

Erratum

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Phylostratigraphic Bias Creates Spurious Patterns of Genome Evolution

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A coding error caused mistakes in figure 3C. The corrected figure is shown below. No deviation in any age group for any expression site is statistically significant, suggesting that, for the genes simulated, phylostratigraphic error does not cause significant over- or under-representation of genes of certain ages at the three expression sites during *Drosophila* embryonic development. Nonetheless, this result may not validate the original claims of Domazet-Lošo and Tautz (2007), because only approximately 40% of the genes originally analyzed have information necessary for our simulation. Future validation of their claims should compare our simulation results to actual phylostratigraphy restricted to the same gene set. We apologize for any inconvenience this may have caused.

