

Article

Genome-Wide Scan for Five Brain Oscillatory Phenotypes Identifies a New QTL Associated with Theta EEG Band

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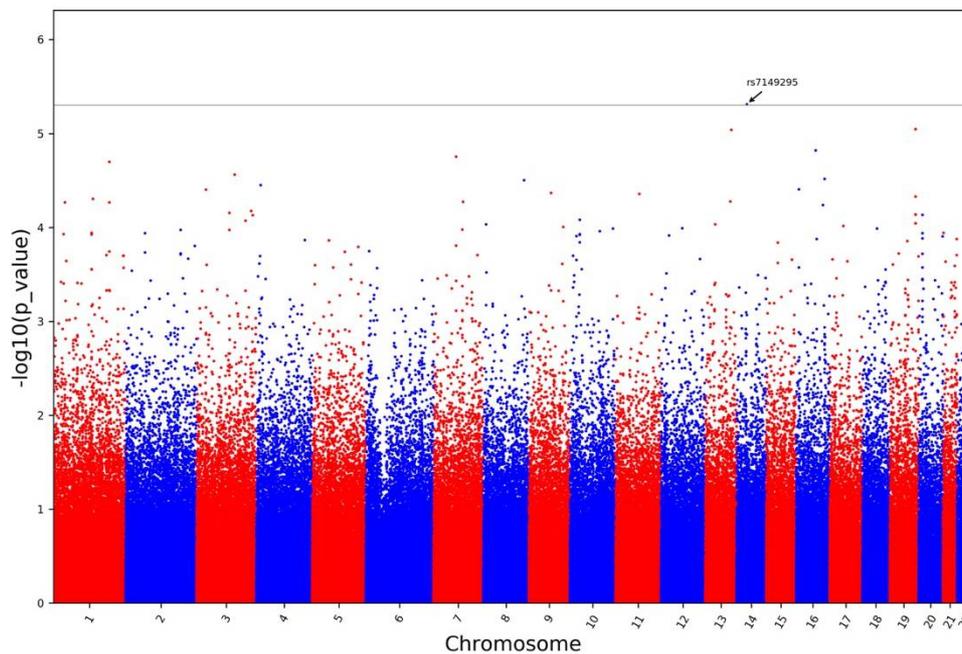
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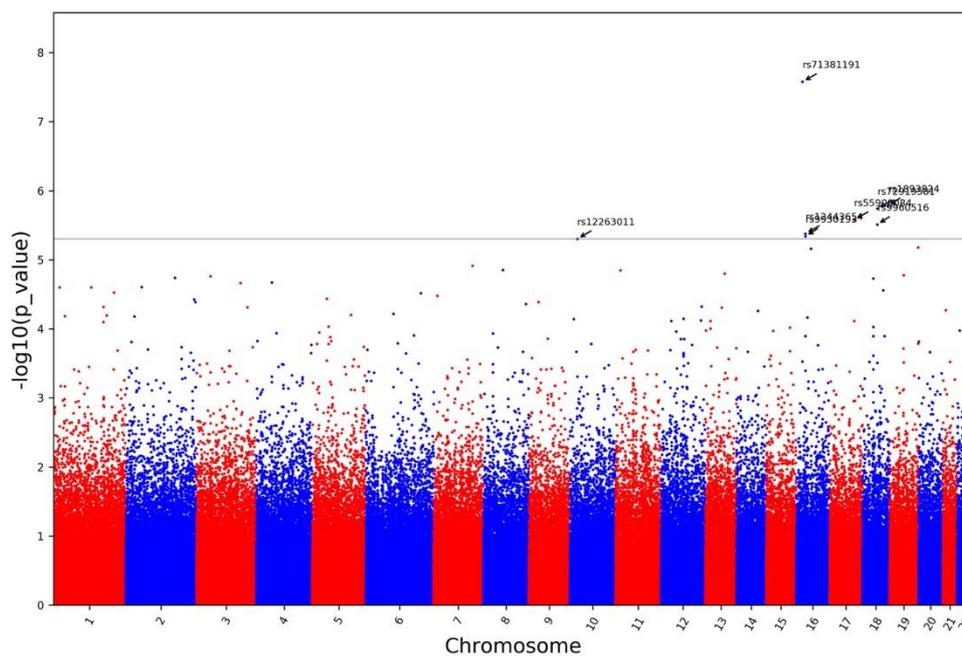
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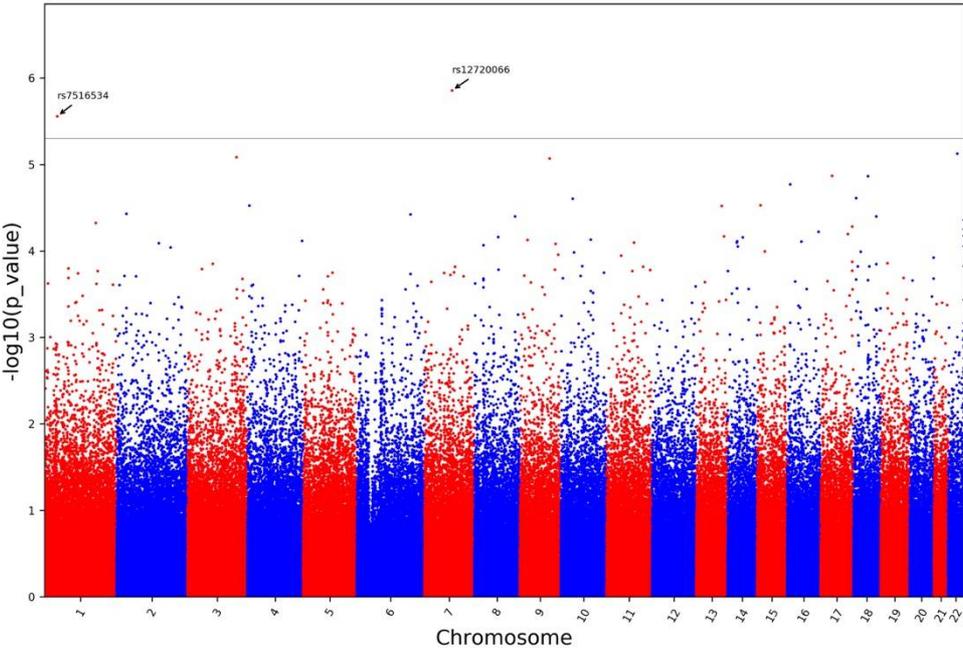
Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1, Figure S1: title, Table S1: title, Video S1: title.



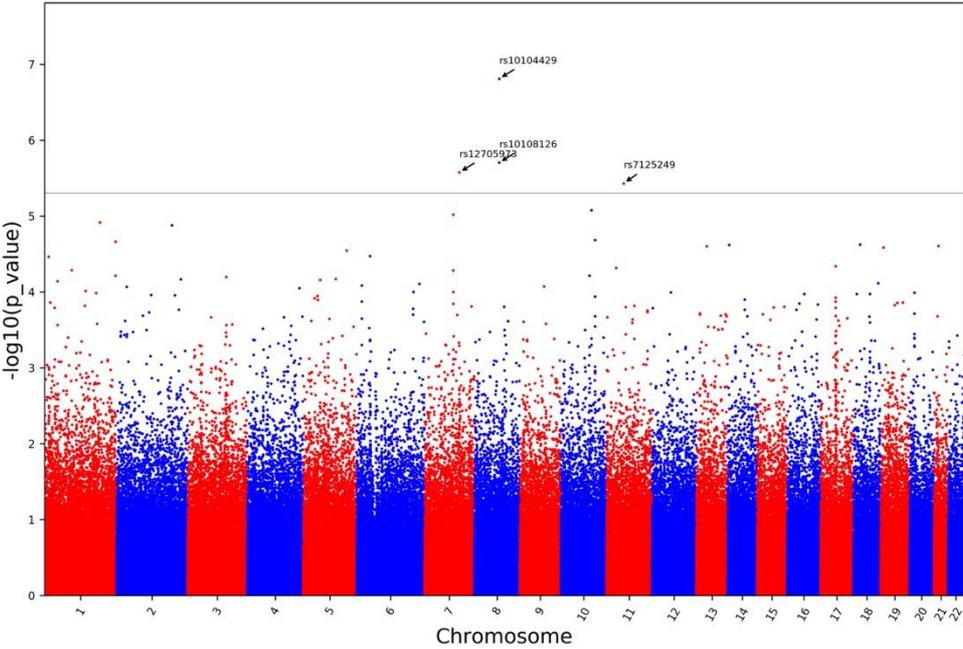
(a)



(b)



(c)



(d)

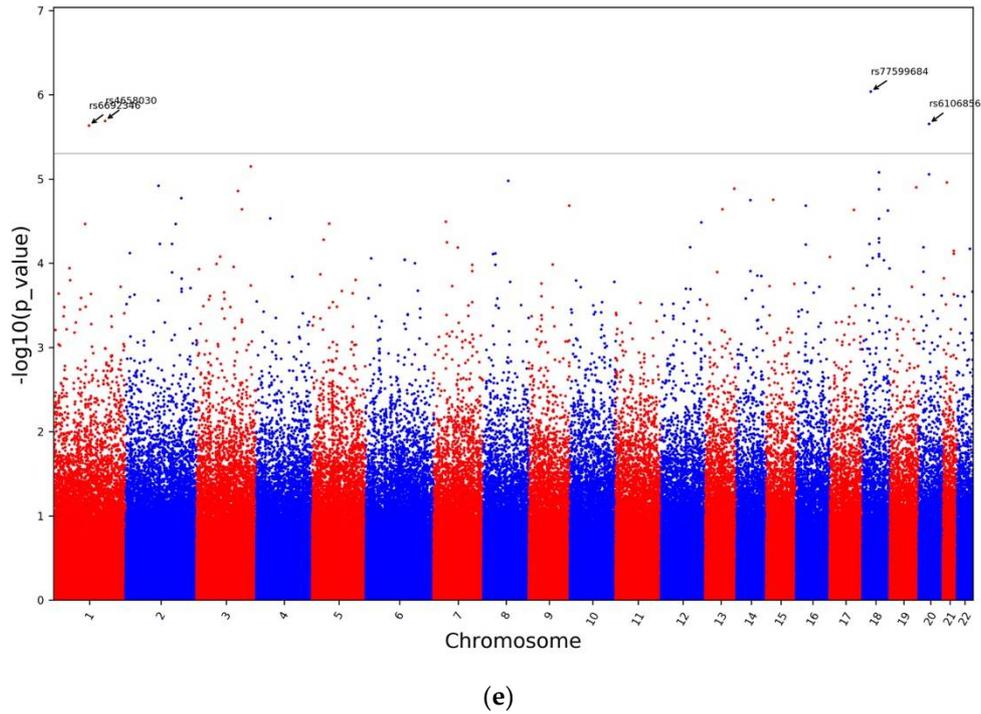


Figure S1. Linear regression *p*-values for each frequency band. Manhattan plot with the log-transformed *p*-values across each chromosome, highlighted by interlaced colors. The grey line marks the custom threshold at 5×10^{-6} . Variants that pass the threshold are highlighted by an arrow and the rsID is displayed. (a) Linear regression *p*-values for the δ frequency band.; (b) Linear regression *p*-values for the θ frequency band.; (c) Linear regression *p*-values for the α frequency band.; (d) Linear regression *p*-values for the β -1 frequency band.; (e) Linear regression *p*-values for the β -2 frequency band.

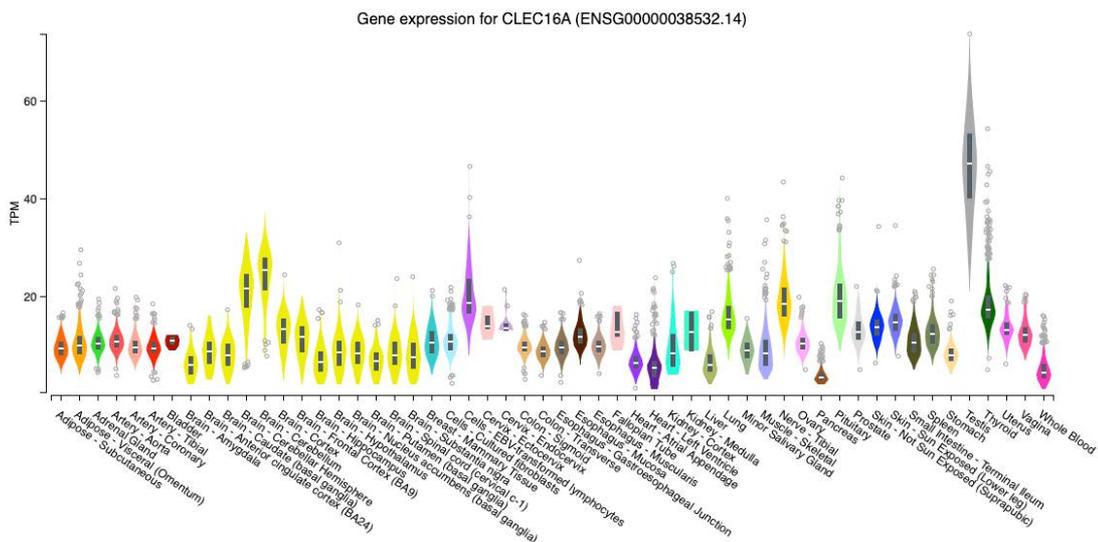


Figure S2. Gene expression for *CLEC16A* in 54 tissues from GTEx v8. Violin plot representing the TPM (transcripts per million) values distribution for each tissue. Every main tissue type is represented with a different color. The dots represent outlying values.

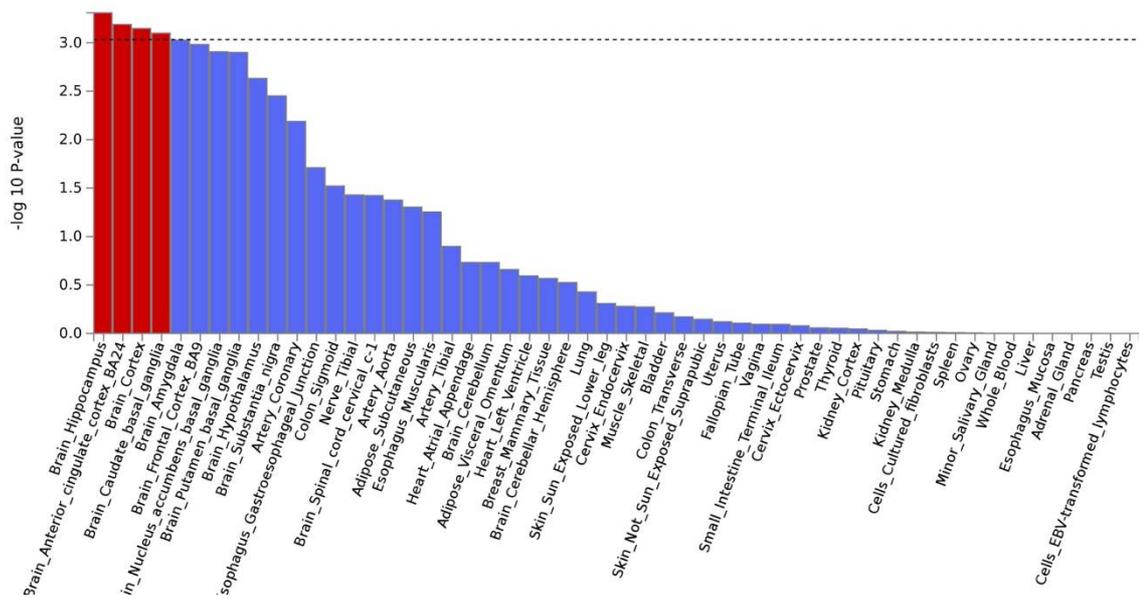


Figure S3. Significantly enriched up-regulated DEGs (differentially expressed genes) for the 15 lead SNPs on GTEx v8 54 tissue types. Log-transformed p -values for the enrichment of up-regulated DEGs in each tissue. Significantly enriched tissues are displayed in red (adjusted p -value ≤ 0.05), otherwise in blue. The dashed line represents the significance threshold.

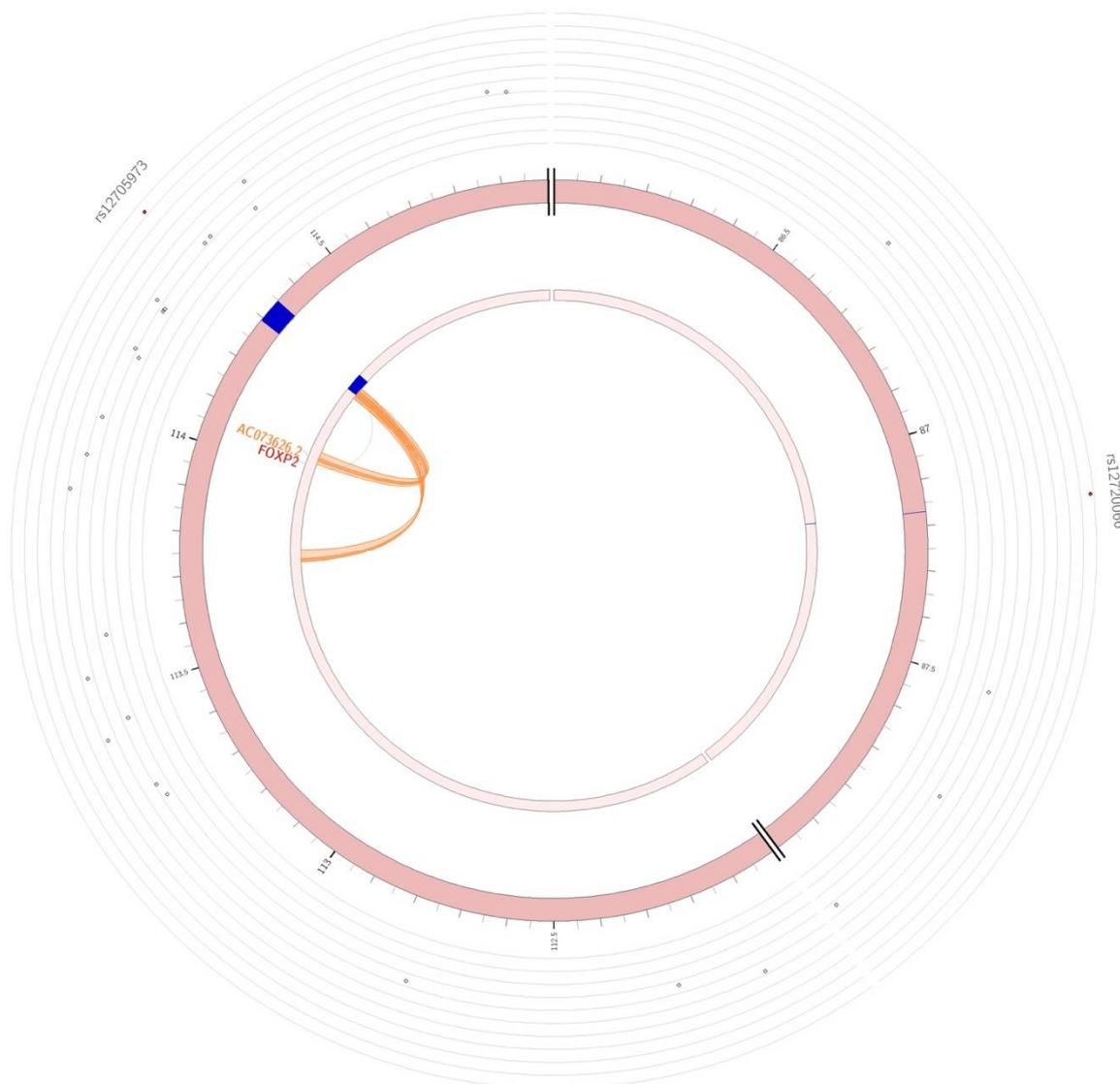


Figure S4. Circos plot for the *rs12705973* genomic associated locus (*FOXP2*). Genomic associated loci are highlighted in blue. Each dot in the outer rings represent a variant. Red dots correspond to variants that pass the defined threshold. If the gene is mapped only by chromatin interactions or only by eQTLs, it is colored orange or green, respectively. When the gene is mapped by both, it is colored red.

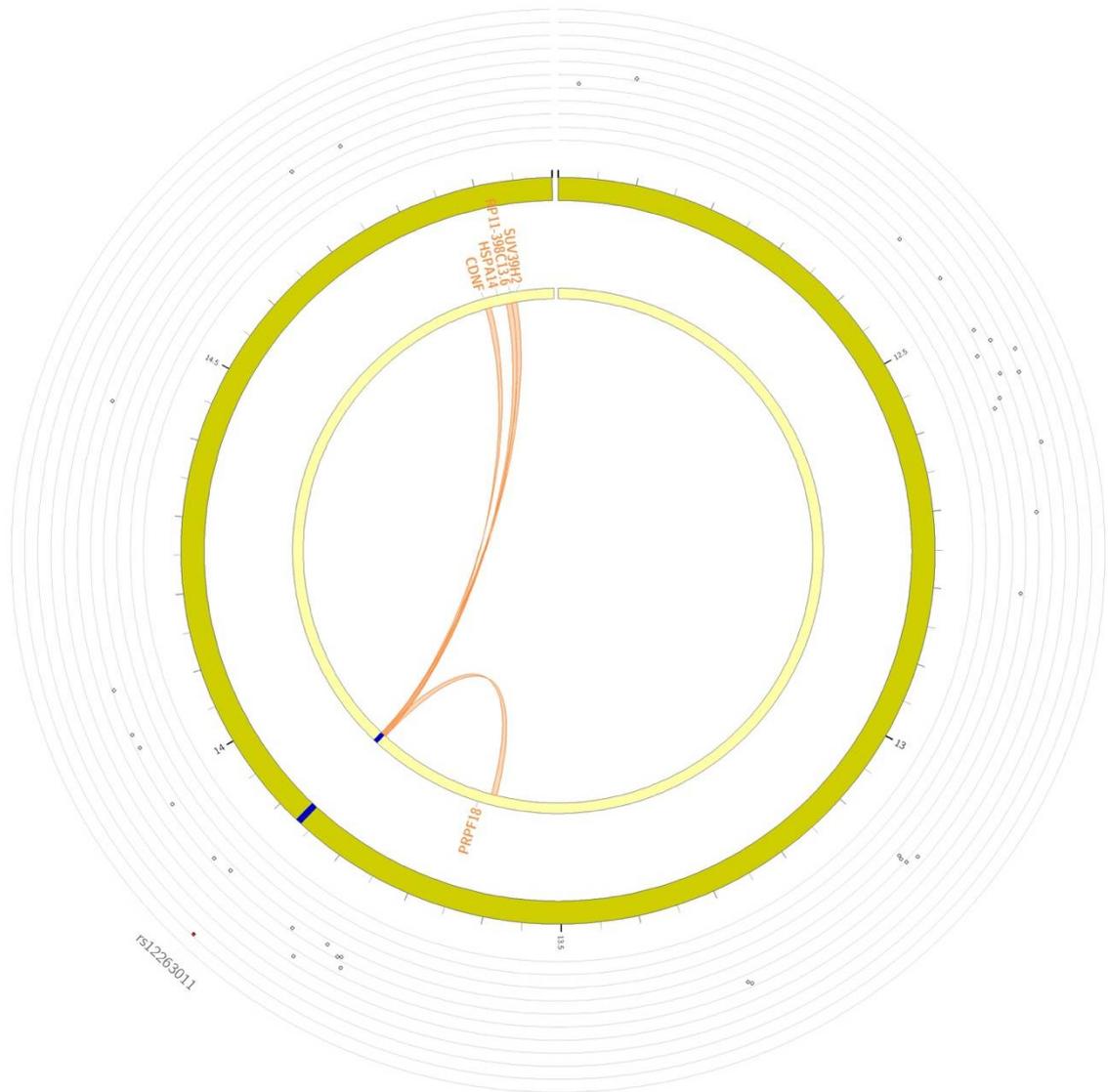


Figure S5. Circos plot for the *rs12705973* genomic associated locus (*FRMD4A*). Genomic associated loci are highlighted in blue. Each dot in the outer rings represent a variant. Red dots correspond to variants that pass the defined threshold. If the gene is mapped only by chromatin interactions or only by eQTLs, it is colored orange or green, respectively. When the gene is mapped by both, it is colored red.

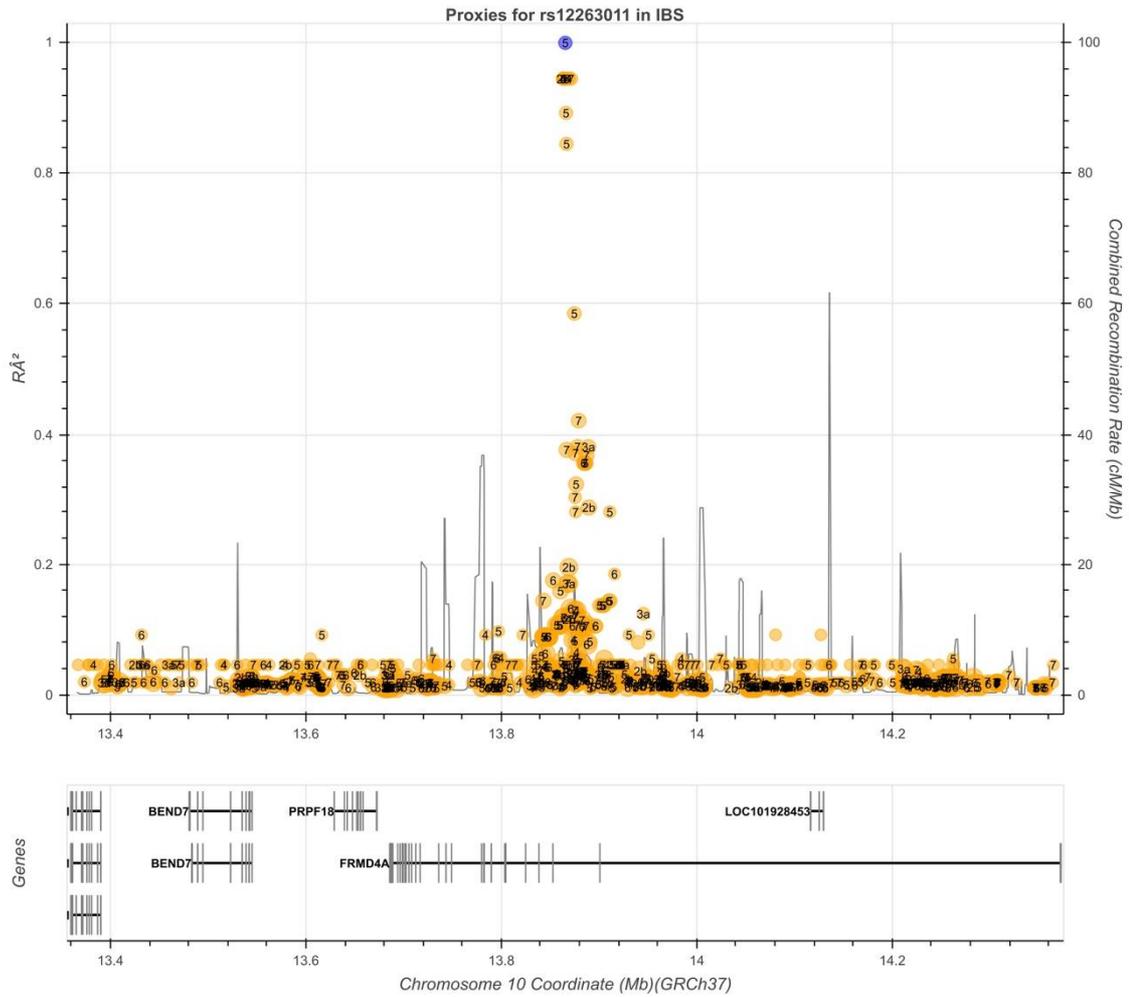


Figure S6. Linkage proxies for the variant *rs12263011*, within *FRMD4A*. Linkage proxies in the 1K Genomes population Iberian in Spain (IBS). The graph displays R^2 (as circles) and combined recombination rate (cM/Mb) (as lines) across chromosome 10 coordinates. The query variant is represented in purple and variants in its vicinity can be classified as non-coding (yellow) or coding (red). The size of the circle is directly proportional to the frequency of the variant. The number inside each circle, if present, indicates the regulatory potential using the scoring scheme of RegulomeDB (<http://www.regulomedb.org/>). Below the main graph with the R^2 scores the genes are mapped to the chromosome coordinates.

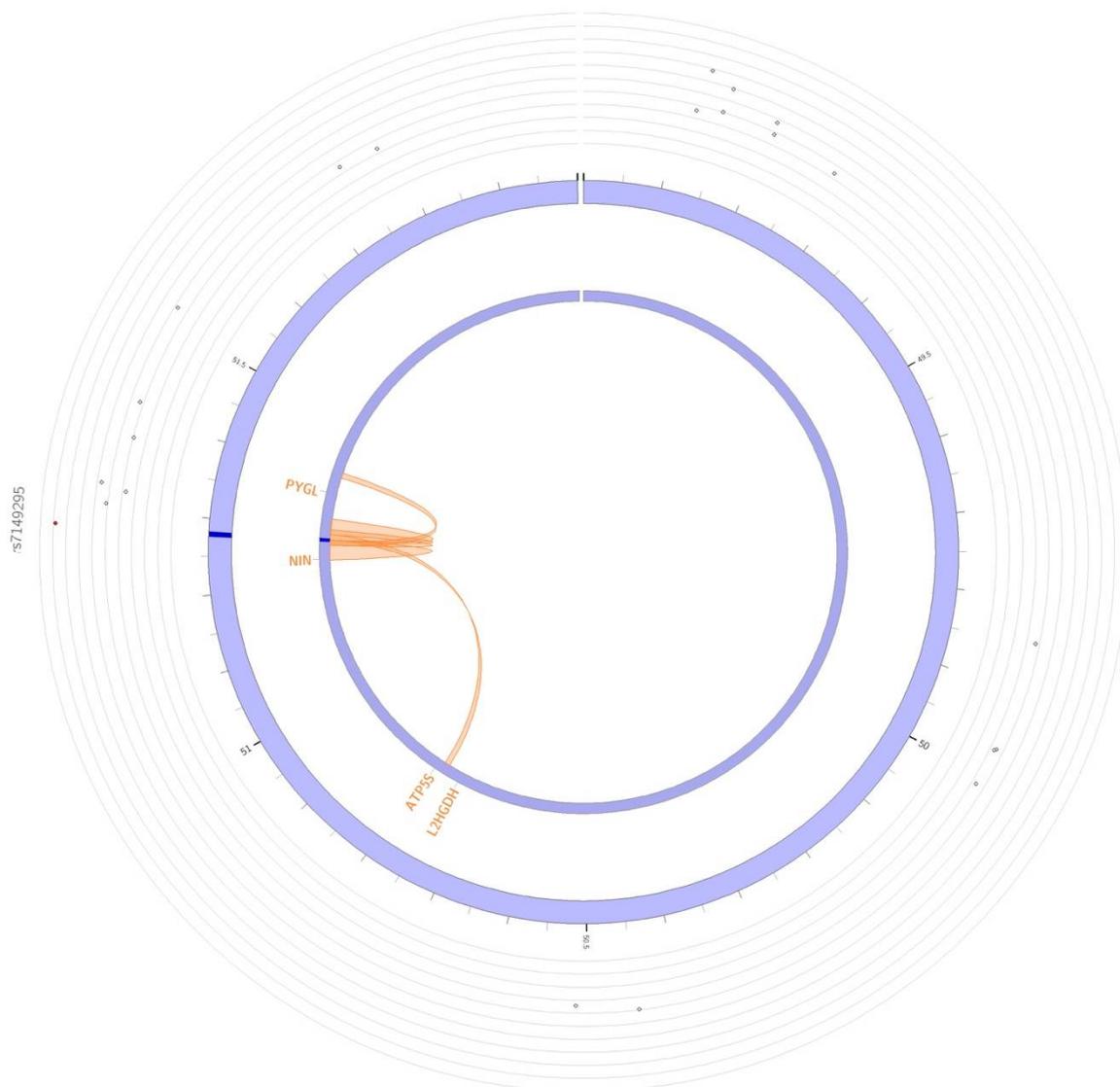


Figure S7. Circos plot for the *rs7149295* genomic associated locus (*L2HGDH*). Genomic associated loci are highlighted in blue. Each dot in the outer rings represent a variant. Red dots correspond to variants that pass the defined threshold. If the gene is mapped only by chromatin interactions or only by eQTLs, it is colored orange or green, respectively. When the gene is mapped by both, it is colored red.

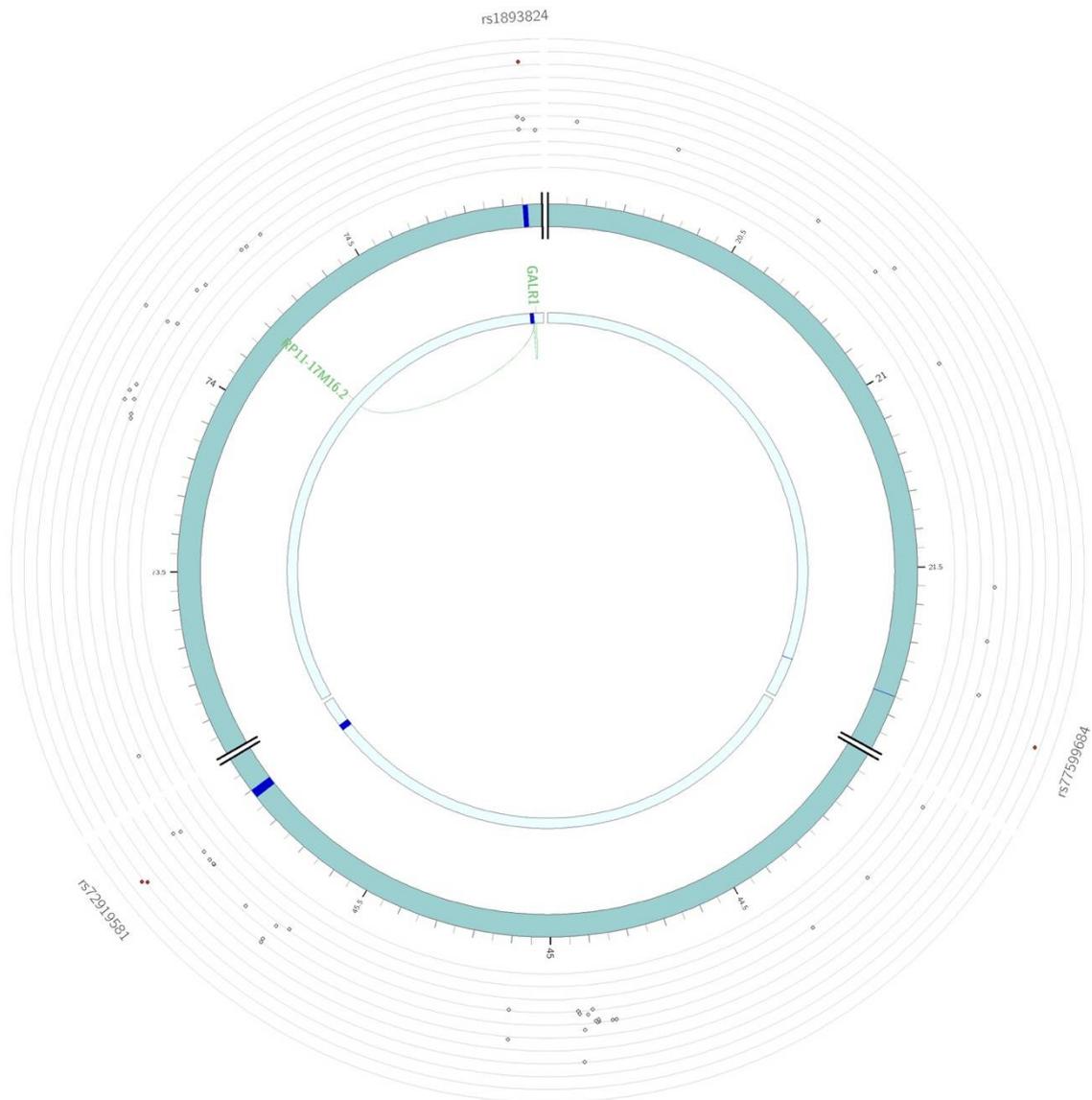


Figure S8. Circos plot for the *rs1893824* genomic associated locus (*GALR1*). Genomic associated loci are highlighted in blue. Each dot in the outer rings represent a variant. Red dots correspond to variants that pass the defined threshold. If the gene is mapped only by chromatin interactions or only by eQTLs, it is colored orange or green, respectively. When the gene is mapped by both, it is colored red.

Table S1. Genescores of genes previously associated with AD. The table displays the number of SNPs mapped to each gene (nSNPs) as well as the computed *p-value* for each gene.

Gene	nSNPs	p-value
<i>CNTNAP2</i>	12.0	8.92×10^{-10}
<i>ALPK2</i>	3.0	4.59×10^{-4}
<i>CLNK</i>	1.0	4.51×10^{-3}
<i>ZCWPW1</i>	1.0	5.95×10^{-3}
<i>ZCWPW1</i>	1.0	5.95×10^{-3}
<i>ADAM10</i>	1.0	7.23×10^{-3}
<i>ECHDC3</i>	1.0	7.26×10^{-3}
<i>ECHDC3</i>	1.0	7.26×10^{-3}
<i>HS3ST1</i>	1.0	7.29×10^{-3}
<i>SLC24A4</i>	1.0	8.57×10^{-3}

Table S2. Genescores of genes previously associated with schizophrenia. The table displays the number of SNPs mapped to each gene (nSNPs) as well as the computed *p-value* for each gene.

Gene	nSNPs	p-value
<i>CNTNAP2</i>	12.0	8.92×10^{-10}
<i>ALPK2</i>	3.0	4.59×10^{-4}
<i>CLNK</i>	1.0	4.51×10^{-3}
<i>ZCWPW1</i>	1.0	5.95×10^{-3}
<i>ZCWPW1</i>	1.0	5.95×10^{-3}
<i>ADAM10</i>	1.0	7.23×10^{-3}
<i>ECHDC3</i>	1.0	7.26×10^{-3}
<i>ECHDC3</i>	1.0	7.26×10^{-3}
<i>HS3ST1</i>	1.0	7.29×10^{-3}
<i>SLC24A4</i>	1.0	8.57×10^{-3}



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