

Figure S1. Multiple protein sequence alignment of several TrxA1 and TrxA2. The sequences are indicated with abbreviations of the organism names: *Nostoc* sp. PCC 7120 TrxA1 (Nostoc_TrxA1), *Synechocystis* sp. PCC 6803 TrxA1 (Synechocystis_TrxA1), *Calothrix* sp. 336/3 TrxA1 (Calothrix_TrxA1), *Scytonema* sp. HK-05 TrxA1 (Scytonema_TrxA1), *Gloeomargarita lithophora* TrxA1 (Gloeomargarita_TrxA1), *Gloeobacter violaceus* TrxA1 (Gloeobacter_TrxA1), *Calothrix* sp. 336/3 TrxA2 (Calothrix_TrxA2), *Scytonema* sp. HK-05 TrxA2 (Scytonema_TrxA2), and *Nostoc* sp. PCC 7120 TrxA2 (Nostoc_TrxA2). The red triangles indicate the unique amino acids that are specific to TrxA2. Blue and cyan color indicate identity or similarity, respectively.

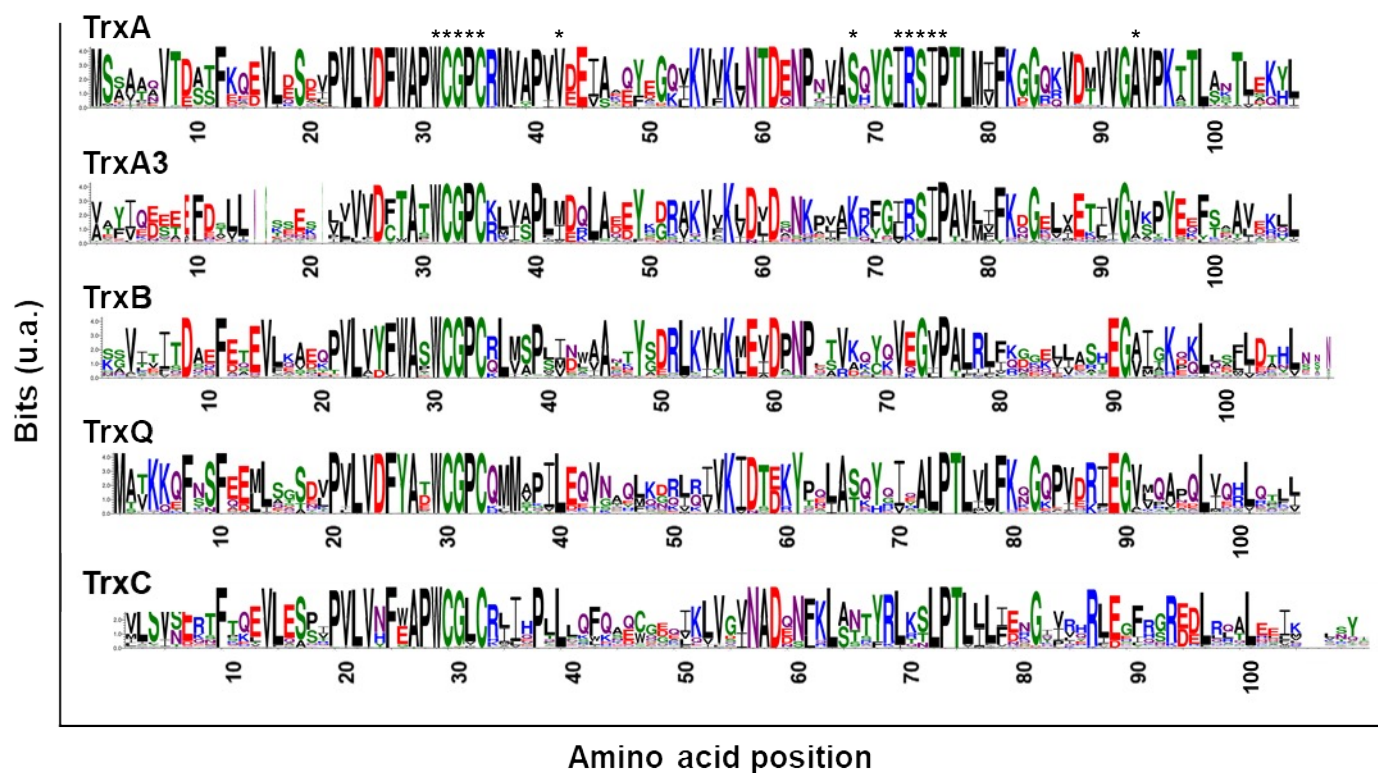


Figure S2. Sequence conservation of TrxA1/2, TrxA3, TrxB, TrxQ and TrxC. Logos were built using blast at IMG and NCBI databases, and manually curated in all cases. The sequences were aligned with Muscle algorithm and the alignment were generated with Weblogo3. The height of each amino acid code for each position indicate the frequency at that position. The numbering corresponds to the respective position in the Trxs of *Nostoc* sp. PCC 7120. Essential amino acids for the formation of the FTR-TrxA complex are marked with asterisks according to Dai et al., 2007.

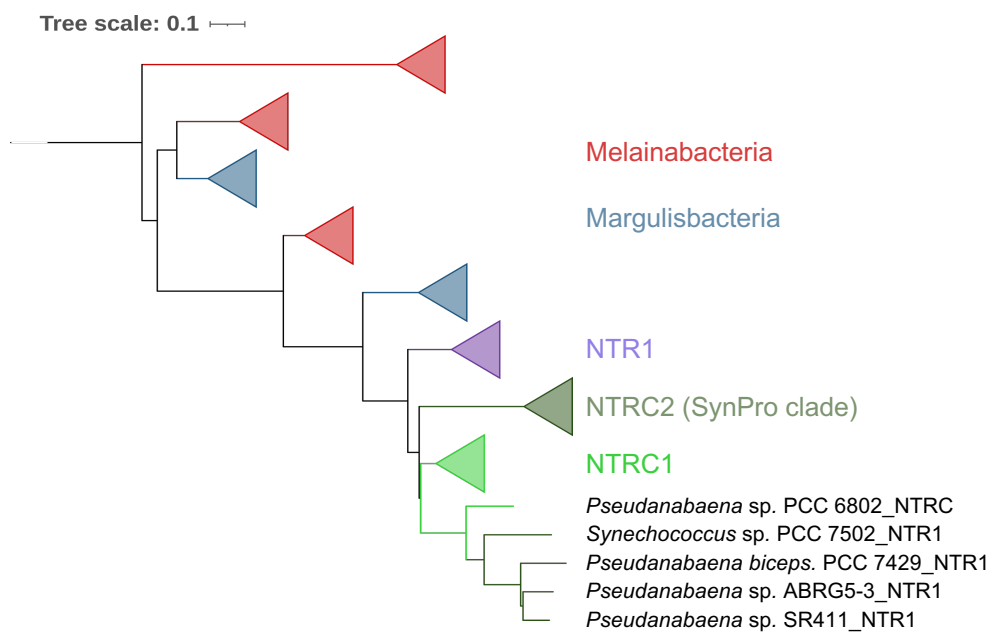


Figure S3. Phylogenetic tree related to NTRC and NTR1 present in Cyanobacteria and close relatives.

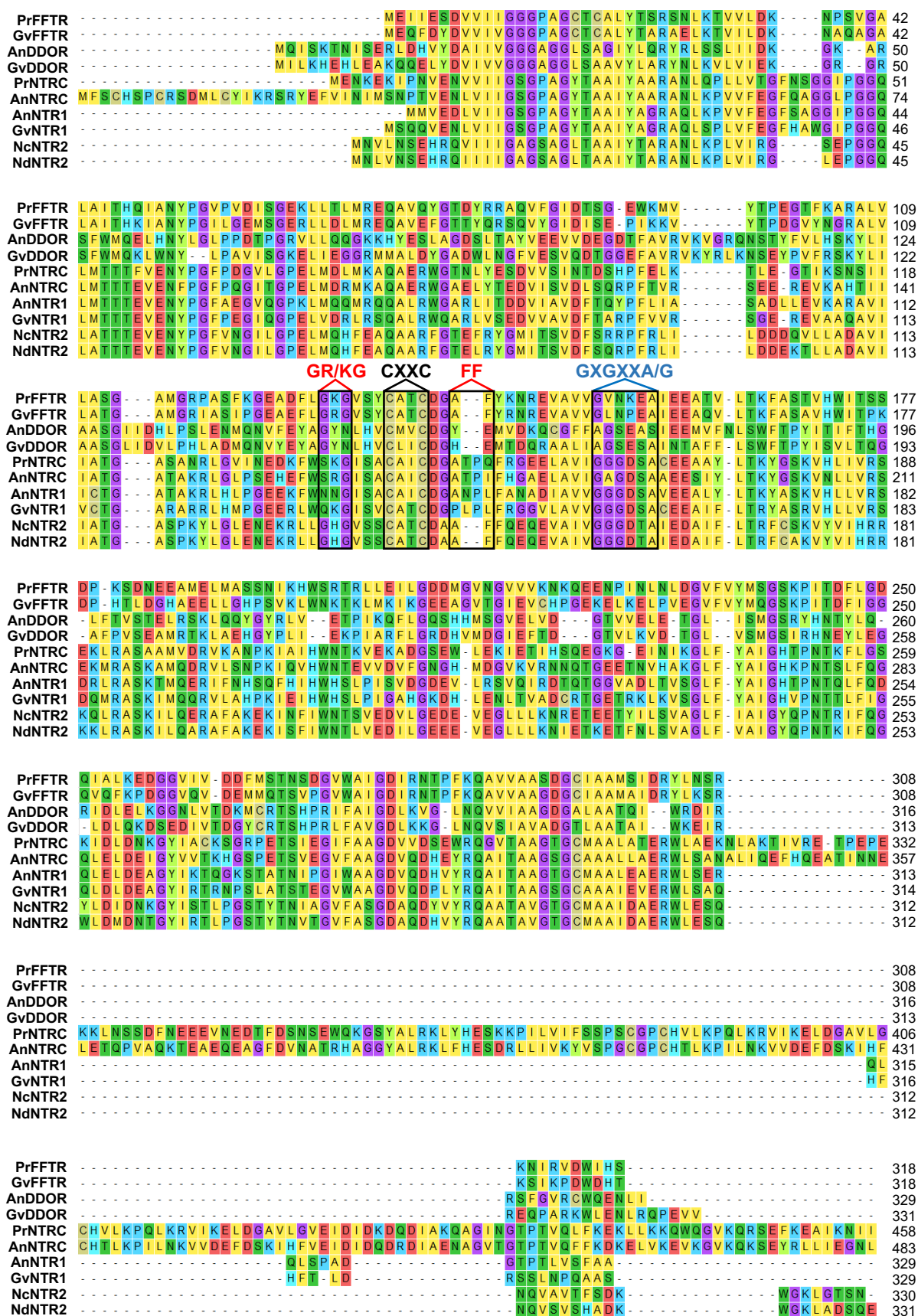


Figure S4. Multiple alignment of full protein sequence of several TR-related enzymes. The sequences are indicated with abbreviations of the organism names as in Figure 3B.

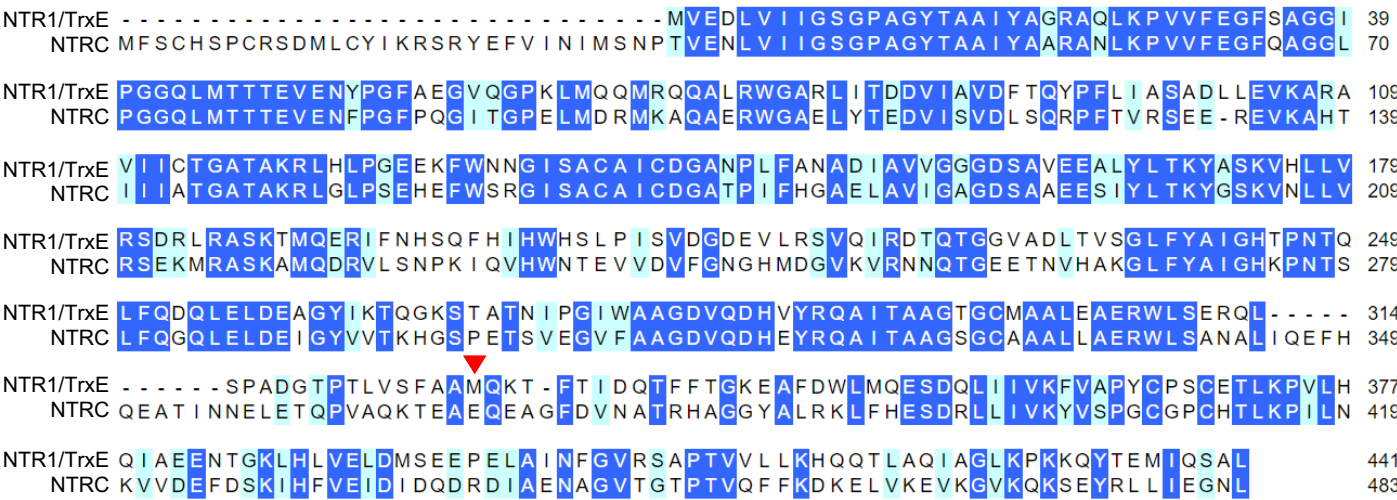


Figure S5. Alignment of the chimeric sequences NTR+TrxE and NTRC. The sequences used correspond to NTRC, NTR1 and TrxE of *Nostoc* sp. PCC 7120. The red triangle indicates the start of the TrxE fragment in the hypothetical chimeric protein. Blue and cyan color indicate identity and similarity, respectively.

ApNTRC	-----MA	VENLV	I	IGSGPAGYTAAIYA	GRANLKP	VVFEG	MEAGGLPGGQ	LMTT	49																																																																
NcNTRC	--MLCYIKRSRYEFVINIM	SNPT	VENLV	I	IGSGPAGYTAAIYA	AARANLKP	VVFEGFQAGGLPGGQ	LMTT	68																																																																
TeNTRC	-----MTPPRI	EN	V	I	IGSGPAGYTAAIYA	AARANLKP	LMFEGYQIGGLPGGQ	LMTT	52																																																																
OsNTRC	-----MSLNNTMTNPA	V	V	I	IGSGPAGFTAIIYA	GRANLKP	VVFEGFQMG	IGGQ	58																																																																
SnNTRC	-----MTEQSR	V	V	I	IGSGPAGFTAIIYA	GRANLKP	VVFEGFQVGGI	IGGQ	53																																																																
PrNTRC	-----MSI	ENLV	I	IGSGPAGYTAAIYA	AARANLQ	PLLITGFERGGI	IGGQ	LMTT	49																																																																
AmNTRC	MQNGSKSQCSIR	SRYLTVLMSEAI	ENLV	V	I	IGSGPAGYTAAIYA	AARANLKP	FMFAGYQAGGLPGGQ	LMTT	70																																																															
ApNTRC	EVENFPGFPEG	I	QGPQLMDR	I	RAQAERWGAD	LIT	EDVTV	VDLSQRPF	TIRSE	SH	EVQAHSI	I	IATGATAK	119																																																											
NcNTRC	EVENFPGFP	Q	I	TGPE	LMDRMKAQA	ERWGAEL	Y	TEDV	I	SV	DL	SQRPF	TVRSE	E	EREVKAHTI	I	IATGATAK	138																																																							
TeNTRC	EVENFPGFPEG	I	QGPQLM	ARMKAQA	ERWG	T	EMV	TEDV	I	QV	D	F	SQRPF	L	I	SSAERQV	Y	AHSV	I	Q	TGATAK	122																																																			
OsNTRC	EVENFPGFPEG	I	TGP	K	LMERMKLQA	QRWGAEL	Y	TEDV	Q	S	VD	L	SQRPF	V	I	RS	D	EREVKAHTV	I	IATGATAK	128																																																				
SnNTRC	EVENFPGFPEG	I	SGPQLM	K	MRQAQA	RWGAEL	Y	P	EDV	T	F	VD	L	SQRPF	V	V	RS	D	EREV	THSL	I	IATGATAK	123																																																		
PrNTRC	FVENFPGFP	D	G	I	MGP	D	LMDLLKAQA	I	RWG	T	K	L	L	E	L	D	A	E	I	D	L	K	Q	N	P	F	R	V	K	T	A	N	Q	S	I	A	A	Q	A	L	I	I	A	T	G	A	R	A	N	119																							
AmNTRC	EVENFPGFP	D	G	I	TGP	Q	LMDRMKLQAL	RWG	S	E	I	V	T	E	D	V	I	S	V	D	F	Q	Q	F	P	F	V	I	Q	S	E	E	R	T	V	K	A	H	S	V	I	A	T	G	A	T	A	K	140																								
ApNTRC	RLHLPGE	E	R	F	W	T	K	G	I	S	A	C	I	D	G	A	T	P	M	F	R	N	A	E	L	A	V	V	G	G	D	S	A	V	E	E	A	I	Y	L	T	K	Y	G	S	K	V	H	L	L	R	S	E	K	M	R	A	S	K	189													
NcNTRC	RLGLPSE	H	E	F	W	S	R	G	I	S	A	C	I	D	G	A	T	P	I	F	H	G	A	E	L	A	V	I	G	A	G	D	S	A	A	E	E	S	I	Y	L	T	K	Y	G	S	K	V	N	L	L	R	S	E	K	M	R	A	S	K	208												
TeNTRC	RLHLPGE	E	Q	Y	W	T	K	G	V	S	A	C	I	D	G	A	T	P	I	F	K	D	V	E	L	A	V	I	G	G	G	D	S	A	A	E	E	A	V	Y	L	T	K	Y	G	S	H	V	H	L	L	R	S	D	K	M	R	A	S	K	192												
OsNTRC	RLGLPSE	H	Q	F	W	S	R	G	V	S	A	C	I	D	G	A	S	P	I	F	K	G	V	S	L	A	V	V	G	G	D	T	A	A	E	E	A	V	Y	L	T	K	Y	G	S	H	V	H	L	L	R	S	E	E	M	R	A	S	K	198													
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PrNTRC	KLGI	P	N	E	N	K	F	W	T	R	G	I	S	A	C	I	D	G	A	T	P	Q	F	R	N	E	L	A	V	V	G	G	D	S	A	C	E	E	A	V	Y	L	T	K	Y	G	S	H	V	H	L	I	R	S	N	Q	L	K	A	S	K	189											
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TeNTRC	MQDR	V	F	A	N	P	K	I	T	V	H	W	Q	T	E	A	R	E	I	L	G	D	G	N	L	M	T	G	L	R	I	I	N	K	A	T	G	E	E	S	L	P	V	R	G	L	F	Y	A	I	G	H	T	P	N	T	Q	L	F	K	D	F	L	E	L	D	262						
OsNTRC	MQDR	V	L	K	N	P	K	I	T	V	H	W	N	T	E	A	V	D	I	F	G	D	R	M	E	G	I	K	V	R	N	I	K	T	G	E	E	T	D	L	Q	V	R	G	L	F	Y	A	I	G	H	T	P	N	T	Q	L	F	K	G	Q	L	E	L	D	268							
SnNTRC	MQDR	V	L	N	H	P	K	I	T	V	H	W	N	T	E	A	V	E	V	I	F	G	D	R	L	T	G	V	K	V	R	N	N	Q	T	G	E	I	R	E	M	A	V	G	L	F	Y	A	I	G	H	K	P	N	T	D	L	F	K	G	Q	L	E	L	D	263							
PrNTRC	MSDR	V	M	A	N	S	Q	I	T	V	H	W	N	T	E	L	I	D	V	E	G	K	-	E	W	I	E	T	L	K	V	K	R	R	G	T	K	Q	E	E	T	I	K	A	K	L	F	Y	A	I	G	H	T	P	N	A	D	L	E	G	Q	L	L	I	N	258							
AmNTRC	MQDR	V	M	R	N	P	K	V	T	V	H	W	Q	T	E	V	D	V	F	G	D	-	T	Q	L	Q	L	G	L	K	I	K	N	R	Q	T	A	E	I	Q	E	L	Q	V	R	G	L	F	Y	A	I	G	H	Q	P	N	T	Q	L	F	T	Q	Q	L	D	279							
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TeNTRC	SVGY	I	V	T	R	H	G	T	-	Q	T	N	V	E	G	V	F	A	A	G	D	V	Q	D	H	E	Y	R	Q	A	V	T	A	A	G	S	G	C	M	A	A	L	D	A	E	R	W	L	S	A	R	G	L	I	Q	E	F	H	C	-	-	-	-	-	R	A	T	326					
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NcNTRC	I	L	N</																																																																						

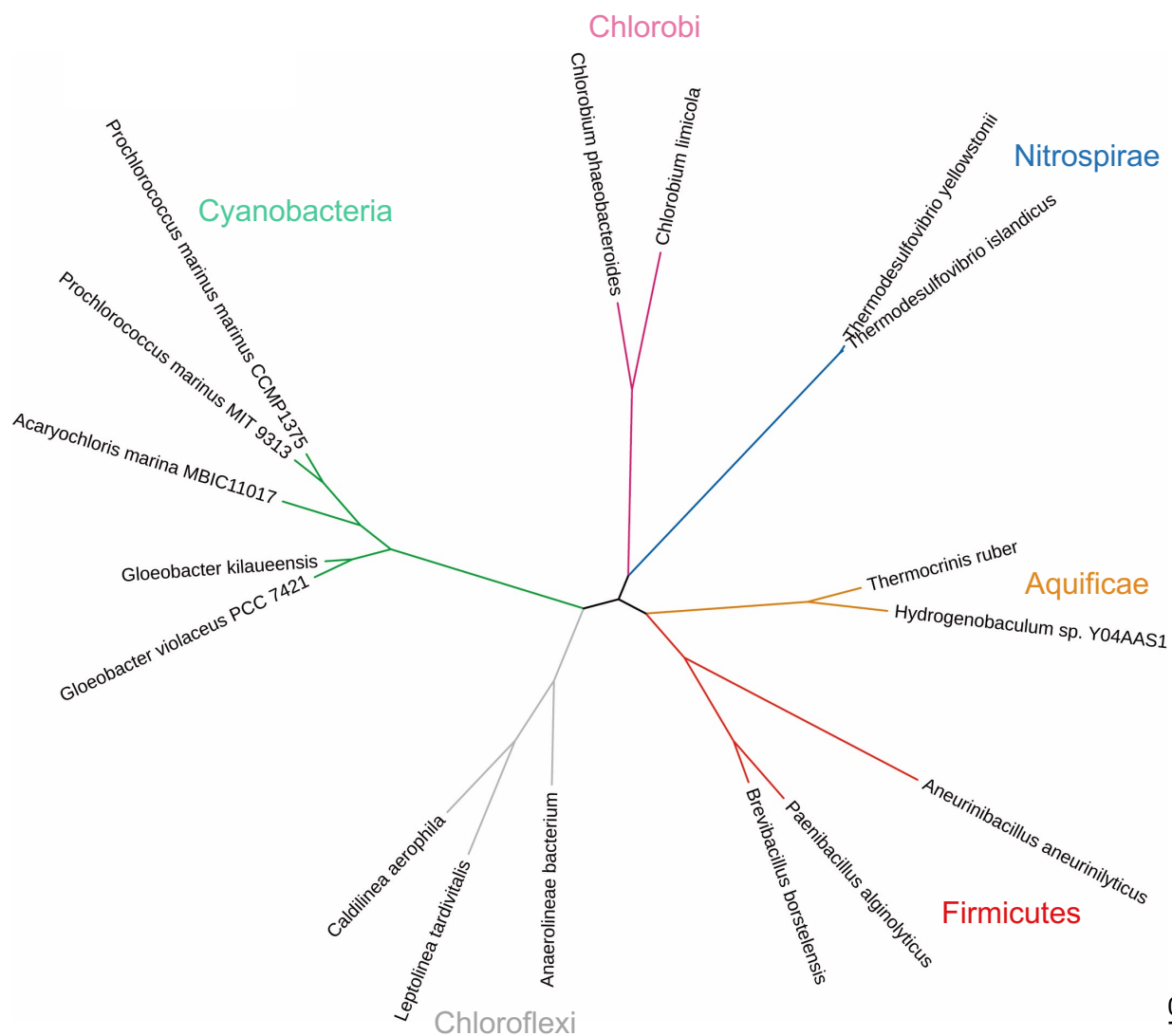


Figure S7. Unrooted tree of FFTR amino acid sequences identified in the IMG and NCBI databases. Branches are colored to represent FFTR amino acid sequences found in the different bacterial phyla: Cyanobacteria (green), Chlorobi (purple), Nitrospirae (blue), Aquificae (brown), Firmicutes (red), and Chloroflexi (grey). Scale bar represents number of substitutions per site.