Supplementary Information

Particulate B-vitamin analyses

Briefly, the cells on the filters were lysed by bead beating in an acidic methanol lysis solution followed by a chloroform liquid phase extraction to reduce signal suppression and negative matrix effects. Analysis of samples was conducted using a Thermo Scientific Quantum Access electrospray ionization triple quadrupole mass spectrometer, coupled to a Thermo Scientific Accela High Speed Liquid Chromatography (LC/MS) system. The LC system used a stable-bond C_{18} reversed-phase column (Discovery HS C_{18} 10cm × 2.1mm, 5μm column, Supelco Analytical), with a methanol:water gradient program (Sanudo-Wilhelmy et al., 2012). Triple injections of each sample were used to increase precision. Quantification was conducted using a stable isotopically labeled riboflavin as an internal standard. Total cobalamin was calculated by summing the mean observed concentrations of adenosyl-, methyl-, hydroxy-, and cyano-cobalamin. The reported standard deviation is the square root of the sum of the variances of each form of cobalamin (Fig. S1). The units used are picomolar (e.g., picomoles of particulate cobalamin per liter of culture).

Consortia RNA read processing and annotation

Reads not recruited to IMS101's reference genome were scanned with SortMeRNA v.2.0 with default settings in order to identify and remove any remaining ribosomal RNA reads (Kopylova et al., 2012). Samples were then concatenated together and co-assembled with Trinity v.2.4.0 with default settings (which included normalization in this version) (Haas et al., 2013). Coding sequences were then identified in these assembled transcripts via Prodigal v.2.6.2 with the –p flag set to 'meta' (Hyatt et al., 2012). Duplicate coding sequences and contaminants were removed with dedupe.sh, available within the BBMap suite of tools (Bushnell, B. sourceforge.net/projects/bbmap/). These remaining coding sequences were utilized as our

reference library for recruiting the original metatranscriptomic reads from each individual sample using Bowtie2, and read counts were then converted to transcripts per million by first normalizing to coding sequence length and then by sample library size. Amino acid sequences of coding sequences were annotated with Kyoto Encyclopedia of Genes and Genomes (KEGG) orthologs (KOs) (Kanehisa et al., 2016). B_{12}-related genes discussed herein were searched against NCBI's RefSeq protein database via BLASTp to identify taxonomy (evalue < 10^{-20}).

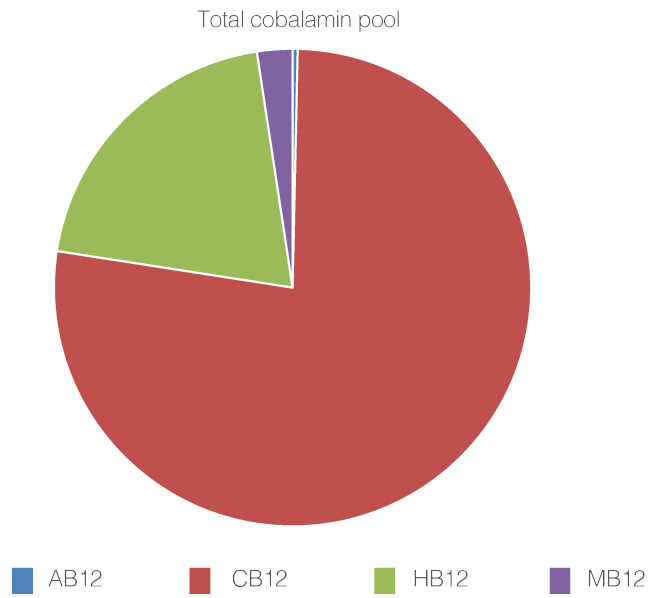

Fig. S1 Distribution of different forms of cobalamin making up the total pool from cultures of *Trichodesmium* IMS101. Cobalamin was extracted from filtered culture samples, and analyzed using LC/MS. The total cobalamin pool is represented including adenosyl- (AB), methyl- (MB), hydroxy- (HB), and cyano- (CB) cobalamin pools and had a mean of 58.4 (+/- 27.1) pM (e.g., picomoles of particulate cobalamin per liter of culture).

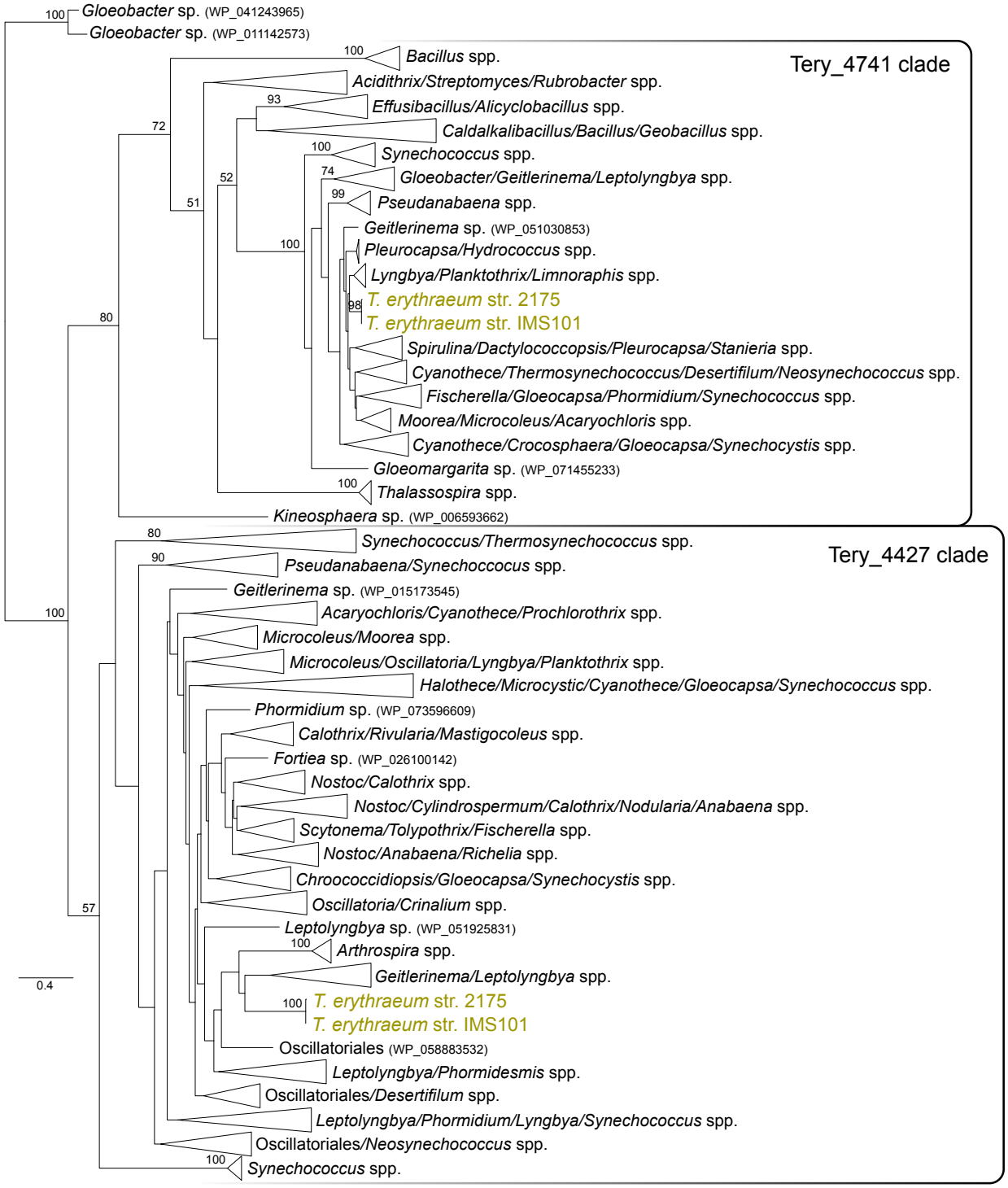

Fig. S2 Maximum likelihood phylogenetic analysis of IMS101 and 2175 *cbiX* genes (Tery_4741 and Tery_4427) and their closest homologs with 100 bootstraps.

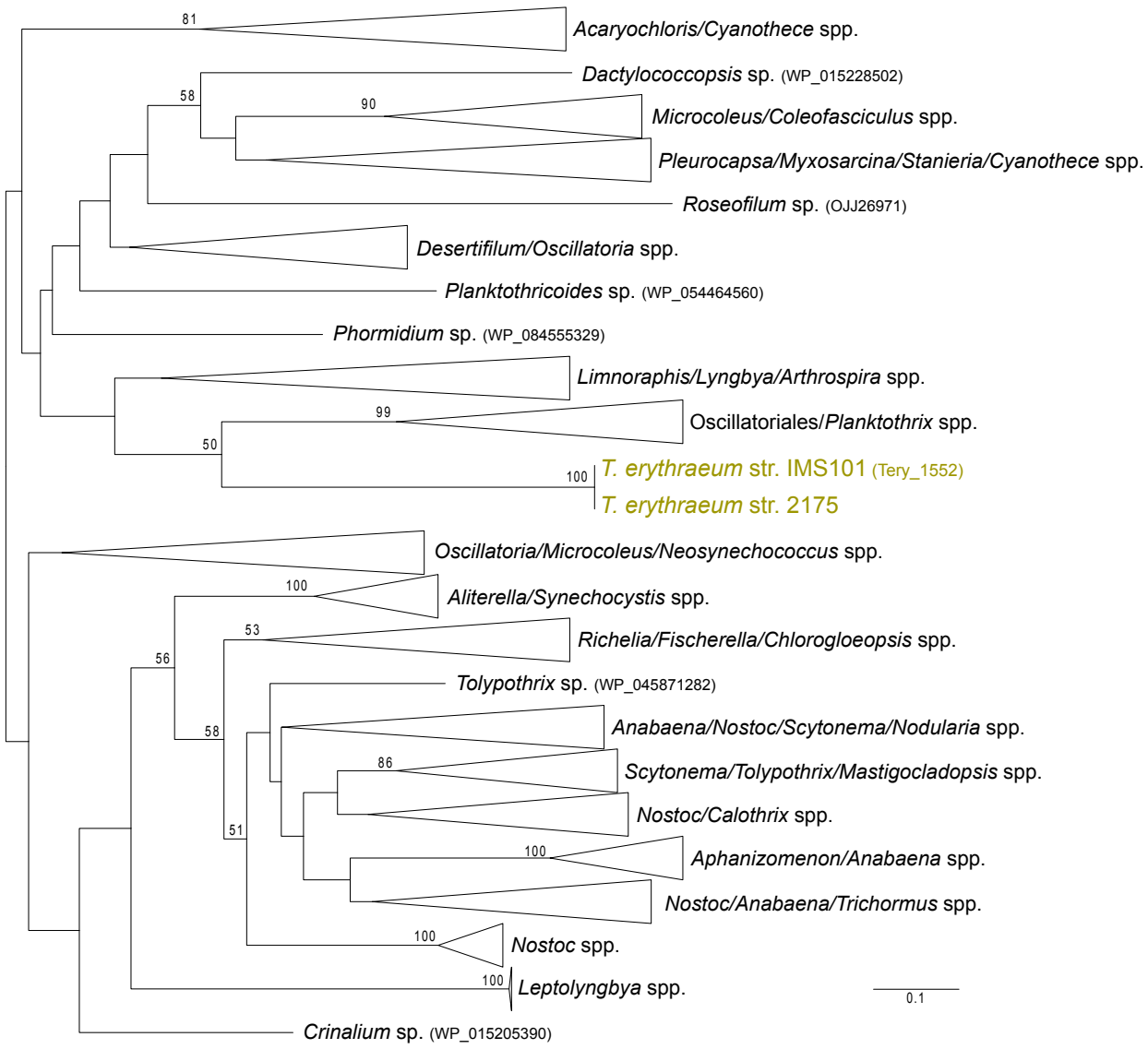

Fig. S3 Maximum likelihood phylogenetic analysis of the *Trichodesmium cbiF* and its closest homologs with 100 bootstraps.

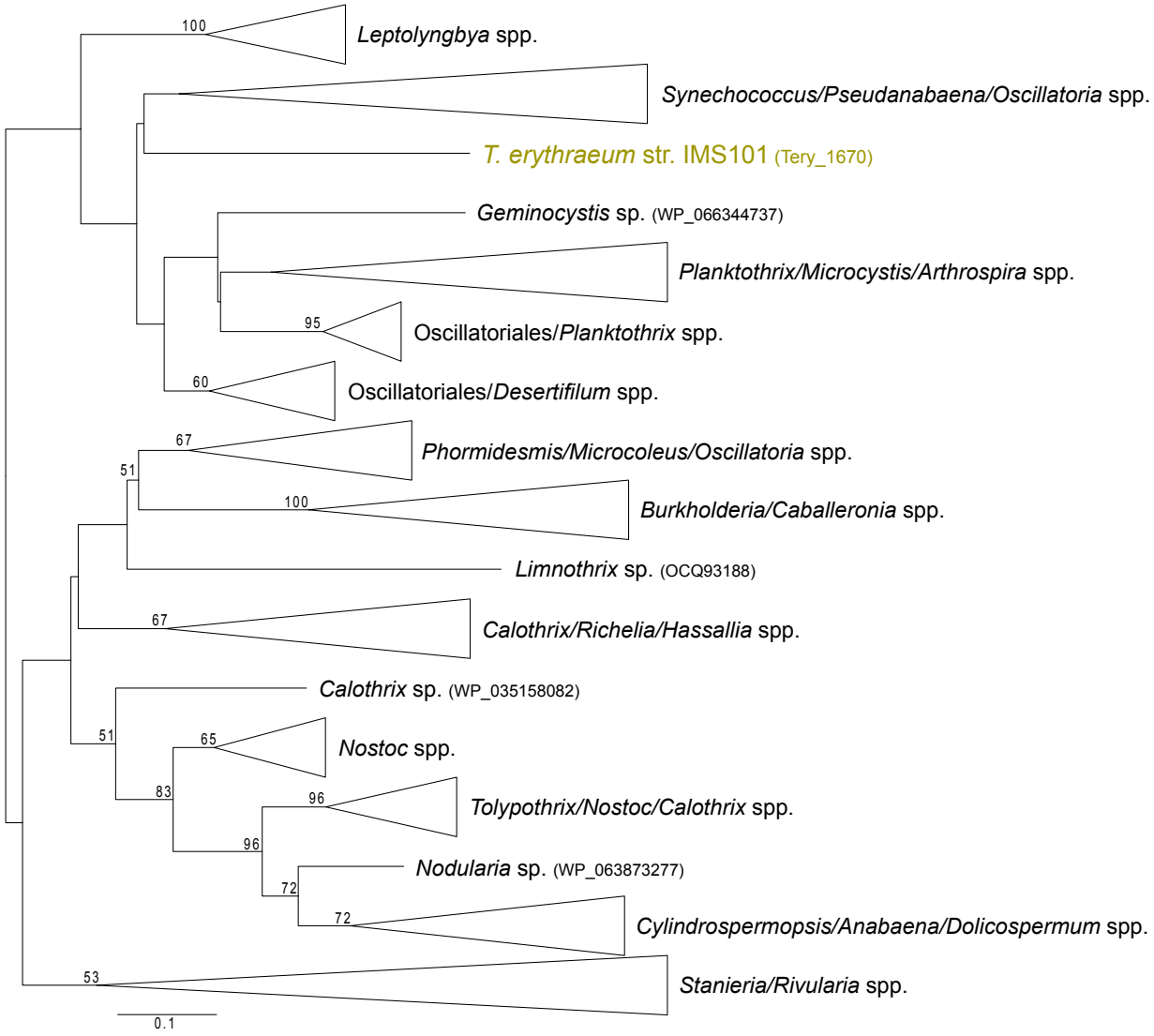

Fig. S4 Maximum likelihood phylogenetic analysis of the *Trichodesmium cbiC* and its closest homologs with 100 bootstraps.

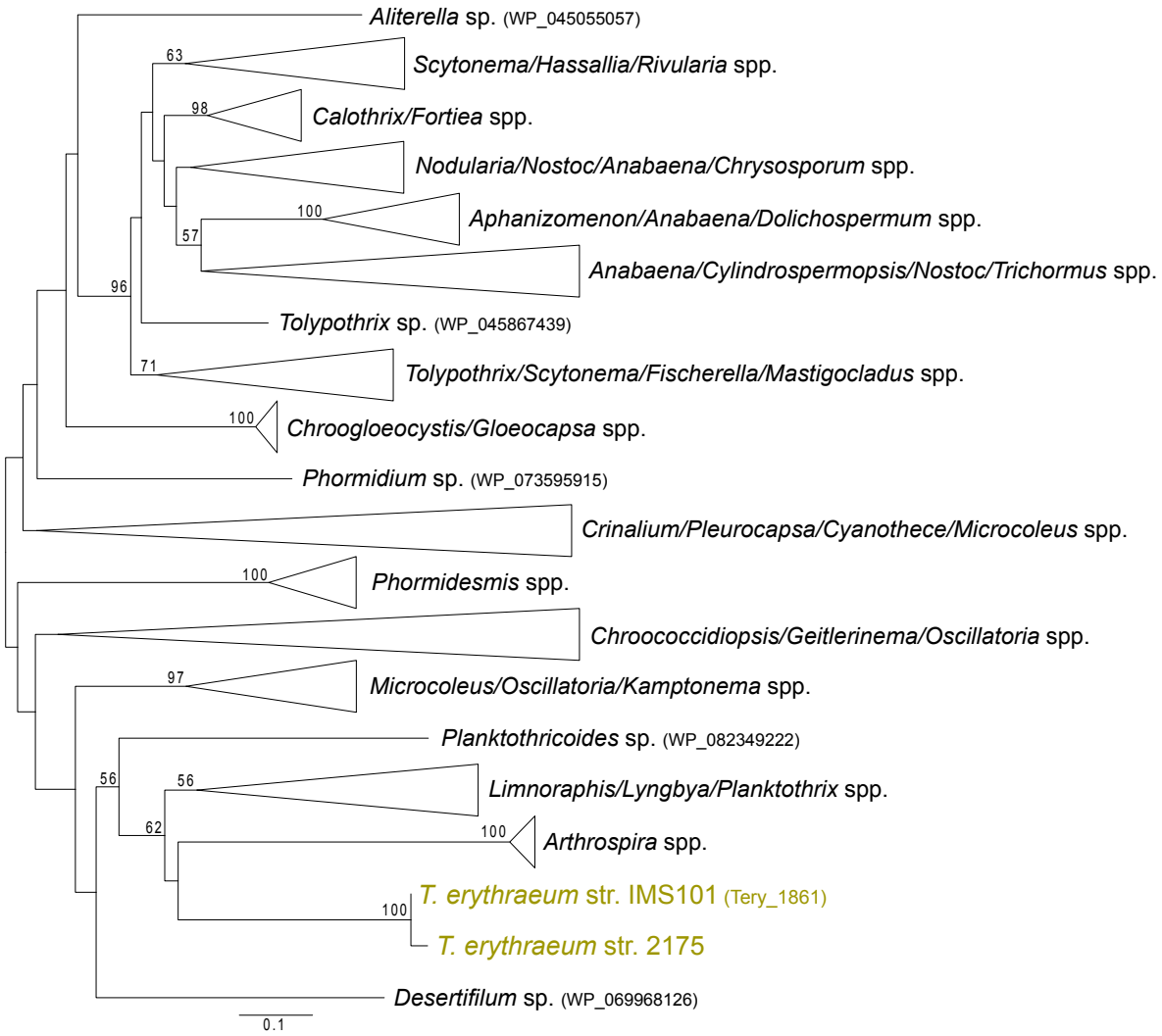

Fig. S5 Maximum likelihood phylogenetic analysis of the *Trichodesmium cobD* and its closest homologs with 100 bootstraps.

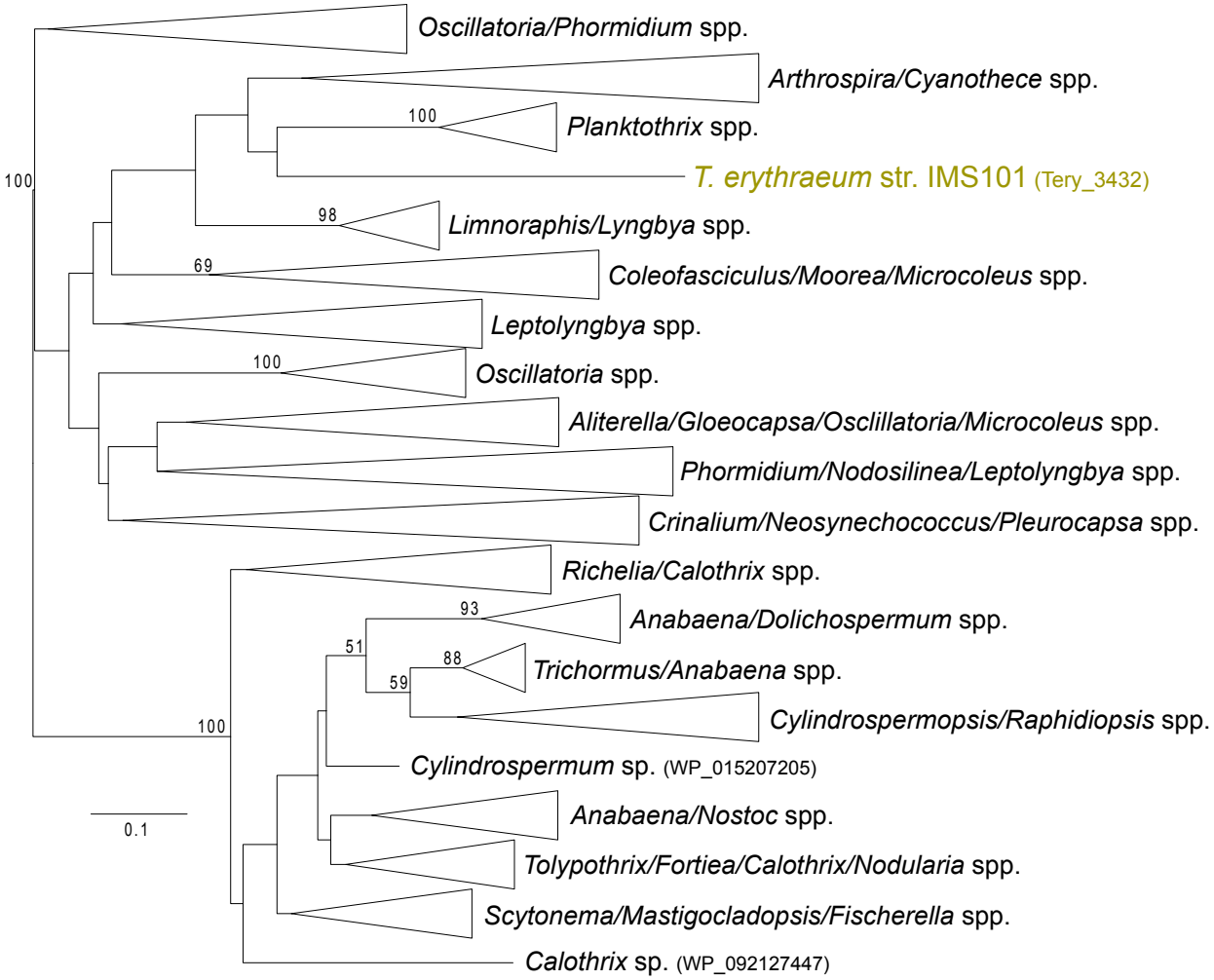

Fig. S6 Maximum likelihood phylogenetic analysis of the *Trichodesmium cobP* and its closest homologs with 100 bootstraps.

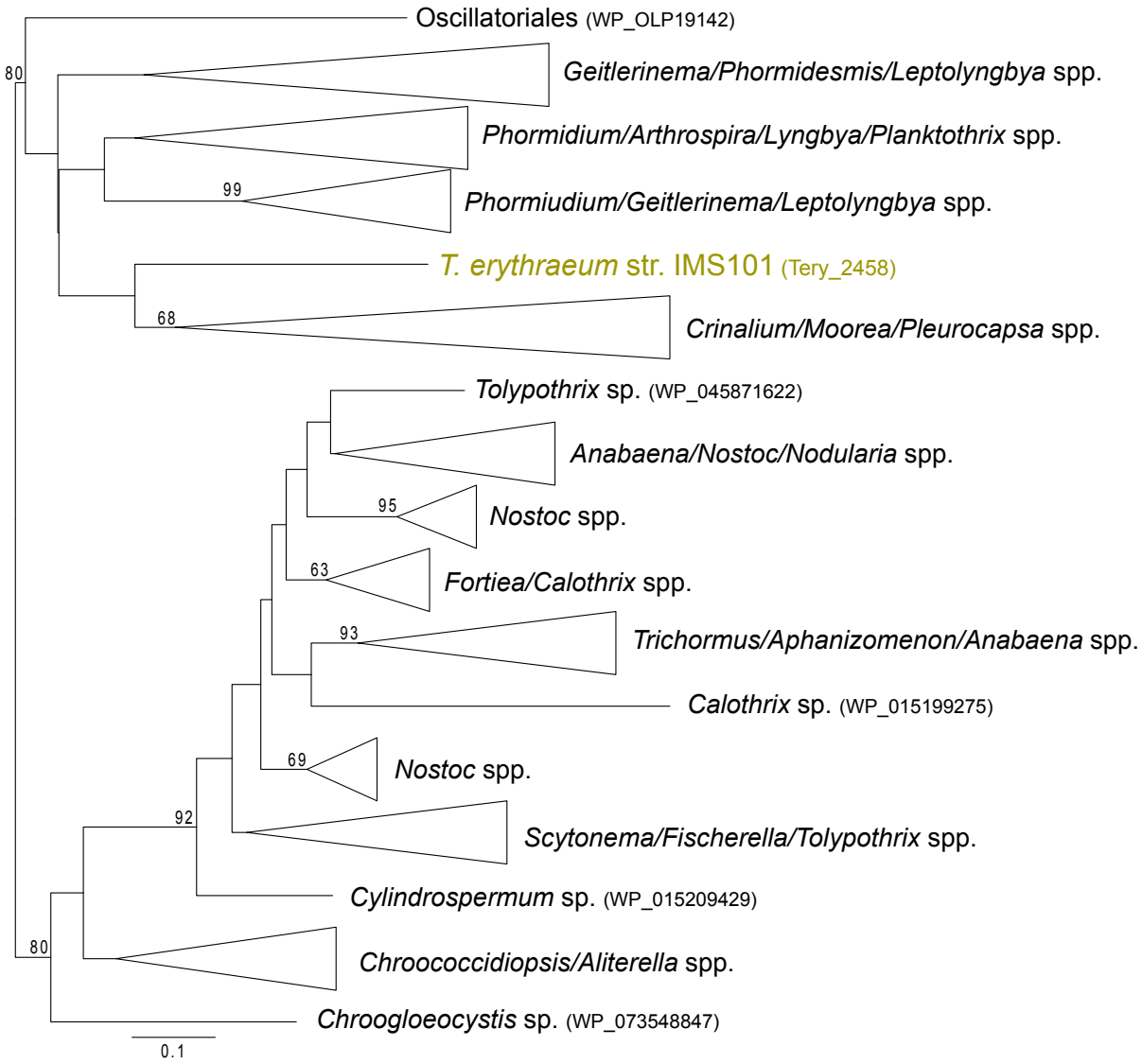

Fig. S7 Maximum likelihood phylogenetic analysis of the *Trichodesmium cobS* and its closest homologs with 100 bootstraps.

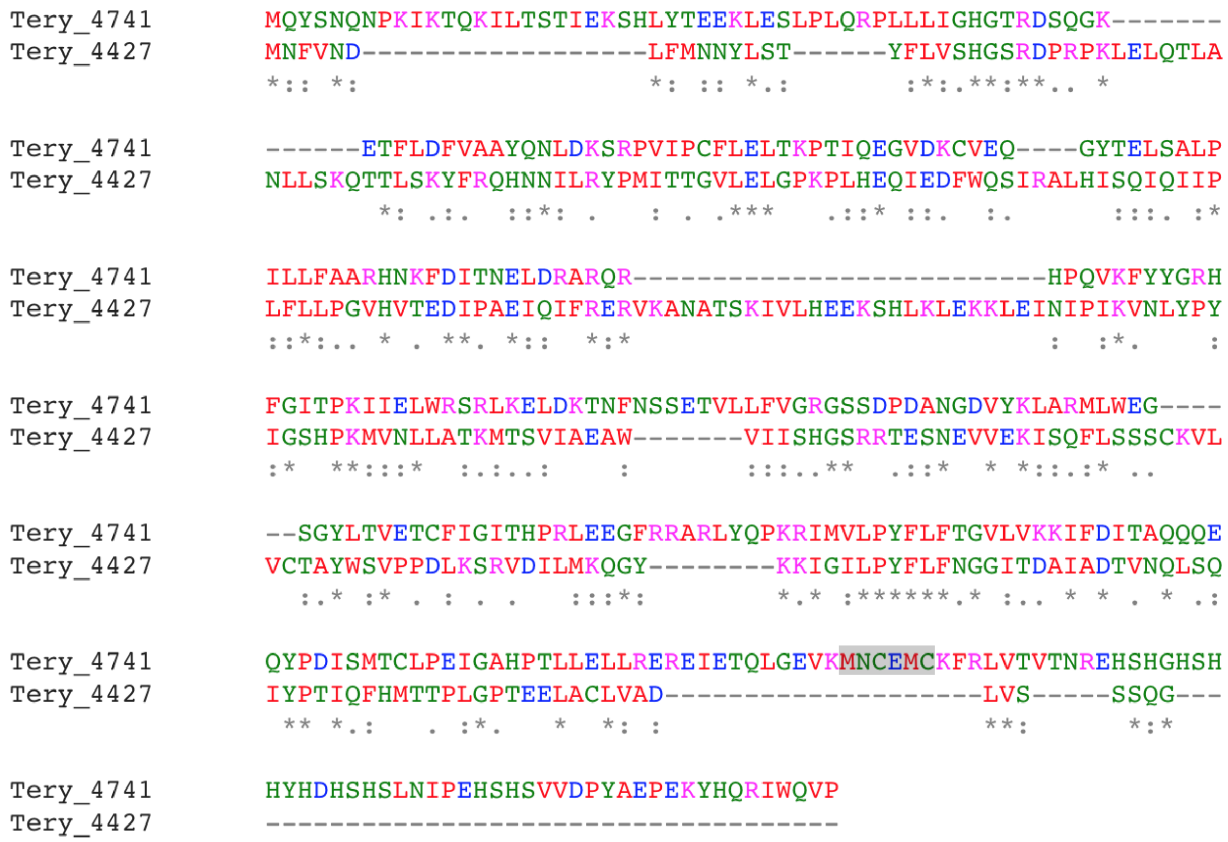

Fig. S8 Multiple sequence alignment of the two CbiX copies from Fig. S2. The metal-binding M*X*C*XX*C motif is denoted in grey in Tery_4741 and is absent in Tery_4427.

Supplementary Data

Table S1: These are the TMM-normalized (Robinson and Oshlack, 2010) expression levels of B_{12} biosynthesis/salvage genes that were sampled midday from the *Trichodesmium* long-term experiment (Walworth et al., 2017). R1 and R2 stand for biological replicate 1 and 2 of the r380 treatment in Walworth et al. 2017 in which cells were grown in nutrient-replete, Aquil medium in 380 ppm CO_2.

		R1	**R2**
Tery_4461	bluB	11.7559833	9.87497621
Tery_0786	btuR	43.16650118	36.25242944
Tery_0517	cbiA	15.82334359	19.06511067
Tery_1861	cbiB	98.79749358	113.6174556
Tery_1670	cbiC	8.633300236	7.312342563
Tery_0905	cbiD	19.05099079	14.6467768
Tery_0210	cbiE	45.23954288	39.65454653
Tery_1552	cbiF	43.6388398	43.29967197
Tery_4366	cbiG	51.90476555	58.36619049
Tery_1175	cbiH	20.41552457	24.89731138
Tery_0768	cbiL	18.00134943	19.06511067
Tery_2739	cbiJ	39.33531019	48.15983924
Tery_3957	cbiP	57.73027513	67.71096663
Tery_1288	cbiT	36.55376057	34.59555424
Tery_4741	cbiX	99.24359116	113.7058223
Tery_4427	cbiX	17.26660047	18.4686356
Tery_2181	cobC	507.5803236	478.8369337
Tery_2458	cobS	14.66873809	15.61881025
Tery_3432	cobU	27.36939862	28.82962853
Tery_3325	cysG	29.20627101	27.96805343
Tery_1666	isiB	1098.948269	1002.69669
Tery_2088	btuR	571.2481888	585.3839262
Tery_4685	btuR	155.9785573	126.5139721

Table S2: These are the normalized spectral counts of B_{12} biosynthesis/salvage proteins that were sampled midday from the *Trichodesmium* long-term experiment (Walworth et al., 2016). R1, R2, and R3 stand for biological replicate 1, 2, and 3 of the r380 treatment in Walworth et al. 2016 in which cells were grown in nutrient-replete, Aquil medium in 380 ppm CO_2.

Id		R1	R2	R3
Tery_3325	CysG	1.8056	2.777	1.7974
Tery_2181	CobC	32.501	31.473	35.947
Tery_3957	CbiP	0.9028	0.92568	0.89868
Tery_4461	BluB	3.6112	3.7027	3.5947
Tery_1666	IsiB	65.905	63.872	65.604
Tery_0786	BtuR	3.6112	1.8514	3.5947
Tery_4366	CbiG	0.9028	1.8514	0.89868
Tery_1552	CbiF	2.7084	3.7027	2.696
Tery_1288	CbiT	0.9028	1.8514	2.696
Tery_2088	BtuR	6.3196	6.4797	5.3921
Tery_4685	BtuR	22.57	21.291	21.568

Table S3: These are the TMM-normalized (Robinson and Oshlack, 2010) expression levels of the B_{12}-dependent *metH* and *nrdJ* and B_{12}-independent *metE* that were sampled midday from the *Trichodesmium* long-term experiment (Walworth et al., 2017). R1 and R2 stand for biological replicate 1 and 2 of the r380 treatment in Walworth et al. 2017 in which cells were grown in nutrient-replete, Aquil medium in 380 ppm CO_2.

RNA		**R1**	**R2**
Tery_0428	nrdJ	164.8174297	149.0907626
Tery_1073	metH	430.0622843	413.826827
Tery_0847	metE	3971.197808	4105.551806

Table S4: These are the normalized spectral counts of the B_{12}-dependent *metH* and *nrdJ* and B_{12}-independent *metE* that were sampled midday from the *Trichodesmium* long-term experiment (Walworth et al., 2016). R1, R2, and R3 stand for biological replicate 1, 2, and 3 of the r380 treatment in Walworth et al. 2016 in which cells were grown in nutrient-replete, Aquil medium in 380 ppm CO_2.

Protein		**R1**	**R3**	**R3**
Tery_1073	MetH	24.376	24.993	35.049
Tery_0847	MetE	146.25	161.07	145.59

Table S5: These are in transcripts per million for the community only (w/o *Trichodesmium* transcripts). These data are from the *Trichodesmium* consortia metatranscriptome as described in Lee et al. 2017(Lee et al., 2017).

	R1	R2	Gene symbol	KO_ID	Kegg deffinition	Blast tax
CDS_44539	24.94	22.41	MMAB/pduO/ btuR	K00798	cob(I)alamin adenosyltransferase	Bacteroidetes (Phaeodactylibacter xiamenensis)
CDS_55643	0.09	0.11	MMAB/pduO/ btuR	K00798	cob(I)alamin adenosyltransferase	Bacteroidetes (Lewinella cohaerens)
CDS_50601	0	0.83	MMAB/pduO/ btuR	K00798	cob(I)alamin adenosyltransferase	Alphaproteobacteria (Ruegeria atlantica)
CDS_71531	0	0.66	MMAB/pduO/ btuR	K00798	cob(I)alamin adenosyltransferase	Synechococcus
CDS_17881	0.13	2.09	btuR/cobA	K19221	cob(I)alamin adenosyltransferase	Synechococcus
CDS_28823	0.19	0	btuR/cobA	K19221	cob(I)alamin adenosyltransferase	Synechococcus
CDS_35672	0	1.03	btuR/cobA	K19221	cob(I)alamin adenosyltransferase	Synechococcus
CDS_62206	1.05	0.16	btuR/cobA	K19221	cob(I)alamin adenosyltransferase	Synechococcus
CDS_51740	1.15	3.86	cbiB/cobD	K02227	adenosylcobinamide-phosphate synthase	Synechococcus

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