Supplementary Fig. S1. Alignments of IsiA and Pcb protein sequences. The black and red arrows indicate the binding sites of the potential and chosen primers to amplify isiA genes, respectively.

		isiA33F (YDWWAG)	isiA348R (IWHTLR)
isiA	IsA_Syn_CC9605_Synce9605_1590 IsA_Syn_WH8109_Sync8109_1040 IsA_Syn_WH8109_Sync8109_1040 IsA_Syn_MTS9504_R512765 IsA_Syn_MTS9508_R508845 IsA_Syn_CC9311_Synce311_2306 IsA_Syn_CC9311_Synce311_2306 IsA_Syn_CC902_Synce902_108420 IsA_Syn_C107_BL07_R506100 IsA_Syn_C107_BL07_R50610 IsA_Syn_D17_B0107_K6	MOSYGSSSVYTYDIWAAGNAG ² VAKRSGSFIÄAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSSVYTDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSSVYTDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSSVYTDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSSVYTDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSSVYDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSVYDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSVYDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSVYDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSVSVDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDG MOSYGNSVSVDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDS MOSYGNSVSVDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDS MOSYGNSVSVDIWAGNSG-VAKRSGSFIAAHAAHAGLIMFWAGAFTLFELARYDS	L PAGLEGERA KERNEL VY SALA SALA SALA SALA SALA SALA SALA SAL
pcb	Pob./HILCJ_CLI4475981 Pob./HILCJ_CLI4475981 Pob./HILCJ_CLI4475981 Pob./HILCJ_CLI4475981 Pob./HILCJ_CLI4475981 Pob./HILLAMM255346 Pob./HATLIA,MM255346 Pob./HATLIA,MM255348 Pob./HATLIA,MM255348 Pob./HATLIA,MM253348 Pob./HATLIA,MM253348 Pob./HATLIA,MM253348 Pob./HATLIA,MM253348 Pob./STL2070,0783 Pob./STL2	VGWAGASG - VANR SGR F AAHVAHAGL VFWAGAF TF FELSREDD YGWAGASG - VANR SGR F AAHVAHAGL VFWAGAF TF FELSREDD WGTYGNDT YGWAGASG - VANR SGR F AAHVAHAGL VFWAGAF TF FELSREDD WGTYGNDT YGWAGAG - VTWK SGR F AAHVAHAGL VFWAGAF TF FELSREDD DYTYGWAGASG - VANR SGR F AAHVAHAGL VFWAGAF TF FELSREDD WGTYGND YTYGWAGAG - VTWK SGR F AAHVAHAGL VFWAGAF TF FELSREDD DYTYGWAGASG - VANR SGR F AAHVAHAGL VFWAGAF TF FELSREDD WGTYGND YTYGWAGAG - VTWK SGR F AAHVAHAGL VFWAGAF TF FELSREDD DYTYGWAGASG - VTWK SGR F AAHVAHAGL VFWAGAF TF FELSREDD WGTYGND YTYGWAGASG - VTWK SGR F AAHVAHAGL VFWAGAF TF FELSREDD WGTYGND YTYGWAGASG - VTWK SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWAGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWAGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWAGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWAGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWAGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGAS - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAAT TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAF TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAAT TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAAT TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL MFFAGAAT TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL AF FAGAAT TF FELSREDD WGTYGND YTYGWYGASG - VTWR SGR F AAHAAHGL AF FAGAAT TF FELSREDD WGTYGND YTYGWYGAAAGA - YWR SGR F AAHAAHGL AF FAGAGAT TF FELSREDD WGTYGND YYGWYGAAAGAG - YWR SGR F AAHAAHGL AF FAGAGAT TF FELSREDD WGTYGND YYGWYGAAAGAG - YWR SGR F AAHAAHGL AF FAGAGAT T	UP MIGNOR LIVE PHILATICS GEPANGE - VMGDT KPV AVA VPLV SKVLANGGL LIST LIPON LUPON - DVGA AKKEN I PMGNOP LIVE PHILATICS GEPANGE - VMGDT KPV AVA VPLV SKVLANGGL LIST LIPON LUPON - DVGA AKKEN I PMGNOP LIVE PHILATICS GEPANGE - VMGDT KPV AVA VPLV SKVLANGGL LIST LIPON LUPON - DVGA AKKEN I PMGNOP LIVE PHILATICS GEPANGE - VMGDT KPV A AK VPLV SKVLANGGL LIST LIPON LUPON - DVGA AKKEN I PMGNOP LIVE PHILATICS GEPANGE - VMGDT KPV A AK VPLV SKVLANGGL LIST LIPON LOPON - VGA AKKEN I PMGNOP LIVE PHILATICS GEPANGE - VMGDT KPV A AK VPLV SKVLANGGL LIST LIPON LOPON - VGA AKKEN I PMGNOP LIVE PHILATICS GEPANGE - VMGDT KPV A AK VPLV SKVLANGGL LIST LIPON LOPON - VGA AKKEN I PMGNOP LIPON - VMGDT KPV A AKKEN I PMGNOP LIPON - DVGT KPV AKKEN I PMGNOP LIPON - DVGT
isiA	ы4.Syn_CC9605_Syncc9605_1590 ы4.Syn_WH8109_Sync3109_1040 ы5.Syn_WH8109_Sync3109_1040 ы4.Syn_WH5500_K512765 ы4.Syn_C1765 ы4.Syn_C17550 ы4.Syn_WH8020_WB44_08420 ы4.Syn_WH8020_WB44_08420 ы4.Syn_BL107_BL107_K50850 ы4.Syn_BL107_BL107_K50850 ы4.Una1KypeA.10C_43_52019 Pab_WH391_P301_P512290 Pab_MH391_P301_P512290	SDKK LTF LGHLIF EGGAN AFV WARNEG YD A GAVRY LENI DGWWGY DDFKLTF LGHLIFEGGAN AFV WARNEG YD ALGAVRY LENI AGNA DDFKLTF LGHLIFEGGAN AFV WARNEG YD ALGAVRY LENI DGWWGY DDFKLTF LGHLIFEGGAN AFV WARNEG YD ALGAVRY LENI AGNA DDFKLTF LGHLIFFAN AFV AGNA DDFKLTF LGHLIFFAN AGNA DDFKLTF LGHLIFFAN AFV AN ANNE	10 AND LESS LEDVWGGHAVLAF LLT LGGWH LLSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSS LEDVWGGHAVLAF LLT LGGWH LLSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LLSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LSYSSLAG VALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LSYSSAG ALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LSYSSAG ALWGFYT ALWCAONT TYN 10 AND LSSSSF AND PEGES PEKKYL LYNG ISS LSYSSAG ALWGFYT ALWCAONT TYN 10 AND LSSSSF AND AND LSSSSF AND TYN ALWCAONT TYN 10 AND LSSSSF AND AND LSSSSF AND TYN ALWCAONT TYN 10 AND LSSSSF AND AND LSSSSF AND TYN ALWCAONT TYN 10 AND LSSSSF AND TYN ALWCAONT TYN ALWCAONT TYN 10 AND LSSSSF AND TYN ALWCAONT TYN ALWCAONT TYN ALWCAONT TYN 10 AND LSSSSF AND TYN ALWCAONT TYN ALWCAO
pcb	PeaA_HNLC_5L3473934.1 PeaA_HNLC_5L347393.1 PeaA_HNLC_5L347393.1 PeaA_HNLC_5L347393.1 PeaA_NATLA_NATL_15561 PeaB_NATLA_NATL35561 PeaB_NATLA_NATL35561 PeaB_NATLA_NATL35561 PeaB_NATLA_NATL35566 PeaH_NATLA_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL4_NATL35566 PeaH_NATL45566 PeaH_NATL45666 PeaH_NATL4566 PeaH_NATL45666 PeaH_NATL45666 PeaH_NATL45666 PeaH_NATL45666 PeaH_NATL45666 PeaH_NATL45666 PeaH_NATL45666 PeaH_NATL45666 PeaH_NATL456666 PeaH_NATL456666 PeaH_NATL45666666 PeaH_NATL45666666666666666666666666666666666666	DEPORT FLCHILLEGAN OF WAARNE VDAALGANGVY VL-ALAK	IG10b111014 D31LE1VMGG IG10b11102LE1VMGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FUNGG IG10b11102LE1VLGG FU
isiA	biA Syn, CC9605, Sync9605, 1590 biA Syn, WH8103 Synca310, 1140 biA Syn, MH8103 Synca310, 1140 biA Syn, MH8300, Bi 1735 biA Syn, MH7350B, BiO8845 biA Syn, CM3502, Sync3902, 1100 biA Syn, CM302, Sync3902, 1100 biA Sync, Sync3902, 1100 biA	WELYGDPLKLNFAFSDYFDT-AL-EGGA	MALR GMGEN FKRVS EALDNMGNSKVSA WHALR GMGEN FKRVSEALENMGNSKVSA WHALR GMGEN FKRVSEALENMGNSKVSA UMHALR GMGEN FKRSVVNAFE SMDKAK IN WHALR SMGEDFKS SVVNAFE SMDKAK IN WHALR SMGEDFKS SVSAFD SMD TMKVN FWHALR SMGEN FKSVSSALE TMD TAKVS WHALR SMGEN FKSVSSALE TMD TAKVS WHALR SMGEN FKSVSSALE TMD TAKVS WHALR SMGEN FKSVSSALE TMD TAKVS WHALR SMGEN FKSVSSALE TMD TAKVS
pcb	Peds/Hit C2 CE194799511 Peds/HIT052 CE194799511 Peds/HIT052 AMM71902 Peds/HIT052 AMM71902 Peds/HIT14/MA253361 Peds/HIT14/MA253361 Peds/HIT14/MA253361 Peds/HIT14/MA253361 Peds/HIT14/MA253361 Peds/HIT16/HIT05216 Peds/HIT167 Peds/HIT0701169 Peds/S120/Pro_1169 Peds/S120/Pro_18	TEFFGEPLELKFS ISP YWYDT-YDL PDGSYTSRAWLANVHYYGFGFFIOGH VEFFGEPLELKFS ISP YWYDT-YDL PDGSYTSRAWLANVHYYGFFFIOGH TEFFGEPLELKFS ISP YWYDT-YDL - DGCAHTARAWLANVHYYGFFFIOGH TEFFGEVLQLKFDFAPYFYDTDPSL-AAGAHTARAWLANVHFYLGFFFIOGH TEFFGDVLQLKFDFAPYFYDTDSSL-ATGAHTARAWLANVHFYLGFFFIOGH TWFGGVLQLKFDFAPYFYDTDSSL-ATGAHTARAWLANVHFYLGFFFIOGH TWFGGVLQLKFDFAPYFYDTDSSL-ATGAHTARAWLANVHFYLGFFFIOGH TWFGGVLQLKFDFAPYFYDTDSSL-ATGAHTARAWLANVHFYLGFFFIOGH TWFGGVLGKFGSSPWIDT-CN	UMALRALGEDEKRYTNAISNIDSATYTLKD UMALRALGEDEKRYTNAISNIDSATYTLKD UMALRAMGEDEKRYTNAISNIDSATYTLKD UMALRAMGEDEKRYGKAEDNMENAKITNG UMALRAMGEDEKRYGKAEDNMENAKITNG UMALRAMGEDEKRYGKAEDNMENAKITNG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAEDNMENAKITAG UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN UMALRAMGEDEKRYGKAETGAISTNN

Supplementary Fig. S2. Results of mapping our PCR primer pair isiA33F & isiA654R and qPCR primer pair isiA33F & isiA348R to a collection of marine Synechococcus and Prochlorococcus genomes (Supplementary S3). The red and green arrows point out the forward and reverse primer binding sites on the genome, respectively. Those Synechococcus genomes with no primer bindings suggest the absent of *isiA* gene, and none of the Prochlorococcus genome generated binding products of the isiA specific qPCR primers (isiA33F & isiA348R).



Supplementary Fig. S3. Neighbor-joining phylogenetic tree of *isiA* gene sequences retrieved from 50 m depth of station SIO, using 3 different primer pairs designed for marine *Synechococcus isiA* genes (see Results). The primer pair (*isiA*33F/*isiA*654R) further used in this study recovered the highest *isiA* diversity among all investigated primer pairs.



* isiA33F and reverse primer pairs *isiA*654R, *isiA*933R and *isiA*1053R

Supplementary Fig. S4. Normal Q-Q plot of the standardized residuals of the regression model Log(isiA:cell) = -0.73 [DFe] + 0.05 [NO3] - 0.33.



Supplementary Fig. S5. Relationships between the relative abundance of *isiA* (expressed as Log(isiA:cell)) and (a) [DFe], (b) [NO₃], (c) temperature, (d) chlorophyll *a* and (e) salinity across all 14 stations (n=24).



Supplementary Fig. S6. Vertical distribution of the *isiA*:cell ratio, *Synechococcus* abundance and *isiA* gene abundance at stations EEP1, SCS, SIO and NIO. Red symbols denote individual measurements at the different stations and black symbols represent the average values over all 4 stations.

