

Cmi_HoxA|FJ824598|1-286881



Cmi_HoxA|FJ824598|1-286881



Cmi_HoxA|FJ824598|1-286881





Cmi_HoxB|FJ824599.1|1-368325 HoxB VISTA alignment with C. milli baseline Cmi_HoxB|FJ824599.1|1-368325



Cmi_HoxB |FJ824599.1|1-368325







Cmi_HoxB|FJ824599.1|1-368325





HoxC VISTA alignment with C. milli baseline























Figure S3: VISTA analyses of ancient CNEs in *Pantodon* and other vertebrates. Five separate

mVISTA alignments using the *C. milli* hox clusters (HoxA, HoxB, HoxC, HoxD) as a baseline were built. Peak height corresponds to conservation level and coloured peaks correspond to conservation levels of >70% over 100bp. Peaks in blue correspond to coding sequence, while peaks in red correspond to noncoding sequence.



Figure S4: Ancient CNE conservation. Histograms showing the number of CNEs identified by multi VISTA alignment using *Callorhinchus milli* as the baseline sequence. The mLAGAN algorithm and a cutoff of 70% identity over 100bp was used. Columns corresponding to pre-TGD sarcopterygian Hox cluster CNE counts are represented in green, the post-TGD clupeocephalan 'a' cluster counts are in red, and the post-TGD clupeocephalan 'b' clusters are in blue. *Pantodon* Hox cluster CNE counts are coloured in gray. While extreme asymmetry in the retention of ancient CNEs between the post-TGD 'a' and 'b' clusters of other teleosts is evident, the hoxbx and hoxby clusters of *Pantodon* retain nearly equal numbers of ancient CNEs (B).