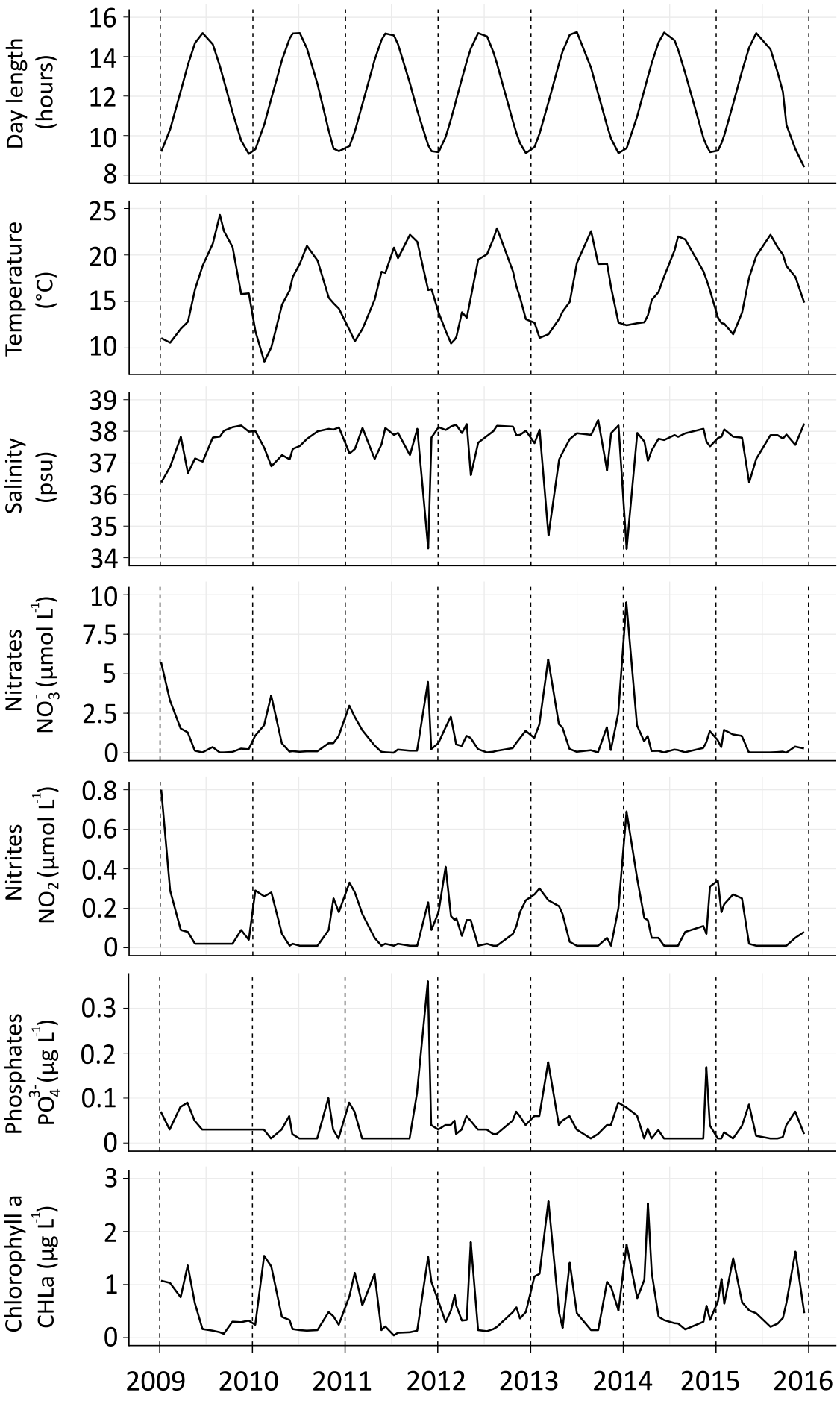


Figure S1: Environmental parameters measured in surface seawaters (3 -meters depth) at SOLA between January 2009 and December 2015.

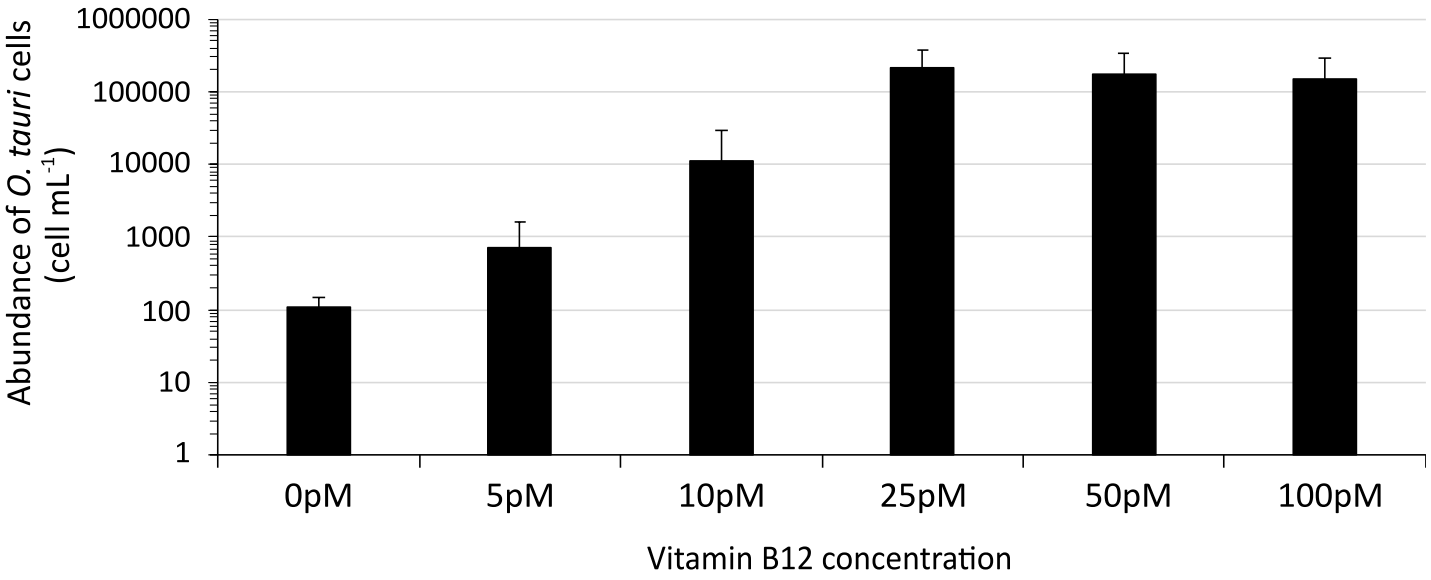


Figure S2: Cell abundances of *Ostreococcus tauri* RCC745 (cell.mL-1 ± SD, n=3) after 6 days of incubation in fresh ASW supplemented with constant B_1 (1 nM) and increasing B_{12} concentrations (between 0 and 100 pM). Deep well microplates were inoculated at 5000 cells.mL-1.

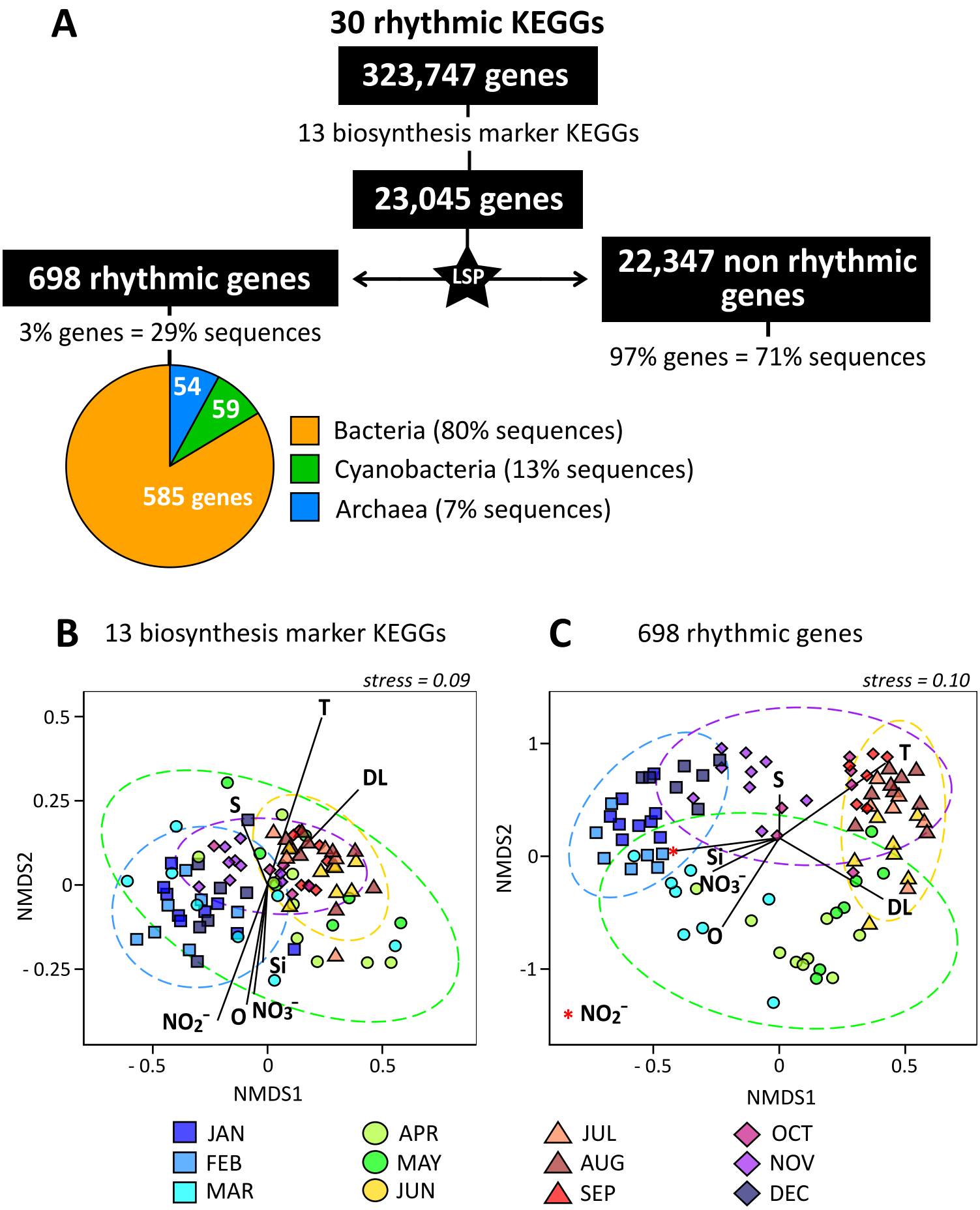


Figure S3: Analysis of the rhythmic KEGGs related to potential B_{12} metabolisms and their associated genes. (A) Schematic of the analysis resulting in the selection of 698 rhythmic genes and their taxonomic composition. (B) NMDS analysis of the 13 rhythmic KEGGs related to B_{12} biosynthesis and (C) of the associated 698 rhythmic genes. Covariance ellipses group the samples by seasons: winter (blue), spring (green), summer (red) and autumn (purple). Environmental variables that significantly impact sample's structure are fitted onto the nMDS: T: temperature; DL: day length; S: salinity; O: dissolved oxygen; Si: silicate ($Si(OH)_4$); NO_2^-: nitrite; NO_3^- : nitrate.

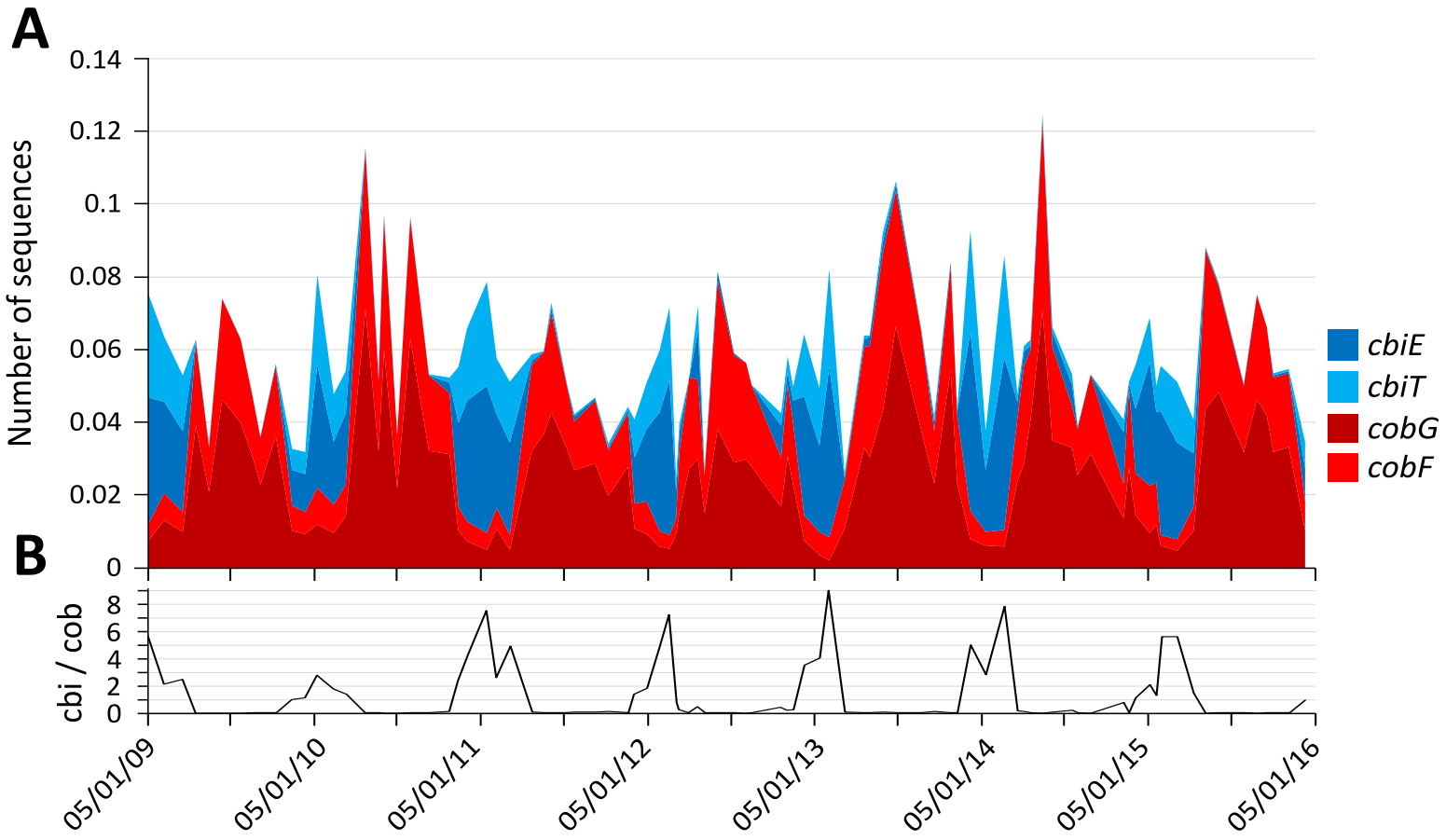


Figure S4: Bacterial and archaeal sequences potentially involved in vitamin B_{12} production at SOLA in winter. (A) Number of sequences associated to *cobF* and *cobG* (aerobic biosynthetic pathway, red), or associated to *cbiE* and *cbiT* (anaerobic biosynthetic pathway, blue). (B) Ratios of archaeal *cbi* (*cbiE* + *cbiT*) to bacterial *cob* (*cobF* + *cobG*) sequence numbers between 2009 and 2015.

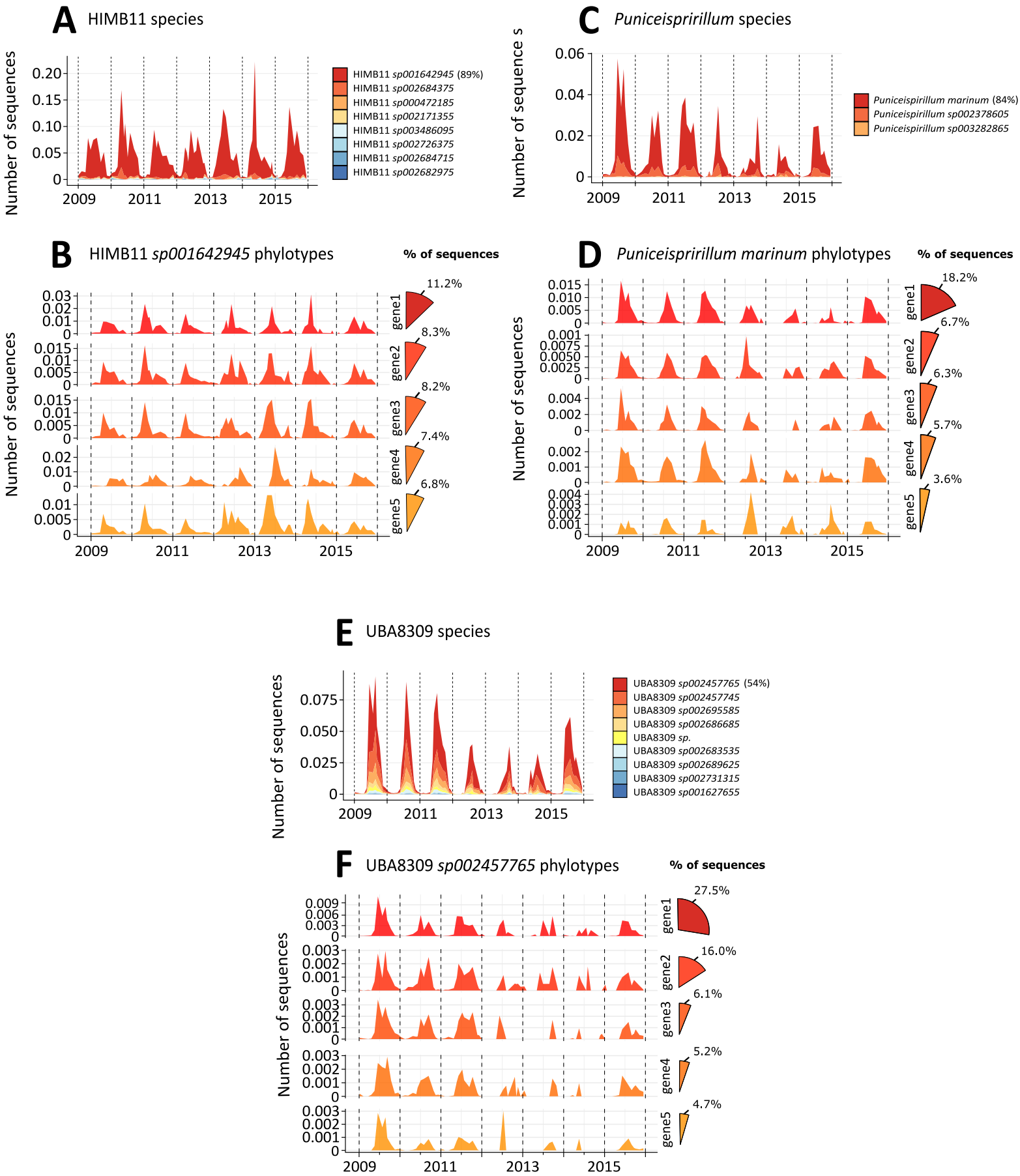
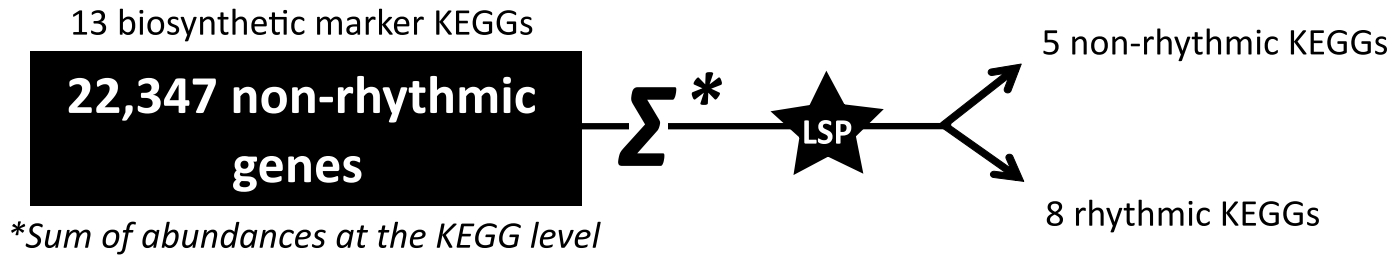


Figure S5: Seasonal abundance of the main bacteria potentially involved in vitamin B_{12} production. HIMB11 (A – B); *Puniceispirillum* (C – D); UBA8309 (E - F) at the species (A, C, E) and unique gene levels (B, D, F). The proportion of sequences represented by the dominant species within each genus is shown in brackets, while the proportion of sequences represented by the 5 dominant genes within their respective species (*i.e.*, phylotypes) is shown in the pie charts in front of density plots.

A



**Sum of abundances at the KEGG level*

B

KEGGs	Number of summed genes	Recovered PNmax	Period (day)	p-value
K04719_bluB	613	23.50	362	5.49E-09
K19712_cobY	263	19.31	362	3.63E-07
K03399_cbiE	466	18.23	373	1.07E-06
K02191_cbiT	276	17.05	373	3.47E-06
K02229_cobG	678	14.44	373	4.75E-05
K02228_cobF	432	11.76	362	6.93E-04
K03839_fldA_nifF_isiB	1061	10.74	362	1.92E-03
K19221_cobA_btuR	3351	10.46	373	2.53E-03
K02234_cobW	2587	9.60	362	5.96E-03
K02226_cobC_phpB	1835	8.08	362	2.71E-02
K13796_cobZ_tcuA	5316	7.98	373	2.99E-02
K02303_cobA	3390	5.14	61	4.05E-01
K05895_cobK_cbiJ	2063	4.31	469	6.98E-01

Rhythm recovered

Rhythm not recovered

Figure S6: Analysis of non-rhythmic genes associated to vitamin B12 biosynthesis. (A) Schematic overview of the analysis performed on the non -rhythmic genes related to our 13 markers. (B) Summary of the results from the analysis of the non -rhythmic genes (PNmax < 10). The number of genes summed for each KEGG and the PNmax they recover are shown. The period (days) and the significance level of the rhythmicity (p-value) are also indicated for KEGGs which recovered rhythm (blue) (PNmax ≥ 10) and also for those which remains non-rhythmic at the KEGG level (PNmax < 10).

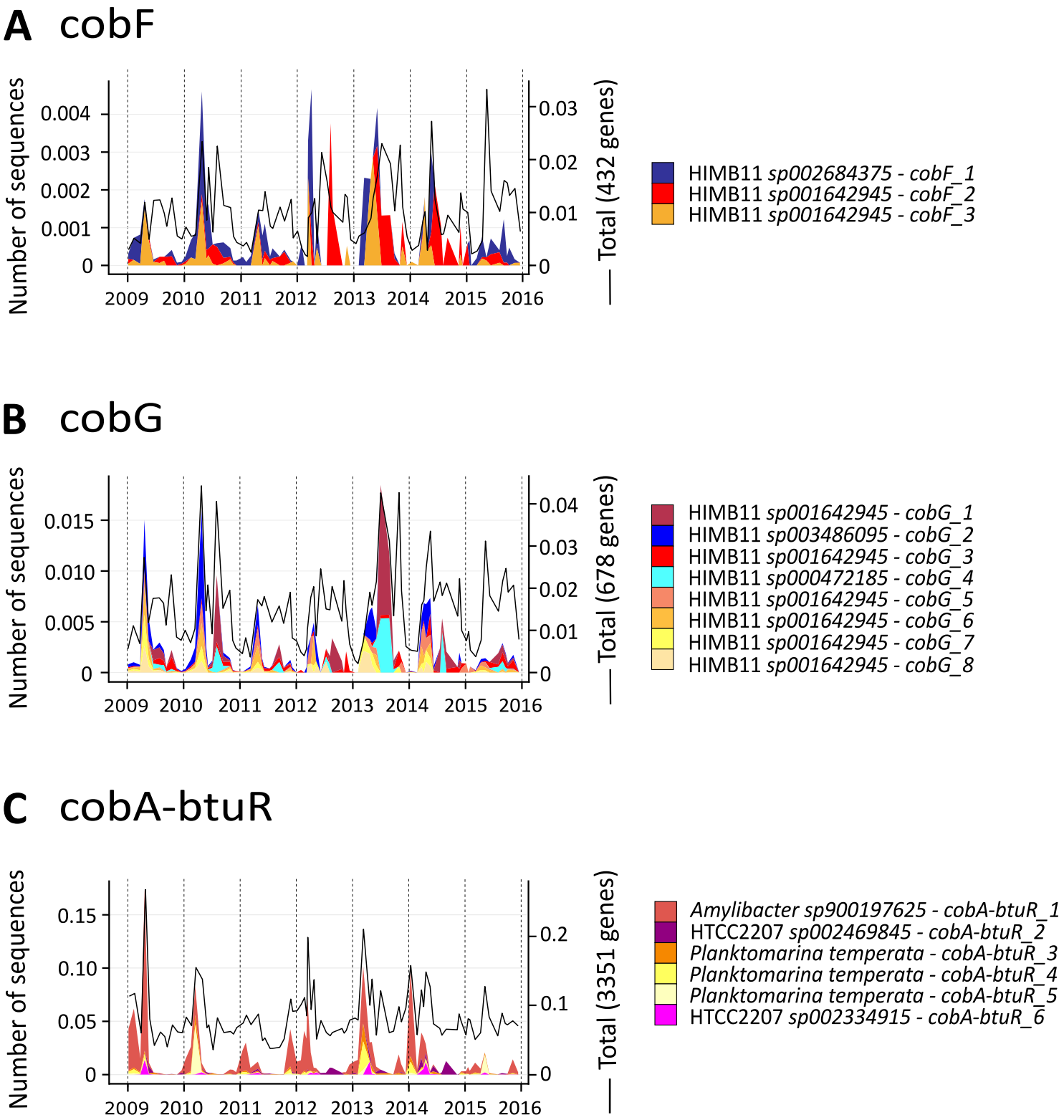


Figure S7: Analysis of non-rhythmic genes associated to three vitamin B12-biosynthesis marker KEGGs involved in the aerobic pathway (A: *cobF*, B: *cobG*) or in the salvage pathway (C: *cobA-btuR*). Density plots shows the relative abundance (number of sequences) of the most abundant and non-rhythmic genes sufficient to recover a rhythm at the KEGG level. The black line shows the sum of all non-rhythmic genes of the respective KEGG.