## Supplementary Material

## Attempt to Predict A/T/N-Based Alzheimer's Disease Cerebrospinal Fluid Biomarkers <br> Using a Peripheral Blood DNA Methylation Clock

Supplementary Figure 1. MDS plot distribution between two groups according to the target of interest (e.g., A+ versus A-, or T+ versus T-).


MDS plot of top 1000 most variable CpG sites revealed no apparent separation in their distribution between the two subgroups regarding the target of interest, $\mathrm{A}+/-\mathrm{in}(\mathrm{A}), \mathrm{T}+/-\mathrm{in}(\mathrm{B})$, and $\mathrm{N}+/-$ in (C). Label " 0 " corresponds to negative (e.g., $\mathrm{A}-$ ) and " 1 " corresponds to positive (e.g., $\mathrm{A}^{+}$).

Supplementary Figure 2. Correlation between the chronological age and the estimated epigenetic age, and correlation between the degree of aging acceleration and the CSF $\mathrm{A} \beta$ value.


The obtained methylation clock shows a clear correlation with the actual chronological age (A, coefficients $=0.692, \mathrm{p}<0.001$ ). After adjustment for sex, APOE genotype, ethnicity, smoking history, CSF A $\beta$, t-tau, and p-tau, there is a weak but significant correlation between the IEAA and $\operatorname{CSF} \mathrm{A} \beta(\mathrm{pg} / \mathrm{mL})($ coefficients $=0.016(\mathrm{p}=0.035)$ in linear regression $)(B$, coefficients $=$ $0.126(p=0.025)$ in Pearson's correlation) and between the EEAA and CSF A $\beta$ value (coefficients $=0.017(p=0.017)$ in linear regression) (data not shown, coefficients $=0.116(p=$ 0.041 ) in Pearson's correlation). However, there is no significant correlation between the IEAA/EEAA and CSF p-tau or t-tau values (data not shown). DNAmAge, methylation clock; IEAA, intrinsic epigenetic aging acceleration; EEAA, extrinsic epigenetic aging acceleration; CSF, cerebrospinal fluid.

Supplementary Table 1. Basic demographics of the included participants categorized according to the $\mathrm{A} / \mathrm{T} / \mathrm{N}$ system

| A/T/N | n | actual age | sex | $\begin{gathered} A P O E \varepsilon 4 \\ \text { allele(s) } \\ {[0: 1: 2]} \end{gathered}$ | ethnicity <br> (white/ <br> others) | education | smoking <br> (yes/no) | baseline diagnosis <br> ( $\mathrm{AD} / \mathrm{MCI} / \mathrm{CN} /$ uncertain) | MMSE | ADAS-cog 13 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| A-T-N- | 43 | 70 (65.75 ~ 76.5) | 21:22 | 41:2:0 | 42:1 | 16 (14 ~ 18) | 15:28 | 3:25:15:0 | 29 (28~30) | $10(8 \sim 13)$ |
| A+T-N- | 26 | 74.4 (70.5 ~ 79.9) | 18:8 | 17: 8:1 | 25:1 | $17(15 \sim 19.75)$ | 10:16 | 0:18:8:0 | 29 (28 ~ 29.75) | $9(6 \sim 15)$ |
| $\mathrm{A}+\mathrm{T}+\mathrm{N}-$ | 77 | 72.7 (67.7 ~ 78.4) | 37:40 | 33:36:8 | 72:4 | 16 (14~18) | 38:39 | 5:52:20:0 | 29 (27 ~ 29) | 13 (9 ~ 16) |
| A+T-N+ | 0 | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| $\mathrm{A}+\mathrm{T}+\mathrm{N}+$ | 91 | 75.6 (71.35 ~ 79.4) | 45:46 | 29:46:16 | 89:2 | 16 (14 ~ 18) | 37:54 | 32:45:13:1 | 26 (24 ~ 28) | 23 (14.5 ~ 30.5) |
| $\mathrm{A}-\mathrm{T}+\mathrm{N}-$ | 67 | 71.7 (67.8 ~ 76.9) | 41:26 | 58:9:0 | 66:0 | 18 (14 ~ 19) | 29:38 | 2:32:31:2 | 29 (28 ~ 30) | $9(7 \sim 12.5)$ |
| A-T-N+ | 1 | 71.3 (71.3 ~ 71.3) | 1:0 | 1:0:0 | 1:0 | 16 (16 ~ 16) | 0:1 | 0:1:0:0 | 29 (29 ~ 29) | $11(11 \sim 11)$ |
| A-T+N+ | 12 | 69.5 (65.9 ~ 77.7) | 5:7 | 9:3:0 | 12:0 | 18 (16 ~ 19) | 4:8 | 1:6:5:0 | 29 (28 ~ 29.25) | 9.5 (7.75 ~ 12.5) |

AD, Alzheimer's disease; MCI, mild cognitive impairment; CN, cognitive normal; MMSE, Mini-Mental Scale Examination; ADAS, Alzheimer's Disease
Assessment Scale

