Extended Data Figure 5: Phylogenetic tree showing X–Y gene conversion in AMELX/AMELY and ZFX/ZFY.

Consensus phylogenies reconstructed by DNAML with 100 bootstrap replicates; scale bars represent the expected number of nucleotide substitutions per site along each branch. Phylogenies of three ancestral X–Y pair genes from the placental-specific X-added region within stratum 2/3 (*USP9X/USP9Y*, *AMELX/AMELY* and *ZFX/ZFY*) are shown. Within each tree, pink and light blue branches highlight the positions of the X and Y homologues, respectively. *USP9X/USP9Y* is a typical stratum 2/3 gene pair; all *USP9Y* genes are more closely related to each other than to any *USP9X* gene. *AMELX/AMELY* and *ZFX/ZFY* show more complex histories. For example, bull *AMELY* is more closely related to bull *AMELX* than to any other *AMELY* orthologue. X–Y gene conversion occurred after stratum formation in multiple lineages. Species abreviations: HAS, human; PTR, chimpanzee; MAQ, rhesus; CJA, marmoset; MUS, mouse; RNO, rat; BTA, bull; MDO, opossum; GGA, chicken; and XTR, *Xenopus tropicalis*.