Gokhale et al., http://www.jcb.org/cgi/content/full/jcb.200906168/DC1

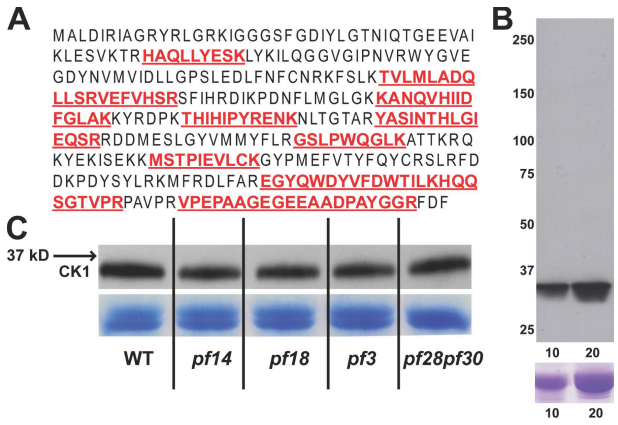

Figure S1. ***C. reinhardtii* CK1.** (A) CK1 amino acid sequence: 15 separate peptides (red and underlined) identified in the *C. reinhardtii* flagellar proteome span the entire sequence. (B) The CK1 antibody identifies a single 36.5-kD band in isolated axonemes (see also Fig. 2 A, left). The two lanes contain 10 and 20 µg of axonemal proteins, and the Coomassie stain below shows tubulin as a loading control. Positions of molecular mass standards are indicated in kD. (C) Axonemes from flagellar structural mutants contain CK1 at wild-type levels, indicating that CK1 assembly is not dependent on the radial spokes (*pf14*), central pair (*pf18*), DRC (*pf3*), I1 dynein, or outer dynein arms (*pf28pf30*). Thus, we conclude that CK1 is localized on the outer doublet microtubules. Coomassie staining of tubulin is shown as a loading control. Black lines delineate lanes of a single gel.

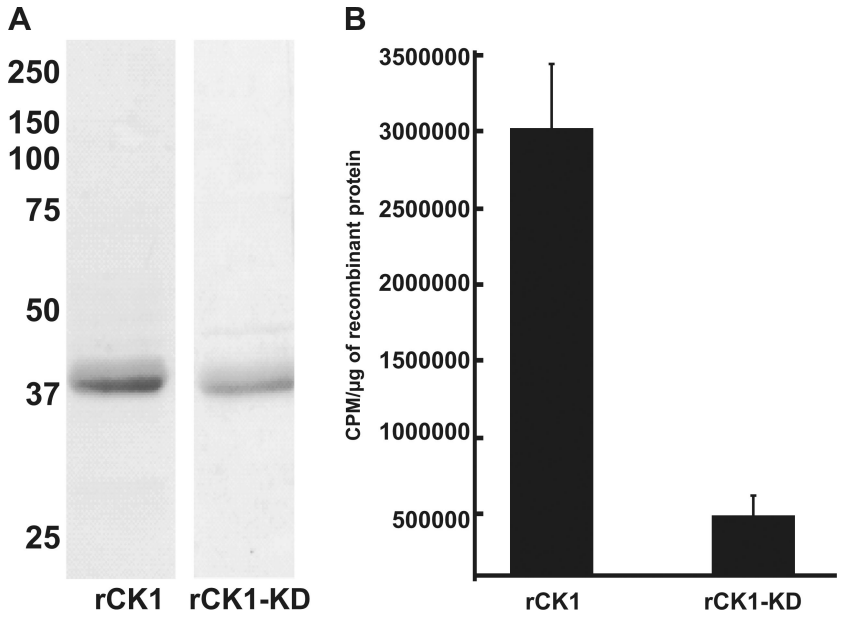

Figure S2. **rCK1 and rCK1-KD are soluble proteins that bind to CK1-depleted axonemes.** (A) Coomassie blue–stained gel of soluble, purified recombinant rCK1 and rCK1-KD. The difference in protein levels obtained with rCK1 and rCK1-KD reflects slightly different levels of induction: an equal amount of each fusion protein was used in each enzymatic and functional assay. Positions of molecular mass standards are indicated in kD. (B) In vitro kinase assays demonstrated that rCK1 and not rCK1-KD displayed kinase activity. The results are expressed as counts per minute per microgram of protein, and the graphs show the mean of four separate measurements and standard error bars.