|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Data subset** | **All** | **Insects** | **Reptiles** | **Birds** | **Mammals** | **Humans** |
| **Coding markers** | **N** | 182 | 33 | 18 | 101 | 30 | n/a |
| **R2** | 0.24 | 0.38 | 0.32 | 0.08 | 0.29 | n/a |
| **P-value** | 1.58×10-12\*\*\* | 1.34×10-4\*\*\* | 1.40×10-2\* | 4.87×10-3\*\* | 2.03×10-3\*\* | n/a |
| **Slope** | -0.28 | -0.25 | -0.24 | -0.19 | -0.33 | n/a |
| **Slope std err** | 0.04 | 0.06 | 0.09 | 0.06 | 0.10 | n/a |
| **Non-SSC****Randomizationa**  | <0.0001\*\*\* | <0.0001\*\*\* | <0.0001\*\*\* | <0.0001\*\*\* | <0.0001\*\*\* | n/a |
| **Non-SSC****H0: s=-1b** | 1.97×10-47\*\*\* | 3.55×10-14\*\*\* | 1.59×10-7\*\*\* | 2.12×10-22\*\*\* | 2.13×10-7\*\*\* | n/a |
| **Non-coding markers** | **N** | 57 | 0 | 2 | 9 | 46 | 26 |
| **R2** | 0.60 | n/a | n/a | 0.67 | 0.57 | 0.69 |
| **P-value** | 1.38×10-12\*\*\* | n/a | n/a | 6.60×10-3\* | 1.50×10-9\*\*\* | 1.51×10-7\*\*\* |
| **Slope** | -0.43 | n/a | n/a | -0.38 | -0.44 | -0.24 |
| **Slope std err** | 0.05 | n/a | n/a | 0.10 | 0.06 | 0.03 |
| **Non-SSC****Randomizationa**  | <0.0001\*\*\* | n/a | n/a | 0.0001\*\*\* | <0.0001\*\*\* | <0.0001\*\*\* |
| **Non-SSC****H0: s=-1b** | 3.88×10-17\*\*\* | n/a | n/a | 4.87×10-4\*\*\* | 3.09×10-12\*\*\* | 5.42×10-18\*\*\* |

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