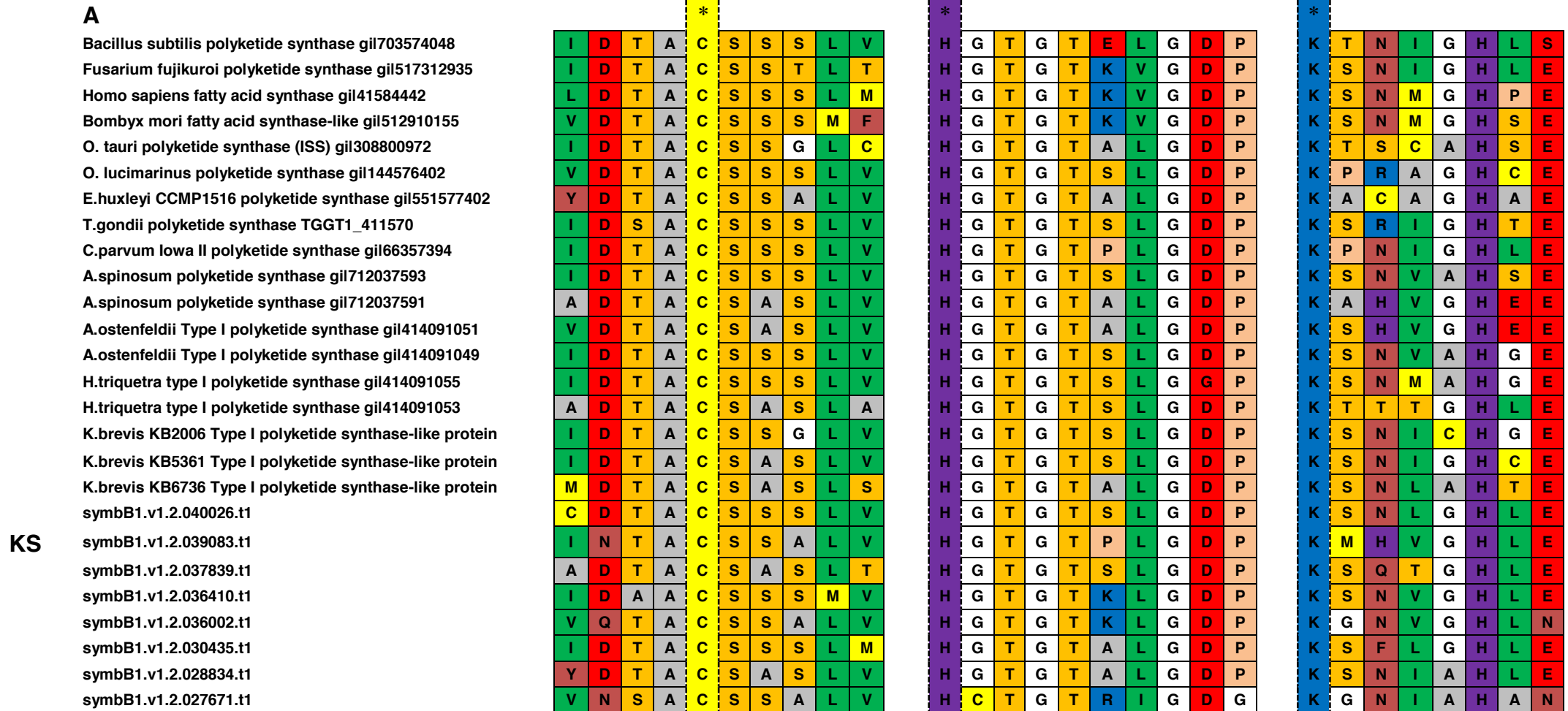


**Figure S3.** (A) Alignment of KS domains with those of other dinoflagellates and animal PKSs and FASs. Asterisks indicate conserved amino acids required for catalytic activity. (B) Additional *Symbiodinium* and *K. brevis* sequences that are consistent with previous reports.



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 symbB1.v1.2.015789.t1  
 symbB1.v1.2.015788.t2  
 symbB1.v1.2.008782.t1  
 symbB1.v1.2.008781.t1  
 symbB1.v1.2.002919.t1  
 symbB1.v1.2.001307.t1  
 symbB1.v1.2.012436.t1

I	S	S	A	C	S	T	G	A	H
I	D	T	A	C	S	A	S	L	V
T	E	T	A	C	S	S	S	L	S
V	N	T	A	C	S	A	S	L	V
C	D	T	A	C	S	A	S	L	T
V	D	T	A	C	S	S	A	L	V
V	D	T	A	C	S	S	T	I	V
M	D	T	A	C	S	S	S	L	V
I	D	T	A	C	S	S	T	L	V
C	D	T	A	C	S	S	S	L	V
L	D	T	A	C	S	S	A	L	V
A	E	T	A	C	S	S	S	L	V
V	D	T	A	C	S	S	S	L	I

H	G	T	S	T	P	I	G	D	V
H	G	T	G	T	A	L	G	D	P
H	G	T	G	T	A	L	G	D	P
H	G	T	G	T	S	L	G	D	P
H	G	T	G	T	S	L	G	D	P
H	G	T	G	T	P	L	G	D	P
H	G	T	G	T	A	L	G	D	P
H	G	T	G	T	A	L	G	D	P
H	G	T	G	T	A	L	G	D	P
H	G	T	G	T	A	L	G	D	P
H	G	T	G	T	A	L	G	D	P
H	G	T	G	T	A	L	G	D	P
H	A	T	G	T	W	F	G	D	Q

K	S	M	S	G	H	A	L
K	S	N	I	G	H	T	E
K	S	N	L	G	H	T	E
K	P	N	L	G	H	L	E
K	S	N	I	G	H	L	E
K	S	N	C	G	H	L	E
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K	T	N	V	G	H	L	E
K	S	V	I	A	H	L	E
K	T	N	I	A	H	L	E
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K	T	N	L	G	H	L	E
K	S	V	L	G	H	H	E

**B**

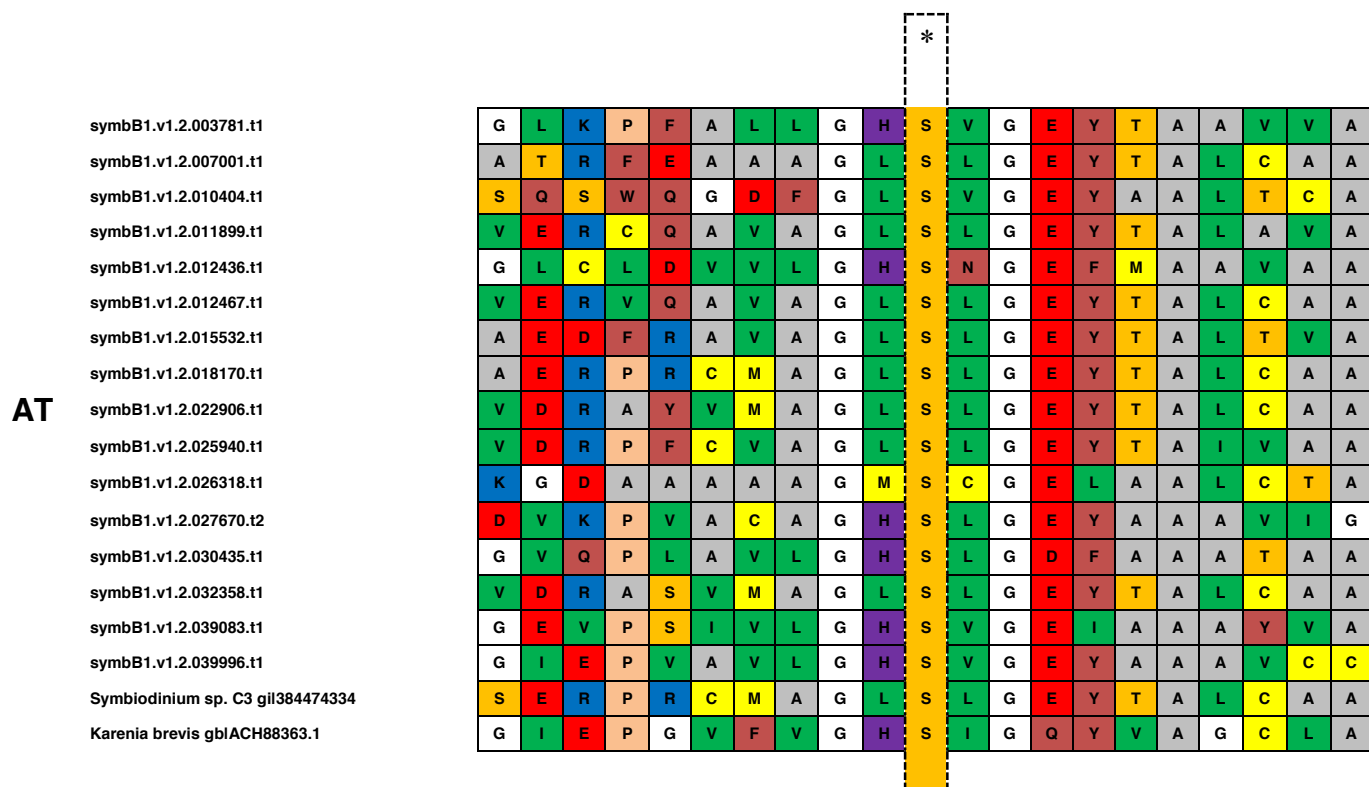
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 K.brevis KB4825 Type I polyketide synthase-like protein  
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 symbB1.v1.2.013880.t1  
 symbB1.v1.2.000535.t1  
 symbB1.v1.2.001928.t1

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I	D	T	D	A	S	S	G	A	T
I	D	C	D	L	S	S	S	A	M
L	D	T	G	C	S	A	S	L	V
C	D	T	D	G	S	S	S	L	T

F	G	D	G	R	F	L	H	E	A
S	G	T	G	H	F	F	C	D	A
Y	G	A	G	A	F	L	P	D	A
H	A	E	G	A	K	L	S	D	S
Q	A	N	G	S	L	L	G	D	P
N	G	Q	G	S	L	L	R	D	A

K	G	S	V	G	D	T	L
K	S	N	V	G	N	S	I
K	S	S	I	G	N	Q	I
K	T	N	T	G	V	Q	R
K	C	N	K	G	H	G	E
K	S	R	M	G	Y	A	T

**Figure S4.** Alignments of motifs within AT, ACP, KR, ER and DH domains. Active sites within the motifs are boxed with dashed lines.



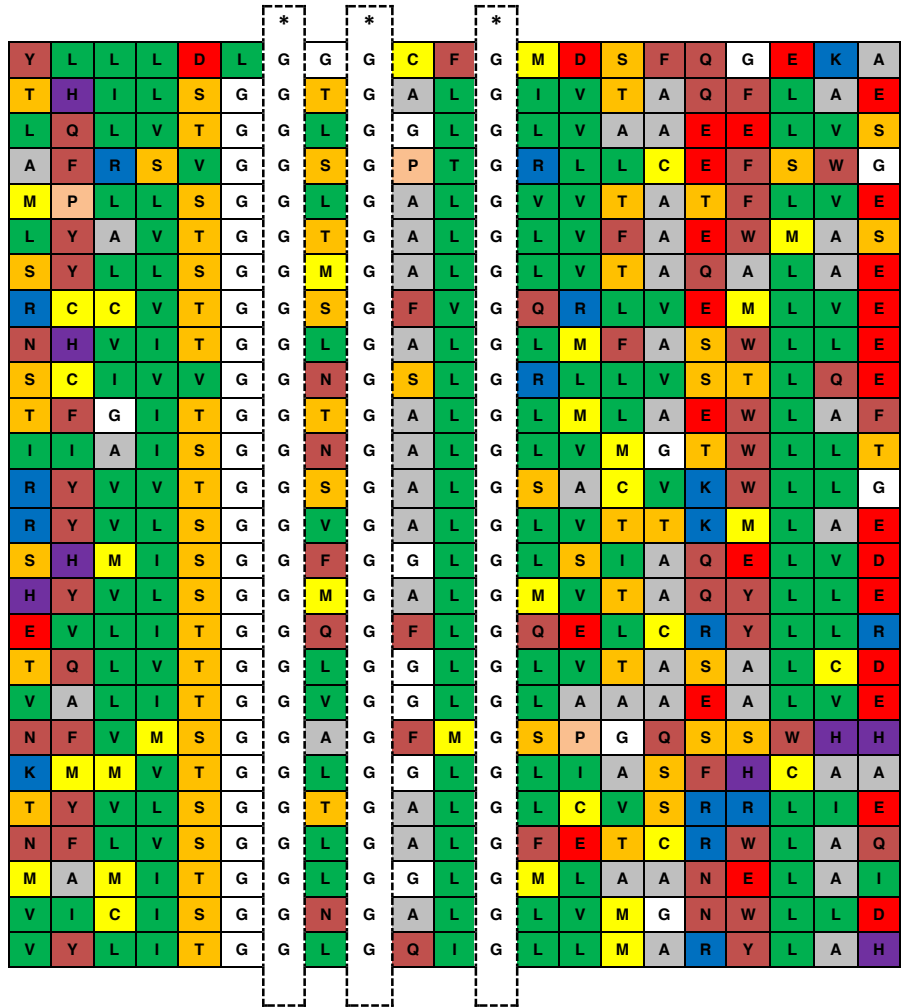
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(PP-binding)

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 symbB1.v1.2.005063.t1  
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 symbB1.v1.2.015788.t1  
 symbB1.v1.2.013531.t1  
 symbB1.v1.2.008780.t1  
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P	L	M	A	A	G	M	D	S	L	S	S	V	E	F	R	N
P	L	M	D	A	G	L	D	S	L	S	M	V	E	F	R	N
P	L	T	T	A	G	M	D	S	L	S	A	V	E	L	R	R
A	L	M	E	S	G	M	D	S	L	S	G	V	E	F	R	N
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P	L	M	E	A	G	I	D	S	L	S	A	V	E	F	R	S
D	L	A	F	I	G	L	D	S	L	Q	A	G	V	L	V	S
T	A	L	M	D	G	I	D	S	L	G	S	T	L	V	I	N
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A	L	M	D	S	G	M	D	S	L	T	A	V	S	F	R	N
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E	F	D	E	L	G	L	D	S	L	S	G	V	E	A	S	R
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R	I	D	I	D	G	L	E	S	L	L	M	K	N	S	A	V
A	L	M	D	A	G	L	D	S	L	A	S	V	E	F	Q	R
A	L	M	D	S	G	M	D	S	L	T	A	V	S	F	R	N
V	L	M	D	S	G	M	D	S	L	T	S	V	A	F	R	N
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D	L	N	E	S	G	L	D	S	L	A	A	A	E	L	S	T
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A	F	I	D	A	G	M	D	S	L	S	G	V	S	L	V	S
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T	F	F	D	Y	G	M	D	S	L	E	L	I	R	V	R	R
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G	F	F	Q	L	G	I	D	S	L	E	M	I	R	V	K	R
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P	L	M	E	A	G	M	D	S	L	S	S	V	Q	L	V	T
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P	L	M	D	I	G	I	N	S	M	N	A	V	V	F	R	R
P	L	M	D	M	G	L	D	S	L	S	A	V	E	F	R	R
T	L	L	R	S	G	M	D	S	L	S	G	V	E	F	R	R
F	V	H	D	L	G	I	D	S	A	G	M	A	G	L	L	G
T	F	E	D	A	G	L	D	S	L	S	L	I	S	L	A	R
V	F	V	E	V	G	V	D	S	I	T	A	V	D	L	V	R

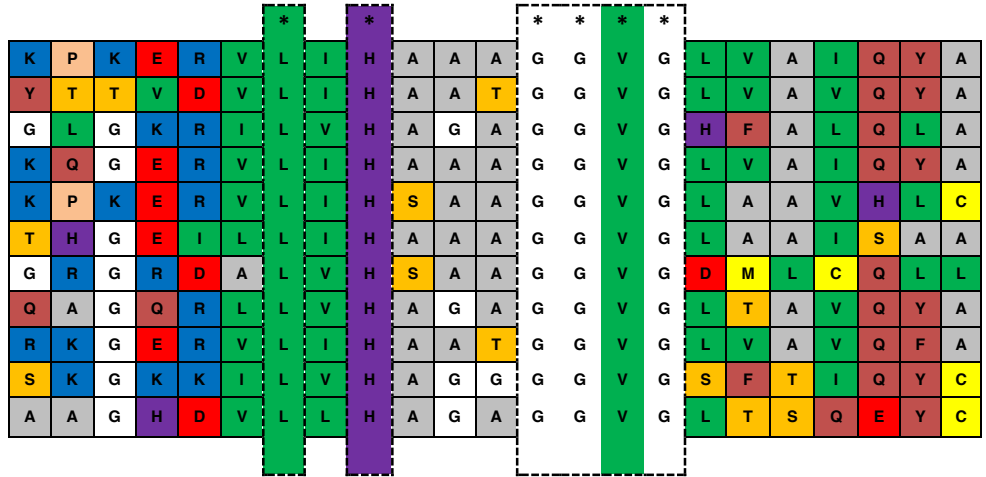
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 symbB1.v1.2.008784.t1  
 symbB1.v1.2.008384.t1  
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 symbB1.v1.2.010308.t1  
 symbB1.v1.2.010776.t2  
 symbB1.v1.2.040601.t1  
 symbB1.v1.2.012436.t1  
 symbB1.v1.2.013218.t1  
 symbB1.v1.2.034858.t1  
 Karenia brevis gblACH88363.1



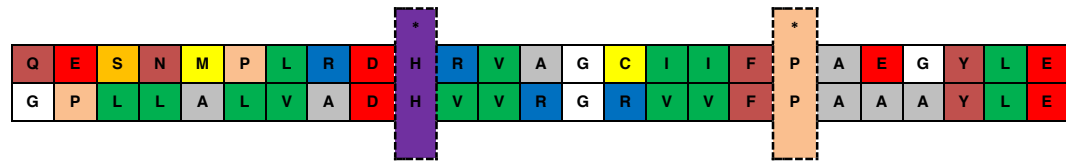
**ER**

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 symbB1.v1.2.001292.t1  
 symbB1.v1.2.007761.t1  
 symbB1.v1.2.040601.t1  
 symbB1.v1.2.008781.t1  
 symbB1.v1.2.005942.t1  
 Emiliana huxleyi CCMP1516 gii551553589



**DH**

symbB1.v1.2.012436.t1  
 Emiliana huxleyi CCMP1516  
 gblEOD11673.1



**Figure S5.** (A) Multiple alignment of the truncated, conserved, N-termini of dinoflagellate KSs (B) Additional Symbiodinium sequences with the divergent signatures. Lower panel: Maximum likelihood tree of the N-termini computed with 1000 bootstrap replicates. Bootstrap values  $\geq 50\%$  are marked at appropriate nodes.

**A**



**B**

