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Supplemental Information

Tropomodulins and Leiomodins: Actin Pointed End Caps and Nucleators in Muscles

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SUPPLEMENTARY FIGURE S1: Alignment of a representative group of Tmod and Lmod sequences

Table showing sequence alignment of Tmod and Lmod sequences. The table consists of multiple columns representing different sequences and rows representing specific residues. Key domains are highlighted with colored boxes: TMS2 (green), DBS (yellow), ABS2 (red), PRD (blue), and WH2 domain (orange). The sequences are grouped into Tmod and Lmod categories, with various subtypes indicated by accession numbers and species names.

FIGURE S1: Alignment of a representative group of Tmod and Lmod sequences. The alignment includes 24 Tmod and 21 Lmod sequences from different species and isoforms. The name of each sequence reflects the specific isoform, organism, and UniProt accession code (in parenthesis). The background is colored according to amino acid conservation (decreasing from dark blue to white), calculated separately for the Tmod and Lmod subfamilies. Boxed regions include: TM-binding sites 1 and 2 (TMBS1 and TMBS2, light green), actin-binding sites 1 and 2 (ABS1 and ABS2, magenta), proline-rich domain (PRD, cyan) and the WASP-Homology 2 domain (WH2, red). The region of Tmod that interacts with the DNase I-binding loop (D-loop) of actin, called here the D-loop-binding site (DBS), is contoured orange. Note that Lmods lack TMBS2, DBS and most of ABS1, whereas Tmods lack the PDR- and WH2-containing C-terminal extension.