Mitochondrial proteomics investigation of a cellular model of impaired dopamine homeostasis, an early step in Parkinson's disease pathogenesis

Supplementary Information

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Captions to Supplemental Figures.

Figure S1: nLC-MS^E data quality evaluation. Analytical reproducibility assessment in SH-SY5Y Control, DA or MPP. Bar charts show: (A,B,C) intensity coefficient of variation (% CV intensity) and (D,E,F) retention time coefficient of variation (%CV RT) reported for EMRTs of peptide samples.

Figure S2: Box-and-whiskers plots for protein amounts calculated from Shotgun experiments that were selected as significant by the paired t-test. The first p value refers to DA vs. Control, whereas the second one refers to MPP vs. Control.

Figure S3: Q-Q plots for all gel pairs included in the analysis.

Figure S4: Box-and-whiskers plots for spots that were selected as significant by the Kruskal-Wallis test. Group A: Control; group B: dopamine; group C: MPP$^+$.

Figure S5: Decrease of VDAC2 in the mitochondrial fraction after dopamine treatment.

FIGURE S1

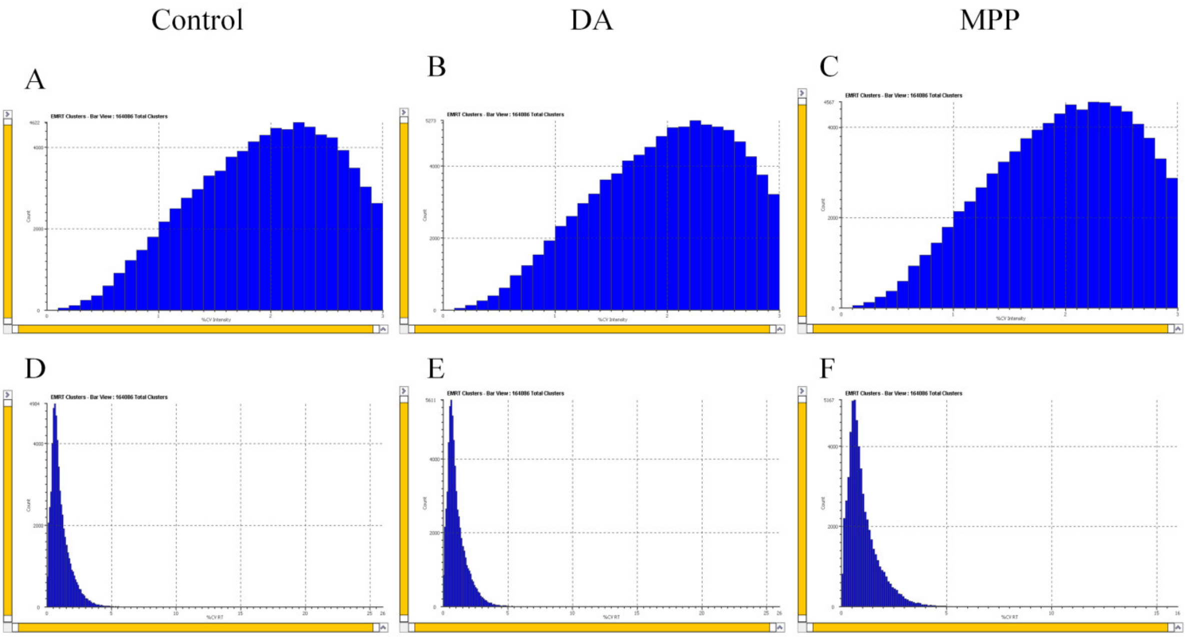
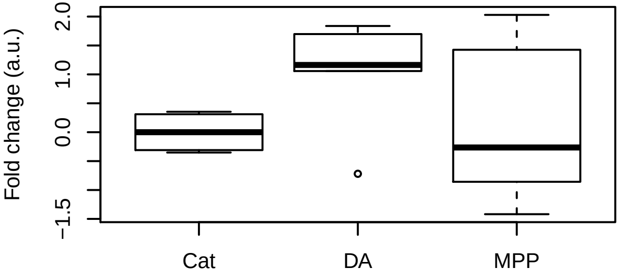
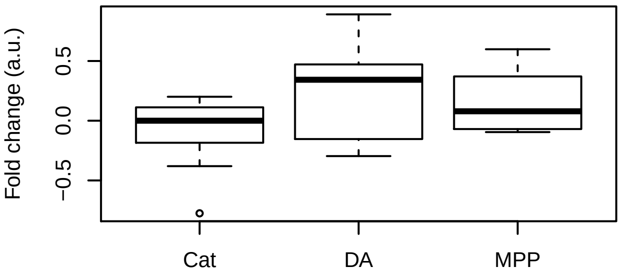

Control
DA
MPP
A
EMRT Clusters - Bar View : 164086 Total Clusters
4622
4000
2000
0
Count
0
1
2
3
%CV Intensity
B
EMRT Clusters - Bar View : 164086 Total Clusters
5273
4000
2000
0
Count
0
1
2
3
%CV Intensity
C
EMRT Clusters - Bar View : 164086 Total Clusters
4567
4000
2000
0
Count
0
1
2
3
%CV Intensity
D
EMRT Clusters - Bar View : 164086 Total Clusters
4984
4000
2000
0
Count
0
5
10
15
20
25
26
%CV RT
E
EMRT Clusters - Bar View : 164086 Total Clusters
5611
4000
2000
0
Count
0
5
10
15
20
25
26
%CV RT
F
EMRT Clusters - Bar View : 164086 Total Clusters
5167
4000
2000
0
Count
0
5
10
15
16
%CV RT

FIGURE S2



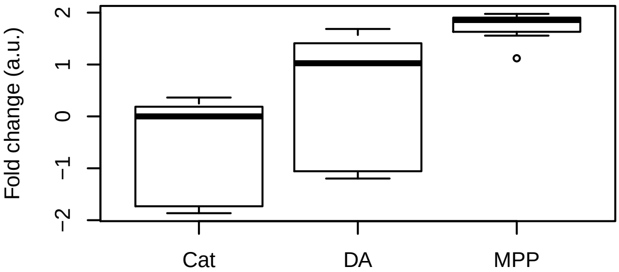
P16104 p= NA , 0.92

Histone H2A x OS Homo sapiens GN H2AFX P



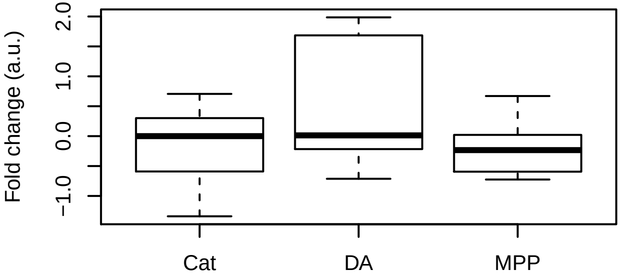
P61604 p= 0.064 , 0.118

10 kDa heat shock protein mitochondrial



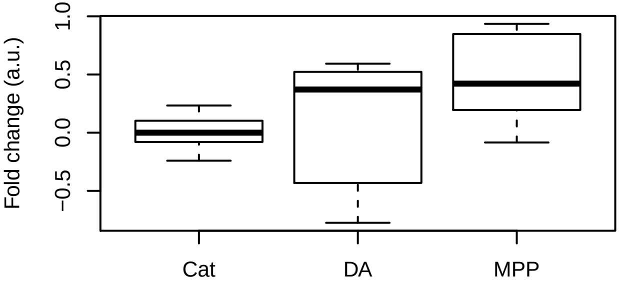
P62805 p= 0.135 , 0

Histone H4 OS Homo sapiens GN HIST1H4A P



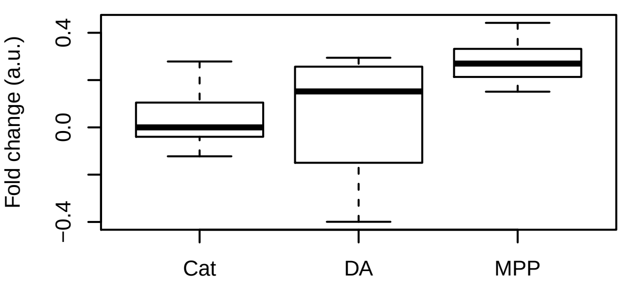
P60709 p= 0.08 , 0.703

Actin cytoplasmic 1 OS Homo sapiens GN A



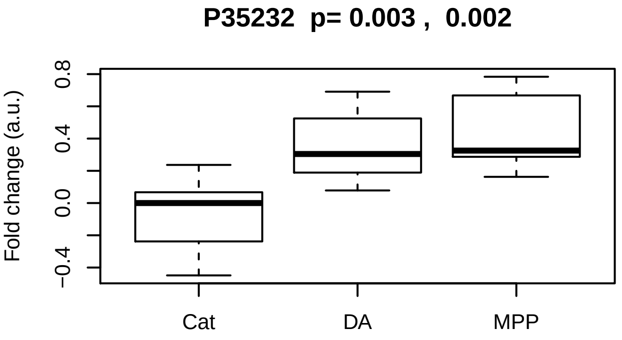
P40926 p= 0.499 , 0.002

Malate dehydrogenase mitochondrial OS Ho

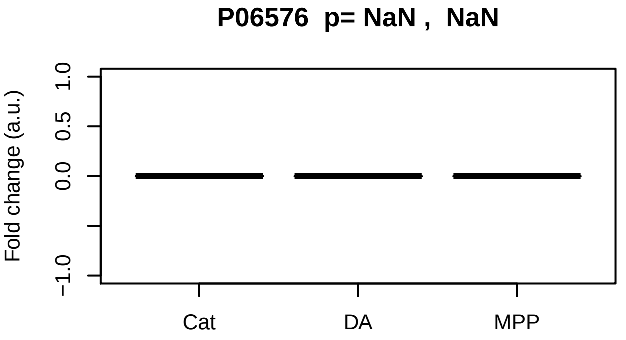


P10809 p= 0.889 , 0.001

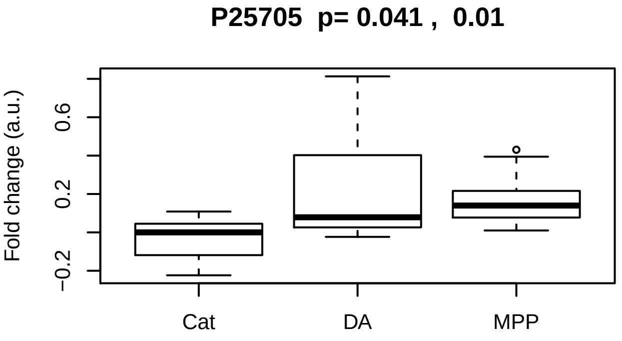
60 kDa heat shock protein mitochondrial



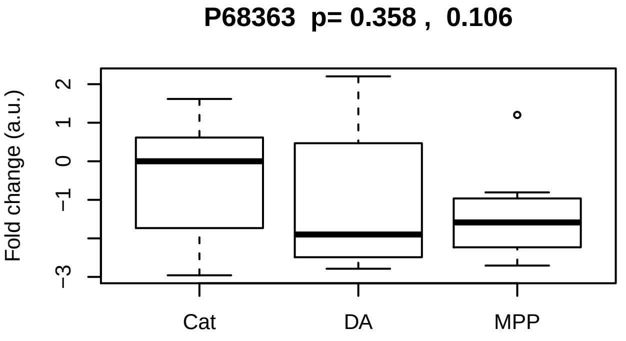
Prohibitin OS Homo sapiens GN PHB PE 1 S



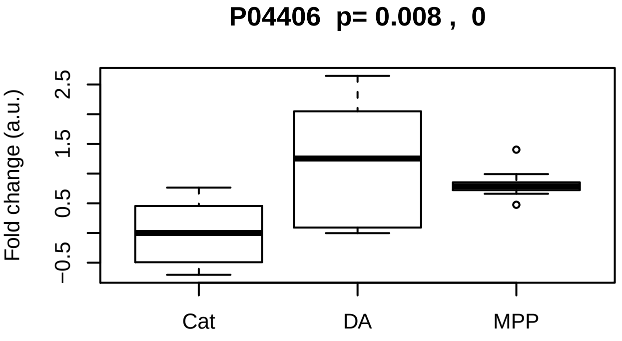
ATP synthase subunit beta mitochondrial



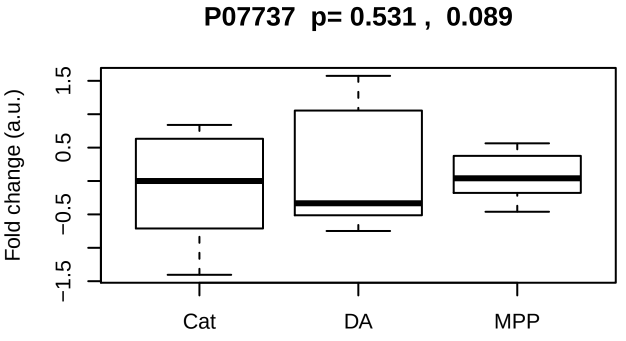
ATP synthase subunit alpha mitochondrial



Tubulin alpha 1B chain OS Homo sapiens G

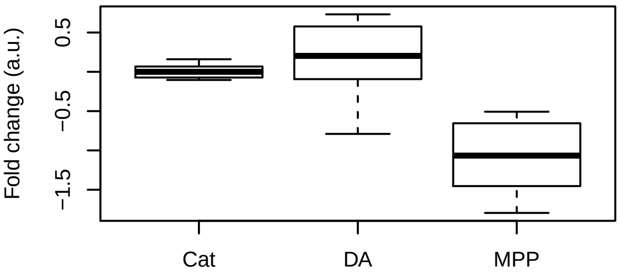


Glyceraldehyde 3 phosphate dehydrogenase



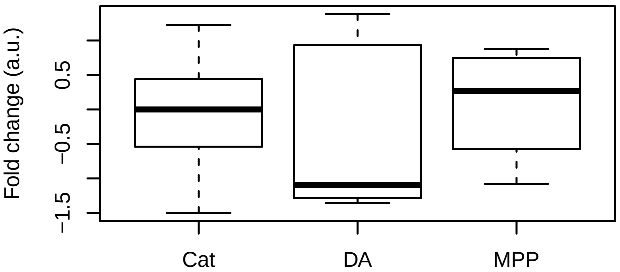
Profilin 1 OS Homo sapiens GN PFN1 PE 1

P49411 p= 0.362 , 0



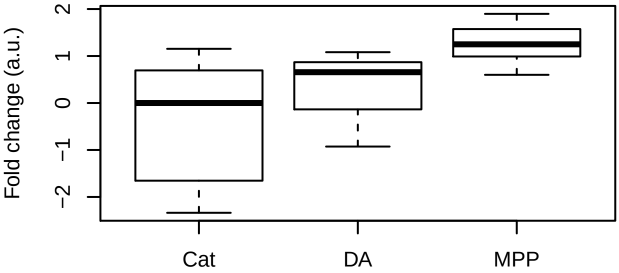
Elongation factor Tu mitochondrial OS Ho

P12236 p= 0.51 , 0.666



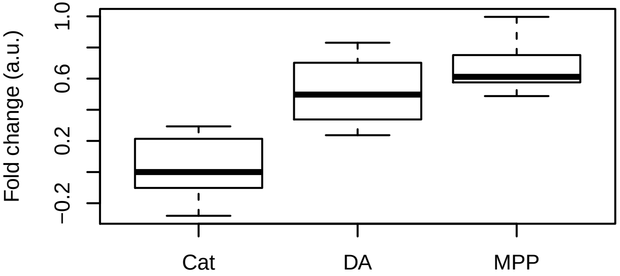
ADP ATP translocase 3 OS Homo sapiens GN

P05141 p= 0.522 , 0.062



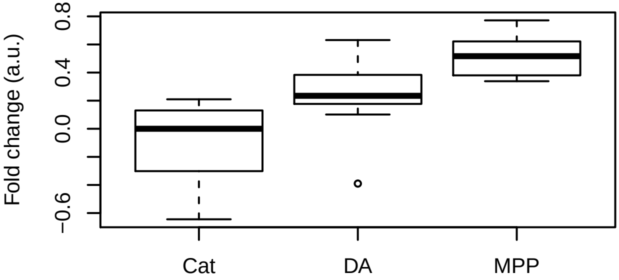
ADP ATP translocase 2 OS Homo sapiens GN

P45880 p= 0.002 , 0



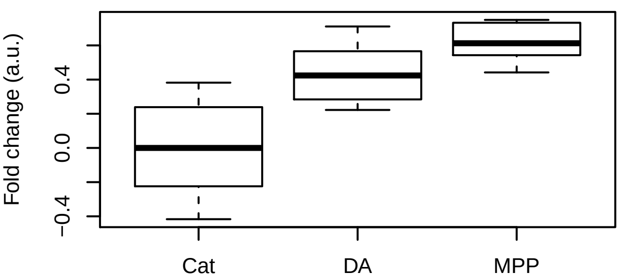
Voltage dependent anion selective channe

Q99623 p= 0.045 , 0



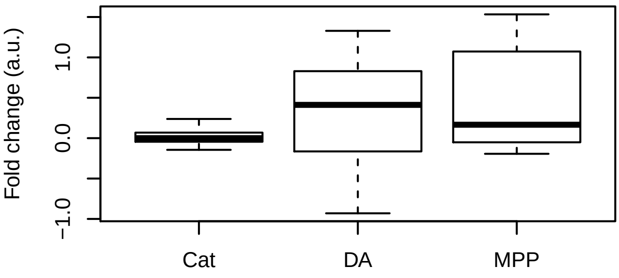
Prohibitin 2 OS Homo sapiens GN PHB2 PE

P21796 p= 0.001 , 0



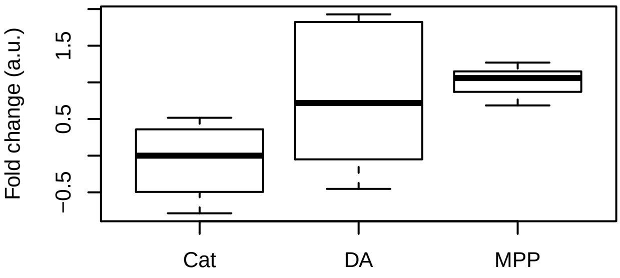
Voltage dependent anion selective channe

P38646 p= 0.292 , 0.037



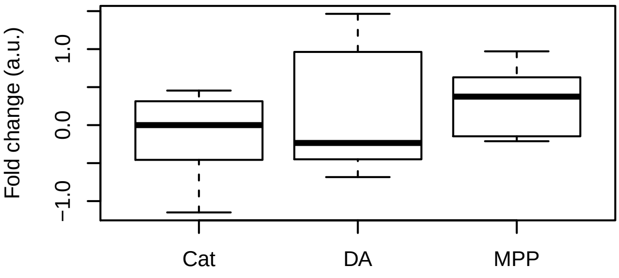
Stress 70 protein mitochondrial OS Homo

P68104 p= 0.016 , 0



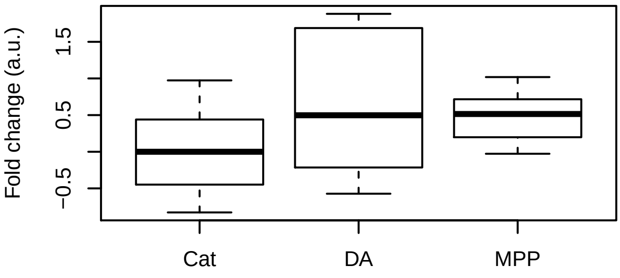
Elongation factor 1 alpha 1 OS Homo sapi

P29966 p= 0.315 , 0.011



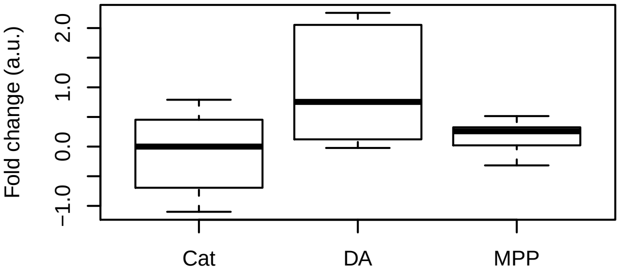
Myristoylated alanine rich C kinase subs

P11142 p= 0.118 , 0.086



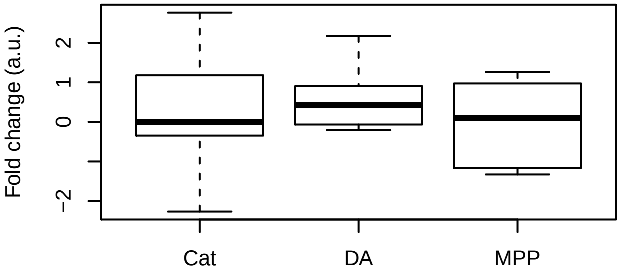
Heat shock cognate 71 kDa protein OS Hom

P14618 p= 0.011 , 0.204

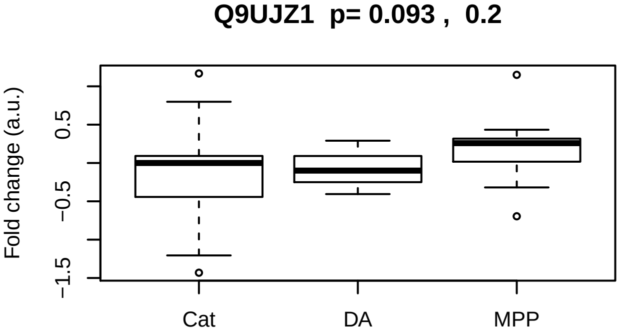


Pyruvate kinase PKM OS Homo sapiens GN P

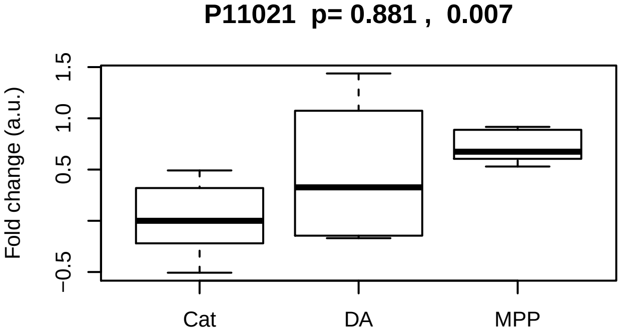
P54652 p= 0.228 , 0.934



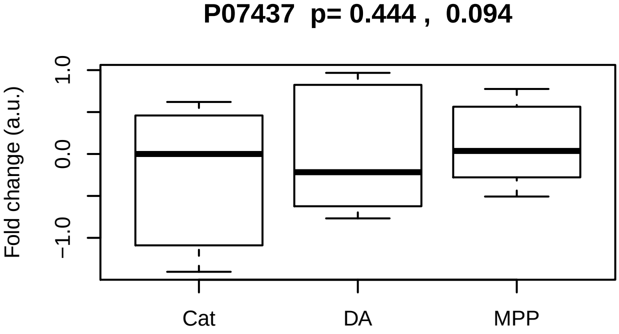
Heat shock related 70 kDa protein 2 OS H



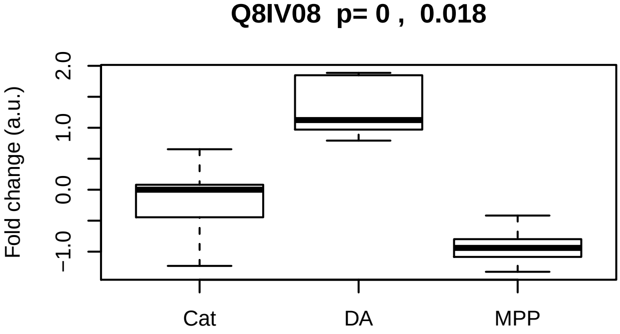
Stomatin like protein 2 mitochondrial OS



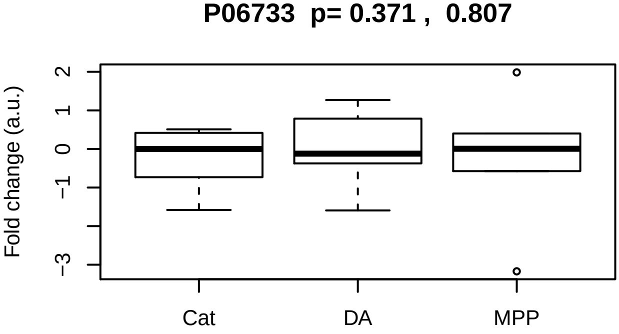
78 kDa glucose regulated protein OS Homo



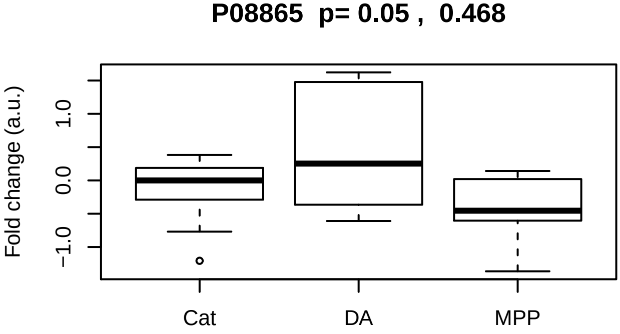
Tubulin beta chain OS Homo sapiens GN TU



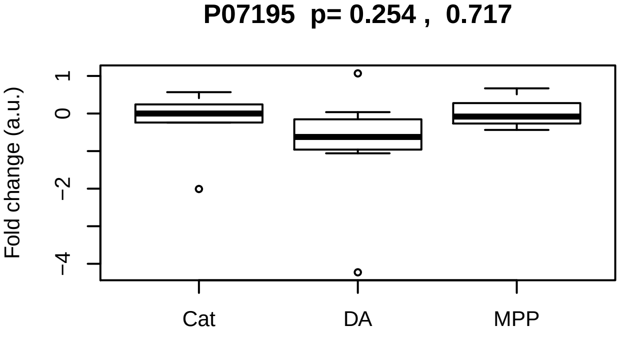
Phospholipase D3 OS Homo sapiens GN PLD3



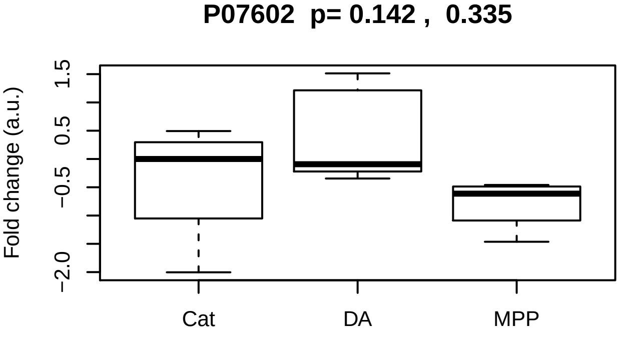
Alpha enolase OS Homo sapiens GN ENO1 PE



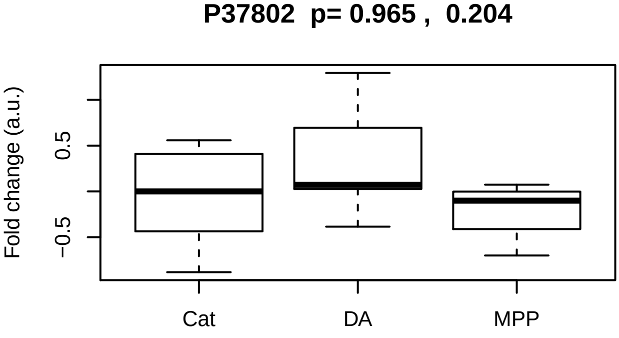
40S ribosomal protein SA OS Homo sapiens



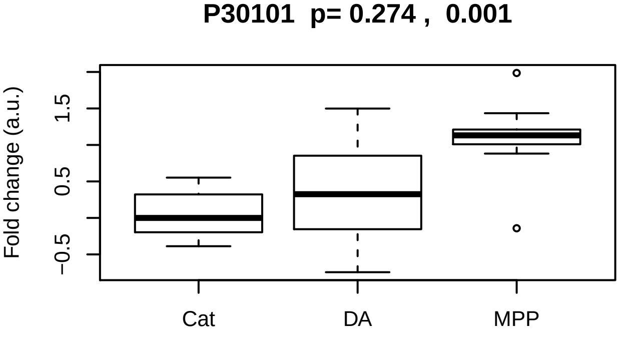
L lactate dehydrogenase B chain OS Homo



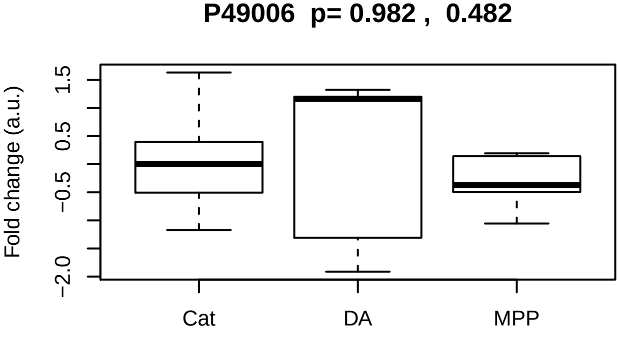
Proactivator polypeptide OS Homo sapiens



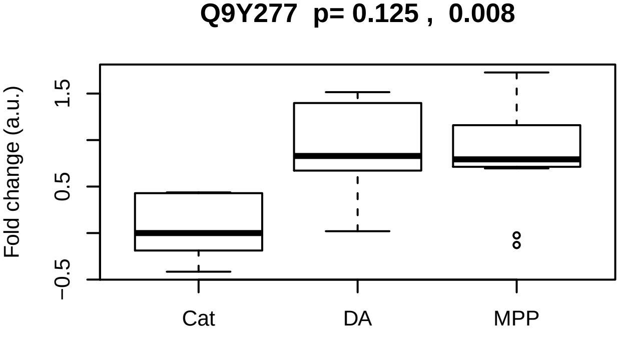
Transgelin 2 OS Homo sapiens GN TAGLN2 P



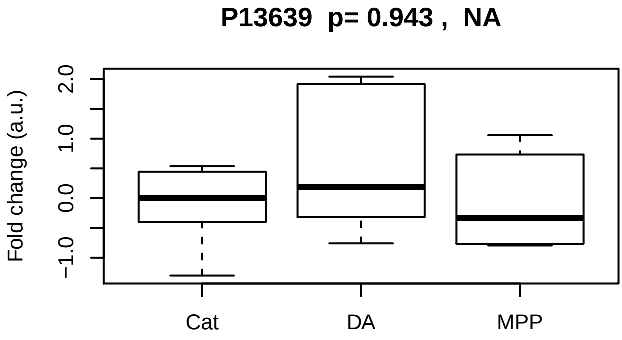
Protein disulfide isomerase A3 OS Homo s



MARCKS related protein OS Homo sapiens G

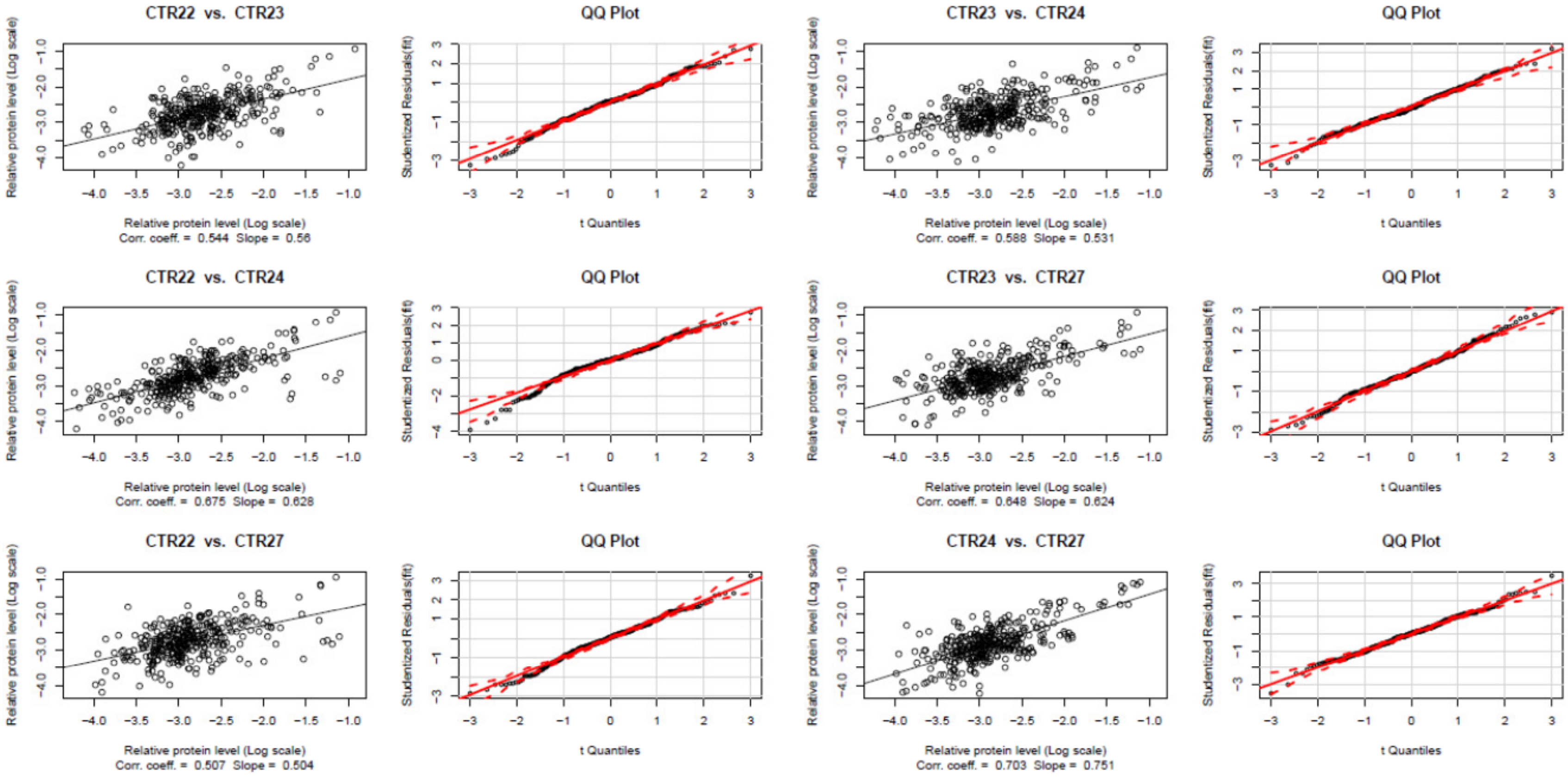


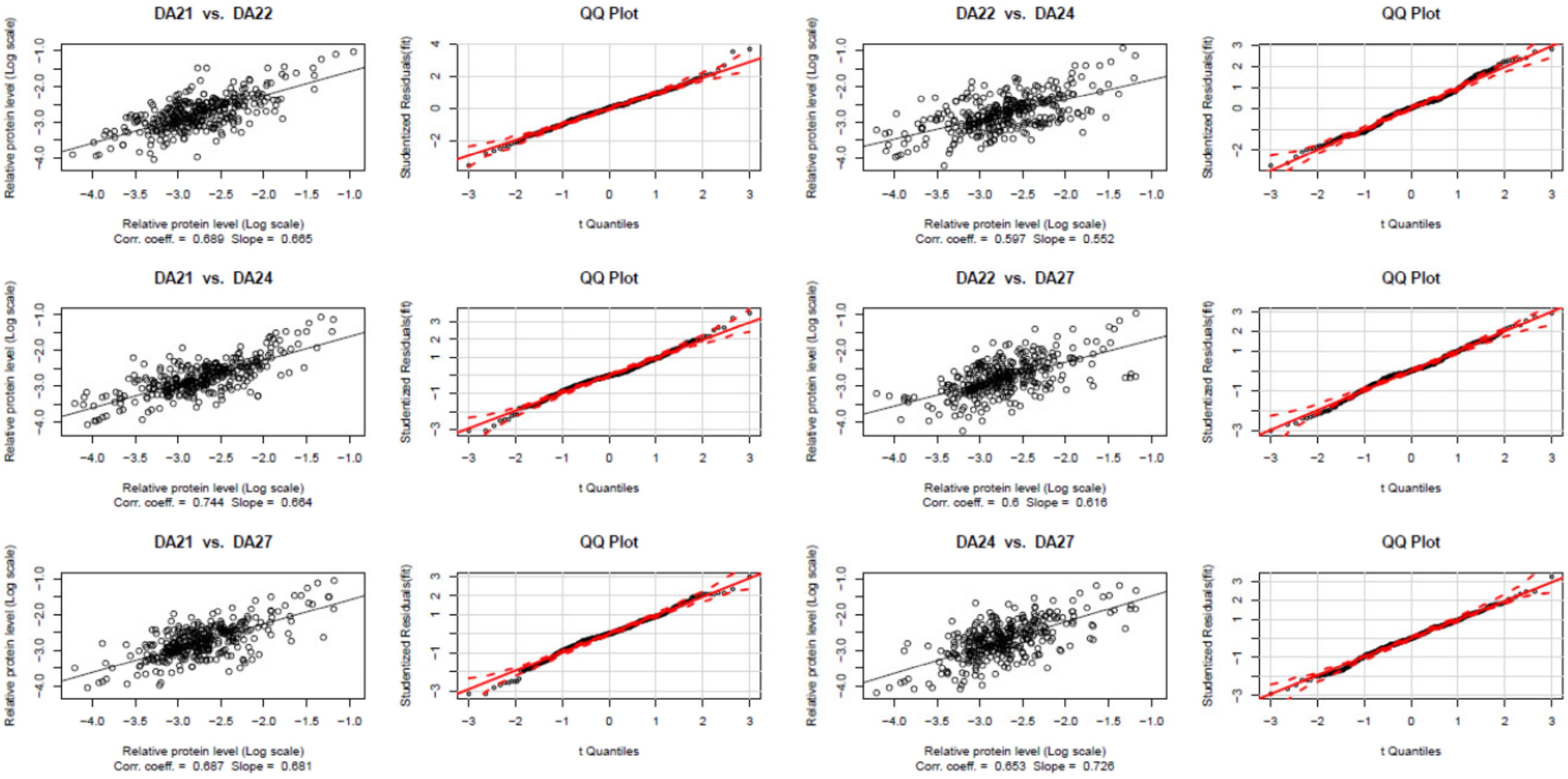
Voltage dependent anion selective channe



Elongation factor 2 OS Homo sapiens GN E

FIGURE S3


CTR22 vs. CTR23
Relative protein level (Log scale)
Corr. coeff. = 0.544 Slope = 0.56
QQ Plot
Studentized Residuals(fit)
t Quantiles
CTR23 vs. CTR24
Relative protein level (Log scale)
Corr. coeff. = 0.588 Slope = 0.531
QQ Plot
CTR22 vs. CTR24
Corr. coeff. = 0.675 Slope = 0.628
CTR23 vs. CTR27
Corr. coeff. = 0.648 Slope = 0.624
CTR22 vs. CTR27
Corr. coeff. = 0.507 Slope = 0.504
CTR24 vs. CTR27
Corr. coeff. = 0.703 Slope = 0.751
-4.0 -3.5 -3.0 -2.5 -2.0 -1.5 -1.0
-3 -2 -1 0 1 2 3


DA21 vs. DA22
Relative protein level (Log scale)
Corr. coeff. = 0.689 Slope = 0.665
QQ Plot
Studentized Residuals(fit)
t Quantiles
DA22 vs. DA24
Relative protein level (Log scale)
Corr. coeff. = 0.597 Slope = 0.552
QQ Plot
Studentized Residuals(fit)
t Quantiles
DA21 vs. DA24
Relative protein level (Log scale)
Corr. coeff. = 0.744 Slope = 0.664
QQ Plot
Studentized Residuals(fit)
t Quantiles
DA22 vs. DA27
Relative protein level (Log scale)
Corr. coeff. = 0.6 Slope = 0.616
QQ Plot
Studentized Residuals(fit)
t Quantiles
DA21 vs. DA27
Relative protein level (Log scale)
Corr. coeff. = 0.687 Slope = 0.681
QQ Plot
Studentized Residuals(fit)
t Quantiles
DA24 vs. DA27
Relative protein level (Log scale)
Corr. coeff. = 0.653 Slope = 0.726
QQ Plot
Studentized Residuals(fit)
t Quantiles
−4.0 −3.5 −3.0 −2.5 −2.0 −1.5 −1.0
−3 −2 −1 0 1 2 3

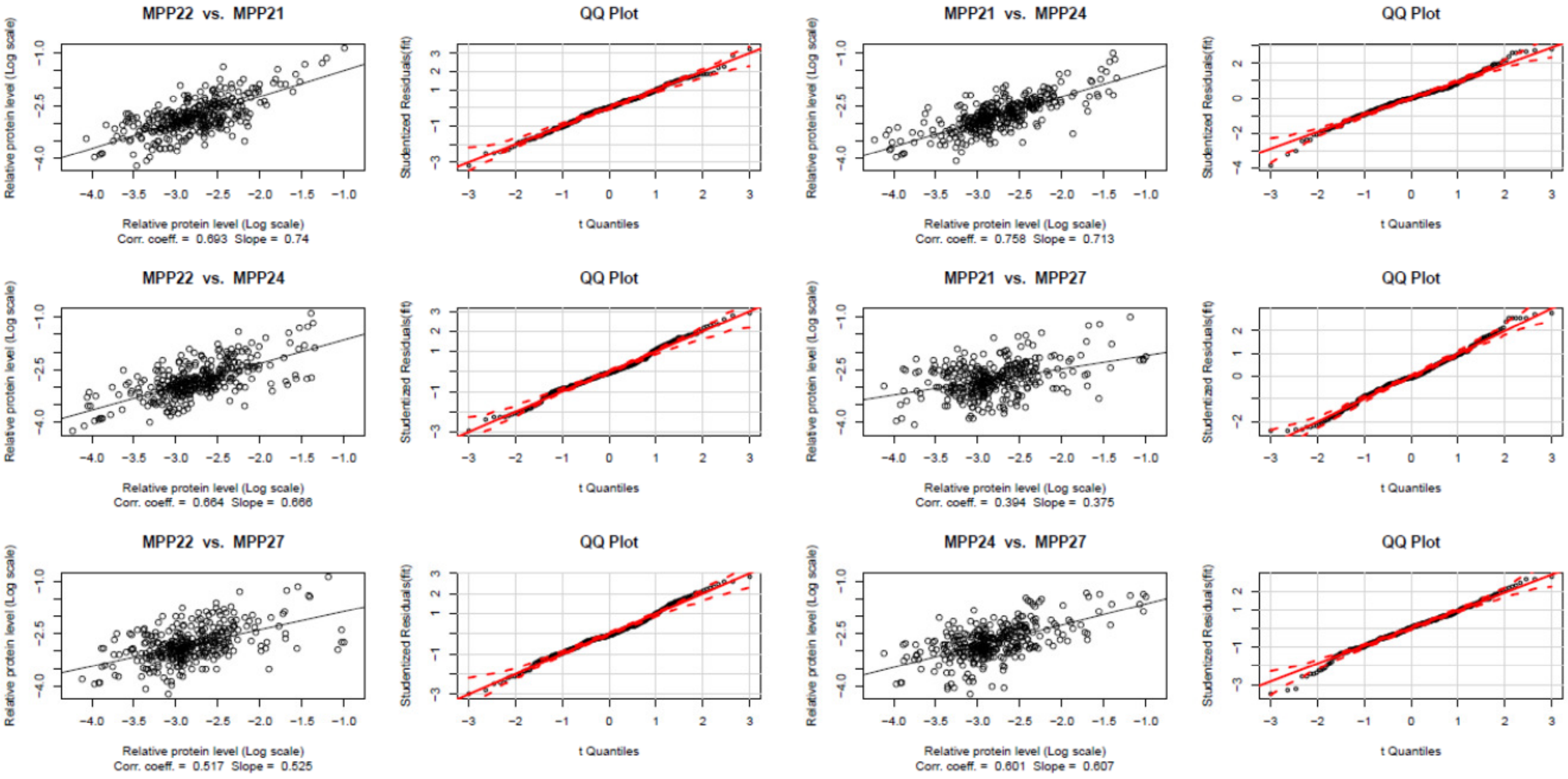
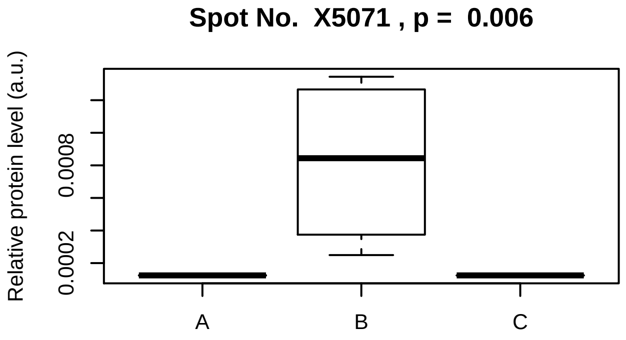
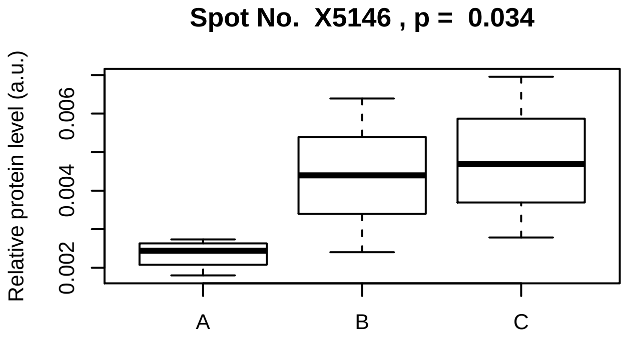
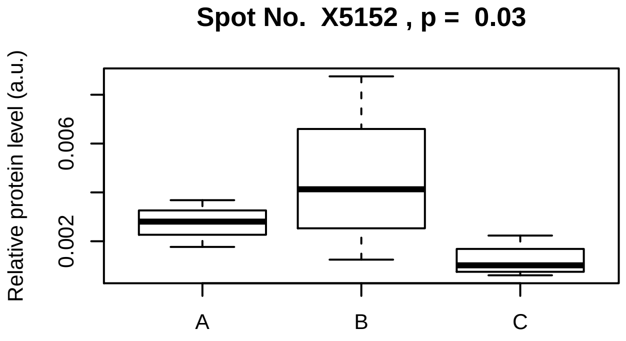
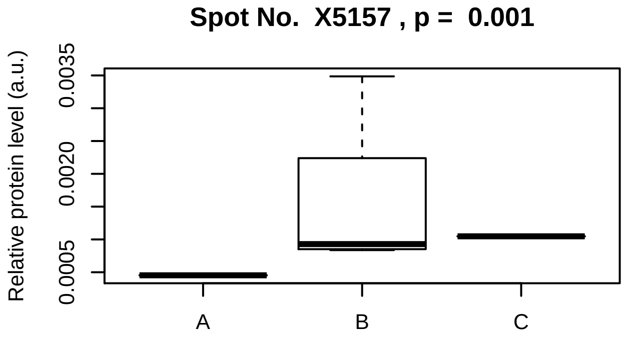

MPP22 vs. MPP21
Relative protein level (Log scale)
Relative protein level (Log scale)
Corr. coeff. = 0.693 Slope = 0.74
QQ Plot
Studentized Residuals(fit)
t Quantiles
MPP21 vs. MPP24
Relative protein level (Log scale)
Relative protein level (Log scale)
Corr. coeff. = 0.758 Slope = 0.713
QQ Plot
Studentized Residuals(fit)
t Quantiles
MPP22 vs. MPP24
Relative protein level (Log scale)
Relative protein level (Log scale)
Corr. coeff. = 0.664 Slope = 0.666
QQ Plot
Studentized Residuals(fit)
t Quantiles
MPP21 vs. MPP27
Relative protein level (Log scale)
Relative protein level (Log scale)
Corr. coeff. = 0.394 Slope = 0.375
QQ Plot
Studentized Residuals(fit)
t Quantiles
MPP22 vs. MPP27
Relative protein level (Log scale)
Relative protein level (Log scale)
Corr. coeff. = 0.517 Slope = 0.525
QQ Plot
Studentized Residuals(fit)
t Quantiles
MPP24 vs. MPP27
Relative protein level (Log scale)
Relative protein level (Log scale)
Corr. coeff. = 0.601 Slope = 0.607
QQ Plot
Studentized Residuals(fit)
t Quantiles

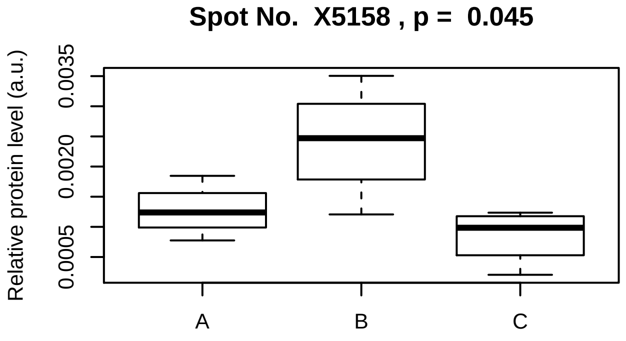
FIGURE S4

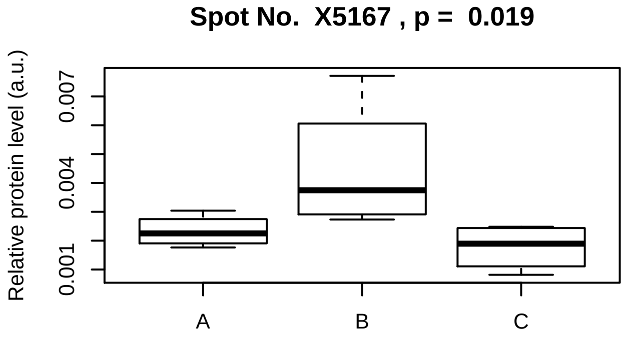

Spot No. X5071 , p = 0.006
Relative protein level (a.u.)
0.0002
0.0008
A
B
C


Spot No. X5146 , p = 0.034
Relative protein level (a.u.)
0.002
0.004
0.006
A
B
C

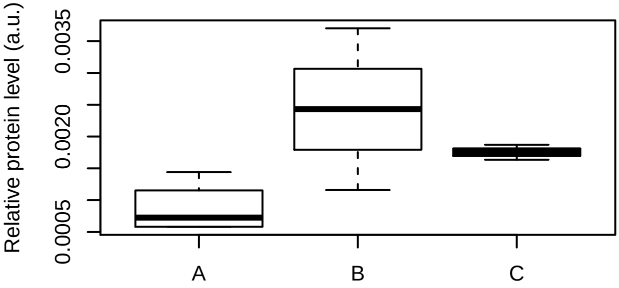

Spot No. X5152 , p = 0.03
Relative protein level (a.u.)
0.002
0.006
A
B
C


Spot No. X5157 , p = 0.001
Relative protein level (a.u.)
0.0005
0.0020
0.0035
A
B
C

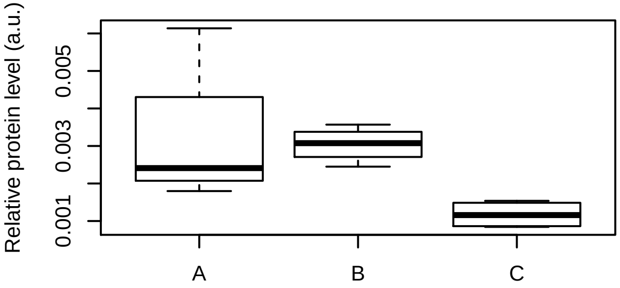

Spot No. X5158 , p = 0.045
Relative protein level (a.u.)
0.0005
0.0020
0.0035
A
B
C


Spot No. X5167 , p = 0.019
Relative protein level (a.u.)
0.001
0.004
0.007
A
B
C

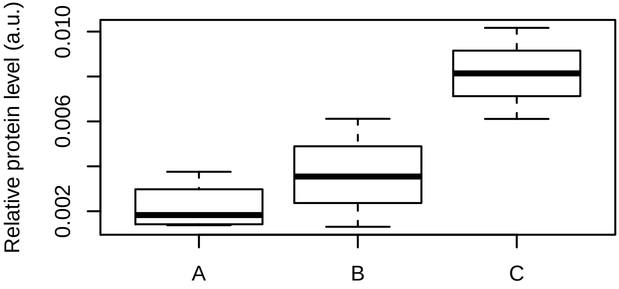
Spot No. X5188 , p = 0.018



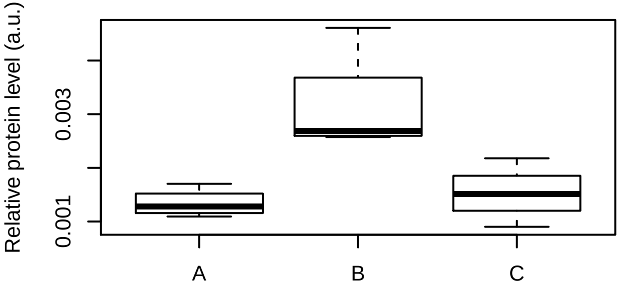
Spot No. X5192 , p = 0.01



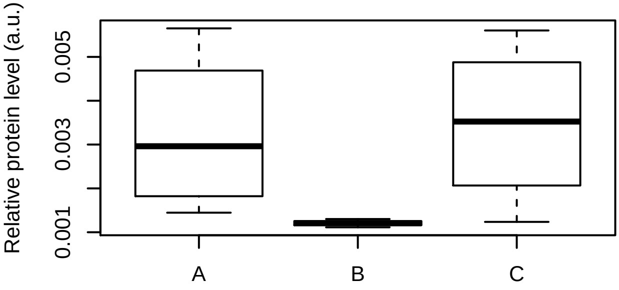
Spot No. X5211 , p = 0.023



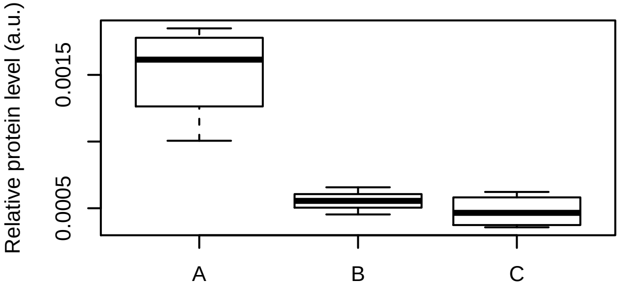
Spot No. X5228 , p = 0.008

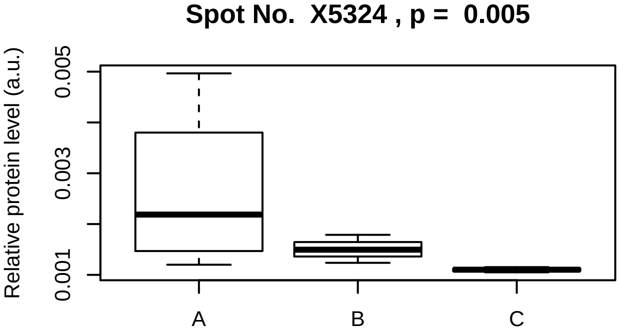


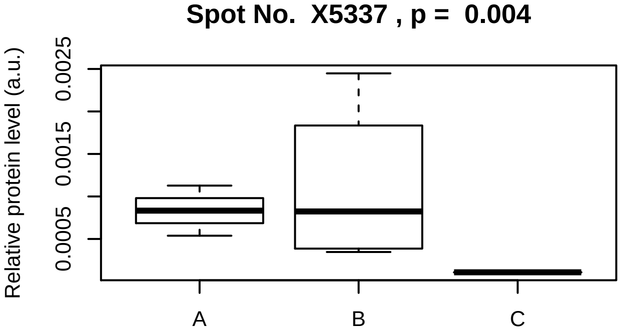
Spot No. X5252 , p = 0.032

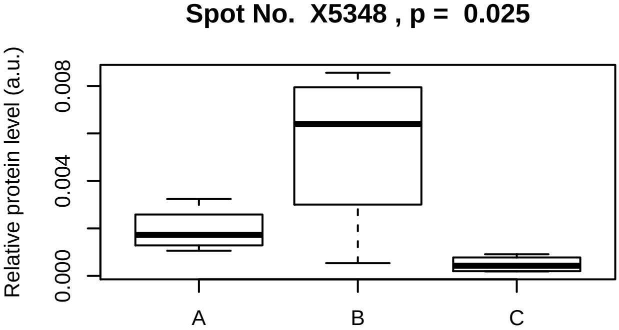


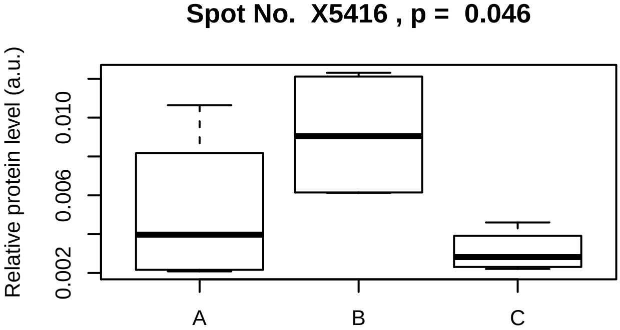
Spot No. X5321 , p = 0.001

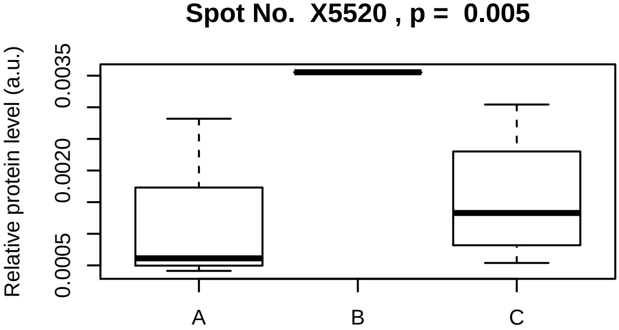


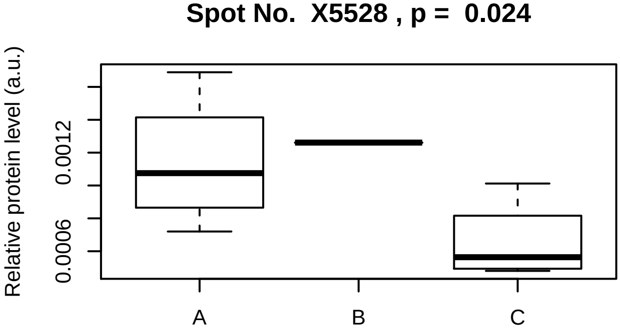

Spot No. X5324 , p = 0.005
Relative protein level (a.u.)
0.001
0.003
0.005
A
B
C

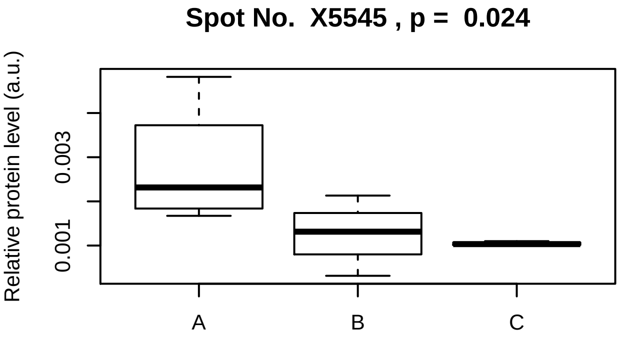

Spot No. X5337 , p = 0.004
Relative protein level (a.u.)
0.0005
0.0015
0.0025
A
B
C

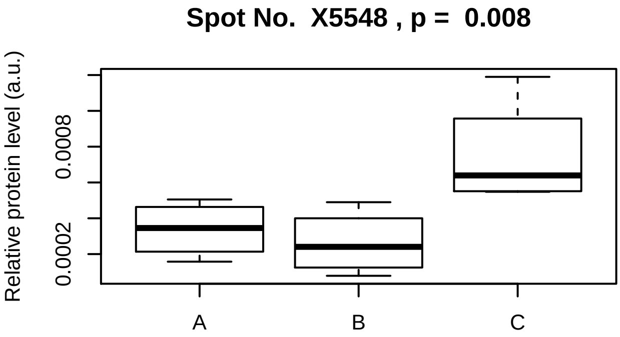

Spot No. X5348 , p = 0.025
Relative protein level (a.u.)
0.000
0.004
0.008
A
B
C

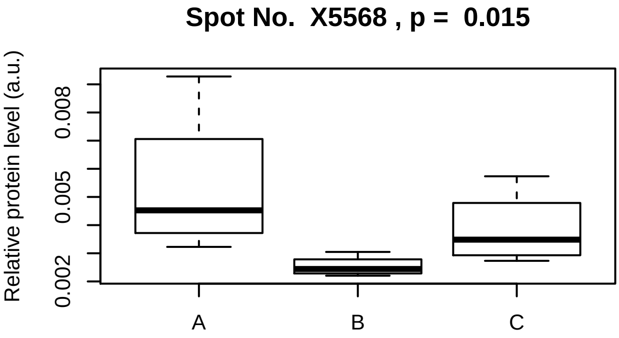

Spot No. X5416 , p = 0.046
Relative protein level (a.u.)
0.002
0.006
0.010
A
B
C

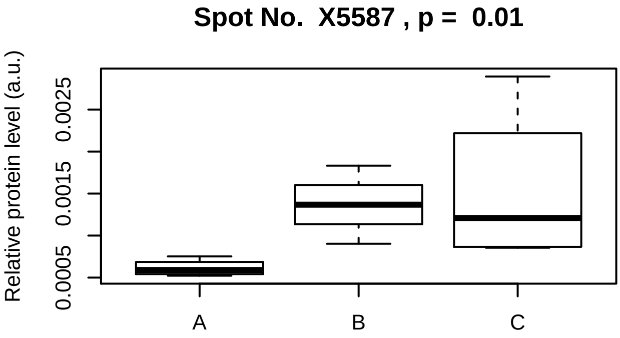

Spot No. X5520 , p = 0.005
Relative protein level (a.u.)
0.0005
0.0020
0.0035
A
B
C

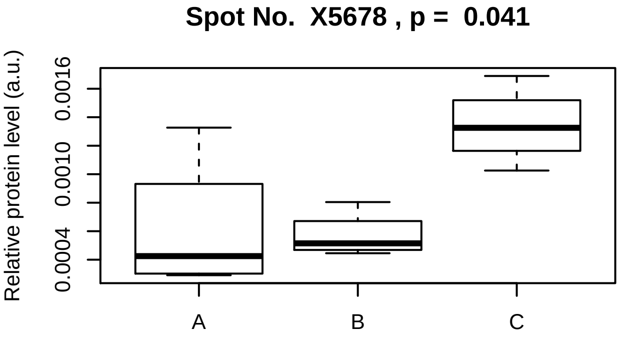

Spot No. X5528 , p = 0.024
Relative protein level (a.u.)
0.0006
0.0012
A
B
C

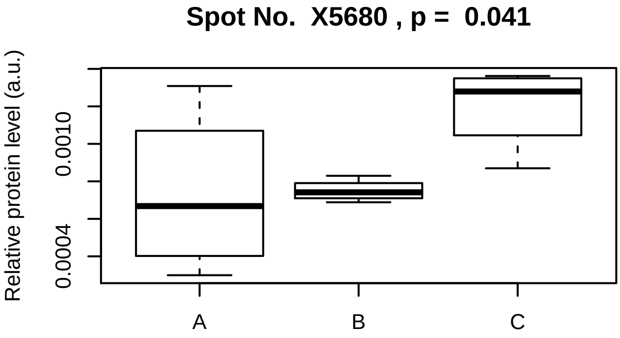

Spot No. X5545 , p = 0.024
Relative protein level (a.u.)
0.001
0.003
A
B
C

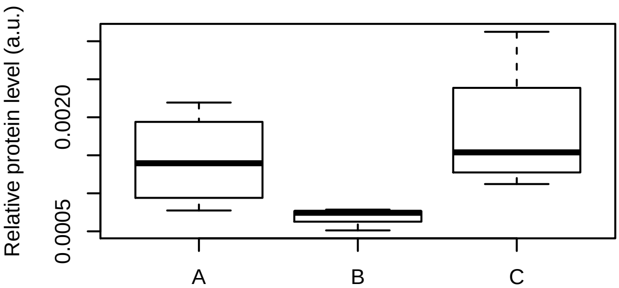

Spot No. X5548 , p = 0.008
Relative protein level (a.u.)
0.0002
0.0008
A
B
C


Spot No. X5568 , p = 0.015
Relative protein level (a.u.)
0.002
0.005
0.008
A
B
C


Spot No. X5587 , p = 0.01
Relative protein level (a.u.)
0.0005
0.0015
0.0025
A
B
C


Spot No. X5678 , p = 0.041
Relative protein level (a.u.)
0.0004
0.0010
0.0016
A
B
C


Spot No. X5680 , p = 0.041
Relative protein level (a.u.)
0.0004
0.0010
A
B
C


Spot No. X5705 , p = 0.014

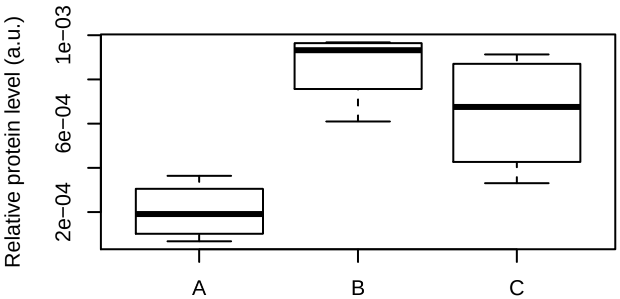

Spot No. X5715 , p = 0.008

FIGURE S5