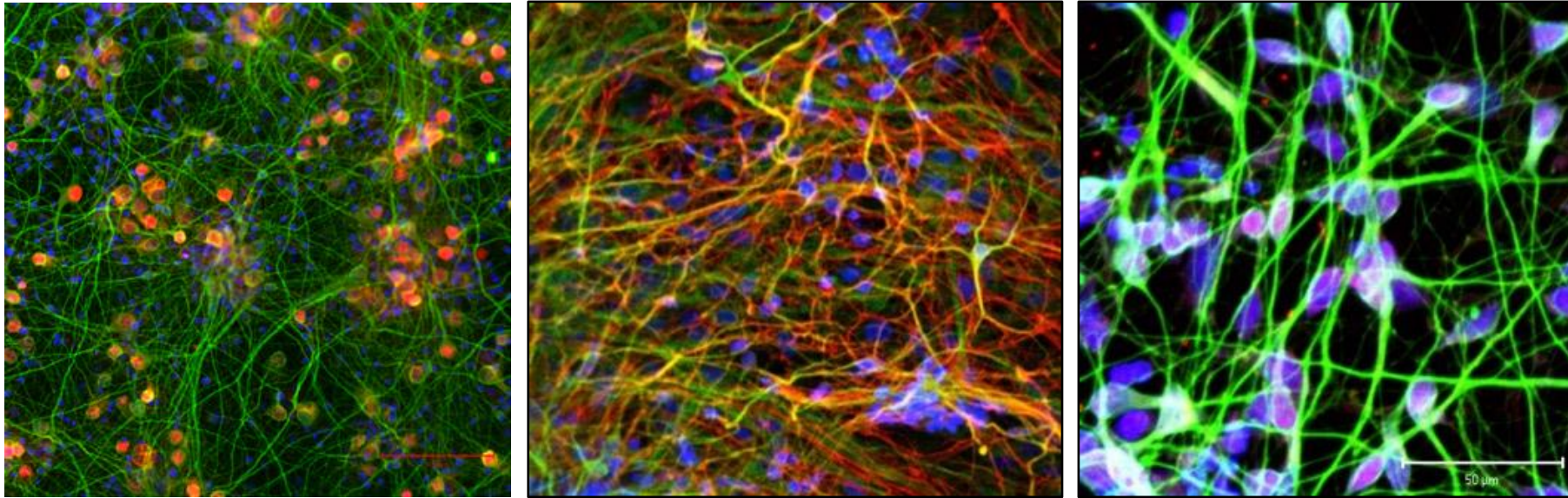


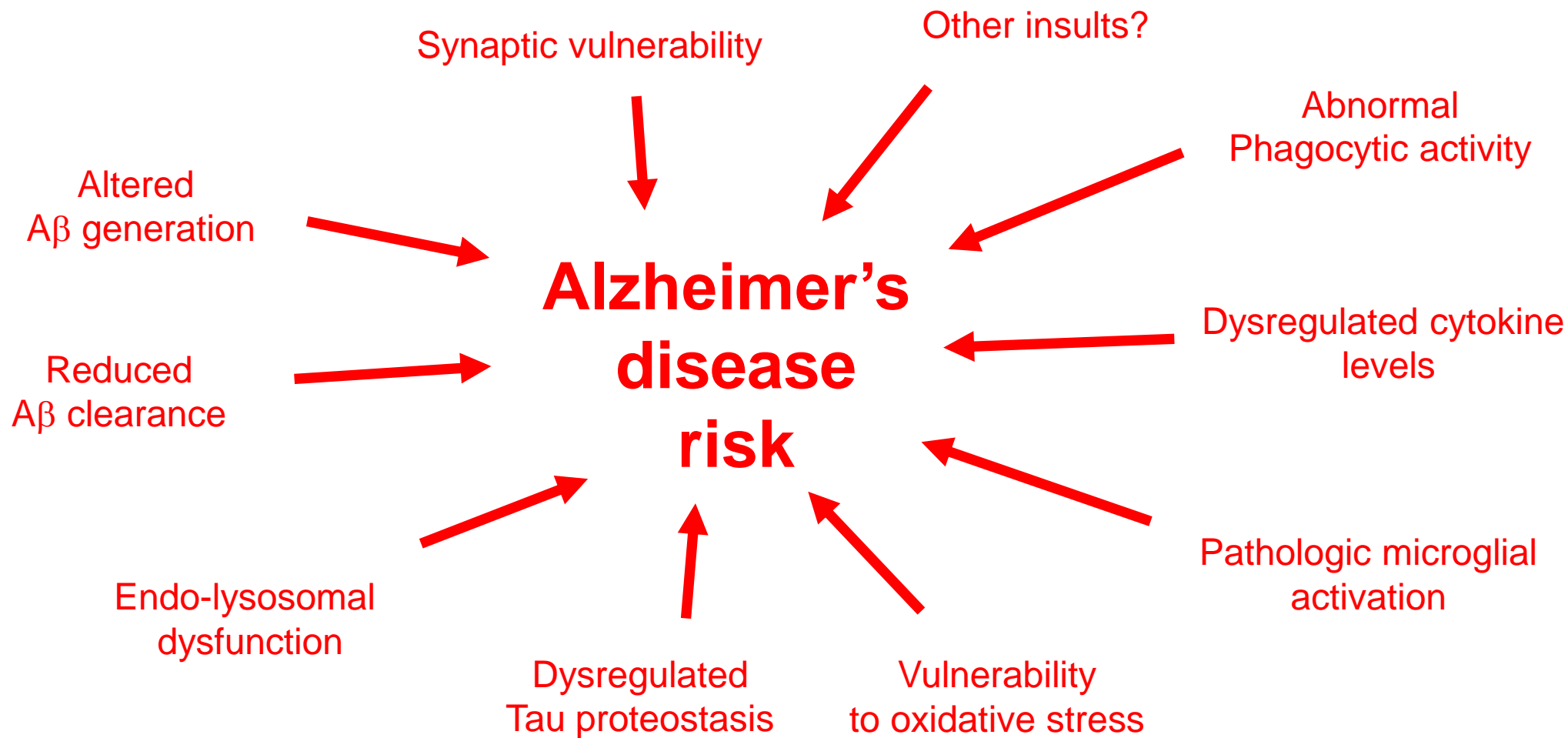


Using iPSCs to Interrogate Heterogeneity in AD and to Develop Assays for Experimental Validation of Novel Targets

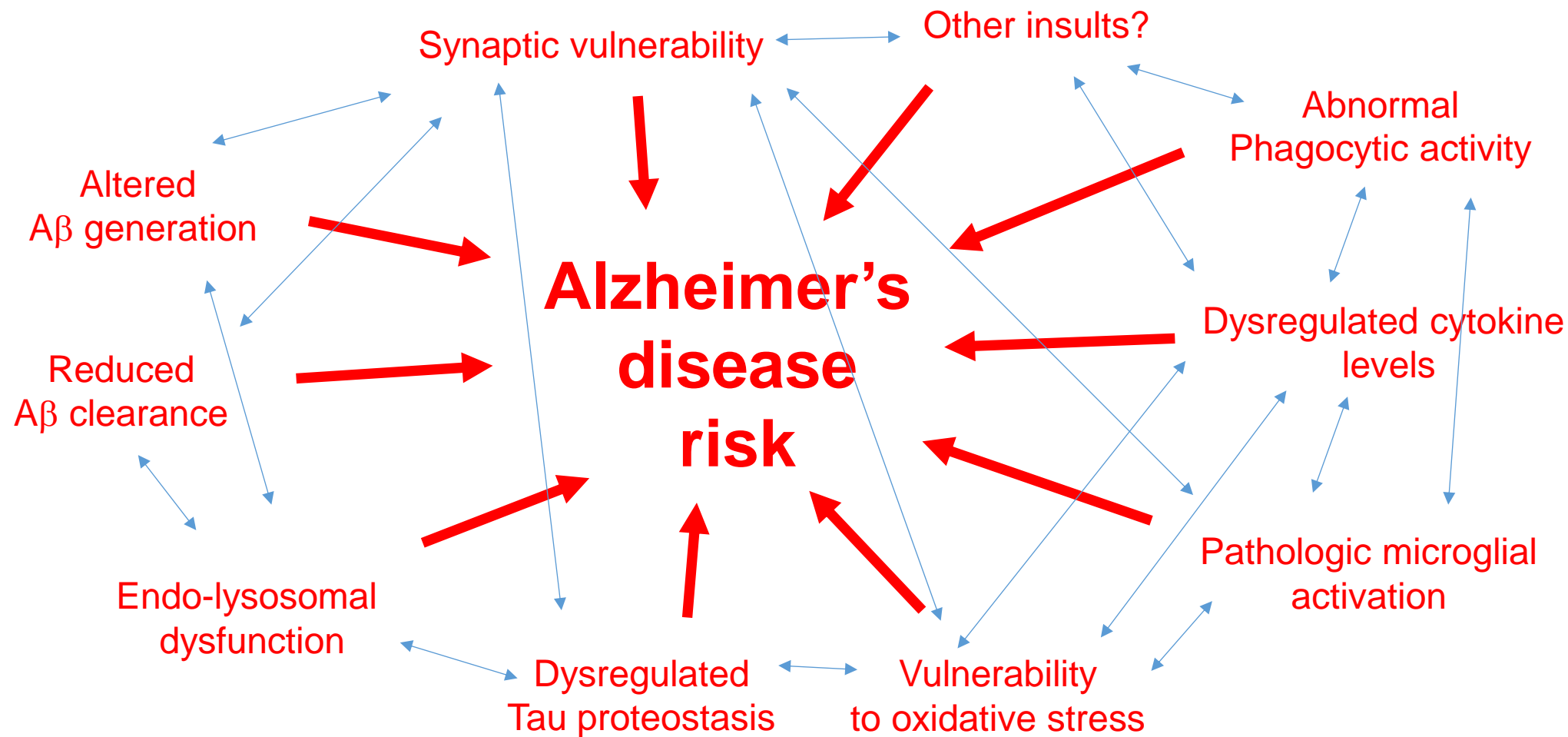


Tracy Young-Pearse, PhD
Associate Professor of Neurology
Ann Romney Center for Neurologic Diseases
Harvard Medical School and Brigham and Women's Hospital

Hypothesis: Alzheimer's disease has multifactorial etiologies that are in part genetically encoded



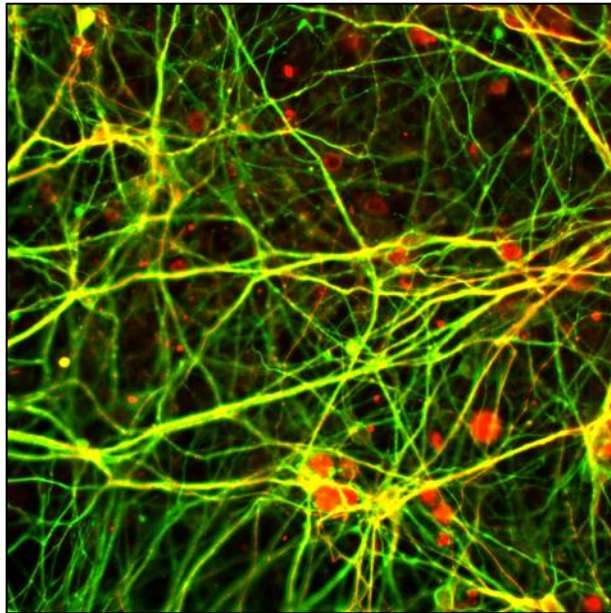
Hypothesis: Alzheimer's disease has multifactorial etiologies that are in part genetically encoded



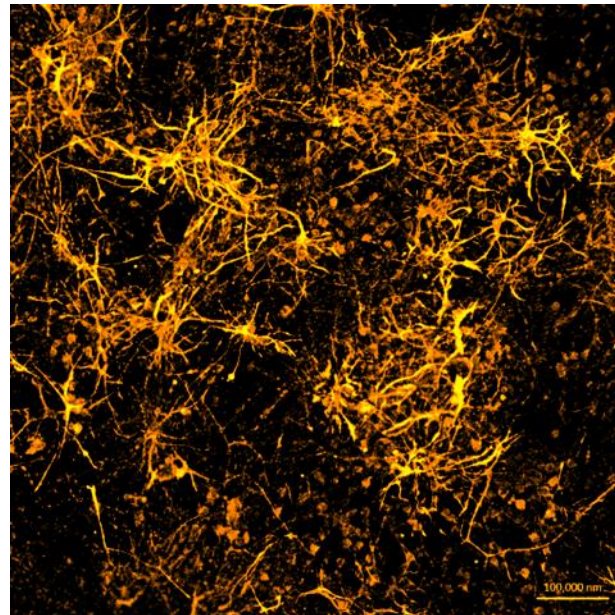
For each new pathway/target identified, which causal process are we trying to rescue?

In which experimental system/cell type(s) should we look?

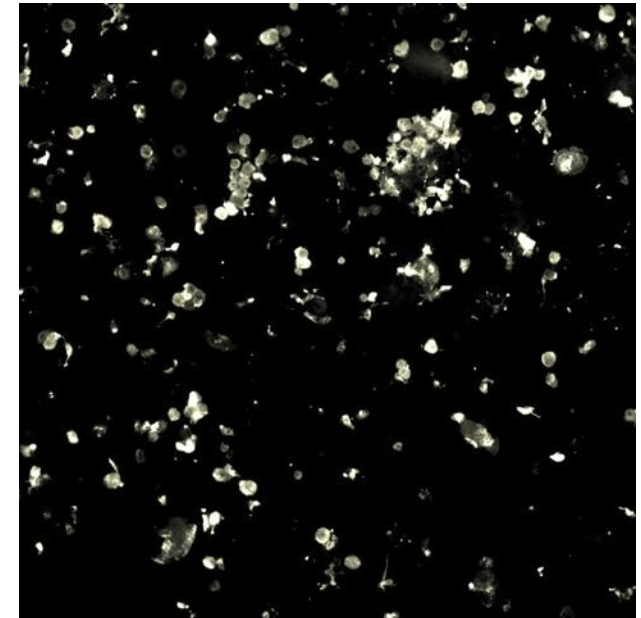
Neurons



Astrocytes



Microglia



Oligodendrocytes?

Pericytes?

Monocytes/macrophages?

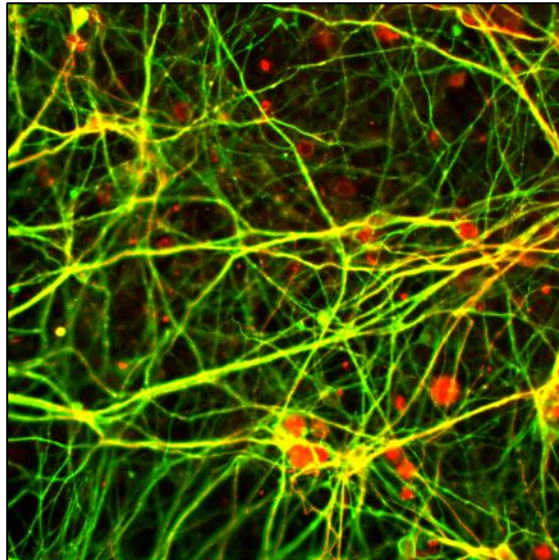
T-cells?

Resources for validating new targets and pathways

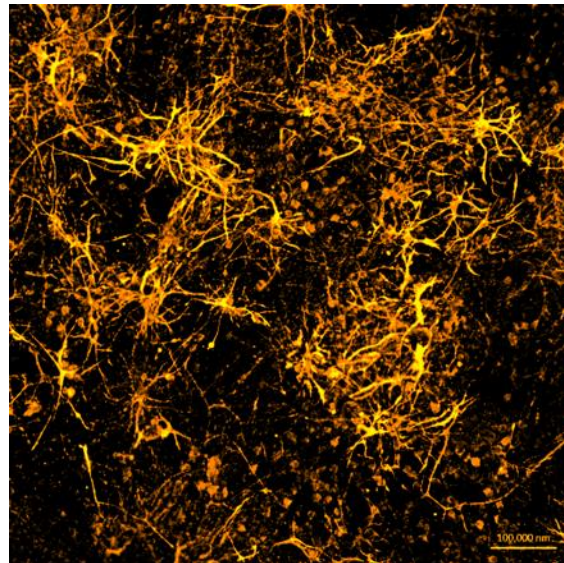
1. A collection of human iPSC lines from ROS and MAP cohorts

2. Cell-based assays

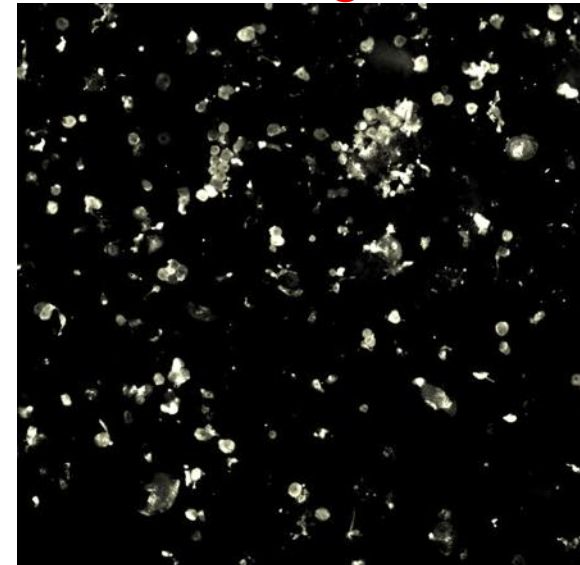
Neurons



Astrocytes



Microglia



Two large cohorts of deeply phenotyped aging Americans

Religious Orders Study (ROS)

- Catholic priests, nuns and brothers
- Started in 1994

Memory and Aging Project (MAP)

- Older men and women in assisted living facilities in the Chicagoland area
- Started in 1997

- Free of dementia at enrollment
- Annual clinical evaluations
- Anatomical Gift Act, donate brains (spinal cords, select nerves and muscles at death)
- 3,087 persons enrolled (July 2018)
- 1,481 autopsies (July 2018)
- Follow-up rate among survivors >90%
- Autopsy rate among deceased >90%



PI: David Bennett



Available data from ROS/MAP cohorts

Longitudinal Clinical Data

Cognitive function
19 tests annually

Clinical and pathological diagnoses for AD and other neurological diseases

Functional evaluation
UPDRS
Neurological exam

Neuroimaging
MRI
fMRI
Post-mortem MRI

Biometric data
Circadian rhythm

Other Medical information

Diabetes
Cardiovascular disease
Hypertension
BMI
Diet
Smoking
Drinking
Cancer
Thyroid disease

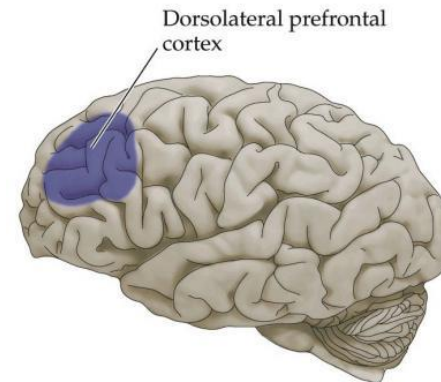
Cell and molecular phenotyping postmortem

Quantitative neuropathology
Amyloid plaques, tangles,
Lewy bodies, TDP43
inclusions, vascular pathology

DNA Methylation
Illumina 450K

Histone Acetylation
H3K9Ac ChIP Seq

miRNA profile
Nanostring codeset



Genotyping

Affy 6.0 1000G imputation
APOE status
Genome sequencing

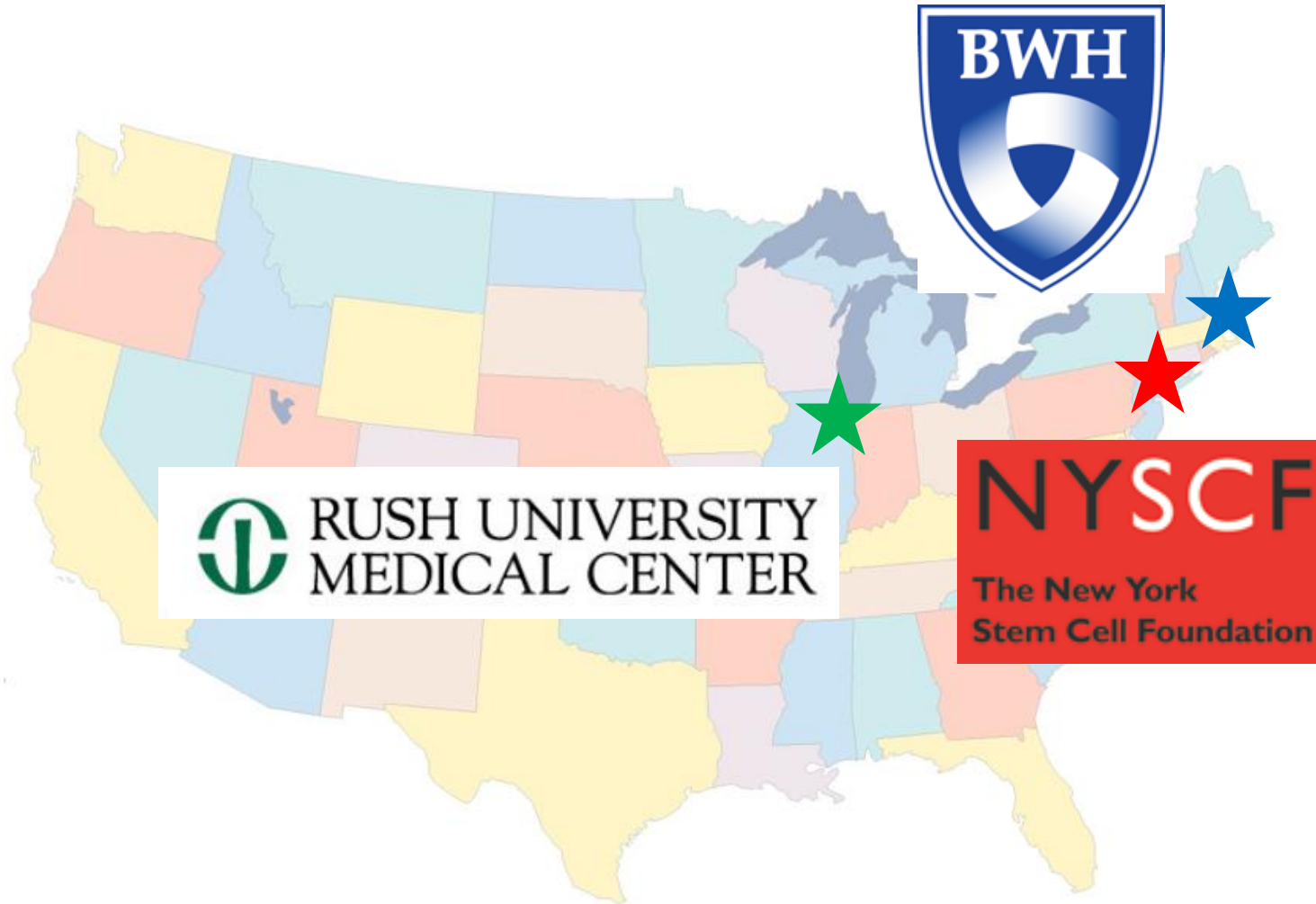
Peripheral blood



RNA profile
miRNA & RNAseq

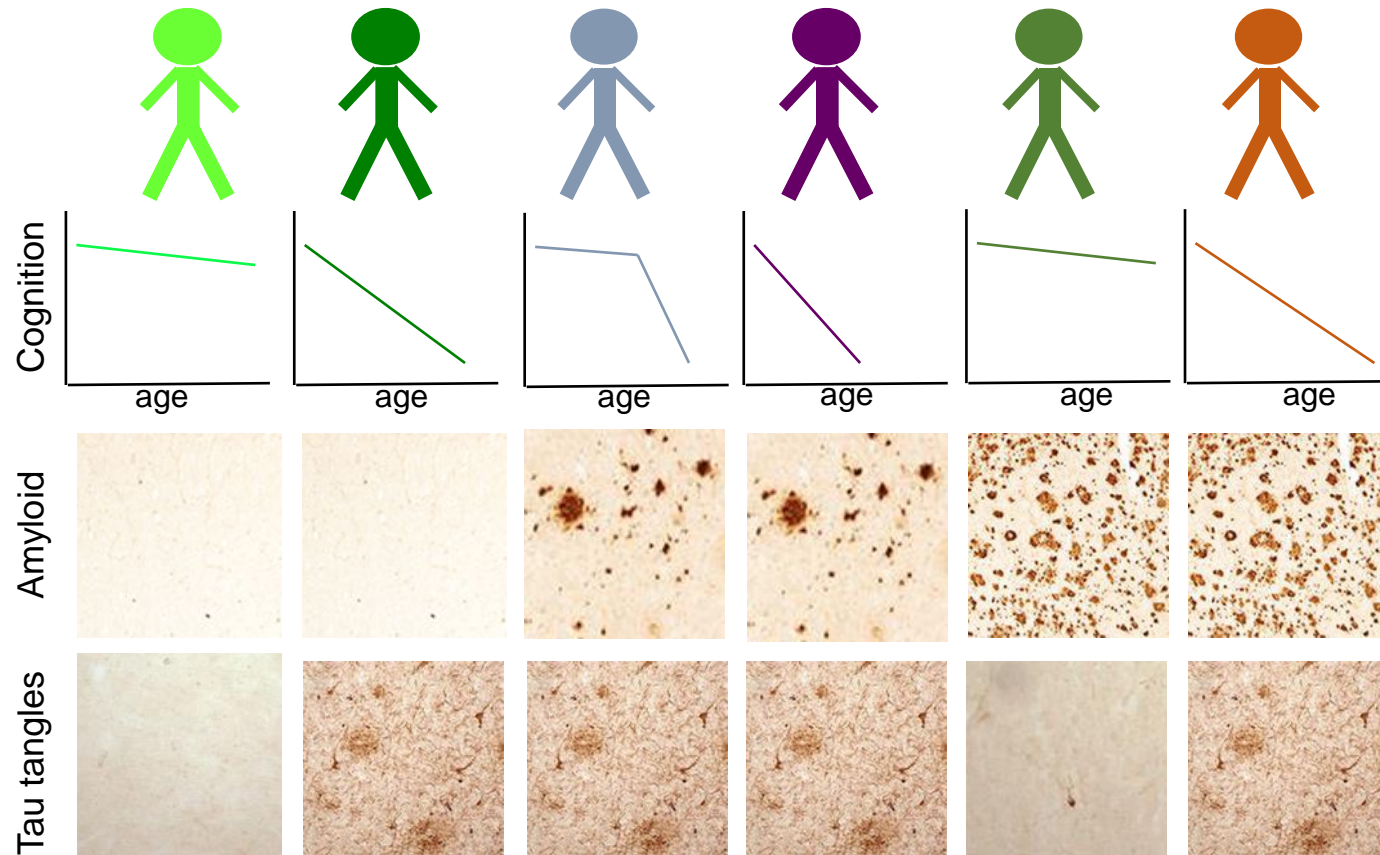
Mass spec profile
Lipids, proteins

Generating iPSC lines from ROS and MAP



- Polyclonal iPSC lines generated from 50 participants using Sendai on PBMCs
- 50 lines generated

A spectrum of cognitive ability and pathology in aging humans

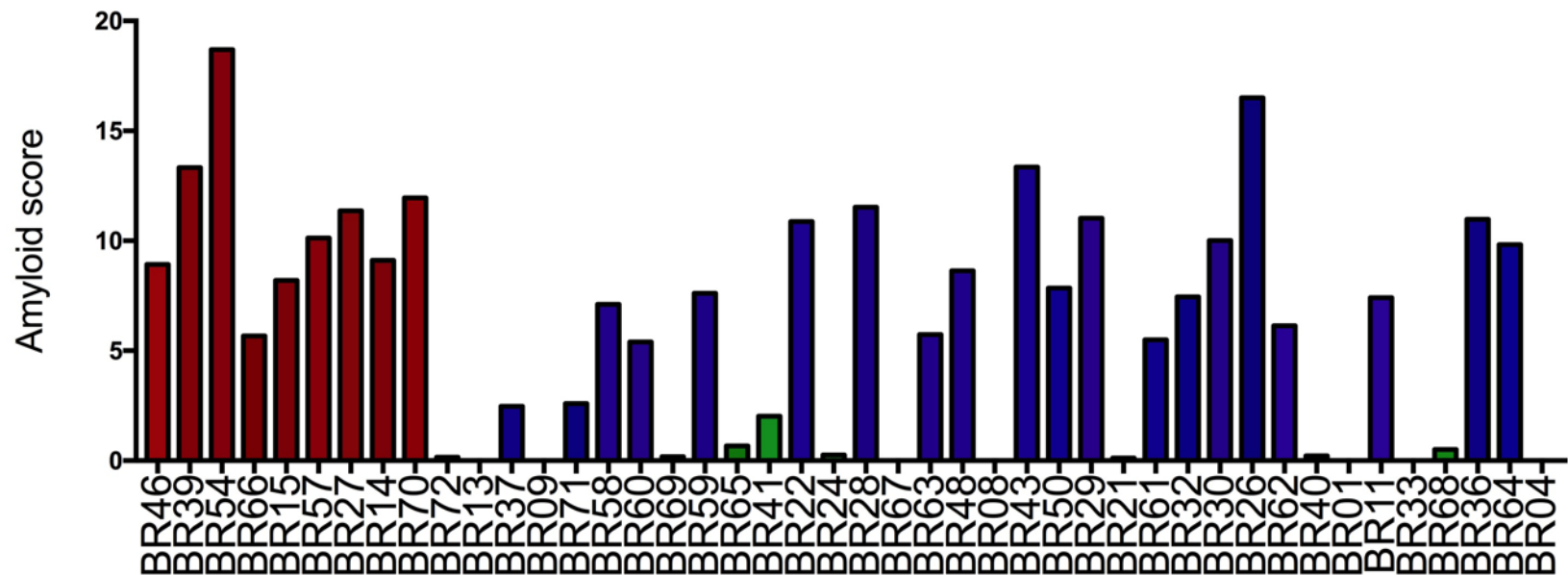
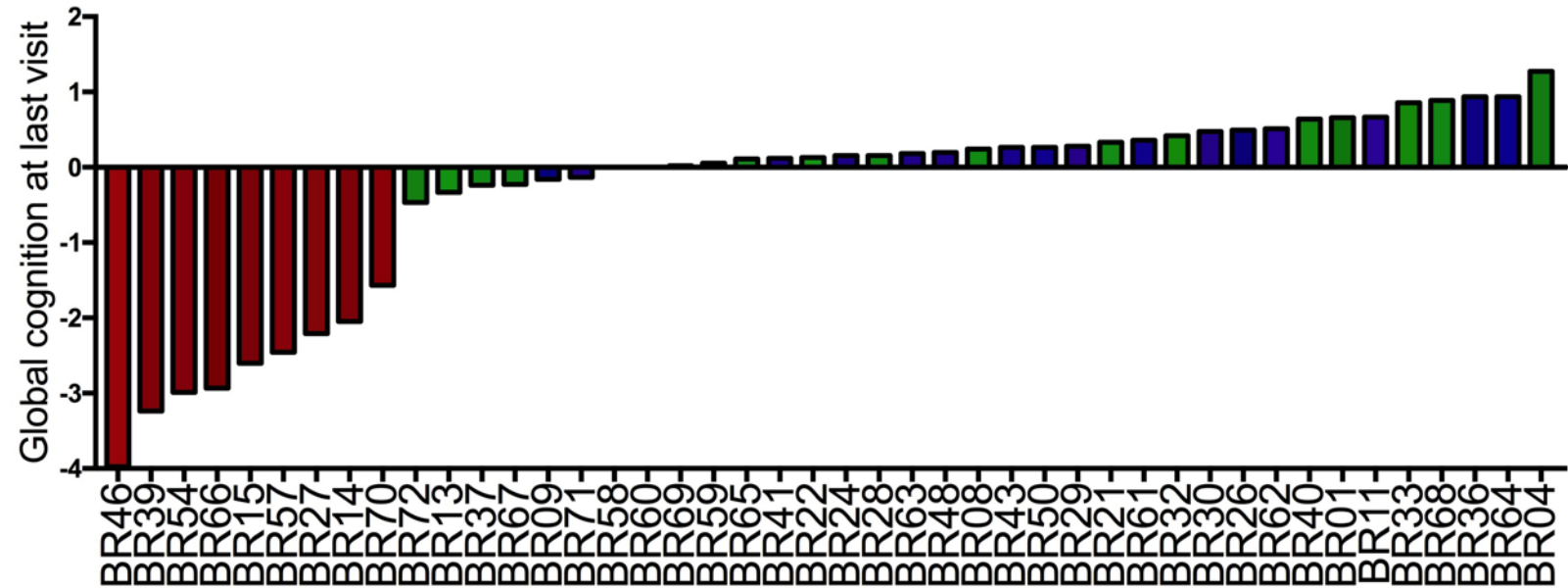
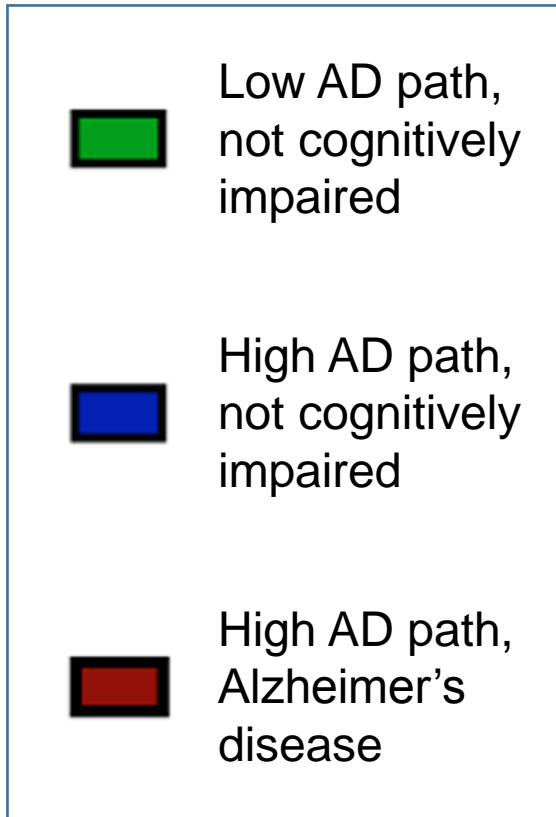


pathology images from Kullmann, *Brain*, 2013

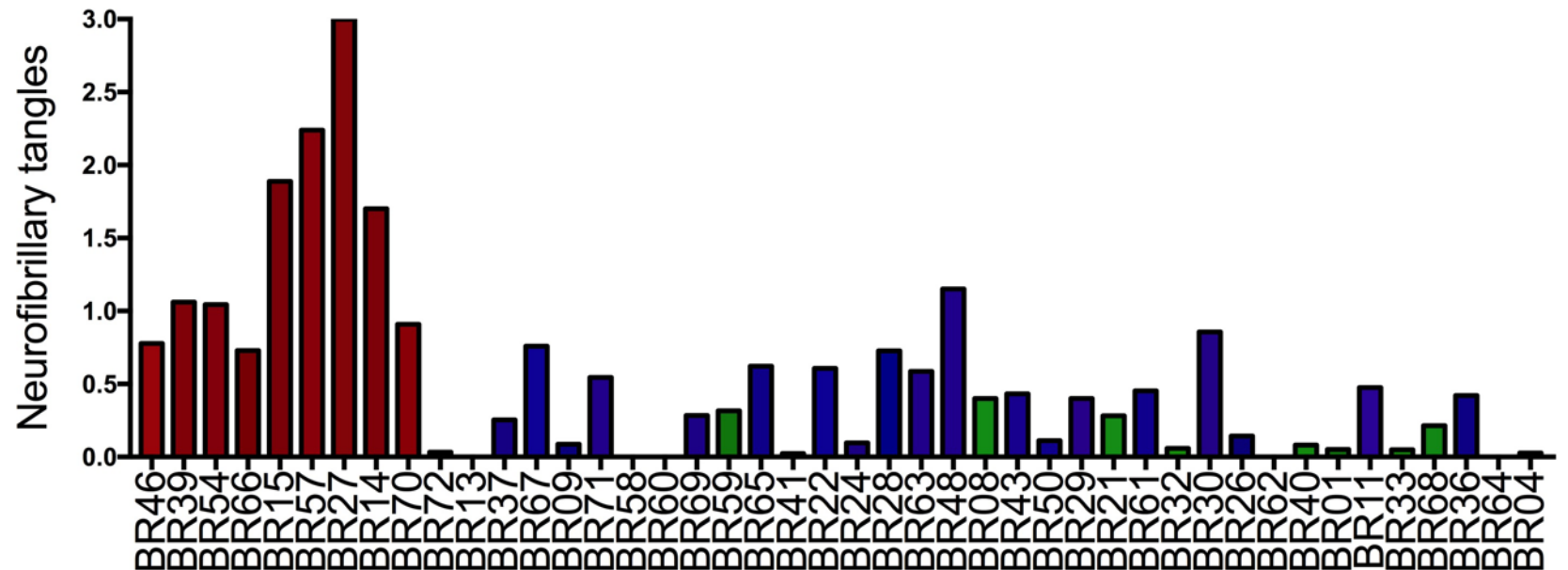
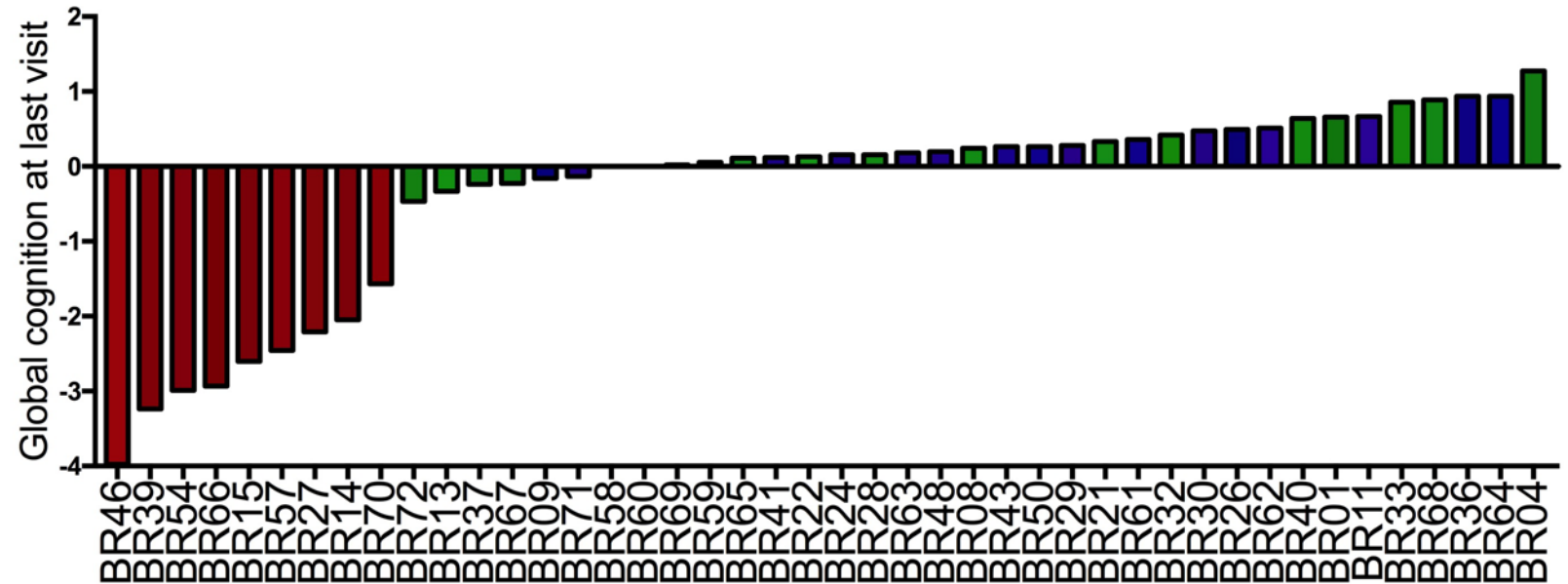
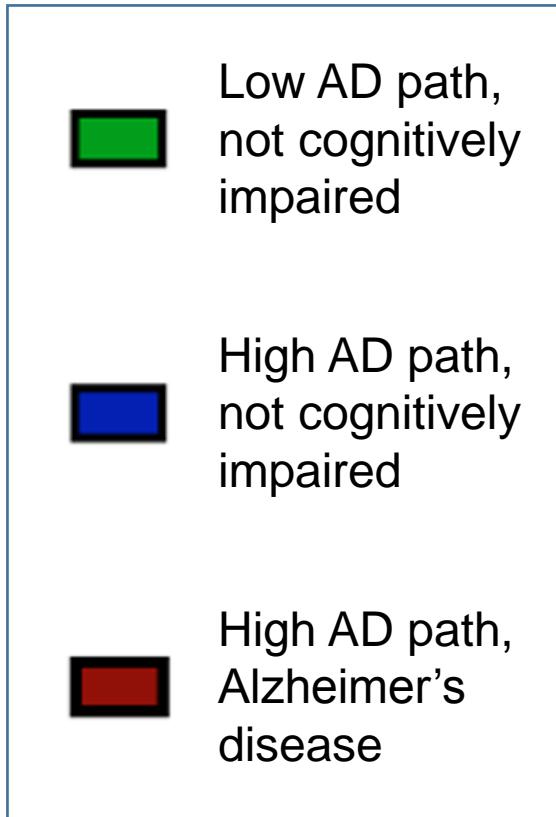
Inclusion/Exclusion criteria (round 1: 50 participants)

- Older age of death
- No hippocampal sclerosis
- No/minimal TDP43 inclusions
- No/minimal Lewy body pathology
- Low/minimal signs of macro and micro infarcts

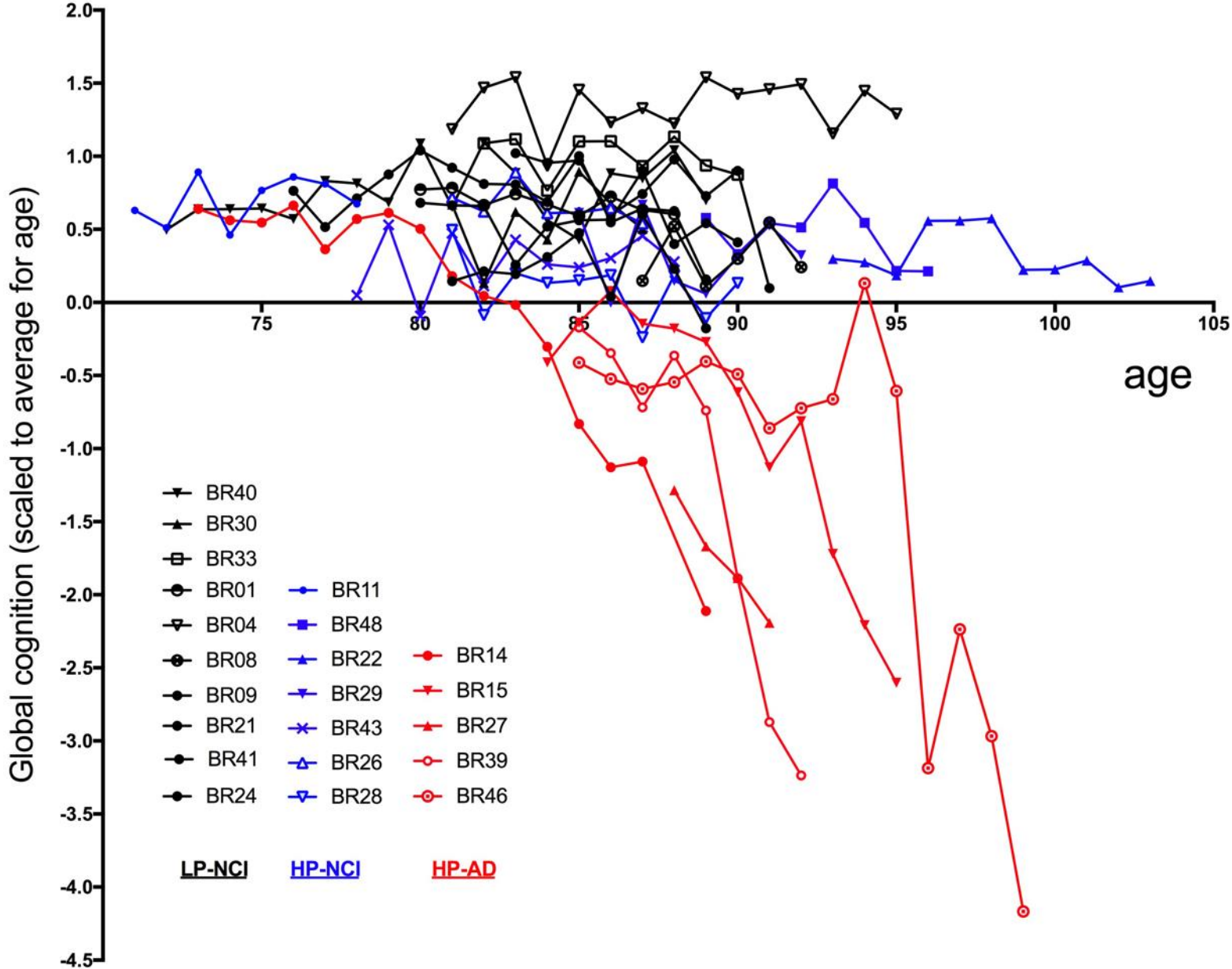
Capturing heterogeneity in brain aging with ROS and MAP cohorts



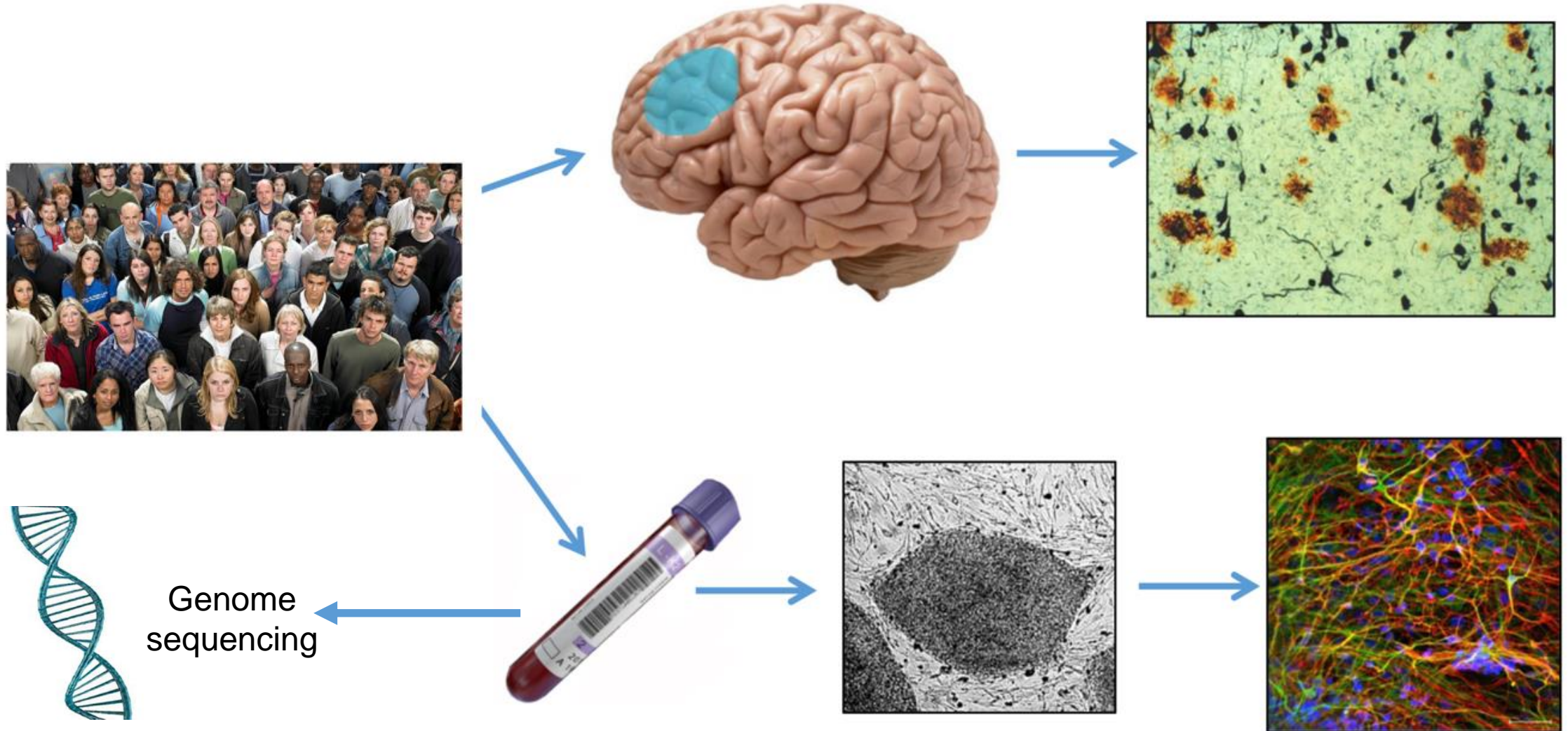
Capturing heterogeneity in brain aging with ROS and MAP cohorts



Global cognitive status over time in the participants represented in the first 21 lines

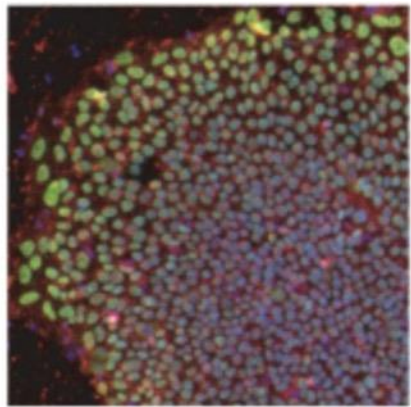


Can iPSC-derived cells predict late-onset “sporadic” Alzheimer’s disease: onset, progression, subtyping and treatment responsiveness?



DAPI/Oct4/SSEA4

iPSCs

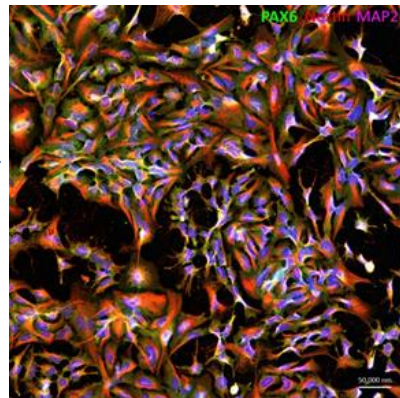


NGN2 direct induction

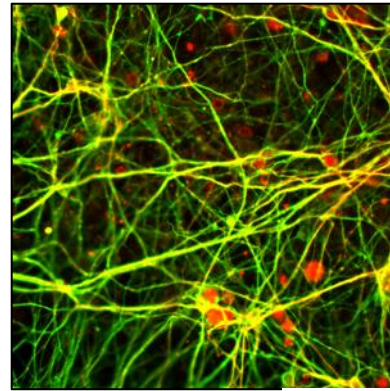
Dual SMAD inh
EB-based

Based on Blurton-Jones lab protocol

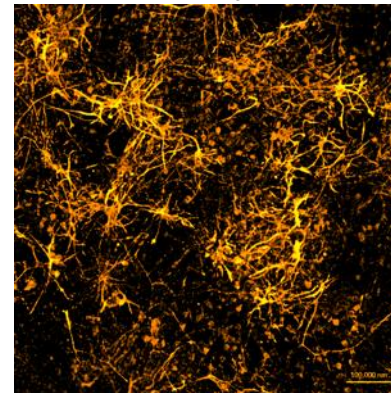
NPCs



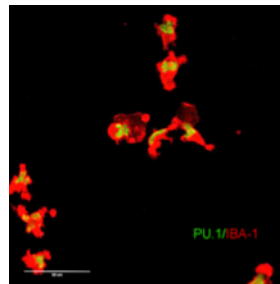
Neurons



Astrocytes



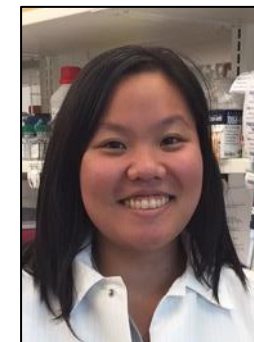
Microglia



Valentina
Lagomarsino



Meichen
Liao, PhD

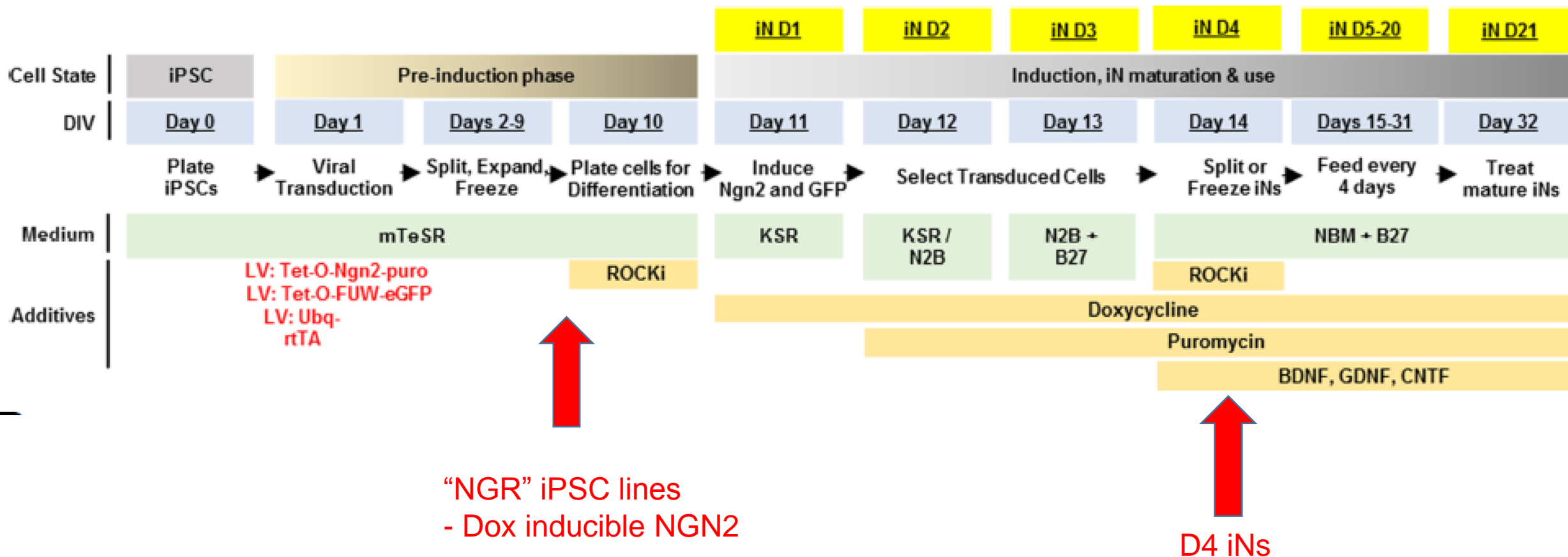


Vicky
Chou

Rapid Single-Step Induction of Functional Neurons from Human Pluripotent Stem Cells

Yingsha Zhang,¹ ChangHui Pak,^{1,6} Yan Han,^{1,6} Henrik Ahlenius,^{3,4} Zhenjie Zhang,⁵ Soham Chanda,^{1,3,4} Samuele Marro,^{3,4} Christopher Patzke,¹ Claudio Acuna,¹ Jason Covy,¹ Wei Xu,^{1,2} Nan Yang,^{3,4} Tamas Danko,^{1,3} Lu Chen,⁵ Marius Wernig,^{3,4} and Thomas C. Südhof^{1,2,5,*}

* Modified by Eggen lab, with minor modifications from TYP lab



Generating and banking stem cells, neurons, and glia from ROS and MAP iPSCs

iPSC
Lines
50

NGR iPSCs:
NGN2 inducible with
Dox addition
43

DAY 4 INs:
Four days post dox
43

NPCs:
Neural progenitor
cells
33

Astrocytes
33

Microglia
3

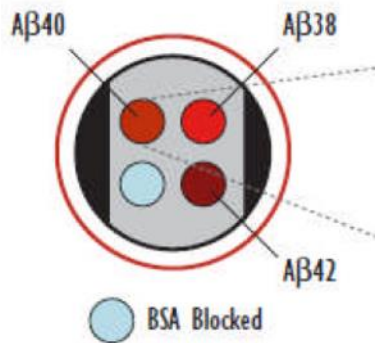
Resources for validating new targets and pathways

1. A collection of human iPSC lines from ROS and MAP cohorts
- 2. Cell-based assays**

Assays developed for human induced neurons from ROS/MAP subjects

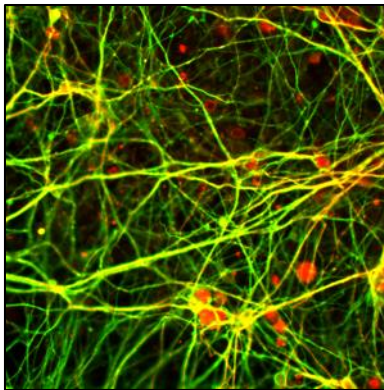
APP processing

$A\beta_{42}$
 $A\beta_{40}$
 $A\beta_{37}$
 $A\beta_{38}$
 $A\beta_{43}$
 Oligomeric $A\beta$
 sAPP β
 sAPP α
 APP holoprotein
 CTFs



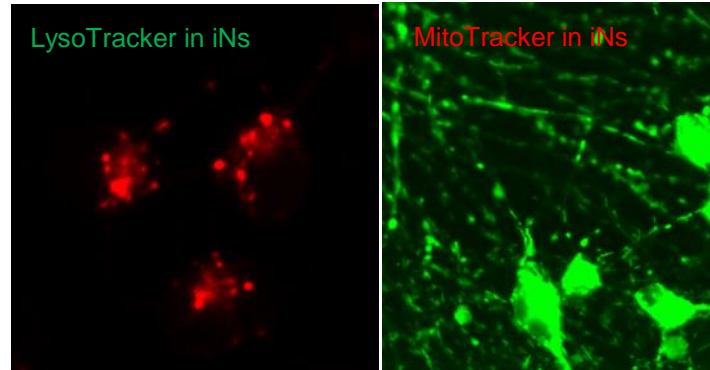
Tau levels

pS202/T205 Tau
 p231 Tau
 P181 Tau
 Tau full length
 Tau N-term
 Tau C-term



Imaging-based assays

Lysosome size, number, localization
 Mitochondria size, number, localization
 Endosome size, number, localization
 Synaptic puncta number
 Oxidative stress



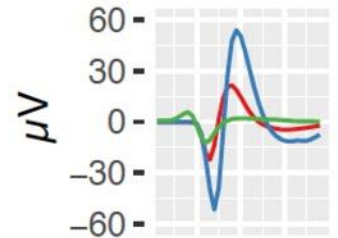
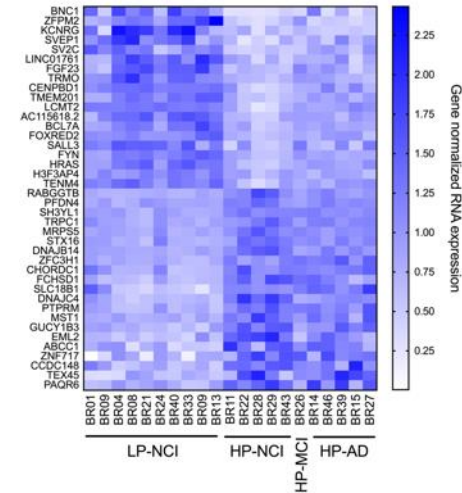
-Omics

RNAseq
 Proteomics

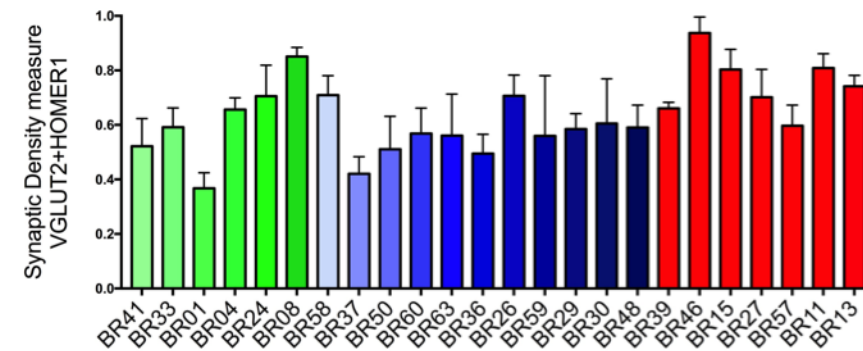
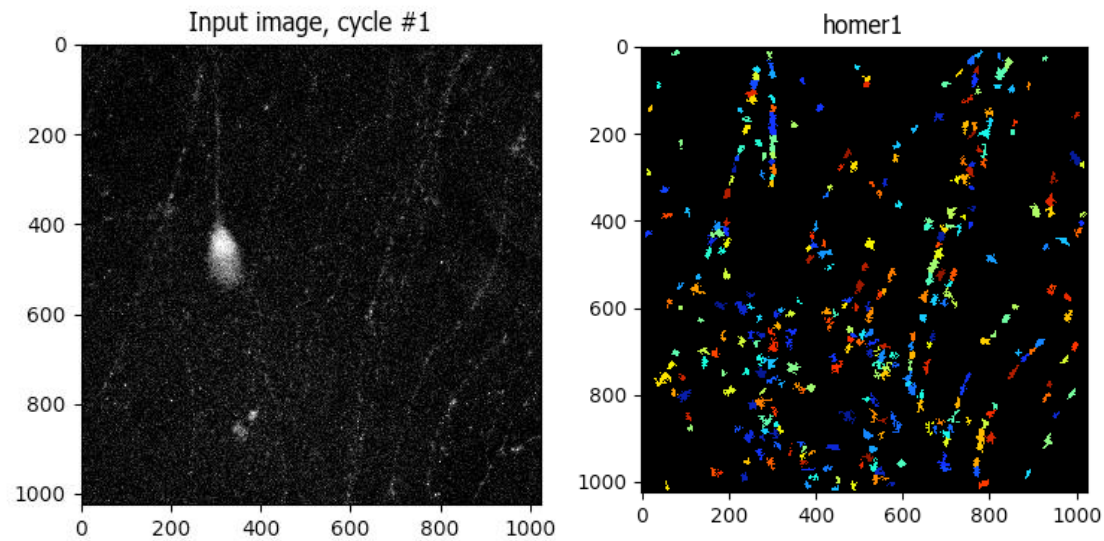
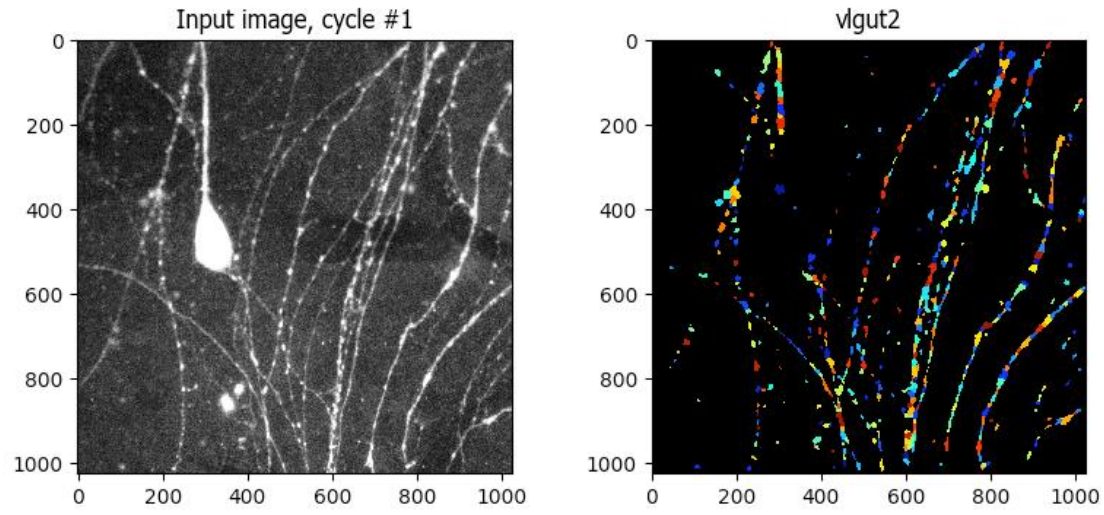
Longitudinal

Incucyte

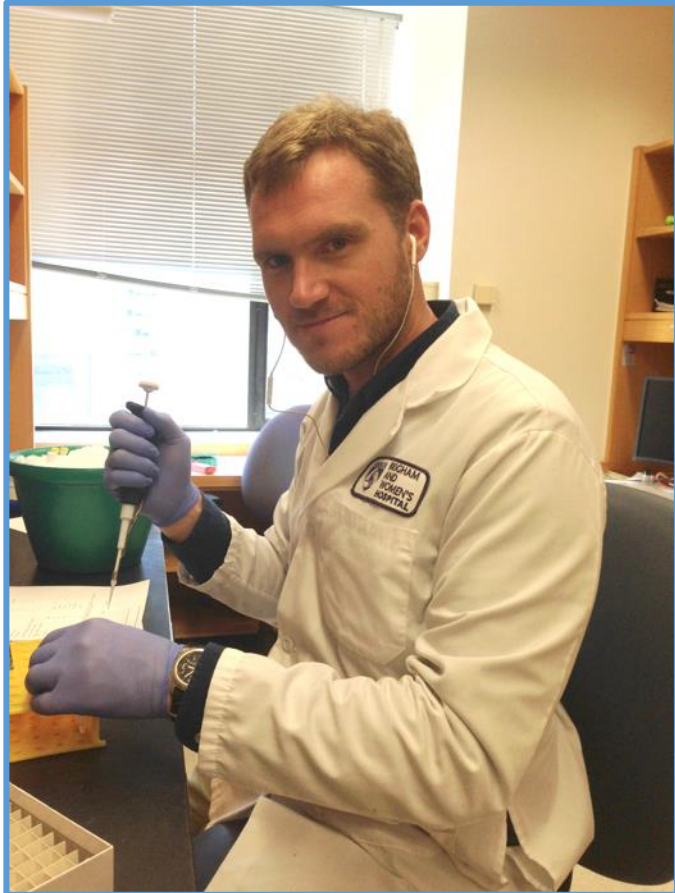
MEA



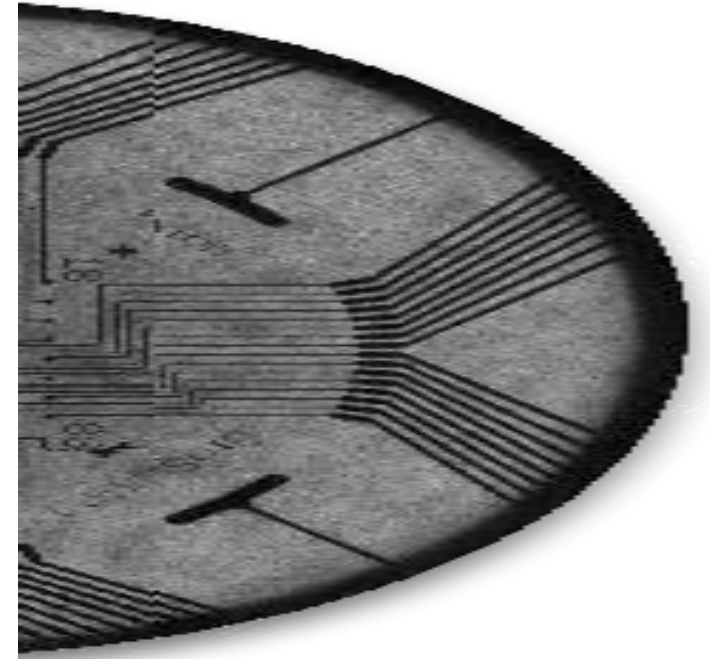
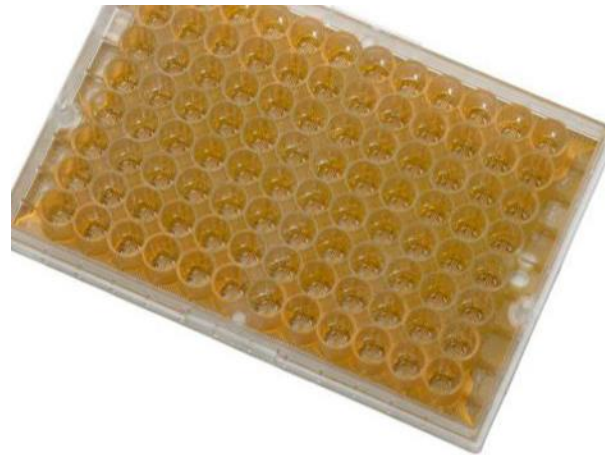
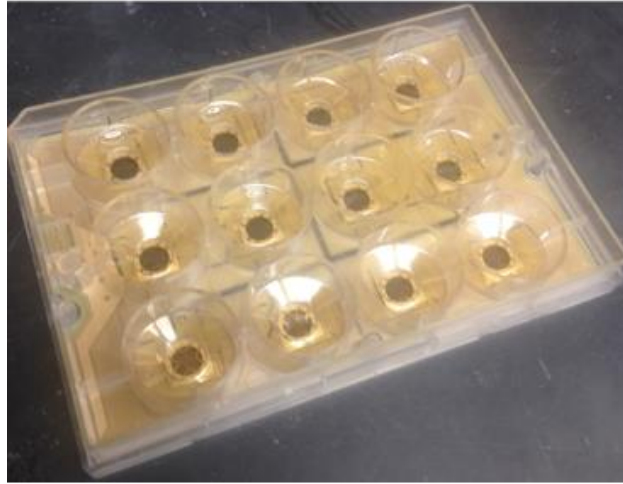
Measuring synaptic puncta number in human iNs



Developing an assay for measuring neuronal activity

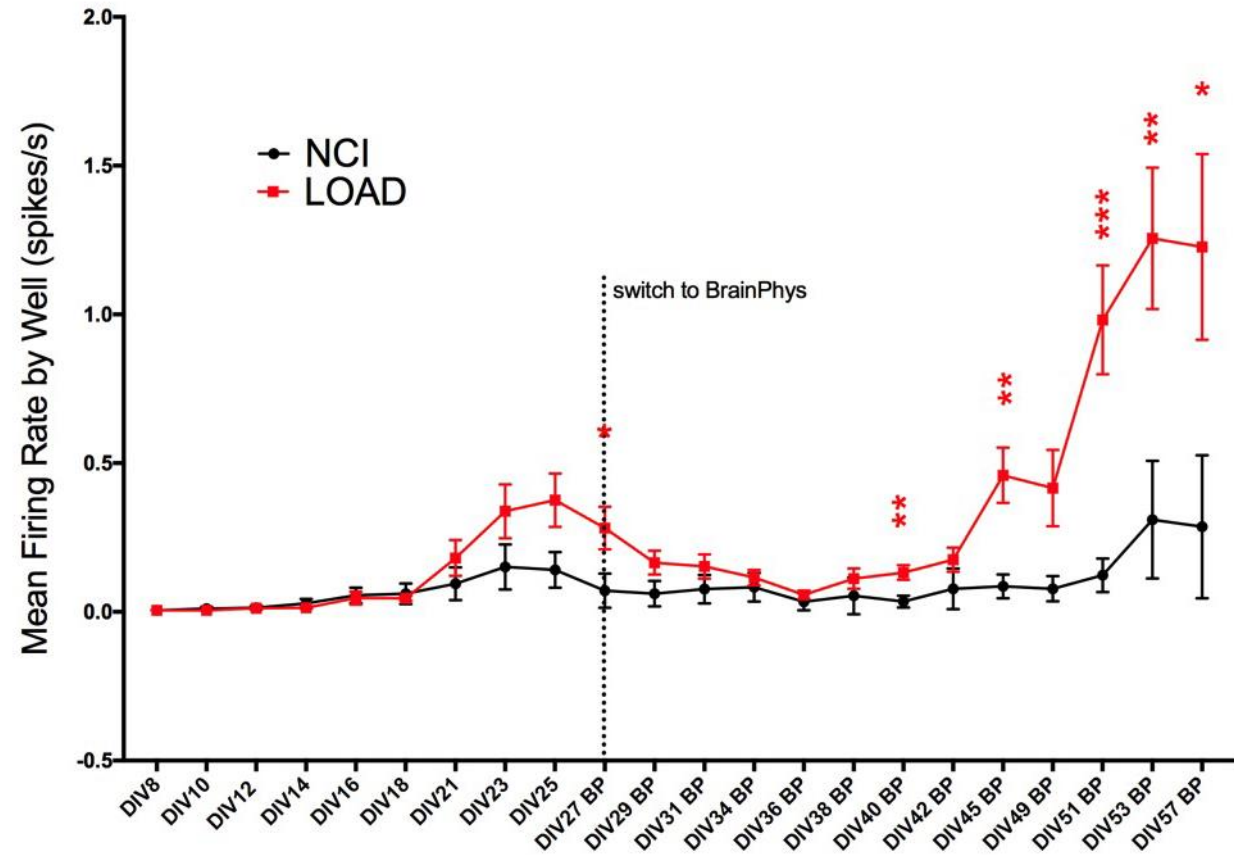
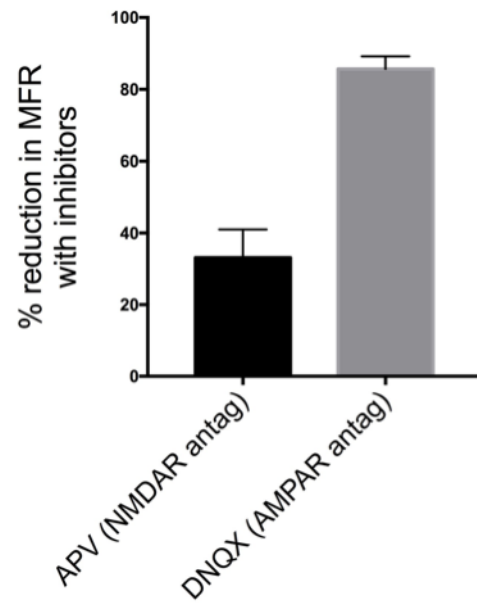


Joe Negri, PhD candidate



Axion Maestro MEA reader

Firing Frequency of control (not cognitively impaired, no pathology) versus LOAD iNs over time Using the Axion Maestro MEA reader



Assays developed for human induced neurons from ROS/MAP subjects

APP processing

A β 42
A β 40
A β 37
A β 38
A β 43

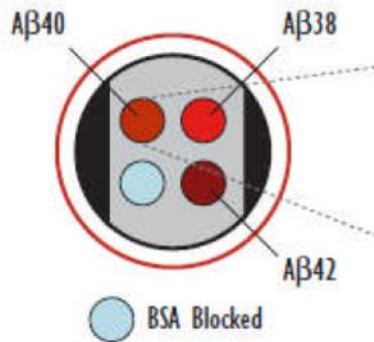
Oligomeric A β

sAPP β

sAPP α

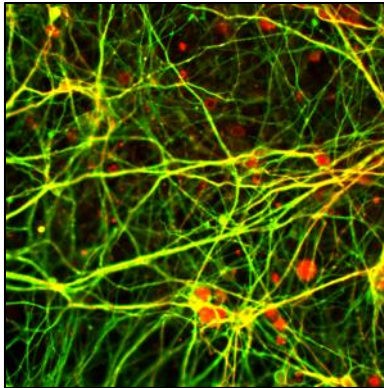
APP holoprotein

CTFs



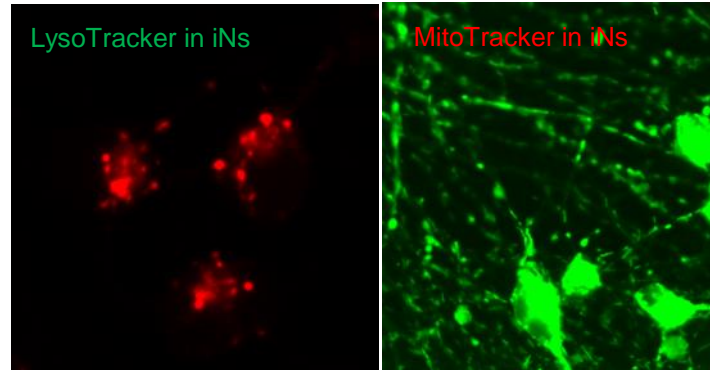
Tau levels

pS202/T205 Tau
p231 Tau
Tau full length
Tau N-term
Tau C-term



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Lysosome size, number, localization
Mitochondria size, number, localization
Endosome size, number, localization
Synaptic puncta number
Oxidative stress



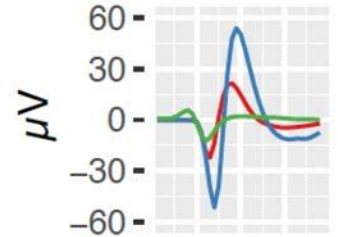
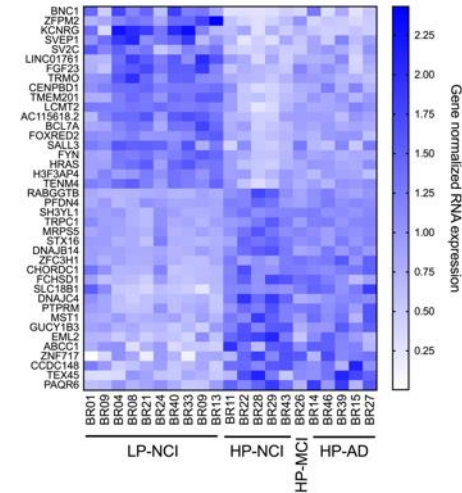
-Omics

RNAseq
Proteomics

Longitudinal

Incucyte

MEA



Assays developed for human induced neurons from ROS/MAP subjects

APP processing

Tau levels

Imaging-based assays

-Omics

Longitudinal

A β 42

A β 40

A β 37

A β 38

A β 41

Oligomer

sAPP

sAPP

APP holop

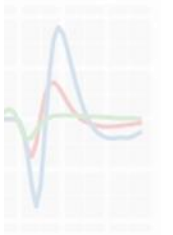
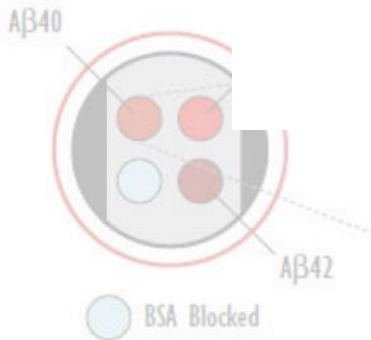
CTF

Changes in these metrics in response to a stimulus:

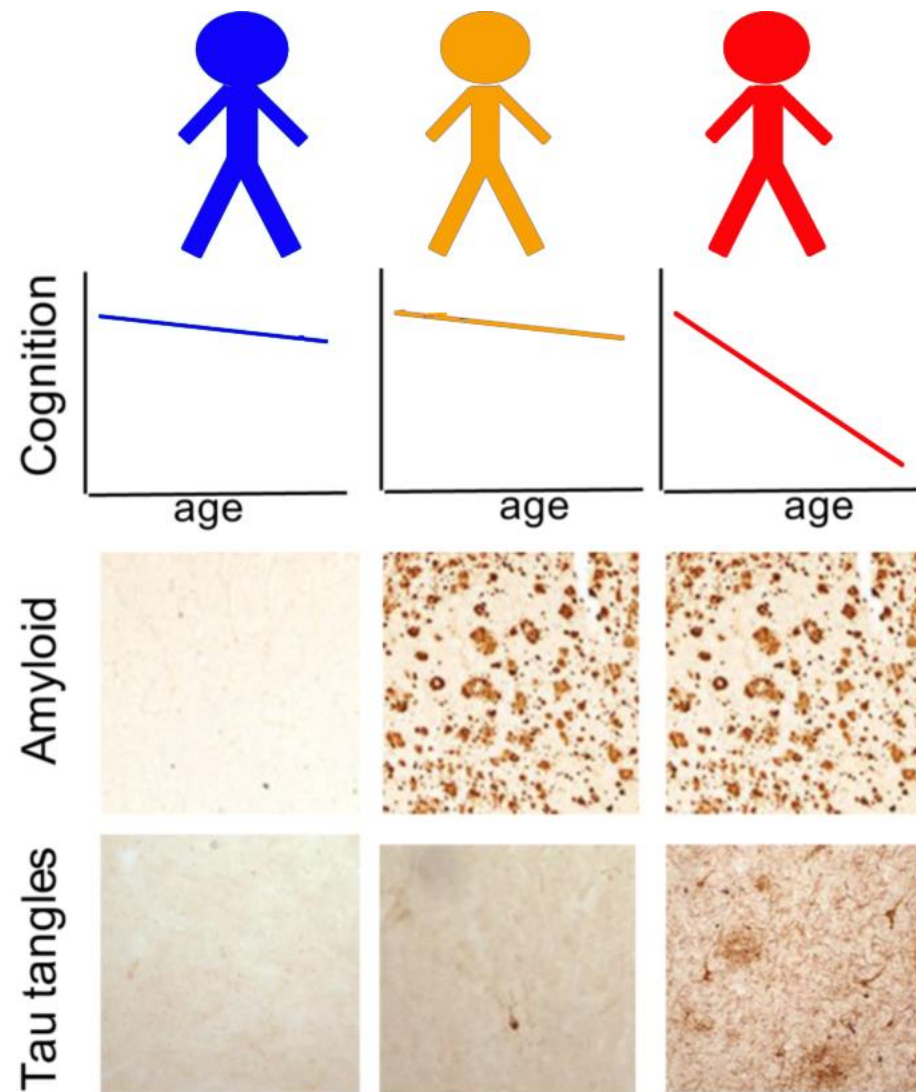
1) genetic perturbation (shRNA, CRISPR-based modulation)

2) chemical treatment (drugs, small molecules)

3) Brain-derived neurotoxic species

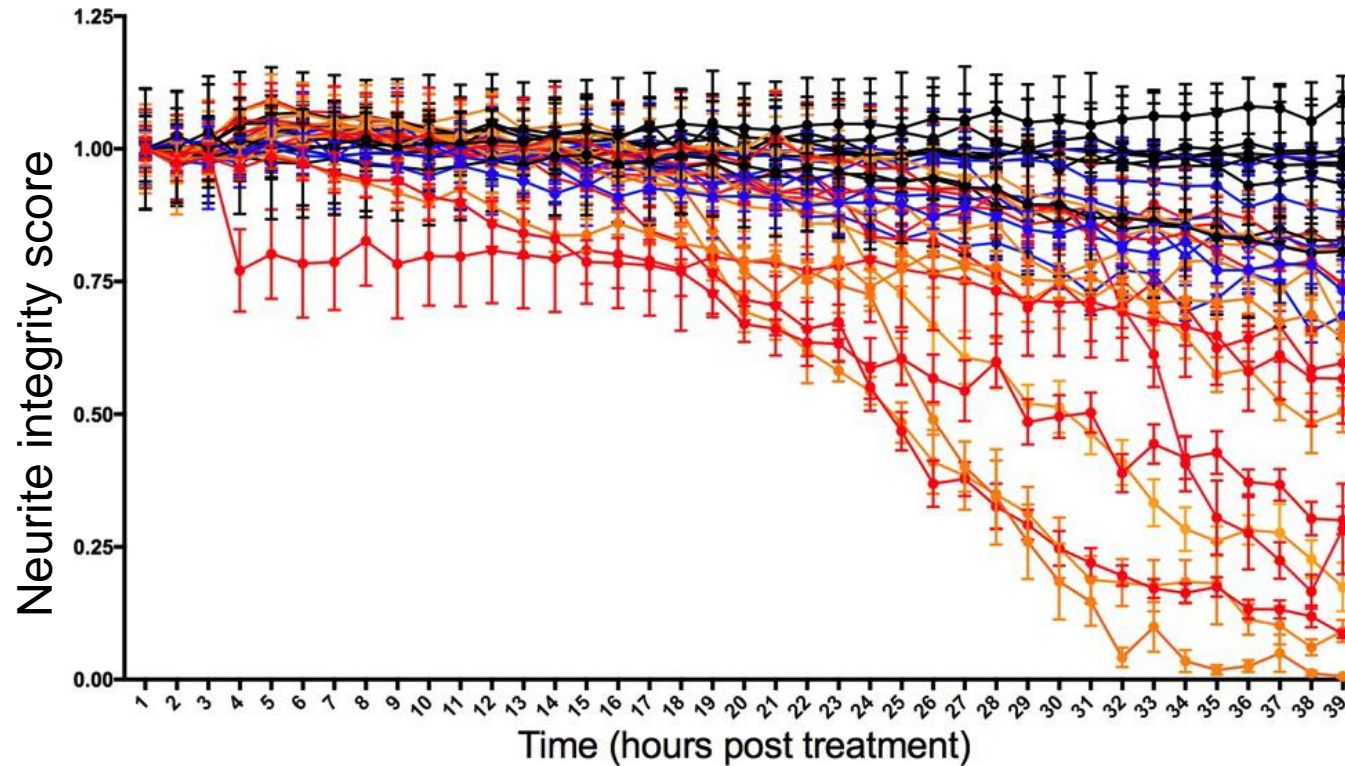


Brain-derived neurotoxic species as a perturbation



Brain extracts from 27
individuals
in ROS/MAP examined

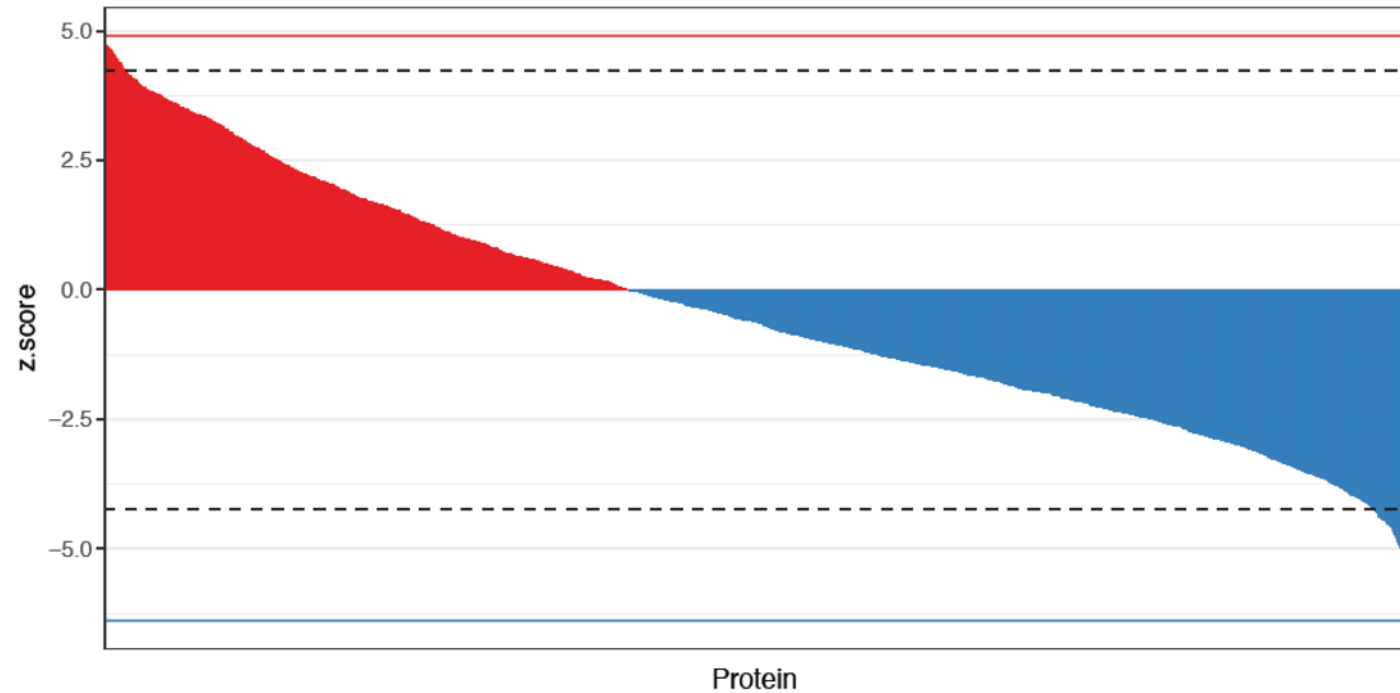
Responsiveness of human iNs to human brain extracts across the clinical and pathological spectrum



Proteomic profiling of human brain extracts and correlations with effects on neurite integrity

EMORY proteomics

3500 proteins identified,
Spearman correlation,
correcting for multiple comparisons
86 proteins significantly correlated

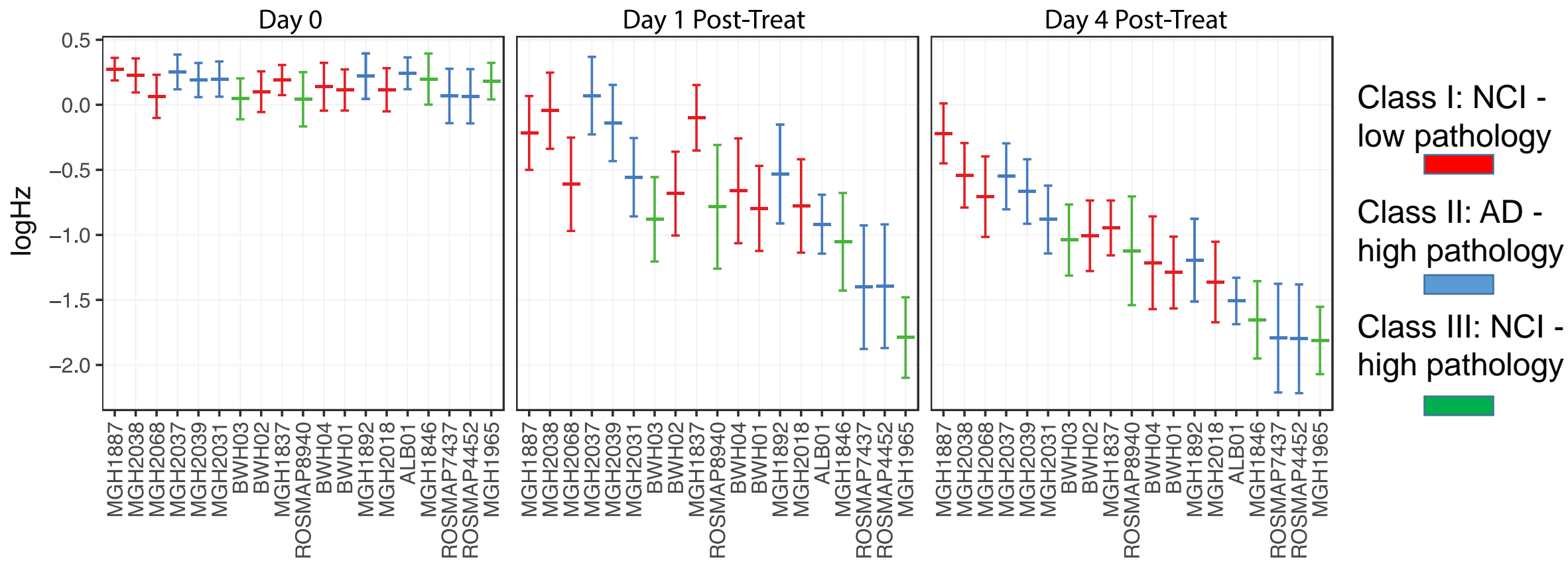


Effects of human brain extracts by diagnosis class; individual, on mean firing rate

Incorporating data from 19 individuals across 22 experiments:

Effect of individual on spontaneous firing

*lme: logHz ~ Individual * Time, random (experiment, well)*

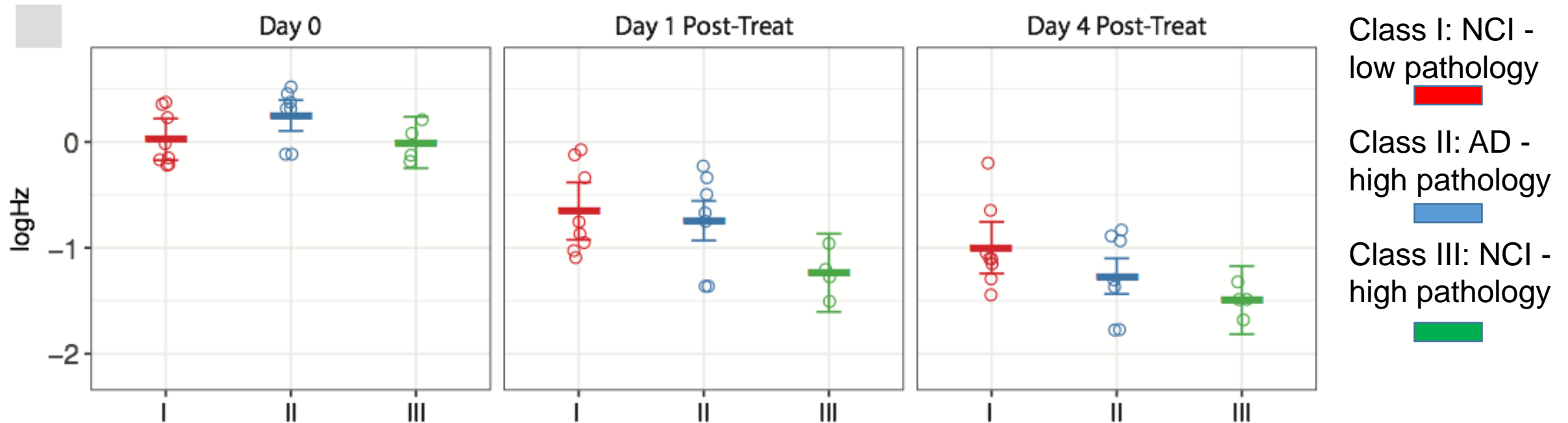


Effects of human brain extracts by diagnosis class; individual, on mean firing rate

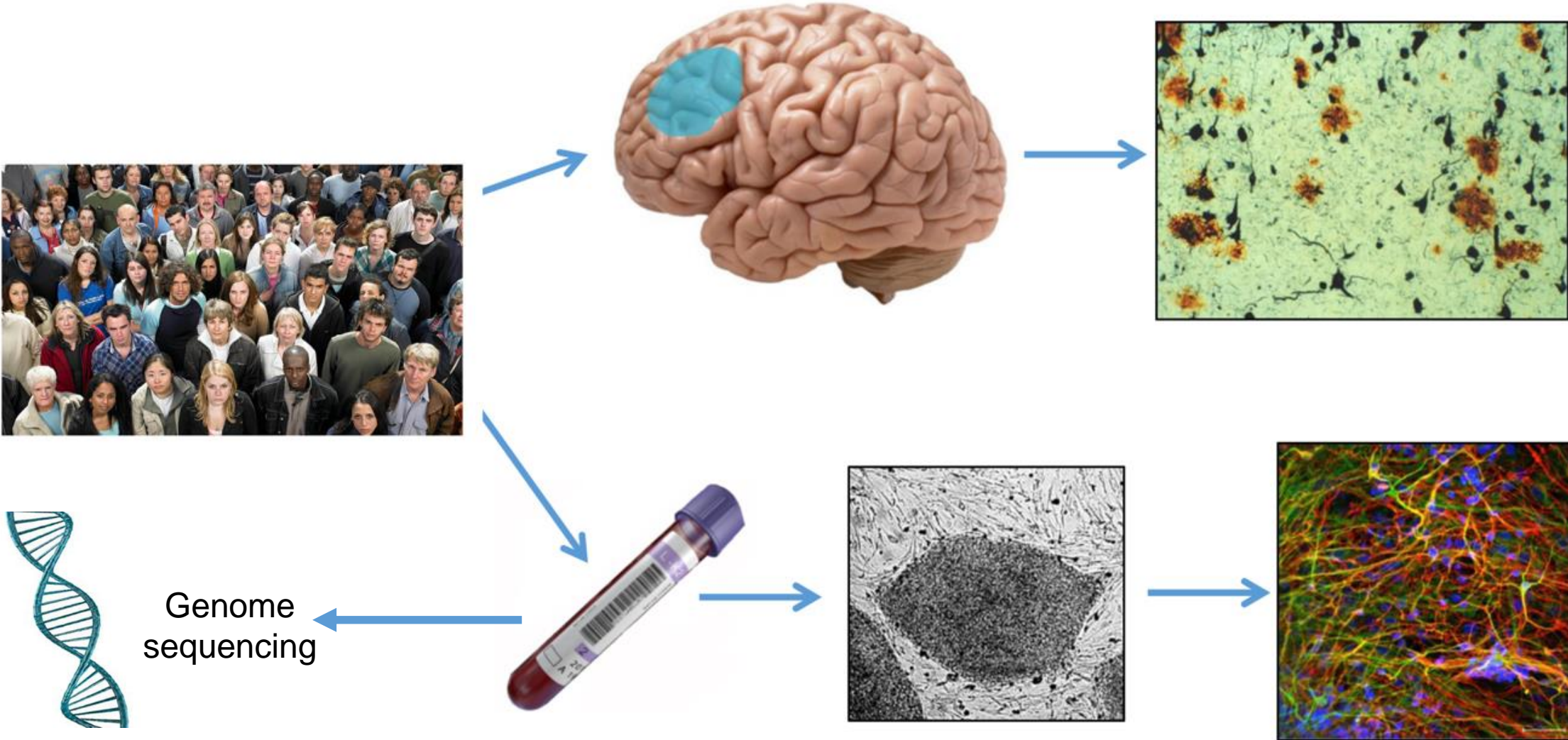
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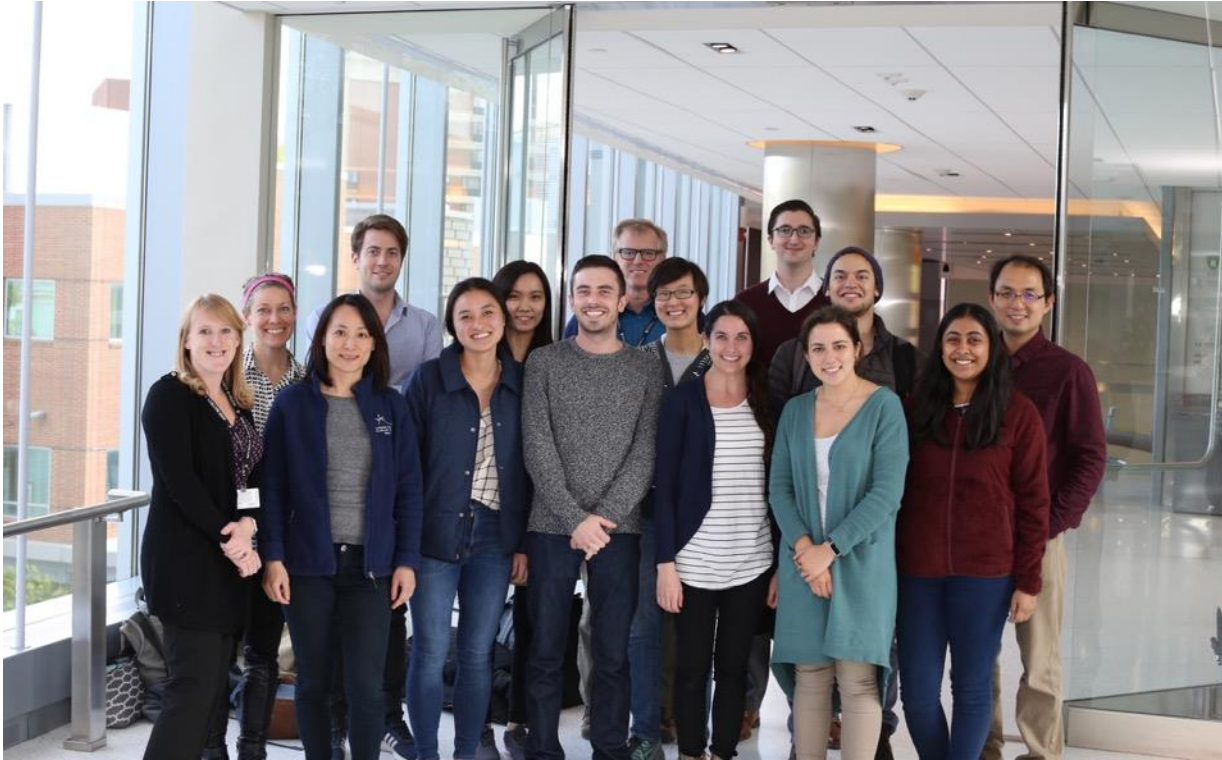
*lme: logHz ~ Individual * Time, random (experiment, well)*



Probing heterogeneity in Alzheimer's disease and the aging human brain using iPSCs



Acknowledgments



Young-Pearse Lab

Christina Muratore, PhD
Meichen Liao, PhD
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Allan Levey, PhD - Emory
Scott Noggle, PhD - NYSCF
Phil De Jager, MD PhD - Columbia
David Bennett, MD - RUSH



**Biggest thank you to the participants of ROS and MAP
and our generous donors who funded the generation of the iPSC lines**