



SUPPLEMENTAL FIGURE 3. Amino acid sequence alignment of the Neh2 domains of various Nrf1/Nrf2-related proteins. Perfectly conserved amino acids are highlighted in black. Red characters indicate lysine residues existing between the DLG and ETGE motifs. The short sequences above the alignment are the DLG and ETGE motifs in mouse Nrf2. Abbreviations are the same as in Fig. 1.