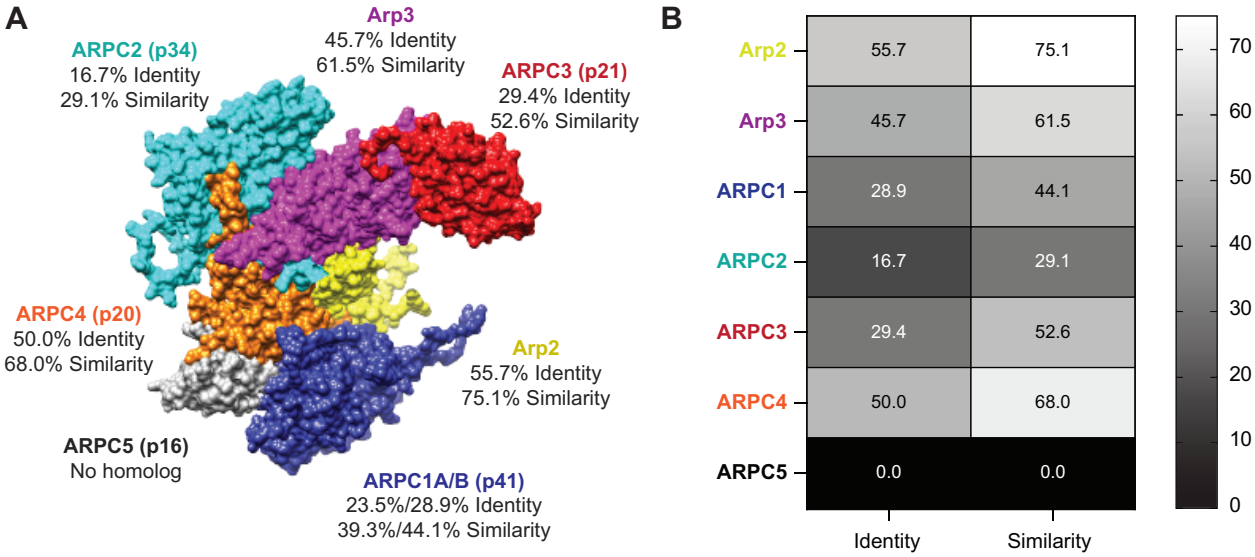
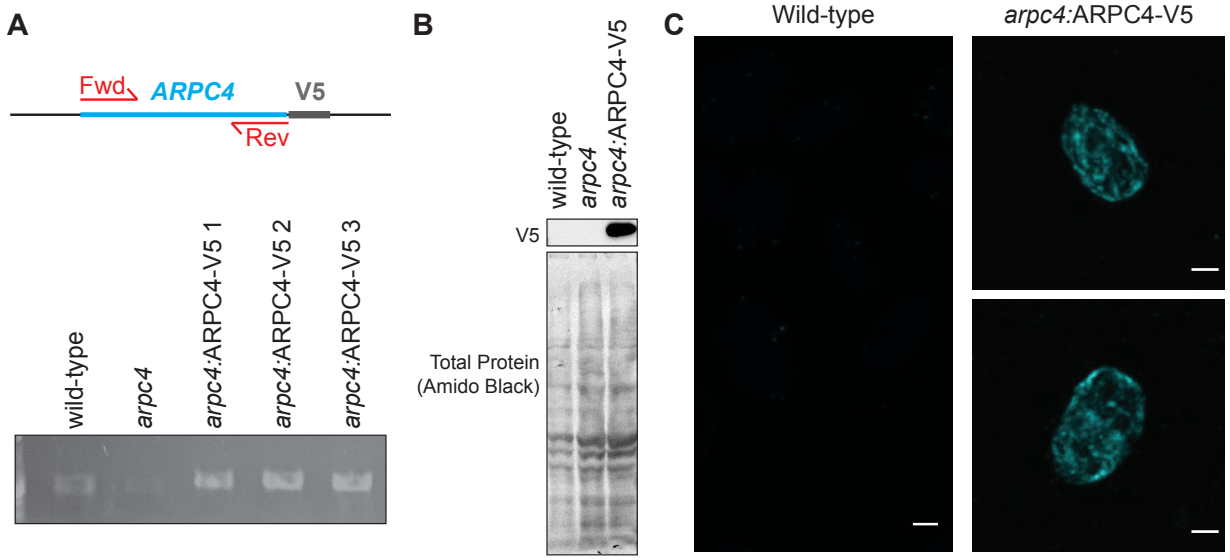
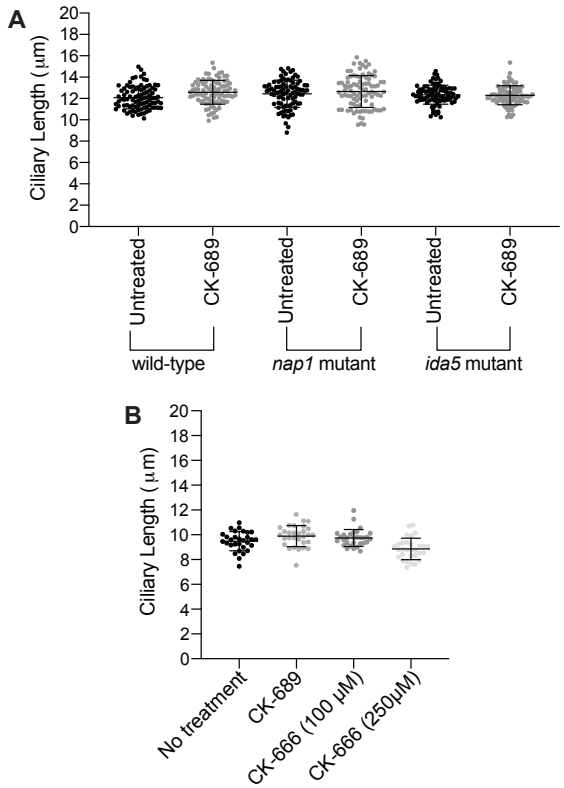
SUPPLEMENTAL MATERIAL:



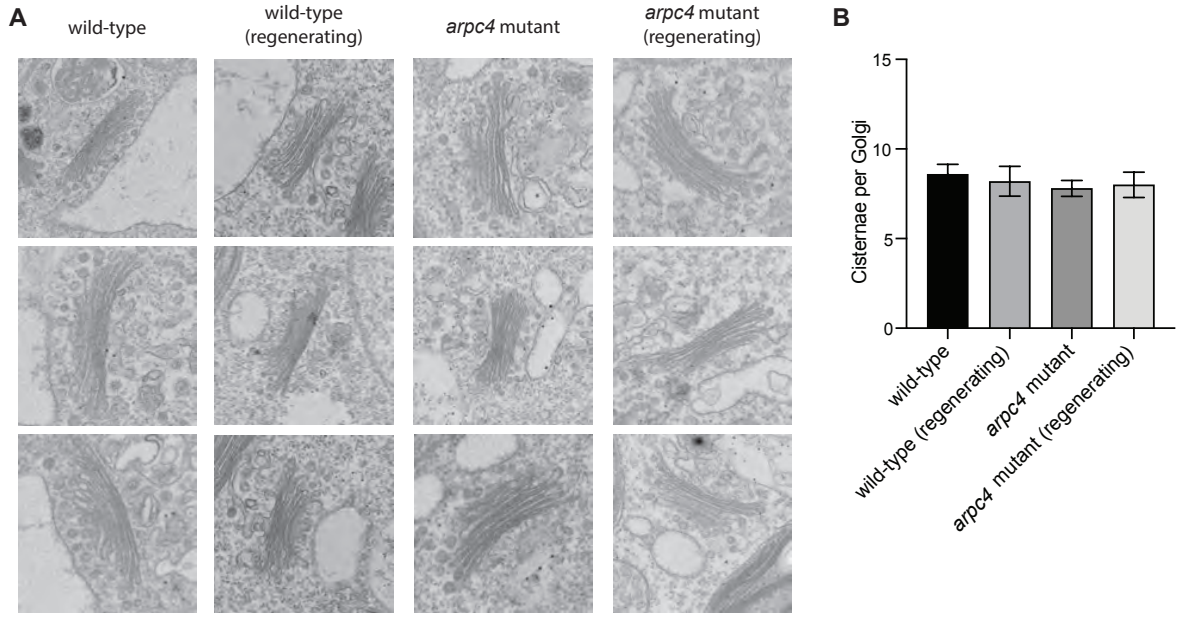
Supplemental Figure 1. Arp2/3 complex conservation in *Chlamydomonas*. A) Homology model of the *Chlamydomonas* Arp2/3 complex based on the bovine Arp2/3 complex (PDB:1K8K). Percent identity and similarity for the protein sequences of the Arp2/3 complex of *Chlamydomonas* compared to the bovine Arp2/3 complex. **B)** Heatmap of sequence identity and similarity of the Arp2/3 complex members of *Chlamydomonas* compared to those of the bovine complex. The ARPC1 isoform used for comparison was ARPC1B as it was more highly conserved to the *Chlamydomonas* ARPC1. Percentages were determined based on a MUSCLE alignment in Geneious.



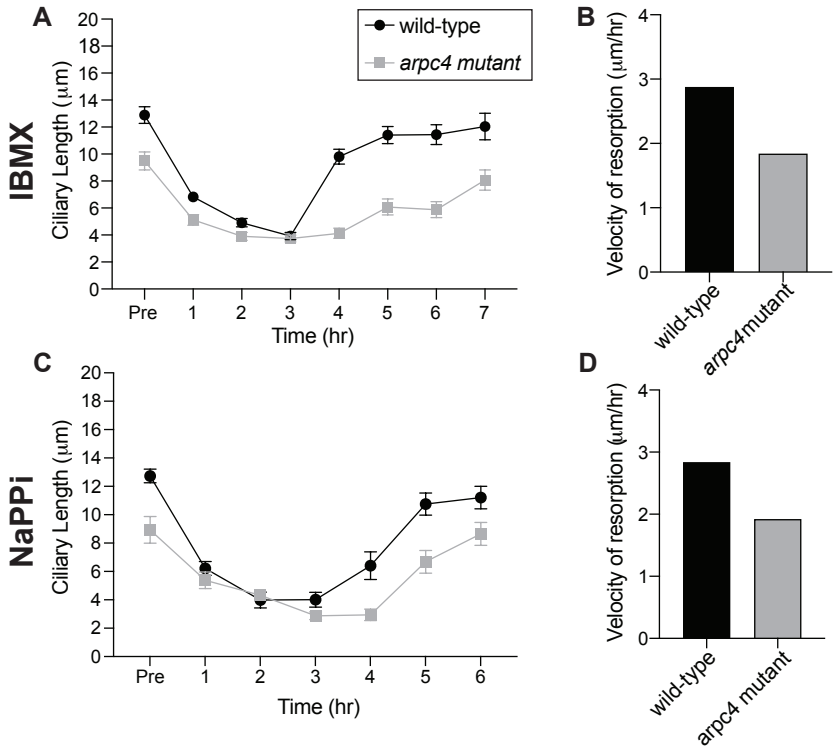
Supplemental Figure 2. Expression of *ARPC4-V5* rescues the *arpc4* mutant. A) PCR gel showing presences of the *ARPC4* gene in wild-type and rescue colonies, but not in the *arpc4* mutant. **B)** Western blot using V5 antibody (Thermo) showing protein expression of V5 in rescues containing *ARPC4-V5*. Total protein was probed using amido black. **C)** Immunofluorescence using the V5 antibody (Thermo). Wild-type cells show little to no signal, while cells expressing *ARPC4-V5* on the *arpc4* mutant background (colony 3) do show signal. Scale bar represents 2μm.



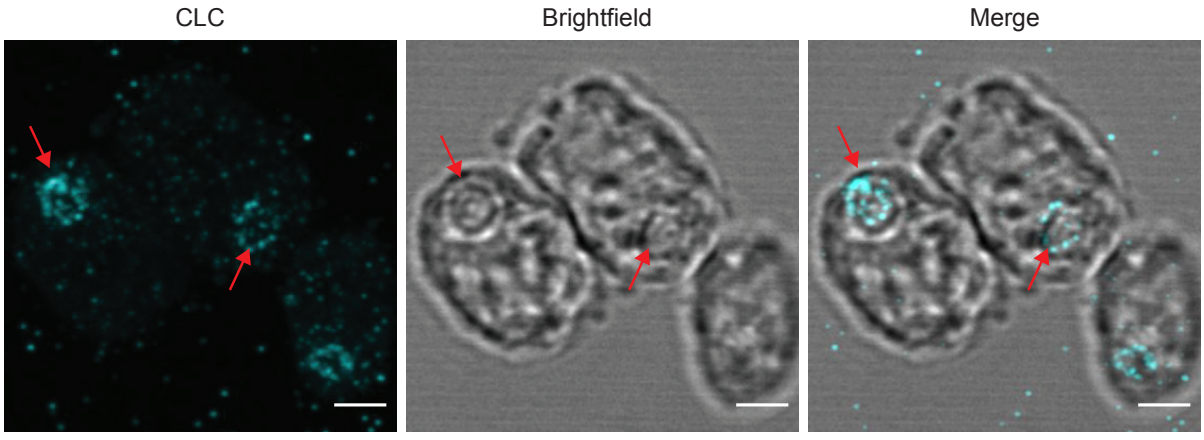
Supplemental Figure 3. Negative controls for the experiment in Figure 3. A) CK-689 (250μM) treated samples for panel 7C. **B)** *arpc4* mutant cells treated with CK-689 (250μM) or CK-666. No change in lengths confirms specify of CK-666.



Supplemental Figure 4. The Arp2/3 complex is not required for Golgi organization or synthesis of new protein. A) Transmission electron micrographs of Golgi found in wild-type or *arpc4* cells. **B)** Number of cisternae per Golgi for each condition. n=5. Error bars represent standard deviation.



Supplemental Figure 5. Resorption of cilia with NaPPi and IBMX is not increased in the *arpc4* mutant as it is with BFA. A) Cells were treated with 1mM IBMX and allowed to resorb their cilia. After 3 hours, IBMX was washed out and cells were allowed to regrow cilia. n=30**. B)** The velocity of IBMX resorption was determined by fitting a line to the first 4 points of the graph in A and determining the slope. **C)** Cells were treated with 20mM NaPPi and allowed to resorb their cilia. After 3 hours, NaPPi was washed out and cilia were allowed to regrow. n=30. **D)** The velocity of NaPPi resorption was determined by fitting a line to the first 4 points of the graph in A and determining the slope. The slightly slower velocities of resorption in the *arpc4* mutant may be due to the fact that these cells start with shorter cilia and therefore have less to resorb or it may be due to problems in endocytosis that is thought to be required for resorption of cilia (Saito et al. 2017).



Supplemental Figure 6. Clathrin light chain accumulation is around the pyrenoid. Cells were stained with a clathrin light chain antibody and imaged using airyscan imaging (left). Brightfiled image is shown in the center, and a merge is shown on the right. Red arrows point to clathrin accumulation and the pyrenoid.