Supplementary Information

Table S1. Fatty acid composition of *Ostreococcus RCC809* (*O. RCC809*) and *F. cylindrus* cultures in stationary phase. Values are the average of three independent experiments (±standard deviation). ND—not detected.

Figure S1. Multiple sequence alignment of Ost809D6 with Δ6-desaturases from *Mantoniella squamata* (*M.squaD6,* CAQ30479.1) [1], *Micromonas pusilla* (*M.pusD6,* XP_002502445.1) [2], *Ostreococcus lucimarinus* (*O.lucD6,* DAA34893.1) [3] and *Ostreococcus tauri* (*O.tauriD6,* XP_003082578.1) [4]. Conserved histidine boxes are shaded in grey. Conserved amino acid residues are indicated with an asterisk. The position of conserved cytochrome b_5 domain motif is marked with a solid line. The alignment was obtained using CLUSTAL W.

Figure S2. Multiple sequence alignment of Ost809D4 with Δ4-desaturases from *Pavlova lutheri* (*P.lutD4*, AAQ98793.1) and *Pavlova salina* (*P.salD4*, AY926606.1) [4], *Isochrysis galbana* (*I.galD4*, AY630574) [5], *Ostreococcus lucimarinus* (*O.lucD4,* XM_001415706.1) [6], and *Emiliania huxleyi* (*E.huxD4*, [7]). Conserved histidine boxes are shaded in grey. Conserved amino acid residues are indicated with an asterisk. The position of conserved cytochrome b_5 domain motif is marked with a solid line. The alignment was obtained using CLUSTAL W. A related Δ4-desaturase from *Thalassiosira pseudonana* (TpD4, AAX14506.1) [8] was omitted from this line-up on the basis of poor alignment.

Figure S3. Multiple sequence alignment of FcElo6 with Δ6-elongasse from *Thalassiosira pseudonana* (TpElo6, AY591337.1) and *Ostreococcus tauri* (OtElo6, AY591335) [5]. Conserved amino acid residues are indicated with an asterisk, whereas conserved motifs are framed. The alignment was obtained using CLUSTAL W.

Figure S4. Codon-optimised nucleotide sequences. (**A**), Ost 809D6; (**B**), Ost809D4; (**C**) Fc ELO6.

Table S1. Fatty acid composition of *Ostreococcus RCC809* (*O. RCC809*) and *F. cylindrus* cultures in stationary phase. Values are the average of three independent experiments (±standard deviation). ND—not detected.

	Composition (Molar %) ± SD	
Fatty Acid	***O. RCC809***	***F. cylindrus***
16:0	20.12 ± 0.6	12.1 ± 0.2
16:1*n*-7	18.1 ± 0.3	24.5 ± 0.1
16:4*n*-3	5.08 ± 0.4	ND
18:0	1.24 ± 0.5	2.4 ± 0.3
18:1*n*-9	8.17 ± 0.2	ND
18:1*n*-7	8.03 ± 0.1	ND
LA	9.12 ± 0.2	0.7 ± 0.3
GLA	3.29 ± 0.3	1 ± 0.4
ALA	3.98 ± 0.4	0.8 ± 0.3
SDA	19.13 ± 0.6	5.7 ± 0.5
20:2*n*-6	0.65 ± 0.4	1 ± 0.2
20:4*n*-3	ND	7.4 ± 0.1
EPA	1.26 ± 0.4	31.4 ± 0.3
DHA	1.83 ± 0.5	2.5 ± 0.1
24:0	ND	1.4 ± 0.2

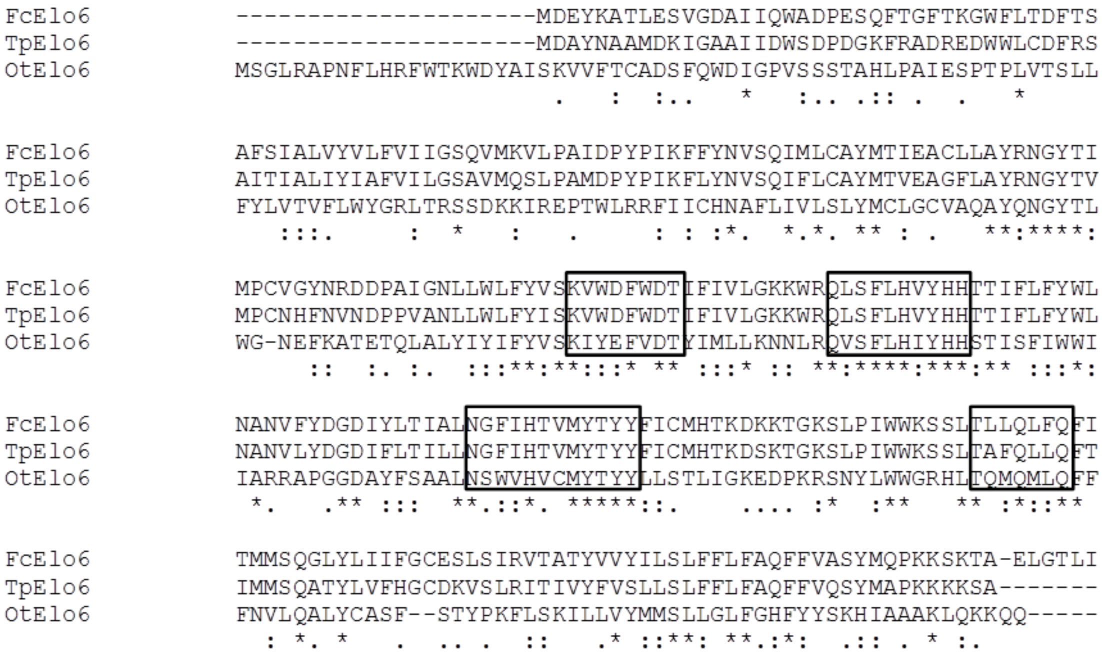
Figure S1. Multiple sequence alignment of Ost809D6 with Δ6-desaturases from *Mantoniella squamata* (*M.squaD6*, CAQ30479.1) [1], *Micromonas pusilla* (*M.pusD6*, XP_002502445.1) [2], *Ostreococcus lucimarinus* (*O.lucD6*, DAA34893.1) [3] and *Ostreococcus tauri* (*O.tauriD6*, XP_003082578.1) [4]. Conserved histidine boxes are shaded in grey. Conserved amino acid residues are indicated with an asterisk. The position of conserved cytochrome b_5 domain motif is marked with a solid line. The alignment was obtained using CLUSTAL W.

```
Ost809D6        -------------------MRVETEDDNVPTVTVGLSEESDGMKGARNPGARAWKSTLEP
O.lucD6         MCVETTEGTSRTMANERTSSSSSLSEGGTPTVTVGMGSE-DAGKKTRNASVTAWTKELEP
O.tauriD6       ------------------MCVETENNDGIPTVEIAFDGE----RERAEANVKLSAEKMEP
M.squaD6        ------------------------------MCPPKESTRKNAGGPLTRGKLSADLAKLEP
M.pusD6         -----------------------------------------MTRGNKAKLDNSKLAKLEP
                                                                         :**

                                         ____
Ost809D6        HAVAKSFDRRWVKVDGVEYDVTDFKHPGGSVIYYMLSNTGADATEAFKEFHYRSKKARKA
O.lucD6         HAIAKTFERRYVTIEGVEYDVTDFKHPGGSVIYYMLSNTGADATEAFKEFHYRSKKARKA
O.tauriD6       AALAKTFARRYVVIEGVEYDVTDFKHPGGTVIFYALSNTGADATEAFKEFHHRSRKARKA
M.squaD6        HKLAQTFDTRWVRVGDVEYDVTNFKHPGGSVIFYMLSNTGADATEAFNEFHMRSPKAWKM
M.pusD6         HKLAQTFEQRWVRIDDVEYDVTNFKHPGGSVIFYMLSNTGADATEAFKEFHMRSPKAWKM
                  :*::*  *:* : .******:******:**:* ************:*** ** ** *

Ost809D6        LAALPQREPEDAS--PVEDANMLKDFAKWRKDLEREGFFKPSPAHVAYRFAELAAMFALG
O.lucD6         LAALPHKPVDAATREPIEDEAMLKDFAQWRKELEREGFFKPSPAHVAYRFAELAAMFALG
O.tauriD6       LAALPSRP---AKTAKVDDAEMLQDFAKWRKELERDGFFKPSPAHVAYRFAELAAMYALG
M.squaD6        LKALPNRPAETPRSQ-DPDGPMLEDFAKWRAQLEKEGFFKPSIAHVAYRIAELAAMFALG
M.pusD6         LKALPQRPAETPRSA-DPDAPMLQDFARWRAELEKEGFFEPSRLHLAYRCLELCATFALG
                * *** :    .      *  **:***:** :**::***:**  *:***  **.* :***

Ost809D6        TALMYARWHATSVFVTACFFGARCGWVQHEGGHSSLTGSIWWDKRIQAFTAGFGLASSGD
O.lucD6         TALMHARWHVASVIVYSCFFGARCGWVQHEGGHNSLTGNIWWDKRIQAFAAGFGLASSGD
O.tauriD6       TYLMYARYVVSSVLVYACFFGARCGWVQHEGGHSSLTGNIWWDKRIQAFTAGFGLAGSGD
M.squaD6        CYIMSLGYPVVASIVFGAFFGARCGWVQHEGGHNSLTGNIWLDKRIQAATCGFGLSTSGD
M.pusD6         TFLMYIGRPLLASIVYGAFFGARCGWVQHEGGHNSLTGSIWWDKRIQAATCGFGLSTSGD
                  :*       : :* ..***************.****.** ****** :.****: ***

Ost809D6        MWNLMHNKHHATPQKVRHDMDLDTTPAVAFFNTAVEENRPRKFSKLWLRVQAWTFVPVTS
O.lucD6         MWNNMHNKHHATPQKVRHDMDLDTTPTVAFFNSAVEENRPRGFSKLWLRLQAWTFVPVTS
O.tauriD6       MWNSMHNKHHATPQKVRHDMDLDTTPAVAFFNTAVEDNRPRGFSKYWLRLQAWTFIPVTS
M.squaD6        MWNQMHNKHHATPQKVRHDMDLDTTPAVAFFKTAVEDNRPRGFSRAWSRAQAWTFVPVTS
M.pusD6         MWNQMHNKHHATPQKVRHDMDLDTTPAVAFFDTAVEDNRPRGFSKTWARAQAWTFVPITS
                *** ***********************:****.:***:**** **: * * *****:*:**

Ost809D6        -GLVLLAWMYLLHPRHIARRKNYEEAAWIVAAHVIRTSVIKAVTGYSWITCYGLFLSTMW
O.lucD6         -GMVLFFWMFVLHPRNALRRKSFEEAAWMFSAHVIRTAVIKAVTGYSWIASYGLFAATMW
O.tauriD6       -GLVLLFWMFFLHPSKALKGGKYEELVWMLAAHVIRTWTIKAVTGFTAMQSYGLFLATSW
M.squaD6        GLLVQMFWIYVLHPRQVARKKNYEEASWMILSHVLRTATIKYAGGYSWPVAYLWFSFGNW
M.pusD6         GVLVQMFWIYVLHPRQVLRKKNYEEASWMFLSHVVRTAVIKLALGCGTAEAYGWFWVGNW
                  :* : *::.*** :  :  .:**  *:. :**:** .** . *     .*  *    *

Ost809D6        VSGCYLFAHFSTSHTHLDVVPSDKHLSWVRYAVDHTIDIDPSKSVVNWLMGYLNCQVIHH
O.lucD6         ASGCYLFAHFSTSHTHLDVVPSDKHLSWVRYAVDHTIDINPNNSVVNWLMGYLNCQVIHH
O.tauriD6       VSGCYLFAHFSTSHTHLDVVPADEHLSWVRYAVDHTIDIDPSQGWVNWLMGYLNCQVIHH
M.squaD6        IAYMYLFAHFSTSHTHLEVVPSDKHISWVNYAVDHTVDIDPSKGYVNWLMGYLNCQVIHH
M.pusD6         IAYMYLFAHFSTSHTHLDVVPSDKHISWVNYAVDHTVDINPRNSIVNWLMGYLNCQVIHH
                 :  *************:***:*:*:***.******:**:* :. ***************

Ost809D6        LFPDMPQFRQPEVSRRFVSFAKKWNLNYKVMSYYGAWKATFGNLNEVGKHYYIQGSQITK
O.lucD6         LFPDMPQFRQPEVSRRFVPFAKKWNLNYKVLTYYGAWKATFGNLNDVGKHYYVHGSQRVK
O.tauriD6       LFPSMPQFRQPEVSRRFVAFAKKWNLNYKVMTYAGAWKATLGNLDNVGKHYYVHGQHSGK
M.squaD6        LFPDMPQFRQPEVSRRFVAFAKKWNLNYKVLTYYGAWKATFTNLDTVGQHYYKHGKAHAH
M.pusD6         LFPDMPQFRQPEVSRRFVAFAEKWNLNYKVLTYYGAWKATFSNLDRVGQHYYVNGKAKAH
                ***.**************.**:********::* ******: **: **:*** :*.   :
```

Figure S2. Multiple sequence alignment of Ost809D4 with Δ4-desaturases from *Pavlova lutheri* (*P.lutD4*, AAQ98793.1) and *Pavlova salina* (*P.salD4*, AY926606.1) [4], *Isochrysis galbana* (*I.galD4*, AY630574) [5], *Ostreococcus lucimarinus* (*O.lucD4*, XM_001415706.1) [6] and *Emiliania huxleyi* (*E.huxD4*, [7]). Conserved histidine boxes are shaded in grey. Conserved amino acid residues are indicated with an asterisk. The position of conserved cytochrome *b*$_5$ domain motif is marked with a solid line. The alignment was obtained using CLUSTAL W. A related Δ4-desaturase from *Thalassiosira pseudonana* (TpD4, AAX14506.1) [8] was omitted from this line-up on the basis of poor alignment.

```
Ost809D4        ---MPTTRSRARVTTPPRETPTRANTVAALDPERKYTRIRGVVYDVTDFASRHPGGAQLL
O.lucD4         --MPSAARSRASKRANATTDVATTAPEATLDPTRAYTRYRGVVYDVTEFQHRHPGGAQLL
P.lutD4         MPPSAASEGGVAELRAAEVAS---YTRKAVDERPDLTIVGDAVYDAKAFRDEHPGGAHFV
P.salD4         MPPSAAKQMGASTGVHAGVTDSSAFTRKDVADRPDLTIVGDSVYDAKAFRSEHPGGAHFV
I.galD4         --------------MCNAAQVETQALRAKEAAKPTWTKIHGRTVDVETFR--HPGGN-IL
EhuxD4          ----------------------MGGAGASEAERPKWTTIHGRHVDVSKFR--HPGGN-II
                                                    *   .   *.  *   ****  ::

Ost809D4        SLCVGRDATILVESHHLRPEVVQKYLKTLPVVEGAAGAFGPEETFPKPLDSDLYRKIQGR
O.lucD4         SLCVGRDATILIESHHLRPEVVRKYMKTLPVVEGAAGAFGKEETFPKPLDSAVYRAIQRR
P.lutD4         SLFGGRDATEAFMEYHRRAWPKARMSKFFVGSLDASEKPTQADSAYLRLCAEVNALLPKG
P.salD4         SLFGGRDATEAFMEYHRRAWPKSRMSRFHVGSLASTEEPVAADEGYLQLCARIAKMVPSV
I.galD4         DLFLGMDATTAFETFHGHHKGAWKMLKTLPEKEVAAADIPAQKEEHVAEMTRLMASWRER
EhuxD4          ELFYGMDSTSAFEQFHGHHKGAWKMLKALPTKEVDPADVPQQPQEHVAEMTRLMTSWRER
                .*  * *:*  .  .* :     :  :        .              : :

Ost809D4        VRKEIVEPLKMTRGREPHGRGWCVLDAGVVLAFFAFALGVYWKTPTVATGCLLGLAGYWS
O.lucD4         VRDEVVEPMKAKSGREAHGRGGCVVDAGVVVLTFVAAMVAYWRAPSALTGCALGLAGYWS
P.lutD4         SGGFAPPSYWLKAA-------------ALVVAAVSIEGYMLLRGKTLLLSVFLGLVFAWI
P.salD4         SSGFAPASYWVKAG-------------LILGSAIALEAYMLYAGKRLLPSIVLGWLFALI
I.galD4         GLFKPRPVASSIYG--------------LCVIFAIAASVACAPYAPVLAGIAVGTCWAQC
EhuxD4          GLFKPRPVASGIYG--------------LAVVAAIVACIACAPHAPVLSGIGLGSCWAQC
                             .              :                    .  :*

Ost809D4        GTGLQHTANHGGLAKSGFWNQFWGWLGNDVAIGKSSVEWRYHHMVSHHSYCNDADLDQDV
O.lucD4         GTGLQHTANHGGLAKSGFWNQFWGWLGNDVAIGKSSVEWRYHHMVSHHSYCNDADLDQDV
P.lutD4         GLNIQHDANHGALSRHSVINYCLGYA--QDWIGGNMVLWLQEHVVMHHLHTNDVDADPDQ
P.salD4         GLNIQHDANHGALSKSASVNLALGLC--QDWIGGSMILWLQEHVVMHHLHTNDVDKDPDQ
I.galD4         G-FLQHMGGHREWGRTWSFAFQHLFEG---LLKGGSASWWRNRHNKHHAKTNVLGEDGD-
EhuxD4          G-FLQHMGGHREWGVRYSFLLQHFFEG---LLKGGSASWWRNRHNKHHAKTNVLGEDGD-
                *  :** ..*   .                 :  .   *  .:   **   *  . * *

Ost809D4        YTALPLLRLDPSQELKWFHRYQAFYAPLMWPMLWLAAQFGDAQNILVDKASPGVEYKGLM
O.lucD4         YTALPLLRLDPSQELKWFHRYQAFYAPLMWPFLWLAAQVGDAQNILIDRASPGVEYKGLM
P.lutD4         K-AHGVLRLKPTDGWMPWHALQQLYILPGEAMYAFKLLFLDALELLAWRWE-GEKISPLA
P.salD4         K-AHGALRLKPTDAWSPMHWLQHLYLLPGETMYAFKLLFLDISELVMWRWE-GEPISKLA
I.galD4         ------LRTTPFFAWDP----TLAKKVPDWSLRTQAFTFLPALGAYVFVFAFTVRKYSVV
EhuxD4          ------LRTTPFFAWDP----TLAKKVPDWSLKTQAFTFLPALGAYVFVFAFTIRKYAVV
                      **  *                   .:      .                   :

Ost809D4        KLEVALYVLGKFLHFSLLLGVPAYLHGFANAIVPFIAYGAFGSFVLCWFFIVSHNLEALT
O.lucD4         KNEIALYLLGKVLHFGLLLGVPAYIHGLSNVIVPFLAYGAFGSFVLCWFFIVSHNLEALT
P.lutD4         RALFAPAVACKLGFWARFVALPLWLQPTVHTALCICATVCTGSFYLAFFFFISHNFDGVG
P.salD4         GYLFMPSLLLKLTFWARFVALPLYLAPSVHTAVCIAATVMTGSFYLAFFFFISHNFEGVA
I.galD4         KRLWHEVALMVAHYALFSWALSAAGASLSSGLTFYCTGYAWQGIYLGFFFGLSHFAVERV
EhuxD4          KKLWHELALMIAHYAMFYYALQLAGASLGSGLAFYCTGYAWQGIYLGFFFGLSHFAVERV
                             .     .:               :     .: * :** :**

Ost809D4        PIN-----LSKSTKNDWGAWQIETSASWGN--GFWSFFSGGLNLQIEHHLFPGCAHNLYP
O.lucD4         PMN-----LSKSTKNDWGAWQIETSASWGN--SFWSFFSGGLNLQIEHHLFPGCAHNLYP
P.lutD4         SVGPKG---SLPRSATFVQRQVETSSNVGG--YWLGVLNGGLNFQIEHHLFPRLHHSYYA
P.salD4         SVGPDGSITSMTRGASFLKRQAETSSNVGG--PLLATLNGGLNYQIEHHLFPRVHHGFYP
I.galD4         PS-----------TATWLESTMMGTVDWGGSSAFCGYLSGFLNIQIEHHMAPQMPMENLR
EhuxD4          PS-----------TATWLESSMIGTVDWGGSSAFCGYVSGFLNIQIEHHMAPQMPMENLR
                .               :       : . *.     . ..* ** *****: *
```

Figure S3. Multiple sequence alignment of FcElo6 with Δ6-elongasse from *Thalassiosira pseudonana* (TpElo6, AY591337.1) and *Ostreococcus tauri* (OtElo6, AY591335) [5]. Conserved amino acid residues are indicated with an asterisk, whereas conserved motifs are framed. The alignment was obtained using CLUSTAL W.



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FcElo6          ---------------------MDEYKATLESVGDAIIQWADPESQFTGFTKGWFLTDFTS
TpElo6          ---------------------MDAYNAAMDKIGAAIIDWSDPDGKFRADREDWWLCDFRS
OtElo6          MSGLRAPNFLHRFWTKWDYAISKVVFTCADSFQWDIGPVSSSTAHLPAIESPTPLVTSLL
                                      .   :  :..   *   :.. .:: .  .   *

FcElo6          AFSIALVYVLFVIIGSQVMKVLPAIDPYPIKFFYNVSQIMLCAYMTIEACLLAYRNGYTI
TpElo6          AITIALIYIAFVILGSAVMQSLPAMDPYPIKFLYNVSQIFLCAYMTVEAGFLAYRNGYTV
OtElo6          FYLVTVFLWYGRLTRSSDKKIREPTWLRRFIICHNAFLIVLSLYMCLGCVAQAYQNGYTL
                   :::.     :  *   :   .     : : :*.  *.*. ** : .   **:****:

FcElo6          MPCVGYNRDDPAIGNLLWLFYVSKVWDFWDTIFIVLGKKWRQLSFLHVYHHTTIFLFYWL
TpElo6          MPCNHFNVNDPPVANLLWLFYISKVWDFWDTIFIVLGKKWRQLSFLHVYHHTTIFLFYWL
OtElo6          WG-NEFKATETQLALYIYIFYVSKIYEFVDTYIMLLKNNLRQVSFLHIYHHSTISFIWWI
                     ::  :. :.  :::**:**:::* ** :::* :: **:****:***:** :::*:

FcElo6          NANVFYDGDIYLTIALNGFIHTVMYTYYFICMHTKDKKTGKSLPIWWKSSLTLLQLFQFI
TpElo6          NANVLYDGDIFLTILLNGFIHTVMYTYYFICMHTKDSKTGKSLPIWWKSSLTAFQLLQFT
OtElo6          IARRAPGGDAYFSAALNSWVHVCMYTYYLLSTLIGKEDPKRSNYLWWGRHLTQMQMLQFF
                 *.   .** :::  **.::*. *****::.    .... :*  :**   ** :*::**

FcElo6          TMMSQGLYLIIFGCESLSIRVTATYVVYILSLFFLFAQFFVASYMQPKKSKTA-ELGTLI
TpElo6          IMMSQATYLVFHGCDKVSLRITIVYFVSLLSLFFLFAQFFVQSYMAPKKKKSA-------
OtElo6          FNVLQALYCASF--STYPKFLSKILLVYMMSLLGLFGHFYYSKHIAAAKLQKKQQ-----
                  : *. *   .  .. .  ::   .* ::**: **.:*:  .:: . * :.
```

Figure S4. Codon-optimised nucleotide sequences. (**A**), Ost 809D6; (**B**), Ost809D4; (**C**) Fc ELO6.

A

```
1 ATGCGTGTGGAAACCGAAGACGATAATGTGCCAACTGTTACTGTGGGATTGTCAGAGGAG

 61 TCCGATGGAATGAAGGGAGCAAGGAACCCCGGAGCACGTGCTTGGAAGTCGACGTTGGAG

 121 CCGCACGCCGTGGCAAAGTCATTCGATCGTAGGTGGGTTAAGGTTGACGGAGTCGAATAC

 181 GACGTAACTGATTTCAAGCATCCCGGAGGATCAGTTATCTACTATATGCTTTCTAACACC

 241 GGAGCTGATGCCACTGAGGCTTTCAAGGAATTTCACTATCGTAGTAAGAAGGCCAGGAAG

 301 GCACTTGCTGCCCTCCCACAACGTGAGCCTGAAGACGCTTCGCCAGTCGAGGATGCCAAT

 361 ATGCTCAAGGACTTCGCAAAGTGGCGTAAGGATTTGGAGAGGGAAGGATTCTTTAAGCCA

 421 AGTCCTGCTCACGTGGCCTACCGTTTCGCCGAACTCGCAGCTATGTTTGCTTTGGGAACT

 481 GCCCTTATGTATGCACGTTGGCATGCTACGTCTGTCTTCGTAACAGCCTGTTTCTTTGGA

 541 GCAAGGTGTGGATGGGTGCAACACGAGGGAGGACATTCTTCCTTGACCGGATCCATCTGG

 601 TGGGATAAGCGTATTCAGGCATTCACTGCTGGATTTGGACTTGCCAGTTCGGGAGACATG

 661 TGGAACCTCATGCACAATAAGCACCATGCAACGCCACAAAAAGTTAGGCATGATATGGAC

 721 CTCGATACCACTCCTGCAGTGGCTTTCTTTAACACAGCTGTTGAGGAAAATCGTCCTAGG

 781 AAGTTCTCTAAGTTGTGGCTTCGTGTCCAGGCCTGGACCTTTGTGCCCGTTACTTCCGGA

 841 TTGGTACTCTTGGCATGGATGTACCTTCTCCACCCGCGTCATATCGCTCGTAGGAAGAAC

 901 TATGAGGAAGCCGCATGGATTGTGGCTGCCCATGTTATCAGGACCTCCGTCATTAAGGCT

 961 GTAACGGGATACAGTTGGATCACATGTTATGGACTCTTCTTGTCGACTATGTGGGTCTCA

 1021 GGATGCTACCTCTTCGCTCACTTTTCAACGTCTCACACACATTTGGACGTGGTTCCATCT

 1081 GATAAGCACCTTTCCTGGGTGCGTTACGCCGTTGATCATACCATCGACATTGATCCTTCC

 1141 AAGAGTGTCGTAAACTGGCTCATGGGATATTTGAACTGTCAGGTTATCCACCATTTGTTC

 1201 CCCGACATGCCGCAATTTCGTCAGCCCGAAGTCAGTCGTAGGTTCGTATCGTTTGCCAAG

 1261 AAGTGGAACCTTAATTACAAGGTCATGTCTTACTATGGAGCCTGGAAGGCAACCTTCGGA

 1321 AATCTCAACGAAGTCGGAAAGCACTACTACATCCAAGGAAGTCAAATCACAAAGAAGACG

 1381 GTTTAG
```

Figure S4. *Cont.*

B

```
1 ATGCCAACTACTCGTTCTCGTGCTCGTGTTACTACTCCACCTCGTGAAACTCCTACTCGT

 61  GCTAATACTGTTGCTGCTTTAGATCCAGAACGTAAATATACACGTATTCGAGGTGTTGTA

 121 TATGATGTTACTGATTTTGCTAGTCGACATCCAGGTGGTGCACAATTATTATCTTTATGT

 181 GTTGGTCGTGATGCTACAATTTTAGTAGAATCACATCATTTACGACCAGAAGTTGTACAA

 241 AAATATTTAAAAACATTACCTGTTGTAGAAGGTGCTGCTGGTGCATTTGGTCCAGAAGAA

 301 ACTTTTCCAAAACCTTTAGATAGTGATTTATATCGTAAAATTCAAGGTCGTGTTCGAAAA

 361 GAAATTGTAGAACCATTAAAAATGACACGTGGTCGAGAACCTCATGGTCGTGGTTGGTGT

 421 GTTTTAGATGCTGGTGTTGTATTAGCTTTCTTTGCTTTTGCATTAGGTGTTTATTGGAAA

 481 ACACCAACTGTAGCTACTGGTTGTTTATTAGGTTTAGCAGGTTATTGGTCTGGTACAGGT

 541 TTACAACATACTGCTAATCATGGTGGTTTAGCAAAATCAGGTTTTTGGAATCAATTTTGG

 601 GGTTGGTTAGGAAATGATGTTGCTATTGGTAAATCAAGTGTAGAATGGCGTTATCATCAT

 661 ATGGTTTCACATCATAGTTATTGTAATGATGCTGATTTAGATCAAGATGTTTATACAGCA

 721 TTACCATTATTACGTTTAGATCCTTCACAAGAATTAAAATGGTTTCATCGTTATCAAGCA

 781 TTTTATGCACCTTTAATGTGGCCTATGTTATGGTTAGCTGCACAATTTGGTGATGCTCAA

 841 AATATTTTAGTTGATAAAGCAAGTCCAGGTGTAGAATATAAAGGTTTAATGAAATTAGAA

 901 GTTGCTTTATATGTATTAGGAAAATTTTTACATTTTTCTTTATTATTAGGTGTTCCTGCA

 961 TATTTACATGGTTTTGCTAATGCAATTGTACCATTTATTGCTTATGGTGCATTTGGTTCA

 1021  TTTGTTTTATGTTGGTTTTTCATTGTAAGTCATAATTTAGAAGCATTAACACCAATTAAT

 1081  TTATCTAAATCAACTAAAAATGATTGGGGTGCTTGGCAAATTGAAACTAGTGCATCTTGG

 1141  GGTAATGGTTTTTGGTCATTTTTCTCAGGTGGTTTAAATTTACAAATTGAACATCATTTA

 1201  TTTCCTGGTTGTGCTCATAATTTATATCCAAAAATGGTTCCTATTATTAAAGAAGAATGT

 1261  GAAAAAGCAGGTGTTACATATACTGGTTATGGTGGTTATTTTGGTTTATTACCAATTACT

 1321  CGTGATATGTTTGCTTATTTATATAAAATGGGTCGTCAATCTAAAAAATCTGCTTAA
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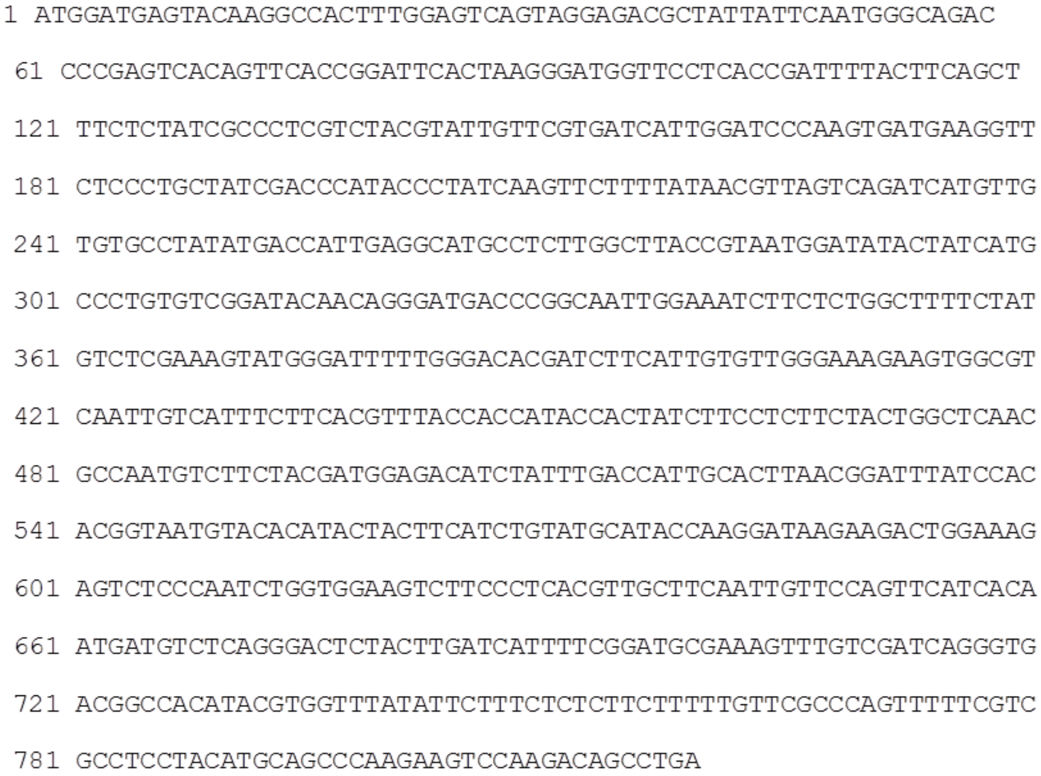
Figure S4. *Cont.*

C



```
1 ATGGATGAGTACAAGGCCACTTTGGAGTCAGTAGGAGACGCTATTATTCAATGGGCAGAC

 61 CCCGAGTCACAGTTCACCGGATTCACTAAGGGATGGTTCCTCACCGATTTTACTTCAGCT

 121 TTCTCTATCGCCCTCGTCTACGTATTGTTCGTGATCATTGGATCCCAAGTGATGAAGGTT

 181 CTCCCTGCTATCGACCCATACCCTATCAAGTTCTTTTATAACGTTAGTCAGATCATGTTG

 241 TGTGCCTATATGACCATTGAGGCATGCCTCTTGGCTTACCGTAATGGATATACTATCATG

 301 CCCTGTGTCGGATACAACAGGGATGACCCGGCAATTGGAAATCTTCTCTGGCTTTTCTAT

 361 GTCTCGAAAGTATGGGATTTTTGGGACACGATCTTCATTGTGTTGGGAAAGAAGTGGCGT

 421 CAATTGTCATTTCTTCACGTTTACCACCATACCACTATCTTCCTCTTCTACTGGCTCAAC

 481 GCCAATGTCTTCTACGATGGAGACATCTATTTGACCATTGCACTTAACGGATTTATCCAC

 541 ACGGTAATGTACACATACTACTTCATCTGTATGCATACCAAGGATAAGAAGACTGGAAAG

 601 AGTCTCCCAATCTGGTGGAAGTCTTCCCTCACGTTGCTTCAATTGTTCCAGTTCATCACA

 661 ATGATGTCTCAGGGACTCTACTTGATCATTTTCGGATGCGAAAGTTTGTCGATCAGGGTG

 721 ACGGCCACATACGTGGTTTATATTCTTTCTCTCTTCTTTTTGTTCGCCCAGTTTTTCGTC

 781 GCCTCCTACATGCAGCCCAAGAAGTCCAAGACAGCCTGA
```

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