

Fig. S2. The Cnidarian Pins/LGN/GPSM2 linker. Sequence alignment at the Pins/LGN/GPSM2 linker region in Cnidaria. Alignment is colored using ClustalX color scheme. Figure is adapted from Jalview 2 (Waterhouse et al., 2009).

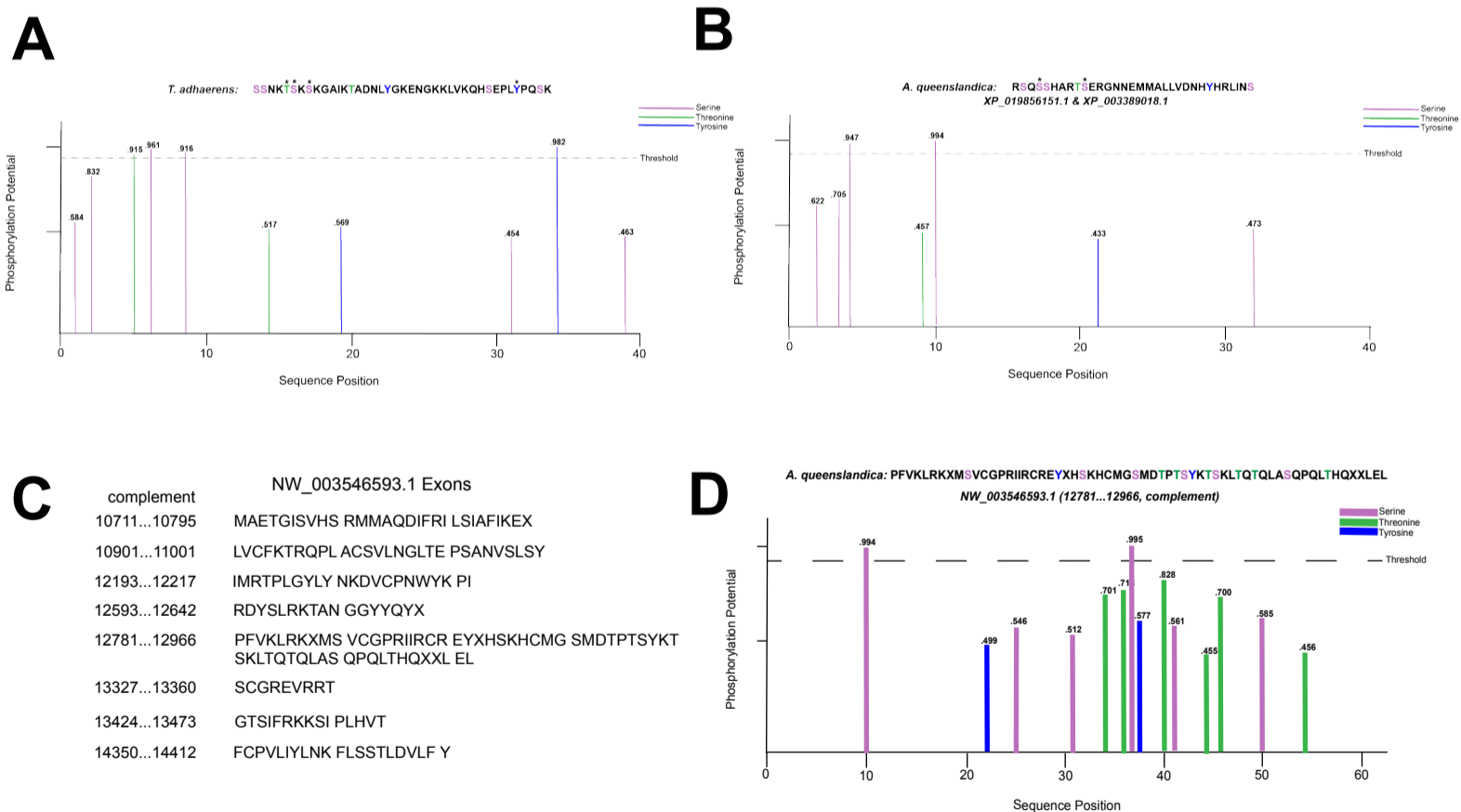


Fig. S3. Phosphorylation site predictions. Predicted phosphorylation potential of **A)** *T. adhaerens* (Placozoa) and **B)** *A. queenslandica* (Porifera) Pins/LGN/GPSM2 linker regions. Asterisks indicate the residues that are predicted to be a phosphorylation site with greater than 90% confidence. Graphs are adapted from NetPhos 3.1 (Blom et al., 1999). **C)** Reverse translated nucleotide sequences of eight regions with high exon character between NW_003546593.1 (14479...19908, complement) and NW_003546593.1 (9550...10710, complement). **D)** Of the eight potential exons identified, only one had predicted phosphorylation sites.