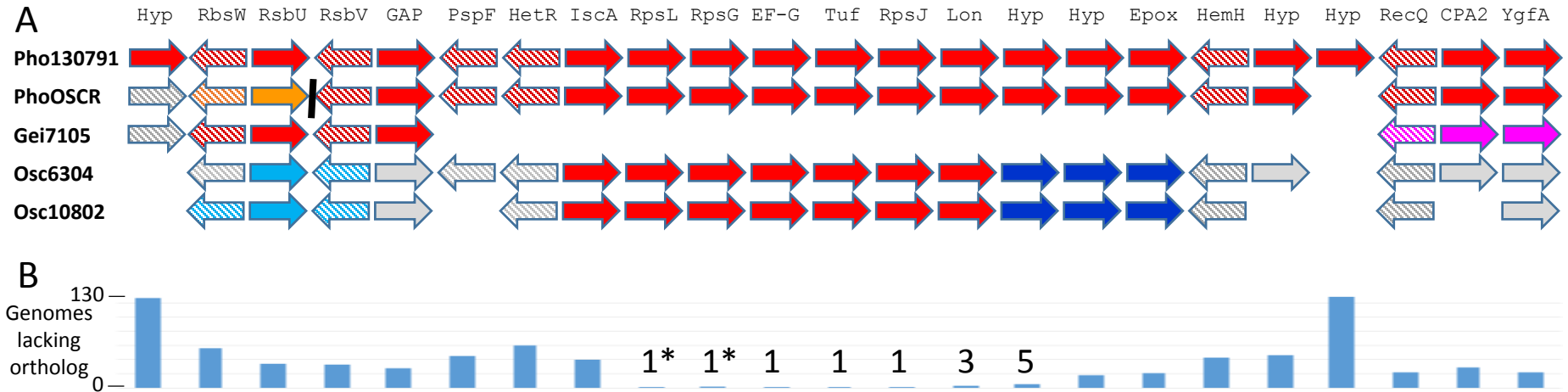


Supporting Information Figure S1

Genetic context of *hetR* in organisms close to *Geitlerinema* PCC 7105



Genetic maps are shown for the *hetR* region in the genomes of *Phormidium* BDU 130791 (Pho130791) and *Phormidium* OSCR (PhoOSCR), the closest available relatives of *Geitlerinema* PCC 7105 (Gei7105), as well as Gei7105 and the two next closest available relatives, *Oscillatoria* PCC 6304 (Osc6304) and *Oscillatoria* PCC 10802 (Osc10802). **(A)** Organism names and other information can be found in Supporting Information Table S1. The genetic maps are not drawn to scale. For each genome, orthologous genes (represented by rightward solid arrows or leftward hatched arrows) are from the same contiguous sequence if they have the same color. Gray arrows are exceptional: they are from different contiguous sequences from colored arrows but are not necessarily from the same contiguous sequences as other gray arrows. The black vertical bar in the genetic map of PhoOSCR indicates the end of two contiguous sequences. The list of genes includes besides *HetR* those that encode five ribosomal proteins (RpsL, RpsG, EF-G, Tuf, and RpsJ). **(B)** Count for each gene of how many of the 130 annotated cyanobacterial genomes in BioBIKE lacking an ortholog of the given protein. The two starred ribosomal proteins have orthologs truncated at the end of a contiguous sequence (RpsL in *Arthrospira maxima* CS 328) or split over two contiguous sequences (RpsG in *Arthrospira maxima* CS 328).