



- GROUPS...CONFIRM WEBSITE

A small toolbar at the top left of the slide contains several icons: a close button (X), a play button (green triangle) with 'A-E' next to it, a list icon (three vertical bars), and a settings icon (gear).

# Autism Spectrum Disorder (ASD)

- ~1% American adults
- Higher recent estimates (1 in 50 births)
- Males 4x more likely
- Familial association
- Possible associated with older parents
- Savant phenotypes ~10%



# ASD Drug Treatments

**NO drugs for specifically treating ASD**

**Antipsychotics and Antidepressants sometime prescribed for symptoms**

■ Telencephalon

Cerebral Cortex

Corpus Collosum

Amygdala

Hippocampus

■ Diencephalon

Thalamus

Hypothalamus

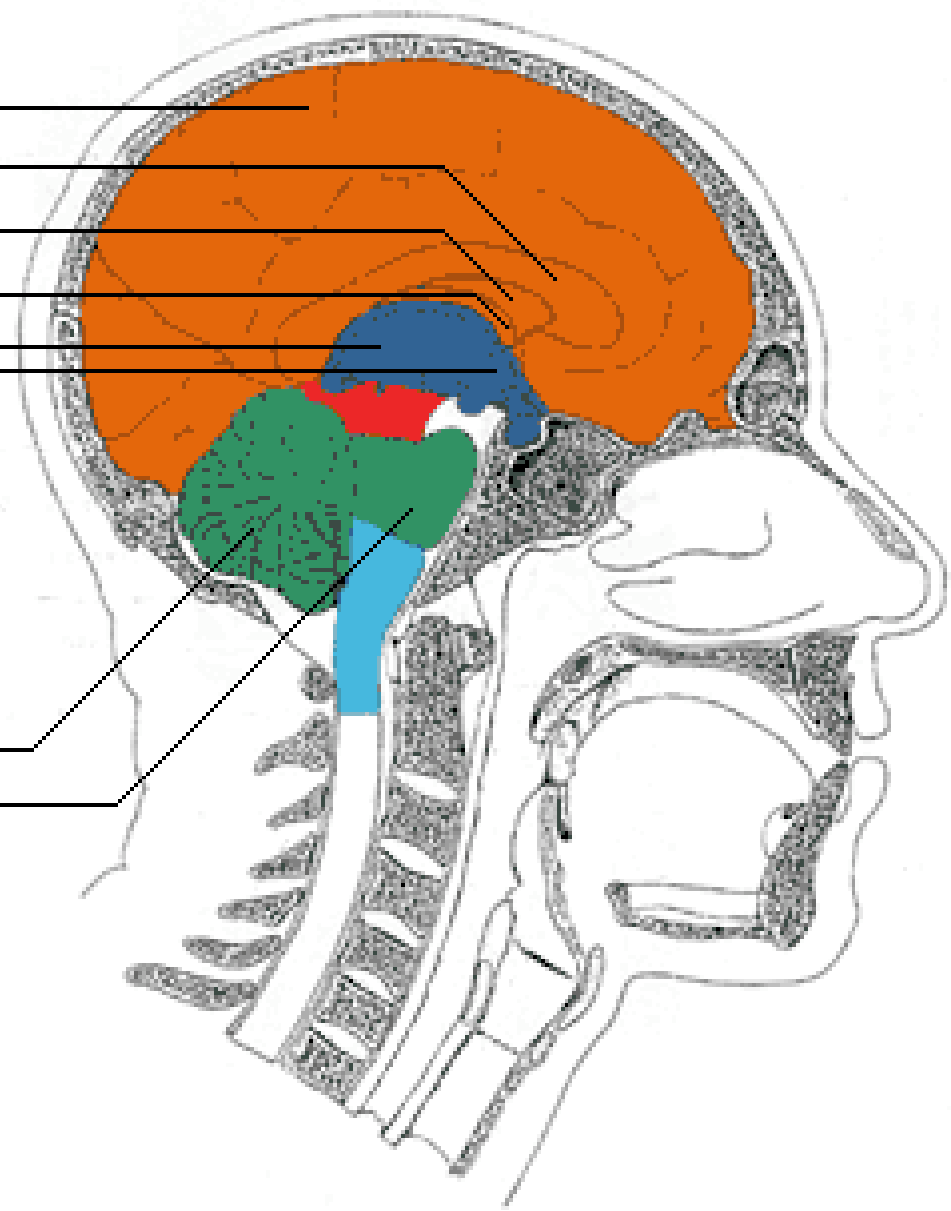
■ Mesencephalon

■ Metencephalon

Cerebellum

Pons

■ Myelencephalon

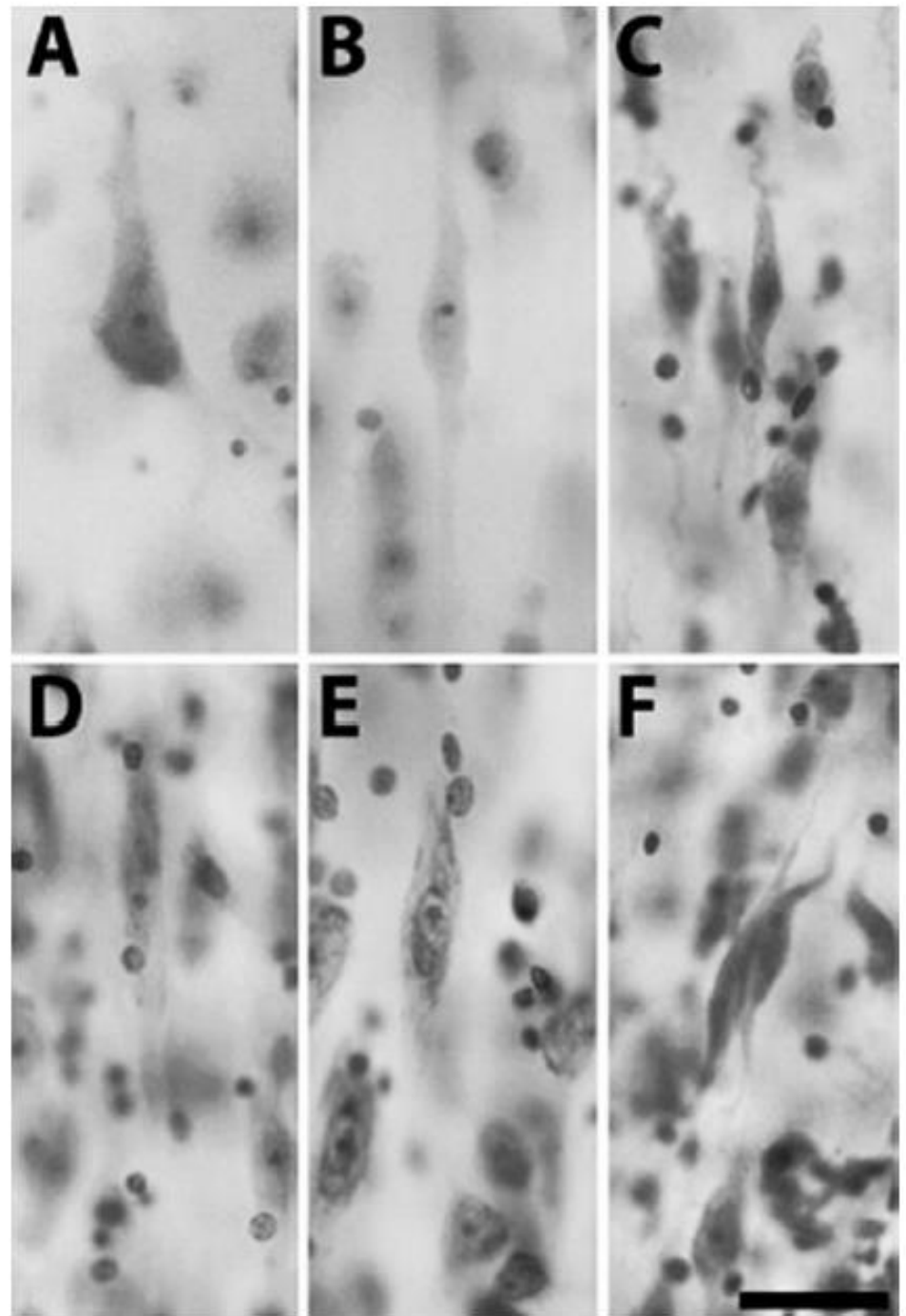




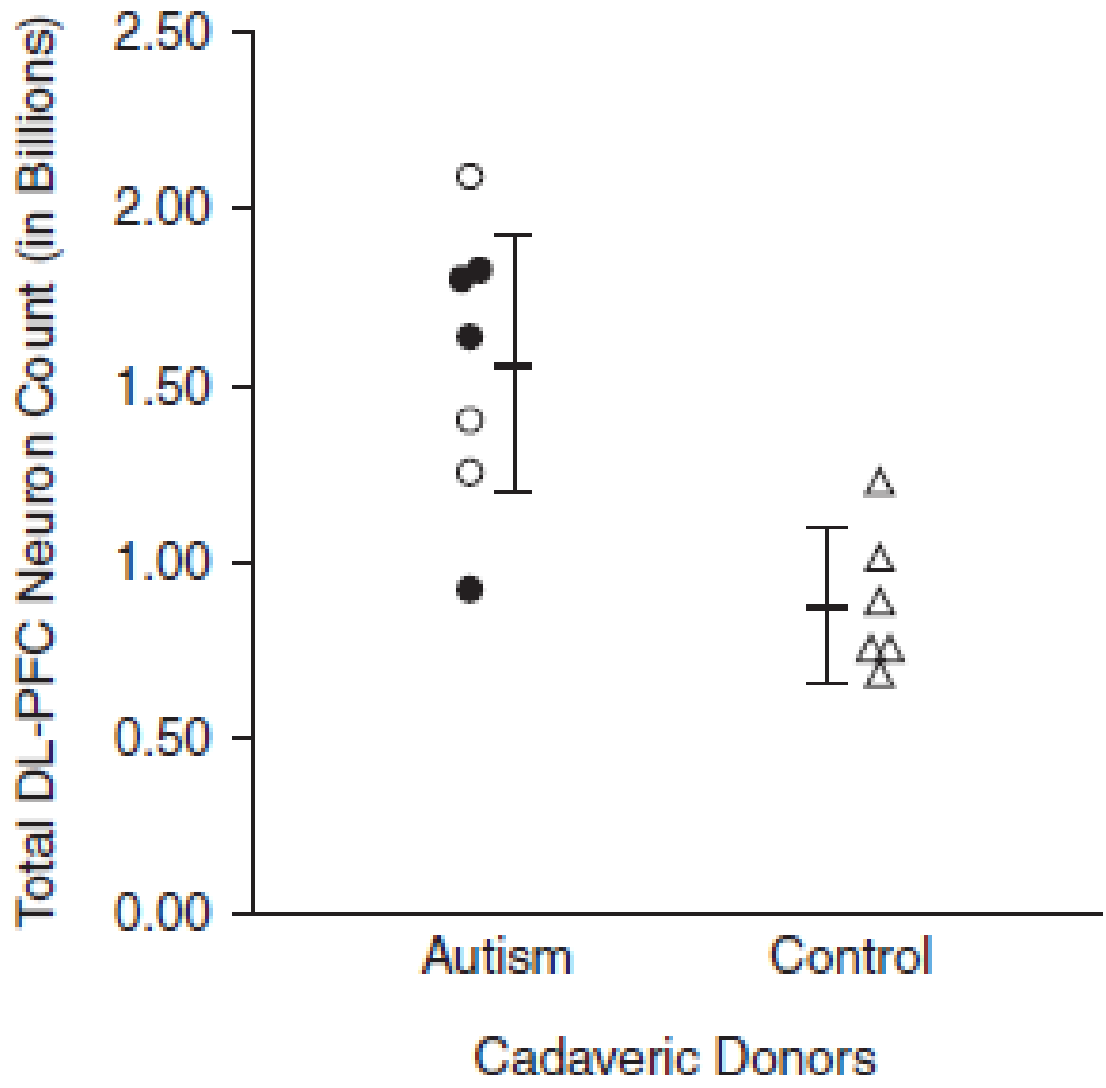
Cell counting using these images is

- A. Objective
- B. Somewhat subjective
- C. Error free
- D. A and C

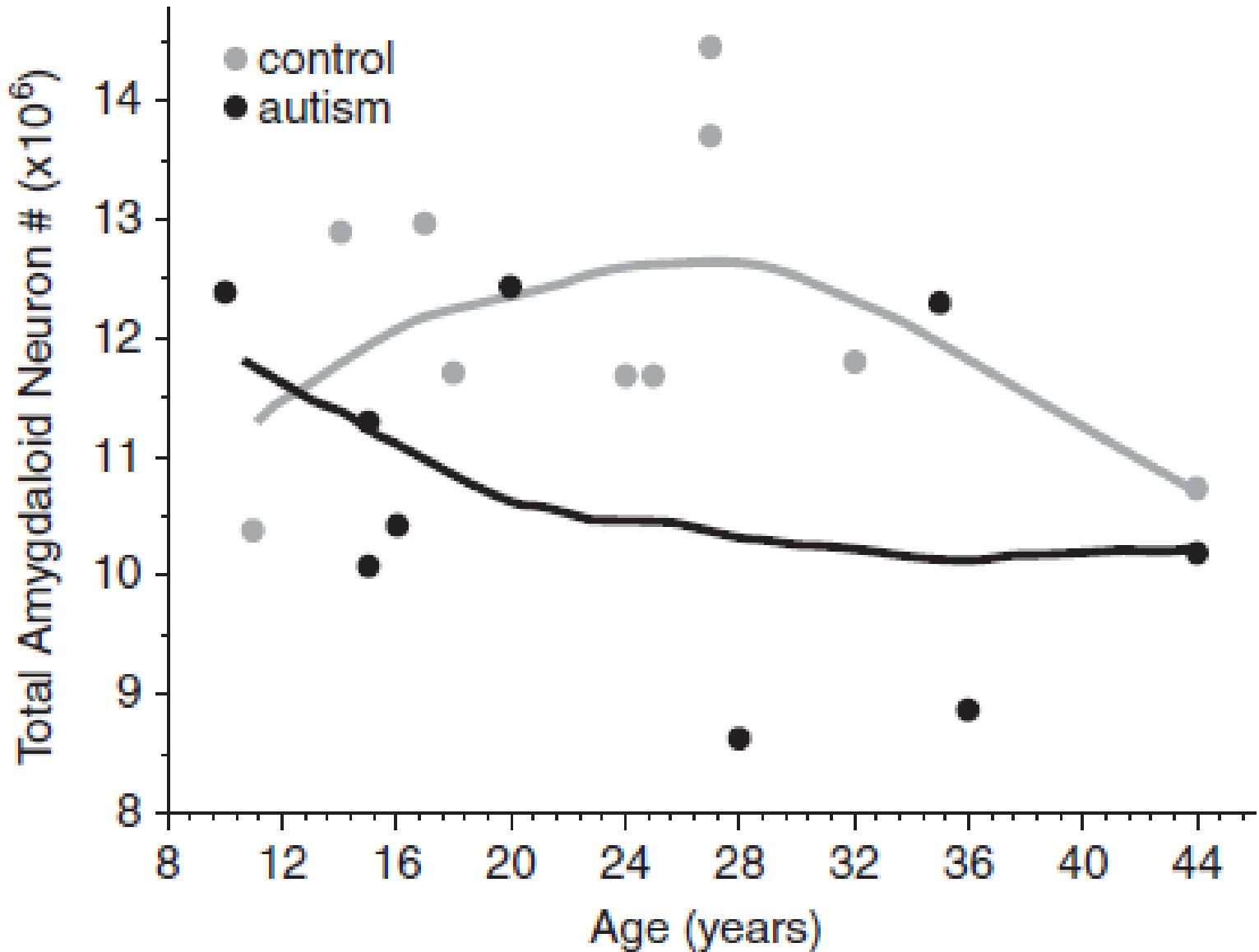
WHY?



### Dorsolateral prefrontal cortex neuron count



Team Workshop 1: How would you fit this data and what conclusions would you make?





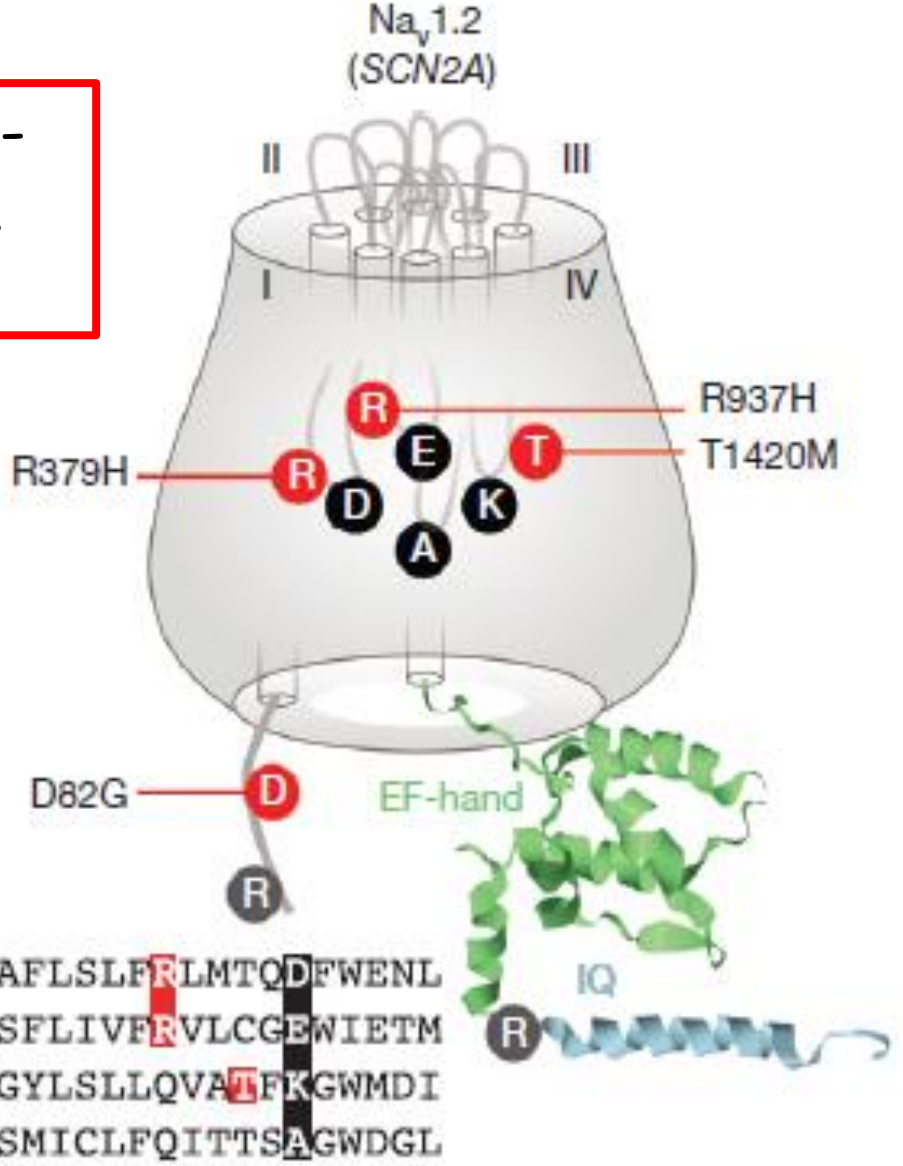
The exome sequence corresponds to

- A. All the DNA of the genome except the introns
- B. Only the intron sequence
- C. Only the protein coding mRNA sequence
- D. Only the major splice variant mRNA sequence
- E. None of the above

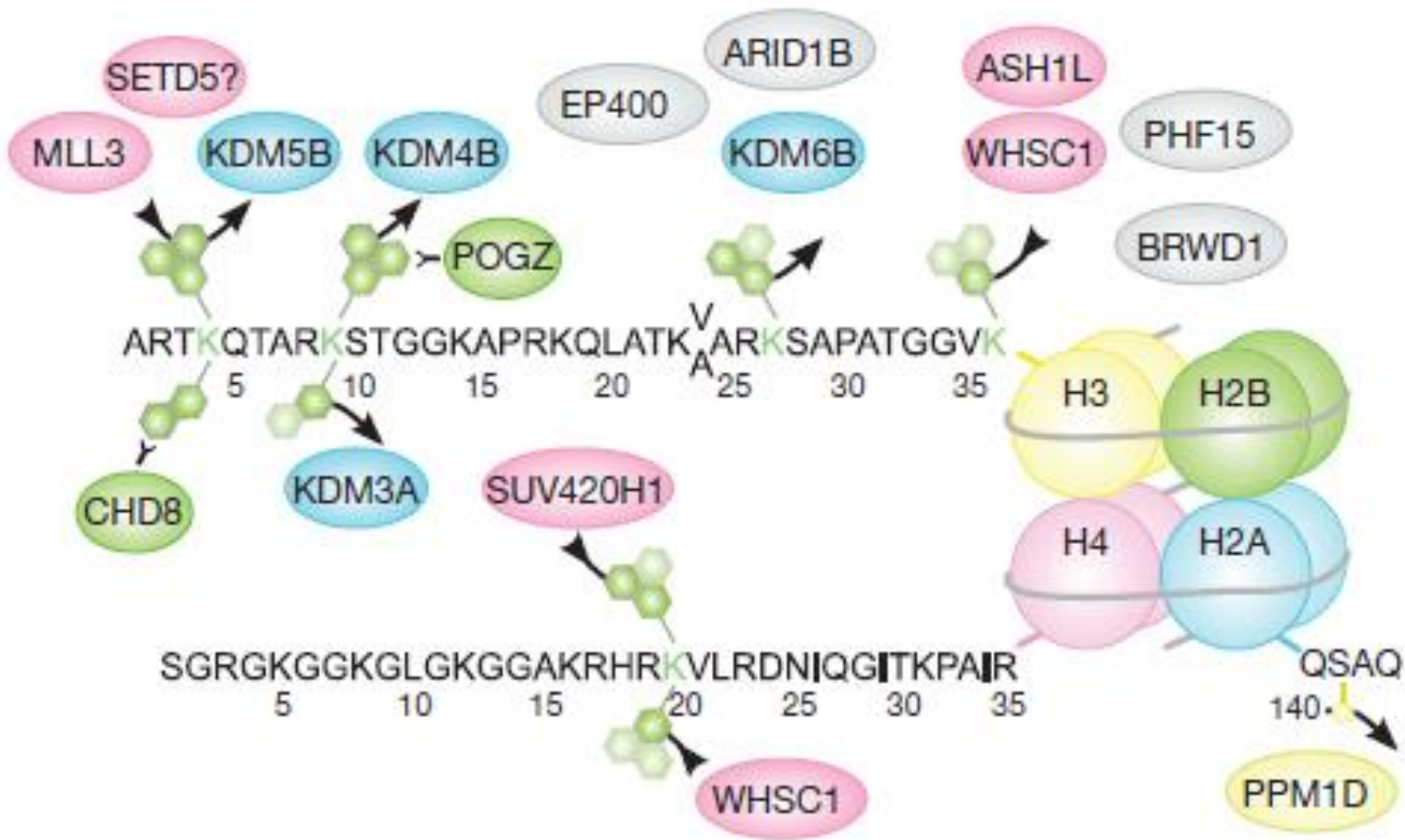


Team Workshop 2: How can ion-selectivity mutations in SCN2A relate to disease

c



- Mutated in this study
- Mutated in previous studies
- Ion-selectivity filter



Team Workshop 3: List the possible outcomes of altered Lysine methylation or demethylation



**Table 1 | ASD risk genes**

dnLoF count	FDR $\leq$ 0.01	0.01 < FDR $\leq$ 0.05	0.05 < FDR $\leq$ 0.1
$\geq 2$	<i>ADNP, ANK2, ARID1B, CHD8, CUL3, DYRK1A, GRIN2B, KATNAL2, POGZ, SCN2A, SUV420H1, SYNGAP1, TBR1</i>	<i>ASXL3, BCL11A, CACNA2D3, MLL3</i>	<i>ASH1L</i>
1		<i>CTTNBP2, GABRB3, PTEN, RELN</i>	<i>APH1A, CD42BPB, ETFB, NAA15, MYO9B, MYT1L, NR3C2, SETD5, TRIO</i>
0		<i>MIB1</i>	<i>VIL1</i>

TADA analysis of LoF and damaging missense variants found to be *de novo* in ASD subjects, inherited by ASD subjects, or present in ASD subjects (versus control subjects). dnLoF, *de novo* LoF events.

Team Workshop 4: Which, if any, of these genes are sex linked?

If so why and if not, why?



# Remember

- Before 12 PM of the next class day:
  - go to [b.socrative.com/student/login](https://b.socrative.com/student/login) and complete the quiz