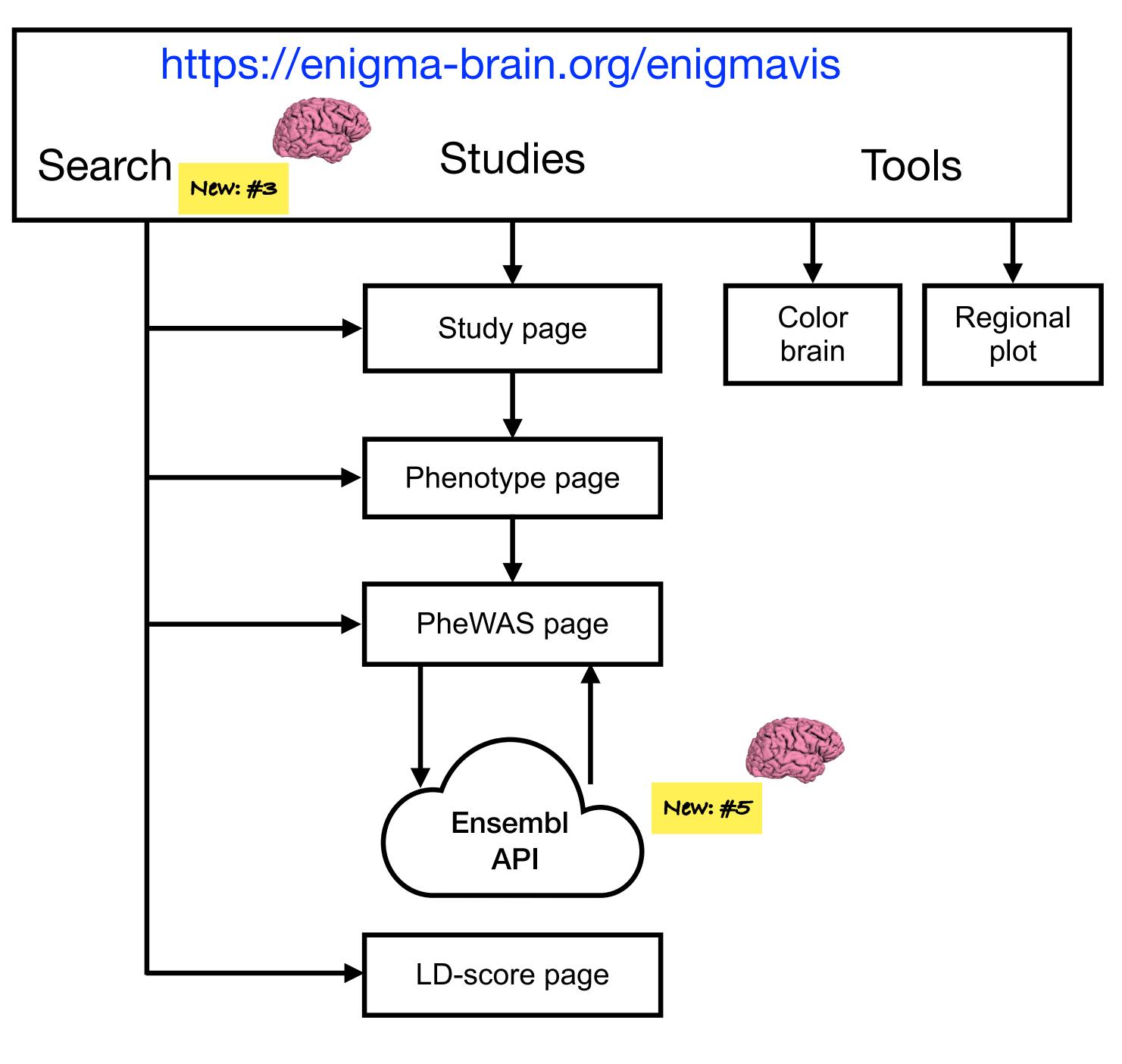
# **Enigma-Vis: a Web Portal to Interact with International Genome-Wide Association Studies (GWAS) of Brain Measures**



# Introduction

We present an update on our ENIGMA Consortium GWAS visualization portal, ENIGMA-Vis (https://enigma-brain.org/enigmavis/). Our portal is a set of browserbased tools to visualize and navigate the GWAS results from the ENIGMA consortium. These GWAS have discovered over 500 common genetic variants associated with brain measures (cortical and subcortical morphometry, sulcal measures, and longitudinal rates of brain growth and atrophy). Users can query and visualize all datasets side by side - to make regional GWAS plots, perform PheWAS analyses, and enable LD data visualization. For cortical data visualization, the portal offers a tool for making 3D color-coded brain maps of SNP effects on the brain. To readily explore the datasets, a search bar is provided at the top of the page. It accepts query input data in the form of the Single Nucleotide Polymorphism Database (dbSNP) id, gene name, phenotype name, and study name. With the recent release of a new GWAS study of brain longitudinal changes (Brouwer et al., 2022), we updated the portal with the top findings from the age-independent meta-analysis and meta-regression. This new data prompted us to add several new features to improve usability. We enhanced the portal to accept a user query by genomic position and upgraded the underlying data reference source to a recent version 155 of dbSNP for the genome assembly GrCh37/hg19. To help with the case when a query SNP entered in the search bar cannot be found in the data reference source, we implemented an additional SNP lookup in the Ensembl API. For a smoother user experience, the PheWAS page was upgraded with an added option to sort data points by p-value.



### Site map

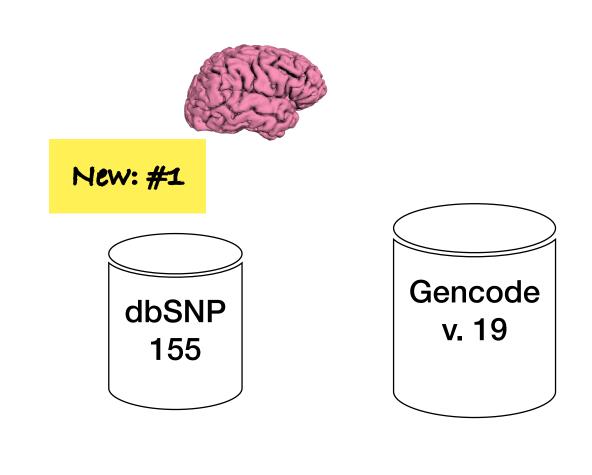
## **Data sources**

#### Publications

rouwer, Rachel M et al. "Genetic variants associated with longitudinal changes in brain structure across the lifespan." Nature neuroscience vol. 25,4 (2022): 421-432. doi:10.1038/s41593-022-01042-4 Grasby, Katrina L et al. "The genetic architecture of the human cerebral cortex." Science (New York, N.Y.) vol. 367,6484 (2020): eaay6690. doi:10.1126/science.aay6690 Adams, Hieab H H et al. "Novel genetic loci underlying human intracranial volume identified through genome-wide association." Nature neuroscience vol. 19,12 (2016): 1569-1582. doi:10.1038/nn.4398 Hibar, Derrek P et al. "Novel genetic loci associated with hippocampal volume." Nature communications vol. 8 13624. 18 Jan. 2017, doi:10.1038/ ncomms13624 Hibar, Derrek P et al. "Common genetic variants influence human subcortical brain structures." *Nature* vol. 520,7546 (2015): 224-9. doi:10.1038/nature14101 Stein, Jason L et al. "Identification of common variants associated with human hippocampal and intracranial volumes." Nature genetics vol. 44,5 552-61. 15 Apr.

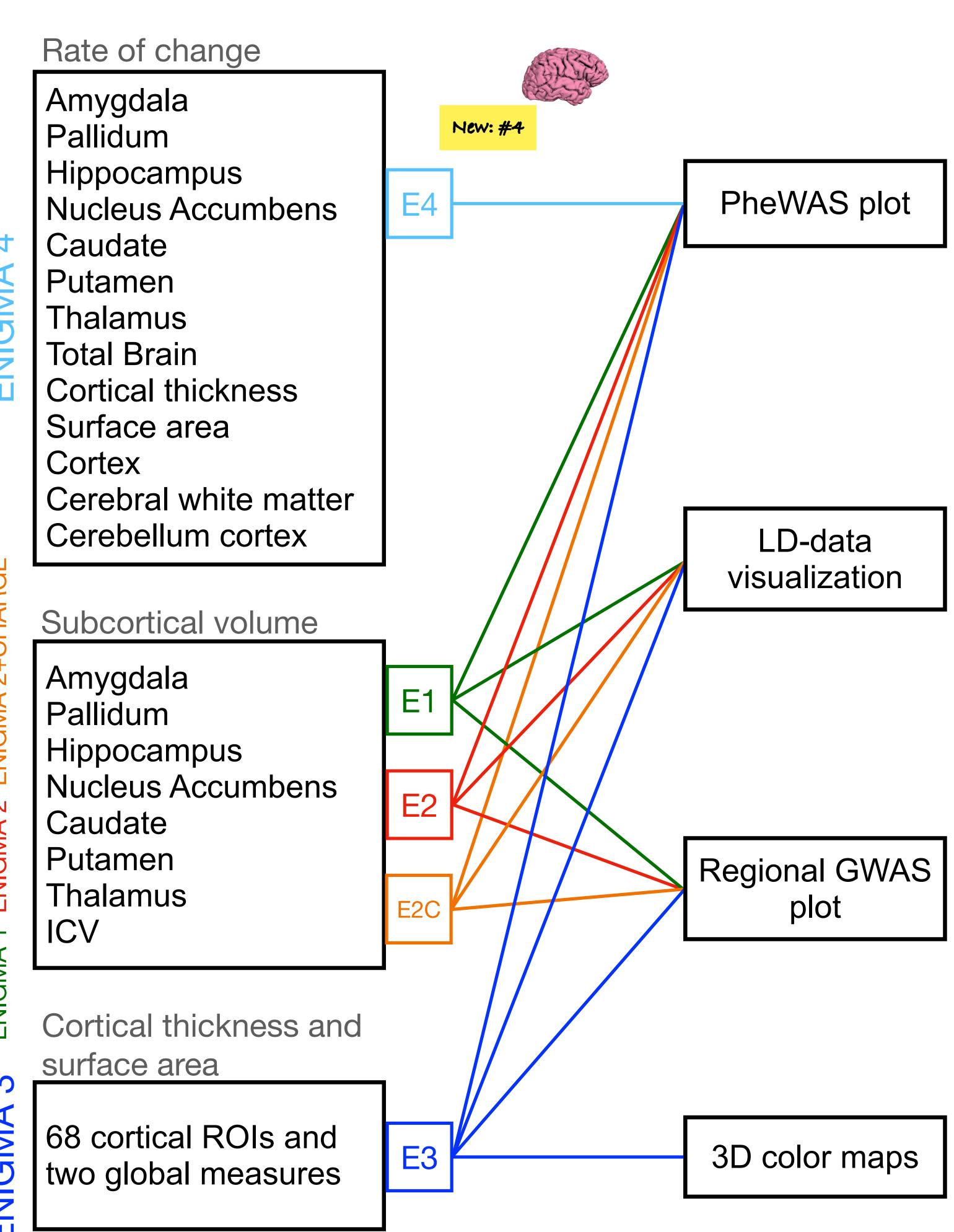
2012, doi:10.1038/ng.2250

Local copies of genomic reference databases



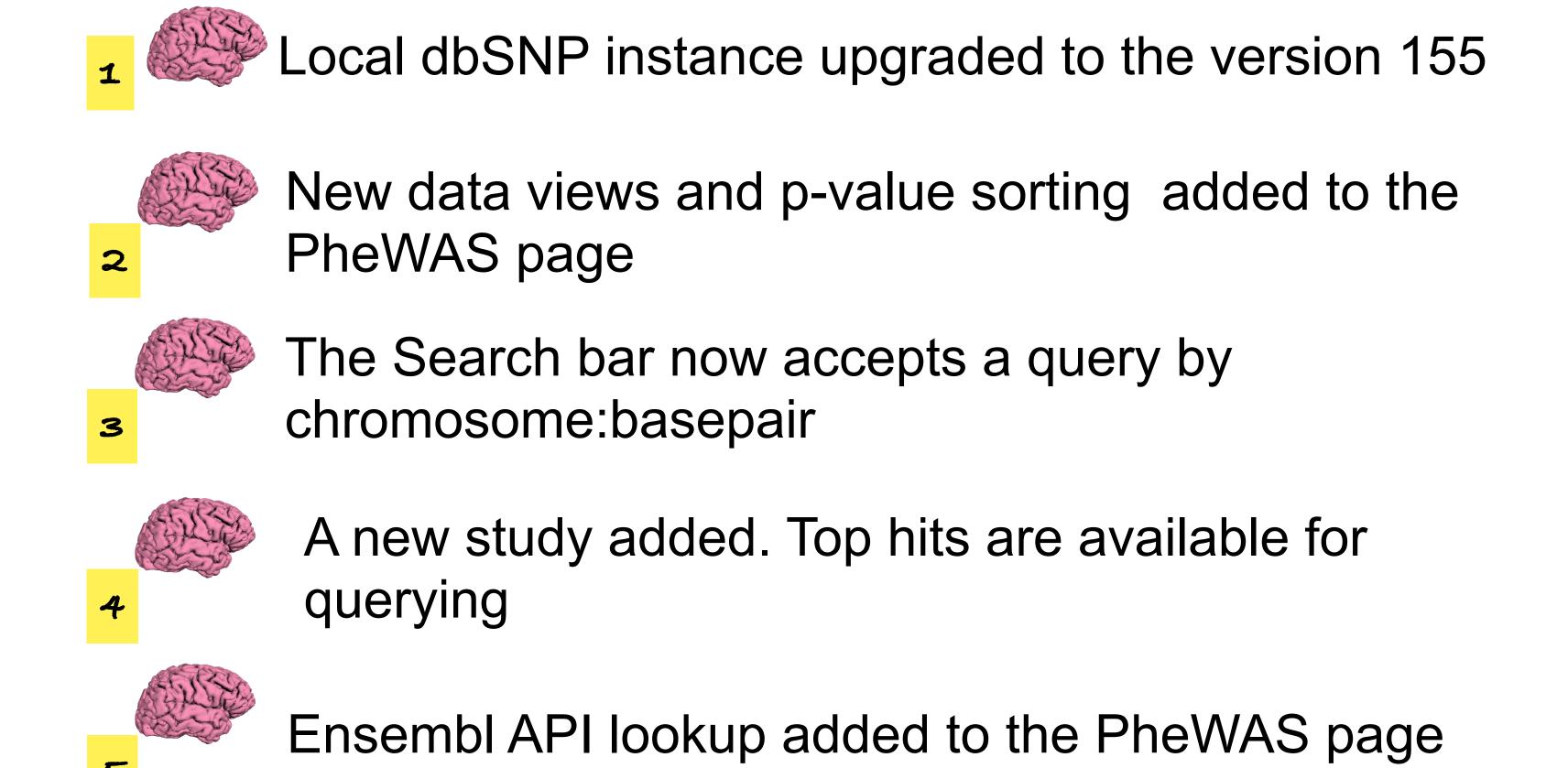
Natalia Shatokhina<sup>1</sup>, Fabrizio Pizzagalli<sup>2</sup>, Rachel M. Brouwer<sup>3</sup>, Hilleke E. Hulshoff Pol<sup>3</sup>, Neda Jahanshad<sup>1</sup>, Jason L. Stein<sup>4</sup>, Sarah E. Medland<sup>5</sup>, ENIGMA GWAS Working Group, Paul M. Thompson<sup>1</sup>

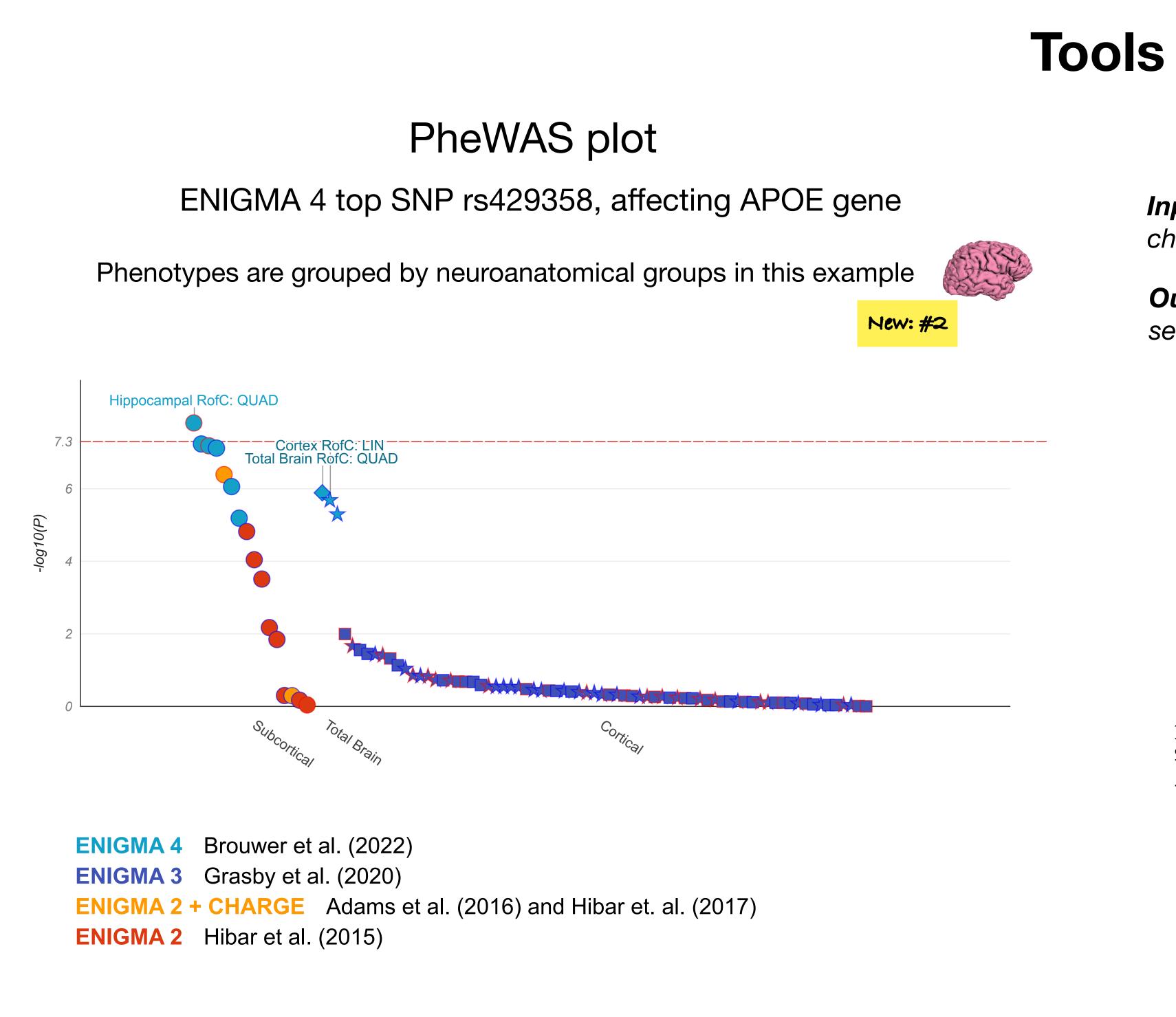
<sup>1</sup> Imaging Genetics Center, Mark and Mary Stevens Neuroimaging and Informatics Institute, University of Southern California, Los Angeles, USA, <sup>2</sup> Department of Neuroscience "Rita Levi Montalcini", University of Turin, Turin, Italy, <sup>3</sup> Department of Psychiatry, Brain Center Rudolf Magnus, University Medical Center, Utrecht, The Netherlands, <sup>4</sup> Department of Genetics & UNC Neuroscience Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA, <sup>5</sup> QIMR Berghofer Medical Research Institute, Brisbane, QLD, Australia



### Datasets

## **New features**





#### 3D color maps of the ENIGMA 3 dataset

SNP rs62101917 (also a top hit for surface area in the ENIGMA 4 dataset)

Input: SNP rs id

**Output:** z-score or p-value textured on 3D brain for surface area or cortical thickness

#### Features:

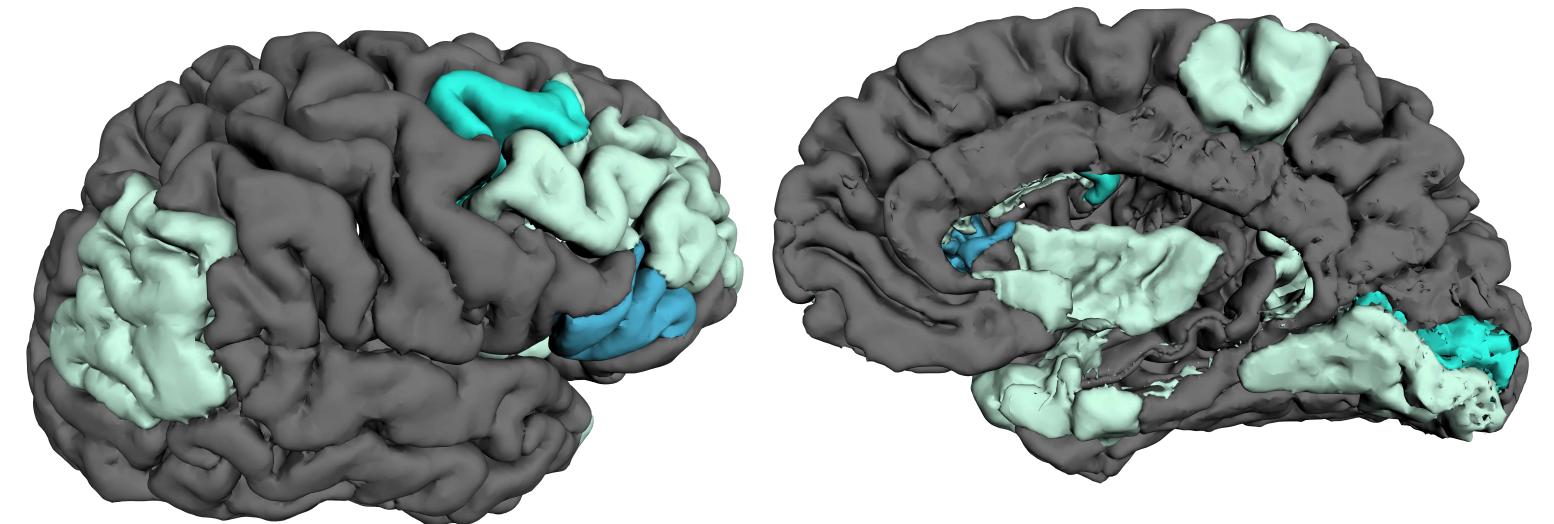
Interactive 3D brain rotation User customizable colorscales Mouse over tooltips Downloadable PNG images

rs62101917 A1: T A2: C Ref: C Category: surface area

full surface area -log10(p): 0 Z-score: 0.05



Right hemisphere (front and back view)



#### USC Mark and Mary Stevens Neuroimaging and Informatics Institute



#### Regional GWAS plot

Input: SNP rs id, gene, a chromosomal region

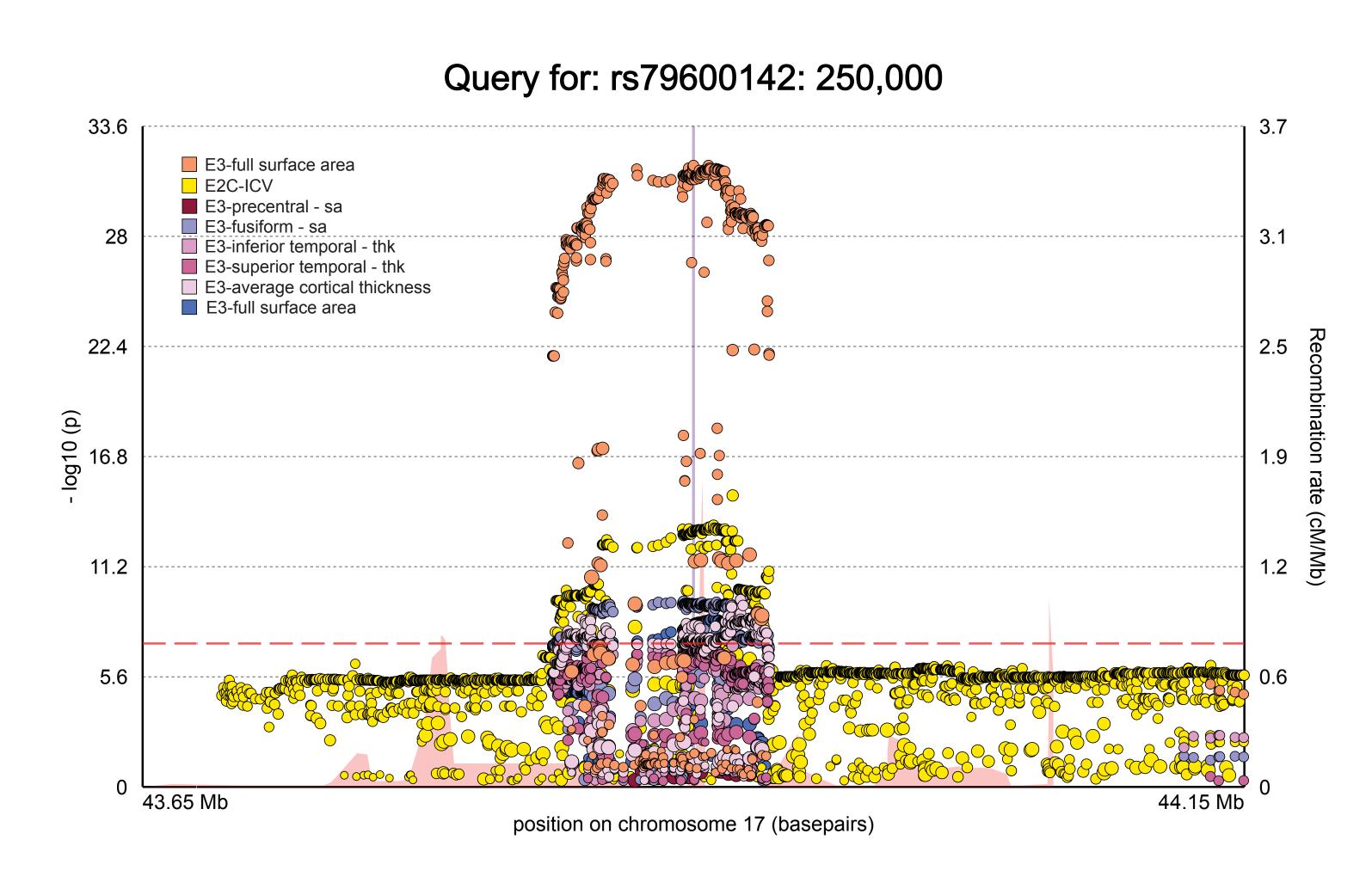
selected phenotypes

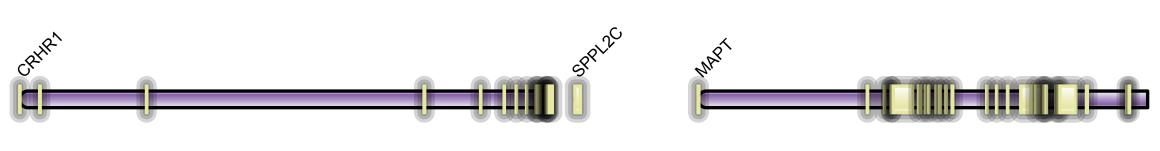
**Output:** Regional plot for user

#### Features:

Multi- phenotypes selection (up to 8) Option to select brain regions on a 3D brain (ENIGMA 3 only) Sliding window

Mouse over tooltips





#### LD data visualization

<b>MAPT</b>		
· ····································	ignificant associations (p < 1.5e-05) for this locus:	
Study	Phenotype	P-value
ENIGMA 3	full surface area	2.33e-32
ENIGMA 2 - CHARGE	icv	1.45e-15
ENIGMA 3	average cortical thickness	2.90e-10
ENIGMA 3	fusiform - surface area	3.48e-10
ENIGMA 2	icv	2.87e-9
ENIGMA 3	superior temporal - cortical thickness	3.03e-8
ENIGMA 3	inferior temporal - cortical thickness	4.49e-8
ENIGMA 3	lingual - surface area	1.68e-7
ENIGMA 3	rostral anterior cingulate - cortical thickness	4.78e-7
ENIGMA 3	middle temporal - cortical thickness	6.24e-7
Showing 1 to 10 of 15 entrie		
	s urface area (ENIGMA 3)	Previous 1 2 Next   LD Population: ALL Save PNG Save SVG
Phenotype: full su		
Phenotype: full su LocusZoom v0.12.2	urface area (ENIGMA 3)	

# Acknowledgements

This work was supported by AI4AD grant. We thank Dr. Peter Kochunov and Sung Yu for hosting the portal.