

Extended Data Figure 4: Phylogenetic analysis of stratum one and stratum two genes.

Consensus phylogenies reconstructed by DNAML with 100 bootstrap replicates; scale bars represent the expected number of nucleotide substitutions per site along each branch. Phylogenies for ancestral X–Y pair genes from the X-conserved region, shared between placental and marsupial mammals are shown. Adjacent to each tree, pink and light blue bars highlight the positions of the X and Y homologues, respectively; red and dark blue bars highlight the position of placental and marsupial homologues, respectively. Among the three gene pairs from stratum one (*SOX3/SRY*, *RBMX/RBMY*, and *HSFX/HSFY*), Y-linked genes are more closely related to each other than their X-linked orthologues. Among the other gene pairs (*KDM5C/KDM5D* and *UBE1X/UBE1Y*), marsupial X–Y pairs are more closely related to each other than they are to placental orthologues, suggesting that a second stratum formed independently in the placental and marsupial lineages. Species abbreviations: HAS, human; PTR, chimpanzee; MAQ, rhesus; CJA, marmoset; MUS, mouse; RNO, rat; BTA, bull; MDO, opossum; and GGA, chicken.