

Figure S1: Neighbor-joining phylogenetic tree of *P. pacificus* Skp1-related proteins.

Phylogenetic tree made from a protein alignment of all *P. pacificus* Skp1-related proteins identified via BLASTp search. Bootstrap values greater than 50 are displayed. Note: the branch leading to PPA33498, PPA39551, PPA10084, PPA10085 and PPA43759 was truncated (diagonal lines) to more easily display the entire phylogeny.

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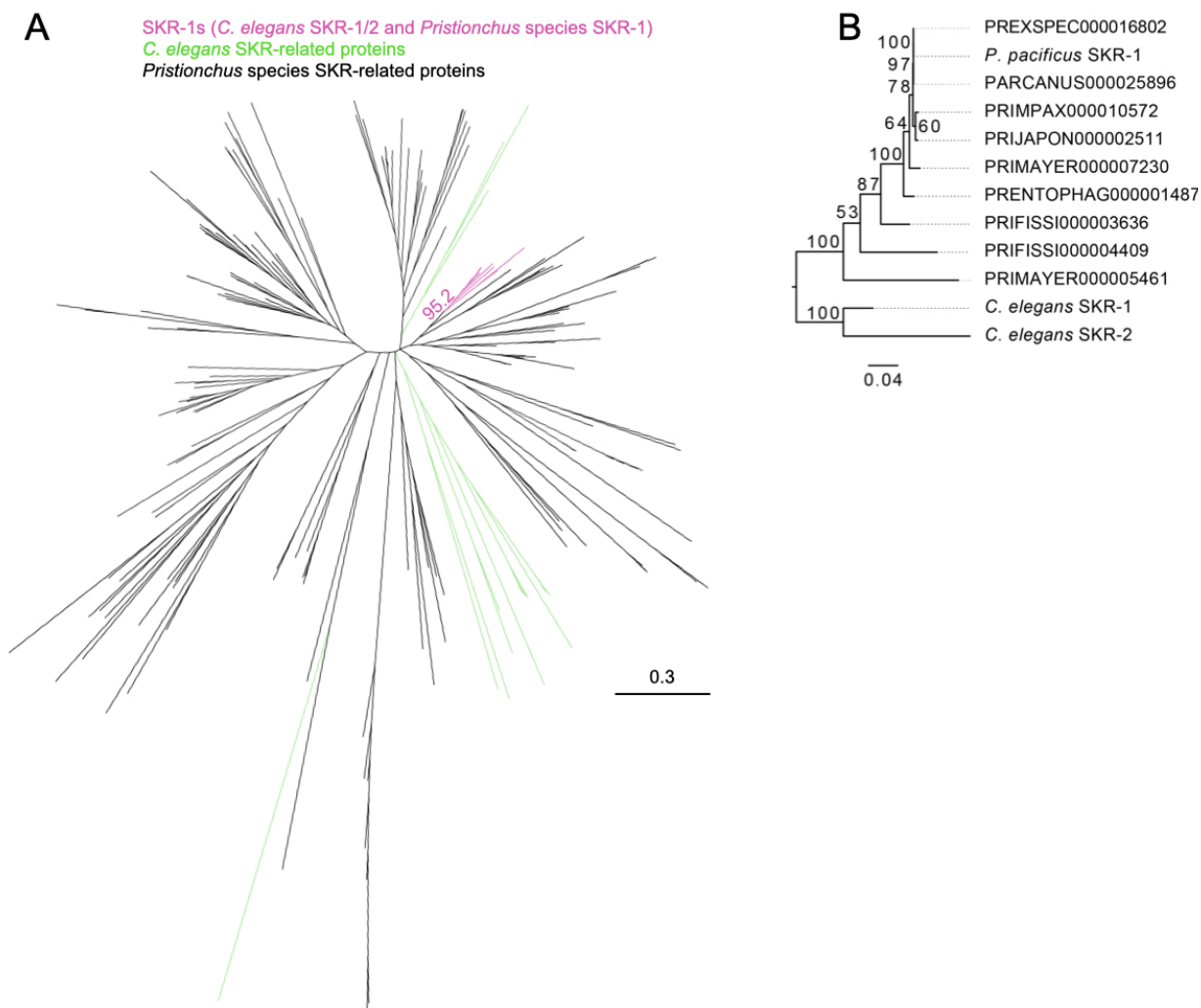


Figure S2: Neighbor-joining phylogenetic tree of *Pristionchus* Skp1-related proteins.

(A) Unrooted phylogenetic tree with 100x bootstrap support made from a protein alignment of all Skp1-related proteins from *C. elegans* and eight *Pristionchus* species. The clade containing *C. elegans* SKR-1/2 and *P. pacificus* SKR-1 has pink branches, all other *C. elegans* SKRs have green branches and all other *Pristionchus* Skp1-related proteins have black branches. The bootstrap support value for the SKR-1 clade is shown. (B) Phylogenetic tree with 100x bootstrap support made from an alignment of the proteins in the SKR-1 clade in (A, pink branches). The tree is rooted on the common ancestor of *Caenorhabditis* and *Pristionchus*.

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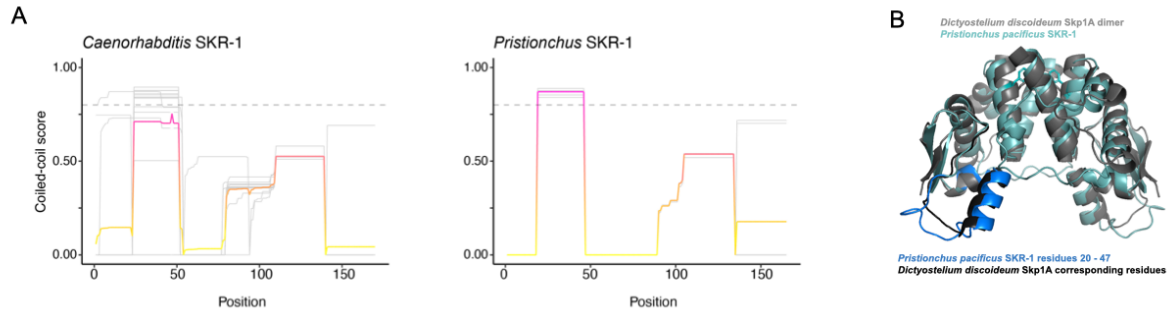


Figure S3: SKR-1 does not contain conserved coiled-coil domains. (A) Plot showing likelihood of coiled-coil domain at every residue in *Caenorhabditis* and *Pristionchus* SKR-1. Individual species are represented by grey lines and the average is shown in a pink to yellow gradient. Higher scores are more likely to be a coiled-coil domain with an arbitrary cut off for a coiled-coil shown in a grey dashed line at 0.8. (B) Structural alignment of *Dictyostelium* Skp1A dimer NMR structure (PDB structure 6V88, gray) and *P. pacificus* SKR-1 (teal) with *P. pacificus* residues 20 – 47 and corresponding residues in *Dictyostelium* labeled in blue and black, respectively.

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