



Figure 3 – figure supplement 2: **Schematic representation and regulatory sequences of the *kaiABC*, *rpaA*, *pecB* and *ftsZ* promoter regions in *Anabaena*.** Highlighted in grey are shown the *in silico* determined RpaA binding sites, with numbers indicating the relative position respect to the transcriptional start site (TSS). Additional TSS (indicated with an asterisk) are shown in the promoter regions. The putative –10 elements are underlined. The table at the bottom shows the output of a FIMO analysis (see Appendix 1 - Supplemental methods), where the p-value of a motif occurrence is defined as the probability of a random sequence of the same length as the motif matching that position of the sequence with as good or better a score; and the q-value as the false discovery rate if the occurrence is accepted as significant.