Table S1 - Contigs >200 bp and >15x coverage from the SRR039878 MIRA assembly

# name	length	av.qual	#-reads	mx.cov.	av.cov	GC%	blast (<10^{-5})
Galdieria_rep_c807	21716	61	21276	172	85.98	43.94	Mt (full)
Galdieria_rep_c808	13012	60	5631	82	39.74	33.4	Cp
Galdieria_rep_c809	4830	59	1608	52	31.11	29.34	Cp
Galdieria_rep_c812	8374	59	2709	54	31.08	24.6	Cp
Galdieria_rep_c811	16987	59	5320	50	29.88	28.1	Cp
Galdieria_rep_c813	7704	59	2447	60	29.84	26.36	Cp
Galdieria_rep_c815	11901	59	3697	56	29.58	26.58	Cp
Galdieria_rep_c819	17564	60	5566	53	29.53	28.06	Cp
Galdieria_rep_c821	8023	60	2511	45	29.36	29.1	Cp
Galdieria_rep_c831	6154	59	1949	47	29.22	27.48	Cp
Galdieria_rep_c816	11927	59	3670	55	28.88	26.84	Cp
Galdieria_rep_c814	9647	60	3082	50	28.71	29.97	Cp
Galdieria_rep_c850	228	55	65	60	28.67	39.47	Mt (repeat region)
Galdieria_rep_c818	7767	59	2390	51	28.44	29.13	Cp
Galdieria_rep_c828	7084	59	2130	43	28.31	26.89	Cp
Galdieria_rep_c824	3770	59	1122	44	27.58	29.77	Cp
Galdieria_rep_c822	4689	59	1365	45	27.57	25.02	Cp
Galdieria_rep_c825	6138	59	1799	46	27.14	27.34	Cp
Galdieria_rep_c829	2561	59	760	47	27.09	27.72	Cp
Galdieria_rep_c820	421	52	114	54	26.99	24.29	Nc (Gasu_62900)
Galdieria_rep_c834	3273	59	953	41	26.8	28.02	Cp
Galdieria_rep_c844	231	52	65	59	26.75	40.26	Mt (repeat region)
Galdieria_rep_c837	1066	58	294	41	26.41	24.77	Cp
Galdieria_rep_c830	1694	57	472	46	26.41	24.79	Cp
Galdieria_rep_c817	6517	59	1827	48	26.21	24.8	Cp
Galdieria_rep_c833	588	58	170	40	25.97	26.7	Cp
Galdieria_rep_c836	744	59	226	50	25.46	34.81	Nc (Gasu_61090)
Galdieria_rep_c823	1891	57	492	51	24.9	26.6	Nc (Gasu_62020)
Galdieria_rep_c826	1672	58	462	41	23.76	28.83	Cp
Galdieria_rep_c810	2549	54	603	92	22.29	31.83	Nc (Gasu_63970)
Galdieria_c804	1925	58	475	60	21.51	35.45	Nc (Gasu_34410)
Galdieria_rep_c840	317	56	63	33	18.36	36.59	Nc (Gasu_63580)
Galdieria_rep_c862	668	55	126	46	17.94	33.88	Nc (Gasu_63970)
Galdieria_rep_c827	3208	58	626	58	16.87	35.66	Nc (Gasu_64790)
Galdieria_rep_c846	1129	56	209	36	16.23	35.43	Nc (Gasu_62440)
Galdieria_rep_c845	821	59	150	38	16.21	35.32	No Match
Galdieria_c797	714	54	143	39	16.13	32.35	Nc (Gasu_65690)
Galdieria_rep_c848	2512	58	481	43	16.04	32.84	No Match
Galdieria_rep_c861	373	56	66	30	15.96	21.98	Cp
Galdieria_rep_c854	1175	56	203	35	15.4	37.11	Nc (Gasu_42170)
Galdieria_rep_c838	3205	58	557	49	15.23	34.1	Nc (Gasu_61670)
Galdieria_rep_c875	488	48	81	40	15.07	25.41	Nc (Gasu_15650)
Galdieria_c388	203	52	33	28	14.73	19.21	Nc (Gasu_63970)
Galdieria_rep_c835	1232	55	201	51	14.5	35.88	Nc (Gasu_61740)

Table S2 - Change in amino acid usage among red algal mitochondrial genomes

	Cyanidiophyceae		Bangiophyceae				Florideophyceae					Median
	Cmer	Gsul	Phai	Ppur	Pumb	Pyez	Ccri	Gand	Glem	Gory	Ppul	AA Freq
A	-1.3	-2.3	1.1	1.1	1.1	1.0	-1.2	1.0	-1.0	-1.0	-1.4	4.9
C	-1.1	1.0	-1.0	1.1	1.4	-1.1	1.1	-1.1	-1.1	-1.0	1.8	1.3
D	1.0	-2.0	1.2	1.4	1.2	1.3	-1.0	-1.0	-1.0	-1.1	-1.1	2.3
E	-1.0	3.2	1.2	1.3	1.0	1.2	-1.1	-1.0	-1.0	-1.0	-1.2	2.8
F	1.0	-3.9	-1.2	-1.3	-1.1	-1.3	1.0	1.1	1.0	-1.0	1.1	9.2
G	-1.2	2.1	1.0	-1.0	1.0	1.0	-1.1	-1.0	-1.0	1.0	-1.1	5.6
H	1.0	-1.4	1.0	1.0	-1.0	1.1	-1.1	-1.0	-1.0	1.0	-1.0	2.0
I	1.2	-1.0	-1.0	-1.1	-1.1	-1.1	1.1	-1.0	1.0	1.0	1.2	10.8
K	1.1	-1.2	1.3	1.2	1.1	1.4	-1.0	-1.1	-1.0	-1.1	-1.0	5.1
L	1.0	-2.2	-1.2	-1.2	-1.1	-1.2	1.0	1.1	1.1	1.0	-1.0	14.1
M	-1.5	3.6	-1.0	-1.1	-1.0	-1.1	-1.0	1.1	1.1	1.1	1.0	2.6
N	1.3	-2.5	1.1	1.1	-1.1	1.1	1.0	-1.0	-1.0	-1.1	-1.0	4.8
P	-1.2	-1.4	1.0	1.1	1.0	1.1	-1.0	1.0	-1.0	-1.0	-1.0	3.3
Q	-1.1	-2.9	1.2	-1.0	1.1	1.1	1.1	1.0	-1.0	-1.0	-1.1	2.5
R	-1.0	2.3	1.3	1.3	1.2	1.4	-1.0	-1.1	-1.0	-1.1	-1.1	2.7
S	-1.1	1.1	-1.0	1.1	1.0	1.0	1.1	-1.1	-1.0	-1.0	-1.0	7.7
T	-1.2	-2.6	-1.0	1.1	1.1	1.0	1.0	-1.0	-1.0	1.0	-1.3	5.2
V	-1.1	1.8	-1.0	1.1	1.1	1.0	-1.1	1.0	-1.0	-1.0	-1.1	5.6
W	-1.2	1.7	-1.1	-1.1	-1.0	-1.1	1.1	1.1	1.0	1.0	-1.0	2.0
Y	1.3	-1.0	-1.0	1.0	1.0	-1.1	-1.1	1.0	-1.0	-1.0	1.3	4.5

X	>1.5-fold increase relative to the median AA frequency
-X	>1.5-fold decrease relative to the median AA frequency

Cmer: *Cyanidioschyzon merolae* ; Gsul: *Galdieria sulphuraria* ; Phai: *Pyropia haitanensis* ; Ppur: *Porphyra purpurea* ; Pumb: *Porphyra umbilicalis* ; Pyez: *Pyropia yezoensis* ; Ccri: *Chondrus crispus* ; Gand: *Gracilariopsis andersonii* ; Glem: *Gracilariopsis lemaneiformis* ; Gory: *Gracilariophila oryzoides* ; Ppul: *Plocamiocolax pulvinata* .

Table S3A - Protein-coding genes in red algal plastid genomes

		Cyanidiophyceae			Bangiophyceae			Florideophyceae			
Gene name	**Synonyms**	**Ccal**	**Cmer**	**Gsul**	**Phai**	**Pyez**	**Ppur**	**Gten**	**Ccri**	**Ctub**	**Gtai**
DNA replication											
dnaB		+	+	+	+	+	+	+	+	+	+
Gene regulation											
hupA	hlpA	-	+	+	-	-	-	-	-	-	-
ntcA	ycf28	+	+	+	+	+	+	+	+	+	+
thdF	trmE, thdH	+	+	-	-	-	-	-	-	-	-
rbcR	lysR, ycf30, trsE	+	+	+	+	+	+	+	+	+	+
dfr	ycf26	+	-	ψ	+	+	+	+	-	+	+
Transcription and mRNA processing											
rpoA		+	+	+	+	+	+	+	+	+	+
rpoB		+	+	+	+	+	+	+	+	+	+
rpoC1	rpoC	+	+	+	+	+	+	+	+	+	+
rpoC2		+	+	+	+	+	+	+	+	+	+
rpoZ	ycf61, rbp6, orf75	+	+	+	+	+	+	+	+	+	+
rne		-	-	-	+	+	+	+	+	+	+
Ribosomal proteins											
rpl1		+	+	+	+	+	+	+	+	+	+
rpl2		+	+	+	+	+	+	+	+	+	+
rpl3		+	+	+	+	+	+	+	+	+	+
rpl4		+	+	+	+	+	+	+	+	+	+
rpl5		+	+	+	+	+	+	+	+	+	+
rpl6		+	+	+	+	+	+	+	+	+	+
rpl9		-	-	+	+	+	+	+	+	+	+
rpl11		+	+	+	+	+	+	+	+	+	+
rpl12		+	+	+	+	+	+	+	+	+	+
rpl13		+	+	+	+	+	+	+	+	+	+
rpl14		+	+	+	+	+	+	+	+	+	+
rpl16		+	+	+	+	+	+	+	+	+	+
rpl18		+	+	+	+	+	+	+	+	+	+
rpl19		+	+	+	+	+	+	+	+	+	+
rpl20		+	+	+	+	+	+	+	+	+	+
rpl21		+	+	+	+	+	+	+	+	+	+
rpl22		+	+	+	+	+	+	+	+	+	+
rpl23		+	+	+	+	+	+	+	+	+	+
rpl24		+	+	-	+	+	+	+	+	+	+
rpl27		+	+	+	+	+	+	+	+	+	+
rpl28		+	+	+	+	+	+	+	+	+	+
rpl29		+	+	+	+	+	+	+	+	+	+
rpl31		+	+	+	+	+	+	+	+	+	+
rpl32		+	+	+	+	+	+	+	+	+	+
rpl33		+	+	+	+	+	+	+	+	+	+
rpl34		+	+	-	+	+	+	+	+	+	+
rpl35		+	+	+	+	+	+	+	+	+	+
rpl36	secX	+	+	+	+	+	+	+	+	+	+
rps1		-	-	-	+	+	+	+	+	+	+
rps2		+	+	+	+	+	+	+	+	+	+
rps3		+	+	+	+	+	+	+	+	+	+
rps4		+	+	+	+	+	+	+	+	+	+
rps5		+	+	+	+	+	+	+	+	+	+
rps6		+	+	+	+	+	+	+	+	+	+
rps7		+	+	+	+	+	+	+	+	+	+
rps8		+	+	+	+	+	+	+	+	+	+
rps9		+	+	+	+	+	+	+	+	+	+
rps10		+	+	+	+	+	+	+	+	+	+
rps11		+	+	+	+	+	+	+	+	+	+
rps12		+	+	+	+	+	+	+	+	+	+
rps13		+	+	+	+	+	+	+	+	+	+
rps14		+	+	+	+	+	+	+	+	+	+
rps16		+	+	+	+	+	+	+	+	+	+

rps17		+	+	+	+	+	+	+	+	+	+
rps18		+	+	+	+	+	+	+	+	+	+
rps19		+	+	+	+	+	+	+	+	+	+
rps20		+	+	+	+	+	+	+	+	+	+
Translation initiation/elongation factors											
infB		-	+	+	+	+	+	+	+	+	+
infC		+	+	+	+	+	+	+	+	+	+
tsf		+	+	+	+	+	+	+	+	+	+
tufA		+	+	+	+	+	+	+	+	+	+
Posttranslational modification											
clpC		+	+	+	+	+	+	+	+	+	+
dnaK	hsp70, ctp70	+	+	+	+	+	+	+	+	+	+
groEL		+	+	+	+	+	+	+	+	+	+
Protein transport											
secA		+	+	+	+	+	+	+	+	+	+
secG	ycf47, orf71c	-	-	+	+	+	+	+	+	+	+
secY		+	+	+	+	+	+	+	+	+	+
tatC	ycf43	+	+	+	+	+	+	+	+	+	+
Energy production (Phycobilisome)											
apcA		+	+	+	+	+	+	+	+	+	+
apcB		+	+	+	+	+	+	+	+	+	+
apcD		+	+	+	+	+	+	+	+	+	+
apcE		+	+	+	+	+	+	+	+	+	+
apcF		+	+	+	+	+	+	+	+	+	+
cpcA	pcyA	+	+	+	+	+	+	+	+	+	+
cpcB	pcyB	+	+	+	+	+	+	+	+	+	+
cpcG	cpcC	+	+	+	+	+	+	+	+	+	+
cpeA	rpeA	-	-	-	+	+	+	+	+	+	+
cpeB	rpeB	-	-	-	+	+	+	+	+	+	+
fabH		-	-	-	+	+	+	+	+	+	+
nblA	ycf18	+	+	+	+	+	+	+	+	+	+
Energy production (Photosynthesis)											
cbbX	cfxQ, cfxX, orf301	+	+	+	+	+	+	+	+	+	+
petA		+	+	+	+	+	+	+	+	+	+
petB		+	+	+	+	+	+	+	+	+	+
petD		+	+	+	+	+	+	+	+	+	+
petF		+	+	+	+	+	+	+	+	+	+
petG		+	+	+	+	+	+	+	+	+	+
petJ		+	+	+	+	+	+	+	+	+	+
petL	ycf7	+	+	+	+	+	+	+	+	+	+
petM	ycf31	+	+	+	+	+	+	+	+	+	+
petN	ycf6, rbp6, orf75	+	+	+	+	+	+	+	+	+	+
psaA		+	+	+	+	+	+	+	+	+	+
psaB		+	+	+	+	+	+	+	+	+	+
psaC		+	+	+	+	+	+	+	+	+	+
psaD		+	+	+	+	+	+	+	+	+	+
psaE		+	+	+	+	+	+	+	+	+	+
psaF		+	+	+	+	+	+	+	+	+	+
psaI		+	+	+	+	+	+	+	+	+	+
psaJ		+	+	+	+	+	+	+	+	+	+
psaK		+	+	+	+	+	+	+	+	+	+
psaL		+	+	+	+	+	+	+	+	+	+
psaM		+	+	+	+	+	+	+	+	+	+
psbA		+	+	+	+	+	+	+	+	+	+
psbB		+	+	+	+	+	+	+	+	+	+
psbC		+	+	+	+	+	+	+	+	+	+
psbD		+	+	+	+	+	+	+	+	+	+
psbE		+	+	+	+	+	+	+	+	+	+
psbF		+	+	+	+	+	+	+	+	+	+
psbH		+	+	+	+	+	+	+	+	+	+
psbI		+	+	+	+	+	+	+	+	+	+
psbJ		+	+	+	+	+	+	+	+	+	+
psbK		+	+	+	+	+	+	+	+	+	+
psbL		+	+	+	+	+	+	+	+	+	+

psbN		+	+	+	+	+	+	+	+	+	+
psbT	ycf8	+	+	+	+	+	+	+	+	+	+
psbV		+	+	+	+	+	+	+	+	+	+
psbW	psb28, ycf79	+	+	+	+	+	+	+	+	+	+
psbX		+	+	+	+	+	+	+	+	+	+
psbY	ycf32	+	+	+	+	+	+	+	+	+	+
psbZ	ycf9	+	+	+	+	+	+	+	+	+	+
psb30	ycf12	+	+	+	+	+	+	+	+	+	+
rbcL	rbcA	+	+	+	+	+	+	+	+	+	+
rbcS		+	+	+	+	+	+	+	+	+	+
Energy production (Respiration)											
atpA		+	+	+	+	+	+	+	+	+	+
atpB		+	+	+	+	+	+	+	+	+	+
atpD		+	+	+	+	+	+	+	+	+	+
atpE		+	+	+	+	+	+	+	+	+	+
atpF		+	+	+	+	+	+	+	+	+	+
atpG		+	+	+	+	+	+	+	+	+	+
atpH		+	+	+	+	+	+	+	+	+	+
atpI		+	+	+	+	+	+	+	+	+	+
odpA	pdhA	+	+	+	+	+	+	+	+	+	+
odpB	pdhB	+	+	+	+	+	+	+	+	+	+
pgmA		-	-	-	+	+	+	+	+	+	+
Detoxification											
bas1	ahpC, ycf42, orf199	-	-	-	+	+	+	+	+	+	+
Amino acid metabolism											
argB		+	+	+	+	+	+	+	+	+	+
carA		+	+	+	+	+	+	+	+	+	+
cysT	mbpY	-	+	+	-	-	-	-	-	-	-
cysW		-	+	+	-	-	-	-	-	-	-
glmS		+	+	-	-	-	-	-	-	-	-
glnB		+	-	-	+	+	+	-	-	-	-
gltB	glsF	+	+	+	+	+	+	+	+	+	+
hisH		+	+	+	-	-	-	-	-	-	-
syh	hisS	-	-	-	+	+	+	+	+	+	+
ilvB		+	+	+	+	+	+	+	+	+	+
ilvH		+	+	+	+	+	+	+	+	+	+
leuC		-	-	-	-	-	-	+	-	-	-
leuD		-	-	-	-	-	-	+	-	-	-
syfB		-	-	-	+	+	+	+	+	+	+
trpA		+	+	+	+	+	+	+	+	+	+
trpG		+	+	+	+	+	+	+	+	+	+
tilS	ycf62, orf327	+	+	+	+	+	+	+	+	+	+
Lipid metabolism											
accA		+	+	+	+	+	+	+	+	+	+
accB		+	+	+	+	+	+	+	+	+	+
accD	ycf11, dedB, zfpA	+	+	+	+	+	+	+	+	+	+
acpP	acpA	+	+	+	+	+	+	+	+	+	+
desA	crtR	+	+	+	-	-	-	-	-	-	-
lpxA		+	+	+	-	-	-	-	-	-	-
lpxC		+	+	-	-	-	-	-	-	-	-
Cofactor metabolism											
acsF	ycf59	+	+	+	+	+	+	+	+	+	+
ccsA	ycf5	+	+	+	+	+	+	+	+	+	+
ccs1	ycf44, orf437	+	+	+	+	+	+	+	+	+	+
chlB		-	-	+	+	+	+	-	-	+	-
chlI		+	+	+	+	+	+	+	+	+	+
chlL	gidB, frxC	-	-	+	+	+	+	-	-	+	-
chlN	gidA	-	-	+	+	+	+	-	-	+	-
cemA	ycf10	+	+	+	+	+	+	+	+	+	+
cobA		+	+	ψ	-	-	-	-	-	-	-
dsbD	ccdA, orf240	-	-	-	+	+	+	+	+	+	+
ftrB	tftrC	+	+	+	+	+	+	+	+	+	+
lipB		+	+	-	-	-	-	-	-	-	-
menA		+	+	-	-	-	-	-	-	-	-

menB		+	+	-	-	-	-	-	-	-	-
menC		+	+	-	-	-	-	-	-	-	-
menD		+	+	-	-	-	-	-	-	-	-
menE		+	+	-	-	-	-	-	-	-	-
menF		+	+	-	-	-	-	-	-	-	-
moeB		+	+	+	+	+	+	+	+	+	+
pbsA		-	-	-	+	+	+	+	+	+	+
preA	crtE	+	+	+	+	+	+	+	+	+	+
sufB	ycf24	+	+	+	+	+	+	+	+	+	+
sufC	ycf16	+	+	+	+	+	+	+	+	+	+
thiG		+	+	+	+	+	+	+	+	+	+
thiS	ycf40, orf71	+	+	+	+	+	+	+	+	+	+
trxA	trxM	+	+	-	+	+	+	+	+	+	+
upp	orf198	-	-	-	+	+	+	+	+	+	+
Plastid division											
ftsH	ycf25	+	+	+	+	+	+	+	+	+	+
minD		-	-	ψ	-	-	-	-	-	-	-
minE		-	-	ψ	-	-	-	-	-	-	-
Conserved hypothetical reading frames											
ycf3		+	+	+	+	+	+	+	+	+	+
ycf4		+	+	+	+	+	+	+	+	+	+
ycf17		+	+	+	+	+	+	+	+	+	+
ycf19		+	+	+	+	+	+	+	+	+	+
ycf20	apcL9.5, orf20	+	+	+	+	+	+	+	+	+	+
ycf21		-	-	-	+	+	+	+	+	+	+
ycf22		-	+	-	+	+	+	+	+	+	+
ycf23		+	+	+	+	+	+	+	+	+	-
ycf27	ompR, orf27	+	+	+	+	+	+	+	+	+	+
ycf29	luxR	+	+	+	+	+	+	+	+	+	+
ycf33		-	+	-	+	+	+	+	+	+	+
ycf34		-	-	-	+	+	+	+	+	-	+
ycf35		-	-	-	+	+	+	+	+	-	+
ycf36		-	-	+	+	+	+	+	+	+	+
ycf37		+	-	+	+	+	+	+	+	+	+
ycf38		-	+	+	+	+	+	+	+	+	+
ycf39		+	+	+	+	+	+	+	+	+	+
ycf41	orf109	-	-	-	-	-	-	+	+	+	-
ycf45	orf565	+	-	+	+	+	+	+	+	+	+
ycf46		-	-	-	+	+	+	+	+	-	+
ycf49		+	+	+	-	-	-	-	-	-	-
ycf52	orf174	+	+	+	+	+	+	+	+	+	+
ycf53	orf238	+	+	ψ	+	+	+	+	+	+	+
ycf54	orf108	+	+	+	+	+	+	+	+	+	+
ycf55		+	+	-	+	+	+	+	+	+	+
ycf56	orf263, rnZ	-	-	+	+	+	+	+	+	+	+
ycf58	cpcS, orf149	+	-	+	+	+	+	+	+	+	+
ycf60	orf203	+	+	+	+	+	+	+	+	+	+
ycf63	ycxr, ORF263	-	+	-	+	+	+	+	+	+	+
ycf64		-	-	-	+	+	+	-	+	-	+
ycf65		+	+	-	+	+	+	+	+	+	+
ycf80	matK, orf450	+	+	+	+	+	+	+	+	+	+
ycf82		+	+	+	-	-	-	-	-	-	-
ycf83	ycf57, orf114, sufA	-	+	+	+	+	+	-	+	-	-
ycf84	yjgP,yjgQ	+	+	+	-	-	-	-	-	-	-
ycf85		+	+	+	-	-	-	-	-	-	-
ycf86	petP, orf68	+	+	+	+	+	+	-	+	-	+
ycf91		-	-	-	+	+	+	+	+	-	+
ycf92	orf245, ORF287	-	-	-	+	+	+	+	+	+	+
Other open reading frames											
orf58		-	-	-	+	+	+	+	+	+	+
orf621		-	-	-	+	+	+	+	-	+	+

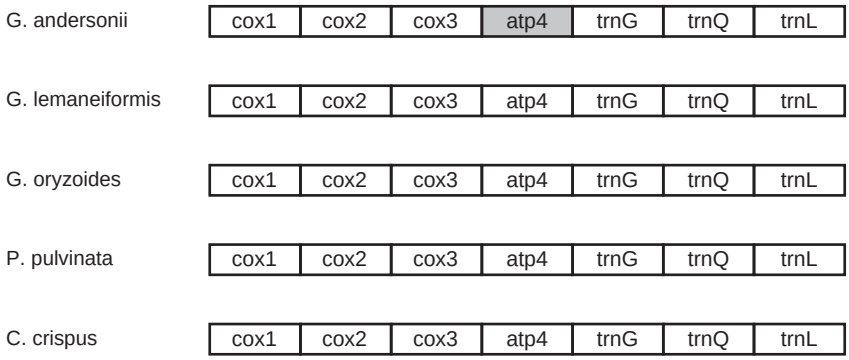
Table S3B - RNA genes in red algal plastid genomes

	Cyanidiophyceae			Bangiophyceae			Florideophyceae			
Gene name	**Ccal**	**Cmer**	**Gsul**	**Phai**	**Pyez**	**Ppur**	**Gten**	**Ccri**	**Ctub**	**Gtai**
Ribosomal RNAs										
rrn5	+	+	+	+	+	+	+	+	+	+
rrn16	+	+	+	+	+	+	+	+	+	+
rrn23	+	+	+	+	+	+	+	+	+	+
Transfer RNAs										
trnA (GGC)	-	-	+	+	+	+	-	-	-	-
trnA (TGC)	+	+	+	+	+	+	+	+	+	+
trnC (GCA)	+	+	+	+	+	+	+	+	+	+
trnD (GTC)	+	+	+	+	+	+	+	+	+	+
trnE (TTC)	+	+	+	+	+	+	+	+	+	+
trnF (GAA)	+	+	+	+	+	+	+	+	+	+
trnG (GCC)	+	+	+	+	+	+	+	+	+	+
trnG (TCC)	+	+	+	+	+	+	+	+	+	+
trnH (GTG)	+	+	+	+	+	+	+	+	+	+
trnI (GAT)	+	+	+	+	+	+	+	+	+	+
trnK (TTT)	+	+	+	+	+	+	+	+	+	+
trnL (CAA)	+	+	+	+	+	+	+	+	+	+
trnL (CAG)	-	-	+	-	-	-	-	-	-	-
trnL (GAG)	+	+	+	+	+	+	-	-	-	-
trnL (TAA)	+	+	+	+	+	+	+	+	+	+
trnL (TAG)	+	+	+	+	+	+	+	+	+	+
trnM-CAT/trnI-CAT	+	+	+	+	+	+	+	+	+	+
trnfM(CAT)	+	+	+	+	+	+	+	+	+	+
trnMe (CAT)	-	-	-	+	+	+	+	+	+	+
trnN (GTT)	+	+	+	+	+	+	+	+	+	+
trnP (TGG)	+	+	+	+	+	+	+	+	+	+
trnQ (TTG)	+	+	+	+	+	+	+	+	+	+
trnR (ACG)	+	+	+	+	+	+	+	+	+	+
trnR (CCG)	+	-	+	+	+	+	+	+	+	+
trnR (CCT)	-	-	+	+	+	+	-	-	-	-
trnR (TCT)	-	+	+	+	+	+	+	+	+	+
trnS (CGA)	-	-	+	+	+	+	-	-	-	-
trnS (GCT)	+	+	+	+	+	+	+	+	+	+
trnS (GGA)	-	+	+	+	+	+	-	-	+	-
trnS (TGA)	+	+	+	+	+	+	+	+	+	+
trnT (CGT)	-	-	+	-	-	-	-	-	-	-
trnT (GGT)	+	+	+	+	+	+	+	+	+	+
trnT (TGT)	+	+	+	+	+	+	+	+	+	+
trnV (GAC)	+	+	+	+	+	+	+	+	+	+
trnV (TAC)	+	+	+	+	+	+	+	+	+	+
trnW (CCA)	+	+	+	+	+	+	+	+	+	+
trnY (GTA)	+	+	+	+	+	+	+	+	+	+
Other RNAs										
ffs	+	+	-	+	+	+	+	+	+	+
rnpB	+	+	+	+	+	+	+	+	+	+
ssrA	-	+	+	+	+	+	+	+	+	+

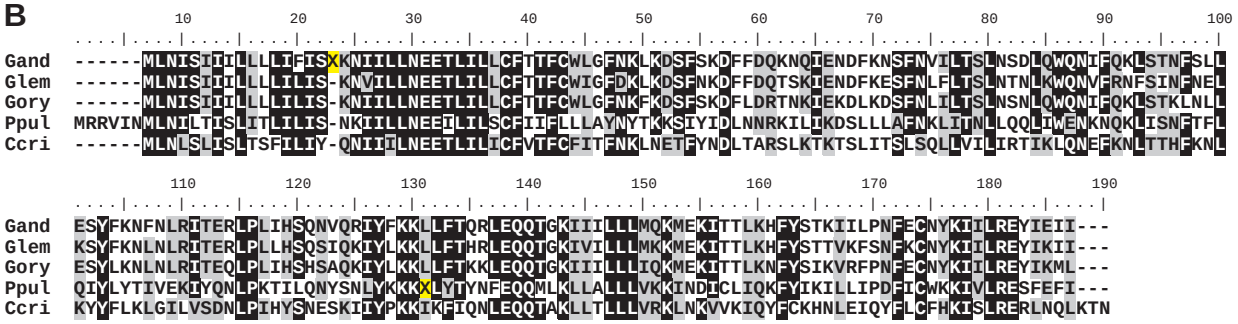
Ccal: *Cyanidium caldarium*; Cmer: *Cyanidioschyzon merolae*; Gsul: *Galdieria sulphuraria*; Phai: *Pyropia haitanensis*; Pyez: *Pyropia yezoensis*; Ppur: *Porphyra purpurea; Gten: Gracilaria tenuistipitata*; Ccri: *Chondrus crispus*; Ctub: *Calliarthron tuberculosum; Gtai: Grateloupia taiwanensis*

Figure S1A - *atp4* gene. A) Gene order map showing the genomic position of the putative *G. andersonii atp4* gene newly identified in this study (shaded in gray). B) Amino acid alignment of *atp4*. Positions with amino acids identical or similar in >75% of sequences are shaded black or gray, respectively. Corrected frameshift mutations are highlighted in yellow and marked with an “X.” C) Nucleotide alignments of the frameshift mutations located in mononucleotide repeat regions. Gaps inserted to correct the reading frame are highlighted in yellow.

A



B



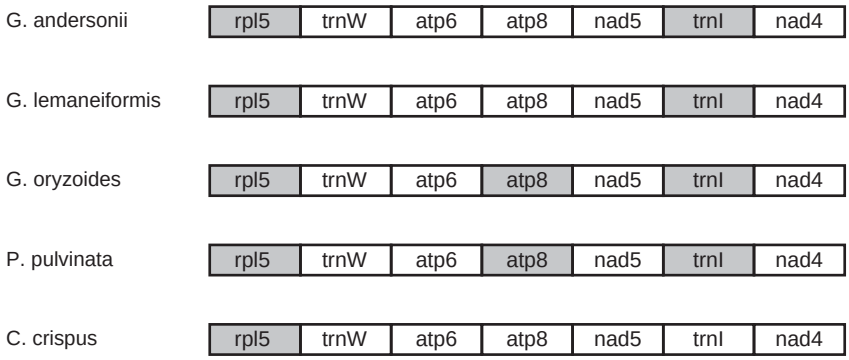
C

```
Gand  TTTATTTCAA--AAAAATATT
       F  I  S  X  K  N  I
Glem  TTAATTTCA---AAAAATGTT
       L  I  S  -  K  N  V
Gory  CTTATTTCA---AAAAATATT
       L  I  S  -  K  N  I
Ppul  TTAATTTCA---AATAAAATA
       L  I  S  -  N  K  I
Ccri  TTAATTTAT---CAGAACATT
       L  I  Y  -  Q  N  I

Gand  TTTAAAAAACTTTTATTTACT
       F  K  K  L  L  F  T
Glem  TTAAAAAAACTTTTATTTACT
       L  K  K  L  L  F  T
Gory  TTAAAAAAACTTTTATTTACT
       L  K  K  L  L  F  T
Ppul  AAAAAAAAA-TTTTATATACA
       K  K  K  X  L  Y  T
Ccri  CCAAAAAAAATCAAATTTATC
       P  K  K  I  K  F  I
```

Figure S1B - *atp8* gene. A) Gene order map showing the genomic position of the putative *atp8* genes newly identified in this study (shaded in gray). The status of *rpl5* is shown in Supplementary Figure S1E, while the status of *trnI*-gau is shown in Supplementary Figure S1H. B) Amino acid alignment of *atp8*. Positions with amino acids identical or similar in >75% of sequences are shaded black or gray, respectively. A corrected frameshift mutation is highlighted in yellow and marked with an “X.” C) Nucleotide alignment of the frameshift mutation located in a mononucleotide repeat region. The gap inserted to correct the reading frame is highlighted in yellow.

A



B

```
          10        20        30        40        50        60        70        80        90        100
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Gand  MPQLDRIIVFSQIFWLFIIFTLFYTILTHFFLPKFIKSLKIRKQILDENSIEISSIAENTLQKQNLLKKILLKDLESVKTLLIQ-HFSNIVKEKSHANTS
Glem  MPQLDRIIVFSQIFWLFIIFTAFYTVLTHFFLPKFIKSLKIRRQIIDANSTEILLMAKNTLLKQNLLKKFLLKDLELIKNLLIQ-YFNNLVKEKSYANTT
Gory  MPQLDRIIVFSQIFWLFIIFTLFYTILTHFFLPKFIKSFKIRKQIIDTNSIEISSIAENTLHKHNLLNFFXLKDLESVKALLAQ-HFSNLVKEKNYANTS
Ppul  MPQLDYTIIFSQIFWLFFIFLFLYTIILHFFLPVFLKSIKIRKELINSLNLEVSKLEEISFKKRTLLYSNVNQQLLIIKKLLKKENFIFLLKKE---NSI
Ccri  MPQLDRIIVFSQIFWLFIIFVLIYIVLTHFFLPKFIKSLKSRKQIIEANDTELSELTSKIINKQLLLKQLLLKNLVMVNISLGH-EFS-ISNTLPKLDIH

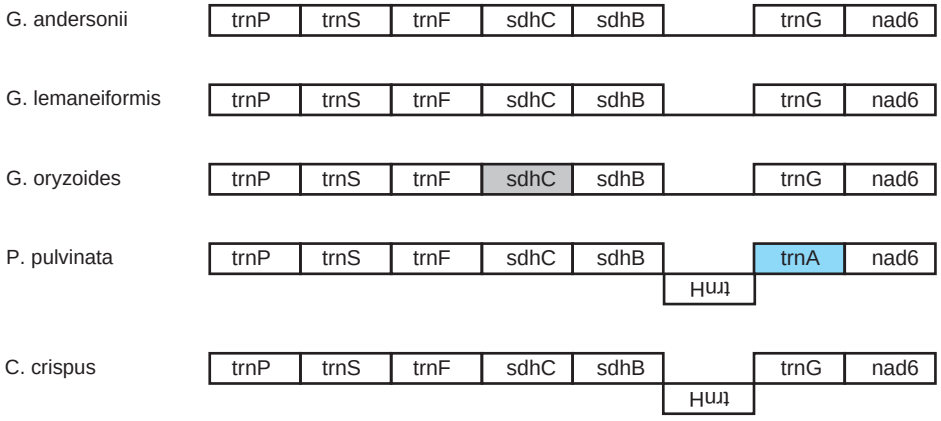
          110       120       130
....|....|....|....|....|....|....|....
Gand  LIDEKISFVIFNTVTYCDLQLLNAIIVYPKVLRYKN---
Glem  LVDEKISSVILNTLMYCDLQLLNAIVVYPKVLKIN----
Gory  LIDEKIGFVILNTLIYCDLQLINAIIVYPKVLEYKN---
Ppul  IIDKKLSIFISNTTKFYNLQIINSIPFSSKILNLLNK--
Ccri  KIDTKISTVTRNVSLYCDVQLFNCIFFYPKLLNITFKPV
```

C

```
Gand  AATTTGTTAAAGAAAATATTG
       N  L  L  K  K  I  L
Glem  AATTTATTAAAAAAATTTTTA
       N  L  L  K  K  F  L
Gory  AACTTGTTAAA-TTTTTTTTA
       N  L  L  X  F  F  L
Ppul  ACTTTATTATATAGTAATGTG
       T  L  L  Y  S  N  V
Ccri  CTTTTGTTAAAACAACTTTTG
       L  L  L  K  Q  L  L
```

Figure S1C - *sdhC* gene. A) Gene order map showing the genomic position of the putative *G. oryzoides sdhC* gene newly identified in this study (shaded in gray). The status of *trnA*-ggc (shaded in blue) is shown in Supplementary Figure S1G. B) Amino acid alignment of *sdhC*. Positions with amino acids identical or similar in >75% of sequences are shaded black or gray, respectively. A corrected frameshift mutation is highlighted in yellow and marked with an “X.” C) Nucleotide alignment of the frameshift mutation located in a mononucleotide repeat region. The gap inserted to correct the reading the frame is highlighted in yellow.

A



B

```
          10        20        30        40        50        60        70        80        90        100
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Gand  ------MYNRPLSPHLTIYKPQVSSLFSIWHRISGIFLTFLIVFYLISSQLFLHITYSKDVLNSLIIQLEYS-FFLQFIYILNTSIFFYHAINGVKHIIW
Glem  ------MYNRPLSPHITIYKPQASSLFSIWHRISGLFLTFLMVFFLISSQLLLFITNSKDILNGLIMQLEVS-FVFQFIYIFNISIFFYHIINGFKHIIW
Gory  ------MYNRPLSPHLTIYKPQPSSLFSIWHRISGFVLTFLIVFYLISLQVLLYIAYSKDILDNLIIQLEFS-XFFQFIYMFNISIFFYHVISGVKHIIW
Ppul  ------MYNRPITPHITIYLPQISSTFSILNRVSSICTIILLLFSILIMKFISNL-YSLYY----SFHYIISNSIYIYIYLIVLINYVYHFFQGFLSILW
Ccri  MFIKFKISNRPIAPHLLVYTPQLSSLFSIWHRISGVGLAFFFTTFLIFIRIILSSNFACNLLT--LISFEISQWIIIYFNLFILLFLFYHLFNGTRHIIW

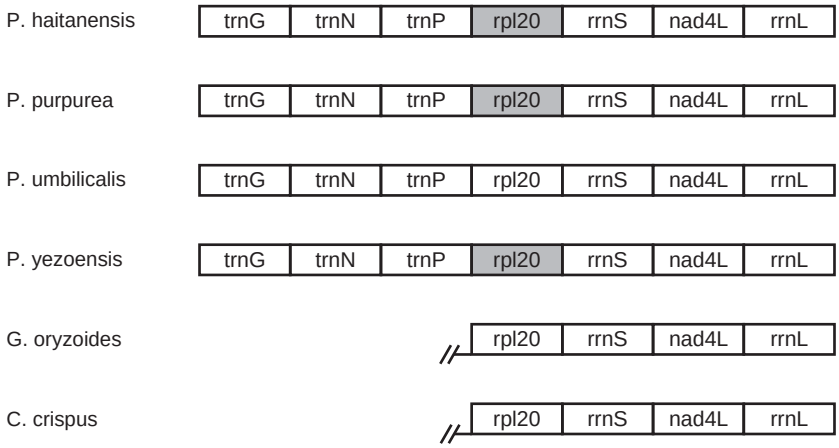
          110       120       130
          ....|....|....|....|....|....|....
Gand  DLGFFPTPKF-WFFLFFNCFLLIIIINVFAAIYK
Glem  DLGFFINQKFLFLFVLFTCFFIFLTILLLL----
Gory  DLGFFITSKFDYLYVLFICFIIVLLL--------
Ppul  SFNIFLNYNNFLINVFKKKPKSN-----------
Ccri  DFGFLLDIKYLSKFSLFLLVSLSLILIFQ-----
```

C

```
Gand  TATTCT---TTCTTTTTACAA
       Y  S  -  F  F  L  Q
Glem  GTTTCT---TTTGTTTTTCAA
       V  S  -  F  V  F  Q
Gory  TTTTCT---TT-TTTTTTCAA
       F  S  -  X  F  F  Q
Ppul  ATATCTAATTCAATATATATA
       I  S  N  S  I  Y  I
Ccri  ATTTCCCAATGAATAATTATT
       I  S  Q  W  I  I  I
```

Figure S1D - *rpl20* gene. A) Gene order map showing the genomic position of all *rpl20* genes newly identified in this study (shaded in gray). A loss of synteny upstream of *rpl20* in *G. oryzoides* and *C. crispus* is marked with a "//." B) Amino acid alignment of *rpl20*. Positions with amino acids identical or similar in >75% of sequences are shaded black or gray, respectively.

A

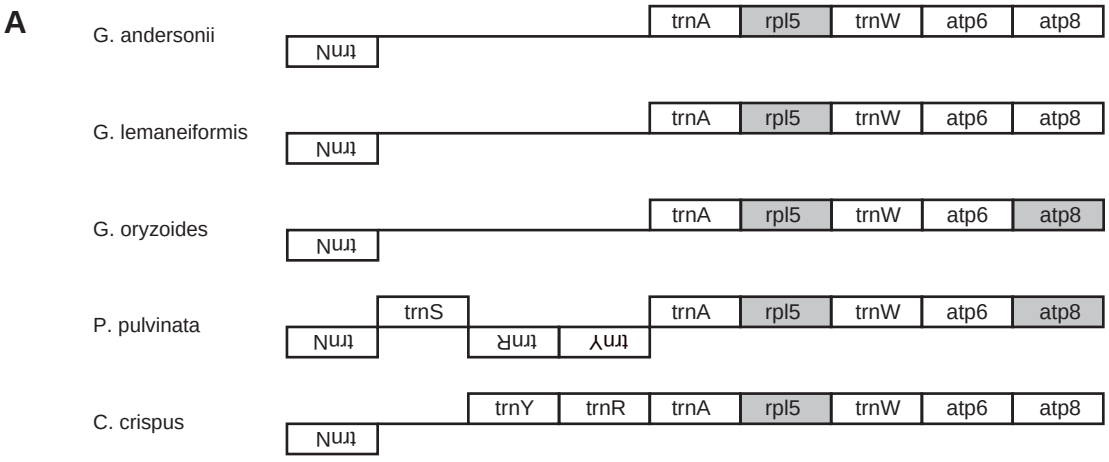


B

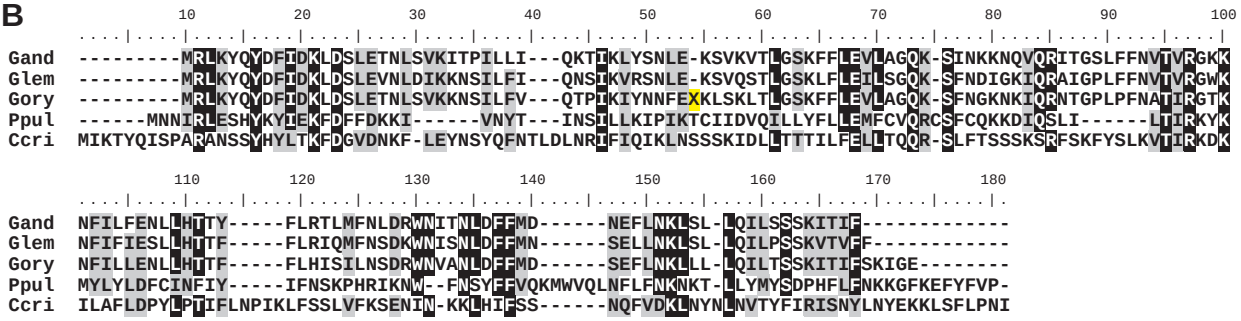
```
          10        20        30        40        50        60        70        80        90
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|..
Phai            MTKKNQKFFLR-------------RIKKYKNFIKTNFIVVNKKILKNLYLYEIGTASALKRWIHLYD
Ppur          MSINKKTSKYFFRERDNYNTH-FLTAKYNKYKNFCRKNSIYLNKRQFKEISIHEVGTATVFVRWIKLYHYG
Pumb          MFINKKTSKYFSREQNIYNTN-FLTIKHTKYKNFCKKNRIHLDKNKSKEIFIYEVGTATILVRWIKMYYYS
Pyez          MNKIKKYRRLLIRGTKLENKL-CSAFKQKKYTTFCKANFILITKRKITNIYIYEIGTASVLARWITLYNQI
Gory     MKKEIYRTKSRRTKKREFYKQNINHIK-VLSGKYSLFNFFVKKQNIRLNKKILSELFITEVGSTFSLMHWNFCYLVV
Ccri  MKTQLKKEFFQTYSRKLKKQNLQQVFTKQINSTINIKYNFLRYFNSNEKIILNRKILSLLFAKESGS---LFSWRNEYVISIKNLLAGVVRLAKILI
```

Figure S1E - *rpl5* gene. A) Gene order map showing the genomic position of all putative *rpl5* genes newly identified in this study (shaded in gray). The status of *atp8* is shown in Supplementary Figure S1B. B) Amino acid alignment of *rpl5*. Positions with amino acids identical or similar in >75% of sequences are shaded black or gray, respectively. A corrected frameshift mutation is highlighted in yellow and marked with an “X.” C) Nucleotide alignment of the frameshift mutation located in the mononucleotide repeat region. Gaps inserted to correct the reading frame are highlighted in yellow.

A



B

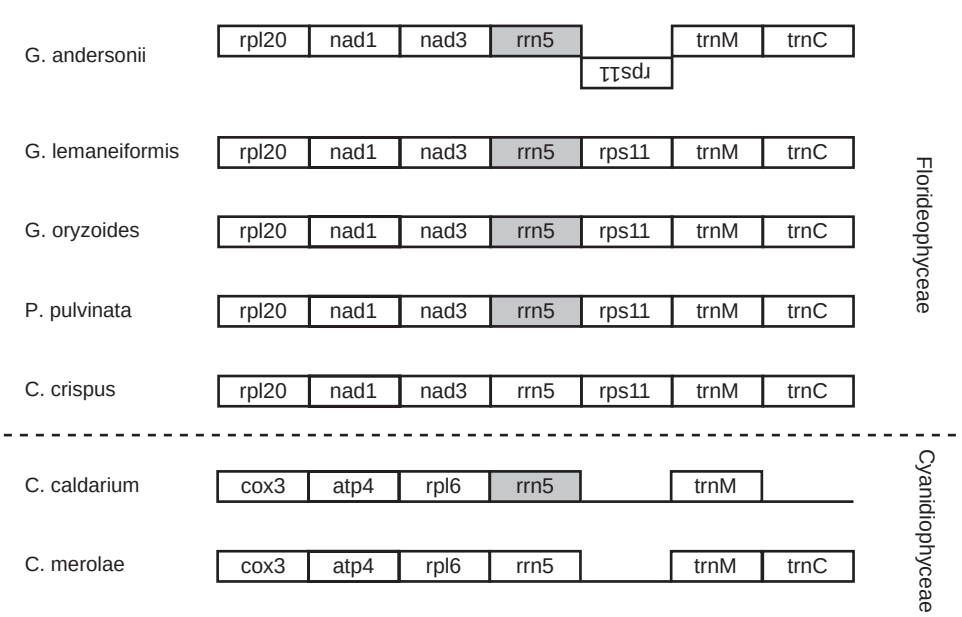


C

```
Gand  AATTTAGAA---AAATCTGTT
       N  L  E     K  S  V
Glem  AACTTAGAA---AAATCTGTT
       N  L  E     K  S  V
Gory  AATTTTGAA--AAAACTTTCA
       N  F  E  X  K  L  S
Ppul  CCTATAAAAACTTGTATTATC
       P  I  K  T  C  I  I
Ccri  AAACTTAATTCTTCCTCCAAA
       K  L  N  S  S  S  K
```

Figure S1F - *rrn5* gene. A) Gene order map showing the genomic position of all *rrn5* genes newly identified in this study (shaded in gray). In parallel, the *rrn5* was also recently identified in the species shown below, as well as all sequenced Bangiales species (Valach et al. 2014). B) Nucleotide alignment of *rrn5*. Positions with nucleotides identical in >75% of sequences are shaded black.

A



B

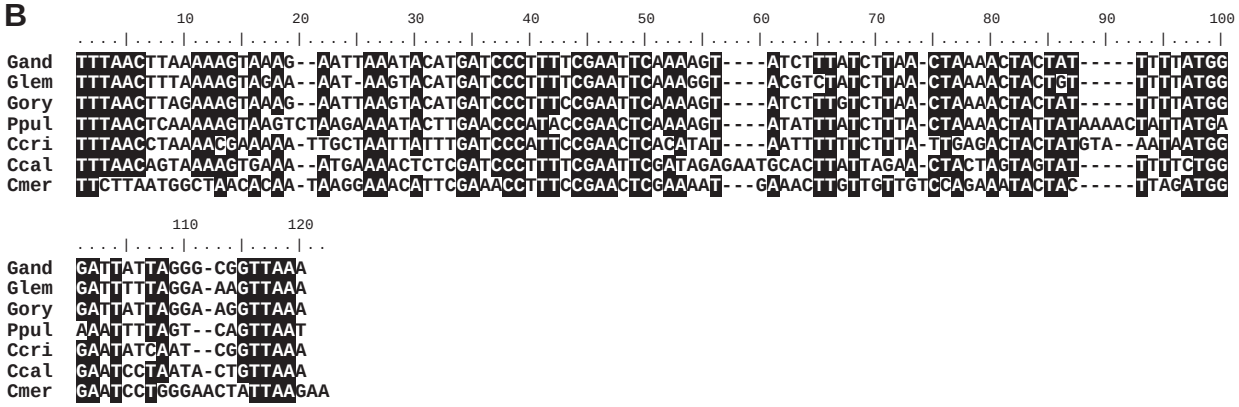
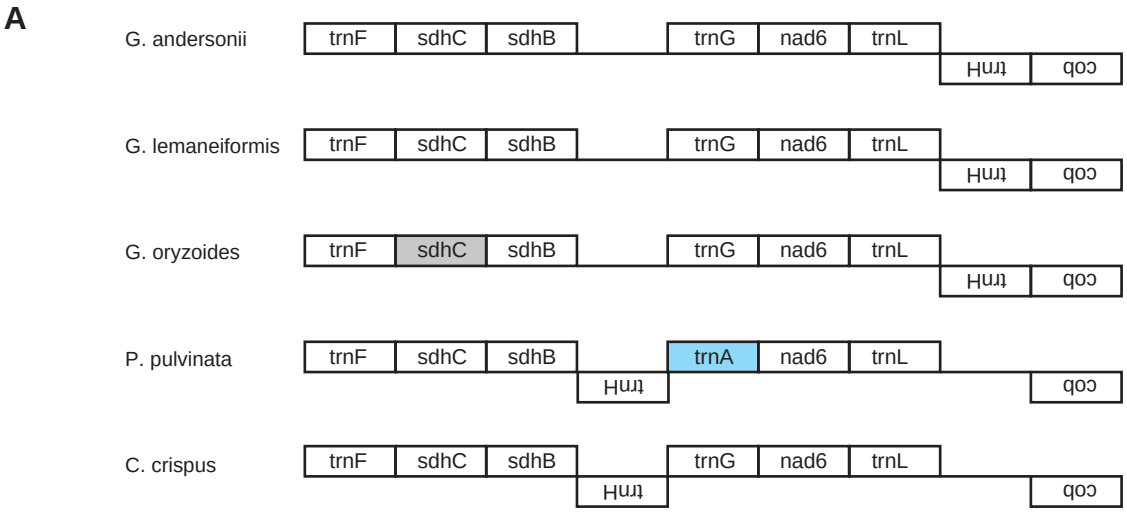


Figure S1G - *trnA*-ggc gene. A) Gene order map showing the genomic position of the *P. pulvinata trnA*-ggc gene (highlighted in blue) and the *trnG*-gcc gene in other Florideophyceae species. The status of *sdhC* is shown in Supplementary Figure S1C. B) Nucleotide alignment of *trnA*-ggc and *trnG*-gcc. Positions with nucleotides identical in >75% of sequences are shaded black. The anticodon mutation is highlighted in blue.



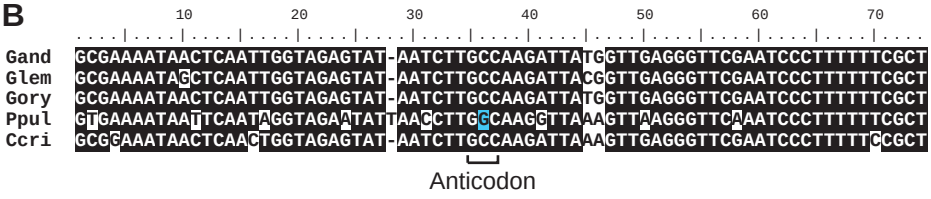
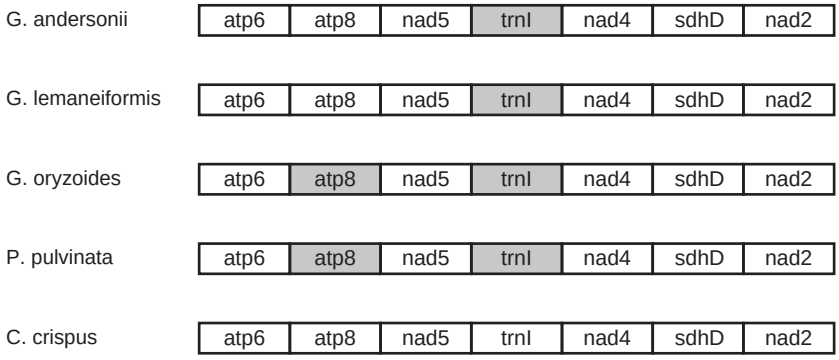


Figure S1H - *trnI*-gau gene and intron. A) Gene order map showing the genomic position of all *trnI*-gau genes newly identified in this study (shaded in gray). The status of *atp8* in *G. oryzoides* and *P. pulvinata* is shown in Supplementary Figure S1B. B) Nucleotide alignment of *trnI*-gau with exon and intron positions highlighted in yellow and brown, respectively. Positions with nucleotides identical in >75% of sequences are shaded black.

A



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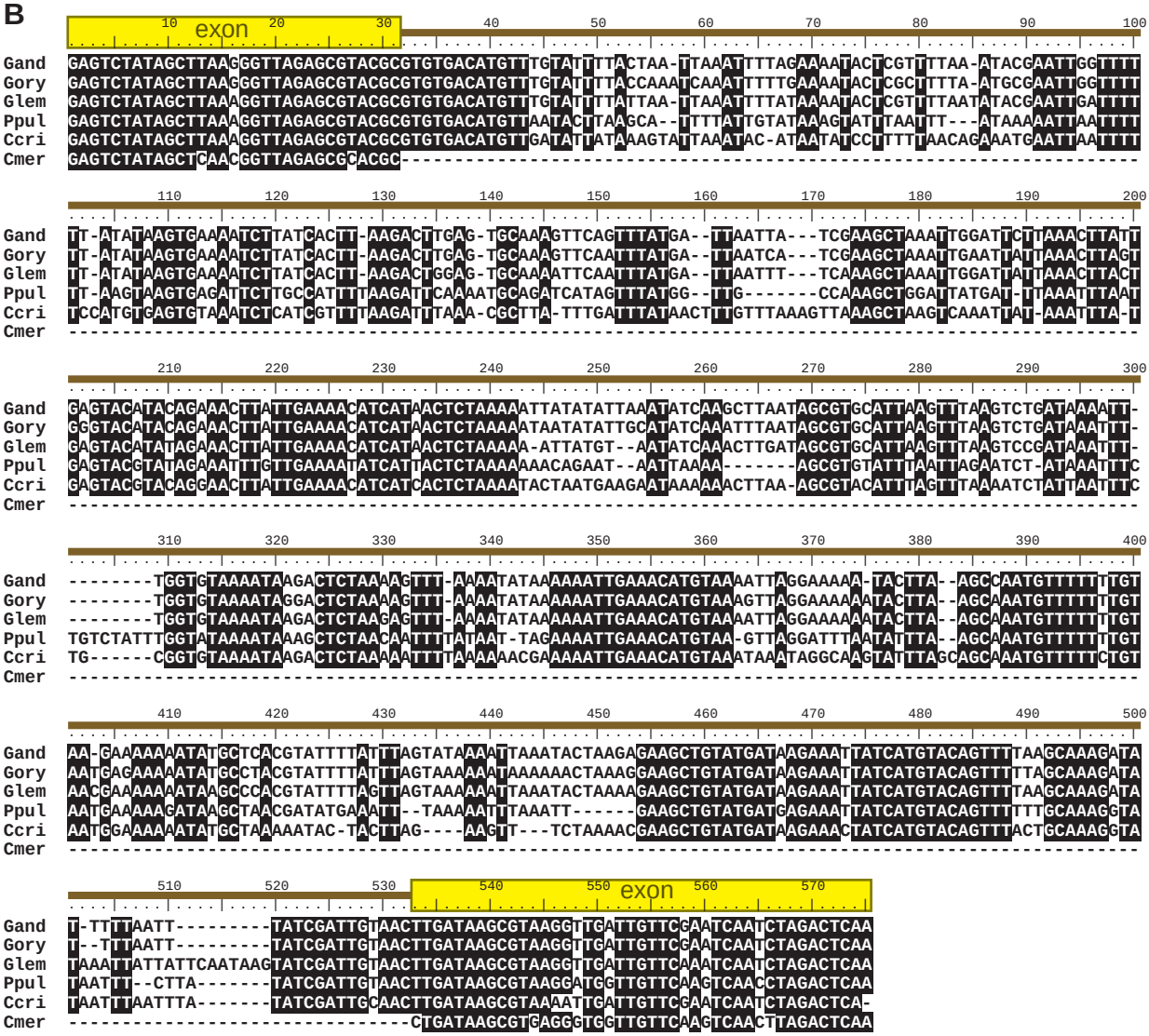
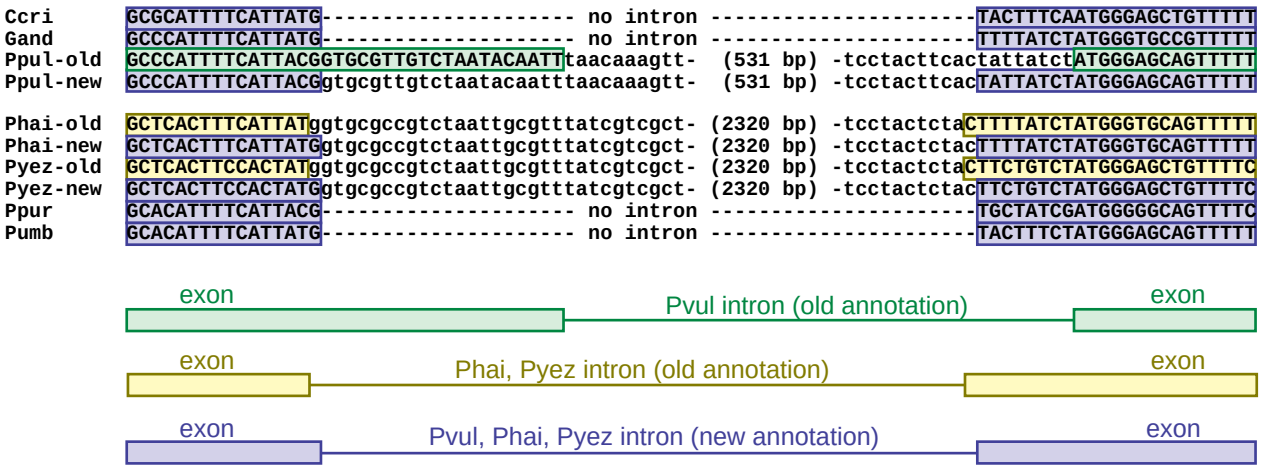


Figure S1I - *cox1* intron. A) *cox1* intron position based on old annotations present in GenBank files (shown in green for *P. pulvinata* and in yellow for *P. haitanensis* and *P. yezoensis*) and new annotations reported here (in purple). The new annotations improve exon similarity compared with intron-lacking species and restore canonical GTGYG–AC intron boundary sequences for all three intron-containing species. B) Sequence alignment of the *cox1* intron from *P. pulvinata* compared to *P. haitanensis* and *P. yezoensis*. The large internal segment of the P. *haitanensis* and *P. yezoensis* introns (encoding the majority of the IEP) is absent from *P. pulvinata* and was excluded from the alignment.

A



B

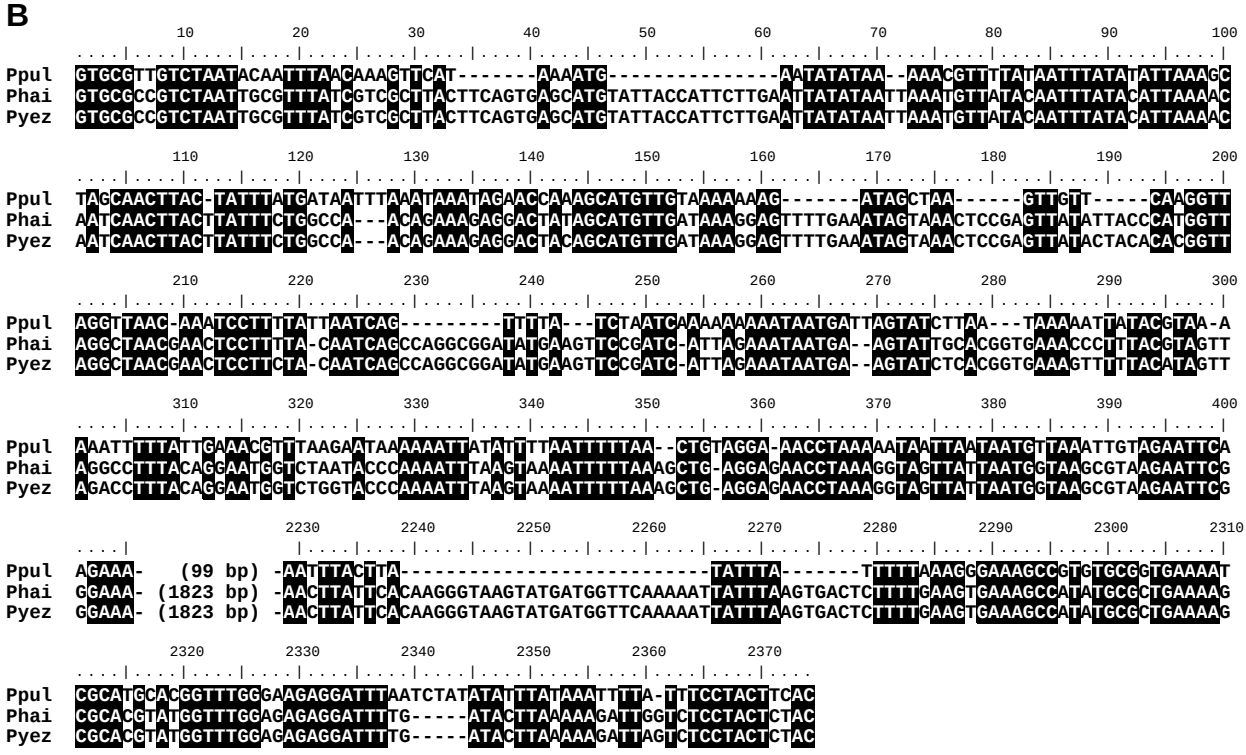


Figure S2 - Predicted stem-loop structures in the *Galdieria sulphuraria* plastid genome. Structures were predicted with the EMBOSS program einverted (http://emboss.bioinformatics.nl/cgi-bin/emboss/einverted), requiring a ≥20 bp stem with ≥80% sequence identity and a ≤20 bp loop.

```
Galdieria-CP: Score 78: 26/26 (100%) matches, 0 gaps
    3547 aaaaaaatatcttgctctatagctat 3572
         ||||||||||||||||||||||||||
    3602 ttttttatagaacgagatatcgata 3577


Galdieria-CP: Score 134: 46/47 ( 97%) matches, 0 gaps
    5036 aataaaaatatggaagttcgtaaataataaccatctattacaaggta 5082
         |||||||||||||||||| |||||||||||||||||||||||||||
    5136 ttatttttataccttcaagtatttattattggtagataatgttccat 5090


Galdieria-CP: Score 75: 25/25 (100%) matches, 0 gaps
    7649 tacataaaaaaatatatggtatctt 7673
         |||||||||||||||||||||||||
    7699 atgtatttttttatataccatagaa 7675


Galdieria-CP: Score 134: 46/47 ( 97%) matches, 0 gaps
   11104 aggtaaagattgattagaaaataaaaataatctagtgtatcttattt 11150
         |||||||||||||||||||| |||||||||||||||||||||||||
   11205 tccatttctaactaatcttttgtttttattagatcacatagaataaa 11159


Galdieria-CP: Score 138: 46/46 (100%) matches, 0 gaps
   19510 aattgtattaaagatagatcagatagaaaataaaaggccatttata 19555
         ||||||||||||||||||||||||||||||||||||||||||||||
   19602 ttaacataatttctatctagtctatcttttattttccggtaaatat 19557


Galdieria-CP: Score 63: 21/21 (100%) matches, 0 gaps
   27947 aagattaaaaaagtggatagt 27967
         |||||||||||||||||||||
   27992 ttctaatttttttcacctatca 27972


Galdieria-CP: Score 147: 49/49 (100%) matches, 0 gaps
   31116 aaactttaaaaagggaaataaaaatagataaaattggattggttctttg 31164
         |||||||||||||||||||||||||||||||||||||||||||||||||
   31218 tttgaaatttttccctttatttttatctattttaacctaaccaagaaac 31170


Galdieria-CP: Score 150: 50/50 (100%) matches, 0 gaps
   48093 aaggaagcattaaaaaacctcaataaatagaaaaagatattatactctaa 48142
         ||||||||||||||||||||||||||||||||||||||||||||||||||
   48193 ttccttcgtaatttttttggagttatttatctttttctataatatgagatt 48144


Galdieria-CP: Score 62: 30/31 ( 96%) matches, 2 gaps
   49807 aataata-ttat-ttgatattttgataatagaa 49837
         || |||| |||| ||||||||||||||||||||
   49880 ttgttatcaatataactataaaactattatctt 49848


Galdieria-CP: Score 59: 21/22 ( 95%) matches, 0 gaps
   53158 taataaataataaataaaaact 53179
         ||| ||||||||||||||||||
   53207 attgtttattatttatttttga 53186


Galdieria-CP: Score 114: 38/38 (100%) matches, 0 gaps
   57756 taaattatatagaataaaaaagaaaataaagtaaatca 57793
         ||||||||||||||||||||||||||||||||||||||
   57834 atttaatatatcttatttttttctttttatttcatttagt 57797


Galdieria-CP: Score 135: 44/44 (100%) matches, 0 gaps
   58808 aatattgaaaaatttcacaaaaatgagctaaagcaaaatgattt 58851
         ||||||||||||||||||||||||||||||||||||||||||||
   58897 ttataacttttttaaagtgtttttactcgatttcgttttactaaa 58854
```

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Galdieria-CP: Score 78: 26/26 (100%) matches, 0 gaps
   59197 aatattatataaatttttatttctta 59222
         ||||||||||||||||||||||||||
   59253 ttataatatatttaaaaataaagaat 59228


Galdieria-CP: Score 66: 22/22 (100%) matches, 0 gaps
   59483 aatataaagaatgagtacaaaa 59504
         ||||||||||||||||||||||
   59531 ttatatttcttactcatgtttt 59510


Galdieria-CP: Score 93: 30/30 (100%) matches, 0 gaps
   60641 ttaattaatacaatcaataaacaaaaatgt 60670
         ||||||||||||||||||||||||||||||
   60702 aattaattatgttagttatttgtttttaca 60673


Galdieria-CP: Score 68: 31/32 ( 96%) matches, 2 gaps
   61424 tattaaagtgataaattataataacaaattatta 61457
         |||| |||| || ||||||||||||||||||||
   61491 ataaattca-ta-ttaatattattgtttaataat 61460


Galdieria-CP: Score 113: 39/40 ( 97%) matches, 0 gaps
   66325 caagcaattaaatatttagtaaaaacaaaacacataacca 66364
         |||||||||||||||||||||||| ||||||||||||||
   66407 gttcgttaatttataaatcatttttattttgtgtattggt 66368


Galdieria-CP: Score 288: 96/96 (100%) matches, 0 gaps
   70875 ttataagaacagaaaattattatcagtatagtaggagaatataatcaaaattctccttgtaaaaaagggtatgtctgaataattactatagttaat 70970
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   71072 aatattcttgtcttttaataatagtcatatcatcctcttatattagttttaagaggaacatttttcccatacagacttattaatgatatcaatta 70977


Galdieria-CP: Score 99: 33/33 (100%) matches, 0 gaps
   89622 ataaatcaataggatataaaacgcttaactttt 89654
         |||||||||||||||||||||||||||||||||
   89692 tatttagttatcctatattttgcgaattgaaaa 89660


Galdieria-CP: Score 146: 50/51 ( 98%) matches, 0 gaps
   92864 taactaatgaataataaataaaattaaaagaagaaataaaatctttgtaag 92914
         |||||| ||||||||||||||||||||||||||||||||||||||||||||
   92971 attgatcacttattatttatttaattttcttcttattttagaaacattc 92921


Galdieria-CP: Score 132: 43/43 (100%) matches, 0 gaps
   96179 aaattaatgtgattgatgttataaatgattatattatatctta 96221
         |||||||||||||||||||||||||||||||||||||||||||
   96266 tttaattacactaactacaatatttactaatataatatagaat 96224


Galdieria-CP: Score 147: 48/48 (100%) matches, 0 gaps
   97529 agaaatccgaatcgtagagacttagaataaaatgaaaagccctagttt 97576
         ||||||||||||||||||||||||||||||||||||||||||||||||
   97626 tctttaggcttagcatctctgaatcttattttacttttcgggatcaaa 97579


Galdieria-CP: Score 129: 43/43 (100%) matches, 0 gaps
   99714 taagatatttatctcataaaatattgatattgatgttataata 99756
         |||||||||||||||||||||||||||||||||||||||||||
   99802 attctataaatagagtattttataactataactacaatattat 99760


Galdieria-CP: Score 232: 79/81 ( 97%) matches, 0 gaps
  101673 tttccatttattagtatggctttgtttttttatttatgttgaacaagaagaaattgggtaatgaagaagacaatctgagtta 101753
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||
  101836 aaaggtaaataatcataccgaaacaaaaaataaatacaacttgttcttctttaaccaattacttcttctgtcagactcaat 101756


Galdieria-CP: Score 111: 37/37 (100%) matches, 0 gaps
  102484 tctataataacataataagaaaatgataataagggct 102520
         |||||||||||||||||||||||||||||||||||||
  102560 agatattattgtattattcttttactattattcccga 102524
```

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Galdieria-CP: Score 161: 55/56 ( 98%) matches, 0 gaps
  107228 tttatttttttccattataatacttcttaactataaacaaataaggacttaaacttt 107283
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||
  107343 aaataaaaaaggtaatattatgaagaattgatattcgtttattcctgaatttgaaa 107288


Galdieria-CP: Score 179: 60/61 ( 98%) matches, 0 gaps
  108167 atatcataataaatccttcaaaattttatattaaaaaatctatagaaaaagttataataat 108227
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  108290 tacagtattatttaggaagttttaaaatataatttttagatatctttttcaatattatta 108230


Galdieria-CP: Score 69: 23/23 (100%) matches, 0 gaps
  115296 aacaaaaatatgttctatttata 115318
         |||||||||||||||||||||||
  115346 ttgtttttatacaagataaatat 115324


Galdieria-CP: Score 150: 49/49 (100%) matches, 0 gaps
  122947 aagttaattacaaaaagaaaattaatatttgtatattattctagtttta 122995
         |||||||||||||||||||||||||||||||||||||||||||||||||
  123046 ttcaattaatgtttttctttttaattataaacatataataagatcaaaat 122998


Galdieria-CP: Score 141: 47/47 (100%) matches, 0 gaps
  137298 catggaaaagaagaaaaacaagaaaaaataagtaattgataacctta 137344
         |||||||||||||||||||||||||||||||||||||||||||||||
  137393 gtacctttttcttcttttgttcttttttattcattaactattggaat 137347


Galdieria-CP: Score 110: 38/39 ( 97%) matches, 0 gaps
  140523 taagtaaattaggttggaataattatgtagaaactacta 140561
         |||||||||||||||||||||||||||||||||||||| ||
  140602 attcatttaatccaaccttattaatacatctttgatcat 140564


Galdieria-CP: Score 153: 51/51 (100%) matches, 0 gaps
  143415 attaatcataaaaaaagatgagagaataacaaataaattattagatataat 143465
         |||||||||||||||||||||||||||||||||||||||||||||||||||
  143524 taattagtatttttttctactctcttattgtttatttaataatctatatta 143474


Galdieria-CP: Score 103: 36/38 ( 94%) matches, 0 gaps
  149605 tataaaataagaaaaatataaaaaacaatattattata 149642
         |||||||||||||||||||||||||||||||||||||  ||
  149682 atattttattcttttatatttttttgttataatataat 149645


Galdieria-CP: Score 81: 27/27 (100%) matches, 0 gaps
  149955 aagatgaaaaaagaaatgaggataaat 149981
         |||||||||||||||||||||||||||
  150010 ttctacttttttctttactcctattta 149984


Galdieria-CP: Score 138: 50/50 (100%) matches, 1 gaps
  151873 tatgaataacaaataaagagatagattgatagattaagttaacaatcggta 151923
         |||||||||||||||||||||||||||||||||||||||| ||||||||||||
  151975 atacttattgtttatttctctatctaactatctaattc-attgttagccat 151926


Galdieria-CP: Score 156: 51/51 (100%) matches, 0 gaps
  154254 tttttatttagatgcctttaagttgggaagctaaaaaaagaacaaagtaaa 154304
         |||||||||||||||||||||||||||||||||||||||||||||||||||
  154357 aaaaataaatctacggaaattcaacccttcgatttttttcttgtttcattt 154307
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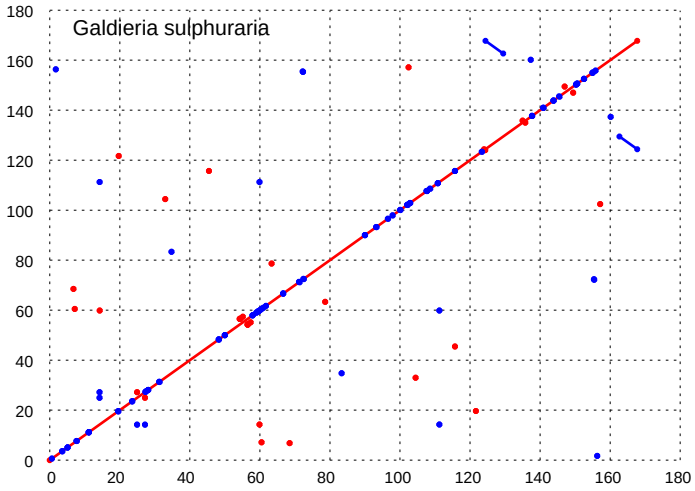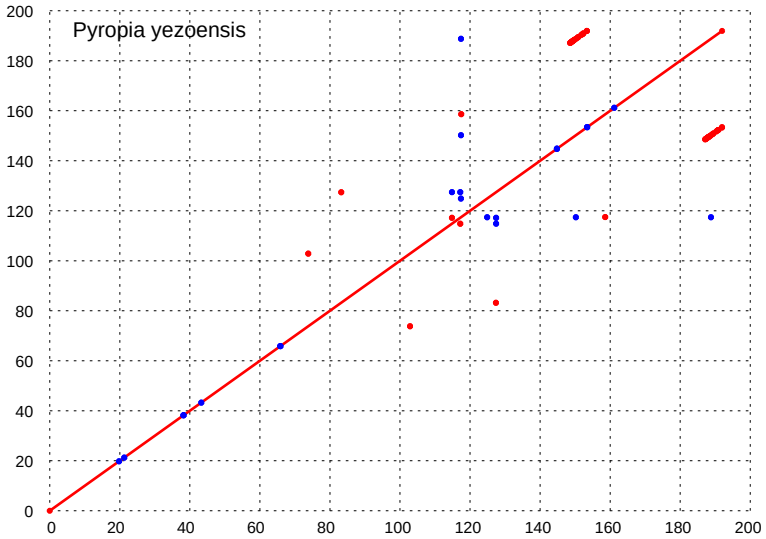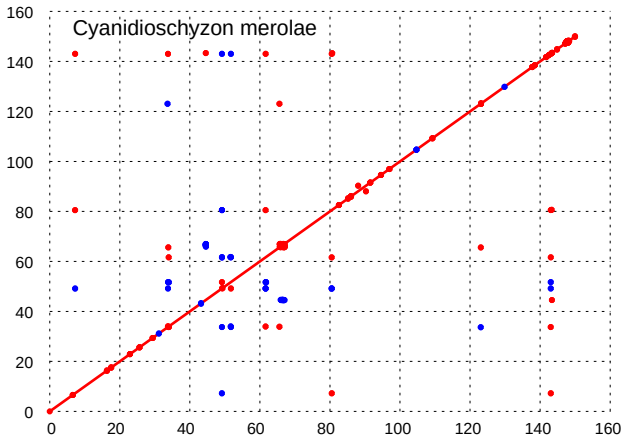
Figure S3 - Dot plot analyses of the plastid genomes of *G. sulphuraria* (top), *P. yezoensis* (middle), and *C. merolae* (bottom). Direct repeats are shown in red. Inverted repeats are shown in blue. Genome sizes are shown in kb.