

SUPPLEMENTARY TABLES

Supplementary Table 1. Associations between accelerated ages of epigenetic and transcriptomic biomarkers and nuclear magnetic resonance biomarkers.

| Biomarker | Aging predictor | Coefficient (95% CI) | P-value |
|-----------|--------------------|---|--------------------------|
| GlycA | GrimAge | 5.71 (4.36, 7.05) | 7.94×10^{-16} * |
| ApoB | GrimAge | 0.10 (-0.35, 0.55) | 0.65 |
| ApoA-1 | GrimAge | -1.03 (-1.42, -0.63) | 5.50×10^{-7} * |
| Glu | GrimAge | -0.12 (-0.82, 0.59) | 0.74 |
| ApoB: A-1 | GrimAge | 0.02 (-0.01, 0.06) | 0.20 |
| GlycA | Hannum Age | 1.81 (0.65, 2.98) | 2.30×10^{-3} |
| ApoB | Hannum Age | -0.06 (-0.42, 0.31) | 0.76 |
| ApoA-1 | Hannum Age | -0.41 (-0.74, -0.08) | 0.01 |
| Glu | Hannum Age | 0.37 (-0.20, 0.94) | 0.21 |
| ApoB: A-1 | Hannum Age | 0.01 (-0.02, 0.04) | 0.47 |
| GlycA | Horvath Age | 0.81 (-0.45, 2.07) | 0.21 |
| ApoB | Horvath Age | -0.19 (-0.58, 0.21) | 0.36 |
| ApoA-1 | Horvath Age | -0.29 (-0.64, 0.07) | 0.12 |
| Glu | Horvath Age | 0.28 (-0.34, 0.89) | 0.37 |
| ApoB: A-1 | Horvath Age | -5.22×10^{-3} (-0.03, 0.02) | 0.73 |
| GlycA | Phenotypic Age | 2.88 (1.91, 3.87) | 1.21×10^{-8} * |
| ApoB | Phenotypic Age | 0.07 (-0.25, 0.39) | 0.67 |
| ApoA-1 | Phenotypic Age | -0.55 (-0.83, -0.26) | 1.58×10^{-4} * |
| Glu | Phenotypic Age | 0.12 (-0.38, 0.61) | 0.64 |
| ApoB: A-1 | Phenotypic Age | 8.96×10^{-3} (-0.01, 0.03) | 0.46 |
| GlycA | Transcriptomic Age | 0.34 (-0.85, 1.53) | 0.57 |
| ApoB | Transcriptomic Age | 0.05 (-0.26, 0.37) | 0.74 |
| ApoA-1 | Transcriptomic Age | 0.34 (0.04, 0.63) | 0.03 |
| Glu | Transcriptomic Age | 0.23 (-0.36, 0.82) | 0.45 |
| ApoB: A-1 | Transcriptomic Age | -1.27×10^{-3} (-5.29×10^{-3} , 2.75×10^{-3}) | 0.54 |

Abbreviation: CI: confidence interval; *indicates Bonferroni significant P-value ($P < 1.43 \times 10^{-3}$).

Supplementary Table 2. Associations between nuclear magnetic resonance biomarkers and multiple adjusted accelerated ages of epigenetic and transcriptomic aging biomarkers.

| Biomarker | Aging predictor adjustment | Aging predictor | Coefficient (95% CI) | P-value |
|-----------|----------------------------|-----------------|--|-------------------------|
| GlycA | Gr + Ha + Ho + Ph + TA | GrimAge | 5.03 (3.01, 7.05) | 1.85×10^{6} * |
| ApoB | Gr + Ha + Ho + Ph + TA | GrimAge | 0.45 (-0.22, 1.11) | 0.19 |
| ApoA-1 | Gr + Ha + Ho + Ph + TA | GrimAge | -1.13 (-1.71, -0.55) | 1.83×10^{-4} * |
| Glu | Gr + Ha + Ho + Ph + TA | GrimAge | -0.09 (-1.16, 0.99) | 0.87 |
| ApoB: A-1 | Gr + Ha + Ho + Ph + TA | GrimAge | 1.04×10^{-2} (2.9×10^{-3} , 0.02) | 6.84×10^{-3} |
| GlycA | Gr + Ha + Ho + Ph + TA | Hannum Age | 1.17 (-0.77, 3.12) | 0.24 |
| ApoB | Gr + Ha + Ho + Ph + TA | Hannum Age | 0.24 (-0.40, 0.88) | 0.46 |
| ApoA-1 | Gr + Ha + Ho + Ph + TA | Hannum Age | -0.60 (-1.16, -0.04) | 0.04 |
| Glu | Gr + Ha + Ho + Ph + TA | Hannum Age | 0.21 (-0.82, 1.25) | 0.68 |
| ApoB: A-1 | Gr + Ha + Ho + Ph + TA | Hannum Age | 6.27×10^{-3} (-9.74×10^{-4} , 0.01) | 0.09 |
| GlycA | Gr + Ha + Ho + Ph + TA | Horvath Age | -2.94 (-4.86, -1.02) | 2.89×10^{-3} |

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|-----------|------------------------|--------------------|---|------|
| ApoB | Gr + Ha + Ho + Ph + TA | Horvath Age | -0.80 (-1.43, -0.16) | 0.01 |
| ApoA-1 | Gr + Ha + Ho + Ph + TA | Horvath Age | -0.12 (-0.67, 0.44) | 0.67 |
| Glu | Gr + Ha + Ho + Ph + TA | Horvath Age | 0.13 (-0.89, 1.15) | 0.80 |
| ApoB: A-1 | Gr + Ha + Ho + Ph + TA | Horvath Age | -6.89×10^{-3} (-0.01, 2.66×10^{-4}) | 0.06 |
| GlycA | Gr + Ha + Ho + Ph + TA | Phenotypic Age* | 2.27 (0.47, 4.06) | 0.01 |
| ApoB | Gr + Ha + Ho + Ph + TA | Phenotypic Age | 0.18 (-0.41, 0.77) | 0.55 |
| ApoA-1 | Gr + Ha + Ho + Ph + TA | Phenotypic Age | 0.28 (-0.24, 0.80) | 0.29 |
| Glu | Gr + Ha + Ho + Ph + TA | Phenotypic Age | 0.33 (-0.62, 1.29) | 0.49 |
| ApoB: A-1 | Gr + Ha + Ho + Ph + TA | Phenotypic Age | -2.30×10^{-4} (-6.93×10^{-3} , 6.47×10^{-3}) | 0.95 |
| GlycA | Gr + Ha + Ho + Ph + TA | Transcriptomic Age | -0.85 (-2.90, 1.13) | 0.39 |
| ApoB | Gr + Ha + Ho + Ph + TA | Transcriptomic Age | 0.08 (-0.58, 0.75) | 0.80 |
| ApoA-1 | Gr + Ha + Ho + Ph + TA | Transcriptomic Age | 0.56 (-0.02, 1.15) | 0.06 |
| Glu | Gr + Ha + Ho + Ph + TA | Transcriptomic Age | -0.13 (-1.20, 0.94) | 0.81 |
| ApoB: A-1 | Gr + Ha + Ho + Ph + TA | Transcriptomic Age | -3.86×10^{-3} (-0.01, 3.66×10^{-3}) | 0.31 |

Abbreviations: Gr: Grim Age; Ha: Hannum Age; Ho: Horvath Age; Ph: Phenotypic Age; TA: Transcriptomic Age; CI: confidence interval. *indicates Bonferroni significant P -value ($P < 1.43 \times 10^{-3}$).

Supplementary Table 3. Associations between nuclear magnetic resonance biomarkers and multiple adjusted accelerated ages of epigenetic aging biomarkers.

| Biomarker | Aging predictor adjustment | Aging predictor | Coefficient (95% CI) | P -value |
|-----------|----------------------------|-----------------|--|-------------------------|
| GlycA | Gr + Ha + Ho + Ph | GrimAge | 5.03 (3.01, 7.05) | 1.83×10^{-6} * |
| ApoB | Gr + Ha + Ho + Ph | GrimAge | 0.45 (-0.22, 1.11) | 0.19 |
| ApoA-1 | Gr + Ha + Ho + Ph | GrimAge | -1.13 (-1.72, -0.54) | 2.02×10^{-4} * |
| Glu | Gr + Ha + Ho + Ph | GrimAge | -0.08 (-1.16, 0.98) | 0.87 |
| ApoB: A-1 | Gr + Ha + Ho + Ph | GrimAge | 0.01 (2.89×10^{-3} , 1.79×10^{-2}) | 6.88×10^{-3} |
| GlycA | Gr + Ha + Ho + Ph | Hannum Age | 1.07 (-0.86, 2.99) | 0.28 |
| ApoB | Gr + Ha + Ho + Ph | Hannum Age | 0.25 (-0.38, 0.89) | 0.43 |
| ApoA-1 | Gr + Ha + Ho + Ph | Hannum Age | -0.53 (-1.09, 0.03) | 0.06 |
| Glu | Gr + Ha + Ho + Ph | Hannum Age | 0.20 (-0.82, 1.22) | 0.70 |
| ApoB: A-1 | Gr + Ha + Ho + Ph | Hannum Age | 5.80×10^{-3} (-1.39×10^{-3} , 0.01) | 0.11 |
| GlycA | Gr + Ha + Ho + Ph | Horvath Age | -2.90 (-4.81, -0.98) | 3.23×10^{-3} |
| ApoB | Gr + Ha + Ho + Ph | Horvath Age | -0.80 (-1.43, -0.17) | 0.01 |
| ApoA-1 | Gr + Ha + Ho + Ph | Horvath Age | -0.14 (-0.70, 0.42) | 0.61 |
| Glu | Gr + Ha + Ho + Ph | Horvath Age | 0.14 (-0.88, 1.15) | 0.79 |
| ApoB: A-1 | Gr + Ha + Ho + Ph | Horvath Age | -6.72×10^{-3} (-0.01, 4.28×10^{-4}) | 0.07 |
| GlycA | Gr + Ha + Ho + Ph | Phenotypic Age | 2.26 (0.46, 4.05) | 0.01 |
| ApoB | Gr + Ha + Ho + Ph | Phenotypic Age | 0.18 (-0.41, 0.77) | 0.55 |
| ApoA-1 | Gr + Ha + Ho + Ph | Phenotypic Age | 0.29 (-0.24, 0.81) | 0.28 |
| Glu | Gr + Ha + Ho + Ph | Phenotypic Age | 0.33 (-0.62, 1.28) | 0.50 |
| ApoB: A-1 | Gr + Ha + Ho + Ph | Phenotypic Age | -2.63×10^{-4} (-7.0×10^{-3} , 6.43×10^{-3}) | 0.94 |

Abbreviations: Gr: Grim Age; Ho: Horvath Age; Ha: Hannum Age; Ph: Phenotypic Age; CI: confidence interval. *indicates Bonferroni significant P -value ($P < 1.43 \times 10^{-3}$).

Supplementary Table 4. Associations between accelerated ages of individual epigenetic and transcriptomic aging predictors and nuclear magnetic resonance multi markers.

| Biomarker | Aging predictor adjustment | Aging predictor | Coefficient (95% CI) | P-value |
|------------------|-----------------------------------|------------------------|--|----------------|
| LP-IR | Grim Age | GrimAge | 0.18 (−0.20, 0.56) | 0.35 |
| DRI | Grim Age | GrimAge | −0.29 (−0.57, −2.03 × 10 ^{−3}) | 0.05 |
| LP-IR | Hannum Age | Hannum Age | 0.15 (−0.16, 0.46) | 0.34 |
| DRI | Hannum Age | Hannum Age | −0.04 (−0.28, 0.19) | 0.72 |
| LP-IR | Horvath Age | Horvath Age | 0.32 (−9.36 × 10 ^{−3} , 0.66) | 0.06 |
| DRI | Horvath Age | Horvath Age | 0.06 (−0.20, 0.31) | 0.67 |
| LP-IR | Phenotypic Age | Phenotypic Age | 0.18 (−0.08, 0.45) | 0.18 |
| DRI | Phenotypic Age | Phenotypic Age | −0.09 (−0.29, 0.15) | 0.40 |
| LP-IR | Transcriptomic Age | Transcriptomic Age | −0.13 (−0.44, 0.18) | 0.40 |
| DRI | Transcriptomic Age | Transcriptomic Age | −0.02 (−0.26, 0.23) | 0.88 |

Abbreviation: CI: confidence interval.

Supplementary Table 5. Associations between nuclear magnetic resonance multi markers and multiple adjusted accelerated ages of epigenetic and transcriptomic aging biomarkers.

| Biomarker | Aging predictor adjustment | Aging predictor | Coefficient (95% CI) | P-value |
|------------------|-----------------------------------|------------------------|-----------------------------|----------------|
| LP-IR | Gr + Ha + Ho + Ph + TA | GrimAge | 0.32 (−0.28, 0.93) | 0.29 |
| DRI | Gr + Ha + Ho + Ph + TA | GrimAge | −0.22 (−0.68, 0.24) | 0.35 |
| LP-IR | Gr + Ha + Ho + Ph + TA | Hannum Age | 0.16 (−0.42, 0.74) | 0.59 |
| DRI | Gr + Ha + Ho + Ph + TA | Hannum Age | −0.01 (−0.46, 0.43) | 0.95 |
| LP-IR | Gr + Ha + Ho + Ph + TA | Horvath Age | 0.13 (−0.44, 0.71) | 0.64 |
| DRI | Gr + Ha + Ho + Ph + TA | Horvath Age | 0.04 (−0.40, 0.48) | 0.87 |
| LP-IR | Gr + Ha + Ho + Ph + TA | Phenotypic Age | −0.12 (−0.66, 0.42) | 0.66 |
| DRI | Gr + Ha + Ho + Ph + TA | Phenotypic Age | −0.10 (−0.51, 0.31) | 0.64 |
| LP-IR | Gr + Ha + Ho + Ph + TA | Transcriptomic Age | −0.11 (−0.72, 0.49) | 0.71 |
| DRI | Gr + Ha + Ho + Ph + TA | Transcriptomic Age | −0.08 (−0.55, 0.38) | 0.72 |

Abbreviations: Gr: Grim Age; Ha: Hannum Age; Ho: Horvath Age; Ph: Phenotypic Age; TA: Transcriptomic Age; CI: confidence interval.

Supplementary Table 6. Associations between nuclear magnetic resonance multi markers and multiple adjusted accelerated ages of epigenetic aging predictors.

| Biomarker | Aging predictor adjustment | Aging predictor | Coefficient (95% CI) | P-value |
|------------------|-----------------------------------|------------------------|-----------------------------|----------------|
| LP-IR | Gr + Ha + Ho + Ph | GrimAge | 0.32 (−0.35, 0.93) | 0.29 |
| DRI | Gr + Ha + Ho + Ph | GrimAge | −0.22 (−0.68, 0.24) | 0.35 |
| LP-IR | Gr + Ha + Ho + Ph | Hannum Age | 0.15 (−0.43, 0.72) | 0.62 |
| DRI | Gr + Ha + Ho + Ph | Hannum Age | −0.03 (−0.46, 0.41) | 0.91 |
| LP-IR | Gr + Ha + Ho + Ph | Horvath Age | 0.14 (−0.43, 0.71) | 0.63 |
| DRI | Gr + Ha + Ho + Ph | Horvath Age | −0.04 (−0.40, 0.48) | 0.85 |
| LP-IR | Gr + Ha + Ho + Ph | Phenotypic Age | −0.12 (−0.65, 0.42) | 0.66 |
| DRI | Gr + Ha + Ho + Ph | Phenotypic Age | −0.10 (−0.51, 0.31) | 0.64 |

Abbreviations: Gr: Grim Age; Ha: Hannum Age; Ho: Horvath Age; Ph: Phenotypic Age; CI: confidence interval.

Supplementary Table 7. Associations between LDL and HDL and accelerated ages of individual epigenetic and transcriptomic aging biomarkers.

| Biomarker | Aging predictor | Coefficient (95% CI) | P-value |
|------------------|------------------------|---------------------------------------|----------------|
| HDL | GrimAge | -0.33 (-0.68, 0.03) | 0.07 |
| LDL | GrimAge | -0.22 (-1.34, 0.90) | 0.70 |
| HDL | Hannum Age | -0.32 (-0.65, 6.28×10^{-3}) | 0.05 |
| LDL | Hannum Age | -1.11 (-2.16, -0.07) | 0.04 |
| HDL | Horvath Age | -0.29 (-0.62, 0.04) | 0.08 |
| LDL | Horvath Age | -1.13 (-2.15, -0.10) | 0.03 |
| HDL | Phenotypic Age | -0.30 (-0.56, -0.04) | 0.03 |
| LDL | Phenotypic Age | -0.74 (-1.56, 0.09) | 0.08 |
| HDL | Transcriptomic Age | -0.18 (-0.12, 0.48) | 0.25 |
| LDL | Transcriptomic Age | 0.24 (-0.61, 1.09) | 0.58 |

Abbreviation: CI: confidence interval.