

Supplemental Figure S6

Genomic sequence of the *V. carteri* *phG* gene

TTGCCCTTCCGAAGCGGCAGGAAGCTACCGACCTGAACATGCTTTTAGGACTTTCAATCTGTGCACCC
GAACACACAAGTTACAATCAACGCTGTAATGCGGGTAAGTTAATAATTAATGCATTTGTCAAGCAATC
GGTGTTTGACATCCGTGATAAAGTCTCTTCAGAATCTGCAGCCCGAGTGTTCAATTTGTTTCAATAAAA
CTTGTGAAAAGTGTATGAATGTGTCTATTTGGCATGTACTTCTGTGTTAATGATACAGCCGGTGATAC
GCGTTTGATAACCACTCGTTATCCGGAACAATCGACCCGTATCGACATGATGTAGATGTCTGGGATCG
CTGATGGATTCCCCAAAATTCTTCTGTTGCTTATCTTCAGAACAAAGTACTTCAATCTTCTATGCTAG
AAATACCAGTGCTCAACGAATGCTCCTGCCTGCCGCCACCACATCTCGCTGTATGTGTGCGCAAAGGCG
GGATCCGCATATTGAACAACACCTTTCTCAATTGACTCCAAGCACCATGTTGCCAATATATTTATTC
AGACATTGCGATATATACTCCAAGGCAAGGAAACGAACGGCATCAATGTCAAGTGCGCTAATGCACGC
ACGGGTCGCGAGCGCTACAATGCTGACGAGCCCATACTTCAATCAGGAGTAAGCGACGAAAGTGAGGA
ATATCGACTAAGCGATGACAGTGAGAAATCGTTAATTGTGCATAACAAGCGTGATTCCCGCTTGAAGG
GTTGTAGCTGCATCTAGCTTTTTGCCCCTGGCAGCAGATGGCAAATATCTACCATCGGCTGTCAAGTA
AATACGGTTTTTGTGCGGGGATTTAAAGTAACGAAAGGTTCAAAGGAACGGAAGGAGCTACACATTGGGC
TGCACGCGACTGATTTCAACCAGCTCCATTGTGCTACTGTACGTTCAAAGTAGTCTGAAGTAAAGCTG
ACTATAAATACGCGGTTGCCAATTATAC**GTTCGAC**ATACTAATTGGGCA**CATAGAGGGCCTAC****ATGCGA**
ACACCAATGAGGAATATACTGCTGGCTGCTCTTTGCGTAGTCGCCGTATTCTCGTAAGTGTCGTTGCT
TACCTTGCTAGGGCCAGCTGCAGGCTTCGATGTACAAGCATGTAGGGTTCGCAGGCTTATTCTTAAAC
GTTTACCTACCTTCTGAGCCATGAGGAGTCGTAGCTTTAATAGCCATGCTGCAATCCGTTTGGCTTAC
GTCGCTTTGGCGGGCAGGGCGCCAGTATCACCCCGTGTGCTTGATCGCTGCGGCTCCCCCATTCTTG
CGAAATTCACCATCATATTTGTAAATGATTGATGACTTGCTGAATCTCTTGCCACCTTGCGCTTATTT
TCCAATCTGCAG**GGCGTCGCACGCGCTGAGTAGTCCGCTGTCGCCCCCGCCGACAAGATACCAGGCAT**
TTCTTACTGCGCAAAATGCGTCGCTTTGGAGCCTATATACCGTCTAAAGCCTGATTTTGCCGGATTT
GGAAATCGCACCTTCTGCTTCACGCTGGAAGTGAATCCTCTCAATGCCGACTTCATGTGCAAGAATGC
ATTAATCTACAAGATGGATGTGAGTATATATCAATTGAACATGTGTTGATGTAGCGCAACTAGCACTT
CGGGCGGTTCTCGAAATCTAGCAGCCTTTTCGCGTTACGGTTGTGCAACGTTAAAGCTTTAGTCAGTCA
CGAGGGCGCGCAACTGTGTGTCACTCCATTTCGAGCAGATTTACCTTGCTGCTTTCATGACATA
GAACATAAGAAGGGTTATCTACTTCCATTTTTTATTATCGTTAACAGCGTTCCCCGGCGAACCCGCAGA
TGCTTCTCAACAAAGGGTGCGGAAGGGATGTTAACGTCAAGGCTTTTCGTAAATGGCGTCTTCACAAGG
AGCTTCACAGAATCTCCACGTTCTGCCGCAAATGGGACTGTGATATTGAACTGAACGATCTGACCGC
GCGACACCTGGGTATCAACAGCAATGGCGCCAGGATTTGCCTTACTATATTGAATGGGGGCAAGGGCA
ACTGCACCACTTTGAGGTCGCTCTGTGCAGACCCTAAGACCACCAACTTCAGAAAGGATAACAACGGC
ACTTACAGAAATACAAATTCCCCAAGAGTGCATGGTTGCGCTATTTCGCCGGGATCGACAGTGGCTCCGA
CCGTACCTGCTGCGACCCCGGTTCTCCCCCATCTCCAACGCCGCCCGCCCTCCTCCAGGGAATTGCA
CGGAGGAGAAGGTCTGTGTCTATCTGACCTTTGGGTTCCGCGAACCG**GACGTC**GCCTTCCCCAACGGC
ACCTGCAATAATTTGGCCAGCCAGATACAGTTTCGACCTCCTCAACTCAAGCGCATCCTACATCTTGCA
GCCCCCGGTAGTTCCACAGATCACTTGCACAGCAGACTTTATCAAAGTTTGCTTAAATTTGGACTTGC
ACGCTAACGCTACAGAGCTGCATTCCGTGGTTGGTGAAGTGGCGGTCCCTGGCTGAATTACGCTCAC
AACTCCACGTGTGCGGCAAGTCGCTCCAACCTACAGCCTACAATTACGGTCGGAGGGGATGGCGACTG
GTCGACTGGCAACGTCTCGTTCCGTTGTTTCAATGCGTCAACTGAAACCAAGTGCCAAGGGCCCTCGA
AGAAATCATGCAAGTGAGTCGAGCAAACCTGGAGGAGGGGGACAAGTATTGCGTGGCGGTGGGGAGTA
AACATGTCTGGCGTTGATCTAATGTGGGATTGCATGCTCGACGCGGATGCATGCACGCATCCACGTAC
GTGTCAGCAGCTACATCTTCTGAGCTACTGGTTTGAATTGGATTTTAGCAGCTTTGTGCCCTCACAT
GATTATCCTTCCAGCTGTATCCCTCTGCTCTCGCCACCTATCCCTTTCCCTCCTTCTCCTTCTCCT
CCGCAG**CTGCAATATGGCGAGGAACATCACCCCTTCGCCGCCTTGCCGACTATGAGCGGTCCCTTCA**
CGGGCCGCAAGAACACGAAGCTGTACTGCTTCAACATCACCGTCGTGAAGCCCATCGAGCCAAATGTG
GGTCGACGCTCGCTGGCGCCCGGTACACCGCATGATAGCATGTGCATGTCCTGGTTGATGTATGT
ATGTATGTATGTGGCCATCTACTGGCTGCGACACGAGCACAGTAGTAGTGCCACATTGACGGCTACAT
CGATTACGCTGTACAGATGTCTAAATGGTGCATGCGGCCACATCTTCTCCAGTAGCACTCCATTAC
GGTTCCCTTGCTATCCAATCCTATCCCTCGCATATCCCCCTTTACAG**AGCACCTGCGGTAAAAGCAA**

SaII, start

AatII

SaII

TGTGCTCGATAAGGTCATCATCTGGGCCAACGACACCAGTTTTTACCGCAGCAGCATCAAGTCCATCG
 CTCTCTACGCTGCGGGCGACACCACCGGAAGTATGTCCCGCCGAGCTGGAACTCGGATAGACAGGAG
 GTGAAGGCAACCAAGATTGGCTGGACTAAGGATAAGGCGAACGGCGGCCCATCTGCCTGGAGCTGGA
 CCAAACGTC AACCTGGCTGACTTTTGCATATGGCGGGGTCCCAAGCAGAAGA ACTCTTGCATGTAAG
 GGCTGGGGATTTATTTGGGGGTTGCCTGCATGCTTGTGCATGCAGTGTGCATGCATGGCGGGATGTGA
 GTGTGCGCGAACTAGGCGGCACTCGGTCGCCATCCCGGCTGCAGAAATGCAGGCATGCACCTAGCTAG
 ACTATTTACGCGTGCTTCCTTGCACATGGTTGAAGAGCTCTCCAATGGCACCCCTAGCCTTGCCTAGC
 TTAGCTTTTCTACTGCTTAGAGGCGCCTCTGGGCCGAGCGTCCTGTCTACCTACCTTATTGTGCGTCC
 CCCATGCCCATGCCCATCTTGCTGAATGCAGGGTTTTACTTTTCGATACATCCTATAGATGCTGCCCC
 ATGTACCGGCCGATGGCGCTTACTACGTAGATGCGTGCCGTACAGCTGGCTAGTCTTGTGCAGAGCA
 TGCACGTTGGATCAGCTGACCTGGTGAGGCGAGGAAGCCCCATCTAAGGTTGTGCGATTGGGCGATTTG
 TGTGTTGCGTGGTAGGATGTAGAATATTTGGTTTGCGAATGTGCTTTGGATAAAATCCATGTTGGTAG
 TTCTTAACTTGTGCACGATGCTGCCCGTGAACAGGGCAGGTAAGGTTGTGTGTTTGAAGTGTTTGG
 AATTACATGGAGGTTATCTCTAAGTTTCAGTGATTAACAGTGCTTAAACAGTCATGTCTGGTTTGC GG
 CTGTTTGCCTGTTCTTACCGGCCGTGTTGCCTGCTGGACCTGCCGCTGCTGCGCAGCC
 TACCCGTGCGATTTTCGCTAGGAAGAATTTCAATTCGTTGTGCAGGTGCGCTTTCTTACTTTTTCAATT
 CTGTCTGTCAGAGGTGCTTGCTTCCTTGCAGCAGGTGGAACCTGATCACCTCGCCGCCGTTTCGATCAT
 TTAAATACCCCTACGTCGCGCAATGATGTGGGGTATCGTAGGCTGCTTTATGCAGCCTCGTTCGCTT
 ATTTGATCGCACCTGCGATTGTAGCAGCTTCATTCATTAGCTGAATCAAGTGAGCGAGCACGCTCGGT
 CGGTCAGGTTTTATAACATGCTGCTTGCTGCTCAAGCTTTTGCTAATATTGTATAGCGCAGGTACGCT
 TTGCTGATTGCTTCTGGGGTCGCCCTAGTTCGGGGCTACTGCTTGCATGCTGTGTGTGGTGAGATAGCA
 GGCTGGCTGCCATTACTGCGGAGTACGCAGCTCTTCAGCCATATATTCATAGTTAGGACGAATTGATT
 AGCCAGCCATGGCGATGTCAGTTCAGTTC AATGTCCATTTTCATACGCGCCTTGCGTTTTGTTTTATG
 GCTGTGAGTCTGCGTGATCACCTTATGTTAGATCGATGCATCCTGCAATCGTTTTGTGCGTTGTAACA
 CTGCGAGCGCGACAGGCAGAGTGTTAGGCGTATTGGCGAGAAATGTCCTGTTTCGGTTAGGGCGGTTTG
 GTTAGGGCAGTTTCTAAAGATCCTCTGCCGGCTGATGGAATATCGGTGTTTATGTGTAGGAAATTTTC
 TCCCGCCCGCCATCCATCCCCAACATTACCGTGTAACATAATCCAACAATCCTTGGCCCATCCTATCC
 TATCCAAGCAGGTCTTCAAGCATACTTTTTTCATCTCCTTCACACTGCAGCCGGCAGCAGGCATGATTC
 CTGCGAAC

stop

NcoI

The sequence depicted here corresponds to the 5244-bp genomic fragment utilized in plasmid pPhG-YFP. The *phG* gene (former common name *phV47*) (von der Heyde and Hallmann, 2020) is located on scaffold 1 (nucleotides 2224937 to 2230180) of the *V. carteri* genome version 2.1 (Prochnik et al., 2010) in Phytozome 12.1.6 (Goodstein et al., 2012) and has the gene ID Vocar.0001s0298. The start codon is at nucleotide position 2225951-2225953 on the forward strand. The gene structure is indicated as follows: Coding sequences are shown with blue background, UTRs with green background and the promoter region with grey background. Start and stop codons are highlighted (violet font). The 5' UTR is just 14 bp in length, while there is a quite long 3' UTR of 1,168 bp. The restriction sites that are shown in Supplemental Figure S4A and B are marked (bold, underlined).

References

- Goodstein, D. M., Shu, S., Howson, R., Neupane, R., Hayes, R. D., Fazo, J., Mitros, T., Dirks, W., Hellsten, U., Putnam, N. et al. (2012) Phytozome: a comparative platform for green plant genomics. *Nucleic Acids Res.* **40**, D1178-1186.
- Prochnik, S. E., Umen, J., Nedelcu, A. M., Hallmann, A., Miller, S. M., Nishii, I., Ferris, P., Kuo, A., Mitros, T., Fritz-Laylin, L. K. et al. (2010) Genomic analysis of organismal complexity in the multicellular green alga *Volvox carteri*. *Science* **329**, 223-226.
- von der Heyde, B. and Hallmann, A. (2020) Targeted migration of pherophorin-S indicates extensive extracellular matrix dynamics in *Volvox carteri*. *Plant J.* **6**, 2301-2317.