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BACKGROUND

- Variations in blood-based biomarkers (BBM) have been reported across different apolipoprotein E (APOE) genotypes along the Alzheimer's disease (AD) continuum.
- These alterations remain understudied in populations with low educational attainment.
- Objectives:** To investigate the association between BBM and APOE genotype across the clinical continuum of AD.

METHODS

- Sample:** 316 individual from Brazilian Cog-Aging cohort
- Clinical groups:** Cognitively unimpaired (CU = 29.8%), Mild cognitive impairment (MCI = 43.7%), dementia of the Alzheimer's type (DAT = 23.9%), and other dementias (2.5%)
- Genetics:** APOE genotyping via real-time PCR, by $\epsilon 4$ allele presence ($\epsilon 4+$ and $\epsilon 4-$).
- Blood biomarkers:** pTau-217, A β 42, A β 40, GFAP, and NfL were quantified using Simoa® technology.
- Statistical Analysis:** The Mann-Whitney U test was employed for hypothesis testing (JASP software).
- Data Visualization:** Clustermaps and hierarchical clustering were performed using Python (Seaborn), grouped by median and standardized by z=score. Genotypes $\epsilon 2/\epsilon 2$ and $\epsilon 2/\epsilon 4$ were excluded due to small sample size.

CONCLUSIONS

- In this cohort from a low- and middle-income country, characterized by low educational attainment, $\epsilon 4$ allele was associated with a distinct BBM expression pattern that is consistent with findings previously reported in high-income populations.
- In the MCI group, these differences suggest that $\epsilon 4$ carriers exhibit a higher reactive astrogliosis, amyloid and Tau disease burden. The NfL results may reflect the limited specificity of this BBM, highlighting the need for further investigation.

The $\epsilon 4$ allele was associated with a distinct BBM expression pattern in a sample with low educational attainment.

RESULTS

Mean age 76.77 years (SD=6.562); median 4 years of schooling (IQR=3); Women (76%); $\epsilon 4+$ (37.1%). In CU groups, no significant differences were found between $\epsilon 4+$ and $\epsilon 4-$ groups. In MCI groups, pTau-217 levels (p<0.001), pTau-217/A β 42 ratio (p<0.001), and GFAP levels (p=0.030) were higher in $\epsilon 4+$ and the A β 42/A β 40 ratio (p=0.006) was lower. In DAT groups, NfL (p=0.026) and A β 42 (p=0.048) levels in $\epsilon 4+$ were lower. (table 1) (figure 1). Cluster analysis showed that $\epsilon 4$ carriers across genotypes exhibited higher pTau-217, pTau-217/A β 42 and GFAP, with lower A β 42 and A β 42/A β 40 ratio, whereas NfL exhibits a distinct pattern (figure 2).

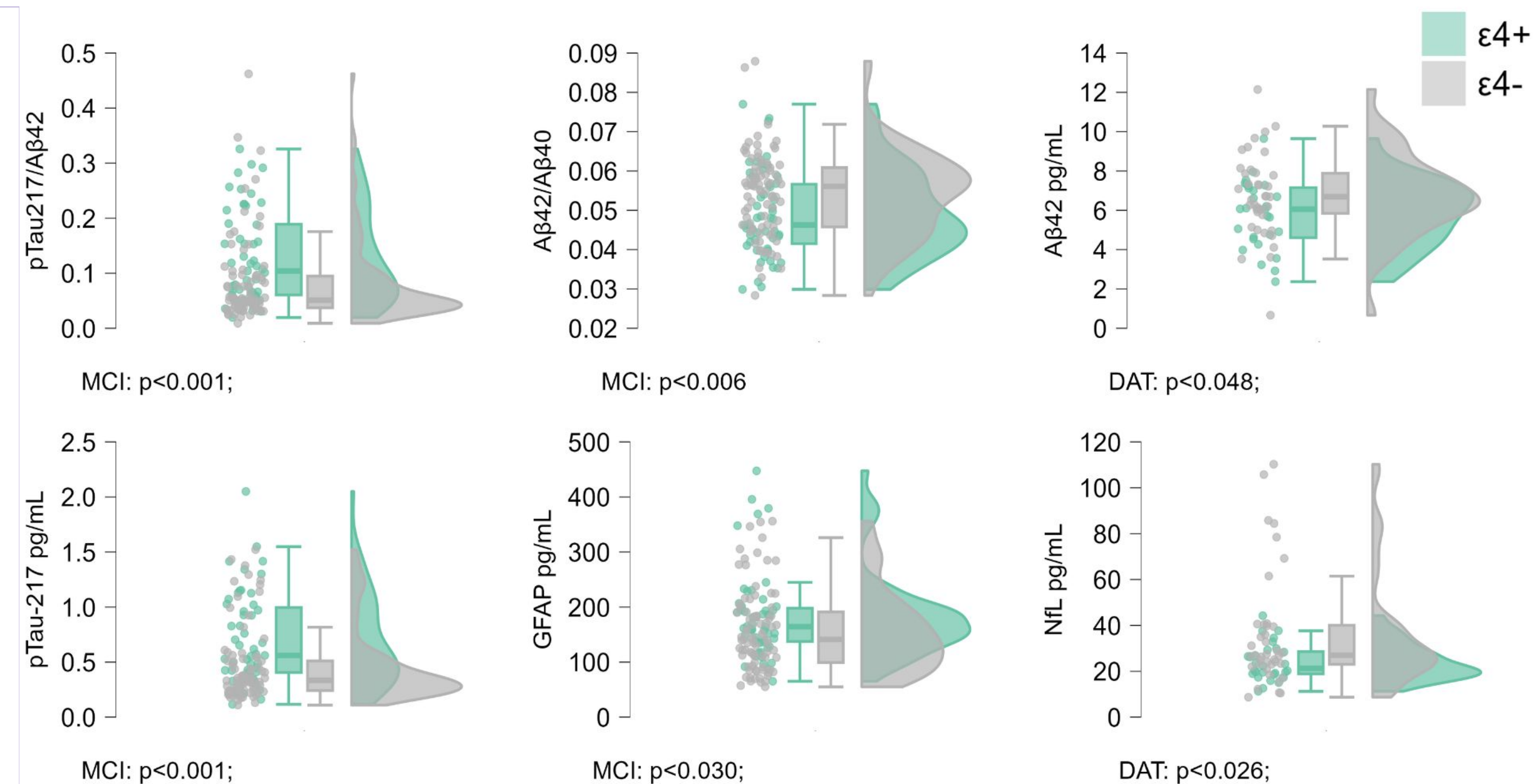


Figure 1.

Table 1.

	CU			MCI			DAT		
	$\epsilon 4+$	$\epsilon 4-$	p-Value	$\epsilon 4+$	$\epsilon 4-$	p-Value	$\epsilon 4+$	$\epsilon 4-$	p-Value
pTau-217 pg/mL (mean±SD)	0.59±0.57	0.36±0.26	0.083	0.70±0.42	0.47±0.34	<0.001**	1.26±0.58	1.11±0.64	0.225
pTau-217/A β 42 (mean±SD)	0.10±0.09	0.06±0.04	0.067	0.13±0.08	0.08±0.08	<0.001**	0.26±0.02	0.21±0.21	0.083
A β 42 pg/mL (mean±SD)	6.33±2.07	6.61±2.66	0.819	5.95±1.93	6.54±2.41	0.107	5.78±1.72	6.75±2.12	0.048*
A β 40 pg/mL (mean±SD)	121.75±24.40	119.55±44.23	0.364	122.65±26.85	119.84±35.70	0.199	126.76±37.58	134.58±38.79	0.222
A β 42/A β 40 (mean±SD)	0.05±0.01	0.06±0.01	0.214	0.05±0.01	0.05±0.01	0.006*	0.05±0.01	0.05±0.01	0.114
GFAP pg/mL (mean±SD)	189.04±137.66	136.46±64.47	0.087	182.73±79.84	158.02±76.18	0.030*	250.02±90.56	259.63±107.17	0.565
NfL pg/mL (mean±SD)	20.02±12.14	18.45±9.46	0.636	21.88±10.07	23.78±18.14	0.859	23.87±8.09	36.57±25.42	0.026*

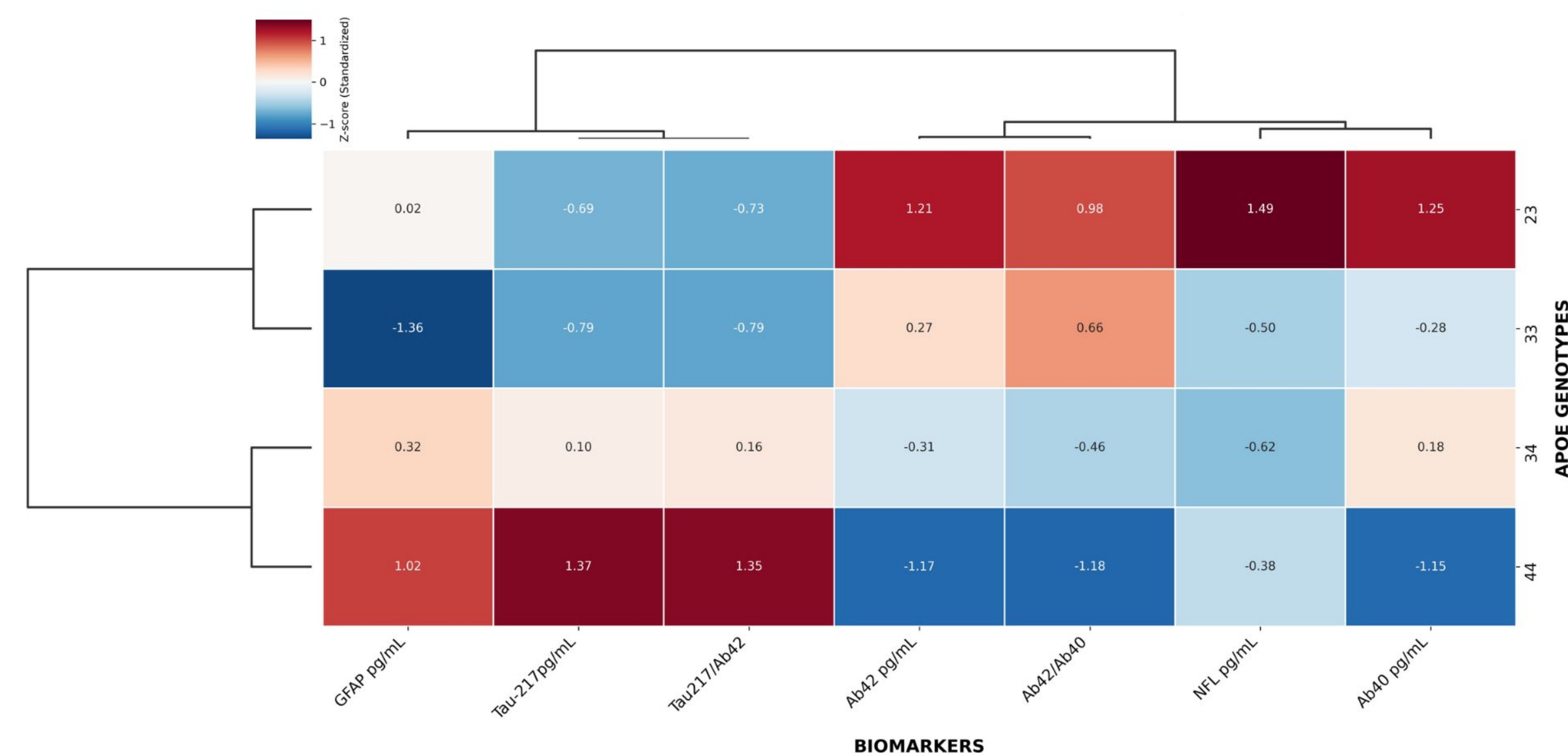


Figure 2.

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