



Figure S3 Alignment of PMK-3 orthologs and locations of *pmk-3(lf)* alleles identified as *rpm-1(lf)* suppressors. The alignment was obtained by the ClustalW multiple-alignment program. MAPK14/p38- α is shown as the PMK-3 ortholog in fly and vertebrates. The positions of nonsense (red) and missense (blue) mutations isolated as *rpm-1(lf)* suppressors in our study are shown above the sequences. Identical and similar residues are highlighted in black and gray, respectively. Kinase domain, based on UniProt, was shaded in yellow. The conserved ATP binding site is shown as a black arrowhead above the sequences. The conserved catalytic loop and activation segment are underlined in green. Species are Ce: *Caenorhabditis elegans*; Dm: *Drosophila melanogaster*; Dr: *Danio rerio*; Mm: *Mus musculus*. Accession numbers in UniProt are Ce PMK-3: O44514; Dm MAPK14: O61443; Dr MAPK14: Q9DGE2; Mm MAPK14: P47811; Ce PMK-1: Q17446; Ce PMK-2: Q8MX14; Ce KGB-1: O44408; Ce KGB-2: H2KZIO.