

Supplemental Figure S1. RNA gel blot and polysome analysis.

(A, B) Schematic representation of the *atpI/H/F/A* (A) and *atpB/E* (B) operons. Transcript maps were generated based on previously reported data (Pfalz et al., 2009; Malik Ghulam et al., 2012). (C, D) RNA gel blot analysis of plastid mRNAs encoding

ATP synthase subunits in the WT and *bfa3* mutant. Total RNA (5 µg/lane) from the leaves of three-week-old plants was size fractionated on denaturing agarose gels and probed with DIG-labeled DNA probes corresponding to plastid *atpA*, *atpF*, *atpH*, *atpI* (C), and *atpB/E* (D) genes. The positions of RNA markers (knt, kilonucleotides) are shown. (E) Polysome association analyses of plastid mRNAs encoding ATP synthase subunits. Total extracts from wild-type and *bfa3-1* leaves were fractionated in 15–55% sucrose gradients under polysome-maintaining conditions. Ten fractions of equal volume were collected from the top to the bottom of the sucrose gradients, and equal proportions of the RNA purified from each fraction were analyzed by RNA gel blotting. rRNAs were detected by EtBr staining. The arrows above the panels indicate sucrose density gradients (from low to high).

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                                     | Predicted cleavage site
AtBFA3 1 ---MA--TSPVQC--FSCNSHHHQREQSGSLWRLGSRVLV-SSSLWKLSPGSLHNRRLTLCVKGDPDPAFKKTVETDRMIDALRDAN-
GmBFA3 1 -MRINAFCVSVSASLYYFPNPH----GALLQDWKLRKHRFSKLTSEPL--NLSCKRRRTPTICANQEADEAFKKTVEIDRLIDMLRAN-
OsBFA3 1 -MSTAAA--ASTSLRPAQS--ALRLAGSPRRWCWGAPALSPARRAF----HADTRRRKTLTYATDKGPEESLKKTEVDRLIDMLRAN-
ZmBFA3 1 ---MATTA--ASTSLRPLSPS--PRLIASLPRRCWGWIPVQSGRSAP----HAQRRRRSTLLCAADKAPESLKKTEVDRLIDMLRAN-
SmBFA3 1 MATMAAASAFCSIRSSNGNH-WASGYVTRPVALRIHSIAE--P-----NLRMCSETRSNFCTICAAADSPQASQSSKEIDRLIDMLRST-
PpBFA3 1 -----MS-----RSTVHVVAASSTKIFRTEVDRLIDMLRST-
CrBFA3 1 -MQVSRANV---CARSSPVRVQAFSSCPVVRVSTCARVVRNSACR-----SAAQPRQRPSRFVGAARSELSDSLKPAALDPLDKLSSAKS

AtBFA3 88 PRQVEKIVVENILAFDEVFVIRLAARSPTCKSDDDKKDYEELATTVMITLVDCVVKTRKIEESTDLKGLLRPAIDG-VEEISWPPRDPFAINL
GmBFA3 86 PREIQKLVVENILAFNPFVWRLAARDTCKSDDDKKDYEELATTVMITLVDCVVKTRKIEESTDVLKGLKRVIDD-EGEIPWPPRDRQATL
OsBFA3 84 PRELDQIVVENVLAFDGFWVRLAARDLCKSDDDKKDYEELANVMNIVDRVHKTDKIEESTDVLKATISVMHE-GENATWPPRDEPAIKL
ZmBFA3 82 PRELDQIVVENVLAFDAGFWVRLAARDLCKSDDDKKDYEELANVMNIVDRVHKTDKIEESTDVLKATISVMHE-GD-VKWPFRDPDTKLL
SmBFA3 87 SQLLQIVAVENVLAFDKFWVRLAARDLCKSDDDKKDYEELANVMNIVDRVHKTDKIEESTDVLKATISVMHE-VAGSKNEIWPFRDEPAIQR
PpBFA3 36 YHMAQIVAVENVLAFDKFWVRLAARDLCKSDDDKKDYEELASQIMSLVVRIVSKTKIEESTDVLKATISVMHE-DNEIWPFRNEASLIE
CrBFA3 83 QQLLQIVAVENVLAFDKFWVRLAARDLCKSDDDKKDYEELASQIMSLVVRIVSKTKIEESTDVLKATISVMHE-QLADSGAVLQDILVAADDDKGE-WYDPLTD-DQVES

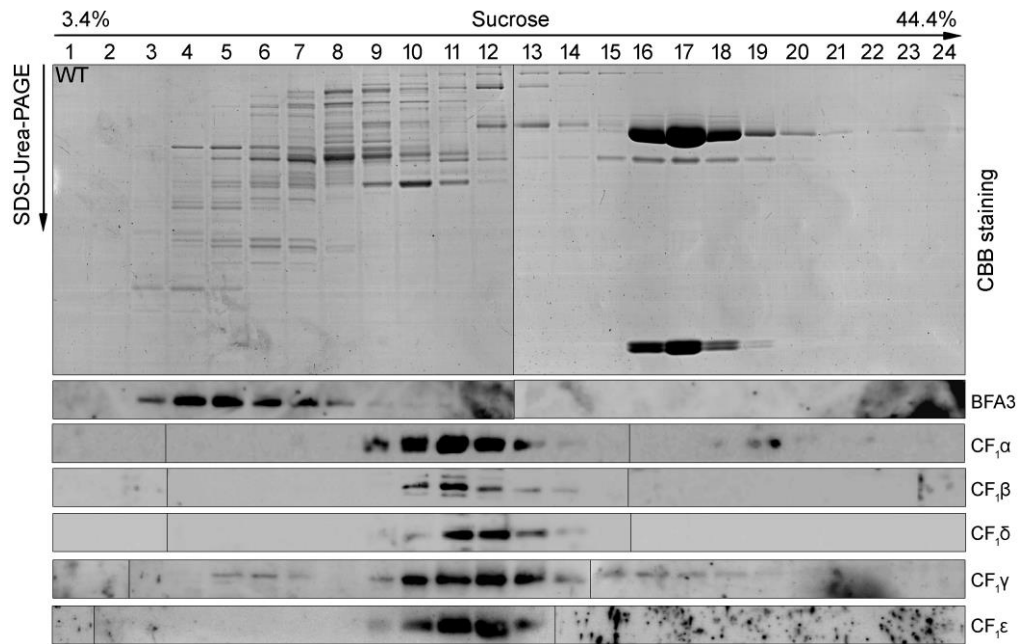
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GmBFA3 180 MKKEISQREKREGQDDEGFLSEVNAQLRQAKEDGDKPGLAMLOKVLQLYASAVLSKRSYAMKCKEVLKDBQLLETLIQAPEQEWSHLITNGLTHG
OsBFA3 178 MKKEISNREKREGQDDEGFLSEVNAQLRQAKQDGDKPGLOAMLOKVLQLYASNFKRSYAYKGGVIVPVSFLSEVHKAPENWNKLLDGLTVG
ZmBFA3 175 MKKEITRREKREGQDDEGFLSEVNAQLRQAKQDGDKPGLOAMLOKVLQLYASKSLKRSYAYKGGVIVPVSFLSEVHKAPENWNKLLDGLTVG
SmBFA3 182 VRKEMHRESGVLDDGFLSEVNAQLRQAKEDKDKPGLAMLOKVLQLYAAFLAKTSYAKRDGVVDEABELLENTISADSEAWDSMIRSGVDLG
PpBFA3 130 MRKEVEKRELENFLEDSFLSEVNAQLRQAKEDKDKPGLAMLOKVLQLYAACLSKRSYAMKRDGVVDKABELLEKMDVDBKWNDDLRRNGFYG
CrBFA3 158 VREAN-N-RHRDRLEBALSNAFWIKKSSBDG-PDGVVQLQDVLQLYAARQLATGE-----TEGVGAVNKLGLSQBQKQWTFPLRLQV--A

AtBFA3 277 KGDITPDEFSAVIKKRIERTLIRTEGGSYQORILTEYLKTEERANRIMKLLQG-----
GmBFA3 275 AGDISAEDLFAVLKKRIERVLRTEGGSYQORILTEYLKTEERABEIVQVLOGRFPQ---
OsBFA3 273 KGNVSPPEFYAVIKKRIERVLRTEGGSYQORILTEYLKTEERAREEVVKVLOGPTI---
ZmBFA3 270 KGDVSPDLYAVINIKKRIERVLRTEGGSYQORILTEYLKTEERAREEVVKVLOGPTI---
SmBFA3 277 GGPVKSVDLRKMAKKRIERTLIRTEGGSYQORILTEYLKTEERASVDMVVAAFSS-----
PpBFA3 225 GGPVPSDEFFKAVDRRIERTLIRTEGGSYQORILTEYLKTEERARASLTAAPQSSPSSR-
CrBFA3 241 EGQLTEAAMPMEALQRKMEGVVGLGLQSGSYAQRVQAEYLKTEERAKRSVFPQETAAASAPKQA

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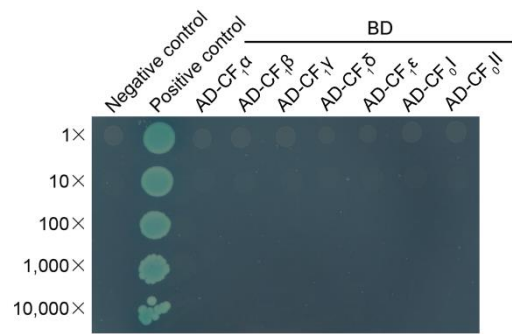
Supplemental Figure S2. Alignment of BFA3 homologs.

Sequences were retrieved from GenBank and aligned with ClustalW2. Identical amino acids are shown as white letters on a black background, and similar amino acids are indicated as black letters on a gray background. The predicted cleavage site of AtBFA3 is indicated by an arrow above the sequence. AtBFA3 (AT2G21385, *Arabidopsis thaliana*), GmBFA3 (XP_006592087.1, *Glycine max*), OsBFA3 (NP_001063753.1, *Oryza sativa*), ZmBFA3 (ACG43670.1, *Zea mays*), SmBFA3 (XP_002992058.1, *Selaginella moellendorffii*), PpBFA3 (XP_001780245.1, *Physcomitrella patens*), CrBFA3 (XP_001701296.1, *Chlamydomonas reinhardtii*)



Supplemental Figure S3. Sucrose density gradient analysis of stromal proteins.

Stromal proteins isolated from wild-type (WT) leaves were fractionated by centrifugation in a linear 3.4–44.4% sucrose gradient. After ultracentrifugation, 24 fractions of equal volume were collected (numbered from top to bottom). ATP synthase subunits and BFA3 were identified by probing with the appropriate antibodies. The arrow above the panels indicates the sucrose density gradient (from low to high). For Coomassie Brilliant Blue (CBB) staining and each immunoblot, the figures were combined from two different gels of a single experiment.



Supplemental Figure S4. Control for yeast two-hybrid analysis. Subunits of the CF₁ subcomplex as well as soluble parts of CF₀I and CF₀II were fused to pGADT7 and the resulting vectors were cotransformed with pGBKT7. AD, GAL4 activation domain; BD, GAL4 DNA-binding domain.

AthCF _β	MRINPTTSSNPEVSIREKKNLGRIAQIIIGFVLDVAFPPGRMKNIYNALVVKGRDITLQEQINVTCEVQC LGNNRRAVAVMSATBGL	85
GmaCF _β	MRINPTTSSGPEVSALEKKNLGRIAQIIIGFVLDVAFPPGRMKNIYNALVVKGRDITVGGQINVTCEVQC LGNNRRAVAVMSATBGL	85
OsaCF _β	MRTNPTTSSRPGVSTIEEKSTGRIDQIIIGFVLDVTFPPGKLFPIYNALVVKSRDITDGQINVTCEVQC LGNNRRAVAVMSATBGL	85
ZmaCF _β	MRTNPTTSSRPGVSTIEEKSVGRIDQIIIGFVLDVTFPPGKLFPIYNALVVKSRDITDGQINVTCEVQC LGNNRRAVAVMSATBGL	85
SmoCF _β	MPIIYNSLTVTGRNPAAGCEINVTCEVQC SLGNNRRAVAVMSATBGL	46
PpaCF _β	MKNDSTRTFGASTVLTKTQNIIGRISQIIIGFVLDVTFPPGRMKNIYNALVVKGRDITLQEQINVTCEVQC LGNNRRAVAVMSATBGL	85
CreCF _β	MPFGILIFLITMSDSIETKNMGRIVQIIIGFVLDVFAKQVFNPIYNALVIRAKNSAGTEMAVTCEVQC LGNNRRAVAVMSATBGL	85
SynCF _β	MVAVKEATNVKGIITQVIGFVILIAQFESGKLFPIYNALVVKGRNSAGNEVAVTCEVQC LGNNRRAVAVMSATBGL	75
NosCF _β	MVITAEKRTNIGYITQIIIGFVVDVVFENGLKFCIYNALVIRKGTNEAGQQLNVTCEVQC LGNNRRAVAVMSATBGL	75
TheCF _β	MVISAERTNVFITQVIGFVVDVVFENGLKFCIYNALVIRKGTNEAGQQLNVTCEVQC LGNNRRAVAVMSATBGL	75
RicCF _β	MVITAEKRTNIGYITQIIIGFVVDVVFENGLKFCIYNALVIRKGTNEAGQQLNVTCEVQC LGNNRRAVAVMSATBGL	75

	I	
	mβ1 mβ2 mβ3 mβ4	
AthCF _β	VRGMDVVDIGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	170
GmaCF _β	VRGMEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	170
OsaCF _β	VRGMEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	170
ZmaCF _β	VRGMEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	170
SmoCF _β	VRGMEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	131
PpaCF _β	VRGMDVVDIGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	170
CreCF _β	VRGMEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	170
SynCF _β	VRGMDVVDIGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	160
NosCF _β	VRGLEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	160
TheCF _β	VRGMEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	160
RicCF _β	VRGMEVDIDGAPP SVVPGGATLGRIFN LGPEVDNIGFVDTRITSPHRSAPAFIEIDTSLIFETGIKV DLLAPYRGGKIGL	160

	II-1	
	mβ5 mβ6 mβ7mβ8 mβ9	
AthCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	255
GmaCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	255
OsaCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	255
ZmaCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	255
SmoCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	216
PpaCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	255
CreCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	255
SynCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	245
NosCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	245
TheCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	245
RicCF _β	FGGAGVGKTVLIMELINNIARKHGGVSVGGVGGERTREGNDLYMEMRESGVINECNLAE SKVALVYGMNEPPGARMRVGLTALT	245

	II-2	
	mβ10	
AthCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	340
GmaCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	340
OsaCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	340
ZmaCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	340
SmoCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	301
PpaCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	340
CreCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	340
SynCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	330
NosCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	330
TheCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	330
RicCF _β	MAEYERDNNQDVLFDNIRFVQAG EVSALLGRMFAVGGQPTLETGGLQERITSTRKGSITSIQAVYVPADLLDPAPA	330

	II-3	
	mβ11 mβ12	
AthCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	425
GmaCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	425
OsaCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	425
ZmaCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	425
SmoCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	386
PpaCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	425
CreCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	425
SynCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	415
NosCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	415
TheCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	415
RicCF _β	TFFAHLDTTVLSRGLARAGIYPAVDPLSTSNLQFRIVGGEHYETACQVKCTLQRYKE QDIAAILGLDELSEEDRLVVRAR	415

AthCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	497
GmaCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	497
OsaCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	497
ZmaCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	497
SmoCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	451
PpaCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	494
CreCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	491
SynCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	483
NosCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	482
TheCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	482
RicCF _β	KIERFLSQFFHVAEVVGTGPGKYVGLAETIRGFKLILSGEDELPEQAFYIVGNIDEATAKATNEMESKIK	483

III

Supplemental Figure S5. Alignment of CF₁β protein sequences.

Amino acid alignment of the CF₁β subunits. Sequences were retrieved from GenBank and aligned with ClustalW2. Identical amino acids are shown as white letters on a black background, and similar amino acids are indicated as black letters on a gray background.

background. Three domains of CF₁β (I, II, and III) and three regions of domain II (II-1, II-2, and II-3) are indicated by different colored lines below the sequences. The positions of the point mutations (mβ1-mβ12) are indicated above the sequences. AthCF₁β (ATCG00480, *Arabidopsis thaliana*), GmaCF₁β (YP_538748.1, *Glycine max*), OsaCF₁β (YP_052756.1, *Oryza sativa*), ZmaCF₁β (NP_043032.1, *Zea mays*), SmoCF₁β (YP_003097494.1, *Selaginella moellendorffii*), PpaCF₁β (NP_904195.1, *Physcomitrella patens*), CreCF₁β (NP_958414.1, *Chlamydomonas reinhardtii*), SynCF₁β (WP_010872712.1, *Synechocystis* sp. PCC 6803), NosCF₁β (WP_010999165.1, *Nostoc* sp. PCC 7120), TheCF₁β (NP_681315.1, *Thermosynechococcus elongatus* BP-1), RinCF₁β (CDN15135.1, *Richelia intracellularis*).

Supplemental Table S1. Phylogenetic analysis of BFA3 and CF₁β

Group	Phylum	Species	BFA3	CF ₁ β						
				ID	β5	β6	β7	β8	β9	
Prokaryotic Algae	Cyanophyta	<i>Synechocystis</i> sp. PCC 6803	-	WP_010872712.1	IM	IQ	N	I	ADKPE	
		<i>Nostoc</i> sp. PCC 7120	-	WP_010999165.1	IM	TQ	N	I	NENLN	
		<i>Thermosynechococcus elongatus</i> BP-1	-	NP_681315.1	IM	TQ	N	I	KDDPS	
		<i>Richelia intracellularis</i>	-	CDN15135.1	IM	TQ	N	I	AENLN	
		<i>Microcystis aeruginosa</i>	-	WP_002760447.1	IM	IQ	N	I	ADNPE	
		<i>Spirulina subsals</i>	-	WP_017303185.1	IM	IN	N	I	PDNLG	
		<i>Scytonema tolypothrichoides</i>	-	WP_048869444.1	IM	TQ	N	I	KDNLN	
		<i>Fischerella muscicola</i>	-	WP_016870242.1	IM	TQ	N	I	KDNLN	
		<i>Calothrix</i> sp. 336/3	-	WP_035156122.1	IM	TE	N	I	KDNLN	
		<i>Leptolyngbya boryana</i>	-	WP_017286658.1	IM	TN	N	I	KDNLN	
		<i>Chlorogloeopsis fritschii</i>	-	WP_016874105.1	IM	TE	N	I	NDNLN	
		<i>Stigonematales</i>	-	WP_026721253.1	IM	TQ	N	I	KDNLN	
		<i>Mastigocladopsis repens</i>	-	WP_017319445.1	IM	TE	N	I	KDNLN	
		<i>Synechococcus</i> sp. NKBG15041c	-	WP_024544923.1	IM	TK	N	I	AENLN	
		<i>Tolypothrix campylonemoides</i>	-	WP_041040374.1	IM	TQ	N	I	KDNLN	
		<i>Raphidiopsis brookii</i>	-	WP_009342625.1	IM	TQ	N	I	KENLN	
		<i>Chamaesiphon minutus</i>	-	WP_015160618.1	IM	TN	N	M	KDNLN	
		<i>Anabaena cylindrica</i>	-	WP_015212783.1	IM	TQ	N	M	KDNLN	
		<i>Chroococcales cyanobacterium</i> CENA595	-	WP_045055788.1	IM	IN	N	K	EENIG	
		<i>Planktothricoides</i> sp. SR001	-	WP_054465960.1	-	II	KA	S	K	EKNLS
		<i>Oscillatoria</i> sp. PCC 10802	-	WP_017716567.1	-	II	KA	N	K	EKNLG
		<i>Gloeocapsa</i> sp. PCC 7428	-	WP_015191148.1	-	II	KE	N	K	EENLN
		Prochlorophyta	<i>Prochlorothrix hollandica</i>	-	WP_017713442.1	LI	KE	N	K	EKNIS
			<i>Prochlorococcus</i> sp. W2	-	WP_019475342.1	LI	KE	E	K	ADDLT
		Rhodophyta	<i>Porphyridium purpureum</i>	-	YP_008965686.1	LI	KA	M	R	ASNLA
			<i>Bangia fuscopurpurea</i>	-	AKE98860.1	LI	KA	M	K	ADNLK
			<i>Gracilariopsis lemaneiformis</i>	-	AJO68470.1	LI	KA	E	K	ASDLK
			<i>Cyanidioschyzon merolae</i> strain 10D	-	NP_849101.1	LI	KA	E	K	SQNLK
<i>Porphyra purpurea</i>	-		NP_053869.1	LI	KA	M	K	EDNLK		
<i>Gracilaria salicornia</i>	-		YP_009019644.1	LI	KA	E	K	ANNLK		
<i>Chondrus crispus</i>	-		YP_007627419.1	LI	KA	E	K	ADKLT		
Phaeophyta	<i>Ectocarpus siliculosus</i>	CBJ49272.1	YP_003289267.1	LI	KA	M	K	EKSLL		
	<i>Sphacelaria plumigera</i>	-	BAR97500.1	LI	KA	M	K	ETNLL		
Bacillariophyta	<i>Undaria pinnatifida</i>	-	YP_009182549.1	LI	KA	M	K	EKNLL		
	<i>Coscinodiscus radiatus</i>	-	YP_009028893.1	LI	KA	E	K	ENNFK		
Eukaryotic Algae	Cryptophyta	<i>Biddulphia tridens</i>	-	AKF18280.1	LI	KA	E	K	EKNFP	
		<i>Phaeodactylum tricorutum</i> CCAP 1055/1	XP_002181618.1	YP_874407.1	LI	KA	E	K	EKNFA	
	Euglenophyta	<i>Guillardia theta</i>	XP_005819851.1	ALG63579.1	LI	KA	M	K	ESNLG	
		<i>Teleaulax amphioxeia</i>	-	YP_009159237.1	LI	KA	M	K	EDNLS	
	Charophyta	<i>Cryptomonas paramecium</i>	-	YP_003359241.1	LI	KA	N	L	LENLC	
		<i>Euglenaformis proxima</i>	-	YP_009032763.1	LI	KA	Q	K	SGNLQ	
		<i>Trachelomonas volvocina</i>	-	YP_009145498.1	LI	KA	Q	K	SSNLK	
	Chlorophyta	<i>Cryptoglena skujai</i>	-	YP_009145387.1	LI	KA	Q	K	SSNLK	
		<i>Chara vulgaris</i>	-	YP_635746.1	LI	KA	M	K	ENISE	
	Gymnosperm	<i>Nitella axilliformis</i>	-	AIC74296.1	LI	KA	M	K	QENIS	
<i>Tolypella boldii</i>		-	AIC74260.1	LI	KA	M	K	QENIS		
Angiosperm	Angiospermae	<i>Chlamydomonas reinhardtii</i>	XP_001701296.1	NP_958414.1	LI	KA	T	K	EKNLS	
		<i>Coccomyxa subellipsoidea</i> C-169	EIE21223.1	YP_004222003.1	LI	KA	A	K	EDNLS	
		<i>Chlorella variabilis</i>	EFN59214.1	YP_004347820.1	LI	KA	M	K	ESNLS	
		<i>Volvox carteri f. nagariensis</i>	XP_002947163.1	ACY05995.1	LI	KA	T	K	EKNLS	
		<i>Auxenochlorella protothecoides</i>	XP_011400029.1	YP_009019317.1	LI	KA	M	K	ESNIA	
		<i>Bathycoccus prasinos</i>	XP_007509545.1	YP_009056877.1	LI	KA	Q	C	KGNLG	
		<i>Ostreococcus tauri</i>	XP_003082051.1	AGW30608.1	LI	KA	Q	C	TANLA	
		<i>Physcomitrella patens</i>	XP_001780245.1	NP_904195.1	LI	KA	M	K	EENIS	
		<i>Selaginella moellendorffii</i>	XP_002964112.1	YP_003097494.1	LI	KA	M	K	AQNIS	
		<i>Picea sitchensis</i>	ABK27019.1	YP_002905096.1	LI	KA	M	K	EQKIS	
Angiosperm	Angiospermae	<i>Oryza sativa</i>	XP_015611535.1	YP_052756.1	LI	KA	M	K	EKNLE	
		<i>Zea mays</i>	ACG43670.1	NP_043032.1	LI	KA	M	K	EKNIE	
		<i>Arabidopsis thaliana</i>	AT2G21385	ATCG00480	LI	KA	M	K	EQNLA	
		<i>Glycine max</i>	XP_006592087.1	YP_538748.1	LI	KA	M	K	EQNIA	
		<i>Eutrema salsugineum</i>	XP_006404584.1	YP_009175682.1	LI	KA	M	K	EQNLA	
		<i>Populus trichocarpa</i>	XP_002306131.2	YP_001109508.1	LI	KA	M	K	EENIA	
		<i>Tarenaya hassleriana</i>	XP_010555273.1	AAK72746.1	LI	KA	M	K	EQNLA	
		<i>Prunus persica</i>	XP_007199184.1	YP_004021672.1	LI	KA	M	K	EQNIA	
		<i>Prunus mume</i>	XP_008236971.1	YP_009020045.1	LI	KA	M	K	EQNIA	
		<i>Citrus sinensis</i>	XP_006487331.1	YP_740482.1	LI	KA	M	K	DQNLS	
<i>Gossypium raimondii</i>	XP_012436293.1	YP_005087700.1	LI	KA	M	K	EQNLA			

BFA3 and CF1 β sequence searches were performed at the NCBI Blast server (<http://www.ncbi.nlm.nih.gov/BLAST/>). “-” indicates no homolog was found during the blast search. The critical CF1 β sites (CF1 β 5, CF1 β 8, and CF1 β 9) for BFA3 binding are in blue. The highly conserved residues in CF1 β 9 are in red.

Supplemental Table S2. Primers used in this work

The following primers were used to detect T-DNA insertion sites:

LBa1: 5' TGGTTCACGTAGTGGGCCATCG 3'

BFA3-sense: 5' TCTGAATTCTCTGGACTCCATTTGAACCG 3'

BFA3-anti: 5' GAGGTCGACCATAATTTTCATTAGCCCTGG 3'

The following primers were used for complementation vector construction:

BFA3-Com-sense: 5' GTCGAATTCCTTGTATGTAATGTC 3'

BFA3-Com-anti: 5' ACGGTCGACACCCTGGAGTAATTTTC 3'

Pr-RbcS-sense: 5' AGATCTAGATGGCTTCTCTATGCTCTC 3'

Pr-RbcS-anti: 5' AGCCTCGAGGGAATCGGTAAGGTCAG 3'

SynATPB-sense: 5' ATACTCGAGATGGTAGCCGTAAAAG 3'

SynATPB-anti: 5' TATACTAGTTTAACCCTCTTTGAGCTTGGCAC 3'

The following primers were used for RT-PCR:

BFA3-RT-sense: 5' TTGGATAAGACTAGCAGCTAGGTC 3'

BFA3-RT-anti: 5' GAGGTCGACCATAATTTTCATTAGCCCTGG 3'

ACT8-sense: 5' AGTGGTCGTACAACCGGTATTGT 3'

ACT8-anti: 5' GAGGATAGCATGTGGAAGTACTGAGAA 3'

The following primers were used to prepare hybridization probes for Northern analysis:

ATPH-Northern-sense: 5' ATGAATCCACTGGTTTCTG 3'

ATPH-Northern-anti: 5' AAAGCGCTAATGCTACAAC 3'

ATPI-Northern-sense: 5' ATCATGTTCCATCAACACAC 3'

ATPI-Northern-anti: 5' CCGCATAAAAATAGGCTAC 3'

ATPA-Northern-sense: 5' GTACCGTGAACAACACACT 3'

ATPA-Northern-anti: 5' GCTTTATCGAGATCAGAAG 3'

ATPF-Northern-sense: 5' TTAGATAACCGAAAGCAGAGG 3'

ATPF-Northern-anti: 5' TTCATCGTACCAAACATCCC 3'

ATPF-in-Northern-sense: 5' TCAAGAATAGGCTGGATTACCCAG 3'

ATPF-in-Northern-anti: 5' TTTGGCTCTCATGCTCACTTATTCC 3'

ATPB/E-Northern-sense: 5' AAATTGGACTATTCGGTGG 3'

ATPB/E-Northern-anti: 5' AAATCGTATTGAGAGCCTCG 3'

The following primers were used for yeast two-hybrid vector construction:

BFA3-BD-sense: 5' TCTGAATTCTCTGGACTCCATTTGAACCG 3'

BFA3-BD-anti: 5' GATGGATCCATAATTTTCATTAGCCCTGGAC 3'

ATPA-AD-sense: 5' ACTCATATGATGGTAACCATTAGAGCCGAC 3'

ATPA-AD-anti: 5' AGCGTCGACTACTTTCTCTGAAGTAGG 3'

ATPB-AD-sense: 5' CGCGAATTCATGAGAACAATCCTAC 3'

ATPB-AD-anti: 5' GCGCTCGAGTTTCTTCAATTTACTC 3'

ATPC-AD-sense: 5' CCACATATGGCGTCTCTTCGTGAG 3'

ATPC-AD-anti: 5' ATCCTCGAGAACCTGTGCATTAGCTC 3'

ATPD-AD-sense: 5' ATACATATGGCCACCGCAGCATCAAG 3'

ATPD-AD-anti: 5' GCGGAATTCAGTAGCTAATTGAATCTCACC 3'
ATPE-AD-sense: 5' CGACATATGATGACCTTAAATCTTTG 3'
ATPE-AD-anti: 5' TATGAATTCAATCGTATTGAGAGCCTCG 3'
ATPF-AD-sense: 5' GCGGGATCCATGATTTATTAGATAACCG 3'
ATPF-AD-anti: 5' AGTCTCGAGATCAGTTATTTCTTTC 3'
ATPG-AD-sense: 5' TATGAATTCCTGCTTGGTAACTTCATGG 3'
ATPG-AD-anti: 5' GATGGATCCAGAAGGAAGAACCTTCTTGACAAT 3'
ATPBI-AD-sense: 5' CGCGAATTCATGAGAACAAATCCTAC 3'
ATPBI-AD-anti: 5' ACTCTCGAGATTTCCCATATCAACCAC 3'
ATPBII-AD-sense: 5' ATGGAATTCCTCTAAGTGTTCAG 3'
ATPBII-AD-anti: 5' AACCTCGAGAGGTTGTAGCATAGTTG 3'
ATPBIII-AD-sense: 5' CTAGAATTCCGAATCGTTGGCGAG 3'
ATPBIII-AD-anti: 5' GCGCTCGAGTTTCTTCAATTTACTC 3'
ATPBII-1-AD-sense: 5' ATGGAATTCCTCTAAGTGTTCAG 3'
ATPBII-1-AD-anti: 5' AATCTCGAGCCCACGACGATAAG 3'
ATPBII-2-AD-sense: 5' CGTGAATTCGAAAAATTGGACTATTTCGG 3'
ATPBII-2-AD-anti: 5' GCGCTCGAGGATATTGTTCGATAAATAG 3'
ATPBII-3-AD-sense: 5' GATGAATTCTTCCGTTTCGTACAAGC 3'
ATPBII-3-AD-anti: 5' AACCTCGAGAGGTTGTAGCATAGTTG 3'
SynATPB-AD-sense: 5' GCAGAATTCATGGTAGCCGTAAGAAGCAAC 3'
SynATPB-AD-anti: 5' TTTGTTCGACACCCTCTTTGAGCTTGGCAC 3'

The following primers used for protein expression vectors construction:

BFA3-GFP-sense: 5' TTCTCTAGAATGGCGGCAATATCCCTG 3'
BFA3-GFP-anti: 5' TTACCGCGGTAACCCTGGAGTAATTTTCAT 3'
ATP11-GFP-sense: 5' ACCGGATCCATGAGAAGAATCGTCG 3'
ATP11-GFP-anti: 5' TCCCCGCGGCACAGAAGAGGCATAT 3'
BFA3-Ab-sense: 5' TCTGAATTCTCTGGACTCCATTTGAACCG 3'
BFA3-Ab-anti: 5' GAGGTCGACCATAATTTATTAGCCCTGG 3'
BFA3-GST-sense: 5' TCTGAATTCTCTGGACTCCATTTGAACCG 3'
BFA3-GST-anti: 5' GAGGTCGACCATAATTTATTAGCCCTGG 3'
ATPA-MBP-sense: 5' ACTCATATGATGGTAACCATTAGAGCCGAC 3'
ATPA-MBP-anti: 5' AGCGTCGACTACTTTCTCCTGAAGTAGG 3'
ATPB-MBP-sense: 5' GCGCATATGATGAGAACAAATCCTAC 3'
ATPB-MBP-anti: 5' CGCGTCGACTTTCTTCAATTTACTC 3'
ATPC-MBP-sense: 5' CCACATATGGCGTCTCTTCGTGAG 3'
ATPC-MBP-anti: 5' ATCCTCGAGAACCTGTGCATTAGCTC 3'
ATPD-MBP-sense: 5' ATACATATGGCCACCGCAGCATCAAG 3'
ATPD-MBP-anti: 5' GCGGAATTCAGTAGCTAATTGAATCTCACC 3'
ATPE-MBP-sense: 5' CGACATATGATGACCTTAAATCTTTG 3'
ATPE-MBP-anti: 5' TATGAATTCAATCGTATTGAGAGCCTCG 3'
ATPF-MBP-sense: 5' GCGGTTCGACGATTTATTAGATAACCG 3'
ATPF-MBP-anti: 5' CGCGAATTCATCAGTTATTTCTTTC 3'
ATPG-MBP-sense: 5' TATGTTCGACCCGCTTGGTAACTTCATGG 3'

ATPG-MBP-anti: 5' GCGGAATTCAGAAGGAAGAACCTTCTTGAC 3'

The following primers were used for mutagenesis of *SynATPB* and *AthATPB*:

SynATPB1-sense: 5' TTAGGCCCCGTGGATACTCGTACAACCTTCTCCATTACCCGTCCC
3'

SynATPB1-anti: 5' AGAAGTTGTACGAGTATCCACGGGGCCTAAGTTGTCAACAGGCTC
3'

SynATPB2-sense: 5' TCTGCTCCCGCTTTTATAGAATTGGAAACCAAGCCC 3'

SynATPB2-anti: 5' TTCTATAAAAGCGGGAGCAGAACGGTGAATGGGGAAAG 3'

SynATPB3-sense: 5' TGGTGGATTTGGATACCAAGTTGCAAGTATTTGAAACC 3'

SynATPB3-anti: 5' CAAATACTTGCAACTTGGTATCCAAATCCACCAATTTGGG 3'

SynATPB4-sense: 5' TGCTTGCTCCCTACCGTCGTGGTGGCAAATCGGTC 3'

SynATPB4-anti: 5' TTTGCCACCACGACGGTAGGGAGCAAGCAGGTCAATTAC 3'

SynATPB5-sense: 5' GGGCAAACCGTACTCATCATGGAATTGATTAAC 3'

SynATPB5-anti: 5' GTTAATCAATTCCATGATGAGTACGGTTTTGCC 3'

SynATPB6-sense: 5' TTAACAACATCGCCAAAGCACATGGTGGTGTATC 3'

SynATPB6-anti: 5' GATACACCACCATGTGCTTTGGCGATGTTGTAA 3'

SynATPB7-sense: 5' GGAATGACCTCTACATGGAAATGATCGAATCCAACGTAATC 3'

SynATPB7-anti: 5' GATTACGTTGGATTCGATCATTTCCATGTAGAGGTCATTCC 3'

SynATPB8-sense: 5' GGAATGACCTCTACAACGAAATGAAGGAATCCAACGTAATC 3'

SynATPB8-anti: 5' GATTACGTTGGATTCCTTCATTTTCGTTGTAGAGGTCATTCC 3'

SynATPB9-sense: 5' CCAACGTAATCAACGAACAAAATCTTGCAGAGTCCAAAATTGC 3'

SynATPB9-anti: 5' GCAATTTTGGACTCTGCAAGATTTTGTTCGTTGATTACGTTGG 3'

SynATPB10-sense: 5' ACTTTAAGTACGGAAATGGGTACTTTGCAAGAGCGTATC 3'

SynATPB10-anti: 5' GCAAAGTACCCATTTCCGTACTTAAAGTGGGCTGGTAAC 3'

SynATPB11-sense: 5' ACCATGCTTCAGCCCCGAATCGTTGGGTCAGAG 3'

SynATPB11-anti: 5' CTCTGACCCAACGATTCGGGGCTGAAGCATGGTG 3'

SynATPB12-sense: 5' ACACCGCTCAACAAGTGAAACAAACCCTGCAACGCTAC 3'

SynATPB12-anti: 5' TTGCAGGGTTTGTTCCTTACTTGTGAGCGGTGTCGTAATG 3'

AthATPB5-sense: 5' GCGTGGGTAAAACAGTAATCATGATGGAATTGATCAAC 3'

AthATPB5-anti: 5' GTTGATCAATTCCATCATGATTACTGTTTTACCCACGC 3'

AthATPB8-AD-sense: 5' GAAATGATCTTTACATGGAAATGATCGAATCTGGAGTCATT 3'

AthATPB8-AD-anti: 5' AATGACTCCAGATTCGATCATTTCCATGTAAAGATCATTTTC 3'

AthATPB9-AD-sense: 5' CTGGAGTCATTAATGCAGATAAACCTGAAGAATCCAAAGTGGCC 3' 5'

AthATPB9-AD-anti: 5' GGCCACTTTGGATTCTTCAGGTTTATCTGCATTAATGACTCCAG
3'