

## INTRODUCTION

Research has examined regulatory converging networks and shared deficiencies in neural growth pathways, including genes targeted by CHD8, a gene strongly associated with ASD (Cotney et al., 2015). One of the most prominent phenotypes in CHD8 is macrocephaly (Bernier et al., 2014; Barnard, Pomaville, & O'Roak, 2015). Despite the relevance of head size to brain development, growth trajectories have not been examined across functional gene classifications.

### METHOD

Head circumference (HC) measurements derived from medical records & medical examination at the research visit were evaluated for 94 participants (female n=39, male n=55) with a disruptive mutation to an ASDassociated gene. Participants were characterized as Macrocephalic or Microcephalic if they met criteria at any time point (i.e. +/- 2 population-based z-scores).



#### **Gene Categorization Criteria** (Cotney et al., 2015; Sugathan 2014)

	CHD8 Target Gene	Other Gene		Non- Ge
CHD8 binding site	$\checkmark$			
CHD8 co- expression	$\checkmark$	Mixed evidence		
Expressed in human brain	$\checkmark$			
Specific	CHD8	ADNP	MYH10	A
genes	ARID1B	ASH1L	NCKAP1	CA
	CTNNB1	CHD1	POGZ	DS
	PTEN	CHD2	SCN2A	GR
	SETBP1	DYRK1A	SETD2	LAF
	TBL1X41	FOXP1	SUB420H1	ST>
	TRIP12	KDM6B	SYNCRIP	TE
		LZTR1	WDFY3	
		MED13L	WDR33	

# A Comparison of Head Circumference **Growth Trajectories** in the Context of the CHD8 Regulatory Network

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Functional gene classifications of CHD8 and its target variants in the CHD8 regulatory network relative to non-targets and to other non-associated genes did not reveal consistent and non-overlapping growth trajectories.

Head circumference growth patterns among individuals with ASD-associated disruptive gene events differ significantly between discrete macrocephalic and microcephalic groups.

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Macrocephaly n=22 Microcephaly n=19

> Target iene

NK2 PN8 CAM IN2B RP4B XBP **3R**1



Best fitting random effect linear models (via MPLUS) indicated that HC increased linearly with a quadratic deceleration with age,  $\beta = -.11$ , SE = .02, p < .001. There was no main effect of CHD8 regulatory group, indicating that all groups exhibited similar growth trajectories.



Barnard, R., Pomaville, M., & O'Roak, B. (2015). Mutations and Modeling of the Chromatin Remodeler CHD8 Define an Emerging Autism Etiology. Frontiers In Neuroscience, 9: 477. Bernier, R., et al. (2014). Disruptive CHD8 Mutations Define a Subtype of Autism Early in Development. Cell, 158(2): 263-276. Cotney, J. et al. (2015). The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nat. Commun. 10(6): 6404. Courchesne, E., Campbell, K., & Solso, S. (2011). Brain growth across the life span in autism: Age-specific changes in anatomical pathology. Brain Research, 1380: 138-145. Shen, M.D. et al. (2013). Early brain enlargement and elevated extra-axial fluid in infants who develop autism spectrum disorder, Brain, 136(9): 2825-2835 Sugathan, A., et al. (2014). CHD8 regulates neurodevelopmental pathways associated with autism spectrum disorder in neural progenitors. Proceedings of the National Academy of Sciences of the United States of America. 111(42):E4468-77.



# RESULTS

	Quadratic		
Effect/Group	β	SE	р
Age	-0.11	0.02	<.001
CHD8 Target	-1.51	0.21	<.001
Non-Target	-1.24	0.65	0.058
Other	-1.2	0.12	<.001
Microcephaly	-0.98	0.19	<.001
Macrocephaly	-1.28	0.21	<.001
Normal HC	-1.29	0.12	<.001

## DISCUSSION

Analyses of functional gene classifications in the context of the CHD8 regulatory network did not reveal significant differences in head circumference growth trajectories.

This functional gene classification may not have sufficient specificity to predict head growth at this time. Other limitations may include the study being underpowered; miscategorization of genes, which could include unknown causal mechanisms in the Other Gene category; and/or that a real effect may be occurring but it is too small to be captured by the current analyses.

Grey matter overgrowth in the first years of life (Courchesne, Campbell, & Solso, 2011) and atypical levels of cerebral fluids (Shen et al., 2013) are common in ASD and may contribute to macro- and microcephalic phenotypes. Further exploration of HC phenotypes and their possible associations with genomic subtypes of ASD may provide clues to the neurobiological and developmental etiology of neurodevelopmental disorders.