



Fig. S1. Phylogenetic analysis of NR2E DBDs

A consensus tree generated from 500 bootstrap replicates and rooted to the *Homo sapiens* retinoic acid receptor gamma DBD outgroup sequence is shown. Further details are provided in Methods. Species abbreviations (used throughout): Ce (or no annotation): *Caenorhabditis elegans*, Cb: *Caenorhabditis briggsae*, Bm: *Brugia malayi*, Pp: *Pristionchus pacificus*, Dm: *Drosophila melanogaster*, Ag: *Anopheles gambiae*, Tc: *Tribolium castaneum*, Sk: *Saccoglossus kowalevskii*, Sp: *Strongylocentrotus purpuratus*, Dr: *Danio rerio*, Xl: *Xenopus laevis*, Mm: *Mus musculus*, Gg: *Gallus gallus*, Hs: *Homo sapiens*, Nv: *Nematostella vectensis*, Aa: *Aedes aegypti*. Tree is proportionally scaled, with the scale bar indicating sequence distance in units of substitutions. Single diamonds identify branchpoints that were supported by >50% of bootstrap replicates; double diamonds identify branchpoints that were supported by >95% of bootstrap replicates. Numbers in red above selected branches show Ka/Ks ratios for the DBD portion only of NRs.

Weber et al., 2012