



**Figure S6** Alignment of ESS-2 homologs. The alignment was obtained by the ClustalW multiple-alignment program. Identical and similar residues are highlighted in black and gray, respectively. Deletion in *ok3569* mutant was confirmed by RT-PCR and is underlined in red. Two coiled-coil domains predicted by the MARCOIL program in *C. elegans* ESS-2 shaded in yellow (See Results). *C. elegans* ESS-2 b isoform has two additional residues, Phe and Ser, in the C-terminus compared to a isoform (shown as FS in red). The names of ESS-2 homologs and accession numbers in UniProt are the same as in Figure 5C.