**Table S1.** Table of all Rab7s and RILP genes examined in this study. Includes gene identifiers (GSPAT and TET IDs in the case of *P. tetraurelia*) and our gene names.

**Figure S1.** Neighbor joining phylogeny showing evolutionary relationships between *P. aurelia* Rab7 coding sequences. *P. tetraurelia* Rab32 gene was designated as an outgroup.

**Figure S2.** The full alignment of all sequences used to make the phylogeny in Figure 1 and detailed in Table S1. Text files of all alignments suitable for analysis by phylogenetics programs are available upon request.

**Figure S3.** The full alignment of all sequences used to make the phylogeny in Figure S2 and detailed in Table S1. Text files of all alignments suitable for analysis by phylogenetics programs are available upon request.

**Figure S4.** Portions of the Rab7 and RILP alignments. A. The C-terminal hypervariable domain (HVD) of Rab7 coding sequences and amino acid alignment. Arrow denotes key amino acid with differential PTMs, as found in Wyroba *et al*. ([16](#_ENREF_16), 17) B. Alignment of the conserved region of the RILP protein sequences. Arrows denote the 17 highly conserved amino acids used in analysis for Table 1.

**Figure S5.** The alignment of RILP protein sequences used to analyze RILP amino acid sequence conservation.