

Supplemental Material to:

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**Discovery of new Longin and Roadblock domains that
form platforms for small GTPases in Ragulator
and TRAPP-II**

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Figure S1. Predicted structure of NPRL proteins. Alignment of secondary structural elements and domains of human NPRL2 and NPRL3, with sheets and helices coloured blue and red. Arrows join segments aligned by HHpred. The whole carboxy-termini contain parts of winged helix-turn-helix repeats (yellow boxes): four in NPRL3, three in NPRL2. By excluding two unstructured loops (asterisks), the N-terminus of NPRL3 can be seen to contain all the elements of an LD (boxed in green), although previously it was previously found to contain only 2 helices and 2 sheets.³²

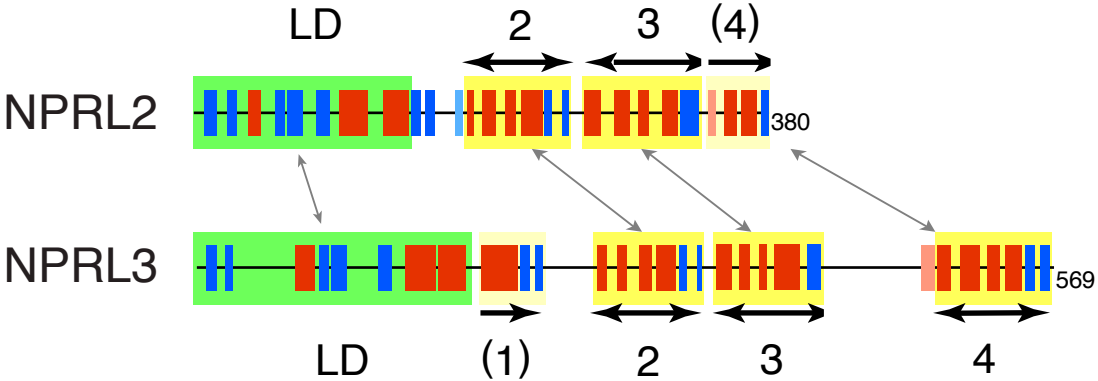


Figure S2. Variation of LD-like features at the N-termini of other long TRAPP subunits. **A.** The N-termini of TRAPPC10 from three model organisms (Fly – *D. melanogaster*, nematode – *C. elegans*, yeast – *S. cerevisiae*) and human were all aligned with NPRL2, as in Fig. 4A. E-values indicate the statistical significance of sequence alignments to NPRL2 across the number of matched columns (in brackets). **B.** Predicted structural elements from the N-termini of human TRAPPC10, TRAPPC9 and TRAPPC8. Compared to TRAPPC10, TRAPPC9 is missing β 1 and has two β sheets inserted between α 2 and α 3. In TRAPPC8 β 1 is replaced by a helix, and α 1 is extended.

