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pdsACFL1(KX910691)          MKHLVFKKDLSDLKNSPLSSLFIGFTSLCETYSLKASEAESCGTDKLTFTLNTYLGKIIEDILKHGGDVLKFAGDALLALWKAEYGGNLDDLTLLINKAIICSIA
pdsACFL2(KY853034)          ------MPRVKHMVGVCMFADISGFTSLCETYSLKASEAESCGTDKLTFTLNTYLGKIIEDILKHGGDVLKFAGDALLALWKAEYGGNLDDLTLLINKAIICSIA
                                     :..: .  : : : *************************************************************************************************

pdsACFL1(KX910691)          IQEECDNYMTDVGVLLRVKIALSVGKMQITHVGVTESKHFDLSGSAVSDVNAAEKWAEPGSIILSLLAFSNCDQSLFLFETIDNGMYYRVAGARVEEESATVSTV
pdsACFL2(KY853034)          IQEECDNYMTDVGVLLRVKIALSVGKMQITHVGVTESKHFDLSGSAVSDVNAAEKWAEPGSIILSLLAFSNCDQSLFLFETIDNGMYYRVAGARVEEESATVSTV
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pdsACFL1(KX910691)          HPTGVQLALMSGVLSTGAVLTSTPSVAKRIFAPHVGTLLSRYYPQMKLPRIYRKKGQSEQKEQICKTTGNLLKSDSCHDPGHRTYIYSKLNDQDIEDLRAYVPKT
pdsACFL2(KY853034)          HPTGVQLALMSGVLSTGAVLTSTPSVAKRIFAPHVGTLLSRYYPQMKLPRIYRKKGQSEQKEQICKTTGNLLKSDSCHDPGHRTYIYSKLNDQDIEDLRAYVPKT
                            ************************************************************************************************************************

pdsACFL1(KX910691)          VLSRIDHGQDLEWLSEMRQVSVLFINMELPIKGNSHSWALQRAFEIHECARRLRGNLNKVFSFDKGCTFIVIFGLPGDKHDDDPTRALKAGHRIMDSLHQIMDIT
pdsACFL2(KY853034)          VLSRIDHGQDLEWLSEMRQVSVLFINMELPIKGNSHSWALQRAFEIHECARRLRGNLNKVFSFDKGCTFIVIFGLPGDKHDDDPTRALKAGHRIMDSLHQIMDIT
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pdsACFL1(KX910691)          TNESIGVTTGRAFCGVVGHRDRHEYTVIGRKVNMAARLMVNYPGTLSCDDDTYRSGKSKLKKEDFMVLPFIKLKGVADPGTVREYNNHHDREEEEEEEYDYPILGR
pdsACFL2(KY853034)          TNESIGVTTGRAFCGVVGHRDRHEYTVIGRKVNMAARLMVNYPGTLSCDDDTYRSGKSKLKKEDFMVLPFIKLKGVADPGTVREYNNHHDREEEEEEEYDYPILGR
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pdsACFL2(KY853034)          REKMFLLNDLLGTHIPPNADFARMDLDKVTTQFHTLLFEIVHQFVVSQPCLFTVDNAQFIDQESWDFIEDLSADSHAILVLSLRPFSSSNPCEAAIRLTGHETTP
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pdsACFL2(KY853034)          KKVKLGGLEASYMSDLACQFMDVMYIPNELDGILREKSHGIASWCEQLIKDMLTSNVIQVVNESQAFLNKESSLDLLSFGGSTTTTISQKHNNASSYLPRPSTLL
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pdsACFL2(KY853034)          QNAHNHHGFYDFNDPVHAQHHGHHHHHHHHQNVASSIHASVYCGCYADEMTKVINLSRLMTPSGPRKHCLYMKFVNTYVQETTYSLWLEDQKKELHERAAMFLES
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pdsACFL1(KX910691)      QAHKCKSCGGGGFVAKKADTLEEQGGHGKRTTEGRSQARVSSKMAKRRRTAEMREKVQSRGAFSSRTHERSSDISEAKHALKTKKLKESPVVNQKAGETEGIGSK
pdsACFL2(KY853034)      QAHKCKSCGGGGFVAKKADTLEEQGGHGKRTTEGRSQARVSSKMAKRRRTAEMREKVQSRGAFSSRTHERSSDISEAKHALKTKKLKESPVVNQKAGETEGIGSK
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pdsACFL1(KX910691)      LILGKKQPKTDFGCYVRLLKEALRHYLHVFLPGYYIGGAGDKSARLIEQSRCLSHLSHVYHSLHLKKWSLMAALQELNAAEEAEENLHELINAYAGVVECSHLVG
pdsACFL2(KY853034)      LILGKKQPKTDFGCYVRLLKEALRHYLHVFLPGYYIGGAGDKSARLIEQSRCLSHLSHVYHSLHLKKWSLMAALQELNAAEEAEENLHELINAYAGVVECSHLVG


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pdsACFL2(KY853034)      WKGWGKTYEKIGKNRCEDPSLYSDPEDMMTVAHLYCVSLAFRLAIGEVSIAINSGKHAFDLAKQVHDQHMMTTCIPLLAQSLLFTAKIPDCIDVLKELNAAALDS
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pdsACFL2(KY853034)     QEDGKNRQNEDEVQKCLKKFKNALNHHPVFDGRRLHLLAYYHLLRGKKDKCKSKLRRCFNKNKNLGLWLEVEWANKSFKEWFISWKESEPNYLGTSMFTLPKPKKD
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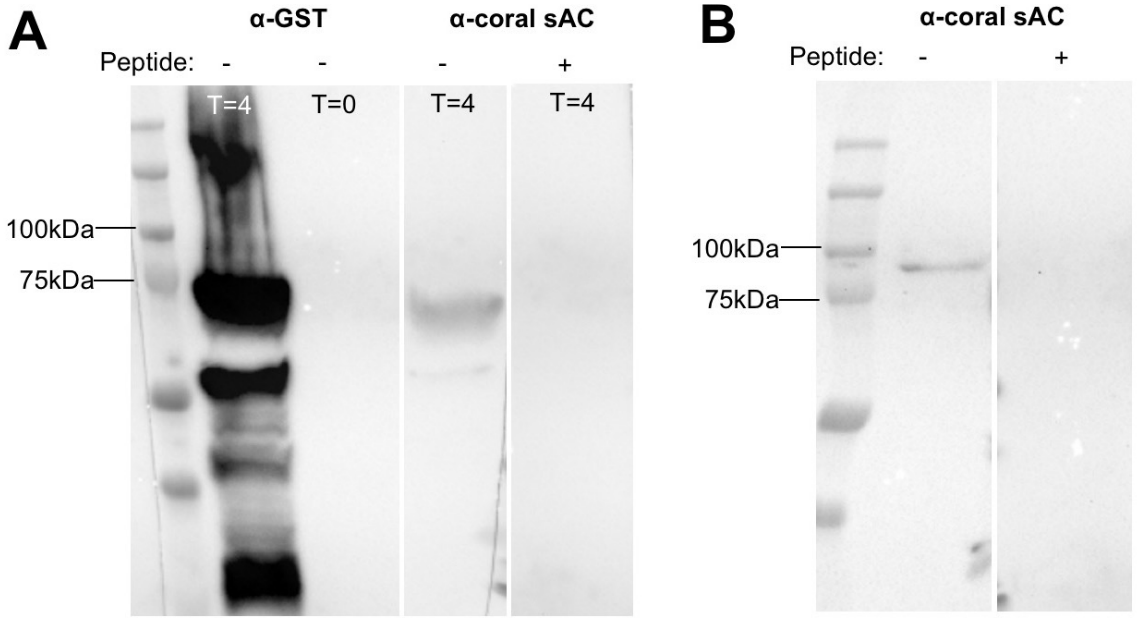
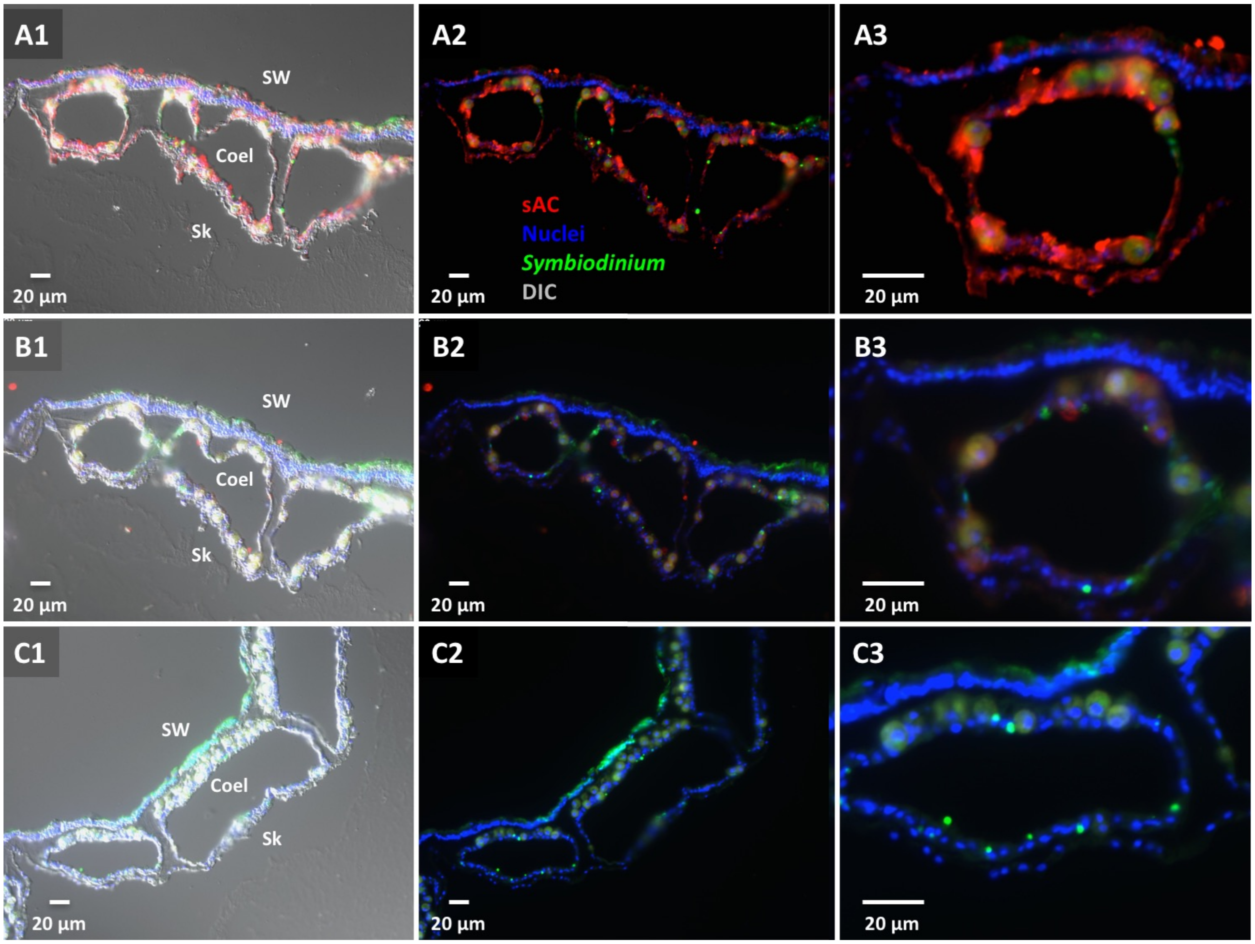
Supplemental Figure 1. Alignment of full length *Pocillopora damicornis* soluble adenylyl cyclases 1 and 2 (pdsACFL1 and pdsACFL1). The two catalytic domains are highlighted in red, the two P-loop motifs in purple, the histidine rich region in light grey, the leucine zipper pattern in dark grey, and the four tertratricopeptide (TPR) like helical domains in green. The 1061 amino acids that are missing in PDsAC94 (Figure 2 in the manuscript) are underlined. Made online using Clustal Omega Multiple Sequence Alignment (http://www.ebi.ac.uk/Tools/msa/clustalo/).

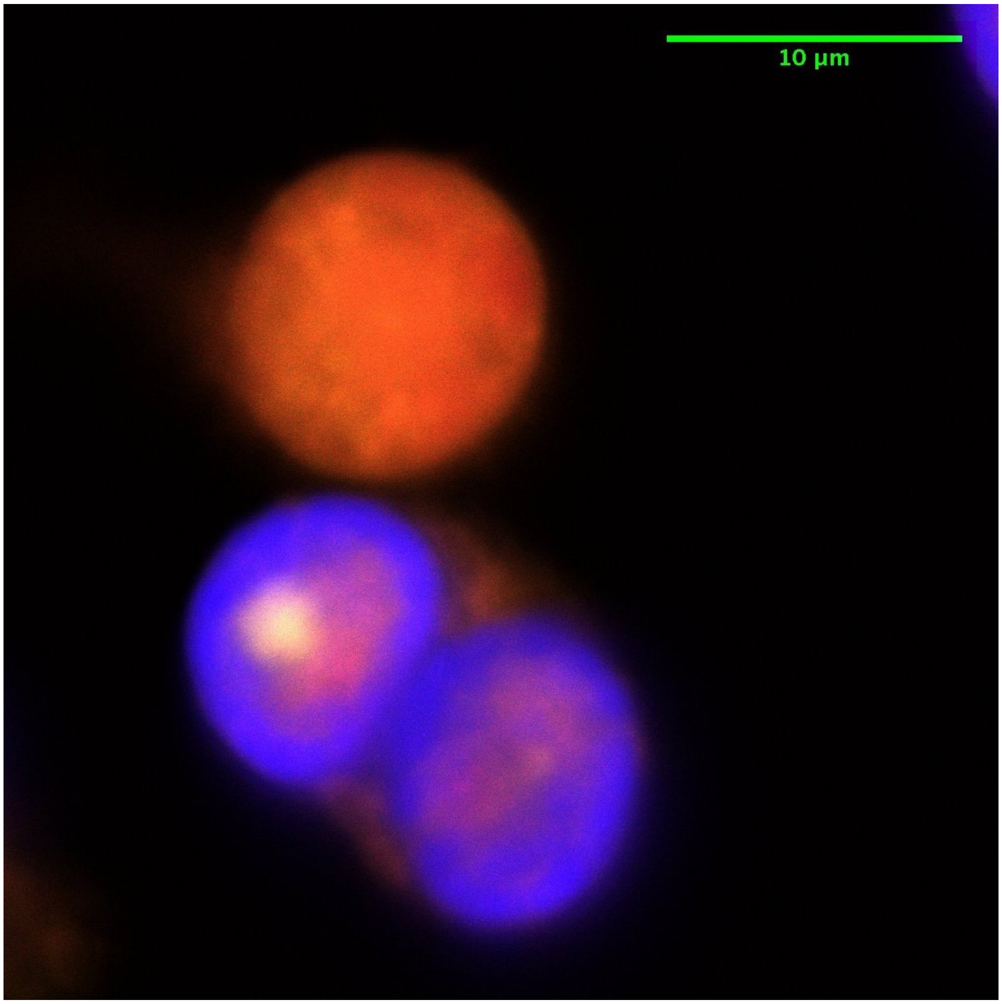
Supplemental Information



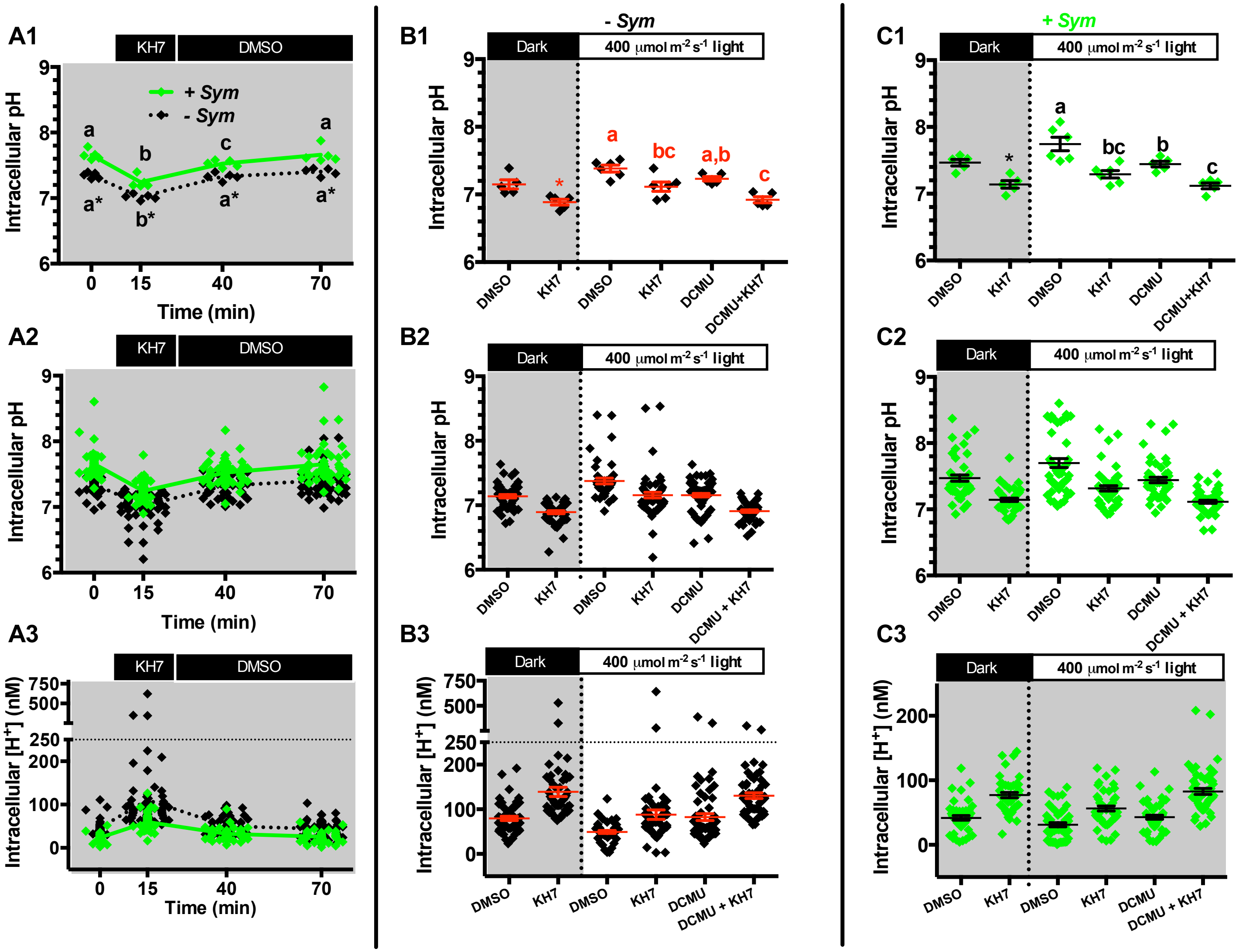
Supplemental Figure 2. Specificity of anti-coral sAC antibodies. A) Western blots with either anti-GST or anti-coral sAC antibodies against recombinant pdsAC$_{94}$ before (T=0) and after (T=4) expression of the protein was induced in *E. coli*. B) Western blots using anti-coral sAC antibodies against native proteins prepared from whole tissue homogenates. Anti-coral sAC antibodies pre-adsorbed with antigen peptide are indicated by +. Molecular weight marker shown in the left-most well with sizes indicated.



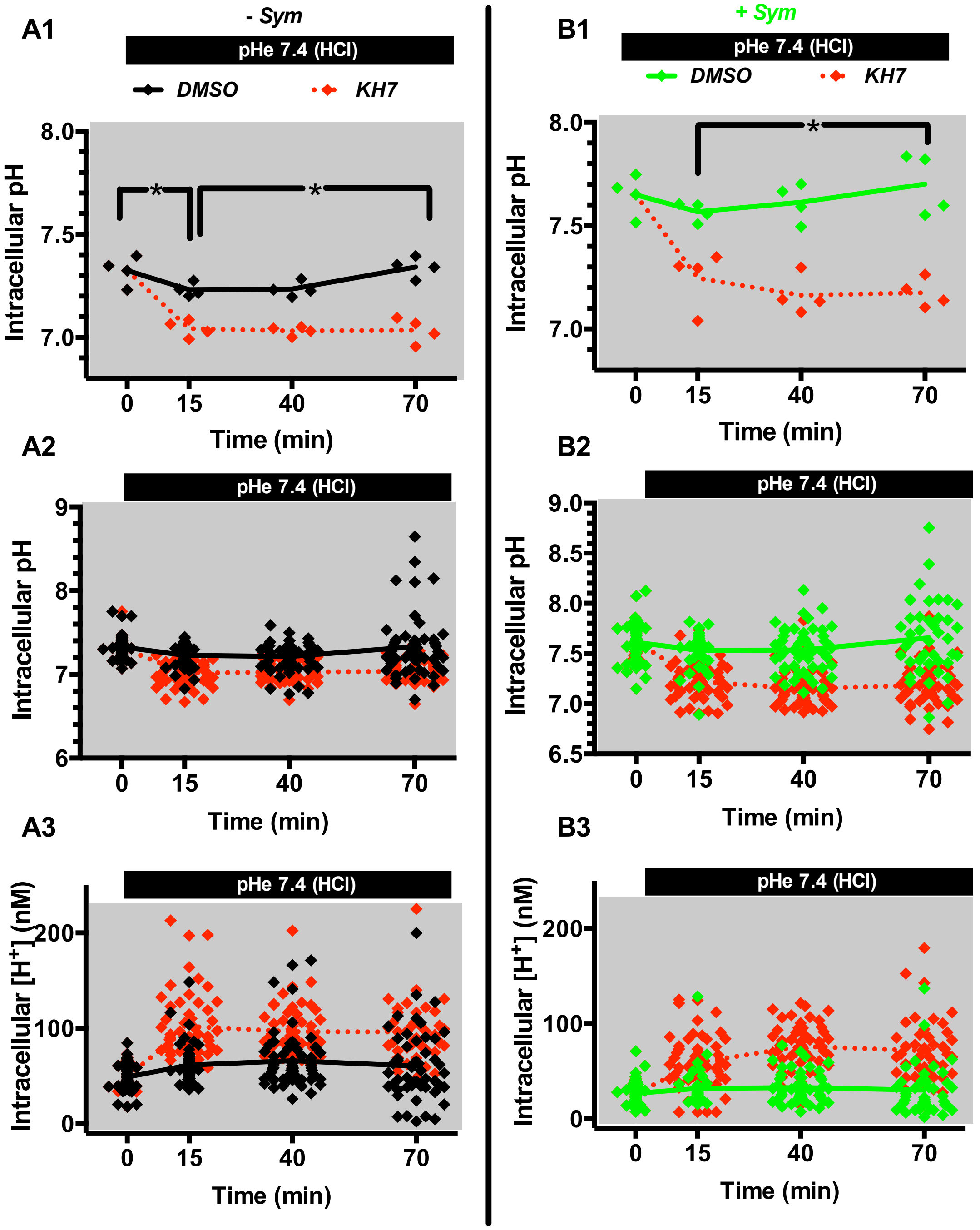
Supplemental Figure 3. Validation of anti-coral sAC antibodies in *P. damicornis*. A) anti-sAC antibodies, B) anti-sAC antibodies preadsorbed with antigen peptide, C) no primary antibody.



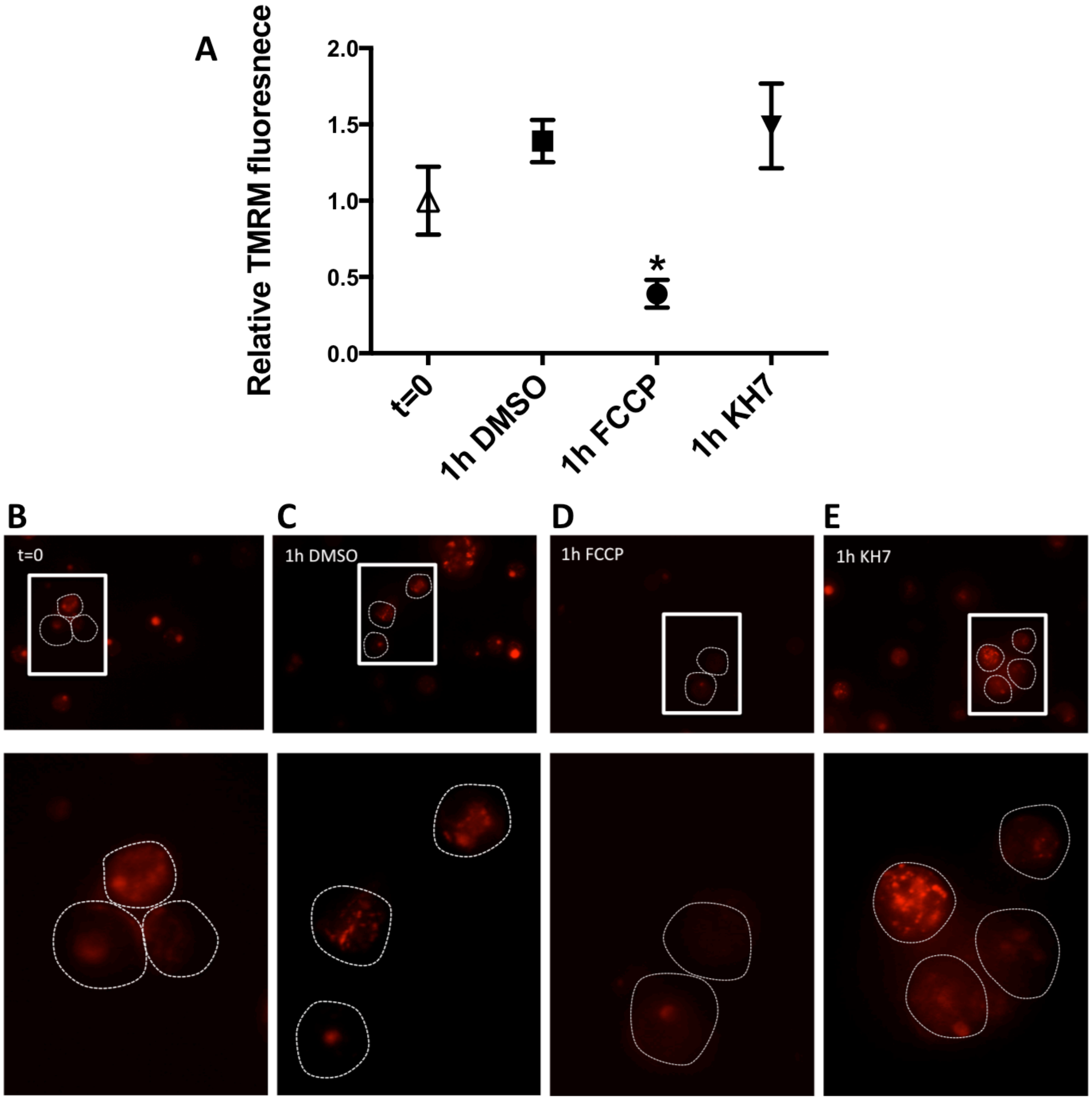
Supplemental Figure 4. Representative image of coral cells with *Symbiodinium* (bottom left) and without *Symbiodinium* (top). Blue indicates *Symbiodinium* chlorophyll autofluorescence. SNARF1 fluorescence is shown in orange.



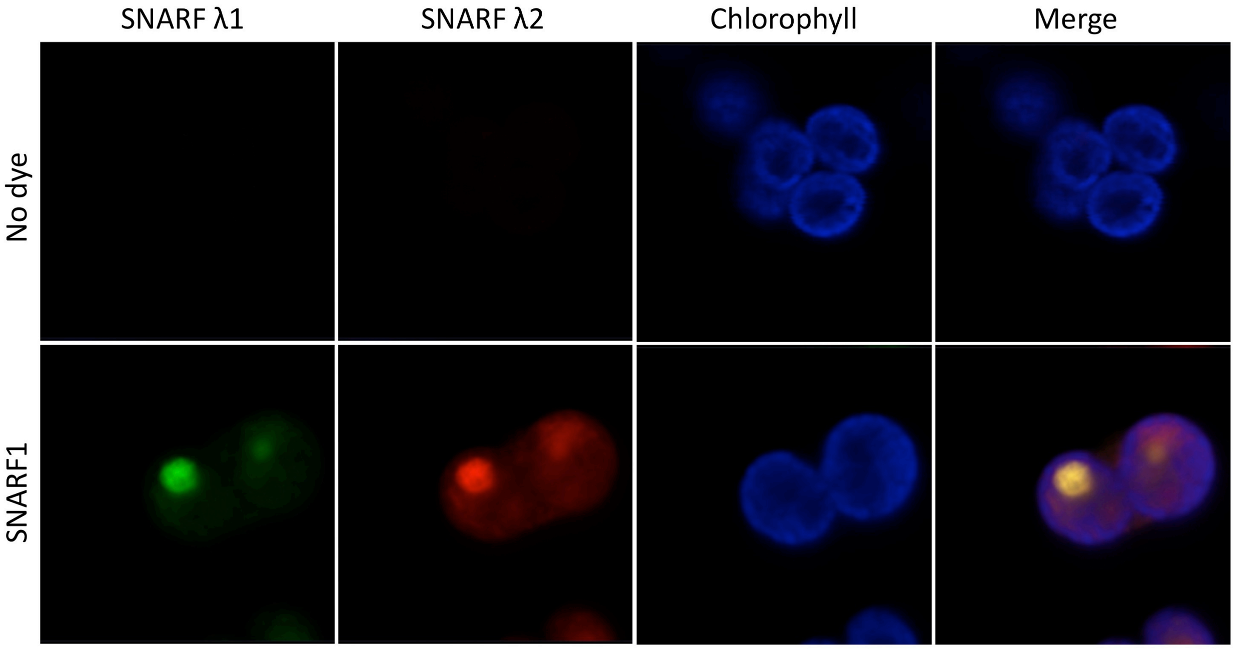
Supplemental Figure 5. Intracellular pH (pHi) and intracellular [H$^+$] in the experiments shown in Figure 4. A1, B1, C1: each point represents the average pHi value from 48-62 (A), 45-53 (B), and 47-67 (C) cells from each of five corals (N=5). A2, B2, C2: Each point represents the pHi value of a cell. A3, B3, C3: Each point is the intracellular [H$^+$] of each cell shown in A2, B2, C2. The shaded boxes indicate dark conditions.



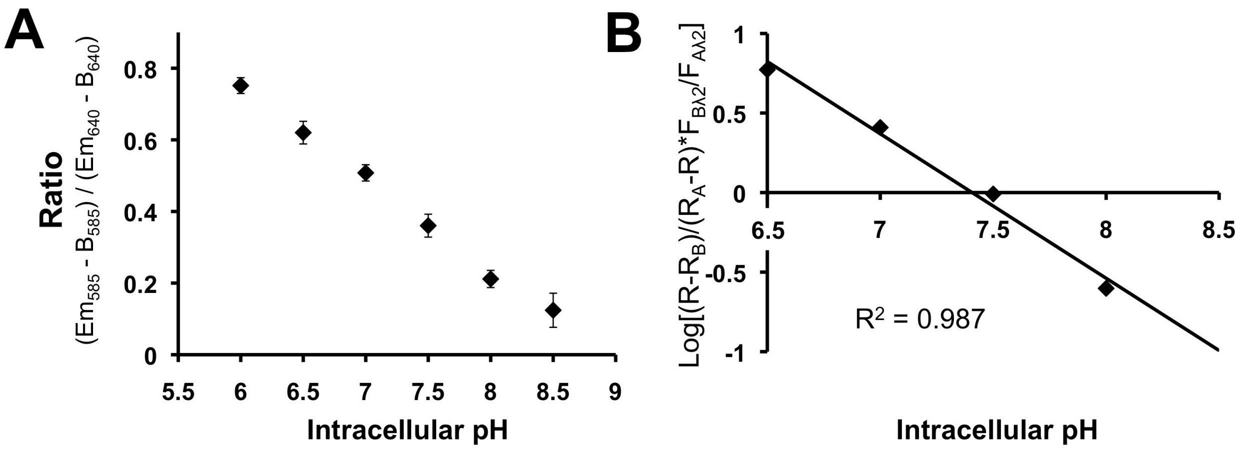
Supplemental Figure 6. Intracellular pH (pHi) and intracellular $[H^+]$ in the experiments shown in Figure 5. External pH (pHe) acidification was achieved by addition of HCl in the dark (indicated by the shadad boxes). A1, B1: each point represents the average pHi value from 50-59 cells from four corals (N=4). A2, B2: Each point is the pHi value of each cell shown in A2, B2. A3, B3: Each point is the intracellular $[H^+]$ of each cell shown in A2, B2, C2.



Supplemental Figure 7. KH7 does not induce mitochondrial uncoupling in isolated coral cells. Coral cells were isolated as described in Methods, incubated with 0.1 µM tetramethylrhodamine methyl ester (TMRE) for 30 min, pelleted down (5 min at 350 xg) and resuspended in filtered seawater to wash away excess dye, and 1 mL aliquots were incubated with either nothing (t=0h), DMSO, 5 µM FCCP (a classic mitochondrial uncoupler that served as positive control), or 50 µM KH7. TMRE accumulation in mitochondria was quantified at t=0 and t=1h using a fluorescence microscope (Zeiss AxioObserver) (magnification=400x, excitation= 550 nm; emission 605 nm). All images were taken with the same exposure settings; for each field of view five z-images were stacked together and analyzed using Image J (National Institute of Health, USA). Per-cell TMRE fluorescence was calculated as the product of fluorescence area and average intensity. **(A)** Summary statistics (Kruskal-Wallis 1-way ANOVA followed by Dunn's multiple comparisons test. Mean ± SEM of 30-34 cells per treatment, the asterisk indicates a significant difference compared to t=0, $p<0.05$). **(B-E)** Representative images of TMRE signal in isolated coral cells from the different treatments, the white squares correspond to the zoomed in images shown in the bottom row.



Supplemental Figure 8. Comparison of endogenous fluorescence with SNARF1 fluorescence in cells isolated from the coral *P. damicornis*. Cells were excited with a 561 nm laser (10% power) and fluorescence emission was collected at 585 +/- 10 nm (SNARF λ1), 640 nm +/- 10 nm (SNARF λ2), and 680 +/- 10 nm (chlorophyll).



Supplemental Figure 9. Calibration of intracellular pH in isolated *P. damicornis* cells loaded with SNARF1-AM.