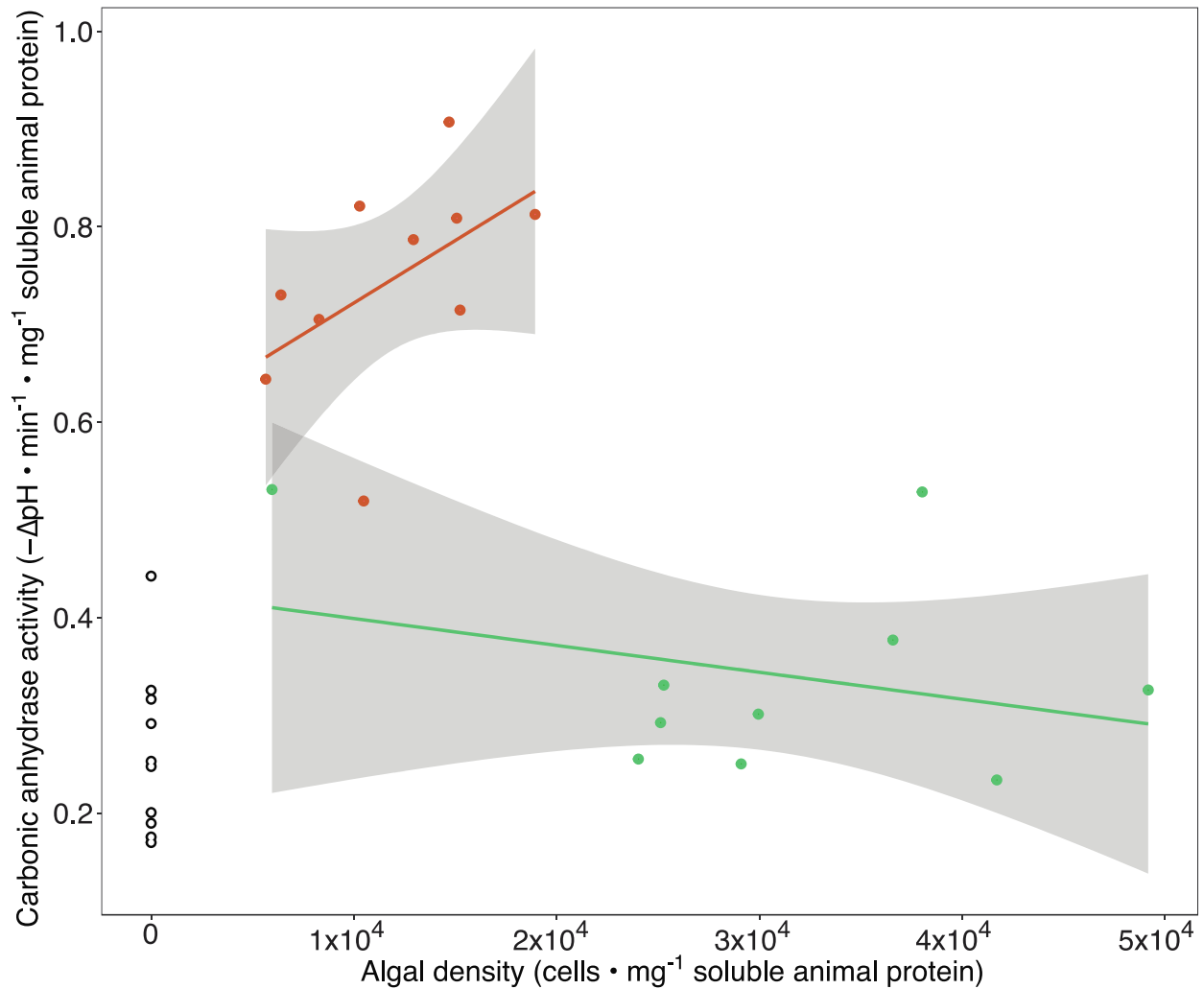SUPPLEMENTARY INFORMATION

SUPPLEMENTARY FIGURES

Figure S1. The relationship between algal density and CA activity from field-collected

brown, green, and aposymbiotic *A. elegantissima*. Each point is the average of triplicate technical

replicates. Colors: brown = brown, green = green, aposymbiotic = white. A linear model was fit for each

set of symbiotic states in the data indicated by a brown or green line (brown: y = 0.000001278x + 0.5942,

adjusted R^2 = 0.1626, F = 2.748, *p* = 0.136; green: y = -0.0000002752x + 0.4266, adjusted R^2 = -0.02078, F

= 0.8168, *p* = 0.3925) with standard error of the model represented by the extent of the gray region

around each line. There is no linear model for the aposymbiotic anemones since all individuals had no
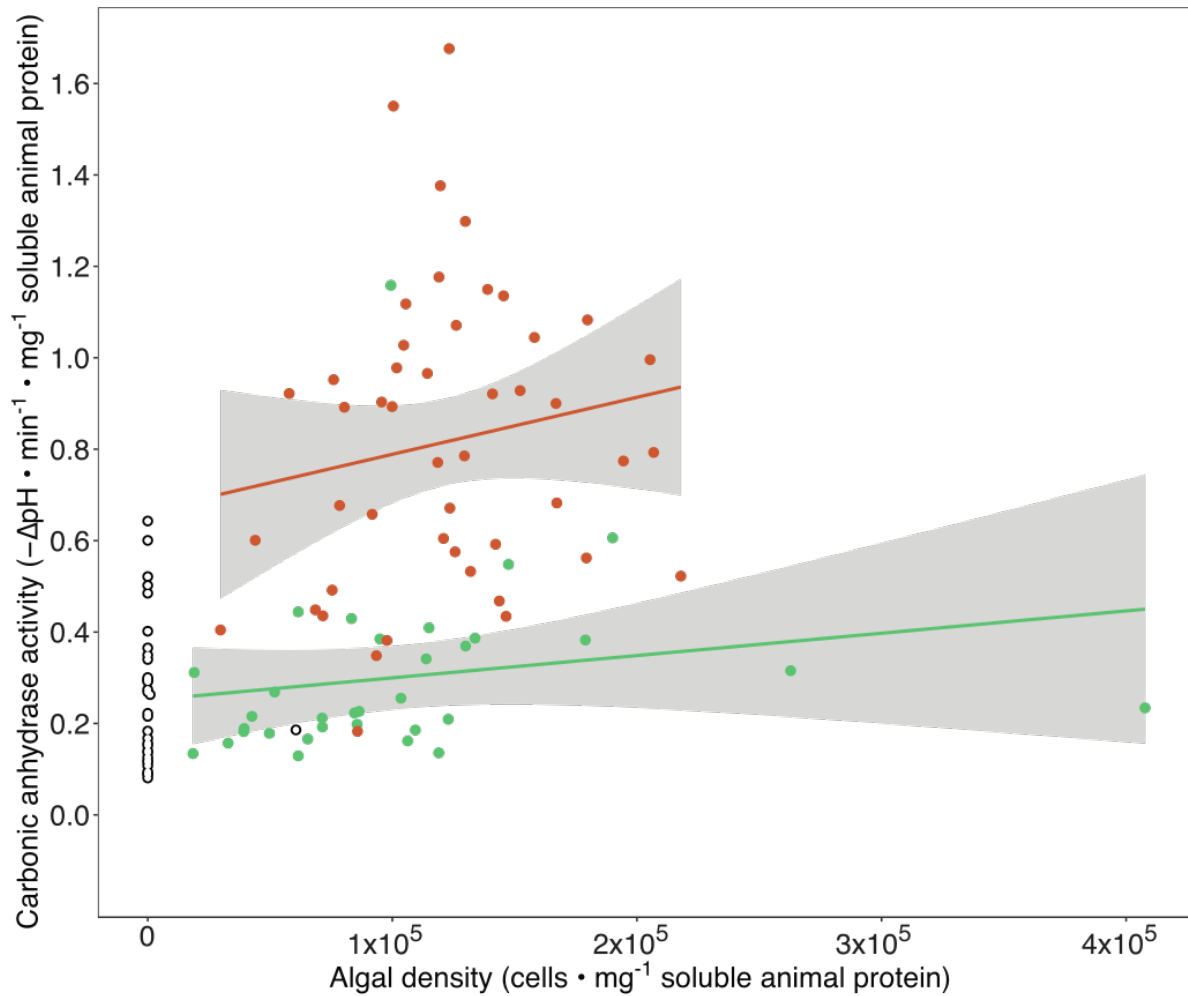
algae present.

Figure S2. The relationship between algal density and CA activity from the light

experiment. Each point is the average of triplicate CA and quadruplicate algal count technical replicates.

Colors: brown = brown, green = green, aposymbiotic = white. A linear model was fit for brown and green

states in the data indicated by a brown or green line, respectively. (brown: y = 0.000001247x + 0.6641,

adjusted R^2 = 0.005193, F = 1.24, *p* = 0.2714; green: y = 0.0000004882x + 0.2509, adjusted R^2 =

0.003974, F = 1.128, *p* = 0.296474) with standard error of the model represented by the extent of the

gray region around each line. There is no linear model for the aposymbiotic anemones because all

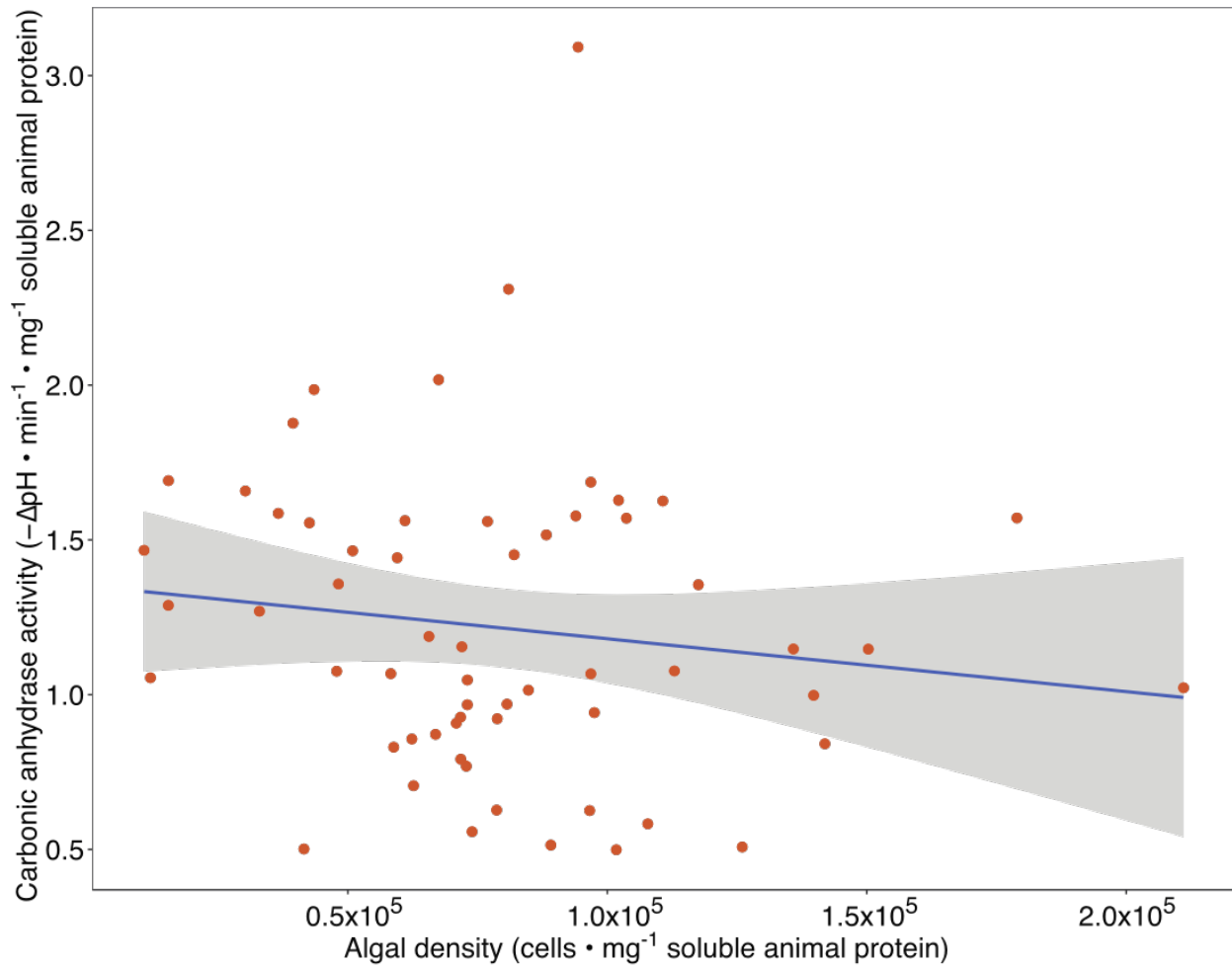individuals except one had no algae present.

Figure S3. The relationship between algal density and CA activity from field-collected

brown *A. elegantissima* of different sizes. Each point is the average of triplicate technical replicates. A

linear model was fit to the data indicated by the blue line (y = -0.0000017x + 1.4, adjusted R^2 = 0.0014, F

= 1.082, *p* = 0.303) with standard error of the model represented by the extent of the gray region around

the line.

SUPPLEMENTARY TABLES

Table S1. Nucleotide and amino acid sequences for AeleCAs used in this study. Signal peptides, where present, are highlighted yellow and were excluded from phylogenetic analyses. Signal peptide with transmembrane regions, where present, are highlighted blue.

Gene	Nucleotide sequences	Protein sequences	Signal peptide?	Transmembrane domain?

AeleCA	Nucleotide:	Amino acid (frame 1, open reading frame 2 frame 1):	Y	N
1	CTTCCGATCTACTTTGCATAAGCTAGCGTCGACTGCTGTTTGTTC CTGCAGAGCTGAGATCCACAACACTCACTTGTAAACCAAGATAT TGAGATGGCTGCACCAAAATGGGGTTATGGTCCTAATAACGGGC CTTCAAAATGGGCCAAGGATTTCCCTGCAGCCGCAGGGGCACG CCAATCACCGATCGACATCAAAACACATGATGCTCAACATGACA GTGCACTCAAAATAAAGCCCTTGAAAATCCAATACAGCCAGGGA AACGACTTCAATGTCACCAATAATGGCTACTCTTTGGTCATATCG CGCAAGACCAGTGAAGGGACTAACTTGAGTGGTGGGCCGTTG GAACATAACTACCGCTTTGAGCAGTTTCATTTCCACTGGGGAAA GACATCTGGAAGTGGCTCGGAGCATTTGCTGGATGGAAAAGCC TTTCCTGCAGAGCTTCATCTTGTTCACTGGAACACAGATCTCTTC AGCAGTTTTGGCGAAGCGGCGTCGAGTAAGAATGGCCTGGCTG TGCTTGGTGCCTTTGTGCAAATTGGTGGTGAAAGTGCTGGTCTG AAGACGATCACCGACATGATCCCCCAAGTCCAGAATATTGGCGA CAAACAAGACCTTAAGGTTCCCTTCAACTTATCGTCGTTGCTACC AAGTAACACTAATGACTACTGGACCTACAGTGGTTCCCTCACCAC CCCTCCCTGCTATGAAAGTGTCTCCTGGTTCGTTTTCAAGGAGC CAATCCACGCAACGGAGAATCAGATGCAGCAGTTCCGTTCACTC AAGGCCAACGATGGTGGATGTATAGTGGACAACTACAGACCAG TCATGGATGGTAGTGGACGCAACGTCAGGGCTTCTTTTGAGTGA AAAGTTTGGCATGAAAAATTAGAAACAAACTCTCGTAATTCTGA CCTTGAAAAGAACGAATGATCGAGGAACGTAGGAAGTATAGTT GTAATTTGTAGCCGAGATGAAGGCTTTTAGAATCTATAGAAATGT TGTAAACAAGAGAGACAGCAAATAAATATGAATTTGCCAAAAAA	==MAAPKWGYGPNNGPSKWAKD== ==FPAAAGA==RQSPIDIKTHDAQHDS ALKIKPLKIQYSQGNDFNVTNNG YSLVISRKTSEGTNLSGGPLEHNY RFEQFHFHWGKTSGSGSEHLLD GKAFPAELHLVHWNTDLFSSFGE AASSKNGLAVLGAFVQIGGESAG LKTITDMIPQVQNIGDKQDLKVP FNLSSLLPSNTNDYWTYSGSLTTP PCYESVSWFVFKEPIHATENQM QQFRSLKANDGGCIVDNYRPVM DGSGRNVRASFE*		

| AeleCA 4 | Nucleotide:

TGTTGCTTACCAAGCTTGAAATATATTATATTAATGAATATGCAAAT AATGTCAGTACAGAAGAAAACATGCTGGAAAAACCAGCAGACA AATGCAAAGTTTGGGAAAATCCCATATAGTTGTTACCTTTCGCTG CTTGCATTCACATCACCCATACTGCATTTAGAGCTTGGTATAAGA CATGCAACAAGCAACAATACCTTCACCAACCTTTCTAAAAATAGC TGTTTATCGGACAACTCGATTACAACAAGACTGCTGCCGTCACA GCGGACAGAATGGTTGTCATGGTGGCGGTCACGAGATAAGATT CGCTGTCTGGTCCCTTATGATCAGCTGCAGTCTTGAAGCTTCTTT TGACGACACGAGAATTCAGAGGTTCAACGGGACGGAAGGTGT CGGTTAGAACACCTCTATCGTTGTCTTTTAGGCTTCGAAGCATGT CGAGCTGAGCTTGGGAGATTGTAGCGTAGTTCTTAAAGACGGT CCAAGTGACAACCTCGTTACAAGTTGGTGTTGTCAAACTACCCT TGTACCTGTAGAAGTCAGTGATGTTGGTTGGGAGTAAAGATGCC AGGTTGTTGGTCATAGACAAACCAGTTACTTTACTAGATGGGTG AGTCACATTGAGTGCGTACTTCAAAAAGGACGTCAGAGCTGTAT TTTCGGTTGTACCAACCTTGAAGATGACGCCTAAAACTGCAAGT CCATCTTCTTGTTTTACGGCTTCACCTATGTTTGAGTACTTTGTGT TGAAGTTCACAAAATGCAACTCAGCCGGGTACTTTGTCCCATCC ACGGTGTGTTCAGATCCCTTATTGTTTTCACTACCCCAGTGGAAA TGAAACTGGAGAGTGGTGAAAGTACCTGGTAACCCTCCTTTGG ACACGAGGAATGTGTTGGGTGTAAAGAACACTGTATAGGAATG ACCATTGTTAGATACATTAAATTTTGCCCCAGTGGGAACAGTGTT GAATTTGGTCAGGGTGAGTTTTTCCAAACTTGCGTCGTATTCAG TTTTAGAGGCTTCAATGTCGATGGGCGACTGGCTTGAACCGTTA CAAAAGCTTGGAAACGTTTTAGCCCAGCCAAGAGGACCATACT TGGTATCTGTGACATTGTAATTGAAACTATTAGAAGCCCCAAGCA TAGGTTGAACCAATGCCAAAATAAGTACACAACTTAGTGAAAGA TTTATTGCCATGTTTCGTGGAGAGAAAAAAGTTTTCATTAAGCA AAAATTACCTTTCGGTATCGTATCTGGTTATTCCTGTCTTTTTCTG TTTTCCTTTTGGCTTCATATAGCTAGTGATTATAGTGTTTCAGTTG TCCATAACTGTTGATTAGACTATTATACTATTCGTTGCCTGTGGAG | Amino acid (frame 3 reverse, open reading frame 13 frame 3):

MKTFFSPRNMAINLSLSCVLILAL VQPMLGASNSFNYNVTDTKYGP LGWAKTFPSFCNGSSQSPIDIEAS KTEYDASLEKLTLTKFNTVPTGAK FNVSNNGHSYTVFFTPNTFLVSK GGLPGTFTTLQFHFHWGSENNK GSEHTVDGTKYPAELHFVNFNTK YSNIGEAVKQEDGLAVLGVIFKV GTTENTALTSFLKYALNVTHPSSK VTGLSMTNNLASLLPTNITDFYR YKGSLTTPTCNEVVTWTVFKNYA TISQAQLDMLRSLKDNDRGVLTD TFRPVEPLNSRVVKRSFKTAADH KGPDSESYLVTATMTTILSAVTAA VLL* | N | Y |

AeleCA 6	Nucleotide: ATATTCCCAAATTCAAGAACATACCAAAATGATCCTCGTGTTTTTC ACGCTTCTTCAAACTTTTCGTGTTTTGATTGATGAGAAACGAAC AGATAAGTAAAACTTTTCACTAATATTTTCTCTACTTTTAATCAGT AGTCATGATTTTATTCTGACACTTTTTCATTCGTGCAGTGTTACTC TTCGCCCGTTGAGGGGTAGGGTAGGTCTGTAGTTGTTGCACATT TTGCCGTGATGGTAGCCATGTGTAGCCTGGAGGGCTCTGAAATT ATTCAGAATTTCTTGGTCAGCAGTGATAGGAGTTCTGAGCACTAT CCATCGAACAGACTCGTAACATCCAGGGGTGGTCAGGGATCCCT TGTATGTGTAGTATGATCTACCACCAGACGATAGACCACCAACCA AGCTATCGAGTCTGACGGCAACTCCAGCTTTCTGAGATCCTTCT GTTATTATTGCATTCAAATTCAGTGAAAACGTCTTAAGTTCTGGT GCTCCAGAAGATCCCTTCTTCAGGAAAGCACCAATCACTGTCAA GCCGTCTGATTTGGTGGCAGCGGTGGAGATGTCGCCATATTTGG CGTTATAGAACACCAAGTGAAGCTCTCCTGGGTAAGATCTGCCA TTGATTGTGTGCTCCGAACCAACATTATCAGTACATCCGAAATGG AAGTGAAACTGAGCAAGGATATATTTCTGACCATTAACTGGATTA TATACACTTGCACTACCTTTCTCAACGTTGAAAGTTGGTGAATGC CCATTGTTGACCAGAGTTCCTTTGACCGTCCCCCAATAATACTGA AACCTTACACGCAGTGGACGGAGGTCGATATCATCACCATCTTT GACTTTAGCACGGACGATGTTTACTGGAGATTGGGAACGAGCA TTGCAATCCTTGGATACGTGACCCCAGTCTGATGGTCCATACACT TGACCATAAGTCTTGCCATAACCCCAAGAACCGGCTGAGGATGC CAGGCCAAAGAATCCAGCACTCAACACTATGATCTGCATCAACA TCATCGTTTTCTTTAATATTCAATGAGAAACGTCGTAAATATCGAA GTAAATAAGGACAAGGTGTTTGAGCGTGATGGCGATAAAGGTT TGTGTTGAGTGCTGGATTCTTTGGCCTGGCATCCTCAGCCGGTT CTTGGGGTTATGGCAAGACTTATGGTCAAGTGTATGGACCATCA GACTGGGGTCACGTATCCAAGGATTGCAATGCTCGTTCCCAATC TCCAGTAAACATCGTCCGTGCTAAAGTCAAAGATGGTGATGATAT CGACCTCCGTCCACTGCGTGTAAGGTTTCAGTATTATTGGGGGA CGGTCAAAGGAACTCTGGTCAACAATGGGCATTCACCAACTTTC	Amino acid (frame 3 reverse, open reading frame 13 frame 3): ==MMLMQIIVLSAGFFGLAS==SAGS WGYGKTYGQVYGPSDWGHVSK DCNARSQSPVNIVRAKVKDGDD IDLRPLRVRFQYYWGTVKGTLVN NGHSPTFNVEKGSASVYNPVNG QKYILAQFHFHFGCTDNVGSEHT INGRSYPGELHLVFYNAKYGDIST AATKSDGLTVIGAFLKKGSSGAPE LKTFSLNLNAIITEGSQKAGVAVR LDSLVGGLSSGGRSYYTYKGSLTT PGCYESVRWIVLRTPITADQEILN NFRALQATHGYHHGKMCNNYR PTLPLNGRRVTLHE*	Y	N

AeleCA	Nucleotide:	Amino acid (frame 3, open reading frame 1 frame 3):	N	N
9	AGGAACTAAGGTAGAGGTAACTGCATCATCTTTCATTGAATTGTT CAACAGAAGTCTCAAATACAAGGATGGCAAACACATTTCTAATT TTCCTAACAGCAGCAATTTTTCAAGTCTCGCTGAGTGTCGATTAC AATTATGAACTTTCAGACACCACCTATGGTCCTCTTGGTTGGCCC AAAACATACAATCCATCCTGTGACGGCTCCAGACAATCACCAATC AACATTAAGCCTTCAGATGCTAGCTATGATGGCTCGTTGGGAGA GCTGAGTTTCAAGAACTATAACCTTCCTGTCGATTCCGTGCTCAA GCTTGGAAACAATGGCAAATCCTACAGAGTGTTCTTCGAACCCA ATACGTACACGATATCCGGAGGAGGGCTGCCTGGTACTTTCTAC ACACATAACTTTCATTTCCACTGGGGTGCAGCTAACACCAAGGG ATCTGAGCATACTATTGATGGAAAGAAGTTCCCACTTGAGCTCCA TTTTGTTAATGTCAACACAAAGTACGCAACTGTTGCAGAAGCTT TACAACAGAAAGATGGGATTGCAGCAGTGGGCATCCTATACGA GGTTGGCGACGAAGATCTAGCGCTTGAACCTTTCTTAAAATACA CAGCTAATGTGACTTACAAAAGGGACATCTCGAATGTGACCGTG ATGGCTCAAGCCCTACAGACCCTTCTACCCCAAAACACCACTGA CTTCTATAGATATAACGGGTCTCTGACAACACCCAACTGCCAAGA AGTTGTCACATGGACTGTGTTTAAGAACTATCGAACAATCTCCCA AGCACAGCTGGATATGCTTCGAAGTCTTAGAGCCACAAACAACG TAACCATGCTGGTAGACACATTCCGCCCTGTTCTACCTCTAGGTT CTCGTGTTGTTAAGAAAACCTTTCACACCAGCCATGGAGAAGCG TATCACGTGACTAACACCATGACGATTATTGCGTTCGTCGTCATG GCAATGGTTATGTCCAAGTAGTTTCACATTTTTTTTGATGTAGTTT GTTTGTTAGCTTTTCAGTGCAAGGCTTTATCATTAAACTGATAAG CGCTTCAAAAAGCAATTTTCTACTTTCACATTCCCCAATACGTTAC AGTTTTTGGGTAACCAGGTTAAAAACAGCCGCAATTATTATGCT GAAGACTGATCAGAAGATGTTAGAAATGCATCTCATAATATAAGA AACAACCAGAAACAAAAAGAAAGAAATTTGCATATTTGGAAAA CTTTTGATATCTCTGCAACAAATTGATATATCAACAAACTGTAAAC GCTATCTGACTTTTTAAAACAACCCTTCCAAGTTACAGTTAAAAC TTGAAGCAAAATATTTCGTTTTAATTCATATAAATTTTGATGAAAT	LHHLSLNCSTEVSNTRMANTFLIF LTAAIFQVSLSVDYNYELSDTTYG PLGWPKTYNPSCDGSRQSPINIK PSDASYDGSLGELSFKNYNLPVD SVLKLGNNGKSYRVFFEPNTYTIS GGGLPGTFYTHNFHFHWGAAN TKGSEHTIDGKKFPLELHFVNVN TKYATVAEALQQKDGIAAVGILYE VGDEDLALEPFLKYTANVTYKRDI SNVTVMAQALQTLLPQNTTDFY RYNGSLTTPNCQEVVTWTVFKN YRTISQAQLDMLRSLRATNNVT MLVDTFRPVLPLGSRVVKKTFHT SHGEAYHVTNTMTIIAFVVMAM VMSK*		

Table S2. Primers for qPCR experiments.

Gene name	Transcriptome identifier	qPCR primers
AeleCA6	comp404_c4_seq3	Forward: 5'-ACC AGA GTT CCT TTG ACC GTC-3'
		Reverse: 5'-CTG GGG TCA CGT ATC CAA GG-3'
AeleCA9	Comp2502_c1_seq3	Forward: 5'-TCG ATT CCG TGC TCA AGC TT-3'
		Reverse: 5'-ATC CCT TGG TGT TAG CTG CA-3'
AeleCA4	comp34611_c0_seq1	Forward: 5'-TAC AAC AAG ACT GCT GCC GT-3'
		Reverse: 5'-CTT CCG TCC CGT TGA ACC TC-3'
AeleCA1	comp7398_c0_seq2	Forward: 5'-CGC CAA TCA CCG ATC GAC AT-3'
		Reverse: 5'-TTC ACT GGT CTT GCG CGA TA-3'
G3PD		Forward: 5'-AGA GGC CTT CTT CAC AGC AC-3'
		Reverse: 5'-GTT GGC AAG GTC ATC CCA GA-3'
NADH		Forward: 5'-ATG GGA TTT GCT GGT CCA CT-3'
		Reverse: 5'-TGG GTA GAC AGG TTC ATC GT-3'