

# Integrative Network Modeling of Cognitive Resilience to Alzheimer's Disease

(R01AG057907)

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# Rationale

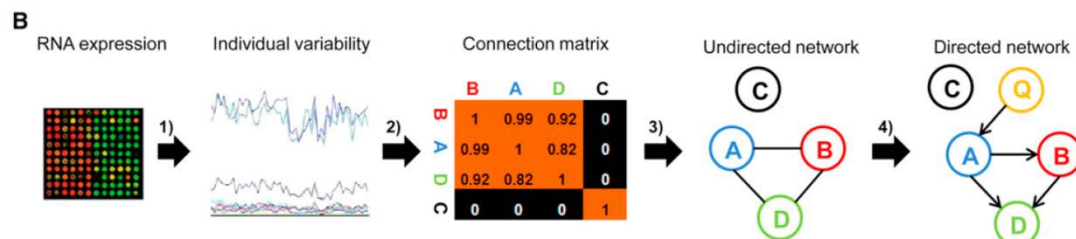
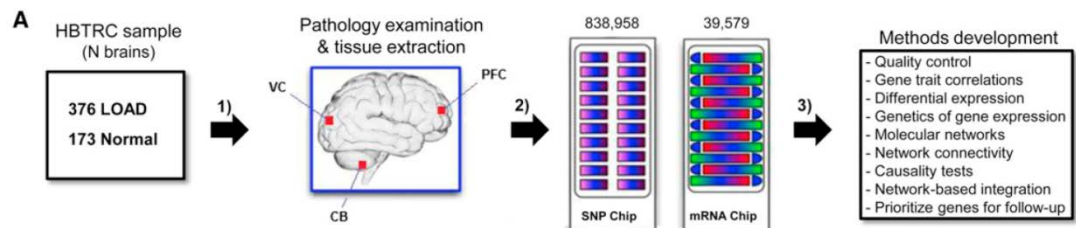
- No effective method is available for preventing and/or treating this devastating disease.
- However, certain individuals of the elder population ( $\geq 85$  years) remain cognitively intact, including some with substantial plaques and neurofibrillary tangle burdens, the two pathological hallmarks for fully symptomatic AD.
- The mechanisms of cognitive resilience and protection against AD in these elderly persons remain elusive.

# Overall Goals

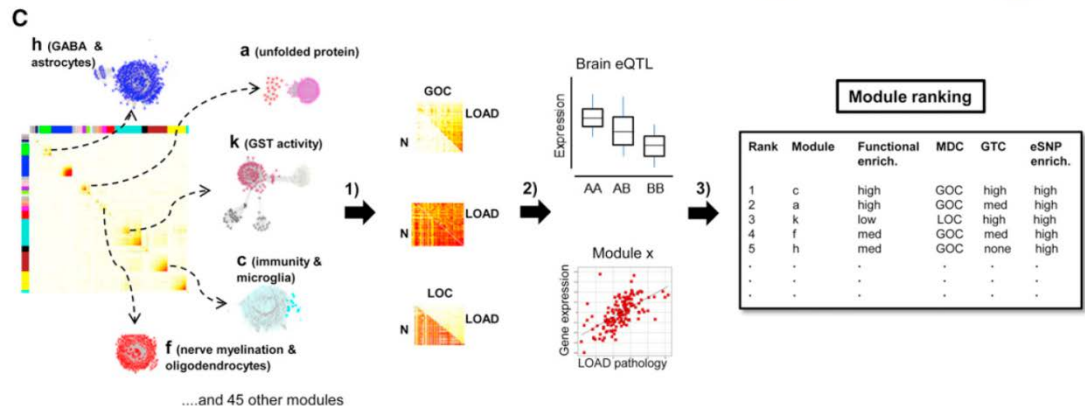
This grant aims to systematically develop and validate molecular network models underlying cognitive resilience to AD risk.

- ❖ Generate and analyze an AD-resilient dataset comprised of matched genetic, transcriptomic and proteomic data from a large number of **very old and AD-resilient human brains**
- ❖ Build network models of cognitive resilience to AD
- ❖ Extensively validate network drivers using *C. elegans* and mouse models.

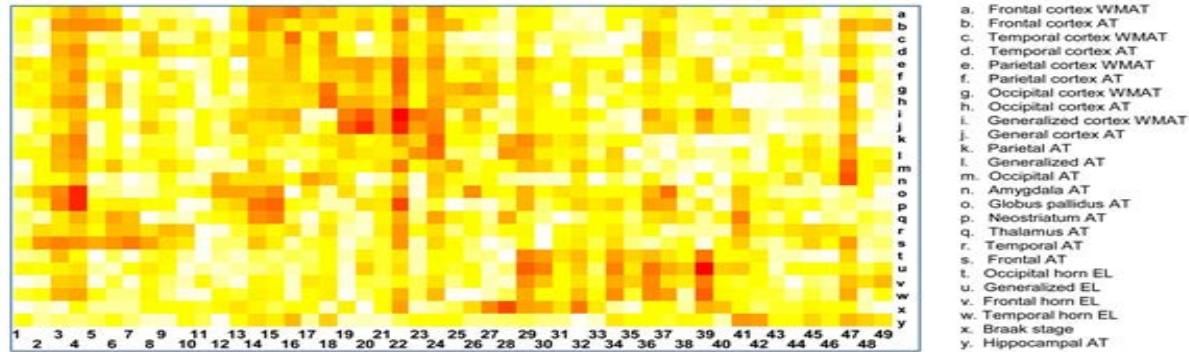
# Overview of HBBAD Cohort and Analysis Flow



subset	samples
Alzh_PFC	310
Alzh_CR	263
Alzh_VC	190
Norm_PFC	153
Norm_CR	128
Norm_VC	121

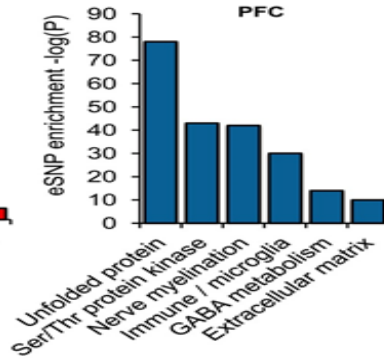
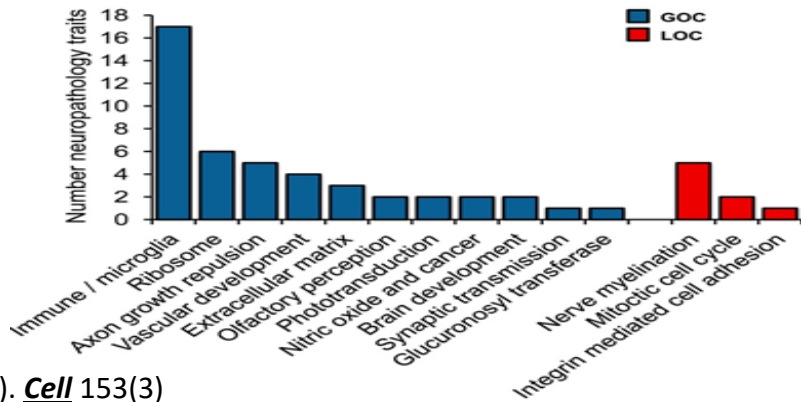
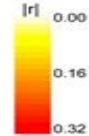


# Gene Modules Associated with AD Pathology



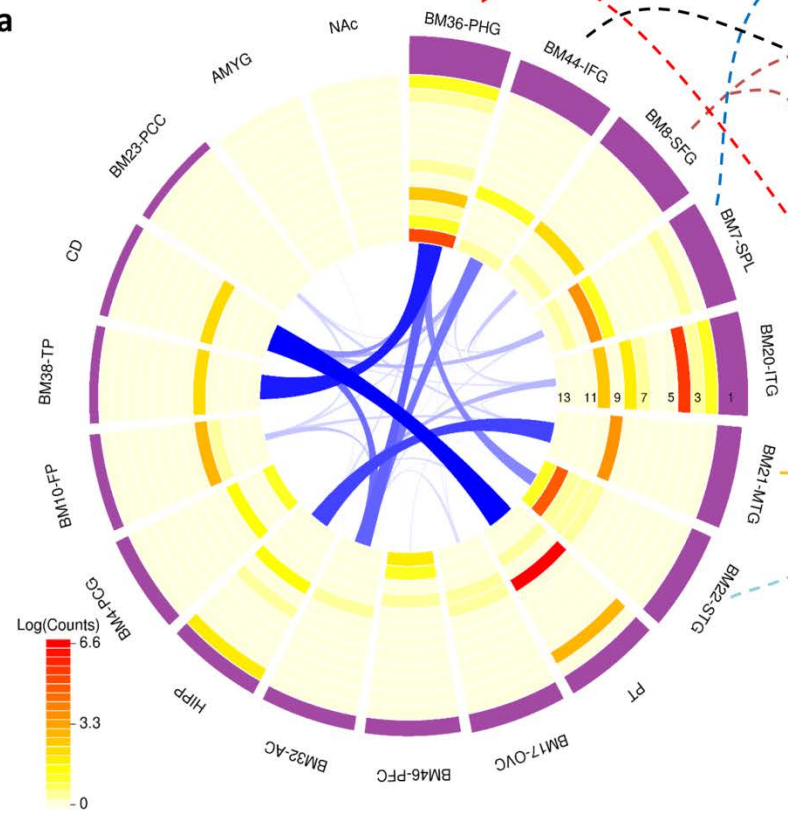
- a. Frontal cortex WMAT
- b. Frontal cortex AT
- c. Temporal cortex WMAT
- d. Temporal cortex AT
- e. Parietal cortex WMAT
- f. Parietal cortex AT
- g. Occipital cortex WMAT
- h. Occipital cortex AT
- i. Generalized cortex WMAT
- j. General cortex AT
- k. Parietal AT
- l. Generalized AT
- m. Occipital AT
- n. Amygdala AT
- o. Globus pallidus AT
- p. Neostriatum AT
- q. Thalamus AT
- r. Temporal AT
- s. Frontal AT
- t. Occipital horn EL
- u. Generalized EL
- v. Frontal horn EL
- w. Temporal horn EL
- x. Braak stage
- y. Hippocampal AT

- 1. Neurotrophin signaling
- 2. Immune / microglia (VC)
- 3. Immune / microglia (CB)
- 4. Immune / microglia (PFC)
- 5. Nerve myelination (VC)
- 6. Vascular development (PFC)
- 7. Nitride oxide
- 8. Cell adhesion
- 9. GABA metabolism / astrocytes
- 10. Biosynthesis of steroids (CB)
- 11. Dorsio-ventral axis formation
- 12. Muscle contraction
- 13. Unfolded protein (CB)
- 14. Response to biotic stimulus
- 15. Regulation of cell growth
- 16. Phototransduction
- 17. Zinc ion biosynthesis
- 18. Osteoblast differentiation
- 19. Nerve myelination (CB)
- 20. Olfactory perception (PFC)
- 21. Biosynthesis of steroids (VC)
- 22. mRNA cleavage factors
- 23. Biosynthesis of steroids (PFC)
- 24. Extracellular matrix / choroid plexus
- 25. Neuropeptide hormone
- 26. Cadherin
- 27. Glucuronosyl transferase
- 28. NAD(P) homeostasis
- 29. Glutathione transferase (PFC)
- 30. Unfolded protein (PFC)
- 31. Unfolded protein (VC)
- 32. Glutathione transferase (VC)
- 33. Ser/Thr kinase receptor
- 34. Neurogenesis
- 35. Calcium ion transportation
- 36. Glutathione transferase (CB)
- 37. Synaptic transmission (VC)
- 38. Nerve myelination (PFC)
- 39. Taste perception
- 40. Vascular development (CB)
- 41. Dynein complex (PFC)
- 42. Olfactory perception (CB)
- 43. Synaptic vesicle transport
- 44. Cytoskeleton organization
- 45. Glucose homeostasis
- 46. Dynein complex (VC)
- 47. Coated vesicle
- 48. Synaptic transmission (PFC)
- 49. Synaptic transmission (CB)

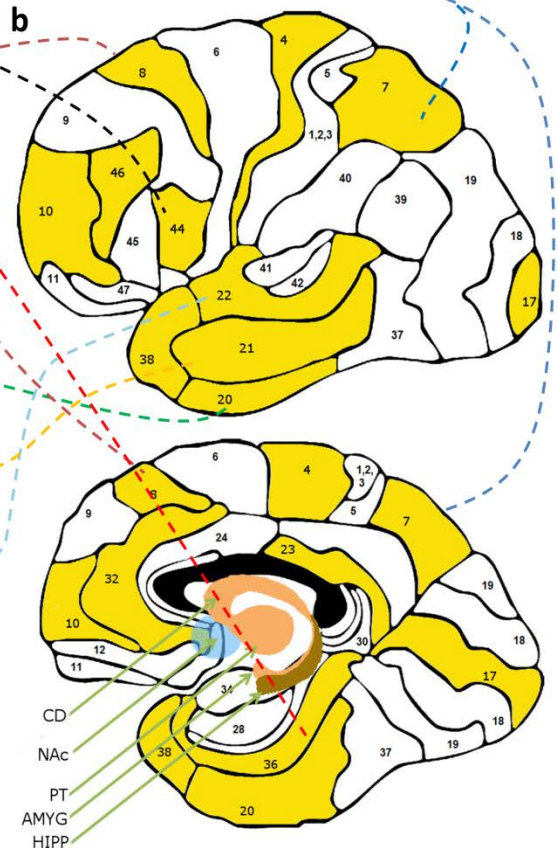


# Brain regions rank-ordered by the relevance to AD pathology

**a**

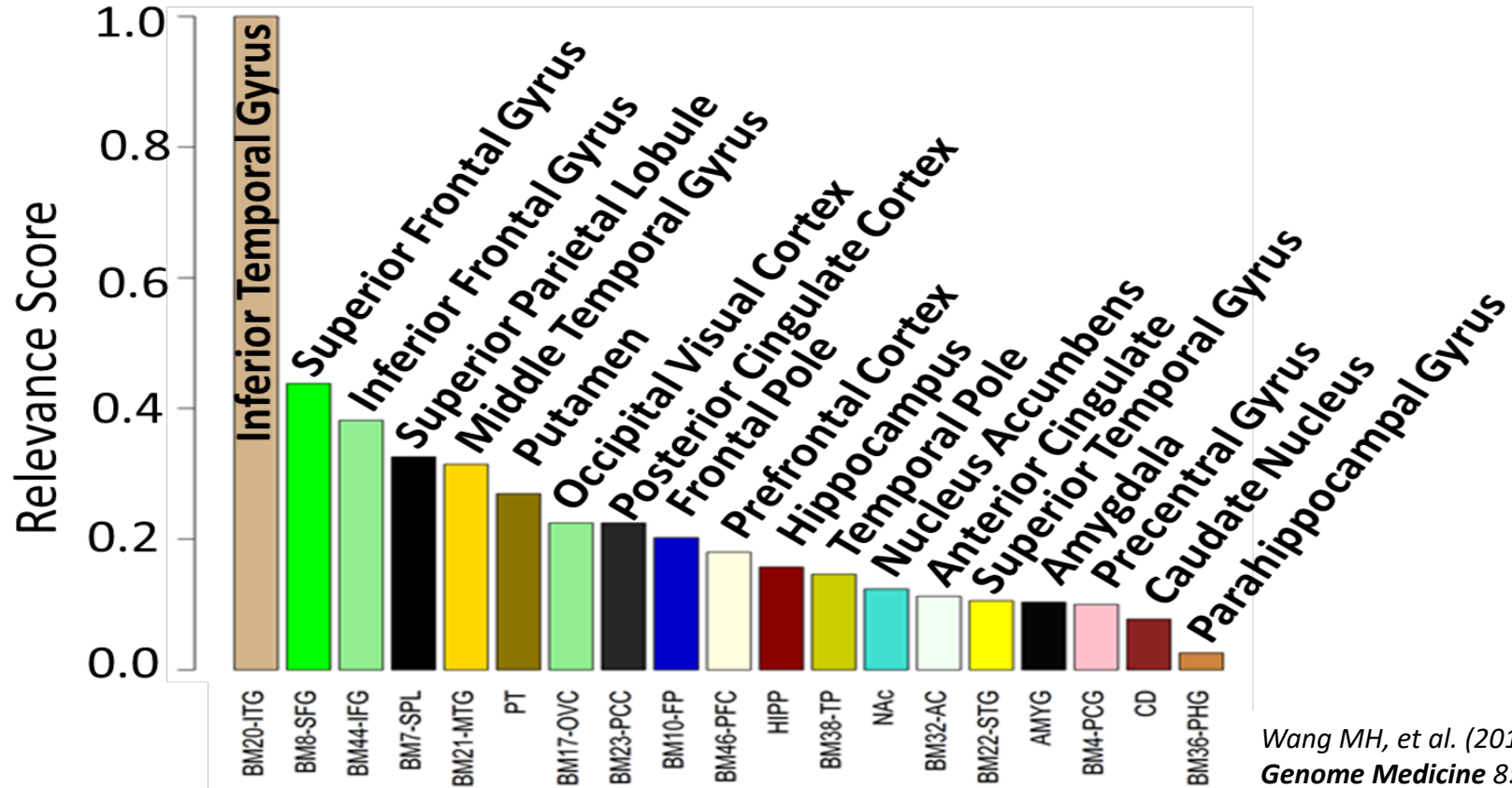


**b**



Region	Full Name
BM10-FP	Frontal Pole
BM17-OVC	Occipital Visual Cortex
BM20-ITG	Inferior Temporal Gyrus
BM21-MTG	Middle Temporal Gyrus
BM22-STG	Superior Temporal Gyrus
BM23-PCC	Posterior Cingulate Cortex
BM32-AC	Anterior Cingulate
BM36-PHG	Parahippocampal Gyrus
BM38-TP	Temporal Pole
BM4-PCG	Precentral Gyrus
BM44-IFG	Inferior Frontal Gyrus
BM46-PFC	Dorsolateral Prefrontal Cortex
BM7-SPL	Superior Parietal Lobule
BM8-FC	Prefrontal Cortex
Bma-AMYG	Amygdala
BMb-CD	Caudate Nucleus
BMc-HIPP	Hippocampus
BMd-NAc	Nucleus Accumbens
Bme-PT	Putamen

# Selective Myelination Vulnerability of 19 Brain Regions to AD

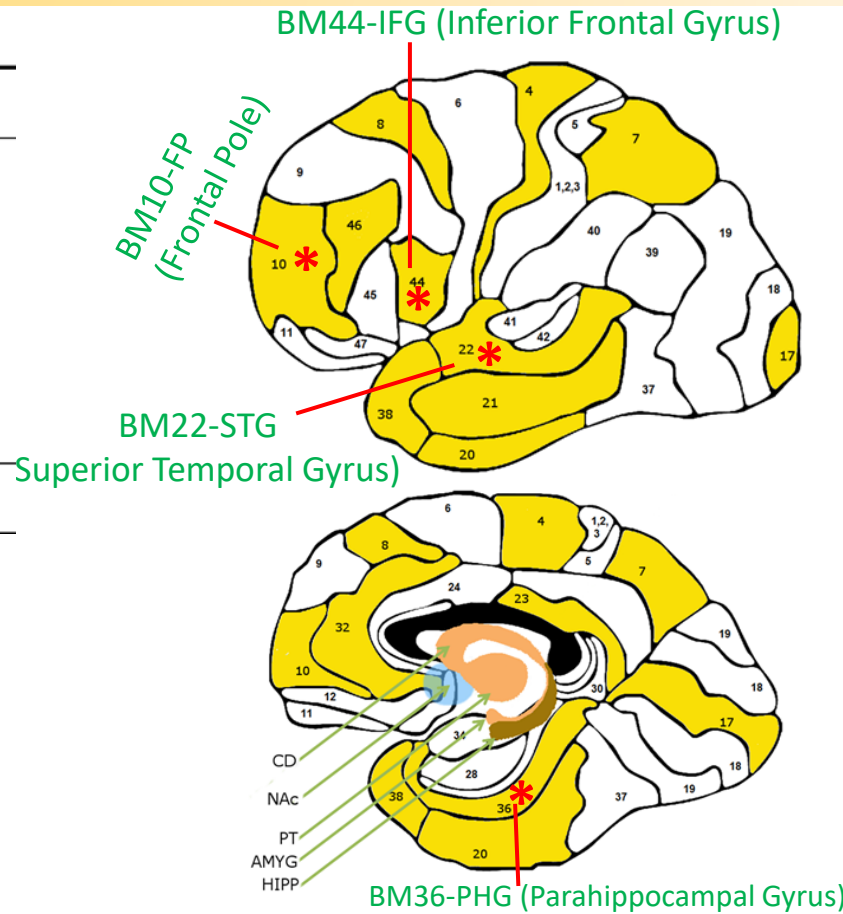


# The Mount Sinai Cohort of Large-scale Genomic, Transcriptomic and Proteomic Data in Alzheimer's Disease

## Demographic characteristics of MSBB AD samples

CDR	N (Sex F/M)	Mean PMI	CDR	Mean Age	Mean Cortical Plaque Density
0	44 (32/12)	590.8	0	82.4	2.06
0.5	47 (24/23)	603.2	0.5	81.7	3.19
1	38 (26/12)	418.6	1	84.9	6.27
2	49 (31/18)	460.3	2	86.5	8.96
3	78 (56/22)	385.2	3	86.4	9.79
4	47 (30/17)	392.8	4	87.6	10.64
5	61 (39/22)	368.3	5	82.3	18.59
All	364 (238/126)	445	2.4	84.7	9.11

- Transcriptomics (RNA-seq) – 4 brain regions
- Proteomics (BM10, BM36 ongoing)
- Whole Exome Sequencing
- Whole Genome Sequencing





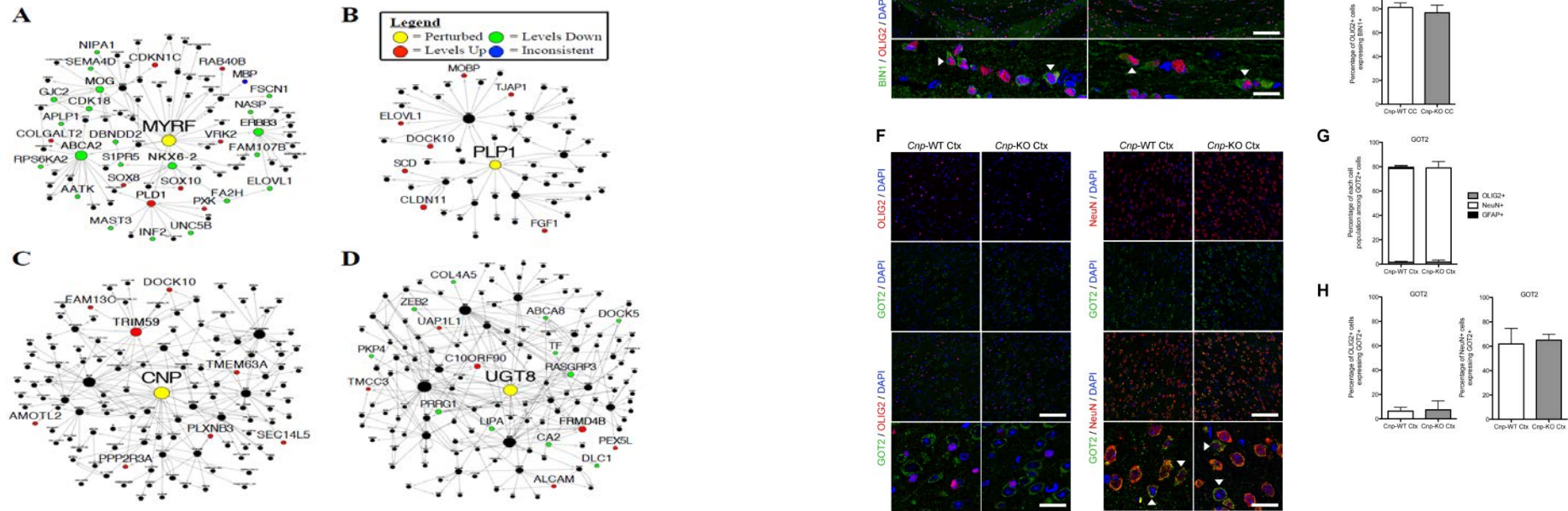
RESEARCH ARTICLE

Open Access



# Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease

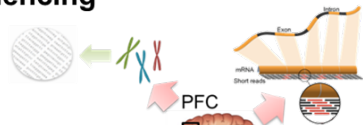
Andrew T. McKenzie<sup>1,2,3</sup>, Sarah Moyon<sup>4,13</sup>, Minghui Wang<sup>1,2</sup>, Igor Katsyv<sup>1,2,3</sup>, Won-Min Song<sup>1,2</sup>, Xianxiao Zhou<sup>1,2</sup>, Eric B. Dammer<sup>5</sup>, Duc M. Duong<sup>6,7</sup>, Joshua Aaker<sup>8</sup>, Yongzhong Zhao<sup>1,2</sup>, Noam Beckmann<sup>1,2</sup>, Pei Wang<sup>1,2</sup>, Jun Zhu<sup>1,2</sup>, James J. Lah<sup>9,10</sup>, Nicholas T. Seyfried<sup>6,7,9</sup>, Allan I. Levey<sup>9,10</sup>, Pavel Katsel<sup>11</sup>, Vahram Haroutunian<sup>2,11,12</sup>, Eric E. Schadt<sup>1,2</sup>, Brian Popko<sup>8</sup>, Patrizia Casaccia<sup>2,4,13\*</sup> and Bin Zhang<sup>1,2\*</sup>



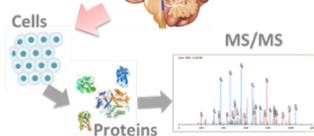
# Approaches

## Aim 1. Data Curation & Generation

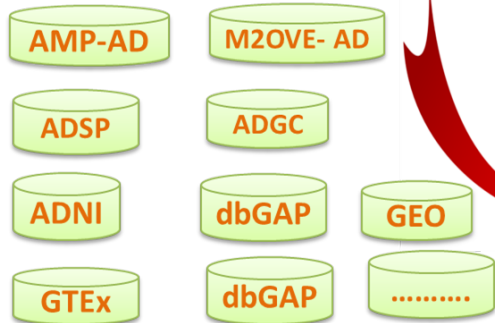
### A. Whole Genome Sequencing B. RNA-sequencing



### C. Proteomics

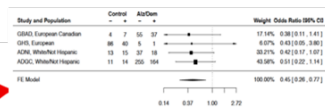


### D. Data Curation

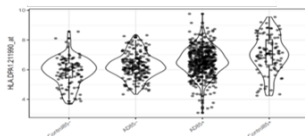


## Aim 2. Multiscale Network Modeling

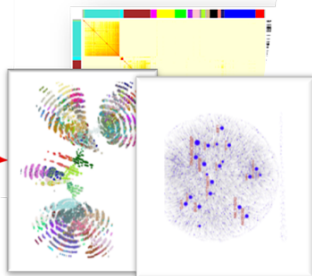
### E. Systems Genetics



### F. Differential Analysis



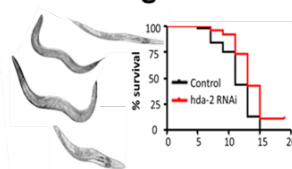
### G. Multiscale Network Analysis



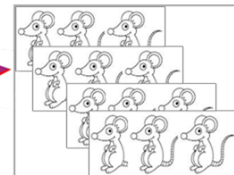
## H. Network Integration

## Aim 3. Target & Network Validation

### I. C. elegans models

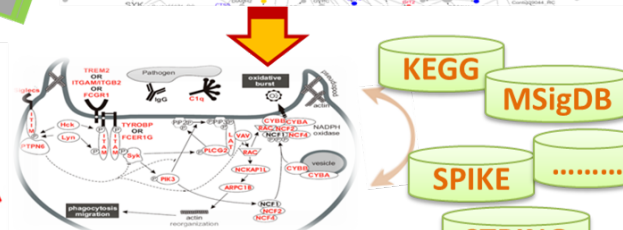
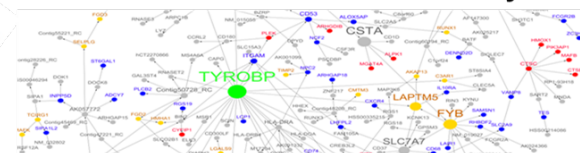


### J. Mouse Models



### K. RNA-sequencing

### L. Validation of Network Connectivity



### M. Construct Signaling Map

# Subgroups of Interest

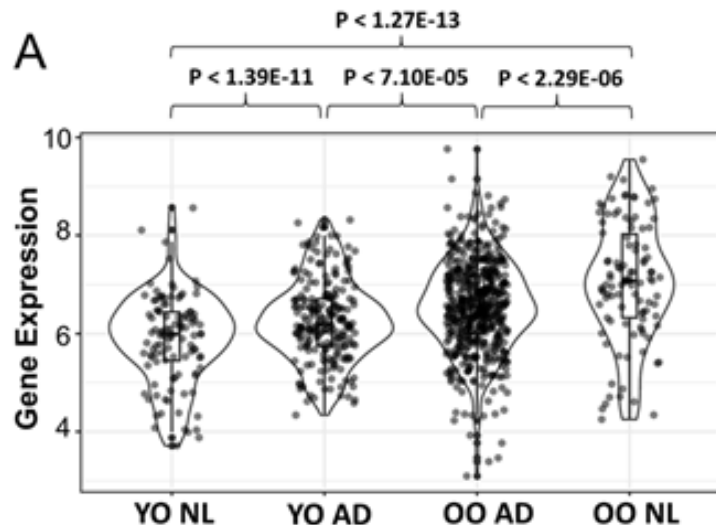
- OONL (oldest/old normal): Very old (age of death (AoD)  $\geq 85$ ) AD-resilient
- YONL (young/old normal): Young (AoD  $< 85$ ) healthy
- OOAD (oldest/old AD): (AoD  $\geq 85$ ) AD
- YOAD (young/old AD): Young (AoD  $< 85$ ) AD.

# Data Generation (Prefrontal Cortex)

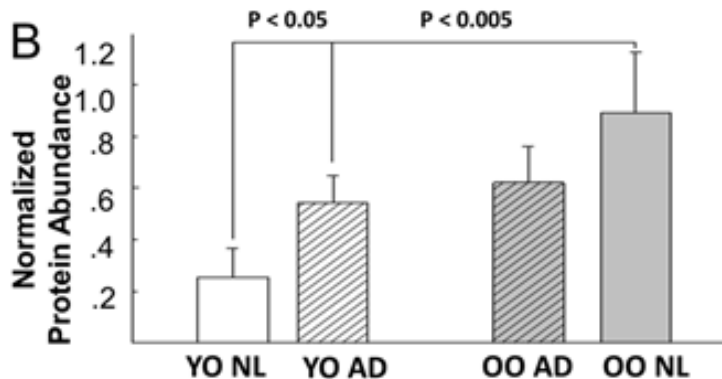
**Table 1. Sample sizes of various groups of interest in the Mount Sinai and ROSMAP brain banks. AoD: age of death, NL: normal healthy brains, AD?: probable or possible AD.**

		MSBB-AD		ROSMAP		Combined		New	Total
		W/ Omics		W/ Omics		W/ Omics			
		Total	Data	Total	Data	Total	Data		
<b>60 ≤ AoD &lt; 85</b>	NL	130	56	127	58	257	<b>114</b>	<b>113</b>	<b>227</b>
	AD	210	83	103	24	313	107		
	AD?	49	27	138	57	187	84		
<b>AoD ≥ 85</b>	NL	72	34	196	79	268	<b>113</b>	<b>137</b>	<b>250</b>
	AD	185	85	348	107	533	192		
	AD?	116	60	479	167	595	227		
<b>Total</b>		762	345	1391	492	2153	837		

# Differential Analysis of the MSBB-AD Data

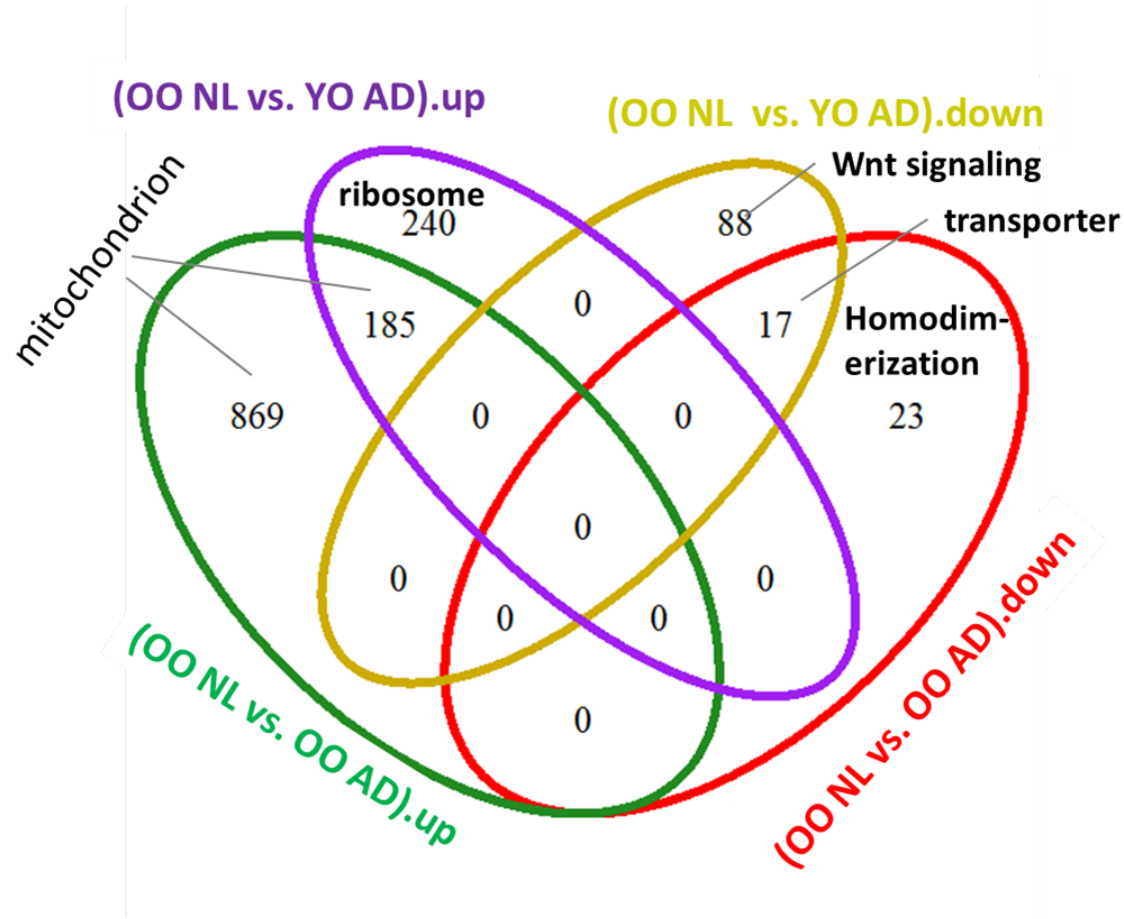


A) Trend analysis identified ***HLA-DPA1*** with the most significant up-regulation trend.



B) Expression of ***HLA-DPA1*** protein in the temporal cortex of young-old and oldest-old persons with and without dementia.

# Differential Analysis of the ROSMAP Data



# Differential Analysis of the ROSMAP Data



Biochimica et Biophysica Acta (BBA) - Molecular Basis  
of Disease

Volume 1802, Issue 1, January 2010, Pages 2-10



Review

## Mitochondrial dysfunction is a trigger of Alzheimer's disease pathophysiology

Paula I. Moreira <sup>a</sup>, Cristina Carvalho <sup>b</sup>, Xiongwei Zhu <sup>c</sup>, Mark A. Smith <sup>c</sup>, George Perry <sup>d</sup> 

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### Abstract

Mitochondria are uniquely poised to play a pivotal role in neuronal cell survival or death because they are regulators of both energy metabolism and cell death pathways. Extensive literature exists supporting a role for mitochondrial dysfunction and oxidative damage in the pathogenesis of Alzheimer's disease. This review discusses evidence indicating that mitochondrial dysfunction has an early and preponderant role in Alzheimer's disease.

# Summary & Future Work

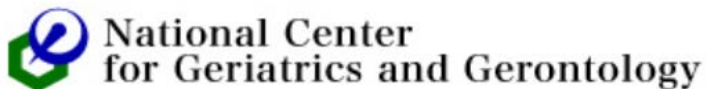
- ❖ The framework of multiscale network modeling of AD has been extensively validated.
- ❖ Preliminary analysis of three large transcriptomic datasets identified novel subnetworks and key regulators of resilience to AD.
- ❖ RNA-sequencing and proteomic profiling of a large number of AD-resilient and contrast groups are undergoing.
- ❖ **Future work**
  - ❖ Integrate multi-Omics data into high-resolution network models of resilience to AD
  - ❖ Screen a large number of candidate drivers *in vivo*



# Team for the AMP-AD U01 Grant



- **Genomics, Informatics, Networks**
  - Bin Zhang, Eric Schadt, Jun Zhu, Minghui Wang, Zhidong Tu, Joel Dudley, Won-min Song
- **Tissue collection and profiling**
  - Vahram Haroutunian
- **Clinical, experimental validation**
  - Sam Gandy, Michelle Ehrlich, Joe Buxbaum, Stephen Salton, Mary Sano, Charles Mobbs (C. elegans), Kristen Brennand and Aiqun Li (stem cells)



- **Fly models**
  - Koichi Iijima

- **High throughput stem cell production and differentiation**
  - Scott Noggle
  - Valentina Fossati



- **Data hosting, sharing, competitions**
  - Lara Mangravite
  - Mette Peters
  - Ben Logsdon

# Team for the Resilience R01 Grant



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## Data Integration

- **Bin Zhang (contact PI)**
- Minghui Wang
- Ali Sharma
- Erming Wang
- Chen Ming
- Ryan Neff
- Shuyu Dan Li
- Rong Chen
- Zhidong Tu
- Li Chen
- Lei Guo

## in vivo Validations

- **Michelle Ehrlich (M-PI)**
- Sam Gandy
- Charles Mobbs
- Mickael Audrain
- Tomas Fanytza
- Ben Shackleton

## Data Generation

- **Vahram Haroutunian (M-PI)**
- Pavel Katsel

## Sample Preparation & Data QC

- **Chris Gaiteri**
- David A Bennett
- Ryan Johnson
- Gregory Klein



## Genetics of Resilience

- **John Kauwe**

## Proteomics

- **Junmin Peng**
- Kaiwen Yu
- Boer Xie



# Acknowledgements



## **AMP-AD Consortium**

R01 AG046170

## **M<sup>2</sup>OVE-AD Consortium**

R01AG057907

**Dr. Suzana Petanceska**