|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Time-slice subset** | **100-104 years** | **101-105 years** | **102-106 years** | **103-107 years** | **104-108 years** | **105-109 years** | **106-109 years** | **107-109 years** | **108-109 years** |
| **Coding markers** | **N** | 1 | 9 | 20 | 132 | 176 | 173 | 162 | 50 | 5 |
| **R2** | 0 | 0.05 | 0.24 | 0.31 | 0.23 | 0.09 | 0.04 | 0.11 | 0.04 |
| **P-value** | n/a | 5.67×10-1 | 2.67×10-2  \* | 3.43×10-12  \*\*\* | 1.48×10-11  \*\*\* | 4.79×10-5  \*\*\* | 1.26×10-2  \* | 1.76×10-2  \* | 7.6×10-1 |
| **Slope** | n/a | -0.33 | -0.34 | -0.37 | -0.29 | -0.20 | -0.15 | -0.34 | 0.36 |
| **Slope std err** | n/a | 0.55 | 0.14 | 0.05 | 0.04 | 0.05 | 0.06 | 0.14 | 1.07 |
| **Non-SSC**  **Randomizationa** | - | 0.137 | <0.0001  \*\*\* | <0.0001  \*\*\* | <0.0001  \*\*\* | <0.0001  \*\*\* | <0.0001  \*\*\* | <0.0001  \*\*\* | 0.1387 |
| **Non-SSC**  **H0: s=-1b** | n/a | 2.60×10-1 | 1.82×10-4 \*\*\* | 7.12×10-26  \*\*\* | 9.12×10-40  \*\*\* | 1.11×10-36  \*\*\* | 6.96×10-31  \*\*\* | 1.52×10-5  \*\*\* | 2.94×10-1 |
| **Non-coding markers** | **N** | 8 | 25 | 27 | 43 | 48 | 31 | 29 | 12 | 1 |
| **R2** | 0.12 | 0.27 | 0.33 | 0.62 | 0.55 | 0.27 | 0.17 | 0.16 | 0 |
| **P-value** | 4.09×10-1 | 7.41×10-3  \* | 1.80×10-3  \*\* | 4.47×10-10  \*\*\* | 1.41×10-9  \*\*\* | 2.58×10-3  \*\* | 2.55×10-2  \* | 2.00×10-1 | n/a |
| **Slope** | 0.08 | -0.34 | -0.36 | -0.48 | -0.49 | -0.58 | -0.53 | -0.89 | n/a |
| **Slope std err** | 0.10 | 0.12 | 0.10 | 0.06 | 0.06 | 0.17 | 0.22 | 0.65 | n/a |
| **Non-SSC**  **Randomizationa** | 0.0023  \*\* | 0.0001  \*\*\* | <0.0001  \*\*\* | <0.0001  \*\*\* | <0.0001  \*\*\* | 0.0098  \*\* | 0.02  \* | 0.4305 | - |
| **Non-SSC**  **H0: s=-1b** | 2.79×10-5  \*\*\* | 9.61×10-6  \*\*\* | 1.31×10-6  \*\*\* | 8.46×10-11  \*\*\* | 4.31×10-10  \*\*\* | 2.20×10-2  \* | 4.39×10-2  \* | 8.64×10-1 | n/a |

aNon-SSC – results of tests against spurious self-correlation using randomized genetic distances to create 10,000 new regressions and inspecting whether the original estimate of the slope falls within the distribution of slopes estimated from the randomized data

bNon-SSC – results of tests against spurious self-correlation using slope s=-1 (average slope for all regressions with randomized genetic distance) as null hypothesis for regression;

\* p<0.05, \*\* p<0.005, \*\*\* p<0.0005.