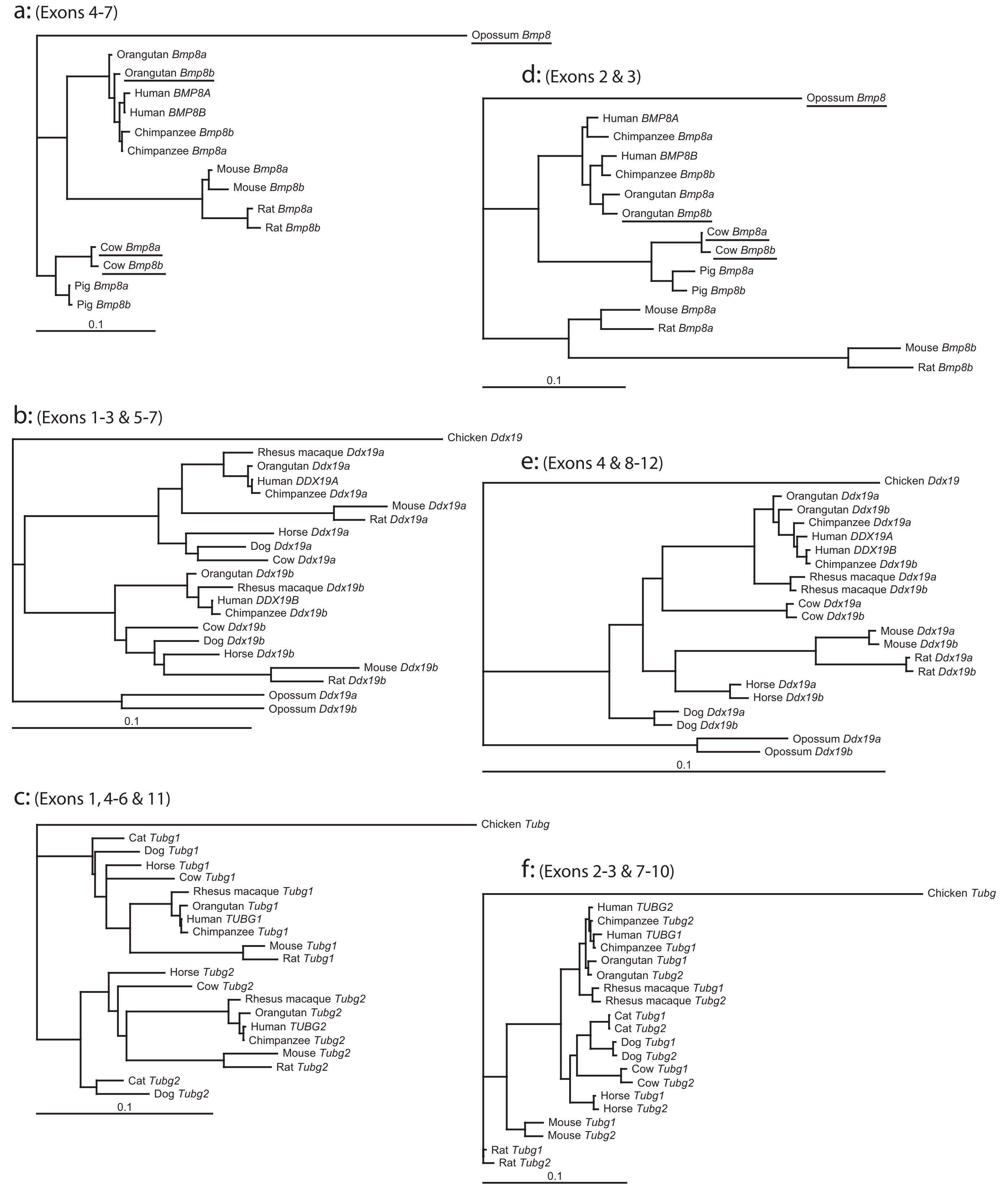

**Additional file 5: Maximum likelihood trees showing mosaic evolution within gene pairs**

Maximum likelihood trees of gene pairs a) and d) *BMP8A/B*, b) and e) *DDX19A/B* and c) and f) *TUBG1/2* were created in PAUP using the likelihood settings from the best-fit model selected by hLRT in MODELTEST (parameters available upon request). Exons were divided into two categories and phylogenetic trees, showing a), b) and c) divergent evolution or d), e) and f) concerted evolution, are illustrated. Like the neighbor-joining trees, opossum *Bmp8*, chicken *Ddx19* and chicken *Tubg* were used as outgroups to root the trees. A distance scale is shown below each tree. Underlined species in a) and d) are missing exon 1, preventing the use of this exon in the phylogenetic analysis.