

Sex-specific transcriptional signatures of depression



Marianne Seney, Ph.D
Assistant Professor
Translational Neuroscience Program
Department of Psychiatry
University of Pittsburgh



Major Depressive Disorder (MDD)

- Chronic, recurrent disease of altered mood regulation
- ~19 million people affected each year in the US (Kessler, 2003)
- ~15% lifetime mortality due to suicide (Mann, 2003)
- Complex disease with many contributing genes that interact with environmental factors

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- Complex disease with many contributing genes that interact with environmental factors
- Very few new pharmacological approaches in the last 50 years

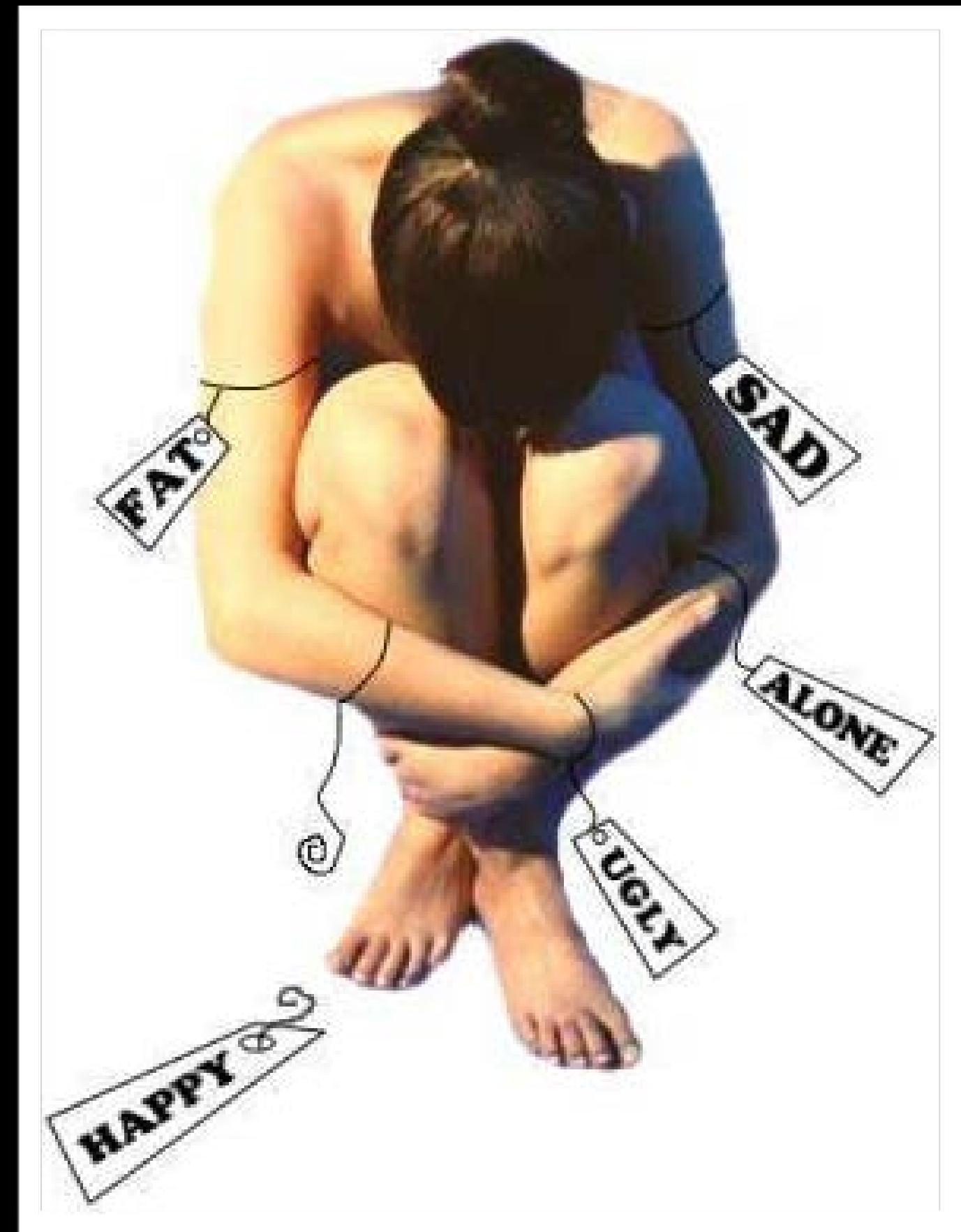
Sex differences in depression

Differences in Incidence

- Females are 2x as likely to have a single episode, and 4x as likely to have recurrent MDD

Differences in Clinical Phenotypes

- Symptom number, severity, subjective distress: F > M
- Hyperphagia and hypersomnia: F > M
- Comorbid anxiety disorder: F > M
- Comorbid substance abuse: M > F



Do these findings reflect sex differences in the biological pathways to MDD and/or sex-specific brain pathology?

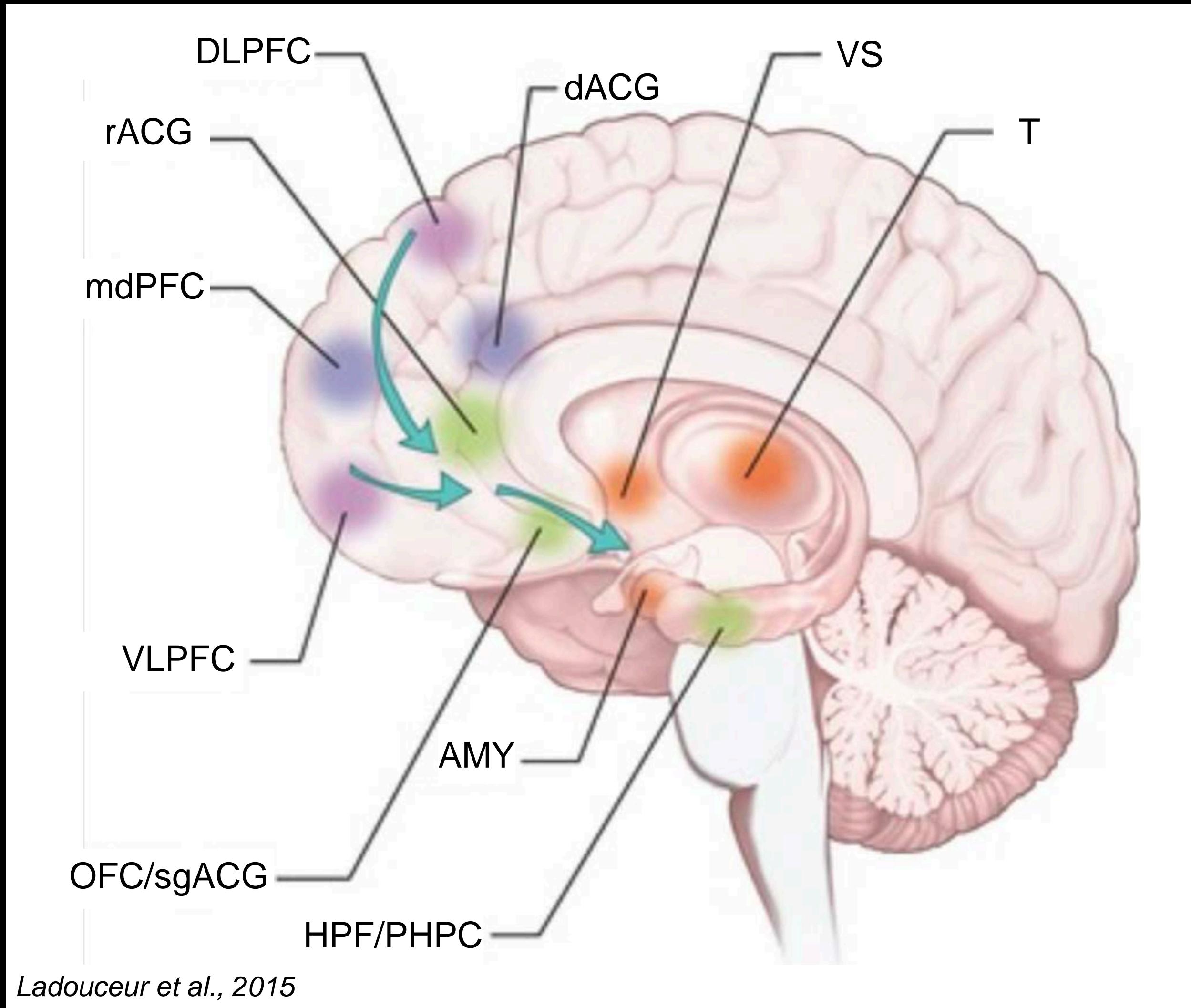
Could such pathways inform sex-specific treatment development?

Molecular pathology in depression: men vs. women

- Hypothesis 1: Men and women have the same pathology, with potential modulation by sex-related factors.
 - Prediction 1: Similar molecular changes in the brains of men and women with MDD.
- Hypothesis 2: The pathology is different in men and women.
 - Prediction 2: Distinct molecular changes in the brains of men and women with MDD.

In either case, knowing the pathology can help us develop novel, possibly sex-specific treatments

Investigate sex differences in gene expression in mood-related brain circuitry



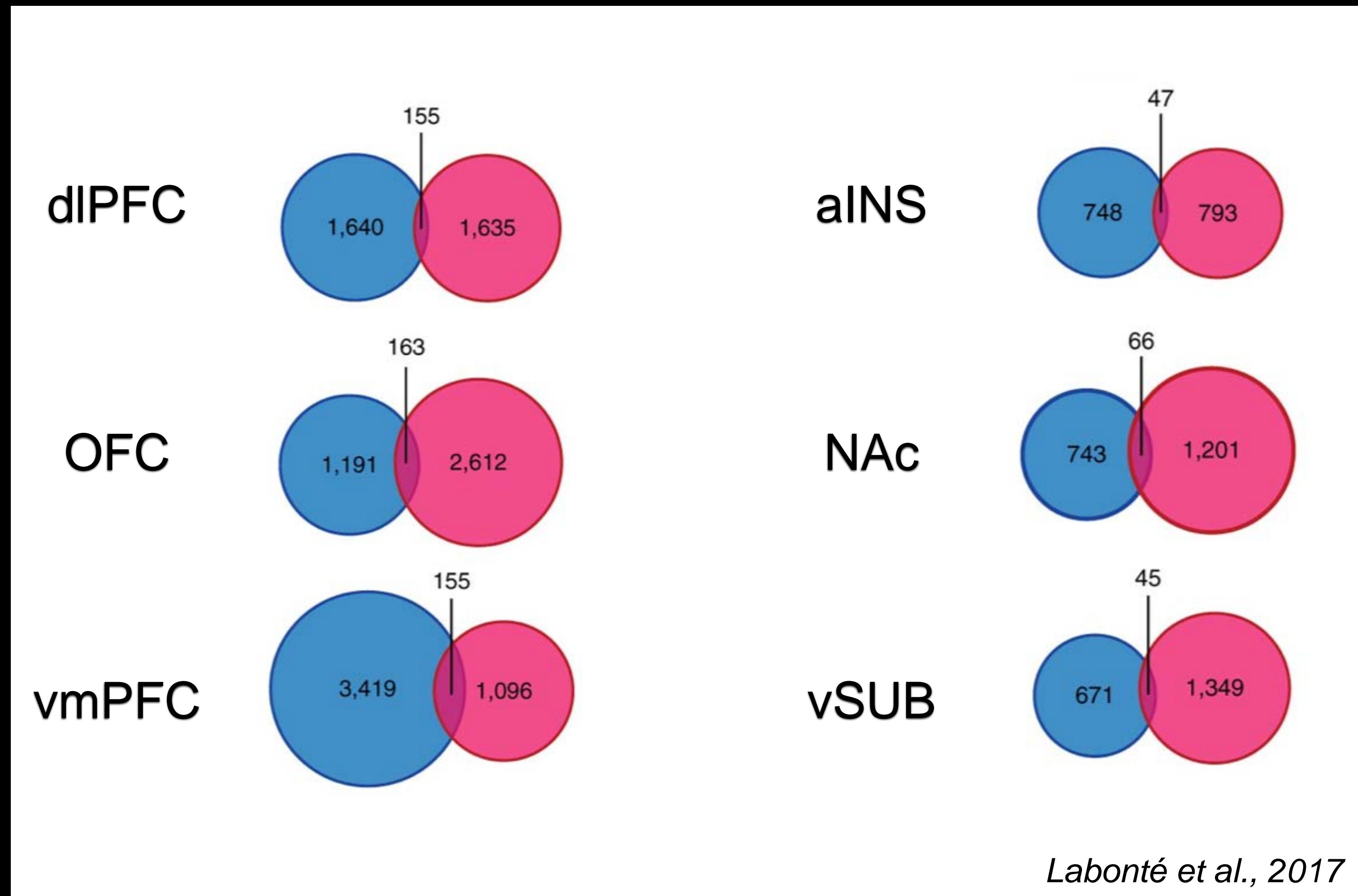
- Human postmortem brain studies: directly examine the diseased organ

Candidate gene vs. large-scale transcriptomics approaches

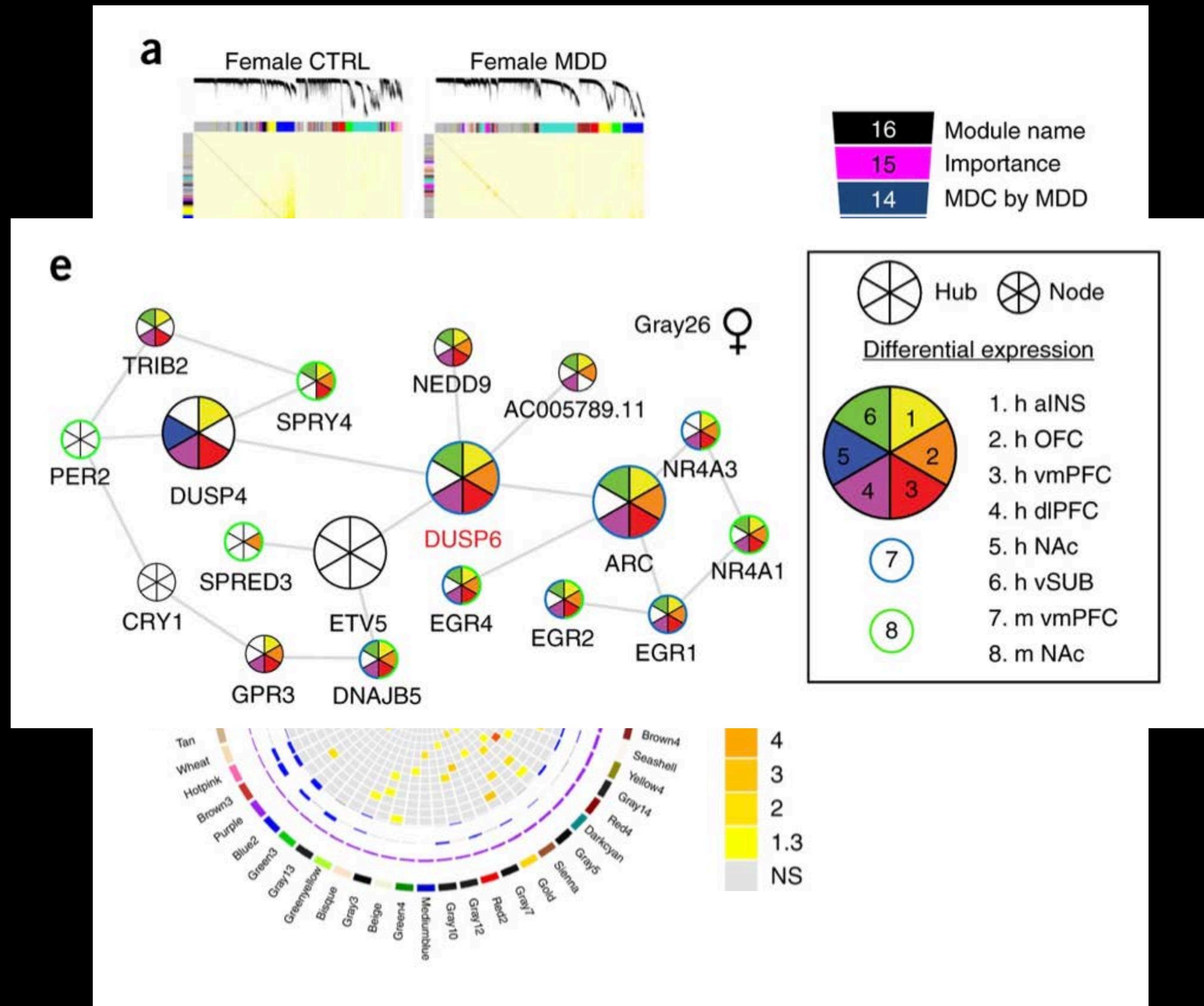
- **Candidate gene studies:** uncovered potential “hits” for MDD molecular alterations - e.g., GABA-, glutamate-, serotonin-, inflammation-related.
 - Presume that we already know the pathways that should be disrupted in MDD.
- **Unbiased large-scale transcriptomics (microarray, RNA-seq):** data can be used for network-based approaches to identify key drivers of transcriptional patterns.
 - Previous studies included only one sex or were not powered to detect sex differences.
 - Conclusions could: 1) be biased towards male-specific alterations; or 2) only detect alterations consistent between males and females.

First large-scale transcriptomics study assessing potential sex-specific MDD pathology

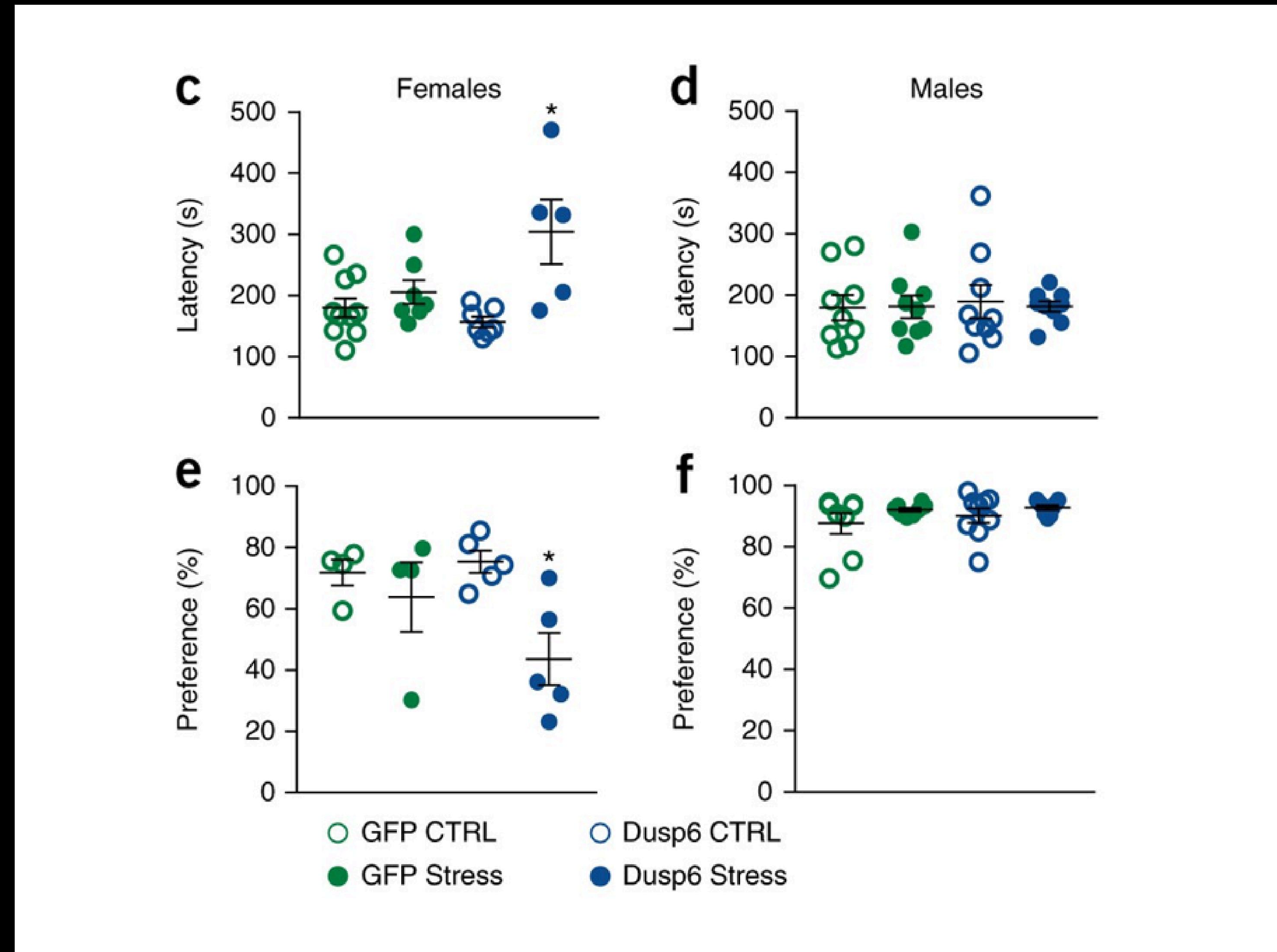
- Labonté et al., *Nature Medicine*, 2017 (Nestler Lab)



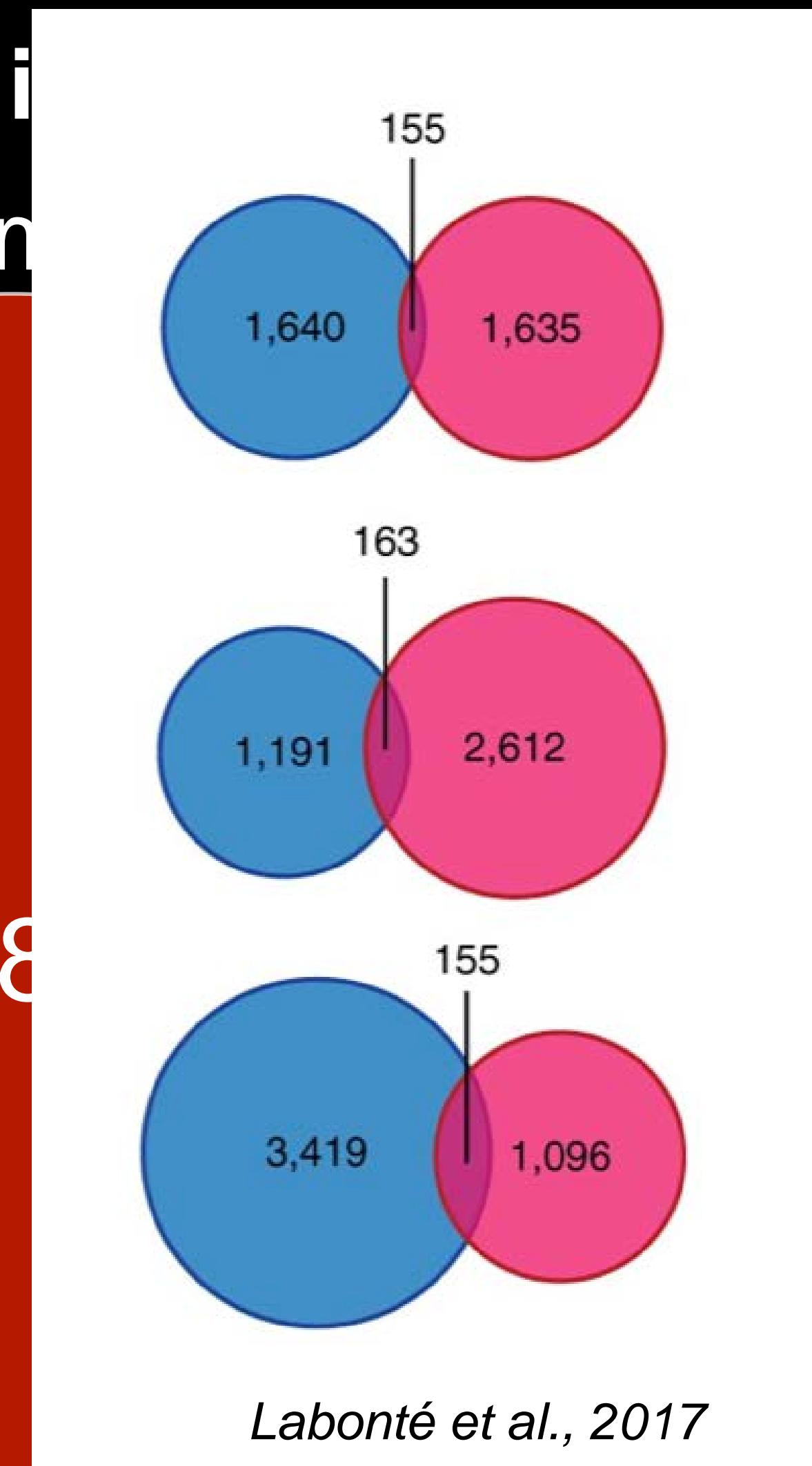
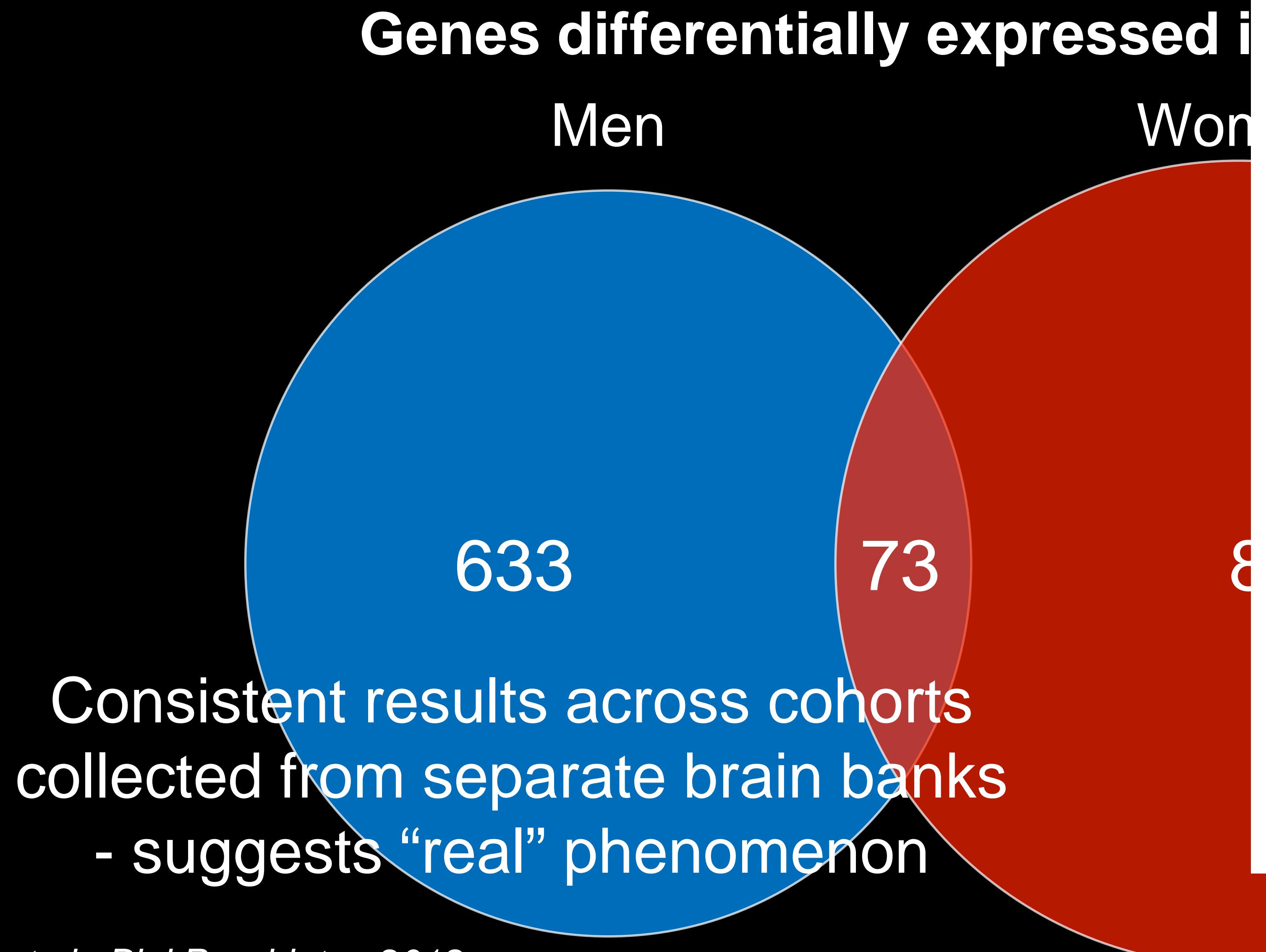
Network-based methods to identify potential upstream drivers of female vulnerability



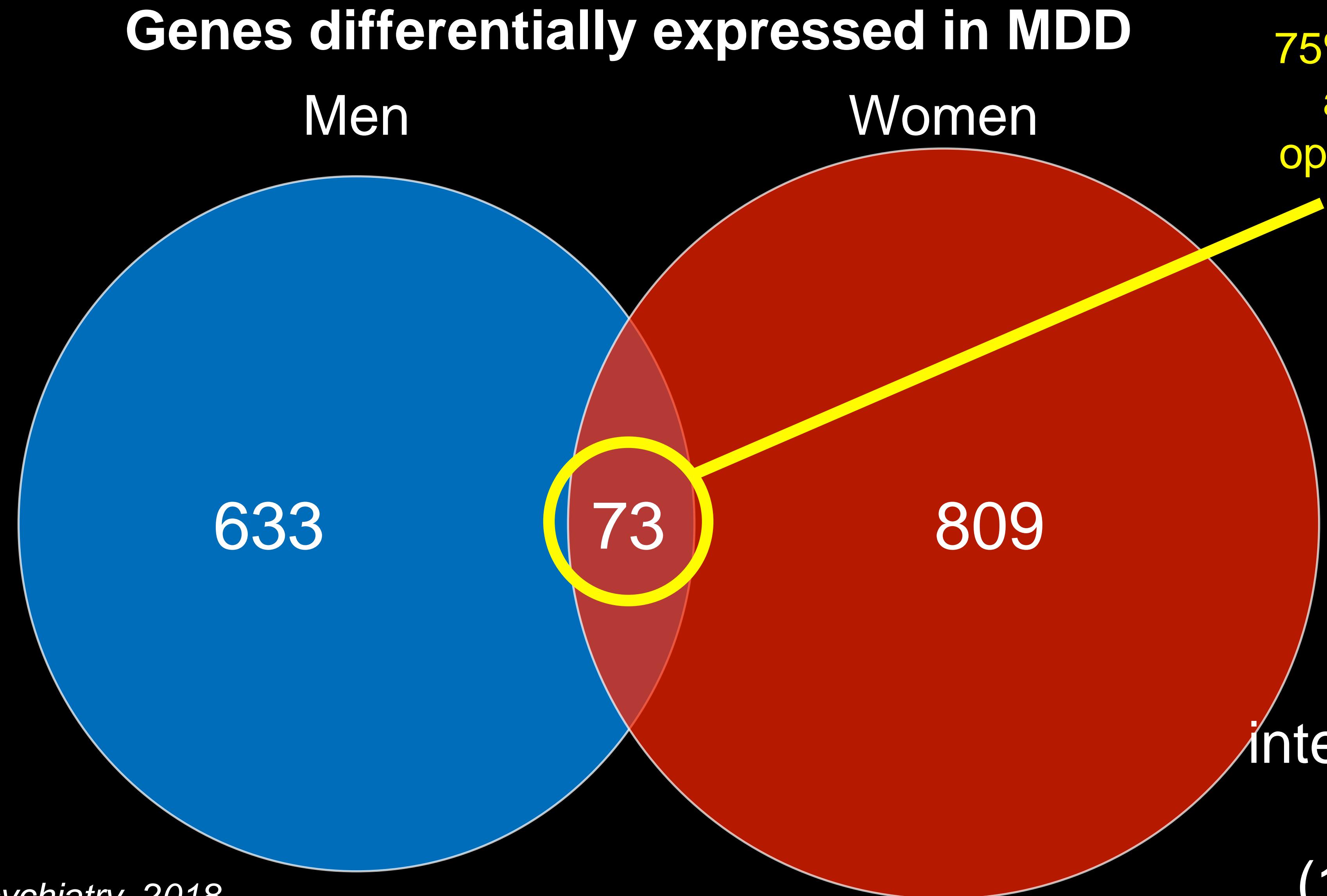
Experimental reduction of *Dusp6* in PFC of mice drives female-specific vulnerability to stress



Distinct molecular signatures of MDD in men and women

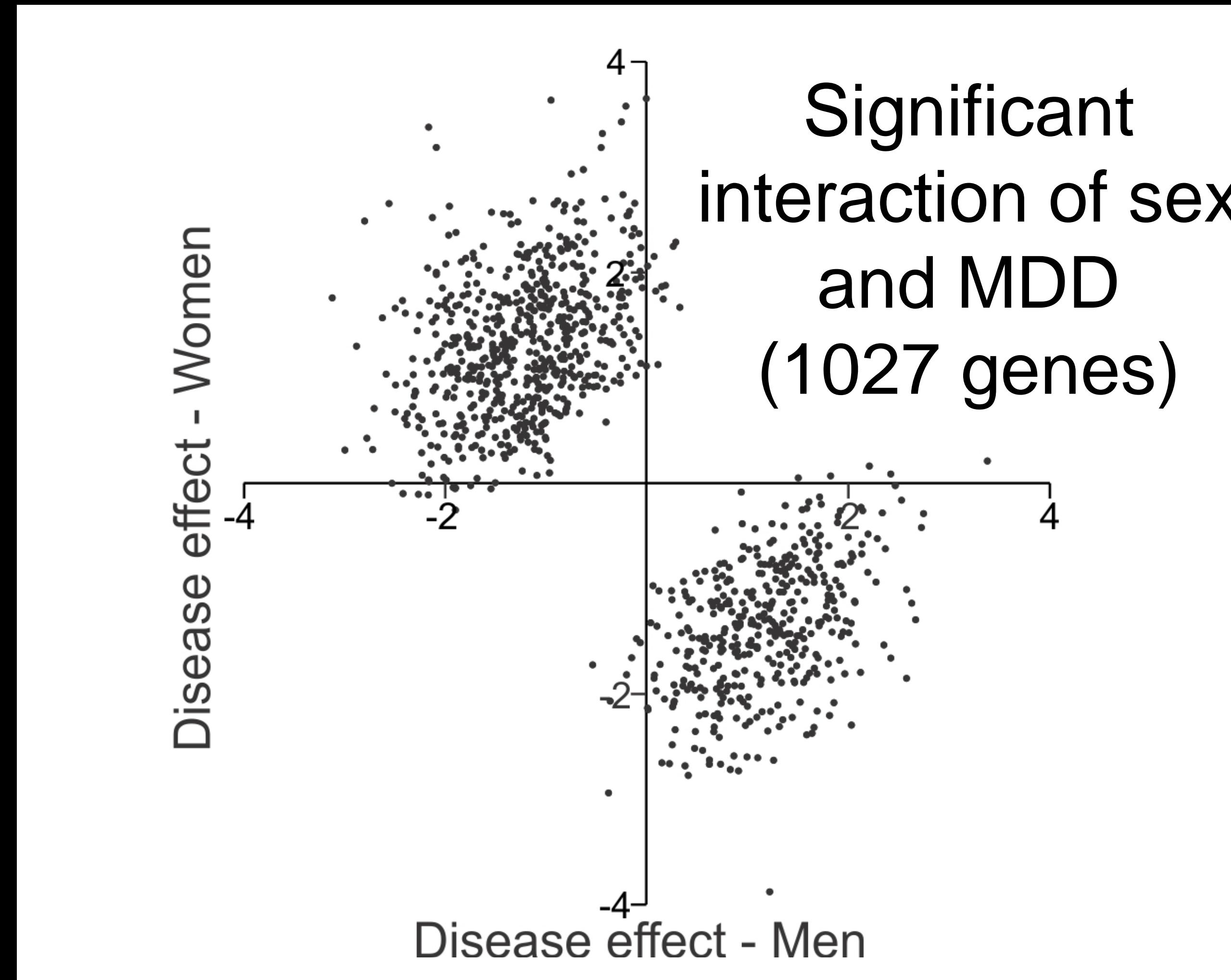


Opposite direction of disease effect in men and women



75% of these genes are changed in opposite directions!

Opposite direction of disease effect in men and women



What pathways and cell types are represented by genes with significant interactions of sex and MDD?

	p-value	Men	Women
		Direction	Direction
Regulation of synapse structure or activity	$< 10^{-8}$	↓	↑
Regulation of synapse organization	$< 10^{-7}$	↓	↑
Neurons	< 0.12	↔	↑
MHC protein complex	$< 10^{-7}$	↑	↓
Antigen processing and presentation	$< 10^{-7}$	↔	↓
Microglia	$< 10^{-7}$	↑	↓

Sex differences in synapse- and immune-related changes in MDD

Take-home messages

- Well-powered, large-scale transcriptional studies have uncovered novel insights into sex-specificity of brain pathological changes in MDD.
- Very little overlap in consistent molecular alterations in depressed men and women.
- Together, these studies have uncovered novel targets for future treatment development - sex specific MDD treatment



Special Thanks!

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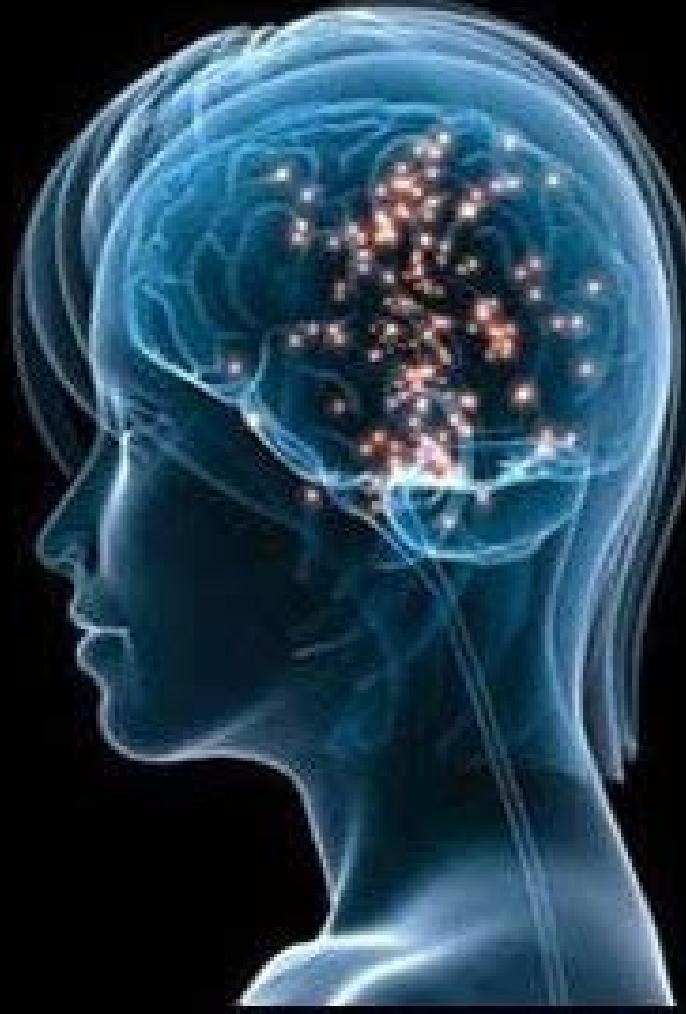
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Kelly Cahill

Rachel Puralewski

Joyce Zhang

Leon French



Collaborators

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Etienne Sibille - University of Toronto, CAMH

Kenneth Fish - University of Pittsburgh

Ryan Logan - University of Pittsburgh

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