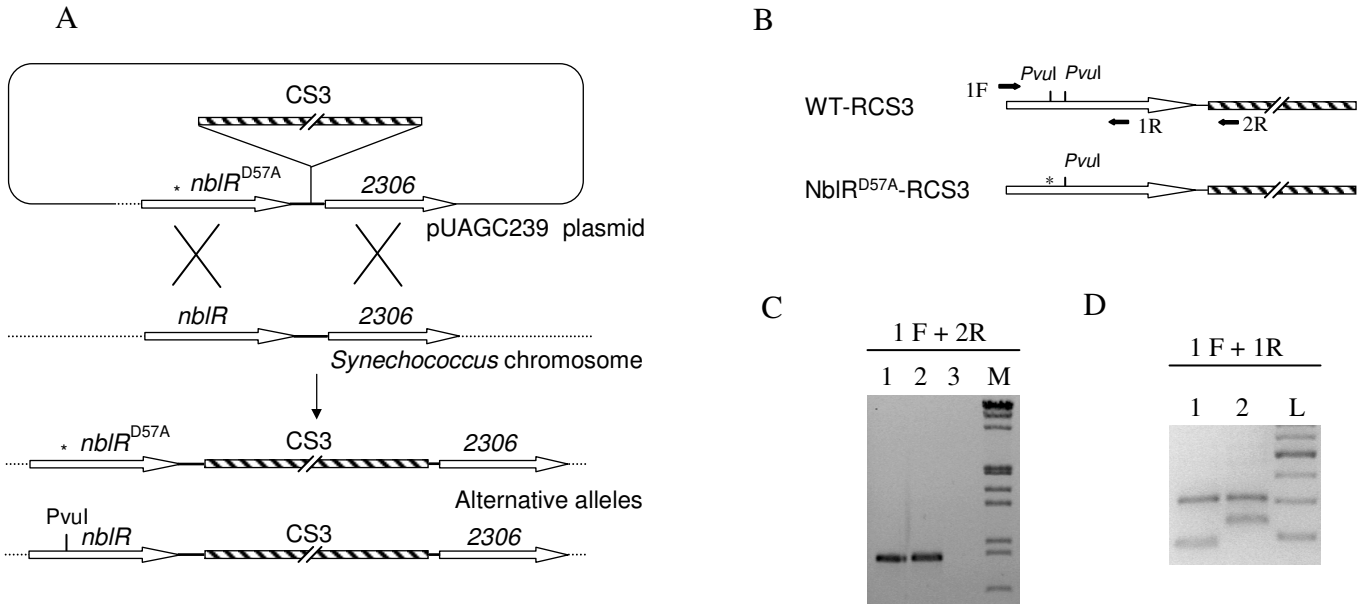

Supplementary Fig 1. Strategy for generation and analysis of strains WT-RCS3 and NblR^{D57A}-RCS3. (A) The integration of the CS3 cassette (hatched bars) in the intergenic region (solid bar) between *nblR* and the downstream ORFs Synpcc7942_2306 (open arrows) by homologous recombination is shown schematically.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