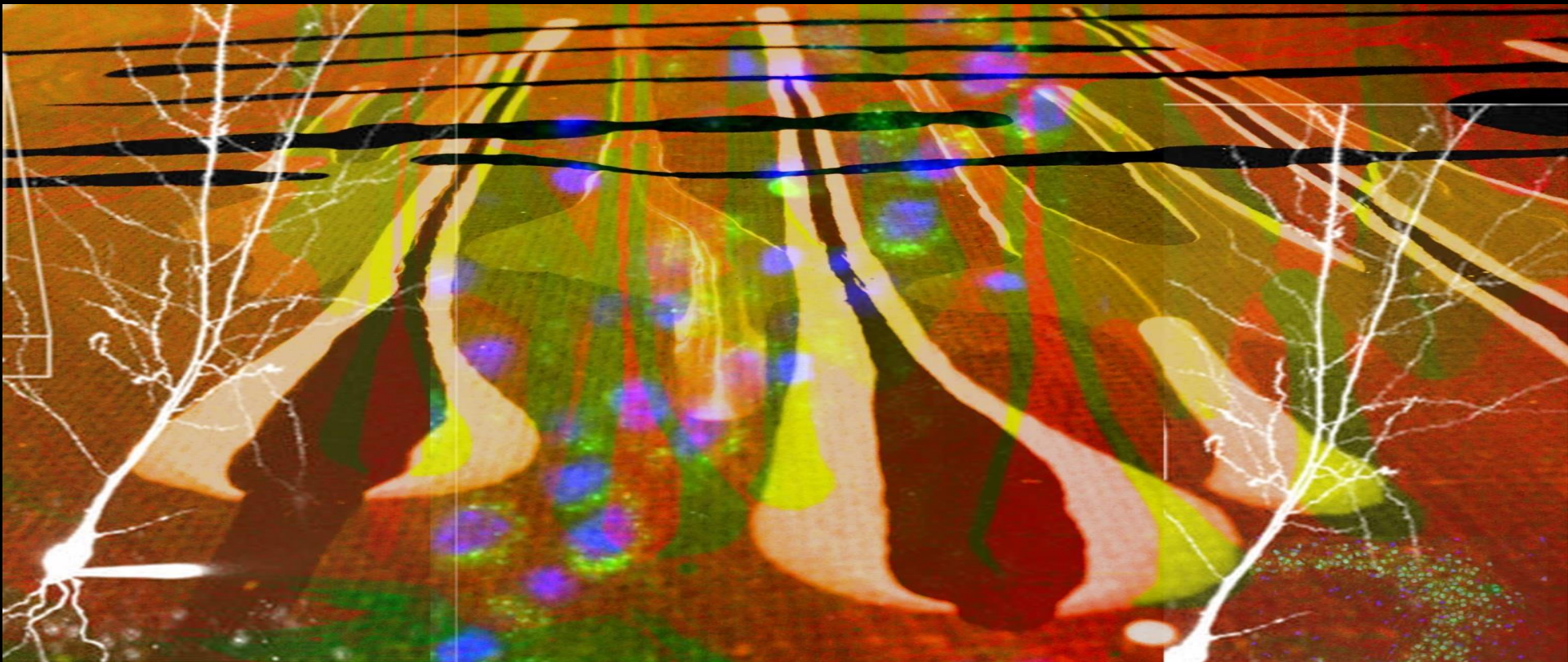


**Overview of the Epigenetics Core, data generated at UF
and UA on aged animals, samples prepped, and general
experimental design for the entire project**

**Tom Foster
Dept of Neuroscience
McKnight Brain Institute
University of Florida**



The Goal: Provide support for bioinformatic analysis of high-throughput RNA sequencing and epigenomics for human and animal studies.

Proof of concept project:

Examine DNA methylation and transcriptome in behaviorally characterized young and aged rats.

- 1) Cognitive tasks**
- 2) Tissue selection**
- 3) Results of RNA analysis (UF)**

Challenges and opportunities in characterizing cognitive aging across species

- 1) Tests of cognitive domains that are age-sensitive in both humans and animal models.
- 2) An understanding of the anatomical substrate for the behavior



Spontaneous
Object
Recognition
(Perirhinal)

Cheese
Board
(Hippocampus)

Spatial
Episodic
Memory
(Hippocampus)

Temporal
Object
Recognition
(Frontal)

Novel
Exploration
(Hippocampus)

Water maze



Set shift
Operant task
(Frontal)

Spatial
Episodic
Memory
(Hippocampus)

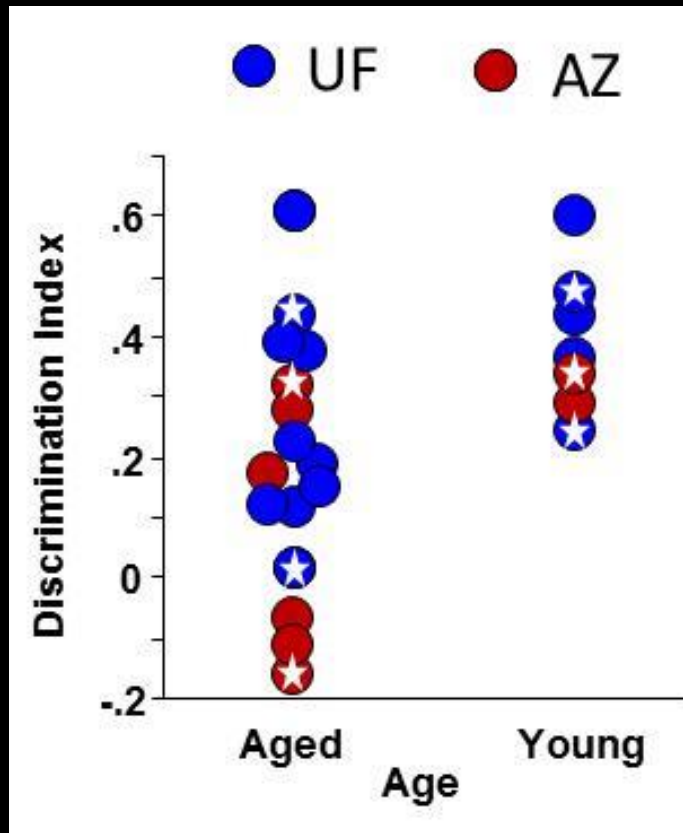
Spontaneous
Object
Recognition
(Perirhinal)

Inhibitory
Avoidance
(Hippocampus &
Amygdala)

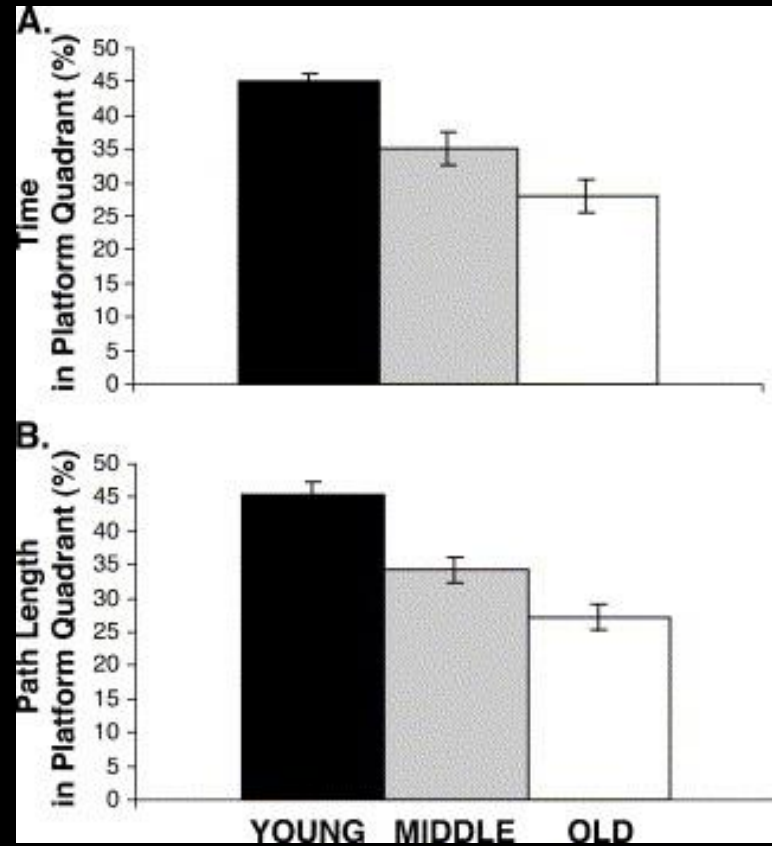
Young 7-8 months
Aged ~20 months

Episodic Spatial Memory on the Water Maze

Reliability

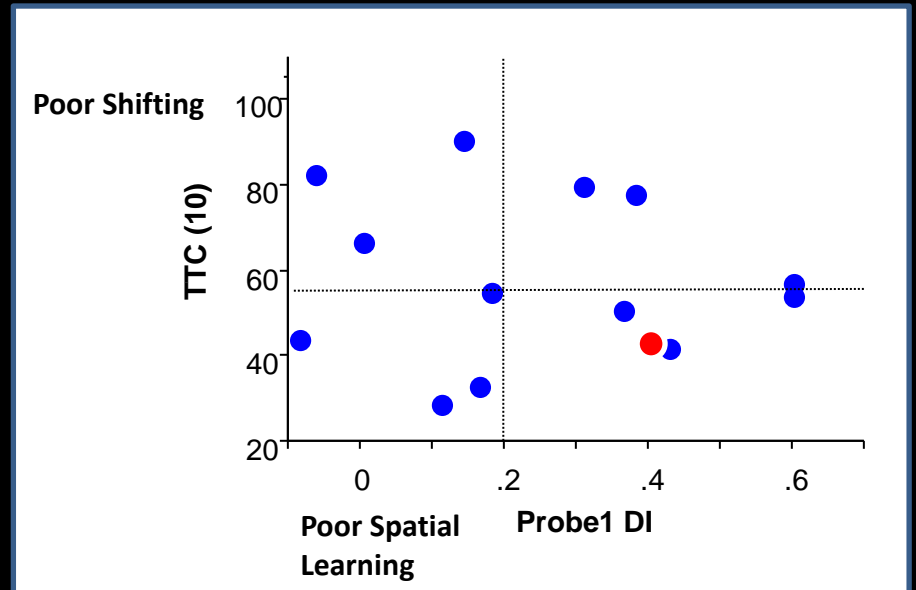
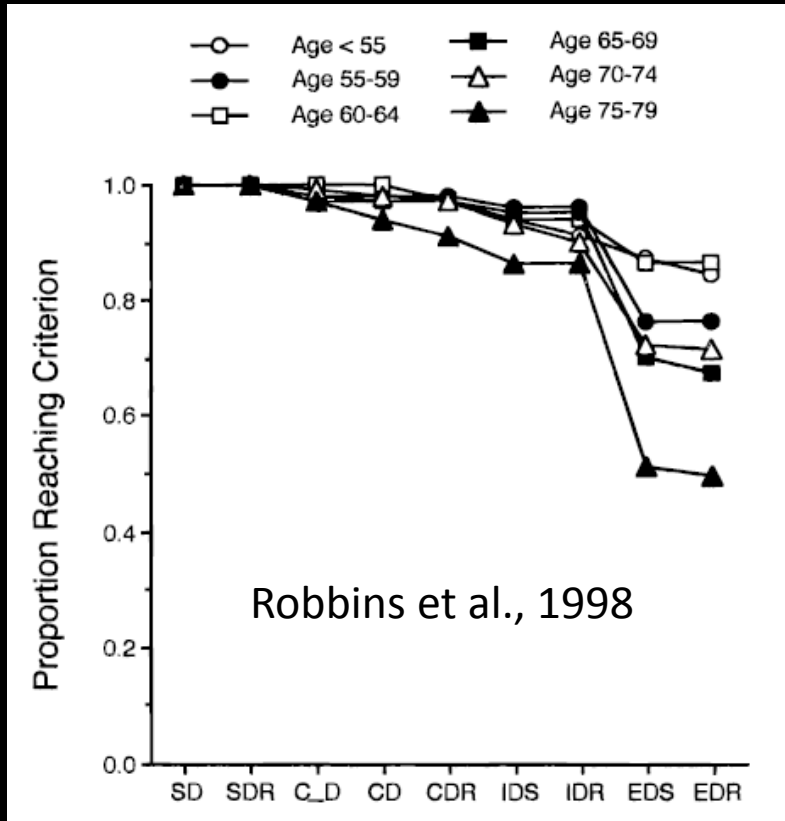
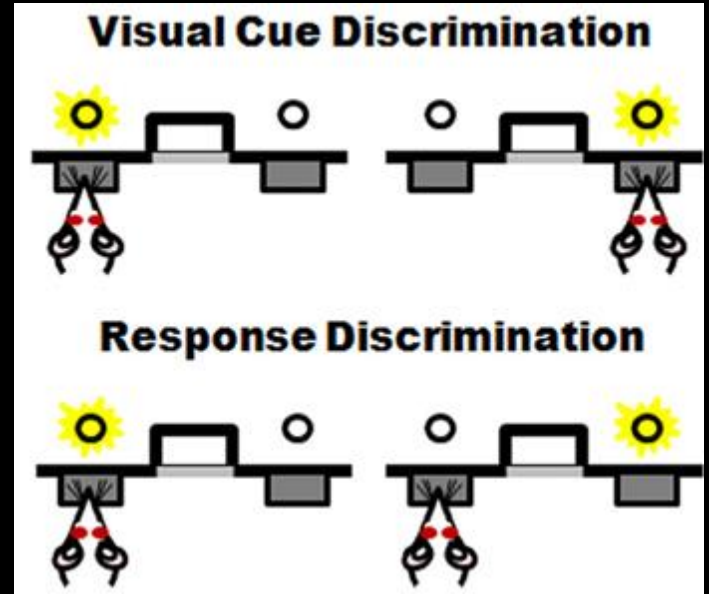


Face Validity

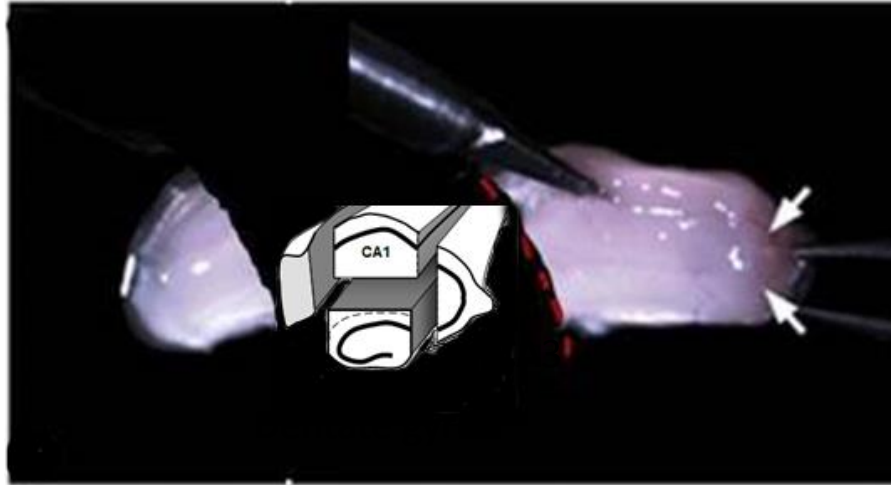


Driscoll et al., 2005

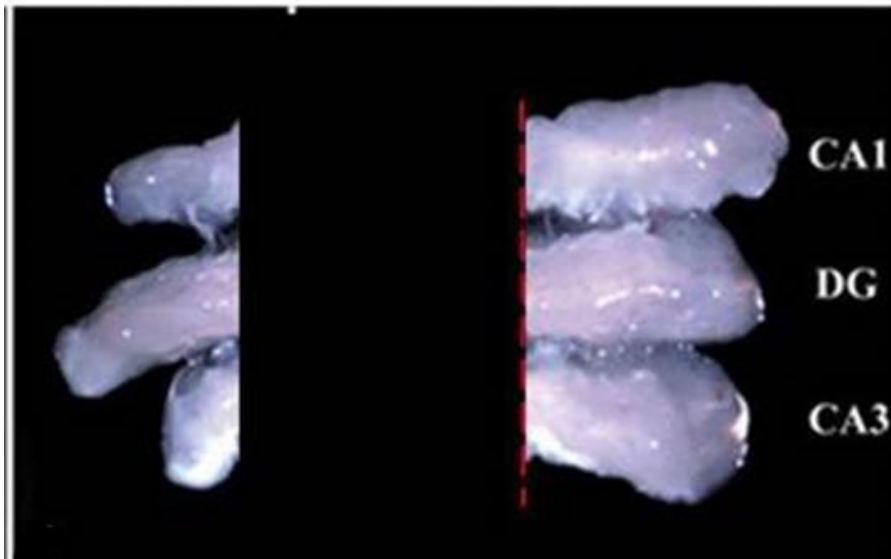
Set shift and frontal cortical function



Hippocampal CA1, CA3, dentate gyrus dissected out and distributed

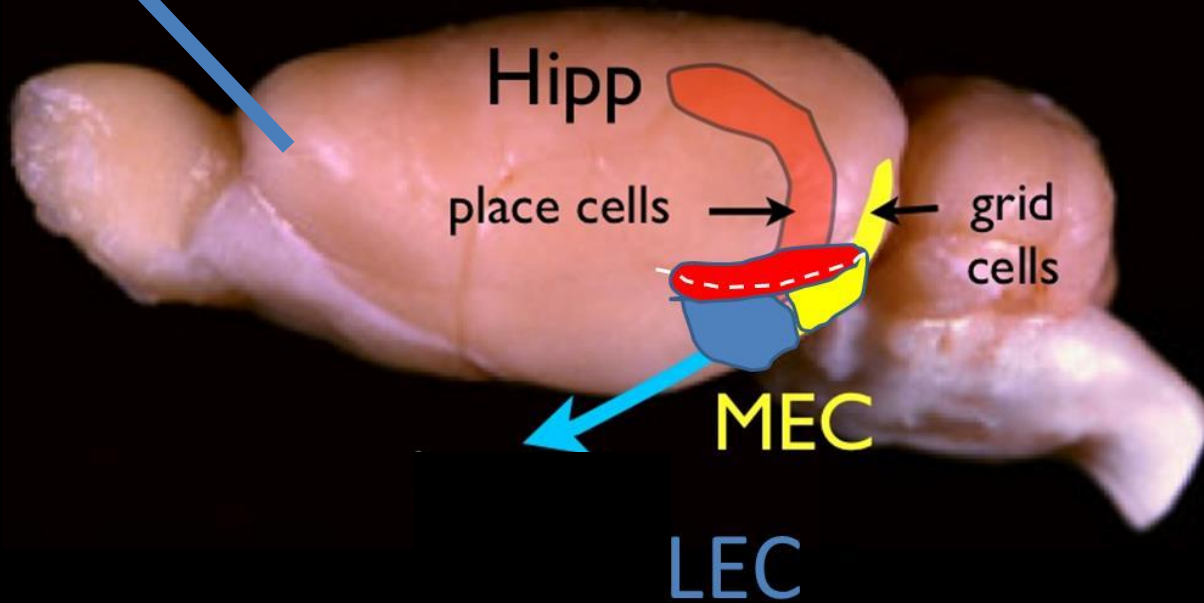
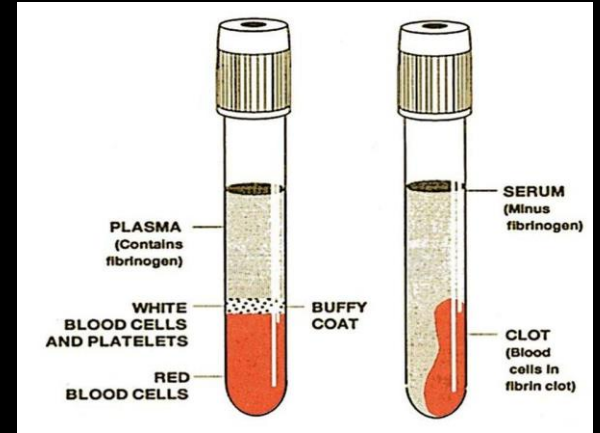
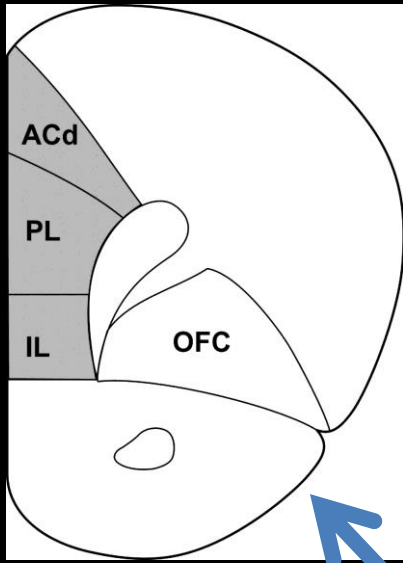


RNA to
three
different
Institutions

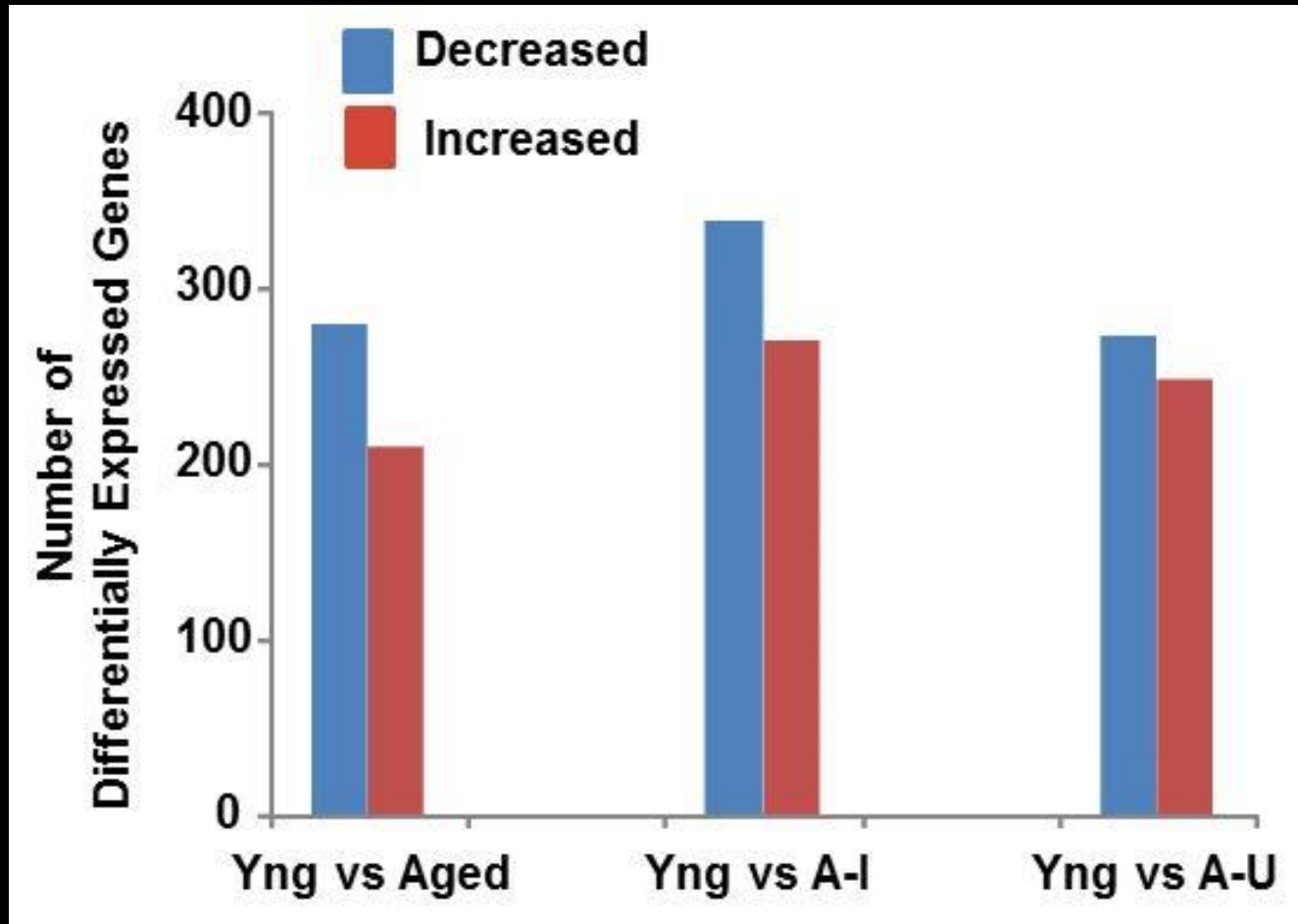


DNA to UAB

Other tissues have been processed or banked



N = 5 young, 11 aged



Decreased

Synaptic Transmission
Regulation of Transcription

Increased

Antigen Processing
Immune Response
Cell Death

Options **Classification Stringency** Medium ▾

Rerun using options

Create Sublist

105 Cluster(s)

[Download File](#)

Annotation Cluster 1		Enrichment Score: 3.01			Count	P_Value	Benjamin
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane part	RT		43	3.8E-4	2.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane	RT		63	1.6E-3	4.2E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	membrane	RT		81	1.6E-3	6.4E-2
Annotation Cluster 2		Enrichment Score: 2.84			Count	P_Value	Benjamin
<input type="checkbox"/>	GOTERM_BP_FAT	synaptic transmission	RT		15	3.3E-5	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	synapse part	RT		16	8.0E-5	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	transmission of nerve impulse	RT		16	1.5E-4	4.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	synapse	RT		19	2.0E-4	2.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	postsynaptic membrane	RT		11	2.0E-4	2.0E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	synapse	RT		13	3.2E-4	2.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cell-cell signaling	RT		16	7.5E-4	1.5E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	postsynaptic cell membrane	RT		9	9.8E-4	5.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cell junction	RT		18	2.8E-3	6.7E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell junction	RT		14	3.7E-3	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	postsynaptic density	RT		6	1.8E-2	2.5E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell membrane	RT		26	1.7E-1	6.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	neurological system process	RT		23	9.9E-1	1.0E0
Annotation Cluster 3		Enrichment Score: 2.79			Count	P_Value	Benjamin
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear lumen	RT		33	3.3E-4	2.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-enclosed lumen	RT		40	5.8E-4	2.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular organelle lumen	RT		38	6.7E-4	2.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoplasm part	RT		19	9.0E-4	2.9E-2



Gene Report

Current Gene List: List_1

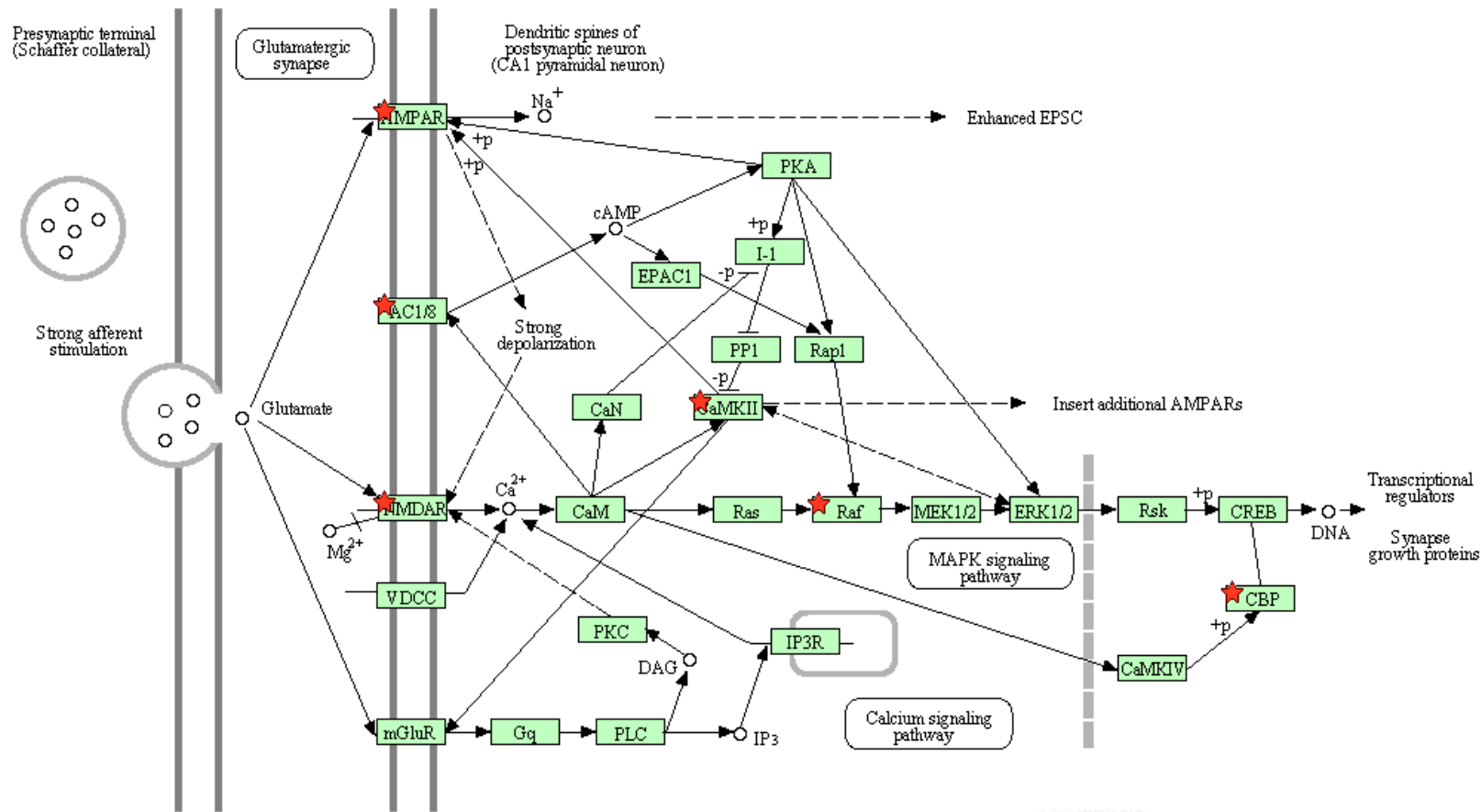
Current Background: *Rattus norvegicus*

352 DAVID IDs

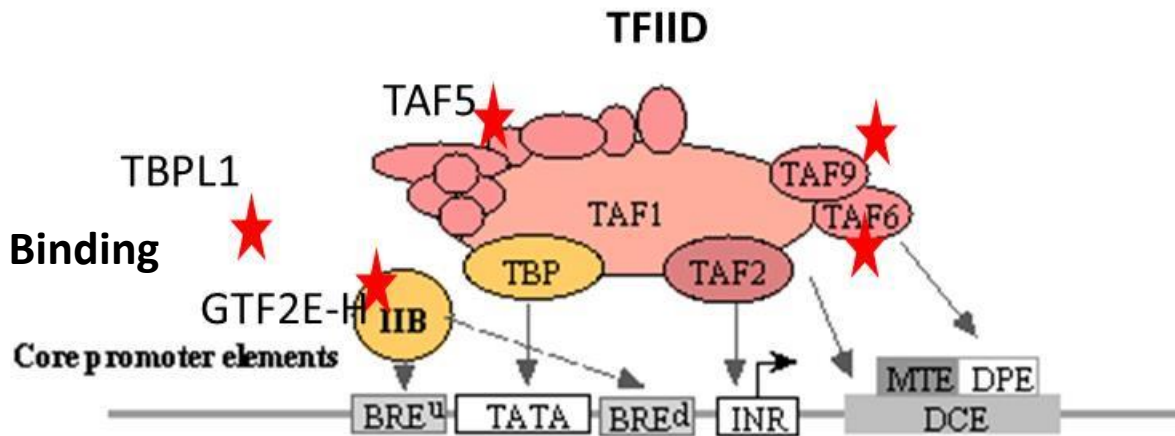
15 record(s)

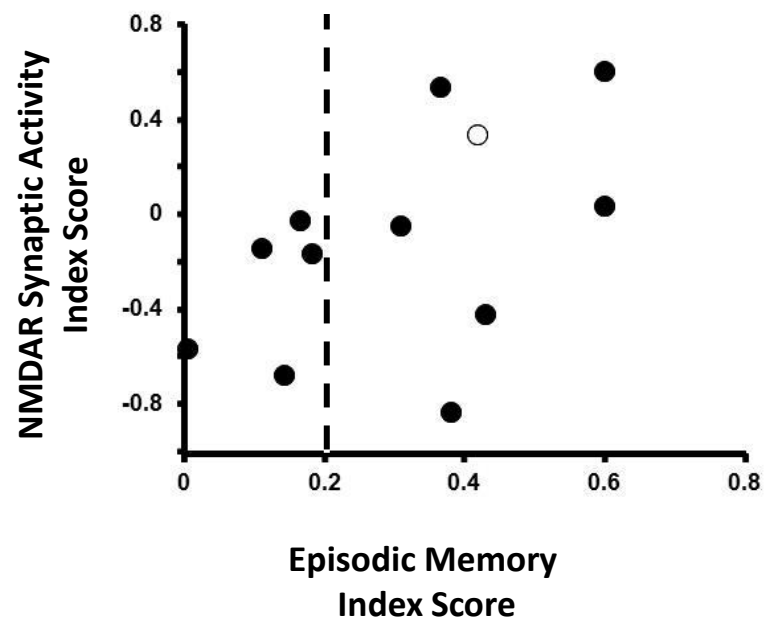
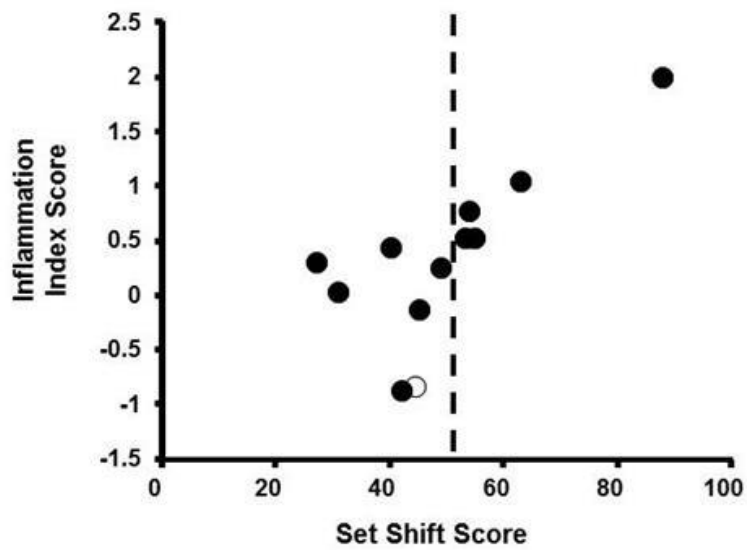
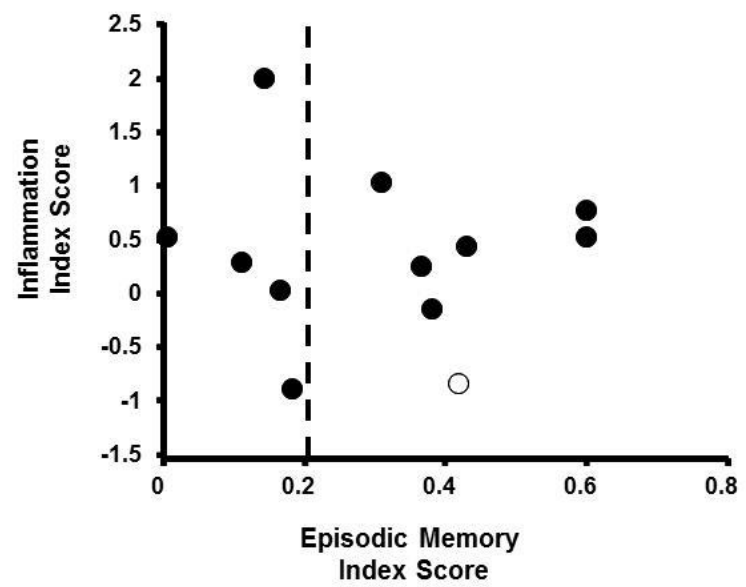
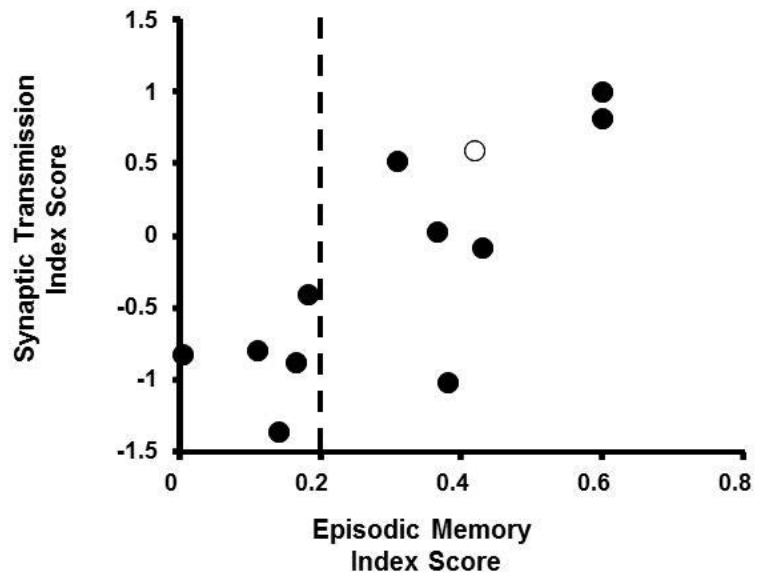
OFFICIAL_GENE_SYMBOL	GENE NAME	Related Genes	
Acp2	acid phosphatase 2, lysosomal	RG	Ratt
Agrn	agrin	RG	Ratt
Atxn1	ataxin 1	RG	Ratt
Ctnna2	catenin (cadherin associated protein), alpha 2	RG	Ratt
Gria1	glutamate receptor, ionotropic, AMPA 1	RG	Ratt
Grin2b	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	RG	Ratt
Grid2	glutamate receptor, ionotropic, delta 2	RG	Ratt
Lin7a	lin-7 homolog a (C. elegans)	RG	Ratt
Ncan	neurocan	RG	Ratt
Nlgn1	neuroligin 1	RG	Ratt
Nlgn3	neuroligin 3	RG	Ratt
Npy	neuropeptide Y	RG	Ratt
Syn3	synapsin III	RG	Ratt
Unc13a	unc-13 homolog A (C. elegans)	RG	Ratt
Unc13b	unc-13 homolog B (C. elegans)	RG	Ratt

Long-Term Potentiation



Transcription Factor Binding





**Behavioral
Characterization**

Asha Rani

Ashok Kumar

Jen Bizon

Barry Setlow

Sofia Beas

Sarah Burke

Drew Maurer

**Transcription &
DNA methylation**

Laura Ianov

Linda Bean

Leonid Moroz

Andrea Kohn

Alberto Riva

Jason Frazier

Scott Harden

**Supported by the McKnight Brain Research Foundation
and NIA**