



Figure S1. Mutations identified by the TILLING method in the zebrafish Nrf2 protein. The amino acid sequence alignment of vertebrate Nrf2 proteins corresponding to the exon 5 region of zebrafish Nrf2. Identical amino acids are highlighted in black. The arrowheads indicate mutated amino acids identified from the screening of the TILLING resulting. Neh1, Neh3, Neh5, and Neh6 domains, and the basic region are indicated by bars. The open circles indicate the positions of heptad repeats of leucine zippers. c, chicken; h, human; m, mouse; x, *X. tropicalis*; z, zebrafish.