**Supplementary Fig 1.** Strategy for generation and analysis of strains WT-RCS3 and NblR\(^{D57A}\)-RCS3. (A) The integration of the CS3 cassette (hatched bars) in the intergenic region (solid bar) between \(nbIR\) and the downstream ORFs Synpcc7942_2306 (open arrows) by homologous recombination is shown schematically. Flanking chromosome regions are represented by dotted lines and plasmid sequences by a continuous line. Depending on specific crossover sites two alternative \(nbIR\) alleles can be generated. Mutant \((nbIR^{D57A})\) and wild type strains differ at the indicated \(PvuI\) site. (B) Schematic representation of the allele structure in strains WT-RCS3 and NblR\(^{D57A}\)-RCS3. Relevant \(PvuI\) sites are shown. Positions of primers used to verify allele structure are indicated by black arrows (C) PCR analysis of WT-RCS3 (lane 1), NblR\(^{D57A}\)-RCS3 (lane 2) and *Synechococcus* sp. PCC7942 (lane3) using primers NblR-1F (1F) and CS3-2R (2R). (D) \(PvuI\) digestion of the PCR fragment generated with primers 1F and NblR-1R (1R). Lane numbers as in (C). M: size marker λ HindIII+EcoRI. L: DNA 100 bp ladder (Fermentas).