

## Overview of neuroimaging phenotypes

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Researchers have used various neuroimaging measurements as quantitative **endophenotypes** in genetic analyses to look for the **biological processes** that underlie functional and structural brain variability.

Neuroimaging endophenotypes are **intermediate steps** between the molecular and behavioural levels, and should be **more easy to relate to biological processes** than behavioural phenotypes.

**Which endophenotypes are available** through neuroimaging and **which biological processes** shape them?

# 2

Two different timescales can be distinguished: The common aspects of brain development, shaped by our **evolutionary history**, and the individual plastic changes, reflecting our **life-long experiences**.

**Heritability** analyses (in twin or extended pedigree studies) suggest that inheritable factors largely determine various structural properties of the brain, supporting the use of neuroimaging endophenotypes in the research for the genetic causes of psychiatric diseases.

# 3

The precise genetic causes of this high heritability remain, however, **largely unknown.**

In the last 10 years, the research for these genetic causes has been tackled through the study of **candidate genes** and biological pathways. More recently, agnostic **genome-wide** association has been successfully used to discover new candidates for brain variability and psychiatric disorders.

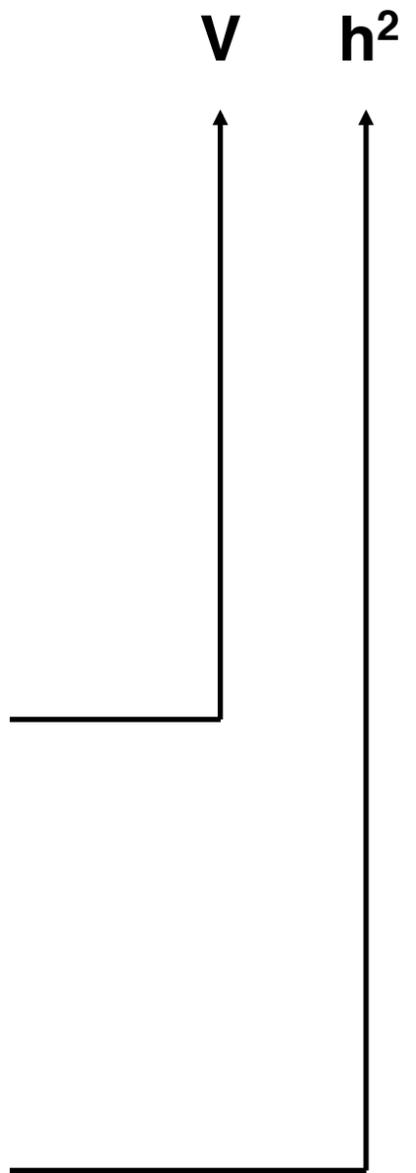
early development  
  rostrocaudal axis  
cortical development  
  mitosis  
  apoptosis  
  neuropil develop.  
connectivity  
  axon growth  
  myelination  
maturation  
  puberty  
  aging  
  plasticity

Gene:  
***MECP2***

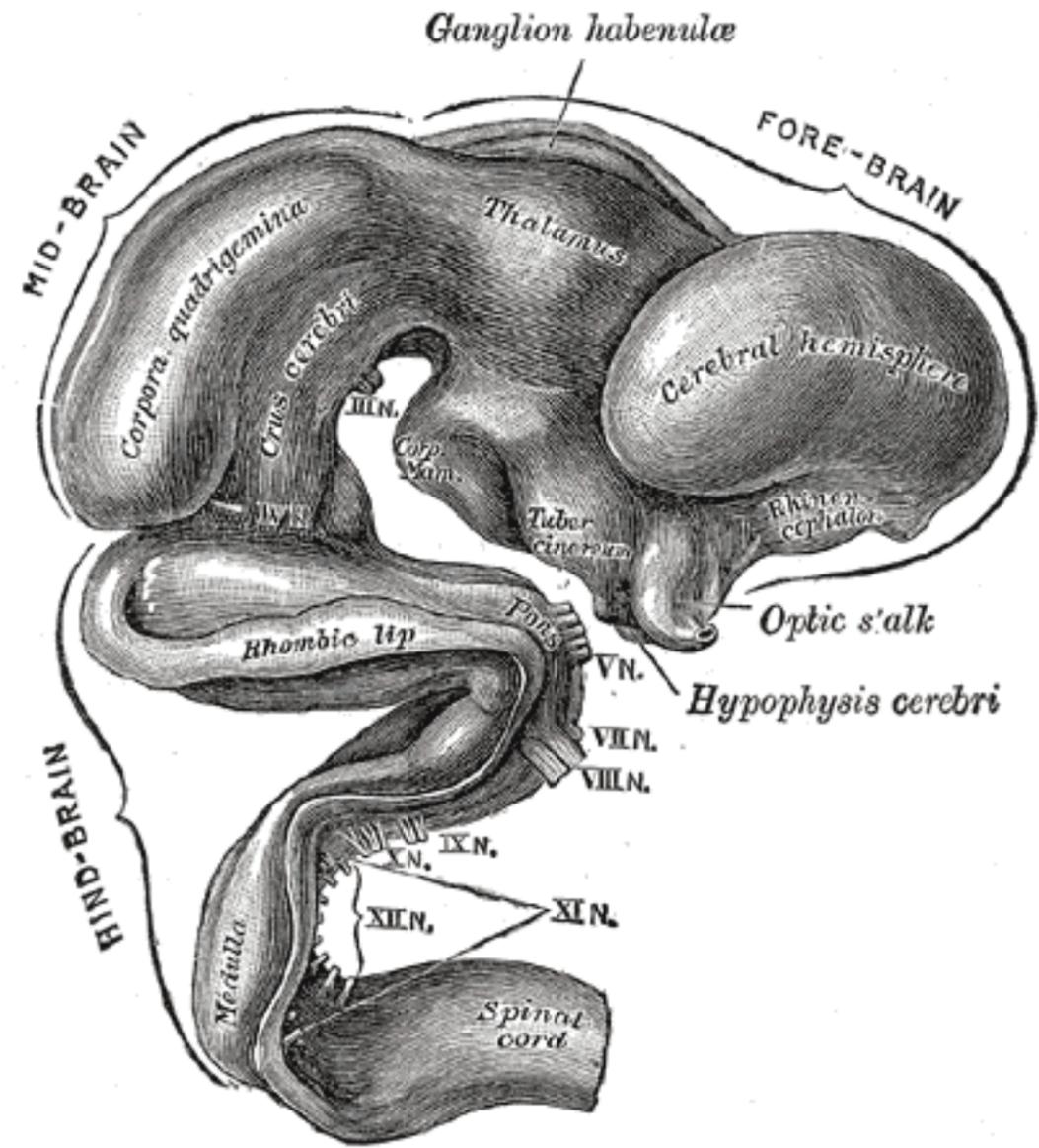
dbSNP:  
rs2266887, rs2266888, rs3027898, rs17435,  
rs2239464)

Gene ontology:  
0000122 negative regulation of transcription  
from RNA polymerase II promoter (214 genes  
in the category)  
0045449 regulation of transcription (978)

Voxel-based morphometry	VBM
Volume	V
Surface	S
Thickness	T
Gyrification	Gy
Diffusion-tensor imaging	DTI
Heritability analysis	$h^2$
Candidate gene/region	C
Genome-wide association study	GW



# Early development



“Brain volumes and surface morphology in monozygotic twins”, White et al, Cereb Cortex 2002

V h<sup>2</sup>

early development  
 rostr-caudal axis

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 aging  
 plasticity

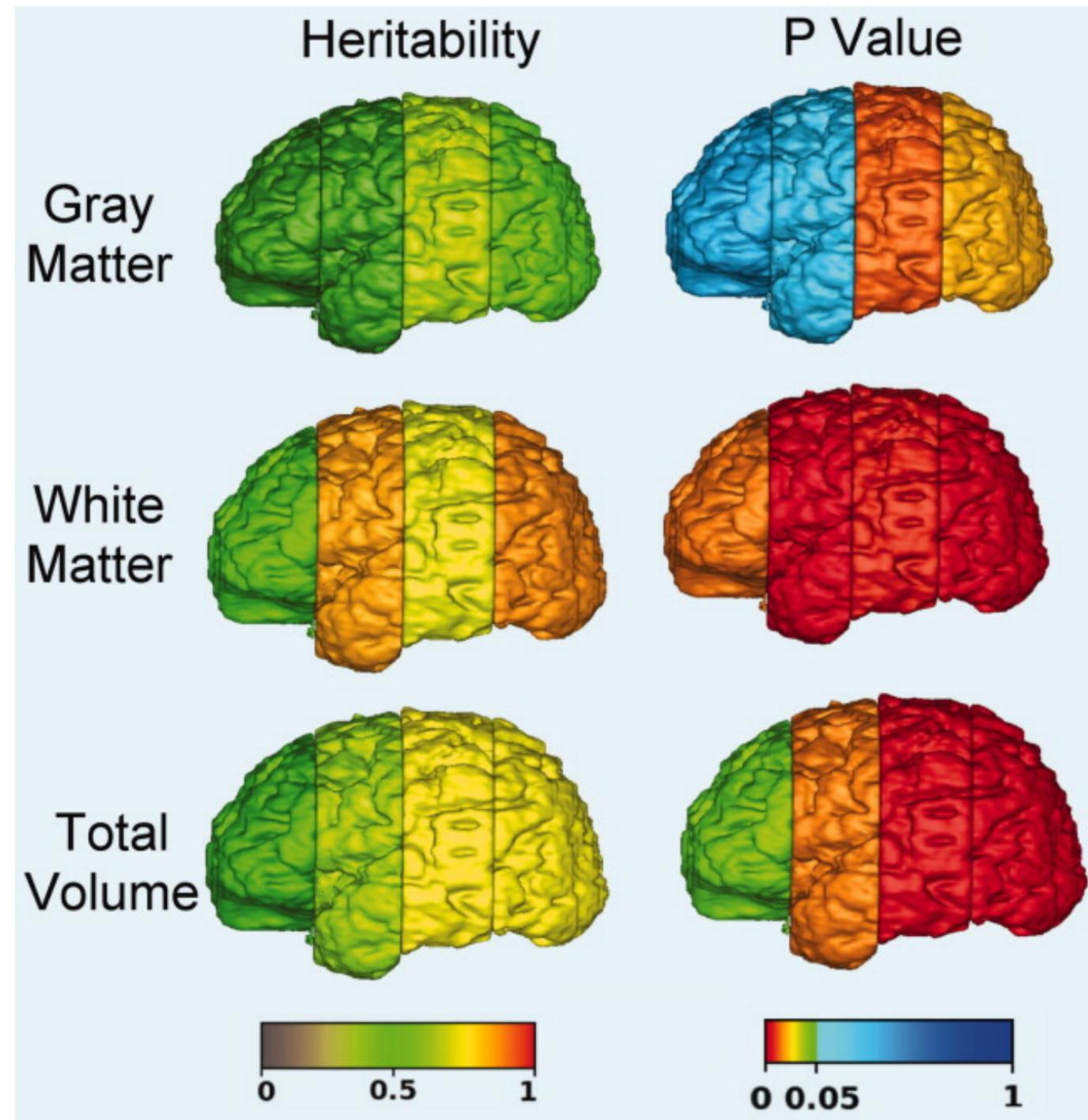
Brain region	r Twins	r Controls
Total brain tissue	0.99	-0.03
Cerebrum	0.99	-0.02
Cerebral GM	0.98	-0.15
Cerebral WM	0.98	0.40
Cortical GM	0.99	-0.14
Ventricles	0.85	0.52
Caudate Nucleus	0.84	-0.17
Putamen	0.75	0.29
Thalamus	0.75	0.0
Cerebellum	0.99	0.20

N=20 (10 MZ, 10 Controls)

“Genetic and environmental contributions to neonatal brain structure: a twin study”,  
 Gilmore et al, Hum Brain Mapp 2010

V h<sup>2</sup>

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N=217 (MZ=2\*21, DZ=2\*50, 35 single)  
 h<sup>2</sup>(ICV)=73%  
 h<sup>2</sup>(WM)=85%  
 h<sup>2</sup>(GM)=56%  
 h<sup>2</sup>(Lateral ventricles)=71%  
 h<sup>2</sup>(Cerebellum)=17%

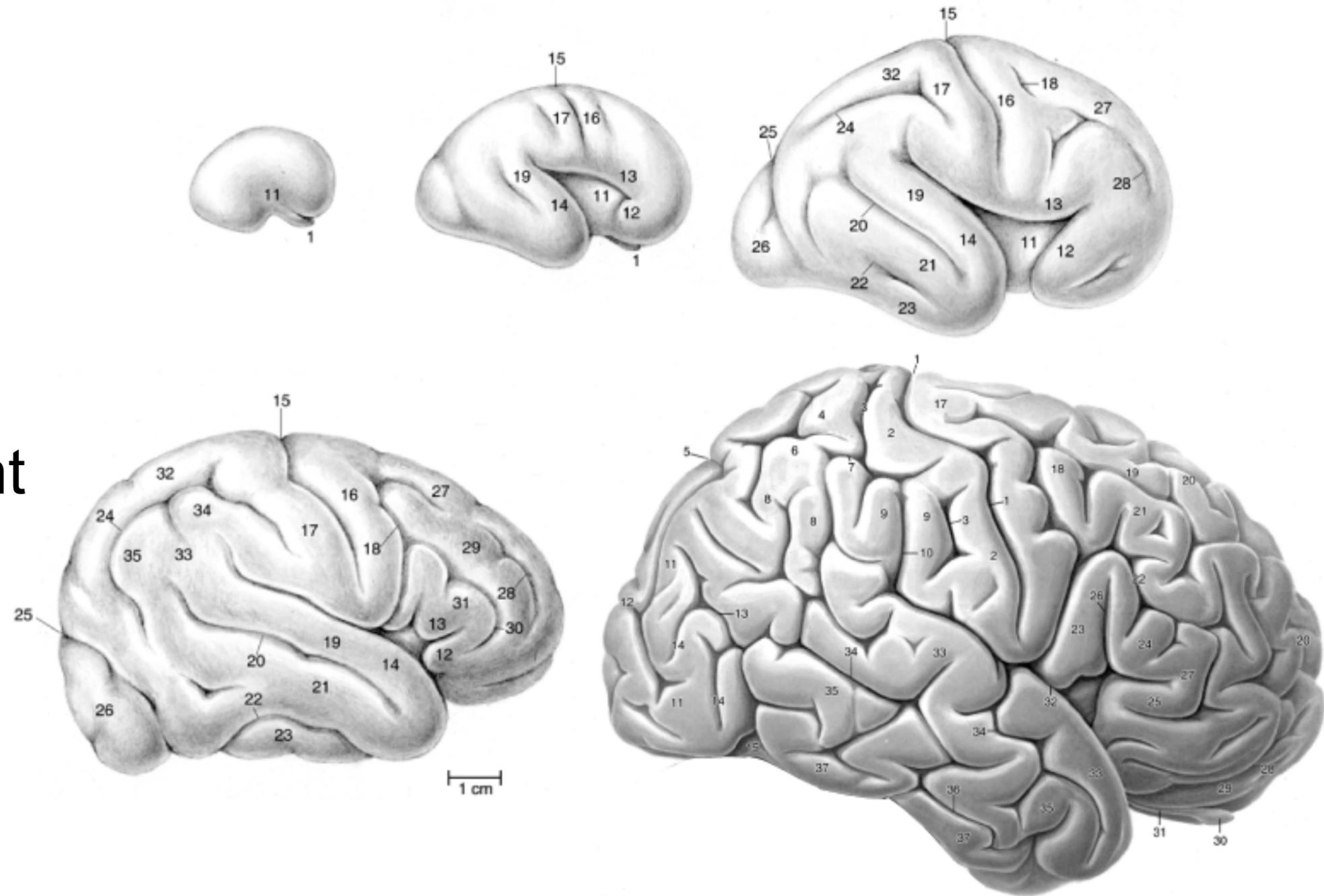
For grey matter, heritability appears higher in posterior regions compared with anterior regions.

White matter heritability appears similar throughout the brain.

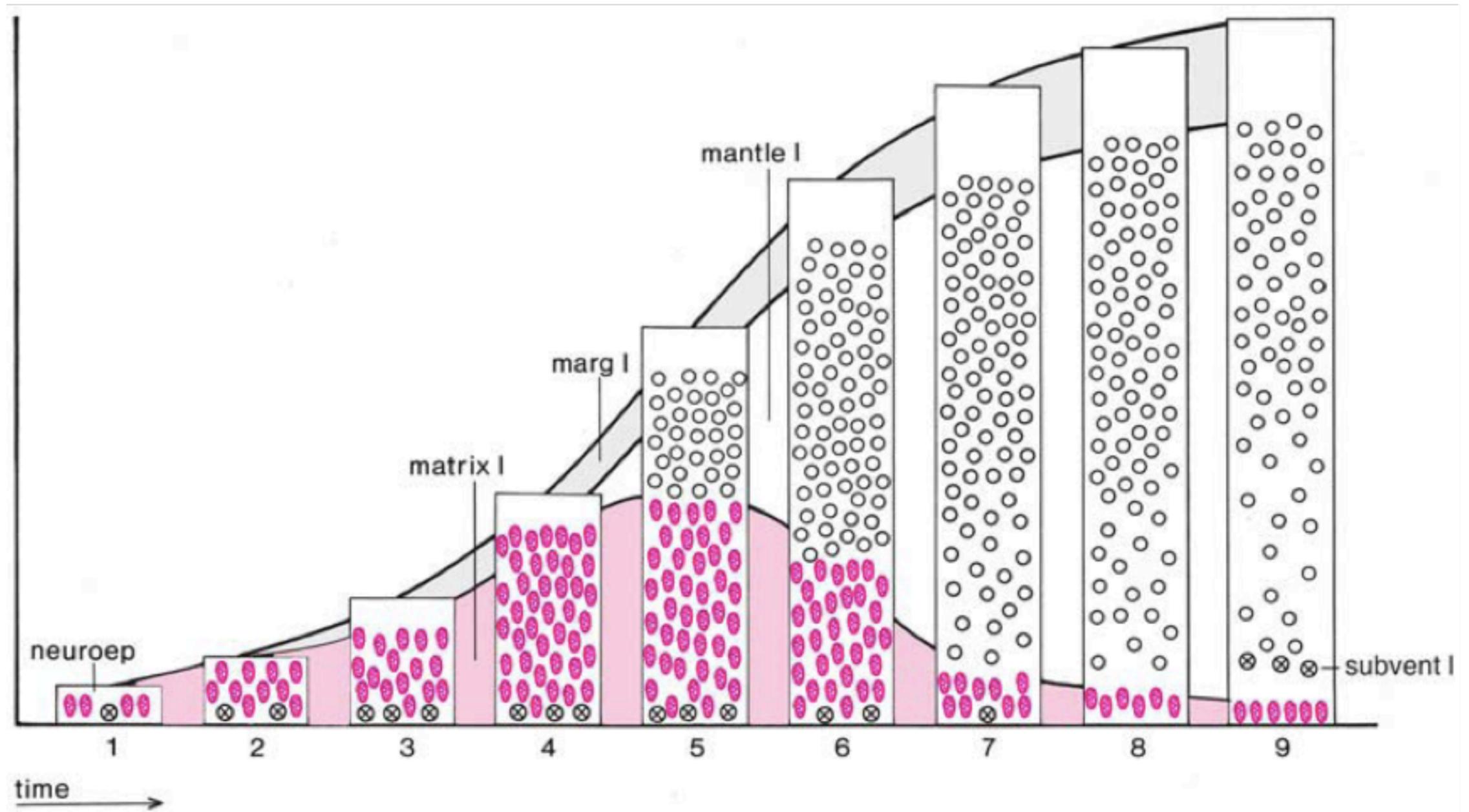
Ventricles appear more heritable in neonates than adults.

Also:  
 “A pediatric twin study of brain morphology”,  
 Wallace et al, J Child Psychol Psyc 2006  
 “The changing impact of genes and environment on brain development during childhood and adolescence: initial findings from a neuroimaging study of pediatric twins”, Lenroot and Giedd, Dev Psychopathol 2008

# Cortical development



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- plasticity



early development

rostrocaudal axis

cortical development

mitosis

apoptosis

neuropil develop.

connectivity

axon growth

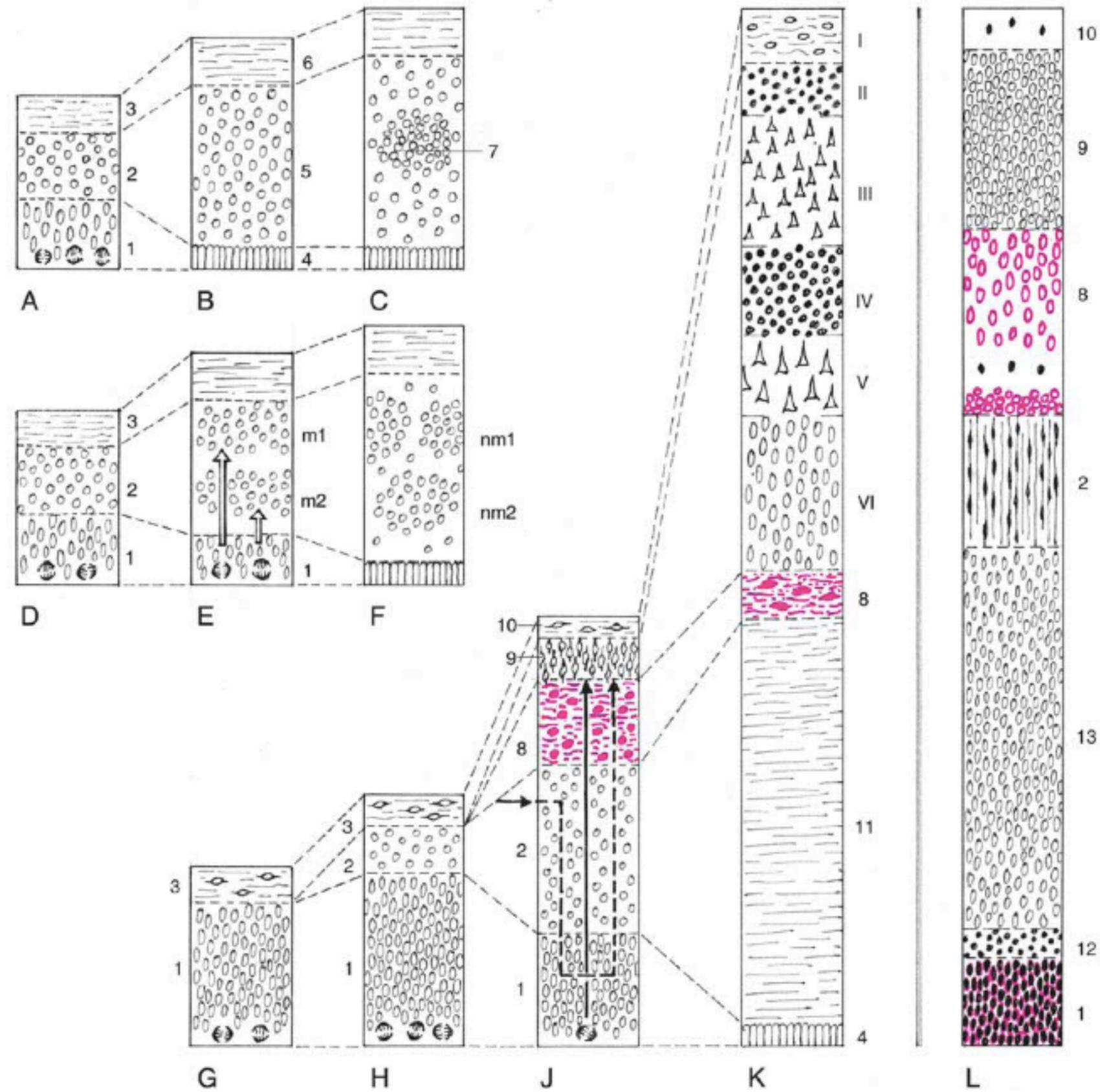
myelination

maturation

puberty

aging

plasticity



“Cortical thickness or gray matter volume? The importance of selecting the phenotype for imaging genetic studies”, Winkler et al, NeuroImage 2009

early development

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apoptosis

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axon growth

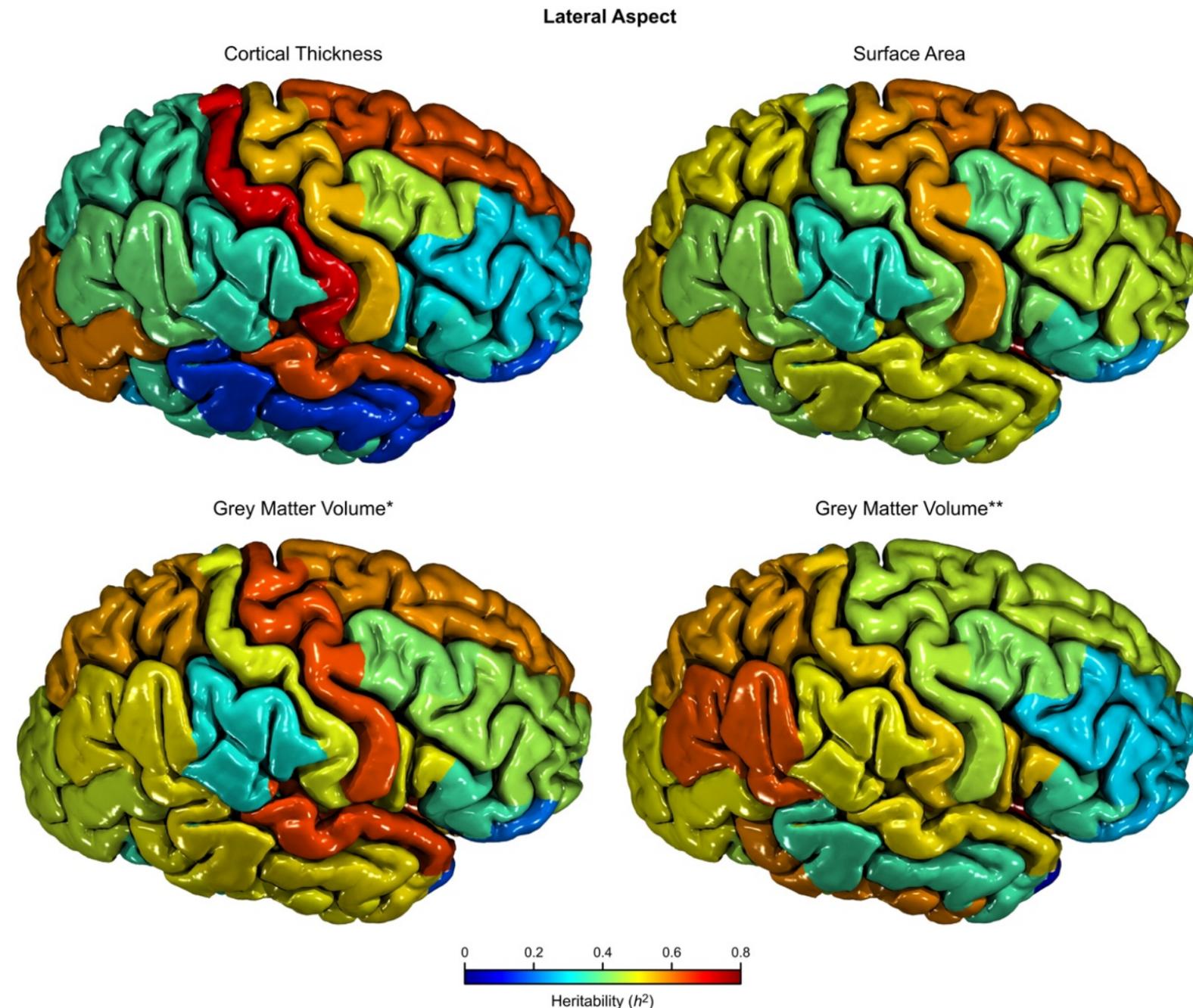
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N=486 (extended pedigrees)  
 $h^2(\text{Brain Vol})=70\%$   
 $h^2(\text{Surf})=70\%$   
 $h^2(\text{Thickn})=69\%$   
 $h^2(\text{GM surf-based})=72\%$   
 $h^2(\text{GM vox-based})=67\%$

The heritability of surface, thickness and grey matter volume were high.

The low genetic correlation between the additive genetic factors of surface and thickness ( $r_g=-0.15$ ) suggests that different genetic mechanisms are at play in their development.

Also:

“Distinct genetic influences on cortical surface and cortical thickness”, Panizzoni et al, Cereb Cortex 2009

“Cortical thickness is influenced by regionally specific genetic factors”, Rimol et al, Biol Psychiatry 2010

“A common MECP2 haplotype associates with reduced cortical surface area in humans in two independent populations”, Joyner et al, PNAS 2009

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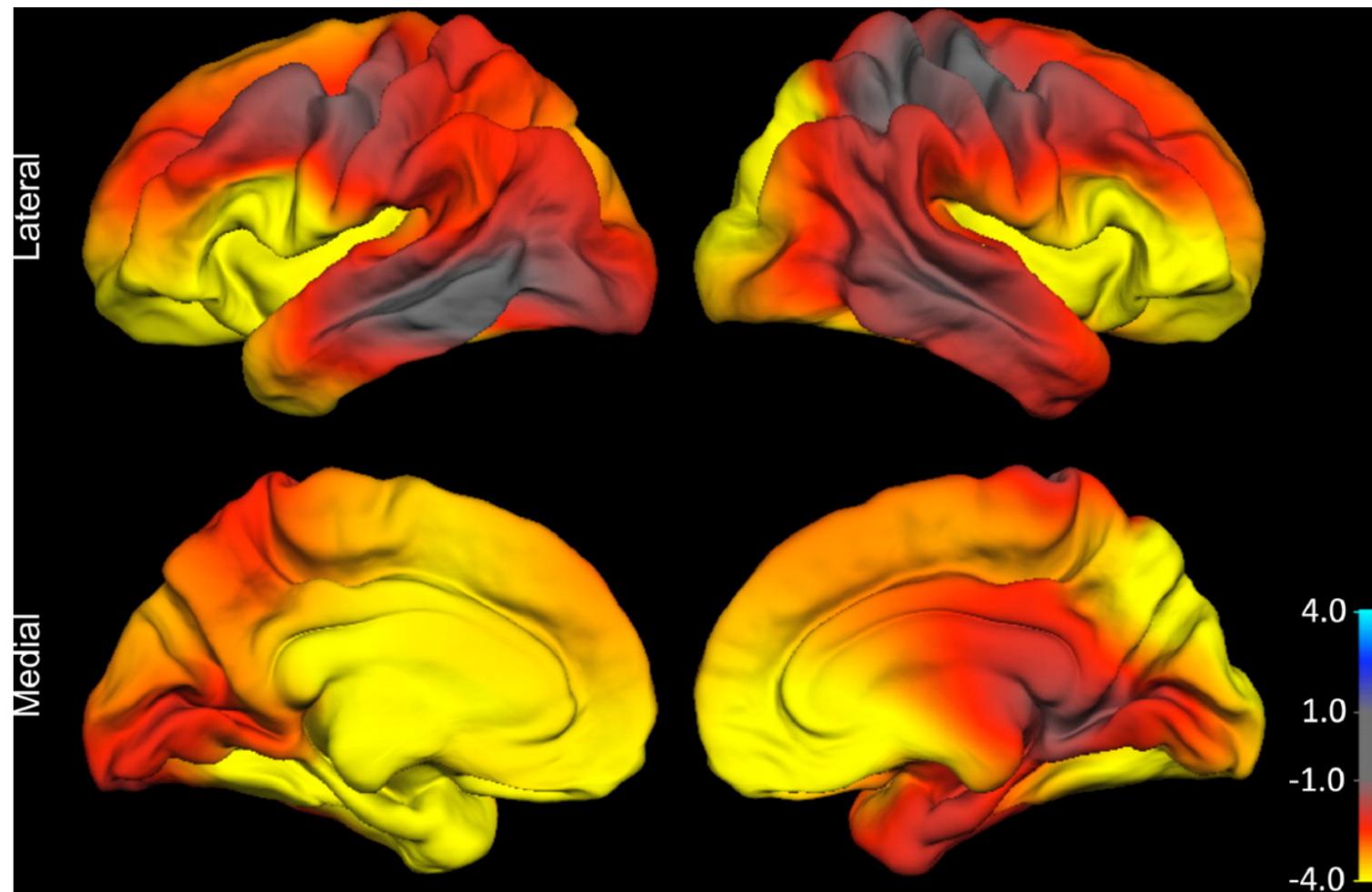
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**MECP2** (rs2266887, rs2266888, rs3027898, rs17435, **rs2239464** [TOP+ADNI])

0000122 negative regulation of transcription from RNA polymerase II promoter (214 genes in the category)

0045449 regulation of transcription (978)

N=289 (TOP) + 655 (ADNI)

Various mutations of MECP2 (located in the X chromosome) have been found in subjects with Rett syndrome (which affects only females).

Here, the association was only found in males.

Reduced surface was found in specific cortical regions (cuneus, fusiform gyrus, pars triangularis). A local effect?

“Sex-dependent association of common microcephaly genes with brain structure” Rimol et al, PNAS 2009

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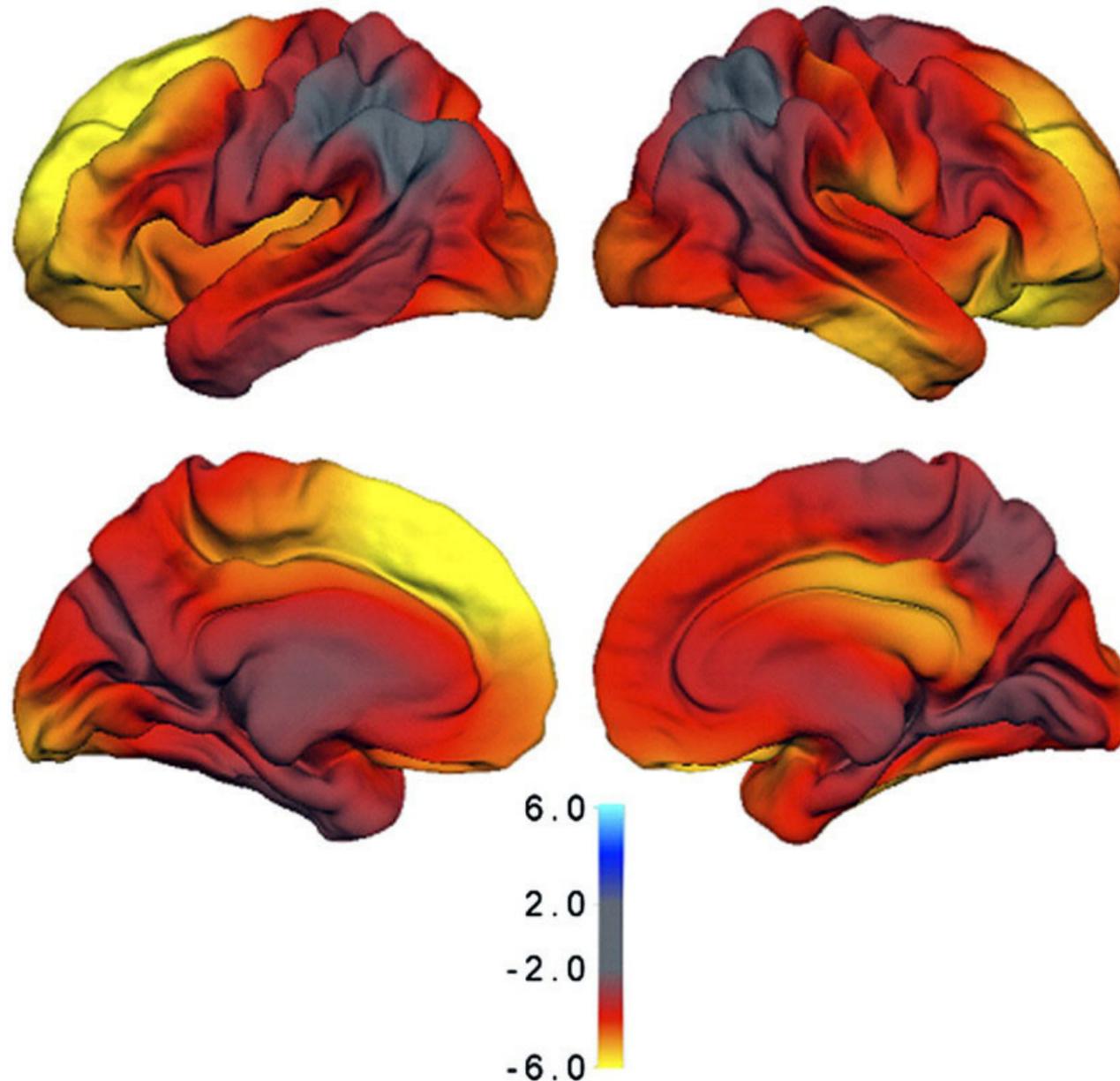
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***CDK5RAP2/MCPH3*** (rs4836817, rs10818453, rs4836819, rs4836820, rs7859743, rs2297453, **rs2282168**, rs1888893, rs914592, rs914593)

0045664 regulation of neuron differentiation (11 genes)  
0007420 brain development (91 genes)

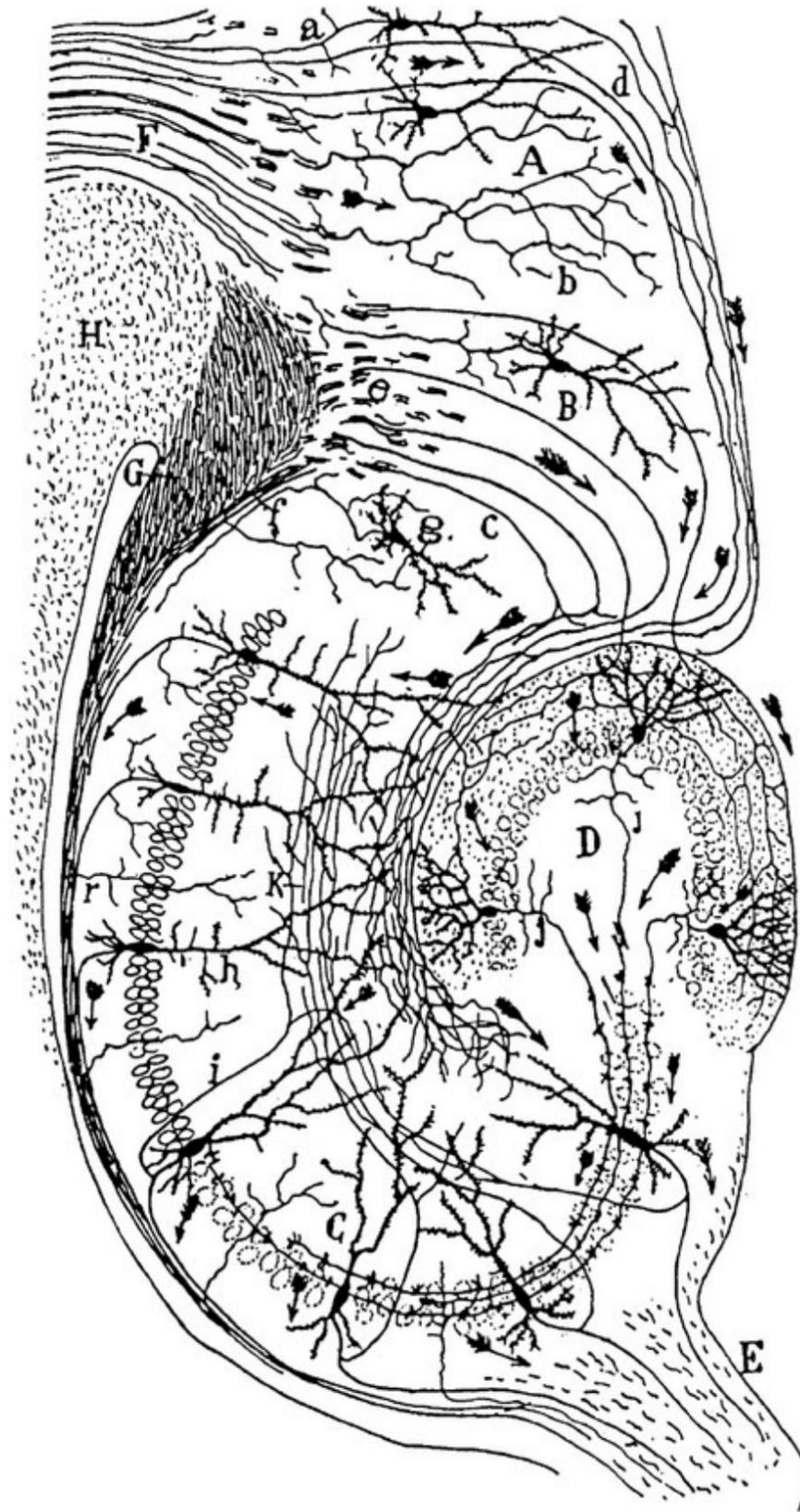
***MCPH1*** (rs2816514, rs2816517, rs11779303, rs11779303)

[no biol. proc. in GO]

***ASPM*** (rs10922168)

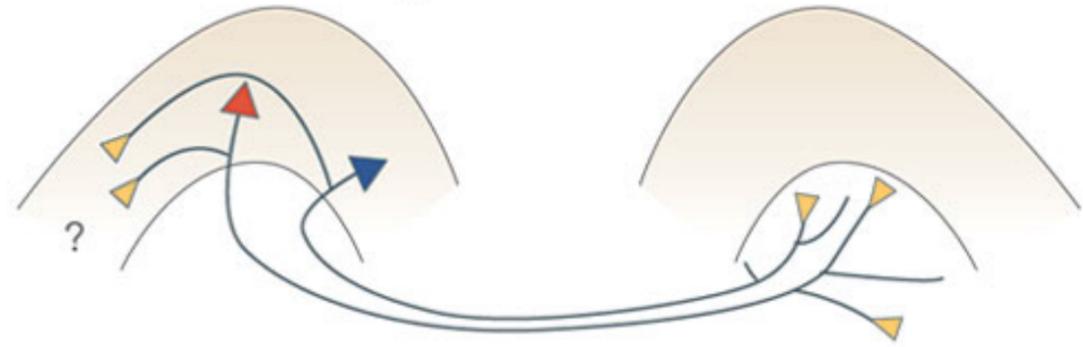
0007049 cell cycle (443 genes)  
0007067 mitosis (171 genes)  
0051301 cell division (221)

# Connectivity

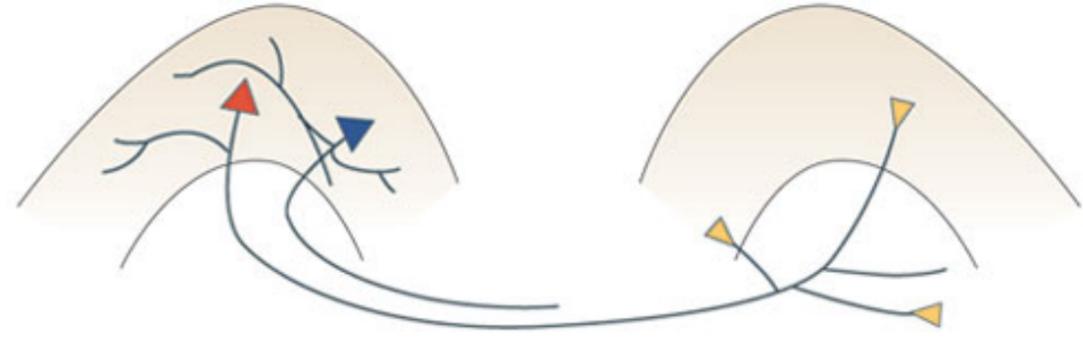


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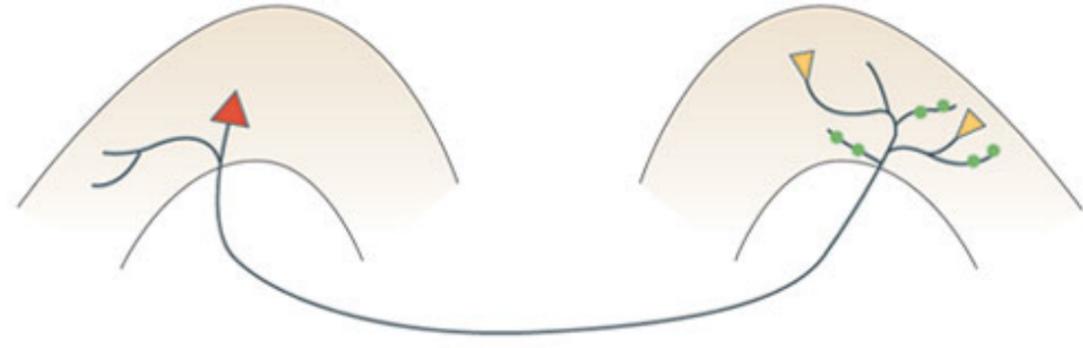
1 Subcortical branching



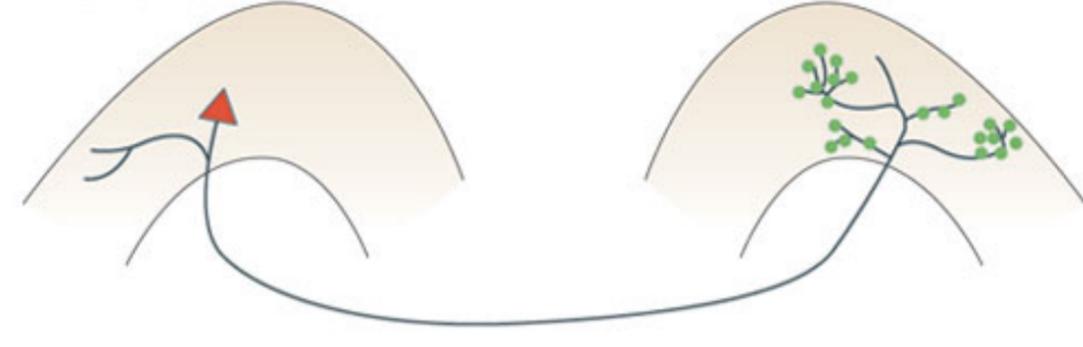
2 Cortical ingrowth



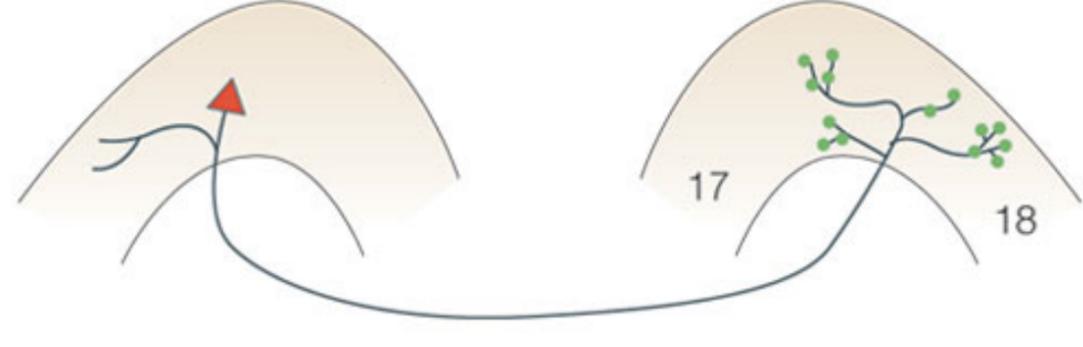
3 Intracortical branching



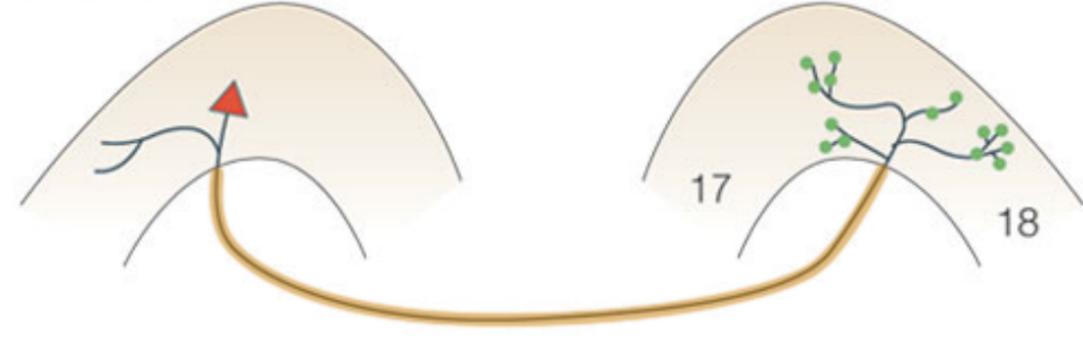
4 Synaptogenesis



5 Synaptic reduction



6 Myelination

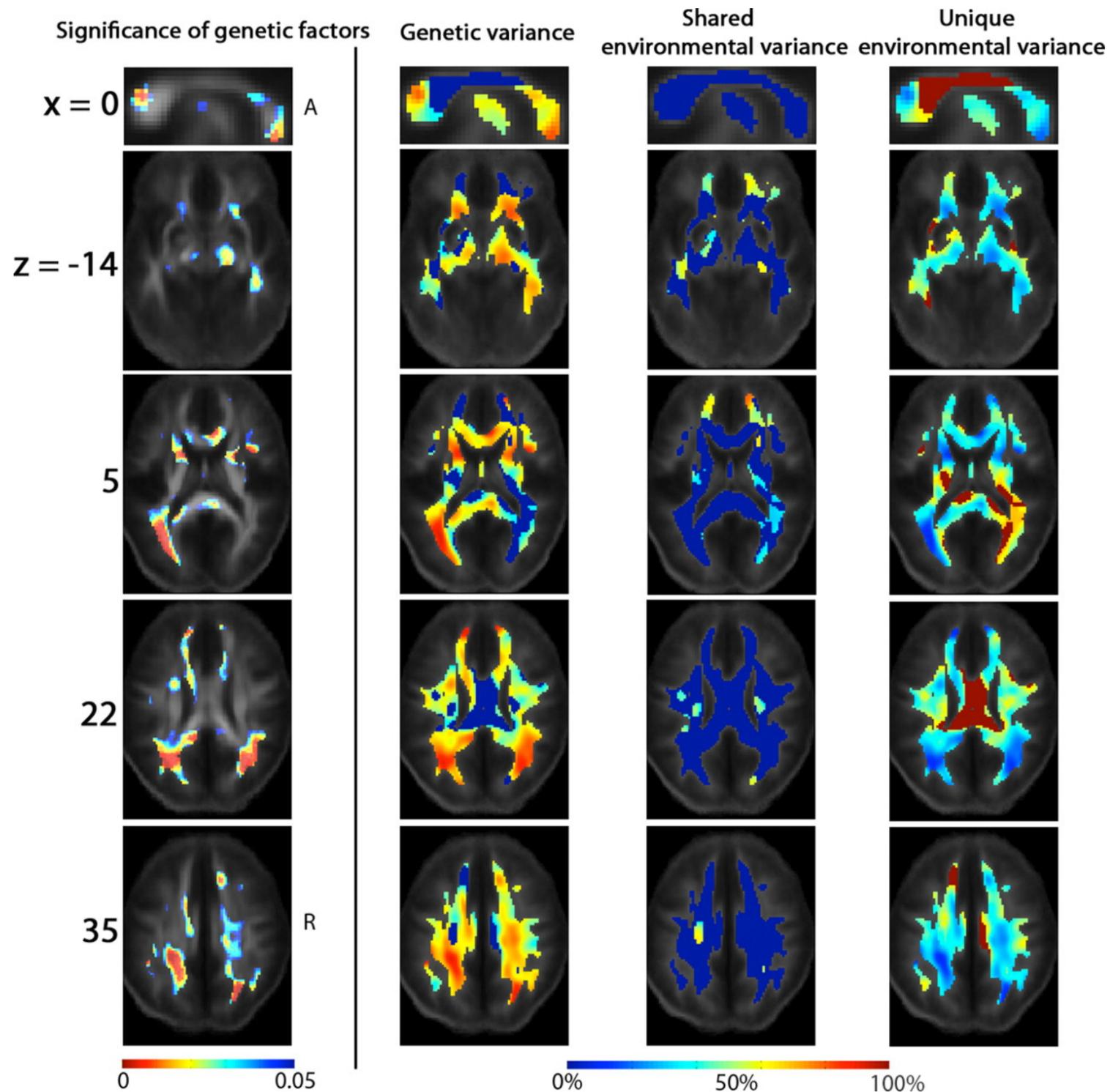


Growth cones	Synapses	Stable projections	Transient projections
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“Genetics of brain fibre architecture and intellectual performance”, Chiang et al,  
 J Neurosci 2009

DTI  $h^2$

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N= 92 (MZ=2\*23, DZ=2\*23)  
 $h^2$ (FA) values between 55% (Frontal left)  
 to 85% (Parietal left)

Common genetic factors mediated the  
 correlation between IQ and white matter  
 integrity.

“Genetic influences on brain asymmetry: a DTI study of 374 twins and siblings”,  
Janhashad et al, NeuroImage 2010

DTI  $h^2$

early development

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neuropil develop.

connectivity

axon growth

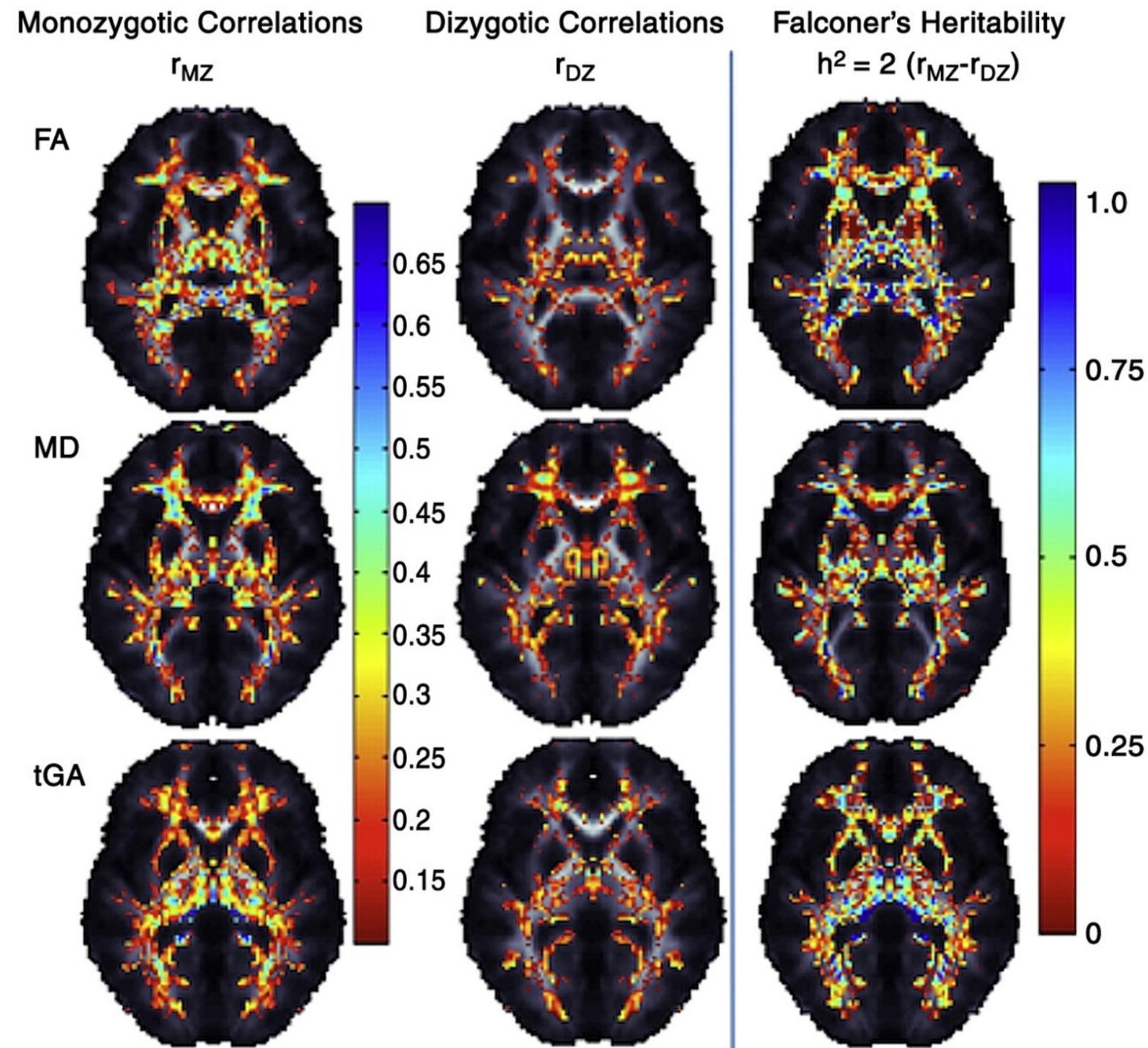
myelination

maturation

puberty

aging

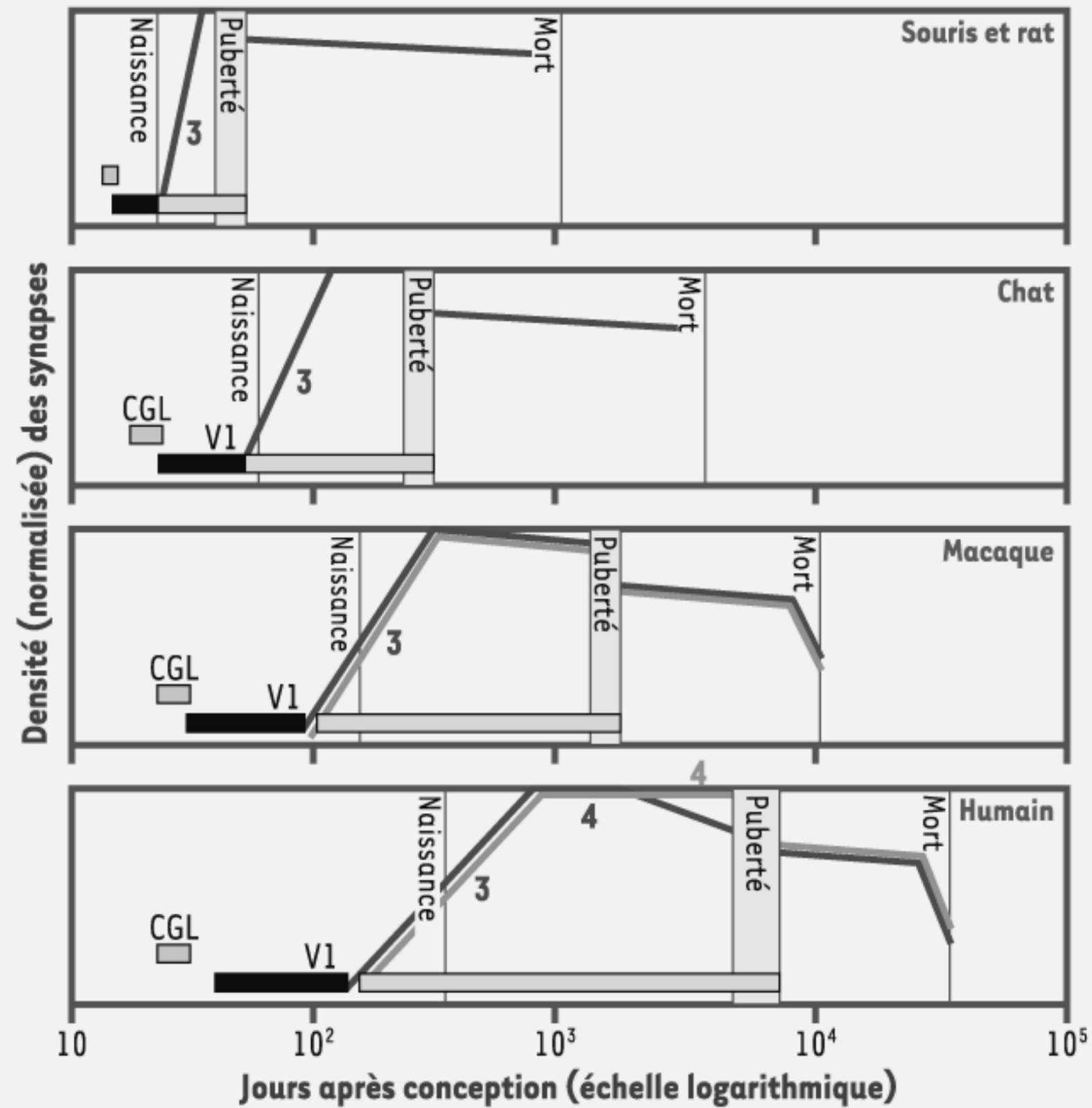
plasticity



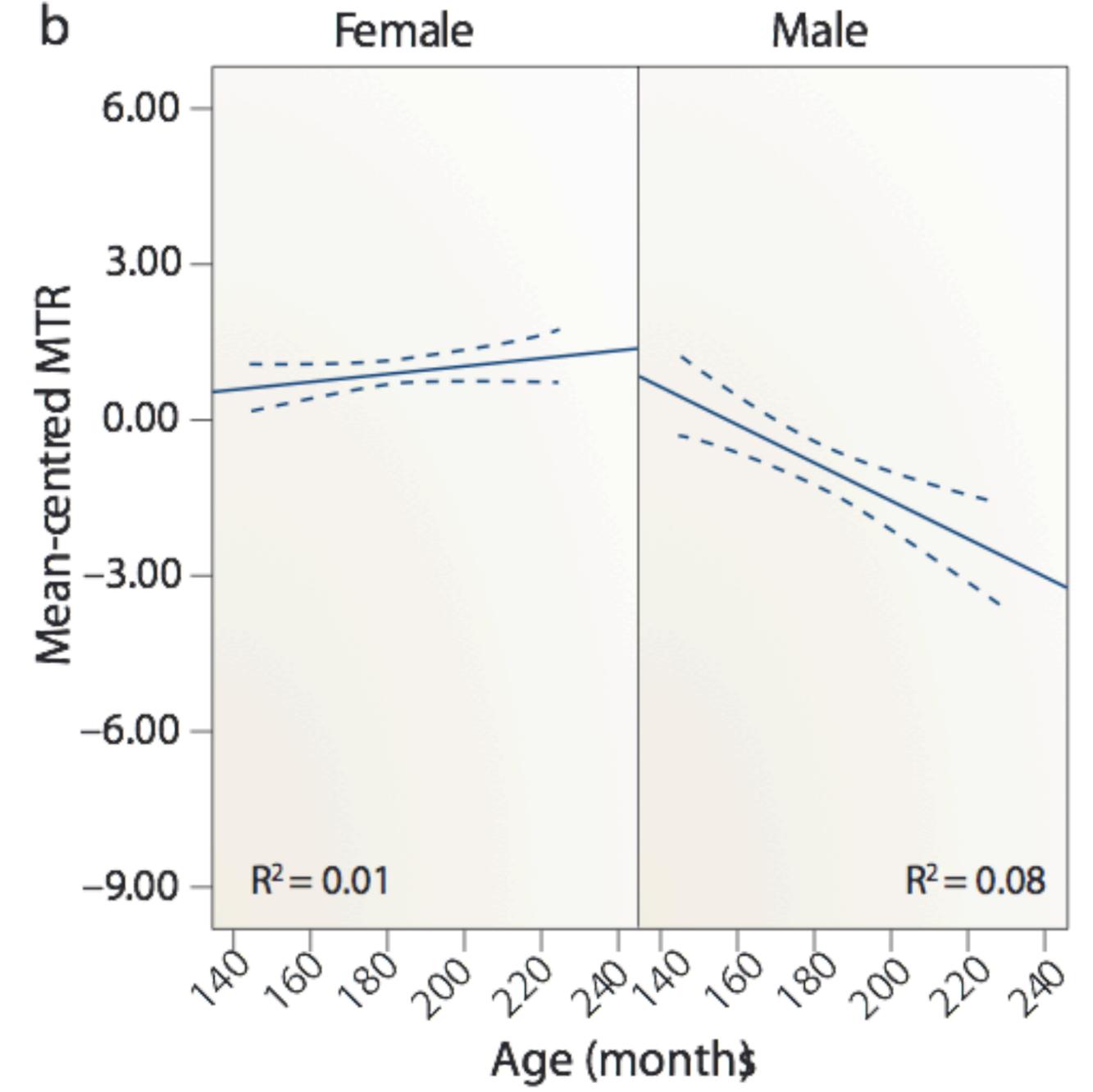
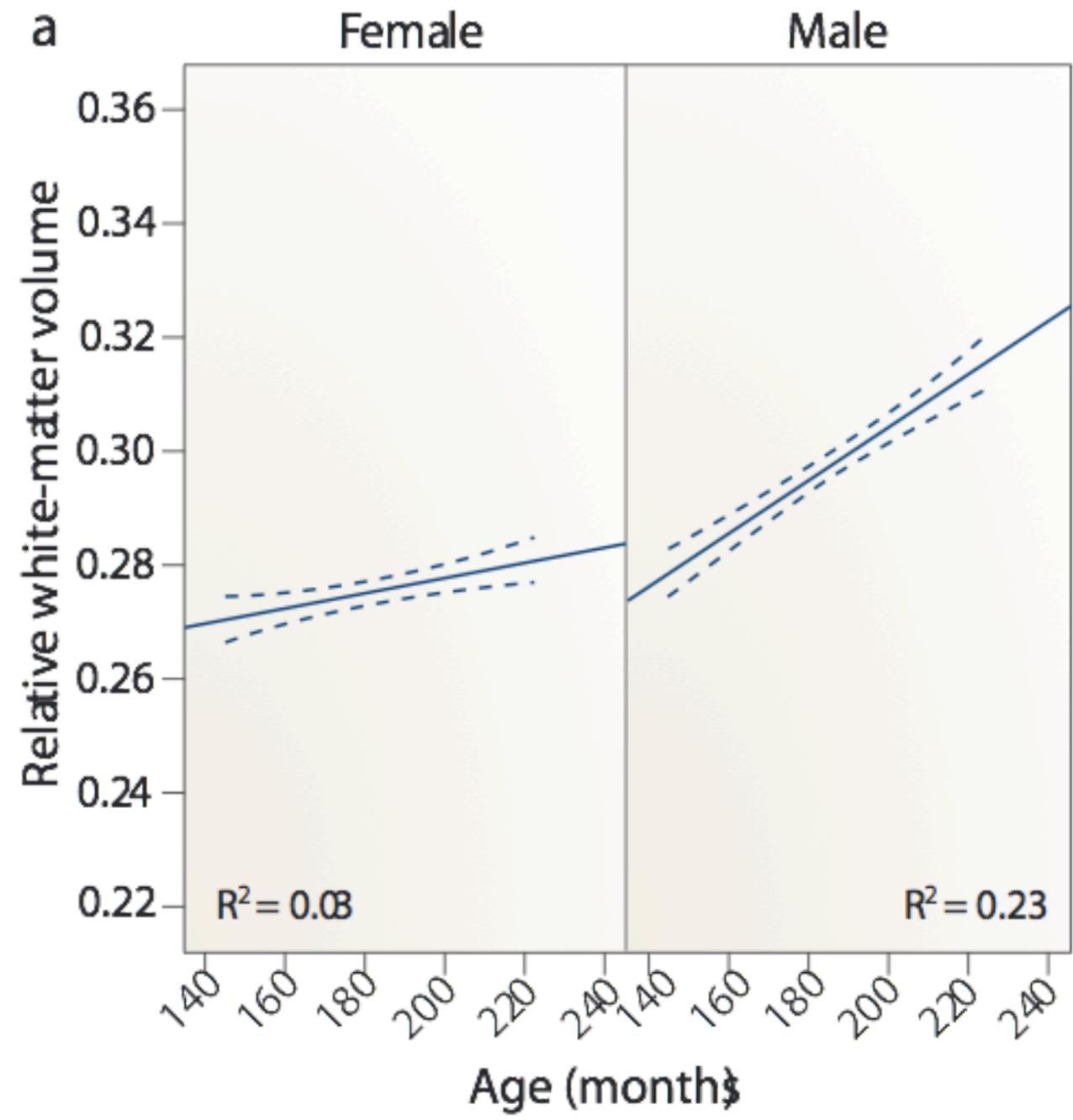
N=374 (MZ=2\*60, DZ=2\*119, 16 sibs)  
 $h^2$ (Asymmetry) values between 10%  
(forceps minor) and 37% (anterior thalamic  
radiation).

There were significant difference in the  
heritability of DTI asymmetry between  
males and females, suggesting a sex-  
dependent mechanism.

# Maturation



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- apoptosis
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“Growth of white matter in the adolescent brain: role of testosterone and androgen receptor”, Perrin et al, J Neurosci 2008

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apoptosis

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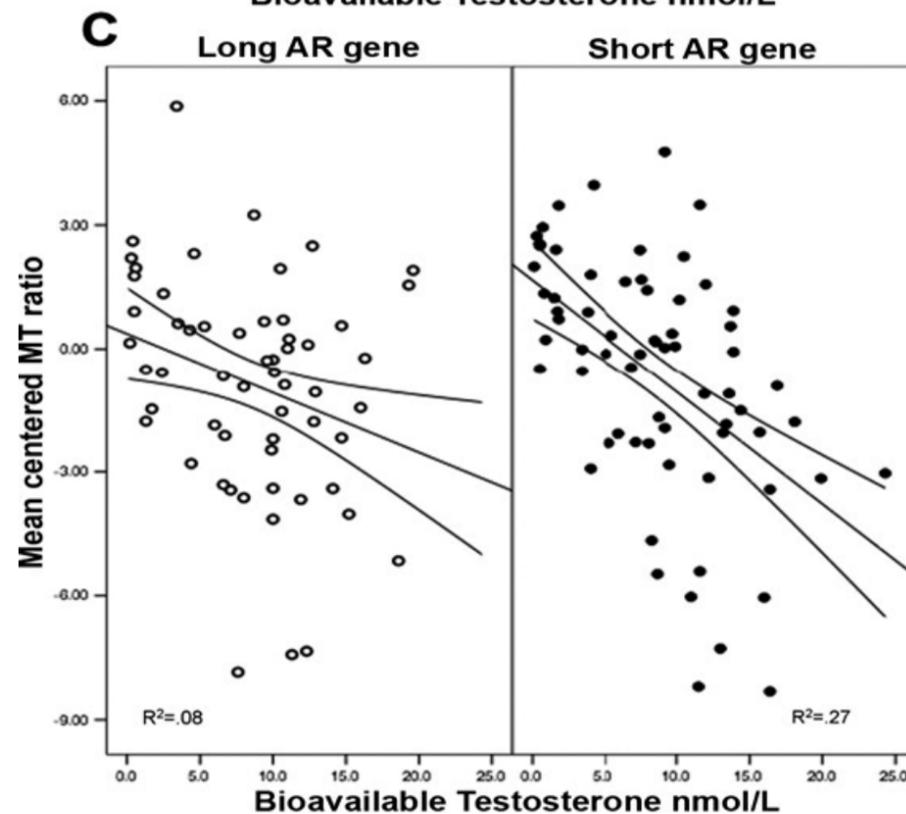
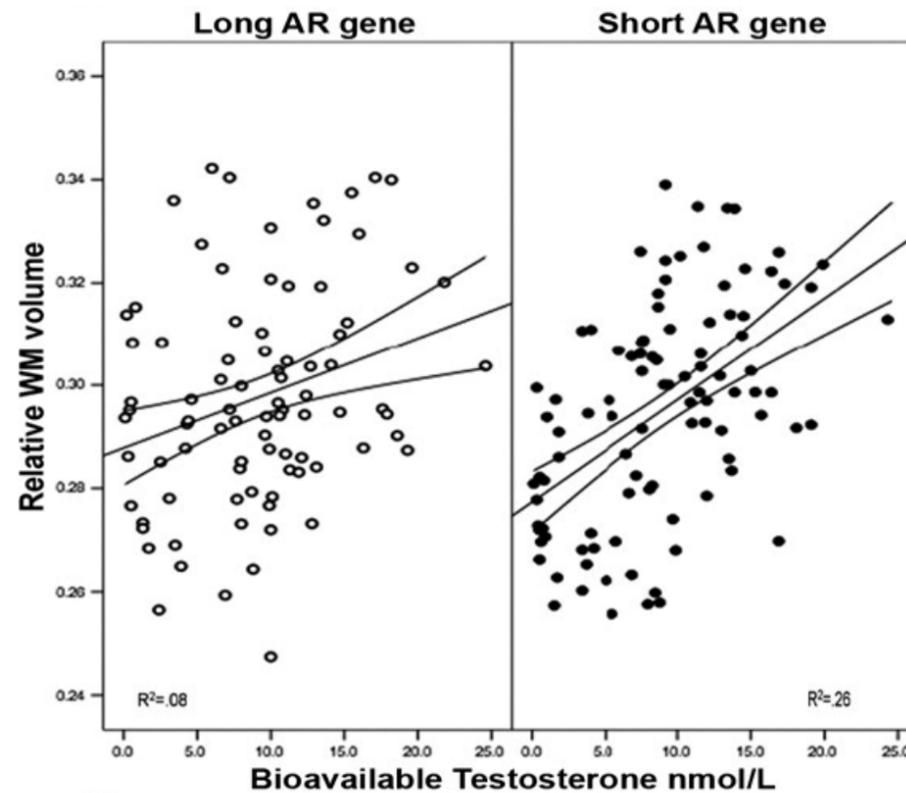
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**AR** (number of CAG repeats in exon 1)  
 0008584 male gonad development (30)  
 0050790 regulation of catalytic activity (8)  
 0001701 in utero embryonic development (103)  
 0030521 androgen receptor signaling pathway (37)  
 0019102 male somatic sex determination (1)  
 0007267 cell-cell signaling (239)  
 0008219 cell death (100)  
 0007548 sex differentiation (18)  
 0008283 cell proliferation (265)  
 0030850 prostate gland development (10)  
 0016049 cell growth (46)  
 + 0045944, 0006810, 0007165

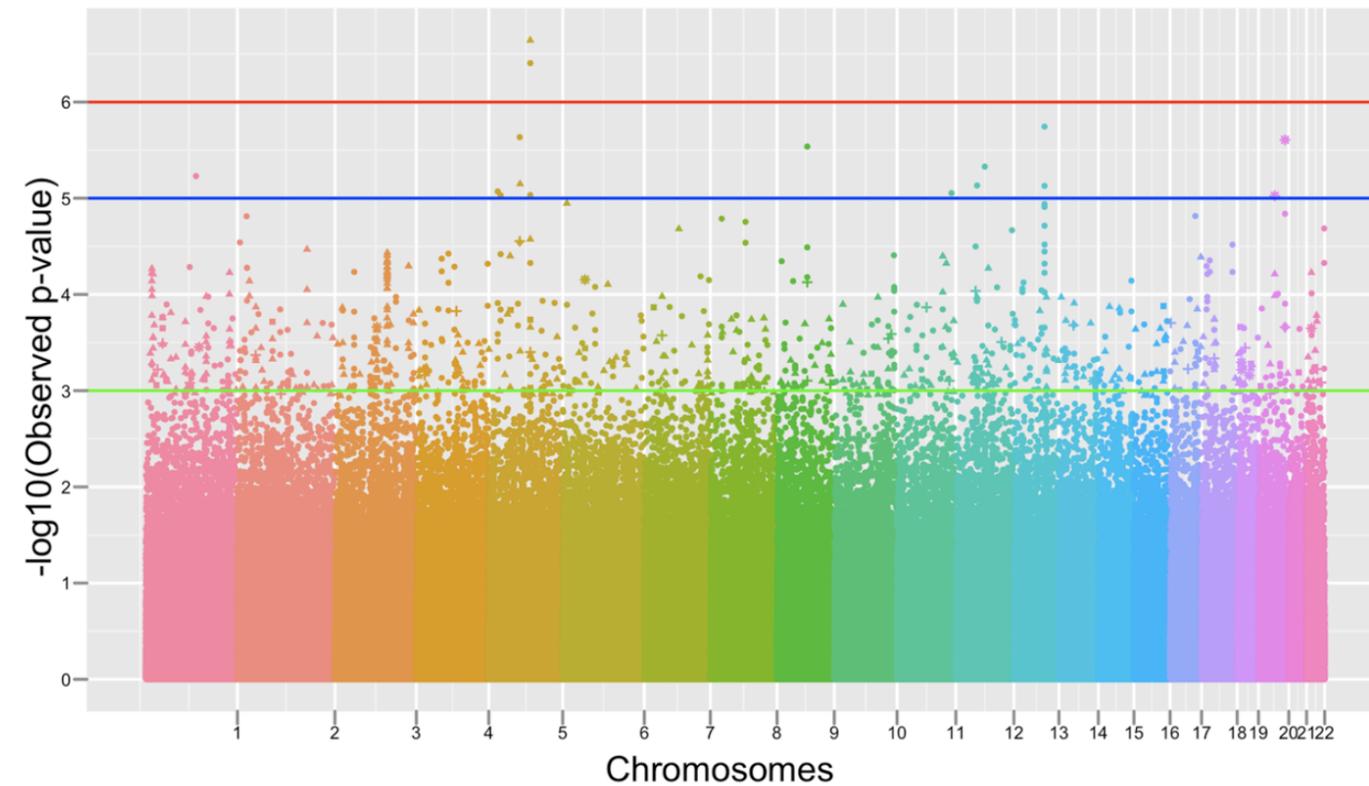
N=408

The number of CAG repeats in Exon 1 believed to be inversely proportional to the AR transcriptional activity.

Testosterone-related increase of WM was stronger in males with the lower number of CAG repeats (R2 of 26% vs 8%)

WM growth does not seem to be due to myelination.

“Hippocampal atrophy as a quantitative trait in a genome-wide association study identifying novel susceptibility genes for Alzheimer’s disease”, Potkin et al, 2009, PLoS One



← TOMM40  
 ← Including APOE, CAND1, MAGI2, ARSB, PRUNE2

N=381 (ADNI)  
 Chip Illumina Human610

Found genes involved in regulation of protein degradation, apoptosis, neuronal loss and neurodevelopment.

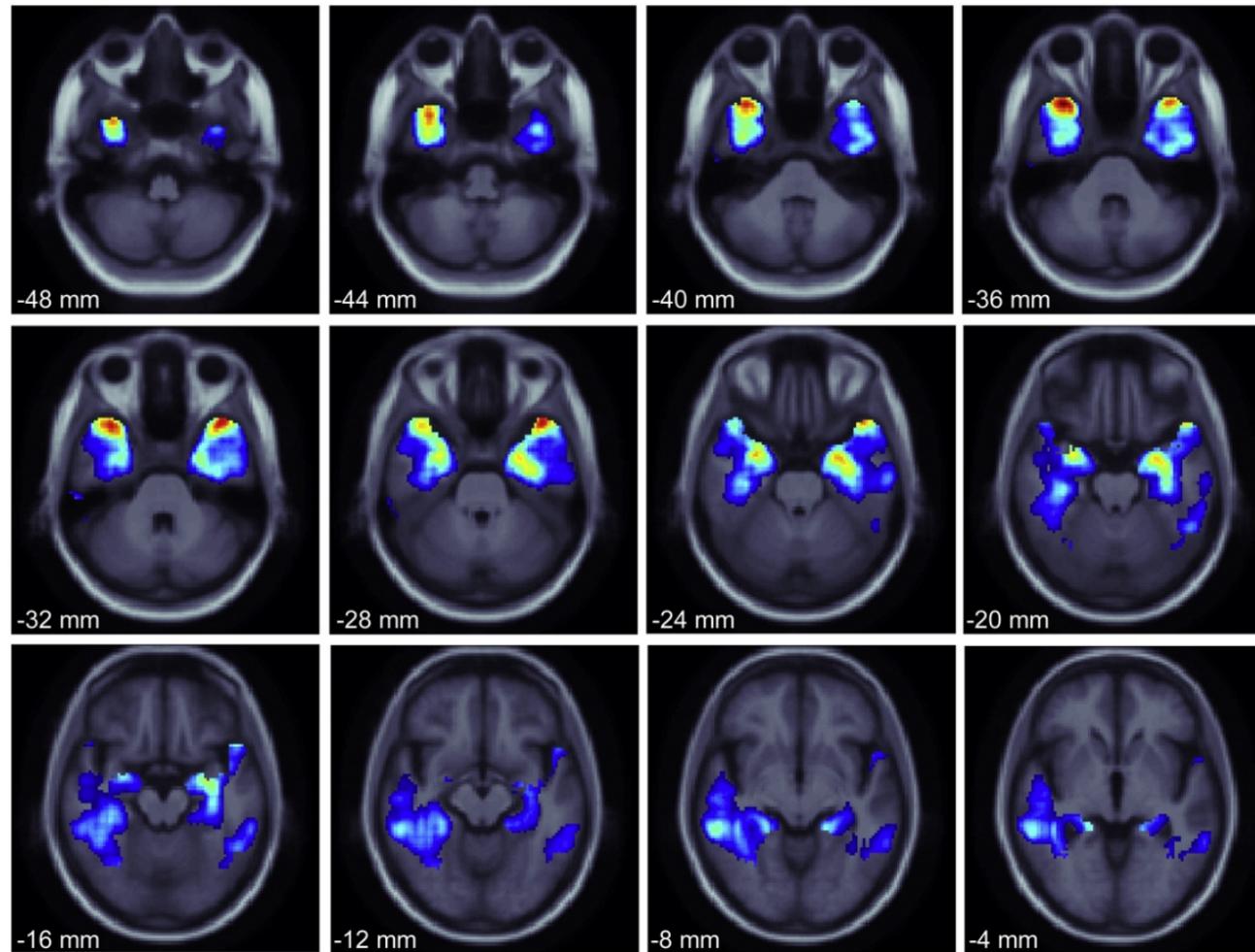
**APOE** (rs429358, rs7412)  
 0001937 negative regulation of endothelial cell proliferation  
 0006916 anti-apoptosis  
 0010468 regulation of gene expression  
 0045471 response to ethanol  
 0007271 synaptic transmission, cholinergic  
 0007010 cytoskeleton organization  
 0006917 induction of apoptosis  
 0048168 regulation of neuronal synaptic plasticity  
 0030516 regulation of axon extension  
 + many more (82 categories in total!)

**TOMM40** (rs2075650, rs11556505, rs157580)  
 0006820 anion transport  
 0015031 protein transport  
 0006626 protein targeting to mitochondrion

Also:  
 Genome-wide association study of CSF biomarkers Abeta1-42, t-tau, and p-tau181p in the ADNI cohort , Kim et al, 2011, Neurology

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“Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease”, Stein et al, 2010, NeuroImage



**GRIN2B** (rs10845840)

- 0007612 learning
- 0007613 memory
- 0009790 embryonic development
- 0060079 regulation of excitatory postsynaptic membrane potential
- 0007215 glutamate signaling pathway
- 0014049 positive regulation of glutamate secretion
- 0045471 response to ethanol
- 0001701 in utero embryonic development
- 0043408 regulation of MAPKKK cascade
- 0048167 regulation of synaptic plasticity
- + 0001662, 0001967, 0006812, 0006816, 0050966, 0048266, 0001964, 0007423

N=742 (ADNI)  
Chip Illumina Human610

Association was stronger with temporal lobe volume than with hippocampal volume (which has been observed to be less heritable)

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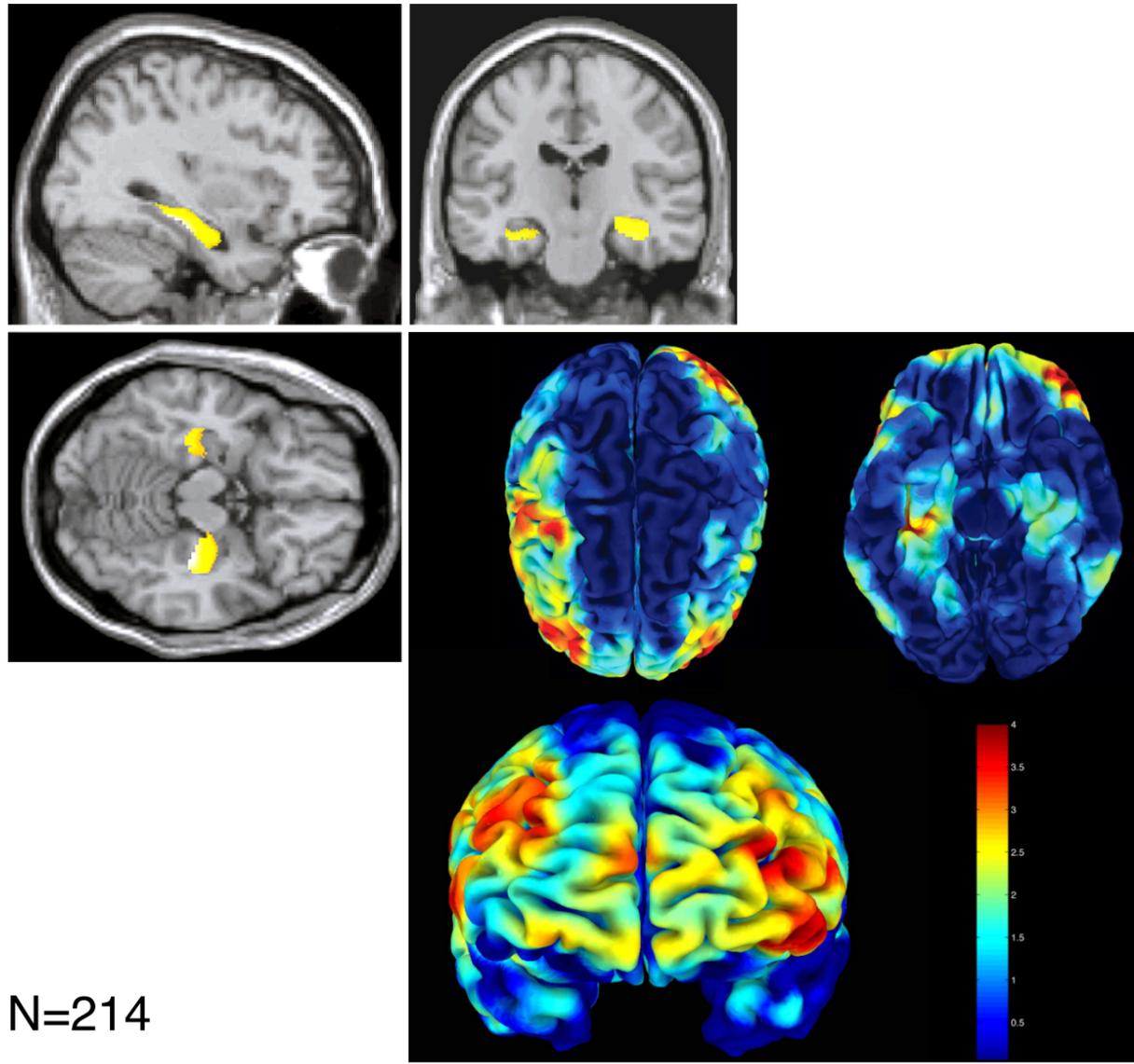
puberty

aging

plasticity

“The brain-derived neurotrophic factor val66met polymorphism and variation in human cortical morphology”, Pezawas et al, J Neurosci, 2004

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N=214

BDNF Val66Met has been associated with variation in human memory and the susceptibility to various psychiatric disorders.

Carriers of the Met allele were observed to have smaller hippocampal volume and prefrontal GM volume compared with Val carriers. A local effect of BDNF?

- BDNF** (rs6265)
- 0014047 glutamate secretion (4)
  - 0007611 learning or memory (22)
  - 0048167 regulation of synaptic plasticity (14)
  - 0007406 negative regulation of neuroblast proliferation (7)
  - 0007411 axon guidance (66)
  - 0007412 axon target recognition (3)
  - 0021675 nerve development (6)
  - 0043524 negative regulation of neuron apoptosis (39)
  - 0045666 positive regulation of neuron differentiation (16)
  - 0046668 regulation of retinal cell programmed cell death (2)
  - 0006916 anti-apoptosis (180)
  - 0016358 dendrite development (19)
  - + 0001657, 0007631, 0048839, 0042596, 0042490, 0042493, 0008038, 0019222

“Brain volumes and Val66Met polymorphism of the BDNF gene: local or global effects?”, Toro et al, Brain Struct Func 2009

V C

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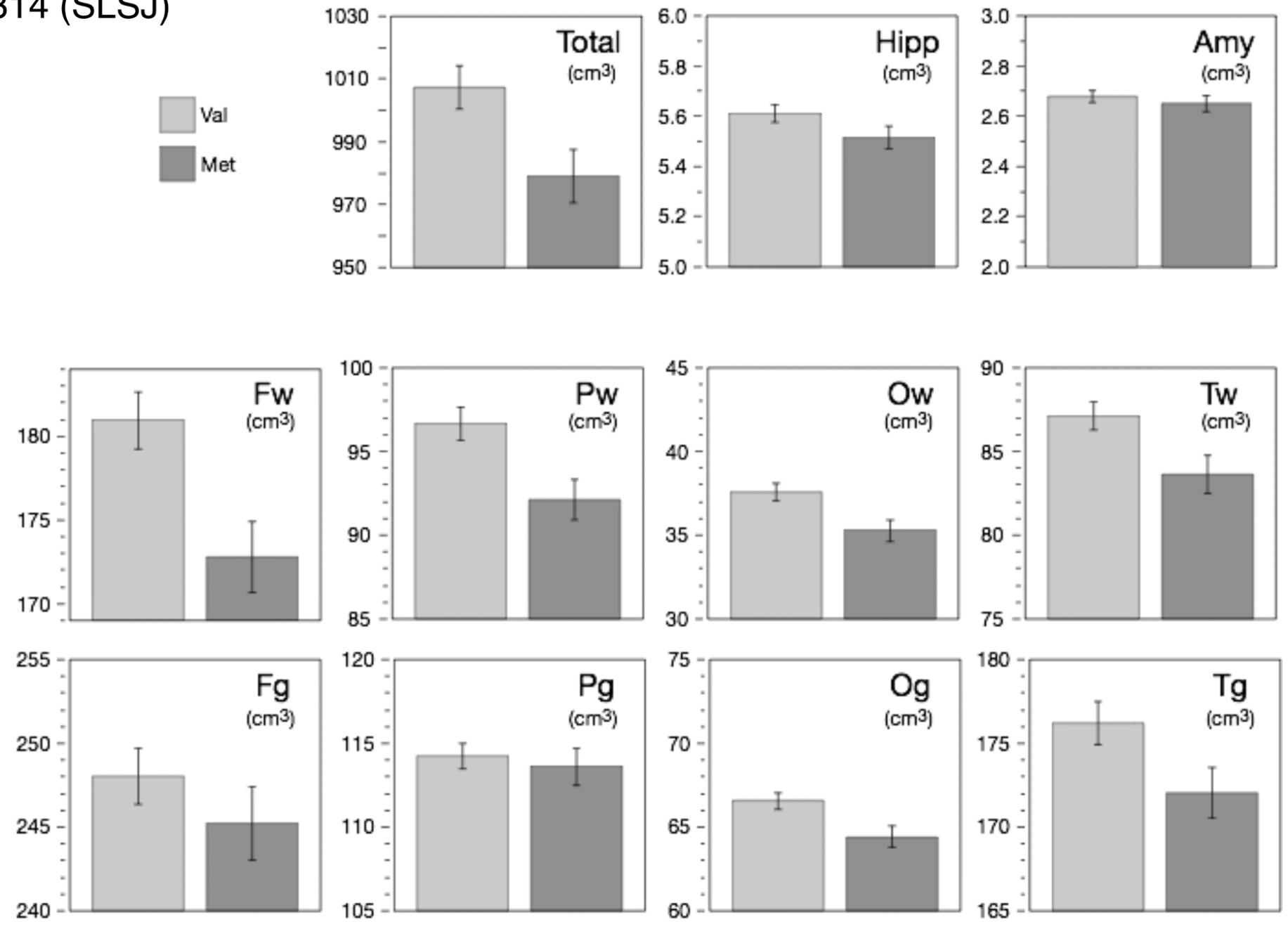
□ Frontal  
 □ Parietal  
 □ Occipital  
 □ Temporal



□ White matter  
 □ Grey matter  
 □ Subcortical

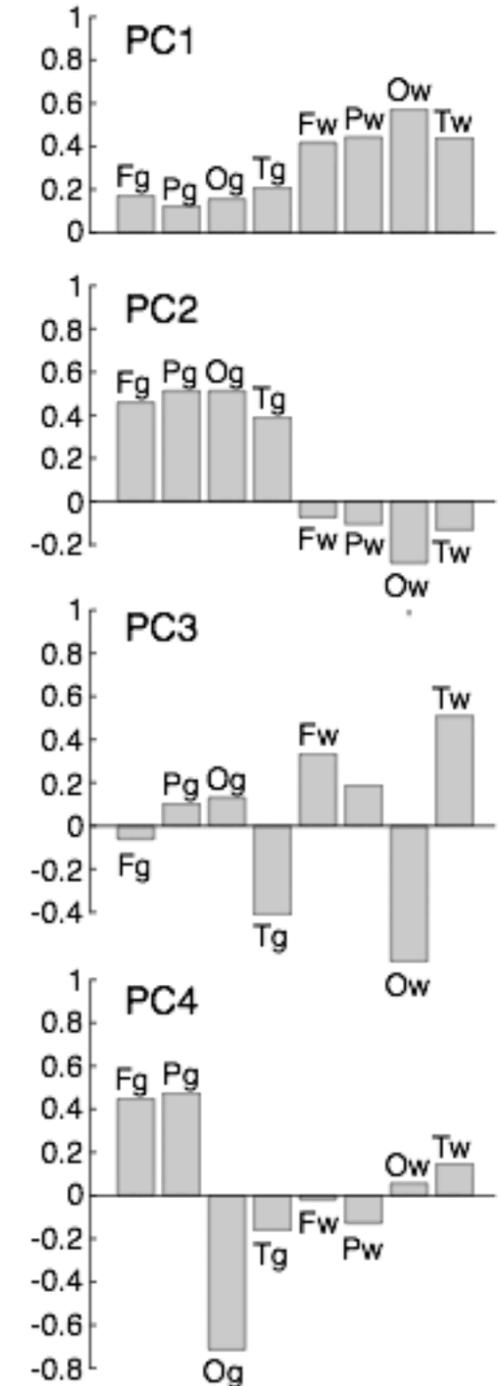
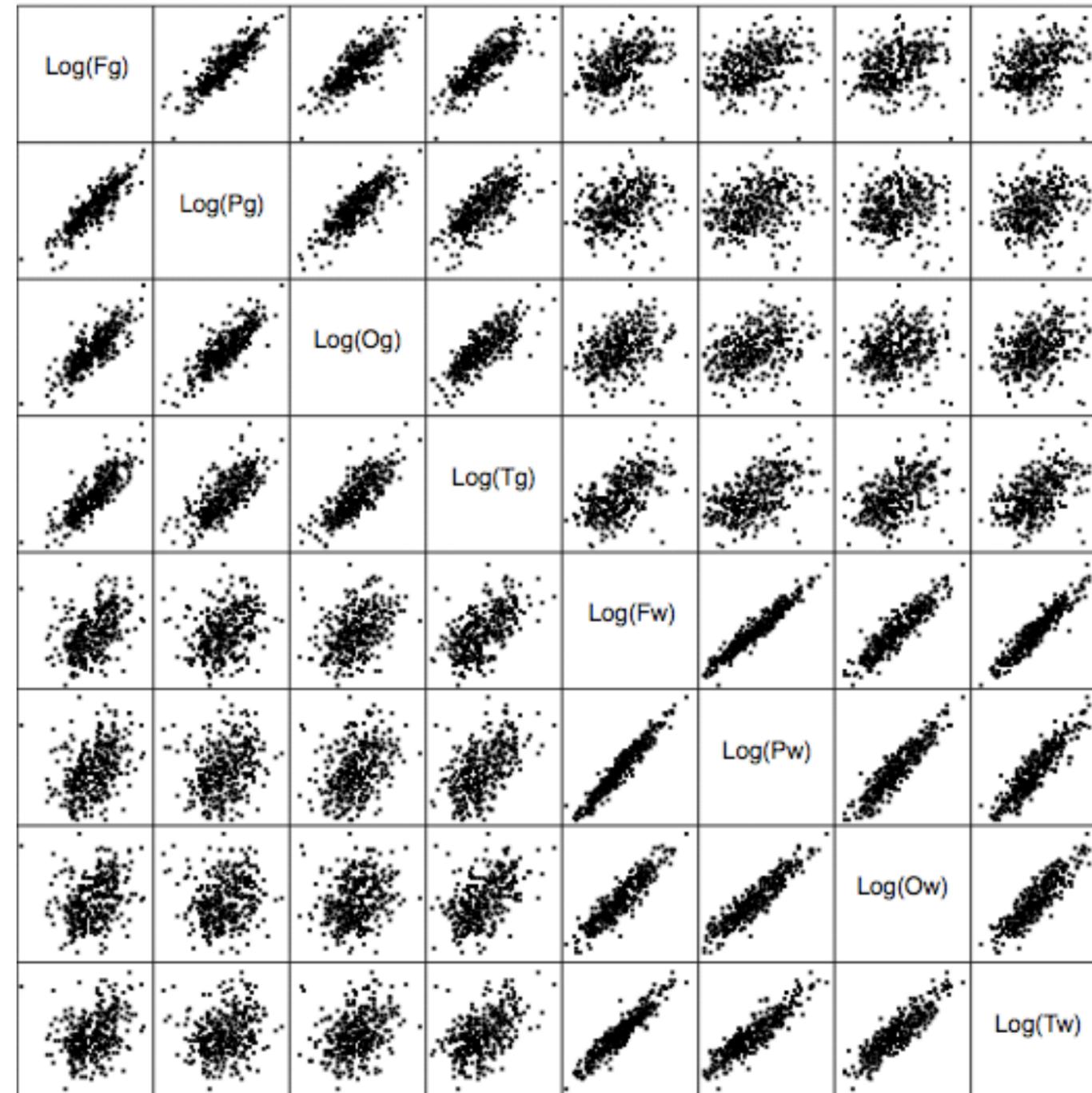
N=314 (SLSJ)

■ Val  
 ■ Met



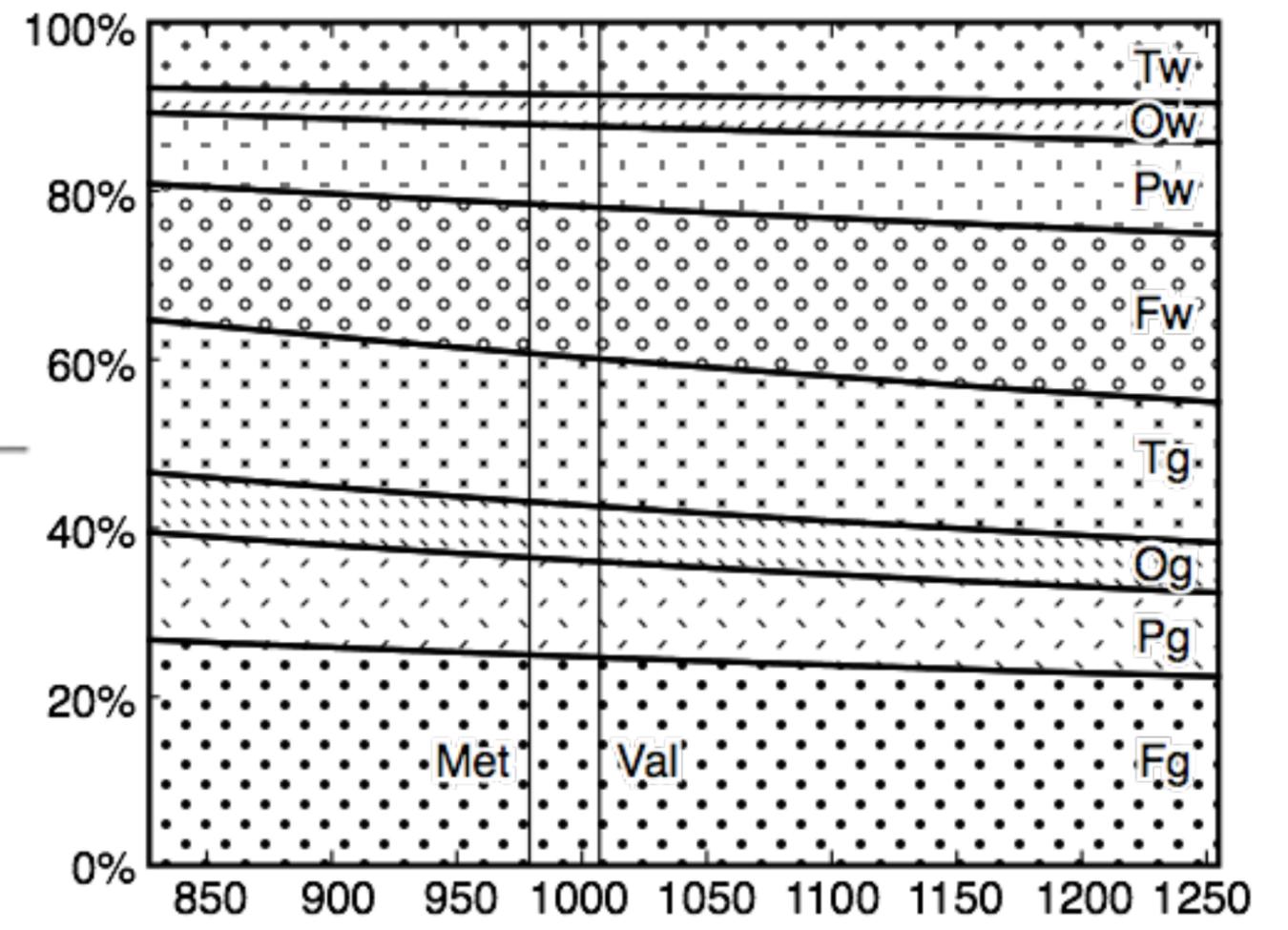
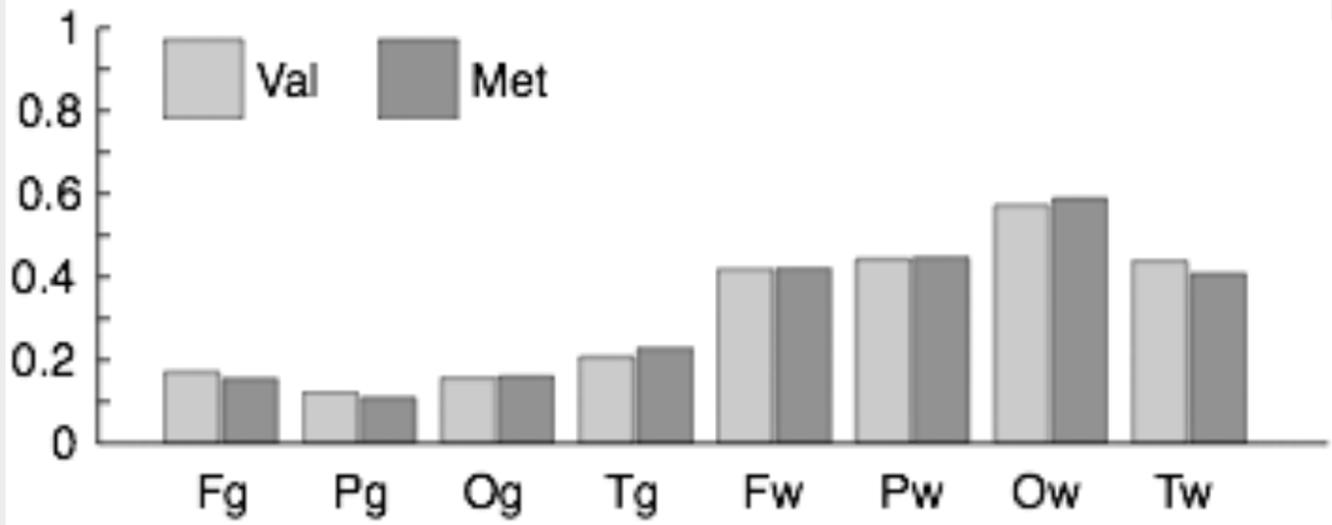
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“Brain volumes and Val66Met polymorphism of the BDNF gene: local or global effects?”, Toro et al, Brain Struct Func 2009

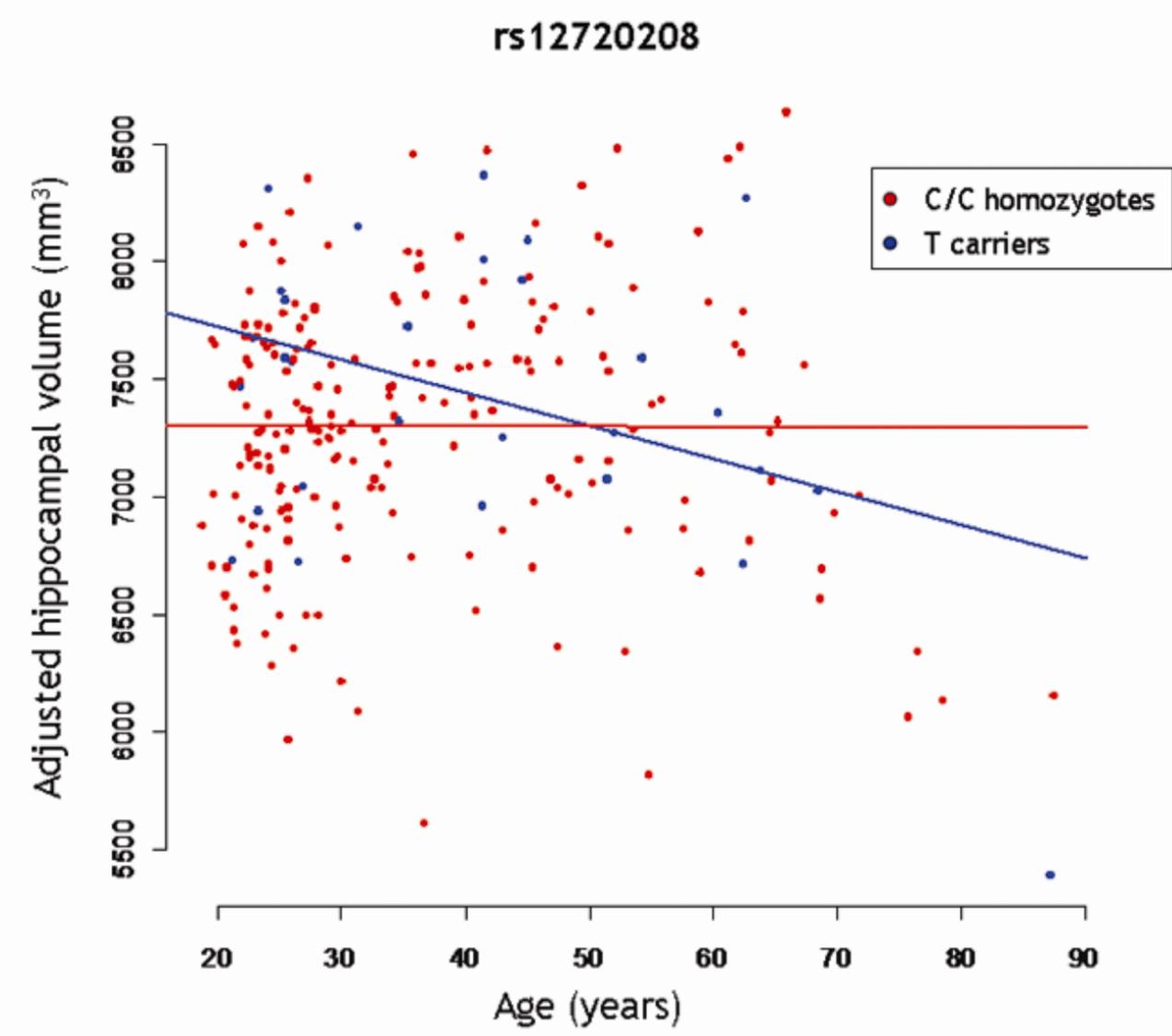
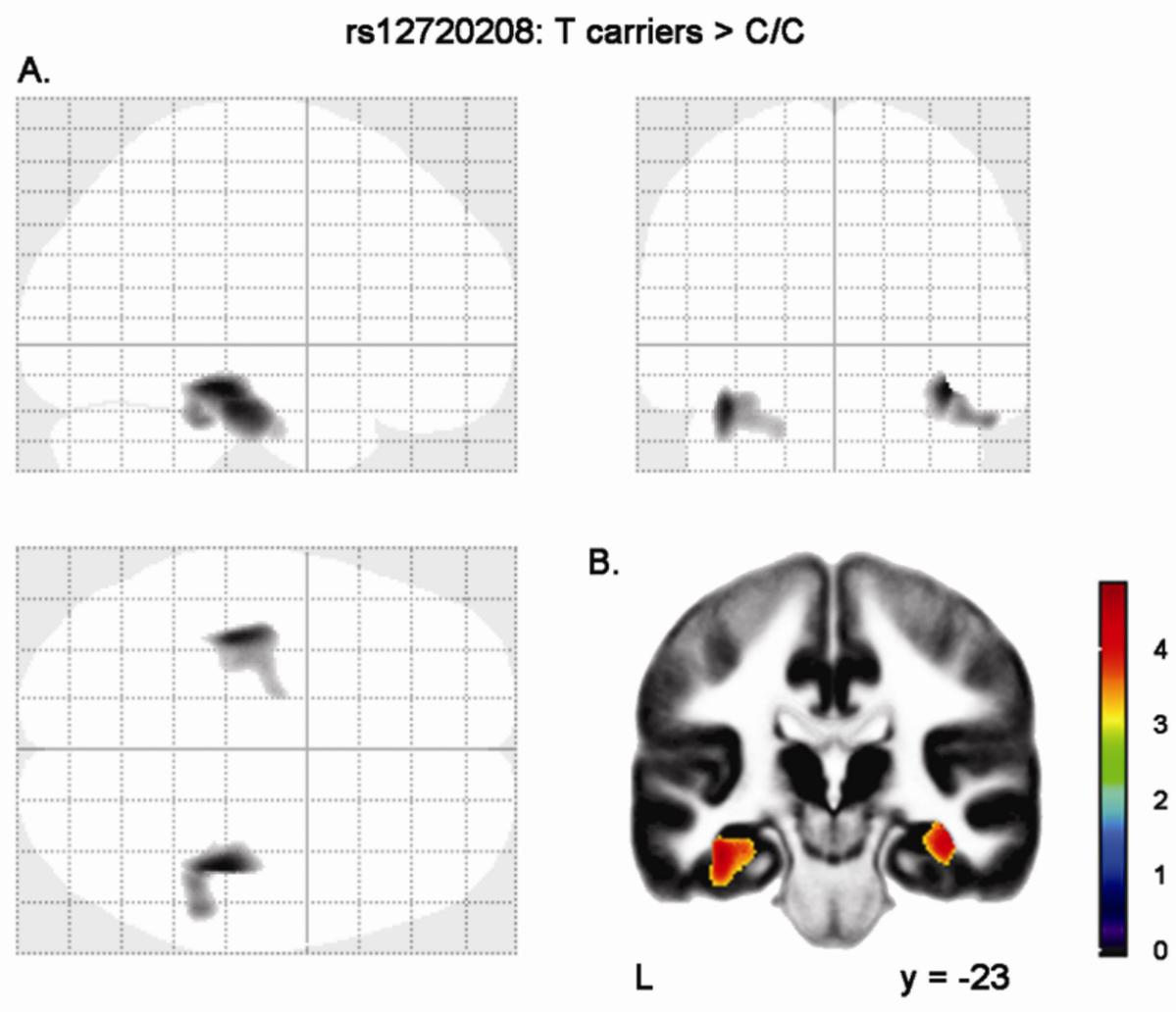
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“Genetic Variation in FGF20 Modulates Hippocampal Biology”,  
Lemaitre et al, Journal of neuroscience 2010

**FGF20**  
rs12720208  
0030154 cell differentiation (486)  
0007267 cell-cell signaling (239)  
0008284 positive regulation of cell proliferation (329)

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summary & discussion

Neuroimaging provides **interesting** and **relevant** endophenotypes to study brain development and psychiatric disorders.

•

Heritability studies show that brain anatomy has a **strong genetic component**. The little variance explained by the current candidate genes suggests the presence of **many genes of small effect**. It is then fundamental to ensure the biological pertinence and the accuracy of the neuroimaging endophenotypes used.

•

Brain morphogenesis is subject to strong **developmental constraints**, understanding this process is essential to understand brain variability

•

Genetic polymorphisms reflect the **diversity of human populations**, but do they encode **neuroanatomical diversity** or the susceptibility to common psychiatric diseases?

# Acknowledgments

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