



Supplemental Fig. 2. Phylogenetic tree of forkhead domains from 6 full sequenced genomes: *Homo sapiens* (Hs), *Xenopus laevis* (Xe), *Gallus gallus* (Ga), *Caenorhabditis elegans* (Ce), *Danio rerio* (Dr) and *Oryzias latipes* (Ol). The construction algorithm and annotations of the tree are same as Fig. 1 The tree was generated with MEGA 5.0 (Tamura et al., 2011) using a maximum likelihood algorithm with a Jones-Taylor-Thornton (JTT) model. Each subclass was represented by red rectangle.