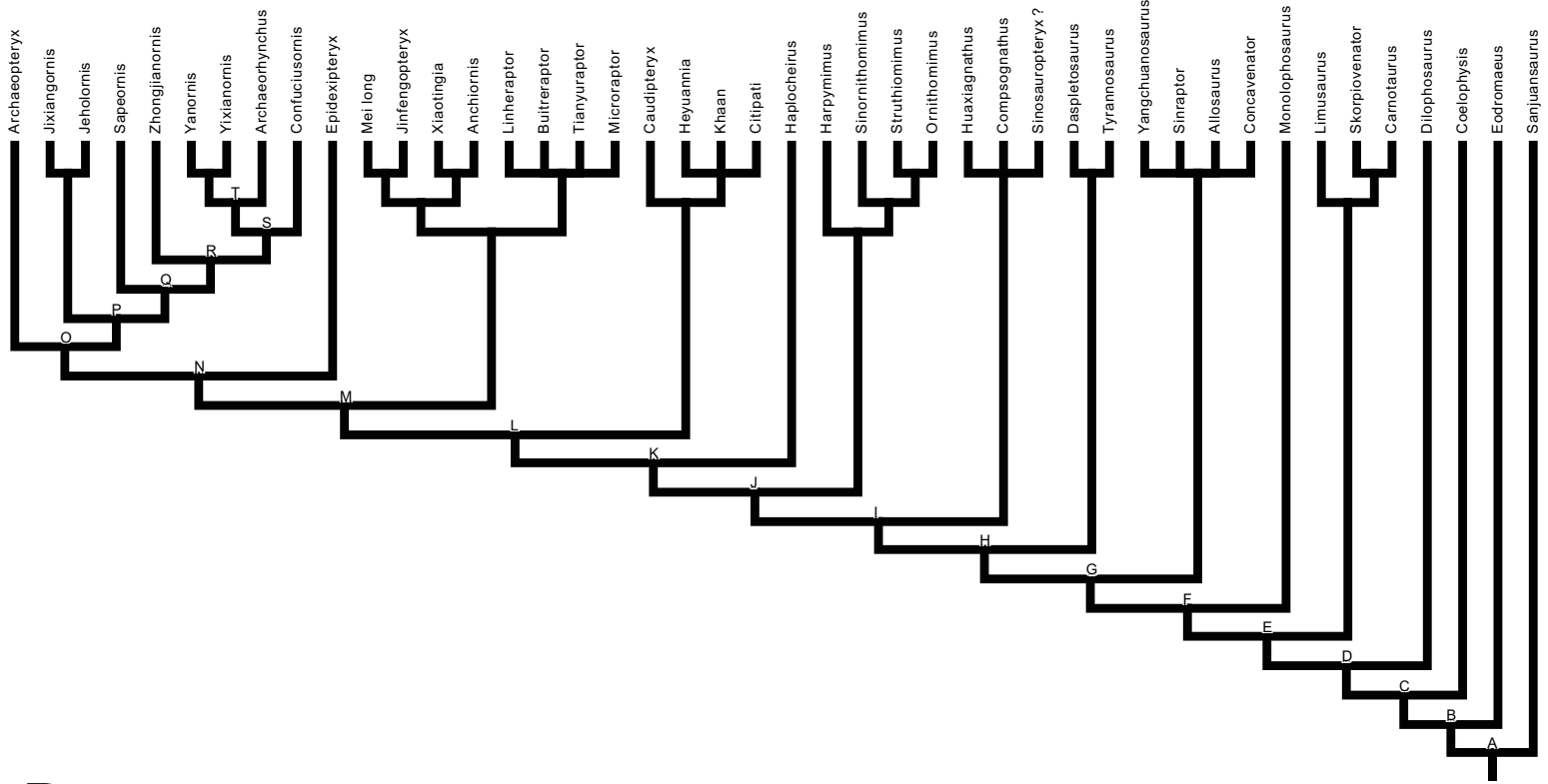
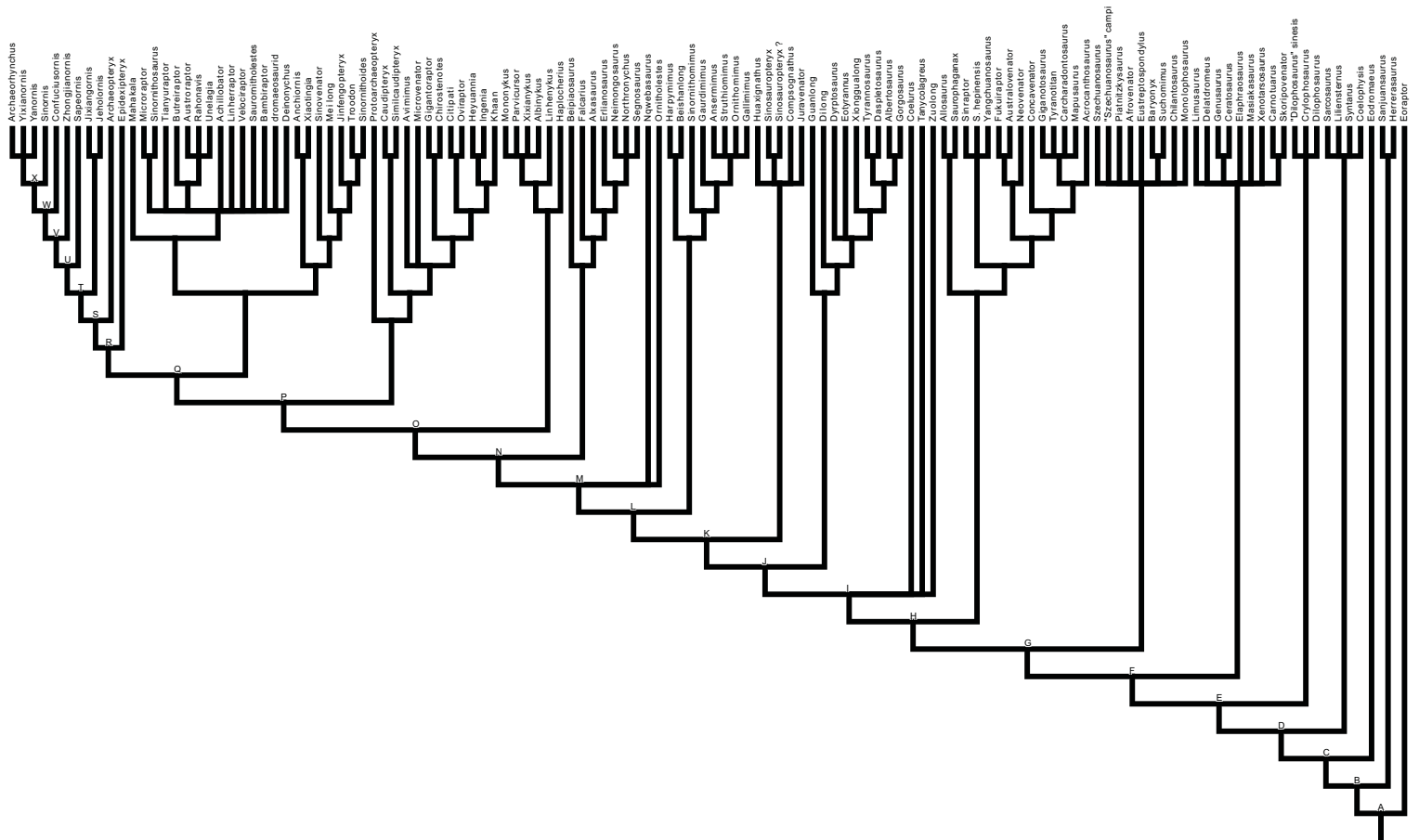


Supplementary Figure 1: Phylogeny used for dataset analysis. Only adult terminal taxa were used in this analysis. Trees based on Carrano et al. 2012, Hu et al. 2009, Li et al. 2010, Mackovicky et al. 2010, Nesbitt et al. 2010, Sereno et al. 2009, Turner et al. 2007, Novas et al. 2009 and Zanno 2010. Three permutations of the placement of *Epidexipteryx* were performed, though only the first is shown. The other two permutations involve *Epidexipteryx* being placed as a Maniraptora outside Paraves (Node L) or placing it after Aves (Node O). A) measured dataset, nodal labels: A- Theropoda, B- Neotheropoda, C-Neotheropoda I, D- Neotheropoda II, E- Ceratosauria, F- Tetanurae, G- Avetheropoda, H- Coelurosauria, I- Coelurosauria I, J- Maniraptoriformes, K- Maniraptora, L- Maniraptora I, M- Paraves, N- Avialae, O- Aves, P- Aves I, Q- Aves II, R- Aves III, S- Pygostylia, T- Ornithothoraces. B) larger dataset: A- Saurischia, B- Theropoda, C- Neotheropoda, D- Neotheropoda I, E- Neotheropoda II, F- Ceratosauria, G- Tetanurae, H- Avetheropoda, I- Coelurosauria, J- Coelurosauria I, K- Coelurosauria II, L- Maniraptoriformes, M- Maniraptora, N- Maniraptora I, O- Maniraptora II, P- Maniraptora III, Q- Paraves, R- Avialae, S- Aves, T- Aves I, U- Aves II, V- Aves III, W- Pygostylia, X- Ornithothoraces

A

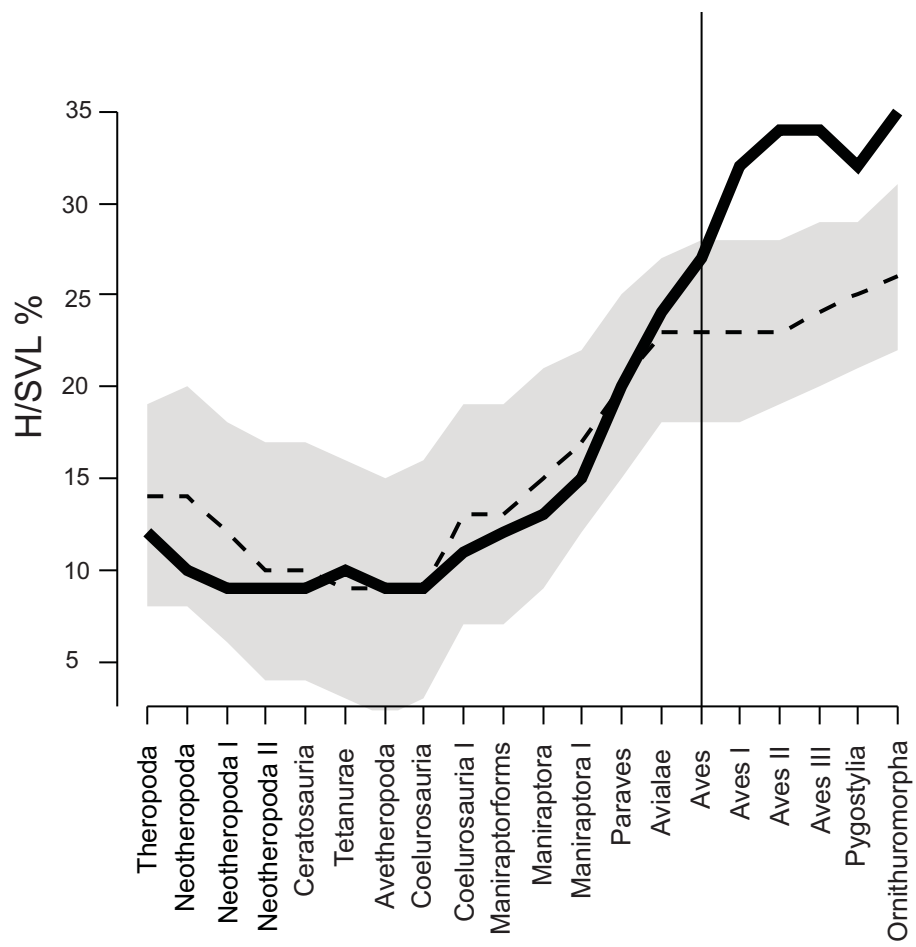


B

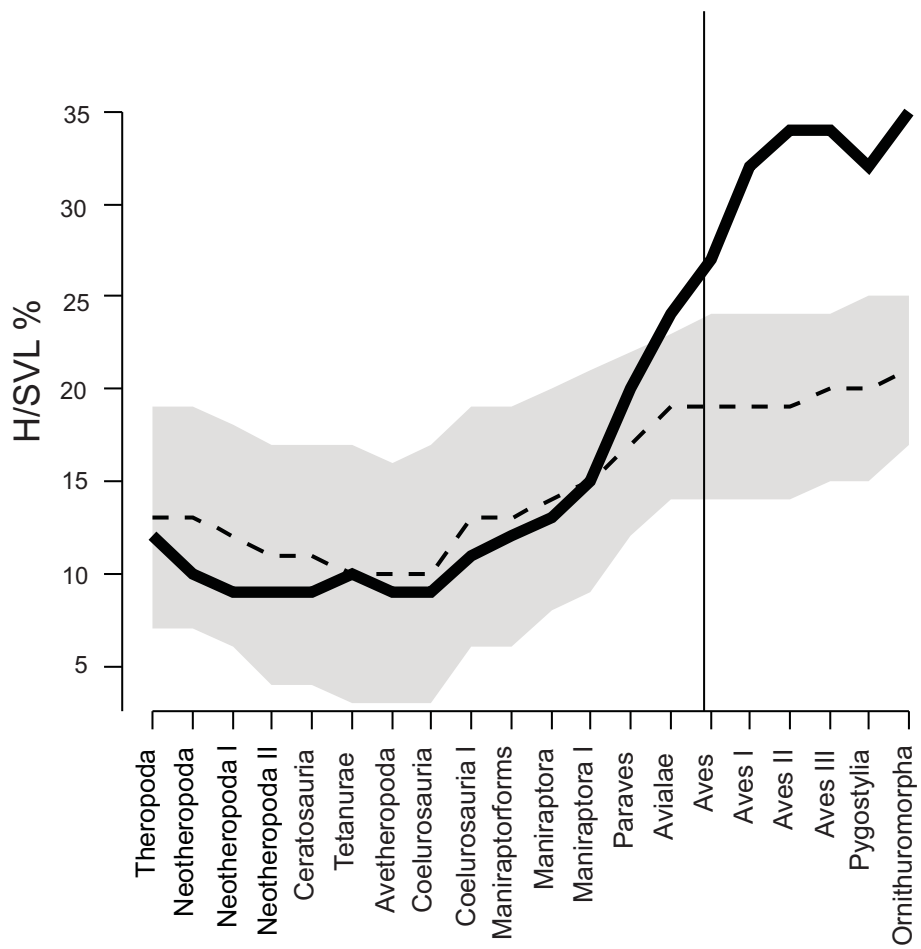


Supplementary Figure 2: Nodal reconstruction (Solid line) for relative H (A,B), FL (C,D) and HL(E, F) lengths using the measured taxon dataset and the *Epidexipteryx* as Avialae tree topology. Estimated expected lengths derived from linear regressions (broken lines) with corresponding error bounds (grey shaded region) using both the total specimens dataset (A, C, E) and adult theropod only dataset (B, D, F). Note the correspondence in lines in pre-Paravian taxa. The node Aves is denoted by a vertical line. Similar patterns occur if using the *Epidexipteryx* as Maniraptora or post *Archaeopteryx* bird topologies (results not shown but see values in Table 5).

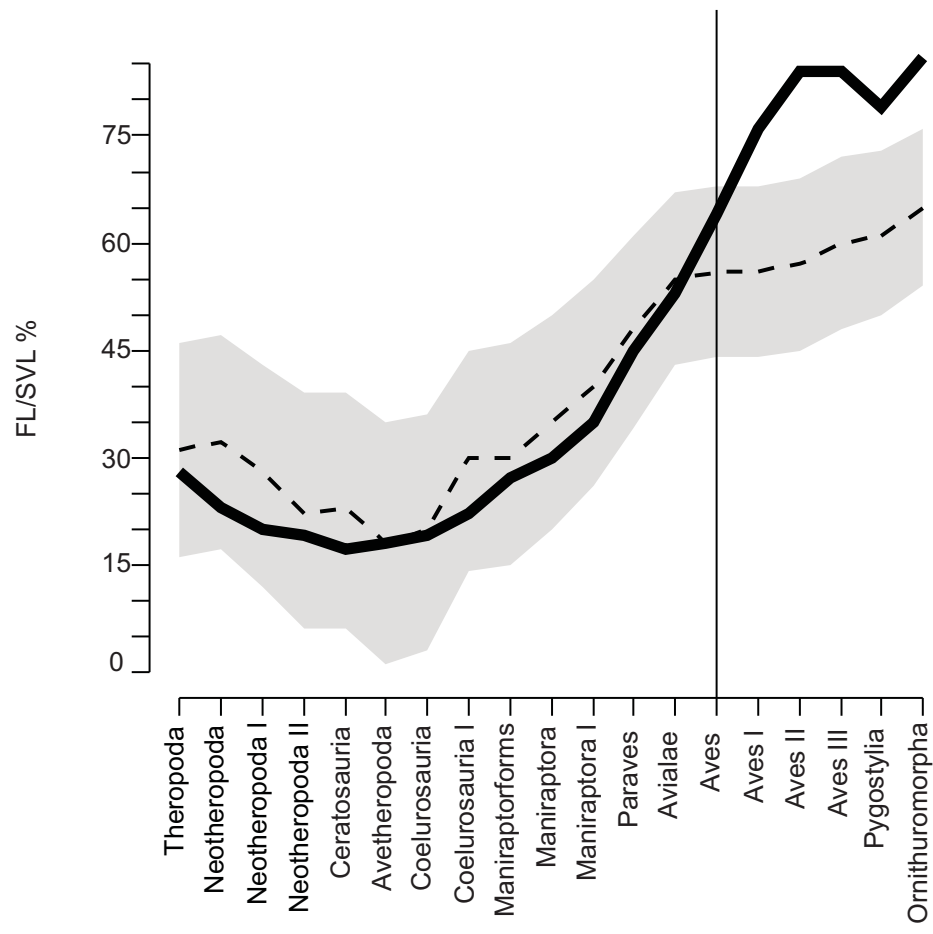
A



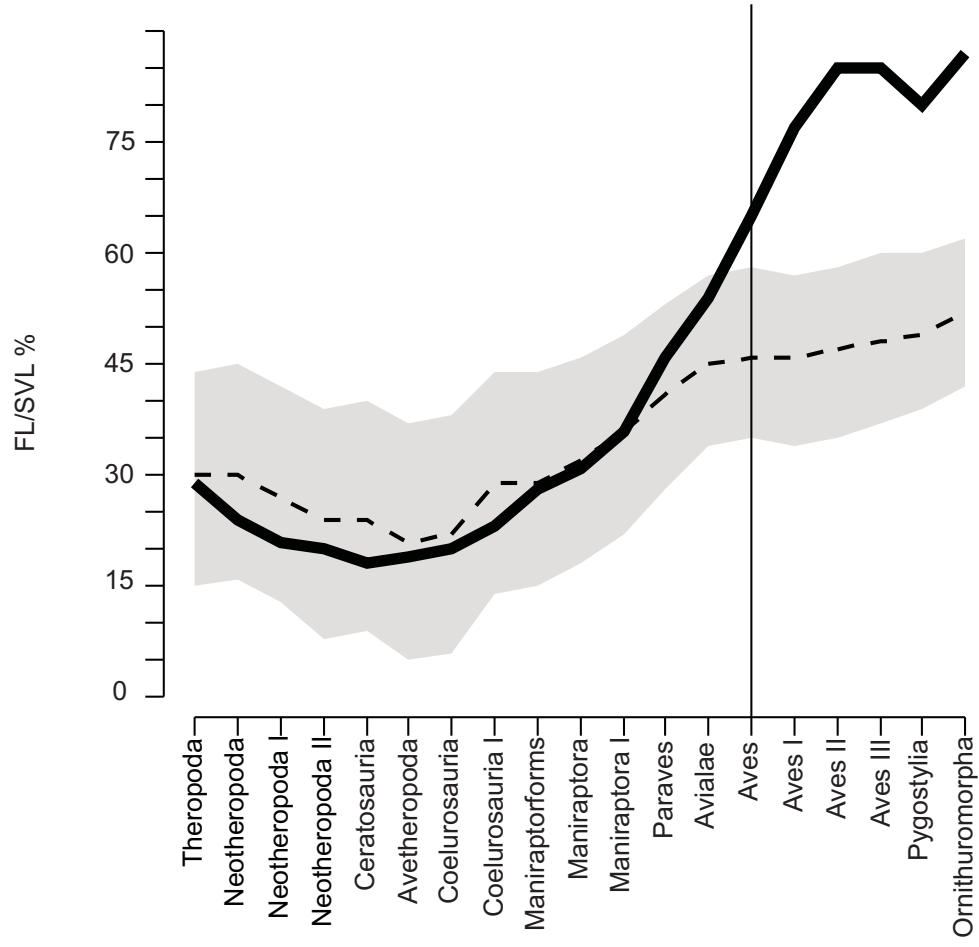
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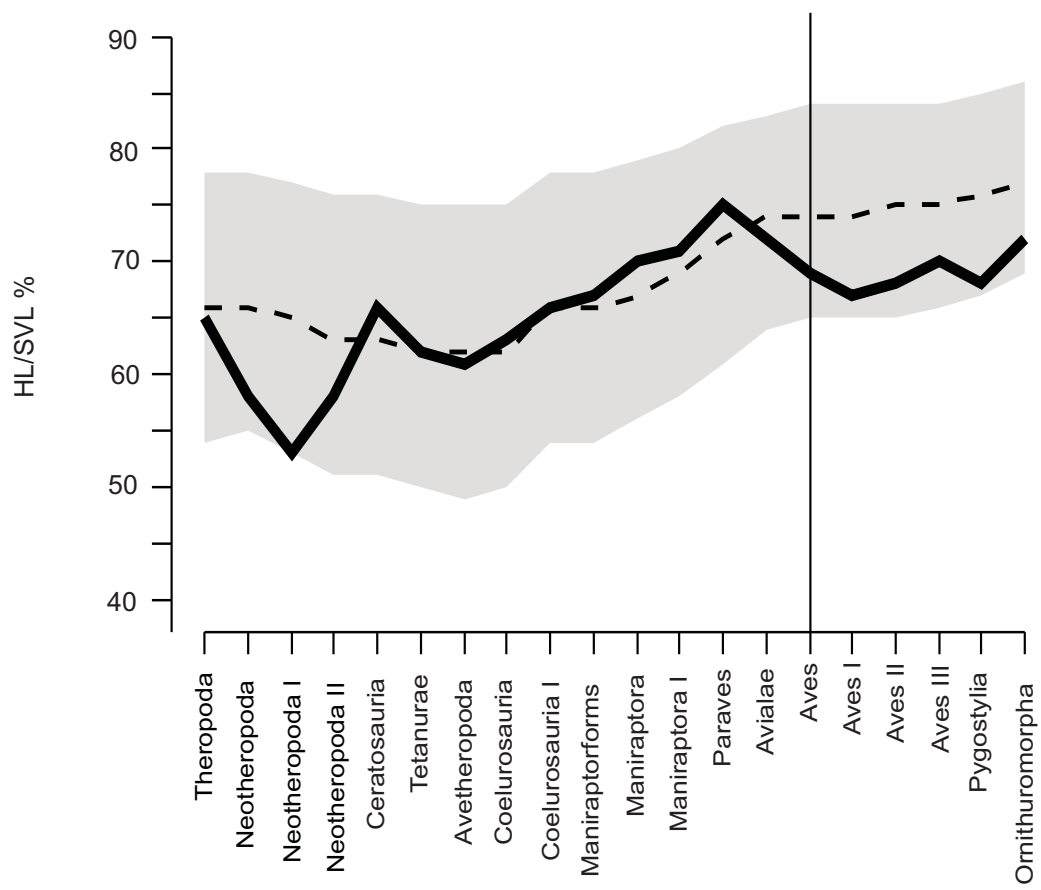
C



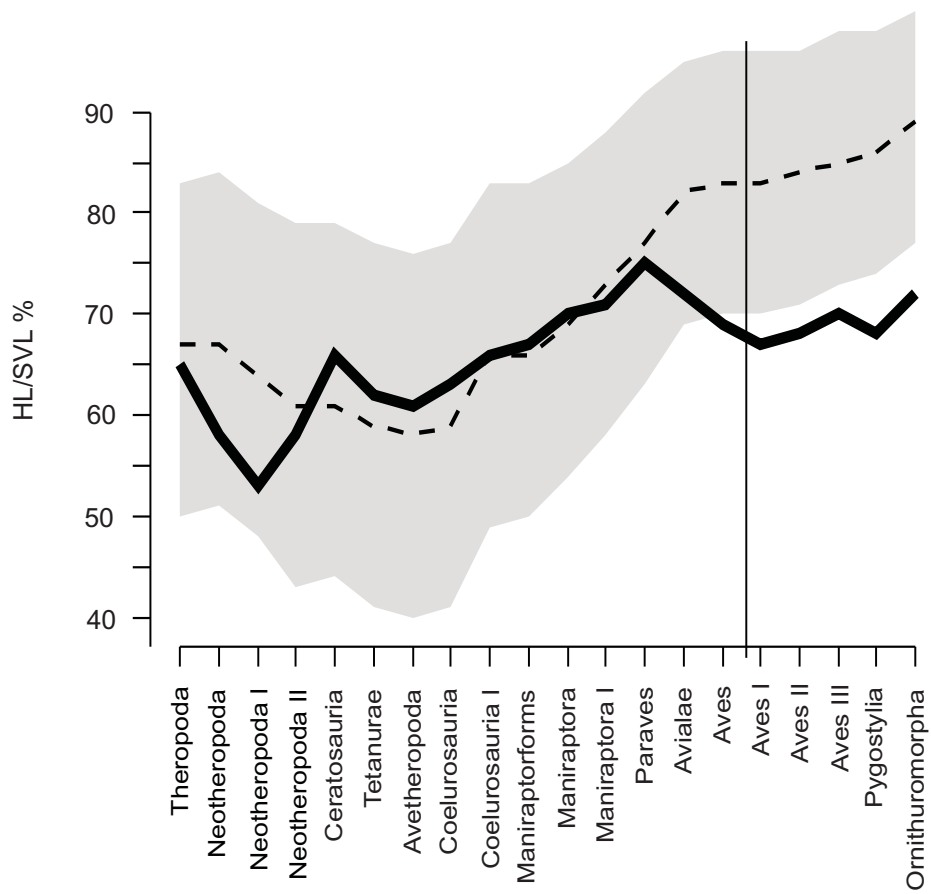
D



E

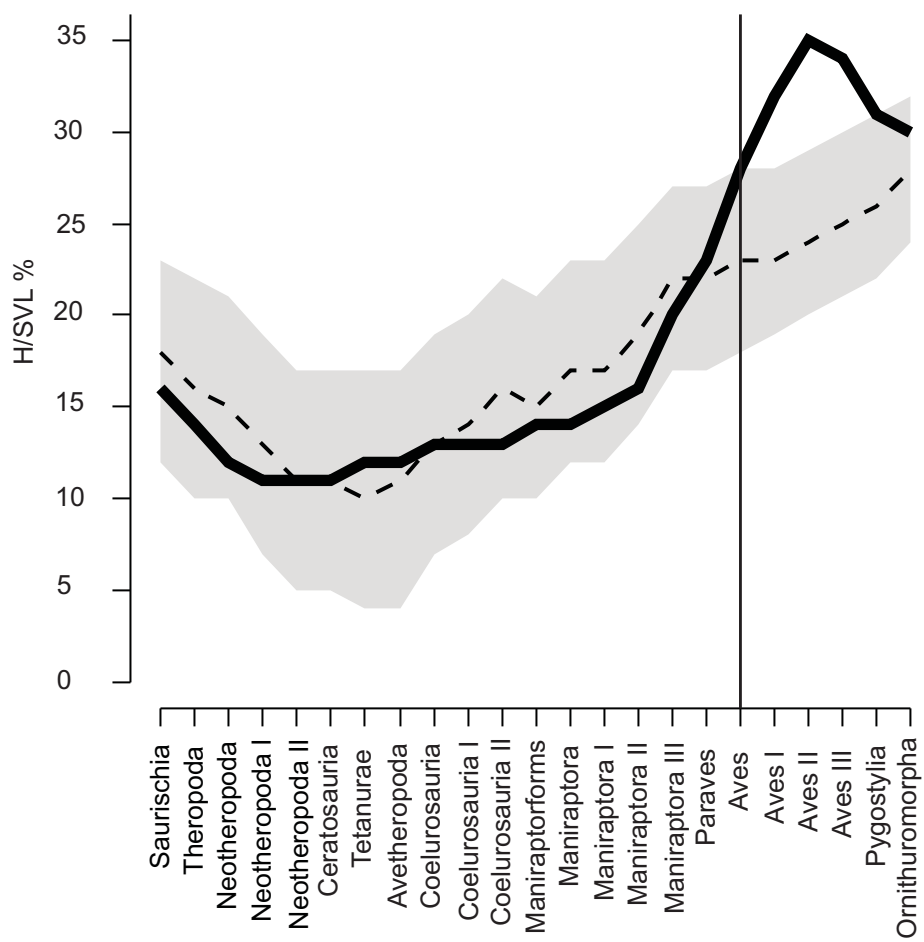


F

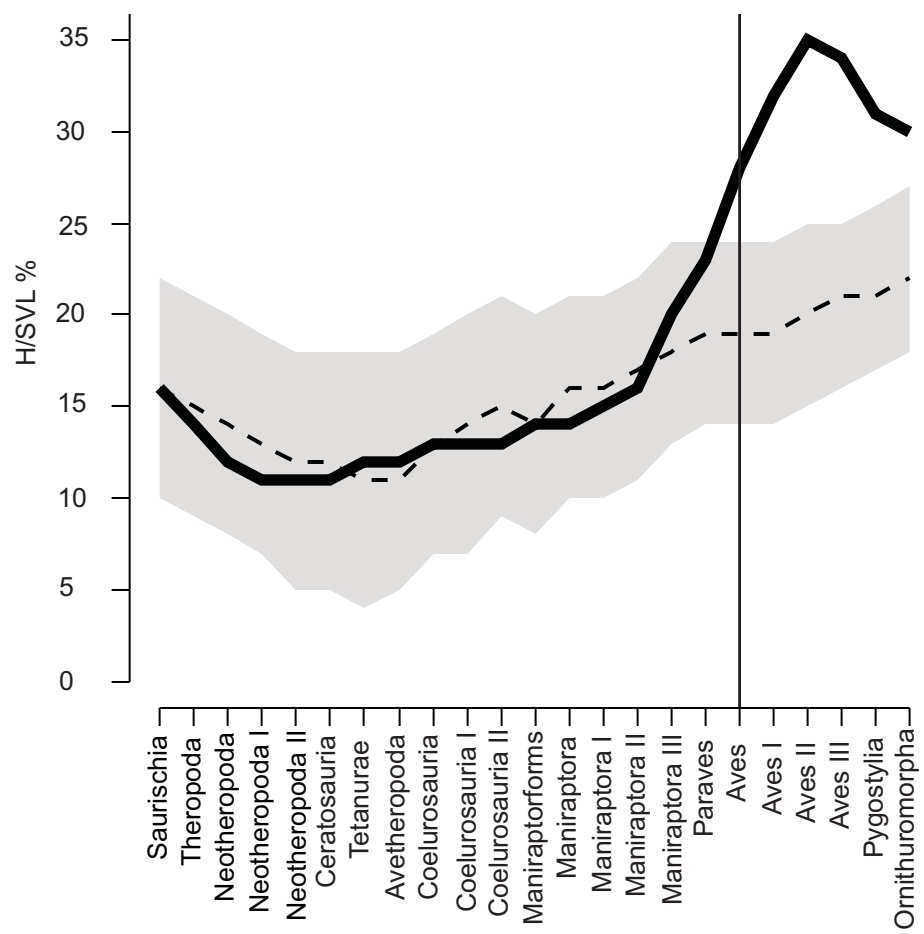


Supplementary Figure 3: Nodal reconstruction (Solid line) for relative H (A,B), FL (C,D) and HL(E, F) lengths using the larger taxon dataset and the *Epidexipteryx* as Avialae tree topology. Estimated expected lengths derived from linear regressions (broken lines) with corresponding error bounds (grey shaded region) using both the total specimens dataset (A, C, E) and adult theropod only dataset (B, D, F). Note the correspondence in lines in pre-Paravian taxa. The node Aves is denoted by a vertical line. Similar patterns occur if using the *Epidexipteryx* as Maniraptora or post *Archaeopteryx* bird topologies (results not shown but see values in Table 5).

A

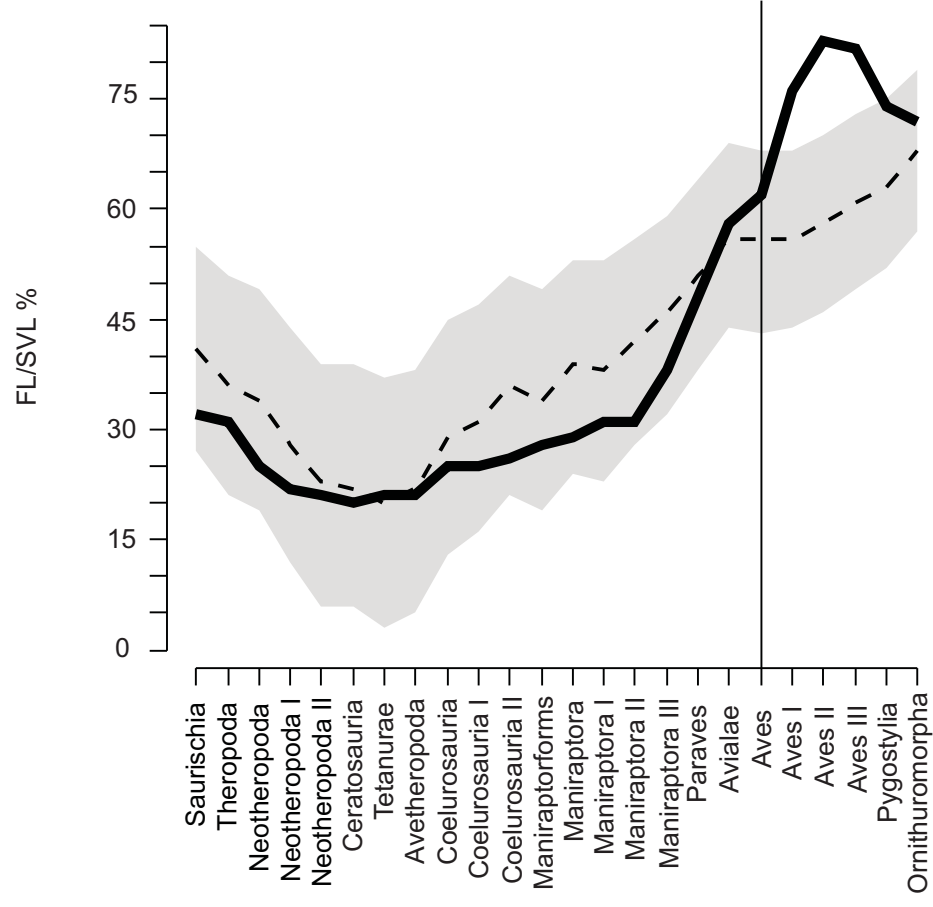


B

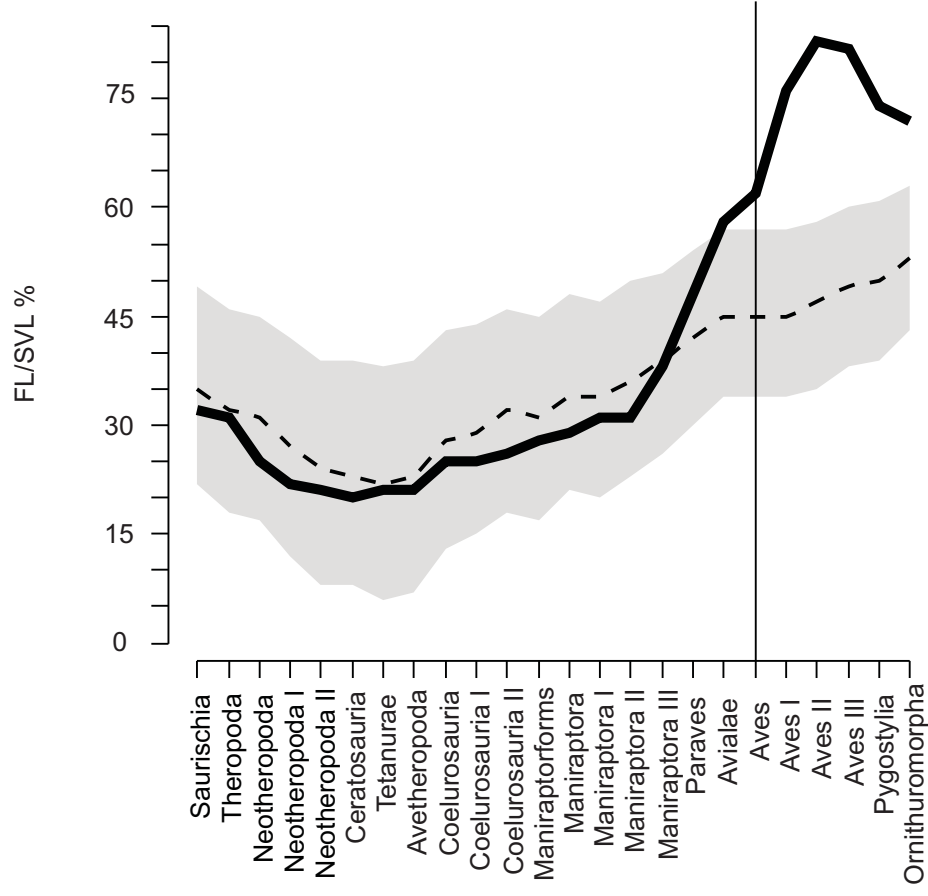




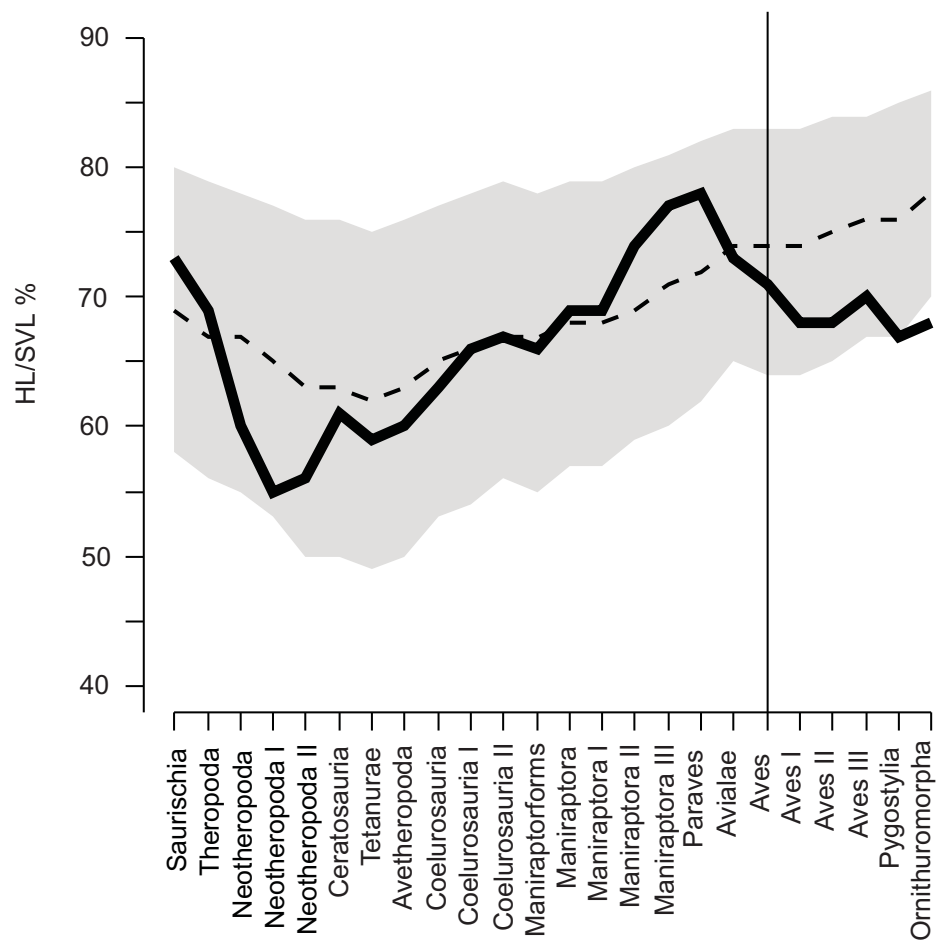
C



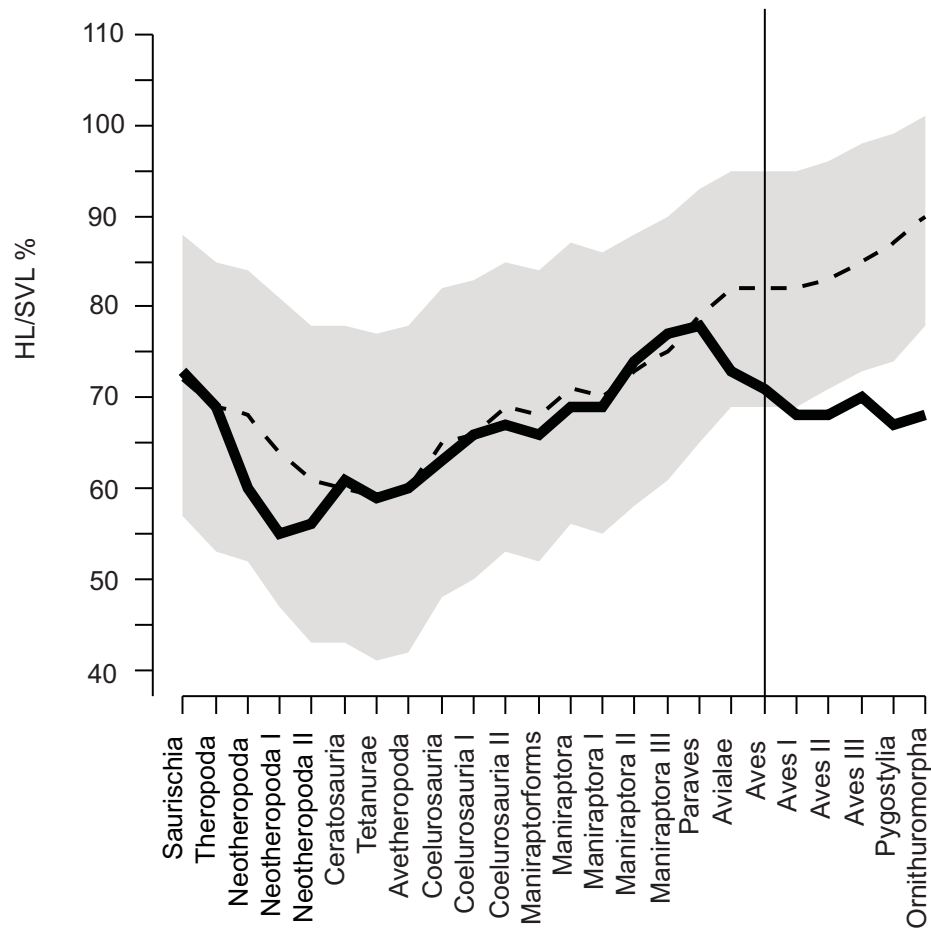
D



E

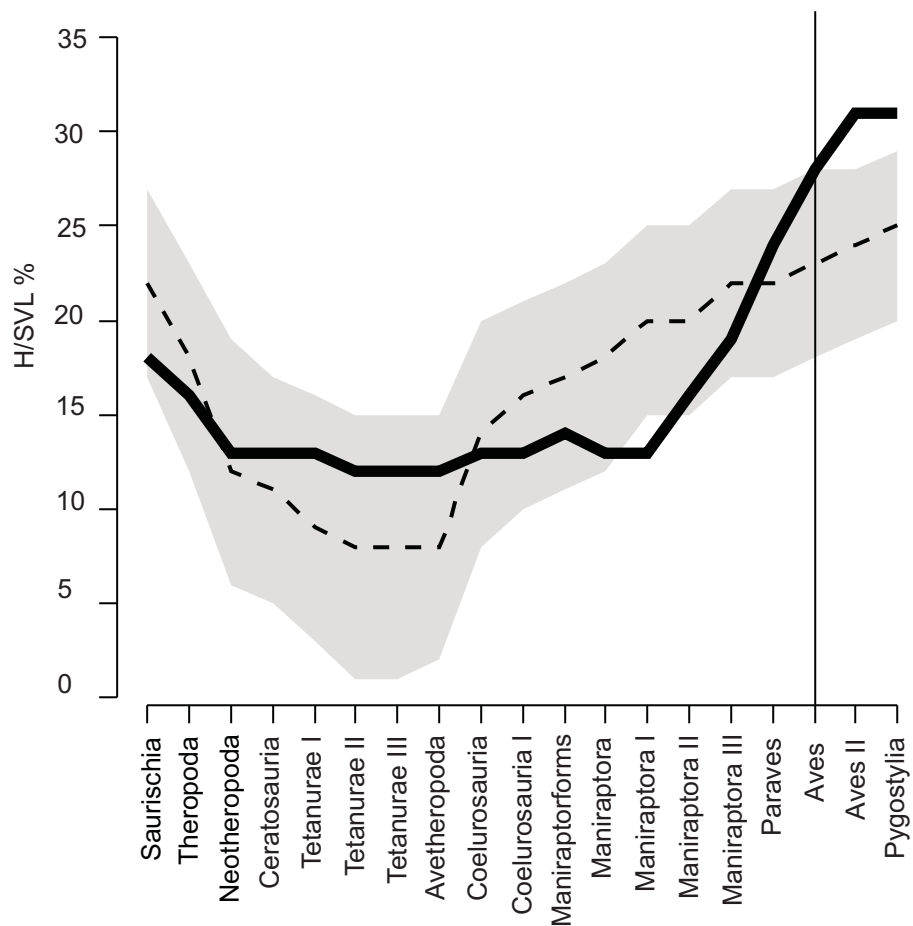


F

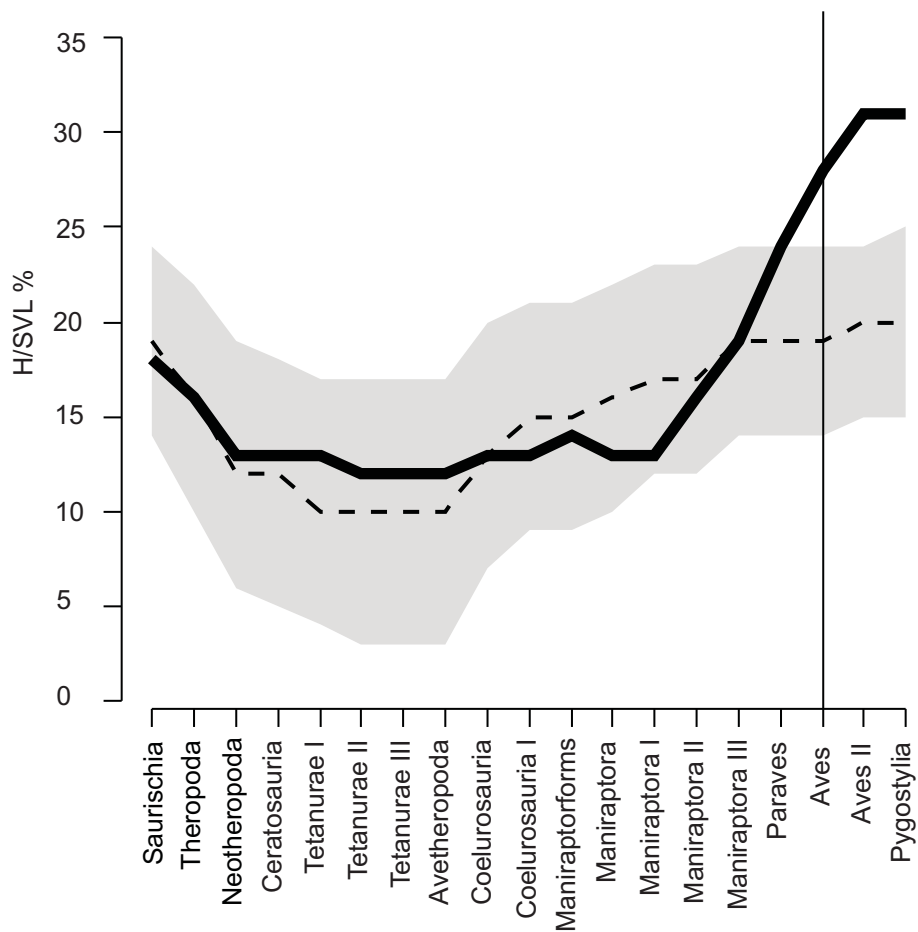


Supplementary Figure 4: Nodal reconstruction (Solid line) for relative H (A,B), FL (C,D) and HL(E, F) lengths using the Xu et al. 2009 topology with unequal branch length. Estimated expected lengths derived from linear regressions (broken lines) with corresponding error bounds (grey shaded region) using both the total specimens dataset (A, C, E) and adult theropod only dataset (B, D, F). Note the correspondence in lines in pre-Paravian taxa. The node Aves is denoted by a vertical line.

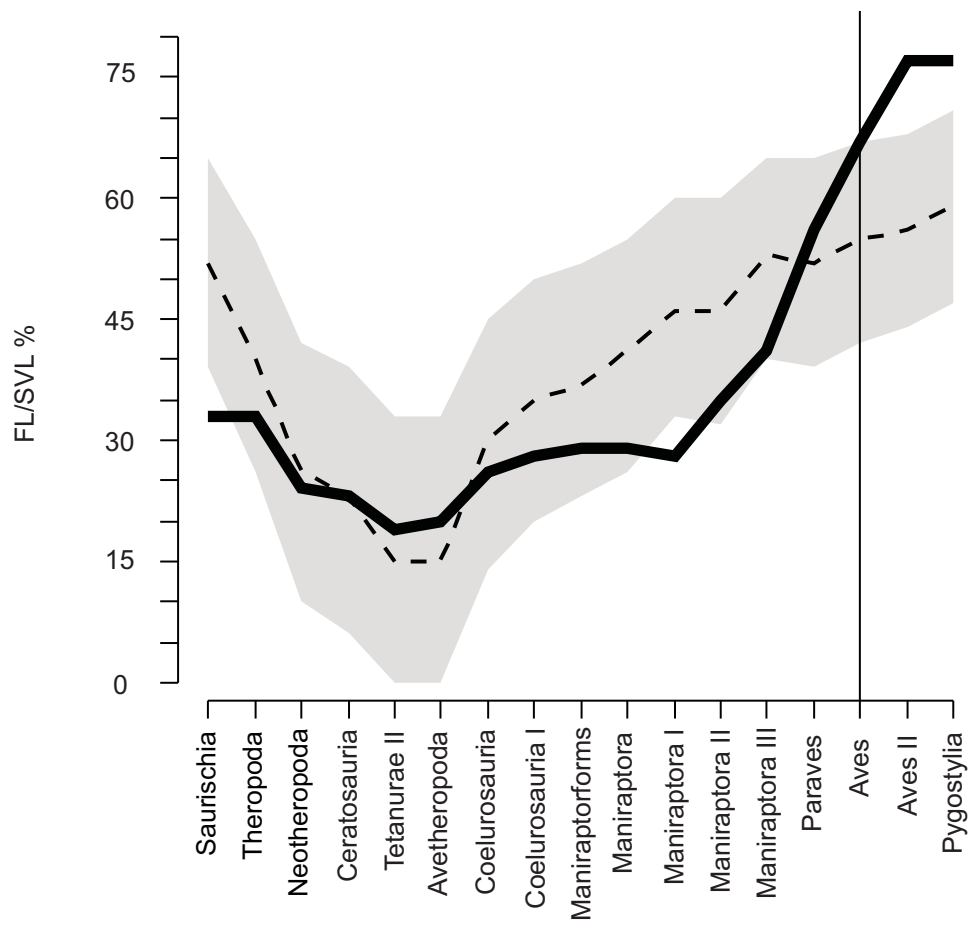
A



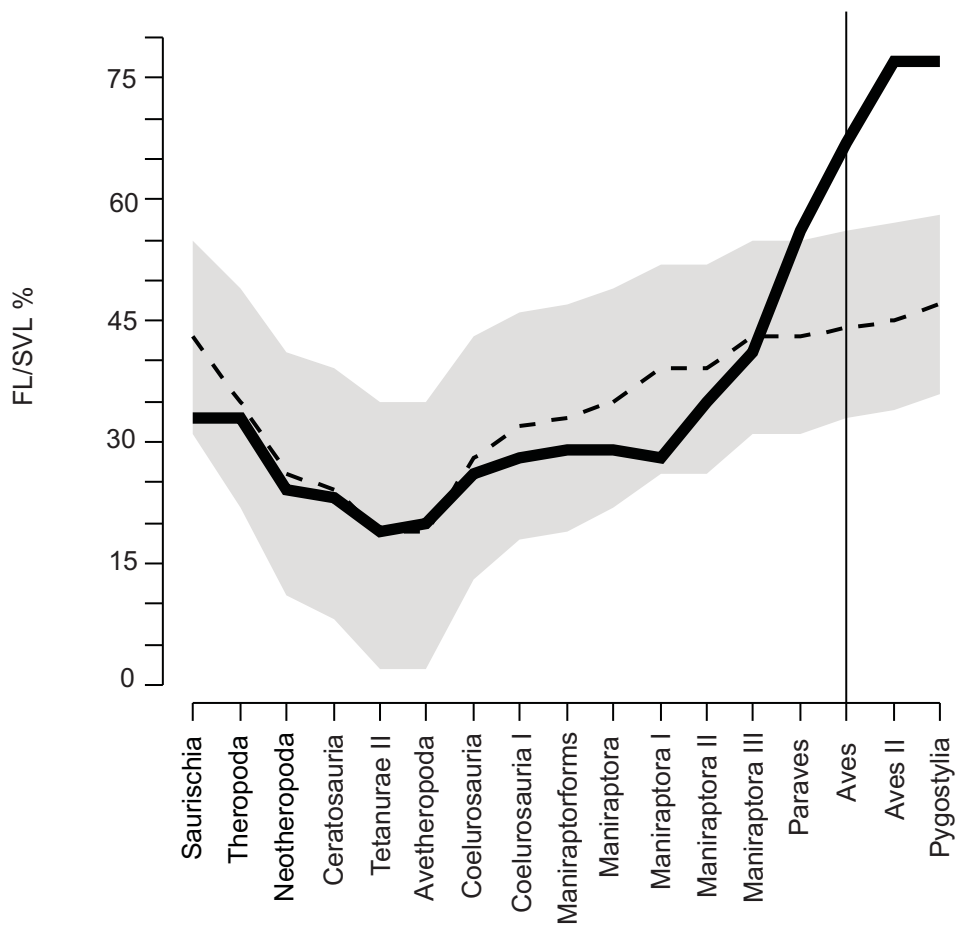
B



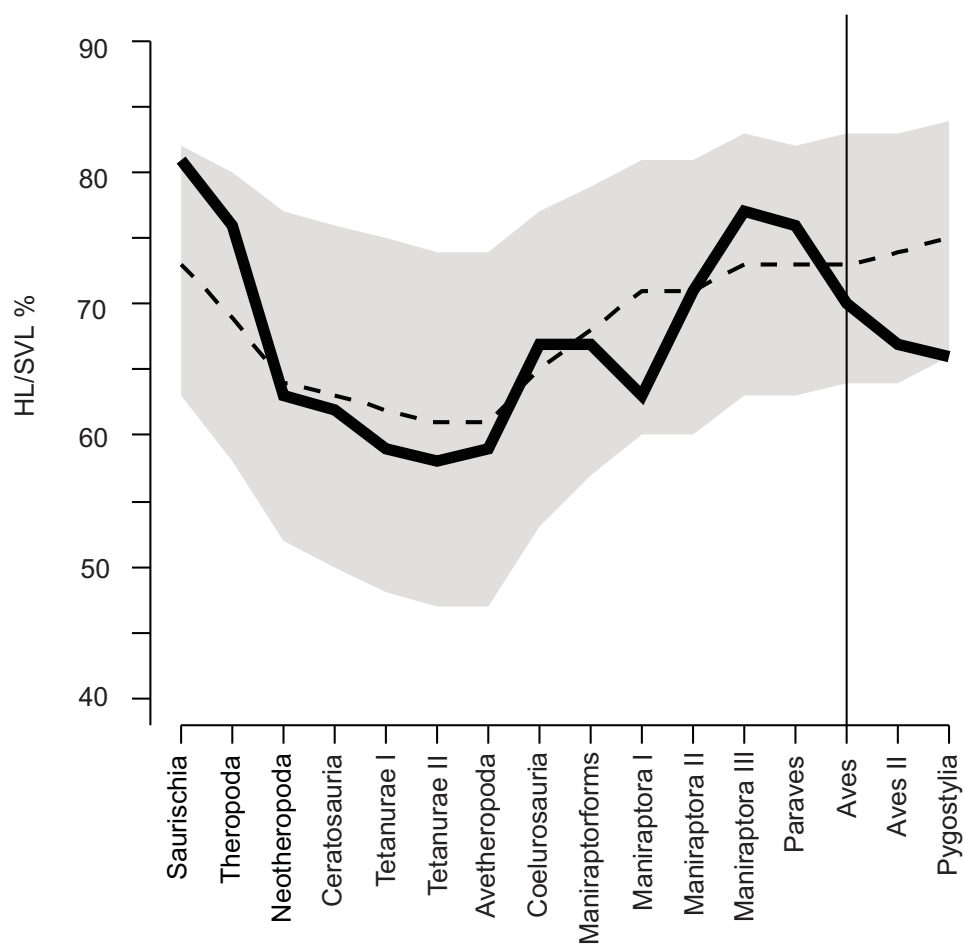
C



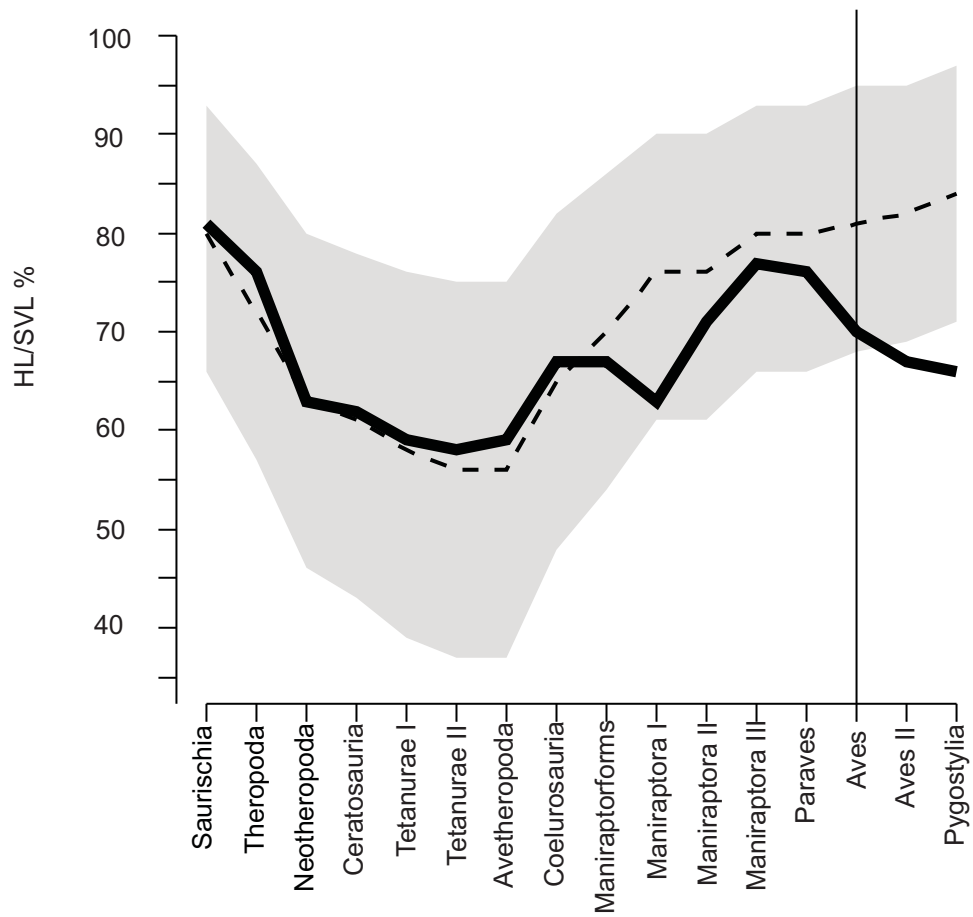
D



E

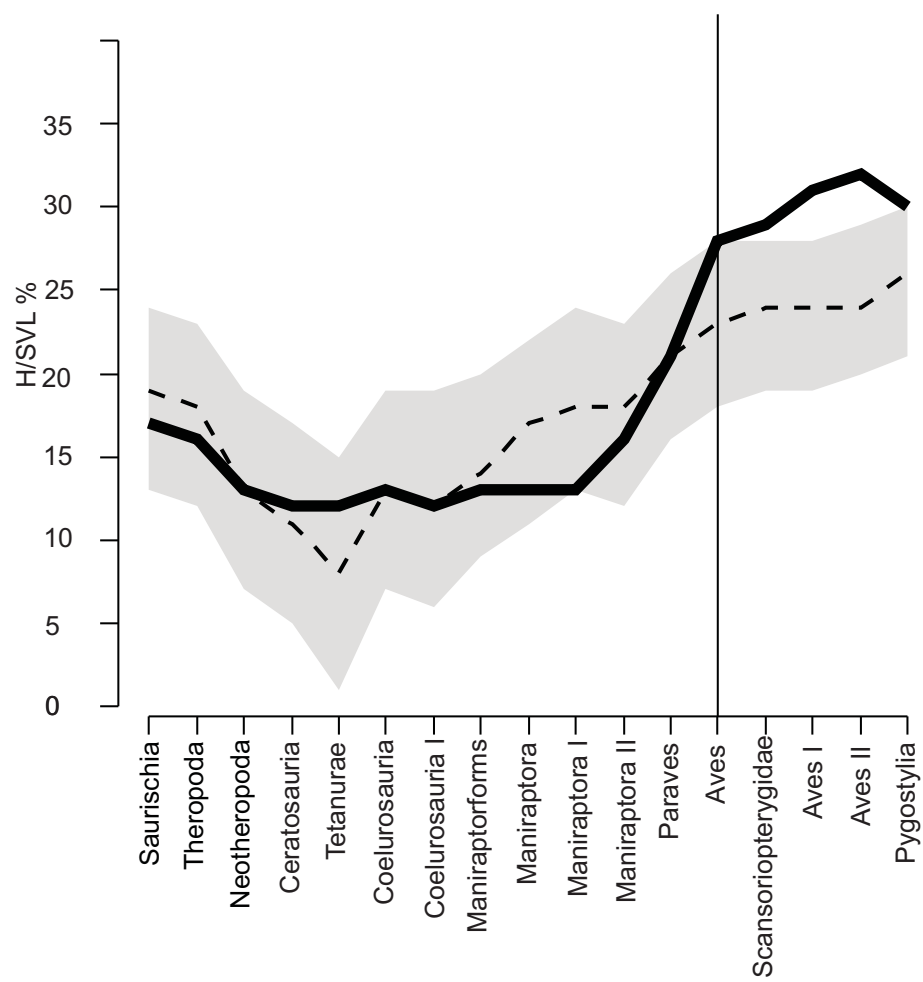


F

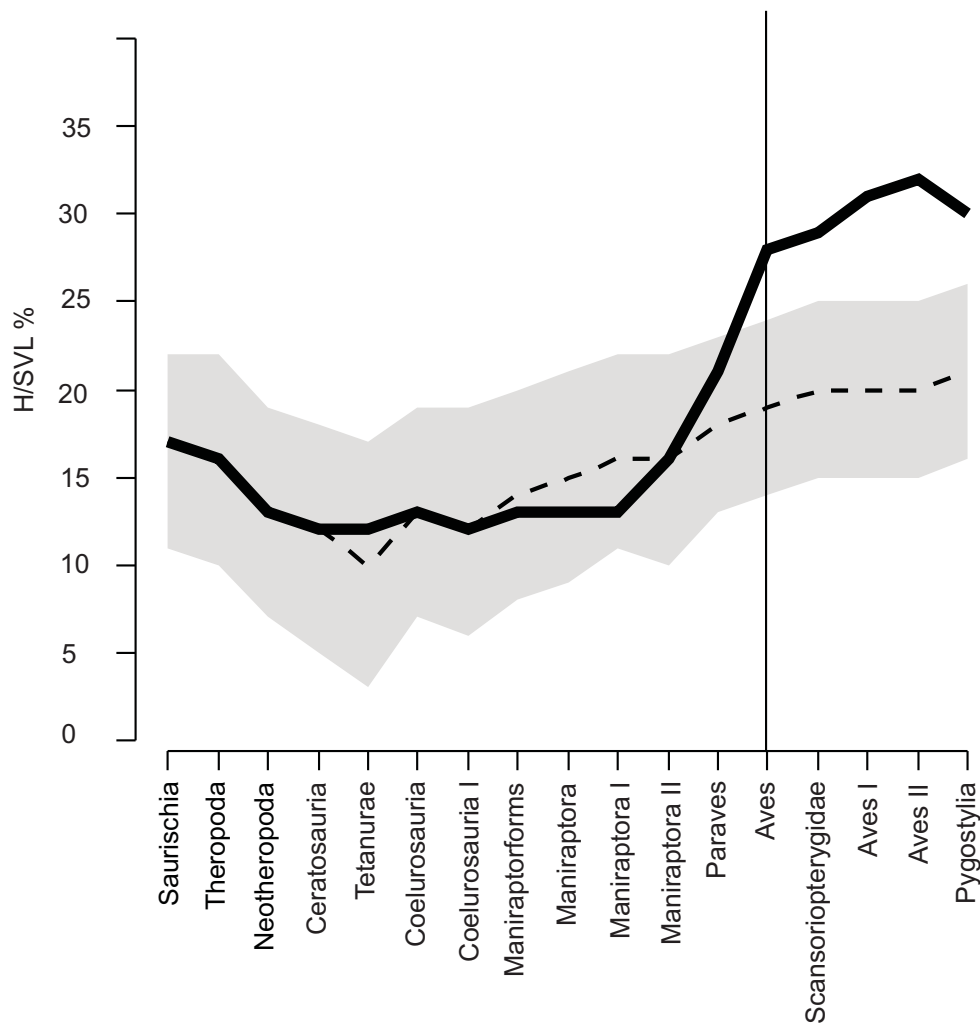


Supplementary Figure 5: Nodal reconstruction (Solid line) for relative H (A,B), FL (C,D) and HL(E, F) lengths using the Choiniere et al. 2010 topology with unequal branch length. Estimated expected lengths derived from linear regressions (broken lines) with corresponding error bounds (grey shaded region) using both the total specimens dataset (A, C, E) and adult theropod only dataset (B, D, F). Note the correspondence in lines in pre-Paravian taxa. The node Aves is denoted by a vertical line.

A

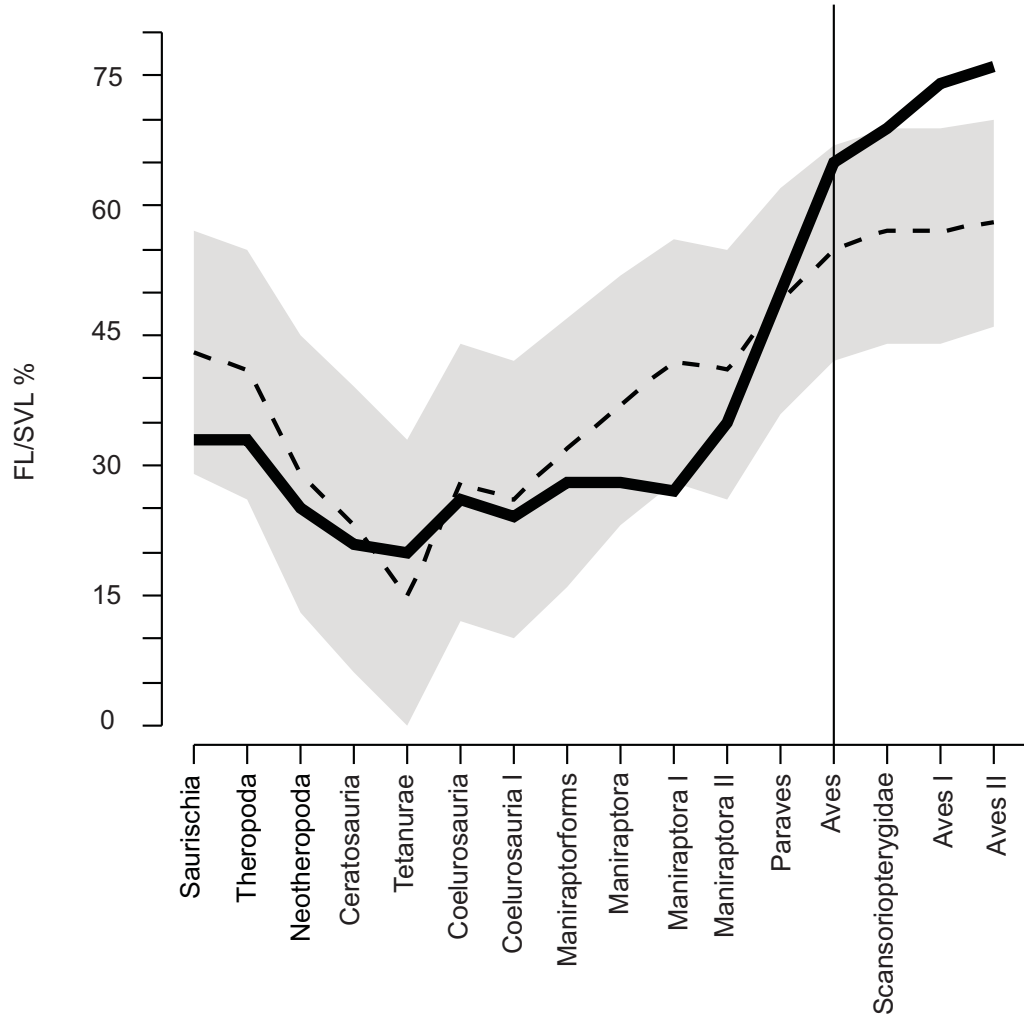


B

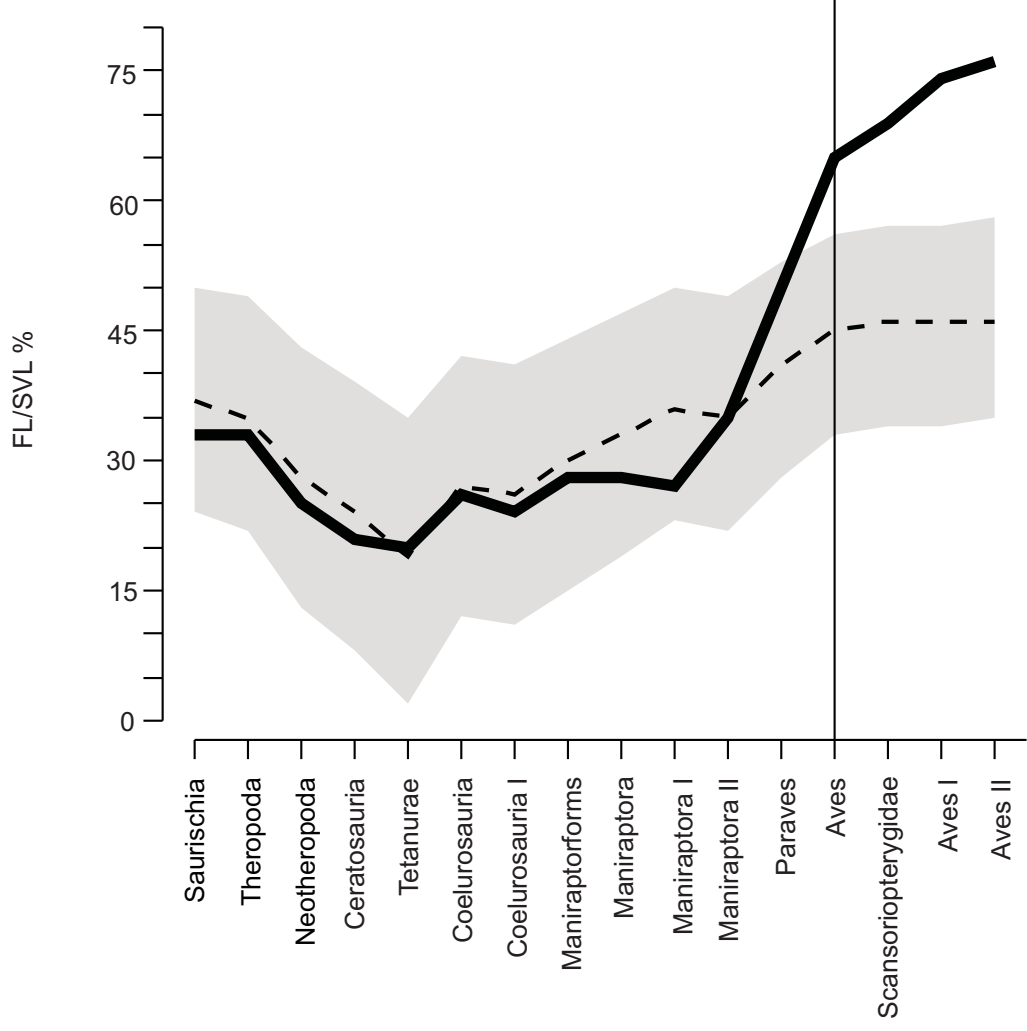




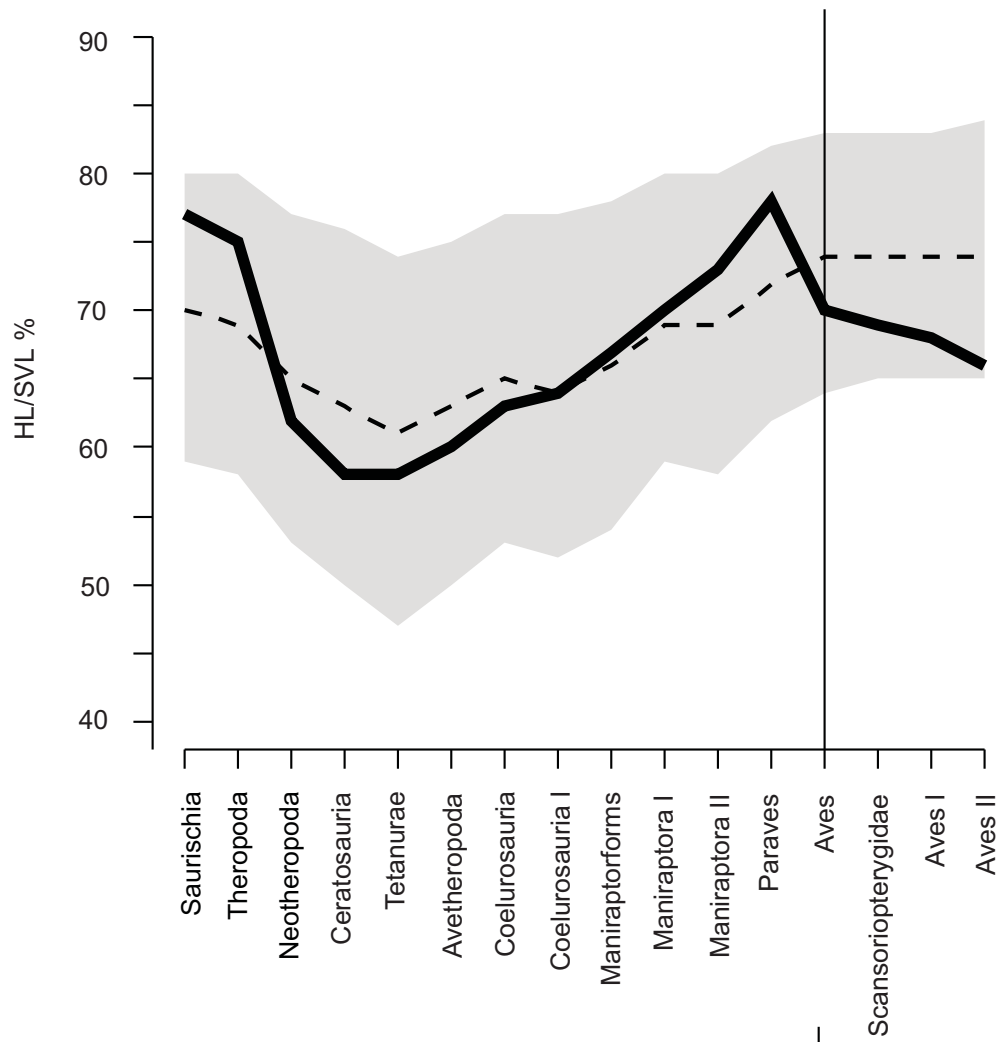
C



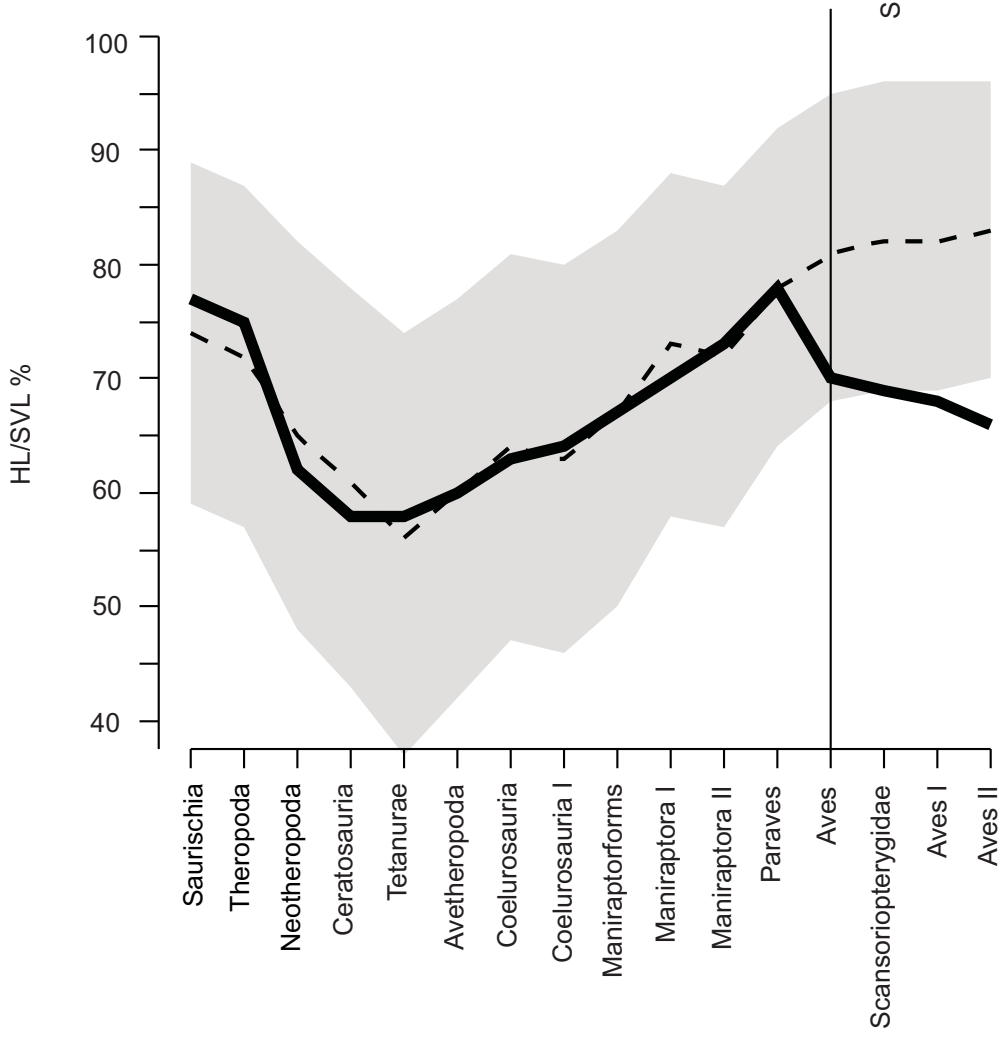
D



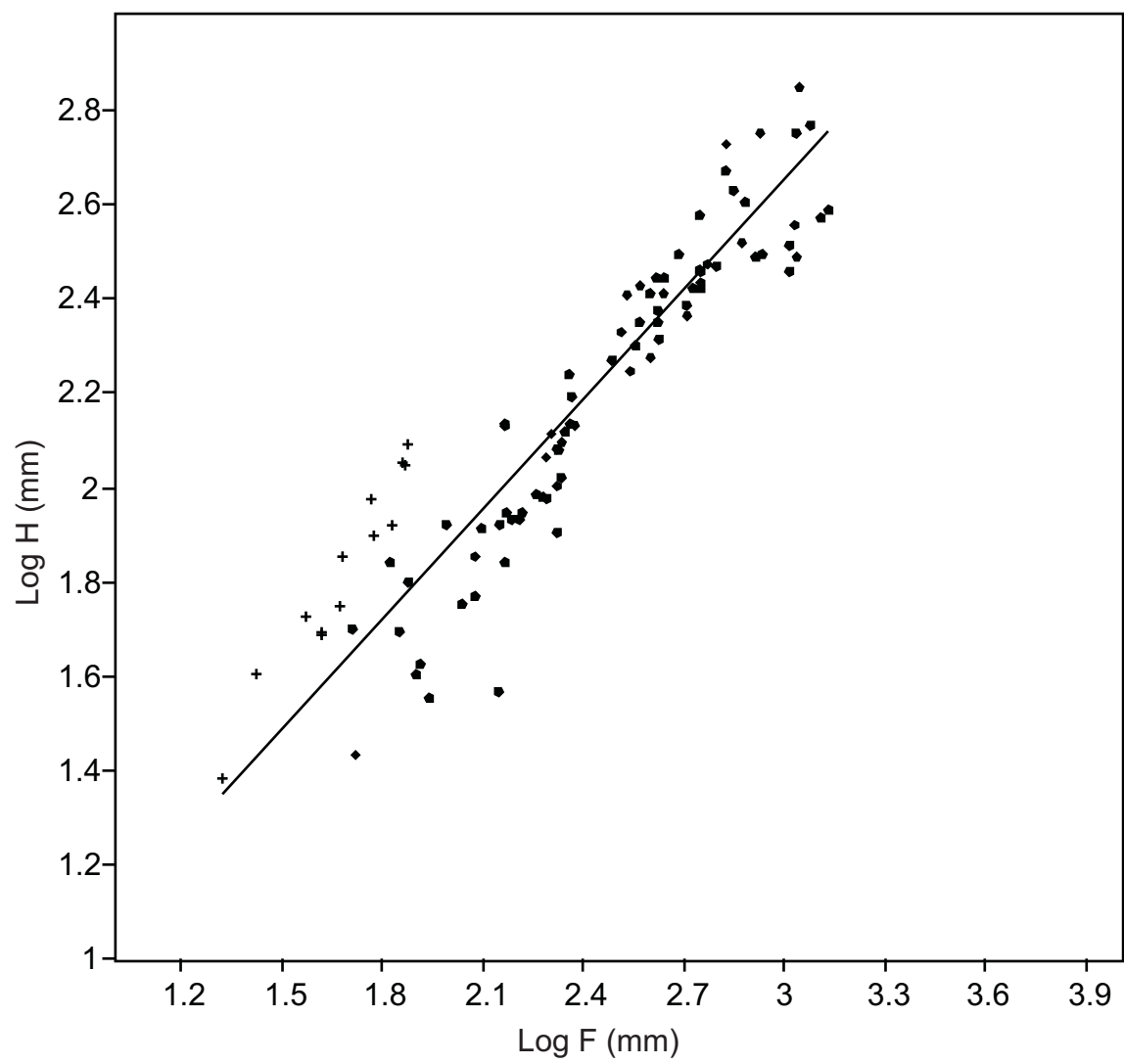
E



F

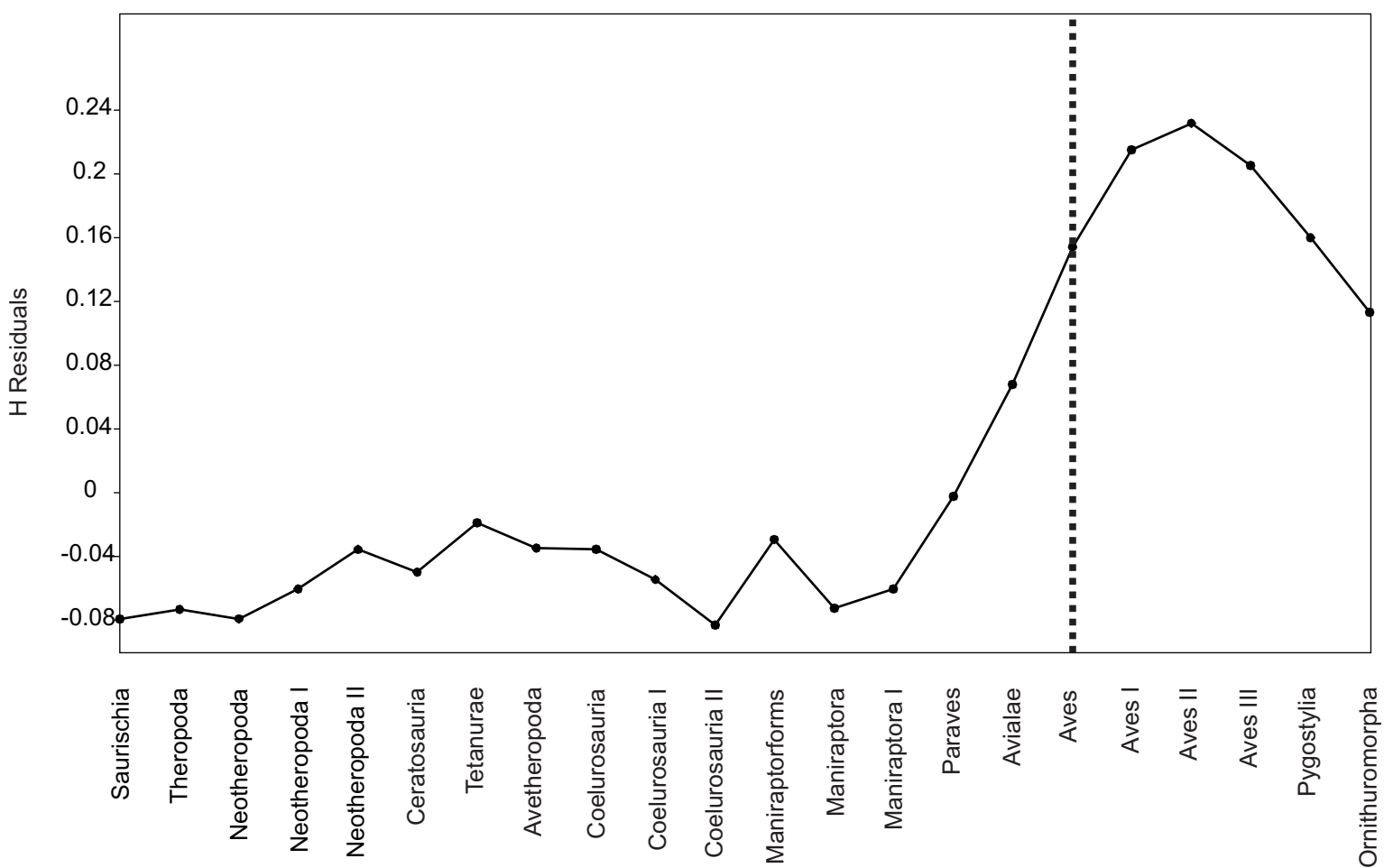


Supplementary Figure 6: Log-log RMA regression of humeral versus femoral for avian and non avian theropods in Table 6.

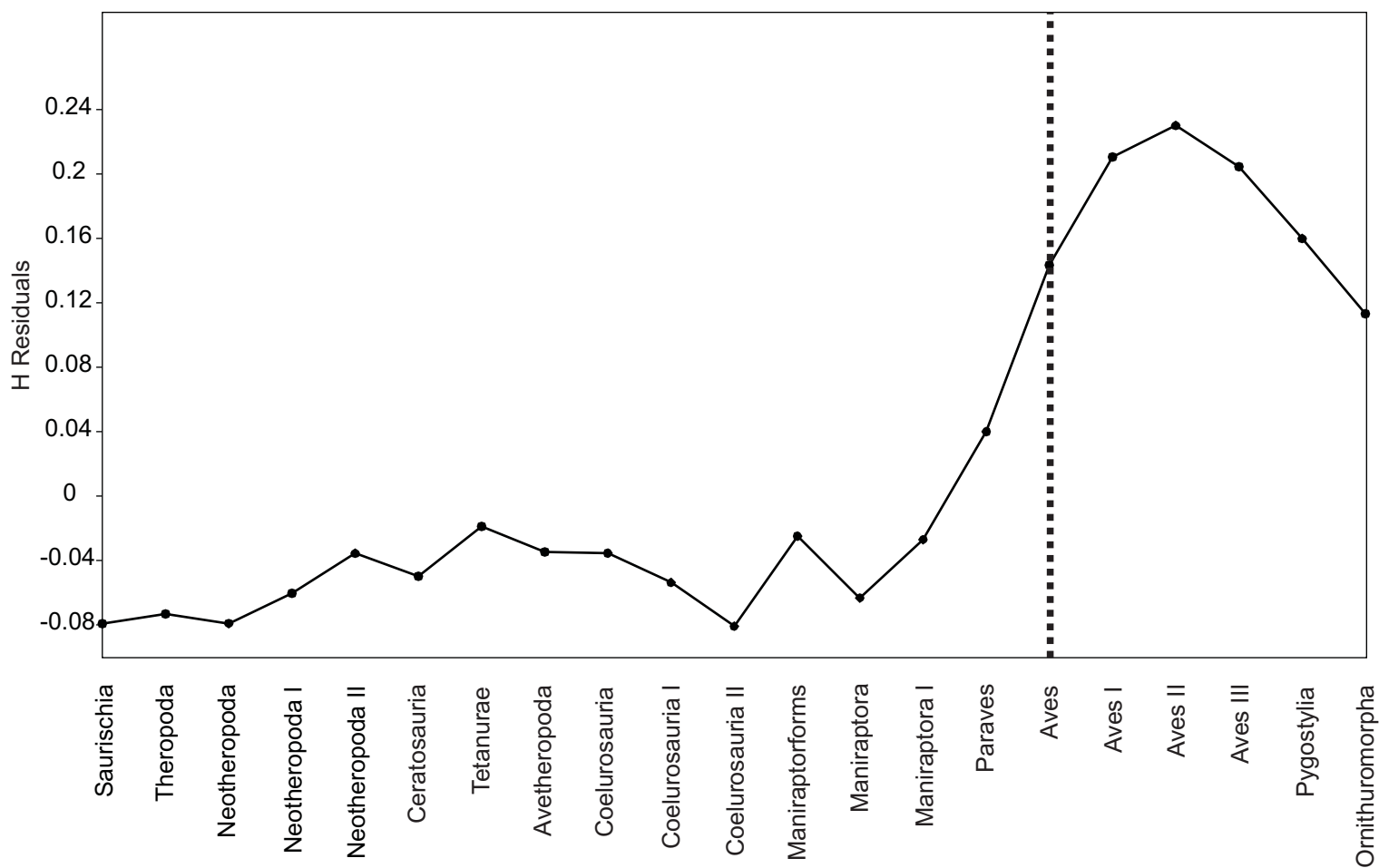


Supplementary Figure 7: Nodal reconstruction for humeral residuals from Figure 6 (See table 6). The node Aves denoted by vertical dashed line. A) Scansoriopterygidae as Avialae B) Scansoriopterygidae as Maniraptorans C) Scansoriopterygidae as Avialae and compsognathids as Maniraptorans.

A



B



C

