Supplemental data

Table S1. Correlations between chronological age and each epigenetic age (predicted age).

| | | Horvath Clock | Hannum Clock | BioAge4HAStatic | DNAmAge SkinBloodClock | DNAmPhenoAge | DNAmGrimAge | DNAmFitAge | DNAmTL |
|---|---|---|---|---|---|---|---|---|---|
| Chronological Age | $r$ | 0.083 | **0.232**** | **0.217**** | **0.317**** | 0.057 | **0.379**** | **0.368**** | -0.139 |
| | $p$ | 0.321 | **0.005** | **0.009** | **< 0.001** | 0.501 | **< 0.001** | **< 0.001** | 0.097 |
| | $n$ | 144 | **144** | **144** | **144** | 144 | **144** | **144** | 144 |

TL, telomere length. Significant correlations at $p < 0.01$ are indicated by **.

Table S2. Correlations between each epigenetic age acceleration and age-adjusted values.

| | | AgeAccelHorvath | AgeAccelHannum | BioAge4HAStatic AdjAge | SkinBloodClock AdjAge | AgeAccelPheno | AgeAccelGrim | FitAgeAccel | DNAmTL AdjAge |
|---|---|---|---|---|---|---|---|---|---|
| AgeAccelHorvath | $r$ | | 0.527** | 0.510** | 0.469** | 0.356** | 0.135 | 0.395** | -0.212* |
| | $p$ | | < 0.001 | < 0.001 | < 0.001 | < 0.001 | 0.107 | < 0.001 | 0.011 |
| | $n$ | | 144 | 144 | 144 | 144 | 144 | 144 | 144 |
| AgeAccelHannum | $r$ | 0.527** | | 0.962** | 0.561** | 0.502** | 0.207* | 0.476** | -0.305** |
| | $p$ | < 0.001 | | < 0.001 | < 0.001 | < 0.001 | 0.013 | < 0.001 | < 0.001 |
| | $n$ | 144 | | 144 | 144 | 144 | 144 | 144 | 144 |
| BioAge4HAStatic AdjAge | $r$ | 0.510** | 0.962** | | 0.538** | 0.526** | 0.211* | 0.492** | -0.336** |
| | $p$ | < 0.001 | < 0.001 | | < 0.001 | < 0.001 | 0.011 | < 0.001 | < 0.001 |
| | $n$ | 144 | 144 | | 144 | 144 | 144 | 144 | 144 |
| SkinBloodClock AdjAge | $r$ | 0.469** | 0.561** | 0.538** | | 0.302** | 0.126 | 0.391** | -0.181* |
| | $p$ | < 0.001 | < 0.001 | < 0.001 | | < 0.001 | 0.132 | < 0.001 | 0.030 |
| | $n$ | 144 | 144 | 144 | | 144 | 144 | 144 | 144 |
| AgeAccelPheno | $r$ | 0.356** | 0.502** | 0.526** | 0.302** | | 0.455** | 0.546** | -0.249** |
| | $p$ | < 0.001 | < 0.001 | < 0.001 | < 0.001 | | < 0.001 | < 0.001 | 0.003 |
| | $n$ | 144 | 144 | 144 | 144 | | 144 | 144 | 144 |
| AgeAccelGrim | $r$ | 0.135 | 0.207* | 0.211* | 0.126 | 0.455** | | 0.744** | -0.208* |
| | $p$ | 0.107 | 0.013 | 0.011 | 0.132 | < 0.001 | | < 0.001 | 0.012 |
| | $n$ | 144 | 144 | 144 | 144 | 144 | | 144 | 144 |
| FitAgeAccel | $r$ | 0.395** | 0.476** | 0.492** | 0.391** | 0.546** | 0.744** | | -0.491** |
| | $p$ | < 0.001 | < 0.001 | < 0.001 | < 0.001 | < 0.001 | < 0.001 | | < 0.001 |
| | $n$ | 144 | 144 | 144 | 144 | 144 | 144 | | 144 |
| DNAmTL AdjAge | $r$ | -0.212* | -0.305** | -0.336** | -0.181* | -0.249** | -0.208* | -0.491** | |
| | $p$ | 0.011 | < 0.001 | < 0.001 | 0.030 | 0.003 | 0.012 | < 0.001 | |
| | $n$ | 144 | 144 | 144 | 144 | 144 | 144 | 144 | |

AgeAccel, age acceleration; AdjAge, age adjusted values; TL, telomere length. Significant correlations at $p < 0.05$ and $p < 0.01$ are indicated by * and **.

Table S3. Association between dietary patterns and epigenetic age acceleration and age-adjusted values by single regression analysis.

| | B | 95%CI | | $p$ | $R^2$ |
|---|---|---|---|---|---|
| *Healthy Japanese dietary pattern* | | | | | |
| AgeAccelHorvath | -4.559 | -12.527 − | 3.409 | 0.260 | 0.009 |
| AgeAccelHannum | -4.293 | -10.846 − | 2.26 | 0.197 | 0.012 |
| BioAge4HAStaticAdjAge | -4.737 | -12.924 − | 3.451 | 0.255 | 0.009 |
| DNAmSkinBloodClockAdjAge | -1.121 | -6.184 − | 3.942 | 0.662 | 0.001 |
| AgeAccelPheno | -10.474 | -20.179 − | -0.769 | **0.035** | 0.031 |
| AgeAccelGrim | -9.152 | -14.635 − | -3.667 | **0.001** | 0.071 |
| FitAgeAccel | -6.488 | -12.314 − | -0.662 | **0.029** | 0.033 |
| DNAmTLAdjAge | 0.372 | 0.071 − | 0.673 | **0.016** | 0.040 |
| *Western-style dietary pattern* | | | | | |
| AgeAccelHorvath | -0.105 | -0.632 − | 0.841 | 0.779 | 0.001 |
| AgeAccelHannum | -0.062 | -0.668 − | 0.545 | 0.841 | 0.0003 |
| BioAge4HAStaticAdjAge | -0.139 | -0.895 − | 0.618 | 0.717 | 0.001 |
| DNAmSkinBloodClockAdjAge | -0.087 | -0.553 − | 0.379 | 0.714 | 0.001 |
| AgeAccelPheno | -0.025 | -0.932 − | 0.882 | 0.957 | 0.00002 |
| AgeAccelGrim | 0.43 | -0.089 − | 0.949 | 0.104 | 0.019 |
| FitAgeAccel | 0.368 | -0.174 − | 0.910 | 0.181 | 0.013 |
| DNAmTLAdjAge | 0.008 | -0.021 − | 0.036 | 0.597 | 0.002 |

AgeAccel, age acceleration; AdjAge, age adjusted values; B: regression coefficient; CI: confidence interval; $R^2$: coefficient of determination: TL, telomere length.

Table S4. Multiple regression analysis of epigenetic age accelerations in the healthy Japanese dietary pattern.

| | B | 95%CI | | $\beta$ | VIF | $p$ |
|---|---|---|---|---|---|---|
| ***AgeAccelGrim**[*1]* | | | | | | |
| Intercept | 3.066 | -7.590 | 13.721 | | | 0.570 |
| $\text{Log}^{10}$ (Healthy Japanese dietary pattern score) | -4.843 | -10.723 | 1.038 | -0.139 | 1.222 | 0.106 |
| BMI | 0.025 | -0.180 | 0.230 | 0.020 | 1.094 | 0.809 |
| Exercise habit | 0.555 | -0.722 | 1.833 | 0.069 | 1.064 | 0.391 |
| Smoking status | -1.793 | -2.688 | -0.898 | -0.326 | 1.127 | **< 0.001** |
| Drinking status | -0.127 | -0.307 | 0.053 | -0.119 | 1.212 | 0.164 |
| Marital status | 1.639 | -1.018 | 4.295 | 0.097 | 1.047 | 0.225 |
| Education status | 0.643 | -2.002 | 3.287 | 0.038 | 1.062 | 0.631 |
| Income status | -0.106 | -0.526 | 0.314 | -0.040 | 1.089 | 0.618 |
| ***FitAgeAccel**[*2]* | | | | | | |
| Intercept | 5.403 | -11.932 | 9.335 | | | 0.365 |
| $\text{Log}^{10}$ (Healthy Japanese dietary pattern score) | -3.379 | -0.322 | 7.650 | -0.093 | 1.222 | 0.305 |
| BMI | -0.169 | -0.168 | 0.242 | -0.127 | 1.094 | 0.140 |
| Exercise habit | 0.544 | -0.806 | 1.738 | 0.064 | 1.064 | 0.447 |
| Smoking status | -1.236 | -0.332 | 0.004 | -0.215 | 1.127 | **0.015** |
| Drinking status | -0.128 | -2.767 | -0.991 | -0.115 | 1.212 | 0.205 |
| Marital status | 1.202 | -0.728 | 4.520 | 0.068 | 1.047 | 0.418 |
| Education status | 0.864 | -2.249 | 3.012 | 0.049 | 1.062 | 0.559 |
| Income status | -0.180 | -0.522 | 0.315 | -0.066 | 1.089 | 0.442 |

AgeAccel, age acceleration; B: partial regression coefficient; BMI: body mass index; CI: confidence interval; $\beta$: standard partial regression coefficient; VIF: variance inflation factor. [*1] $R^2 = 0.215$, adjusted $R^2 = 0.167$; [*2] $R^2 = 0.120$, adjusted $R^2 = 0.066$.

Table S5. Multiple regression analysis of epigenetic age accelerations in the western-style dietary pattern.

| | B | 95%CI | $\beta$ | VIF | $p$ |
|---|---|---|---|---|---|
| **AgeAccelGrim[*1]** | | | | | |
| Intercept | -1.298 | -11.932 − 9.335 | | | 0.810 |
| $Log^{10}$ (Western-style dietary pattern score) | 3.664 | -0.322 − 7.650 | 0.142 | 1.027 | 0.071 |
| BMI | 0.037 | -0.168 − 0.242 | 0.029 | 1.104 | 0.724 |
| Exercise habit | 0.466 | -0.806 − 1.738 | 0.058 | 1.059 | 0.470 |
| Smoking status | -1.879 | -2.767 − -0.991 | -0.341 | 1.115 | **< 0.001** |
| Drinking status | -0.164 | -0.332 − 0.004 | -0.154 | 1.064 | 0.056 |
| Marital status | 1.896 | -0.728 − 4.520 | 0.112 | 1.027 | 0.155 |
| Education status | 0.382 | -2.249 − 3.012 | 0.023 | 1.056 | 0.755 |
| Income status | -0.104 | -0.522 − 0.315 | -0.039 | 1.088 | 0.625 |
| **FitAgeAccel[*2]** | | | | | |
| Intercept | 2.334 | -9.412 − 14.079 | | | 0.695 |
| $Log^{10}$ (Western-style dietary pattern score) | 2.594 | -1.808 − 6.997 | 0.097 | 1.027 | 0.246 |
| BMI | -0.161 | -0.387 − 0.065 | -0.121 | 1.104 | 0.162 |
| Exercise habit | 0.481 | -0.924 − 1.886 | 0.057 | 1.059 | 0.499 |
| Smoking status | -1.295 | -2.276 − -0.315 | -0.226 | 1.115 | **0.010** |
| Drinking status | -0.153 | -0.339 − 0.032 | -0.138 | 1.064 | 0.105 |
| Marital status | 1.381 | -1.517 − 4.280 | 0.078 | 1.027 | 0.348 |
| Education status | 0.681 | -2.224 − 3.586 | 0.039 | 1.056 | 0.644 |
| Income status | -0.179 | -0.641 − 0.284 | -0.065 | 1.088 | 0.446 |

AgeAccel, age acceleration; B: partial regression coefficient; BMI: body mass index; CI: confidence interval; $\beta$: standard partial regression coefficient; VIF: variance inflation factor. [*1] $R^2 = 0.219$, adjusted $R^2 = 0.171$; [*2] $R^2 = 0.122$, adjusted $R^2 = 0.068$.
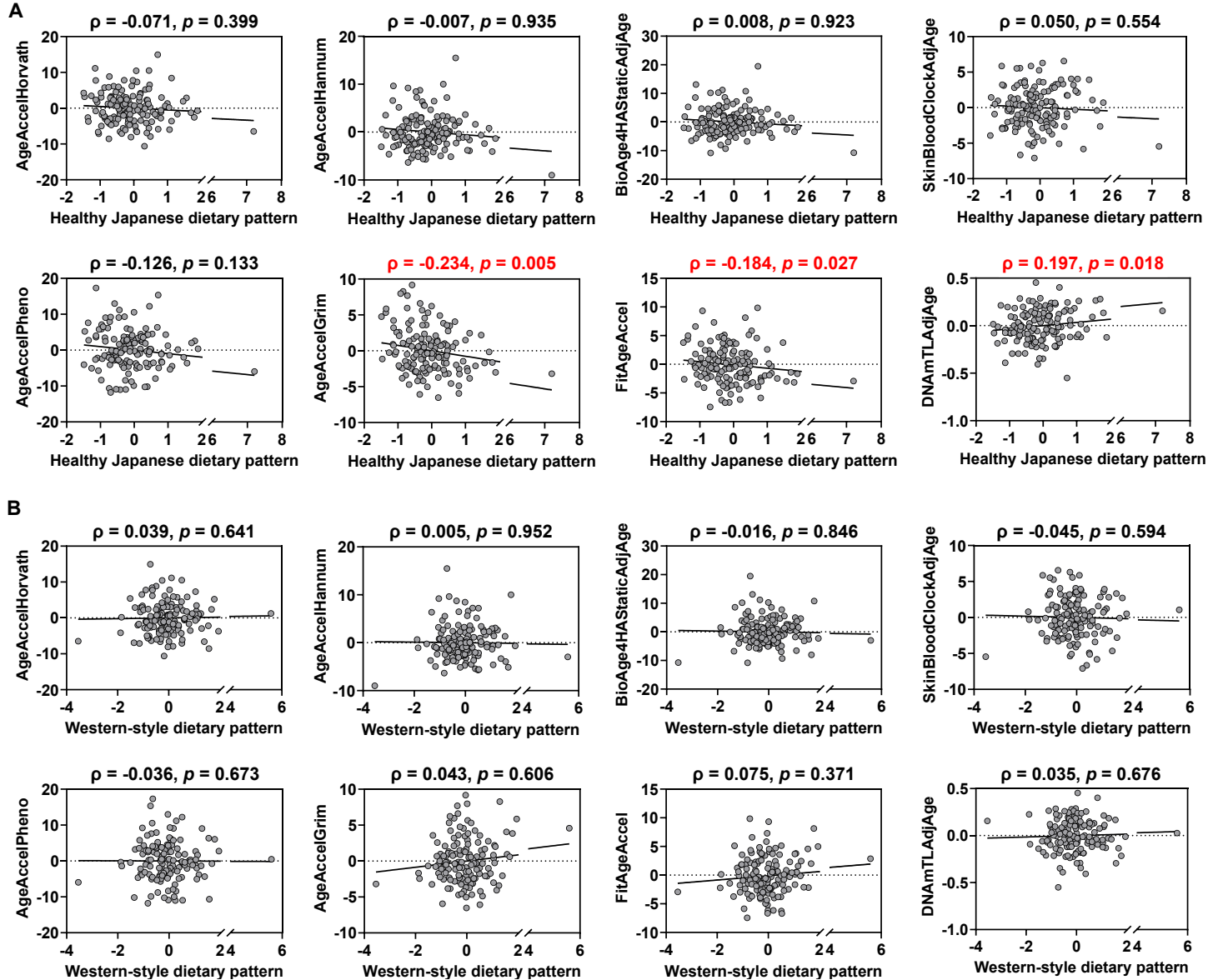
**Figure S1. Spearman correlation scatterplots. A)** Correlation between healthy Japanese dietary pattern scores and age acceleration (AgeAccel) and age adjusted (AdjAge) values for each epigenetic clock. **B)** Correlation between Western-style dietary pattern scores and AgeAccel and AdjAge. values for each epigenetic clock. Red letters indicate that the correlation is significant.
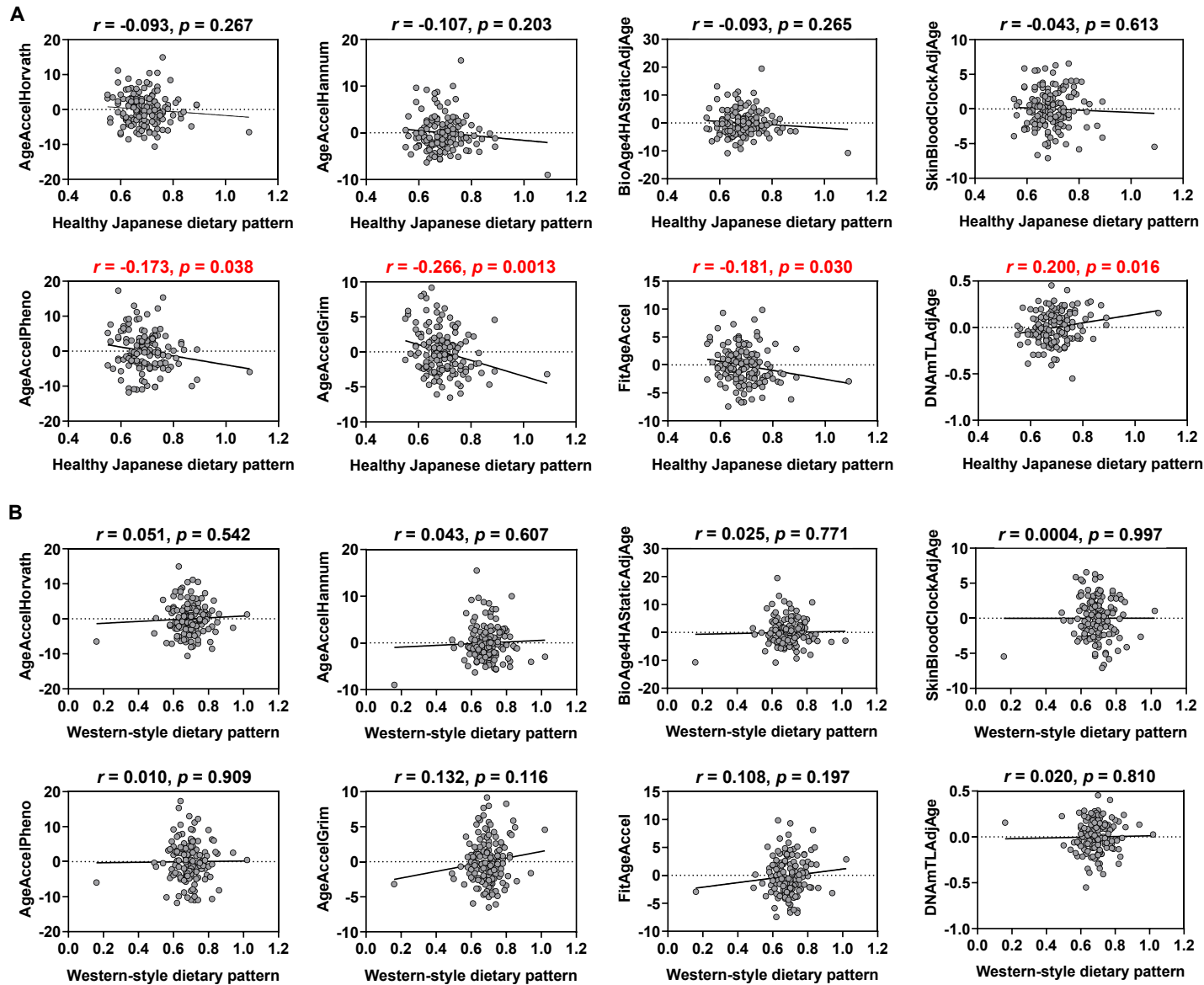
**Figure S2. Pearson correlation scatterplots.**
**A)** Correlation between log10 (healthy Japanese dietary pattern scores) and age acceleration (AgeAccel) and age adjusted (AdjAge) values for each epigenetic clock. **B)** Correlation between log10 (western-style dietary pattern scores) and AgeAccel and AdjAge. values for each epigenetic clock. Red letters indicate that the correlation is significant.