

# Supplementary Information

## Multi-ancestry versus European signals

S. Goovaerts et al.

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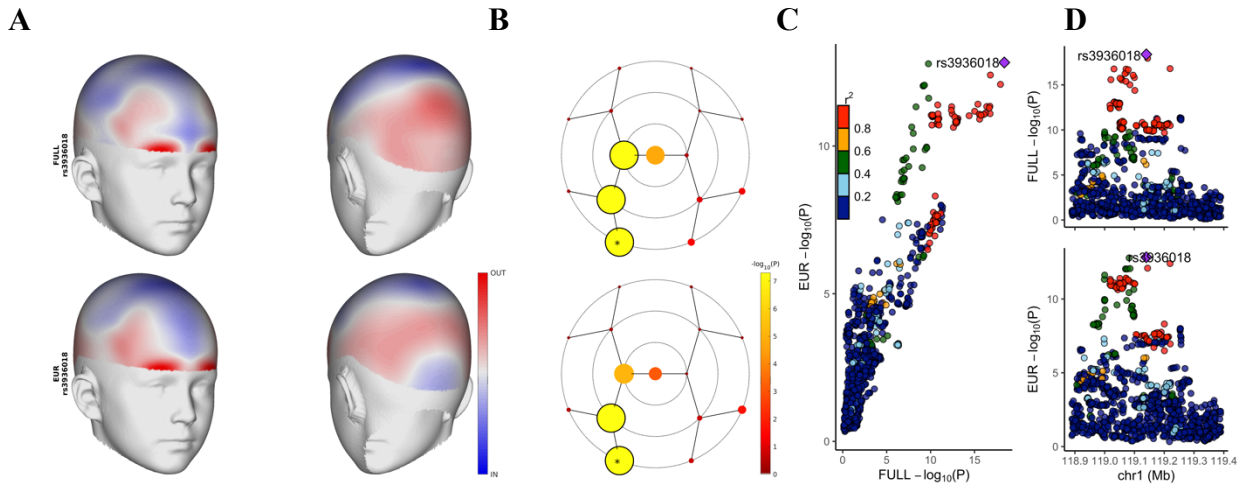
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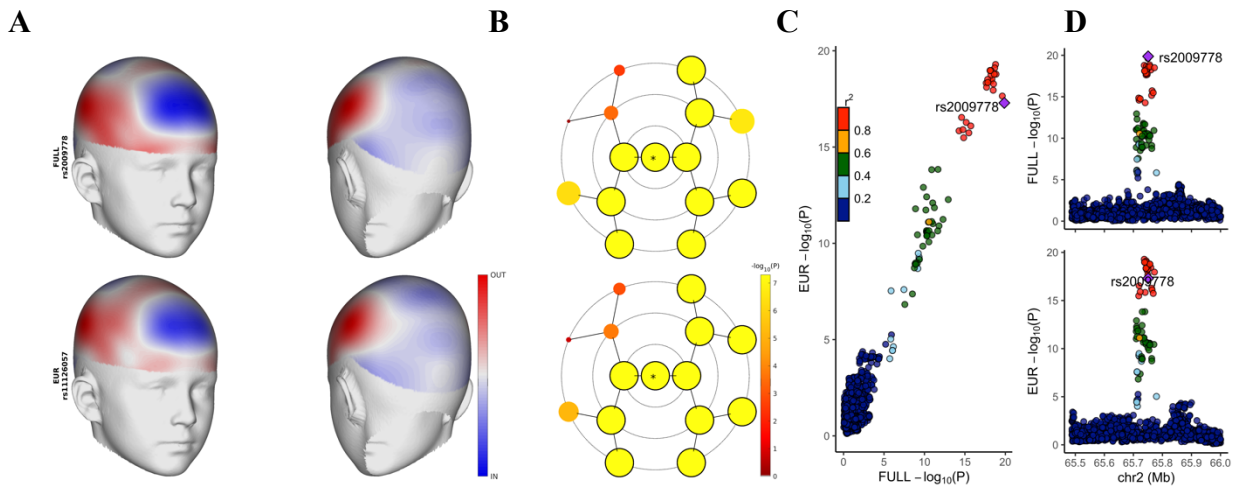
**Comparison of multi-ancestry and European shape associations at the joint set of loci.** **A**, Shape associated with lead SNPs from the full multi-ancestry GWAS (FULL;  $n = 6,772$ ) and European subset GWAS (EUR;  $n = 4,198$ ). Bold rsID labels indicate that the SNP was a lead SNP in the respective GWAS; regular type rsID labels indicate that the SNP was not genome-wide significant but had the lowest P-value among all SNPs within 200kb or in LD ( $r^2 > 0.2$ ). Blue and red indicate inward depression and outward protrusion respectively. **B**,  $-\log_{10}(\text{P-values})$  (one-sided chi-square) across hierarchical cranial vault segments. Genome-wide significant ( $P < 5e-8$ ) segments are indicated with a black circle. The strongest association across all segments is indicated with '\*'. **C**, LocusCompare<sup>1</sup> plot of minimal P-values across hierarchical segments. Colors indicate LD with the most significant SNP across the FULL and EUR GWAS (purple diamond). If that SNP was not found in the 1000 Genomes dataset, the next most significant SNP was chosen. **D**, LocusZoom<sup>2</sup> plots of minimal P-values across hierarchical segments. Panel legend matches with C.

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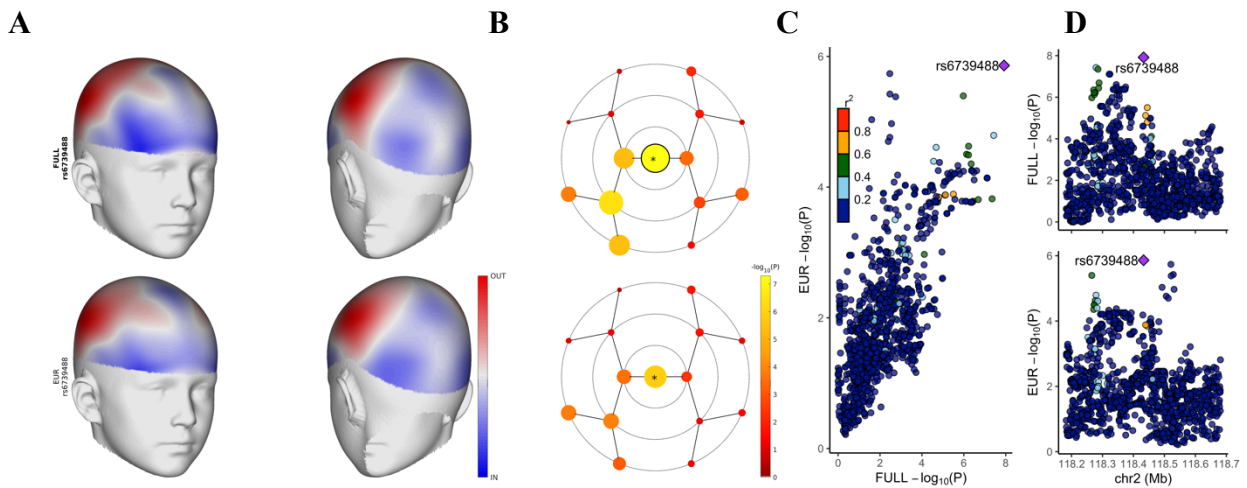
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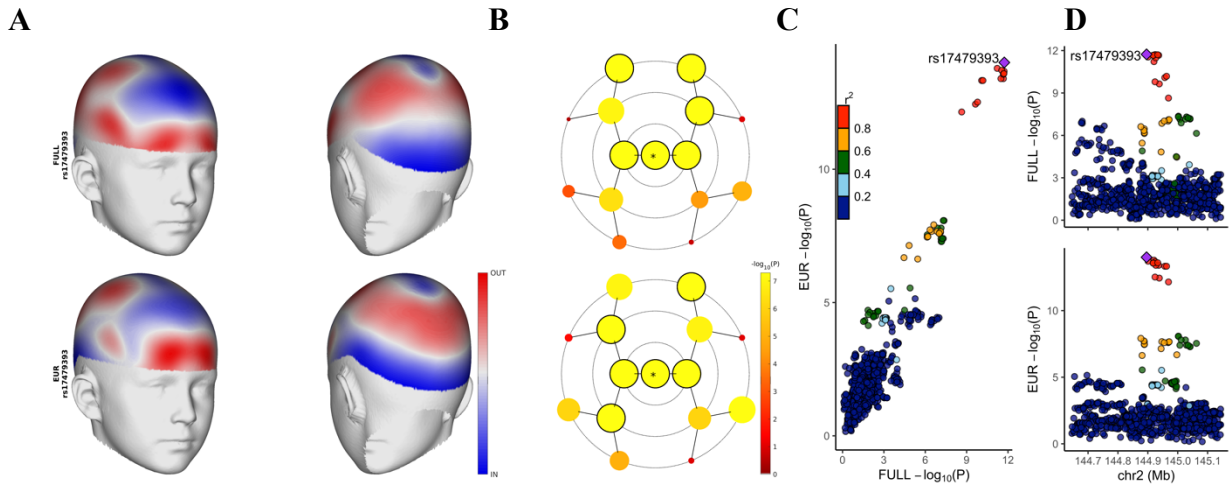


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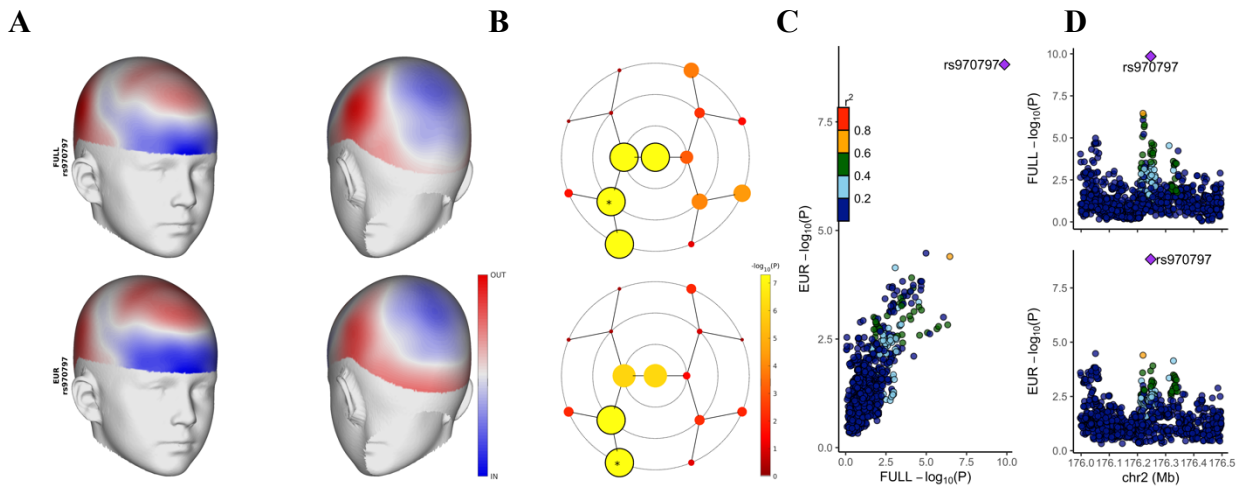


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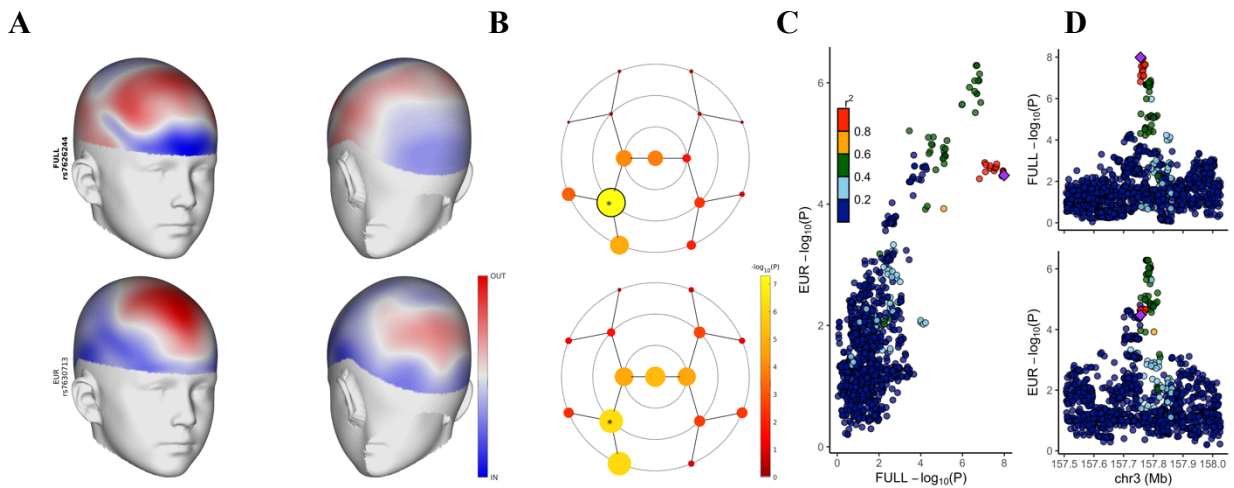
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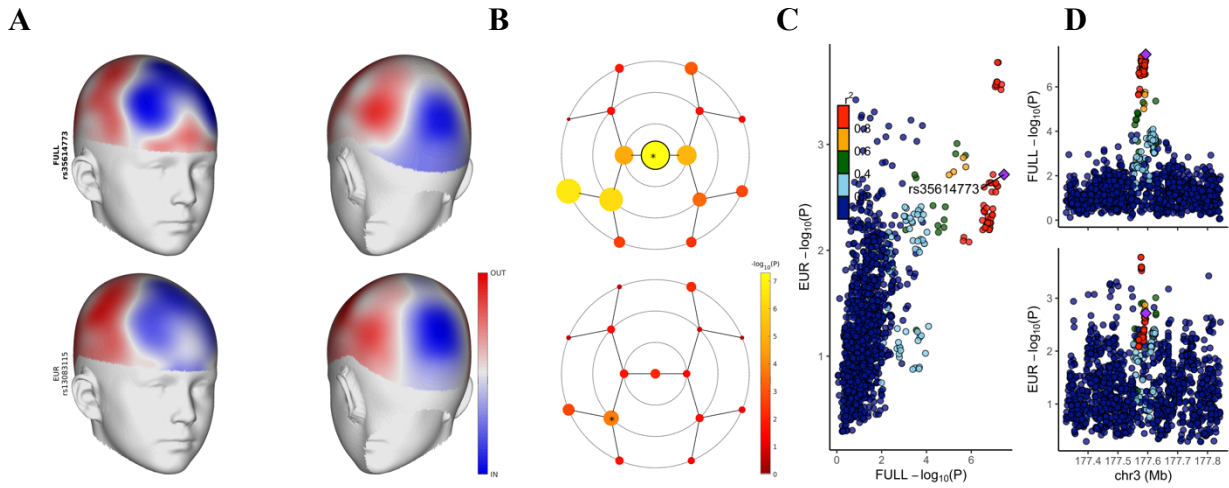
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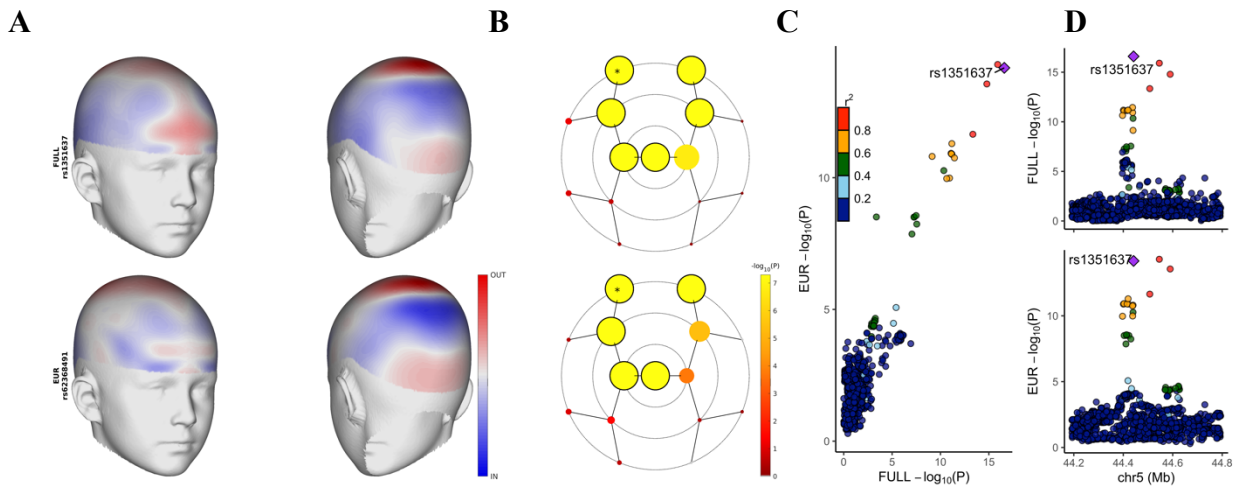
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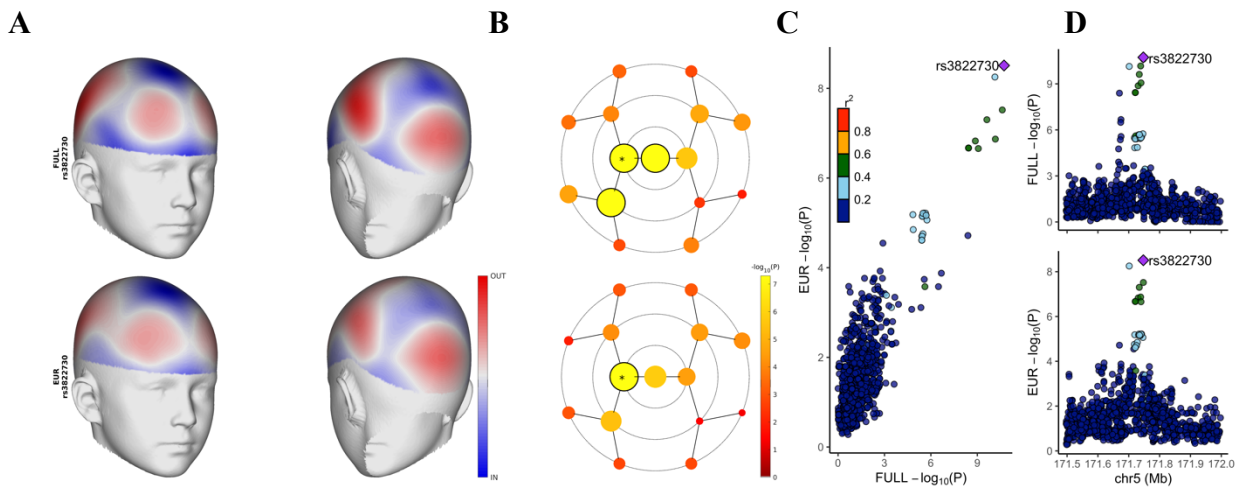
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**rs62368491 – rs1351637**

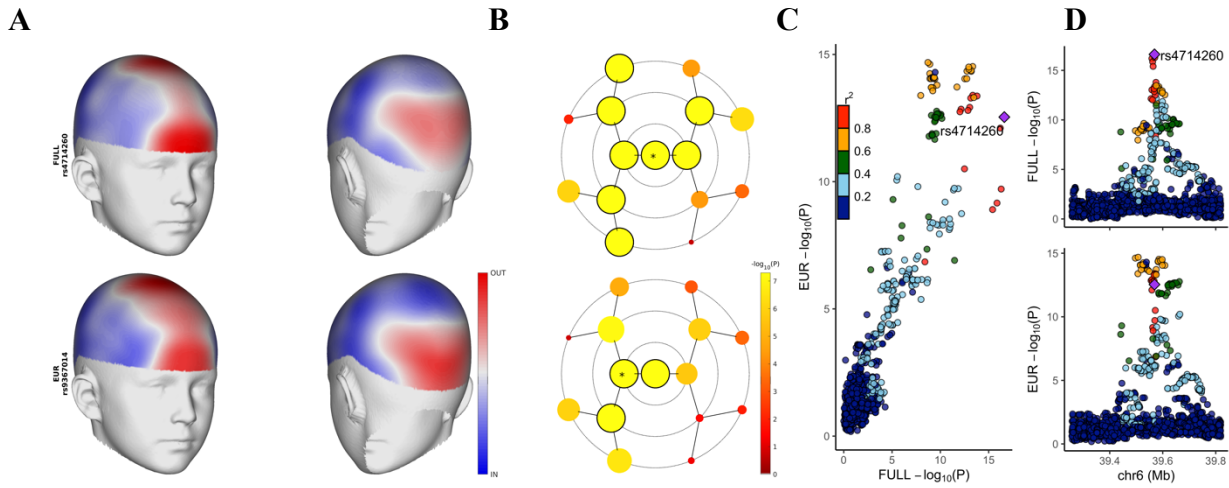


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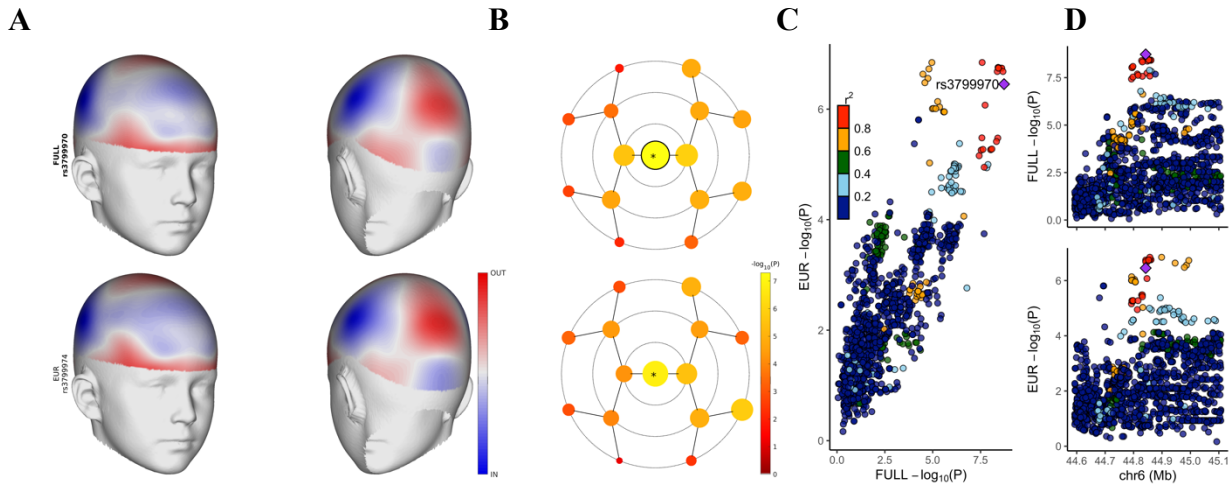


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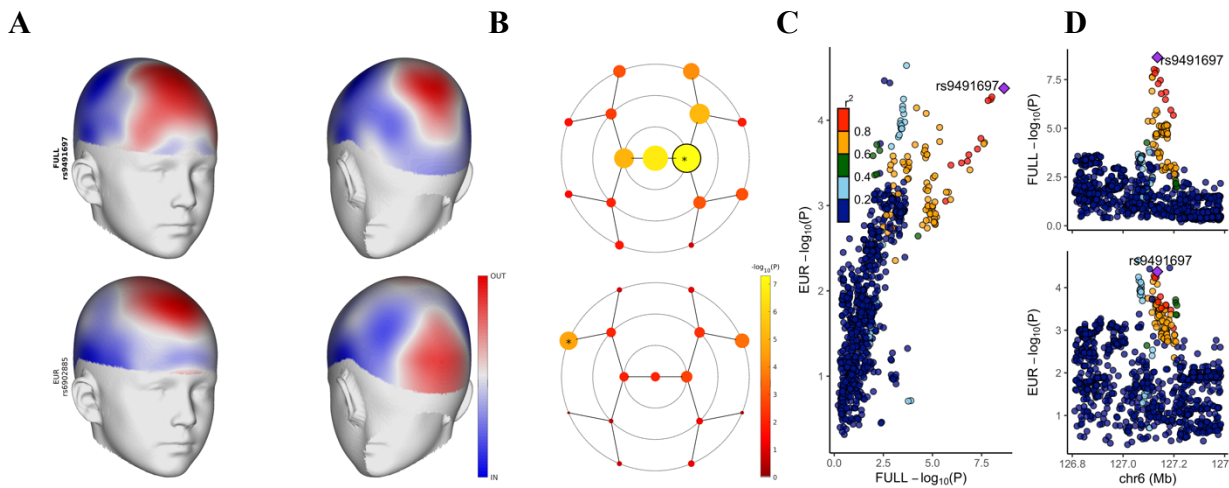
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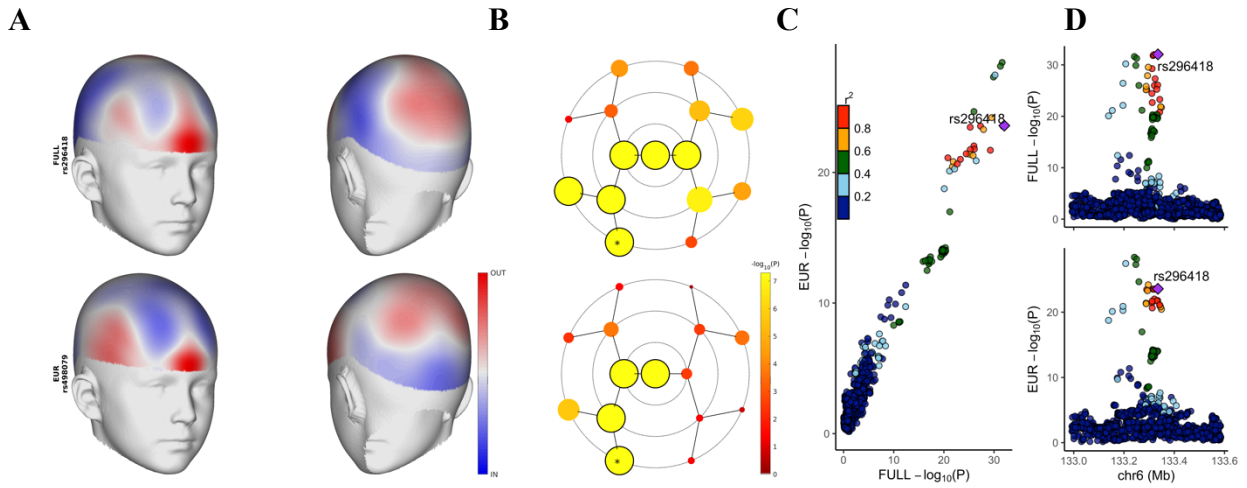


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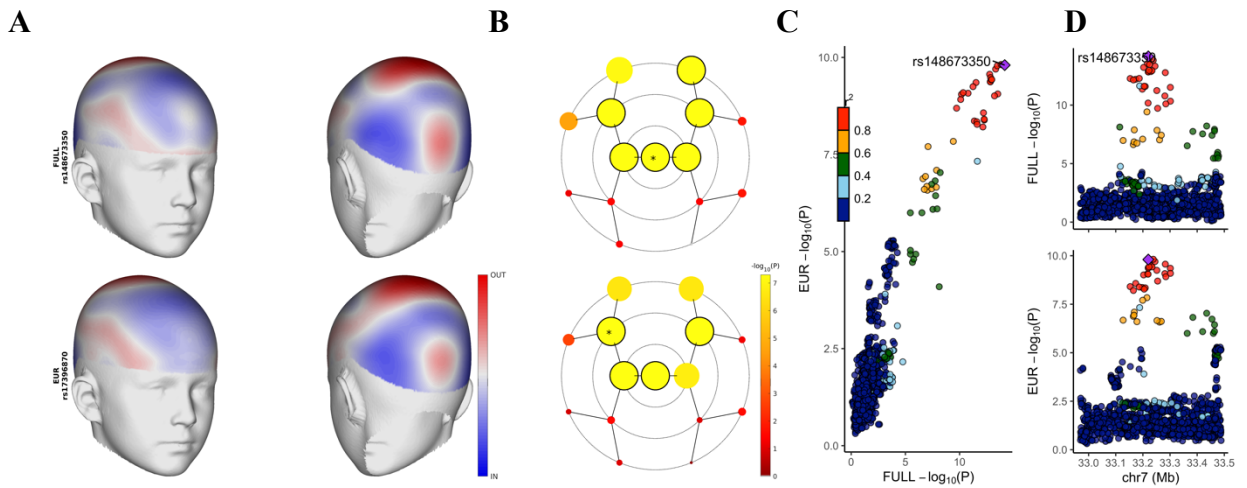


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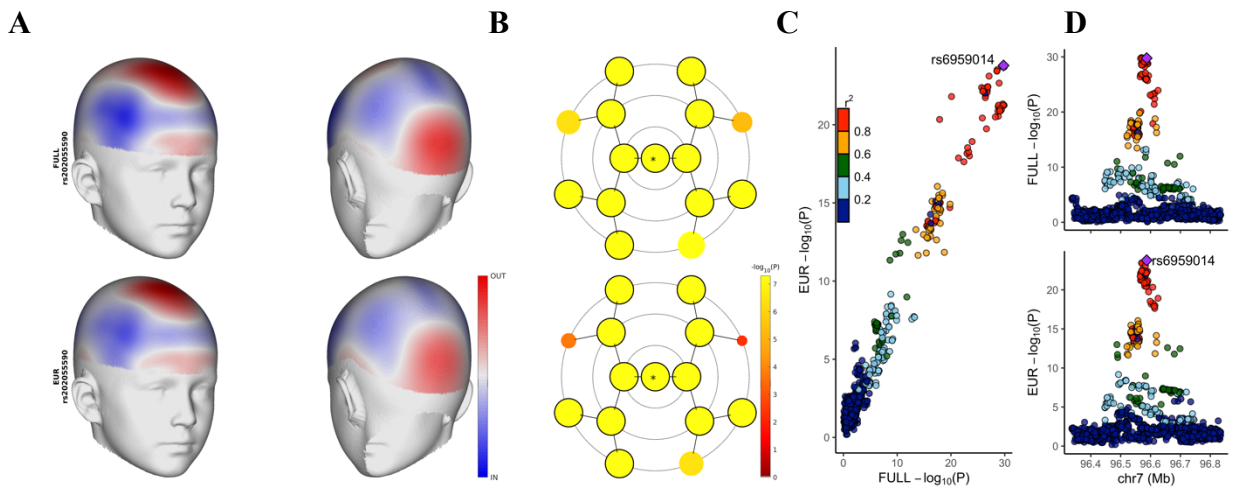
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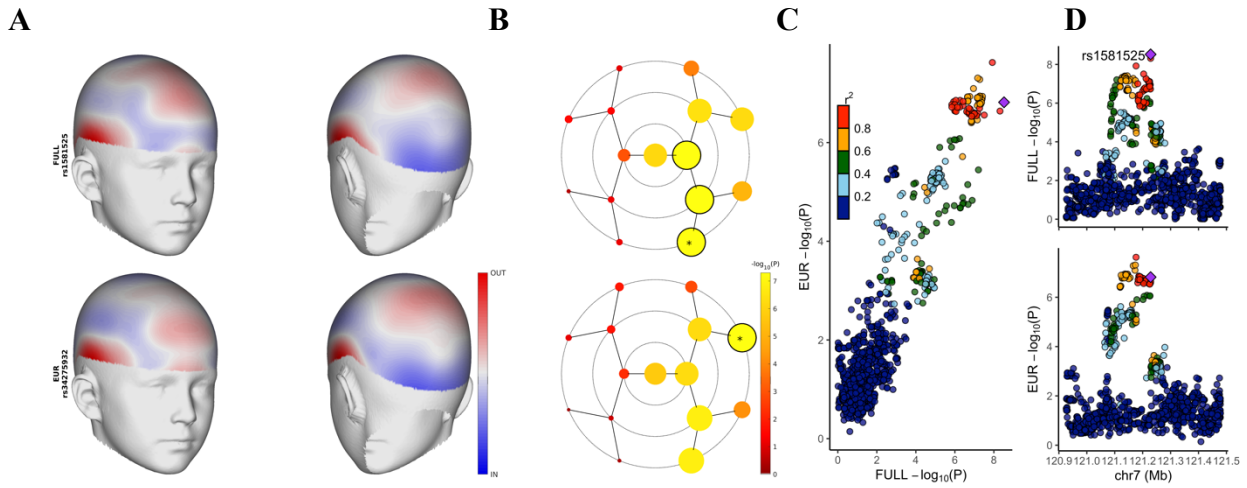


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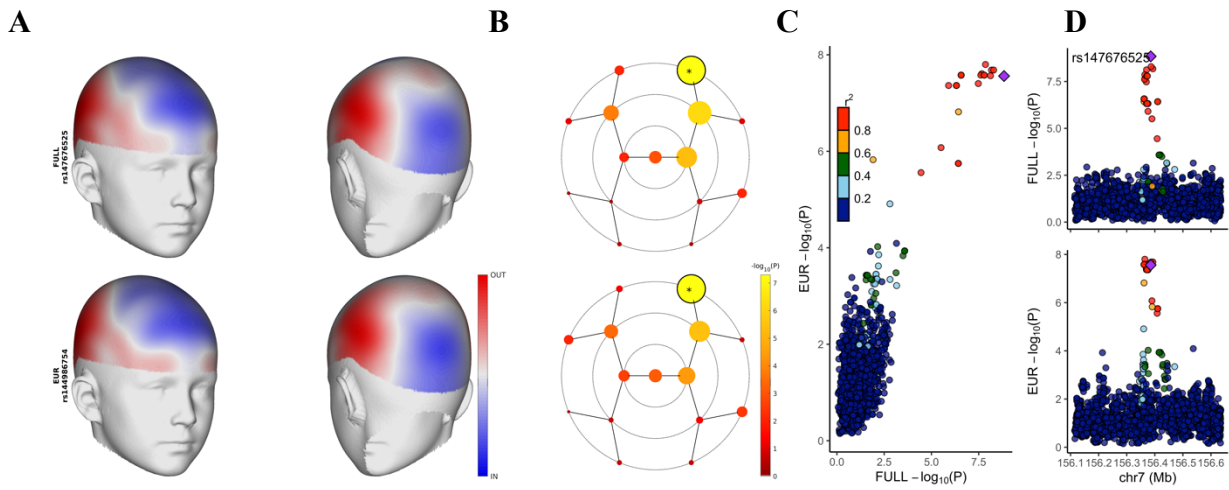


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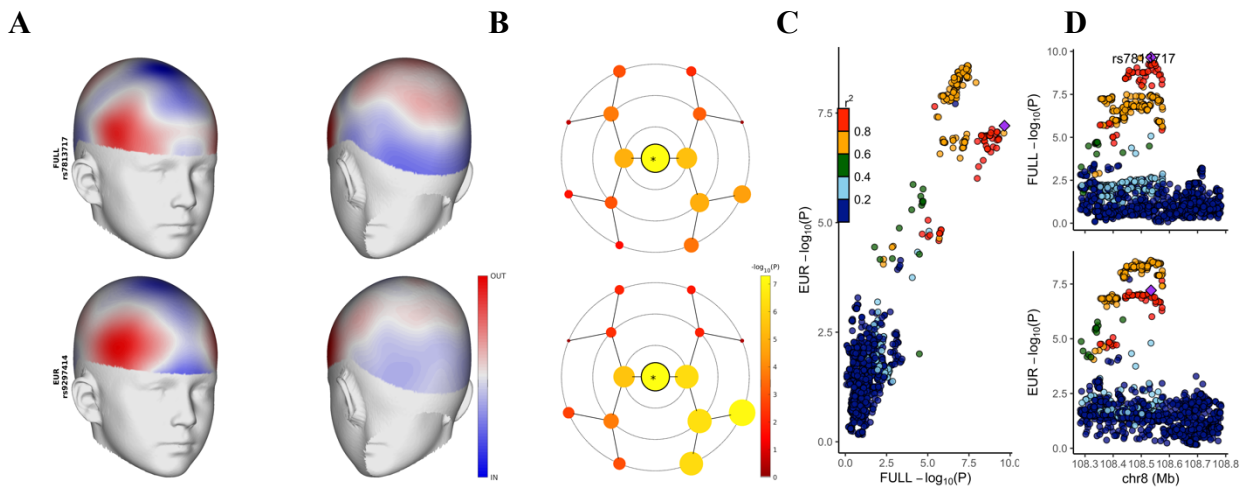
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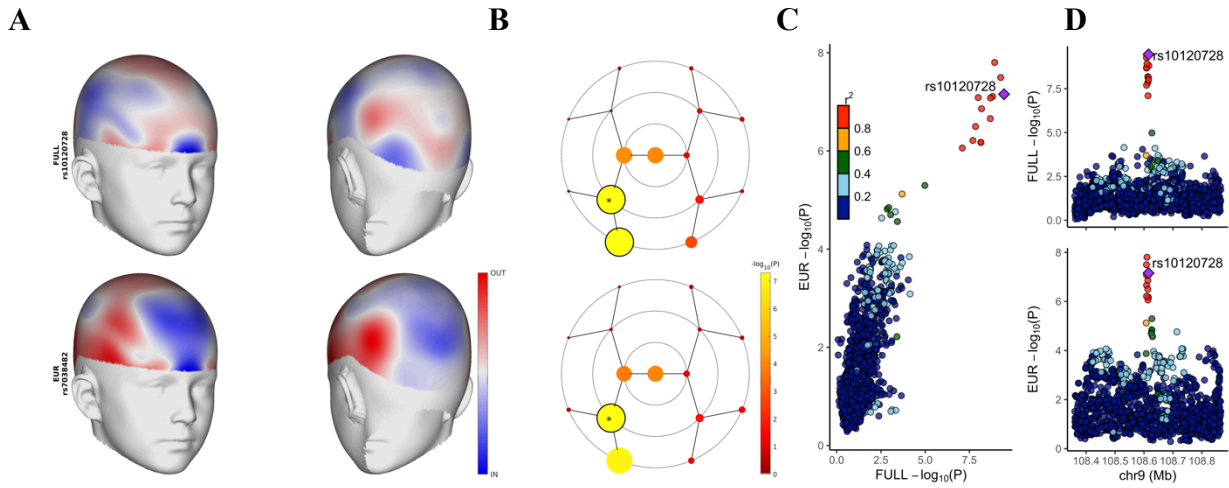
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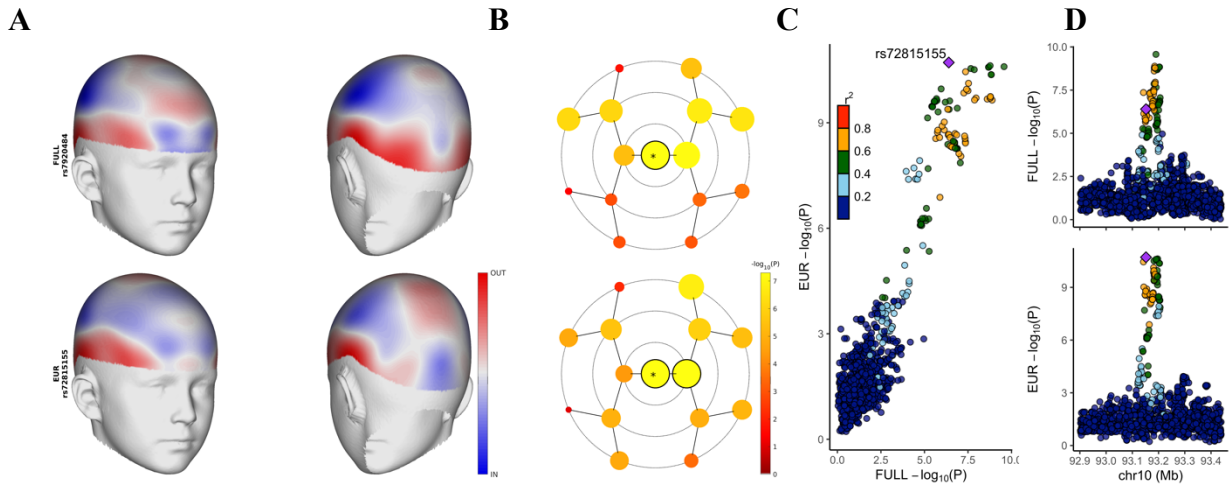


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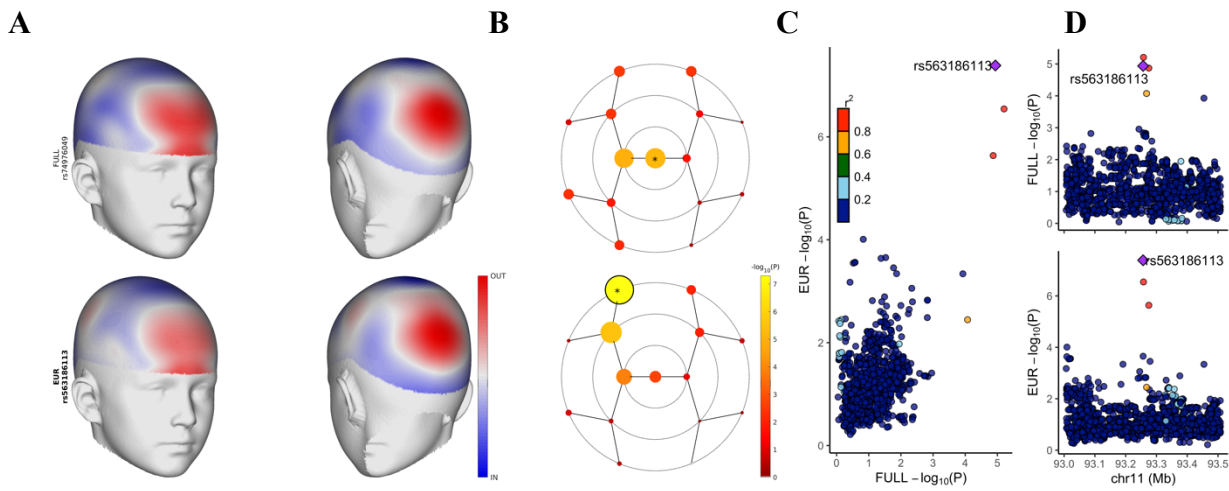
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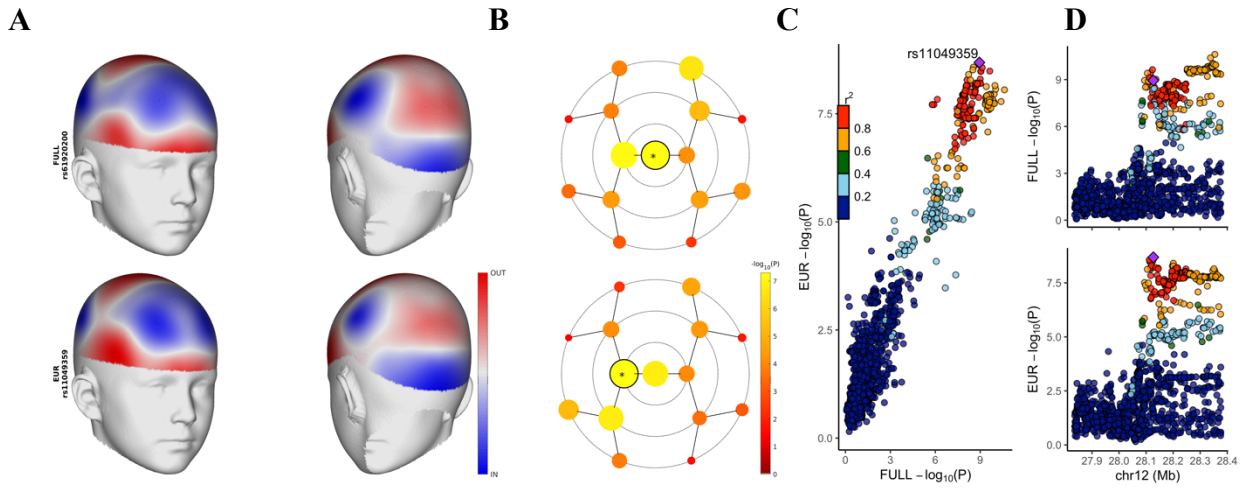


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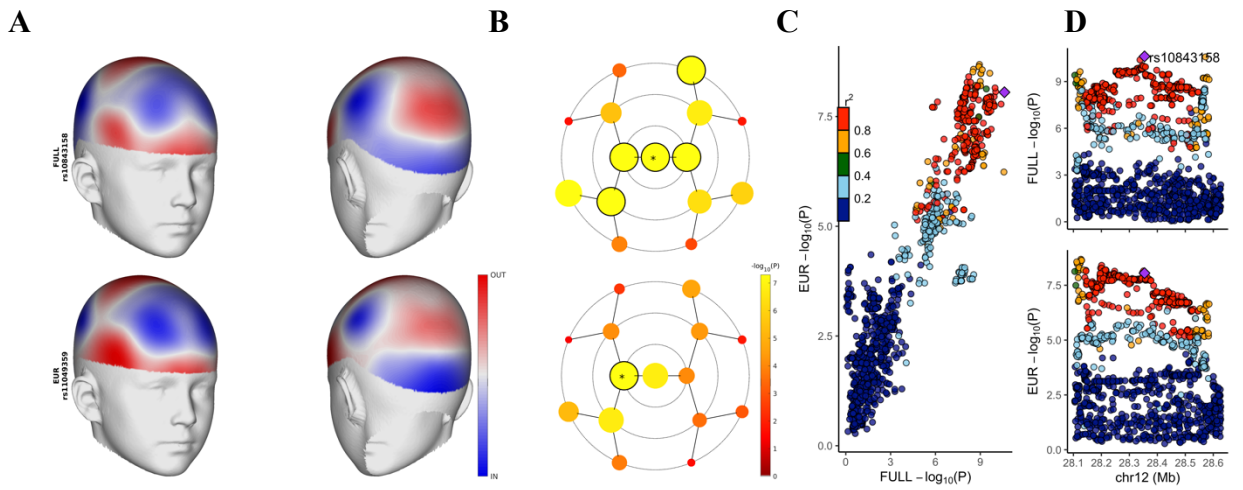


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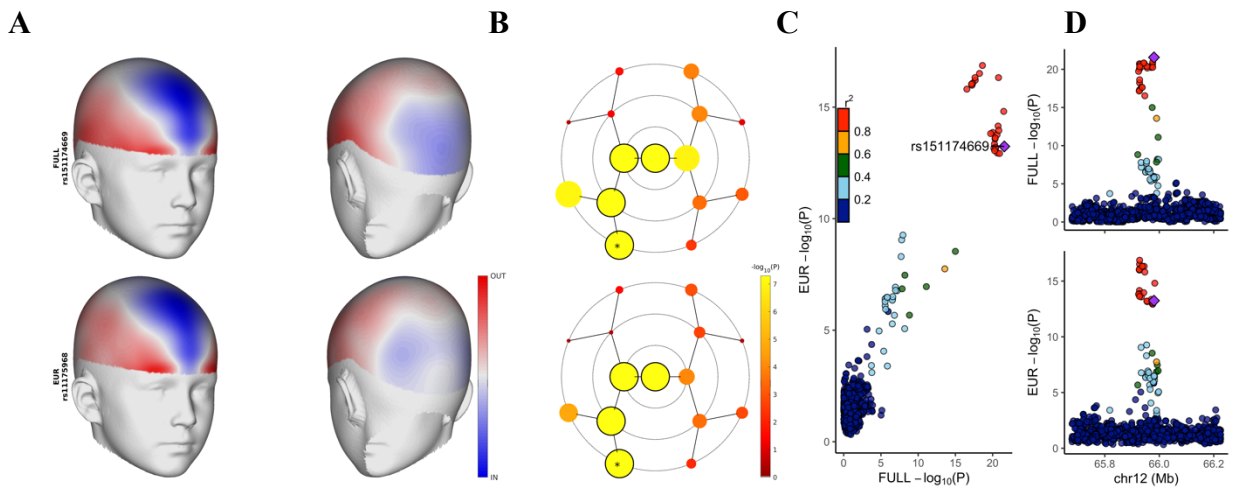
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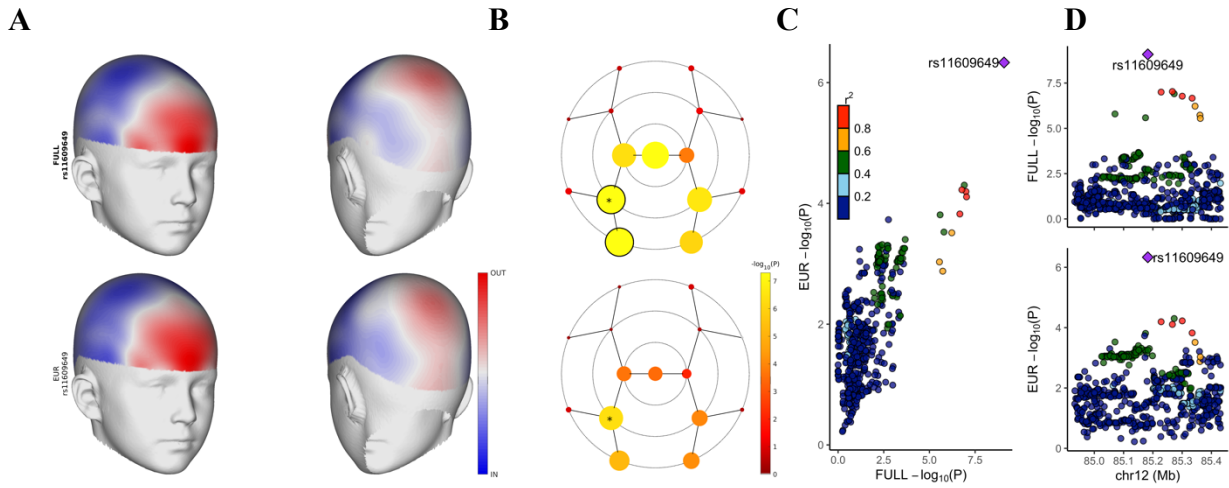


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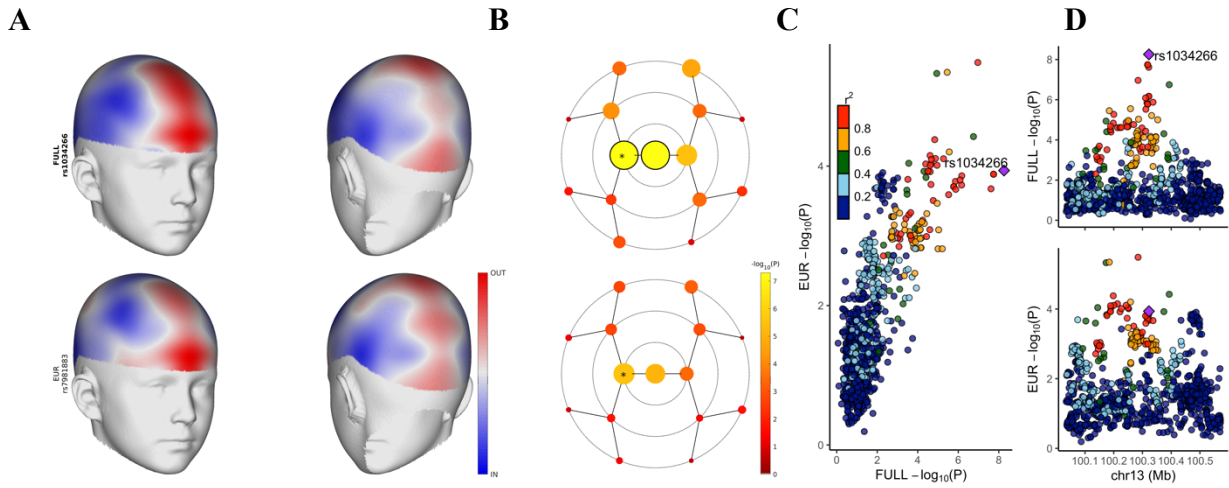


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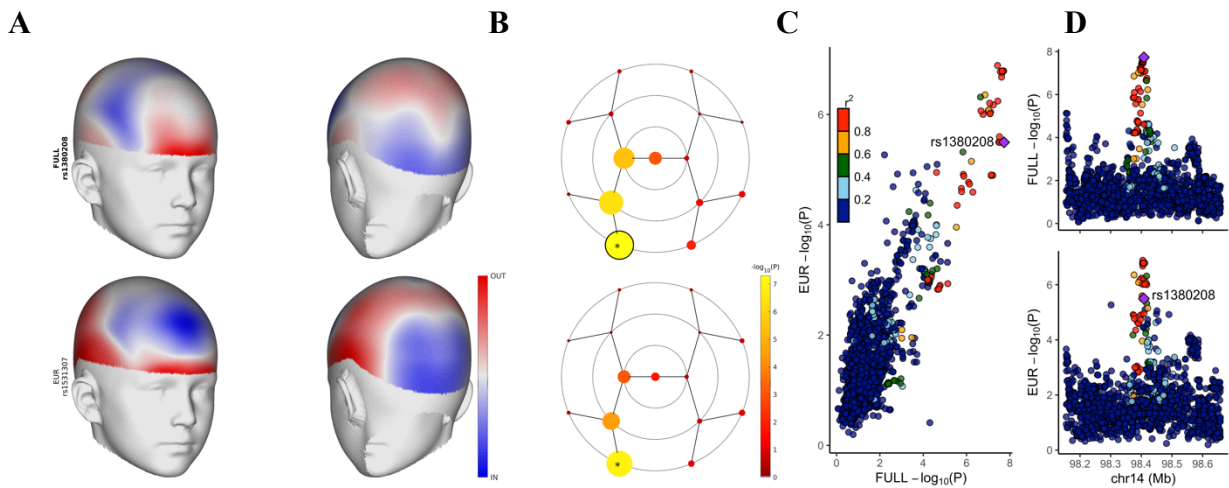
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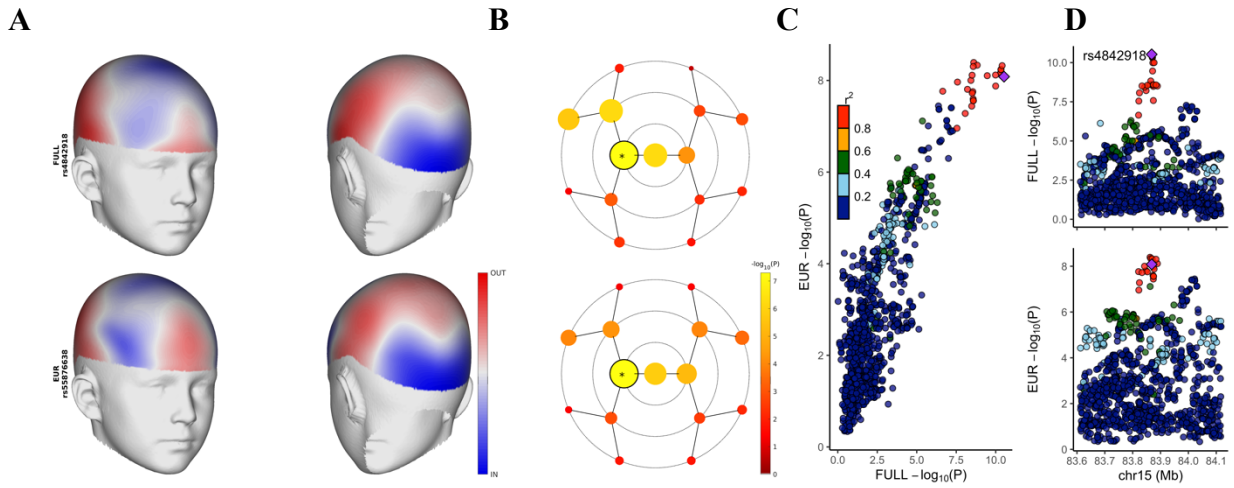
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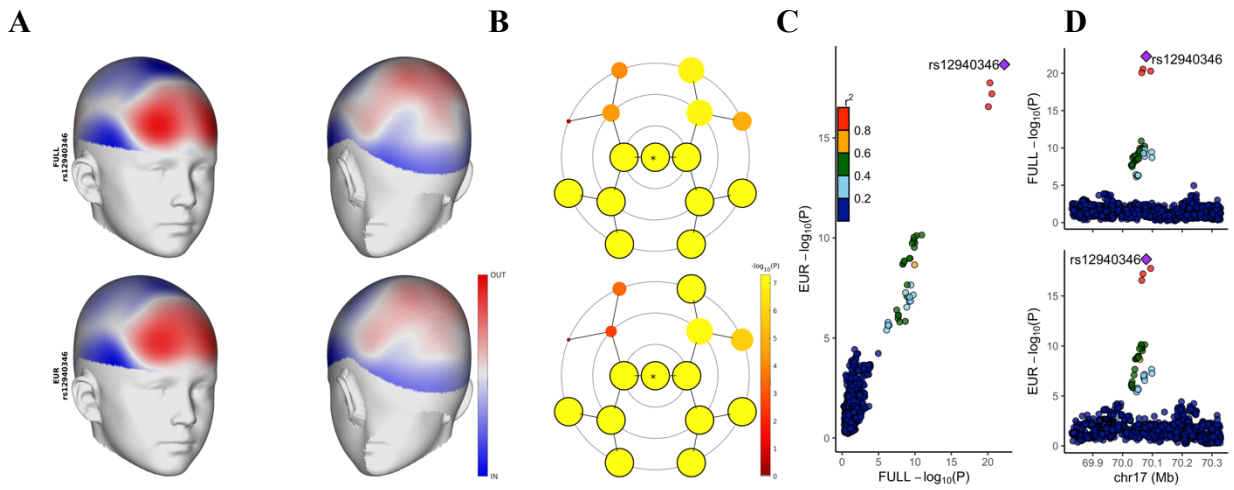
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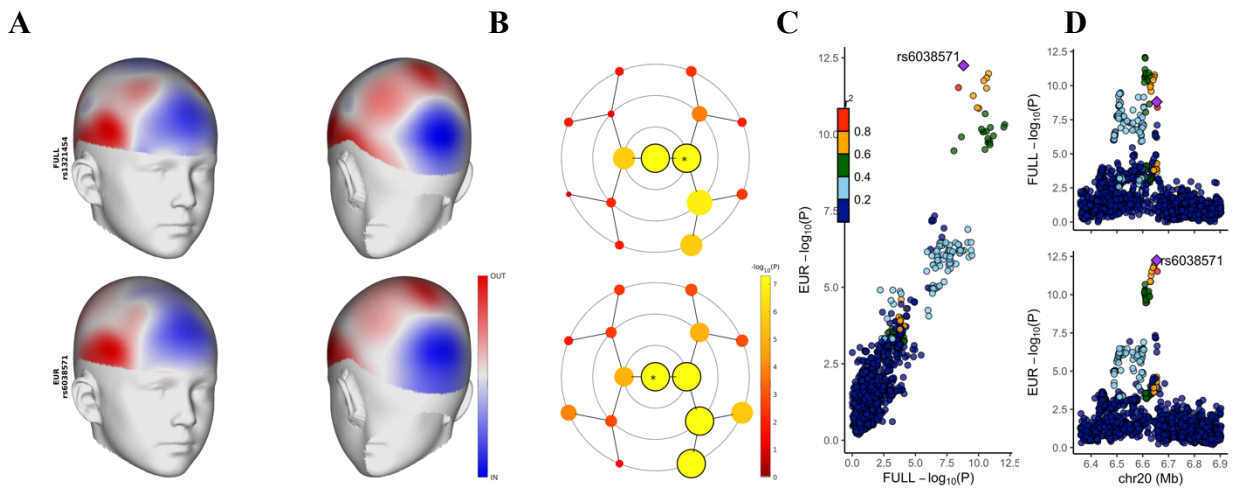
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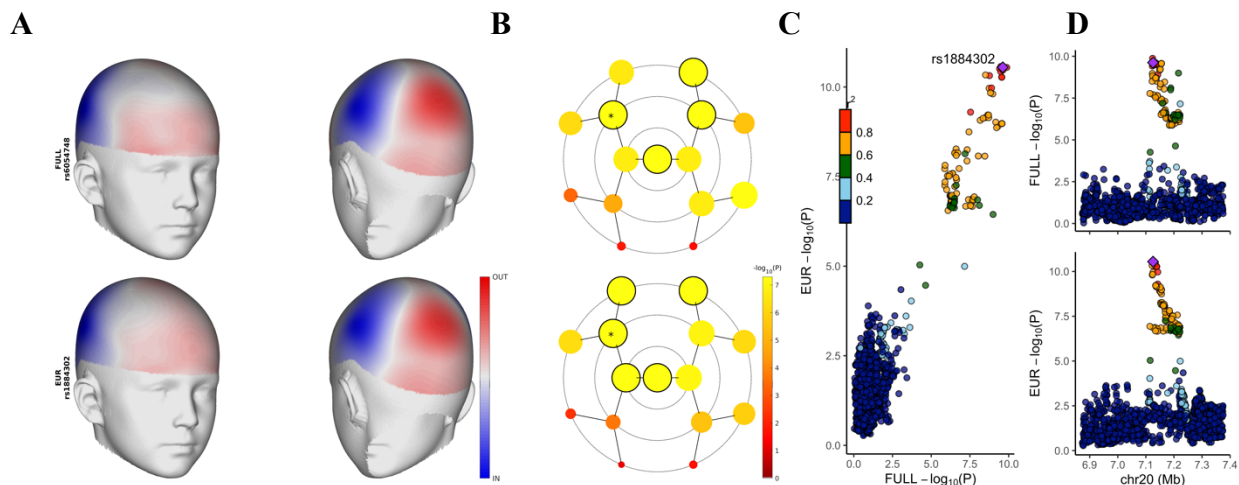
**rs12940346 – rs12940346**



**rs6038571 – rs1321454**



rs1884302 – rs6054748



References

1. Liu, B., Gludemans, M. J., Rao, A. S., Ingelsson, E. & Montgomery, S. B. Abundant associations with gene expression complicate GWAS follow-up. *Nat. Genet.* **51**, 768–769 (2019).
2. Pruim, R. J. *et al.* LocusZoom: regional visualization of genome-wide association scan results. *Bioinformatics* **26**, 2336–2337 (2010).