**Supplemental Table 1:** List of primers used for cloning. Column 1: Primer designation. Column 2: Nucleotide sequence of each individual primer. Column 3: Indication of the presence or absence of a restriction site sequence engineered into the primer. See materials and methods section for additional details.

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| --- | --- | --- |
| Name | Sequence (5’ to 3’) | Restriction Site |
| AT7 | ATG GTG AGC AAG GGC GAG GAG CTG | N/A |
| AT95 | GGT TCT GGT TCT GGT TCT ATG GTG AGC AAG GGC GAG GAG CTG | N/A |
| AT109 | GAT AAT AAT GGT TTC TTA GAC GTG TCG ATC GAC TCT AGA GGA TCA GAA AAT TAT C | N/A |
| AT110 | GAA AAG TGC CAC CTG ACG TGC ATT ACT AAT AGA AAG GAT TAT TTC ACT TCT AAT TAC ACA AAT TCC G | N/A |
| AT139 | AGA ACC AGA ACC AGA ACC CTC CTT TAA CAT ATC AGC AAC GGA CAT TTC AAC | N/A |
| AT147 | GAC ATT CCT TTT ACC CGG G TTA CTT GTA CAG CTC GTC CAT GCC GAG | N/A |
| AT168 | GTC GCT TTG TTA AAT CAT ACC ACC ATG GCC GCC ACT CTC GTC TCT CCG CC | Xho1 |
| AT262 | GTT AAA TCA TAC CTC GAG GGA TCC ACC ATG AGG TCT AAG TCG ATG CGA TTG AGG | BamH1 |
| AT264 | GTT AAA TCA TAC CTC GAG GGA TCC ACC ATG GCC GCT CAG AAA TCT GAA TCT TCT | BamH1 |
| AT266 | GTT AAA TCA TAC CTC GAG GGA TCC ACC ATG GCG AGA ATT AAG GTG ATT GGT GTC GGT G | BamH1 |
| AT268 | GTT AAA TCA TAC CTC GAG GGA TCC ACC ATG GCG AGG ATT AAG GTT ATT GGT GTG GG | BamH1 |
| AT285 | CTC GCC CTT GCT CAC CAT CTG CAT GAA GCC TGT GGC GAT TAT CGT TAC ATG | N/A |
| AT287 | CTC GCC CTT GCT CAC CAT CTG CAT GAA ACC CGT AGC TAT CAG GGT TAT GC | N/A |
| AT297 | GAC ATT CCT TTT ACC CGG GGA TCC TTA CTT GTA CAG CTC GTC CAT GCC GAG | BamH1 |
| AT298 | CTC GCC CTT GCT CAC CAT CTG CAT GAA GAA AAG TCT ACG GGG AGA AGA | N/A |
| AT299 | CTC GCC CTT GCT CAC CAT CTG CAT GAC TCG GGG ATA ACG AGA GCT | N/A |
| AT310 | GTT AAA TCA TAC CTC GAG GGA TCC ACC ATG GTG AGC AAG GGC GAG GAG CTG | BamH1 |

**Supplemental Figure Legends**

**Supplemental Figure 1: Multiple Sequence alignment of FtsZ proteins.** Multiple protein alignment was performed using for FtsZ homologs from *Arabidopsis thaliana* (FtsZ1 - NP\_200339.1 and FtsZ2 - NP\_565839.1), *Ostreococcus tauri* (FtsZ1 - XP\_003080788.1 and FtsZ2 - XP\_003080256.1), *Cyanidioschyzon merolae* (FtsZ1 - BAC87808.1 and FtsZ2 - BAC87807.1), *Synechococcus elongatus PCC 7942* (FtsZ - AAC26227.1), *Escherichia coli* (FtsZ - YP\_851294.1), and *Bacillus subtilis* (FtsZ - AAA22457.1) using the MUSCLE algorithm within MEGA5 (Edgar, 2004a; Edgar, 2004b; Tamura, et al., 2011) and graphic generated using ESPript 3.0 with a %Equivalent and global score of 0.7 sequence similarity depiction parameter (Robert & Gouet, 2014). Alignment identified the highly conserved GTP-binding and hydrolysis domain (blue bar) and conserved C-terminal peptide among FtsZ2/FtsZA and bacterial FtsZs (grey box). The later is consistent with previous reports highlighting the absence of C-terminal peptides in FtsZ1’s of land plants and green algae (TerBush, et al., 2013). Illustrative of FtsZ divergence, *Galdieria sulphuraria* FtsZB lacks a large portion of the C-terminal region while FtsZA possesses the highly conserved C-terminal peptide. The C-terminal variable region (CTV) (Buske & Levin, 2012) is indicated by a magenta box.

**Supplemental Figure 2: Graph comparing fluorescence recovery of FtsZ2 alone and when coexpressed with ARC6.** Normalized average fluorescence recovery vs time for FtsZ2FL-eCFP alone (red circle) and in the presence of ARC6stromal-mVenus (green diamond). Data in each graph were normalized to the pre-bleach fluorescence intensity (1 on the y-axis) and the fluorescence intensity at the time of photobleaching (0 on the y-axis). Error bars indicate SEM at each time point.