

Clinical workpackage



AETIONOMY PD cohort

Towards mechanism-based classification

Partners: ICM (JC Corvol)



Novartis (A Graf)



UKB (M Heneka, U Wuellner)



BBRC (JL Molinuevo)

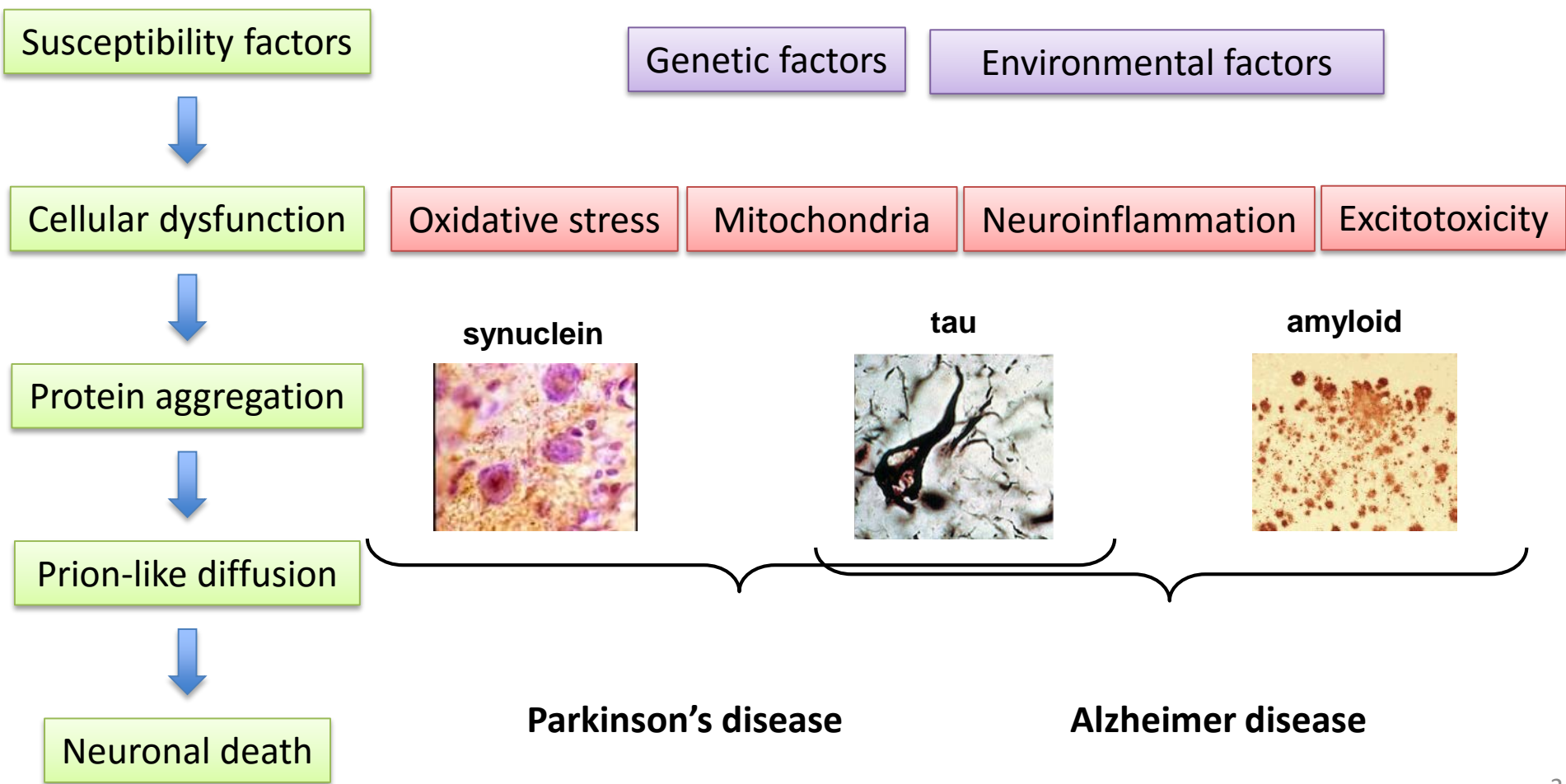


KI (P Svenningsson)



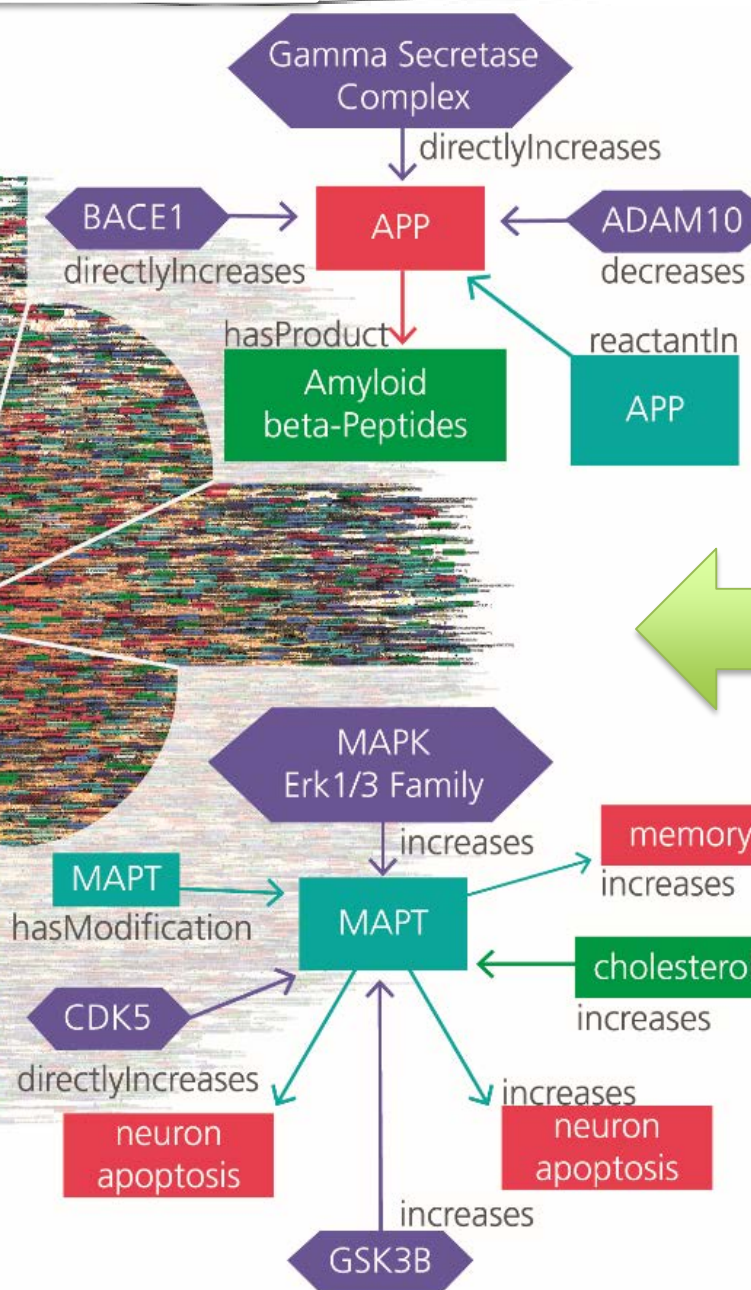
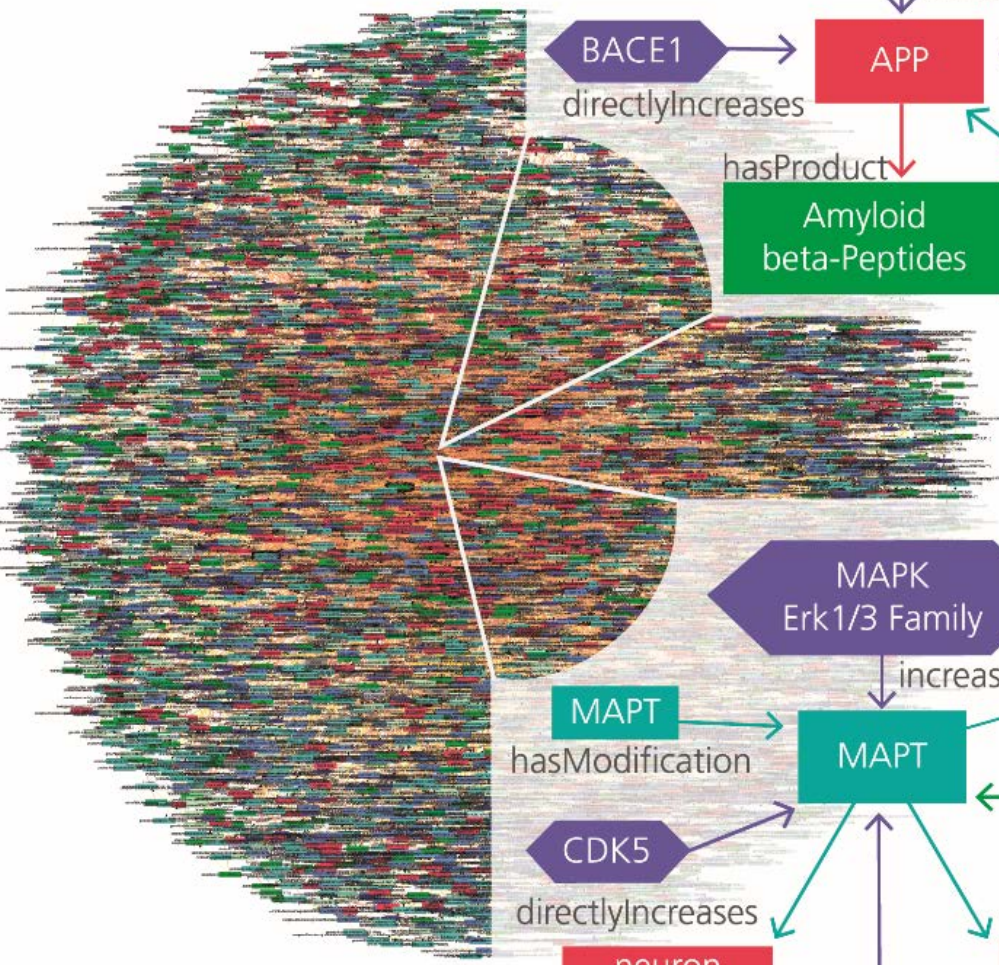


Neurodegenerative diseases



OpenBEL model for Alzheimer's Disease

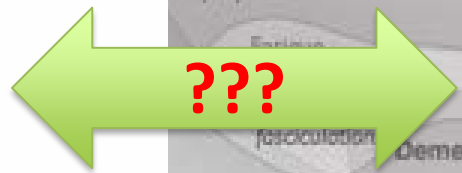
"diseased"



of molecular dysfunction,
disease
signs and symptoms

Diseases
and
medical
treatments

| | | |
|-------------------------|--------------|------------|
| Anxiety | bradykinesia | Epilepsy |
| blurry vision | weight loss | Diabetes |
| polyuria | | |
| Emesis | atrophy | ALS |
| fasciculation | Dementia | |
| | pneumonia | Alzheimer |
| orthostatic hypotension | | Huntington |
| rigid muscle | Tremor | Parkinson |
| REM behavior disorder | | |



g links

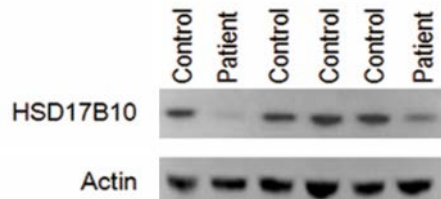
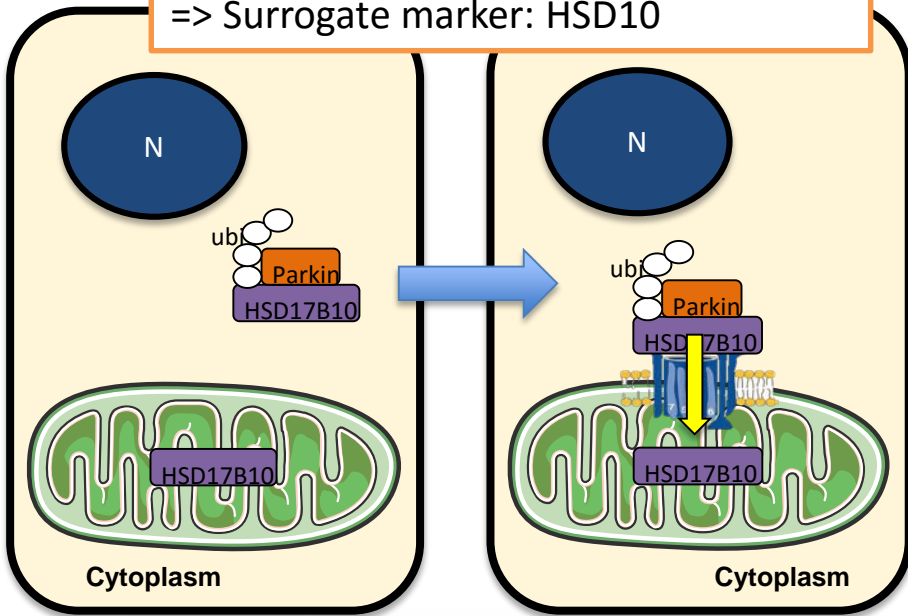
Medical Ontologies



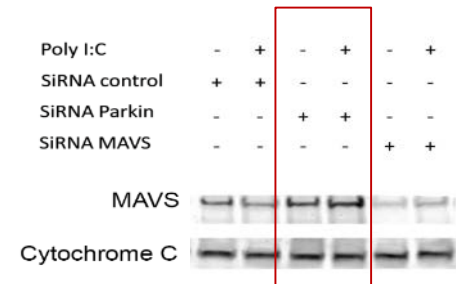
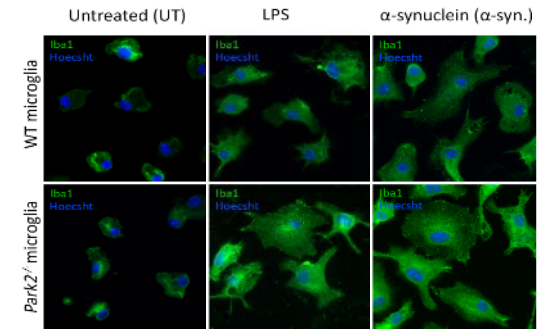
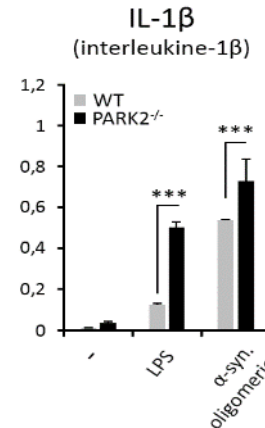
PD: Cross-talk mitophagy - neuroinflammation

Parkin-dependent mitophagy => PD
=> Surrogate marker: HSD10

Parkin-dependent microglia over-activation
=> Surrogate marker: TFAM



1/ *PARK2*^{-/-} microglia are over-activated

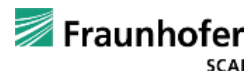


2/ Inflammasome-related cytokine over-production

3/ Parkin contributes to MAVS degradation

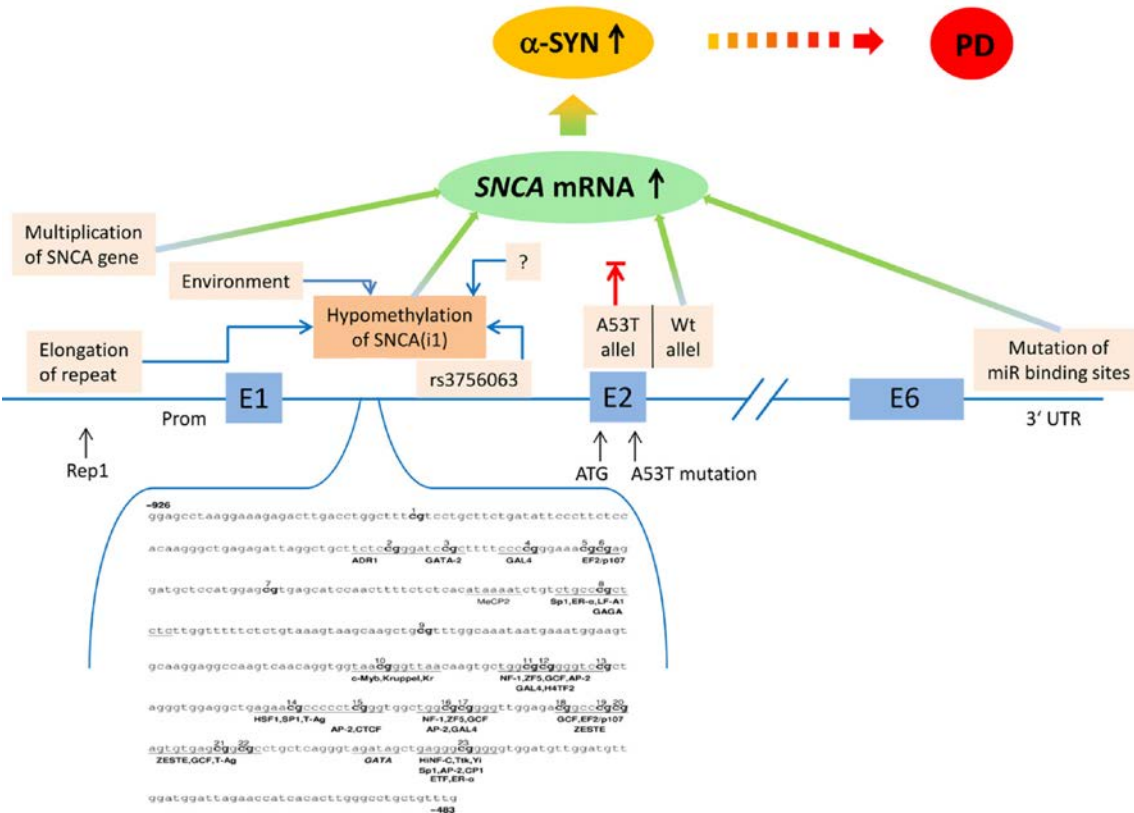
Bertolin et al., 2015

Mouton-Liger, Glia 2018⁴

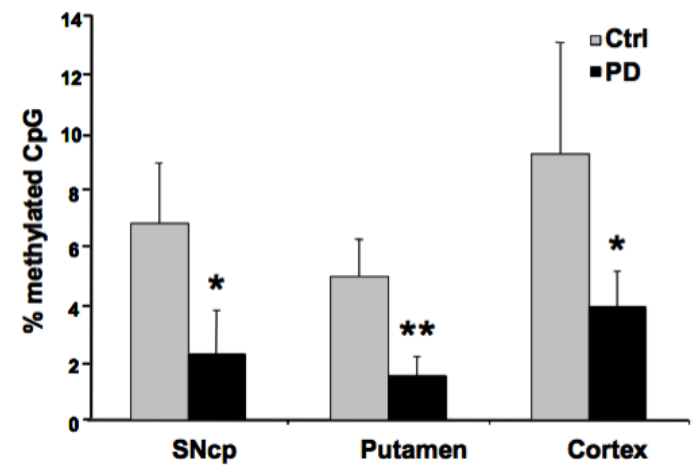




PD: Epigenetics hypothesis



SNCA methylation in the CNS

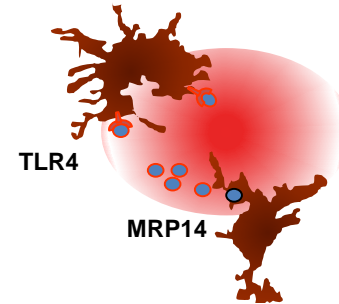
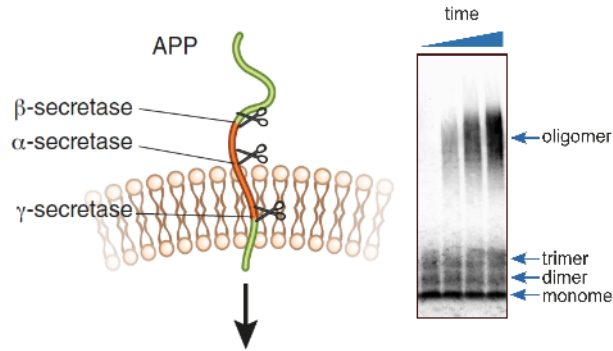


Wullner et al., J Neurochem 2016

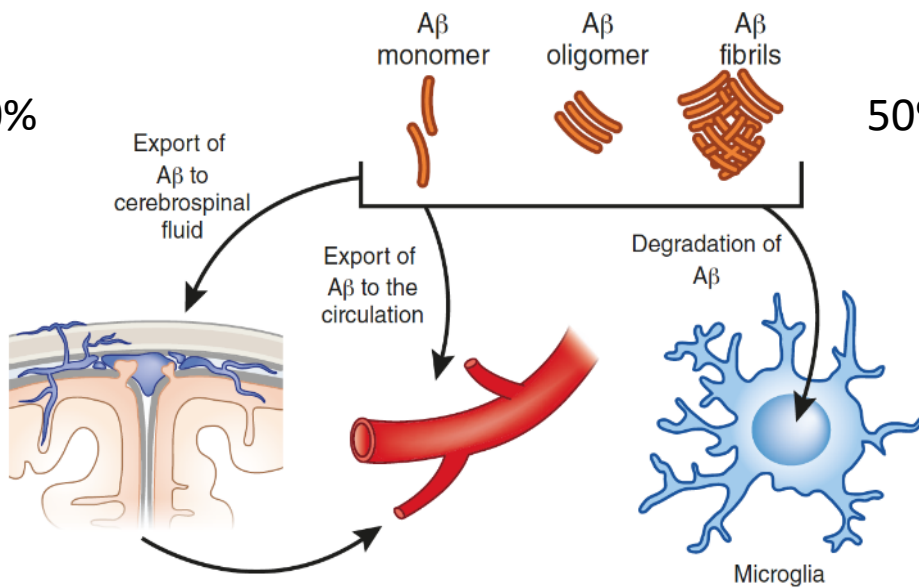




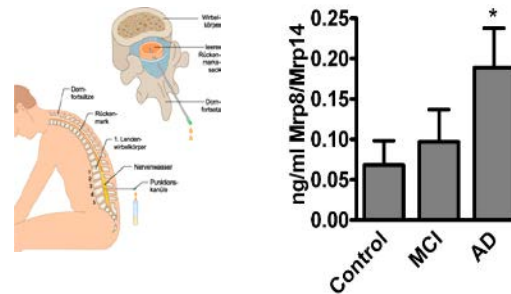
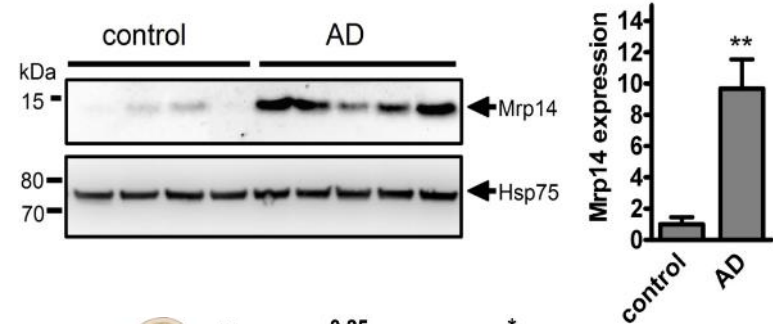
AD: Neuroinflammation hypothesis



50%



50%



Heneka et al. *Nat Immunol*, 2015

Kummer et al. *J. Neurosci.* 2012

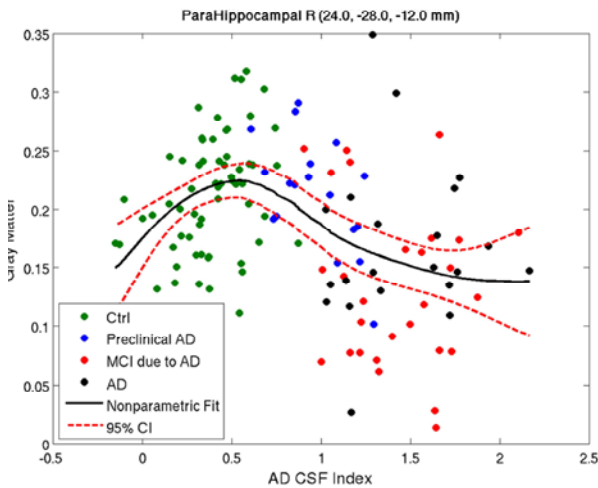
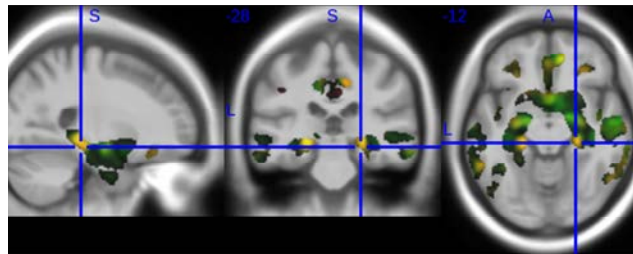
Heneka et al. *Lancet Neurol*, 2015





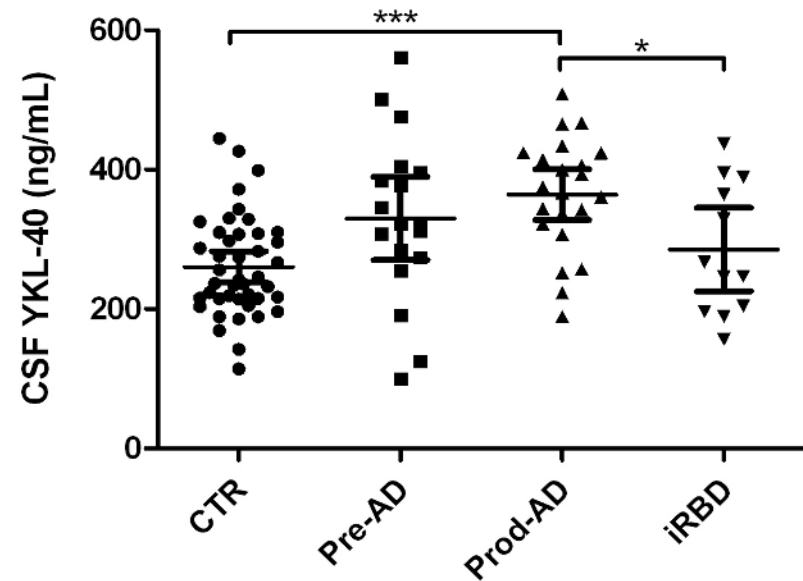
AD: glial inflammatory response, YKL40 as a biomarker

Nonlinear cerebral atrophy patterns across the Alzheimer's Disease continuum



Gispert et al., Neurobiol Aging (2015)

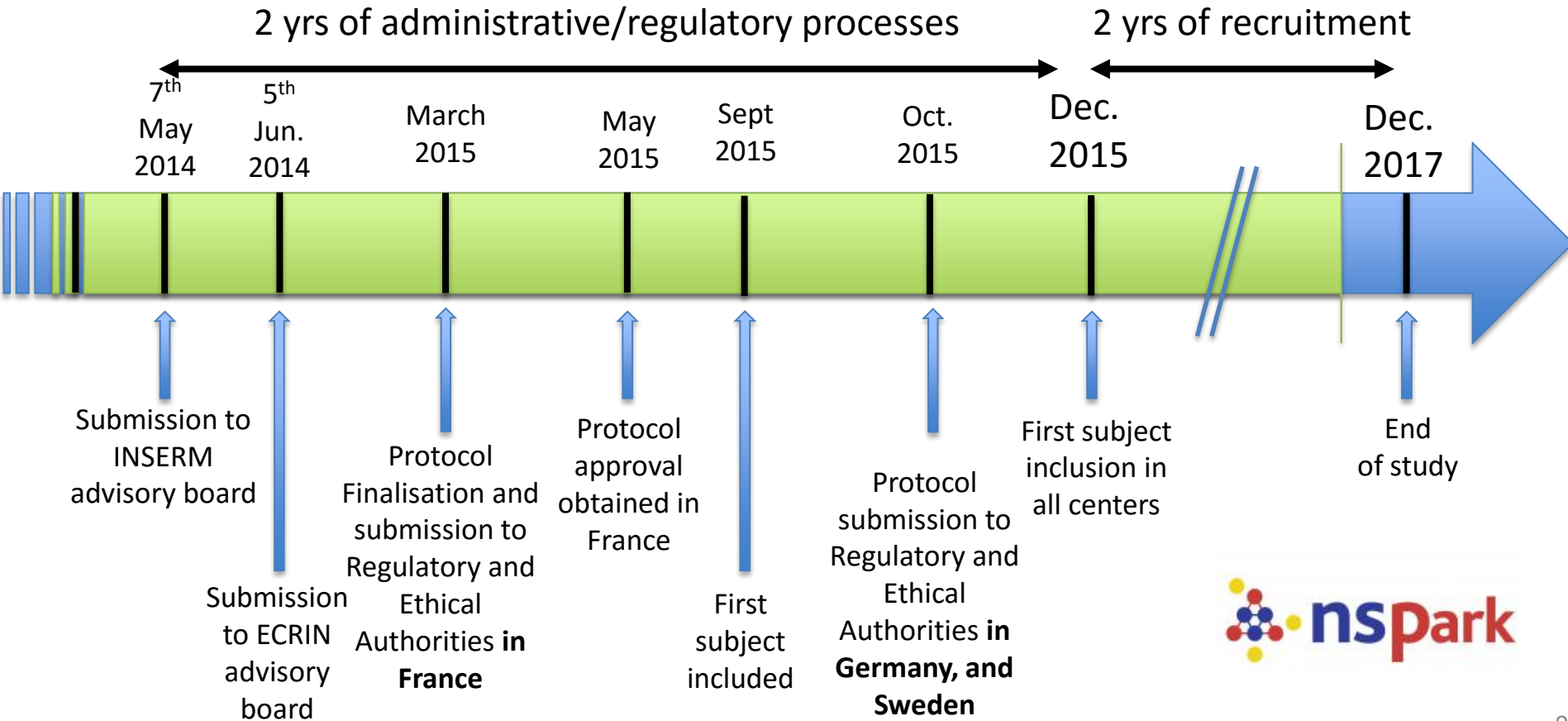
YKL40: glial inflammatory response in AD





European multicenter study – ECRIN

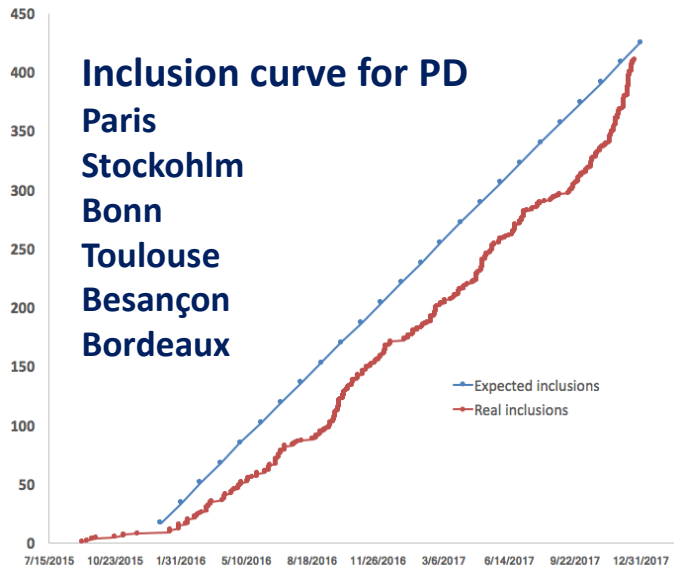
ICM, INSERM, Paris
 Cécile Gaudebout
 Stéphanie Carvalho





AETIONOMY: unique dataset across neurodegenerative diseases

| Origin | Total n | PD | | | | | | AD | | |
|-------------------------|---------|------------------------------|-------------------------------|-----------------------------|-------------------------|-------------------------|--------------------------|---------------------------|-----------------------------|--------------------------|
| | | DNA | CSF | Plasma | Serum | Fibroblasts | MRI | DNA | CSF | MRI |
| AETIONOMY-CS (PD group) | 405 | 396 | 99 | 391 | 391 | 160 | 30 | | | |
| External cohorts | 1556 | 645 | 84 | 230 | | | 14 | 436 | 380 | 23 |
| TOTAL samples | | 1041 ^{0,1,4} | 183 ^{0,2,3,6} | 621 ^{0,3,5} | 391 ⁰ | 160 ⁰ | 44 ^{0,7} | 436 ^{0,1} | 380 ^{0,2,6} | 23 ^{0,7} |

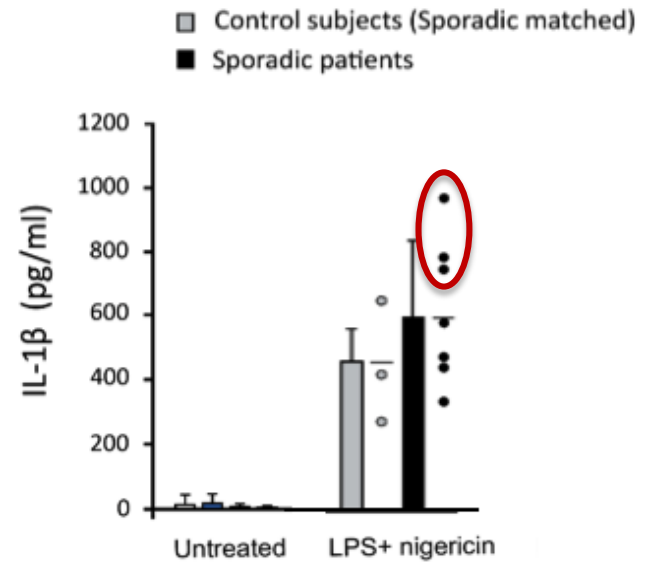
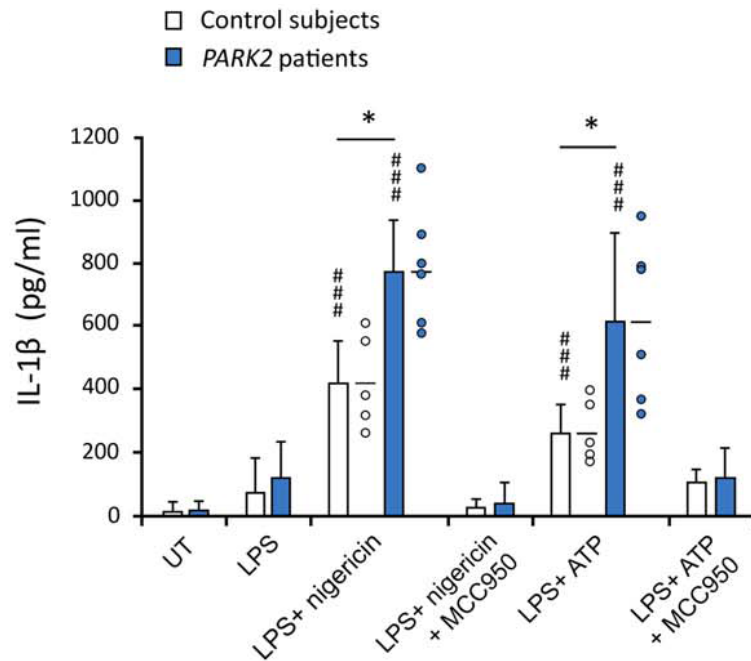
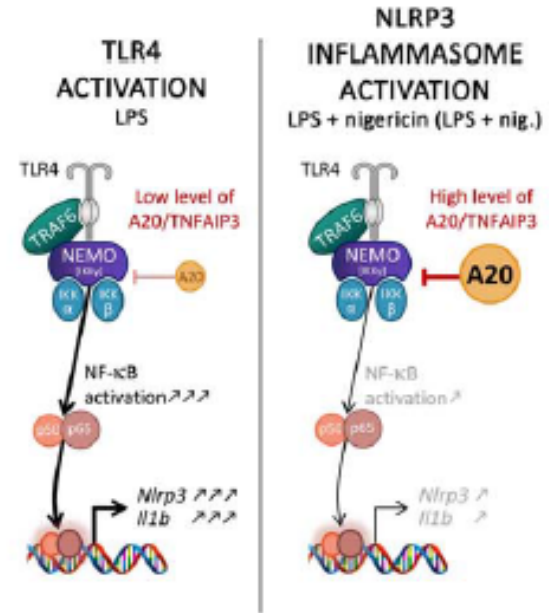
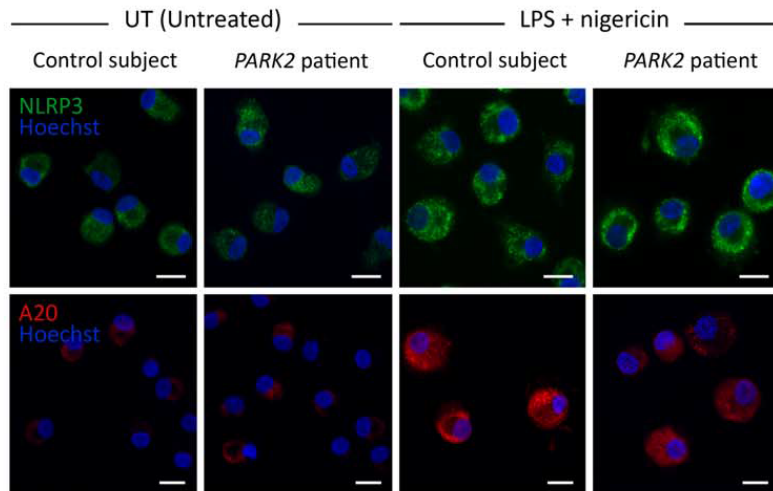


Available associated data:

- ⁰ Clinical Data
- ¹ Genomics (ICM)
- ² Inflammatory (IDIBAPS/UKB)
- ³ Proteomics (KI)
- ⁴ Methylation (UKB)
- ⁵ Cholesterol (UKB)
- ⁶ Insuline resistance pathway (SARD)
- ⁷ Brain imaging (BBRC)

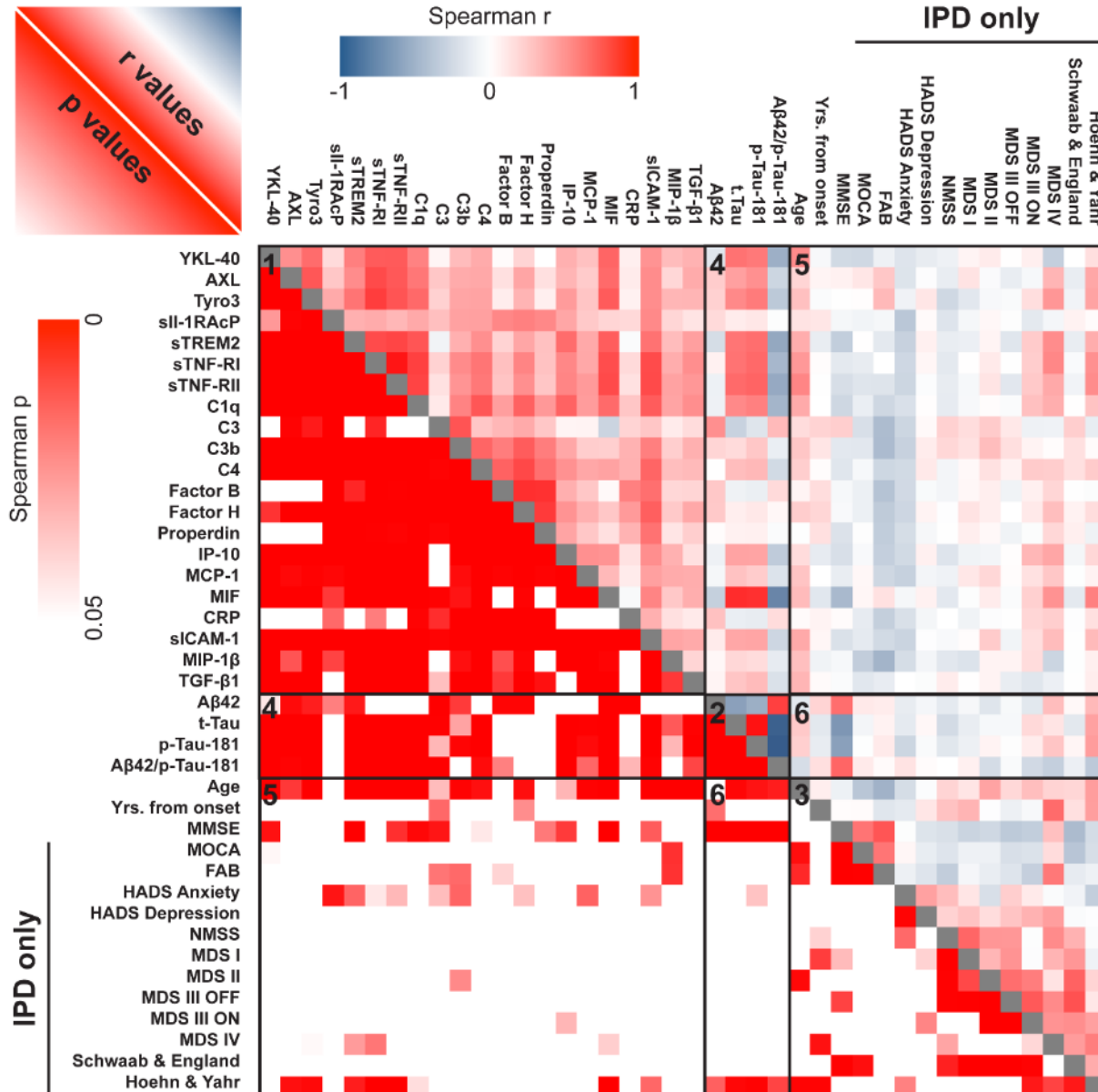
| | Genetic PD (N = 25) | Idiopathic PD (N = 251) | At Risk for PD (N = 39) | Healthy Control (N = 90) |
|--|--------------------------------|------------------------------------|------------------------------------|-------------------------------------|
| Age (years)* | 58.72 ± 14.89 | 64.07 ± 8.64 | 63.26 ± 11.05 | 62.83 ± 9.22 |
| Female, n (%) | 11 (44.00) | 80 (31.87) | 13 (33.33) | 59 (65.56) |
| Ethnicity, n (%) | | | | |
| Caucasian/White | 19 (76.0) | 245 (97.61) | 32 (80.0) | 85 (93.41) |
| Black | 1 (4.0) | 3 (1.2) | 2 (5.0) | 1 (1.1) |
| Asian | 1 (4.0) | 0 | 1 (2.5) | 2 (2.2) |
| North African/Arabic | 4 (16.0) | 3 (1.2) | 3 (7.5) | 1 (1.1) |
| Other | 0 | 0 | 2 (5.0) | 2 (2.2) |
| Weight (kg)* | 67.42 ± 12.26 | 77.03 ± 15.51 | 74.33 ± 13.86 | 71.88 ± 14.46 |
| Smoking, n (%) | | | | |
| Current | 3 (12.00) | 17 (6.85) | 5 (12.82) | 7 (7.95) |
| Past | 7 (28.00) | 101 (40.37) | 18 (46.15) | 40 (45.45) |
| Never | 15 (60.00) | 130 (52.42) | 16 (41.03) | 41 (46.59) |
| Age at onset (years)* | 45.42 ± 15.78 | 60.47 ± 8.71 | N/A | N/A |
| Disease duration (months) ⁺ | 28.5 (43.0) | 144.0 (125.0) | N/A | N/A |
| MDS-UPDRS Score* | | | | |
| Part I | 12.72 ± 6.56 | 8.73 ± 4.91 | 7.13 ± 3.44 | 3.48 ± 3.33 |
| Part II | 15.0 ± 9.05 | 8.99 ± 5.38 | 1.14 ± 1.59 | 0.58 ± 1.21 |
| Part III | 45.16 ± 17.75 | 30.4 ± 14.51 | 9.64 ± 5.36 | 2.13 ± 3.17 |
| Part IV | 5.56 ± 4.28 | 1.39 ± 2.61 | 0 ± 0 | 0 ± 0 |
| HADS* | | | | |
| Anxiety Score | 7.77 ± 4.25 | 5.68 ± 3.72 | 6.92 ± 3.37 | 4.87 ± 3.29 |
| Depression Score | 4.77 ± 3.25 | 4.03 ± 3.45 | 3.18 ± 2.99 | 2.21 ± 3.02 |
| NMSS total score* | 9.9 ± 5.35 | 9.18 ± 4.67 | 7.59 ± 4.30 | 2.89 ± 3.42 |
| MMSE total score * | 28.43 ± 1.69 | 28.38 ± 1.68 | 29.18 ± 0.9 | 28.93 ± 1.33 |
| MoCA total score* | 25.74 ± 4.28 | 26.07 ± 2.9 | 26.95 ± 2.55 | 26.69 ± 2.75 |
| RBANS total score* | 92.57 ± 20.4 | 91.95 ± 16.51 | 102.11 ± 13.63 | 100.9 ± 15.57 |
| Family history of PD, n (%) | 16 (64.00) | 14 (5.62) | 15 (39.47) | 5 (5.81) |

Crosstalk between mitochondria dysfunction and inflammation in PD

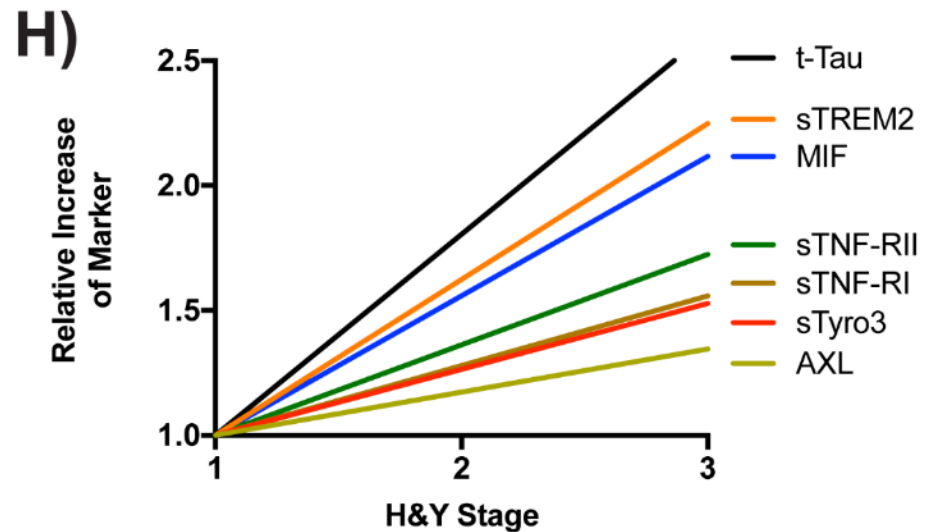
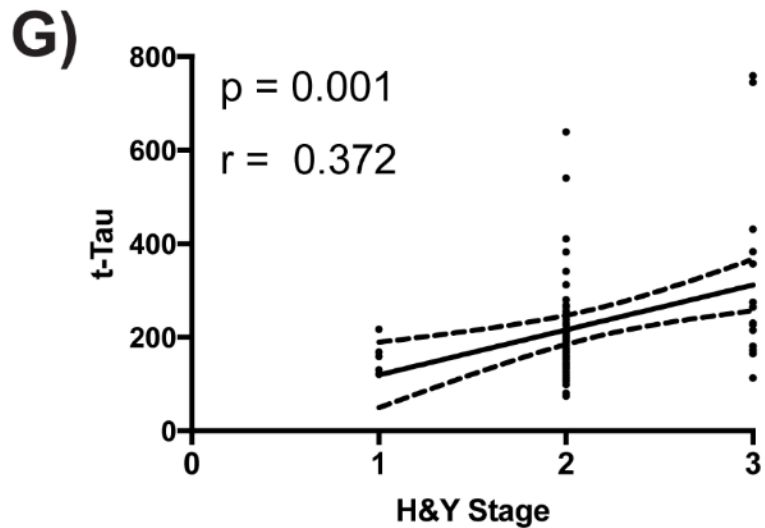
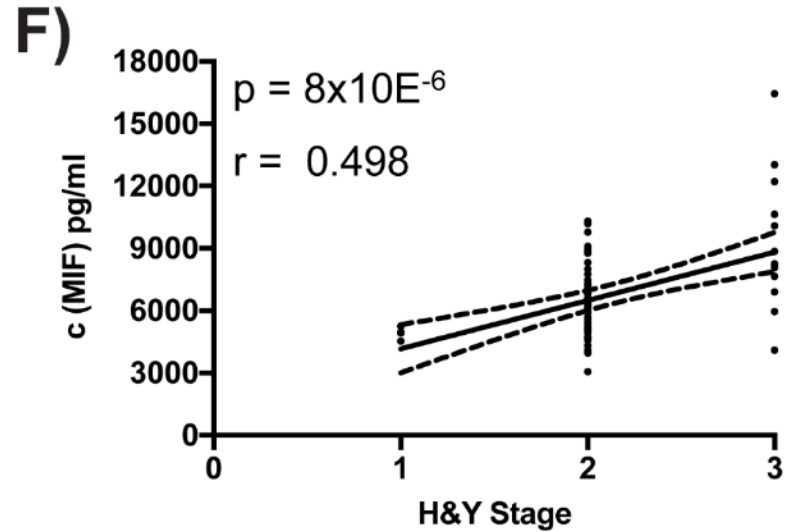
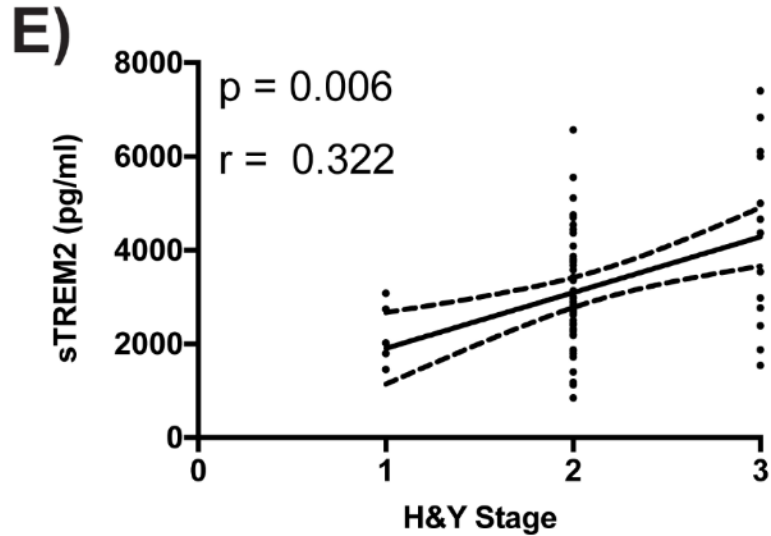


Immune biomarkers associates with AD markers and symptoms

UKB, Bonn
 Micheal Heneka
 Frederic Brosseron



Immune response depends on neuronal damage independently of the disease



WM microstructure gets altered with age and amyloid markers whatever the underlying pathology

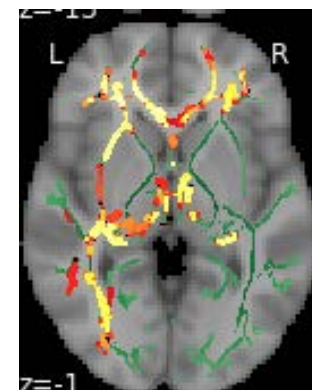
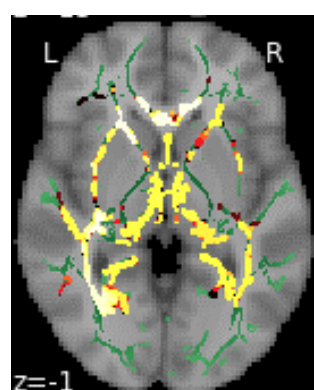
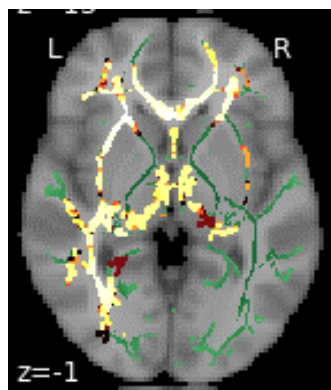
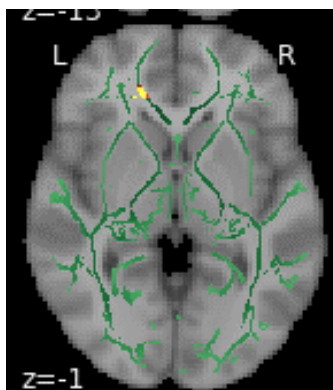
Age

↘FA

↗MD

↗AxD

↗RD



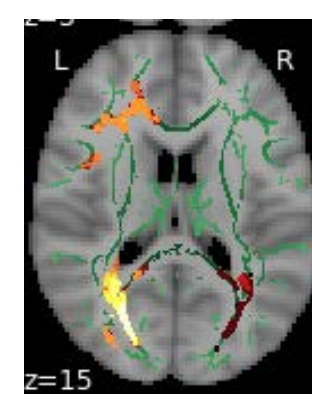
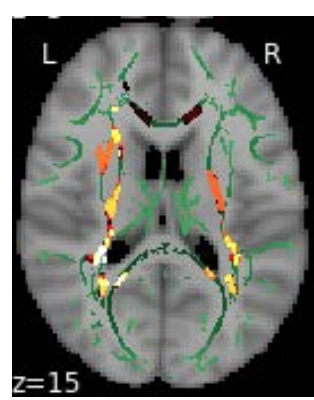
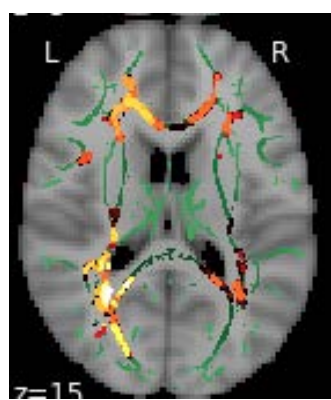
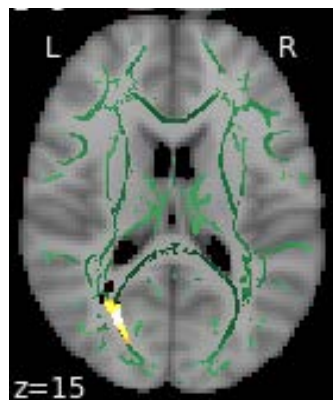
A β 42

Positive with FA

Negative with MD

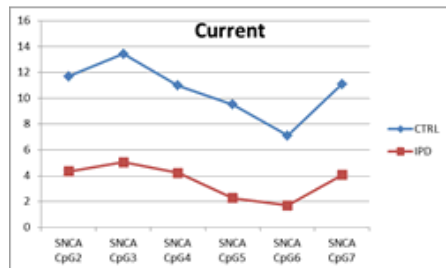
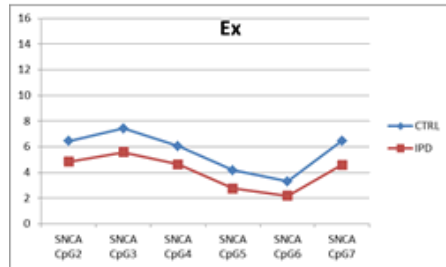
Negative with AxD

Negative with RD

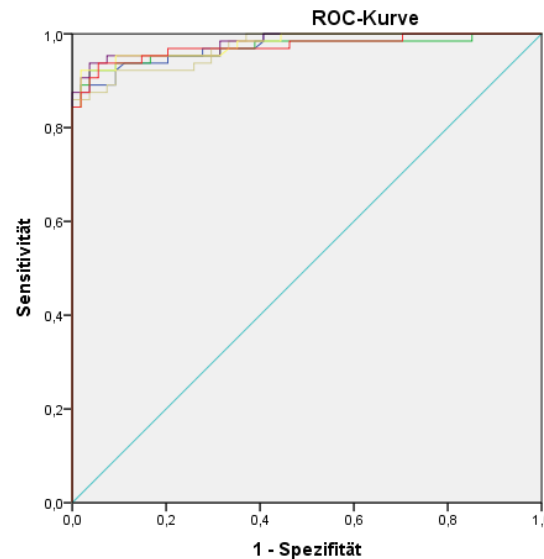




α -Synuclein: methylation *and* smoking



**ROC curve IPD vs. HC
(current smokers)**



Diagonale Segmente ergeben sich aus Bindungen.

**AUC IPD vs. HC
(current smokers)**

| Variable(n) für Testergebnis | Fläche |
|------------------------------|--------|
| SNCA CpG2 | ,975 |
| SNCA CpG3 | ,970 |
| SNCA CpG4 | ,971 |
| SNCA CpG5 | ,981 |
| SNCA CpG6 | ,978 |
| SNCA CpG7 | ,973 |

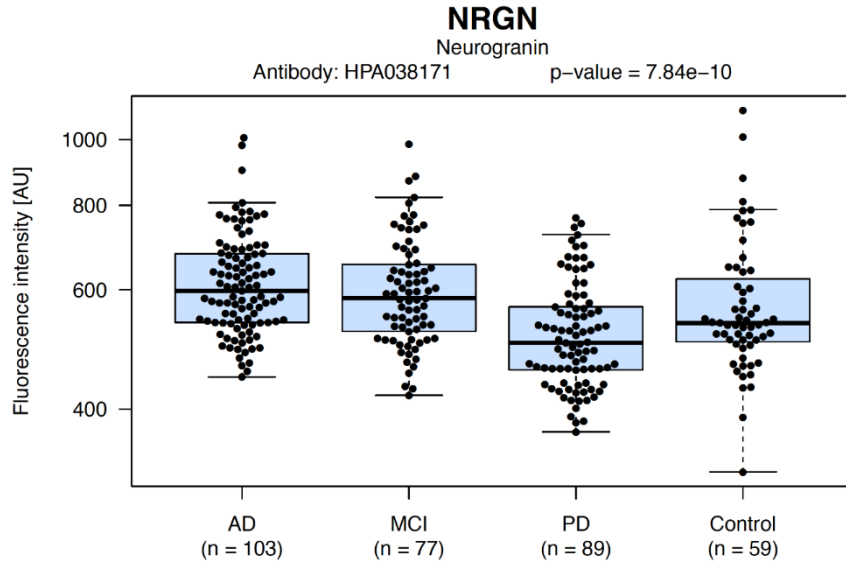
UKB, Bonn
Ullrich Wuellner
Ina Schmitt
Sandra Roeske

Proteomic analysis in CSF



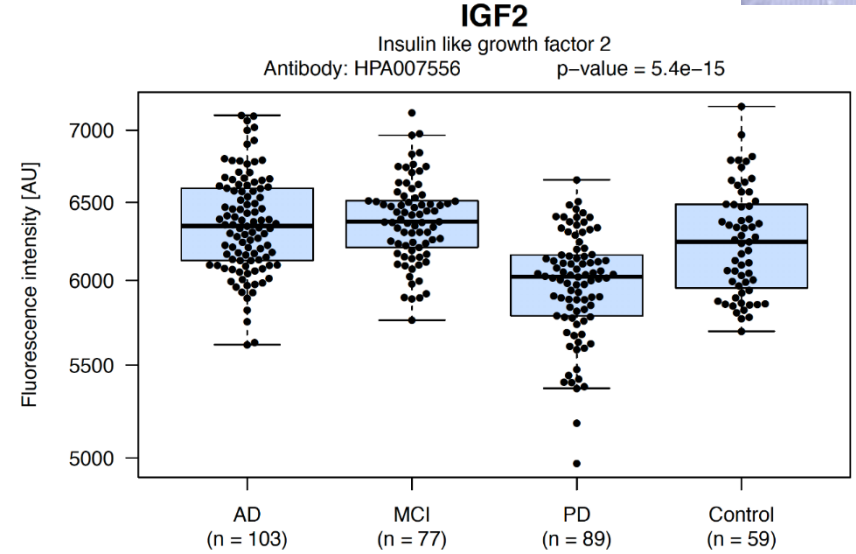
NRGN

Neurogranin



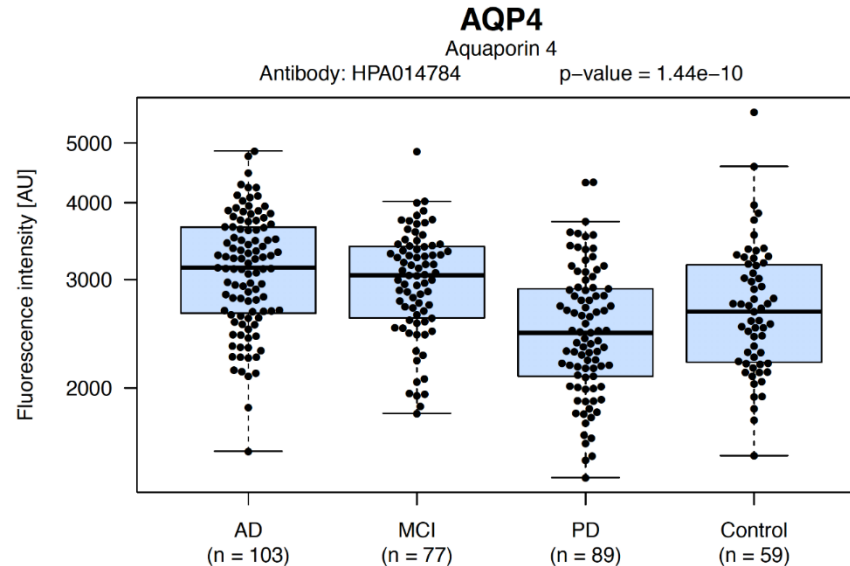
IGF2

Insulin like growth factor 2



AQP4

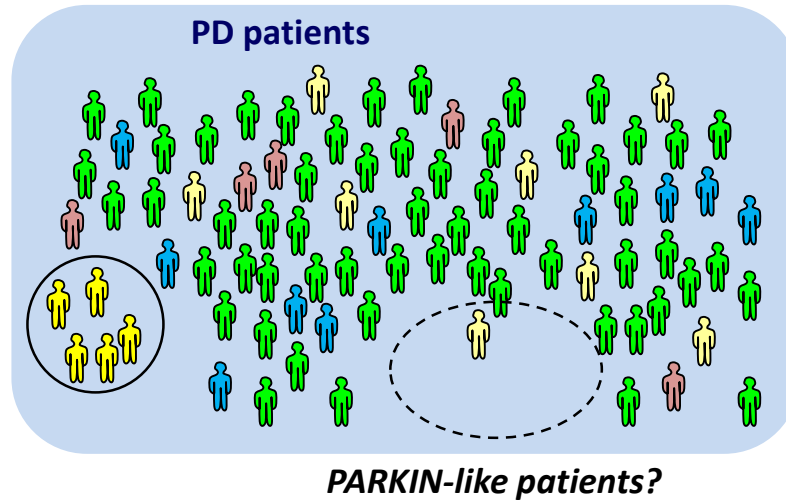
Inflammation



KI, Stockholm
P Svenningsson
I Markaki
P Tsitsi
P Nilsson
S Berström

Is it possible to stratify patients according to their underlying mechanism ?

AETIO $\frac{N/O}{M/Y}$



imi innovative medicines initiative

Genomic-based stratification

Biological validation

Replication in independant cohorts

PD subpopulation ready for therapeutic intervention targeting specific mechanisms

Analysis pipeline

5 candidate mechanisms

Mitochondria dysfunction
Epigenetic of SNCA
Neuro-inflammation
Insuline pathway
Stress-induced comorbidity

Genotyping

NeuroChips: 400 k backbone +
200 k custum SNPs
Imputation of > 10 M variants
Selection of relevant variants



Discovery

DIGPD
N=416 PD



Clinical phenotype



Replication

AETIONOMY
N=224 PD



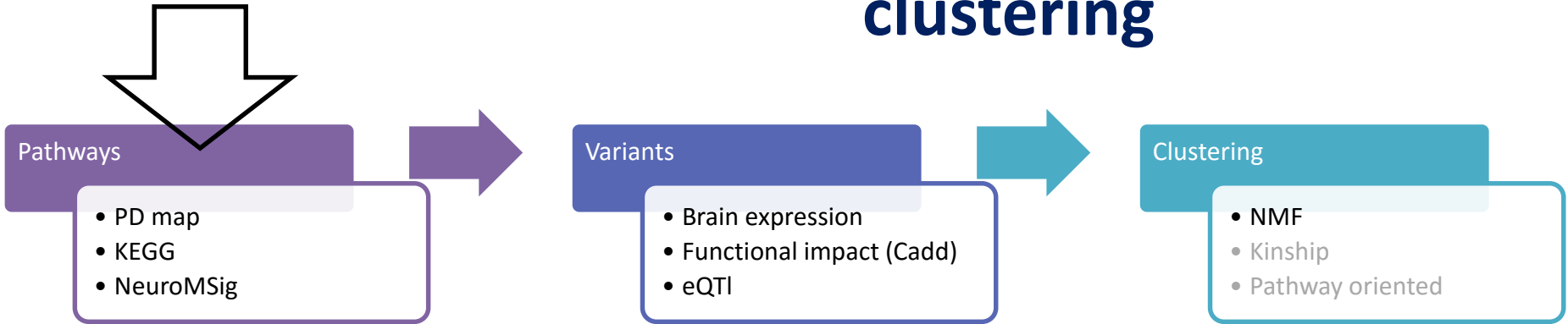
Clinical phenotype



Biological data in CSF

Genetic variant selection and clustering

**5 candidate
MECHANISMS**

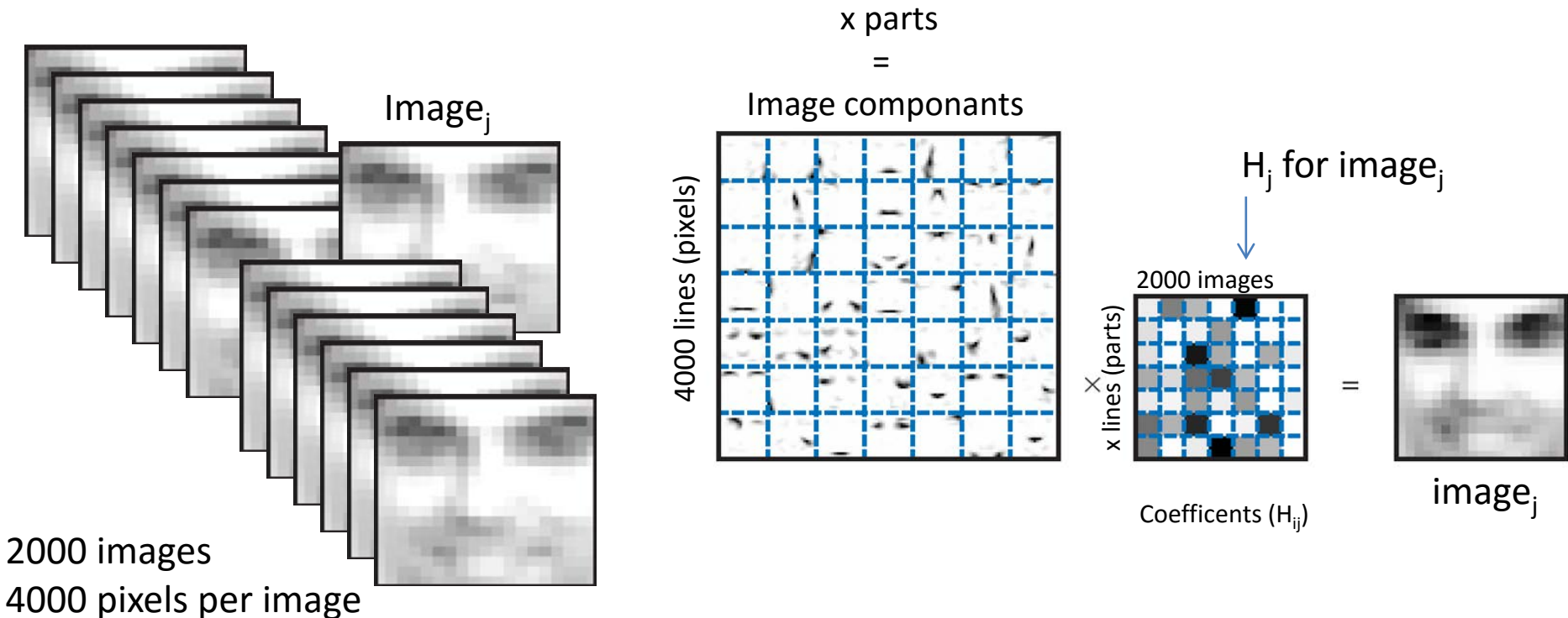


| | N | Astroglial Inflammation | Insulin Signal Transduction | Mitochondrial Dysfunction | SNCA Methylation | Stress Induced Comorbidity |
|-------------------------------------|----------|------------------------------------|--|--------------------------------------|-----------------------------|---------------------------------------|
| Total number of variants | 956 | 354 | 221 | 285 | 237 | 76 |
| Not shared | | 303 | 142 | 168 | 113 | 22 |
| Common in 2 mechanisms | | 27 | 0 | 22 | 19 | 28 |
| Common in 3 mechanisms | | 10 | 79 | 81 | 91 | 12 |
| Common in 4 mechanisms | | 14 | 0 | 14 | 14 | 14 |

Non-negative Matrix Factorisation method

- NMF provides a parts-based representation of data:

$$H_{1j} \times \text{Part}_1 + H_{2j} \times \text{Part}_2 + \dots = \text{Image}_j$$



NMF: application to AETIONOMY

ICM, Paris

François-Xavier Lejeune

Fabrice Danjou

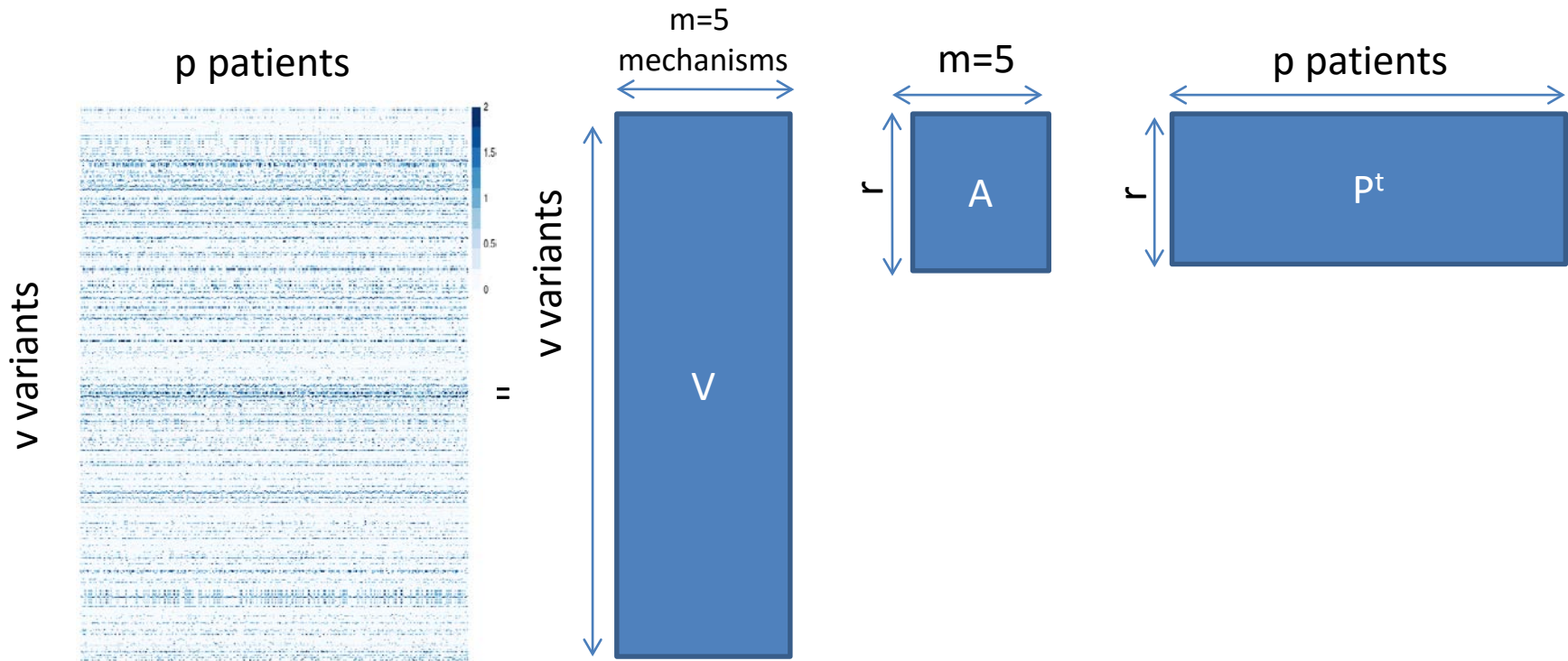
Boris Labrador

UCB

Holger Froehlich

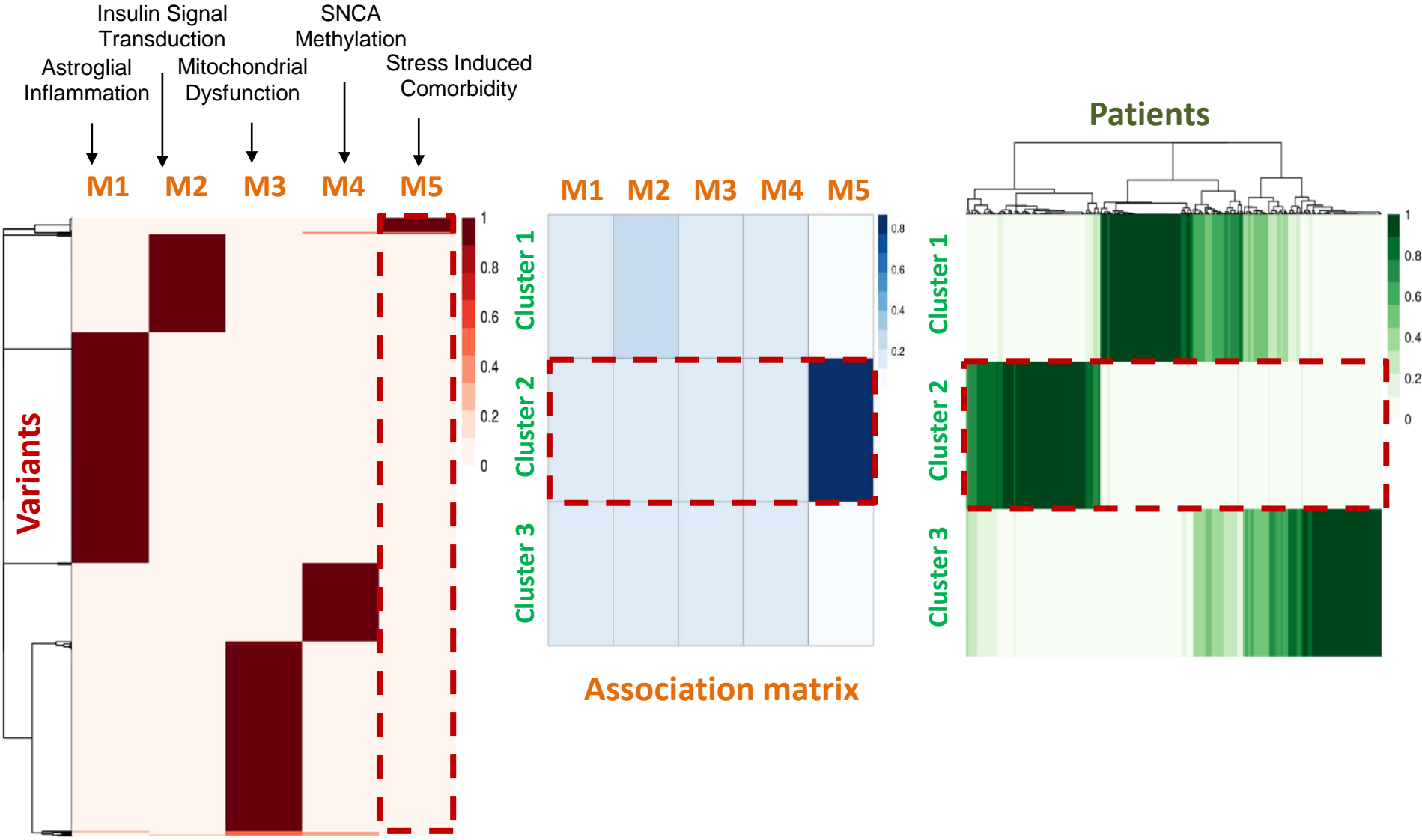
$$X \approx V \times A \times P^t$$

$$(v,p) = (v,m) \times (m,r) \times (r,p)$$



$$\min_{V,A,P} F(V,A,P) = \min_{V,A,P} ||X - V A P^t||^2 + \text{Pen}(V)$$

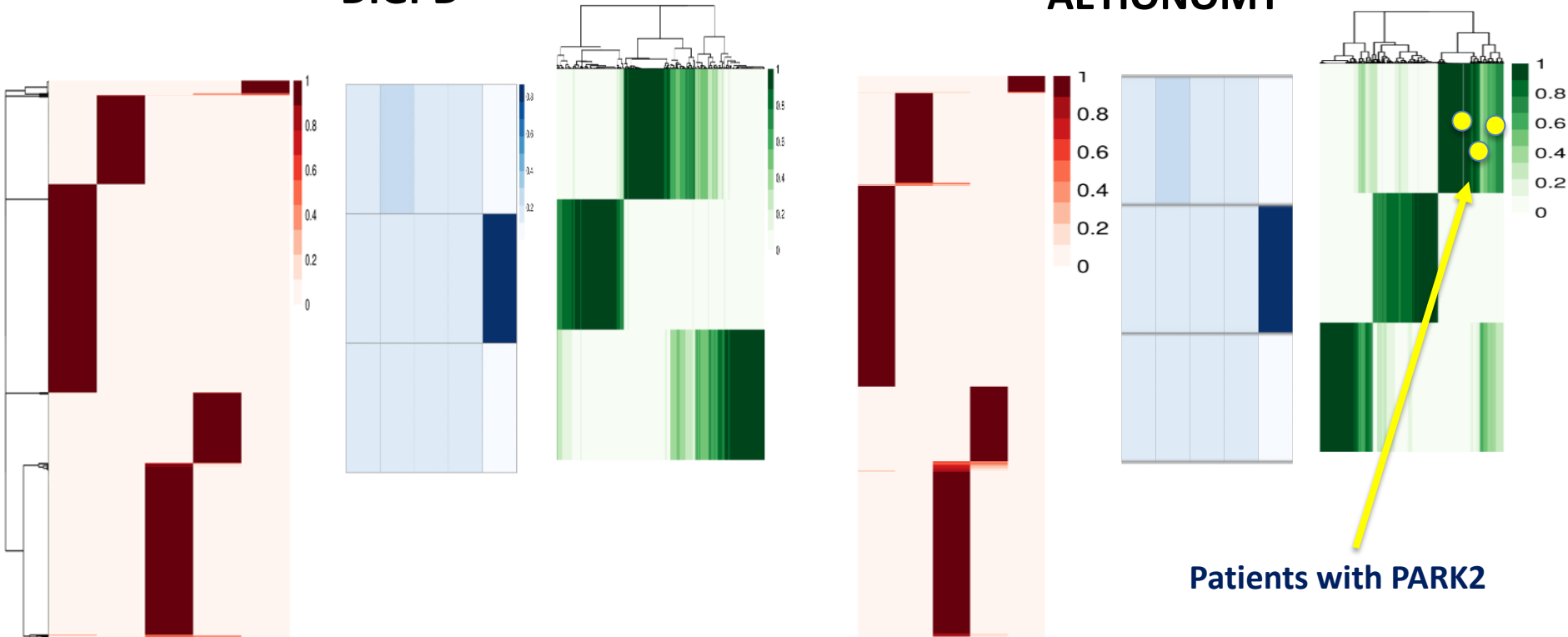
NMF in PD patients from the DIGPD cohort



Replication in the AETIONOMY cohort

DIGPD

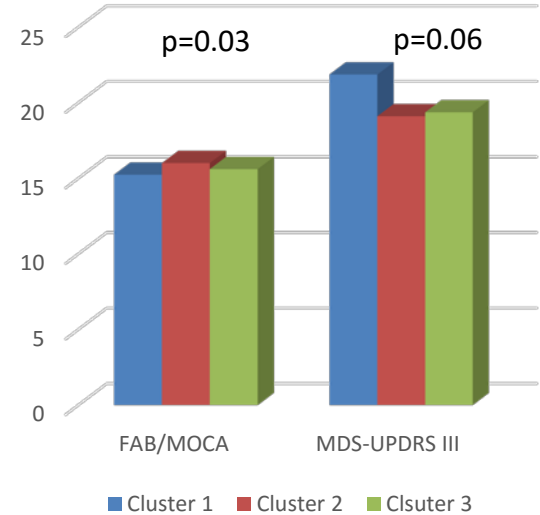
AETIONOMY



Similar variant map profile
Similar number of patients in clusters
Similar relationship with mechanisms

DIGPD (n=407)

| | Cluster 1 | Cluster 2 | Cluster 3 | P-value |
|---------------------------|----------------------|---------------------|----------------------|-------------|
| N | 130 (32) | 145 (36) | 132 (32) | |
| Age | 62.59 ± 10.64 | 61.8 ± 10.17 | 62.62 ± 8.63 | 0.79 |
| Female (%) | 52 (40%) | 55 (37.93%) | 58 (43.94%) | 0.59 |
| FAB/MOCA | 15.25 ± 2.66 | 16.02 ± 2.15 | 15.62 ± 2.19 | 0.03 |
| MMSE | 28.2 ± 1.82 | 28.3 ± 1.84 | 28.08 ± 2.01 | 0.68 |
| Non motor | 7.41 ± 4.66 | 7.66 ± 4.8 | 7.24 ± 4.35 | 0.87 |
| MDS-UPDRS I | 8.27 ± 5.07 | 7.87 ± 4.94 | 7.82 ± 4.31 | 0.81 |
| MDS-UPDRS II | 8 ± 4.75 | 7.08 ± 4.47 | 7.68 ± 4.67 | 0.3 |
| MDS-UPDRS III | 21.88 ± 10.85 | 19.12 ± 9.2 | 19.38 ± 10.76 | 0.06 |
| MDS-UPDRS IV | 0.7 ± 1.99 | 0.49 ± 1.33 | 0.51 ± 1.62 | 0.79 |
| Anxiety/depression | 4.77 ± 3.11 | 4.63 ± 3.35 | 4.51 ± 3.03 | 0.77 |



Regression model

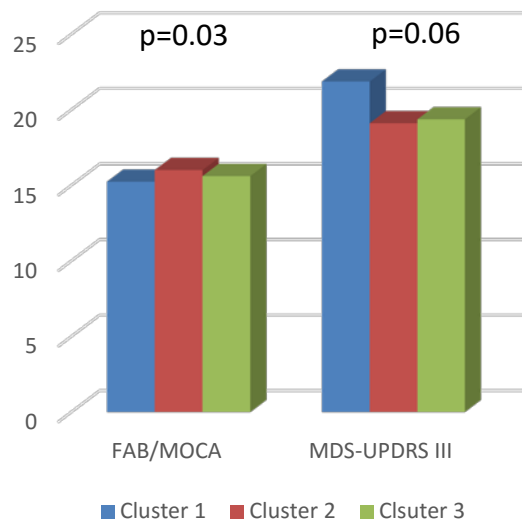
| Variable | Age inclusion | Age diagnosis | Sexe | Groupe |
|----------------------|---------------|---------------|--------|---------|
| MDS-UPDRS III | <0.0001 * | <0.0001 * | 0.7645 | 0.0385* |
| FAB | 0.0066* | 0.0426* | 0.1947 | 0.0246* |

DIGPD (n=407)

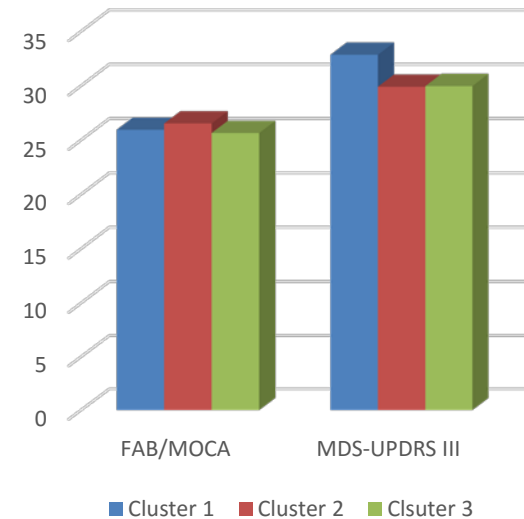
AETIONOMY (n=224)

| | Cluster 1 | Cluster 2 | Cluster 3 | P-value | Cluster 1 | Cluster 2 | Cluster 3 | P-value |
|---------------------------|----------------------|---------------------|----------------------|-------------|----------------------|----------------------|----------------------|-------------|
| N | 130 (32) | 145 (36) | 132 (32) | | 81 (36) | 63 (28) | 80 (35) | |
| Age | 62.59 ± 10.64 | 61.8 ± 10.17 | 62.62 ± 8.63 | 0.79 | 63.52 ± 7.88 | 65 ± 7.57 | 63.89 ± 10.02 | 0.45 |
| Female (%) | 52 (40%) | 55 (37.93%) | 58 (43.94%) | 0.59 | 25 (30.86%) | 17 (26.98%) | 26 (32.5%) | 0.77 |
| FAB/MOCA | 15.25 ± 2.66 | 16.02 ± 2.15 | 15.62 ± 2.19 | 0.03 | 25.95 ± 3.09 | 26.53 ± 2.58 | 25.65 ± 3.04 | 0.29 |
| MMSE | 28.2 ± 1.82 | 28.3 ± 1.84 | 28.08 ± 2.01 | 0.68 | 28.28 ± 1.73 | 28.72 ± 1.44 | 28.25 ± 1.86 | 0.25 |
| Non motor | 7.41 ± 4.66 | 7.66 ± 4.8 | 7.24 ± 4.35 | 0.87 | 10.39 ± 4.47 | 8.4 ± 4.77 | 8.49 ± 4.55 | 0.01 |
| MDS-UPDRS I | 8.27 ± 5.07 | 7.87 ± 4.94 | 7.82 ± 4.31 | 0.81 | 9.04 ± 5.12 | 8.35 ± 4.67 | 8.24 ± 4.9 | 0.54 |
| MDS-UPDRS II | 8 ± 4.75 | 7.08 ± 4.47 | 7.68 ± 4.67 | 0.3 | 9.53 ± 5.68 | 8.5 ± 5.03 | 9.21 ± 5.45 | 0.52 |
| MDS-UPDRS III | 21.88 ± 10.85 | 19.12 ± 9.2 | 19.38 ± 10.76 | 0.06 | 32.85 ± 14.81 | 29.91 ± 16.07 | 29.97 ± 12.71 | 0.29 |
| MDS-UPDRS IV | 0.7 ± 1.99 | 0.49 ± 1.33 | 0.51 ± 1.62 | 0.79 | 1.54 ± 2.82 | 1.18 ± 2.33 | 1.13 ± 2.3 | 0.81 |
| Anxiety/depression | 4.77 ± 3.11 | 4.63 ± 3.35 | 4.51 ± 3.03 | 0.77 | 4.96 ± 3.97 | 3.79 ± 3.05 | 3.42 ± 3.3 | 0.03 |

DIGPD



AETIONOMY

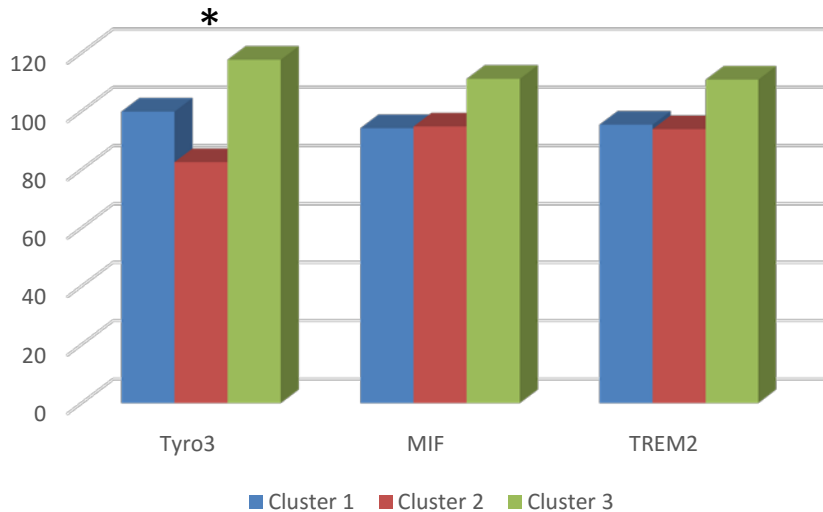


Immune markers and methylome profiles

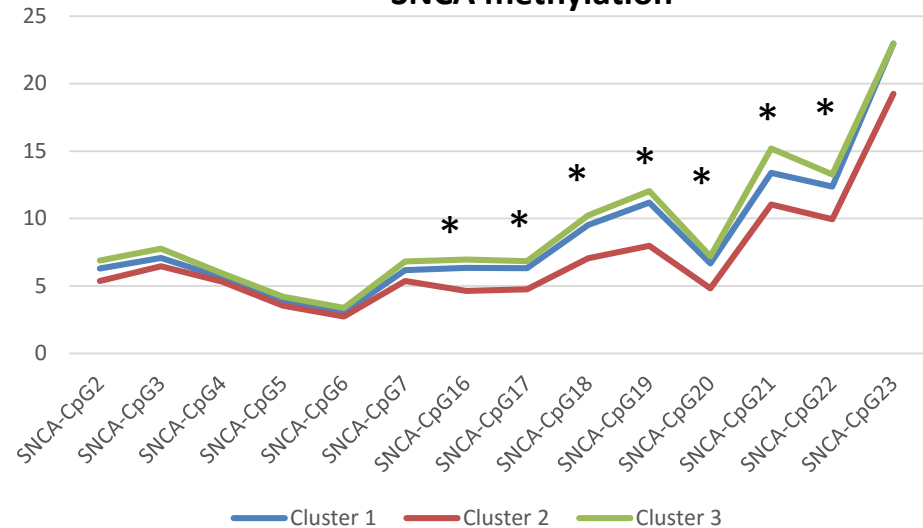
| | Cluster 1 | Cluster 2 | Cluster 3 | p-value |
|------------------|-------------------|--------------------|--------------------|---------|
| n | 22 (36,07%) | 16 (26,23%) | 23 (37,7%) | |
| Tyro3 | 2858.06 ± 987.28 | 2362.4 ± 831.82 | 3367.07 ± 1068.86 | 0.01 |
| Properdin | 18.73 ± 13 | 19.05 ± 10.75 | 13.16 ± 6.89 | 0.07 |
| MIF | 9167.03 ± 2328.36 | 9224.26 ± 4205 | 10812.88 ± 3653.66 | 0.1 |
| C4 | 683.47 ± 364.5 | 827.27 ± 283.79 | 666.36 ± 279.18 | 0.12 |
| TNFR_I | 273.18 ± 71.21 | 253.45 ± 70.07 | 289.12 ± 70.45 | 0.16 |
| Factor_B | 670.86 ± 374.49 | 683.91 ± 287.24 | 559.48 ± 288.86 | 0.18 |
| CRP | 9036.66 ± 13345.2 | 8097.73 ± 18559.51 | 3579.72 ± 2926.23 | 0.22 |
| TREM2 | 5823.23 ± 3142.85 | 5730.11 ± 2672.96 | 6766.13 ± 2842.98 | 0.26 |
| Factor_H | 673.45 ± 282.12 | 688.45 ± 262.09 | 588.84 ± 186.11 | 0.33 |
| TNFR_II | 147.36 ± 43.81 | 134.96 ± 44.52 | 147.43 ± 40.97 | 0.35 |
| TGF_b1 | 36.58 ± 6.51 | 34.65 ± 4.54 | 36.56 ± 5.18 | 0.35 |
| MCP_1 | 309.77 ± 93.16 | 333.11 ± 79.55 | 303.51 ± 76.08 | 0.42 |
| C3 | 1354.68 ± 1579.78 | 1315.42 ± 1484.42 | 1075.14 ± 1069.76 | 0.7 |
| IP_10 | 253.85 ± 121.72 | 309.51 ± 211.77 | 305.06 ± 200.79 | 0.72 |
| AXL | 19.1 ± 4.25 | 18.42 ± 4.78 | 19.46 ± 4.77 | 0.76 |
| C1q | 290.88 ± 90.9 | 274.76 ± 81.2 | 285.09 ± 80.39 | 0.79 |
| ICAM_1 | 2915.91 ± 1074.36 | 2830.26 ± 1221.11 | 2722.75 ± 714.47 | 0.84 |
| IL1RAcP | 1342.47 ± 877.63 | 1216.78 ± 776.73 | 1312.15 ± 836.71 | 0.9 |
| C3b | 834.5 ± 1293.52 | 744.68 ± 648.18 | 581.53 ± 265.22 | 0.91 |
| MIP_1b | 10.08 ± 4.07 | 9.93 ± 3.7 | 9.28 ± 2.74 | 0.91 |

| | Cluster 1 | Cluster 2 | Cluster 3 | p-value |
|-------------------|-----------|-----------|-----------|---------|
| n | 24 (32%) | 30 (40%) | 21 (28%) | |
| SNCA-CpG2 | 6.29 | 5.38 | 6.9 | 0.09 |
| SNCA-CpG3 | 7.09 | 6.47 | 7.77 | 0.38 |
| SNCA-CpG4 | 5.63 | 5.33 | 5.94 | 0.68 |
| SNCA-CpG5 | 3.92 | 3.54 | 4.21 | 0.52 |
| SNCA-CpG6 | 3.04 | 2.74 | 3.38 | 0.45 |
| SNCA-CpG7 | 6.18 | 5.38 | 6.82 | 0.11 |
| SNCA-CpG16 | 6.35 | 4.64 | 6.97 | 0.0002 |
| SNCA-CpG17 | 6.32 | 4.76 | 6.84 | 0.003 |
| SNCA-CpG18 | 9.52 | 7.06 | 10.23 | 0.0001 |
| SNCA-CpG19 | 11.18 | 7.99 | 12.04 | 0.00003 |
| SNCA-CpG20 | 6.68 | 4.83 | 7.2 | 0.0006 |
| SNCA-CpG21 | 13.4 | 11.03 | 15.19 | 0.0004 |
| SNCA-CpG22 | 12.37 | 9.95 | 13.28 | 0.004 |
| SNCA-CpG23 | 22.97 | 19.25 | 22.98 | 0.08 |

Immune markers



SNCA methylation





Conclusions and perspectives

- Neurodegenerative & neuro-immune **biomarkers are associated with neurodegeneration (and aging) across diseases**
- **Specific profiles** of biomarkers can however be found to **discriminate AD from PD** and/or **patients from controls**
- **Mechanism-based stratification** may be achieved by using genomic information, but association with **relevant biomarkers must be further explored**
- **Prospective longitudinal datasets are needed** for testing their association with disease progression
- **AETIONOMY: unique dataset** combining clinical, biological, and genetic data made available for the scientific community



Thank you for your attention

ICM

JC Corvol

A Brice

O Corti

F Danjou

FX Lejeune

G Mangone

C Dongmo

S Carvalho

C Gaudebout

B Labrador

S Bekadar

B Dubois

S Epelbaum

UKB

M Heneka

F Brosseron

P Tacik

U Wuellner

I Schmitt

KI

P Svenningsson

I Markaki

P Tsitsi

P Nilsson

S Berström

IDIBAPS/BBRC

R Sanchez-Valle

B Bosch

A Antonell

JL Molinuevo

G Operto

SARD

L Canard

E Boitier

D Ibghi

Novartis

A Graf

C Dongmo
S Carvalho
C Gaudebout
B Labrador
S Bekadar
B Dubois
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P Cordis

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T Rechmann

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H Froehlich

