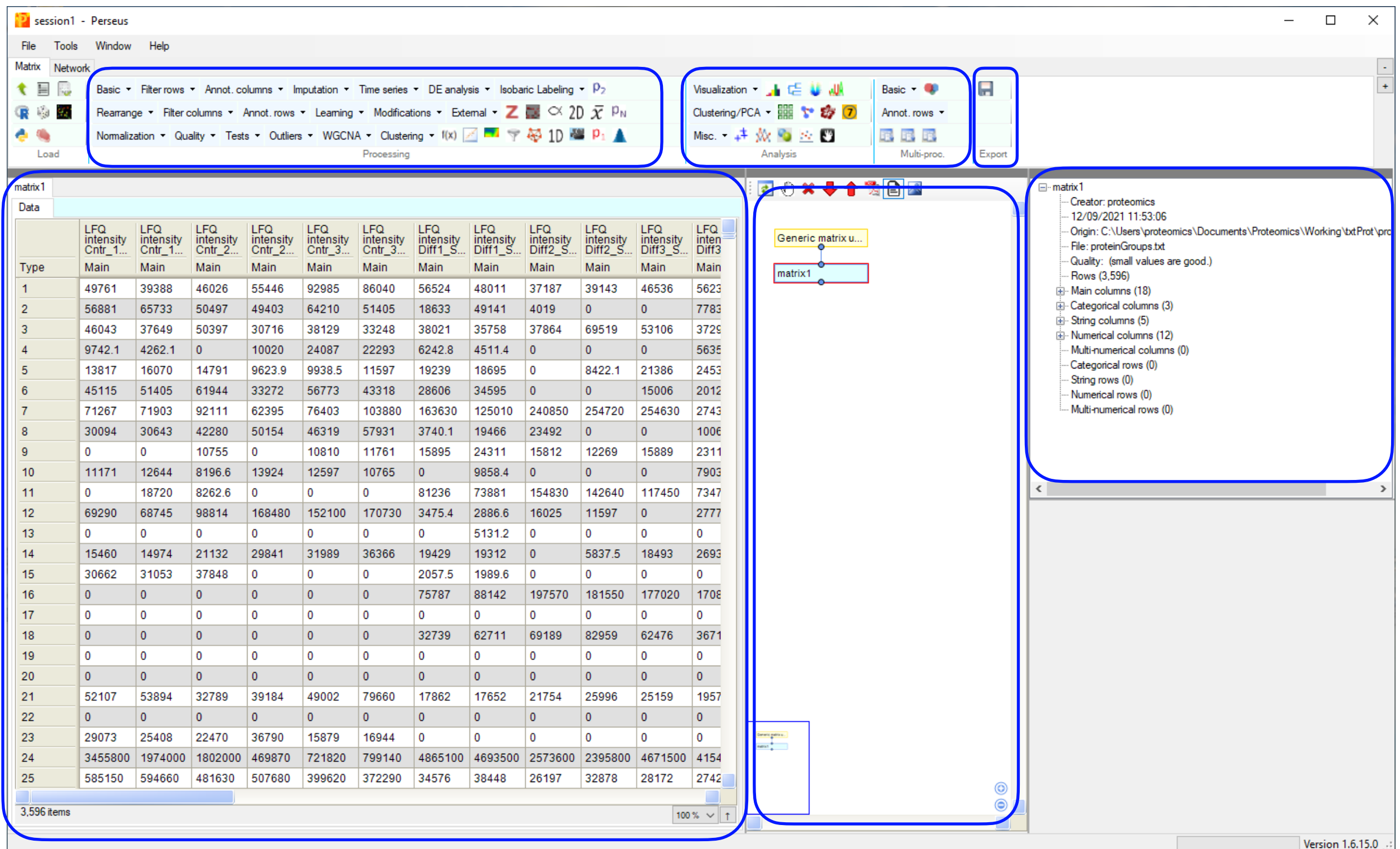
- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,596)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Generic matrix u...

matrix1

Version 1.6.15.0

Start Perseus and Load Data: proteinGroups.txt



The screenshot shows the Perseus software interface with the 'Load' step selected. The 'Data' tab is active, displaying a table of protein groups. The 'Matrix' tab is also visible, showing a network diagram. The 'Processing' and 'Analysis' tabs are also visible.

Matrix

- Basic
- Filter rows
- Annot. columns
- Imputation
- Time series
- DE analysis
- Isobaric Labeling
- P₂
- Rearrange
- Filter columns
- Annot. rows
- Learning
- Modifications
- External
- Z
- 2D
- X
- P_N
- Normalization
- Quality
- Tests
- Outliers
- WGCNA
- Clustering
- f(x)
- 1D
- P₁
- Analysis
- Multi-proc.
- Export

matrix1

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,596 items

Version 1.6.15.0

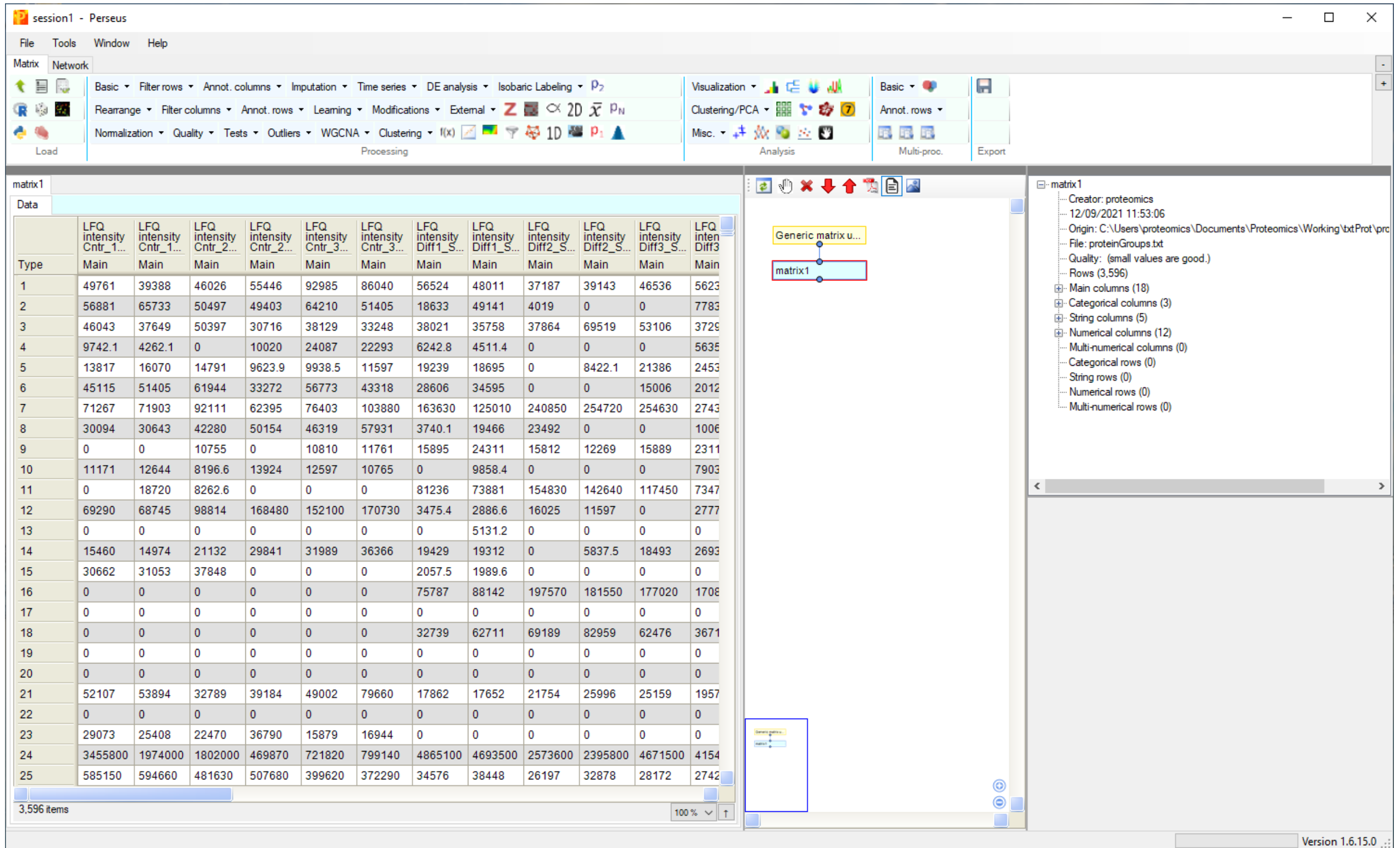


Filter rows (proteins) which are not relevant : **Filter rows > on categorical column**

Proteins, that are identified in the reverse database search and only by site (by a modification)

Filter rows (proteins) which are not relevant : **Filter rows > on categorical column**

Proteins, that are identified in the reverse database search and only by site (by a modification)



The screenshot displays the Perseus software interface, version 1.6.15.0, with a session named 'session1'. The main window shows a data matrix with 25 rows and 13 columns. The columns are labeled 'Type', 'LFQ intensity Cntr_1...', 'LFQ intensity Cntr_2...', 'LFQ intensity Cntr_3...', 'LFQ intensity Diff1_S...', 'LFQ intensity Diff2_S...', and 'LFQ intensity Diff3_S...'. The rows are numbered 1 to 25. The status bar at the bottom indicates '3,596 items'.

On the right side, the 'matrix1' panel shows a workflow diagram with two nodes: 'Generic matrix u...' and 'matrix1'. The 'matrix1' node is highlighted with a red box. Below the workflow, a summary of the matrix data is displayed:

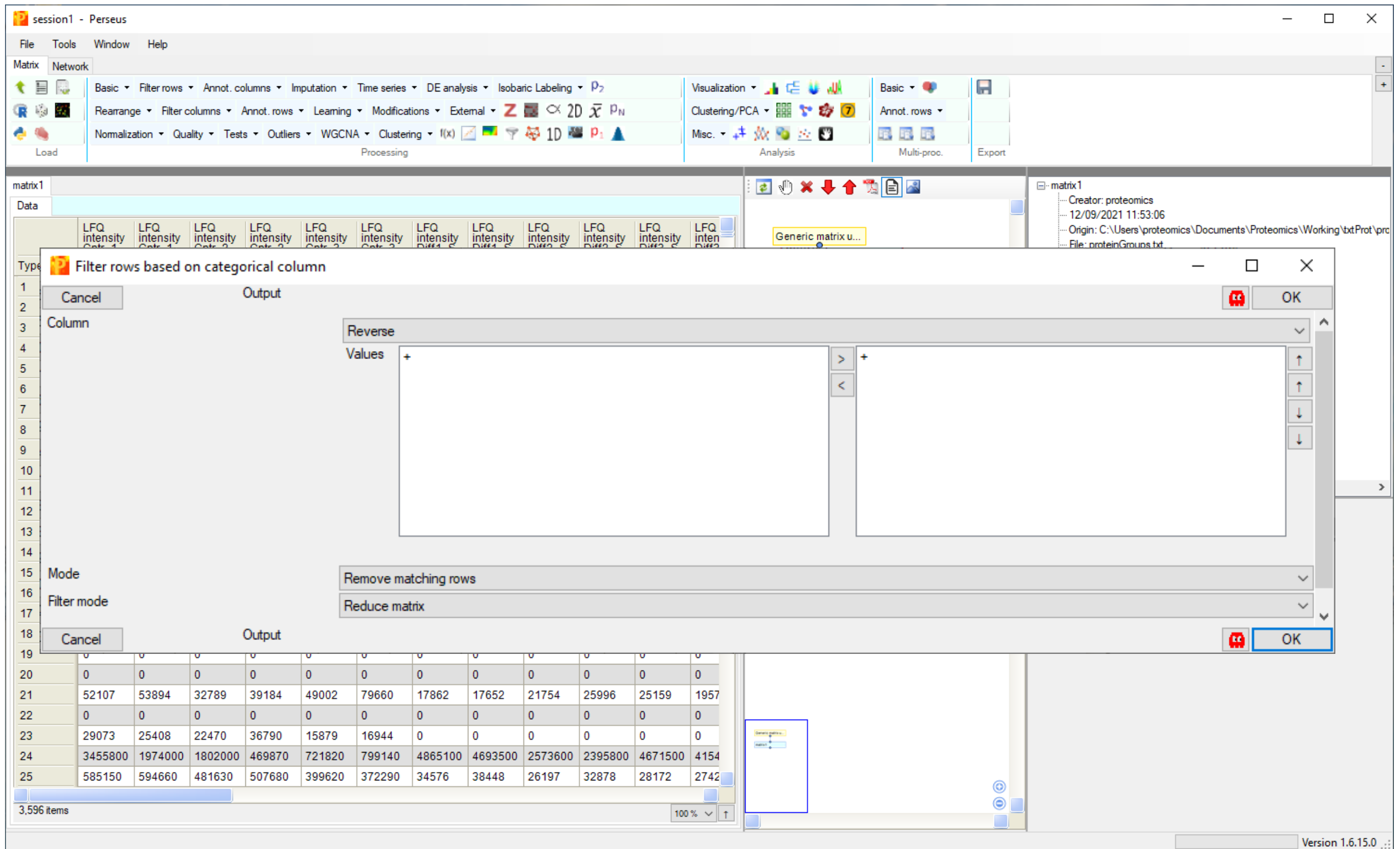
- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,596)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Proteins, that are identified in the reverse database search and only by site (by a modification)

The screenshot displays the Perseus software interface. At the top, there is a menu bar with 'File', 'Tools', 'Window', and 'Help'. Below this is a toolbar with various icons for file operations and analysis. The main window is divided into several panels. On the left, there is a 'matrix1' panel showing a data matrix with columns labeled 'Type', 'Main', and 'LFQ intensity'. The matrix contains numerical data for 25 rows. In the center, a 'Filter rows' menu is open, listing several filtering options: 'Filter rows based on categorical column', 'Filter rows based on numerical/main column', 'Filter rows based on text column', 'Filter rows based on valid values', 'Filter rows based on duplicate values', and 'Filter rows based on random sampling'. On the right, there is a 'Visualization' panel with icons for different visualization methods, and a 'Basic' panel with icons for basic analysis tools. At the bottom right, there is a 'matrix1' panel showing a summary of the data matrix, including the number of rows (3,596) and columns (18), and a list of column types (Main, Categorical, String, Numerical, Multi-numerical).

Filter rows (proteins) which are not relevant : **Filter rows > on categorical column**

Proteins, that are identified in the reverse database search and only by site (by a modification)

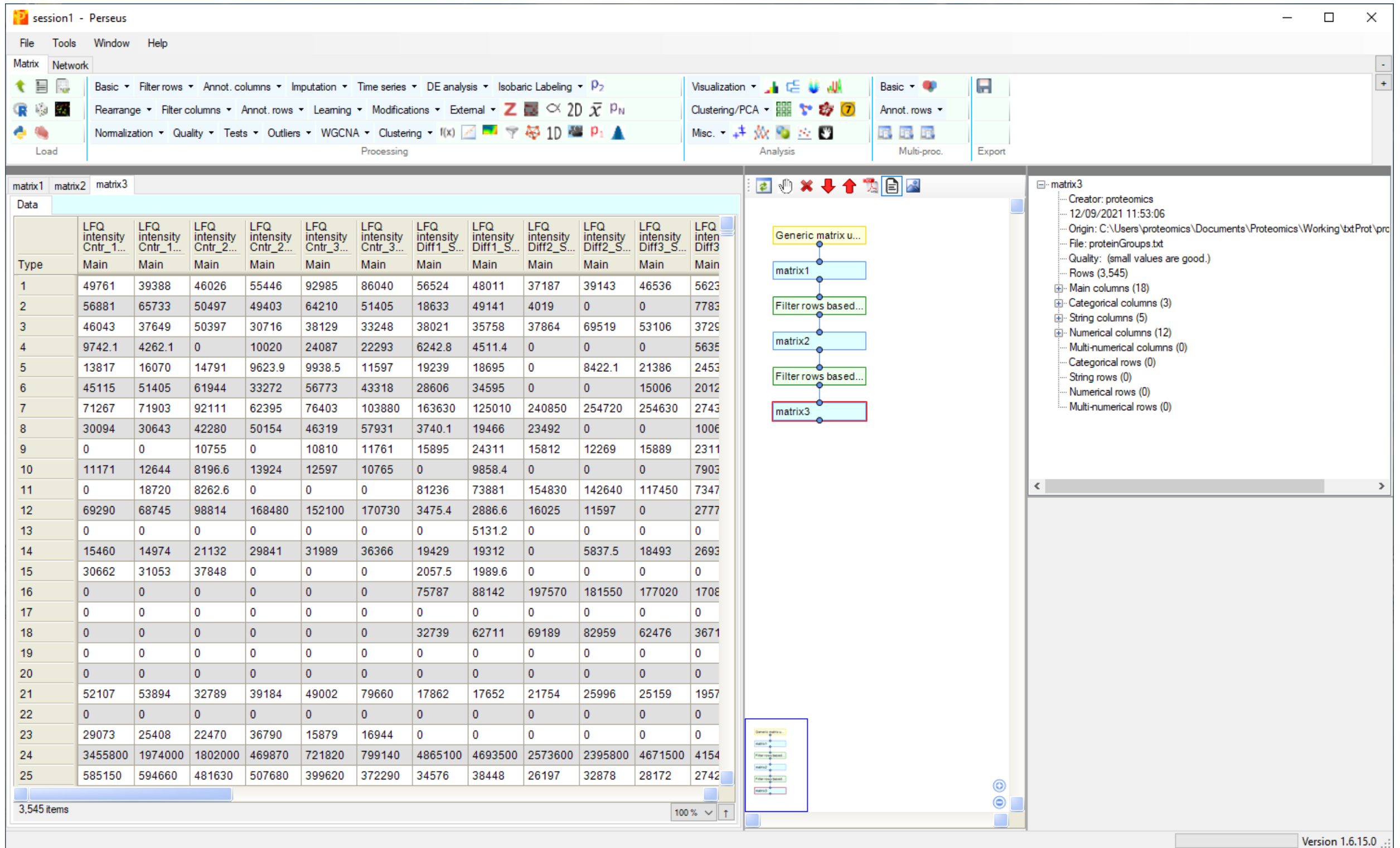


The screenshot shows the Perseus software interface with a dialog box titled "Filter rows based on categorical column" open. The dialog box has a "Cancel" button and an "OK" button. It contains a "Column" dropdown menu set to "Reverse", a "Values" input field with a "+" sign, and a "Mode" dropdown menu set to "Remove matching rows". The "Filter mode" dropdown menu is set to "Reduce matrix". The background shows a data table with columns for LFQ intensity and various modifications. The status bar at the bottom indicates "3,596 items" and "Version 1.6.15.0".

Type	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity	LFQ intensity
1	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0
3	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
4	0	0	0	0	0	0	0	0	0	0	0	0
5	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
6	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
7	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

Filter rows (proteins) which are not relevant : **Filter rows > on categorical column**

Proteins, that are identified in the reverse database search and only by site (by a modification)



The screenshot displays the Perseus software interface, version 1.6.15.0. The main window shows a data matrix with 25 rows and 13 columns. The columns are labeled 'Type', 'LFQ intensity Cntr_1...', 'LFQ intensity Cntr_2...', 'LFQ intensity Cntr_3...', 'LFQ intensity Diff1_S...', 'LFQ intensity Diff2_S...', and 'LFQ intensity Diff3_S...'. The rows are numbered 1 to 25. The matrix is titled 'matrix3'.

On the right side, there is a workflow diagram showing the process of filtering rows based on categorical columns. The workflow starts with 'Generic matrix u...' and proceeds through 'matrix1', 'Filter rows based...', 'matrix2', 'Filter rows based...', and finally 'matrix3'.

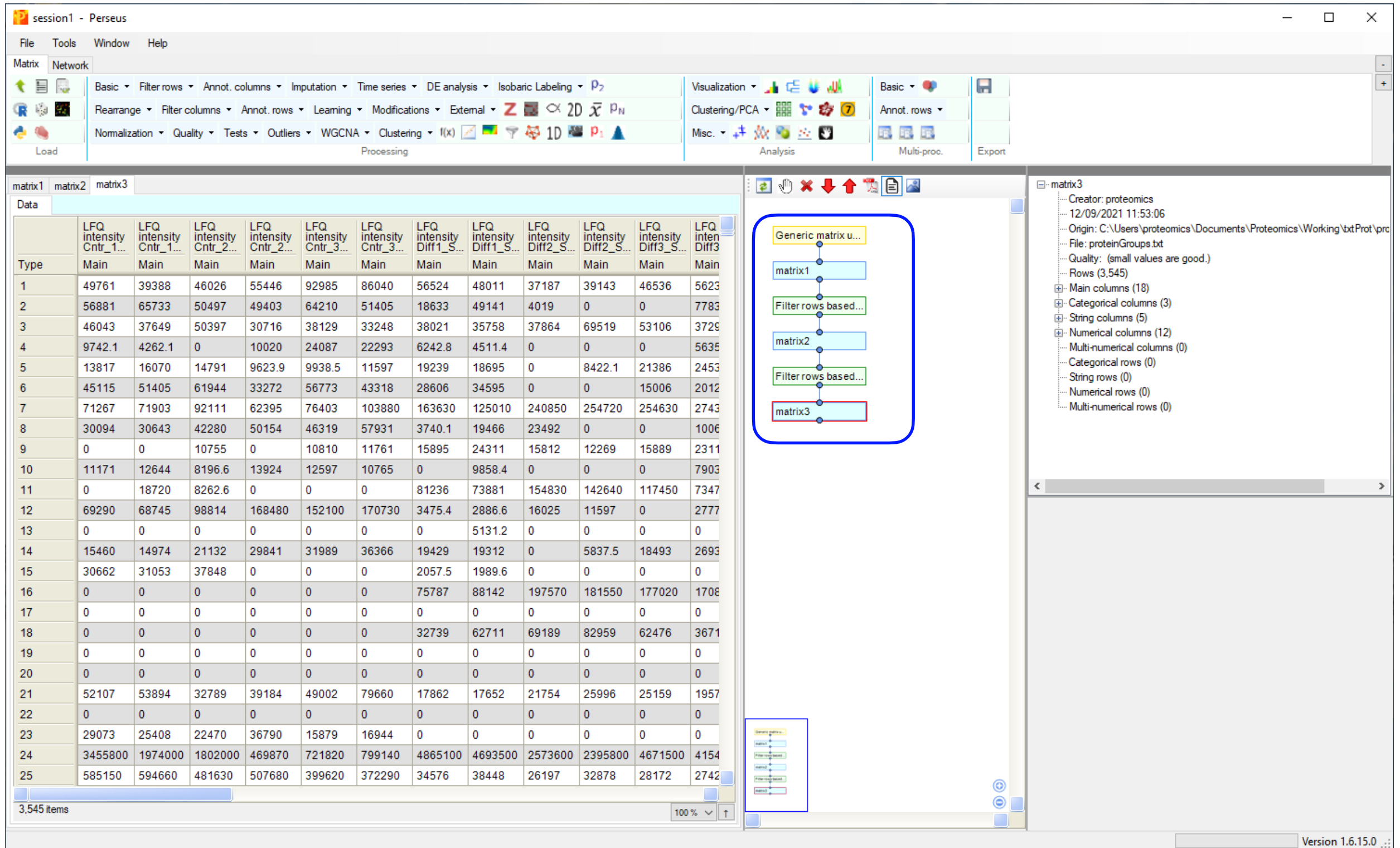
Below the workflow diagram, there is a summary of the matrix statistics:

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,545)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

The bottom status bar indicates '3,545 items' and '100%' zoom.

Filter rows (proteins) which are not relevant : **Filter rows > on categorical column**

Proteins, that are identified in the reverse database search and only by site (by a modification)



The screenshot displays the Perseus software interface, version 1.6.15.0. The main window shows a data matrix with 25 rows and 13 columns. The columns are labeled 'LFQ intensity Cntr_1...' through 'LFQ intensity Cntr_13...'. The rows are numbered 1 to 25. The matrix is currently selected, and the 'Filter rows' button is highlighted in the 'Processing' tab.

On the right side, the 'matrix3' panel shows a workflow diagram. The diagram starts with 'Generic matrix u...' and proceeds through 'matrix1', 'Filter rows based...', 'matrix2', 'Filter rows based...', and finally 'matrix3'. The 'matrix3' panel also displays a summary of the data: 3,545 items, 18 main columns, 3 categorical columns, 5 string columns, 12 numerical columns, 0 multi-numerical columns, 0 categorical rows, 0 string rows, 0 numerical rows, and 0 multi-numerical rows.

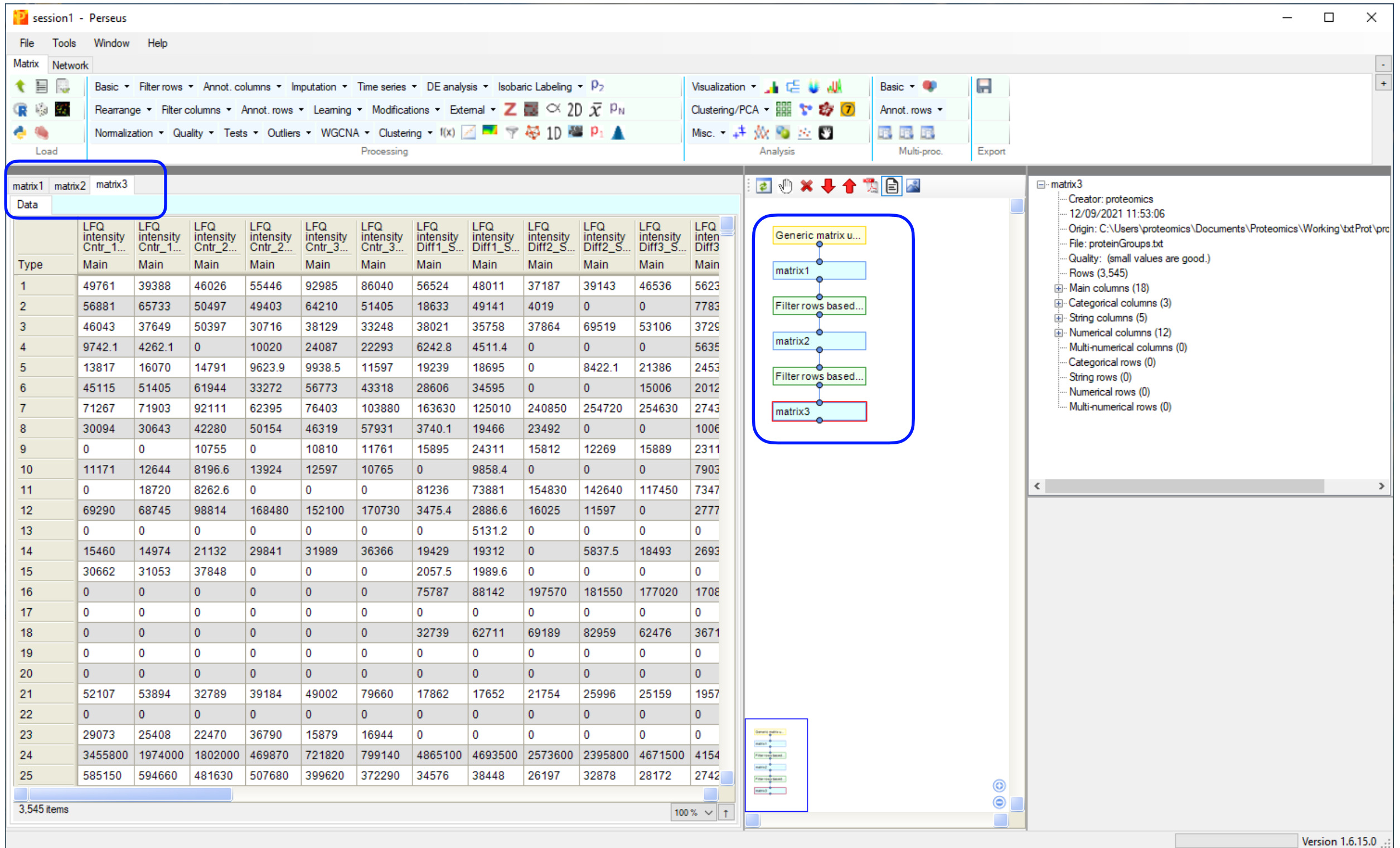
Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,545 items

Version 1.6.15.0

Filter rows (proteins) which are not relevant : **Filter rows > on categorical column**

Proteins, that are identified in the reverse database search and only by site (by a modification)



The screenshot displays the Perseus software interface, version 1.6.15.0. The main window shows a data matrix with 25 rows and 13 columns. The columns are labeled 'Type', 'LFQ intensity Cntr_1...', 'LFQ intensity Cntr_2...', 'LFQ intensity Cntr_3...', 'LFQ intensity Diff1_S...', 'LFQ intensity Diff2_S...', and 'LFQ intensity Diff3_S...'. The rows are numbered 1 to 25. The 'Type' column contains values like 'Main', 'Main'.

On the right side, there is a workflow diagram showing the process of filtering rows based on categorical columns. The workflow starts with 'Generic matrix u...' and proceeds through 'matrix1', 'Filter rows based...', 'matrix2', 'Filter rows based...', and finally 'matrix3'. The 'matrix3' node is highlighted with a red border.

Below the workflow diagram, there is a summary of the data matrix statistics:

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,545)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

The bottom status bar indicates '3,545 items' and '100%' zoom.



Convert the Statistical Distribution of Intensity Values into a Gaußsche Normal Distribution: **Basic > Transform > log2(x)**

t-Test and ANOVA test require normal distributed data

t-Test and ANOVA test require normal distributed data

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1 matrix2 matrix3

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2	56881	65733	50497	49403	64210	51405	18633	49141	4019	0	0	7783
3	46043	37649	50397	30716	38129	33248	38021	35758	37864	69519	53106	3729
4	9742.1	4262.1	0	10020	24087	22293	6242.8	4511.4	0	0	0	5635
5	13817	16070	14791	9623.9	9938.5	11597	19239	18695	0	8422.1	21386	2453
6	45115	51405	61944	33272	56773	43318	28606	34595	0	0	15006	2012
7	71267	71903	92111	62395	76403	103880	163630	125010	240850	254720	254630	2743
8	30094	30643	42280	50154	46319	57931	3740.1	19466	23492	0	0	1006
9	0	0	10755	0	10810	11761	15895	24311	15812	12269	15889	2311
10	11171	12644	8196.6	13924	12597	10765	0	9858.4	0	0	0	7903
11	0	18720	8262.6	0	0	0	81236	73881	154830	142640	117450	7347
12	69290	68745	98814	168480	152100	170730	3475.4	2886.6	16025	11597	0	2777
13	0	0	0	0	0	0	0	5131.2	0	0	0	0
14	15460	14974	21132	29841	31989	36366	19429	19312	0	5837.5	18493	2693
15	30662	31053	37848	0	0	0	2057.5	1989.6	0	0	0	0
16	0	0	0	0	0	0	75787	88142	197570	181550	177020	1708
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	32739	62711	69189	82959	62476	3671
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742

3,545 items

100 %

Generic matrix u...

matrix1

Filter rows based...

matrix2

Filter rows based...

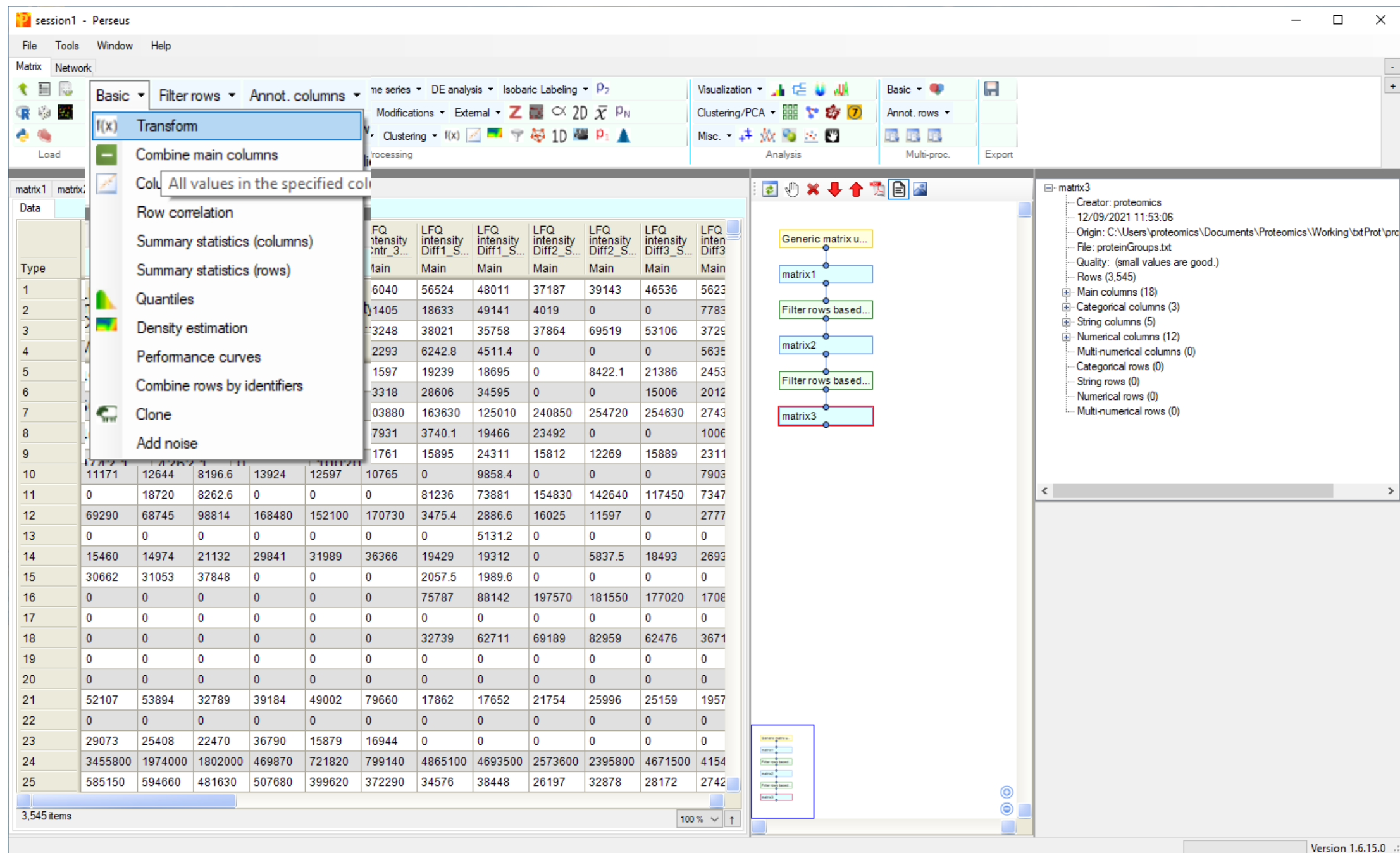
matrix3

matrix3

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\btProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,545)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

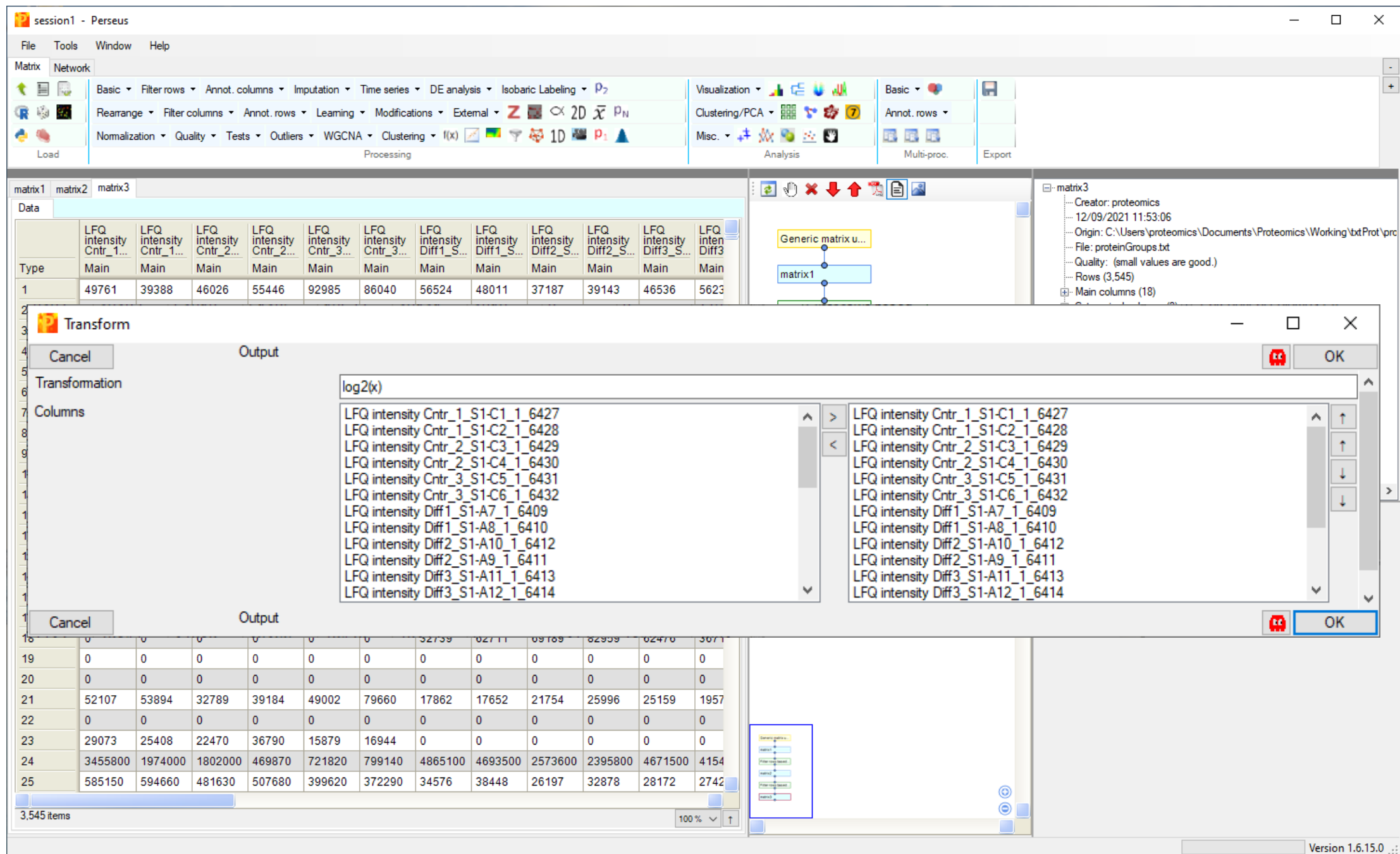
Version 1.6.15.0

t-Test and ANOVA test require normal distributed data



Convert the Statistical Distribution of Intensity Values into a Gaußsche Normal Distribution: **Basic > Transform > log2(x)**

t-Test and ANOVA test require normal distributed data



The screenshot shows the Perseus software interface with the 'Transform' dialog box open. The 'Transformation' field is set to 'log2(x)'. The 'Columns' list on the right includes various intensity and difference values. The background shows a data matrix with columns labeled 'LFQ intensity Cntr_1...', 'LFQ intensity Cntr_2...', 'LFQ intensity Cntr_3...', 'LFQ intensity Diff1_S...', 'LFQ intensity Diff2_S...', and 'LFQ intensity Diff3_S...'. The status bar at the bottom indicates '3,545 items' and 'Version 1.6.15.0'.

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...
1	49761	39388	46026	55446	92985	86040	56524	48011	37187	39143	46536	5623
2												
3												
4												
5												
6												
7												
8												
9												
10												
11												
12												
13												
14												
15												
16												
17												
18												
19	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0
21	52107	53894	32789	39184	49002	79660	17862	17652	21754	25996	25159	1957
22	0	0	0	0	0	0	0	0	0	0	0	0
23	29073	25408	22470	36790	15879	16944	0	0	0	0	0	0
24	3455800	1974000	1802000	469870	721820	799140	4865100	4693500	2573600	2395800	4671500	4154
25	585150	594660	481630	507680	399620	372290	34576	38448	26197	32878	28172	2742



Sample Grouping (technical and biological replicates !): **Annot. Rows >**
Categorical Annotation Row

Sample Grouping (technical and biological replicates !): **Annot. Rows > Categorical Annotation Row**

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing Analysis Multi-proc. Export

matrix1 matrix2 matrix3 matrix4

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
1	15.6027	15.2655	15.4902	15.7588	16.5047	16.3927	15.7866	15.5511	15.1825	15.2565	15.5061	15.7
2	15.7957	16.0043	15.6239	15.5923	15.9705	15.6496	14.1856	15.5846	11.9726	NaN	NaN	16.2
3	15.4907	15.2003	15.621	14.9067	15.2186	15.021	15.2145	15.126	15.2085	16.0851	15.6966	15.1
4	13.25	12.0573	NaN	13.2906	14.556	14.4443	12.608	12.1394	NaN	NaN	NaN	12.4
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	NaN	13.04	14.3844	14.5
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	NaN	NaN	13.8733	14.2
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	NaN	NaN	13.2
9	NaN	NaN	13.3927	NaN	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	NaN	13.2671	NaN	NaN	NaN	12.9
11	NaN	14.1923	13.0124	NaN	NaN	NaN	16.3098	16.1729	17.2403	17.122	16.8417	16.1
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	NaN	11.4
13	NaN	NaN	NaN	NaN	NaN	NaN	NaN	12.3251	NaN	NaN	NaN	NaN
14	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	NaN	12.5111	14.1747	14.7
15	14.9042	14.9224	15.2079	NaN	NaN	NaN	11.0067	10.9583	NaN	NaN	NaN	NaN
16	NaN	NaN	NaN	NaN	NaN	NaN	16.2097	16.4275	17.592	17.47	17.4336	17.3
17	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
18	NaN	NaN	NaN	NaN	NaN	NaN	14.9987	15.9364	16.0783	16.3401	15.931	15.1
19	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
20	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
21	15.6692	15.7178	15.0009	15.258	15.5806	16.2816	14.1246	14.1075	14.409	14.666	14.6188	14.2
22	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
23	14.8274	14.633	14.4557	15.167	13.9548	14.0485	NaN	NaN	NaN	NaN	NaN	NaN
24	21.7206	20.9127	20.7812	18.8419	19.4613	19.6081	22.214	22.1622	21.2954	21.1921	22.1555	21.9
25	19.1584	19.1817	18.8776	18.9536	18.6083	18.5061	15.0775	15.2306	14.6771	15.0048	14.782	14.7

3,545 items

100 %

matrix4

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,545)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (0)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Generic matrix u...

matrix1

Filter rows based...

matrix2

Filter rows based...

matrix3

Transform

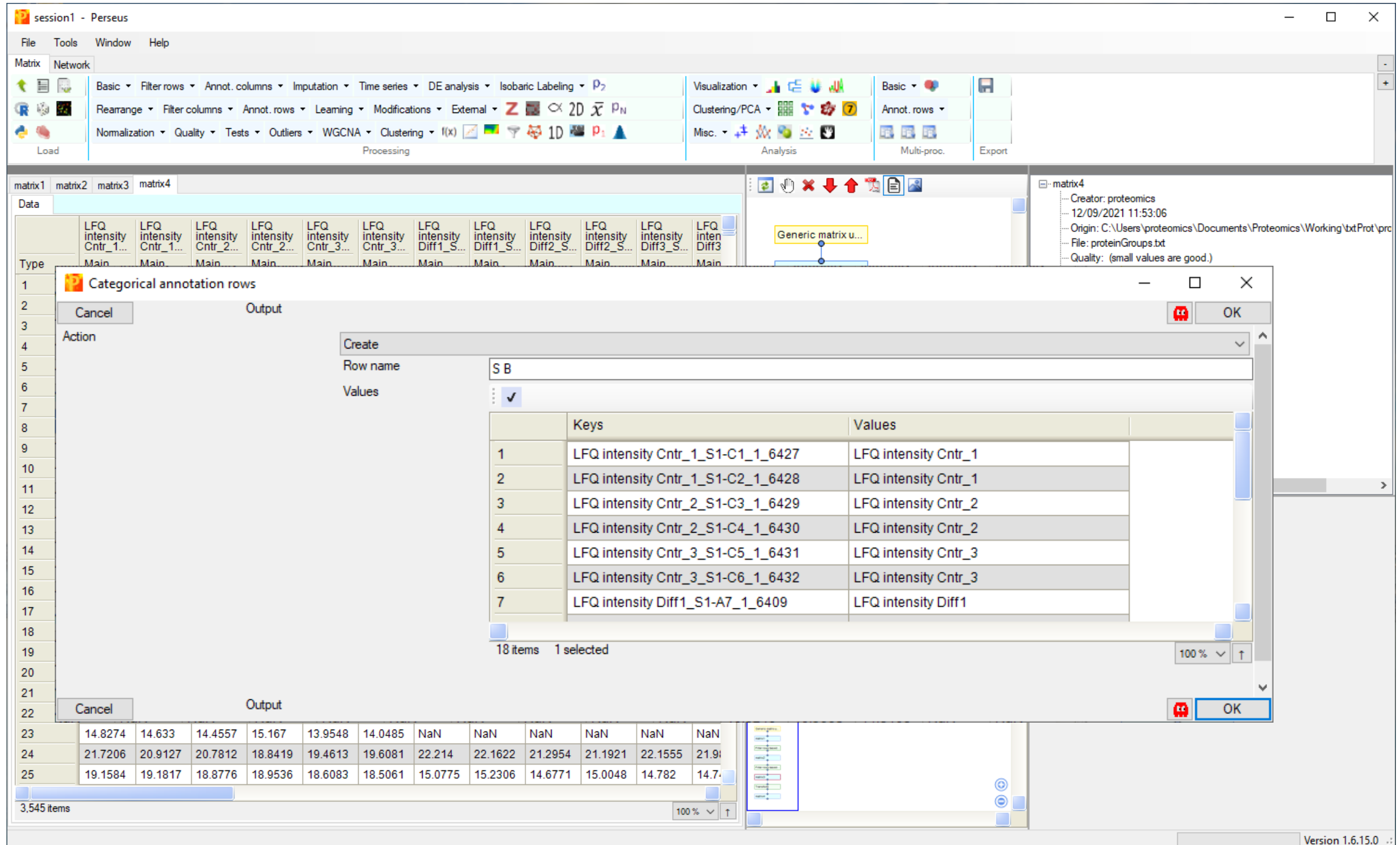
matrix4

Version 1.6.15.0

Sample Grouping (technical and biological replicates !): **Annot. Rows > Categorical Annotation Row**

The screenshot displays the Perseus software interface. The main window shows a data matrix with columns for LFQ intensity and various annotations. A context menu is open over the matrix, offering options like 'Categorical annotation rows', 'Correlate', 'Join terms in categorical row', and 'Extract to matrix'. On the right, a workflow diagram shows the sequence of operations: 'Generic matrix u...' leading to 'matrix1', 'matrix2', 'matrix3', and 'matrix4', with intermediate steps like 'Filter rows based...' and 'Transform'. The bottom right corner indicates the software version is 1.6.15.0.

Sample Grouping (technical and biological replicates !): **Annot. Rows > Categorical Annotation Row**

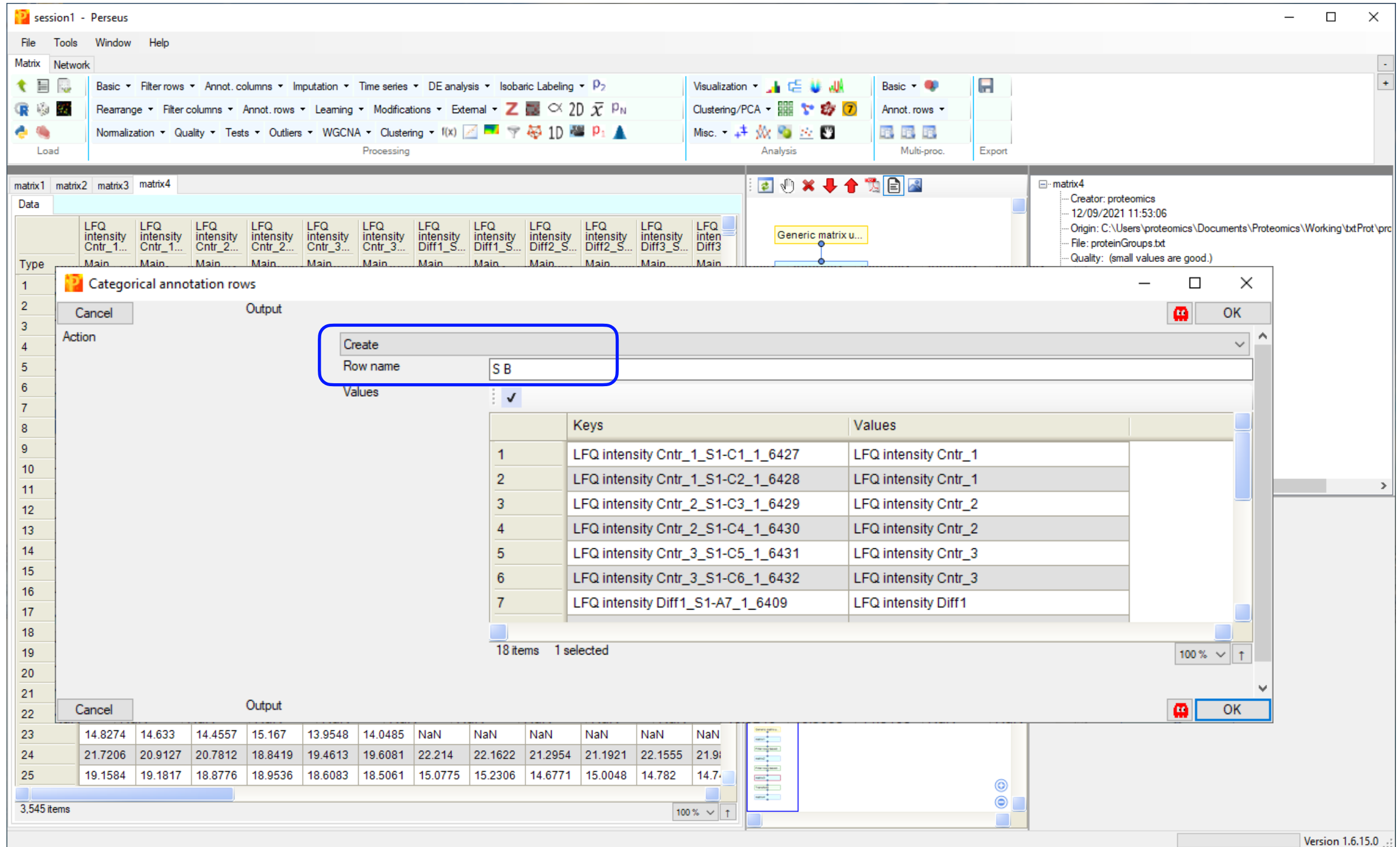


The screenshot shows the Perseus software interface with the 'Categorical annotation rows' dialog box open. The dialog box has a 'Create' button and a 'Row name' field set to 'S B'. The 'Values' field is checked. Below this is a table with 7 rows and 2 columns: 'Keys' and 'Values'.

	Keys	Values
1	LFQ intensity Cntr_1_S1-C1_1_6427	LFQ intensity Cntr_1
2	LFQ intensity Cntr_1_S1-C2_1_6428	LFQ intensity Cntr_1
3	LFQ intensity Cntr_2_S1-C3_1_6429	LFQ intensity Cntr_2
4	LFQ intensity Cntr_2_S1-C4_1_6430	LFQ intensity Cntr_2
5	LFQ intensity Cntr_3_S1-C5_1_6431	LFQ intensity Cntr_3
6	LFQ intensity Cntr_3_S1-C6_1_6432	LFQ intensity Cntr_3
7	LFQ intensity Diff1_S1-A7_1_6409	LFQ intensity Diff1

At the bottom of the dialog box, it says '18 items 1 selected'. The background shows the main Perseus interface with a data table and various toolbars.

Sample Grouping (technical and biological replicates !): **Annot. Rows > Categorical Annotation Row**

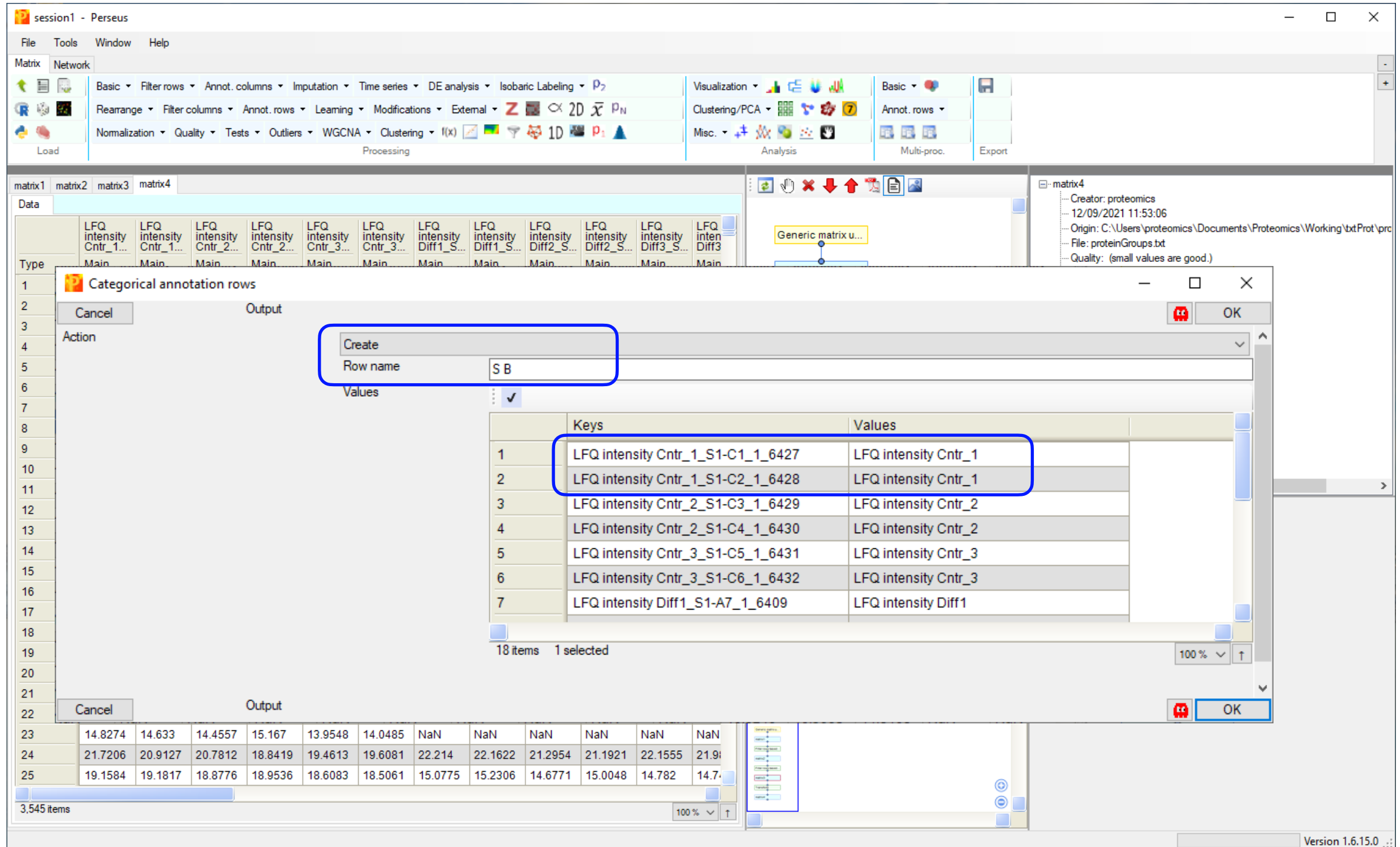


The screenshot shows the Perseus software interface with the 'Categorical annotation rows' dialog box open. The dialog box has a 'Create' button highlighted with a blue box. Below it, the 'Row name' field contains 'S B'. The 'Values' section shows a list of keys and values for the annotation row.

Keys	Values
1 LFQ intensity Cntr_1_S1-C1_1_6427	LFQ intensity Cntr_1
2 LFQ intensity Cntr_1_S1-C2_1_6428	LFQ intensity Cntr_1
3 LFQ intensity Cntr_2_S1-C3_1_6429	LFQ intensity Cntr_2
4 LFQ intensity Cntr_2_S1-C4_1_6430	LFQ intensity Cntr_2
5 LFQ intensity Cntr_3_S1-C5_1_6431	LFQ intensity Cntr_3
6 LFQ intensity Cntr_3_S1-C6_1_6432	LFQ intensity Cntr_3
7 LFQ intensity Diff1_S1-A7_1_6409	LFQ intensity Diff1

The dialog box also shows a list of 18 items, with 1 selected. The 'OK' button is highlighted with a blue box.

Sample Grouping (technical and biological replicates !): **Annot. Rows > Categorical Annotation Row**

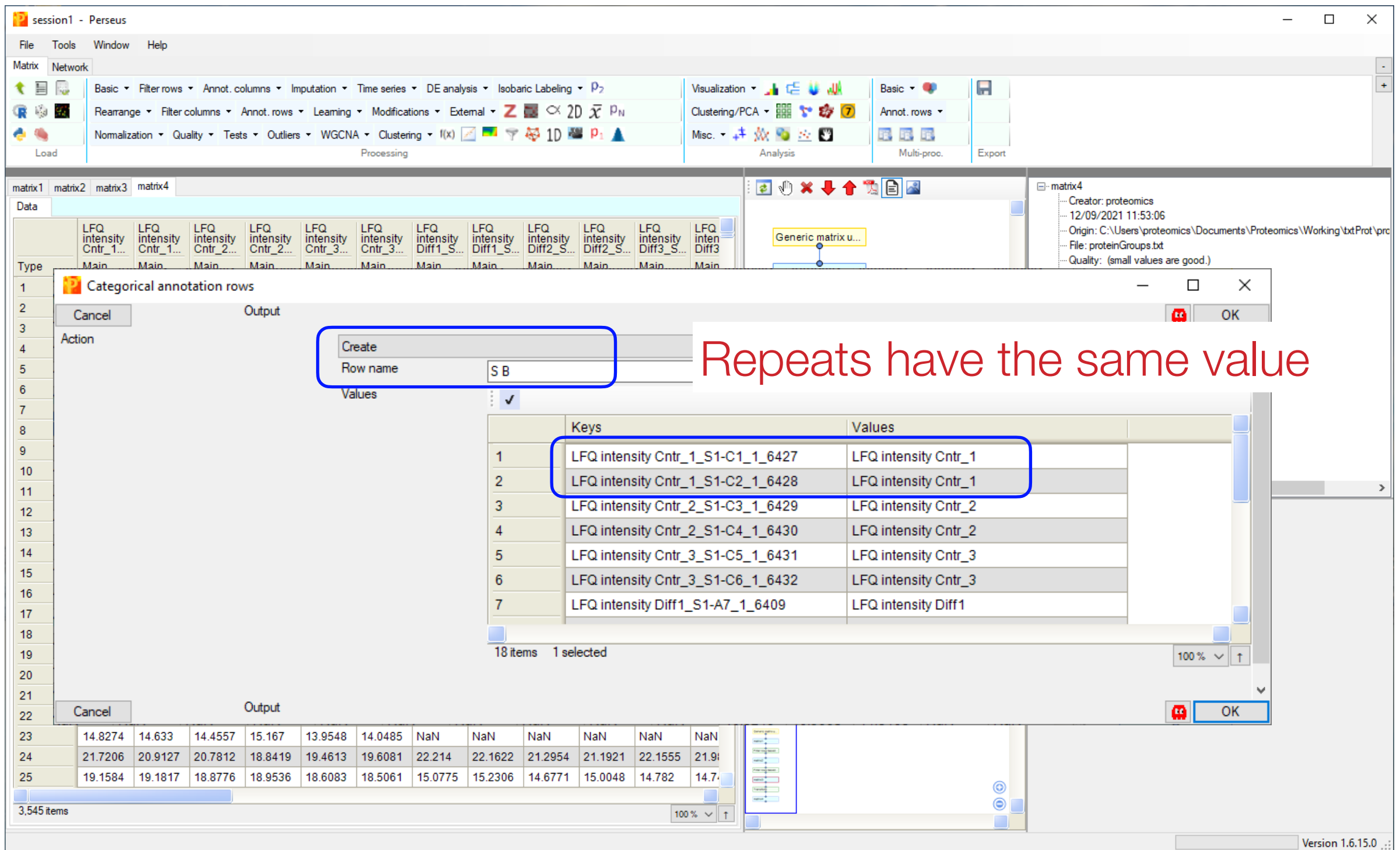


The screenshot displays the Perseus software interface. The 'Categorical annotation rows' dialog box is open, showing the 'Create' tab. The 'Row name' field is set to 'S B'. Below this, a table lists keys and values for the new row. The first two rows are highlighted with a blue box.

	Keys	Values
1	LFQ intensity Cntr_1_S1-C1_1_6427	LFQ intensity Cntr_1
2	LFQ intensity Cntr_1_S1-C2_1_6428	LFQ intensity Cntr_1
3	LFQ intensity Cntr_2_S1-C3_1_6429	LFQ intensity Cntr_2
4	LFQ intensity Cntr_2_S1-C4_1_6430	LFQ intensity Cntr_2
5	LFQ intensity Cntr_3_S1-C5_1_6431	LFQ intensity Cntr_3
6	LFQ intensity Cntr_3_S1-C6_1_6432	LFQ intensity Cntr_3
7	LFQ intensity Diff1_S1-A7_1_6409	LFQ intensity Diff1

The background window shows the main Perseus interface with a menu bar (File, Tools, Window, Help) and a toolbar. The 'Matrix' tab is active, displaying a data matrix with columns labeled 'LFQ intensity Cntr_1...', 'LFQ intensity Cntr_2...', 'LFQ intensity Cntr_3...', 'LFQ intensity Diff1_S1...', 'LFQ intensity Diff2_S1...', 'LFQ intensity Diff3_S1...', and 'LFQ intensity Diff3'. The 'Data' tab is also visible, showing a table of values for the selected row.

Sample Grouping (technical and biological replicates !): **Annot. Rows > Categorical Annotation Row**



session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering I(x) 1D P₁

Load Processing Analysis Multi-proc. Export

matrix1 matrix2 matrix3 matrix4

Data

Type

1 LfQ intensity Cntr_1... Main

2 LfQ intensity Cntr_1... Main

3 LfQ intensity Cntr_2... Main

4 LfQ intensity Cntr_2... Main

5 LfQ intensity Cntr_3... Main

6 LfQ intensity Cntr_3... Main

7 LfQ intensity Diff1_S... Main

8 LfQ intensity Diff1_S... Main

9 LfQ intensity Diff2_S... Main

10 LfQ intensity Diff2_S... Main

11 LfQ intensity Diff3_S... Main

12 LfQ intensity Diff3_S... Main

13 LfQ intensity Diff3_S... Main

14 LfQ intensity Diff3_S... Main

15 LfQ intensity Diff3_S... Main

16 LfQ intensity Diff3_S... Main

17 LfQ intensity Diff3_S... Main

18 LfQ intensity Diff3_S... Main

19 LfQ intensity Diff3_S... Main

20 LfQ intensity Diff3_S... Main

21 LfQ intensity Diff3_S... Main

22 LfQ intensity Diff3_S... Main

23 14.8274 14.633 14.4557 15.167 13.9548 14.0485 NaN NaN NaN NaN NaN NaN

24 21.7206 20.9127 20.7812 18.8419 19.4613 19.6081 22.214 22.1622 21.2954 21.1921 22.1555 21.9

25 19.1584 19.1817 18.8776 18.9536 18.6083 18.5061 15.0775 15.2306 14.6771 15.0048 14.782 14.7

3,545 items

100 %

Version 1.6.15.0

Categorical annotation rows

Cancel Output

Action

Create

Row name S B

Values

Keys Values

1	LfQ intensity Cntr_1_S1-C1_1_6427	LfQ intensity Cntr_1
2	LfQ intensity Cntr_1_S1-C2_1_6428	LfQ intensity Cntr_1
3	LfQ intensity Cntr_2_S1-C3_1_6429	LfQ intensity Cntr_2
4	LfQ intensity Cntr_2_S1-C4_1_6430	LfQ intensity Cntr_2
5	LfQ intensity Cntr_3_S1-C5_1_6431	LfQ intensity Cntr_3
6	LfQ intensity Cntr_3_S1-C6_1_6432	LfQ intensity Cntr_3
7	LfQ intensity Diff1_S1-A7_1_6409	LfQ intensity Diff1

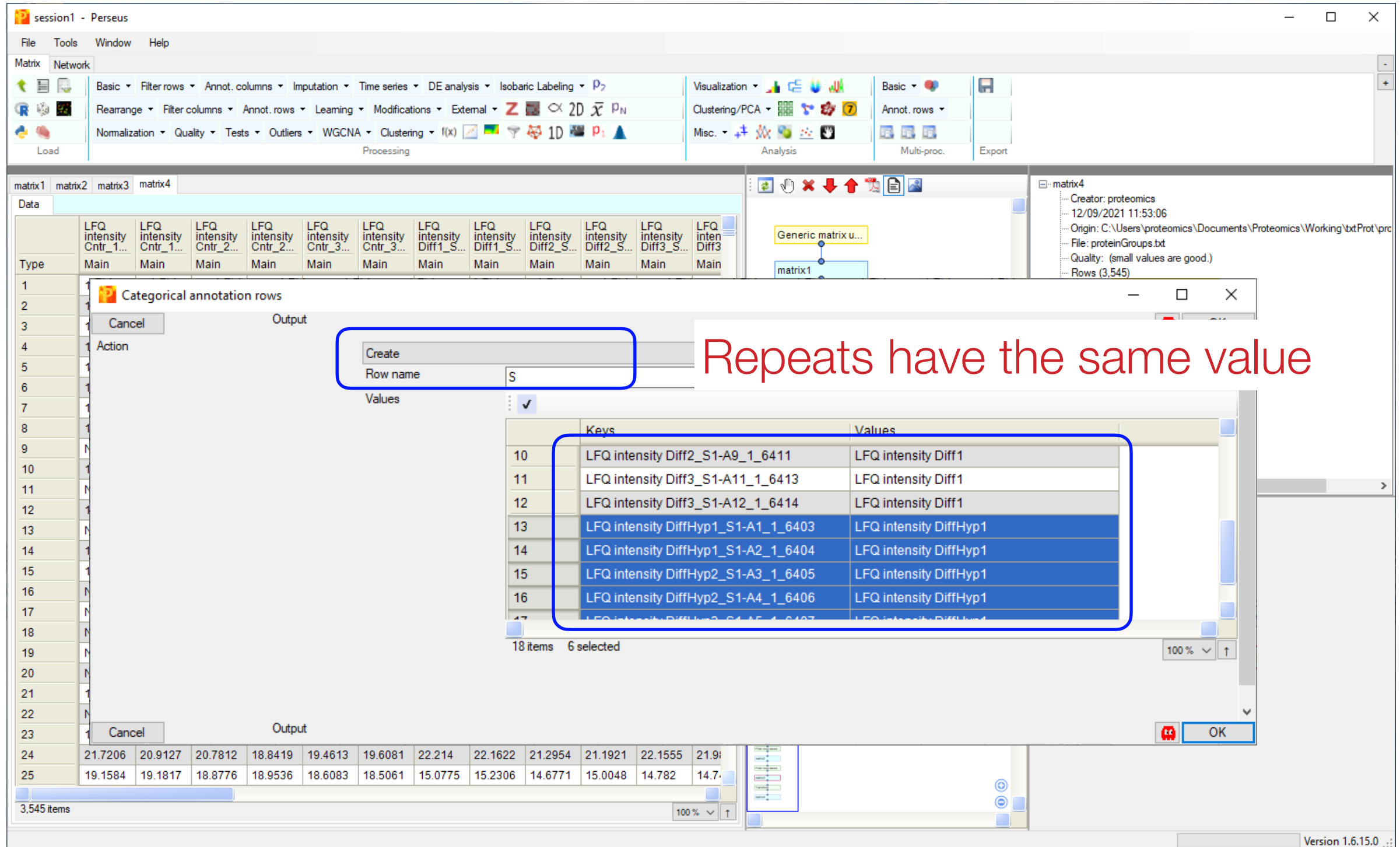
18 items 1 selected

100 %

OK

Repeats have the same value

Sample Grouping (technical and biological replicates !): **Annot. Rows > Categorical Annotation Row**



session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing Analysis Multi-proc. Export

matrix1 matrix2 matrix3 matrix4

Data

Type Main Main Main Main Main Main Main Main Main Main Main Main

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25

21.7206 20.9127 20.7812 18.8419 19.4613 19.6081 22.214 22.1622 21.2954 21.1921 22.1555 21.91

19.1584 19.1817 18.8776 18.9536 18.6083 18.5061 15.0775 15.2306 14.6771 15.0048 14.782 14.7

3,545 items

100 %

Version 1.6.15.0

Categorical annotation rows

Cancel Output

Action

Create

Row name S

Values

✓

Keys Values

10 LFQ intensity Diff2_S1-A9_1_6411 LFQ intensity Diff1

11 LFQ intensity Diff3_S1-A11_1_6413 LFQ intensity Diff1

12 LFQ intensity Diff3_S1-A12_1_6414 LFQ intensity Diff1

13 LFQ intensity DiffHyp1_S1-A1_1_6403 LFQ intensity DiffHyp1

14 LFQ intensity DiffHyp1_S1-A2_1_6404 LFQ intensity DiffHyp1

15 LFQ intensity DiffHyp2_S1-A3_1_6405 LFQ intensity DiffHyp1

16 LFQ intensity DiffHyp2_S1-A4_1_6406 LFQ intensity DiffHyp1

17 LFQ intensity DiffHyp2_S1-A5_1_6407 LFQ intensity DiffHyp1

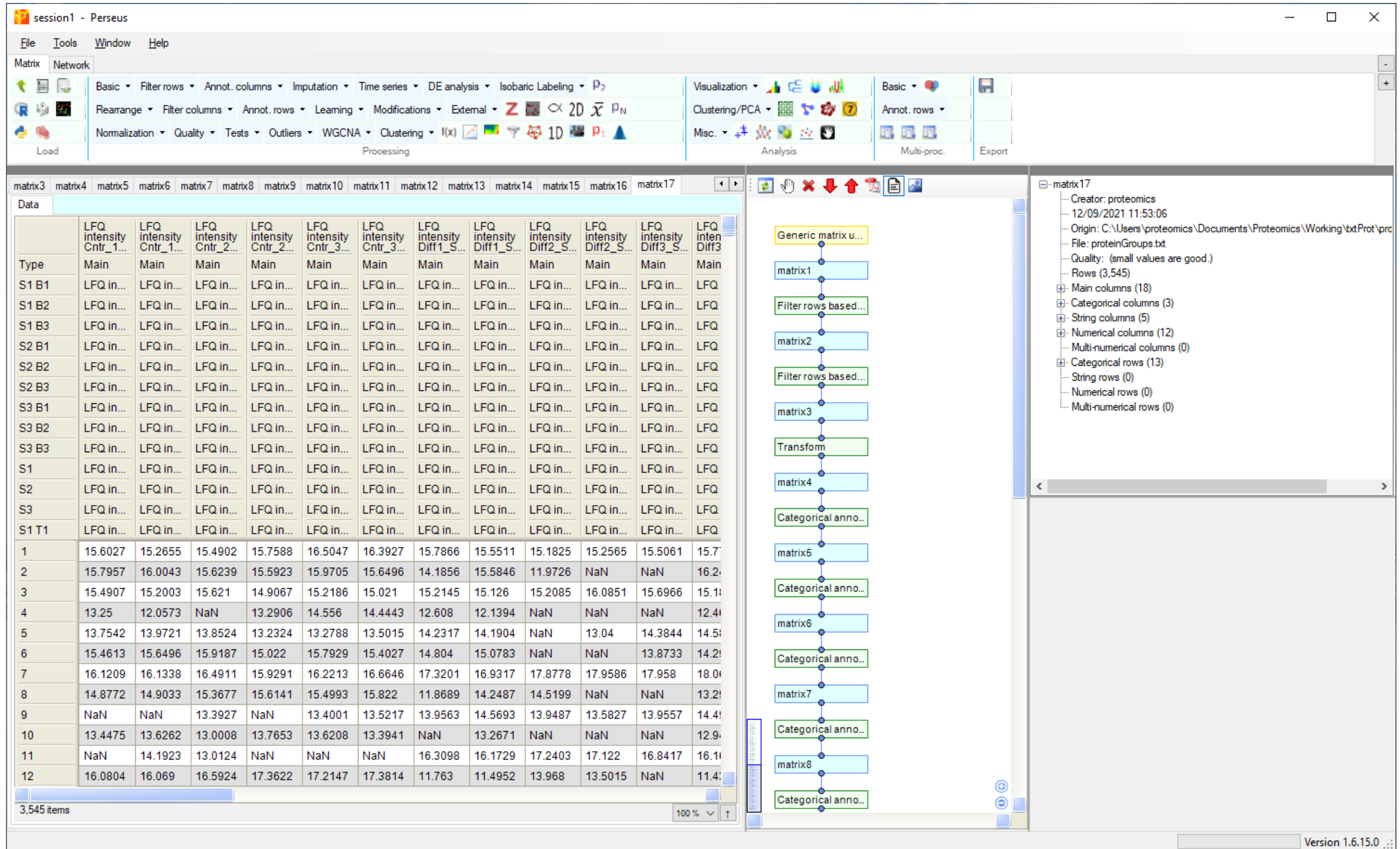
18 items 6 selected

100 %

OK

Repeats have the same value

Data Quality: **Filter Rows > Filter rows based on valid numbers**



The screenshot displays the Perseus software interface, version 1.6.15.0, showing a data processing workflow and a data table.

Workflow (Matrix 17):

- Generic matrix u...
- matrix1
- Filter rows based...
- matrix2
- Filter rows based...
- matrix3
- Transform
- matrix4
- Categorical anno...
- matrix5
- Categorical anno...
- matrix6
- Categorical anno...
- matrix7
- Categorical anno...
- matrix8
- Categorical anno...

Data Table (Matrix 17):

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
S1 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 T1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588	16.5047	16.3927	15.7866	15.5511	15.1825	15.2565	15.5061	15.7...
2	15.7957	16.0043	15.6239	15.5923	15.9705	15.6496	14.1856	15.5846	11.9726	NaN	NaN	16.2...
3	15.4907	15.2003	15.621	14.9067	15.2186	15.021	15.2145	15.126	15.2085	16.0851	15.6966	15.1...
4	13.25	12.0573	NaN	13.2906	14.556	14.4443	12.608	12.1394	NaN	NaN	NaN	12.4...
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	NaN	13.04	14.3844	14.5...
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	NaN	NaN	13.8733	14.2...
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0...
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	NaN	NaN	13.2...
9	NaN	NaN	13.3927	NaN	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4...
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	NaN	13.2671	NaN	NaN	NaN	12.9...
11	NaN	14.1923	13.0124	NaN	NaN	NaN	16.3098	16.1729	17.2403	17.122	16.8417	16.1...
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	NaN	11.4...

3,545 items

Data Quality: **Filter Rows > Filter rows based on valid numbers**

The screenshot shows the Perseus software interface. The 'Filter Rows' menu is open, displaying options: 'Filter rows based on categorical column', 'Filter rows based on numerical/main column', 'Filter rows based on text column', 'Filter rows based on valid values' (highlighted), and 'Filter rows based on duplicate values'. Below the menu, a tooltip states: 'Rows of the matrix are filtered to contain at least one value that are valid in the specified way.'

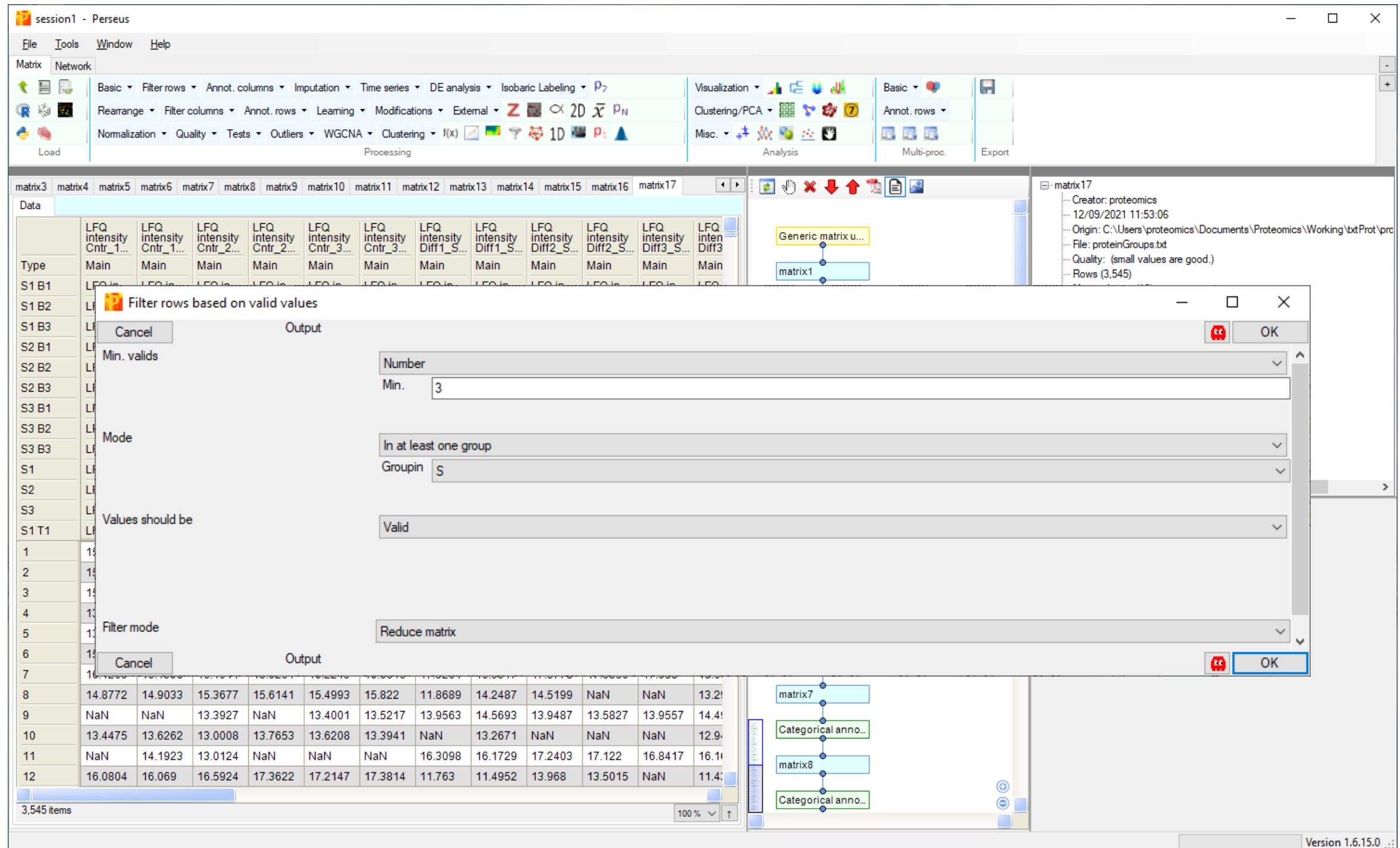
The main data matrix is visible, showing columns for 'Type' and 'LFQ intensity' (Main, Diff1_S, Diff2_S, Diff3_S, Diff3). The 'Type' column lists various sample types (S1 B1, S1 B2, S1 B3, S2 B1, S2 B2, S2 B3, S3 B1, S3 B2, S3 B3, S1, S2, S3, S1 T1). The 'LFQ intensity' columns contain numerical values, with some cells showing 'NaN'.

On the right side, the 'matrix17' panel displays a workflow diagram with steps: 'Generic matrix u...', 'matrix1', 'Filter rows based...', 'matrix2', 'Filter rows based...', 'matrix3', 'Transform', 'matrix4', 'Categorical anno...', 'matrix5', 'Categorical anno...', 'matrix6', 'Categorical anno...', 'matrix7', 'Categorical anno...', 'matrix8', and 'Categorical anno...'. Below the workflow, a summary of matrix statistics is shown:

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (3,545)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (13)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

The bottom status bar indicates '3,545 items' and 'Version 1.6.15.0'.

Data Quality: **Filter Rows > Filter rows based on valid numbers**

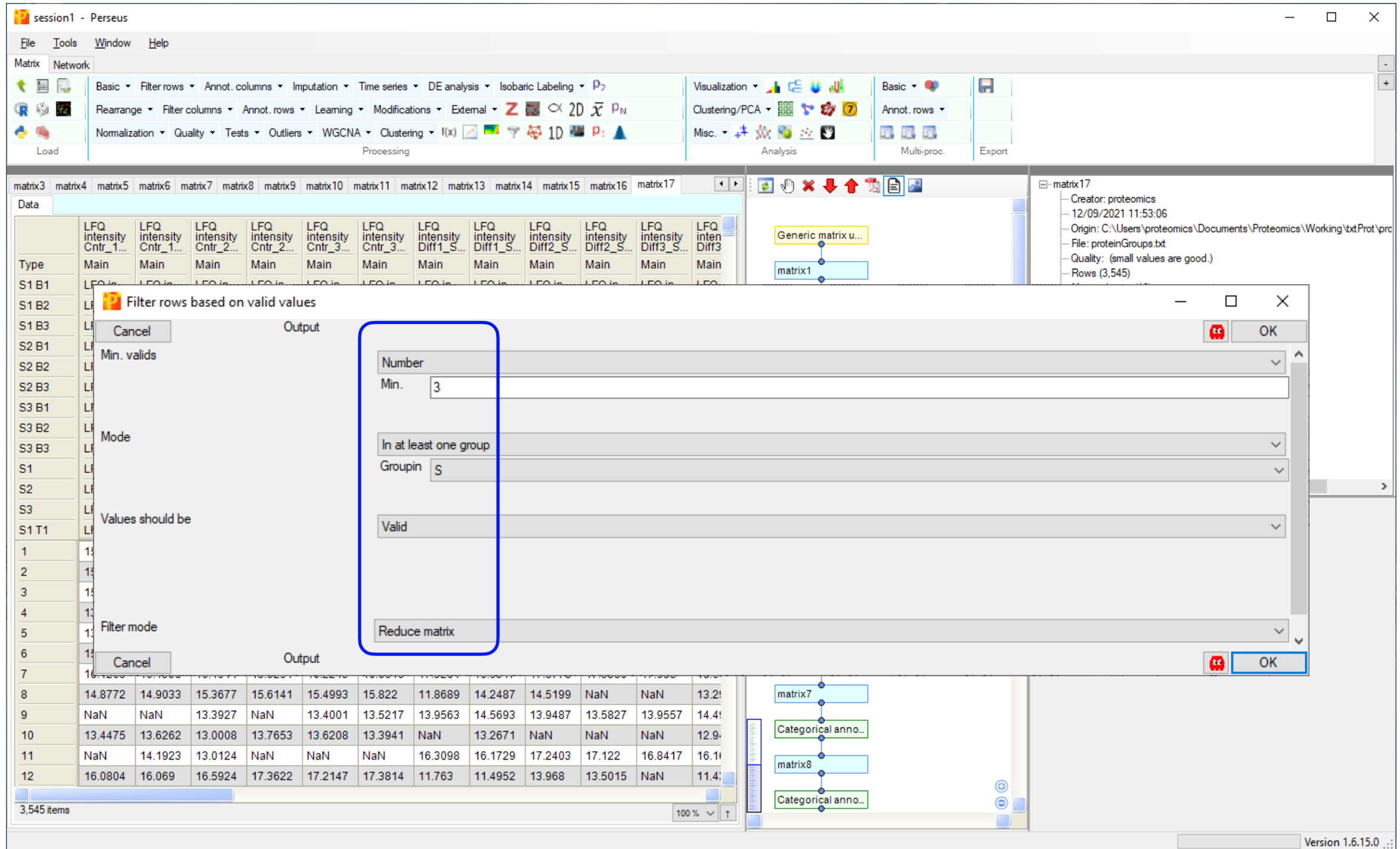


The screenshot displays the Perseus software interface. A dialog box titled "Filter rows based on valid values" is open, allowing users to filter data based on the number of valid values in each row. The dialog includes the following settings:

- Min. valids:** Number (3)
- Mode:** In at least one group
- Values should be:** Valid
- Filter mode:** Reduce matrix

The background shows a data matrix with columns labeled "LFQ intensity Cntr_1...", "LFQ intensity Cntr_2...", "LFQ intensity Cntr_3...", "LFQ intensity Diff1_S...", "LFQ intensity Diff2_S...", "LFQ intensity Diff3_S...", and "LFQ intensity Diff3". The rows are labeled with sample types: S1 B1, S1 B2, S1 B3, S2 B1, S2 B2, S2 B3, S3 B1, S3 B2, S3 B3, S1, S2, S3, S1 T1, and a list of numerical values (1-12). The status bar at the bottom indicates "3,545 items" and "Version 1.6.15.0".

Data Quality: **Filter Rows > Filter rows based on valid numbers**



The screenshot displays the Perseus software interface with a data table and a dialog box for filtering rows based on valid values.

Dialog Box: Filter rows based on valid values

- Cancel** (top left)
- Output** (top right)
- Min. valids**: Number (dropdown), Min. (input field: 3)
- Mode**: In at least one group (dropdown)
- Groupin**: S (dropdown)
- Values should be**: Valid (dropdown)
- Filter mode**: Reduce matrix (dropdown)
- Cancel** (bottom left)
- Output** (bottom right)
- OK** (bottom right)

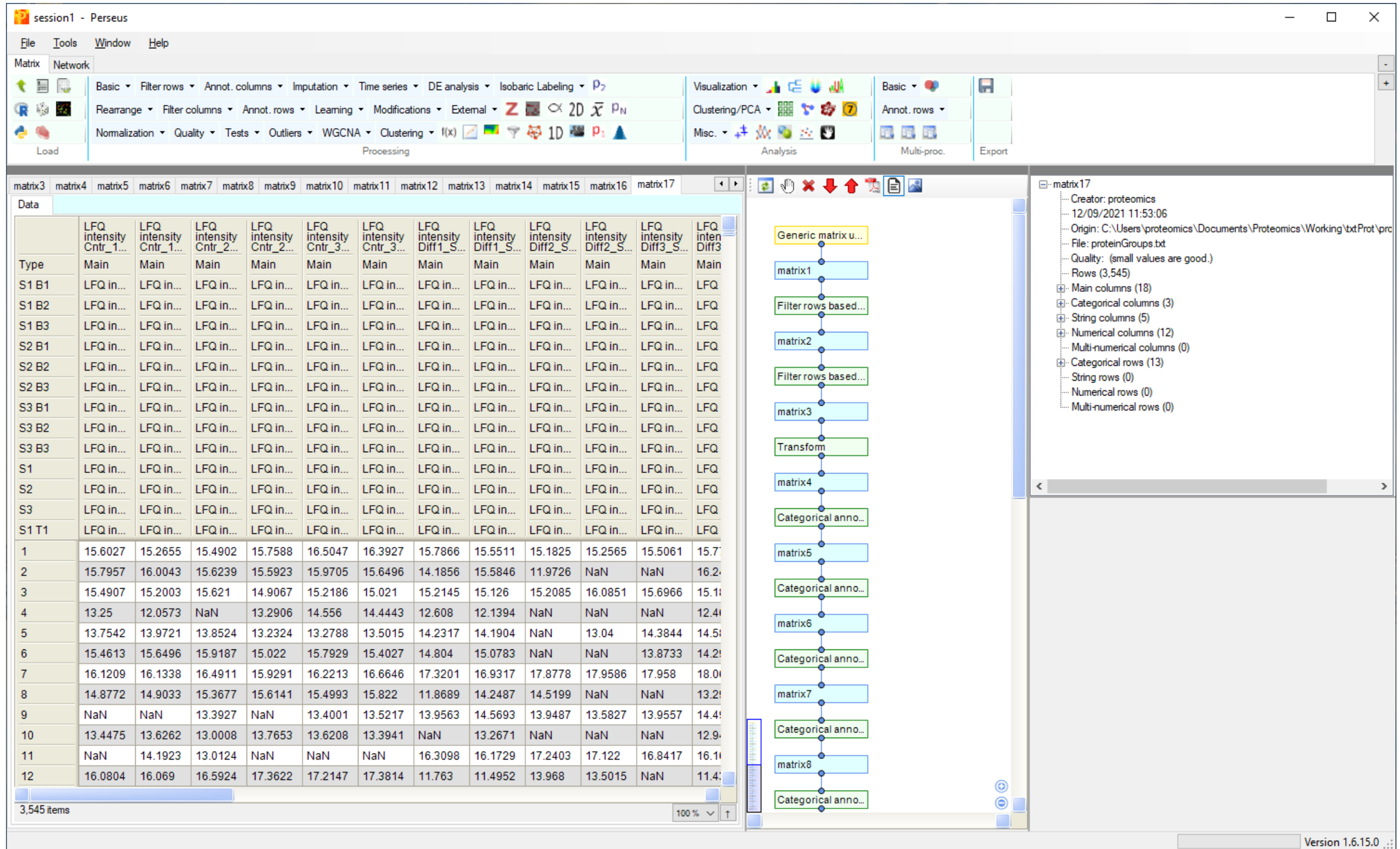
Data Table (matrix17):

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
S1 B1	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689
S1 B2	NaN	NaN	13.3927	NaN	13.4001	13.5217	13.9563
S1 B3	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	NaN
S2 B1	NaN	14.1923	13.0124	NaN	NaN	NaN	16.3098
S2 B2	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763
S2 B3							
S3 B1							
S3 B2							
S3 B3							
S1 T1							
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							

3,545 items

Version 1.6.15.0

Data Quality - Fill in missing values : **Imputation > Replace missing values from normal distribution**



The screenshot displays the Perseus software interface, version 1.6.15.0. The main window is titled "session1 - Perseus". The interface is divided into several sections:

- Menu Bar:** File, Tools, Window, Help.
- Matrix Network:** A toolbar with icons for various data processing steps, including Load, Rearrange, Filter rows, Annot. columns, Imputation, Time series, DE analysis, Isobaric Labeling, Visualization, Clustering/PCA, Misc., Analysis, Multi-proc., Export, and Annot. rows.
- Data Table:** A table with 13 columns (matrix3 to matrix17) and 13 rows (S1 B1 to S1 T1). The table contains numerical values, with some cells showing "NaN".
- Workflow Diagram:** A vertical flowchart on the right side of the interface, showing a sequence of steps: Generic matrix u..., matrix1, Filter rows based..., matrix2, Filter rows based..., matrix3, Transform, matrix4, Categorical anno..., matrix5, Categorical anno..., matrix6, Categorical anno..., matrix7, Categorical anno..., matrix8, and Categorical anno....
- Matrix Properties Panel:** A panel on the far right showing details for "matrix17", including Creator (proteomics), Origin (C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro), File (proteinGroups.txt), Quality (small values are good.), Rows (3,545), Main columns (18), Categorical columns (3), String columns (5), Numerical columns (12), Multi-numerical columns (0), Categorical rows (13), String rows (0), Numerical rows (0), and Multi-numerical rows (0).

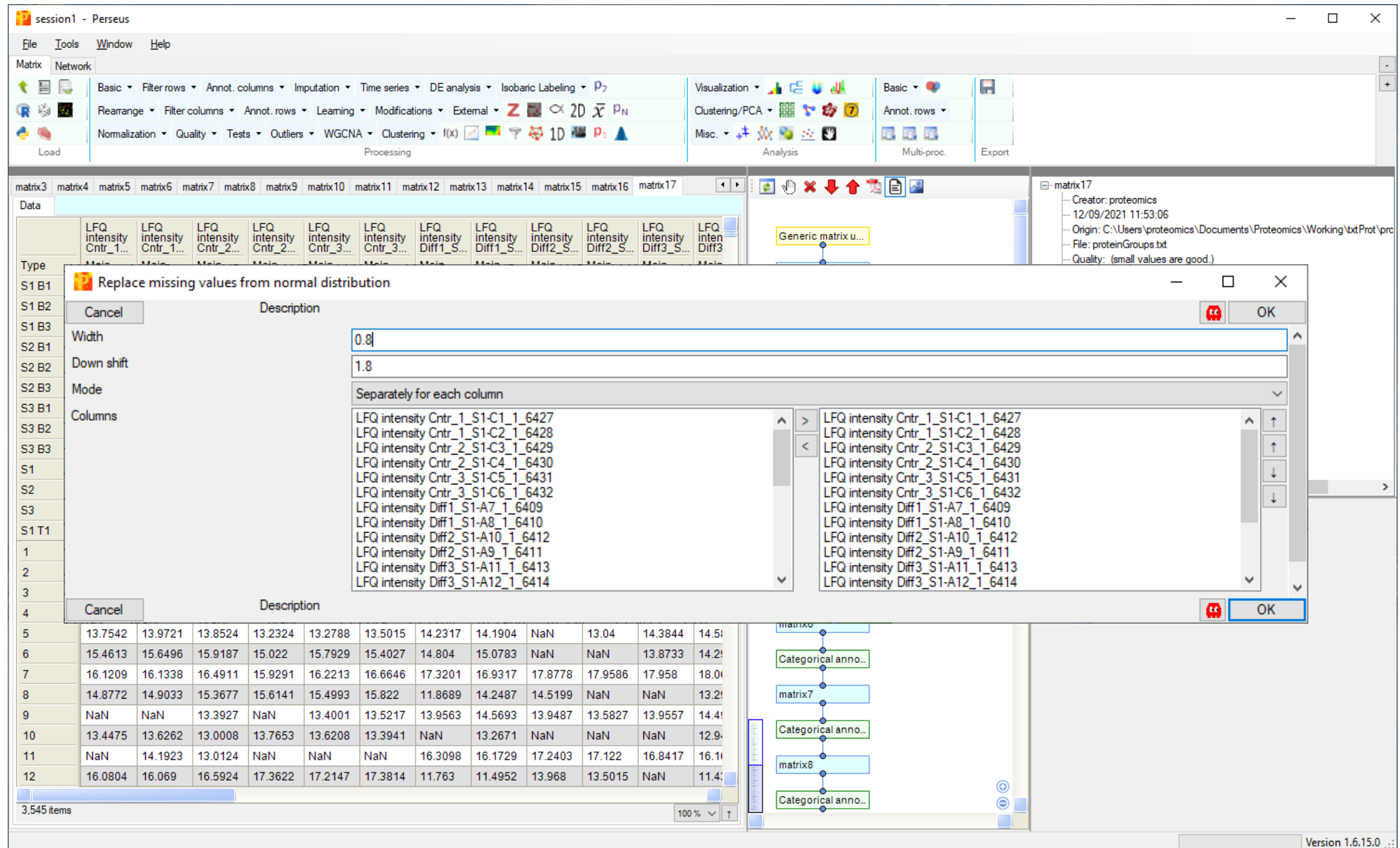
The bottom status bar indicates "3,545 items" and "100 %".

Data Quality - Fill in missing values : **Imputation > Replace missing values from normal distribution**

The screenshot shows the Perseus software interface. The 'Imputation' menu is open, highlighting the option 'Replace missing values from normal distribution'. A tooltip explains: 'Missing values will be replaced by random numbers. The parameters of this distribution can be optimized for the region that the missing values would have if they were present.' The main window displays a data matrix with columns for LFQ intensity and various difference scores. The matrix is organized into a workflow on the right, showing a sequence of matrices (matrix1 to matrix8) and processing steps like 'Filter rows based...' and 'Transform'. The bottom status bar indicates '3,545 items' and 'Version 1.6.15.0'.

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
S1 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 T1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588	16.5047	16.3927	15.7866	15.5511	15.1825	15.2565	15.5061	15.7...
2	15.7957	16.0043	15.6239	15.5923	15.9705	15.6496	14.1856	15.5846	11.9726	NaN	NaN	16.2...
3	15.4907	15.2003	15.621	14.9067	15.2186	15.021	15.2145	15.126	15.2085	16.0851	15.6966	15.1...
4	13.25	12.0573	NaN	13.2906	14.556	14.4443	12.608	12.1394	NaN	NaN	NaN	12.4...
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	NaN	13.04	14.3844	14.5...
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	NaN	NaN	13.8733	14.2...
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0...
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	NaN	NaN	13.2...
9	NaN	NaN	13.3927	NaN	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4...
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	NaN	13.2671	NaN	NaN	NaN	12.9...
11	NaN	14.1923	13.0124	NaN	NaN	NaN	16.3098	16.1729	17.2403	17.122	16.8417	16.1...
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	NaN	11.4...

Data Quality - Fill in missing values : **Imputation > Replace missing values from normal distribution**



The screenshot shows the Perseus software interface with a session titled 'session1 - Perseus'. The 'Matrix' tab is active, displaying a data matrix with columns labeled 'matrix3' through 'matrix17'. The 'Data' section shows a list of columns with descriptions like 'LFQ intensity Cntr_1...', 'LFQ intensity Cntr_2...', 'LFQ intensity Cntr_3...', 'LFQ intensity Diff1_S...', 'LFQ intensity Diff2_S...', and 'LFQ intensity Diff3_S...'. The 'Type' section shows a list of sample types: S1 B1, S1 B2, S1 B3, S2 B1, S2 B2, S2 B3, S3 B1, S3 B2, S3 B3, S1, S2, S3, S1 T1, 1, 2, 3, 4.

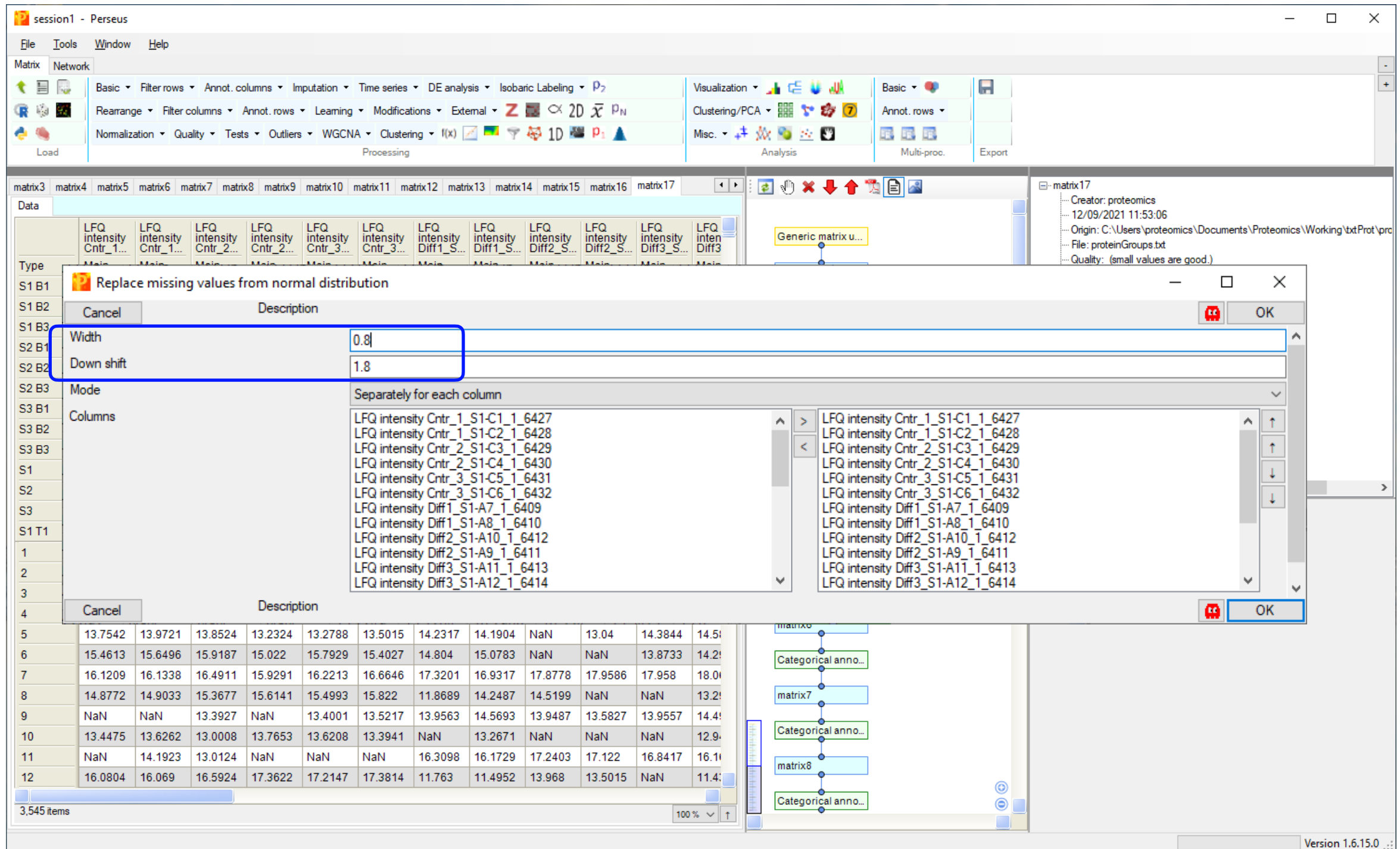
A dialog box titled 'Replace missing values from normal distribution' is open, showing the following settings:

- Width:** 0.8
- Down shift:** 1.8
- Mode:** Separately for each column
- Columns:** A list of columns to be processed, including 'LFQ intensity Cntr_1_S1-C1_1_6427', 'LFQ intensity Cntr_1_S1-C2_1_6428', 'LFQ intensity Cntr_2_S1-C3_1_6429', 'LFQ intensity Cntr_2_S1-C4_1_6430', 'LFQ intensity Cntr_3_S1-C5_1_6431', 'LFQ intensity Cntr_3_S1-C6_1_6432', 'LFQ intensity Diff1_S1-A7_1_6409', 'LFQ intensity Diff1_S1-A8_1_6410', 'LFQ intensity Diff2_S1-A10_1_6412', 'LFQ intensity Diff2_S1-A9_1_6411', 'LFQ intensity Diff3_S1-A11_1_6413', and 'LFQ intensity Diff3_S1-A12_1_6414'.

The dialog box has 'Cancel' and 'OK' buttons. The 'OK' button is highlighted in blue.

The background interface shows a 'Processing' section with various tools like 'Basic', 'Filter rows', 'Annot. columns', 'Imputation', 'Time series', 'DE analysis', 'Isobaric Labeling', 'Visualization', 'Clustering/PCA', 'Misc.', 'Analysis', 'Multi-proc.', and 'Export'. The 'Data' section shows a table with 12 rows and 12 columns of numerical data. The status bar at the bottom indicates '3,545 items' and 'Version 1.6.15.0'.

Data Quality - Fill in missing values : **Imputation > Replace missing values from normal distribution**



The screenshot shows the Perseus software interface with the 'Replace missing values from normal distribution' dialog box open. The dialog box has a 'Width' field set to 0.8 and a 'Down shift' field set to 1.8. The 'Mode' is set to 'Separately for each column'. The 'Columns' list includes various LFQ intensity and difference values. The background shows a data table with 12 rows and 13 columns, and a network diagram on the right.

Dialog Box: Replace missing values from normal distribution

- Width: 0.8
- Down shift: 1.8
- Mode: Separately for each column
- Columns:
 - LFQ intensity Cntr_1_S1-C1_1_6427
 - LFQ intensity Cntr_1_S1-C2_1_6428
 - LFQ intensity Cntr_2_S1-C3_1_6429
 - LFQ intensity Cntr_2_S1-C4_1_6430
 - LFQ intensity Cntr_3_S1-C5_1_6431
 - LFQ intensity Cntr_3_S1-C6_1_6432
 - LFQ intensity Diff1_S1-A7_1_6409
 - LFQ intensity Diff1_S1-A8_1_6410
 - LFQ intensity Diff2_S1-A10_1_6412
 - LFQ intensity Diff2_S1-A9_1_6411
 - LFQ intensity Diff3_S1-A11_1_6413
 - LFQ intensity Diff3_S1-A12_1_6414

Data Table (Matrix 17):

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
S1 B1												
S1 B2												
S1 B3												
S2 B1												
S2 B2												
S2 B3												
S3 B1												
S3 B2												
S3 B3												
S1												
S2												
S3												
S1 T1												
1												
2												
3												
4												
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	NaN	13.04	14.3844	14.51
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	NaN	NaN	13.8733	14.21
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.01
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	NaN	NaN	13.21
9	NaN	NaN	13.3927	NaN	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.41
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	NaN	13.2671	NaN	NaN	NaN	12.91
11	NaN	14.1923	13.0124	NaN	NaN	NaN	16.3098	16.1729	17.2403	17.122	16.8417	16.11
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	NaN	11.41

3,545 items

Version 1.6.15.0

Data Quality - Normal distributed values ? : **Visualisation - Histogram**

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix5 matrix6 matrix7 matrix8 matrix9 matrix10 matrix11 matrix12 matrix13 matrix14 matrix15 matrix16 matrix17 matrix26 matrix27

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
S1 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 T1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
4	13.25	12.0573	13.2664	13.2906	14.556	14.4443	12.608	12.1394	13.7824	11.6769	13.6862	12.4
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	11.2877	13.04	14.3844	14.5
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	13.5567	11.1301	13.8733	14.2
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	12.1056	12.494	13.2
9	13.5942	10.0977	13.3927	9.5969	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	10.0339	13.2671	12.4006	13.4661	11.6896	12.9
11	11.5438	14.1923	13.0124	9.87217	10.5357	9.02876	16.3098	16.1729	17.2403	17.122	16.8417	16.1
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	13.2817	11.4
13	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	11.4146	12.5111	14.1747	14.7
14	14.9042	14.9224	15.2079	11.0139	13.3988	10.797	11.0067	10.9583	13.4384	13.5095	11.4338	11.5
15	11.3495	11.4932	14.279	12.9967	10.8642	13.0463	16.2097	16.4275	17.592	17.47	17.4336	17.3

2,920 items

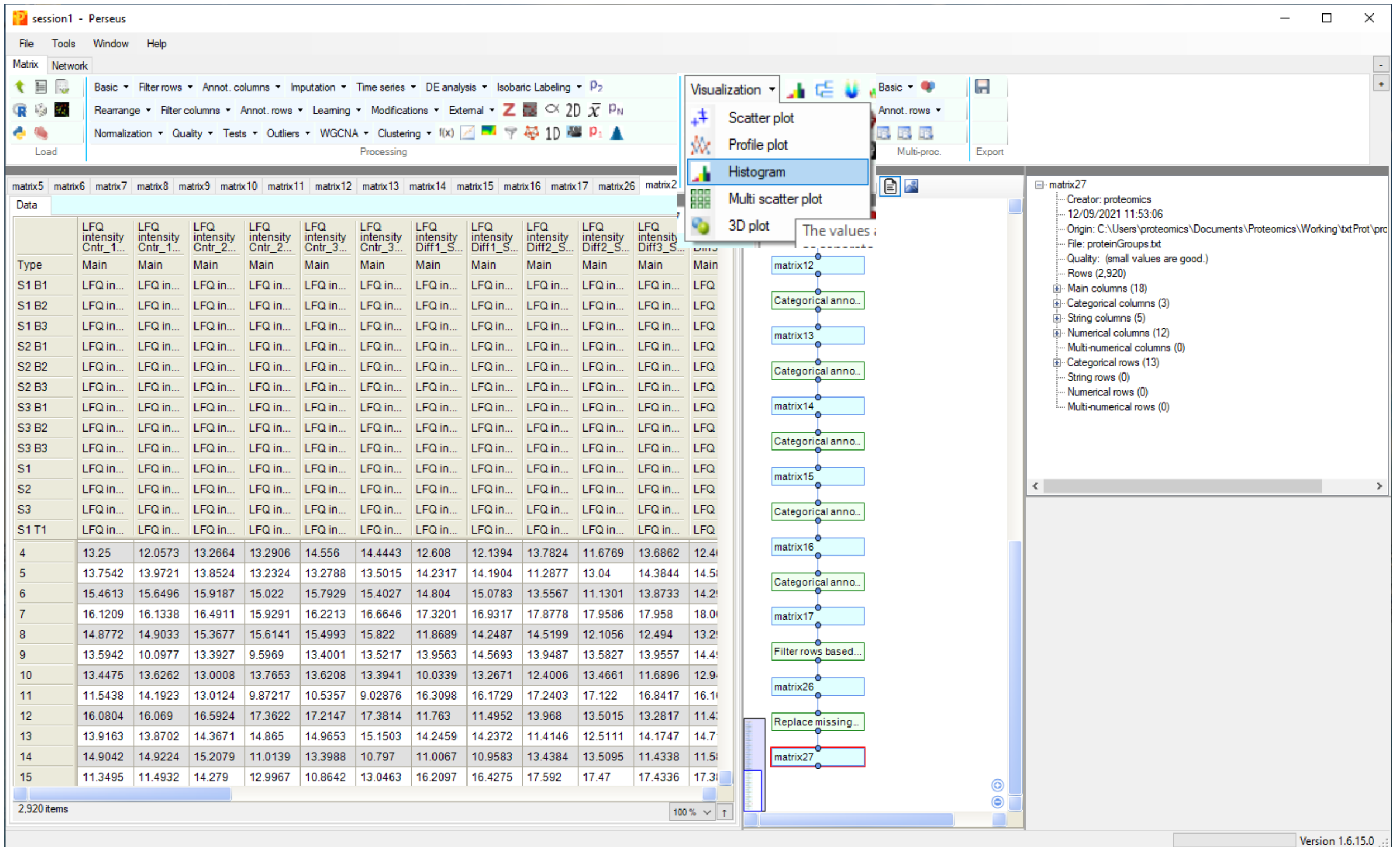
100% ↑

matrix27

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (2,920)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (13)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Version 1.6.15.0

Data Quality - Normal distributed values ? : **Visualisation - Histogram**



The screenshot displays the Perseus software interface. The main window shows a data matrix with columns labeled 'LFQ intensity' and 'LFQ intensity Diff'. The 'Visualization' menu is open, showing options for 'Scatter plot', 'Profile plot', 'Histogram', 'Multi scatter plot', and '3D plot'. The 'Histogram' option is highlighted. The right panel shows a summary of the data matrix, including the number of rows (2,920) and columns (18).

Matrix Summary:

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (2,920)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (13)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Data Matrix (Sample Rows):

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
S1 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 T1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
4	13.25	12.0573	13.2664	13.2906	14.556	14.4443	12.608	12.1394	13.7824	11.6769	13.6862	12.4
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	11.2877	13.04	14.3844	14.5
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	13.5567	11.1301	13.8733	14.2
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	12.1056	12.494	13.2
9	13.5942	10.0977	13.3927	9.5969	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	10.0339	13.2671	12.4006	13.4661	11.6896	12.9
11	11.5438	14.1923	13.0124	9.87217	10.5357	9.02876	16.3098	16.1729	17.2403	17.122	16.8417	16.1
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	13.2817	11.4
13	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	11.4146	12.5111	14.1747	14.7
14	14.9042	14.9224	15.2079	11.0139	13.3988	10.797	11.0067	10.9583	13.4384	13.5095	11.4338	11.5
15	11.3495	11.4932	14.279	12.9967	10.8642	13.0463	16.2097	16.4275	17.592	17.47	17.4336	17.3

2,920 items

Version 1.6.15.0

Data Quality - Normal distributed values ? : **Visualisation - Histogram**

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix5 matrix6 matrix7 matrix8 matrix9 matrix10 matrix11 matrix12 matrix13 matrix14 matrix15 matrix16 matrix17 matrix26 matrix27

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
S1 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3 B3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S2	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S3	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 T1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
4	13.25	12.0573	13.2664	13.2906	14.556	14.4443	12.608	12.1394	13.7824	11.6769	13.6862	12.4
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	11.2877	13.04	14.3844	14.5
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	13.5567	11.1301	13.8733	14.2
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	12.1056	12.494	13.2
9	13.5942	10.0977	13.3927	9.5969	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	10.0339	13.2671	12.4006	13.4661	11.6896	12.9
11	11.5438	14.1923	13.0124	9.87217	10.5357	9.02876	16.3098	16.1729	17.2403	17.122	16.8417	16.1
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	13.2817	11.4
13	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	11.4146	12.5111	14.1747	14.7
14	14.9042	14.9224	15.2079	11.0139	13.3988	10.797	11.0067	10.9583	13.4384	13.5095	11.4338	11.5
15	11.3495	11.4932	14.279	12.9967	10.8642	13.0463	16.2097	16.4275	17.592	17.47	17.4336	17.3

2,920 items

100% ↑

matrix27

- Creator: proteomics
- 12/09/2021 11:53:06
- Origin: C:\Users\proteomics\Documents\Proteomics\Working\txtProt\pro
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (2,920)
- Main columns (18)
- Categorical columns (3)
- String columns (5)
- Numerical columns (12)
- Multi-numerical columns (0)
- Categorical rows (13)
- String rows (0)
- Numerical rows (0)
- Multi-numerical rows (0)

Version 1.6.15.0

Data Quality - Normal distributed values ? : **Visualisation - Histogram**

session1 - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D x P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing Analysis Multi-proc. Export

matrix5 matrix6 matrix7 matrix8 matrix9 matrix10 matrix11 matrix12 matrix13 matrix14 matrix15 matrix16 matrix17 matrix26 matrix27

Data

	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...
Type	Main	Main	Main	Main	Main	Main	Main	Main	Main	Main	Main	Main
S1 B1	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S1 B2												
S1 B3												
S2 B1												
S2 B2												
S2 B3												
S3 B1												
S3 B2												
S3 B3												
S1												
S2												
S3												
S1 T1												
4												
5												
6												
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	12.1056	12.494	13.2
9	13.5942	10.0977	13.3927	9.5969	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	10.0339	13.2671	12.4006	13.4661	11.6896	12.9
11	11.5438	14.1923	13.0124	9.87217	10.5357	9.02876	16.3098	16.1729	17.2403	17.122	16.8417	16.1
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	13.2817	11.4
13	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	11.4146	12.5111	14.1747	14.7
14	14.9042	14.9224	15.2079	11.0139	13.3988	10.797	11.0067	10.9583	13.4384	13.5095	11.4338	11.5
15	11.3495	11.4932	14.279	12.9967	10.8642	13.0463	16.2097	16.4275	17.592	17.47	17.4336	17.3

2,920 items

100% ↑

Histogram

Cancel Description OK

Columns

LFQ intensity Cntr_1_S1-C1_1_6427
LFQ intensity Cntr_1_S1-C2_1_6428
LFQ intensity Cntr_2_S1-C3_1_6429
LFQ intensity Cntr_2_S1-C4_1_6430
LFQ intensity Cntr_3_S1-C5_1_6431
LFQ intensity Cntr_3_S1-C6_1_6432
LFQ intensity Diff1_S1-A7_1_6409
LFQ intensity Diff1_S1-A8_1_6410
LFQ intensity Diff2_S1-A10_1_6412
LFQ intensity Diff2_S1-A9_1_6411
LFQ intensity Diff3_S1-A11_1_6413
LFQ intensity Diff3_S1-A12_1_6414

LFQ intensity Cntr_1_S1-C1_1_6427
LFQ intensity Cntr_1_S1-C2_1_6428
LFQ intensity Cntr_2_S1-C3_1_6429
LFQ intensity Cntr_2_S1-C4_1_6430
LFQ intensity Cntr_3_S1-C5_1_6431
LFQ intensity Cntr_3_S1-C6_1_6432
LFQ intensity Diff1_S1-A7_1_6409
LFQ intensity Diff1_S1-A8_1_6410
LFQ intensity Diff2_S1-A10_1_6412
LFQ intensity Diff2_S1-A9_1_6411
LFQ intensity Diff3_S1-A11_1_6413
LFQ intensity Diff3_S1-A12_1_6414

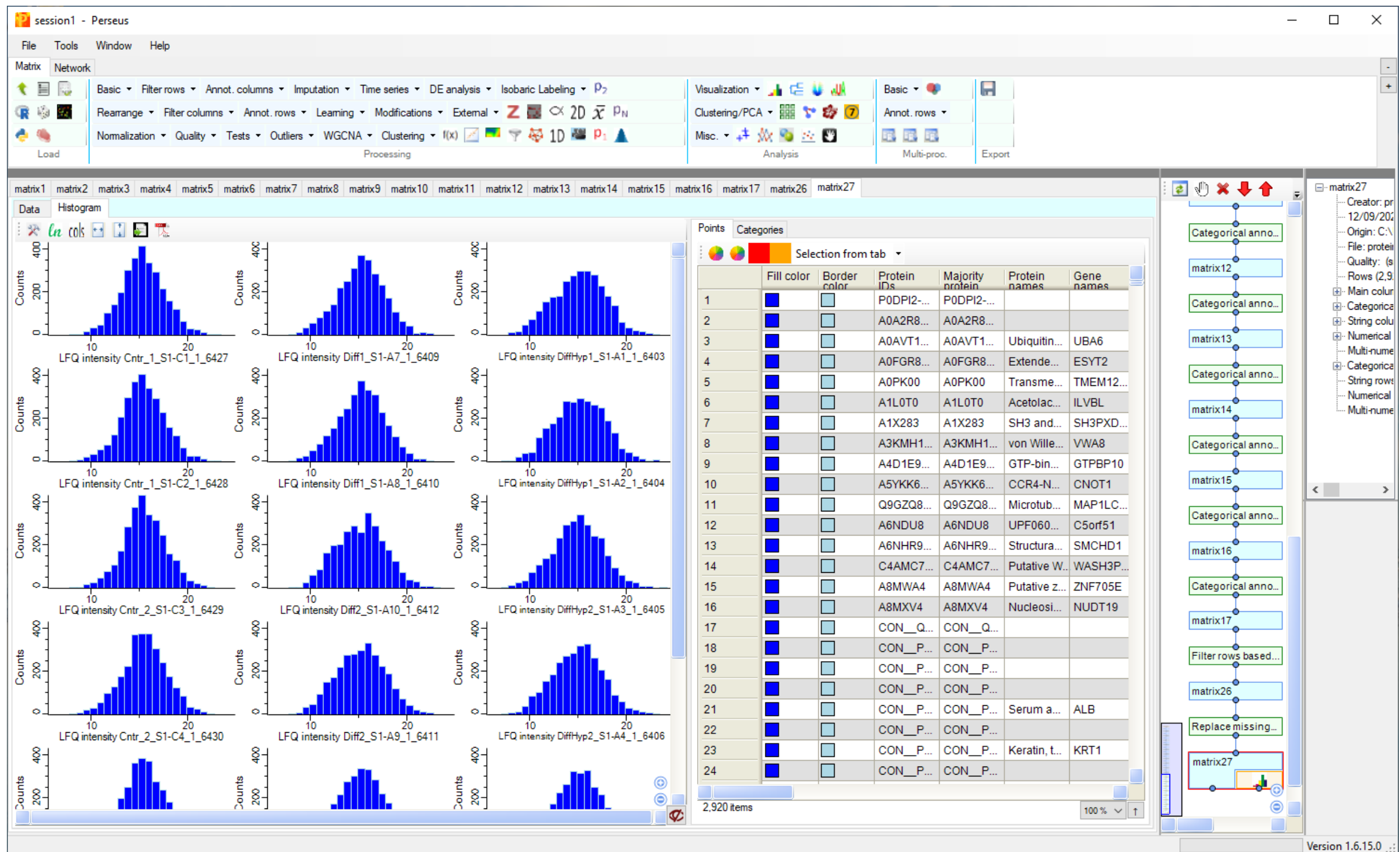
Cancel Description OK

matrix17
Filter rows based...
matrix26
Replace missing...
matrix27

Version 1.6.15.0

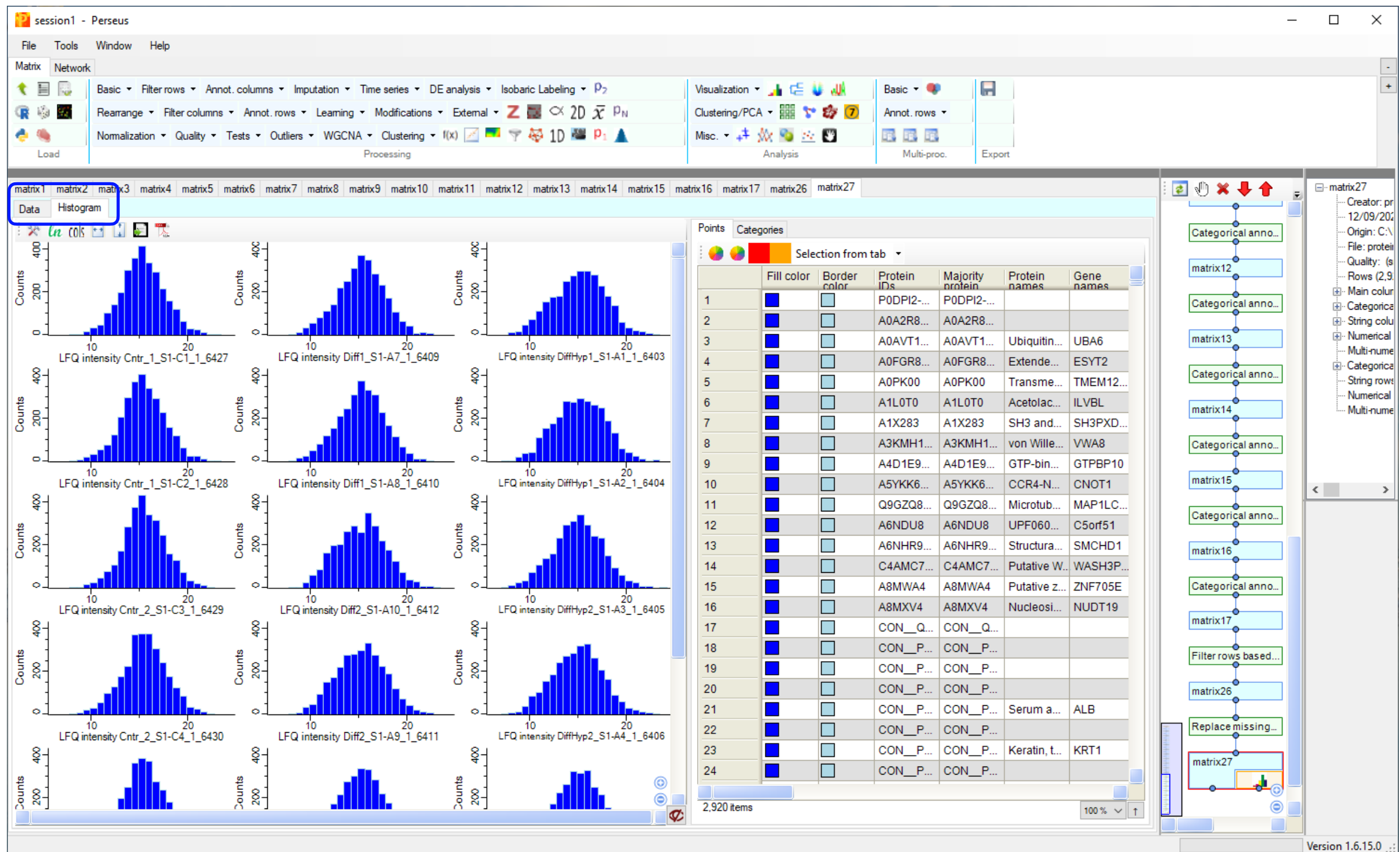
Data Quality - Distribution of the intensity values of the different proteins? :

Visualisation - Histogram



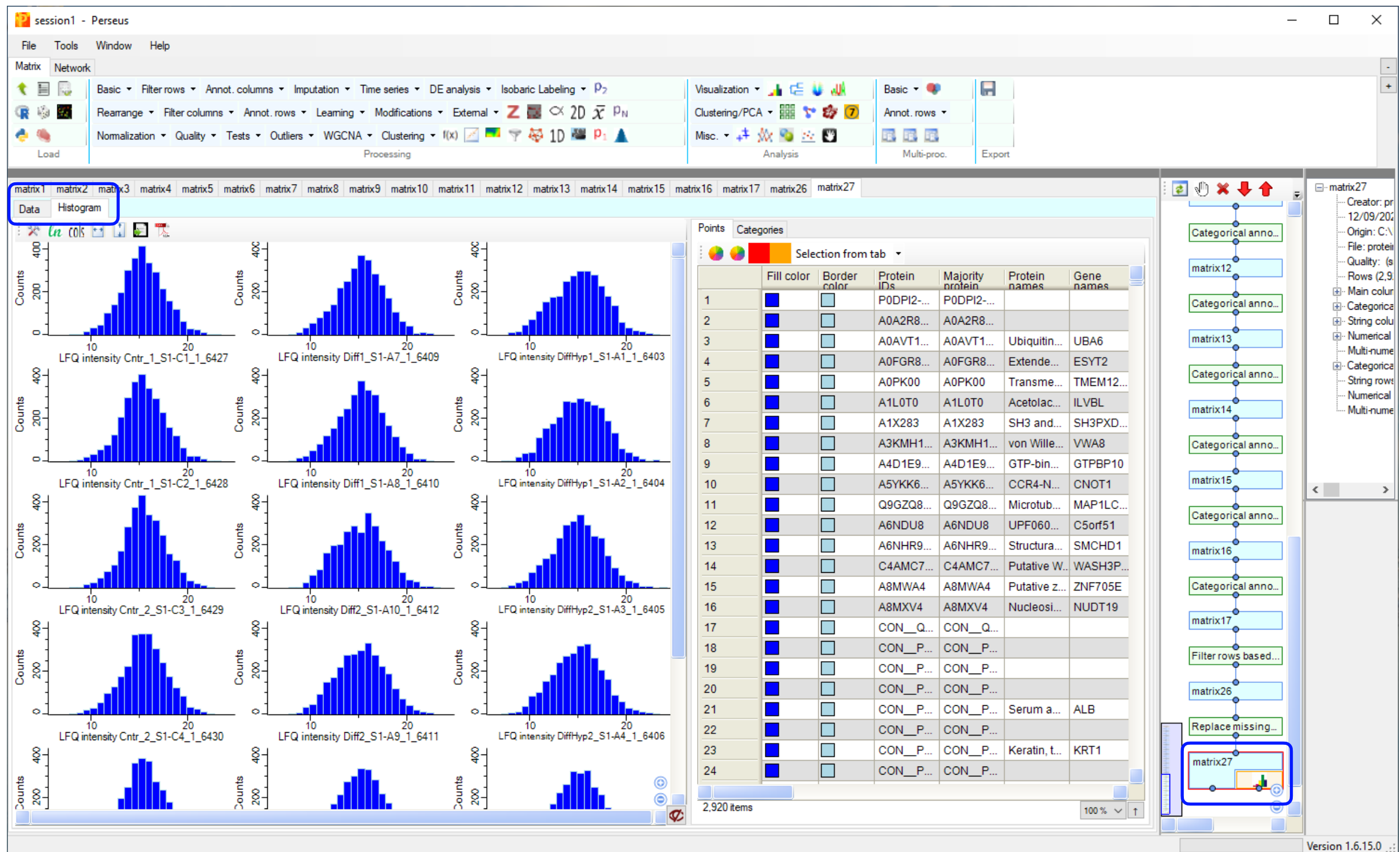
Data Quality - Distribution of the intensity values of the different proteins? :

Visualisation - Histogram



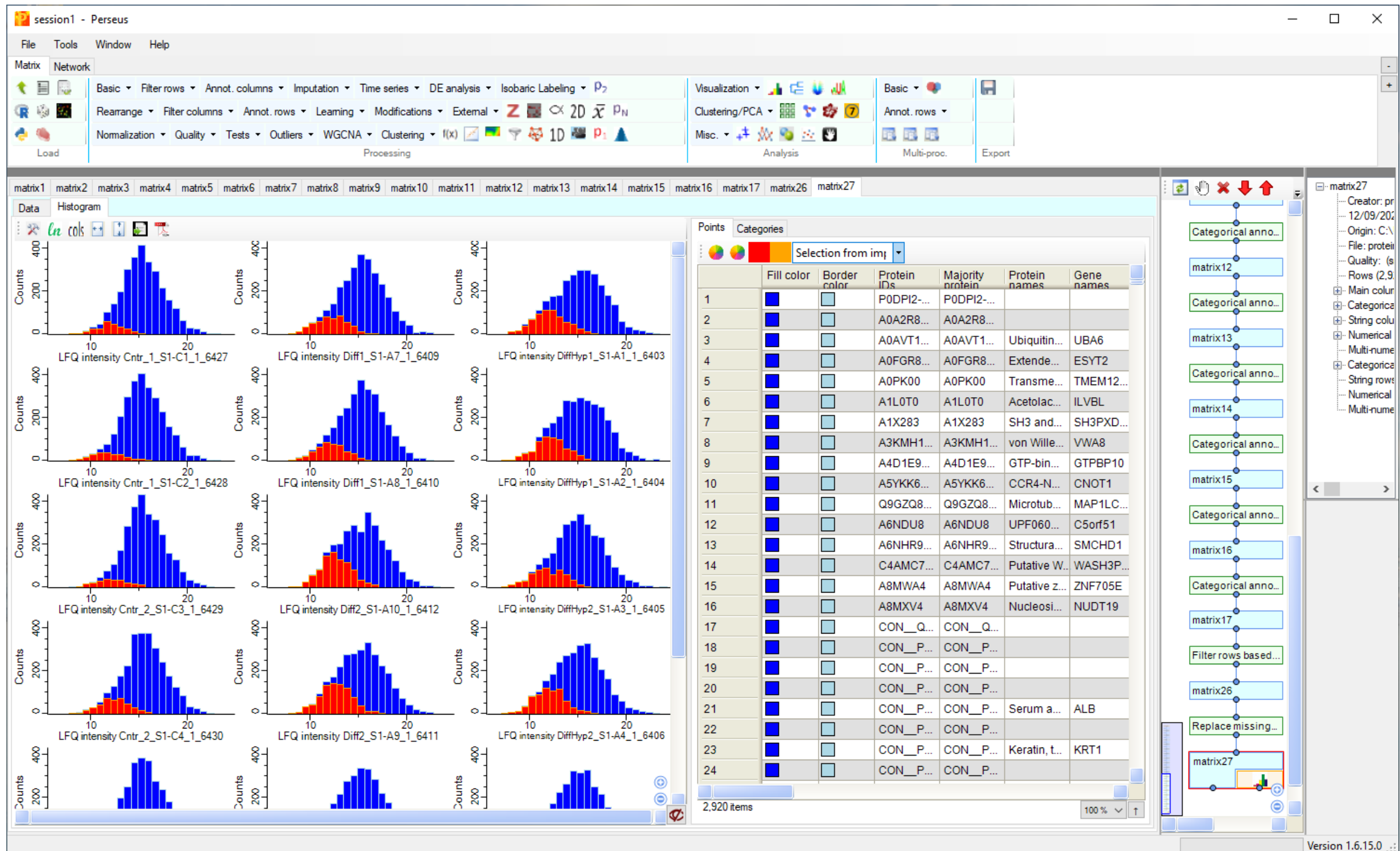
Data Quality - Distribution of the intensity values of the different proteins? :

Visualisation - Histogram

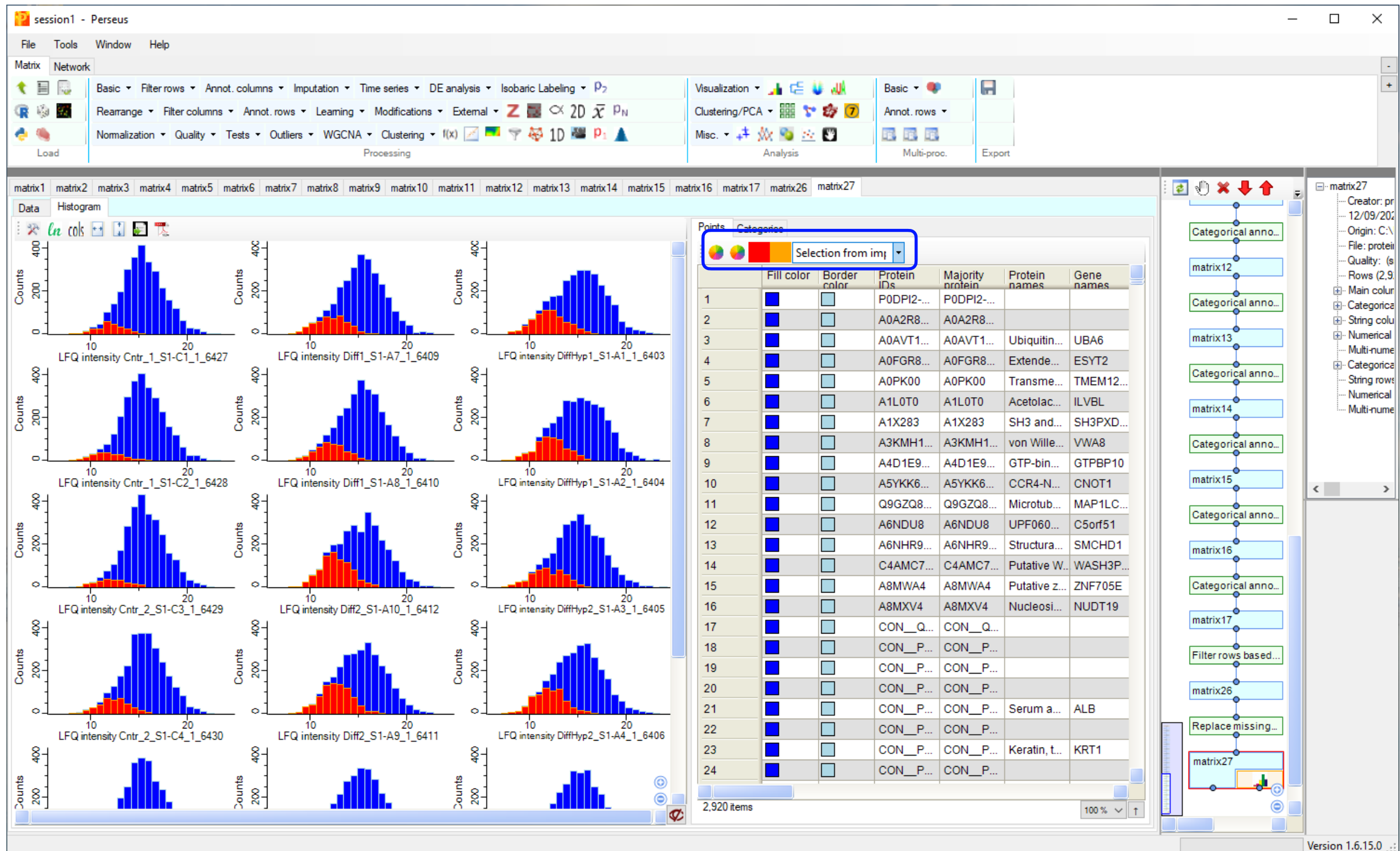


Data Quality - Distribution of the intensity values of the different proteins? :

Visualisation - Histogram

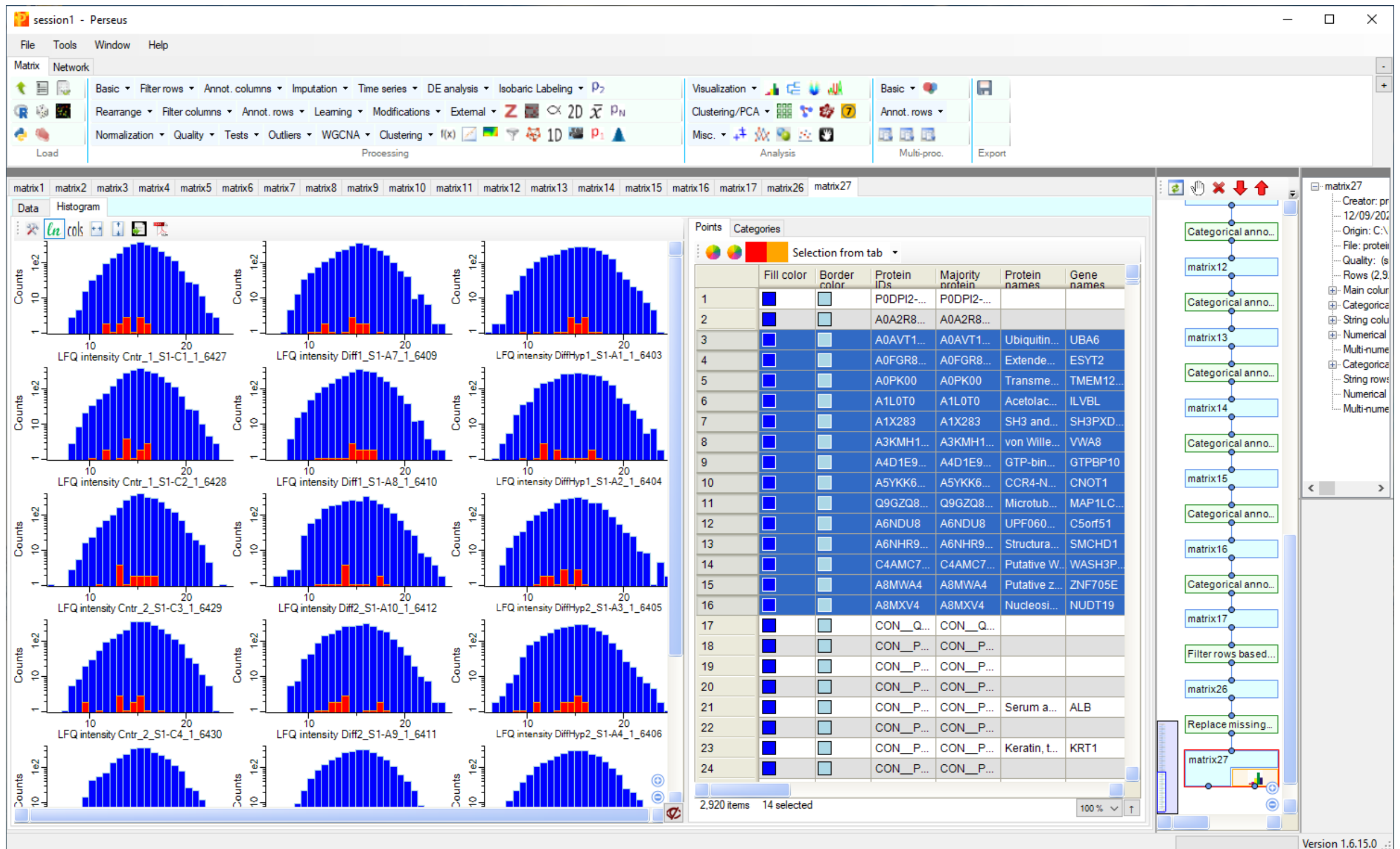


Visualisation - Histogram



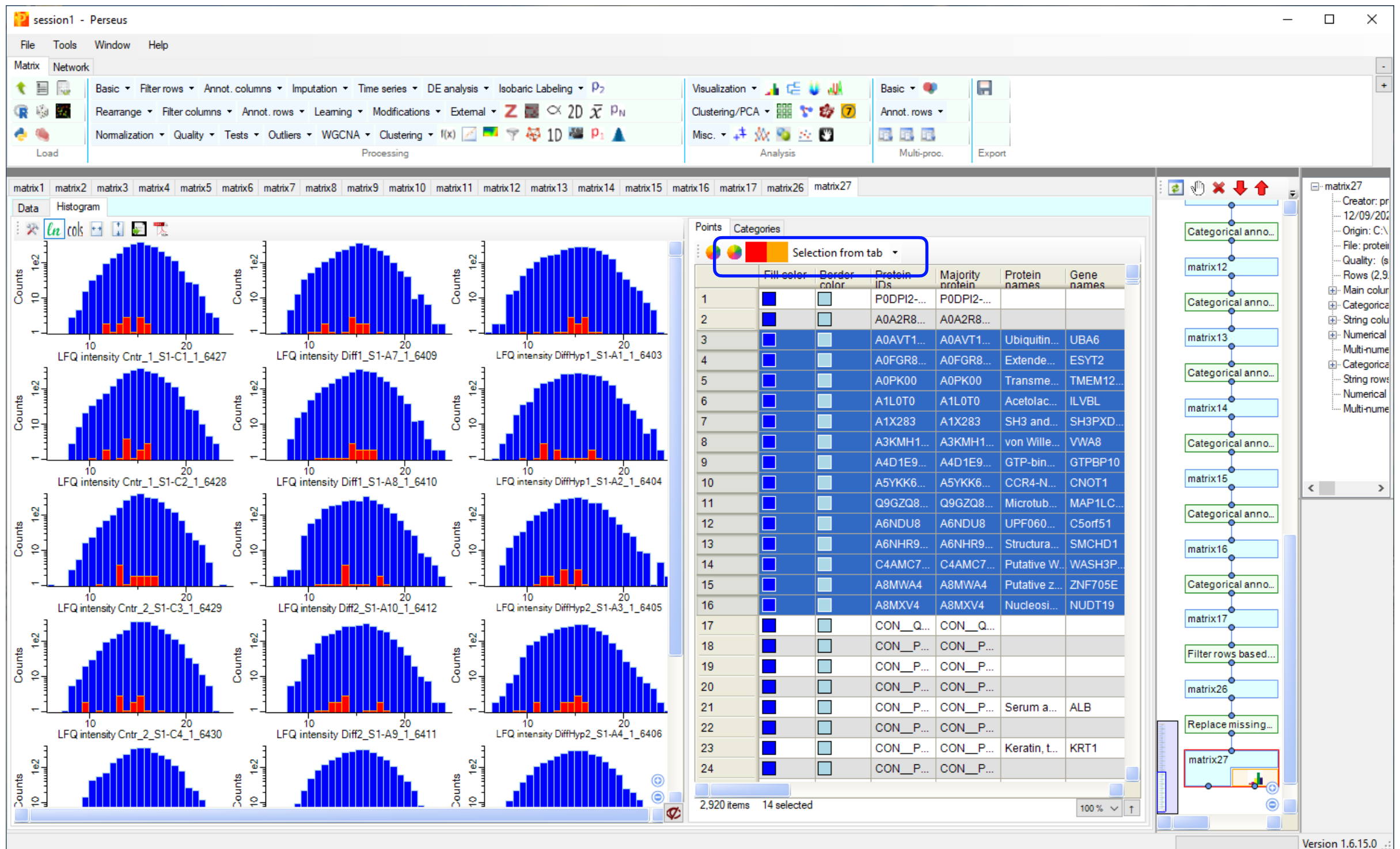
Data Quality - Distribution of the intensity values of the different proteins? :

Visualisation - Histogram



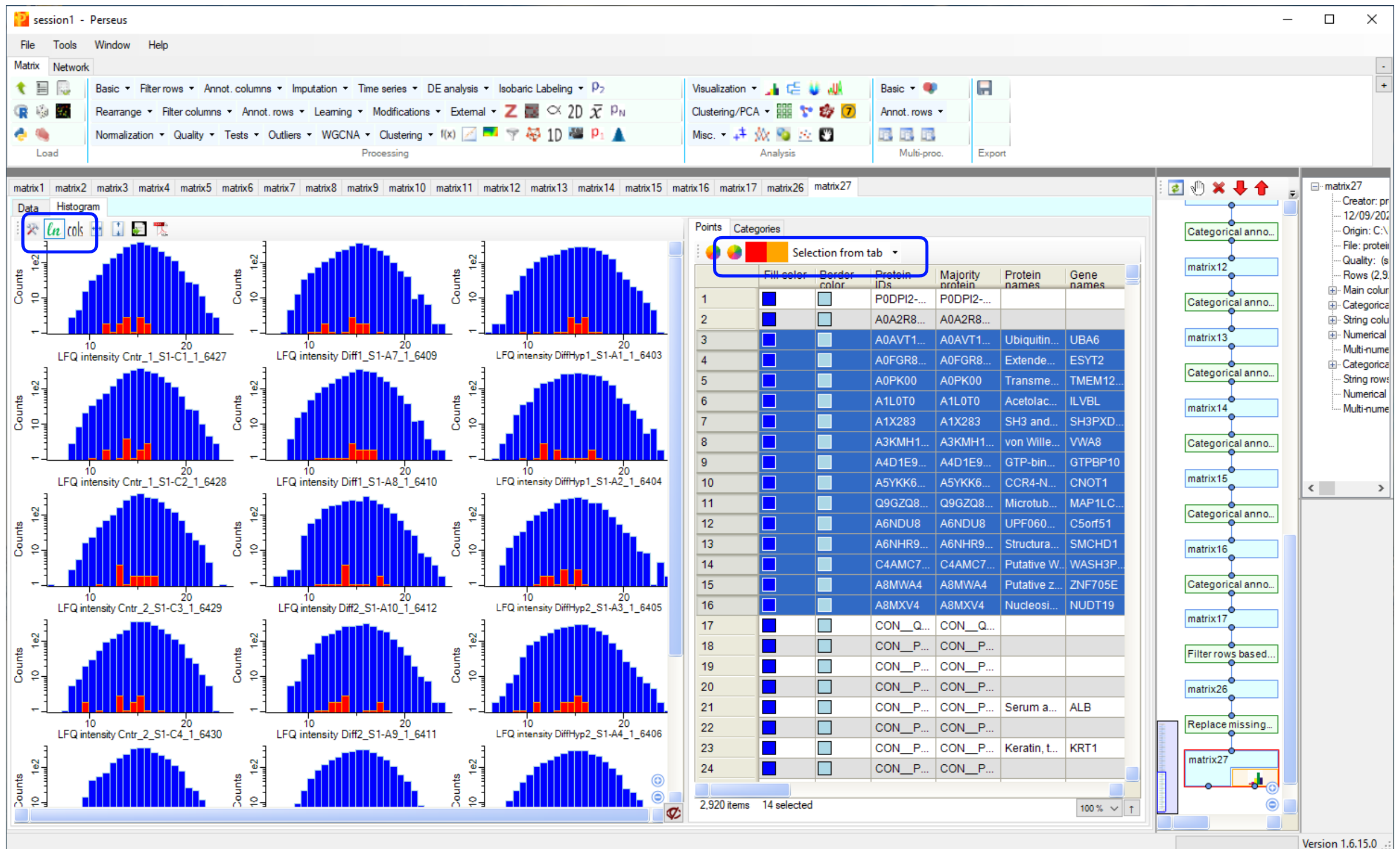
Data Quality - Distribution of the intensity values of the different proteins? :

Visualisation - Histogram

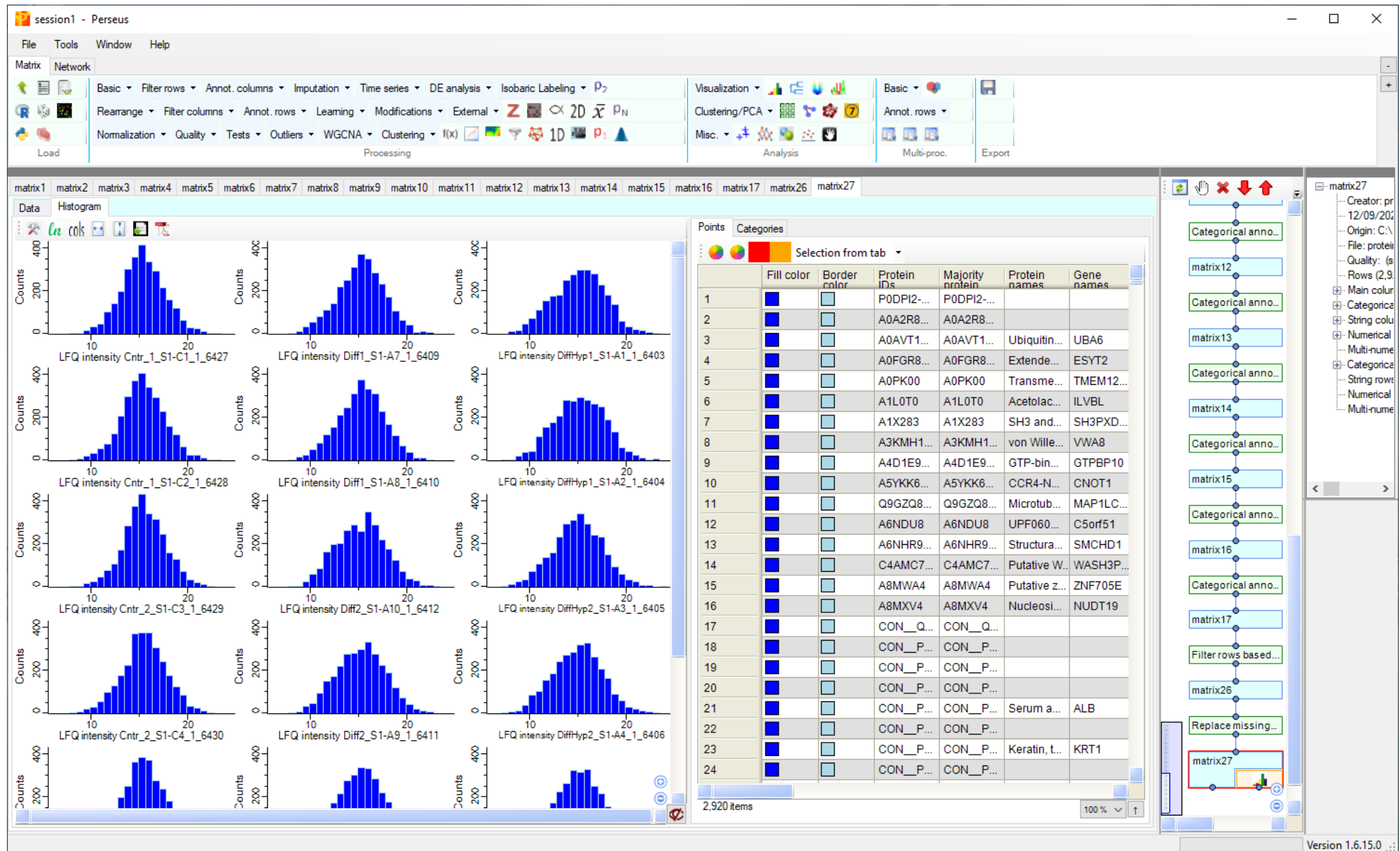


Data Quality - Distribution of the intensity values of the different proteins? :

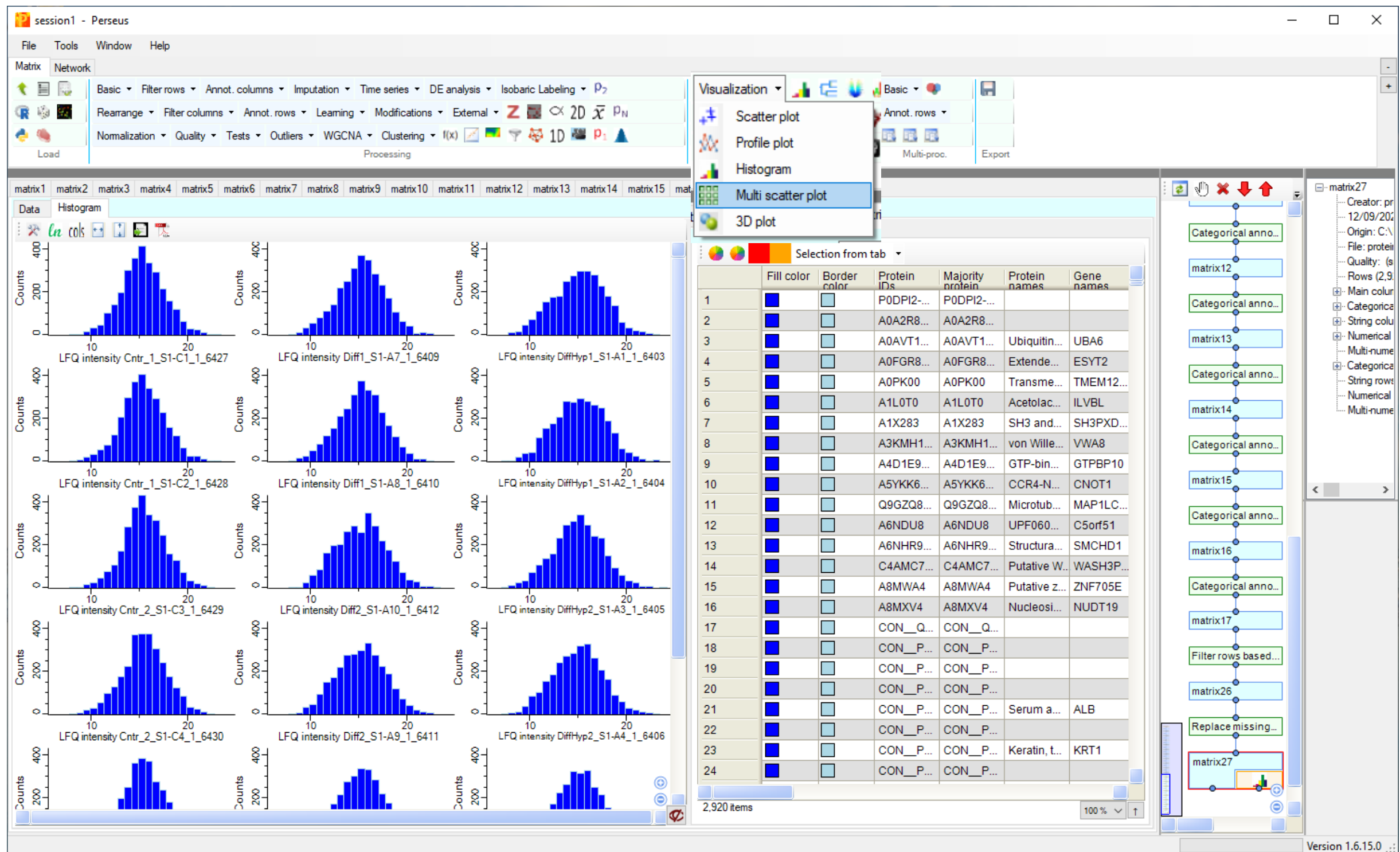
Visualisation - Histogram



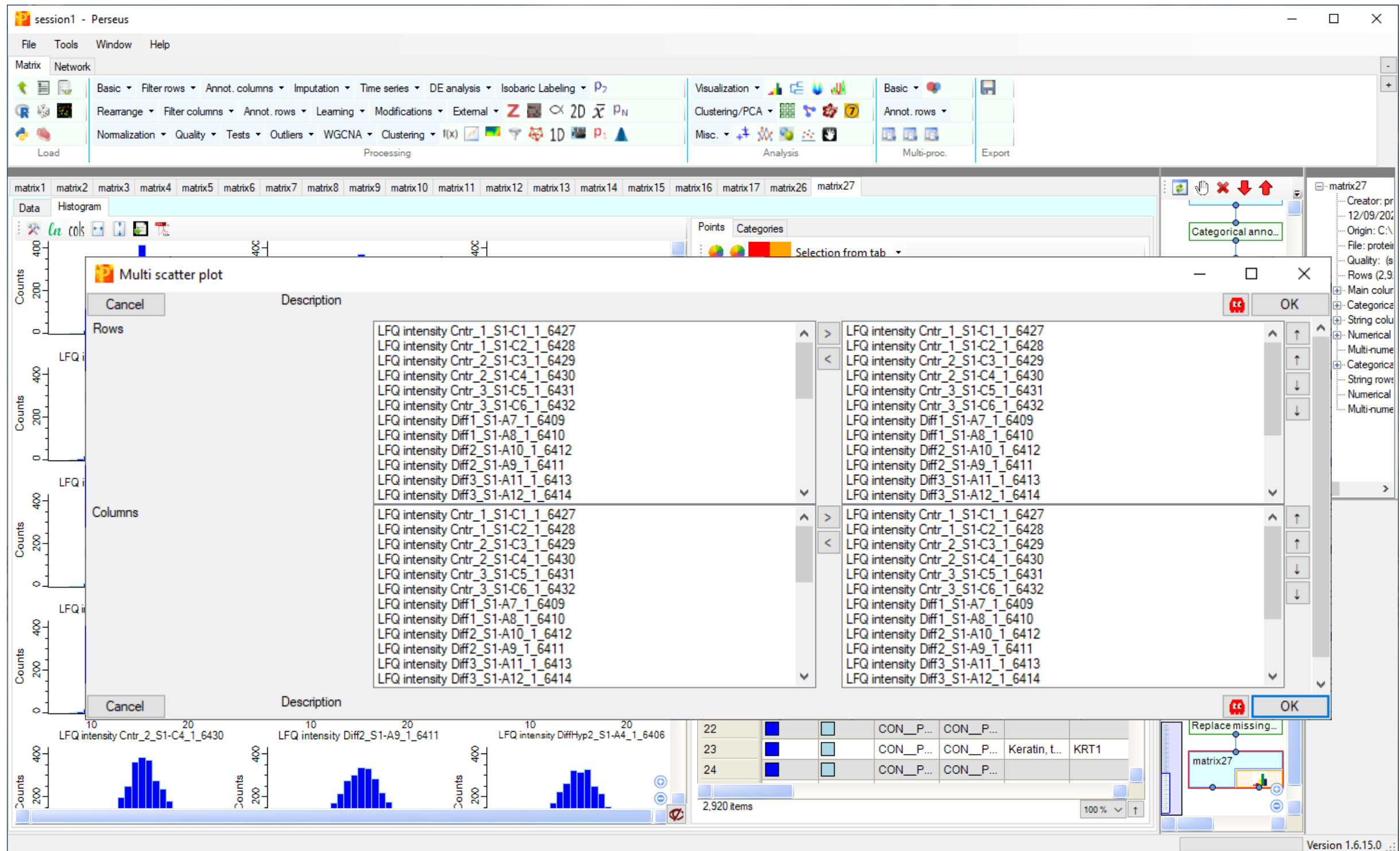
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



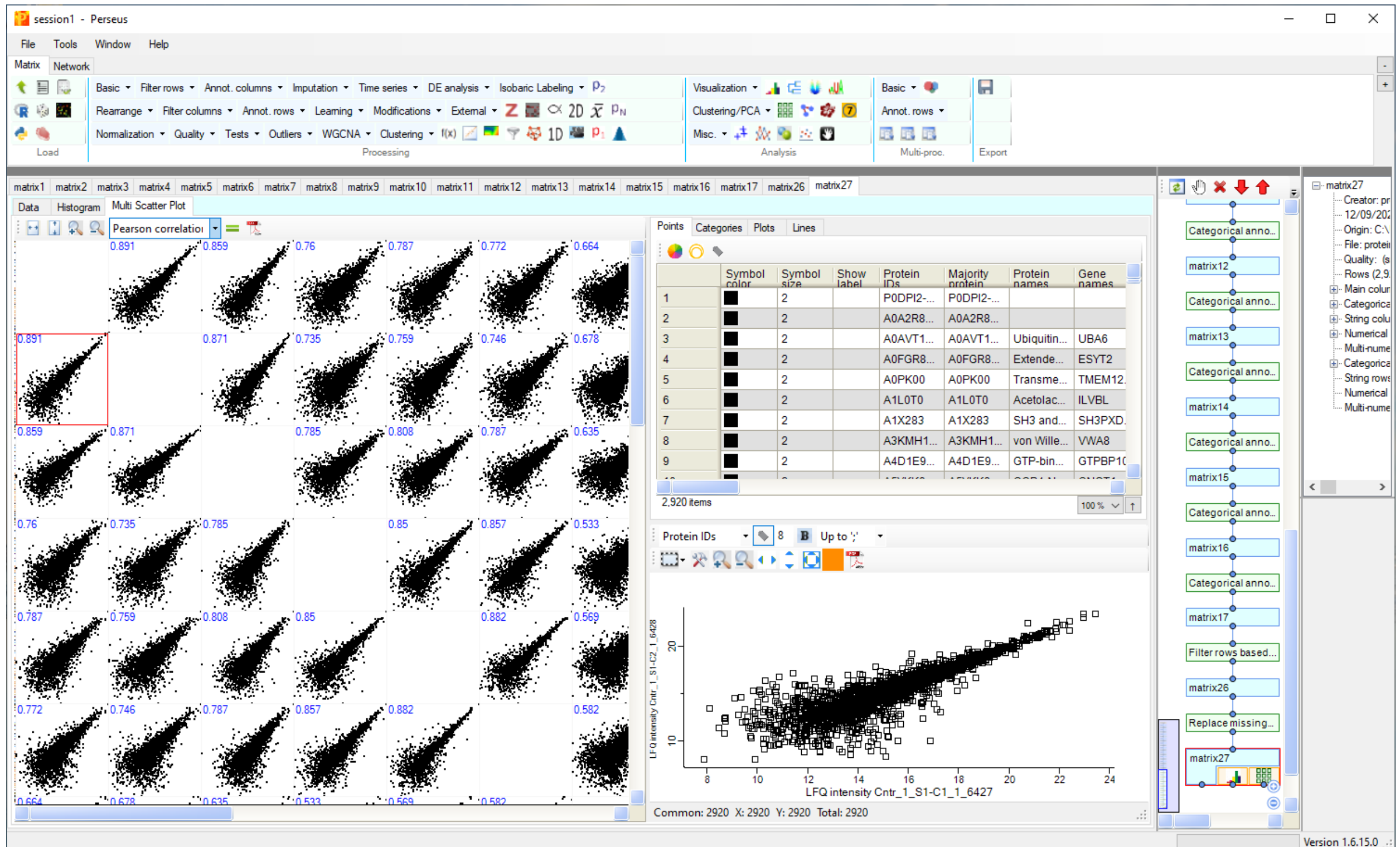
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



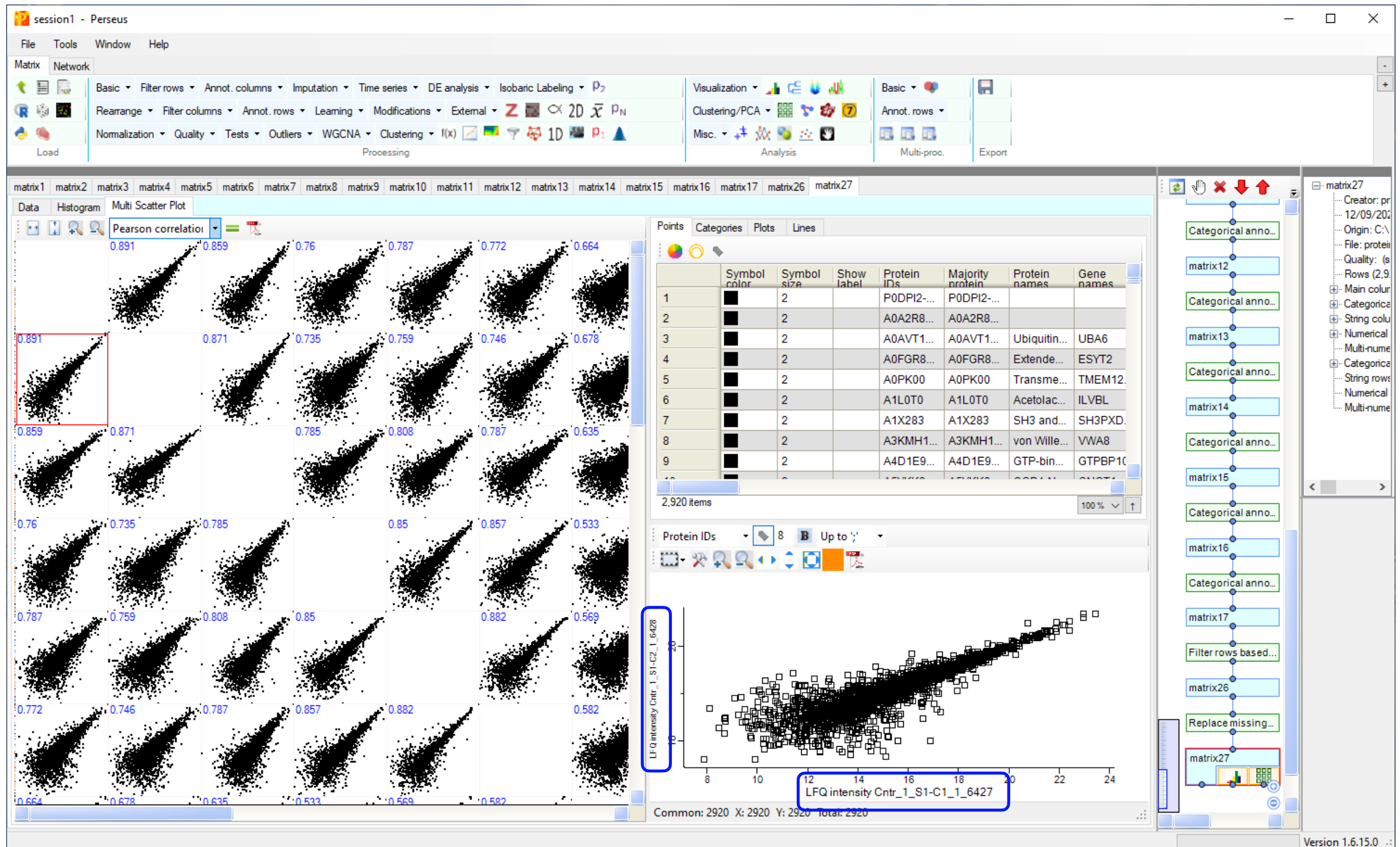
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



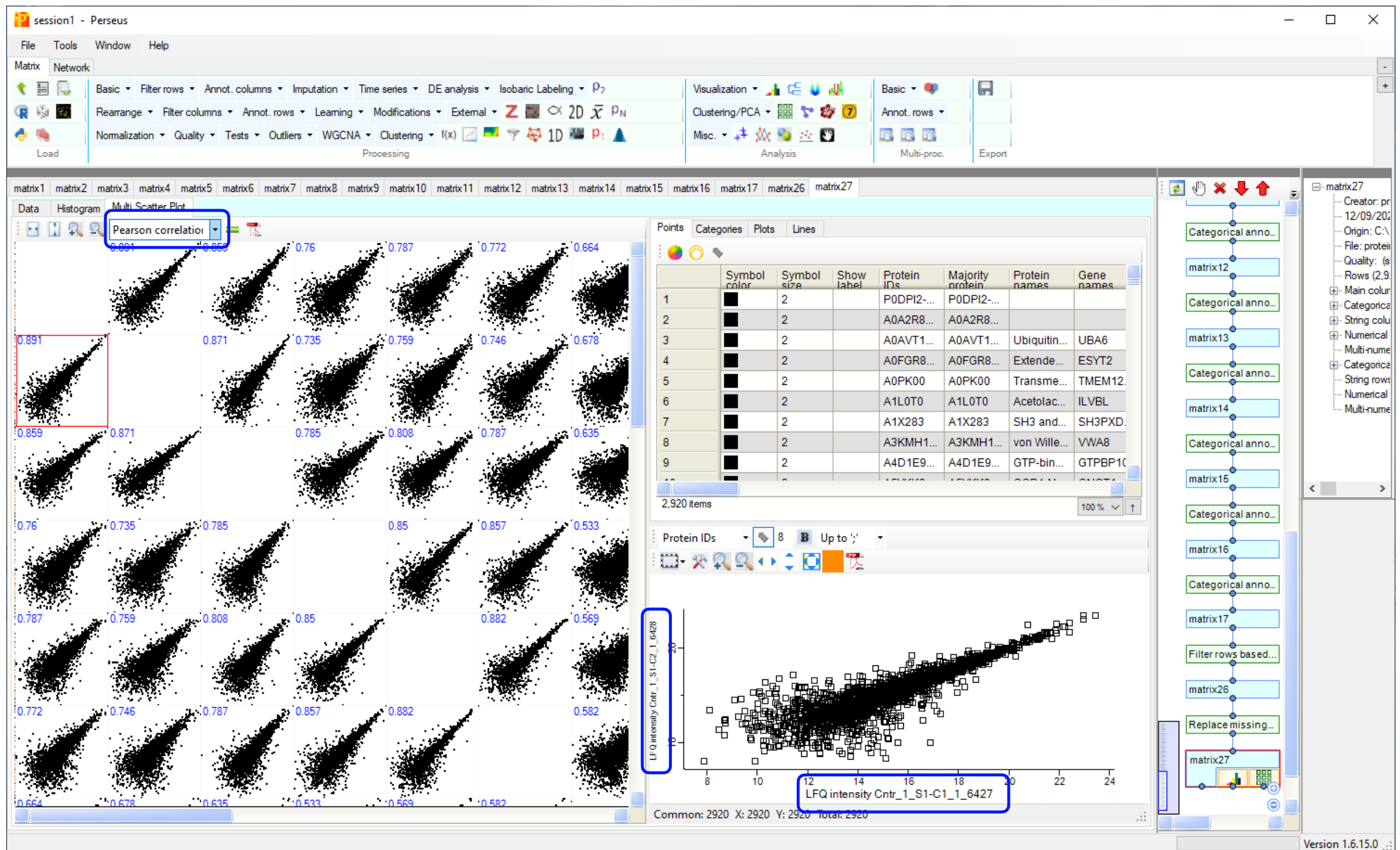
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



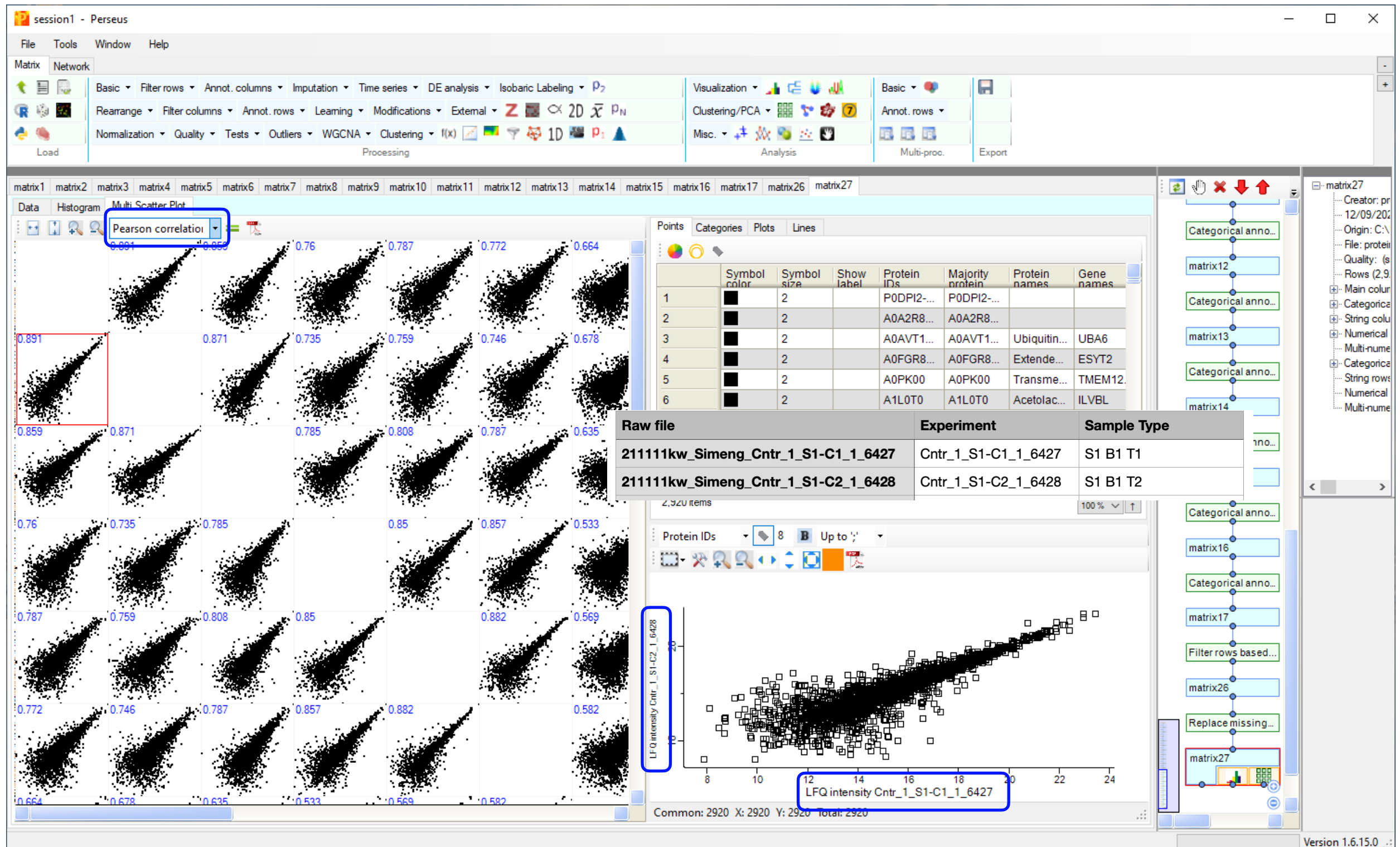
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



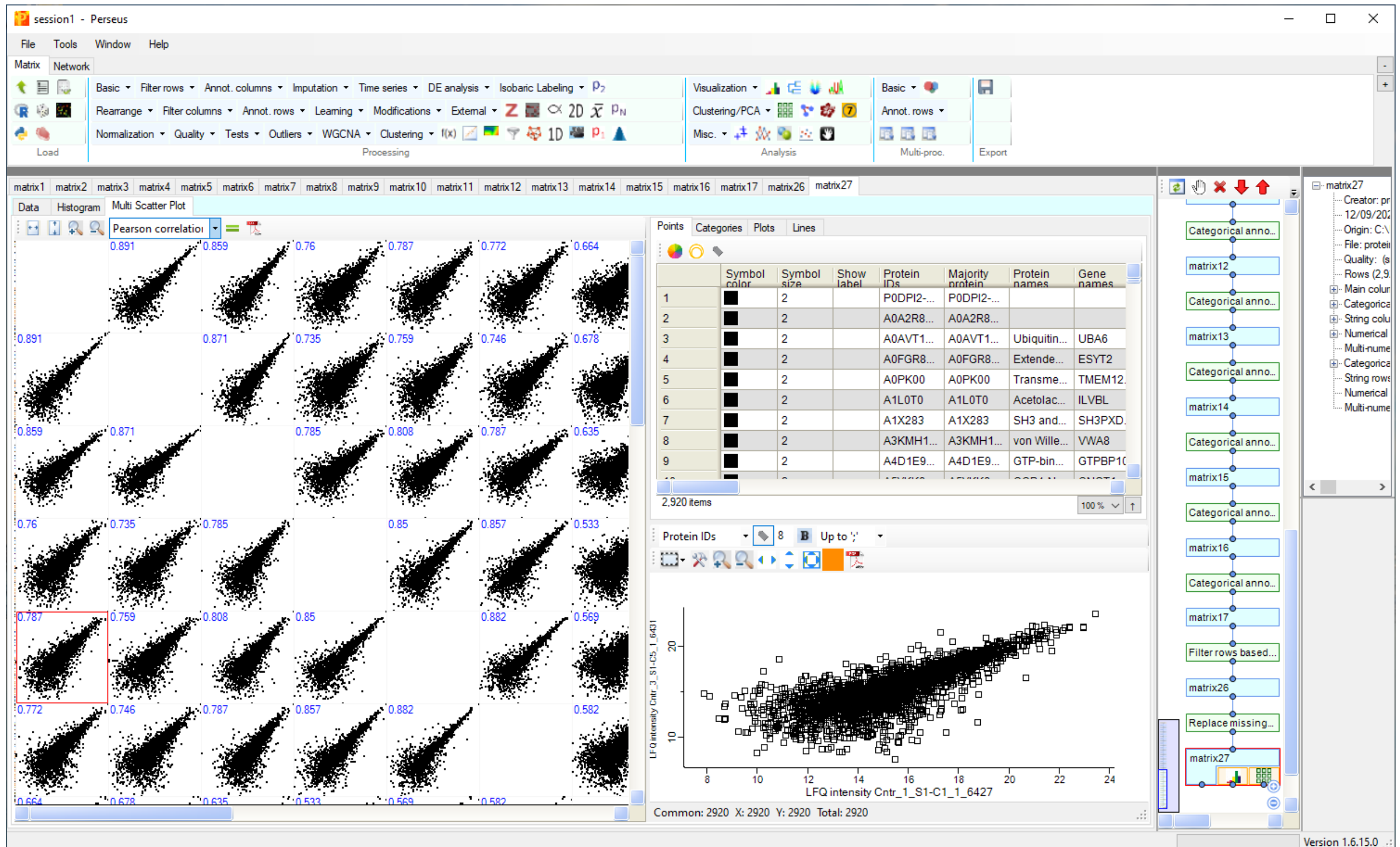
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



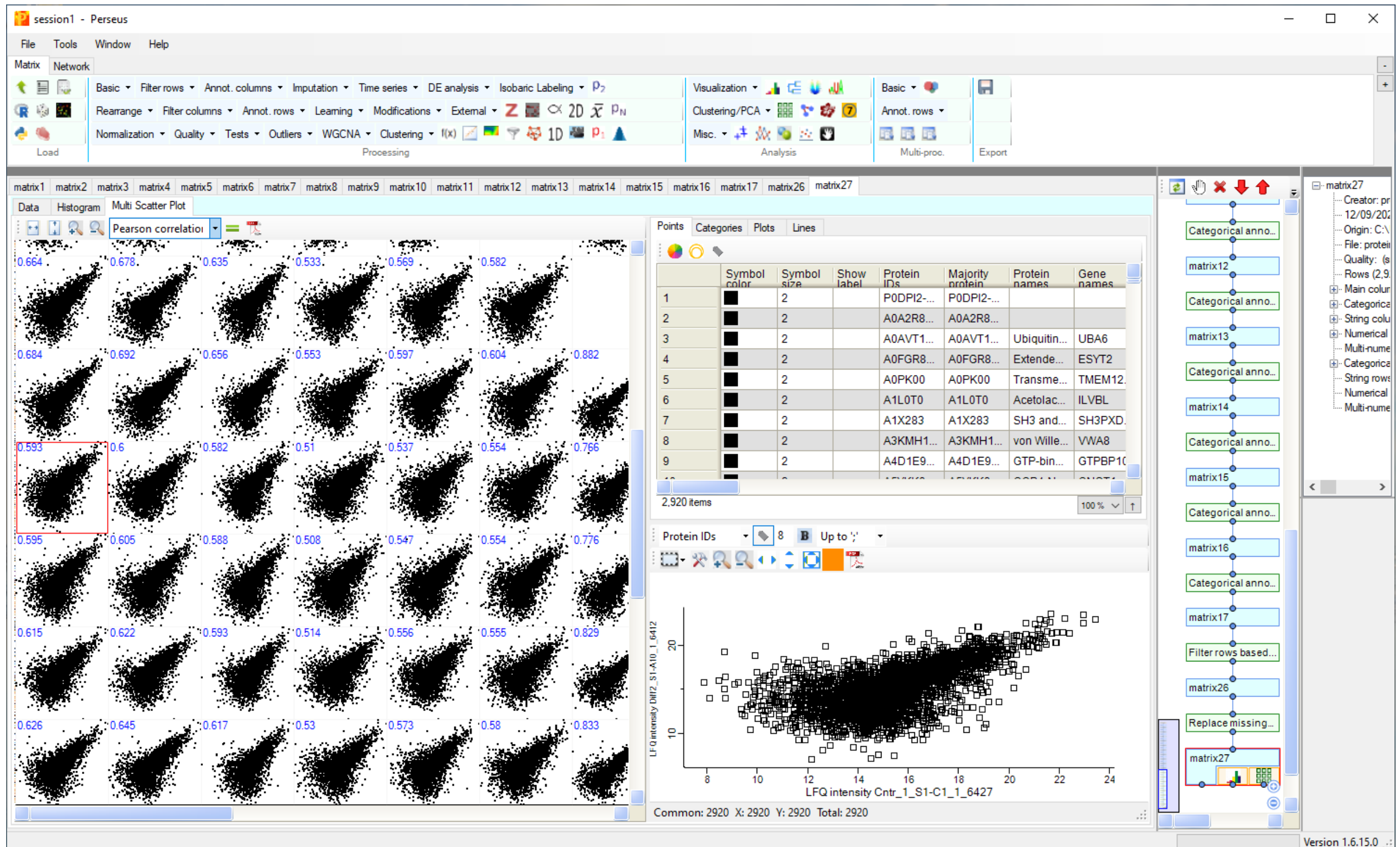
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



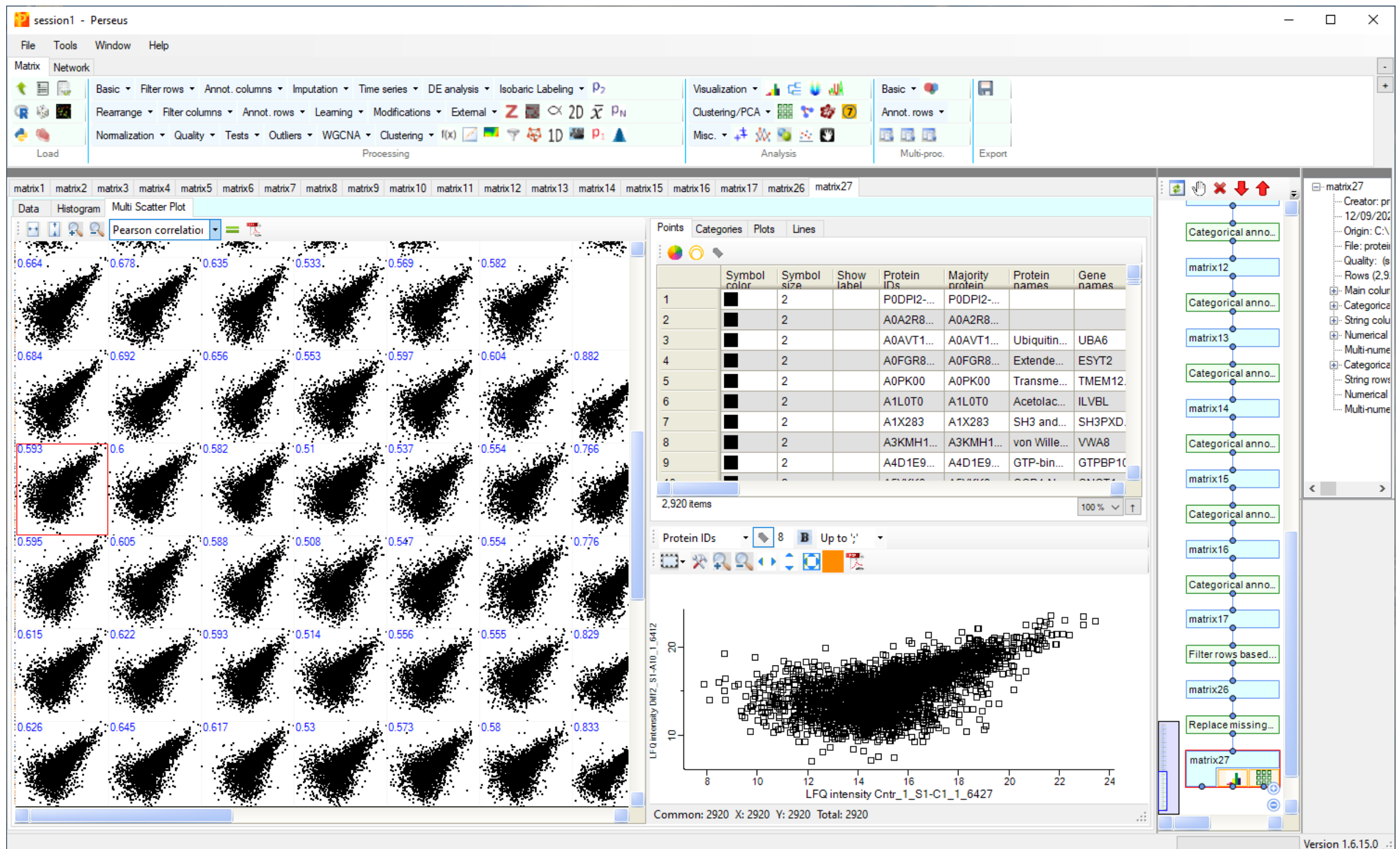
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



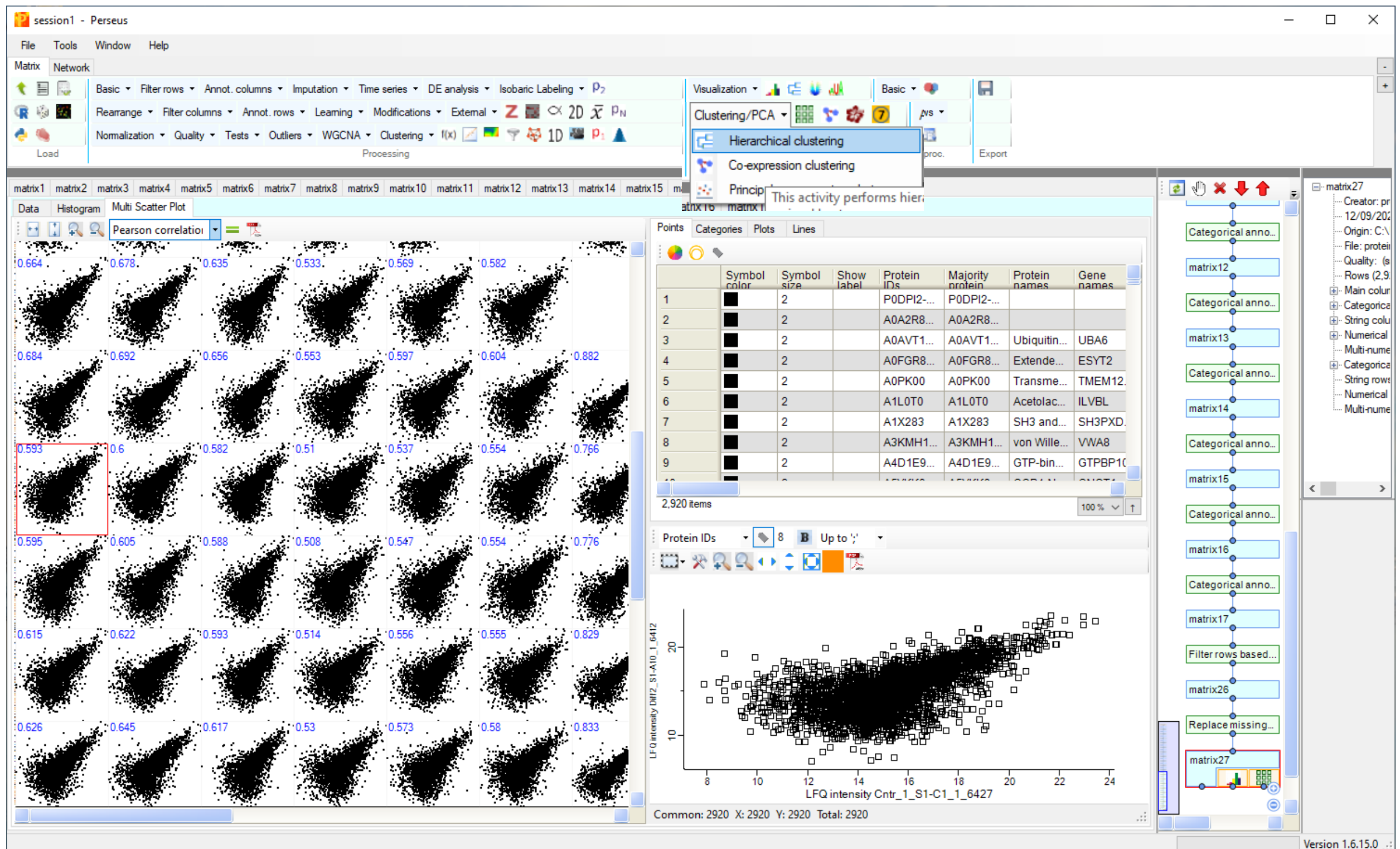
Statistical Data Analysis - Data Quality : **Visualisation - Multi Scatter Plot**



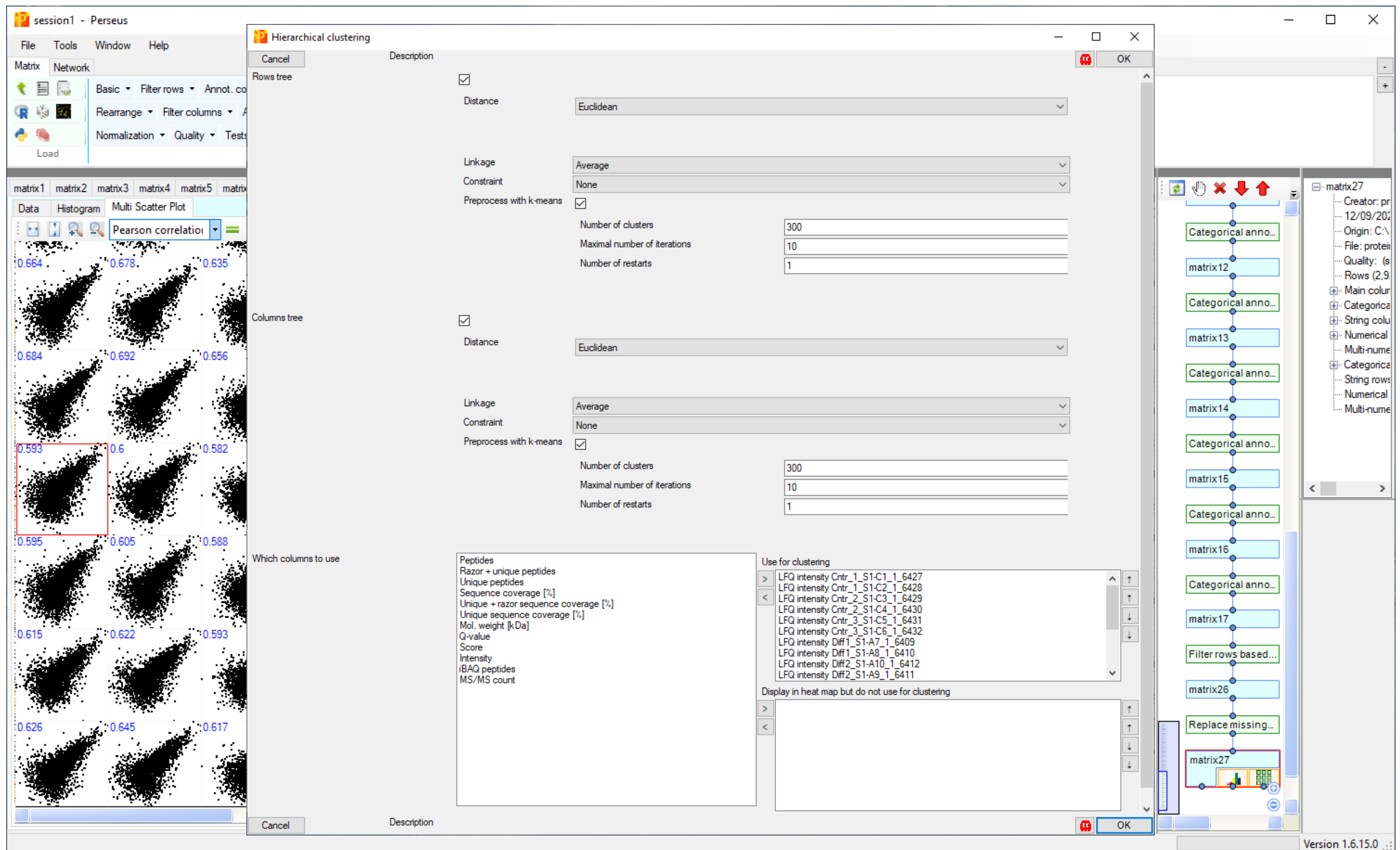
Statistical Data Analysis - Data Quality : **Clustering/PCA - Hierarchical Cluster**



Statistical Data Analysis - Data Quality : **Clustering/PCA - Hierarchical Cluster**



Statistical Data Analysis - Data Quality : **Clustering/PCA - Hierarchical Cluster**



The screenshot displays the Perseus software interface, specifically the 'Hierarchical clustering' dialog box and the main data matrix view.

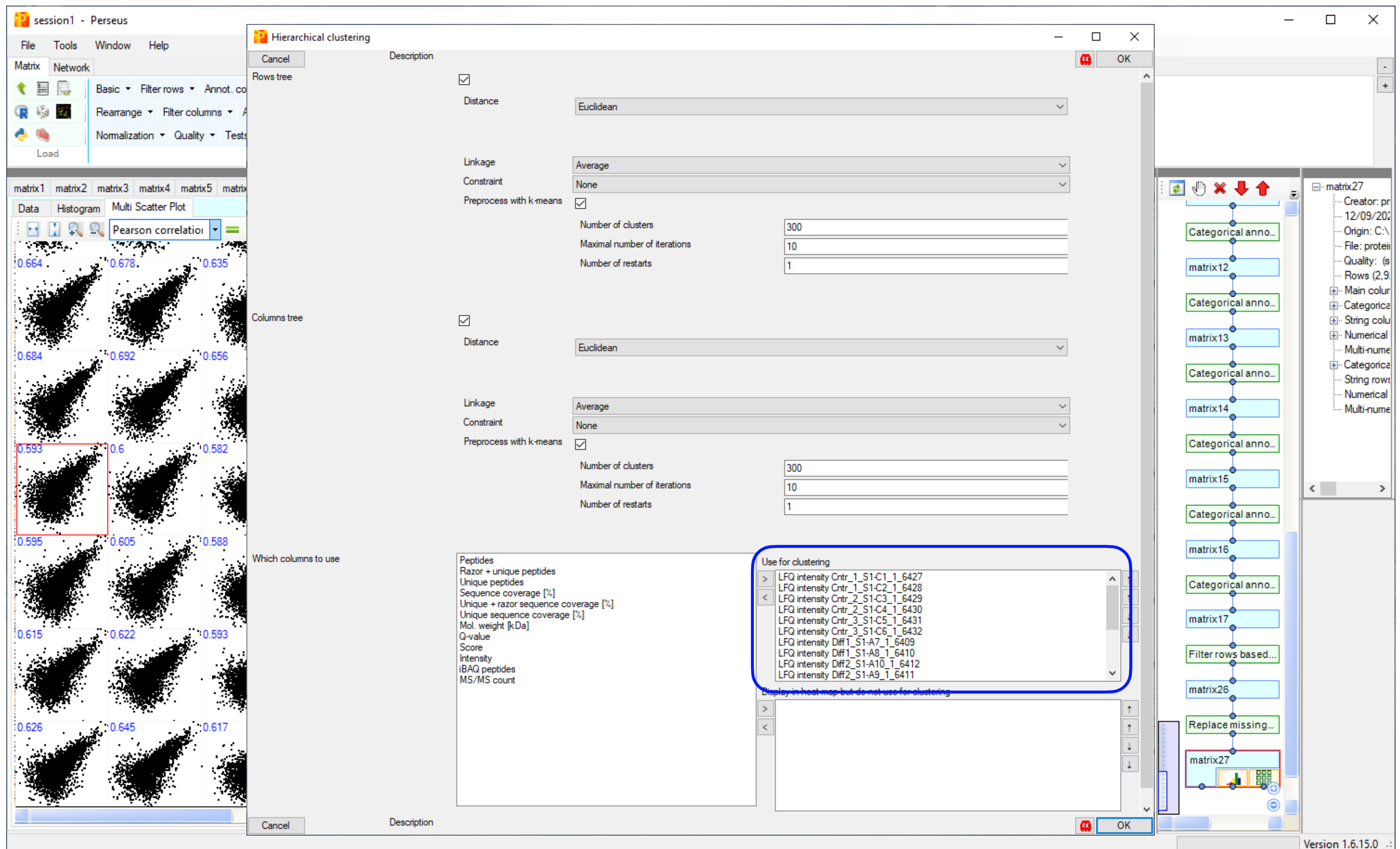
Hierarchical clustering dialog box:

- Rows tree:** Distance: Euclidean, Linkage: Average, Constraint: None, Preprocess with k-means: ☒. Parameters: Number of clusters: 300, Maximal number of iterations: 10, Number of restarts: 1.
- Columns tree:** Distance: Euclidean, Linkage: Average, Constraint: None, Preprocess with k-means: ☒. Parameters: Number of clusters: 300, Maximal number of iterations: 10, Number of restarts: 1.
- Which columns to use:**
 - Peptides
 - Razor + unique peptides
 - Unique peptides
 - Sequence coverage [%]
 - Unique + razor sequence coverage [%]
 - Unique sequence coverage [%]
 - Mol. weight [kDa]
 - Q-value
 - Score
 - Intensity
 - iBAQ peptides
 - MS/MS count
- Use for clustering:**
 - LFQ intensity Cntr_1_S1-C1_1_6427
 - LFQ intensity Cntr_1_S1-C2_1_6428
 - LFQ intensity Cntr_2_S1-C3_1_6429
 - LFQ intensity Cntr_2_S1-C4_1_6430
 - LFQ intensity Cntr_3_S1-C5_1_6431
 - LFQ intensity Cntr_3_S1-C6_1_6432
 - LFQ intensity Diff1_S1-A7_1_6409
 - LFQ intensity Diff1_S1-A8_1_6410
 - LFQ intensity Diff2_S1-A10_1_6412
 - LFQ intensity Diff2_S1-A9_1_6411
- Display in heat map but do not use for clustering:** (Empty list)

Main data matrix view:

- Matrix:** matrix1, matrix2, matrix3, matrix4, matrix5, matrix6, matrix7, matrix8, matrix9, matrix10, matrix11, matrix12, matrix13, matrix14, matrix15, matrix16, matrix17, matrix18, matrix19, matrix20, matrix21, matrix22, matrix23, matrix24, matrix25, matrix26, matrix27.
- Data:** Pearson correlation (0.664, 0.678, 0.635, 0.684, 0.692, 0.656, 0.593, 0.6, 0.582, 0.595, 0.605, 0.588, 0.615, 0.622, 0.593, 0.626, 0.645, 0.617).
- Columns tree:** Categorical anno..., matrix12, Categorical anno..., matrix13, Categorical anno..., matrix14, Categorical anno..., matrix15, Categorical anno..., matrix16, Categorical anno..., matrix17, Filter rows based..., matrix26, Replace missing..., matrix27.
- Version:** 1.6.15.0

Statistical Data Analysis - Data Quality : **Clustering/PCA - Hierarchical Cluster**



The screenshot displays the Perseus software interface, specifically the 'Hierarchical clustering' dialog box and the main data matrix view.

Hierarchical clustering dialog box:

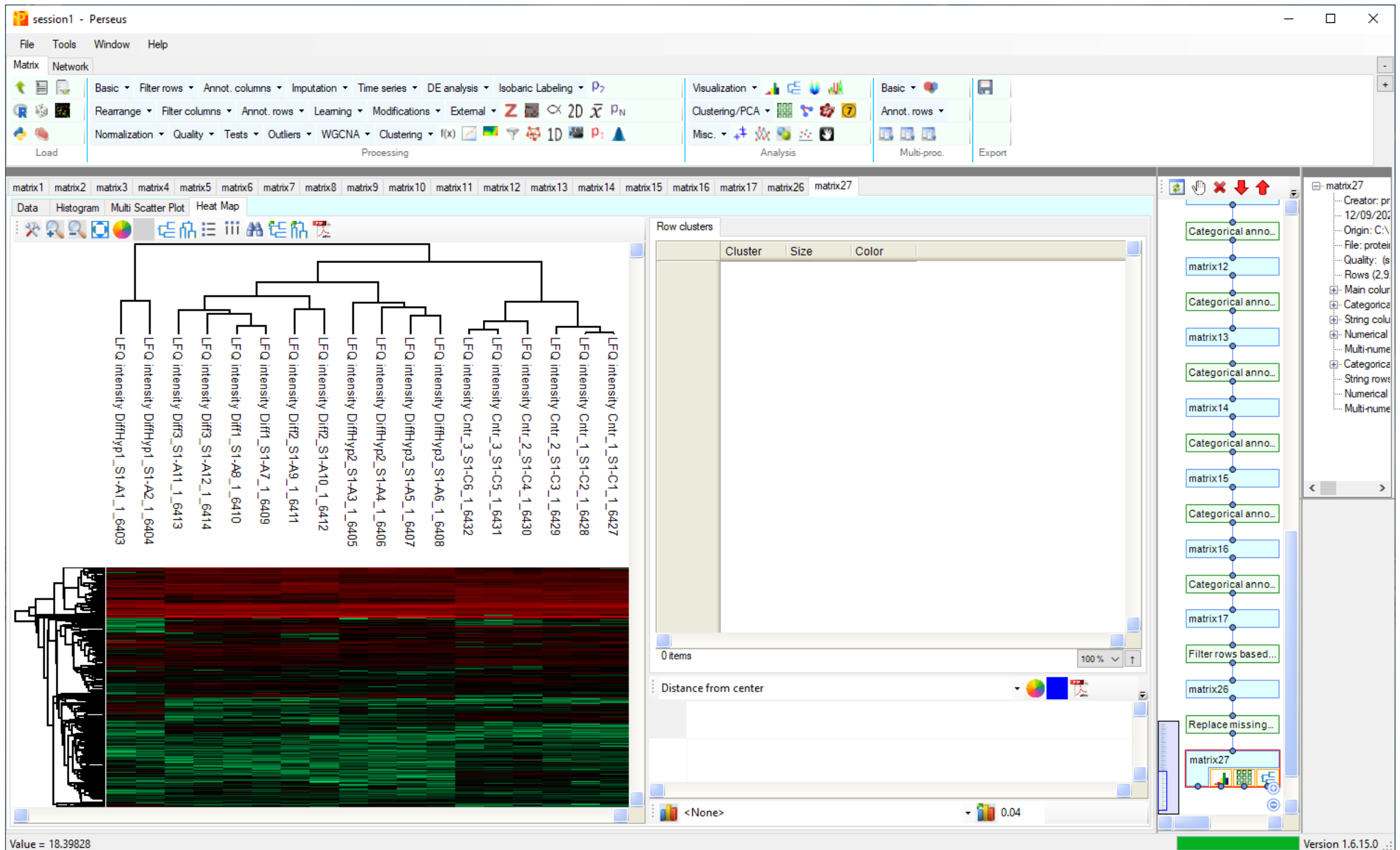
- Distance:** Euclidean
- Linkage:** Average
- Constraint:** None
- Preprocess with k-means:** ☒
 - Number of clusters: 300
 - Maximal number of iterations: 10
 - Number of restarts: 1

Main data matrix view:

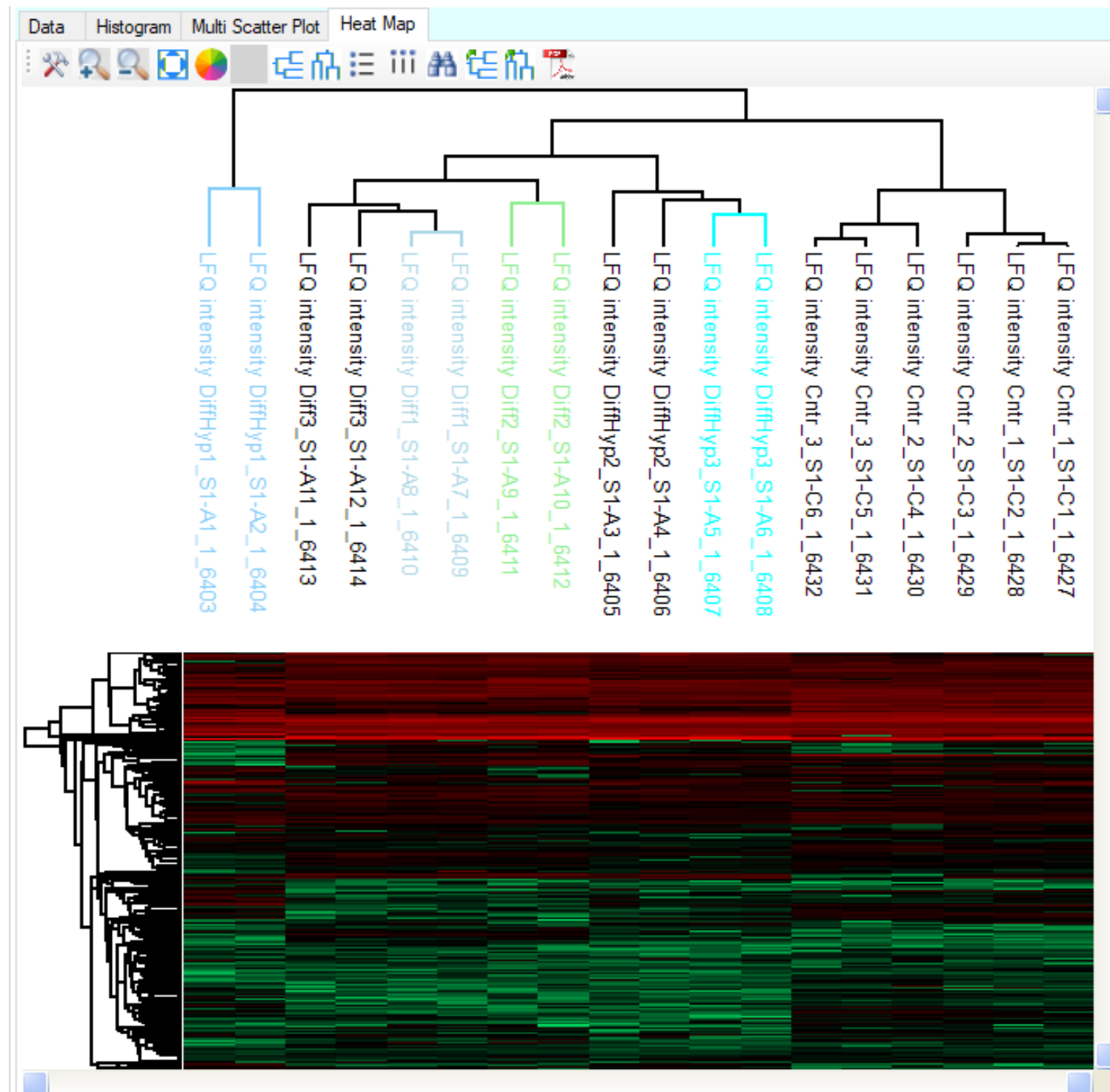
- Columns tree:** A list of columns is shown, including 'Peptides', 'Razor + unique peptides', 'Unique peptides', 'Sequence coverage [%]', 'Unique + razor sequence coverage [%]', 'Unique sequence coverage [%]', 'Mol. weight [kDa]', 'Q-value', 'Score', 'Intensity', 'iBAQ peptides', and 'MS/MS count'.
- Which columns to use:** A list of columns is shown, including 'Peptides', 'Razor + unique peptides', 'Unique peptides', 'Sequence coverage [%]', 'Unique + razor sequence coverage [%]', 'Unique sequence coverage [%]', 'Mol. weight [kDa]', 'Q-value', 'Score', 'Intensity', 'iBAQ peptides', and 'MS/MS count'.
- Use for clustering:** A list of columns is shown, including 'LFQ intensity Cntr_1_S1-C1_1_6427', 'LFQ intensity Cntr_1_S1-C2_1_6428', 'LFQ intensity Cntr_2_S1-C3_1_6429', 'LFQ intensity Cntr_2_S1-C4_1_6430', 'LFQ intensity Cntr_3_S1-C5_1_6431', 'LFQ intensity Cntr_3_S1-C6_1_6432', 'LFQ intensity Diff1_S1-A7_1_6409', 'LFQ intensity Diff1_S1-A8_1_6410', 'LFQ intensity Diff2_S1-A10_1_6412', and 'LFQ intensity Diff2_S1-A9_1_6411'.

The main data matrix view shows a grid of scatter plots with Pearson correlation values. A red box highlights a specific cluster of data points.

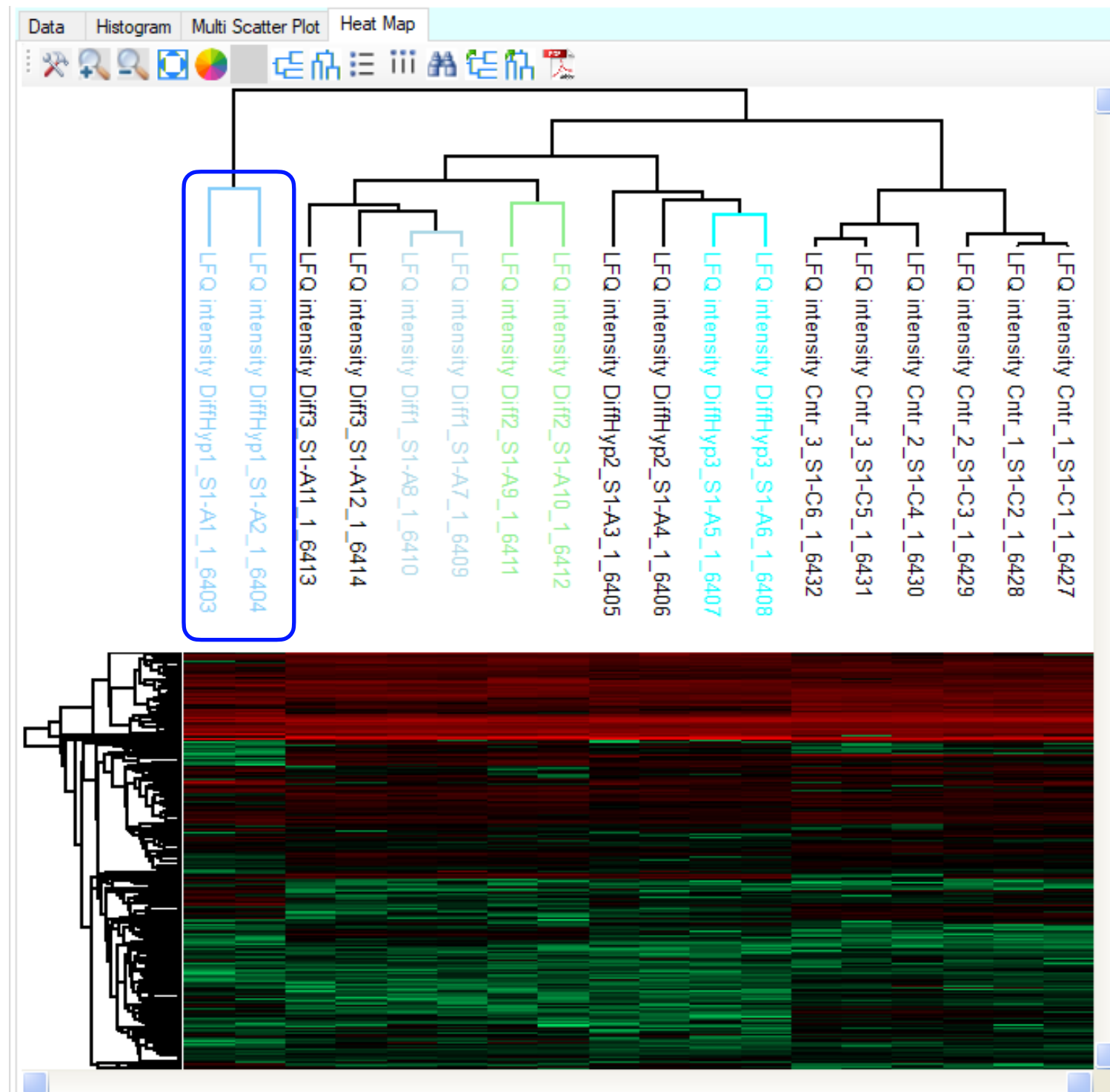
Cluster



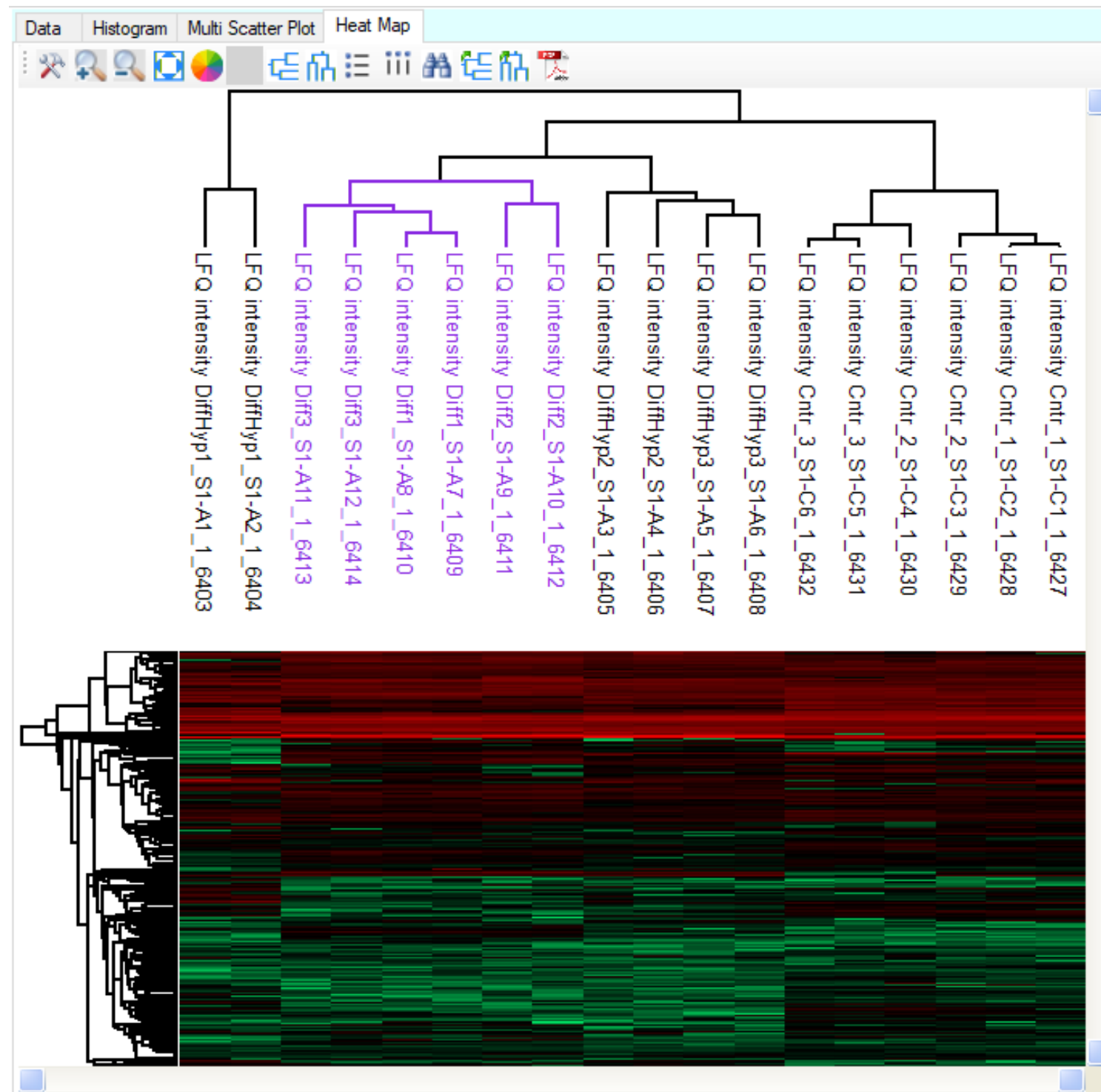
Statistical Data Analysis - Data Quality : **Clustering/PCA - Hierarchical Cluster**



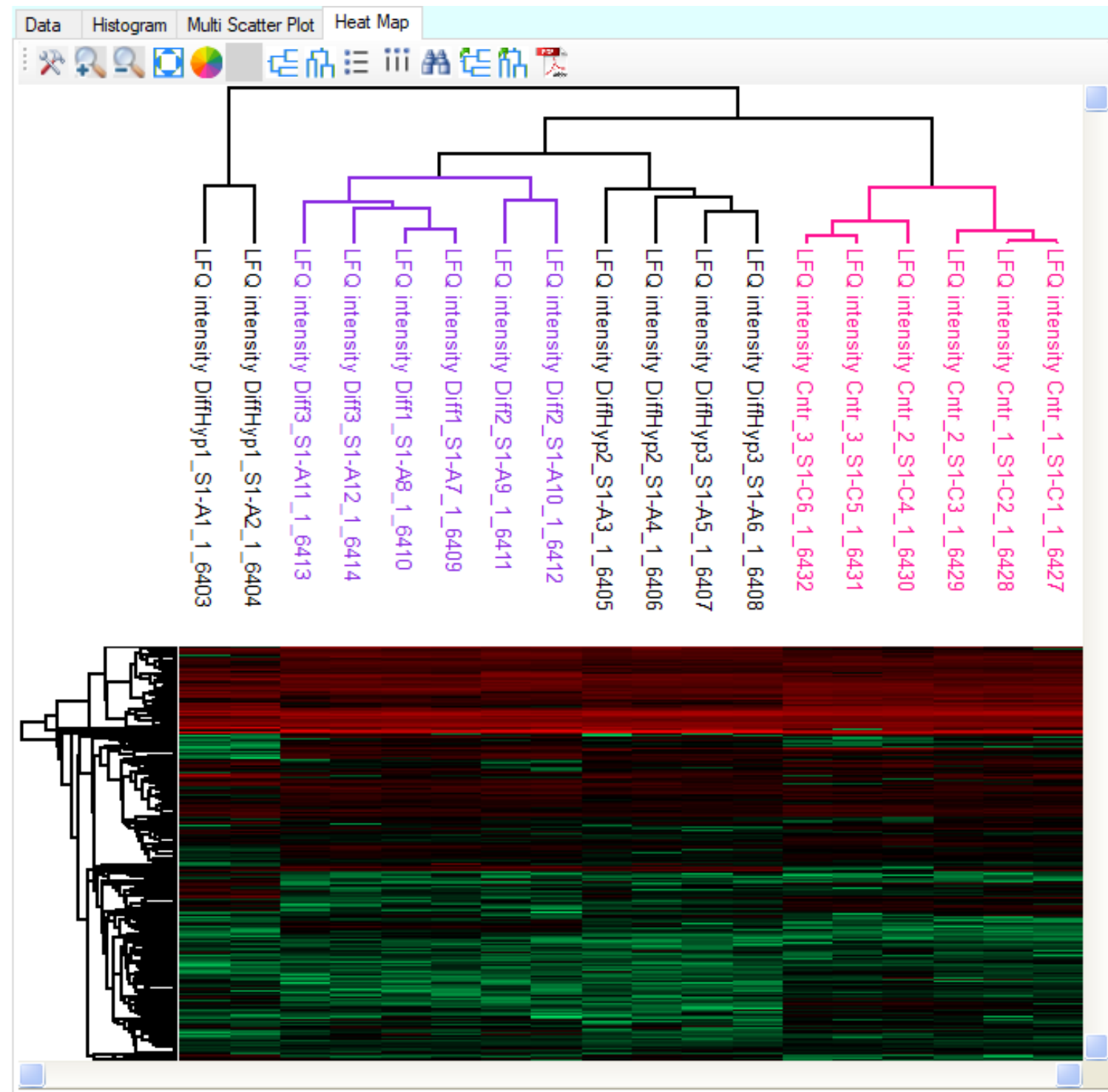
Statistical Data Analysis - Data Quality : **Clustering/PCA - Hierarchical Cluster**



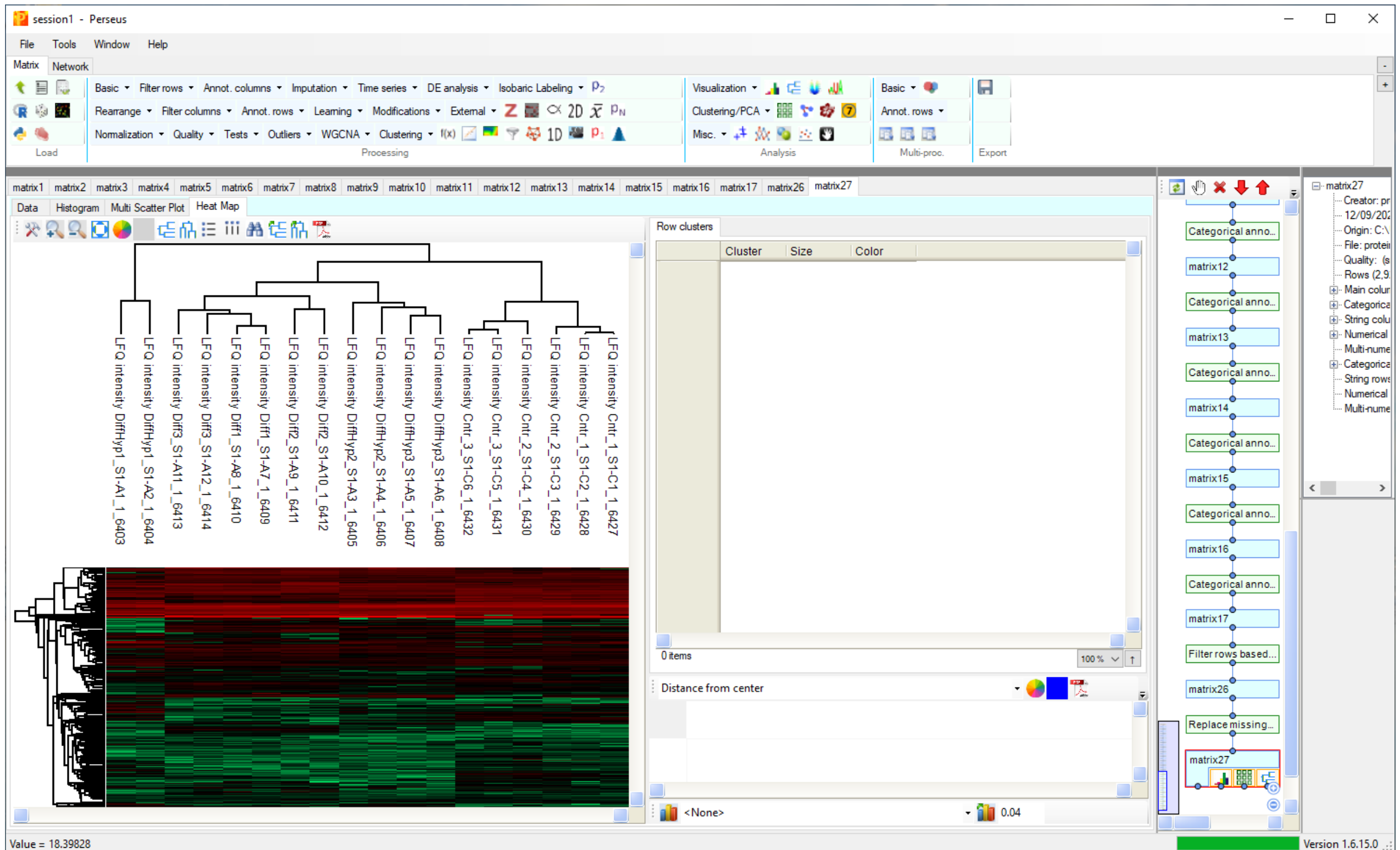
Statistical Data Analysis - Data Quality : **Clustering/PCA - Hierarchical Cluster**



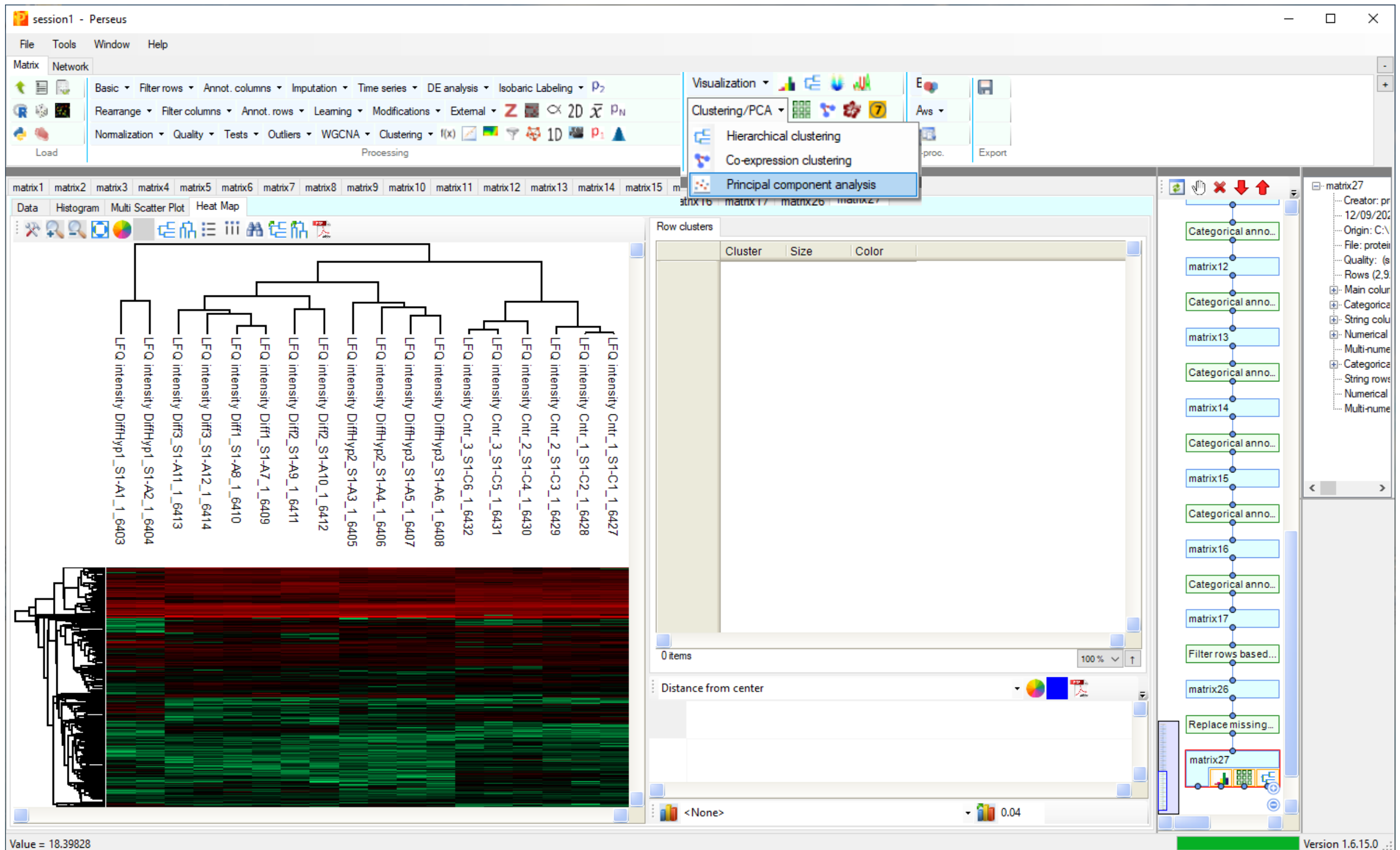
Cluster



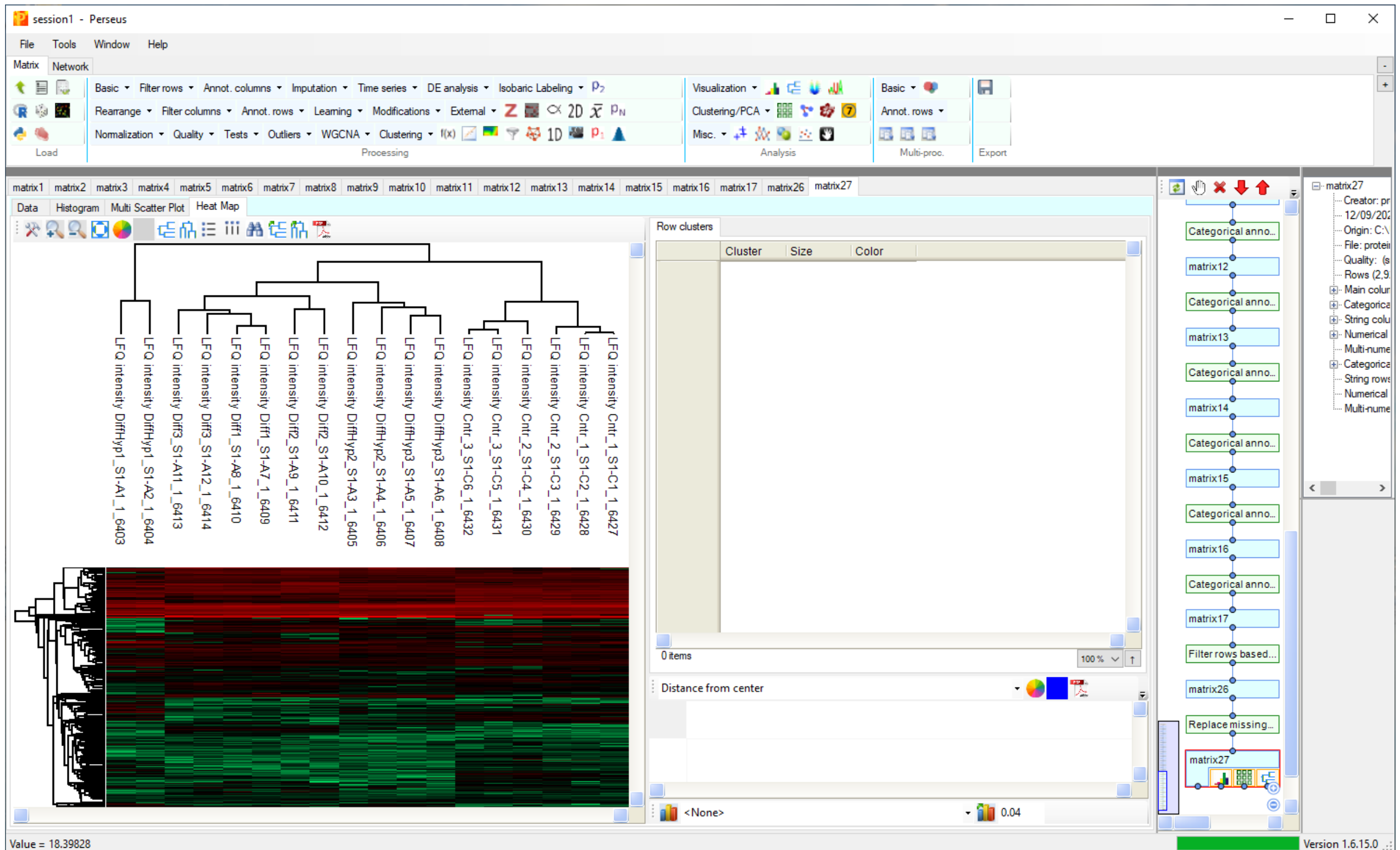
Statistical Data Analysis - Data Quality : **Clustering/PCA - Principal Component Analysis**



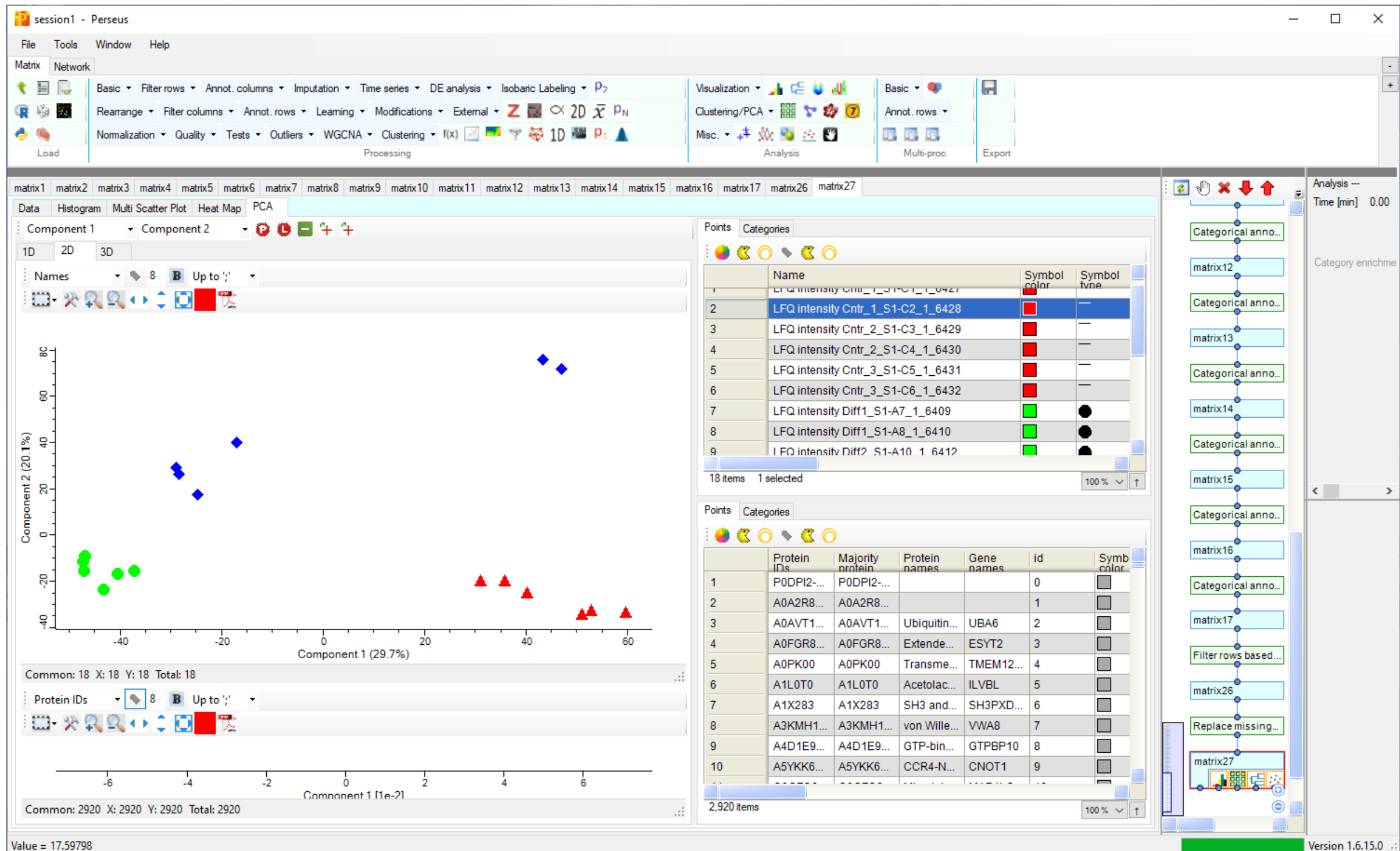
Statistical Data Analysis - Data Quality : **Clustering/PCA - Principal Component Analysis**



Statistical Data Analysis - Data Quality : **Clustering/PCA - Principal Component Analysis**



Statistical Data Analysis - Data Quality : **Clustering/PCA - Principal Component Analysis**





Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7 matrix8

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588	16.5047	16.3927	15.7866	15.5511	15.1825	15.2565	15.5061	15.7792	15.5861	14.628	15.0796	15.3716	15.3609	15.6501
2	15.7957	16.0043	15.6239	15.5923	15.9705	15.6496	14.1856	15.5846	11.9726	12.8582	11.4426	16.2481	10.1735	12.4288	15.4047	9.27313	15.5808	12.8713
3	15.4907	15.2003	15.621	14.9067	15.2186	15.021	15.2145	15.126	15.2085	16.0851	15.6966	15.1867	17.5363	17.4853	15.2908	15.0416	15.3305	15.2065
4	13.25	12.0573	12.1402	13.2906	14.556	14.4443	12.608	12.1394	13.3981	11.8589	14.5212	12.4602	15.8372	15.2094	14.0748	13.7629	13.6459	13.3462
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	12.001	13.04	14.3844	14.5827	9.42047	12.9801	12.39	13.4134	13.9552	13.3053
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	12.4117	10.929	13.8733	14.2966	16.4678	16.2123	13.2848	10.1267	12.3721	8.70416
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0657	12.4342	11.5343	14.2558	13.9408	12.8668	13.7572
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	14.0138	12.6136	13.2975	12.1952	13.1518	9.76304	12.8855	13.4764	8.16214
9	13.5336	10.9555	13.3927	9.5643	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4968	13.9336	12.3454	12.5808	13.3988	15.0613	11.9149
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	14.2596	13.2671	14.5327	14.2152	14.852	12.9483	14.7926	14.3779	12.0392	12.6415	10.3462	10.3343
11	11.4667	14.1923	13.0124	12.8779	10.5208	7.93972	16.3098	16.1729	17.2403	17.122	16.8417	16.165	16.2099	16.8026	14.9837	15.8051	16.0069	15.9548
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	12.7369	11.4397	16.1709	16.6458	15.357	14.9057	15.3776	15.3389
13	11.2708	11.5649	12.1723	13.0609	11.4062	10.531	11.5048	12.3251	15.3369	12.2581	12.8887	10.9838	12.5511	14.0792	14.293	12.6436	14.1591	11.7696
14	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	12.9986	12.5111	14.1747	14.7171	13.028	13.3694	9.58924	16.2516	10.249	13.6763
15	14.9042	14.9224	15.2079	13.7669	12.5769	12.4224	11.0067	10.9583	12.9499	10.8134	12.4726	11.4379	9.56079	13.6875	10.0139	8.61217	10.181	13.7832
16	12.2094	12.2637	13.8553	12.3034	14.5747	12.8217	16.2097	16.4275	17.592	17.47	17.4336	17.3825	12.502	9.14356	15.7249	16.2154	16.2608	15.9374
17	14.3318	12.407	12.5811	12.0068	11.0157	12.666	13.1222	12.6189	11.7982	16.1451	14.4791	9.77786	16.5249	16.3995	14.8108	13.3565	11.6479	13.0395
18	10.164	12.4989	10.8944	14.8757	11.985	10.9919	14.9987	15.9364	16.0783	16.3401	15.931	15.1639	11.659	13.8909	13.8479	14.3207	13.9426	14.4976
19	15.6692	15.7178	15.0009	15.258	15.5806	16.2816	14.1246	14.1075	14.409	14.666	14.6188	14.2565	14.0755	12.5335	15.1889	15.8176	15.3053	15.1008
20	14.8274	14.633	14.4557	15.167	13.9548	14.0485	14.8536	9.51972	14.26	11.2201	13.5946	10.8934	14.8706	15.2273	10.7979	13.4724	10.2021	14.3512
21	21.7206	20.9127	20.7812	18.8419	19.4613	19.6081	22.214	22.1622	21.2954	21.1021	22.1555	21.9863	22.1854	18.4826	22.3537	23.1808	23.107	22.8554

3,142 items 1 selected

Value = 13.01437

Version 1.6.15.0

Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P_2

Rearrange Filter columns Annot. rows Learning Modifications External Z α $2D$ $\bar{x}$ P_N

Normalization Quality Tests Outliers WGCNA Clustering $f(x)$ p_1 p_2 p_N

Visualization Clustering/PCA Misc. Analysis Multi-proc. Export

matrix1 matrix2 matrix3 matrix4 matrix5

Data

Type Main Main Main

S B LFQ in... LFQ in... LFQ in...

S LFQ in... LFQ in... LFQ in...

1 15.6027 15.2655 15.4902 15.7588 16.5047 16.3927 15.7866 15.5511 15.1825 15.2565 15.5061 15.7792 15.5861 14.628 15.0796 15.3716 15.3609 15.6501

2 15.7957 16.0043 15.6239 15.5923 15.9705 15.6496 14.1856 15.5846 11.9726 12.8582 11.4426 16.2481 10.1735 12.4288 15.4047 9.27313 15.5808 12.8713

3 15.4907 15.2003 15.621 14.9067 15.2186 15.021 15.2145 15.126 15.2085 16.0851 15.6966 15.1867 17.5363 17.4853 15.2908 15.0416 15.3305 15.2065

4 13.25 12.0573 12.1402 13.2906 14.556 14.4443 12.608 12.1394 13.3981 11.8589 14.5212 12.4602 15.8372 15.2094 14.0748 13.7629 13.6459 13.3462

5 13.7542 13.9721 13.8524 13.2324 13.2788 13.5015 14.2317 14.1904 12.001 13.04 14.3844 14.5827 9.42047 12.9801 12.39 13.4134 13.9552 13.3053

6 15.4613 15.6496 15.9187 15.022 15.7929 15.4027 14.804 15.0783 12.4117 10.929 13.8733 14.2966 16.4678 16.2123 13.2848 10.1267 12.3721 8.70416

7 16.1209 16.1338 16.4911 15.9291 16.2213 16.6646 17.3201 16.9317 17.8778 17.9586 17.958 18.0657 12.4342 11.5343 14.2558 13.9408 12.8668 13.7572

8 14.8772 14.9033 15.3677 15.6141 15.4993 15.822 11.8689 14.2487 14.5199 14.0138 12.6136 13.2975 12.1952 13.1518 9.76304 12.8855 13.4764 8.16214

9 13.5336 10.9555 13.3927 9.5643 13.4001 13.5217 13.9563 14.5693 13.9487 13.5827 13.9557 14.4968 13.9336 12.3454 12.5808 13.3988 15.0613 11.9149

10 13.4475 13.6262 13.0008 13.7653 13.6208 13.3941 14.2596 13.2671 14.5327 14.2152 14.852 12.9483 14.7926 14.3779 12.0392 12.6415 10.3462 10.3343

11 11.4667 14.1923 13.0124 12.8779 10.5208 7.93972 16.3098 16.1729 17.2403 17.122 16.8417 16.165 16.2099 16.8026 14.9837 15.8051 16.0069 15.9548

12 16.0804 16.069 16.5924 17.3622 17.2147 17.3814 11.763 11.4952 13.968 13.5015 12.7369 11.4397 16.1709 16.6458 15.357 14.9057 15.3776 15.3389

13 11.2708 11.5649 12.1723 13.0609 11.4062 10.531 11.5048 12.3251 15.3369 12.2581 12.8887 10.9838 12.5511 14.0792 14.293 12.6436 14.1591 11.7696

14 13.9163 13.8702 14.3671 14.865 14.9653 15.1503 14.2459 14.2372 12.9986 12.5111 14.1747 14.7171 13.028 13.3694 9.58924 16.2516 10.249 13.6763

15 14.9042 14.9224 15.2079 13.7669 12.5769 12.4224 11.0067 10.9583 12.9499 10.8134 12.4726 11.4379 9.56079 13.6875 10.0139 8.61217 10.181 13.7832

16 12.2094 12.2637 13.8553 12.3034 14.5747 12.8217 16.2097 16.4275 17.592 17.47 17.4336 17.3825 12.502 9.14356 15.7249 16.2154 16.2608 15.9374

17 14.3318 12.407 12.5811 12.0068 11.0157 12.666 13.1222 12.6189 11.7982 16.1451 14.4791 9.77786 16.5249 16.3995 14.8108 13.3565 11.6479 13.0395

18 10.164 12.4989 10.8944 14.8757 11.985 10.9919 14.9987 15.9364 16.0783 16.3401 15.931 15.1639 11.659 13.8909 13.8479 14.3207 13.9426 14.4976

19 15.6692 15.7178 15.0009 15.258 15.5806 16.2816 14.1246 14.1075 14.409 14.666 14.6188 14.2565 14.0755 12.5335 15.1889 15.8176 15.3053 15.1008

20 14.8274 14.633 14.4557 15.167 13.9548 14.0485 14.8536 9.51972 14.26 11.2201 13.5946 10.8934 14.8706 15.2273 10.7979 13.4724 10.2021 14.3512

21 21.7206 20.9127 20.7812 18.8419 19.4613 19.6081 22.214 22.1622 21.2954 21.1021 22.1555 21.9863 22.1854 18.1826 22.3537 23.1808 23.107 22.8554

3,142 items 1 selected

Value = 13.01437

Version 1.6.15.0



Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P_2

Rearrange Filter columns Annot. rows Learning Modifications External Z χ^2 P_N

Normalization Quality Tests Outliers WGCNA Clustering $f(x)$ 1D P_1

Load Processing

Visualization Clustering/PCA Misc. Analysis

Basic Annot. rows Multi-proc. Export

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7 matrix8

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588	16.5047	16.3927	15.7866	15.5511	15.1825	15.2565	15.5061	15.7792	15.5861	14.628	15.0796	15.3716	15.3609	15.6501
2	15.7957	16.0043	15.6239	15.5923	15.9705	15.6496	14.1856	15.5846	11.9726	12.8582	11.4426	16.2481	10.1735	12.4288	15.4047	9.27313	15.5808	12.8713
3	15.4907	15.2003	15.621	14.9067	15.2186	15.021	15.2145	15.126	15.2085	16.0851	15.6966	15.1867	17.5363	17.4853	15.2908	15.0416	15.3305	15.2065
4	13.25	12.0573	12.1402	13.2906	14.556	14.4443	12.608	12.1394	13.3981	11.8589	14.5212	12.4602	15.8372	15.2094	14.0748	13.7629	13.6459	13.3462
5	13.7542	13.9721	13.8524	13.2324	13.2788	13.5015	14.2317	14.1904	12.001	13.04	14.3844	14.5827	9.42047	12.9801	12.39	13.4134	13.9552	13.3053
6	15.4613	15.6496	15.9187	15.022	15.7929	15.4027	14.804	15.0783	12.4117	10.929	13.8733	14.2966	16.4678	16.2123	13.2848	10.1267	12.3721	8.70416
7	16.1209	16.1338	16.4911	15.9291	16.2213	16.6646	17.3201	16.9317	17.8778	17.9586	17.958	18.0657	12.4342	11.5343	14.2558	13.9408	12.8668	13.7572
8	14.8772	14.9033	15.3677	15.6141	15.4993	15.822	11.8689	14.2487	14.5199	14.0138	12.6136	13.2975	12.1952	13.1518	9.76304	12.8855	13.4764	8.16214
9	13.5336	10.9555	13.3927	9.5643	13.4001	13.5217	13.9563	14.5693	13.9487	13.5827	13.9557	14.4968	13.9336	12.3454	12.5808	13.3988	15.0613	11.9149
10	13.4475	13.6262	13.0008	13.7653	13.6208	13.3941	14.2596	13.2671	14.5327	14.2152	14.852	12.9483	14.7926	14.3779	12.0392	12.6415	10.3462	10.3343
11	11.4667	14.1923	13.0124	12.8779	10.5208	7.93972	16.3098	16.1729	17.2403	17.122	16.8417	16.165	16.2099	16.8026	14.9837	15.8051	16.0069	15.9548
12	16.0804	16.069	16.5924	17.3622	17.2147	17.3814	11.763	11.4952	13.968	13.5015	12.7369	11.4397	16.1709	16.6458	15.357	14.9057	15.3776	15.3389
13	11.2708	11.5649	12.1723	13.0609	11.4062	10.531	11.5048	12.3251	15.3369	12.2581	12.8887	10.9838	12.5511	14.0792	14.293	12.6436	14.1591	11.7696
14	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	12.9986	12.5111	14.1747	14.7171	13.028	13.3694	9.58924	16.2516	10.249	13.6763
15	14.9042	14.9224	15.2079	13.7669	12.5769	12.4224	11.0067	10.9583	12.9499	10.8134	12.4726	11.4379	9.56079	13.6875	10.0139	8.61217	10.181	13.7832
16	12.2094	12.2637	13.8553	12.3034	14.5747	12.8217	16.2097	16.4275	17.592	17.47	17.4336	17.3825	12.502	9.14356	15.7249	16.2154	16.2608	15.9374
17	14.3318	12.407	12.5811	12.0068	11.0157	12.666	13.1222	12.6189	11.7982	16.1451	14.4791	9.77786	16.5249	16.3995	14.8108	13.3565	11.6479	13.0395
18	10.164	12.4989	10.8944	14.8757	11.985	10.9919	14.9987	15.9364	16.0783	16.3401	15.931	15.1639	11.659	13.8909	13.8479	14.3207	13.9426	14.4976
19	15.6692	15.7178	15.0009	15.258	15.5806	16.2816	14.1246	14.1075	14.409	14.666	14.6188	14.2565	14.0755	12.5335	15.1889	15.8176	15.3053	15.1008
20	14.8274	14.633	14.4557	15.167	13.9548	14.0485	14.8536	9.51972	14.26	11.2201	13.5946	10.8934	14.8706	15.2273	10.7979	13.4724	10.2021	14.3512
21	21.7206	20.9127	20.7812	18.8419	19.4613	19.6081	22.214	22.1622	21.2954	21.1021	22.1555	21.9863	22.1854	18.4826	22.3537	23.1808	23.107	22.8554

3,142 items 1 selected

Value = 13.01437

Version 1.6.15.0

Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Im
Rearrange Filter columns Annot. rows
Normalization Quality Tests Outliers

Load

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588
2	15.7957	16.0043	15.6239	15.5923
3	15.4907	15.2003	15.621	14.9067
4	13.25	12.0573	12.1402	13.2906
5	13.7542	13.9721	13.8524	13.2324
6	15.4613	15.6496	15.9187	15.022
7	16.1209	16.1338	16.4911	15.9291
8	14.8772	14.9033	15.3677	15.6141
9	13.5336	10.9555	13.3927	9.5643
10	13.4475	13.6262	13.0008	13.7653
11	11.4667	14.1923	13.0124	12.8779
12	16.0804	16.069	16.5924	17.3622
13	11.2708	11.5649	12.1723	13.0609
14	13.9163	13.8702	14.3671	14.865
15	14.9042	14.9224	15.2079	13.7669
16	12.2094	12.2637	13.8553	12.3034
17	14.3318	12.407	12.5811	12.0068
18	10.164	12.4989	10.8944	14.8757
19	15.6692	15.7178	15.0009	15.258
20	14.8274	14.633	14.4557	15.167
21	21.7206	20.9127	20.7812	18.8410

3,142 items 1 selected

Value = 13.01437

Two-sample tests

Cancel Suppl. table 1 OK

First group (right)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Second groups mode

Specify individual groups

Second group (left)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Paired ☐

Test

Student's T-test

S0 2

Side Both

☒ Valid value filter

Min. number of valid values 1

Min. number mode In total

Min. percentage of valid values 0

Min. percentage mode In total

Use for truncation

Permutation-based FDR

FDR 0.01

Report q-value ☒

Number of randomizations 250

Preserve grouping in randomizations <None>

Calculate combined score ☐

-Log10 p-value

☒ Suffix

matrix4

Categorical anno...

matrix5

Categorical anno...

matrix6

Filter rows based...

matrix7

Replace missing...

matrix8

Version 1.6.15.0

Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Im
Rearrange Filter columns Annot. rows
Normalization Quality Tests Outliers

Load

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588
2	15.7957	16.0043	15.6239	15.5923
3	15.4907	15.2003	15.621	14.9067
4	13.25	12.0573	12.1402	13.2906
5	13.7542	13.9721	13.8524	13.2324
6	15.4613	15.6496	15.9187	15.022
7	16.1209	16.1338	16.4911	15.9291
8	14.8772	14.9033	15.3677	15.6141
9	13.5336	10.9555	13.3927	9.5643
10	13.4475	13.6262	13.0008	13.7653
11	11.4667	14.1923	13.0124	12.8779
12	16.0804	16.069	16.5924	17.3622
13	11.2708	11.5649	12.1723	13.0609
14	13.9163	13.8702	14.3671	14.865
15	14.9042	14.9224	15.2079	13.7669
16	12.2094	12.2637	13.8553	12.3034
17	14.3318	12.407	12.5811	12.0068
18	10.164	12.4989	10.8944	14.8757
19	15.6692	15.7178	15.0009	15.258
20	14.8274	14.633	14.4557	15.167
21	21.7206	20.9127	20.7812	18.8410

3,142 items 1 selected

Value = 13.01437

Two-sample tests

Cancel Suppl. table 1 OK

First group (right)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Second groups mode

Specify individual groups

Second group (left)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Paired ☐

Student's T-test

S0 2

Side Both

☒ Valid value filter

Min. number of valid values 1

Min. number mode In total

Min. percentage of valid values 0

Min. percentage mode In total

Use for truncation

Permutation-based FDR

FDR 0.01

Report q-value ☒

Number of randomizations 250

Preserve grouping in randomizations <None>

Calculate combined score ☐

-Log10 p-value

Suffix

matrix4
Categorical anno...
matrix5
Categorical anno...
matrix6
Filter rows based...
matrix7
Replace missing...
matrix8

Version 1.6.15.0

Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Im
Rearrange Filter columns Annot. rows
Normalization Quality Tests Outliers

Load

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588
2	15.7957	16.0043	15.6239	15.5923
3	15.4907	15.2003	15.621	14.9067
4	13.25	12.0573	12.1402	13.2906
5	13.7542	13.9721	13.8524	13.2324
6	15.4613	15.6496	15.9187	15.022
7	16.1209	16.1338	16.4911	15.9291
8	14.8772	14.9033	15.3677	15.6141
9	13.5336	10.9555	13.3927	9.5643
10	13.4475	13.6262	13.0008	13.7653
11	11.4667	14.1923	13.0124	12.8779
12	16.0804	16.069	16.5924	17.3622
13	11.2708	11.5649	12.1723	13.0609
14	13.9163	13.8702	14.3671	14.865
15	14.9042	14.9224	15.2079	13.7669
16	12.2094	12.2637	13.8553	12.3034
17	14.3318	12.407	12.5811	12.0068
18	10.164	12.4989	10.8944	14.8757
19	15.6692	15.7178	15.0009	15.258
20	14.8274	14.633	14.4557	15.167
21	21.7206	20.9127	20.7812	18.8410

Test

Valid value filter

Use for truncation

Calculate combined score

-Log10 p-value

Suffix

Two-sample tests

Cancel Suppl. table 1 OK

First group (right)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Second groups mode

Specify individual groups

Second group (left)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Paired

Student's T-test

S0 2

Side Both

Min. number of valid values 1

Min. number mode In total

Min. percentage of valid values 0

Min. percentage mode In total

Permutation-based FDR

FDR 0.01

Report q-value

Number of randomizations 250

Preserve grouping in randomizations <None>

Value = 13.01437

Version 1.6.15.0

Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Im
Rearrange Filter columns Annot. rows
Normalization Quality Tests Outliers

Load

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588
2	15.7957	16.0043	15.6239	15.5923
3	15.4907	15.2003	15.621	14.9067
4	13.25	12.0573	12.1402	13.2906
5	13.7542	13.9721	13.8524	13.2324
6	15.4613	15.6496	15.9187	15.022
7	16.1209	16.1338	16.4911	15.9291
8	14.8772	14.9033	15.3677	15.6141
9	13.5336	10.9555	13.3927	9.5643
10	13.4475	13.6262	13.0008	13.7653
11	11.4667	14.1923	13.0124	12.8779
12	16.0804	16.069	16.5924	17.3622
13	11.2708	11.5649	12.1723	13.0609
14	13.9163	13.8702	14.3671	14.865
15	14.9042	14.9224	15.2079	13.7669
16	12.2094	12.2637	13.8553	12.3034
17	14.3318	12.407	12.5811	12.0068
18	10.164	12.4989	10.8944	14.8757
19	15.6692	15.7178	15.0009	15.258
20	14.8274	14.633	14.4557	15.167
21	21.7206	20.9127	20.7812	18.8410

3,142 items 1 selected

Value = 13.01437

Two-sample tests

Cancel Suppl. table 1 OK

First group (right)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Second groups mode

Specify individual groups

Second group (left)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Paired ☐

Test

Student's T-test

S0 2

Side Both

Valid value filter

☒ Min. number of valid values 1

Min. number mode In total

Min. percentage of valid values 0

Min. percentage mode In total

Use for truncation

Permutation-based FDR

FDR 0.01

Report q-value ☒

Number of randomizations 250

Preserve grouping in randomizations <None>

Calculate combined score ☐

-Log10 p-value

Suffix

matrix4
Categorical anno...
matrix5
Categorical anno...
matrix6
Filter rows based...
matrix7
Replace missing...
matrix8

Version 1.6.15.0

Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Im
Rearrange Filter columns Annot. rows
Normalization Quality Tests Outliers

Load

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588
2	15.7957	16.0043	15.6239	15.5923
3	15.4907	15.2003	15.621	14.9067
4	13.25	12.0573	12.1402	13.2906
5	13.7542	13.9721	13.8524	13.2324
6	15.4613	15.6496	15.9187	15.022
7	16.1209	16.1338	16.4911	15.9291
8	14.8772	14.9033	15.3677	15.6141
9	13.5336	10.9555	13.3927	9.5643
10	13.4475	13.6262	13.0008	13.7653
11	11.4667	14.1923	13.0124	12.8779
12	16.0804	16.069	16.5924	17.3622
13	11.2708	11.5649	12.1723	13.0609
14	13.9163	13.8702	14.3671	14.865
15	14.9042	14.9224	15.2079	13.7669
16	12.2094	12.2637	13.8553	12.3034
17	14.3318	12.407	12.5811	12.0068
18	10.164	12.4989	10.8944	14.8757
19	15.6692	15.7178	15.0009	15.258
20	14.8274	14.633	14.4557	15.167
21	21.7206	20.9127	20.7812	18.8410

3,142 items 1 selected

Value = 13.01437

Two-sample tests

Cancel Suppl. table 1 OK

First group (right)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Second groups mode

Specify individual groups

Second group (left)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Paired ☐

Test

Student's T-test

S0 2

Side Both

Valid value filter

☒ Min. number of valid values 1

Min. number mode In total

Min. percentage of valid values 0

Min. percentage mode In total

Use for truncation

Permutation-based FDR

FDR 0.01

Report q-value ☒

Number of randomizations 250

Preserve grouping in randomizations <None>

Calculate combined score ☐

-Log10 p-value

Suffix

matrix4
Categorical anno...
matrix5
Categorical anno...
matrix6
Filter rows based...
matrix7
Replace missing...
matrix8

Version 1.6.15.0

Statistical Data Analysis - Enrichment Test : t-Test

Processing > Tests > Two samples tests

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Im
Rearrange Filter columns Annot. rows
Normalization Quality Tests Outliers

Load

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7

Data

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...
S B	LFQ in...	LFQ in...	LFQ in...	LFQ in...
S	LFQ in...	LFQ in...	LFQ in...	LFQ in...
1	15.6027	15.2655	15.4902	15.7588
2	15.7957	16.0043	15.6239	15.5923
3	15.4907	15.2003	15.621	14.9067
4	13.25	12.0573	12.1402	13.2906
5	13.7542	13.9721	13.8524	13.2324
6	15.4613	15.6496	15.9187	15.022
7	16.1209	16.1338	16.4911	15.9291
8	14.8772	14.9033	15.3677	15.6141
9	13.5336	10.9555	13.3927	9.5643
10	13.4475	13.6262	13.0008	13.7653
11	11.4667	14.1923	13.0124	12.8779
12	16.0804	16.069	16.5924	17.3622
13	11.2708	11.5649	12.1723	13.0609
14	13.9163	13.8702	14.3671	14.865
15	14.9042	14.9224	15.2079	13.7669
16	12.2094	12.2637	13.8553	12.3034
17	14.3318	12.407	12.5811	12.0068
18	10.164	12.4989	10.8944	14.8757
19	15.6692	15.7178	15.0009	15.258
20	14.8274	14.633	14.4557	15.167
21	21.7206	20.9127	20.7812	18.8410

Test

Valid value filter

Use for truncation

Calculate combined score

-Log10 p-value

Suffix

Two-sample tests

Cancel Suppl. table 1

First group (right)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Second groups mode

Specify individual groups

Second group (left)

LFQ intensity Cntr
LFQ intensity Diff
LFQ intensity DiffHyp

Required fold change for hits to be considered

Student's T-test

S0

Side

Both

Min. number of valid values

1

Min. number mode

In total

Min. percentage of valid values

0

Min. percentage mode

In total

Permutation-based FDR

FDR

0.01

Report q-value

Number of randomizations

250

Preserve grouping in randomizations

<None>

matrix4

Categorical anno...

matrix6

Filter rows based...

matrix7

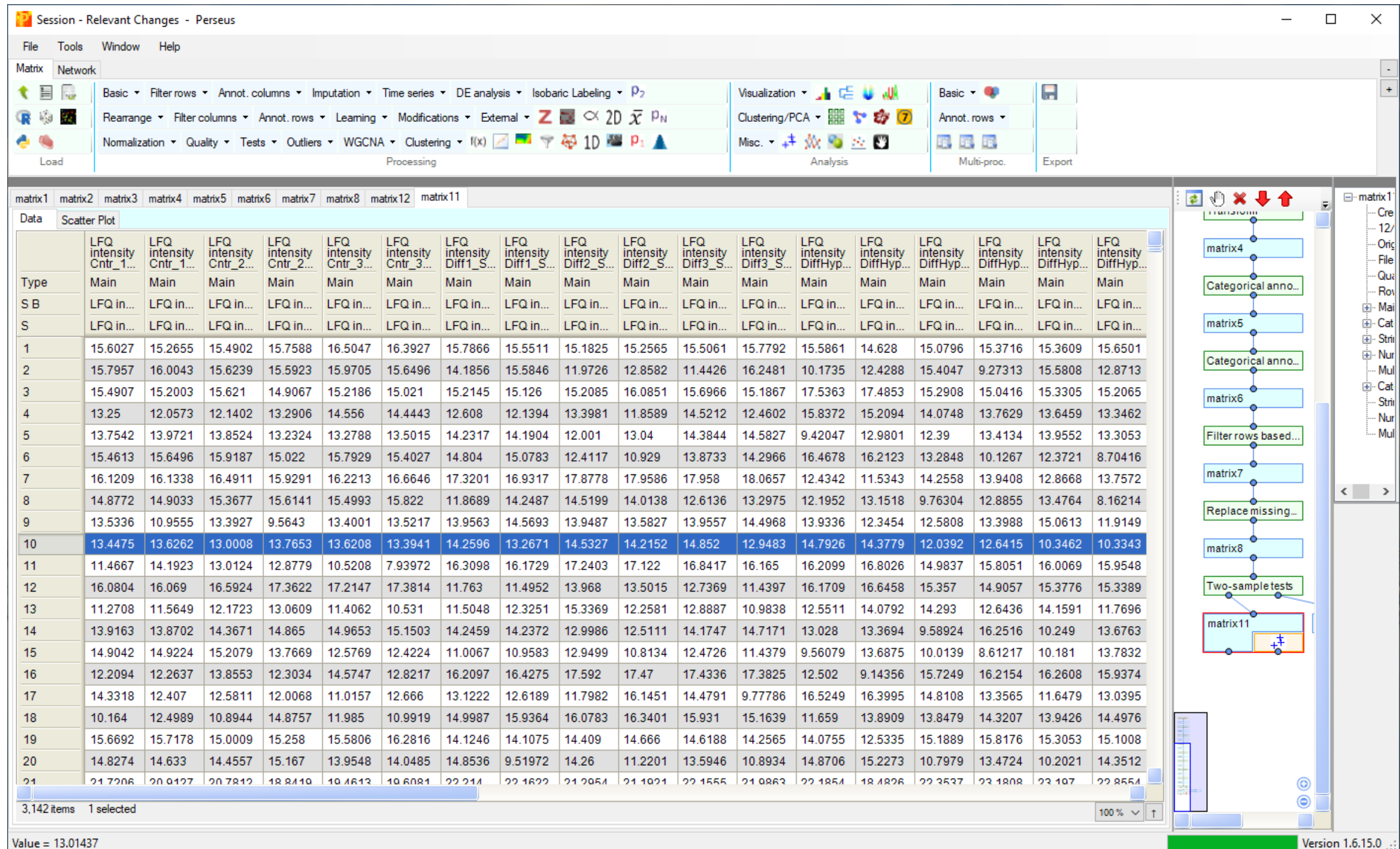
Replace missing...

matrix8

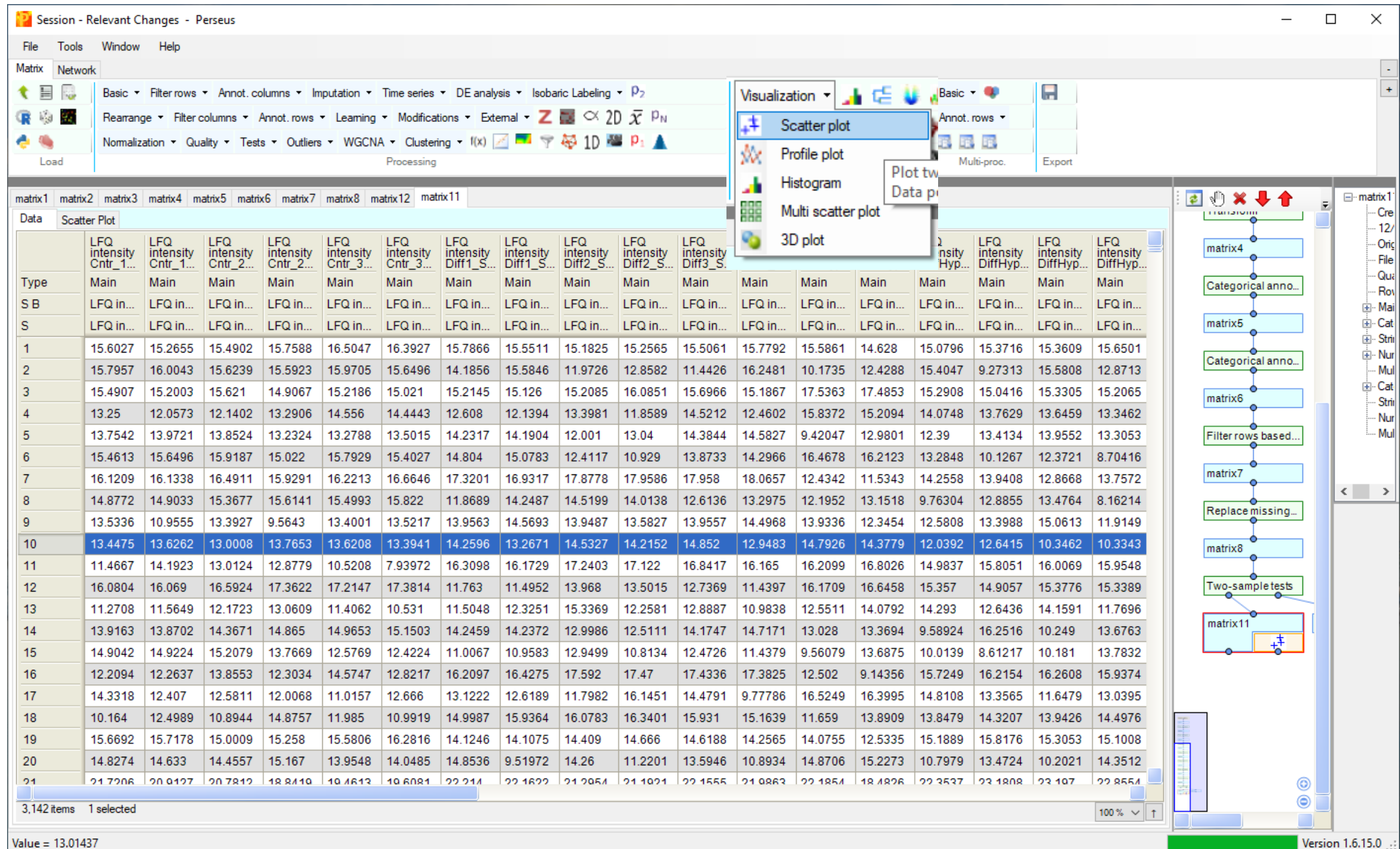
Value = 13.01437

Version 1.6.15.0

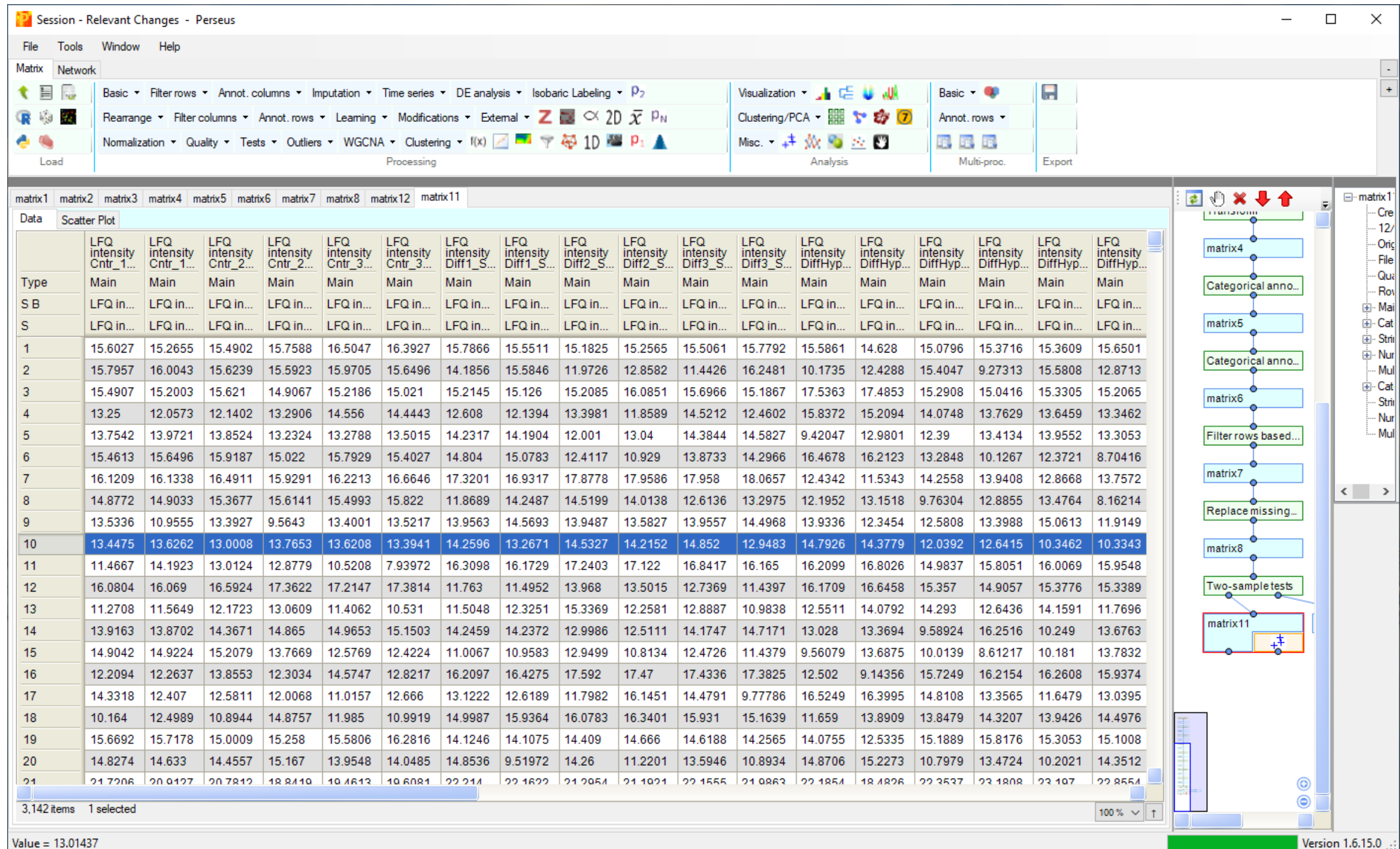
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Visualisation > Scatter Plot**



Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Visualisation > Scatter Plot**



Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Visualisation > Scatter Plot**



Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Visualisation > Scatter Plot**

Session - Relevant Changes - Perseus

File Tools Window Help

Matrix Network

Basic Filter rows Annot. columns Imputation Time series DE analysis Isobaric Labeling P₂

Rearrange Filter columns Annot. rows Learning Modifications External Z 2D X P_N

Normalization Quality Tests Outliers WGCNA Clustering f(x) 1D P₁

Visualization Clustering/PCA Misc. Basic Annot. rows Multi-proc. Export

matrix1 matrix2 matrix3 matrix4 matrix5 matrix6 matrix7 matrix8 matrix12 matrix11

Data Scatter Plot

Type	LFQ intensity Cntr_1...	LFQ intensity Cntr_1...	LFQ intensity Cntr_2...	LFQ intensity Cntr_2...	LFQ intensity Cntr_3...	LFQ intensity Cntr_3...	LFQ intensity Diff1_S...	LFQ intensity Diff1_S...	LFQ intensity Diff2_S...	LFQ intensity Diff2_S...	LFQ intensity Diff3_S...	LFQ intensity Diff3_S...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...	LFQ intensity DiffHyp...
1	15.6027	15.2655	15.4902	15.7588	16.5047	16.3927	15.7866	15.5511	15.1825	15.2565	15.5061	15.7792	15.5861	14.628	15.0796	15.3716	15.3609	15.6501
2	15.7957	16.0043	15.6239	15.5923	15.9705	15.6496	14.1856	15.5846	11.9726	12.8582	11.4426	16.2481	10.1735	12.4288	15.4047	9.27313	15.5808	12.8713
3	15.4907	15.2003	15.621	14.9067	15.2186	15.021	15.2145	15.126	15.2085	16.0851	15.6966	15.1867	17.5363	17.4853	15.2908	15.0416	15.3305	15.2065
4	11.2708	11.5649	12.1723	13.0609	11.4062	10.531	11.5048	12.3251	15.3369	12.2581	12.8887	10.9838	12.5511	14.0792	14.293	12.6436	14.1591	11.7696
5	13.9163	13.8702	14.3671	14.865	14.9653	15.1503	14.2459	14.2372	12.9986	12.5111	14.1747	14.7171	13.028	13.3694	9.58924	16.2516	10.249	13.6763
6	14.9042	14.9224	15.2079	13.7669	12.5769	12.4224	11.0067	10.9583	12.9499	10.8134	12.4726	11.4379	9.56079	13.6875	10.0139	8.61217	10.181	13.7832
7	12.2094	12.2637	13.8553	12.3034	14.5747	12.8217	16.2097	16.4275	17.592	17.47	17.4336	17.3825	12.502	9.14356	15.7249	16.2154	16.2608	15.9374
8	14.3318	12.407	12.5811	12.0068	11.0157	12.666	13.1222	12.6189	11.7982	16.1451	14.4791	9.77786	16.5249	16.3995	14.8108	13.3565	11.6479	13.0395
9	10.164	12.4989	10.8944	14.8757	11.985	10.9919	14.9987	15.9364	16.0783	16.3401	15.931	15.1639	11.659	13.8909	13.8479	14.3207	13.9426	14.4976
10	15.6692	15.7178	15.0009	15.258	15.5806	16.2816	14.1246	14.1075	14.409	14.666	14.6188	14.2565	14.0755	12.5335	15.1889	15.8176	15.3053	15.1008
11	14.8274	14.633	14.4557	15.167	13.9548	14.0485	14.8536	9.51972	14.26	11.2201	13.5946	10.8934	14.8706	15.2273	10.7979	13.4724	10.2021	14.3512
12	21.7206	20.9127	20.7812	18.8410	19.4613	19.6081	22.214	22.1622	21.2054	21.1921	22.1555	21.0863	22.1854	18.4826	22.3537	23.1808	23.107	22.8554

3,142 items 1 selected

Value = 13.01437

Scatter plot

Cancel Description

Matrix access Columns

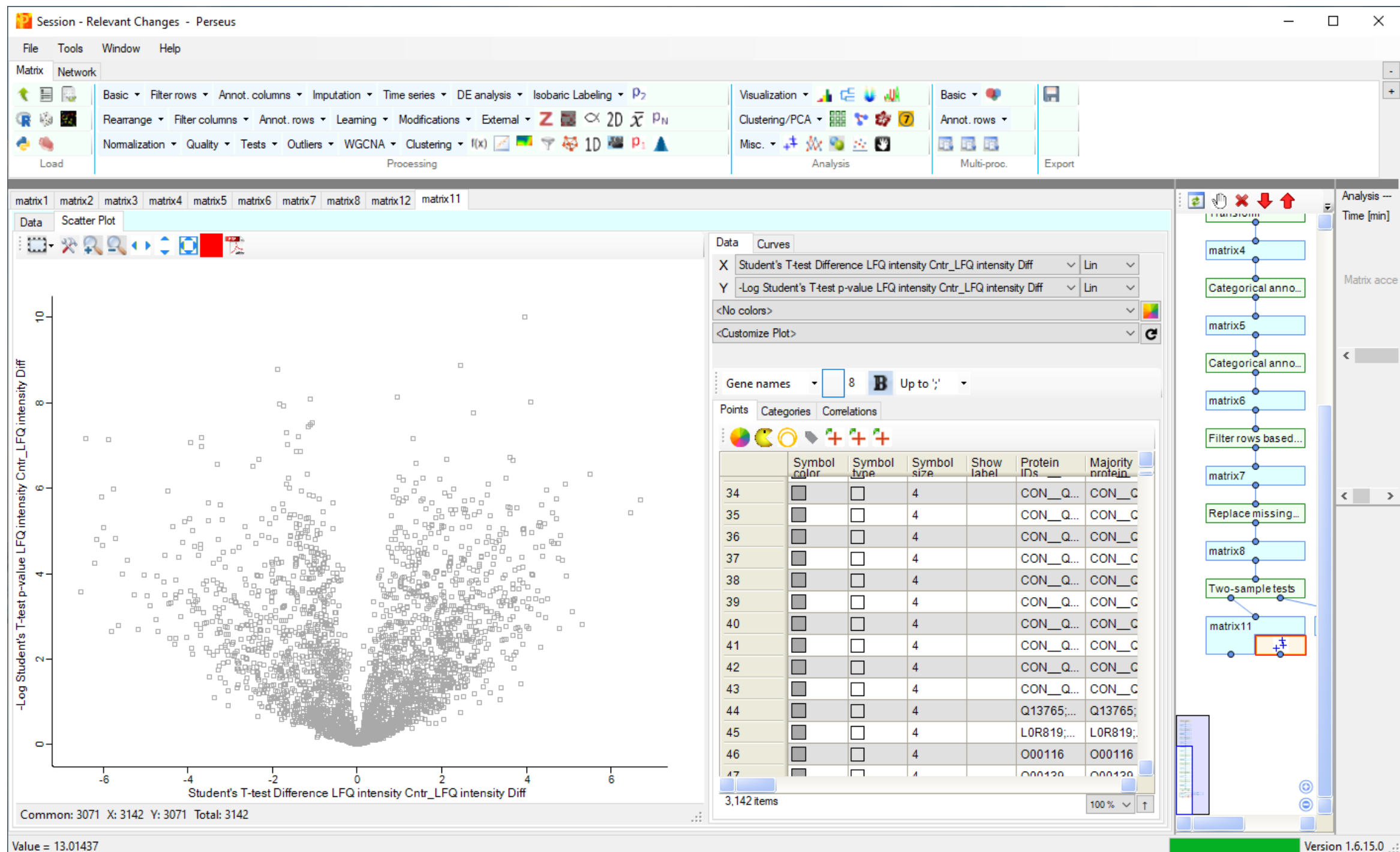
Cancel Description

OK

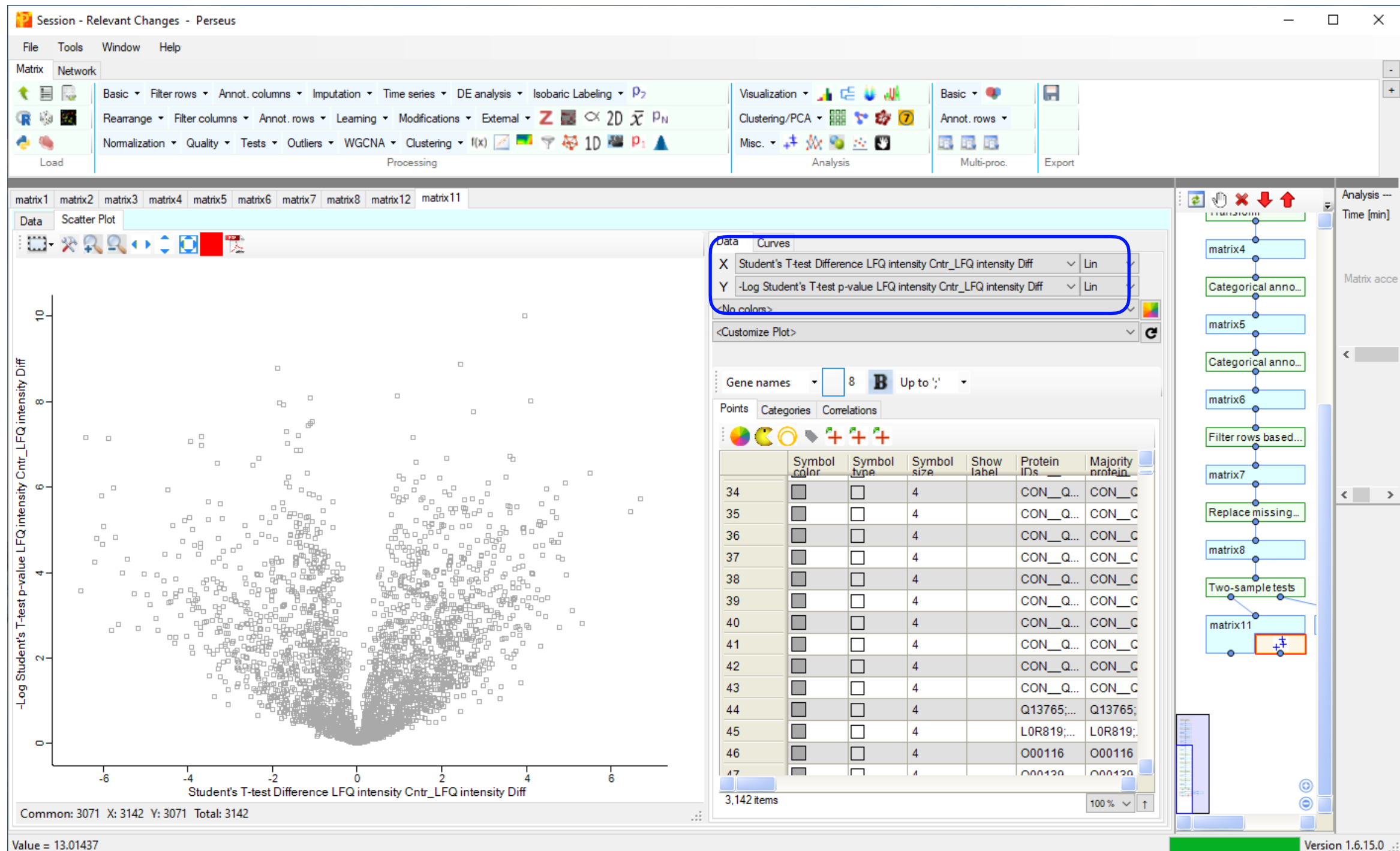
OK

Version 1.6.15.0

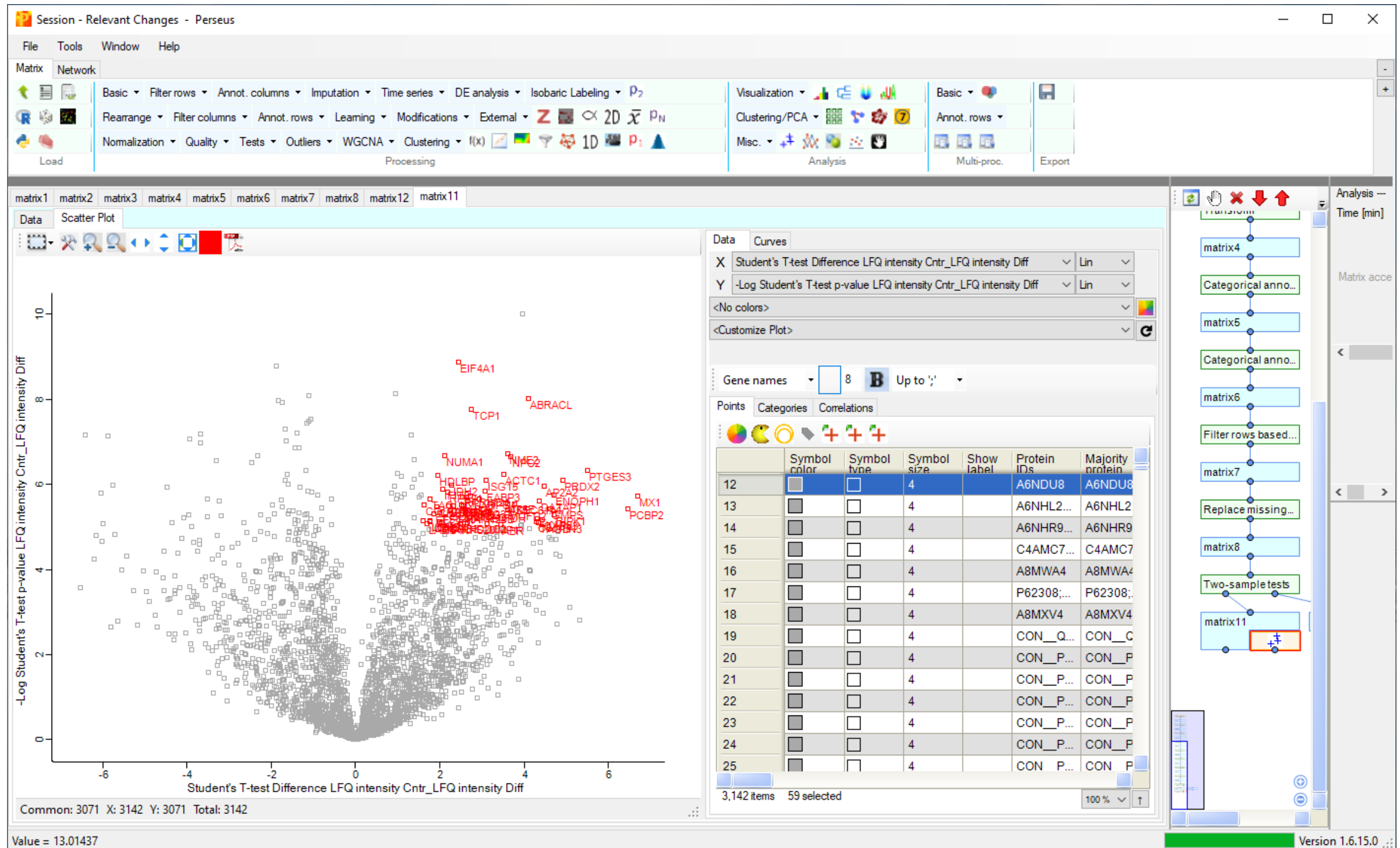
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Visualisation > Scatter Plot**



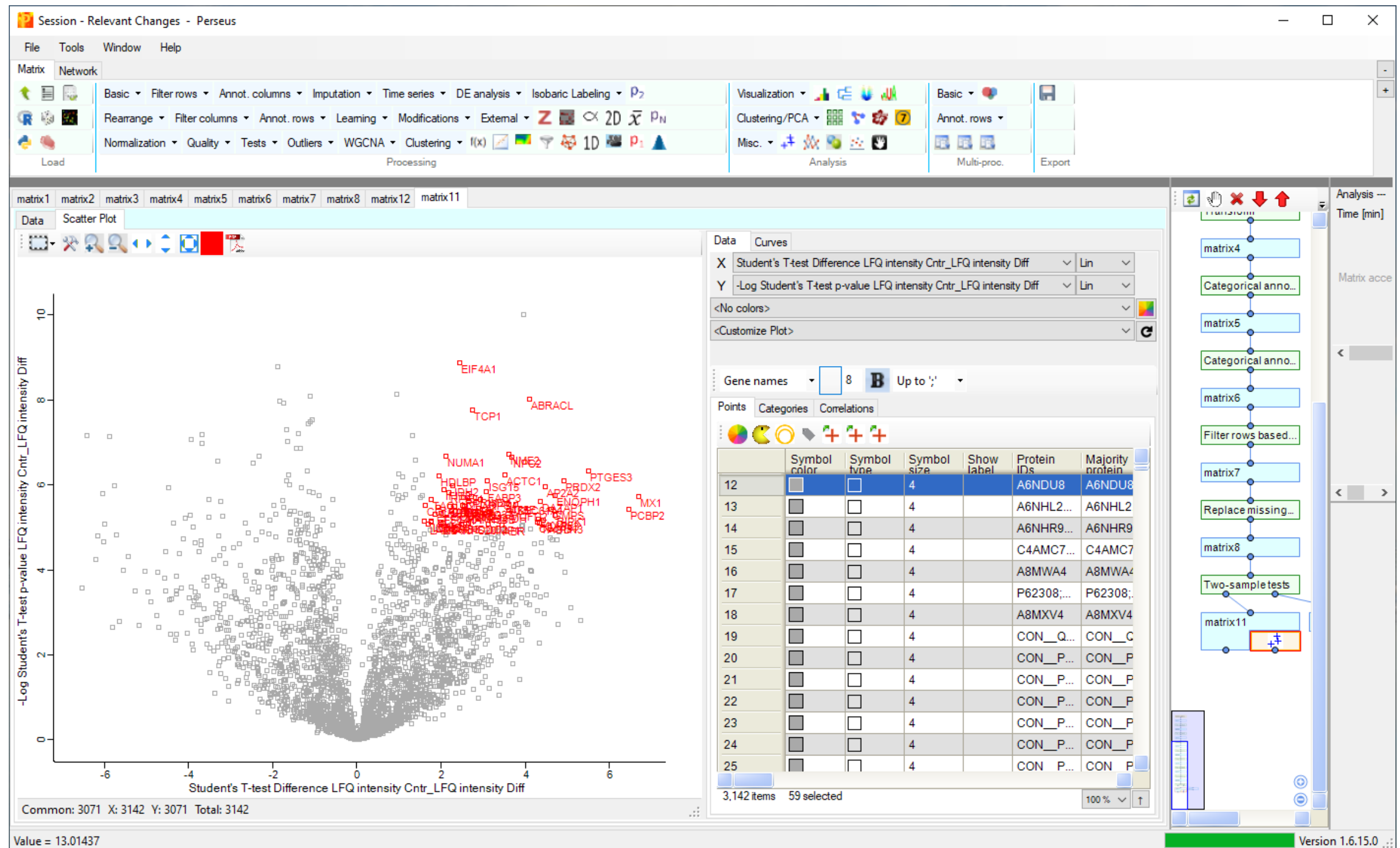
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Visualisation > Scatter Plot**



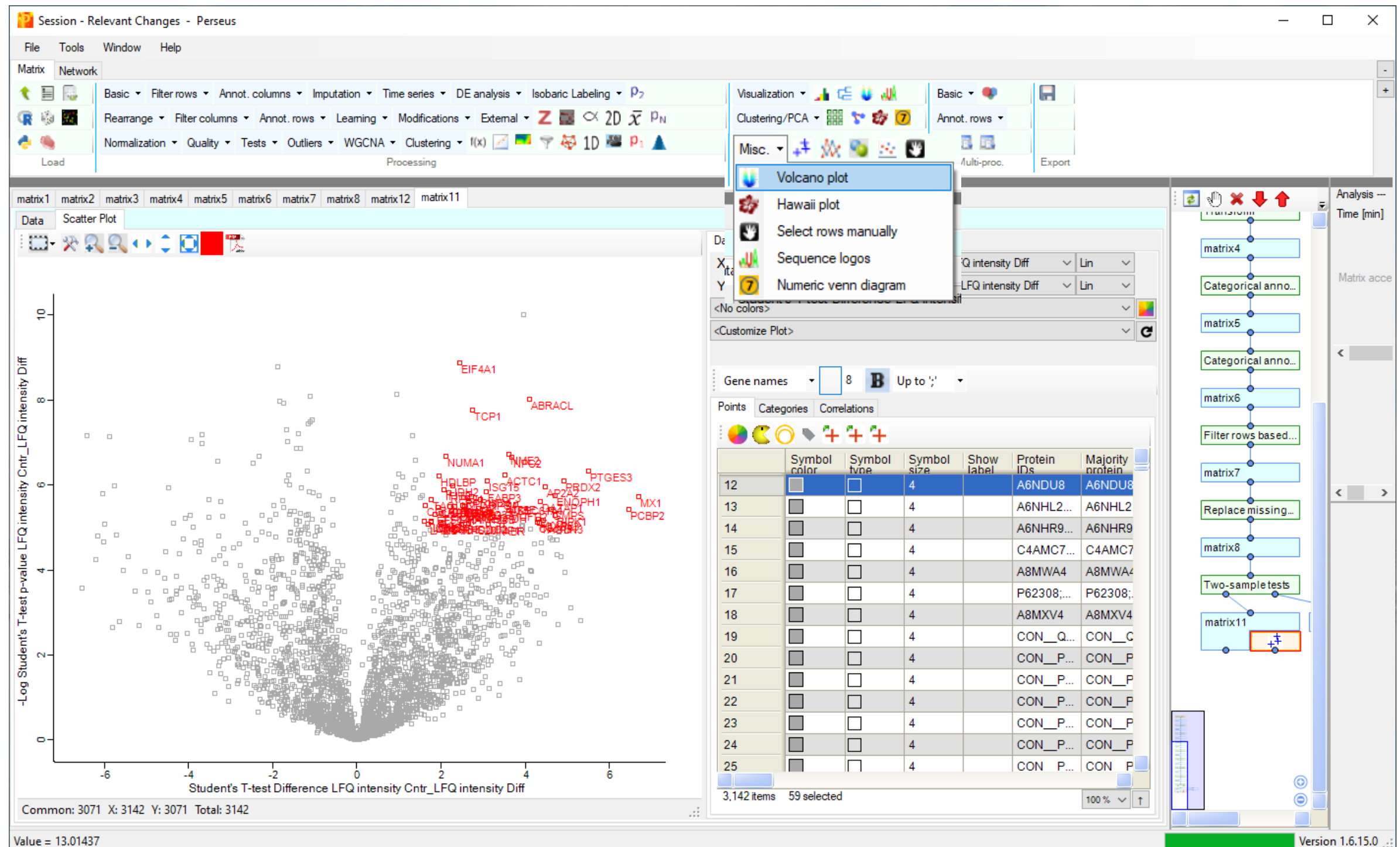
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Visualisation > Scatter Plot**



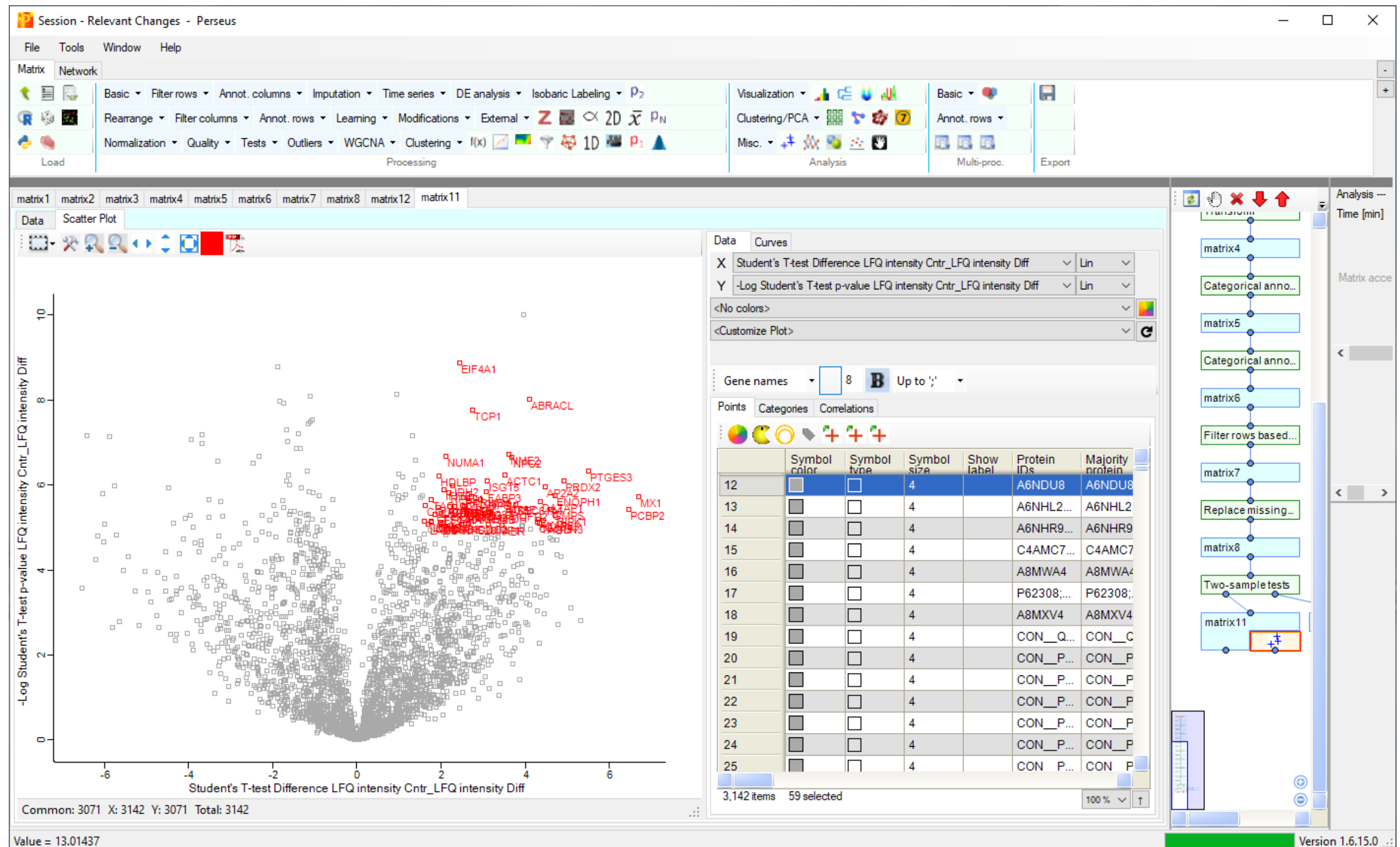
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



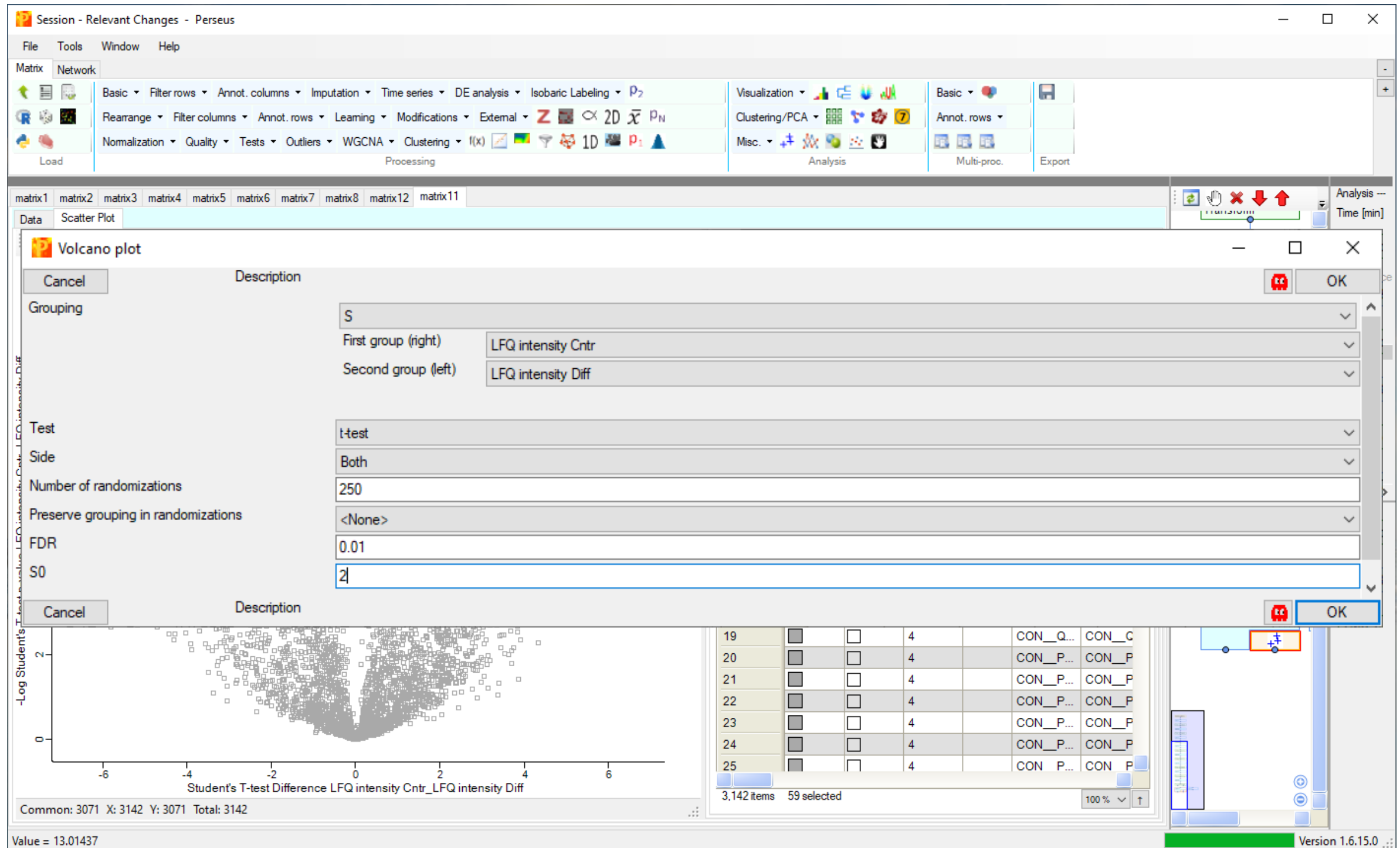
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



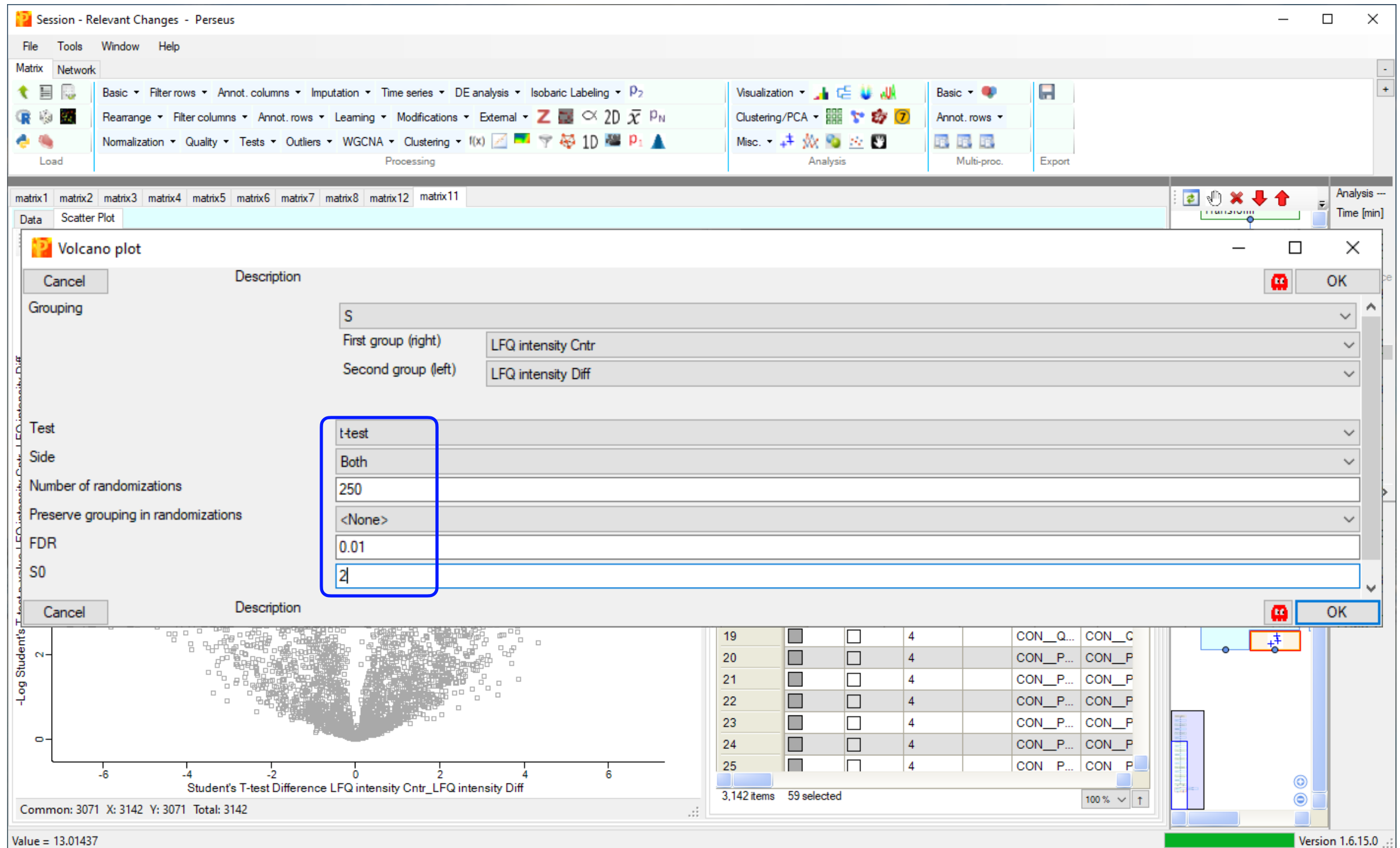
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



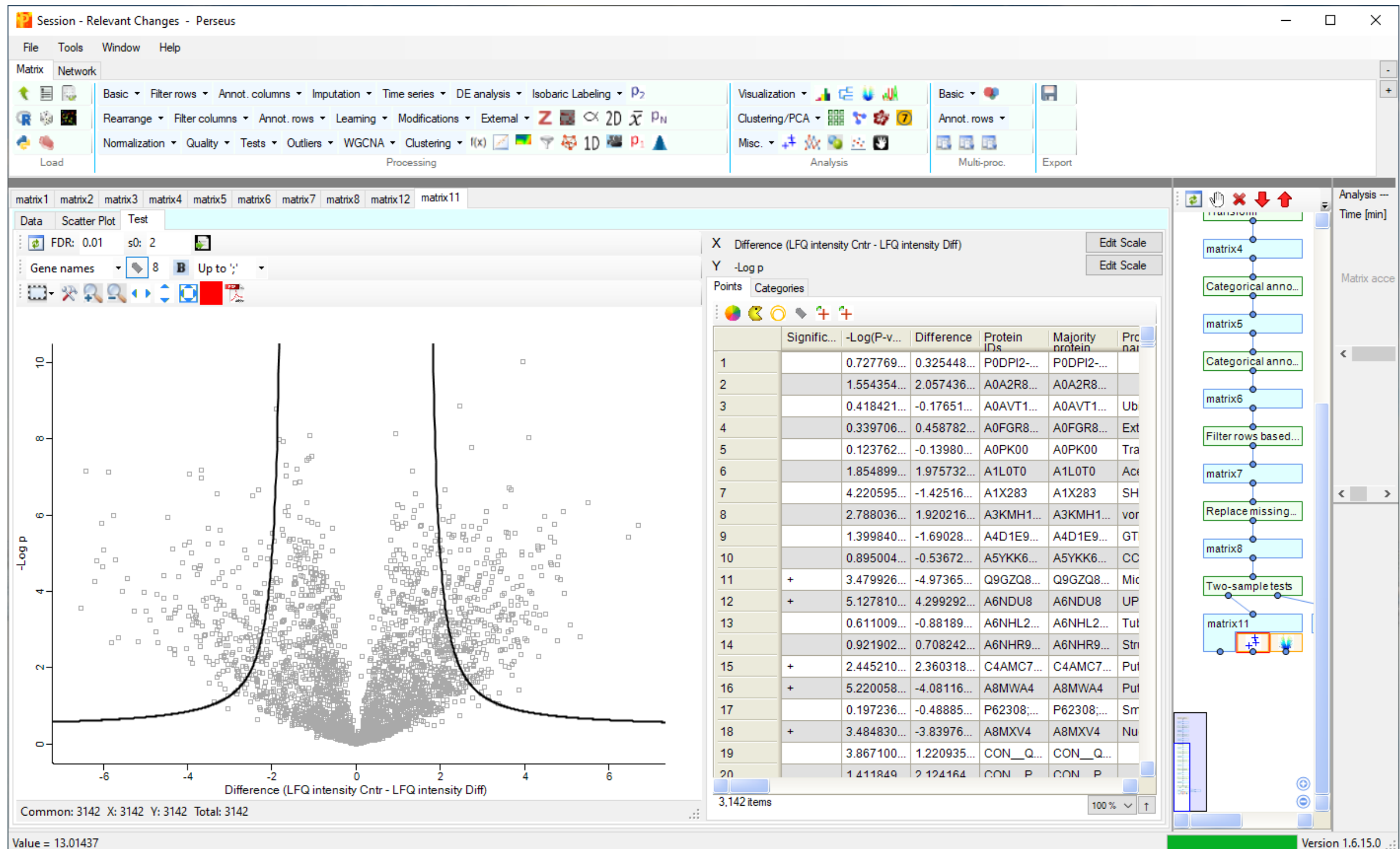
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



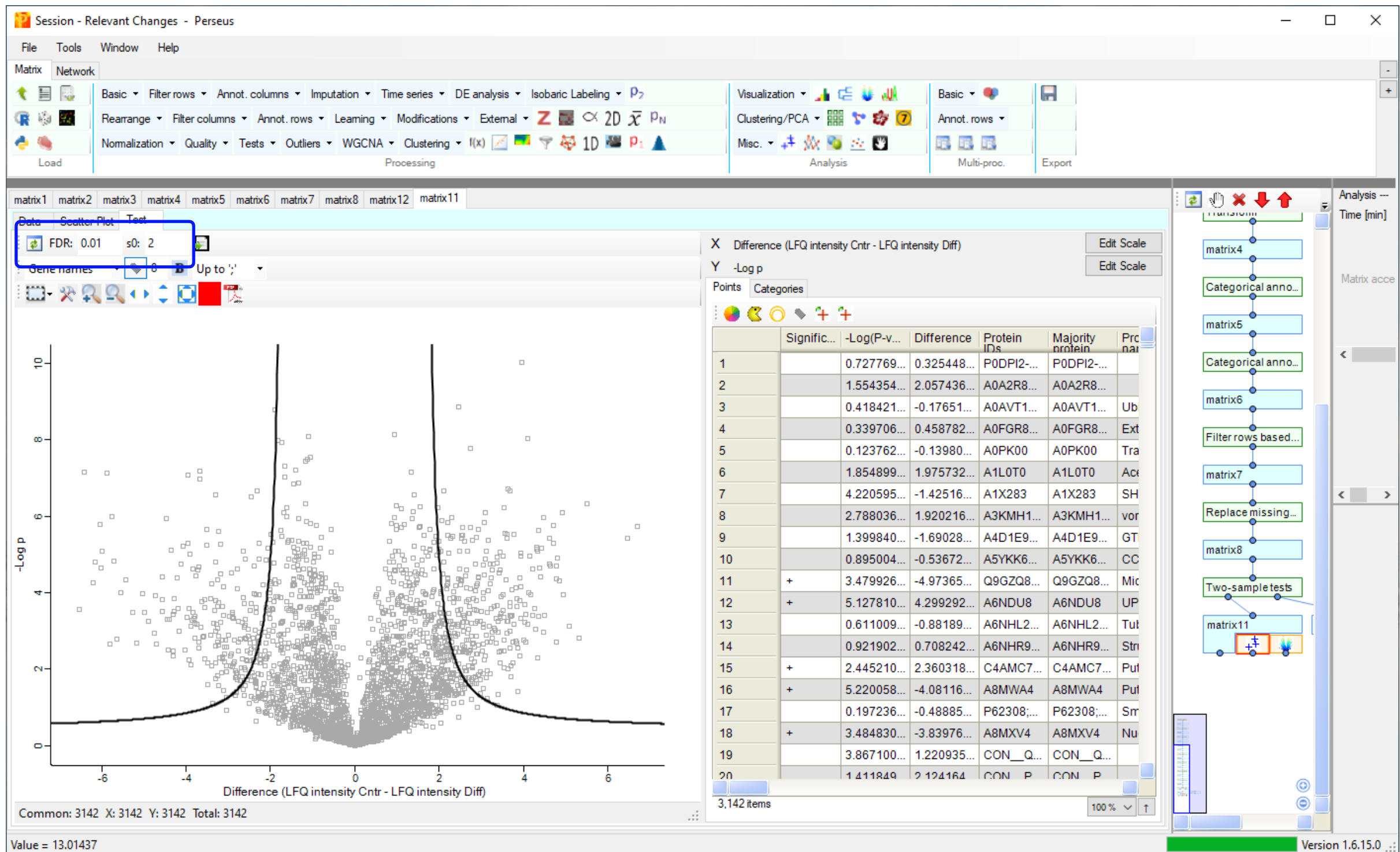
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



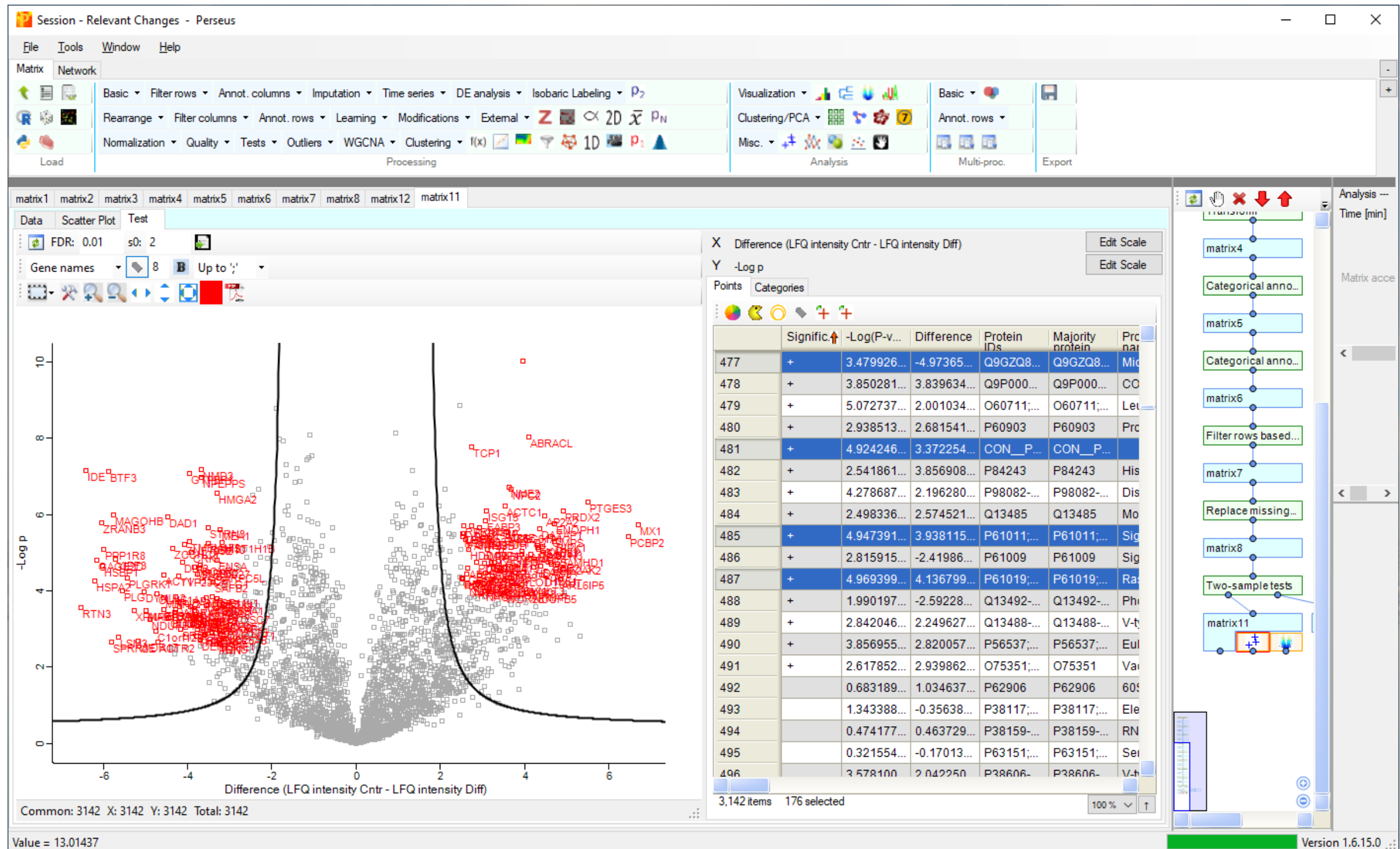
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



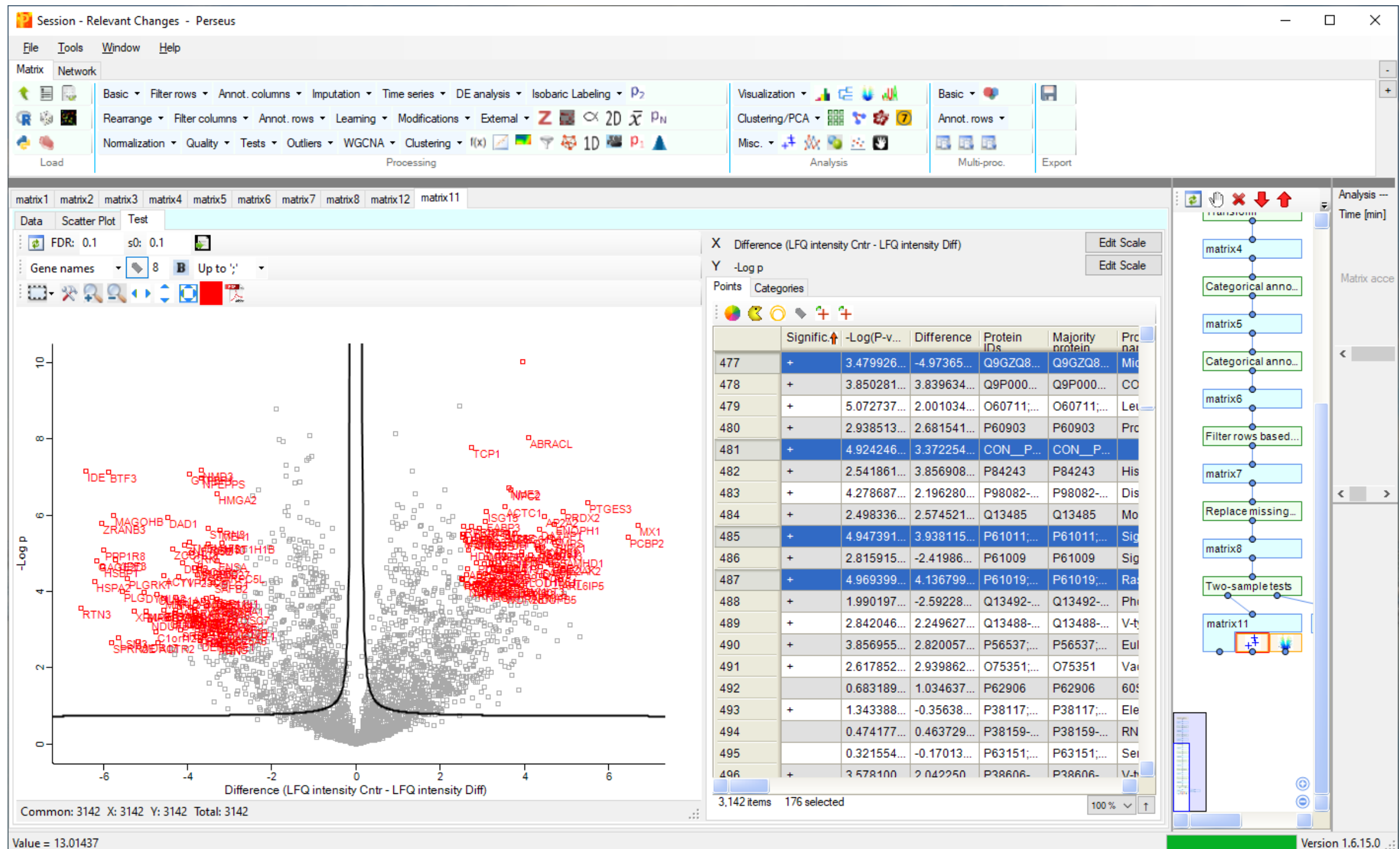
Significance - **Misc. > Volcano plot**



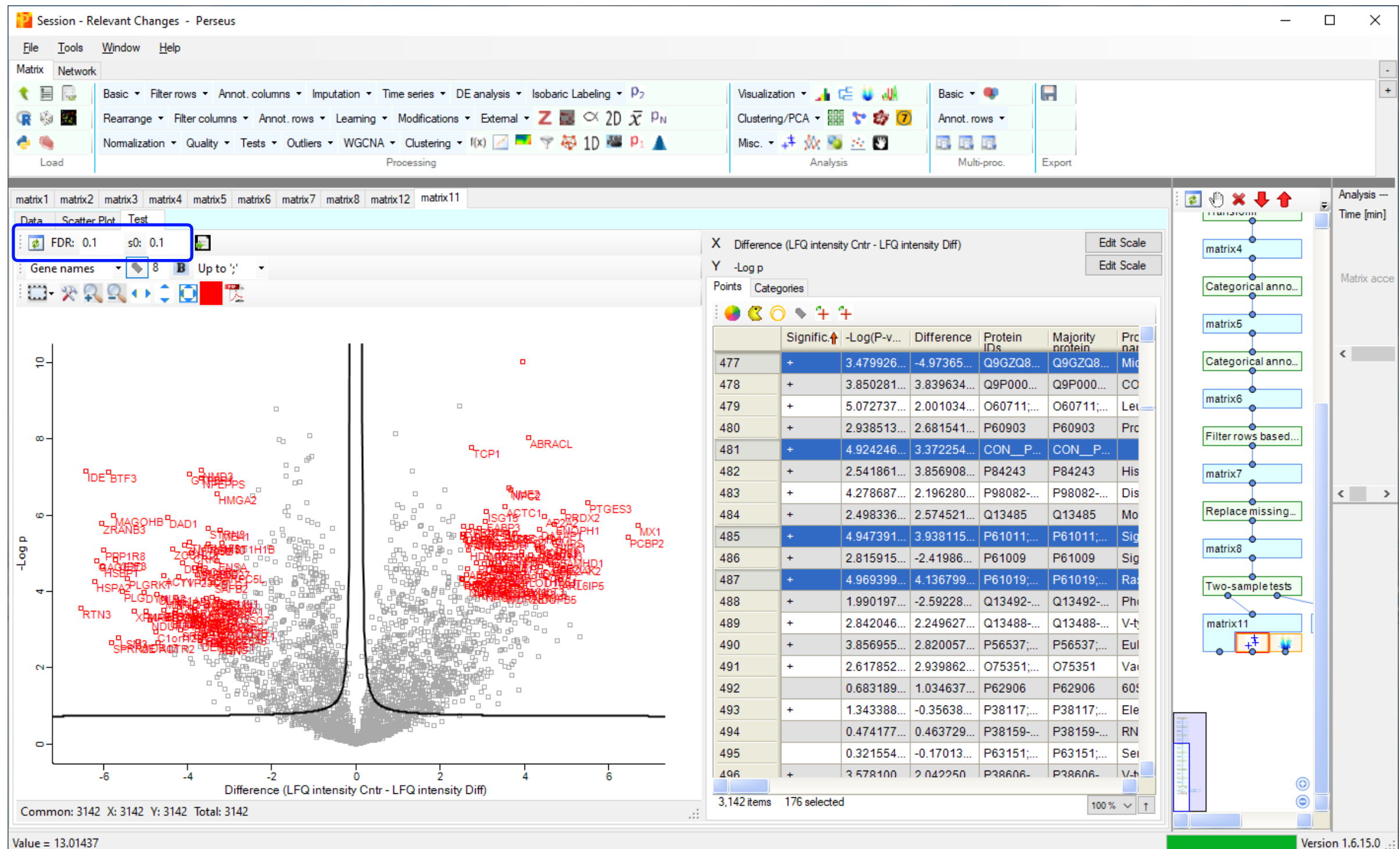
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



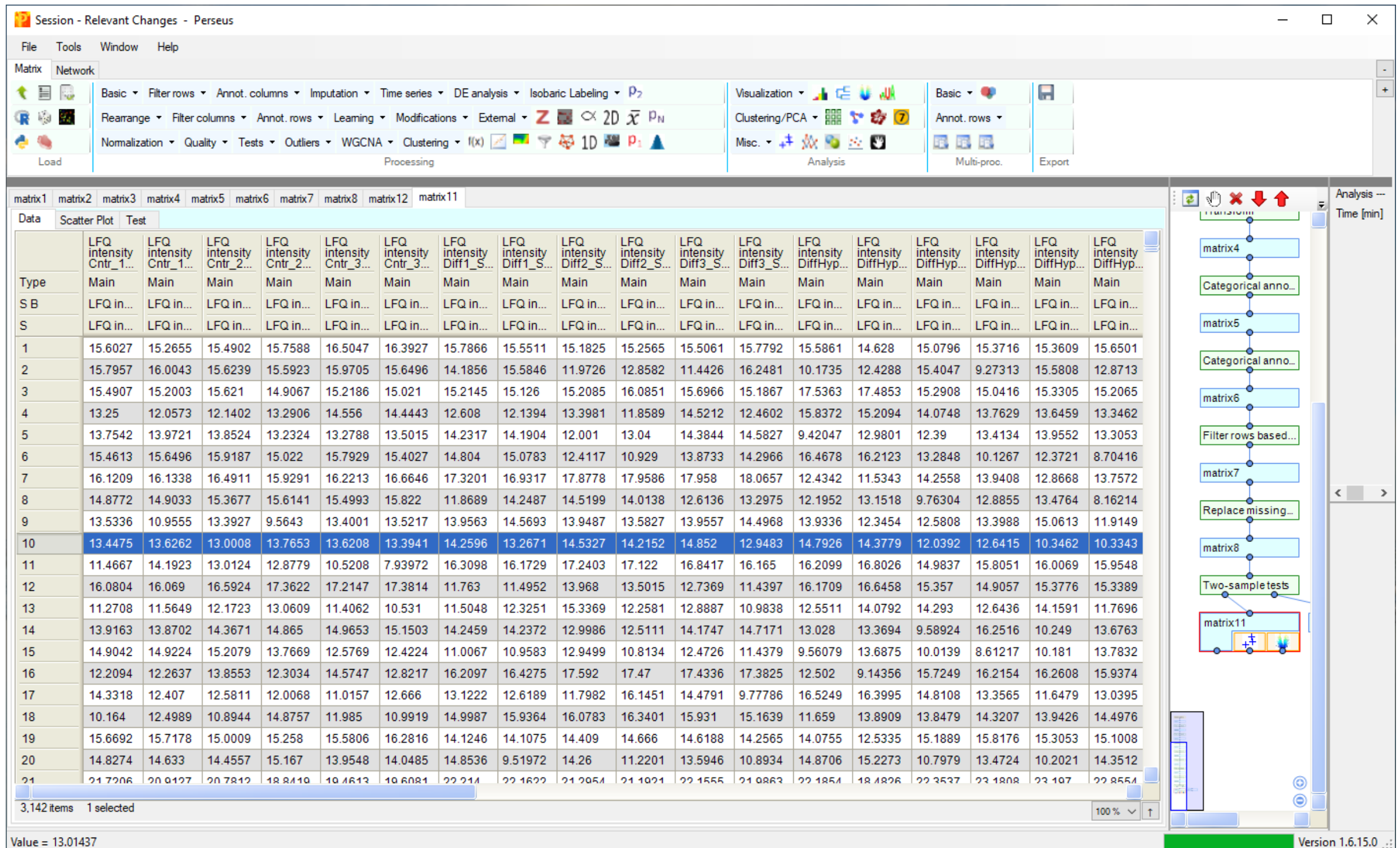
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



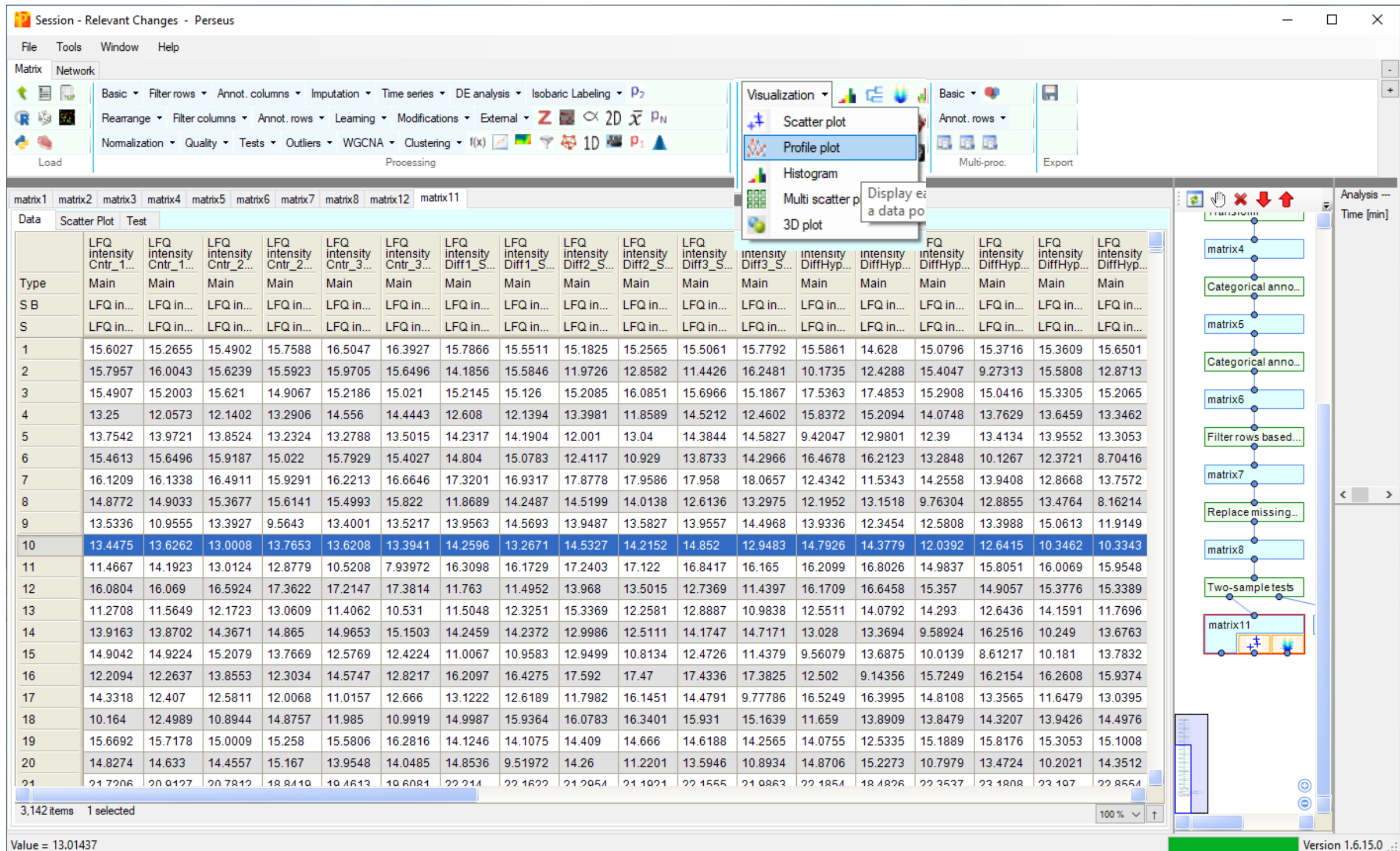
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



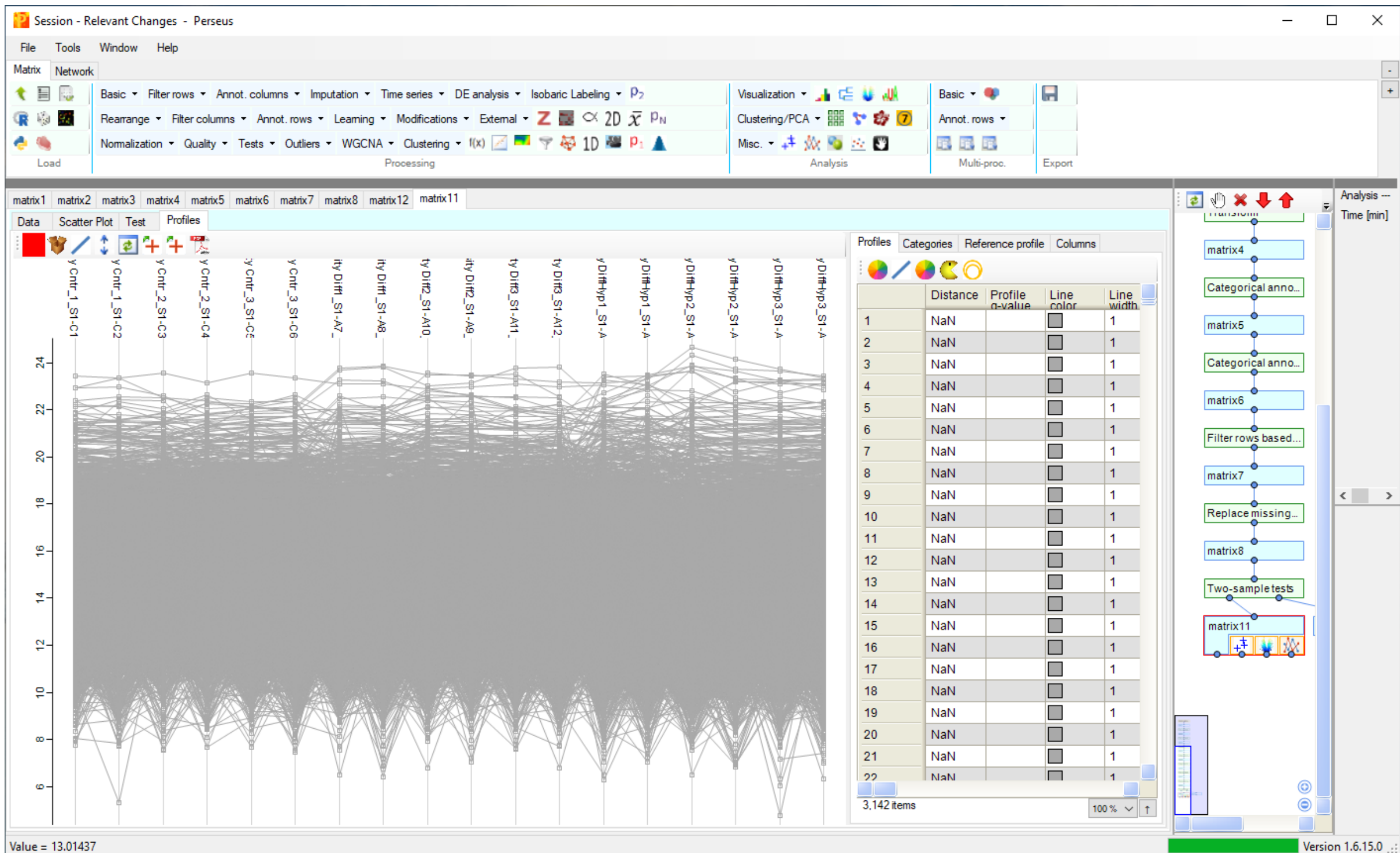
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



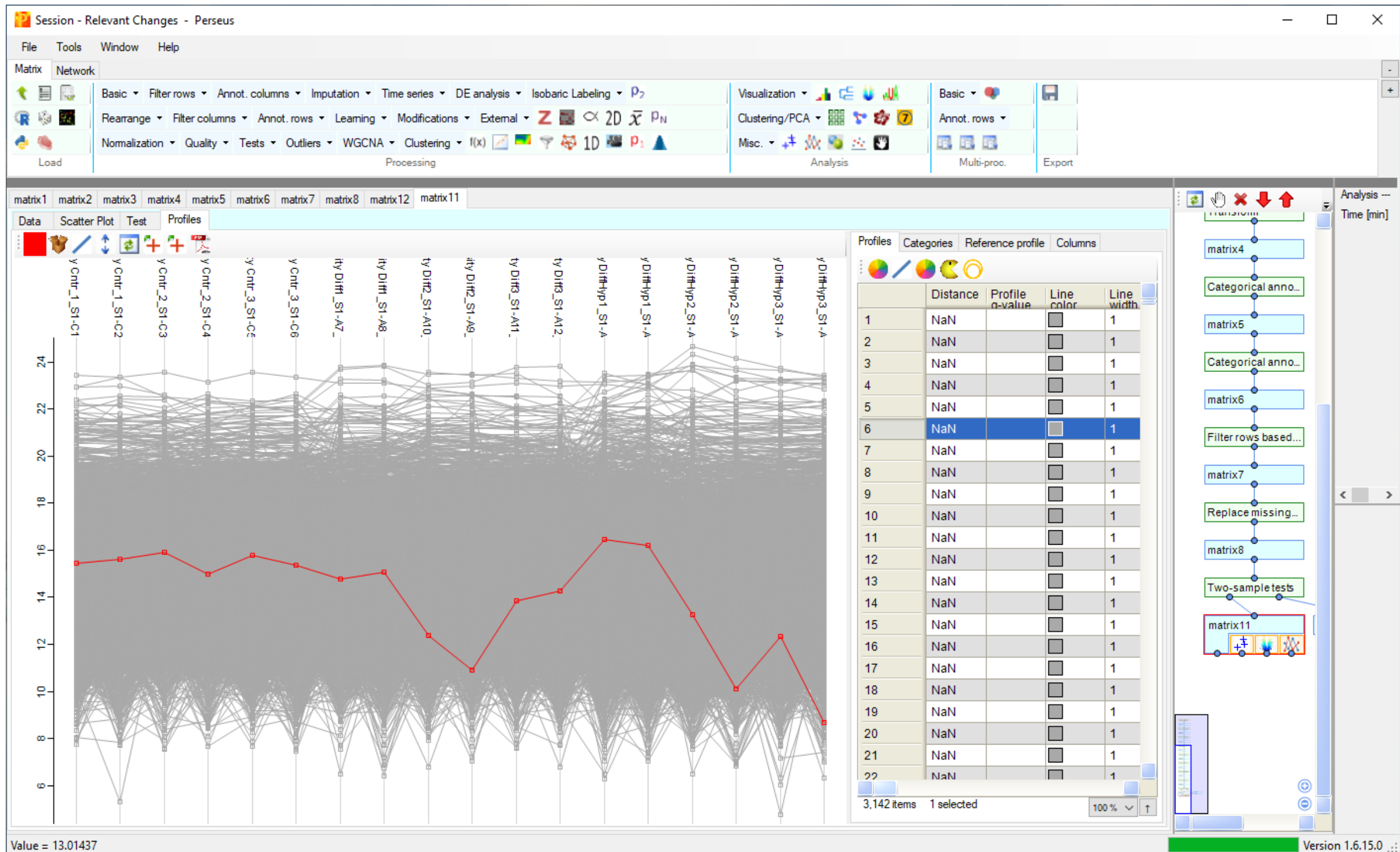
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



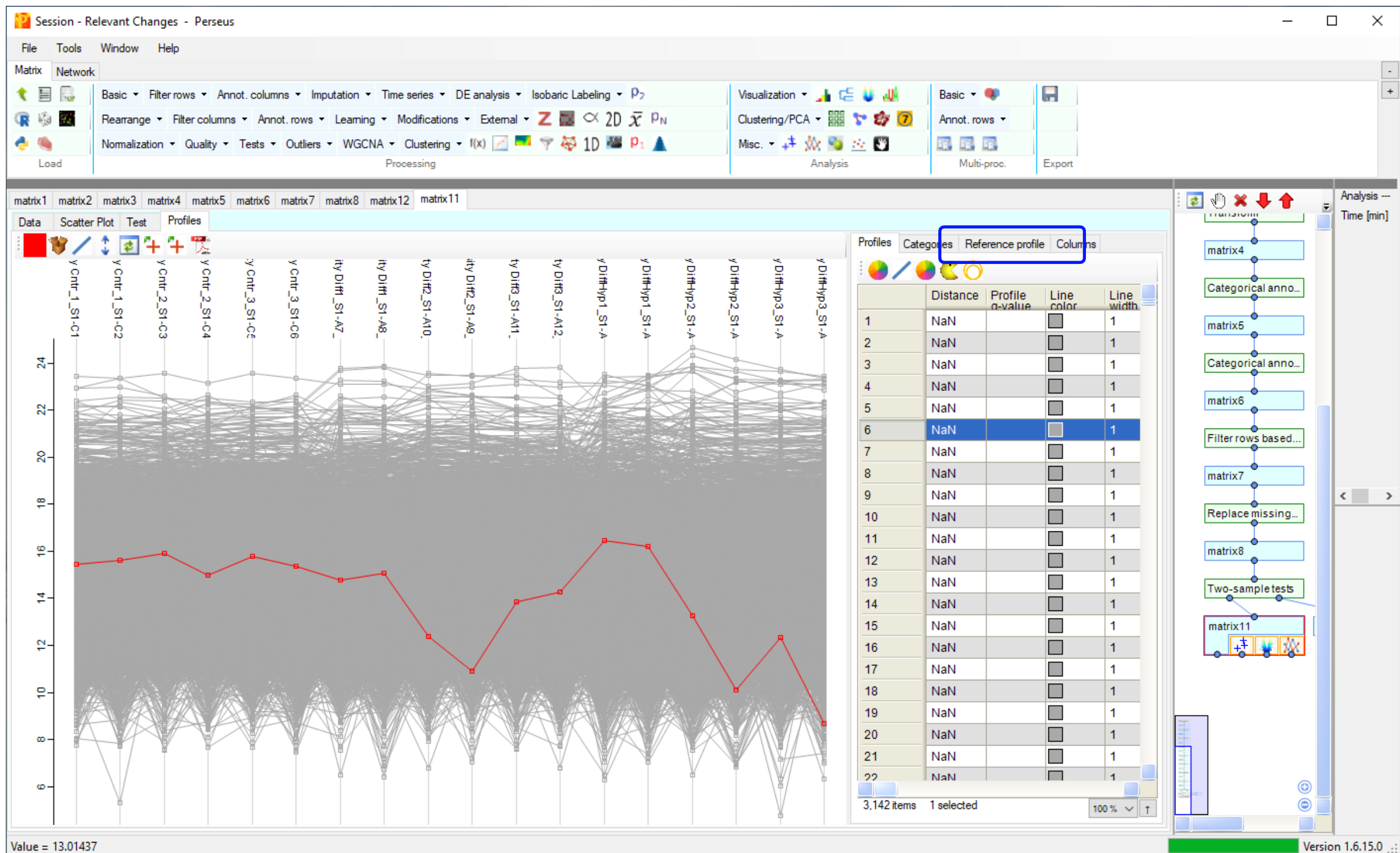
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



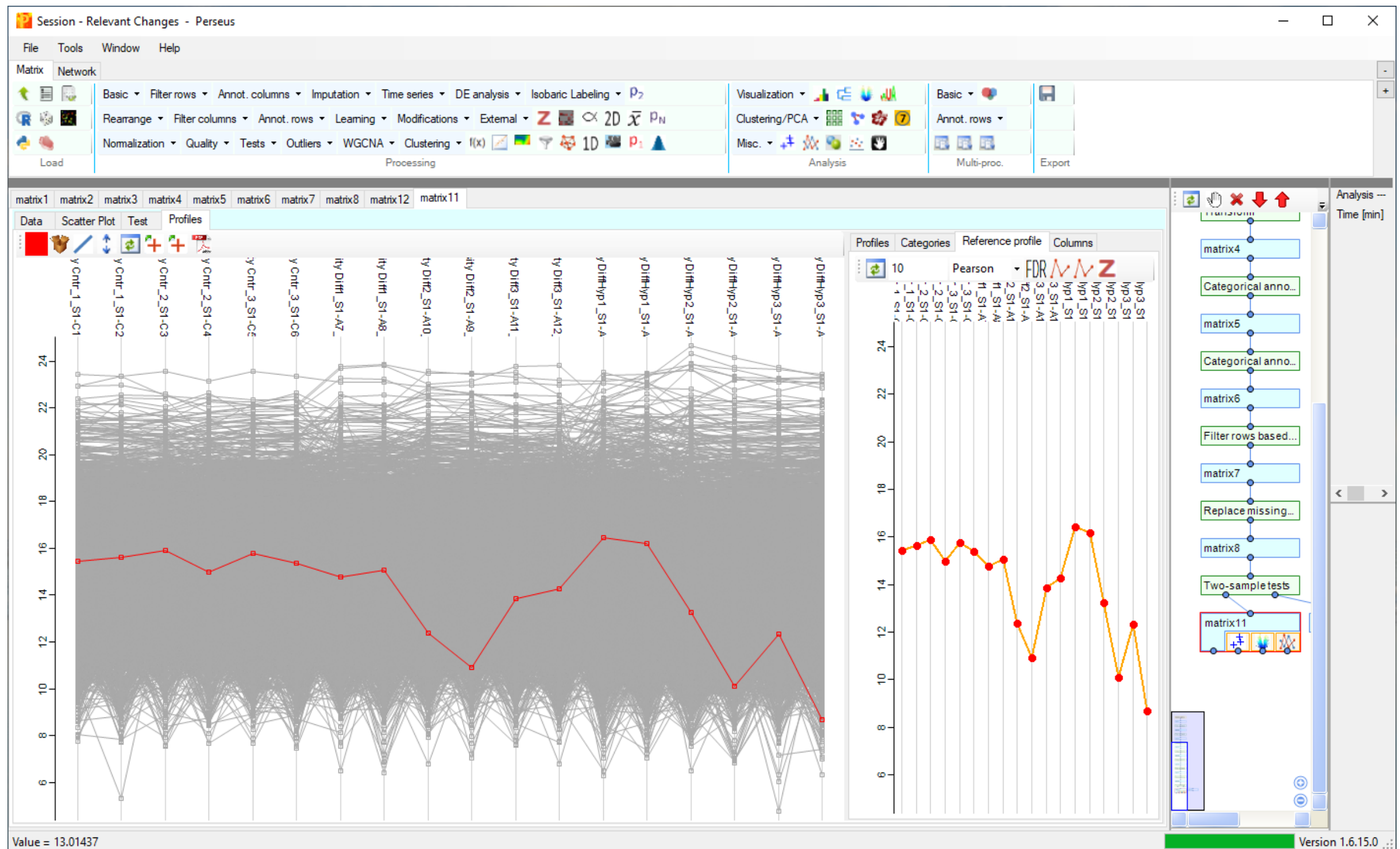
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



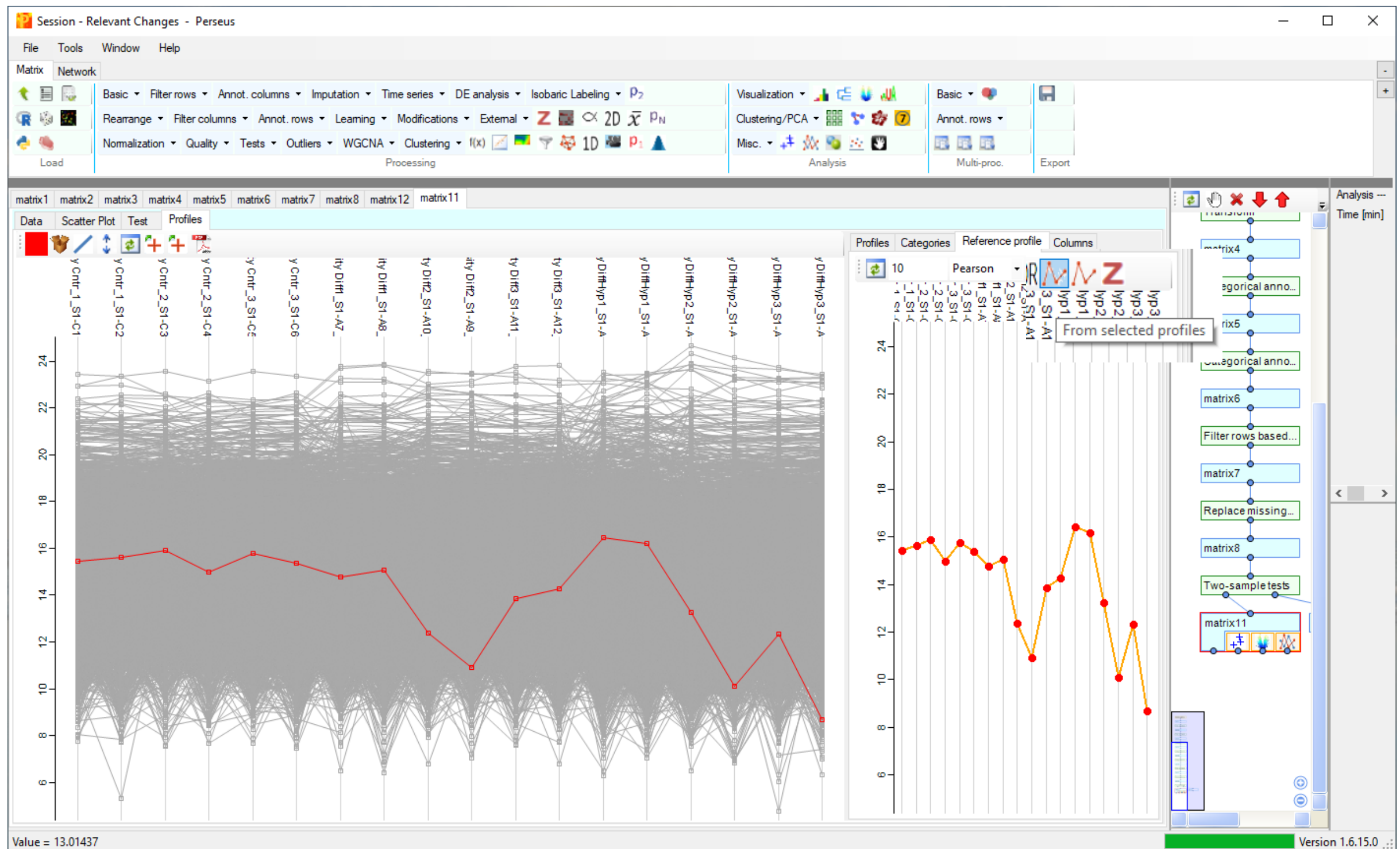
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



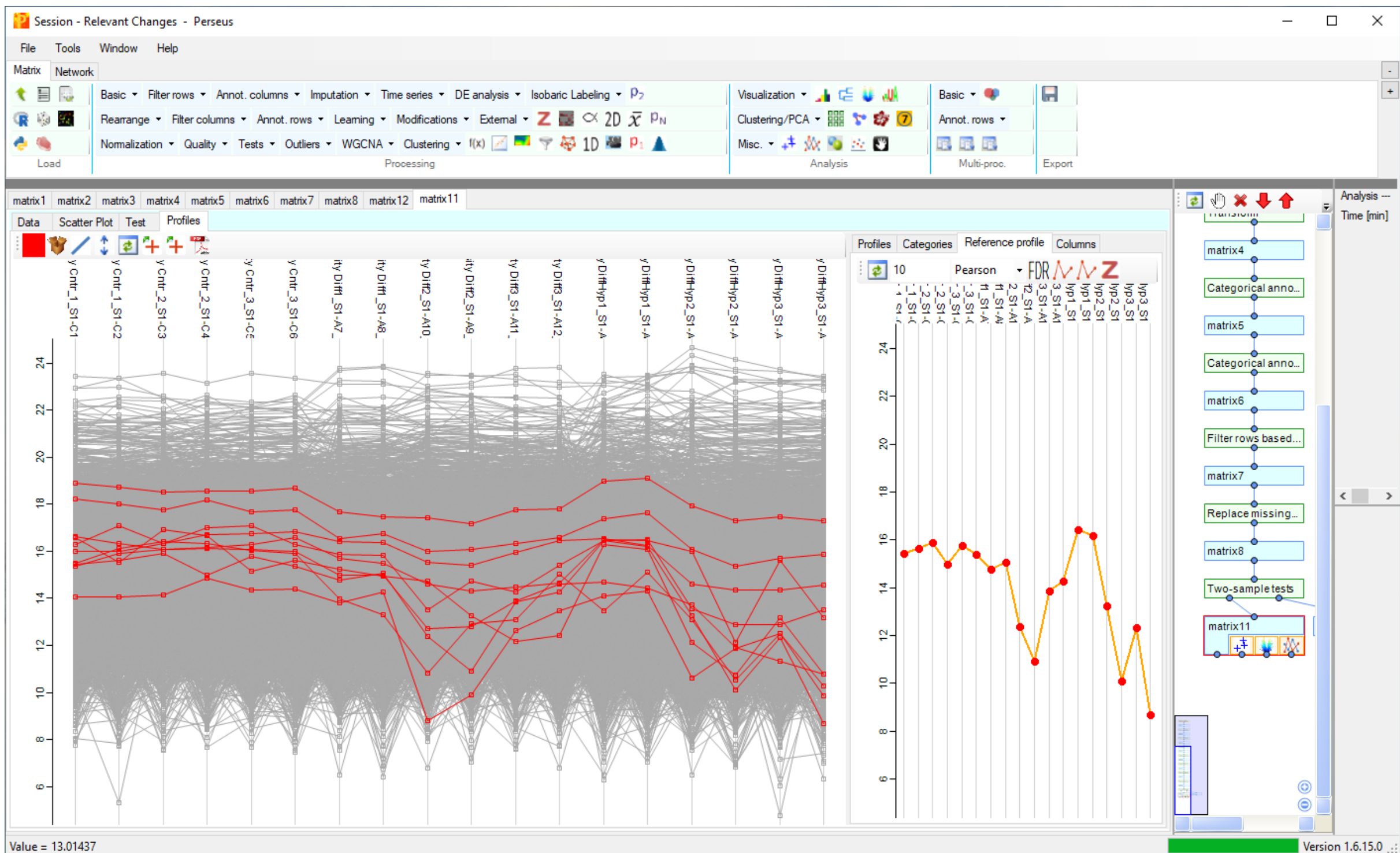
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



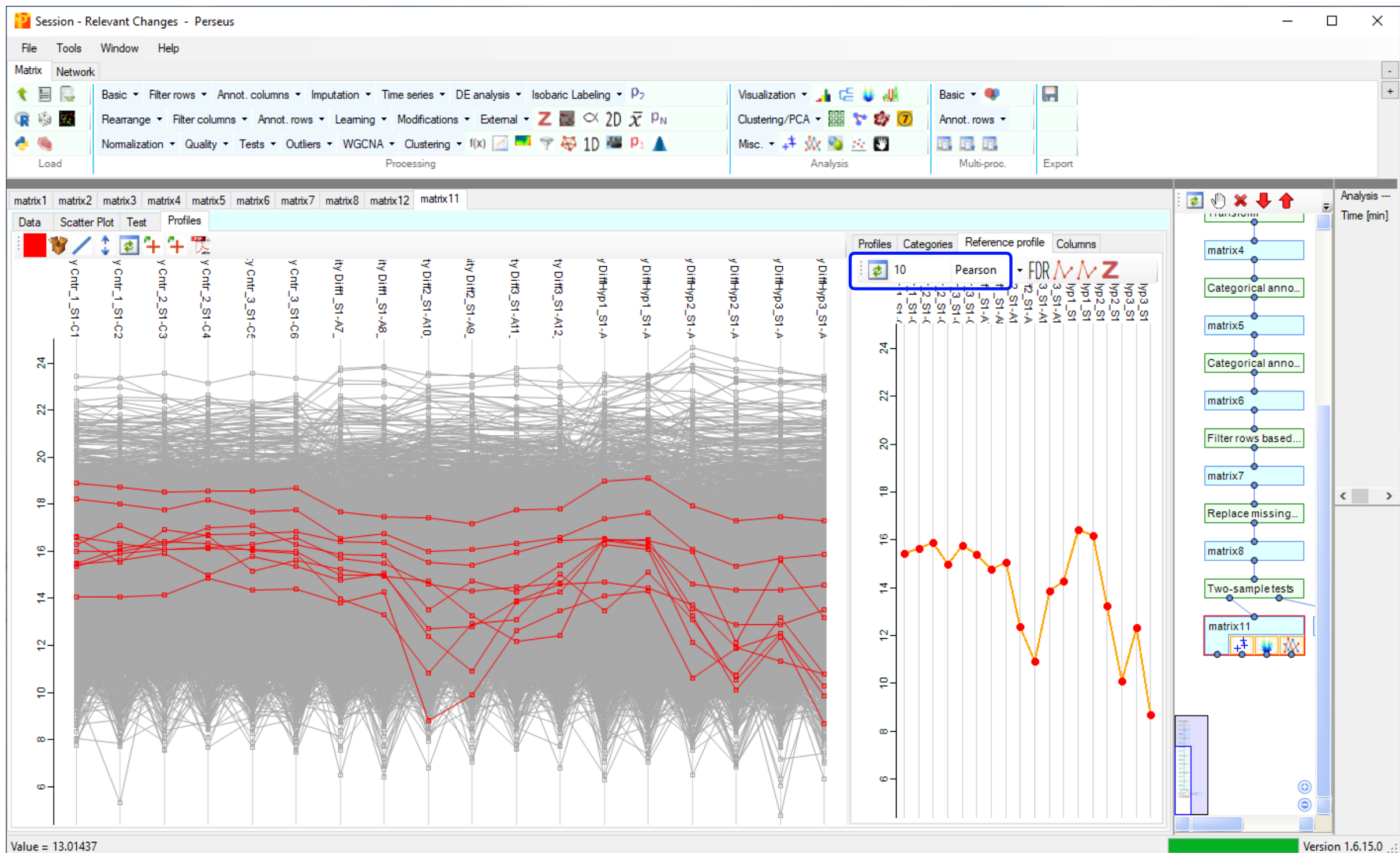
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



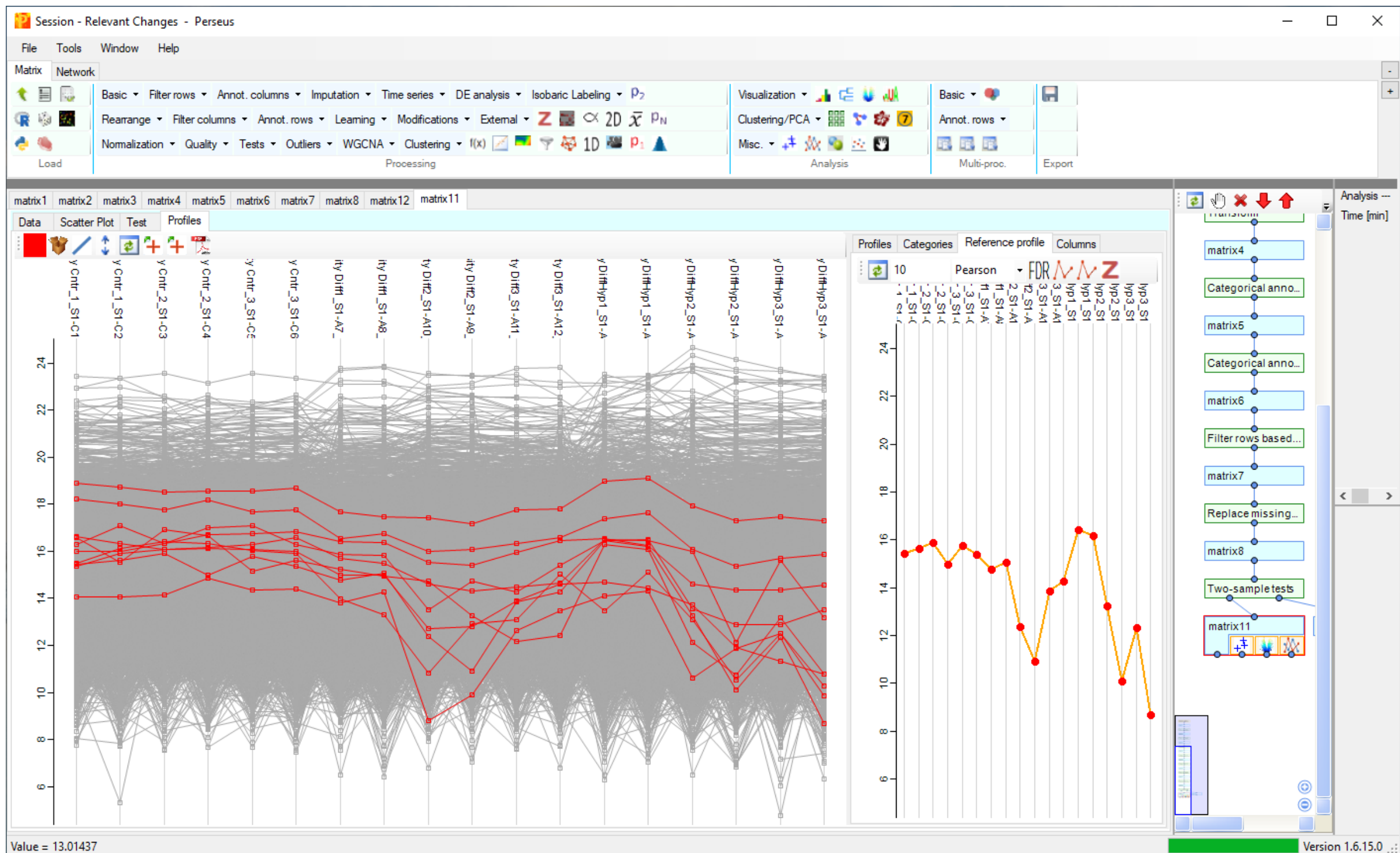
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



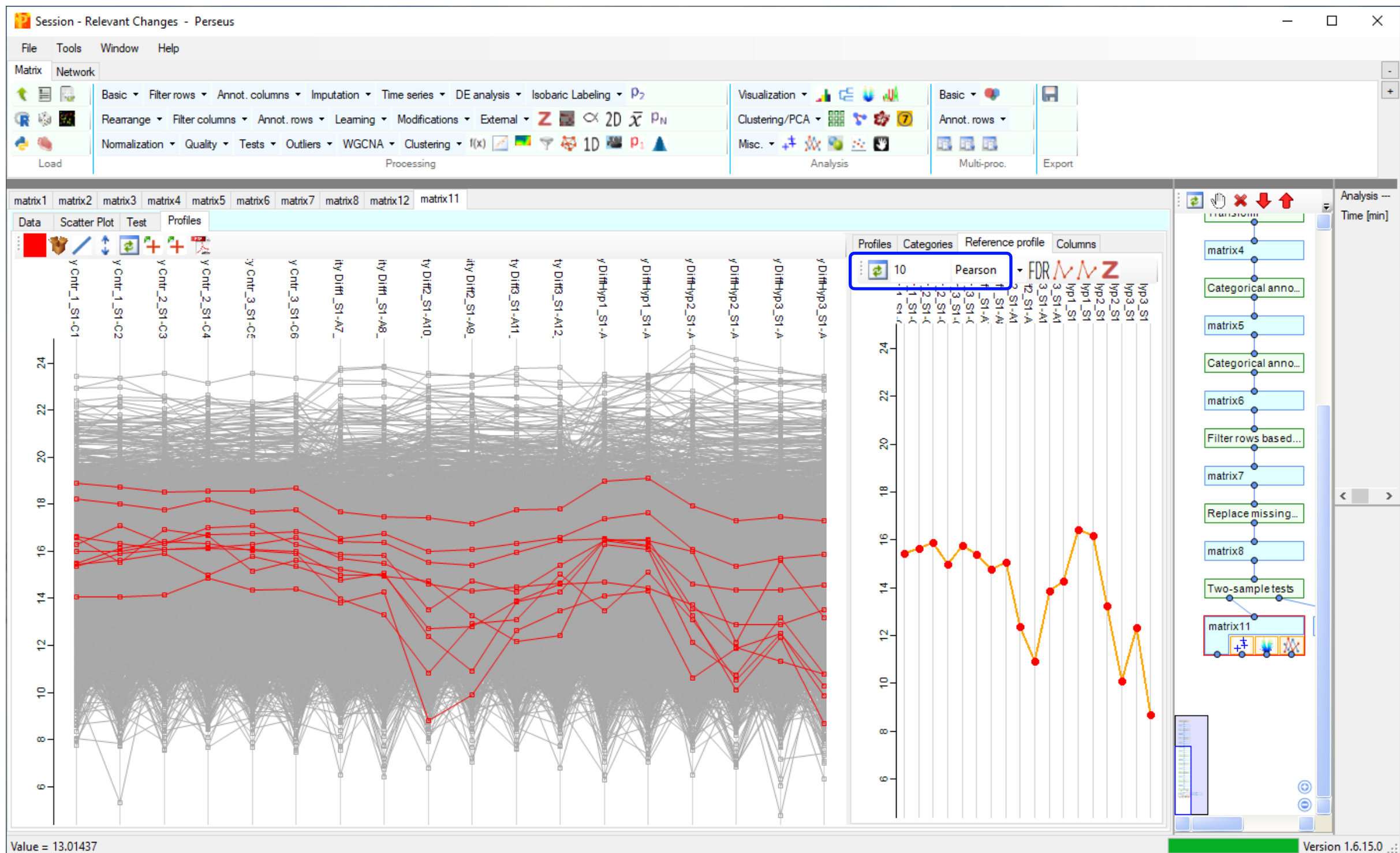
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



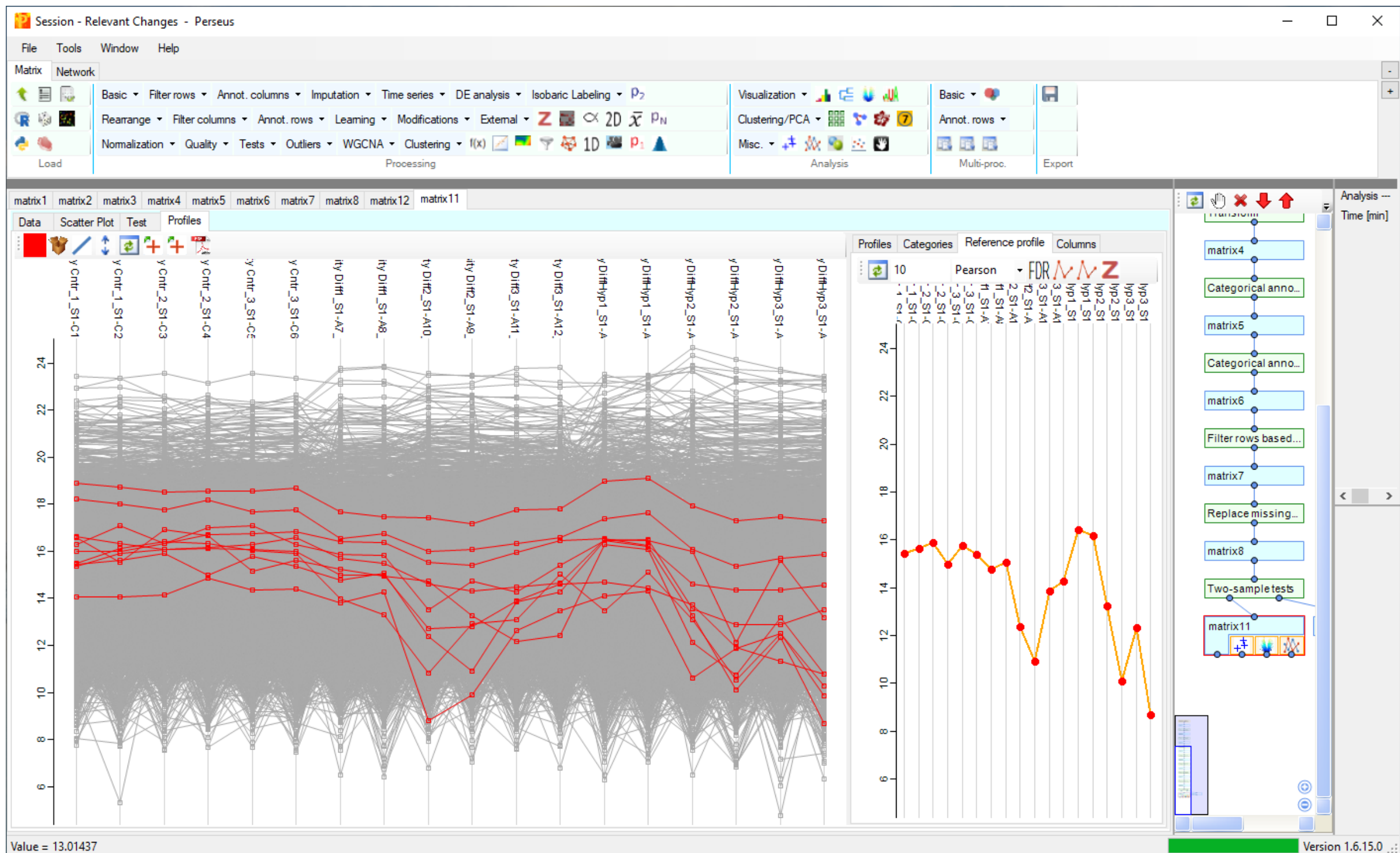
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



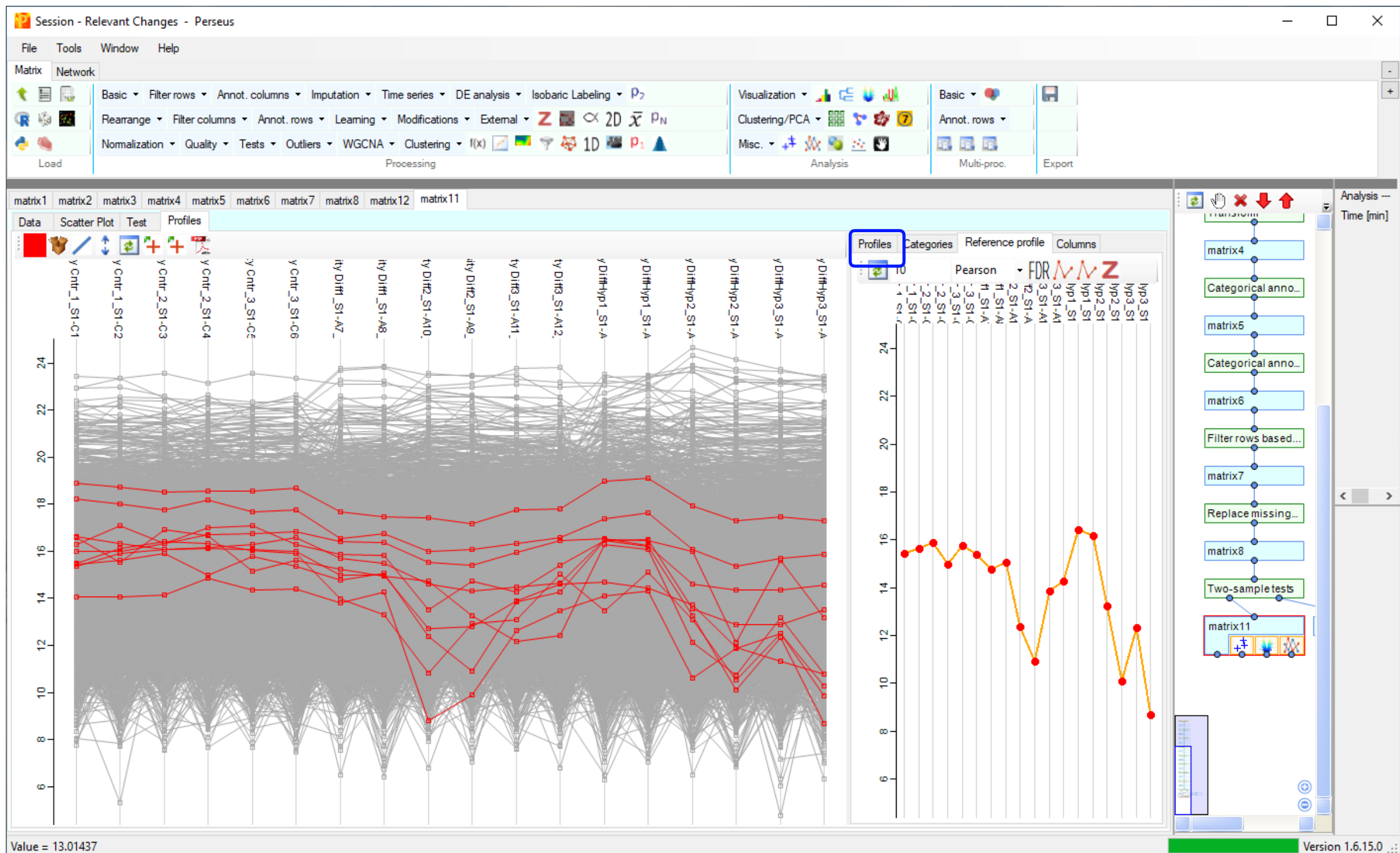
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



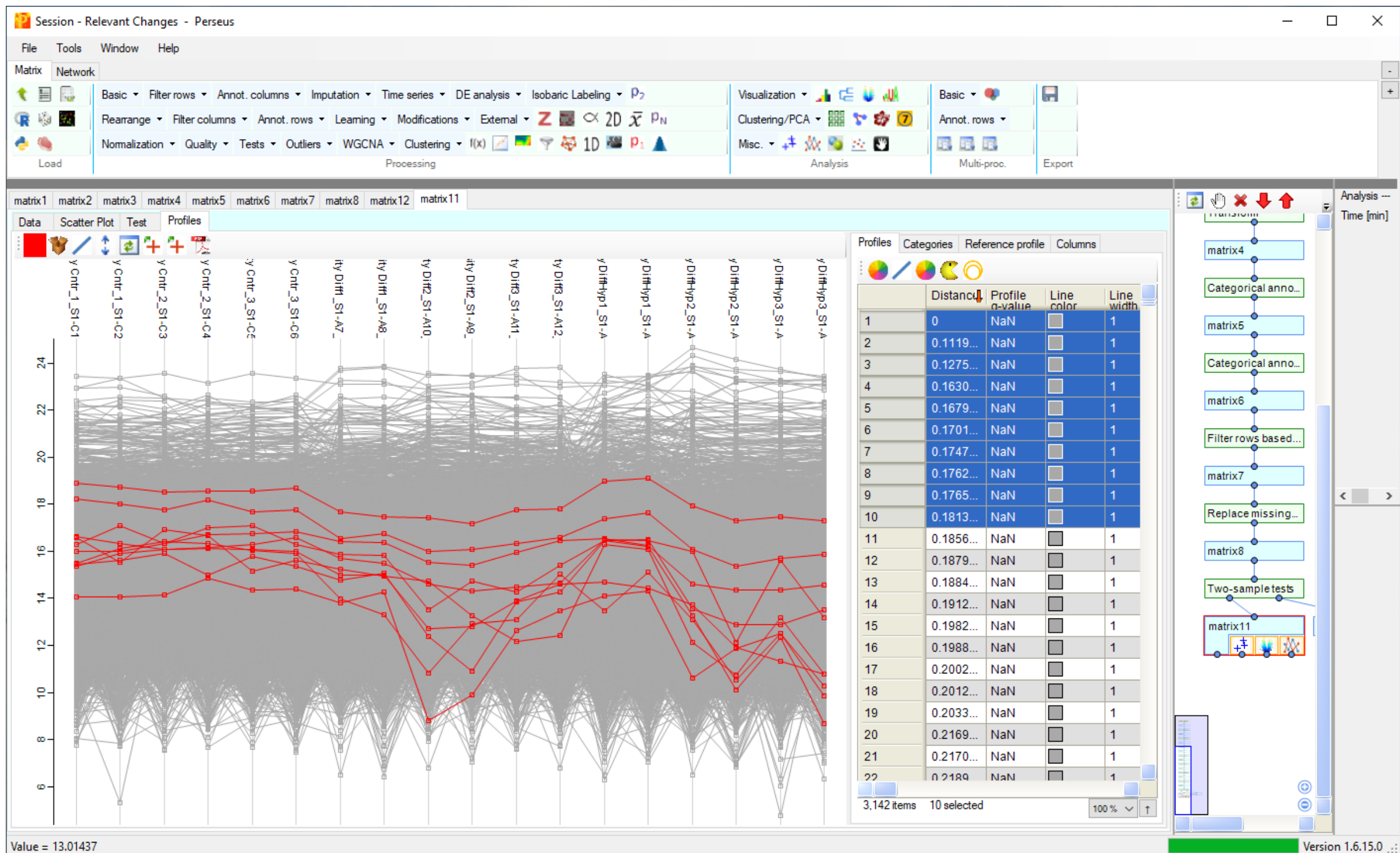
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



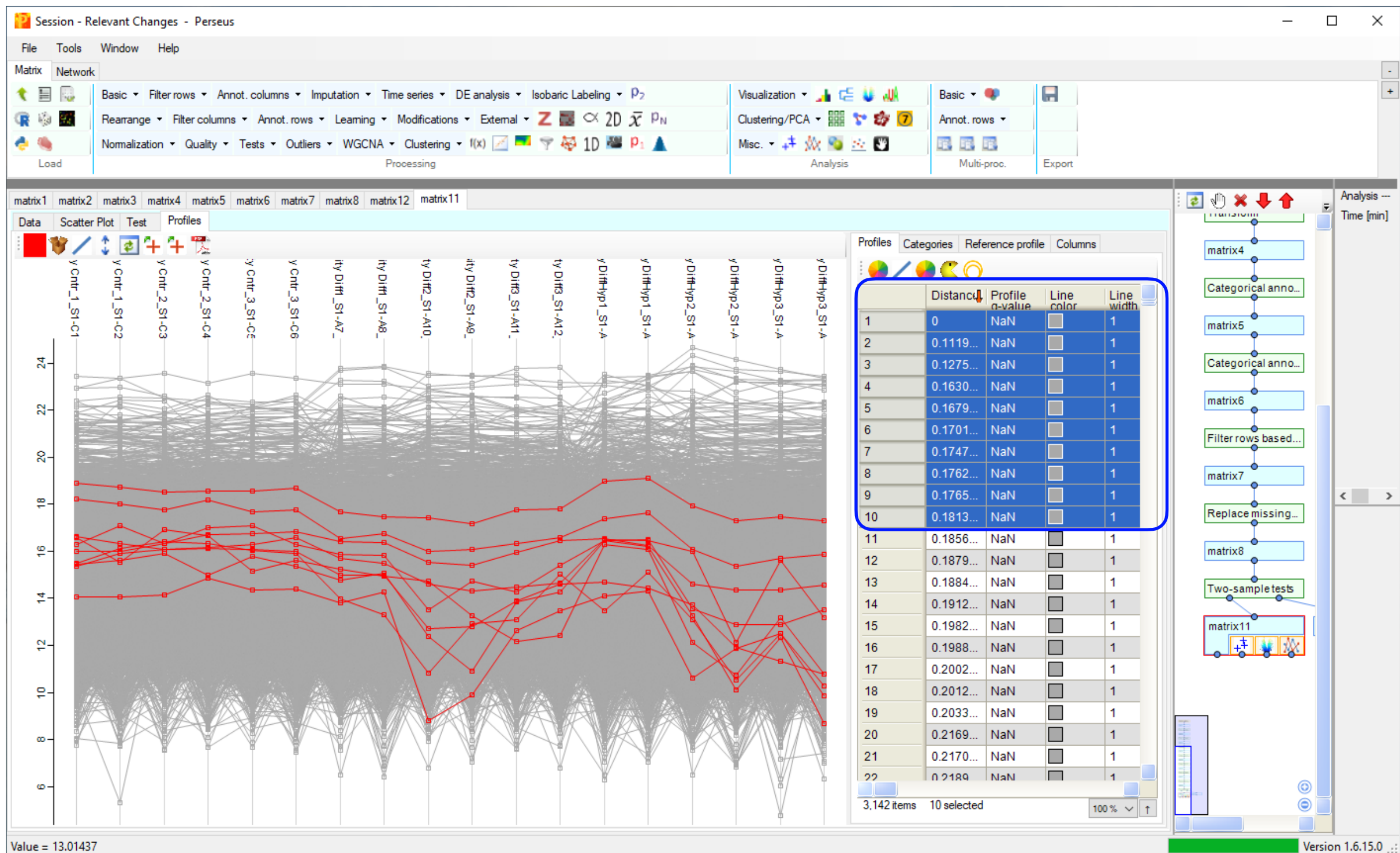
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



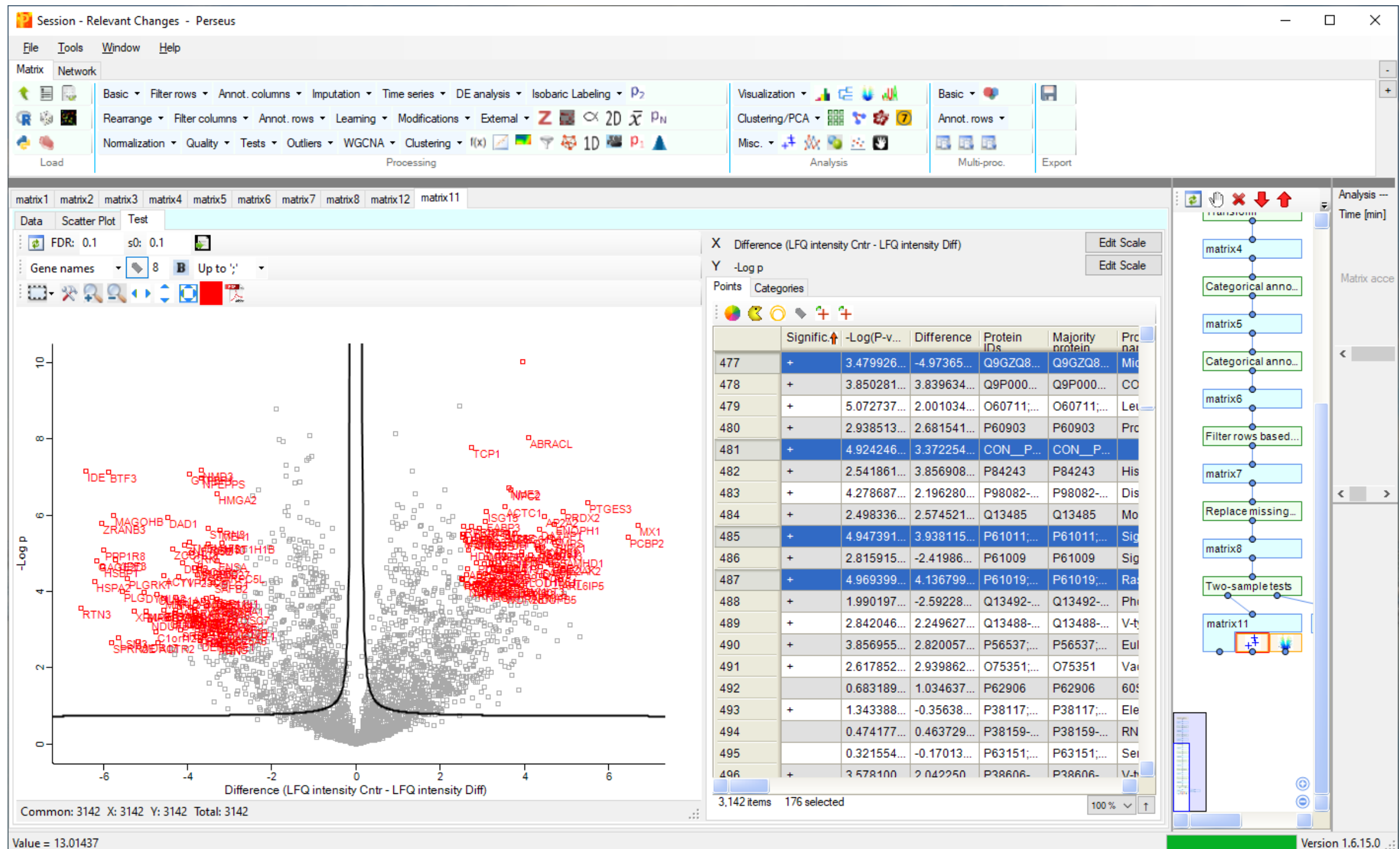
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



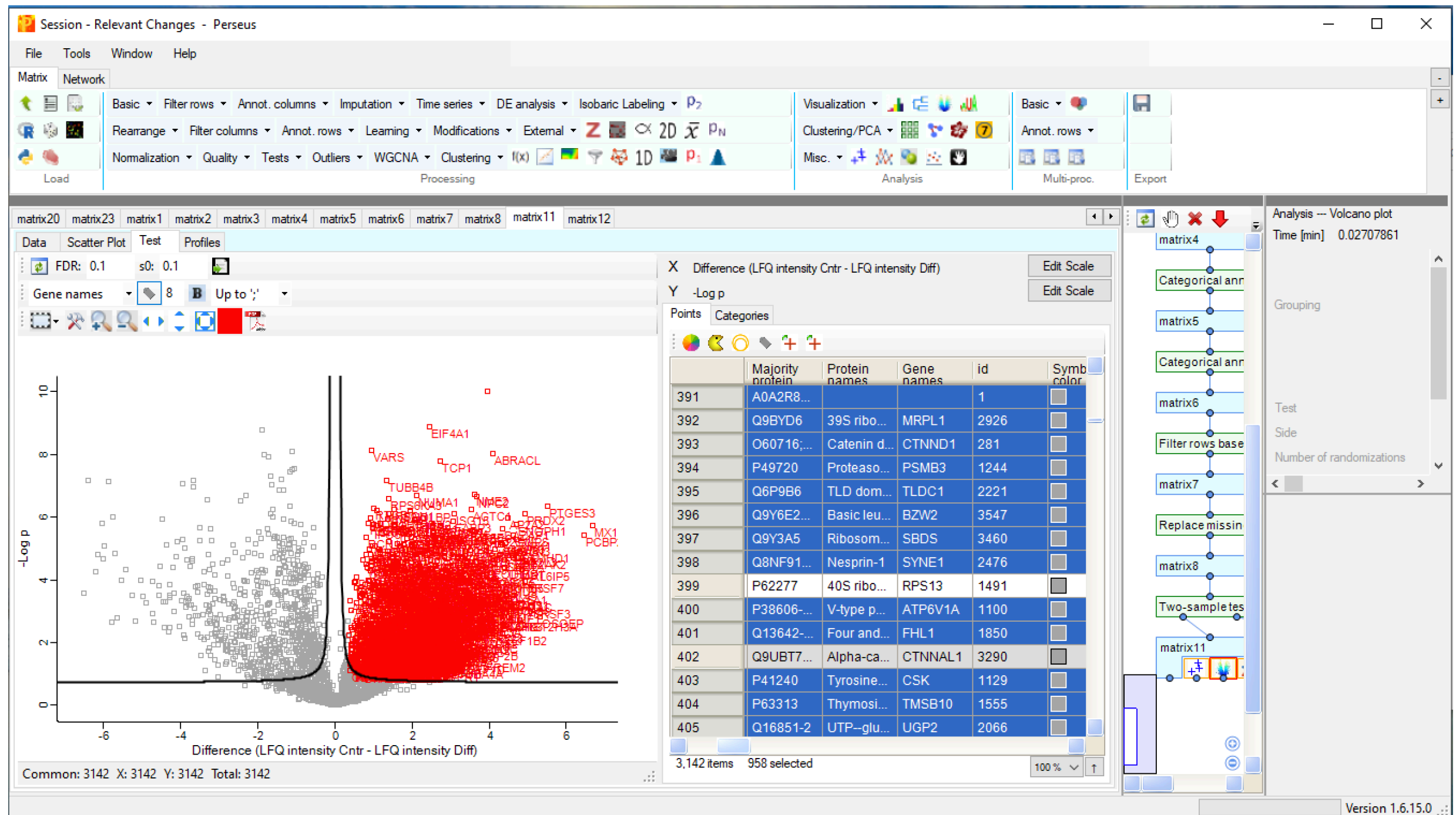
Statistical Data Analysis - Visualisation: Time Course Analysis - **Visualisation.** > **Profile Plot**



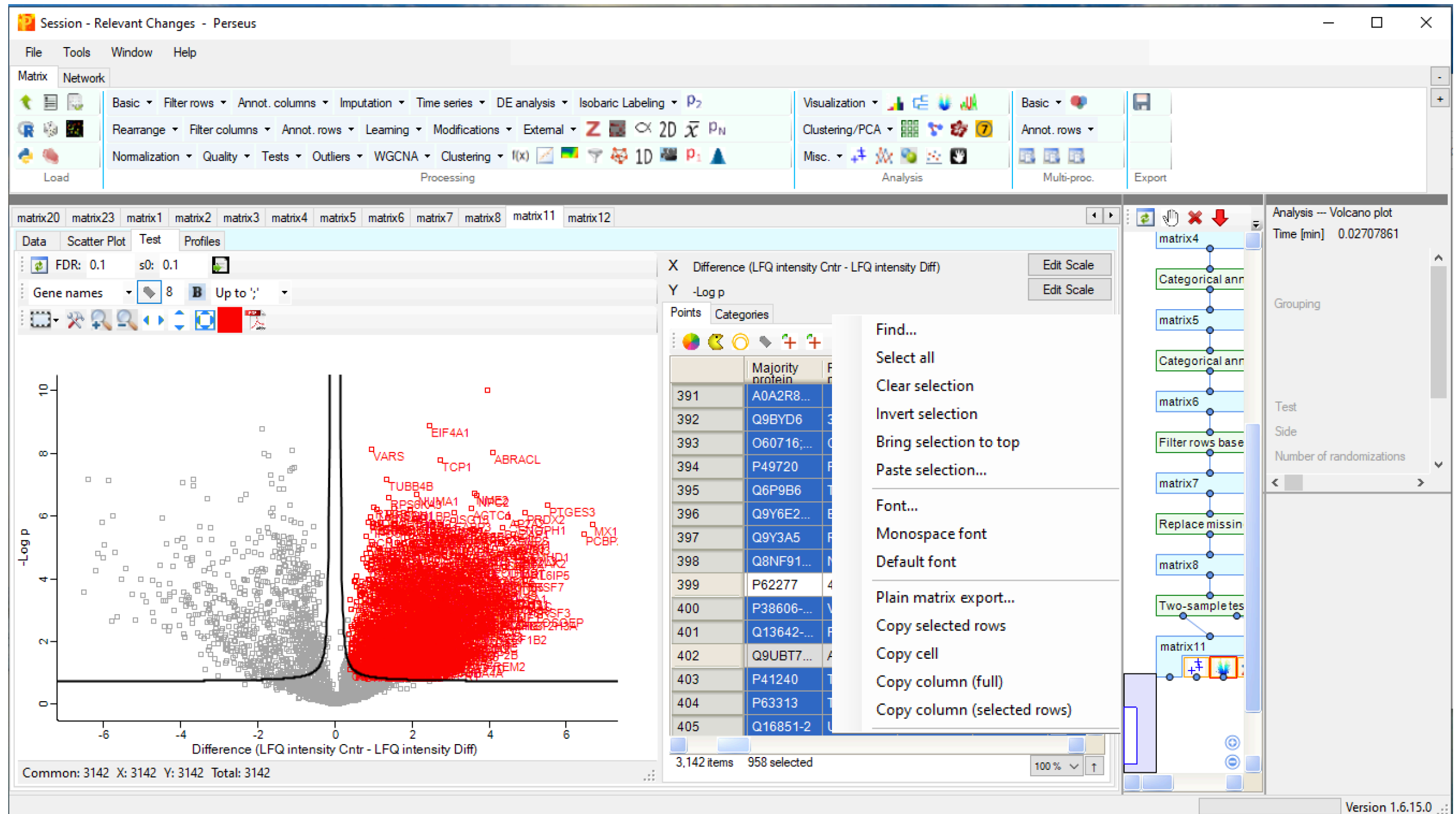
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Misc. > Volcano plot**



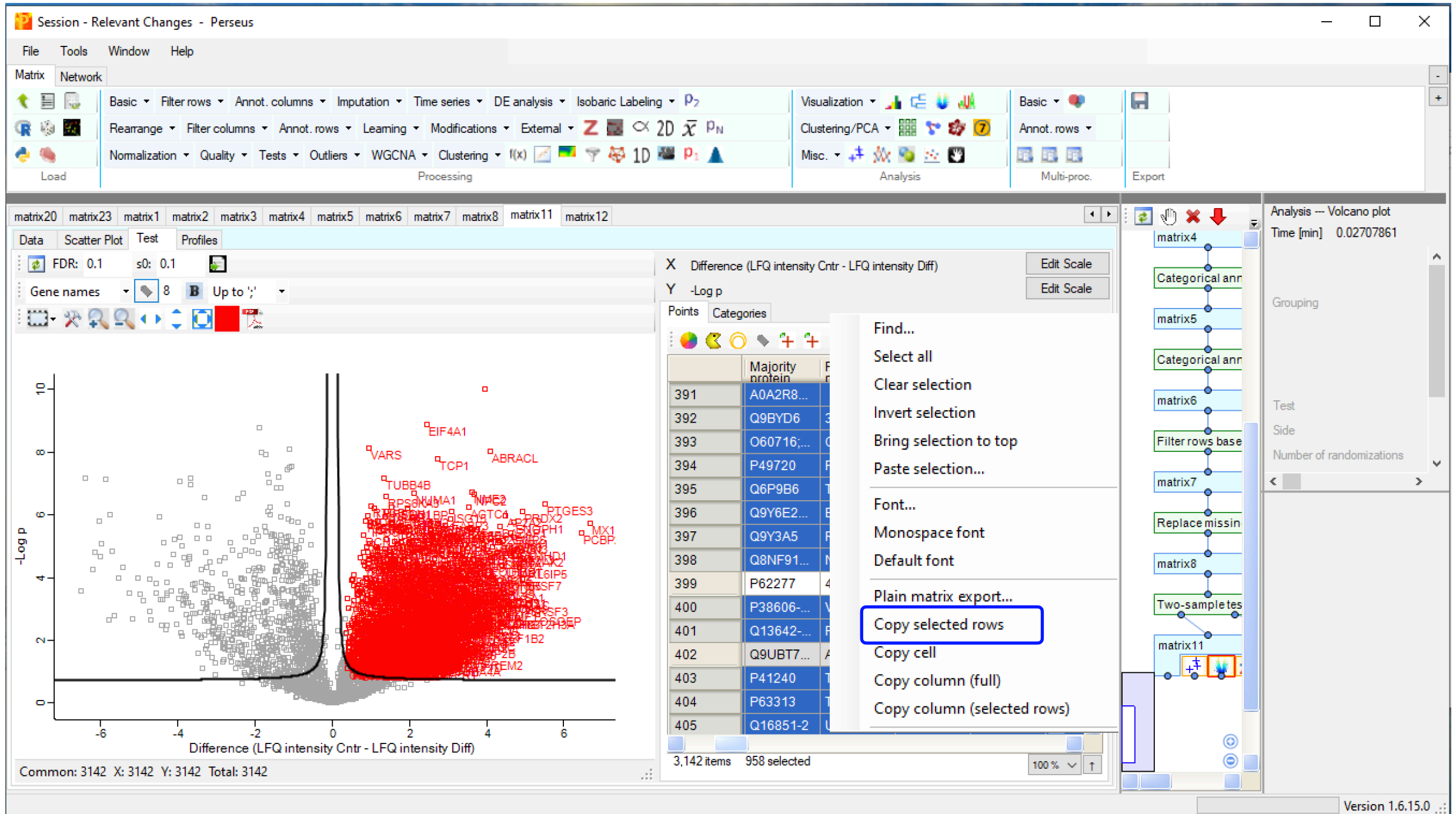
Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Right Click onto the Table > Copy Selected Rows**



Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Right Click onto the Table > Copy Selected Rows**



Statistical Data Analysis - Visualisation: Intensity Difference - Statistical Significance - **Right Click onto the Table > Copy Selected Rows**





Statistical Data Analysis - Visualisation: Network & Pathway Analysis

AutoSave OFF

Book1

Search

HomeInsertDrawPage LayoutFormulasDataReviewViewAcrobatTell me

ThemesAa Fonts

Colours

MarginsOrientationSizePrint AreaBreaksBackgroundPrint TitlesPage Setup

Width: AutomaticHeight: Automatic

GridlinesViewPrintHeadingsViewPrint

ShareComments

K13fx4

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	Significant	#NAME?	Difference	Protein IDs	Majority prot	Protein name	Gene names id		Symbol color	Symbol type	Symbol size	Show label	Only identifi	Reverse	Potential cor	Student's T-t	Student's T-t	Peptides	Razor + uniq	Unique
2	+	1.55435499	2.05743663	A0A2R8Y619	A0A2R8Y619			1	Color2 [A=25	1	4							3	1	
3	+	1.85489919	1.97573217	A1L0T0	A1L0T0	Acetolactate	ILVBL	5	Color2 [A=25	1	4							5	5	
4	+	2.78803617	1.9202164	A3KMH1;A3K	A3KMH1;A3K	von Willebra	VWA8	7	Color2 [A=25	1	4							2	2	
5	+	5.1278101	4.29929225	A6NDU8	A6NDU8	UPF0600 pro	C5orf51	11	Color2 [A=25	1	4					+	LFQ intensity	4	4	
6	+	2.44521016	2.36031882	C4AMC7;Q6V	C4AMC7;Q6V	Putative WA	WASH3P;WA	14	Color2 [A=25	1	4					+	LFQ intensity	1	1	
7	+	3.86710013	1.22093582	CON_Q3MH	CON_Q3MH	CON_Q3MHN5;CON	ENSEMBL:ENSE	20	Color2 [A=25	1	4				+			4	4	
8	+	1.41184962	2.1241649	CON_P0073	CON_P0073			22	Color2 [A=25	1	4				+			3	3	
9	+	10.0185073	3.96177419	CON_P0196	CON_P0196			24	Color2 [A=25	1	4				+	+	LFQ intensity	7	7	
10	+	5.04489656	3.93767436	CON_P0686	CON_P0686			29	Color2 [A=25	1	4				+	+	LFQ intensity	17	15	
11	+	4.92424699	3.37225405	CON_P1549	CON_P1549			32	Color2 [A=25	1	4				+	+	LFQ intensity	9	9	
12	+	1.84467521	2.31118377	CON_P4136	CON_P4136			37	Color2 [A=25	1	4				+			1	1	
13	+	5.15537224	1.61123244	CON_Q294	CON_Q294	CON_Q0IIK2		39	Color2 [A=25	1	4				+			9	9	
14	+	3.49571552	2.00845734	Q13765;E9P	Q13765;E9P	Nascent poly	NACA	51	Color2 [A=25	1	4							4	4	
15	+	4.58161475	0.95561965	O00116	O00116	Alkyldihydro	AGPS	54	Color2 [A=25	1	4							13	13	
16	+	1.95904664	0.4355154	O00170	O00170	AH receptor	AIP	61	Color2 [A=25	1	4							6	6	
17	+	3.71947306	1.97502708	O00232;O00	O00232;O00	26S proteasc	PSMD12	67	Color2 [A=25	1	4							7	7	
18	+	1.51348841	2.22553317	O00233;O00	O00233;O00	26S proteasc	PSMD9	68	Color2 [A=25	1	4							4	4	
19	+	2.9569985	3.39298932	O00267-2;O	O00267-2;O	Transcriptio	SUPT5H	71	Color2 [A=25	1	4					+	LFQ intensity	2	2	
20	+	3.25523113	2.96861712	O00303	O00303	Eukaryotic tr	EIF3F	75	Color2 [A=25	1	4					+	LFQ intensity	2	2	
21	+	5.66810714	0.97534752	O00410;O00	O00410;O00	Importin-5	IPOS	78	Color2 [A=25	1	4							34	34	
22	+	3.12436179	1.93475405	O00560;O00	O00560;O00	Syntenin-1	SDCBP	94	Color2 [A=25	1	4							7	7	
23	+	4.36021901	2.20206674	O00571-2;O	O00571-2;O	ATP-depende	DDX3X	97	Color2 [A=25	1	4					+	LFQ intensity	15	15	
24	+	2.44005413	1.92432197	O00743-2;O	O00743-2;O	Serine/threo	PPP6C	100	Color2 [A=25	1	4							3	3	
25	+	3.44940553	0.68289375	O14617;O14	O14617;O14	AP-3 comple	AP3D1	107	Color2 [A=25	1	4							13	13	
26	+	3.57808911	1.34338919	O14727-5;O	O14727-5;O	Apoptotic pr	APAF1	113	Color2 [A=25	1	4							1	1	
27	+	1.38523056	0.49817276	O14879	O14879	Interferon-in	IFIT3	125	Color2 [A=25	1	4							9	9	
28	+	1.82799793	1.64875571	O14880	O14880	Microsomal	MGST3	126	Color2 [A=25	1	4							4	4	
29	+	4.37027036	2.47093328	O14950;P19	O14950;P19	Myosin regul	MYL12B;MYL	132	Color2 [A=25	1	4					+	LFQ intensity	11	11	
30	+	2.34330316	3.08777857	O14974-5;O	O14974-5;O	Protein phos	PPP1R12A	135	Color2 [A=25	1	4					+	LFQ intensity	8	8	
31	+	2.47962476	1.24199581	O14981-2;O	O14981-2;O	TATA-binding	BTA1	138	Color2 [A=25	1	4							1	1	
32	+	1.34839273	1.33280754	O15013-7;O	O15013-7;O	Rho guanine	ARHGEF10	139	Color2 [A=25	1	4							3	3	
33	+	1.88596943	3.03884776	O15067	O15067	Phosphoribo	PFAS	143	Color2 [A=25	1	4					+	LFQ intensity	7	7	
34	+	1.45805292	2.24850003	O15116	O15116	U6 snRNA-as	LSM1	146	Color2 [A=25	1	4							2	2	
35	+	2.76787081	1.09159056	O15143	O15143	Actin-relatec	ARPC1B	151	Color2 [A=25	1	4							13	13	
36	+	2.86102121	0.97764524	O15144	O15144	Actin-relatec	ARPC2	152	Color2 [A=25	1	4							13	13	
37	+	4.97028583	0.8936828	O15145	O15145	Actin-relatec	ARPC3	153	Color2 [A=25	1	4							6	6	
38	+	1.36422025	2.12705612	O15160-2;O	O15160-2;O	DNA-directe	POLR1C	155	Color2 [A=25	1	4							3	3	
39	+	3.89564801	1.82343992	O15182	O15182	Centrin-3	CETN3	158	Color2 [A=25	1	4							1	1	

Sheet1

ReadyAccessibility: Good to go

100%



Statistical Data Analysis - Visualisation: Network & Pathway Analysis

Book1																			
Home Insert Draw Page Layout Formulas Data Review View Acrobat Tell me																			
Themes Aa Colours Margins Orientation Size Print Area Breaks Background Print Titles Page Setup Width: Automatic Height: Automatic Gridlines View View Print Print																			
G1 fx Gene names																			
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	Significant	#NAME?	Difference	Protein IDs	Majority prot	Protein nam	Gene names	id	Symbol color	Symbol type	Symbol size	Show label	Only identifi	Reverse	Potential cor	Student's T-t	Student's T-t	Peptides	Razor + uniq l
2	+	1.55435499	2.05743663	A0A2R8Y619	A0A2R8Y619			1	Color2 [A=25	1	4							3	1
3	+	1.85489919	1.97573217	A1L0T0	A1L0T0	Acetolactate	ILVBL	5	Color2 [A=25	1	4							5	5
4	+	2.78803617	1.9202164	A3KMH1;A3K	A3KMH1;A3K	von Willebra	VWA8	7	Color2 [A=25	1	4							2	2
5	+	5.1278101	4.29929225	A6NDU8	A6NDU8	UPF0600 pro	C5orf51	11	Color2 [A=25	1	4				+		LFQ intensity	4	4
6	+	2.44521016	2.36031882	C4AMC7;Q6V	C4AMC7;Q6V	Putative WA	WASH3P;WASH2P;V	14	Color2 [A=25	1	4				+		LFQ intensity	1	1
7	+	3.86710013	1.22093582	CON_Q3MH	CON_Q3MH	CON_Q3MHN5;CON_E	SEMBL:ENSBTAP00	20	Color2 [A=25	1	4				+			4	4
8	+	1.41184962	2.1241649	CON_P0073	CON_P0073			22	Color2 [A=25	1	4				+			3	3
9	+	10.0185073	3.96177419	CON_P0196	CON_P0196			24	Color2 [A=25	1	4				+	+	LFQ intensity	7	7
10	+	5.04489656	3.93767436	CON_P0686	CON_P0686			29	Color2 [A=25	1	4				+	+	LFQ intensity	17	15
11	+	4.92424699	3.37225405	CON_P1545	CON_P15497			32	Color2 [A=25	1	4				+	+	LFQ intensity	9	9
12	+	1.84467521	2.31118377	CON_P4136	CON_P41361			37	Color2 [A=25	1	4				+			1	1
13	+	5.15537224	1.61123244	CON_Q294	CON_Q29443;CON_Q01	K2		39	Color2 [A=25	1	4				+			9	9
14	+	3.49571552	2.00845734	Q13765;E9P	Q13765;E9P	Nascent poly	NACA	51	Color2 [A=25	1	4							4	4
15	+	4.58161475	0.95561965	O00116	O00116	Alkyldihydro	AGPS	54	Color2 [A=25	1	4							13	13
16	+	1.95904664	0.4355154	O00170	O00170	AH receptor	AIP	61	Color2 [A=25	1	4							6	6
17	+	3.71947306	1.97502708	O00232;O00	O00232;O00	26S protease	PSMD12	67	Color2 [A=25	1	4							7	7
18	+	1.51348841	2.22553317	O00233;O00	O00233;O00	26S protease	PSMD9	68	Color2 [A=25	1	4							4	4
19	+	2.9569985	3.39298932	O00267-2;O	O00267-2;O	Transcription	SUPT5H	71	Color2 [A=25	1	4				+		LFQ intensity	2	2
20	+	3.25523113	2.96861712	O00303	O00303	Eukaryotic tr	EIF3F	75	Color2 [A=25	1	4				+		LFQ intensity	2	2
21	+	5.66810714	0.97534752	O00410;O00	O00410;O00	Importin-5	IPOS	78	Color2 [A=25	1	4							34	34
22	+	3.12436179	1.93475405	O00560;O00	O00560;O00	Syntenin-1	SDCBP	94	Color2 [A=25	1	4							7	7
23	+	4.36021901	2.20206674	O00571-2;O	O00571-2;O	ATP-depende	DDX3X	97	Color2 [A=25	1	4				+		LFQ intensity	15	15
24	+	2.44005413	1.92432197	O00743-2;O	O00743-2;O	Serine/threo	PPP6C	100	Color2 [A=25	1	4							3	3
25	+	3.44940553	0.68289375	O14617;O14	O14617;O14	AP-3 comple	AP3D1	107	Color2 [A=25	1	4							13	13
26	+	3.57808911	1.34338919	O14727-5;O	O14727-5;O	Apoptotic pr	APAF1	113	Color2 [A=25	1	4							1	1
27	+	1.38523056	0.49817276	O14879	O14879	Interferon-in	IFIT3	125	Color2 [A=25	1	4							9	9
28	+	1.82799793	1.64875571	O14880	O14880	Microsomal	MGST3	126	Color2 [A=25	1	4							4	4
29	+	4.37027036	2.47093328	O14950;P19	O14950;P19	Myosin regu	MYL12B;MYL12A	132	Color2 [A=25	1	4				+		LFQ intensity	11	11
30	+	2.34330316	3.08777857	O14974-5;O	O14974-5;O	Protein phos	PPP1R12A	135	Color2 [A=25	1	4				+		LFQ intensity	8	8
31	+	2.47962476	1.24199581	O14981-2;O	O14981-2;O	TATA-bindin	BTAF1	138	Color2 [A=25	1	4							1	1
32	+	1.34839273	1.33280754	O15013-7;O	O15013-7;O	Rho guanine	ARHGEF10	139	Color2 [A=25	1	4							3	3
33	+	1.88596943	3.03884776	O15067	O15067	Phosphoribo	PFAS	143	Color2 [A=25	1	4				+		LFQ intensity	7	7
34	+	1.45805292	2.24850003	O15116	O15116	U6 snRNA-a	LSM1	146	Color2 [A=25	1	4							2	2
35	+	2.76787081	1.09159056	O15143	O15143	Actin-relate	ARPC1B	151	Color2 [A=25	1	4							13	13
36	+	2.86102121	0.97764524	O15144	O15144	Actin-relate	ARPC2	152	Color2 [A=25	1	4							13	13
37	+	4.97028583	0.8936828	O15145	O15145	Actin-relate	ARPC3	153	Color2 [A=25	1	4							6	6
38	+	1.36422025	2.12705612	O15160-2;O	O15160-2;O	DNA-directe	POLR1C	155	Color2 [A=25	1	4							3	3
39	+	3.89564801	1.87343992	O15182	O15182	Centrin-3	CETN3	158	Color2 [A=25	1	4							1	1

AutoSave

OFF

Home

Insert

Draw

Page Layout

Formulas

Data

Review

View

Acrobat

Tell me

Aa

Themes

Colours

Aa

Fonts

Margins

Orientation

Size

Print Area

Page Setup

Width: Automatic

Height: Automatic

Gridlines

View

Print

Headings

View

Print

G1

fx

Gene names

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	Significant	#NAME?	Difference	Protein IDs	Majority	Gene names	Symbol color	Symbol type	Symbol size	Show label	Only identifier	Reverse	Potential correlation	Student's T-test	Student's T-test	Peptides	Razor + unique		
2	+	1.55435499	2.05743663	A0A2R8Y6G9	A0A2R8Y6G9		1	Color2	[A=25	1	4							3	1
3	+	1.85489919	1.97573217	A1L0T0	A1L0T0		5	Color2	[A=25	1	4							5	5
4	+	2.78803617	1.9202164	A3KMH1;A3K	A3KMH1;A3K		7	Color2	[A=25	1	4							2	2
5	+	5.1278101	4.29929225	A6NDU8	A6NDU8		11	Color2	[A=25	1	4			+		LFQ intensity	4	4	
6	+	2.44521016	2.36031882	C4AMC7;Q6V	C4AMC7;Q6V		14	Color2	[A=25	1	4			+		LFQ intensity	1	1	
7	+	3.86710013	1.22093582	CON_Q3MH	CON_Q3MHNS;CO		20	Color2	[A=25	1	4		+				4	4	
8	+	1.41184962	2.1241649	CON_P0073	CON_P00735		22	Color2	[A=25	1	4		+				3	3	
9	+	10.0185073	3.96177419	CON_P0196	CON_P01966		24	Color2	[A=25	1	4		+		+	LFQ intensity	7	7	
10	+	5.04489656	3.93767436	CON_P0686	CON_P06868		29	Color2	[A=25	1	4		+		+	LFQ intensity	17	15	
11	+	4.92424699	3.37225405	CON_P1549	CON_P15497		32	Color2	[A=25	1	4		+		+	LFQ intensity	9	9	
12	+	1.84467521	2.31118377	CON_P4136	CON_P41361		37	Color2	[A=25	1	4		+				1	1	
13	+	5.15537224	1.61123244	CON_Q2944	CON_Q29443;CON_Q01K2		39	Color2	[A=25	1	4		+				9	9	
14	+	3.49571552	2.00845734	Q13765;E9P	Q13765;E9P	Nascent polypeptide	51	Color2	[A=25	1	4						4	4	
15	+	4.58161475	0.95561965	O00116	O00116	Alkyl dihydroxy	54	Color2	[A=25	1	4						13	13	
16	+	1.95904664	0.4355154	O00170	O00170	AH receptor	61	Color2	[A=25	1	4						6	6	
17	+	3.71947306	1.97502708	O00232;O00	O00232;O00	26S proteasome	67	Color2	[A=25	1	4						7	7	
18	+	1.51348841	2.22553317	O00233;O00	O00233;O00	26S proteasome	68	Color2	[A=25	1	4						4	4	
19	+	2.9569985	3.39298932	O00267-2;O	O00267-2;O	Transcription	71	Color2	[A=25	1	4			+		LFQ intensity	2	2	
20	+	3.25523113	2.96861712	O00303	O00303	Eukaryotic tr	75	Color2	[A=25	1	4			+		LFQ intensity	2	2	
21	+	5.66810714	0.97534752	O00410;O00	O00410;O00	Importin-5	78	Color2	[A=25	1	4						34	34	
22	+	3.12436179	1.93475405	O00560;O00	O00560;O00	Syntenin-1	94	Color2	[A=25	1	4						7	7	
23	+	4.36021901	2.20206674	O00571-2;O	O00571-2;O	ATP-dependent	97	Color2	[A=25	1	4			+		LFQ intensity	15	15	
24	+	2.44005413	1.92432197	O00743-2;O	O00743-2;O	Serine/thre	100	Color2	[A=25	1	4						3	3	
25	+	3.44940553	0.68289375	O14617;O14	O14617;O14	AP-3 complex	107	Color2	[A=25	1	4						13	13	
26	+	3.57808911	1.34338919	O															

Statistical Data Analysis - Visualisation: Network & Pathway Analysis

Version: 11.5

LOGIN | REGISTER | SURVEY

 **STRING**

Search | Download | Help | My Data

Protein by name >

Protein by sequence >

Multiple proteins >

Multiple sequences >

Proteins with Values/Ranks >

Protein families ("COGs") >

Organisms >

Examples >

Random entry >

SEARCH

Multiple Proteins by Names / Identifiers

List Of Names: (one-per-line or CSV; examples: #1 #2 #3)

... or, upload a file:

Browse ...

Organisms:

auto-detect

✕ ▼

[Advanced Settings](#)

SEARCH

Statistical Data Analysis - Visualisation: Network & Pathway Analysis

Version: 11.5

LOGIN | REGISTER | SURVEY

 **STRING**

Search | Download | Help | My Data

Protein by name >

Protein by sequence >

Multiple proteins >

Multiple sequences >

Proteins with Values/Ranks >

Protein families ("COGs") >

Organisms >

Examples >

Random entry >

SEARCH

Multiple Proteins by Names / Identifiers

List Of Names: (one-per-line or CSV; examples: #1 #2 #3)

... or, upload a file:

Browse ...

Organisms:

auto-detect

✕ ▼

[Advanced Settings](#)

SEARCH

Statistical Data Analysis - Visualisation: Network & Pathway Analysis

Version: 11.5

LOGIN | REGISTER | SURVEY

 **STRING**

Search | Download | Help | My Data

Protein by name >

Protein by sequence >

Multiple proteins >

Multiple sequences >

Proteins with Values/Ranks >

Protein families ("COGs") >

Organisms >

Examples >

Random entry >

SEARCH

Multiple Proteins by Names / Identifiers

List Of Names: (one-per-line or CSV; examples: #1 #2 #3)

... or, upload a file:

Browse ...

Organisms:

auto-detect

✕ ▼

[Advanced Settings](#)

SEARCH

Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Search**

Version: 11.5

LOGIN | REGISTER | SURVEY

 **STRING**

Search | Download | Help | My Data

Protein by name >

Protein by sequence >

Multiple proteins >

Multiple sequences >

Proteins with Values/Ranks >

Protein families ("COGs") >

Organisms >

Examples >

Random entry >

SEARCH

Multiple Proteins by Names / Identifiers

List Of Names: (one-per-line or CSV; examples: #1 #2 #3)

HDAC6
CLIP2
TJP2
DNAJB4
VTI1B
STK39
LIMD1

... or, upload a file:

Browse ...

Organisms:

auto-detect

✕ ▼

[Advanced Settings](#)

SEARCH

Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Search**

Version: 11.5

LOGIN | REGISTER | SURVEY

 **STRING**

Search | Download | Help | My Data

Protein by name >

Protein by sequence >

Multiple proteins >

Multiple sequences >

Proteins with Values/Ranks >

Protein families ("COGs") >

Organisms >

Examples >

Random entry >

SEARCH

Multiple Proteins by Names / Identifiers

List Of Names: (one-per-line or CSV; examples: #1 #2 #3)

HDAC6
CLIP2
TJP2
DNAJB4
VTI1B
STK39
LIMD1

... or, upload a file:

Browse ...

Organisms:

auto-detect

✕ ▼

[Advanced Settings](#)

SEARCH

Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Continue**

Version: 11.5

LOGIN | REGISTER | SURVEY



Search Download Help My Data

The following proteins in *Homo sapiens* appear to match your input. Please review the list, then click 'Continue' to proceed.

<- BACK

↓ MAPPING

CONTINUE ->

950 query items

showing page 1 of 48 • first • previous • next • last

1) 'Gene names':

-- Sorry, STRING found no proteins by this name in *Homo sapiens* --

2) 'ILVBL':

☒ **ILVBL** - Acetolactate synthase-like protein; ilvB acetolactate synthase like

3) 'VWA8':

☒ **VWA8** - Von Willebrand factor A domain-containing protein 8; Exhibits ATPase activity in vitro

4) 'C5orf51':

☒ **C5orf51** - UPF0600 protein **C5orf51**; Chromosome 5 open reading frame 51; Belongs to the UPF0600 family

5) 'WASH3P;WASH2P;WASH1':

-- Sorry, STRING found no proteins by this name in *Homo sapiens* --

6) 'NACA':

☒ **NACA** - Nascent polypeptide-associated complex subunit alpha, muscle-specific form; Cardiac- and muscle-specific transcription factor. May act to regulate the expression of genes involved in the development of myotubes. Plays a critical role in ventricular cardiomyocyte expansion and regulates postnatal skeletal muscle growth and regeneration. Involved in the organized assembly of thick and thin filaments of myofibril sarcomeres (By similarity)

☐ **BTF3** - Transcription factor BTF3; When associated with **NACA**, prevents inappropriate targeting of non-secretory polypeptides to the endoplasmic reticulum (ER). Binds to nascent polypeptide chains as they emerge from the ribosome and blocks their interaction with the signal recognition particle (SRP), which normally targets nascent secretory peptides to the ER. BTF3 is also a general transcription factor that can form a stable complex with RNA polymerase II. Required for the initiation of transcription [*a.k.a. LOC102724313, NACB, OK/SW-cl.8*]

7) 'AGPS':

☒ **AGPS** - Alkylldihydroxyacetonephosphate synthase, peroxisomal; Catalyzes the exchange of an acyl for a long-chain alkyl group and the formation of the ether bond in the biosynthesis of ether phospholipids; Belongs to the FAD-binding oxidoreductase/transferase type 4 family

8) 'AIP':

☒ **AIP** - AH receptor-interacting protein; May play a positive role in AHR-mediated (aromatic hydrocarbon receptor) signaling, possibly by influencing its receptivity for ligand and/or its nuclear targeting; FKBP prolyl isomerases

Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Continue**

Version: 11.5

LOGIN | REGISTER | SURVEY

 Search Download Help My Data

The following proteins in *Homo sapiens* appear to match your input. Please review the list, then click 'Continue' to proceed.

[<- BACK](#) [↑ MAPPING](#) [CONTINUE ->](#)

950 query items

showing page 1 of 48 • first • previous • next • last

1) 'Gene names':

-- Sorry, STRING found no proteins by this name in Homo sapiens --

2) 'ILVBL':

☒ [ILVBL](#) - Acetolactate synthase-like protein; ilvB acetolactate synthase like

3) 'VWA8':

☒ [VWA8](#) - Von Willebrand factor A domain-containing protein 8; Exhibits ATPase activity in vitro

4) 'C5orf51':

☒ [C5orf51](#) - UPF0600 protein [C5orf51](#); Chromosome 5 open reading frame 51; Belongs to the UPF0600 family

5) 'WASH3P;WASH2P;WASH1':

-- Sorry, STRING found no proteins by this name in Homo sapiens --

6) 'NACA':

☒ [NACA](#) - Nascent polypeptide-associated complex subunit alpha, muscle-specific form; Cardiac- and muscle-specific transcription factor. May act to regulate the expression of genes involved in the development of myotubes. Plays a critical role in ventricular cardiomyocyte expansion and regulates postnatal skeletal muscle growth and regeneration. Involved in the organized assembly of thick and thin filaments of myofibril sarcomeres (By similarity)

☐ BTF3 - Transcription factor BTF3; When associated with [NACA](#), prevents inappropriate targeting of non-secretory polypeptides to the endoplasmic reticulum (ER). Binds to nascent polypeptide chains as they emerge from the ribosome and blocks their interaction with the signal recognition particle (SRP), which normally targets nascent secretory peptides to the ER. BTF3 is also a general transcription factor that can form a stable complex with RNA polymerase II. Required for the initiation of transcription [a.k.a. LOC102724313, NACB, OK/SW-cl.8]

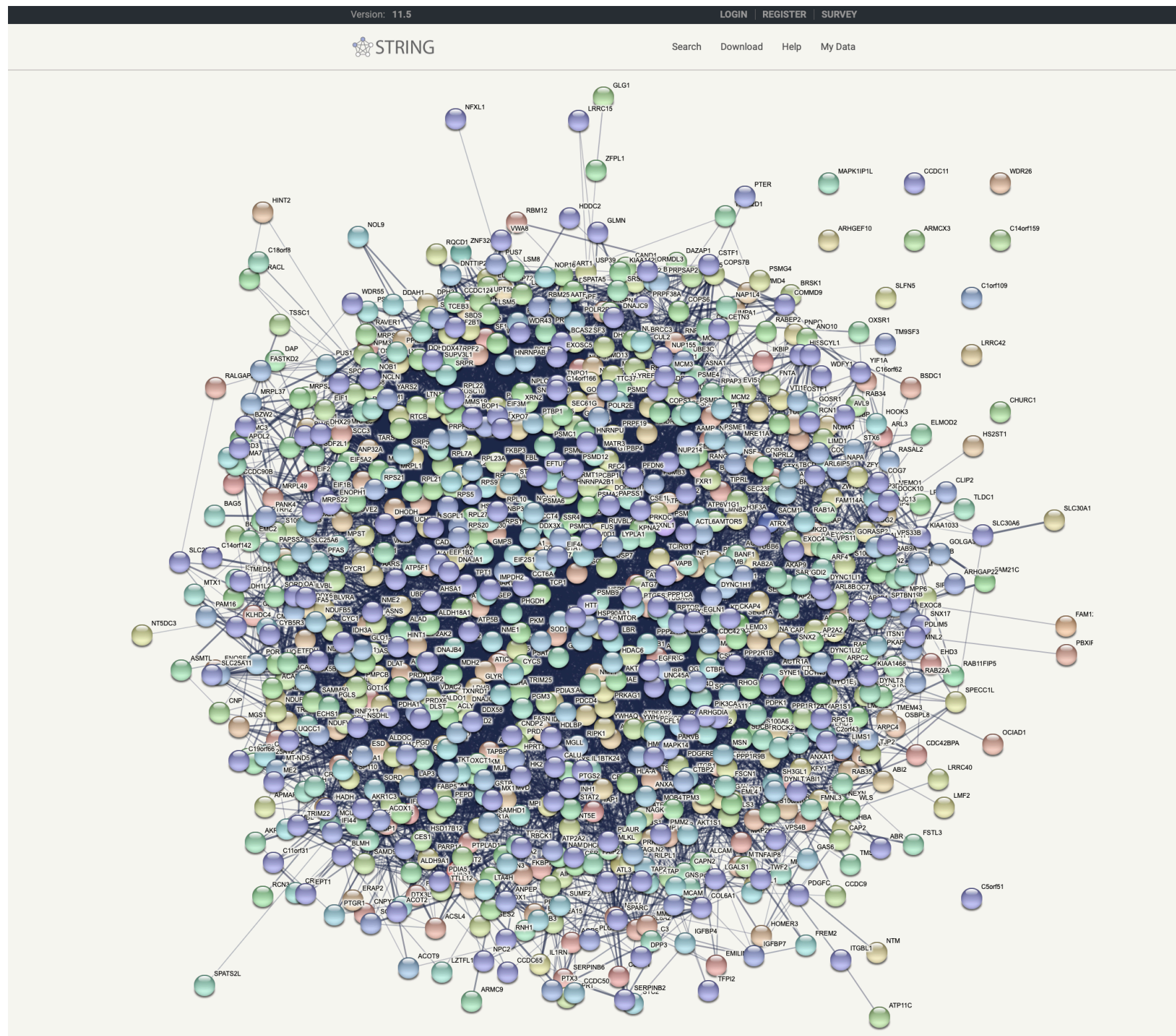
7) 'AGPS':

☒ [AGPS](#) - Alkyldihydroxyacetonephosphate synthase, peroxisomal; Catalyzes the exchange of an acyl for a long-chain alkyl group and the formation of the ether bond in the biosynthesis of ether phospholipids; Belongs to the FAD-binding oxidoreductase/transferase type 4 family

8) 'AIP':

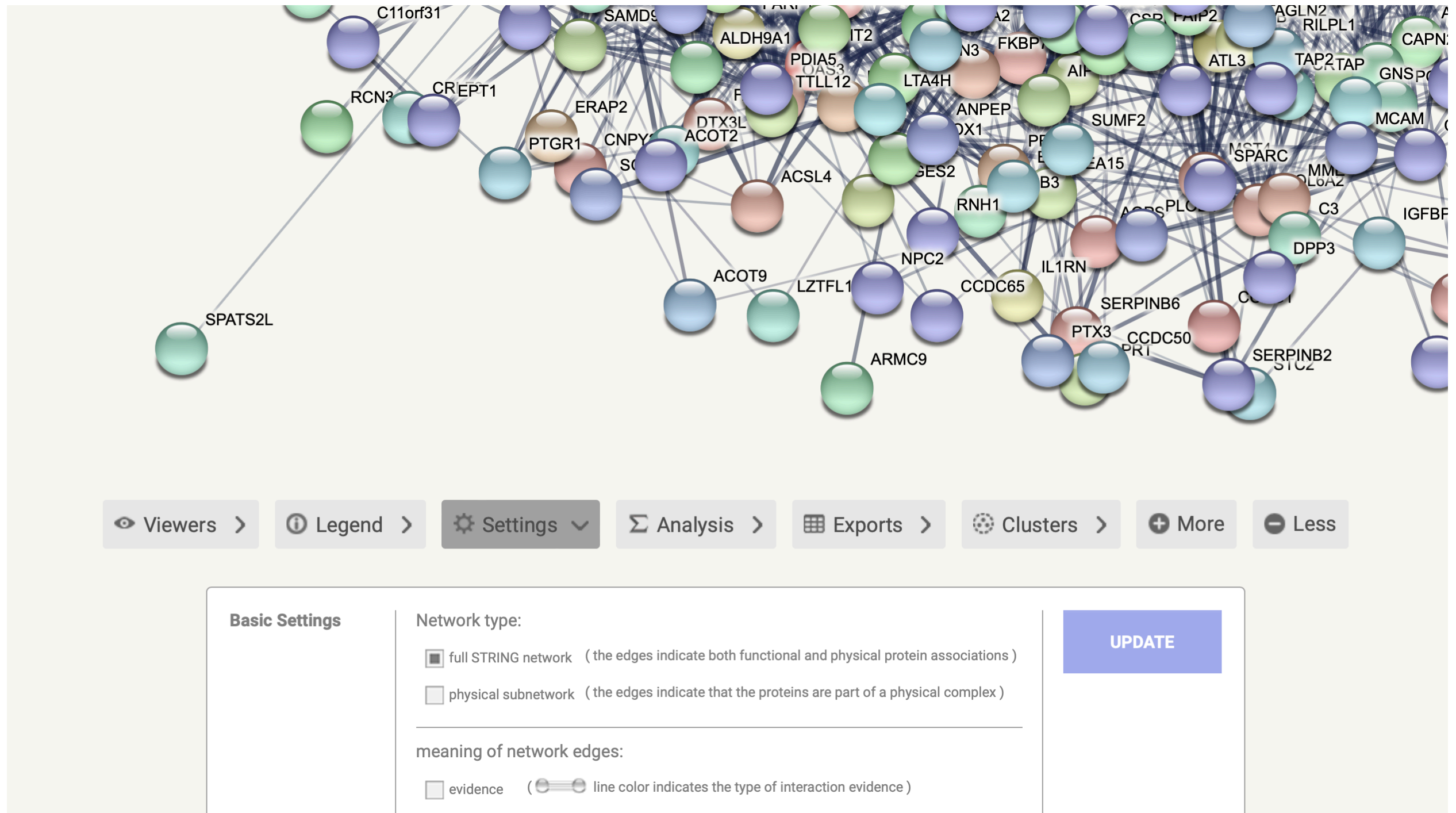
☒ [AIP](#) - AH receptor-interacting protein; May play a positive role in AHR-mediated (aromatic hydrocarbon receptor) signaling, possibly by influencing its receptivity for ligand and/or its nuclear targeting; FKBP prolyl isomerases

Statistical Data Analysis - Visualisation: Network & Pathway Analysis



String : <https://string-db.org/>

Statistical Data Analysis - Visualisation: Network & Pathway Analysis



Network visualization showing protein-protein interactions. The network is composed of numerous nodes (proteins) and edges (interactions). The nodes are colored based on their function or interaction type. The edges are colored based on the type of interaction evidence.

Toolbar buttons: Viewers, Legend, Settings, Analysis, Exports, Clusters, More, Less.

Basic Settings:

- Network type:
 - ☒ full STRING network (the edges indicate both functional and physical protein associations)
 - ☐ physical subnetwork (the edges indicate that the proteins are part of a physical complex)
- meaning of network edges:
 - ☐ evidence (line color indicates the type of interaction evidence)

UPDATE

Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Settings**

>

Legend >

Settings ▾

Analysis >

Exports >

Clusters >

+ More

-

Basic Settings

Network type:

☒ full STRING network (the edges indicate both functional and physical protein associations)

☐ physical subnetwork (the edges indicate that the proteins are part of a physical complex)

meaning of network edges:

☐ evidence ( line color indicates the type of interaction evidence)

☒ confidence ( line thickness indicates the strength of data support)

active interaction sources:

☒ Textmining ☒ Experiments ☒ Databases ☒ Co-expression

☒ Neighborhood ☒ Gene Fusion ☒ Co-occurrence

minimum required interaction score:

highest confidence (0.900) ▴ ▾

max number of interactors to show:

1st shell: - none / query proteins only - ▴ ▾

2nd shell: - none - ▴ ▾

Advanced Settings

network display mode:

☐ static png ( network is a simple bitmap image; not interactive)

☒ interactive svg ( network is a scalable vector graphic [SVG]; interactive)

network display options:

☒ disable structure previews inside network bubbles

☒ hide disconnected nodes in the network

☐ show input protein names

☐ hide protein names

UPDATE

String : <https://string-db.org/>



Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Settings**

>

Legend >

Settings ▾

Analysis >

Exports >

Clusters >

+ More

-

Basic Settings

Network type:

☒ full STRING network (the edges indicate both functional and physical protein associations)

☐ physical subnetwork (the edges indicate that the proteins are part of a physical complex)

meaning of network edges:

☐ evidence ( line color indicates the type of interaction evidence)

☒ confidence ( line thickness indicates the strength of data support)

active interaction sources:

☒ Textmining ☒ Experiments ☒ Databases ☒ Co-expression

☒ Neighborhood ☒ Gene Fusion ☒ Co-occurrence

minimum required interaction score:

highest confidence (0.900) ▴ ▾

max number of interactors to show:

1st shell: - none / query proteins only - ▴ ▾

2nd shell: - none - ▴ ▾

Advanced Settings

network display mode:

☐ static png ( network is a simple bitmap image; not interactive)

☒ interactive svg ( network is a scalable vector graphic [SVG]; interactive)

network display options:

☒ disable structure previews inside network bubbles

☒ hide disconnected nodes in the network

☐ show input protein names

☐ hide protein names

UPDATE

String : <https://string-db.org/>



Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Settings**

>

Legend >

Settings ▾

Analysis >

Exports >

Clusters >

+ More

-

Basic Settings

Network type:

☒ full STRING network (the edges indicate both functional and physical protein associations)

☐ physical subnetwork (the edges indicate that the proteins are part of a physical complex)

meaning of network edges:

☐ evidence ( line color indicates the type of interaction evidence)

☒ confidence ( line thickness indicates the strength of data support)

active interaction sources:

☒ Textmining ☒ Experiments ☒ Databases ☒ Co-expression

☒ Neighborhood ☒ Gene Fusion ☒ Co-occurrence

minimum required interaction score:

highest confidence (0.900) ▴ ▾

max number of interactors to show:

1st shell: - none / query proteins only - ▴ ▾

2nd shell: - none - ▴ ▾

Advanced Settings

network display mode:

☐ static png ( network is a simple bitmap image; not interactive)

☒ interactive svg ( network is a scalable vector graphic [SVG]; interactive)

network display options:

☒ disable structure previews inside network bubbles

☒ hide disconnected nodes in the network

☐ show input protein names

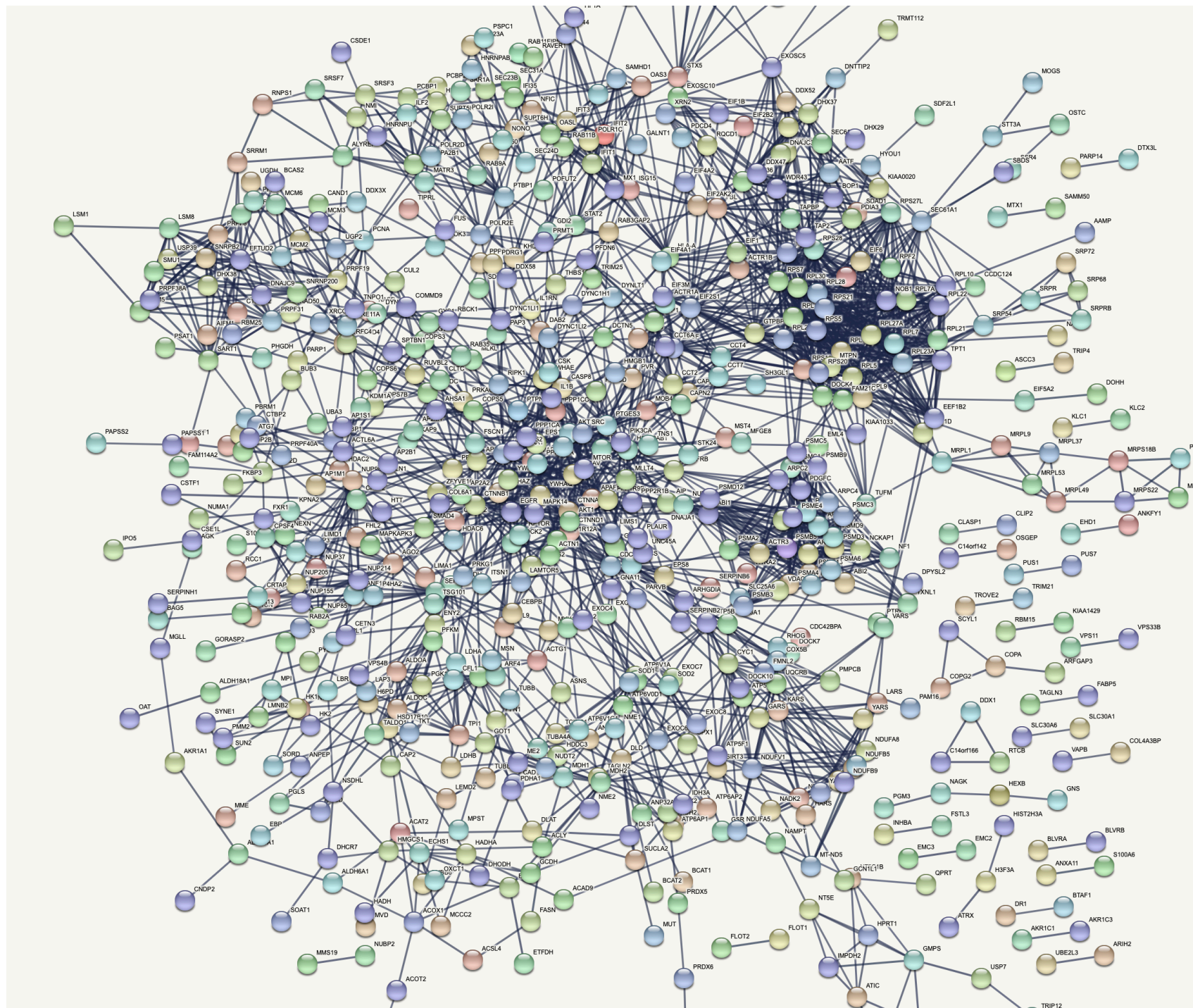
☐ hide protein names

UPDATE

String : <https://string-db.org/>



Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Settings**



Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Analysis**

Viewers > Legend > Settings > **Analysis** > Exports > Clusters > More > Less

Network Stats

number of nodes: 915	expected number of edges: 1740
number of edges: 2321	PPI enrichment p-value: < 1.0e-16
average node degree: 5.07	<i>your network has significantly more interactions</i>
avg. local clustering coefficient: 0.46	<i>than expected (what does that mean?)</i>

Functional enrichments in your network

[explain columns](#)

> Biological Process (Gene Ontology)				
GO-term	description	count in network	strength	false discovery rate
GO:1905323	Telomerase holoenzyme complex assembly	3 of 4	1.21	0.0416
GO:0046967	Cytosol to endoplasmic reticulum transport	3 of 4	1.21	0.0416
GO:0035711	T-helper 1 cell activation	3 of 4	1.21	0.0416
GO:0019322	Pentose biosynthetic process	3 of 4	1.21	0.0416
GO:0009051	Pentose-phosphate shunt, oxidative branch	3 of 4	1.21	0.0416

(more ...)

> Molecular Function (Gene Ontology)				
GO-term	description	count in network	strength	false discovery rate
GO:0015433	ATPase-coupled peptide antigen transmembrane transport...	3 of 3	1.33	0.0481
GO:0046977	TAP binding	4 of 7	1.09	0.0353
GO:0016615	Malate dehydrogenase activity	4 of 8	1.03	0.0453
GO:0016668	Oxidoreductase activity, acting on a sulfur group of donors, ...	5 of 12	0.95	0.0256
GO:0043024	Ribosomal small subunit binding	6 of 15	0.93	0.0103

(more ...)

> Cellular Component (Gene Ontology)				
GO-term	description	count in network	strength	false discovery rate
GO:0042824	MHC class I peptide loading complex	5 of 7	1.18	0.0016
GO:0030122	AP-2 adaptor complex	5 of 8	1.13	0.0025
GO:0005832	Chaperonin-containing t-complex	6 of 10	1.11	0.00072
GO:0005638	Lamin filament	3 of 5	1.11	0.0364
GO:0016600	Flotillin complex	4 of 8	1.03	0.0156

(more ...)

Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Analysis**

> KEGG Pathways				
<i>pathway</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
hsa00920	Sulfur metabolism	4 of 10	0.93	0.0145
hsa03060	Protein export	8 of 23	0.87	0.00051
hsa03050	Proteasome	14 of 43	0.84	4.46e-06
hsa00051	Fructose and mannose metabolism	10 of 32	0.82	0.00019
hsa00020	Citrate cycle (TCA cycle)	9 of 29	0.82	0.00040

(more ...)

> Reactome Pathways				
<i>pathway</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
HSA-2408550	Metabolism of ingested H ₂ SeO ₄ and H ₂ SeO ₃ into H ₂ Se	4 of 4	1.33	0.0020
HSA-9686347	Microbial modulation of RIPK1-mediated regulated necrosis	3 of 4	1.21	0.0177
HSA-390450	Folding of actin by CCT/TriC	6 of 10	1.11	0.00042
HSA-77350	Beta oxidation of hexanoyl-CoA to butanoyl-CoA	3 of 5	1.11	0.0258
HSA-77348	Beta oxidation of octanoyl-CoA to hexanoyl-CoA	3 of 5	1.11	0.0258

(more ...)

> WikiPathways				
<i>pathway</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
WP4629	Aerobic glycolysis	8 of 12	1.15	6.26e-05
WP4804	Cholesterol biosynthesis with skeletal dysplasias	4 of 7	1.09	0.0176
WP134	Pentose phosphate metabolism	4 of 7	1.09	0.0176
WP5049	Glycolysis in senescence	6 of 11	1.07	0.0021
WP2453	TCA cycle and deficiency of pyruvate dehydrogenase compl...	7 of 16	0.97	0.0017

(more ...)

> Disease-gene associations (DISEASES)				
<i>disease</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
DOID:5212	Congenital disorder of glycosylation	12 of 58	0.65	0.0208
DOID:2978	Carbohydrate metabolic disorder	20 of 135	0.5	0.0096
DOID:700	Mitochondrial metabolism disease	23 of 173	0.45	0.0102
DOID:655	Inherited metabolic disorder	76 of 726	0.35	1.02e-06
DOID:0014667	Disease of metabolism	91 of 997	0.29	7.48e-06

(more ...)

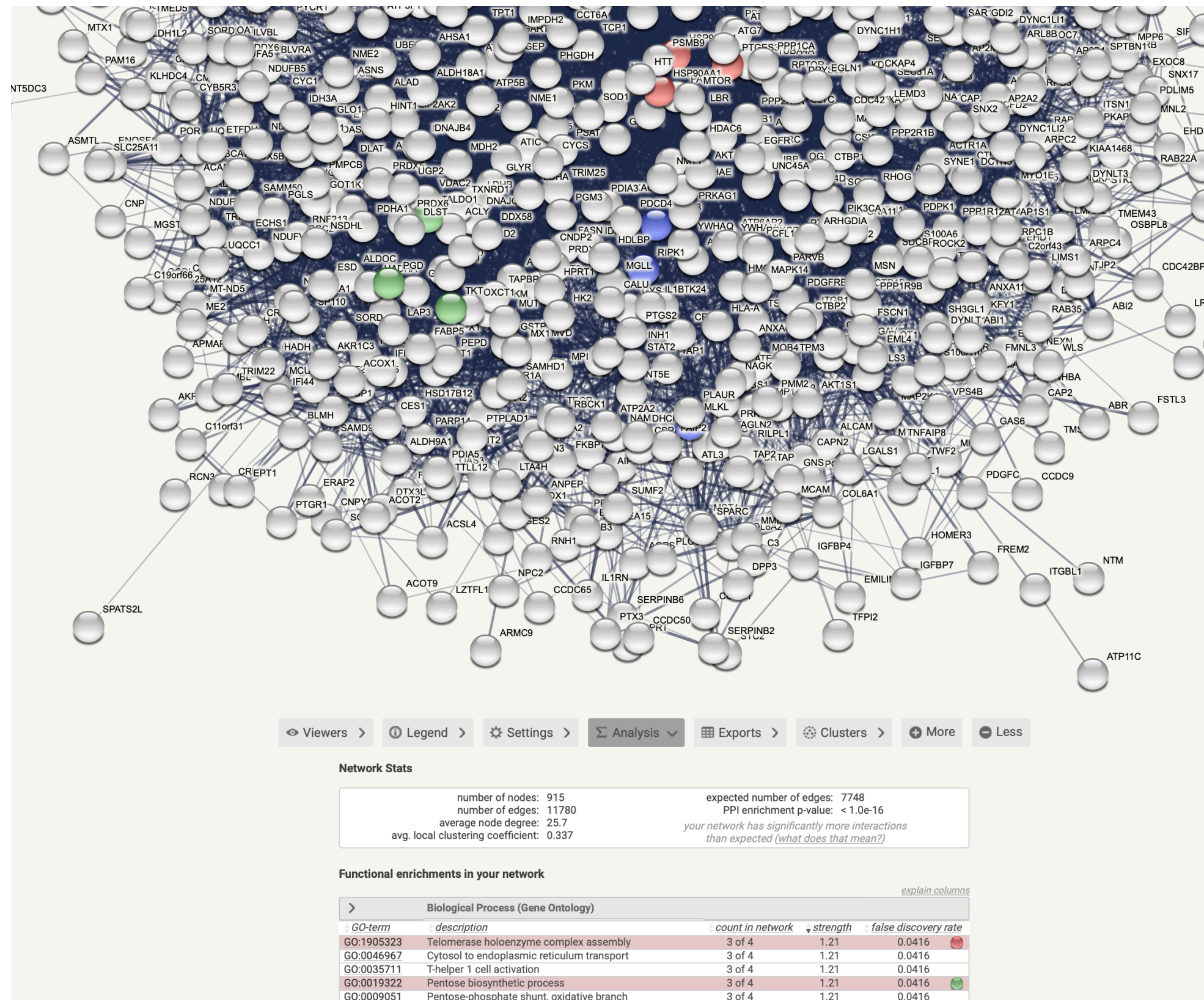
> Tissue expression (TISSUES)				
<i>tissue</i>	<i>description</i>	<i>count in network</i>	<i>strength</i>	<i>false discovery rate</i>
BTO:0003914	Interstitial cell of cajal	5 of 15	0.85	0.0239
BTO:0000772	Lymphoblast	73 of 235	0.82	5.42e-31
BTO:0001702	Left atrium	19 of 61	0.82	4.52e-08
BTO:0004238	Interstitial cell	18 of 64	0.78	4.24e-07
BTO:0000862	Heart ventricle	23 of 84	0.77	7.89e-09

(more ...)

String : <https://string-db.org/>

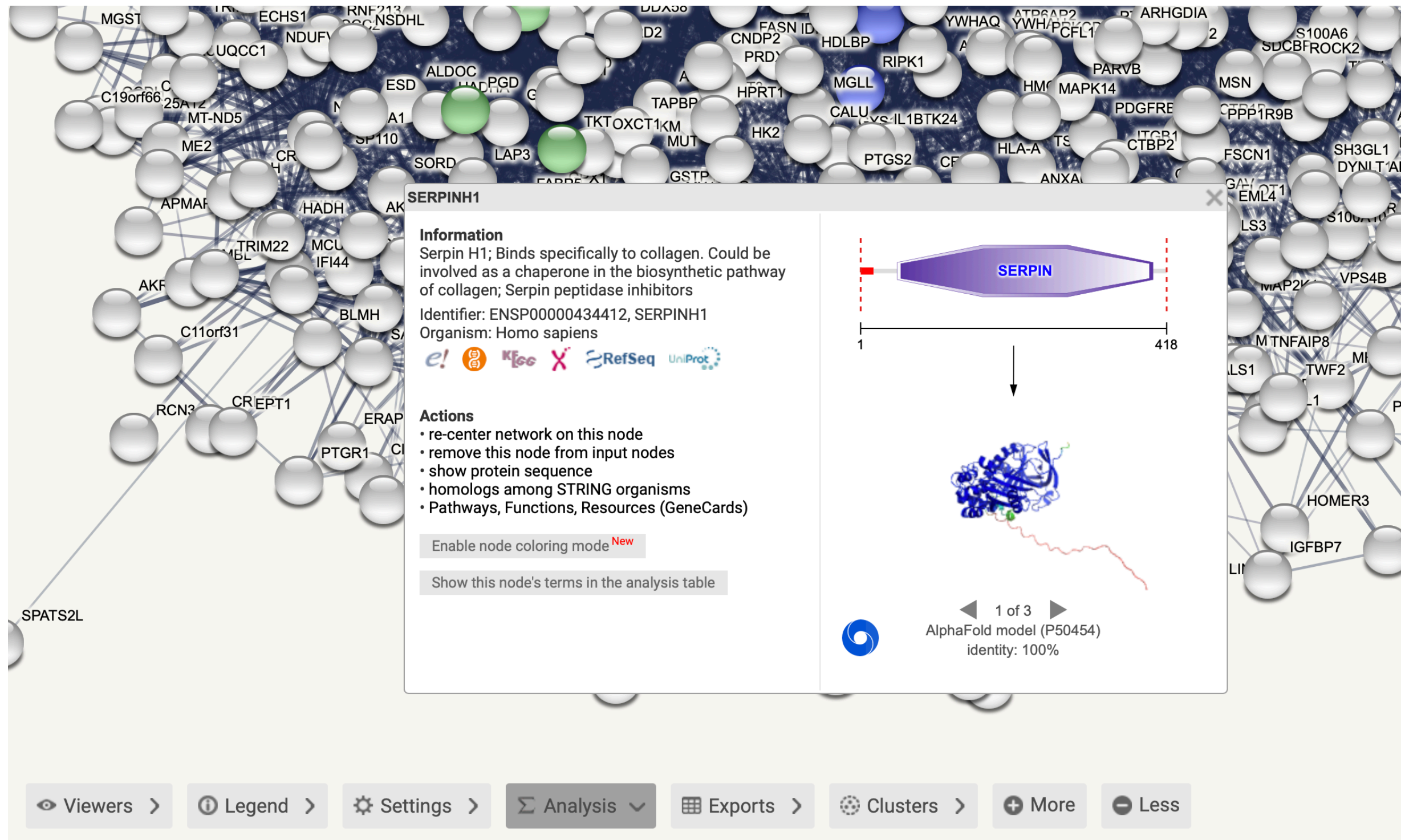


Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Analysis**



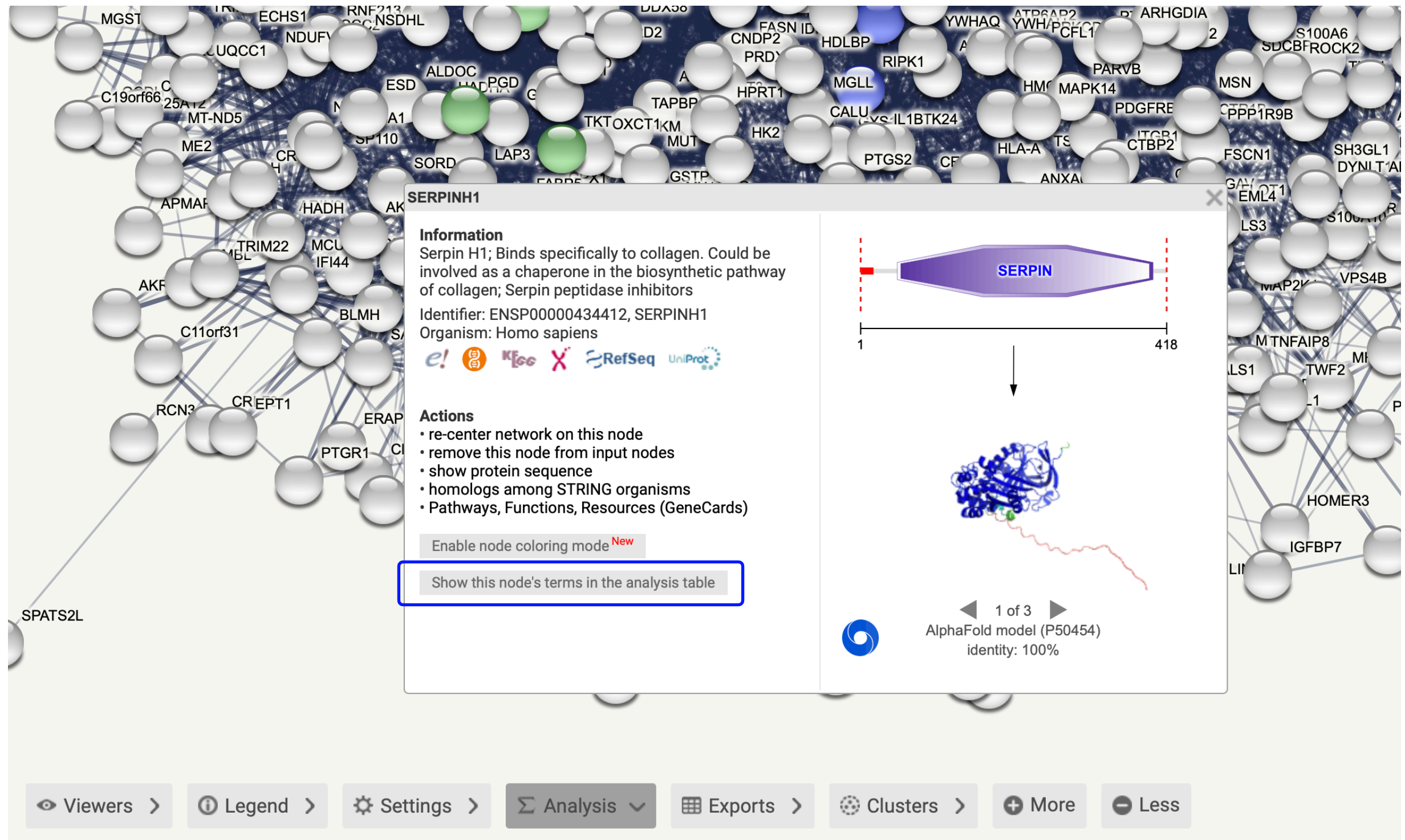
String : <https://string-db.org/>

Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Analysis**



String : <https://string-db.org/>

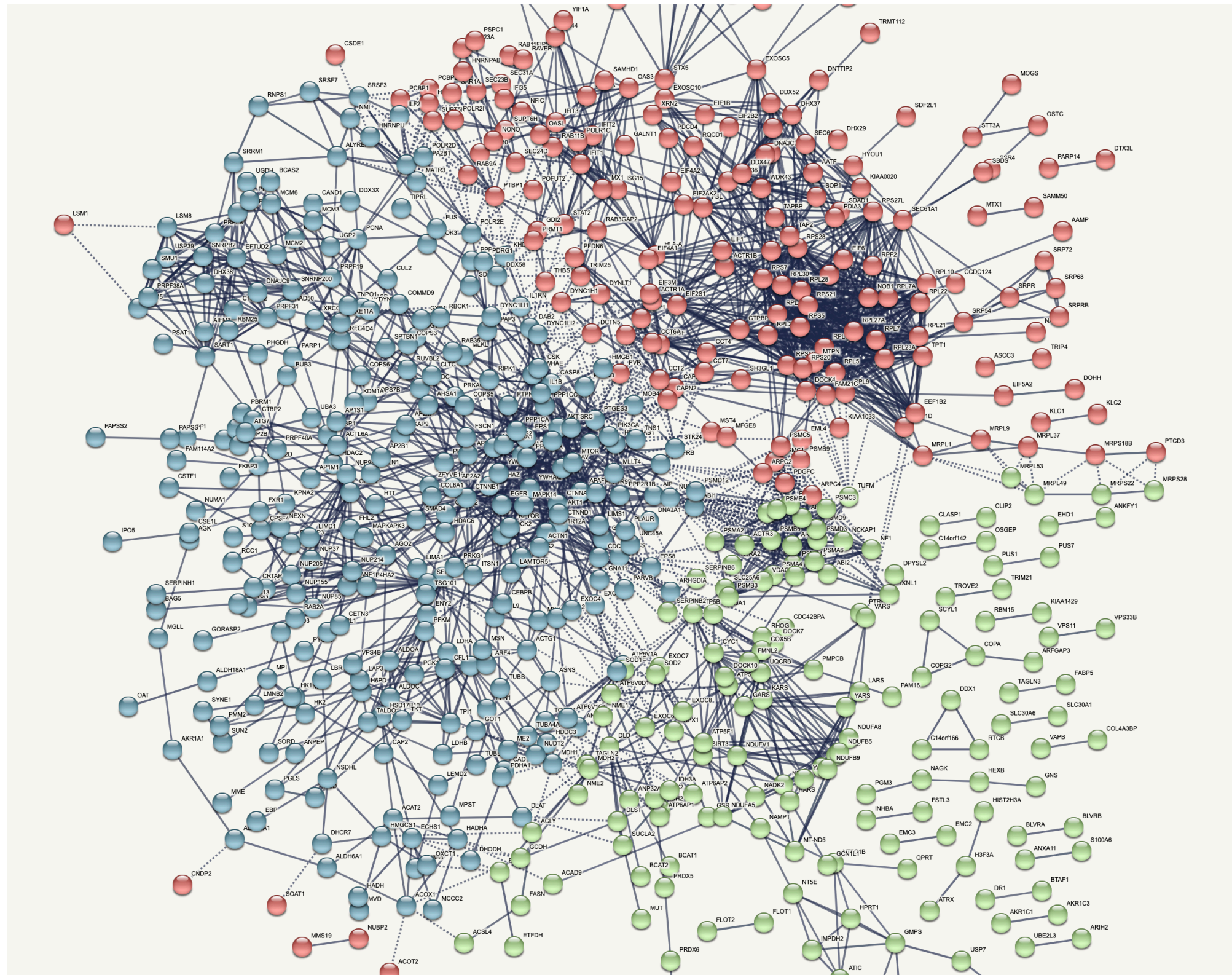
Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Analysis**



String : <https://string-db.org/>



Statistical Data Analysis - Visualisation: Network & Pathway Analysis - **Cluster**



End

