



Fig. S1. Normalized residue conservation scores for full-length cytochrome *b* sequences from 632 mammalian species (Castresana 2001). Sequences were aligned using Clustal X (Thompson et al. 1994). Higher scores (grey bars) are indicative of a higher degree of conservation. Locations of the substitutions occurring at the stem of the *P. maniculatus* species complex (indicated by large arrows) and within *P. maniculatus* (indicated by smaller arrows) are among the most variable sites in the alignment of mammalian *cytb* sequences.

References

- Castresana J (2001). Cytochrome *b* phylogeny and the taxonomy of great apes and mammals. *Mol Biol Evol* 18: 465–471.
- Thompson JD, Higgins DG, Gibson TJ (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignments through sequence weighting, position specific gap penalties and weight matrix choice. *Nucl Acids Res* 22: 4673–4680.