Palaeogene can thus not be interpreted with confidence as a "residuum of the primitive torsion between humeral head and elbow condyle"8.

Rougier et al. remark that we excluded other relevant fossil taxa from our analysis, such as Gobiconodon<sup>6</sup> and Henkelotherium<sup>5</sup>. Regarding the former, our initial study<sup>16</sup> showed that inclusion of its fragmentary pectoral girdle in the analysis has no effect on our results. Regarding the latter, which was published after our initial analysis, only a single, partial, crushed pectoral girdle is available. Finally, the small fossa on the distal end of the scapular blade in tritylodonts (absent in known multituberculates) may be homologous with some part of the broad crescentic fossa of therians, as Rougier et al. suggest. The presence of this distal fossa is, nevertheless, highly variable among therian outgroups (present in distant forms such as Cynognathus<sup>17</sup>, but absent in forms undeniably closer to mammals such as Probainognathus and Probelesodon<sup>18</sup>). In our comparative figure, we failed to note that the distal end of the scapular blade of Morganucodon is based on a complete scapula of a close relative, the tritheledontid Pachygenelus, which is remarkably similar to the former where these bones overlap.

We join Rougier et al. in encouraging future attempts to re-evaluate multituberculate relationships on a broader sampling of taxa and characters. Indeed, this is the only means available to test whether the structural changes we outlined in the pectoral girdle in multituberculates and therians actually constitute key evidence for their common ancestry.

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MENG AND WYSS REPLY - Rougier et al.'s underlying objection stems from a misperception that our paper<sup>2</sup> and its comments concerning the placement of multituberculates was intended as an

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exhaustive phylogenetic analysis of the major groups of mammals. The aim of our presentation of new anatomical information for the auditory apparatus in Lambdopsalis, in relation to several competing hypotheses of currently multituberculate relationships, was of necessarily limited scope. Attention was given to major taxa for which ear ossicles are currently known.

Moreover, their criticisms of 3 of the 16 anatomical features we presented are unsubstantiated and self-contradictory. First, the previously described fragmentary incus and malleus<sup>12</sup> are displaced (as noted in our Fig. 3 legend<sup>2</sup>). Thus, there is no basis for regarding the incus as having had a posterior position in Lambdopsalis. That the incus lies dorsal to the malleus (given the position of the fossa for the incuidal articulation) is no more in doubt than the possession of a brain by mammoths - a supposition that has "yet to be documented" directly.

Second, Rougier et al. assert that the horizontal ectotympanic shared by Lambdopsalis and monotremes is primitive for placentals (and therefore Mammalia) as well. This contradicts not only a recent analysis arguing against the homology of this feature in therians<sup>19</sup> and monotremes, but also their own polarity assessment of this feature<sup>3</sup>, in which an inclined ectotympanic was considered to characterize Theria ancestrally. Their assumption that orientation of the oval window predicts ectotympanic inclination has been contradicted repeatedly - not just by our specimen (V10777.3), in which the oval window inclines more than 30°, but also in other studies (for example, a ventromedially facing oval window in Lambdopsalis<sup>20</sup>, a vertical ectotympanic coexisting with an inclined oval window in Morganucodon<sup>4</sup>, and a horizontal ectotympanic occurring with an anteroventrolateral oval window in Scutisorex (AMNH 48474)).

Third, the statement that the pterygoid is a broken piece (V10777.1) is incorrect. widely appreciated problematic The homology of the monotreme-multituberculate 'pterygoid' bone was signified in our paper by its placement in inverted commas in the figure legend. The claim that the monotreme 'pterygoid' is neo-

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morphic is supported neither by phylo-genetic studies<sup>3,4</sup> nor by ontogenetic studies of the platypus skull<sup>21,22</sup>. Even if one assumes this structure to be a neomorph in monotremes, this alone would not rule out its homology in multituberculates.

Finally, we would be the last to question the desirability of bringing to bear all available data in evaluating this, or any, phylogenetic question.

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## Taxonomy of the **Iberian** lynx

SIR - The Iberian lynx, Lynx pardinus, is considered the most vulnerable cat in the world, yet its taxonomic status and relationship to other lynx species are controversial<sup>1,2</sup>. Given that the Iberian lynx is listed as endangered and its populations are highly fragmented<sup>3</sup>, an understanding of its relationship to other taxa of Lvnx is important for the development of an effective conservation plan. Here we report the first detailed molecular phylogenetic assessment of Lvnx relationships. Our data suggest that the Iberian lynx is a distinct species relative to its European and North American counterparts.

The complete mitochondrial control region (D-loop) was sequenced for the Iberian lynx, Eurasian lynx (Lynx lynx), Canadian lynx (Lynx canadensis), bobcat (Lynx rufus) and related felid species (caracal, serval, jaguarundi and ocelot). Phylogenetic analyses of the D-loop performed using both maximum parsimony



Phylogeny derived using a maximum-parsimony analysis (branch and bound option) of aligned sequences. The single most parsimonious tree had a length of 410, a consistency index of 0.670 and a retention index of 0.791. Bootstrap values (1,000 replicates) are shown along branches, with the number of extra tree lengths needed to collapse a node separated by a slash. All specimens are unrelated individuals. The Iberian lynxes are from two different populations in Spain. Specific details of primers and experimental procedures are available from the authors on request.