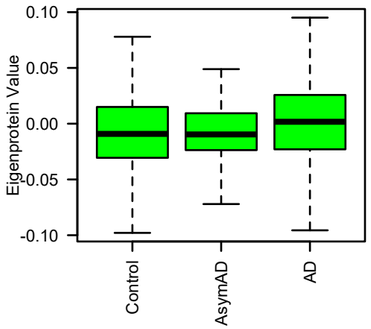
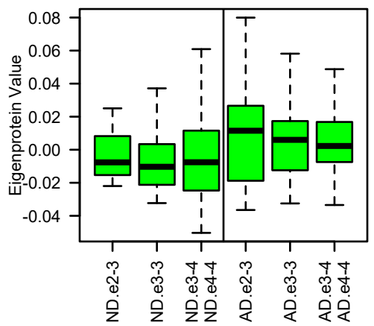
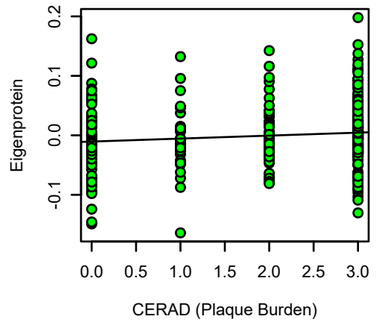
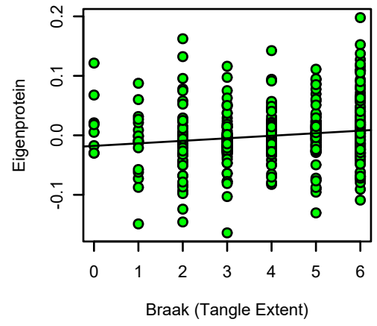
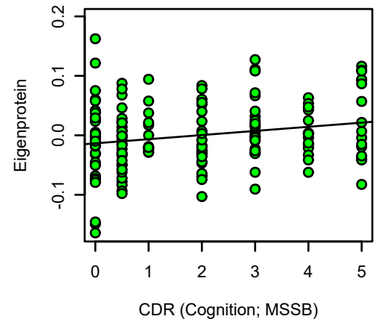
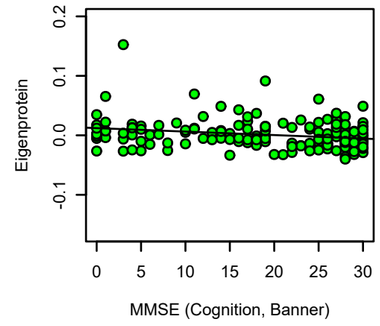

M5 green
K-W p = 0.012
Eigenprotein Value
Control
AsymAD
AD

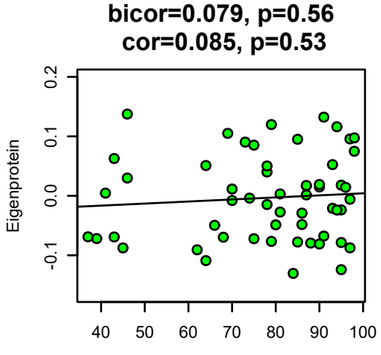

M5 green
ND K-W p = 0.75 | AD K-W p = 0.98
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

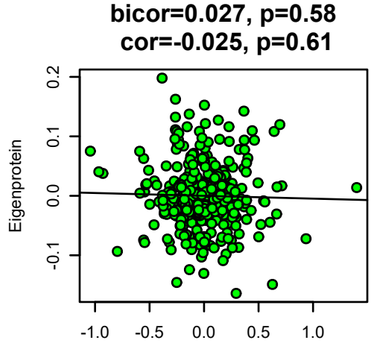

bicor=0.1, p=0.032
cor=0.12, p=0.014
Eigenprotein
CERAD (Plaque Burden)

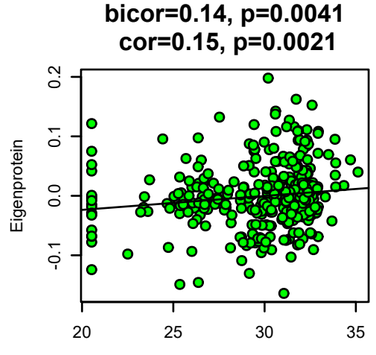

bicor=0.14, p=0.0052
cor=0.14, p=0.0041
Eigenprotein
Braak (Tangle Extent)

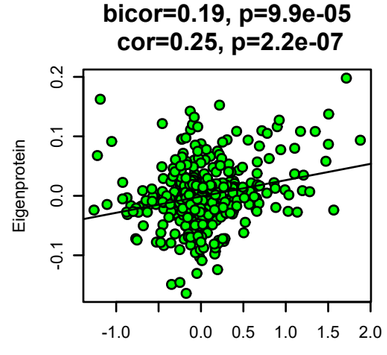

bicor=0.19, p=0.019
cor=0.21, p=0.0079
Eigenprotein
CDR (Cognition; MSSB)

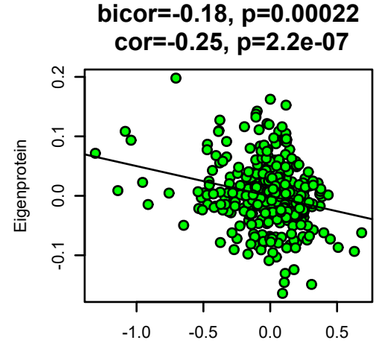

bicor=-0.22, p=0.0047
cor=-0.24, p=0.0018
Eigenprotein
MMSE (Cognition, Banner)

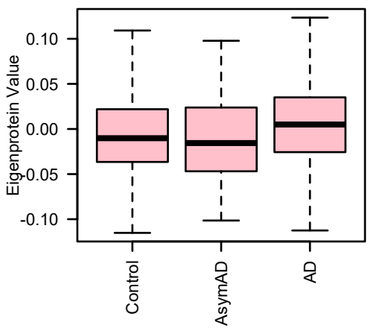

bicor=0.079, p=0.56
cor=0.085, p=0.53
Eigenprotein
CASI (Cognition, ACT)

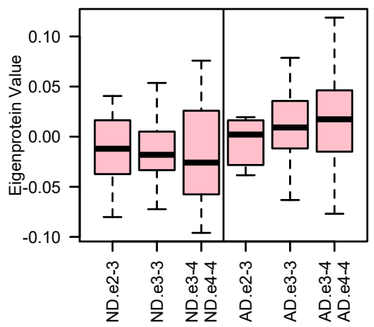

bicor=0.027, p=0.58
cor=-0.025, p=0.61
Eigenprotein
TDP-43 LFQ

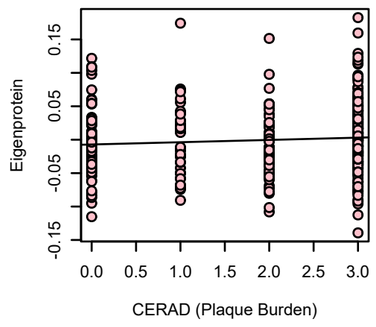

bicor=0.14, p=0.0041
cor=0.15, p=0.0021
Eigenprotein
ABETA 2-peptide LFQ

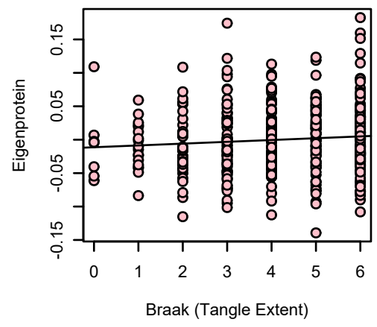

bicor=0.19, p=9.9e-05
cor=0.25, p=2.2e-07
Eigenprotein
Tau MTBR LFQ

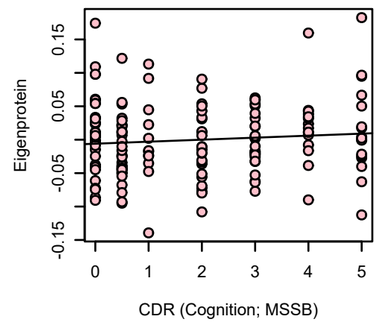

bicor=-0.18, p=0.00022
cor=-0.25, p=2.2e-07
Eigenprotein
alpha Synuclein LFQ

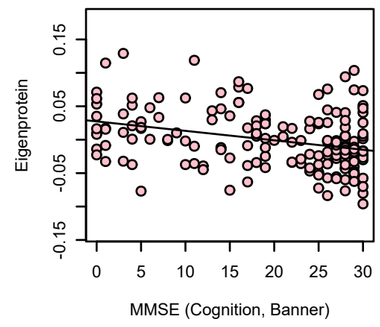

M8 pink
K-W p = 0.016
Eigenprotein Value
Control
AsymAD
AD

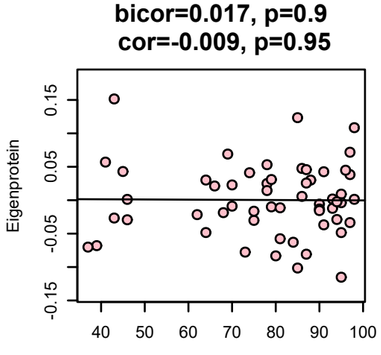

M8 pink
ND K-W p = 0.9 | AD K-W p = 0.47
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

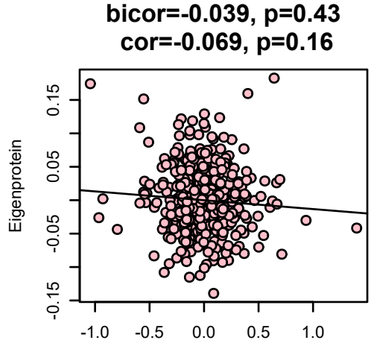

bicor=0.092, p=0.059
cor=0.082, p=0.094
Eigenprotein
CERAD (Plaque Burden)

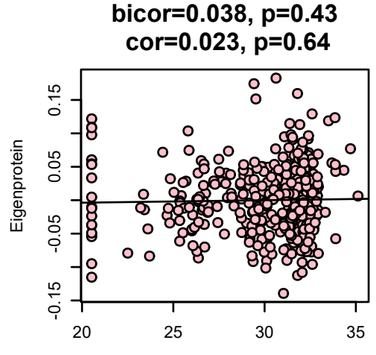

bicor=0.09, p=0.065
cor=0.089, p=0.069
Eigenprotein
Braak (Tangle Extent)

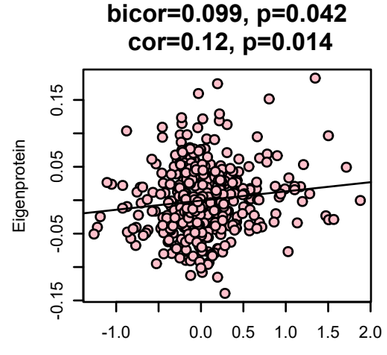

bicor=0.091, p=0.25
cor=0.093, p=0.24
Eigenprotein
CDR (Cognition; MSSB)

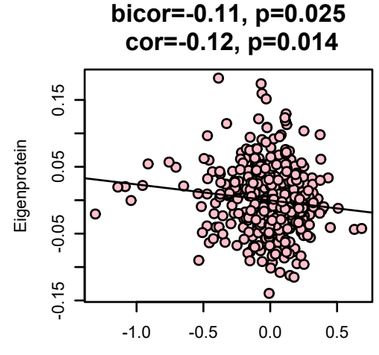

bicor=-0.32, p=3.4e-05
cor=-0.32, p=2.5e-05
Eigenprotein
MMSE (Cognition, Banner)

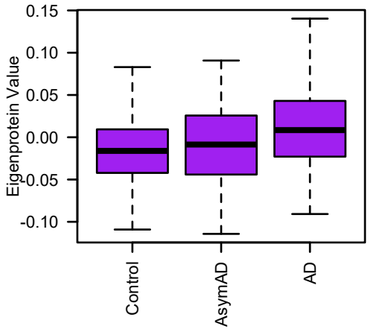

bicor=0.017, p=0.9
cor=-0.009, p=0.95
Eigenprotein
CASI (Cognition, ACT)

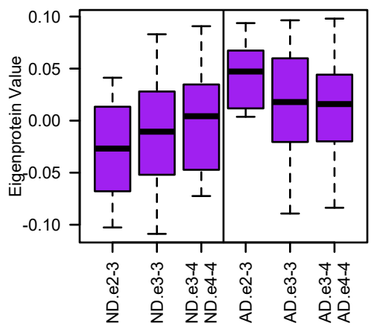

bicor=-0.039, p=0.43
cor=-0.069, p=0.16
Eigenprotein
TDP-43 LFQ

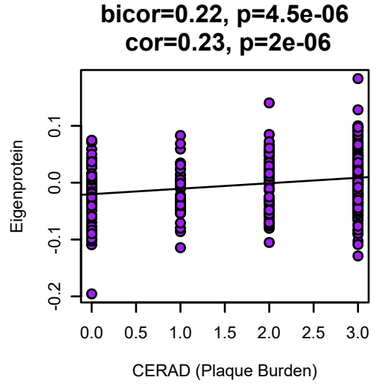

bicor=0.038, p=0.43
cor=0.023, p=0.64
Eigenprotein
ABETA 2-peptide LFQ

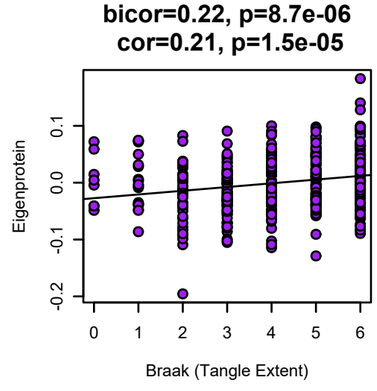

bicor=0.099, p=0.042
cor=0.12, p=0.014
Eigenprotein
Tau MTBR LFQ

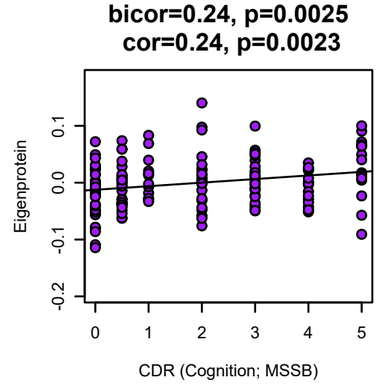

bicor=-0.11, p=0.025
cor=-0.12, p=0.014
Eigenprotein
alpha Synuclein LFQ

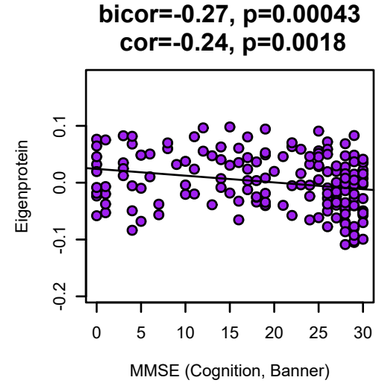

M10 purple
K-W p = 4.7e-07
Eigenprotein Value
Control
AsymAD
AD

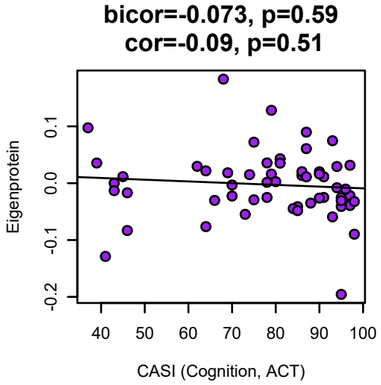

M10 purple
ND K-W p = 0.24 | AD K-W p = 0.46
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

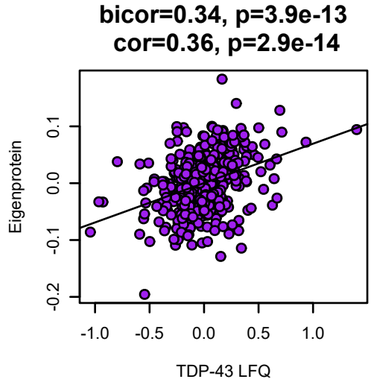

bicor=0.22, p=4.5e-06
cor=0.23, p=2e-06
Eigenprotein
CERAD (Plaque Burden)

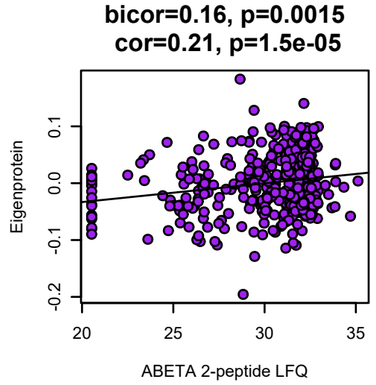

bicor=0.22, p=8.7e-06
cor=0.21, p=1.5e-05
Eigenprotein
Braak (Tangle Extent)

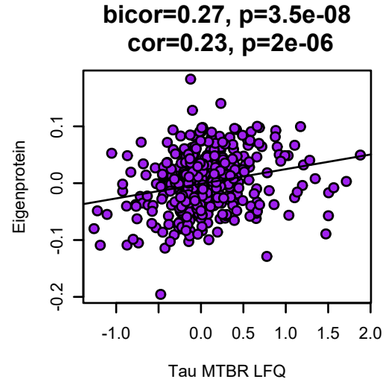

bicor=0.24, p=0.0025
cor=0.24, p=0.0023
Eigenprotein
CDR (Cognition; MSSB)

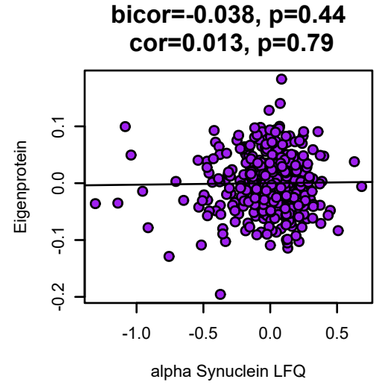

bicor=-0.27, p=0.00043
cor=-0.24, p=0.0018
Eigenprotein
MMSE (Cognition, Banner)

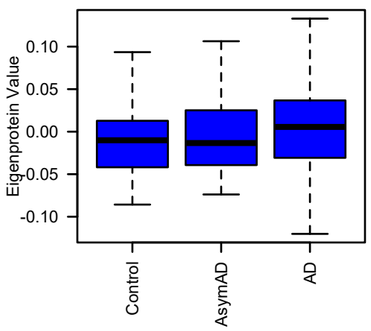

bicor=-0.073, p=0.59
cor=-0.09, p=0.51
Eigenprotein
CASI (Cognition, ACT)

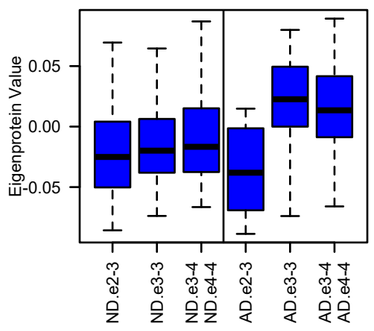

bicor=0.34, p=3.9e-13
cor=0.36, p=2.9e-14
Eigenprotein
TDP-43 LFQ

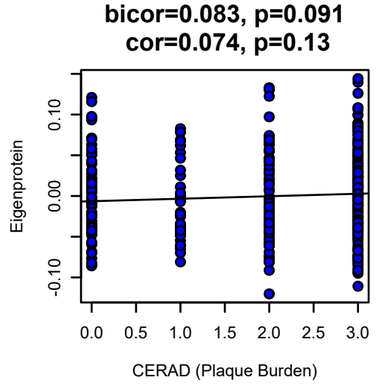

bicor=0.16, p=0.0015
cor=0.21, p=1.5e-05
Eigenprotein
ABETA 2-peptide LFQ

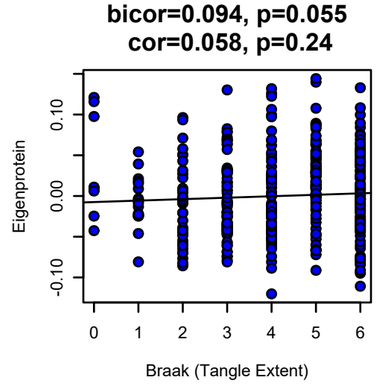

bicor=0.27, p=3.5e-08
cor=0.23, p=2e-06
Eigenprotein
Tau MTBR LFQ

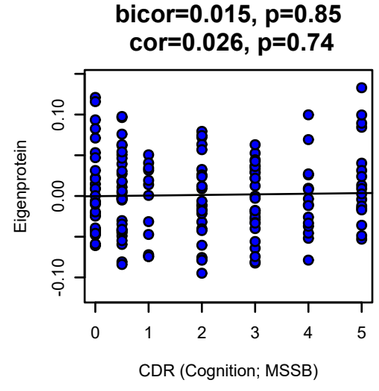

bicor=-0.038, p=0.44
cor=0.013, p=0.79
Eigenprotein
alpha Synuclein LFQ

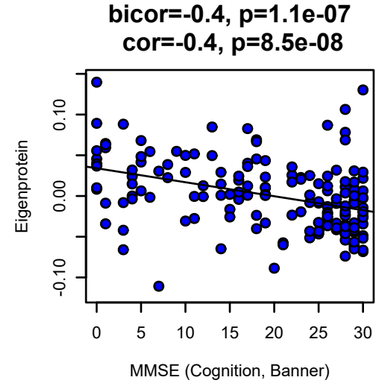

M2 blue
K-W p = 0.11
Eigenprotein Value
Control
AsymAD
AD

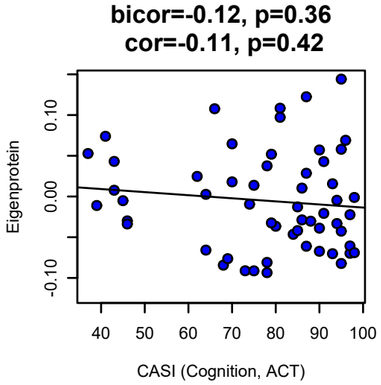

M2 blue
ND K-W p = 0.65 | AD K-W p = 0.0061
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

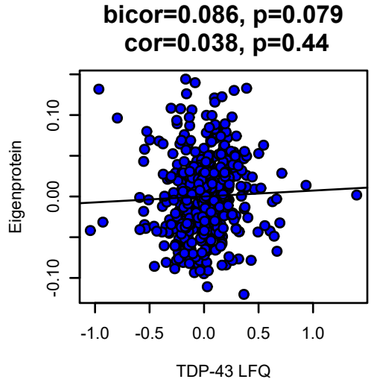

bicor=0.083, p=0.091
cor=0.074, p=0.13
Eigenprotein
CERAD (Plaque Burden)

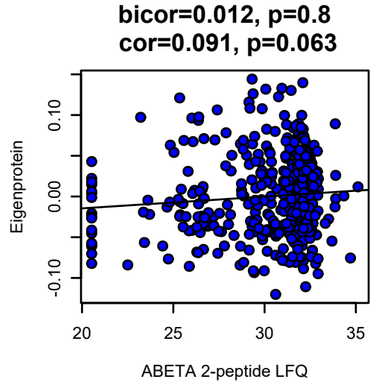

bicor=0.094, p=0.055
cor=0.058, p=0.24
Eigenprotein
Braak (Tangle Extent)

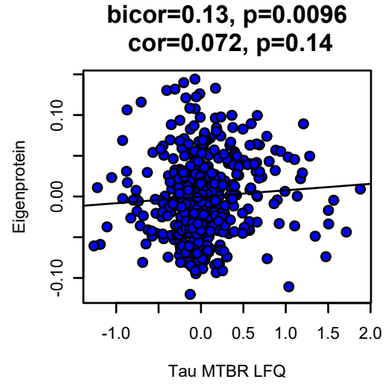

bicor=0.015, p=0.85
cor=0.026, p=0.74
Eigenprotein
CDR (Cognition; MSSB)

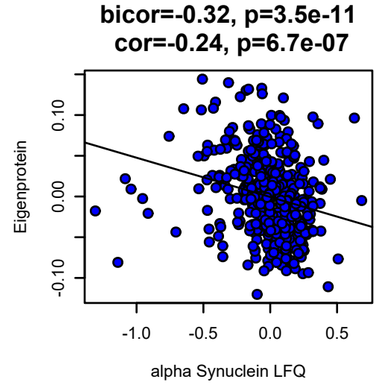

bicor=-0.4, p=1.1e-07
cor=-0.4, p=8.5e-08
Eigenprotein
MMSE (Cognition, Banner)

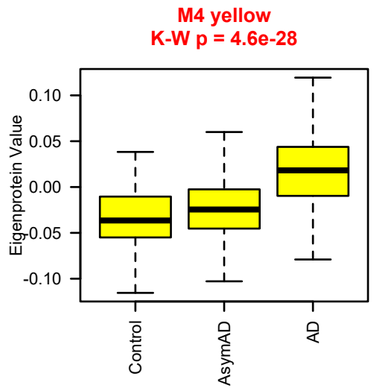

bicor=-0.12, p=0.36
cor=-0.11, p=0.42
Eigenprotein
CASI (Cognition, ACT)

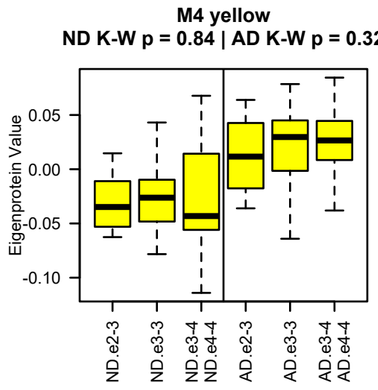

bicor=0.086, p=0.079
cor=0.038, p=0.44
Eigenprotein
TDP-43 LFQ

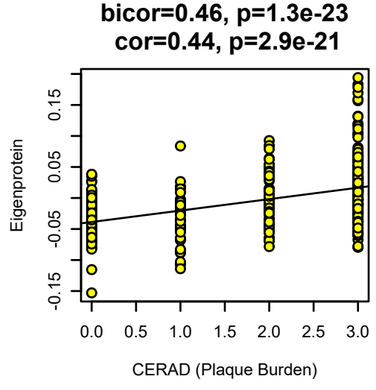

bicor=0.012, p=0.8
cor=0.091, p=0.063
Eigenprotein
ABETA 2-peptide LFQ

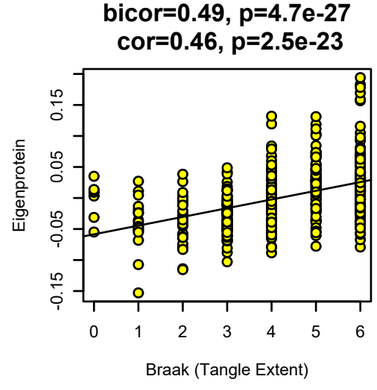

bicor=0.13, p=0.0096
cor=0.072, p=0.14
Eigenprotein
Tau MTBR LFQ

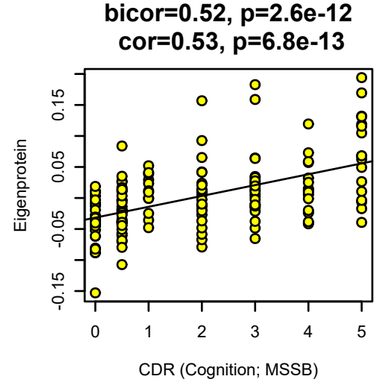

bicor=-0.32, p=3.5e-11
cor=-0.24, p=6.7e-07
Eigenprotein
alpha Synuclein LFQ

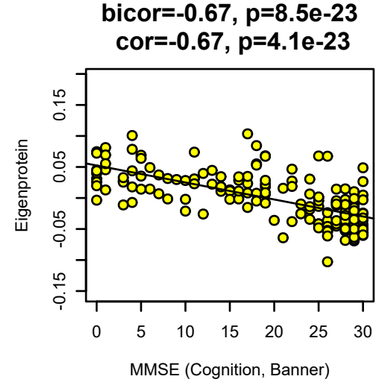

M4 yellow
K-W p = 4.6e-28
Eigenprotein Value
Control
AsymAD
AD

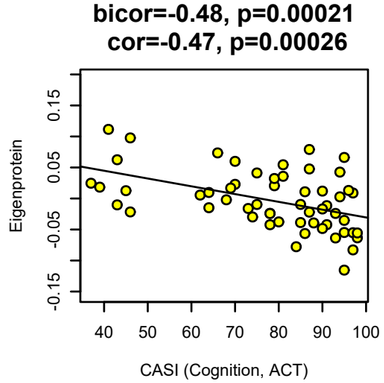

M4 yellow
ND K-W p = 0.84 | AD K-W p = 0.32
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

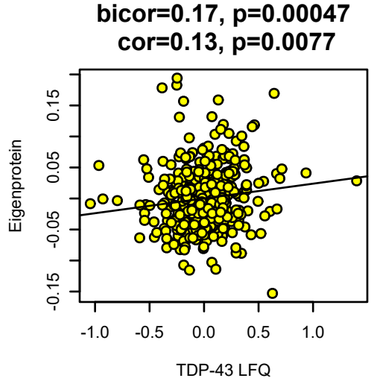

bicor=0.46, p=1.3e-23
cor=0.44, p=2.9e-21
Eigenprotein
CERAD (Plaque Burden)

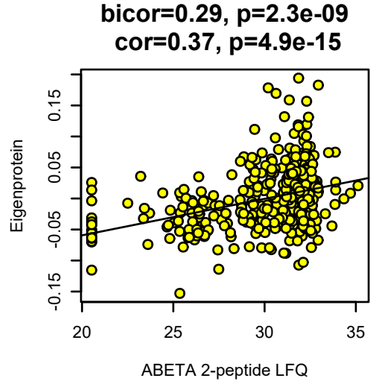

bicor=0.49, p=4.7e-27
cor=0.46, p=2.5e-23
Eigenprotein
Braak (Tangle Extent)

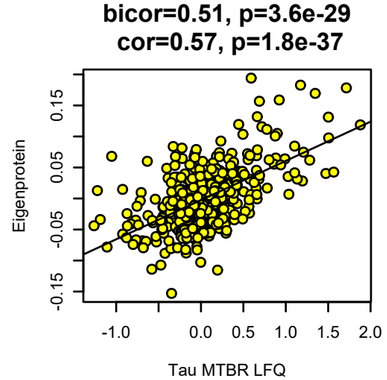

bicor=0.52, p=2.6e-12
cor=0.53, p=6.8e-13
Eigenprotein
CDR (Cognition; MSSB)

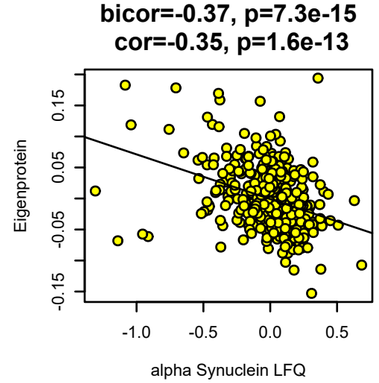

bicor=-0.67, p=8.5e-23
cor=-0.67, p=4.1e-23
Eigenprotein
MMSE (Cognition, Banner)

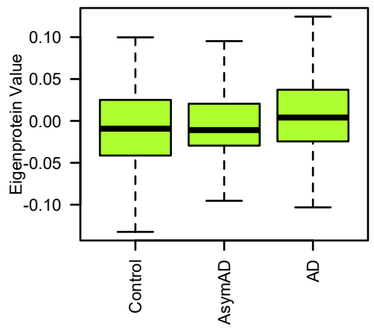

bicor=-0.48, p=0.00021
cor=-0.47, p=0.00026
Eigenprotein
CASI (Cognition, ACT)

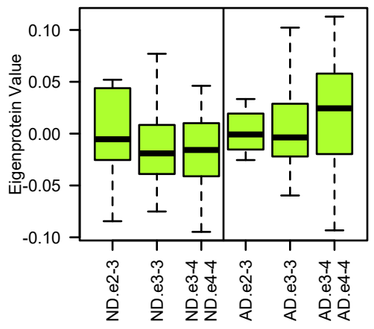

bicor=0.17, p=0.00047
cor=0.13, p=0.0077
Eigenprotein
TDP-43 LFQ

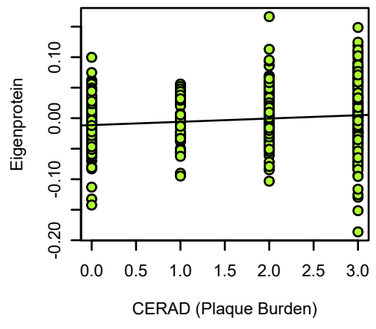

bicor=0.29, p=2.3e-09
cor=0.37, p=4.9e-15
Eigenprotein
ABETA 2-peptide LFQ

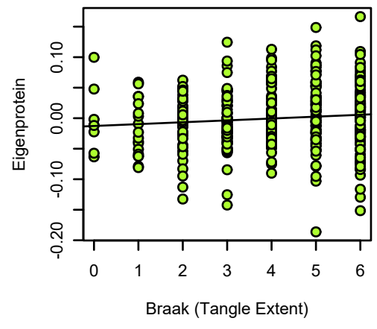

bicor=0.51, p=3.6e-29
cor=0.57, p=1.8e-37
Eigenprotein
Tau MTBR LFQ

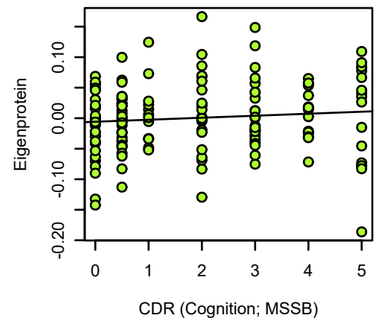

bicor=-0.37, p=7.3e-15
cor=-0.35, p=1.6e-13
Eigenprotein
alpha Synuclein LFQ

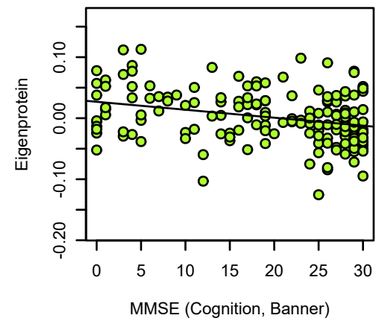

M11 greenyellow
K-W p = 0.0032
Eigenprotein Value
Control
AsymAD
AD

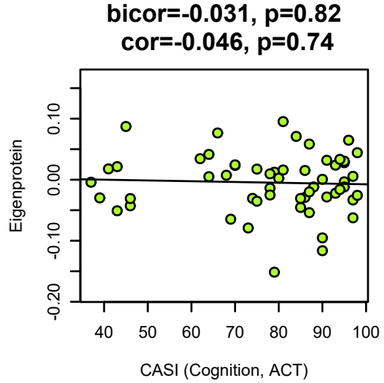

M11 greenyellow
ND K-W p = 0.46 | AD K-W p = 0.13
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

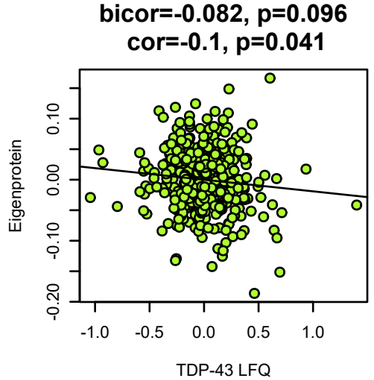

bicor=0.13, p=0.0064
cor=0.13, p=0.0077
Eigenprotein
CERAD (Plaque Burden)

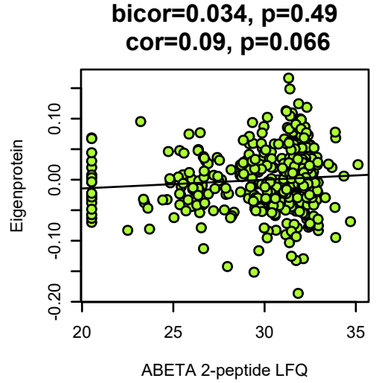

bicor=0.11, p=0.02
cor=0.1, p=0.041
Eigenprotein
Braak (Tangle Extent)

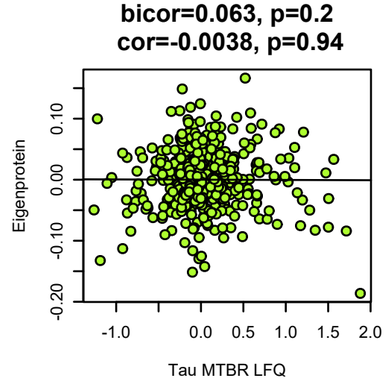

bicor=0.11, p=0.17
cor=0.099, p=0.21
Eigenprotein
CDR (Cognition; MSSB)

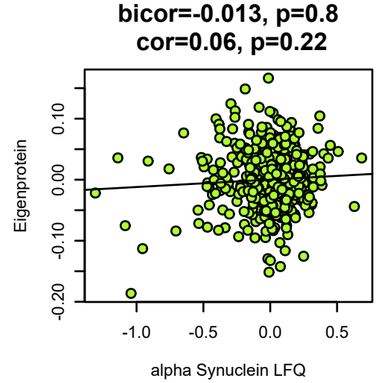

bicor=-0.33, p=1.1e-05
cor=-0.3, p=8.2e-05
Eigenprotein
MMSE (Cognition, Banner)

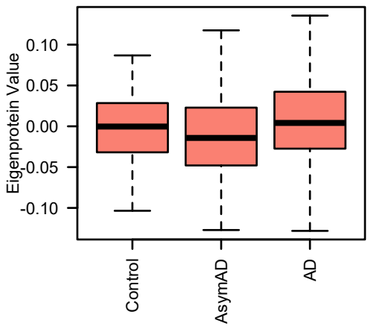

bicor=-0.031, p=0.82
cor=-0.046, p=0.74
Eigenprotein
CASI (Cognition, ACT)

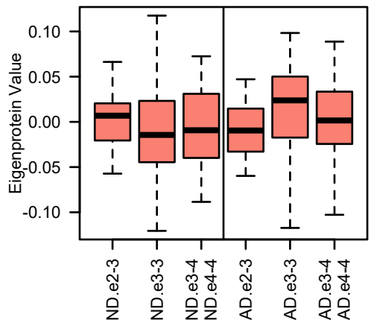

bicor=-0.082, p=0.096
cor=-0.1, p=0.041
Eigenprotein
TDP-43 LFQ

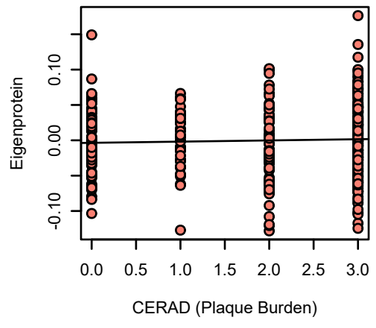

bicor=0.034, p=0.49
cor=0.09, p=0.066
Eigenprotein
ABETA 2-peptide LFQ

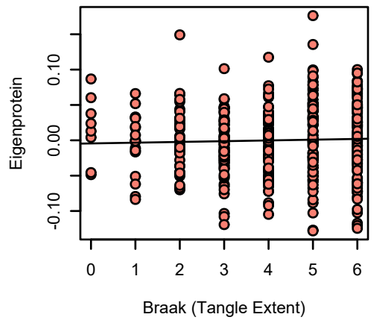

bicor=0.063, p=0.2
cor=-0.0038, p=0.94
Eigenprotein
Tau MTBR LFQ

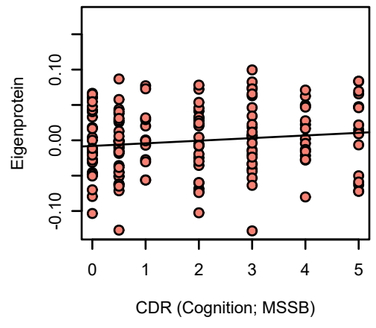

bicor=-0.013, p=0.8
cor=0.06, p=0.22
Eigenprotein
alpha Synuclein LFQ

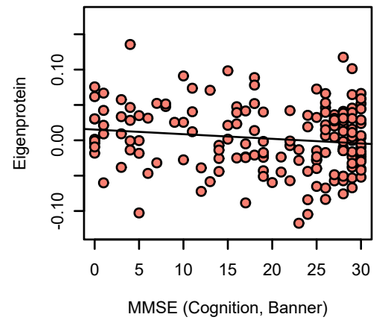

M13 salmon
K-W p = 0.012
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

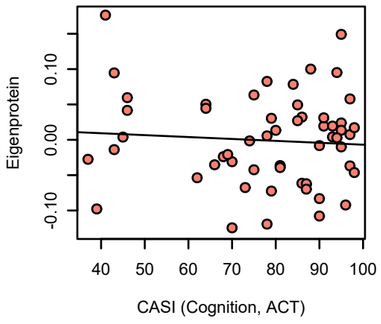

M13 salmon
ND K-W p = 0.56 | AD K-W p = 0.24
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

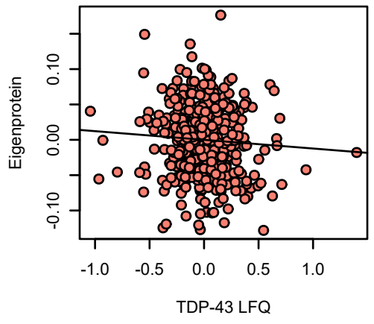

bicor=0.041, p=0.4
cor=0.041, p=0.4
Eigenprotein
0.10
0.00
-0.10
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD (Plaque Burden)

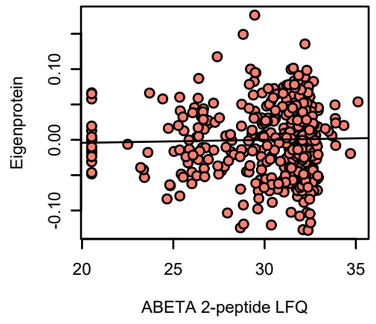

bicor=0.05, p=0.3
cor=0.035, p=0.47
Eigenprotein
0.10
0.00
-0.10
0
1
2
3
4
5
6
Braak (Tangle Extent)

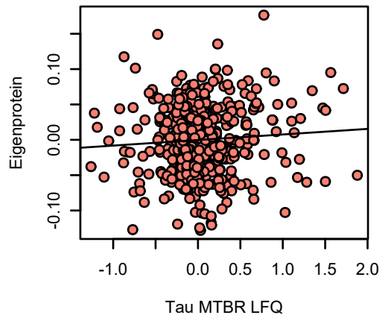

bicor=0.13, p=0.099
cor=0.13, p=0.1
Eigenprotein
0.10
0.00
-0.10
0
1
2
3
4
5
CDR (Cognition; MSSB)

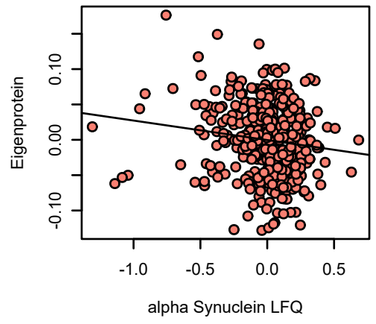

bicor=-0.14, p=0.08
cor=-0.14, p=0.071
Eigenprotein
0.10
0.00
-0.10
0
5
10
15
20
25
30
MMSE (Cognition, Banner)

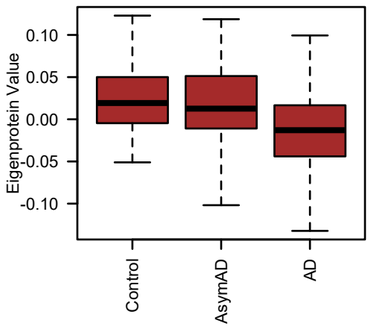

bicor=-0.015, p=0.91
cor=-0.074, p=0.59
Eigenprotein
0.10
0.00
-0.10
40
50
60
70
80
90
100
CASI (Cognition, ACT)

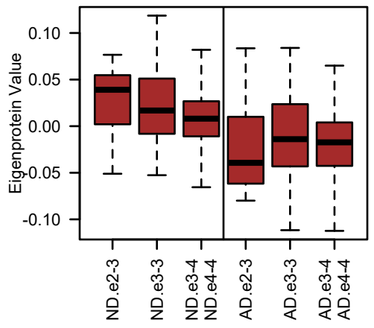

bicor=-0.056, p=0.25
cor=-0.064, p=0.19
Eigenprotein
0.10
0.00
-0.10
-1.0
-0.5
0.0
0.5
1.0
TDP-43 LFQ

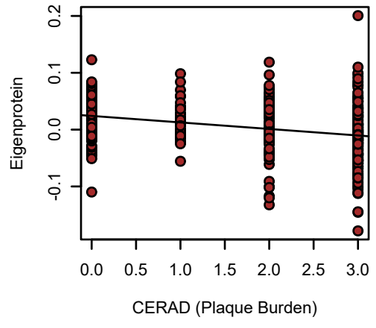

bicor=0.0092, p=0.85
cor=0.027, p=0.58
Eigenprotein
0.10
0.00
-0.10
20
25
30
35
ABETA 2-peptide LFQ

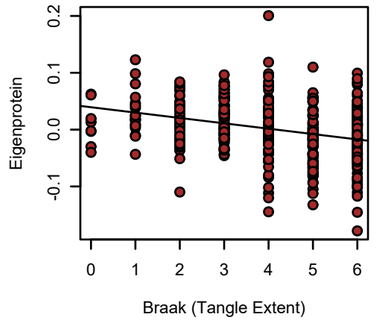

bicor=0.049, p=0.31
cor=0.071, p=0.15
Eigenprotein
0.10
0.00
-0.10
-1.0
0.0
0.5
1.0
1.5
2.0
Tau MTBR LFQ

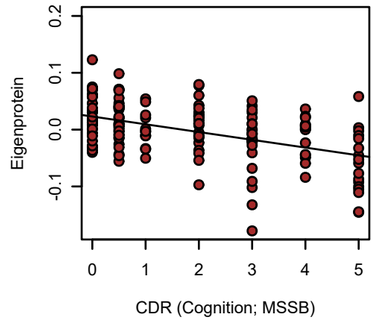

bicor=-0.15, p=0.0021
cor=-0.14, p=0.0041
Eigenprotein
0.10
0.00
-0.10
-1.0
-0.5
0.0
0.5
alpha Synuclein LFQ

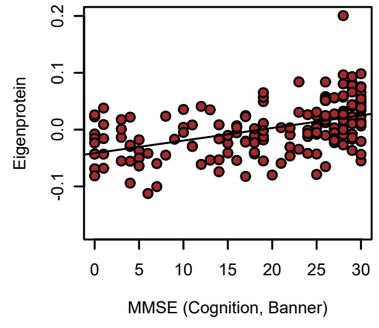

M3 brown
K-W p = 4.4e-12
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

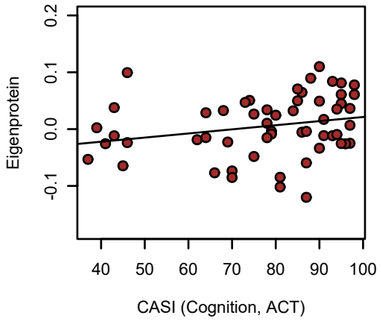

M3 brown
ND K-W p = 0.44 | AD K-W p = 0.58
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

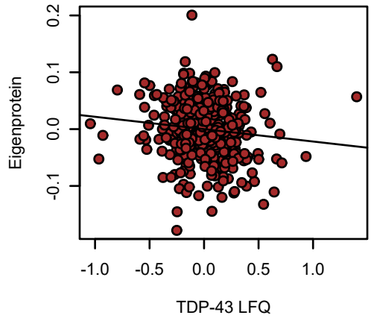

bicor=-0.3, p=5.4e-10
cor=-0.28, p=5.5e-09
Eigenprotein
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD (Plaque Burden)

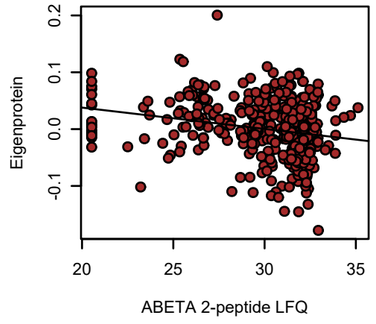

bicor=-0.33, p=6.5e-12
cor=-0.31, p=8.8e-11
Eigenprotein
0.2
0.1
0.0
-0.1
0
1
2
3
4
5
6
Braak (Tangle Extent)

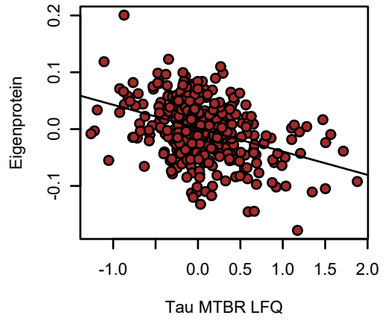

bicor=-0.44, p=5.1e-09
cor=-0.47, p=4.1e-10
Eigenprotein
0.2
0.1
0.0
-0.1
0
1
2
3
4
5
CDR (Cognition; MSSB)

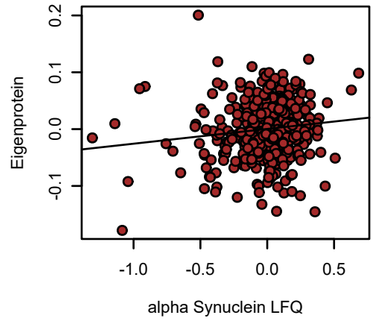

bicor=0.47, p=1.8e-10
cor=0.47, p=1.5e-10
Eigenprotein
0.2
0.1
0.0
-0.1
0
5
10
15
20
25
30
MMSE (Cognition, Banner)

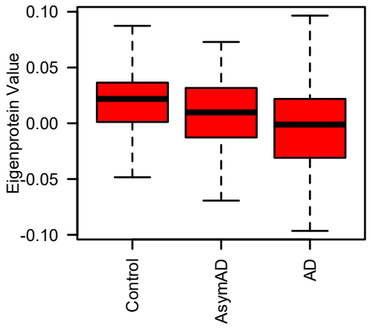

bicor=0.24, p=0.069
cor=0.24, p=0.075
Eigenprotein
0.2
0.1
0.0
-0.1
40
50
60
70
80
90
100
CASI (Cognition, ACT)

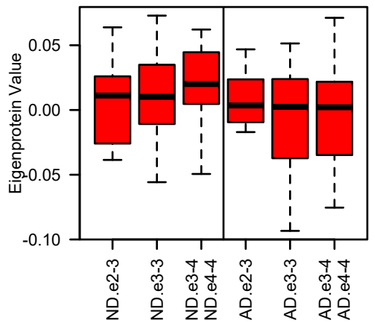

bicor=-0.15, p=0.0018
cor=-0.11, p=0.024
Eigenprotein
0.2
0.1
0.0
-0.1
-1.0
-0.5
0.0
0.5
1.0
TDP-43 LFQ

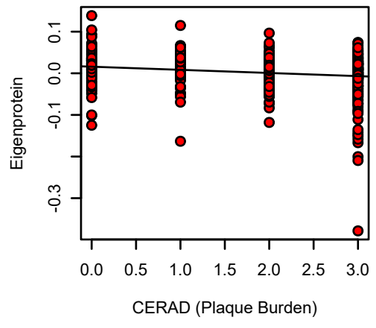

bicor=-0.22, p=7.9e-06
cor=-0.24, p=6.7e-07
Eigenprotein
0.2
0.1
0.0
-0.1
20
25
30
35
ABETA 2-peptide LFQ

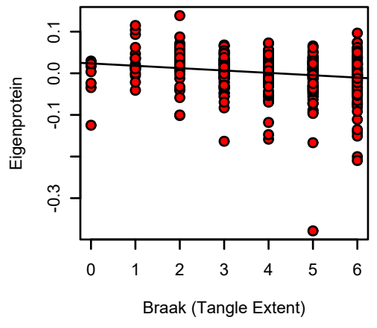

bicor=-0.33, p=4e-12
cor=-0.37, p=4.9e-15
Eigenprotein
0.2
0.1
0.0
-0.1
-1.0
0.0
0.5
1.0
1.5
2.0
Tau MTBR LFQ

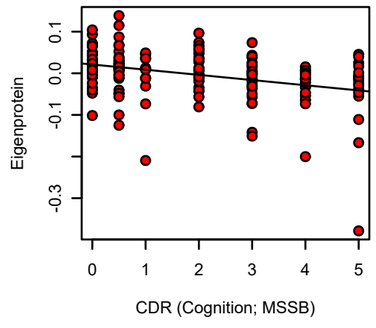

bicor=0.12, p=0.011
cor=0.13, p=0.0077
Eigenprotein
0.2
0.1
0.0
-0.1
-1.0
-0.5
0.0
0.5
alpha Synuclein LFQ

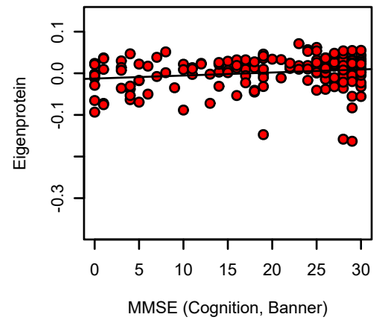

M6 red
K-W p = 2.2e-05
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

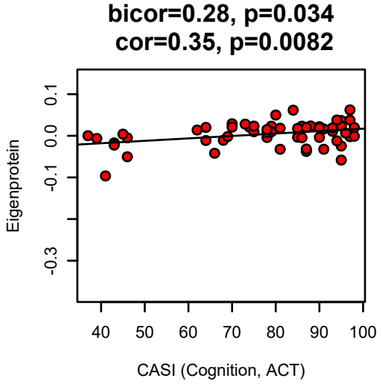

M6 red
ND K-W p = 0.48 | AD K-W p = 0.57
Eigenprotein Value
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

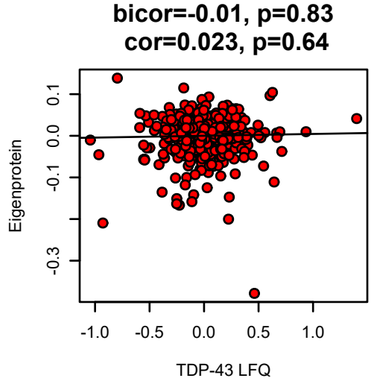

bicor=-0.18, p=3e-04
cor=-0.18, p=0.00021
Eigenprotein
CERAD (Plaque Burden)

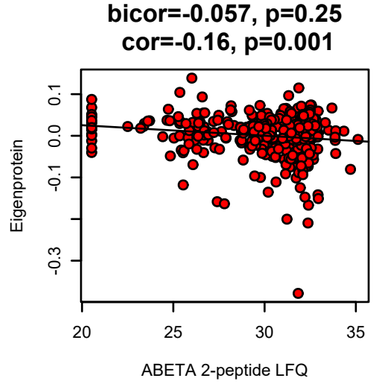

bicor=-0.2, p=3.1e-05
cor=-0.19, p=9.1e-05
Eigenprotein
Braak (Tangle Extent)

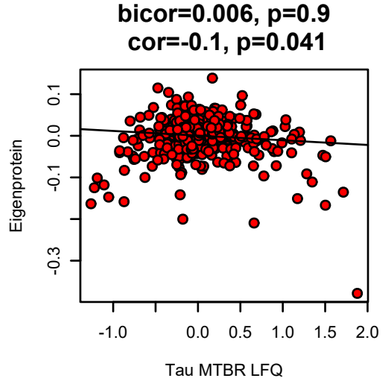

bicor=-0.33, p=2.5e-05
cor=-0.34, p=1.2e-05
Eigenprotein
CDR (Cognition; MSSB)

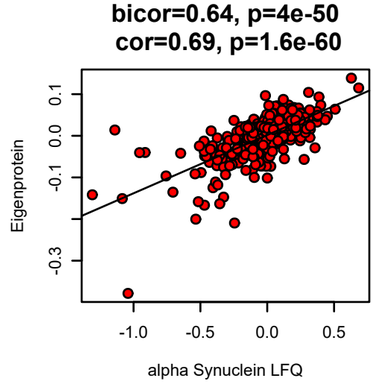

bicor=0.25, p=0.0013
cor=0.18, p=0.02
Eigenprotein
MMSE (Cognition, Banner)

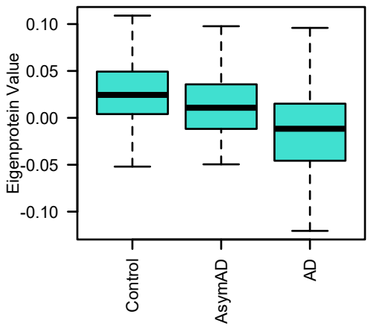

bicor=0.28, p=0.034
cor=0.35, p=0.0082
Eigenprotein
CASI (Cognition, ACT)

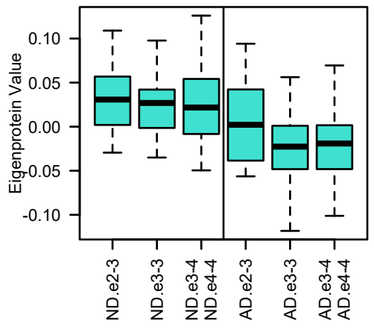

bicor=-0.01, p=0.83
cor=0.023, p=0.64
Eigenprotein
TDP-43 LFQ

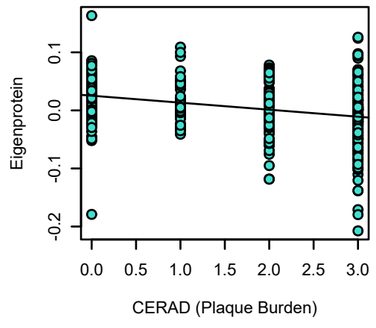

bicor=-0.057, p=0.25
cor=-0.16, p=0.001
Eigenprotein
ABETA 2-peptide LFQ

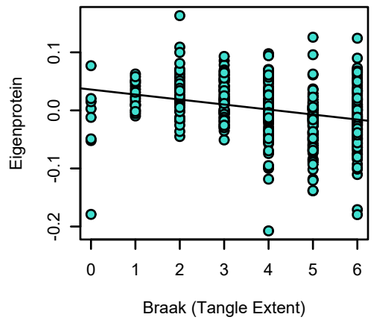

bicor=0.006, p=0.9
cor=-0.1, p=0.041
Eigenprotein
Tau MTBR LFQ

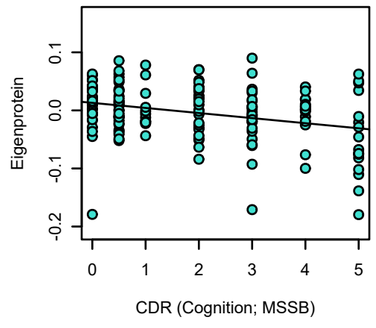

bicor=0.64, p=4e-50
cor=0.69, p=1.6e-60
Eigenprotein
alpha Synuclein LFQ

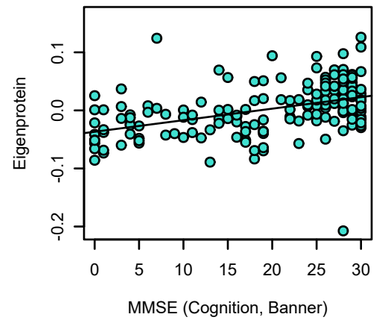

M1 turquoise
K-W p = 2.8e-11
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

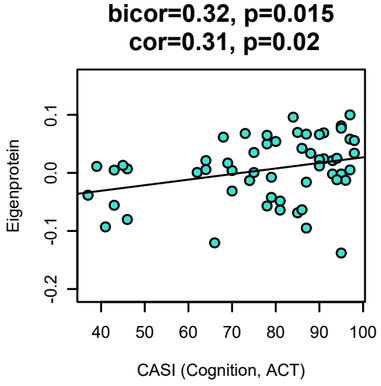

M1 turquoise
ND K-W p = 0.32 | AD K-W p = 0.17
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

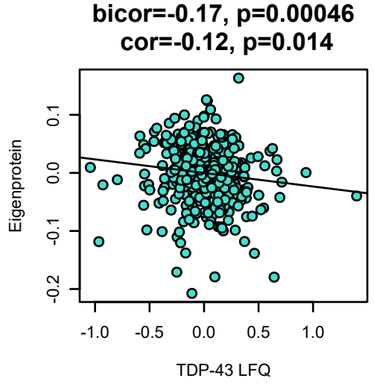

bicor=-0.31, p=5e-11
cor=-0.29, p=1.5e-09
Eigenprotein
CERAD (Plaque Burden)

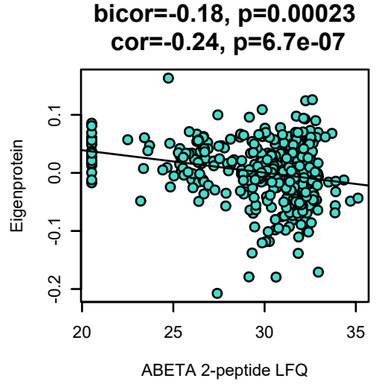

bicor=-0.33, p=3.1e-12
cor=-0.28, p=5.5e-09
Eigenprotein
Braak (Tangle Extent)

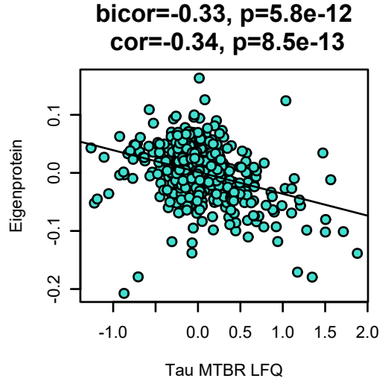

bicor=-0.28, p=0.00029
cor=-0.31, p=7e-05
Eigenprotein
CDR (Cognition; MSSB)

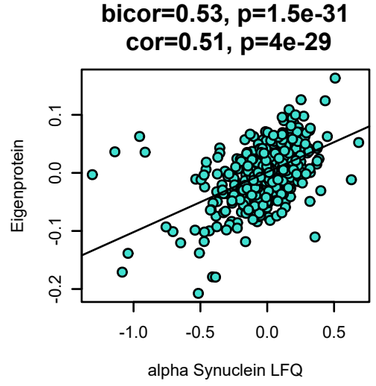

bicor=0.47, p=9.8e-11
cor=0.44, p=2.7e-09
Eigenprotein
MMSE (Cognition, Banner)

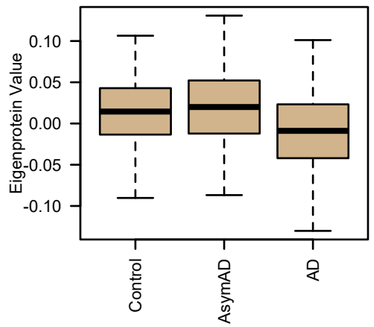

bicor=0.32, p=0.015
cor=0.31, p=0.02
Eigenprotein
CASI (Cognition, ACT)

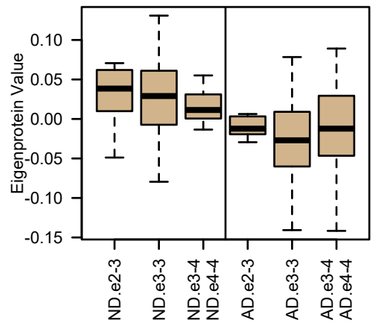

bicor=-0.17, p=0.00046
cor=-0.12, p=0.014
Eigenprotein
TDP-43 LFQ

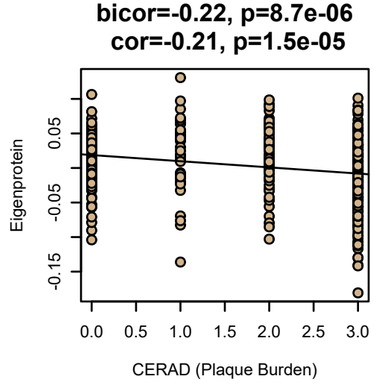

bicor=-0.18, p=0.00023
cor=-0.24, p=6.7e-07
Eigenprotein
ABETA 2-peptide LFQ

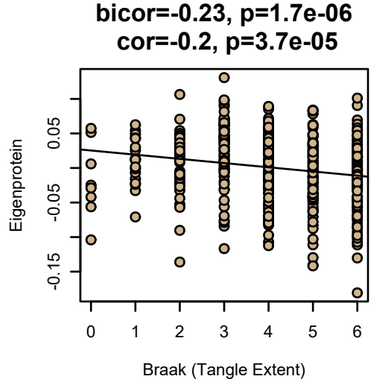

bicor=-0.33, p=5.8e-12
cor=-0.34, p=8.5e-13
Eigenprotein
Tau MTBR LFQ

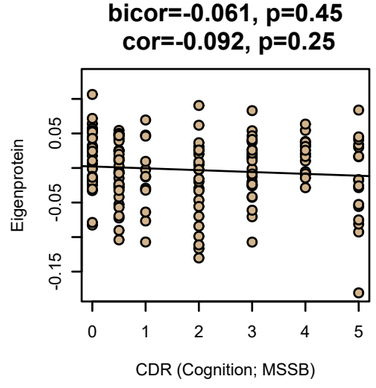

bicor=0.53, p=1.5e-31
cor=0.51, p=4e-29
Eigenprotein
alpha Synuclein LFQ

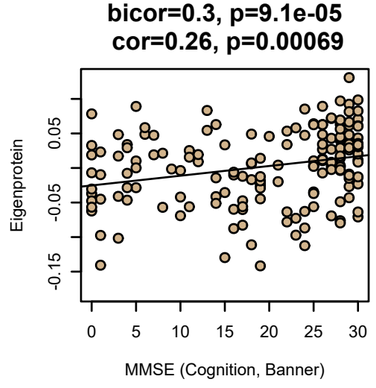

M12 tan
K-W p = 1.3e-06
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

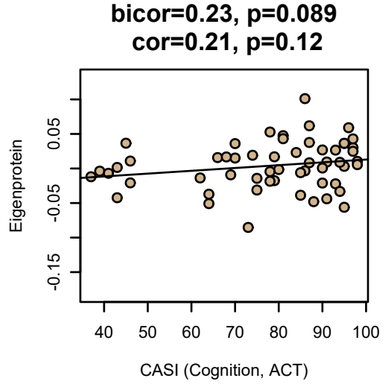

M12 tan
ND K-W p = 0.27 | AD K-W p = 0.21
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
-0.15
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

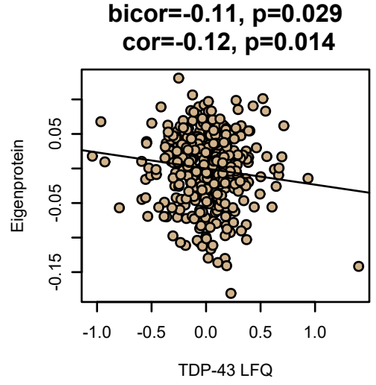

bicor=-0.22, p=8.7e-06
cor=-0.21, p=1.5e-05
Eigenprotein
0.05
-0.05
-0.15
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD (Plaque Burden)

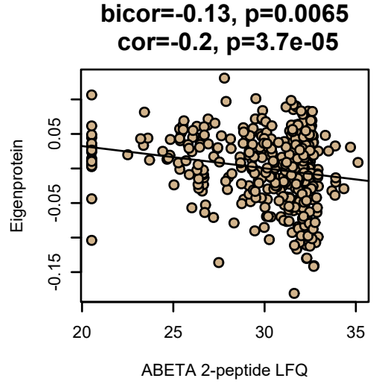

bicor=-0.23, p=1.7e-06
cor=-0.2, p=3.7e-05
Eigenprotein
0.05
-0.05
-0.15
0
1
2
3
4
5
6
Braak (Tangle Extent)

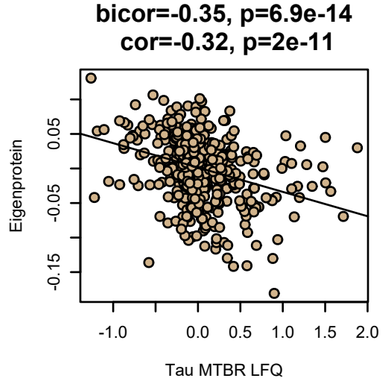

bicor=-0.061, p=0.45
cor=-0.092, p=0.25
Eigenprotein
0.05
-0.05
-0.15
0
1
2
3
4
5
CDR (Cognition; MSSB)

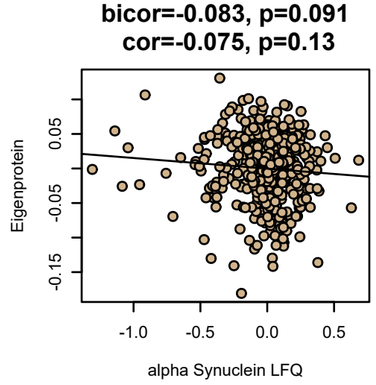

bicor=0.3, p=9.1e-05
cor=0.26, p=0.00069
Eigenprotein
0.05
-0.05
-0.15
0
5
10
15
20
25
30
MMSE (Cognition, Banner)

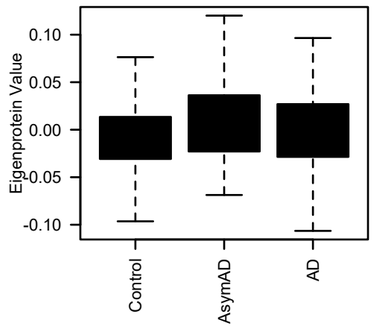

bicor=0.23, p=0.089
cor=0.21, p=0.12
Eigenprotein
0.05
-0.05
-0.15
40
50
60
70
80
90
100
CASI (Cognition, ACT)

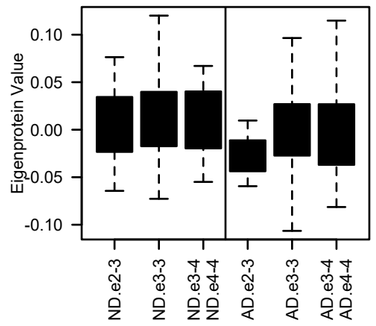

bicor=-0.11, p=0.029
cor=-0.12, p=0.014
Eigenprotein
0.05
-0.05
-0.15
-1.0
-0.5
0.0
0.5
1.0
TDP-43 LFQ

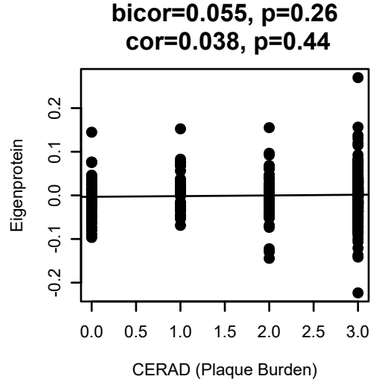

bicor=-0.13, p=0.0065
cor=-0.2, p=3.7e-05
Eigenprotein
0.05
-0.05
-0.15
20
25
30
35
ABETA 2-peptide LFQ

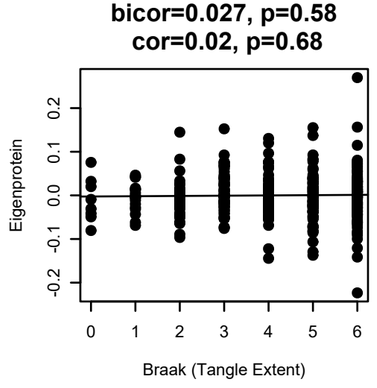

bicor=-0.35, p=6.9e-14
cor=-0.32, p=2e-11
Eigenprotein
0.05
-0.05
-0.15
-1.0
0.0
0.5
1.0
1.5
2.0
Tau MTBR LFQ

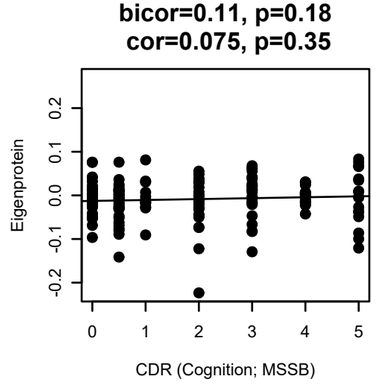

bicor=-0.083, p=0.091
cor=-0.075, p=0.13
Eigenprotein
0.05
-0.05
-0.15
-1.0
-0.5
0.0
0.5
alpha Synuclein LFQ

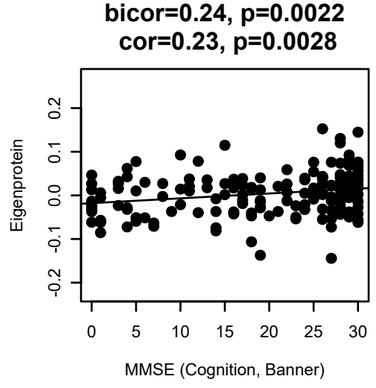

M7 black
K-W p = 0.18
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

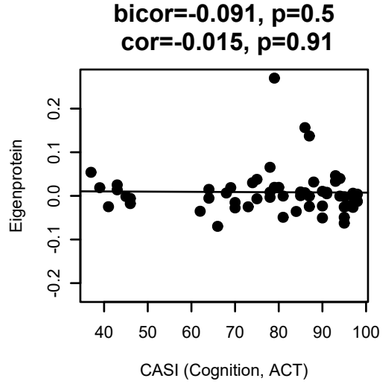

M7 black
ND K-W p = 0.59 | AD K-W p = 0.47
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

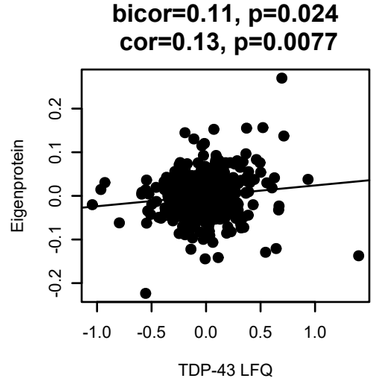

bicor=0.055, p=0.26
cor=0.038, p=0.44
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD (Plaque Burden)

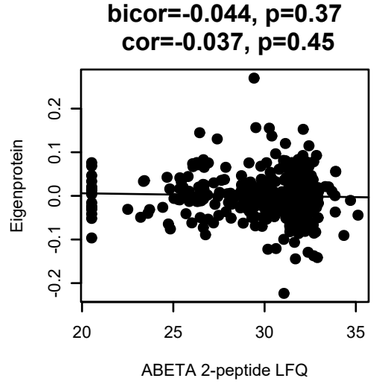

bicor=0.027, p=0.58
cor=0.02, p=0.68
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
1
2
3
4
5
6
Braak (Tangle Extent)

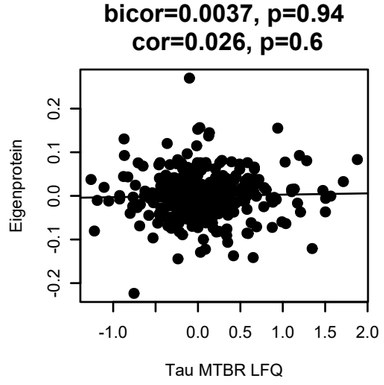

bicor=0.11, p=0.18
cor=0.075, p=0.35
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
1
2
3
4
5
CDR (Cognition; MSSB)

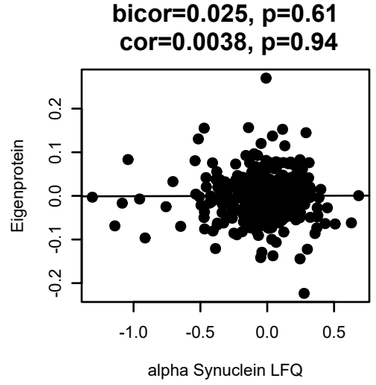

bicor=0.24, p=0.0022
cor=0.23, p=0.0028
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
5
10
15
20
25
30
MMSE (Cognition, Banner)

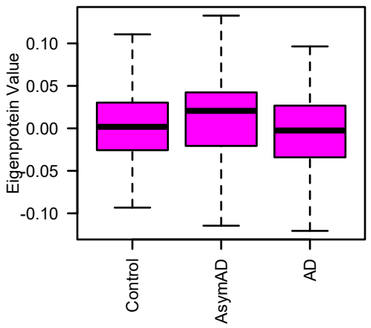

bicor=-0.091, p=0.5
cor=-0.015, p=0.91
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
40
50
60
70
80
90
100
CASI (Cognition, ACT)

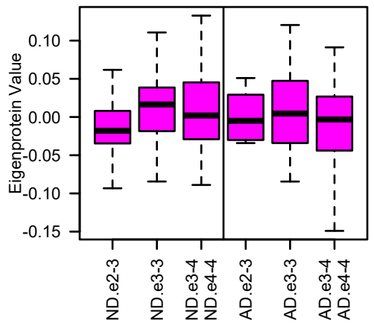

bicor=0.11, p=0.024
cor=0.13, p=0.0077
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-1.0
-0.5
0.0
0.5
1.0
TDP-43 LFQ

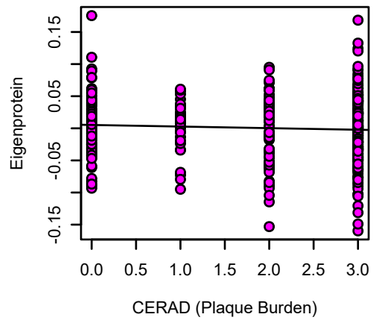

bicor=-0.044, p=0.37
cor=-0.037, p=0.45
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
20
25
30
35
ABETA 2-peptide LFQ

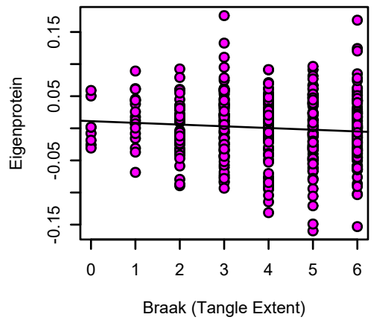

bicor=0.0037, p=0.94
cor=0.026, p=0.6
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-1.0
0.0
0.5
1.0
1.5
2.0
Tau MTBR LFQ

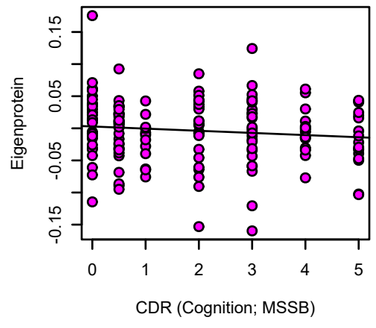

bicor=0.025, p=0.61
cor=0.0038, p=0.94
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-1.0
-0.5
0.0
0.5
alpha Synuclein LFQ

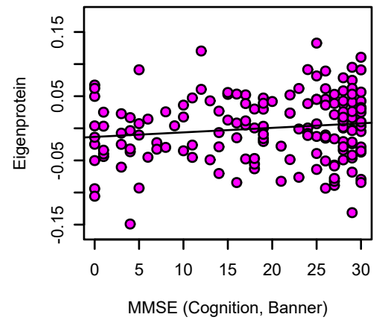

M9 magenta
K-W p = 0.05
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

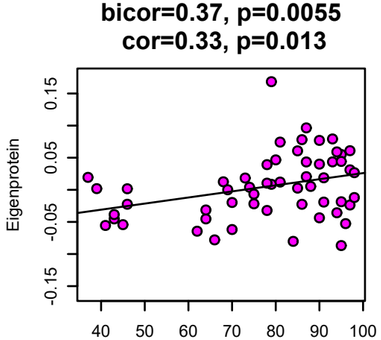

M9 magenta
ND K-W p = 0.35 | AD K-W p = 0.41
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
-0.15
ND.e2-3
ND.e3-3
ND.e3-4
ND.e4-4
AD.e2-3
AD.e3-3
AD.e3-4
AD.e4-4

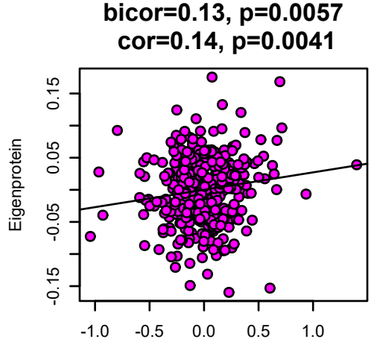

bicor=-0.055, p=0.26
cor=-0.06, p=0.22
Eigenprotein
0.15
0.05
-0.05
-0.15
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD (Plaque Burden)

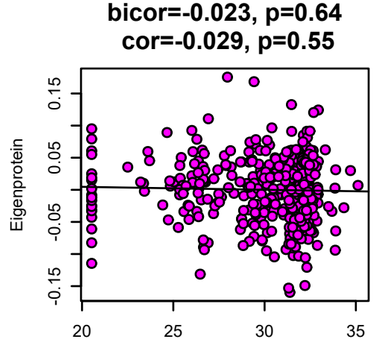

bicor=-0.094, p=0.054
cor=-0.087, p=0.075
Eigenprotein
0.15
0.05
-0.05
-0.15
0
1
2
3
4
5
6
Braak (Tangle Extent)

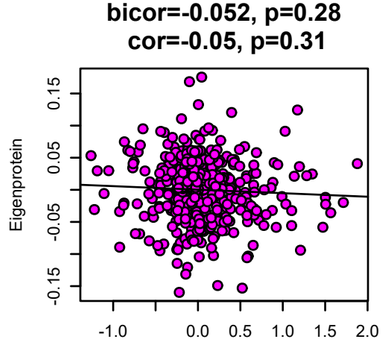

bicor=-0.1, p=0.2
cor=-0.12, p=0.13
Eigenprotein
0.15
0.05
-0.05
-0.15
0
1
2
3
4
5
CDR (Cognition; MSSB)

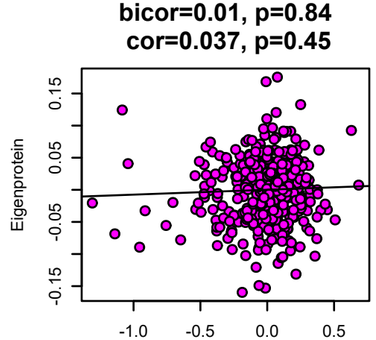

bicor=0.13, p=0.095
cor=0.14, p=0.071
Eigenprotein
0.15
0.05
-0.05
-0.15
0
5
10
15
20
25
30
MMSE (Cognition, Banner)


bicor=0.37, p=0.0055
cor=0.33, p=0.013
Eigenprotein
0.15
0.05
-0.05
-0.15
40
50
60
70
80
90
100
CASI (Cognition, ACT)


bicor=0.13, p=0.0057
cor=0.14, p=0.0041
Eigenprotein
0.15
0.05
-0.05
-0.15
-1.0
-0.5
0.0
0.5
1.0
TDP-43 LFQ

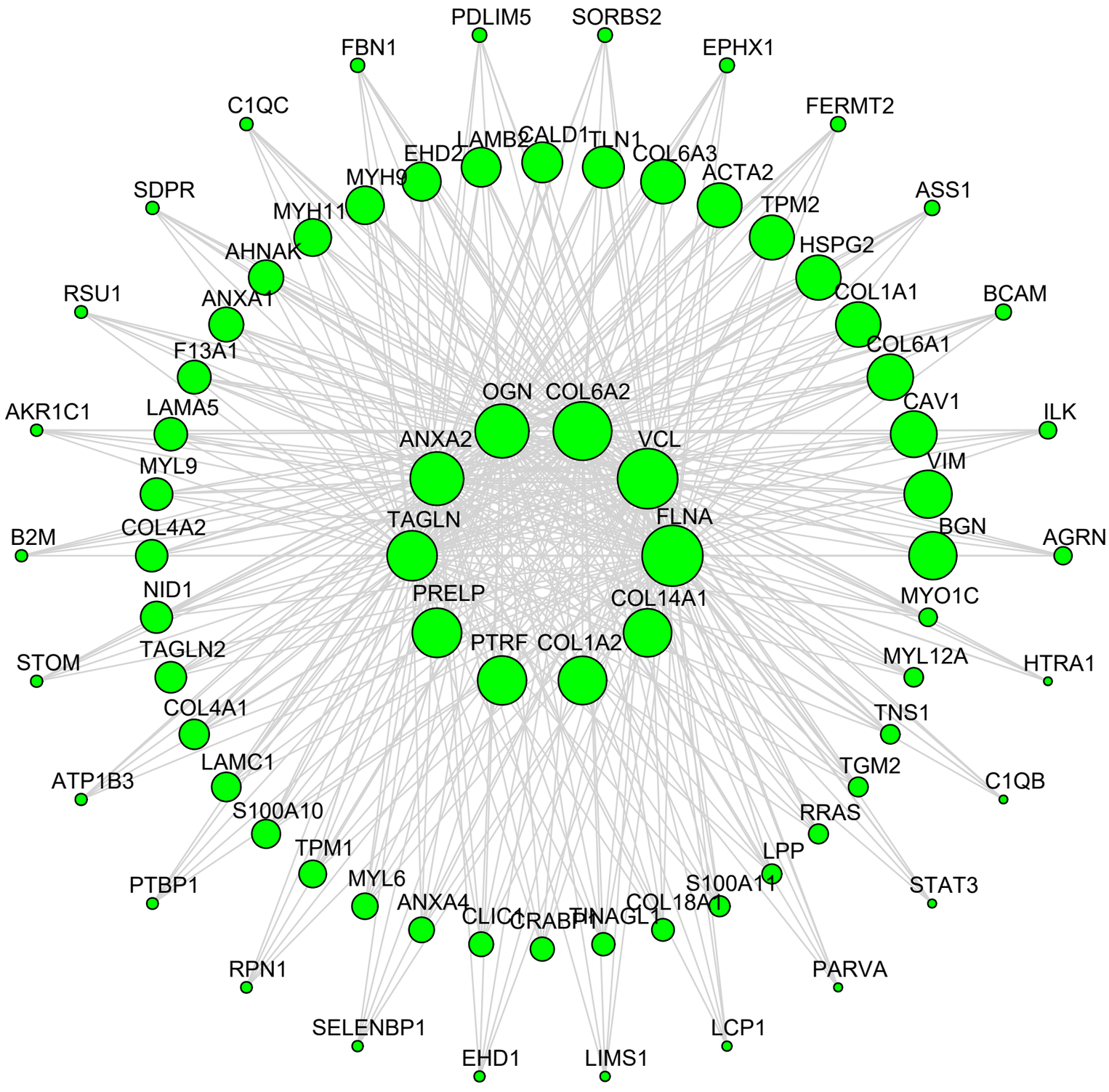

bicor=-0.023, p=0.64
cor=-0.029, p=0.55
Eigenprotein
0.15
0.05
-0.05
-0.15
20
25
30
35
ABETA 2-peptide LFQ


bicor=-0.052, p=0.28
cor=-0.05, p=0.31
Eigenprotein
0.15
0.05
-0.05
-0.15
-1.0
0.0
0.5
1.0
1.5
2.0
Tau MTBR LFQ

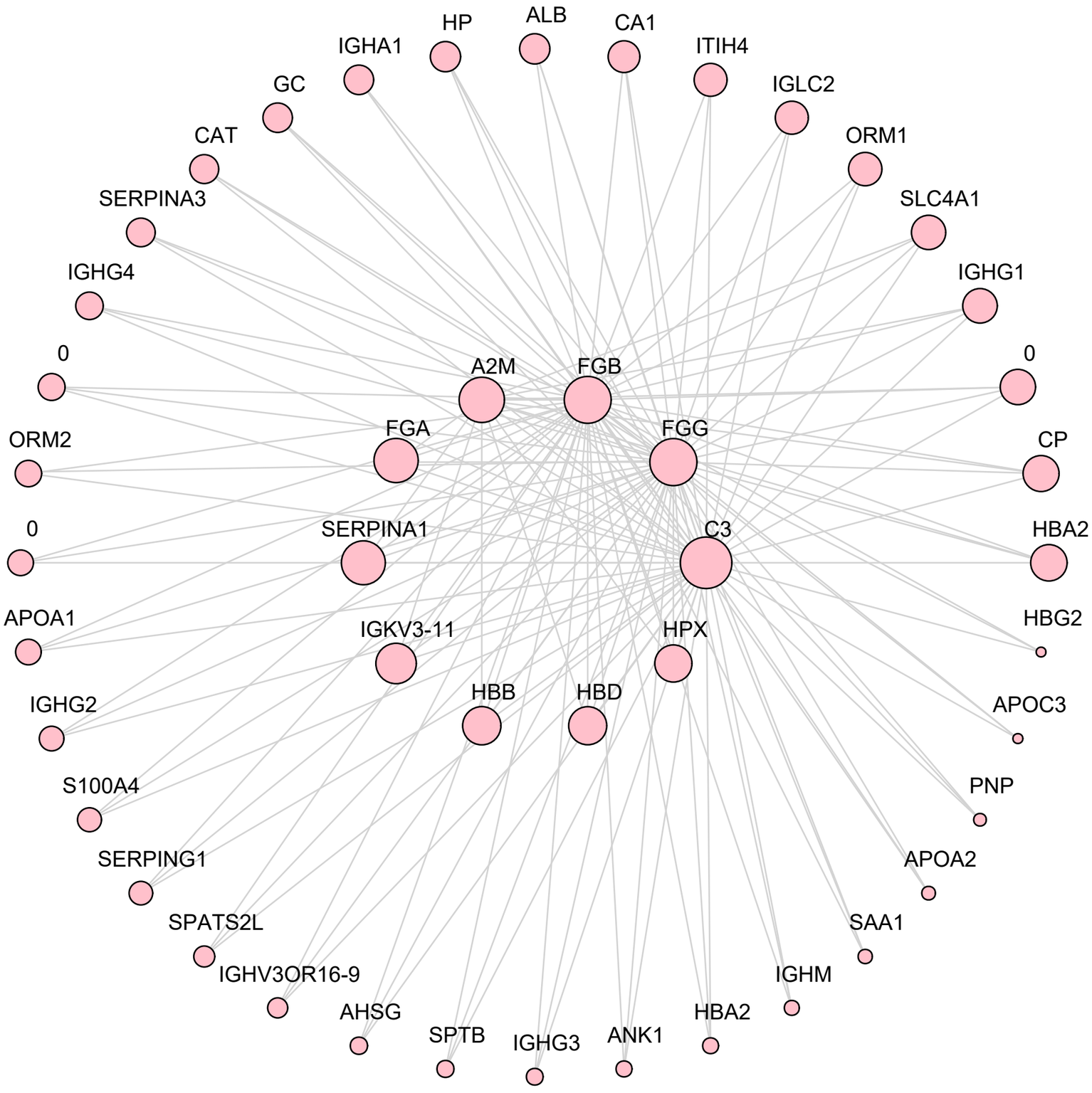

bicor=0.01, p=0.84
cor=0.037, p=0.45
Eigenprotein
0.15
0.05
-0.05
-0.15
-1.0
-0.5
0.0
0.5
alpha Synuclein LFQ

Supplementary Figure 1. AD Network Module Phenotype Correlations. Each module eigenprotein was assessed for group differences by case status and *APOE* genotype, and correlated to genetic, neuropathological, cognitive/functional, and molecular traits (*n*=419 independent case sample traits after network connectivity outlier removal except for cognitive measures, where *n*=167 MMSE, *n*=159 CDR, and *n*=56 CASI). *APOE* genotype information is from the Banner and BLSA cohorts. Control (*n*=91) and AsymAD (*n*=98) cases were grouped into non-demented (ND) in the *APOE* analysis for sufficient statistical power (ND: *n*=16 E2/3, *n*=68 E3/3, *n*=22 E3/4 and E4/4; AD: *n*=8 E2/3, *n*=38 E3/3, *n*=54 E3/4 and E4/4). E2/2 (*n*=1 AsymAD) and E2/4 (*n*=1 AsymAD) were excluded from the analysis. Eigenprotein differences by case status or *APOE* genotype were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Statistical significance at $p < 0.05$ for case status is highlighted in red. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

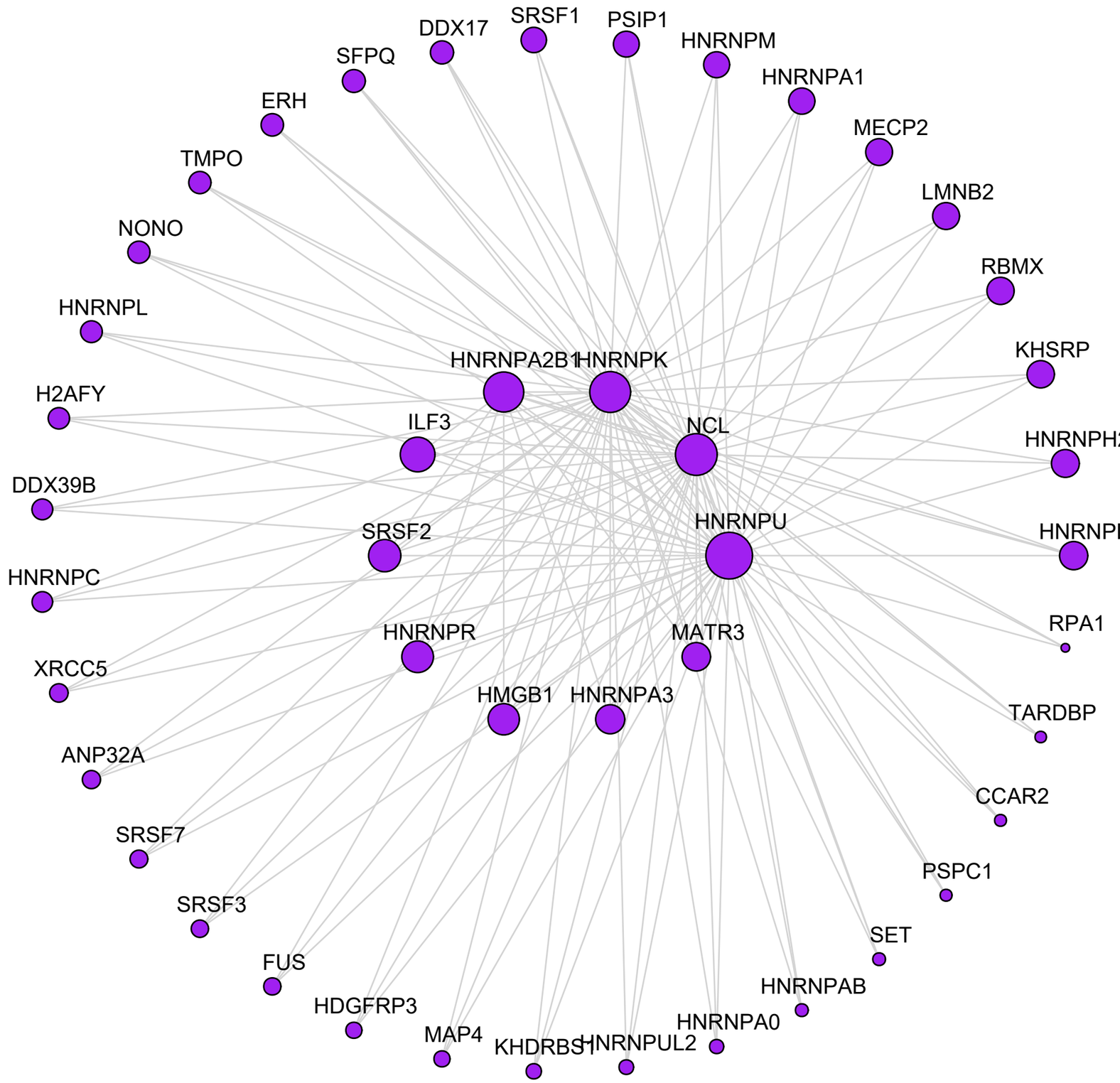
M5 Extracellular Matrix



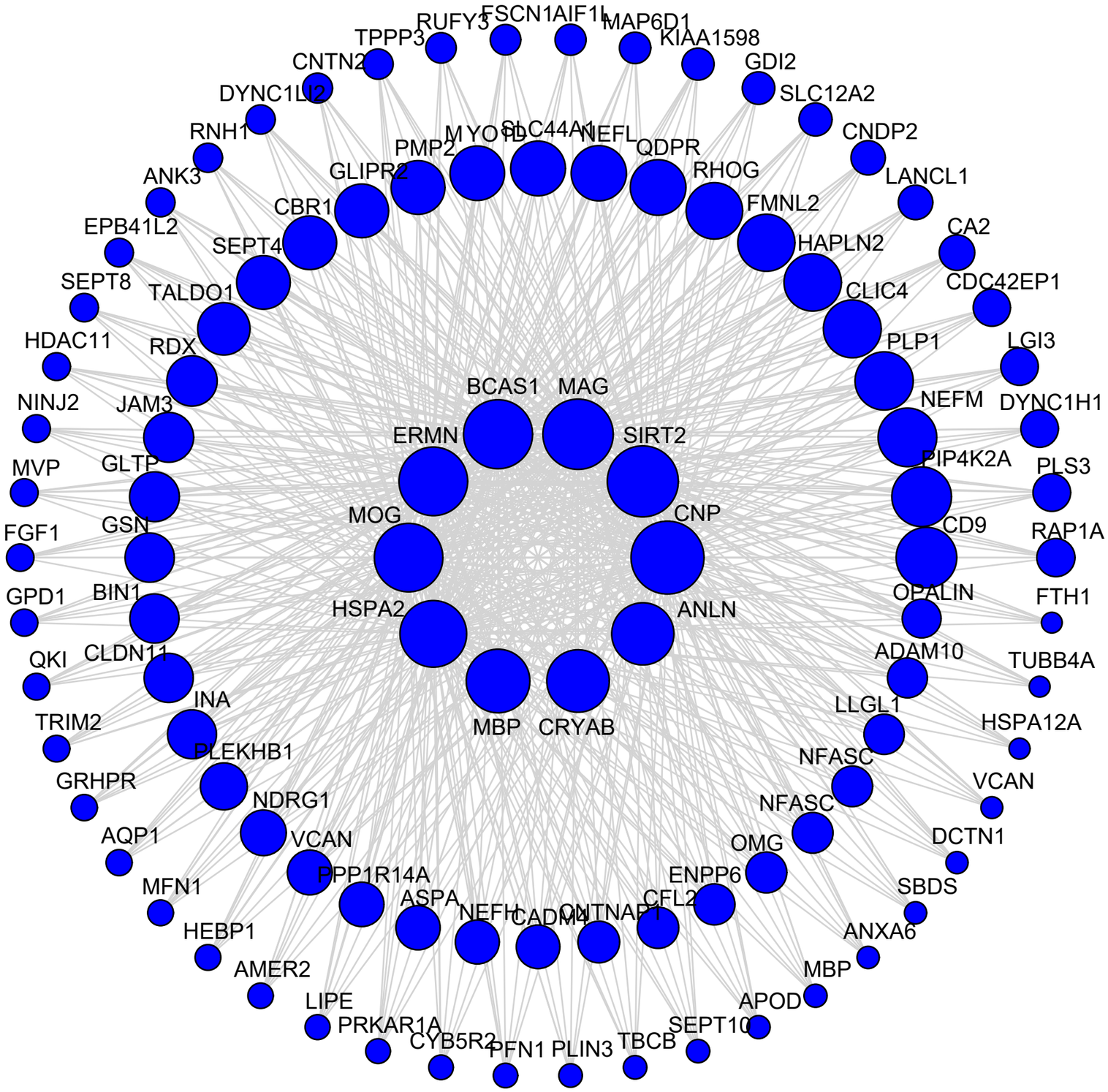
M8 Blood


HP
ALB
CA1
IGHA1
ITIH4
GC
IGLC2
CAT
ORM1
SERPINA3
SLC4A1
IGHG4
IGHG1
0
A2M
FGB
0
FGA
FGG
ORM2
CP
0
SERPINA1
C3
HBA2
APOA1
IGKV3-11
HPX
HBG2
IGHG2
HBB
HBD
APOC3
S100A4
PNP
SERPING1
APOA2
SPATS2L
SAA1
IGHV3OR16-9
IGHM
AHSG
HBA2
SPTB
IGHG3
ANK1

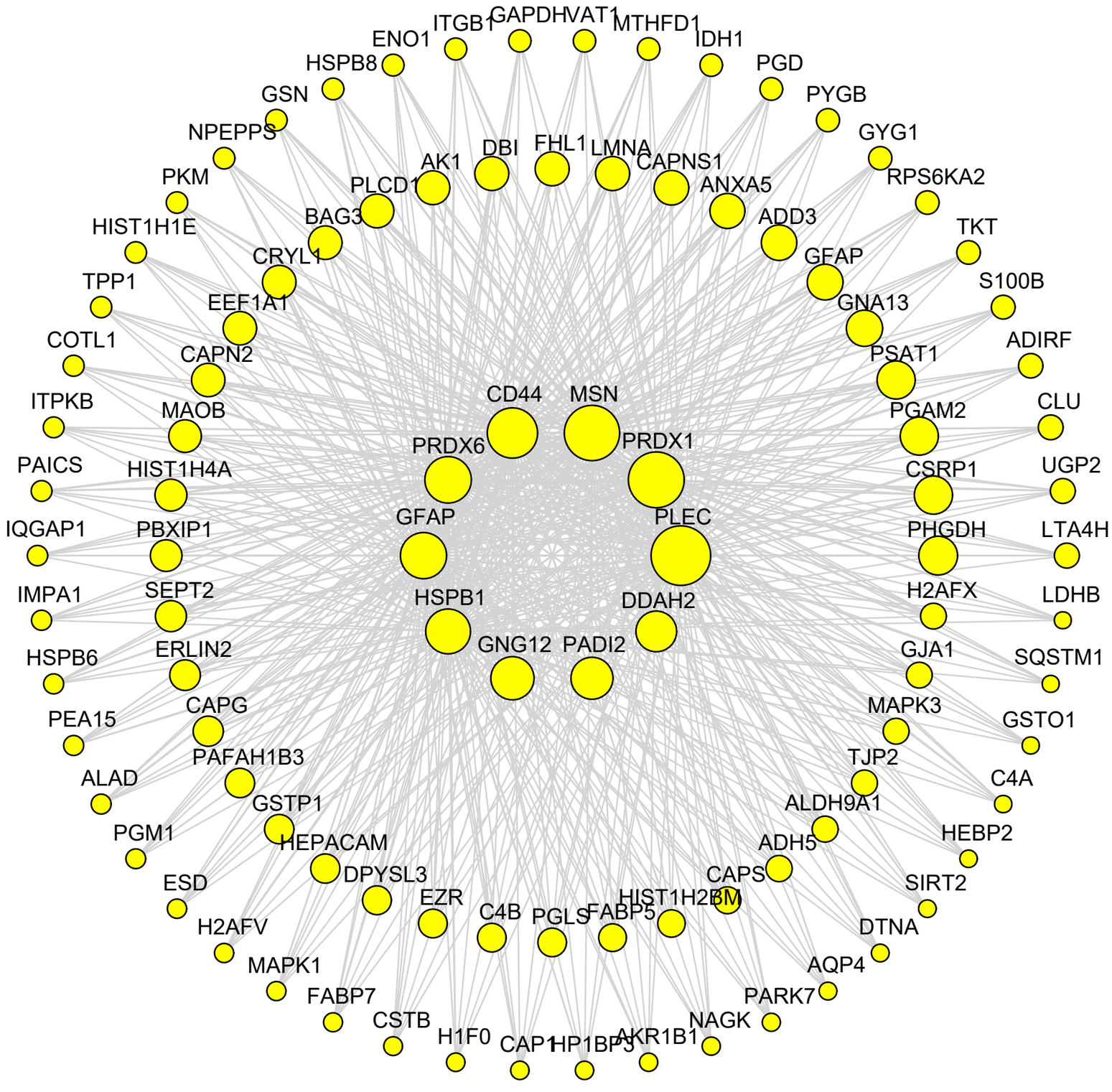
M10 RNA Binding/Splicing



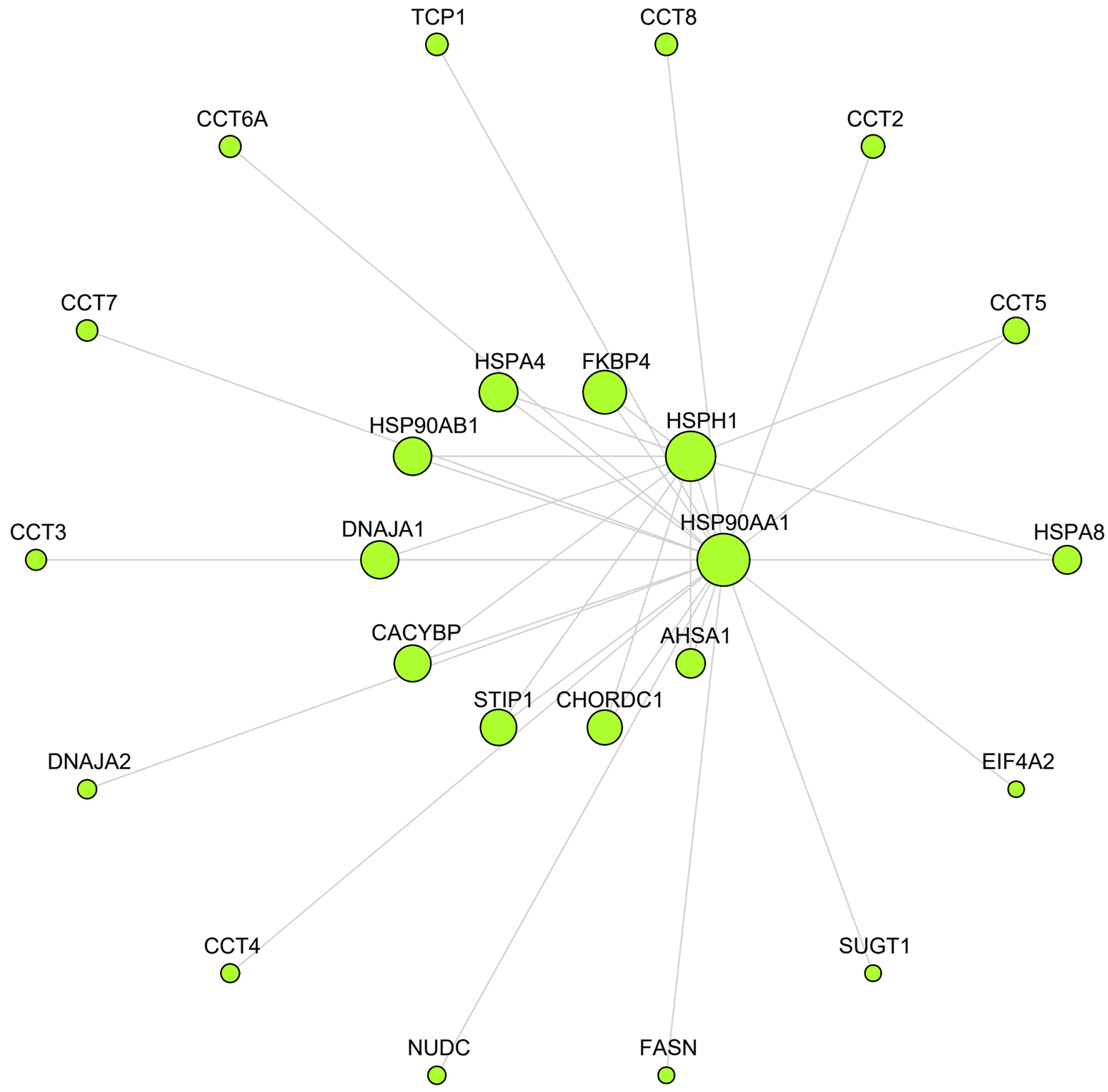
M2 Myelin/Oligodendrocyte



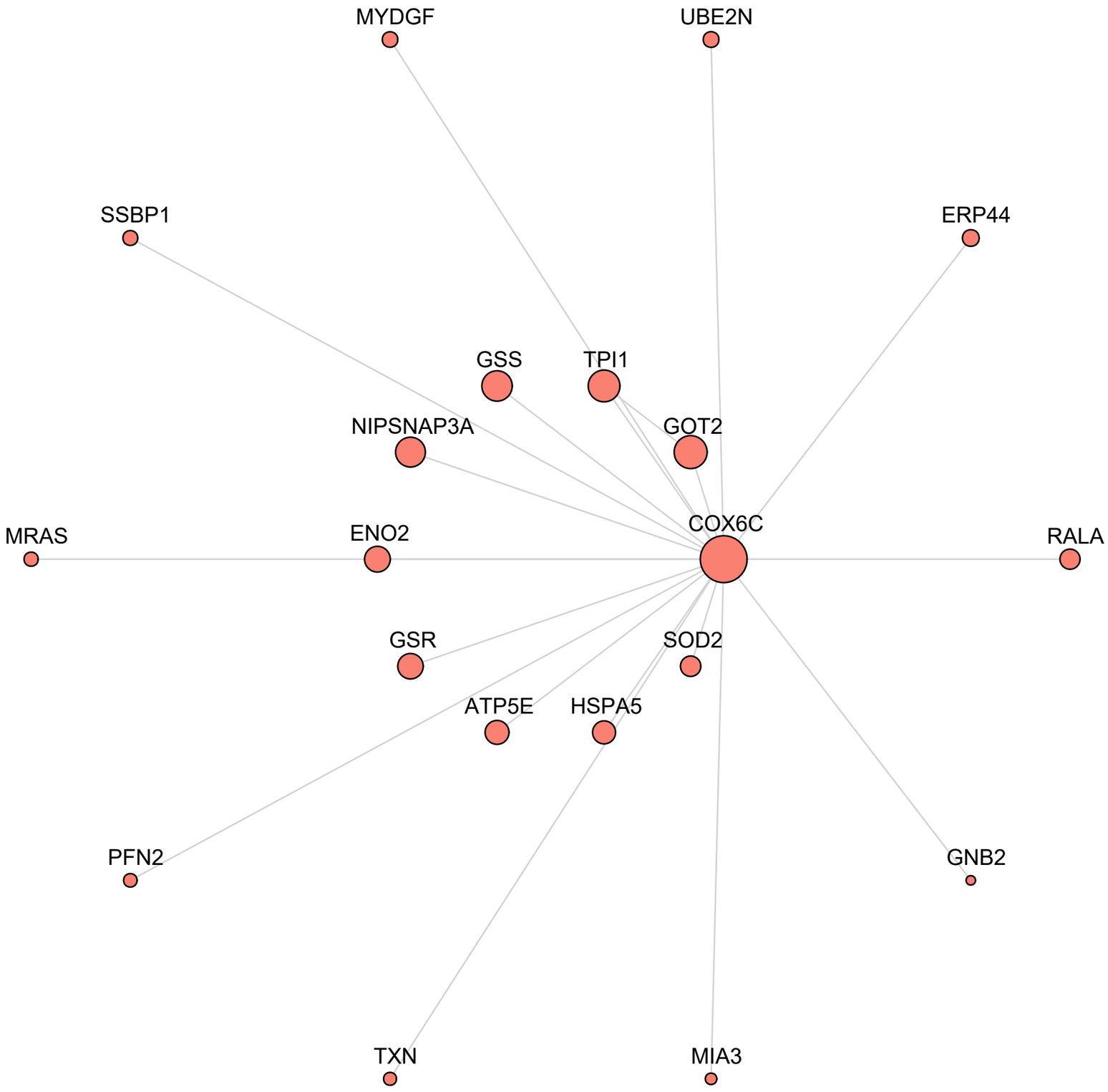
M4 Sugar Metabolism



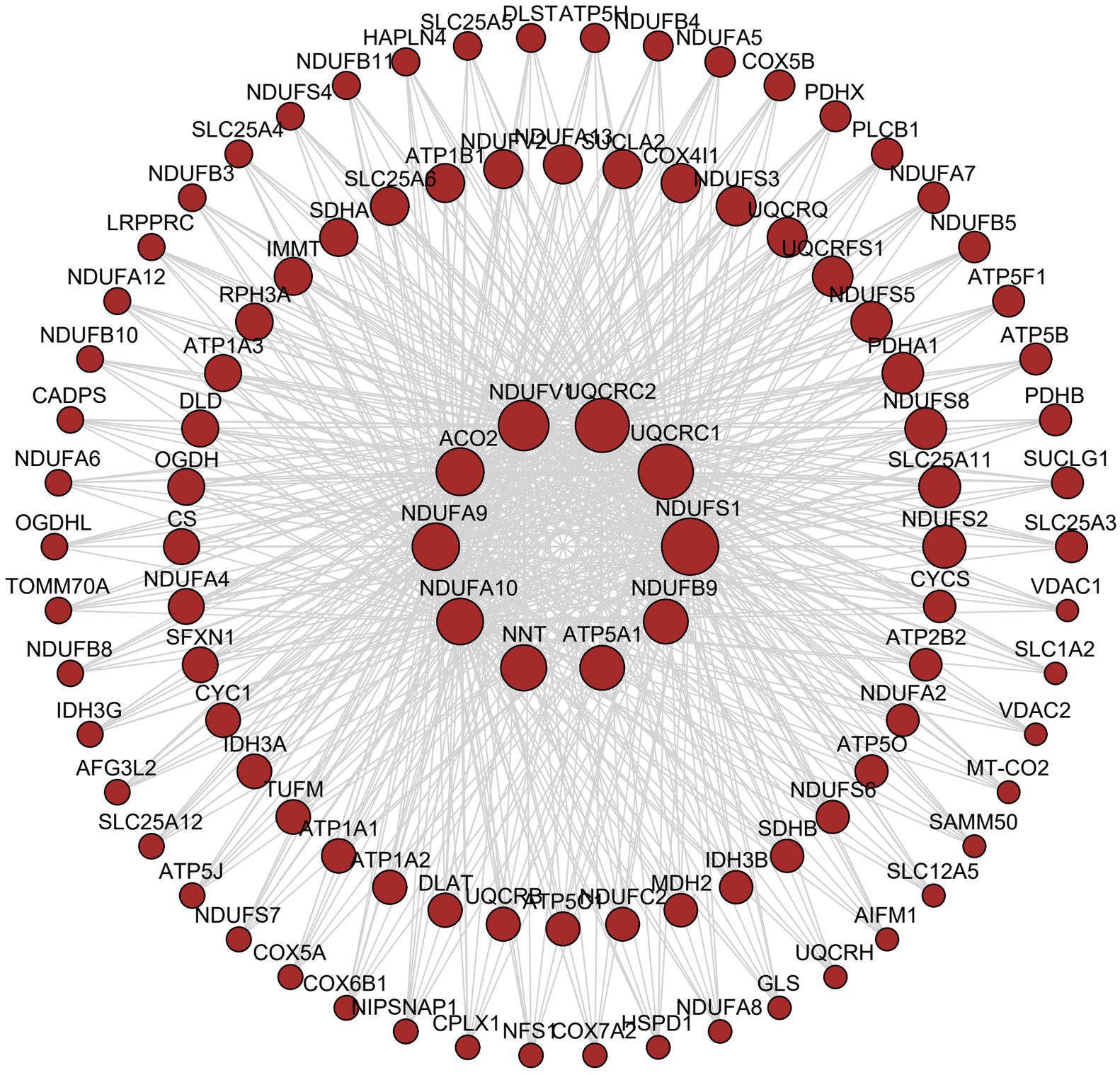
M11 Chaperone/Protein Folding



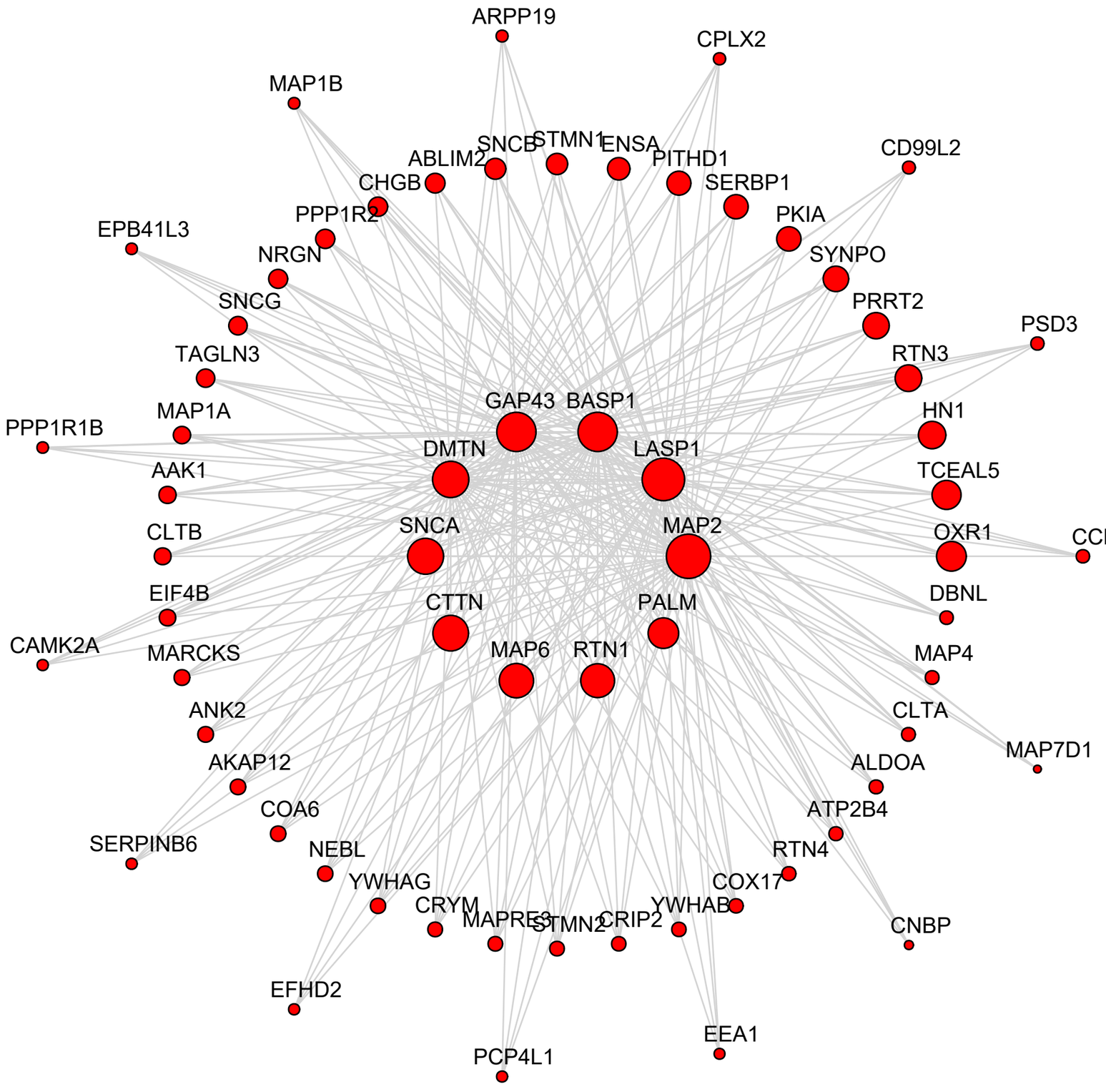
M13 Unknown


MYDGF
UBE2N
SSBP1
ERP44
GSS
TPI1
NIPSNAP3A
GOT2
MRAS
ENO2
COX6C
RALA
GSR
SOD2
ATP5E
HSPA5
PFN2
GNB2
TXN
MIA3

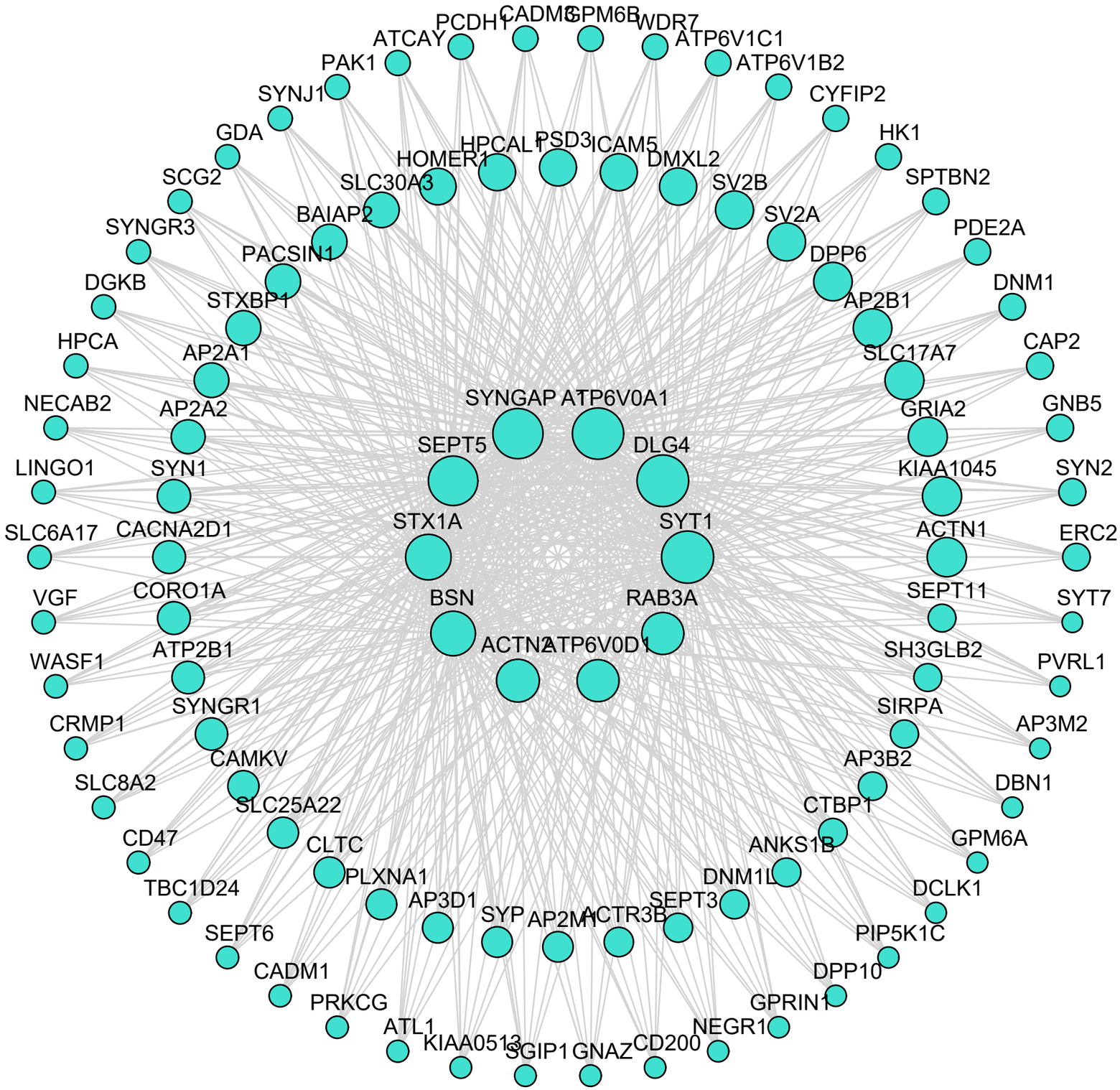
M3 Mitochondrial



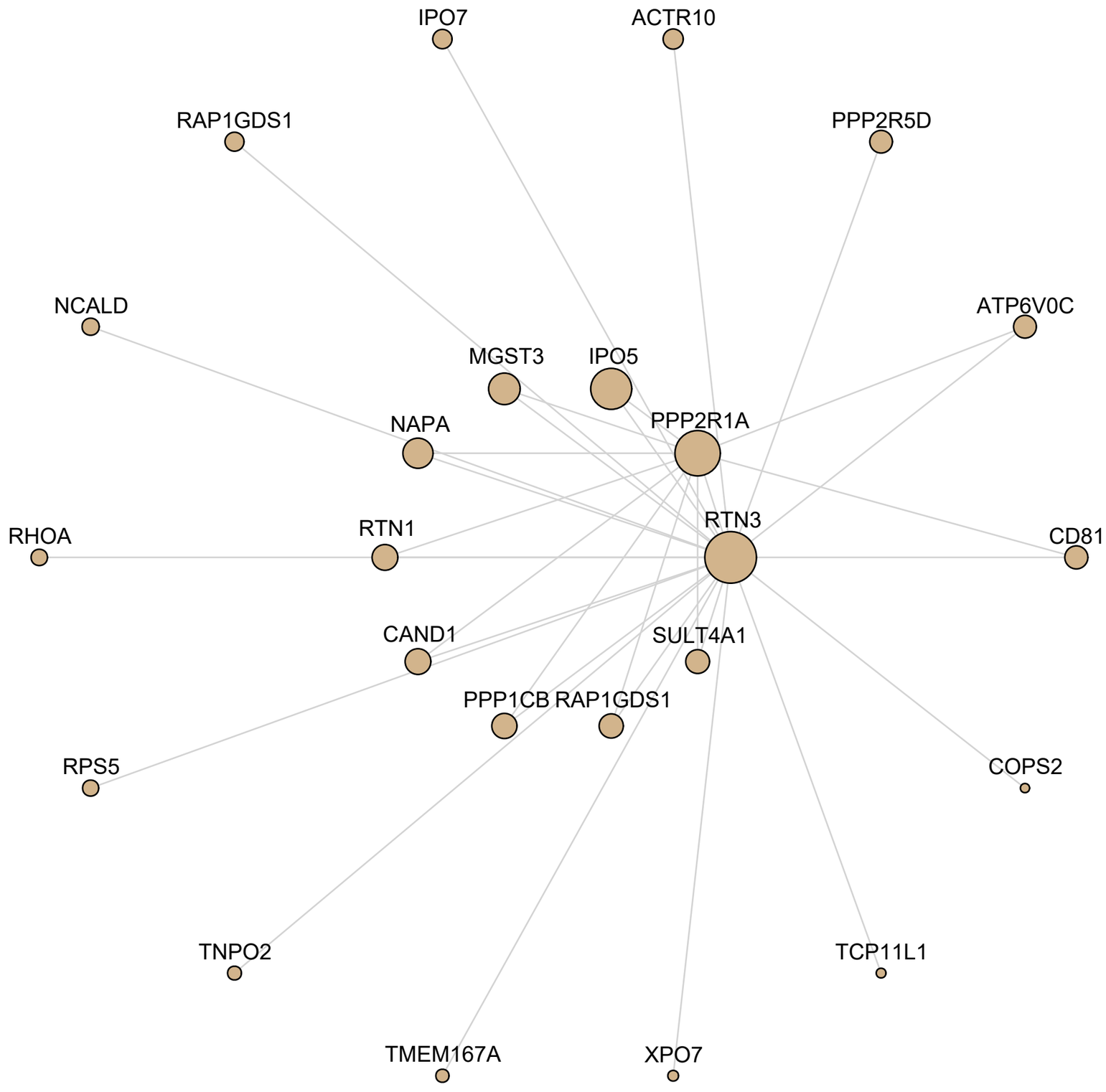
M6 Cytoskeleton



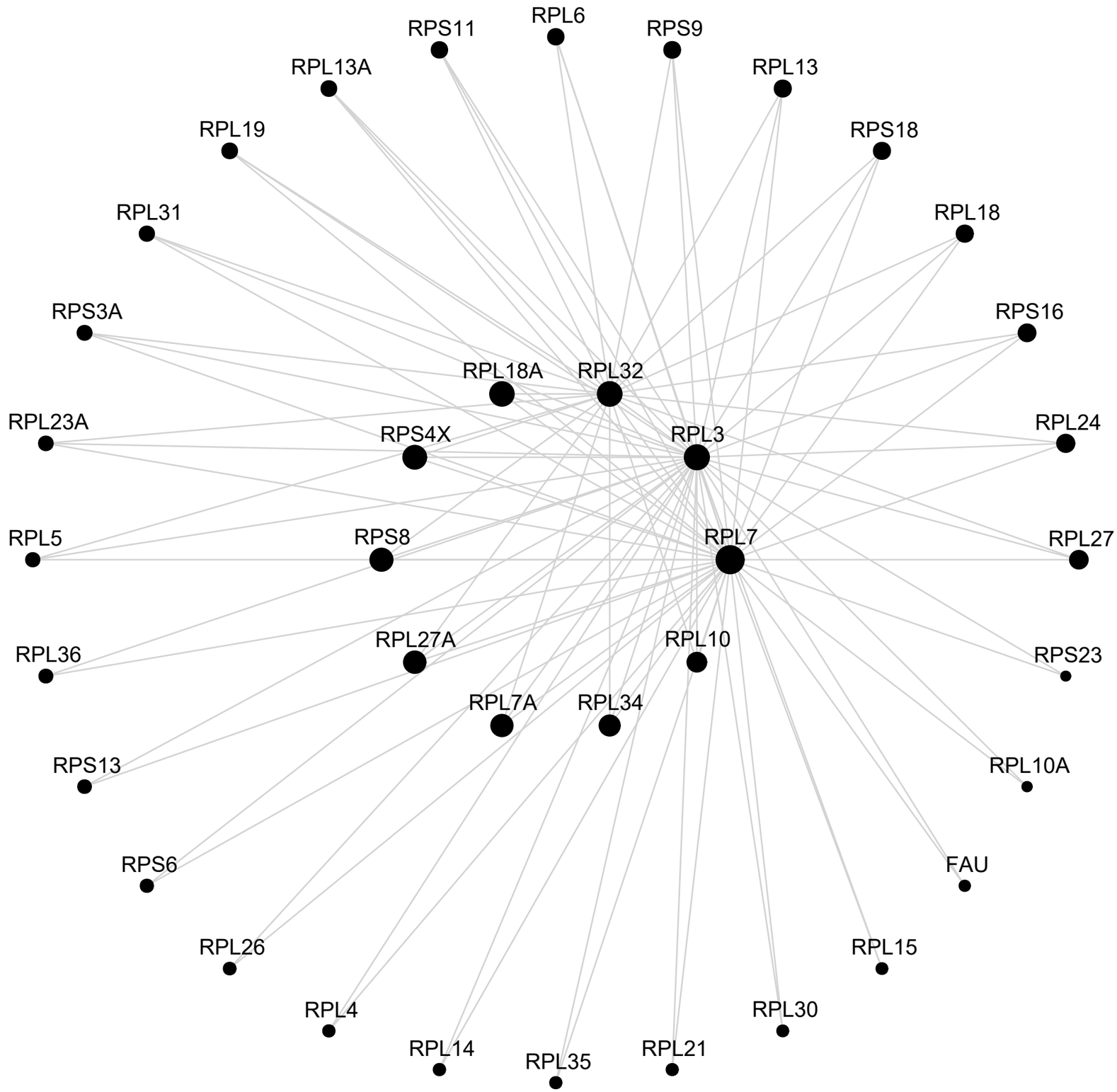
M1 Synapse


PCDH1
CADM3
GPM6B
WDR7
ATP6V1C1
ATCAY
PAK1
ATP6V1B2
SYNJ1
CYFIP2
GDA
HK1
HPCAL1
PSD3
ICAM5
HOMER1
DMXL2
SCG2
SLC30A3
SV2B
SPTBN2
BAIAP2
SV2A
SYNGR3
PDE2A
PACSIN1
DPP6
DGKB
DNM1
STXBP1
AP2B1
HPCA
AP2A1
SLC17A7
CAP2
NECAB2
AP2A2
SYNGAP
ATP6V0A1
GRIA2
GNB5
SEPT5
DLG4
LINGO1
SYN1
KIAA1045
SYN2
STX1A
SYT1
SLC6A17
CACNA2D1
ACTN1
ERC2
CORO1A
SEPT11
VGF
BSN
RAB3A
SYT7
ACTN2
ATP6V0D1
SH3GLB2
ATP2B1
PVRL1
WASF1
SYNGR1
SIRPA
CRMP1
AP3M2
CAMKV
AP3B2
SLC8A2
DBN1
SLC25A22
CTBP1
CD47
CLTC
ANKS1B
GPM6A
PLXNA1
DNM1L
TBC1D24
AP3D1
SEPT3
DCLK1
SYP
AP2M1
ACTR3B
SEPT6
PIP5K1C
CADM1
DPP10
PRKCG
GPRIN1
ATL1
NEGR1
KIAA0513
SGIP1
GNAZ
CD200

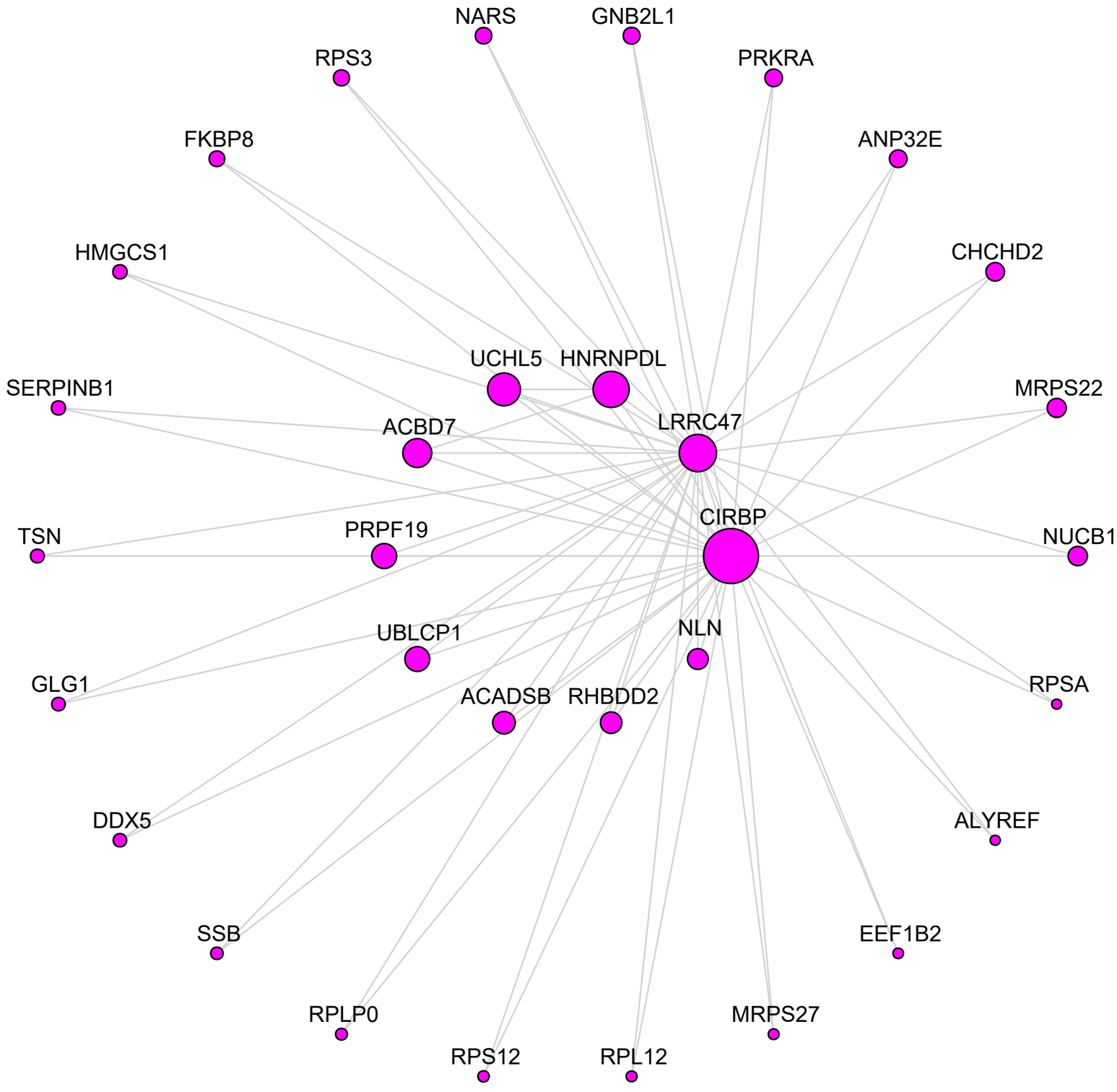
M12 Unknown


IPO7
ACTR10
RAP1GDS1
PPP2R5D
NCALD
ATP6V0C
MGST3
IPO5
NAPA
PPP2R1A
RHOA
RTN1
RTN3
CD81
CAND1
SULT4A1
PPP1CB
RAP1GDS1
RPS5
COPS2
TNPO2
TCP11L1
TMEM167A
XPO7

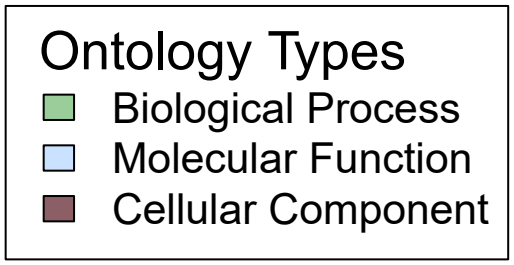
M7 Translation/Ribosome

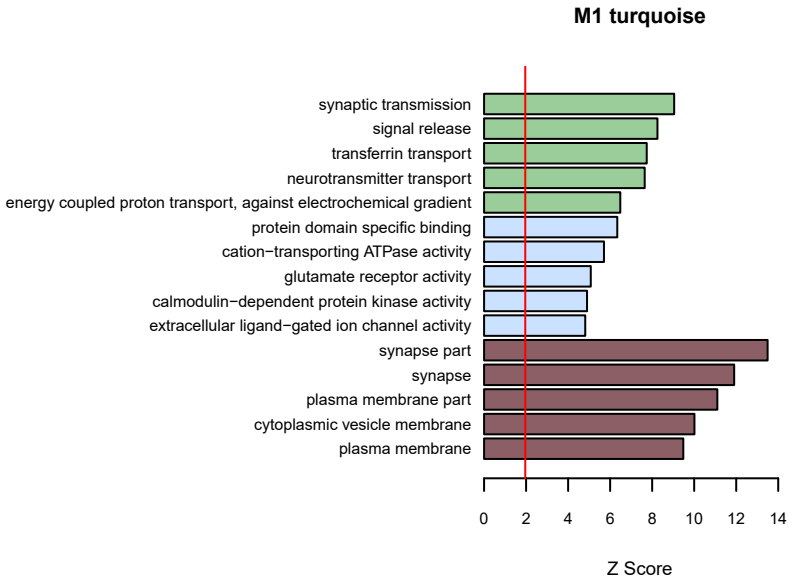


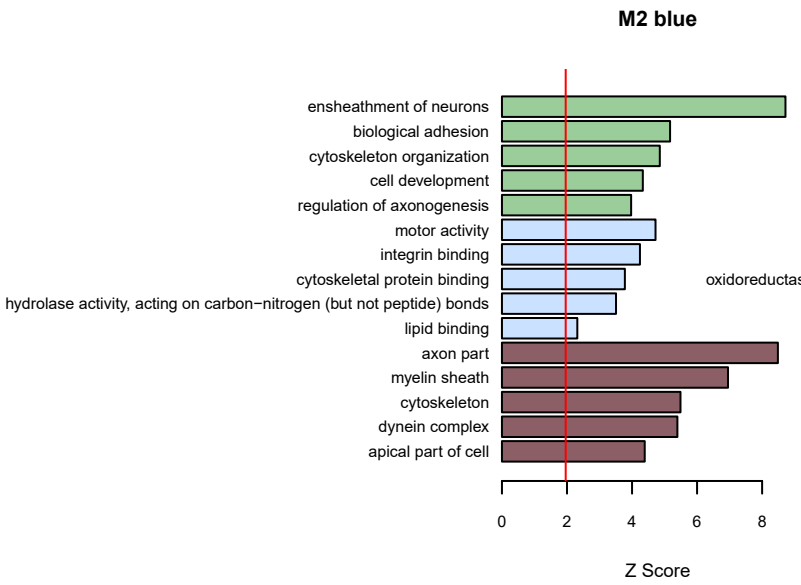
M9 Translation/Ribosome

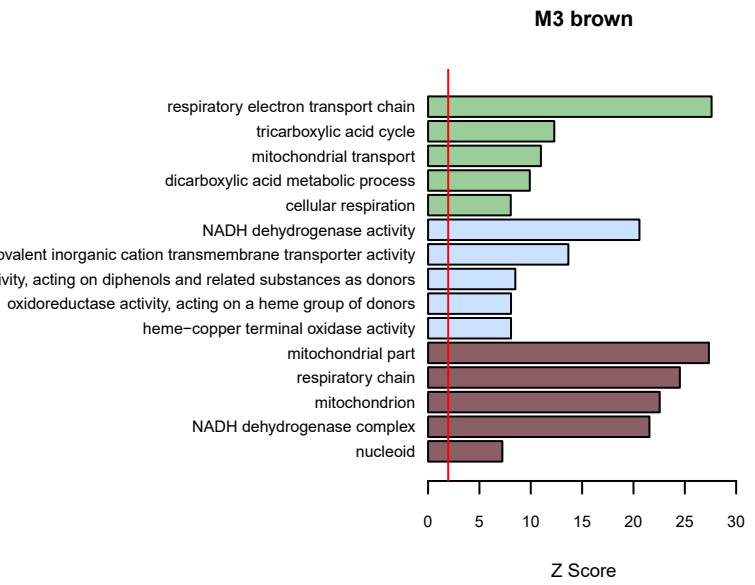


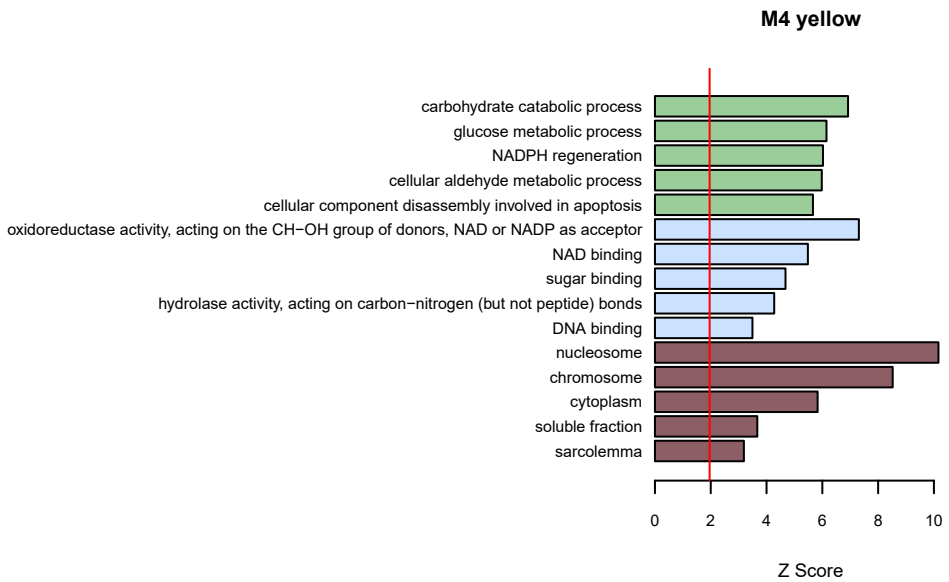
Supplementary Figure 2. AD Network Module Protein Memberships. The top 100 proteins by module eigenprotein correlation value (kME) in each AD protein network module. The size of each circle indicates the relative kME. Those proteins with the largest kME are considered “hub” proteins within the module, and explain the largest variance in module expression.

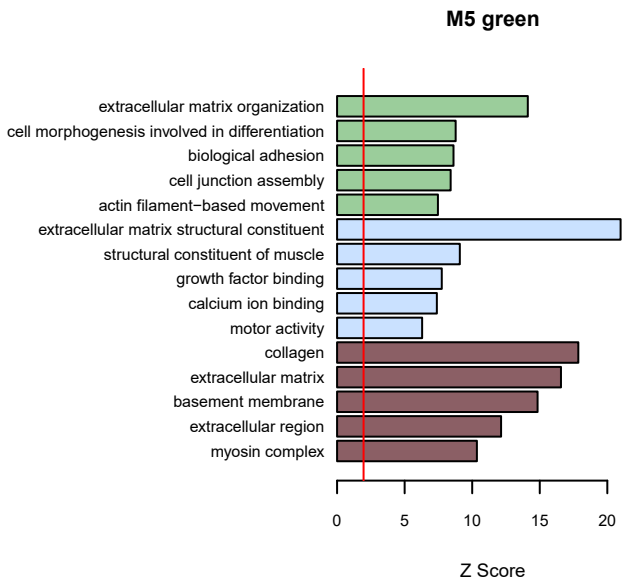

Ontology Types
Biological Process
Molecular Function
Cellular Component

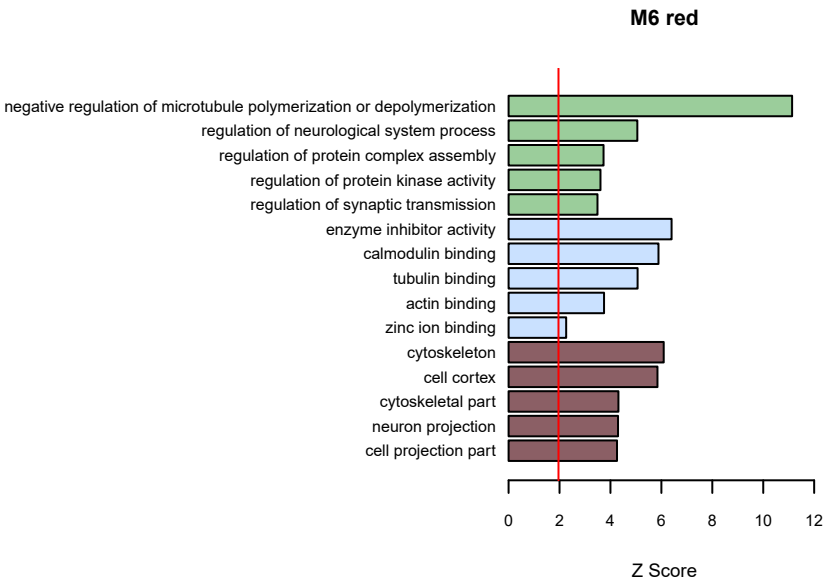

M1 turquoise
synaptic transmission
signal release
transferrin transport
neurotransmitter transport
energy coupled proton transport, against electrochemical gradient
protein domain specific binding
cation−transporting ATPase activity
glutamate receptor activity
calmodulin−dependent protein kinase activity
extracellular ligand−gated ion channel activity
synapse part
synapse
plasma membrane part
cytoplasmic vesicle membrane
plasma membrane
0 2 4 6 8 10 12 14
Z Score

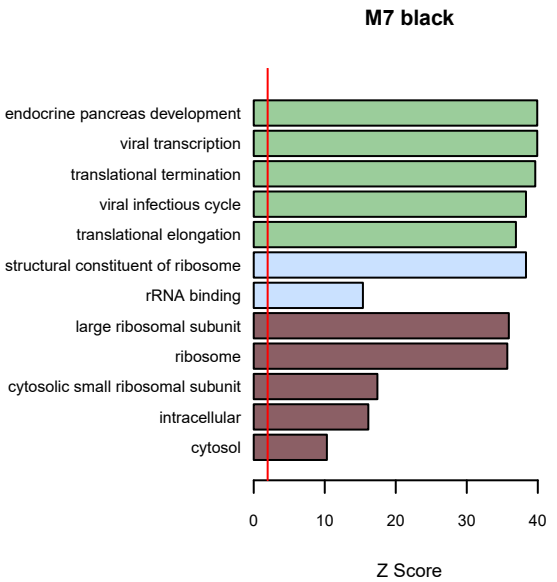

M2 blue
ensheathment of neurons
biological adhesion
cytoskeleton organization
cell development
regulation of axonogenesis
motor activity
integrin binding
cytoskeletal protein binding
hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
lipid binding
axon part
myelin sheath
cytoskeleton
dynein complex
apical part of cell
0 2 4 6 8
Z Score

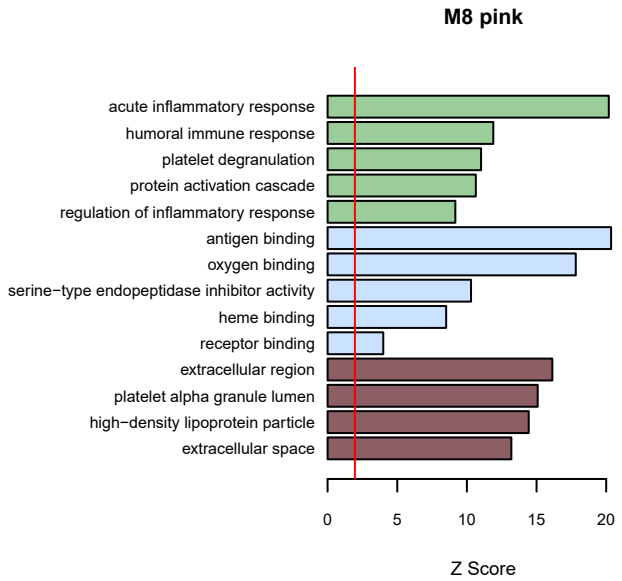

M3 brown
respiratory electron transport chain
tricarboxylic acid cycle
mitochondrial transport
dicarboxylic acid metabolic process
cellular respiration
NADH dehydrogenase activity
monovalent inorganic cation transmembrane transporter activity
oxidoreductase activity, acting on diphenols and related substances as donors
oxidoreductase activity, acting on a heme group of donors
heme−copper terminal oxidase activity
mitochondrial part
respiratory chain
mitochondrion
NADH dehydrogenase complex
nucleoid
0 5 10 15 20 25 30
Z Score

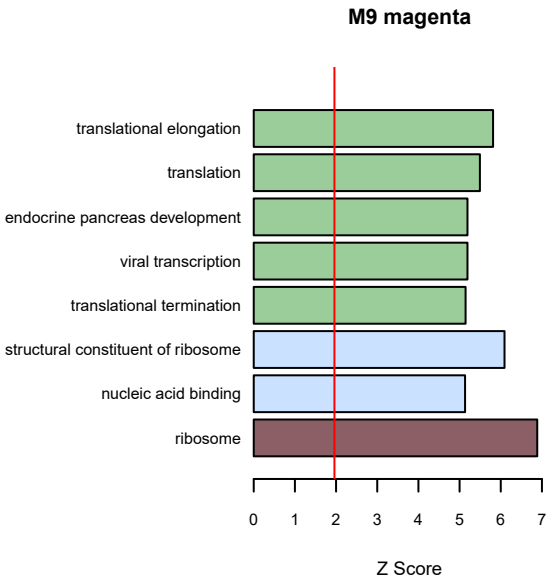

M4 yellow
carbohydrate catabolic process
glucose metabolic process
NADPH regeneration
cellular aldehyde metabolic process
cellular component disassembly involved in apoptosis
oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP as acceptor
NAD binding
sugar binding
hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
DNA binding
nucleosome
chromosome
cytoplasm
soluble fraction
sarcolemma
0 2 4 6 8 10
Z Score

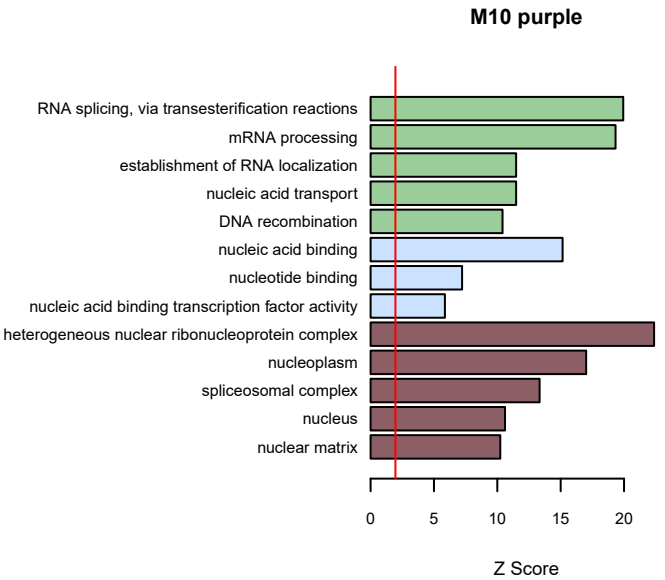

M5 green
extracellular matrix organization
cell morphogenesis involved in differentiation
biological adhesion
cell junction assembly
actin filament−based movement
extracellular matrix structural constituent
structural constituent of muscle
growth factor binding
calcium ion binding
motor activity
collagen
extracellular matrix
basement membrane
extracellular region
myosin complex
0 5 10 15 20
Z Score

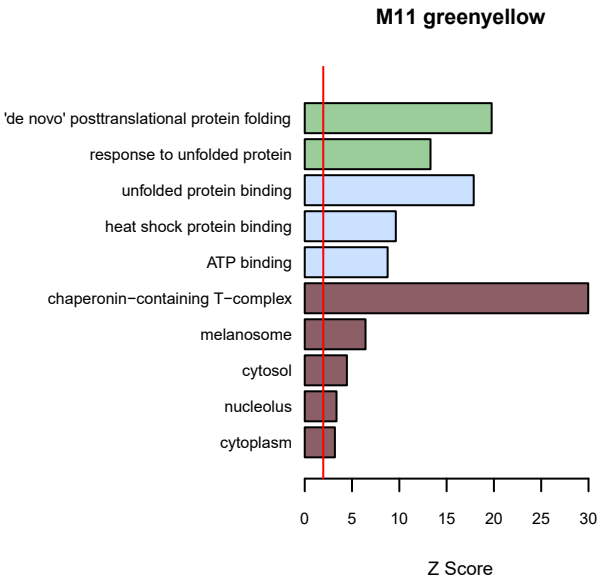

M6 red
negative regulation of microtubule polymerization or depolymerization
regulation of neurological system process
regulation of protein complex assembly
regulation of protein kinase activity
regulation of synaptic transmission
enzyme inhibitor activity
calmodulin binding
tubulin binding
actin binding
zinc ion binding
cytoskeleton
cell cortex
cytoskeletal part
neuron projection
cell projection part
0 2 4 6 8 10 12
Z Score

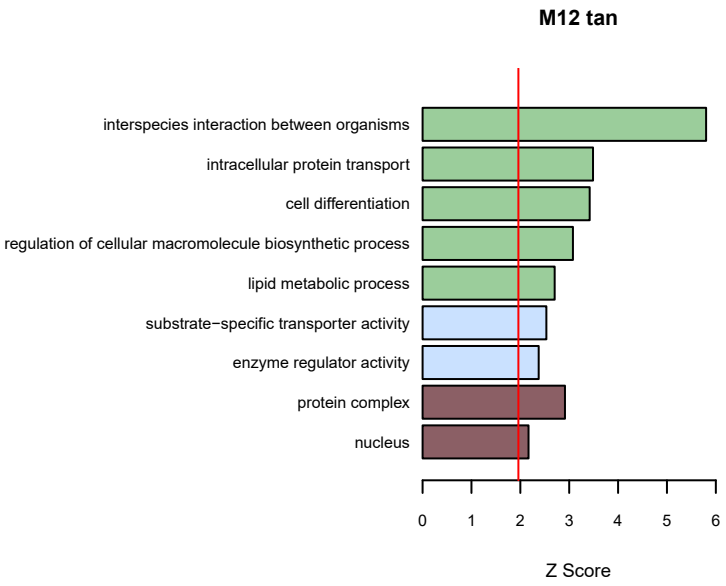

M7 black
endocrine pancreas development
viral transcription
translational termination
viral infectious cycle
translational elongation
structural constituent of ribosome
rRNA binding
large ribosomal subunit
ribosome
cytosolic small ribosomal subunit
intracellular
cytosol
0 10 20 30 40
Z Score

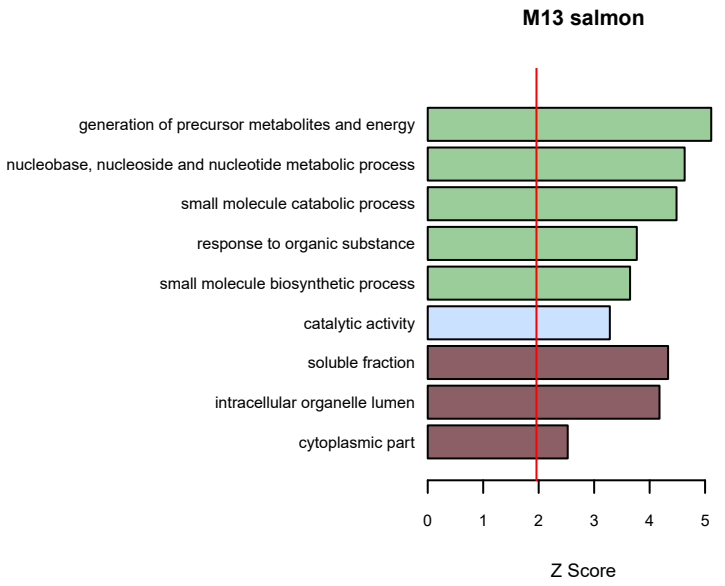

M8 pink
acute inflammatory response
humoral immune response
platelet degranulation
protein activation cascade
regulation of inflammatory response
antigen binding
oxygen binding
serine−type endopeptidase inhibitor activity
heme binding
receptor binding
extracellular region
platelet alpha granule lumen
high−density lipoprotein particle
extracellular space
0 5 10 15 20
Z Score


M9 magenta
translational elongation
translation
endocrine pancreas development
viral transcription
translational termination
structural constituent of ribosome
nucleic acid binding
ribosome
0 1 2 3 4 5 6 7
Z Score

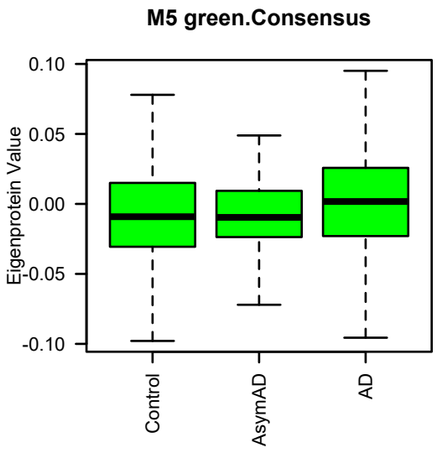

M10 purple
RNA splicing, via transesterification reactions
mRNA processing
establishment of RNA localization
nucleic acid transport
DNA recombination
nucleic acid binding
nucleotide binding
nucleic acid binding transcription factor activity
heterogeneous nuclear ribonucleoprotein complex
nucleoplasm
spliceosomal complex
nucleus
nuclear matrix
0 5 10 15 20
Z Score

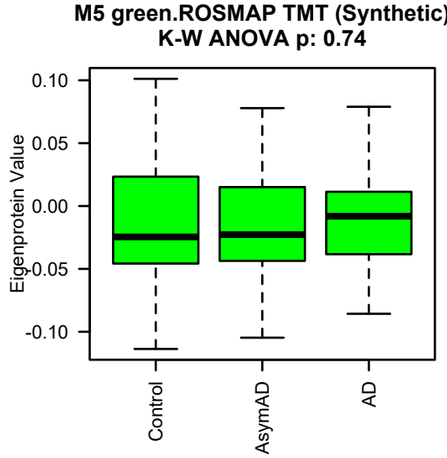

M11 greenyellow
'de novo' posttranslational protein folding
response to unfolded protein
unfolded protein binding
heat shock protein binding
ATP binding
chaperonin−containing T−complex
melanosome
cytosol
nucleolus
cytoplasm
0 5 10 15 20 25 30
Z Score

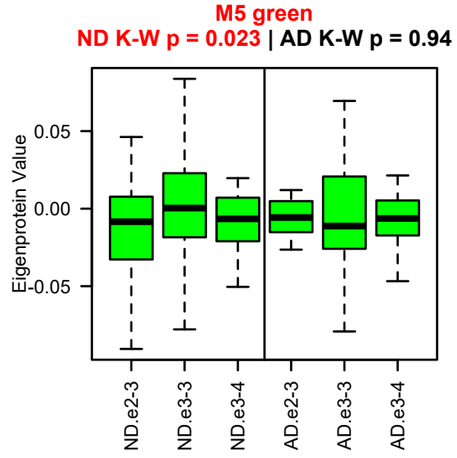

M12 tan
interspecies interaction between organisms
intracellular protein transport
cell differentiation
regulation of cellular macromolecule biosynthetic process
lipid metabolic process
substrate−specific transporter activity
enzyme regulator activity
protein complex
nucleus
0
1
2
3
4
5
6
Z Score

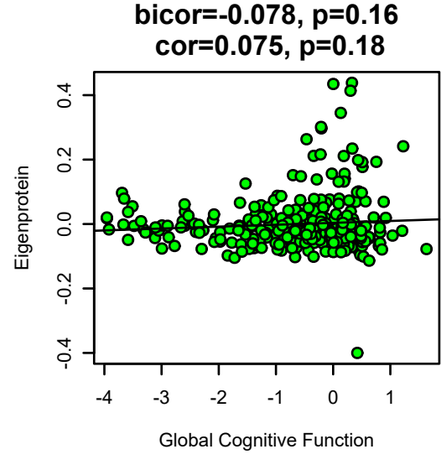

M13 salmon
generation of precursor metabolites and energy
nucleobase, nucleoside and nucleotide metabolic process
small molecule catabolic process
response to organic substance
small molecule biosynthetic process
catalytic activity
soluble fraction
intracellular organelle lumen
cytoplasmic part
0
1
2
3
4
5
Z Score

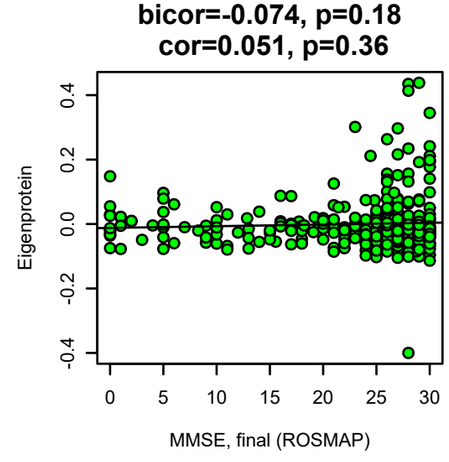
Supplementary Figure 3. GO Analysis on AD Network Modules. Gene ontology (GO) analysis was performed to gain insight into the biological meaning of each AD protein network module. Enrichment for a given ontology is shown by *z* score.

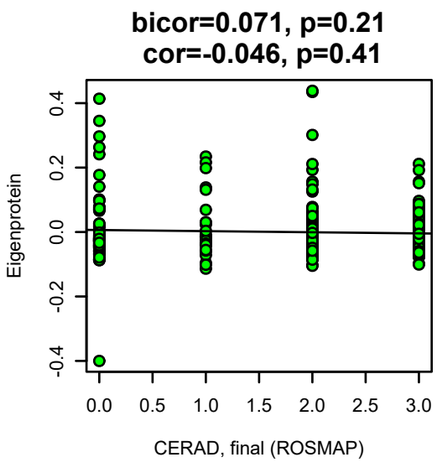

M5 green.Consensus
Eigenprotein Value
Control
AsymAD
AD

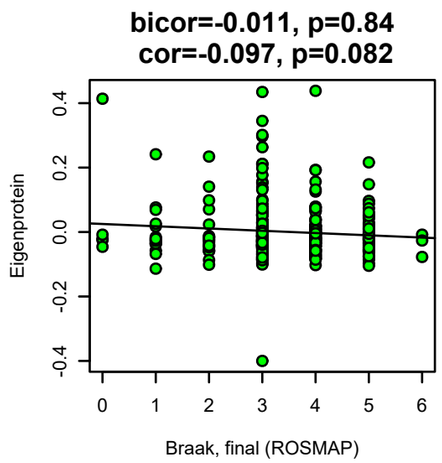

M5 green.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.74
Eigenprotein Value
Control
AsymAD
AD

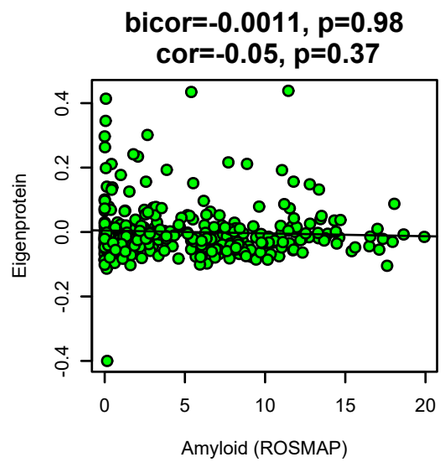

M5 green
ND K-W p = 0.023 | AD K-W p = 0.94
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

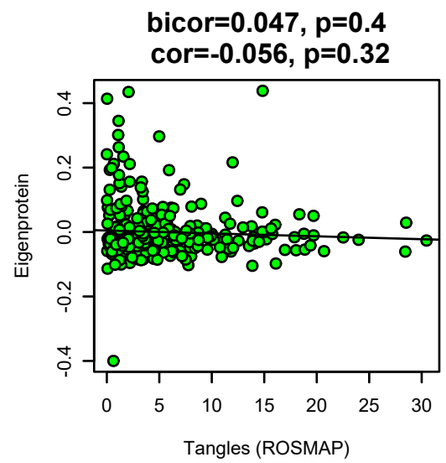

bicor=-0.078, p=0.16
cor=0.075, p=0.18
Eigenprotein
Global Cognitive Function

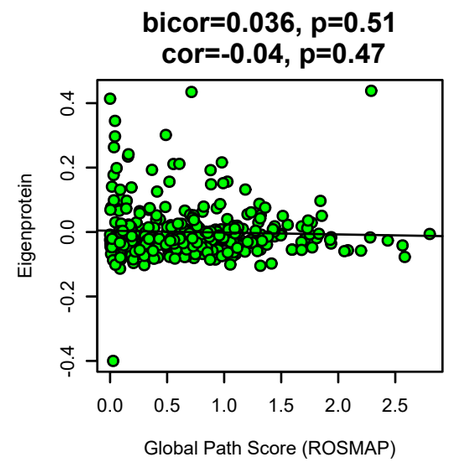

bicor=-0.074, p=0.18
cor=0.051, p=0.36
Eigenprotein
MMSE, final (ROSMAP)

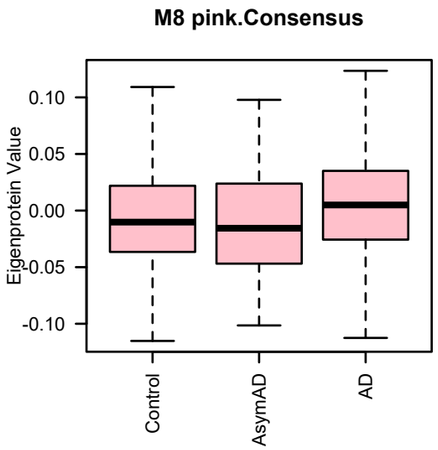

bicor=0.071, p=0.21
cor=-0.046, p=0.41
Eigenprotein
CERAD, final (ROSMAP)

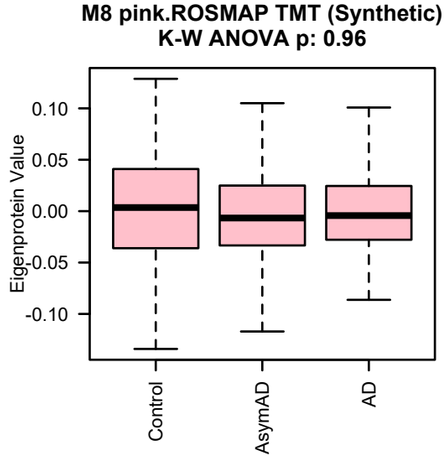

bicor=-0.011, p=0.84
cor=-0.097, p=0.082
Eigenprotein
Braak, final (ROSMAP)

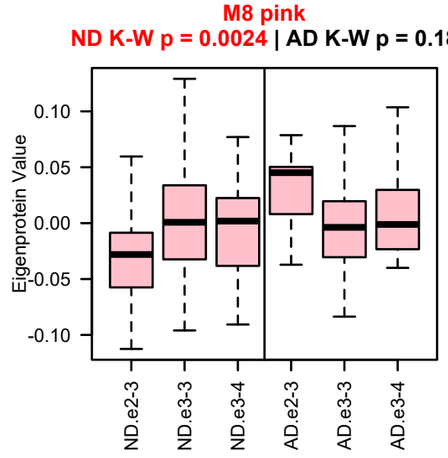

bicor=-0.0011, p=0.98
cor=-0.05, p=0.37
Eigenprotein
Amyloid (ROSMAP)

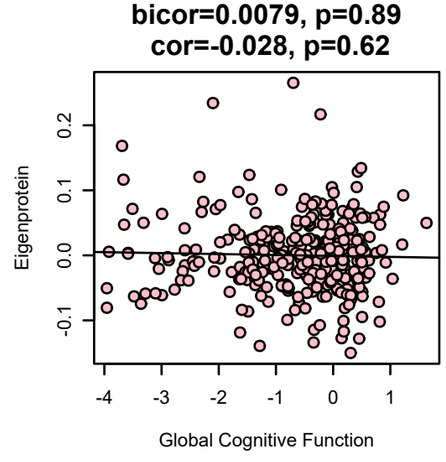

bicor=0.047, p=0.4
cor=-0.056, p=0.32
Eigenprotein
Tangles (ROSMAP)

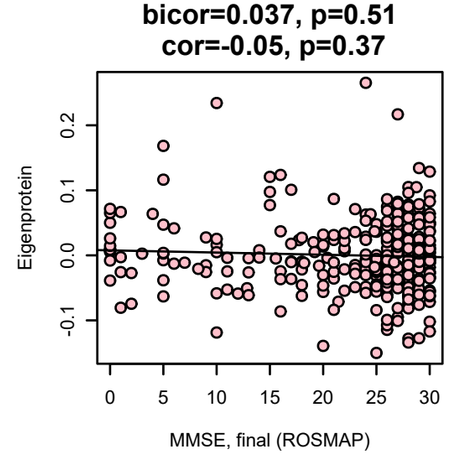

bicor=0.036, p=0.51
cor=-0.04, p=0.47
Eigenprotein
Global Path Score (ROSMAP)

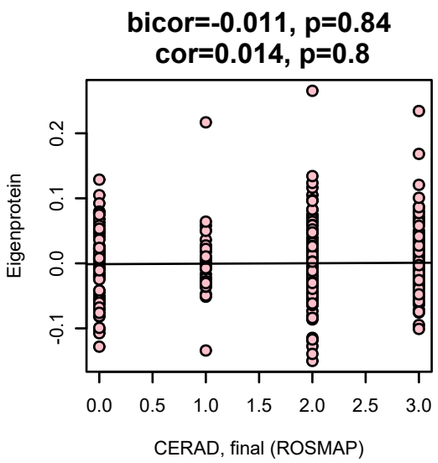

M8 pink.Consensus
Eigenprotein Value
Control
AsymAD
AD

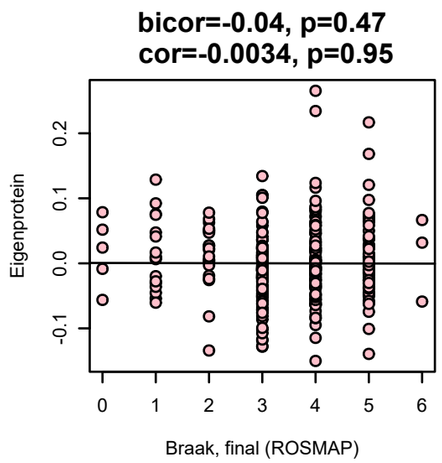

M8 pink.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.96
Eigenprotein Value
Control
AsymAD
AD

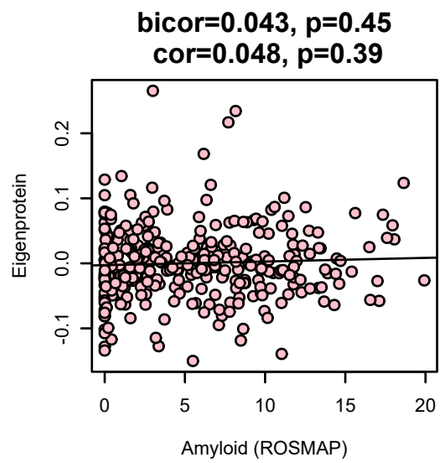

M8 pink
ND K-W p = 0.0024 | AD K-W p = 0.18
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

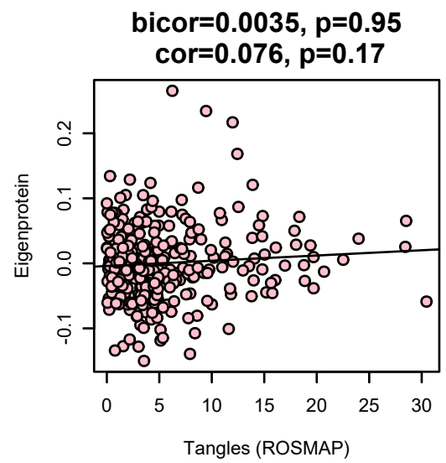

bicor=0.0079, p=0.89
cor=-0.028, p=0.62
Eigenprotein
Global Cognitive Function

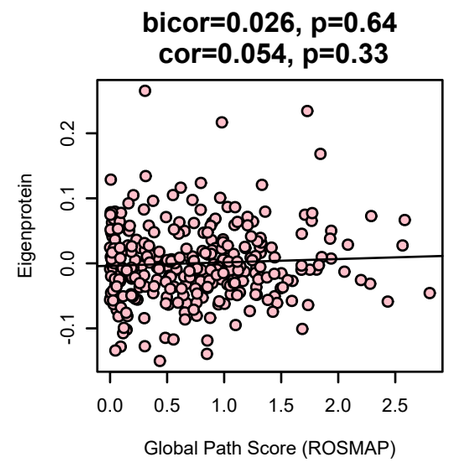

bicor=0.037, p=0.51
cor=-0.05, p=0.37
Eigenprotein
MMSE, final (ROSMAP)

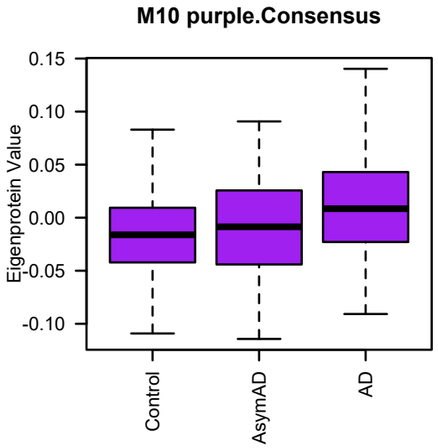

bicor=-0.011, p=0.84
cor=0.014, p=0.8
Eigenprotein
CERAD, final (ROSMAP)

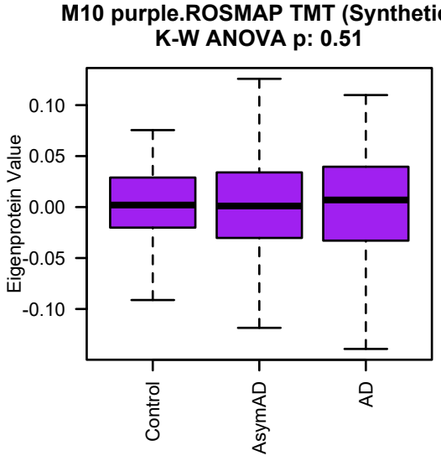

bicor=-0.04, p=0.47
cor=-0.0034, p=0.95
Eigenprotein
Braak, final (ROSMAP)

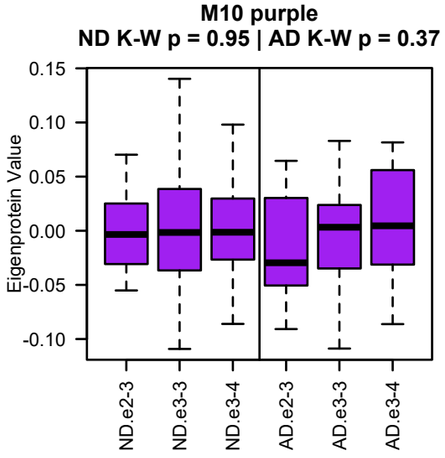

bicor=0.043, p=0.45
cor=0.048, p=0.39
Eigenprotein
Amyloid (ROSMAP)

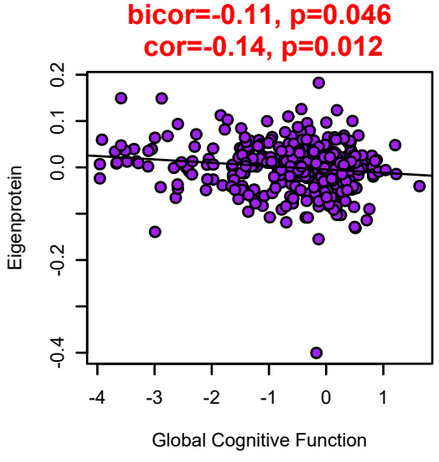

bicor=0.0035, p=0.95
cor=0.076, p=0.17
Eigenprotein
Tangles (ROSMAP)

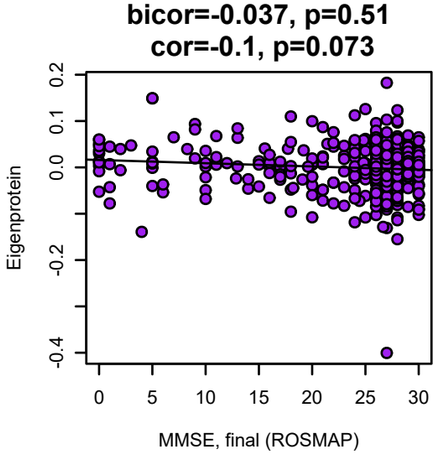

bicor=0.026, p=0.64
cor=0.054, p=0.33
Eigenprotein
Global Path Score (ROSMAP)

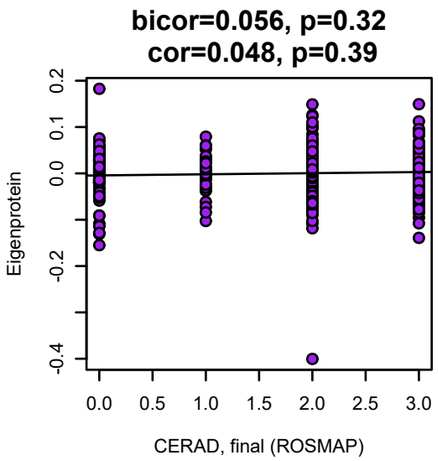

M10 purple.Consensus
Eigenprotein Value
Control
AsymAD
AD

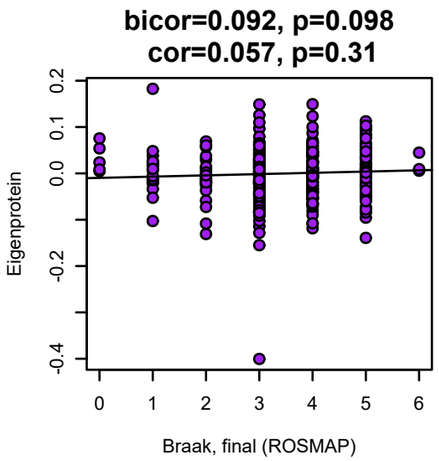

M10 purple.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.51
Eigenprotein Value
Control
AsymAD
AD

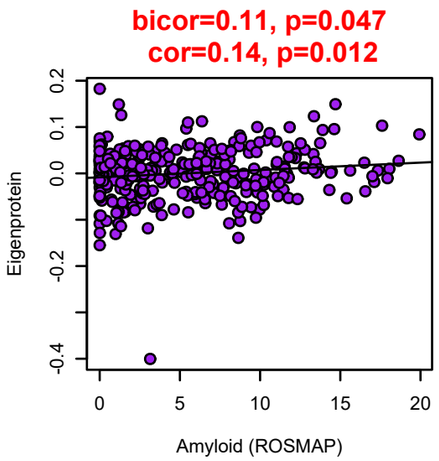

M10 purple
ND K-W p = 0.95 | AD K-W p = 0.37
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

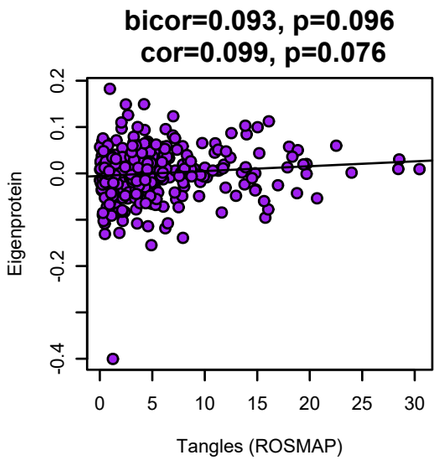

bicor=-0.11, p=0.046
cor=-0.14, p=0.012
Eigenprotein
Global Cognitive Function

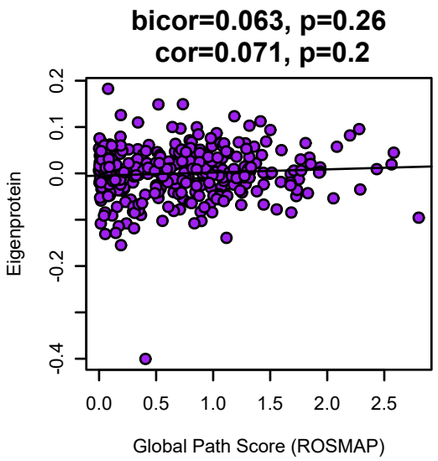

bicor=-0.037, p=0.51
cor=-0.1, p=0.073
Eigenprotein
MMSE, final (ROSMAP)

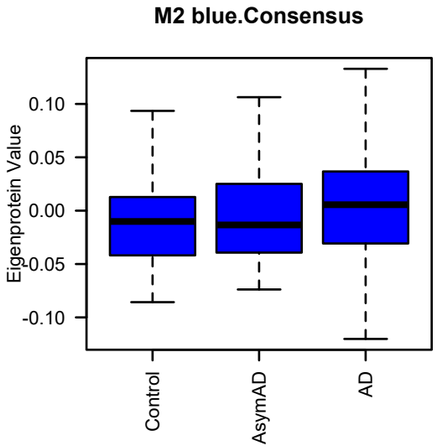

bicor=0.056, p=0.32
cor=0.048, p=0.39
Eigenprotein
CERAD, final (ROSMAP)

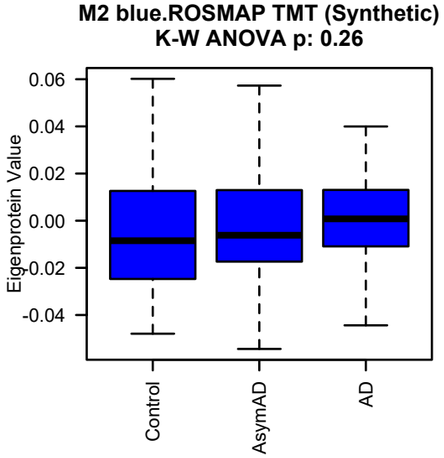

bicor=0.092, p=0.098
cor=0.057, p=0.31
Eigenprotein
Braak, final (ROSMAP)

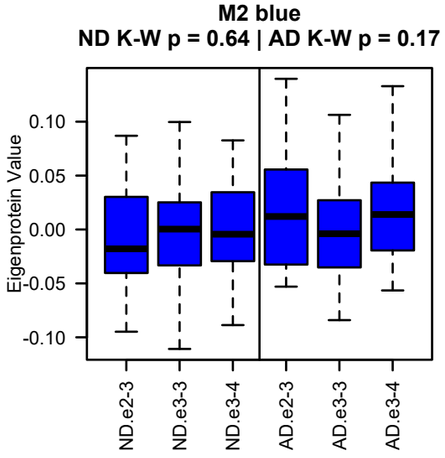

bicor=0.11, p=0.047
cor=0.14, p=0.012
Eigenprotein
Amyloid (ROSMAP)

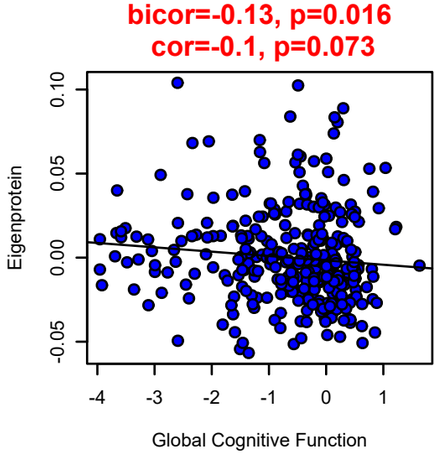

bicor=0.093, p=0.096
cor=0.099, p=0.076
Eigenprotein
Tangles (ROSMAP)

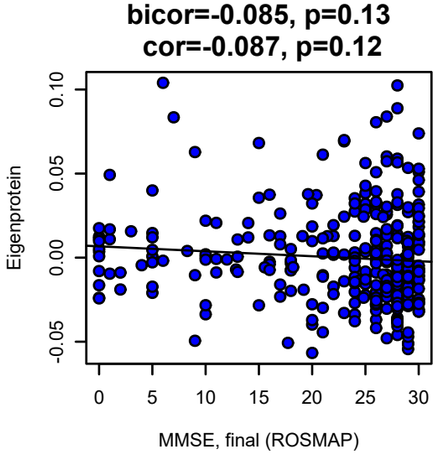

bicor=0.063, p=0.26
cor=0.071, p=0.2
Eigenprotein
Global Path Score (ROSMAP)

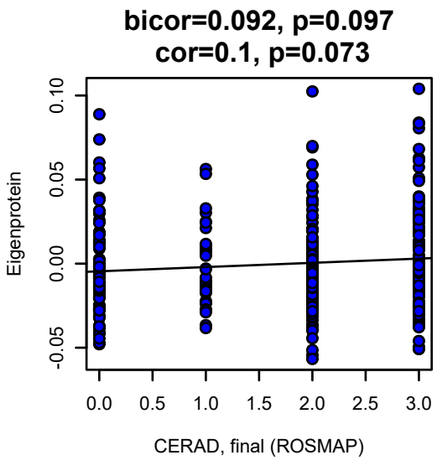

M2 blue.Consensus
Eigenprotein Value
Control
AsymAD
AD

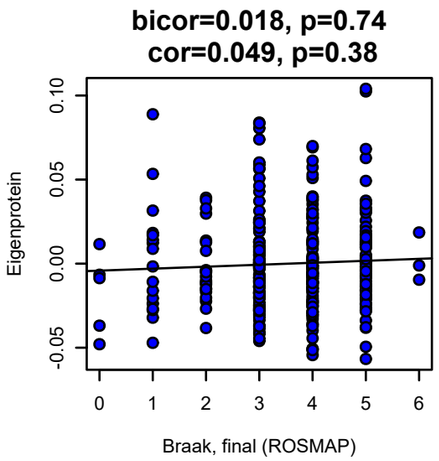

M2 blue.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.26
Eigenprotein Value
Control
AsymAD
AD

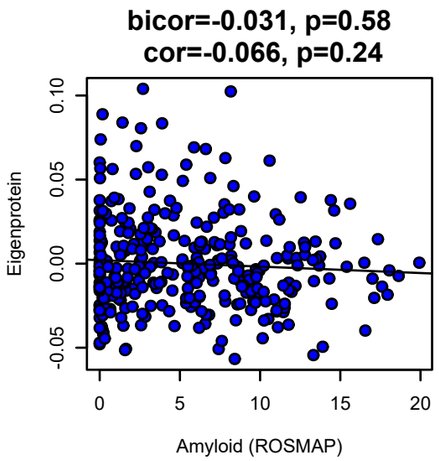

M2 blue
ND K-W p = 0.64 | AD K-W p = 0.17
Eigenprotein Value
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

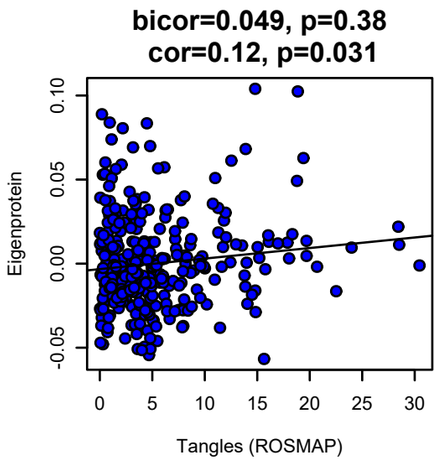

bicor=-0.13, p=0.016
cor=-0.1, p=0.073
Eigenprotein
Global Cognitive Function

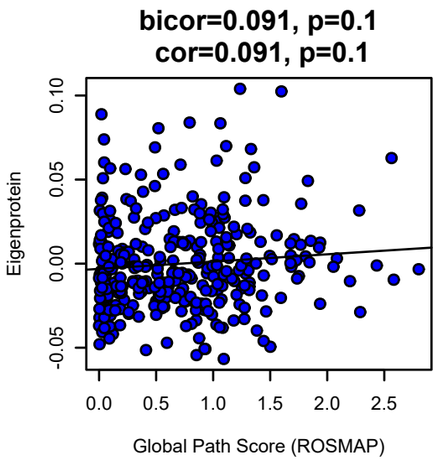

bicor=-0.085, p=0.13
cor=-0.087, p=0.12
Eigenprotein
MMSE, final (ROSMAP)

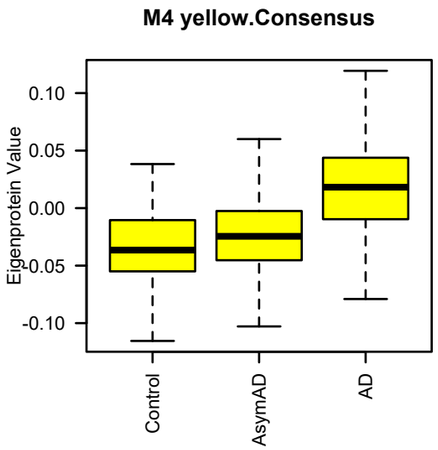

bicor=0.092, p=0.097
cor=0.1, p=0.073
Eigenprotein
CERAD, final (ROSMAP)

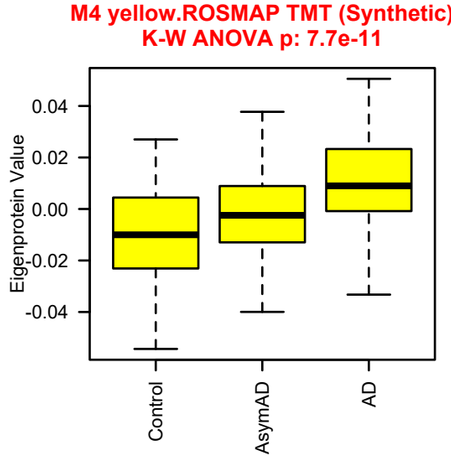

bicor=0.018, p=0.74
cor=0.049, p=0.38
Eigenprotein
Braak, final (ROSMAP)

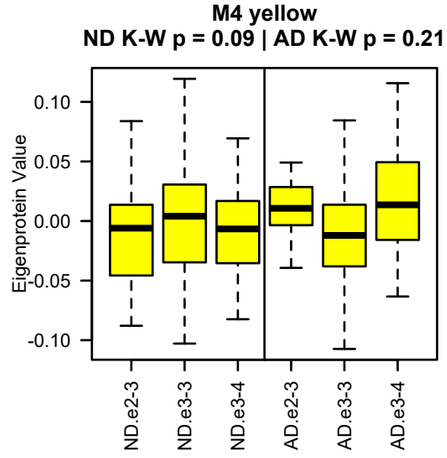

bicor=-0.031, p=0.58
cor=-0.066, p=0.24
Eigenprotein
Amyloid (ROSMAP)

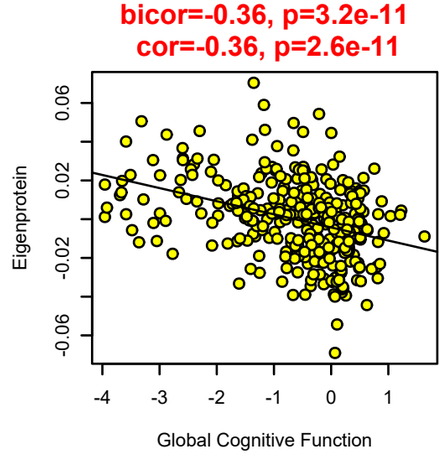

bicor=0.049, p=0.38
cor=0.12, p=0.031
Eigenprotein
Tangles (ROSMAP)

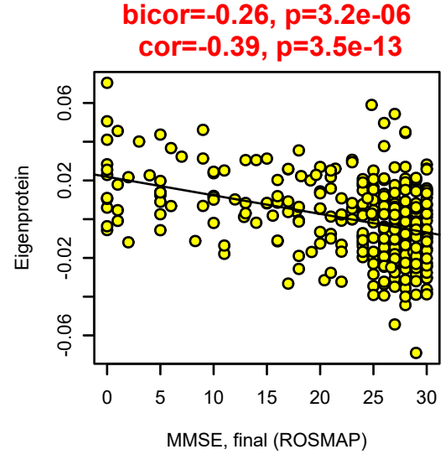

bicor=0.091, p=0.1
cor=0.091, p=0.1
Eigenprotein
Global Path Score (ROSMAP)

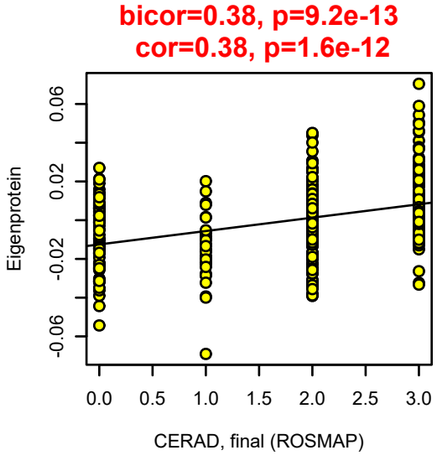

M4 yellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

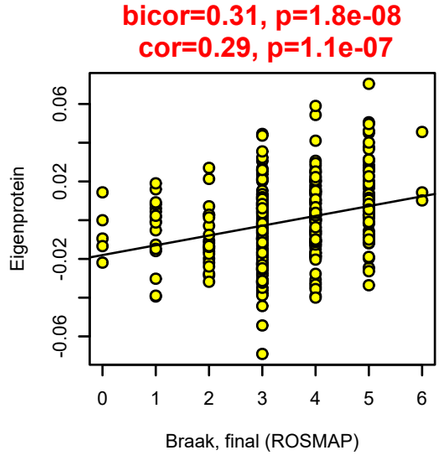

M4 yellow.ROSMAP TMT (Synthetic)
K-W ANOVA p: 7.7e-11
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
AsymAD
AD

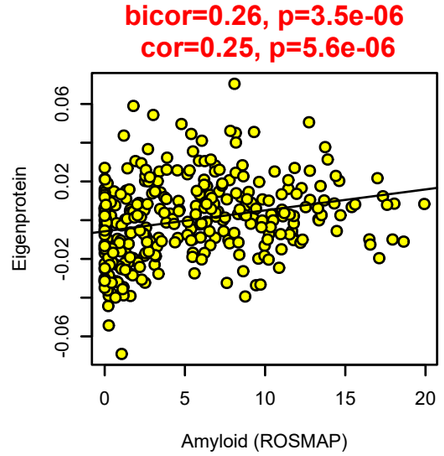

M4 yellow
ND K-W p = 0.09 | AD K-W p = 0.21
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

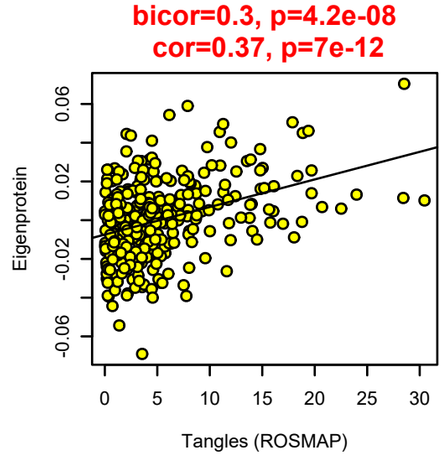

bicor=-0.36, p=3.2e-11
cor=-0.36, p=2.6e-11
Eigenprotein
0.06
0.02
-0.02
-0.06
-4
-3
-2
-1
0
1
Global Cognitive Function

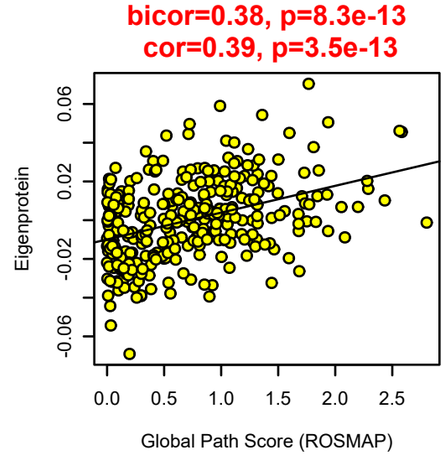

bicor=-0.26, p=3.2e-06
cor=-0.39, p=3.5e-13
Eigenprotein
0.06
0.02
-0.02
-0.06
0
5
10
15
20
25
30
MMSE, final (ROSMAP)

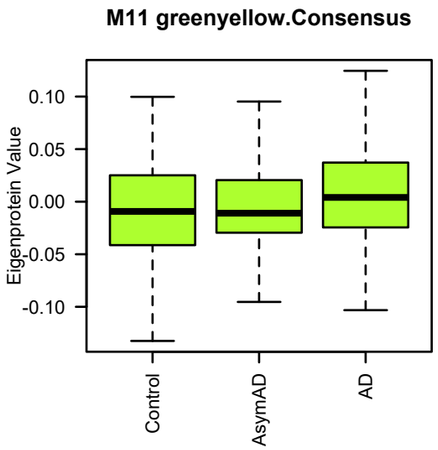

bicor=0.38, p=9.2e-13
cor=0.38, p=1.6e-12
Eigenprotein
0.06
0.02
-0.02
-0.06
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

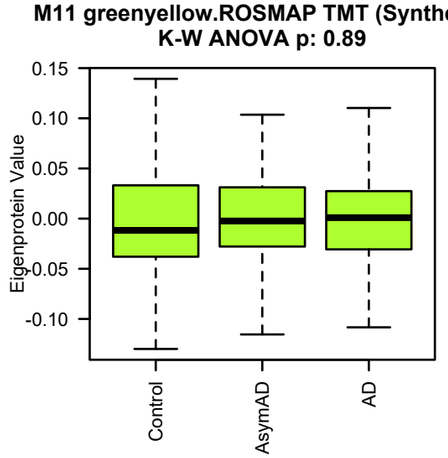

bicor=0.31, p=1.8e-08
cor=0.29, p=1.1e-07
Eigenprotein
0.06
0.02
-0.02
-0.06
0
1
2
3
4
5
6
Braak, final (ROSMAP)

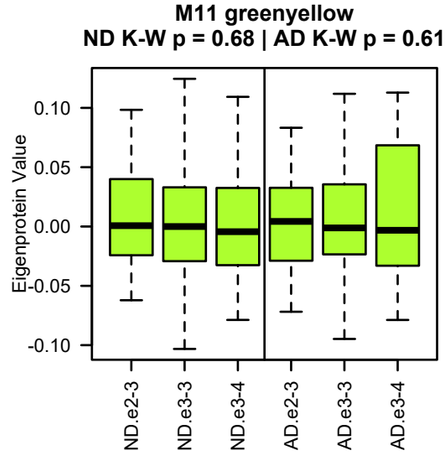

bicor=0.26, p=3.5e-06
cor=0.25, p=5.6e-06
Eigenprotein
0.06
0.02
-0.02
-0.06
0
5
10
15
20
Amyloid (ROSMAP)

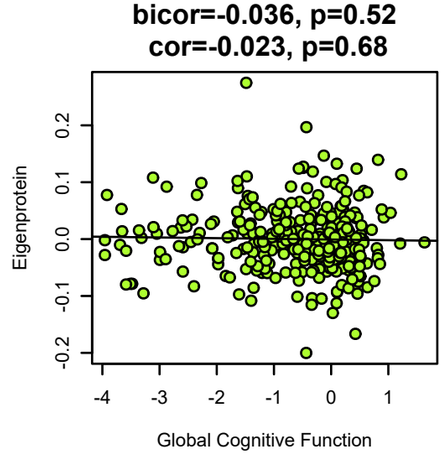

bicor=0.3, p=4.2e-08
cor=0.37, p=7e-12
Eigenprotein
0.06
0.02
-0.02
-0.06
0
5
10
15
20
25
30
Tangles (ROSMAP)

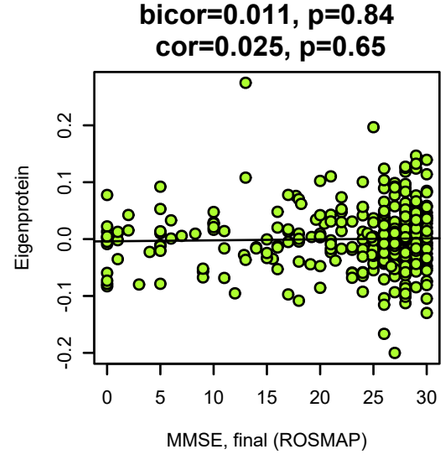

bicor=0.38, p=8.3e-13
cor=0.39, p=3.5e-13
Eigenprotein
0.06
0.02
-0.02
-0.06
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

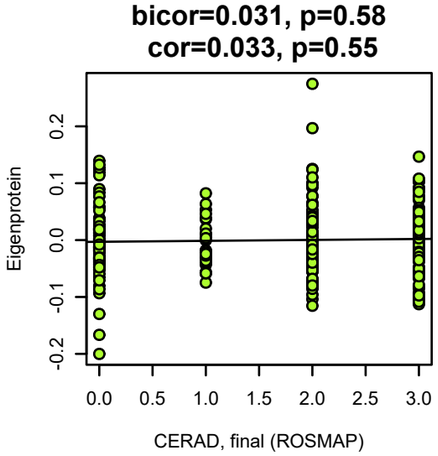

M11 greenyellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

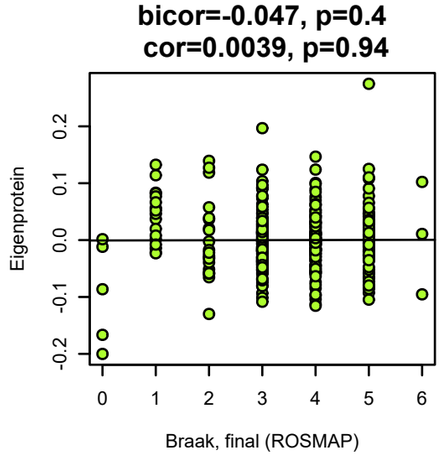

M11 greenyellow.ROSMAP TMT (Synthetic
K-W ANOVA p: 0.89
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

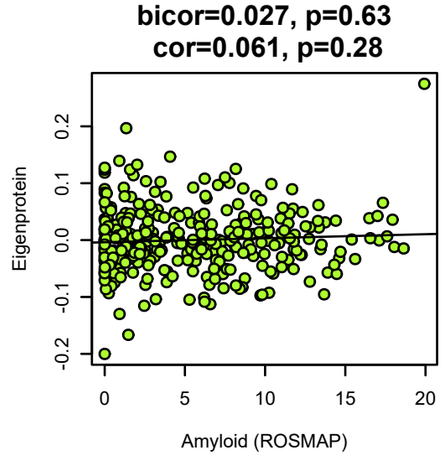

M11 greenyellow
ND K-W p = 0.68 | AD K-W p = 0.61
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

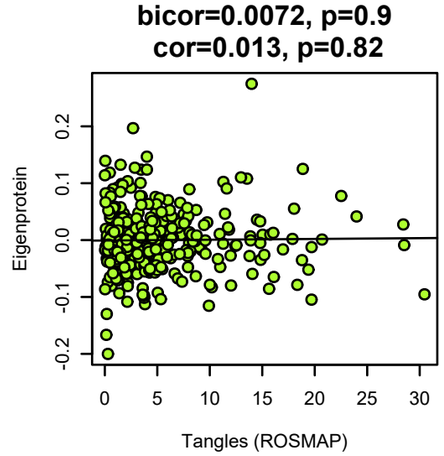

bicor=-0.036, p=0.52
cor=-0.023, p=0.68
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-4
-3
-2
-1
0
1
Global Cognitive Function

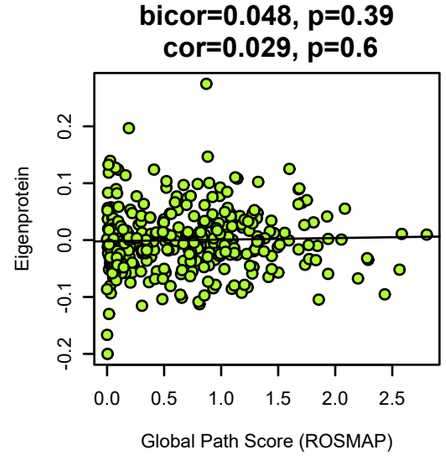

bicor=0.011, p=0.84
cor=0.025, p=0.65
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
5
10
15
20
25
30
MMSE, final (ROSMAP)

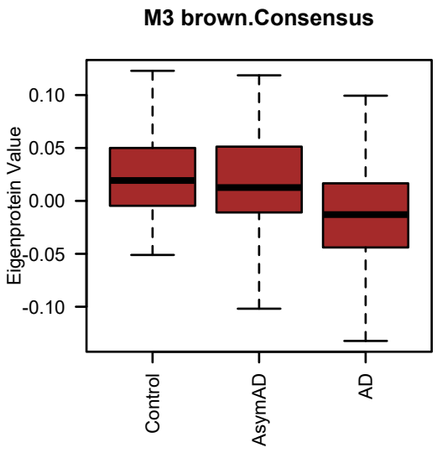

bicor=0.031, p=0.58
cor=0.033, p=0.55
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

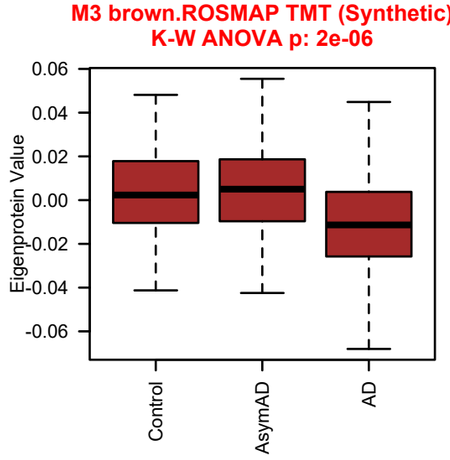

bicor=-0.047, p=0.4
cor=0.0039, p=0.94
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
1
2
3
4
5
6
Braak, final (ROSMAP)

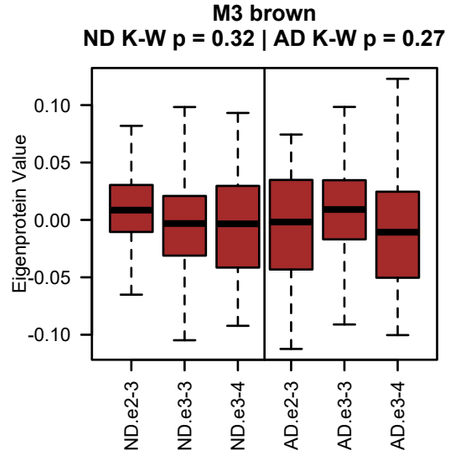

bicor=0.027, p=0.63
cor=0.061, p=0.28
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
5
10
15
20
Amyloid (ROSMAP)

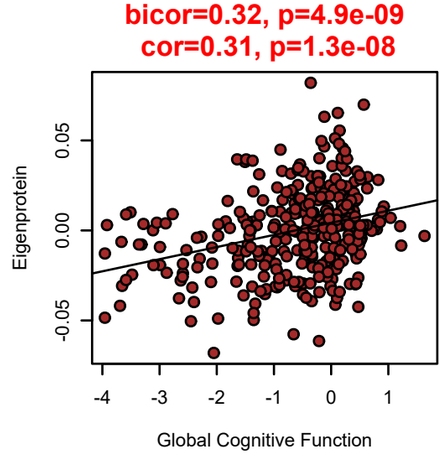

bicor=0.0072, p=0.9
cor=0.013, p=0.82
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
5
10
15
20
25
30
Tangles (ROSMAP)

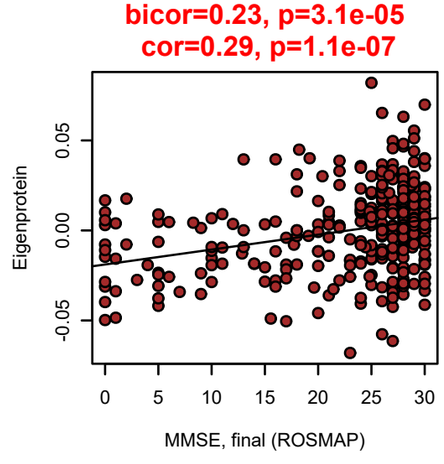

bicor=0.048, p=0.39
cor=0.029, p=0.6
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

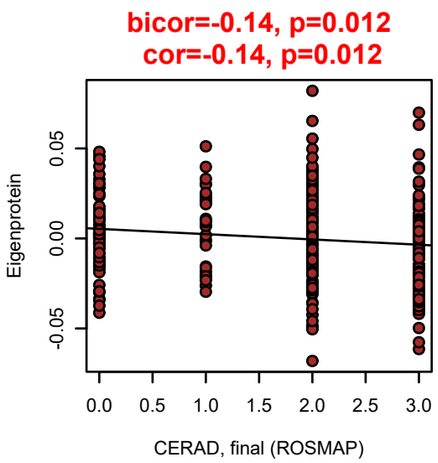

M3 brown.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

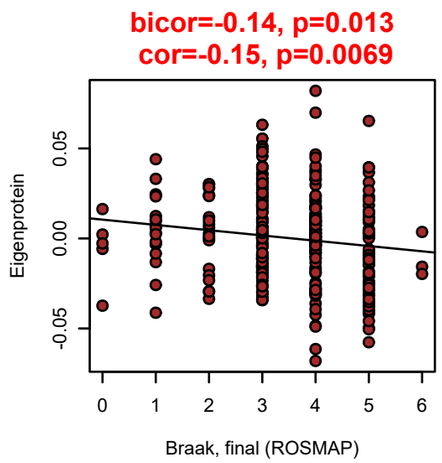

M3 brown.ROSMAP TMT (Synthetic)
K-W ANOVA p: 2e-06
Eigenprotein Value
0.06
0.04
0.02
0.00
-0.02
-0.04
-0.06
Control
AsymAD
AD

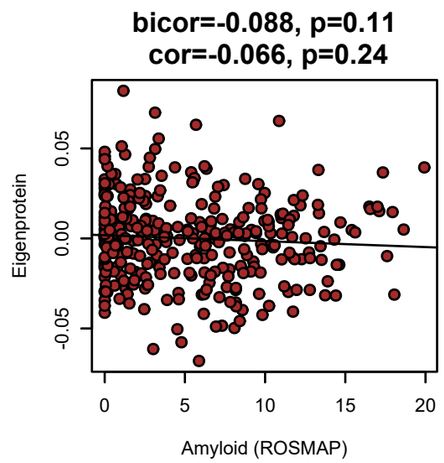

M3 brown
ND K-W p = 0.32 | AD K-W p = 0.27
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

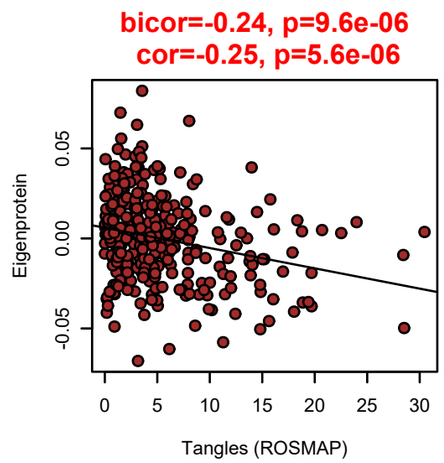

bicor=0.32, p=4.9e-09
cor=0.31, p=1.3e-08
Eigenprotein
0.05
0.00
-0.05
-4
-3
-2
-1
0
1
Global Cognitive Function

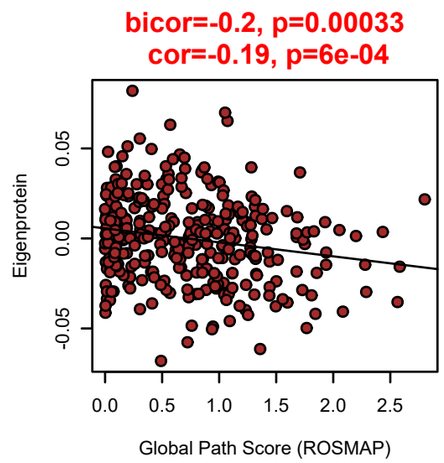

bicor=0.23, p=3.1e-05
cor=0.29, p=1.1e-07
Eigenprotein
0.05
0.00
-0.05
0
5
10
15
20
25
30
MMSE, final (ROSMAP)

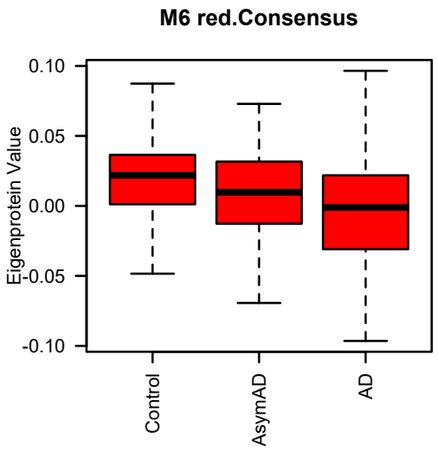

bicor=-0.14, p=0.012
cor=-0.14, p=0.012
Eigenprotein
0.05
0.00
-0.05
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

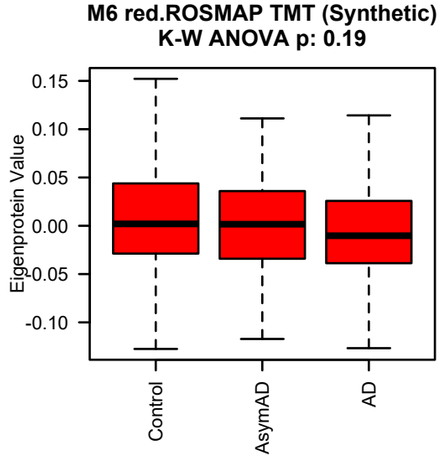

bicor=-0.14, p=0.013
cor=-0.15, p=0.0069
Eigenprotein
0.05
0.00
-0.05
0
1
2
3
4
5
6
Braak, final (ROSMAP)

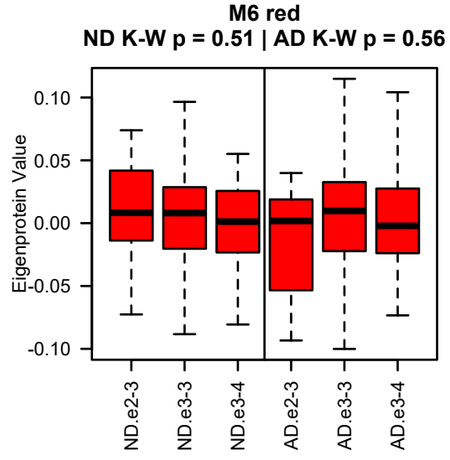

bicor=-0.088, p=0.11
cor=-0.066, p=0.24
Eigenprotein
0.05
0.00
-0.05
0
5
10
15
20
Amyloid (ROSMAP)

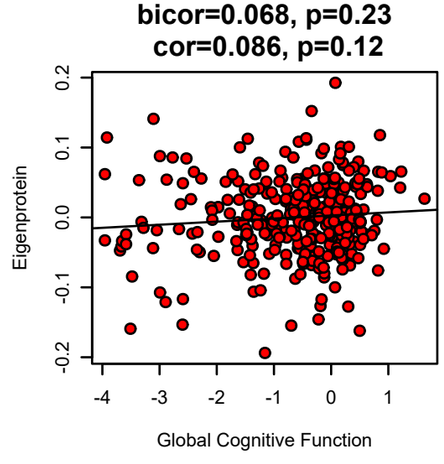

bicor=-0.24, p=9.6e-06
cor=-0.25, p=5.6e-06
Eigenprotein
0.05
0.00
-0.05
0
5
10
15
20
25
30
Tangles (ROSMAP)

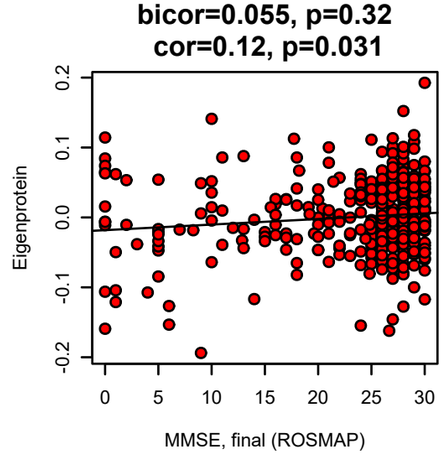

bicor=-0.2, p=0.00033
cor=-0.19, p=6e-04
Eigenprotein
0.05
0.00
-0.05
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

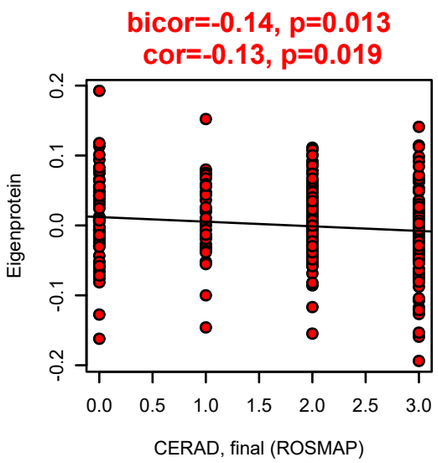

M6 red.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

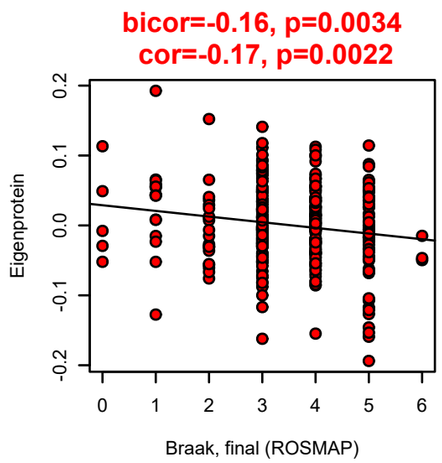

M6 red.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.19
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

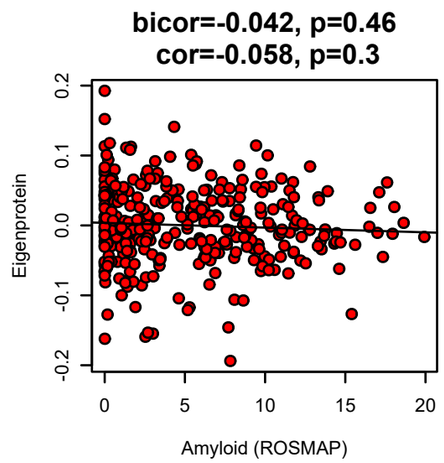

M6 red
ND K-W p = 0.51 | AD K-W p = 0.56
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

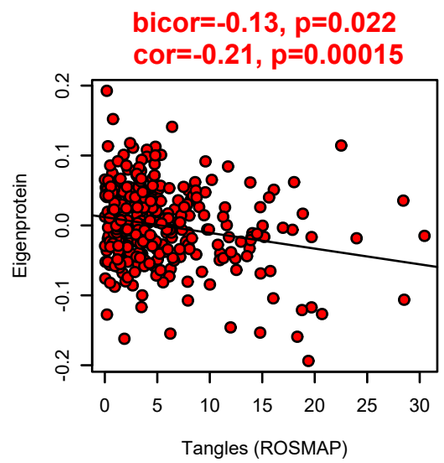

bicor=0.068, p=0.23
cor=0.086, p=0.12
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-4
-3
-2
-1
0
1
Global Cognitive Function

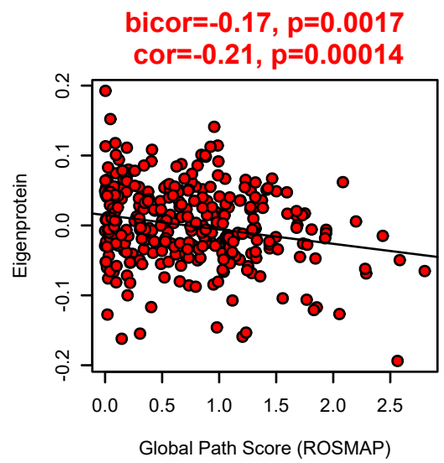

bicor=0.055, p=0.32
cor=0.12, p=0.031
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
5
10
15
20
25
30
MMSE, final (ROSMAP)

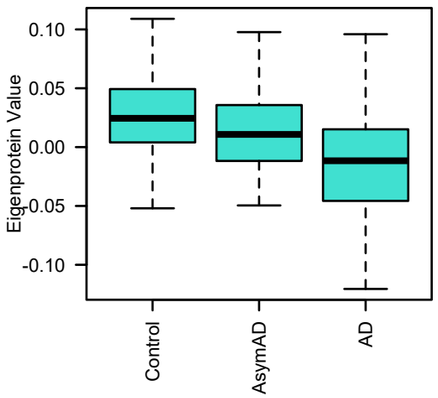

bicor=-0.14, p=0.013
cor=-0.13, p=0.019
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

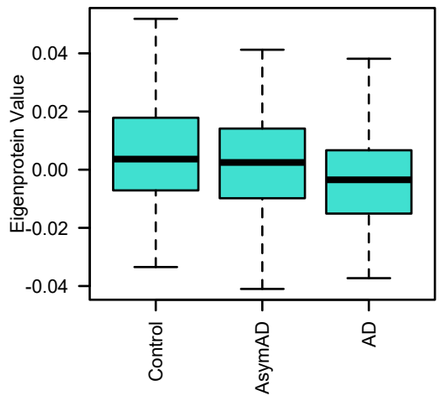

bicor=-0.16, p=0.0034
cor=-0.17, p=0.0022
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
1
2
3
4
5
6
Braak, final (ROSMAP)

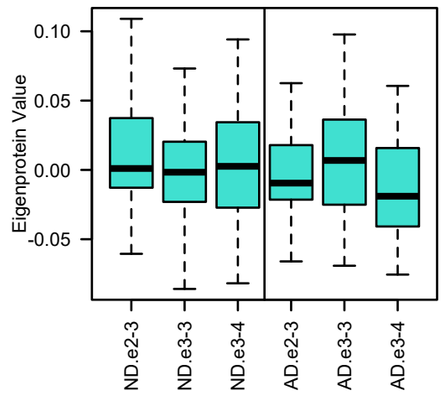

bicor=-0.042, p=0.46
cor=-0.058, p=0.3
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
5
10
15
20
Amyloid (ROSMAP)

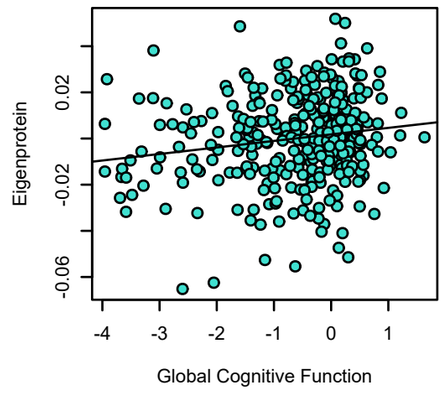

bicor=-0.13, p=0.022
cor=-0.21, p=0.00015
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0
5
10
15
20
25
30
Tangles (ROSMAP)

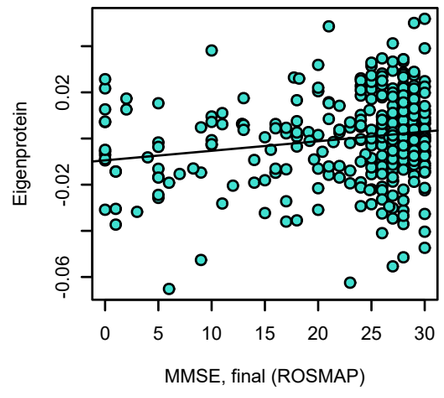

bicor=-0.17, p=0.0017
cor=-0.21, p=0.00014
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

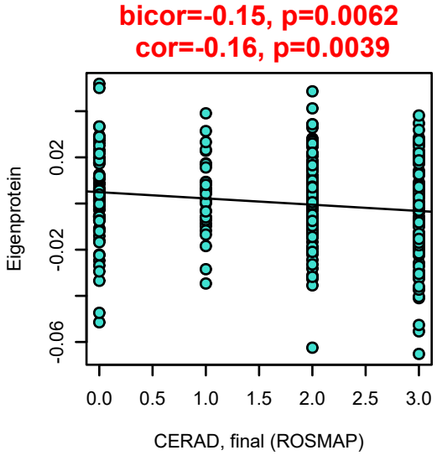

M1 turquoise.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

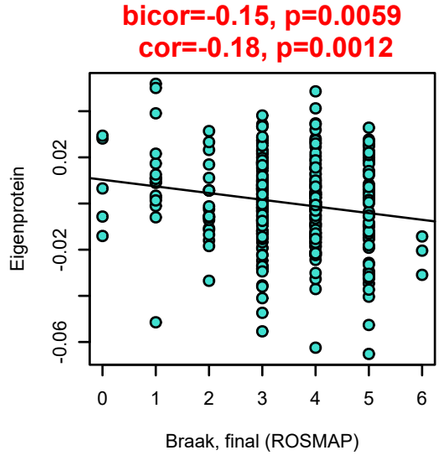

M1 turquoise.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.0044
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
AsymAD
AD

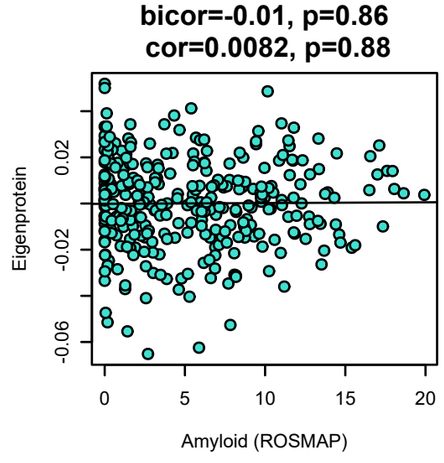

M1 turquoise
ND K-W p = 0.22 | AD K-W p = 0.23
Eigenprotein Value
0.10
0.05
0.00
-0.05
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

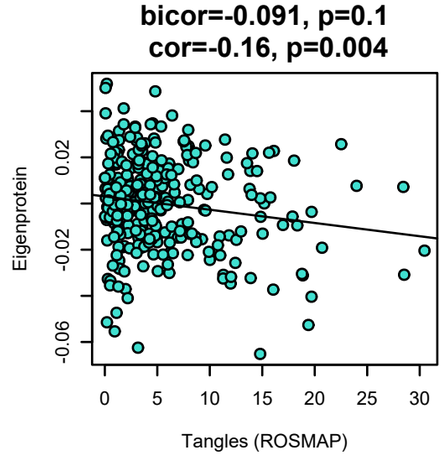

bicor=0.15, p=0.0062
cor=0.16, p=0.0039
Eigenprotein
0.02
-0.02
-0.06
-4
-3
-2
-1
0
1
Global Cognitive Function

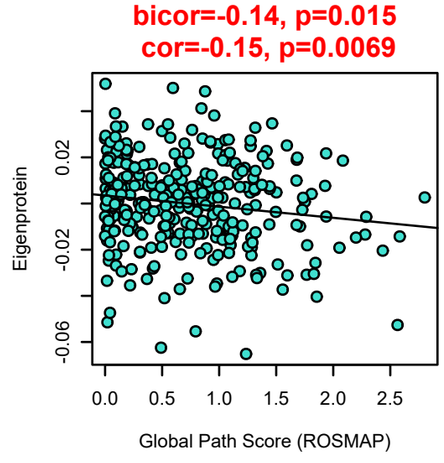

bicor=0.13, p=0.018
cor=0.18, p=0.0012
Eigenprotein
0.02
-0.02
-0.06
0
5
10
15
20
25
30
MMSE, final (ROSMAP)

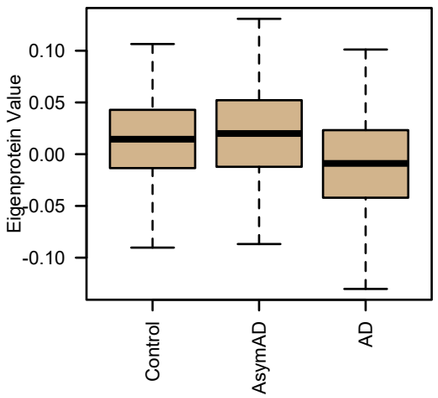

bicor=-0.15, p=0.0062
cor=-0.16, p=0.0039
Eigenprotein
0.02
-0.02
-0.06
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

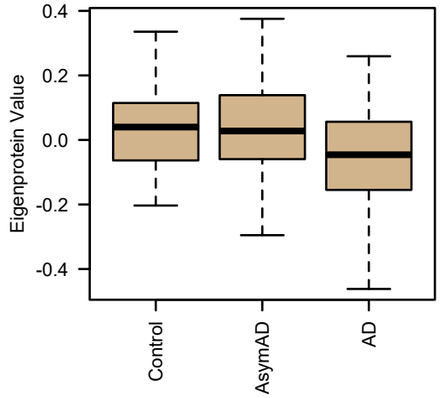

bicor=-0.15, p=0.0059
cor=-0.18, p=0.0012
Eigenprotein
0.02
-0.02
-0.06
0
1
2
3
4
5
6
Braak, final (ROSMAP)

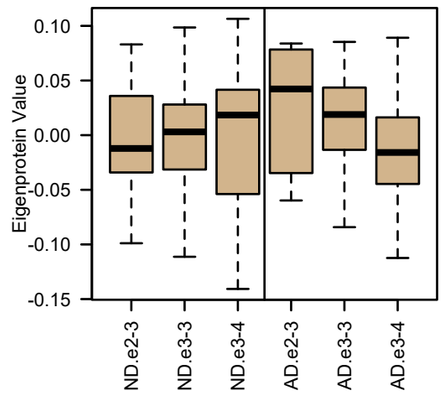

bicor=-0.01, p=0.86
cor=0.0082, p=0.88
Eigenprotein
0.02
-0.02
-0.06
0
5
10
15
20
Amyloid (ROSMAP)

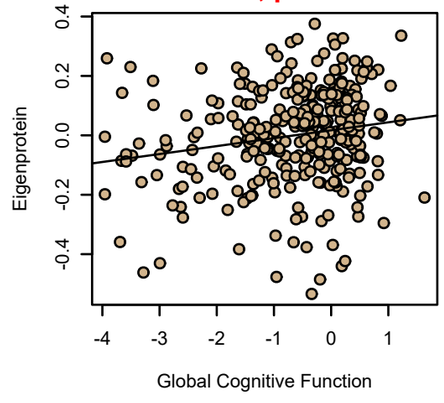

bicor=-0.091, p=0.1
cor=-0.16, p=0.004
Eigenprotein
0.02
-0.02
-0.06
0
5
10
15
20
25
30
Tangles (ROSMAP)

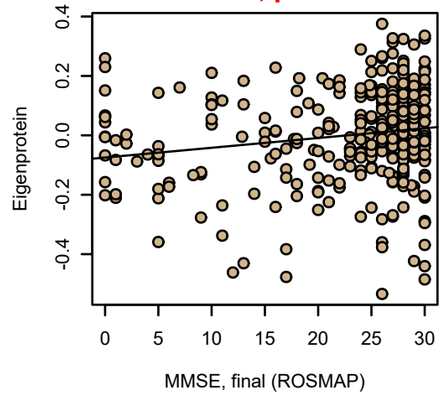

bicor=-0.14, p=0.015
cor=-0.15, p=0.0069
Eigenprotein
0.02
-0.02
-0.06
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

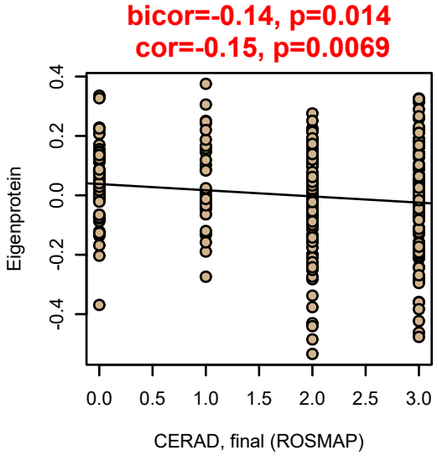

M12 tan.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

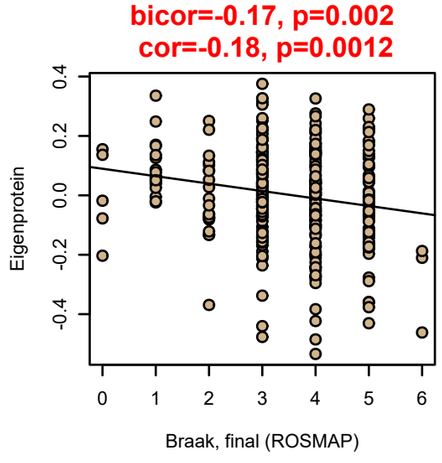

M12 tan.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.00047
Eigenprotein Value
0.4
0.2
0.0
-0.2
-0.4
Control
AsymAD
AD

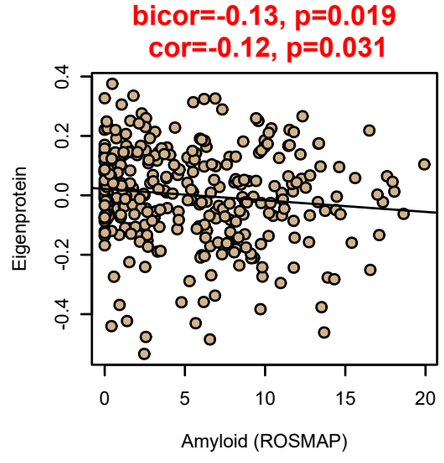

M12 tan
ND K-W p = 0.92 | AD K-W p = 0.14
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
-0.15
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

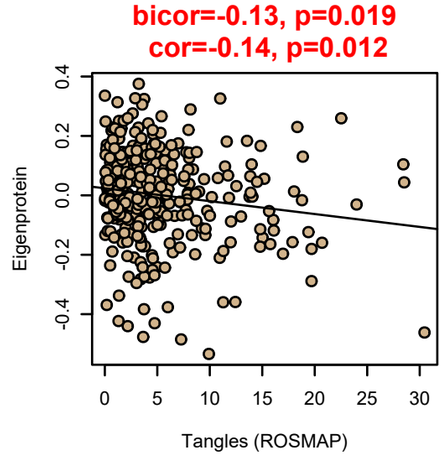

bicor=0.18, p=0.00087
cor=0.18, p=0.0012
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
-4
-3
-2
-1
0
1
Global Cognitive Function

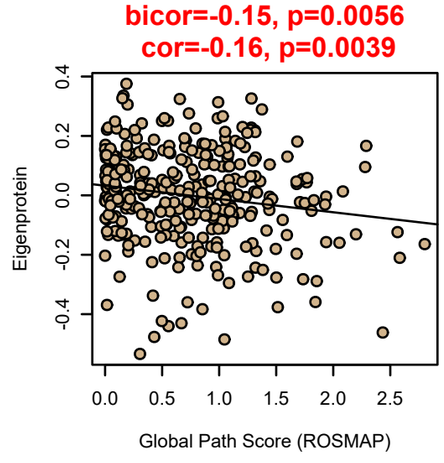

bicor=0.19, p=0.00045
cor=0.17, p=0.0022
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0
5
10
15
20
25
30
MMSE, final (ROSMAP)

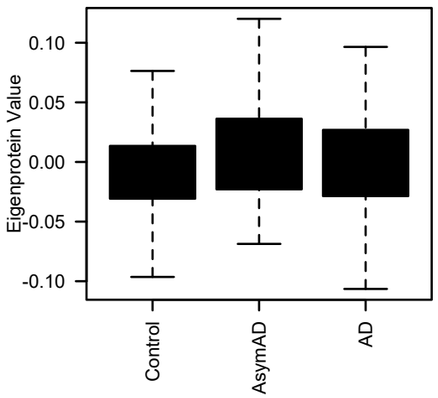

bicor=-0.14, p=0.014
cor=-0.15, p=0.0069
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

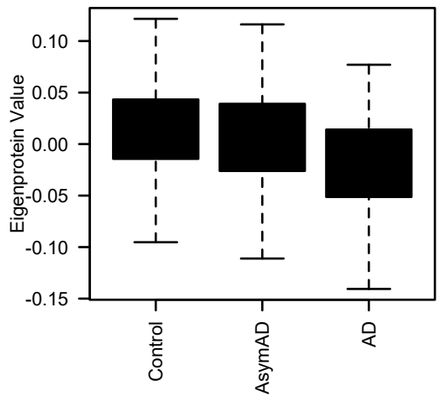

bicor=-0.17, p=0.002
cor=-0.18, p=0.0012
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0
1
2
3
4
5
6
Braak, final (ROSMAP)

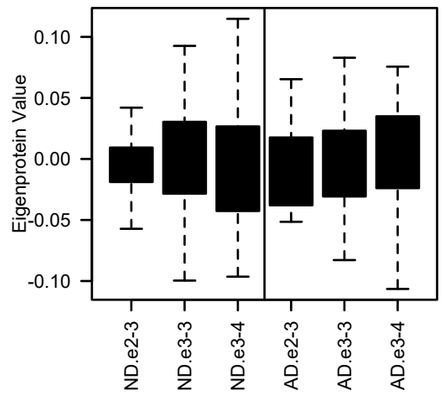

bicor=-0.13, p=0.019
cor=-0.12, p=0.031
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0
5
10
15
20
Amyloid (ROSMAP)

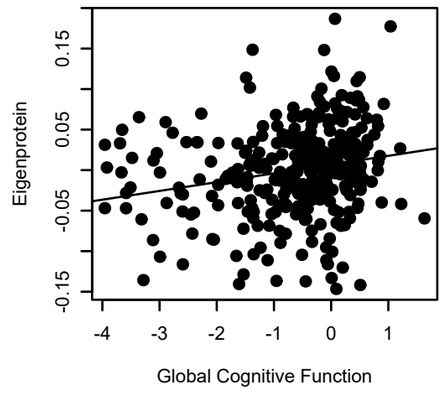

bicor=-0.13, p=0.019
cor=-0.14, p=0.012
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0
5
10
15
20
25
30
Tangles (ROSMAP)

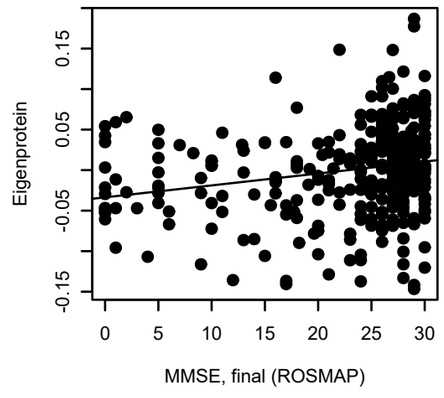

bicor=-0.15, p=0.0056
cor=-0.16, p=0.0039
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

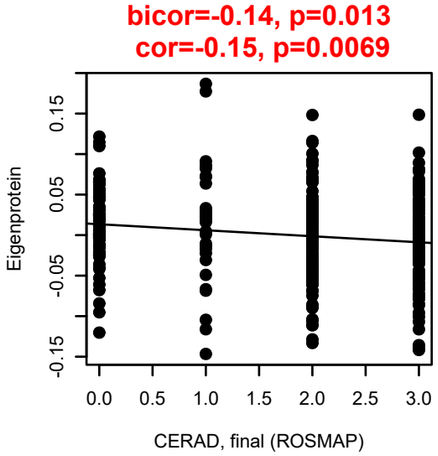

M7 black.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

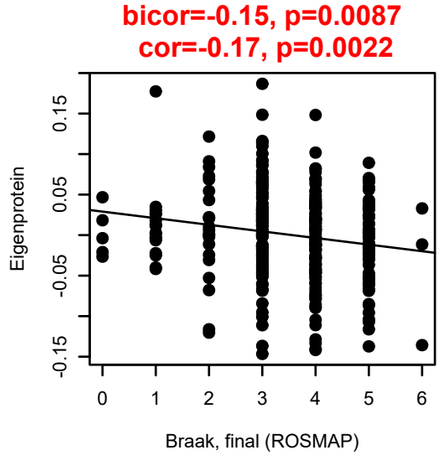

M7 black.ROSMAP TMT (Synthetic)
K-W ANOVA p: 1.5e-05
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
AsymAD
AD

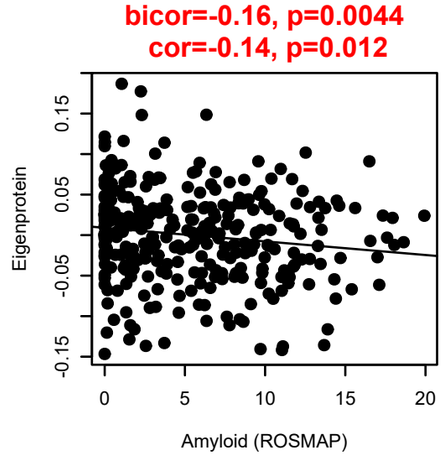

M7 black
ND K-W p = 0.58 | AD K-W p = 0.96
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

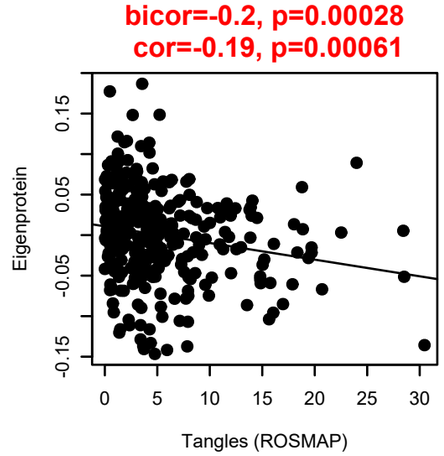

bicor=0.25, p=3.7e-06
cor=0.21, p=0.00014
Eigenprotein
0.15
0.05
-0.05
-0.15
-4
-3
-2
-1
0
1
Global Cognitive Function

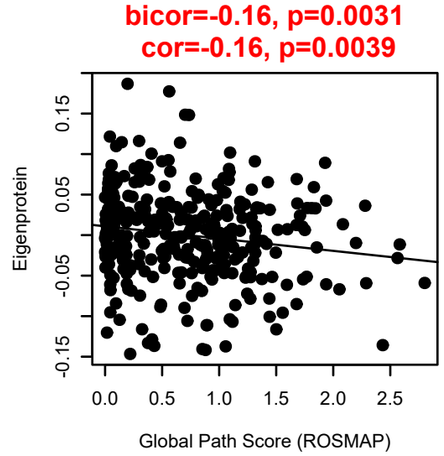

bicor=0.27, p=1.3e-06
cor=0.22, p=6.7e-05
Eigenprotein
0.15
0.05
-0.05
-0.15
0
5
10
15
20
25
30
MMSE, final (ROSMAP)

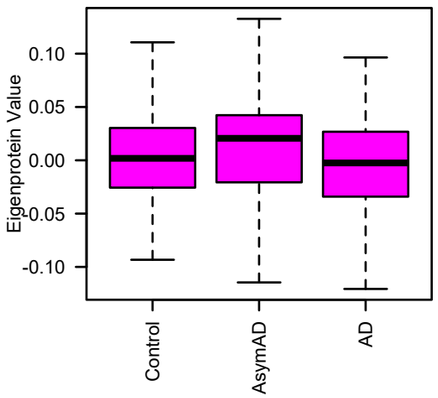

bicor=-0.14, p=0.013
cor=-0.15, p=0.0069
Eigenprotein
0.15
0.05
-0.05
-0.15
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

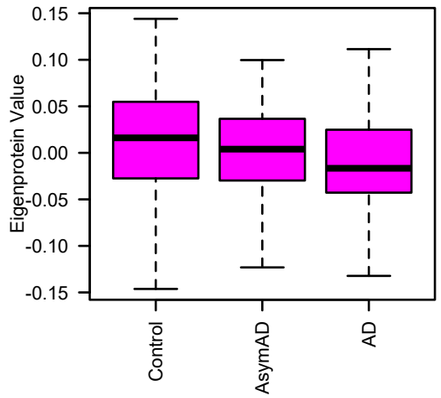

bicor=-0.15, p=0.0087
cor=-0.17, p=0.0022
Eigenprotein
0.15
0.05
-0.05
-0.15
0
1
2
3
4
5
6
Braak, final (ROSMAP)

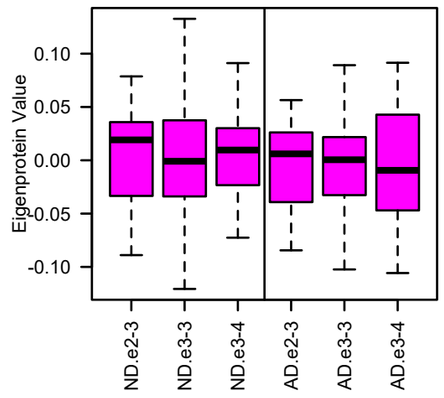

bicor=-0.16, p=0.0044
cor=-0.14, p=0.012
Eigenprotein
0.15
0.05
-0.05
-0.15
0
5
10
15
20
Amyloid (ROSMAP)

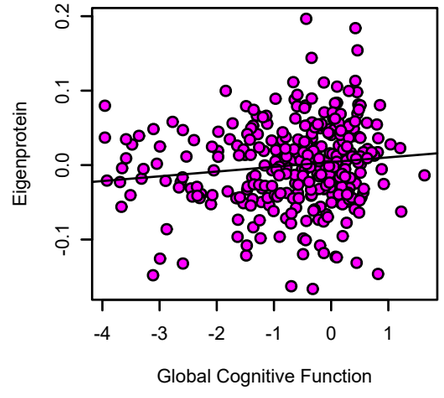

bicor=-0.2, p=0.00028
cor=-0.19, p=0.00061
Eigenprotein
0.15
0.05
-0.05
-0.15
0
5
10
15
20
25
30
Tangles (ROSMAP)

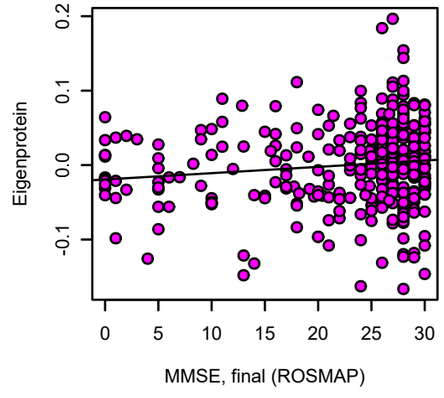

bicor=-0.16, p=0.0031
cor=-0.16, p=0.0039
Eigenprotein
0.15
0.05
-0.05
-0.15
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

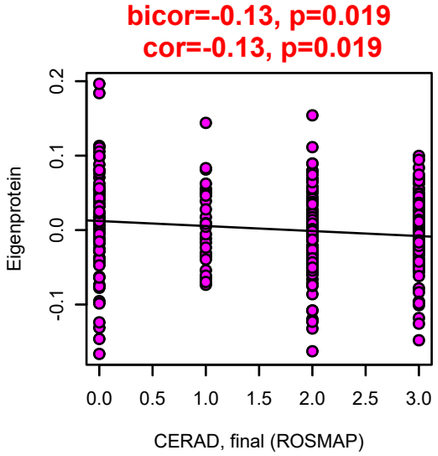

M9 magenta.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

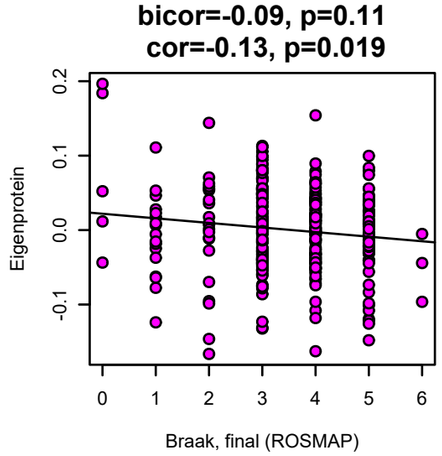

M9 magenta.ROSMAP TMT (Synthetic)
K-W ANOVA p: 0.0073
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
AsymAD
AD

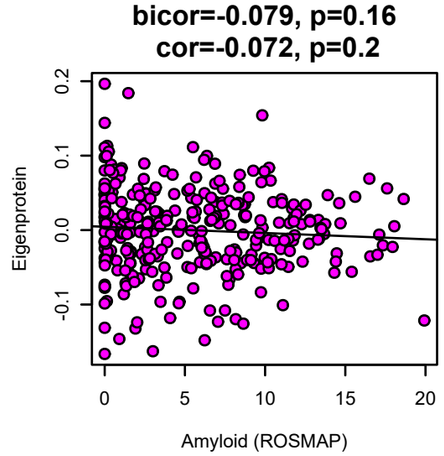

M9 magenta
ND K-W p = 0.74 | AD K-W p = 0.96
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
ND.e2-3
ND.e3-3
ND.e3-4
AD.e2-3
AD.e3-3
AD.e3-4

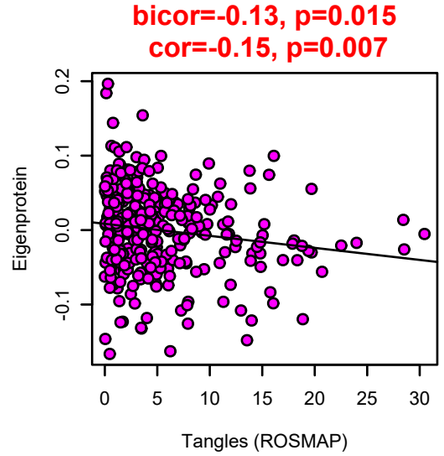

bicor=0.15, p=0.0075
cor=0.12, p=0.031
Eigenprotein
0.2
0.1
0.0
-0.1
-4
-3
-2
-1
0
1
Global Cognitive Function

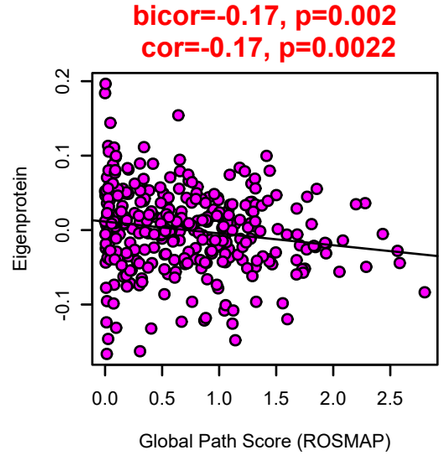

bicor=0.13, p=0.025
cor=0.13, p=0.019
Eigenprotein
0.2
0.1
0.0
-0.1
0
5
10
15
20
25
30
MMSE, final (ROSMAP)


bicor=-0.13, p=0.019
cor=-0.13, p=0.019
Eigenprotein
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD, final (ROSMAP)

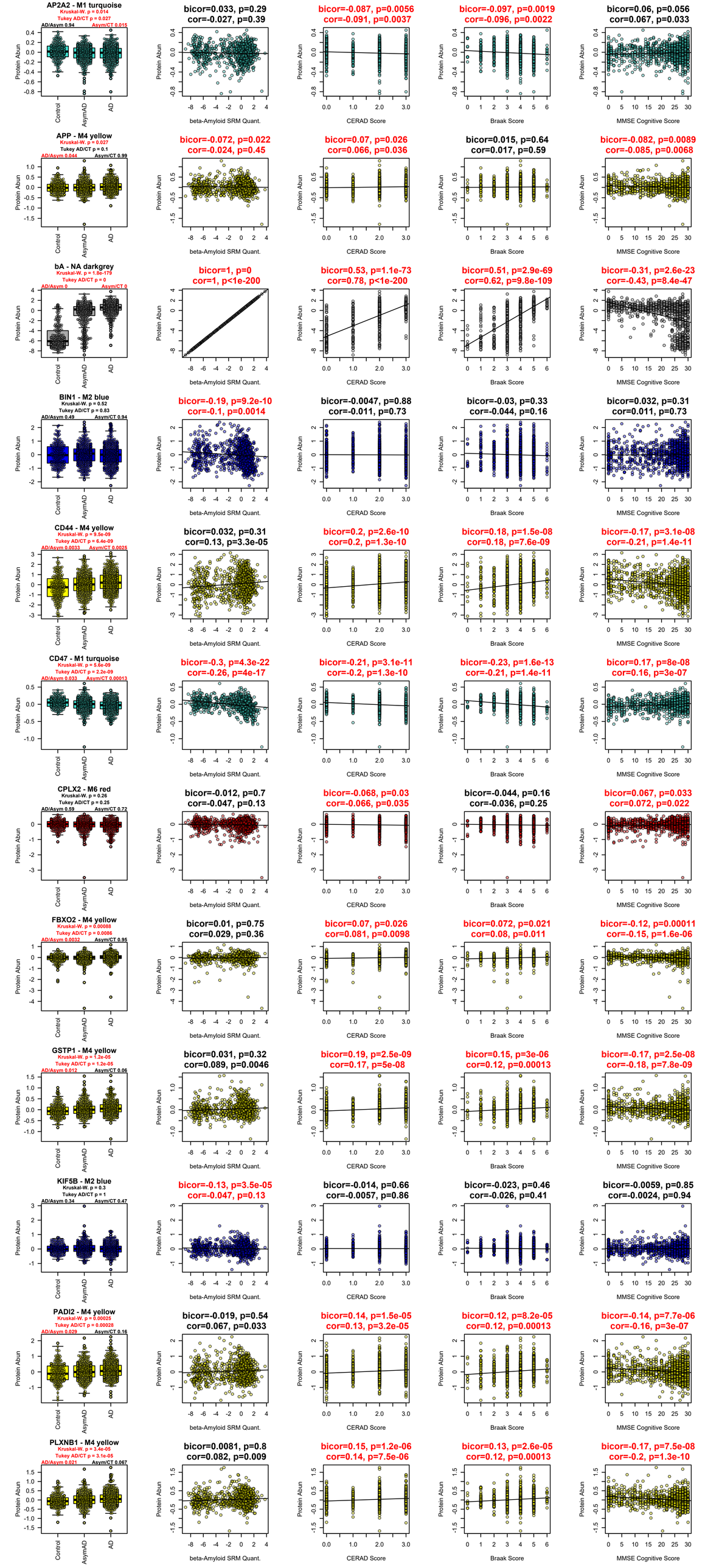

bicor=-0.09, p=0.11
cor=-0.13, p=0.019
Eigenprotein
0.2
0.1
0.0
-0.1
0
1
2
3
4
5
6
Braak, final (ROSMAP)

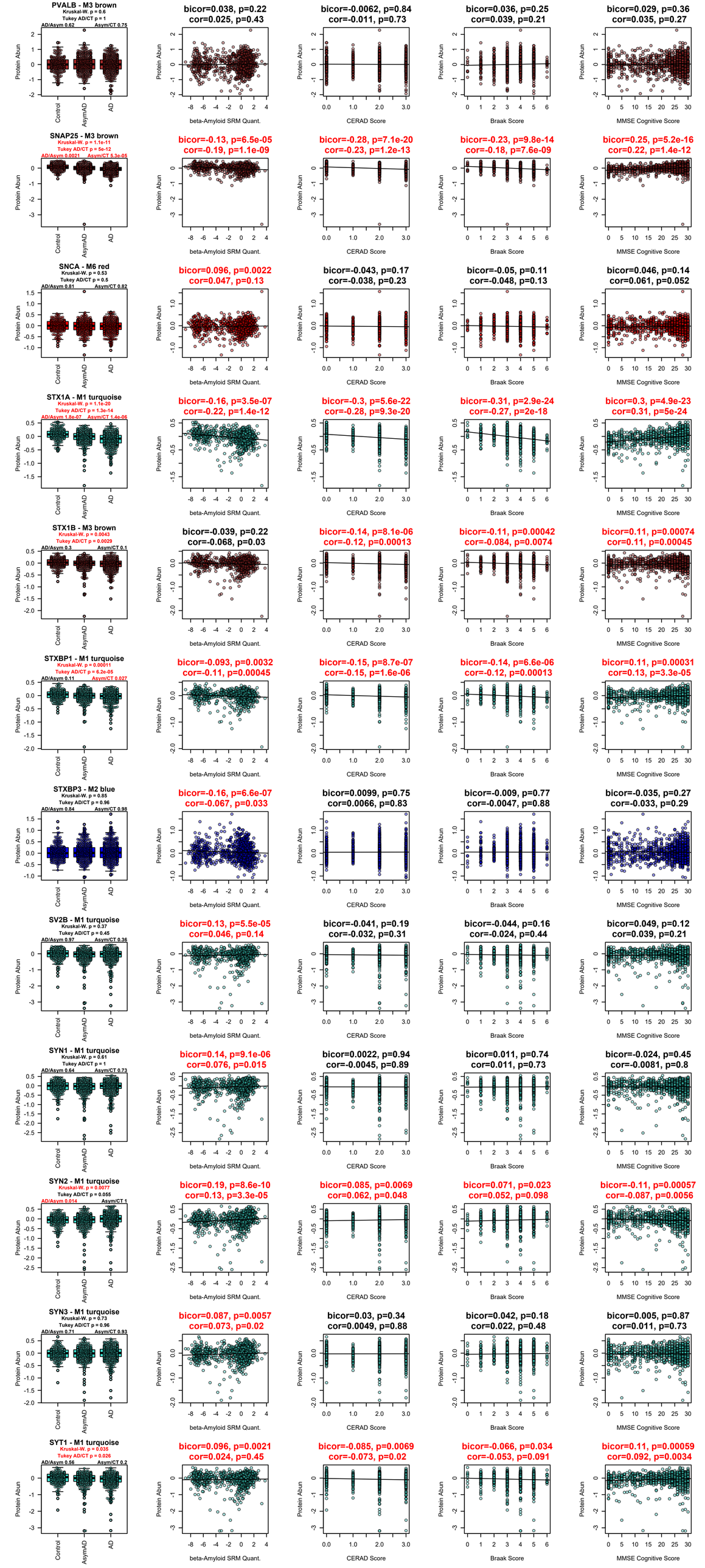

bicor=-0.079, p=0.16
cor=-0.072, p=0.2
Eigenprotein
0.2
0.1
0.0
-0.1
0
5
10
15
20
Amyloid (ROSMAP)

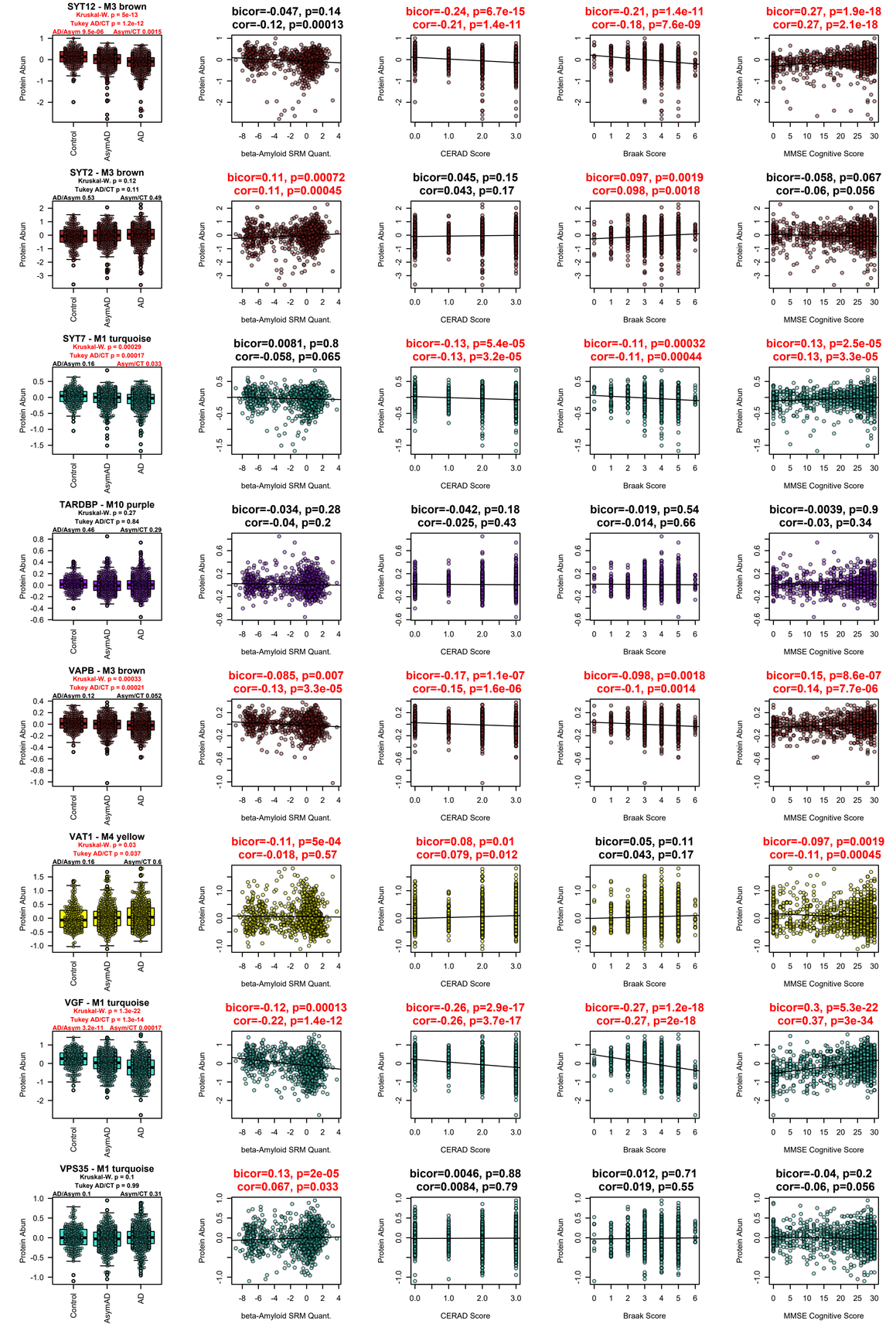

bicor=-0.13, p=0.015
cor=-0.15, p=0.007
Eigenprotein
0.2
0.1
0.0
-0.1
0
5
10
15
20
25
30
Tangles (ROSMAP)


bicor=-0.17, p=0.002
cor=-0.17, p=0.0022
Eigenprotein
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
Global Path Score (ROSMAP)

Supplementary Figure 4. AD Network Validation in ROS/MAP. The top 20% of proteins by kME value in each AD brain protein network module was used to create a synthetic eigenprotein, which was then measured by case status in ROS/MAP and correlated with different traits as assessed in the ROS/MAP cohorts (*n*=323 independent case samples after network connectivity outlier removal). The first boxplot for each module is the AD network eigenprotein by case status, given as reference for the second boxplot, which is the synthetic eigenprotein in the ROS/MAP cohorts (control, *n*=78; AsymAD, *n*=142; AD, *n*=103). Control and AsymAD cases were grouped into non-demented (ND) in the *APOE* analysis for sufficient statistical power (ND: *n*=31 E2/3, *n*=144 E3/3, *n*=36 E3/4; AD: *n*=10 E2/3, *n*=65 E3/3, *n*=25 E3/4). E2/2 (*n*=2 control, *n*=1 AsymAD) and E2/4 (*n*=6 AsymAD, *n*=3 AD) were excluded from the analysis. Synthetic eigenprotein differences by case status or *APOE* genotype in ROS/MAP were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

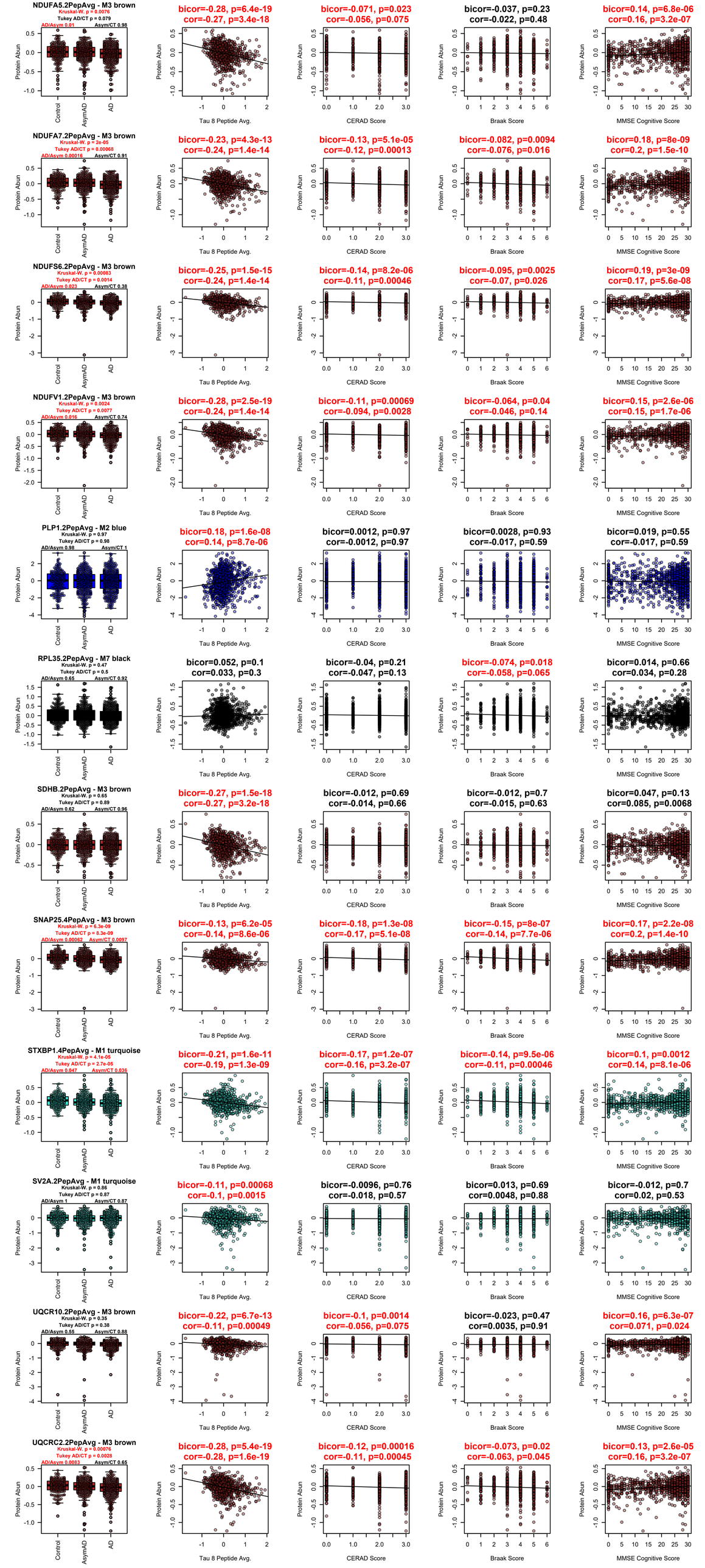

AP2A2 - M1 turquoise
Kruskal-W. p = 0.014
Tukey AD/CT p = 0.027
AD/Asym 0.94
Asym/CT 0.015
bicor=0.033, p=0.29
cor=-0.027, p=0.39
bicor=-0.087, p=0.0056
cor=-0.091, p=0.0037
bicor=-0.097, p=0.0019
cor=-0.096, p=0.0022
bicor=0.06, p=0.056
cor=0.067, p=0.033
APP - M4 yellow
Kruskal-W. p = 0.027
Tukey AD/CT p = 0.1
AD/Asym 0.044
Asym/CT 0.99
bicor=-0.072, p=0.022
cor=-0.024, p=0.45
bicor=0.07, p=0.026
cor=0.066, p=0.036
bicor=0.015, p=0.64
cor=0.017, p=0.59
bicor=-0.082, p=0.0089
cor=-0.085, p=0.0068
bA - NA darkgrey
Kruskal-W. p = 1.8e-179
Tukey AD/CT p = 0
AD/Asym 0
Asym/CT 0
bicor=1, p=0
cor=1, p<1e-200
bicor=0.53, p=1.1e-73
cor=0.78, p<1e-200
bicor=0.51, p=2.9e-69
cor=0.62, p=9.8e-109
bicor=-0.31, p=2.6e-23
cor=-0.43, p=8.4e-47
BIN1 - M2 blue
Kruskal-W. p = 0.52
Tukey AD/CT p = 0.83
AD/Asym 0.49
Asym/CT 0.94
bicor=-0.19, p=9.2e-10
cor=-0.1, p=0.0014
bicor=-0.0047, p=0.88
cor=-0.011, p=0.73
bicor=-0.03, p=0.33
cor=-0.044, p=0.16
bicor=0.032, p=0.31
cor=0.011, p=0.73
CD44 - M4 yellow
Kruskal-W. p = 9.5e-09
Tukey AD/CT p = 6.4e-09
AD/Asym 0.0033
Asym/CT 0.0025
bicor=0.032, p=0.31
cor=0.13, p=3.3e-05
bicor=0.2, p=2.6e-10
cor=0.2, p=1.3e-10
bicor=0.18, p=1.5e-08
cor=0.18, p=7.6e-09
bicor=-0.17, p=3.1e-08
cor=-0.21, p=1.4e-11
CD47 - M1 turquoise
Kruskal-W. p = 5.6e-09
Tukey AD/CT p = 2.2e-09
AD/Asym 0.033
Asym/CT 0.00013
bicor=-0.3, p=4.3e-22
cor=-0.26, p=4e-17
bicor=-0.21, p=3.1e-11
cor=-0.2, p=1.3e-10
bicor=-0.23, p=1.6e-13
cor=-0.21, p=1.4e-11
bicor=0.17, p=8e-08
cor=0.16, p=3e-07
CPLX2 - M6 red
Kruskal-W. p = 0.26
Tukey AD/CT p = 0.25
AD/Asym 0.59
Asym/CT 0.72
bicor=-0.012, p=0.7
cor=-0.047, p=0.13
bicor=-0.068, p=0.03
cor=-0.066, p=0.035
bicor=-0.044, p=0.16
cor=-0.036, p=0.25
bicor=0.067, p=0.033
cor=0.072, p=0.022
FBXO2 - M4 yellow
Kruskal-W. p = 0.00088
Tukey AD/CT p = 0.0086
AD/Asym 0.0032
Asym/CT 0.95
bicor=0.01, p=0.75
cor=0.029, p=0.36
bicor=0.07, p=0.026
cor=0.081, p=0.0098
bicor=0.072, p=0.021
cor=0.08, p=0.011
bicor=-0.12, p=0.00011
cor=-0.15, p=1.6e-06
GSTP1 - M4 yellow
Kruskal-W. p = 1.2e-05
Tukey AD/CT p = 1.2e-05
AD/Asym 0.012
Asym/CT 0.06
bicor=0.031, p=0.32
cor=0.089, p=0.0046
bicor=0.19, p=2.5e-09
cor=0.17, p=5e-08
bicor=0.15, p=3e-06
cor=0.12, p=0.00013
bicor=-0.17, p=2.5e-08
cor=-0.18, p=7.8e-09
KIF5B - M2 blue
Kruskal-W. p = 0.3
Tukey AD/CT p = 1
AD/Asym 0.34
Asym/CT 0.47
bicor=-0.13, p=3.5e-05
cor=-0.047, p=0.13
bicor=-0.014, p=0.66
cor=-0.0057, p=0.86
bicor=-0.023, p=0.46
cor=-0.026, p=0.41
bicor=-0.0059, p=0.85
cor=-0.0024, p=0.94
PADI2 - M4 yellow
Kruskal-W. p = 0.00025
Tukey AD/CT p = 0.00028
AD/Asym 0.029
Asym/CT 0.16
bicor=-0.019, p=0.54
cor=0.067, p=0.033
bicor=0.14, p=1.5e-05
cor=0.13, p=3.2e-05
bicor=0.12, p=8.2e-05
cor=0.12, p=0.00013
bicor=-0.14, p=7.7e-06
cor=-0.16, p=3e-07
PLXNB1 - M4 yellow
Kruskal-W. p = 3.4e-05
Tukey AD/CT p = 3.1e-05
AD/Asym 0.021
Asym/CT 0.067
bicor=0.0081, p=0.8
cor=0.082, p=0.009
bicor=0.15, p=1.2e-06
cor=0.14, p=7.5e-06
bicor=0.13, p=2.6e-05
cor=0.12, p=0.00013
bicor=-0.17, p=7.5e-08
cor=-0.2, p=1.3e-10
Protein Abun
Control
AsymAD
AD
beta-Amyloid SRM Quant.
CERAD Score
Braak Score
MMSE Cognitive Score

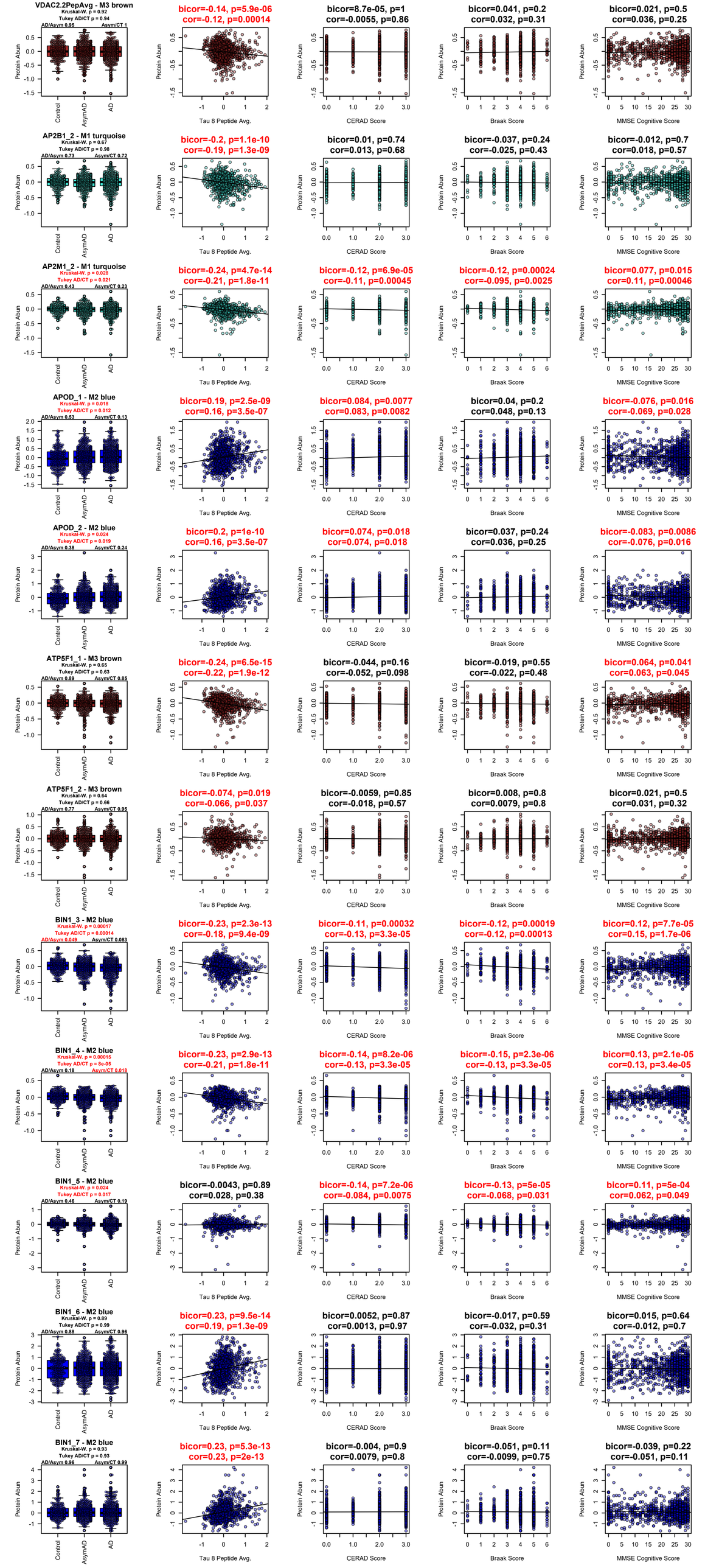

PVALB - M3 brown
Kruskal-W. p = 0.6
Tukey AD/CT p = 1
AD/Asym 0.62
Asym/CT 0.75
bicor=0.038, p=0.22
cor=0.025, p=0.43
bicor=-0.0062, p=0.84
cor=-0.011, p=0.73
bicor=0.036, p=0.25
cor=0.039, p=0.21
bicor=0.029, p=0.36
cor=0.035, p=0.27
SNAP25 - M3 brown
Kruskal-W. p = 1.1e-11
Tukey AD/CT p = 5e-12
AD/Asym 0.0021
Asym/CT 5.3e-05
bicor=-0.13, p=6.5e-05
cor=-0.19, p=1.1e-09
bicor=-0.28, p=7.1e-20
cor=-0.23, p=1.2e-13
bicor=-0.23, p=9.8e-14
cor=-0.18, p=7.6e-09
bicor=0.25, p=5.2e-16
cor=0.22, p=1.4e-12
SNCA - M6 red
Kruskal-W. p = 0.53
Tukey AD/CT p = 0.5
AD/Asym 0.81
Asym/CT 0.82
bicor=0.096, p=0.0022
cor=0.047, p=0.13
bicor=-0.043, p=0.17
cor=-0.038, p=0.23
bicor=-0.05, p=0.11
cor=-0.048, p=0.13
bicor=0.046, p=0.14
cor=0.061, p=0.052
STX1A - M1 turquoise
Kruskal-W. p = 1.1e-20
Tukey AD/CT p = 1.3e-14
AD/Asym 1.8e-07
Asym/CT 1.4e-06
bicor=-0.16, p=3.5e-07
cor=-0.22, p=1.4e-12
bicor=-0.3, p=5.6e-22
cor=-0.28, p=9.3e-20
bicor=-0.31, p=2.9e-24
cor=-0.27, p=2e-18
bicor=0.3, p=4.9e-23
cor=0.31, p=5e-24
STX1B - M3 brown
Kruskal-W. p = 0.0043
Tukey AD/CT p = 0.0029
AD/Asym 0.3
Asym/CT 0.1
bicor=-0.039, p=0.22
cor=-0.068, p=0.03
bicor=-0.14, p=8.1e-06
cor=-0.12, p=0.00013
bicor=-0.11, p=0.00042
cor=-0.084, p=0.0074
bicor=0.11, p=0.00074
cor=0.11, p=0.00045
STXBP1 - M1 turquoise
Kruskal-W. p = 0.00011
Tukey AD/CT p = 6.2e-05
AD/Asym 0.11
Asym/CT 0.027
bicor=-0.093, p=0.0032
cor=-0.11, p=0.00045
bicor=-0.15, p=8.7e-07
cor=-0.15, p=1.6e-06
bicor=-0.14, p=6.6e-06
cor=-0.12, p=0.00013
bicor=0.11, p=0.00031
cor=0.13, p=3.3e-05
STXBP3 - M2 blue
Kruskal-W. p = 0.85
Tukey AD/CT p = 0.96
AD/Asym 0.84
Asym/CT 0.98
bicor=-0.16, p=6.6e-07
cor=-0.067, p=0.033
bicor=0.0099, p=0.75
cor=0.0066, p=0.83
bicor=-0.009, p=0.77
cor=-0.0047, p=0.88
bicor=-0.035, p=0.27
cor=-0.033, p=0.29
SV2B - M1 turquoise
Kruskal-W. p = 0.37
Tukey AD/CT p = 0.45
AD/Asym 0.97
Asym/CT 0.36
bicor=0.13, p=5.5e-05
cor=0.046, p=0.14
bicor=-0.041, p=0.19
cor=-0.032, p=0.31
bicor=-0.044, p=0.16
cor=-0.024, p=0.44
bicor=0.049, p=0.12
cor=0.039, p=0.21
SYN1 - M1 turquoise
Kruskal-W. p = 0.61
Tukey AD/CT p = 1
AD/Asym 0.64
Asym/CT 0.73
bicor=0.14, p=9.1e-06
cor=0.076, p=0.015
bicor=0.0022, p=0.94
cor=-0.0045, p=0.89
bicor=0.011, p=0.74
cor=0.011, p=0.73
bicor=-0.024, p=0.45
cor=-0.0081, p=0.8
SYN2 - M1 turquoise
Kruskal-W. p = 0.0077
Tukey AD/CT p = 0.055
AD/Asym 0.014
Asym/CT 1
bicor=0.19, p=8.6e-10
cor=0.13, p=3.3e-05
bicor=0.085, p=0.0069
cor=0.062, p=0.048
bicor=0.071, p=0.023
cor=0.052, p=0.098
bicor=-0.11, p=0.00057
cor=-0.087, p=0.0056
SYN3 - M1 turquoise
Kruskal-W. p = 0.73
Tukey AD/CT p = 0.96
AD/Asym 0.71
Asym/CT 0.93
bicor=0.087, p=0.0057
cor=0.073, p=0.02
bicor=0.03, p=0.34
cor=0.0049, p=0.88
bicor=0.042, p=0.18
cor=0.022, p=0.48
bicor=0.005, p=0.87
cor=0.011, p=0.73
SYT1 - M1 turquoise
Kruskal-W. p = 0.035
Tukey AD/CT p = 0.026
AD/Asym 0.56
Asym/CT 0.2
bicor=0.096, p=0.0021
cor=0.024, p=0.45
bicor=-0.085, p=0.0069
cor=-0.073, p=0.02
bicor=-0.066, p=0.034
cor=-0.053, p=0.091
bicor=0.11, p=0.00059
cor=0.092, p=0.0034
Protein Abun
Control
AsymAD
AD
beta-Amyloid SRM Quant.
CERAD Score
Braak Score
MMSE Cognitive Score

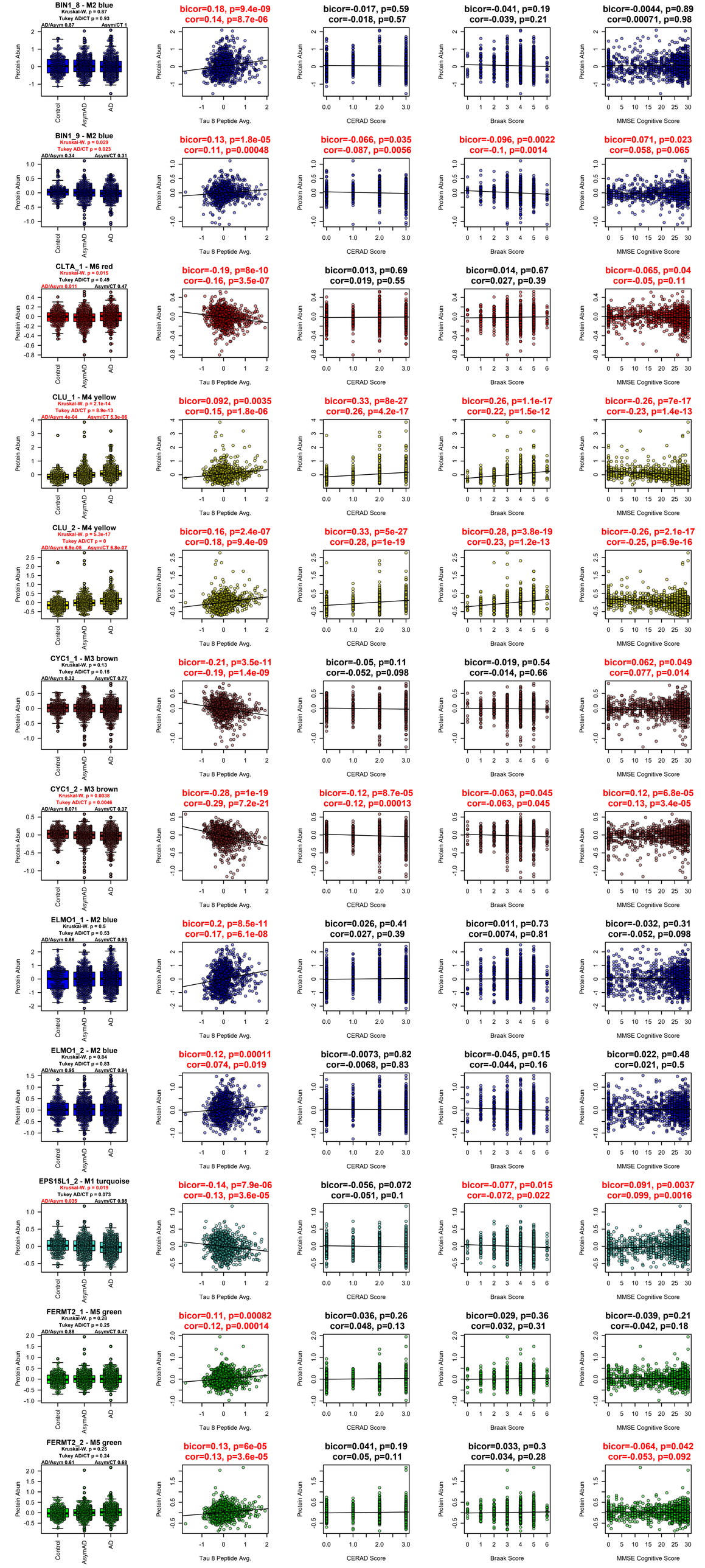

SYT12 - M3 brown
Kruskal-W. p = 5e-13
Tukey AD/CT p = 1.2e-12
AD/Asym 9.5e-06
Asym/CT 0.0015
bicor=-0.047, p=0.14
cor=-0.12, p=0.00013
bicor=-0.24, p=6.7e-15
cor=-0.21, p=1.4e-11
bicor=-0.21, p=1.4e-11
cor=-0.18, p=7.6e-09
bicor=0.27, p=1.9e-18
cor=0.27, p=2.1e-18
SYT2 - M3 brown
Kruskal-W. p = 0.12
Tukey AD/CT p = 0.11
AD/Asym 0.53
Asym/CT 0.49
bicor=0.11, p=0.00072
cor=0.11, p=0.00045
bicor=0.045, p=0.15
cor=0.043, p=0.17
bicor=0.097, p=0.0019
cor=0.098, p=0.0018
bicor=-0.058, p=0.067
cor=-0.06, p=0.056
SYT7 - M1 turquoise
Kruskal-W. p = 0.00029
Tukey AD/CT p = 0.00017
AD/Asym 0.16
Asym/CT 0.033
bicor=0.0081, p=0.8
cor=-0.058, p=0.065
bicor=-0.13, p=5.4e-05
cor=-0.13, p=3.2e-05
bicor=-0.11, p=0.00032
cor=-0.11, p=0.00044
bicor=0.13, p=2.5e-05
cor=0.13, p=3.3e-05
TARDBP - M10 purple
Kruskal-W. p = 0.27
Tukey AD/CT p = 0.84
AD/Asym 0.46
Asym/CT 0.29
bicor=-0.034, p=0.28
cor=-0.04, p=0.2
bicor=-0.042, p=0.18
cor=-0.025, p=0.43
bicor=-0.019, p=0.54
cor=-0.014, p=0.66
bicor=-0.0039, p=0.9
cor=-0.03, p=0.34
VAPB - M3 brown
Kruskal-W. p = 0.00033
Tukey AD/CT p = 0.00021
AD/Asym 0.12
Asym/CT 0.052
bicor=-0.085, p=0.007
cor=-0.13, p=3.3e-05
bicor=-0.17, p=1.1e-07
cor=-0.15, p=1.6e-06
bicor=-0.098, p=0.0018
cor=-0.1, p=0.0014
bicor=0.15, p=8.6e-07
cor=0.14, p=7.7e-06
VAT1 - M4 yellow
Kruskal-W. p = 0.03
Tukey AD/CT p = 0.037
AD/Asym 0.16
Asym/CT 0.6
bicor=-0.11, p=5e-04
cor=-0.018, p=0.57
bicor=0.08, p=0.01
cor=0.079, p=0.012
bicor=0.05, p=0.11
cor=0.043, p=0.17
bicor=-0.097, p=0.0019
cor=-0.11, p=0.00045
VGF - M1 turquoise
Kruskal-W. p = 1.3e-22
Tukey AD/CT p = 1.3e-14
AD/Asym 3.2e-11
Asym/CT 0.00017
bicor=-0.12, p=0.00013
cor=-0.22, p=1.4e-12
bicor=-0.26, p=2.9e-17
cor=-0.26, p=3.7e-17
bicor=-0.27, p=1.2e-18
cor=-0.27, p=2e-18
bicor=0.3, p=5.3e-22
cor=0.37, p=3e-34
VPS35 - M1 turquoise
Kruskal-W. p = 0.1
Tukey AD/CT p = 0.99
AD/Asym 0.1
Asym/CT 0.31
bicor=0.13, p=2e-05
cor=0.067, p=0.033
bicor=0.0046, p=0.88
cor=0.0084, p=0.79
bicor=0.012, p=0.71
cor=0.019, p=0.55
bicor=-0.04, p=0.2
cor=-0.06, p=0.056
Protein Abun
Control
AsymAD
AD
beta-Amyloid SRM Quant.
CERAD Score
Braak Score
MMSE Cognitive Score

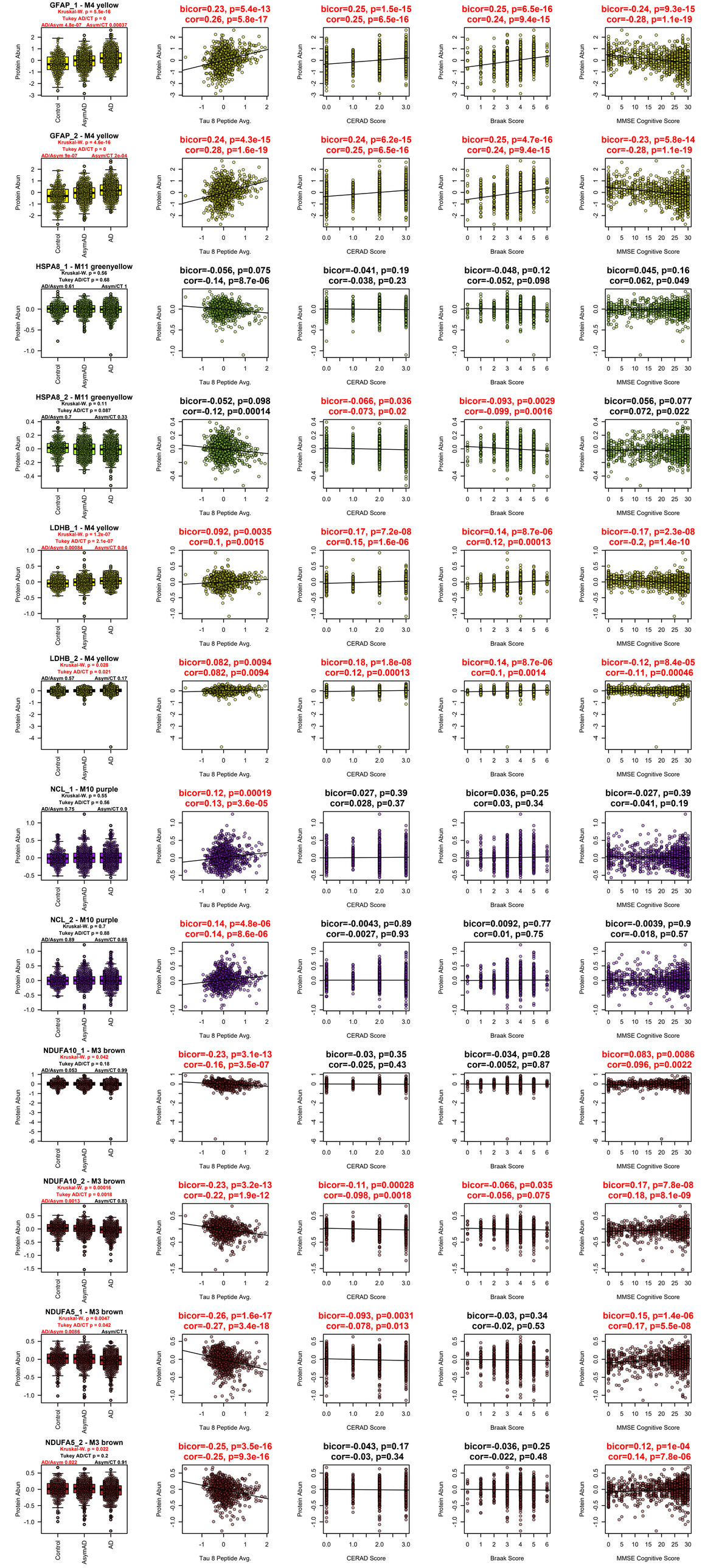
Supplementary Figure 5. Round 1 Targeted Measurements of AD Network Proteins in ROS/MAP. Levels of 67 proteins were measured by selected reaction monitoring (SRM) mass spectrometry across 1016 ROS/MAP cases (control, *n*=139; AsymAD, *n*=384; AD, *n*=439 independent case samples). One peptide per protein was selected for measurement. Peptide sequences can be found at https://www.synapse.org/#!Synapse:syn10468856. Protein levels were correlated to Aβ levels as measured by SRM, CERAD score, Braak stage, and MMSE. Protein level differences by case status were assessed by Kruskal-Wallis (K-W) one-way ANOVA with Tukey test. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Data for each protein is colored by the AD network module in which it resides. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

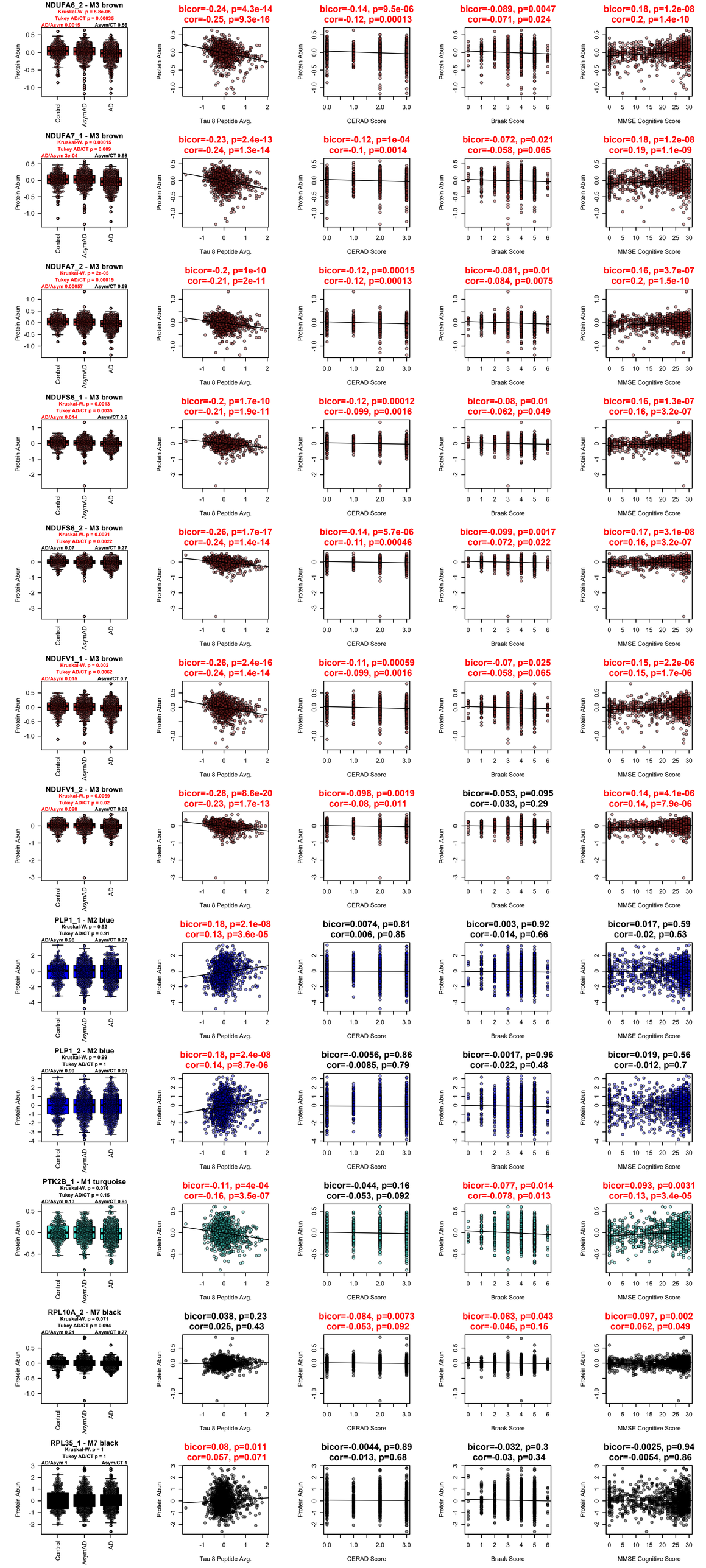
APOD.2PepAvg - M2 blue Kruskal-W. p = 0.019 Tukey AD/CT p = 0.014 AD/Asym 0.44 Asym/CT 0.17	**bicor=0.2, p=4.6e-10** **cor=0.16, p=3.5e-07**	**bicor=0.079, p=0.011** **cor=0.079, p=0.012**	**bicor=0.039, p=0.22** **cor=0.043, p=0.17**	**bicor=-0.076, p=0.016** **cor=-0.074, p=0.019**
ATP5F1.2PepAvg - M3 brown Kruskal-W. p = 0.6 Tukey AD/CT p = 0.59 AD/Asym 0.81 Asym/CT 0.89	**bicor=-0.16, p=5.4e-07** **cor=-0.15, p=1.8e-06**	**bicor=-0.032, p=0.31** **cor=-0.037, p=0.24**	**bicor=-0.0041, p=0.9** **cor=-0.0055, p=0.86**	**bicor=0.053, p=0.093** **cor=0.05, p=0.11**
BIN1.7PepAvg - M2 blue Kruskal-W. p = 0.3 Tukey AD/CT p = 0.32 AD/Asym 0.54 Asym/CT 0.84	**bicor=0.23, p=1e-13** **cor=0.19, p=1.6e-09**	**bicor=-0.042, p=0.18** **cor=-0.047, p=0.14**	**bicor=-0.074, p=0.019** **cor=-0.077, p=0.015**	**bicor=0.024, p=0.45** **cor=0.019, p=0.55**
CLU.2PepAvg - M4 yellow Kruskal-W. p = 2.2e-16 Tukey AD/CT p = 8.8e-13 AD/Asym 0.00012 Asym/CT 9.4e-07	**bicor=0.13, p=3.8e-05** **cor=0.17, p=6.2e-08**	**bicor=0.34, p=2.6e-29** **cor=0.28, p=1.1e-19**	**bicor=0.28, p=4.7e-20** **cor=0.23, p=1.3e-13**	**bicor=-0.27, p=5e-18** **cor=-0.24, p=1.1e-14**
CYC1.2PepAvg - M3 brown Kruskal-W. p = 0.019 Tukey AD/CT p = 0.023 AD/Asym 0.14 Asym/CT 0.52	**bicor=-0.26, p=7.5e-17** **cor=-0.25, p=9.9e-16**	**bicor=-0.09, p=0.0044** **cor=-0.087, p=0.0056**	**bicor=-0.045, p=0.15** **cor=-0.04, p=0.2**	**bicor=0.1, p=0.0011** **cor=0.11, p=0.00046**
ELMO1.2PepAvg - M2 blue Kruskal-W. p = 0.85 Tukey AD/CT p = 0.87 AD/Asym 0.9 Asym/CT 0.99	**bicor=0.18, p=6.5e-09** **cor=0.14, p=8.7e-06**	**bicor=0.015, p=0.63** **cor=0.015, p=0.63**	**bicor=-0.0055, p=0.86** **cor=-0.012, p=0.7**	**bicor=-0.0049, p=0.88** **cor=-0.026, p=0.41**
FERMT2.2PepAvg - M5 green Kruskal-W. p = 0.21 Tukey AD/CT p = 0.18 AD/Asym 0.71 Asym/CT 0.51	**bicor=0.12, p=0.00014** **cor=0.14, p=8.6e-06**	**bicor=0.038, p=0.23** **cor=0.054, p=0.086**	**bicor=0.028, p=0.37** **cor=0.036, p=0.25**	**bicor=-0.054, p=0.088** **cor=-0.052, p=0.098**
GFAP.2PepAvg - M4 yellow Kruskal-W. p = 3.2e-16 Tukey AD/CT p = 0 AD/Asym 5.5e-07 Asym/CT 0.00024	**bicor=0.24, p=3.4e-14** **cor=0.27, p=3.2e-18**	**bicor=0.24, p=2.7e-15** **cor=0.25, p=6.5e-16**	**bicor=0.25, p=4e-16** **cor=0.24, p=9.4e-15**	**bicor=-0.24, p=1.6e-14** **cor=-0.28, p=1.1e-19**
HSPA8.2PepAvg - M11 greenyellov Kruskal-W. p = 0.24 Tukey AD/CT p = 0.23 AD/Asym 0.63 Asym/CT 0.65	**bicor=-0.06, p=0.058** **cor=-0.14, p=8.7e-06**	**bicor=-0.055, p=0.08** **cor=-0.064, p=0.042**	**bicor=-0.076, p=0.016** **cor=-0.084, p=0.0075**	**bicor=0.058, p=0.064** **cor=0.074, p=0.019**
LDHB.2PepAvg - M4 yellow Kruskal-W. p = 2.3e-05 Tukey AD/CT p = 1.7e-05 AD/Asym 0.032 Asym/CT 0.037	**bicor=0.11, p=0.00075** **cor=0.11, p=0.00049**	**bicor=0.2, p=1.1e-10** **cor=0.16, p=3.2e-07**	**bicor=0.16, p=1.7e-07** **cor=0.13, p=3.4e-05**	**bicor=-0.18, p=4.4e-09** **cor=-0.18, p=8.5e-09**
NCL.2PepAvg - M10 purple Kruskal-W. p = 0.72 Tukey AD/CT p = 0.71 AD/Asym 0.99 Asym/CT 0.78	**bicor=0.14, p=1e-05** **cor=0.14, p=8.6e-06**	**bicor=0.0096, p=0.76** **cor=0.013, p=0.68**	**bicor=0.025, p=0.43** **cor=0.021, p=0.5**	**bicor=-0.015, p=0.63** **cor=-0.031, p=0.32**
NDUFA10.2PepAvg - M3 brown Kruskal-W. p = 0.0016 Tukey AD/CT p = 0.016 AD/Asym 0.0045 Asym/CT 0.98	**bicor=-0.25, p=1.5e-15** **cor=-0.21, p=1.8e-11**	**bicor=-0.072, p=0.022** **cor=-0.062, p=0.048**	**bicor=-0.057, p=0.072** **cor=-0.029, p=0.36**	**bicor=0.13, p=3e-05** **cor=0.15, p=1.6e-06**

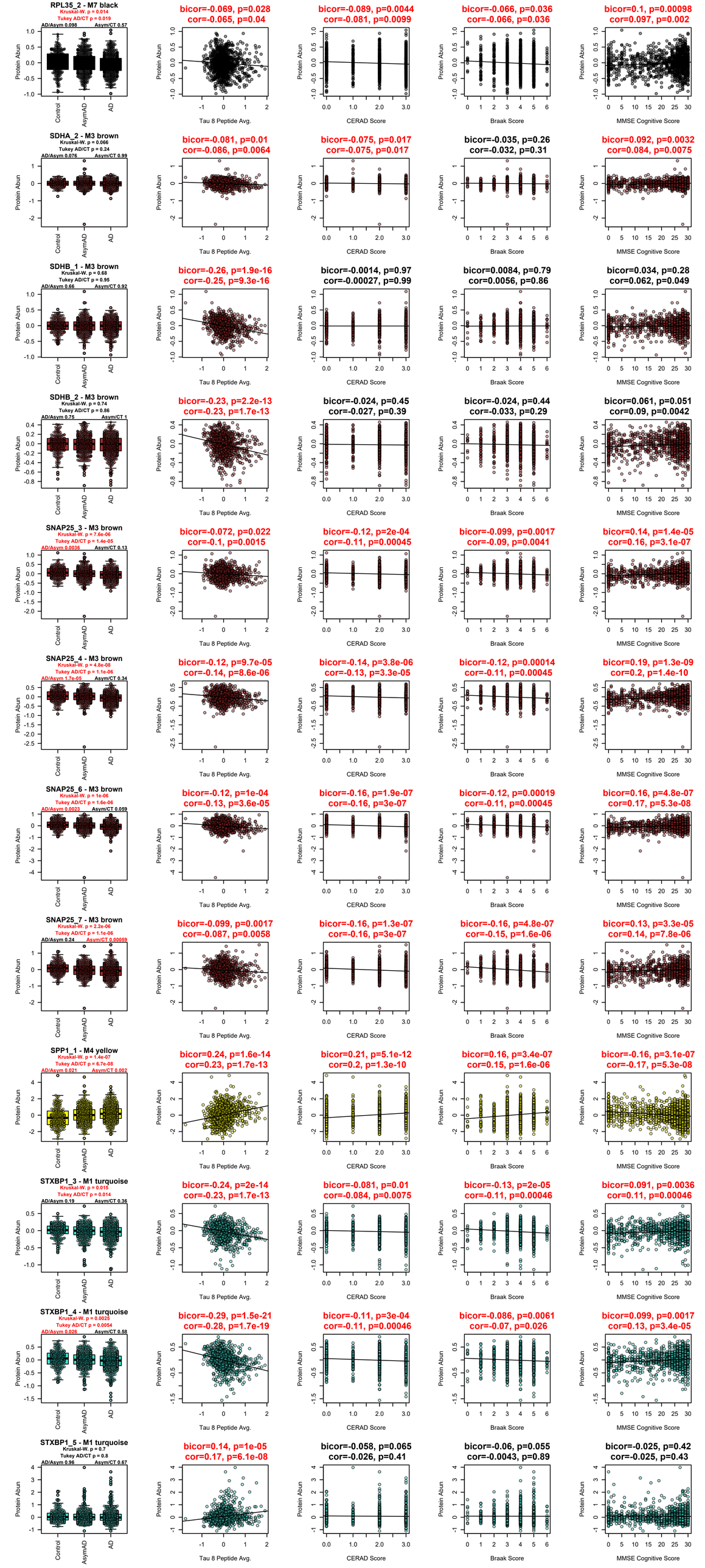

NDUFA5.2PepAvg - M3 brown
Kruskal-W. p = 0.0076
Tukey AD/CT p = 0.079
AD/Asym 0.01
Asym/CT 0.98
bicor=-0.28, p=6.4e-19
cor=-0.27, p=3.4e-18
bicor=-0.071, p=0.023
cor=-0.056, p=0.075
bicor=-0.037, p=0.23
cor=-0.022, p=0.48
bicor=0.14, p=6.8e-06
cor=0.16, p=3.2e-07
NDUFA7.2PepAvg - M3 brown
Kruskal-W. p = 2e-05
Tukey AD/CT p = 0.00068
AD/Asym 0.00016
Asym/CT 0.91
bicor=-0.23, p=4.3e-13
cor=-0.24, p=1.4e-14
bicor=-0.13, p=5.1e-05
cor=-0.12, p=0.00013
bicor=-0.082, p=0.0094
cor=-0.076, p=0.016
bicor=0.18, p=8e-09
cor=0.2, p=1.5e-10
NDUFS6.2PepAvg - M3 brown
Kruskal-W. p = 0.00083
Tukey AD/CT p = 0.0014
AD/Asym 0.023
Asym/CT 0.38
bicor=-0.25, p=1.5e-15
cor=-0.24, p=1.4e-14
bicor=-0.14, p=8.2e-06
cor=-0.11, p=0.00046
bicor=-0.095, p=0.0025
cor=-0.07, p=0.026
bicor=0.19, p=3e-09
cor=0.17, p=5.6e-08
NDUFV1.2PepAvg - M3 brown
Kruskal-W. p = 0.0024
Tukey AD/CT p = 0.0077
AD/Asym 0.016
Asym/CT 0.74
bicor=-0.28, p=2.5e-19
cor=-0.24, p=1.4e-14
bicor=-0.11, p=0.00069
cor=-0.094, p=0.0028
bicor=-0.064, p=0.04
cor=-0.046, p=0.14
bicor=0.15, p=2.6e-06
cor=0.15, p=1.7e-06
PLP1.2PepAvg - M2 blue
Kruskal-W. p = 0.97
Tukey AD/CT p = 0.98
AD/Asym 0.98
Asym/CT 1
bicor=0.18, p=1.6e-08
cor=0.14, p=8.7e-06
bicor=0.0012, p=0.97
cor=-0.0012, p=0.97
bicor=0.0028, p=0.93
cor=-0.017, p=0.59
bicor=0.019, p=0.55
cor=-0.017, p=0.59
RPL35.2PepAvg - M7 black
Kruskal-W. p = 0.47
Tukey AD/CT p = 0.6
AD/Asym 0.65
Asym/CT 0.92
bicor=0.052, p=0.1
cor=0.033, p=0.3
bicor=-0.04, p=0.21
cor=-0.047, p=0.13
bicor=-0.074, p=0.018
cor=-0.058, p=0.065
bicor=0.014, p=0.66
cor=0.034, p=0.28
SDHB.2PepAvg - M3 brown
Kruskal-W. p = 0.65
Tukey AD/CT p = 0.89
AD/Asym 0.62
Asym/CT 0.96
bicor=-0.27, p=1.5e-18
cor=-0.27, p=3.2e-18
bicor=-0.012, p=0.69
cor=-0.014, p=0.66
bicor=-0.012, p=0.7
cor=-0.015, p=0.63
bicor=0.047, p=0.13
cor=0.085, p=0.0068
SNAP25.4PepAvg - M3 brown
Kruskal-W. p = 6.3e-09
Tukey AD/CT p = 8.3e-09
AD/Asym 0.00062
Asym/CT 0.0097
bicor=-0.13, p=6.2e-05
cor=-0.14, p=8.6e-06
bicor=-0.18, p=1.3e-08
cor=-0.17, p=5.1e-08
bicor=-0.15, p=8e-07
cor=-0.14, p=7.7e-06
bicor=0.17, p=2.2e-08
cor=0.2, p=1.4e-10
STXBP1.4PepAvg - M1 turquoise
Kruskal-W. p = 4.1e-05
Tukey AD/CT p = 2.7e-05
AD/Asym 0.047
Asym/CT 0.036
bicor=-0.21, p=1.6e-11
cor=-0.19, p=1.3e-09
bicor=-0.17, p=1.2e-07
cor=-0.16, p=3.2e-07
bicor=-0.14, p=9.5e-06
cor=-0.11, p=0.00046
bicor=0.1, p=0.0012
cor=0.14, p=8.1e-06
SV2A.2PepAvg - M1 turquoise
Kruskal-W. p = 0.86
Tukey AD/CT p = 0.87
AD/Asym 1
Asym/CT 0.87
bicor=-0.11, p=0.00068
cor=-0.1, p=0.0015
bicor=-0.0096, p=0.76
cor=-0.018, p=0.57
bicor=0.013, p=0.69
cor=0.0048, p=0.88
bicor=-0.012, p=0.7
cor=0.02, p=0.53
UQCR10.2PepAvg - M3 brown
Kruskal-W. p = 0.35
Tukey AD/CT p = 0.38
AD/Asym 0.55
Asym/CT 0.88
bicor=-0.22, p=6.7e-13
cor=-0.11, p=0.00049
bicor=-0.1, p=0.0014
cor=-0.056, p=0.075
bicor=-0.023, p=0.47
cor=0.0035, p=0.91
bicor=0.16, p=6.3e-07
cor=0.071, p=0.024
UQCRC2.2PepAvg - M3 brown
Kruskal-W. p = 0.00076
Tukey AD/CT p = 0.0028
AD/Asym 0.0083
Asym/CT 0.65
bicor=-0.28, p=5.4e-19
cor=-0.28, p=1.6e-19
bicor=-0.12, p=0.00016
cor=-0.11, p=0.00045
bicor=-0.073, p=0.02
cor=-0.063, p=0.045
bicor=0.13, p=2.6e-05
cor=0.16, p=3.2e-07
Protein Abun
Control
AsymAD
AD
Tau 8 Peptide Avg.
CERAD Score
Braak Score
MMSE Cognitive Score

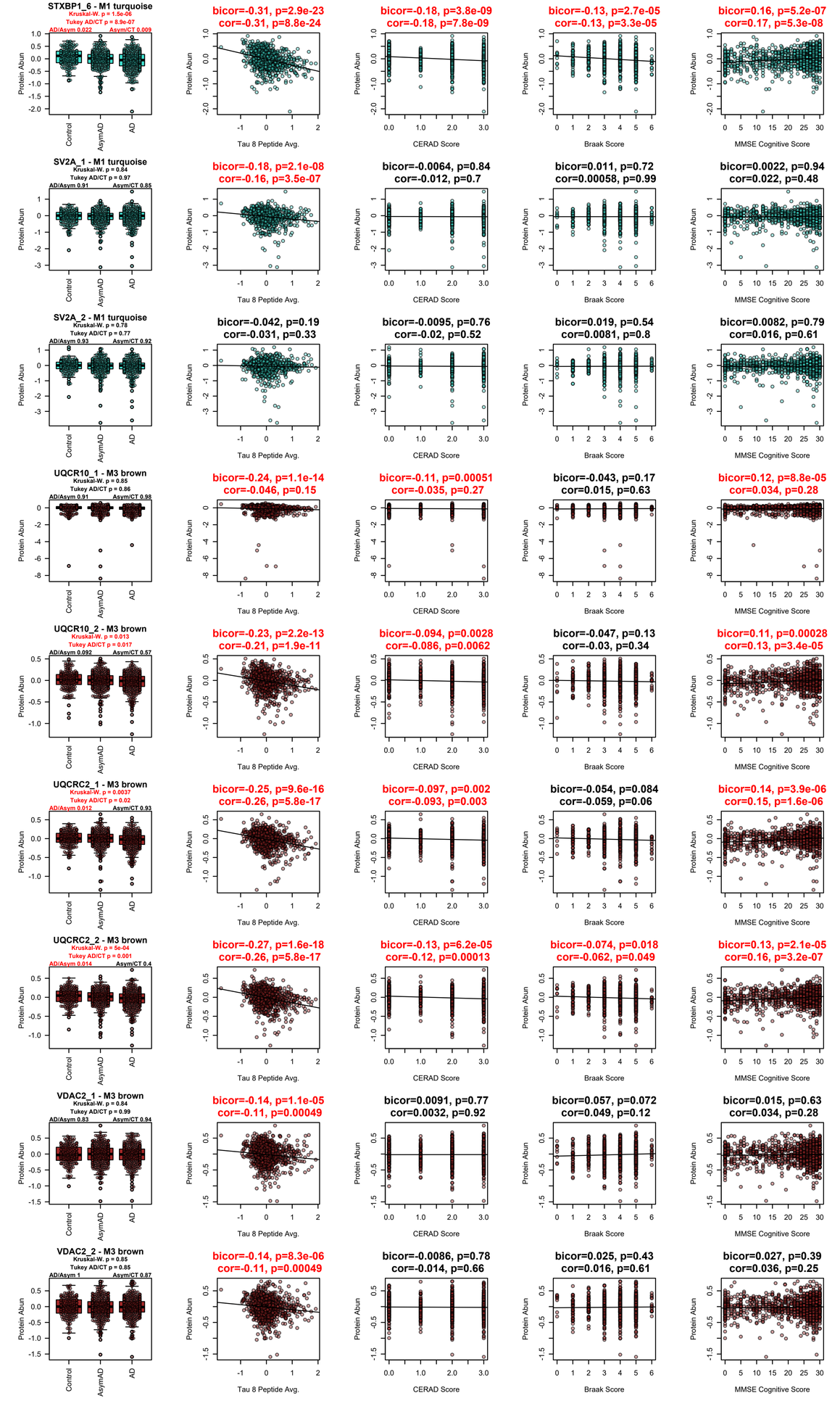

VDAC2.2PepAvg - M3 brown
Kruskal-W. p = 0.92
Tukey AD/CT p = 0.94
AD/Asym 0.95
Asym/CT 1
bicor=-0.14, p=5.9e-06
cor=-0.12, p=0.00014
bicor=8.7e-05, p=1
cor=-0.0055, p=0.86
bicor=0.041, p=0.2
cor=0.032, p=0.31
bicor=0.021, p=0.5
cor=0.036, p=0.25
AP2B1_2 - M1 turquoise
Kruskal-W. p = 0.67
Tukey AD/CT p = 0.98
AD/Asym 0.73
Asym/CT 0.72
bicor=-0.2, p=1.1e-10
cor=-0.19, p=1.3e-09
bicor=0.01, p=0.74
cor=0.013, p=0.68
bicor=-0.037, p=0.24
cor=-0.025, p=0.43
bicor=-0.012, p=0.7
cor=0.018, p=0.57
AP2M1_2 - M1 turquoise
Kruskal-W. p = 0.028
Tukey AD/CT p = 0.021
AD/Asym 0.43
Asym/CT 0.23
bicor=-0.24, p=4.7e-14
cor=-0.21, p=1.8e-11
bicor=-0.12, p=6.9e-05
cor=-0.11, p=0.00045
bicor=-0.12, p=0.00024
cor=-0.095, p=0.0025
bicor=0.077, p=0.015
cor=0.11, p=0.00046
APOD_1 - M2 blue
Kruskal-W. p = 0.018
Tukey AD/CT p = 0.012
AD/Asym 0.53
Asym/CT 0.13
bicor=0.19, p=2.5e-09
cor=0.16, p=3.5e-07
bicor=0.084, p=0.0077
cor=0.083, p=0.0082
bicor=0.04, p=0.2
cor=0.048, p=0.13
bicor=-0.076, p=0.016
cor=-0.069, p=0.028
APOD_2 - M2 blue
Kruskal-W. p = 0.024
Tukey AD/CT p = 0.019
AD/Asym 0.38
Asym/CT 0.24
bicor=0.2, p=1e-10
cor=0.16, p=3.5e-07
bicor=0.074, p=0.018
cor=0.074, p=0.018
bicor=0.037, p=0.24
cor=0.036, p=0.25
bicor=-0.083, p=0.0086
cor=-0.076, p=0.016
ATP5F1_1 - M3 brown
Kruskal-W. p = 0.65
Tukey AD/CT p = 0.63
AD/Asym 0.89
Asym/CT 0.85
bicor=-0.24, p=6.5e-15
cor=-0.22, p=1.9e-12
bicor=-0.044, p=0.16
cor=-0.052, p=0.098
bicor=-0.019, p=0.55
cor=-0.022, p=0.48
bicor=0.064, p=0.041
cor=0.063, p=0.045
ATP5F1_2 - M3 brown
Kruskal-W. p = 0.64
Tukey AD/CT p = 0.66
AD/Asym 0.77
Asym/CT 0.95
bicor=-0.074, p=0.019
cor=-0.066, p=0.037
bicor=-0.0059, p=0.85
cor=-0.018, p=0.57
bicor=0.008, p=0.8
cor=0.0079, p=0.8
bicor=0.021, p=0.5
cor=0.031, p=0.32
BIN1_3 - M2 blue
Kruskal-W. p = 0.00017
Tukey AD/CT p = 0.00014
AD/Asym 0.049
Asym/CT 0.083
bicor=-0.23, p=2.3e-13
cor=-0.18, p=9.4e-09
bicor=-0.11, p=0.00032
cor=-0.13, p=3.3e-05
bicor=-0.12, p=0.00019
cor=-0.12, p=0.00013
bicor=0.12, p=7.7e-05
cor=0.15, p=1.7e-06
BIN1_4 - M2 blue
Kruskal-W. p = 0.00015
Tukey AD/CT p = 8e-05
AD/Asym 0.18
Asym/CT 0.018
bicor=-0.23, p=2.9e-13
cor=-0.21, p=1.8e-11
bicor=-0.14, p=8.2e-06
cor=-0.13, p=3.3e-05
bicor=-0.15, p=2.3e-06
cor=-0.13, p=3.3e-05
bicor=0.13, p=2.1e-05
cor=0.13, p=3.4e-05
BIN1_5 - M2 blue
Kruskal-W. p = 0.024
Tukey AD/CT p = 0.017
AD/Asym 0.46
Asym/CT 0.19
bicor=-0.0043, p=0.89
cor=0.028, p=0.38
bicor=-0.14, p=7.2e-06
cor=-0.084, p=0.0075
bicor=-0.13, p=5e-05
cor=-0.068, p=0.031
bicor=0.11, p=5e-04
cor=0.062, p=0.049
BIN1_6 - M2 blue
Kruskal-W. p = 0.89
Tukey AD/CT p = 0.99
AD/Asym 0.88
Asym/CT 0.96
bicor=0.23, p=9.5e-14
cor=0.19, p=1.3e-09
bicor=0.0052, p=0.87
cor=0.0013, p=0.97
bicor=-0.017, p=0.59
cor=-0.032, p=0.31
bicor=0.015, p=0.64
cor=-0.012, p=0.7
BIN1_7 - M2 blue
Kruskal-W. p = 0.93
Tukey AD/CT p = 0.93
AD/Asym 0.96
Asym/CT 0.99
bicor=0.23, p=5.3e-13
cor=0.23, p=2e-13
bicor=-0.004, p=0.9
cor=0.0079, p=0.8
bicor=-0.051, p=0.11
cor=-0.0099, p=0.75
bicor=-0.039, p=0.22
cor=-0.051, p=0.11
Protein Abun
Control
AsymAD
AD
Tau 8 Peptide Avg.
CERAD Score
Braak Score
MMSE Cognitive Score


BIN1_8 - M2 blue
Kruskal-W. p = 0.87
Tukey AD/CT p = 0.93
AD/Asym 0.87
Asym/CT 1
bicor=0.18, p=9.4e-09
cor=0.14, p=8.7e-06
bicor=-0.017, p=0.59
cor=-0.018, p=0.57
bicor=-0.041, p=0.19
cor=-0.039, p=0.21
bicor=-0.0044, p=0.89
cor=0.00071, p=0.98
BIN1_9 - M2 blue
Kruskal-W. p = 0.029
Tukey AD/CT p = 0.023
AD/Asym 0.34
Asym/CT 0.31
bicor=0.13, p=1.8e-05
cor=0.11, p=0.00048
bicor=-0.066, p=0.035
cor=-0.087, p=0.0056
bicor=-0.096, p=0.0022
cor=-0.1, p=0.0014
bicor=0.071, p=0.023
cor=0.058, p=0.065
CLTA_1 - M6 red
Kruskal-W. p = 0.015
Tukey AD/CT p = 0.49
AD/Asym 0.011
Asym/CT 0.47
bicor=-0.19, p=8e-10
cor=-0.16, p=3.5e-07
bicor=0.013, p=0.69
cor=0.019, p=0.55
bicor=0.014, p=0.67
cor=0.027, p=0.39
bicor=-0.065, p=0.04
cor=-0.05, p=0.11
CLU_1 - M4 yellow
Kruskal-W. p = 2.1e-14
Tukey AD/CT p = 8.9e-13
AD/Asym 4e-04
Asym/CT 5.3e-06
bicor=0.092, p=0.0035
cor=0.15, p=1.8e-06
bicor=0.33, p=8e-27
cor=0.26, p=4.2e-17
bicor=0.26, p=1.1e-17
cor=0.22, p=1.5e-12
bicor=-0.26, p=7e-17
cor=-0.23, p=1.4e-13
CLU_2 - M4 yellow
Kruskal-W. p = 5.3e-17
Tukey AD/CT p = 0
AD/Asym 6.9e-05
Asym/CT 6.8e-07
bicor=0.16, p=2.4e-07
cor=0.18, p=9.4e-09
bicor=0.33, p=5e-27
cor=0.28, p=1e-19
bicor=0.28, p=3.8e-19
cor=0.23, p=1.2e-13
bicor=-0.26, p=2.1e-17
cor=-0.25, p=6.9e-16
CYC1_1 - M3 brown
Kruskal-W. p = 0.13
Tukey AD/CT p = 0.15
AD/Asym 0.32
Asym/CT 0.77
bicor=-0.21, p=3.5e-11
cor=-0.19, p=1.4e-09
bicor=-0.05, p=0.11
cor=-0.052, p=0.098
bicor=-0.019, p=0.54
cor=-0.014, p=0.66
bicor=0.062, p=0.049
cor=0.077, p=0.014
CYC1_2 - M3 brown
Kruskal-W. p = 0.0038
Tukey AD/CT p = 0.0046
AD/Asym 0.071
Asym/CT 0.37
bicor=-0.28, p=1e-19
cor=-0.29, p=7.2e-21
bicor=-0.12, p=8.7e-05
cor=-0.12, p=0.00013
bicor=-0.063, p=0.045
cor=-0.063, p=0.045
bicor=0.12, p=6.8e-05
cor=0.13, p=3.4e-05
ELMO1_1 - M2 blue
Kruskal-W. p = 0.5
Tukey AD/CT p = 0.53
AD/Asym 0.66
Asym/CT 0.93
bicor=0.2, p=8.5e-11
cor=0.17, p=6.1e-08
bicor=0.026, p=0.41
cor=0.027, p=0.39
bicor=0.011, p=0.73
cor=0.0074, p=0.81
bicor=-0.032, p=0.31
cor=-0.052, p=0.098
ELMO1_2 - M2 blue
Kruskal-W. p = 0.84
Tukey AD/CT p = 0.83
AD/Asym 0.95
Asym/CT 0.94
bicor=0.12, p=0.00011
cor=0.074, p=0.019
bicor=-0.0073, p=0.82
cor=-0.0068, p=0.83
bicor=-0.045, p=0.15
cor=-0.044, p=0.16
bicor=0.022, p=0.48
cor=0.021, p=0.5
EPS15L1_2 - M1 turquoise
Kruskal-W. p = 0.019
Tukey AD/CT p = 0.073
AD/Asym 0.035
Asym/CT 0.98
bicor=-0.14, p=7.9e-06
cor=-0.13, p=3.6e-05
bicor=-0.056, p=0.072
cor=-0.051, p=0.1
bicor=-0.077, p=0.015
cor=-0.072, p=0.022
bicor=0.091, p=0.0037
cor=0.099, p=0.0016
FERMT2_1 - M5 green
Kruskal-W. p = 0.28
Tukey AD/CT p = 0.25
AD/Asym 0.88
Asym/CT 0.47
bicor=0.11, p=0.00082
cor=0.12, p=0.00014
bicor=0.036, p=0.26
cor=0.048, p=0.13
bicor=0.029, p=0.36
cor=0.032, p=0.31
bicor=-0.039, p=0.21
cor=-0.042, p=0.18
FERMT2_2 - M5 green
Kruskal-W. p = 0.25
Tukey AD/CT p = 0.24
AD/Asym 0.61
Asym/CT 0.68
bicor=0.13, p=6e-05
cor=0.13, p=3.6e-05
bicor=0.041, p=0.19
cor=0.05, p=0.11
bicor=0.033, p=0.3
cor=0.034, p=0.28
bicor=-0.064, p=0.042
cor=-0.053, p=0.092
Protein Abun
Control
AsymAD
AD
Tau 8 Peptide Avg.
CERAD Score
Braak Score
MMSE Cognitive Score

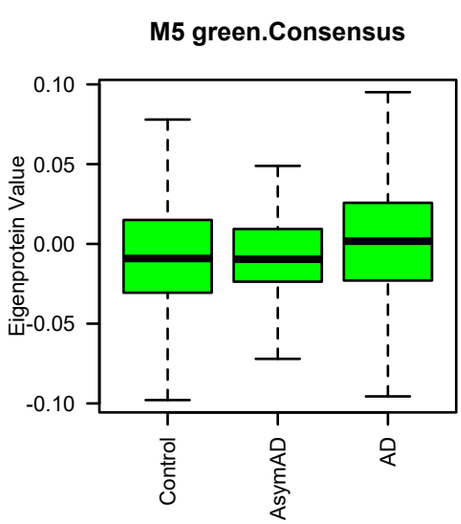

GFAP_1 - M4 yellow
Kruskal-W. p = 5.5e-16
Tukey AD/CT p = 0
AD/Asym 4.8e-07
Asym/CT 0.00037
bicor=0.23, p=5.4e-13
cor=0.26, p=5.8e-17
bicor=0.25, p=1.5e-15
cor=0.25, p=6.5e-16
bicor=0.25, p=6.5e-16
cor=0.24, p=9.4e-15
bicor=-0.24, p=9.3e-15
cor=-0.28, p=1.1e-19
GFAP_2 - M4 yellow
Kruskal-W. p = 4.5e-16
Tukey AD/CT p = 0
AD/Asym 9e-07
Asym/CT 2e-04
bicor=0.24, p=4.3e-15
cor=0.28, p=1.6e-19
bicor=0.24, p=6.2e-15
cor=0.25, p=6.5e-16
bicor=0.25, p=4.7e-16
cor=0.24, p=9.4e-15
bicor=-0.23, p=5.8e-14
cor=-0.28, p=1.1e-19
HSPA8_1 - M11 greenyellow
Kruskal-W. p = 0.56
Tukey AD/CT p = 0.68
AD/Asym 0.61
Asym/CT 1
bicor=-0.056, p=0.075
cor=-0.14, p=8.7e-06
bicor=-0.041, p=0.19
cor=-0.038, p=0.23
bicor=-0.048, p=0.12
cor=-0.052, p=0.098
bicor=0.045, p=0.16
cor=0.062, p=0.049
HSPA8_2 - M11 greenyellow
Kruskal-W. p = 0.11
Tukey AD/CT p = 0.087
AD/Asym 0.7
Asym/CT 0.33
bicor=-0.052, p=0.098
cor=-0.12, p=0.00014
bicor=-0.066, p=0.036
cor=-0.073, p=0.02
bicor=-0.093, p=0.0029
cor=-0.099, p=0.0016
bicor=0.056, p=0.077
cor=0.072, p=0.022
LDHB_1 - M4 yellow
Kruskal-W. p = 1.2e-07
Tukey AD/CT p = 2.1e-07
AD/Asym 0.00084
Asym/CT 0.04
bicor=0.092, p=0.0035
cor=0.1, p=0.0015
bicor=0.17, p=7.2e-08
cor=0.15, p=1.6e-06
bicor=0.14, p=8.7e-06
cor=0.12, p=0.00013
bicor=-0.17, p=2.3e-08
cor=-0.2, p=1.4e-10
LDHB_2 - M4 yellow
Kruskal-W. p = 0.028
Tukey AD/CT p = 0.021
AD/Asym 0.57
Asym/CT 0.17
bicor=0.082, p=0.0094
cor=0.082, p=0.0094
bicor=0.18, p=1.8e-08
cor=0.12, p=0.00013
bicor=0.14, p=8.7e-06
cor=0.1, p=0.0014
bicor=-0.12, p=8.4e-05
cor=-0.11, p=0.00046
NCL_1 - M10 purple
Kruskal-W. p = 0.55
Tukey AD/CT p = 0.56
AD/Asym 0.75
Asym/CT 0.9
bicor=0.12, p=0.00019
cor=0.13, p=3.6e-05
bicor=0.027, p=0.39
cor=0.028, p=0.37
bicor=0.036, p=0.25
cor=0.03, p=0.34
bicor=-0.027, p=0.39
cor=-0.041, p=0.19
NCL_2 - M10 purple
Kruskal-W. p = 0.7
Tukey AD/CT p = 0.88
AD/Asym 0.89
Asym/CT 0.68
bicor=0.14, p=4.8e-06
cor=0.14, p=8.6e-06
bicor=-0.0043, p=0.89
cor=-0.0027, p=0.93
bicor=0.0092, p=0.77
cor=0.01, p=0.75
bicor=-0.0039, p=0.9
cor=-0.018, p=0.57
NDUFA10_1 - M3 brown
Kruskal-W. p = 0.042
Tukey AD/CT p = 0.18
AD/Asym 0.053
Asym/CT 0.99
bicor=-0.23, p=3.1e-13
cor=-0.16, p=3.5e-07
bicor=-0.03, p=0.35
cor=-0.025, p=0.43
bicor=-0.034, p=0.28
cor=-0.0052, p=0.87
bicor=0.083, p=0.0086
cor=0.096, p=0.0022
NDUFA10_2 - M3 brown
Kruskal-W. p = 0.00016
Tukey AD/CT p = 0.0018
AD/Asym 0.0013
Asym/CT 0.83
bicor=-0.23, p=3.2e-13
cor=-0.22, p=1.9e-12
bicor=-0.11, p=0.00028
cor=-0.098, p=0.0018
bicor=-0.066, p=0.035
cor=-0.056, p=0.075
bicor=0.17, p=7.8e-08
cor=0.18, p=8.1e-09
NDUFA5_1 - M3 brown
Kruskal-W. p = 0.0047
Tukey AD/CT p = 0.042
AD/Asym 0.0086
Asym/CT 1
bicor=-0.26, p=1.6e-17
cor=-0.27, p=3.4e-18
bicor=-0.093, p=0.0031
cor=-0.078, p=0.013
bicor=-0.03, p=0.34
cor=-0.02, p=0.53
bicor=0.15, p=1.4e-06
cor=0.17, p=5.5e-08
NDUFA5_2 - M3 brown
Kruskal-W. p = 0.022
Tukey AD/CT p = 0.2
AD/Asym 0.022
Asym/CT 0.91
bicor=-0.25, p=3.5e-16
cor=-0.25, p=9.3e-16
bicor=-0.043, p=0.17
cor=-0.03, p=0.34
bicor=-0.036, p=0.25
cor=-0.022, p=0.48
bicor=0.12, p=1e-04
cor=0.14, p=7.8e-06
Protein Abun
Control
AsymAD
AD
Tau 8 Peptide Avg.
CERAD Score
Braak Score
MMSE Cognitive Score

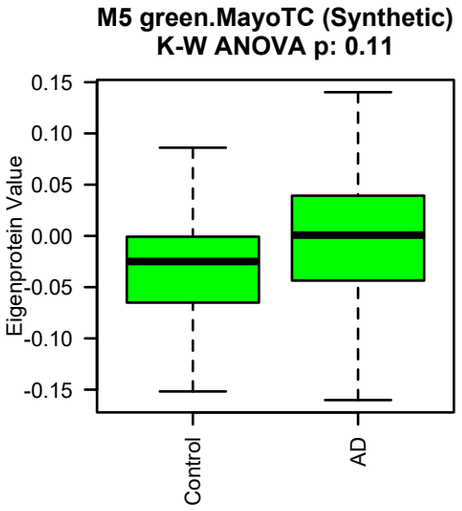

NDUFA6_2 - M3 brown
Kruskal-W. p = 5.8e-05
Tukey AD/CT p = 0.00035
AD/Asym 0.0015
Asym/CT 0.56
bicor=-0.24, p=4.3e-14
cor=-0.25, p=9.3e-16
bicor=-0.14, p=9.5e-06
cor=-0.12, p=0.00013
bicor=-0.089, p=0.0047
cor=-0.071, p=0.024
bicor=0.18, p=1.2e-08
cor=0.2, p=1.4e-10
NDUFA7_1 - M3 brown
Kruskal-W. p = 0.00015
Tukey AD/CT p = 0.009
AD/Asym 3e-04
Asym/CT 0.98
bicor=-0.23, p=2.4e-13
cor=-0.24, p=1.3e-14
bicor=-0.12, p=1e-04
cor=-0.1, p=0.0014
bicor=-0.072, p=0.021
cor=-0.058, p=0.065
bicor=0.18, p=1.2e-08
cor=0.19, p=1.1e-09
NDUFA7_2 - M3 brown
Kruskal-W. p = 2e-05
Tukey AD/CT p = 0.00019
AD/Asym 0.00057
Asym/CT 0.59
bicor=-0.2, p=1e-10
cor=-0.21, p=2e-11
bicor=-0.12, p=0.00015
cor=-0.12, p=0.00013
bicor=-0.081, p=0.01
cor=-0.084, p=0.0075
bicor=0.16, p=3.7e-07
cor=0.2, p=1.5e-10
NDUFS6_1 - M3 brown
Kruskal-W. p = 0.0013
Tukey AD/CT p = 0.0035
AD/Asym 0.014
Asym/CT 0.6
bicor=-0.2, p=1.7e-10
cor=-0.21, p=1.9e-11
bicor=-0.12, p=0.00012
cor=-0.099, p=0.0016
bicor=-0.08, p=0.01
cor=-0.062, p=0.049
bicor=0.16, p=1.3e-07
cor=0.16, p=3.2e-07
NDUFS6_2 - M3 brown
Kruskal-W. p = 0.0021
Tukey AD/CT p = 0.0022
AD/Asym 0.07
Asym/CT 0.27
bicor=-0.26, p=1.7e-17
cor=-0.24, p=1.4e-14
bicor=-0.14, p=5.7e-06
cor=-0.11, p=0.00046
bicor=-0.099, p=0.0017
cor=-0.072, p=0.022
bicor=0.17, p=3.1e-08
cor=0.16, p=3.2e-07
NDUFV1_1 - M3 brown
Kruskal-W. p = 0.002
Tukey AD/CT p = 0.0062
AD/Asym 0.015
Asym/CT 0.7
bicor=-0.26, p=2.4e-16
cor=-0.24, p=1.4e-14
bicor=-0.11, p=0.00059
cor=-0.099, p=0.0016
bicor=-0.07, p=0.025
cor=-0.058, p=0.065
bicor=0.15, p=2.2e-06
cor=0.15, p=1.7e-06
NDUFV1_2 - M3 brown
Kruskal-W. p = 0.0069
Tukey AD/CT p = 0.02
AD/Asym 0.028
Asym/CT 0.82
bicor=-0.28, p=8.6e-20
cor=-0.23, p=1.7e-13
bicor=-0.098, p=0.0019
cor=-0.08, p=0.011
bicor=-0.053, p=0.095
cor=-0.033, p=0.29
bicor=0.14, p=4.1e-06
cor=0.14, p=7.9e-06
PLP1_1 - M2 blue
Kruskal-W. p = 0.92
Tukey AD/CT p = 0.91
AD/Asym 0.98
Asym/CT 0.97
bicor=0.18, p=2.1e-08
cor=0.13, p=3.6e-05
bicor=0.0074, p=0.81
cor=0.006, p=0.85
bicor=0.003, p=0.92
cor=-0.014, p=0.66
bicor=0.017, p=0.59
cor=-0.02, p=0.53
PLP1_2 - M2 blue
Kruskal-W. p = 0.99
Tukey AD/CT p = 1
AD/Asym 0.99
Asym/CT 0.99
bicor=0.18, p=2.4e-08
cor=0.14, p=8.7e-06
bicor=-0.0056, p=0.86
cor=-0.0085, p=0.79
bicor=-0.0017, p=0.96
cor=-0.022, p=0.48
bicor=0.019, p=0.56
cor=-0.012, p=0.7
PTK2B_1 - M1 turquoise
Kruskal-W. p = 0.076
Tukey AD/CT p = 0.15
AD/Asym 0.13
Asym/CT 0.95
bicor=-0.11, p=4e-04
cor=-0.16, p=3.5e-07
bicor=-0.044, p=0.16
cor=-0.053, p=0.092
bicor=-0.077, p=0.014
cor=-0.078, p=0.013
bicor=0.093, p=0.0031
cor=0.13, p=3.4e-05
RPL10A_2 - M7 black
Kruskal-W. p = 0.071
Tukey AD/CT p = 0.094
AD/Asym 0.21
Asym/CT 0.77
bicor=0.038, p=0.23
cor=0.025, p=0.43
bicor=-0.084, p=0.0073
cor=-0.053, p=0.092
bicor=-0.063, p=0.043
cor=-0.045, p=0.15
bicor=0.097, p=0.002
cor=0.062, p=0.049
RPL35_1 - M7 black
Kruskal-W. p = 1
Tukey AD/CT p = 1
AD/Asym 1
Asym/CT 1
bicor=0.08, p=0.011
cor=0.057, p=0.071
bicor=-0.0044, p=0.89
cor=-0.013, p=0.68
bicor=-0.032, p=0.3
cor=-0.03, p=0.34
bicor=-0.0025, p=0.94
cor=-0.0054, p=0.86
Protein Abun
Control
AsymAD
AD
Tau 8 Peptide Avg.
CERAD Score
Braak Score
MMSE Cognitive Score

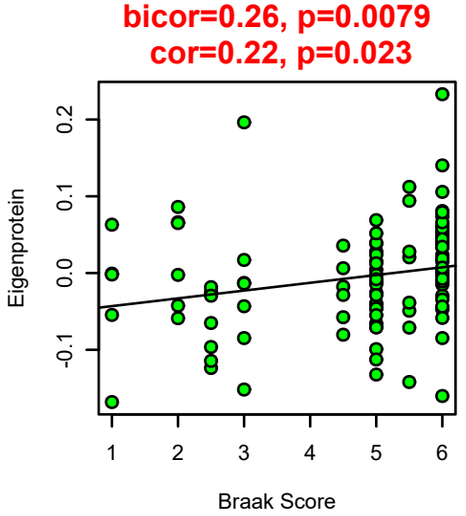

RPL35_2 - M7 black
Kruskal-W. p = 0.014
Tukey AD/CT p = 0.019
AD/Asym 0.098
Asym/CT 0.57
bicor=-0.069, p=0.028
cor=-0.065, p=0.04
bicor=-0.089, p=0.0044
cor=-0.081, p=0.0099
bicor=-0.066, p=0.036
cor=-0.066, p=0.036
bicor=0.1, p=0.00098
cor=0.097, p=0.002
SDHA_2 - M3 brown
Kruskal-W. p = 0.066
Tukey AD/CT p = 0.24
AD/Asym 0.076
Asym/CT 0.99
bicor=-0.081, p=0.01
cor=-0.086, p=0.0064
bicor=-0.075, p=0.017
cor=-0.075, p=0.017
bicor=-0.035, p=0.26
cor=-0.032, p=0.31
bicor=0.092, p=0.0032
cor=0.084, p=0.0075
SDHB_1 - M3 brown
Kruskal-W. p = 0.68
Tukey AD/CT p = 0.95
AD/Asym 0.66
Asym/CT 0.92
bicor=-0.26, p=1.9e-16
cor=-0.25, p=9.3e-16
bicor=-0.0014, p=0.97
cor=-0.00027, p=0.99
bicor=0.0084, p=0.79
cor=0.0056, p=0.86
bicor=0.034, p=0.28
cor=0.062, p=0.049
SDHB_2 - M3 brown
Kruskal-W. p = 0.74
Tukey AD/CT p = 0.86
AD/Asym 0.75
Asym/CT 1
bicor=-0.23, p=2.2e-13
cor=-0.23, p=1.7e-13
bicor=-0.024, p=0.45
cor=-0.027, p=0.39
bicor=-0.024, p=0.44
cor=-0.033, p=0.29
bicor=0.061, p=0.051
cor=0.09, p=0.0042
SNAP25_3 - M3 brown
Kruskal-W. p = 7.6e-06
Tukey AD/CT p = 1.4e-05
AD/Asym 0.0036
Asym/CT 0.13
bicor=-0.072, p=0.022
cor=-0.1, p=0.0015
bicor=-0.12, p=2e-04
cor=-0.11, p=0.00045
bicor=-0.099, p=0.0017
cor=-0.09, p=0.0041
bicor=0.14, p=1.4e-05
cor=0.16, p=3.1e-07
SNAP25_4 - M3 brown
Kruskal-W. p = 4.8e-08
Tukey AD/CT p = 1.1e-06
AD/Asym 1.7e-05
Asym/CT 0.34
bicor=-0.12, p=9.7e-05
cor=-0.14, p=8.6e-06
bicor=-0.14, p=3.8e-06
cor=-0.13, p=3.3e-05
bicor=-0.12, p=0.00014
cor=-0.11, p=0.00045
bicor=0.19, p=1.3e-09
cor=0.2, p=1.4e-10
SNAP25_6 - M3 brown
Kruskal-W. p = 1e-06
Tukey AD/CT p = 1.6e-06
AD/Asym 0.0023
Asym/CT 0.059
bicor=-0.12, p=1e-04
cor=-0.13, p=3.6e-05
bicor=-0.16, p=1.9e-07
cor=-0.16, p=3e-07
bicor=-0.12, p=0.00019
cor=-0.11, p=0.00045
bicor=0.16, p=4.8e-07
cor=0.17, p=5.3e-08
SNAP25_7 - M3 brown
Kruskal-W. p = 2.2e-06
Tukey AD/CT p = 1.1e-06
AD/Asym 0.24
Asym/CT 0.00059
bicor=-0.099, p=0.0017
cor=-0.087, p=0.0058
bicor=-0.16, p=1.3e-07
cor=-0.16, p=3e-07
bicor=-0.16, p=4.8e-07
cor=-0.15, p=1.6e-06
bicor=0.13, p=3.3e-05
cor=0.14, p=7.8e-06
SPP1_1 - M4 yellow
Kruskal-W. p = 1.4e-07
Tukey AD/CT p = 6.7e-08
AD/Asym 0.021
Asym/CT 0.002
bicor=0.24, p=1.6e-14
cor=0.23, p=1.7e-13
bicor=0.21, p=5.1e-12
cor=0.2, p=1.3e-10
bicor=0.16, p=3.4e-07
cor=0.15, p=1.6e-06
bicor=-0.16, p=3.1e-07
cor=-0.17, p=5.3e-08
STXBP1_3 - M1 turquoise
Kruskal-W. p = 0.015
Tukey AD/CT p = 0.014
AD/Asym 0.19
Asym/CT 0.36
bicor=-0.24, p=2e-14
cor=-0.23, p=1.7e-13
bicor=-0.081, p=0.01
cor=-0.084, p=0.0075
bicor=-0.13, p=2e-05
cor=-0.11, p=0.00046
bicor=0.091, p=0.0036
cor=0.11, p=0.00046
STXBP1_4 - M1 turquoise
Kruskal-W. p = 0.0025
Tukey AD/CT p = 0.0054
AD/Asym 0.026
Asym/CT 0.58
bicor=-0.29, p=1.5e-21
cor=-0.28, p=1.7e-19
bicor=-0.11, p=3e-04
cor=-0.11, p=0.00046
bicor=-0.086, p=0.0061
cor=-0.07, p=0.026
bicor=0.099, p=0.0017
cor=0.13, p=3.4e-05
STXBP1_5 - M1 turquoise
Kruskal-W. p = 0.7
Tukey AD/CT p = 0.8
AD/Asym 0.96
Asym/CT 0.67
bicor=0.14, p=1e-05
cor=0.17, p=6.1e-08
bicor=-0.058, p=0.065
cor=-0.026, p=0.41
bicor=-0.06, p=0.055
cor=-0.0043, p=0.89
bicor=-0.025, p=0.42
cor=-0.025, p=0.43
Protein Abun
Control
AsymAD
AD
Tau 8 Peptide Avg.
CERAD Score
Braak Score
MMSE Cognitive Score

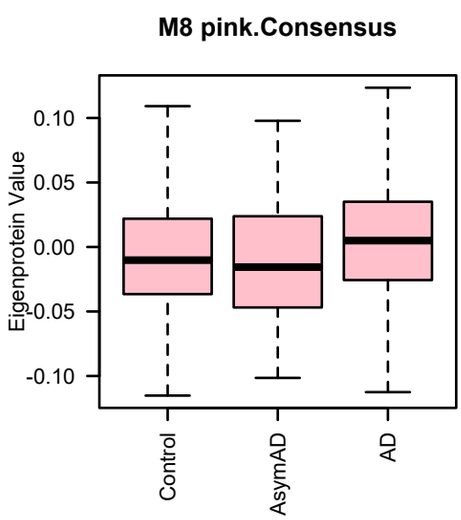

STXBP1_6 - M1 turquoise
Kruskal-W. p = 1.5e-06
Tukey AD/CT p = 8.9e-07
AD/Asym 0.022
Asym/CT 0.009
bicor=-0.31, p=2.9e-23
cor=-0.31, p=8.8e-24
bicor=-0.18, p=3.8e-09
cor=-0.18, p=7.8e-09
bicor=-0.13, p=2.7e-05
cor=-0.13, p=3.3e-05
bicor=0.16, p=5.2e-07
cor=0.17, p=5.3e-08
SV2A_1 - M1 turquoise
Kruskal-W. p = 0.84
Tukey AD/CT p = 0.97
AD/Asym 0.91
Asym/CT 0.85
bicor=-0.18, p=2.1e-08
cor=-0.16, p=3.5e-07
bicor=-0.0064, p=0.84
cor=-0.012, p=0.7
bicor=0.011, p=0.72
cor=0.00058, p=0.99
bicor=0.0022, p=0.94
cor=0.022, p=0.48
SV2A_2 - M1 turquoise
Kruskal-W. p = 0.78
Tukey AD/CT p = 0.77
AD/Asym 0.93
Asym/CT 0.92
bicor=-0.042, p=0.19
cor=-0.031, p=0.33
bicor=-0.0095, p=0.76
cor=-0.02, p=0.52
bicor=0.019, p=0.54
cor=0.0081, p=0.8
bicor=0.0082, p=0.79
cor=0.016, p=0.61
UQCR10_1 - M3 brown
Kruskal-W. p = 0.85
Tukey AD/CT p = 0.86
AD/Asym 0.91
Asym/CT 0.98
bicor=-0.24, p=1.1e-14
cor=-0.046, p=0.15
bicor=-0.11, p=0.00051
cor=-0.035, p=0.27
bicor=-0.043, p=0.17
cor=0.015, p=0.63
bicor=0.12, p=8.8e-05
cor=0.034, p=0.28
UQCR10_2 - M3 brown
Kruskal-W. p = 0.013
Tukey AD/CT p = 0.017
AD/Asym 0.092
Asym/CT 0.57
bicor=-0.23, p=2.2e-13
cor=-0.21, p=1.9e-11
bicor=-0.094, p=0.0028
cor=-0.086, p=0.0062
bicor=-0.047, p=0.13
cor=-0.03, p=0.34
bicor=0.11, p=0.00028
cor=0.13, p=3.4e-05
UQCRC2_1 - M3 brown
Kruskal-W. p = 0.0037
Tukey AD/CT p = 0.02
AD/Asym 0.012
Asym/CT 0.93
bicor=-0.25, p=9.6e-16
cor=-0.26, p=5.8e-17
bicor=-0.097, p=0.002
cor=-0.093, p=0.003
bicor=-0.054, p=0.084
cor=-0.059, p=0.06
bicor=0.14, p=3.9e-06
cor=0.15, p=1.6e-06
UQCRC2_2 - M3 brown
Kruskal-W. p = 5e-04
Tukey AD/CT p = 0.001
AD/Asym 0.014
Asym/CT 0.4
bicor=-0.27, p=1.6e-18
cor=-0.26, p=5.8e-17
bicor=-0.13, p=6.2e-05
cor=-0.12, p=0.00013
bicor=-0.074, p=0.018
cor=-0.062, p=0.049
bicor=0.13, p=2.1e-05
cor=0.16, p=3.2e-07
VDAC2_1 - M3 brown
Kruskal-W. p = 0.84
Tukey AD/CT p = 0.99
AD/Asym 0.83
Asym/CT 0.94
bicor=-0.14, p=1.1e-05
cor=-0.11, p=0.00049
bicor=0.0091, p=0.77
cor=0.0032, p=0.92
bicor=0.057, p=0.072
cor=0.049, p=0.12
bicor=0.015, p=0.63
cor=0.034, p=0.28
VDAC2_2 - M3 brown
Kruskal-W. p = 0.85
Tukey AD/CT p = 0.85
AD/Asym 1
Asym/CT 0.87
bicor=-0.14, p=8.3e-06
cor=-0.11, p=0.00049
bicor=-0.0086, p=0.78
cor=-0.014, p=0.66
bicor=0.025, p=0.43
cor=0.016, p=0.61
bicor=0.027, p=0.39
cor=0.036, p=0.25
Protein Abun
Control
AsymAD
AD
Tau 8 Peptide Avg.
CERAD Score
Braak Score
MMSE Cognitive Score

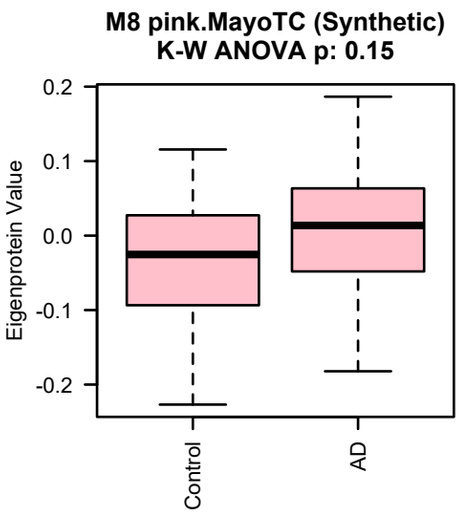
Supplementary Figure 6. Round 2 Targeted Measurements in ROS/MAP. Levels of 37 proteins were measured by selected reaction monitoring (SRM) mass spectrometry across 1016 ROS/MAP cases (control, *n*=139; AsymAD, *n*=384; AD, *n*=439 independent case samples). Most proteins were measured with at least two peptides per protein, and therefore protein level measurements for these proteins are calculated as the average of the individual peptide measurements. Individual peptide measurements are shown after the protein level measurements. Peptide sequences can be found at https://www.synapse.org/#!Synapse:syn10468856. Protein and peptide levels were correlated to tau levels as measured by SRM, CERAD score, Braak stage, and MMSE. Differences in levels by case status were assessed by Kruskal-Wallis (K-W) one-way ANOVA with Tukey test. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Data for each protein and peptide is colored by the AD network module in which it resides. Statistical significance at p <0.05 is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

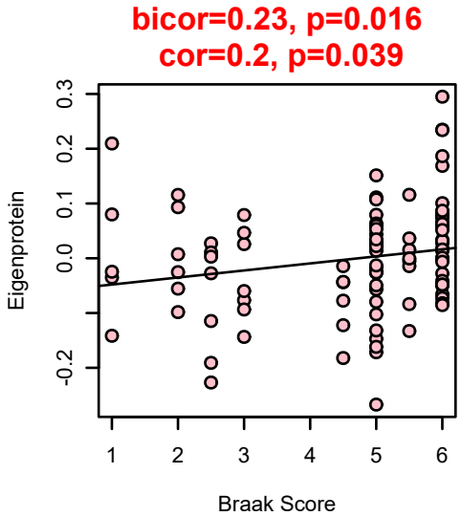

M5 green.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

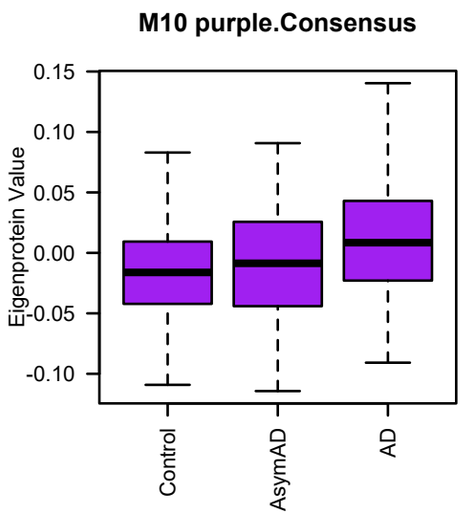

M5 green.MayoTC (Synthetic)
K-W ANOVA p: 0.11
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
AD

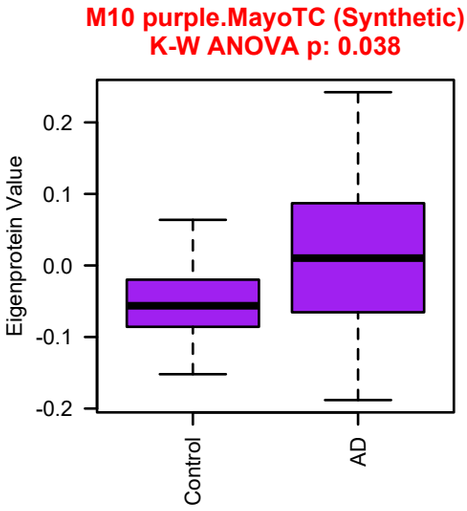

bicor=0.26, p=0.0079
cor=0.22, p=0.023
Eigenprotein
0.2
0.1
0.0
-0.1
1
2
3
4
5
6
Braak Score

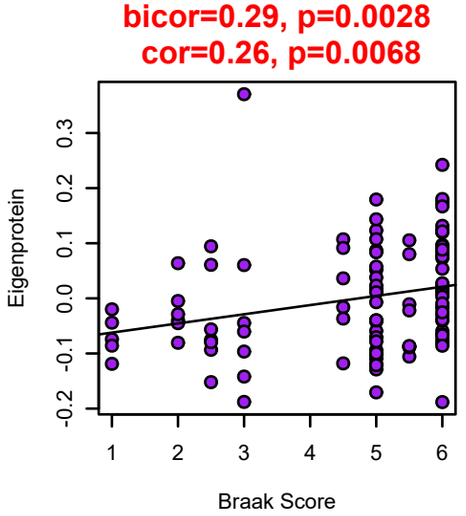

M8 pink.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

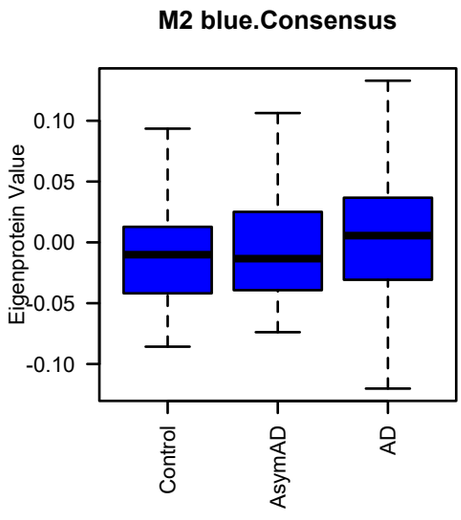

M8 pink.MayoTC (Synthetic)
K-W ANOVA p: 0.15
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

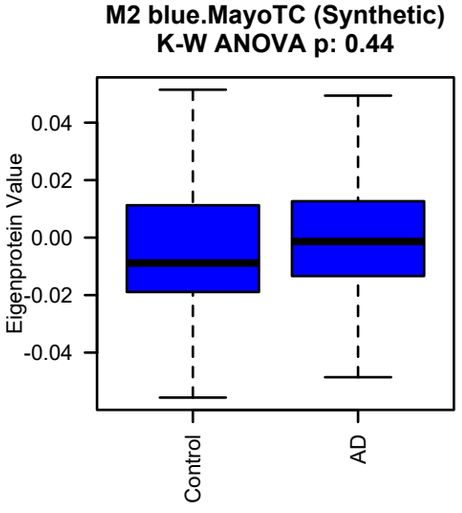

bicor=0.23, p=0.016
cor=0.2, p=0.039
Eigenprotein
0.3
0.2
0.1
0.0
-0.2
1
2
3
4
5
6
Braak Score

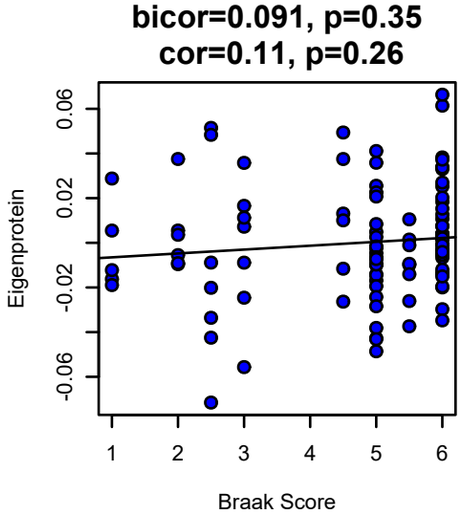

M10 purple.Consensus
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

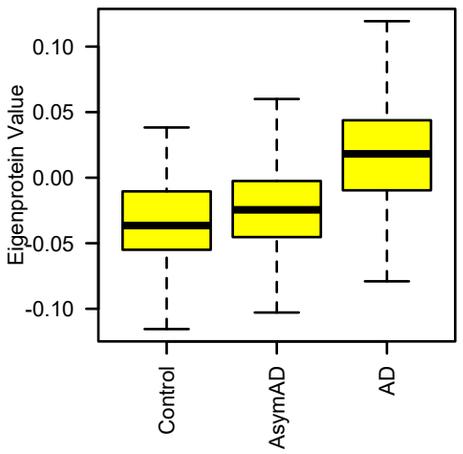

M10 purple.MayoTC (Synthetic)
K-W ANOVA p: 0.038
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

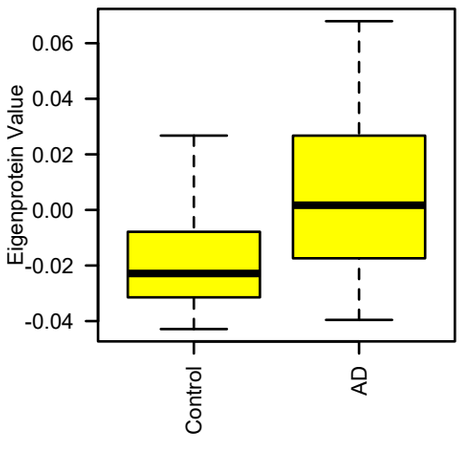

bicor=0.29, p=0.0028
cor=0.26, p=0.0068
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
1
2
3
4
5
6
Braak Score

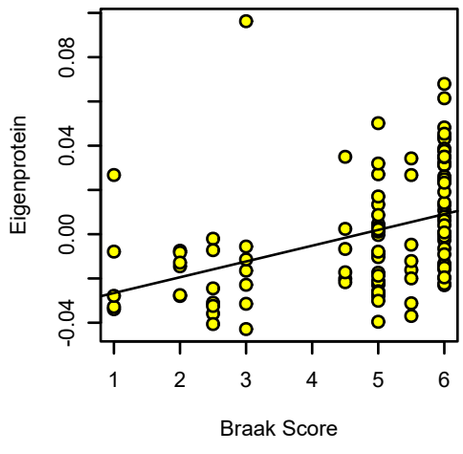

M2 blue.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

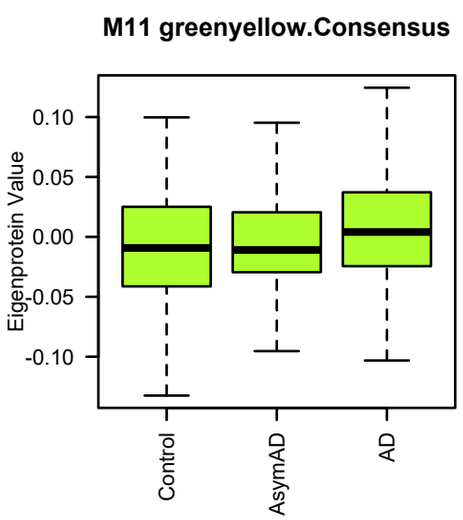

M2 blue.MayoTC (Synthetic)
K-W ANOVA p: 0.44
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
AD

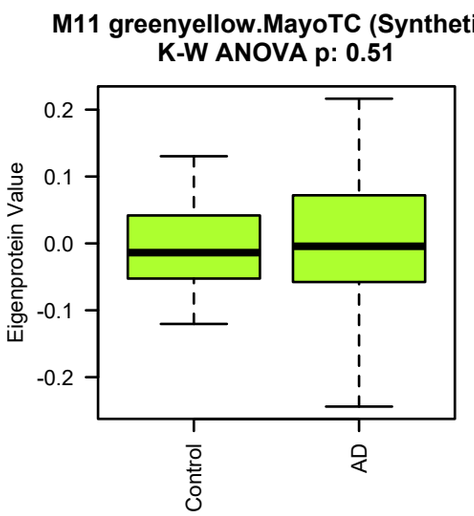

bicor=0.091, p=0.35
cor=0.11, p=0.26
Eigenprotein
0.06
0.02
-0.02
-0.06
1
2
3
4
5
6
Braak Score

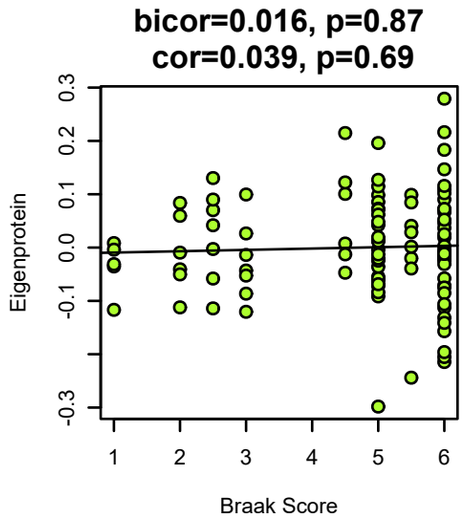

M4 yellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

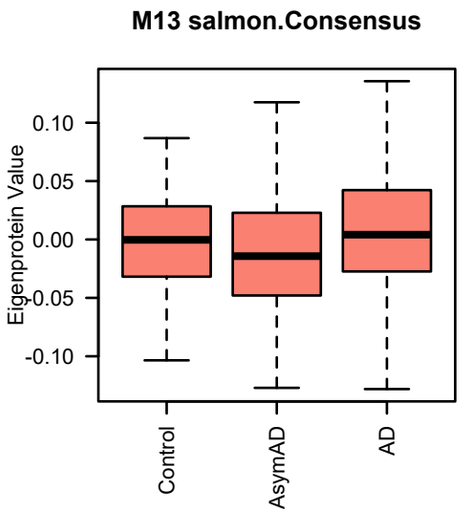

M4 yellow.MayoTC (Synthetic)
K-W ANOVA p: 0.0011
Eigenprotein Value
0.06
0.04
0.02
0.00
-0.02
-0.04
Control
AD

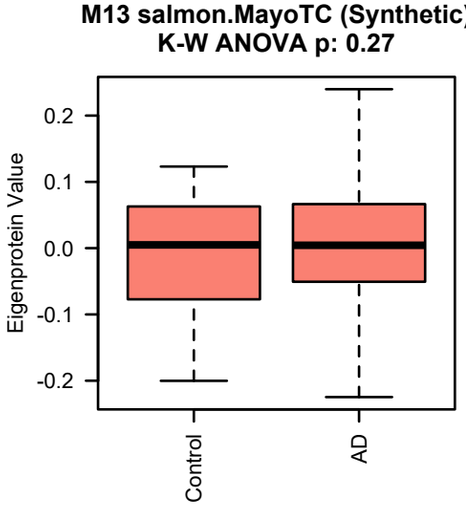

bicor=0.45, p=1.5e-06
cor=0.39, p=3.3e-05
Eigenprotein
0.08
0.04
0.00
-0.04
1
2
3
4
5
6
Braak Score

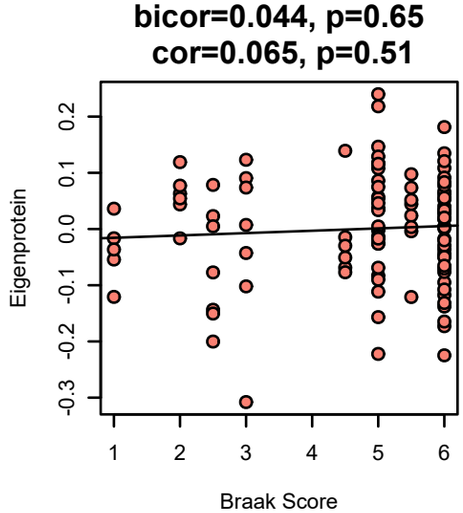

M11 greenyellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

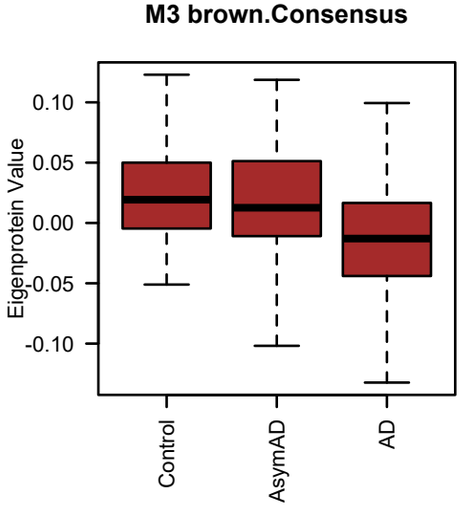

M11 greenyellow.MayoTC (Synthetic)
K-W ANOVA p: 0.51
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

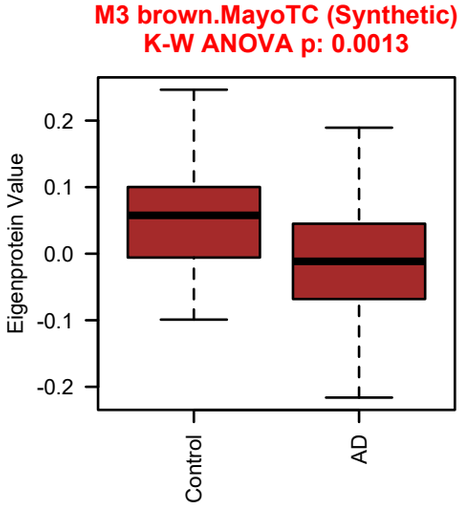

bicor=0.016, p=0.87
cor=0.039, p=0.69
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.3
1
2
3
4
5
6
Braak Score

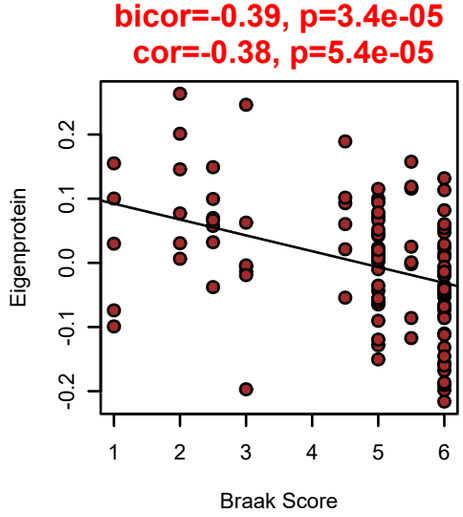

M13 salmon.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

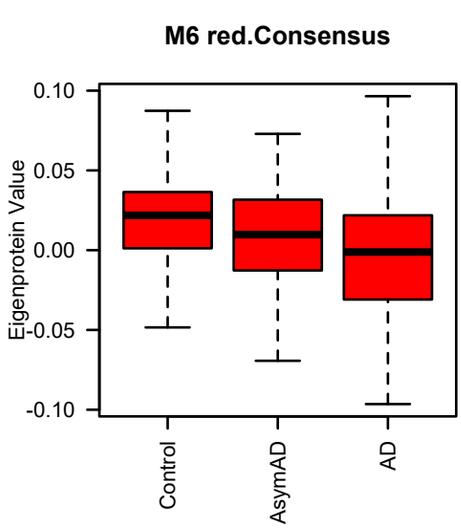

M13 salmon.MayoTC (Synthetic)
K-W ANOVA p: 0.27
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

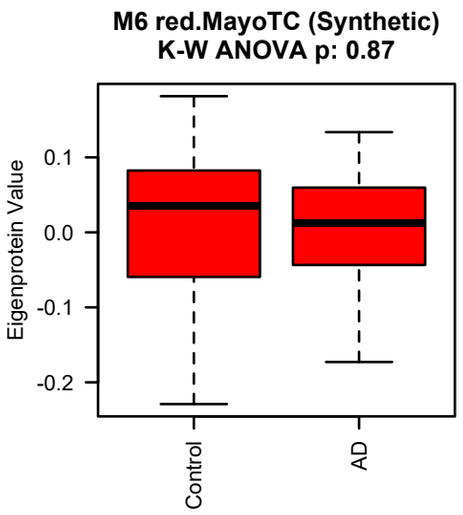

bicor=0.044, p=0.65
cor=0.065, p=0.51
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-0.3
1
2
3
4
5
6
Braak Score

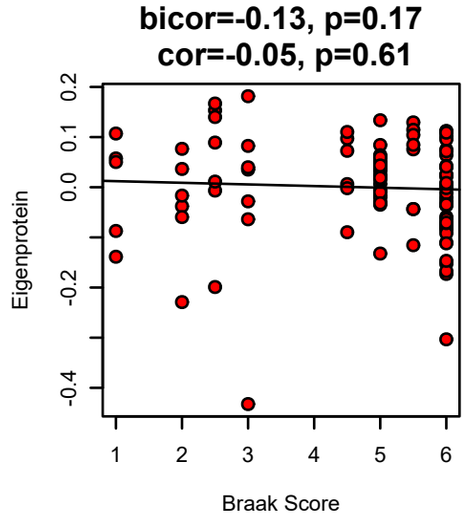

M3 brown.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

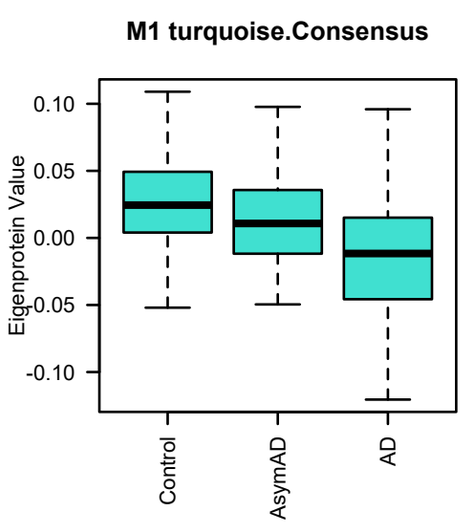

M3 brown.MayoTC (Synthetic)
K-W ANOVA p: 0.0013
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

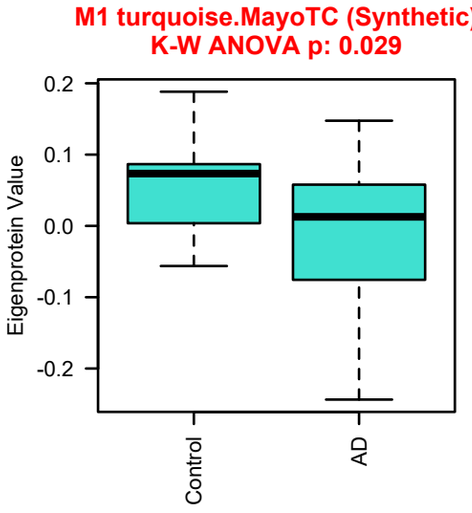

bicor=-0.39, p=3.4e-05
cor=-0.38, p=5.4e-05
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
1
2
3
4
5
6
Braak Score

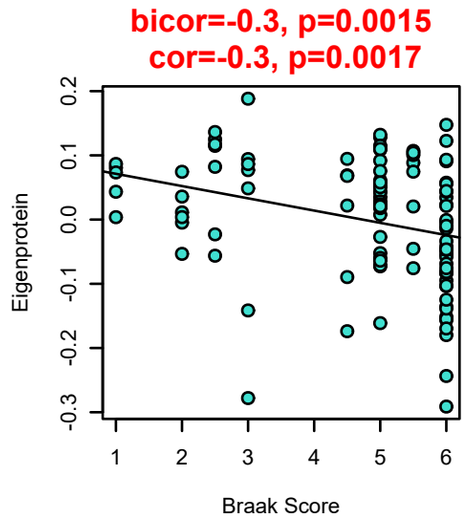

M6 red.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

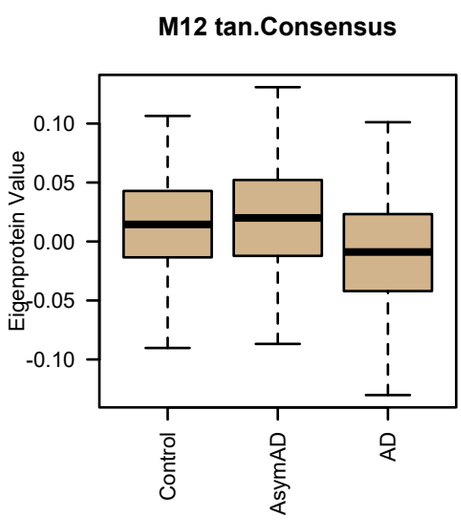

M6 red.MayoTC (Synthetic)
K-W ANOVA p: 0.87
Eigenprotein Value
0.1
0.0
-0.1
-0.2
Control
AD

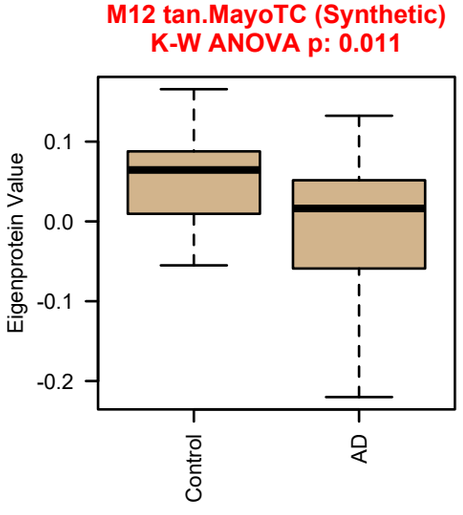

bicor=-0.13, p=0.17
cor=-0.05, p=0.61
Eigenprotein
0.2
0.1
0.0
-0.2
-0.4
1
2
3
4
5
6
Braak Score

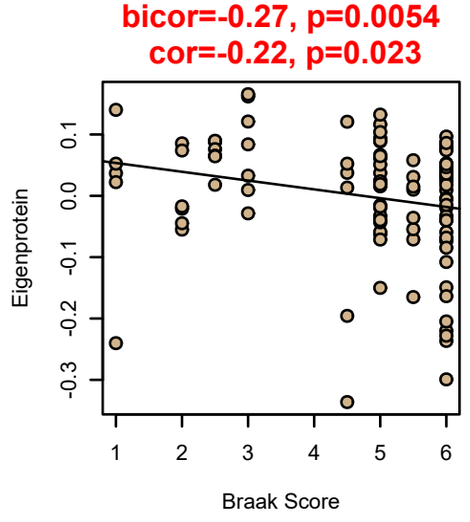

M1 turquoise.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

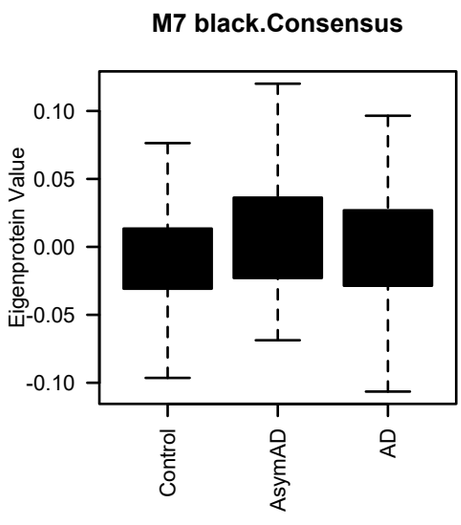

M1 turquoise.MayoTC (Synthetic)
K-W ANOVA p: 0.029
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

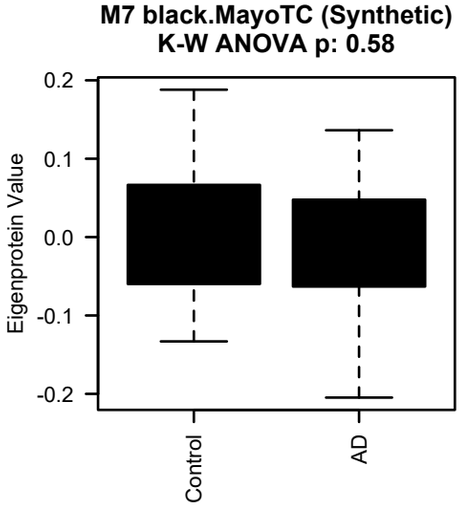

bicor=-0.3, p=0.0015
cor=-0.3, p=0.0017
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-0.3
1
2
3
4
5
6
Braak Score

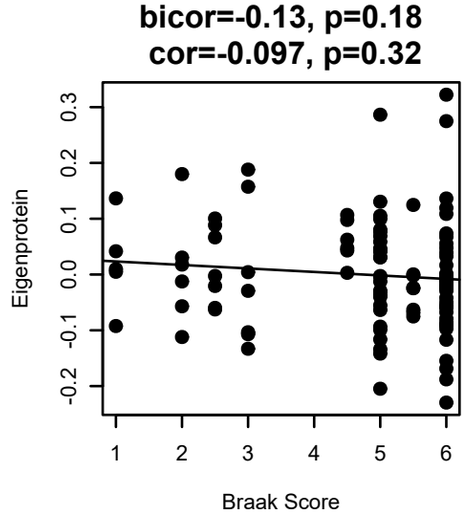

M12 tan.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

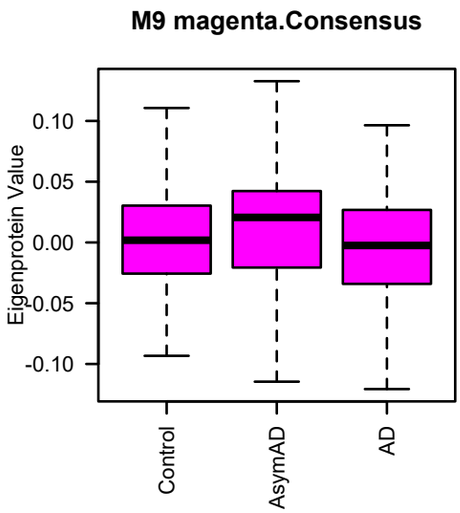

M12 tan.MayoTC (Synthetic)
K-W ANOVA p: 0.011
Eigenprotein Value
0.1
0.0
-0.1
-0.2
Control
AD

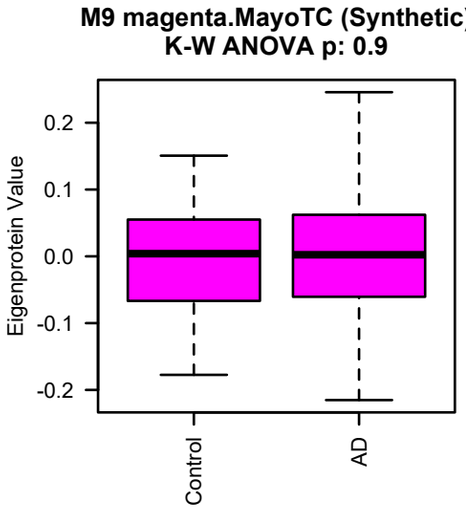

bicor=-0.27, p=0.0054
cor=-0.22, p=0.023
Eigenprotein
0.1
0.0
-0.1
-0.2
-0.3
1
2
3
4
5
6
Braak Score

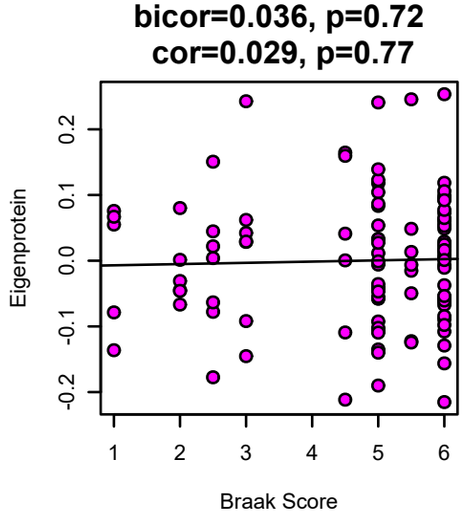

M7 black.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD


M7 black.MayoTC (Synthetic)
K-W ANOVA p: 0.58
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

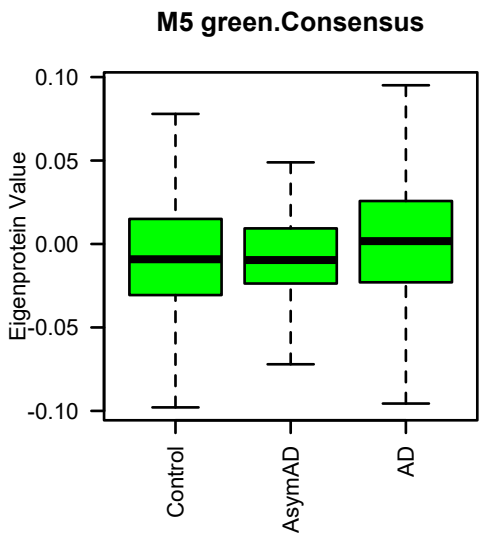

bicor=-0.13, p=0.18
cor=-0.097, p=0.32
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
1
2
3
4
5
6
Braak Score

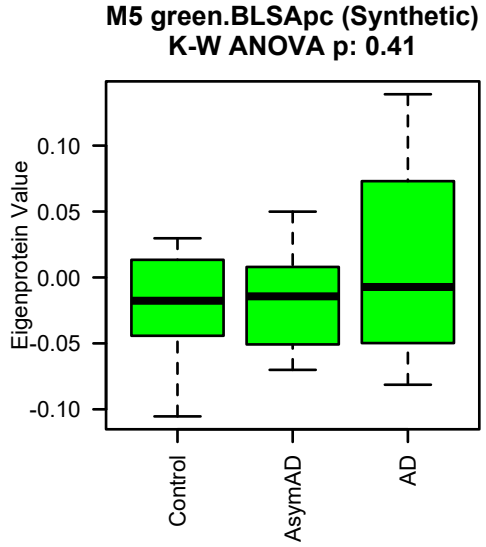

M9 magenta.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

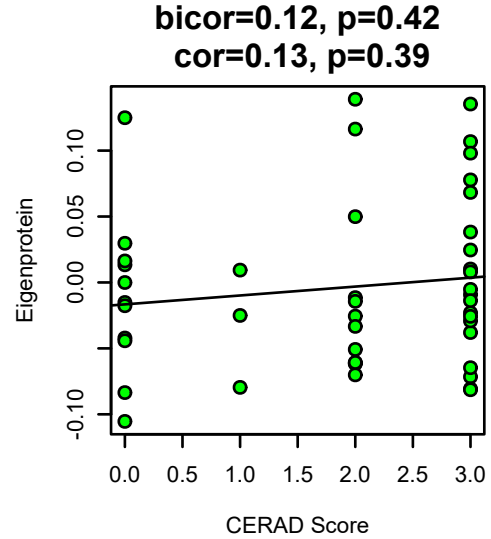

M9 magenta.MayoTC (Synthetic)
K-W ANOVA p: 0.9
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD

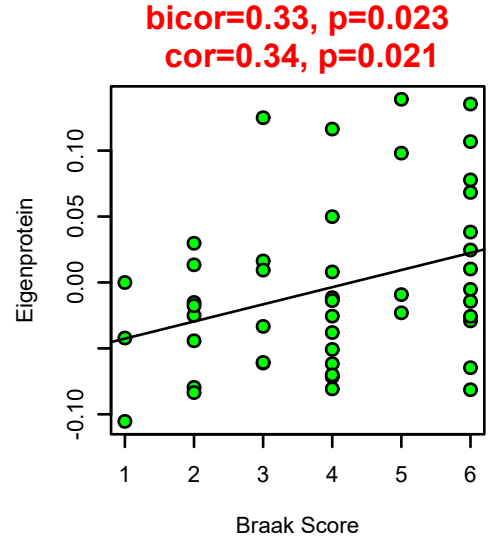

bicor=0.036, p=0.72
cor=0.029, p=0.77
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
1
2
3
4
5
6
Braak Score

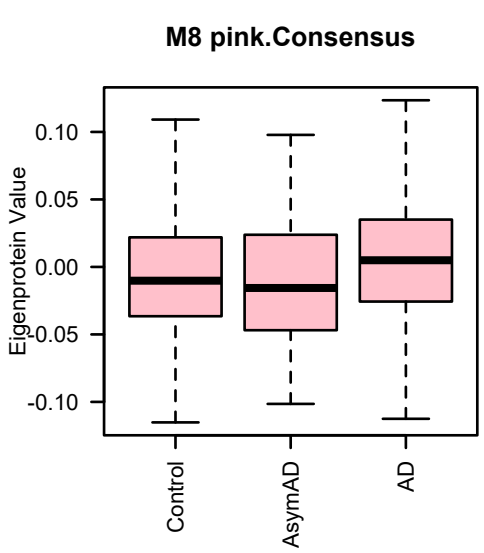
Supplementary Figure 7. AD Network Modules in Temporal Cortex. The top 20% of proteins by kME value in each AD brain protein network module was used to create a synthetic eigenprotein, which was then measured by case status in the Mayo cohort (temporal cortex) and correlated with Braak score (*n*=107 independent case samples after network connectivity outlier removal). The first boxplot for each module is the AD network eigenprotein by case status, given as reference for the second boxplot, which is the synthetic eigenprotein in the Mayo cohort (control, *n*=25; AD, *n*=82). Synthetic eigenprotein differences by case status in the Mayo cohort were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

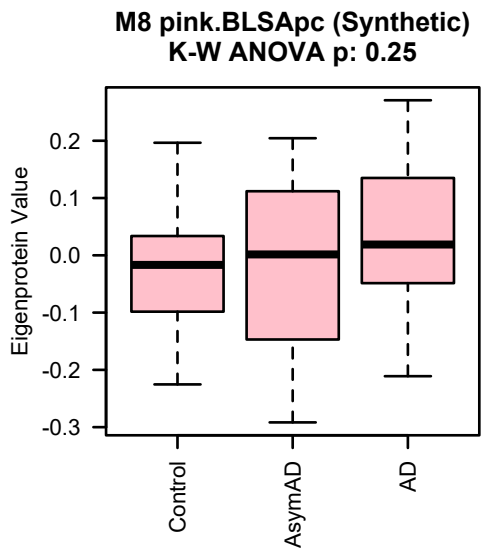

M5 green.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

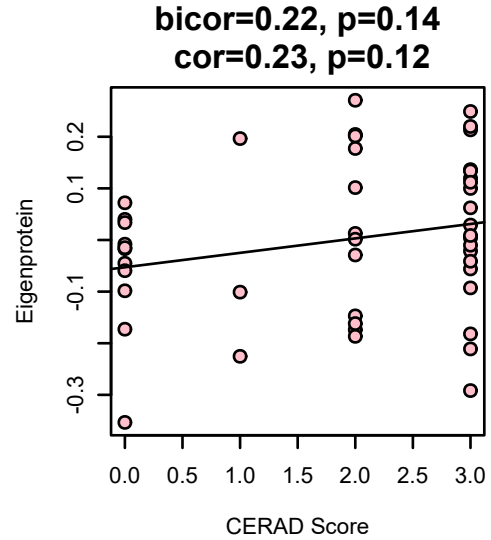

M5 green.BLSApc (Synthetic)
K-W ANOVA p: 0.41
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

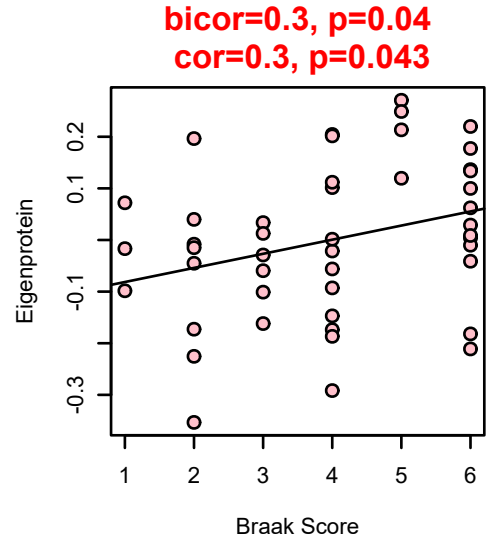

bicor=0.12, p=0.42
cor=0.13, p=0.39
Eigenprotein
0.10
0.05
0.00
-0.10
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

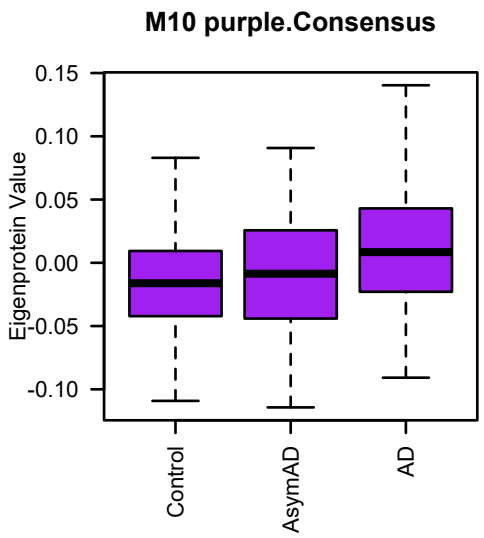

bicor=0.33, p=0.023
cor=0.34, p=0.021
Eigenprotein
0.10
0.05
0.00
-0.10
1
2
3
4
5
6
Braak Score

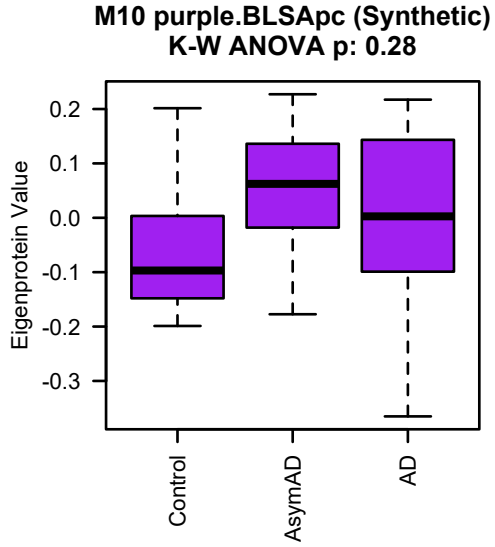

M8 pink.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

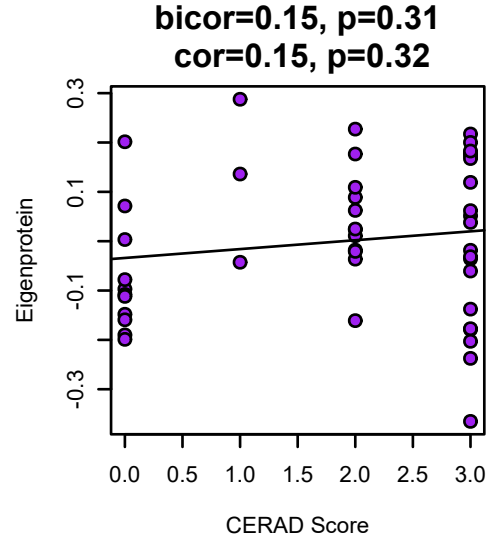

M8 pink.BLSApc (Synthetic)
K-W ANOVA p: 0.25
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AsymAD
AD

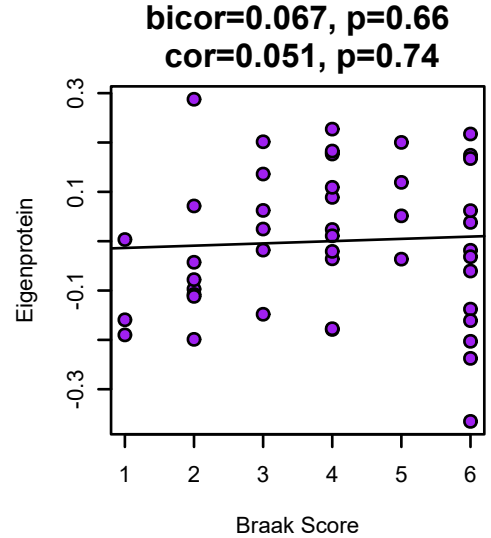

bicor=0.22, p=0.14
cor=0.23, p=0.12
Eigenprotein
0.2
0.1
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

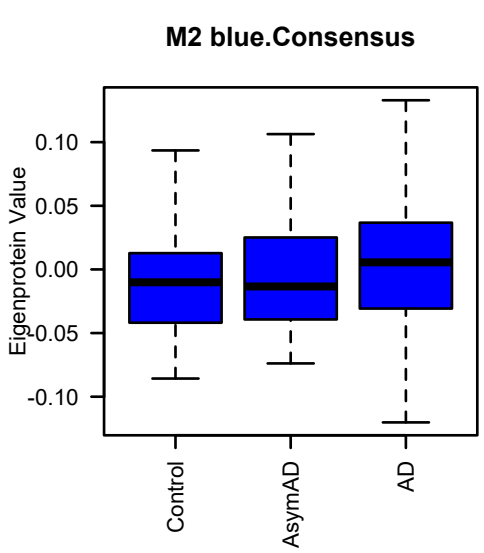

bicor=0.3, p=0.04
cor=0.3, p=0.043
Eigenprotein
0.2
0.1
-0.1
-0.3
1
2
3
4
5
6
Braak Score

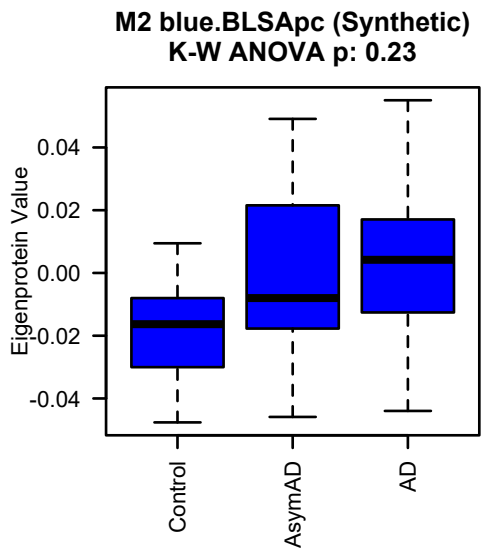

M10 purple.Consensus
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

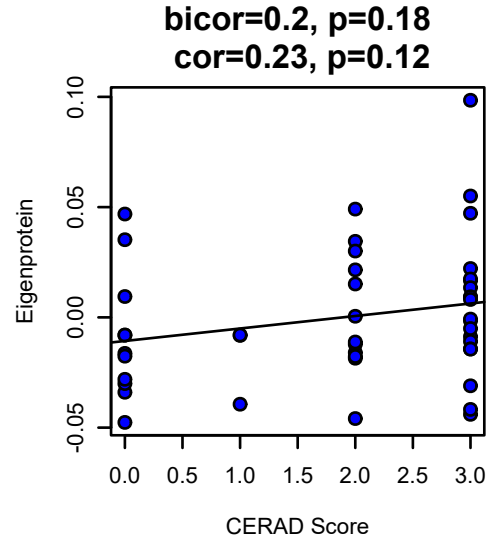

M10 purple.BLSApc (Synthetic)
K-W ANOVA p: 0.28
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AsymAD
AD

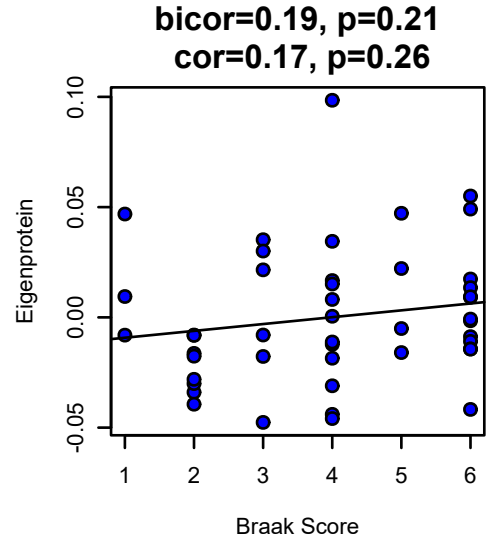

bicor=0.15, p=0.31
cor=0.15, p=0.32
Eigenprotein
0.3
0.1
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

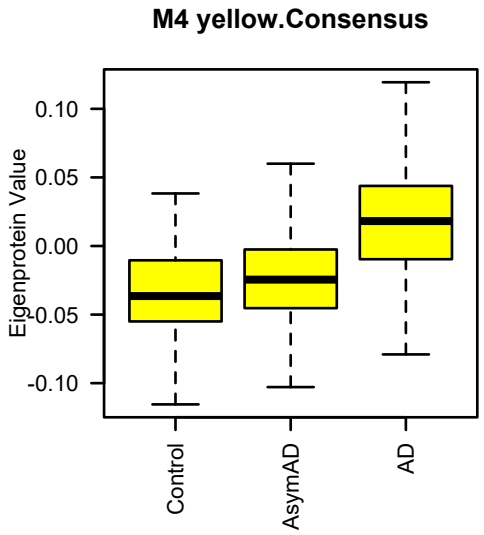

bicor=0.067, p=0.66
cor=0.051, p=0.74
Eigenprotein
0.3
0.1
-0.1
-0.3
1
2
3
4
5
6
Braak Score

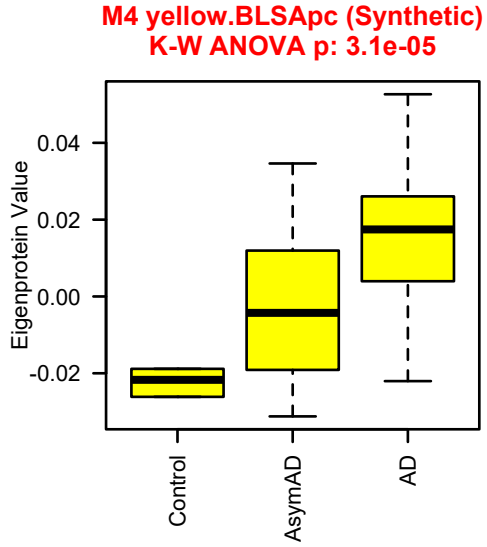

M2 blue.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

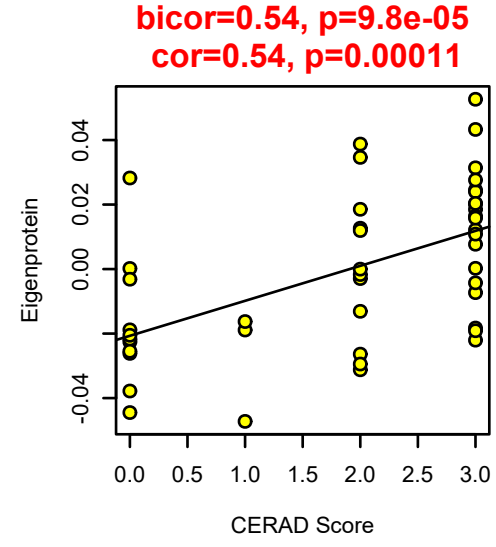

M2 blue.BLSApc (Synthetic)
K-W ANOVA p: 0.23
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
AsymAD
AD

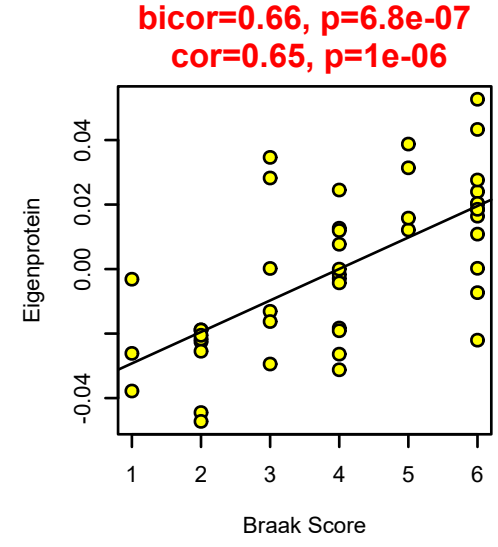

bicor=0.2, p=0.18
cor=0.23, p=0.12
Eigenprotein
0.10
0.05
0.00
-0.05
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

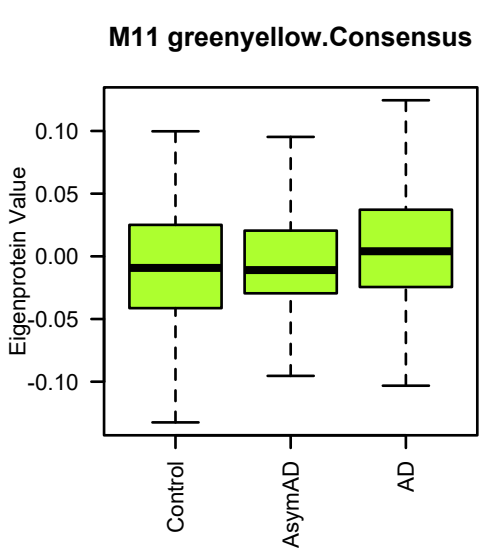

bicor=0.19, p=0.21
cor=0.17, p=0.26
Eigenprotein
0.10
0.05
0.00
-0.05
1
2
3
4
5
6
Braak Score

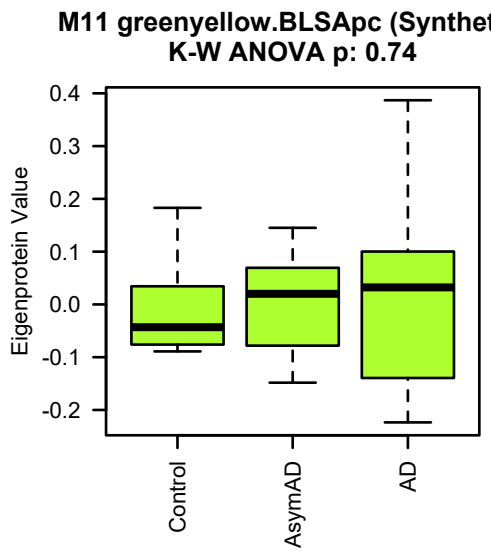

M4 yellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

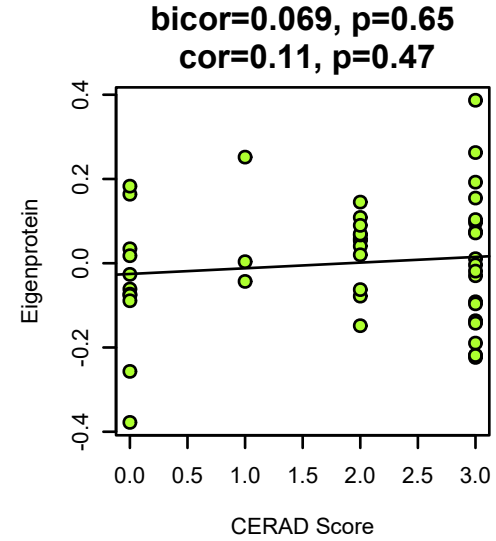

M4 yellow.BLSApc (Synthetic)
K-W ANOVA p: 3.1e-05
Eigenprotein Value
0.04
0.02
0.00
-0.02
Control
AsymAD
AD

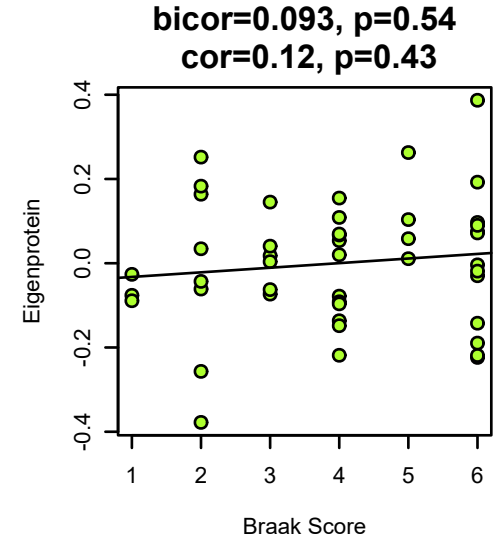

bicor=0.54, p=9.8e-05
cor=0.54, p=0.00011
Eigenprotein
0.04
0.02
0.00
-0.04
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

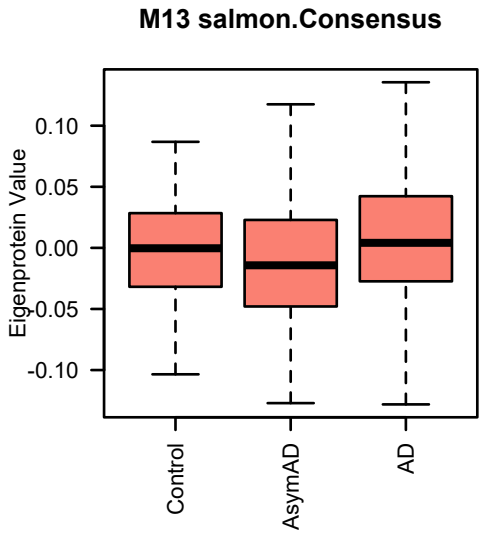

bicor=0.66, p=6.8e-07
cor=0.65, p=1e-06
Eigenprotein
0.04
0.02
0.00
-0.04
1
2
3
4
5
6
Braak Score

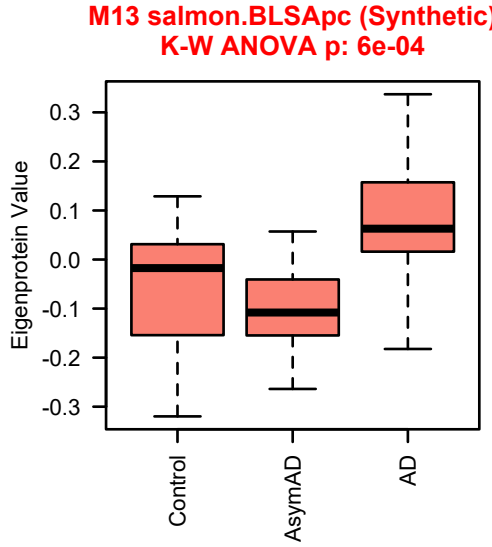

M11 greenyellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

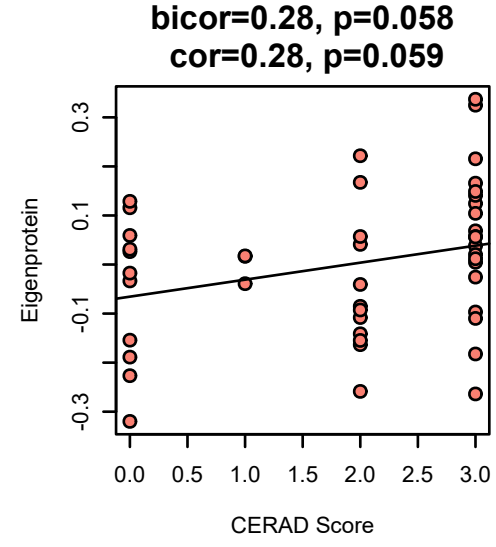

M11 greenyellow.BLSApc (Synthetic)
K-W ANOVA p: 0.74
Eigenprotein Value
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
Control
AsymAD
AD

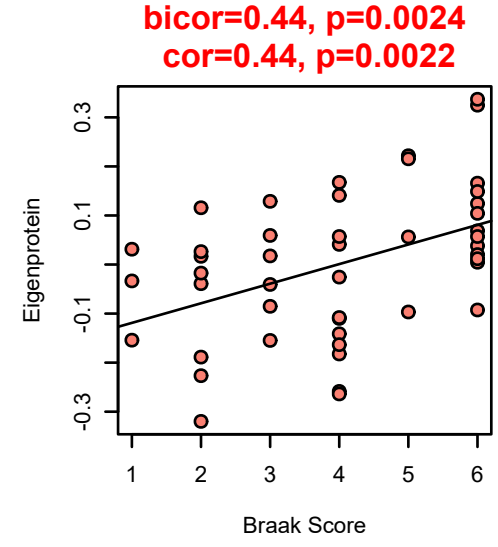

bicor=0.069, p=0.65
cor=0.11, p=0.47
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

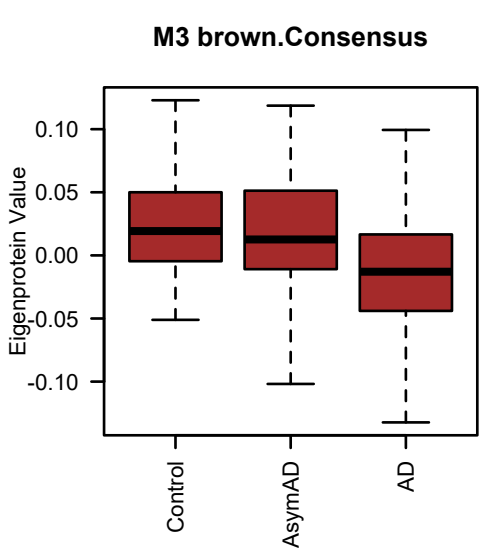

bicor=0.093, p=0.54
cor=0.12, p=0.43
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
1
2
3
4
5
6
Braak Score

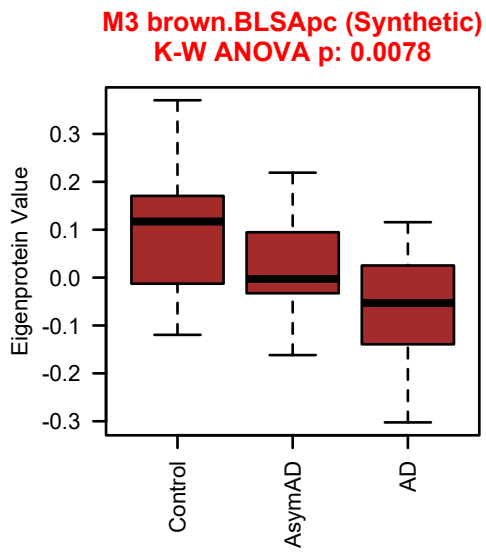

M13 salmon.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

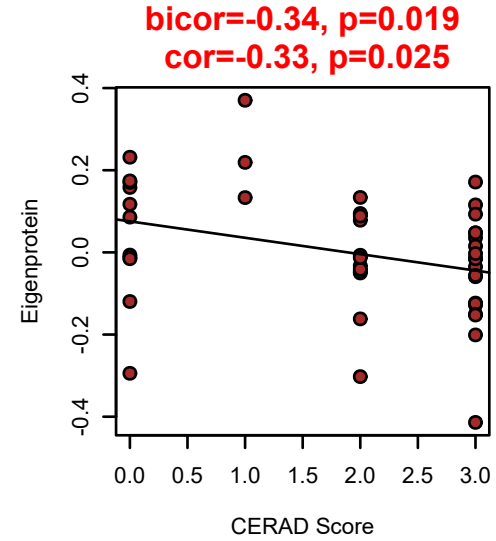

M13 salmon.BLSApc (Synthetic)
K-W ANOVA p: 6e-04
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AsymAD
AD

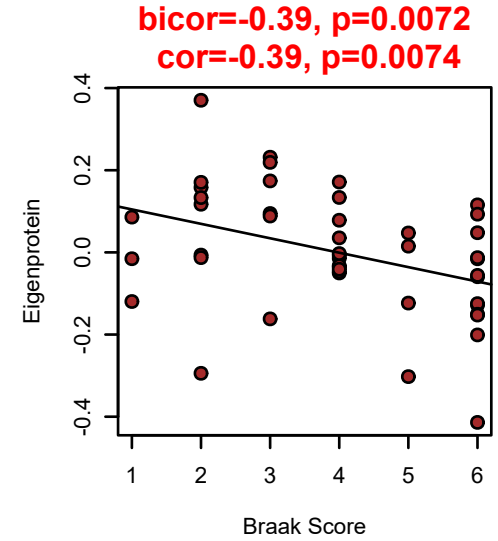

bicor=0.28, p=0.058
cor=0.28, p=0.059
Eigenprotein
0.3
0.1
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

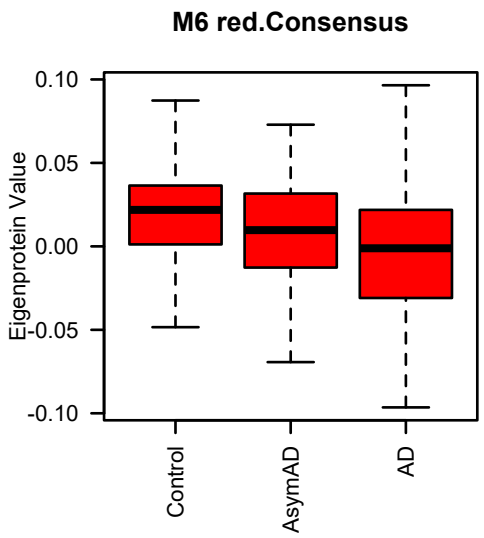

bicor=0.44, p=0.0024
cor=0.44, p=0.0022
Eigenprotein
0.3
0.1
-0.1
-0.3
1
2
3
4
5
6
Braak Score

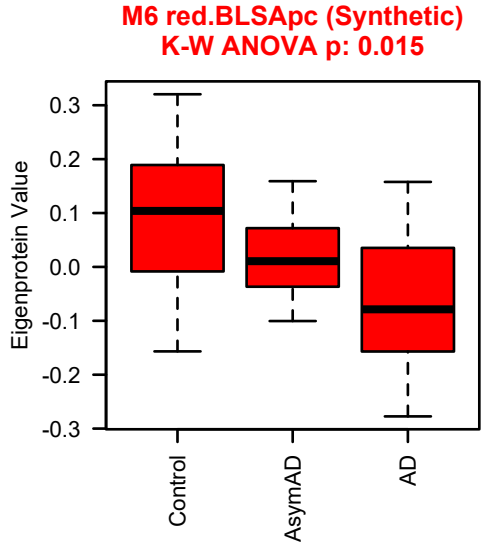

M3 brown.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

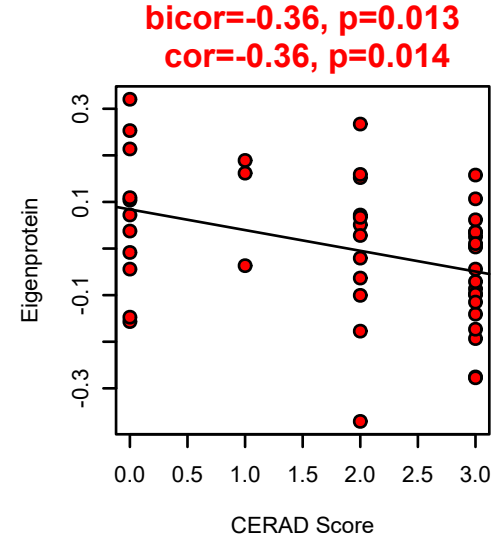

M3 brown.BLSApc (Synthetic)
K-W ANOVA p: 0.0078
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AsymAD
AD

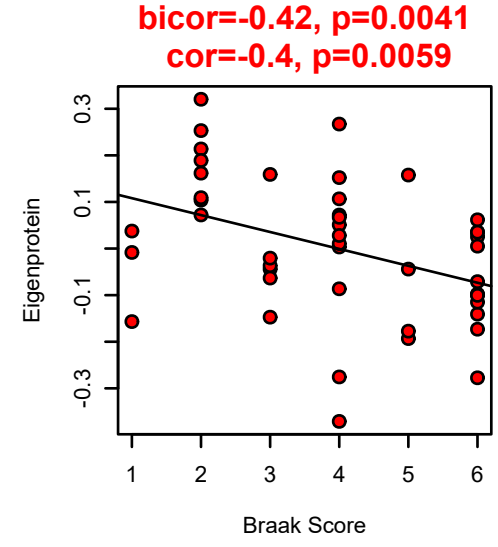

bicor=-0.34, p=0.019
cor=-0.33, p=0.025
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

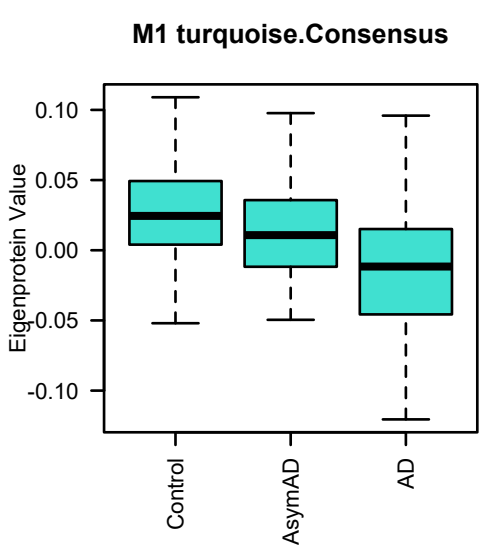

bicor=-0.39, p=0.0072
cor=-0.39, p=0.0074
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
1
2
3
4
5
6
Braak Score

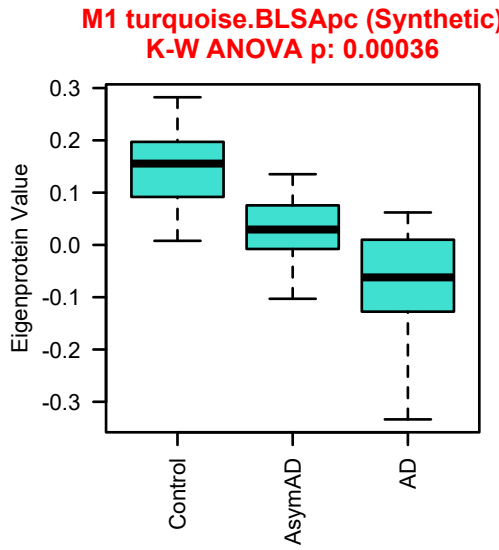

M6 red.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

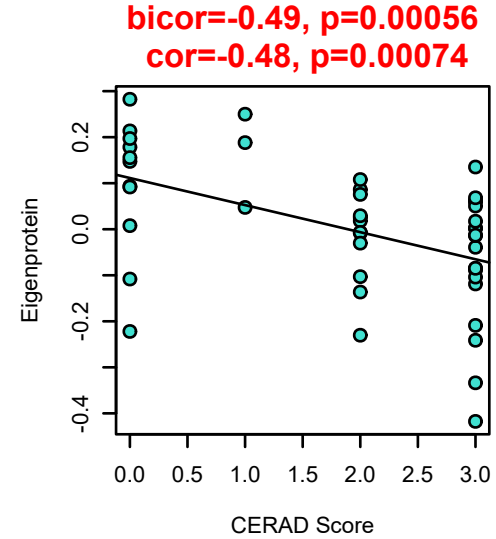

M6 red.BLSApc (Synthetic)
K-W ANOVA p: 0.015
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AsymAD
AD

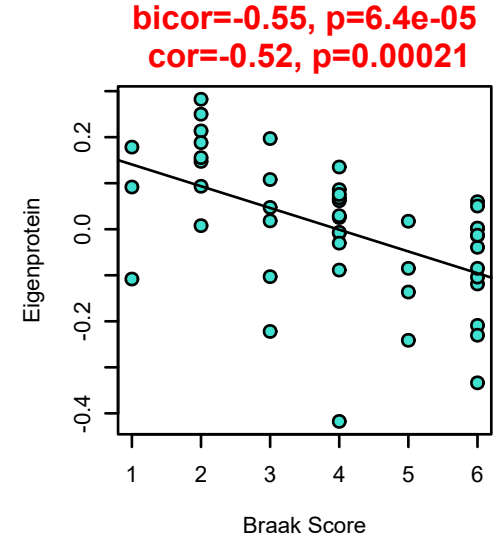

bicor=-0.36, p=0.013
cor=-0.36, p=0.014
Eigenprotein
0.3
0.1
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

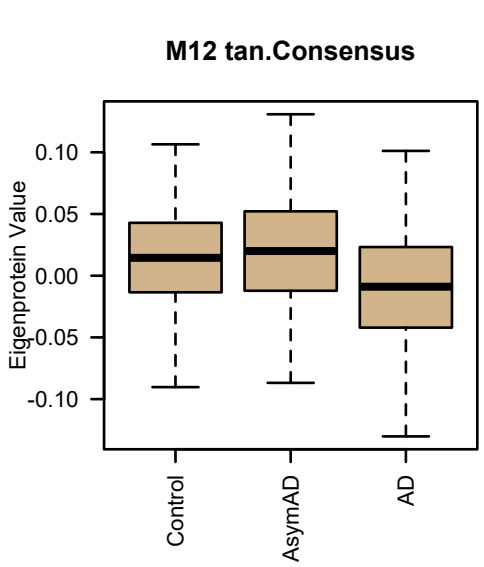

bicor=-0.42, p=0.0041
cor=-0.4, p=0.0059
Eigenprotein
0.3
0.1
-0.1
-0.3
1
2
3
4
5
6
Braak Score

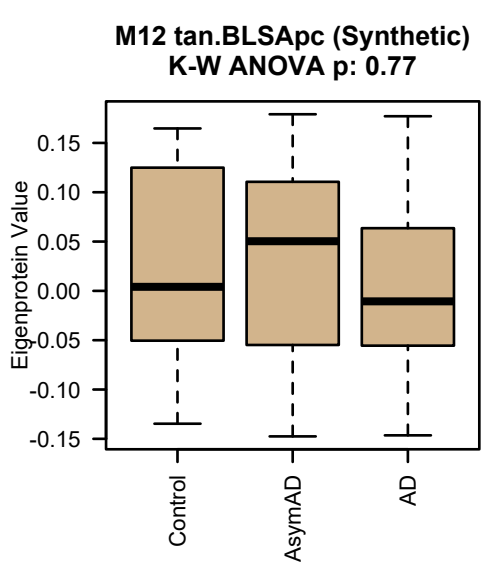

M1 turquoise.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

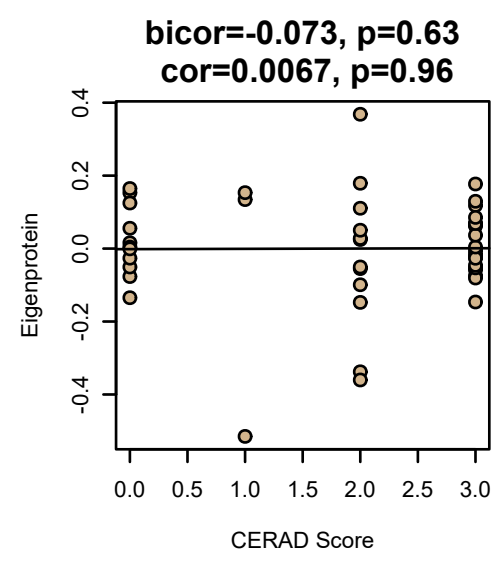

M1 turquoise.BLSApc (Synthetic)
K-W ANOVA p: 0.00036
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AsymAD
AD

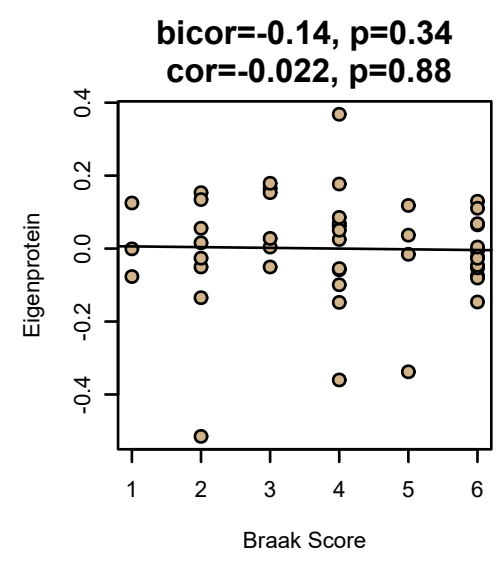

bicor=-0.49, p=0.00056
cor=-0.48, p=0.00074
Eigenprotein
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

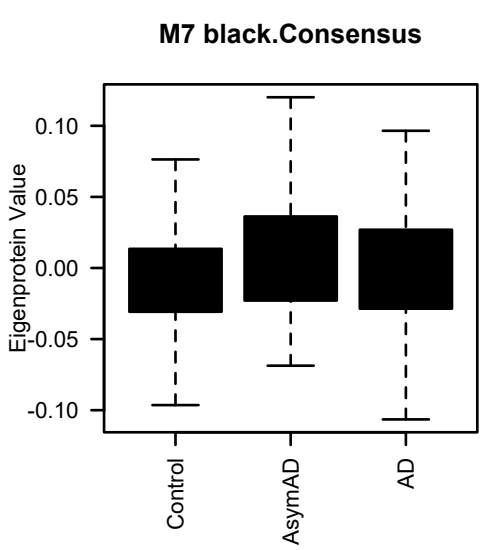

bicor=-0.55, p=6.4e-05
cor=-0.52, p=0.00021
Eigenprotein
0.2
0.0
-0.2
-0.4
1
2
3
4
5
6
Braak Score

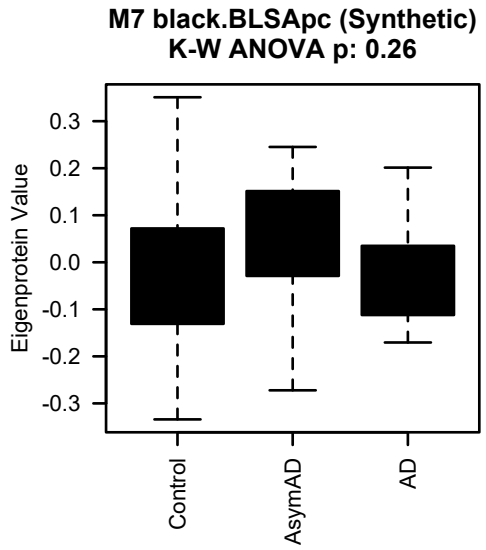

M12 tan.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

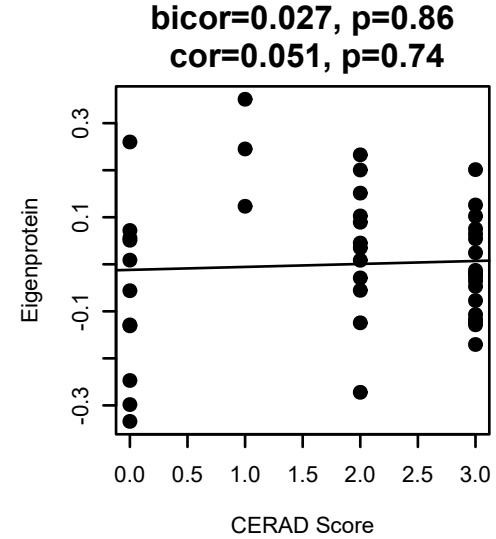

M12 tan.BLSApc (Synthetic)
K-W ANOVA p: 0.77
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
AsymAD
AD

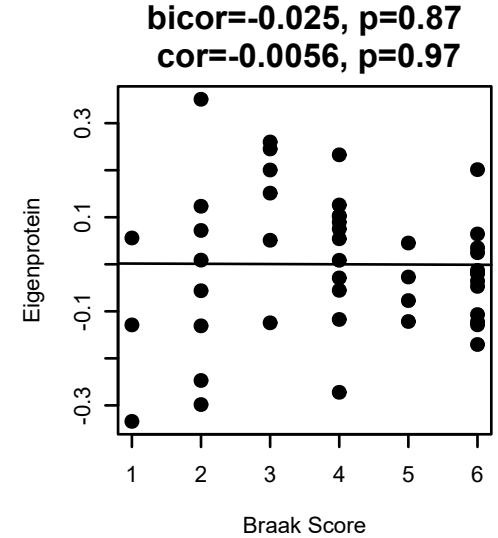

bicor=-0.073, p=0.63
cor=0.0067, p=0.96
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

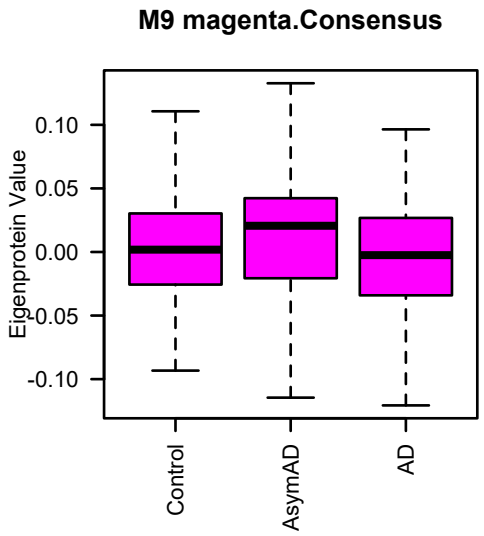

bicor=-0.14, p=0.34
cor=-0.022, p=0.88
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
1
2
3
4
5
6
Braak Score

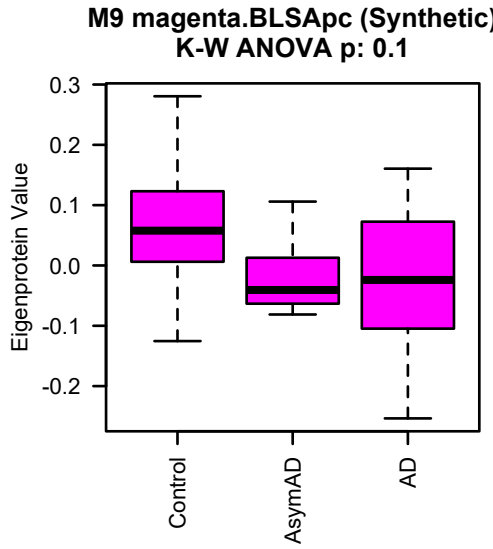

M7 black.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

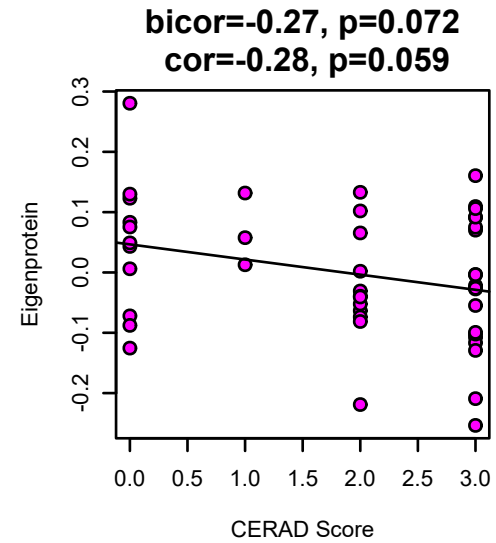

M7 black.BLSApc (Synthetic)
K-W ANOVA p: 0.26
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AsymAD
AD

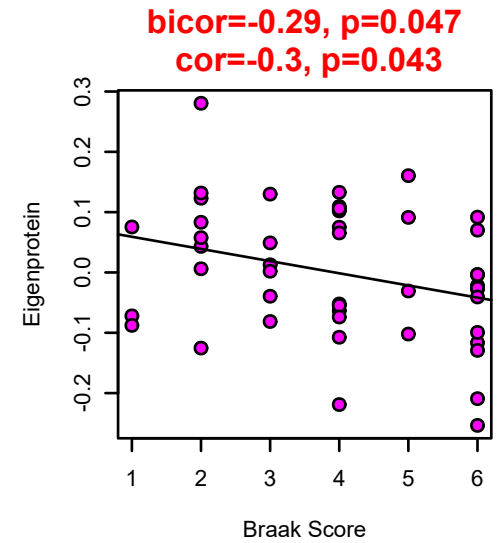

bicor=0.027, p=0.86
cor=0.051, p=0.74
Eigenprotein
0.3
0.1
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score


bicor=-0.025, p=0.87
cor=-0.0056, p=0.97
Eigenprotein
0.3
0.1
-0.1
-0.3
1
2
3
4
5
6
Braak Score

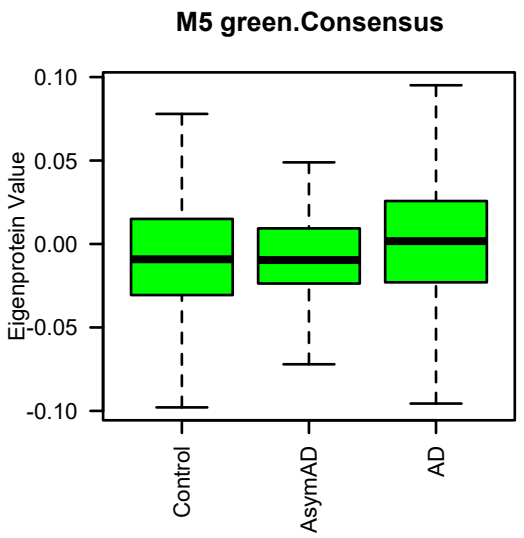

M9 magenta.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

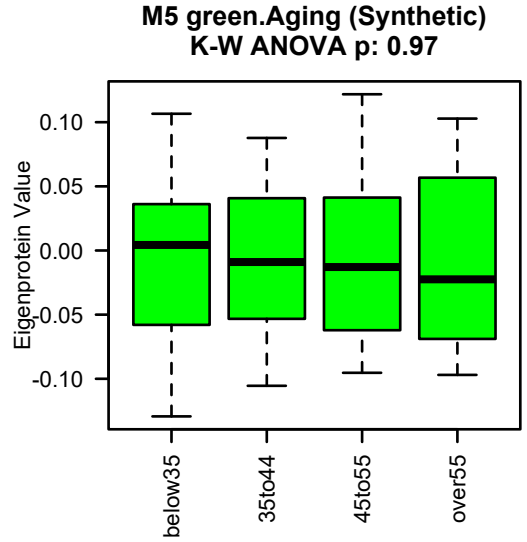

M9 magenta.BLSApc (Synthetic)
K-W ANOVA p: 0.1
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
Control
AsymAD
AD

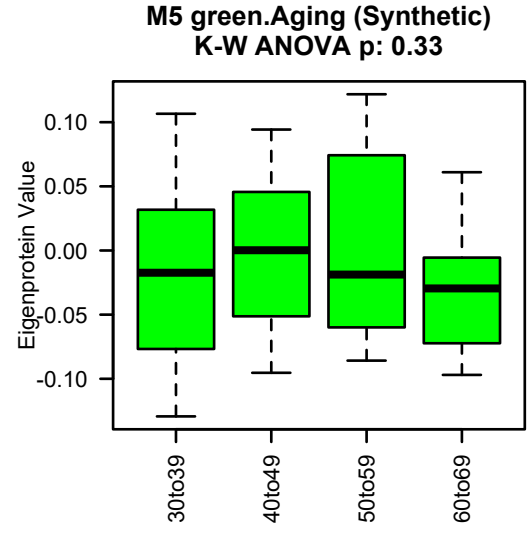

bicor=-0.27, p=0.072
cor=-0.28, p=0.059
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

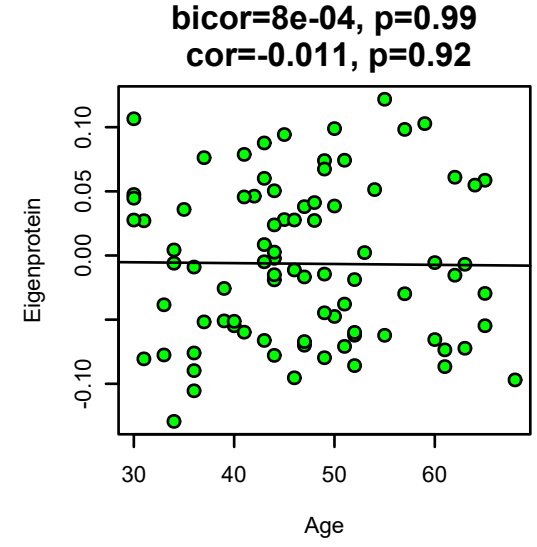

bicor=-0.29, p=0.047
cor=-0.3, p=0.043
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
1
2
3
4
5
6
Braak Score

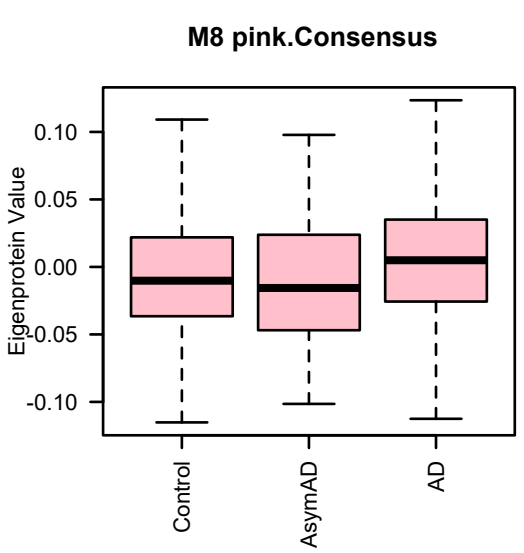
Supplementary Figure 8. AD Network Modules in Precuneus. The top 20% of proteins by kME value in each AD brain protein network module was used to create a synthetic eigenprotein, which was then measured by case status in the BLSA cohort (precuneus) and correlated with CERAD and Braak scores (*n*=46 independent case samples). The first boxplot for each module is the AD network eigenprotein by case status, given as reference for the second boxplot, which is the synthetic eigenprotein in the BLSA precuneus cohort (control, *n*=13; AsymAD, *n*=13; AD, *n*=20). Synthetic eigenprotein differences by case status in the BLSA precuneus cohort were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

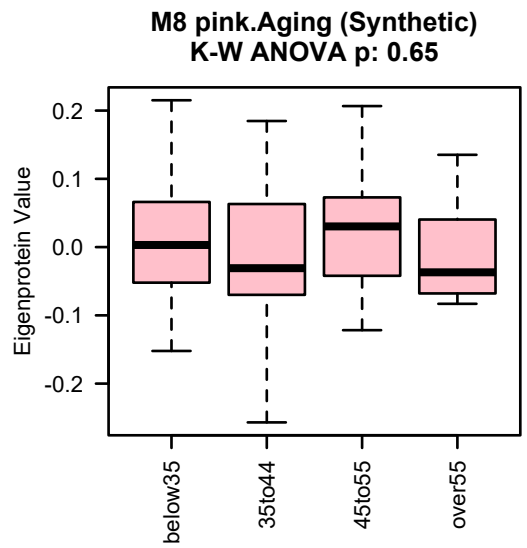

M5 green.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

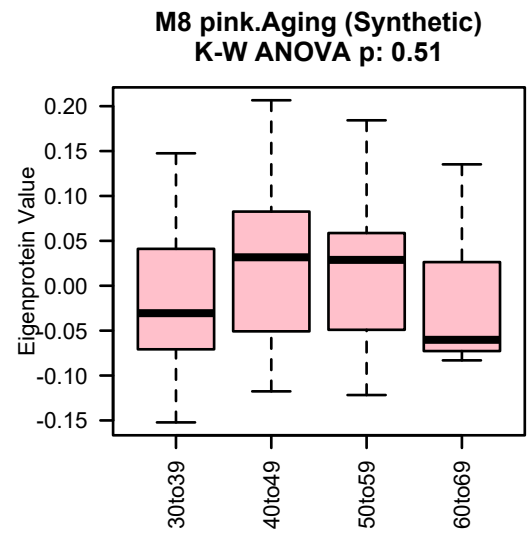

M5 green.Aging (Synthetic)
K-W ANOVA p: 0.97
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
below35
35to44
45to55
over55

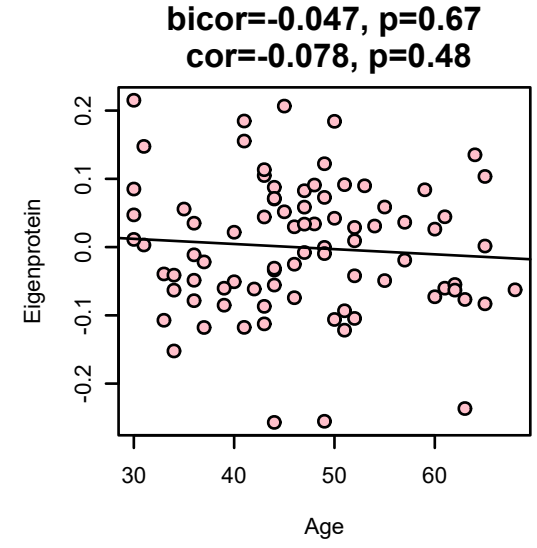

M5 green.Aging (Synthetic)
K-W ANOVA p: 0.33
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
30to39
40to49
50to59
60to69

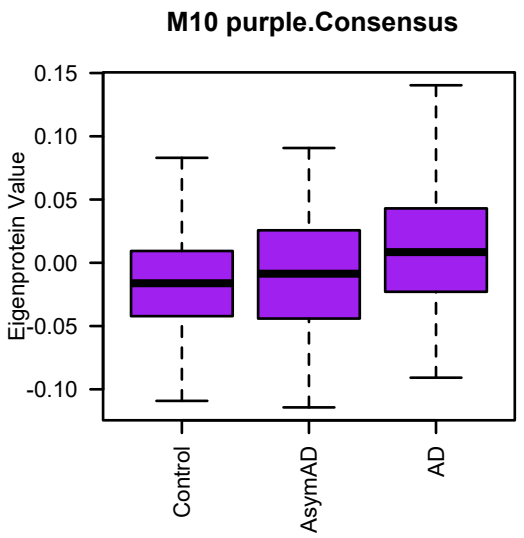

bicor=8e-04, p=0.99
cor=-0.011, p=0.92
Eigenprotein
0.10
0.05
0.00
-0.10
30
40
50
60
Age

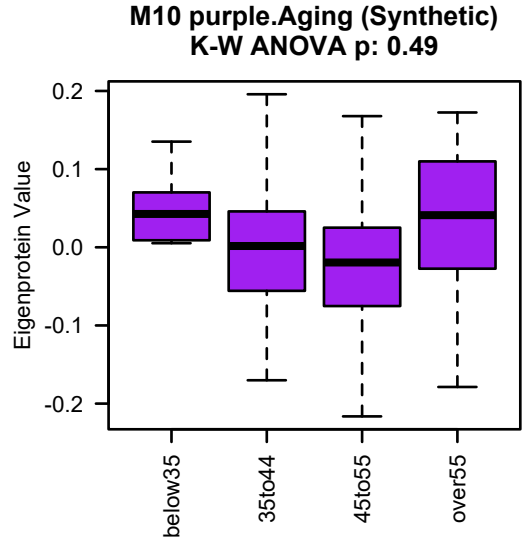

M8 pink.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

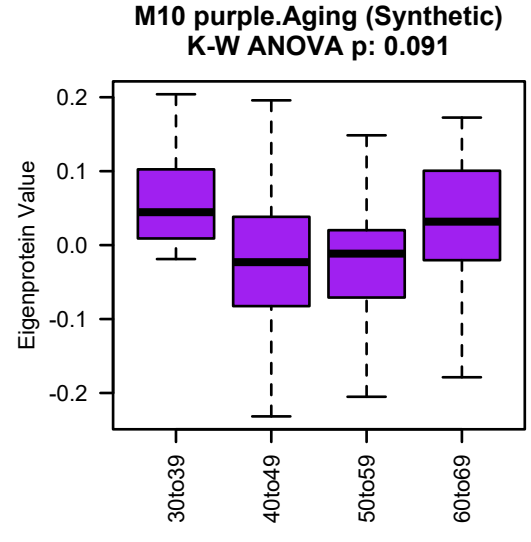

M8 pink.Aging (Synthetic)
K-W ANOVA p: 0.65
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
below35
35to44
45to55
over55

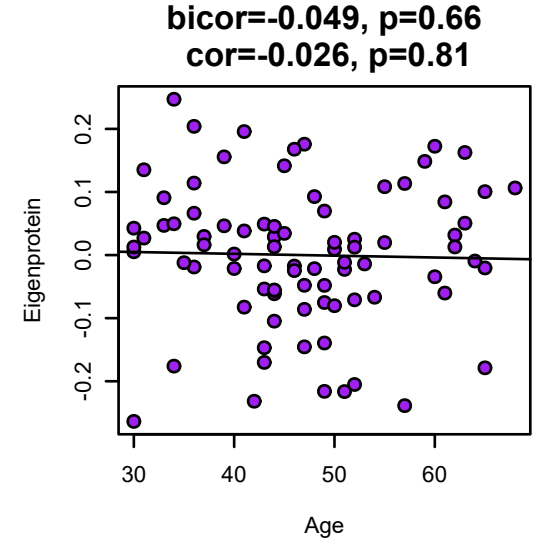

M8 pink.Aging (Synthetic)
K-W ANOVA p: 0.51
Eigenprotein Value
0.20
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
30to39
40to49
50to59
60to69

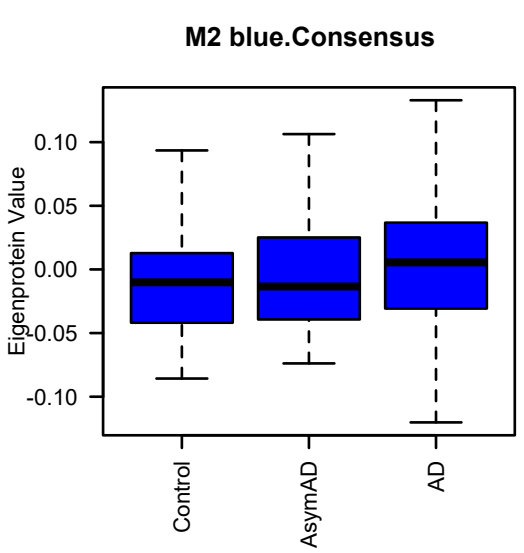

bicor=-0.047, p=0.67
cor=-0.078, p=0.48
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
30
40
50
60
Age

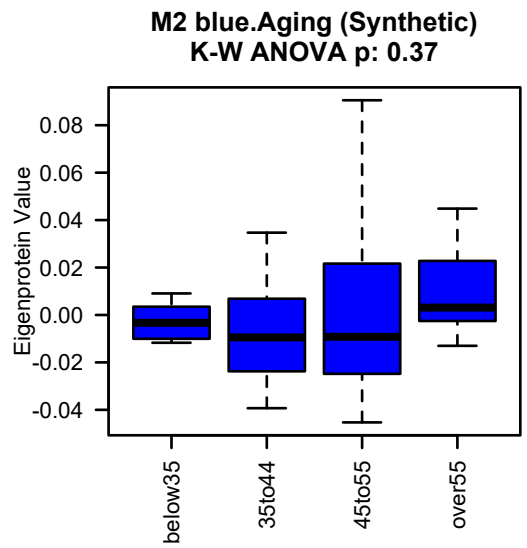

M10 purple.Consensus
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

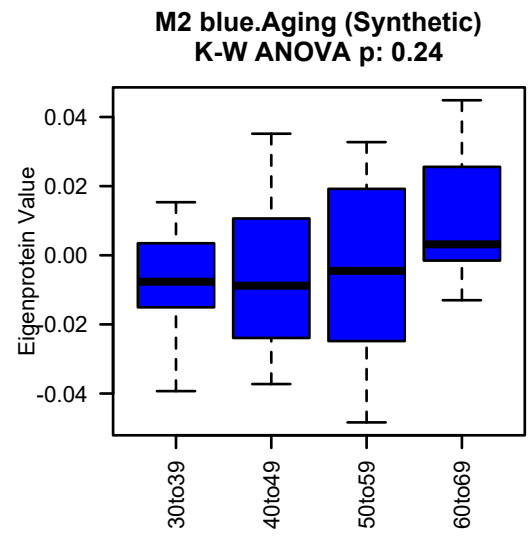

M10 purple.Aging (Synthetic)
K-W ANOVA p: 0.49
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
below35
35to44
45to55
over55

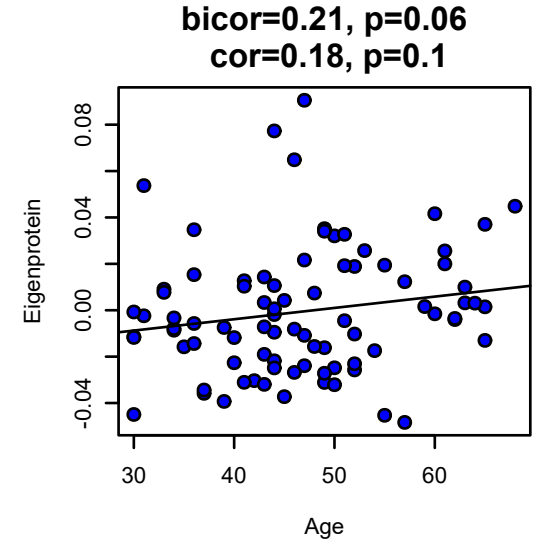

M10 purple.Aging (Synthetic)
K-W ANOVA p: 0.091
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
30to39
40to49
50to59
60to69

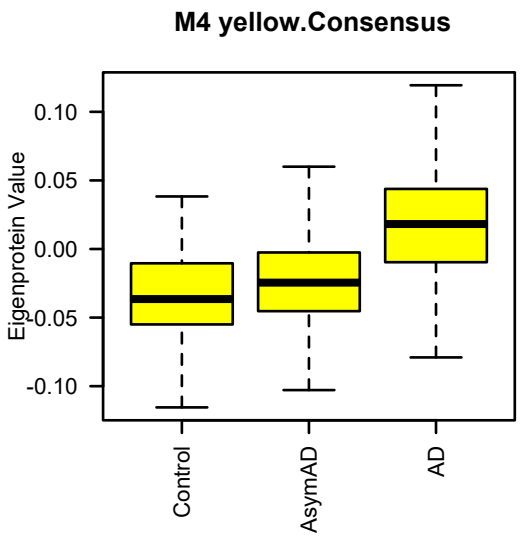

bicor=-0.049, p=0.66
cor=-0.026, p=0.81
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
30
40
50
60
Age

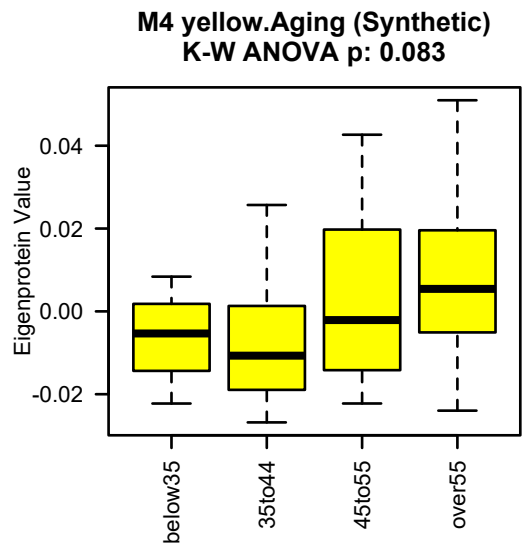

M2 blue.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

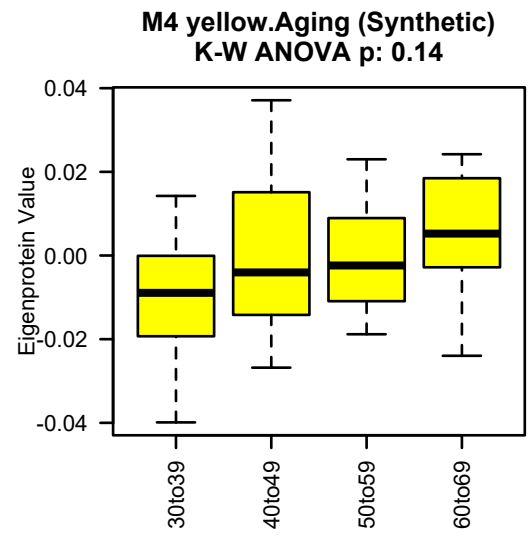

M2 blue.Aging (Synthetic)
K-W ANOVA p: 0.37
Eigenprotein Value
0.08
0.06
0.04
0.02
0.00
-0.02
-0.04
below35
35to44
45to55
over55

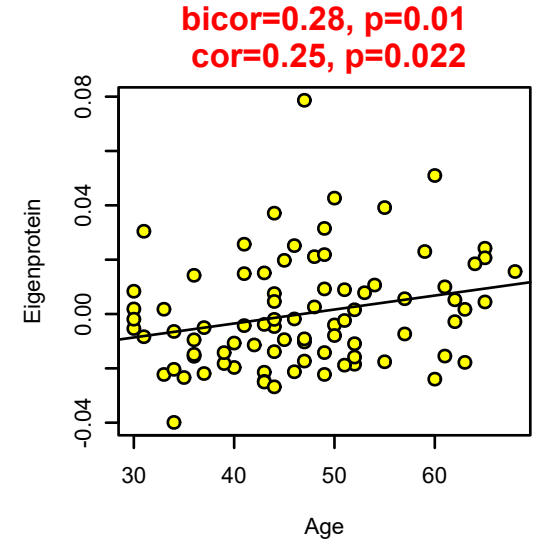

M2 blue.Aging (Synthetic)
K-W ANOVA p: 0.24
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
30to39
40to49
50to59
60to69

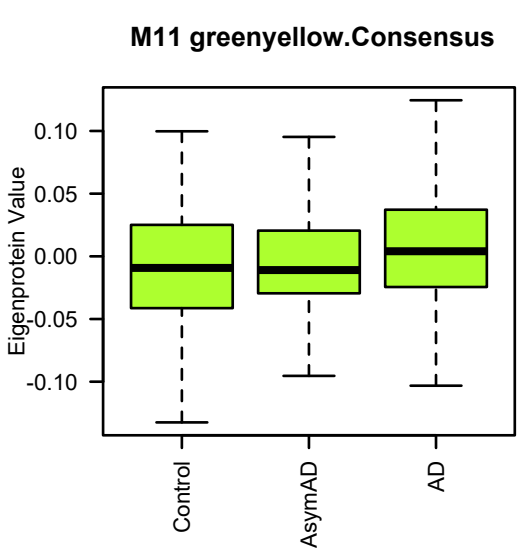

bicor=0.21, p=0.06
cor=0.18, p=0.1
Eigenprotein
0.08
0.04
0.00
-0.04
30
40
50
60
Age

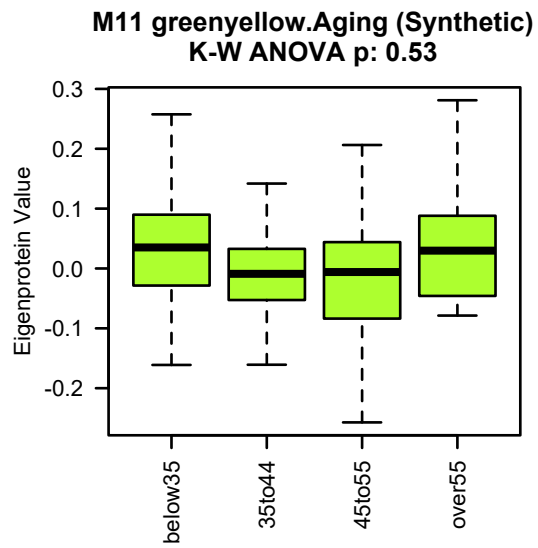

M4 yellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

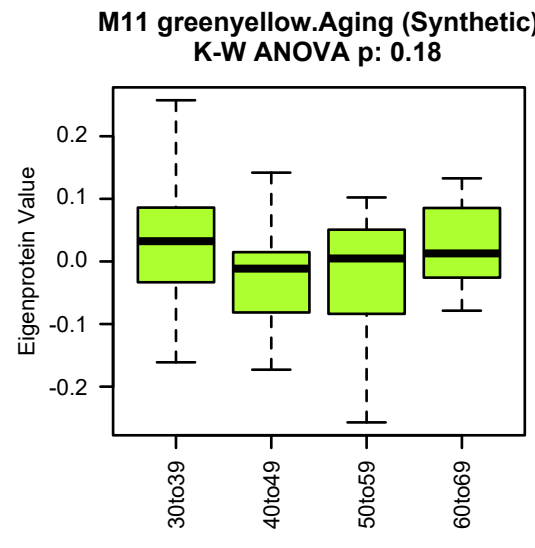

M4 yellow.Aging (Synthetic)
K-W ANOVA p: 0.083
Eigenprotein Value
0.04
0.02
0.00
-0.02
below35
35to44
45to55
over55

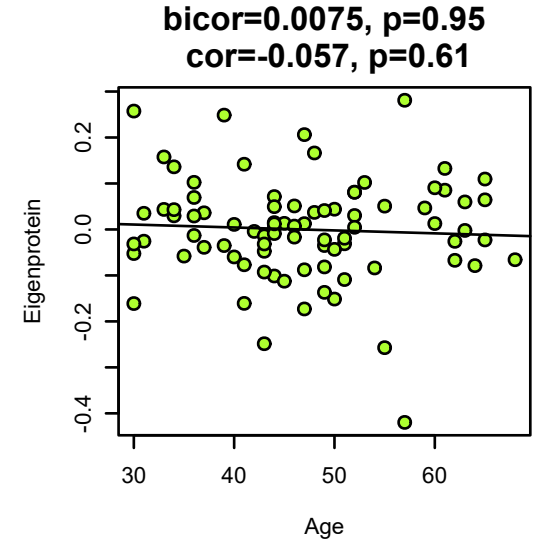

M4 yellow.Aging (Synthetic)
K-W ANOVA p: 0.14
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
30to39
40to49
50to59
60to69

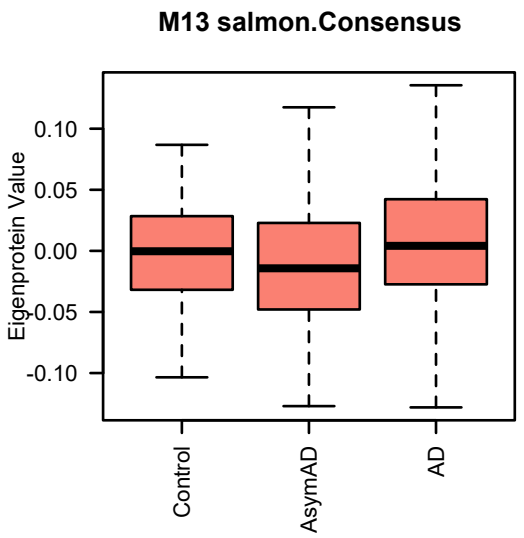

bicor=0.28, p=0.01
cor=0.25, p=0.022
Eigenprotein
0.08
0.04
0.00
-0.04
30
40
50
60
Age

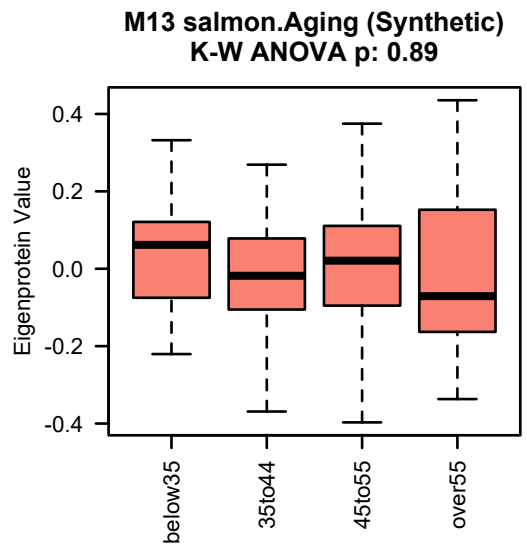

M11 greenyellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

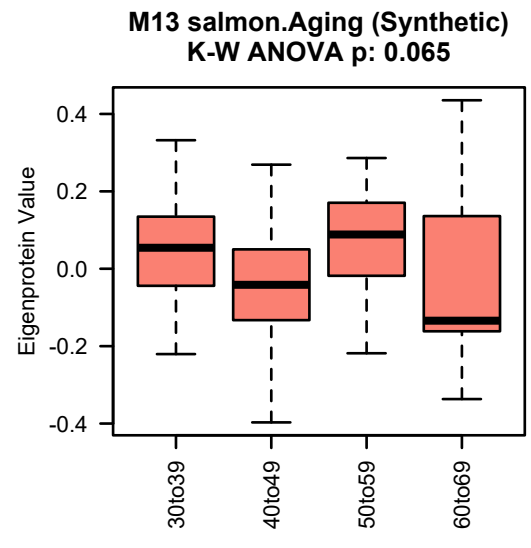

M11 greenyellow.Aging (Synthetic)
K-W ANOVA p: 0.53
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
below35
35to44
45to55
over55

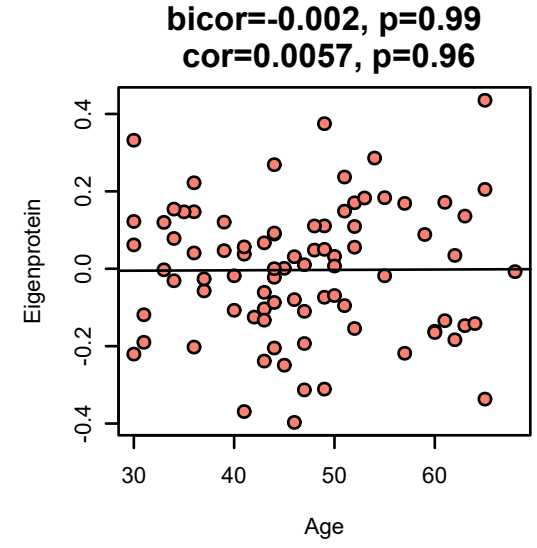

M11 greenyellow.Aging (Synthetic)
K-W ANOVA p: 0.18
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
30to39
40to49
50to59
60to69

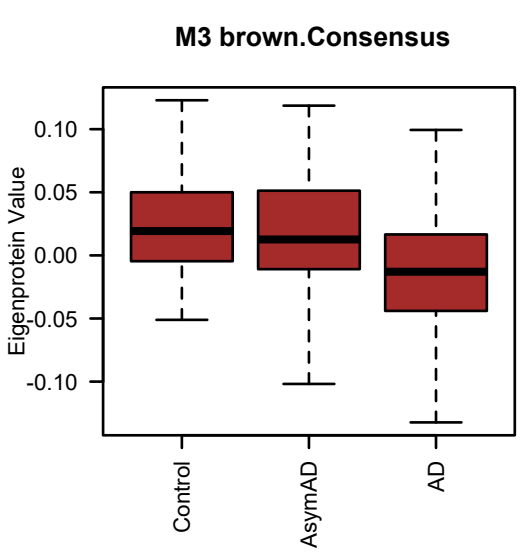

bicor=0.0075, p=0.95
cor=-0.057, p=0.61
Eigenprotein
0.2
0.0
-0.2
-0.4
30
40
50
60
Age

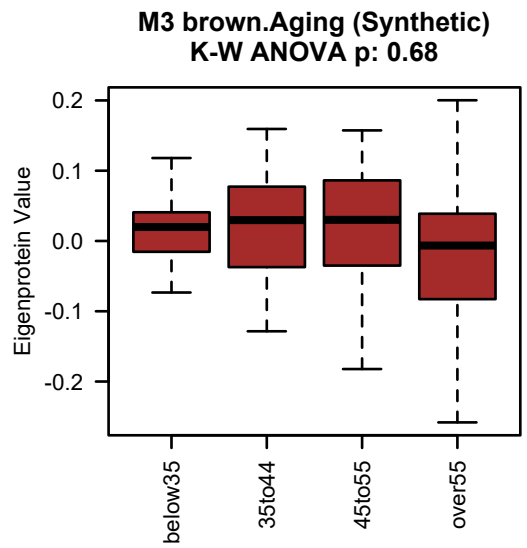

M13 salmon.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

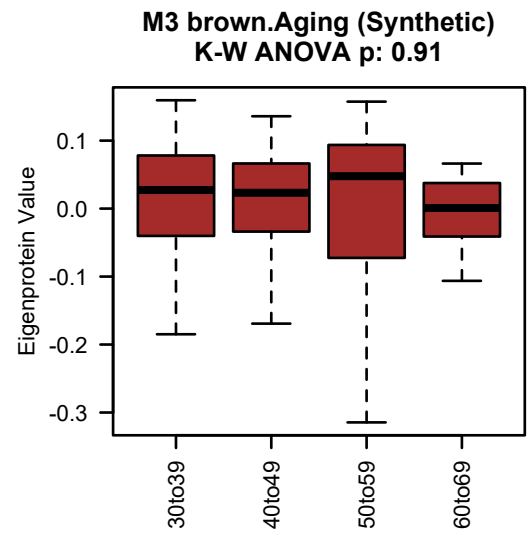

M13 salmon.Aging (Synthetic)
K-W ANOVA p: 0.89
Eigenprotein Value
0.4
0.2
0.0
-0.2
-0.4
below35
35to44
45to55
over55

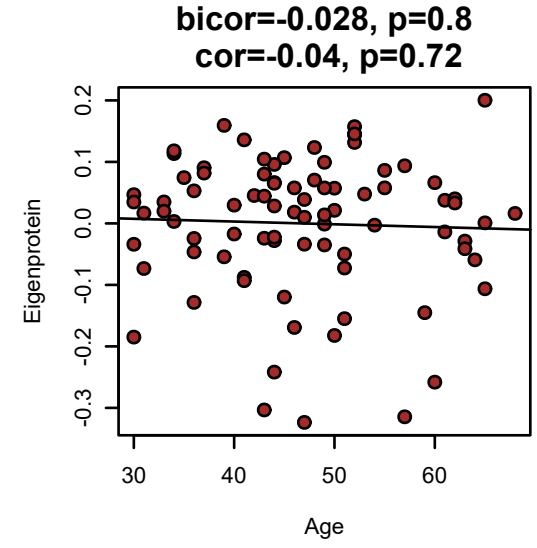

M13 salmon.Aging (Synthetic)
K-W ANOVA p: 0.065
Eigenprotein Value
0.4
0.2
0.0
-0.2
-0.4
30to39
40to49
50to59
60to69

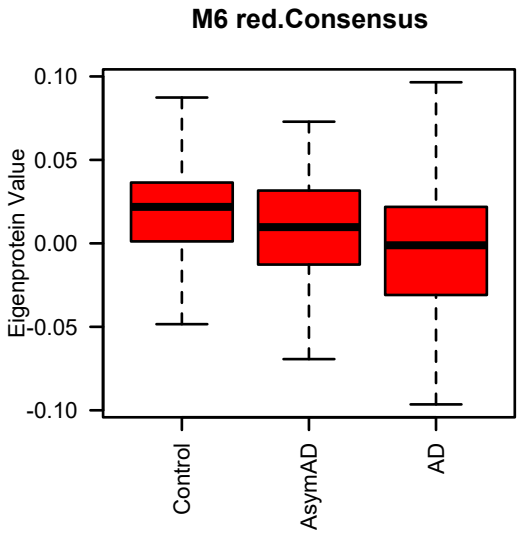

bicor=-0.002, p=0.99
cor=0.0057, p=0.96
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
30
40
50
60
Age

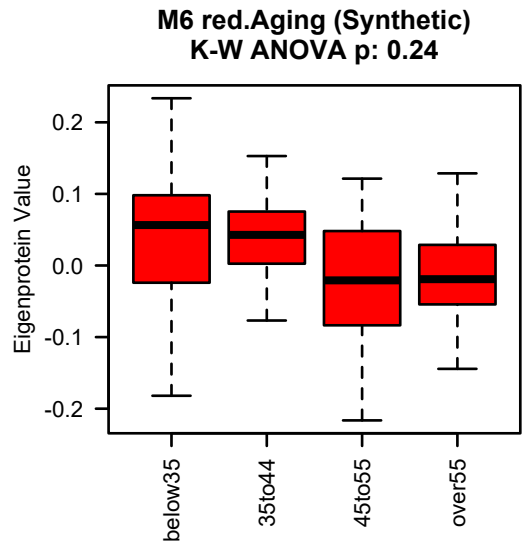

M3 brown.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

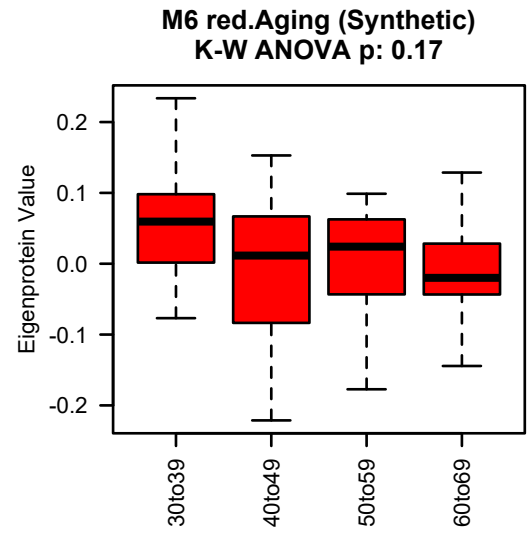

M3 brown.Aging (Synthetic)
K-W ANOVA p: 0.68
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
below35
35to44
45to55
over55

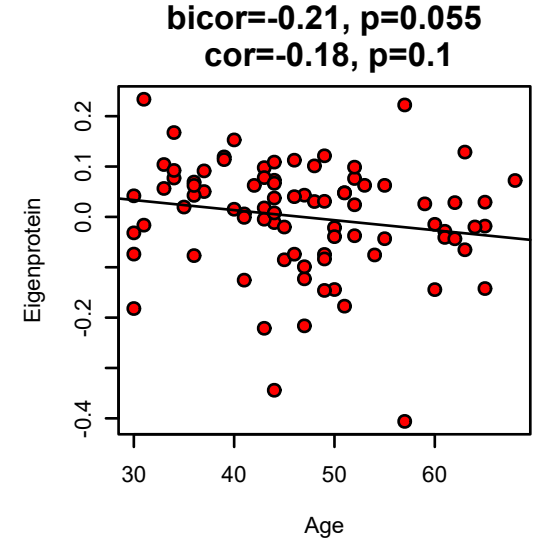

M3 brown.Aging (Synthetic)
K-W ANOVA p: 0.91
Eigenprotein Value
0.1
0.0
-0.1
-0.2
-0.3
30to39
40to49
50to59
60to69

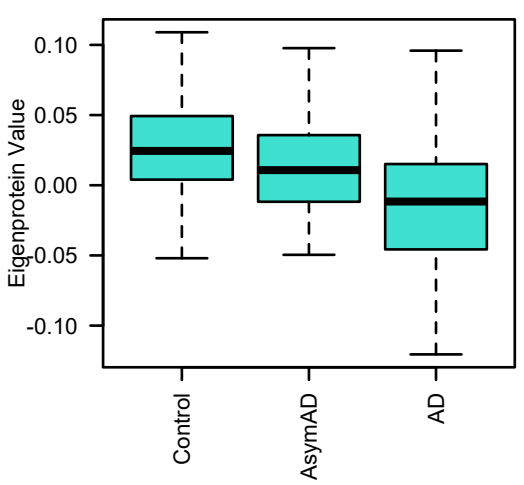

bicor=-0.028, p=0.8
cor=-0.04, p=0.72
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
-0.3
30
40
50
60
Age

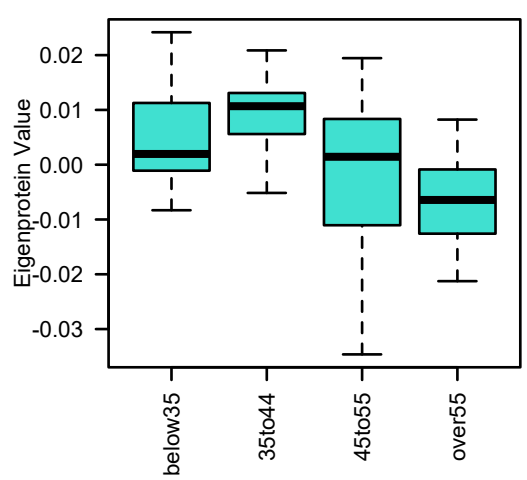

M6 red.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

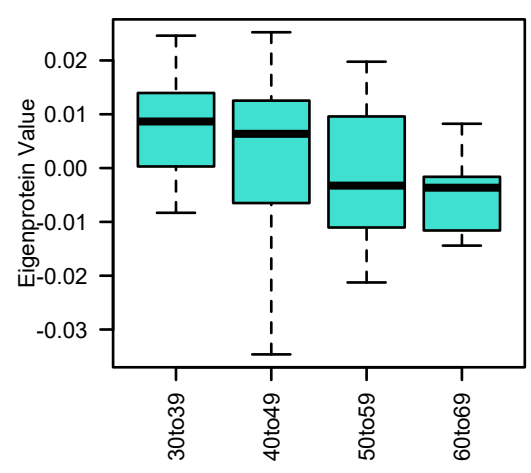

M6 red.Aging (Synthetic)
K-W ANOVA p: 0.24
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
below35
35to44
45to55
over55

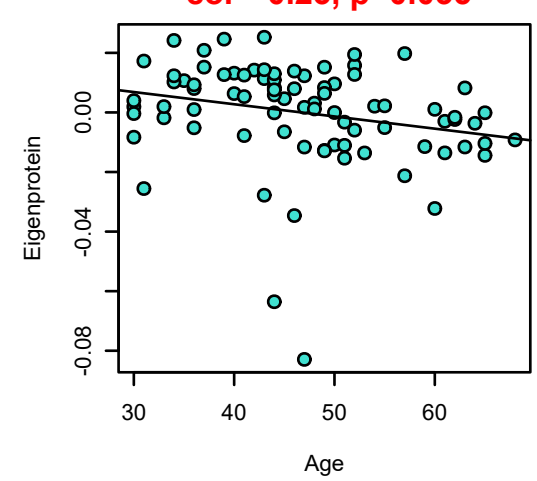

M6 red.Aging (Synthetic)
K-W ANOVA p: 0.17
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
30to39
40to49
50to59
60to69

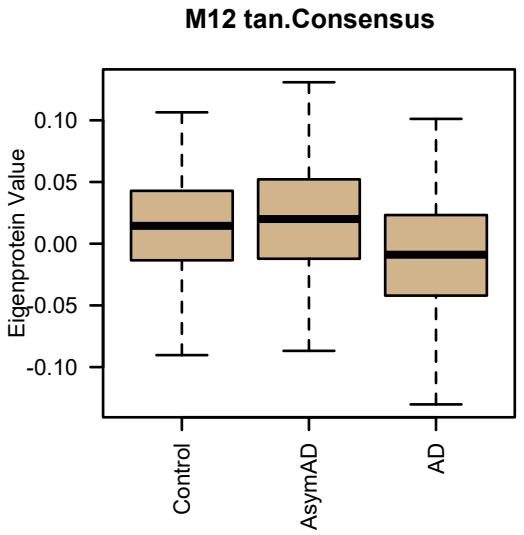

bicor=-0.21, p=0.055
cor=-0.18, p=0.1
Eigenprotein
0.2
0.1
0.0
-0.2
-0.4
30
40
50
60
Age

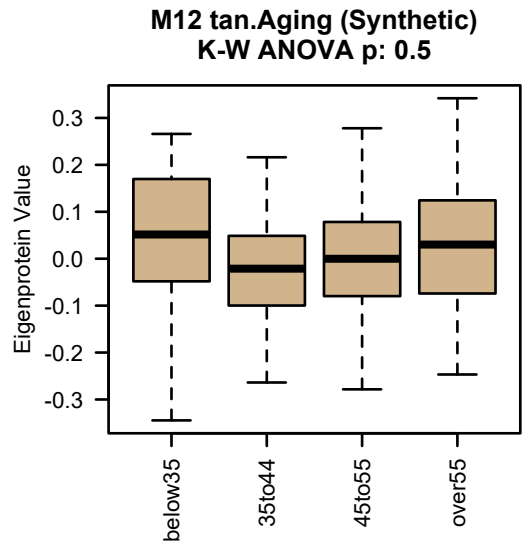

M1 turquoise.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

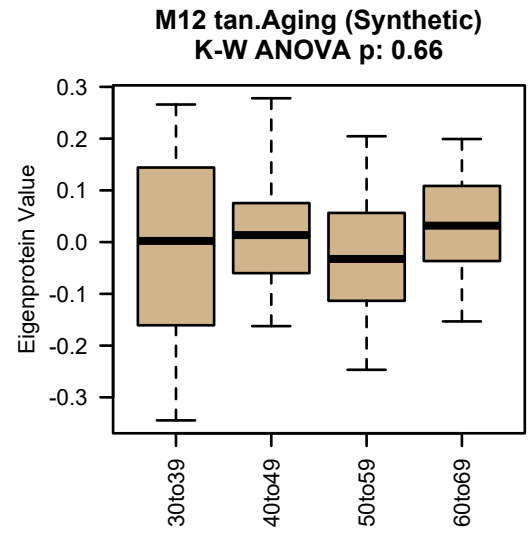

M1 turquoise.Aging (Synthetic)
K-W ANOVA p: 0.074
Eigenprotein Value
0.02
0.01
0.00
-0.01
-0.02
-0.03
below35
35to44
45to55
over55

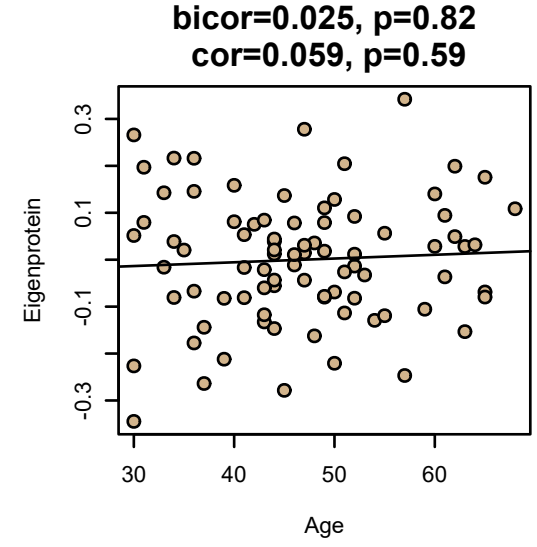

M1 turquoise.Aging (Synthetic)
K-W ANOVA p: 0.15
Eigenprotein Value
0.02
0.01
0.00
-0.01
-0.02
-0.03
30to39
40to49
50to59
60to69

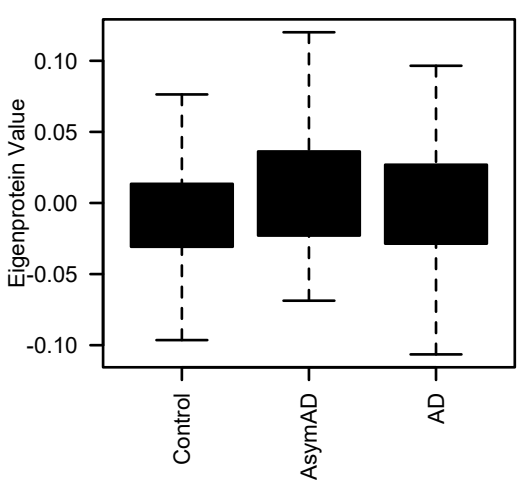

bicor=-0.35, p=0.001
cor=-0.23, p=0.035
Eigenprotein
0.00
-0.04
-0.08
30
40
50
60
Age

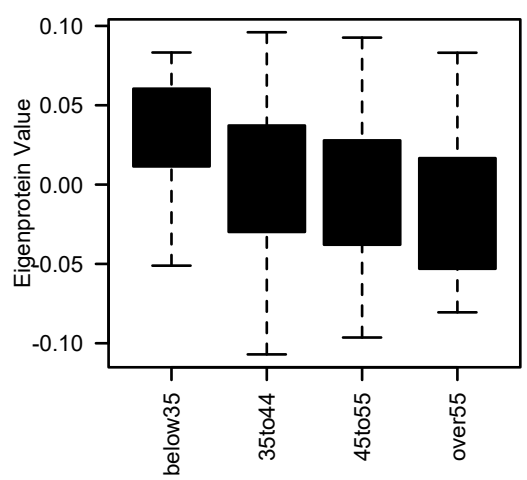

M12 tan.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

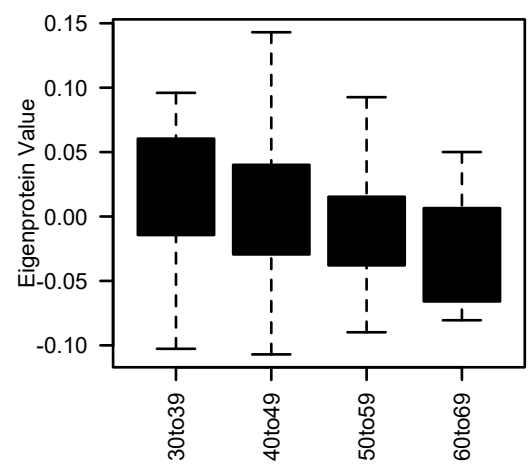

M12 tan.Aging (Synthetic)
K-W ANOVA p: 0.5
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
below35
35to44
45to55
over55

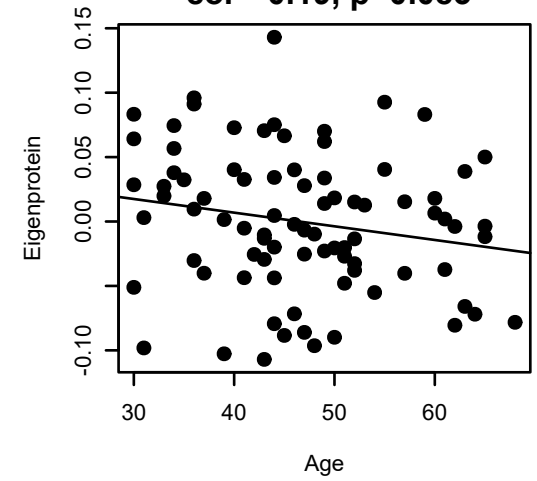

M12 tan.Aging (Synthetic)
K-W ANOVA p: 0.66
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
30to39
40to49
50to59
60to69

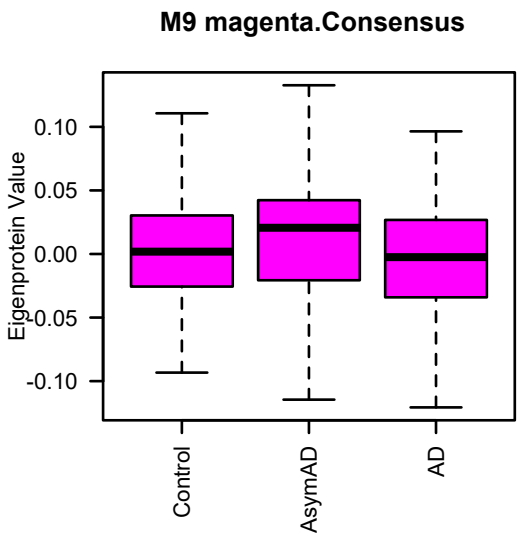

bicor=0.025, p=0.82
cor=0.059, p=0.59
Eigenprotein
0.3
0.1
-0.1
-0.3
30
40
50
60
Age

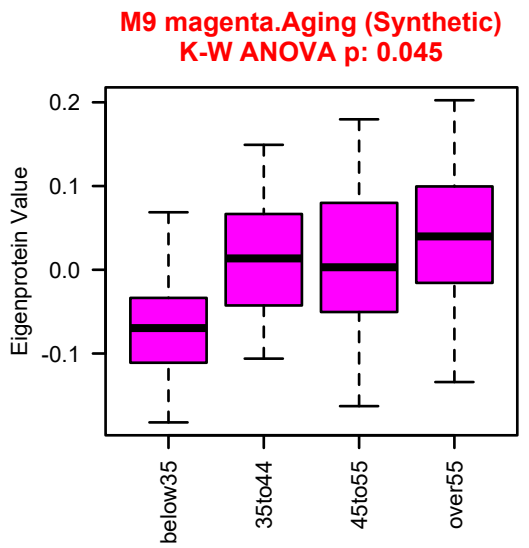

M7 black.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

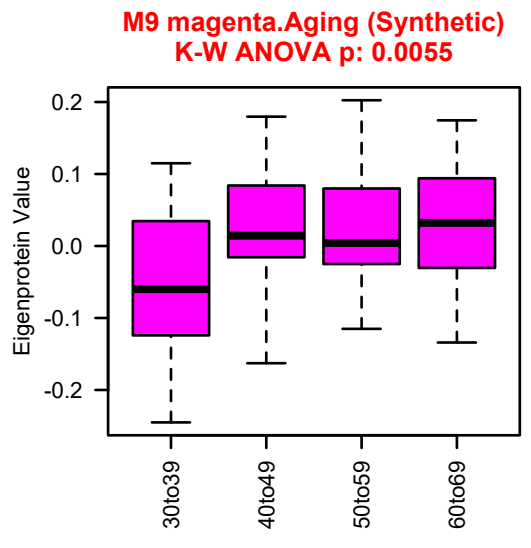

M7 black.Aging (Synthetic)
K-W ANOVA p: 0.3
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
below35
35to44
45to55
over55

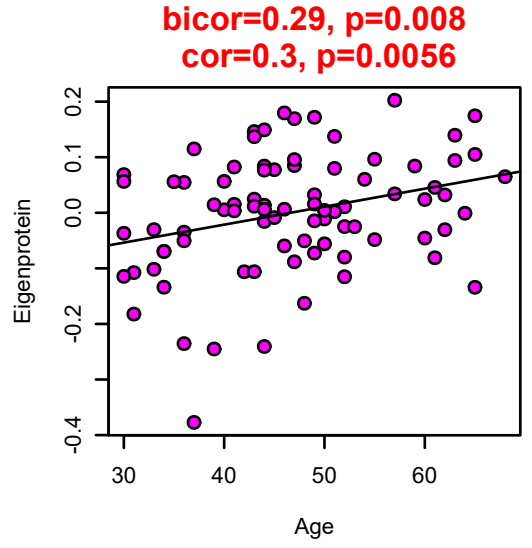

M7 black.Aging (Synthetic)
K-W ANOVA p: 0.33
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
30to39
40to49
50to59
60to69


bicor=-0.2, p=0.071
cor=-0.19, p=0.083
Eigenprotein
0.15
0.10
0.05
0.00
-0.10
30
40
50
60
Age

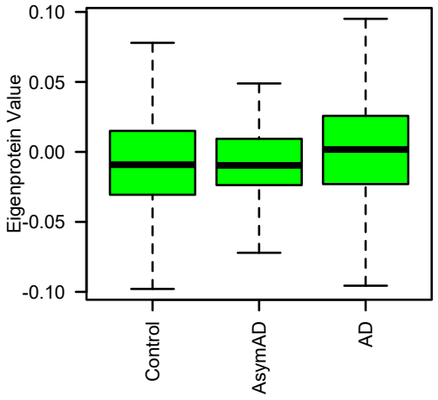

M9 magenta.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

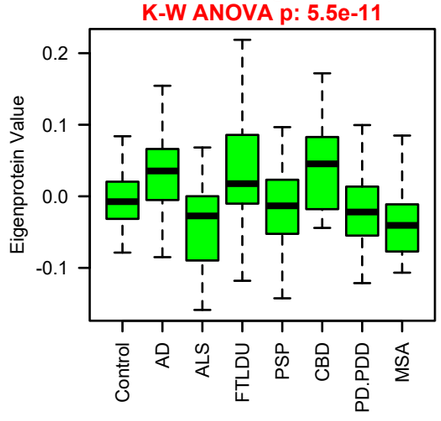

M9 magenta.Aging (Synthetic)
K-W ANOVA p: 0.045
Eigenprotein Value
0.2
0.1
0.0
-0.1
below35
35to44
45to55
over55

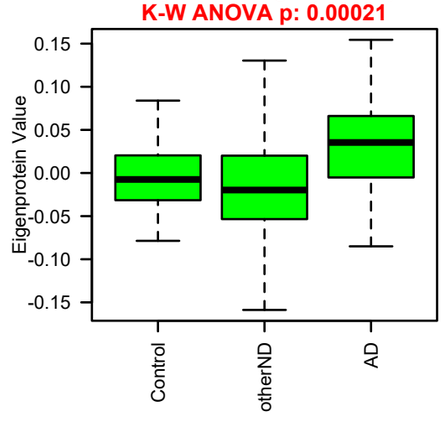

M9 magenta.Aging (Synthetic)
K-W ANOVA p: 0.0055
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
30to39
40to49
50to59
60to69

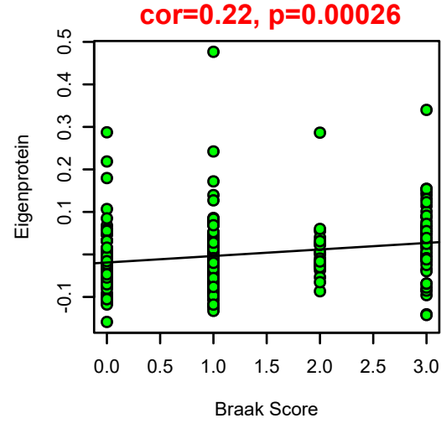

bicor=0.29, p=0.008
cor=0.3, p=0.0056
Eigenprotein
0.2
0.1
0.0
-0.2
-0.4
30
40
50
60
Age

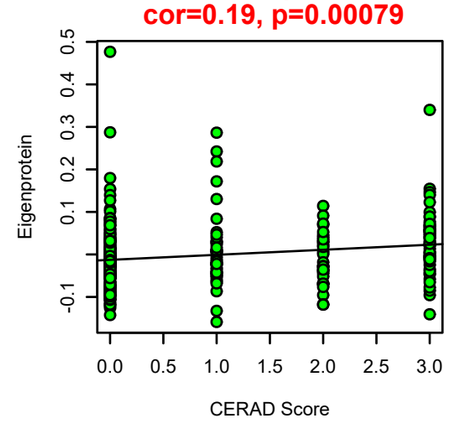
Supplementary Figure 9. Effect of Aging on AD Network Modules. The top 20% of proteins by kME value in each AD brain protein network module was used to create a synthetic eigenprotein, which was then measured by age grouping and correlated with age in the aging cohort from the Baltimore coroner's office (*n*=84 independent case samples). The first boxplot for each module is the AD network eigenprotein by case status, given as reference for the second and third boxplots, which is the synthetic eigenprotein in the BLSA precuneus cohort measured in two different age groupings (age below 35, *n*=11; age 35-44, *n*=27; age 45-55, *n*=30; age over 55, *n*=16; age 30-39, *n*=20; age 40-49, *n*=34; age 50-59, *n*=17; age 60-69, *n*=13;). Synthetic eigenproteins were also correlated directly with age, using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Synthetic eigenprotein differences by case status were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

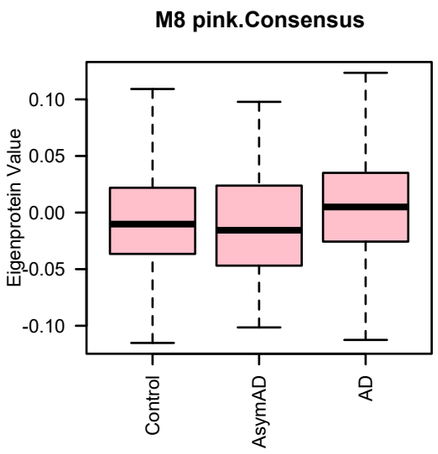

M5 green.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

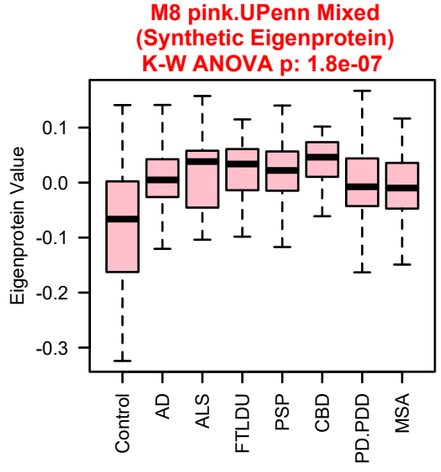

M5 green.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 5.5e-11
Eigenprotein Value
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

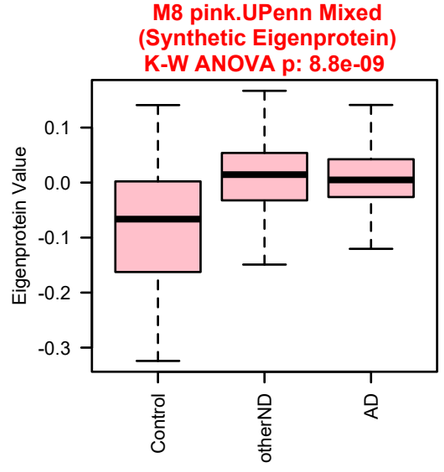

M5 green.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.00021
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
otherND
AD

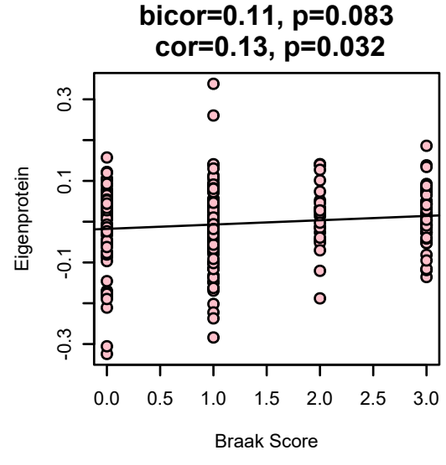

bicor=0.27, p=5e-06
cor=0.22, p=0.00026
Eigenprotein
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

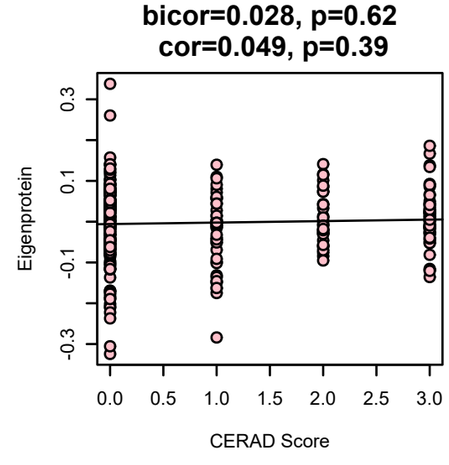

bicor=0.24, p=2.6e-05
cor=0.19, p=0.00079
Eigenprotein
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

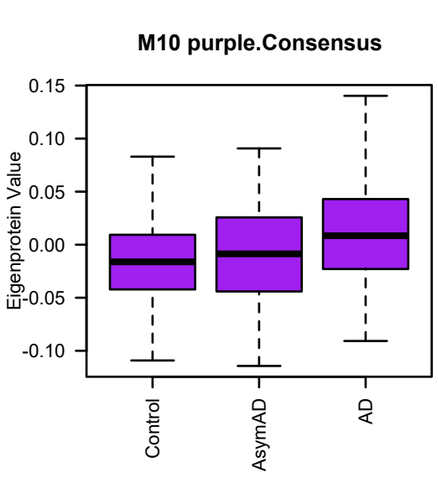

M8 pink.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

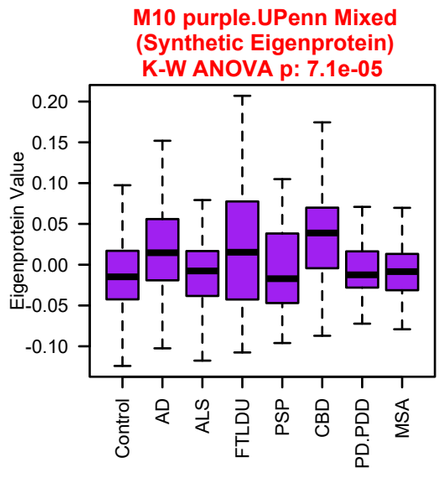

M8 pink.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 1.8e-07
Eigenprotein Value
0.1
0.0
-0.1
-0.2
-0.3
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

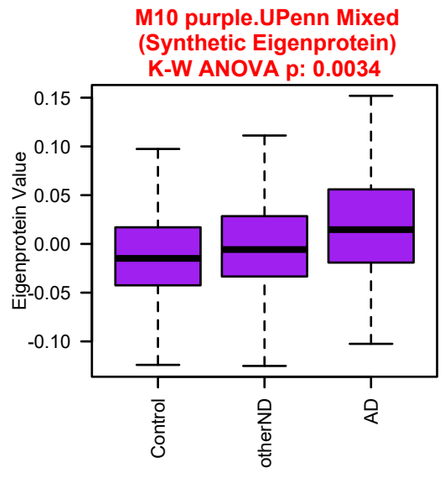

M8 pink.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 8.8e-09
Eigenprotein Value
0.1
0.0
-0.1
-0.2
-0.3
Control
otherND
AD

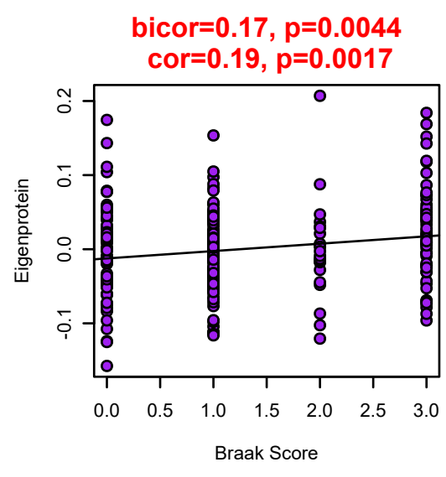

bicor=0.11, p=0.083
cor=0.13, p=0.032
Eigenprotein
0.3
0.1
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

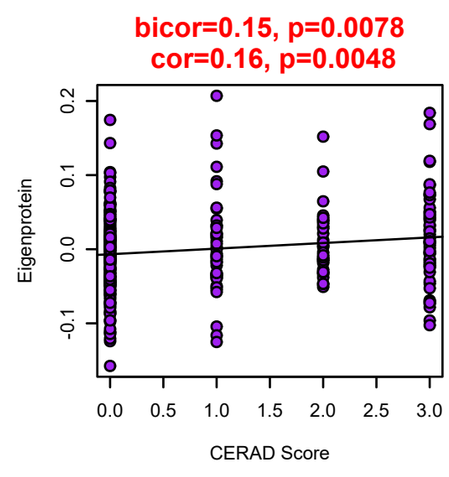

bicor=0.028, p=0.62
cor=0.049, p=0.39
Eigenprotein
0.3
0.1
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

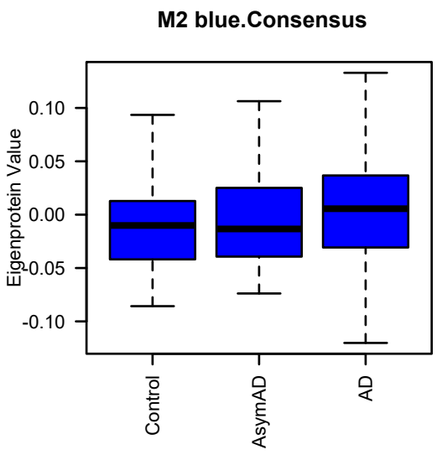

M10 purple.Consensus
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

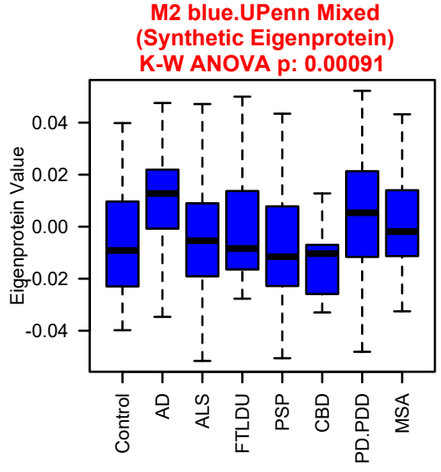

M10 purple.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 7.1e-05
Eigenprotein Value
0.20
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

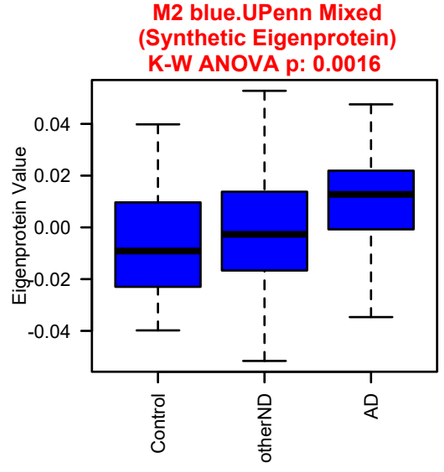

M10 purple.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.0034
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
otherND
AD

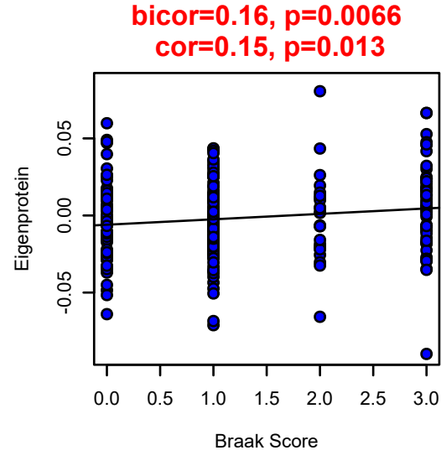

bicor=0.17, p=0.0044
cor=0.19, p=0.0017
Eigenprotein
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

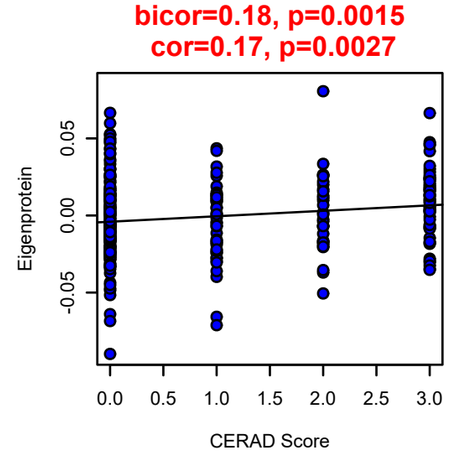

bicor=0.15, p=0.0078
cor=0.16, p=0.0048
Eigenprotein
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

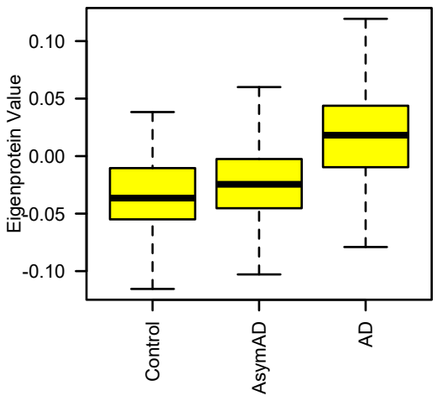

M2 blue.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

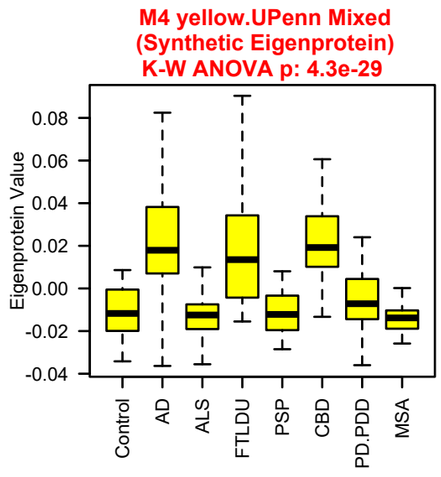

M2 blue.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.00091
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

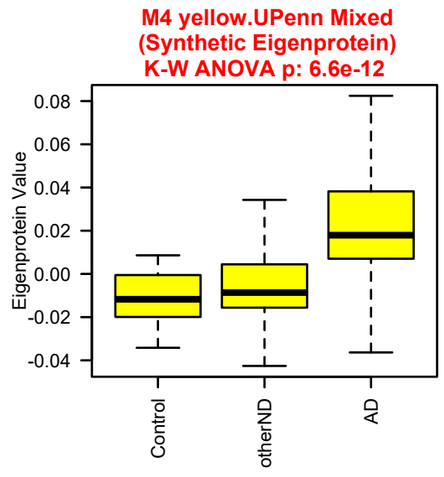

M2 blue.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.0016
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
otherND
AD

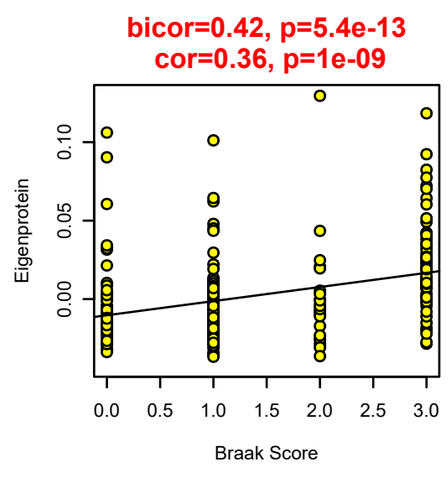

bicor=0.16, p=0.0066
cor=0.15, p=0.013
Eigenprotein
0.05
0.00
-0.05
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

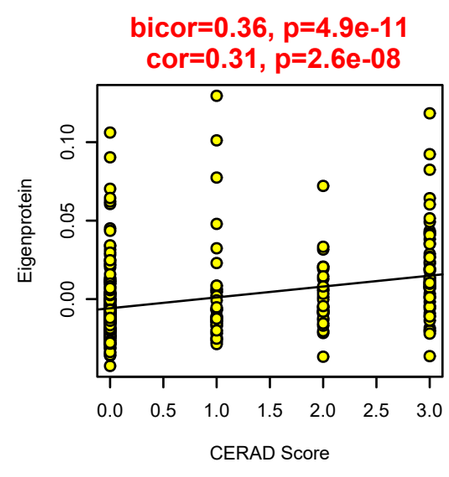

bicor=0.18, p=0.0015
cor=0.17, p=0.0027
Eigenprotein
0.05
0.00
-0.05
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

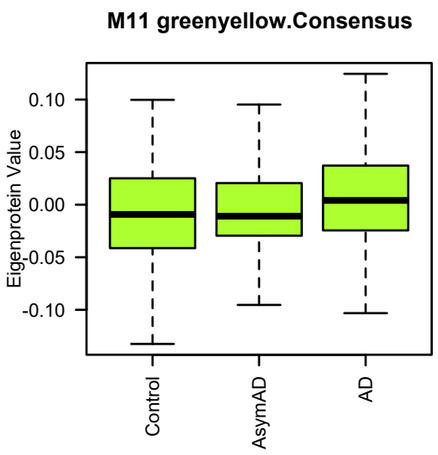

M4 yellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

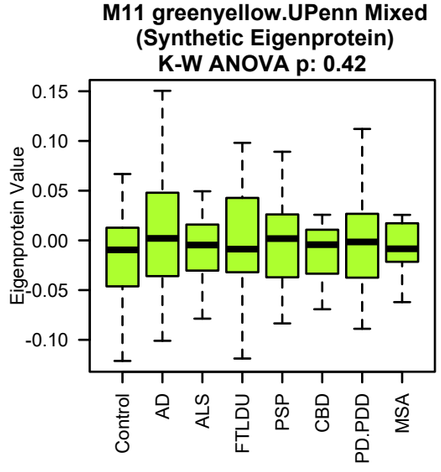

M4 yellow.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 4.3e-29
Eigenprotein Value
0.08
0.06
0.04
0.02
0.00
-0.02
-0.04
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

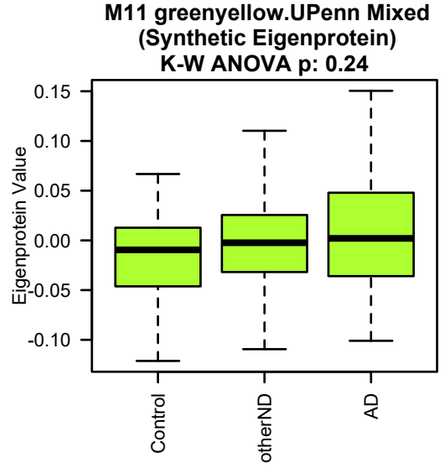

M4 yellow.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 6.6e-12
Eigenprotein Value
0.08
0.06
0.04
0.02
0.00
-0.02
-0.04
Control
otherND
AD

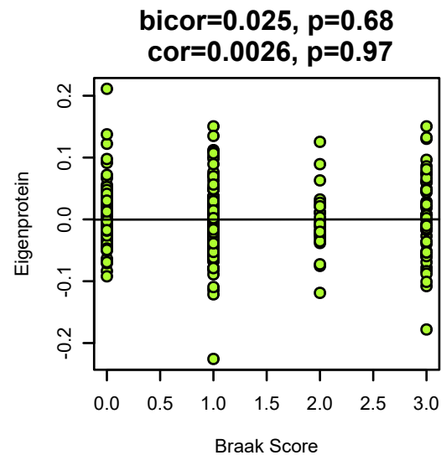

bicor=0.42, p=5.4e-13
cor=0.36, p=1e-09
Eigenprotein
0.10
0.05
0.00
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

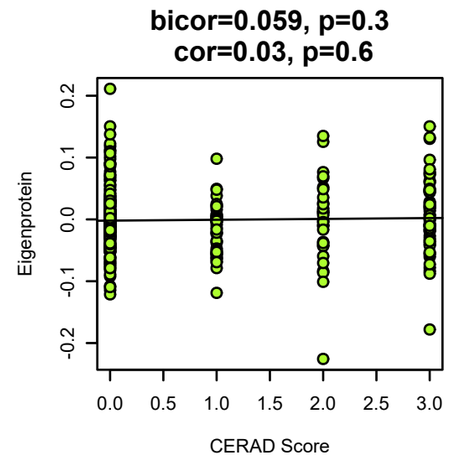

bicor=0.36, p=4.9e-11
cor=0.31, p=2.6e-08
Eigenprotein
0.10
0.05
0.00
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

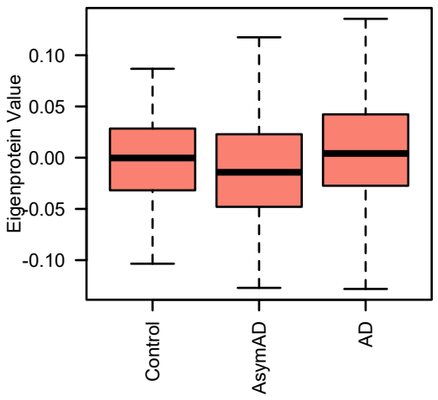

M11 greenyellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

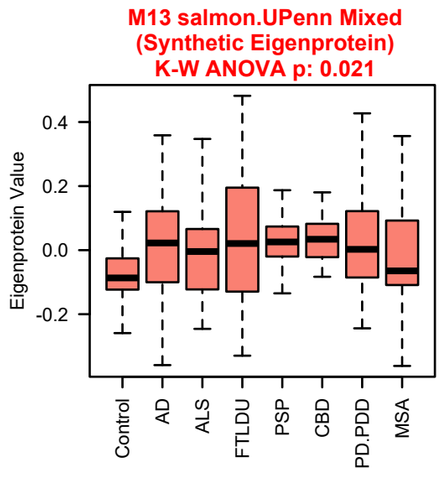

M11 greenyellow.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.42
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

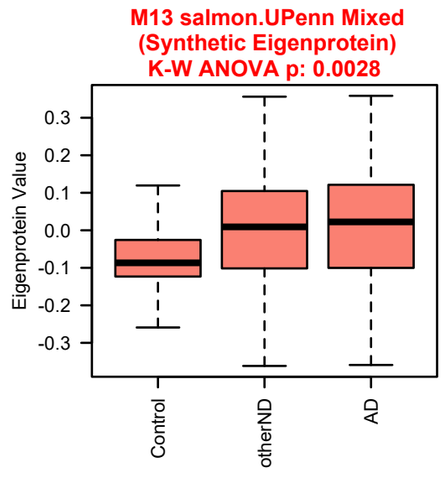

M11 greenyellow.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.24
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
otherND
AD

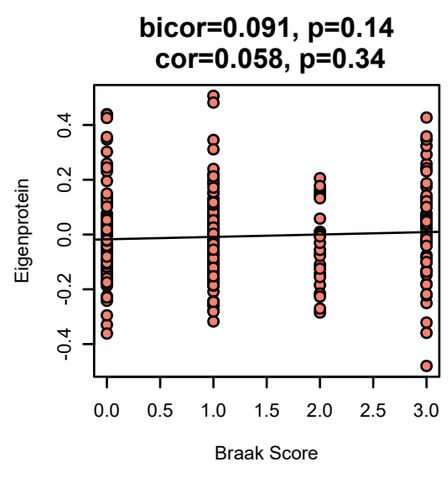

bicor=0.025, p=0.68
cor=0.0026, p=0.97
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

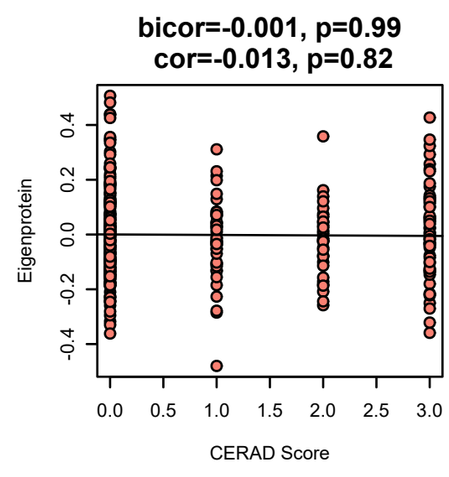

bicor=0.059, p=0.3
cor=0.03, p=0.6
Eigenprotein
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

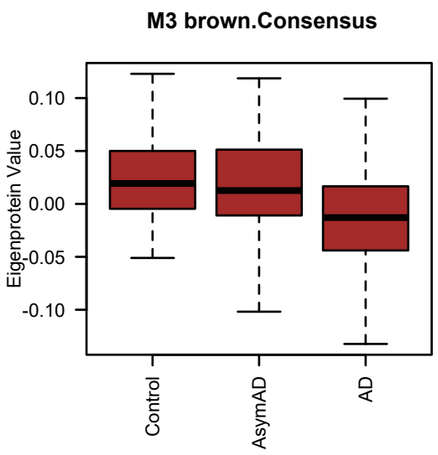

M13 salmon.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

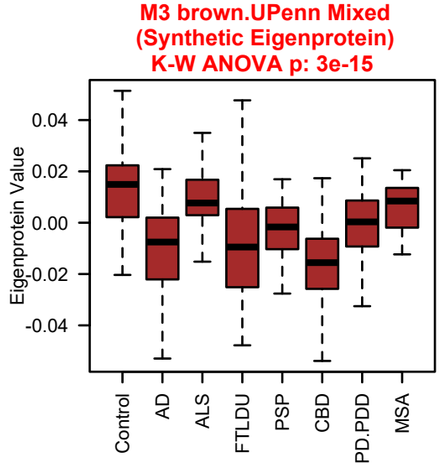

M13 salmon.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.021
Eigenprotein Value
0.4
0.2
0.0
-0.2
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

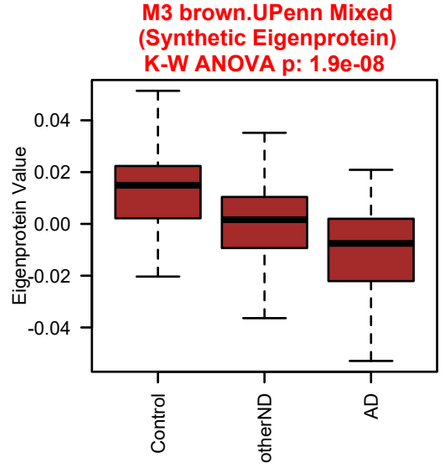

M13 salmon.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.0028
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
otherND
AD

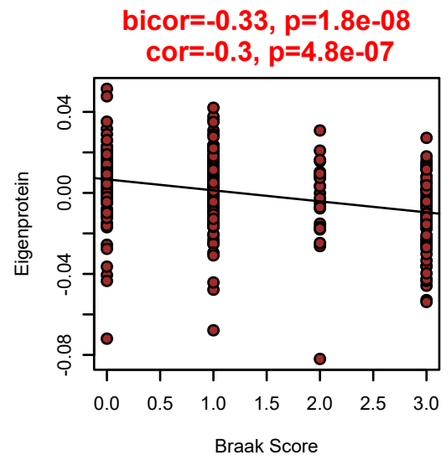

bicor=0.091, p=0.14
cor=0.058, p=0.34
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

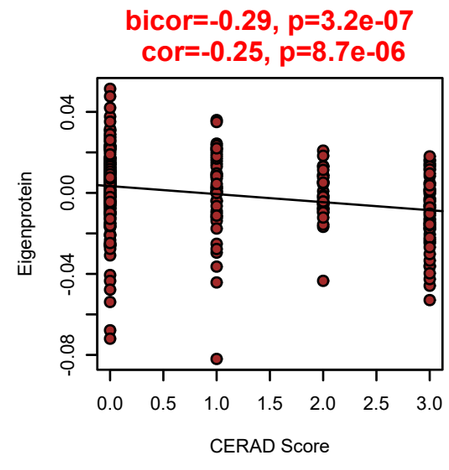

bicor=-0.001, p=0.99
cor=-0.013, p=0.82
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

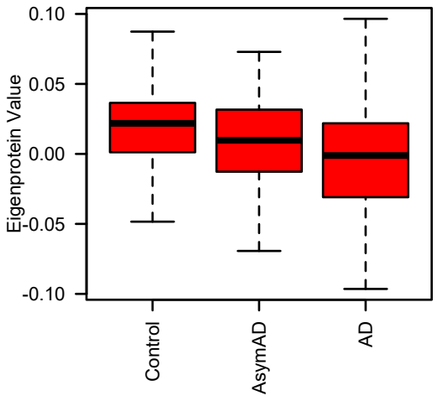

M3 brown.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

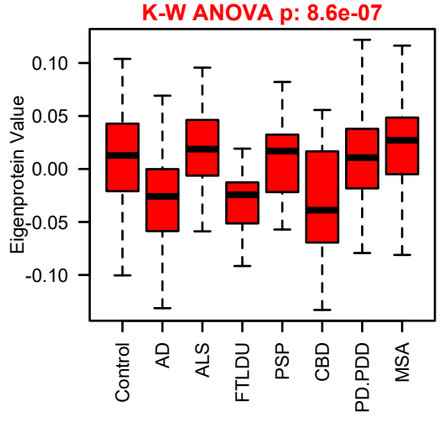

M3 brown.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 3e-15
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

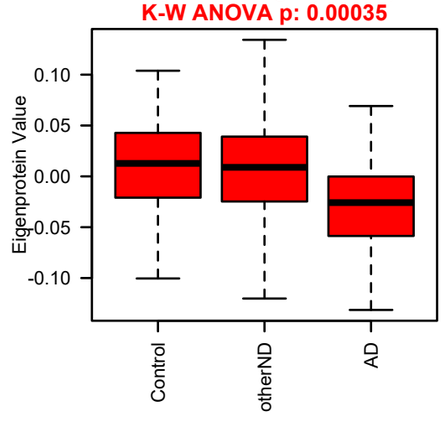

M3 brown.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 1.9e-08
Eigenprotein Value
0.04
0.02
0.00
-0.02
-0.04
Control
otherND
AD

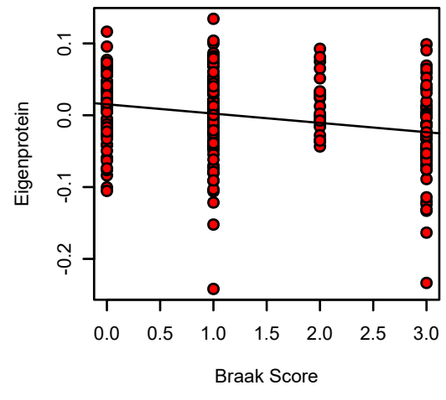

bicor=-0.33, p=1.8e-08
cor=-0.3, p=4.8e-07
Eigenprotein
0.04
0.00
-0.04
-0.08
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

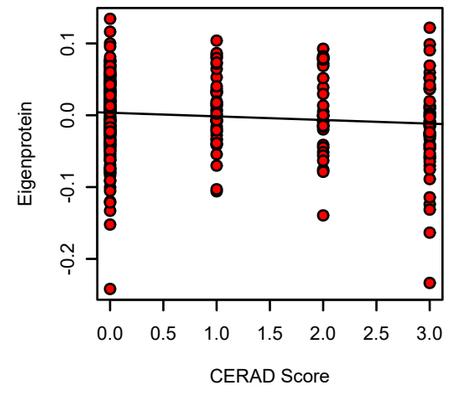

bicor=-0.29, p=3.2e-07
cor=-0.25, p=8.7e-06
Eigenprotein
0.04
0.00
-0.04
-0.08
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

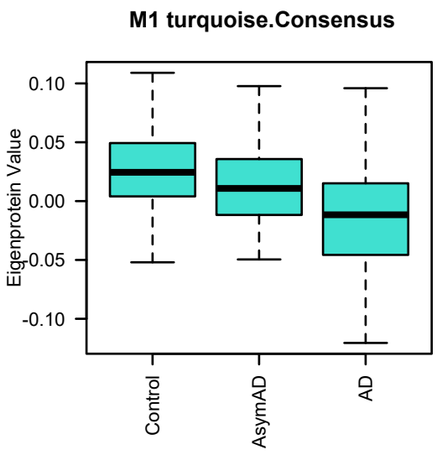

M6 red.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

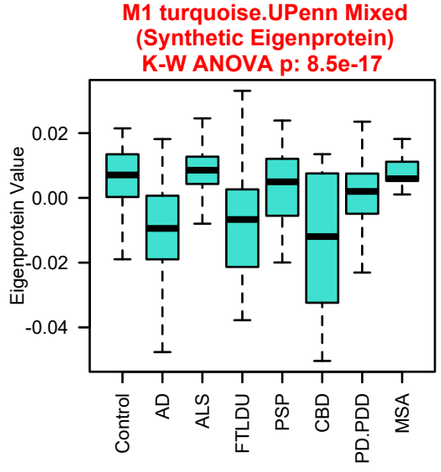

M6 red.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 8.6e-07
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

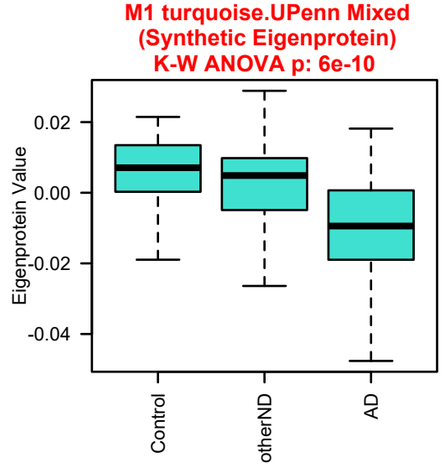

M6 red.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.00035
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
otherND
AD

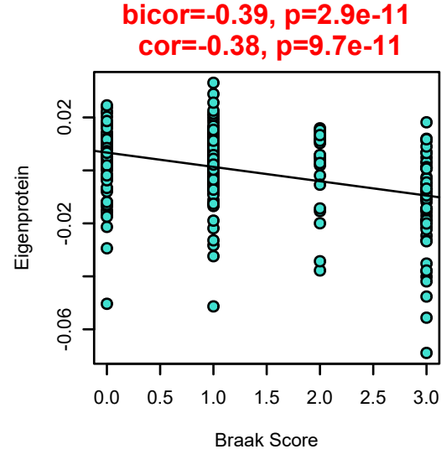

bicor=-0.25, p=4.3e-05
cor=-0.25, p=3.1e-05
Eigenprotein
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

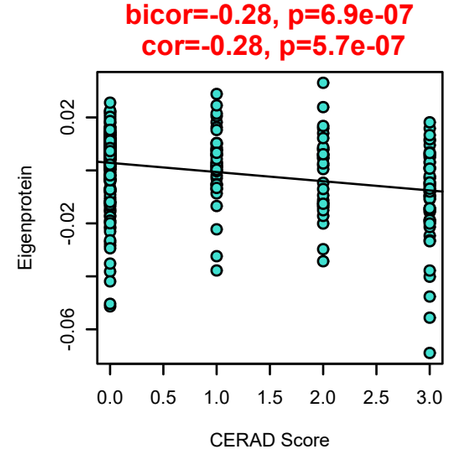

bicor=-0.11, p=0.062
cor=-0.11, p=0.053
Eigenprotein
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

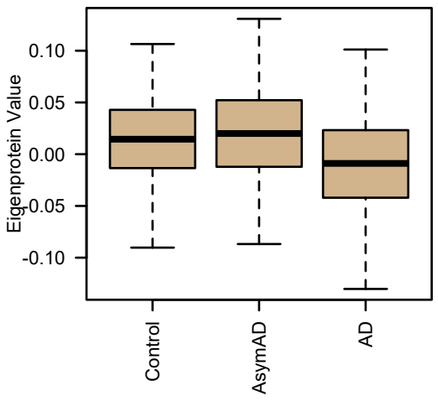

M1 turquoise.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

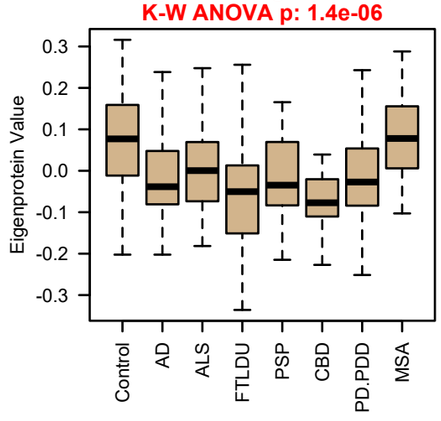

M1 turquoise.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 8.5e-17
Eigenprotein Value
0.02
0.00
-0.02
-0.04
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

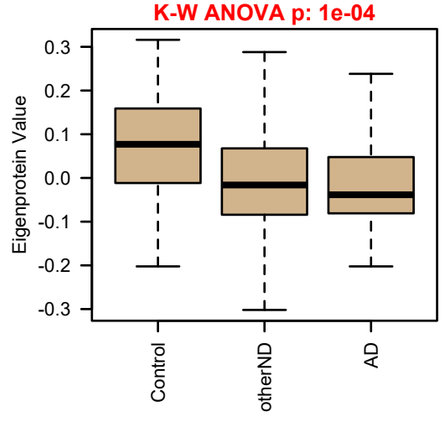

M1 turquoise.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 6e-10
Eigenprotein Value
0.02
0.00
-0.02
-0.04
Control
otherND
AD

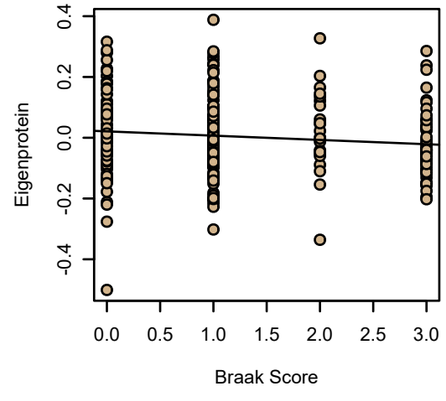

bicor=-0.39, p=2.9e-11
cor=-0.38, p=9.7e-11
Eigenprotein
0.02
-0.02
-0.06
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

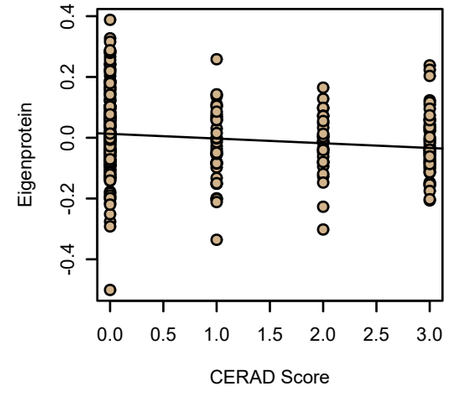

bicor=-0.28, p=6.9e-07
cor=-0.28, p=5.7e-07
Eigenprotein
0.02
-0.02
-0.06
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

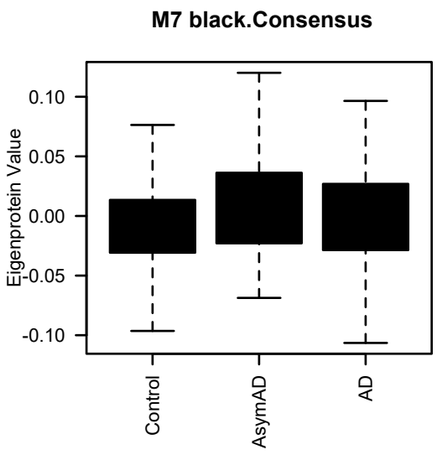

M12 tan.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

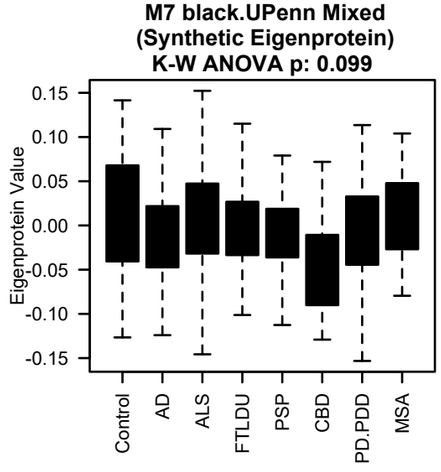

M12 tan.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 1.4e-06
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

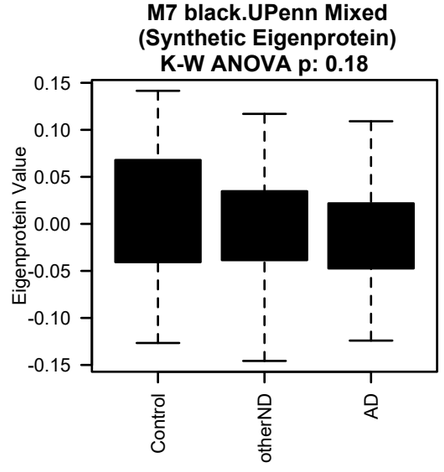

M12 tan.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 1e-04
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
otherND
AD

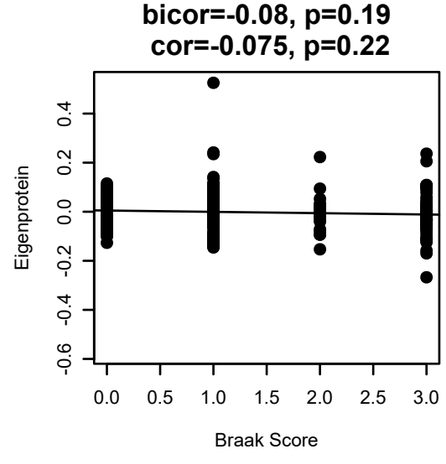

bicor=-0.12, p=0.056
cor=-0.12, p=0.048
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

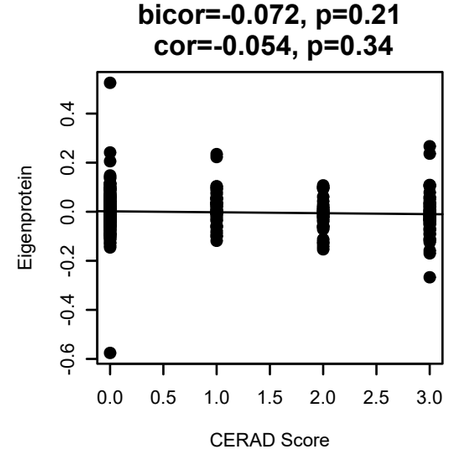

bicor=-0.15, p=0.0073
cor=-0.15, p=0.0083
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

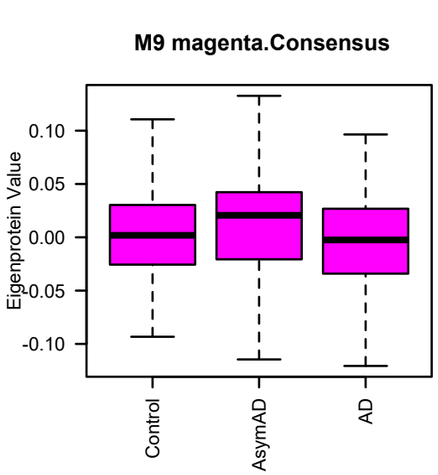

M7 black.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

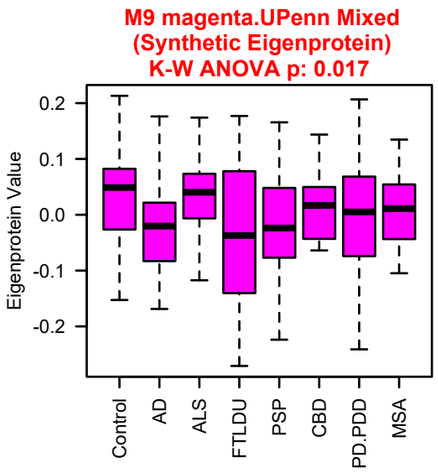

M7 black.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.099
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

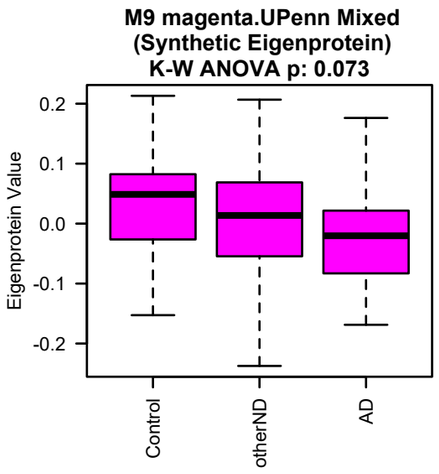

M7 black.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.18
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
otherND
AD

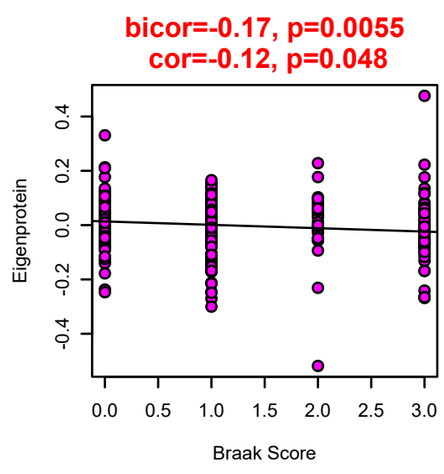

bicor=-0.08, p=0.19
cor=-0.075, p=0.22
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

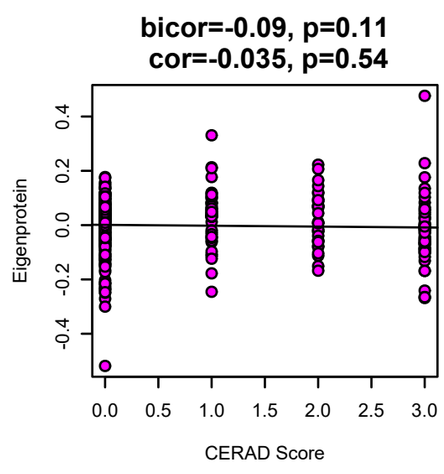

bicor=-0.072, p=0.21
cor=-0.054, p=0.34
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score


M9 magenta.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

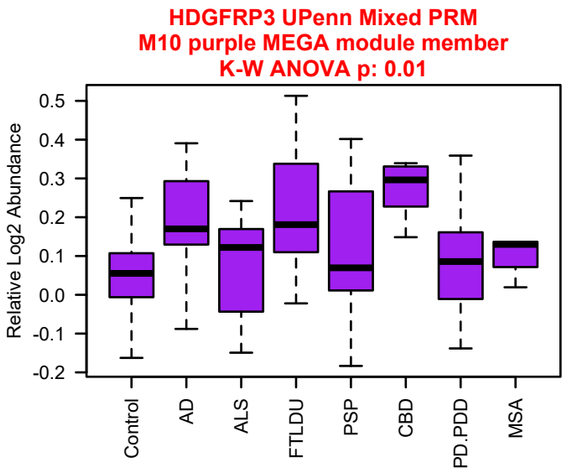

M9 magenta.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.017
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

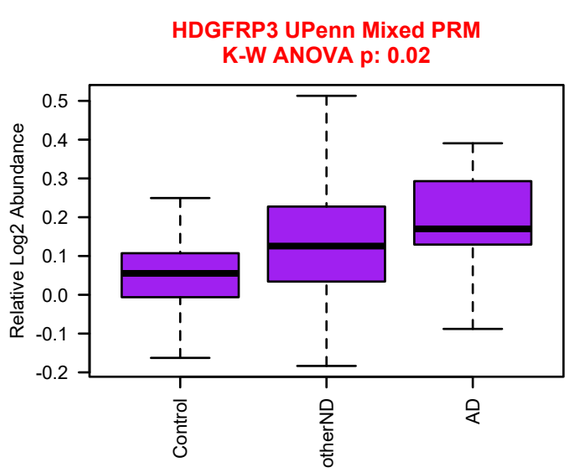

M9 magenta.UPenn Mixed
(Synthetic Eigenprotein)
K-W ANOVA p: 0.073
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
otherND
AD

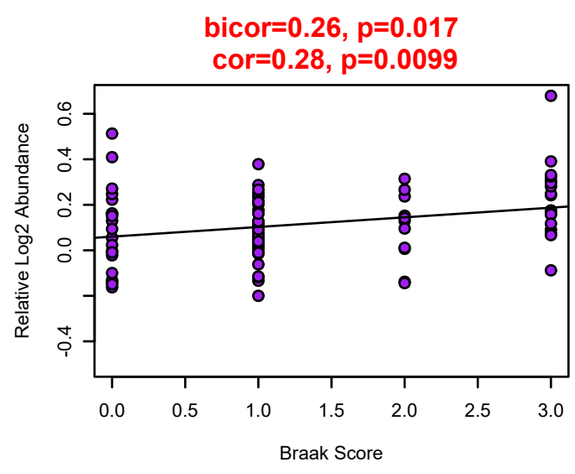

bicor=-0.17, p=0.0055
cor=-0.12, p=0.048
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

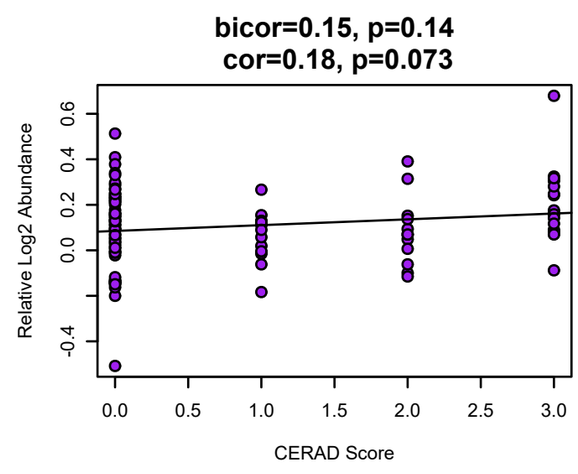

bicor=-0.09, p=0.11
cor=-0.035, p=0.54
Eigenprotein
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

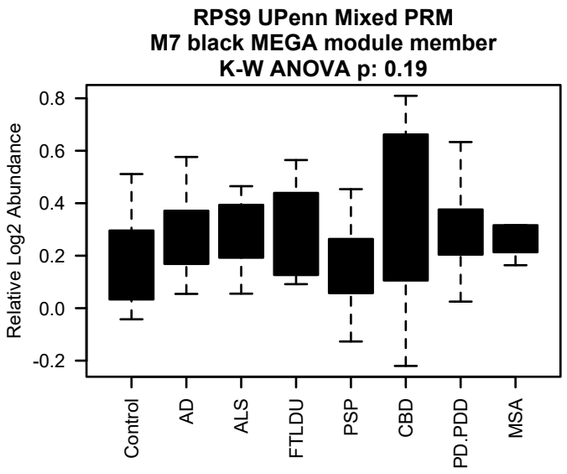
Supplementary Figure 10. AD Protein Network Module Changes in Other Neurodegenerative Diseases. The top 20% of proteins by kME value in each AD brain protein network module was used to create a synthetic eigenprotein, which was then measured in different neurodegenerative diseases in the UPenn cohort (*n*=330 independent case samples after network connectivity outlier removal). The first boxplot for each module is the AD network eigenprotein by case status, given as reference for the second and third boxplots (control *n*=46, AD *n*=49, amyotrophic lateral sclerosis (ALS) *n*=59, frontotemporal lobar degeneration with TAR DNA-binding protein 43 inclusions (FTLD-TDP) *n*=29, progressive supranuclear palsy (PSP) *n*=27, corticobasal degeneration (CBD) *n*=17, Parkinson's disease and Parkinsons's disease dementia (PD/PDD) *n*=80, and multiple system atrophy (MSA) *n*=23). Other neurodegenerative diseases (otherND) include these non-AD diseases. Synthetic eigenproteins were also correlated with CERAD and Braak scores, using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Synthetic eigenprotein differences by case status were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Differences between AD and other case groups were assessed by two-sided Dunnett's test and are provided in **Supplementary Table 4**. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

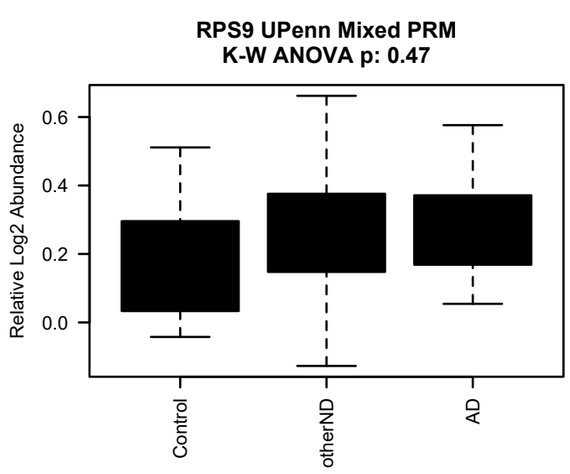

HDGFRP3 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.01
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

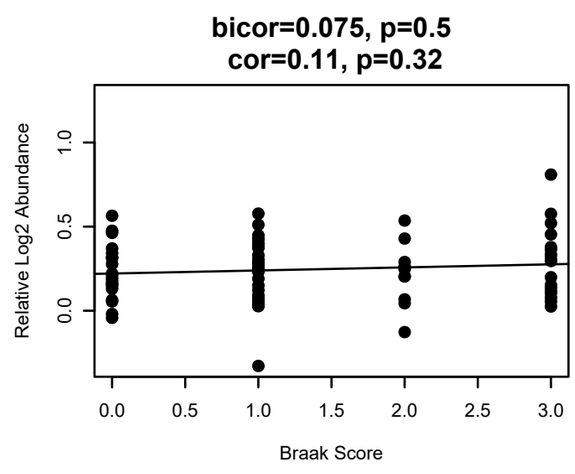

HDGFRP3 UPenn Mixed PRM
K-W ANOVA p: 0.02
Relative Log2 Abundance
Control
otherND
AD

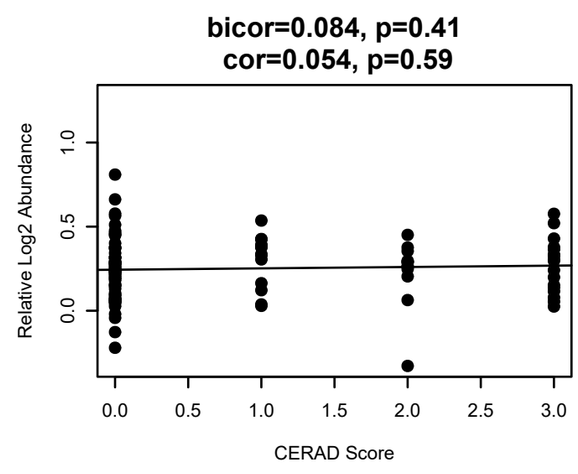

bicor=0.26, p=0.017
cor=0.28, p=0.0099
Relative Log2 Abundance
Braak Score

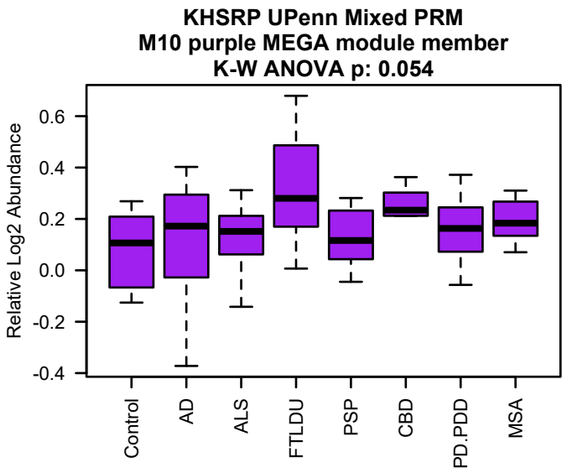

bicor=0.15, p=0.14
cor=0.18, p=0.073
Relative Log2 Abundance
CERAD Score

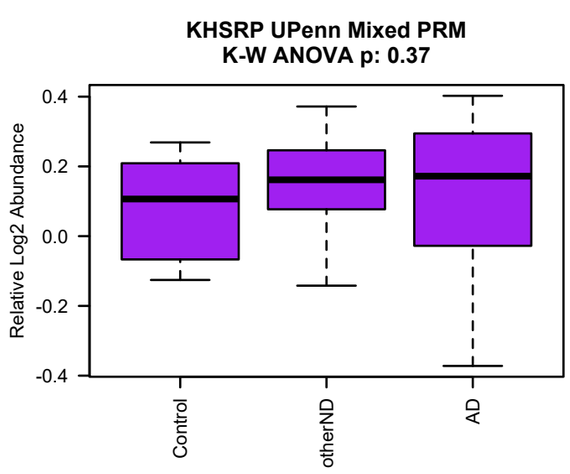

RPS9 UPenn Mixed PRM
M7 black MEGA module member
K-W ANOVA p: 0.19
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

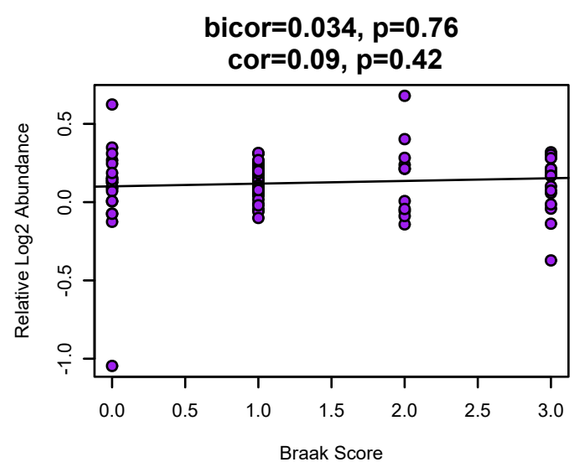

RPS9 UPenn Mixed PRM
K-W ANOVA p: 0.47
Relative Log2 Abundance
Control
otherND
AD

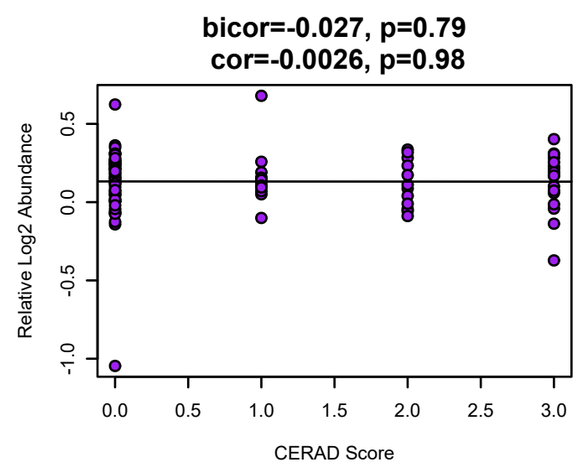

bicor=0.075, p=0.5
cor=0.11, p=0.32
Relative Log2 Abundance
Braak Score

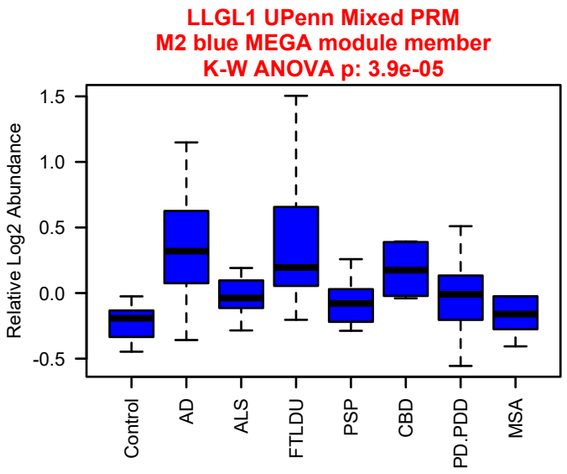

bicor=0.084, p=0.41
cor=0.054, p=0.59
Relative Log2 Abundance
CERAD Score

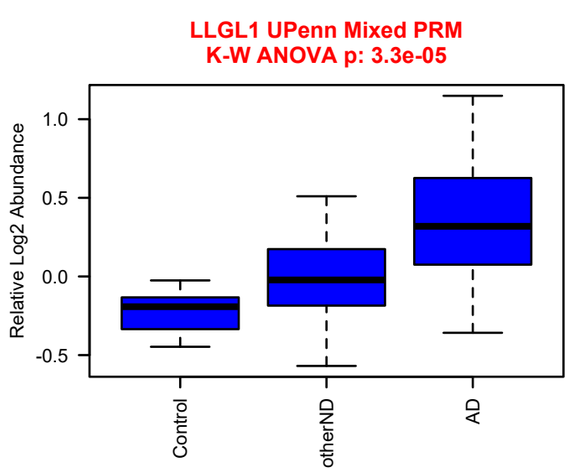

KHSRP UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.054
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

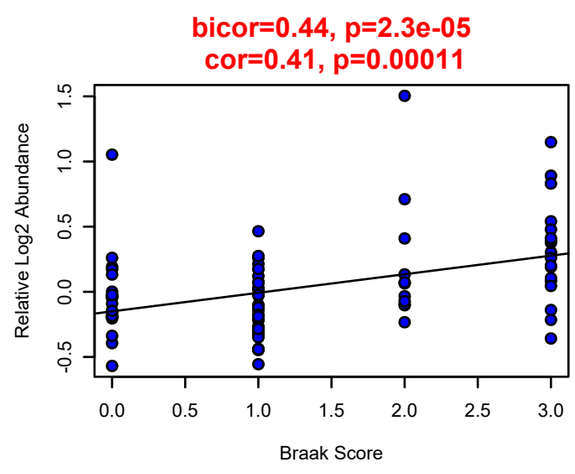

KHSRP UPenn Mixed PRM
K-W ANOVA p: 0.37
Relative Log2 Abundance
Control
otherND
AD

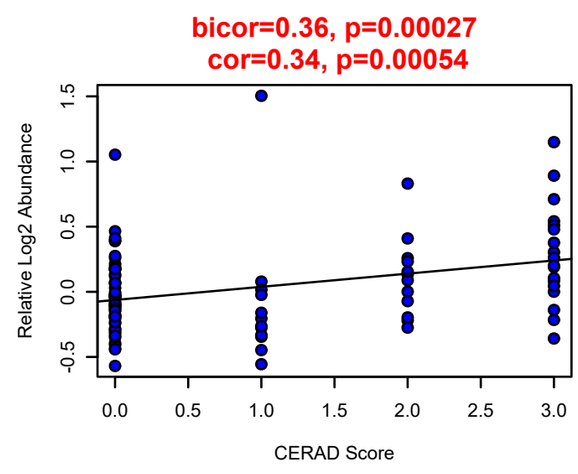

bicor=0.034, p=0.76
cor=0.09, p=0.42
Relative Log2 Abundance
Braak Score

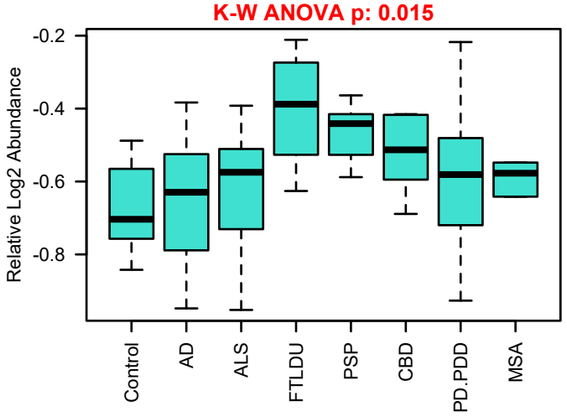

bicor=-0.027, p=0.79
cor=-0.0026, p=0.98
Relative Log2 Abundance
CERAD Score

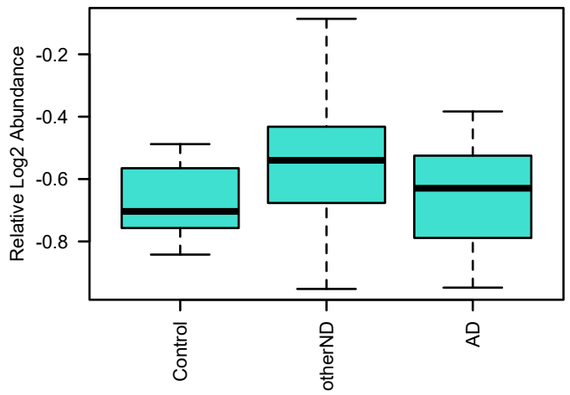

LLGL1 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 3.9e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

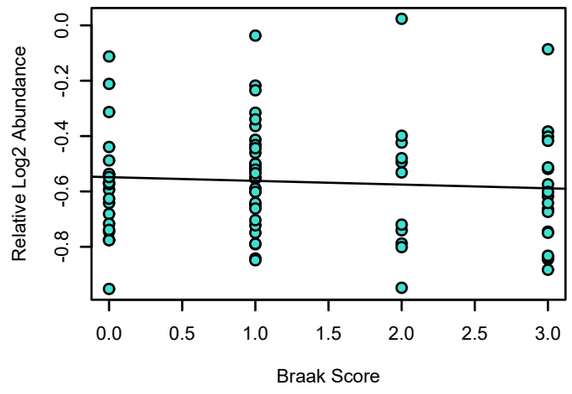

LLGL1 UPenn Mixed PRM
K-W ANOVA p: 3.3e-05
Relative Log2 Abundance
Control
otherND
AD

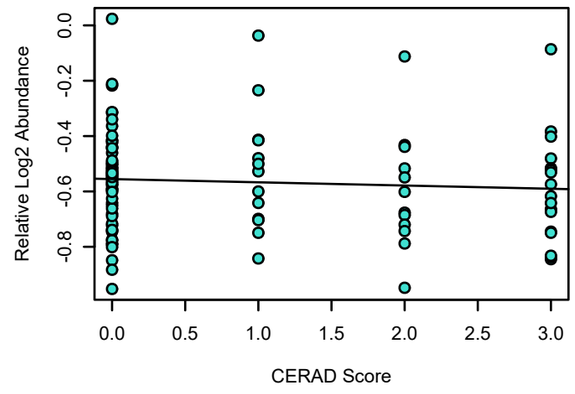

bicor=0.44, p=2.3e-05
cor=0.41, p=0.00011
Relative Log2 Abundance
Braak Score

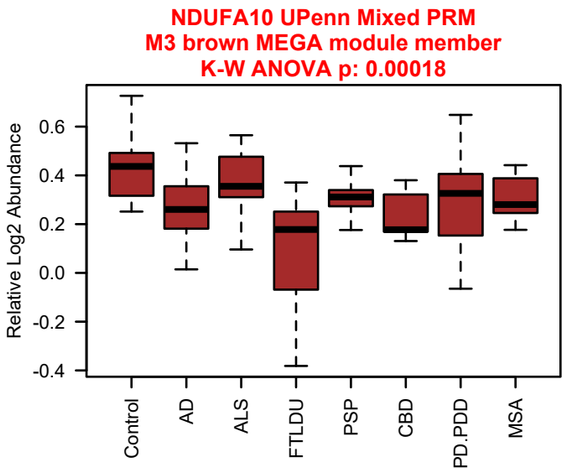

bicor=0.36, p=0.00027
cor=0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

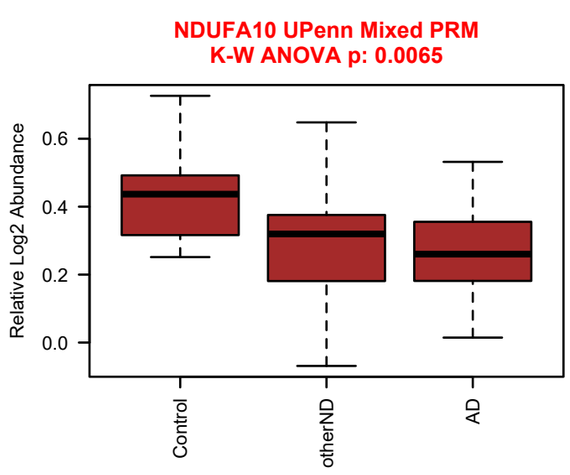

SYN2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.015
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

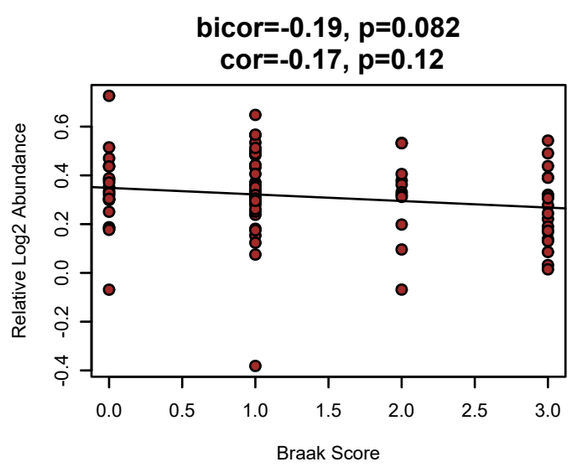

SYN2 UPenn Mixed PRM
K-W ANOVA p: 0.0095
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
Control
otherND
AD

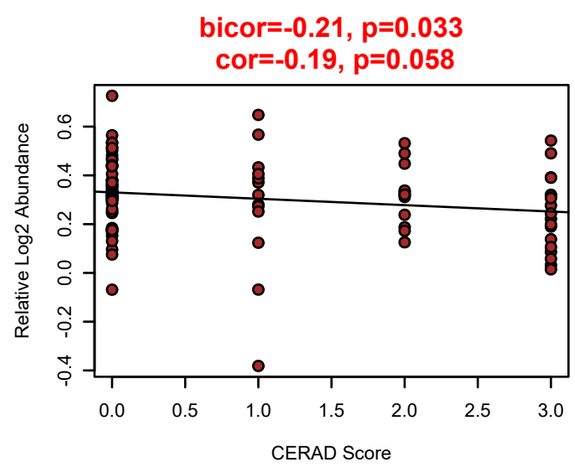

bicor=-0.096, p=0.39
cor=-0.072, p=0.52
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

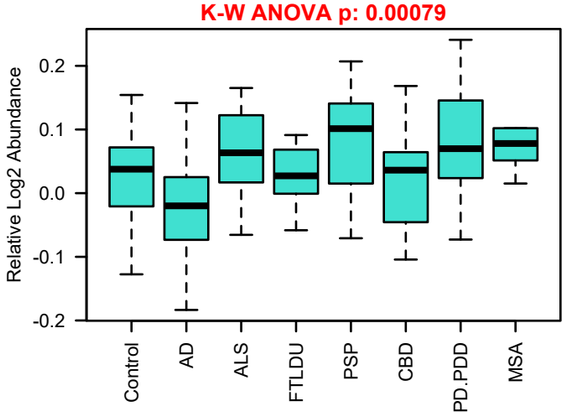

bicor=-0.088, p=0.39
cor=-0.074, p=0.46
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

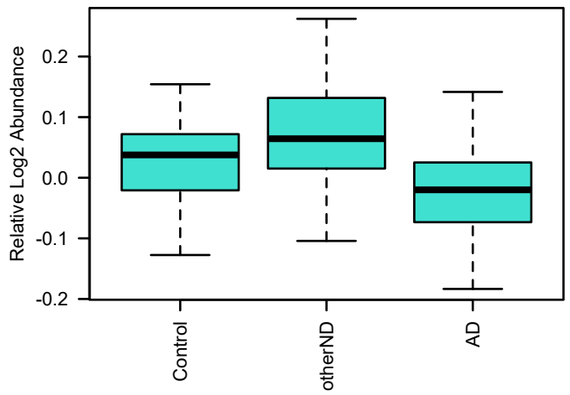

NDUFA10 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.00018
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

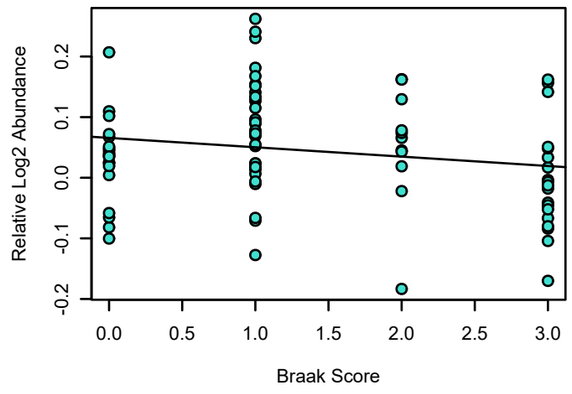

NDUFA10 UPenn Mixed PRM
K-W ANOVA p: 0.0065
Relative Log2 Abundance
0.6
0.4
0.2
0.0
Control
otherND
AD

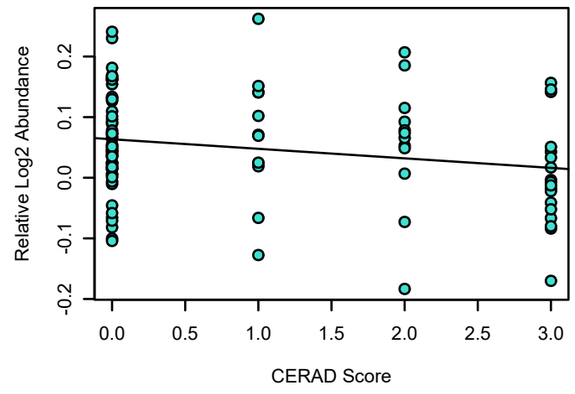

bicor=-0.19, p=0.082
cor=-0.17, p=0.12
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

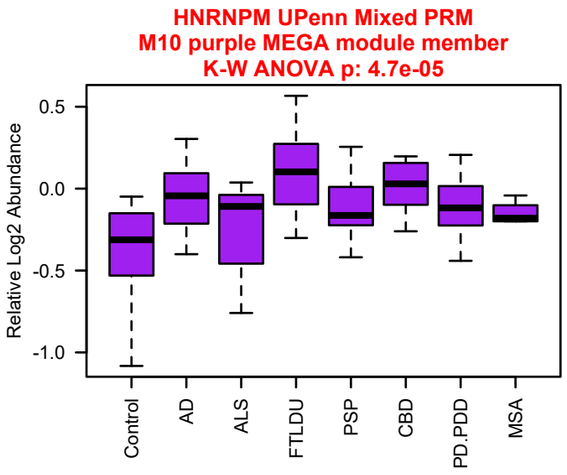

bicor=-0.21, p=0.033
cor=-0.19, p=0.058
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

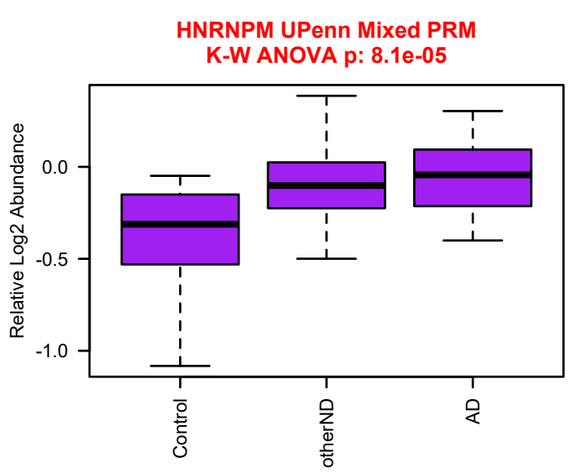

AP2M1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00079
Relative Log2 Abundance
0.2
0.1
0.0
-0.1
-0.2
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

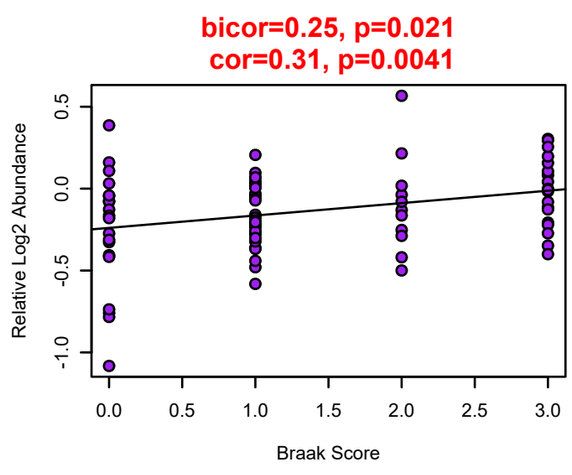

AP2M1 UPenn Mixed PRM
K-W ANOVA p: 5e-05
Relative Log2 Abundance
0.2
0.1
0.0
-0.1
-0.2
Control
otherND
AD

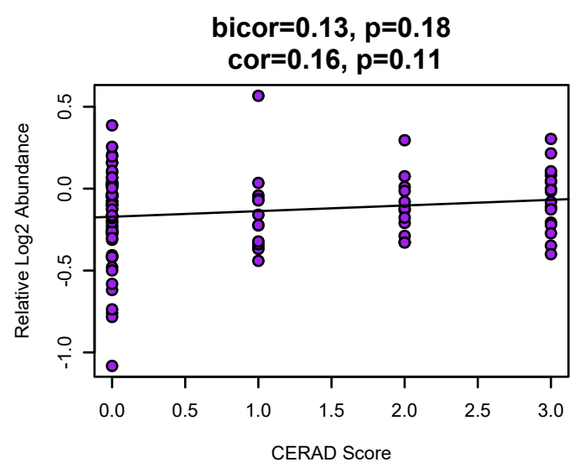

bicor=-0.16, p=0.14
cor=-0.19, p=0.083
Relative Log2 Abundance
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

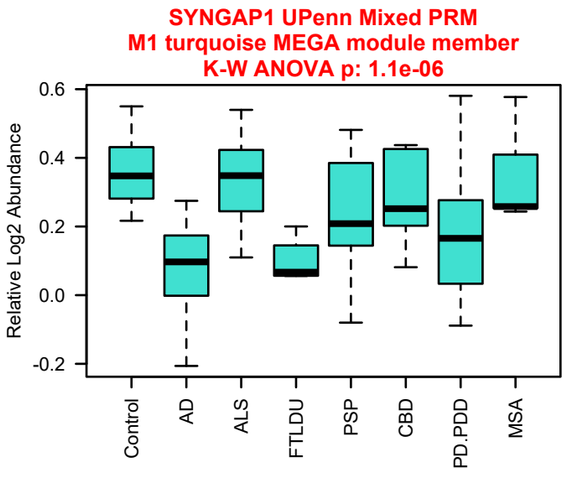

bicor=-0.21, p=0.037
cor=-0.21, p=0.036
Relative Log2 Abundance
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

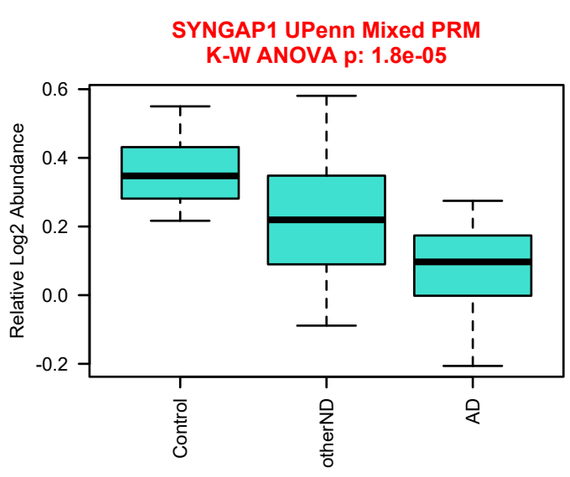

HNRNPM UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 4.7e-05
Relative Log2 Abundance
0.5
0.0
-0.5
-1.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

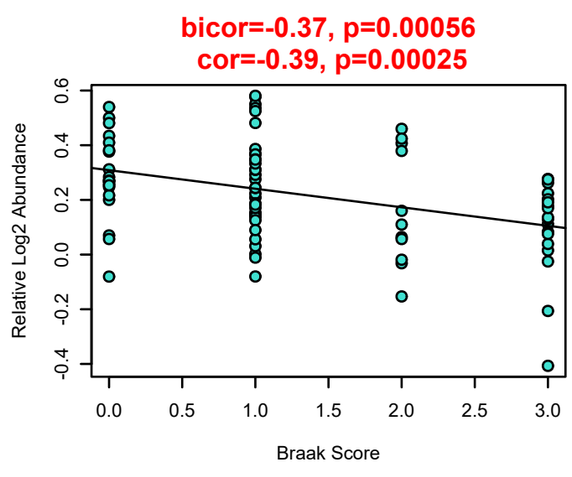

HNRNPM UPenn Mixed PRM
K-W ANOVA p: 8.1e-05
Relative Log2 Abundance
0.0
-0.5
-1.0
Control
otherND
AD

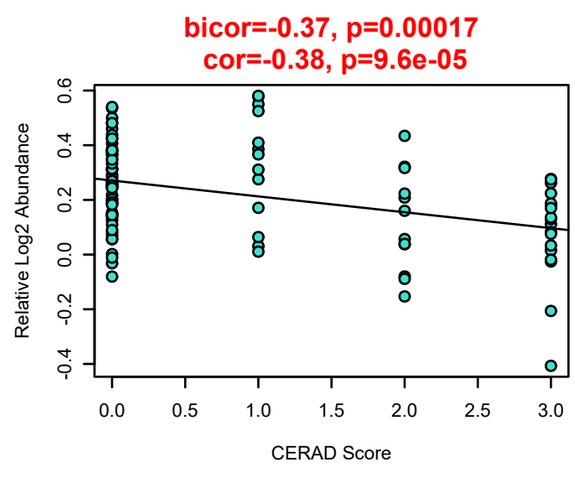

bicor=0.25, p=0.021
cor=0.31, p=0.0041
Relative Log2 Abundance
0.5
0.0
-0.5
-1.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

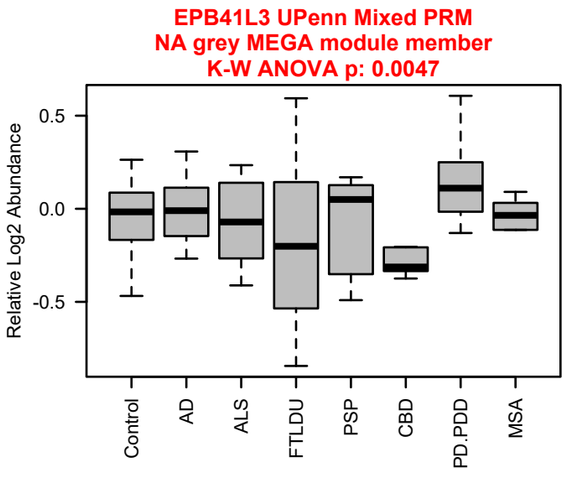

bicor=0.13, p=0.18
cor=0.16, p=0.11
Relative Log2 Abundance
0.5
0.0
-0.5
-1.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

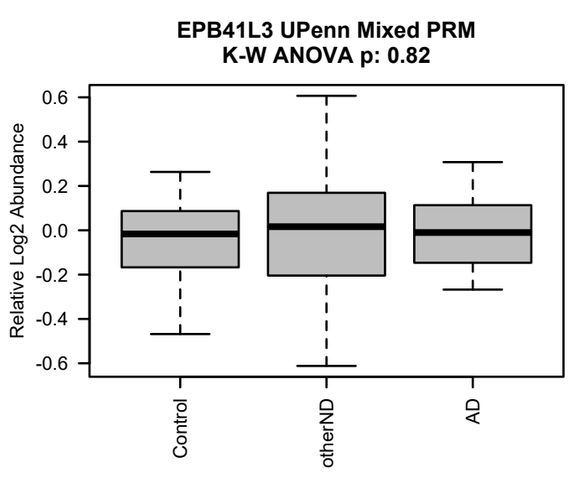

SYNGAP1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 1.1e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

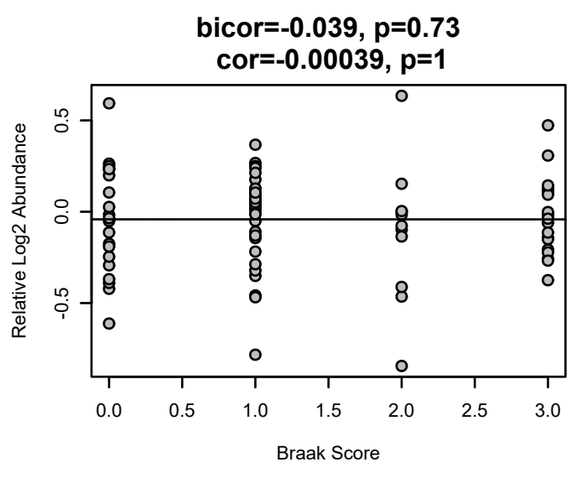

SYNGAP1 UPenn Mixed PRM
K-W ANOVA p: 1.8e-05
Relative Log2 Abundance
Control
otherND
AD

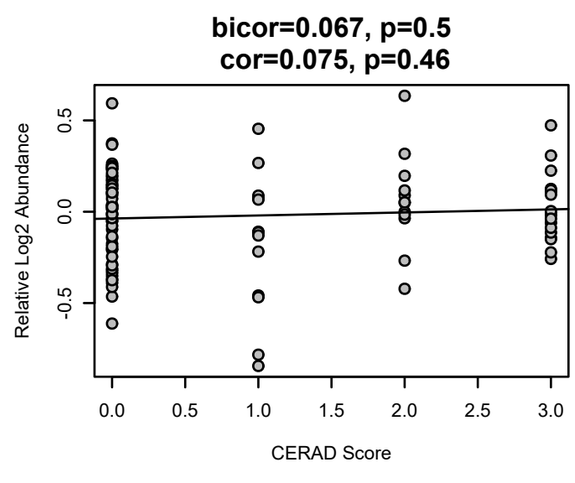

bicor=-0.37, p=0.00056
cor=-0.39, p=0.00025
Relative Log2 Abundance
Braak Score

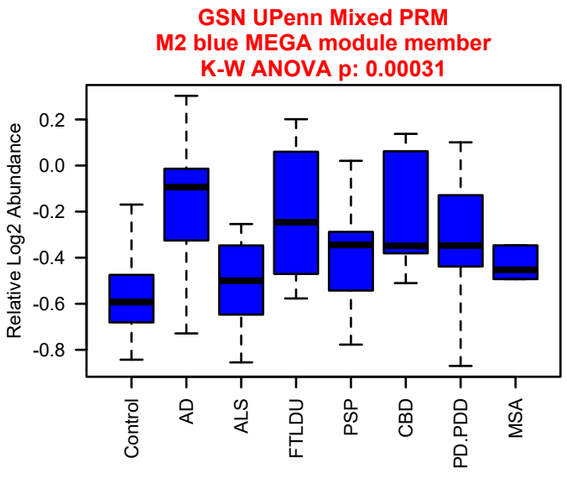

bicor=-0.37, p=0.00017
cor=-0.38, p=9.6e-05
Relative Log2 Abundance
CERAD Score

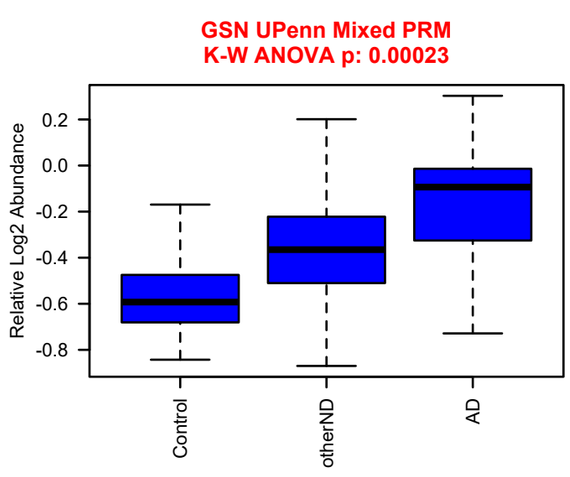

EPB41L3 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.0047
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

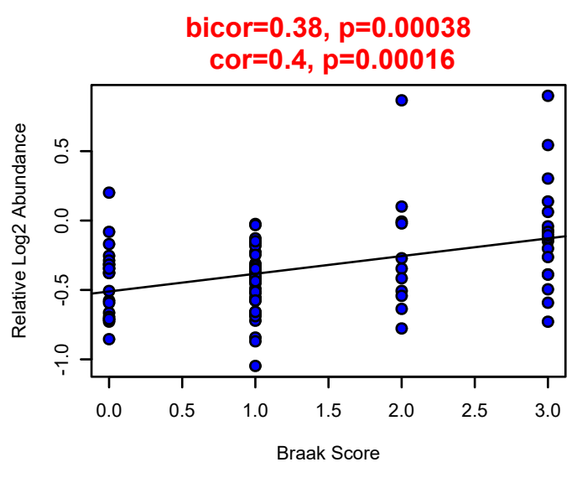

EPB41L3 UPenn Mixed PRM
K-W ANOVA p: 0.82
Relative Log2 Abundance
Control
otherND
AD

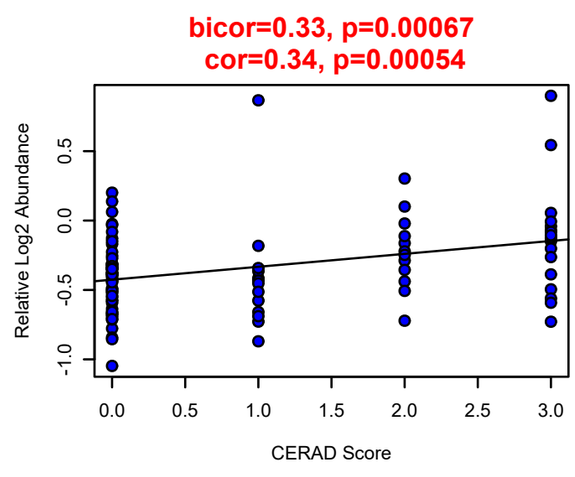

bicor=-0.039, p=0.73
cor=-0.00039, p=1
Relative Log2 Abundance
Braak Score

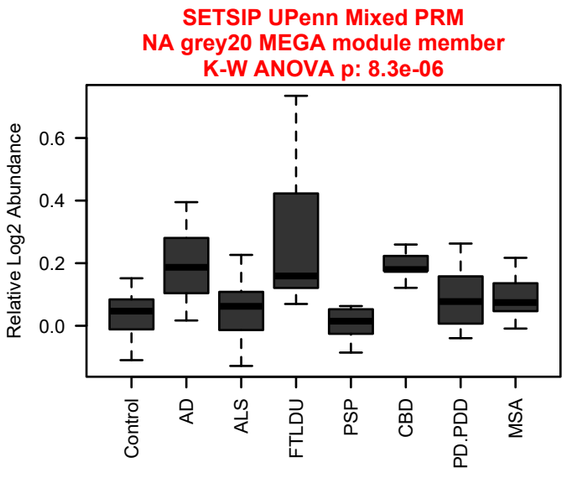

bicor=0.067, p=0.5
cor=0.075, p=0.46
Relative Log2 Abundance
CERAD Score

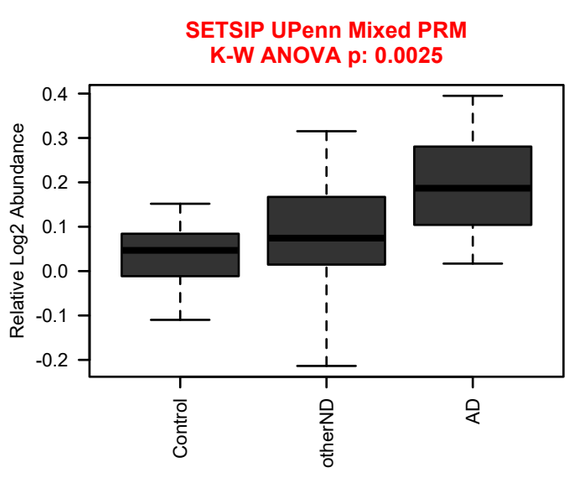

GSN UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.00031
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

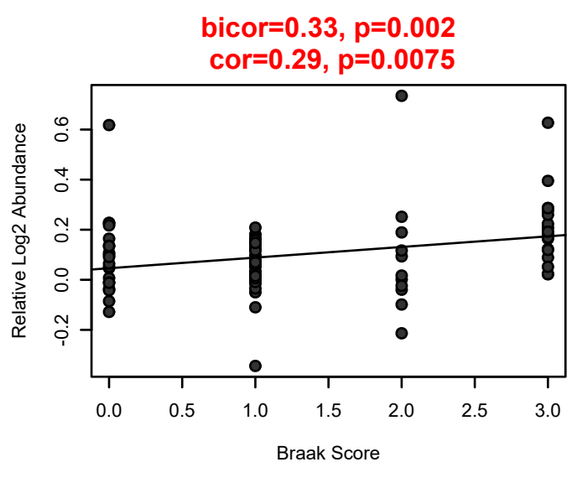

GSN UPenn Mixed PRM
K-W ANOVA p: 0.00023
Relative Log2 Abundance
Control
otherND
AD

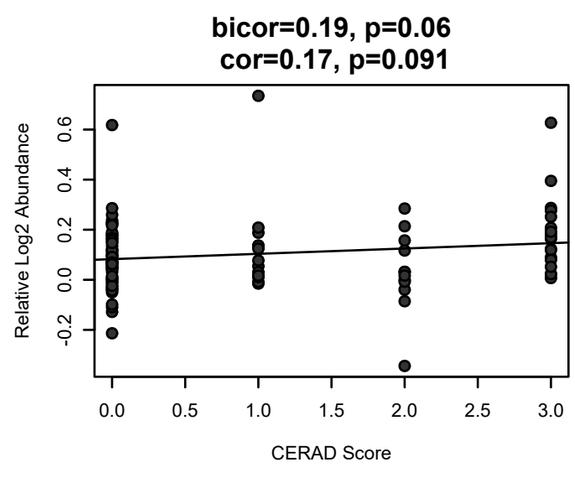

bicor=0.38, p=0.00038
cor=0.4, p=0.00016
Relative Log2 Abundance
Braak Score

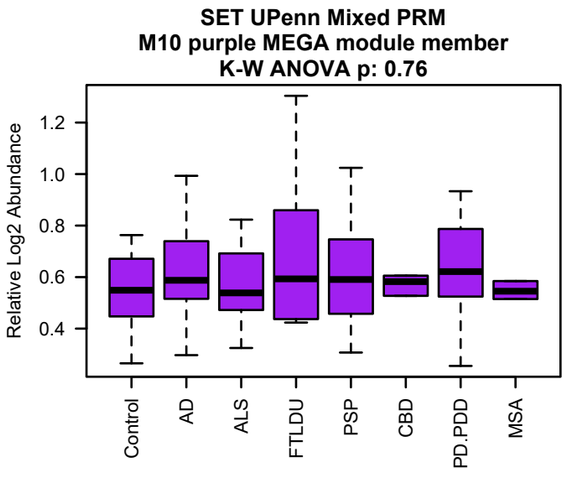

bicor=0.33, p=0.00067
cor=0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

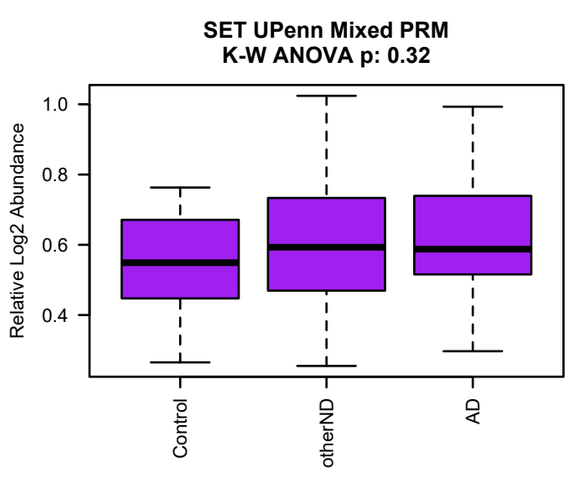

SETSIP UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 8.3e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

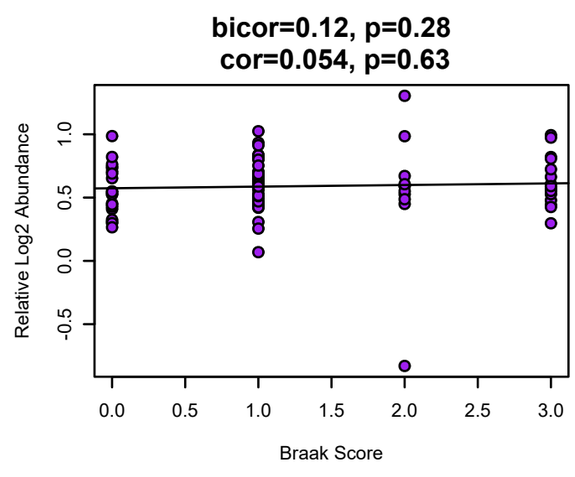

SETSIP UPenn Mixed PRM
K-W ANOVA p: 0.0025
Relative Log2 Abundance
Control
otherND
AD

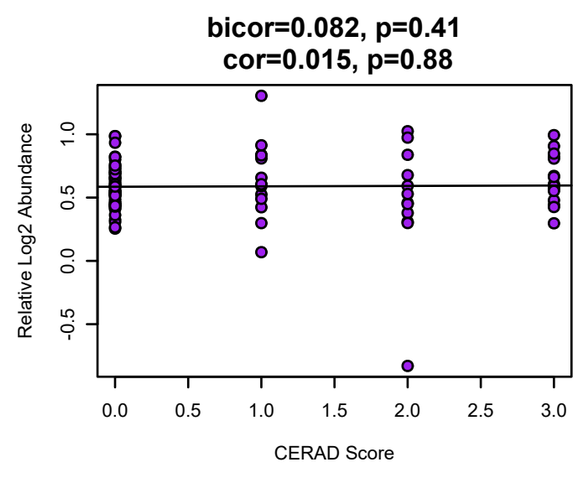

bicor=0.33, p=0.002
cor=0.29, p=0.0075
Relative Log2 Abundance
Braak Score

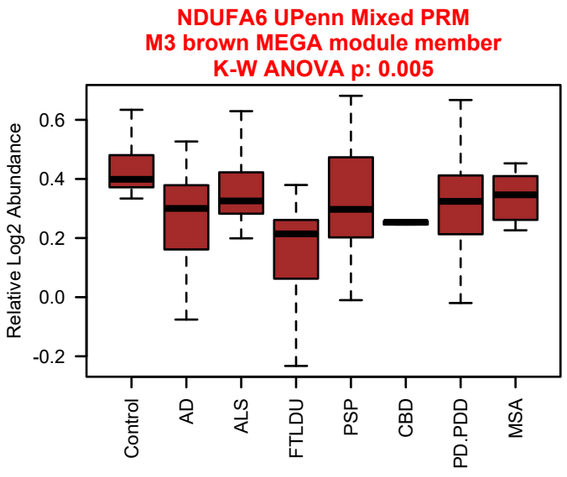

bicor=0.19, p=0.06
cor=0.17, p=0.091
Relative Log2 Abundance
CERAD Score

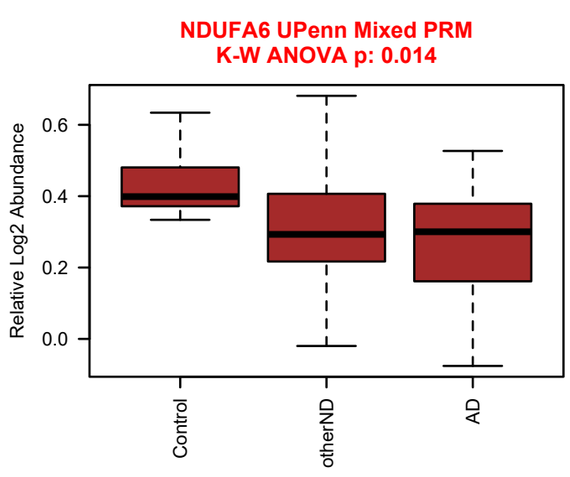

SET UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.76
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

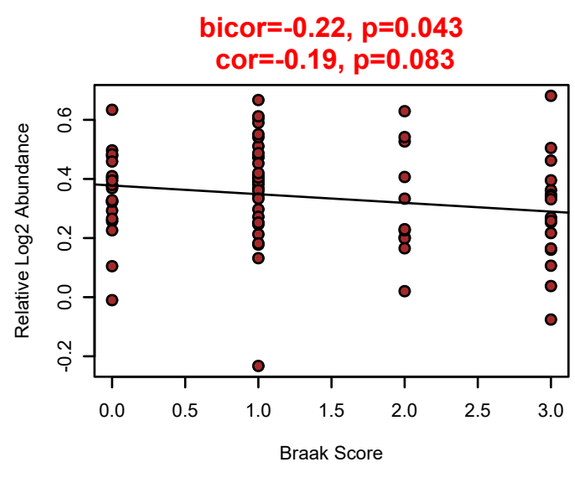

SET UPenn Mixed PRM
K-W ANOVA p: 0.32
Relative Log2 Abundance
Control
otherND
AD

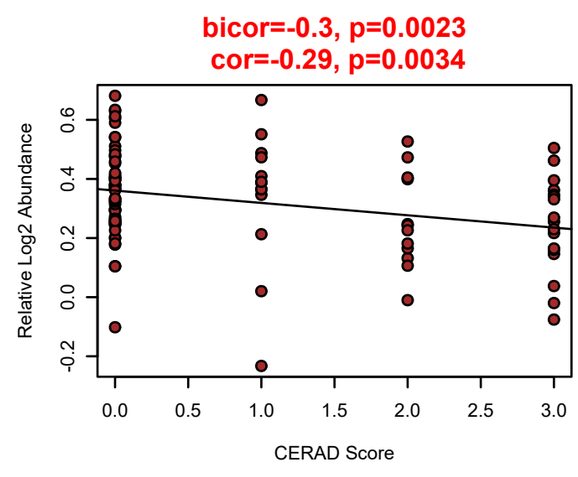

bicor=0.12, p=0.28
cor=0.054, p=0.63
Relative Log2 Abundance
Braak Score

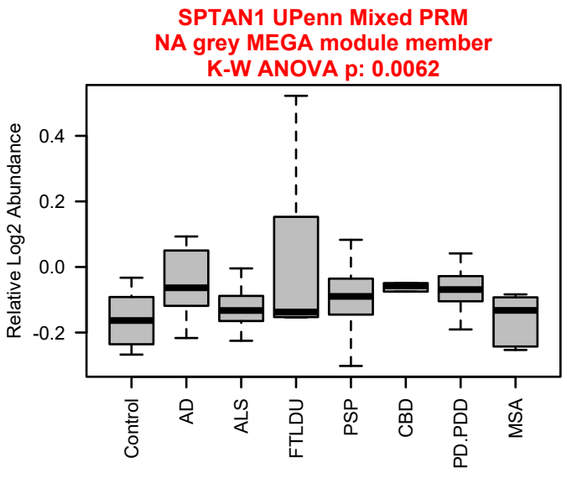

bicor=0.082, p=0.41
cor=0.015, p=0.88
Relative Log2 Abundance
CERAD Score

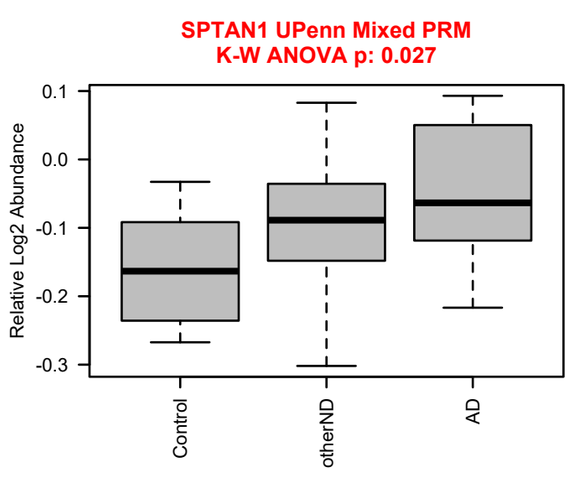

NDUFA6 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.005
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

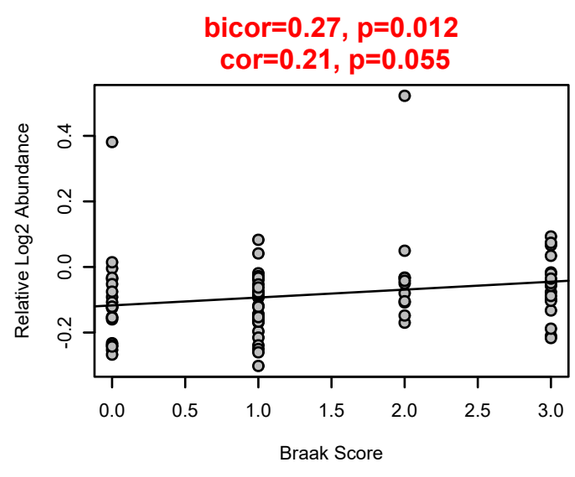

NDUFA6 UPenn Mixed PRM
K-W ANOVA p: 0.014
Relative Log2 Abundance
Control
otherND
AD

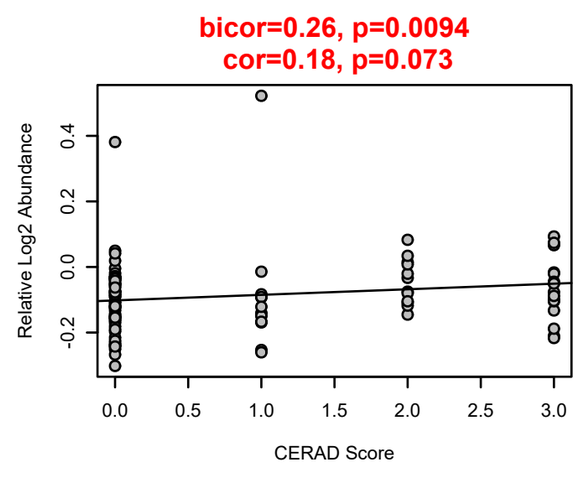

bicor=-0.22, p=0.043
cor=-0.19, p=0.083
Relative Log2 Abundance
Braak Score

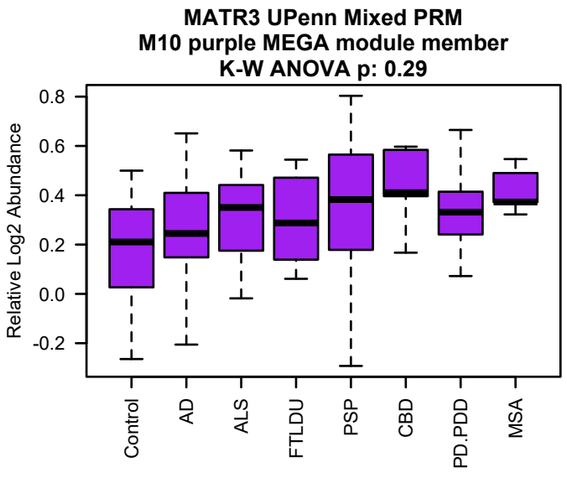

bicor=-0.3, p=0.0023
cor=-0.29, p=0.0034
Relative Log2 Abundance
CERAD Score

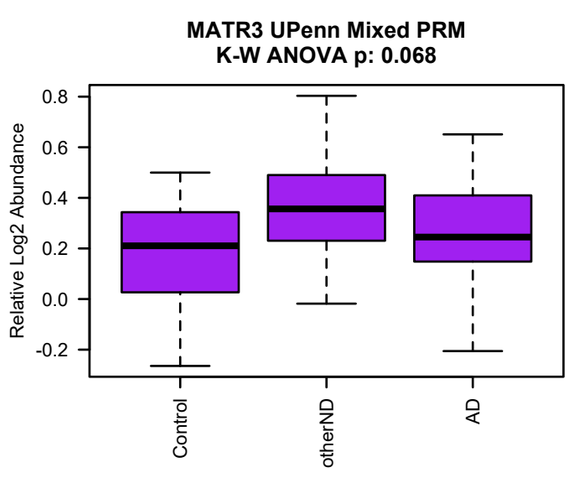

SPTAN1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.0062
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

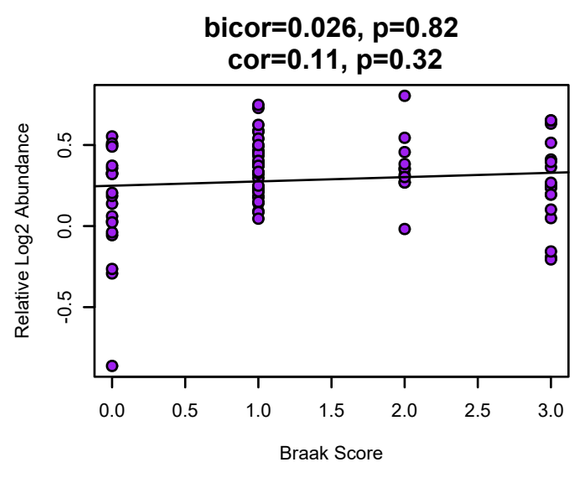

SPTAN1 UPenn Mixed PRM
K-W ANOVA p: 0.027
Relative Log2 Abundance
Control
otherND
AD

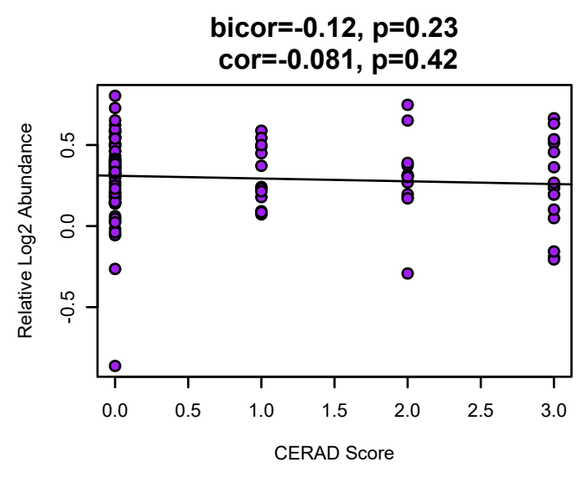

bicor=0.27, p=0.012
cor=0.21, p=0.055
Relative Log2 Abundance
Braak Score

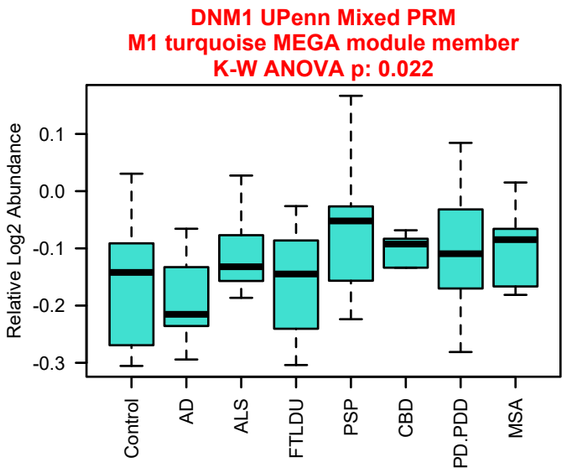

bicor=0.26, p=0.0094
cor=0.18, p=0.073
Relative Log2 Abundance
CERAD Score

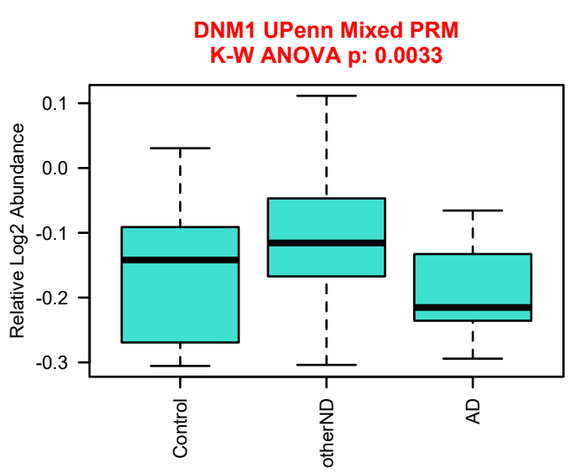

MATR3 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.29
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

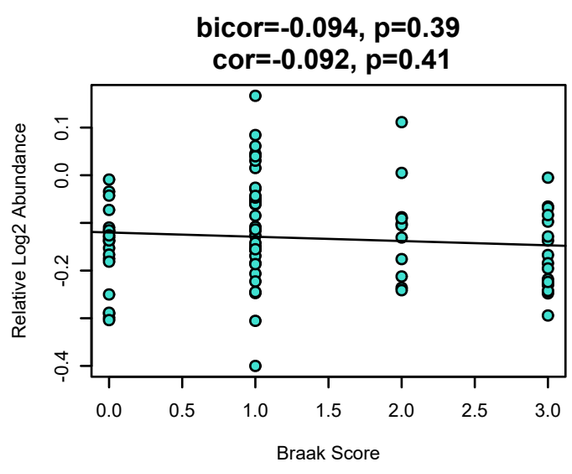

MATR3 UPenn Mixed PRM
K-W ANOVA p: 0.068
Relative Log2 Abundance
Control
otherND
AD

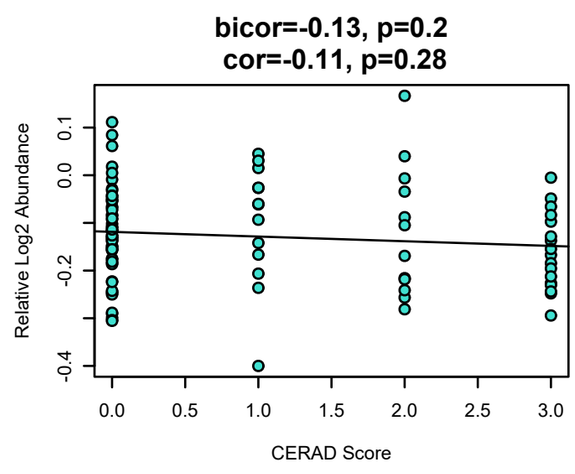

bicor=0.026, p=0.82
cor=0.11, p=0.32
Relative Log2 Abundance
Braak Score

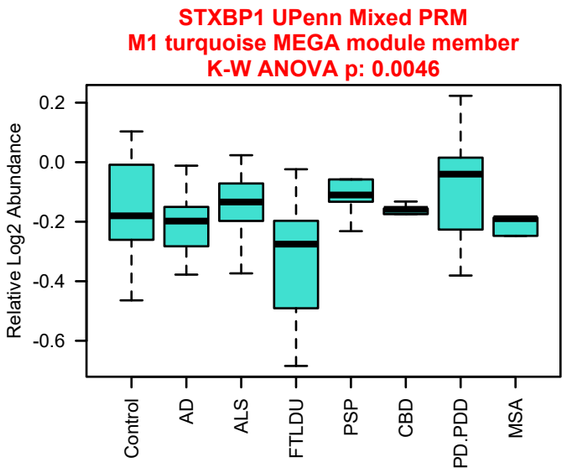

bicor=-0.12, p=0.23
cor=-0.081, p=0.42
Relative Log2 Abundance
CERAD Score

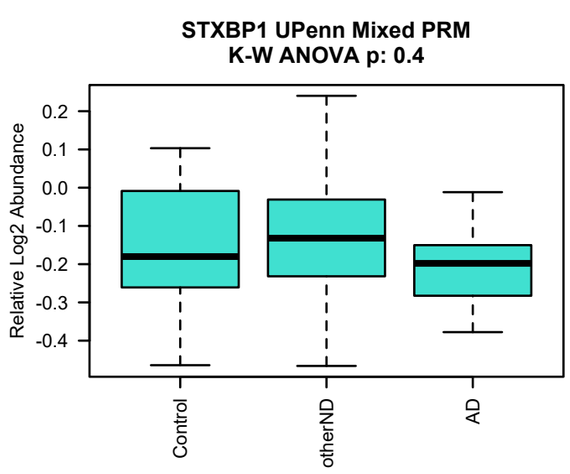

DNM1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.022
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

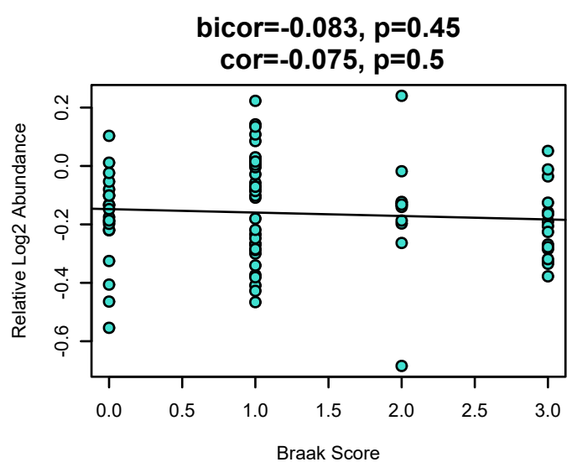

DNM1 UPenn Mixed PRM
K-W ANOVA p: 0.0033
Relative Log2 Abundance
Control
otherND
AD

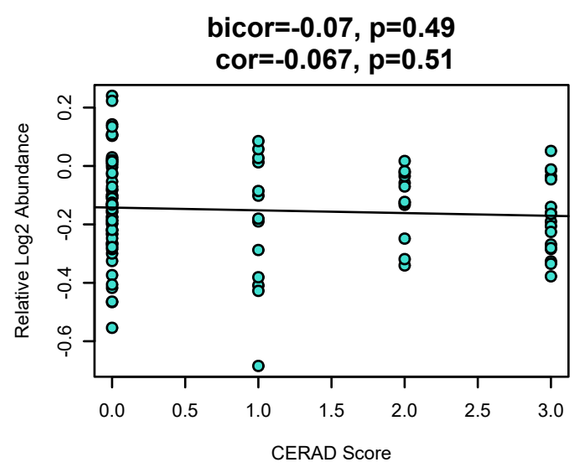

bicor=-0.094, p=0.39
cor=-0.092, p=0.41
Relative Log2 Abundance
Braak Score

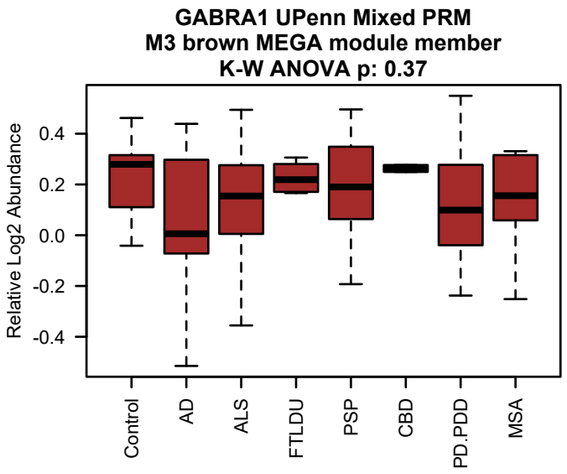

bicor=-0.13, p=0.2
cor=-0.11, p=0.28
Relative Log2 Abundance
CERAD Score

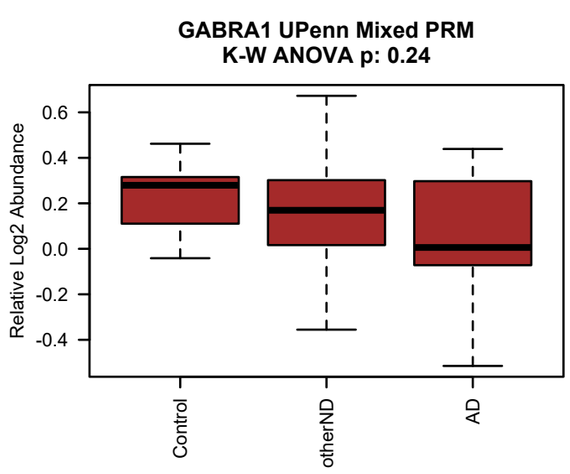

STXBP1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0046
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

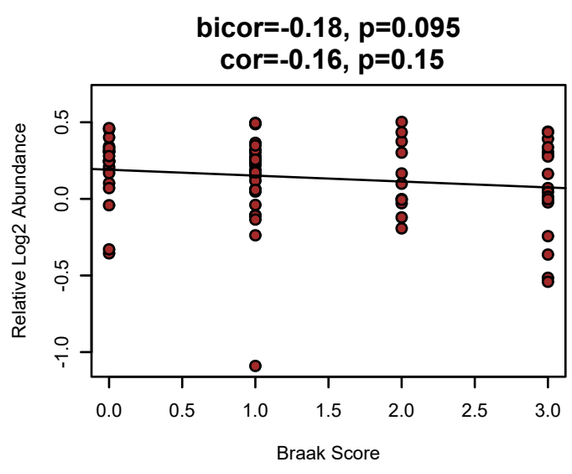

STXBP1 UPenn Mixed PRM
K-W ANOVA p: 0.4
Relative Log2 Abundance
Control
otherND
AD

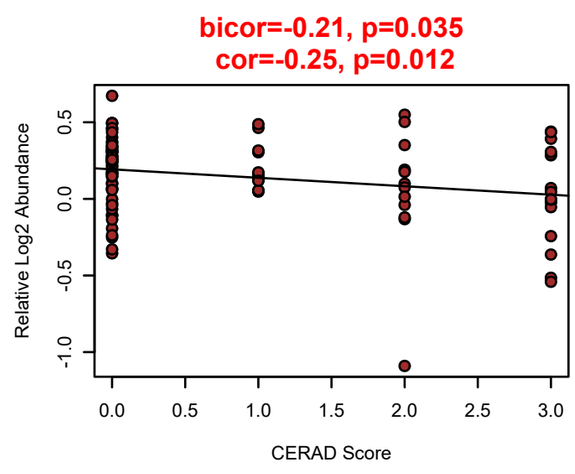

bicor=-0.083, p=0.45
cor=-0.075, p=0.5
Relative Log2 Abundance
Braak Score

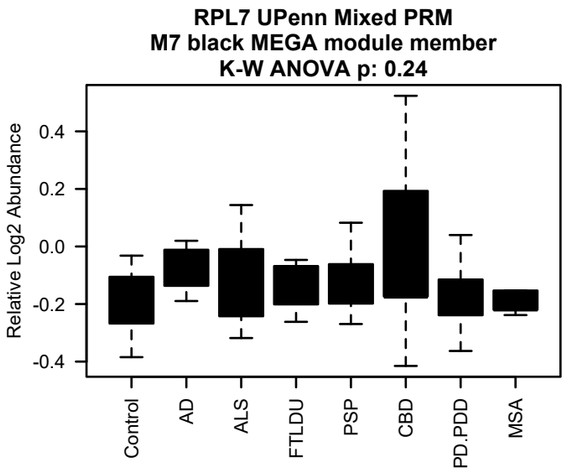

bicor=-0.07, p=0.49
cor=-0.067, p=0.51
Relative Log2 Abundance
CERAD Score

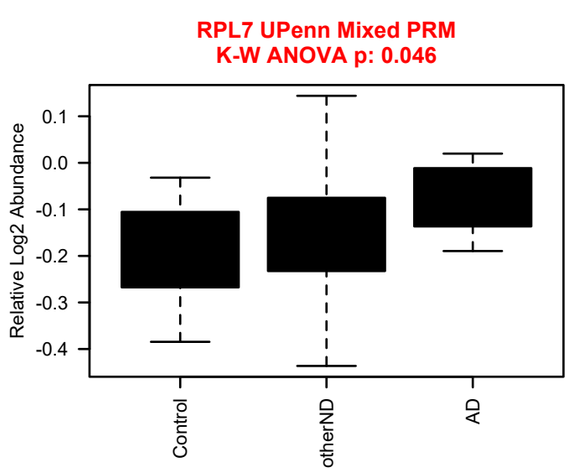

GABRA1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.37
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

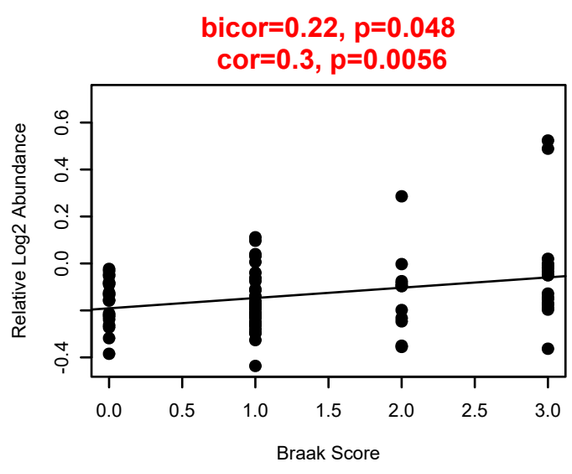

GABRA1 UPenn Mixed PRM
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
otherND
AD

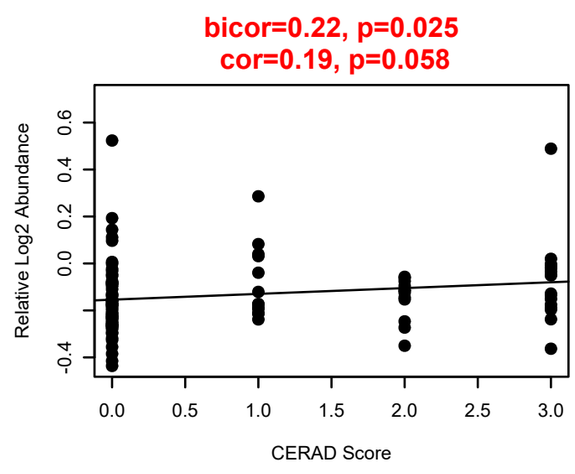

bicor=-0.18, p=0.095
cor=-0.16, p=0.15
Relative Log2 Abundance
Braak Score

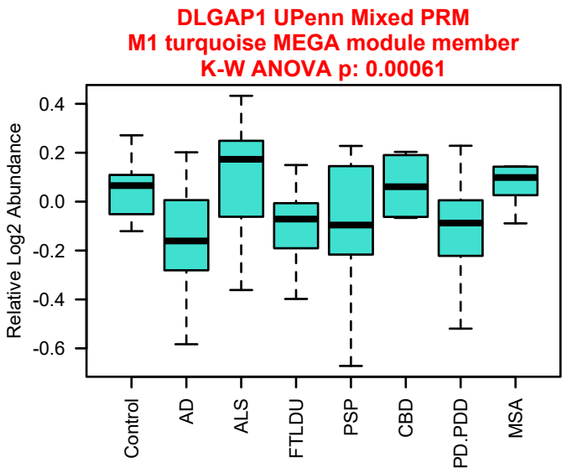

bicor=-0.21, p=0.035
cor=-0.25, p=0.012
Relative Log2 Abundance
CERAD Score

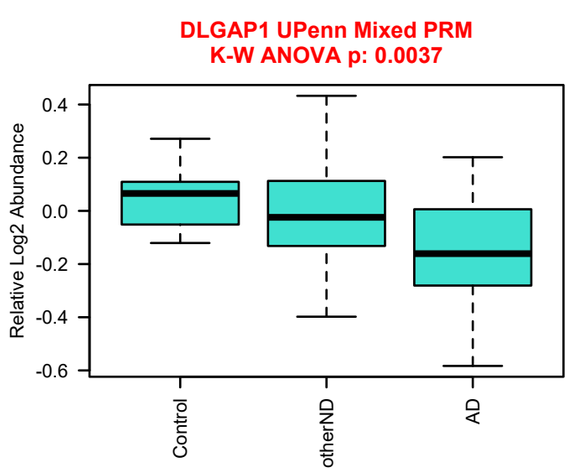

RPL7 UPenn Mixed PRM
M7 black MEGA module member
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

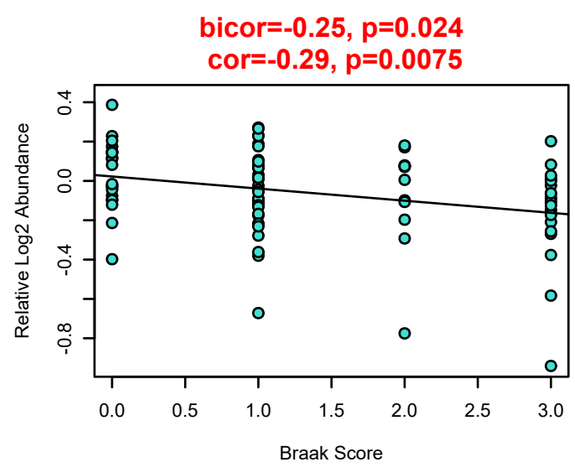

RPL7 UPenn Mixed PRM
K-W ANOVA p: 0.046
Relative Log2 Abundance
Control
otherND
AD

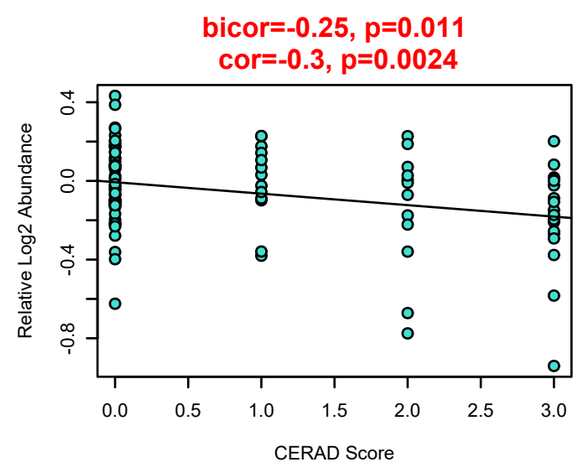

bicor=0.22, p=0.048
cor=0.3, p=0.0056
Relative Log2 Abundance
Braak Score

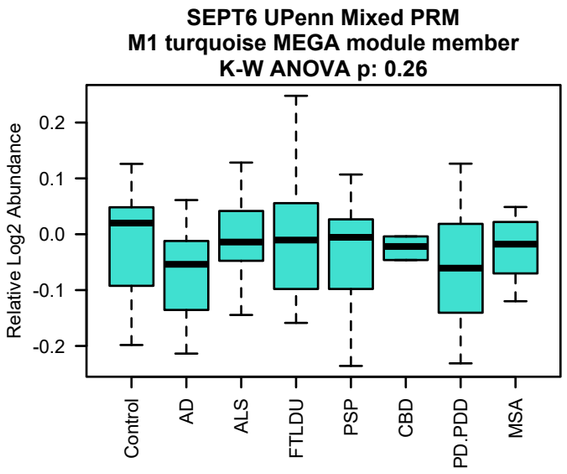

bicor=0.22, p=0.025
cor=0.19, p=0.058
Relative Log2 Abundance
CERAD Score

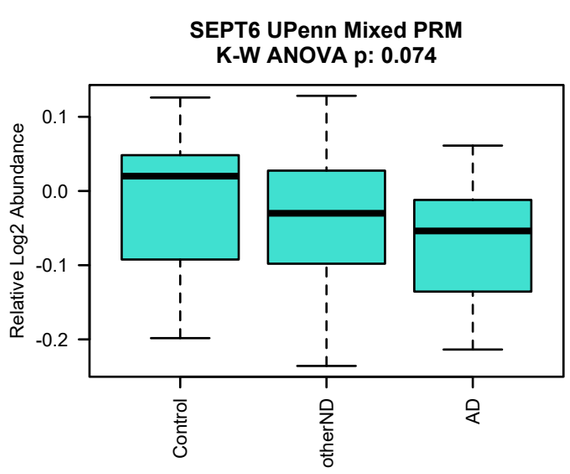

DLGAP1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00061
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

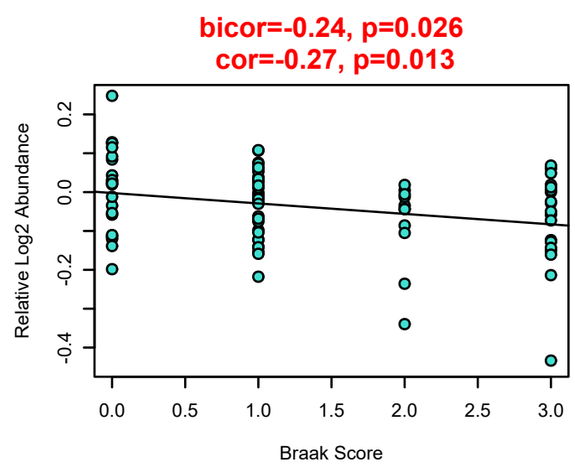

DLGAP1 UPenn Mixed PRM
K-W ANOVA p: 0.0037
Relative Log2 Abundance
Control
otherND
AD

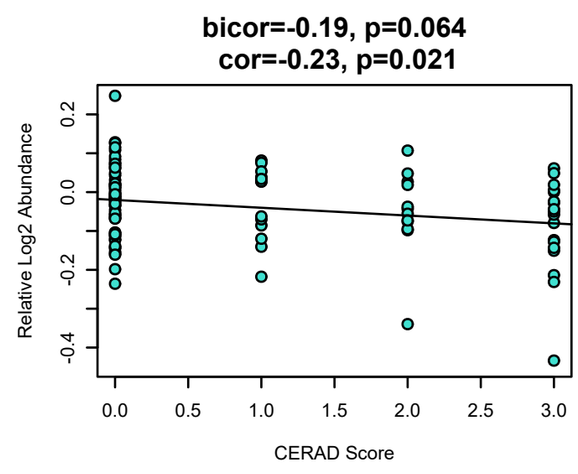

bicor=-0.25, p=0.024
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

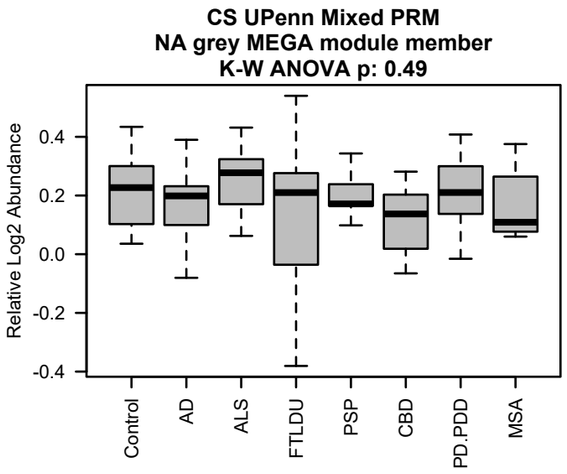

bicor=-0.25, p=0.011
cor=-0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

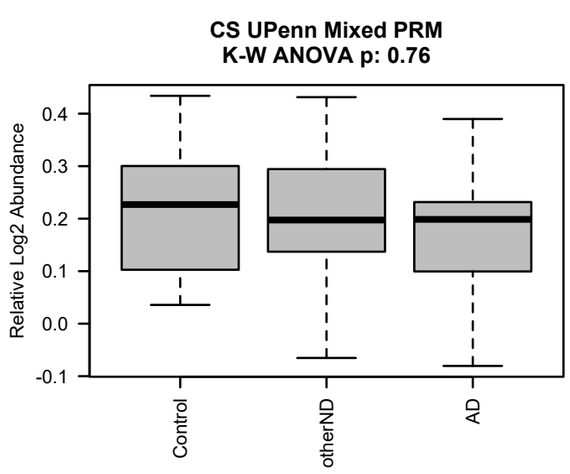

SEPT6 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.26
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

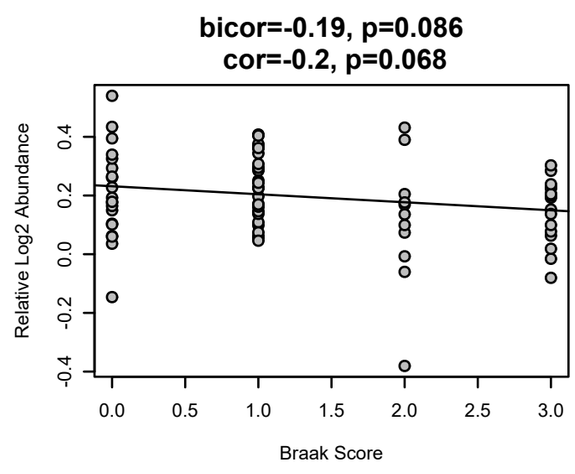

SEPT6 UPenn Mixed PRM
K-W ANOVA p: 0.074
Relative Log2 Abundance
Control
otherND
AD

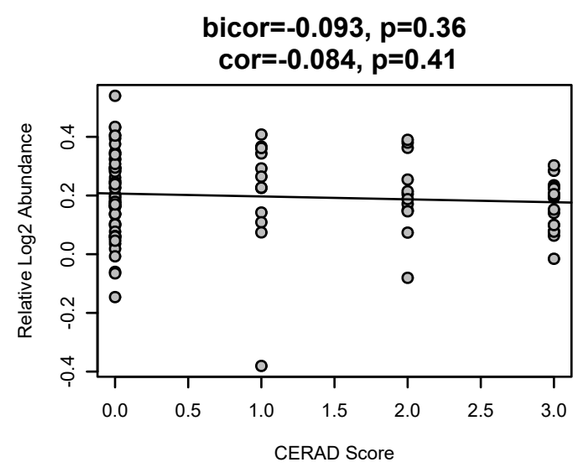

bicor=-0.24, p=0.026
cor=-0.27, p=0.013
Relative Log2 Abundance
Braak Score

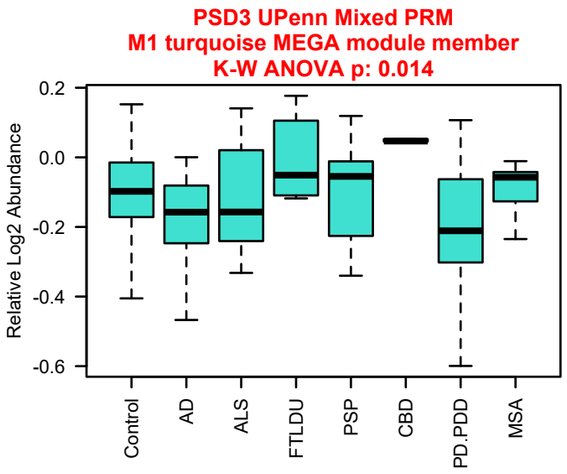

bicor=-0.19, p=0.064
cor=-0.23, p=0.021
Relative Log2 Abundance
CERAD Score

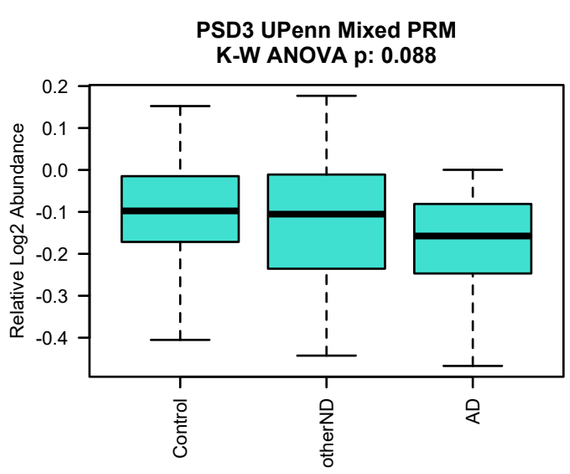

CS UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.49
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

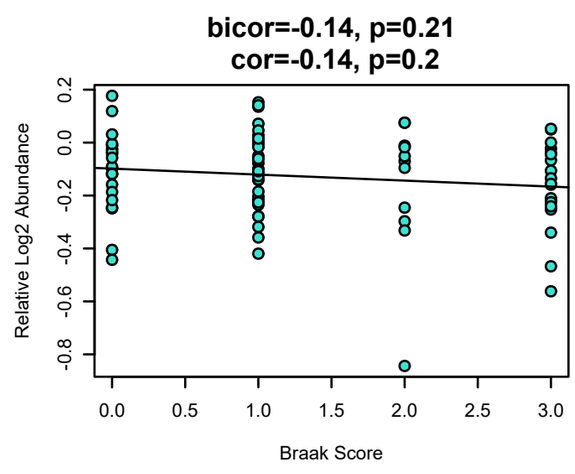

CS UPenn Mixed PRM
K-W ANOVA p: 0.76
Relative Log2 Abundance
Control
otherND
AD

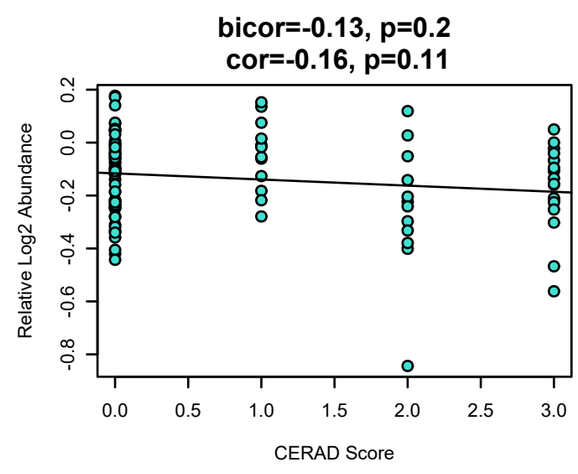

bicor=-0.19, p=0.086
cor=-0.2, p=0.068
Relative Log2 Abundance
Braak Score

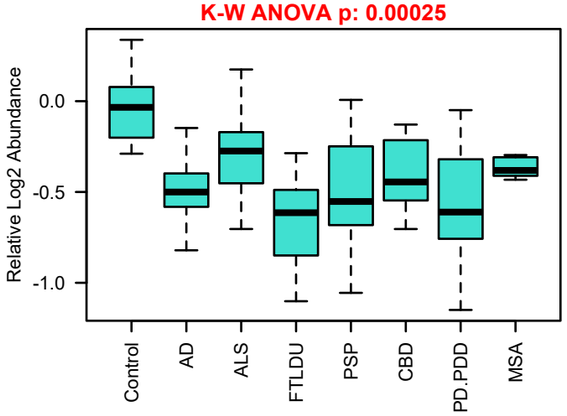

bicor=-0.093, p=0.36
cor=-0.084, p=0.41
Relative Log2 Abundance
CERAD Score

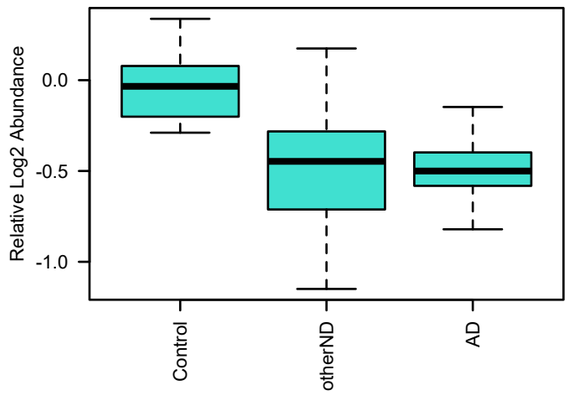

PSD3 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.014
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

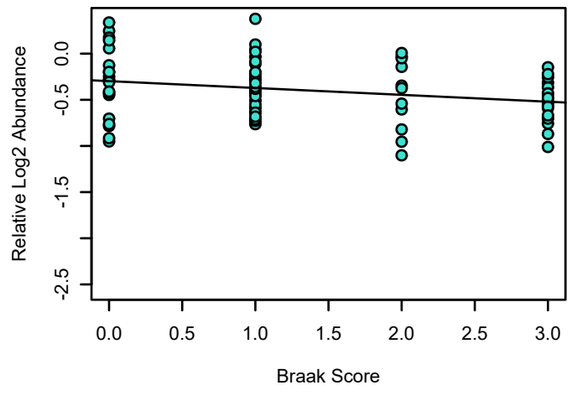

PSD3 UPenn Mixed PRM
K-W ANOVA p: 0.088
Relative Log2 Abundance
Control
otherND
AD

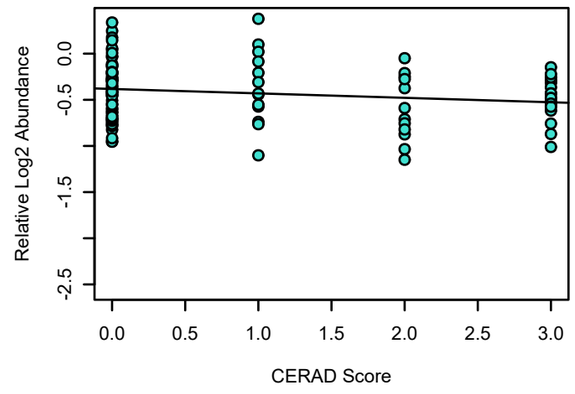

bicor=-0.14, p=0.21
cor=-0.14, p=0.2
Relative Log2 Abundance
Braak Score

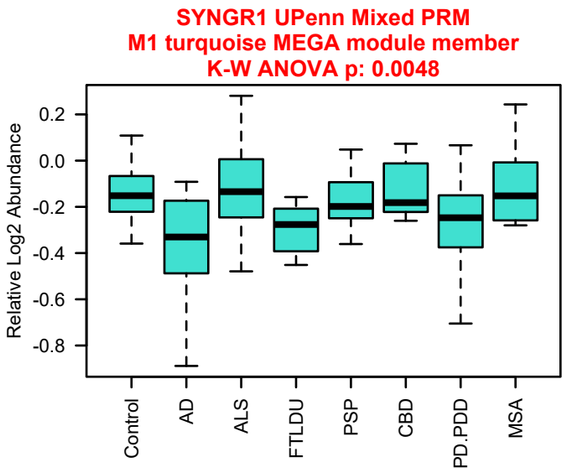

bicor=-0.13, p=0.2
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

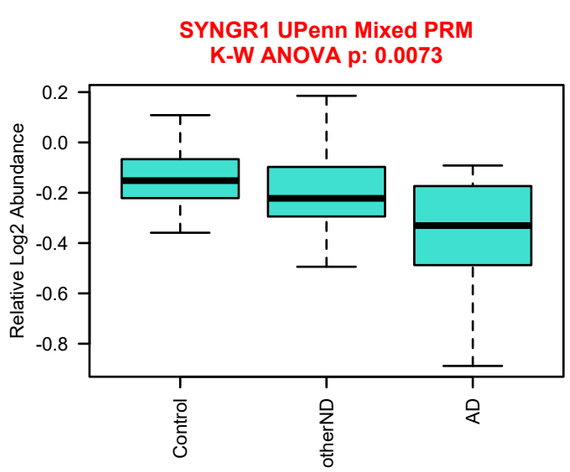

DGKB UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00025
Relative Log2 Abundance
0.0
-0.5
-1.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

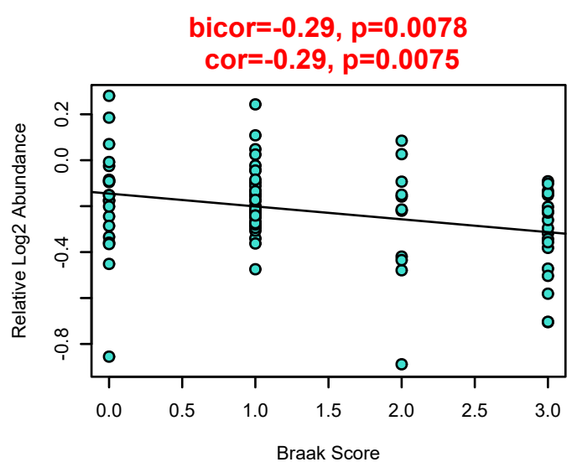

DGKB UPenn Mixed PRM
K-W ANOVA p: 8.3e-05
Relative Log2 Abundance
0.0
-0.5
-1.0
Control
otherND
AD

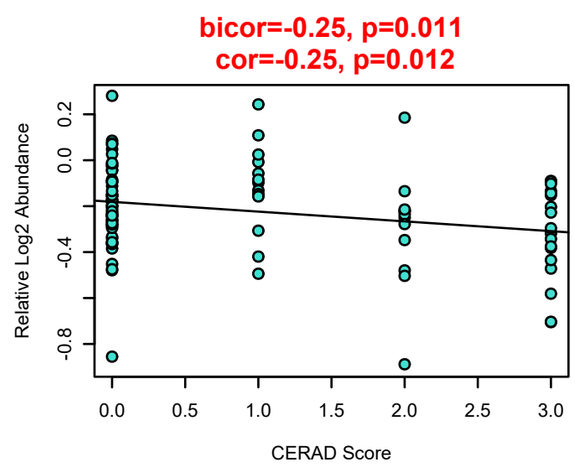

bicor=-0.23, p=0.039
cor=-0.25, p=0.022
Relative Log2 Abundance
0.0
-0.5
-1.5
-2.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

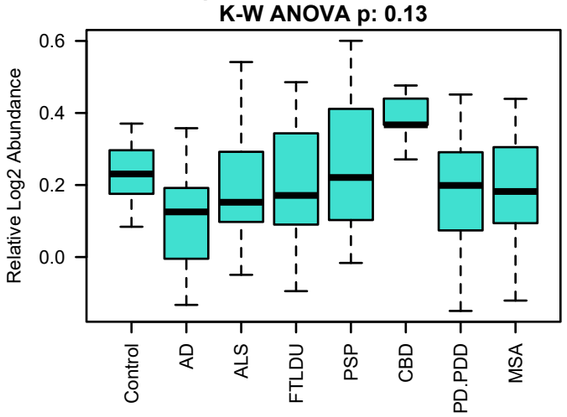

bicor=-0.17, p=0.089
cor=-0.18, p=0.073
Relative Log2 Abundance
0.0
-0.5
-1.5
-2.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

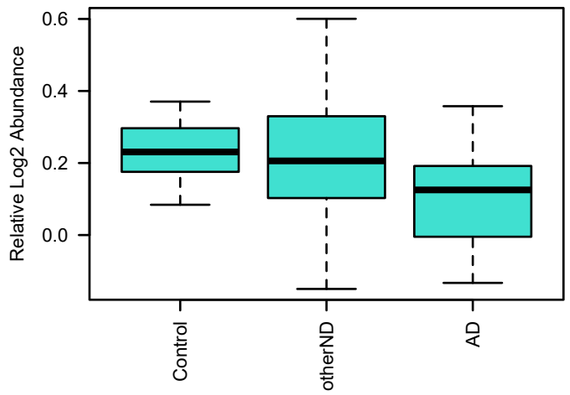

SYNGR1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0048
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
-0.8
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

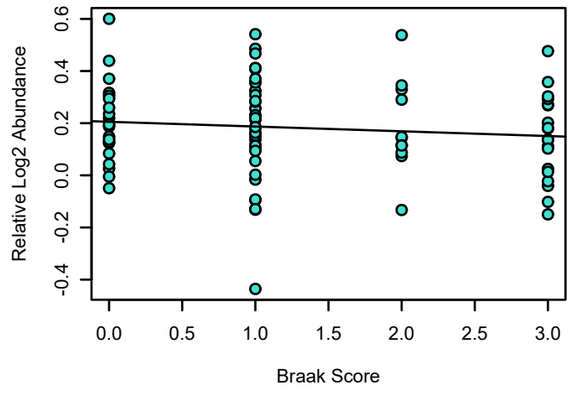

SYNGR1 UPenn Mixed PRM
K-W ANOVA p: 0.0073
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
-0.8
Control
otherND
AD

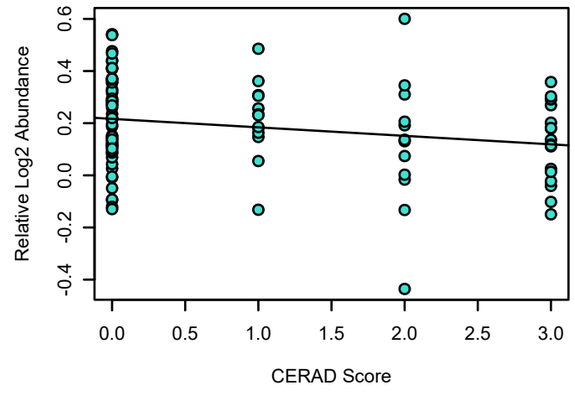

bicor=-0.29, p=0.0078
cor=-0.29, p=0.0075
Relative Log2 Abundance
0.2
0.0
-0.4
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

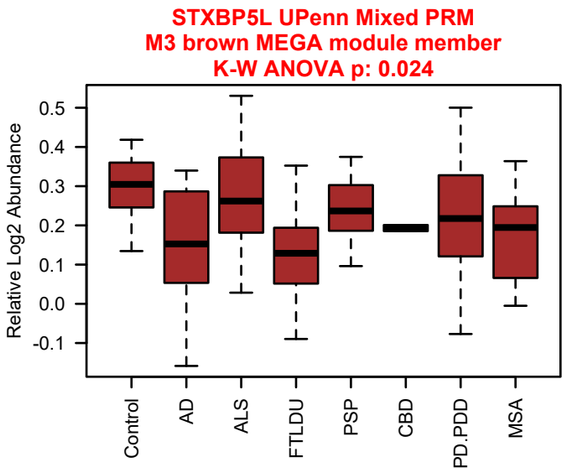

bicor=-0.25, p=0.011
cor=-0.25, p=0.012
Relative Log2 Abundance
0.2
0.0
-0.4
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

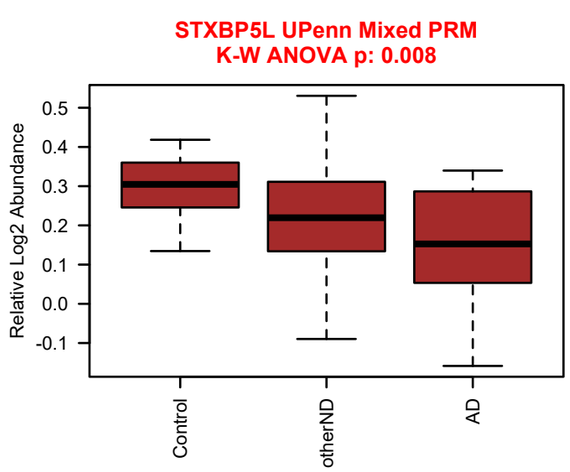

GPM6B UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.13
Relative Log2 Abundance
0.6
0.4
0.2
0.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

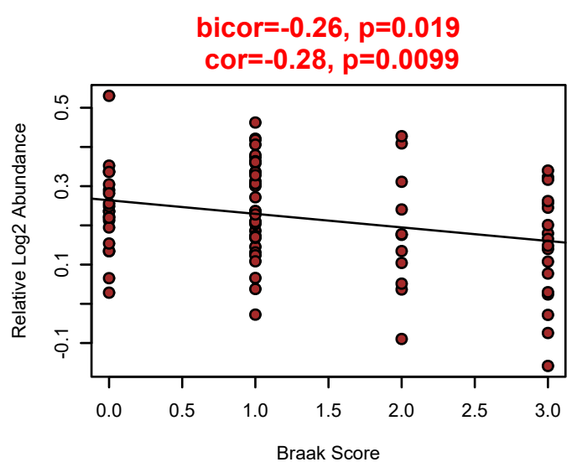

GPM6B UPenn Mixed PRM
K-W ANOVA p: 0.094
Relative Log2 Abundance
0.6
0.4
0.2
0.0
Control
otherND
AD

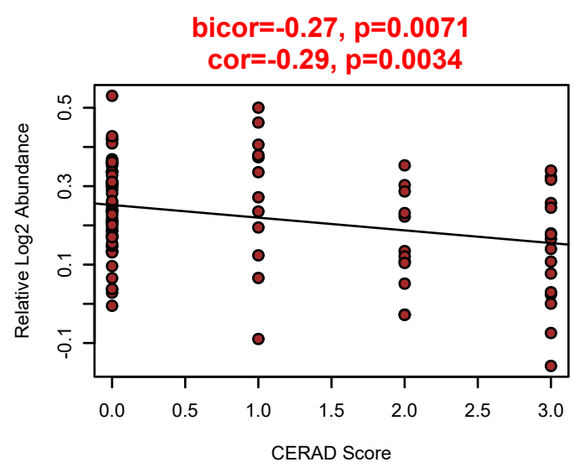

bicor=-0.1, p=0.35
cor=-0.11, p=0.32
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

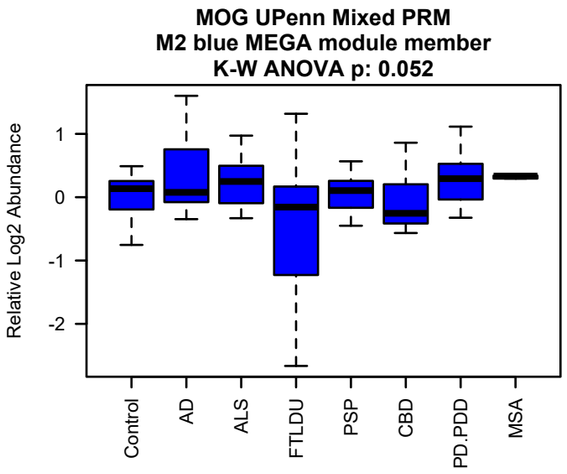

bicor=-0.21, p=0.033
cor=-0.22, p=0.028
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

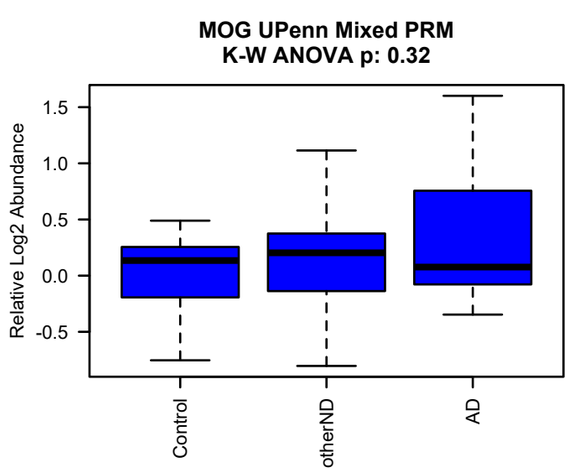

STXBP5L UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.024
Relative Log2 Abundance
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

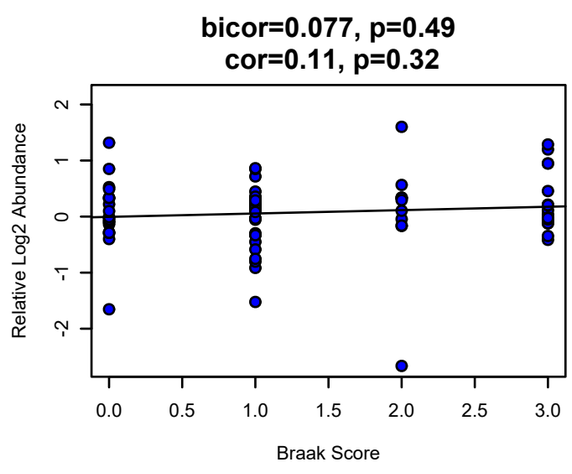

STXBP5L UPenn Mixed PRM
K-W ANOVA p: 0.008
Relative Log2 Abundance
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
Control
otherND
AD

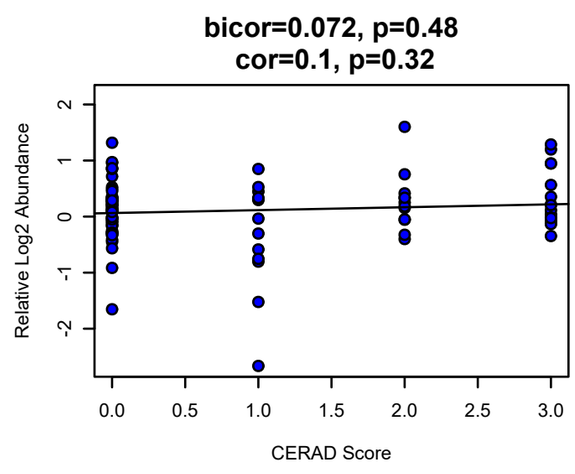

bicor=-0.26, p=0.019
cor=-0.28, p=0.0099
Relative Log2 Abundance
0.5
0.3
0.1
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

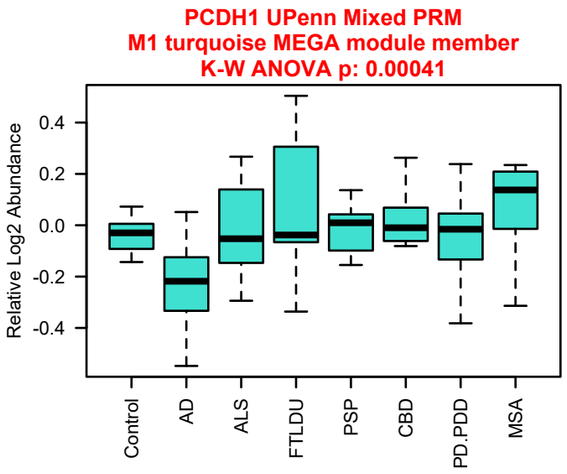

bicor=-0.27, p=0.0071
cor=-0.29, p=0.0034
Relative Log2 Abundance
0.5
0.3
0.1
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

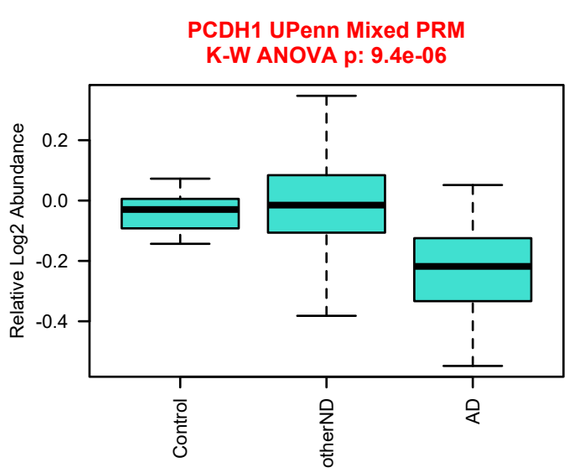

MOG UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.052
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

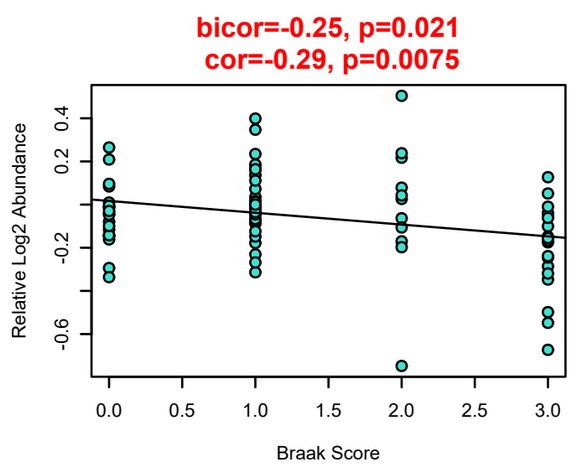

MOG UPenn Mixed PRM
K-W ANOVA p: 0.32
Relative Log2 Abundance
Control
otherND
AD

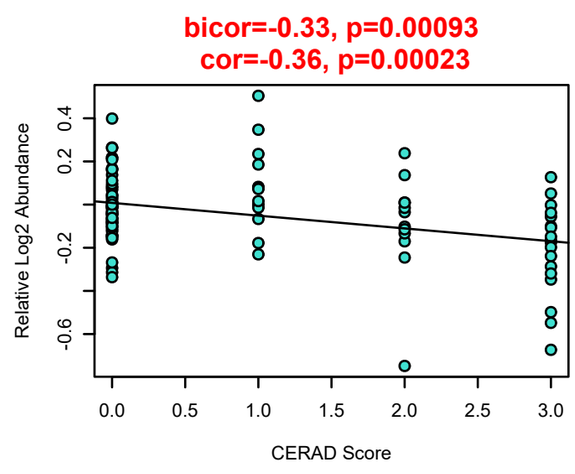

bicor=0.077, p=0.49
cor=0.11, p=0.32
Relative Log2 Abundance
Braak Score

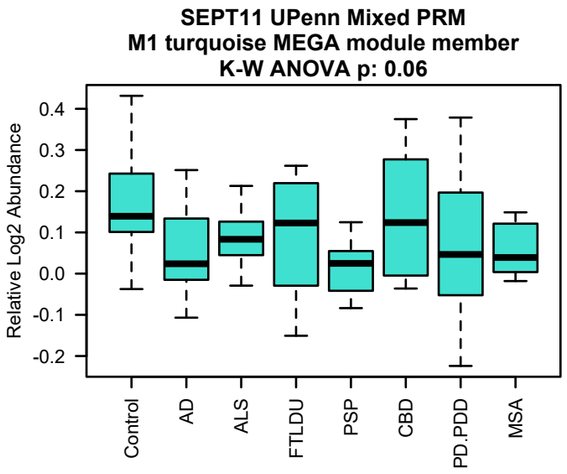

bicor=0.072, p=0.48
cor=0.1, p=0.32
Relative Log2 Abundance
CERAD Score

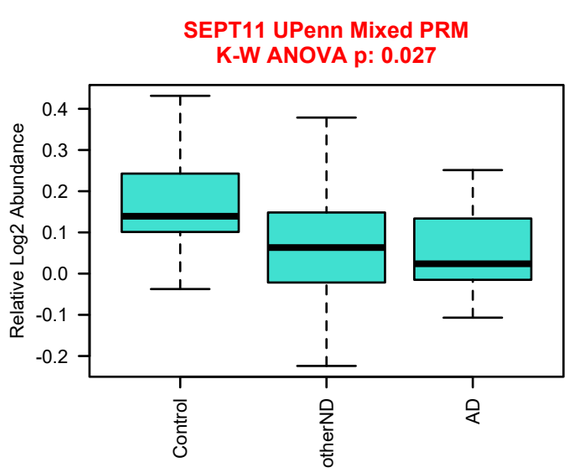

PCDH1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00041
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

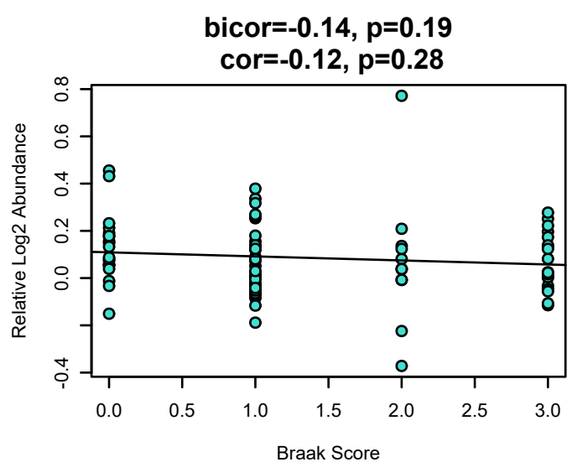

PCDH1 UPenn Mixed PRM
K-W ANOVA p: 9.4e-06
Relative Log2 Abundance
Control
otherND
AD

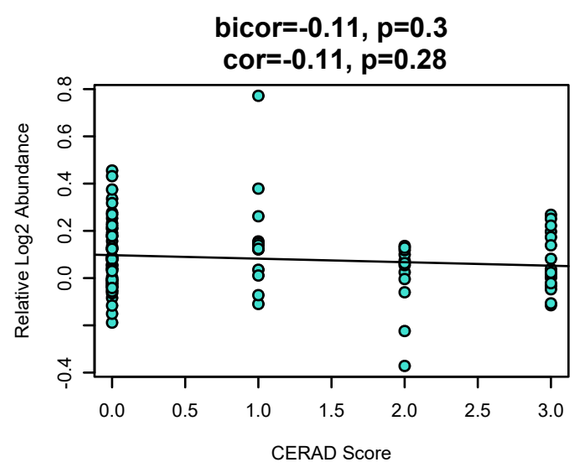

bicor=-0.25, p=0.021
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

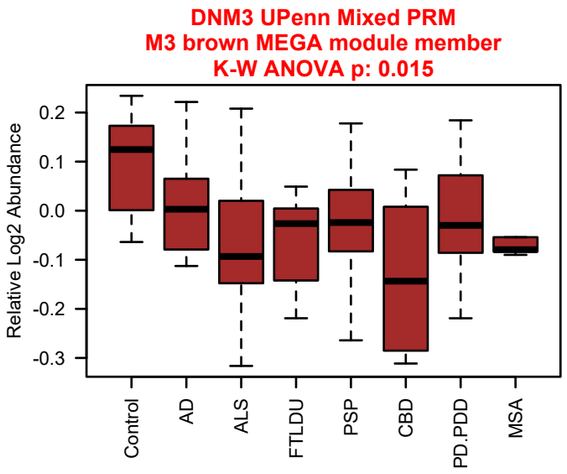

bicor=-0.33, p=0.00093
cor=-0.36, p=0.00023
Relative Log2 Abundance
CERAD Score

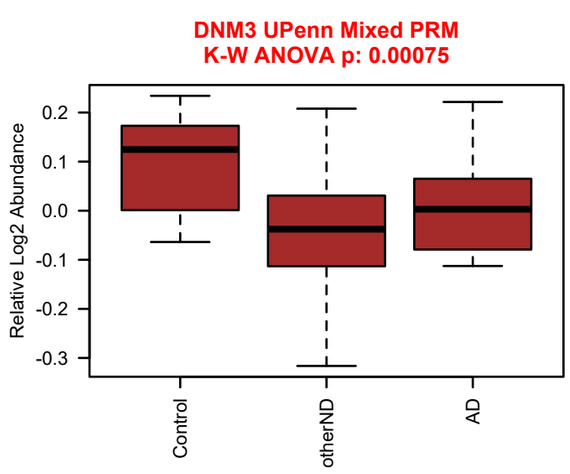

SEPT11 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

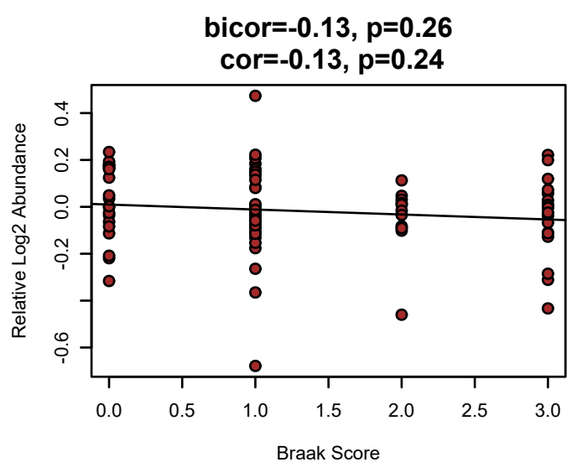

SEPT11 UPenn Mixed PRM
K-W ANOVA p: 0.027
Relative Log2 Abundance
Control
otherND
AD

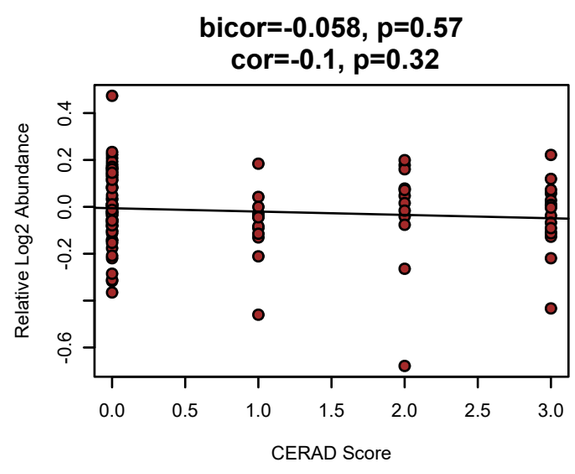

bicor=-0.14, p=0.19
cor=-0.12, p=0.28
Relative Log2 Abundance
Braak Score

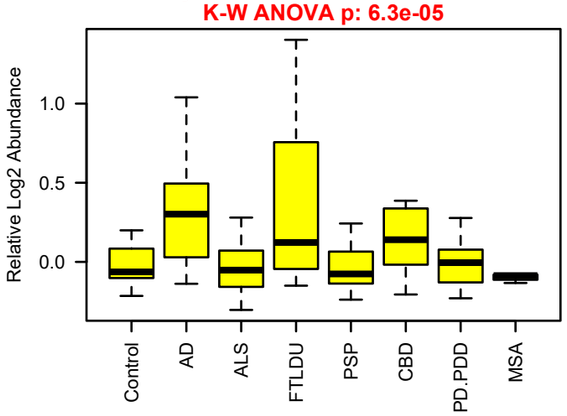

bicor=-0.11, p=0.3
cor=-0.11, p=0.28
Relative Log2 Abundance
CERAD Score

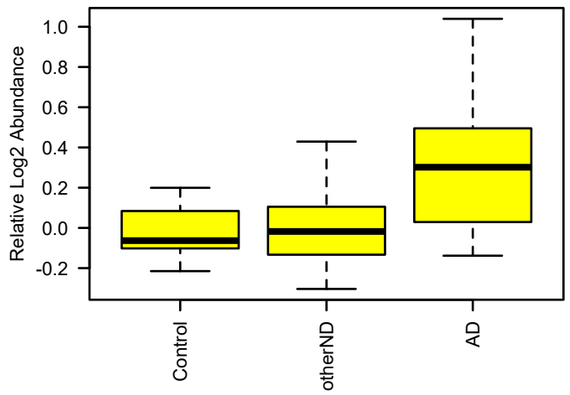

DNM3 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.015
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

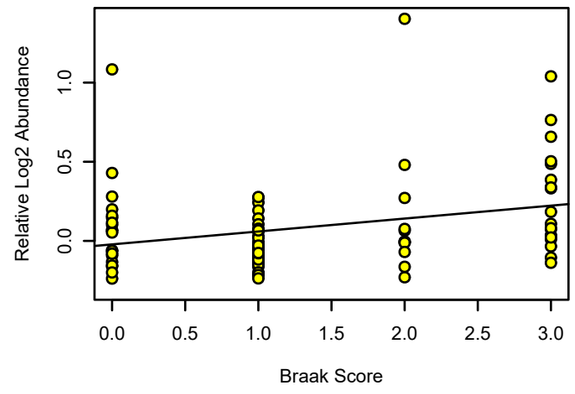

DNM3 UPenn Mixed PRM
K-W ANOVA p: 0.00075
Relative Log2 Abundance
Control
otherND
AD

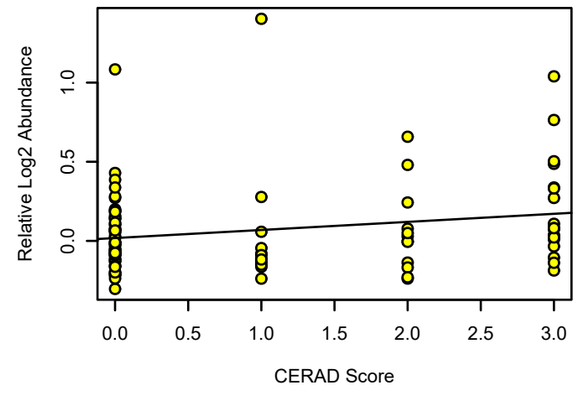

bicor=-0.13, p=0.26
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

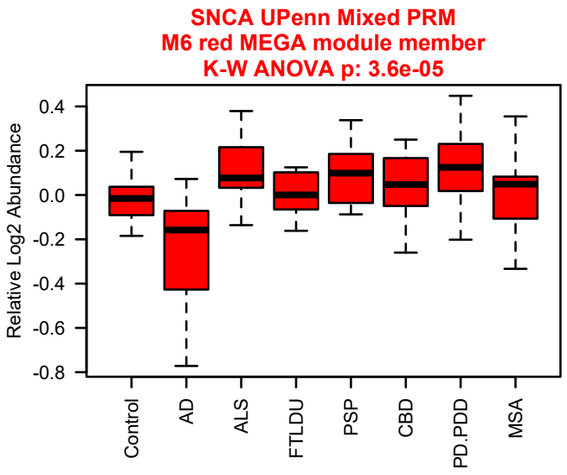

bicor=-0.058, p=0.57
cor=-0.1, p=0.32
Relative Log2 Abundance
CERAD Score

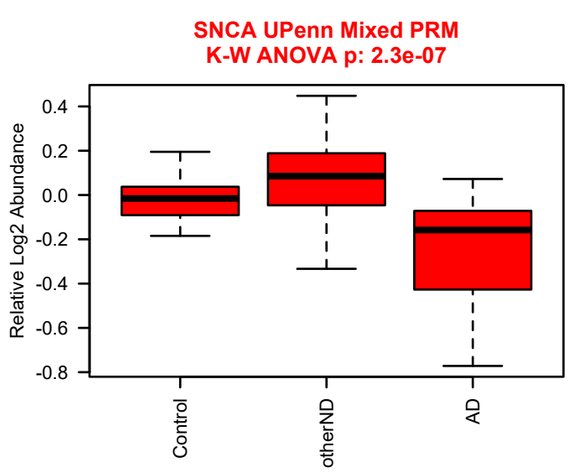

ERLIN2 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 6.3e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

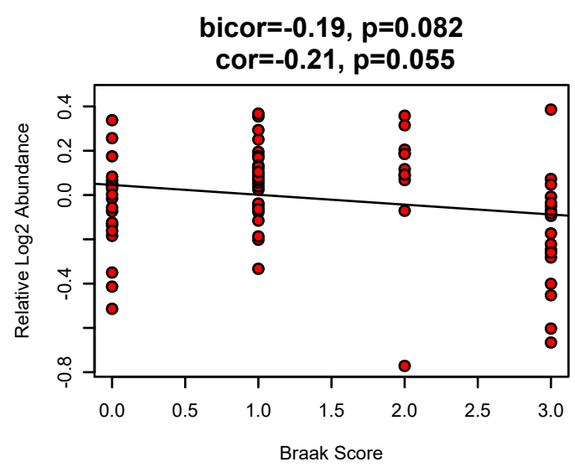

ERLIN2 UPenn Mixed PRM
K-W ANOVA p: 0.00073
Relative Log2 Abundance
Control
otherND
AD

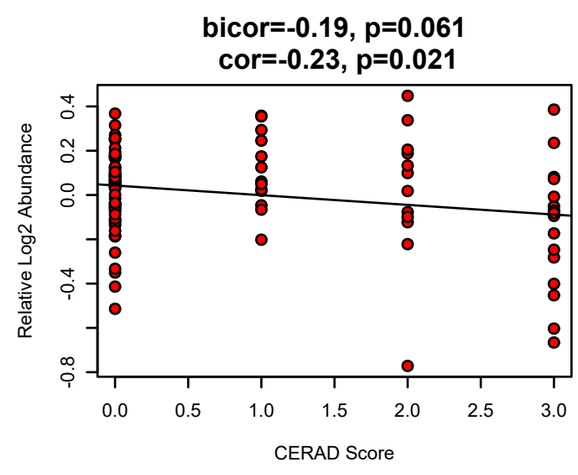

bicor=0.32, p=0.0027
cor=0.3, p=0.0056
Relative Log2 Abundance
Braak Score

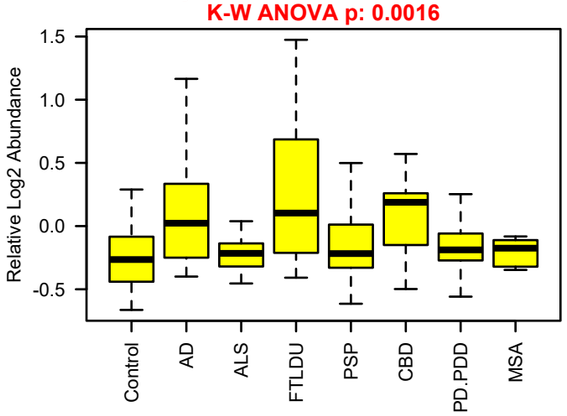

bicor=0.17, p=0.083
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

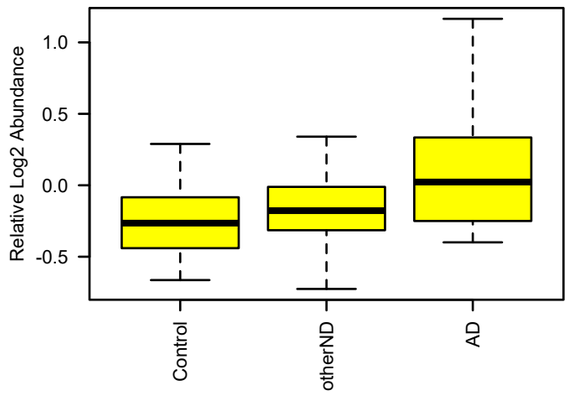

SNCA UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 3.6e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

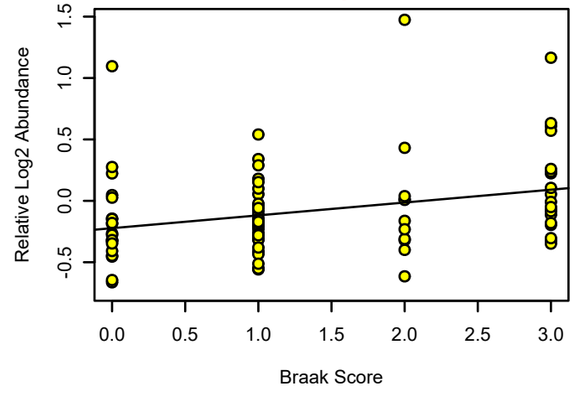

SNCA UPenn Mixed PRM
K-W ANOVA p: 2.3e-07
Relative Log2 Abundance
Control
otherND
AD

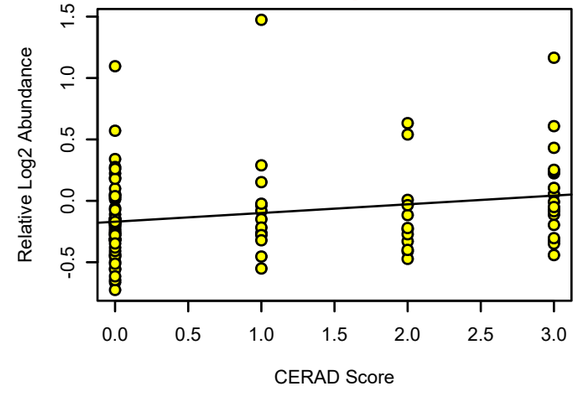

bicor=-0.19, p=0.082
cor=-0.21, p=0.055
Relative Log2 Abundance
Braak Score

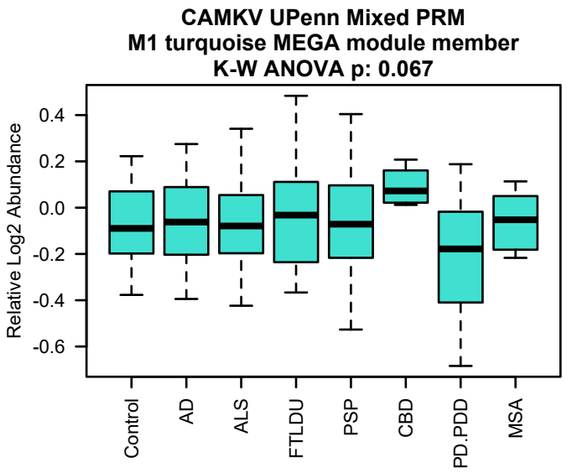

bicor=-0.19, p=0.061
cor=-0.23, p=0.021
Relative Log2 Abundance
CERAD Score

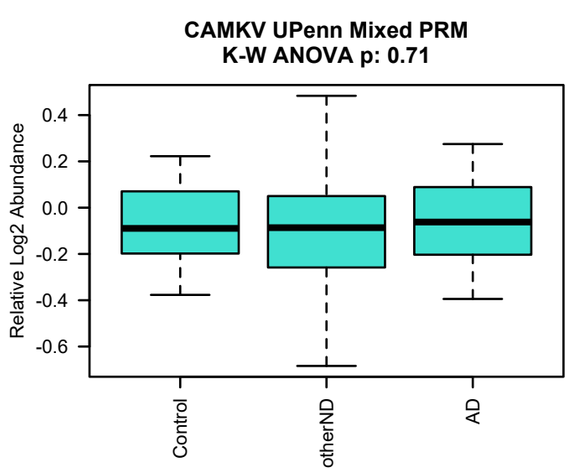

EZR UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.0016
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

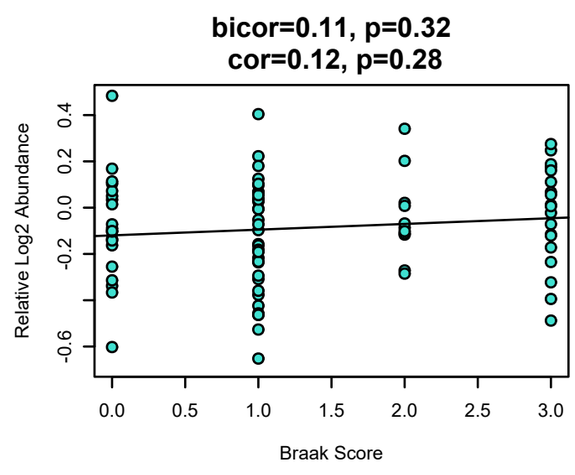

EZR UPenn Mixed PRM
K-W ANOVA p: 0.014
Relative Log2 Abundance
Control
otherND
AD

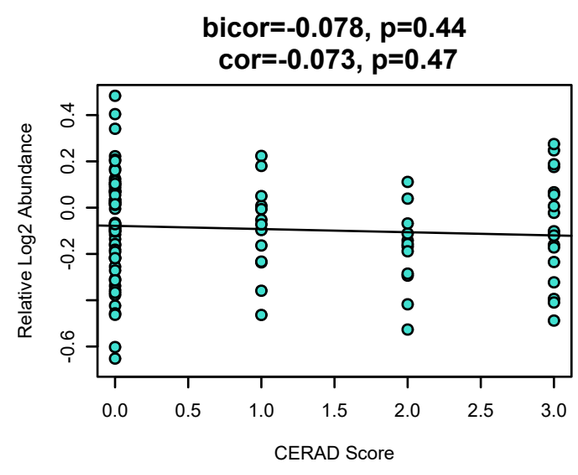

bicor=0.32, p=0.0027
cor=0.29, p=0.0075
Relative Log2 Abundance
Braak Score

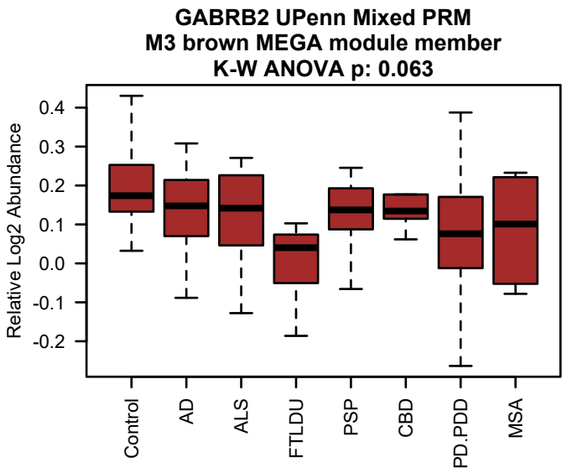

bicor=0.23, p=0.023
cor=0.23, p=0.021
Relative Log2 Abundance
CERAD Score

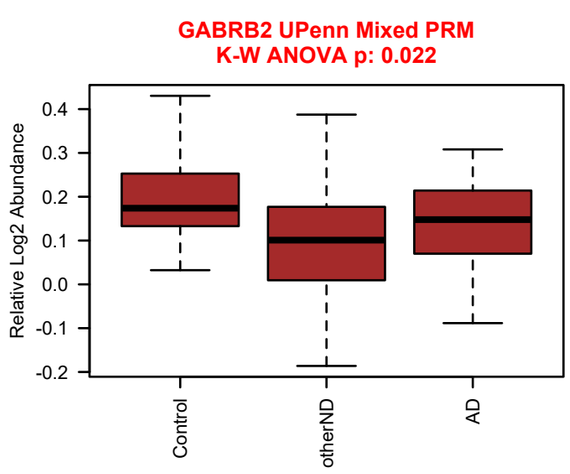

CAMKV UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.067
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

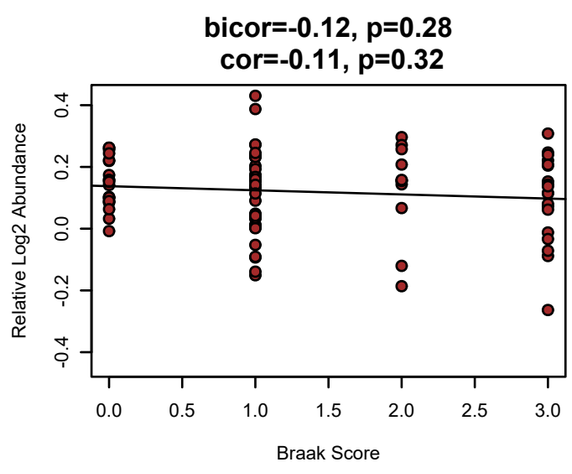

CAMKV UPenn Mixed PRM
K-W ANOVA p: 0.71
Relative Log2 Abundance
Control
otherND
AD

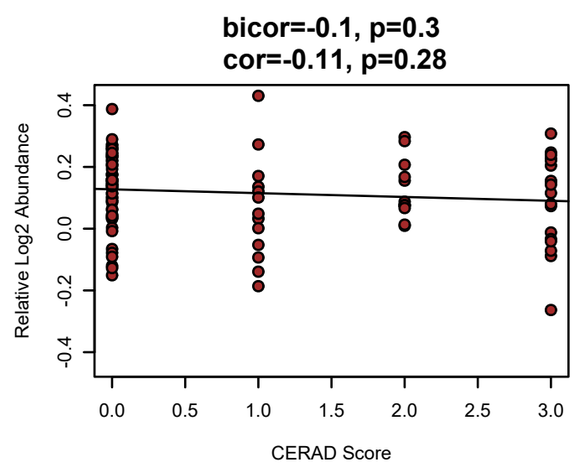

bicor=0.11, p=0.32
cor=0.12, p=0.28
Relative Log2 Abundance
Braak Score

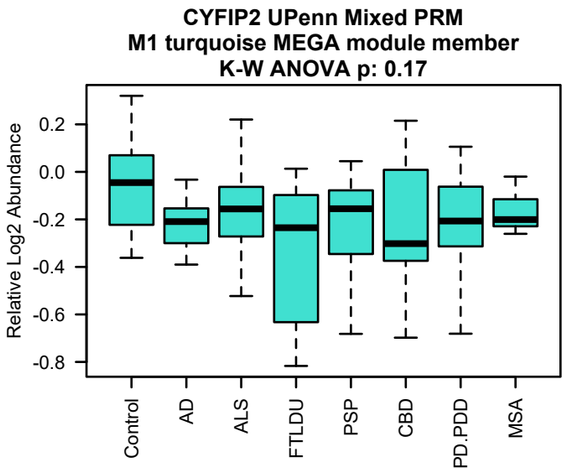

bicor=-0.078, p=0.44
cor=-0.073, p=0.47
Relative Log2 Abundance
CERAD Score

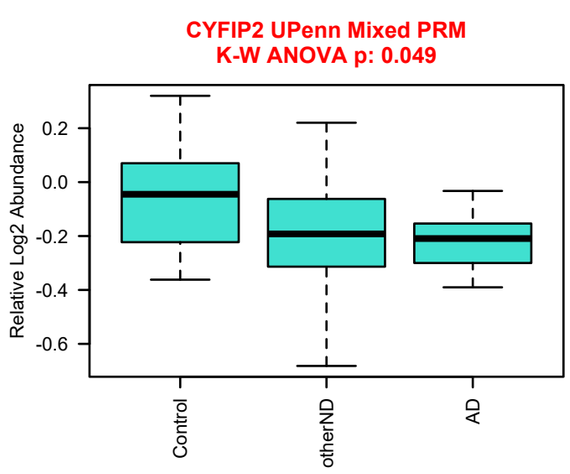

GABRB2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.063
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

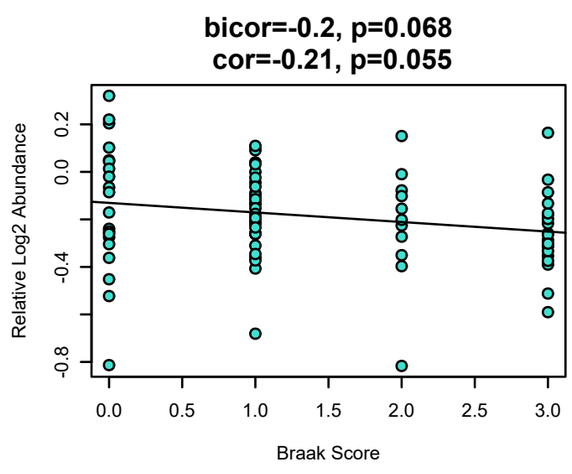

GABRB2 UPenn Mixed PRM
K-W ANOVA p: 0.022
Relative Log2 Abundance
Control
otherND
AD

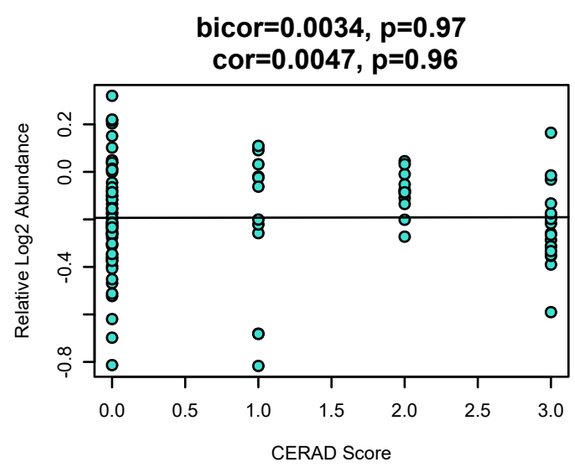

bicor=-0.12, p=0.28
cor=-0.11, p=0.32
Relative Log2 Abundance
Braak Score

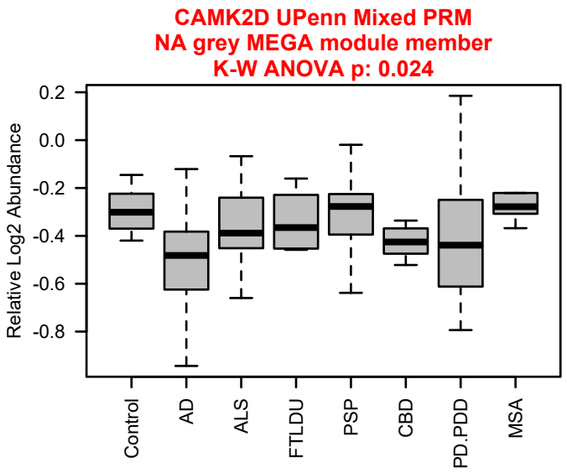

bicor=-0.1, p=0.3
cor=-0.11, p=0.28
Relative Log2 Abundance
CERAD Score

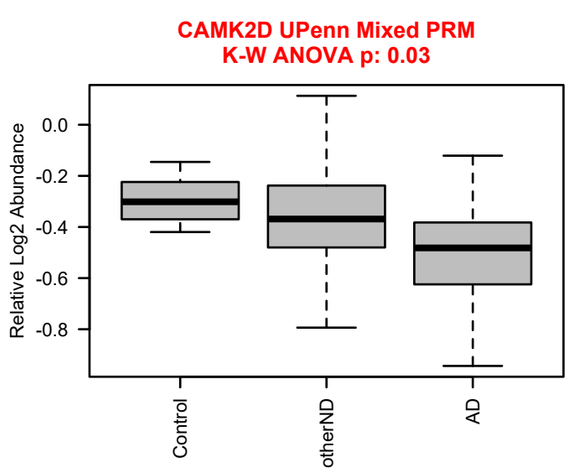

CYFIP2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.17
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

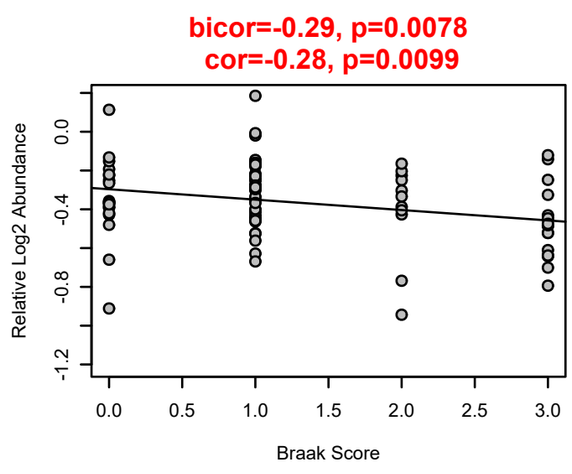

CYFIP2 UPenn Mixed PRM
K-W ANOVA p: 0.049
Relative Log2 Abundance
Control
otherND
AD

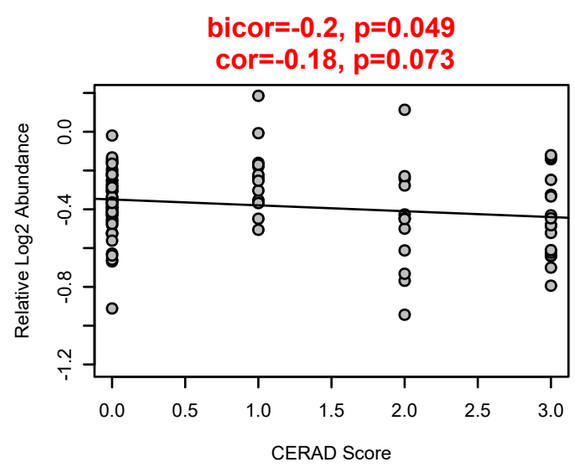

bicor=-0.2, p=0.068
cor=-0.21, p=0.055
Relative Log2 Abundance
Braak Score

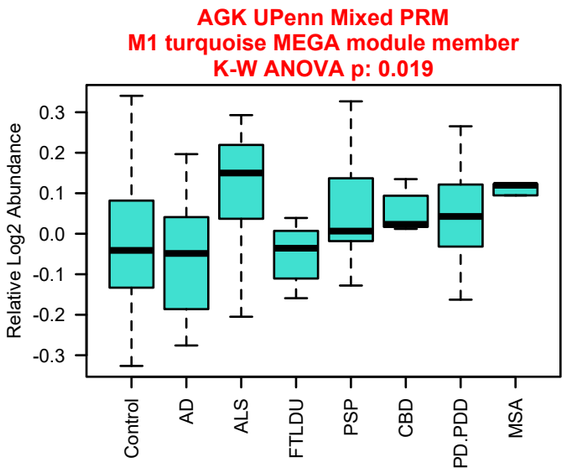

bicor=0.0034, p=0.97
cor=0.0047, p=0.96
Relative Log2 Abundance
CERAD Score

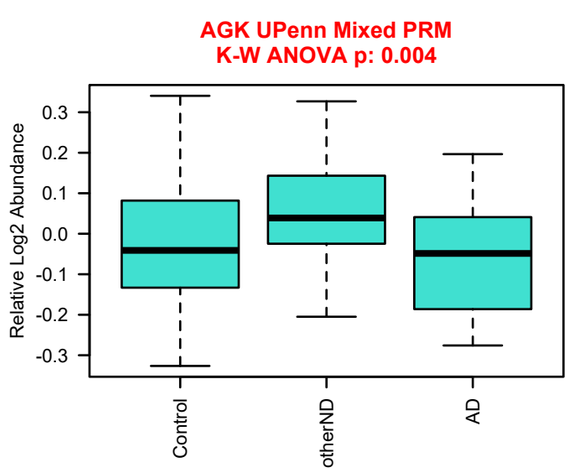

CAMK2D UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.024
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

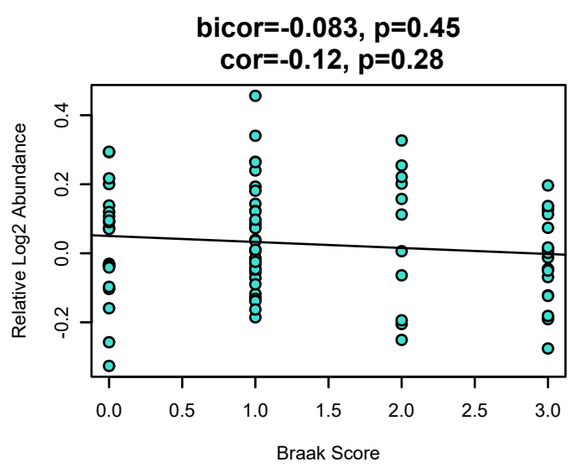

CAMK2D UPenn Mixed PRM
K-W ANOVA p: 0.03
Relative Log2 Abundance
Control
otherND
AD

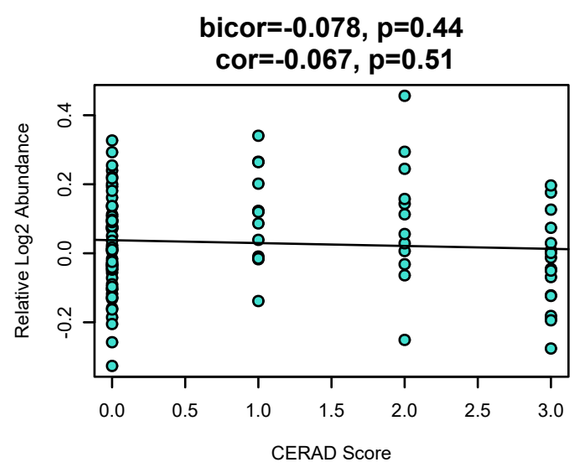

bicor=-0.29, p=0.0078
cor=-0.28, p=0.0099
Relative Log2 Abundance
Braak Score

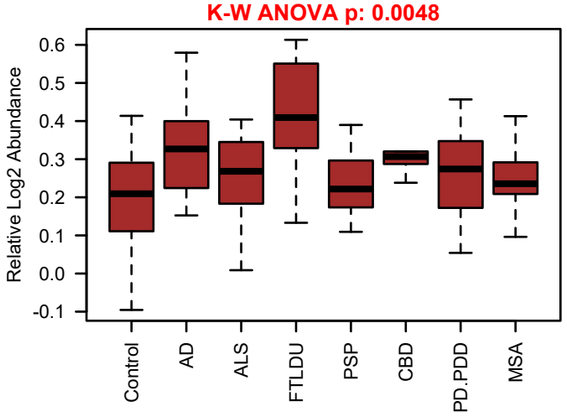

bicor=-0.2, p=0.049
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

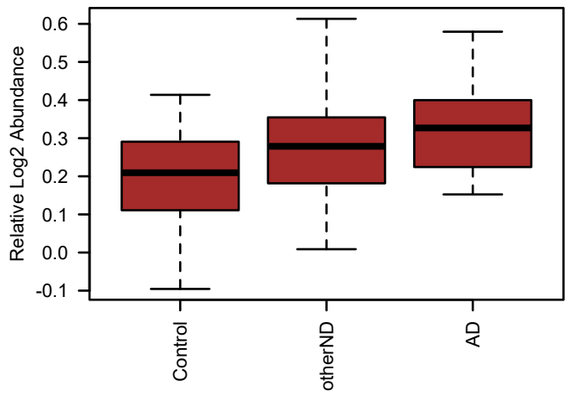

AGK UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.019
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

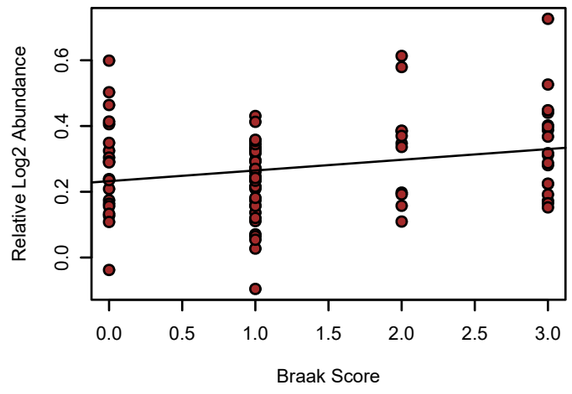

AGK UPenn Mixed PRM
K-W ANOVA p: 0.004
Relative Log2 Abundance
Control
otherND
AD

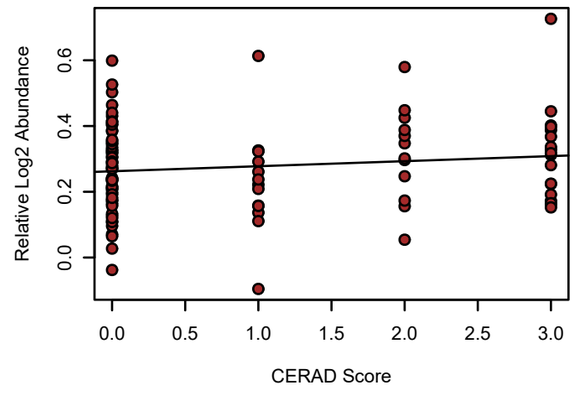

bicor=-0.083, p=0.45
cor=-0.12, p=0.28
Relative Log2 Abundance
Braak Score

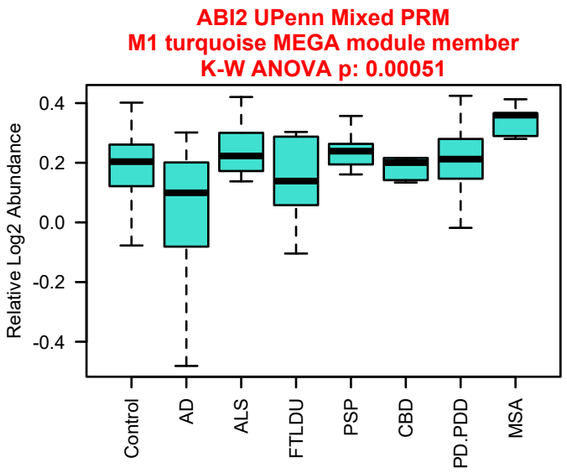

bicor=-0.078, p=0.44
cor=-0.067, p=0.51
Relative Log2 Abundance
CERAD Score

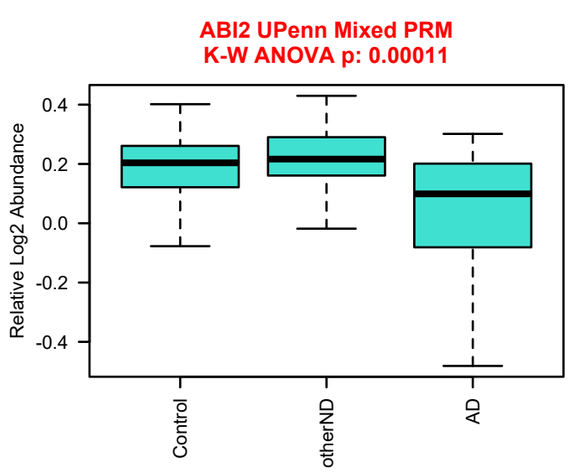

OGDH UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0048
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

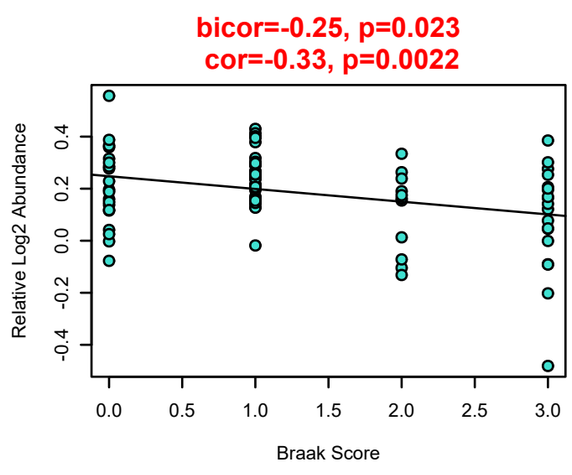

OGDH UPenn Mixed PRM
K-W ANOVA p: 0.0071
Relative Log2 Abundance
Control
otherND
AD

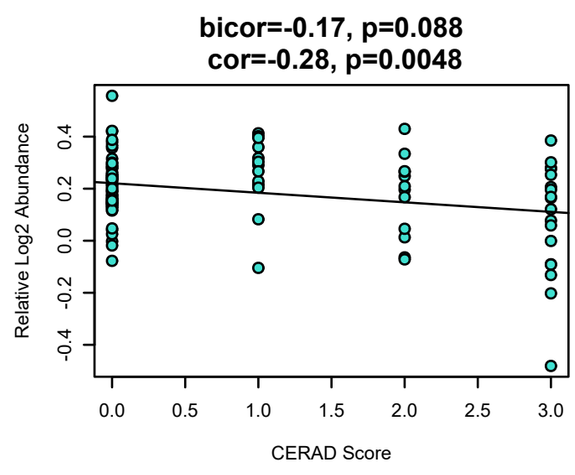

bicor=0.22, p=0.04
cor=0.24, p=0.028
Relative Log2 Abundance
Braak Score

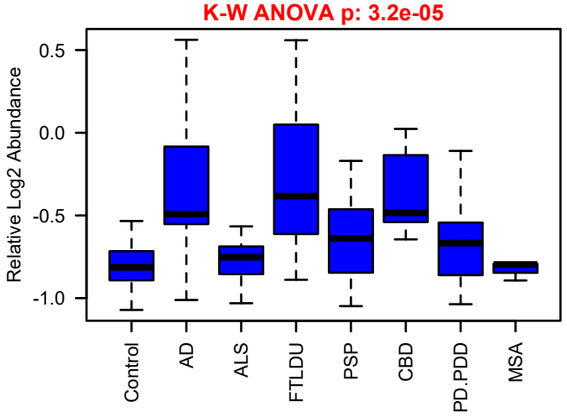

bicor=0.12, p=0.25
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

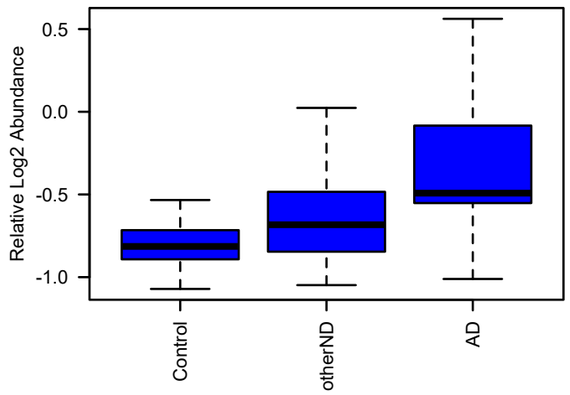

ABI2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00051
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

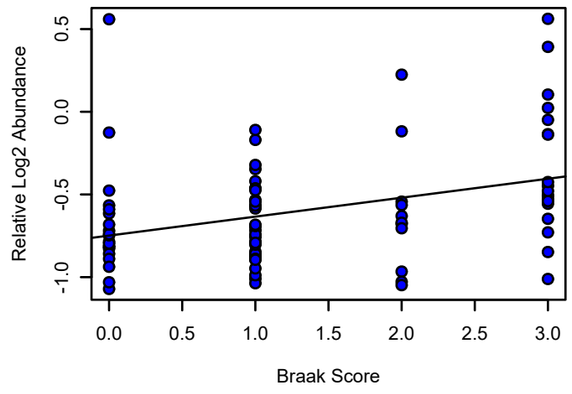

ABI2 UPenn Mixed PRM
K-W ANOVA p: 0.00011
Relative Log2 Abundance
Control
otherND
AD

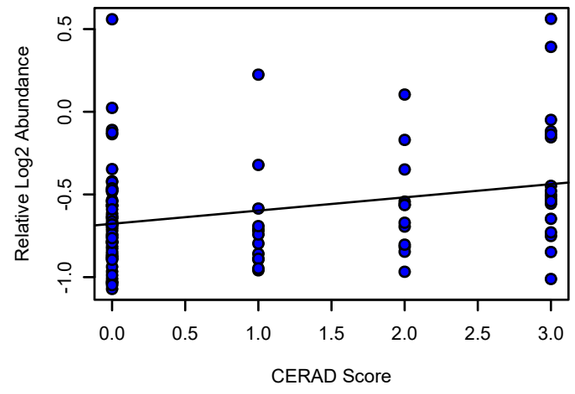

bicor=-0.25, p=0.023
cor=-0.33, p=0.0022
Relative Log2 Abundance
Braak Score

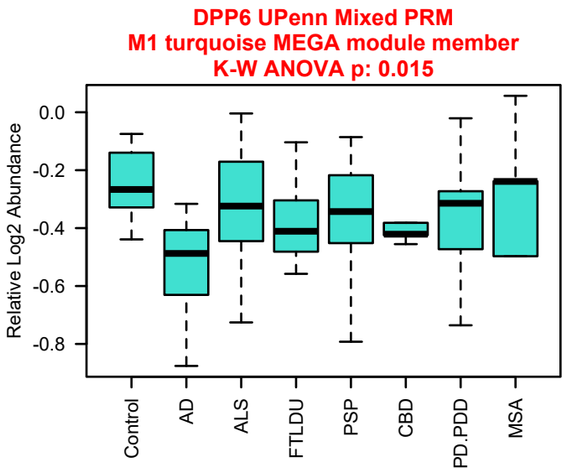

bicor=-0.17, p=0.088
cor=-0.28, p=0.0048
Relative Log2 Abundance
CERAD Score

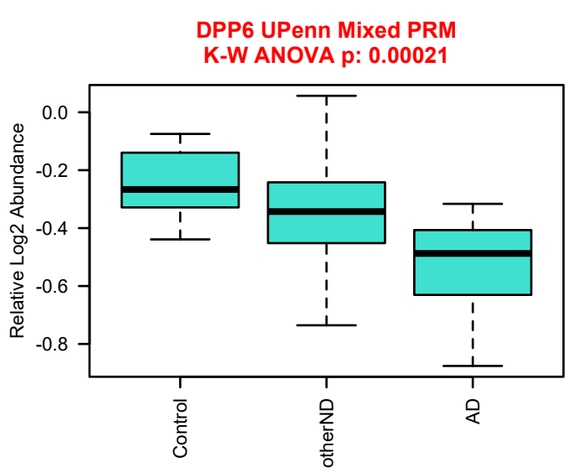

VCAN UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 3.2e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

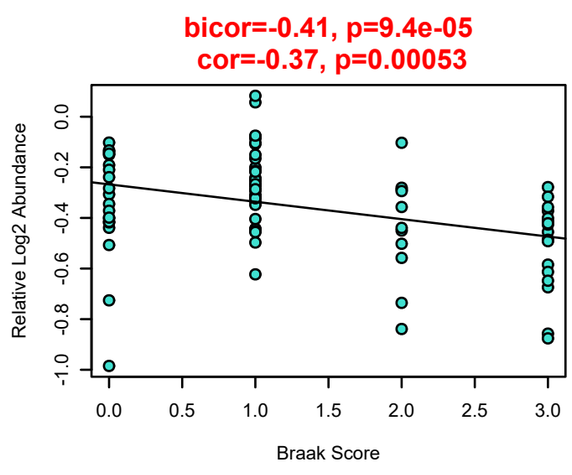

VCAN UPenn Mixed PRM
K-W ANOVA p: 0.00049
Relative Log2 Abundance
Control
otherND
AD

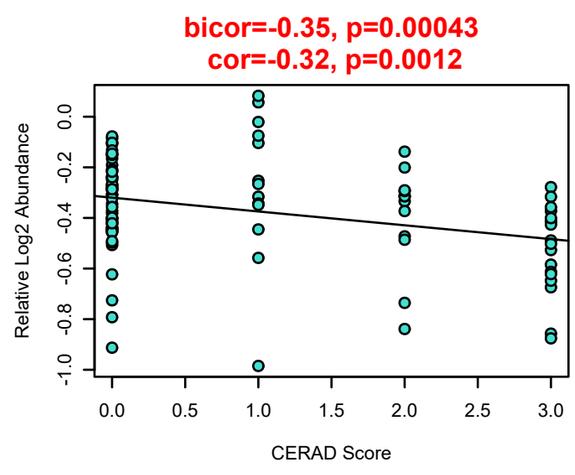

bicor=0.39, p=0.00026
cor=0.35, p=0.0011
Relative Log2 Abundance
Braak Score

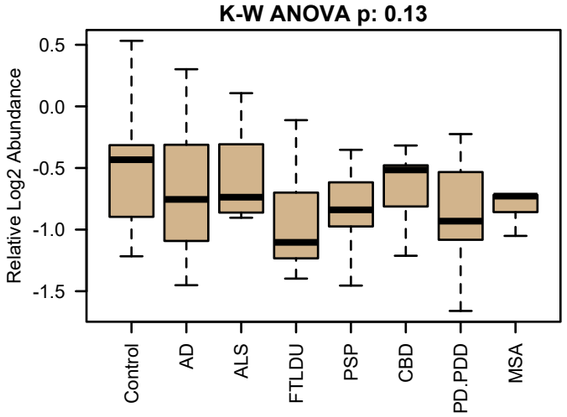

bicor=0.27, p=0.0071
cor=0.28, p=0.0048
Relative Log2 Abundance
CERAD Score

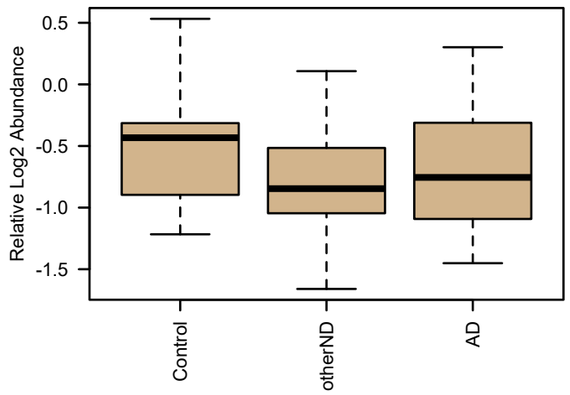

DPP6 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.015
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

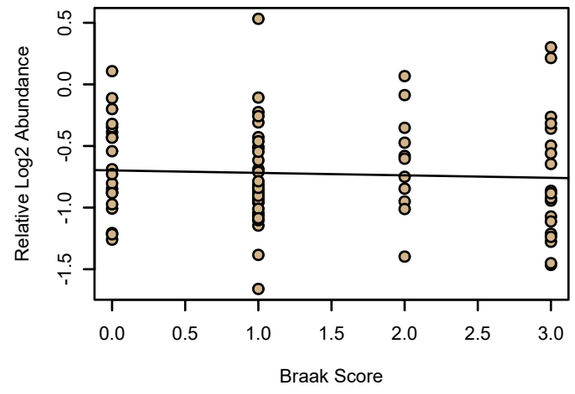

DPP6 UPenn Mixed PRM
K-W ANOVA p: 0.00021
Relative Log2 Abundance
Control
otherND
AD

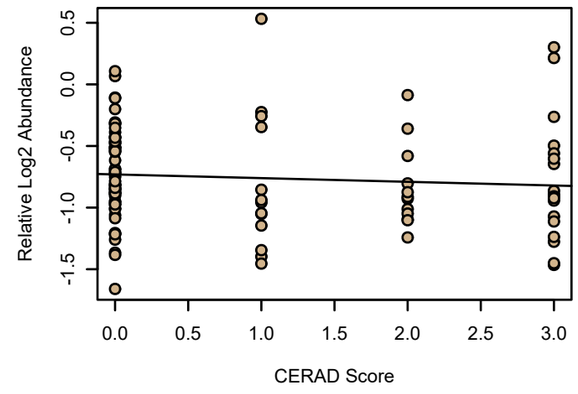

bicor=-0.41, p=9.4e-05
cor=-0.37, p=0.00053
Relative Log2 Abundance
Braak Score

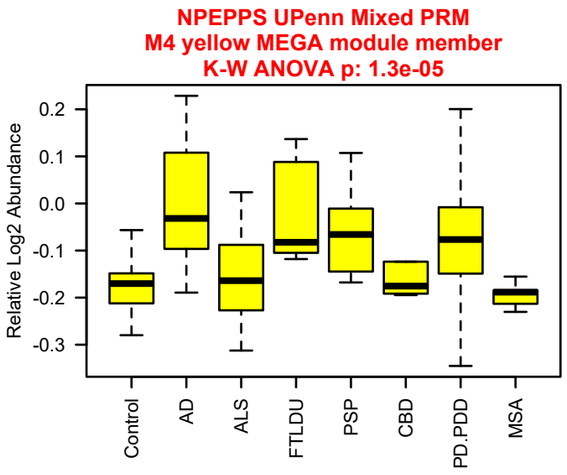

bicor=-0.35, p=0.00043
cor=-0.32, p=0.0012
Relative Log2 Abundance
CERAD Score

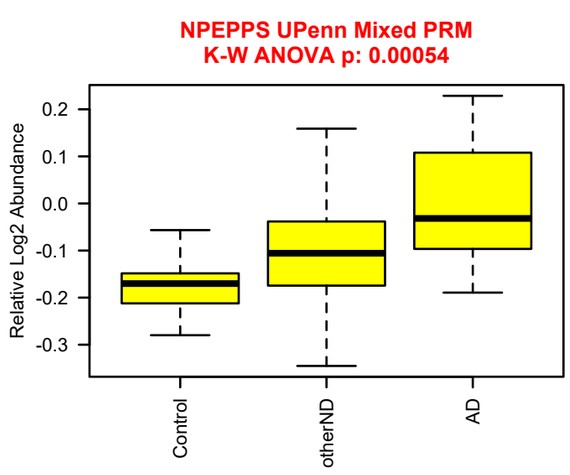

CD81 UPenn Mixed PRM
M12 tan MEGA module member
K-W ANOVA p: 0.13
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

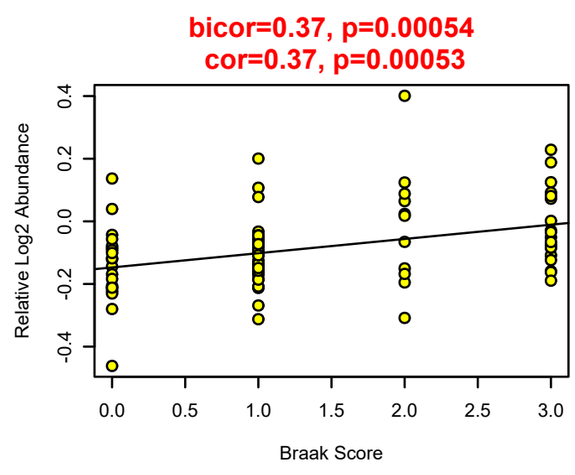

CD81 UPenn Mixed PRM
K-W ANOVA p: 0.1
Relative Log2 Abundance
Control
otherND
AD

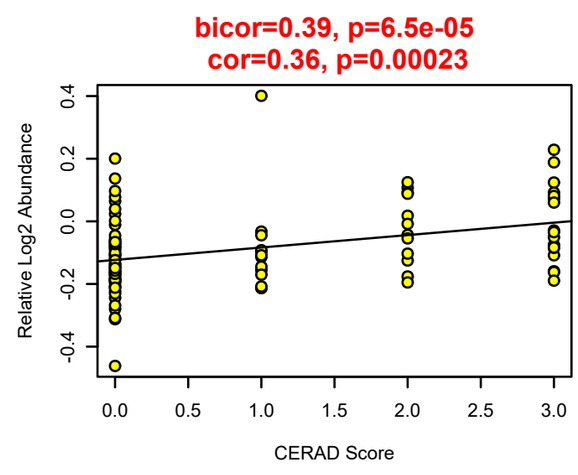

bicor=-0.0055, p=0.96
cor=-0.051, p=0.65
Relative Log2 Abundance
Braak Score

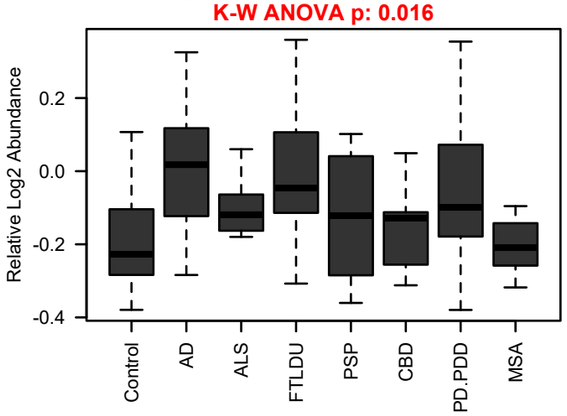

bicor=-0.13, p=0.21
cor=-0.086, p=0.39
Relative Log2 Abundance
CERAD Score

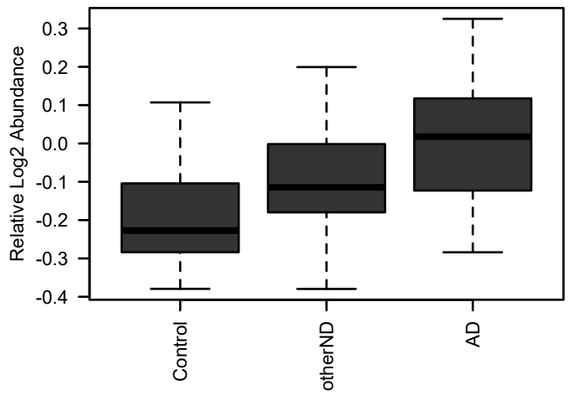

NPEPPS UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1.3e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

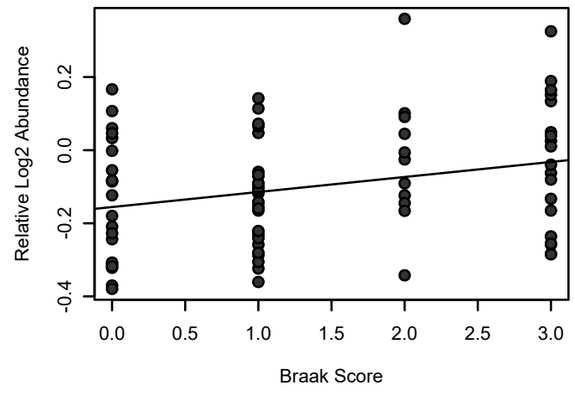

NPEPPS UPenn Mixed PRM
K-W ANOVA p: 0.00054
Relative Log2 Abundance
Control
otherND
AD

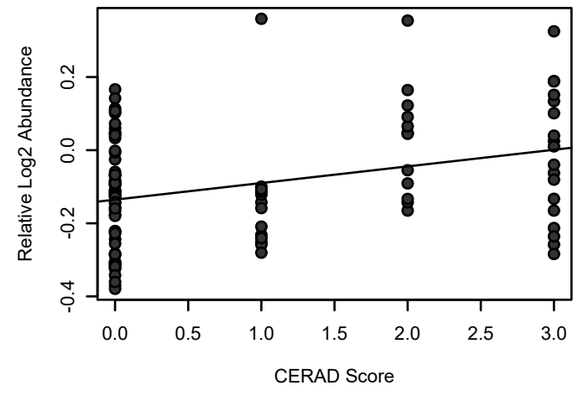

bicor=0.37, p=0.00054
cor=0.37, p=0.00053
Relative Log2 Abundance
Braak Score

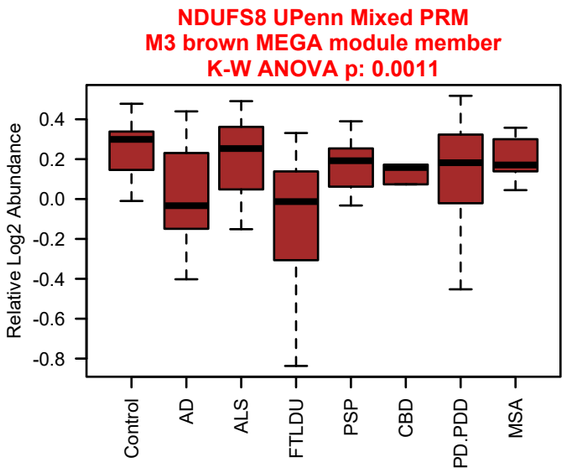

bicor=0.39, p=6.5e-05
cor=0.36, p=0.00023
Relative Log2 Abundance
CERAD Score

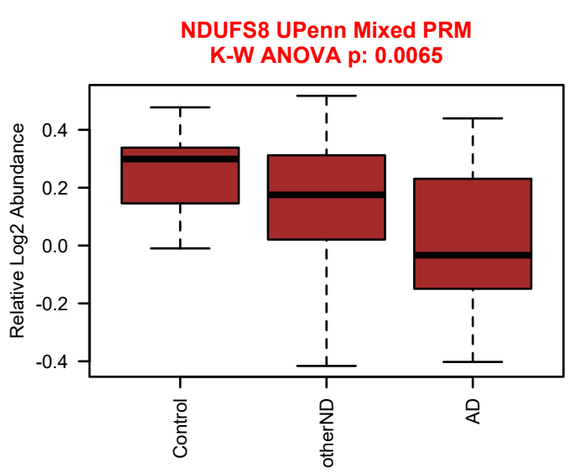

NPEPPSL1 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.016
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

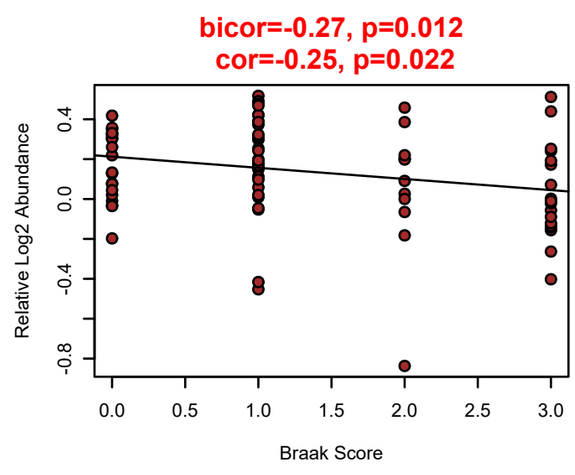

NPEPPSL1 UPenn Mixed PRM
K-W ANOVA p: 0.0073
Relative Log2 Abundance
Control
otherND
AD

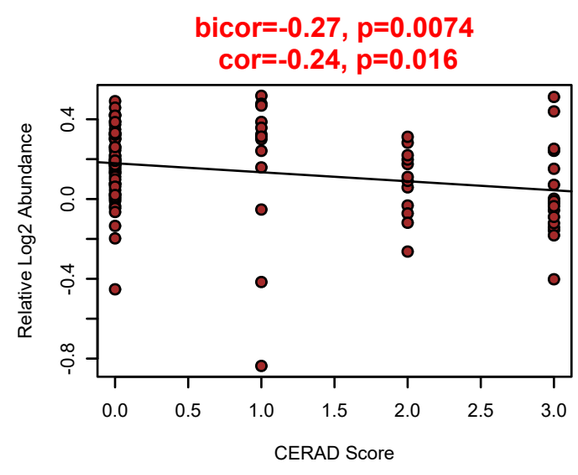

bicor=0.27, p=0.015
cor=0.27, p=0.013
Relative Log2 Abundance
Braak Score

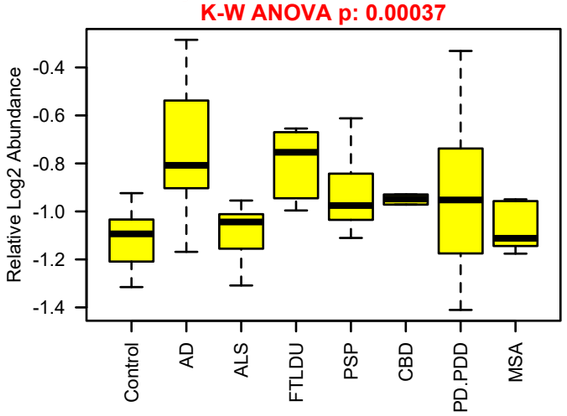

bicor=0.32, p=0.0012
cor=0.33, p=8e-04
Relative Log2 Abundance
CERAD Score

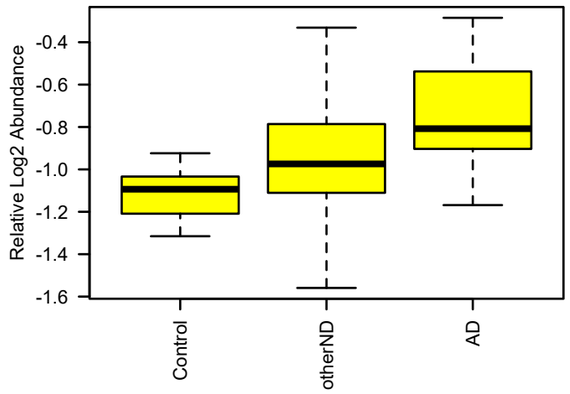

NDUFS8 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0011
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

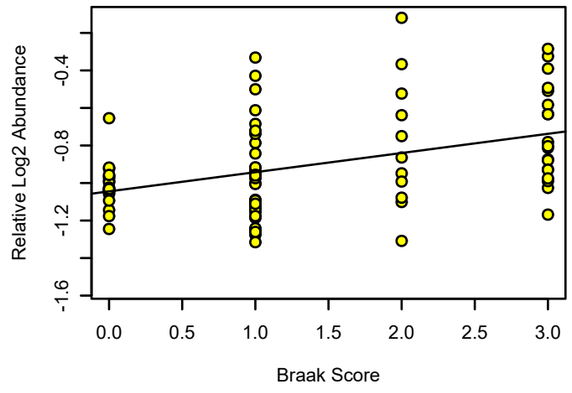

NDUFS8 UPenn Mixed PRM
K-W ANOVA p: 0.0065
Relative Log2 Abundance
Control
otherND
AD

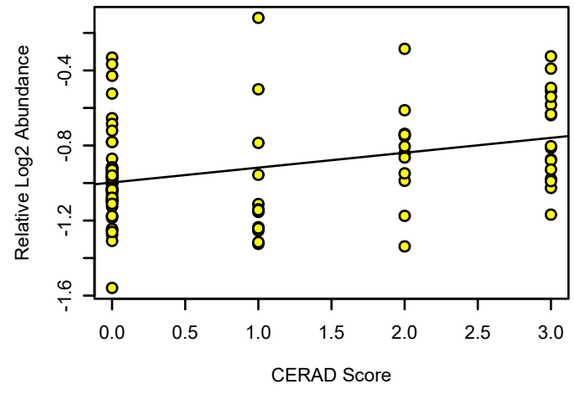

bicor=-0.27, p=0.012
cor=-0.25, p=0.022
Relative Log2 Abundance
Braak Score

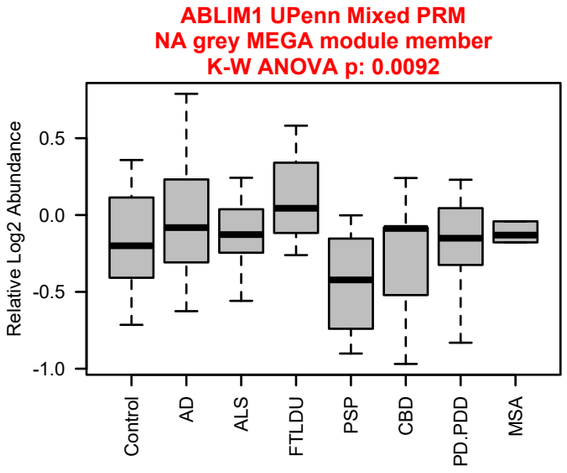

bicor=-0.27, p=0.0074
cor=-0.24, p=0.016
Relative Log2 Abundance
CERAD Score

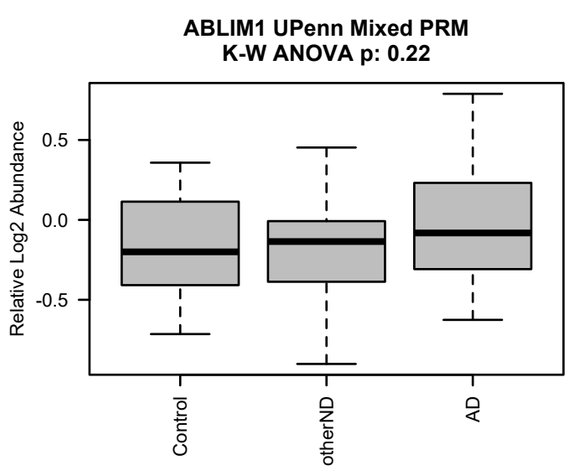

MAPK3 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.00037
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

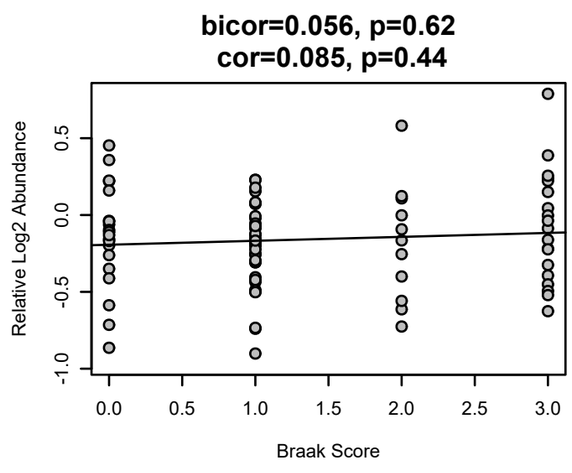

MAPK3 UPenn Mixed PRM
K-W ANOVA p: 0.00034
Relative Log2 Abundance
Control
otherND
AD

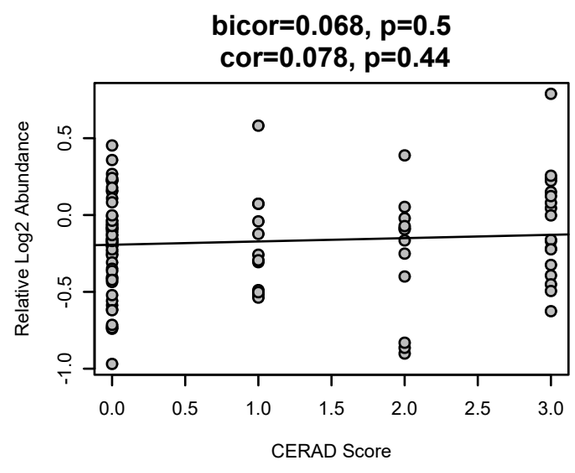

bicor=0.44, p=2.4e-05
cor=0.42, p=7e-05
Relative Log2 Abundance
Braak Score

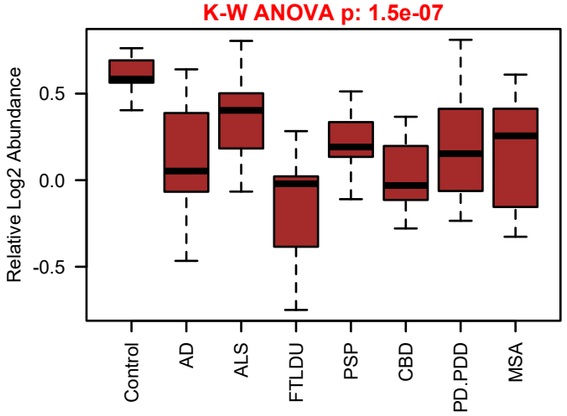

bicor=0.38, p=9.9e-05
cor=0.35, p=0.00036
Relative Log2 Abundance
CERAD Score

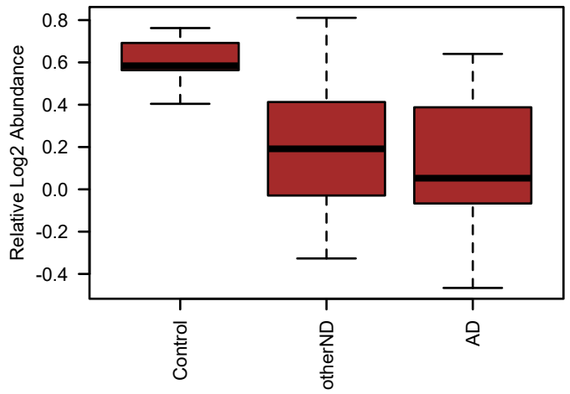

ABLIM1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.0092
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

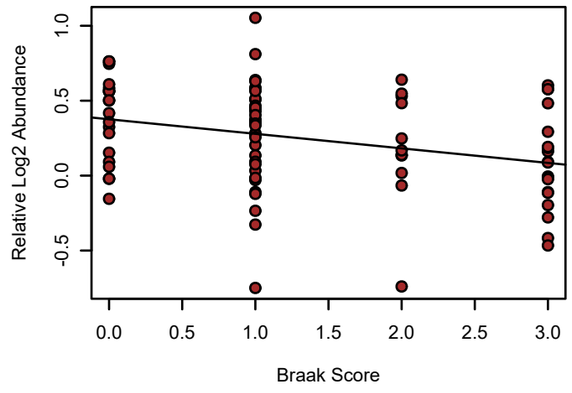

ABLIM1 UPenn Mixed PRM
K-W ANOVA p: 0.22
Relative Log2 Abundance
Control
otherND
AD

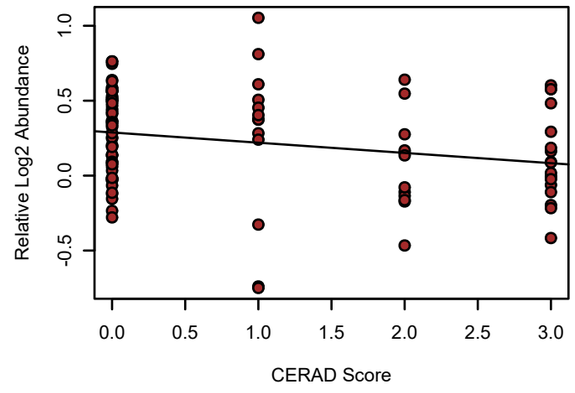

bicor=0.056, p=0.62
cor=0.085, p=0.44
Relative Log2 Abundance
Braak Score

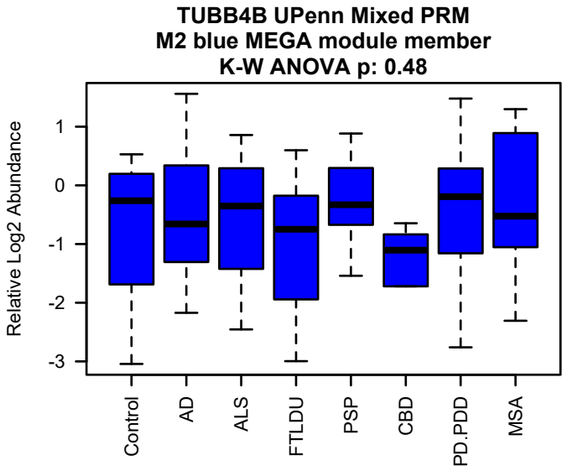

bicor=0.068, p=0.5
cor=0.078, p=0.44
Relative Log2 Abundance
CERAD Score

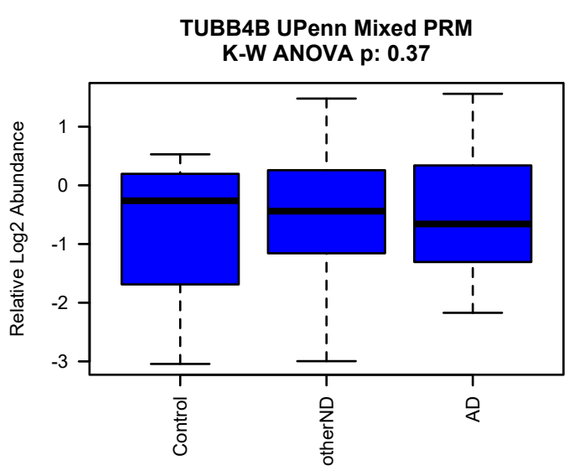

NDUFV1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 1.5e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

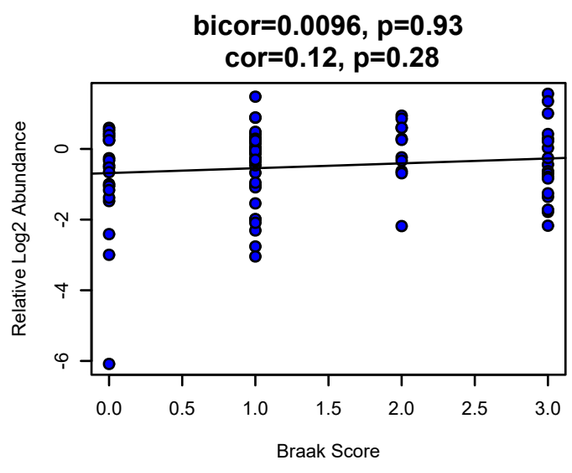

NDUFV1 UPenn Mixed PRM
K-W ANOVA p: 1.7e-06
Relative Log2 Abundance
Control
otherND
AD

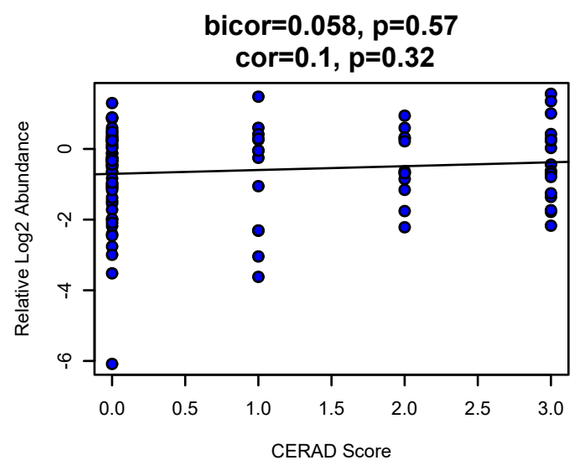

bicor=-0.32, p=0.0029
cor=-0.3, p=0.0056
Relative Log2 Abundance
Braak Score

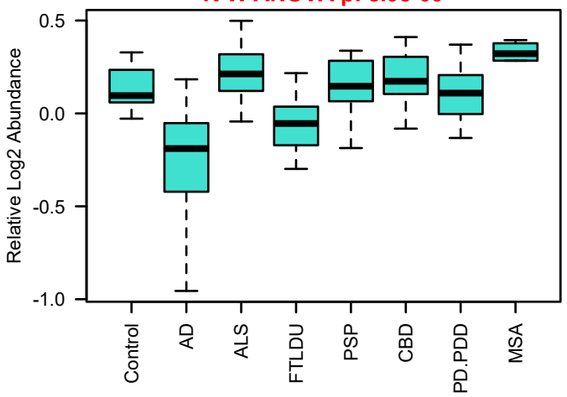

bicor=-0.25, p=0.011
cor=-0.24, p=0.016
Relative Log2 Abundance
CERAD Score

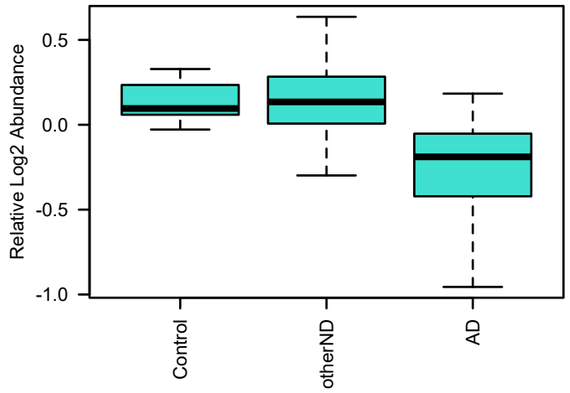

TUBB4B UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.48
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

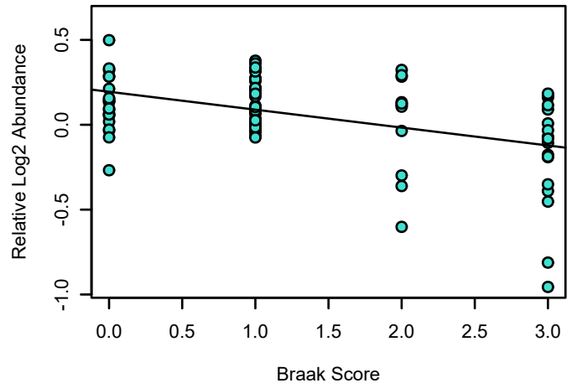

TUBB4B UPenn Mixed PRM
K-W ANOVA p: 0.37
Relative Log2 Abundance
Control
otherND
AD

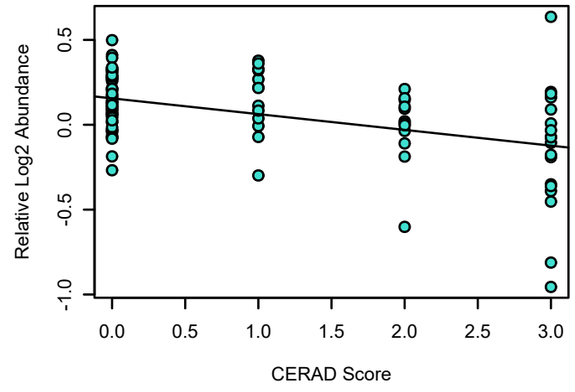

bicor=0.0096, p=0.93
cor=0.12, p=0.28
Relative Log2 Abundance
Braak Score

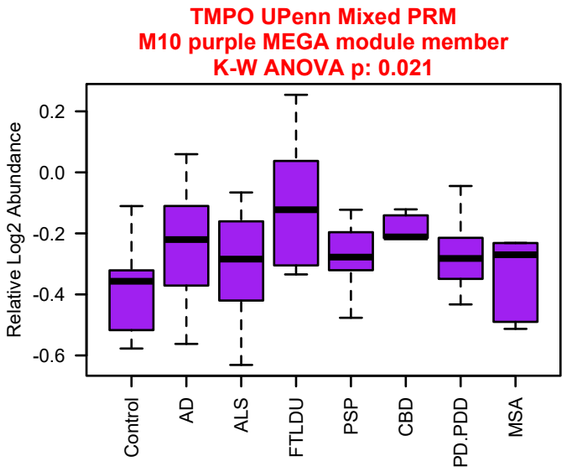

bicor=0.058, p=0.57
cor=0.1, p=0.32
Relative Log2 Abundance
CERAD Score

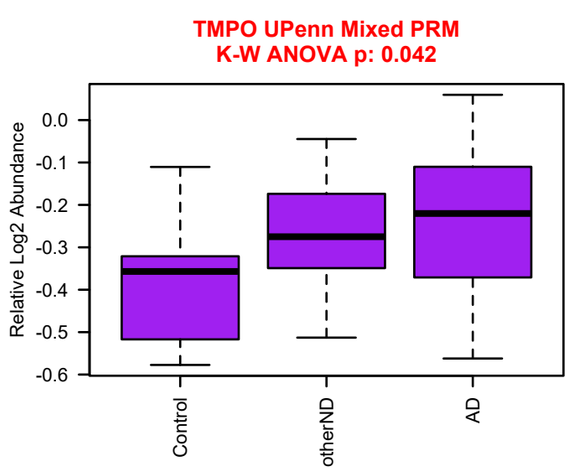

SEPT5 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 8.9e-09
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

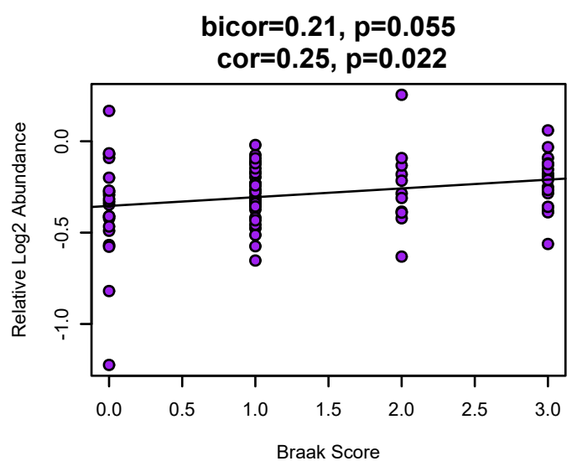

SEPT5 UPenn Mixed PRM
K-W ANOVA p: 2.2e-09
Relative Log2 Abundance
Control
otherND
AD

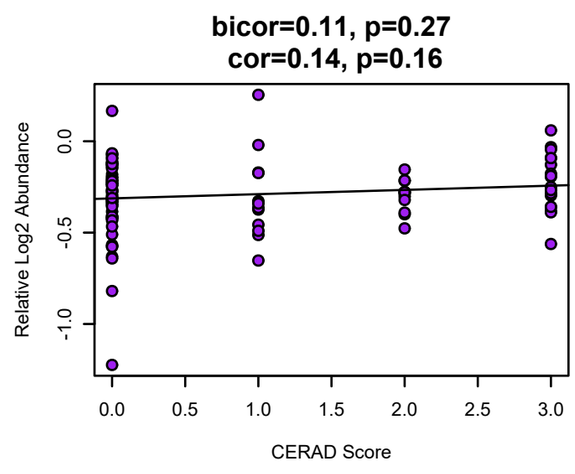

bicor=-0.38, p=0.00037
cor=-0.46, p=1.1e-05
Relative Log2 Abundance
Braak Score

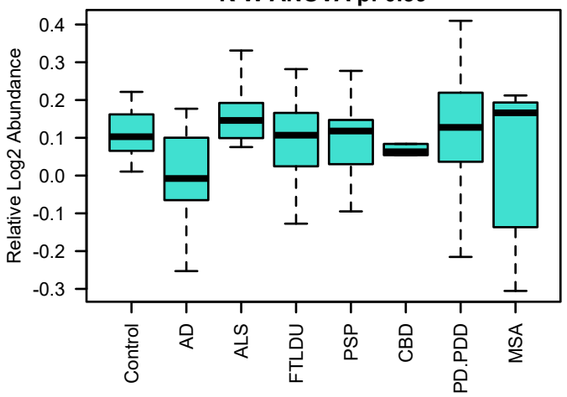

bicor=-0.39, p=6.4e-05
cor=-0.45, p=2.6e-06
Relative Log2 Abundance
CERAD Score

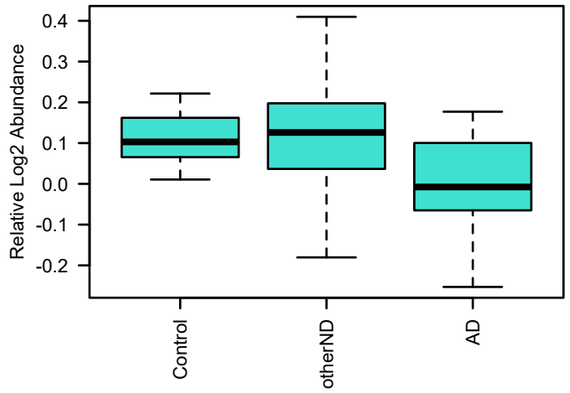

TMPO UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.021
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

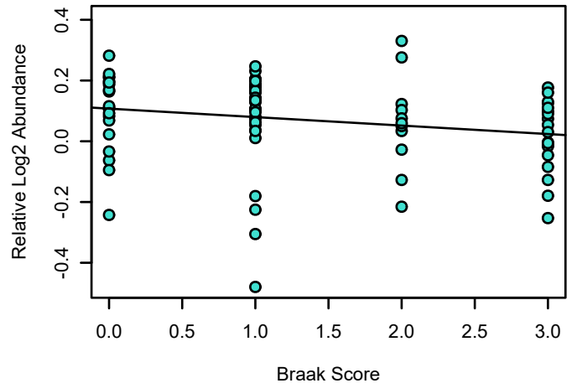

TMPO UPenn Mixed PRM
K-W ANOVA p: 0.042
Relative Log2 Abundance
Control
otherND
AD

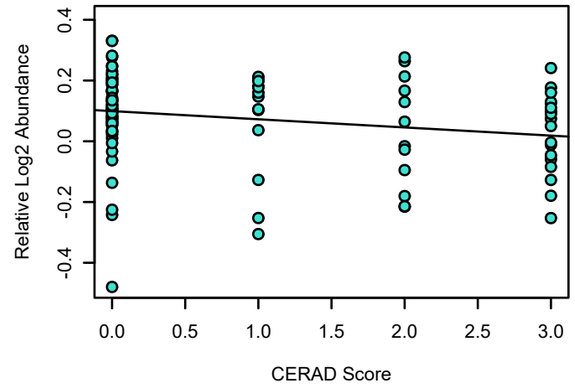

bicor=0.21, p=0.055
cor=0.25, p=0.022
Relative Log2 Abundance
Braak Score

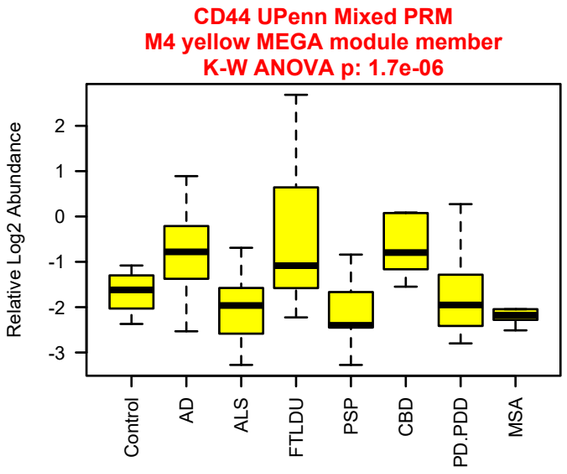

bicor=0.11, p=0.27
cor=0.14, p=0.16
Relative Log2 Abundance
CERAD Score

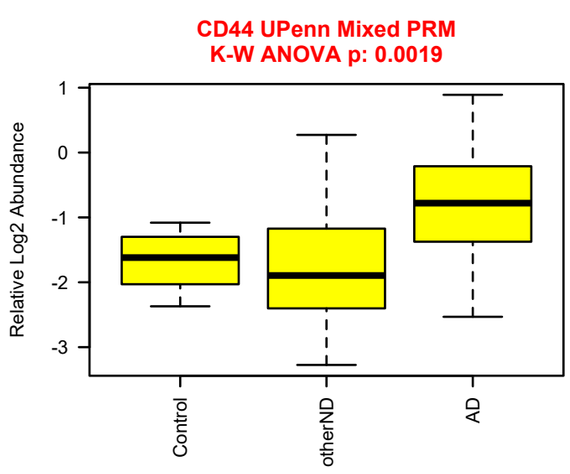

DNM1L UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.39
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

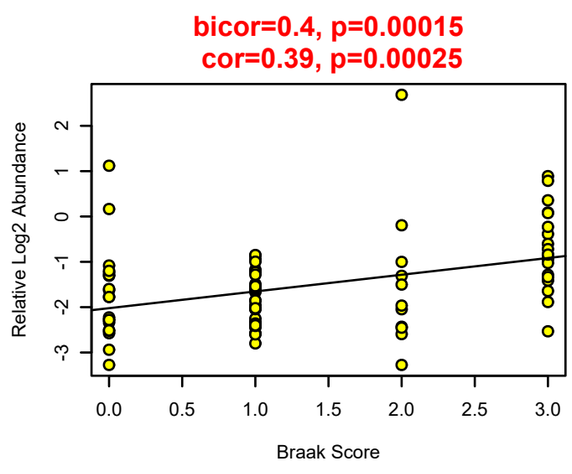

DNM1L UPenn Mixed PRM
K-W ANOVA p: 0.086
Relative Log2 Abundance
Control
otherND
AD

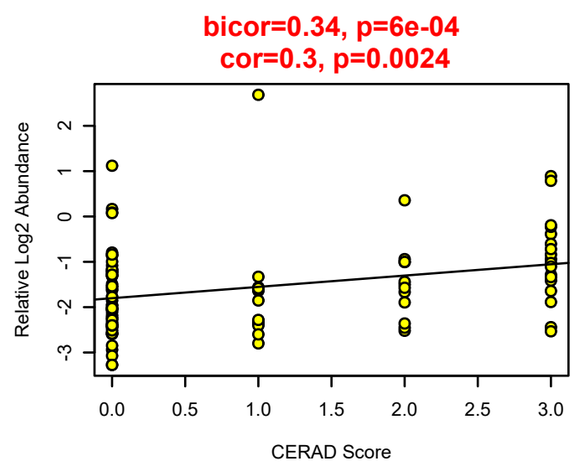

bicor=-0.32, p=0.0029
cor=-0.21, p=0.055
Relative Log2 Abundance
Braak Score

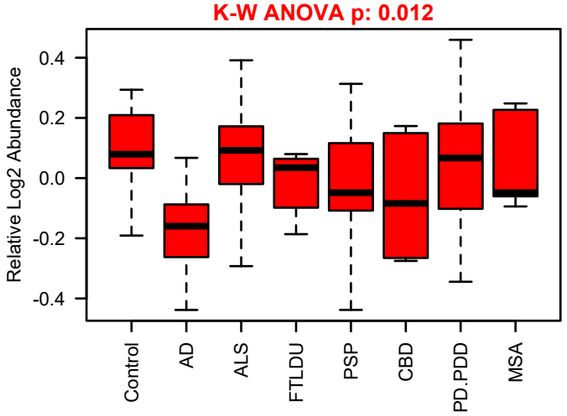

bicor=-0.27, p=0.0074
cor=-0.21, p=0.036
Relative Log2 Abundance
CERAD Score

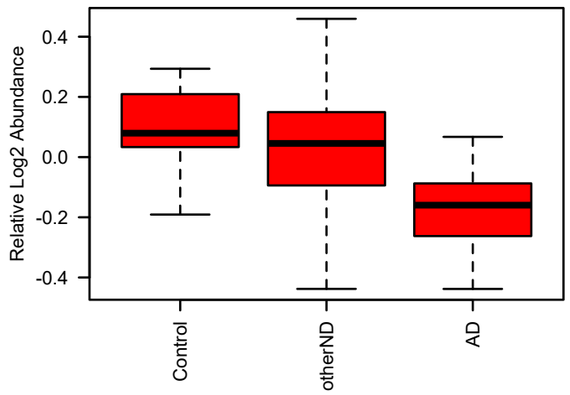

CD44 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1.7e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

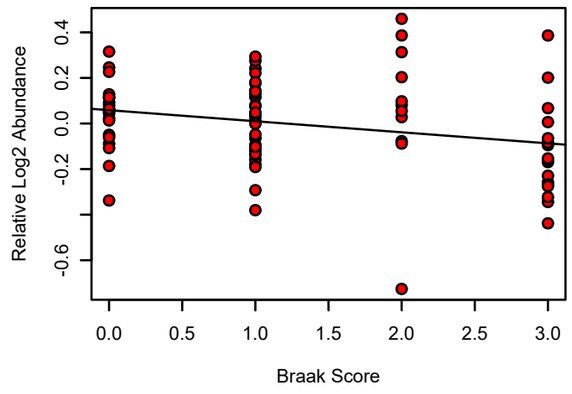

CD44 UPenn Mixed PRM
K-W ANOVA p: 0.0019
Relative Log2 Abundance
Control
otherND
AD

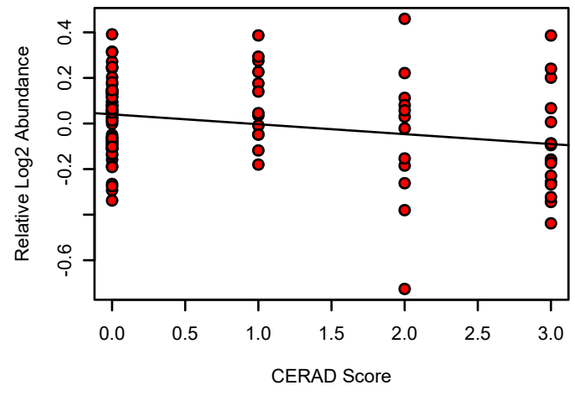

bicor=0.4, p=0.00015
cor=0.39, p=0.00025
Relative Log2 Abundance
Braak Score

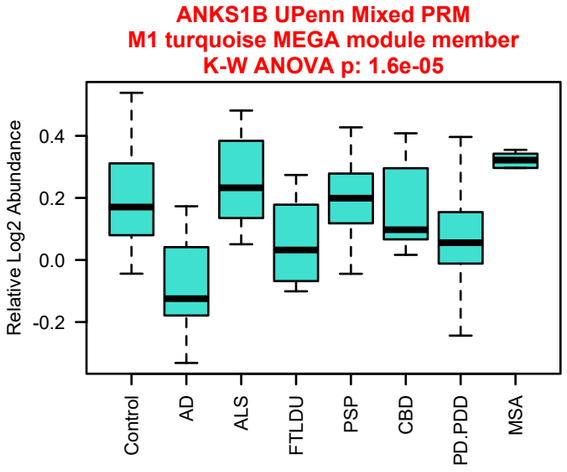

bicor=0.34, p=6e-04
cor=0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

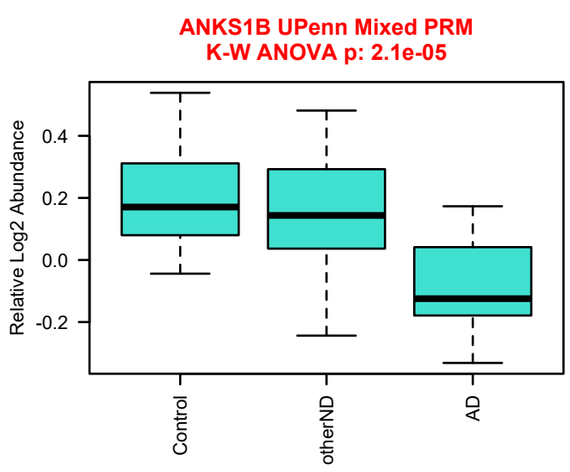

CRIP2 UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.012
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

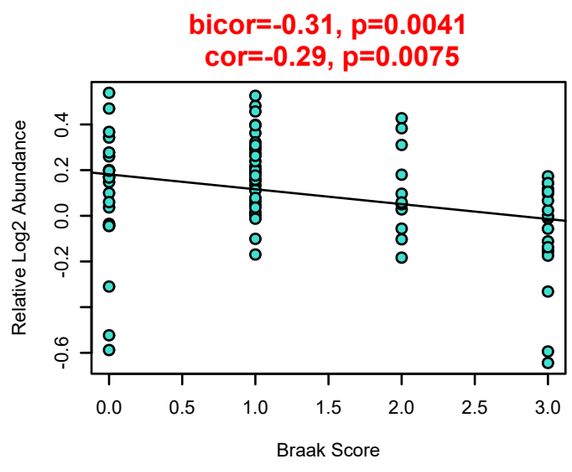

CRIP2 UPenn Mixed PRM
K-W ANOVA p: 0.00041
Relative Log2 Abundance
Control
otherND
AD

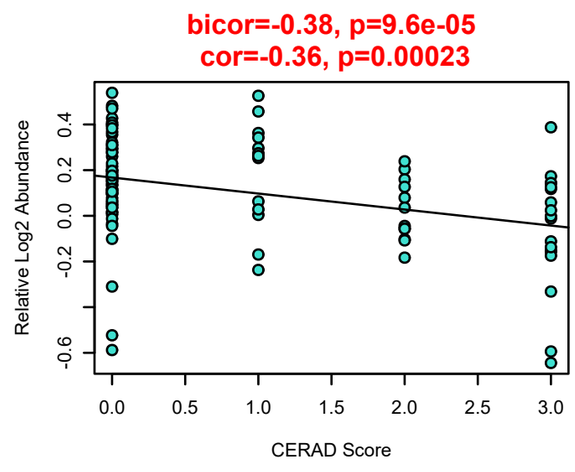

bicor=-0.28, p=0.0094
cor=-0.26, p=0.017
Relative Log2 Abundance
Braak Score

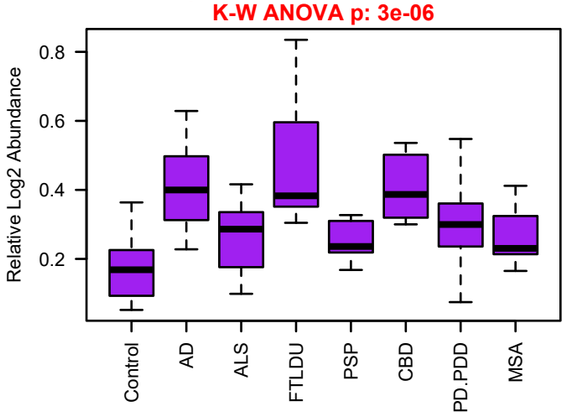

bicor=-0.25, p=0.012
cor=-0.26, p=0.009
Relative Log2 Abundance
CERAD Score

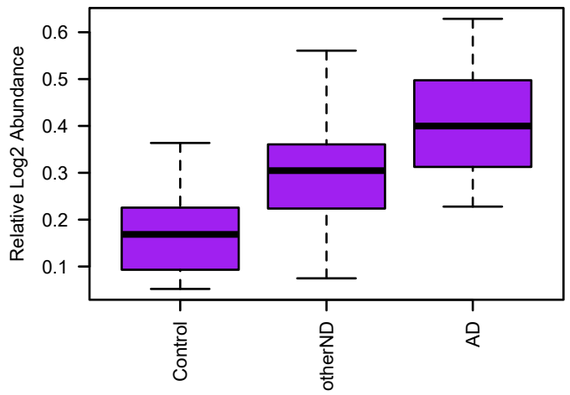

ANKS1B UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 1.6e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

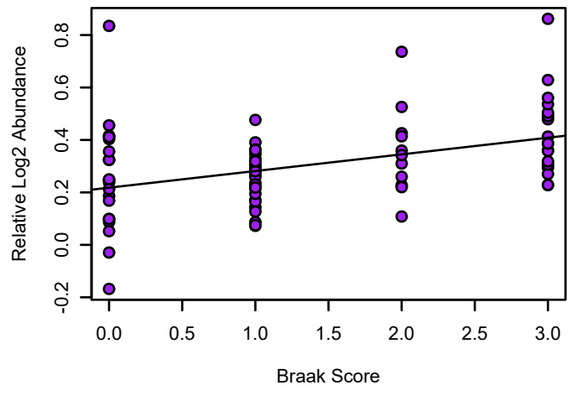

ANKS1B UPenn Mixed PRM
K-W ANOVA p: 2.1e-05
Relative Log2 Abundance
Control
otherND
AD

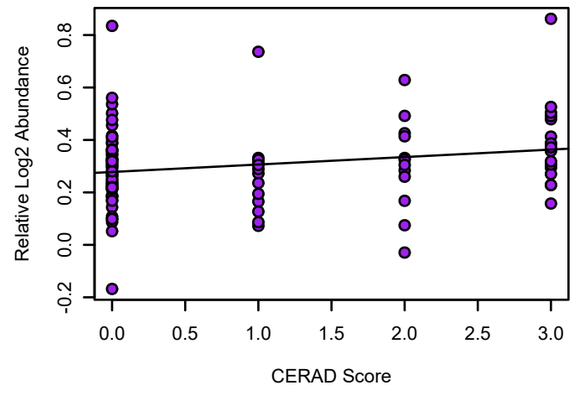

bicor=-0.31, p=0.0041
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

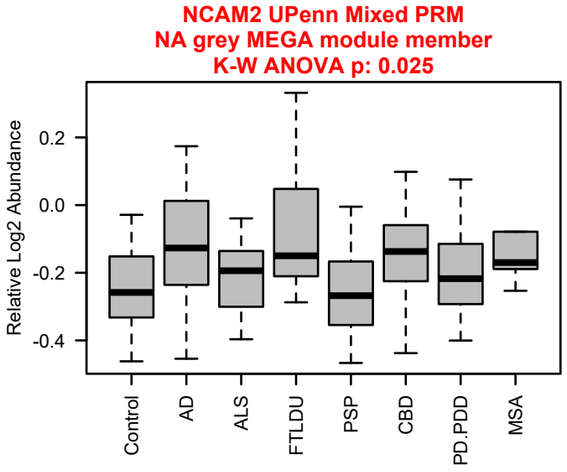

bicor=-0.38, p=9.6e-05
cor=-0.36, p=0.00023
Relative Log2 Abundance
CERAD Score

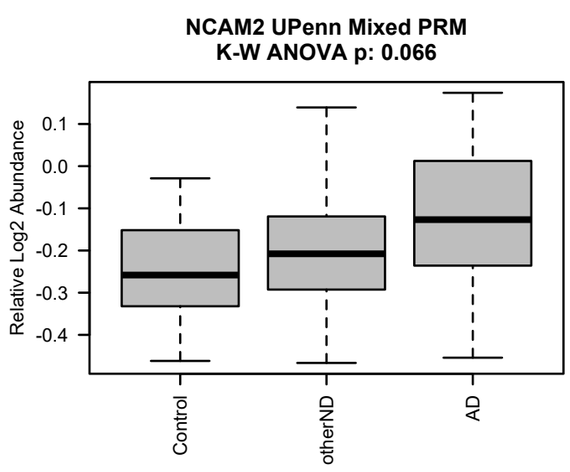

ANP32A UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 3e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

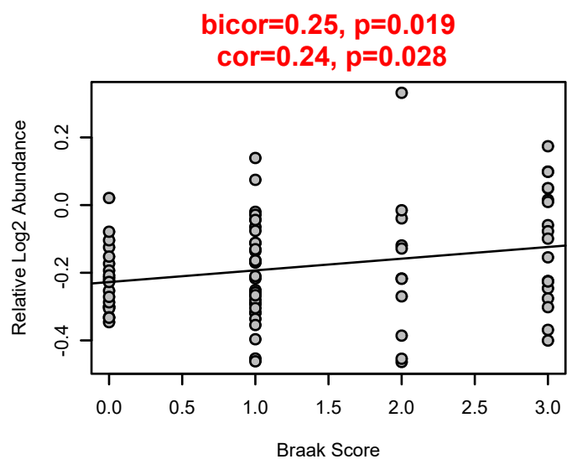

ANP32A UPenn Mixed PRM
K-W ANOVA p: 2.8e-05
Relative Log2 Abundance
Control
otherND
AD

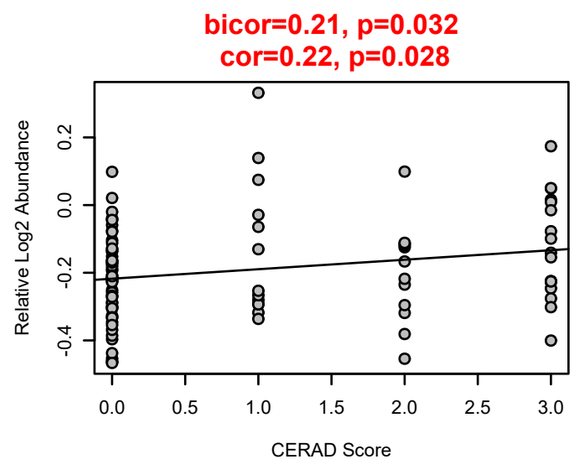

bicor=0.43, p=4.9e-05
cor=0.41, p=0.00011
Relative Log2 Abundance
Braak Score

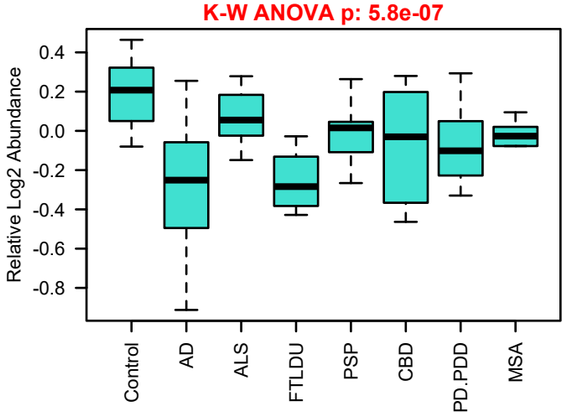

bicor=0.23, p=0.023
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

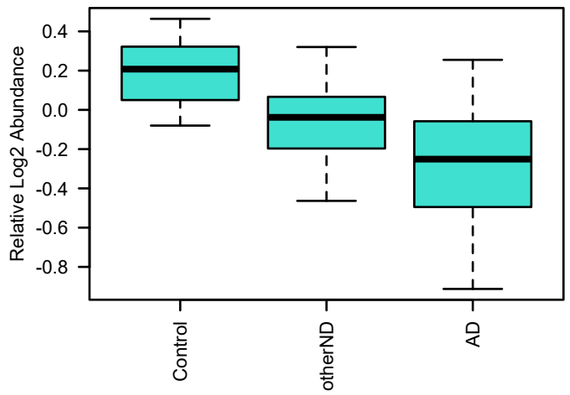

NCAM2 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.025
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

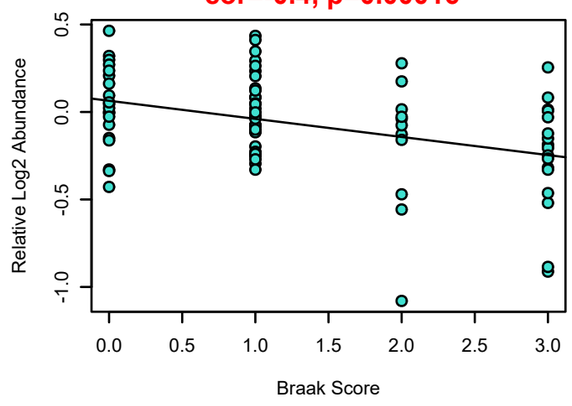

NCAM2 UPenn Mixed PRM
K-W ANOVA p: 0.066
Relative Log2 Abundance
Control
otherND
AD

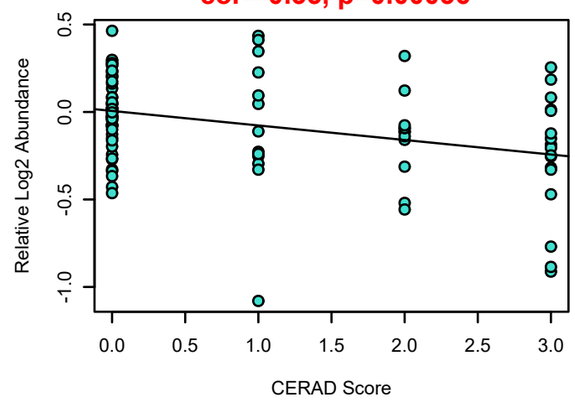

bicor=0.25, p=0.019
cor=0.24, p=0.028
Relative Log2 Abundance
Braak Score

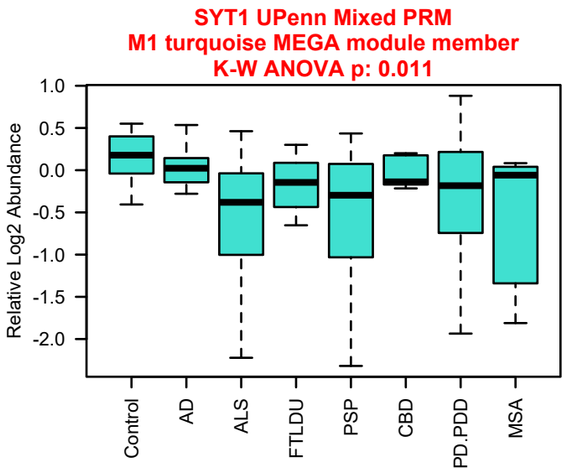

bicor=0.21, p=0.032
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

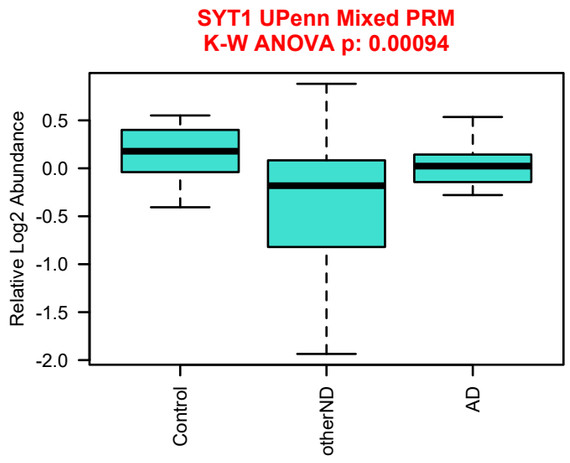

ACTN1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 5.8e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

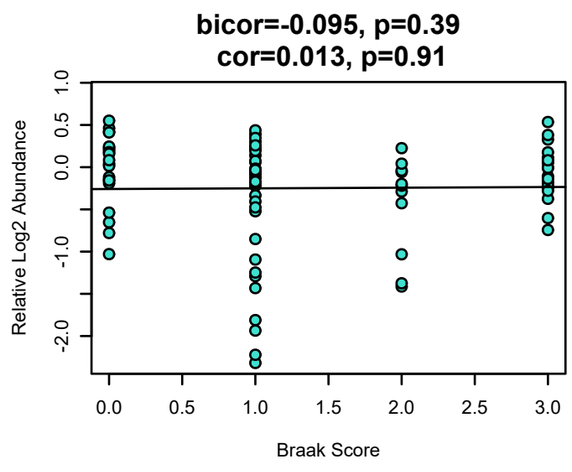

ACTN1 UPenn Mixed PRM
K-W ANOVA p: 2.7e-06
Relative Log2 Abundance
Control
otherND
AD

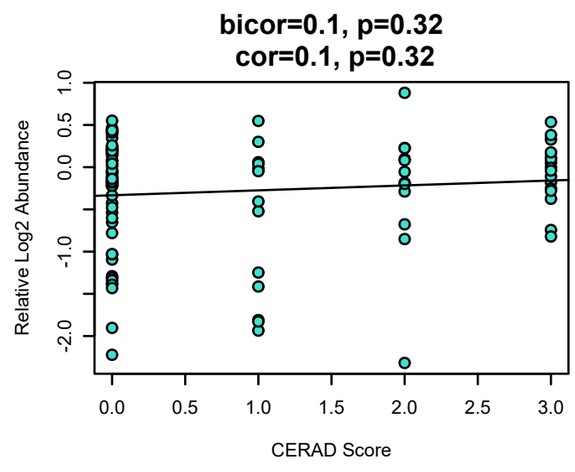

bicor=-0.36, p=0.00076
cor=-0.4, p=0.00016
Relative Log2 Abundance
Braak Score

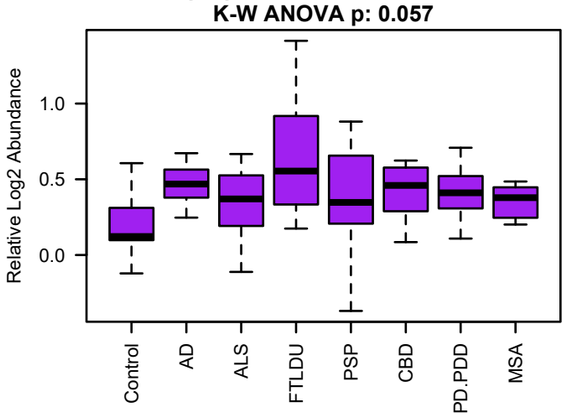

bicor=-0.34, p=0.00055
cor=-0.35, p=0.00036
Relative Log2 Abundance
CERAD Score

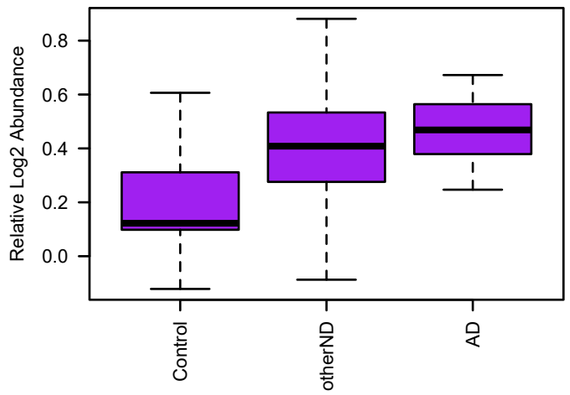

SYT1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.011
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

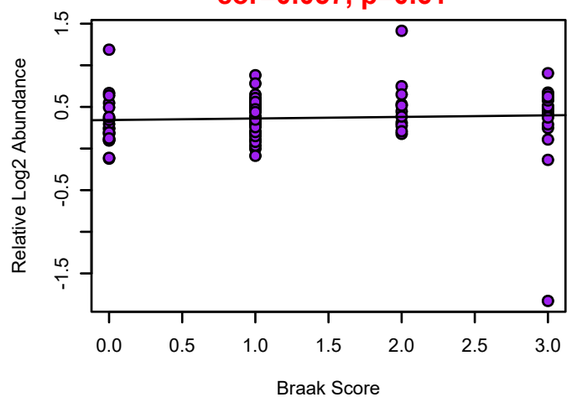

SYT1 UPenn Mixed PRM
K-W ANOVA p: 0.00094
Relative Log2 Abundance
Control
otherND
AD

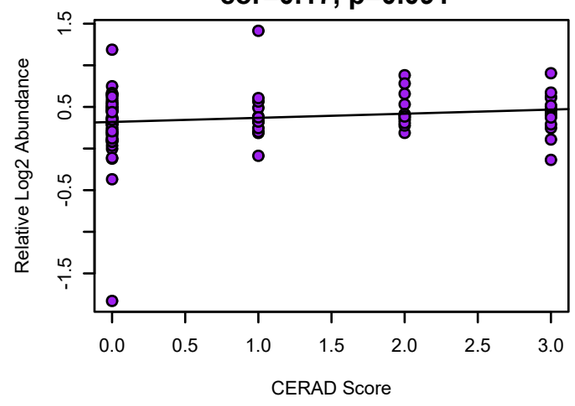

bicor=-0.095, p=0.39
cor=0.013, p=0.91
Relative Log2 Abundance
Braak Score

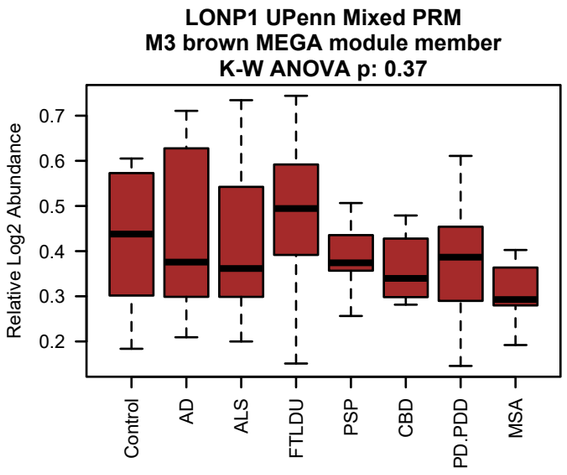

bicor=0.1, p=0.32
cor=0.1, p=0.32
Relative Log2 Abundance
CERAD Score

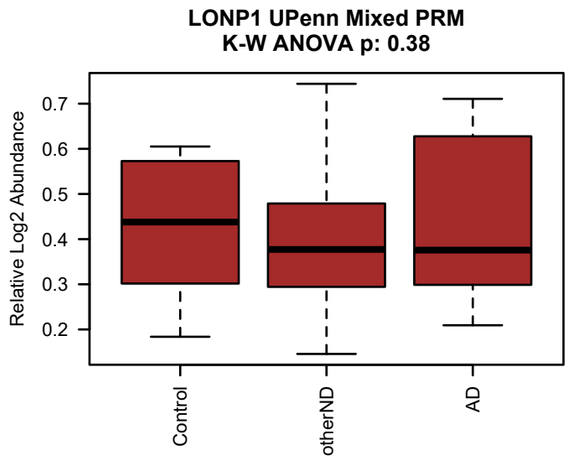

SRSF2 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.057
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

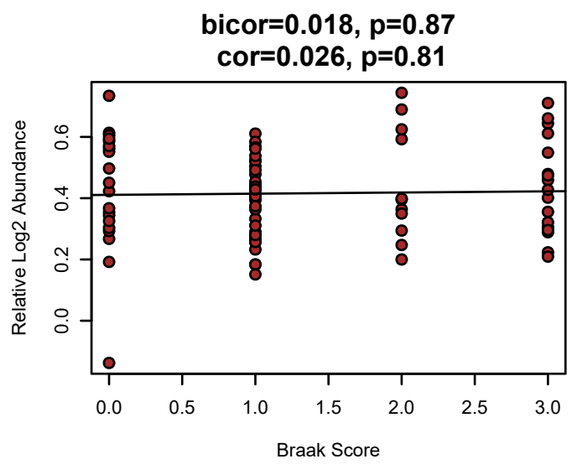

SRSF2 UPenn Mixed PRM
K-W ANOVA p: 0.063
Relative Log2 Abundance
Control
otherND
AD

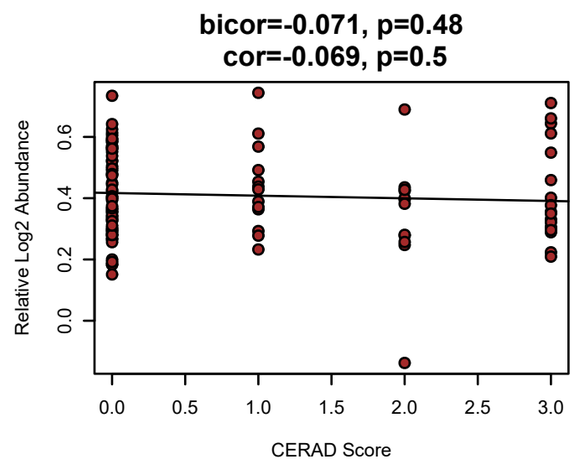

bicor=0.27, p=0.012
cor=0.057, p=0.61
Relative Log2 Abundance
Braak Score

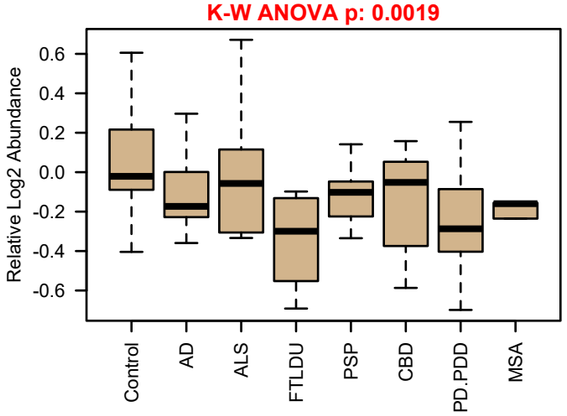

bicor=0.19, p=0.056
cor=0.17, p=0.091
Relative Log2 Abundance
CERAD Score

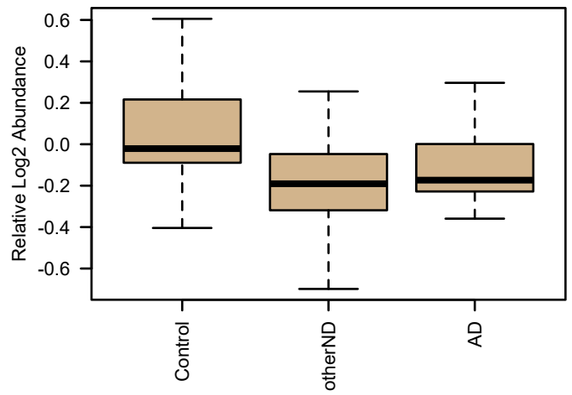

LONP1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.37
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

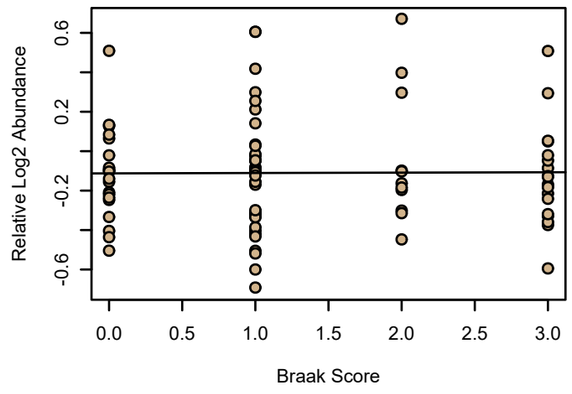

LONP1 UPenn Mixed PRM
K-W ANOVA p: 0.38
Relative Log2 Abundance
Control
otherND
AD

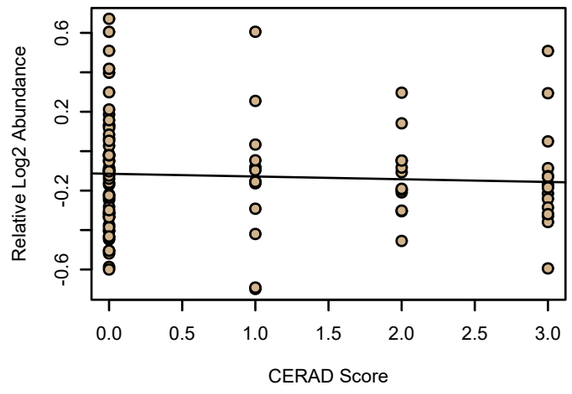

bicor=0.018, p=0.87
cor=0.026, p=0.81
Relative Log2 Abundance
Braak Score

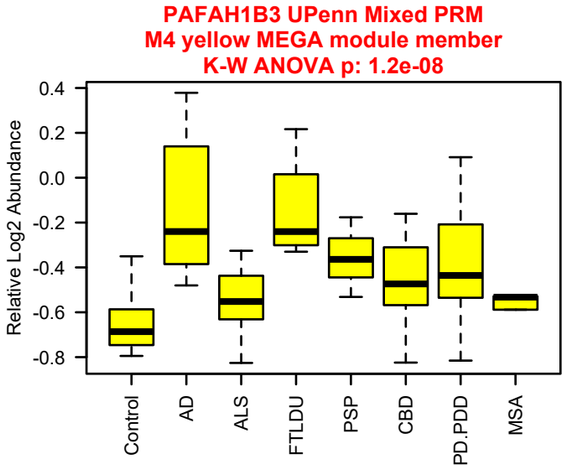

bicor=-0.071, p=0.48
cor=-0.069, p=0.5
Relative Log2 Abundance
CERAD Score

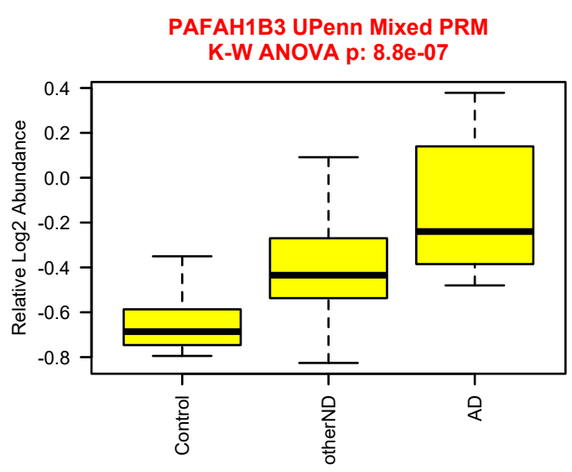

RPS5 UPenn Mixed PRM
M12 tan MEGA module member
K-W ANOVA p: 0.0019
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

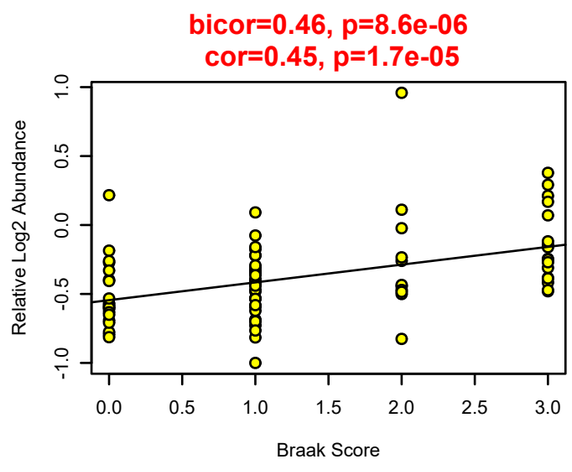

RPS5 UPenn Mixed PRM
K-W ANOVA p: 0.0019
Relative Log2 Abundance
Control
otherND
AD

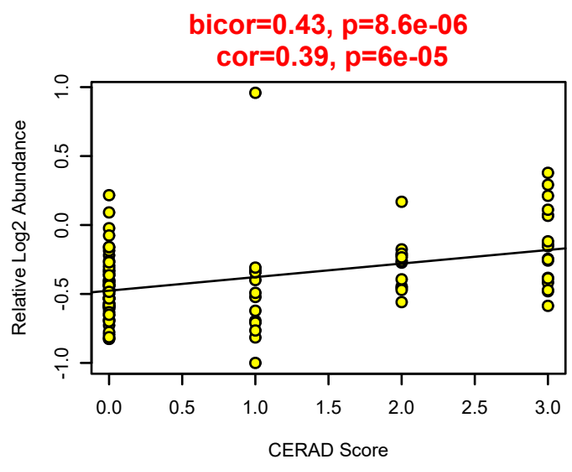

bicor=0.0041, p=0.97
cor=0.0071, p=0.95
Relative Log2 Abundance
Braak Score

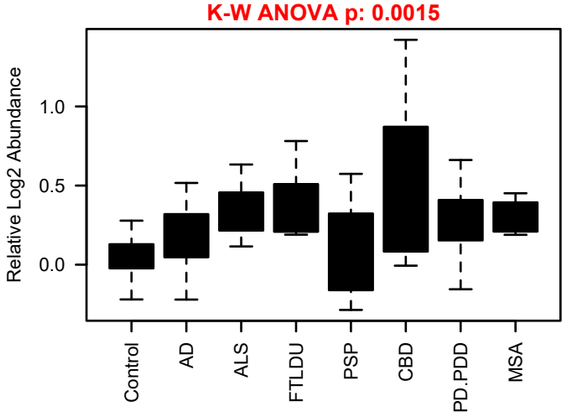

bicor=-0.055, p=0.59
cor=-0.059, p=0.56
Relative Log2 Abundance
CERAD Score

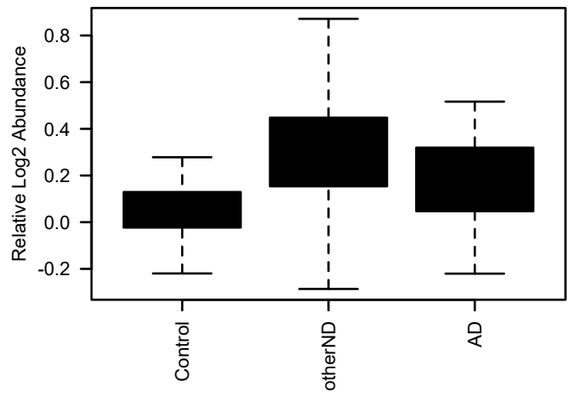

PAFAH1B3 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1.2e-08
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

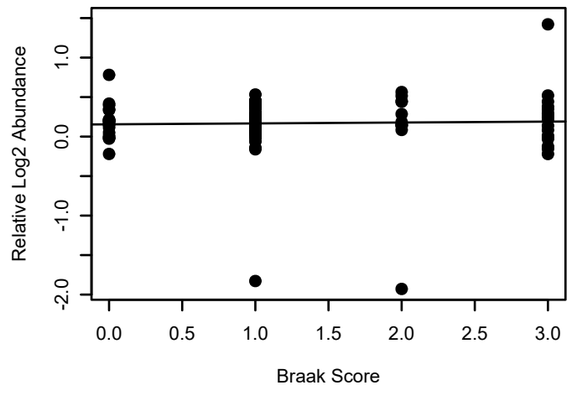

PAFAH1B3 UPenn Mixed PRM
K-W ANOVA p: 8.8e-07
Relative Log2 Abundance
Control
otherND
AD

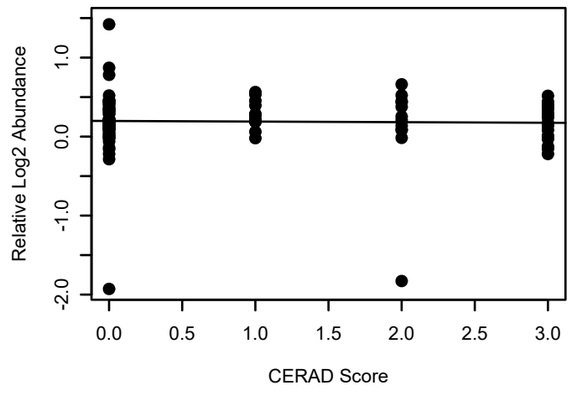

bicor=0.46, p=8.6e-06
cor=0.45, p=1.7e-05
Relative Log2 Abundance
Braak Score

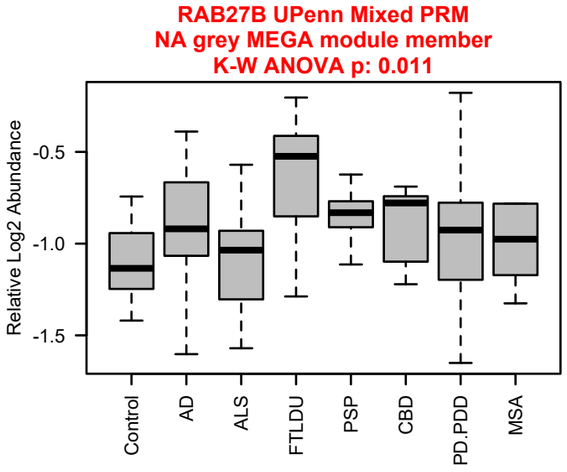

bicor=0.43, p=8.6e-06
cor=0.39, p=6e-05
Relative Log2 Abundance
CERAD Score

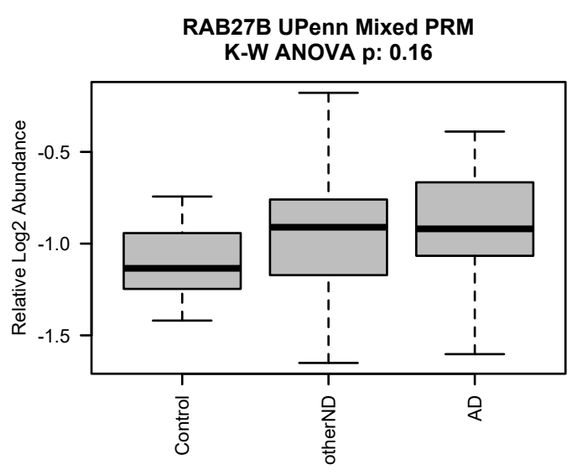

RPL18A UPenn Mixed PRM
M7 black MEGA module member
K-W ANOVA p: 0.0015
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

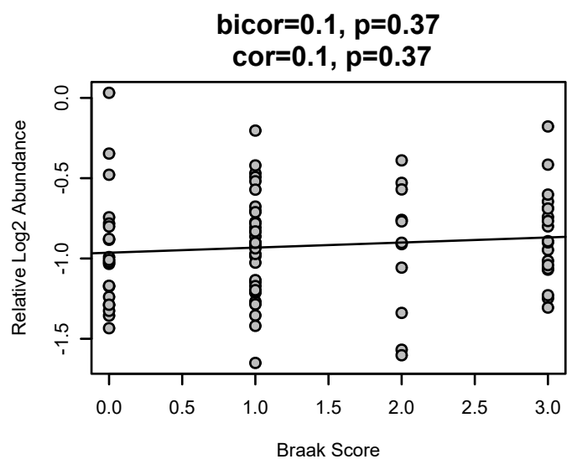

RPL18A UPenn Mixed PRM
K-W ANOVA p: 0.15
Relative Log2 Abundance
Control
otherND
AD

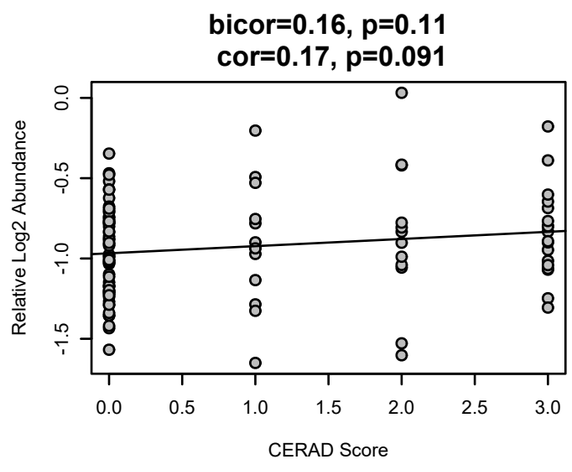

bicor=0.016, p=0.89
cor=0.031, p=0.78
Relative Log2 Abundance
Braak Score

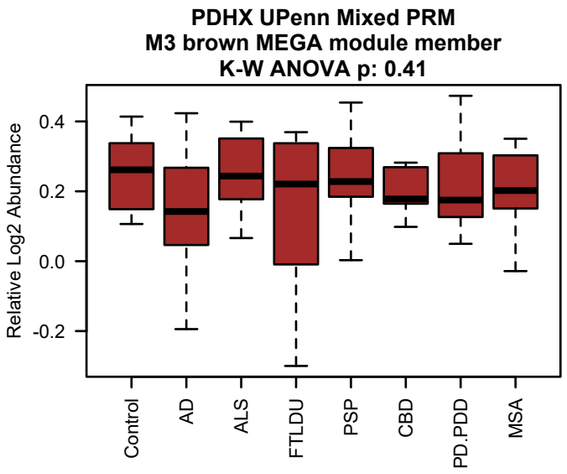

bicor=0.033, p=0.74
cor=-0.024, p=0.81
Relative Log2 Abundance
CERAD Score

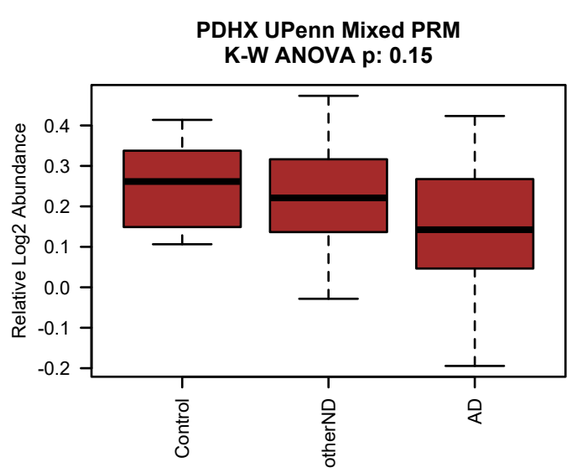

RAB27B UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.011
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

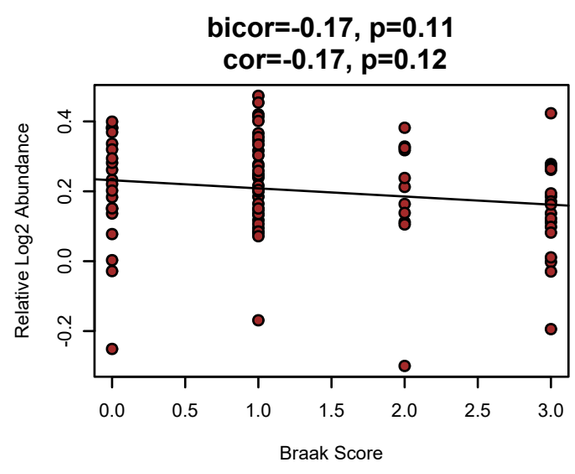

RAB27B UPenn Mixed PRM
K-W ANOVA p: 0.16
Relative Log2 Abundance
Control
otherND
AD

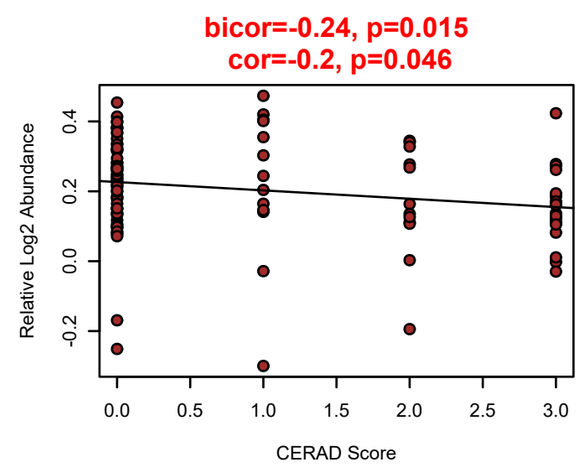

bicor=0.1, p=0.37
cor=0.1, p=0.37
Relative Log2 Abundance
Braak Score

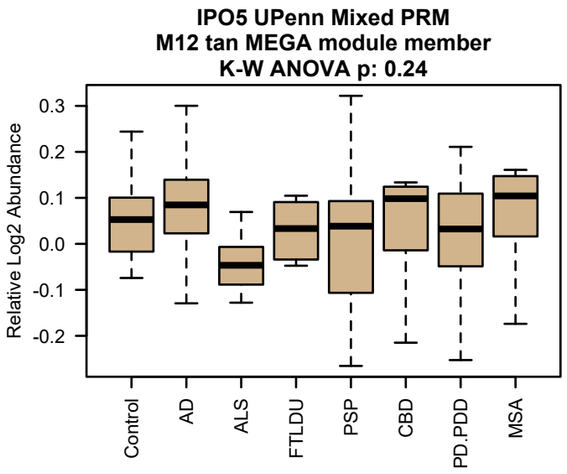

bicor=0.16, p=0.11
cor=0.17, p=0.091
Relative Log2 Abundance
CERAD Score

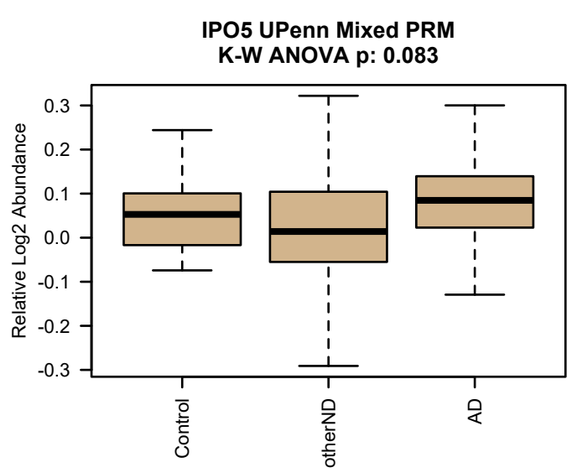

PDHX UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.41
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

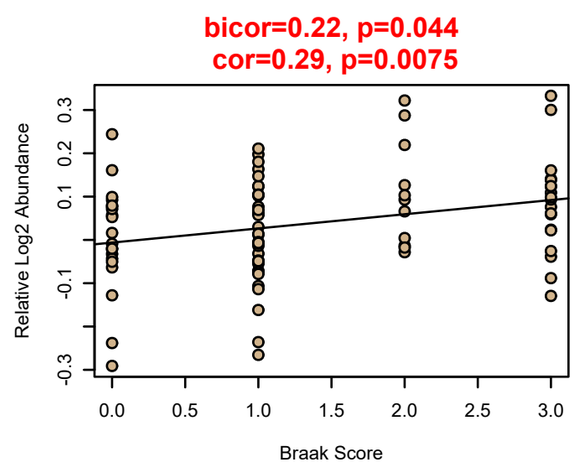

PDHX UPenn Mixed PRM
K-W ANOVA p: 0.15
Relative Log2 Abundance
Control
otherND
AD

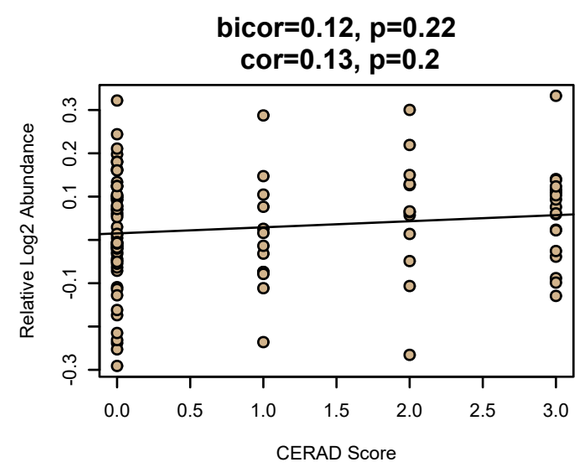

bicor=-0.17, p=0.11
cor=-0.17, p=0.12
Relative Log2 Abundance
Braak Score

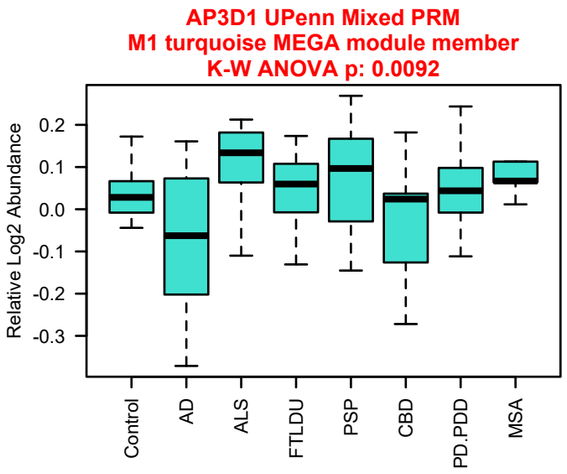

bicor=-0.24, p=0.015
cor=-0.2, p=0.046
Relative Log2 Abundance
CERAD Score

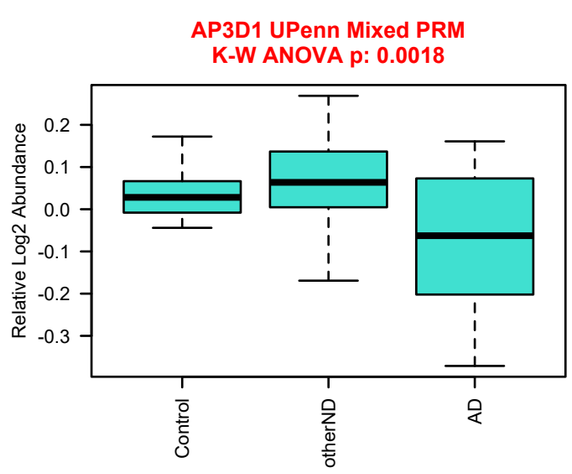

IPO5 UPenn Mixed PRM
M12 tan MEGA module member
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

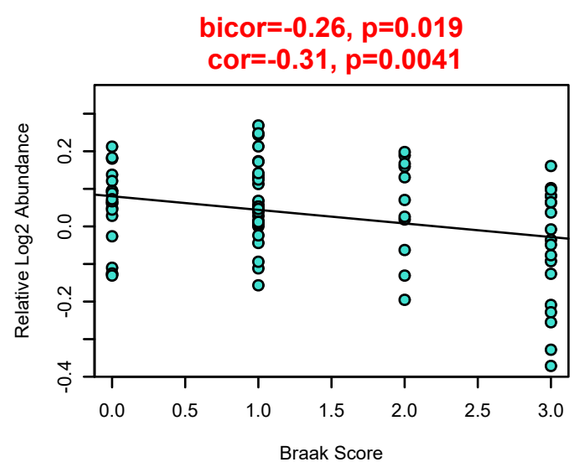

IPO5 UPenn Mixed PRM
K-W ANOVA p: 0.083
Relative Log2 Abundance
Control
otherND
AD

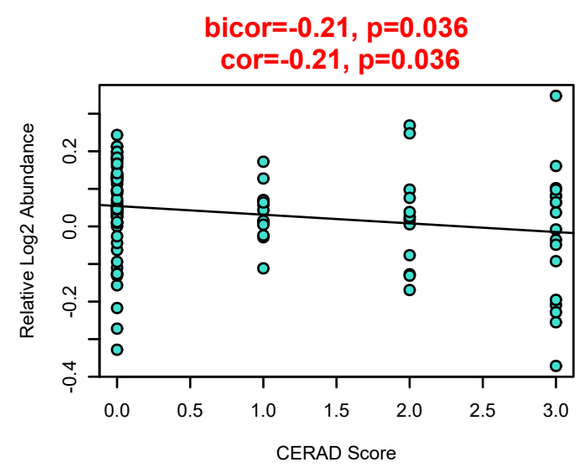

bicor=0.22, p=0.044
cor=0.29, p=0.0075
Relative Log2 Abundance
Braak Score

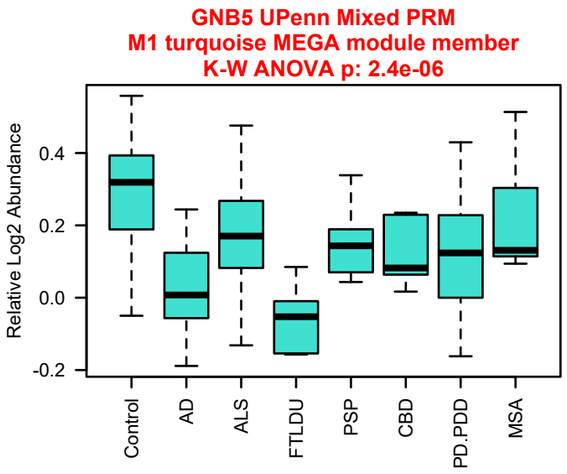

bicor=0.12, p=0.22
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

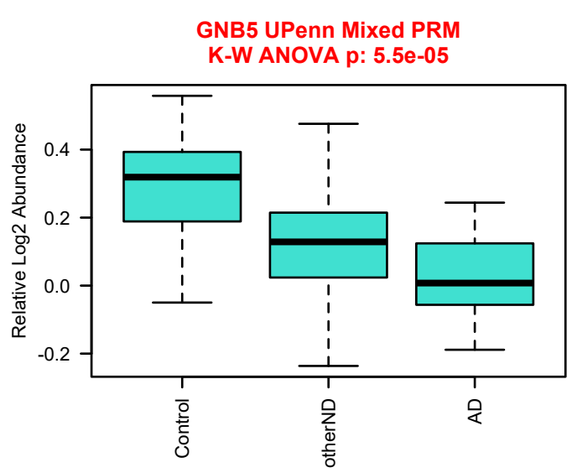

AP3D1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0092
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

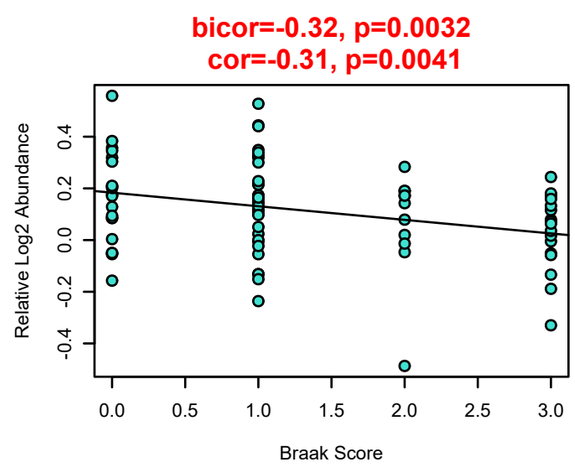

AP3D1 UPenn Mixed PRM
K-W ANOVA p: 0.0018
Relative Log2 Abundance
Control
otherND
AD

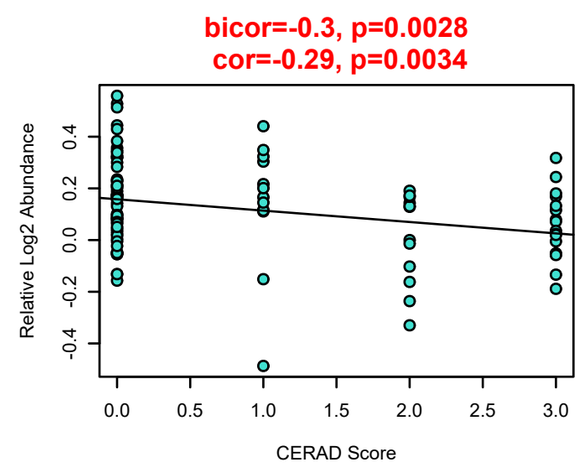

bicor=-0.26, p=0.019
cor=-0.31, p=0.0041
Relative Log2 Abundance
Braak Score

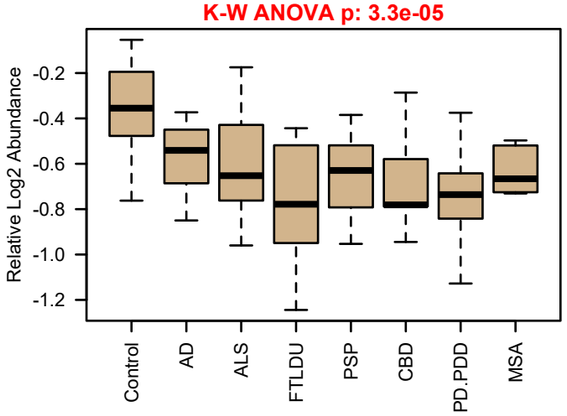

bicor=-0.21, p=0.036
cor=-0.21, p=0.036
Relative Log2 Abundance
CERAD Score

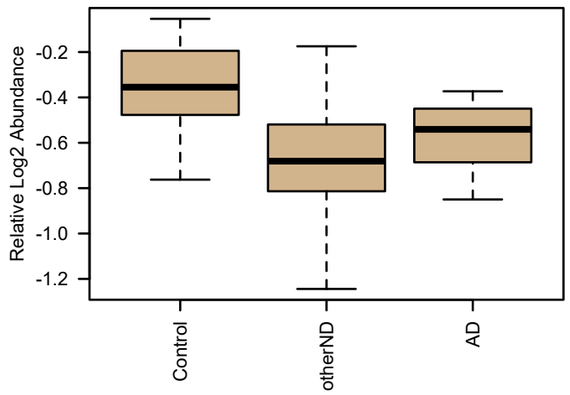

GNB5 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2.4e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

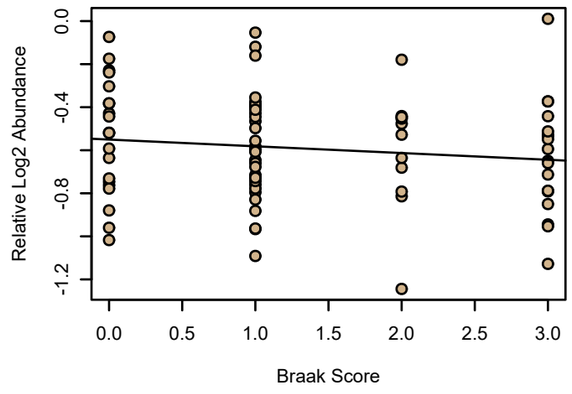

GNB5 UPenn Mixed PRM
K-W ANOVA p: 5.5e-05
Relative Log2 Abundance
Control
otherND
AD

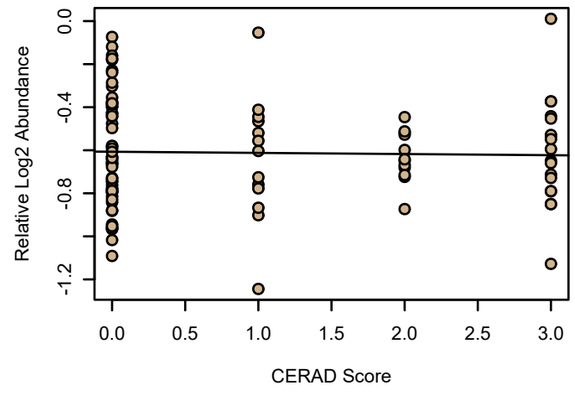

bicor=-0.32, p=0.0032
cor=-0.31, p=0.0041
Relative Log2 Abundance
Braak Score

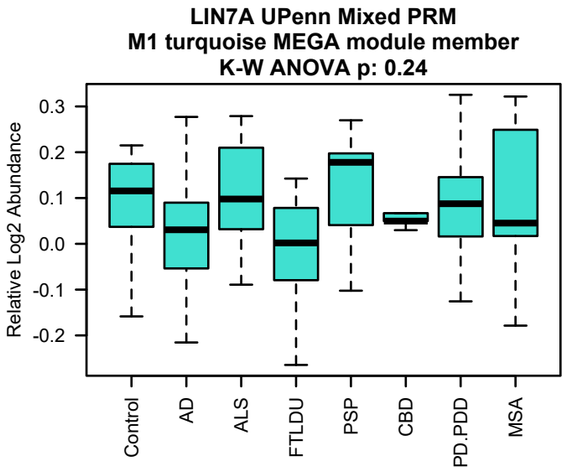

bicor=-0.3, p=0.0028
cor=-0.29, p=0.0034
Relative Log2 Abundance
CERAD Score

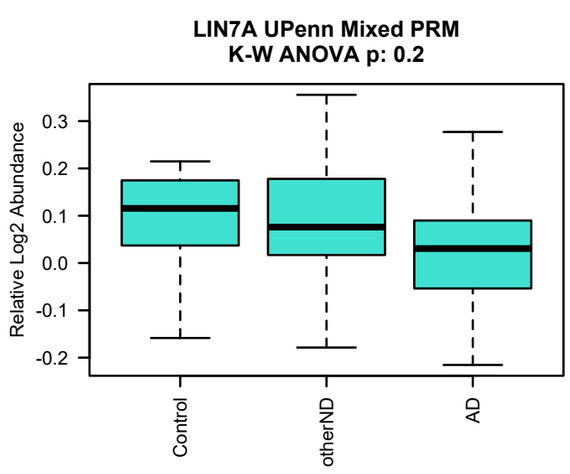

MGST3 UPenn Mixed PRM
M12 tan MEGA module member
K-W ANOVA p: 3.3e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

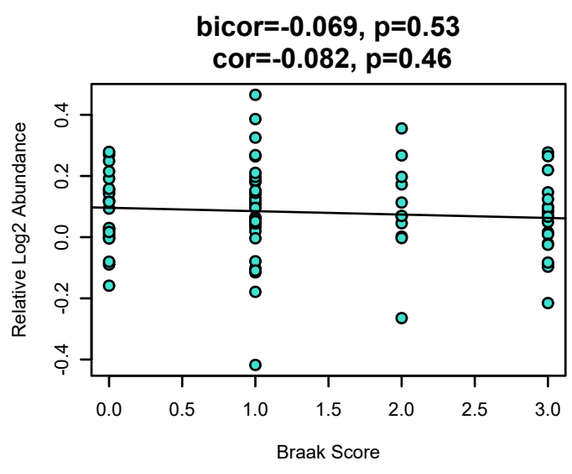

MGST3 UPenn Mixed PRM
K-W ANOVA p: 1.2e-06
Relative Log2 Abundance
Control
otherND
AD

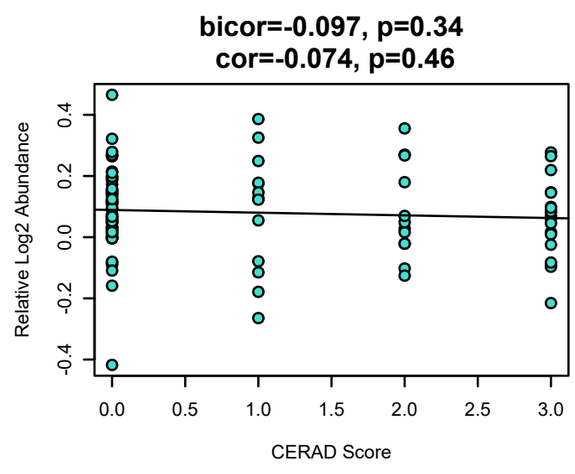

bicor=-0.12, p=0.26
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

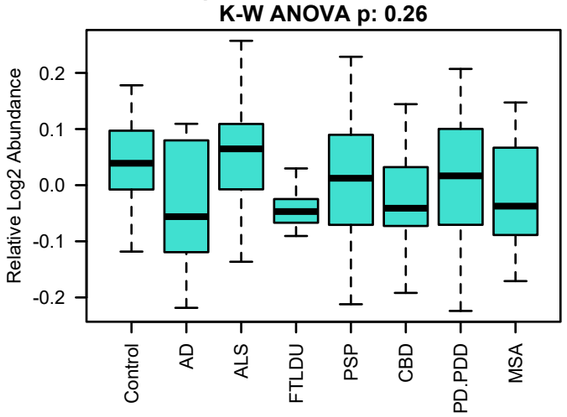

bicor=-0.023, p=0.82
cor=-0.026, p=0.8
Relative Log2 Abundance
CERAD Score

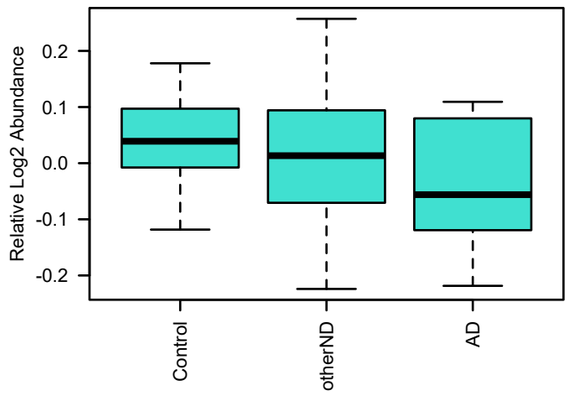

LIN7A UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

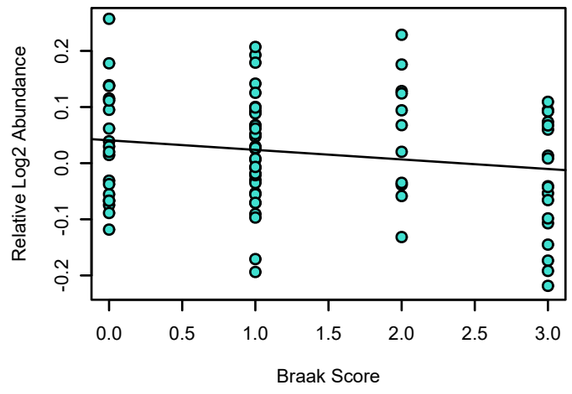

LIN7A UPenn Mixed PRM
K-W ANOVA p: 0.2
Relative Log2 Abundance
Control
otherND
AD

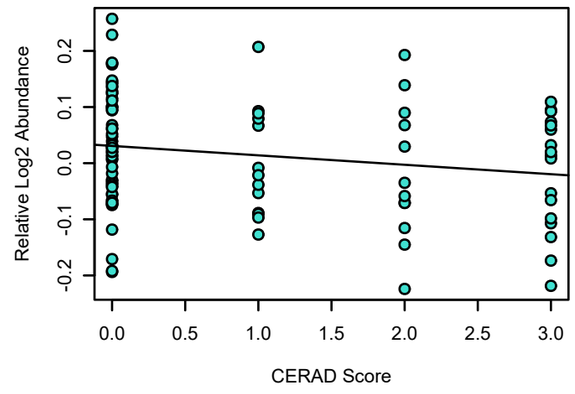

bicor=-0.069, p=0.53
cor=-0.082, p=0.46
Relative Log2 Abundance
Braak Score

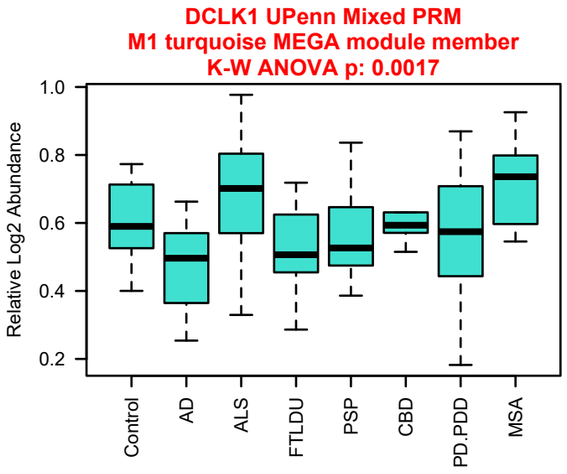

bicor=-0.097, p=0.34
cor=-0.074, p=0.46
Relative Log2 Abundance
CERAD Score

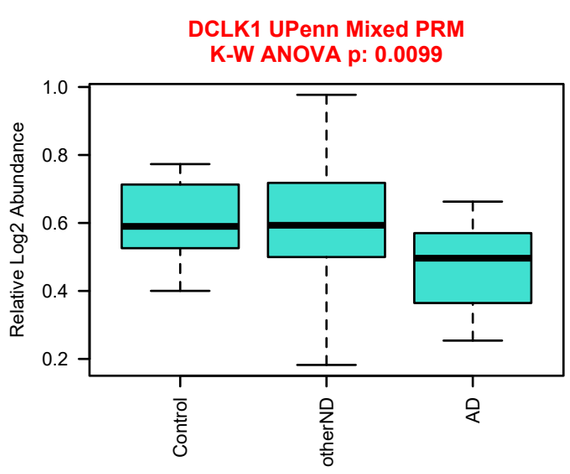

SPTBN2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.26
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

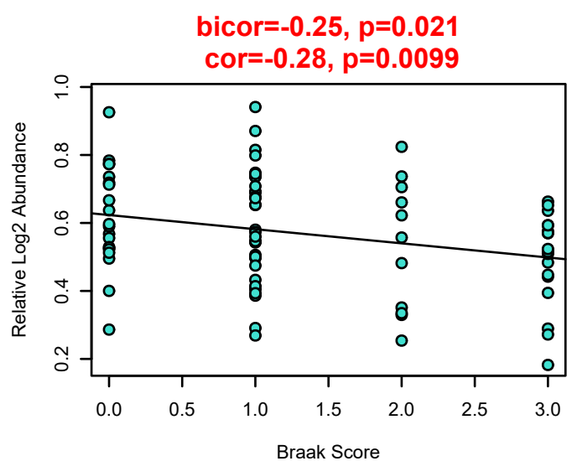

SPTBN2 UPenn Mixed PRM
K-W ANOVA p: 0.15
Relative Log2 Abundance
Control
otherND
AD

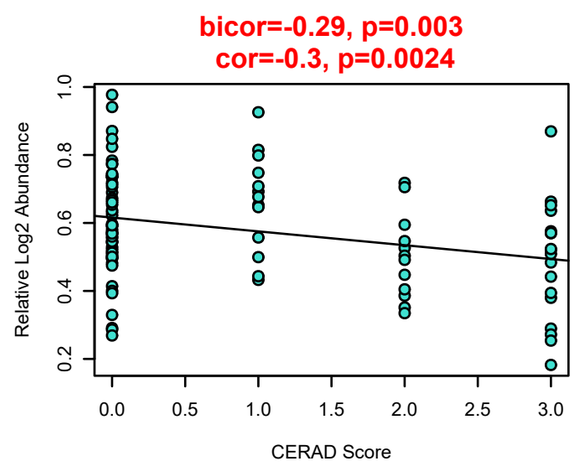

bicor=-0.16, p=0.16
cor=-0.18, p=0.1
Relative Log2 Abundance
Braak Score

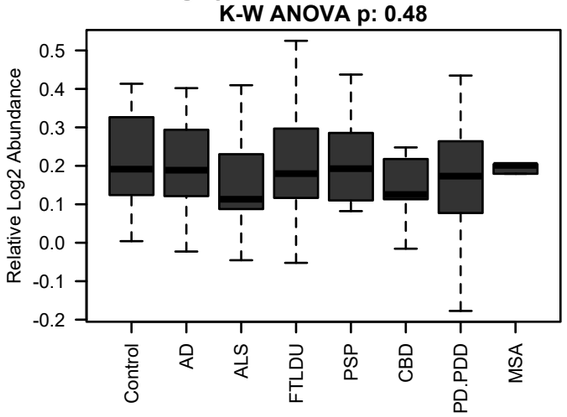

bicor=-0.18, p=0.068
cor=-0.19, p=0.058
Relative Log2 Abundance
CERAD Score

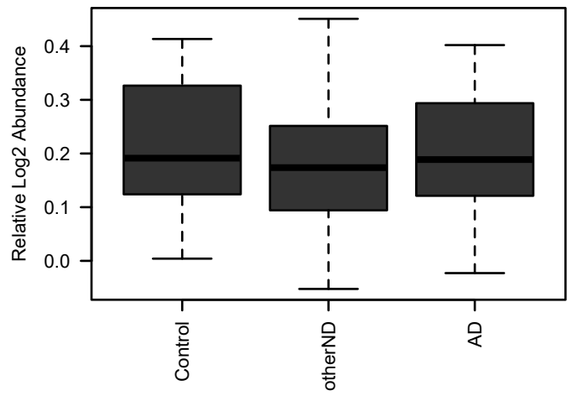

DCLK1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0017
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

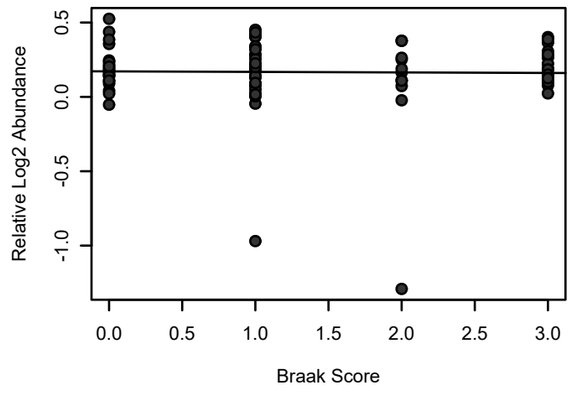

DCLK1 UPenn Mixed PRM
K-W ANOVA p: 0.0099
Relative Log2 Abundance
Control
otherND
AD

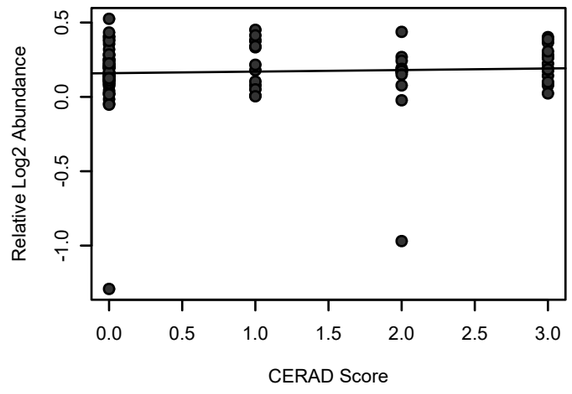

bicor=-0.25, p=0.021
cor=-0.28, p=0.0099
Relative Log2 Abundance
Braak Score

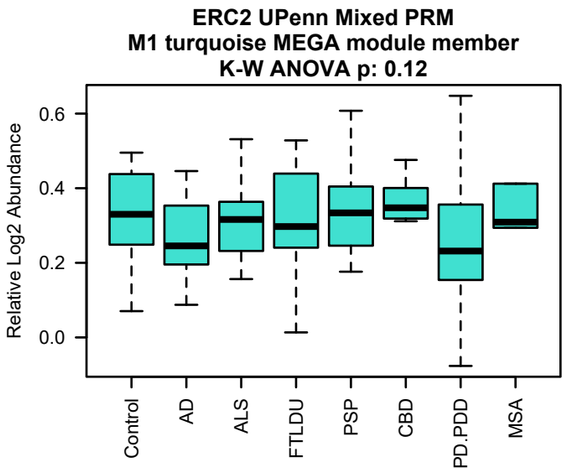

bicor=-0.29, p=0.003
cor=-0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

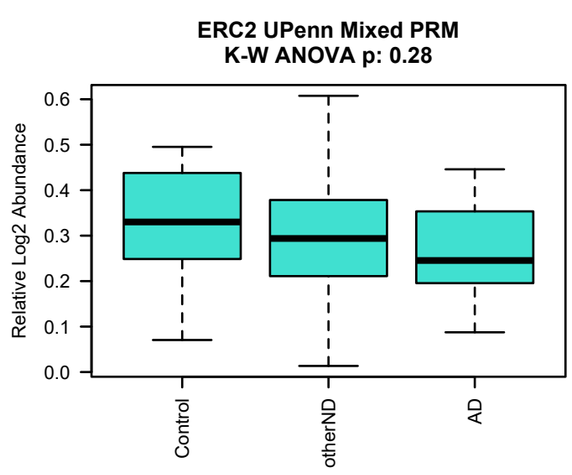

ERC1 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.48
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

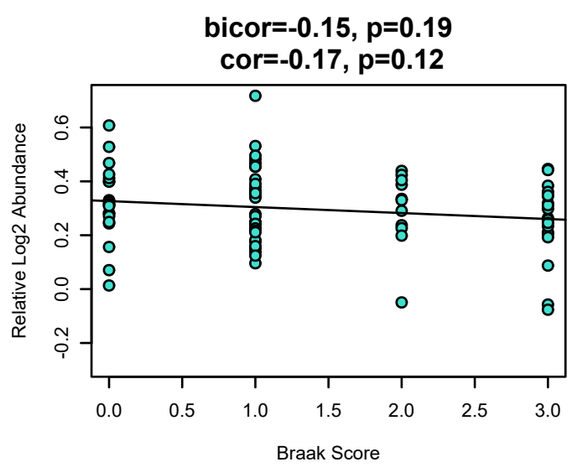

ERC1 UPenn Mixed PRM
K-W ANOVA p: 0.56
Relative Log2 Abundance
Control
otherND
AD

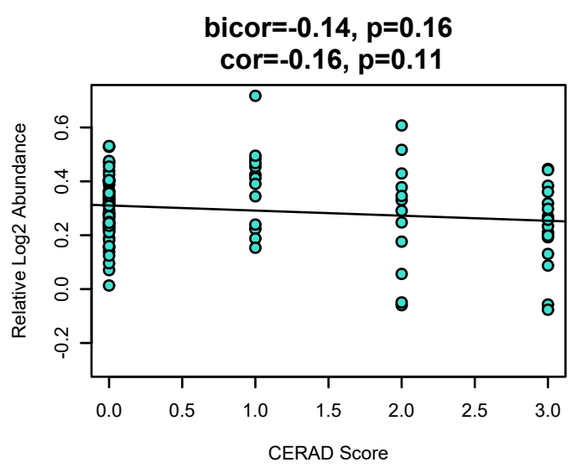

bicor=0.051, p=0.65
cor=-0.016, p=0.89
Relative Log2 Abundance
Braak Score

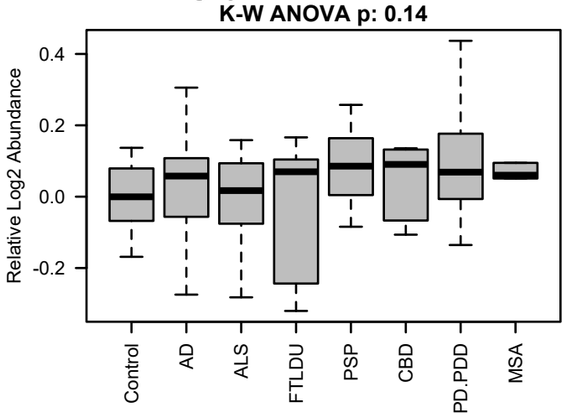

bicor=0.11, p=0.28
cor=0.056, p=0.58
Relative Log2 Abundance
CERAD Score

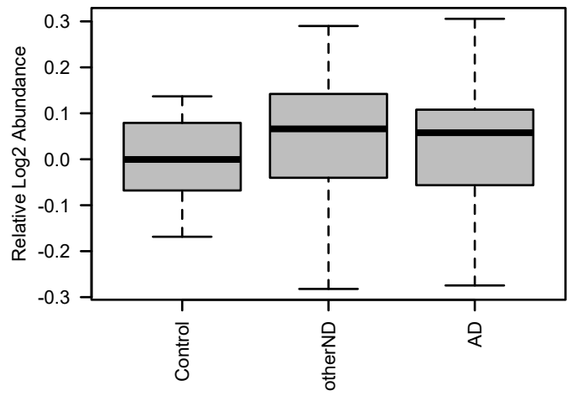

ERC2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.12
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

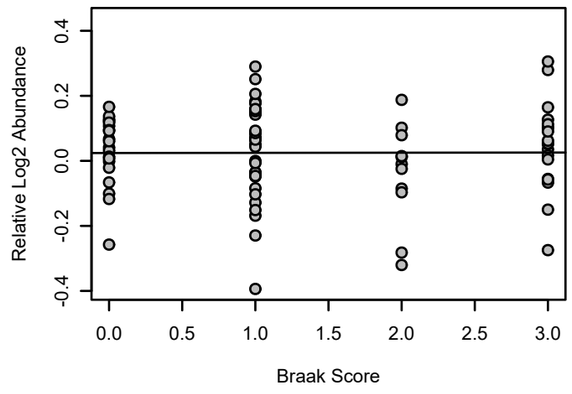

ERC2 UPenn Mixed PRM
K-W ANOVA p: 0.28
Relative Log2 Abundance
Control
otherND
AD

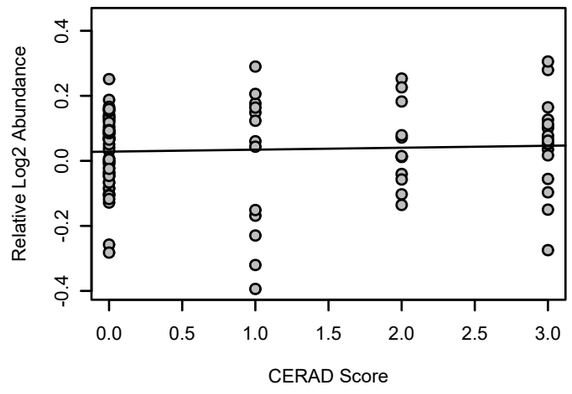

bicor=-0.15, p=0.19
cor=-0.17, p=0.12
Relative Log2 Abundance
Braak Score

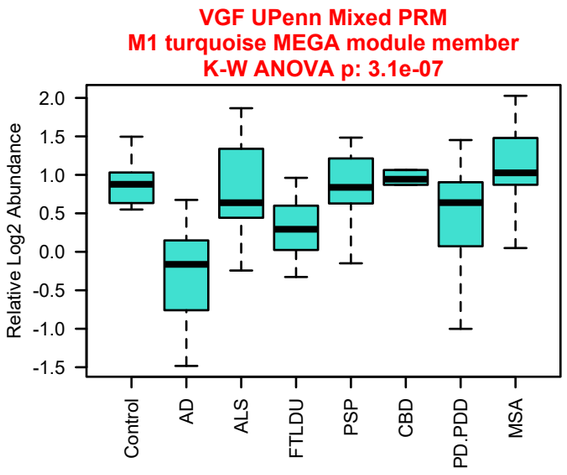

bicor=-0.14, p=0.16
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

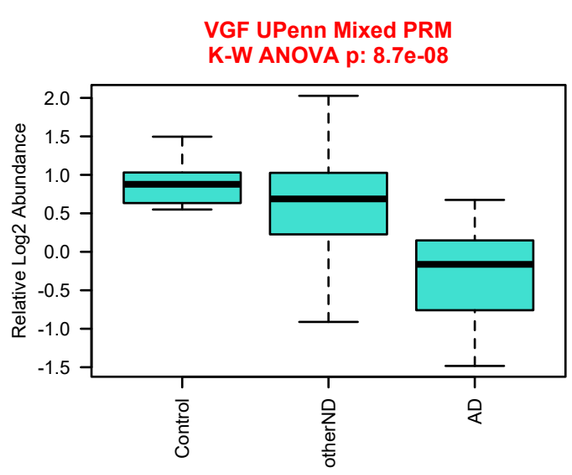

PFDN6 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.14
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

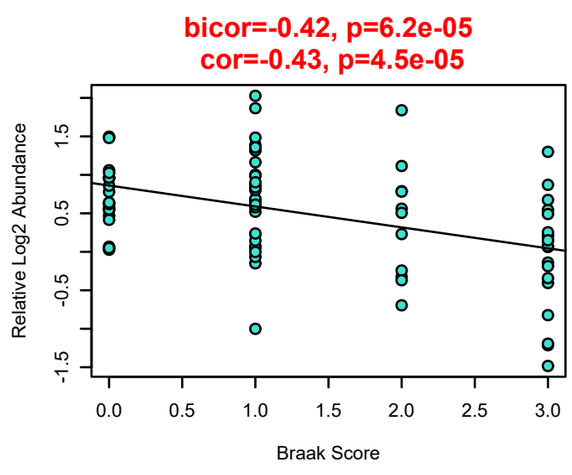

PFDN6 UPenn Mixed PRM
K-W ANOVA p: 0.21
Relative Log2 Abundance
Control
otherND
AD

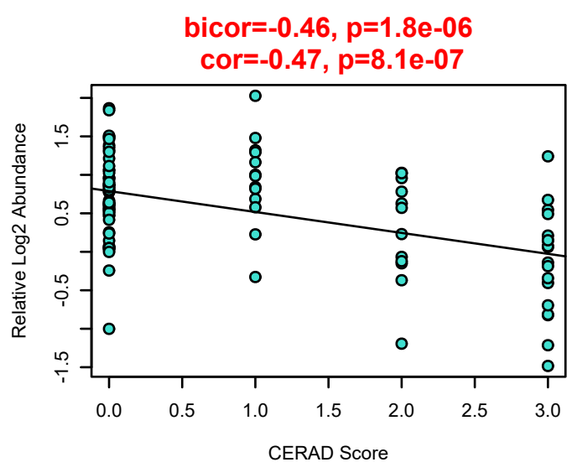

bicor=-0.038, p=0.73
cor=0.0037, p=0.97
Relative Log2 Abundance
Braak Score

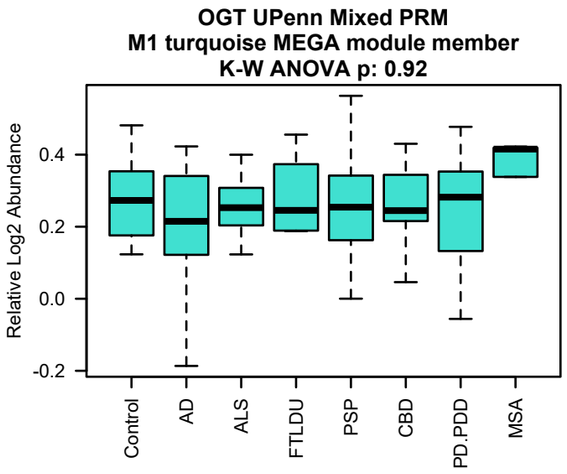

bicor=0.063, p=0.53
cor=0.054, p=0.59
Relative Log2 Abundance
CERAD Score

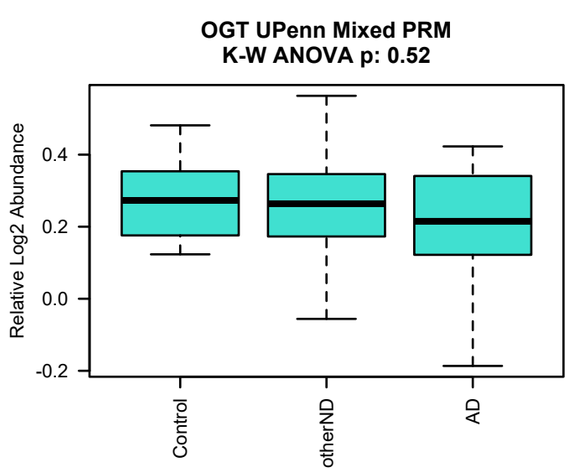

VGF UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 3.1e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

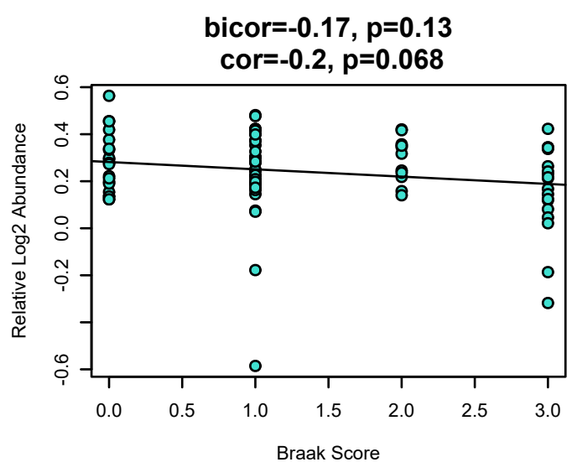

VGF UPenn Mixed PRM
K-W ANOVA p: 8.7e-08
Relative Log2 Abundance
Control
otherND
AD

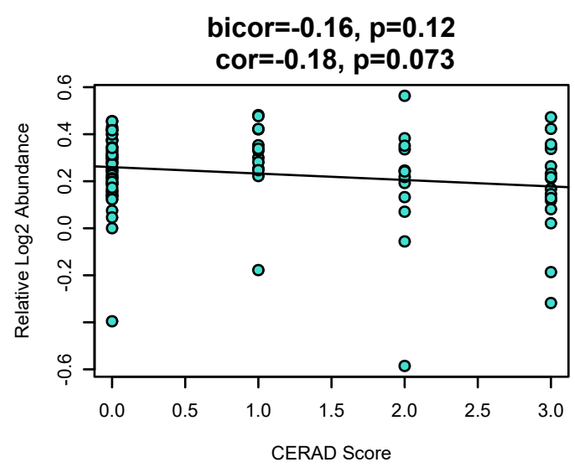

bicor=-0.42, p=6.2e-05
cor=-0.43, p=4.5e-05
Relative Log2 Abundance
Braak Score

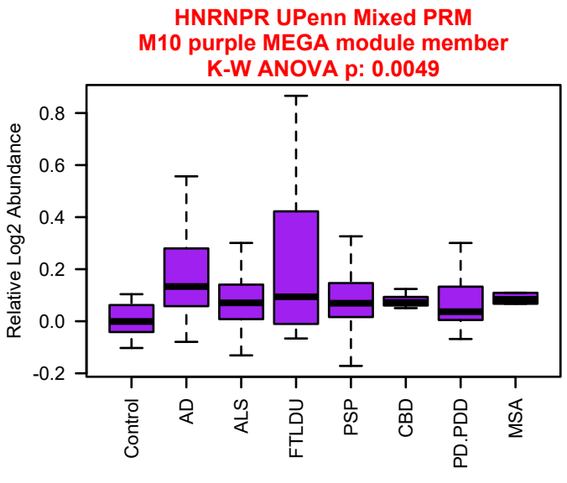

bicor=-0.46, p=1.8e-06
cor=-0.47, p=8.1e-07
Relative Log2 Abundance
CERAD Score

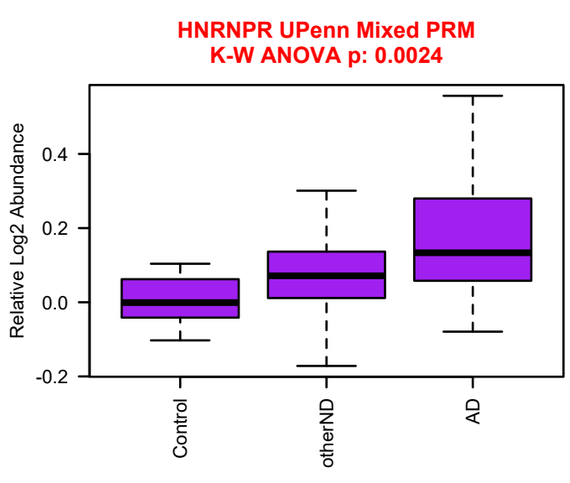

OGT UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.92
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

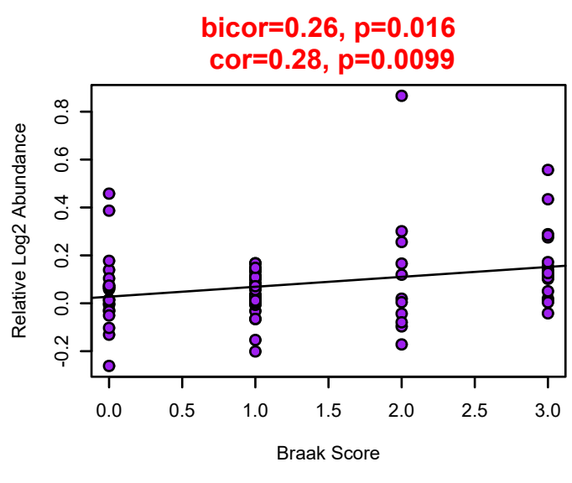

OGT UPenn Mixed PRM
K-W ANOVA p: 0.52
Relative Log2 Abundance
Control
otherND
AD

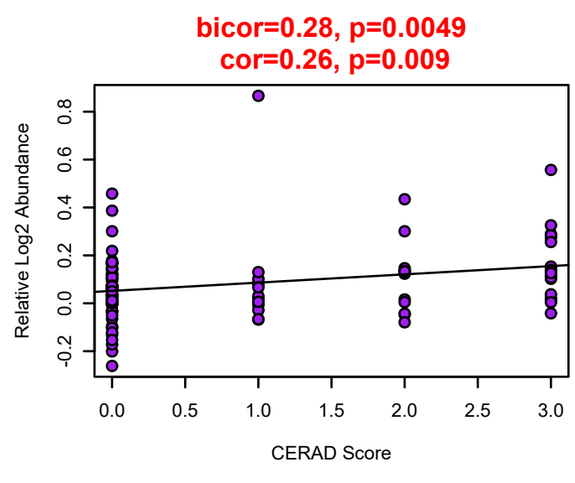

bicor=-0.17, p=0.13
cor=-0.2, p=0.068
Relative Log2 Abundance
Braak Score

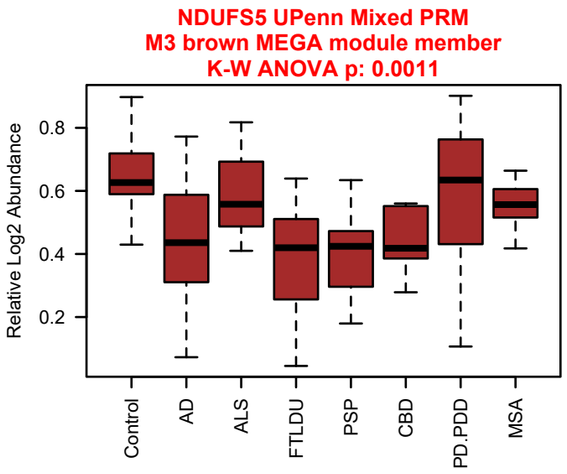

bicor=-0.16, p=0.12
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

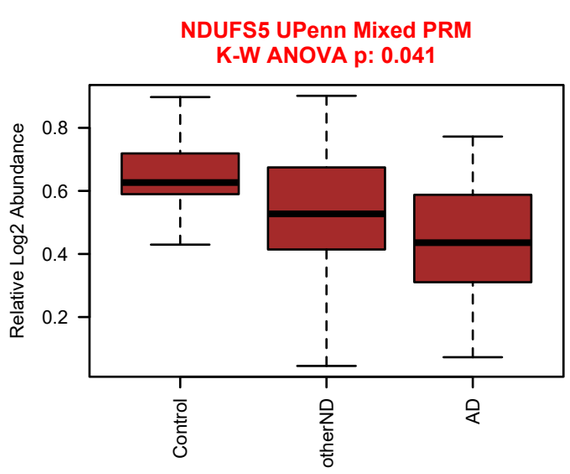

HNRNPR UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.0049
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

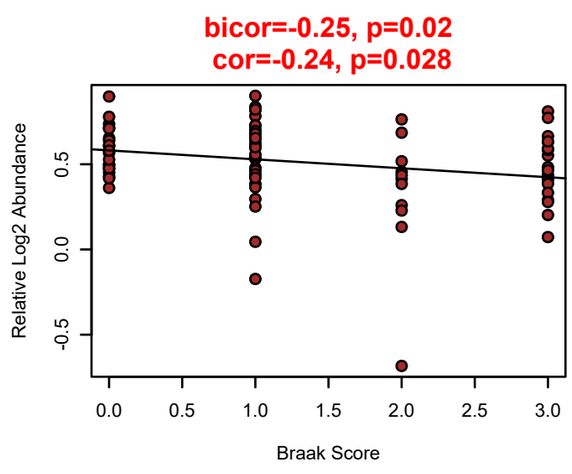

HNRNPR UPenn Mixed PRM
K-W ANOVA p: 0.0024
Relative Log2 Abundance
Control
otherND
AD

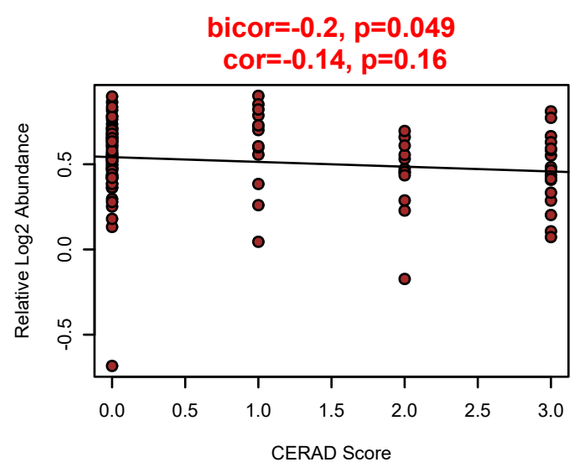

bicor=0.26, p=0.016
cor=0.28, p=0.0099
Relative Log2 Abundance
Braak Score

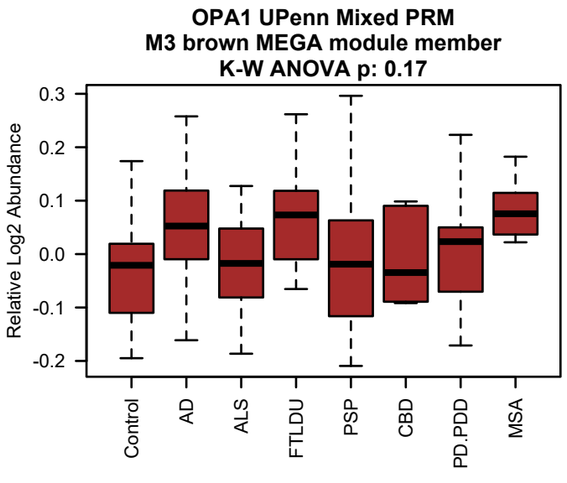

bicor=0.28, p=0.0049
cor=0.26, p=0.009
Relative Log2 Abundance
CERAD Score

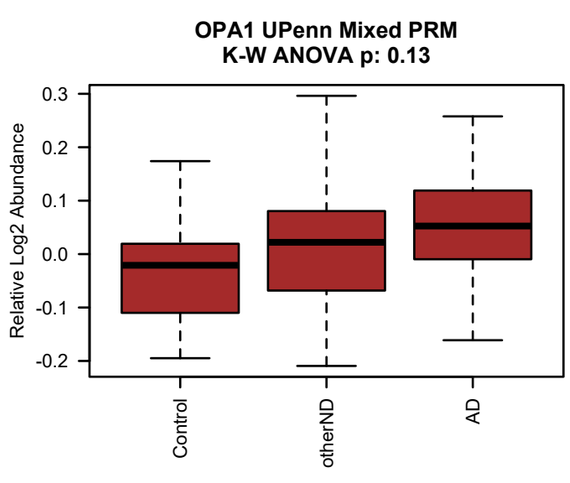

NDUFS5 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0011
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

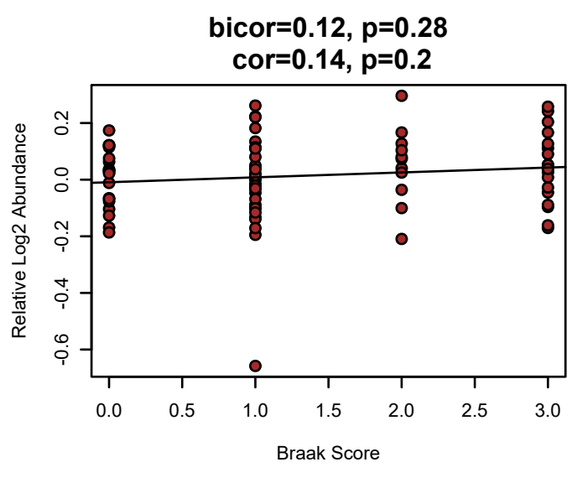

NDUFS5 UPenn Mixed PRM
K-W ANOVA p: 0.041
Relative Log2 Abundance
Control
otherND
AD

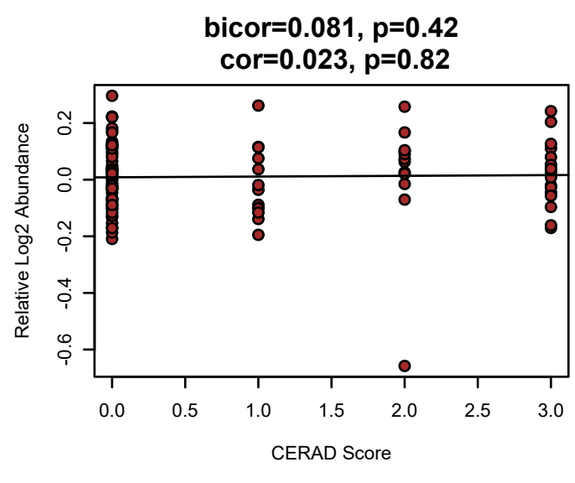

bicor=-0.25, p=0.02
cor=-0.24, p=0.028
Relative Log2 Abundance
Braak Score

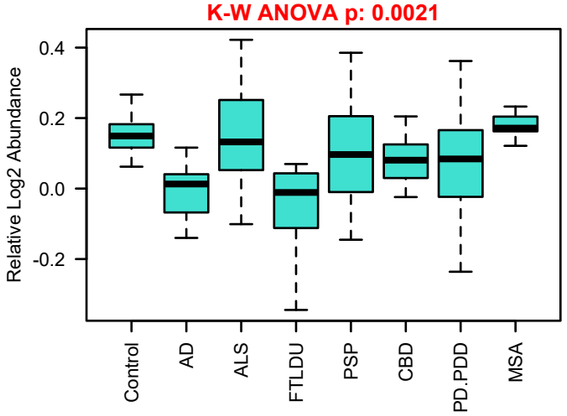

bicor=-0.2, p=0.049
cor=-0.14, p=0.16
Relative Log2 Abundance
CERAD Score

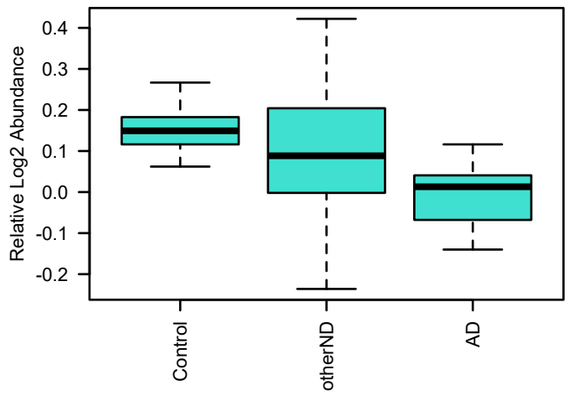

OPA1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.17
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

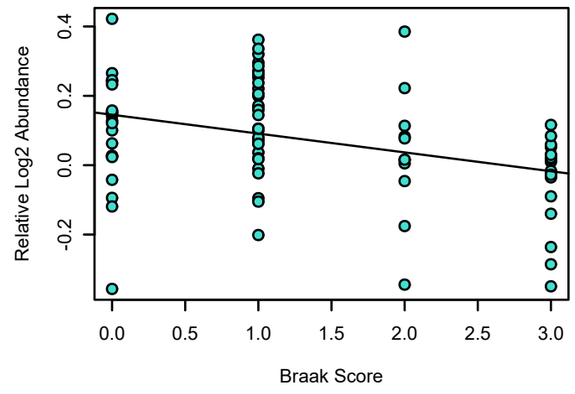

OPA1 UPenn Mixed PRM
K-W ANOVA p: 0.13
Relative Log2 Abundance
Control
otherND
AD

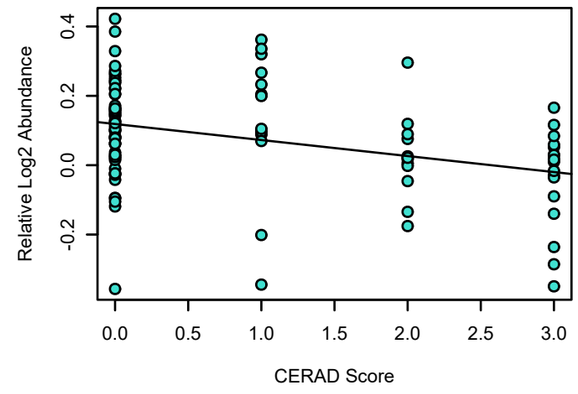

bicor=0.12, p=0.28
cor=0.14, p=0.2
Relative Log2 Abundance
Braak Score

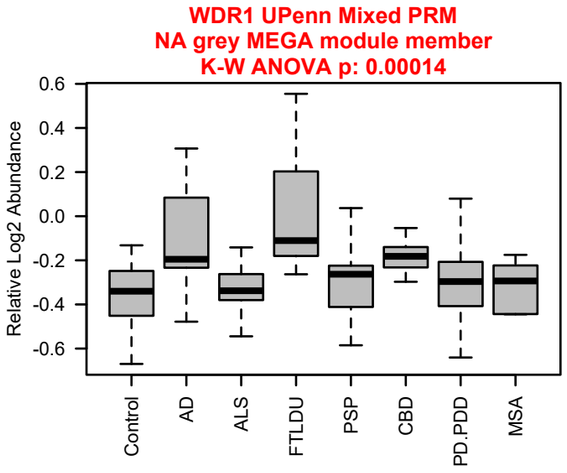

bicor=0.081, p=0.42
cor=0.023, p=0.82
Relative Log2 Abundance
CERAD Score

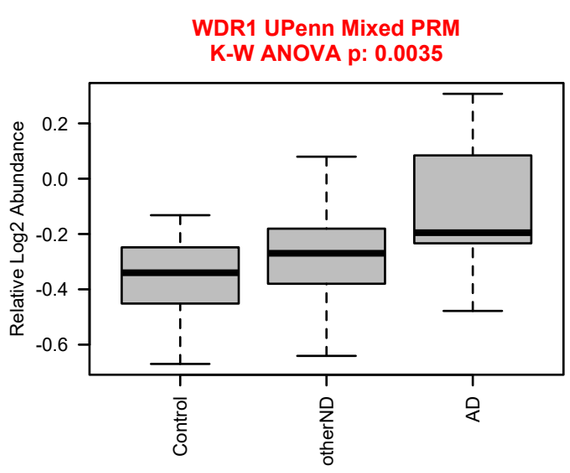

DNAJC6 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0021
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

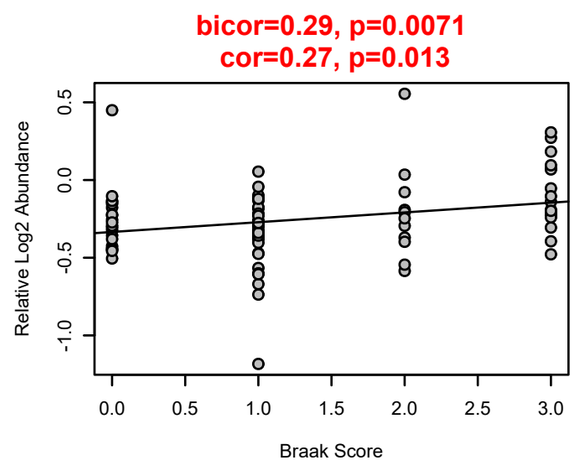

DNAJC6 UPenn Mixed PRM
K-W ANOVA p: 0.0045
Relative Log2 Abundance
Control
otherND
AD

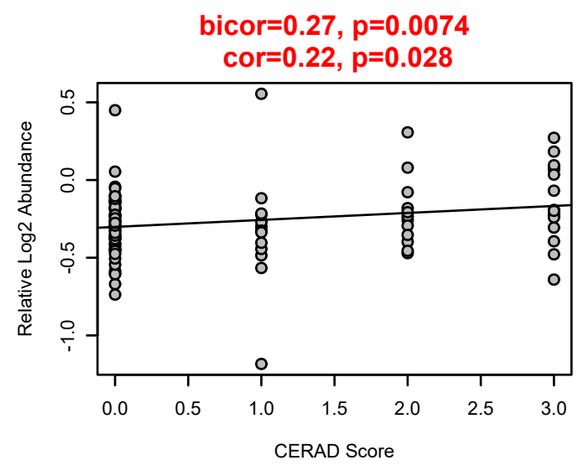

bicor=-0.35, p=0.00098
cor=-0.36, p=0.00077
Relative Log2 Abundance
Braak Score

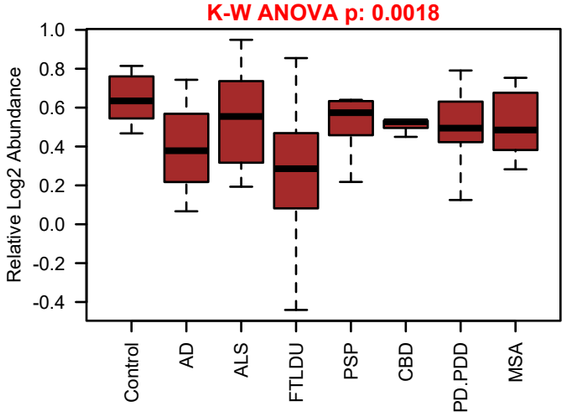

bicor=-0.37, p=0.00014
cor=-0.35, p=0.00036
Relative Log2 Abundance
CERAD Score

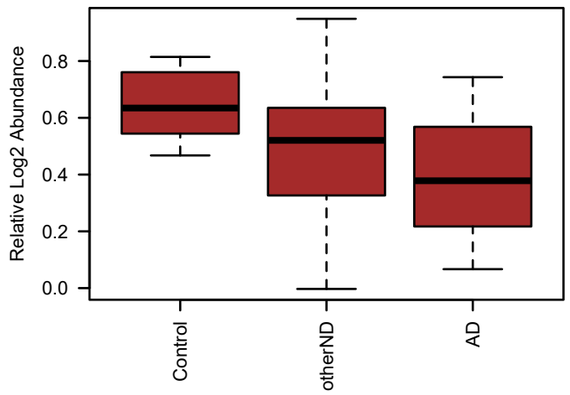

WDR1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.00014
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

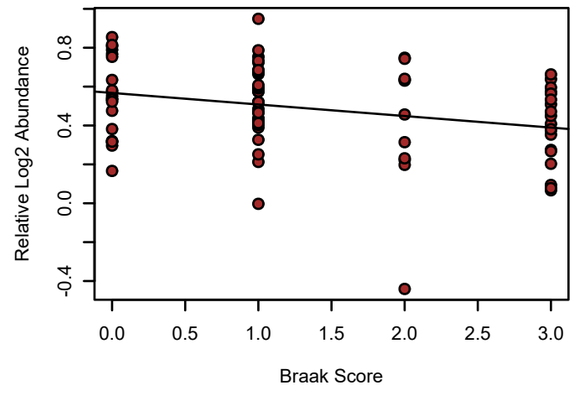

WDR1 UPenn Mixed PRM
K-W ANOVA p: 0.0035
Relative Log2 Abundance
Control
otherND
AD

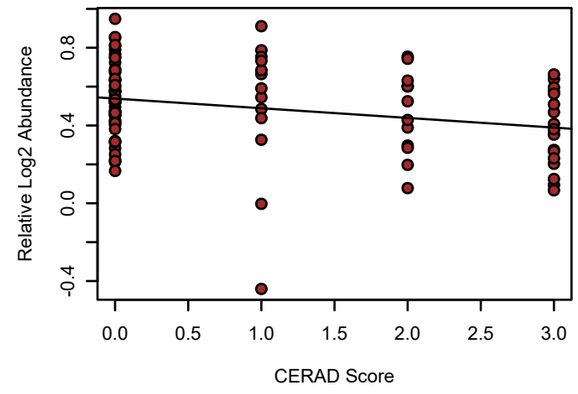

bicor=0.29, p=0.0071
cor=0.27, p=0.013
Relative Log2 Abundance
Braak Score

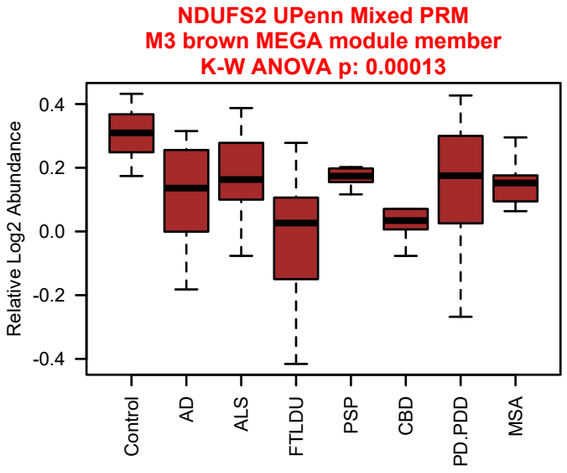

bicor=0.27, p=0.0074
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

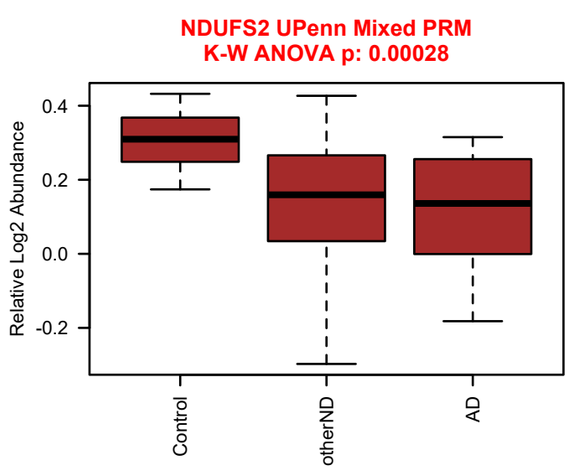

NDUFS7 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0018
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

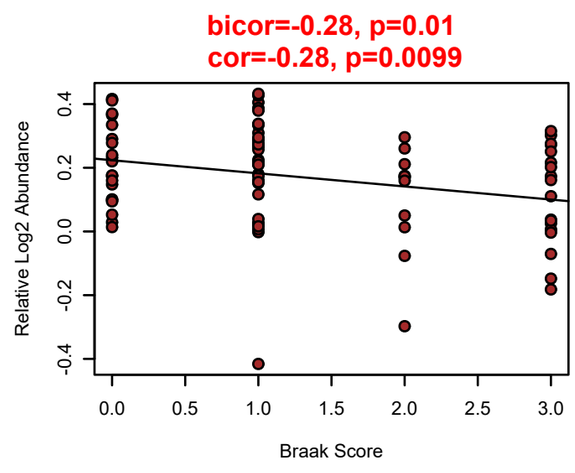

NDUFS7 UPenn Mixed PRM
K-W ANOVA p: 0.0031
Relative Log2 Abundance
Control
otherND
AD

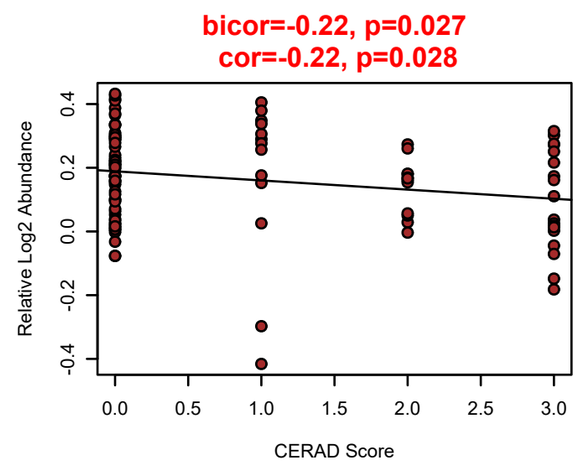

bicor=-0.3, p=0.0058
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

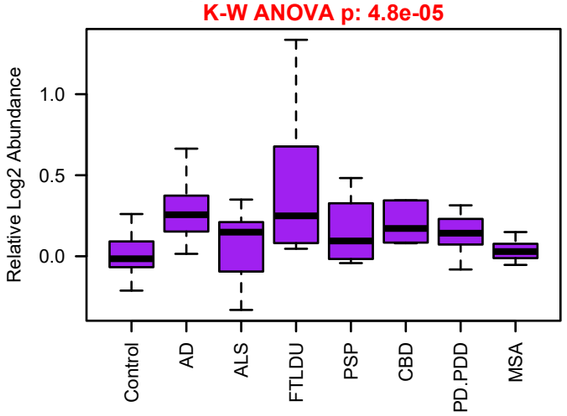

bicor=-0.28, p=0.005
cor=-0.27, p=0.0066
Relative Log2 Abundance
CERAD Score

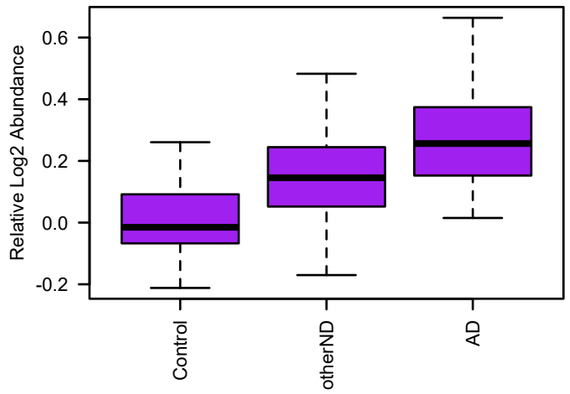

NDUFS2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.00013
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

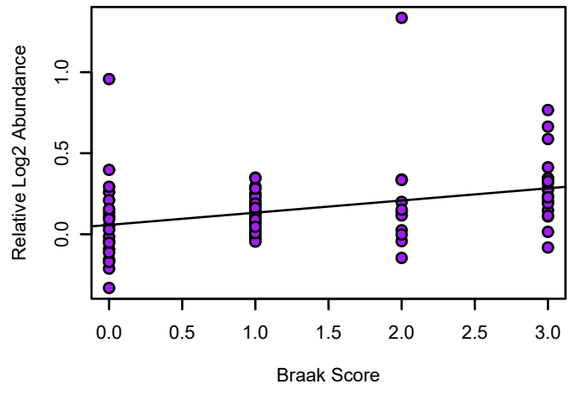

NDUFS2 UPenn Mixed PRM
K-W ANOVA p: 0.00028
Relative Log2 Abundance
Control
otherND
AD

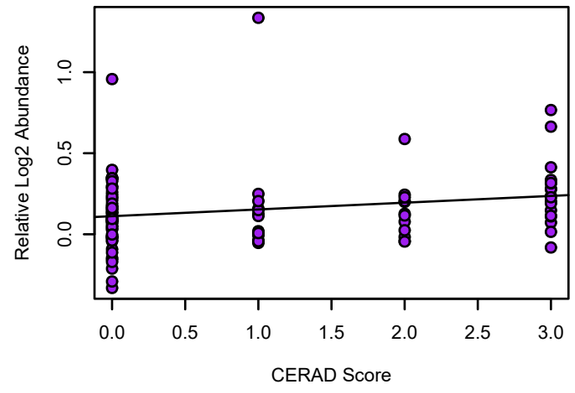

bicor=-0.28, p=0.01
cor=-0.28, p=0.0099
Relative Log2 Abundance
Braak Score

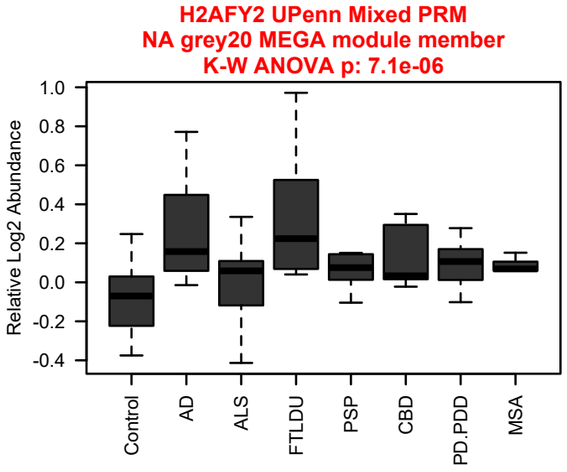

bicor=-0.22, p=0.027
cor=-0.22, p=0.028
Relative Log2 Abundance
CERAD Score

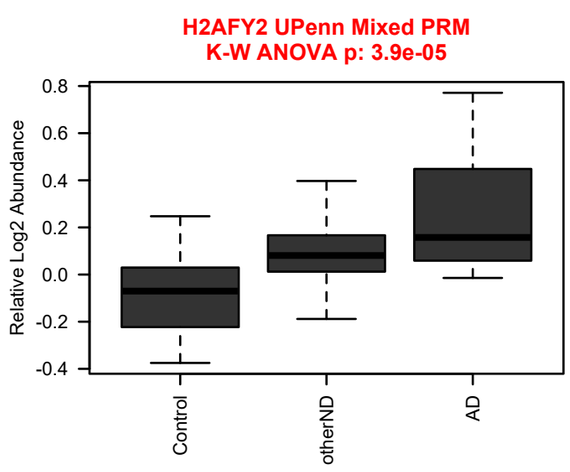

H2AFY UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 4.8e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

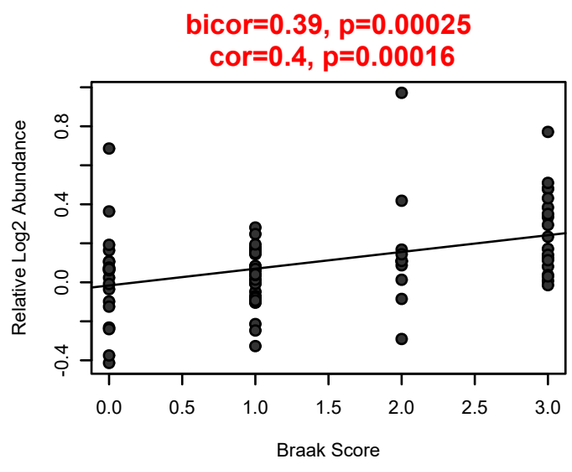

H2AFY UPenn Mixed PRM
K-W ANOVA p: 0.00093
Relative Log2 Abundance
Control
otherND
AD

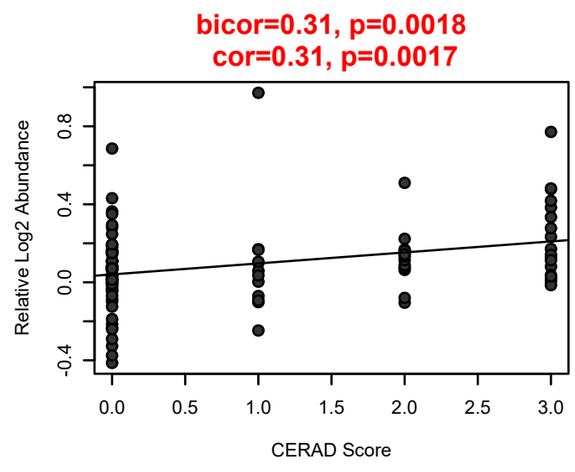

bicor=0.41, p=0.00012
cor=0.34, p=0.0016
Relative Log2 Abundance
Braak Score

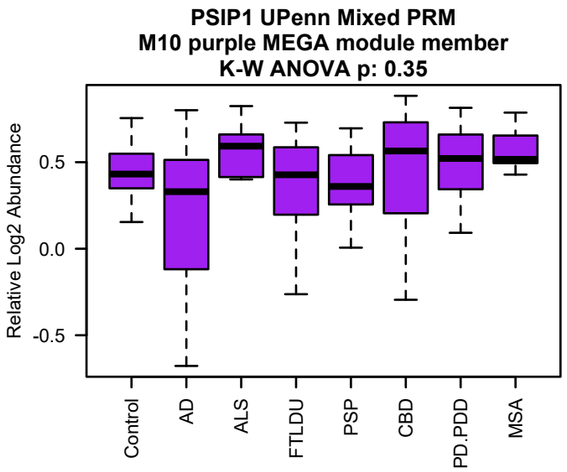

bicor=0.26, p=0.0081
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

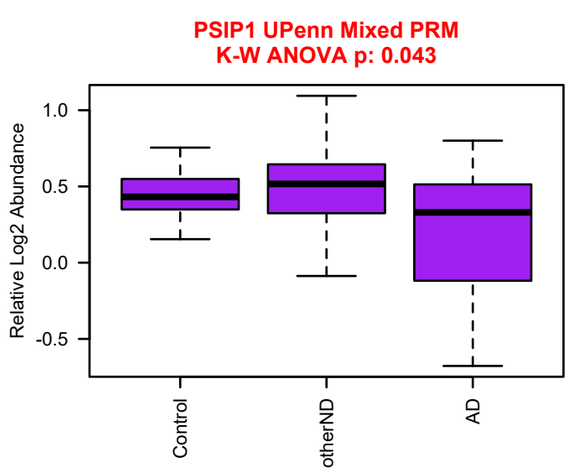

H2AFY2 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 7.1e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

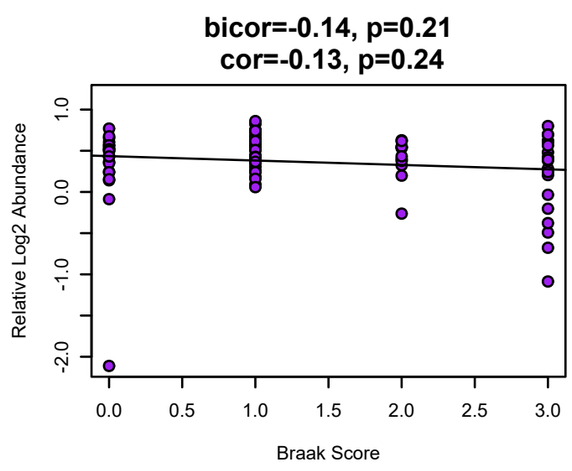

H2AFY2 UPenn Mixed PRM
K-W ANOVA p: 3.9e-05
Relative Log2 Abundance
Control
otherND
AD

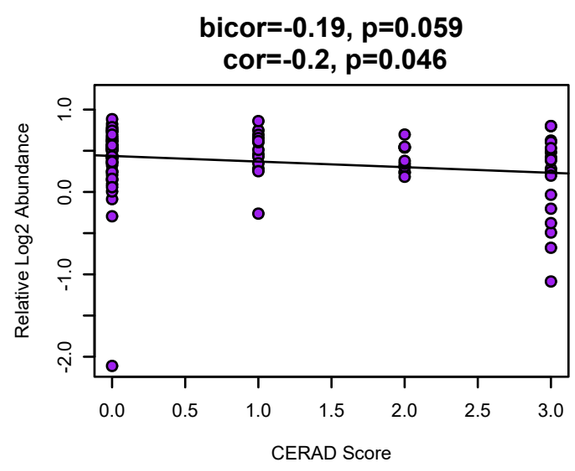

bicor=0.39, p=0.00025
cor=0.4, p=0.00016
Relative Log2 Abundance
Braak Score

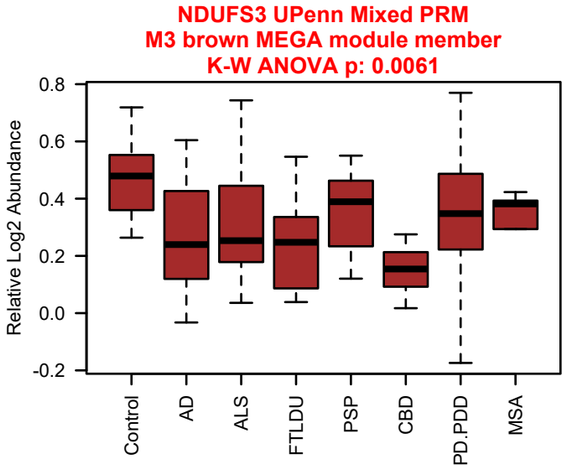

bicor=0.31, p=0.0018
cor=0.31, p=0.0017
Relative Log2 Abundance
CERAD Score

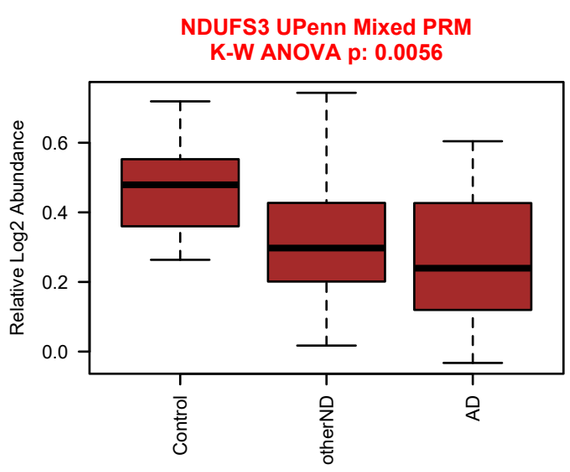

PSIP1 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.35
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

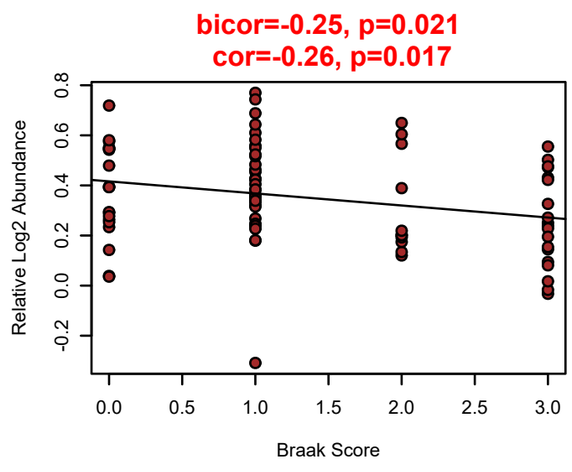

PSIP1 UPenn Mixed PRM
K-W ANOVA p: 0.043
Relative Log2 Abundance
Control
otherND
AD

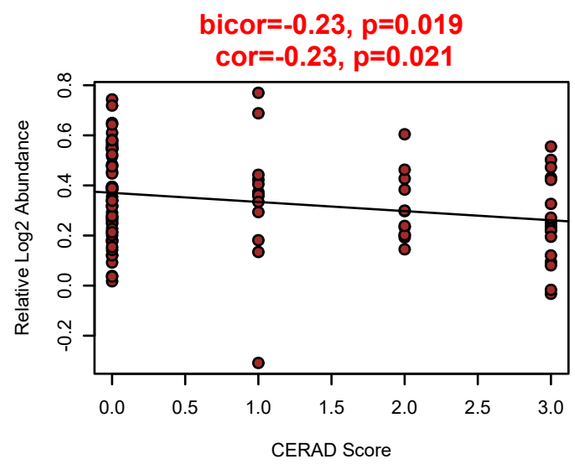

bicor=-0.14, p=0.21
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

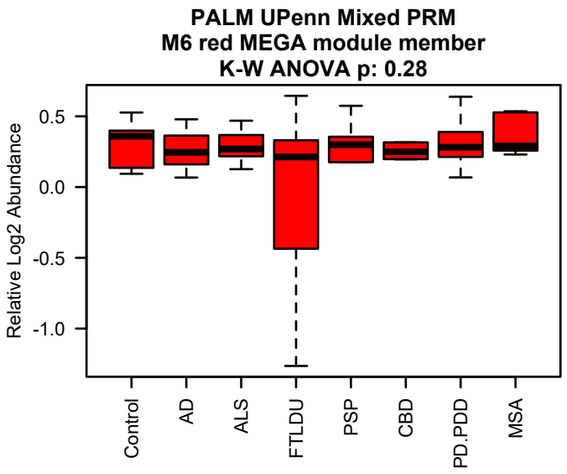

bicor=-0.19, p=0.059
cor=-0.2, p=0.046
Relative Log2 Abundance
CERAD Score

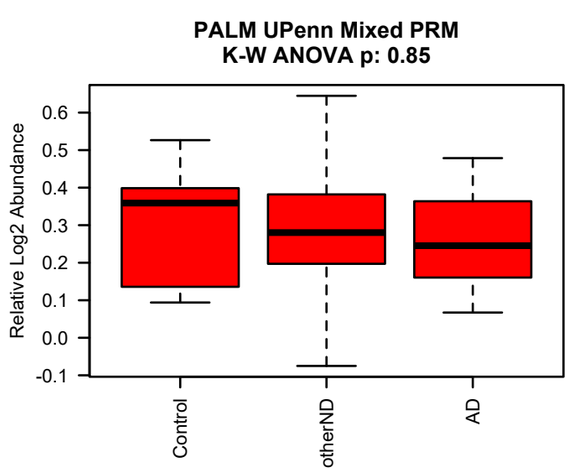

NDUFS3 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0061
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

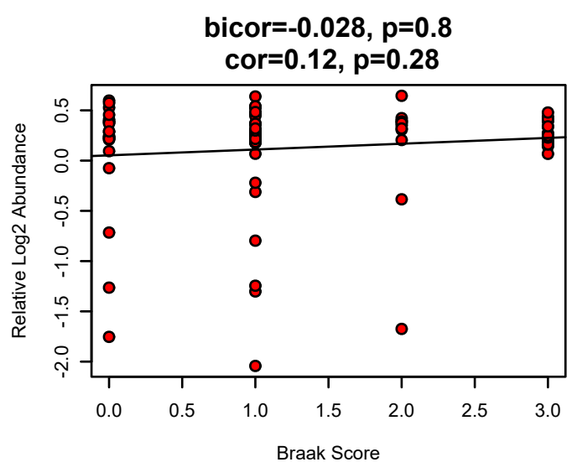

NDUFS3 UPenn Mixed PRM
K-W ANOVA p: 0.0056
Relative Log2 Abundance
Control
otherND
AD

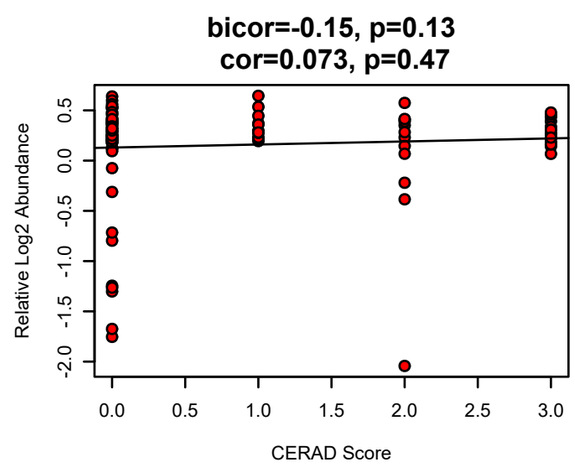

bicor=-0.25, p=0.021
cor=-0.26, p=0.017
Relative Log2 Abundance
Braak Score

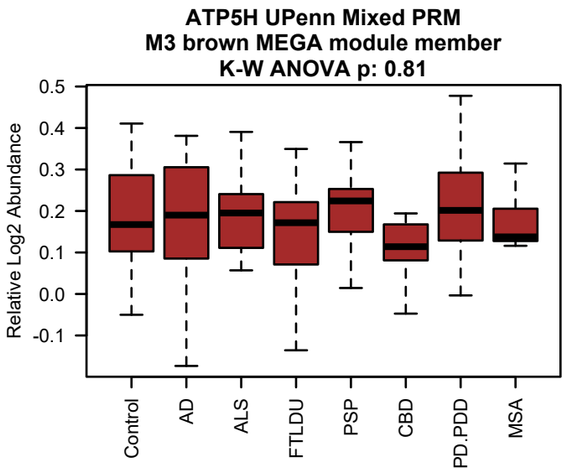

bicor=-0.23, p=0.019
cor=-0.23, p=0.021
Relative Log2 Abundance
CERAD Score

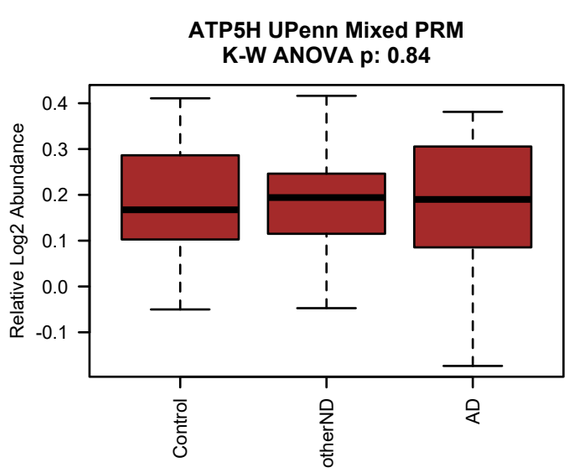

PALM UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.28
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

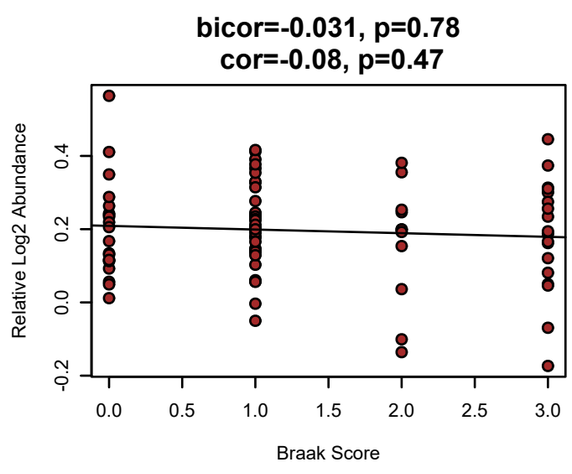

PALM UPenn Mixed PRM
K-W ANOVA p: 0.85
Relative Log2 Abundance
Control
otherND
AD

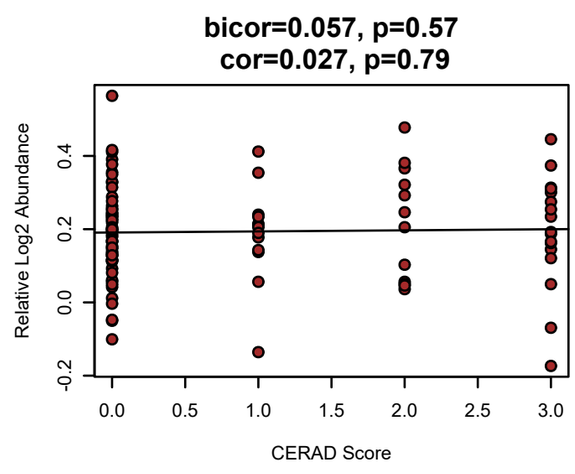

bicor=-0.028, p=0.8
cor=0.12, p=0.28
Relative Log2 Abundance
Braak Score

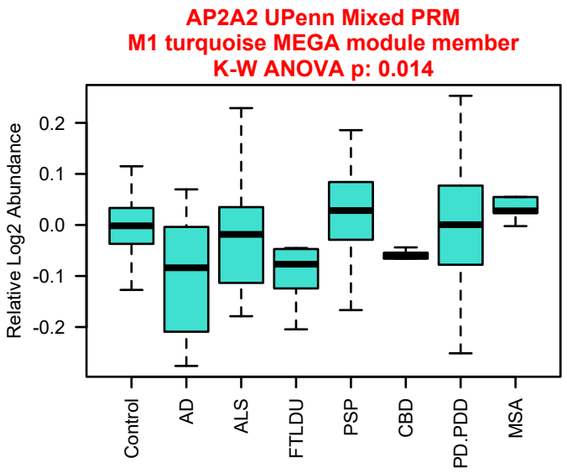

bicor=-0.15, p=0.13
cor=0.073, p=0.47
Relative Log2 Abundance
CERAD Score

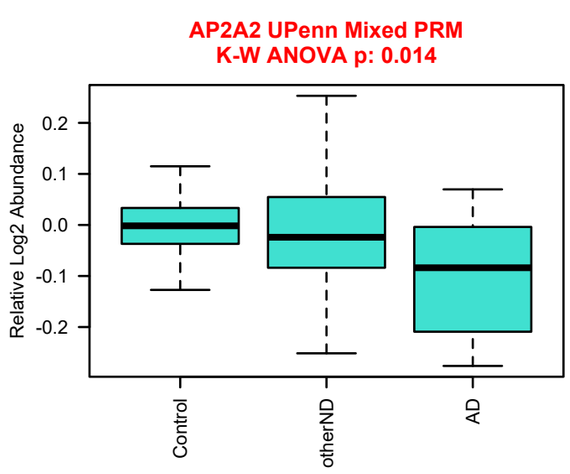

ATP5H UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.81
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

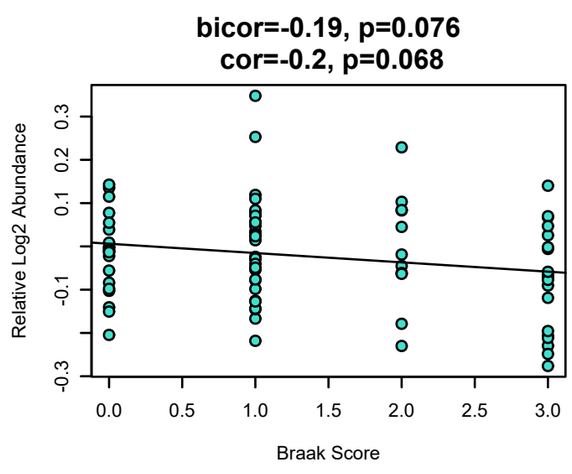

ATP5H UPenn Mixed PRM
K-W ANOVA p: 0.84
Relative Log2 Abundance
Control
otherND
AD

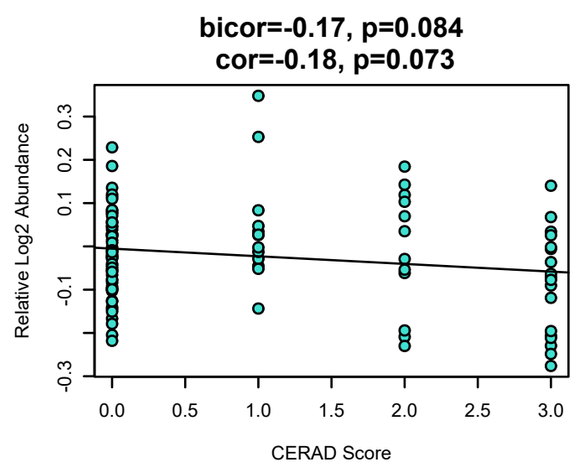

bicor=-0.031, p=0.78
cor=-0.08, p=0.47
Relative Log2 Abundance
Braak Score

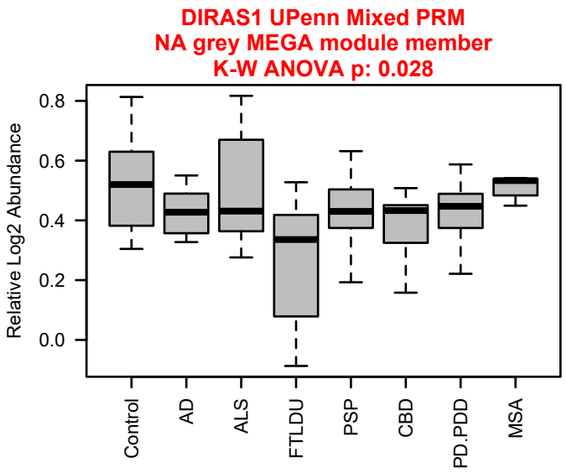

bicor=0.057, p=0.57
cor=0.027, p=0.79
Relative Log2 Abundance
CERAD Score

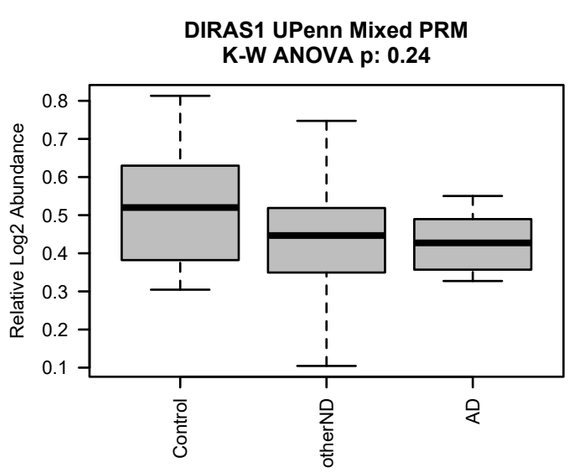

AP2A2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.014
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

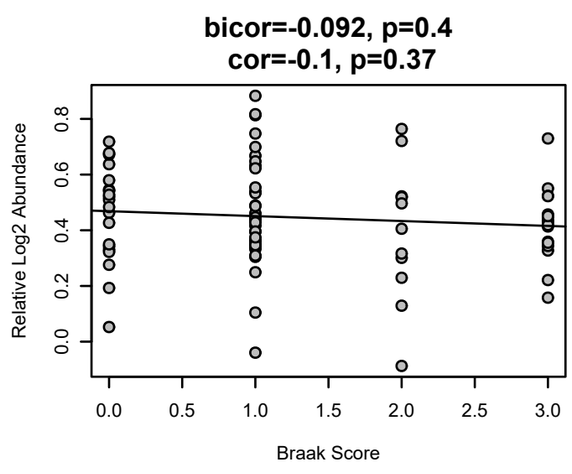

AP2A2 UPenn Mixed PRM
K-W ANOVA p: 0.014
Relative Log2 Abundance
Control
otherND
AD

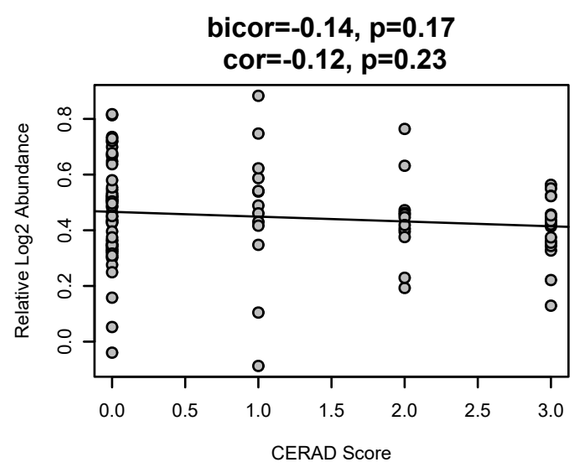

bicor=-0.19, p=0.076
cor=-0.2, p=0.068
Relative Log2 Abundance
Braak Score

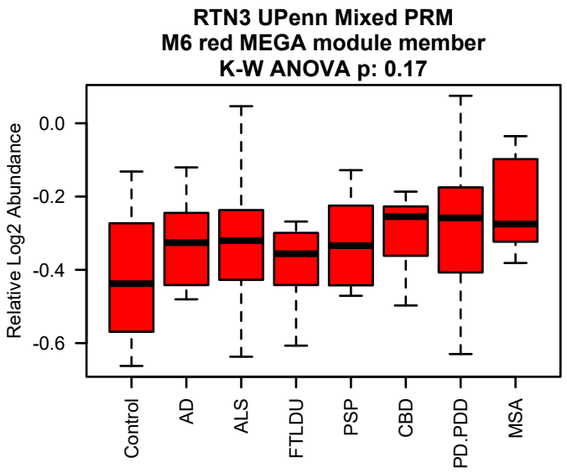

bicor=-0.17, p=0.084
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

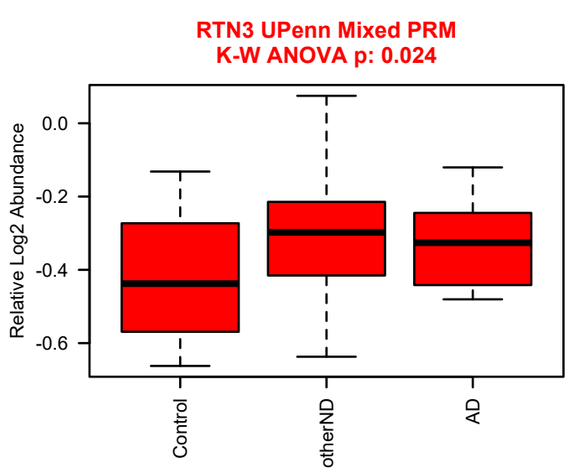

DIRAS1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.028
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

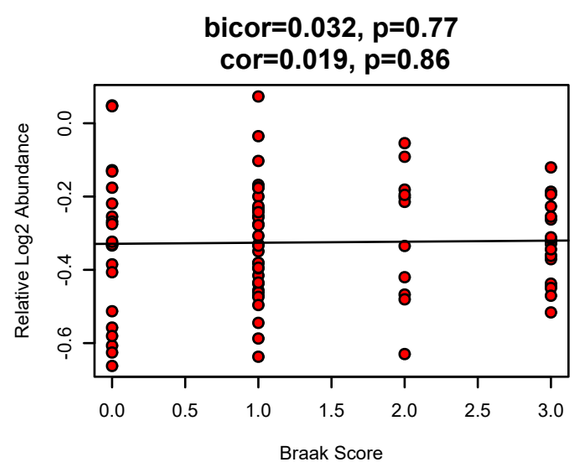

DIRAS1 UPenn Mixed PRM
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
otherND
AD

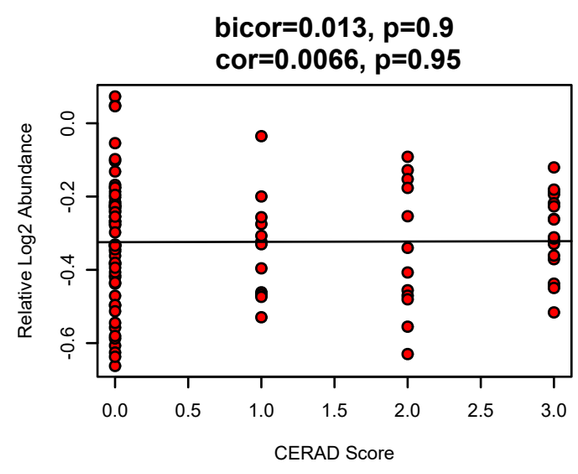

bicor=-0.092, p=0.4
cor=-0.1, p=0.37
Relative Log2 Abundance
Braak Score

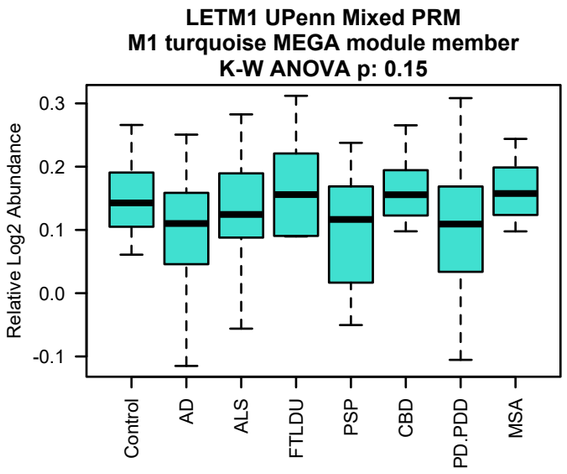

bicor=-0.14, p=0.17
cor=-0.12, p=0.23
Relative Log2 Abundance
CERAD Score

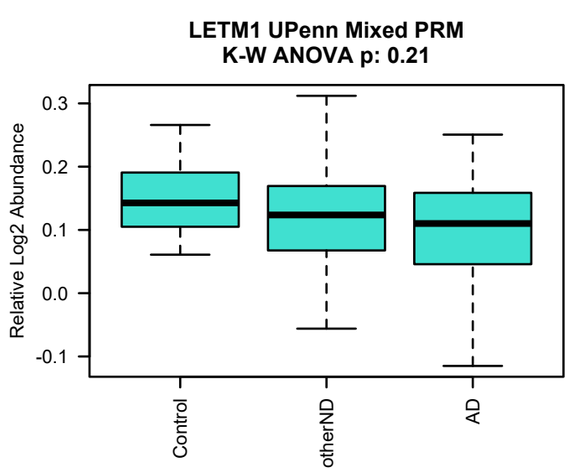

RTN3 UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.17
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

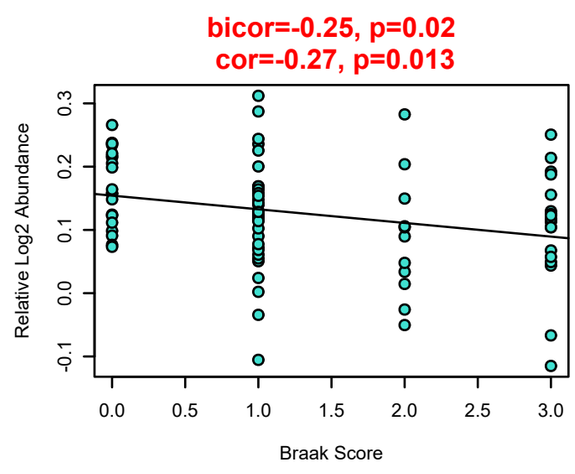

RTN3 UPenn Mixed PRM
K-W ANOVA p: 0.024
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
Control
otherND
AD

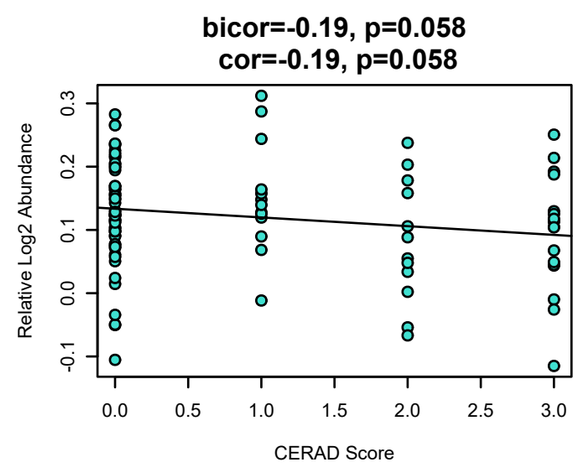

bicor=0.032, p=0.77
cor=0.019, p=0.86
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

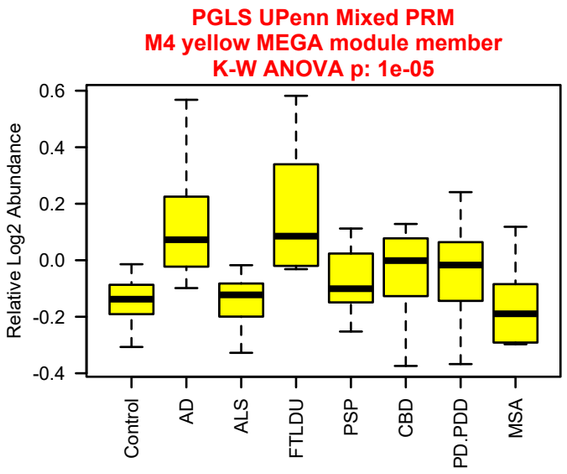

bicor=0.013, p=0.9
cor=0.0066, p=0.95
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

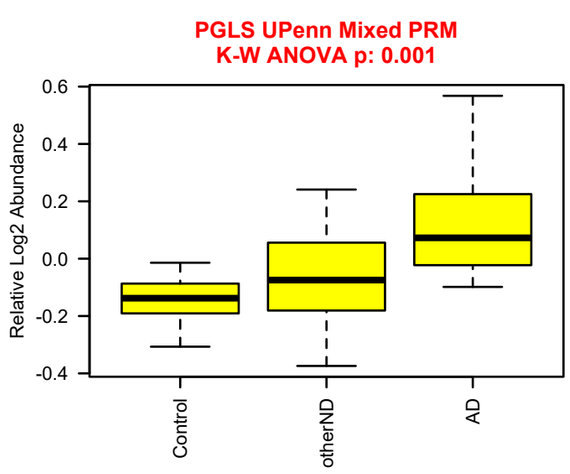

LETM1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.15
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

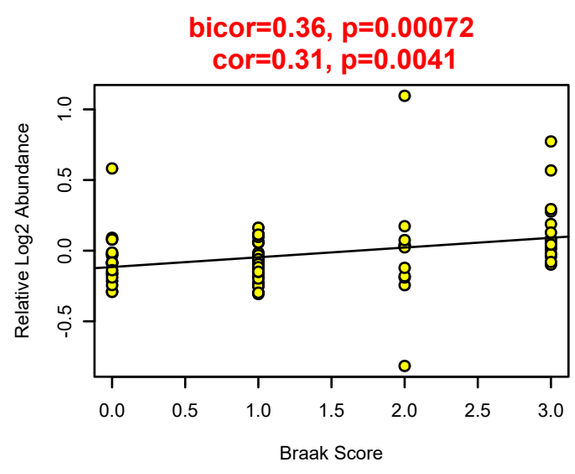

LETM1 UPenn Mixed PRM
K-W ANOVA p: 0.21
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
Control
otherND
AD

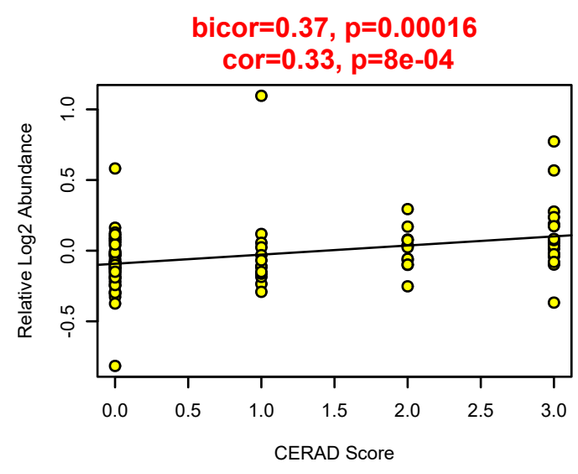

bicor=-0.25, p=0.02
cor=-0.27, p=0.013
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

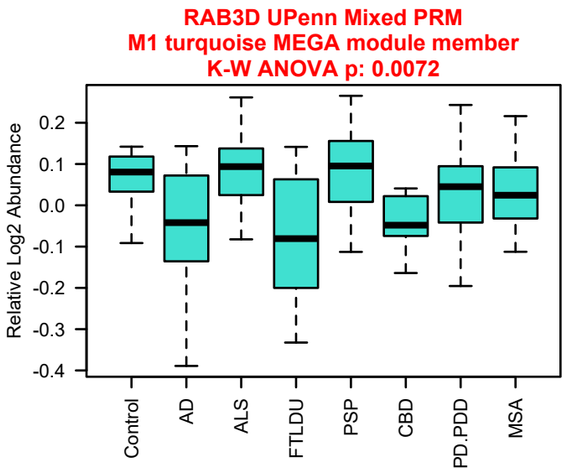

bicor=-0.19, p=0.058
cor=-0.19, p=0.058
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

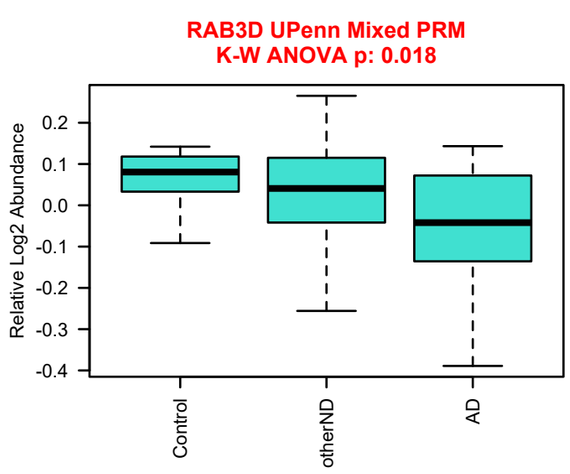

PGLS UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1e-05
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

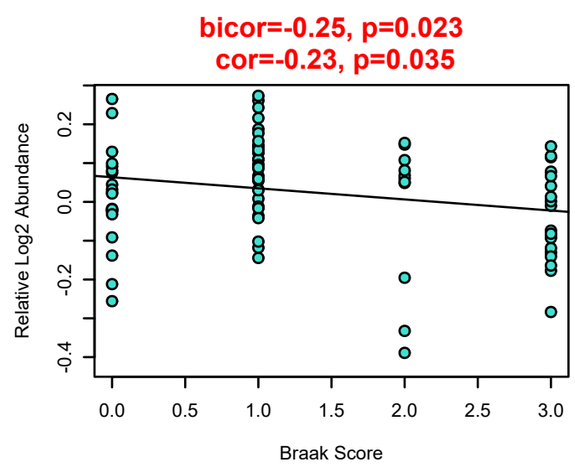

PGLS UPenn Mixed PRM
K-W ANOVA p: 0.001
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
Control
otherND
AD

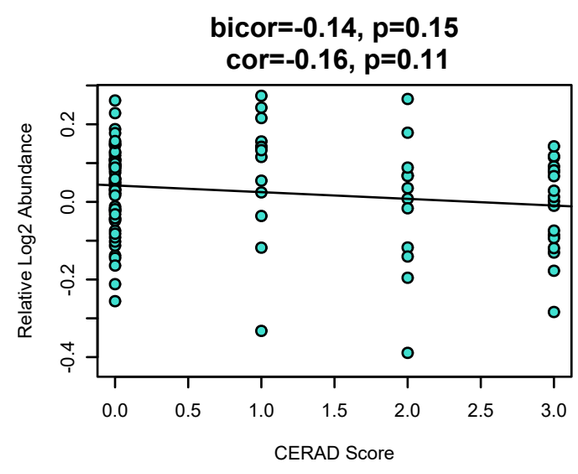

bicor=0.36, p=0.00072
cor=0.31, p=0.0041
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

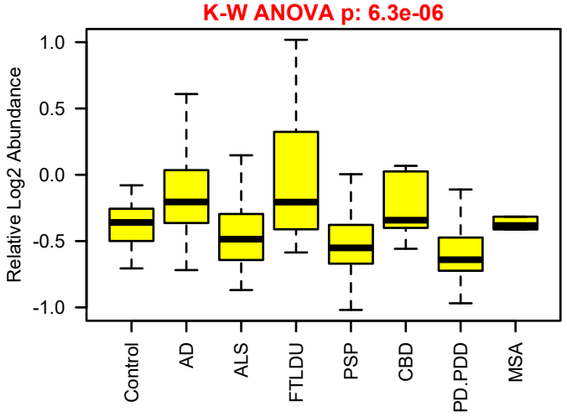

bicor=0.37, p=0.00016
cor=0.33, p=8e-04
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

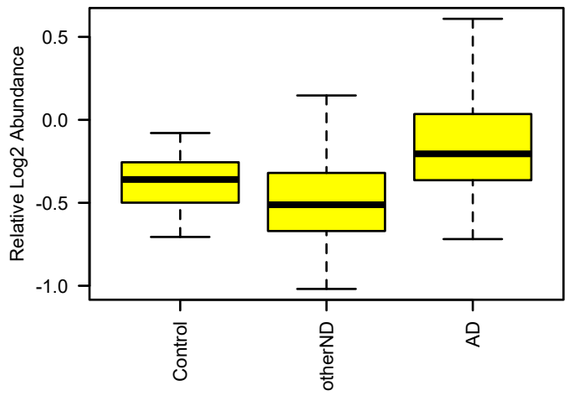

RAB3D UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0072
Relative Log2 Abundance
0.2
0.1
0.0
-0.1
-0.2
-0.3
-0.4
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

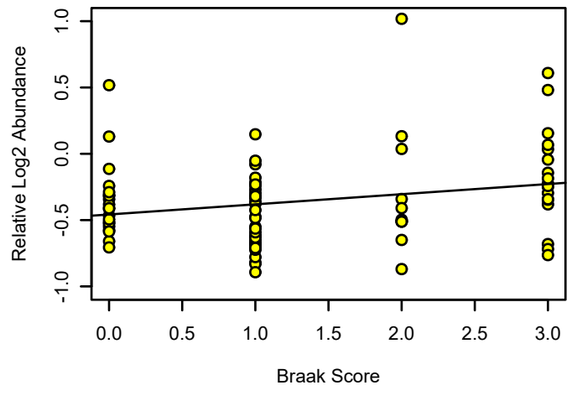

RAB3D UPenn Mixed PRM
K-W ANOVA p: 0.018
Relative Log2 Abundance
0.2
0.1
0.0
-0.1
-0.2
-0.3
-0.4
Control
otherND
AD

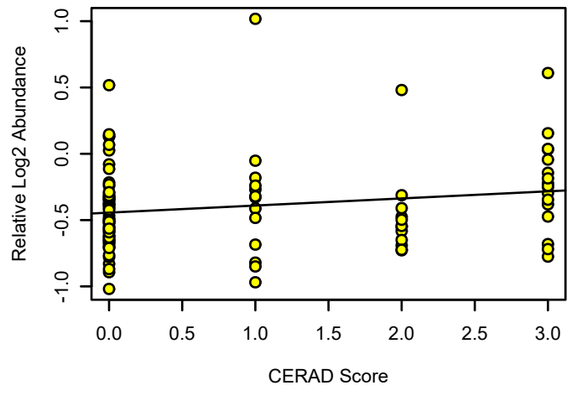

bicor=-0.25, p=0.023
cor=-0.23, p=0.035
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

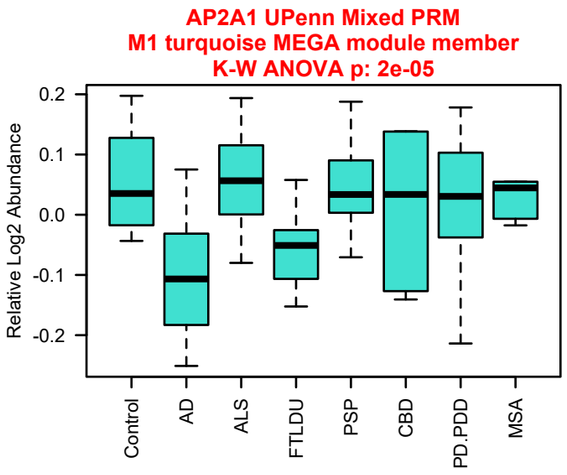

bicor=-0.14, p=0.15
cor=-0.16, p=0.11
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

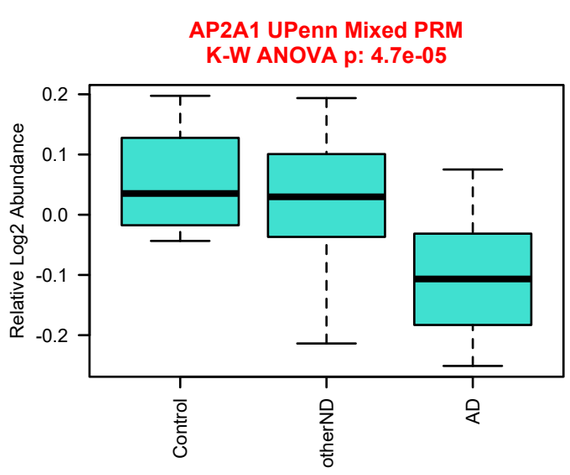

CPNE6 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 6.3e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

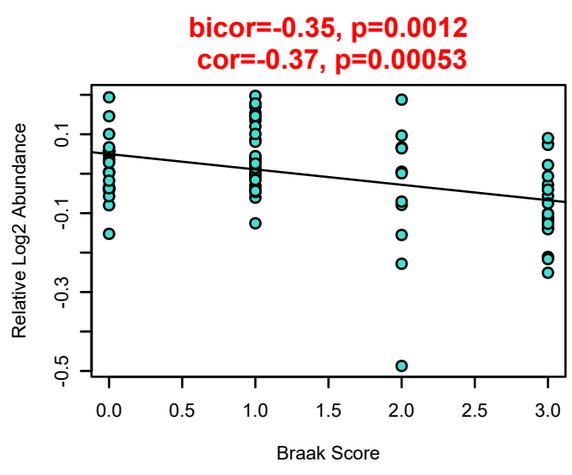

CPNE6 UPenn Mixed PRM
K-W ANOVA p: 0.0038
Relative Log2 Abundance
Control
otherND
AD

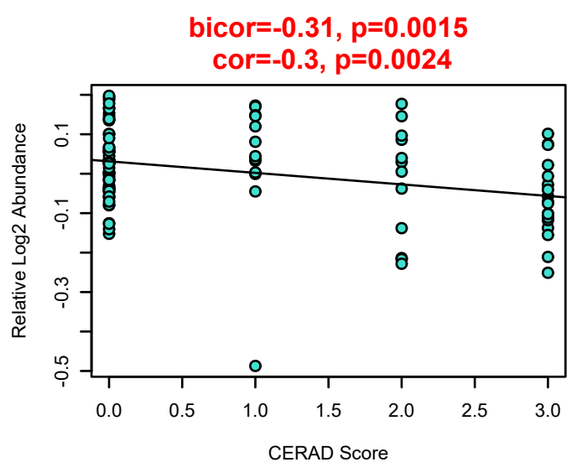

bicor=0.21, p=0.051
cor=0.24, p=0.028
Relative Log2 Abundance
Braak Score

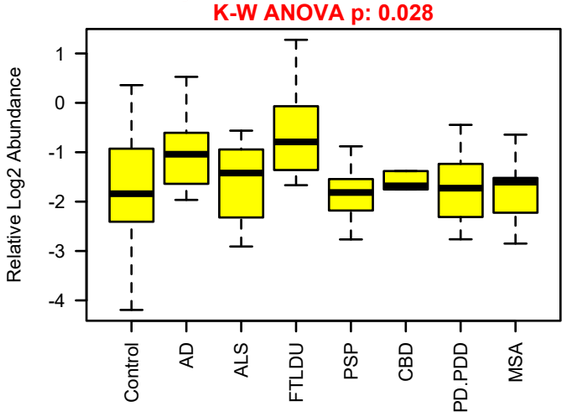

bicor=0.2, p=0.05
cor=0.19, p=0.058
Relative Log2 Abundance
CERAD Score

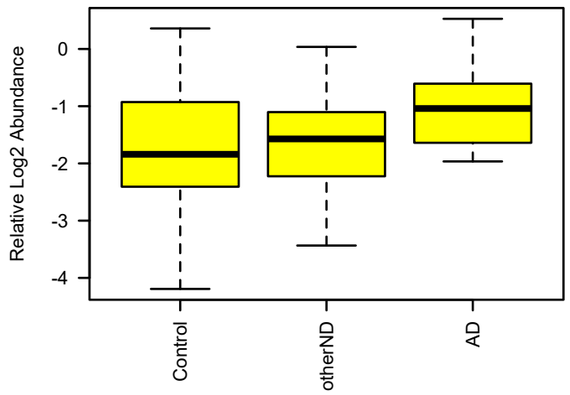

AP2A1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

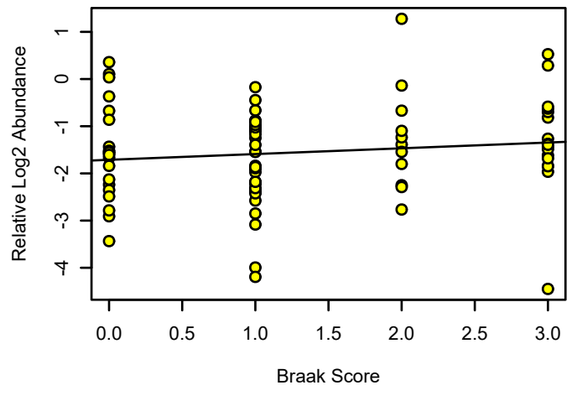

AP2A1 UPenn Mixed PRM
K-W ANOVA p: 4.7e-05
Relative Log2 Abundance
Control
otherND
AD

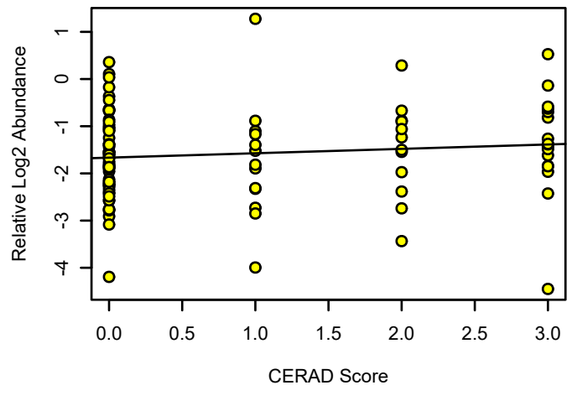

bicor=-0.35, p=0.0012
cor=-0.37, p=0.00053
Relative Log2 Abundance
Braak Score

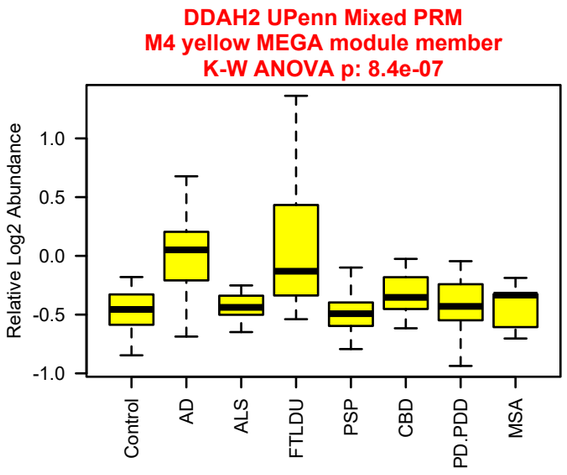

bicor=-0.31, p=0.0015
cor=-0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

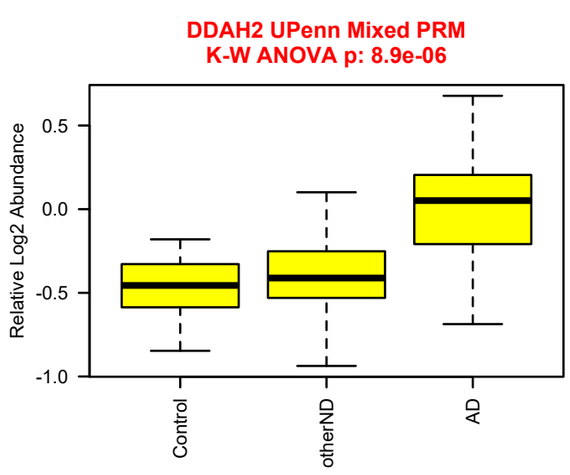

BAG3 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.028
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

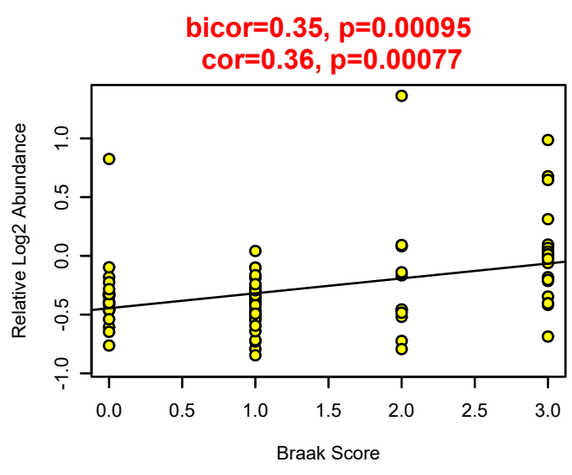

BAG3 UPenn Mixed PRM
K-W ANOVA p: 0.15
Relative Log2 Abundance
Control
otherND
AD

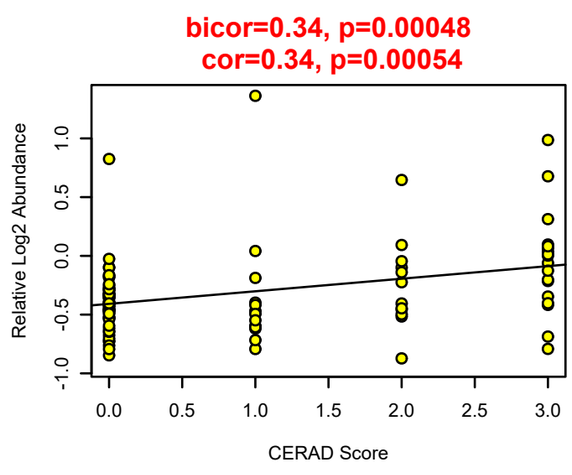

bicor=0.15, p=0.18
cor=0.13, p=0.24
Relative Log2 Abundance
Braak Score

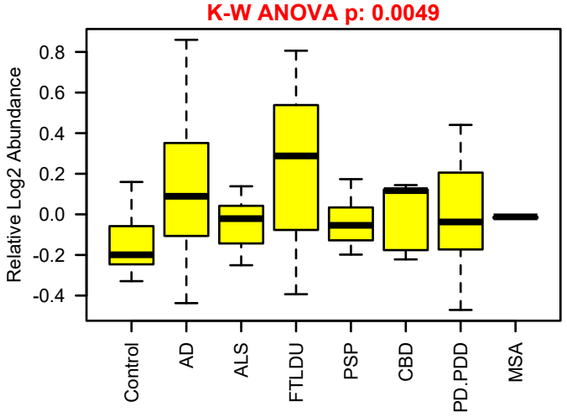

bicor=0.14, p=0.15
cor=0.11, p=0.28
Relative Log2 Abundance
CERAD Score

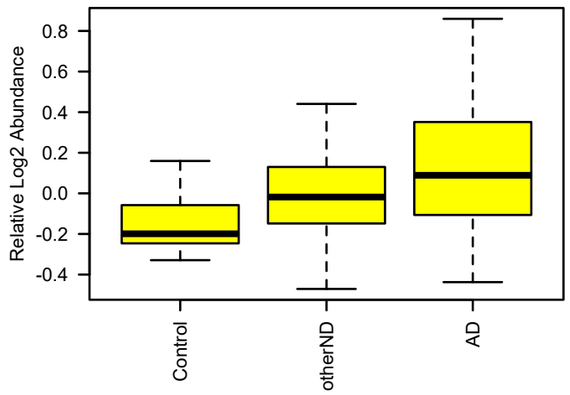

DDAH2 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 8.4e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

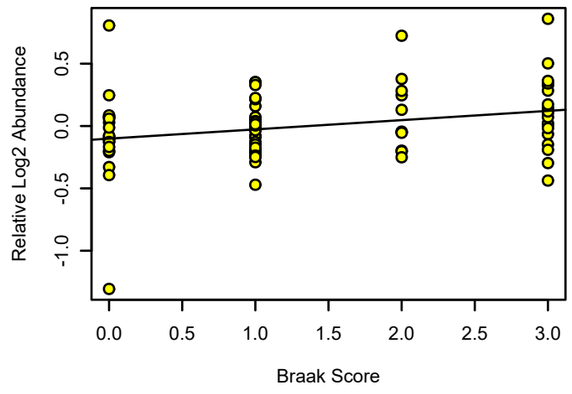

DDAH2 UPenn Mixed PRM
K-W ANOVA p: 8.9e-06
Relative Log2 Abundance
Control
otherND
AD

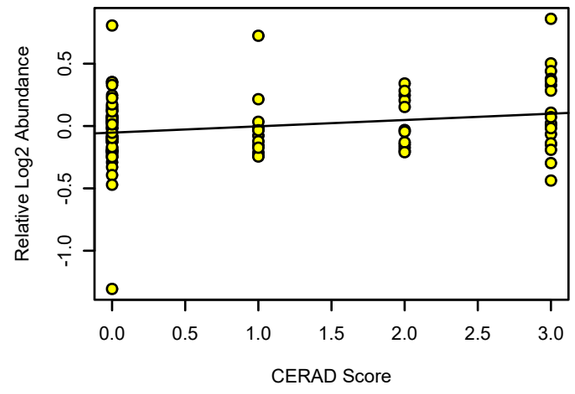

bicor=0.35, p=0.00095
cor=0.36, p=0.00077
Relative Log2 Abundance
Braak Score

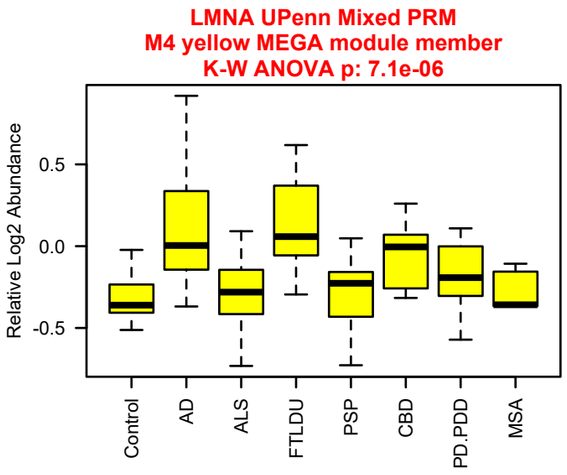

bicor=0.34, p=0.00048
cor=0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

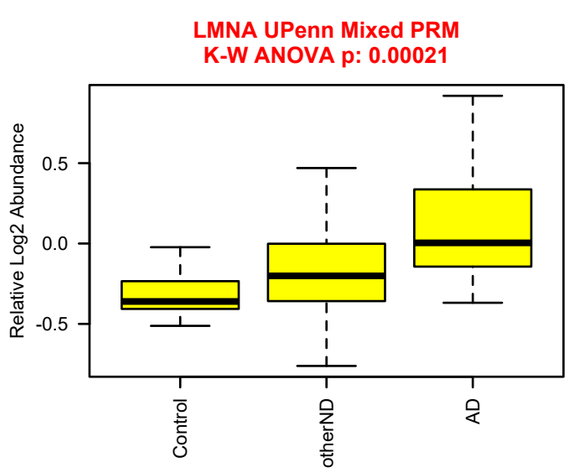

AK1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.0049
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

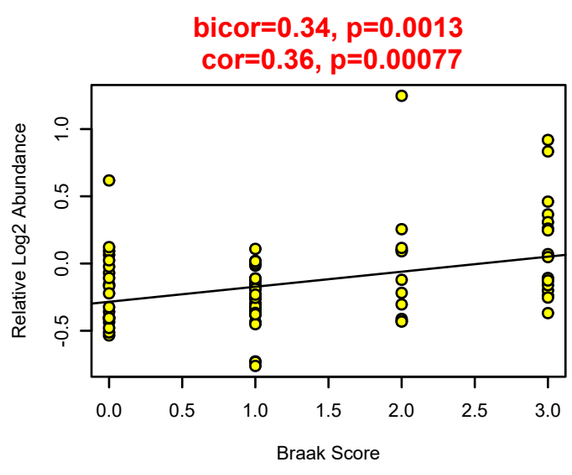

AK1 UPenn Mixed PRM
K-W ANOVA p: 0.0014
Relative Log2 Abundance
Control
otherND
AD

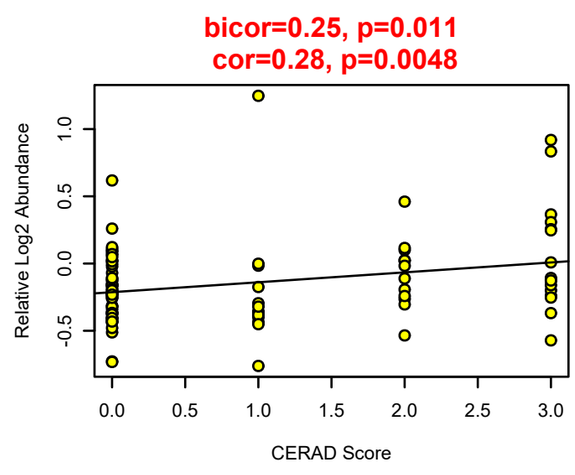

bicor=0.27, p=0.015
cor=0.28, p=0.0099
Relative Log2 Abundance
Braak Score

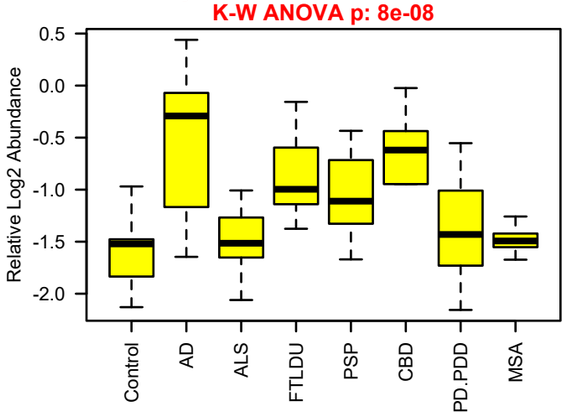

bicor=0.19, p=0.057
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

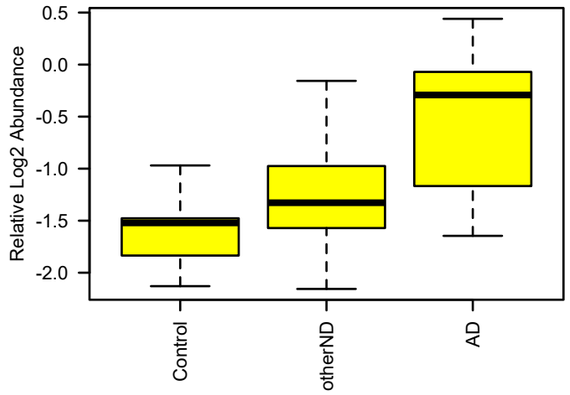

LMNA UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 7.1e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

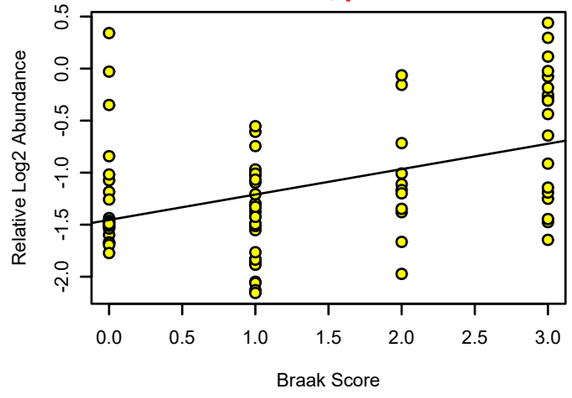

LMNA UPenn Mixed PRM
K-W ANOVA p: 0.00021
Relative Log2 Abundance
Control
otherND
AD

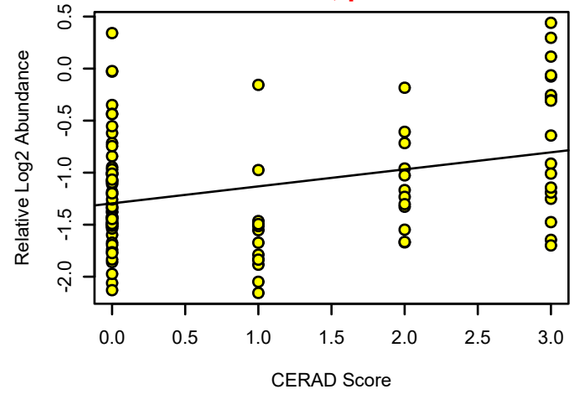

bicor=0.34, p=0.0013
cor=0.36, p=0.00077
Relative Log2 Abundance
Braak Score

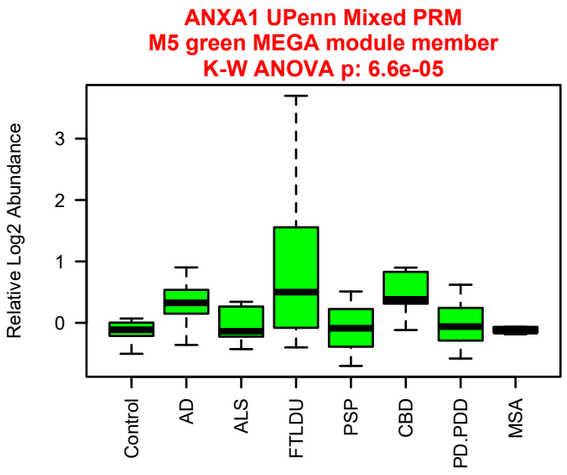

bicor=0.25, p=0.011
cor=0.28, p=0.0048
Relative Log2 Abundance
CERAD Score

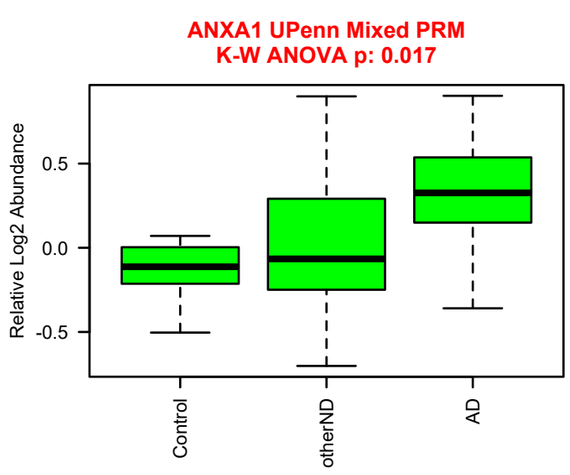

CSTB UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 8e-08
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

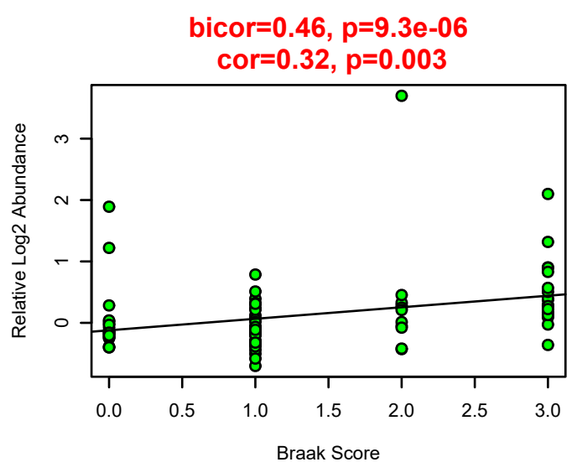

CSTB UPenn Mixed PRM
K-W ANOVA p: 7.8e-08
Relative Log2 Abundance
Control
otherND
AD

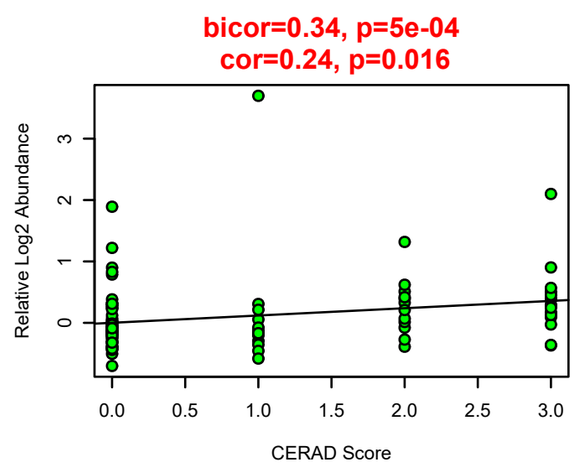

bicor=0.43, p=5.4e-05
cor=0.42, p=7e-05
Relative Log2 Abundance
Braak Score

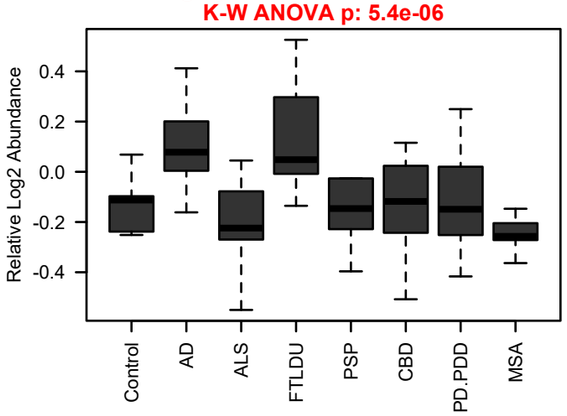

bicor=0.29, p=0.0032
cor=0.33, p=8e-04
Relative Log2 Abundance
CERAD Score

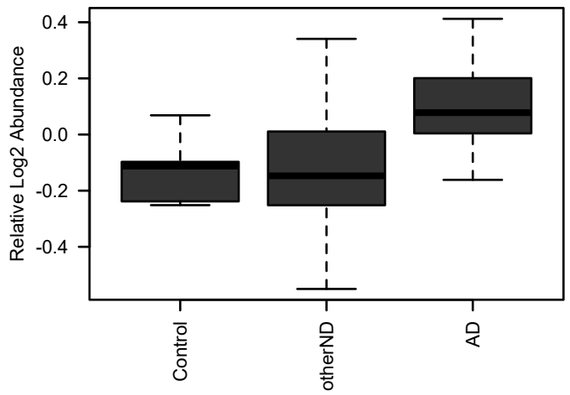

ANXA1 UPenn Mixed PRM
M5 green MEGA module member
K-W ANOVA p: 6.6e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

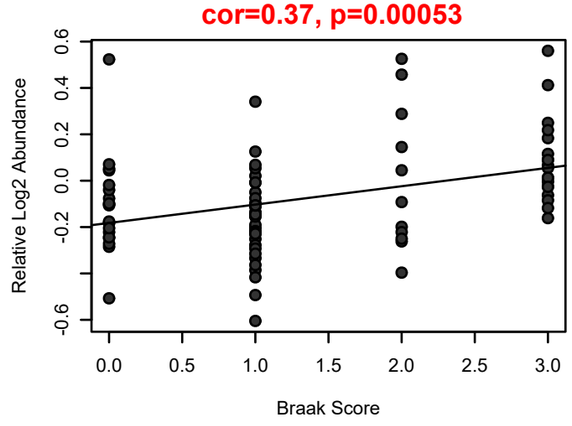

ANXA1 UPenn Mixed PRM
K-W ANOVA p: 0.017
Relative Log2 Abundance
Control
otherND
AD

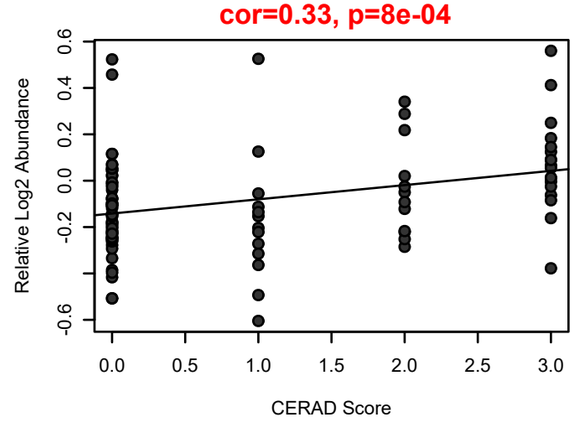

bicor=0.46, p=9.3e-06
cor=0.32, p=0.003
Relative Log2 Abundance
Braak Score

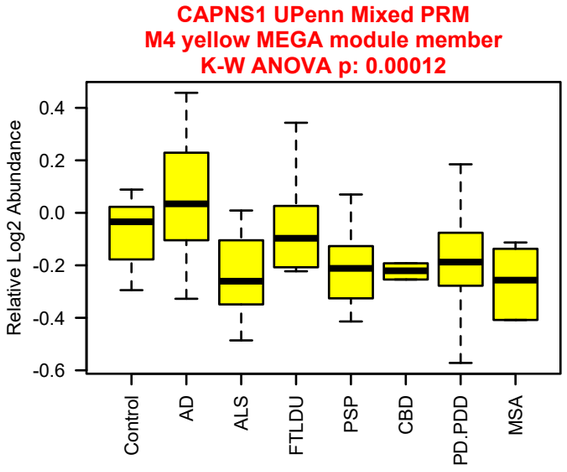

bicor=0.34, p=5e-04
cor=0.24, p=0.016
Relative Log2 Abundance
CERAD Score

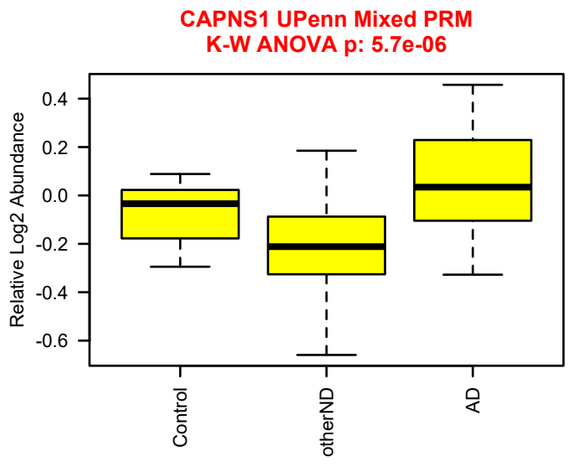

CAPNS2 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 5.4e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

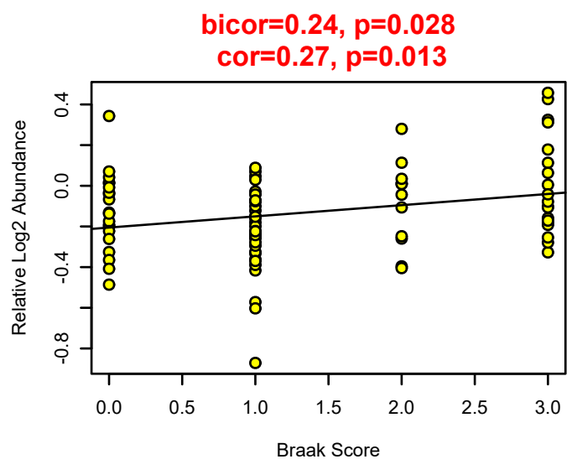

CAPNS2 UPenn Mixed PRM
K-W ANOVA p: 0.00012
Relative Log2 Abundance
Control
otherND
AD

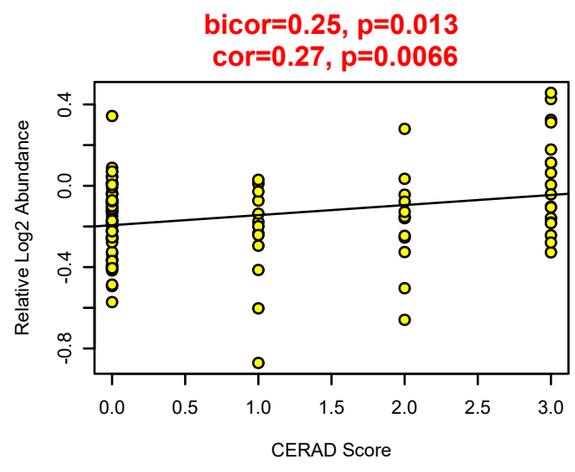

bicor=0.4, p=0.00013
cor=0.37, p=0.00053
Relative Log2 Abundance
Braak Score

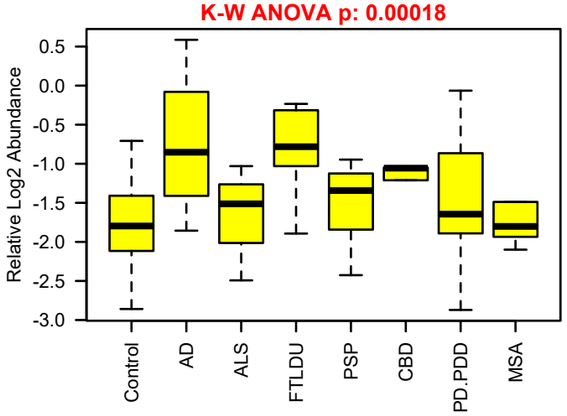

bicor=0.36, p=0.00025
cor=0.33, p=8e-04
Relative Log2 Abundance
CERAD Score

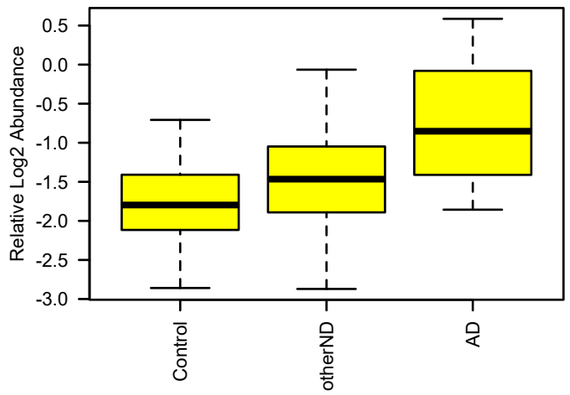

CAPNS1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.00012
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

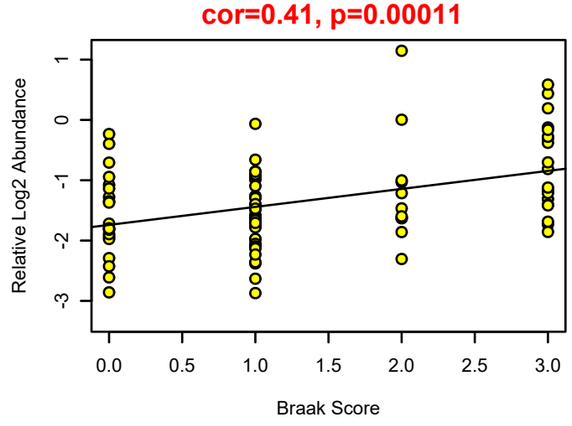

CAPNS1 UPenn Mixed PRM
K-W ANOVA p: 5.7e-06
Relative Log2 Abundance
Control
otherND
AD

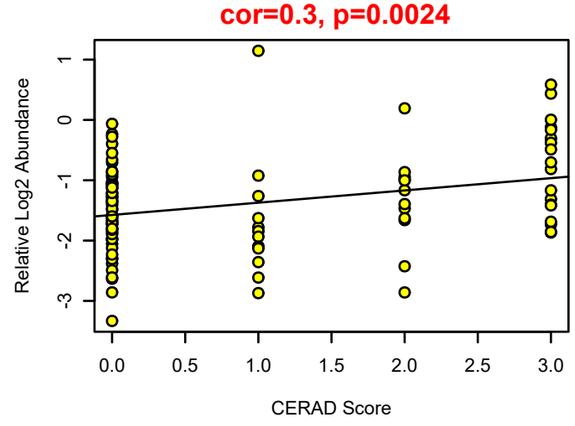

bicor=0.24, p=0.028
cor=0.27, p=0.013
Relative Log2 Abundance
Braak Score

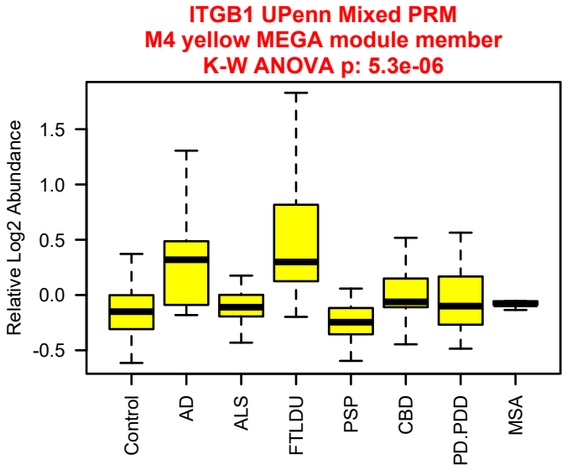

bicor=0.25, p=0.013
cor=0.27, p=0.0066
Relative Log2 Abundance
CERAD Score

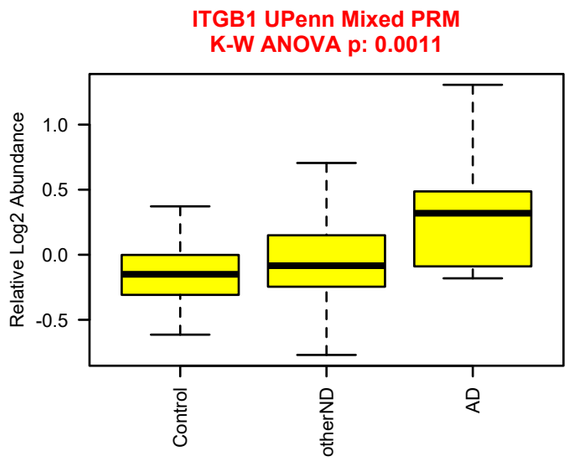

HSPB1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.00018
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

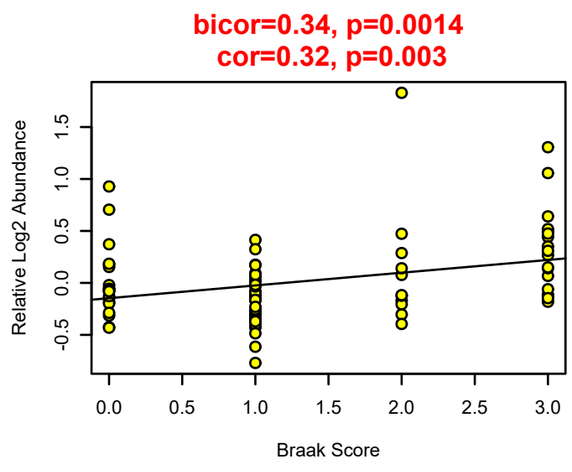

HSPB1 UPenn Mixed PRM
K-W ANOVA p: 3e-04
Relative Log2 Abundance
Control
otherND
AD

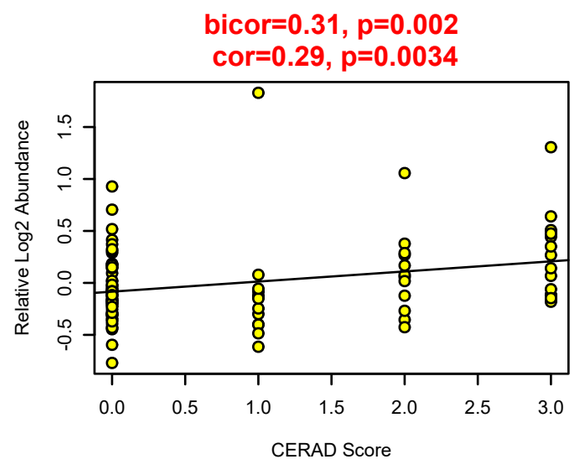

bicor=0.39, p=0.00024
cor=0.41, p=0.00011
Relative Log2 Abundance
Braak Score

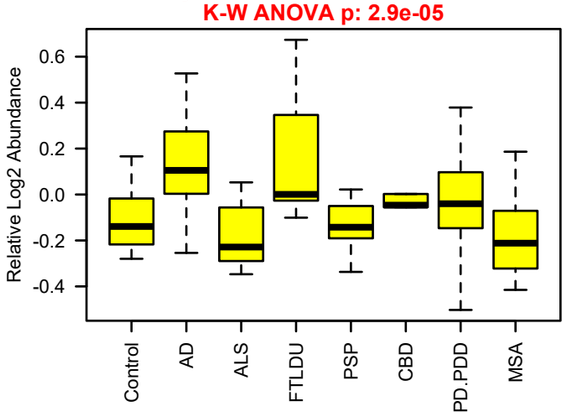

bicor=0.29, p=0.003
cor=0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

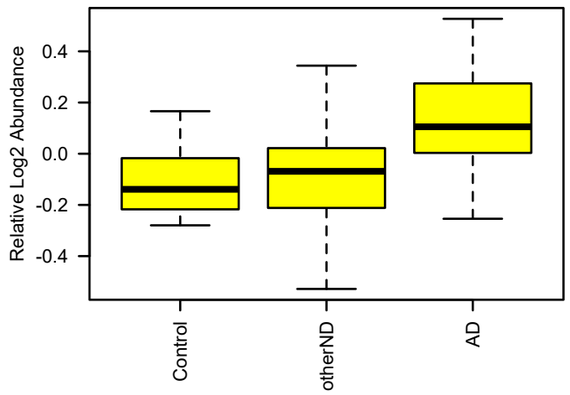

ITGB1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 5.3e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

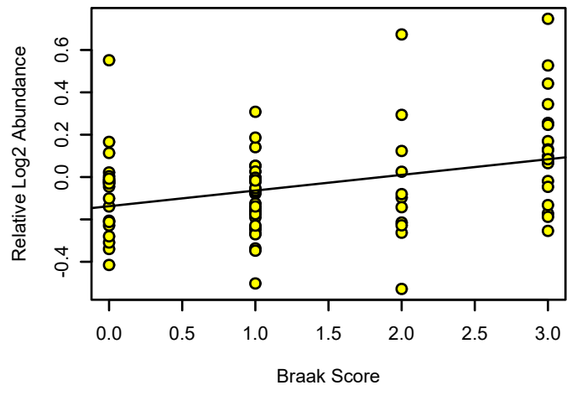

ITGB1 UPenn Mixed PRM
K-W ANOVA p: 0.0011
Relative Log2 Abundance
Control
otherND
AD


bicor=0.34, p=0.0014
cor=0.32, p=0.003
Relative Log2 Abundance
Braak Score


bicor=0.31, p=0.002
cor=0.29, p=0.0034
Relative Log2 Abundance
CERAD Score


ENO1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 2.9e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA


ENO1 UPenn Mixed PRM
K-W ANOVA p: 7e-04
Relative Log2 Abundance
Control
otherND
AD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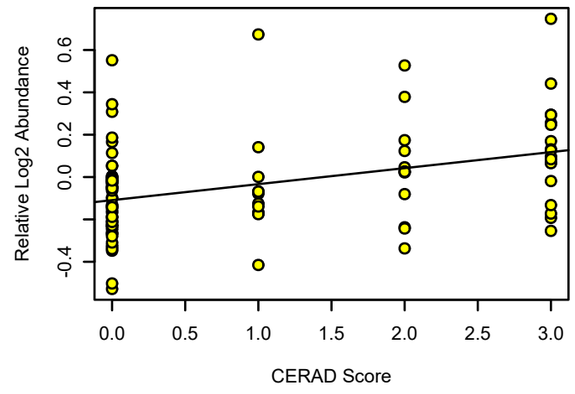
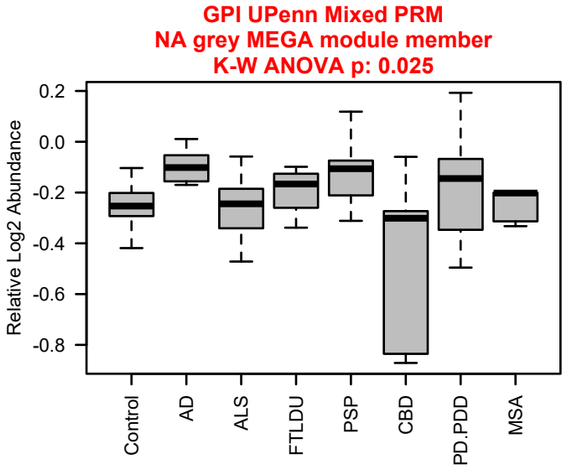
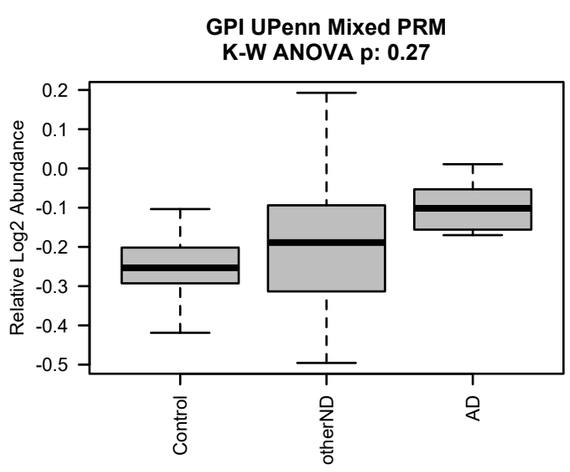
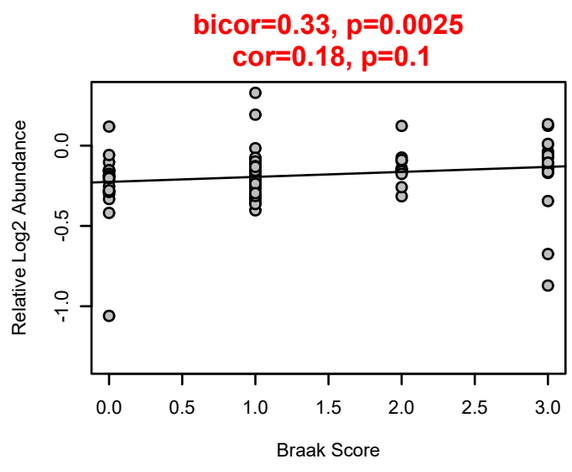
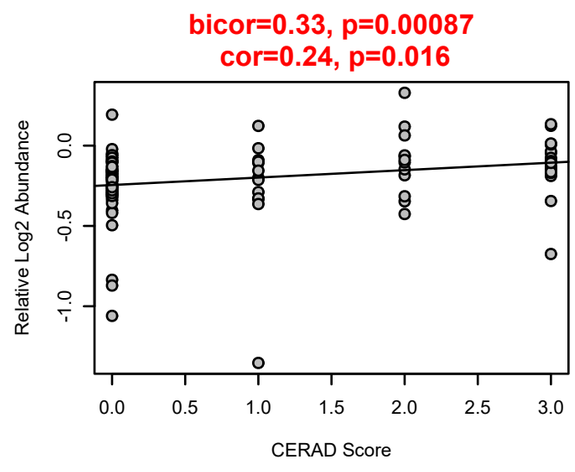
cor=0.34, p=0.0016
Relative Log2 Abundance
Braak Score

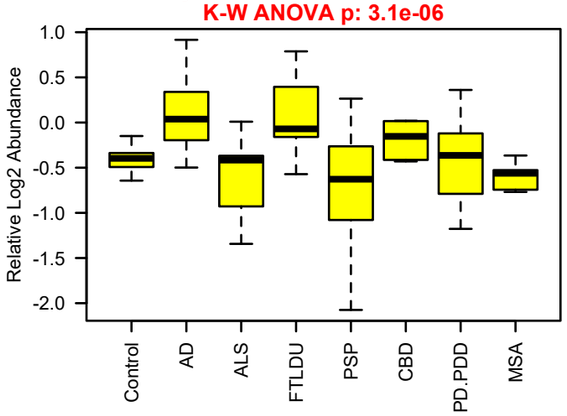

bicor=0.4, p=3.1e-05
cor=0.39, p=6e-05
Relative Log2 Abundance
CERAD Score

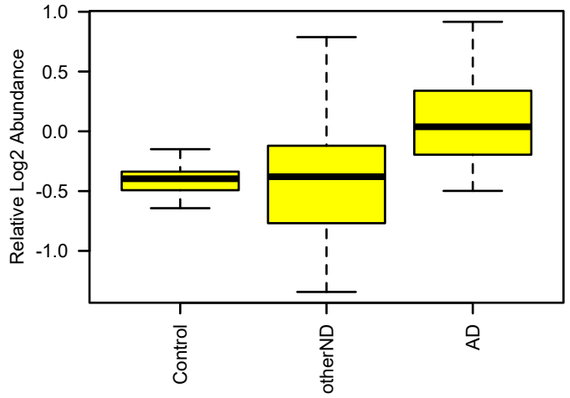

GPI UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.025
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

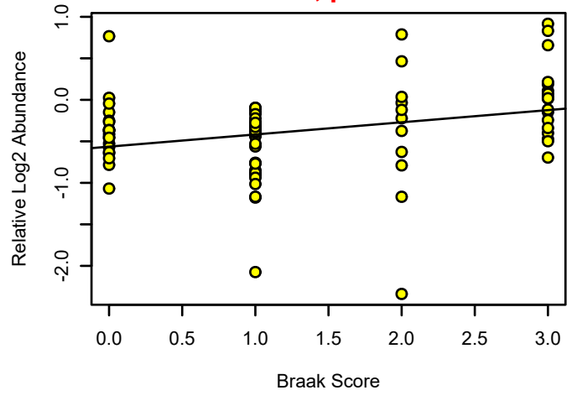

GPI UPenn Mixed PRM
K-W ANOVA p: 0.27
Relative Log2 Abundance
Control
otherND
AD

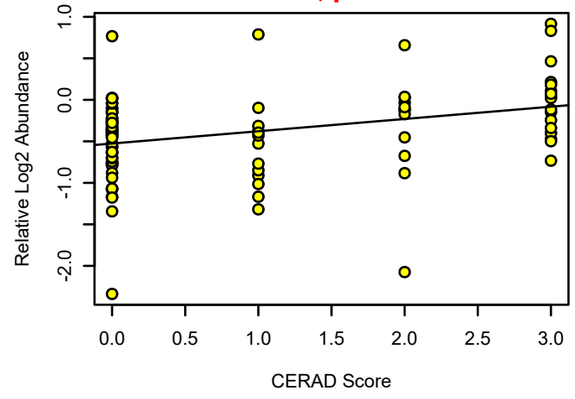

bicor=0.33, p=0.0025
cor=0.18, p=0.1
Relative Log2 Abundance
Braak Score

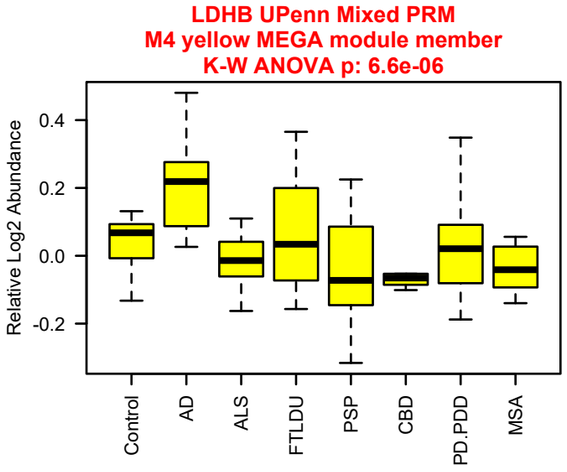

bicor=0.33, p=0.00087
cor=0.24, p=0.016
Relative Log2 Abundance
CERAD Score

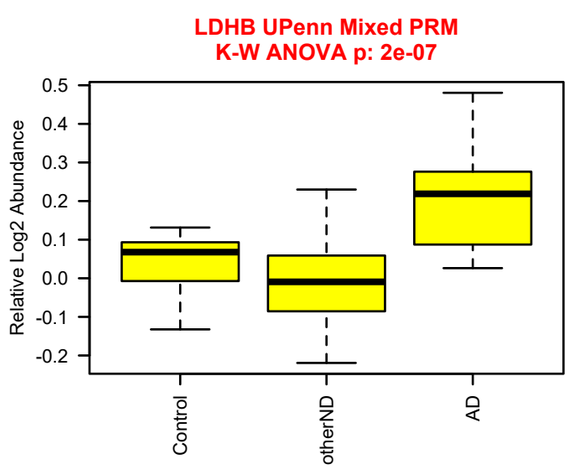

DBI UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 3.1e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

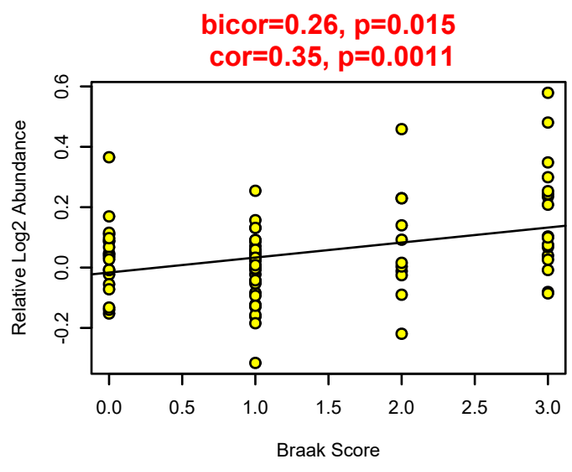

DBI UPenn Mixed PRM
K-W ANOVA p: 0.00011
Relative Log2 Abundance
Control
otherND
AD

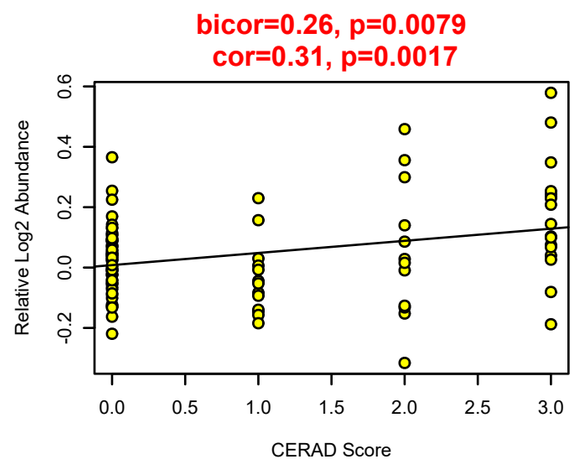

bicor=0.38, p=0.00044
cor=0.3, p=0.0056
Relative Log2 Abundance
Braak Score

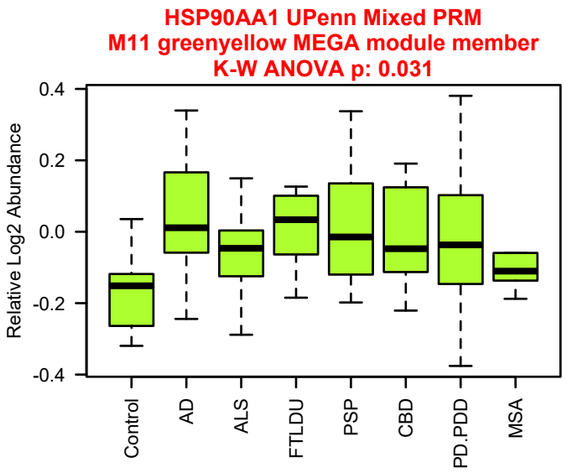

bicor=0.39, p=6.8e-05
cor=0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

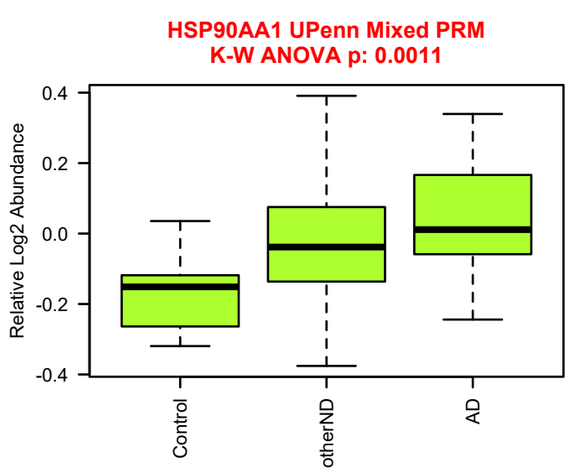

LDHB UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 6.6e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

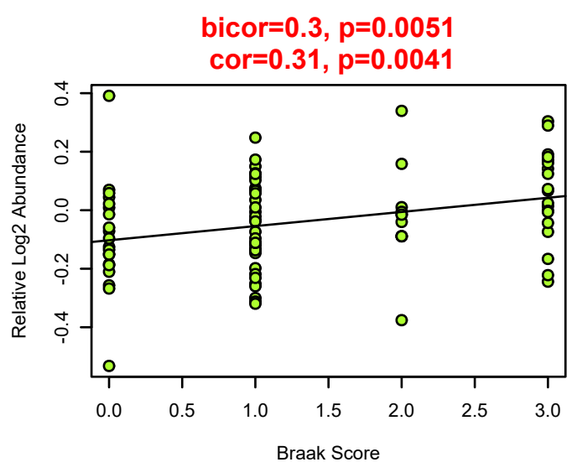

LDHB UPenn Mixed PRM
K-W ANOVA p: 2e-07
Relative Log2 Abundance
Control
otherND
AD

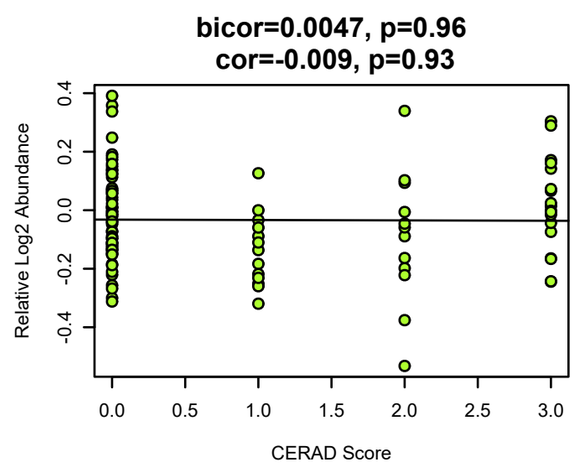

bicor=0.26, p=0.015
cor=0.35, p=0.0011
Relative Log2 Abundance
Braak Score

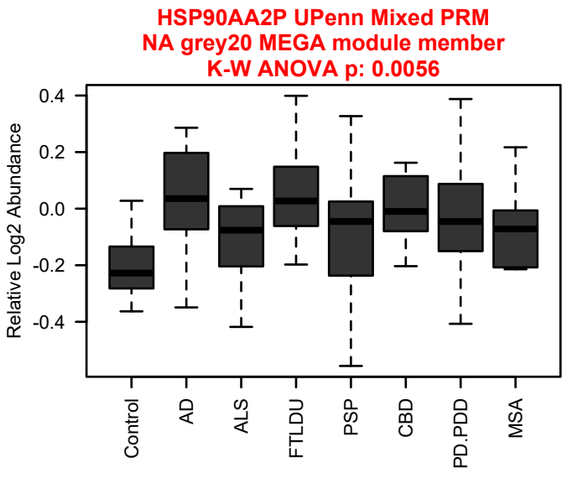

bicor=0.26, p=0.0079
cor=0.31, p=0.0017
Relative Log2 Abundance
CERAD Score

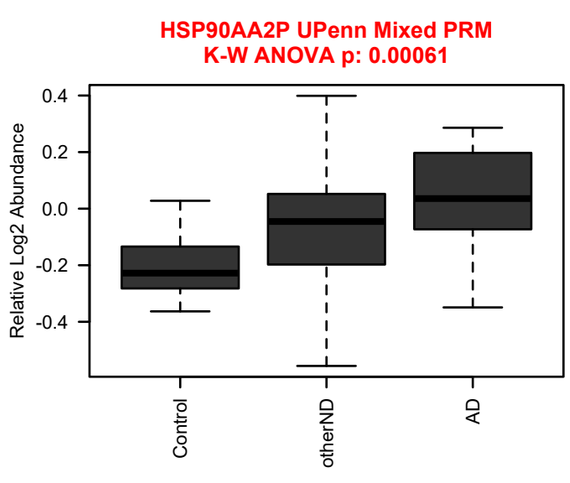

HSP90AA1 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 0.031
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

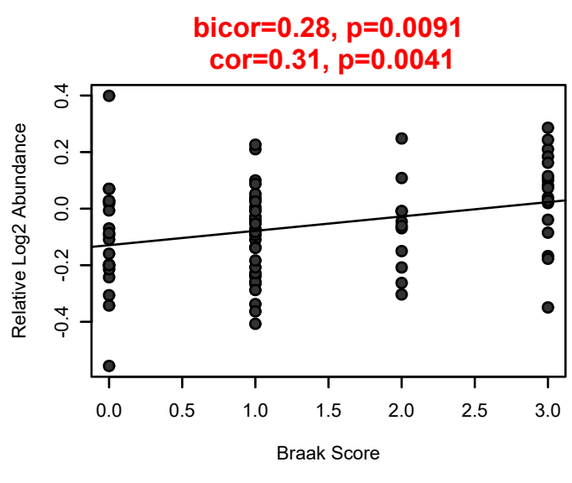

HSP90AA1 UPenn Mixed PRM
K-W ANOVA p: 0.0011
Relative Log2 Abundance
Control
otherND
AD

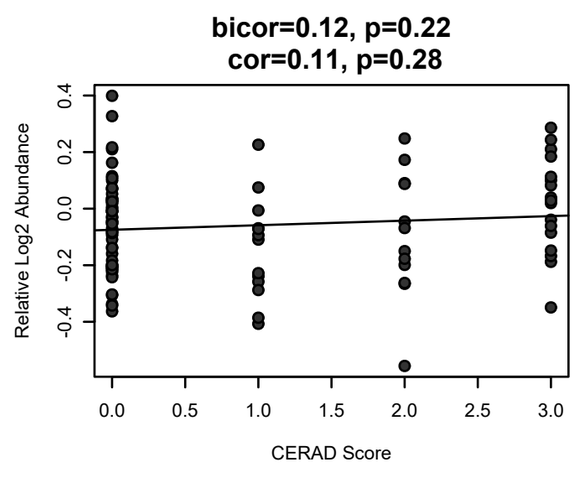

bicor=0.3, p=0.0051
cor=0.31, p=0.0041
Relative Log2 Abundance
Braak Score

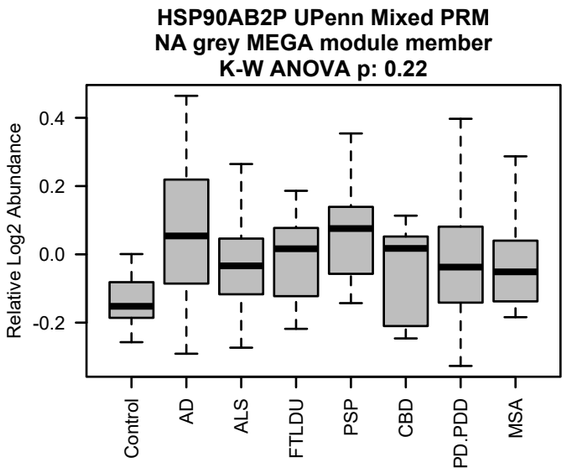

bicor=0.0047, p=0.96
cor=-0.009, p=0.93
Relative Log2 Abundance
CERAD Score

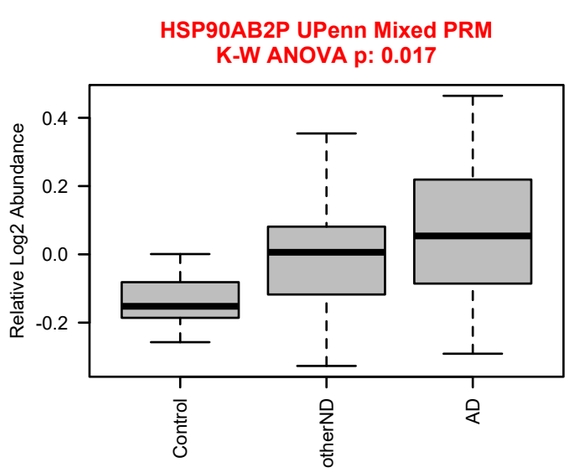

HSP90AA2P UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.0056
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

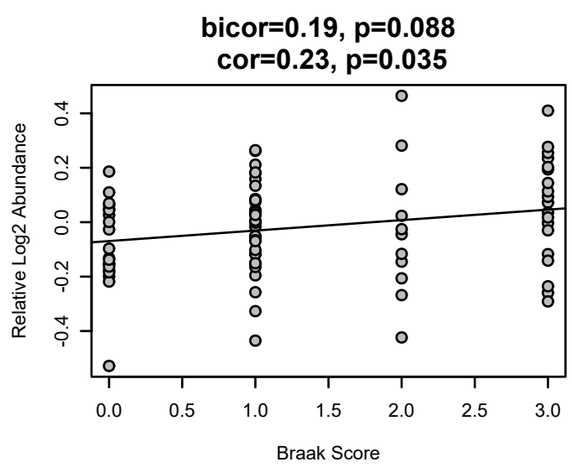

HSP90AA2P UPenn Mixed PRM
K-W ANOVA p: 0.00061
Relative Log2 Abundance
Control
otherND
AD

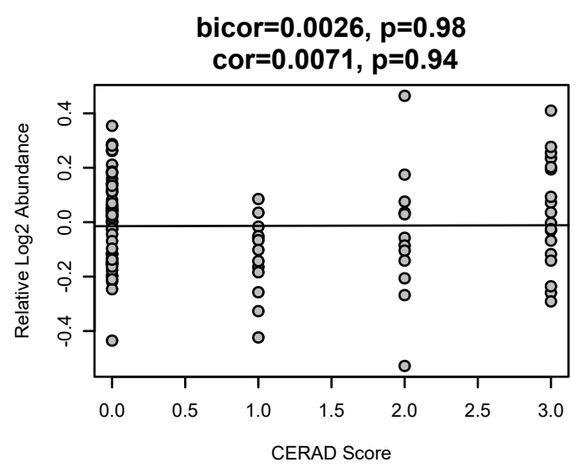

bicor=0.28, p=0.0091
cor=0.31, p=0.0041
Relative Log2 Abundance
Braak Score

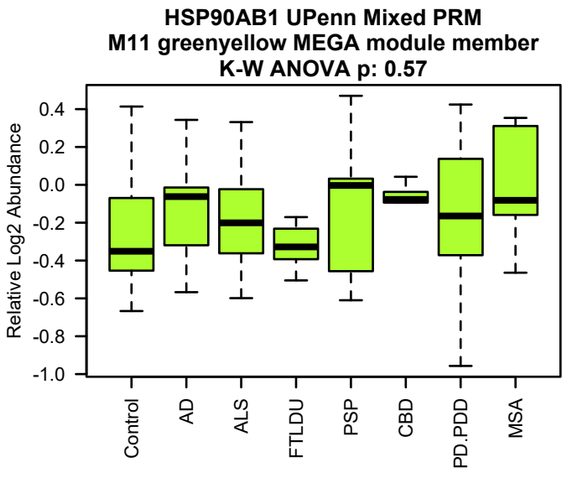

bicor=0.12, p=0.22
cor=0.11, p=0.28
Relative Log2 Abundance
CERAD Score

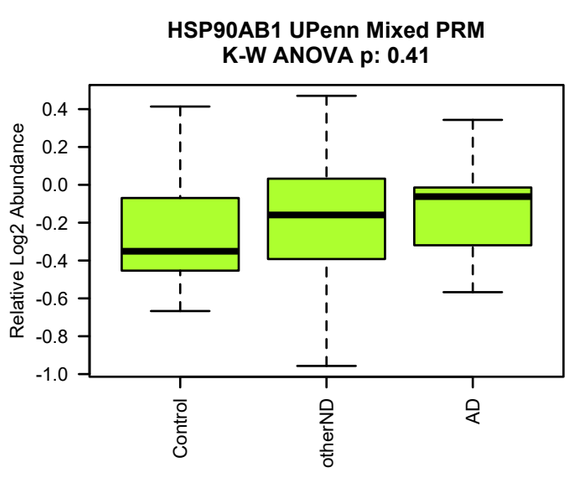

HSP90AB2P UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.22
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

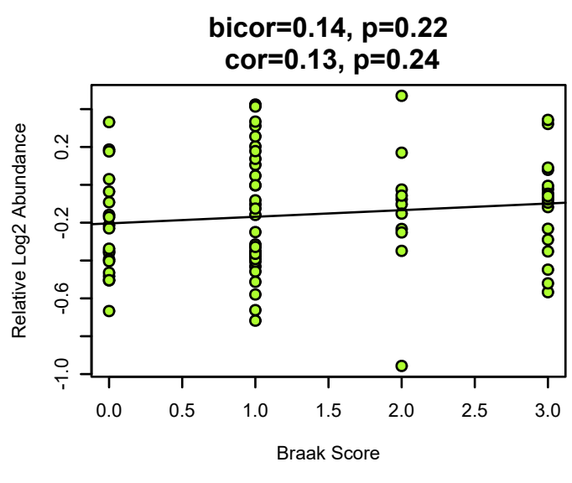

HSP90AB2P UPenn Mixed PRM
K-W ANOVA p: 0.017
Relative Log2 Abundance
Control
otherND
AD

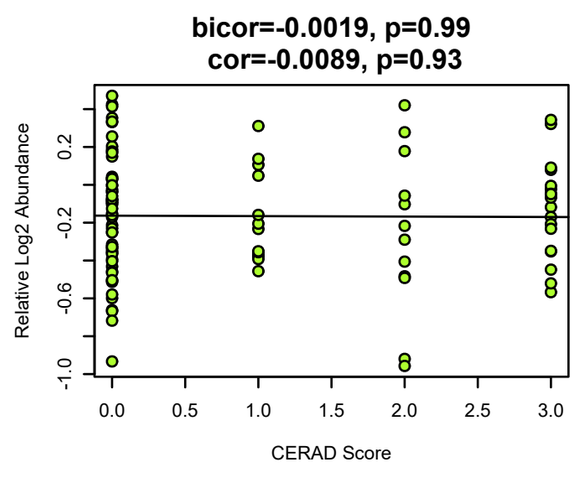

bicor=0.19, p=0.088
cor=0.23, p=0.035
Relative Log2 Abundance
Braak Score

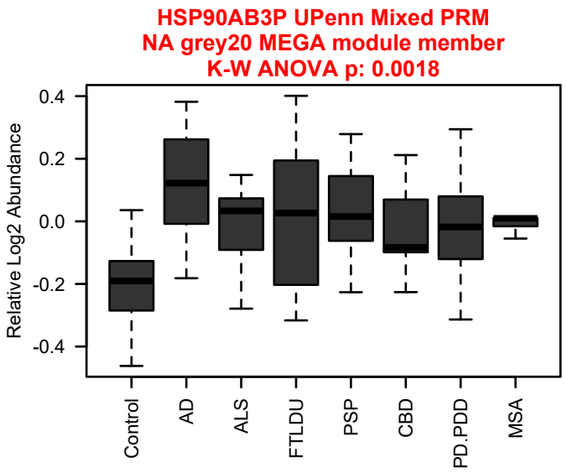

bicor=0.0026, p=0.98
cor=0.0071, p=0.94
Relative Log2 Abundance
CERAD Score

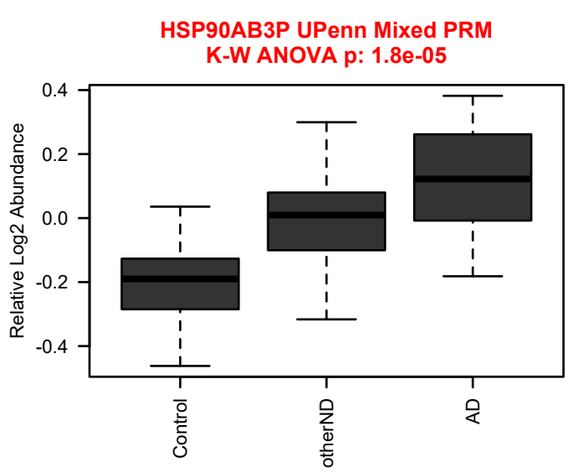

HSP90AB1 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 0.57
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

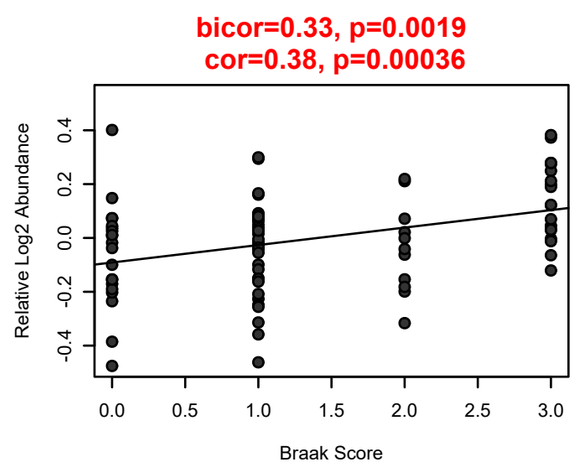

HSP90AB1 UPenn Mixed PRM
K-W ANOVA p: 0.41
Relative Log2 Abundance
Control
otherND
AD

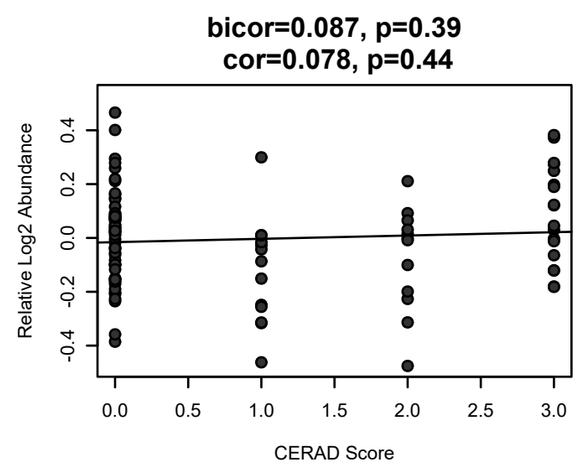

bicor=0.14, p=0.22
cor=0.13, p=0.24
Relative Log2 Abundance
Braak Score

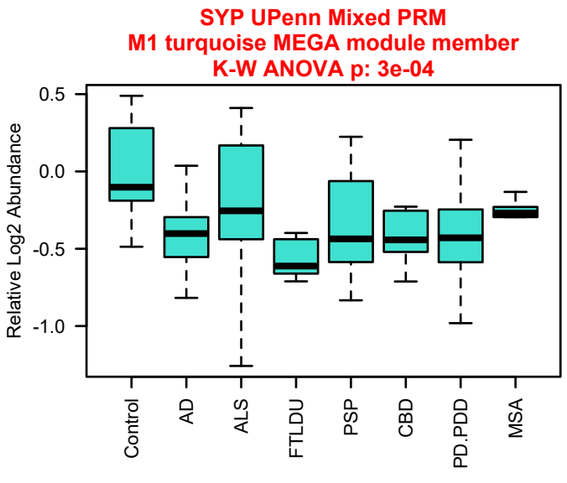

bicor=-0.0019, p=0.99
cor=-0.0089, p=0.93
Relative Log2 Abundance
CERAD Score

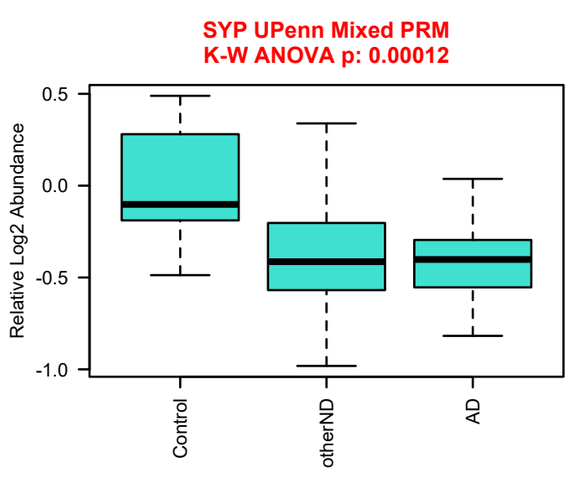

HSP90AB3P UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.0018
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

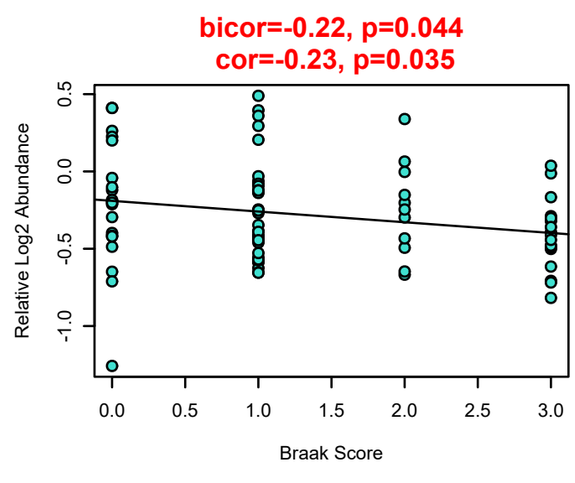

HSP90AB3P UPenn Mixed PRM
K-W ANOVA p: 1.8e-05
Relative Log2 Abundance
Control
otherND
AD

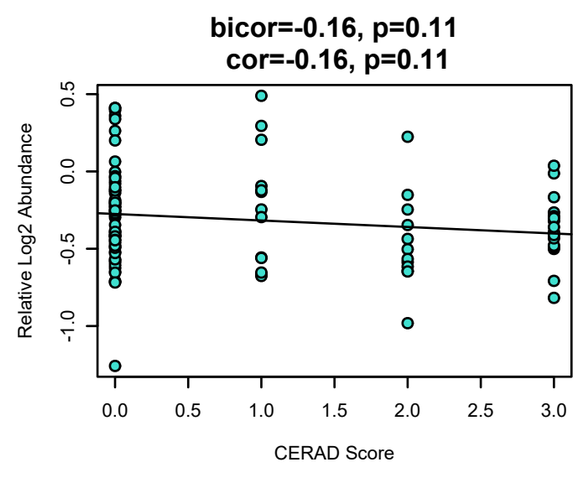

bicor=0.33, p=0.0019
cor=0.38, p=0.00036
Relative Log2 Abundance
Braak Score

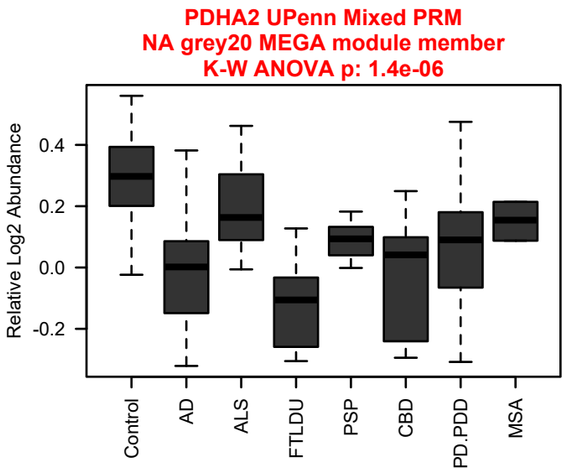

bicor=0.087, p=0.39
cor=0.078, p=0.44
Relative Log2 Abundance
CERAD Score

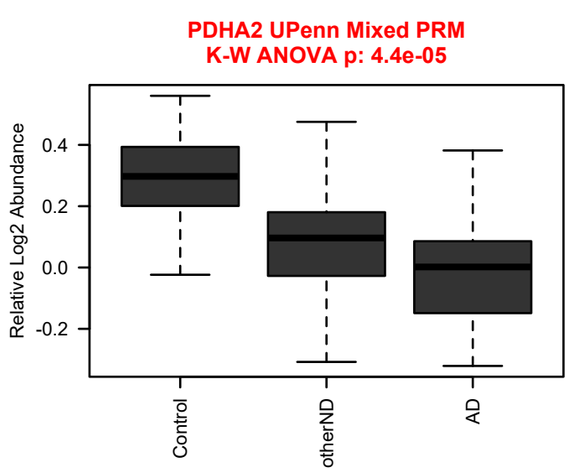

SYP UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 3e-04
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

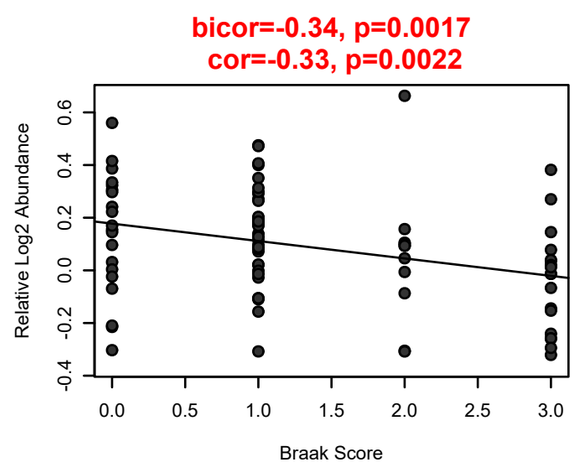

SYP UPenn Mixed PRM
K-W ANOVA p: 0.00012
Relative Log2 Abundance
Control
otherND
AD

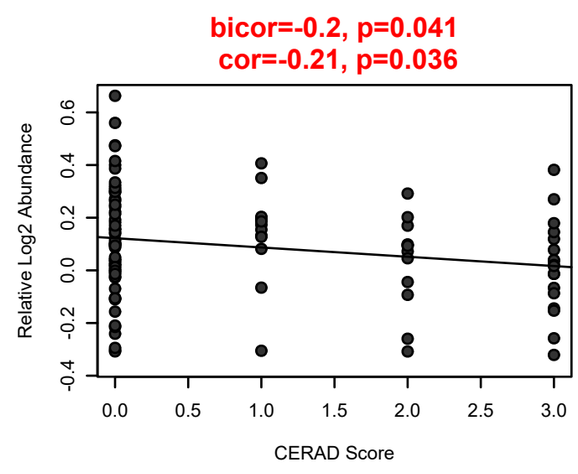

bicor=-0.22, p=0.044
cor=-0.23, p=0.035
Relative Log2 Abundance
Braak Score

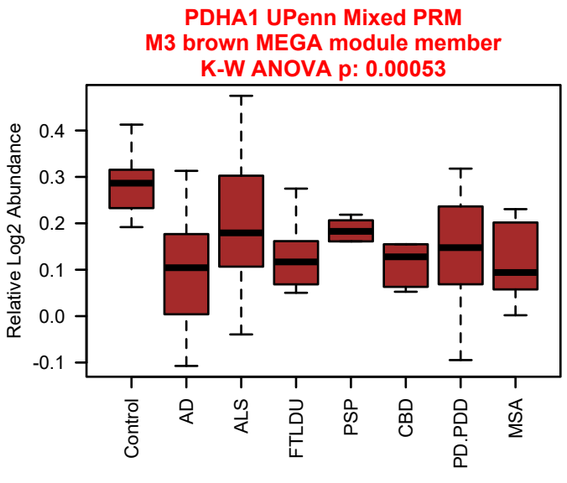

bicor=-0.16, p=0.11
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

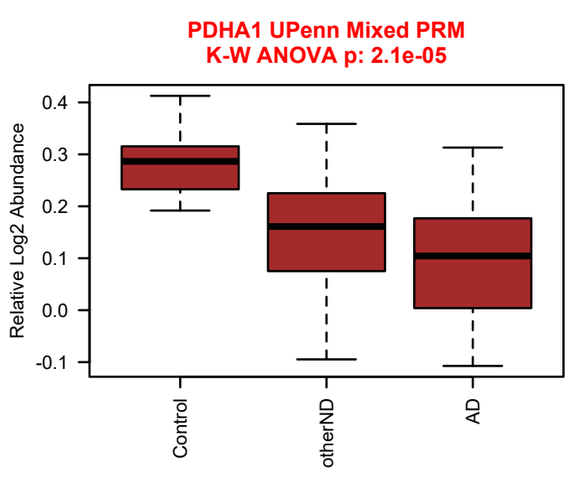

PDHA2 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 1.4e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

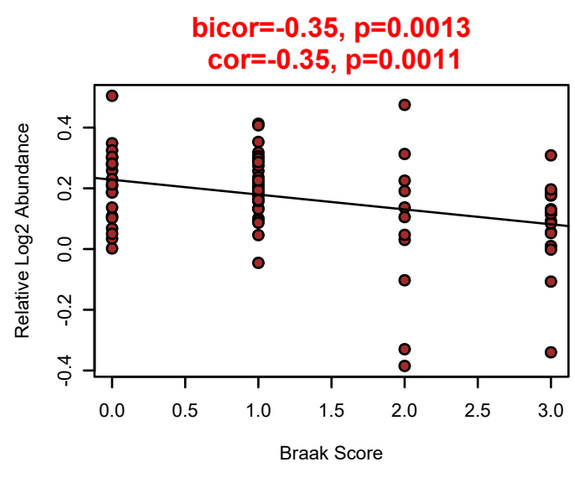

PDHA2 UPenn Mixed PRM
K-W ANOVA p: 4.4e-05
Relative Log2 Abundance
Control
otherND
AD

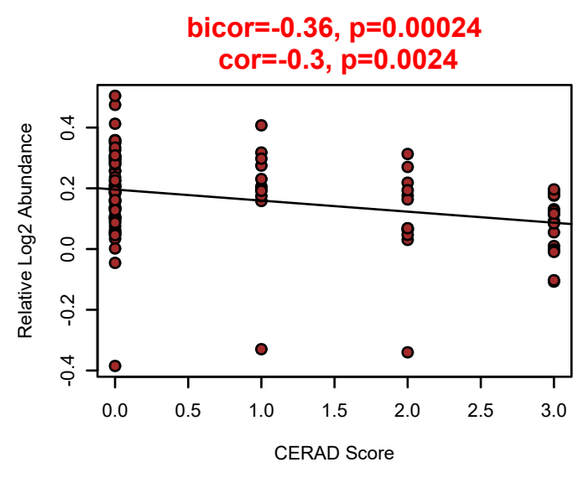

bicor=-0.34, p=0.0017
cor=-0.33, p=0.0022
Relative Log2 Abundance
Braak Score

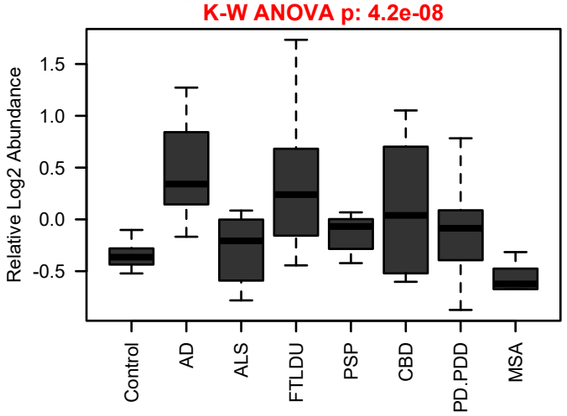

bicor=-0.2, p=0.041
cor=-0.21, p=0.036
Relative Log2 Abundance
CERAD Score

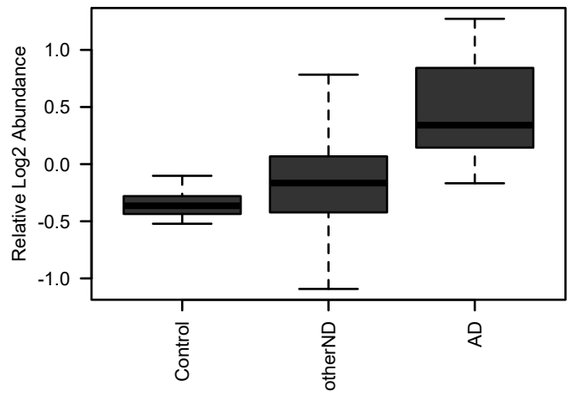

PDHA1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.00053
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

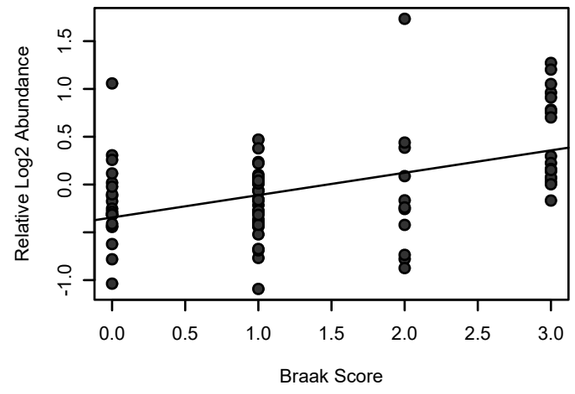

PDHA1 UPenn Mixed PRM
K-W ANOVA p: 2.1e-05
Relative Log2 Abundance
Control
otherND
AD

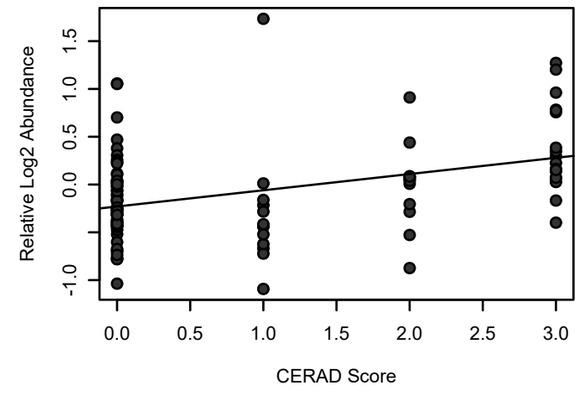

bicor=-0.35, p=0.0013
cor=-0.35, p=0.0011
Relative Log2 Abundance
Braak Score

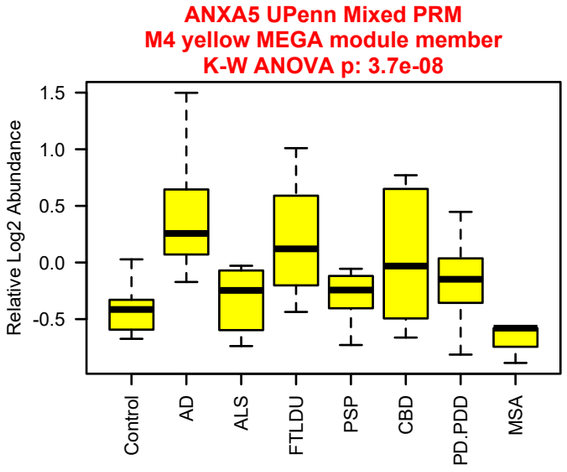

bicor=-0.36, p=0.00024
cor=-0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

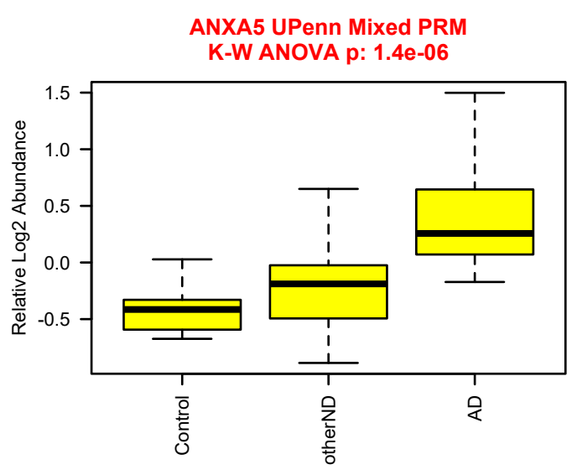

HPS6 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 4.2e-08
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

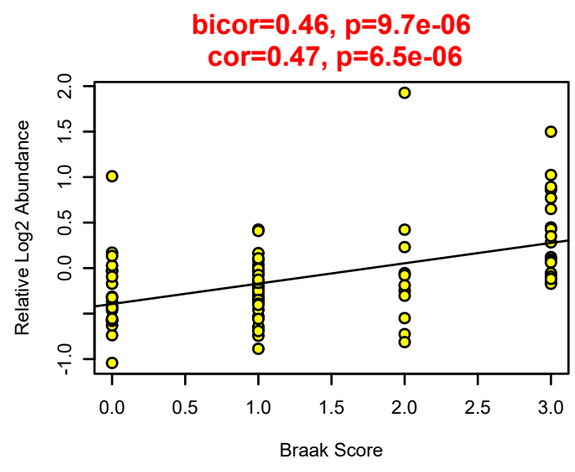

HPS6 UPenn Mixed PRM
K-W ANOVA p: 1.1e-06
Relative Log2 Abundance
Control
otherND
AD

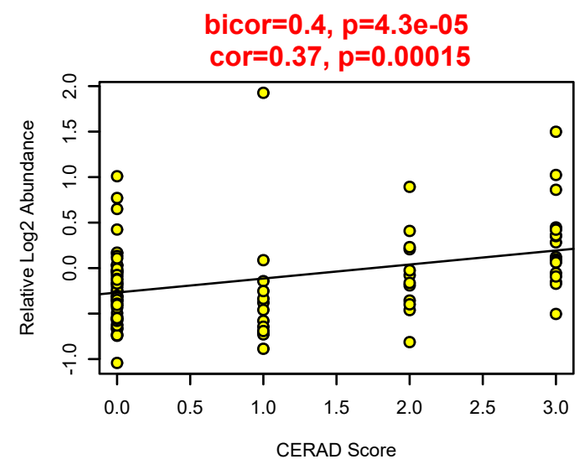

bicor=0.47, p=6.2e-06
cor=0.47, p=6.5e-06
Relative Log2 Abundance
Braak Score

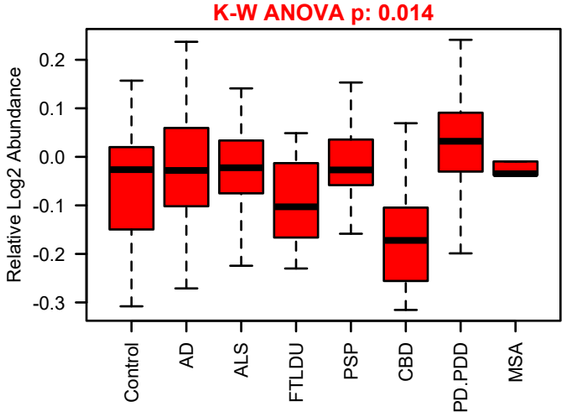

bicor=0.42, p=1.7e-05
cor=0.39, p=6e-05
Relative Log2 Abundance
CERAD Score

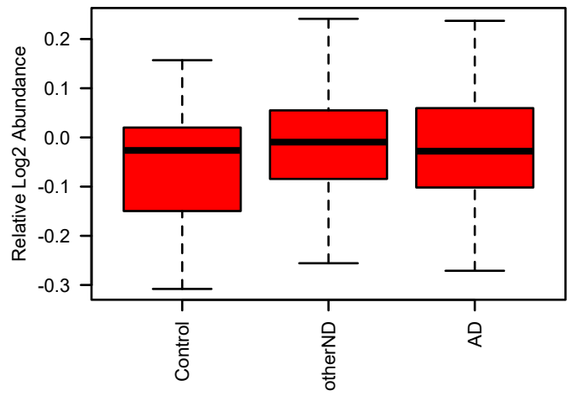

ANXA5 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 3.7e-08
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

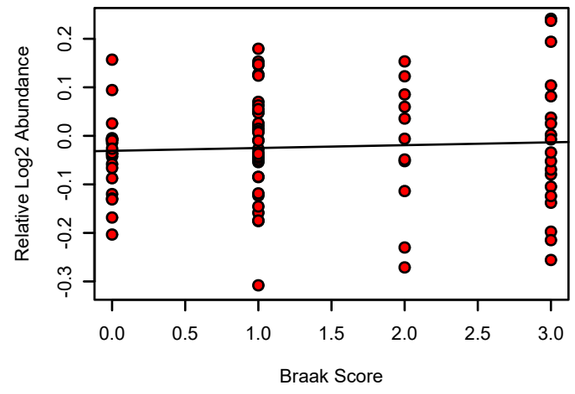

ANXA5 UPenn Mixed PRM
K-W ANOVA p: 1.4e-06
Relative Log2 Abundance
Control
otherND
AD

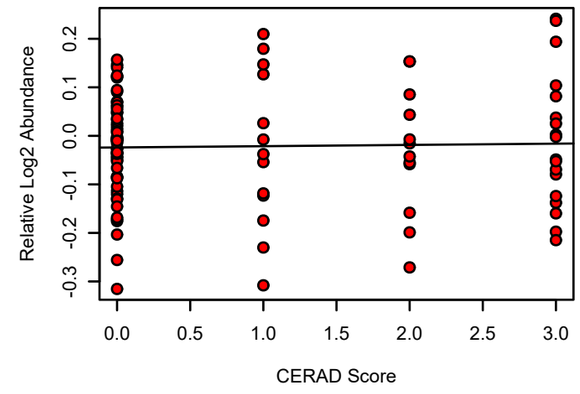

bicor=0.46, p=9.7e-06
cor=0.47, p=6.5e-06
Relative Log2 Abundance
Braak Score

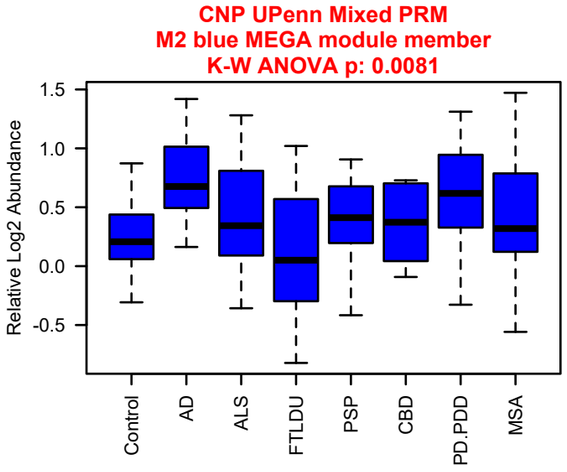

bicor=0.4, p=4.3e-05
cor=0.37, p=0.00015
Relative Log2 Abundance
CERAD Score

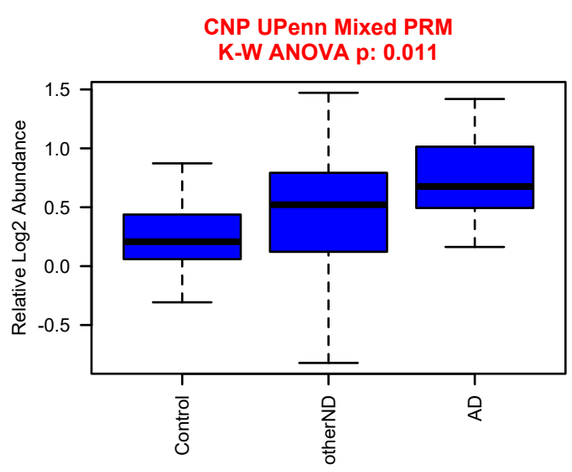

CLTA UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.014
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

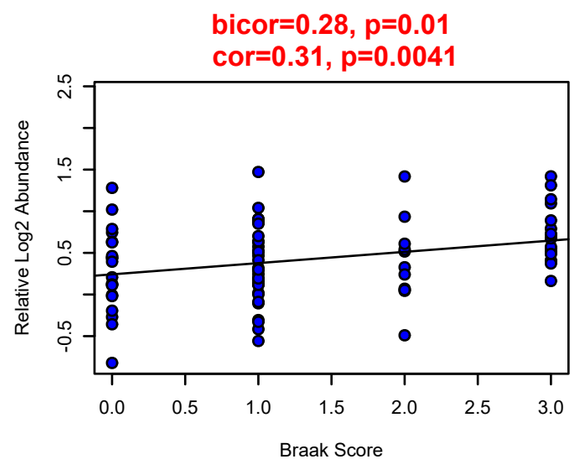

CLTA UPenn Mixed PRM
K-W ANOVA p: 0.51
Relative Log2 Abundance
Control
otherND
AD

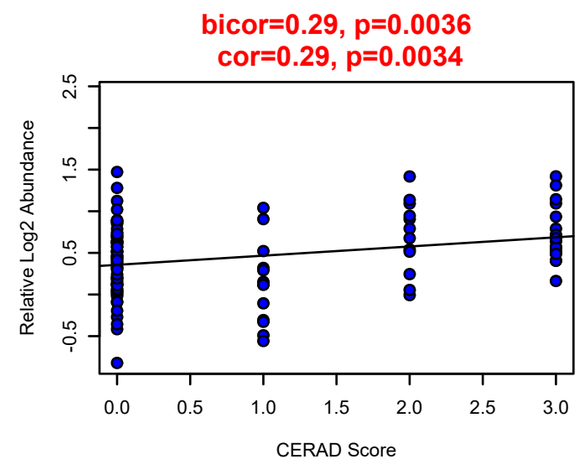

bicor=0.056, p=0.61
cor=0.054, p=0.63
Relative Log2 Abundance
Braak Score

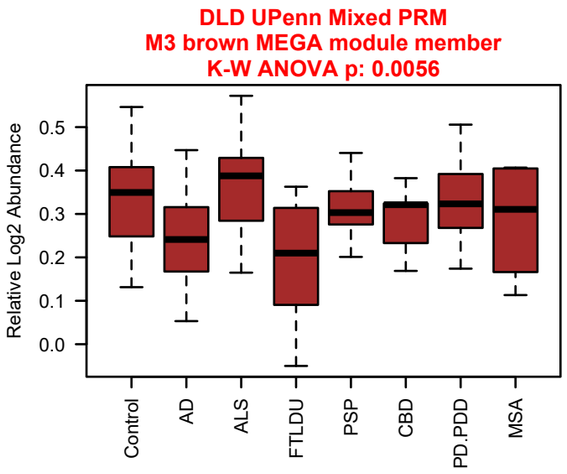

bicor=0.0069, p=0.95
cor=0.026, p=0.8
Relative Log2 Abundance
CERAD Score

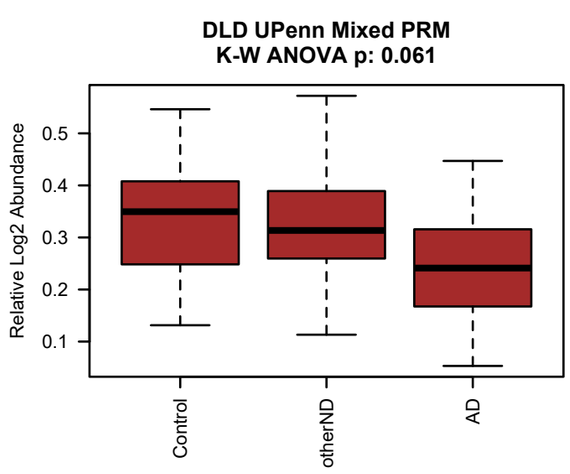

CNP UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.0081
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

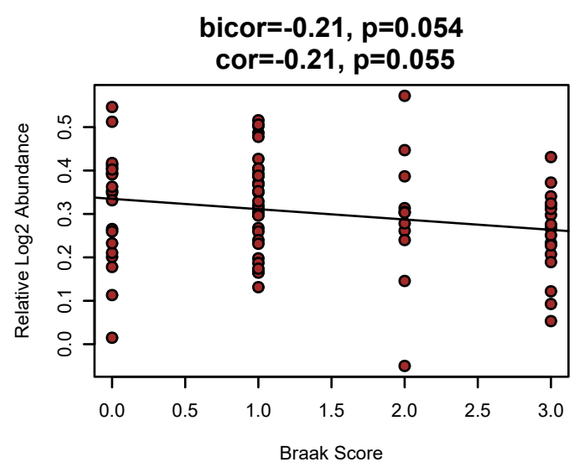

CNP UPenn Mixed PRM
K-W ANOVA p: 0.011
Relative Log2 Abundance
Control
otherND
AD

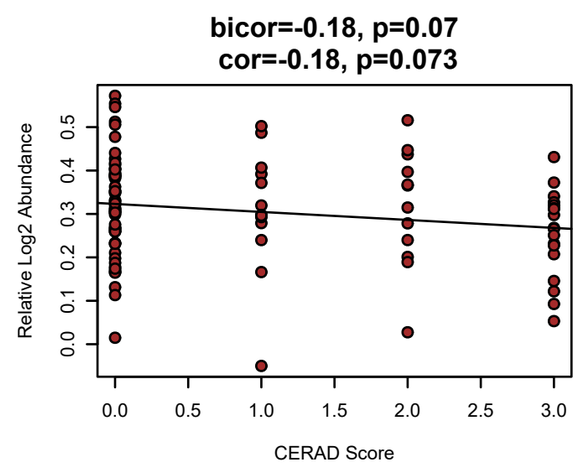

bicor=0.28, p=0.01
cor=0.31, p=0.0041
Relative Log2 Abundance
Braak Score

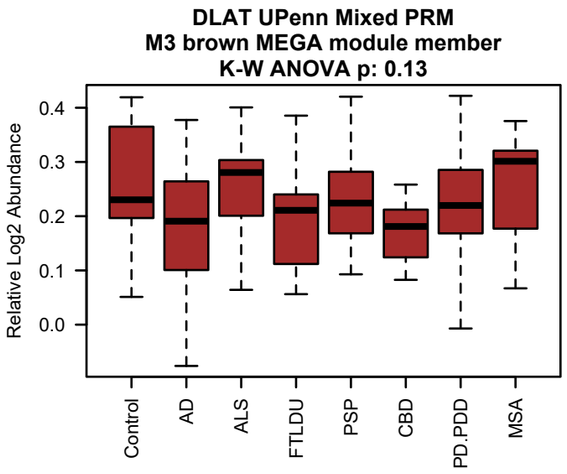

bicor=0.29, p=0.0036
cor=0.29, p=0.0034
Relative Log2 Abundance
CERAD Score

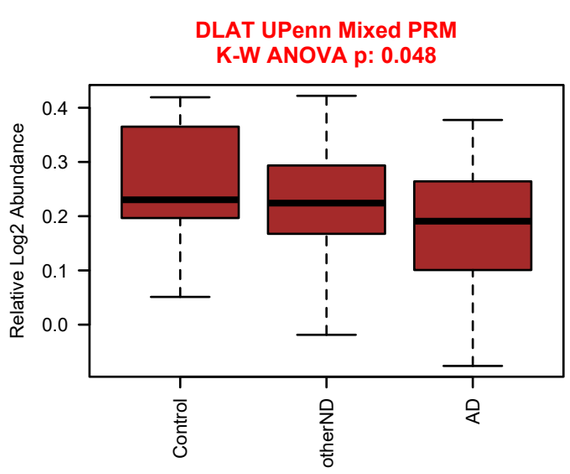

DLD UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0056
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

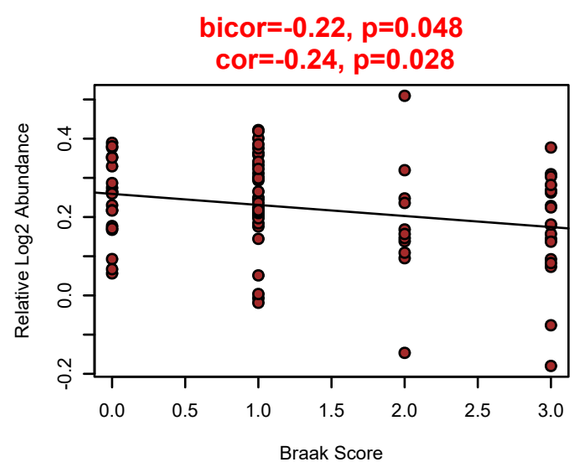

DLD UPenn Mixed PRM
K-W ANOVA p: 0.061
Relative Log2 Abundance
Control
otherND
AD

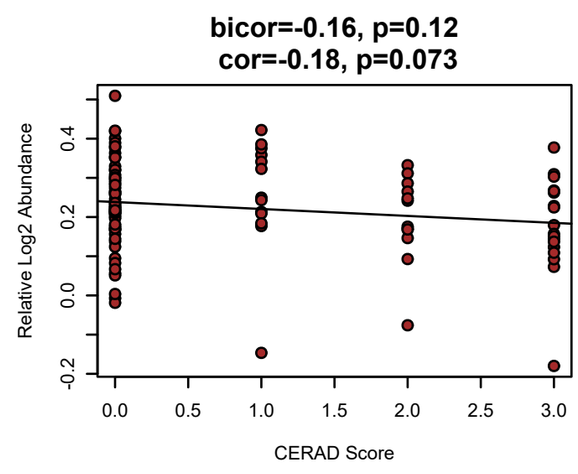

bicor=-0.21, p=0.054
cor=-0.21, p=0.055
Relative Log2 Abundance
Braak Score

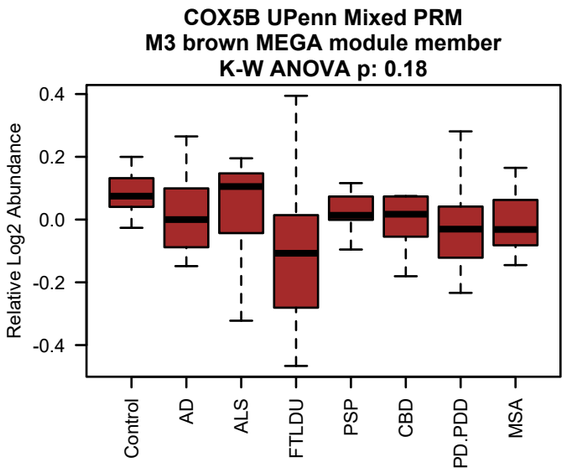

bicor=-0.18, p=0.07
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

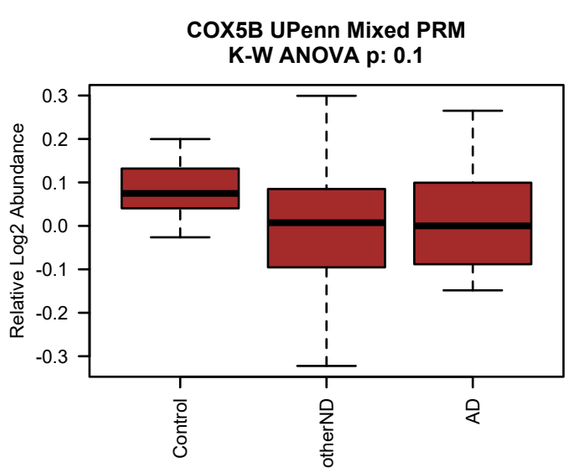

DLAT UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.13
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

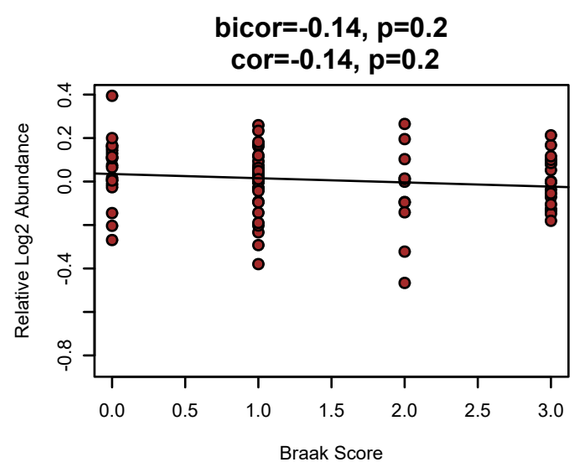

DLAT UPenn Mixed PRM
K-W ANOVA p: 0.048
Relative Log2 Abundance
Control
otherND
AD

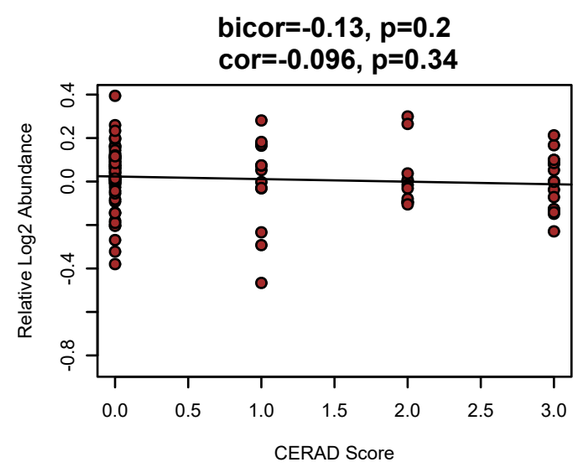

bicor=-0.22, p=0.048
cor=-0.24, p=0.028
Relative Log2 Abundance
Braak Score

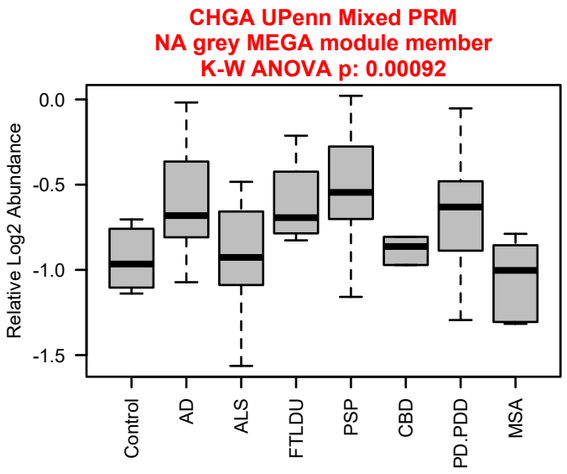

bicor=-0.16, p=0.12
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

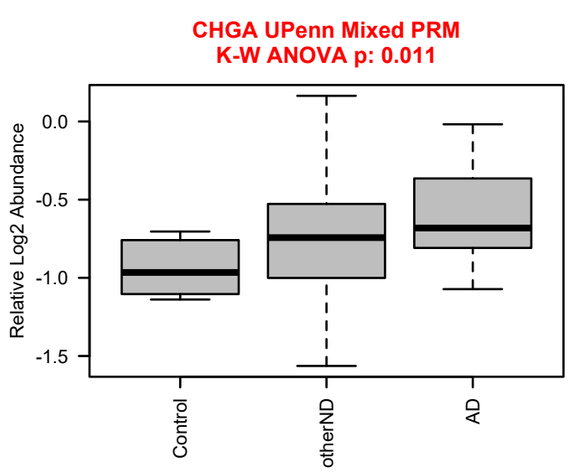

COX5B UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.18
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

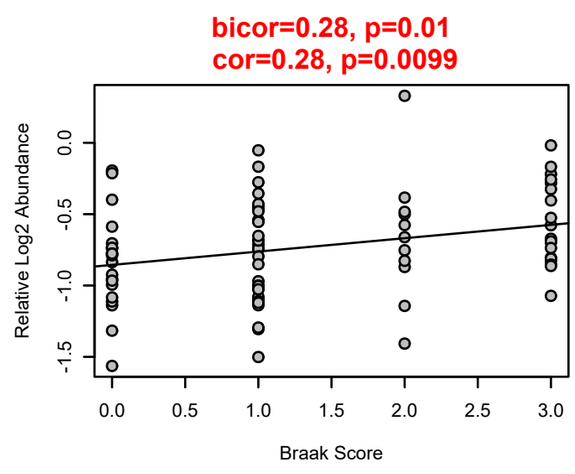

COX5B UPenn Mixed PRM
K-W ANOVA p: 0.1
Relative Log2 Abundance
Control
otherND
AD

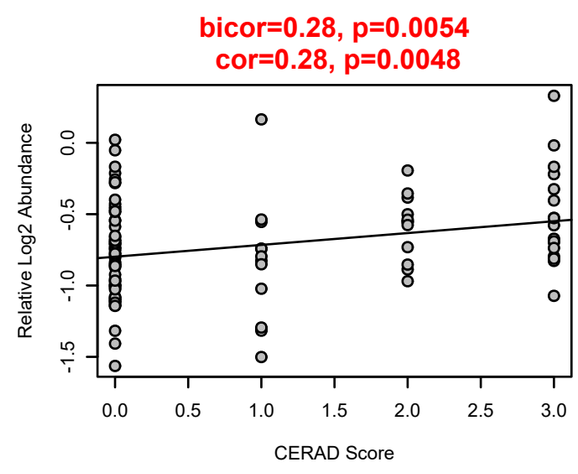

bicor=-0.14, p=0.2
cor=-0.14, p=0.2
Relative Log2 Abundance
Braak Score

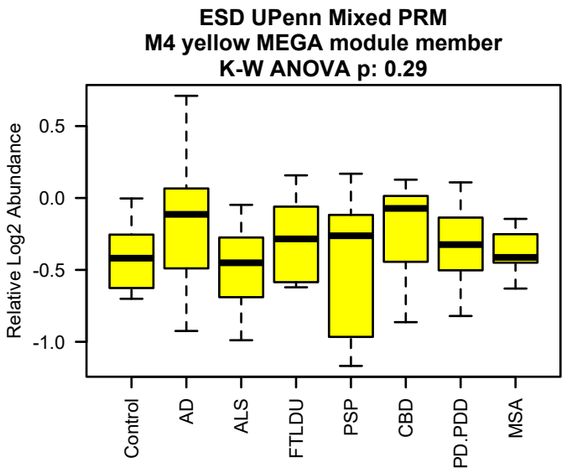

bicor=-0.13, p=0.2
cor=-0.096, p=0.34
Relative Log2 Abundance
CERAD Score

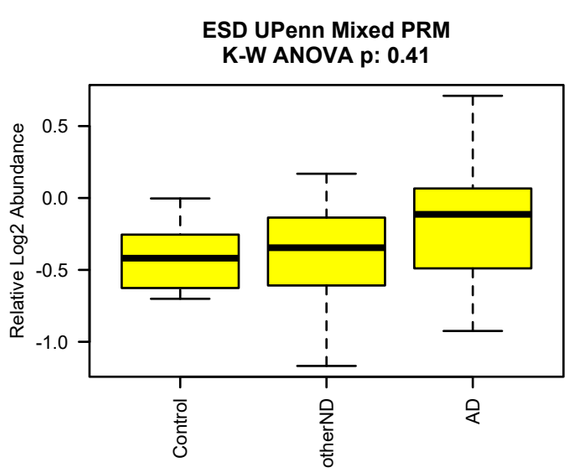

CHGA UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.00092
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

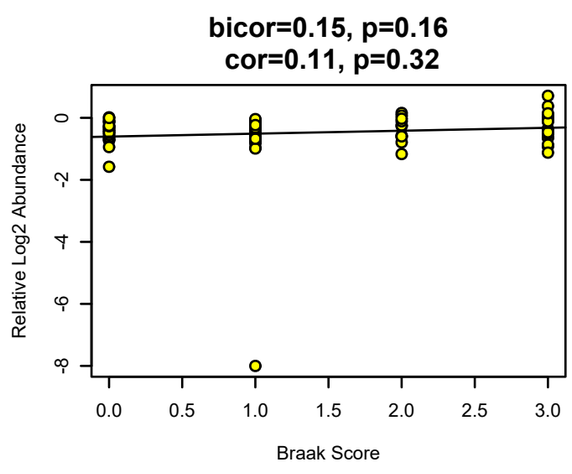

CHGA UPenn Mixed PRM
K-W ANOVA p: 0.011
Relative Log2 Abundance
Control
otherND
AD

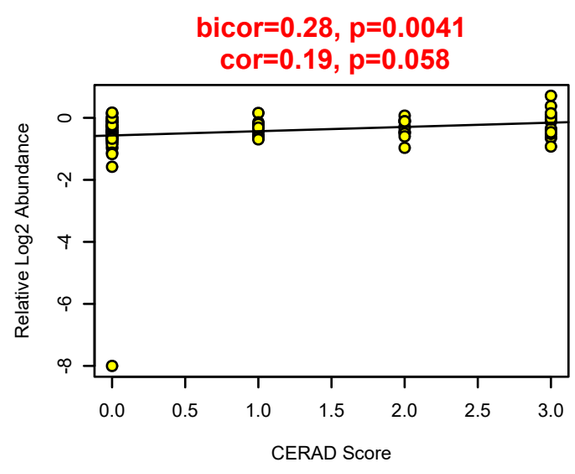

bicor=0.28, p=0.01
cor=0.28, p=0.0099
Relative Log2 Abundance
Braak Score

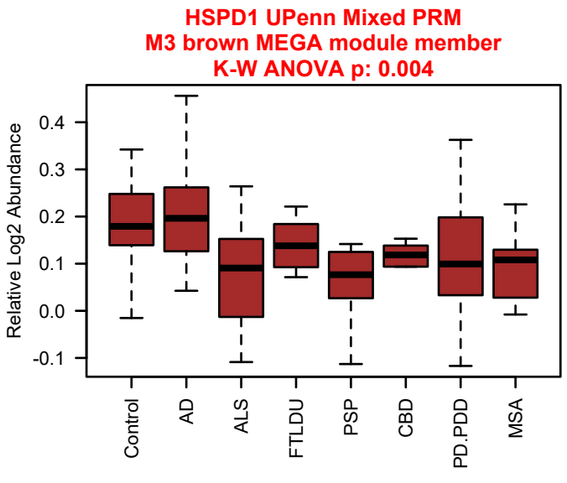

bicor=0.28, p=0.0054
cor=0.28, p=0.0048
Relative Log2 Abundance
CERAD Score

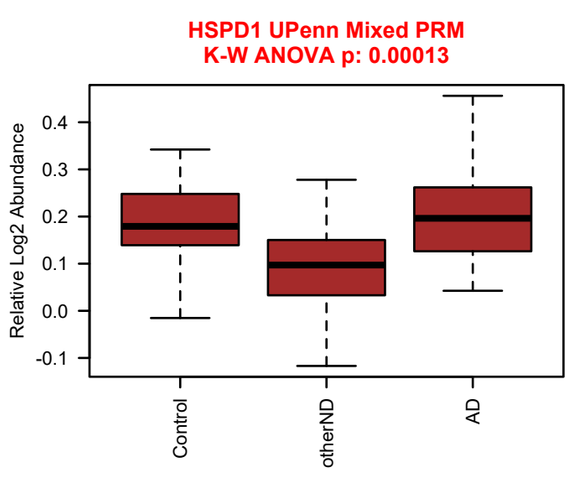

ESD UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.29
Relative Log2 Abundance
0.5
0.0
-0.5
-1.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

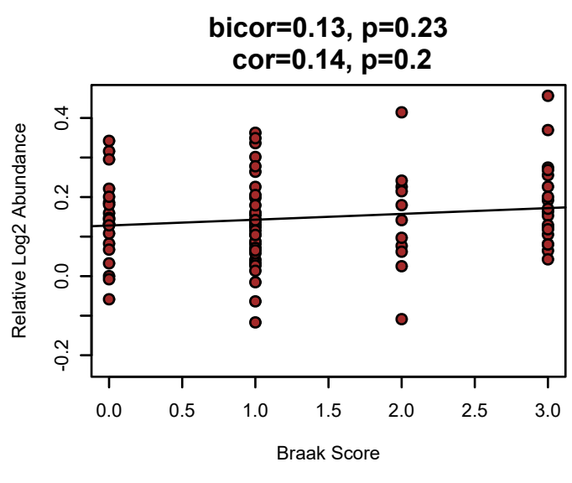

ESD UPenn Mixed PRM
K-W ANOVA p: 0.41
Relative Log2 Abundance
0.5
0.0
-0.5
-1.0
Control
otherND
AD

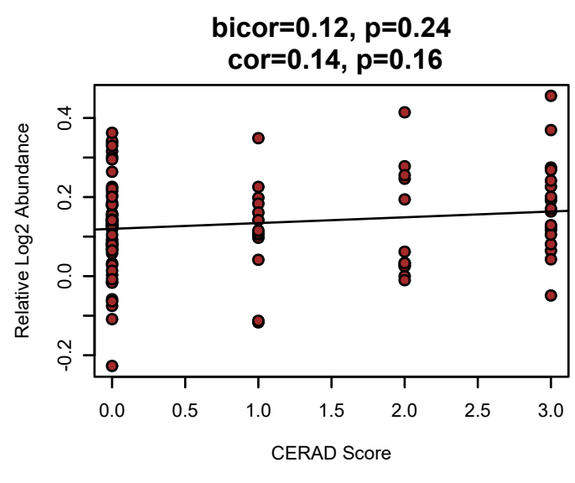

bicor=0.15, p=0.16
cor=0.11, p=0.32
Relative Log2 Abundance
0
-2
-4
-6
-8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

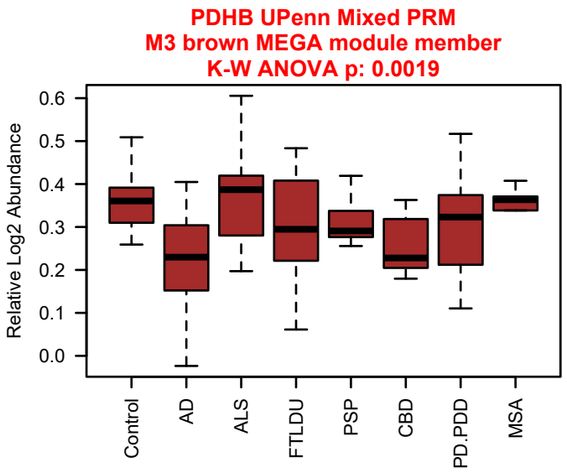

bicor=0.28, p=0.0041
cor=0.19, p=0.058
Relative Log2 Abundance
0
-2
-4
-6
-8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

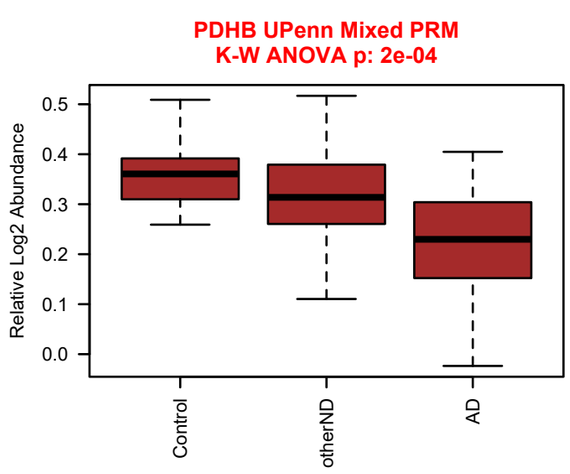

HSPD1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.004
Relative Log2 Abundance
0.4
0.3
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

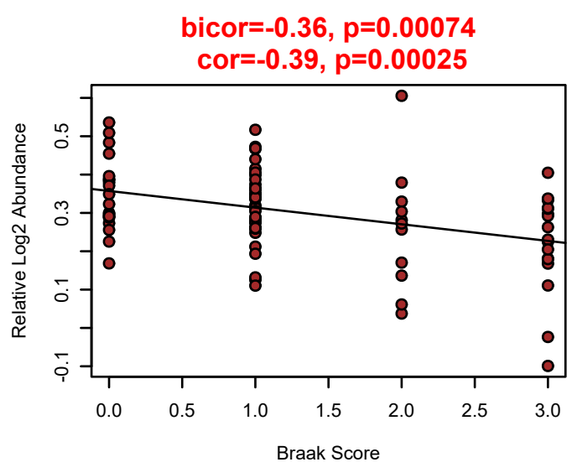

HSPD1 UPenn Mixed PRM
K-W ANOVA p: 0.00013
Relative Log2 Abundance
0.4
0.3
0.2
0.1
0.0
-0.1
Control
otherND
AD

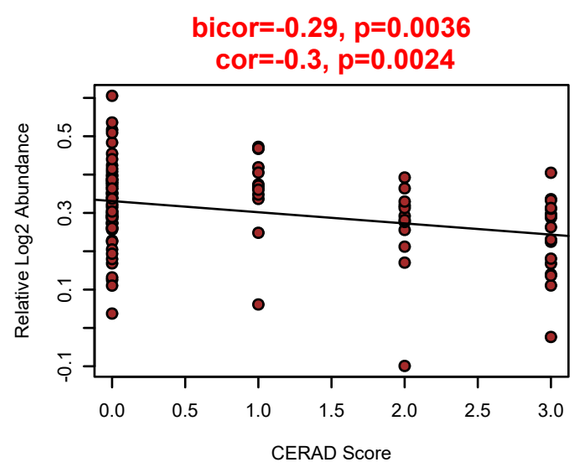

bicor=0.13, p=0.23
cor=0.14, p=0.2
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

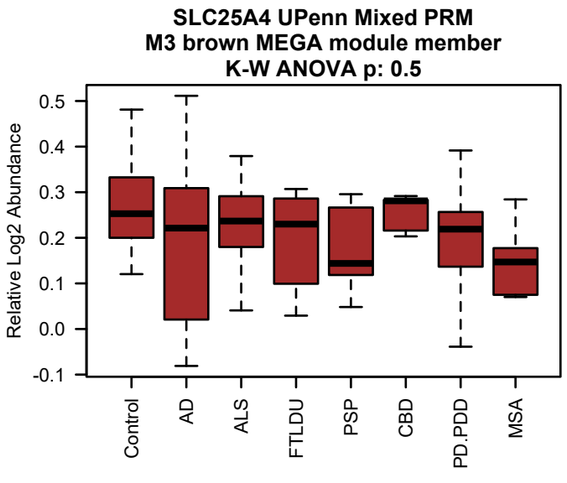

bicor=0.12, p=0.24
cor=0.14, p=0.16
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

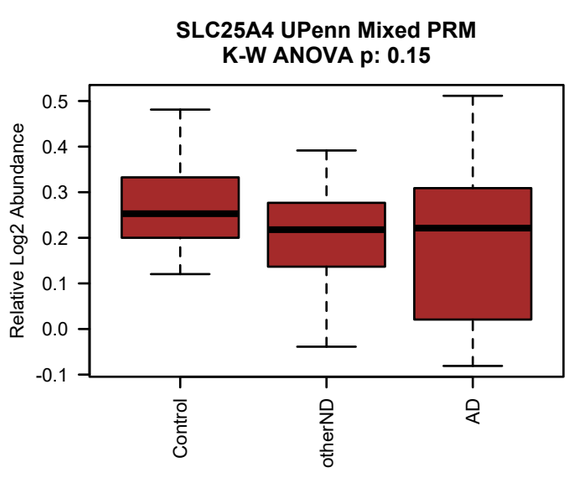

PDHB UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0019
Relative Log2 Abundance
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

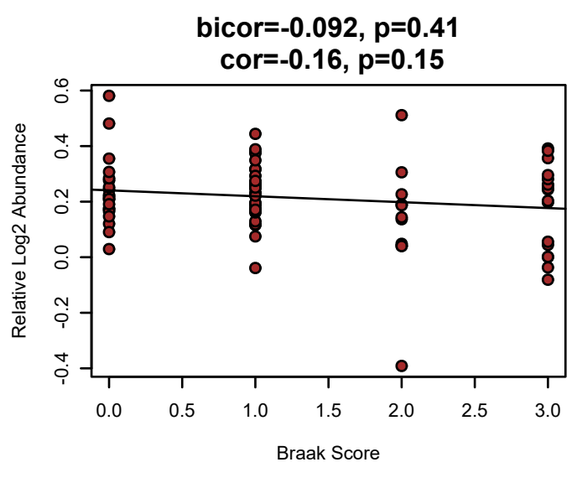

PDHB UPenn Mixed PRM
K-W ANOVA p: 2e-04
Relative Log2 Abundance
0.5
0.4
0.3
0.2
0.1
0.0
Control
otherND
AD

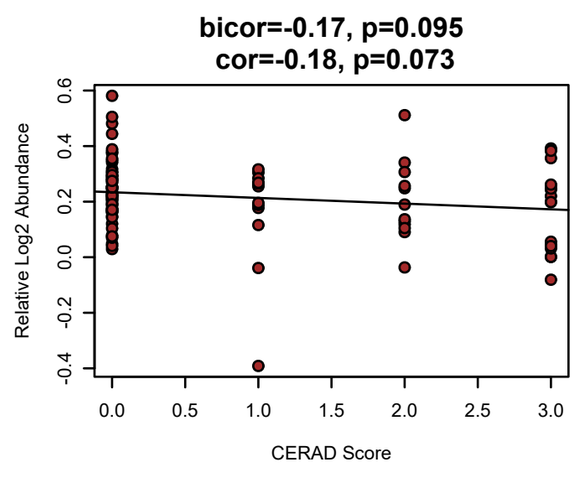

bicor=-0.36, p=0.00074
cor=-0.39, p=0.00025
Relative Log2 Abundance
0.5
0.3
0.1
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

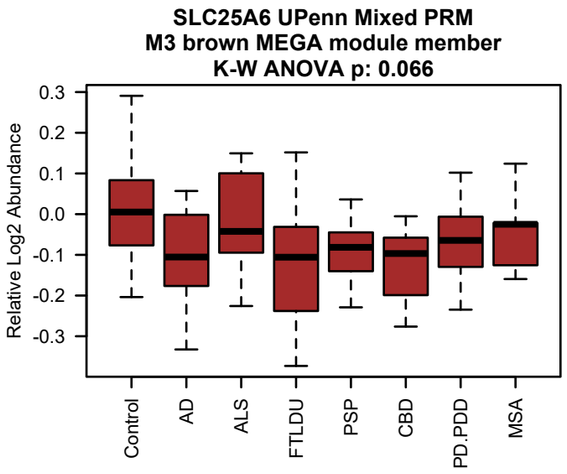

bicor=-0.29, p=0.0036
cor=-0.3, p=0.0024
Relative Log2 Abundance
0.5
0.3
0.1
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

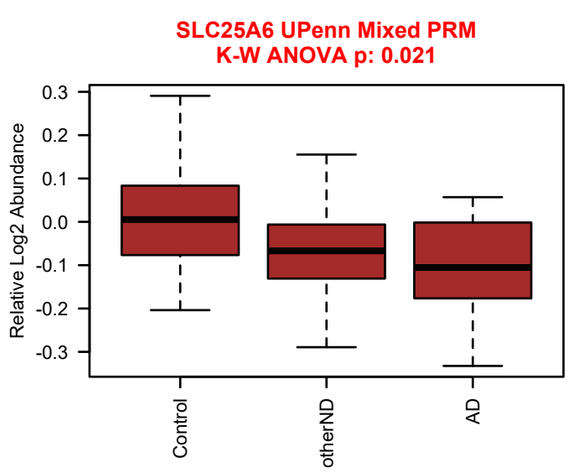

SLC25A4 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.5
Relative Log2 Abundance
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

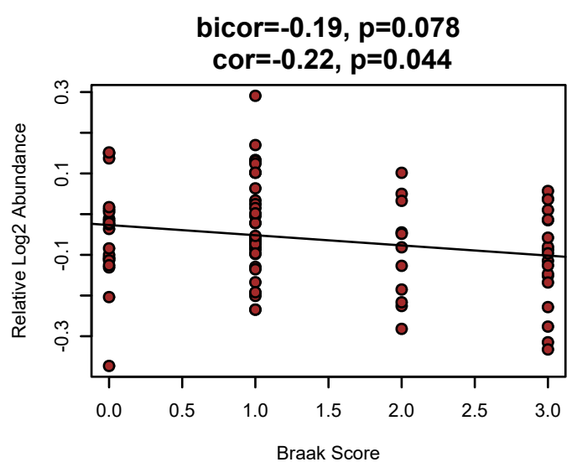

SLC25A4 UPenn Mixed PRM
K-W ANOVA p: 0.15
Relative Log2 Abundance
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
Control
otherND
AD

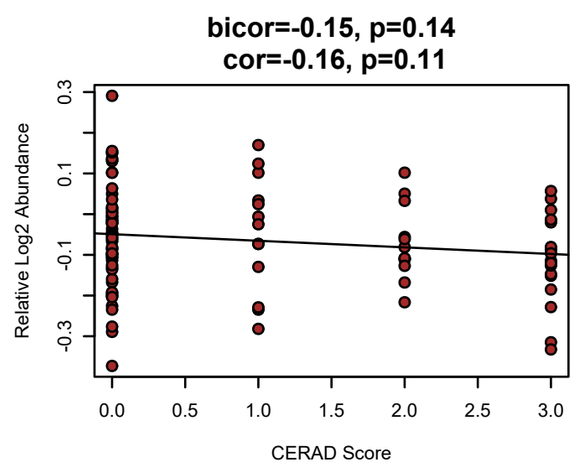

bicor=-0.092, p=0.41
cor=-0.16, p=0.15
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

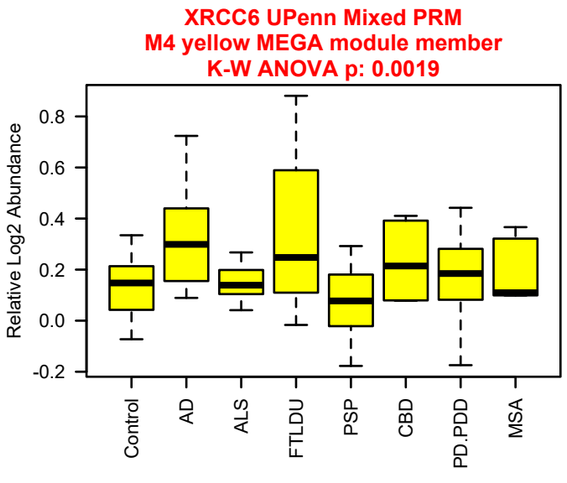

bicor=-0.17, p=0.095
cor=-0.18, p=0.073
Relative Log2 Abundance
0.6
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

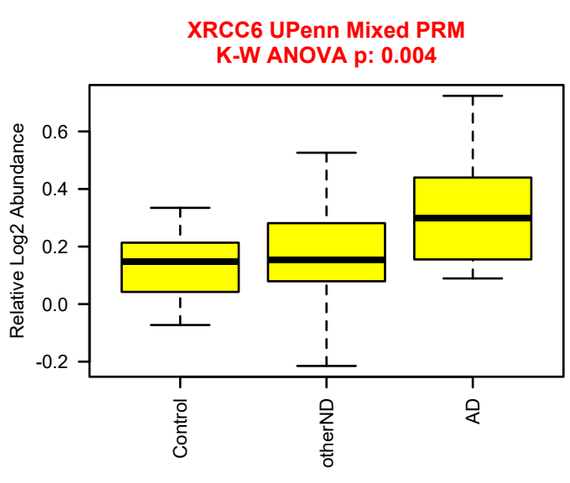

SLC25A6 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.066
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

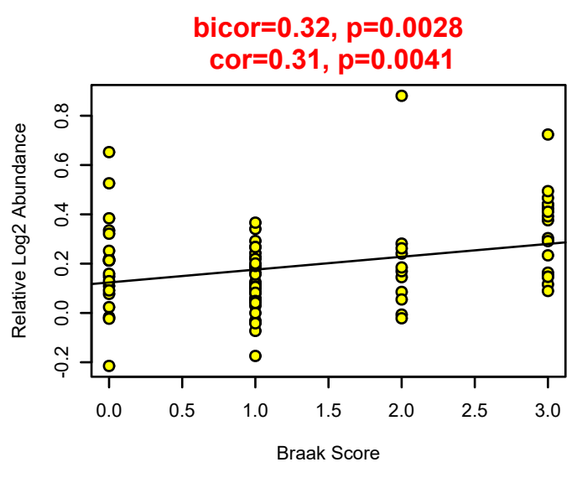

SLC25A6 UPenn Mixed PRM
K-W ANOVA p: 0.021
Relative Log2 Abundance
Control
otherND
AD

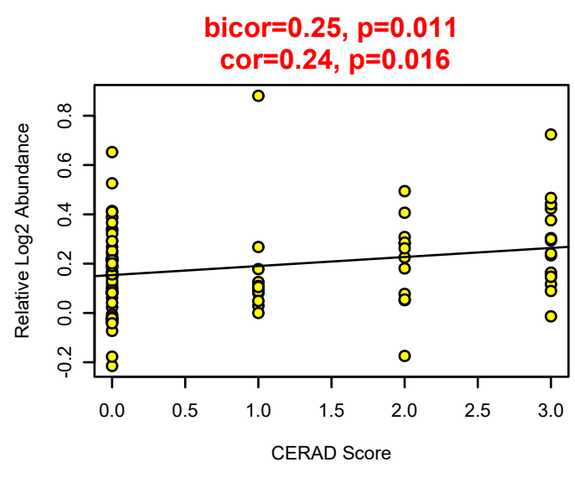

bicor=-0.19, p=0.078
cor=-0.22, p=0.044
Relative Log2 Abundance
Braak Score

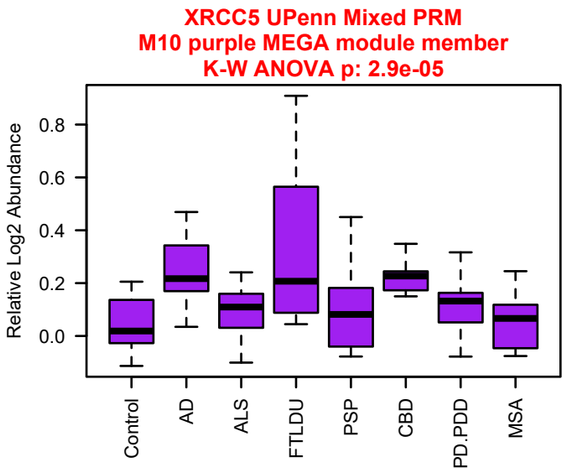

bicor=-0.15, p=0.14
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

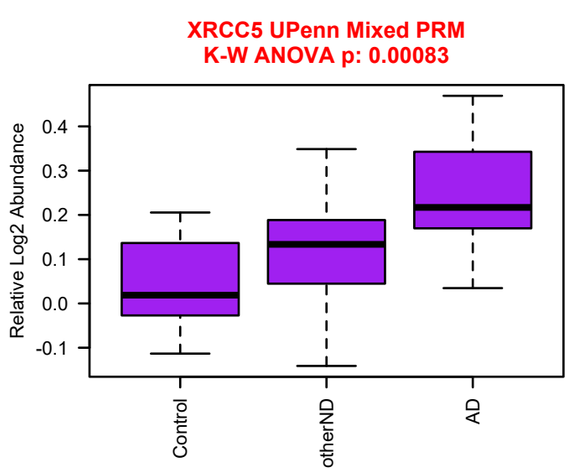

XRCC6 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.0019
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

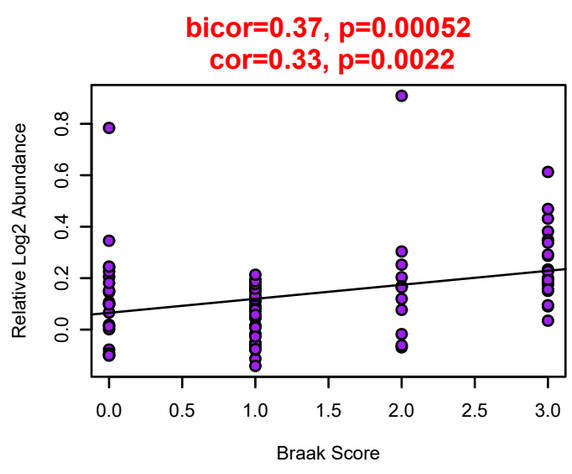

XRCC6 UPenn Mixed PRM
K-W ANOVA p: 0.004
Relative Log2 Abundance
Control
otherND
AD

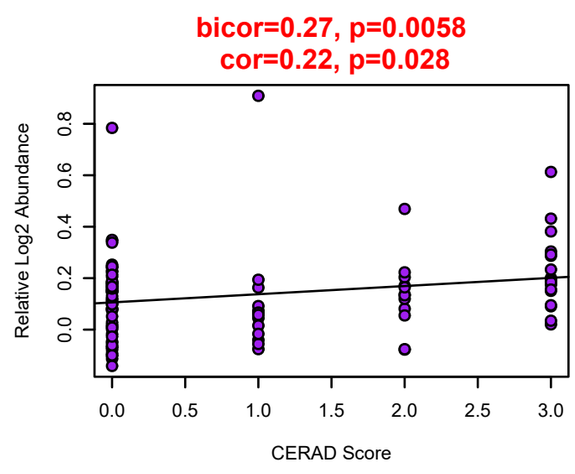

bicor=0.32, p=0.0028
cor=0.31, p=0.0041
Relative Log2 Abundance
Braak Score

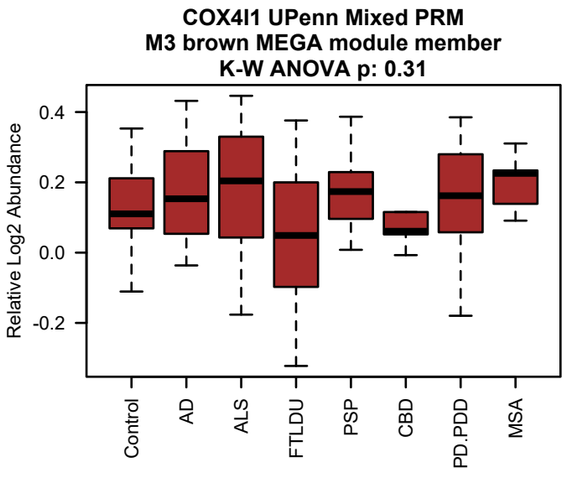

bicor=0.25, p=0.011
cor=0.24, p=0.016
Relative Log2 Abundance
CERAD Score

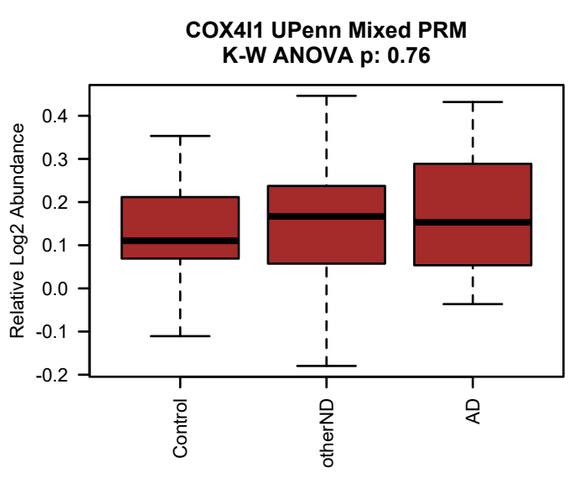

XRCC5 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 2.9e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

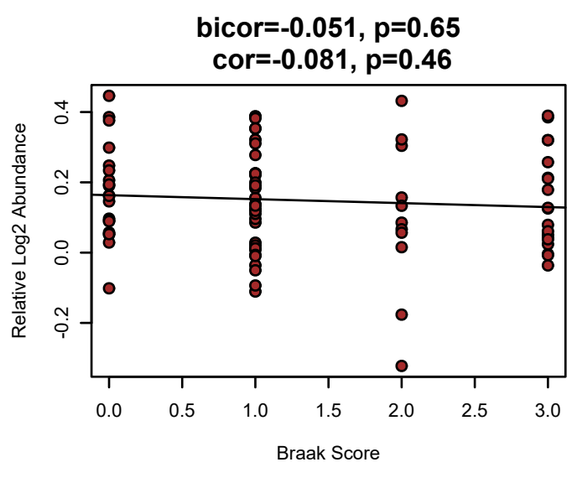

XRCC5 UPenn Mixed PRM
K-W ANOVA p: 0.00083
Relative Log2 Abundance
Control
otherND
AD

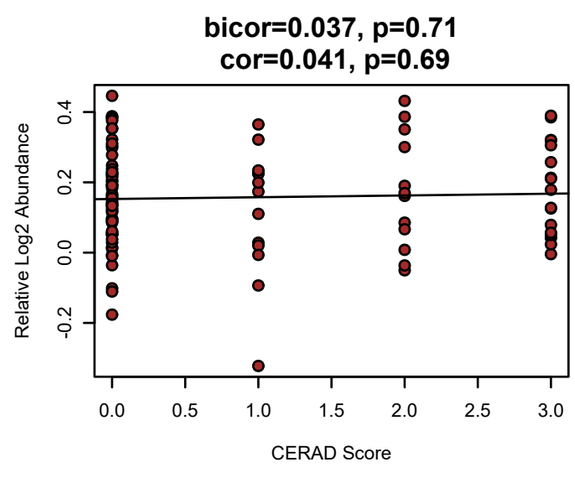

bicor=0.37, p=0.00052
cor=0.33, p=0.0022
Relative Log2 Abundance
Braak Score

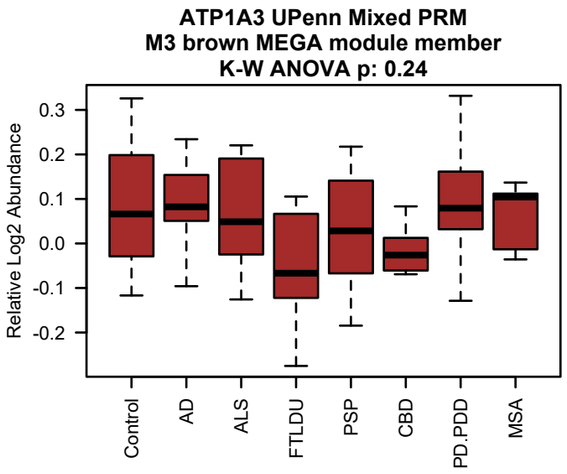

bicor=0.27, p=0.0058
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

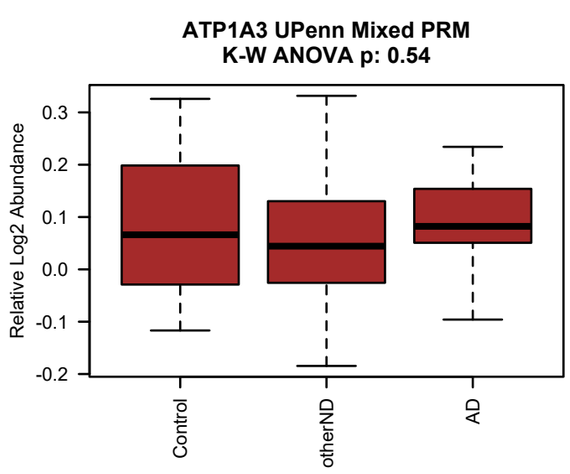

COX4I1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.31
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

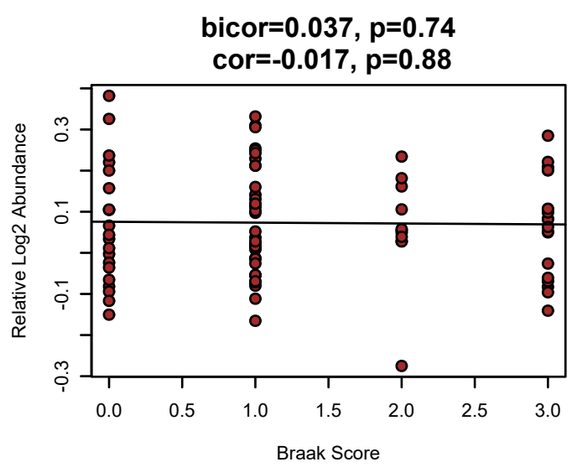

COX4I1 UPenn Mixed PRM
K-W ANOVA p: 0.76
Relative Log2 Abundance
Control
otherND
AD

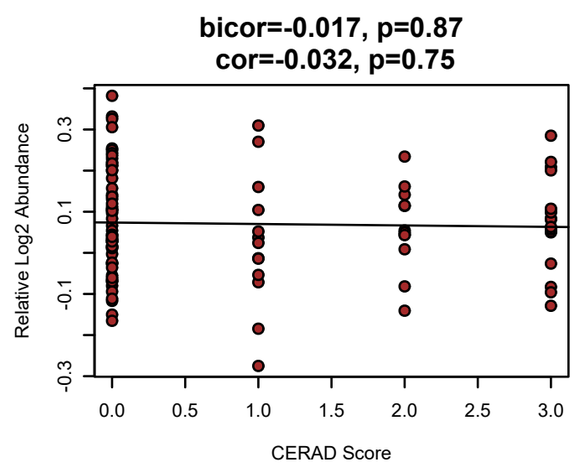

bicor=-0.051, p=0.65
cor=-0.081, p=0.46
Relative Log2 Abundance
Braak Score

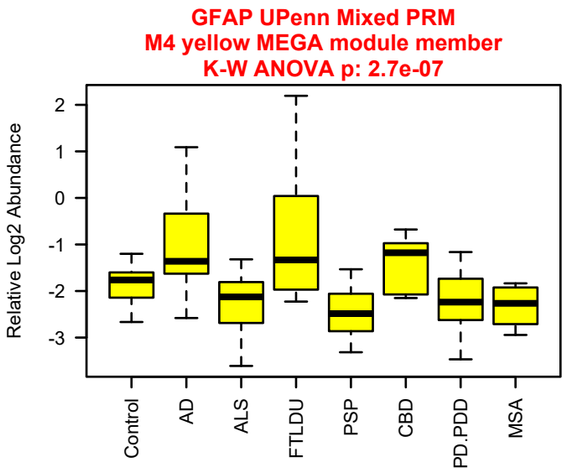

bicor=0.037, p=0.71
cor=0.041, p=0.69
Relative Log2 Abundance
CERAD Score

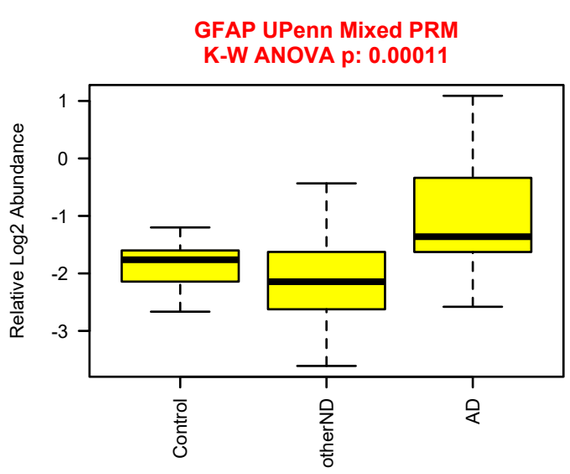

ATP1A3 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

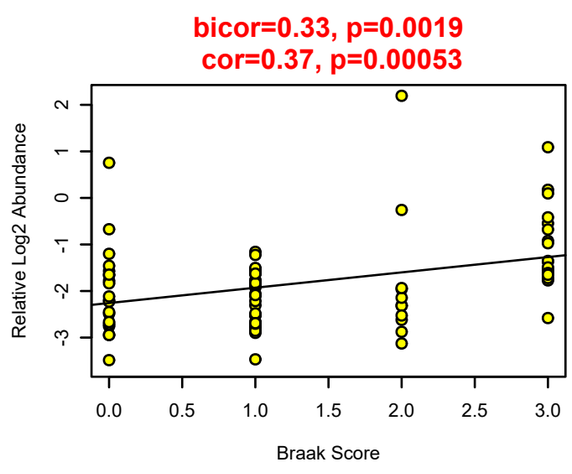

ATP1A3 UPenn Mixed PRM
K-W ANOVA p: 0.54
Relative Log2 Abundance
Control
otherND
AD

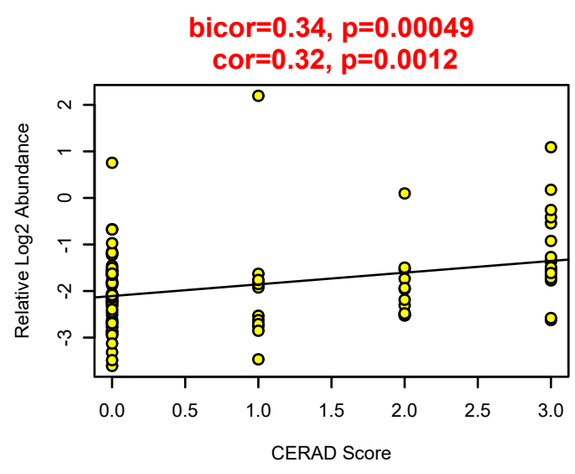

bicor=0.037, p=0.74
cor=-0.017, p=0.88
Relative Log2 Abundance
Braak Score

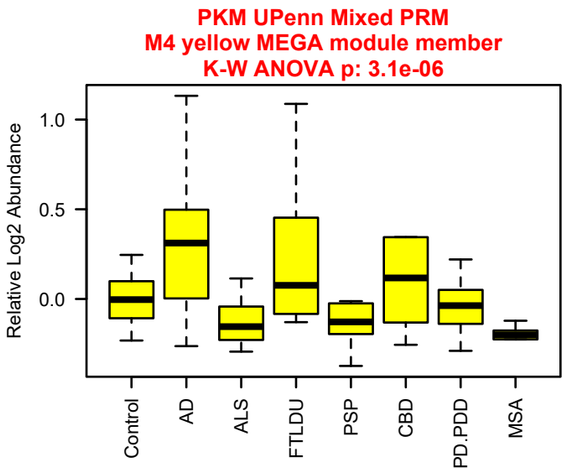

bicor=-0.017, p=0.87
cor=-0.032, p=0.75
Relative Log2 Abundance
CERAD Score

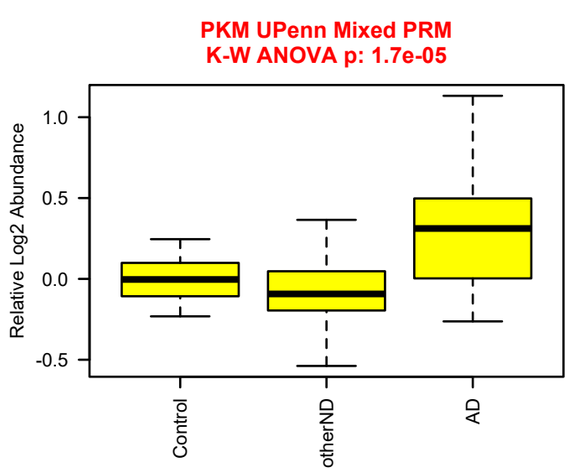

GFAP UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 2.7e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

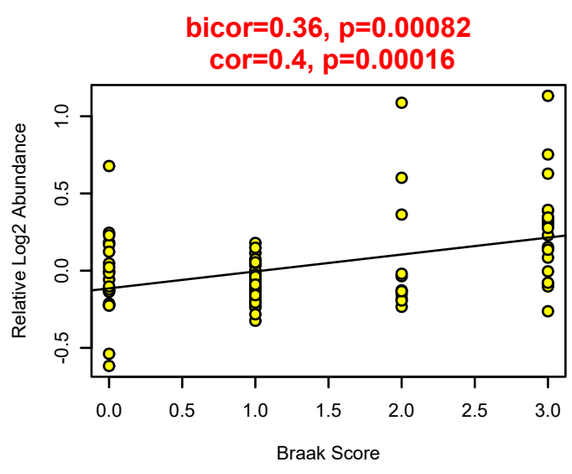

GFAP UPenn Mixed PRM
K-W ANOVA p: 0.00011
Relative Log2 Abundance
Control
otherND
AD

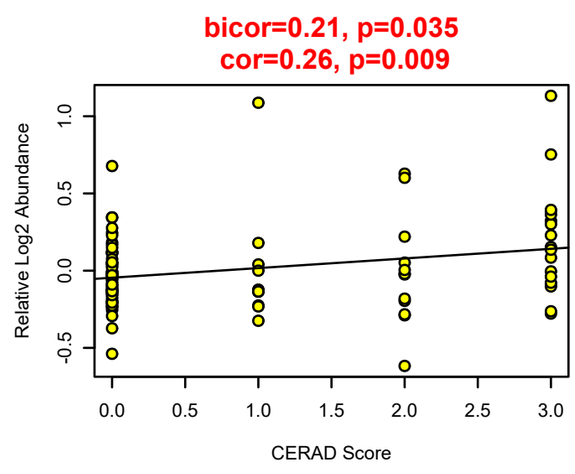

bicor=0.33, p=0.0019
cor=0.37, p=0.00053
Relative Log2 Abundance
Braak Score

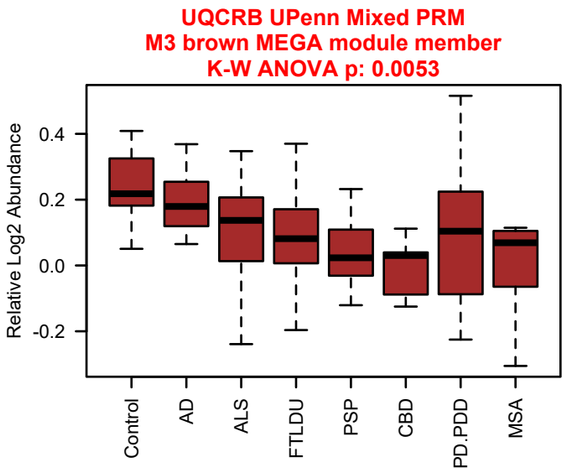

bicor=0.34, p=0.00049
cor=0.32, p=0.0012
Relative Log2 Abundance
CERAD Score

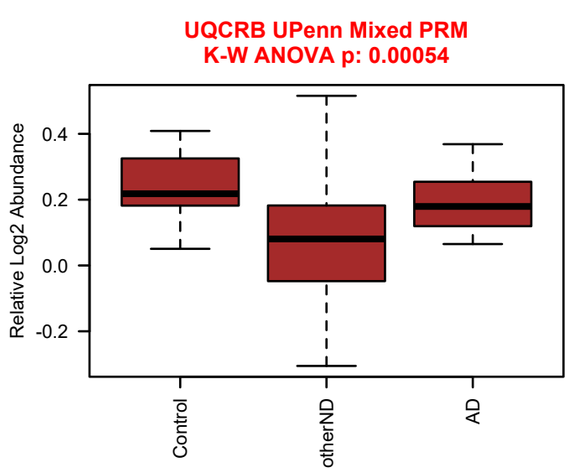

PKM UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 3.1e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

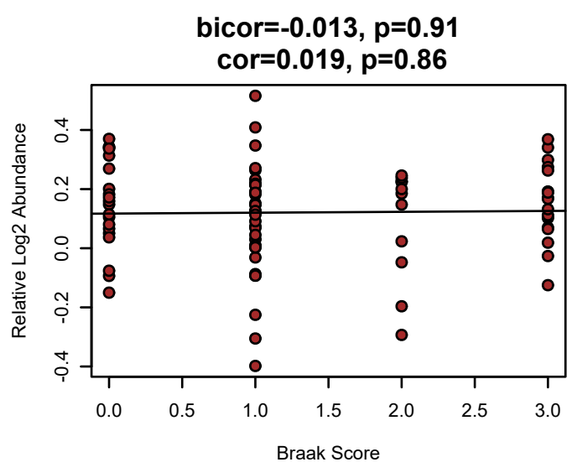

PKM UPenn Mixed PRM
K-W ANOVA p: 1.7e-05
Relative Log2 Abundance
Control
otherND
AD

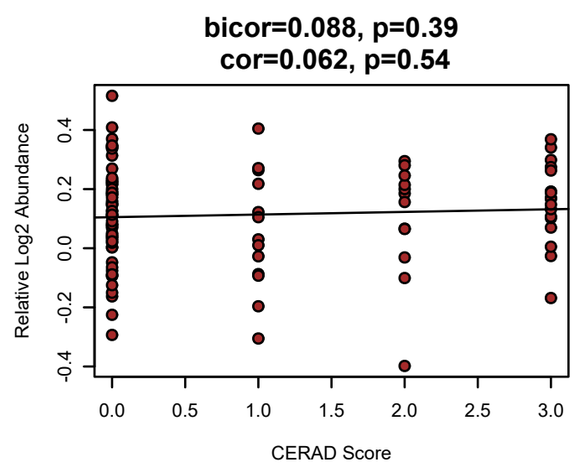

bicor=0.36, p=0.00082
cor=0.4, p=0.00016
Relative Log2 Abundance
Braak Score

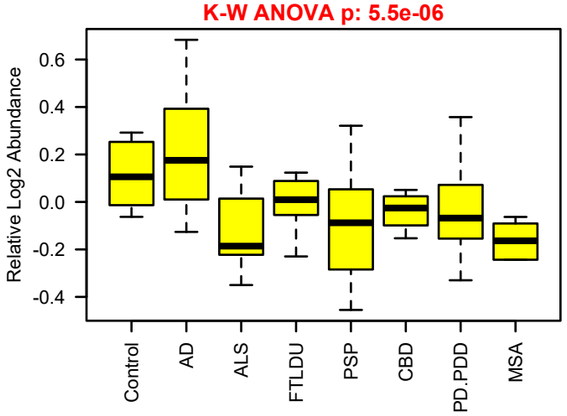

bicor=0.21, p=0.035
cor=0.26, p=0.009
Relative Log2 Abundance
CERAD Score

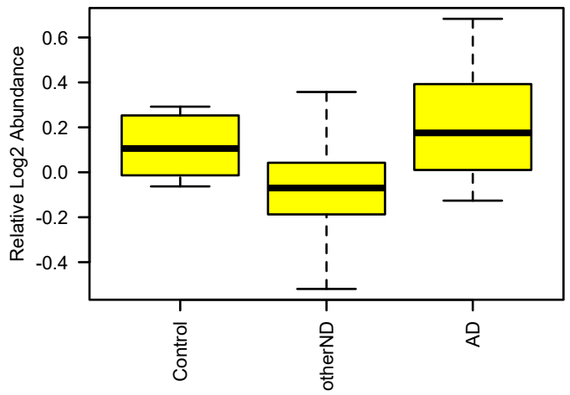

UQCRB UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0053
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

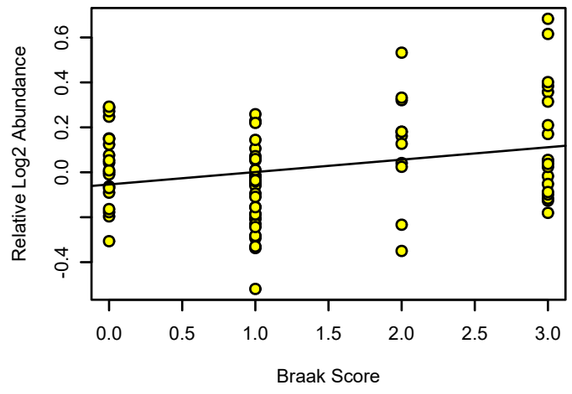

UQCRB UPenn Mixed PRM
K-W ANOVA p: 0.00054
Relative Log2 Abundance
Control
otherND
AD

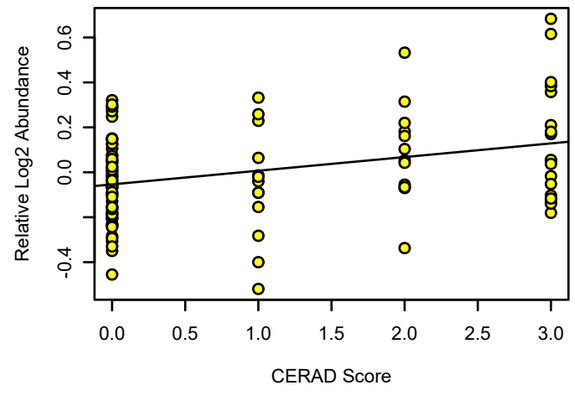

bicor=-0.013, p=0.91
cor=0.019, p=0.86
Relative Log2 Abundance
Braak Score

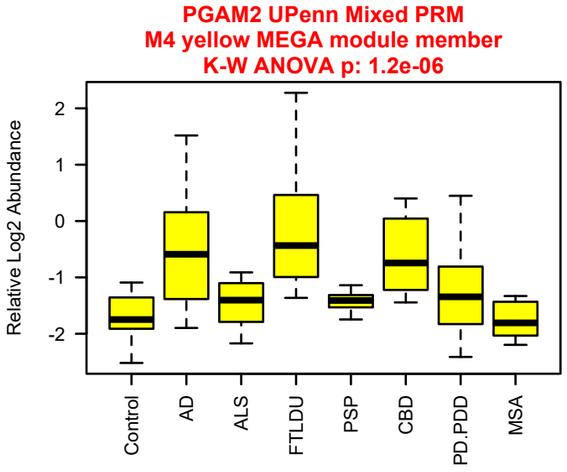

bicor=0.088, p=0.39
cor=0.062, p=0.54
Relative Log2 Abundance
CERAD Score

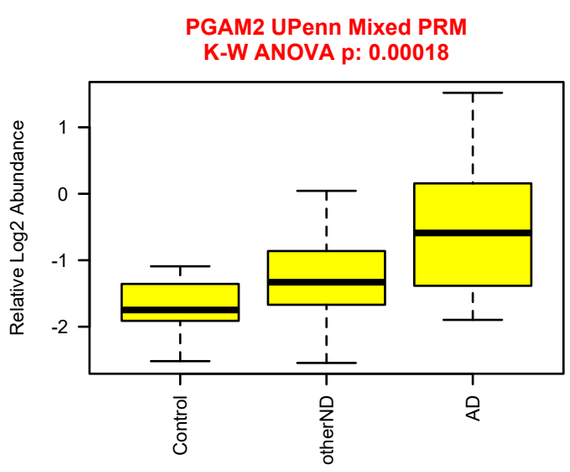

AKR1B1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 5.5e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

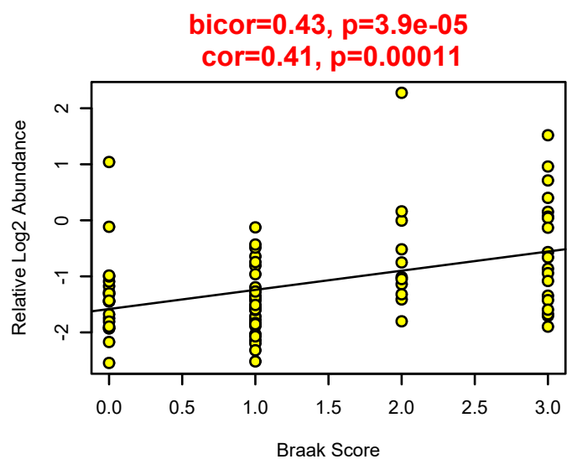

AKR1B1 UPenn Mixed PRM
K-W ANOVA p: 2.6e-07
Relative Log2 Abundance
Control
otherND
AD

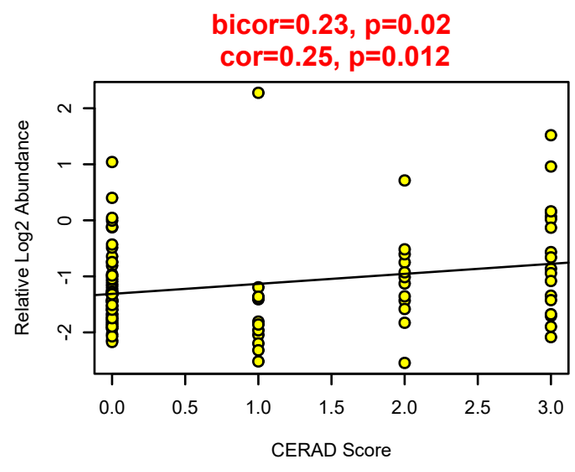

bicor=0.24, p=0.031
cor=0.27, p=0.013
Relative Log2 Abundance
Braak Score

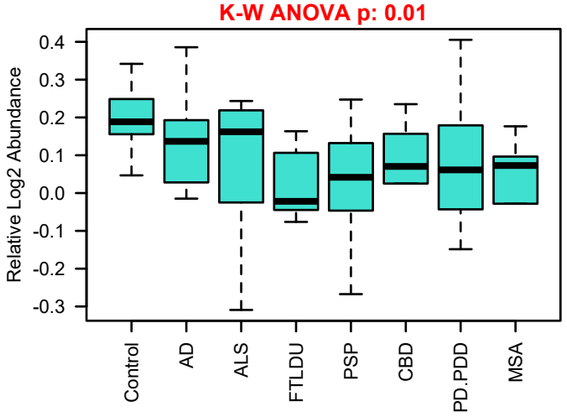

bicor=0.29, p=0.003
cor=0.33, p=8e-04
Relative Log2 Abundance
CERAD Score

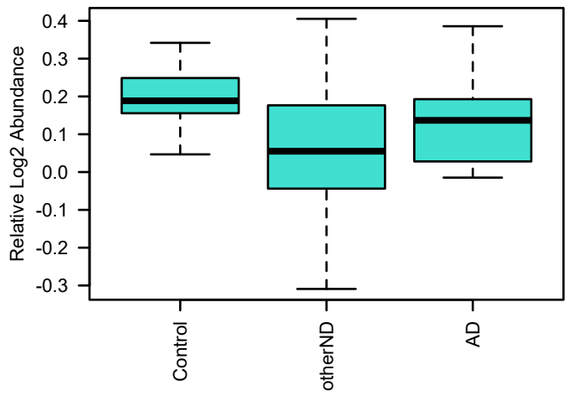

PGAM2 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1.2e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

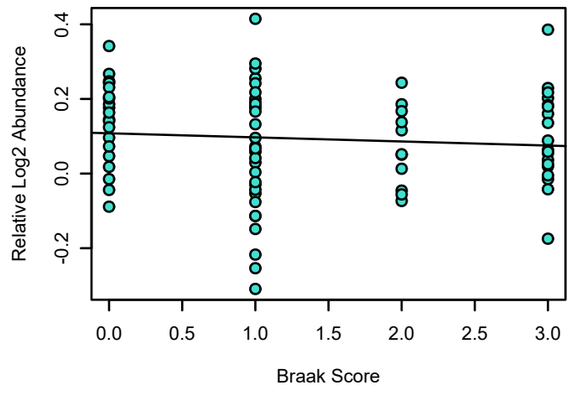

PGAM2 UPenn Mixed PRM
K-W ANOVA p: 0.00018
Relative Log2 Abundance
Control
otherND
AD

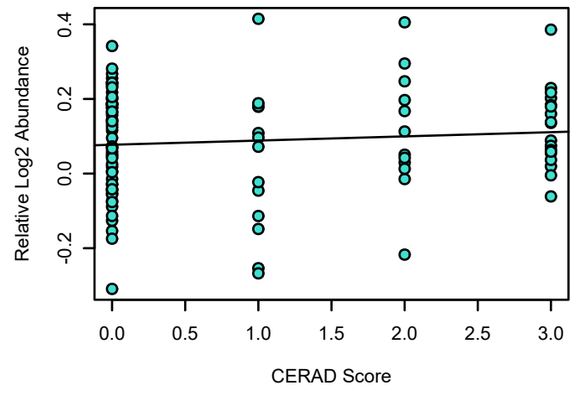

bicor=0.43, p=3.9e-05
cor=0.41, p=0.00011
Relative Log2 Abundance
Braak Score

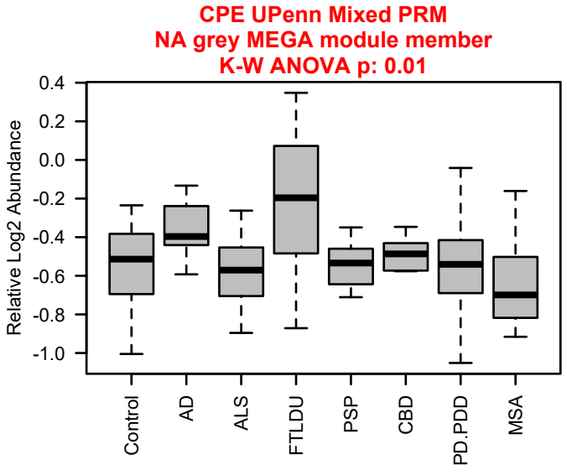

bicor=0.23, p=0.02
cor=0.25, p=0.012
Relative Log2 Abundance
CERAD Score

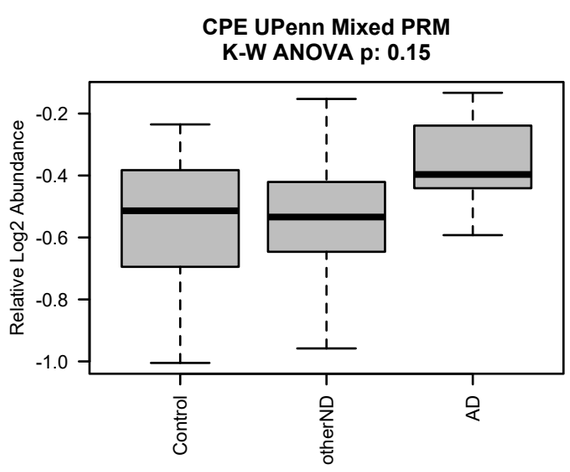

ATP2A2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.01
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

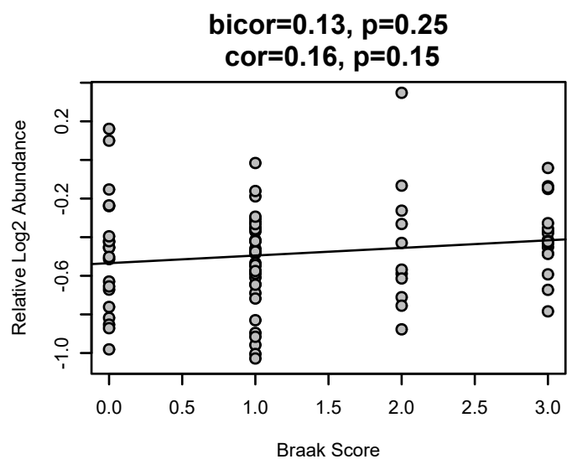

ATP2A2 UPenn Mixed PRM
K-W ANOVA p: 0.00043
Relative Log2 Abundance
Control
otherND
AD

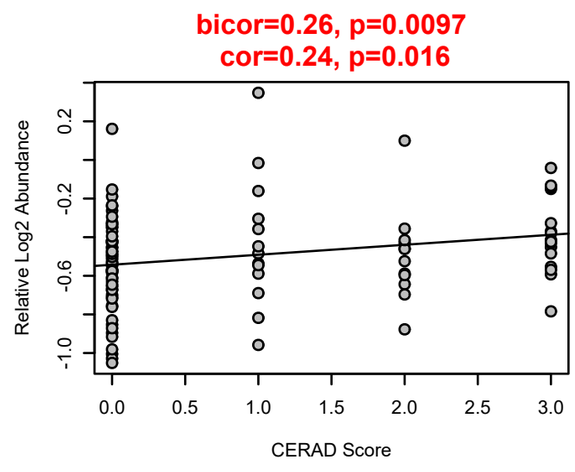

bicor=-0.13, p=0.26
cor=-0.085, p=0.44
Relative Log2 Abundance
Braak Score

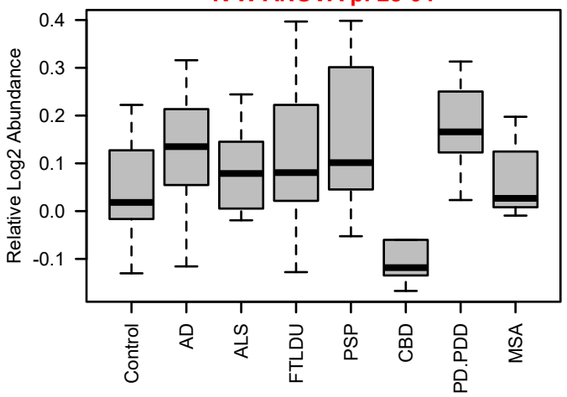

bicor=0.082, p=0.42
cor=0.093, p=0.36
Relative Log2 Abundance
CERAD Score

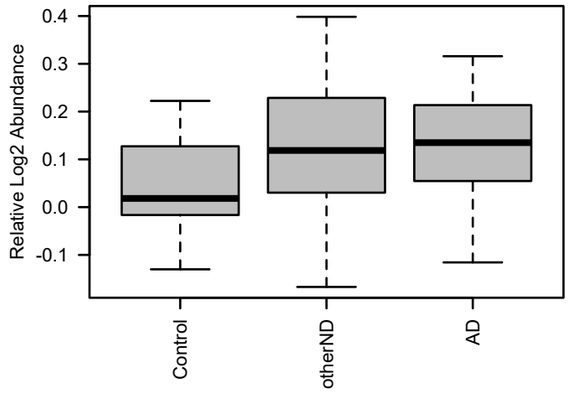

CPE UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.01
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

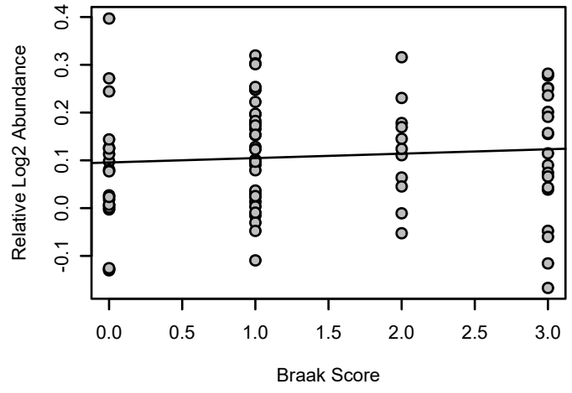

CPE UPenn Mixed PRM
K-W ANOVA p: 0.15
Relative Log2 Abundance
Control
otherND
AD

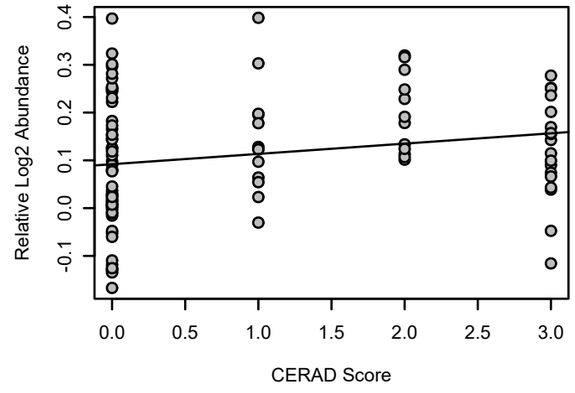

bicor=0.13, p=0.25
cor=0.16, p=0.15
Relative Log2 Abundance
Braak Score

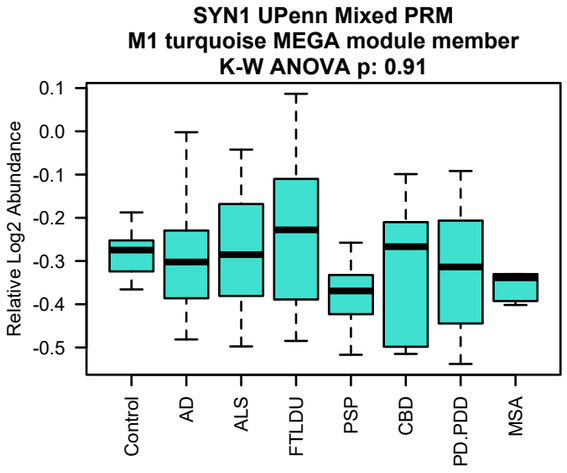

bicor=0.26, p=0.0097
cor=0.24, p=0.016
Relative Log2 Abundance
CERAD Score

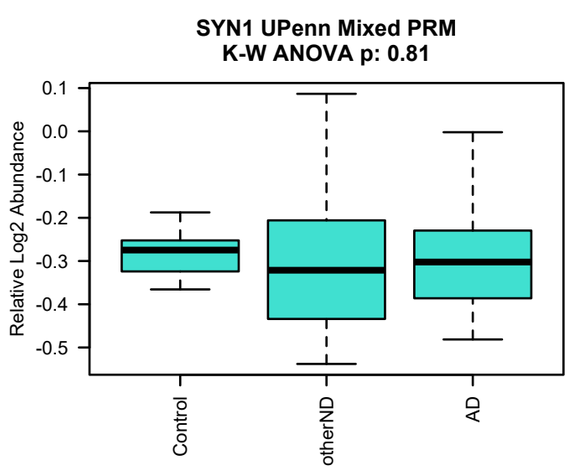

GOT1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 2e-04
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

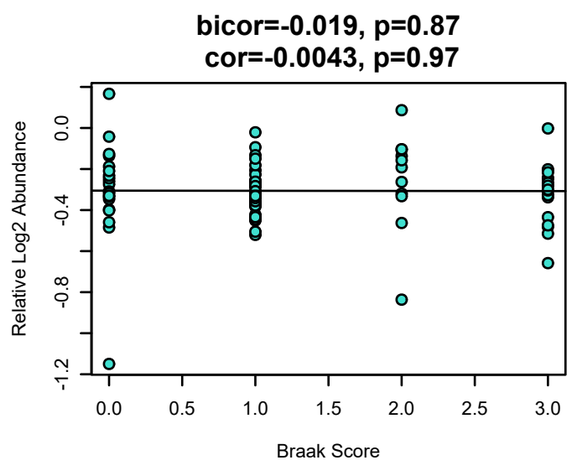

GOT1 UPenn Mixed PRM
K-W ANOVA p: 0.06
Relative Log2 Abundance
Control
otherND
AD

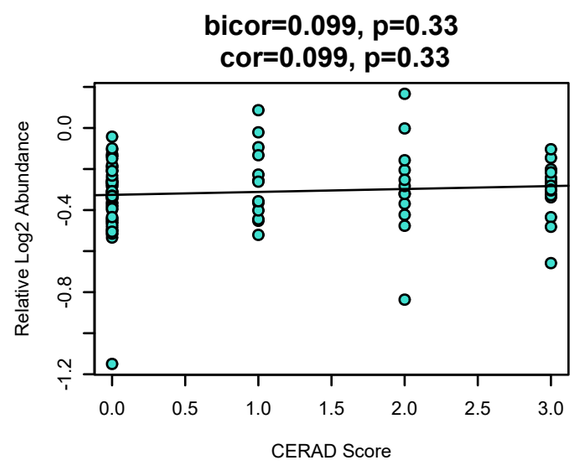

bicor=0.088, p=0.43
cor=0.081, p=0.46
Relative Log2 Abundance
Braak Score

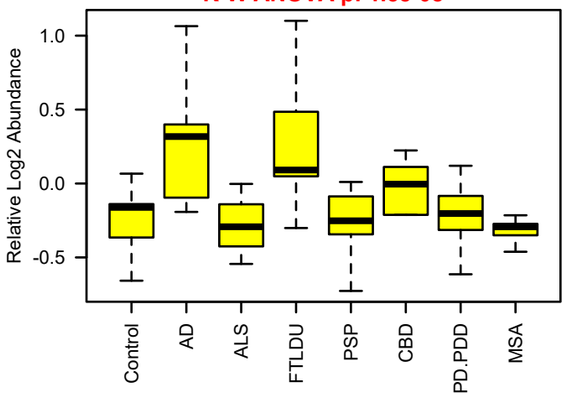

bicor=0.21, p=0.037
cor=0.2, p=0.046
Relative Log2 Abundance
CERAD Score

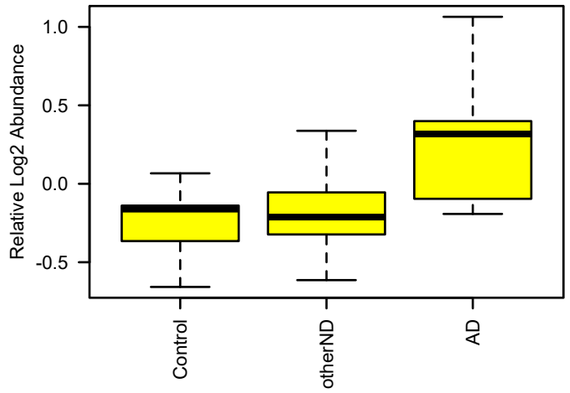

SYN1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.91
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

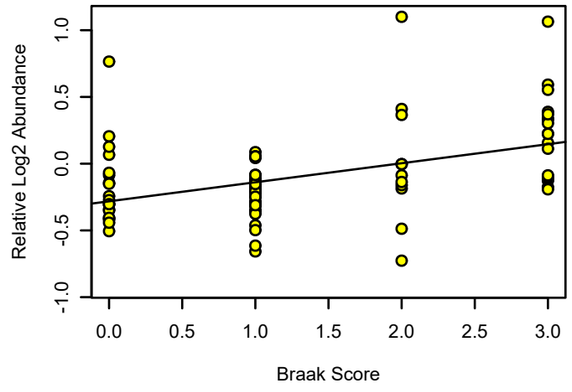

SYN1 UPenn Mixed PRM
K-W ANOVA p: 0.81
Relative Log2 Abundance
Control
otherND
AD

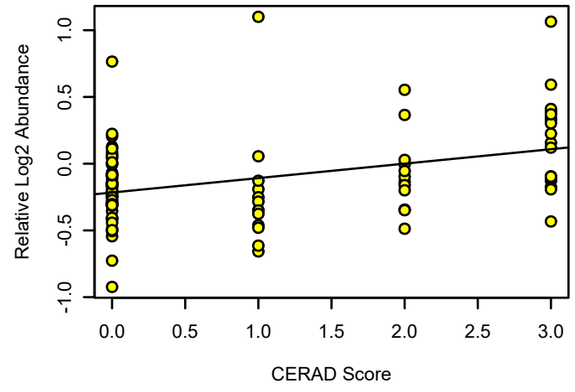

bicor=-0.019, p=0.87
cor=-0.0043, p=0.97
Relative Log2 Abundance
Braak Score

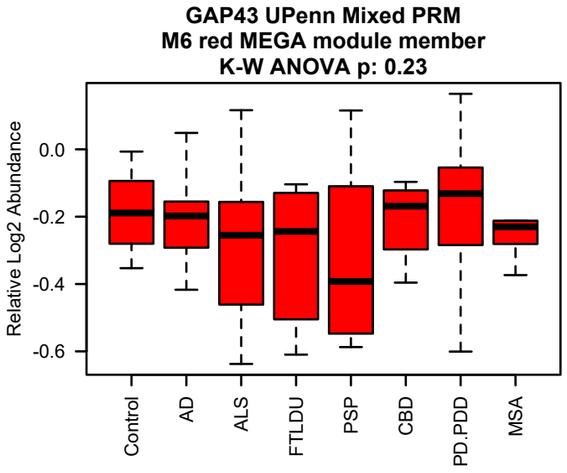

bicor=0.099, p=0.33
cor=0.099, p=0.33
Relative Log2 Abundance
CERAD Score

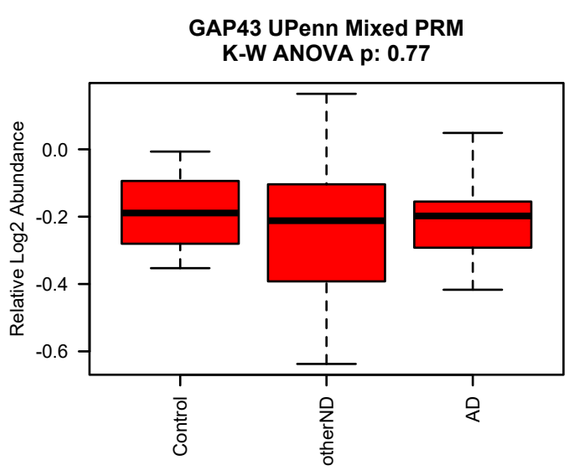

CAPN2 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1.5e-08
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

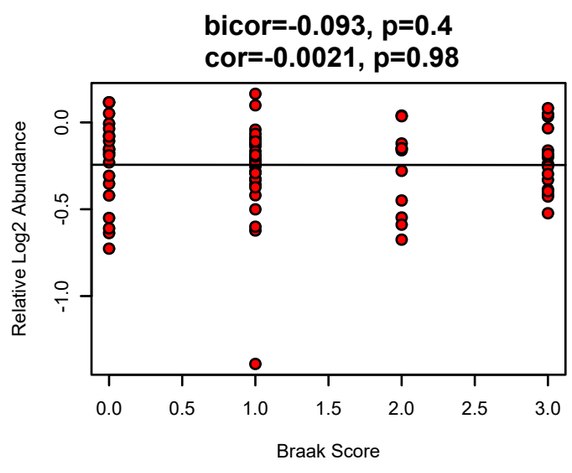

CAPN2 UPenn Mixed PRM
K-W ANOVA p: 9.1e-07
Relative Log2 Abundance
Control
otherND
AD

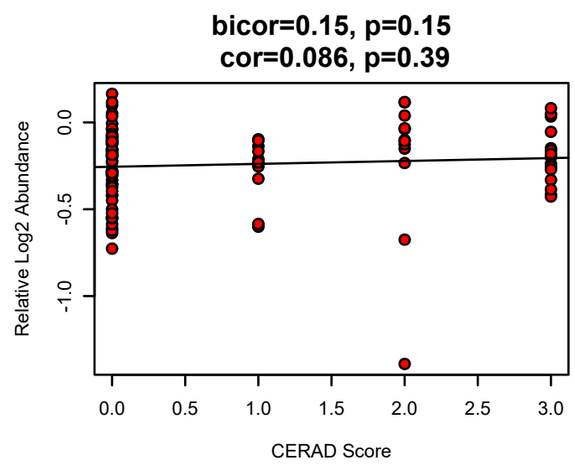

bicor=0.49, p=2.9e-06
cor=0.46, p=1.1e-05
Relative Log2 Abundance
Braak Score

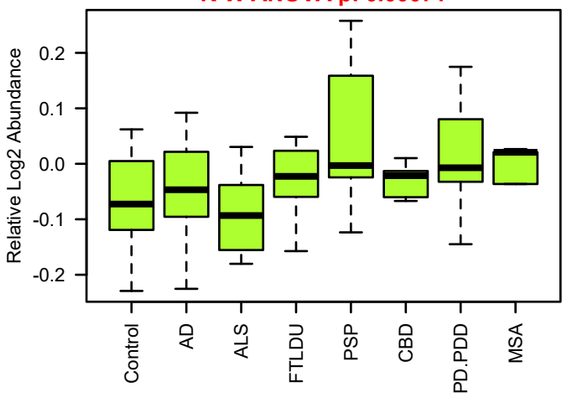

bicor=0.39, p=7.6e-05
cor=0.39, p=6e-05
Relative Log2 Abundance
CERAD Score

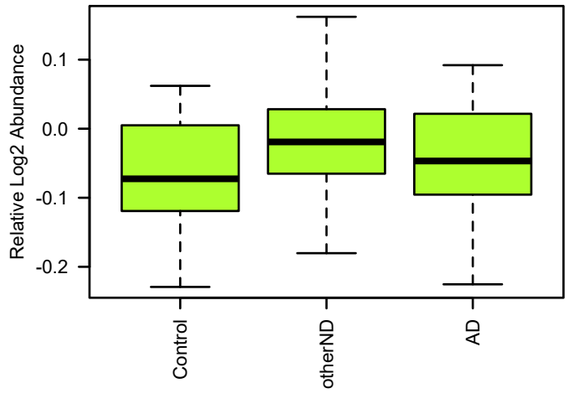

GAP43 UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.23
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

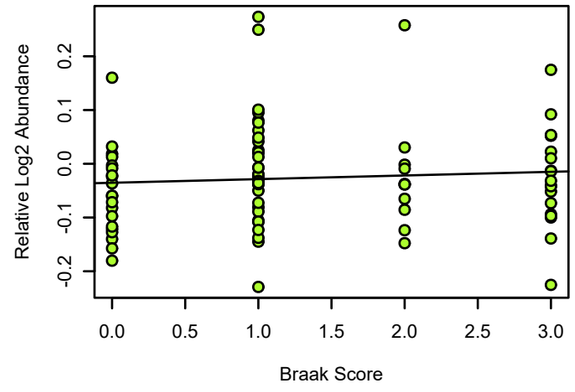

GAP43 UPenn Mixed PRM
K-W ANOVA p: 0.77
Relative Log2 Abundance
Control
otherND
AD

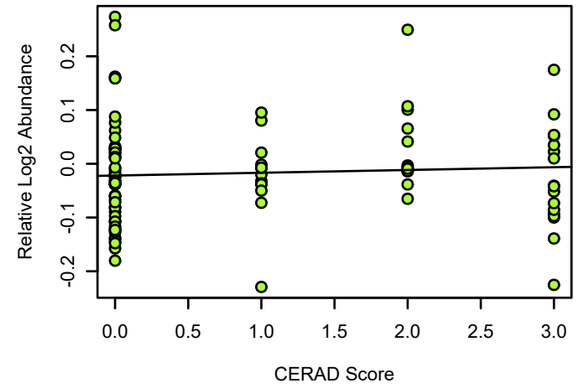

bicor=-0.093, p=0.4
cor=-0.0021, p=0.98
Relative Log2 Abundance
Braak Score

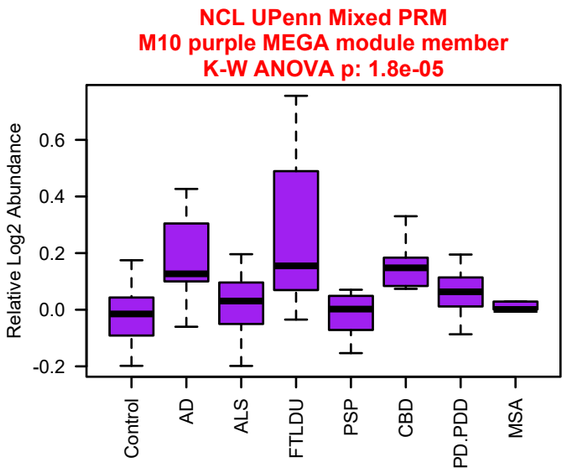

bicor=0.15, p=0.15
cor=0.086, p=0.39
Relative Log2 Abundance
CERAD Score

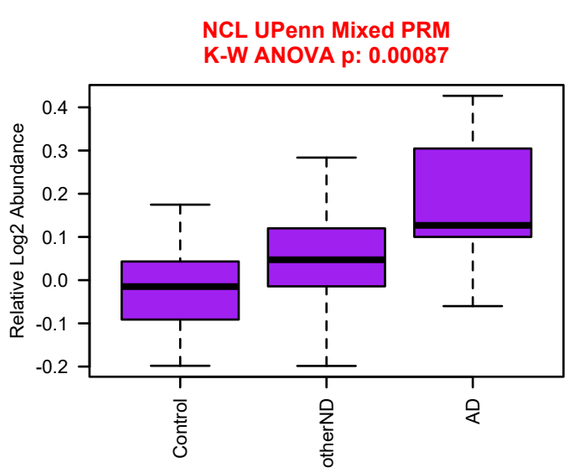

TCP1 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 0.00071
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

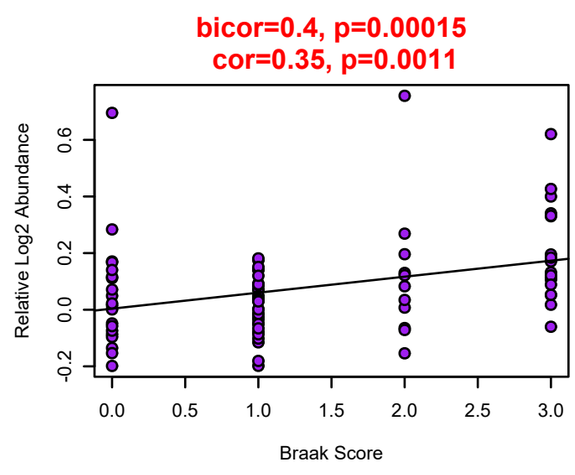

TCP1 UPenn Mixed PRM
K-W ANOVA p: 0.047
Relative Log2 Abundance
Control
otherND
AD

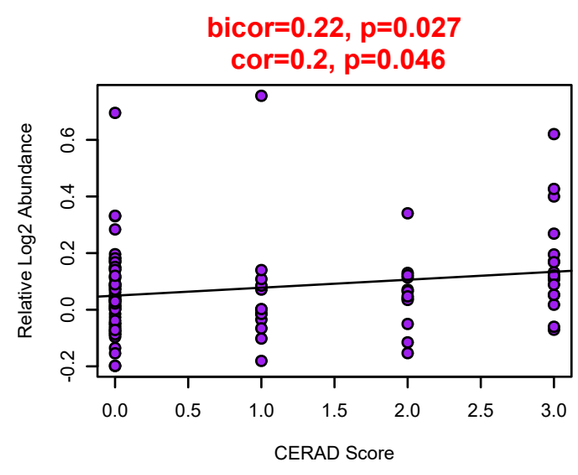

bicor=0.1, p=0.36
cor=0.077, p=0.49
Relative Log2 Abundance
Braak Score

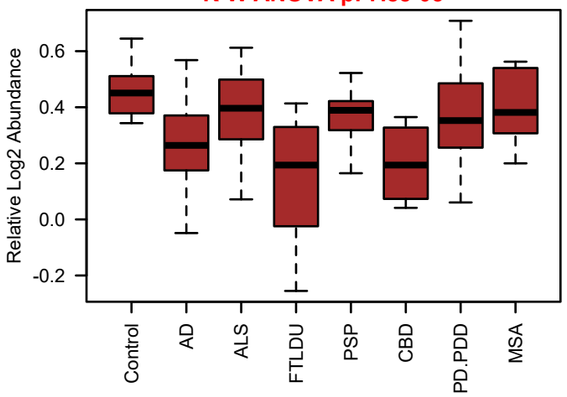

bicor=0.11, p=0.3
cor=0.066, p=0.51
Relative Log2 Abundance
CERAD Score

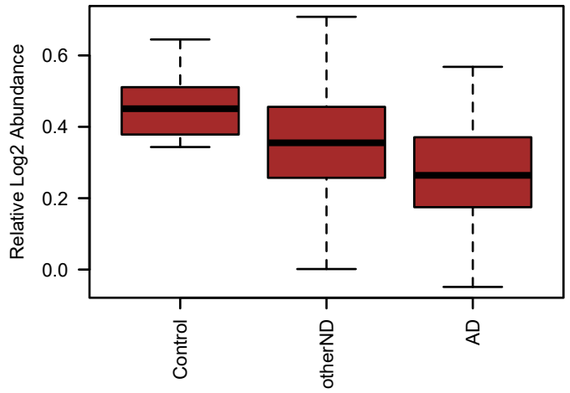

NCL UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 1.8e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

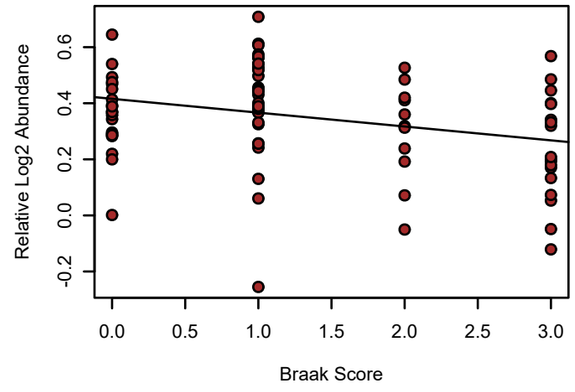

NCL UPenn Mixed PRM
K-W ANOVA p: 0.00087
Relative Log2 Abundance
Control
otherND
AD

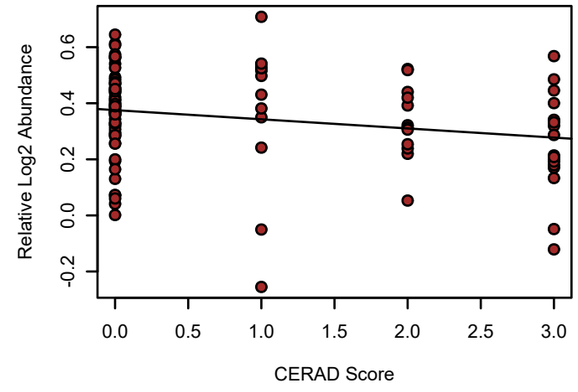

bicor=0.4, p=0.00015
cor=0.35, p=0.0011
Relative Log2 Abundance
Braak Score

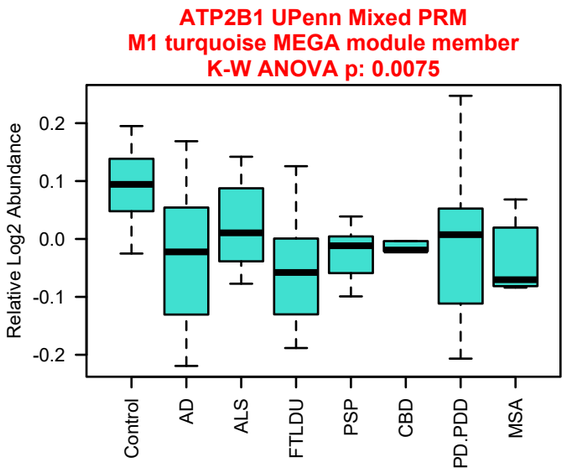

bicor=0.22, p=0.027
cor=0.2, p=0.046
Relative Log2 Abundance
CERAD Score

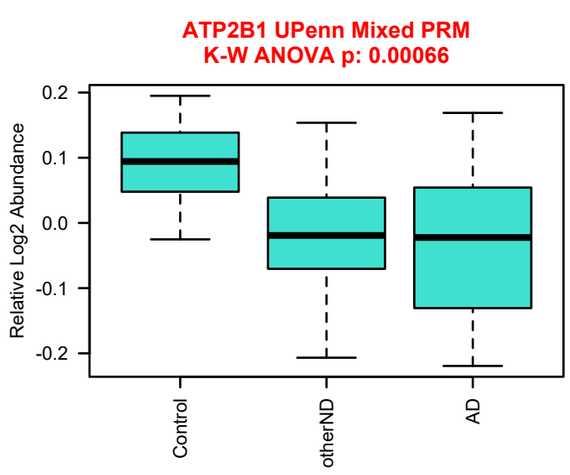

NDUFV2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 7.8e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

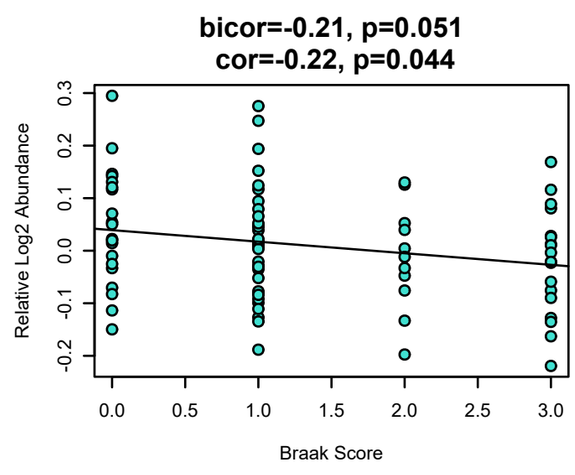

NDUFV2 UPenn Mixed PRM
K-W ANOVA p: 0.0025
Relative Log2 Abundance
Control
otherND
AD

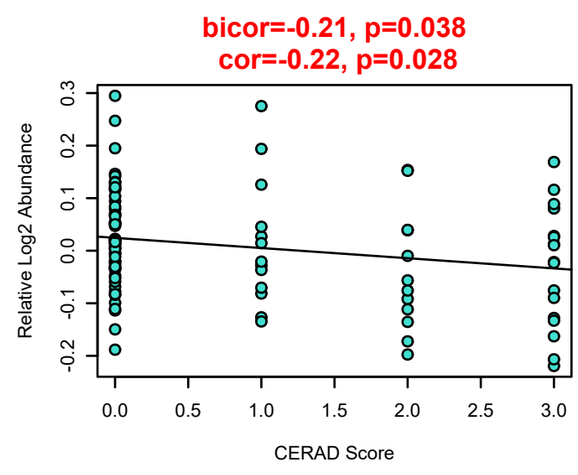

bicor=-0.31, p=0.0036
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

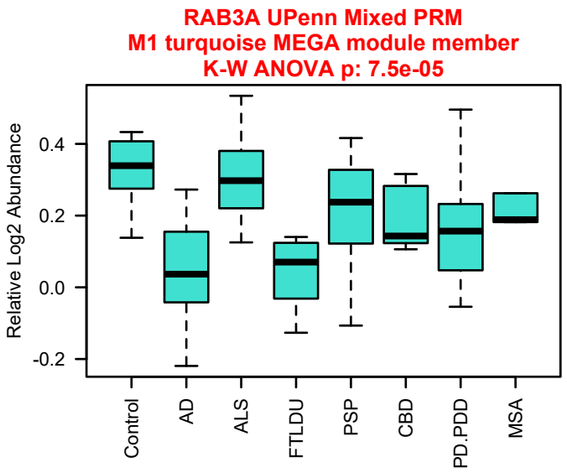

bicor=-0.23, p=0.02
cor=-0.22, p=0.028
Relative Log2 Abundance
CERAD Score

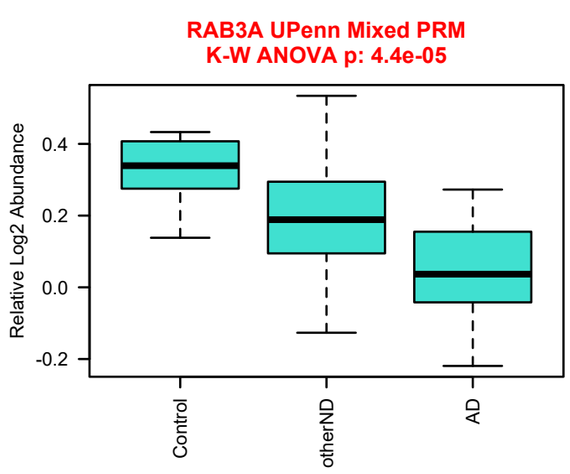

ATP2B1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0075
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

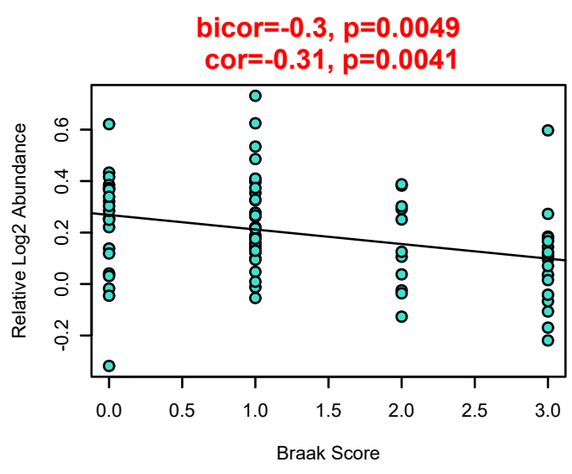

ATP2B1 UPenn Mixed PRM
K-W ANOVA p: 0.00066
Relative Log2 Abundance
Control
otherND
AD

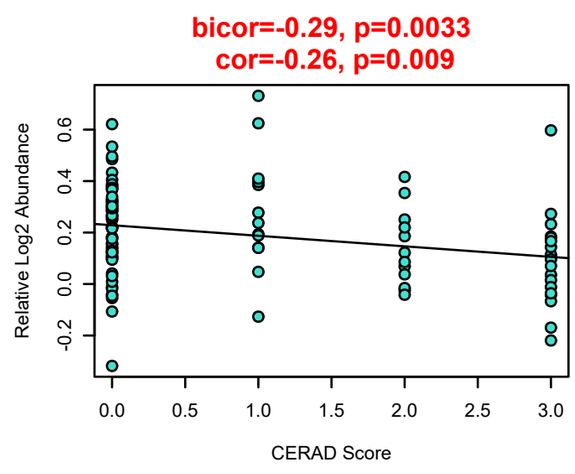

bicor=-0.21, p=0.051
cor=-0.22, p=0.044
Relative Log2 Abundance
Braak Score

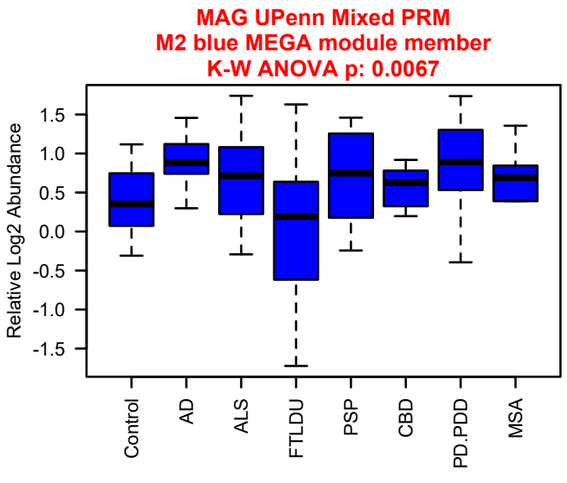

bicor=-0.21, p=0.038
cor=-0.22, p=0.028
Relative Log2 Abundance
CERAD Score

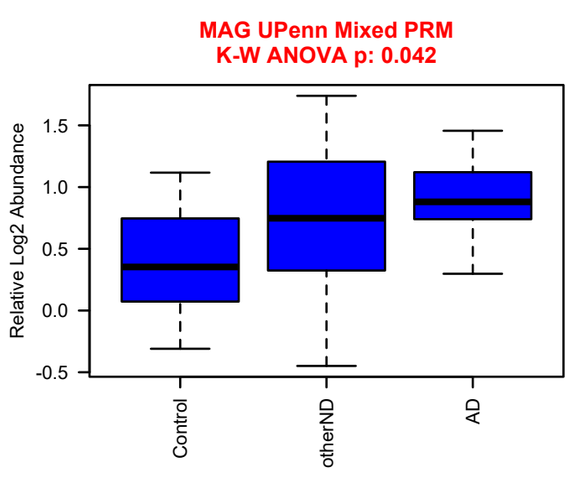

RAB3A UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 7.5e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

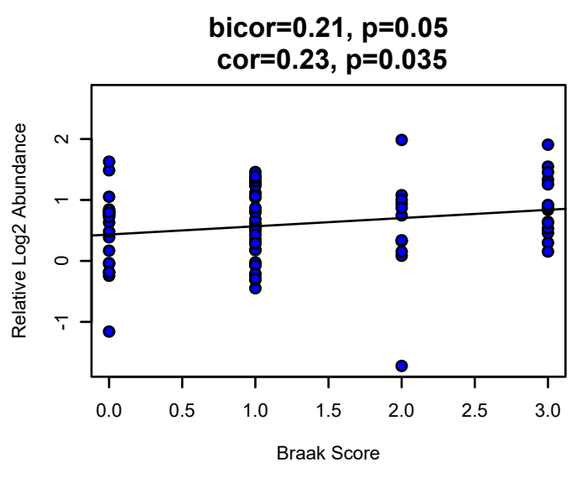

RAB3A UPenn Mixed PRM
K-W ANOVA p: 4.4e-05
Relative Log2 Abundance
Control
otherND
AD

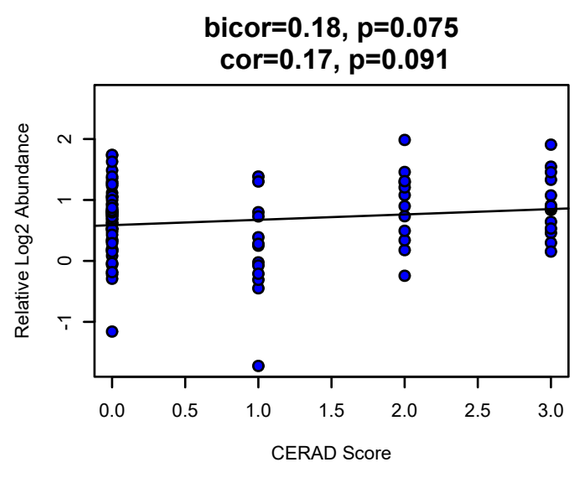

bicor=-0.3, p=0.0049
cor=-0.31, p=0.0041
Relative Log2 Abundance
Braak Score

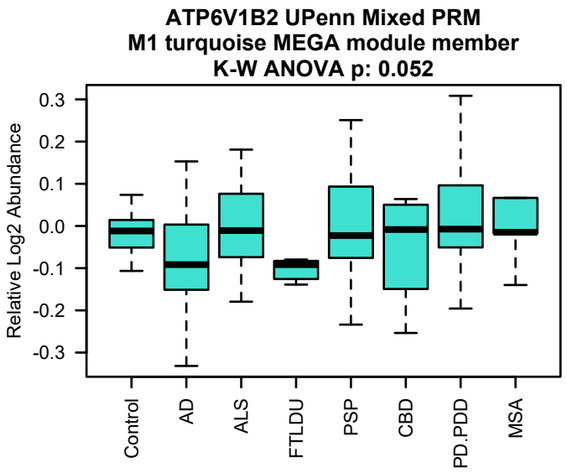

bicor=-0.29, p=0.0033
cor=-0.26, p=0.009
Relative Log2 Abundance
CERAD Score

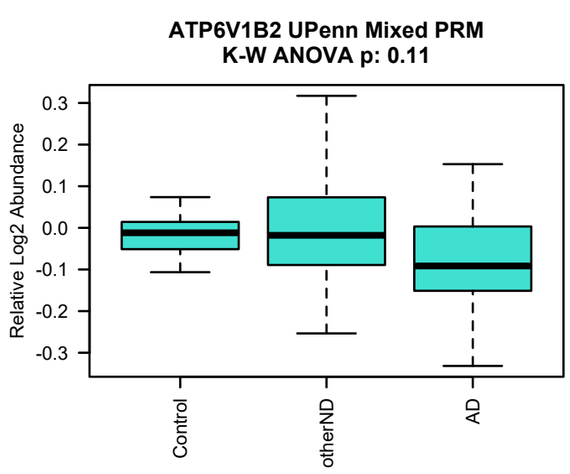

MAG UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.0067
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

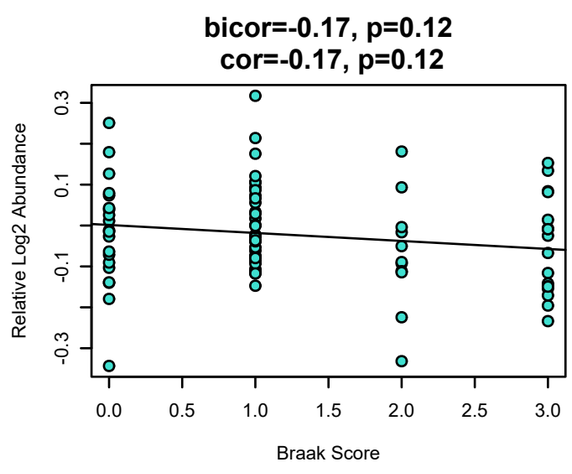

MAG UPenn Mixed PRM
K-W ANOVA p: 0.042
Relative Log2 Abundance
Control
otherND
AD

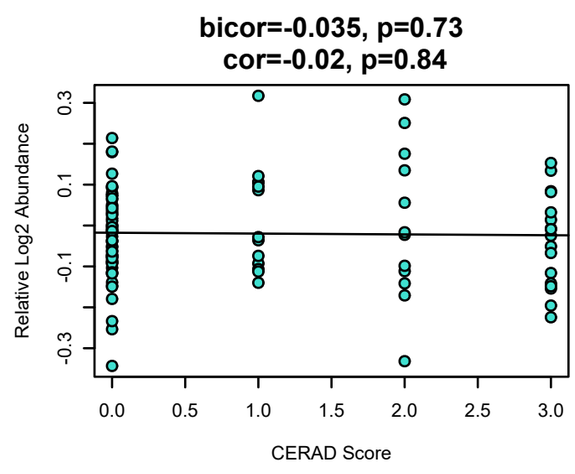

bicor=0.21, p=0.05
cor=0.23, p=0.035
Relative Log2 Abundance
Braak Score

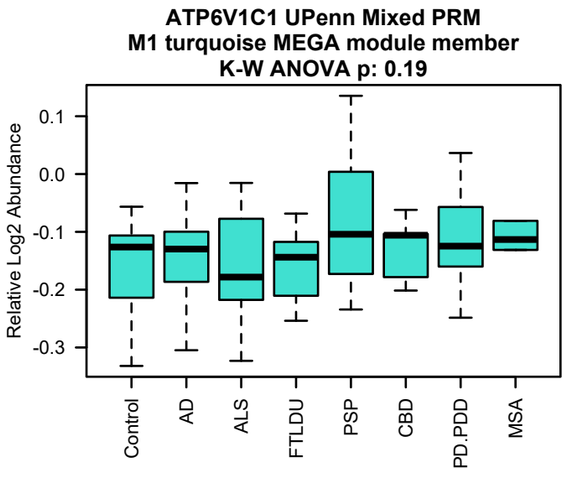

bicor=0.18, p=0.075
cor=0.17, p=0.091
Relative Log2 Abundance
CERAD Score

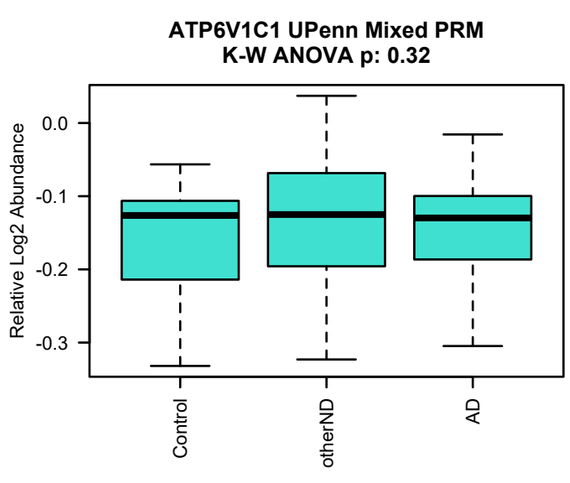

ATP6V1B2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.052
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

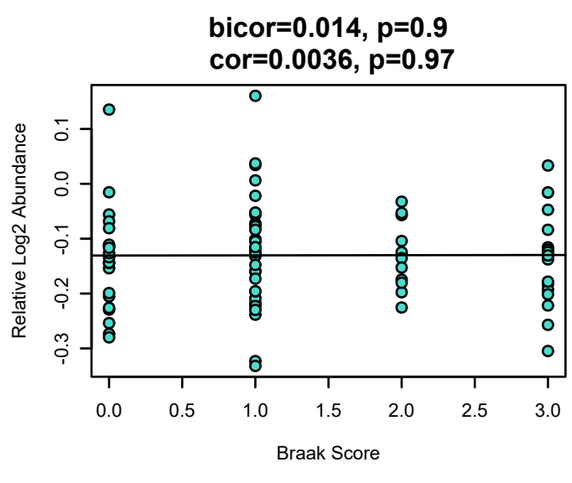

ATP6V1B2 UPenn Mixed PRM
K-W ANOVA p: 0.11
Relative Log2 Abundance
Control
otherND
AD

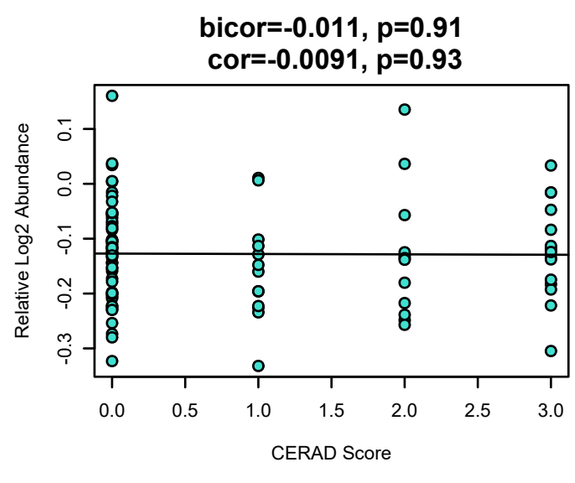

bicor=-0.17, p=0.12
cor=-0.17, p=0.12
Relative Log2 Abundance
Braak Score

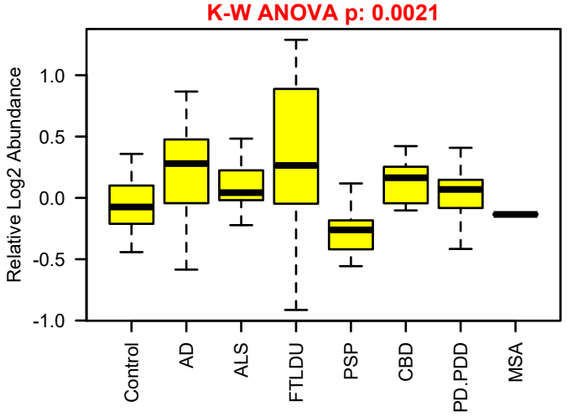

bicor=-0.035, p=0.73
cor=-0.02, p=0.84
Relative Log2 Abundance
CERAD Score

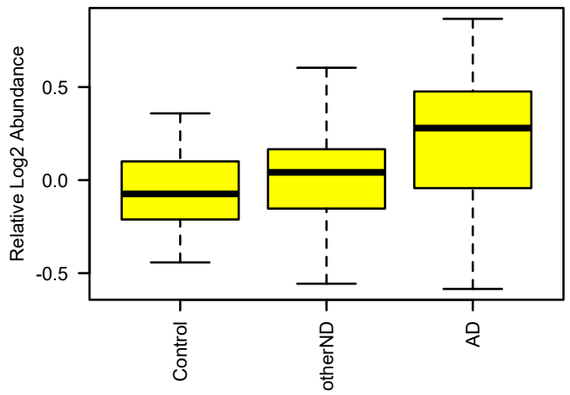

ATP6V1C1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.19
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

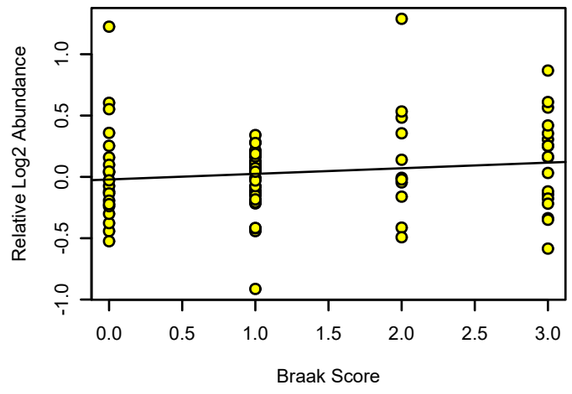

ATP6V1C1 UPenn Mixed PRM
K-W ANOVA p: 0.32
Relative Log2 Abundance
Control
otherND
AD

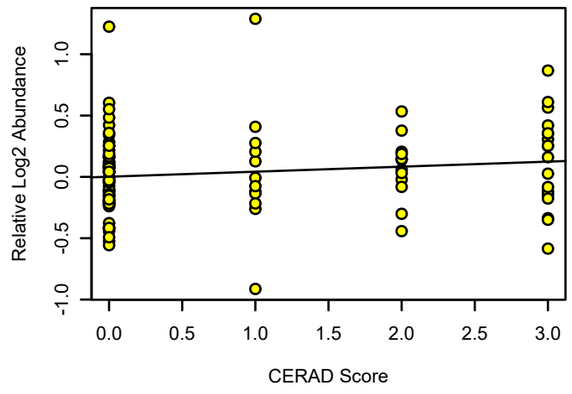

bicor=0.014, p=0.9
cor=0.0036, p=0.97
Relative Log2 Abundance
Braak Score

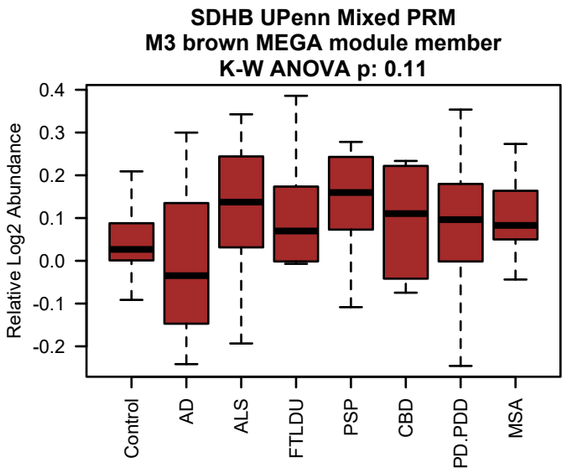

bicor=-0.011, p=0.91
cor=-0.0091, p=0.93
Relative Log2 Abundance
CERAD Score

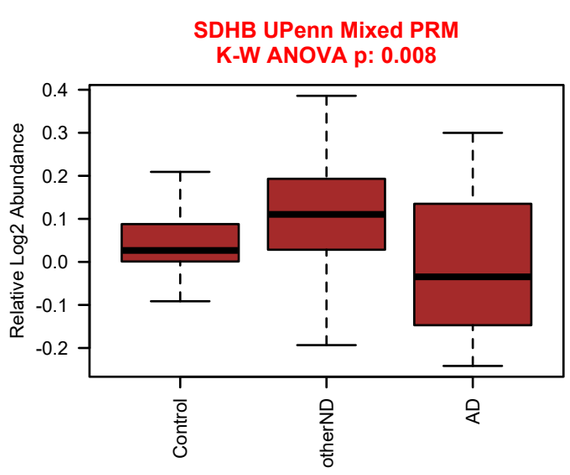

CSRP1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.0021
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

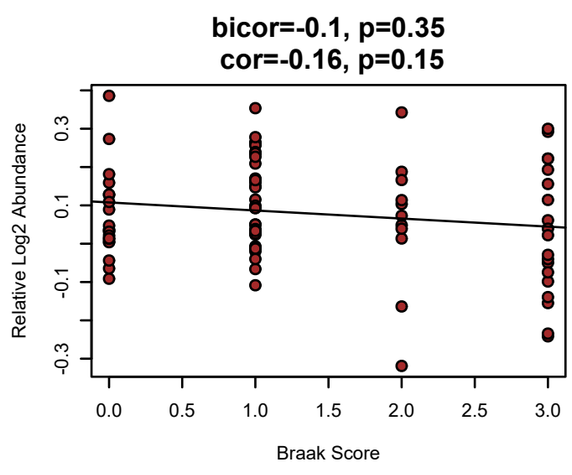

CSRP1 UPenn Mixed PRM
K-W ANOVA p: 0.08
Relative Log2 Abundance
Control
otherND
AD

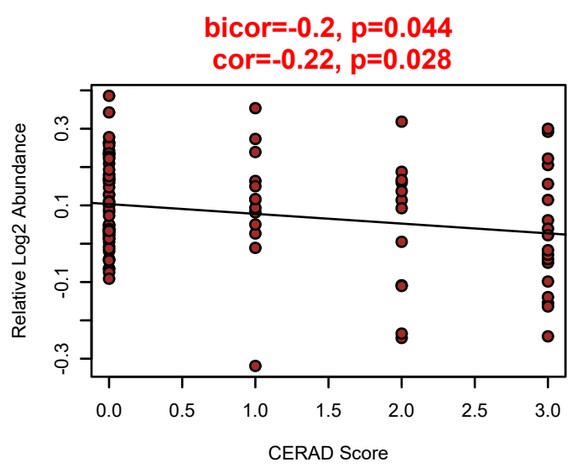

bicor=0.15, p=0.18
cor=0.14, p=0.2
Relative Log2 Abundance
Braak Score

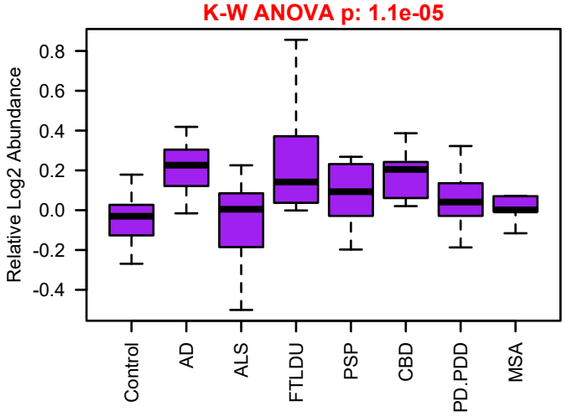

bicor=0.17, p=0.084
cor=0.14, p=0.16
Relative Log2 Abundance
CERAD Score

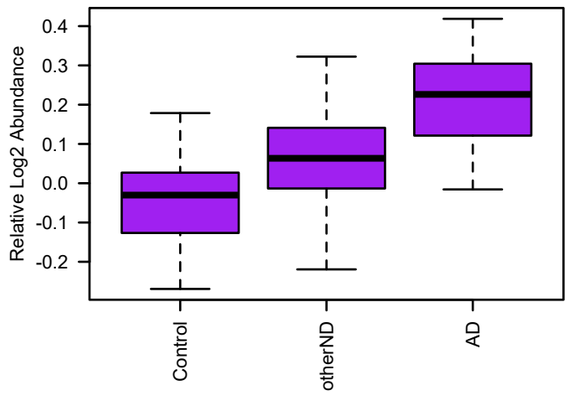

SDHB UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.11
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

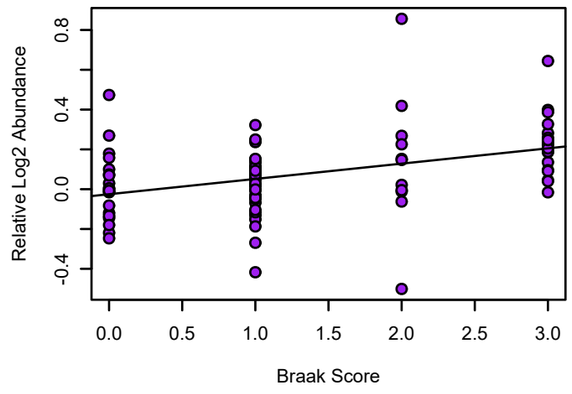

SDHB UPenn Mixed PRM
K-W ANOVA p: 0.008
Relative Log2 Abundance
Control
otherND
AD

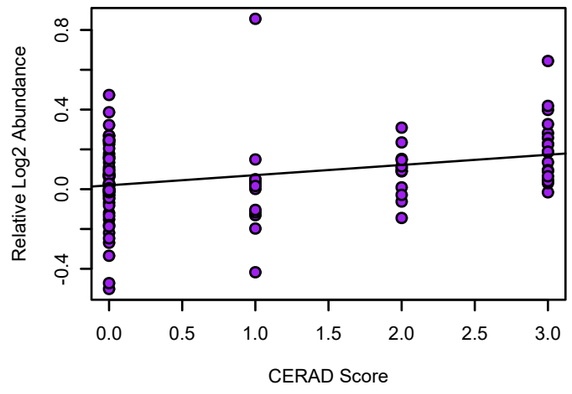

bicor=-0.1, p=0.35
cor=-0.16, p=0.15
Relative Log2 Abundance
Braak Score

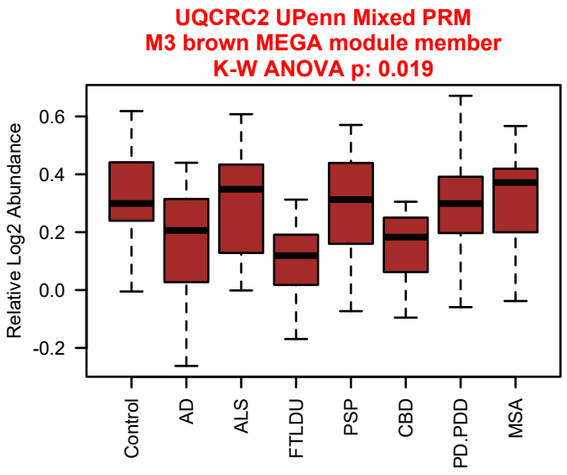

bicor=-0.2, p=0.044
cor=-0.22, p=0.028
Relative Log2 Abundance
CERAD Score

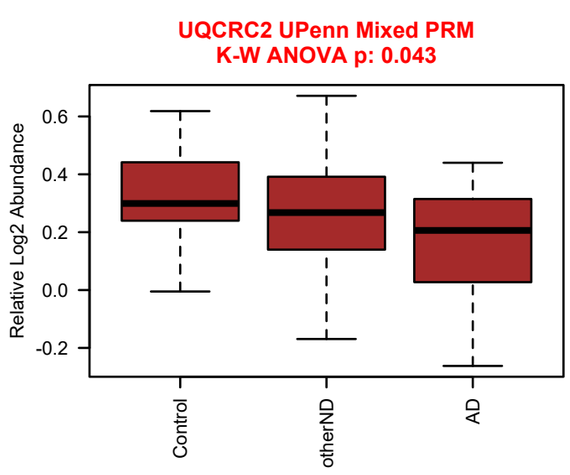

HNRNPA2B1 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 1.1e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

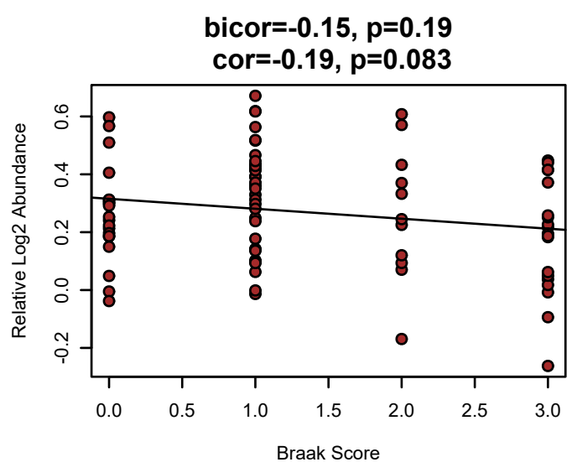

HNRNPA2B1 UPenn Mixed PRM
K-W ANOVA p: 2e-04
Relative Log2 Abundance
Control
otherND
AD

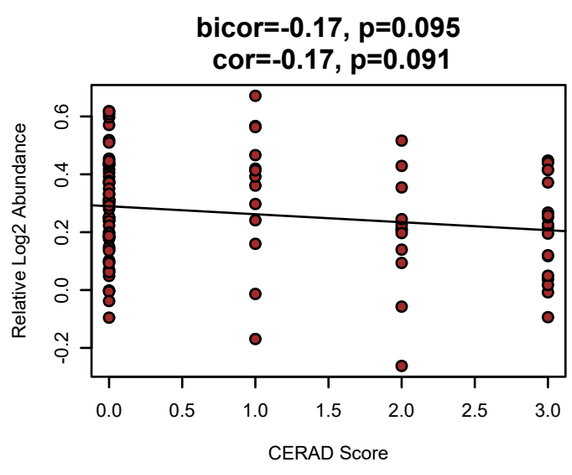

bicor=0.45, p=1.7e-05
cor=0.41, p=0.00011
Relative Log2 Abundance
Braak Score

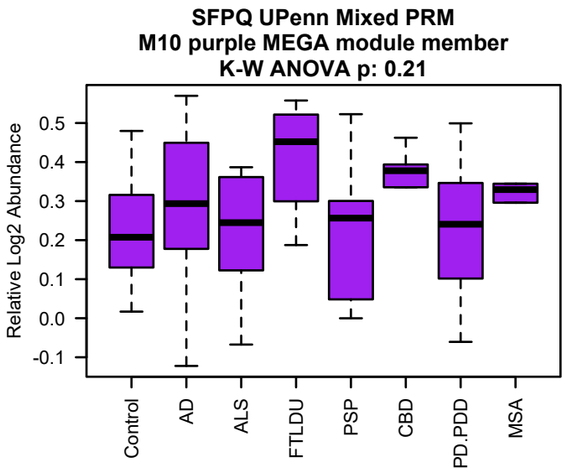

bicor=0.31, p=0.0019
cor=0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

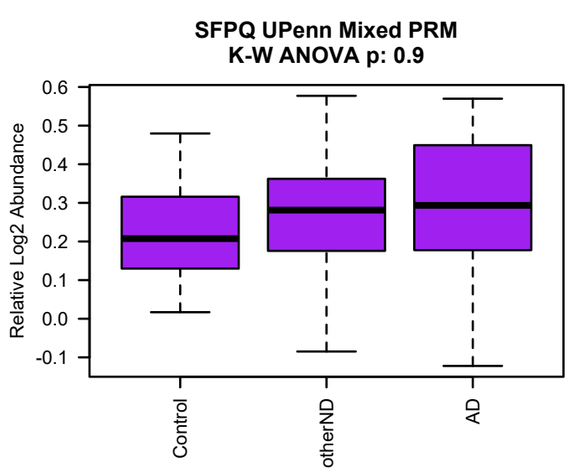

UQCRC2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.019
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

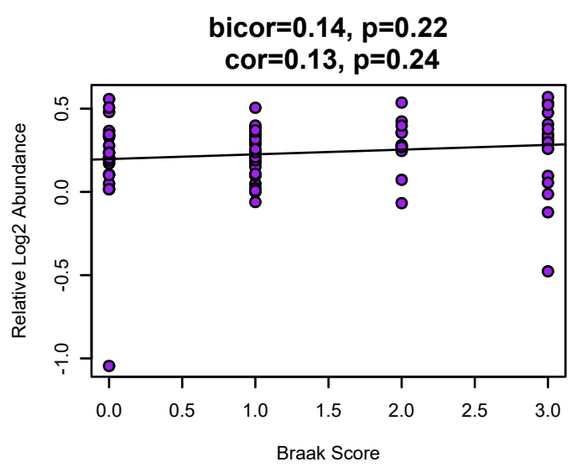

UQCRC2 UPenn Mixed PRM
K-W ANOVA p: 0.043
Relative Log2 Abundance
Control
otherND
AD

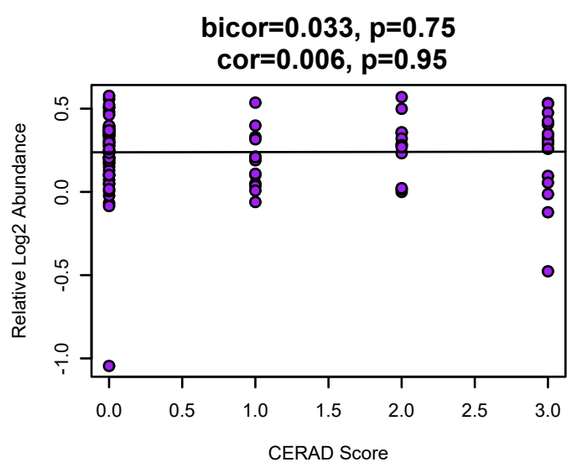

bicor=-0.15, p=0.19
cor=-0.19, p=0.083
Relative Log2 Abundance
Braak Score

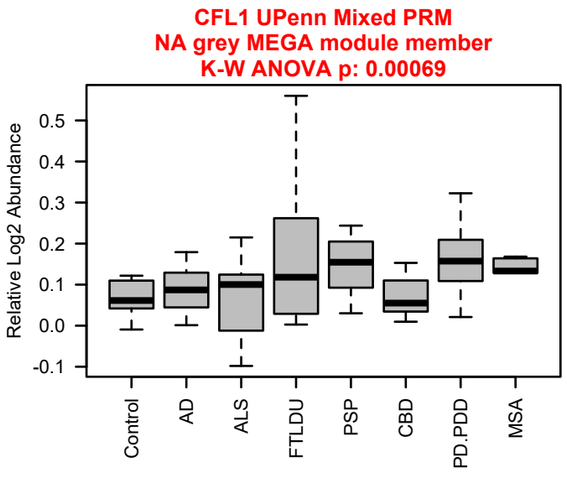

bicor=-0.17, p=0.095
cor=-0.17, p=0.091
Relative Log2 Abundance
CERAD Score

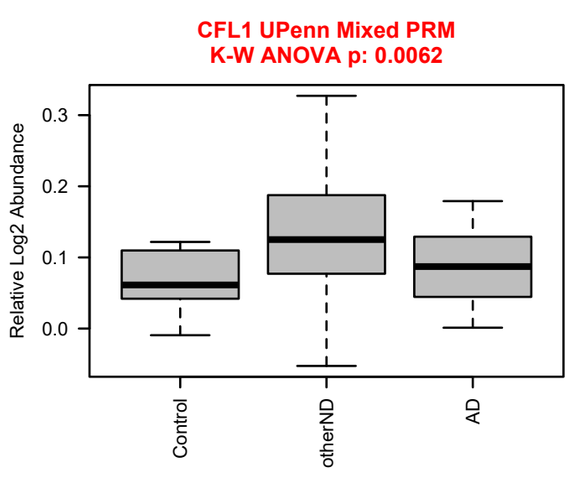

SFPQ UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.21
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

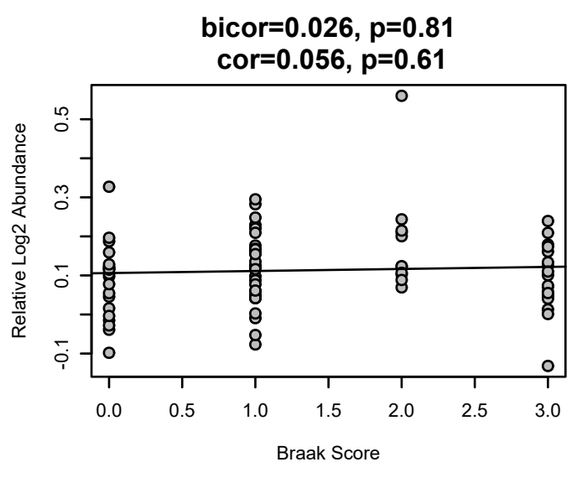

SFPQ UPenn Mixed PRM
K-W ANOVA p: 0.9
Relative Log2 Abundance
Control
otherND
AD

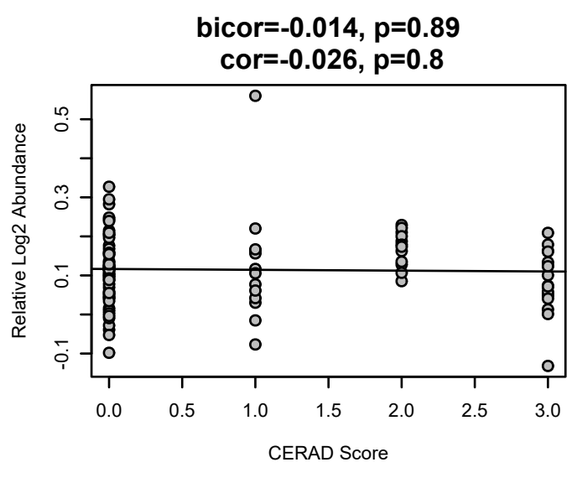

bicor=0.14, p=0.22
cor=0.13, p=0.24
Relative Log2 Abundance
Braak Score

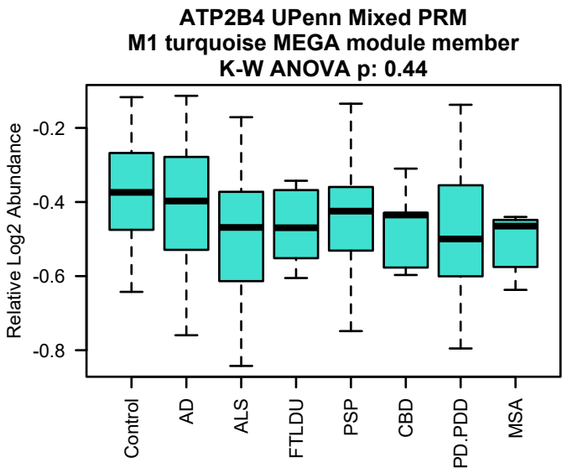

bicor=0.033, p=0.75
cor=0.006, p=0.95
Relative Log2 Abundance
CERAD Score

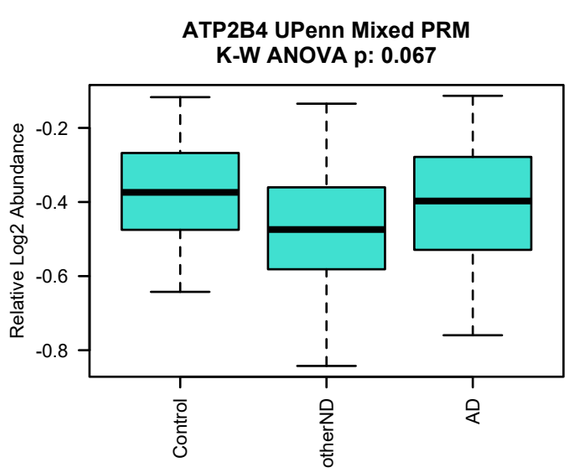

CFL1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.00069
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

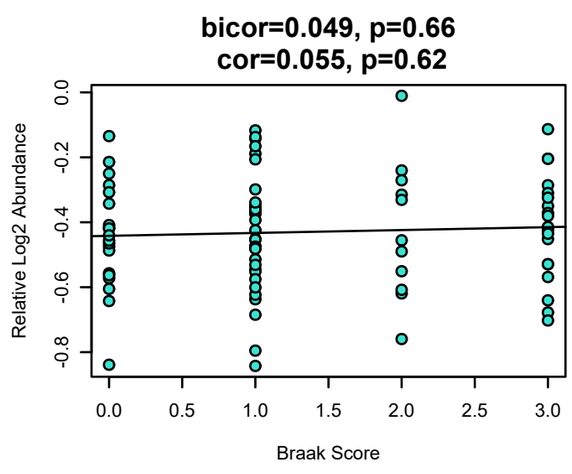

CFL1 UPenn Mixed PRM
K-W ANOVA p: 0.0062
Relative Log2 Abundance
Control
otherND
AD

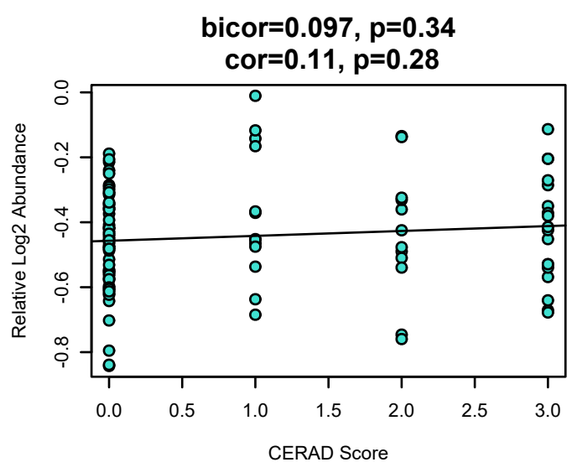

bicor=0.026, p=0.81
cor=0.056, p=0.61
Relative Log2 Abundance
Braak Score

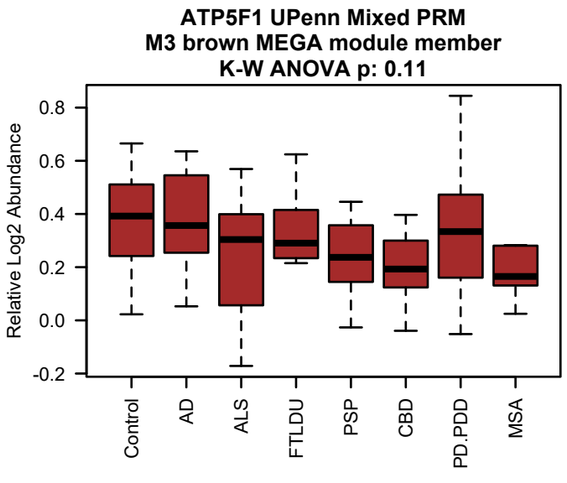

bicor=-0.014, p=0.89
cor=-0.026, p=0.8
Relative Log2 Abundance
CERAD Score

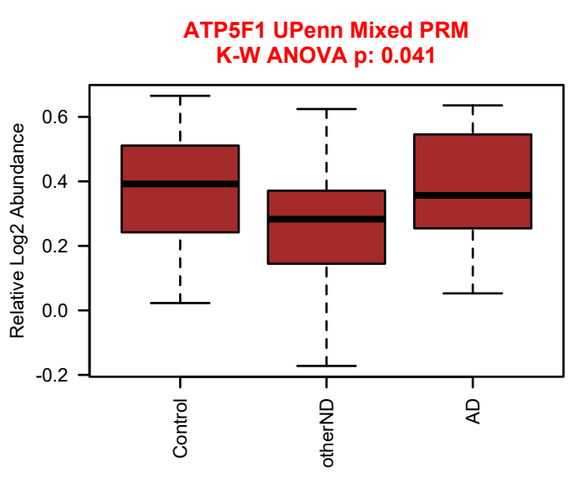

ATP2B4 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.44
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

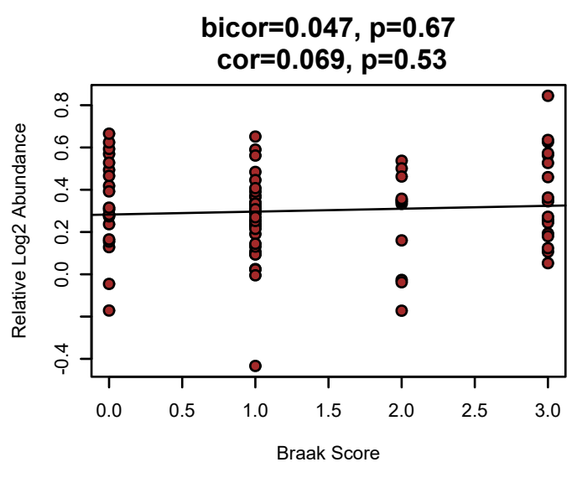

ATP2B4 UPenn Mixed PRM
K-W ANOVA p: 0.067
Relative Log2 Abundance
Control
otherND
AD

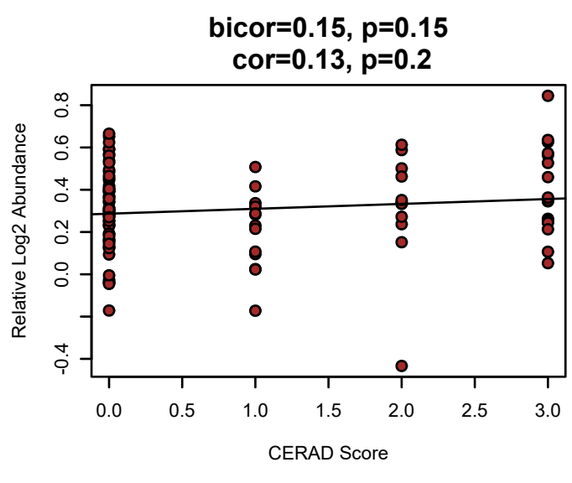

bicor=0.049, p=0.66
cor=0.055, p=0.62
Relative Log2 Abundance
Braak Score

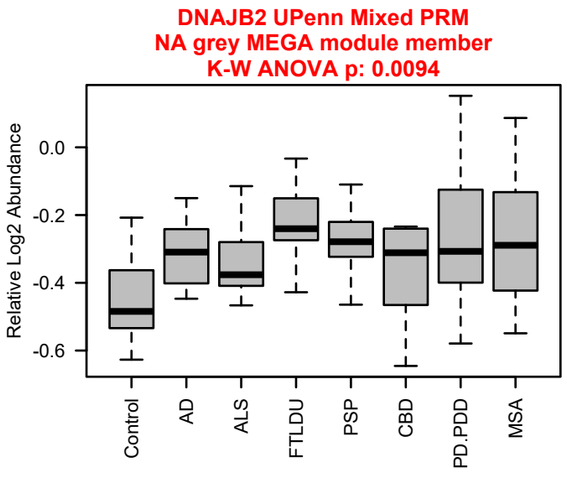

bicor=0.097, p=0.34
cor=0.11, p=0.28
Relative Log2 Abundance
CERAD Score

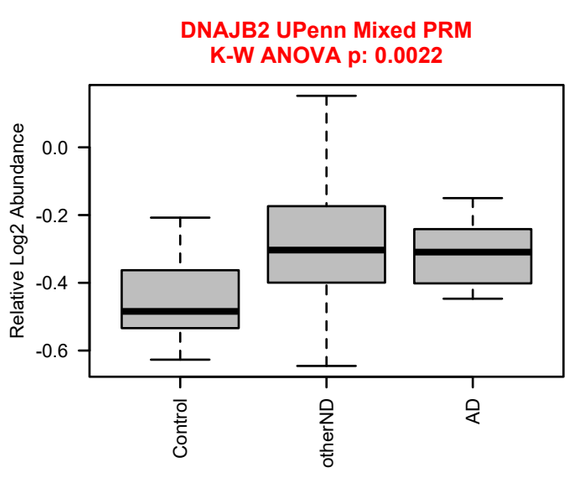

ATP5F1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.11
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

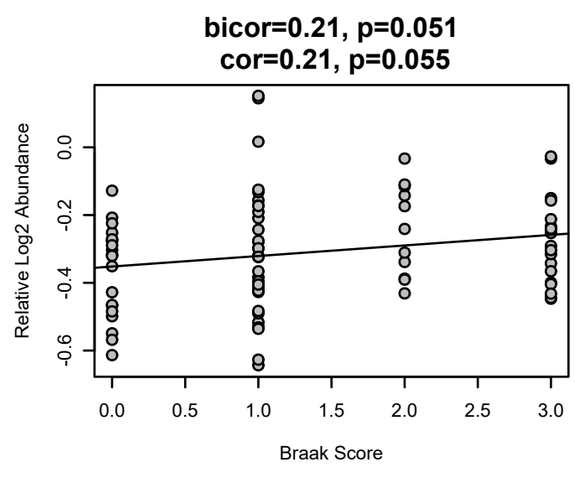

ATP5F1 UPenn Mixed PRM
K-W ANOVA p: 0.041
Relative Log2 Abundance
Control
otherND
AD

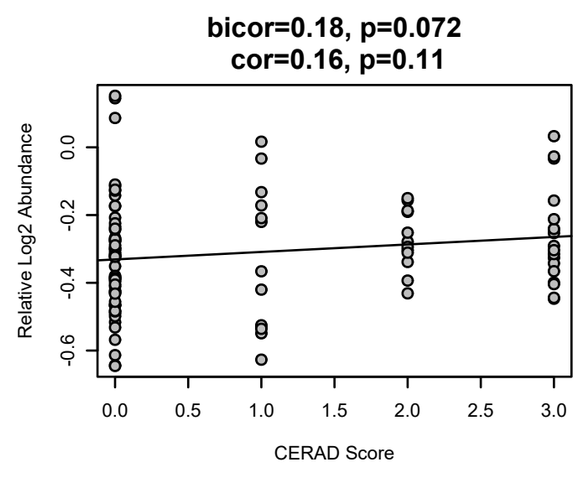

bicor=0.047, p=0.67
cor=0.069, p=0.53
Relative Log2 Abundance
Braak Score

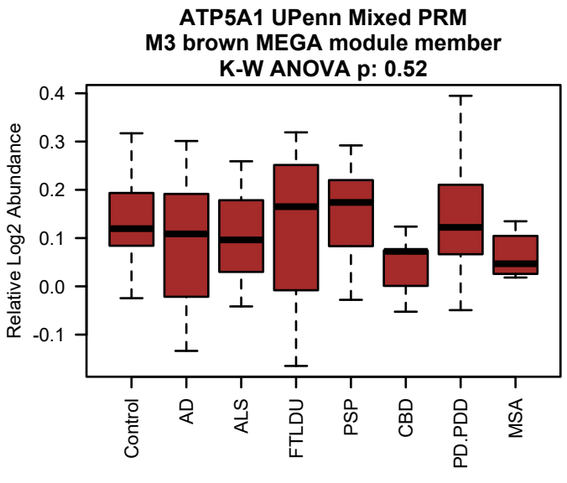

bicor=0.15, p=0.15
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

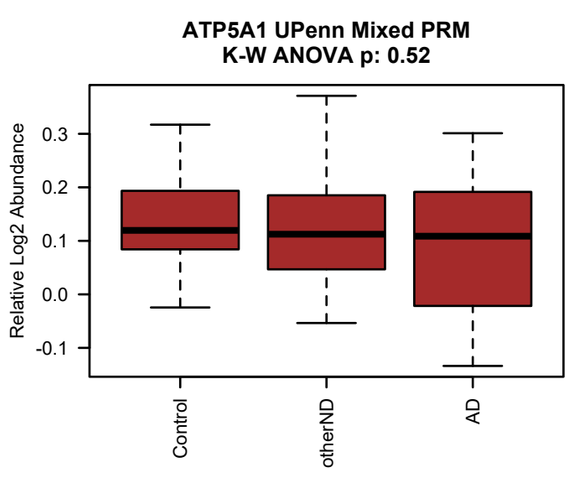

DNAJB2 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.0094
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

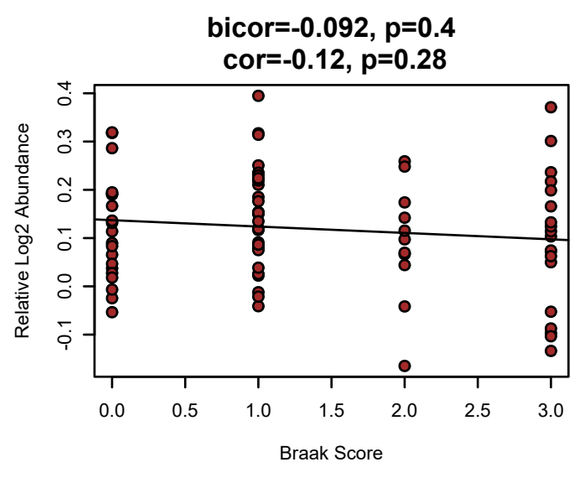

DNAJB2 UPenn Mixed PRM
K-W ANOVA p: 0.0022
Relative Log2 Abundance
Control
otherND
AD

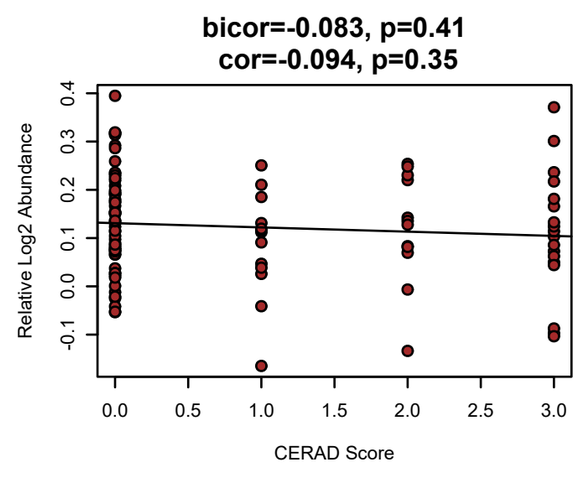

bicor=0.21, p=0.051
cor=0.21, p=0.055
Relative Log2 Abundance
Braak Score

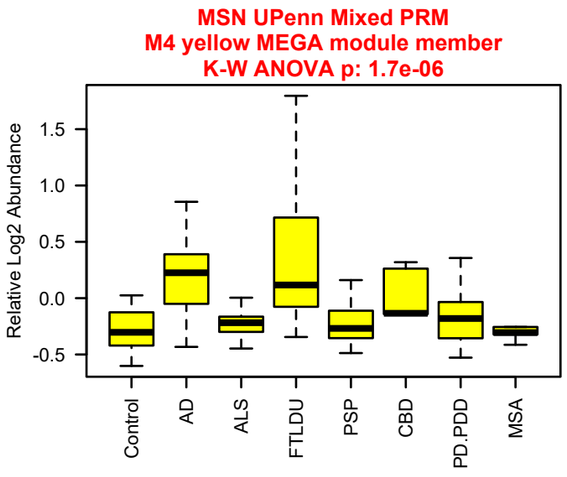

bicor=0.18, p=0.072
cor=0.16, p=0.11
Relative Log2 Abundance
CERAD Score

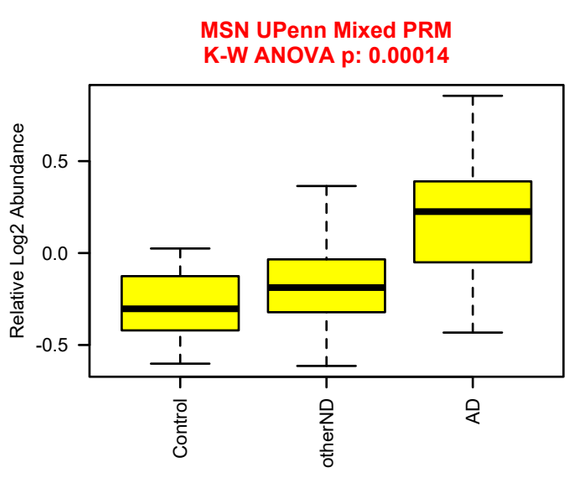

ATP5A1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.52
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

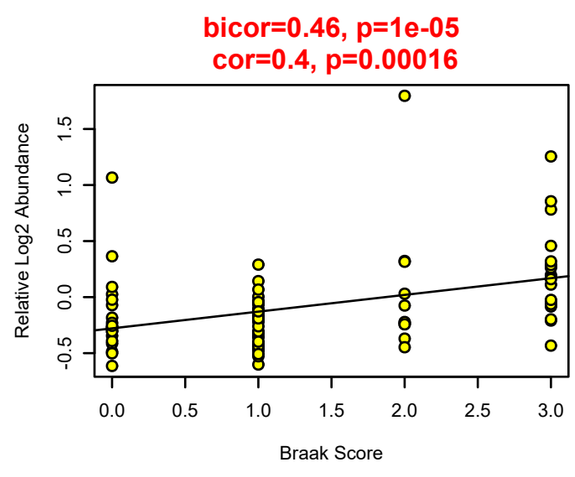

ATP5A1 UPenn Mixed PRM
K-W ANOVA p: 0.52
Relative Log2 Abundance
Control
otherND
AD

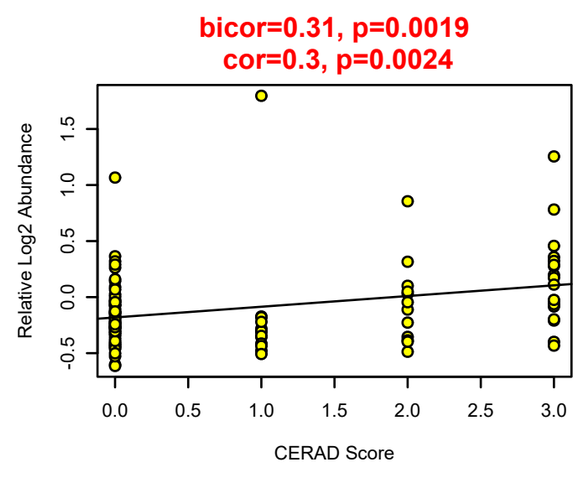

bicor=-0.092, p=0.4
cor=-0.12, p=0.28
Relative Log2 Abundance
Braak Score

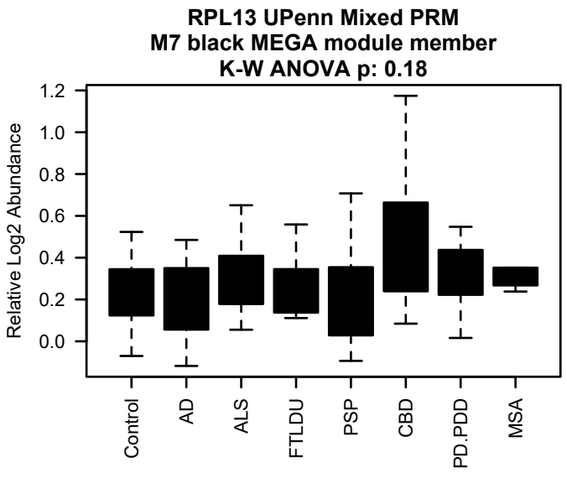

bicor=-0.083, p=0.41
cor=-0.094, p=0.35
Relative Log2 Abundance
CERAD Score

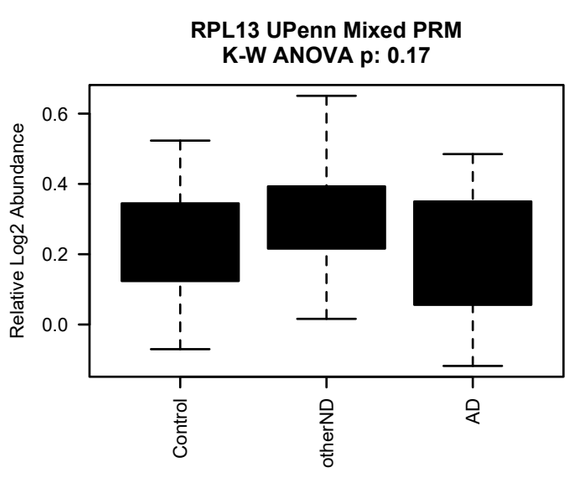

MSN UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1.7e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

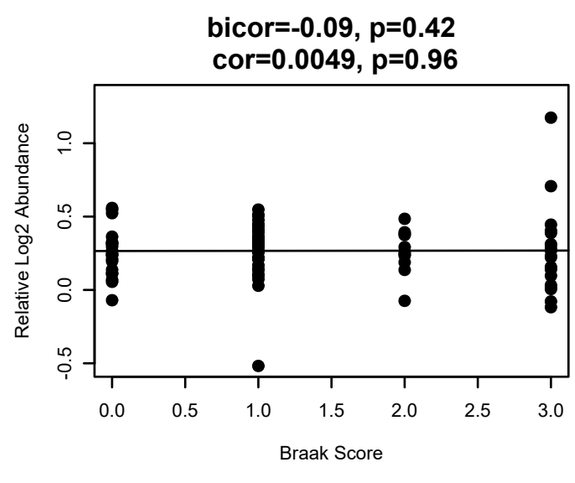

MSN UPenn Mixed PRM
K-W ANOVA p: 0.00014
Relative Log2 Abundance
Control
otherND
AD

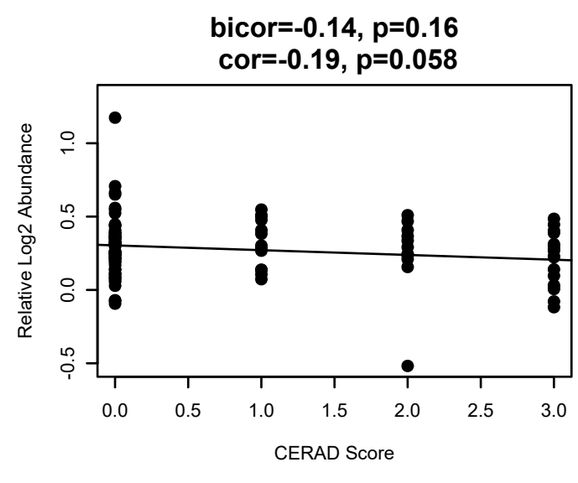

bicor=0.46, p=1e-05
cor=0.4, p=0.00016
Relative Log2 Abundance
Braak Score

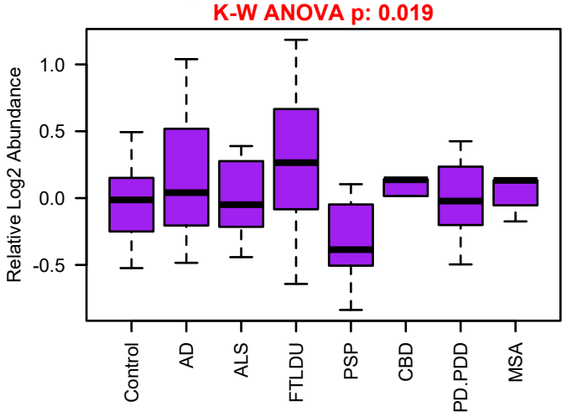

bicor=0.31, p=0.0019
cor=0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

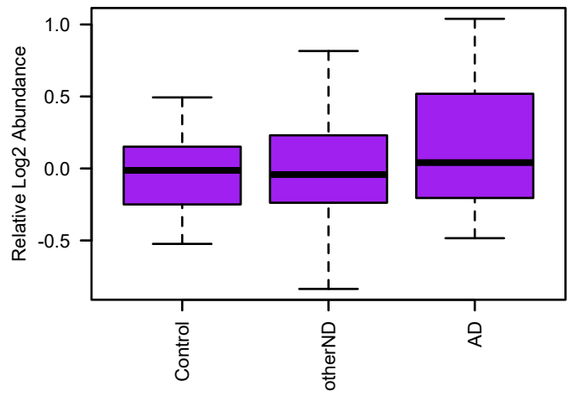

RPL13 UPenn Mixed PRM
M7 black MEGA module member
K-W ANOVA p: 0.18
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

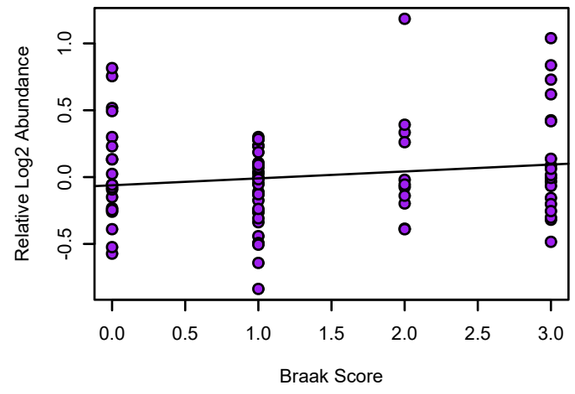

RPL13 UPenn Mixed PRM
K-W ANOVA p: 0.17
Relative Log2 Abundance
Control
otherND
AD

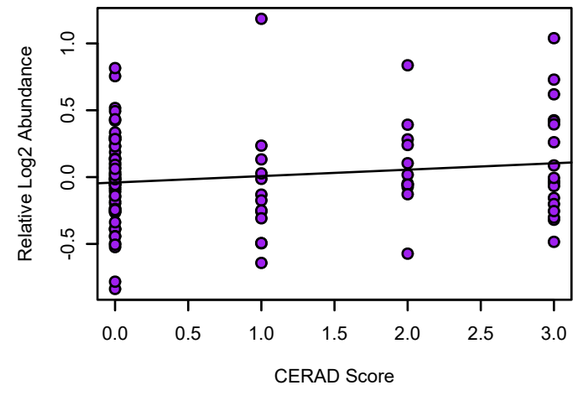

bicor=-0.09, p=0.42
cor=0.0049, p=0.96
Relative Log2 Abundance
Braak Score

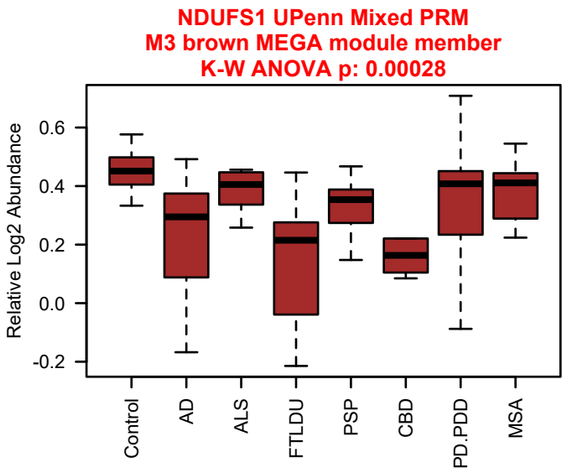

bicor=-0.14, p=0.16
cor=-0.19, p=0.058
Relative Log2 Abundance
CERAD Score

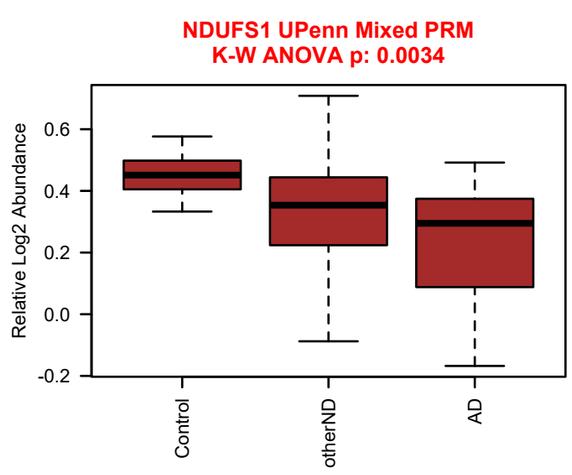

MAP4 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.019
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

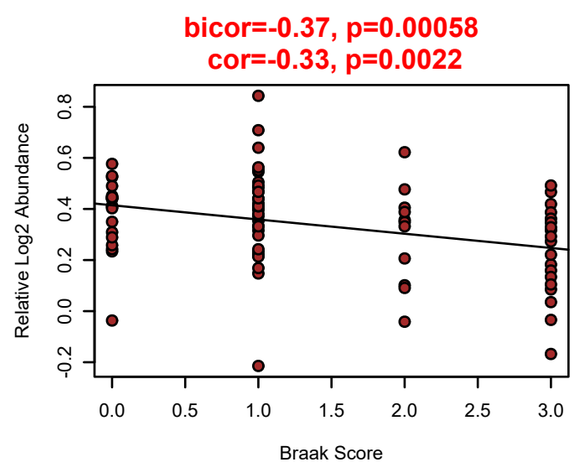

MAP4 UPenn Mixed PRM
K-W ANOVA p: 0.2
Relative Log2 Abundance
Control
otherND
AD

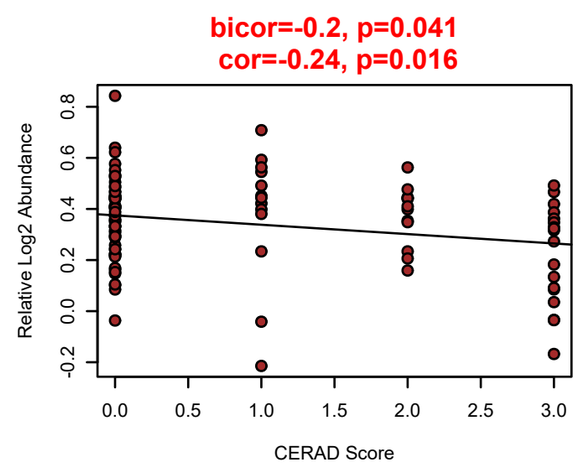

bicor=0.13, p=0.24
cor=0.15, p=0.17
Relative Log2 Abundance
Braak Score

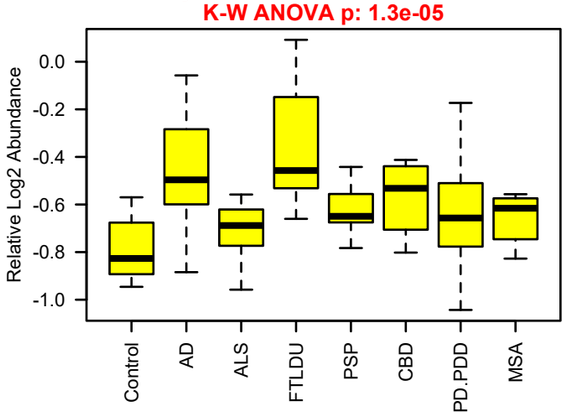

bicor=0.13, p=0.2
cor=0.15, p=0.14
Relative Log2 Abundance
CERAD Score

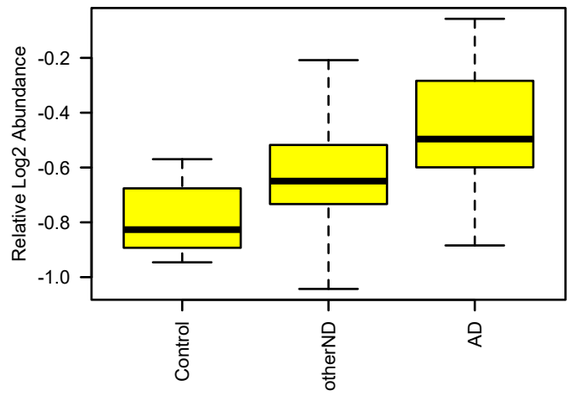

NDUFS1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.00028
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

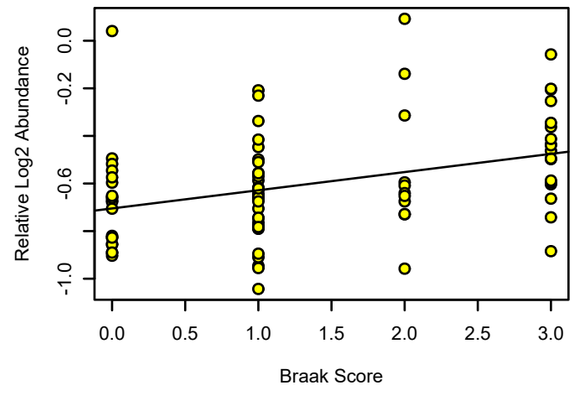

NDUFS1 UPenn Mixed PRM
K-W ANOVA p: 0.0034
Relative Log2 Abundance
Control
otherND
AD

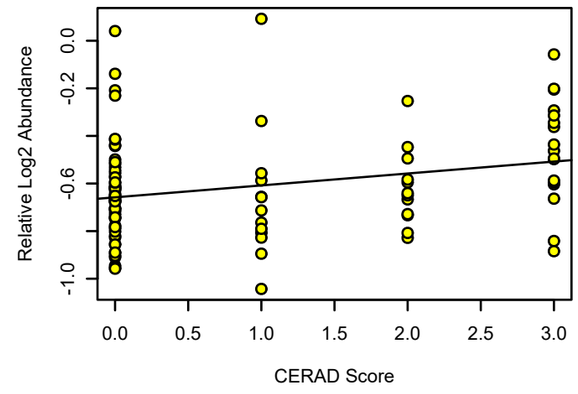

bicor=-0.37, p=0.00058
cor=-0.33, p=0.0022
Relative Log2 Abundance
Braak Score

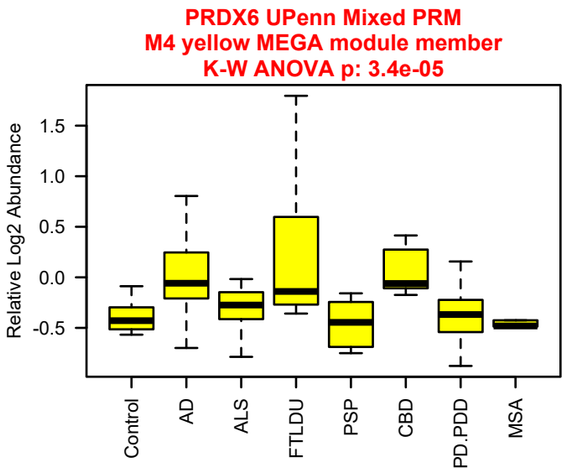

bicor=-0.2, p=0.041
cor=-0.24, p=0.016
Relative Log2 Abundance
CERAD Score

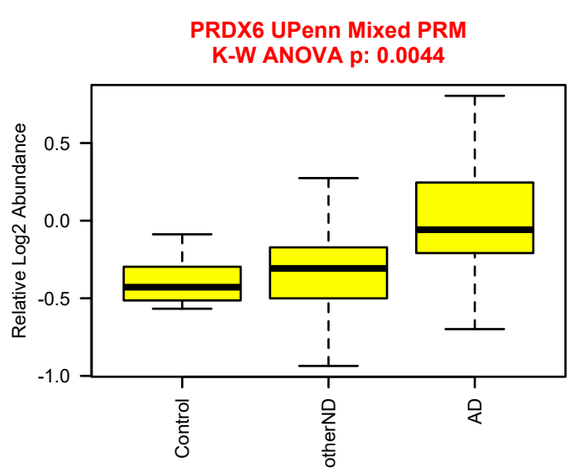

MAPK1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 1.3e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

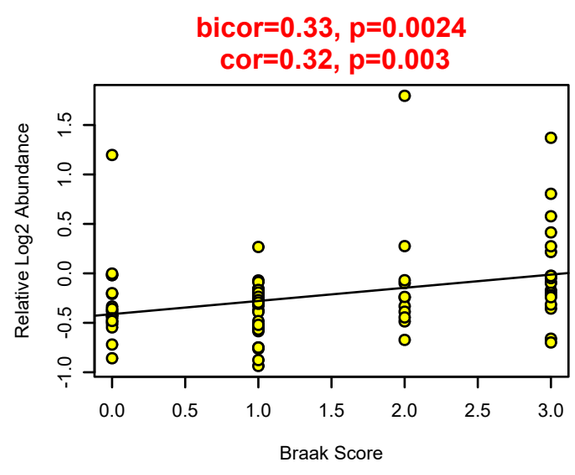

MAPK1 UPenn Mixed PRM
K-W ANOVA p: 9.7e-05
Relative Log2 Abundance
Control
otherND
AD

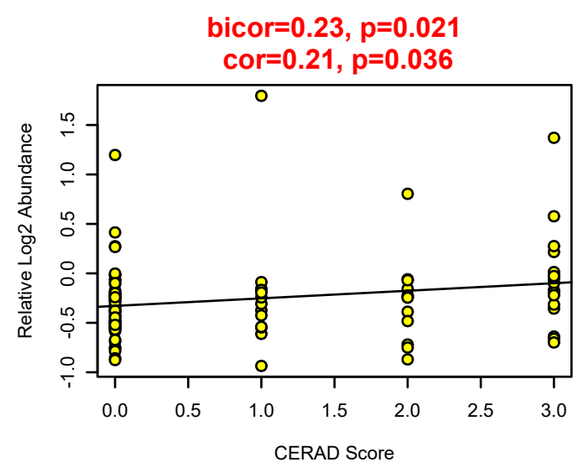

bicor=0.41, p=0.00012
cor=0.36, p=0.00077
Relative Log2 Abundance
Braak Score

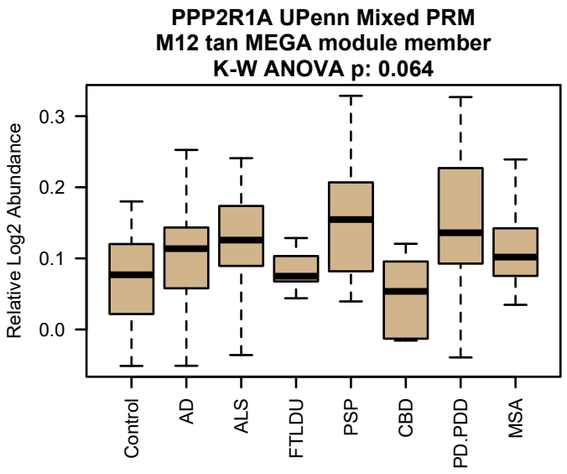

bicor=0.3, p=0.0022
cor=0.27, p=0.0066
Relative Log2 Abundance
CERAD Score

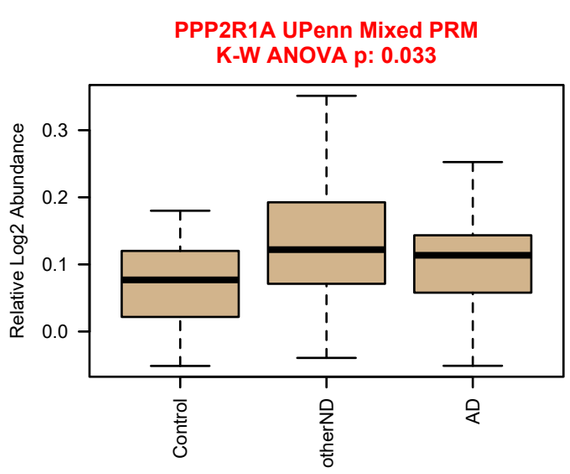

PRDX6 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 3.4e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

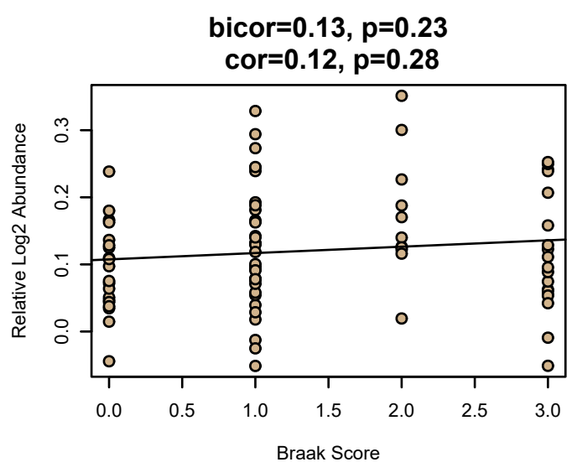

PRDX6 UPenn Mixed PRM
K-W ANOVA p: 0.0044
Relative Log2 Abundance
Control
otherND
AD

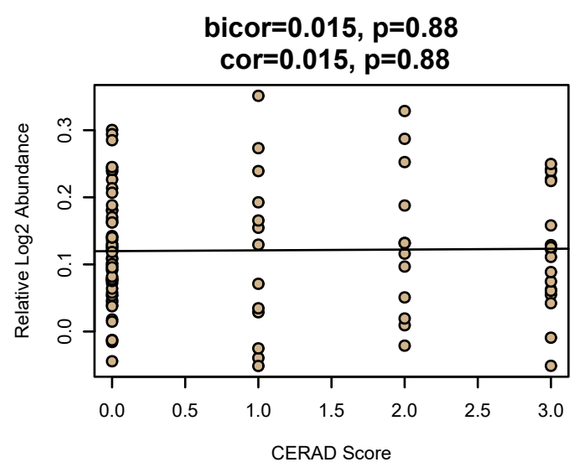

bicor=0.33, p=0.0024
cor=0.32, p=0.003
Relative Log2 Abundance
Braak Score

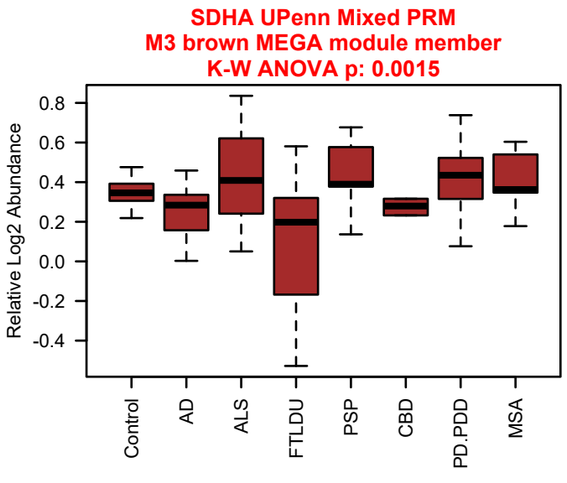

bicor=0.23, p=0.021
cor=0.21, p=0.036
Relative Log2 Abundance
CERAD Score

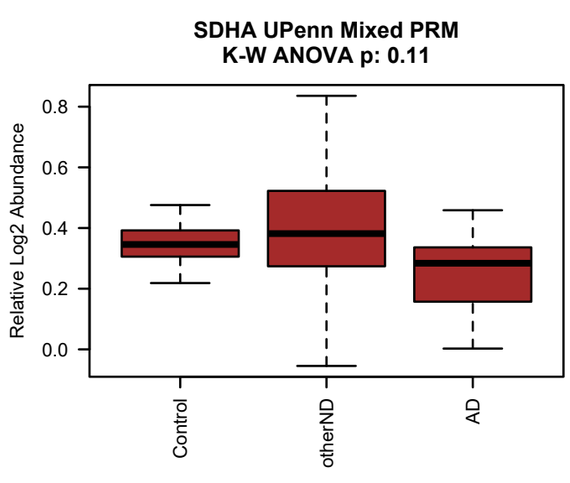

PPP2R1A UPenn Mixed PRM
M12 tan MEGA module member
K-W ANOVA p: 0.064
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

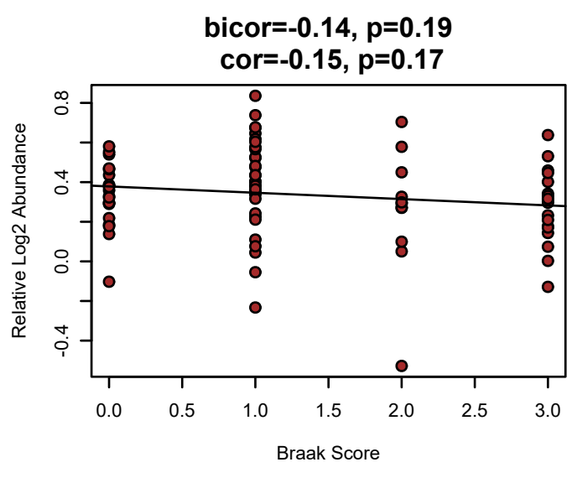

PPP2R1A UPenn Mixed PRM
K-W ANOVA p: 0.033
Relative Log2 Abundance
Control
otherND
AD

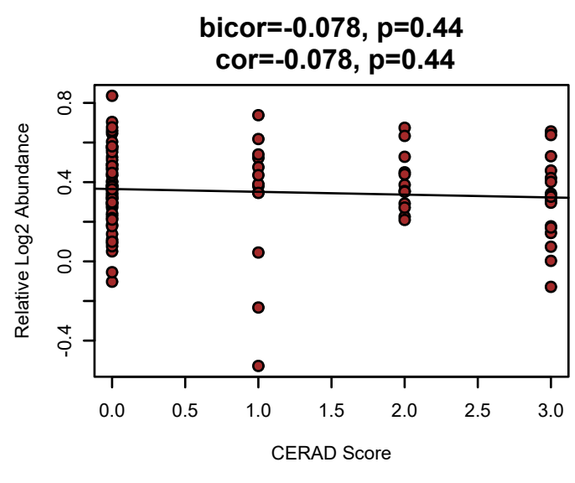

bicor=0.13, p=0.23
cor=0.12, p=0.28
Relative Log2 Abundance
Braak Score

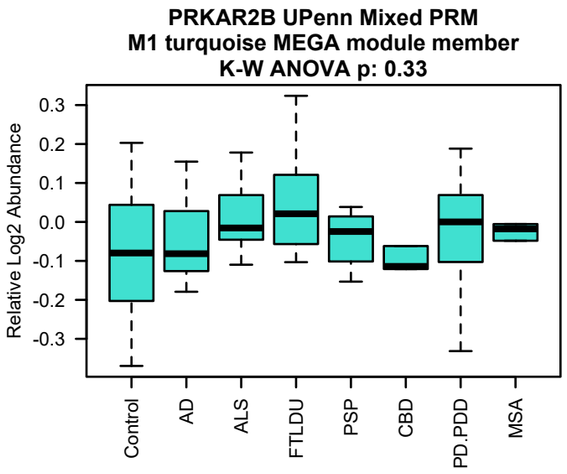

bicor=0.015, p=0.88
cor=0.015, p=0.88
Relative Log2 Abundance
CERAD Score

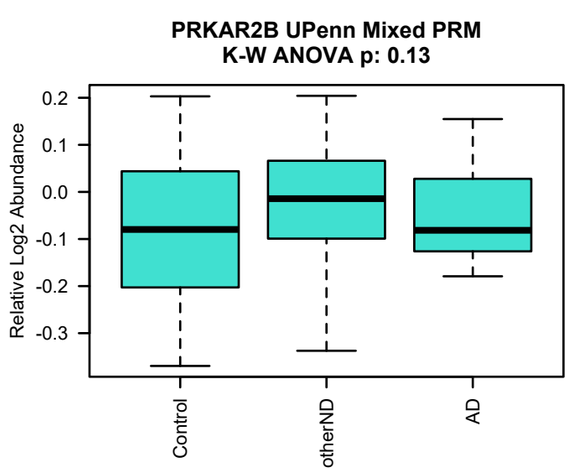

SDHA UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0015
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

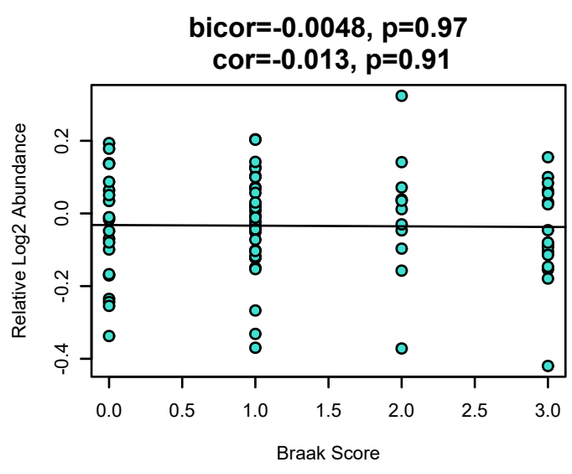

SDHA UPenn Mixed PRM
K-W ANOVA p: 0.11
Relative Log2 Abundance
Control
otherND
AD

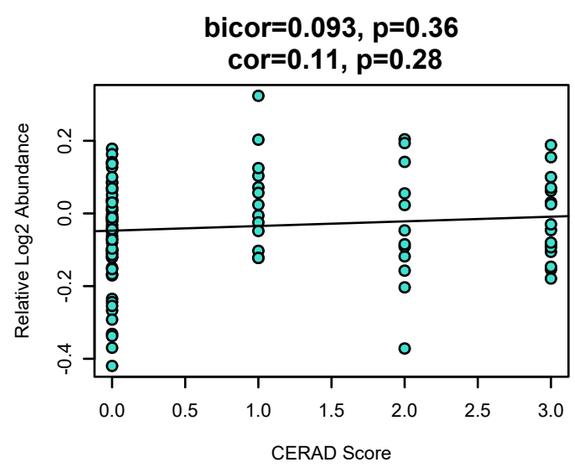

bicor=-0.14, p=0.19
cor=-0.15, p=0.17
Relative Log2 Abundance
Braak Score

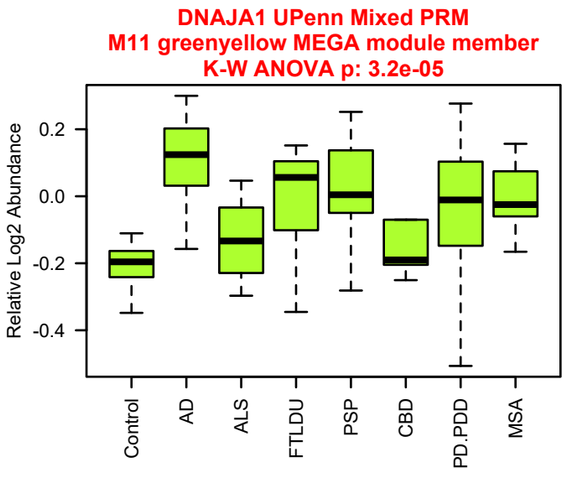

bicor=-0.078, p=0.44
cor=-0.078, p=0.44
Relative Log2 Abundance
CERAD Score

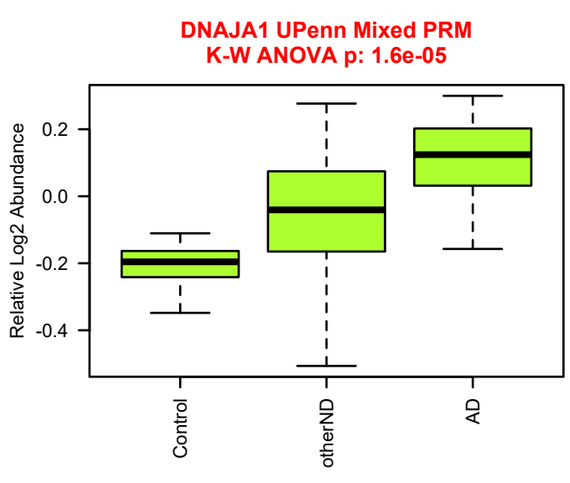

PRKAR2B UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.33
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

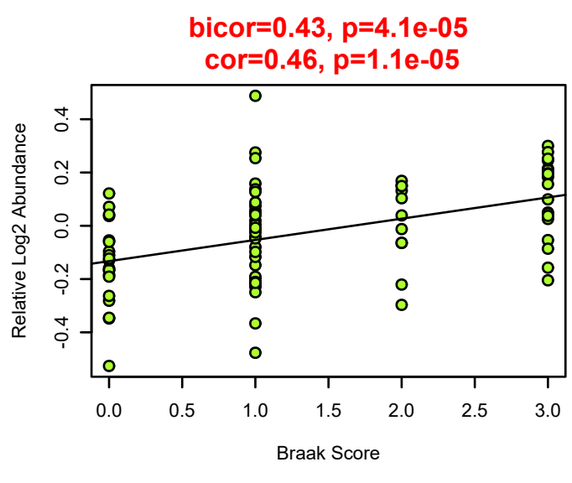

PRKAR2B UPenn Mixed PRM
K-W ANOVA p: 0.13
Relative Log2 Abundance
Control
otherND
AD

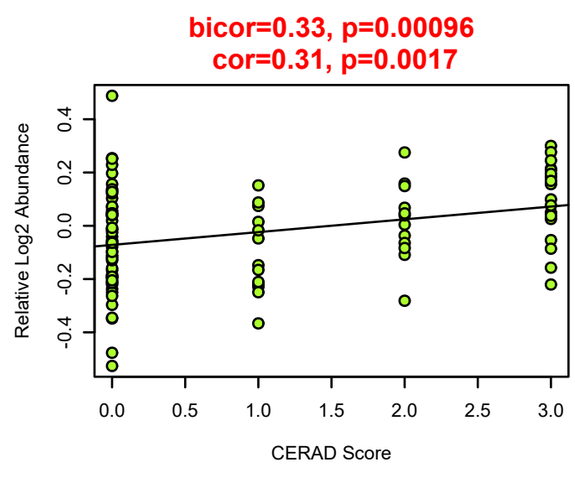

bicor=-0.0048, p=0.97
cor=-0.013, p=0.91
Relative Log2 Abundance
Braak Score

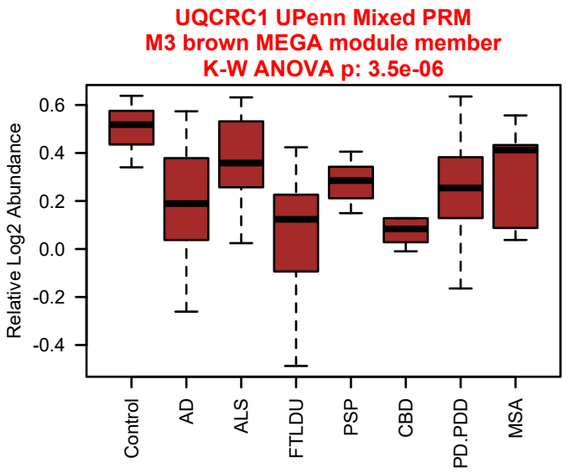

bicor=0.093, p=0.36
cor=0.11, p=0.28
Relative Log2 Abundance
CERAD Score

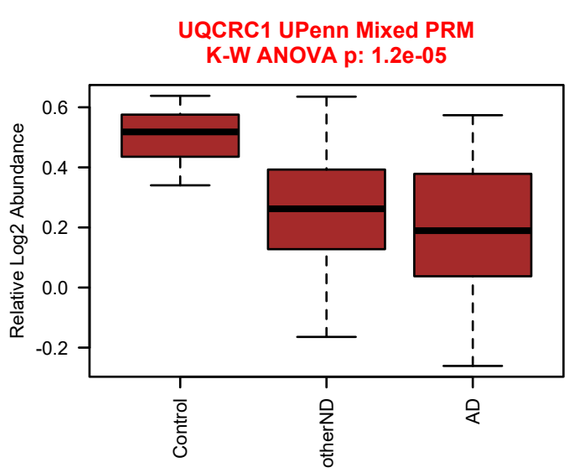

DNAJA1 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 3.2e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

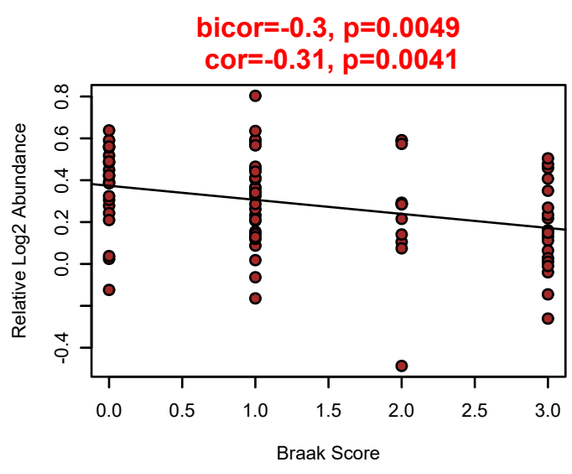

DNAJA1 UPenn Mixed PRM
K-W ANOVA p: 1.6e-05
Relative Log2 Abundance
Control
otherND
AD

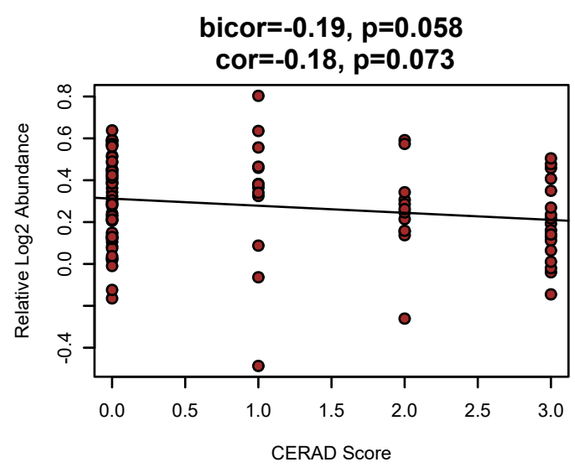

bicor=0.43, p=4.1e-05
cor=0.46, p=1.1e-05
Relative Log2 Abundance
Braak Score

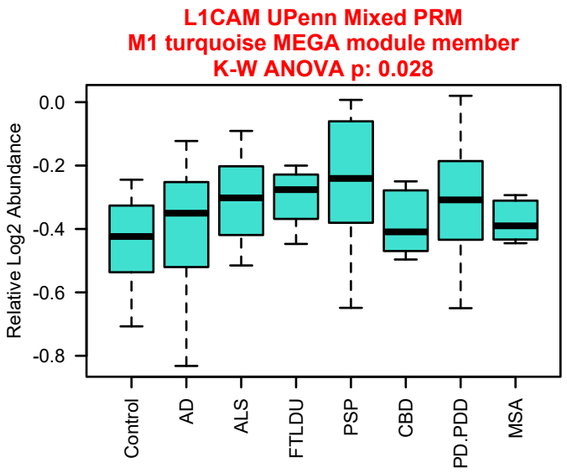

bicor=0.33, p=0.00096
cor=0.31, p=0.0017
Relative Log2 Abundance
CERAD Score

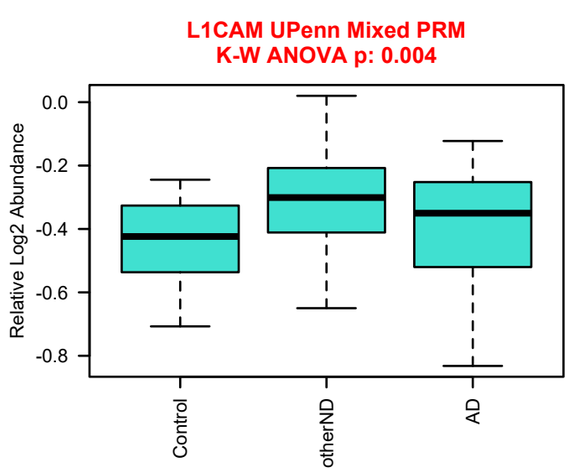

UQCRC1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 3.5e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

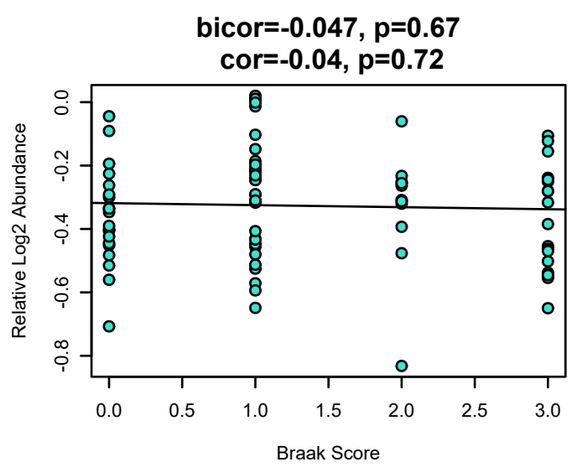

UQCRC1 UPenn Mixed PRM
K-W ANOVA p: 1.2e-05
Relative Log2 Abundance
Control
otherND
AD

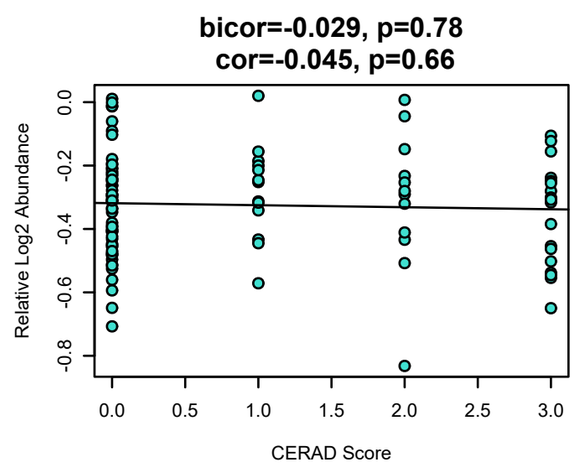

bicor=-0.3, p=0.0049
cor=-0.31, p=0.0041
Relative Log2 Abundance
Braak Score

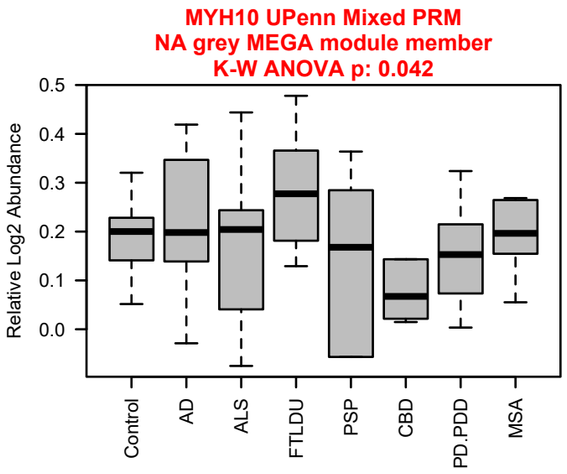

bicor=-0.19, p=0.058
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

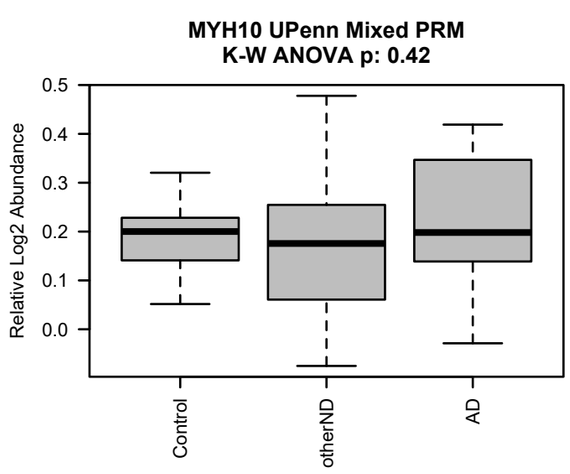

L1CAM UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.028
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

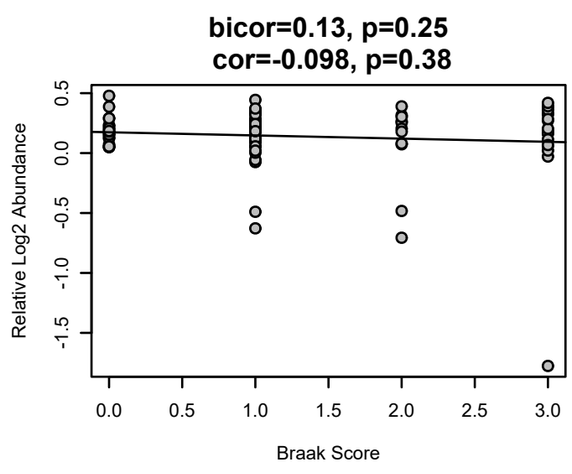

L1CAM UPenn Mixed PRM
K-W ANOVA p: 0.004
Relative Log2 Abundance
Control
otherND
AD

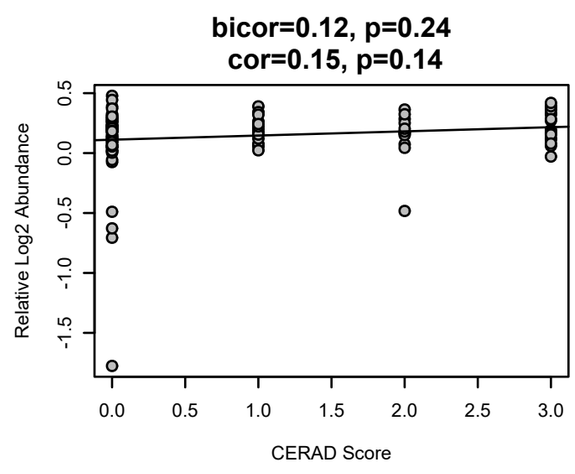

bicor=-0.047, p=0.67
cor=-0.04, p=0.72
Relative Log2 Abundance
Braak Score

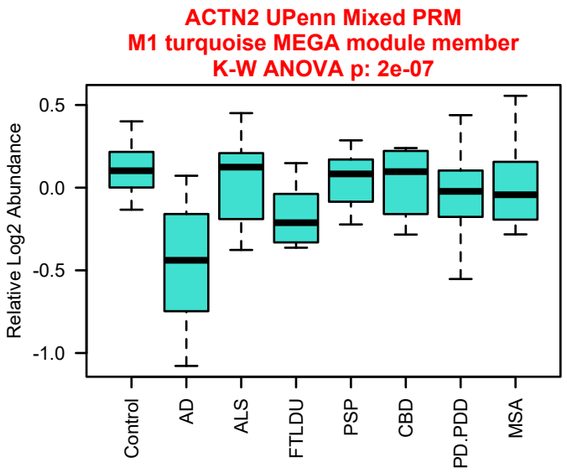

bicor=-0.029, p=0.78
cor=-0.045, p=0.66
Relative Log2 Abundance
CERAD Score

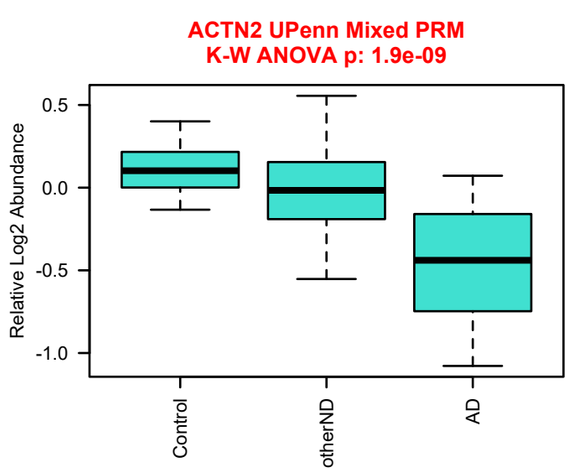

MYH10 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.042
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

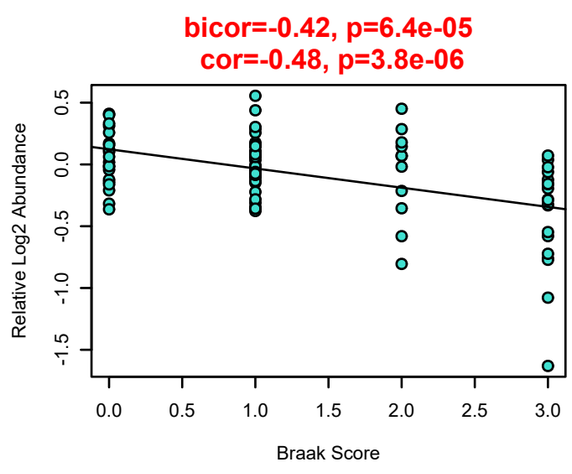

MYH10 UPenn Mixed PRM
K-W ANOVA p: 0.42
Relative Log2 Abundance
Control
otherND
AD

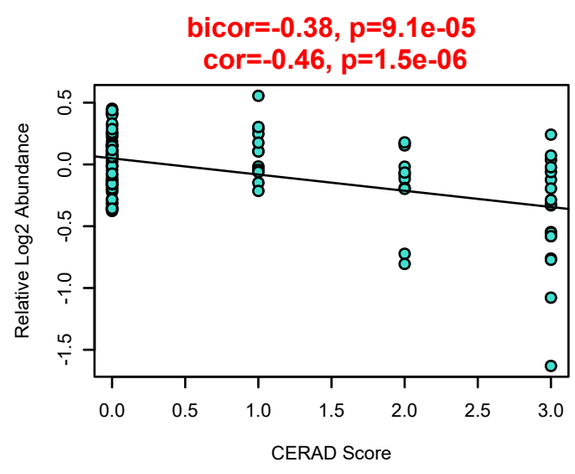

bicor=0.13, p=0.25
cor=-0.098, p=0.38
Relative Log2 Abundance
Braak Score

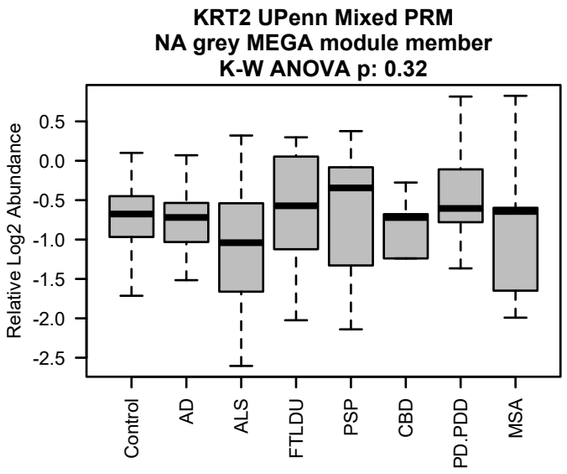

bicor=0.12, p=0.24
cor=0.15, p=0.14
Relative Log2 Abundance
CERAD Score

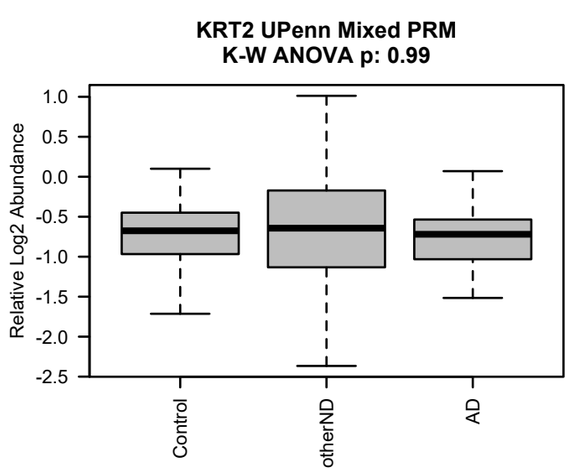

ACTN2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

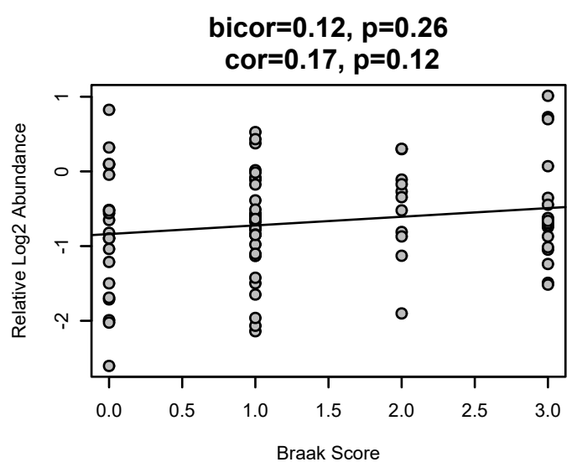

ACTN2 UPenn Mixed PRM
K-W ANOVA p: 1.9e-09
Relative Log2 Abundance
Control
otherND
AD

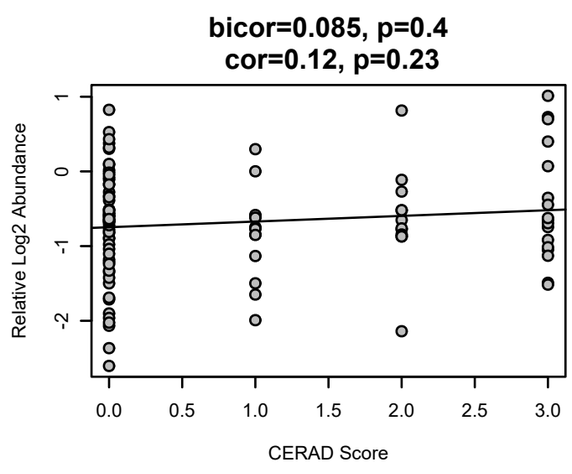

bicor=-0.42, p=6.4e-05
cor=-0.48, p=3.8e-06
Relative Log2 Abundance
Braak Score

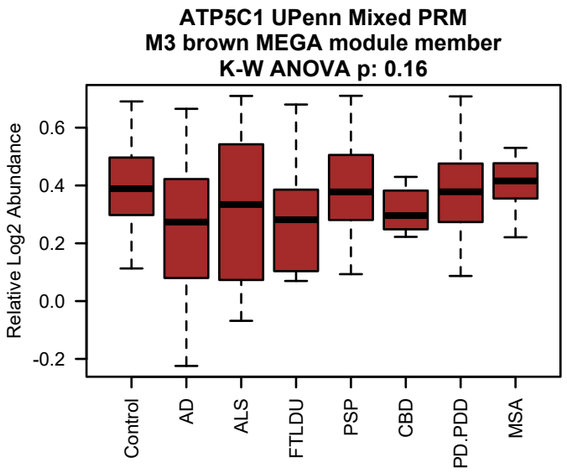

bicor=-0.38, p=9.1e-05
cor=-0.46, p=1.5e-06
Relative Log2 Abundance
CERAD Score

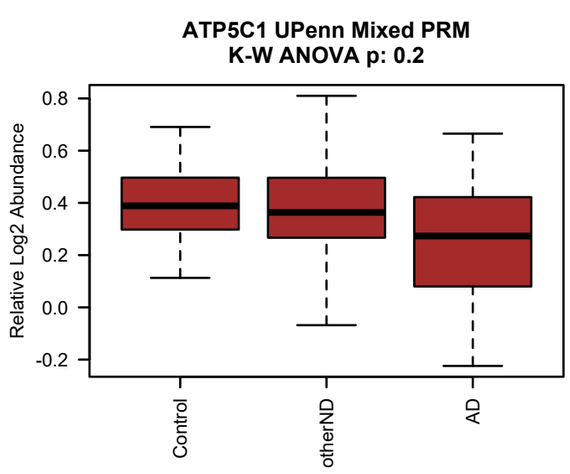

KRT2 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.32
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

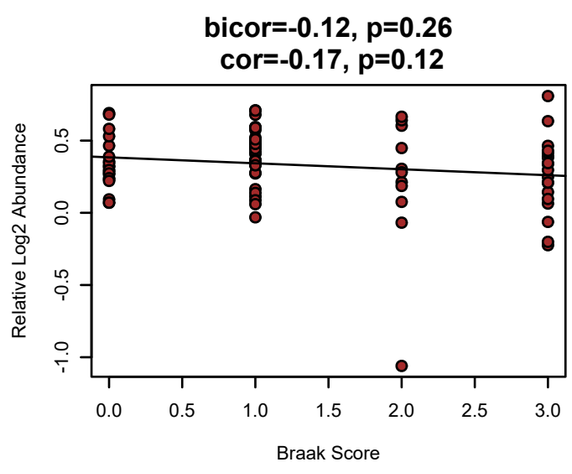

KRT2 UPenn Mixed PRM
K-W ANOVA p: 0.99
Relative Log2 Abundance
Control
otherND
AD

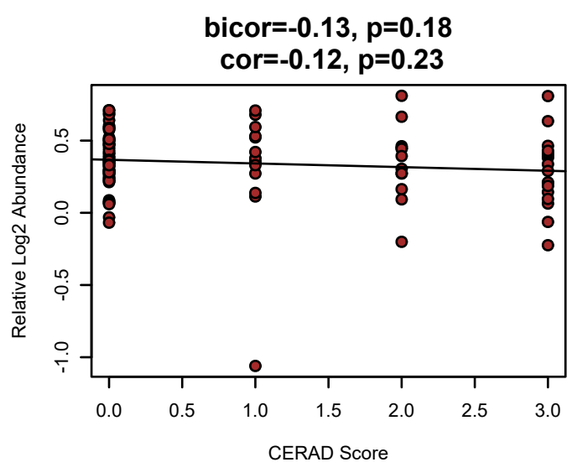

bicor=0.12, p=0.26
cor=0.17, p=0.12
Relative Log2 Abundance
Braak Score

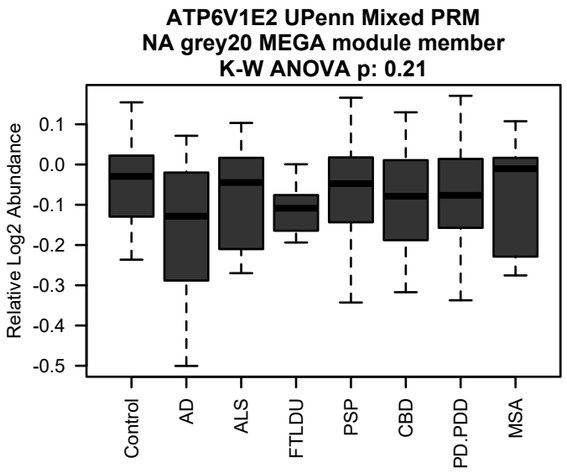

bicor=0.085, p=0.4
cor=0.12, p=0.23
Relative Log2 Abundance
CERAD Score

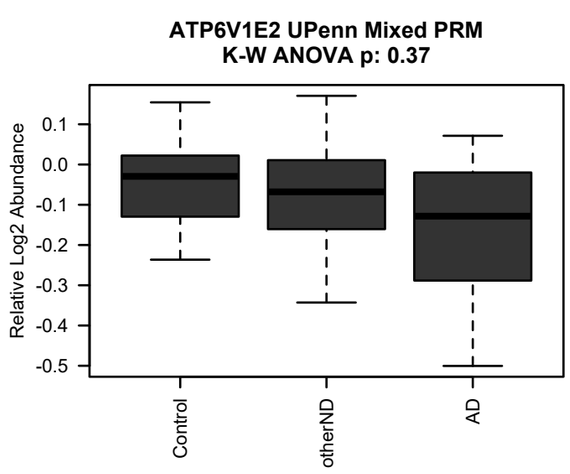

ATP5C1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.16
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

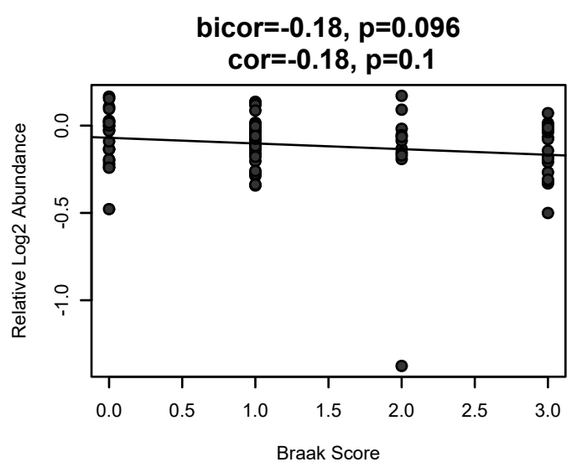

ATP5C1 UPenn Mixed PRM
K-W ANOVA p: 0.2
Relative Log2 Abundance
Control
otherND
AD

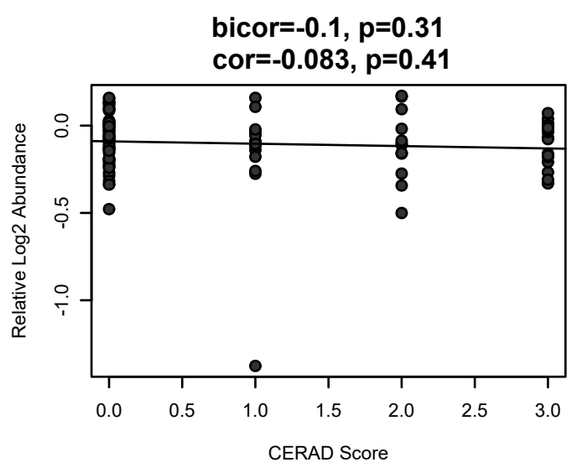

bicor=-0.12, p=0.26
cor=-0.17, p=0.12
Relative Log2 Abundance
Braak Score

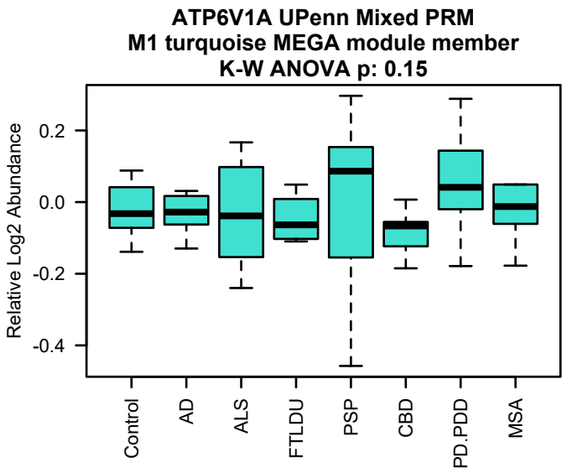

bicor=-0.13, p=0.18
cor=-0.12, p=0.23
Relative Log2 Abundance
CERAD Score

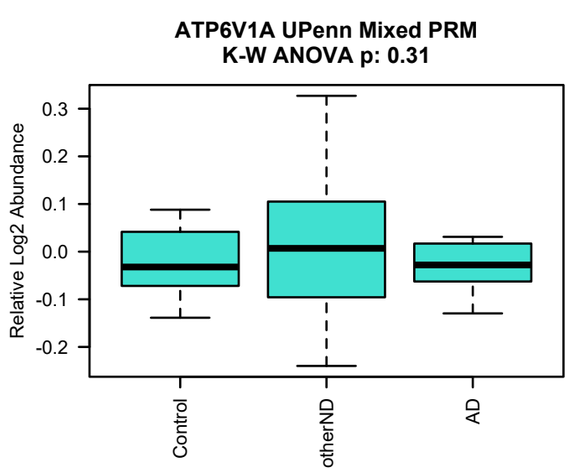

ATP6V1E2 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.21
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

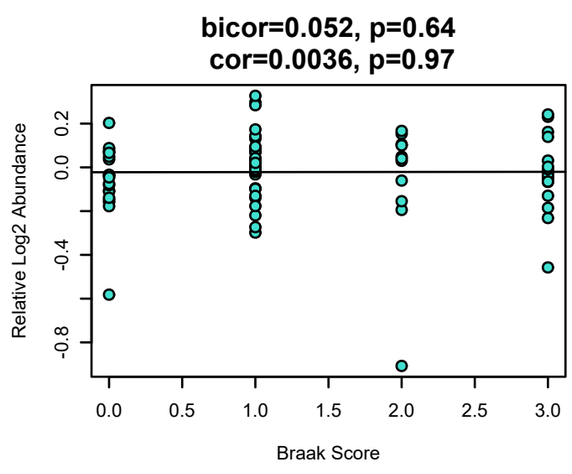

ATP6V1E2 UPenn Mixed PRM
K-W ANOVA p: 0.37
Relative Log2 Abundance
Control
otherND
AD

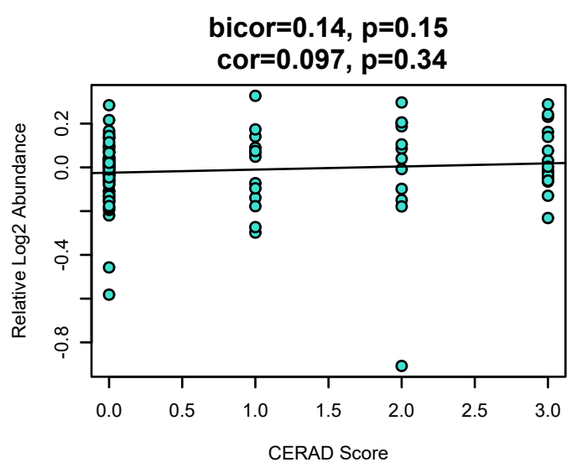

bicor=-0.18, p=0.096
cor=-0.18, p=0.1
Relative Log2 Abundance
Braak Score

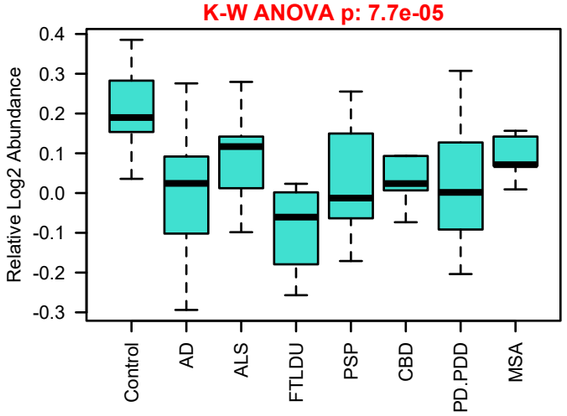

bicor=-0.1, p=0.31
cor=-0.083, p=0.41
Relative Log2 Abundance
CERAD Score

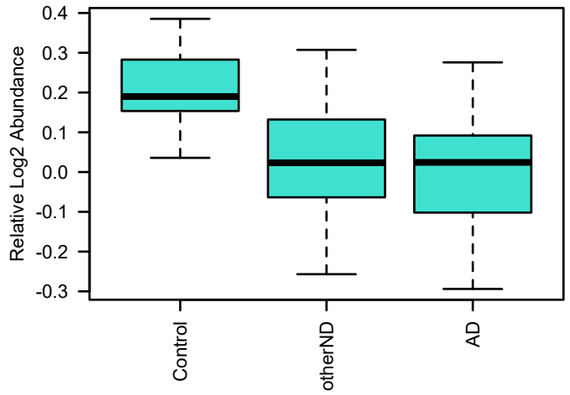

ATP6V1A UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.15
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

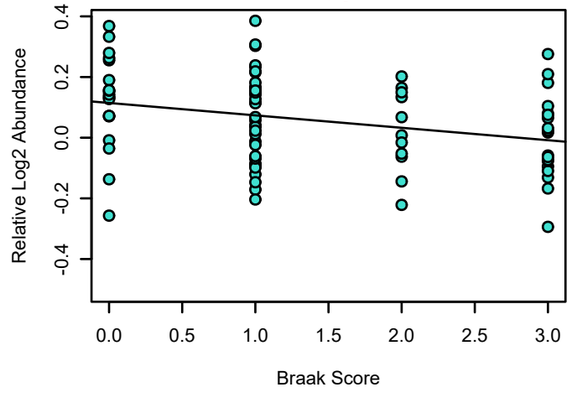

ATP6V1A UPenn Mixed PRM
K-W ANOVA p: 0.31
Relative Log2 Abundance
Control
otherND
AD

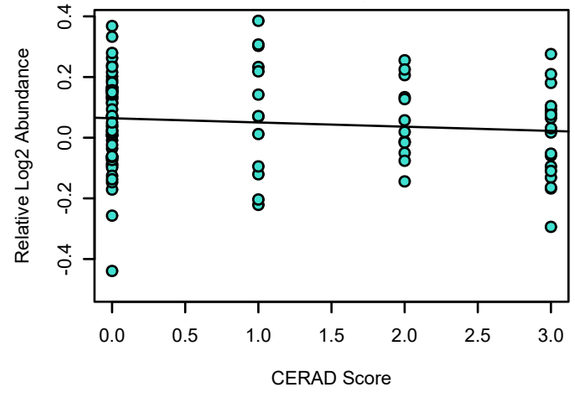

bicor=0.052, p=0.64
cor=0.0036, p=0.97
Relative Log2 Abundance
Braak Score

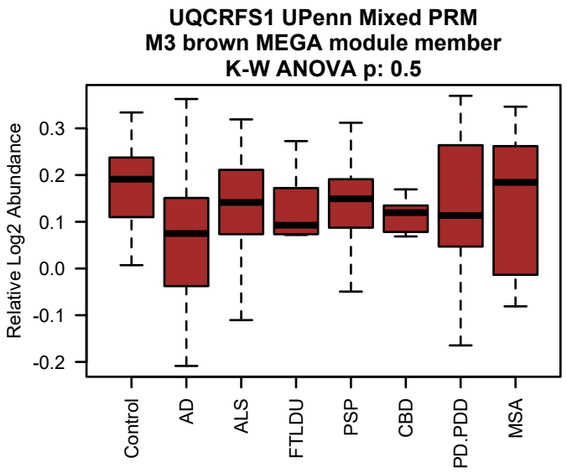

bicor=0.14, p=0.15
cor=0.097, p=0.34
Relative Log2 Abundance
CERAD Score

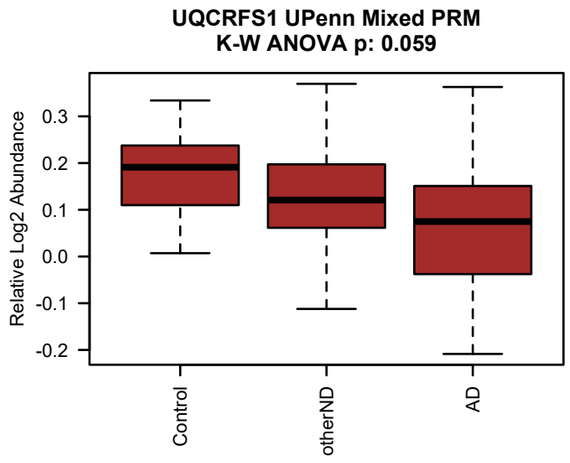

GRIA2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 7.7e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

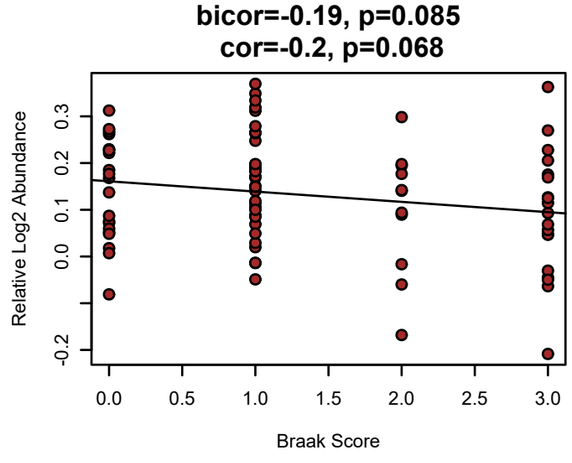

GRIA2 UPenn Mixed PRM
K-W ANOVA p: 3.4e-05
Relative Log2 Abundance
Control
otherND
AD

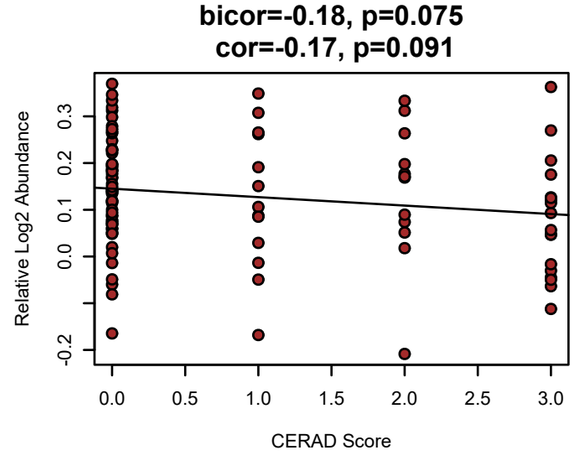

bicor=-0.3, p=0.005
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

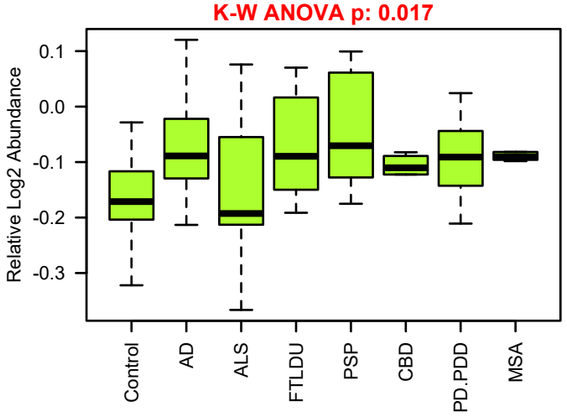

bicor=-0.12, p=0.25
cor=-0.11, p=0.28
Relative Log2 Abundance
CERAD Score

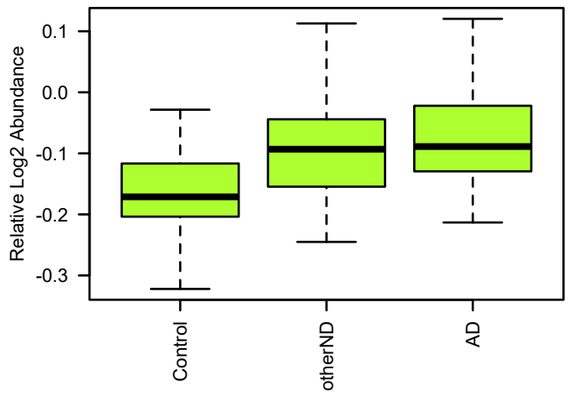

UQCRFS1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.5
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

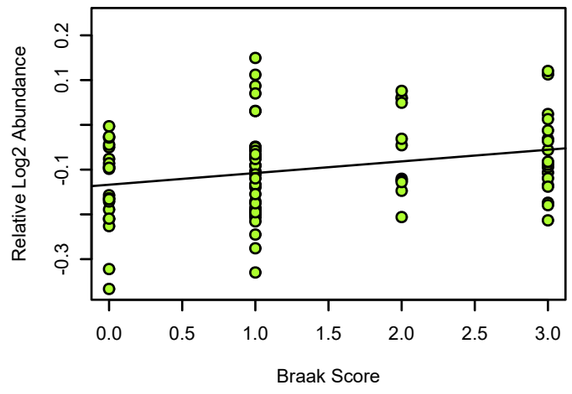

UQCRFS1 UPenn Mixed PRM
K-W ANOVA p: 0.059
Relative Log2 Abundance
Control
otherND
AD

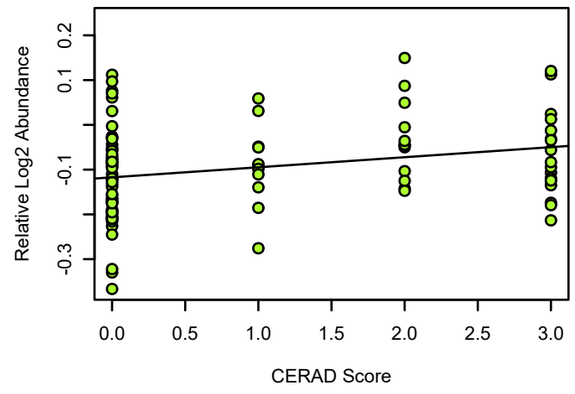

bicor=-0.19, p=0.085
cor=-0.2, p=0.068
Relative Log2 Abundance
Braak Score

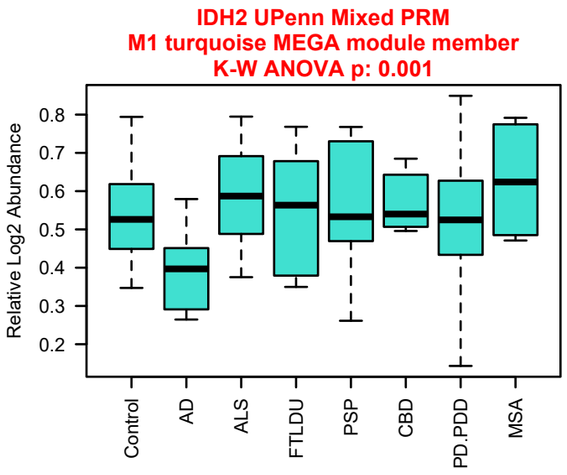

bicor=-0.18, p=0.075
cor=-0.17, p=0.091
Relative Log2 Abundance
CERAD Score

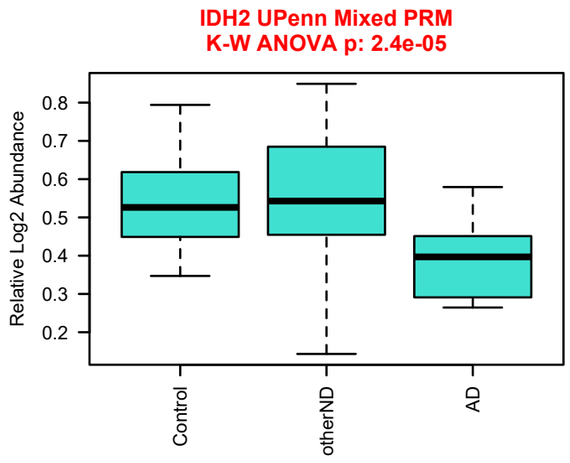

CCT5 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 0.017
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

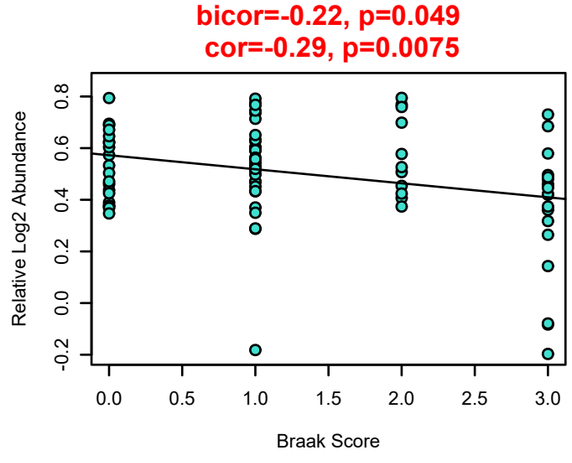

CCT5 UPenn Mixed PRM
K-W ANOVA p: 0.042
Relative Log2 Abundance
Control
otherND
AD

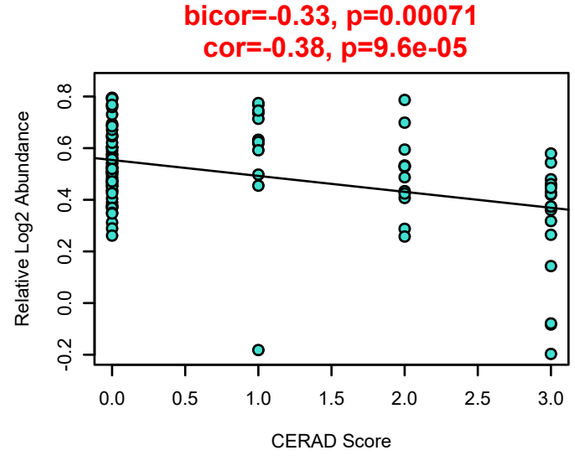

bicor=0.24, p=0.025
cor=0.27, p=0.013
Relative Log2 Abundance
Braak Score

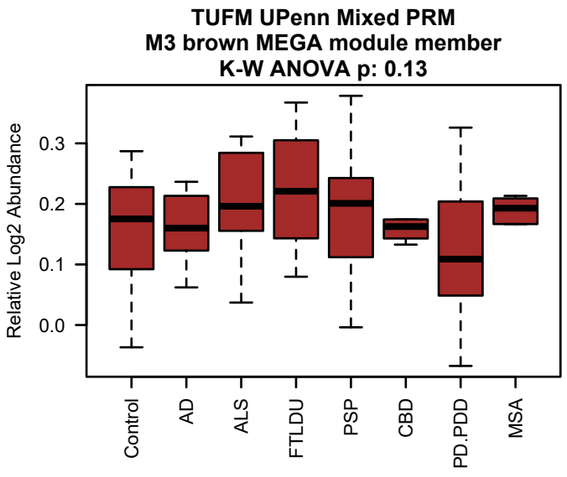

bicor=0.26, p=0.0084
cor=0.27, p=0.0066
Relative Log2 Abundance
CERAD Score

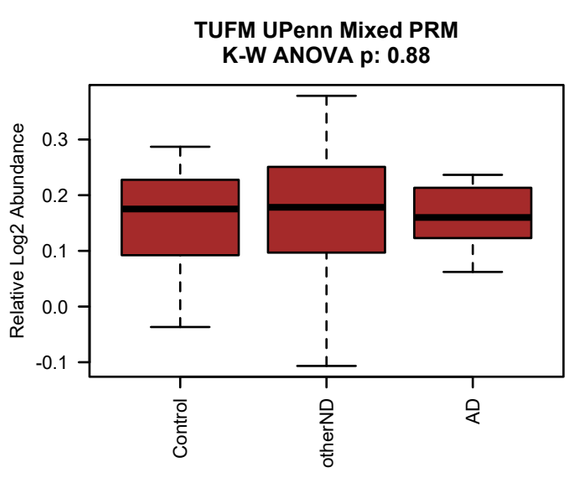

IDH2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.001
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

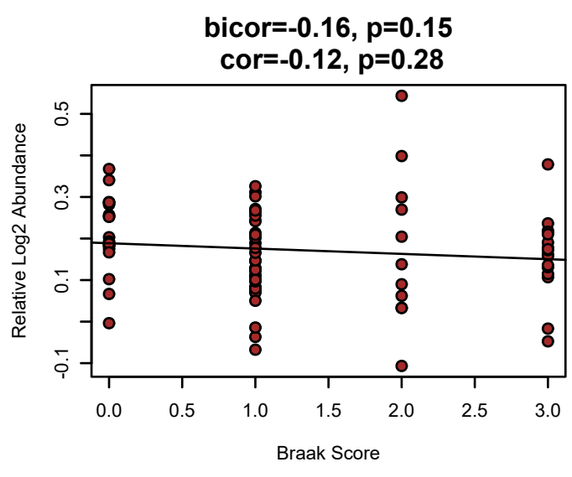

IDH2 UPenn Mixed PRM
K-W ANOVA p: 2.4e-05
Relative Log2 Abundance
Control
otherND
AD

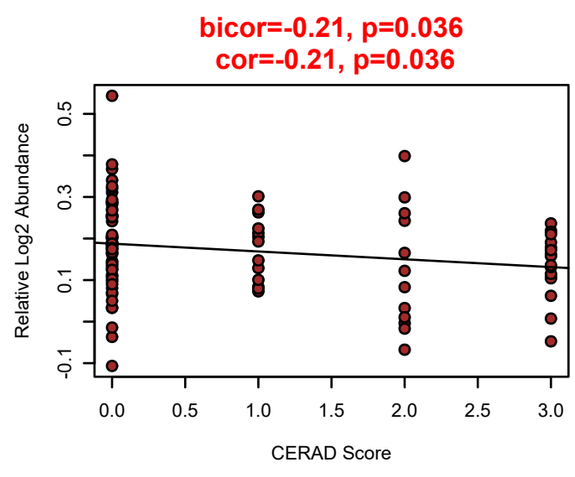

bicor=-0.22, p=0.049
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

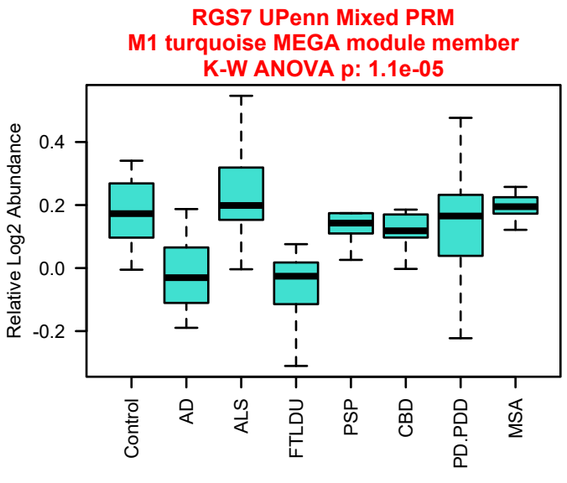

bicor=-0.33, p=0.00071
cor=-0.38, p=9.6e-05
Relative Log2 Abundance
CERAD Score

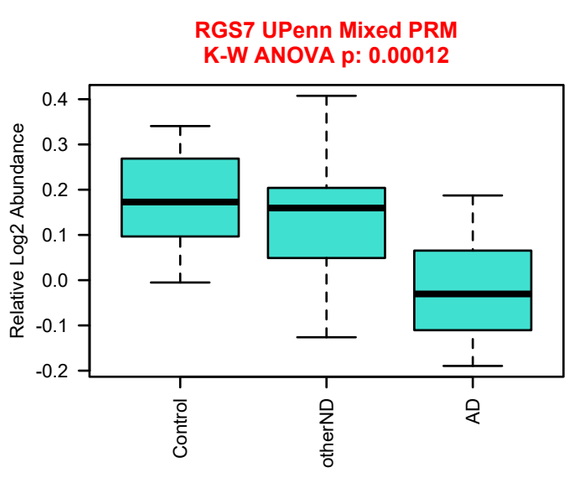

TUFM UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.13
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

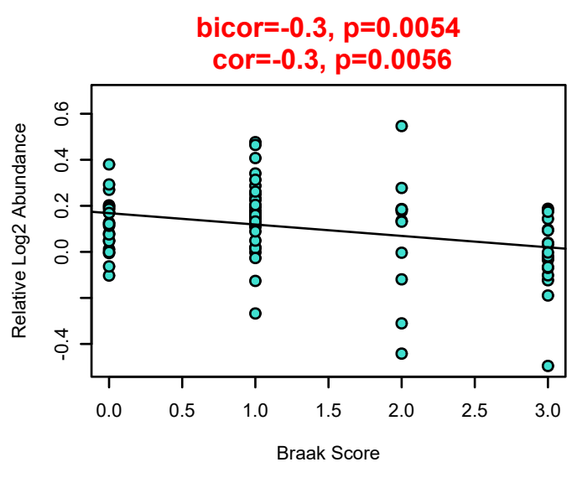

TUFM UPenn Mixed PRM
K-W ANOVA p: 0.88
Relative Log2 Abundance
Control
otherND
AD

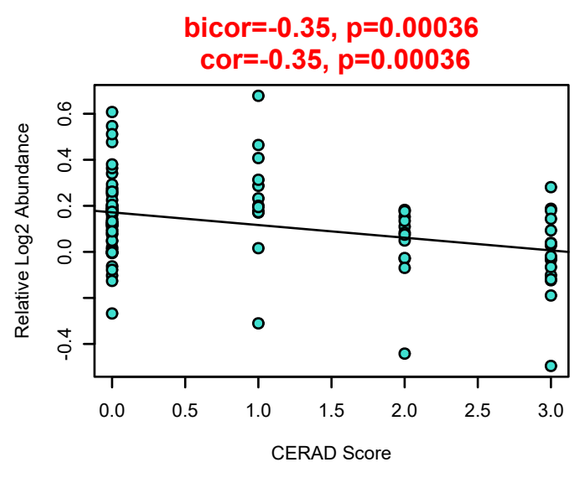

bicor=-0.16, p=0.15
cor=-0.12, p=0.28
Relative Log2 Abundance
Braak Score

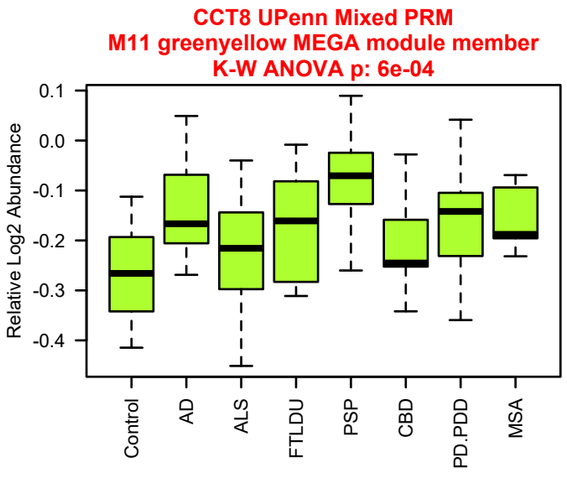

bicor=-0.21, p=0.036
cor=-0.21, p=0.036
Relative Log2 Abundance
CERAD Score

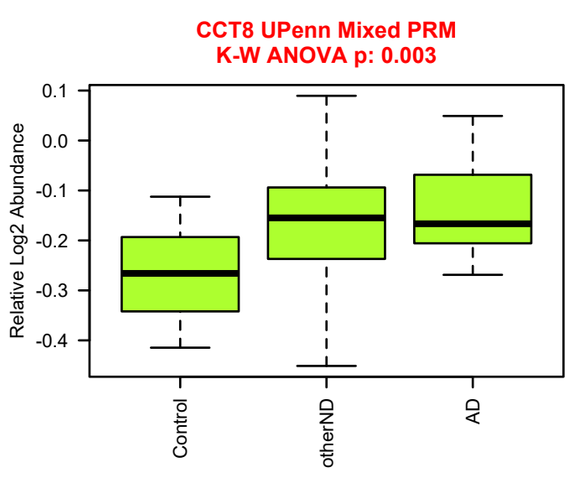

RGS7 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 1.1e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

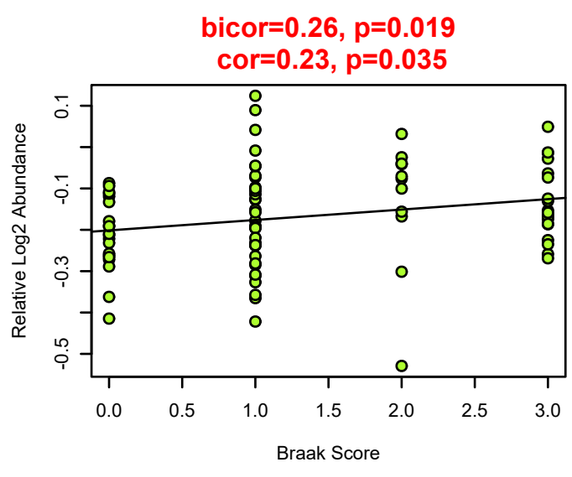

RGS7 UPenn Mixed PRM
K-W ANOVA p: 0.00012
Relative Log2 Abundance
Control
otherND
AD

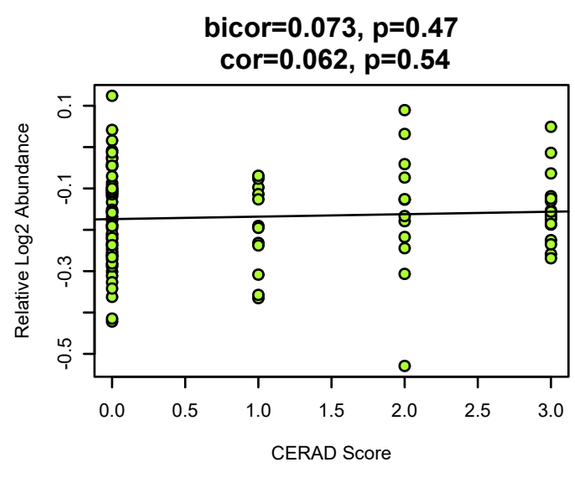

bicor=-0.3, p=0.0054
cor=-0.3, p=0.0056
Relative Log2 Abundance
Braak Score

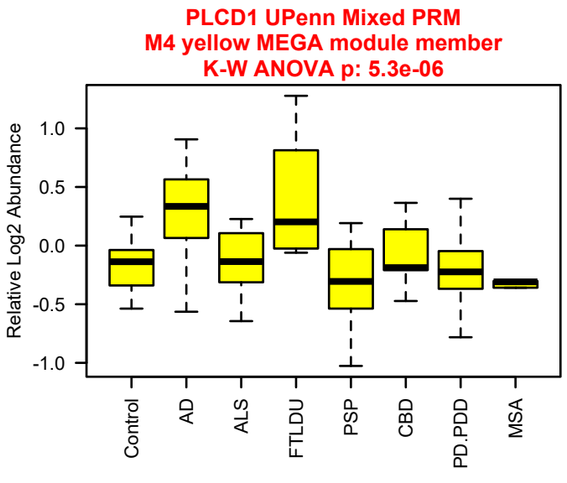

bicor=-0.35, p=0.00036
cor=-0.35, p=0.00036
Relative Log2 Abundance
CERAD Score

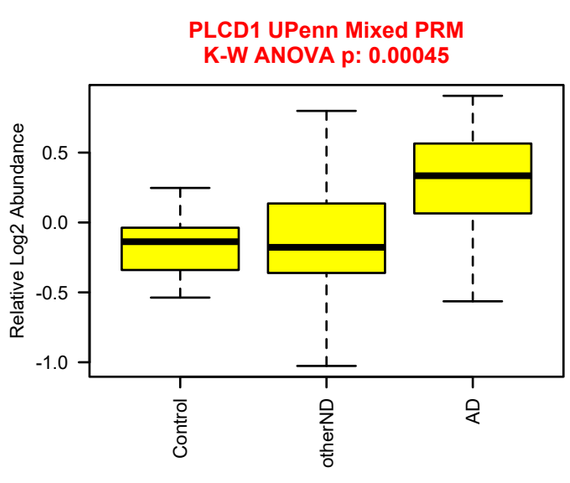

CCT8 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 6e-04
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

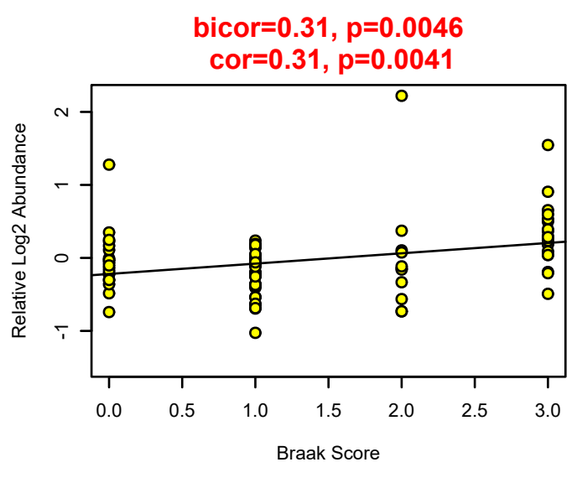

CCT8 UPenn Mixed PRM
K-W ANOVA p: 0.003
Relative Log2 Abundance
Control
otherND
AD

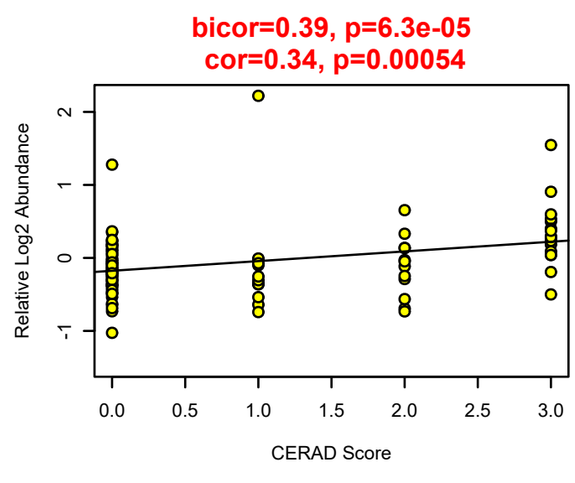

bicor=0.26, p=0.019
cor=0.23, p=0.035
Relative Log2 Abundance
Braak Score

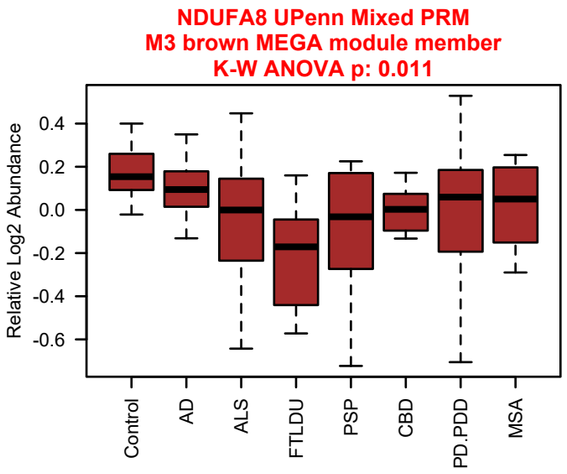

bicor=0.073, p=0.47
cor=0.062, p=0.54
Relative Log2 Abundance
CERAD Score

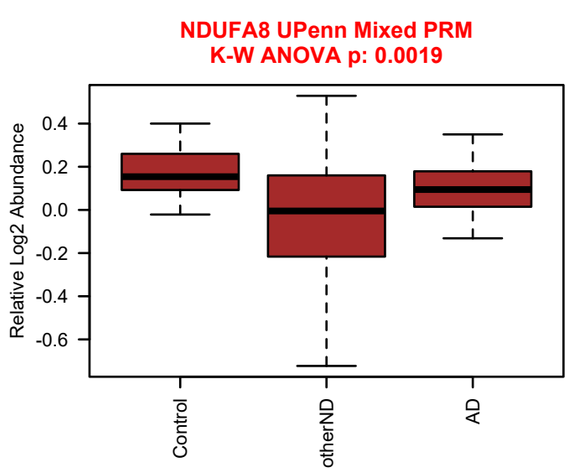

PLCD1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 5.3e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

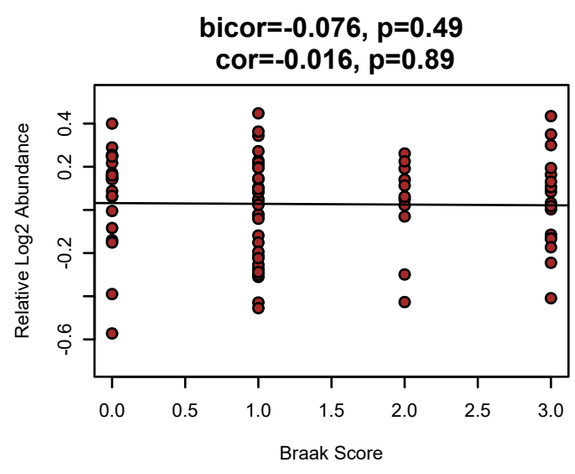

PLCD1 UPenn Mixed PRM
K-W ANOVA p: 0.00045
Relative Log2 Abundance
Control
otherND
AD

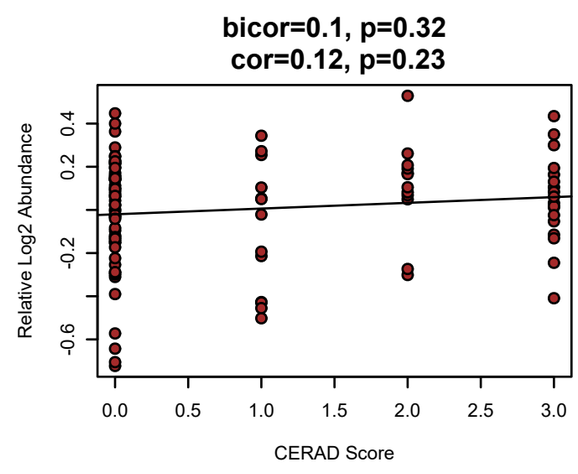

bicor=0.31, p=0.0046
cor=0.31, p=0.0041
Relative Log2 Abundance
Braak Score

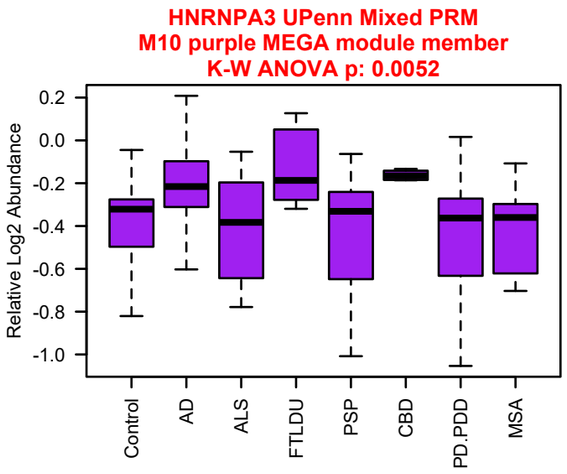

bicor=0.39, p=6.3e-05
cor=0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

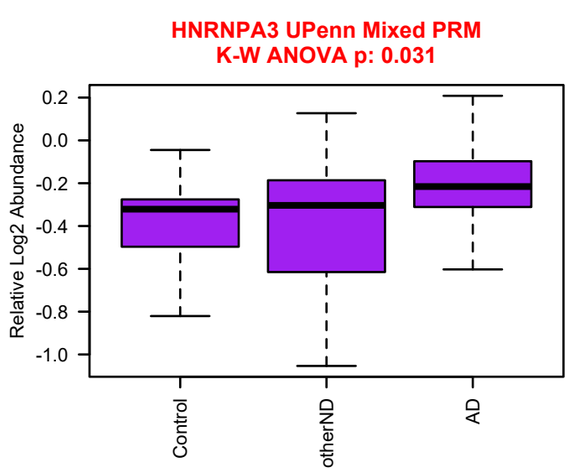

NDUFA8 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.011
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

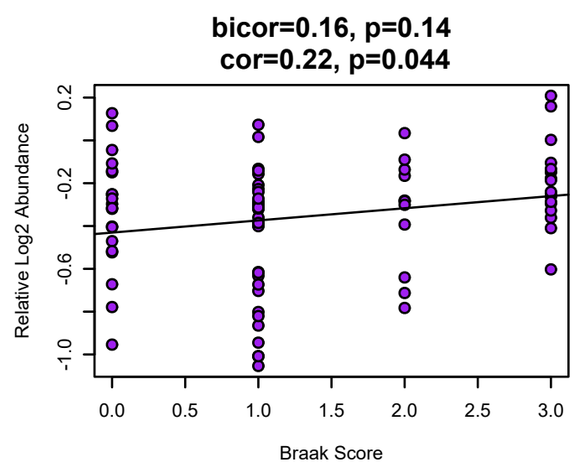

NDUFA8 UPenn Mixed PRM
K-W ANOVA p: 0.0019
Relative Log2 Abundance
Control
otherND
AD

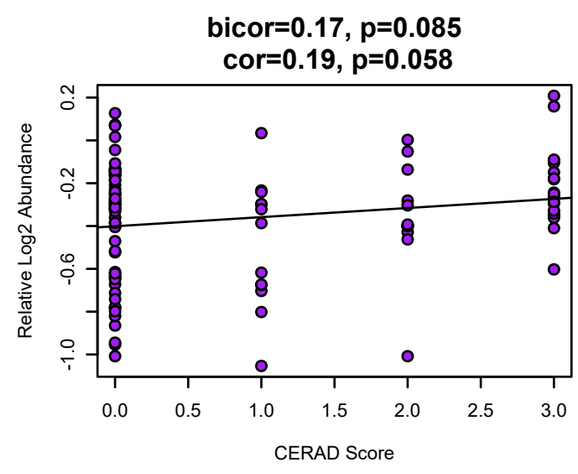

bicor=-0.076, p=0.49
cor=-0.016, p=0.89
Relative Log2 Abundance
Braak Score

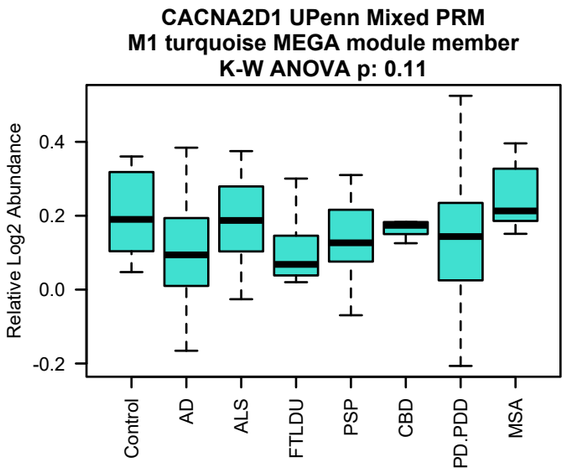

bicor=0.1, p=0.32
cor=0.12, p=0.23
Relative Log2 Abundance
CERAD Score

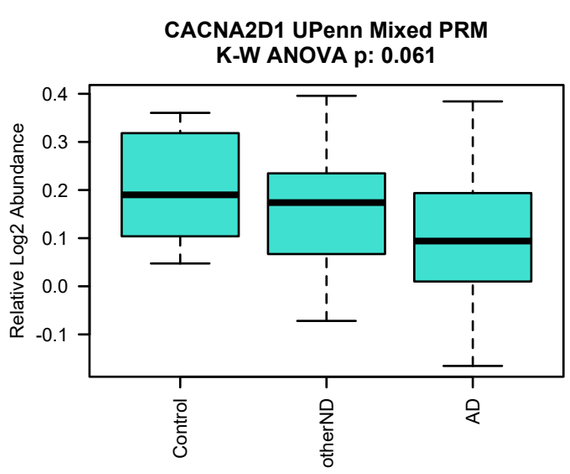

HNRNPA3 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.0052
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

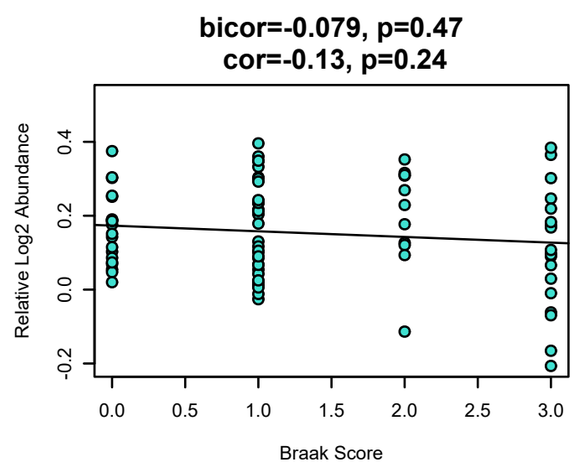

HNRNPA3 UPenn Mixed PRM
K-W ANOVA p: 0.031
Relative Log2 Abundance
Control
otherND
AD

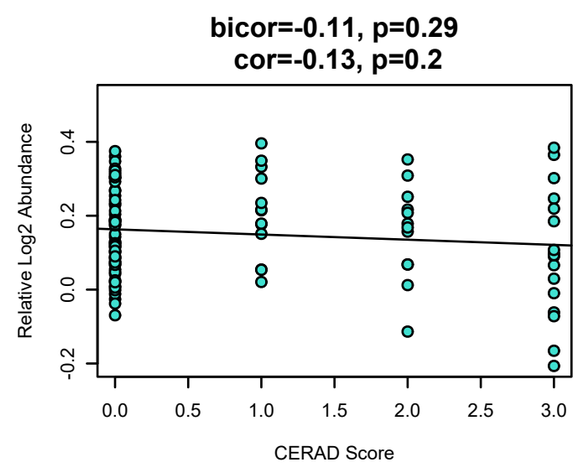

bicor=0.16, p=0.14
cor=0.22, p=0.044
Relative Log2 Abundance
Braak Score

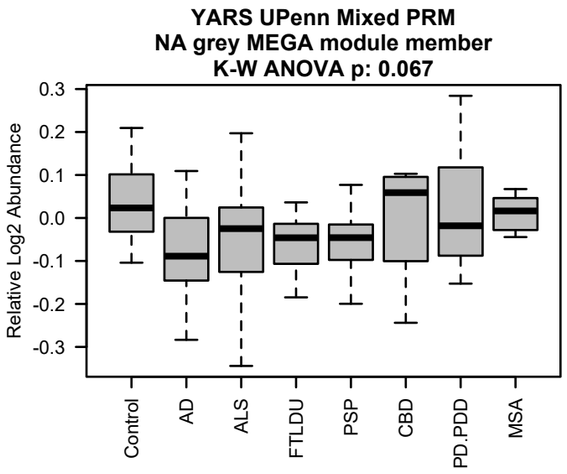

bicor=0.17, p=0.085
cor=0.19, p=0.058
Relative Log2 Abundance
CERAD Score

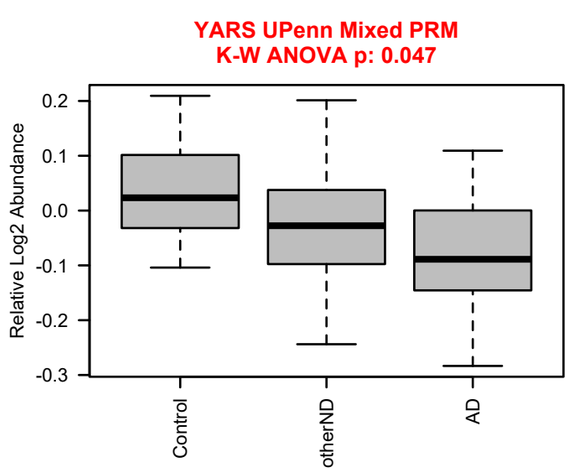

CACNA2D1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.11
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

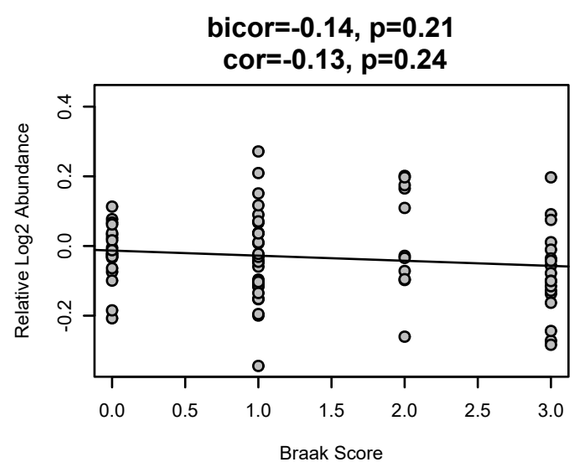

CACNA2D1 UPenn Mixed PRM
K-W ANOVA p: 0.061
Relative Log2 Abundance
Control
otherND
AD

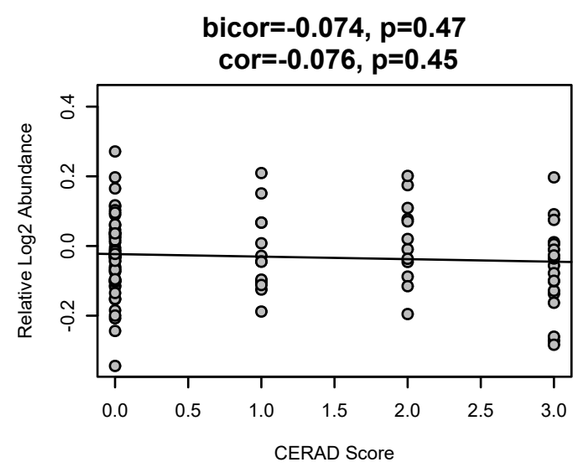

bicor=-0.079, p=0.47
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

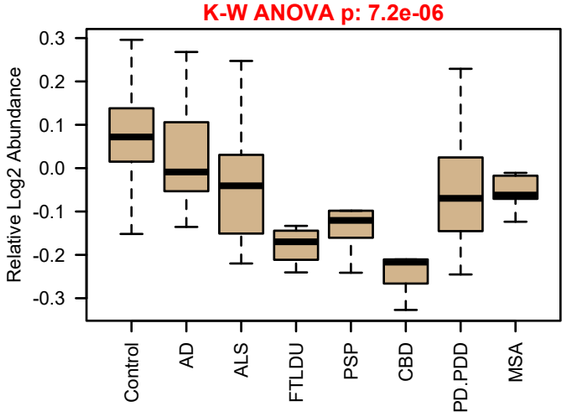

bicor=-0.11, p=0.29
cor=-0.13, p=0.2
Relative Log2 Abundance
CERAD Score

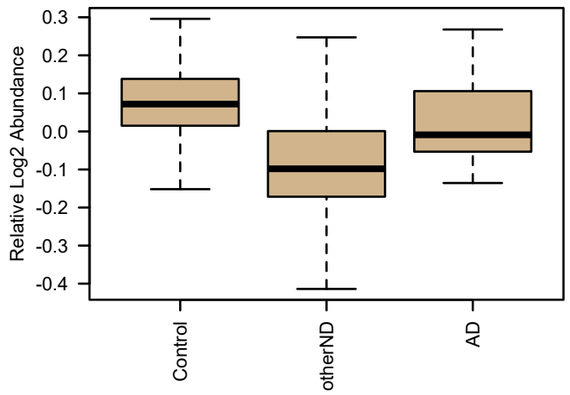

YARS UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.067
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

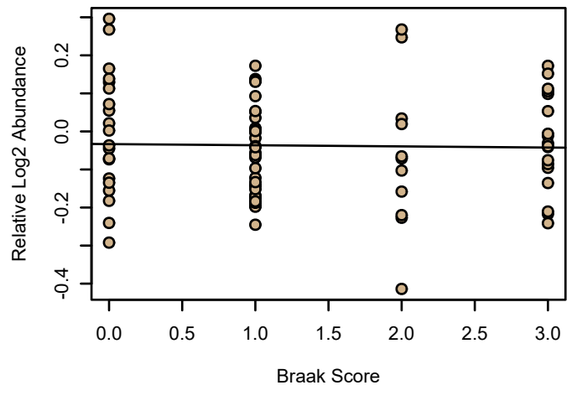

YARS UPenn Mixed PRM
K-W ANOVA p: 0.047
Relative Log2 Abundance
Control
otherND
AD

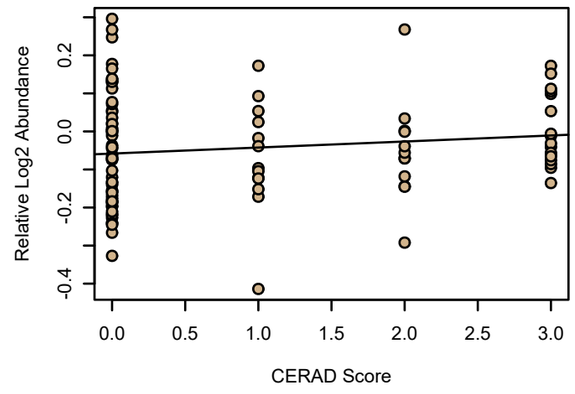

bicor=-0.14, p=0.21
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

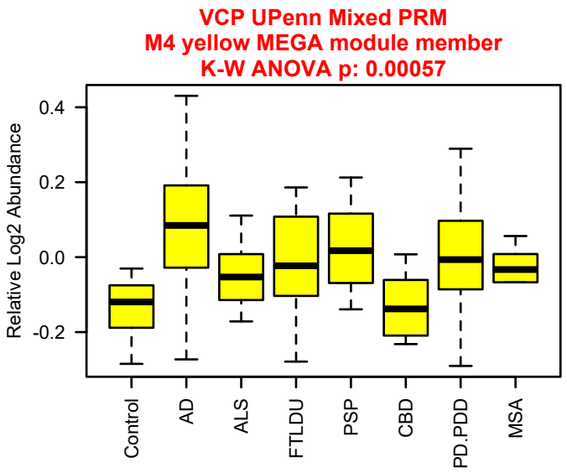

bicor=-0.074, p=0.47
cor=-0.076, p=0.45
Relative Log2 Abundance
CERAD Score

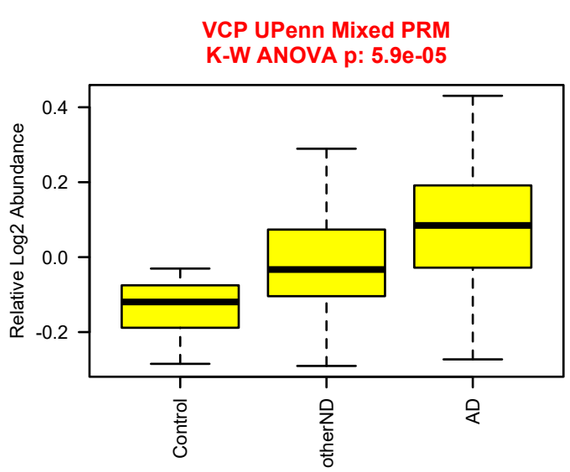

NAPA UPenn Mixed PRM
M12 tan MEGA module member
K-W ANOVA p: 7.2e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

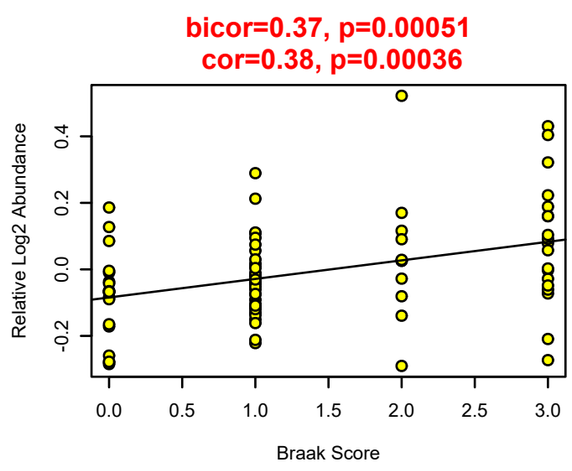

NAPA UPenn Mixed PRM
K-W ANOVA p: 7e-06
Relative Log2 Abundance
Control
otherND
AD

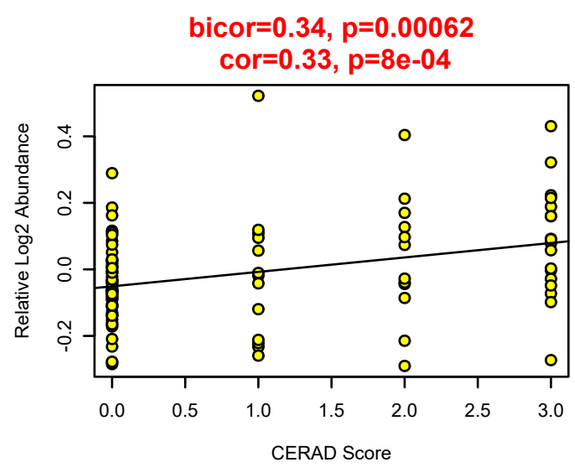

bicor=-0.01, p=0.93
cor=-0.023, p=0.84
Relative Log2 Abundance
Braak Score

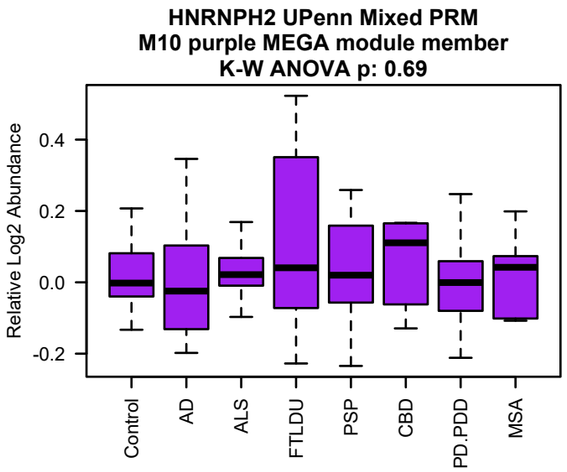

bicor=0.15, p=0.13
cor=0.14, p=0.16
Relative Log2 Abundance
CERAD Score

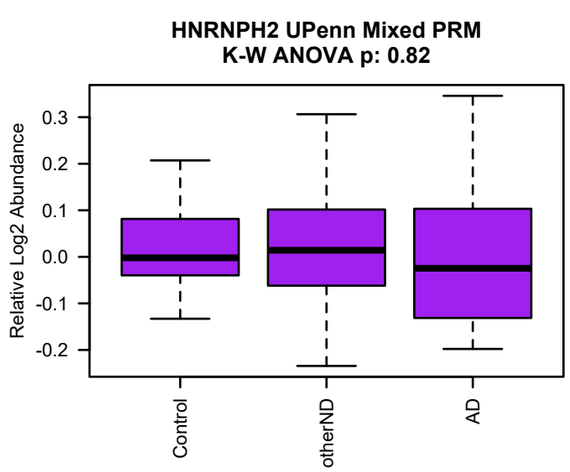

VCP UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.00057
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

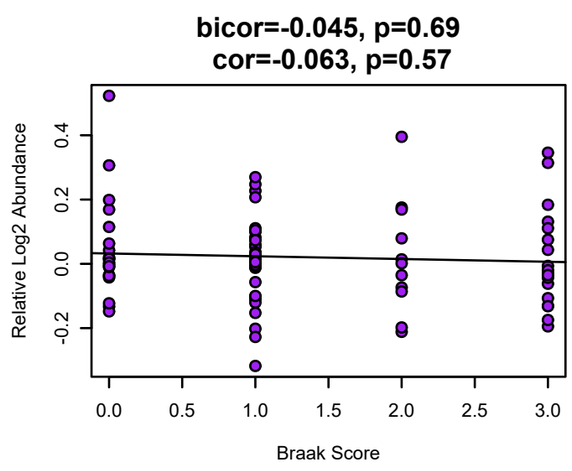

VCP UPenn Mixed PRM
K-W ANOVA p: 5.9e-05
Relative Log2 Abundance
Control
otherND
AD

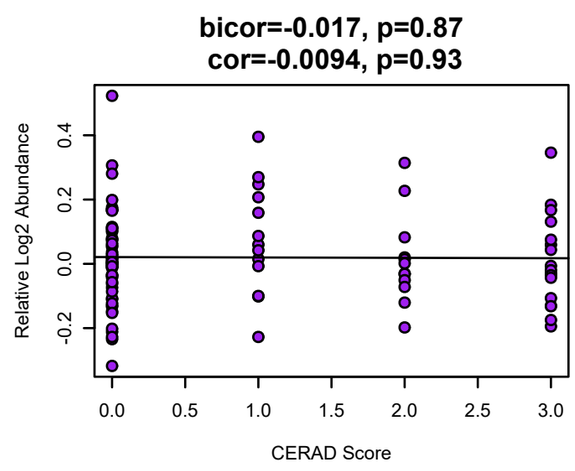

bicor=0.37, p=0.00051
cor=0.38, p=0.00036
Relative Log2 Abundance
Braak Score

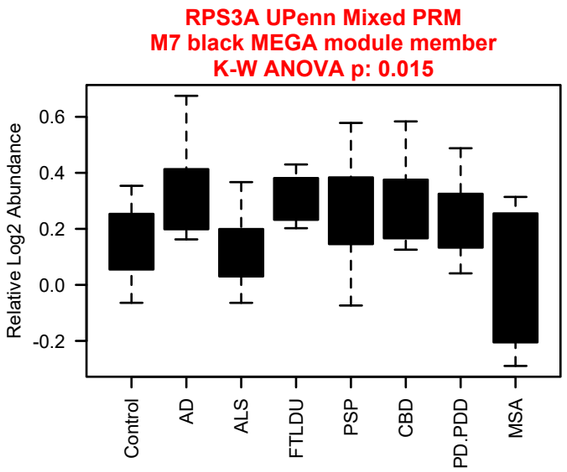

bicor=0.34, p=0.00062
cor=0.33, p=8e-04
Relative Log2 Abundance
CERAD Score

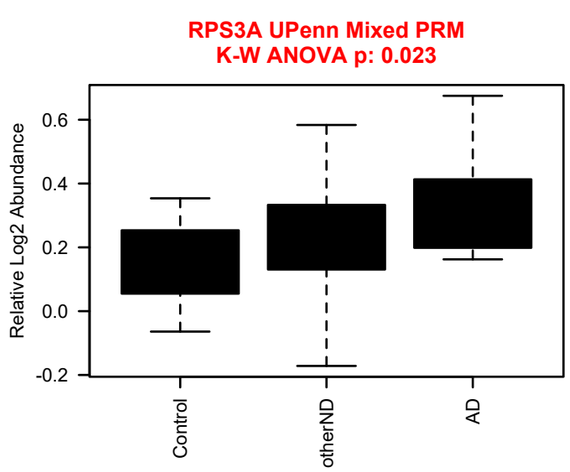

HNRNPH2 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.69
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

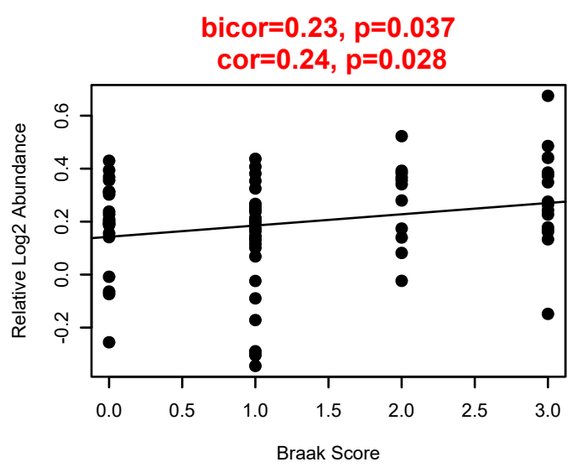

HNRNPH2 UPenn Mixed PRM
K-W ANOVA p: 0.82
Relative Log2 Abundance
Control
otherND
AD

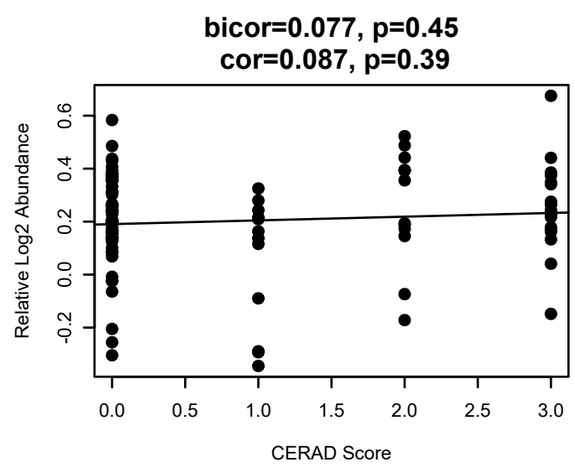

bicor=-0.045, p=0.69
cor=-0.063, p=0.57
Relative Log2 Abundance
Braak Score

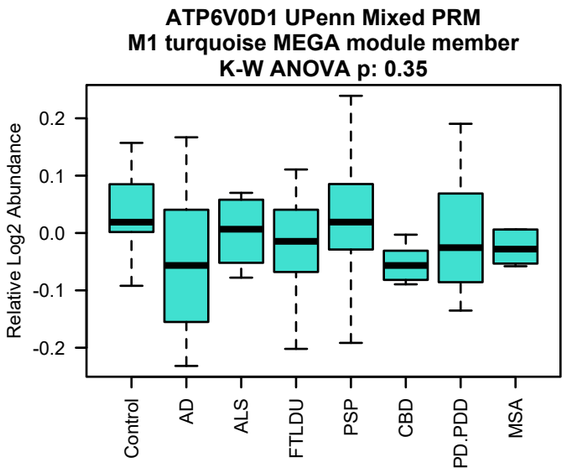

bicor=-0.017, p=0.87
cor=-0.0094, p=0.93
Relative Log2 Abundance
CERAD Score

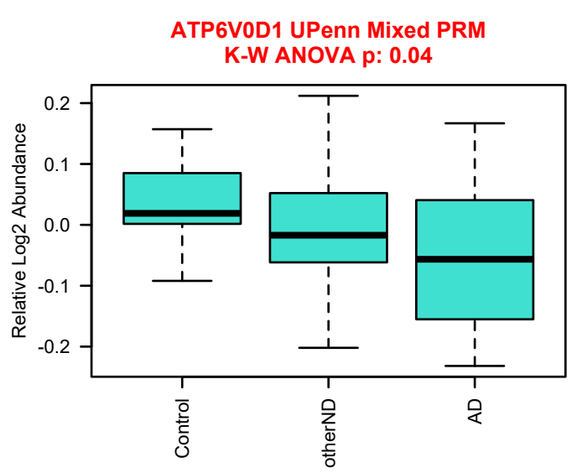

RPS3A UPenn Mixed PRM
M7 black MEGA module member
K-W ANOVA p: 0.015
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

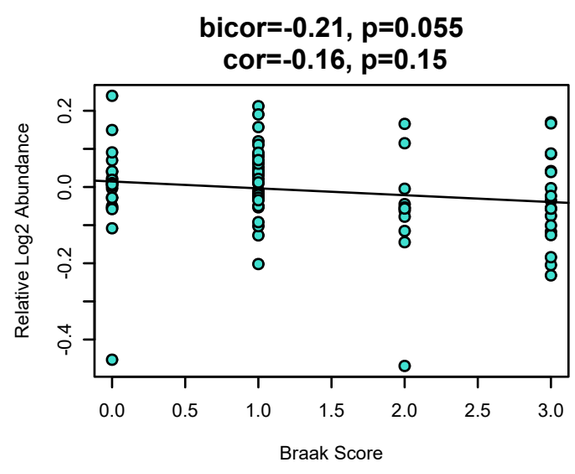

RPS3A UPenn Mixed PRM
K-W ANOVA p: 0.023
Relative Log2 Abundance
Control
otherND
AD

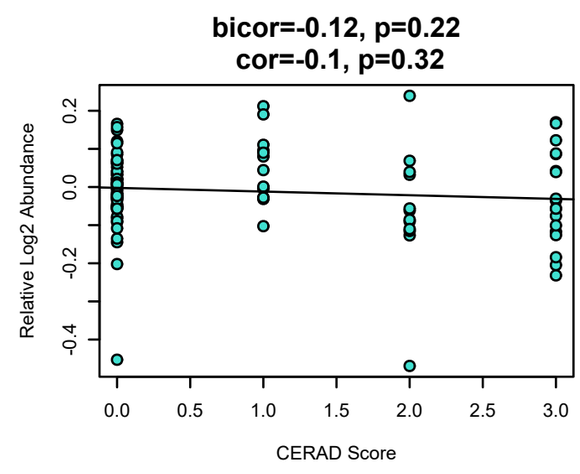

bicor=0.23, p=0.037
cor=0.24, p=0.028
Relative Log2 Abundance
Braak Score

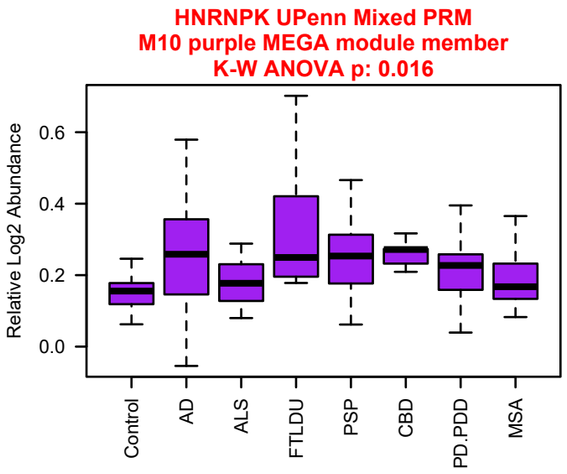

bicor=0.077, p=0.45
cor=0.087, p=0.39
Relative Log2 Abundance
CERAD Score

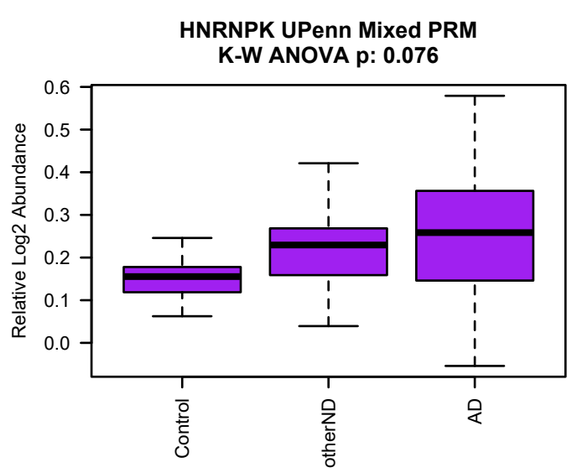

ATP6V0D1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.35
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

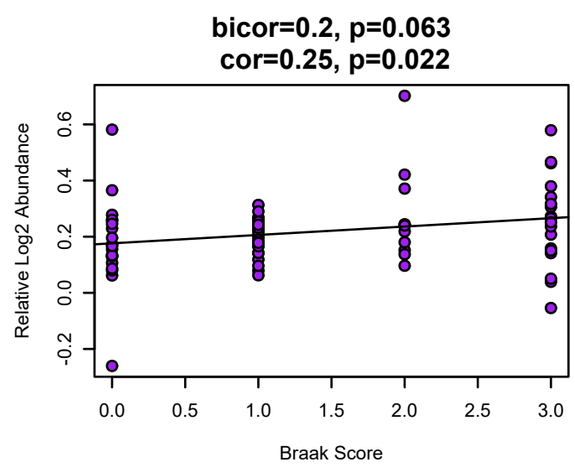

ATP6V0D1 UPenn Mixed PRM
K-W ANOVA p: 0.04
Relative Log2 Abundance
Control
otherND
AD

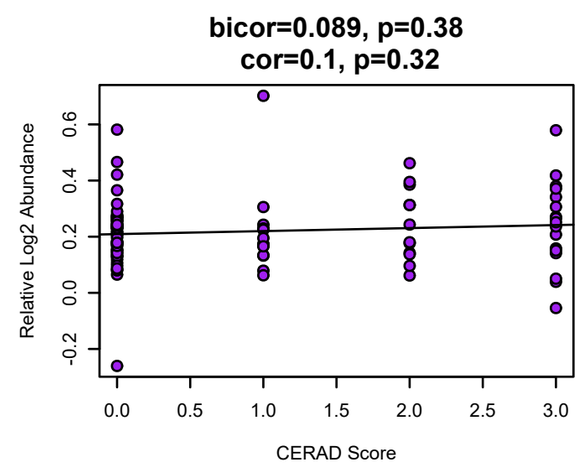

bicor=-0.21, p=0.055
cor=-0.16, p=0.15
Relative Log2 Abundance
Braak Score

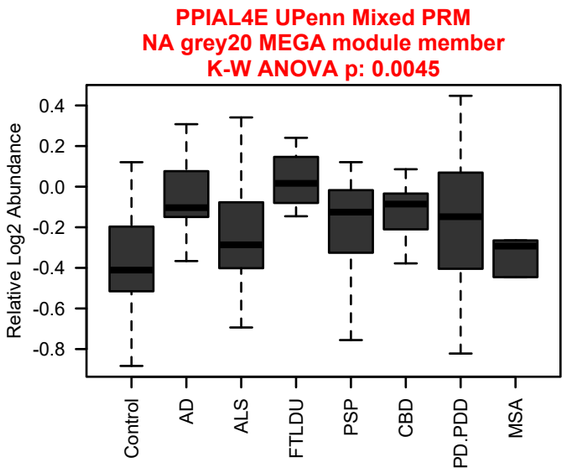

bicor=-0.12, p=0.22
cor=-0.1, p=0.32
Relative Log2 Abundance
CERAD Score

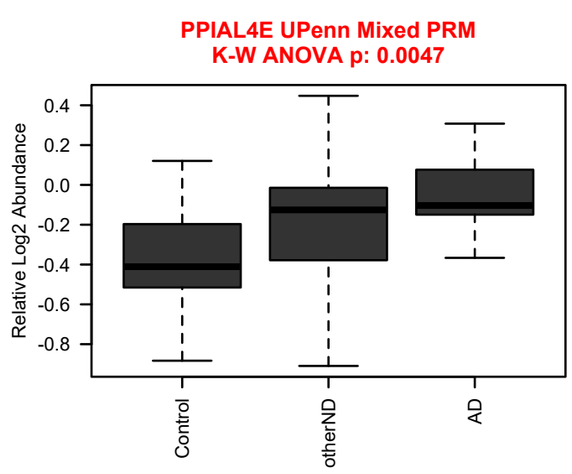

HNRNPK UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.016
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

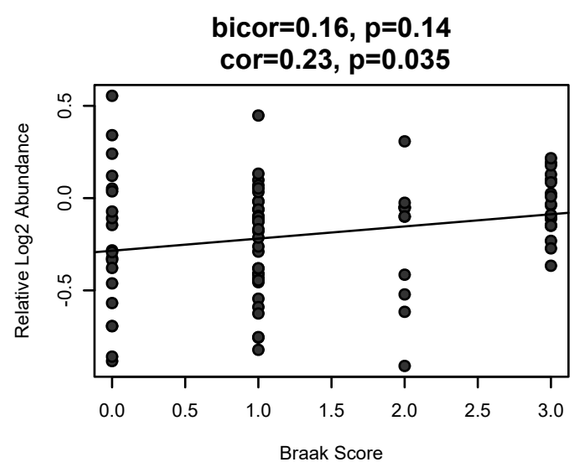

HNRNPK UPenn Mixed PRM
K-W ANOVA p: 0.076
Relative Log2 Abundance
Control
otherND
AD

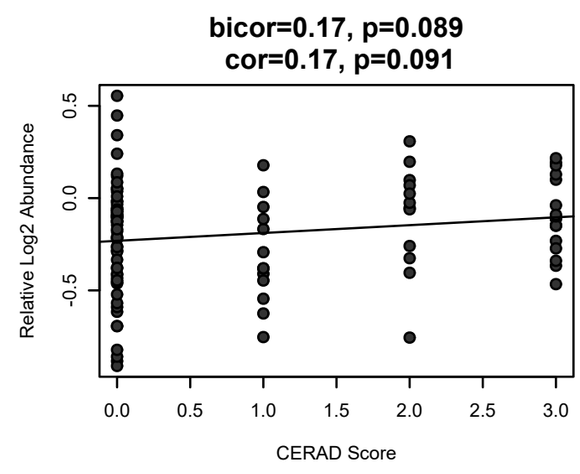

bicor=0.2, p=0.063
cor=0.25, p=0.022
Relative Log2 Abundance
Braak Score

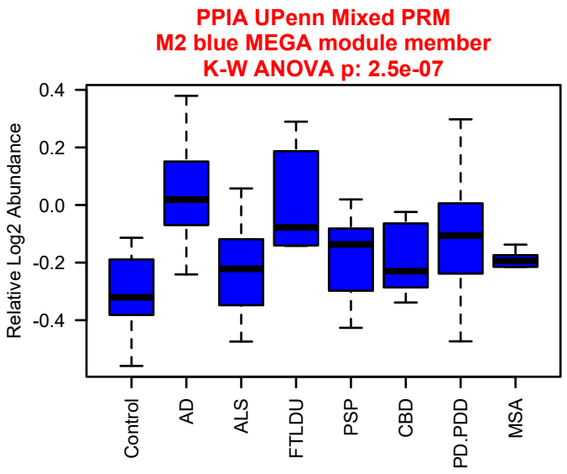

bicor=0.089, p=0.38
cor=0.1, p=0.32
Relative Log2 Abundance
CERAD Score

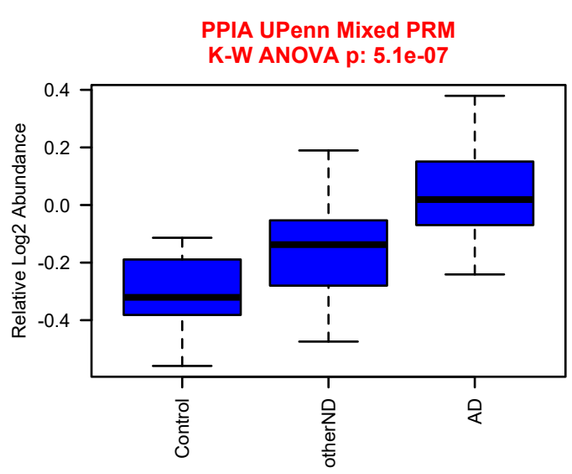

PPIAL4E UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.0045
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

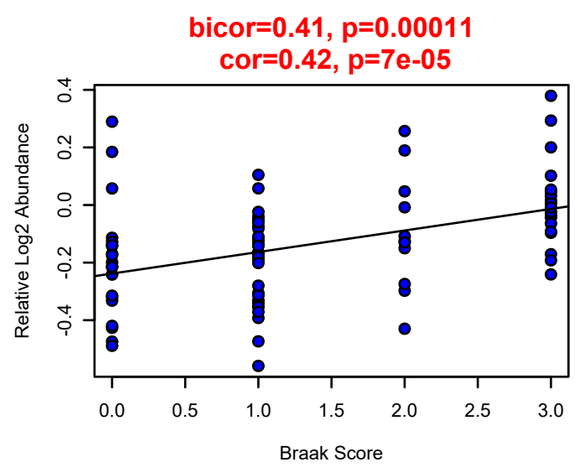

PPIAL4E UPenn Mixed PRM
K-W ANOVA p: 0.0047
Relative Log2 Abundance
Control
otherND
AD

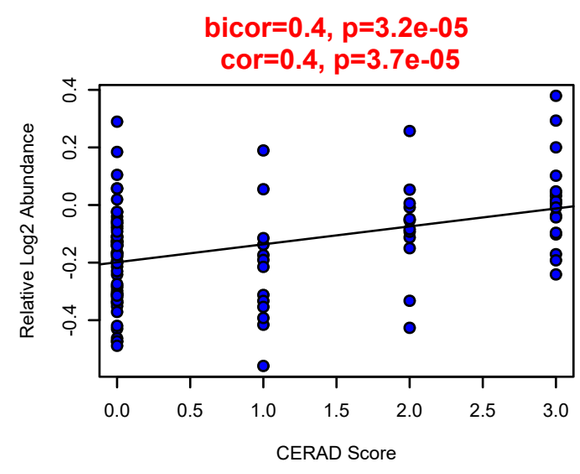

bicor=0.16, p=0.14
cor=0.23, p=0.035
Relative Log2 Abundance
Braak Score

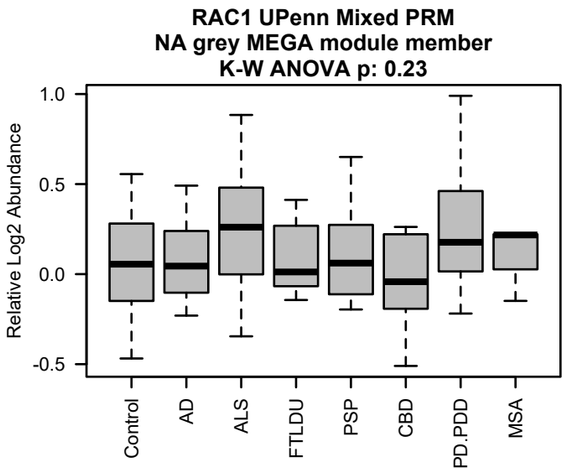

bicor=0.17, p=0.089
cor=0.17, p=0.091
Relative Log2 Abundance
CERAD Score

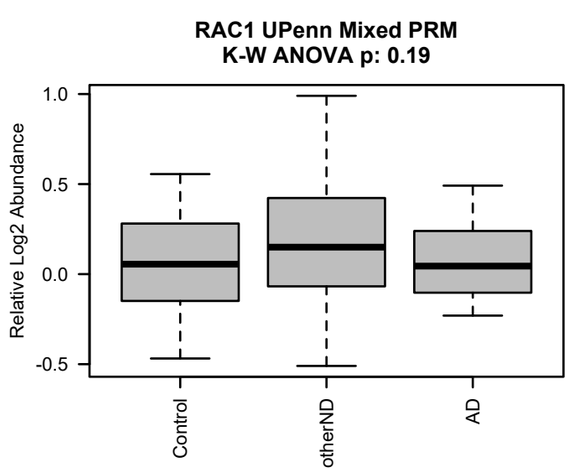

PPIA UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 2.5e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

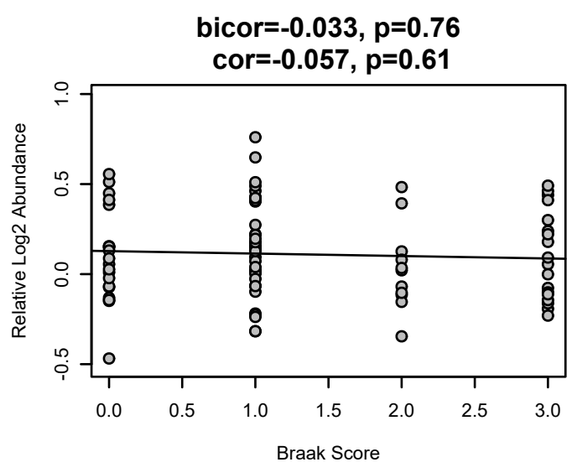

PPIA UPenn Mixed PRM
K-W ANOVA p: 5.1e-07
Relative Log2 Abundance
Control
otherND
AD

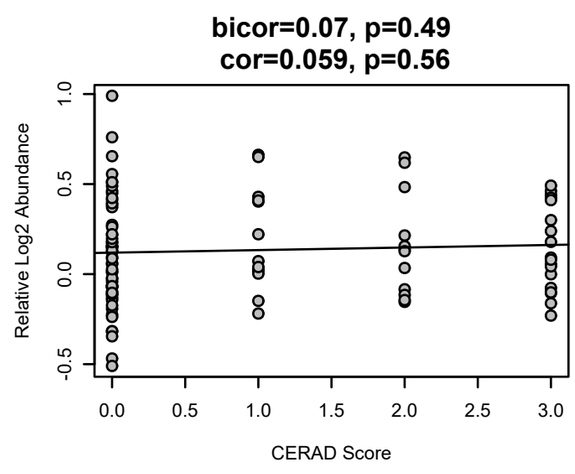

bicor=0.41, p=0.00011
cor=0.42, p=7e-05
Relative Log2 Abundance
Braak Score

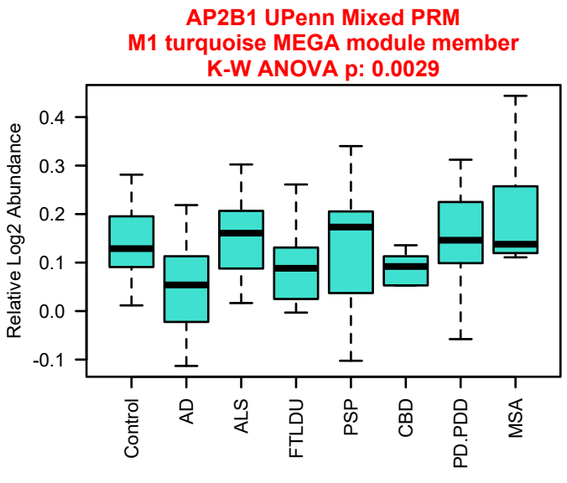

bicor=0.4, p=3.2e-05
cor=0.4, p=3.7e-05
Relative Log2 Abundance
CERAD Score

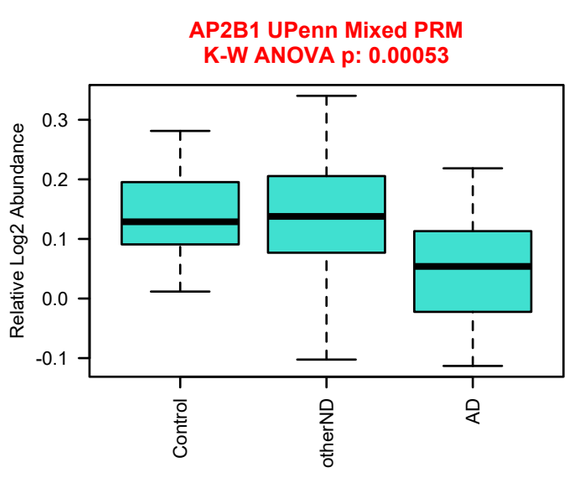

RAC1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.23
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

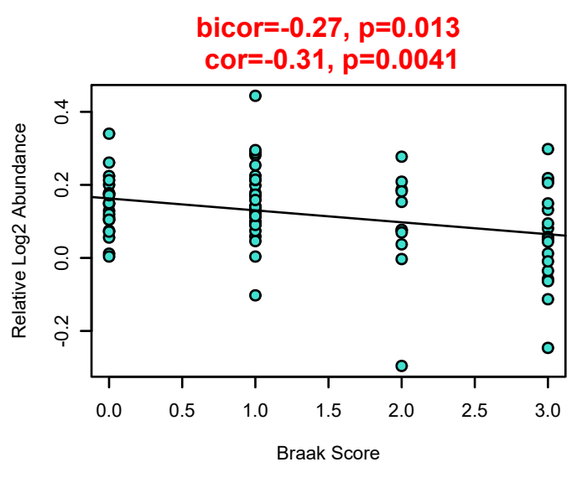

RAC1 UPenn Mixed PRM
K-W ANOVA p: 0.19
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
Control
otherND
AD

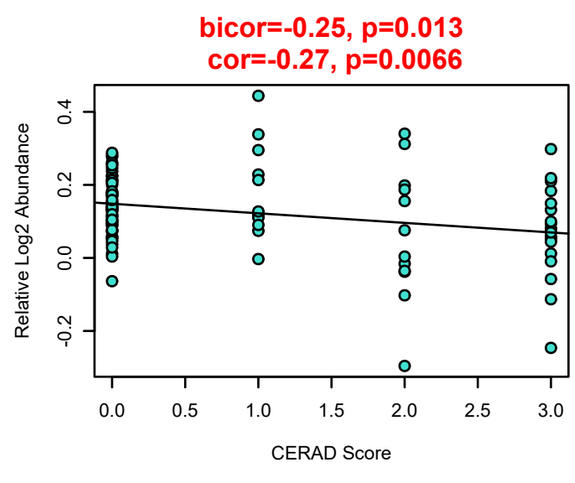

bicor=-0.033, p=0.76
cor=-0.057, p=0.61
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

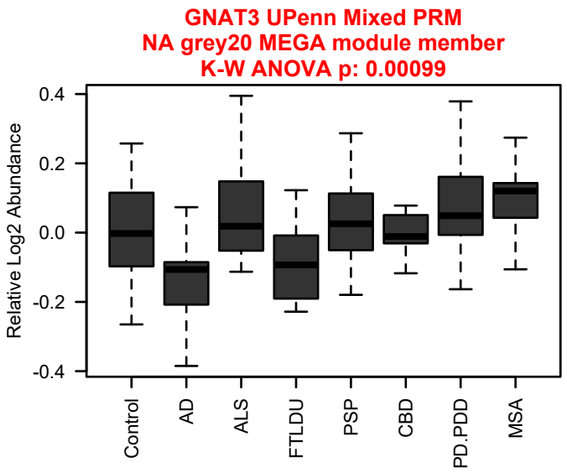

bicor=0.07, p=0.49
cor=0.059, p=0.56
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

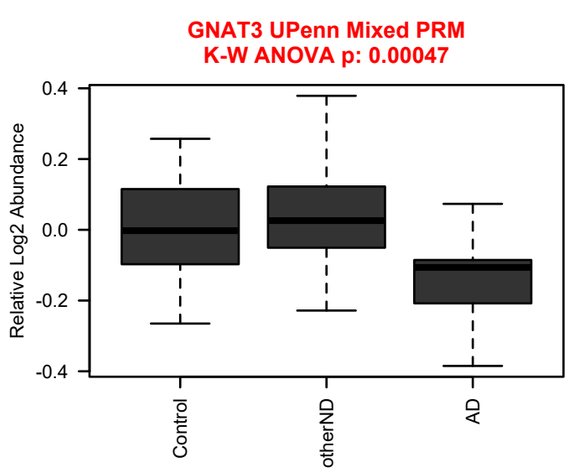

AP2B1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0029
Relative Log2 Abundance
0.4
0.3
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

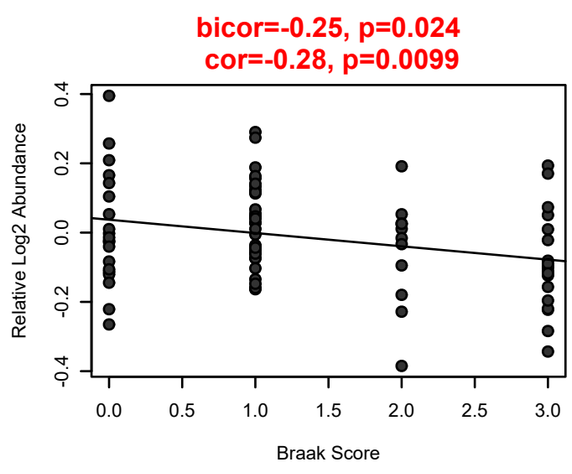

AP2B1 UPenn Mixed PRM
K-W ANOVA p: 0.00053
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
Control
otherND
AD

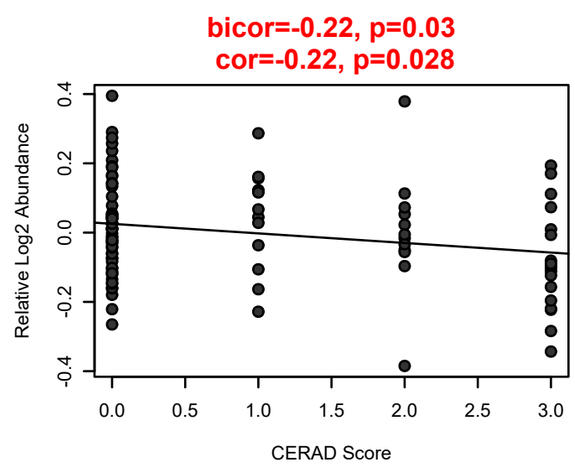

bicor=-0.27, p=0.013
cor=-0.31, p=0.0041
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

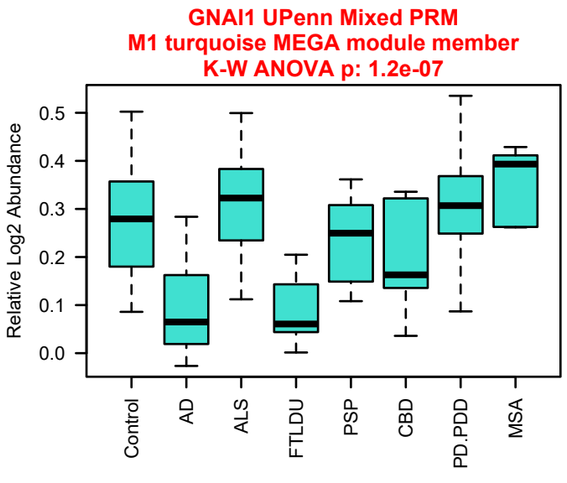

bicor=-0.25, p=0.013
cor=-0.27, p=0.0066
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

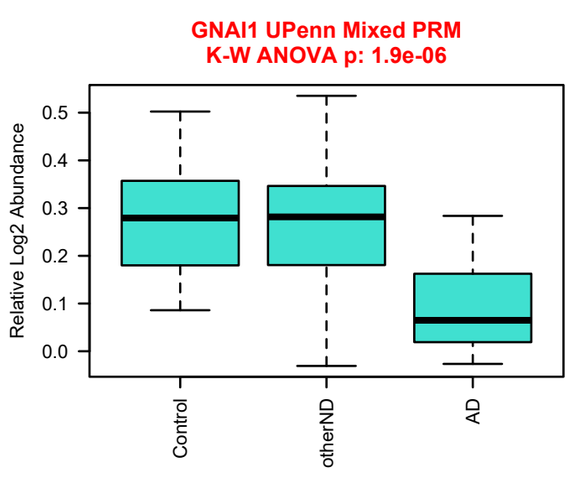

GNAT3 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.00099
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
-0.4
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

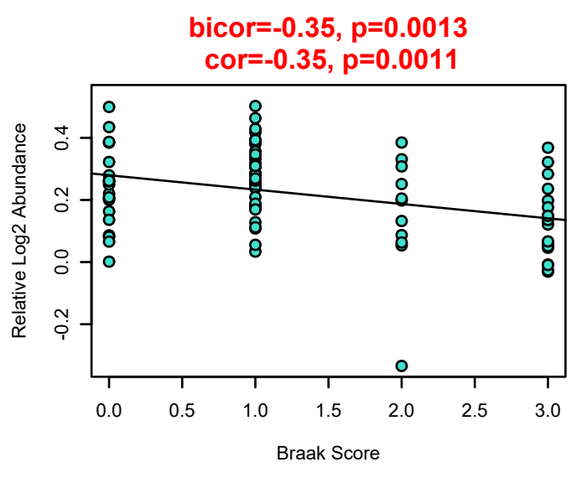

GNAT3 UPenn Mixed PRM
K-W ANOVA p: 0.00047
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
-0.4
Control
otherND
AD

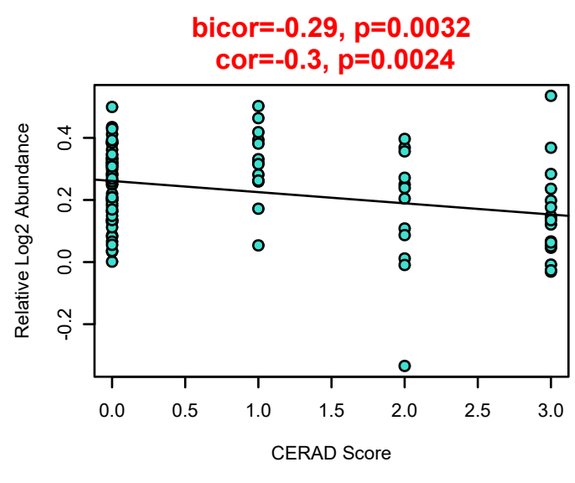

bicor=-0.25, p=0.024
cor=-0.28, p=0.0099
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

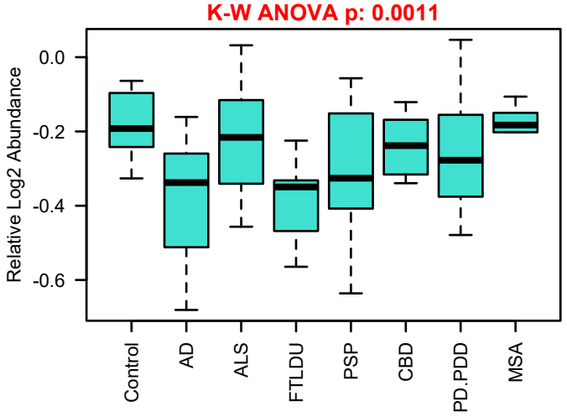

bicor=-0.22, p=0.03
cor=-0.22, p=0.028
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

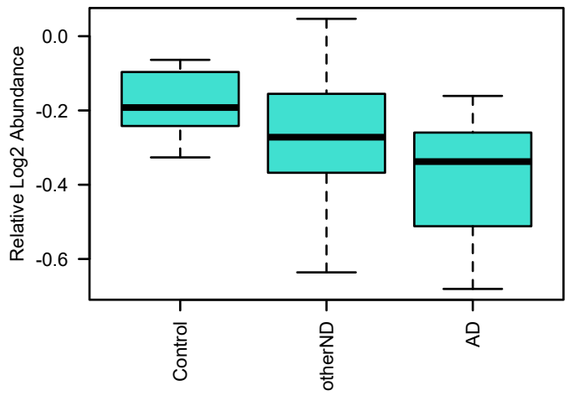

GNAI1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 1.2e-07
Relative Log2 Abundance
0.5
0.4
0.3
0.2
0.1
0.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

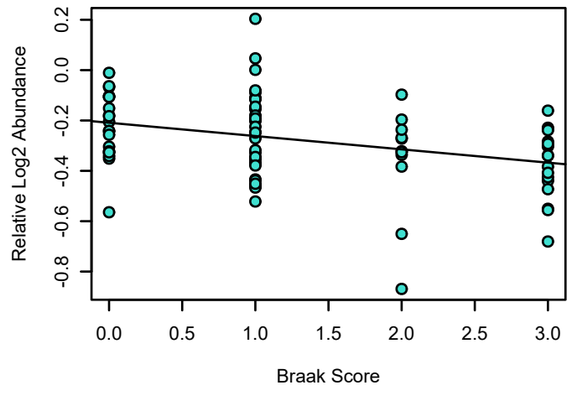

GNAI1 UPenn Mixed PRM
K-W ANOVA p: 1.9e-06
Relative Log2 Abundance
0.5
0.4
0.3
0.2
0.1
0.0
Control
otherND
AD

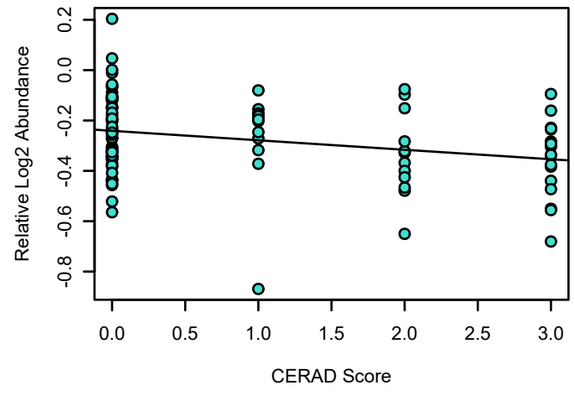

bicor=-0.35, p=0.0013
cor=-0.35, p=0.0011
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

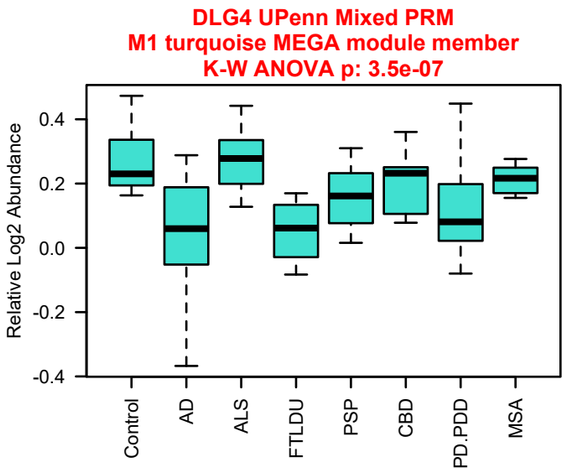

bicor=-0.29, p=0.0032
cor=-0.3, p=0.0024
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

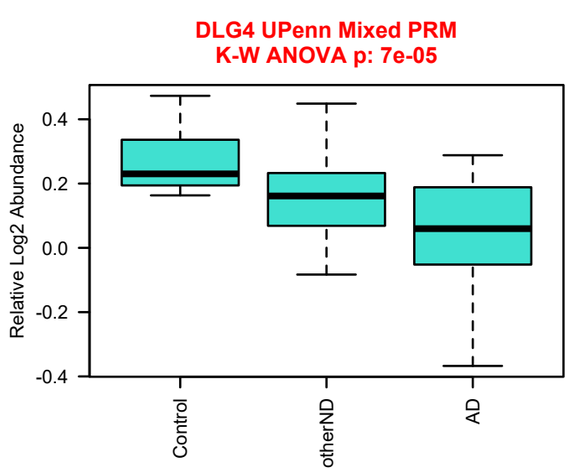

SIRPA UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0011
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

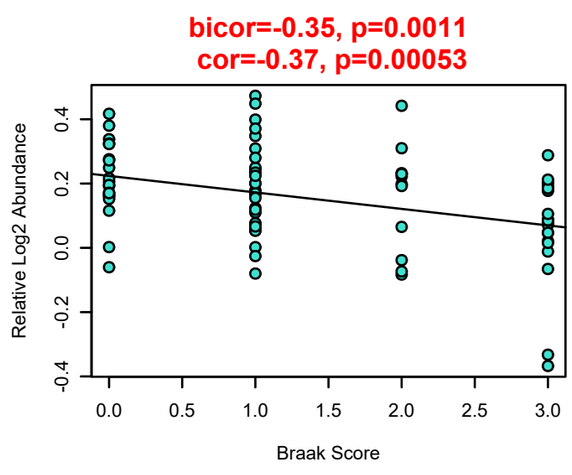

SIRPA UPenn Mixed PRM
K-W ANOVA p: 0.0013
Relative Log2 Abundance
Control
otherND
AD

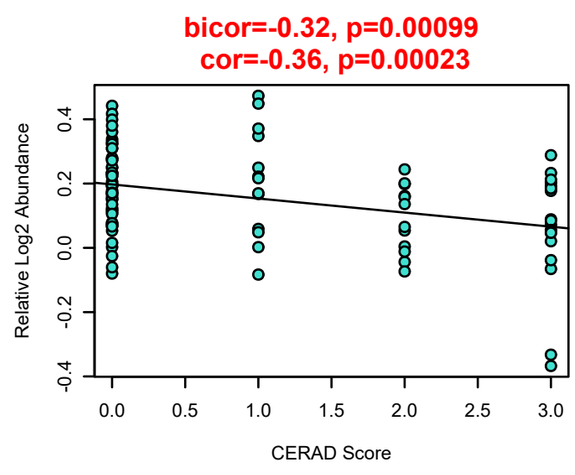

bicor=-0.34, p=0.0014
cor=-0.34, p=0.0016
Relative Log2 Abundance
Braak Score

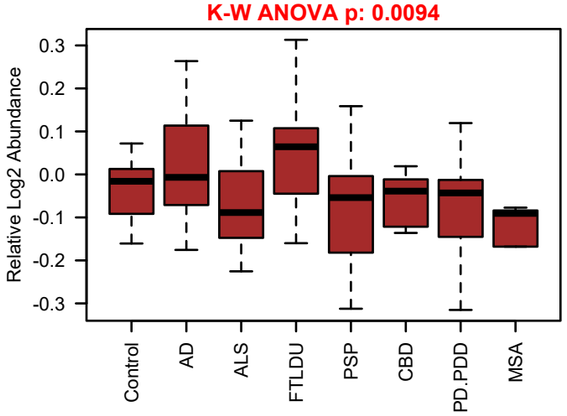

bicor=-0.28, p=0.0054
cor=-0.28, p=0.0048
Relative Log2 Abundance
CERAD Score

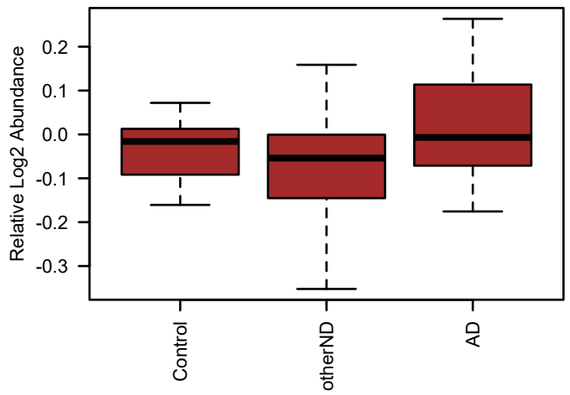

DLG4 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 3.5e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

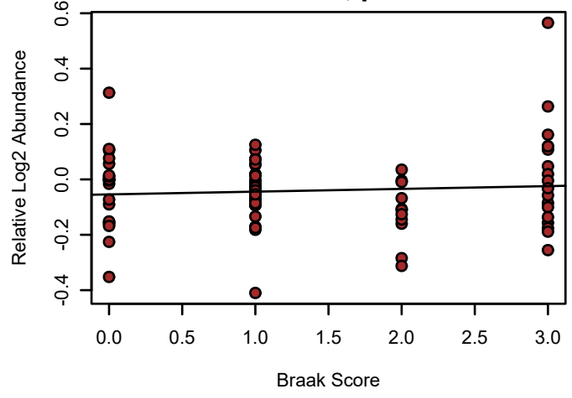

DLG4 UPenn Mixed PRM
K-W ANOVA p: 7e-05
Relative Log2 Abundance
Control
otherND
AD

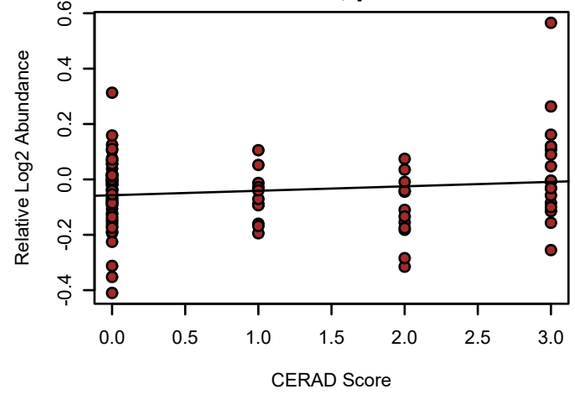

bicor=-0.35, p=0.0011
cor=-0.37, p=0.00053
Relative Log2 Abundance
Braak Score

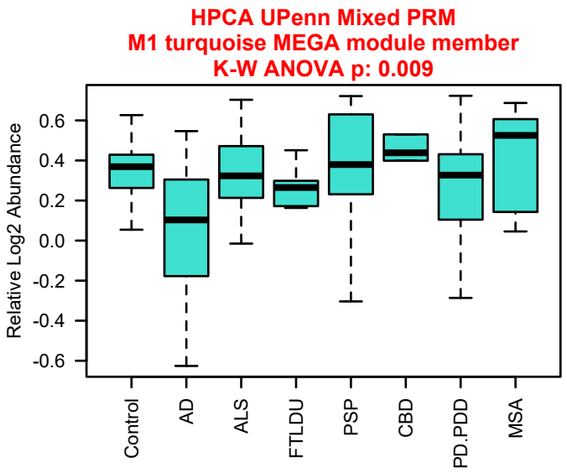

bicor=-0.32, p=0.00099
cor=-0.36, p=0.00023
Relative Log2 Abundance
CERAD Score

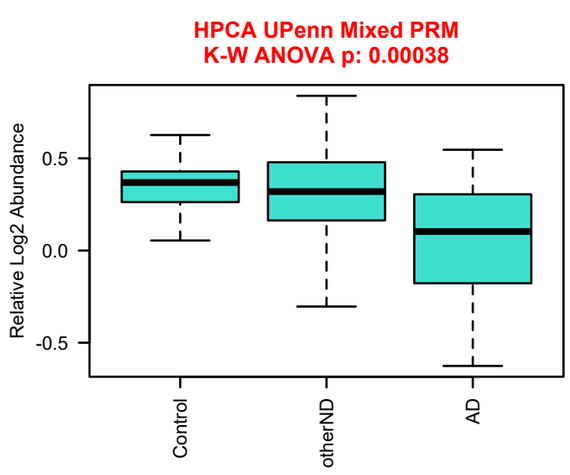

ABAT UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0094
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

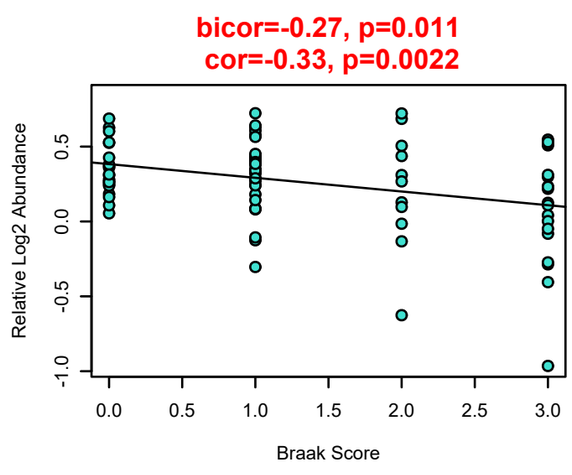

ABAT UPenn Mixed PRM
K-W ANOVA p: 0.01
Relative Log2 Abundance
Control
otherND
AD

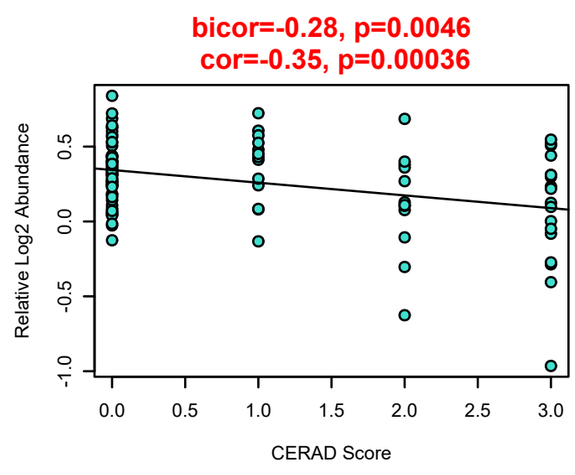

bicor=-0.051, p=0.64
cor=0.077, p=0.49
Relative Log2 Abundance
Braak Score

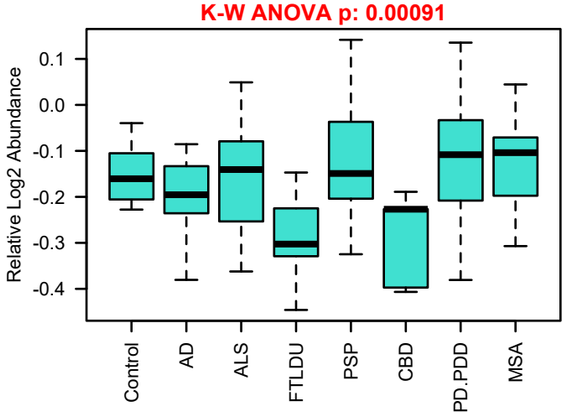

bicor=0.056, p=0.58
cor=0.14, p=0.16
Relative Log2 Abundance
CERAD Score

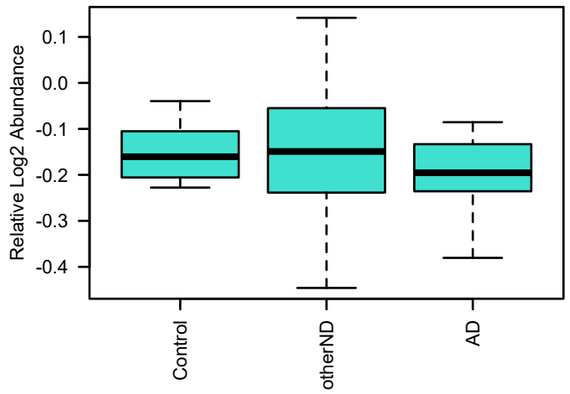

HPCA UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.009
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

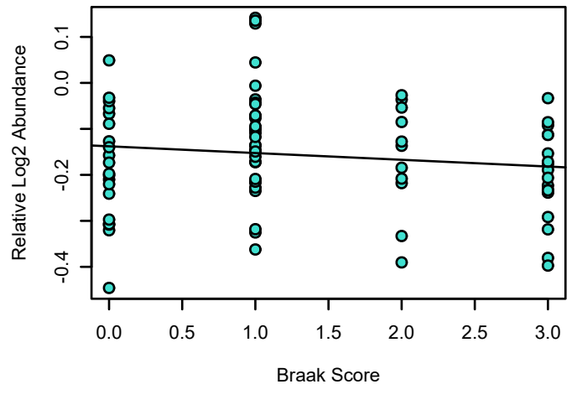

HPCA UPenn Mixed PRM
K-W ANOVA p: 0.00038
Relative Log2 Abundance
Control
otherND
AD

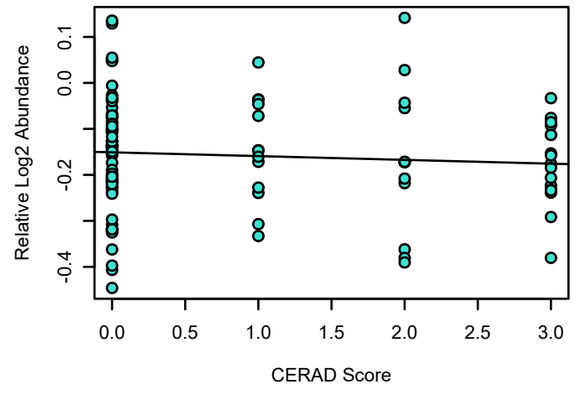

bicor=-0.27, p=0.011
cor=-0.33, p=0.0022
Relative Log2 Abundance
Braak Score

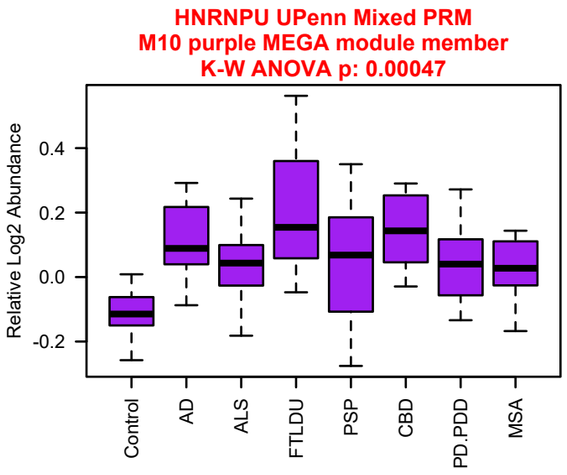

bicor=-0.28, p=0.0046
cor=-0.35, p=0.00036
Relative Log2 Abundance
CERAD Score

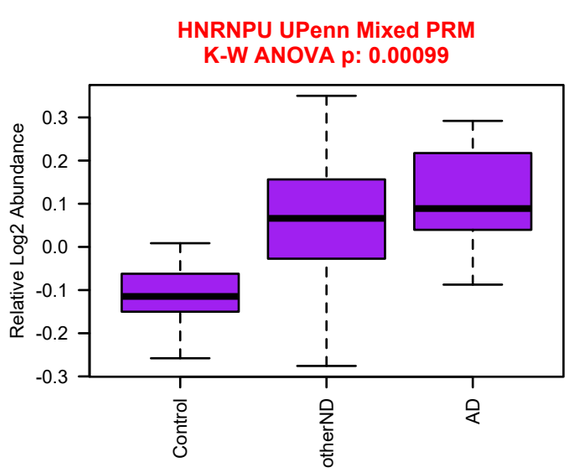

CLTC UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00091
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

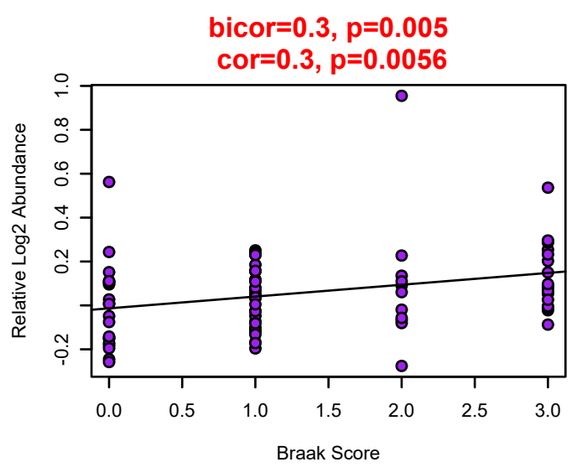

CLTC UPenn Mixed PRM
K-W ANOVA p: 0.32
Relative Log2 Abundance
Control
otherND
AD

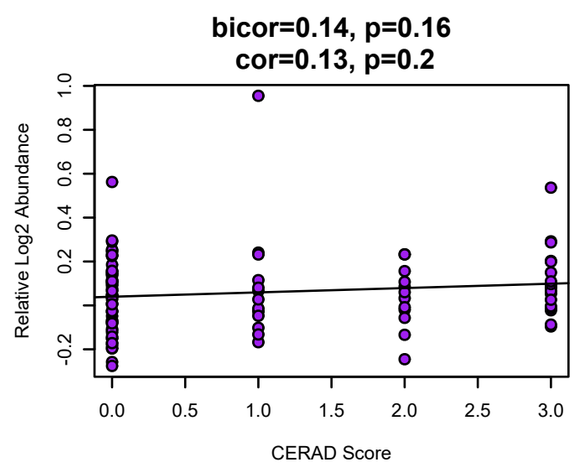

bicor=-0.14, p=0.2
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

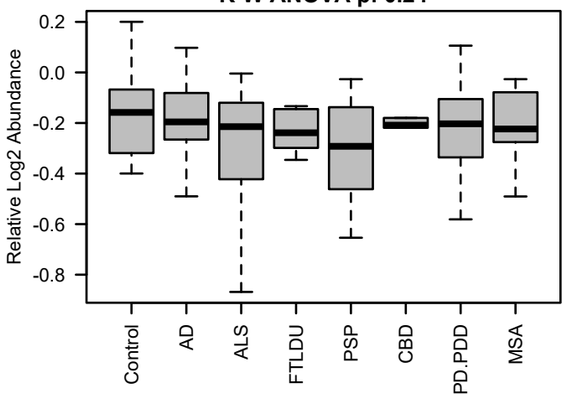

bicor=-0.088, p=0.39
cor=-0.08, p=0.43
Relative Log2 Abundance
CERAD Score

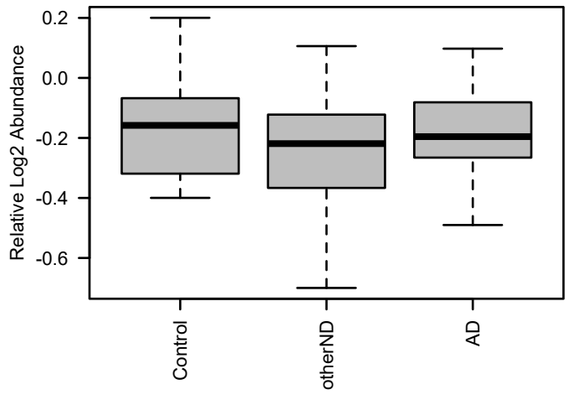

HNRNPU UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.00047
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

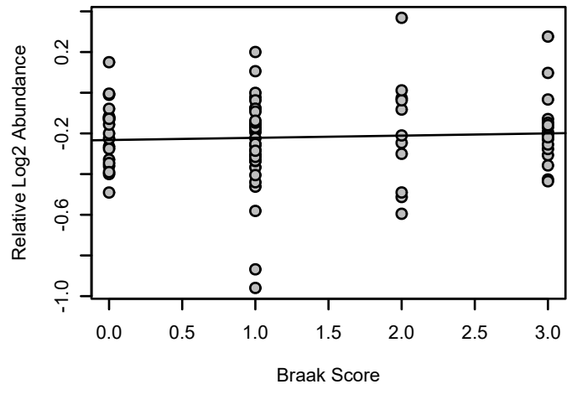

HNRNPU UPenn Mixed PRM
K-W ANOVA p: 0.00099
Relative Log2 Abundance
Control
otherND
AD

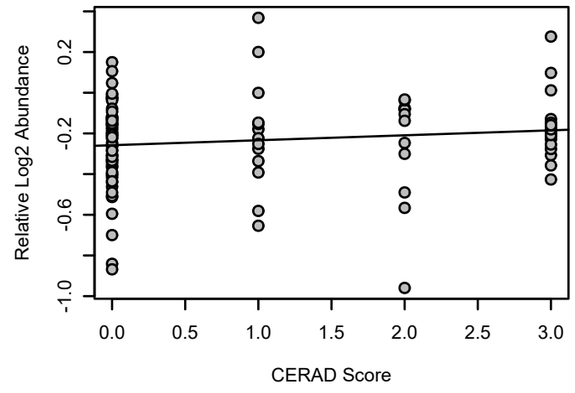

bicor=0.3, p=0.005
cor=0.3, p=0.0056
Relative Log2 Abundance
Braak Score

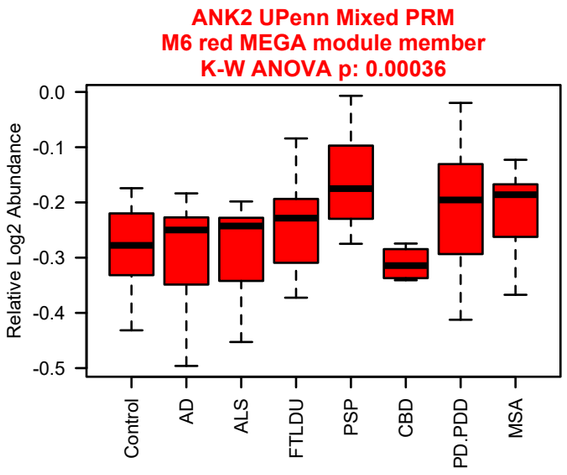

bicor=0.14, p=0.16
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

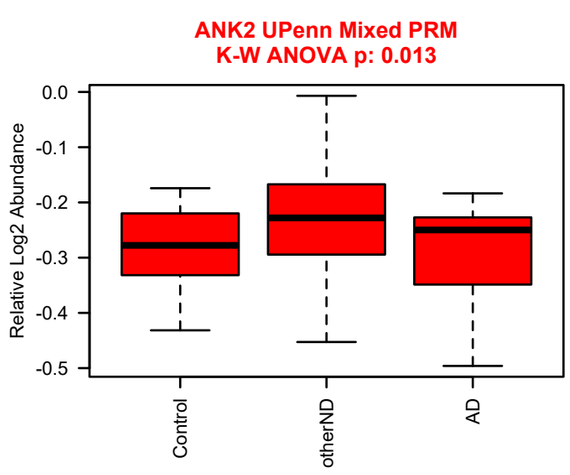

SPTBN1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

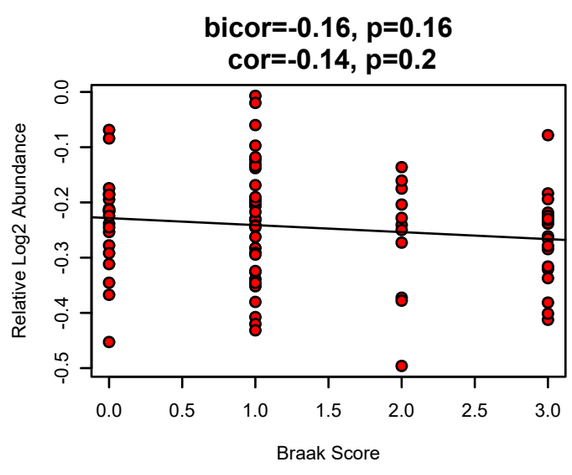

SPTBN1 UPenn Mixed PRM
K-W ANOVA p: 0.11
Relative Log2 Abundance
Control
otherND
AD

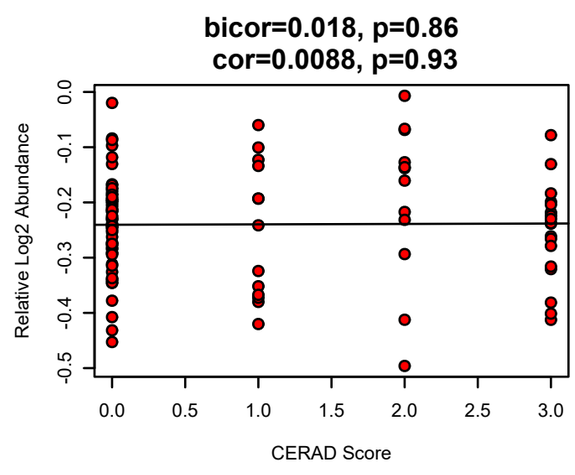

bicor=0.015, p=0.89
cor=0.056, p=0.61
Relative Log2 Abundance
Braak Score

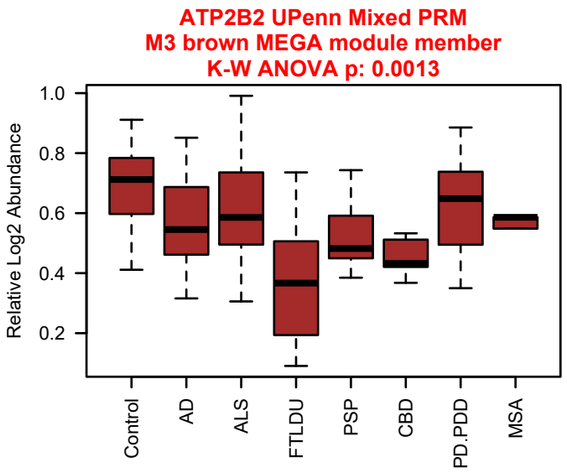

bicor=0.14, p=0.16
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

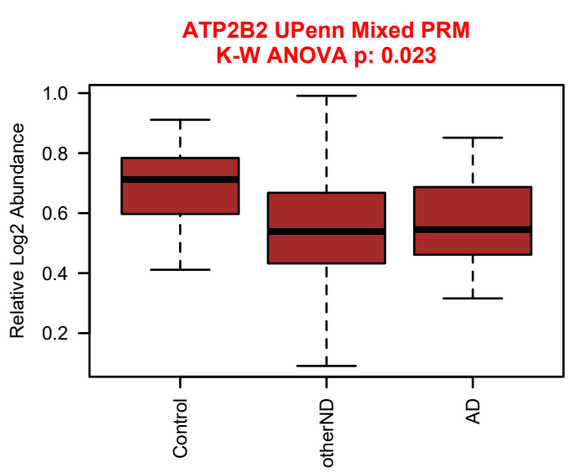

ANK2 UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.00036
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

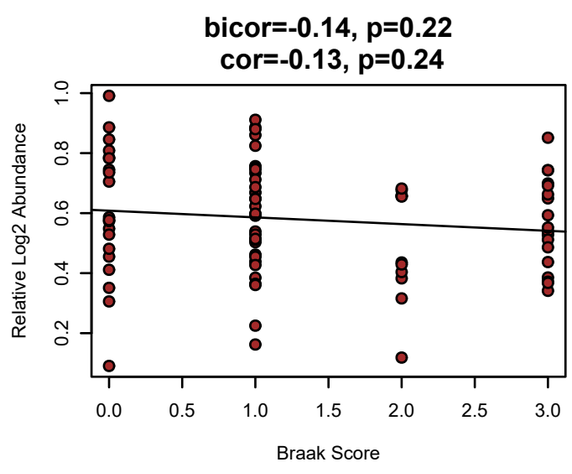

ANK2 UPenn Mixed PRM
K-W ANOVA p: 0.013
Relative Log2 Abundance
Control
otherND
AD

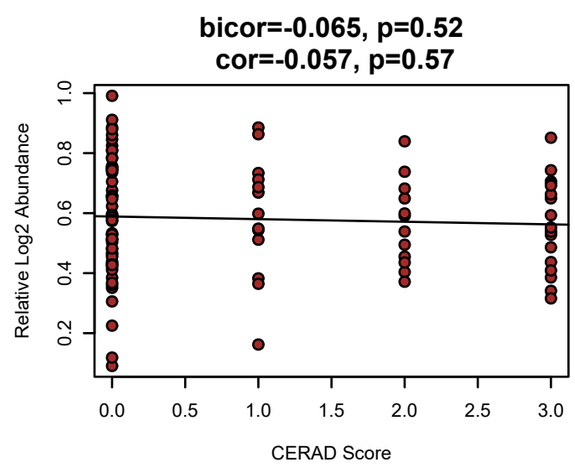

bicor=-0.16, p=0.16
cor=-0.14, p=0.2
Relative Log2 Abundance
Braak Score

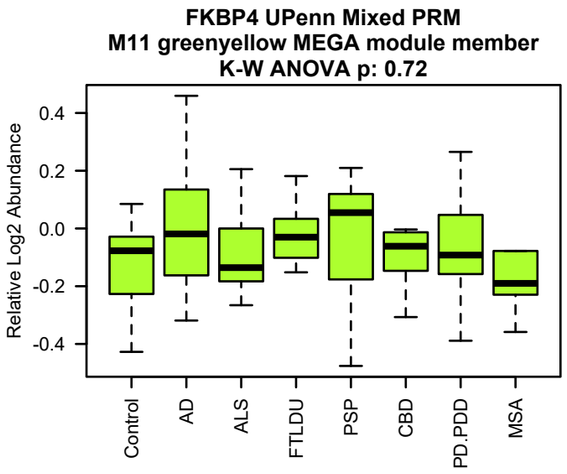

bicor=0.018, p=0.86
cor=0.0088, p=0.93
Relative Log2 Abundance
CERAD Score

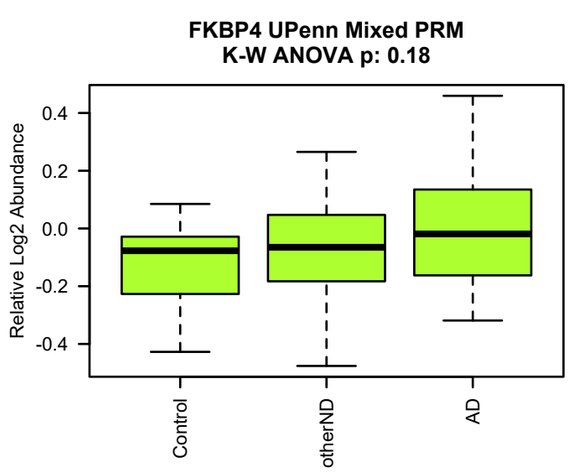

ATP2B2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0013
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

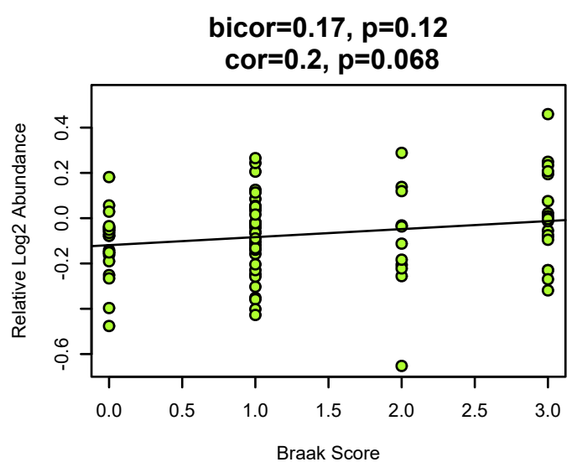

ATP2B2 UPenn Mixed PRM
K-W ANOVA p: 0.023
Relative Log2 Abundance
Control
otherND
AD

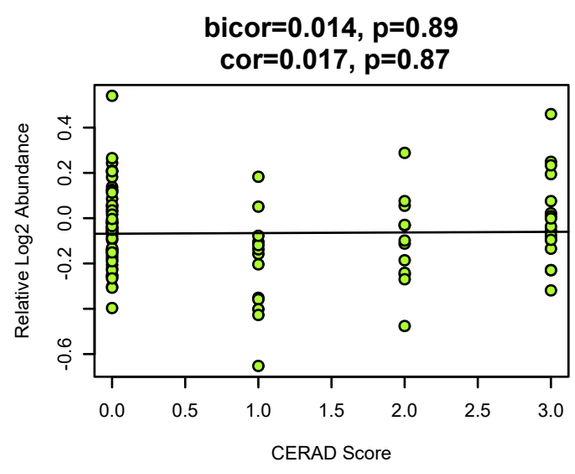

bicor=-0.14, p=0.22
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

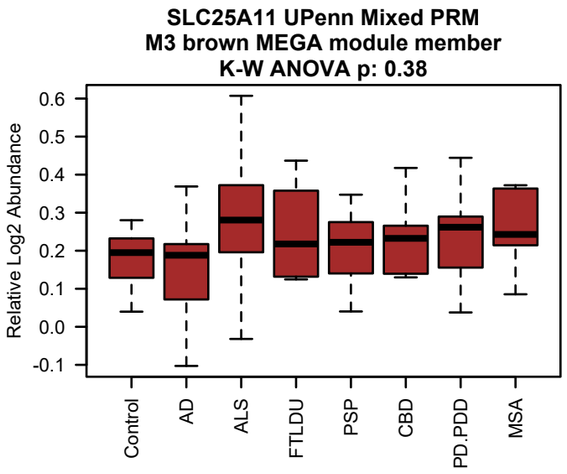

bicor=-0.065, p=0.52
cor=-0.057, p=0.57
Relative Log2 Abundance
CERAD Score

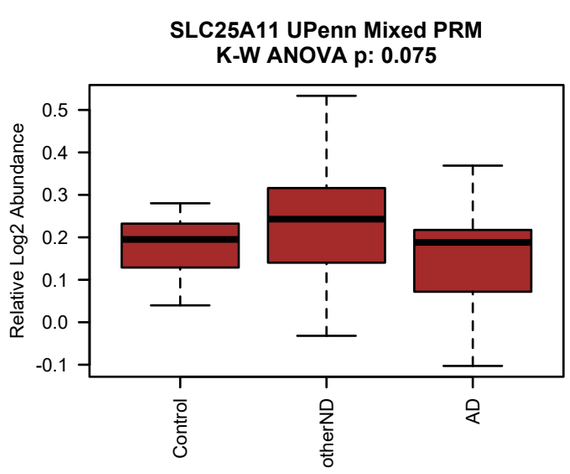

FKBP4 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 0.72
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

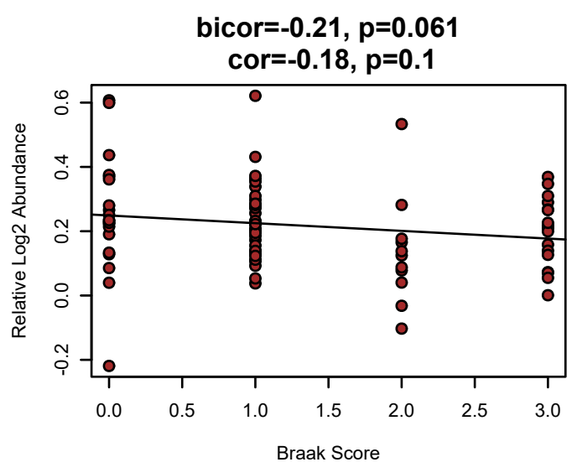

FKBP4 UPenn Mixed PRM
K-W ANOVA p: 0.18
Relative Log2 Abundance
Control
otherND
AD

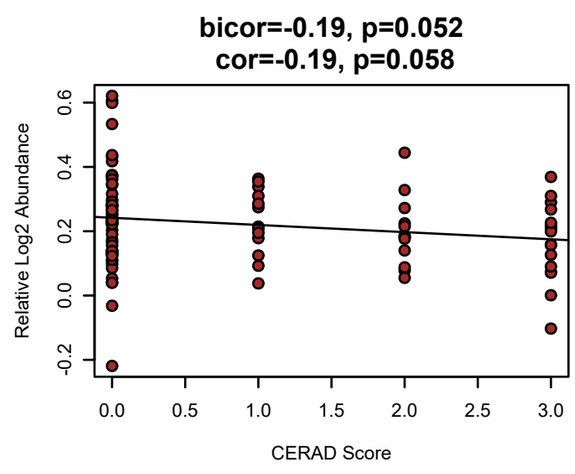

bicor=0.17, p=0.12
cor=0.2, p=0.068
Relative Log2 Abundance
Braak Score

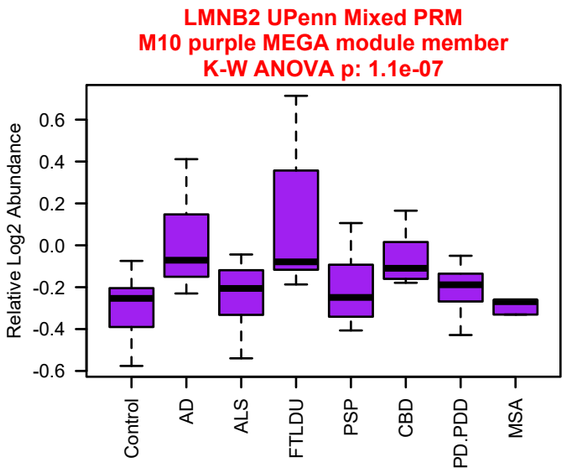

bicor=0.014, p=0.89
cor=0.017, p=0.87
Relative Log2 Abundance
CERAD Score

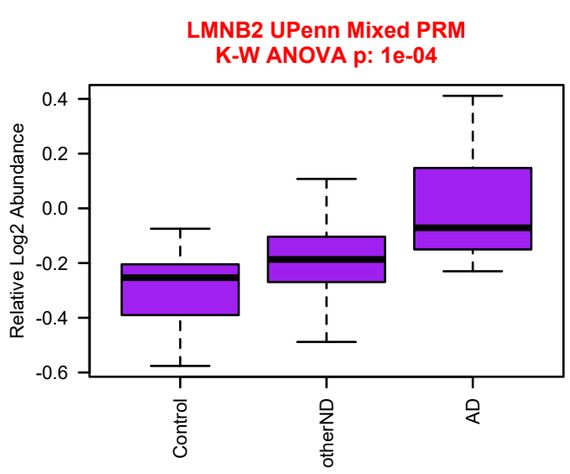

SLC25A11 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.38
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

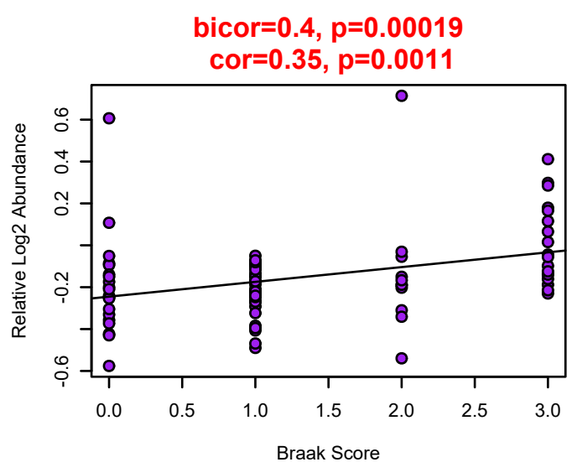

SLC25A11 UPenn Mixed PRM
K-W ANOVA p: 0.075
Relative Log2 Abundance
Control
otherND
AD

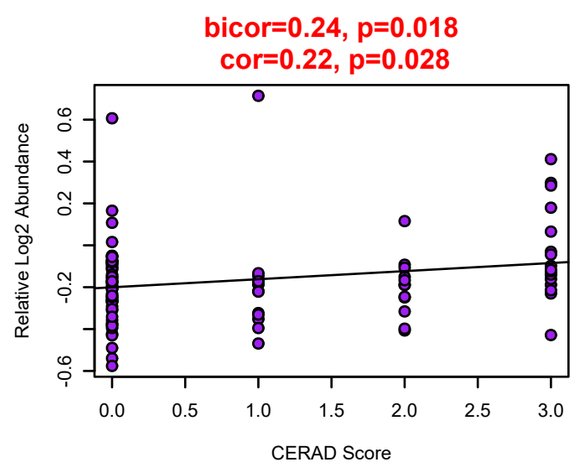

bicor=-0.21, p=0.061
cor=-0.18, p=0.1
Relative Log2 Abundance
Braak Score

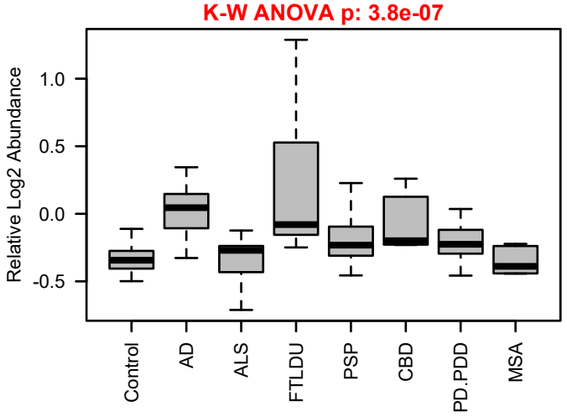

bicor=-0.19, p=0.052
cor=-0.19, p=0.058
Relative Log2 Abundance
CERAD Score

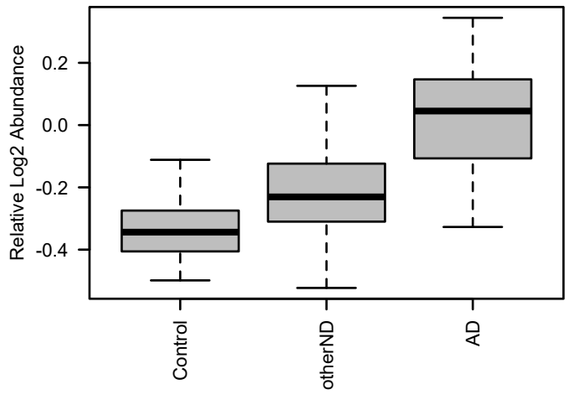

LMNB2 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 1.1e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

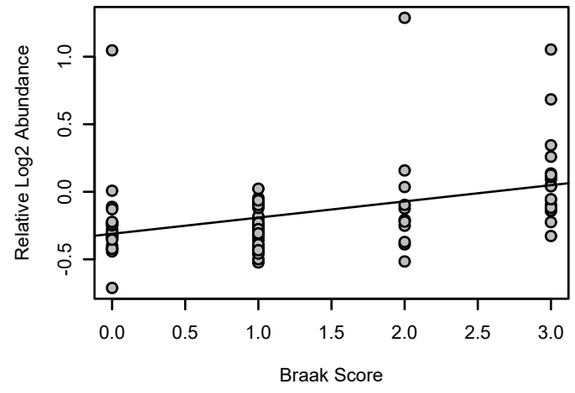

LMNB2 UPenn Mixed PRM
K-W ANOVA p: 1e-04
Relative Log2 Abundance
Control
otherND
AD

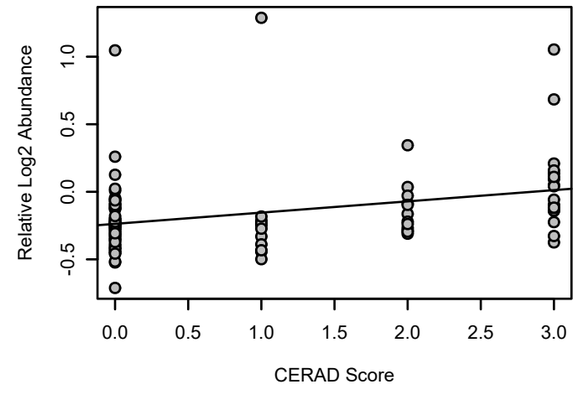

bicor=0.4, p=0.00019
cor=0.35, p=0.0011
Relative Log2 Abundance
Braak Score

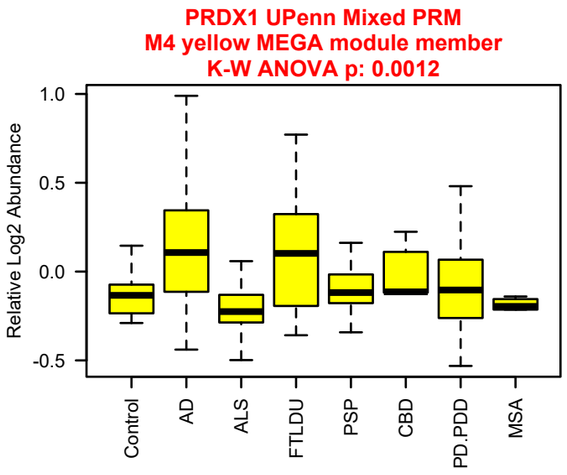

bicor=0.24, p=0.018
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

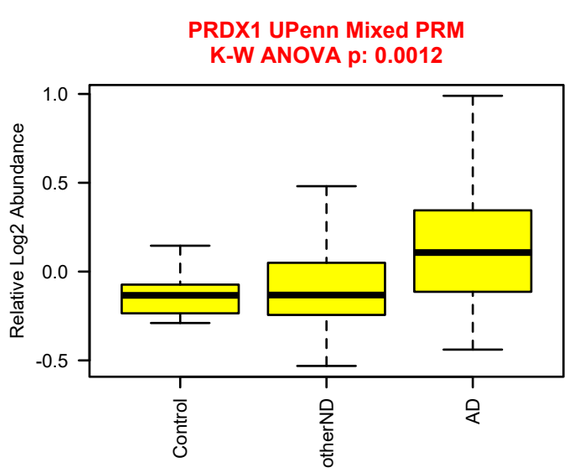

PRDX4 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 3.8e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

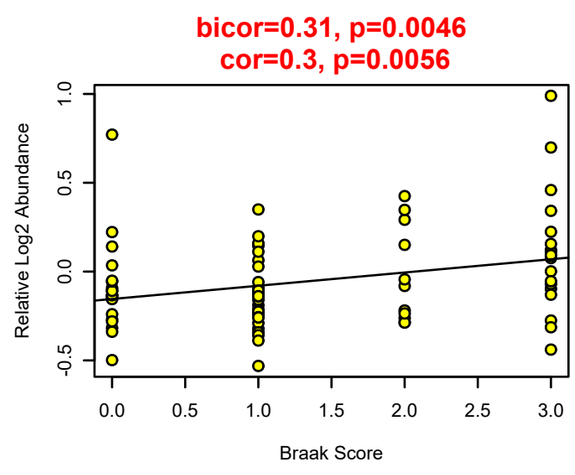

PRDX4 UPenn Mixed PRM
K-W ANOVA p: 0.00012
Relative Log2 Abundance
Control
otherND
AD

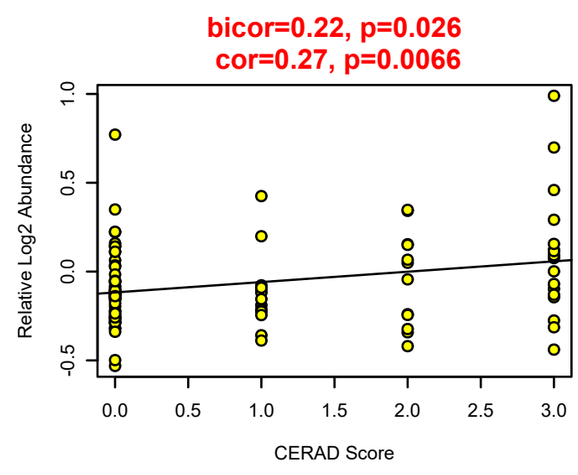

bicor=0.53, p=2.7e-07
cor=0.4, p=0.00016
Relative Log2 Abundance
Braak Score

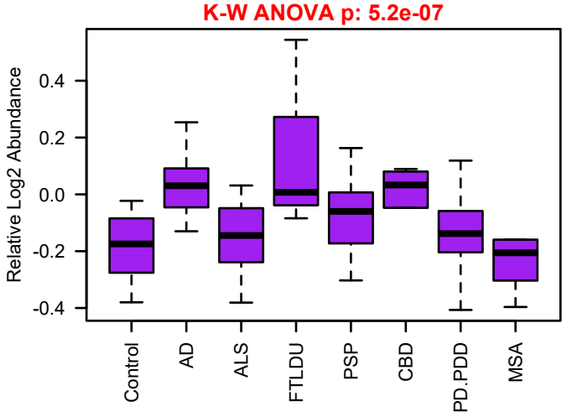

bicor=0.39, p=6.3e-05
cor=0.32, p=0.0012
Relative Log2 Abundance
CERAD Score

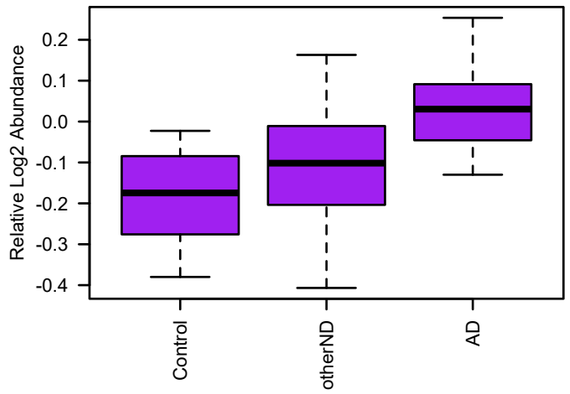

PRDX1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.0012
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

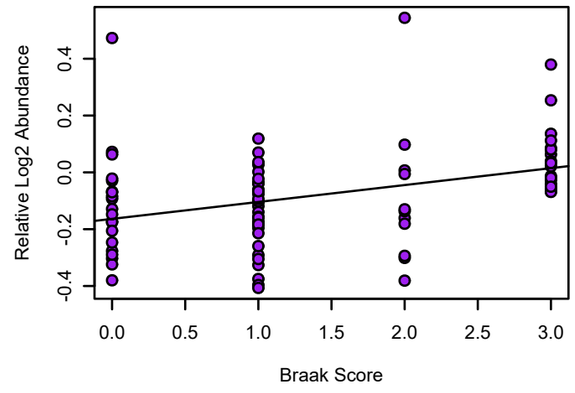

PRDX1 UPenn Mixed PRM
K-W ANOVA p: 0.0012
Relative Log2 Abundance
Control
otherND
AD

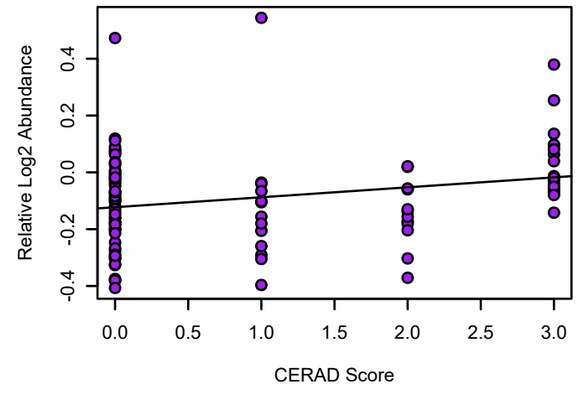

bicor=0.31, p=0.0046
cor=0.3, p=0.0056
Relative Log2 Abundance
Braak Score

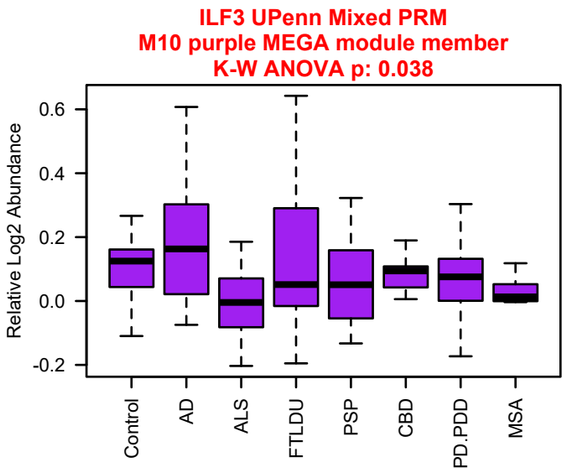

bicor=0.22, p=0.026
cor=0.27, p=0.0066
Relative Log2 Abundance
CERAD Score

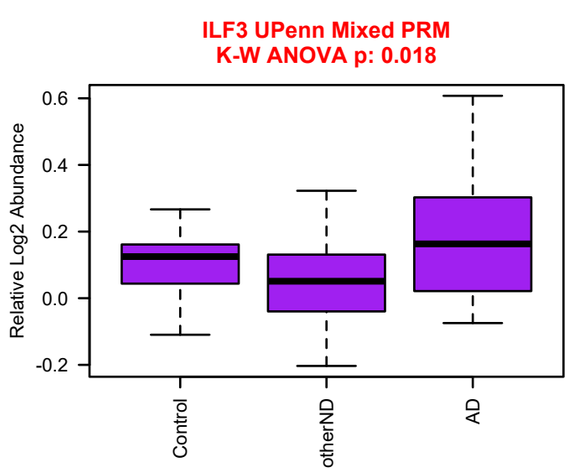

SRSF1 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 5.2e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

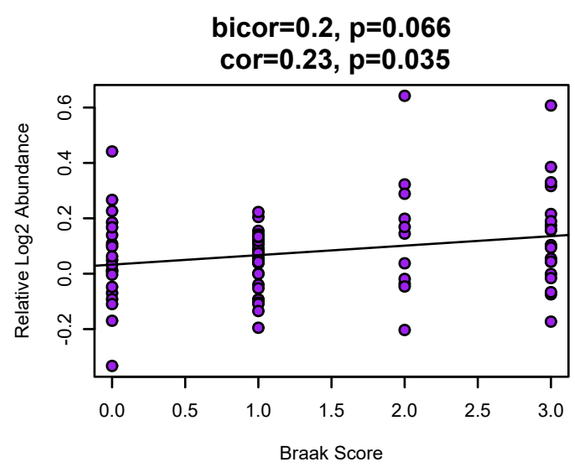

SRSF1 UPenn Mixed PRM
K-W ANOVA p: 0.00017
Relative Log2 Abundance
Control
otherND
AD

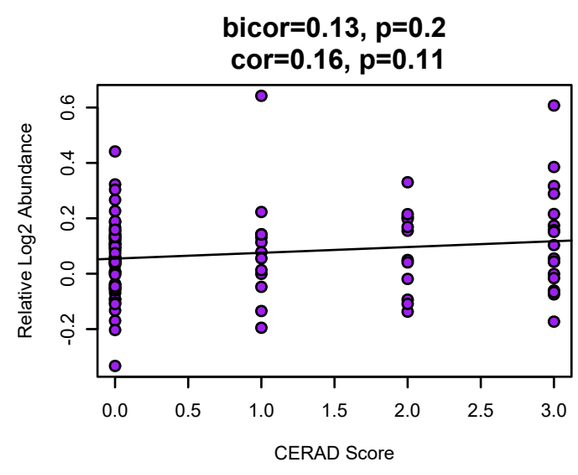

bicor=0.36, p=0.00067
cor=0.36, p=0.00077
Relative Log2 Abundance
Braak Score

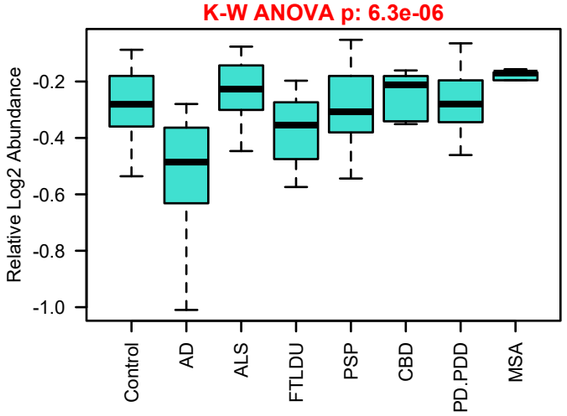

bicor=0.28, p=0.0055
cor=0.25, p=0.012
Relative Log2 Abundance
CERAD Score

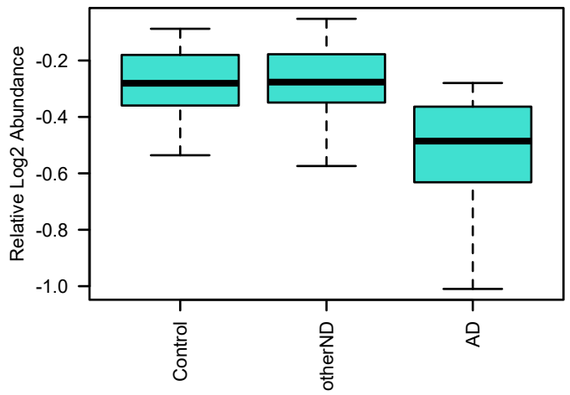

ILF3 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.038
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

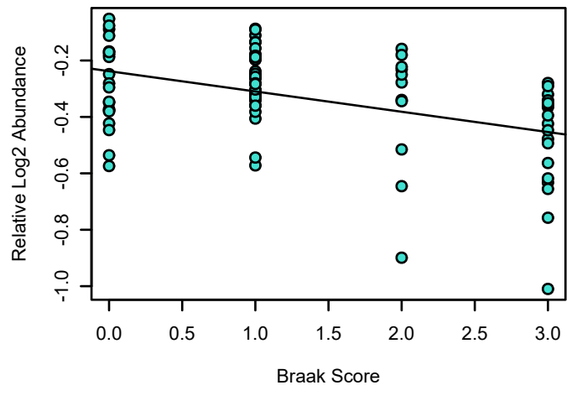

ILF3 UPenn Mixed PRM
K-W ANOVA p: 0.018
Relative Log2 Abundance
Control
otherND
AD

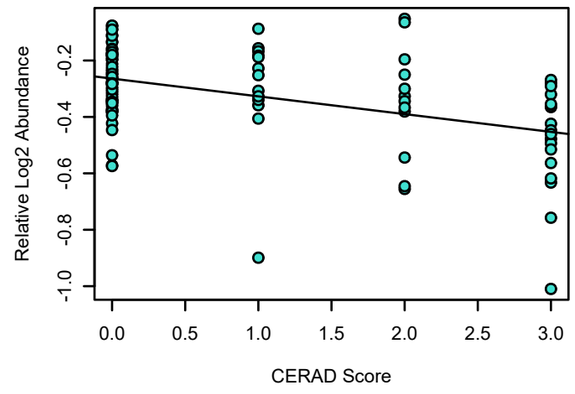

bicor=0.2, p=0.066
cor=0.23, p=0.035
Relative Log2 Abundance
Braak Score

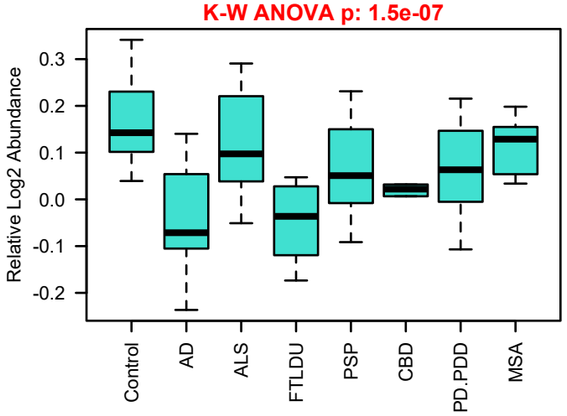

bicor=0.13, p=0.2
cor=0.16, p=0.11
Relative Log2 Abundance
CERAD Score

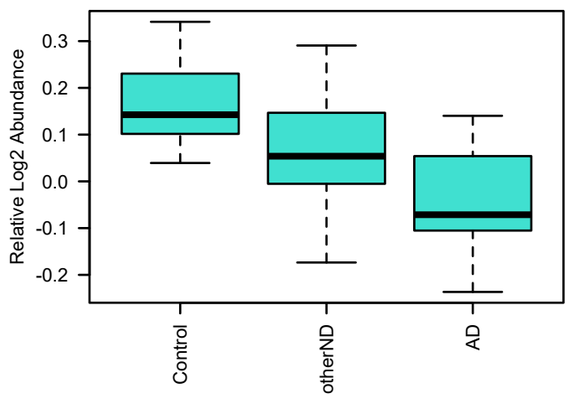

PAK1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 6.3e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

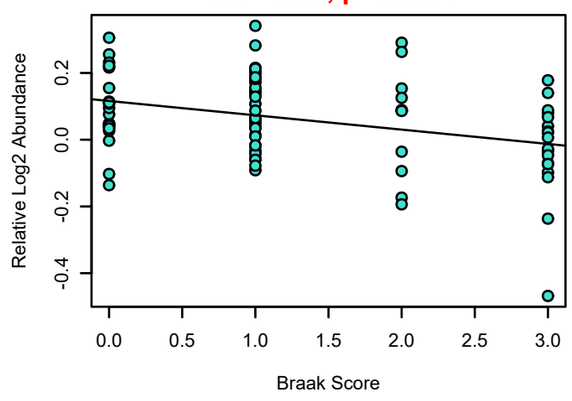

PAK1 UPenn Mixed PRM
K-W ANOVA p: 1.4e-06
Relative Log2 Abundance
Control
otherND
AD

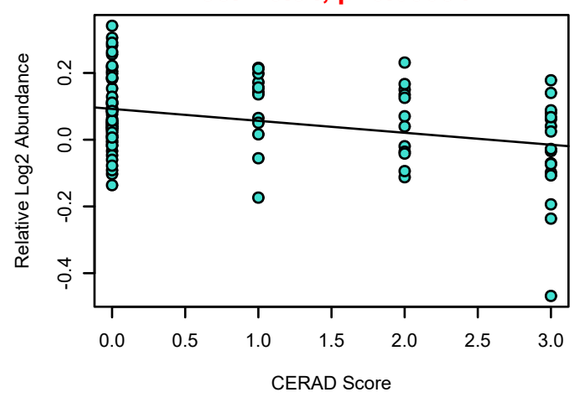

bicor=-0.37, p=0.00056
cor=-0.44, p=2.8e-05
Relative Log2 Abundance
Braak Score

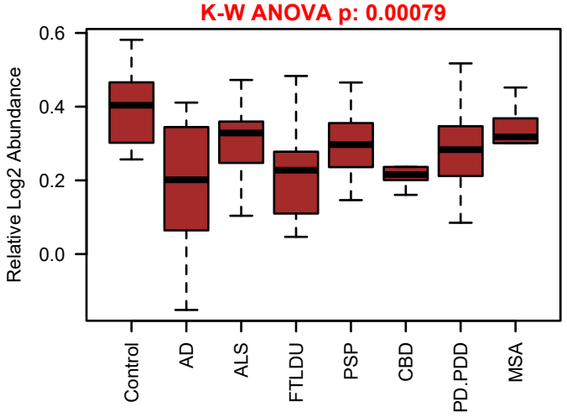

bicor=-0.42, p=1.5e-05
cor=-0.44, p=4.6e-06
Relative Log2 Abundance
CERAD Score

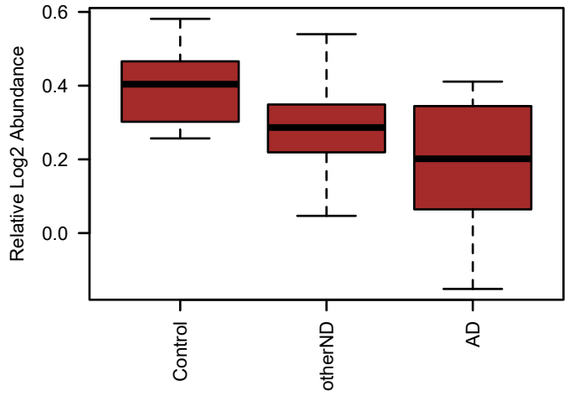

AP3B2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 1.5e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

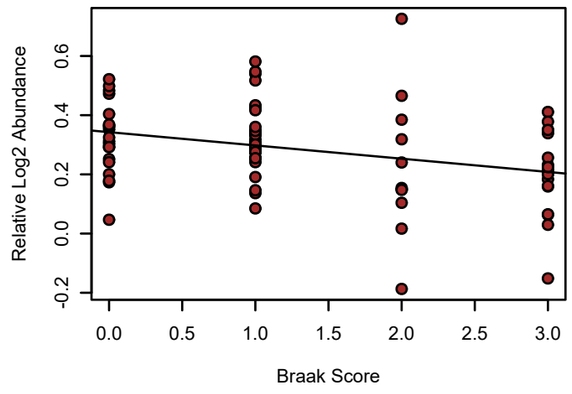

AP3B2 UPenn Mixed PRM
K-W ANOVA p: 2.8e-07
Relative Log2 Abundance
Control
otherND
AD

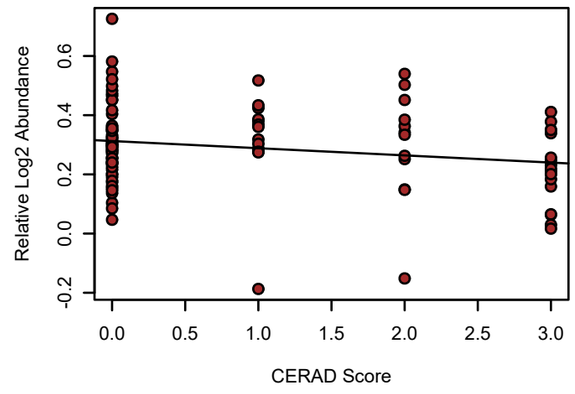

bicor=-0.31, p=0.0047
cor=-0.35, p=0.0011
Relative Log2 Abundance
Braak Score

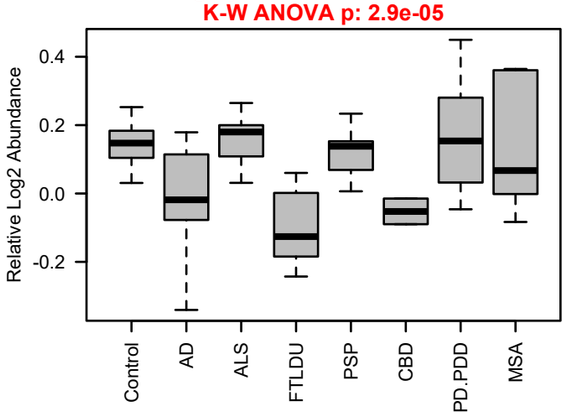

bicor=-0.29, p=0.0032
cor=-0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

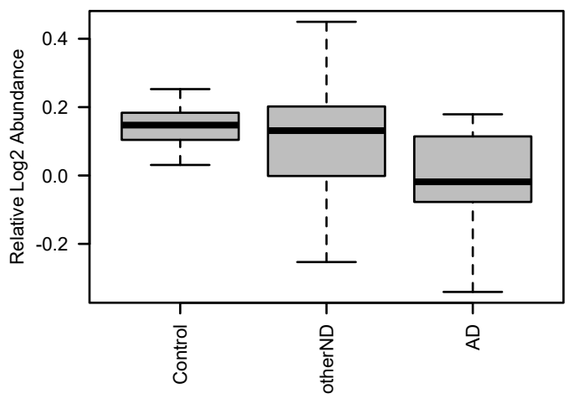

NNT UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.00079
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

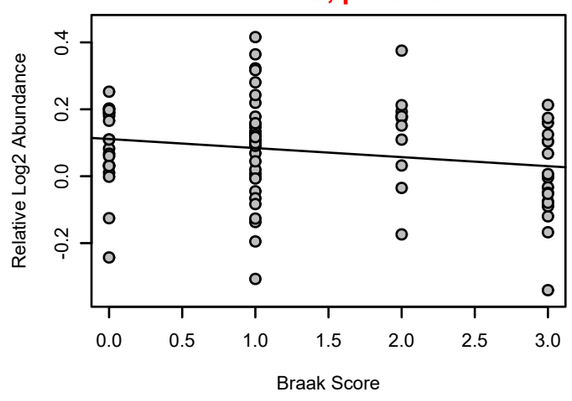

NNT UPenn Mixed PRM
K-W ANOVA p: 0.00018
Relative Log2 Abundance
Control
otherND
AD

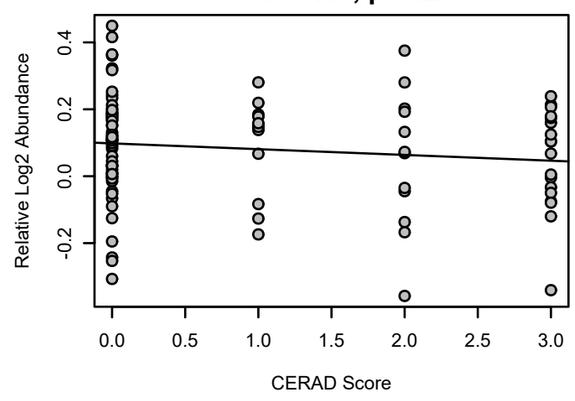

bicor=-0.34, p=0.0017
cor=-0.32, p=0.003
Relative Log2 Abundance
Braak Score

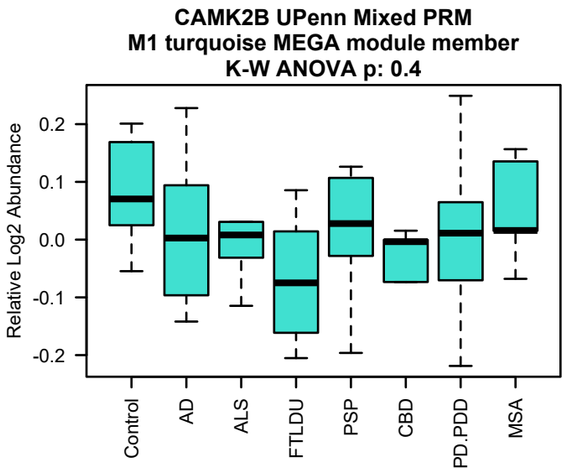

bicor=-0.18, p=0.074
cor=-0.2, p=0.046
Relative Log2 Abundance
CERAD Score

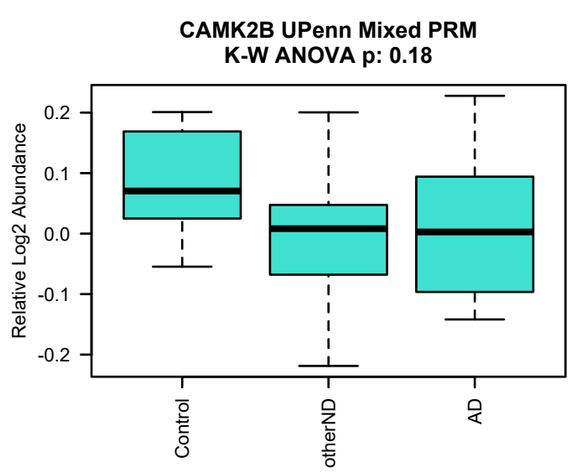

TUBB3 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 2.9e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

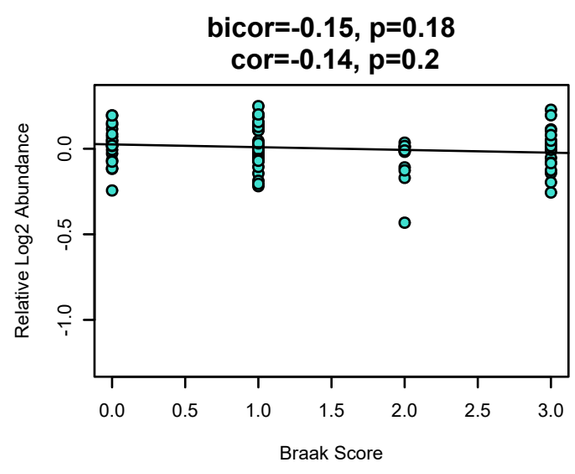

TUBB3 UPenn Mixed PRM
K-W ANOVA p: 0.016
Relative Log2 Abundance
Control
otherND
AD

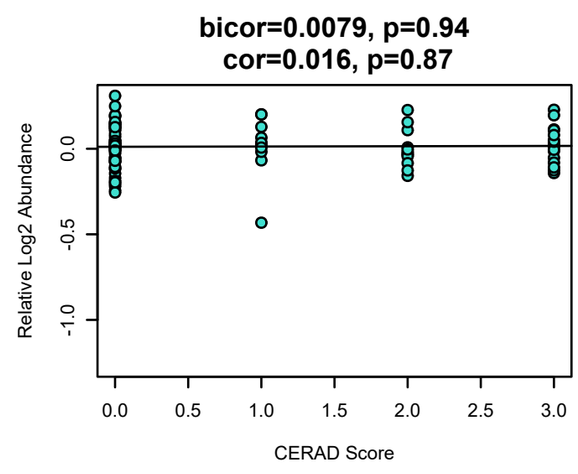

bicor=-0.24, p=0.03
cor=-0.2, p=0.068
Relative Log2 Abundance
Braak Score

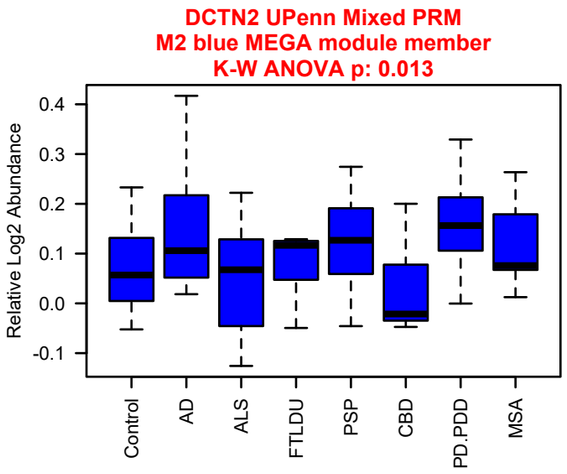

bicor=-0.11, p=0.26
cor=-0.13, p=0.2
Relative Log2 Abundance
CERAD Score

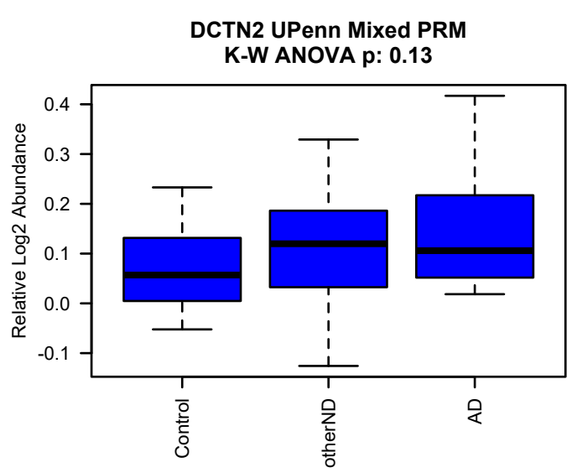

CAMK2B UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.4
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

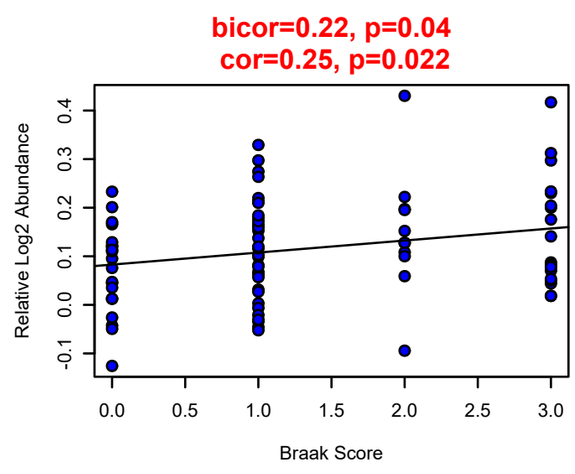

CAMK2B UPenn Mixed PRM
K-W ANOVA p: 0.18
Relative Log2 Abundance
Control
otherND
AD

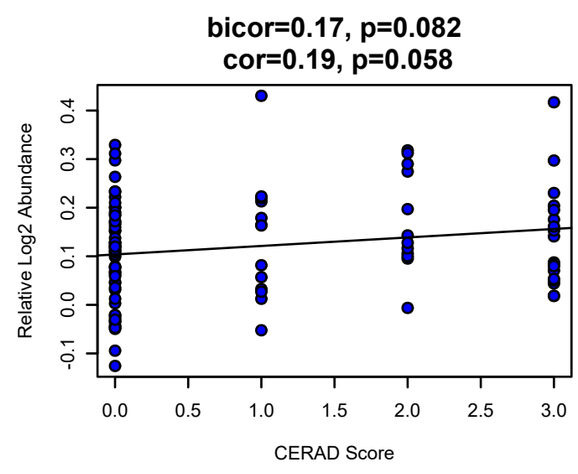

bicor=-0.15, p=0.18
cor=-0.14, p=0.2
Relative Log2 Abundance
Braak Score

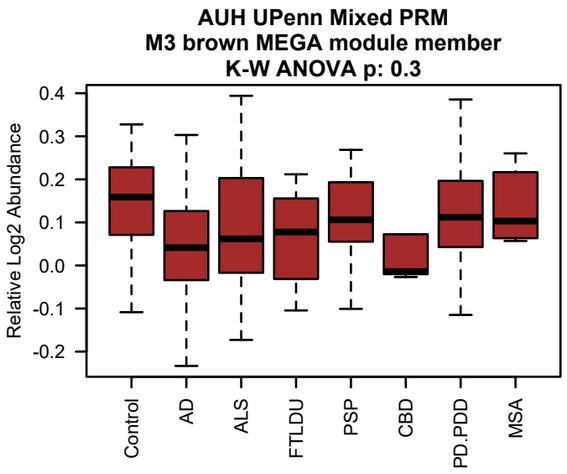

bicor=0.0079, p=0.94
cor=0.016, p=0.87
Relative Log2 Abundance
CERAD Score

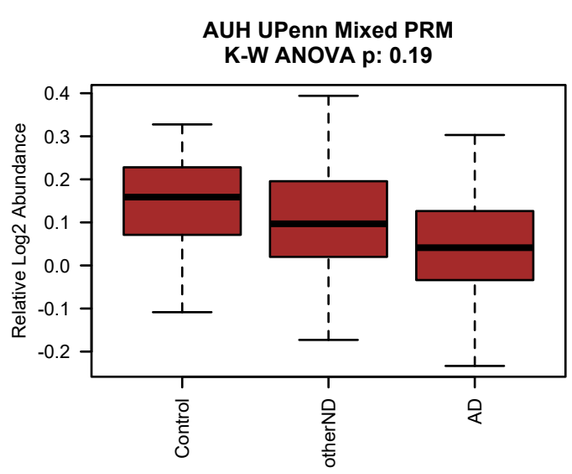

DCTN2 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.013
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

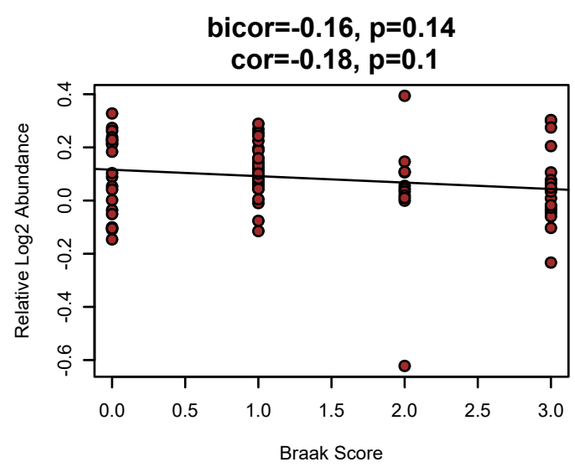

DCTN2 UPenn Mixed PRM
K-W ANOVA p: 0.13
Relative Log2 Abundance
Control
otherND
AD

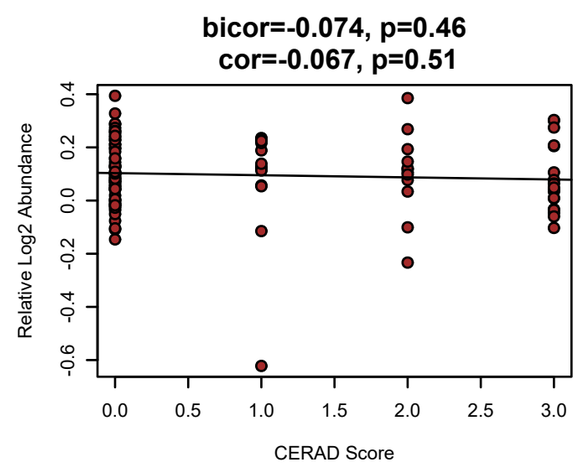

bicor=0.22, p=0.04
cor=0.25, p=0.022
Relative Log2 Abundance
Braak Score

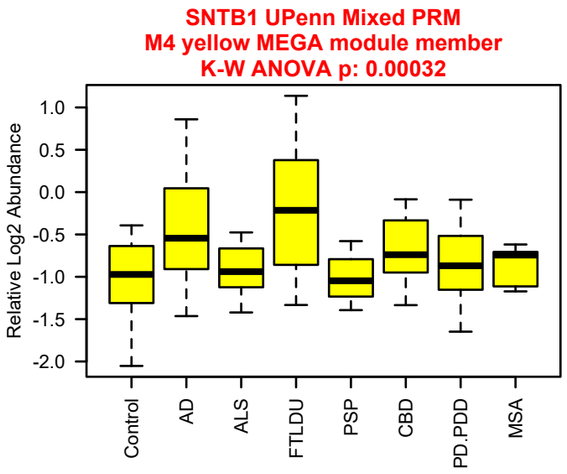

bicor=0.17, p=0.082
cor=0.19, p=0.058
Relative Log2 Abundance
CERAD Score

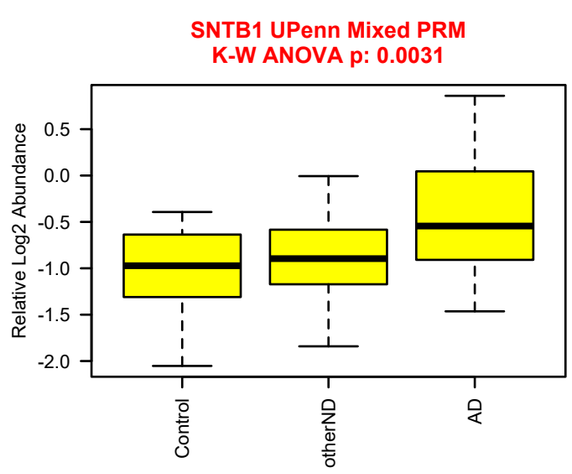

AUH UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.3
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

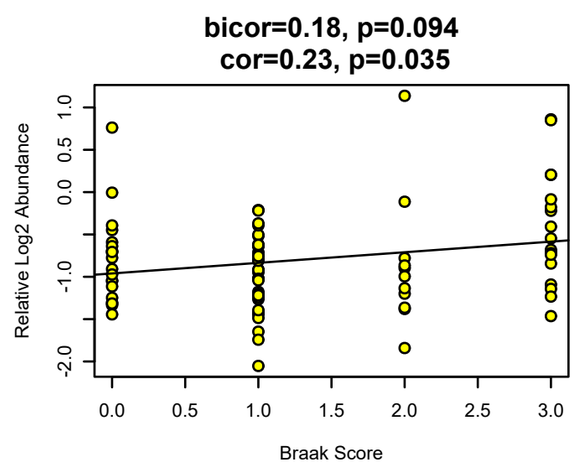

AUH UPenn Mixed PRM
K-W ANOVA p: 0.19
Relative Log2 Abundance
Control
otherND
AD

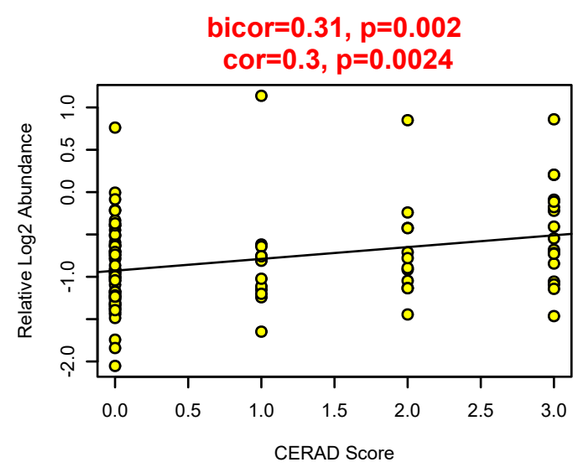

bicor=-0.16, p=0.14
cor=-0.18, p=0.1
Relative Log2 Abundance
Braak Score

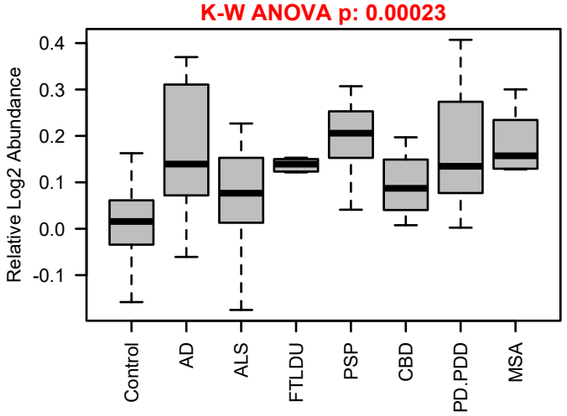

bicor=-0.074, p=0.46
cor=-0.067, p=0.51
Relative Log2 Abundance
CERAD Score

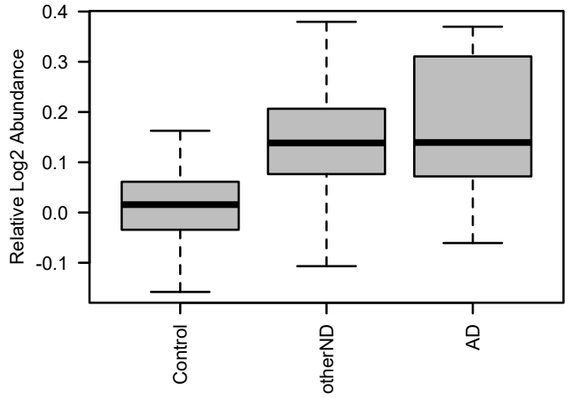

SNTB1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.00032
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

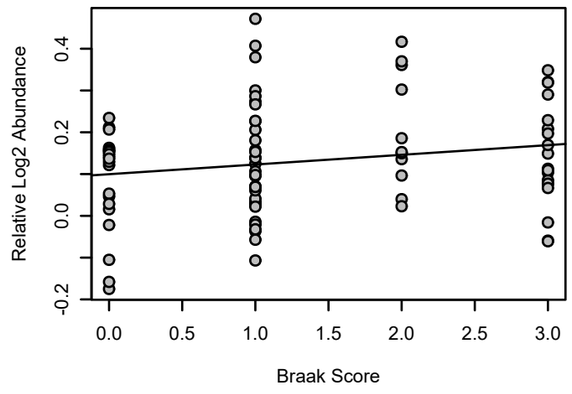

SNTB1 UPenn Mixed PRM
K-W ANOVA p: 0.0031
Relative Log2 Abundance
Control
otherND
AD

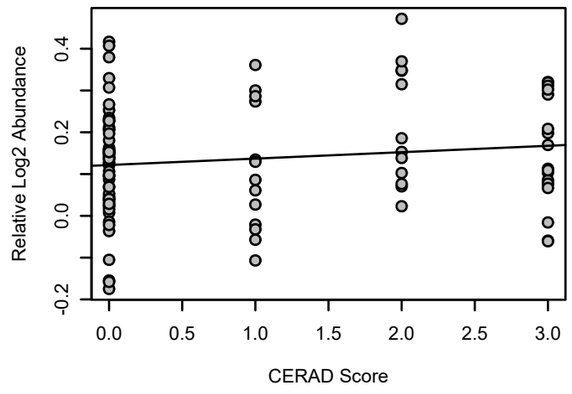

bicor=0.18, p=0.094
cor=0.23, p=0.035
Relative Log2 Abundance
Braak Score

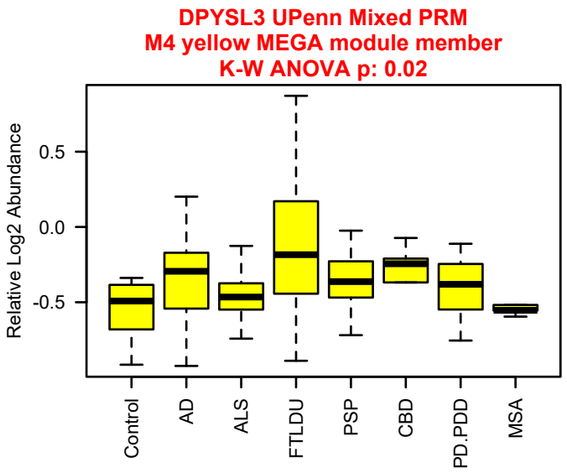

bicor=0.31, p=0.002
cor=0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

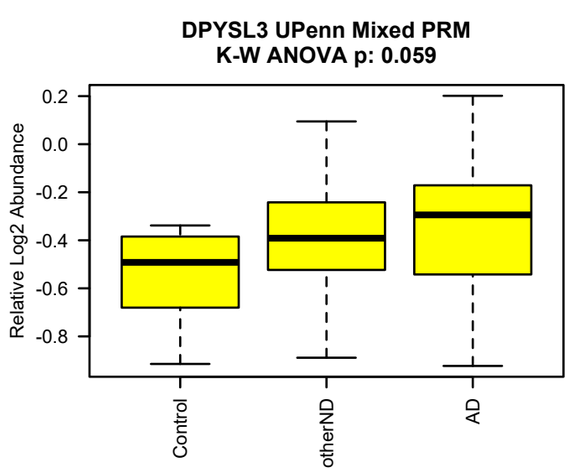

CKAP5 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.00023
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

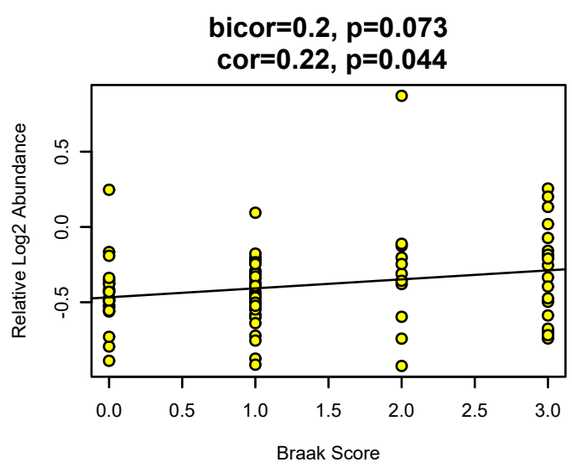

CKAP5 UPenn Mixed PRM
K-W ANOVA p: 0.001
Relative Log2 Abundance
Control
otherND
AD

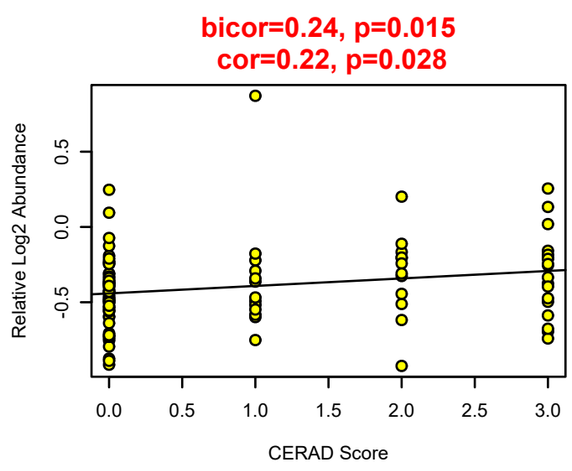

bicor=0.17, p=0.12
cor=0.19, p=0.083
Relative Log2 Abundance
Braak Score

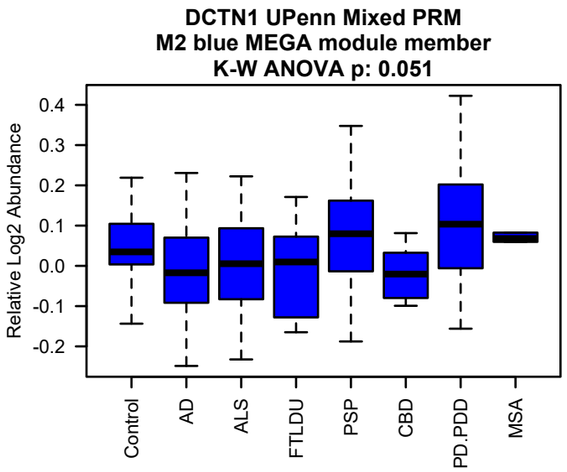

bicor=0.13, p=0.2
cor=0.14, p=0.16
Relative Log2 Abundance
CERAD Score

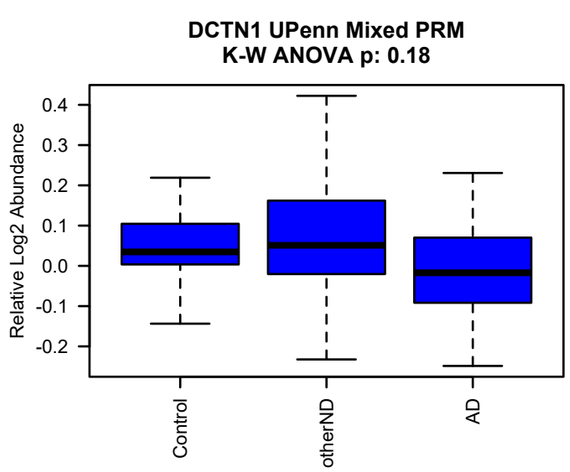

DPYSL3 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.02
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

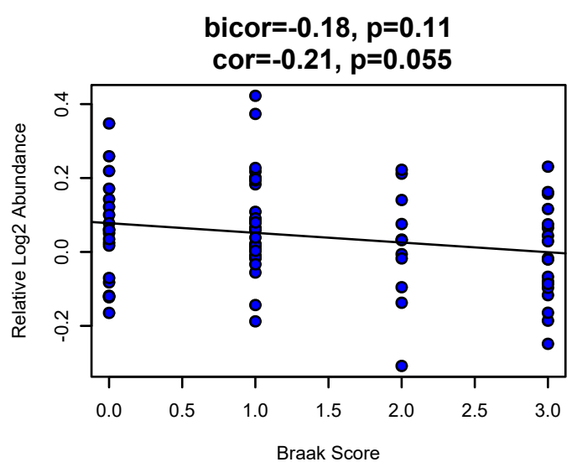

DPYSL3 UPenn Mixed PRM
K-W ANOVA p: 0.059
Relative Log2 Abundance
Control
otherND
AD

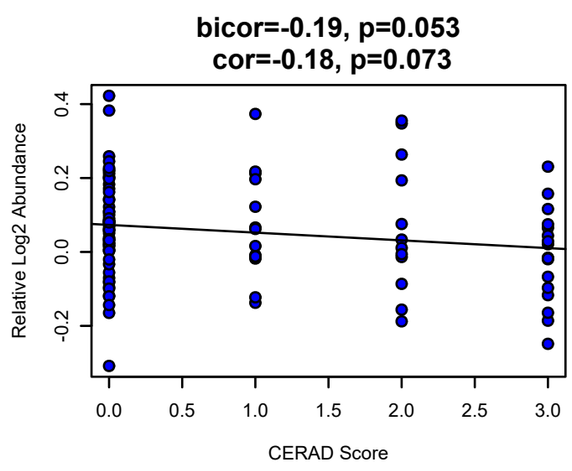

bicor=0.2, p=0.073
cor=0.22, p=0.044
Relative Log2 Abundance
Braak Score

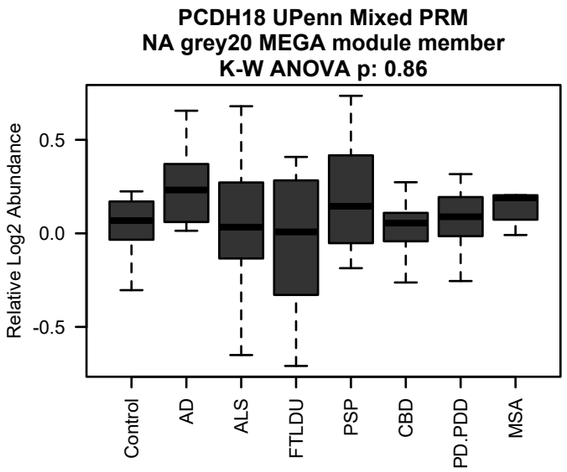

bicor=0.24, p=0.015
cor=0.22, p=0.028
Relative Log2 Abundance
CERAD Score

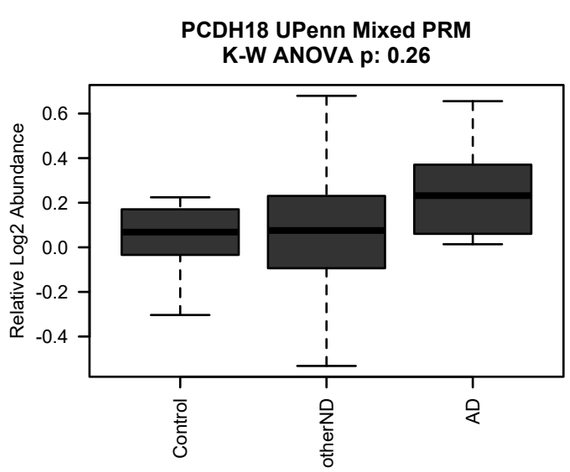

DCTN1 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.051
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

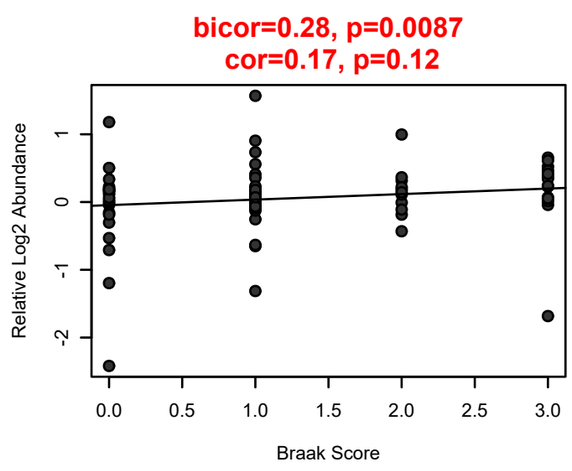

DCTN1 UPenn Mixed PRM
K-W ANOVA p: 0.18
Relative Log2 Abundance
Control
otherND
AD

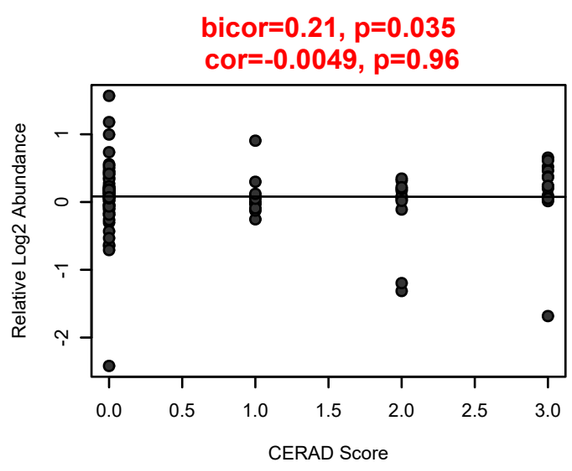

bicor=-0.18, p=0.11
cor=-0.21, p=0.055
Relative Log2 Abundance
Braak Score

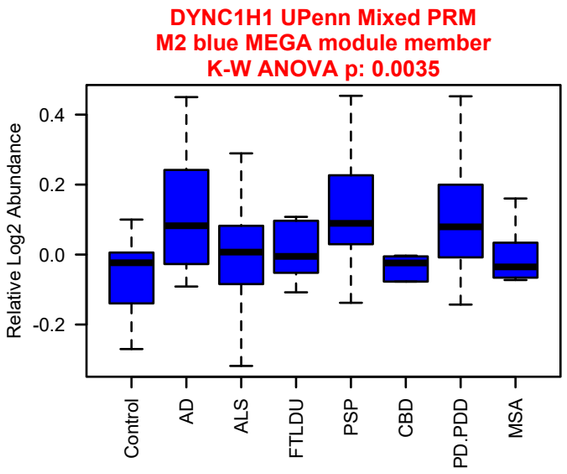

bicor=-0.19, p=0.053
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

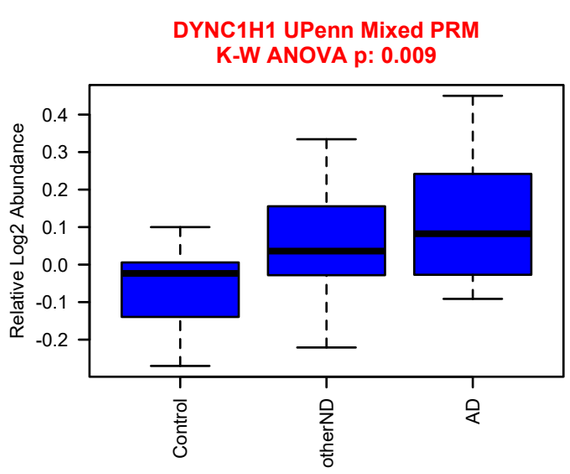

PCDH18 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.86
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

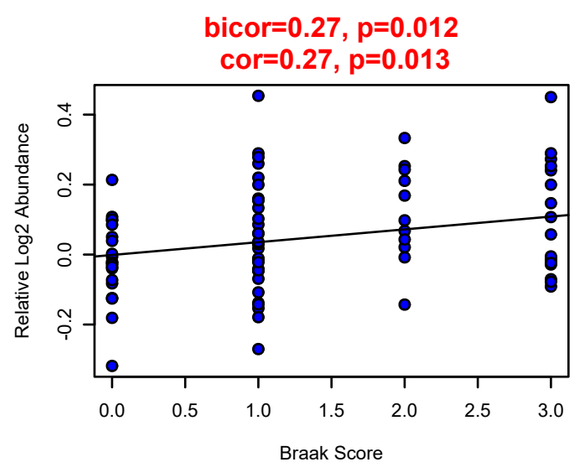

PCDH18 UPenn Mixed PRM
K-W ANOVA p: 0.26
Relative Log2 Abundance
Control
otherND
AD

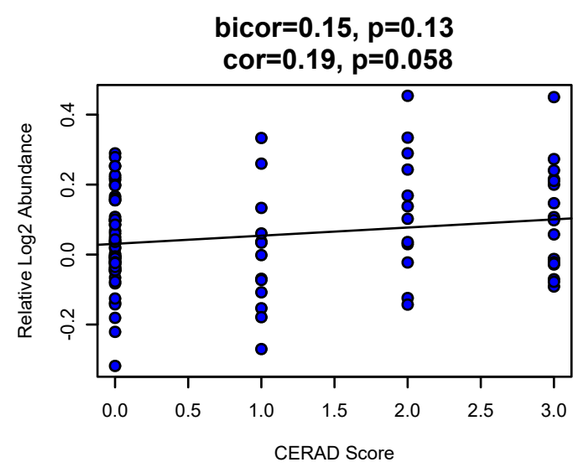

bicor=0.28, p=0.0087
cor=0.17, p=0.12
Relative Log2 Abundance
Braak Score

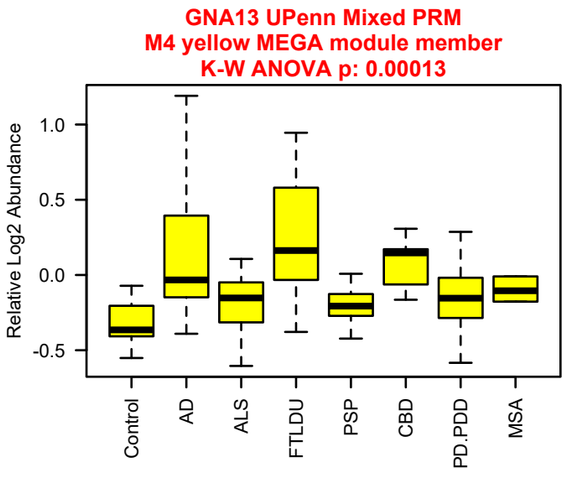

bicor=0.21, p=0.035
cor=-0.0049, p=0.96
Relative Log2 Abundance
CERAD Score

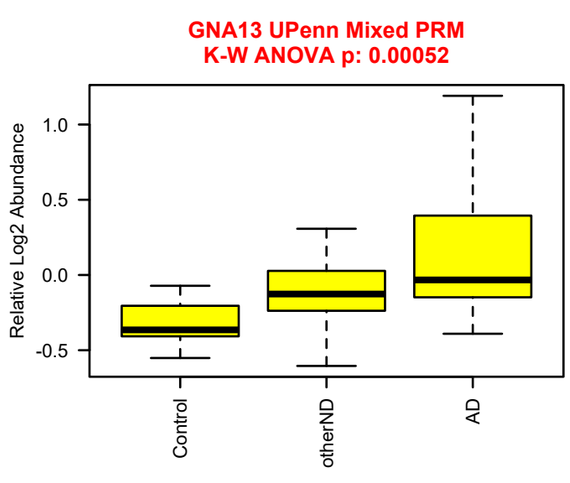

DYNC1H1 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.0035
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

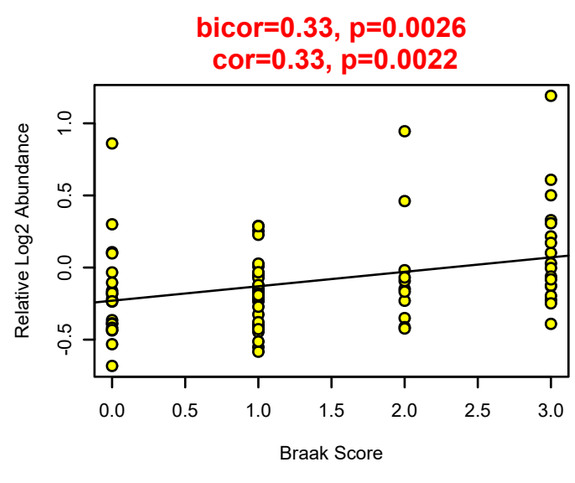

DYNC1H1 UPenn Mixed PRM
K-W ANOVA p: 0.009
Relative Log2 Abundance
Control
otherND
AD

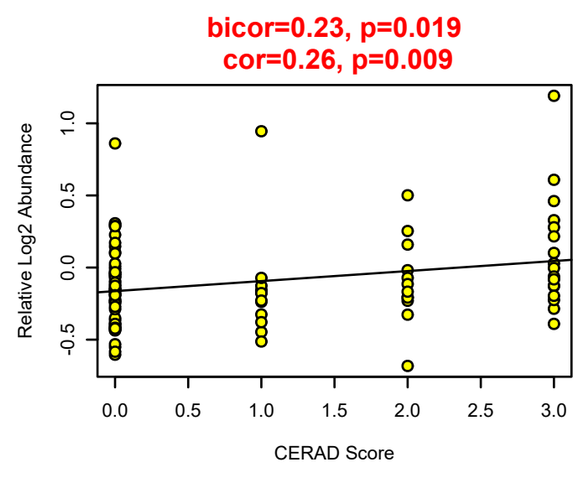

bicor=0.27, p=0.012
cor=0.27, p=0.013
Relative Log2 Abundance
Braak Score

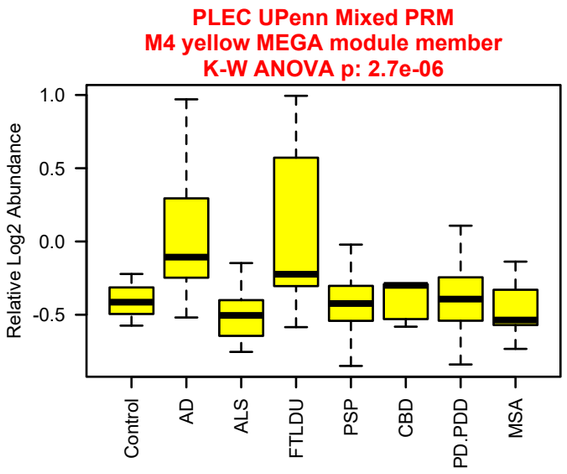

bicor=0.15, p=0.13
cor=0.19, p=0.058
Relative Log2 Abundance
CERAD Score

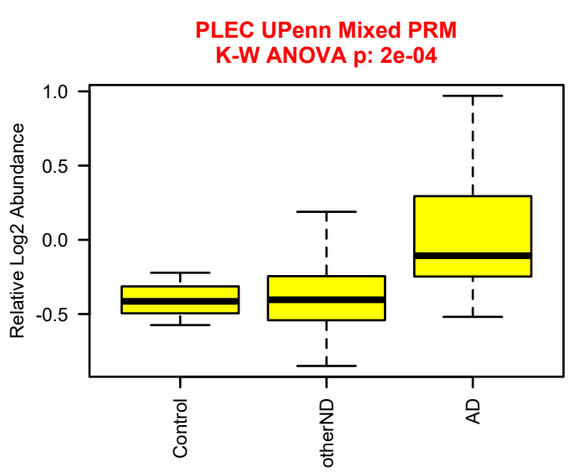

GNA13 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.00013
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

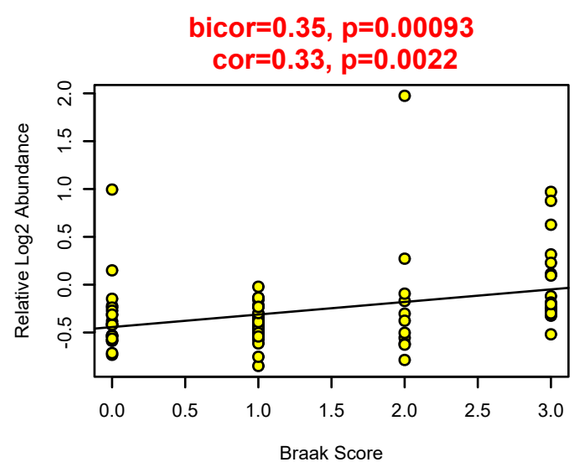

GNA13 UPenn Mixed PRM
K-W ANOVA p: 0.00052
Relative Log2 Abundance
Control
otherND
AD

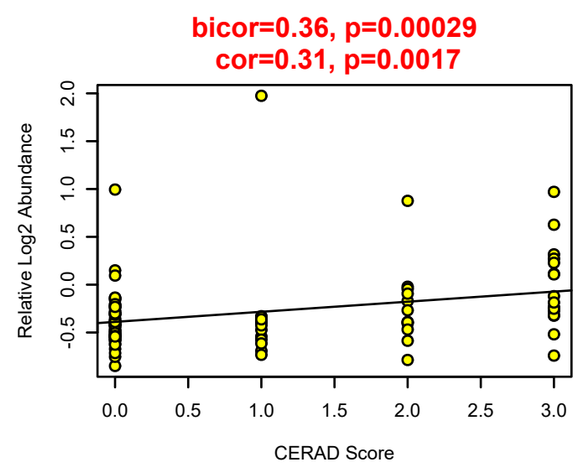

bicor=0.33, p=0.0026
cor=0.33, p=0.0022
Relative Log2 Abundance
Braak Score

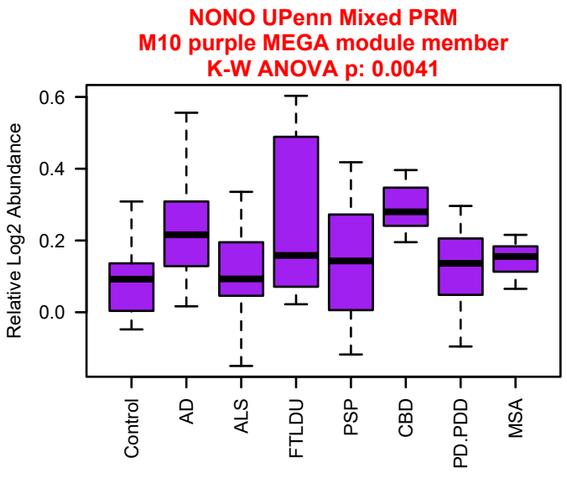

bicor=0.23, p=0.019
cor=0.26, p=0.009
Relative Log2 Abundance
CERAD Score

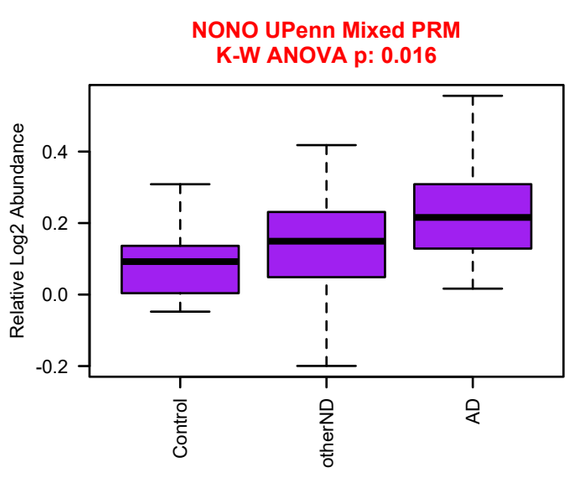

PLEC UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 2.7e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

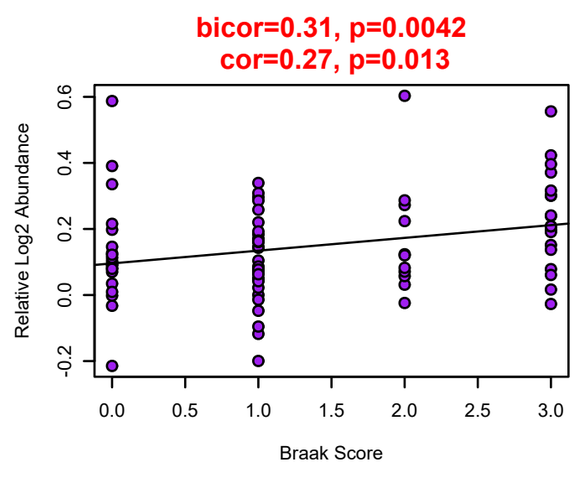

PLEC UPenn Mixed PRM
K-W ANOVA p: 2e-04
Relative Log2 Abundance
Control
otherND
AD

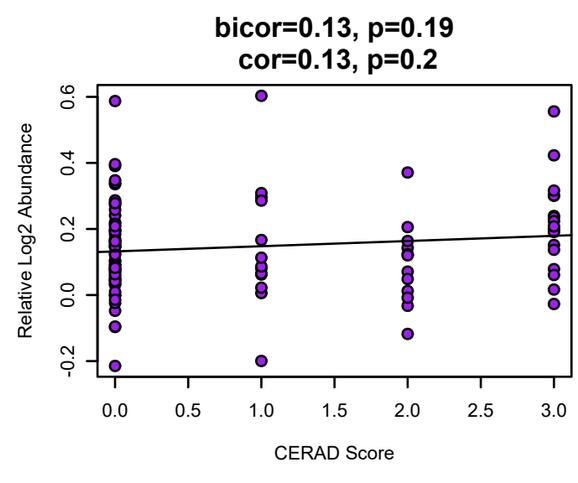

bicor=0.35, p=0.00093
cor=0.33, p=0.0022
Relative Log2 Abundance
Braak Score

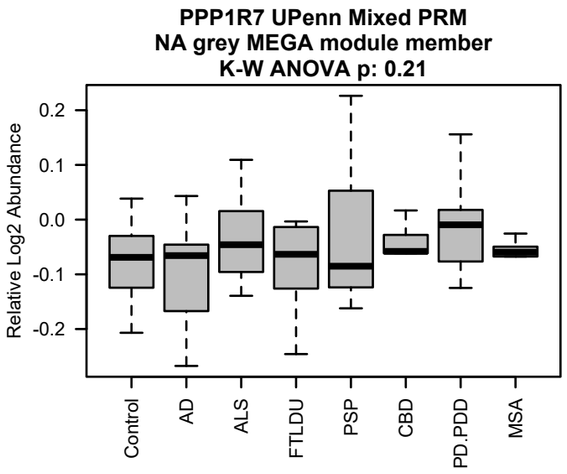

bicor=0.36, p=0.00029
cor=0.31, p=0.0017
Relative Log2 Abundance
CERAD Score

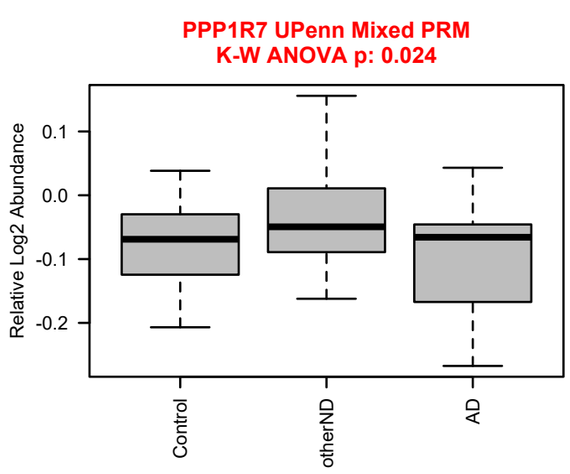

NONO UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.0041
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

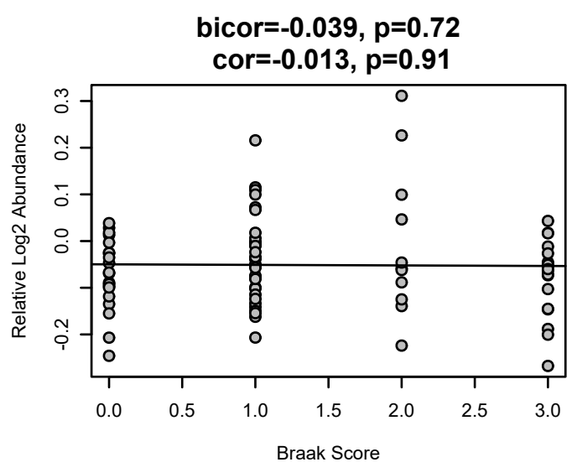

NONO UPenn Mixed PRM
K-W ANOVA p: 0.016
Relative Log2 Abundance
Control
otherND
AD

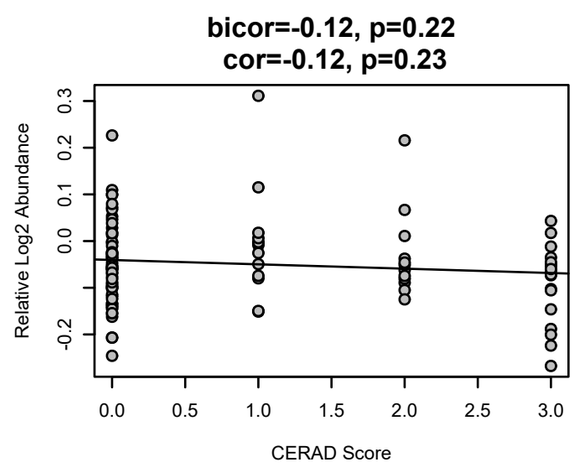

bicor=0.31, p=0.0042
cor=0.27, p=0.013
Relative Log2 Abundance
Braak Score

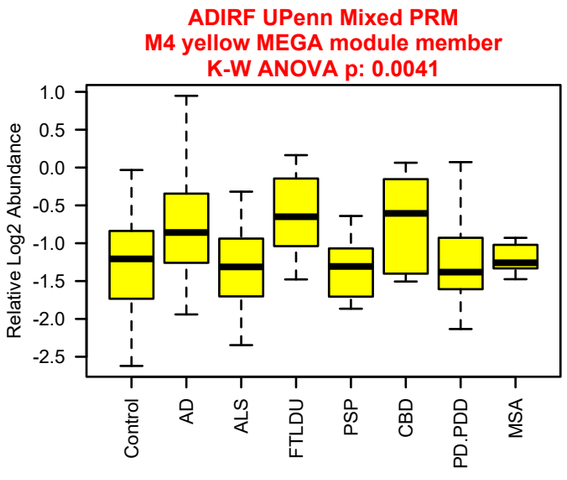

bicor=0.13, p=0.19
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

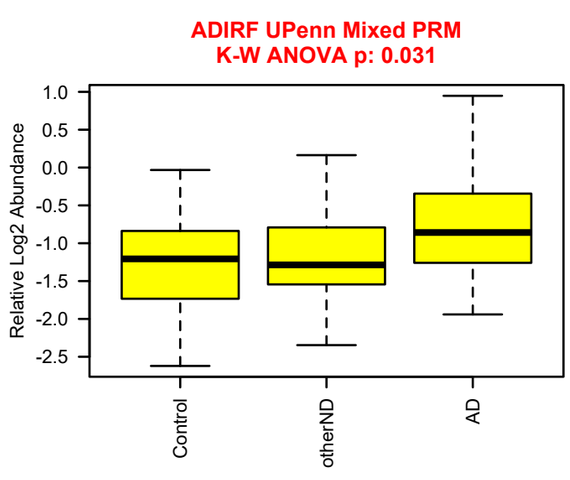

PPP1R7 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.21
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

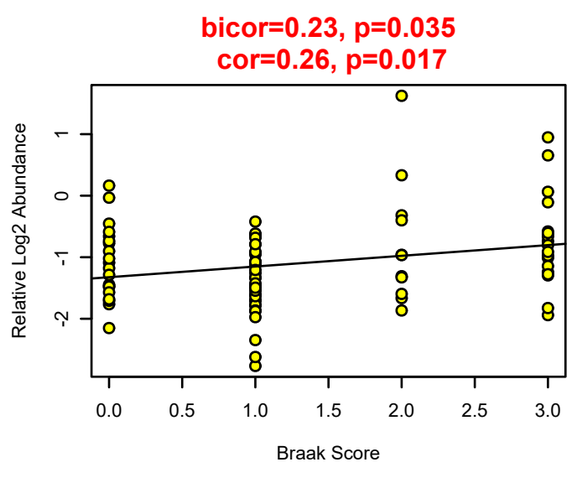

PPP1R7 UPenn Mixed PRM
K-W ANOVA p: 0.024
Relative Log2 Abundance
Control
otherND
AD

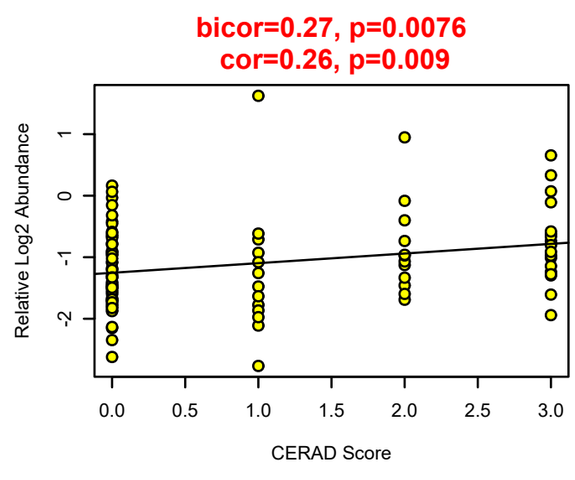

bicor=-0.039, p=0.72
cor=-0.013, p=0.91
Relative Log2 Abundance
Braak Score

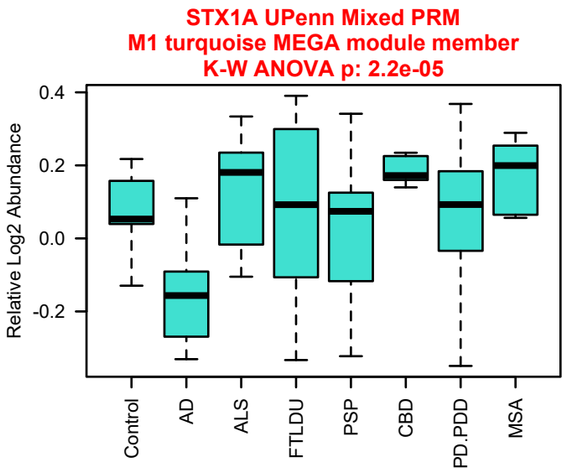

bicor=-0.12, p=0.22
cor=-0.12, p=0.23
Relative Log2 Abundance
CERAD Score

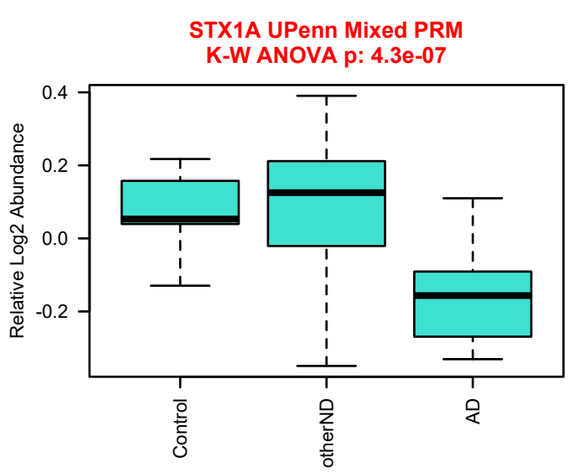

ADIRF UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.0041
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

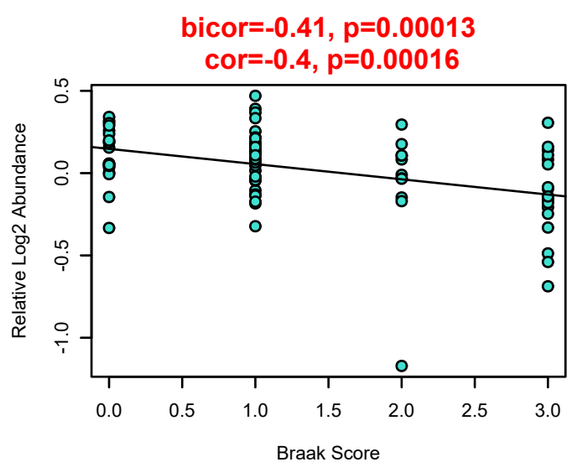

ADIRF UPenn Mixed PRM
K-W ANOVA p: 0.031
Relative Log2 Abundance
Control
otherND
AD

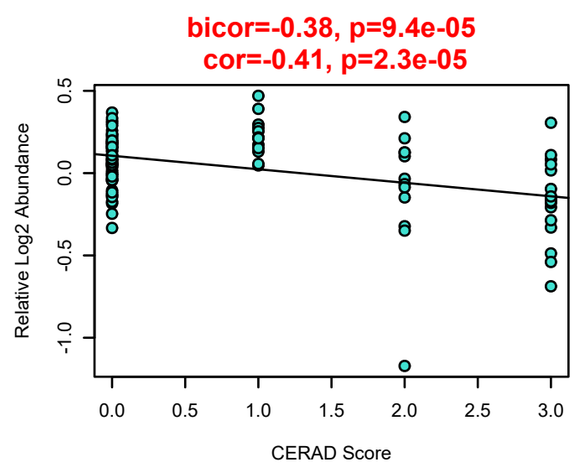

bicor=0.23, p=0.035
cor=0.26, p=0.017
Relative Log2 Abundance
Braak Score

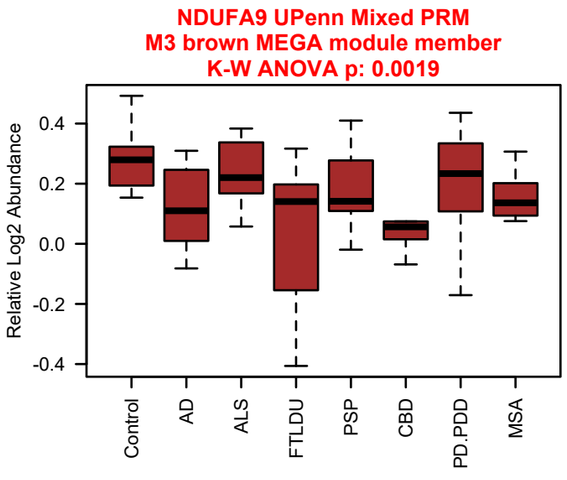

bicor=0.27, p=0.0076
cor=0.26, p=0.009
Relative Log2 Abundance
CERAD Score

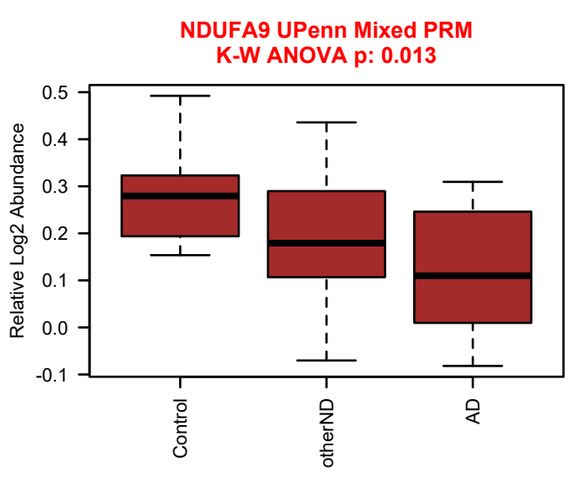

STX1A UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2.2e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

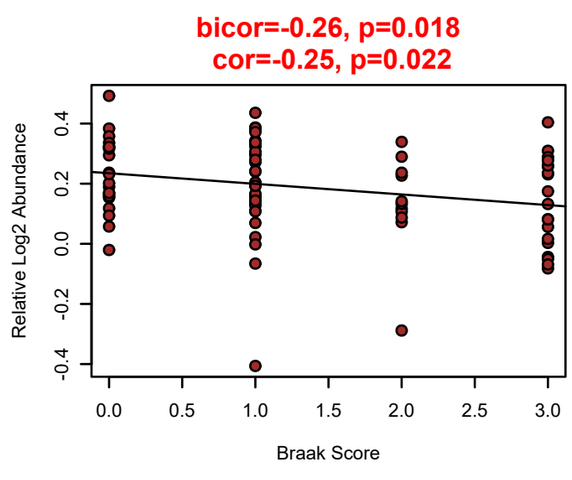

STX1A UPenn Mixed PRM
K-W ANOVA p: 4.3e-07
Relative Log2 Abundance
Control
otherND
AD

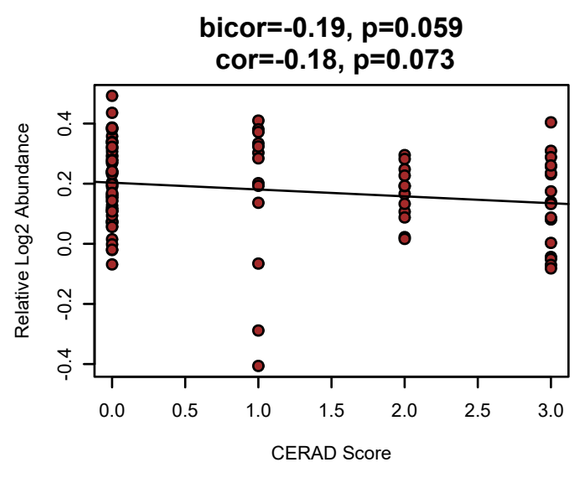

bicor=-0.41, p=0.00013
cor=-0.4, p=0.00016
Relative Log2 Abundance
Braak Score

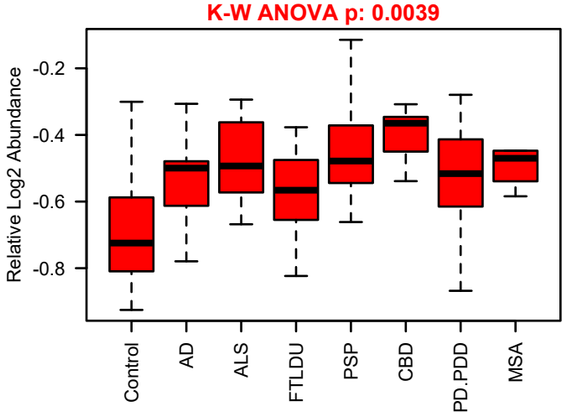

bicor=-0.38, p=9.4e-05
cor=-0.41, p=2.3e-05
Relative Log2 Abundance
CERAD Score

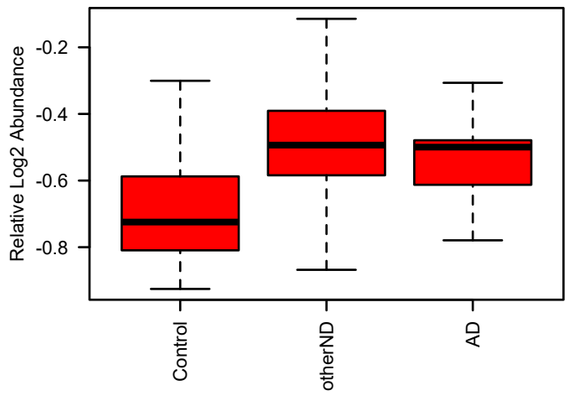

NDUFA9 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0019
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

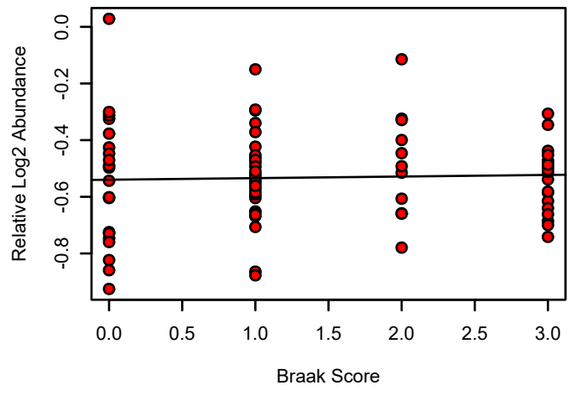

NDUFA9 UPenn Mixed PRM
K-W ANOVA p: 0.013
Relative Log2 Abundance
Control
otherND
AD

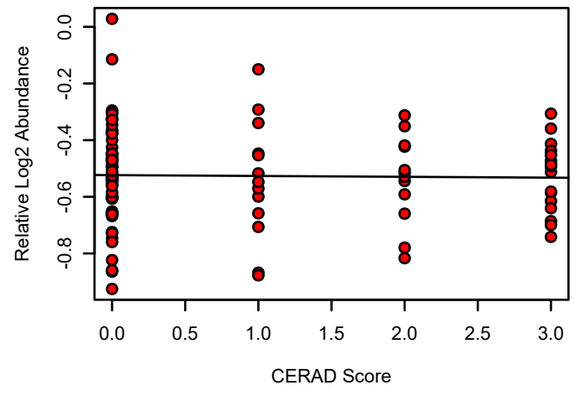

bicor=-0.26, p=0.018
cor=-0.25, p=0.022
Relative Log2 Abundance
Braak Score

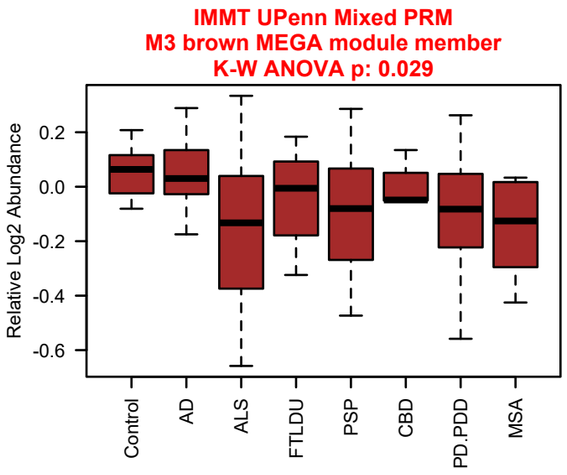

bicor=-0.19, p=0.059
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

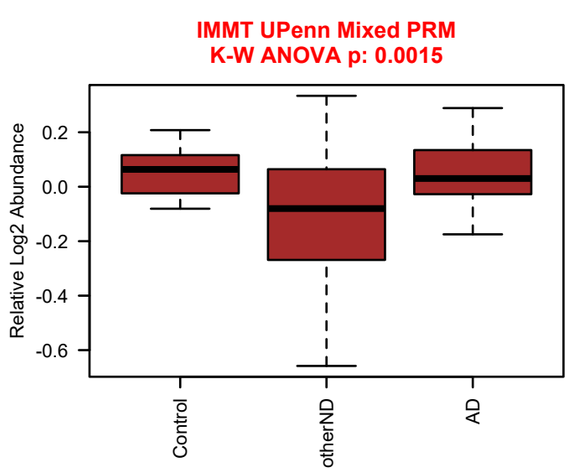

RTN1 UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.0039
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

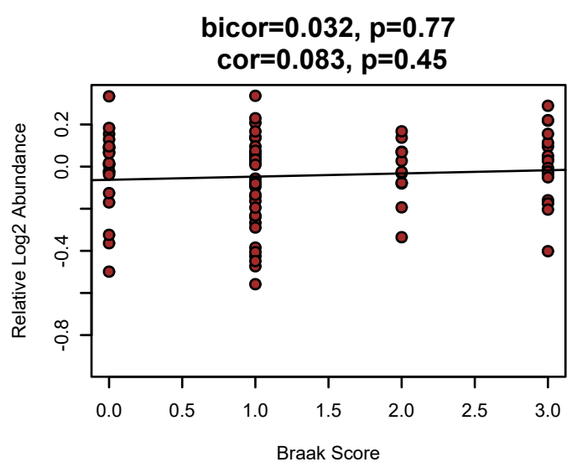

RTN1 UPenn Mixed PRM
K-W ANOVA p: 0.00056
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
Control
otherND
AD

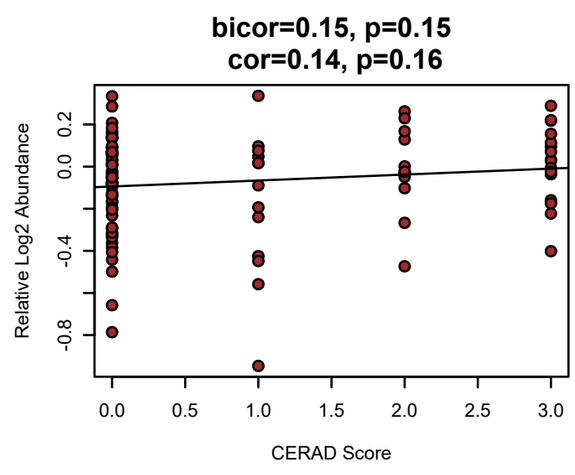

bicor=0.021, p=0.85
cor=0.036, p=0.75
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

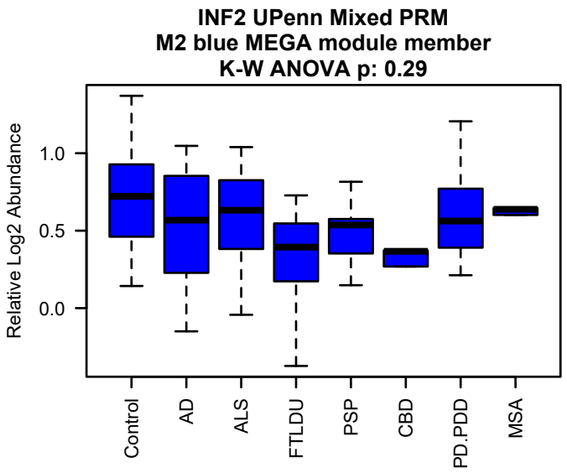

bicor=-0.011, p=0.91
cor=-0.021, p=0.84
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

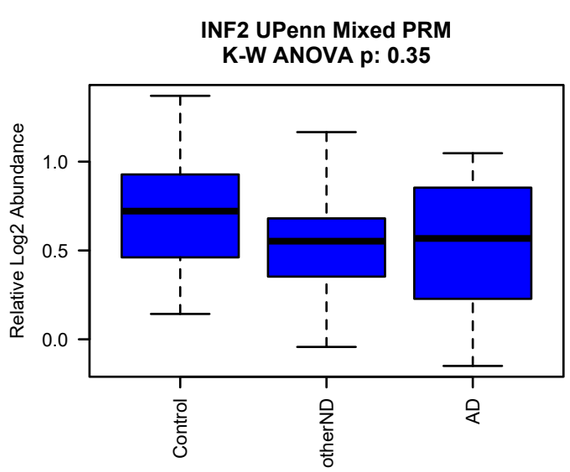

IMMT UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.029
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

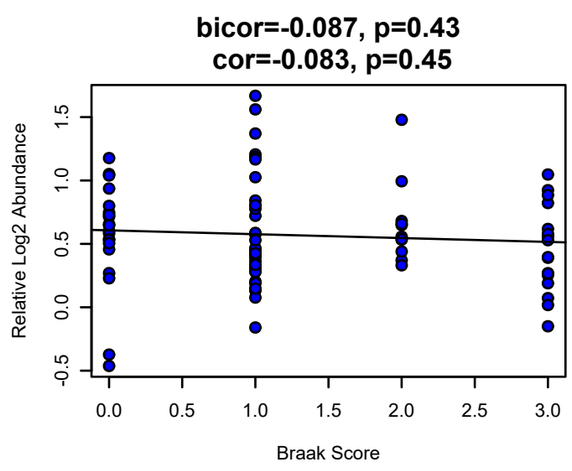

IMMT UPenn Mixed PRM
K-W ANOVA p: 0.0015
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
Control
otherND
AD

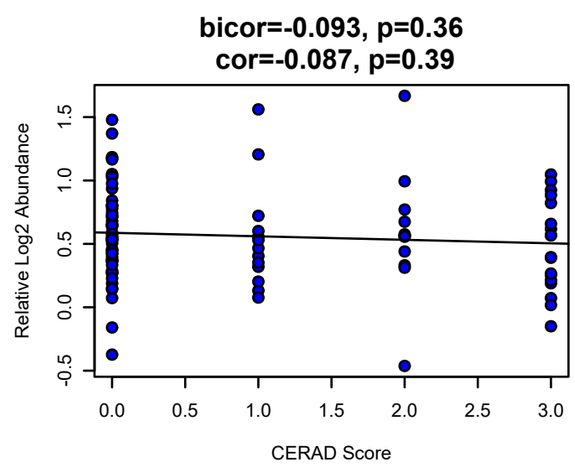

bicor=0.032, p=0.77
cor=0.083, p=0.45
Relative Log2 Abundance
0.2
0.0
-0.4
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

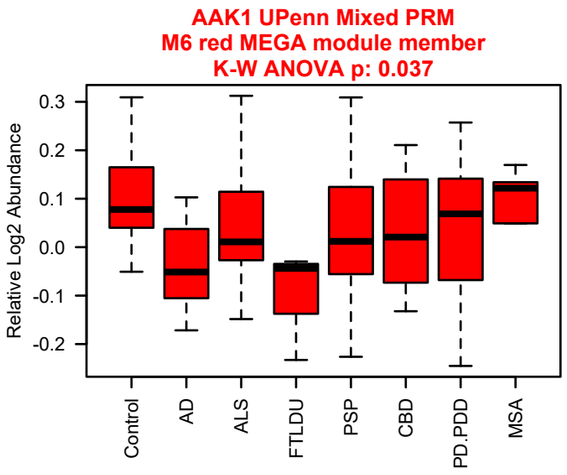

bicor=0.15, p=0.15
cor=0.14, p=0.16
Relative Log2 Abundance
0.2
0.0
-0.4
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

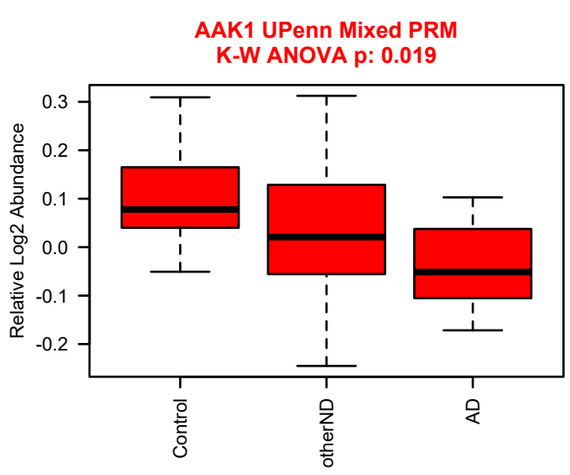

INF2 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.29
Relative Log2 Abundance
1.0
0.5
0.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

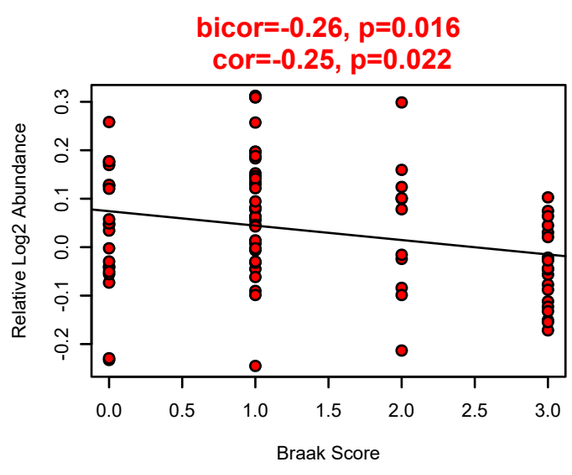

INF2 UPenn Mixed PRM
K-W ANOVA p: 0.35
Relative Log2 Abundance
1.0
0.5
0.0
Control
otherND
AD

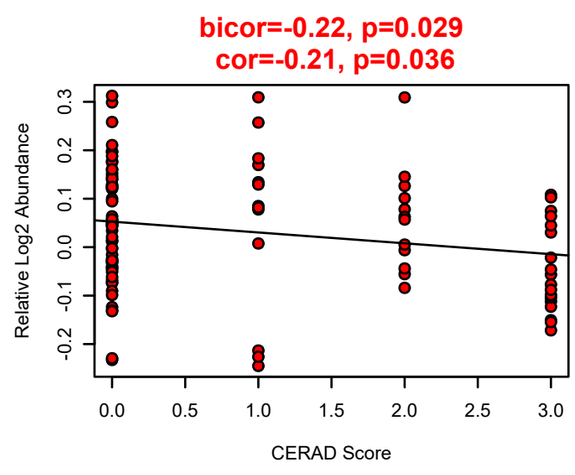

bicor=-0.087, p=0.43
cor=-0.083, p=0.45
Relative Log2 Abundance
1.5
1.0
0.5
0.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

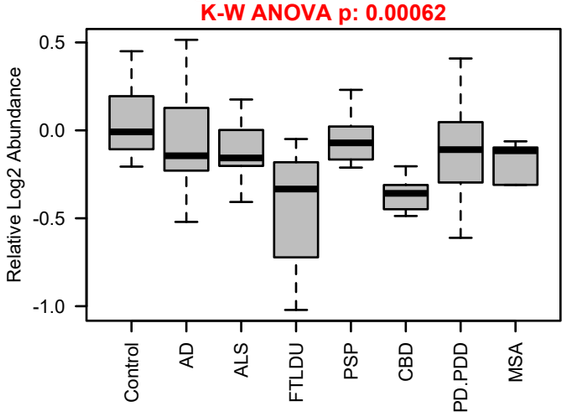

bicor=-0.093, p=0.36
cor=-0.087, p=0.39
Relative Log2 Abundance
1.5
1.0
0.5
0.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

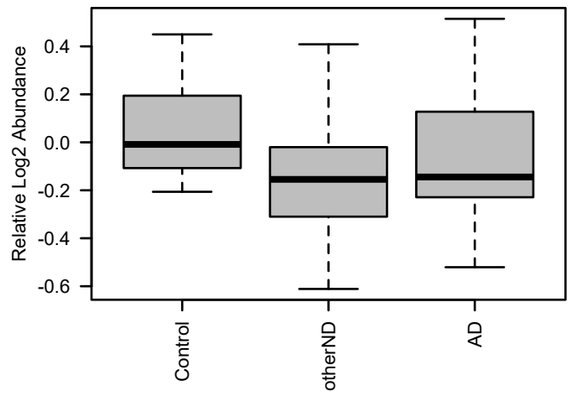

AAK1 UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.037
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
-0.2
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

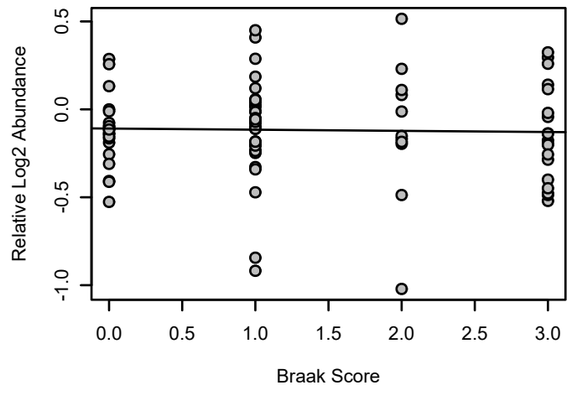

AAK1 UPenn Mixed PRM
K-W ANOVA p: 0.019
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
-0.2
Control
otherND
AD

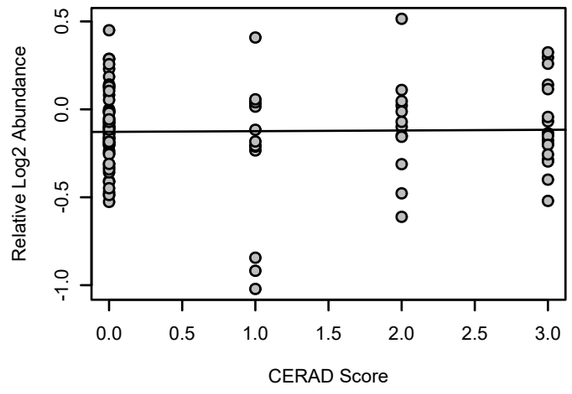

bicor=-0.26, p=0.016
cor=-0.25, p=0.022
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

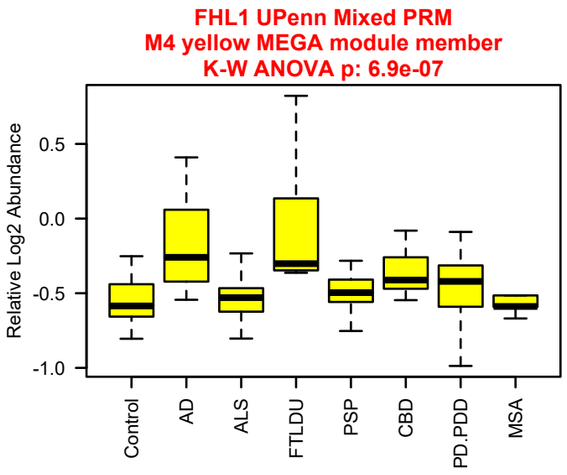

bicor=-0.22, p=0.029
cor=-0.21, p=0.036
Relative Log2 Abundance
0.3
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

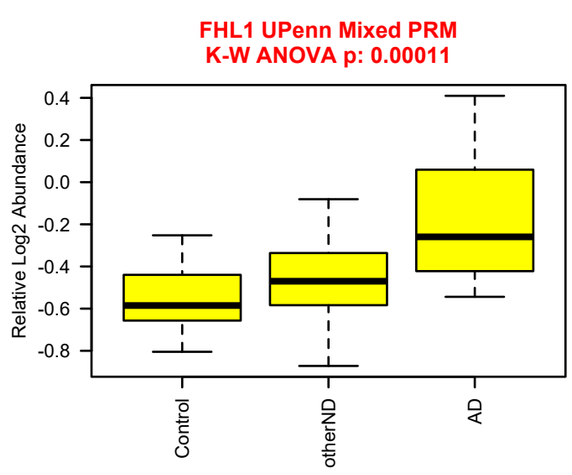

PREPL UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.00062
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

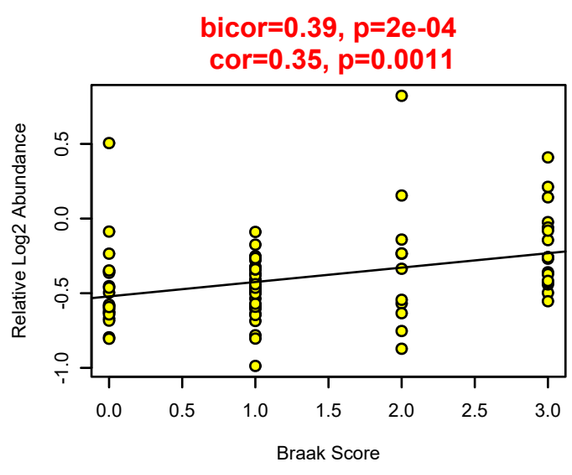

PREPL UPenn Mixed PRM
K-W ANOVA p: 0.0089
Relative Log2 Abundance
Control
otherND
AD

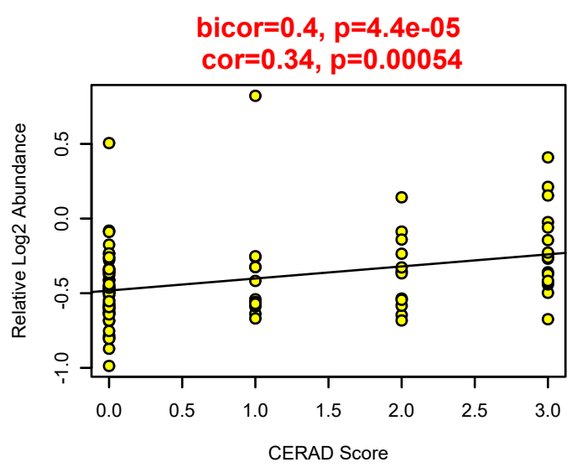

bicor=-0.015, p=0.89
cor=-0.026, p=0.81
Relative Log2 Abundance
Braak Score

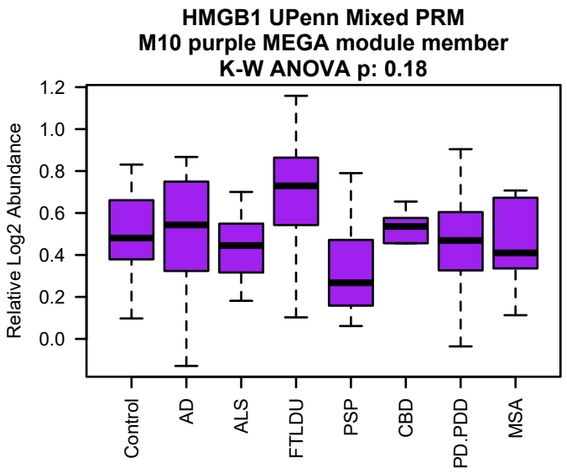

bicor=0.016, p=0.87
cor=0.017, p=0.87
Relative Log2 Abundance
CERAD Score

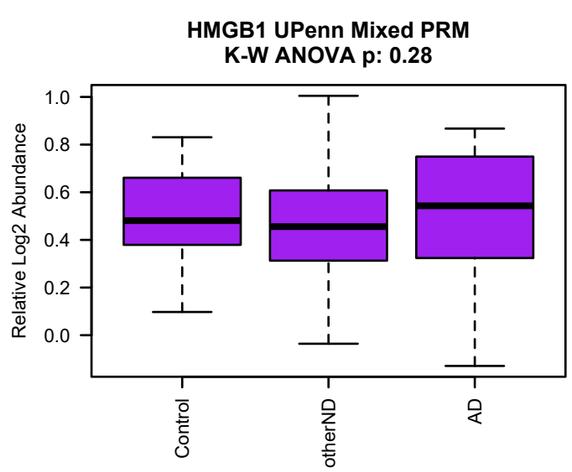

FHL1 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 6.9e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

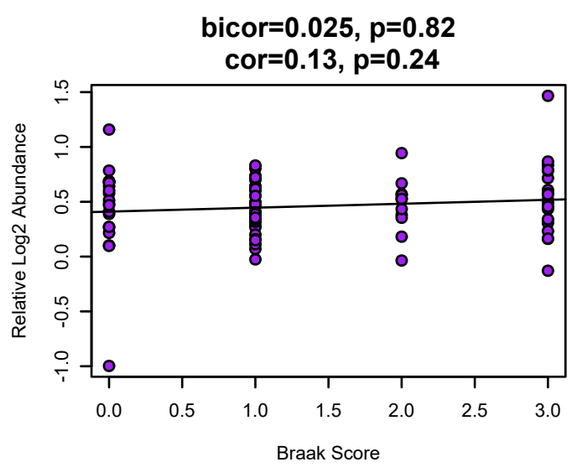

FHL1 UPenn Mixed PRM
K-W ANOVA p: 0.00011
Relative Log2 Abundance
Control
otherND
AD

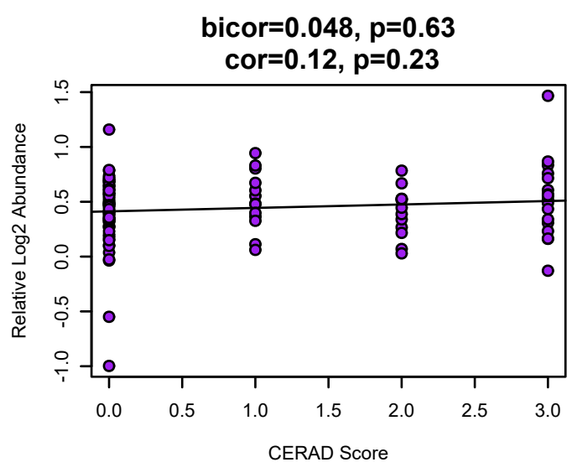

bicor=0.39, p=2e-04
cor=0.35, p=0.0011
Relative Log2 Abundance
Braak Score

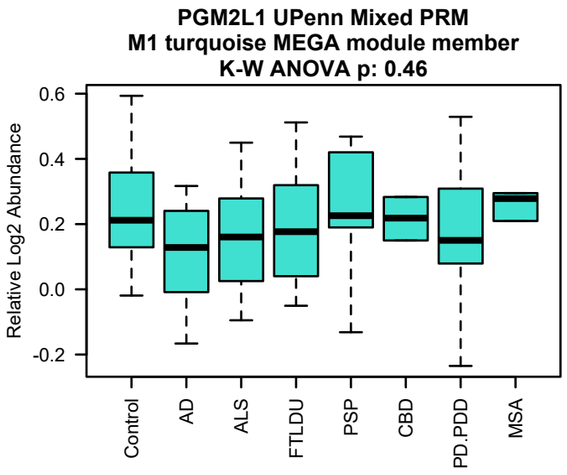

bicor=0.4, p=4.4e-05
cor=0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

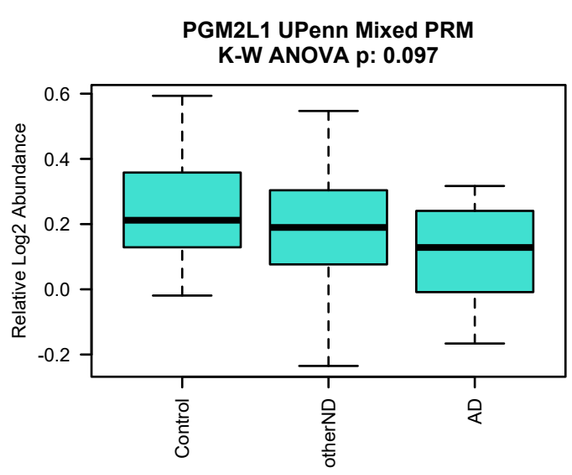

HMGB1 UPenn Mixed PRM
M10 purple MEGA module member
K-W ANOVA p: 0.18
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

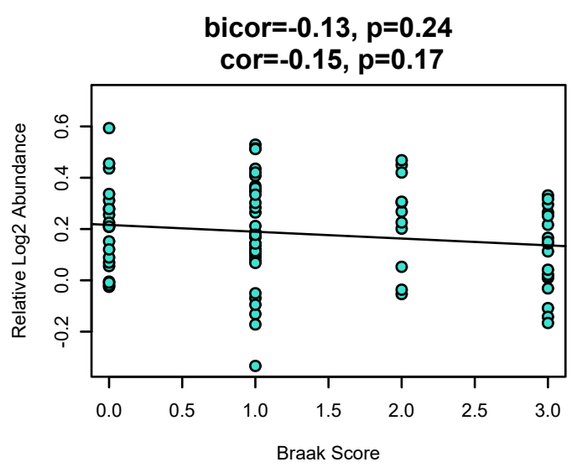

HMGB1 UPenn Mixed PRM
K-W ANOVA p: 0.28
Relative Log2 Abundance
Control
otherND
AD

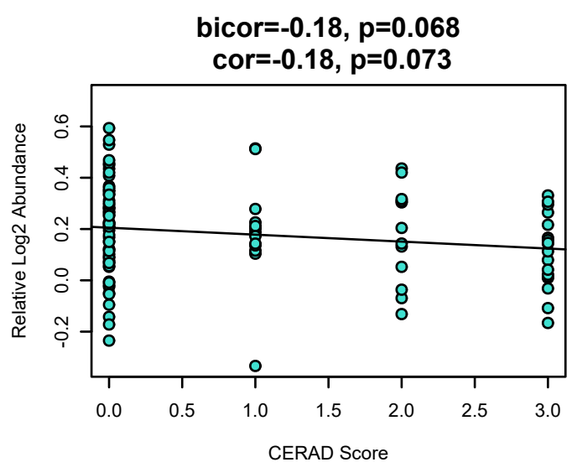

bicor=0.025, p=0.82
cor=0.13, p=0.24
Relative Log2 Abundance
Braak Score

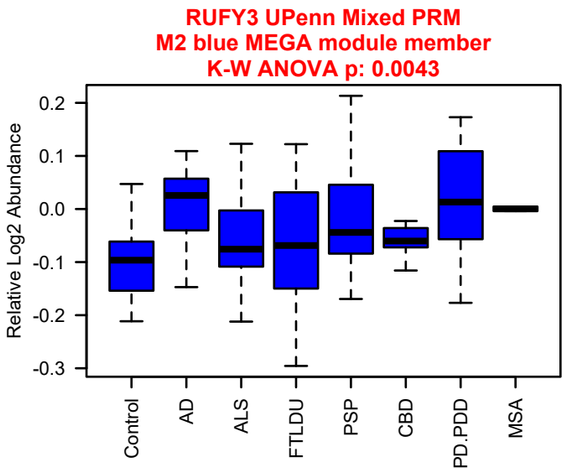

bicor=0.048, p=0.63
cor=0.12, p=0.23
Relative Log2 Abundance
CERAD Score

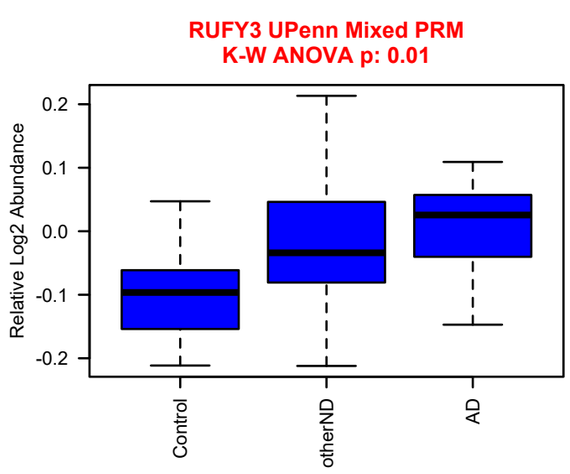

PGM2L1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.46
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

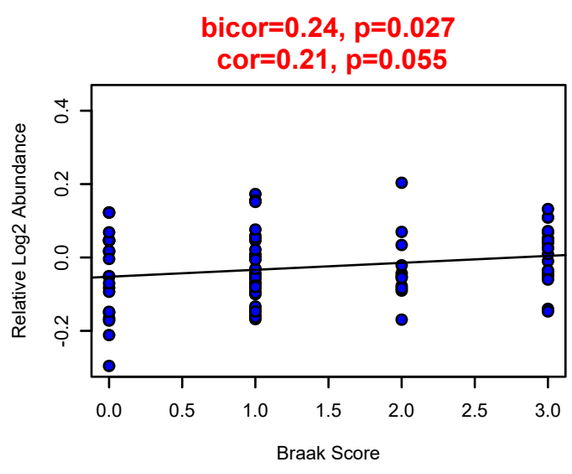

PGM2L1 UPenn Mixed PRM
K-W ANOVA p: 0.097
Relative Log2 Abundance
Control
otherND
AD

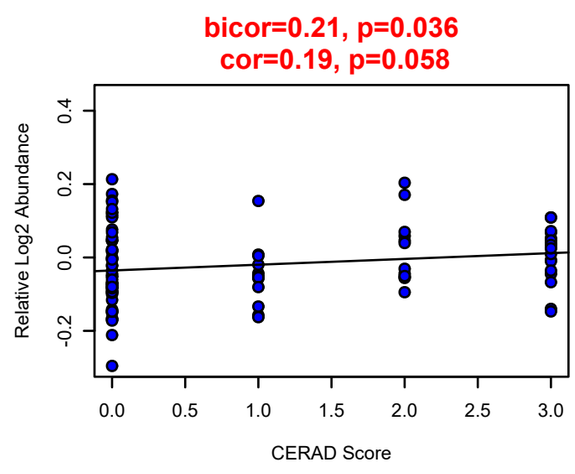

bicor=-0.13, p=0.24
cor=-0.15, p=0.17
Relative Log2 Abundance
Braak Score

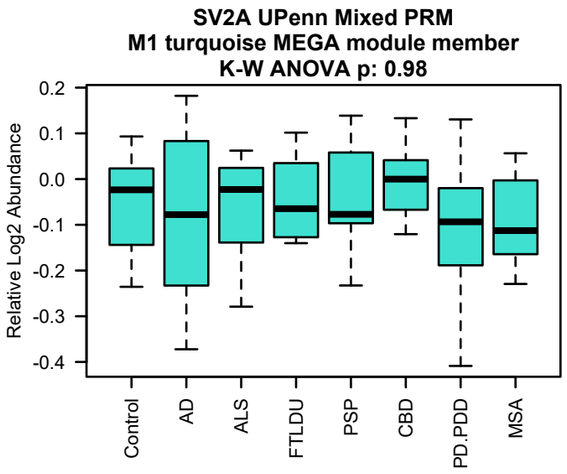

bicor=-0.18, p=0.068
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

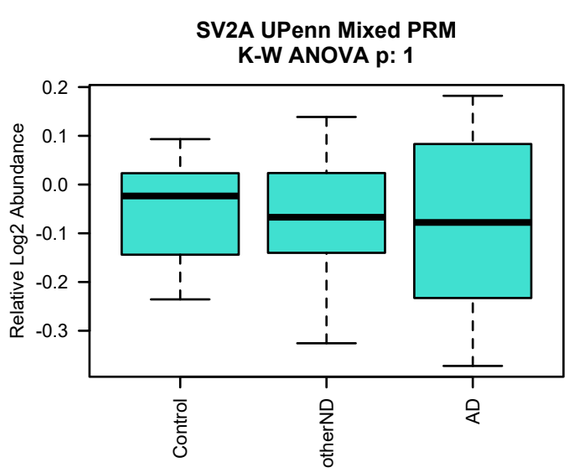

RUFY3 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.0043
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

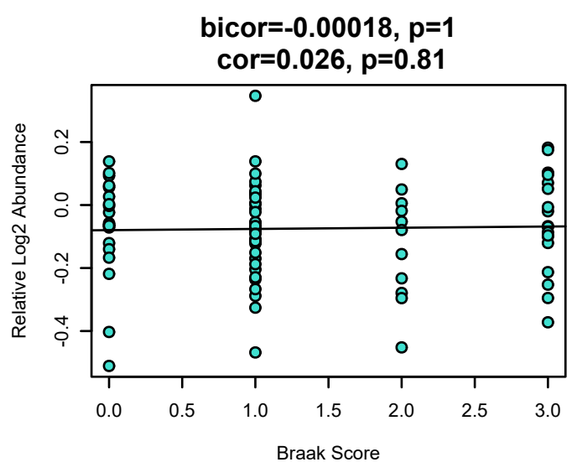

RUFY3 UPenn Mixed PRM
K-W ANOVA p: 0.01
Relative Log2 Abundance
Control
otherND
AD

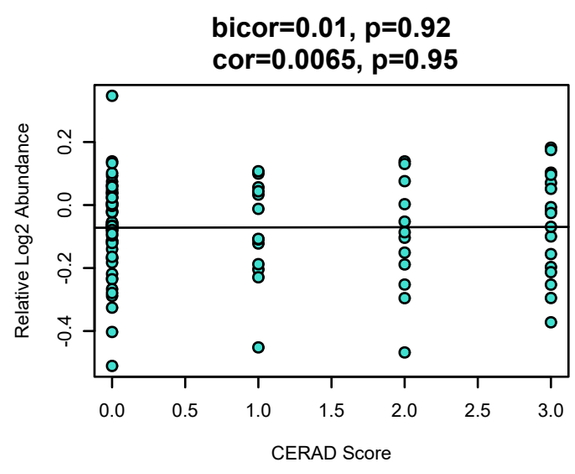

bicor=0.24, p=0.027
cor=0.21, p=0.055
Relative Log2 Abundance
Braak Score

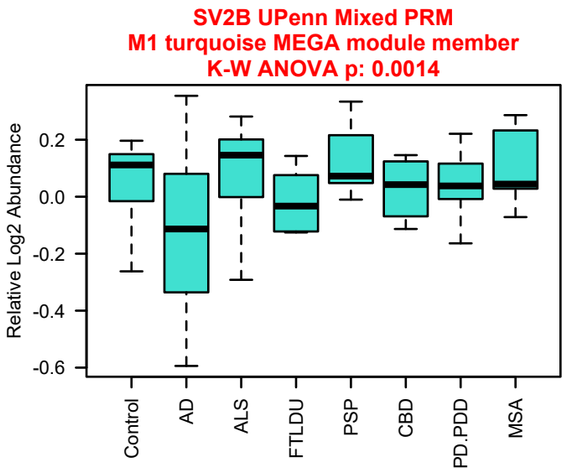

bicor=0.21, p=0.036
cor=0.19, p=0.058
Relative Log2 Abundance
CERAD Score

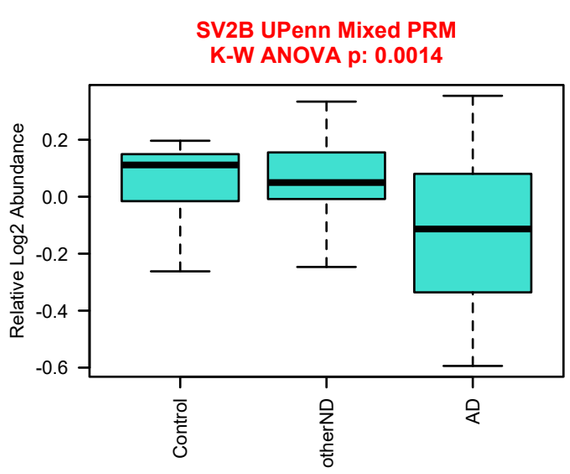

SV2A UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.98
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

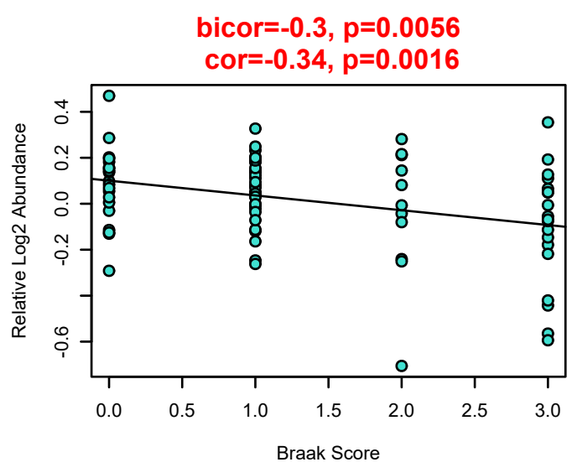

SV2A UPenn Mixed PRM
K-W ANOVA p: 1
Relative Log2 Abundance
Control
otherND
AD

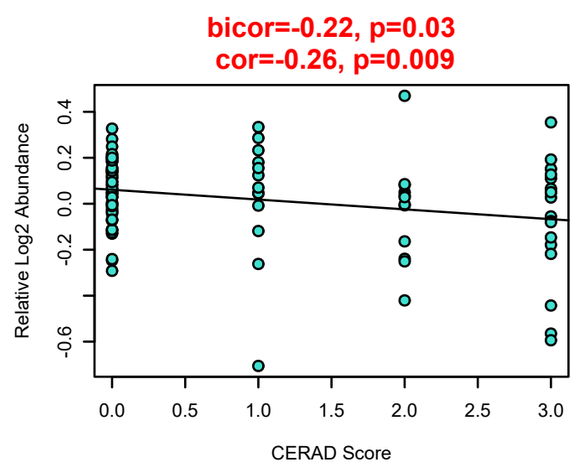

bicor=-0.00018, p=1
cor=0.026, p=0.81
Relative Log2 Abundance
Braak Score

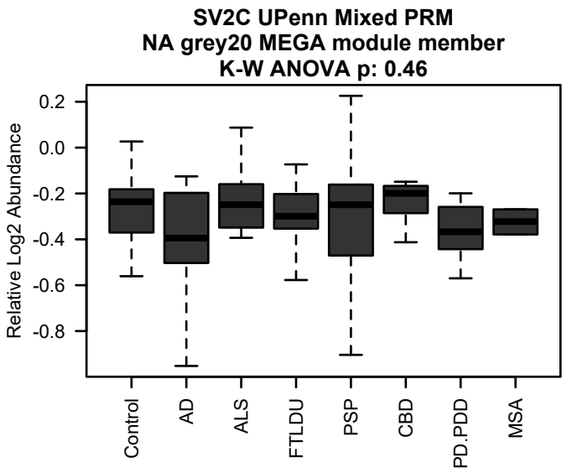

bicor=0.01, p=0.92
cor=0.0065, p=0.95
Relative Log2 Abundance
CERAD Score

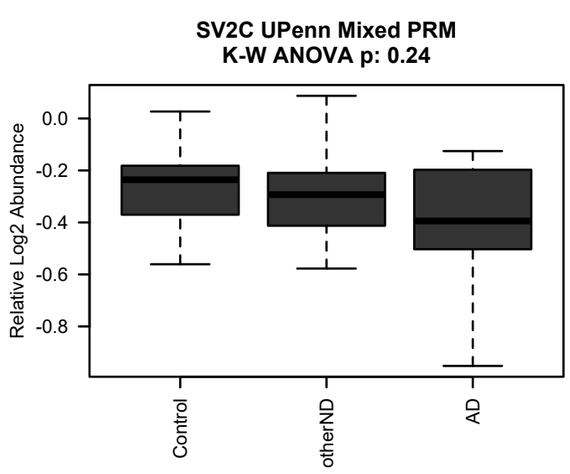

SV2B UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0014
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

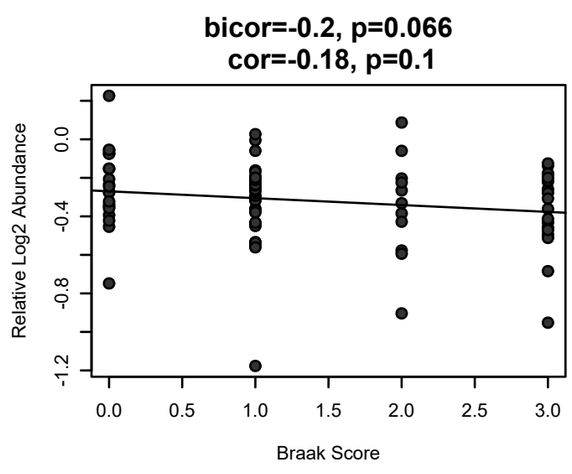

SV2B UPenn Mixed PRM
K-W ANOVA p: 0.0014
Relative Log2 Abundance
Control
otherND
AD

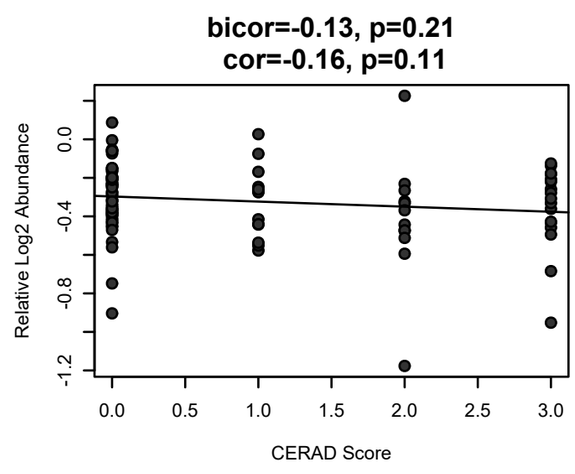

bicor=-0.3, p=0.0056
cor=-0.34, p=0.0016
Relative Log2 Abundance
Braak Score

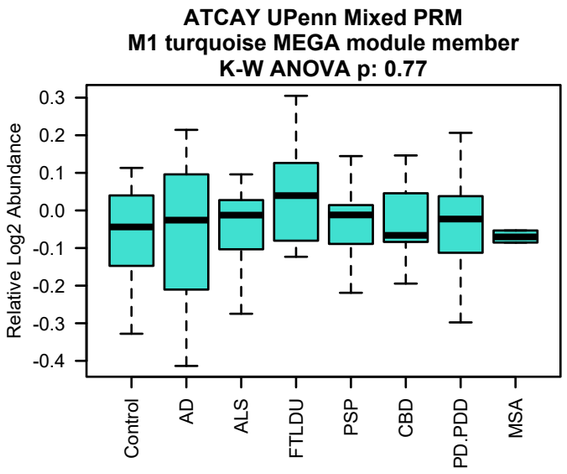

bicor=-0.22, p=0.03
cor=-0.26, p=0.009
Relative Log2 Abundance
CERAD Score

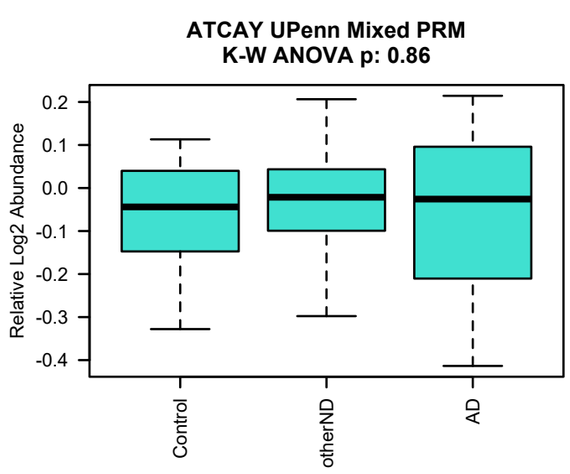

SV2C UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.46
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

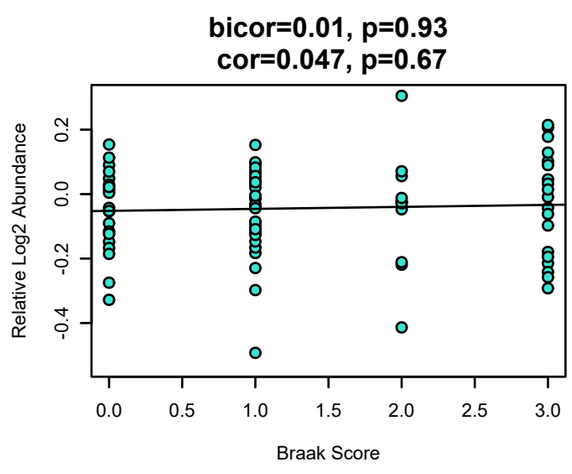

SV2C UPenn Mixed PRM
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
otherND
AD

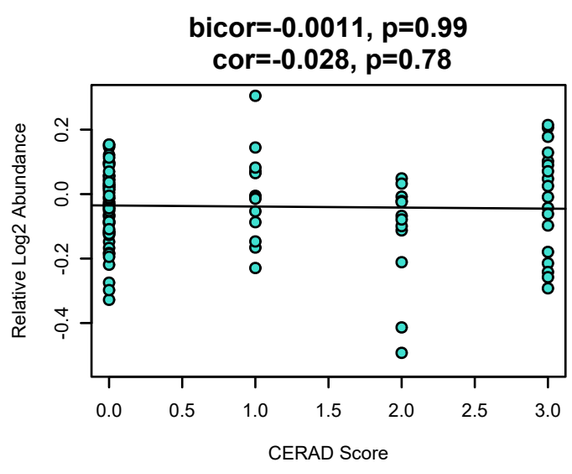

bicor=-0.2, p=0.066
cor=-0.18, p=0.1
Relative Log2 Abundance
Braak Score

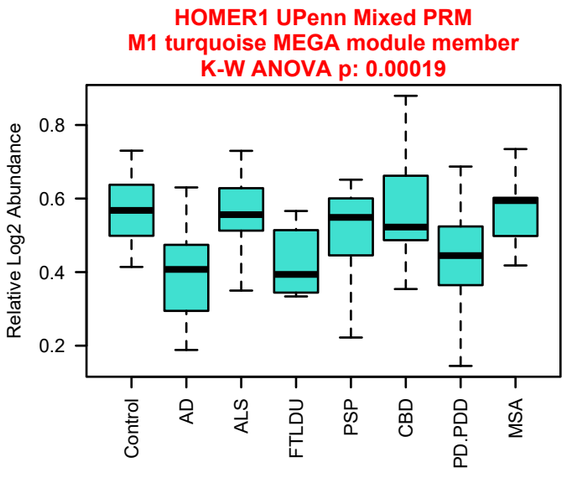

bicor=-0.13, p=0.21
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

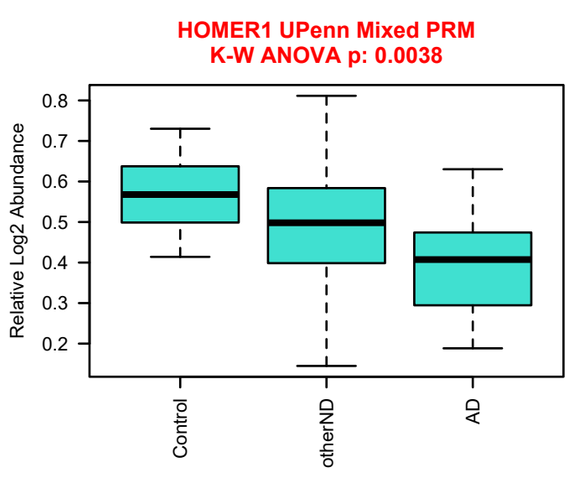

ATCAY UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.77
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

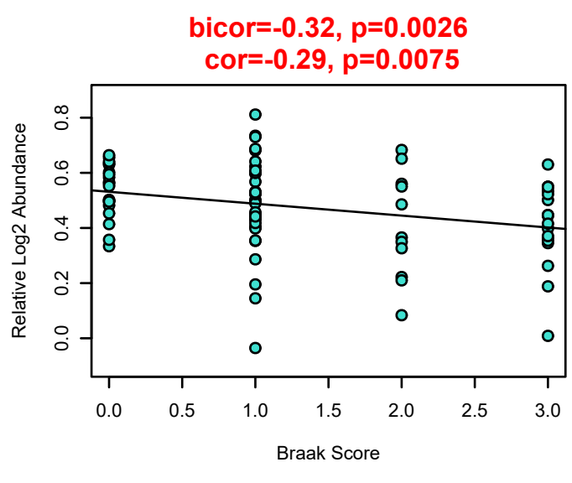

ATCAY UPenn Mixed PRM
K-W ANOVA p: 0.86
Relative Log2 Abundance
Control
otherND
AD

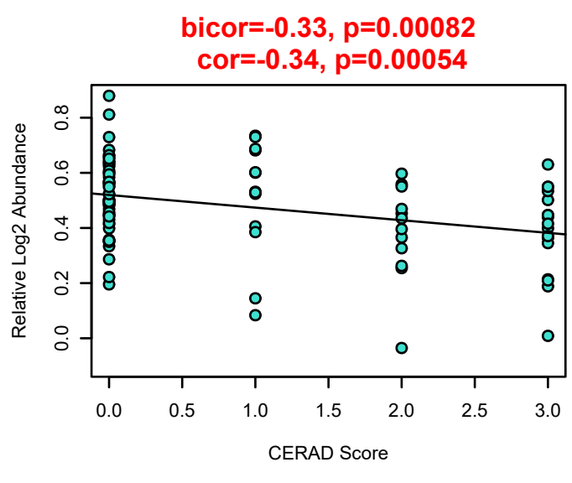

bicor=0.01, p=0.93
cor=0.047, p=0.67
Relative Log2 Abundance
Braak Score

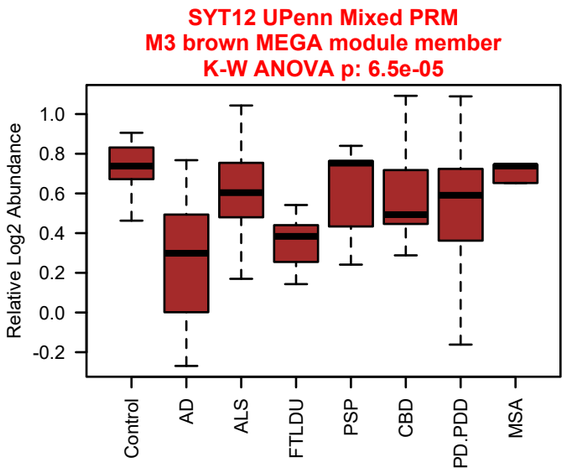

bicor=-0.0011, p=0.99
cor=-0.028, p=0.78
Relative Log2 Abundance
CERAD Score

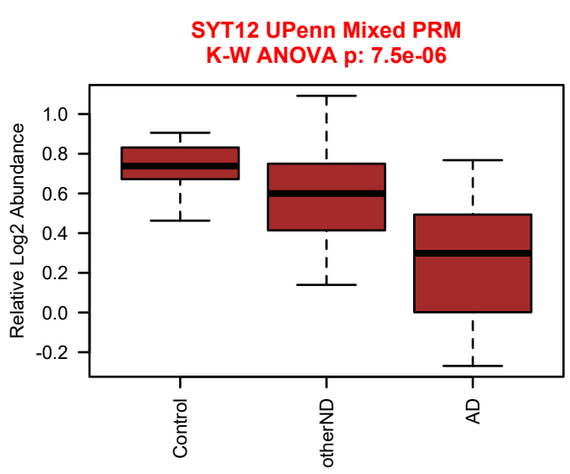

HOMER1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00019
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

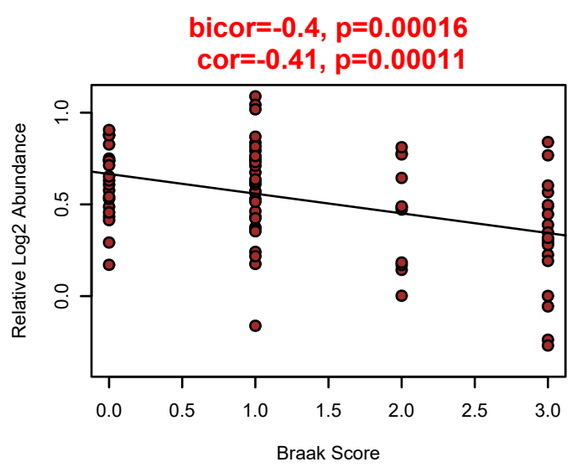

HOMER1 UPenn Mixed PRM
K-W ANOVA p: 0.0038
Relative Log2 Abundance
Control
otherND
AD

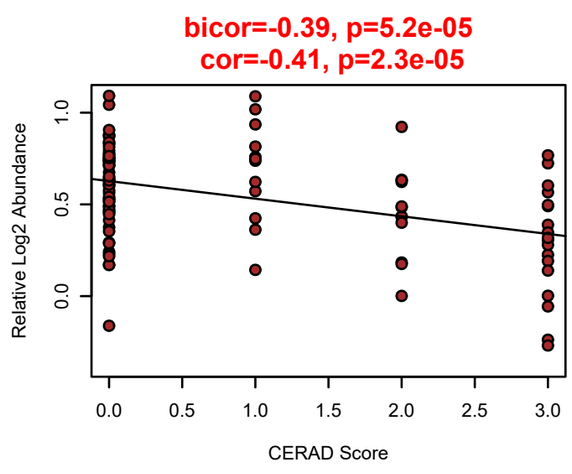

bicor=-0.32, p=0.0026
cor=-0.29, p=0.0075
Relative Log2 Abundance
Braak Score

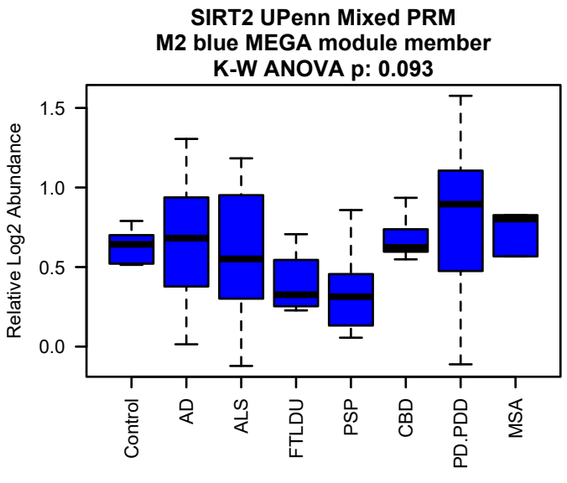

bicor=-0.33, p=0.00082
cor=-0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

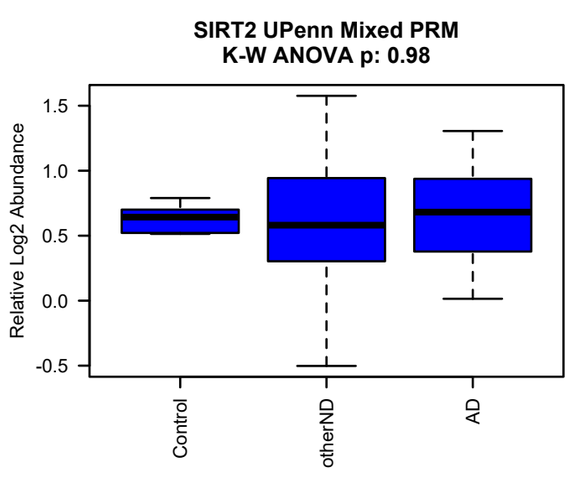

SYT12 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 6.5e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

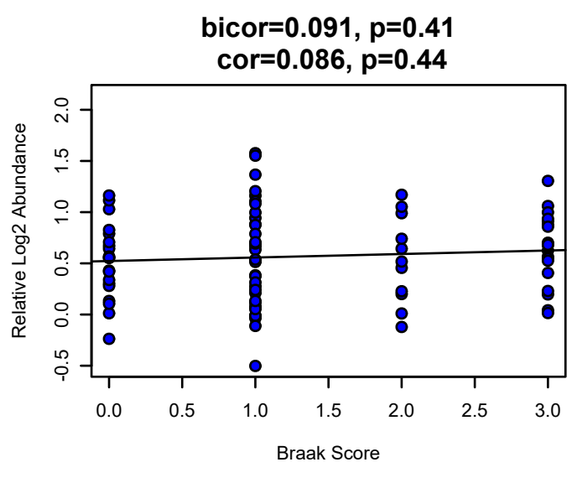

SYT12 UPenn Mixed PRM
K-W ANOVA p: 7.5e-06
Relative Log2 Abundance
Control
otherND
AD

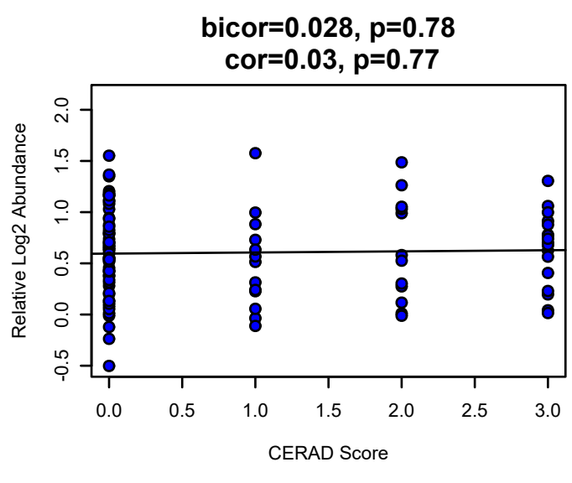

bicor=-0.4, p=0.00016
cor=-0.41, p=0.00011
Relative Log2 Abundance
Braak Score

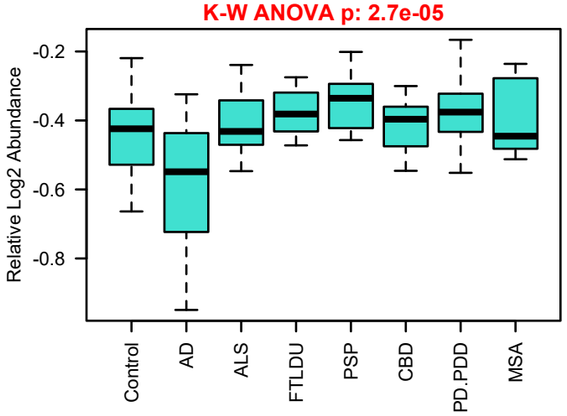

bicor=-0.39, p=5.2e-05
cor=-0.41, p=2.3e-05
Relative Log2 Abundance
CERAD Score

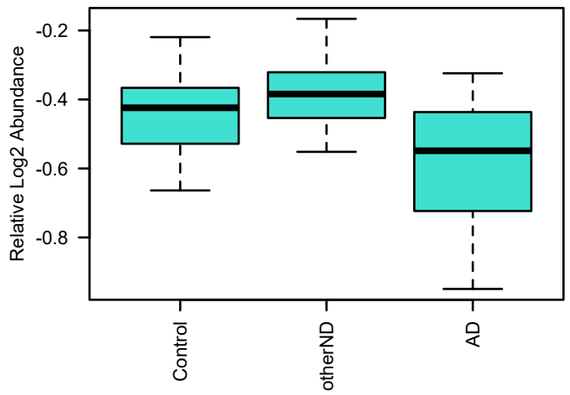

SIRT2 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.093
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

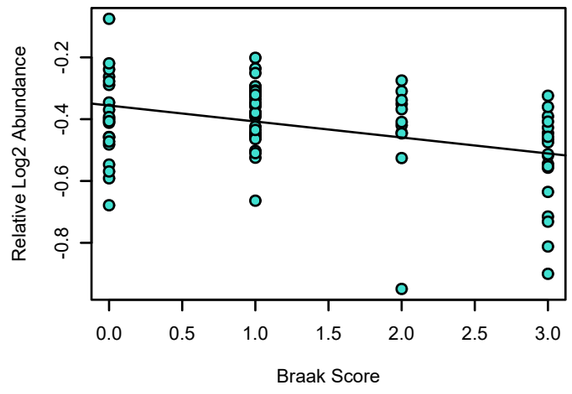

SIRT2 UPenn Mixed PRM
K-W ANOVA p: 0.98
Relative Log2 Abundance
Control
otherND
AD

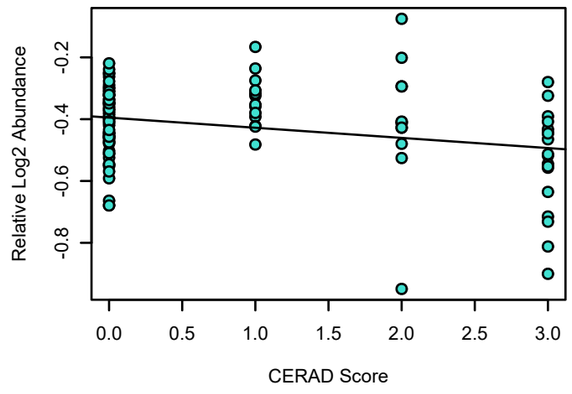

bicor=0.091, p=0.41
cor=0.086, p=0.44
Relative Log2 Abundance
Braak Score

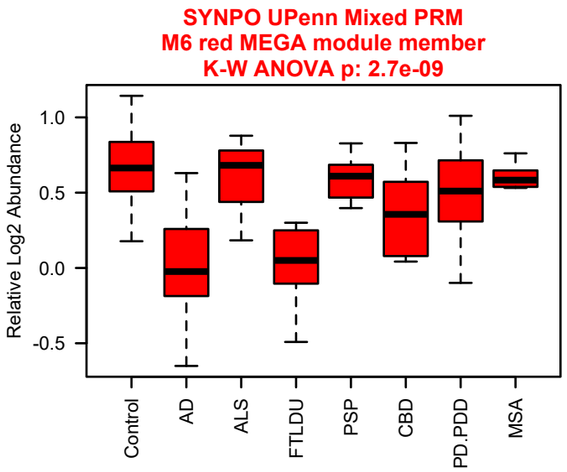

bicor=0.028, p=0.78
cor=0.03, p=0.77
Relative Log2 Abundance
CERAD Score

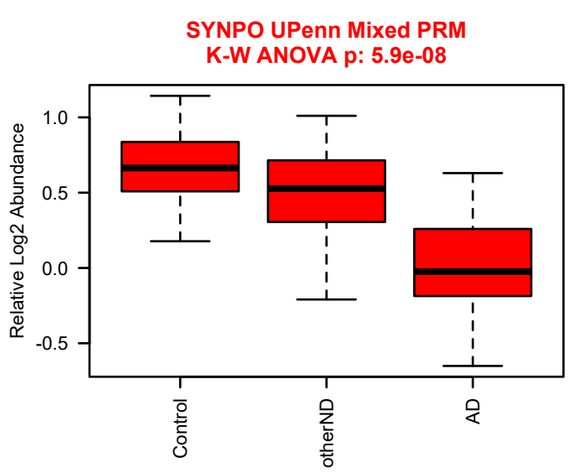

CADM3 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2.7e-05
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

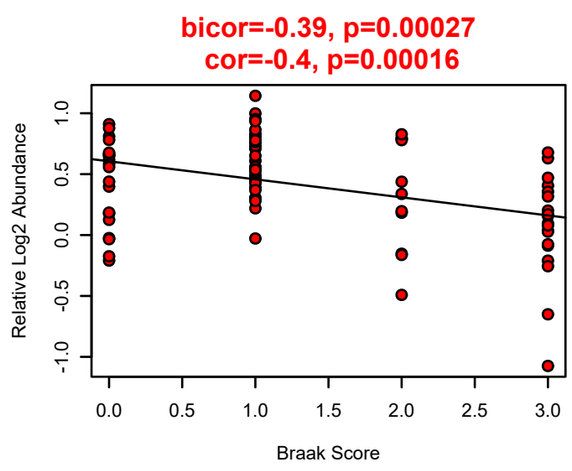

CADM3 UPenn Mixed PRM
K-W ANOVA p: 1.9e-07
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
Control
otherND
AD

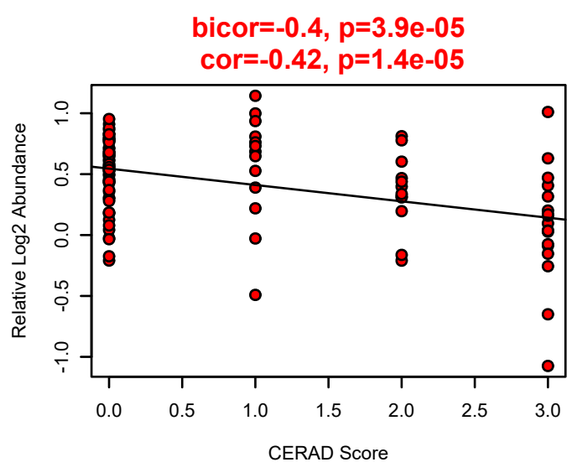

bicor=-0.34, p=0.0014
cor=-0.38, p=0.00036
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

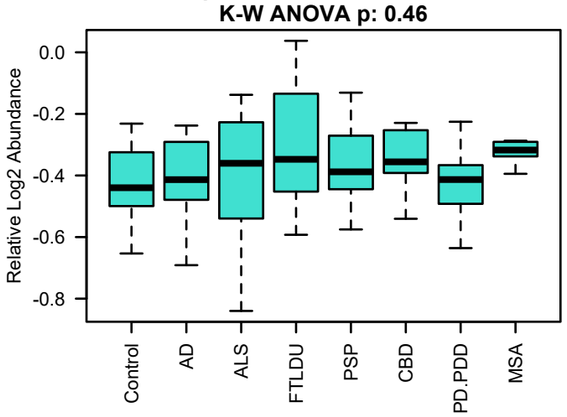

bicor=-0.23, p=0.021
cor=-0.27, p=0.0066
Relative Log2 Abundance
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

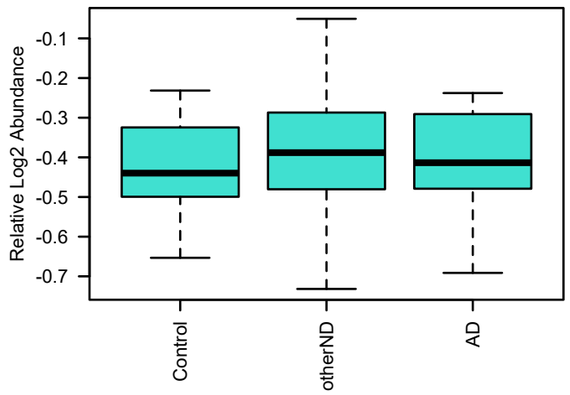

SYNPO UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 2.7e-09
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

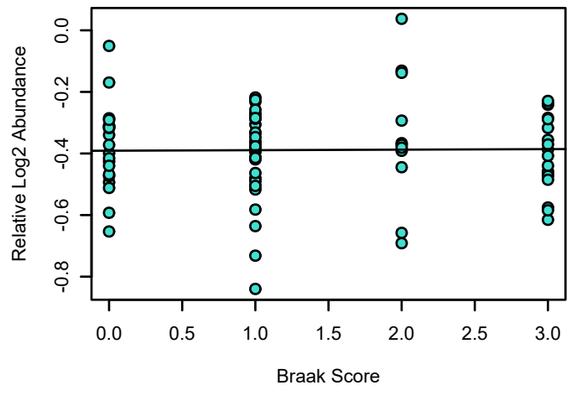

SYNPO UPenn Mixed PRM
K-W ANOVA p: 5.9e-08
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
Control
otherND
AD

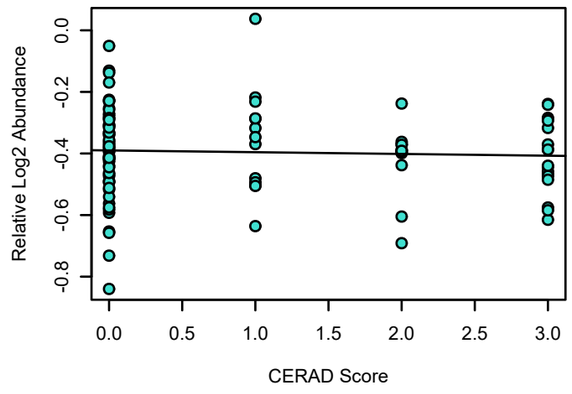

bicor=-0.39, p=0.00027
cor=-0.4, p=0.00016
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
-1.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

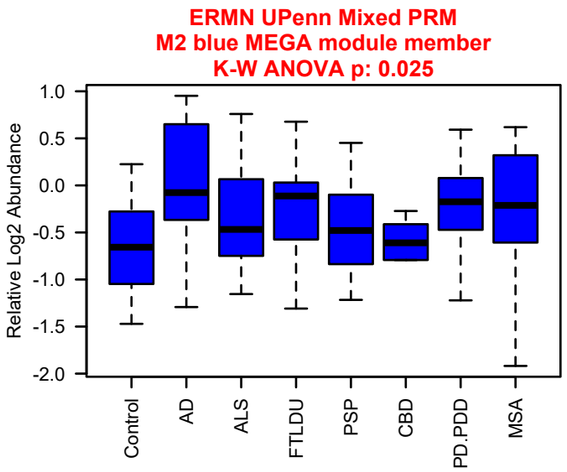

bicor=-0.4, p=3.9e-05
cor=-0.42, p=1.4e-05
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
-1.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

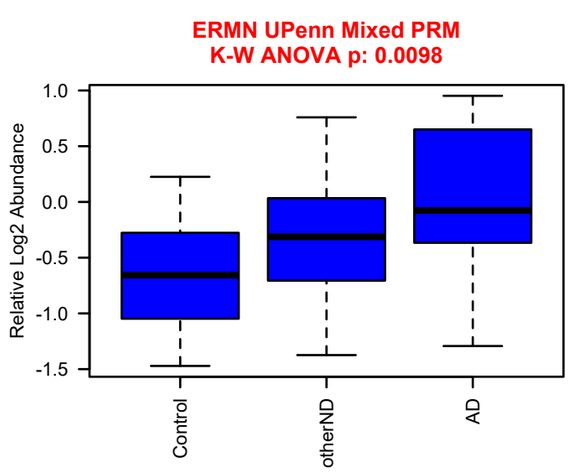

DPP10 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.46
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
-0.8
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

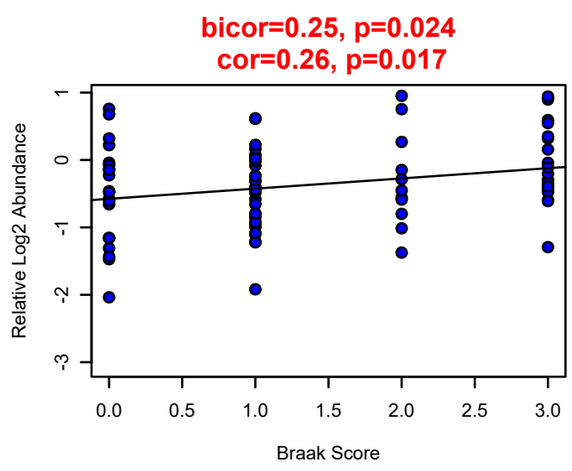

DPP10 UPenn Mixed PRM
K-W ANOVA p: 0.62
Relative Log2 Abundance
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
Control
otherND
AD

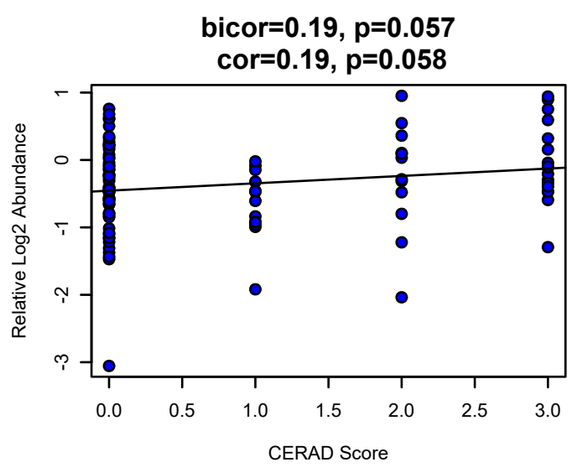

bicor=-8.1e-05, p=1
cor=0.013, p=0.91
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

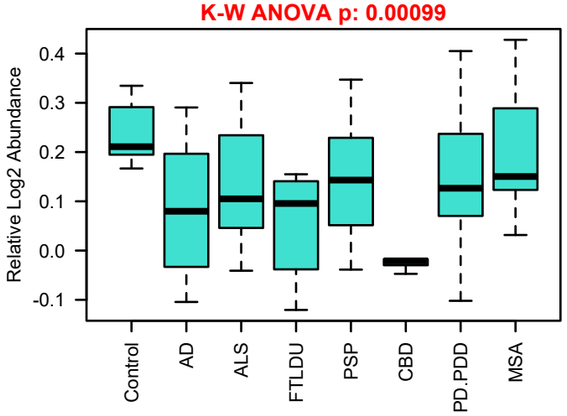

bicor=-0.063, p=0.53
cor=-0.048, p=0.64
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
-0.8
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

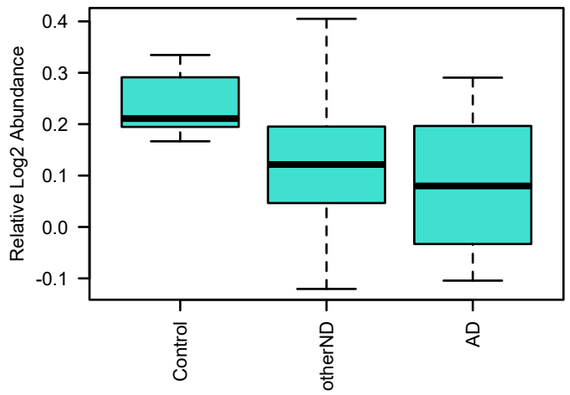

ERMN UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 0.025
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
-1.0
-1.5
-2.0
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

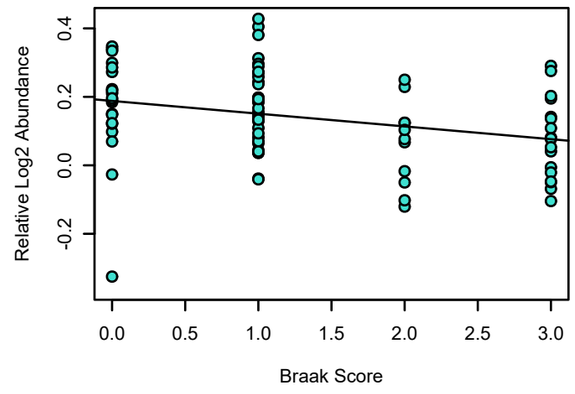

ERMN UPenn Mixed PRM
K-W ANOVA p: 0.0098
Relative Log2 Abundance
1.0
0.5
0.0
-0.5
-1.0
-1.5
Control
otherND
AD

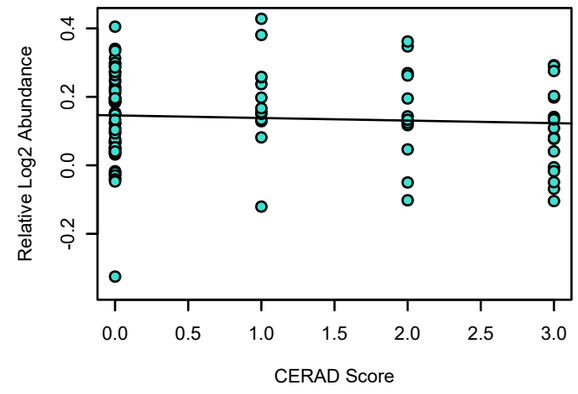

bicor=0.25, p=0.024
cor=0.26, p=0.017
Relative Log2 Abundance
1
0
-1
-2
-3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

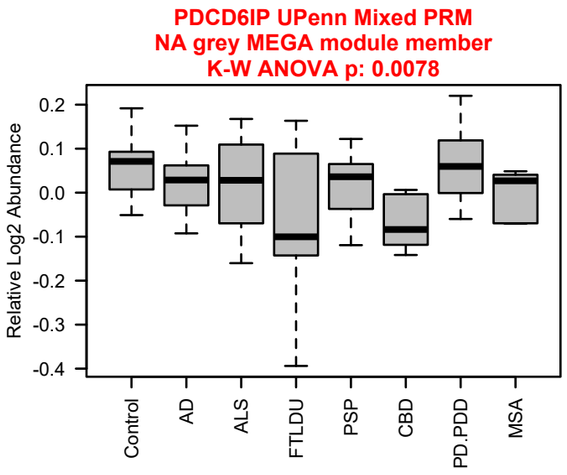

bicor=0.19, p=0.057
cor=0.19, p=0.058
Relative Log2 Abundance
1
0
-1
-2
-3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

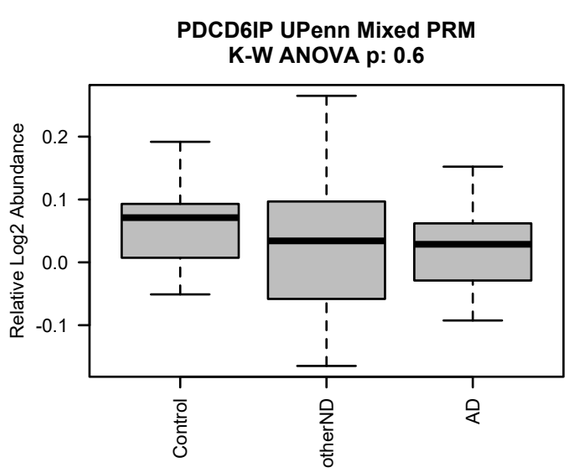

DMXL2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00099
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

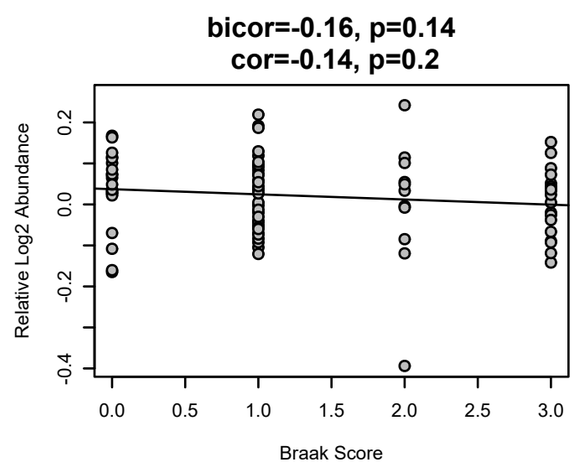

DMXL2 UPenn Mixed PRM
K-W ANOVA p: 0.0023
Relative Log2 Abundance
Control
otherND
AD

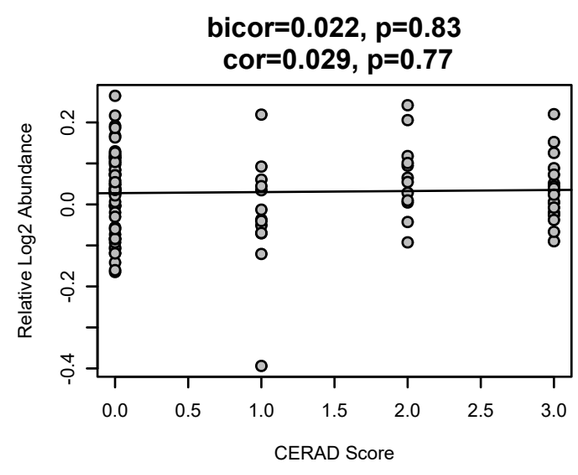

bicor=-0.34, p=0.0017
cor=-0.3, p=0.0056
Relative Log2 Abundance
Braak Score

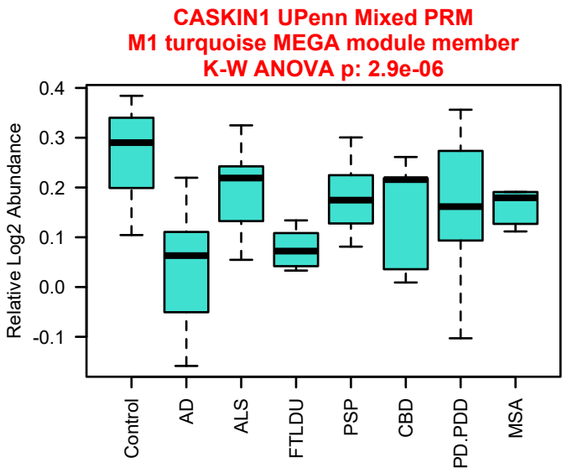

bicor=-0.083, p=0.41
cor=-0.069, p=0.5
Relative Log2 Abundance
CERAD Score

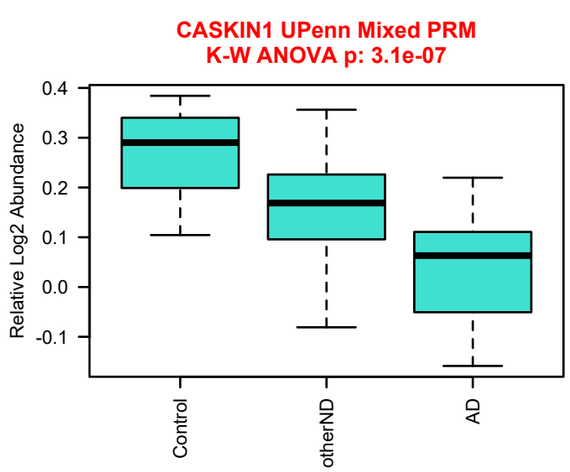

PDCD6IP UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.0078
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

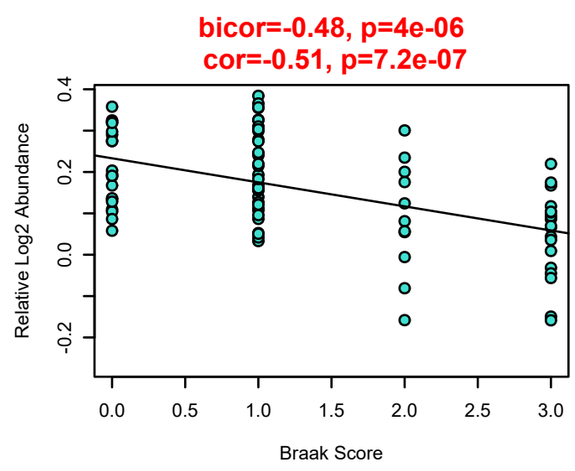

PDCD6IP UPenn Mixed PRM
K-W ANOVA p: 0.6
Relative Log2 Abundance
Control
otherND
AD

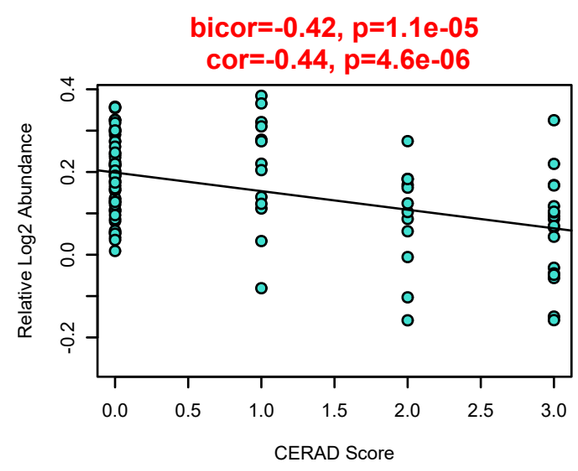

bicor=-0.16, p=0.14
cor=-0.14, p=0.2
Relative Log2 Abundance
Braak Score

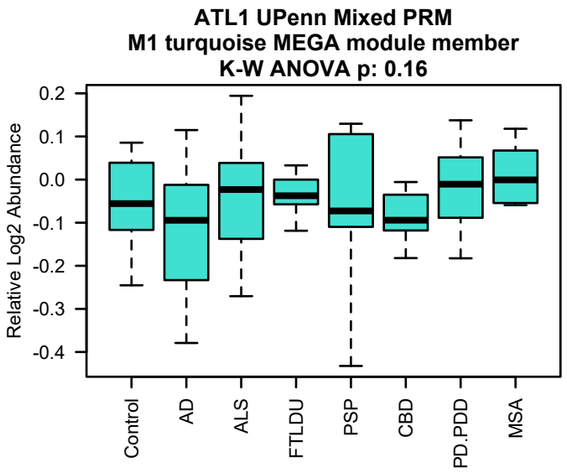

bicor=0.022, p=0.83
cor=0.029, p=0.77
Relative Log2 Abundance
CERAD Score

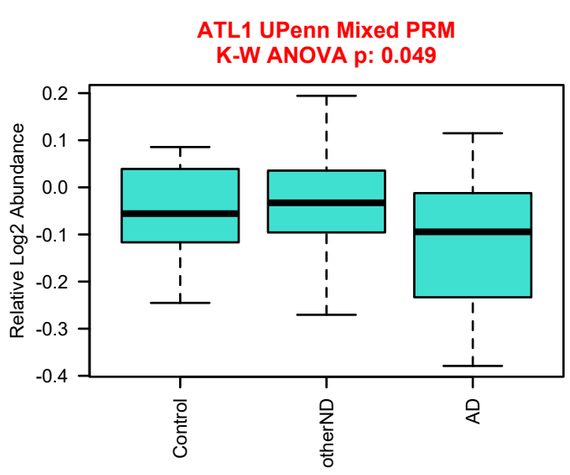

CASKIN1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2.9e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

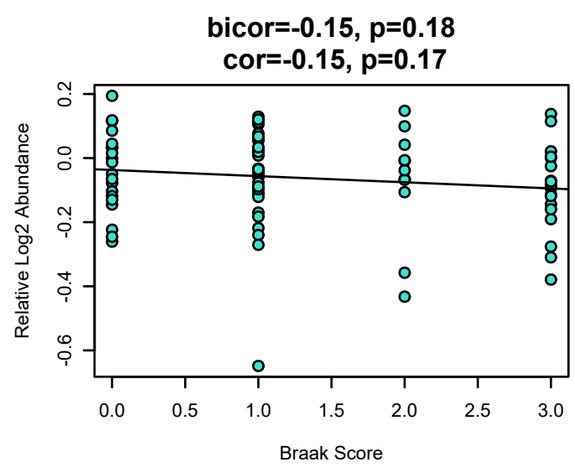

CASKIN1 UPenn Mixed PRM
K-W ANOVA p: 3.1e-07
Relative Log2 Abundance
Control
otherND
AD

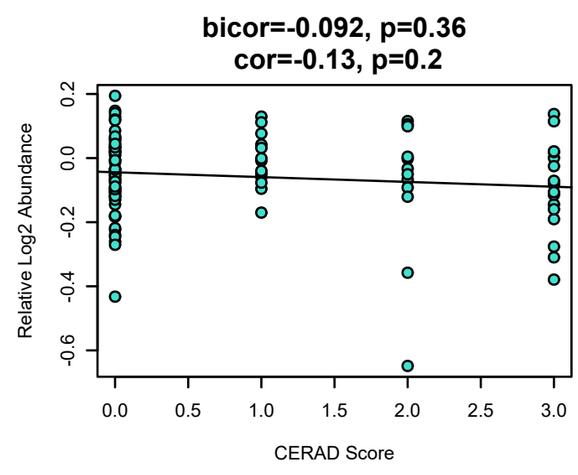

bicor=-0.48, p=4e-06
cor=-0.51, p=7.2e-07
Relative Log2 Abundance
Braak Score

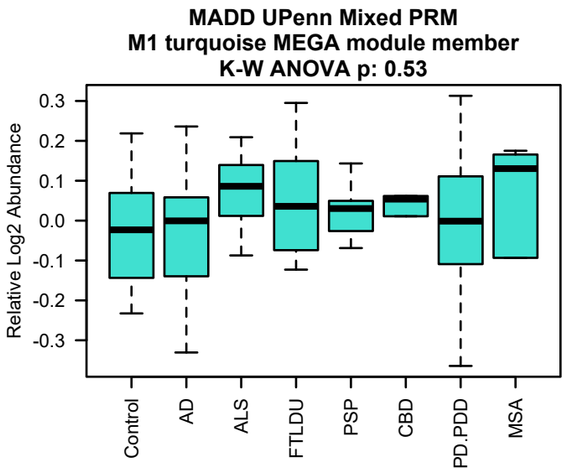

bicor=-0.42, p=1.1e-05
cor=-0.44, p=4.6e-06
Relative Log2 Abundance
CERAD Score

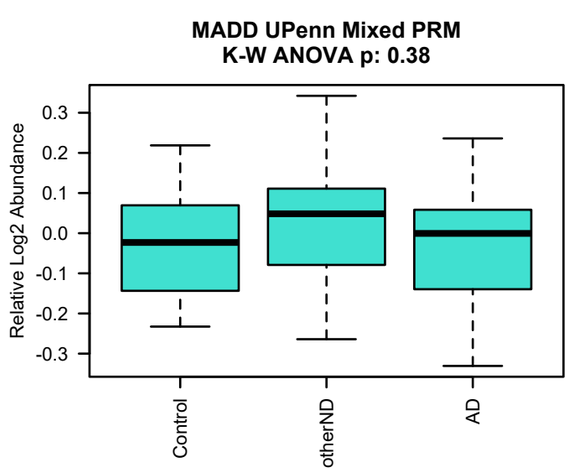

ATL1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.16
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

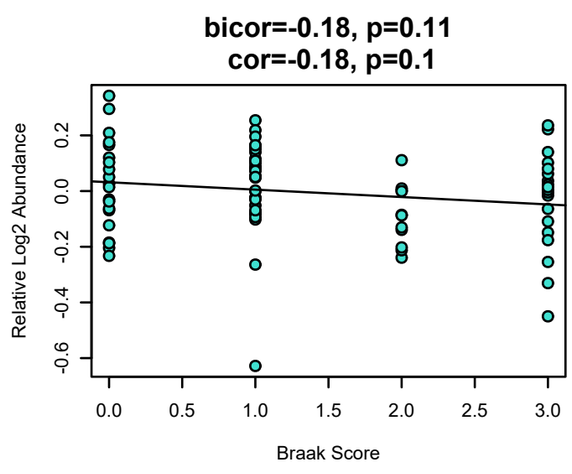

ATL1 UPenn Mixed PRM
K-W ANOVA p: 0.049
Relative Log2 Abundance
Control
otherND
AD

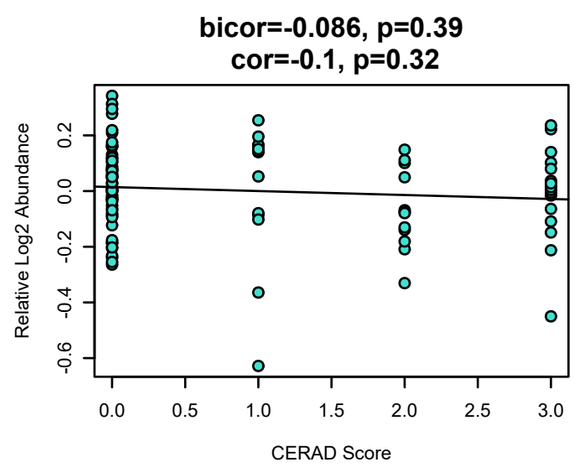

bicor=-0.15, p=0.18
cor=-0.15, p=0.17
Relative Log2 Abundance
Braak Score

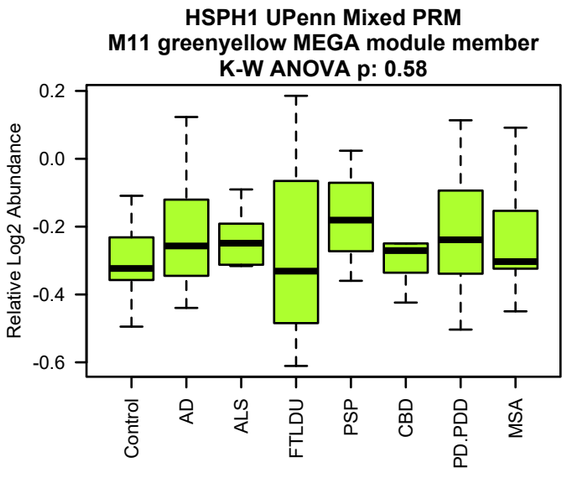

bicor=-0.092, p=0.36
cor=-0.13, p=0.2
Relative Log2 Abundance
CERAD Score

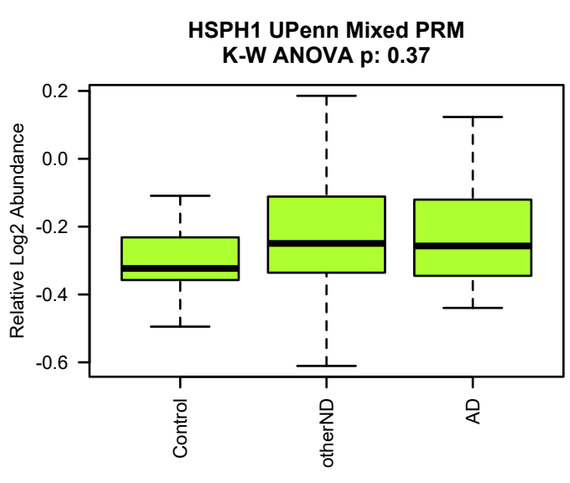

MADD UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.53
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

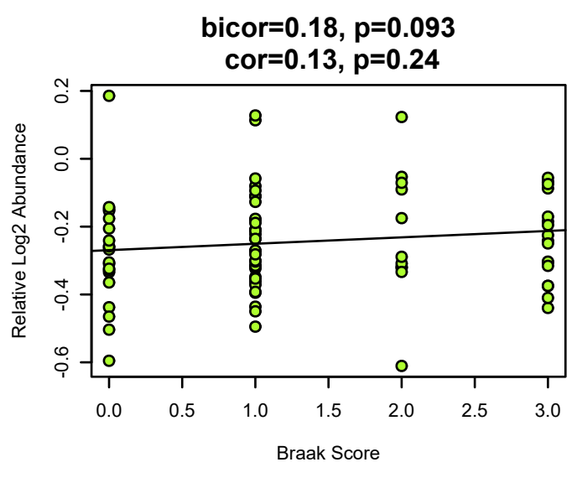

MADD UPenn Mixed PRM
K-W ANOVA p: 0.38
Relative Log2 Abundance
Control
otherND
AD

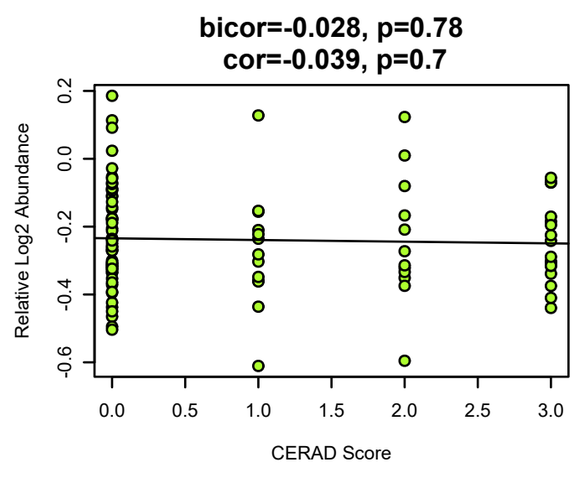

bicor=-0.18, p=0.11
cor=-0.18, p=0.1
Relative Log2 Abundance
Braak Score

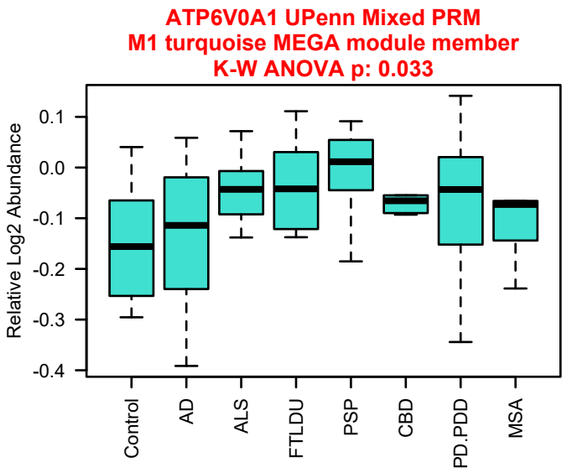

bicor=-0.086, p=0.39
cor=-0.1, p=0.32
Relative Log2 Abundance
CERAD Score

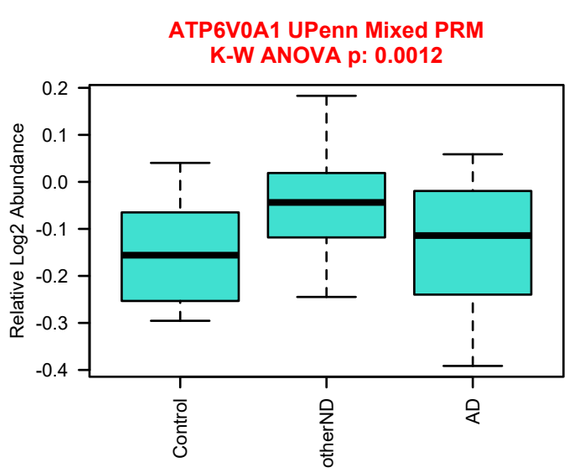

HSPH1 UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 0.58
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

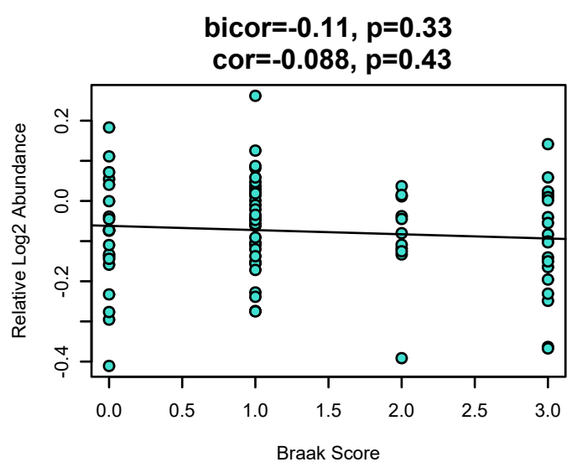

HSPH1 UPenn Mixed PRM
K-W ANOVA p: 0.37
Relative Log2 Abundance
Control
otherND
AD

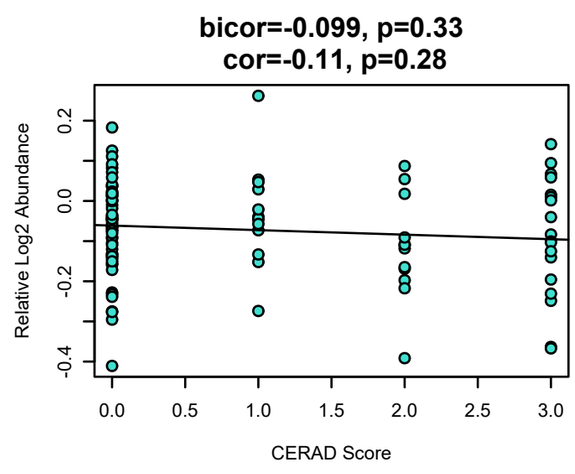

bicor=0.18, p=0.093
cor=0.13, p=0.24
Relative Log2 Abundance
Braak Score

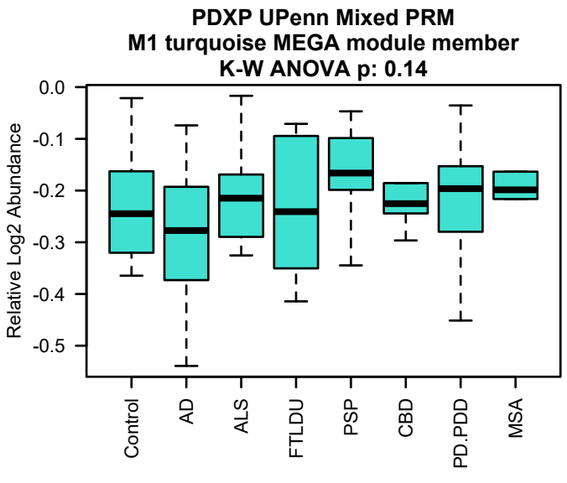

bicor=-0.028, p=0.78
cor=-0.039, p=0.7
Relative Log2 Abundance
CERAD Score

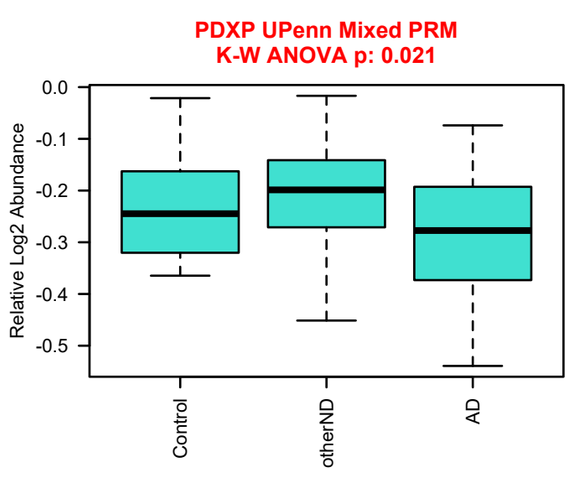

ATP6V0A1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.033
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

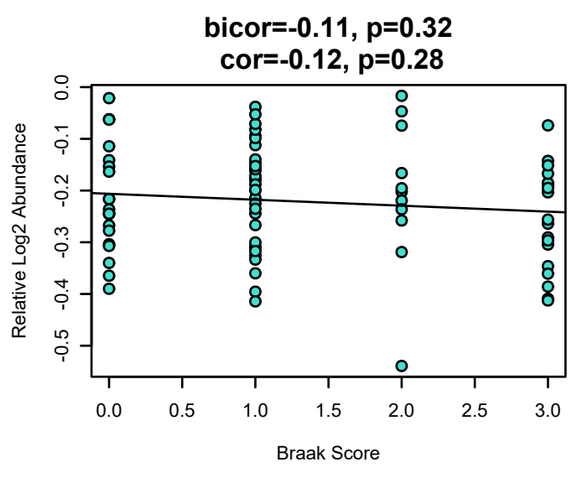

ATP6V0A1 UPenn Mixed PRM
K-W ANOVA p: 0.0012
Relative Log2 Abundance
Control
otherND
AD

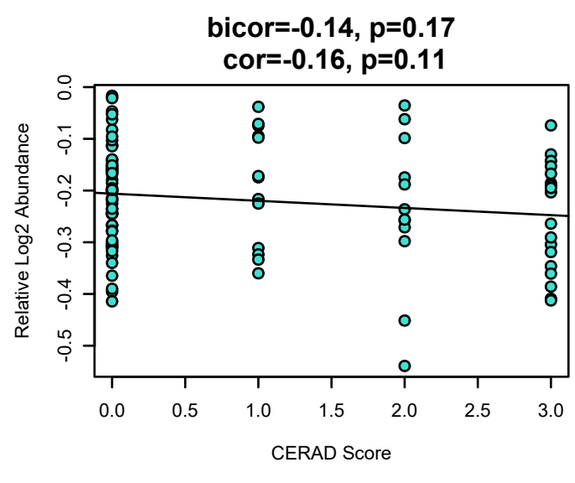

bicor=-0.11, p=0.33
cor=-0.088, p=0.43
Relative Log2 Abundance
Braak Score

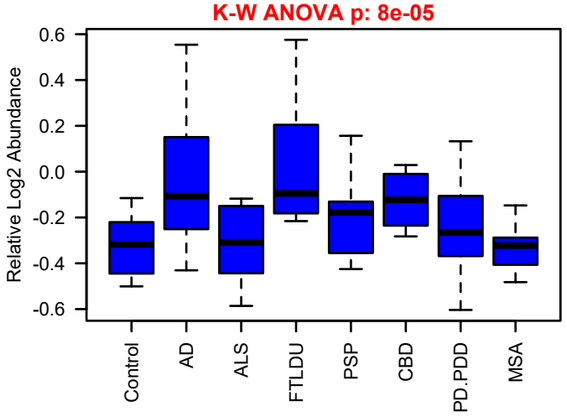

bicor=-0.099, p=0.33
cor=-0.11, p=0.28
Relative Log2 Abundance
CERAD Score

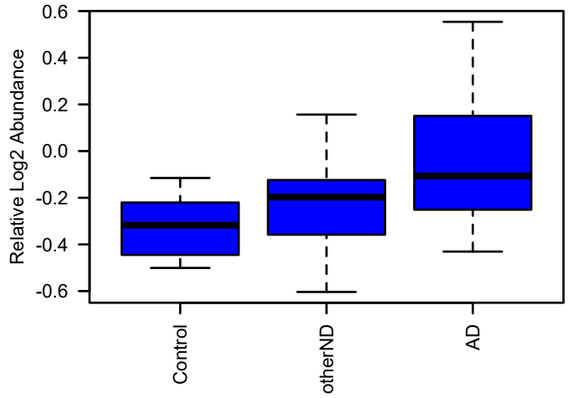

PDXP UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.14
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

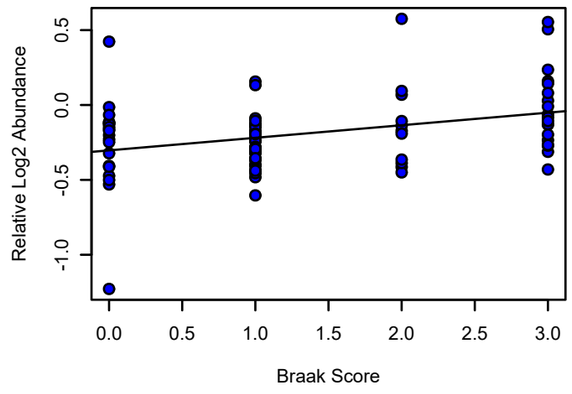

PDXP UPenn Mixed PRM
K-W ANOVA p: 0.021
Relative Log2 Abundance
Control
otherND
AD

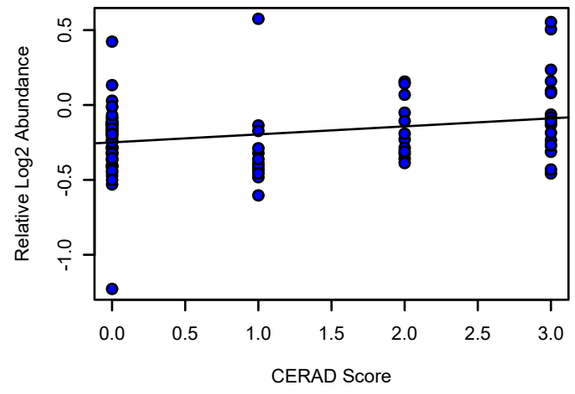

bicor=-0.11, p=0.32
cor=-0.12, p=0.28
Relative Log2 Abundance
Braak Score

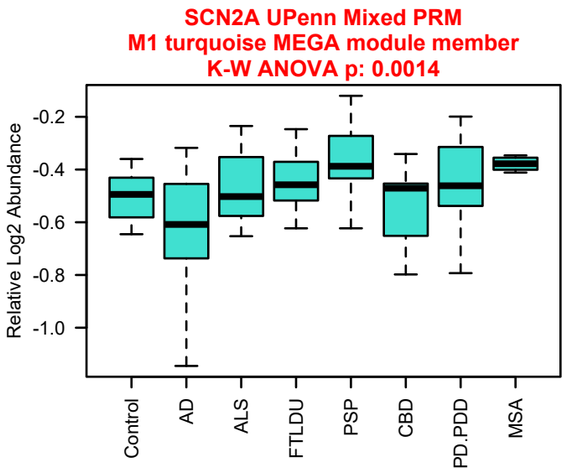

bicor=-0.14, p=0.17
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

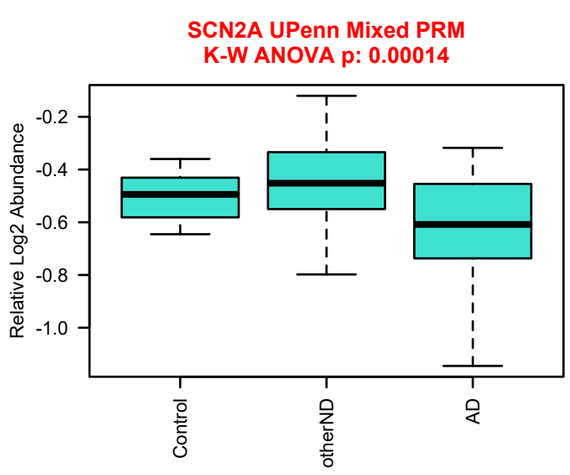

CNDP2 UPenn Mixed PRM
M2 blue MEGA module member
K-W ANOVA p: 8e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

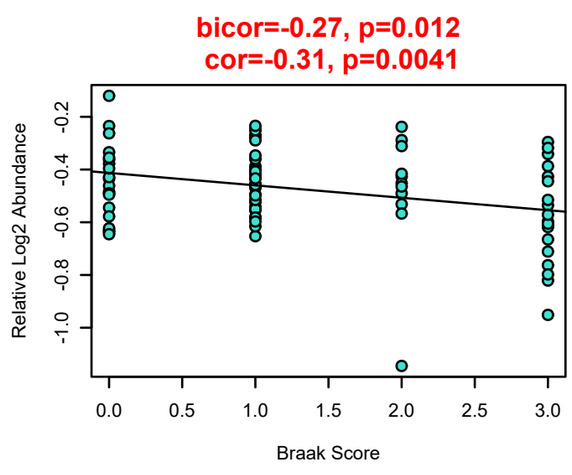

CNDP2 UPenn Mixed PRM
K-W ANOVA p: 0.00022
Relative Log2 Abundance
Control
otherND
AD

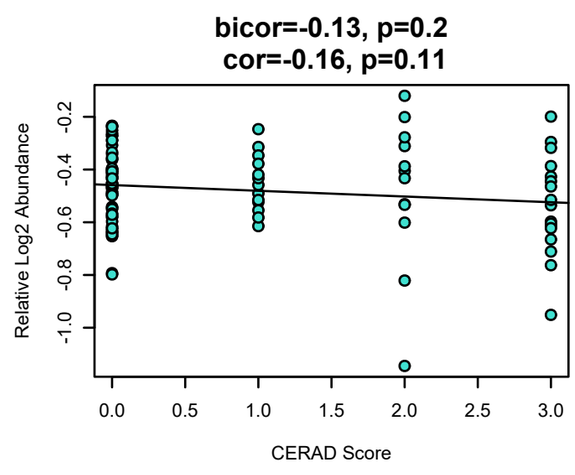

bicor=0.28, p=0.011
cor=0.35, p=0.0011
Relative Log2 Abundance
Braak Score

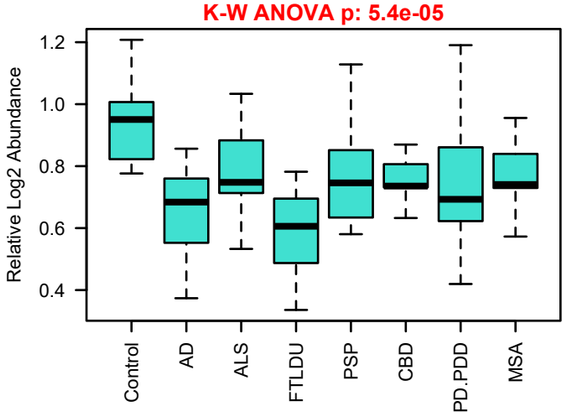

bicor=0.21, p=0.034
cor=0.26, p=0.009
Relative Log2 Abundance
CERAD Score

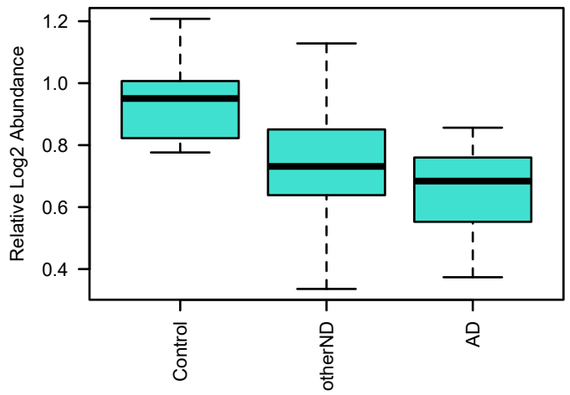

SCN2A UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0014
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

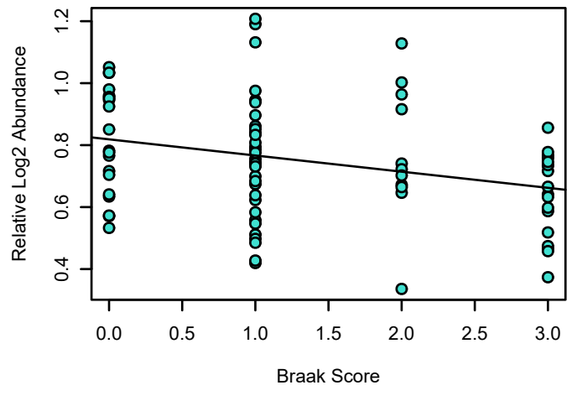

SCN2A UPenn Mixed PRM
K-W ANOVA p: 0.00014
Relative Log2 Abundance
Control
otherND
AD

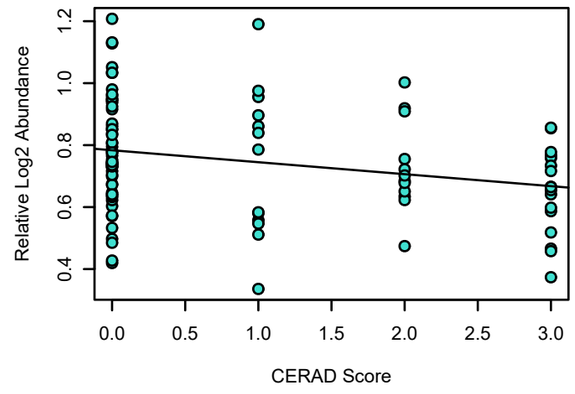

bicor=-0.27, p=0.012
cor=-0.31, p=0.0041
Relative Log2 Abundance
Braak Score

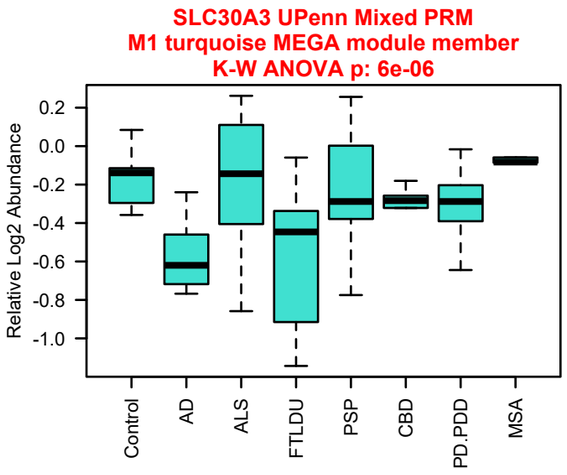

bicor=-0.13, p=0.2
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

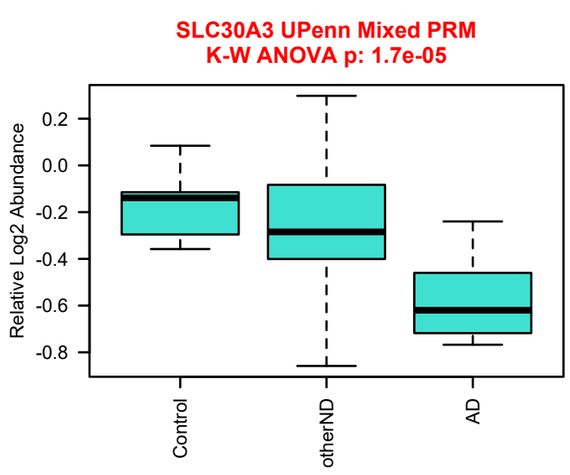

MGLL UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 5.4e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

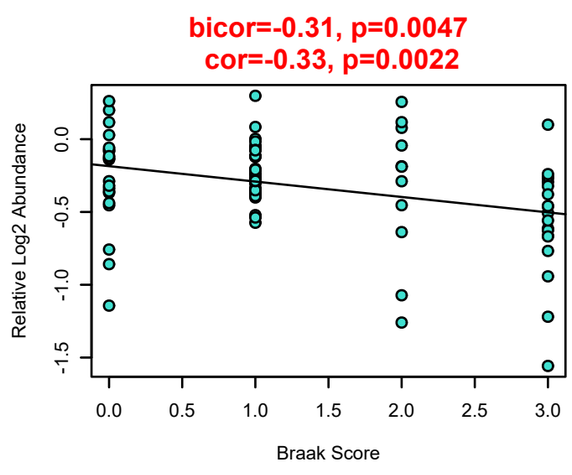

MGLL UPenn Mixed PRM
K-W ANOVA p: 1.7e-05
Relative Log2 Abundance
Control
otherND
AD

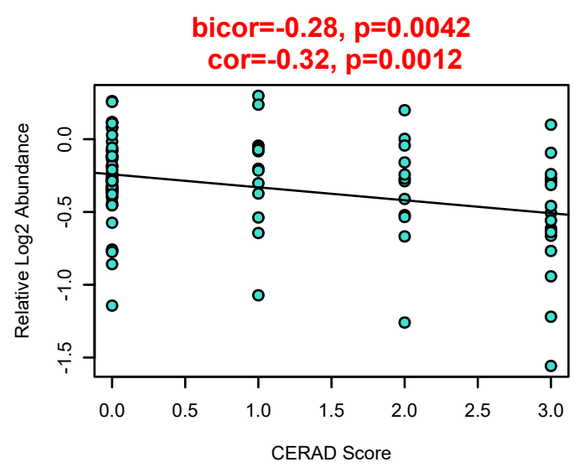

bicor=-0.28, p=0.0091
cor=-0.3, p=0.0056
Relative Log2 Abundance
Braak Score

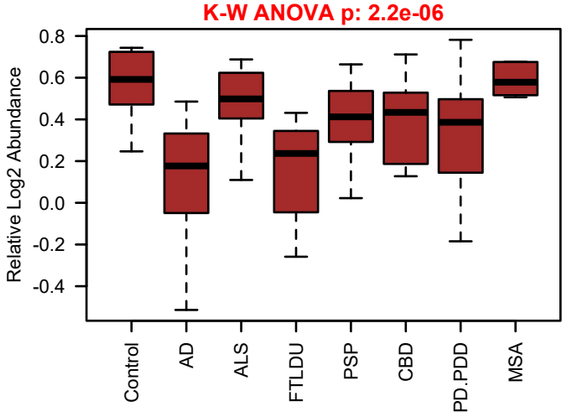

bicor=-0.26, p=0.0092
cor=-0.26, p=0.009
Relative Log2 Abundance
CERAD Score

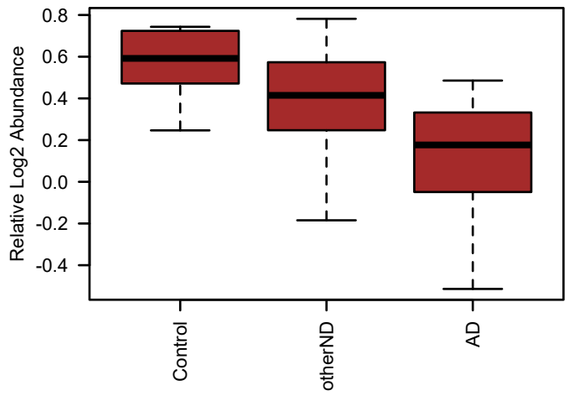

SLC30A3 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 6e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

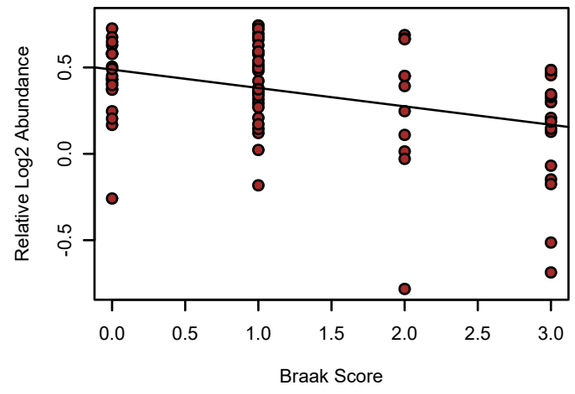

SLC30A3 UPenn Mixed PRM
K-W ANOVA p: 1.7e-05
Relative Log2 Abundance
Control
otherND
AD

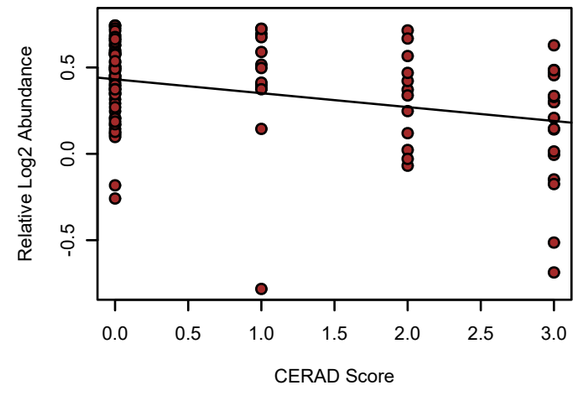

bicor=-0.31, p=0.0047
cor=-0.33, p=0.0022
Relative Log2 Abundance
Braak Score

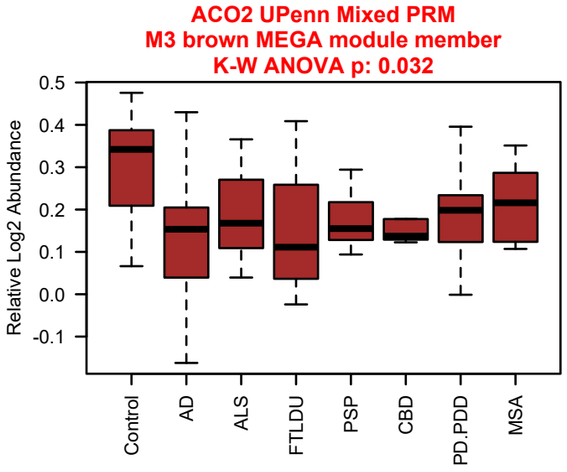

bicor=-0.28, p=0.0042
cor=-0.32, p=0.0012
Relative Log2 Abundance
CERAD Score

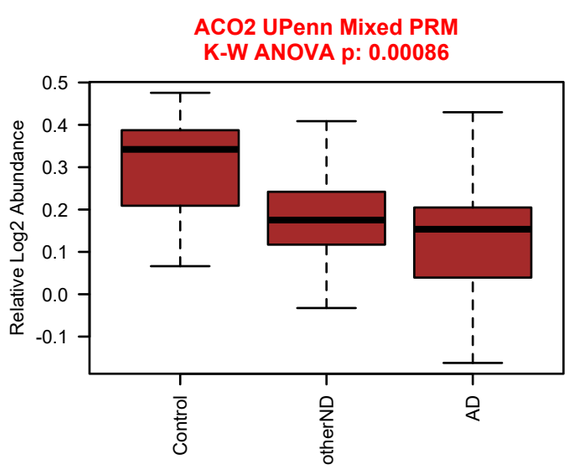

OLFM1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 2.2e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

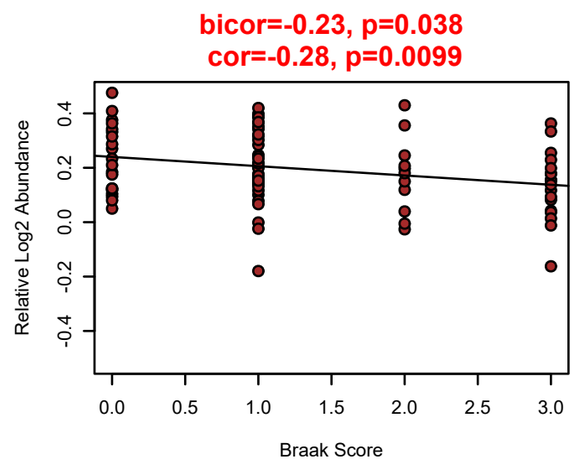

OLFM1 UPenn Mixed PRM
K-W ANOVA p: 1.3e-05
Relative Log2 Abundance
Control
otherND
AD

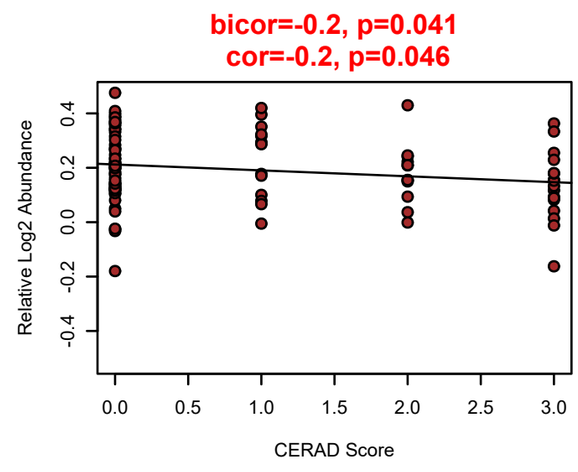

bicor=-0.37, p=0.00053
cor=-0.38, p=0.00036
Relative Log2 Abundance
Braak Score

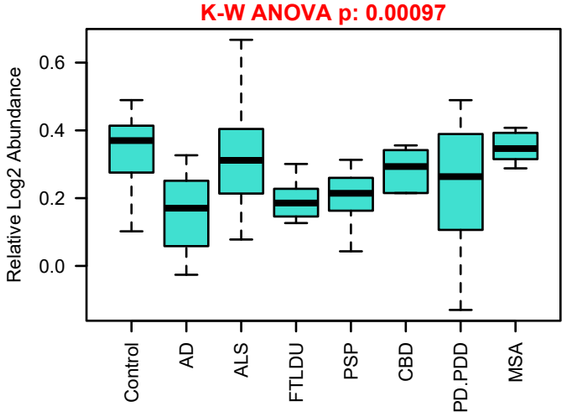

bicor=-0.3, p=0.0021
cor=-0.33, p=8e-04
Relative Log2 Abundance
CERAD Score

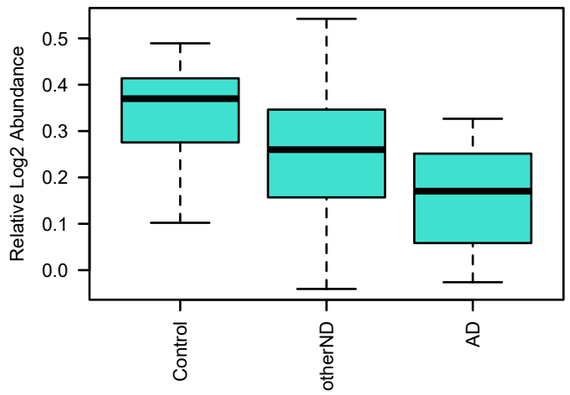

ACO2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.032
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

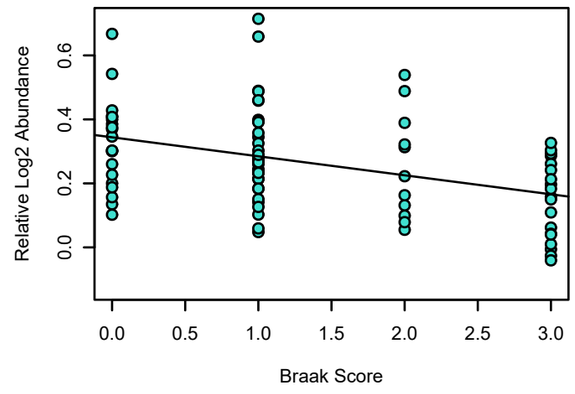

ACO2 UPenn Mixed PRM
K-W ANOVA p: 0.00086
Relative Log2 Abundance
Control
otherND
AD

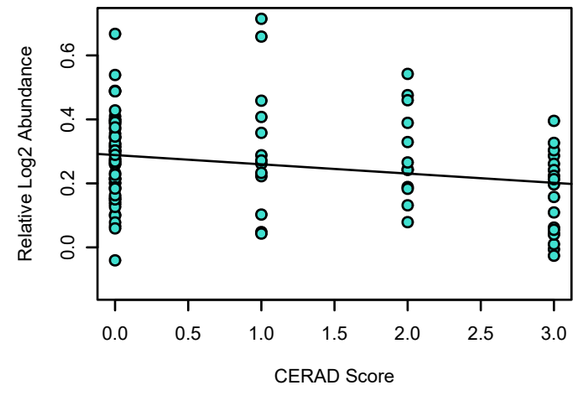

bicor=-0.23, p=0.038
cor=-0.28, p=0.0099
Relative Log2 Abundance
Braak Score

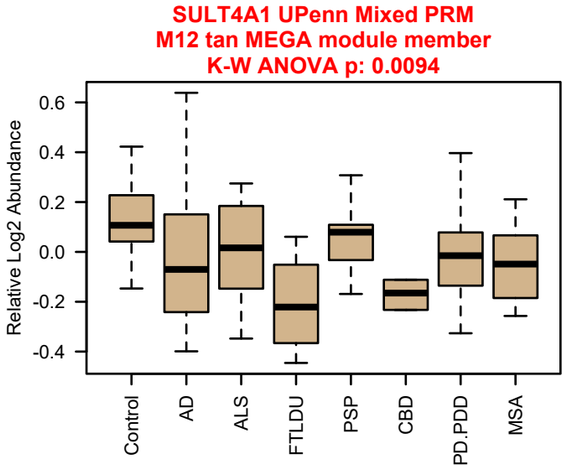

bicor=-0.2, p=0.041
cor=-0.2, p=0.046
Relative Log2 Abundance
CERAD Score

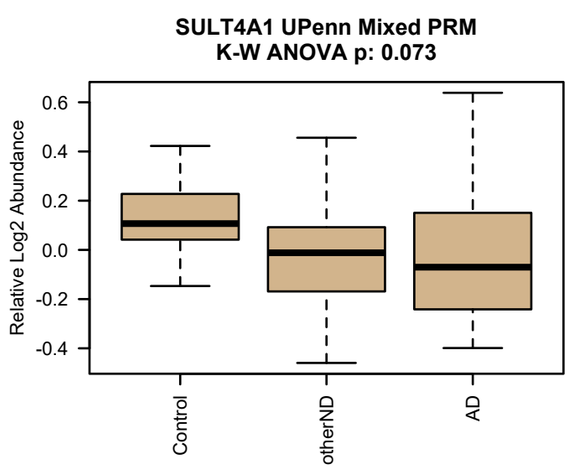

SGIP1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00097
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

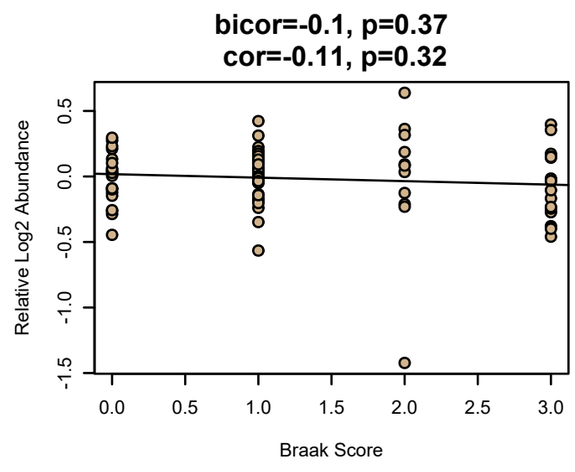

SGIP1 UPenn Mixed PRM
K-W ANOVA p: 0.00022
Relative Log2 Abundance
Control
otherND
AD

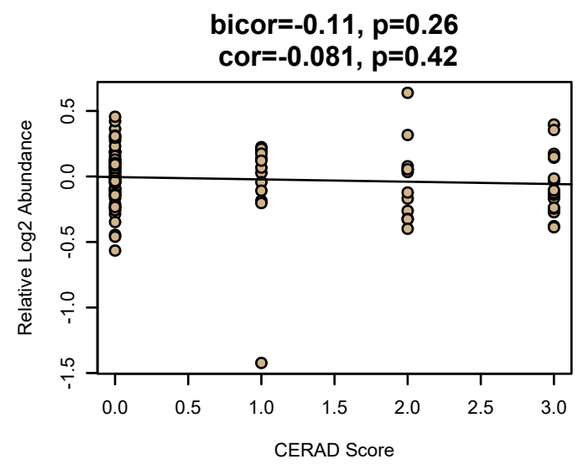

bicor=-0.4, p=2e-04
cor=-0.41, p=0.00011
Relative Log2 Abundance
Braak Score

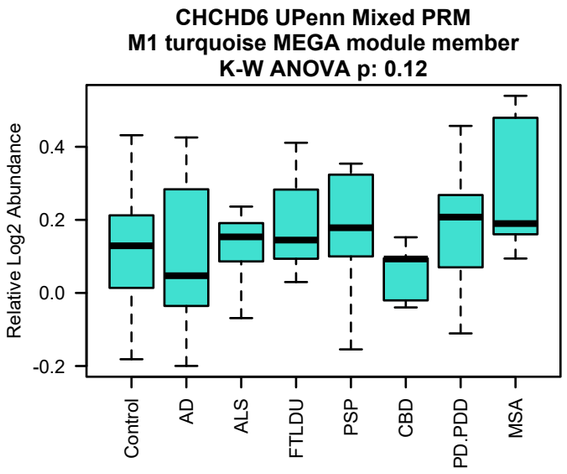

bicor=-0.24, p=0.018
cor=-0.23, p=0.021
Relative Log2 Abundance
CERAD Score

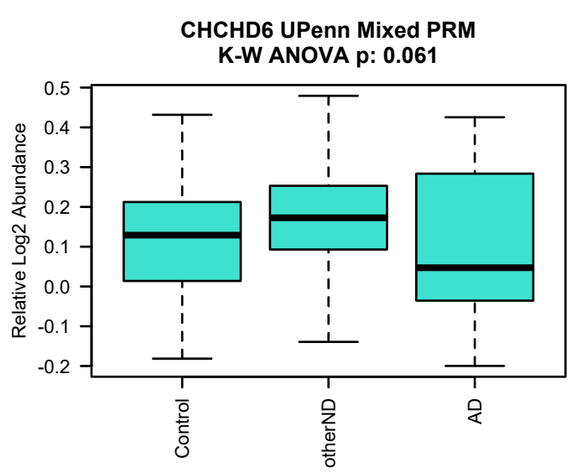

SULT4A1 UPenn Mixed PRM
M12 tan MEGA module member
K-W ANOVA p: 0.0094
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

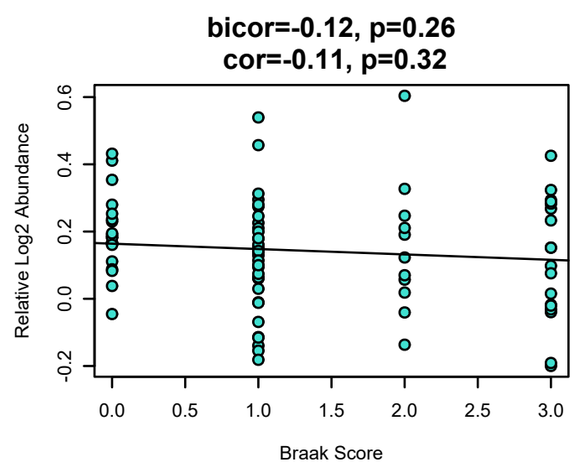

SULT4A1 UPenn Mixed PRM
K-W ANOVA p: 0.073
Relative Log2 Abundance
Control
otherND
AD

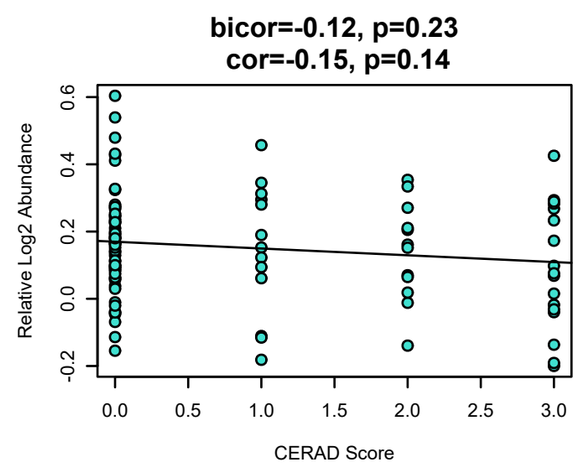

bicor=-0.1, p=0.37
cor=-0.11, p=0.32
Relative Log2 Abundance
Braak Score

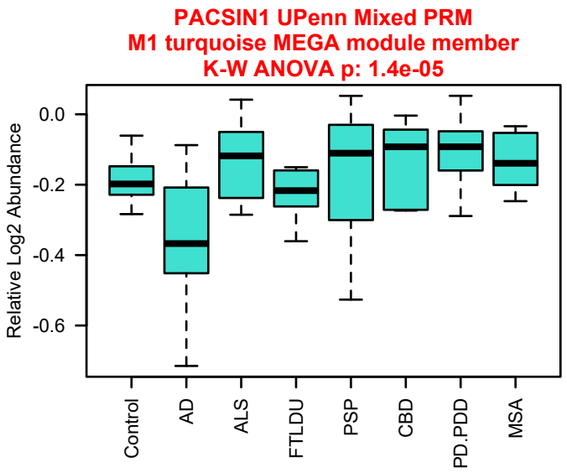

bicor=-0.11, p=0.26
cor=-0.081, p=0.42
Relative Log2 Abundance
CERAD Score

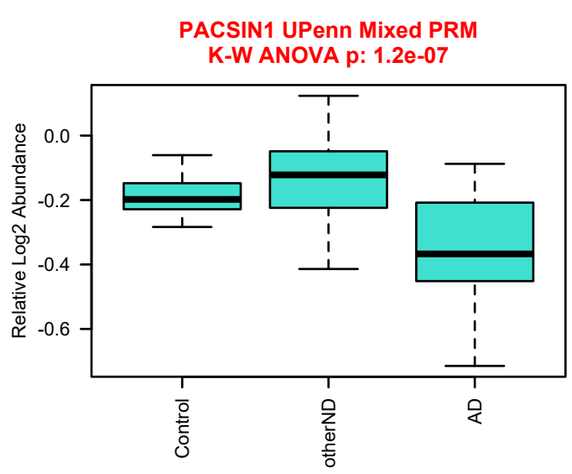

CHCHD6 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.12
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

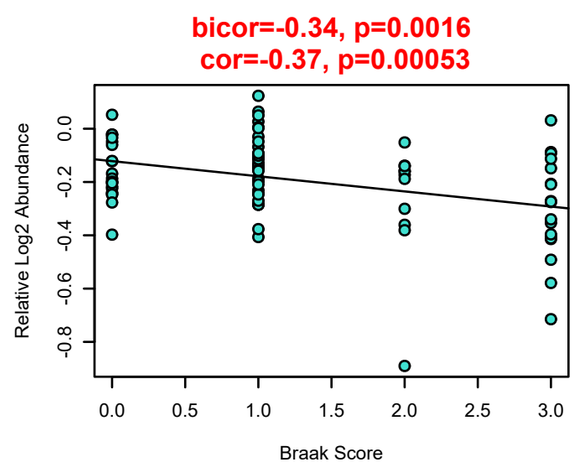

CHCHD6 UPenn Mixed PRM
K-W ANOVA p: 0.061
Relative Log2 Abundance
Control
otherND
AD

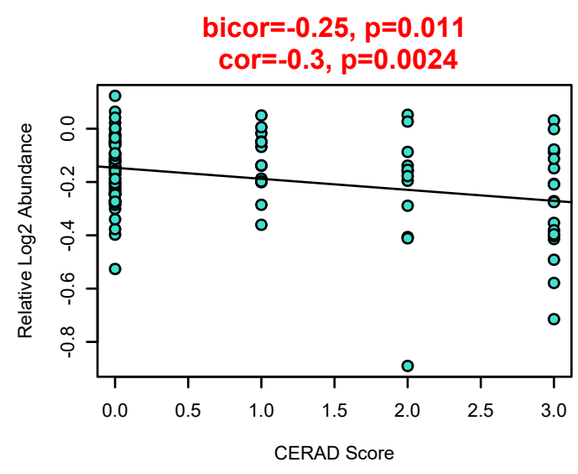

bicor=-0.12, p=0.26
cor=-0.11, p=0.32
Relative Log2 Abundance
Braak Score

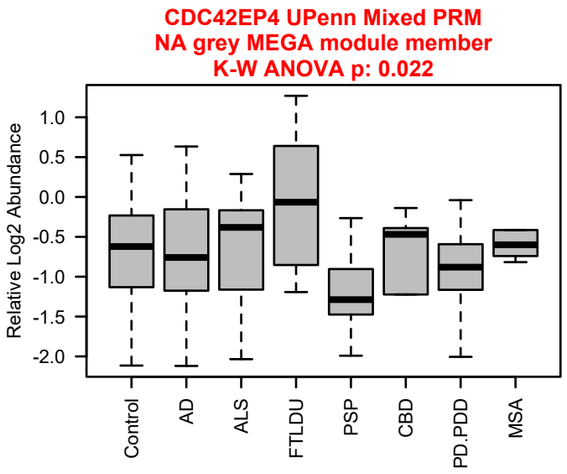

bicor=-0.12, p=0.23
cor=-0.15, p=0.14
Relative Log2 Abundance
CERAD Score

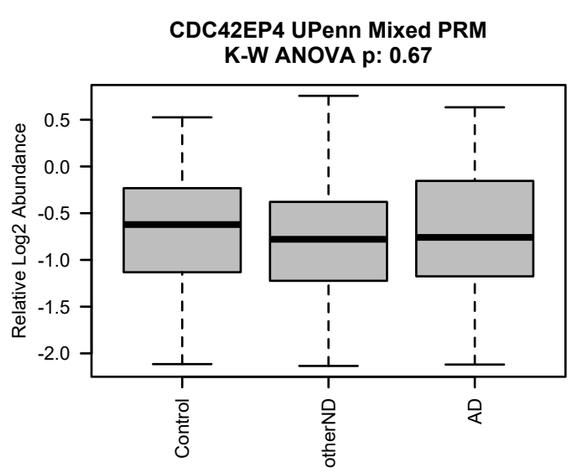

PACSIN1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 1.4e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

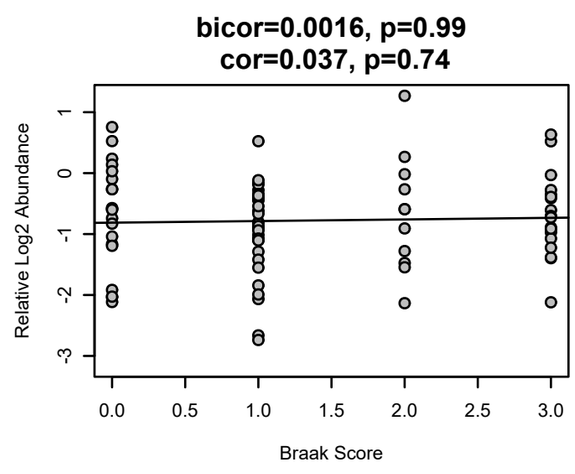

PACSIN1 UPenn Mixed PRM
K-W ANOVA p: 1.2e-07
Relative Log2 Abundance
Control
otherND
AD

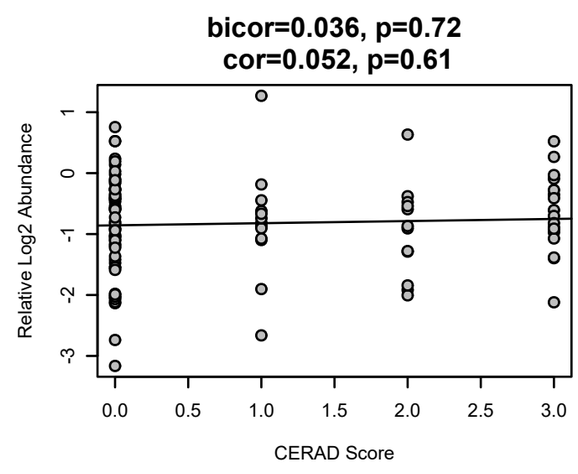

bicor=-0.34, p=0.0016
cor=-0.37, p=0.00053
Relative Log2 Abundance
Braak Score

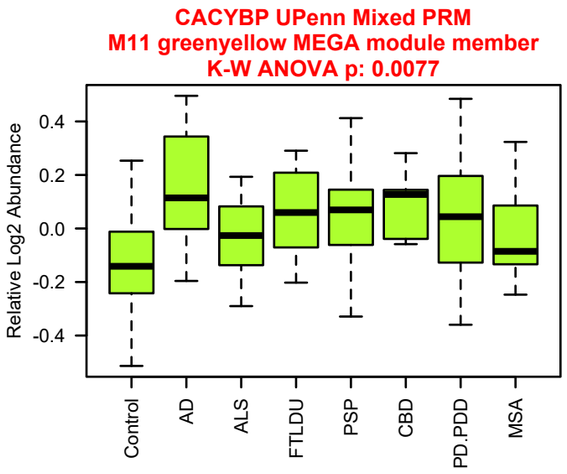

bicor=-0.25, p=0.011
cor=-0.3, p=0.0024
Relative Log2 Abundance
CERAD Score

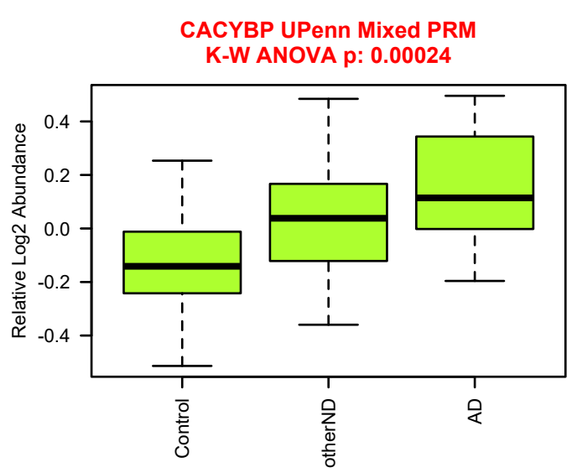

CDC42EP4 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.022
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

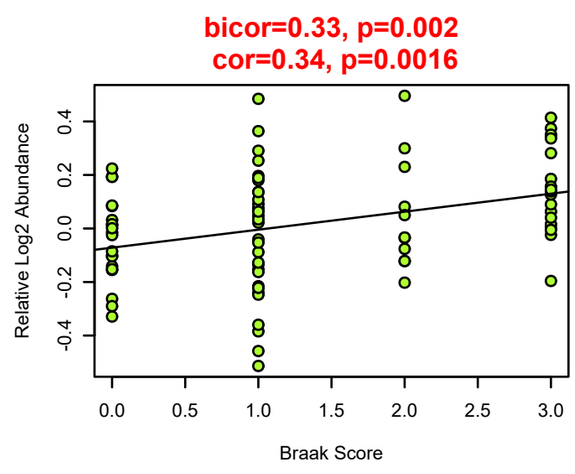

CDC42EP4 UPenn Mixed PRM
K-W ANOVA p: 0.67
Relative Log2 Abundance
Control
otherND
AD

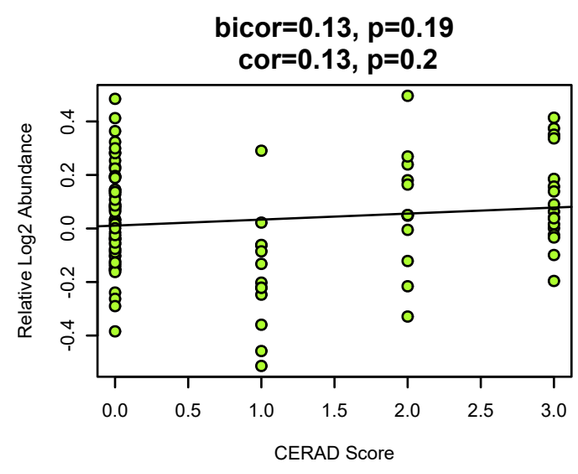

bicor=0.0016, p=0.99
cor=0.037, p=0.74
Relative Log2 Abundance
Braak Score

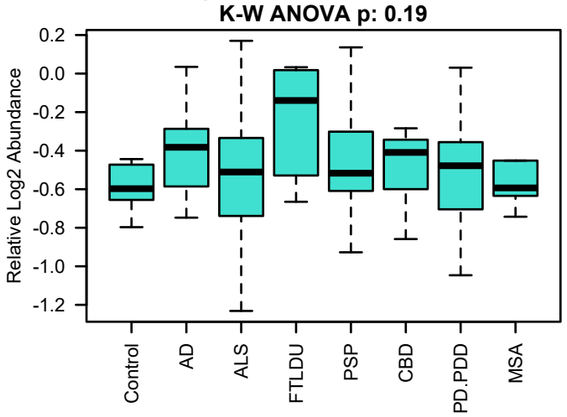

bicor=0.036, p=0.72
cor=0.052, p=0.61
Relative Log2 Abundance
CERAD Score

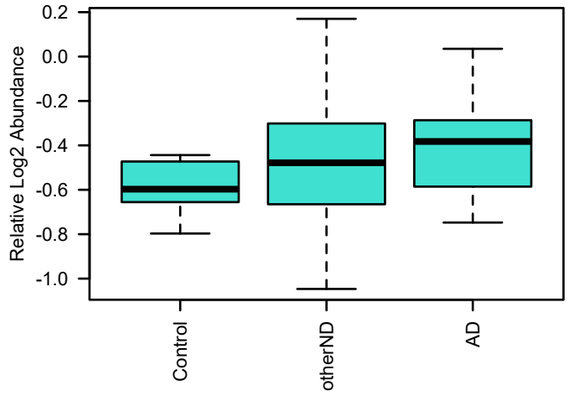

CACYBP UPenn Mixed PRM
M11 greenyellow MEGA module member
K-W ANOVA p: 0.0077
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

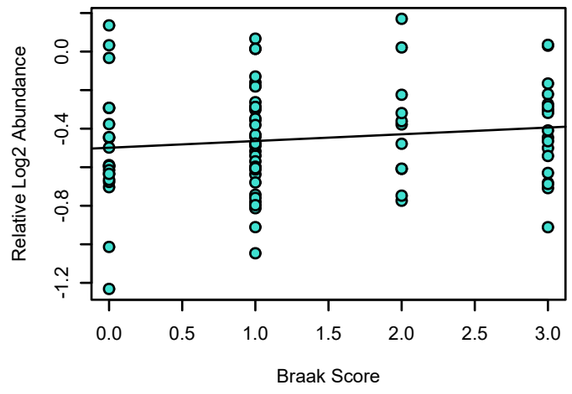

CACYBP UPenn Mixed PRM
K-W ANOVA p: 0.00024
Relative Log2 Abundance
Control
otherND
AD

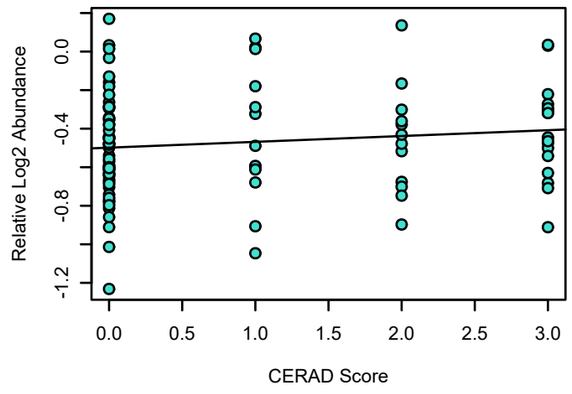

bicor=0.33, p=0.002
cor=0.34, p=0.0016
Relative Log2 Abundance
Braak Score

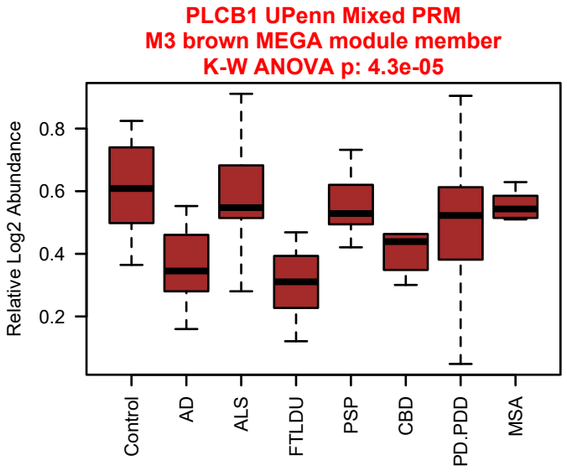

bicor=0.13, p=0.19
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

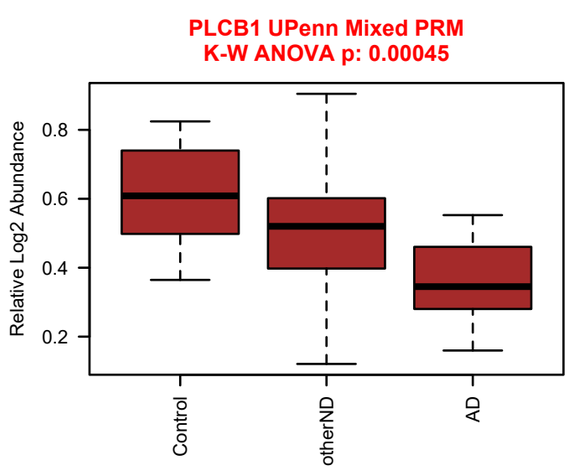

VAT1L UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.19
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

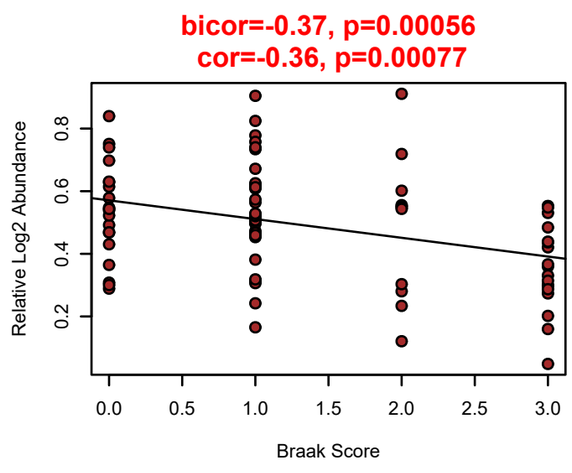

VAT1L UPenn Mixed PRM
K-W ANOVA p: 0.42
Relative Log2 Abundance
Control
otherND
AD

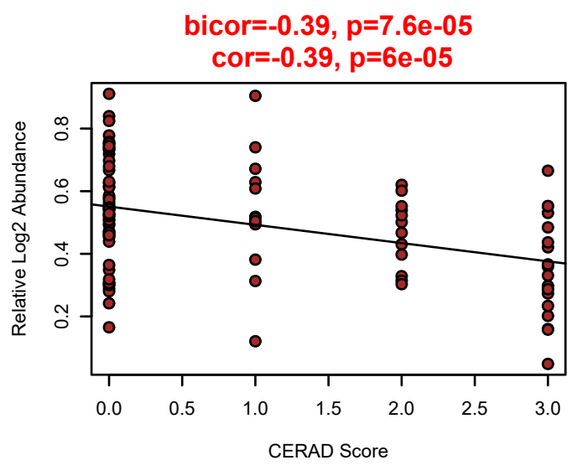

bicor=0.15, p=0.18
cor=0.13, p=0.24
Relative Log2 Abundance
Braak Score

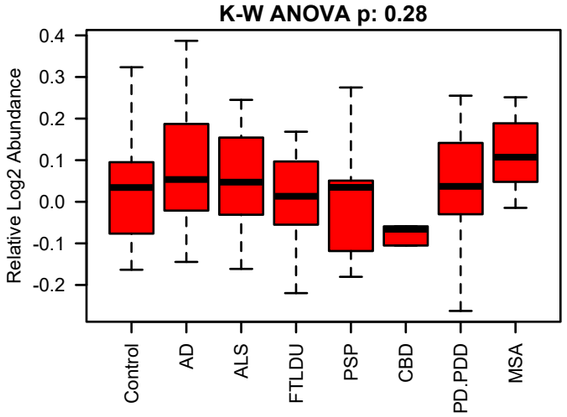

bicor=0.14, p=0.18
cor=0.13, p=0.2
Relative Log2 Abundance
CERAD Score

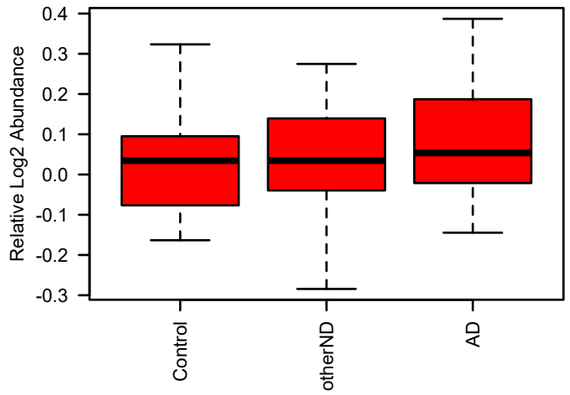

PLCB1 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 4.3e-05
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

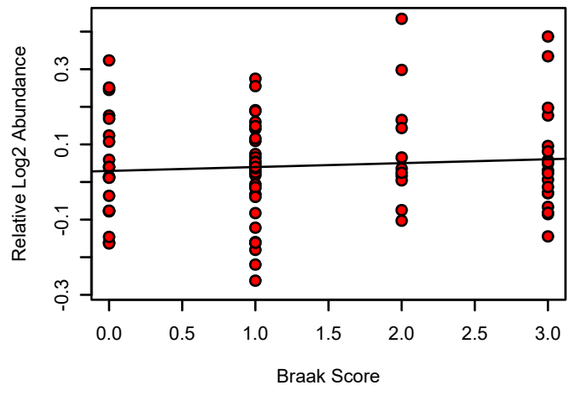

PLCB1 UPenn Mixed PRM
K-W ANOVA p: 0.00045
Relative Log2 Abundance
Control
otherND
AD

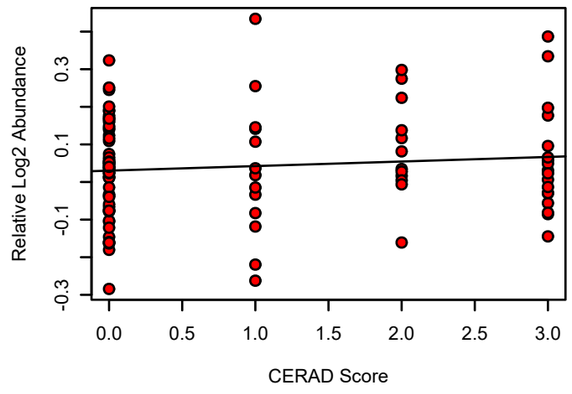

bicor=-0.37, p=0.00056
cor=-0.36, p=0.00077
Relative Log2 Abundance
Braak Score

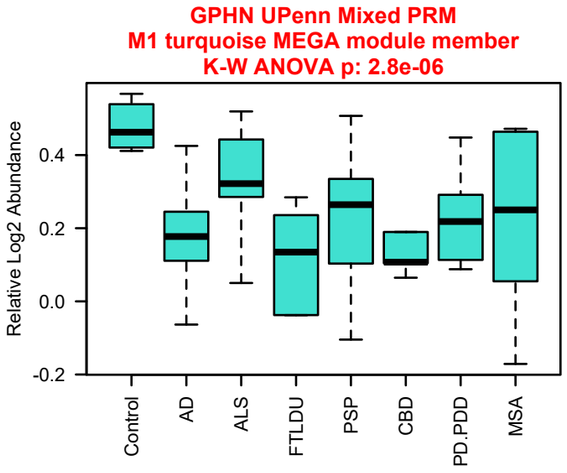

bicor=-0.39, p=7.6e-05
cor=-0.39, p=6e-05
Relative Log2 Abundance
CERAD Score

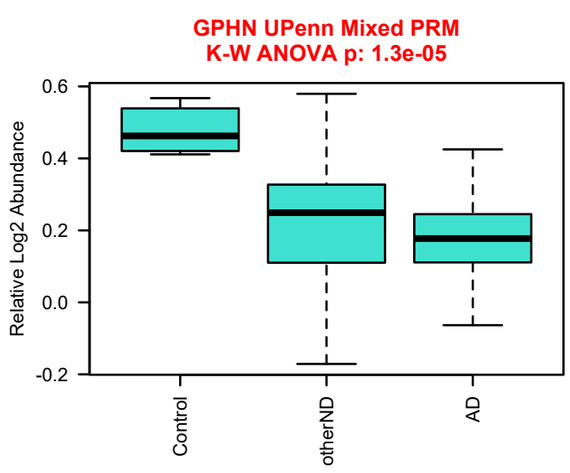

RTN4 UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.28
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

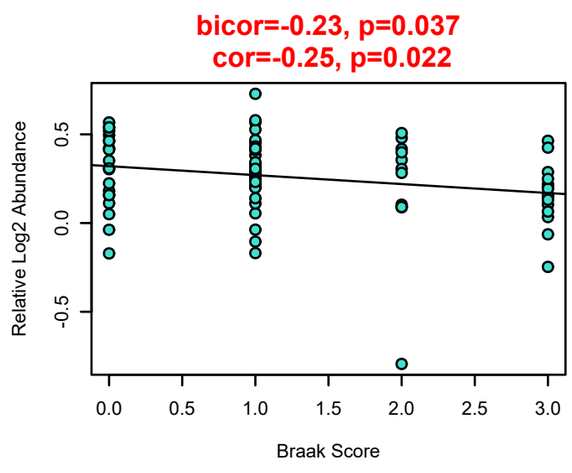

RTN4 UPenn Mixed PRM
K-W ANOVA p: 0.39
Relative Log2 Abundance
Control
otherND
AD

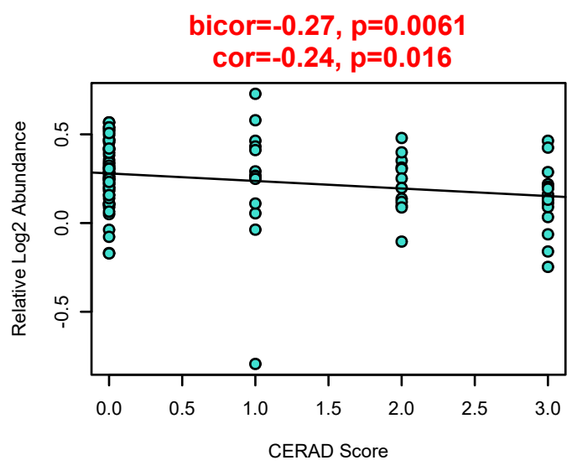

bicor=0.062, p=0.57
cor=0.08, p=0.47
Relative Log2 Abundance
Braak Score

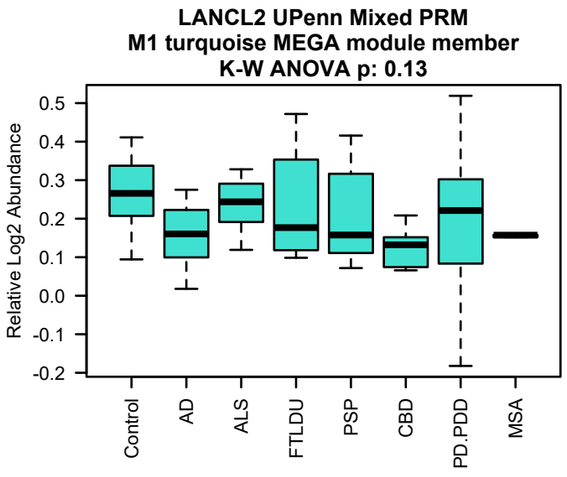

bicor=0.085, p=0.4
cor=0.1, p=0.32
Relative Log2 Abundance
CERAD Score

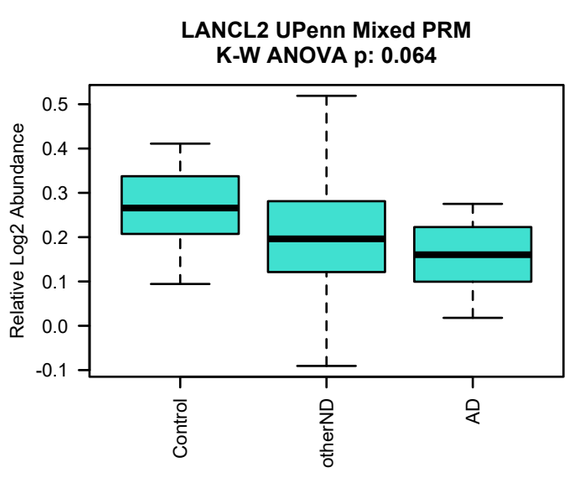

GPHN UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2.8e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

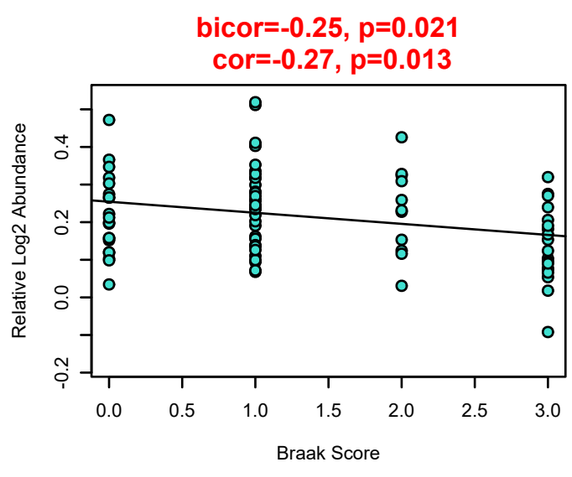

GPHN UPenn Mixed PRM
K-W ANOVA p: 1.3e-05
Relative Log2 Abundance
Control
otherND
AD

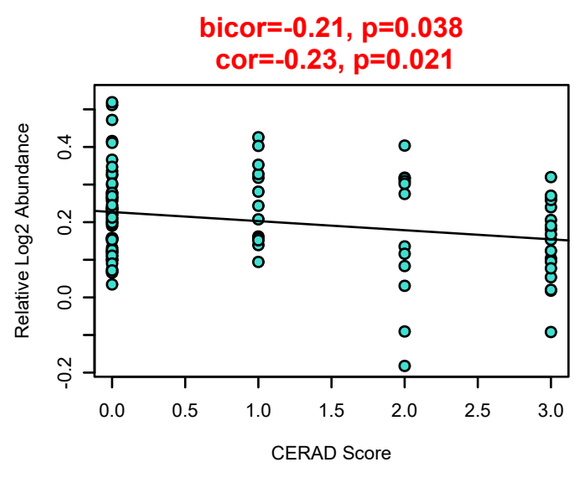

bicor=-0.23, p=0.037
cor=-0.25, p=0.022
Relative Log2 Abundance
Braak Score

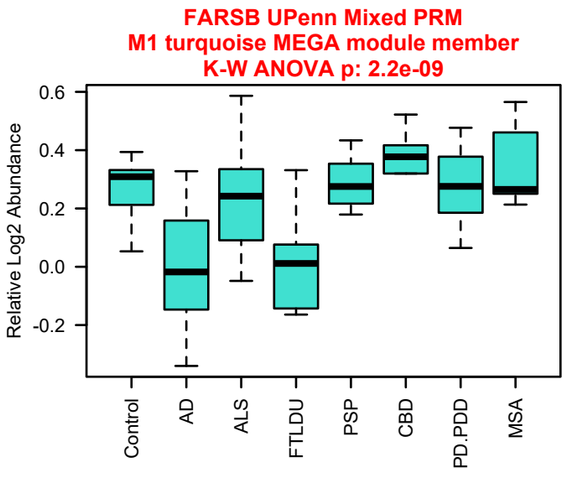

bicor=-0.27, p=0.0061
cor=-0.24, p=0.016
Relative Log2 Abundance
CERAD Score

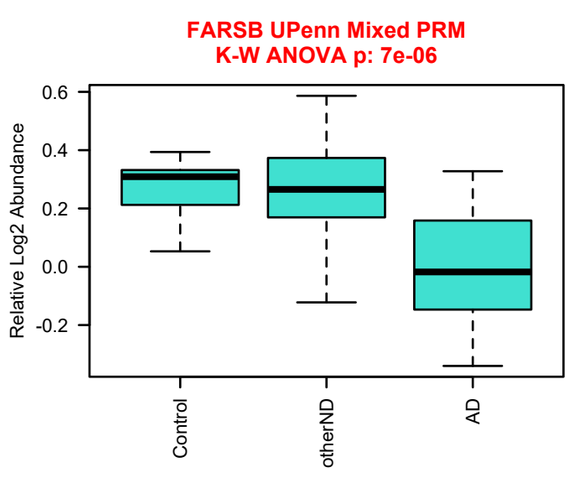

LANCL2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.13
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

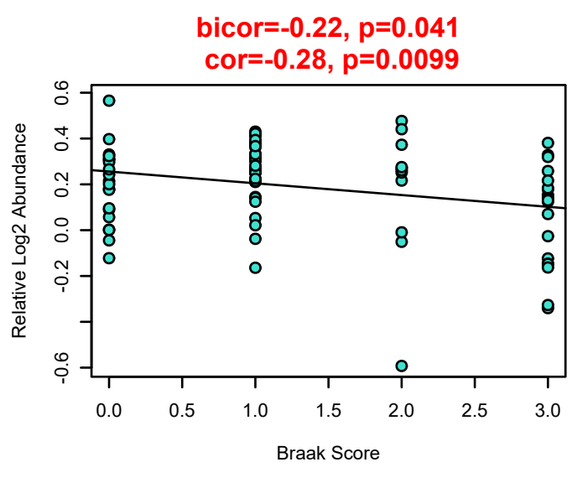

LANCL2 UPenn Mixed PRM
K-W ANOVA p: 0.064
Relative Log2 Abundance
Control
otherND
AD

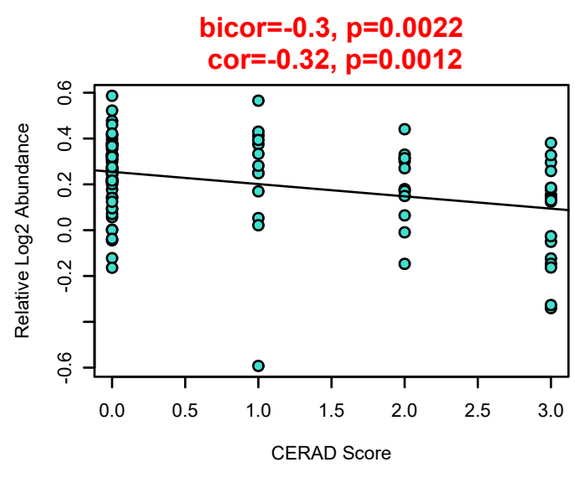

bicor=-0.25, p=0.021
cor=-0.27, p=0.013
Relative Log2 Abundance
Braak Score

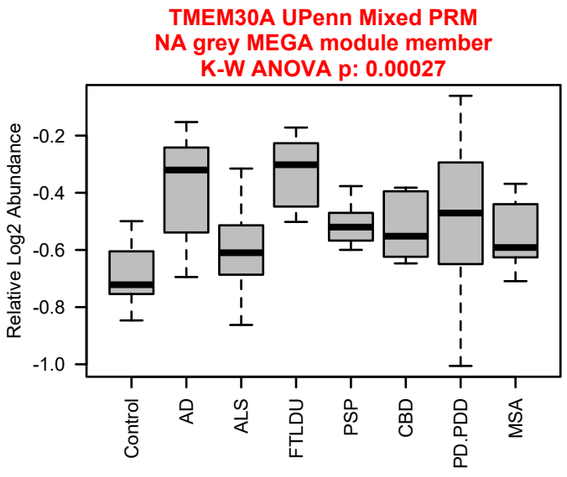

bicor=-0.21, p=0.038
cor=-0.23, p=0.021
Relative Log2 Abundance
CERAD Score

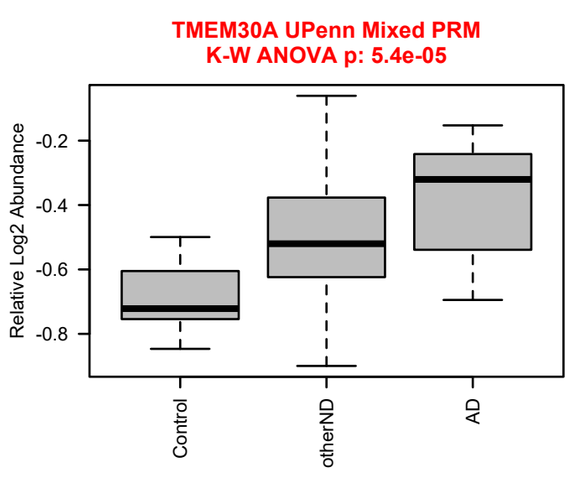

FARSB UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 2.2e-09
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

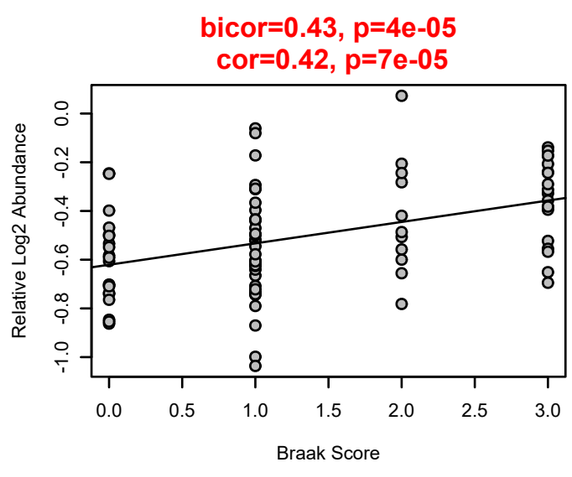

FARSB UPenn Mixed PRM
K-W ANOVA p: 7e-06
Relative Log2 Abundance
Control
otherND
AD

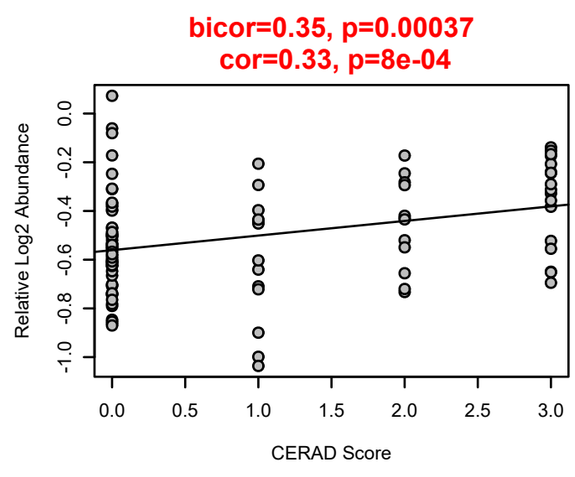

bicor=-0.22, p=0.041
cor=-0.28, p=0.0099
Relative Log2 Abundance
Braak Score

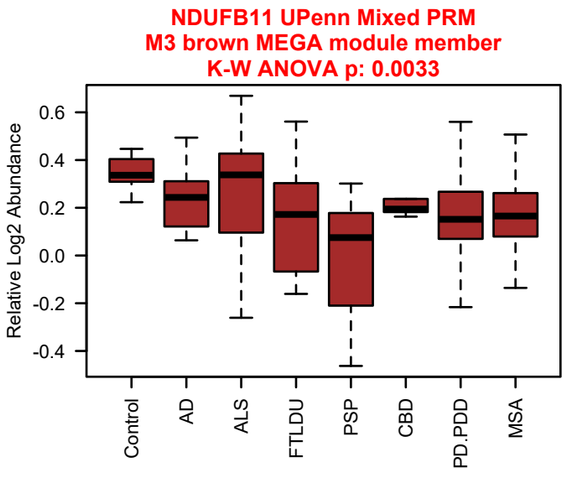

bicor=-0.3, p=0.0022
cor=-0.32, p=0.0012
Relative Log2 Abundance
CERAD Score

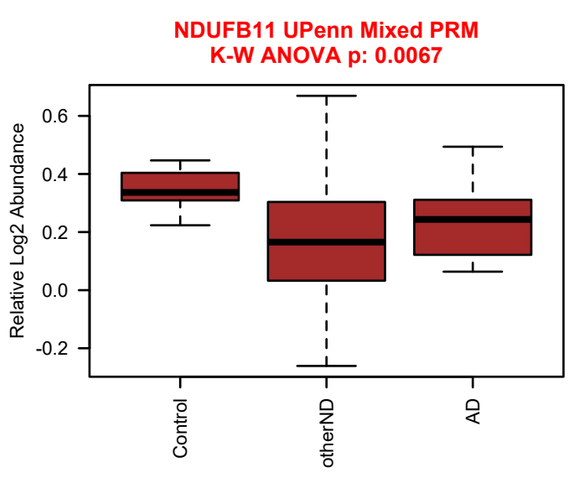

TMEM30A UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.00027
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

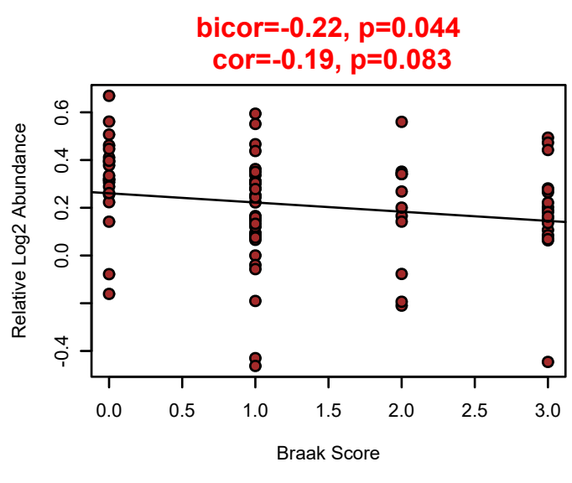

TMEM30A UPenn Mixed PRM
K-W ANOVA p: 5.4e-05
Relative Log2 Abundance
Control
otherND
AD

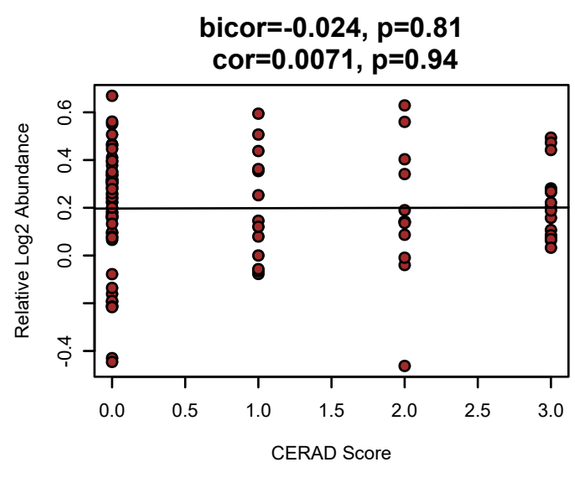

bicor=0.43, p=4e-05
cor=0.42, p=7e-05
Relative Log2 Abundance
Braak Score

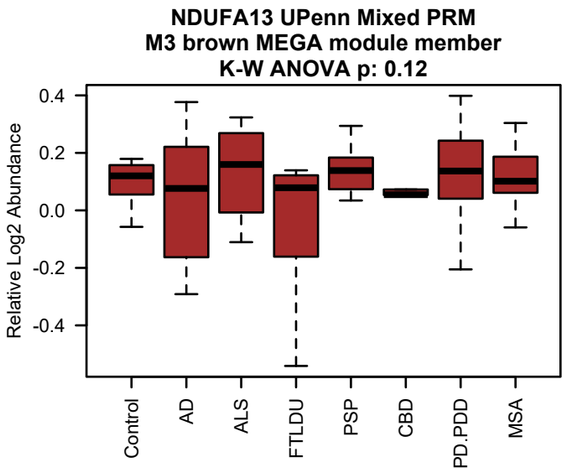

bicor=0.35, p=0.00037
cor=0.33, p=8e-04
Relative Log2 Abundance
CERAD Score

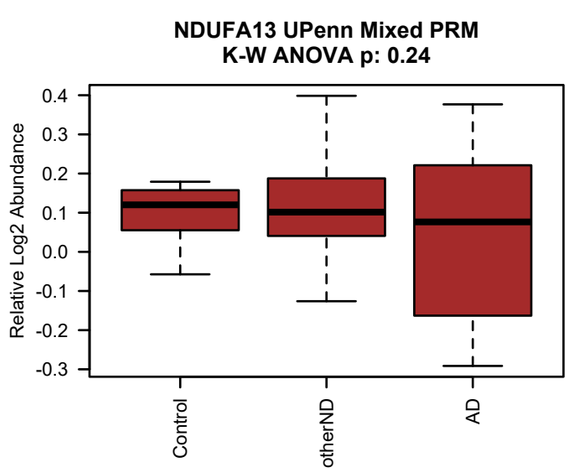

NDUFB11 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.0033
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

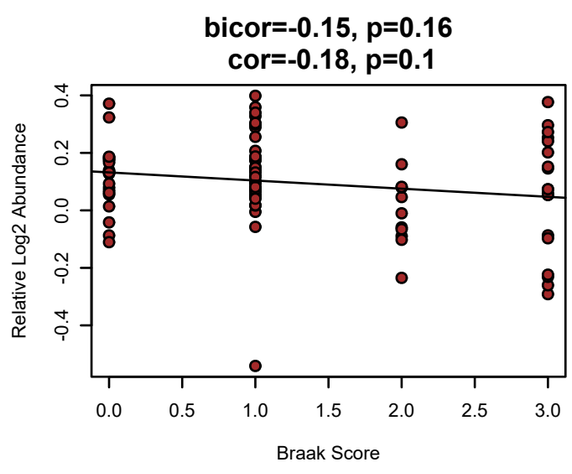

NDUFB11 UPenn Mixed PRM
K-W ANOVA p: 0.0067
Relative Log2 Abundance
Control
otherND
AD

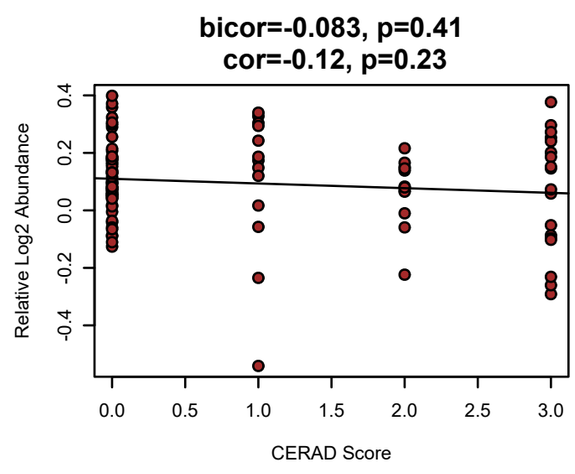

bicor=-0.22, p=0.044
cor=-0.19, p=0.083
Relative Log2 Abundance
Braak Score

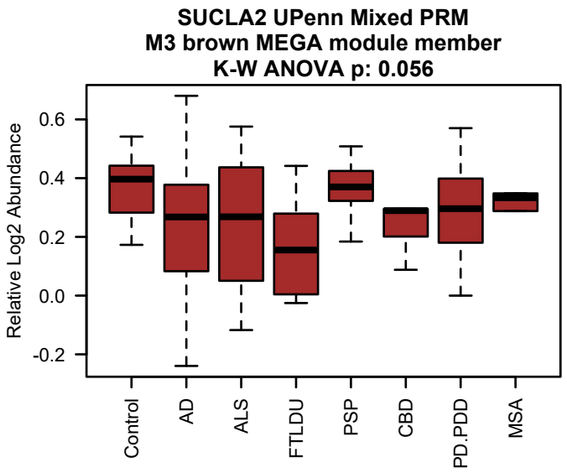

bicor=-0.024, p=0.81
cor=0.0071, p=0.94
Relative Log2 Abundance
CERAD Score

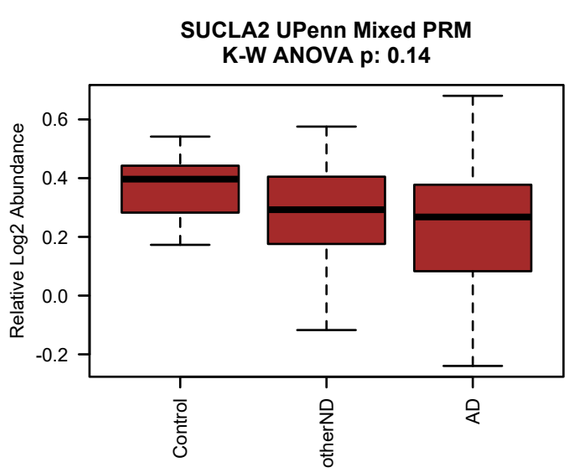

NDUFA13 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.12
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

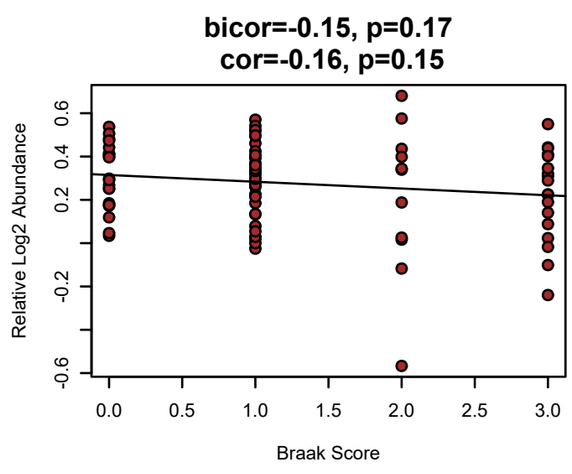

NDUFA13 UPenn Mixed PRM
K-W ANOVA p: 0.24
Relative Log2 Abundance
Control
otherND
AD

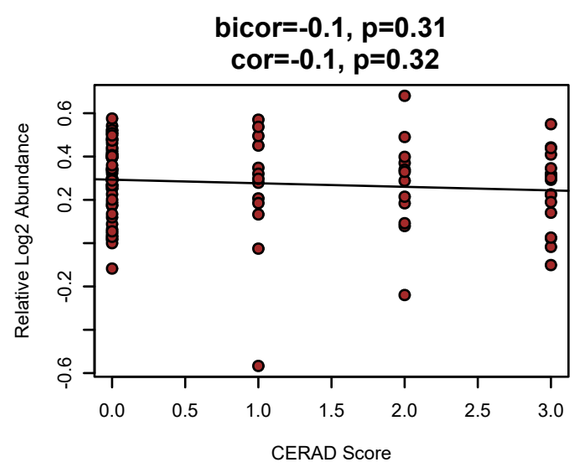

bicor=-0.15, p=0.16
cor=-0.18, p=0.1
Relative Log2 Abundance
Braak Score

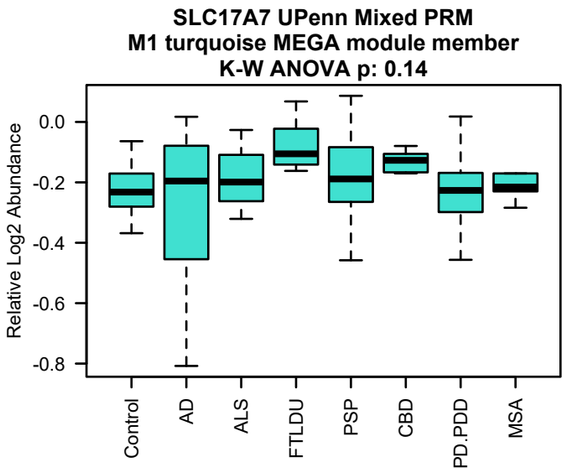

bicor=-0.083, p=0.41
cor=-0.12, p=0.23
Relative Log2 Abundance
CERAD Score

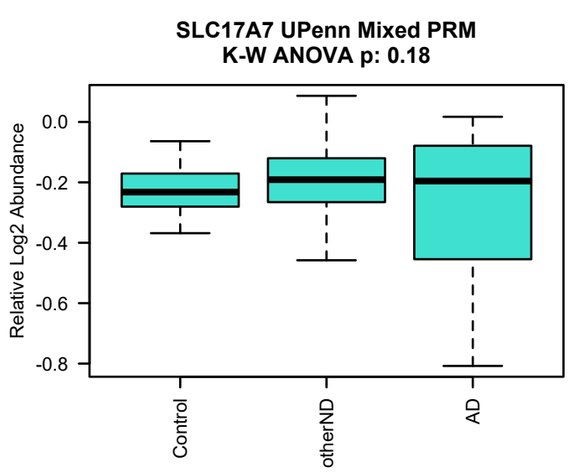

SUCLA2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.056
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

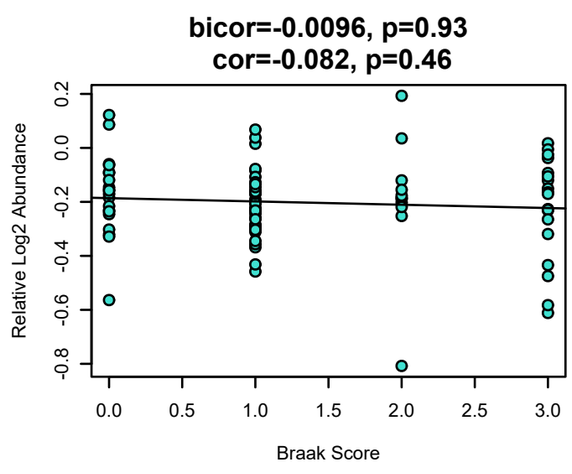

SUCLA2 UPenn Mixed PRM
K-W ANOVA p: 0.14
Relative Log2 Abundance
Control
otherND
AD

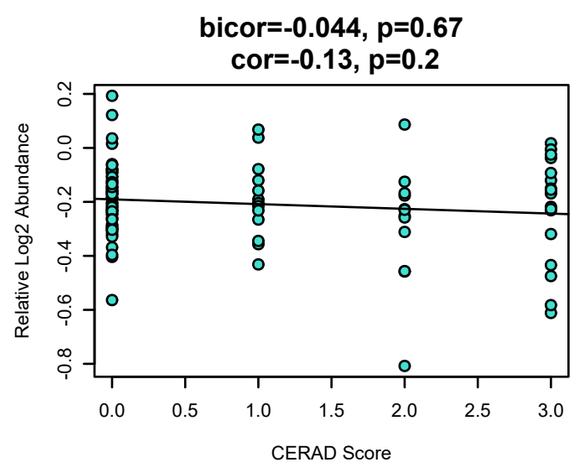

bicor=-0.15, p=0.17
cor=-0.16, p=0.15
Relative Log2 Abundance
Braak Score

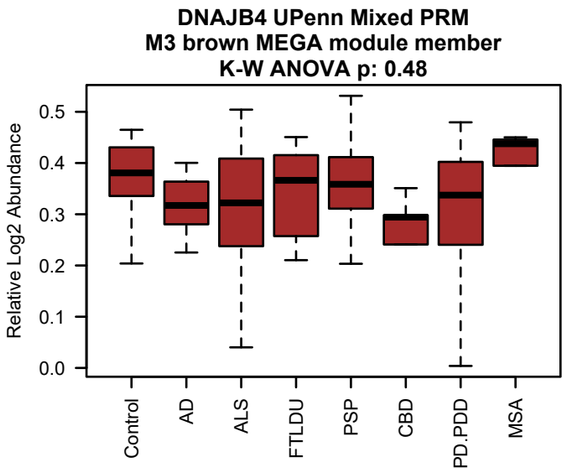

bicor=-0.1, p=0.31
cor=-0.1, p=0.32
Relative Log2 Abundance
CERAD Score

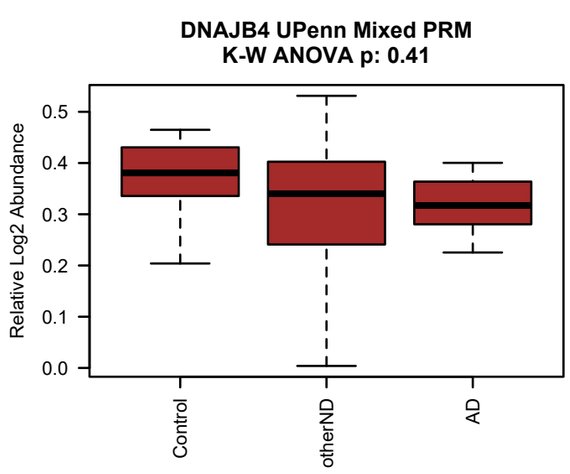

SLC17A7 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.14
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

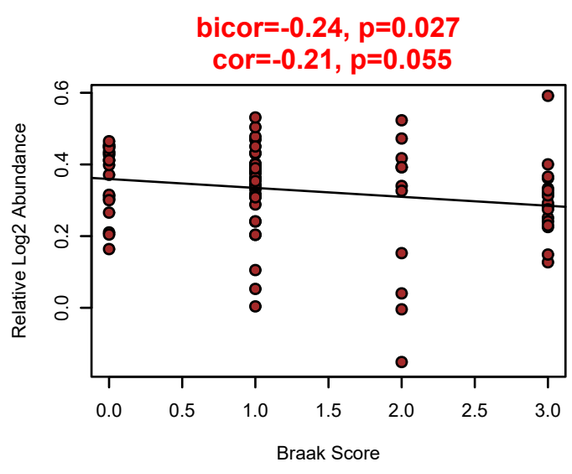

SLC17A7 UPenn Mixed PRM
K-W ANOVA p: 0.18
Relative Log2 Abundance
Control
otherND
AD

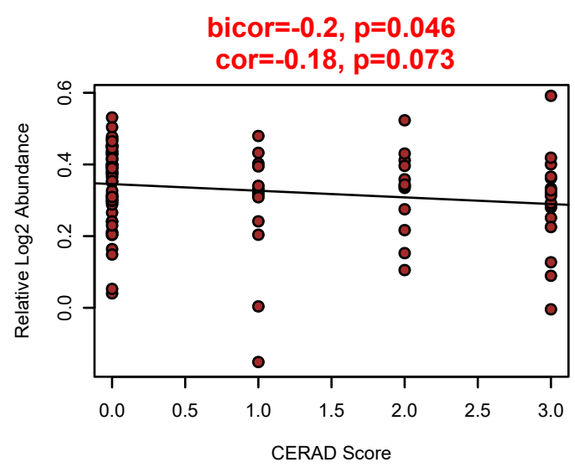

bicor=-0.0096, p=0.93
cor=-0.082, p=0.46
Relative Log2 Abundance
Braak Score

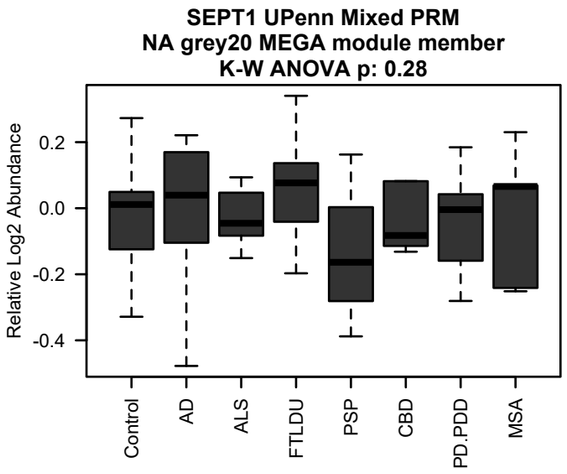

bicor=-0.044, p=0.67
cor=-0.13, p=0.2
Relative Log2 Abundance
CERAD Score

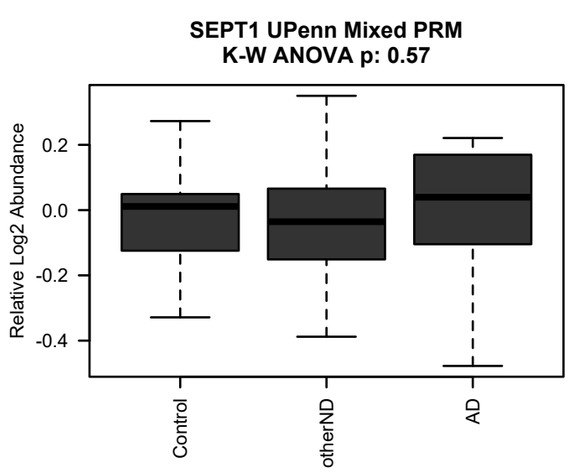

DNAJB4 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.48
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

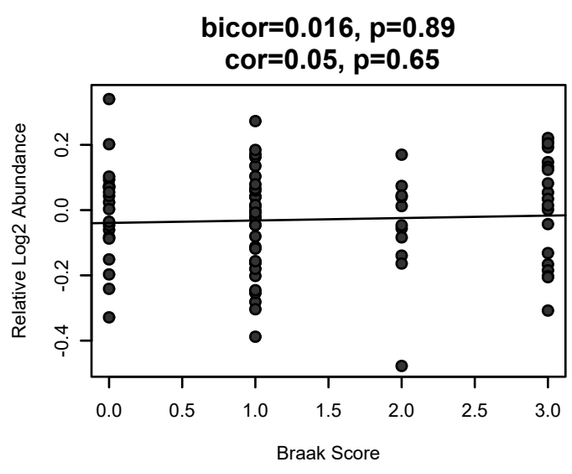

DNAJB4 UPenn Mixed PRM
K-W ANOVA p: 0.41
Relative Log2 Abundance
Control
otherND
AD

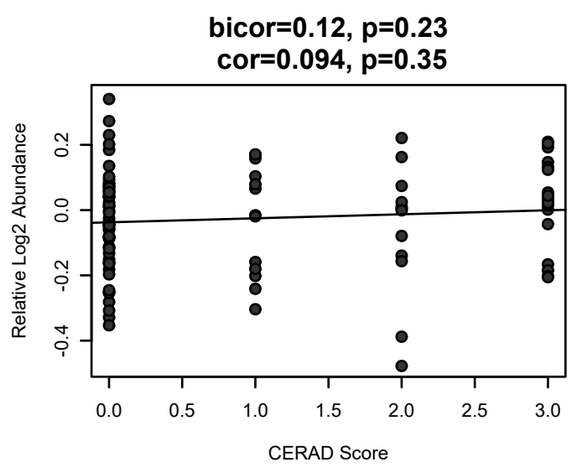

bicor=-0.24, p=0.027
cor=-0.21, p=0.055
Relative Log2 Abundance
Braak Score

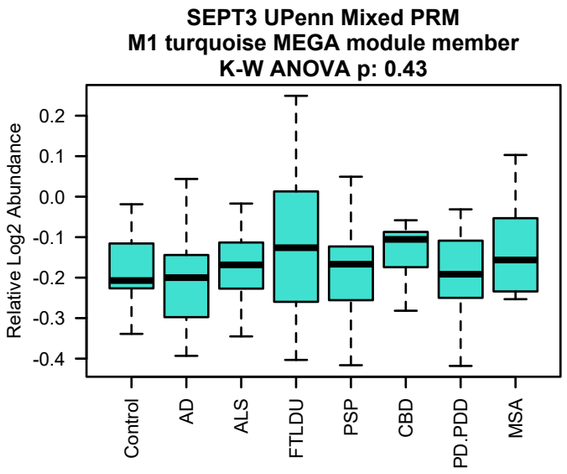

bicor=-0.2, p=0.046
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

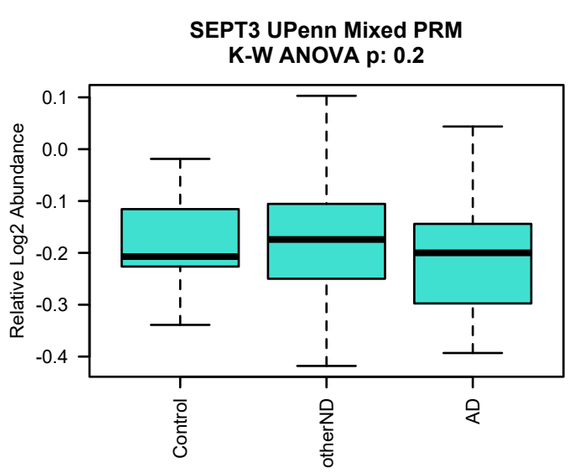

SEPT1 UPenn Mixed PRM
NA grey20 MEGA module member
K-W ANOVA p: 0.28
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

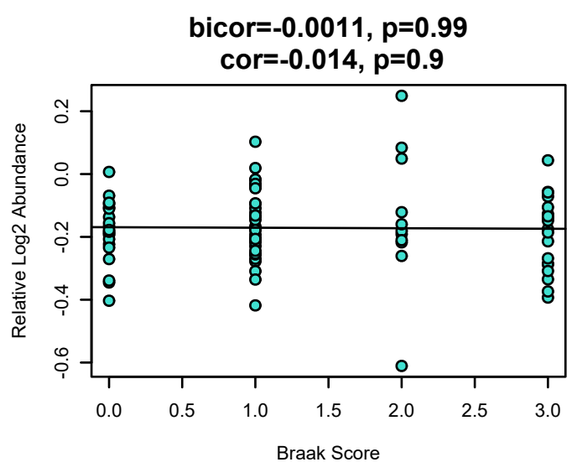

SEPT1 UPenn Mixed PRM
K-W ANOVA p: 0.57
Relative Log2 Abundance
Control
otherND
AD

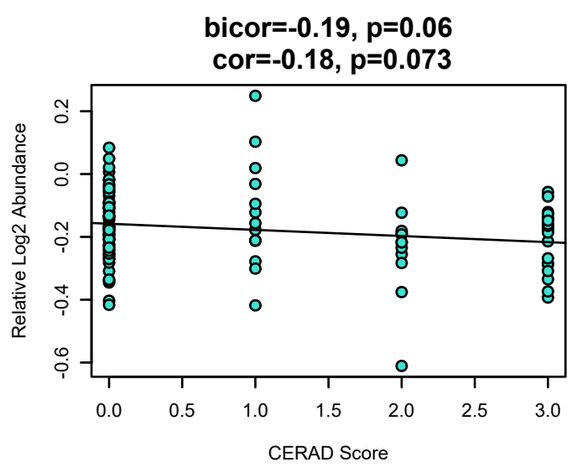

bicor=0.016, p=0.89
cor=0.05, p=0.65
Relative Log2 Abundance
Braak Score

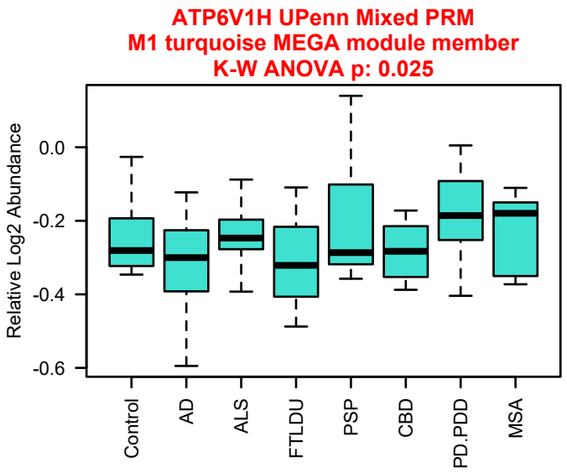

bicor=0.12, p=0.23
cor=0.094, p=0.35
Relative Log2 Abundance
CERAD Score

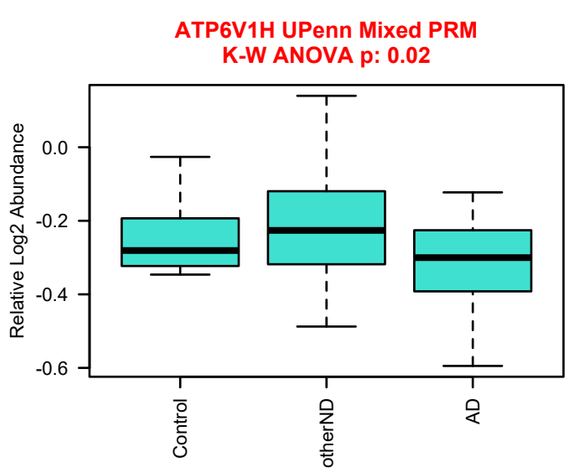

SEPT3 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.43
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

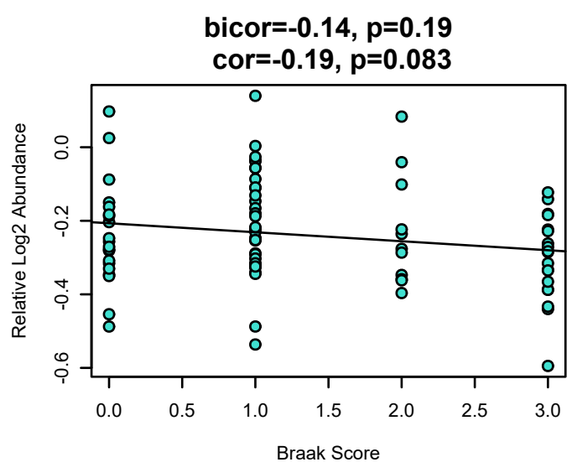

SEPT3 UPenn Mixed PRM
K-W ANOVA p: 0.2
Relative Log2 Abundance
Control
otherND
AD

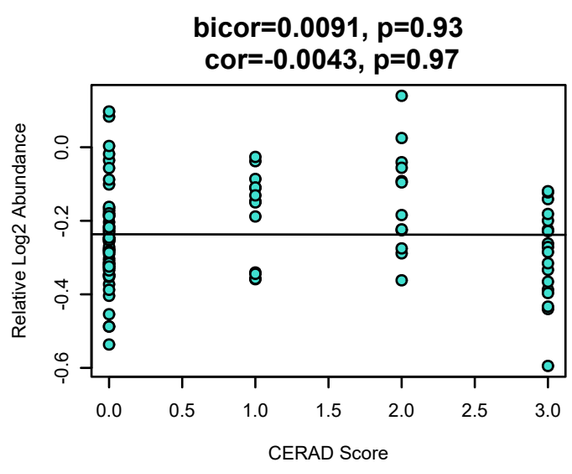

bicor=-0.0011, p=0.99
cor=-0.014, p=0.9
Relative Log2 Abundance
Braak Score

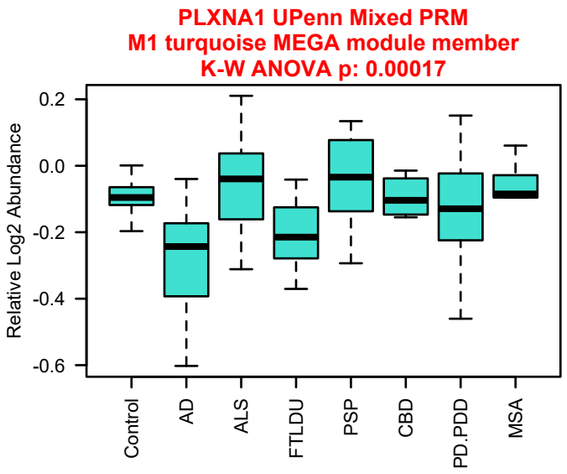

bicor=-0.19, p=0.06
cor=-0.18, p=0.073
Relative Log2 Abundance
CERAD Score

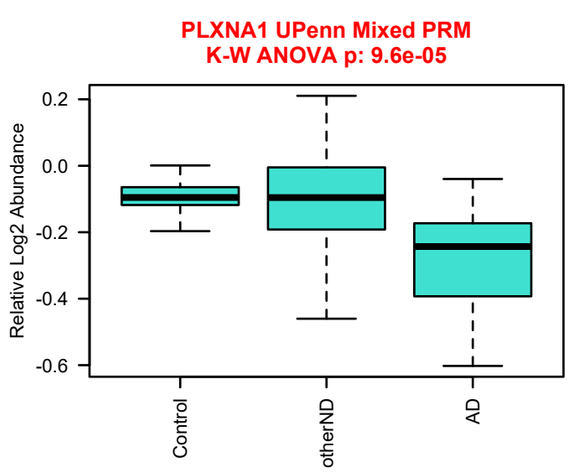

ATP6V1H UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.025
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

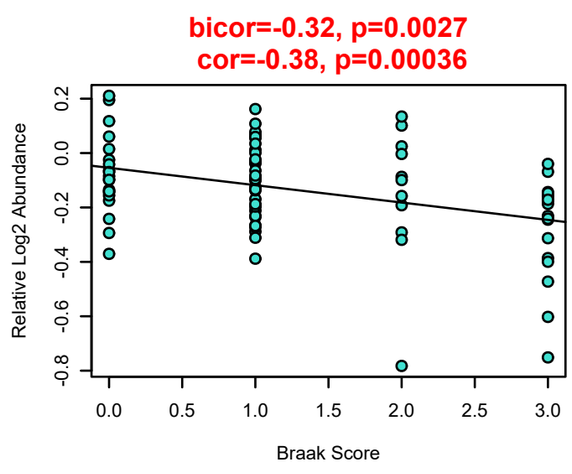

ATP6V1H UPenn Mixed PRM
K-W ANOVA p: 0.02
Relative Log2 Abundance
Control
otherND
AD

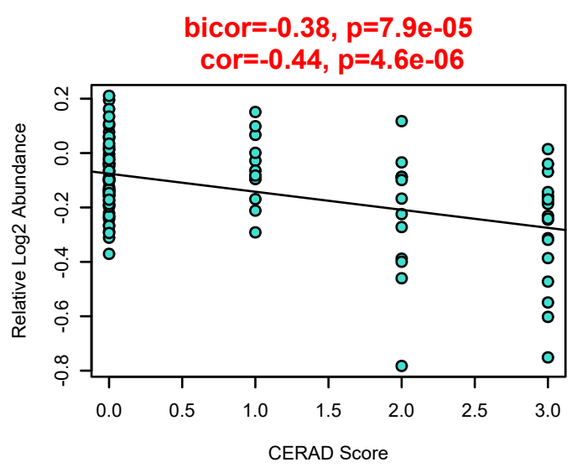

bicor=-0.14, p=0.19
cor=-0.19, p=0.083
Relative Log2 Abundance
Braak Score

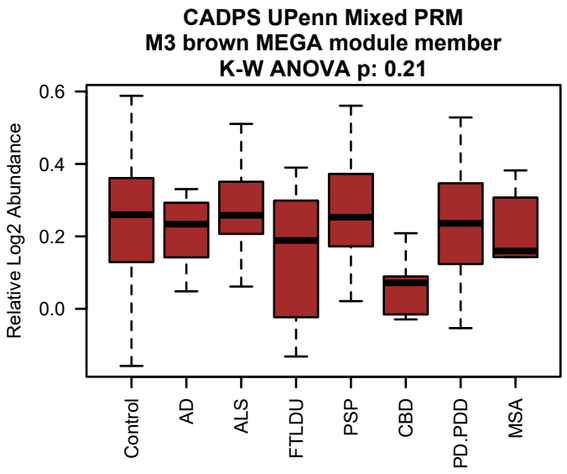

bicor=0.0091, p=0.93
cor=-0.0043, p=0.97
Relative Log2 Abundance
CERAD Score

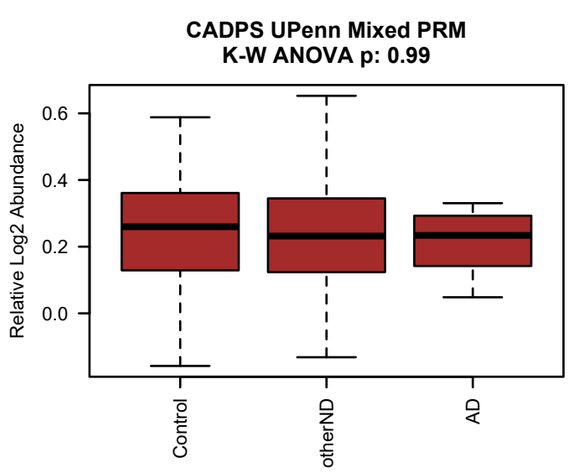

PLXNA1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00017
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

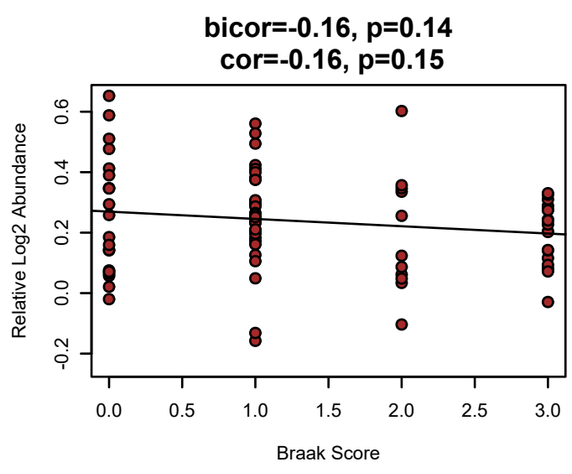

PLXNA1 UPenn Mixed PRM
K-W ANOVA p: 9.6e-05
Relative Log2 Abundance
Control
otherND
AD

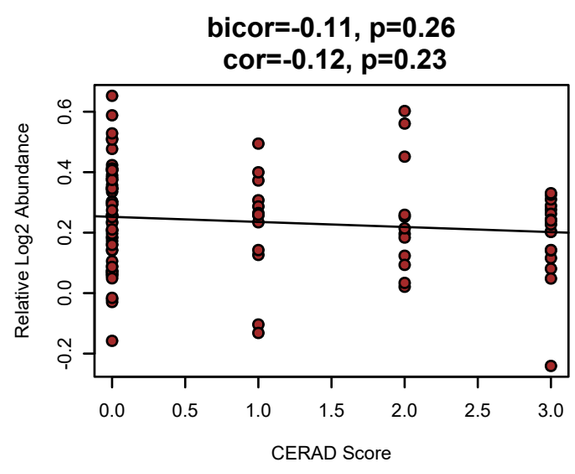

bicor=-0.32, p=0.0027
cor=-0.38, p=0.00036
Relative Log2 Abundance
Braak Score

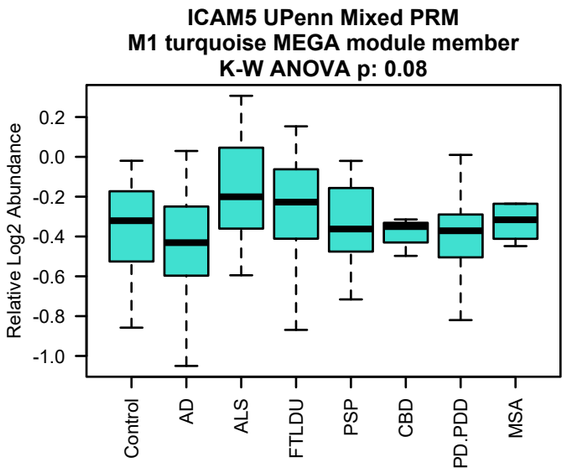

bicor=-0.38, p=7.9e-05
cor=-0.44, p=4.6e-06
Relative Log2 Abundance
CERAD Score

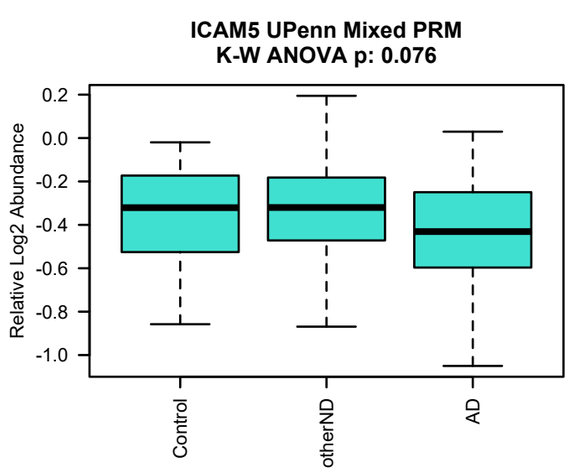

CADPS UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.21
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

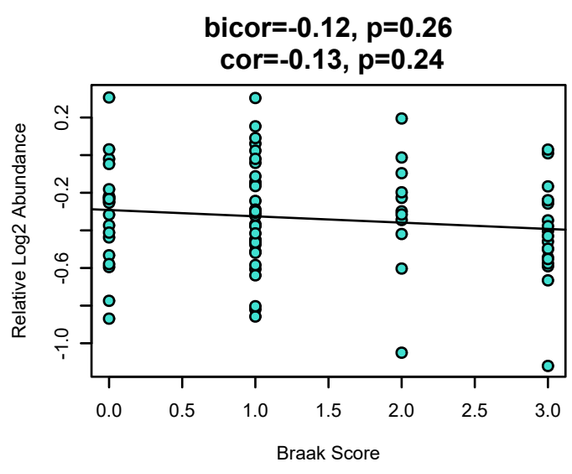

CADPS UPenn Mixed PRM
K-W ANOVA p: 0.99
Relative Log2 Abundance
Control
otherND
AD

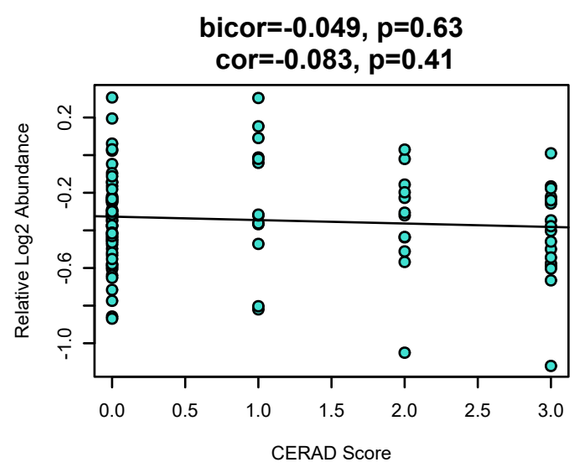

bicor=-0.16, p=0.14
cor=-0.16, p=0.15
Relative Log2 Abundance
Braak Score

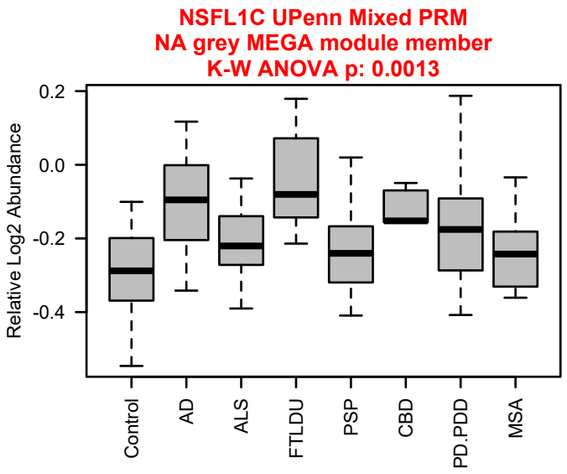

bicor=-0.11, p=0.26
cor=-0.12, p=0.23
Relative Log2 Abundance
CERAD Score

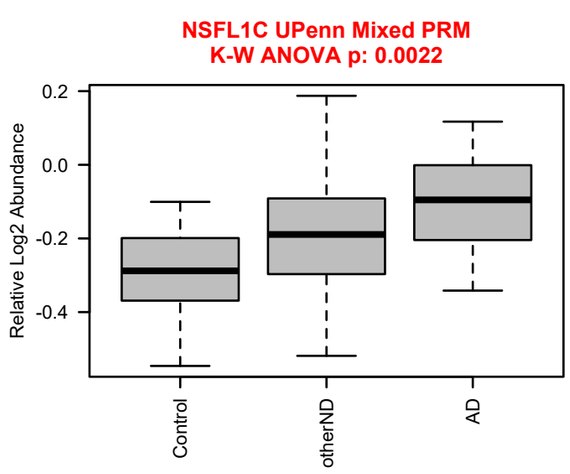

ICAM5 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.08
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

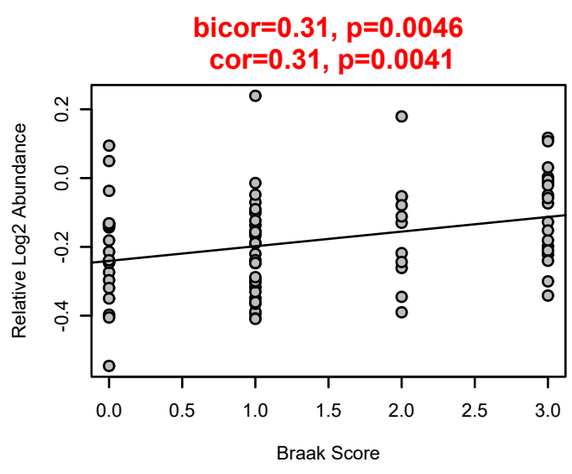

ICAM5 UPenn Mixed PRM
K-W ANOVA p: 0.076
Relative Log2 Abundance
Control
otherND
AD

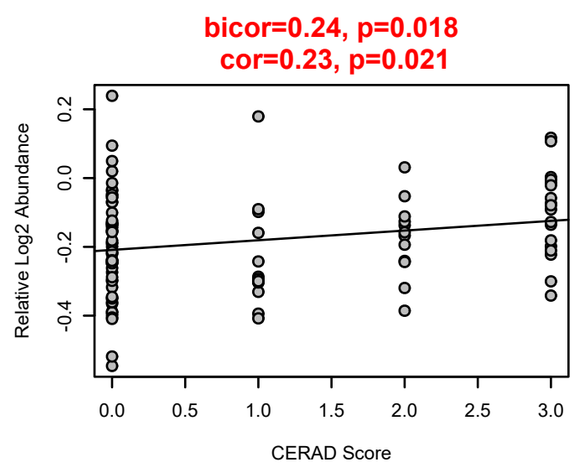

bicor=-0.12, p=0.26
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

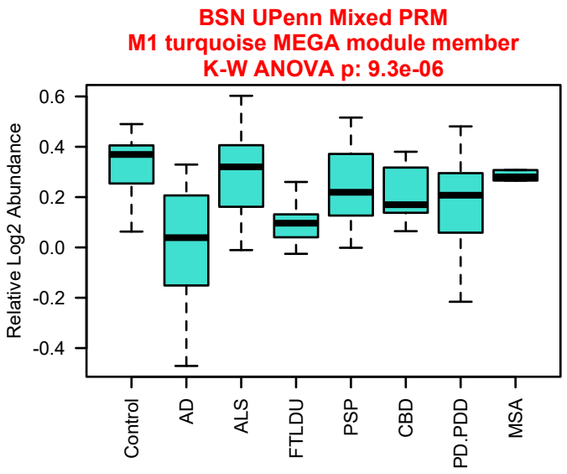

bicor=-0.049, p=0.63
cor=-0.083, p=0.41
Relative Log2 Abundance
CERAD Score

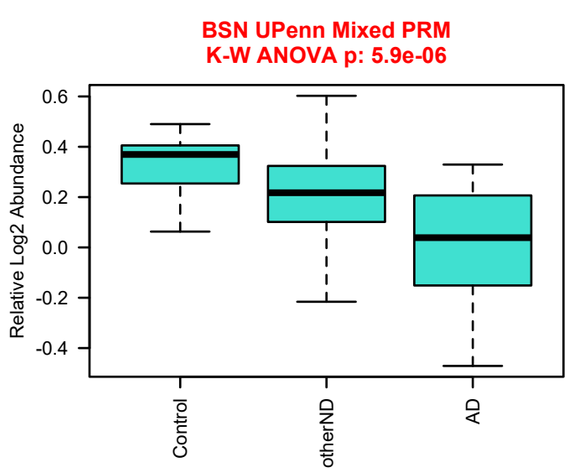

NSFL1C UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.0013
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

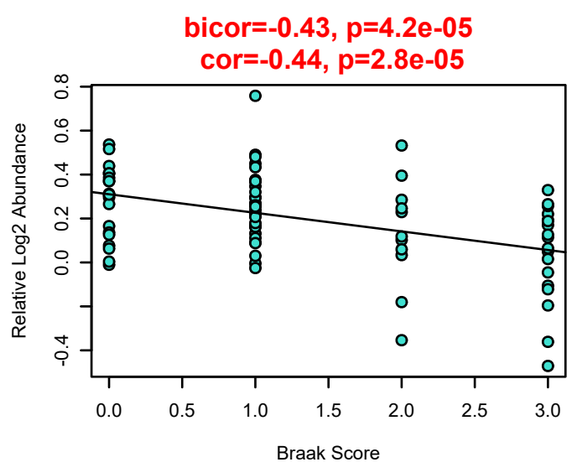

NSFL1C UPenn Mixed PRM
K-W ANOVA p: 0.0022
Relative Log2 Abundance
Control
otherND
AD

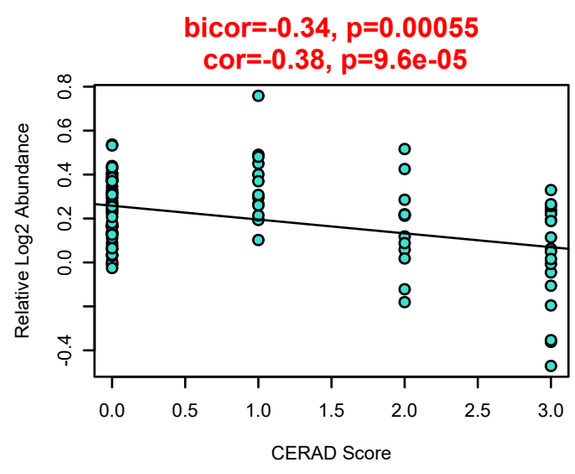

bicor=0.31, p=0.0046
cor=0.31, p=0.0041
Relative Log2 Abundance
Braak Score

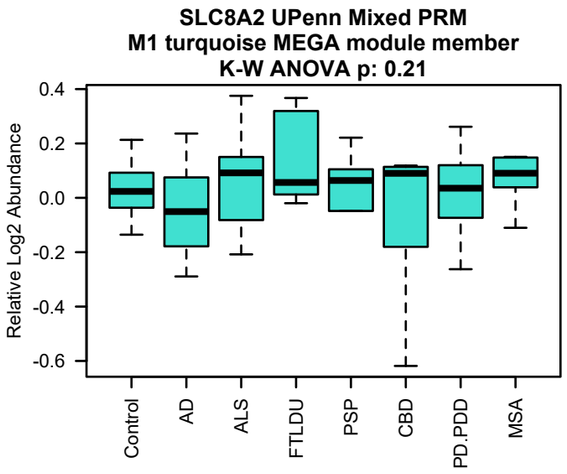

bicor=0.24, p=0.018
cor=0.23, p=0.021
Relative Log2 Abundance
CERAD Score

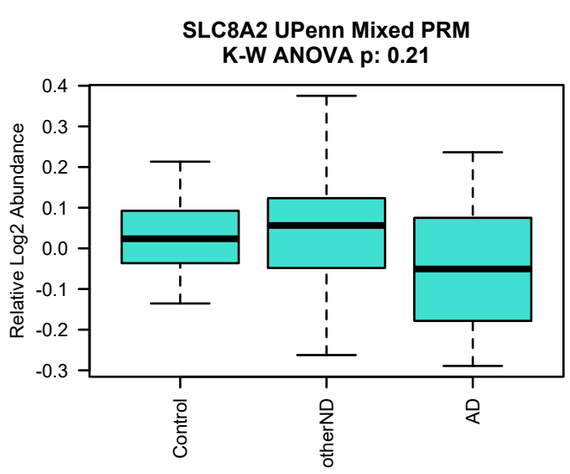

BSN UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 9.3e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

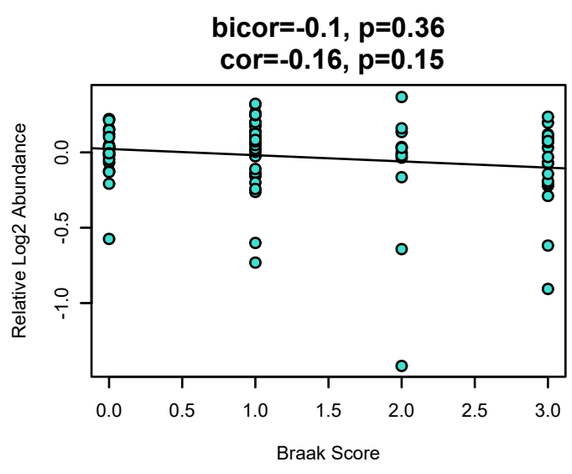

BSN UPenn Mixed PRM
K-W ANOVA p: 5.9e-06
Relative Log2 Abundance
Control
otherND
AD

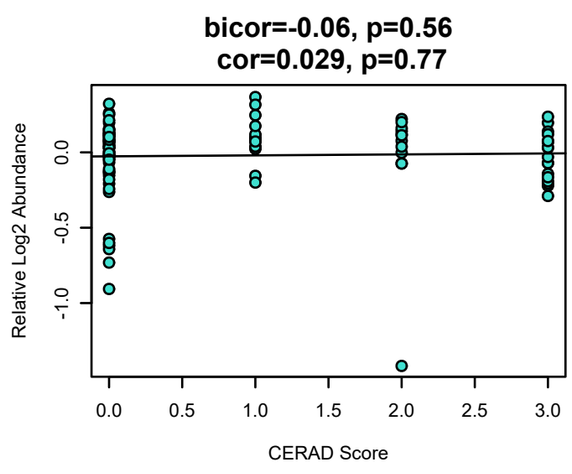

bicor=-0.43, p=4.2e-05
cor=-0.44, p=2.8e-05
Relative Log2 Abundance
Braak Score

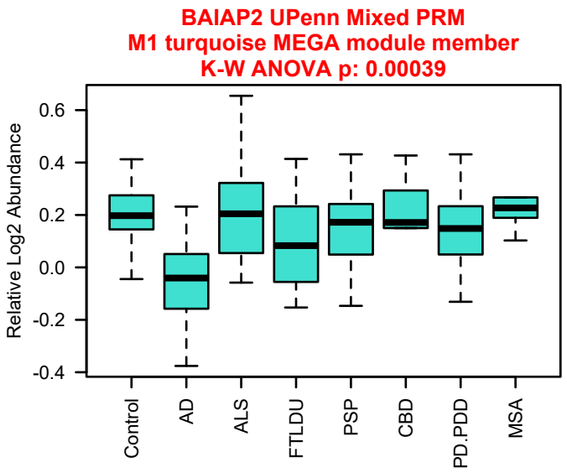

bicor=-0.34, p=0.00055
cor=-0.38, p=9.6e-05
Relative Log2 Abundance
CERAD Score

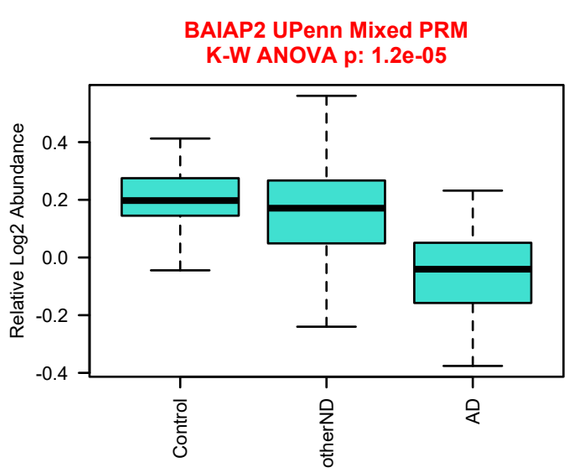

SLC8A2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.21
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

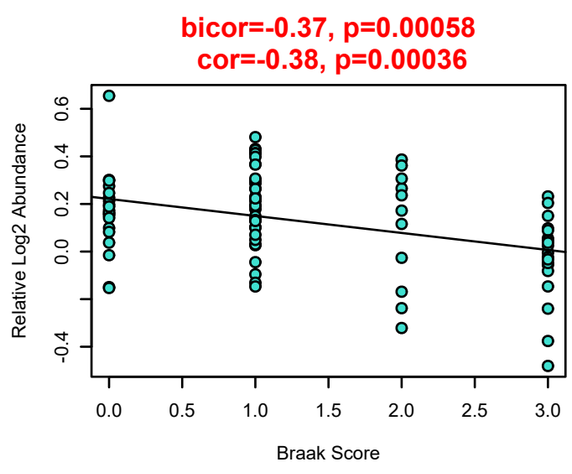

SLC8A2 UPenn Mixed PRM
K-W ANOVA p: 0.21
Relative Log2 Abundance
Control
otherND
AD

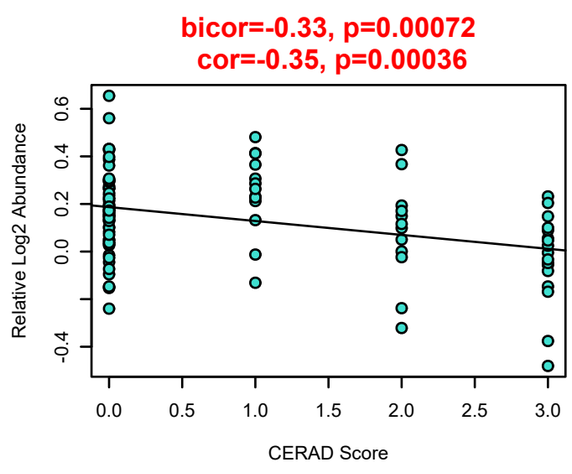

bicor=-0.1, p=0.36
cor=-0.16, p=0.15
Relative Log2 Abundance
Braak Score

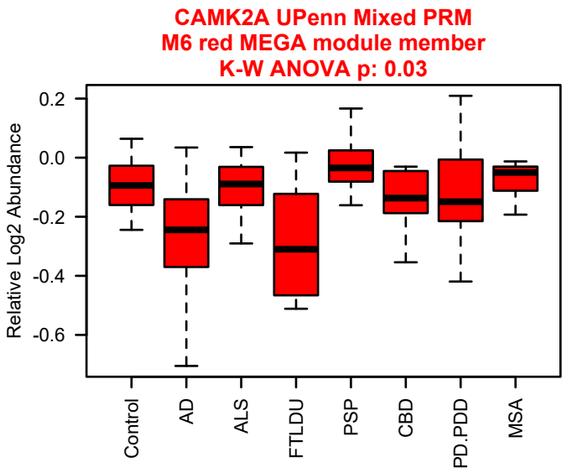

bicor=-0.06, p=0.56
cor=0.029, p=0.77
Relative Log2 Abundance
CERAD Score

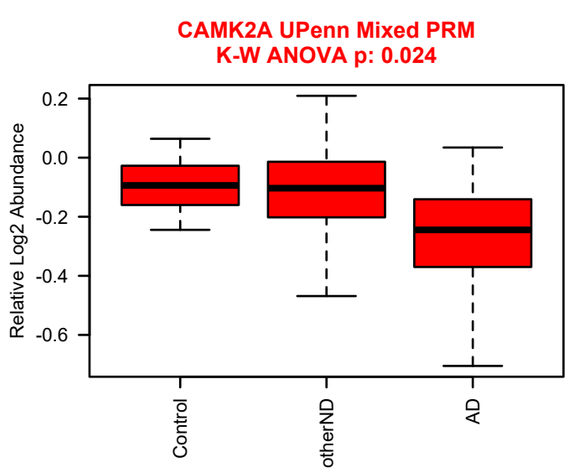

BAIAP2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.00039
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

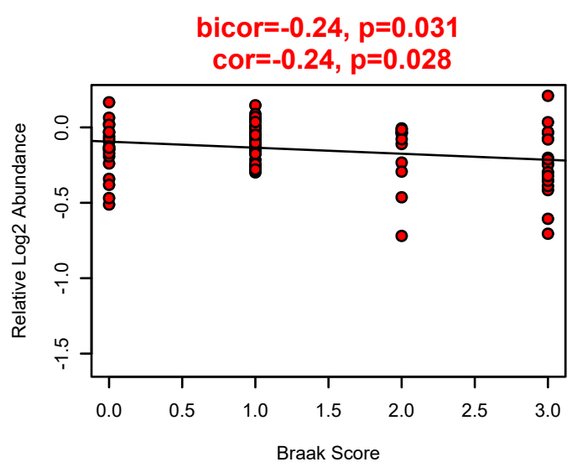

BAIAP2 UPenn Mixed PRM
K-W ANOVA p: 1.2e-05
Relative Log2 Abundance
Control
otherND
AD

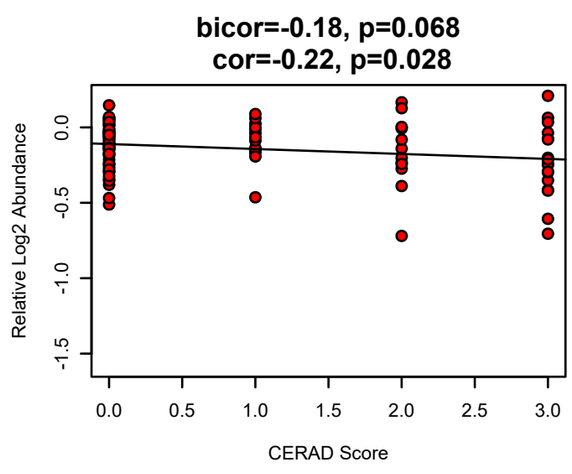

bicor=-0.37, p=0.00058
cor=-0.38, p=0.00036
Relative Log2 Abundance
Braak Score

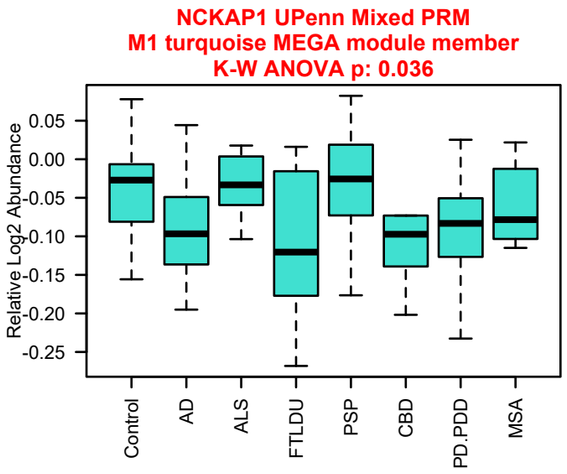

bicor=-0.33, p=0.00072
cor=-0.35, p=0.00036
Relative Log2 Abundance
CERAD Score

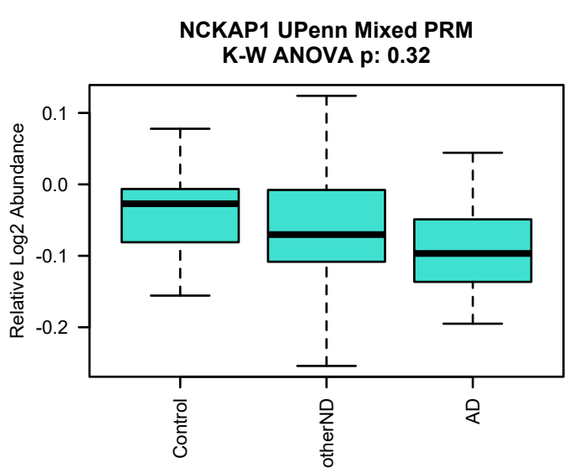

CAMK2A UPenn Mixed PRM
M6 red MEGA module member
K-W ANOVA p: 0.03
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

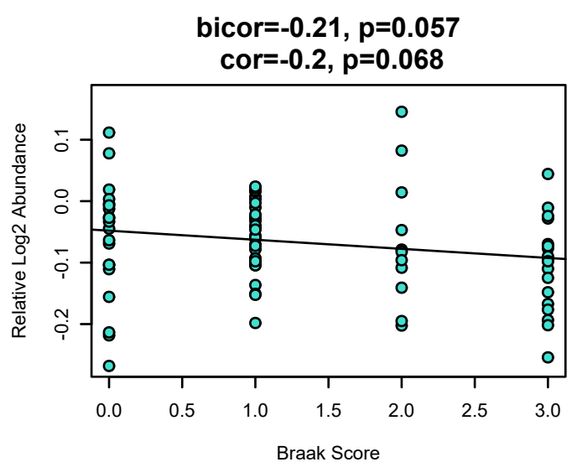

CAMK2A UPenn Mixed PRM
K-W ANOVA p: 0.024
Relative Log2 Abundance
Control
otherND
AD

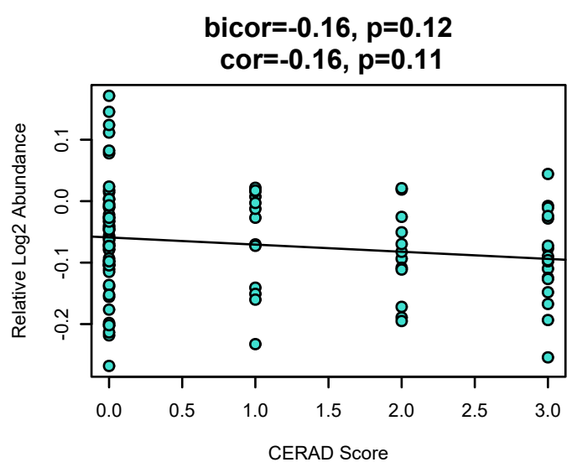

bicor=-0.24, p=0.031
cor=-0.24, p=0.028
Relative Log2 Abundance
Braak Score

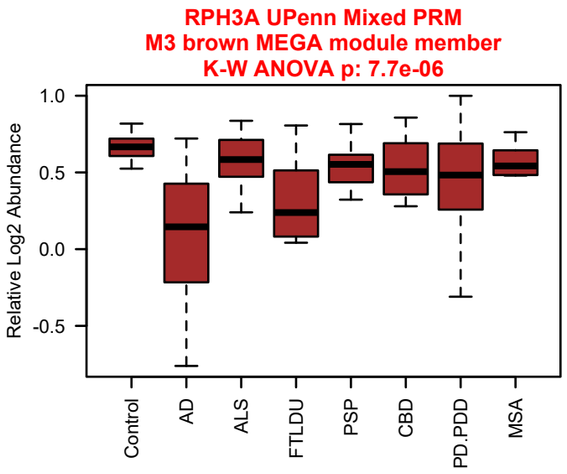

bicor=-0.18, p=0.068
cor=-0.22, p=0.028
Relative Log2 Abundance
CERAD Score

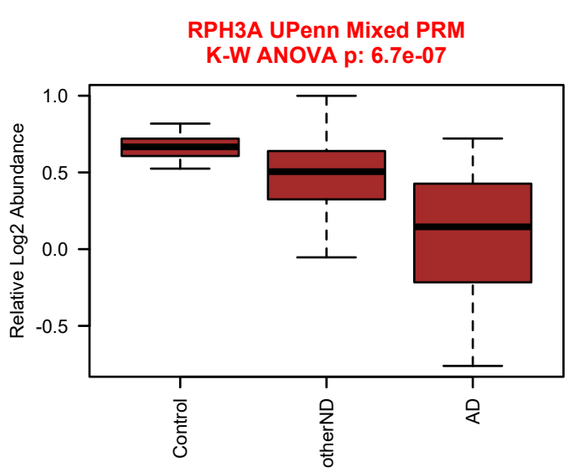

NCKAP1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.036
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

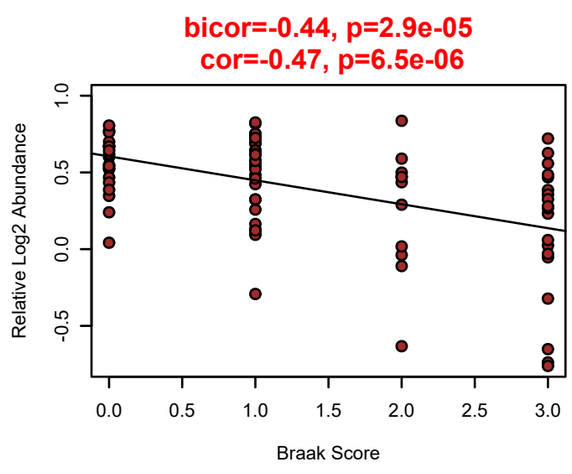

NCKAP1 UPenn Mixed PRM
K-W ANOVA p: 0.32
Relative Log2 Abundance
Control
otherND
AD

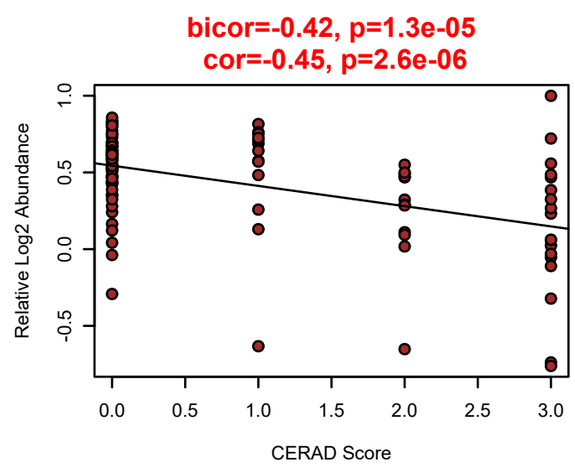

bicor=-0.21, p=0.057
cor=-0.2, p=0.068
Relative Log2 Abundance
Braak Score

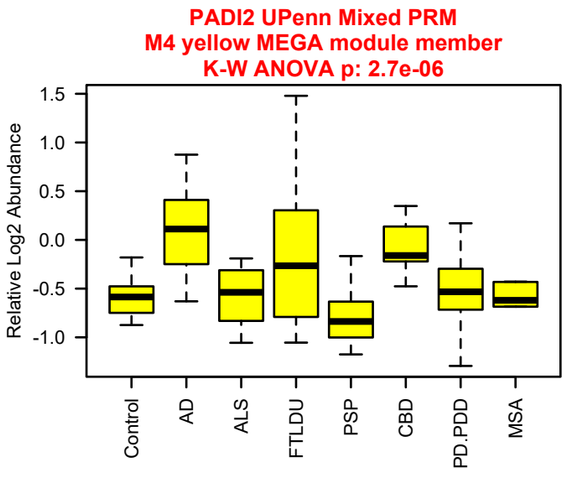

bicor=-0.16, p=0.12
cor=-0.16, p=0.11
Relative Log2 Abundance
CERAD Score

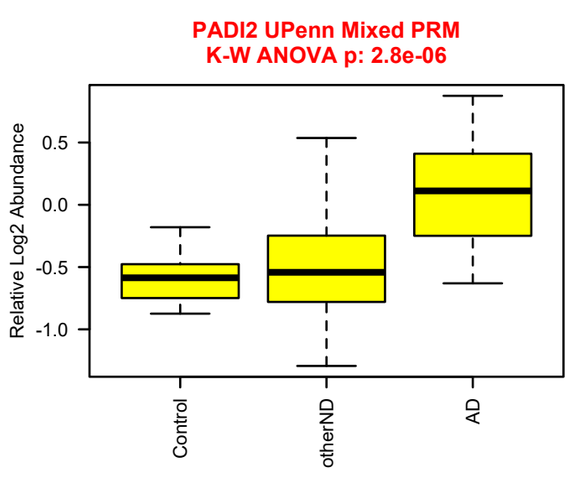

RPH3A UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 7.7e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

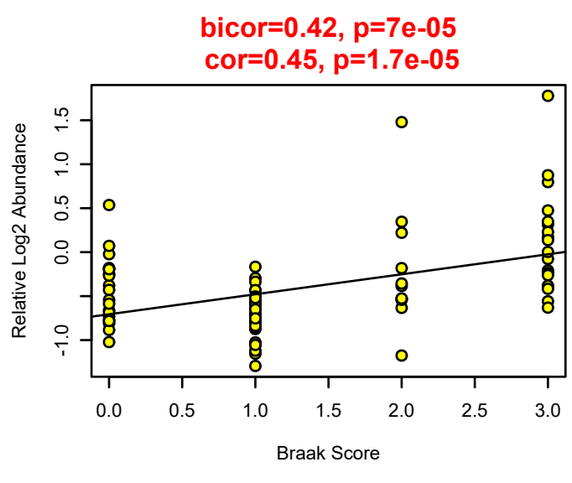

RPH3A UPenn Mixed PRM
K-W ANOVA p: 6.7e-07
Relative Log2 Abundance
Control
otherND
AD

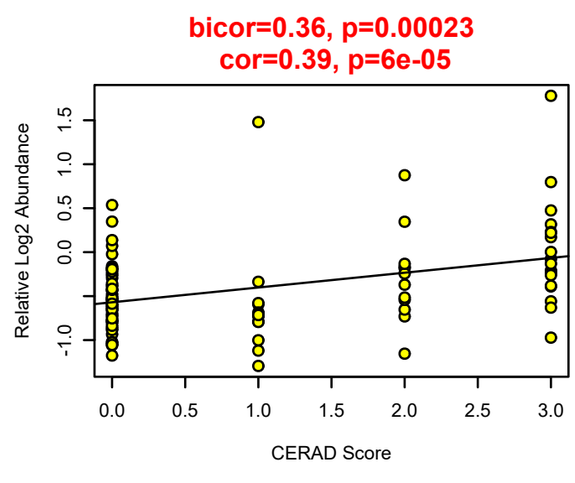

bicor=-0.44, p=2.9e-05
cor=-0.47, p=6.5e-06
Relative Log2 Abundance
Braak Score

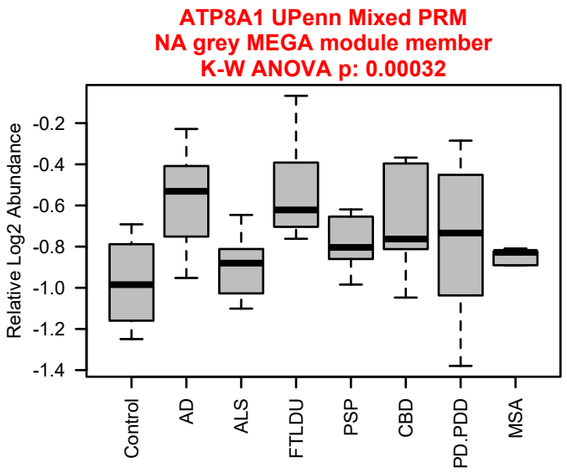

bicor=-0.42, p=1.3e-05
cor=-0.45, p=2.6e-06
Relative Log2 Abundance
CERAD Score

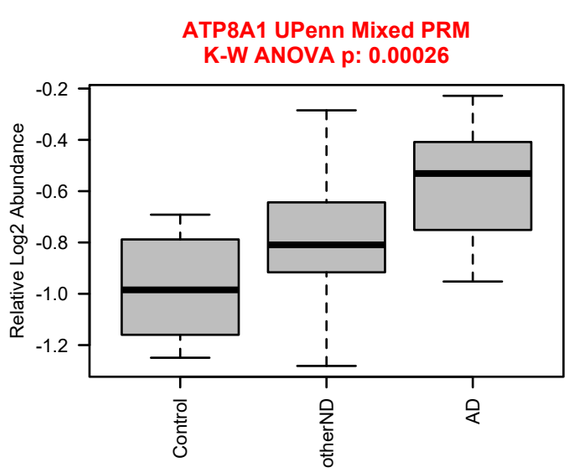

PADI2 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 2.7e-06
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

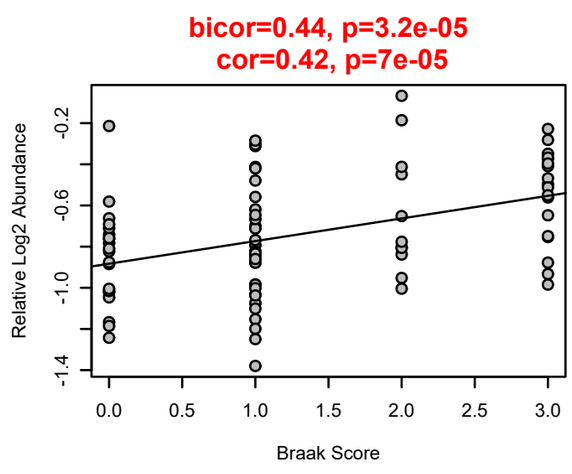

PADI2 UPenn Mixed PRM
K-W ANOVA p: 2.8e-06
Relative Log2 Abundance
Control
otherND
AD

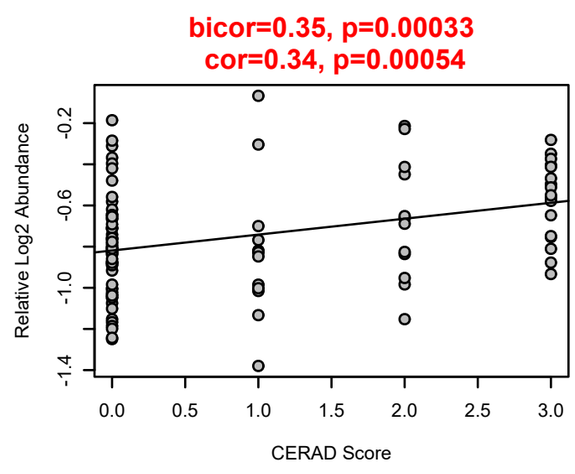

bicor=0.42, p=7e-05
cor=0.45, p=1.7e-05
Relative Log2 Abundance
Braak Score

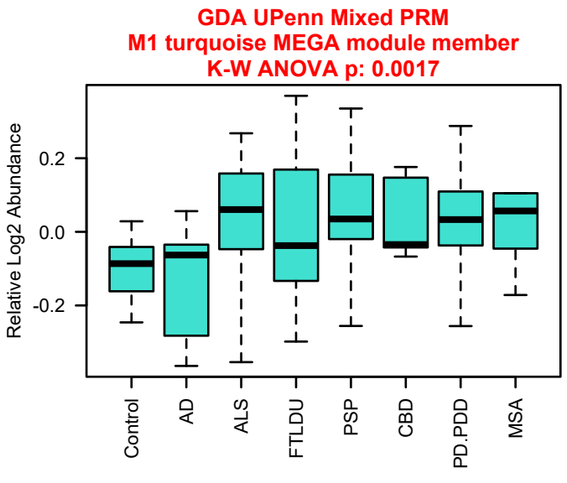

bicor=0.36, p=0.00023
cor=0.39, p=6e-05
Relative Log2 Abundance
CERAD Score

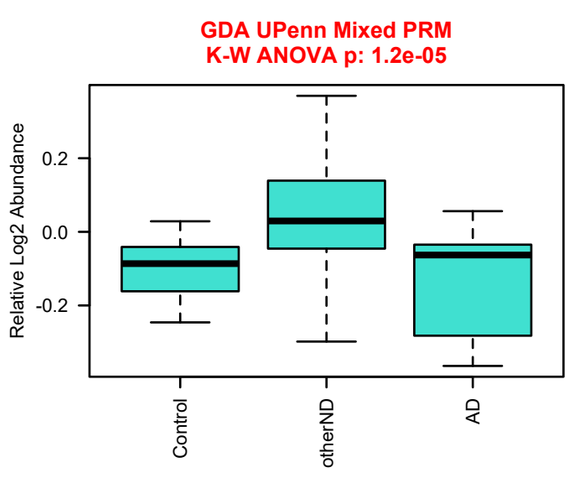

ATP8A1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.00032
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

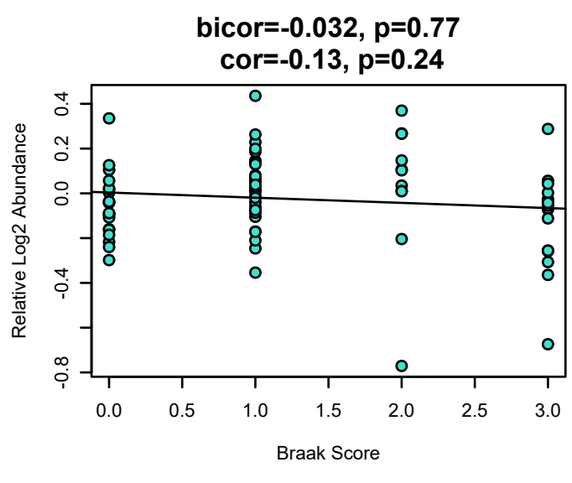

ATP8A1 UPenn Mixed PRM
K-W ANOVA p: 0.00026
Relative Log2 Abundance
Control
otherND
AD

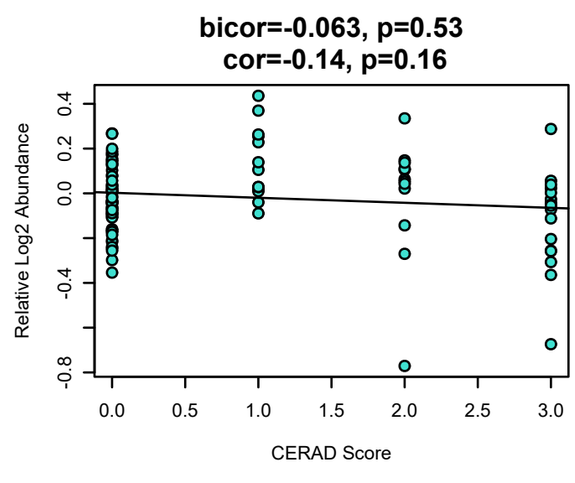

bicor=0.44, p=3.2e-05
cor=0.42, p=7e-05
Relative Log2 Abundance
Braak Score

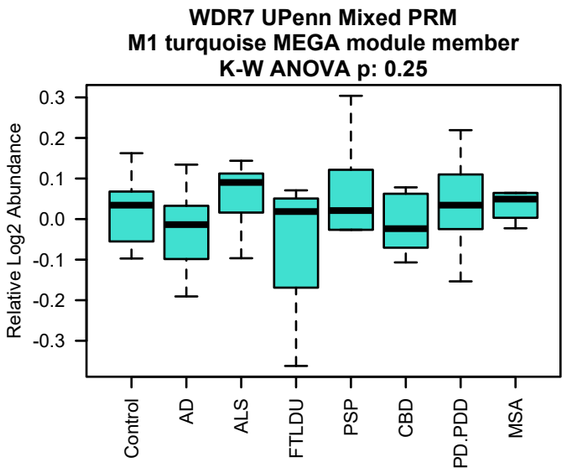

bicor=0.35, p=0.00033
cor=0.34, p=0.00054
Relative Log2 Abundance
CERAD Score

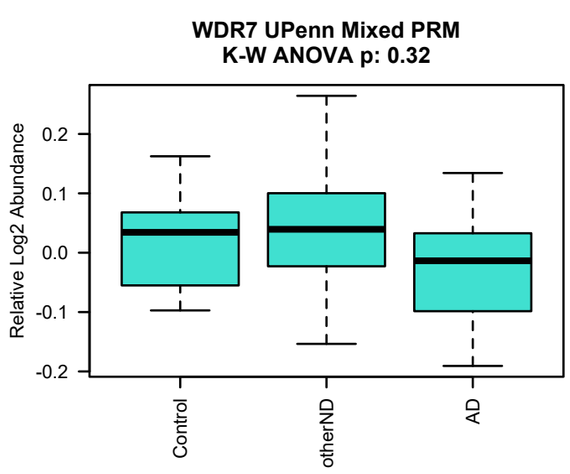

GDA UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0017
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

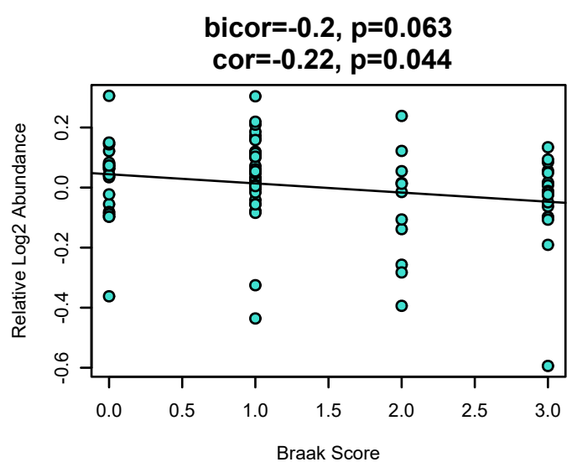

GDA UPenn Mixed PRM
K-W ANOVA p: 1.2e-05
Relative Log2 Abundance
Control
otherND
AD

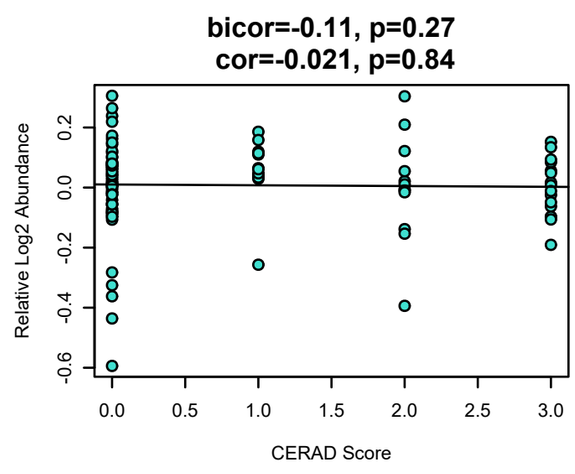

bicor=-0.032, p=0.77
cor=-0.13, p=0.24
Relative Log2 Abundance
Braak Score

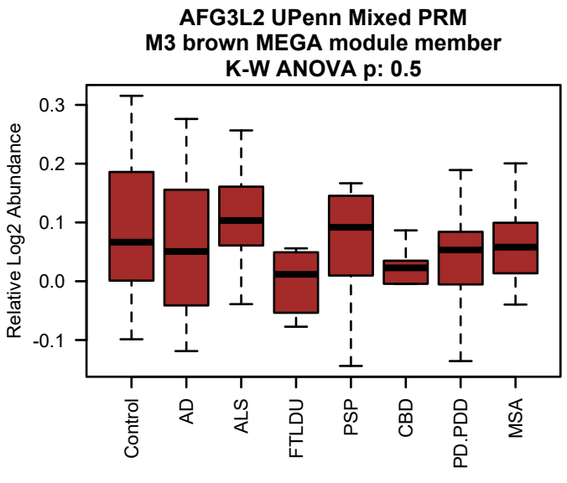

bicor=-0.063, p=0.53
cor=-0.14, p=0.16
Relative Log2 Abundance
CERAD Score

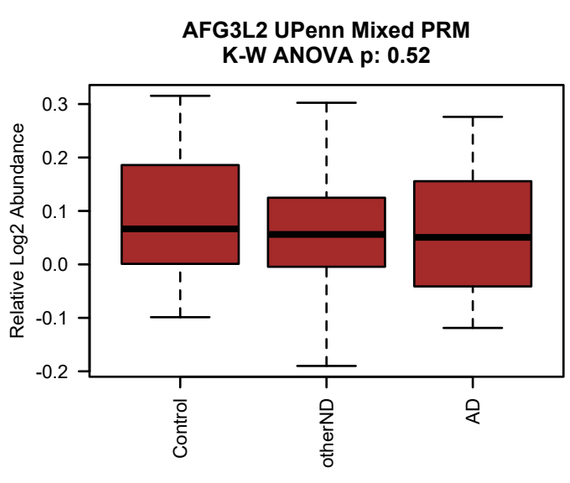

WDR7 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.25
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

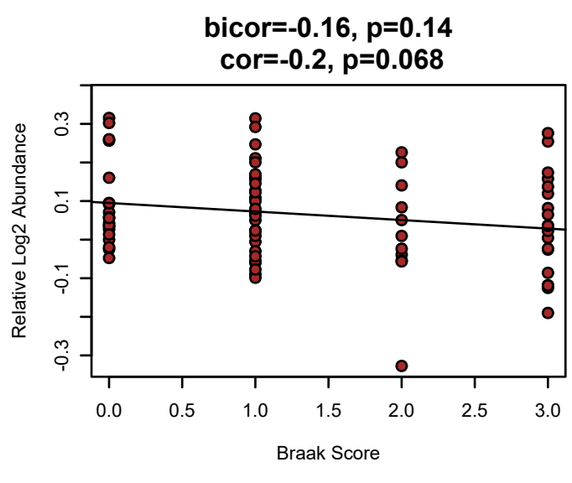

WDR7 UPenn Mixed PRM
K-W ANOVA p: 0.32
Relative Log2 Abundance
Control
otherND
AD

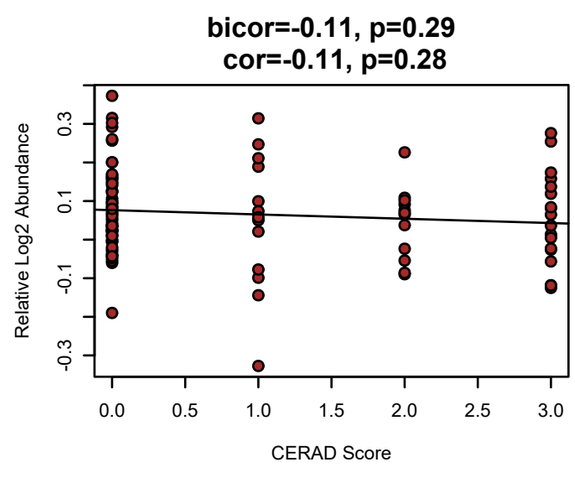

bicor=-0.2, p=0.063
cor=-0.22, p=0.044
Relative Log2 Abundance
Braak Score

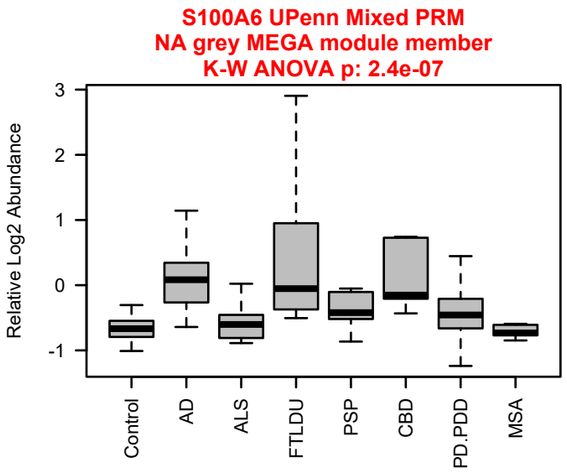

bicor=-0.11, p=0.27
cor=-0.021, p=0.84
Relative Log2 Abundance
CERAD Score

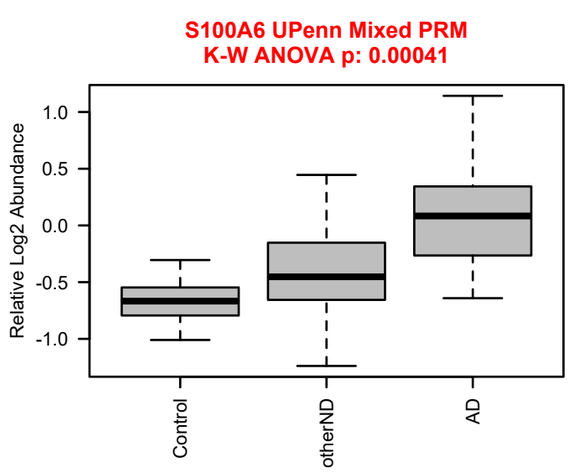

AFG3L2 UPenn Mixed PRM
M3 brown MEGA module member
K-W ANOVA p: 0.5
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

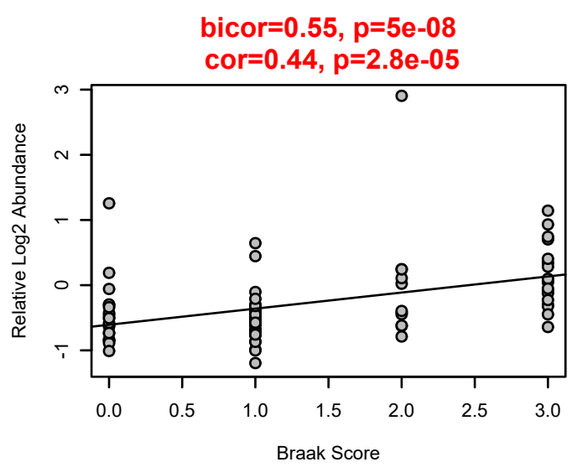

AFG3L2 UPenn Mixed PRM
K-W ANOVA p: 0.52
Relative Log2 Abundance
Control
otherND
AD

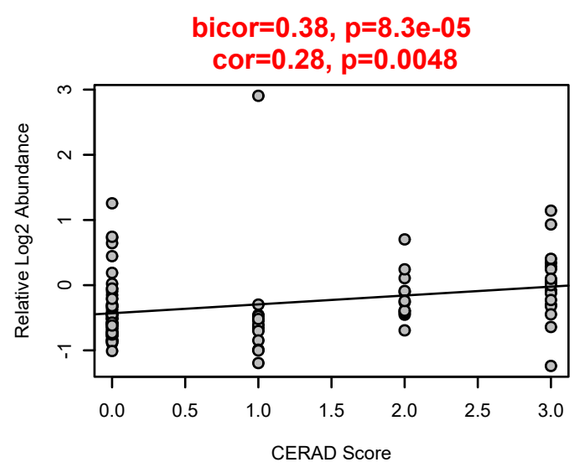

bicor=-0.16, p=0.14
cor=-0.2, p=0.068
Relative Log2 Abundance
Braak Score

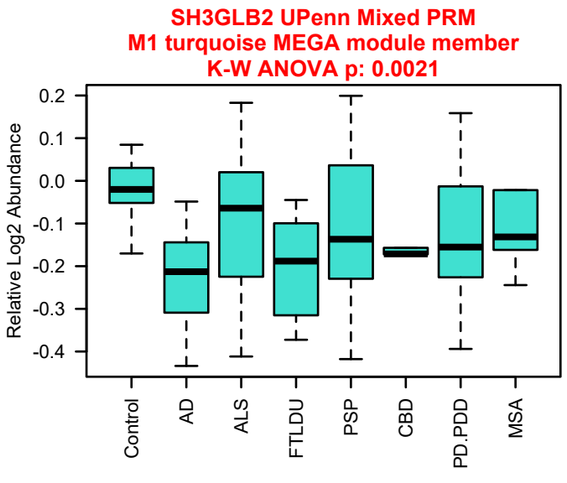

bicor=-0.11, p=0.29
cor=-0.11, p=0.28
Relative Log2 Abundance
CERAD Score

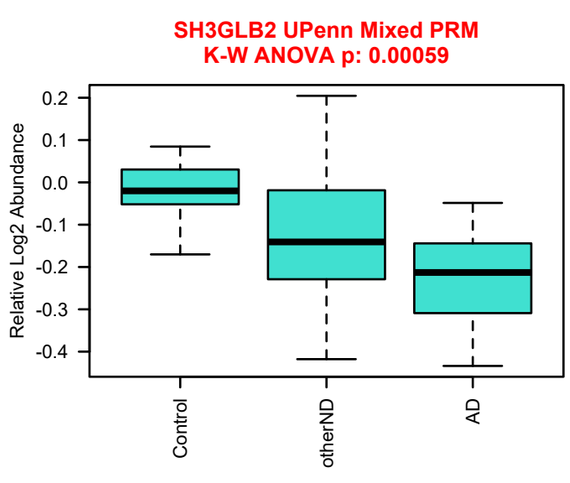

S100A6 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 2.4e-07
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

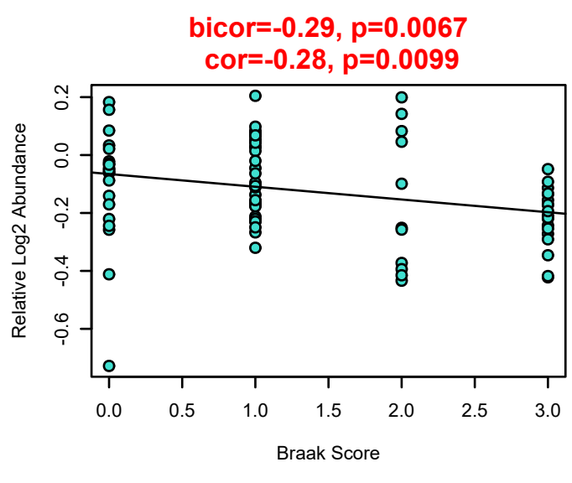

S100A6 UPenn Mixed PRM
K-W ANOVA p: 0.00041
Relative Log2 Abundance
Control
otherND
AD

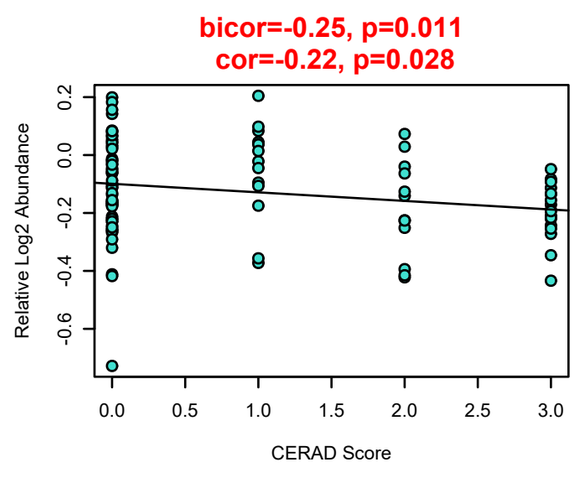

bicor=0.55, p=5e-08
cor=0.44, p=2.8e-05
Relative Log2 Abundance
Braak Score

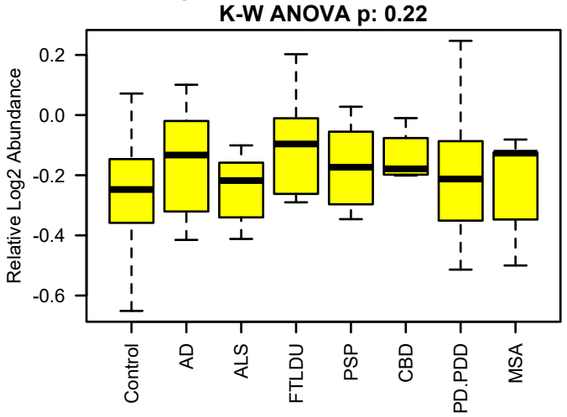

bicor=0.38, p=8.3e-05
cor=0.28, p=0.0048
Relative Log2 Abundance
CERAD Score

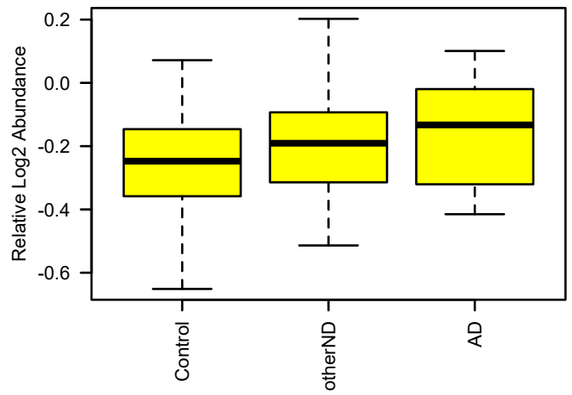

SH3GLB2 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.0021
Relative Log2 Abundance
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

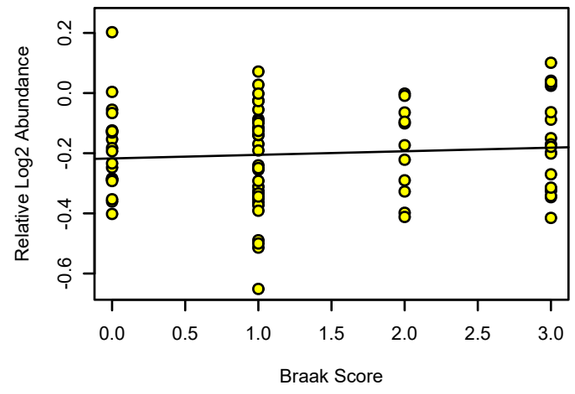

SH3GLB2 UPenn Mixed PRM
K-W ANOVA p: 0.00059
Relative Log2 Abundance
Control
otherND
AD

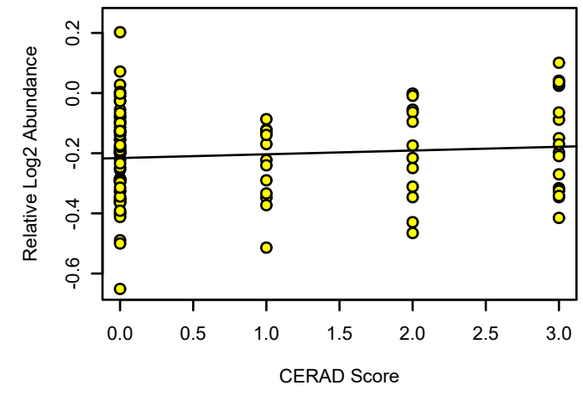

bicor=-0.29, p=0.0067
cor=-0.28, p=0.0099
Relative Log2 Abundance
Braak Score

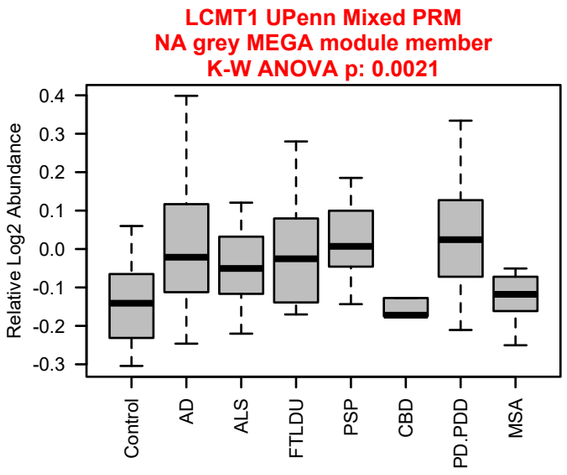

bicor=-0.25, p=0.011
cor=-0.22, p=0.028
Relative Log2 Abundance
CERAD Score

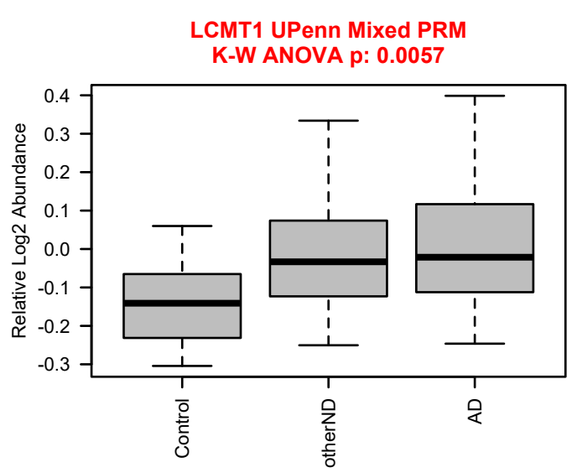

GLOD4 UPenn Mixed PRM
M4 yellow MEGA module member
K-W ANOVA p: 0.22
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

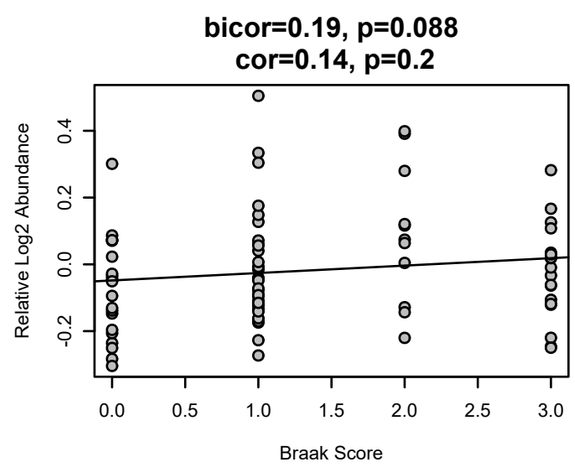

GLOD4 UPenn Mixed PRM
K-W ANOVA p: 0.14
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
Control
otherND
AD

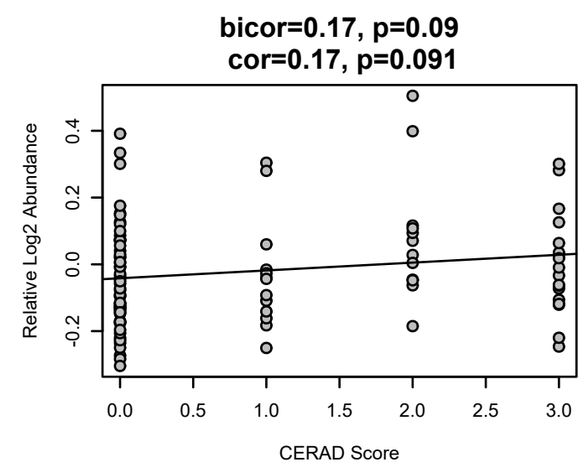

bicor=0.059, p=0.59
cor=0.081, p=0.46
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

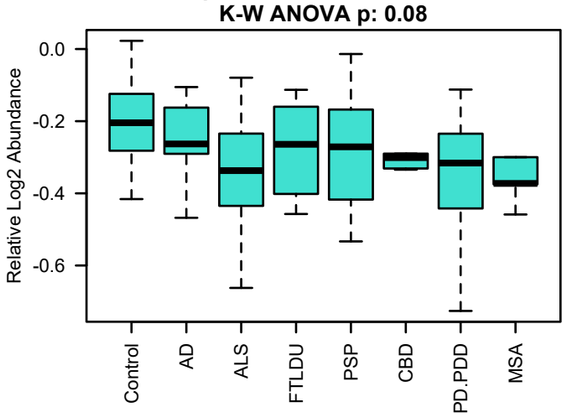

bicor=0.09, p=0.37
cor=0.096, p=0.34
Relative Log2 Abundance
0.2
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

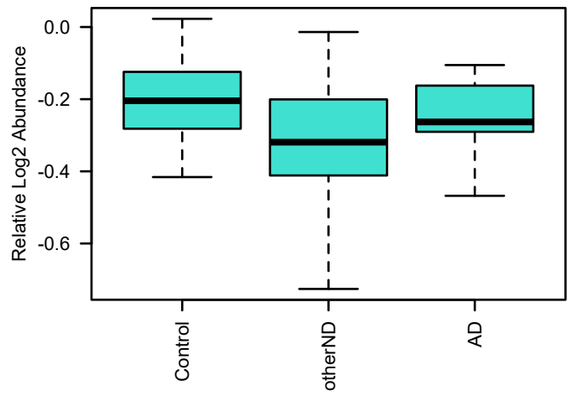

LCMT1 UPenn Mixed PRM
NA grey MEGA module member
K-W ANOVA p: 0.0021
Relative Log2 Abundance
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

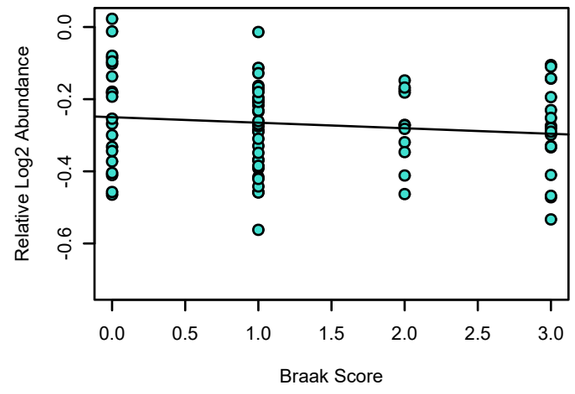

LCMT1 UPenn Mixed PRM
K-W ANOVA p: 0.0057
Relative Log2 Abundance
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
otherND
AD

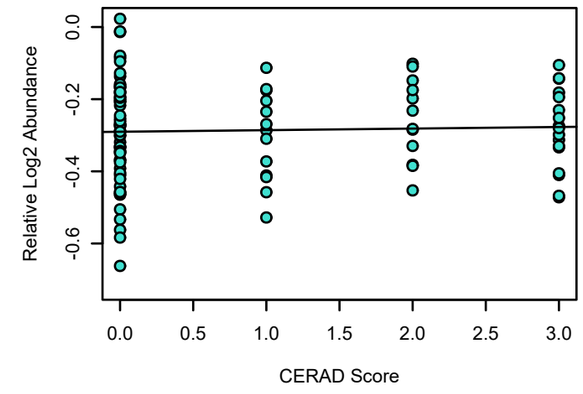

bicor=0.19, p=0.088
cor=0.14, p=0.2
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score


bicor=0.17, p=0.09
cor=0.17, p=0.091
Relative Log2 Abundance
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

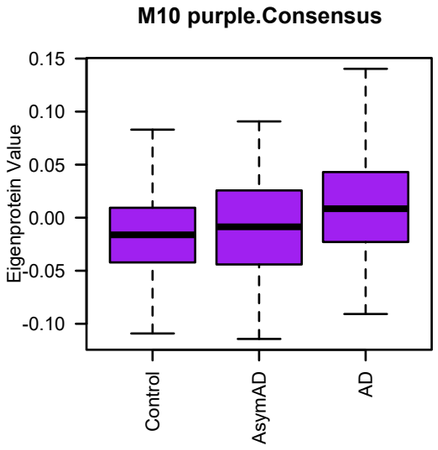

CADM1 UPenn Mixed PRM
M1 turquoise MEGA module member
K-W ANOVA p: 0.08
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

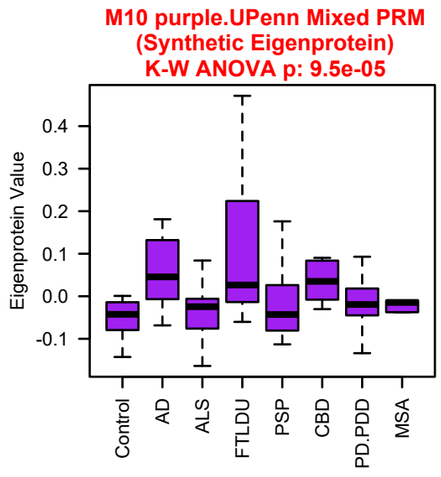

CADM1 UPenn Mixed PRM
K-W ANOVA p: 0.0049
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
Control
otherND
AD

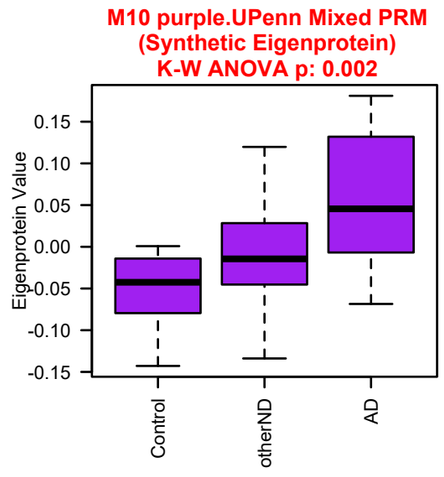

bicor=-0.11, p=0.32
cor=-0.13, p=0.24
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

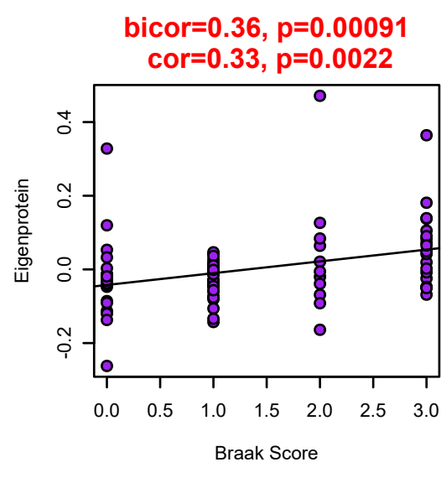

bicor=0.035, p=0.73
cor=0.039, p=0.7
Relative Log2 Abundance
0.0
-0.2
-0.4
-0.6
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

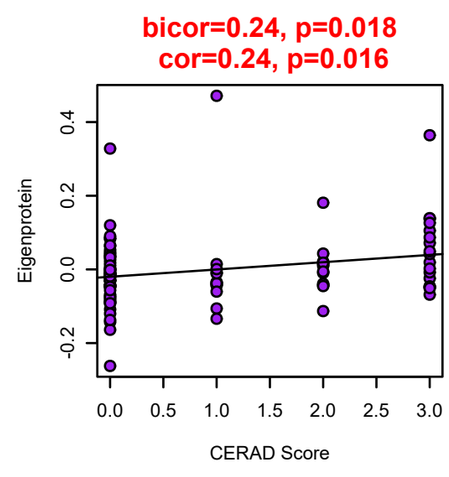
Supplementary Figure 11. Targeted Individual Protein Measurements in Other Neurodegenerative Diseases. Peptides from proteins across all modules in the AD network were targeted for measurement by parallel reaction monitoring mass spectrometry (PRM) in a subset of cases in the UPenn cohort encompassing all disease groups (*n*=108 independent case samples; control *n*=15, AD *n*=16, amyotrophic lateral sclerosis (ALS) *n*=16, frontotemporal lobar degeneration with TAR DNA-binding protein 43 inclusions (FTLD-TDP) *n*=8, progressive supranuclear palsy (PSP) *n*=13, corticobasal degeneration (CBD) *n*=5, Parkinson's disease and Parkinsons's disease dementia (PD/PDD) *n*=30, and multiple system atrophy (MSA) *n*=5). Other neurodegenerative diseases (otherND) include these non-AD diseases. Protein levels were correlated with CERAD and Braak scores, using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Protein level differences by case status were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Differences between AD and other case groups were assessed by two-sided Dunnett's test and are provided in **Supplementary Table 4**. Data for each protein is colored by the AD network module in which it resides. Statistical significance at p <0.05 is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

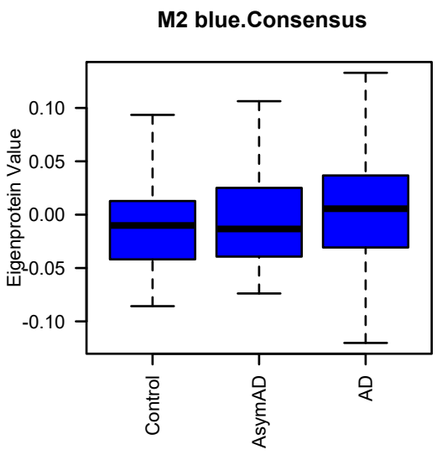

M10 purple.Consensus
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

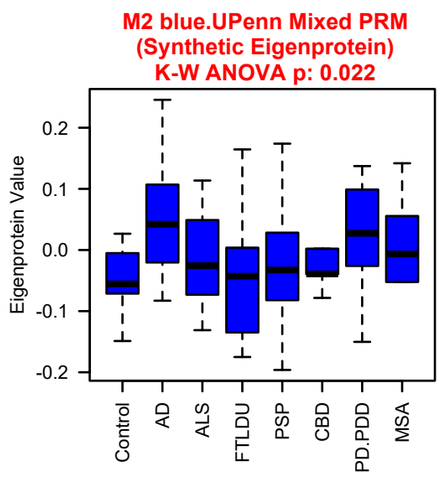

M10 purple.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 9.5e-05
Eigenprotein Value
0.4
0.3
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

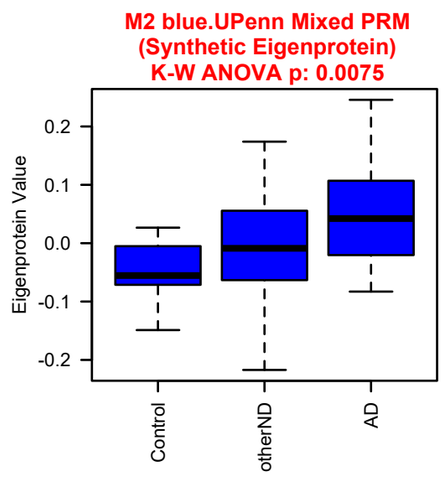

M10 purple.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.002
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
otherND
AD

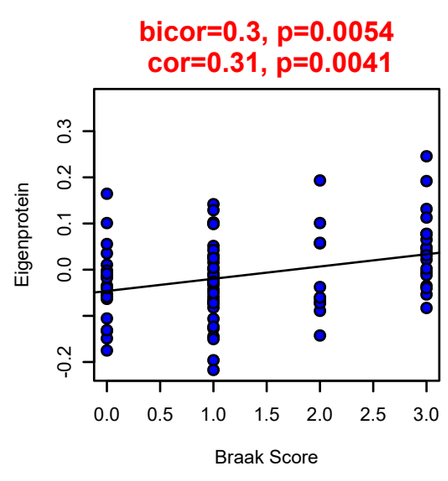

bicor=0.36, p=0.00091
cor=0.33, p=0.0022
Eigenprotein
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

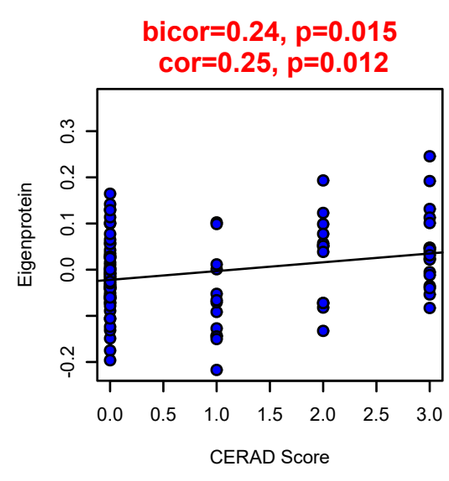

bicor=0.24, p=0.018
cor=0.24, p=0.016
Eigenprotein
0.4
0.2
0.0
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

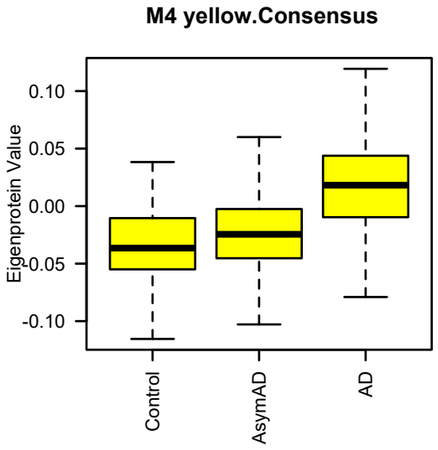

M2 blue.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

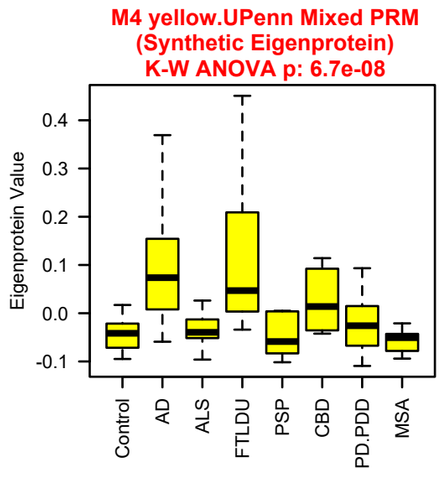

M2 blue.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.022
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

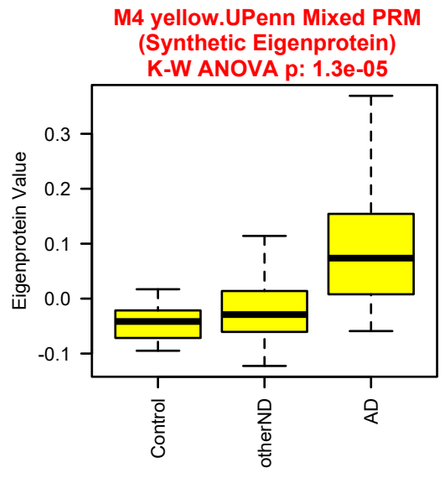

M2 blue.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.0075
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
otherND
AD

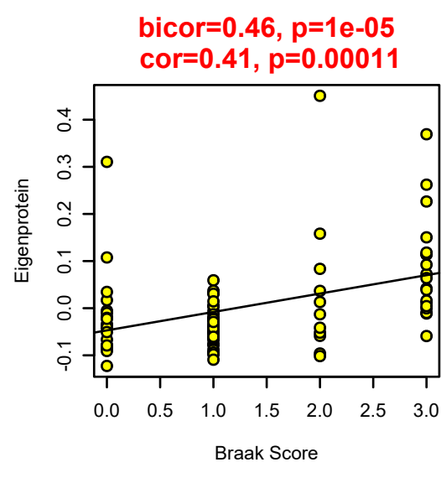

bicor=0.3, p=0.0054
cor=0.31, p=0.0041
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

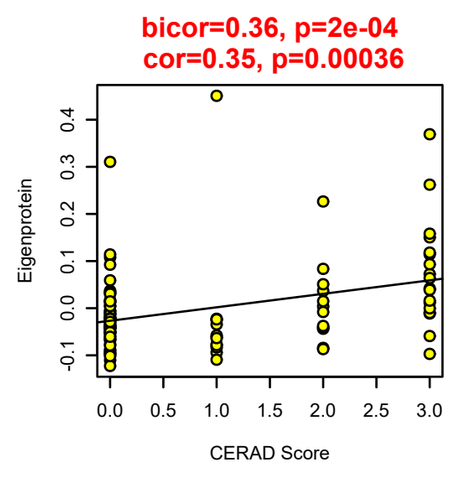

bicor=0.24, p=0.015
cor=0.25, p=0.012
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

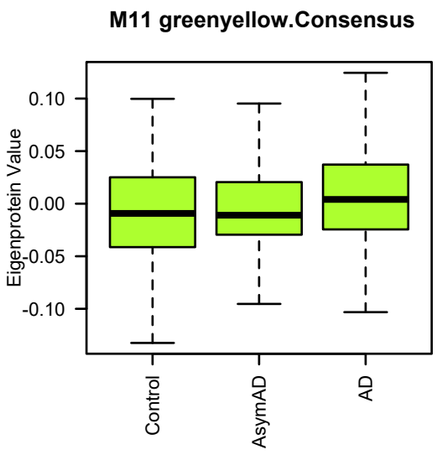

M4 yellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

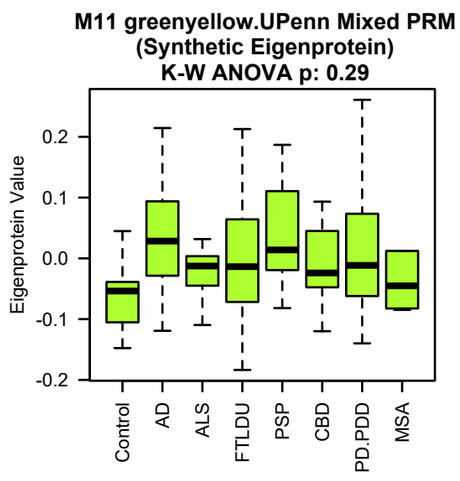

M4 yellow.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 6.7e-08
Eigenprotein Value
0.4
0.3
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

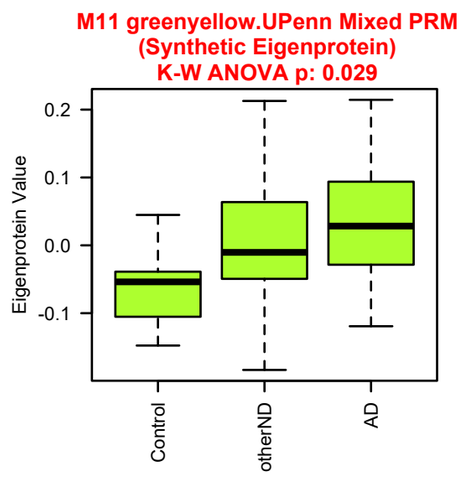

M4 yellow.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 1.3e-05
Eigenprotein Value
0.3
0.2
0.1
0.0
-0.1
Control
otherND
AD

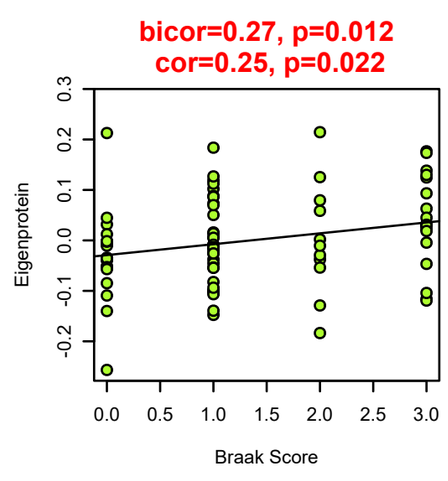

bicor=0.46, p=1e-05
cor=0.41, p=0.00011
Eigenprotein
0.4
0.3
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

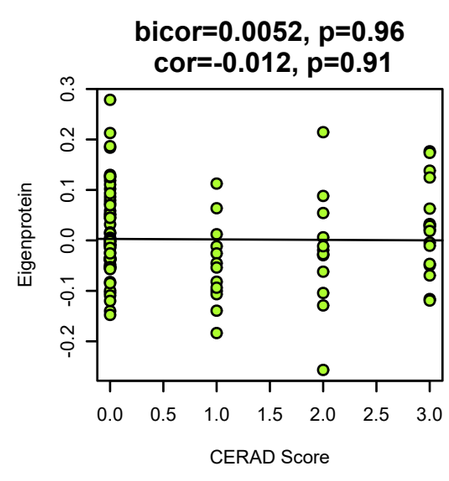

bicor=0.36, p=2e-04
cor=0.35, p=0.00036
Eigenprotein
0.4
0.3
0.2
0.1
0.0
-0.1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

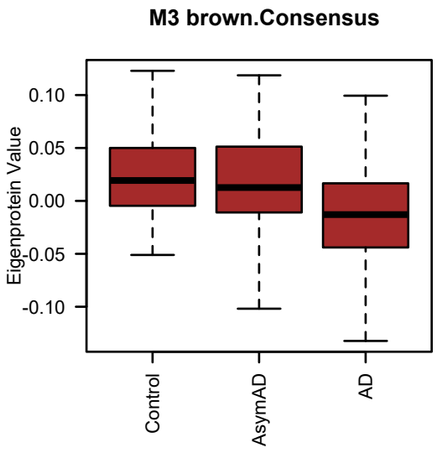

M11 greenyellow.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

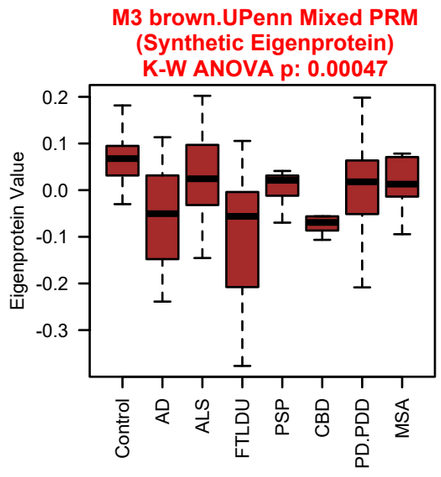

M11 greenyellow.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.29
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

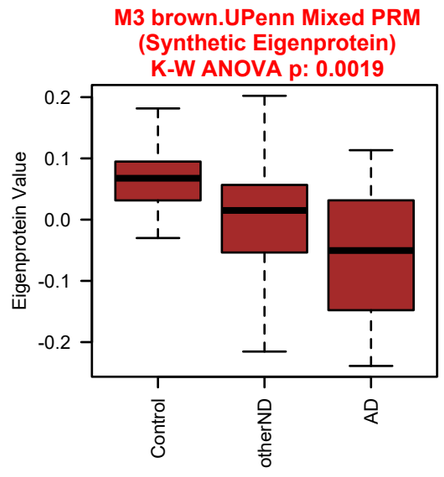

M11 greenyellow.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.029
Eigenprotein Value
0.2
0.1
0.0
-0.1
Control
otherND
AD

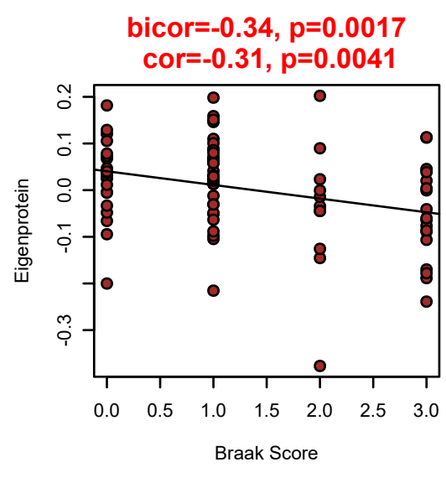

bicor=0.27, p=0.012
cor=0.25, p=0.022
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

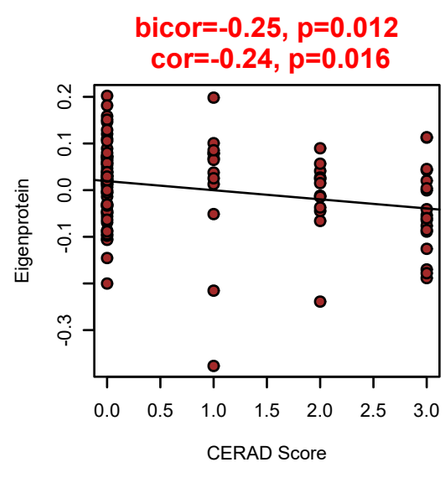

bicor=0.0052, p=0.96
cor=-0.012, p=0.91
Eigenprotein
0.3
0.2
0.1
0.0
-0.1
-0.2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

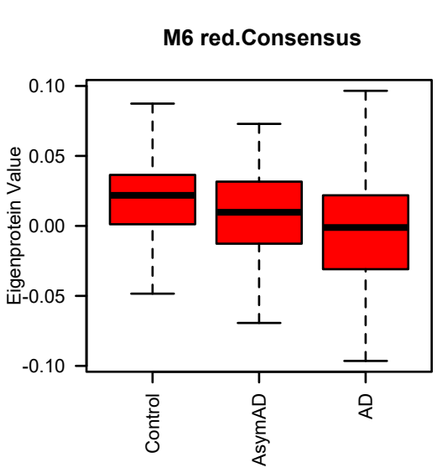

M3 brown.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

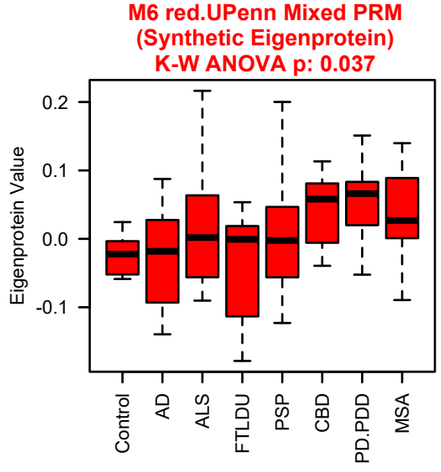

M3 brown.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.00047
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
-0.3
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

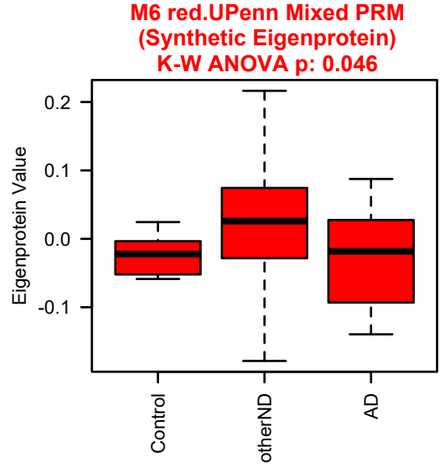

M3 brown.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.0019
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
otherND
AD

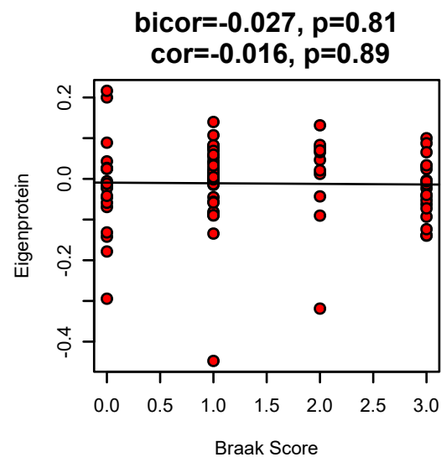

bicor=-0.34, p=0.0017
cor=-0.31, p=0.0041
Eigenprotein
0.2
0.1
0.0
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

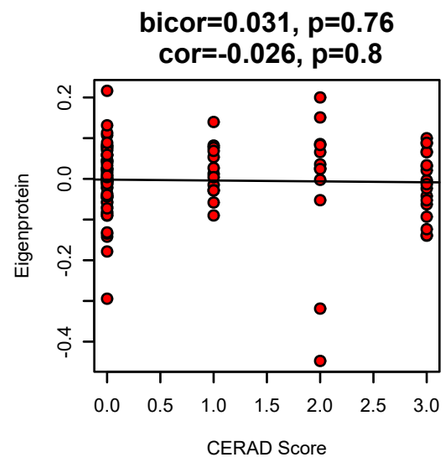

bicor=-0.25, p=0.012
cor=-0.24, p=0.016
Eigenprotein
0.2
0.1
0.0
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

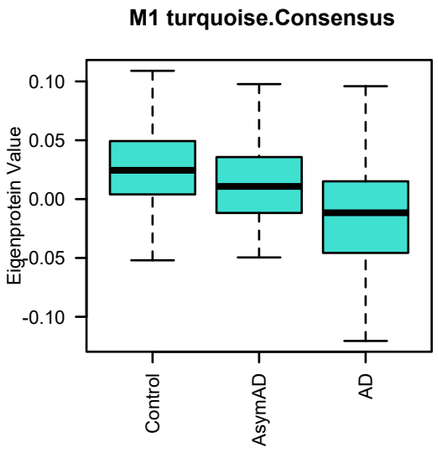

M6 red.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

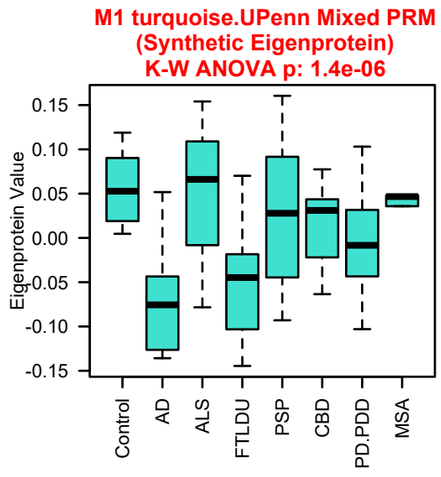

M6 red.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.037
Eigenprotein Value
0.2
0.1
0.0
-0.1
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

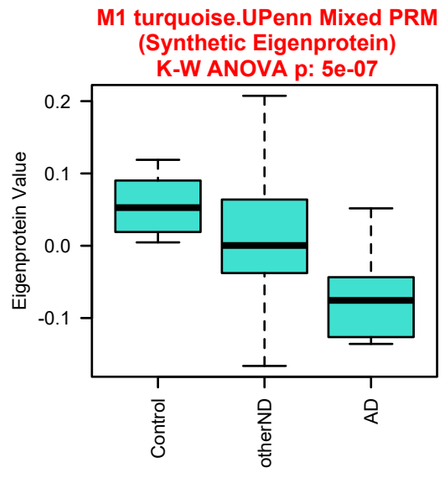

M6 red.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 0.046
Eigenprotein Value
0.2
0.1
0.0
-0.1
Control
otherND
AD

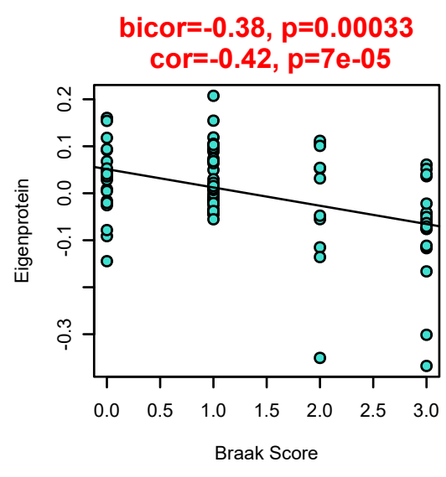

bicor=-0.027, p=0.81
cor=-0.016, p=0.89
Eigenprotein
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

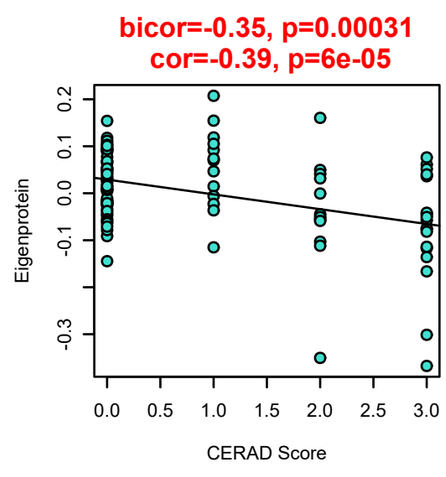

bicor=0.031, p=0.76
cor=-0.026, p=0.8
Eigenprotein
0.2
0.0
-0.2
-0.4
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

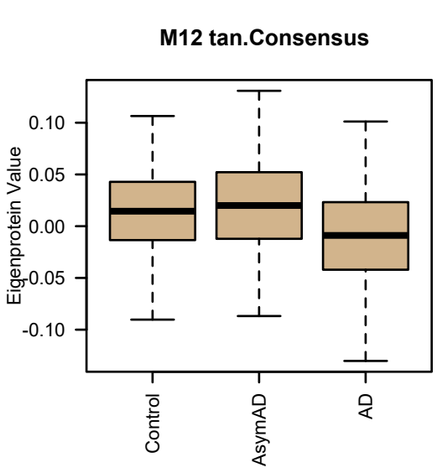

M1 turquoise.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD

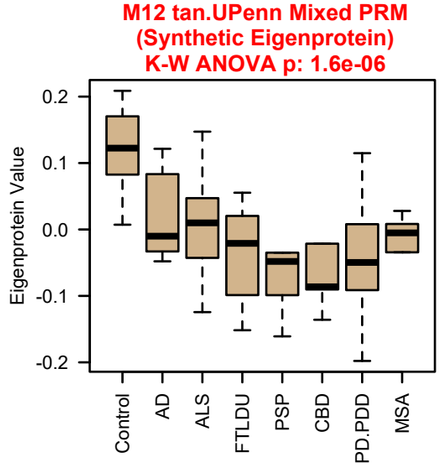

M1 turquoise.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 1.4e-06
Eigenprotein Value
0.15
0.10
0.05
0.00
-0.05
-0.10
-0.15
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

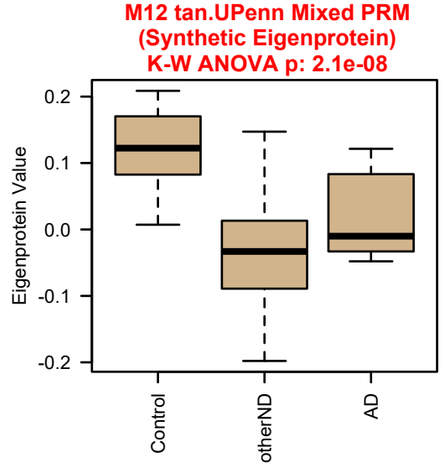

M1 turquoise.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 5e-07
Eigenprotein Value
0.2
0.1
0.0
-0.1
Control
otherND
AD

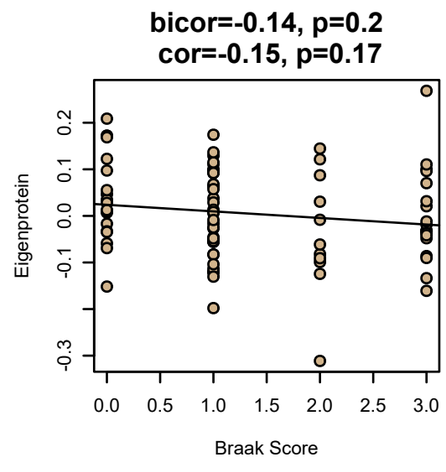

bicor=-0.38, p=0.00033
cor=-0.42, p=7e-05
Eigenprotein
0.2
0.1
0.0
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

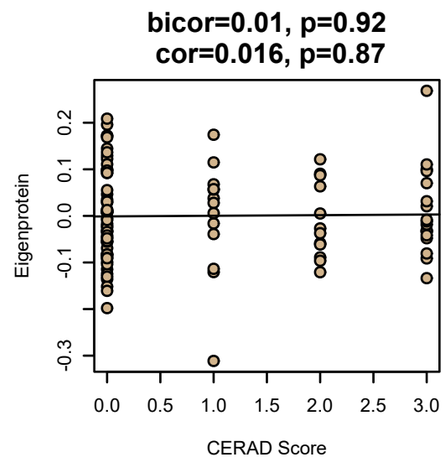

bicor=-0.35, p=0.00031
cor=-0.39, p=6e-05
Eigenprotein
0.2
0.1
0.0
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score


M12 tan.Consensus
Eigenprotein Value
0.10
0.05
0.00
-0.05
-0.10
Control
AsymAD
AD


M12 tan.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 1.6e-06
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
AD
ALS
FTLDU
PSP
CBD
PD.PDD
MSA

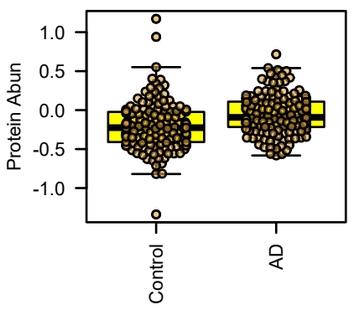

M12 tan.UPenn Mixed PRM
(Synthetic Eigenprotein)
K-W ANOVA p: 2.1e-08
Eigenprotein Value
0.2
0.1
0.0
-0.1
-0.2
Control
otherND
AD


bicor=-0.14, p=0.2
cor=-0.15, p=0.17
Eigenprotein
0.2
0.1
0.0
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Braak Score

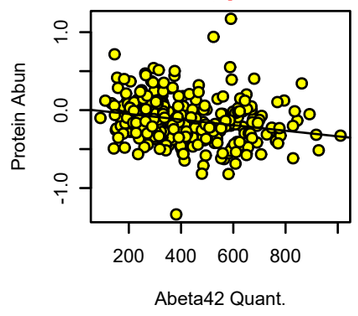

bicor=0.01, p=0.92
cor=0.016, p=0.87
Eigenprotein
0.2
0.1
0.0
-0.1
-0.3
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CERAD Score

Supplementary Figure 12. AD Network Module Changes in Other Neurodegenerative Diseases by Targeted Mass Spectrometry Measurements. A synthetic eigenprotein for each AD network module was created from proteins measured by parallel reaction monitoring mass spectrometry (PRM) that mapped to an AD network module (see **Supplementary Table 4**). Individual protein measurements by disease group are provided in **Supplementary Figure 11**. The first boxplot for each module is the AD network eigenprotein by case status, given as reference for the second and third boxplots (control *n*=46, AD *n*=49, amyotrophic lateral sclerosis (ALS) *n*=59, frontotemporal lobar degeneration with TAR DNA-binding protein 43 inclusions (FTLD-TDP) *n*=29, progressive supranuclear palsy (PSP) *n*=27, corticobasal degeneration (CBD) *n*=17, Parkinson's disease and Parkinsons's disease dementia (PD/PDD) *n*=80, and multiple system atrophy (MSA) *n*=23). Other neurodegenerative diseases (otherND) include these non-AD diseases. Synthetic eigenproteins were correlated with CERAD and Braak scores, using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Synthetic eigenprotein differences by case status were assessed by Kruskal-Wallis (K-W) one-way ANOVA. Differences between AD and other case groups were assessed by two-sided Dunnett's test and are provided in **Supplementary Table 4**. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles.

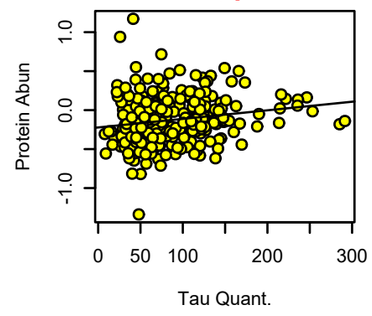
PARK7|K7ELW0
T-test AD/CT p = 5.5e-06



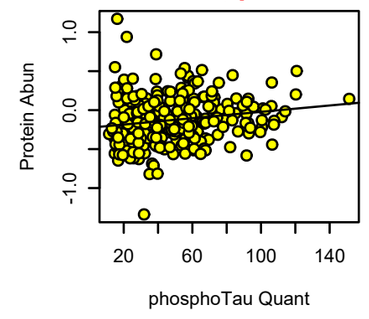
bicor=-0.26, p=4.6e-06
cor=-0.22, p=0.00014



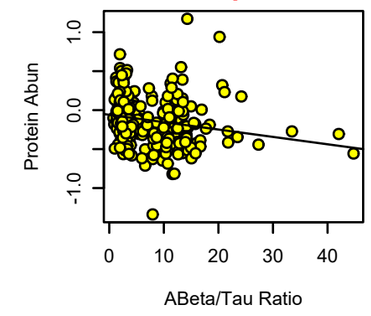
bicor=0.23, p=8.4e-05
cor=0.18, p=0.0019



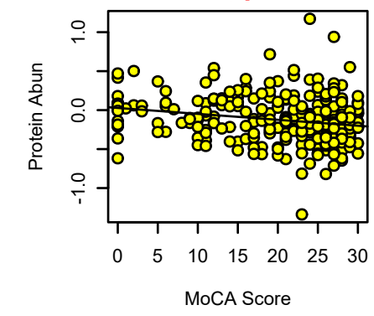
bicor=0.22, p=0.00014
cor=0.17, p=0.0034



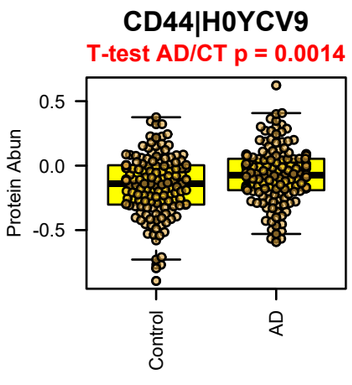
bicor=-0.24, p=3e-05
cor=-0.2, p=0.00055



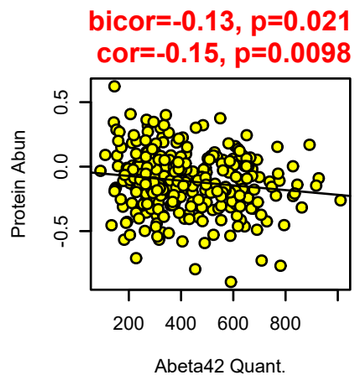
bicor=-0.25, p=1.3e-05
cor=-0.21, p=0.00028



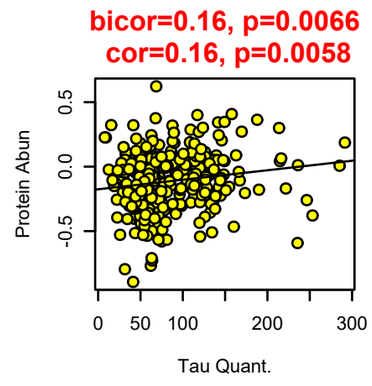
CD44|H0YCV9
T-test AD/CT p = 0.0014



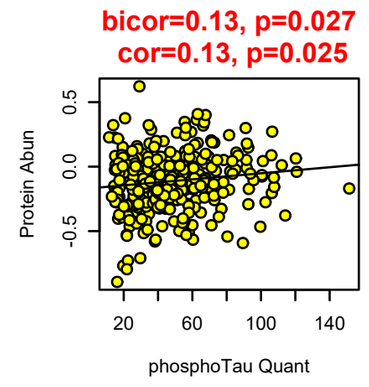
bicor=-0.13, p=0.021
cor=-0.15, p=0.0098



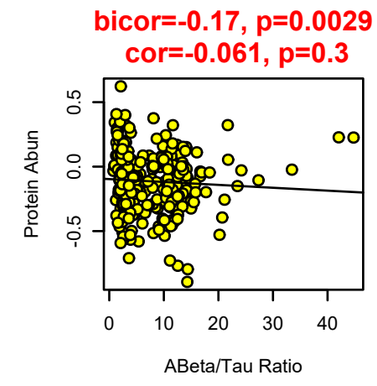
bicor=0.16, p=0.0066
cor=0.16, p=0.0058



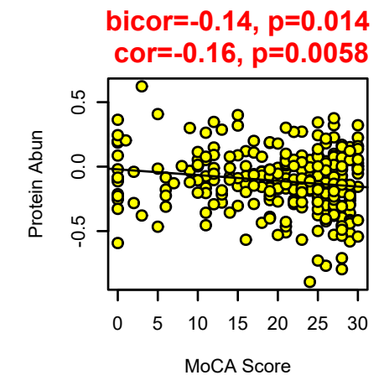
bicor=0.13, p=0.027
cor=0.13, p=0.025



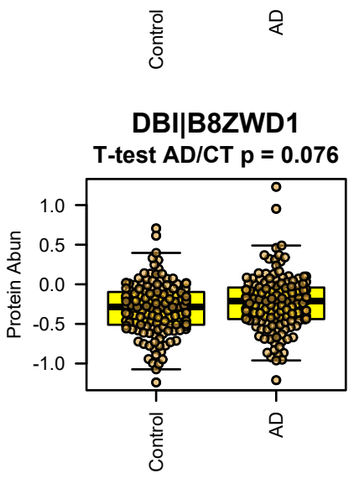
bicor=-0.17, p=0.0029
cor=-0.061, p=0.3



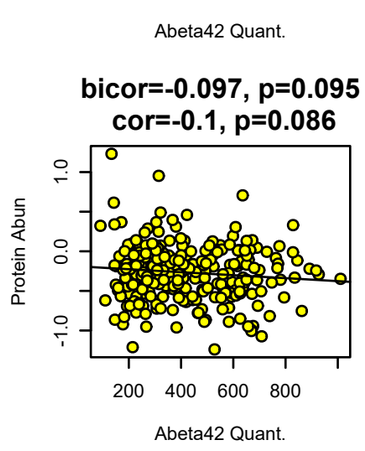
bicor=-0.14, p=0.014
cor=-0.16, p=0.0058



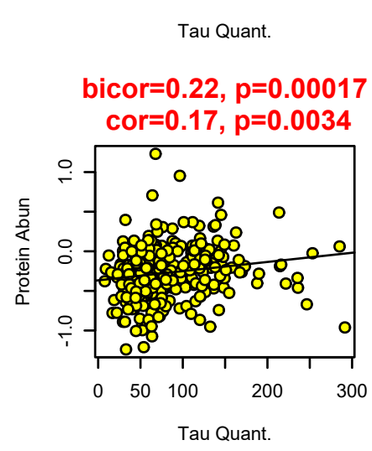
DBI|B8ZWD1
T-test AD/CT p = 0.076



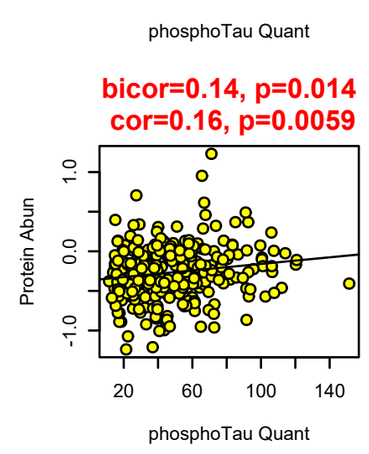
bicor=-0.097, p=0.095
cor=-0.1, p=0.086



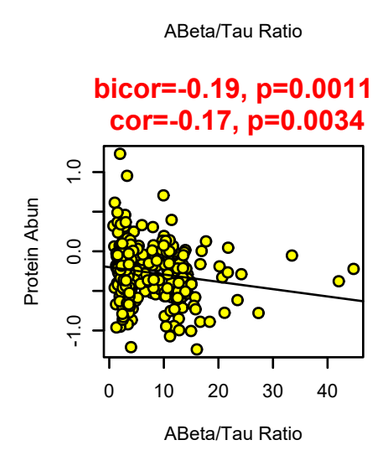
bicor=0.22, p=0.00017
cor=0.17, p=0.0034



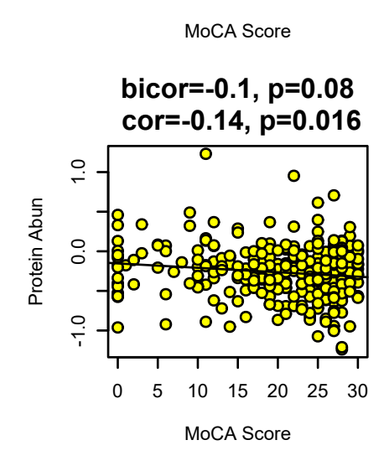
bicor=0.14, p=0.014
cor=0.16, p=0.0059



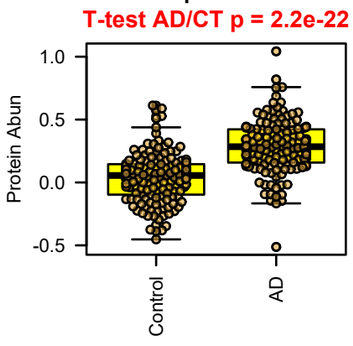
bicor=-0.19, p=0.0011
cor=-0.17, p=0.0034



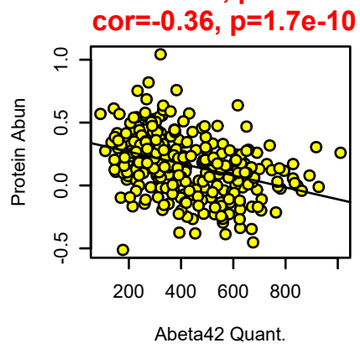
bicor=-0.1, p=0.08
cor=-0.14, p=0.016



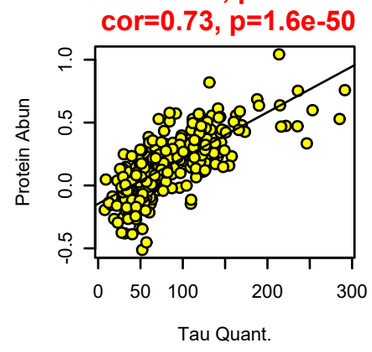
PKM|P14618-2
T-test AD/CT p = 2.2e-22



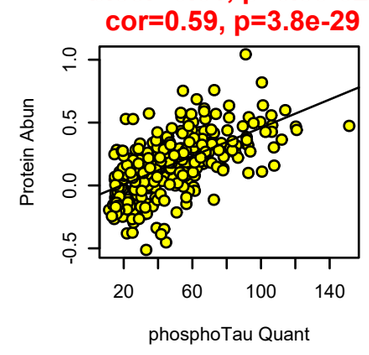
bicor=-0.39, p=4.2e-12
cor=-0.36, p=1.7e-10



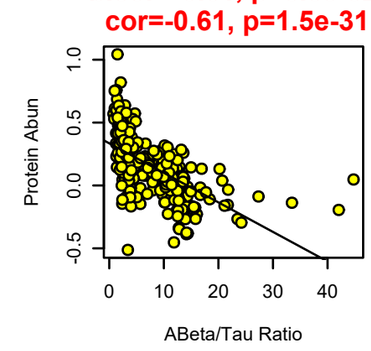
bicor=0.73, p=4.3e-50
cor=0.73, p=1.6e-50



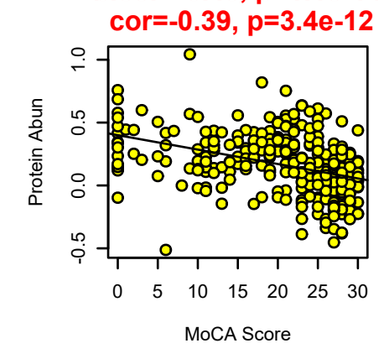
bicor=0.61, p=6.8e-32
cor=0.59, p=3.8e-29



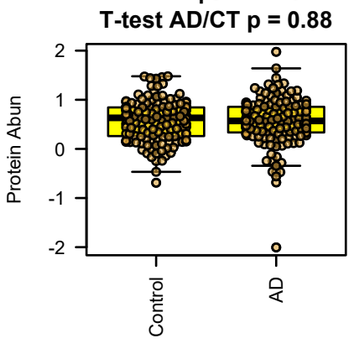
bicor=-0.61, p=5.5e-32
cor=-0.61, p=1.5e-31



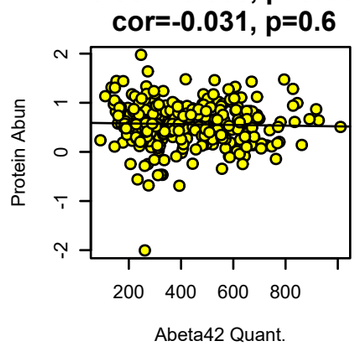
bicor=-0.43, p=1.1e-14
cor=-0.39, p=3.4e-12



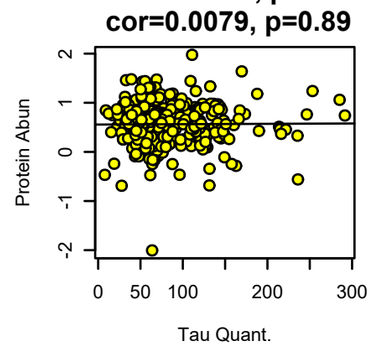
TPP1|O14773
T-test AD/CT p = 0.88



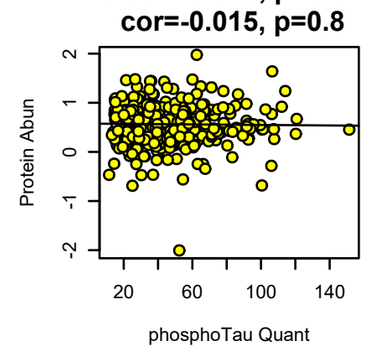
bicor=-0.068, p=0.24
cor=-0.031, p=0.6



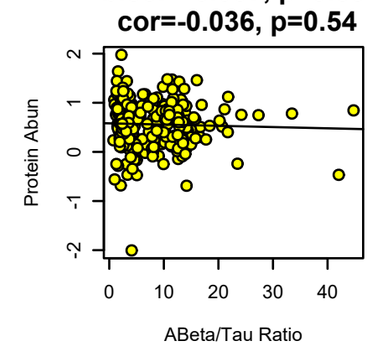
bicor=-0.032, p=0.58
cor=0.0079, p=0.89



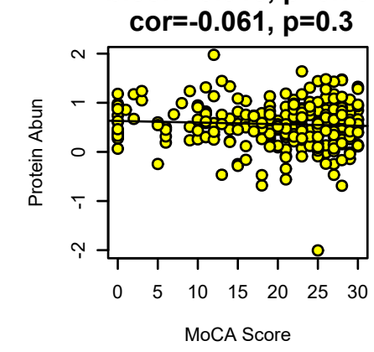
bicor=-0.027, p=0.64
cor=-0.015, p=0.8



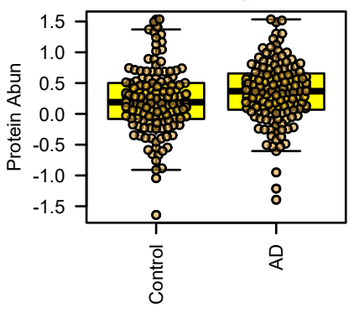
bicor=-0.037, p=0.53
cor=-0.036, p=0.54



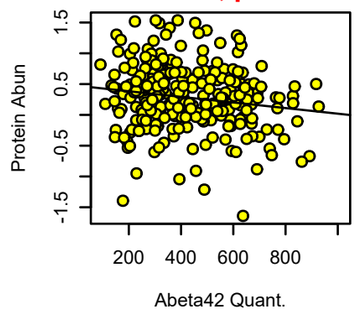
bicor=-0.018, p=0.76
cor=-0.061, p=0.3



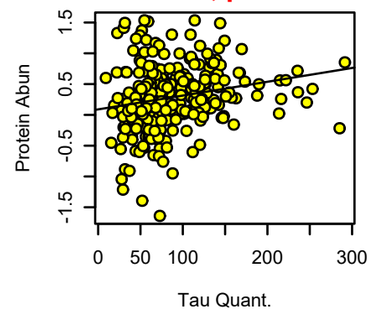
DDAH2|Q5SRR8
T-test AD/CT p = 0.025



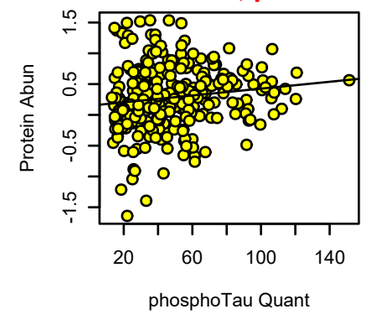
bicor=-0.15, p=0.013
cor=-0.16, p=0.0075



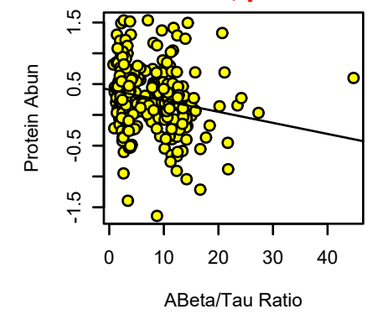
bicor=0.26, p=1.1e-05
cor=0.21, p=0.00042



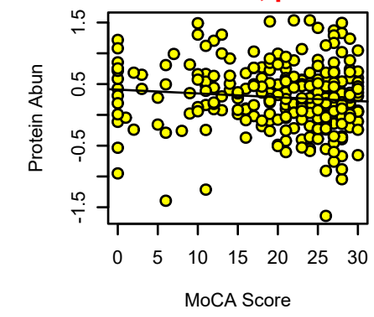
bicor=0.15, p=0.011
cor=0.14, p=0.02



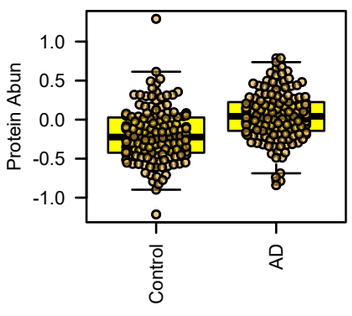
bicor=-0.21, p=0.00034
cor=-0.2, p=8e-04



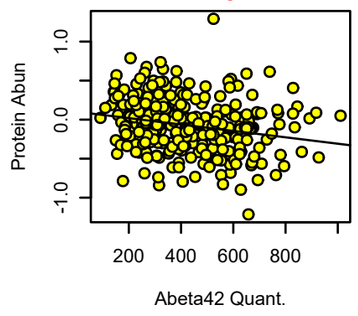
bicor=-0.14, p=0.019
cor=-0.097, p=0.11



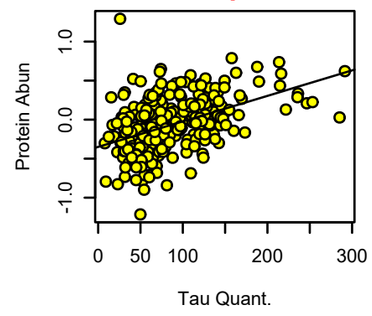
SPP1|P10451
T-test AD/CT p = 2.4e-10



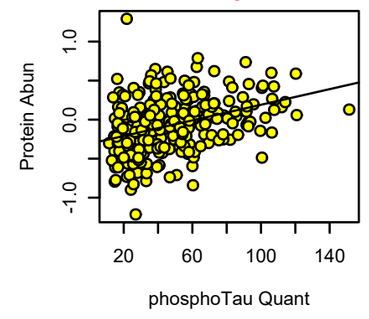
bicor=-0.24, p=2.2e-05
cor=-0.22, p=0.00014



bicor=0.46, p=8.9e-17
cor=0.46, p=6.6e-17



bicor=0.39, p=2.8e-12
cor=0.37, p=4.9e-11



bicor=-0.4, p=4.3e-13
cor=-0.36, p=1.7e-10

bicor=-0.34, p=2.2e-09
cor=-0.31, p=5.2e-08

GSN|P06396
T-test AD/CT p = 0.9

bicor=0.027, p=0.64
cor=-0.0027, p=0.96

bicor=-0.082, p=0.16
cor=-0.079, p=0.18

bicor=-0.095, p=0.1
cor=-0.081, p=0.16

bicor=0.093, p=0.11
cor=0.0044, p=0.94

bicor=-0.049, p=0.4
cor=-0.074, p=0.2

APP|P05067
T-test AD/CT p = 0.54

bicor=0.096, p=0.1
cor=0.086, p=0.14

bicor=0.28, p=7.7e-07
cor=0.28, p=9.8e-07

bicor=0.23, p=8.5e-05
cor=0.24, p=3e-05

bicor=-0.14, p=0.019
cor=-0.16, p=0.0058

bicor=0.042, p=0.47
cor=0.027, p=0.64

LDHB|P07195
T-test AD/CT p = 1.2e-13

bicor=-0.29, p=5.7e-07
cor=-0.27, p=2.4e-06

bicor=0.6, p=1.3e-30
cor=0.54, p=8.4e-24

bicor=0.49, p=5.1e-19
cor=0.43, p=9.5e-15

bicor=-0.48, p=3.2e-18
cor=-0.49, p=2.8e-19

bicor=-0.38, p=9e-12
cor=-0.36, p=1.7e-10

SPP1|P10451-3
T-test AD/CT p = 0.16

bicor=-0.031, p=0.61
cor=-0.0076, p=0.9

bicor=-0.13, p=0.041
cor=-0.12, p=0.052

bicor=-0.045, p=0.47
cor=-0.076, p=0.22

bicor=0.0092, p=0.88
cor=0.092, p=0.14

bicor=0.028, p=0.65
cor=0.028, p=0.65

GAPDH|P04406
T-test AD/CT p = 2.9e-09

bicor=-0.31, p=5e-08
cor=-0.29, p=4e-07

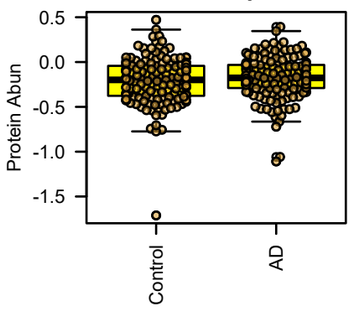
bicor=0.32, p=2.2e-08
cor=0.28, p=1e-06

bicor=0.33, p=7.8e-09
cor=0.31, p=5.4e-08

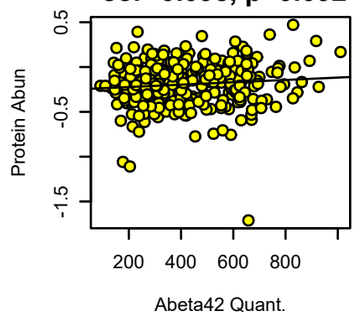
bicor=-0.37, p=3e-11
cor=-0.26, p=6e-06

bicor=-0.3, p=1.5e-07
cor=-0.28, p=1e-06

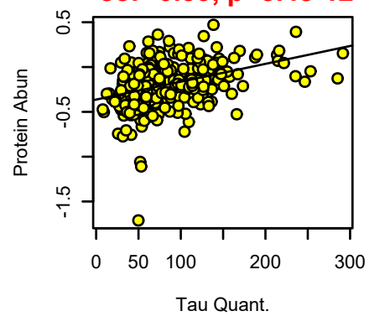
DKK3|F6SYF8
T-test AD/CT p = 0.18



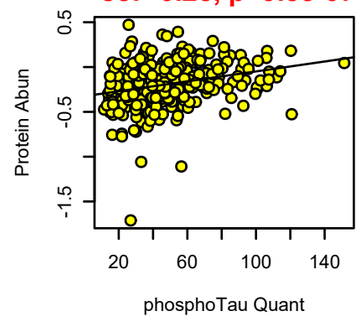
bicor=0.1, p=0.085
cor=0.098, p=0.092



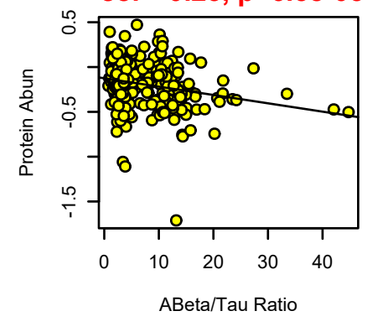
bicor=0.4, p=8.7e-13
cor=0.39, p=3.4e-12



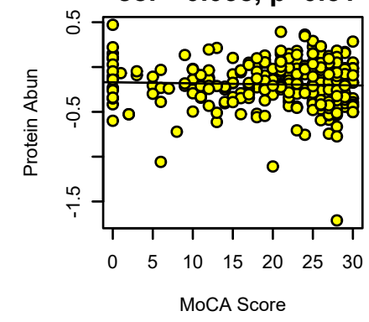
bicor=0.31, p=4e-08
cor=0.28, p=9.8e-07



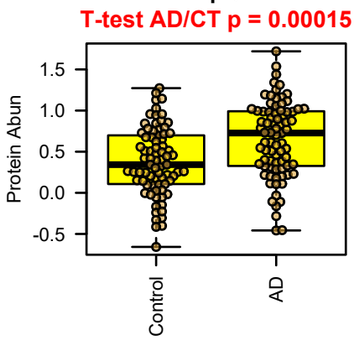
bicor=-0.17, p=0.0027
cor=-0.23, p=6.5e-05



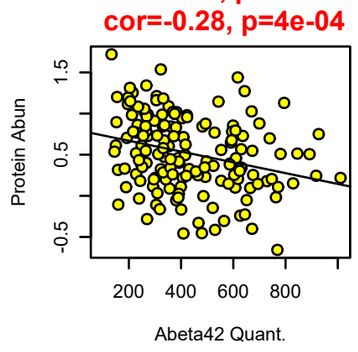
bicor=-0.027, p=0.64
cor=-0.038, p=0.51



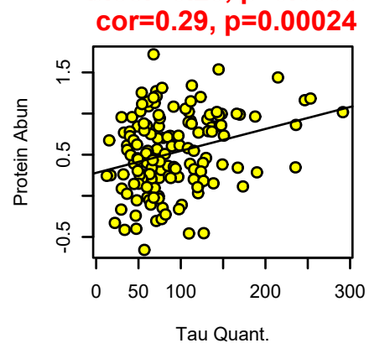
PRDX1|Q06830
T-test AD/CT p = 0.00015



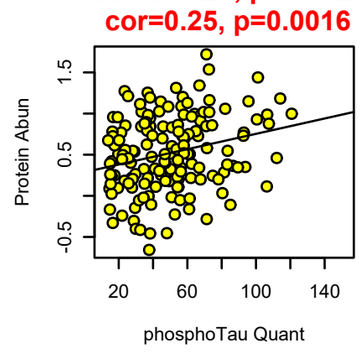
bicor=-0.27, p=0.00054
cor=-0.28, p=4e-04



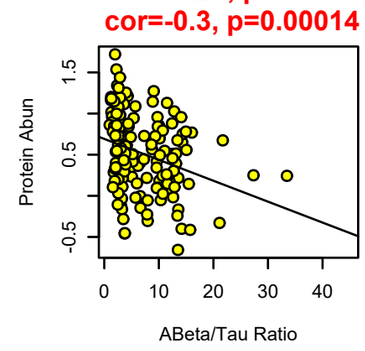
bicor=0.23, p=0.0038
cor=0.29, p=0.00024



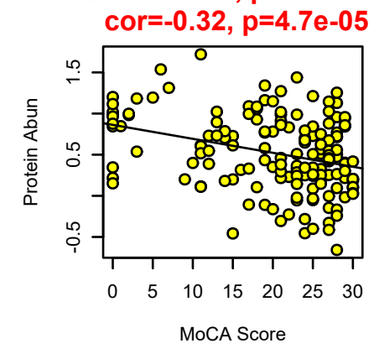
bicor=0.25, p=0.002
cor=0.25, p=0.0016



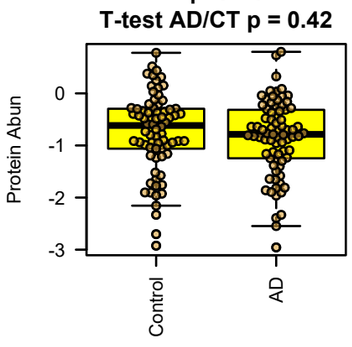
bicor=-0.28, p=0.00042
cor=-0.3, p=0.00014



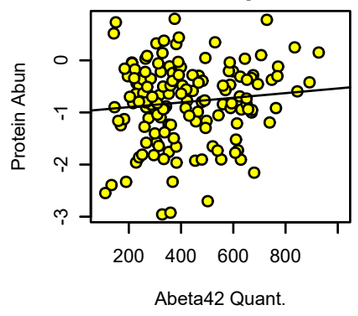
bicor=-0.31, p=9.3e-05
cor=-0.32, p=4.7e-05



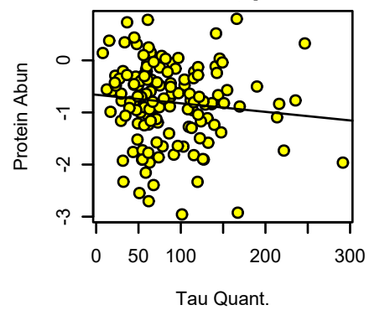
C4A|P0C0L4
T-test AD/CT p = 0.42



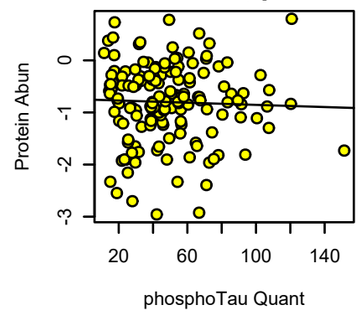
bicor=0.057, p=0.49
cor=0.11, p=0.18



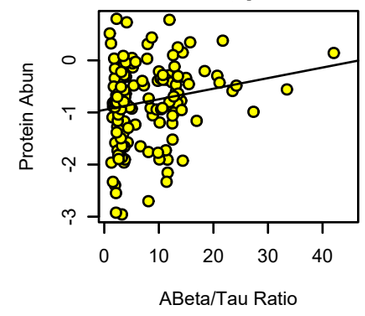
bicor=-0.11, p=0.16
cor=-0.11, p=0.18



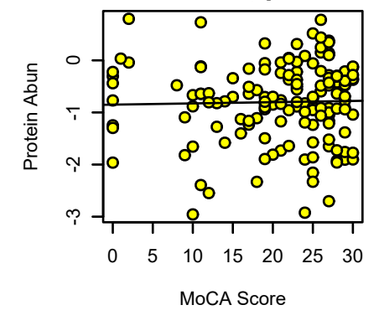
bicor=-0.049, p=0.55
cor=-0.036, p=0.66



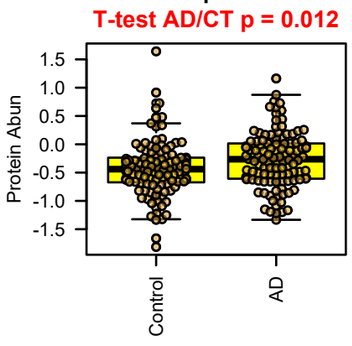
bicor=0.044, p=0.59
cor=0.18, p=0.027



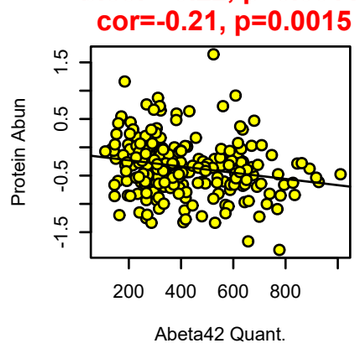
bicor=0.066, p=0.42
cor=0.025, p=0.76



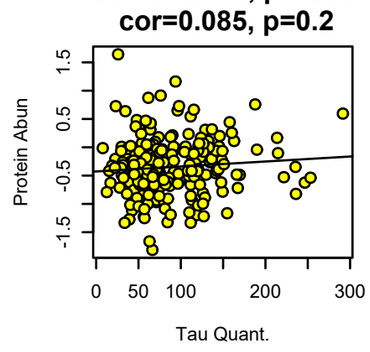
ENO1|P06733
T-test AD/CT p = 0.012



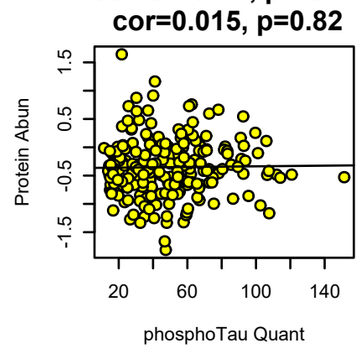
bicor=-0.22, p=0.0011
cor=-0.21, p=0.0015



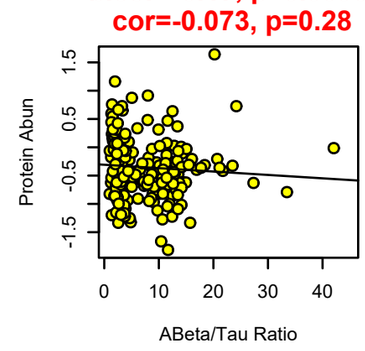
bicor=0.098, p=0.14
cor=0.085, p=0.2



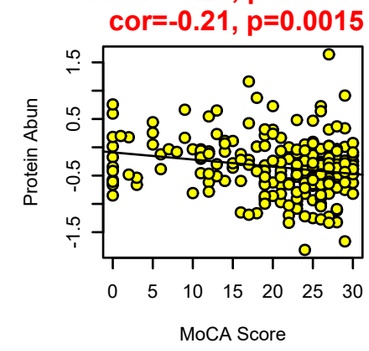
bicor=0.057, p=0.39
cor=0.015, p=0.82



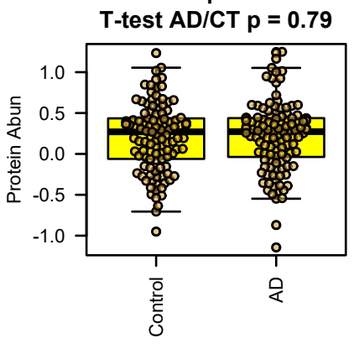
bicor=-0.17, p=0.0096
cor=-0.073, p=0.28



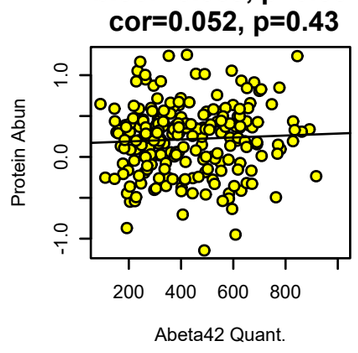
bicor=-0.23, p=0.00055
cor=-0.21, p=0.0015



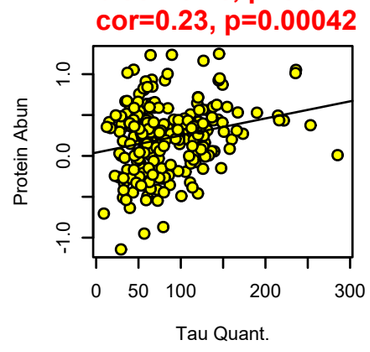
COTL1|H3BT58
T-test AD/CT p = 0.79



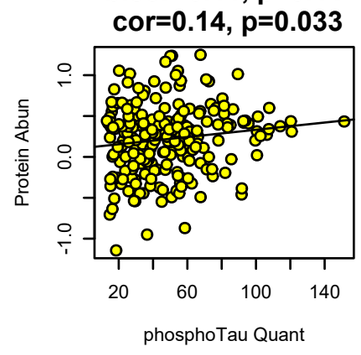
bicor=0.039, p=0.55
cor=0.052, p=0.43



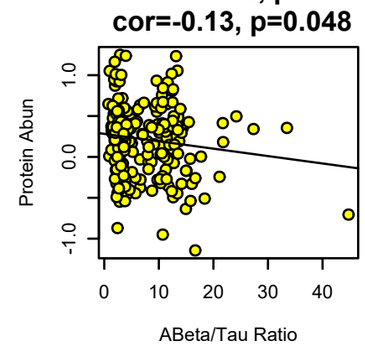
bicor=0.16, p=0.012
cor=0.23, p=0.00042



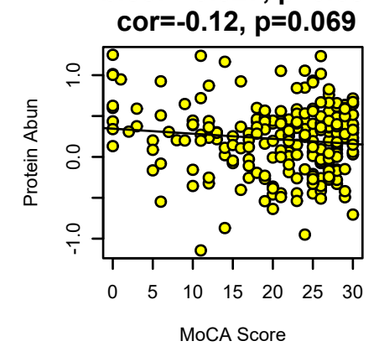
bicor=0.11, p=0.11
cor=0.14, p=0.033



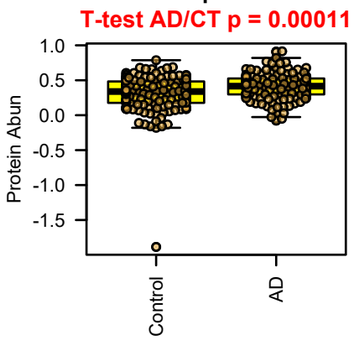
bicor=-0.098, p=0.14
cor=-0.13, p=0.048



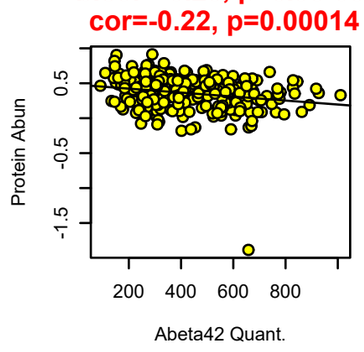
bicor=-0.027, p=0.68
cor=-0.12, p=0.069



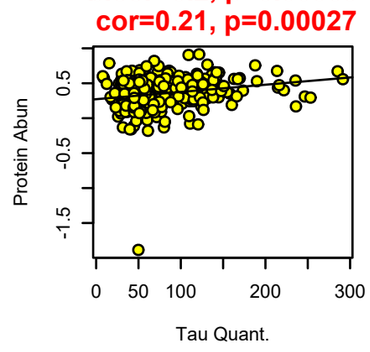
NPC2|P61916
T-test AD/CT p = 0.00011



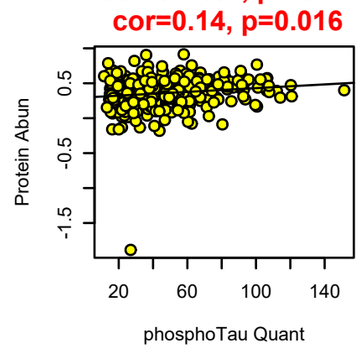
bicor=-0.23, p=6.9e-05
cor=-0.22, p=0.00014



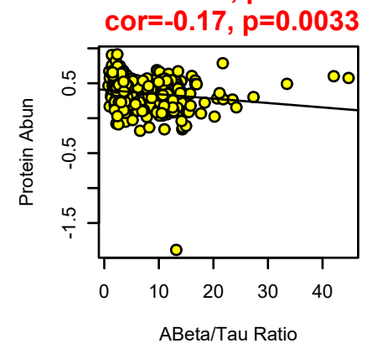
bicor=0.2, p=0.00063
cor=0.21, p=0.00027



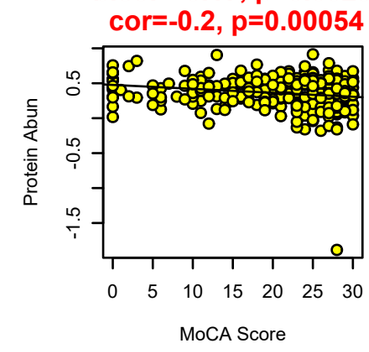
bicor=0.13, p=0.03
cor=0.14, p=0.016



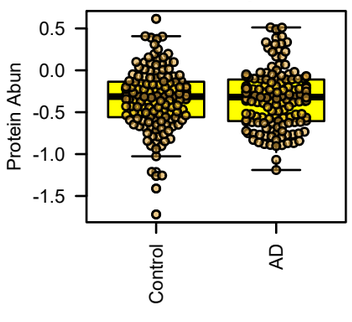
bicor=-0.29, p=4.9e-07
cor=-0.17, p=0.0033



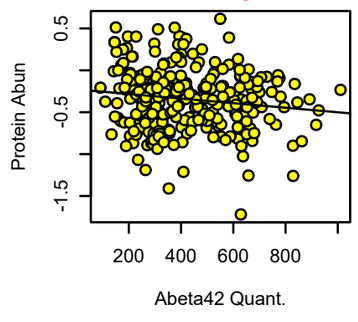
bicor=-0.17, p=0.0029
cor=-0.2, p=0.00054



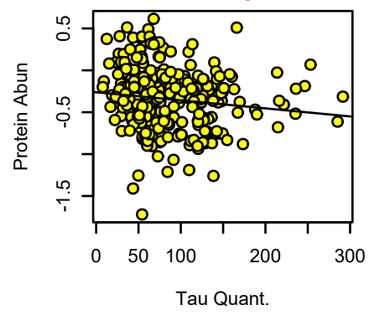
C4B|P0C0L5
T-test AD/CT p = 0.87



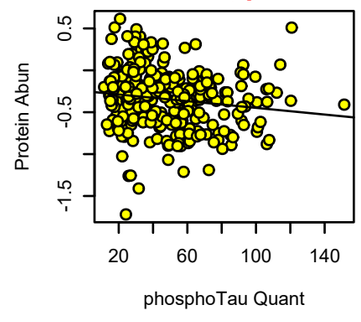
bicor=-0.14, p=0.019
cor=-0.14, p=0.016



bicor=-0.2, p=0.00067
cor=-0.13, p=0.025



bicor=-0.19, p=0.00075
cor=-0.14, p=0.016



bicor=-0.0012, p=0.98
cor=0.098, p=0.092

bicor=-0.054, p=0.35
cor=-0.094, p=0.11

CD99|H7C2F2
T-test AD/CT p = 0.35

bicor=-0.015, p=0.85
cor=-0.12, p=0.13

bicor=-0.04, p=0.62
cor=0.017, p=0.83

bicor=0.026, p=0.74
cor=0.1, p=0.21

bicor=0.056, p=0.48
cor=-0.045, p=0.57

bicor=0.078, p=0.32
cor=-0.013, p=0.87

CLU|P10909
T-test AD/CT p = 0.79

bicor=0.095, p=0.1
cor=0.058, p=0.32

bicor=-0.005, p=0.93
cor=0.042, p=0.47

bicor=-0.014, p=0.8
cor=0.037, p=0.53

bicor=0.058, p=0.32
cor=-0.007, p=0.9

bicor=-0.0045, p=0.94
cor=-0.052, p=0.37

CTSD|P07339
T-test AD/CT p = 0.098

bicor=-0.12, p=0.037
cor=-0.14, p=0.016

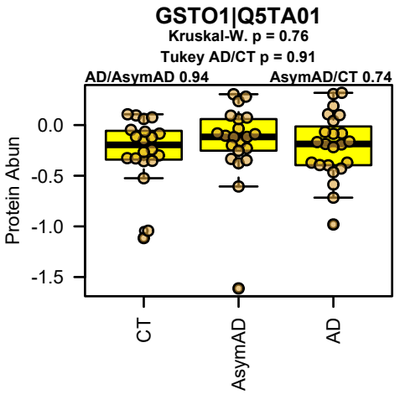
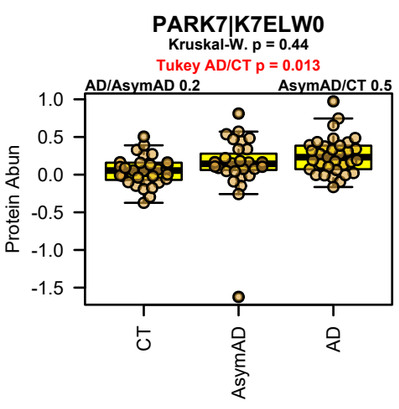
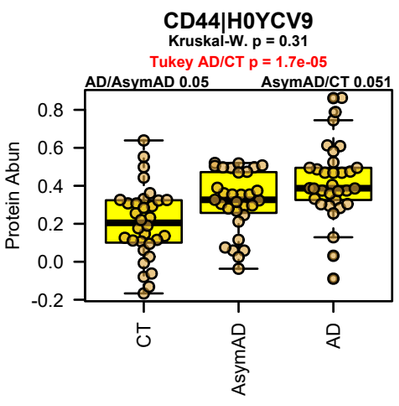
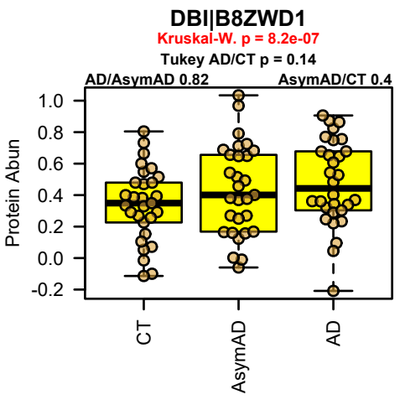
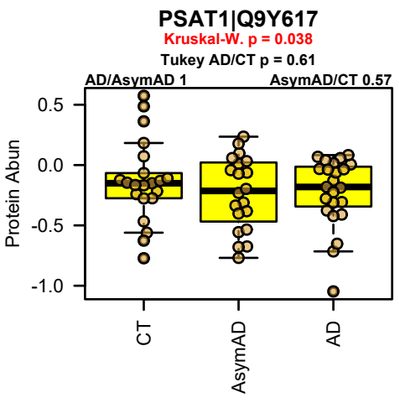
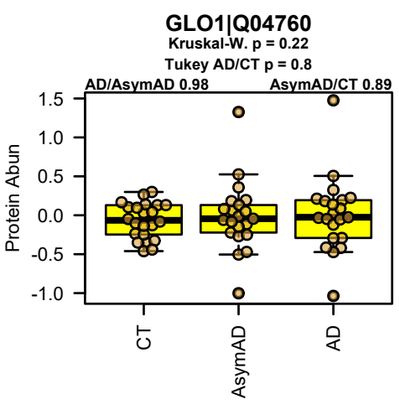
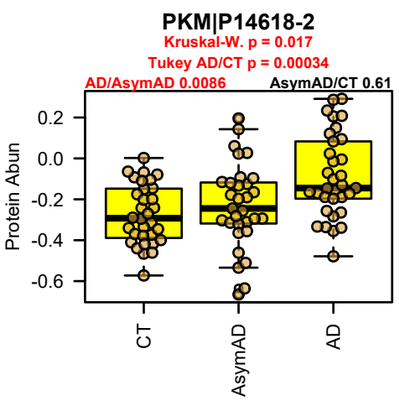
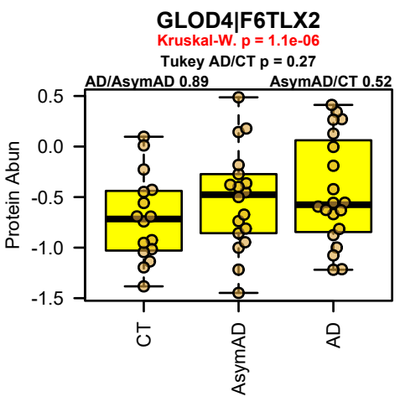
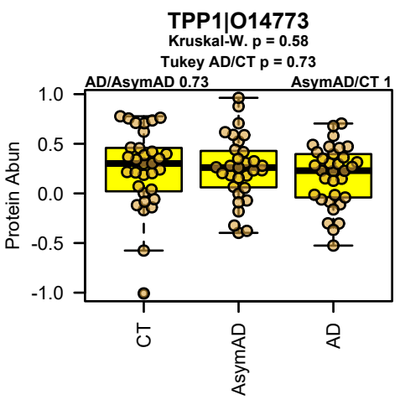
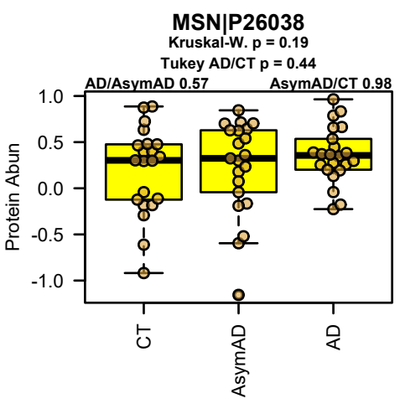
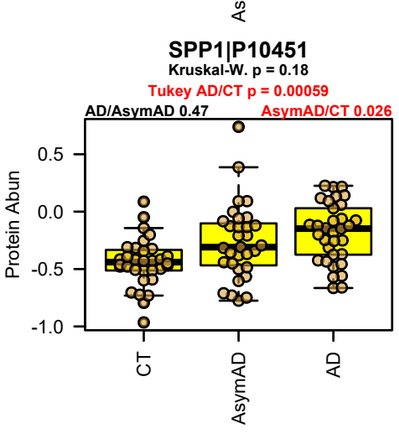
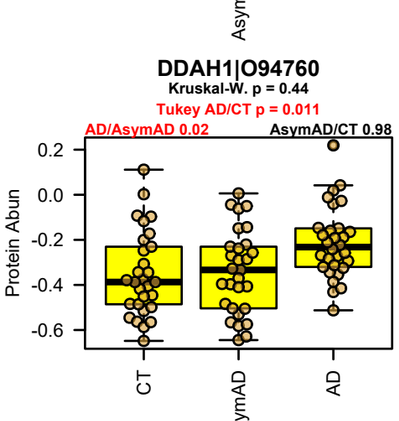
bicor=-0.32, p=2.8e-08
cor=-0.33, p=6e-09

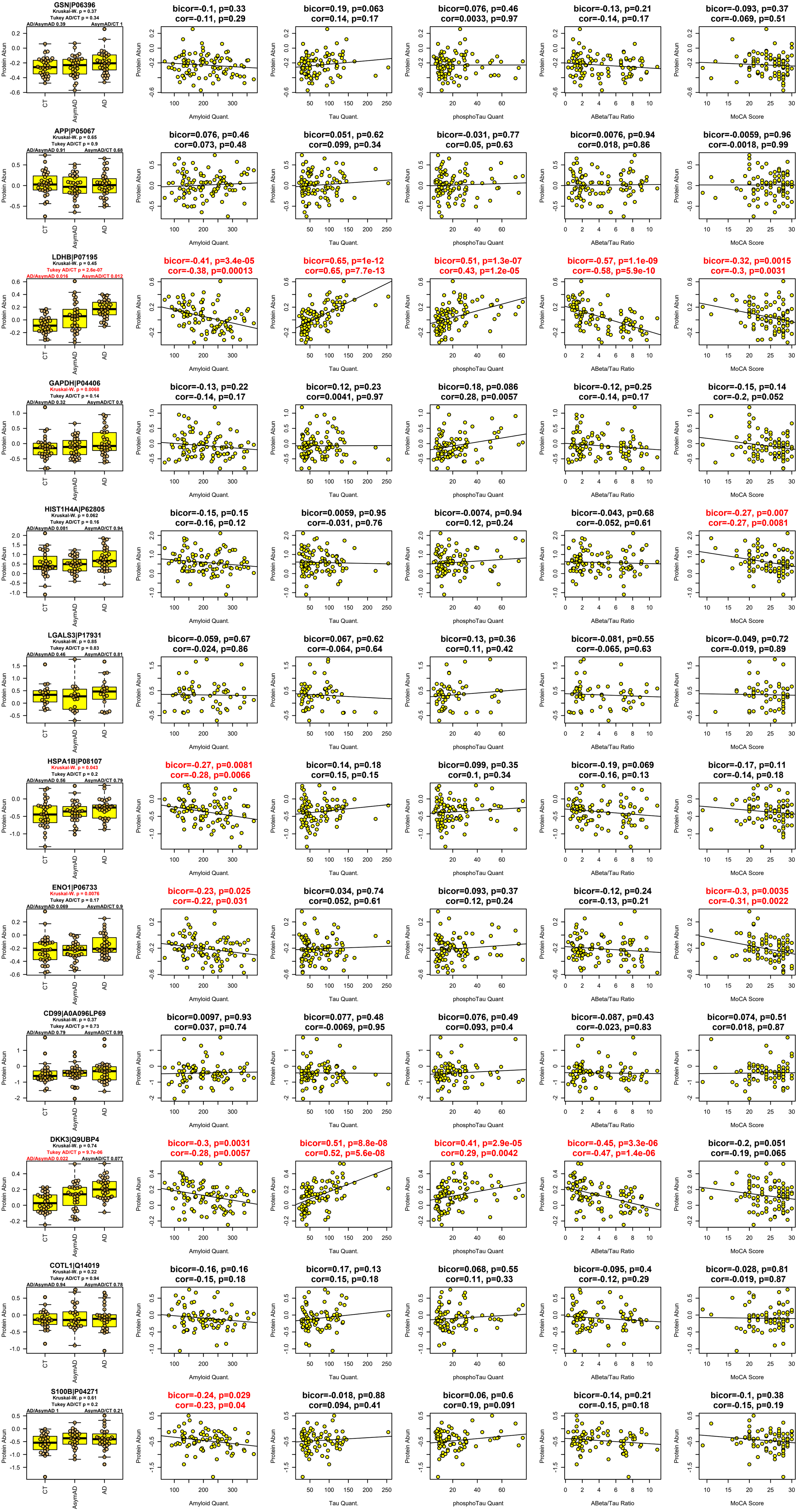
bicor=-0.25, p=1.5e-05
cor=-0.22, p=0.00014

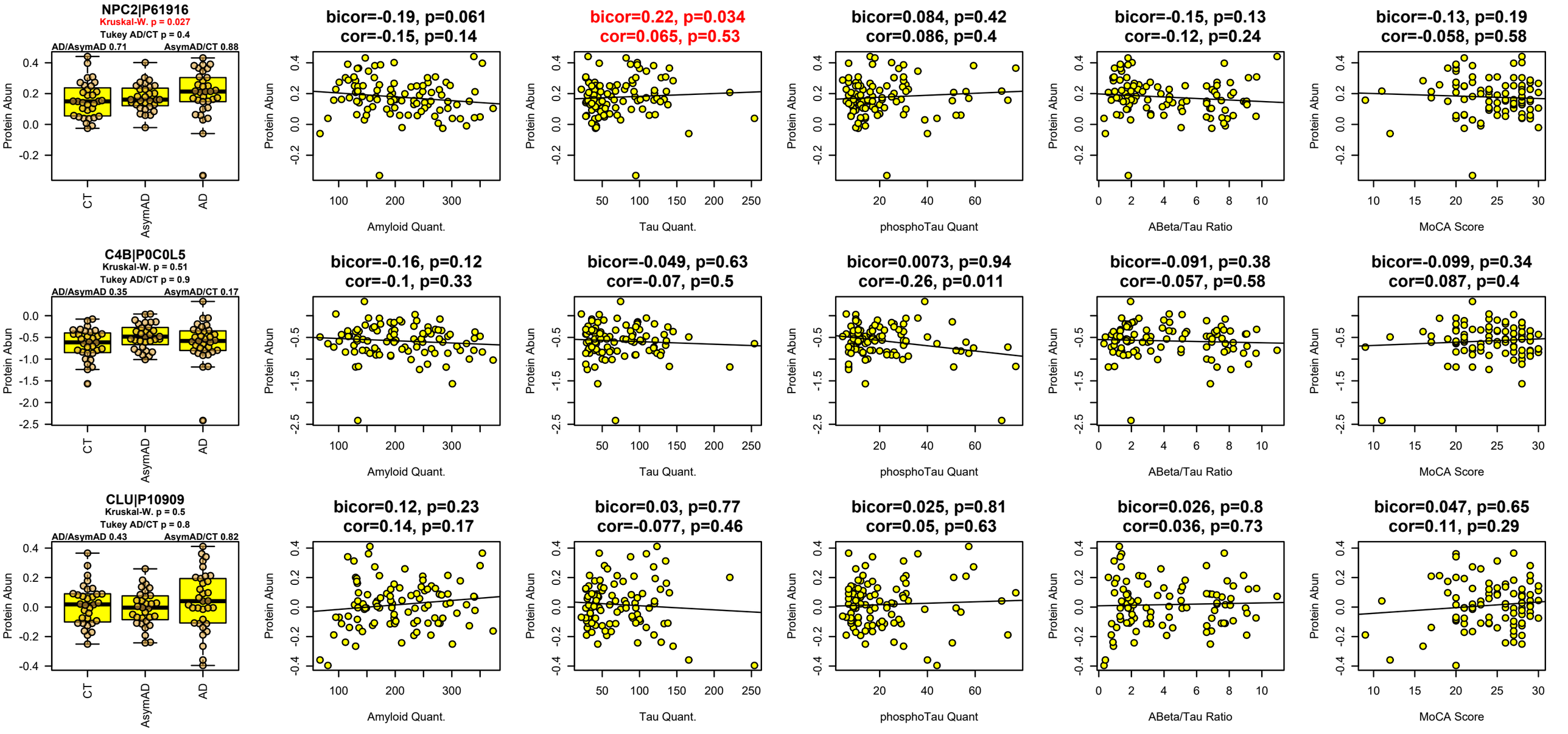
bicor=0.1, p=0.075
cor=0.2, p=0.00054

bicor=0.044, p=0.45
cor=0.052, p=0.37

Supplementary Figure 13. Relative Levels and Trait Correlations of Module M4 Proteins in AD CSF Cohort 1. Relative levels of each protein were measured in control (*n*=150 independent case samples) and AD (*n*=147 independent case samples) CSF by tandem mass tag mass spectrometry (TMT-MS), and correlated with ELISA measurements of Aβ42, Tau, and phosphorylated tau, as well as Aβ42/Tau ratio and MoCA score. The number of missing values for each protein measurement is provided at https://www.synapse.org/consensus. ELISA measurements are given in pg/mL. Differences in protein levels were assessed by two-sided Welch's *t* test. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles. MoCA, Montreal Cognitive Assessment (higher scores represent better cognitive function).

GSTO1|Q5TA01 Kruskal-W. p = 0.76 Tukey AD/CT p = 0.91 AD/AsymAD 0.94 AsymAD/CT 0.74		**bicor=-0.13, p=0.31** **cor=-0.14, p=0.27**	**bicor=0.046, p=0.72** **cor=0.081, p=0.52**	**bicor=-0.041, p=0.75** **cor=-0.051, p=0.69**	**bicor=-0.1, p=0.42** **cor=-0.11, p=0.39**	**bicor=0.015, p=0.91** **cor=-0.038, p=0.77**
PARK7|K7ELW0 Kruskal-W. p = 0.44 Tukey AD/CT p = 0.013 AD/AsymAD 0.2 AsymAD/CT 0.5		**bicor=-0.27, p=0.0078** **cor=-0.2, p=0.051**	**bicor=0.33, p=0.00085** **cor=0.17, p=0.098**	**bicor=0.3, p=0.0032** **cor=0.22, p=0.031**	**bicor=-0.31, p=0.002** **cor=-0.22, p=0.031**	**bicor=-0.13, p=0.19** **cor=-0.13, p=0.21**
CD44|H0YCV9 Kruskal-W. p = 0.31 Tukey AD/CT p = 1.7e-05 AD/AsymAD 0.05 AsymAD/CT 0.051		**bicor=-0.41, p=3.4e-05** **cor=-0.39, p=8.6e-05**	**bicor=0.33, p=0.0011** **cor=0.29, p=0.0042**	**bicor=0.36, p=0.00028** **cor=0.3, p=0.003**	**bicor=-0.42, p=2.3e-05** **cor=-0.39, p=8.6e-05**	**bicor=-0.24, p=0.02** **cor=-0.22, p=0.032**
DBI|B8ZWD1 Kruskal-W. p = 8.2e-07 Tukey AD/CT p = 0.14 AD/AsymAD 0.82 AsymAD/CT 0.4		**bicor=-0.15, p=0.15** **cor=-0.17, p=0.11**	**bicor=0.27, p=0.01** **cor=0.29, p=0.0061**	**bicor=0.37, p=0.00037** **cor=0.34, p=0.0012**	**bicor=-0.23, p=0.032** **cor=-0.29, p=0.0061**	**bicor=-0.087, p=0.42** **cor=-0.089, p=0.41**
PSAT1|Q9Y617 Kruskal-W. p = 0.038 Tukey AD/CT p = 0.61 AD/AsymAD 1 AsymAD/CT 0.57		**bicor=-0.0022, p=0.99** **cor=0.032, p=0.8**	**bicor=-0.089, p=0.49** **cor=-0.12, p=0.34**	**bicor=-0.1, p=0.43** **cor=-0.11, p=0.39**	**bicor=0.032, p=0.8** **cor=0.062, p=0.63**	**bicor=-0.11, p=0.38** **cor=-0.11, p=0.39**
GLO1|Q04760 Kruskal-W. p = 0.22 Tukey AD/CT p = 0.8 AD/AsymAD 0.98 AsymAD/CT 0.89		**bicor=-0.14, p=0.28** **cor=-0.17, p=0.18**	**bicor=-0.049, p=0.7** **cor=-0.065, p=0.61**	**bicor=0.038, p=0.76** **cor=0.085, p=0.5**	**bicor=-0.018, p=0.89** **cor=-0.033, p=0.8**	**bicor=-0.023, p=0.86** **cor=-0.063, p=0.62**
PKM|P14618-2 Kruskal-W. p = 0.017 Tukey AD/CT p = 0.00034 AD/AsymAD 0.0086 AsymAD/CT 0.61		**bicor=-0.31, p=0.0021** **cor=-0.31, p=0.0021**	**bicor=0.53, p=3e-08** **cor=0.63, p=6.1e-12**	**bicor=0.4, p=5.2e-05** **cor=0.42, p=2e-05**	**bicor=-0.46, p=2.5e-06** **cor=-0.46, p=2.4e-06**	**bicor=-0.23, p=0.023** **cor=-0.25, p=0.015**
GLOD4|F6TLX2 Kruskal-W. p = 1.1e-06 Tukey AD/CT p = 0.27 AD/AsymAD 0.89 AsymAD/CT 0.52		**bicor=-0.15, p=0.28** **cor=-0.16, p=0.25**	**bicor=0.27, p=0.045** **cor=0.29, p=0.033**	**bicor=0.14, p=0.32** **cor=0.095, p=0.49**	**bicor=-0.16, p=0.25** **cor=-0.22, p=0.11**	**bicor=-0.13, p=0.36** **cor=-0.1, p=0.48**
TPP1|O14773 Kruskal-W. p = 0.58 Tukey AD/CT p = 0.73 AD/AsymAD 0.73 AsymAD/CT 1		**bicor=-0.015, p=0.88** **cor=-0.034, p=0.74**	**bicor=-0.23, p=0.026** **cor=-0.097, p=0.35**	**bicor=-0.25, p=0.015** **cor=-0.099, p=0.34**	**bicor=0.095, p=0.36** **cor=0.084, p=0.42**	**bicor=0.00075, p=0.99** **cor=0.0029, p=0.98**
MSN|P26038 Kruskal-W. p = 0.19 Tukey AD/CT p = 0.44 AD/AsymAD 0.57 AsymAD/CT 0.98		**bicor=-0.031, p=0.81** **cor=-0.032, p=0.8**	**bicor=-0.01, p=0.94** **cor=0.06, p=0.64**	**bicor=0.2, p=0.12** **cor=0.1, p=0.43**	**bicor=-0.1, p=0.42** **cor=-0.082, p=0.52**	**bicor=-0.036, p=0.77** **cor=-0.099, p=0.44**
SPP1|P10451 Kruskal-W. p = 0.18 Tukey AD/CT p = 0.00059 AD/AsymAD 0.47 AsymAD/CT 0.026		**bicor=-0.34, p=0.00065** **cor=-0.33, p=0.001**	**bicor=0.49, p=3.5e-07** **cor=0.44, p=7.3e-06**	**bicor=0.39, p=7.2e-05** **cor=0.31, p=0.0021**	**bicor=-0.4, p=5.1e-05** **cor=-0.42, p=2e-05**	**bicor=-0.2, p=0.051** **cor=-0.15, p=0.15**
DDAH1|O94760 Kruskal-W. p = 0.44 Tukey AD/CT p = 0.011 AD/AsymAD 0.02 AsymAD/CT 0.98		**bicor=-0.28, p=0.0081** **cor=-0.28, p=0.0082**	**bicor=0.33, p=0.0018** **cor=0.38, p=0.00026**	**bicor=0.36, p=0.00056** **cor=0.33, p=0.0017**	**bicor=-0.34, p=0.0014** **cor=-0.35, p=0.00083**	**bicor=-0.28, p=0.0077** **cor=-0.29, p=0.0064**


GSN|P06396
Kruskal-W. p = 0.37
Tukey AD/CT p = 0.34
AD/AsymAD 0.39
AsymAD/CT 1
bicor=-0.1, p=0.33
cor=-0.11, p=0.29
bicor=0.19, p=0.063
cor=0.14, p=0.17
bicor=0.076, p=0.46
cor=0.0033, p=0.97
bicor=-0.13, p=0.21
cor=-0.14, p=0.17
bicor=-0.093, p=0.37
cor=-0.069, p=0.51
APP|P05067
Kruskal-W. p = 0.65
Tukey AD/CT p = 0.9
AD/AsymAD 0.91
AsymAD/CT 0.68
bicor=0.076, p=0.46
cor=0.073, p=0.48
bicor=0.051, p=0.62
cor=0.099, p=0.34
bicor=-0.031, p=0.77
cor=0.05, p=0.63
bicor=0.0076, p=0.94
cor=0.018, p=0.86
bicor=-0.0059, p=0.96
cor=-0.0018, p=0.99
LDHB|P07195
Kruskal-W. p = 0.45
Tukey AD/CT p = 2.6e-07
AD/AsymAD 0.016
AsymAD/CT 0.012
bicor=-0.41, p=3.4e-05
cor=-0.38, p=0.00013
bicor=0.65, p=1e-12
cor=0.65, p=7.7e-13
bicor=0.51, p=1.3e-07
cor=0.43, p=1.2e-05
bicor=-0.57, p=1.1e-09
cor=-0.58, p=5.9e-10
bicor=-0.32, p=0.0015
cor=-0.3, p=0.0031
GAPDH|P04406
Kruskal-W. p = 0.0068
Tukey AD/CT p = 0.14
AD/AsymAD 0.32
AsymAD/CT 0.9
bicor=-0.13, p=0.22
cor=-0.14, p=0.17
bicor=0.12, p=0.23
cor=0.0041, p=0.97
bicor=0.18, p=0.086
cor=0.28, p=0.0057
bicor=-0.12, p=0.25
cor=-0.14, p=0.17
bicor=-0.15, p=0.14
cor=-0.2, p=0.052
HIST1H4A|P62805
Kruskal-W. p = 0.062
Tukey AD/CT p = 0.16
AD/AsymAD 0.081
AsymAD/CT 0.94
bicor=-0.15, p=0.15
cor=-0.16, p=0.12
bicor=0.0059, p=0.95
cor=-0.031, p=0.76
bicor=-0.0074, p=0.94
cor=0.12, p=0.24
bicor=-0.043, p=0.68
cor=-0.052, p=0.61
bicor=-0.27, p=0.007
cor=-0.27, p=0.0081
LGALS3|P17931
Kruskal-W. p = 0.85
Tukey AD/CT p = 0.83
AD/AsymAD 0.46
AsymAD/CT 0.81
bicor=-0.059, p=0.67
cor=-0.024, p=0.86
bicor=0.067, p=0.62
cor=-0.064, p=0.64
bicor=0.13, p=0.36
cor=0.11, p=0.42
bicor=-0.081, p=0.55
cor=-0.065, p=0.63
bicor=-0.049, p=0.72
cor=-0.019, p=0.89
HSPA1B|P08107
Kruskal-W. p = 0.043
Tukey AD/CT p = 0.2
AD/AsymAD 0.56
AsymAD/CT 0.79
bicor=-0.27, p=0.0081
cor=-0.28, p=0.0066
bicor=0.14, p=0.18
cor=0.15, p=0.15
bicor=0.099, p=0.35
cor=0.1, p=0.34
bicor=-0.19, p=0.069
cor=-0.16, p=0.13
bicor=-0.17, p=0.11
cor=-0.14, p=0.18
ENO1|P06733
Kruskal-W. p = 0.0076
Tukey AD/CT p = 0.17
AD/AsymAD 0.069
AsymAD/CT 0.9
bicor=-0.23, p=0.025
cor=-0.22, p=0.031
bicor=0.034, p=0.74
cor=0.052, p=0.61
bicor=0.093, p=0.37
cor=0.12, p=0.24
bicor=-0.12, p=0.24
cor=-0.13, p=0.21
bicor=-0.3, p=0.0035
cor=-0.31, p=0.0022
CD99|A0A096LP69
Kruskal-W. p = 0.37
Tukey AD/CT p = 0.73
AD/AsymAD 0.79
AsymAD/CT 0.99
bicor=0.0097, p=0.93
cor=0.037, p=0.74
bicor=0.077, p=0.48
cor=-0.0069, p=0.95
bicor=0.076, p=0.49
cor=0.093, p=0.4
bicor=-0.087, p=0.43
cor=-0.023, p=0.83
bicor=0.074, p=0.51
cor=0.018, p=0.87
DKK3|Q9UBP4
Kruskal-W. p = 0.74
Tukey AD/CT p = 9.7e-06
AD/AsymAD 0.022
AsymAD/CT 0.077
bicor=-0.3, p=0.0031
cor=-0.28, p=0.0057
bicor=0.51, p=8.8e-08
cor=0.52, p=5.6e-08
bicor=0.41, p=2.9e-05
cor=0.29, p=0.0042
bicor=-0.45, p=3.3e-06
cor=-0.47, p=1.4e-06
bicor=-0.2, p=0.051
cor=-0.19, p=0.065
COTL1|Q14019
Kruskal-W. p = 0.22
Tukey AD/CT p = 0.94
AD/AsymAD 0.94
AsymAD/CT 0.78
bicor=-0.16, p=0.16
cor=-0.15, p=0.18
bicor=0.17, p=0.13
cor=0.15, p=0.18
bicor=0.068, p=0.55
cor=0.11, p=0.33
bicor=-0.095, p=0.4
cor=-0.12, p=0.29
bicor=-0.028, p=0.81
cor=-0.019, p=0.87
S100B|P04271
Kruskal-W. p = 0.61
Tukey AD/CT p = 0.2
AD/AsymAD 1
AsymAD/CT 0.21
bicor=-0.24, p=0.029
cor=-0.23, p=0.04
bicor=-0.018, p=0.88
cor=0.094, p=0.41
bicor=0.06, p=0.6
cor=0.19, p=0.091
bicor=-0.14, p=0.21
cor=-0.15, p=0.18
bicor=-0.1, p=0.38
cor=-0.15, p=0.19
Protein Abun
CT
AsymAD
AD
Amyloid Quant.
Tau Quant.
phosphoTau Quant
ABeta/Tau Ratio
MoCA Score


NPC2|P61916
Kruskal-W. p = 0.027
Tukey AD/CT p = 0.4
AD/AsymAD 0.71
AsymAD/CT 0.88
bicor=-0.19, p=0.061
cor=-0.15, p=0.14
bicor=0.22, p=0.034
cor=0.065, p=0.53
bicor=0.084, p=0.42
cor=0.086, p=0.4
bicor=-0.15, p=0.13
cor=-0.12, p=0.24
bicor=-0.13, p=0.19
cor=-0.058, p=0.58
C4B|P0C0L5
Kruskal-W. p = 0.51
Tukey AD/CT p = 0.9
AD/AsymAD 0.35
AsymAD/CT 0.17
bicor=-0.16, p=0.12
cor=-0.1, p=0.33
bicor=-0.049, p=0.63
cor=-0.07, p=0.5
bicor=0.0073, p=0.94
cor=-0.26, p=0.011
bicor=-0.091, p=0.38
cor=-0.057, p=0.58
bicor=-0.099, p=0.34
cor=0.087, p=0.4
CLU|P10909
Kruskal-W. p = 0.5
Tukey AD/CT p = 0.8
AD/AsymAD 0.43
AsymAD/CT 0.82
bicor=0.12, p=0.23
cor=0.14, p=0.17
bicor=0.03, p=0.77
cor=-0.077, p=0.46
bicor=0.025, p=0.81
cor=0.05, p=0.63
bicor=0.026, p=0.8
cor=0.036, p=0.73
bicor=0.047, p=0.65
cor=0.11, p=0.29
CTSD|P07339
Kruskal-W. p = 0.23
Tukey AD/CT p = 0.076
AD/AsymAD 0.44
AsymAD/CT 0.61
bicor=0.063, p=0.54
cor=0.038, p=0.71
bicor=-0.35, p=0.00039
cor=-0.4, p=5.4e-05
bicor=-0.3, p=0.0029
cor=-0.28, p=0.0057
bicor=0.29, p=0.0043
cor=0.26, p=0.011
bicor=0.063, p=0.54
cor=0.085, p=0.41
Protein Abun
CT
AsymAD
AD
Amyloid Quant.
Tau Quant.
phosphoTau Quant
ABeta/Tau Ratio
MoCA Score

Supplementary Figure 14. Relative Levels and Trait Correlations of Module M4 Proteins in AsymAD and AD CSF Cohort 2. Relative levels of each protein were measured in control (*n*=32 independent case samples), AsymAD (*n*=31 independent case samples), and AD (*n*=33 independent case samples) CSF by tandem mass tag mass spectrometry (TMT-MS), and correlated with ELISA measurements of Aβ42, Tau, and phosphorylated tau, as well as Aβ42/Tau ratio and MoCA score. The number of missing values for each protein measurement is provided at https://www.synapse.org/consensus. ELISA measurements are given in pg/mL. Differences in protein levels were assessed by Kruskal-Wallis (K-W) one-way ANOVA with Tukey test. Correlations were performed using both Pearson correlation (cor) and biweight midcorrelation (bicor), which is more robust to outliers. Statistical significance at $p < 0.05$ is highlighted in red. Boxplots represent the median, 25th, and 75th percentiles, and whiskers represent measurements to the 5th and 95th percentiles. MoCA, Montreal Cognitive Assessment (higher scores represent better cognitive function).