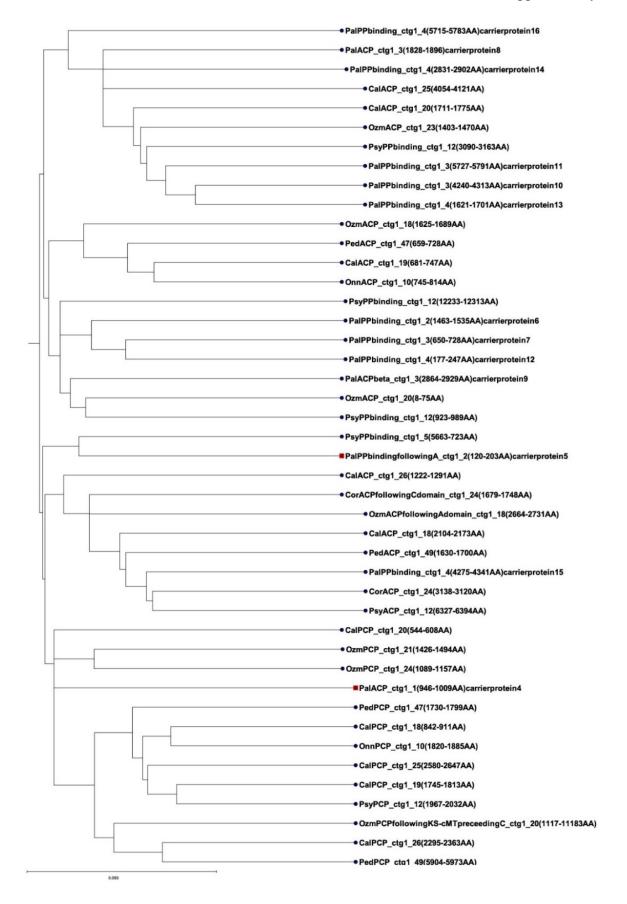


Supplementary Material



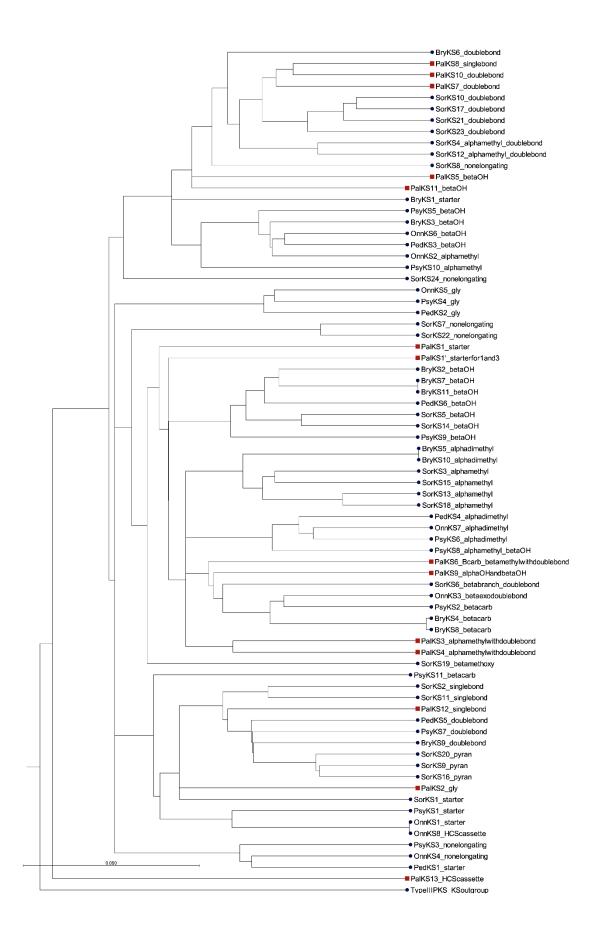
Supplementary Figure 1. Phylogenetic tree demonstrating the relationship between the third and fourth carrier proteins in the *pal* BGC with acyl-carrier proteins (ACPs) and peptidyl-carrier proteins (PCPs) from other hybrid PKS-NRPS systems. Though, an ACP would be expected at the end of module 1 (carrier protein 4) while a PCP would be expected at the end of module 2 (carrier protein 5), this is not what is observed bioinformatically. Carrier protein 4 was initially annotated as an ACP; however, is in the same clade as PCPs. Carrier protein 5 falls within the Pfam 00550.24 as a phosphopanthetheine attachment site and is within the clade associated with ACPs.

		20		40		60		80	
paIACP_ctg1_1(946-1009AA)carrierprotein4			IERLLOA						
palPPbindingfollowingA ctg1 2(120-203AA)carrierprotein5			AGSVVQAKLK	KEDAARS	GEIGLDSIR		VEGVSMEEAK	FFEL KSLR	GVARELAT
palPPbinding_ctg1_2(120205AA)carrierprotein6			VREALQA	EEDELGVDAT	FESMGVDSII	AVELVETLNA	KMAVKLRSAD	VENY ASIM	RLARRITA
palPPbinding_ctg1_2(1403-1333AA)carrierprotein7				ETSDLSAETS	FDRLGVDSIV				
palACP ctg1 3(1828-1896)carrierprotein8		ETVRVL	LASVLKL	SPORLHOTTP	FTDYGVDSIL	VLKENERLAE	LLP - EVSKTL		
palACPbeta ctg1 3(2864-2929AA)carrierprotein9				DPVGEDGQTA	FRDLGLDSIL	SVEFINGLNR	AFREREDASI		
palPPbinding ctg1 3(4240-4313AA)carrierprotein10		TOMEDELKSR	FAELTRI	PIDRIKGHEA		VMSETRRLEE	DFG-PLSKSL		ALASHEATR-
palPPbinding_ctg1_3(4240-4313A-4carrierprotein10 palPPbinding_ctg1_3(5727-5791AA)carrierprotein11			FCELTKL	PREQVYADEP		VTSFAOMLER	DLG-ELSKTL		KVADEL
palPPbinding_ctg1_5(5727-5751AA)carrierprotein12				APGDLDVKSP	FSEYGVDSIV	GVAEVNELNR		LFDH ASVE	RLATEIVG
palPPbinding ctg1 4(1621-1701AA)carrierprotein13		MALLPWLTTR	FSELVKL	PVERIOPMDA		VMDFTRRLEV	DFG-ELSKTL		ELAEYLVAQ -
palPPbinding_ctg1_4(1821-1701A4)carrierprotein13				PAEQIDDEOR	FDEMGVDSIV	VNDVNOREER	DLG-NVPKTL	LEEH ANIR	KLARHLVAH-
palPPbinding_ctg1_4(2275-4341AA)carrierprotein15			AAGVLKL	DPVLLDPEID	SAEYGEDSMT	FTSLANEVGR	ALALEVTPAM	FFEHRT LA	EFGDYL
pallPPbinding_ctg1_4(5715-5783AA)carrierprotein16			FAELSKV	AAGKIRPTES		AVEFSORIGK	VYG-EVSQAV	VEEH SSIE	ALCAYLENR -
calPCP ctg1 18(842-911AA)			WEDLLGI	MDISLEDG	FLEAGGNSLL	AISLIERINK	TEGCSLTTTT	LFKYPSIK	ELSAHLAAT -
calACP ctg1 18(2104-2173AA)				GIDDLDPISP	FNEFGEDSVS	LISEANRLNQ	EYDEDLKPMV		SETTYLVE
calACP_ctg1_16(2104-2173AA)		A		PPEKINCDKH		GTOLIRGLEK	AFSCKVYGRD	LLAH PSIN	ALSAFLAQQL
calPCP_ctg1_19(01-7477A)			WKSMLSI	DAISTIDG	FFEVGGDSLR	AVLLAERIGK	REGVSETTTE	VERH ASVQ	AMAQKIAS
calPCP_ctg1_20(544-608AA)			FGEALNW		LEDVGATSET		HEGISVPIDV	FLDQ PTVA	ALAEYL
calACP_ctg1_20(1711-1775AA)		T		PISRLNERAT	FDTYGLTSAM		DLG-ECSKTM	FFEY QSIQ	DLADYLAA
calPCP_ctg1_25(2580-2647AA)			WRTVLQI	DNIALDDA	FFEVGGDSLN	AVILAEKIQE	REGEDETAAL		AVADY LAD
calACP_ctg1_25(2560-26477A)		LVSGV	LADTTRS	AREKIRPEMS	FEOLGVDSIL	OMSVIEALEK	VTG-ELPKTL		ELVDHLIA
calACP_ctg1_25(4054-4121AA)			VALQLGQ	PIERIEAGHG	YLEVGLOSRG	LVALVQGVSH			AFADYLADQ -
calPCP_ctg1_26(1222-1291AA)		ETKLAGI	WOEVLGO	VRIGVDDH	FFELGGHSLL	GLOLLTKIDR	IFGRNLPLST		ELAARIEQ
corACPfollowingCdomain ctg1 24(1679-1748AA)			AASMLGM	GPEQLOPTAT	FAQAGENSVT	LTALRARLLE	RLSVQVDPPA		ALAAHLAER-
corACP ctg1 24(3138-3120AA)		DEVRHI	VAGLLQL	EPASLOPRKD		ETELATALNT	AFGSELTPAN	FFELTPPSLD	ALVAHLRER -
onnACP ctg1 10(745-814AA)				PANELKMOCH		GMRLCRGLTE	REGVEVLGRE	MERH PTID	SLSAYLAQ
onnPCP_ctg1_10(143-8144A)			WODILKI	DNISPTOG	FFALGGNSVL	AVREAERIAO	TLGMPENPTA	LEKH ASIR	EIGHY
ozmACP ctg1 18(1625-1689AA)		GD	INTATLK		LSDYGFDSLS	GMKLAAVLEE	DLGVRLRLSD		ELSDHIG
ozmACPfollowingAdomain ctg1 18(2664-2731AA)			AGILGT	DAAEVPVDVP		ETVLSTRVSE	RYGTEVLPTL	EYRR PTVA	AVAAHLGE
ozmACP ctg1 20(8-75AA)				ATPERVSAAP	FEDLGLDLAR	AVELTEEINS	REGTTLSTGA	VTGA ADLD	GLARHVSEH -
ozmPCPfollowingKS-cMTpreceedingC_ctg1_20(0-75/A)			WREVLGW	TSVRPEDD	FOEVGGDSTL	ATOISRERS	GEPEELELGE	LFQA RTLA	DMVELLEA
ozmPCP ctg1 21(1426-1494AA)		EHLLAEL	WAEVLGV		FFELGGDSIH	TIHVVAKARQ	RGLE - FAPOL	VERH GTVA	ALAAALDER -
ozmACP ctg1 23(1403-1470AA)				DPDELDLRVP	FDRYGIDSLV	TRENTEER	HFD - DLPKTL	FFEY ATLQ	ELAEYFAAE -
ozmPCP_ctg1_24(1089-1157AA)		ERRISAI	WQSALGP		FFDAGGDSLR	LTHVVARLRA	ELRPSESRED	MERH PTIR	TMARHLAG
pedACP ctg1 47(659-728AA)				PVERIDPQQH	LYDLGVDSIV	AMKLERNEAR	AFGIPVRGRD	LLQY STVQ	ALSRHLAQ
pedPCP ctg1 47(1730-1799AA)			WRSLLAV	GIGVSVG	FFEVGGNSIL	SVMLAQQISE	AFGIREAATD		DISLLIGET -
pedACP ctg1 49(1630-1700AA)			IAELMKE	ELEDLDVETO	LTDYGENSIT	LTDESNRLNQ	OYSLEMTPTV	FFEYPTVS	EFAGWLSTE-
pedPCP_ctg1_49(5904-5973AA)			WRRVLDI	DRVGVHDS	FFDLGGHSLL	ALREMSALKO	GLGYELPISS		AQAELLGOD -
psyPPbinding ctg1 5(5663-723AA)			REVRSEEL	DETAFAWDRP		LLQLGERVAS	AFGVSPDPAF	FETH NTCK	KILA
psyPPbinding_ctg1 12(923-989AA)		RUVKI	FTDRLGL	AREELAEDES	FMAMGLSSIN	VVEFLEHINQ	CFOLTLSTGL	IFEHDTLH	ALAAHI
psyPCP ctg1 12(1967-2032AA)		RKILAI	WODLLKI	EKLSTTDG	FFEVGGSSVL	AVVLADRICO	AFDVAFTAPE	LEKY SSVQ	ALAAHL
psylect		AQVEDQURRE	FADVMRL	SVDDVDVQAP	LESFGLDSVV	VTYLNORERD	AFG-EVSATL	FYEY RTLA	DLADFLAA
psyl + binding_ctg1_12(6350-5105/4) psvACP_ctg1_12(6327-6394AA)			VARVQKI	OPEKIRLNRE		ETTLANALNE	AYDISIMPTI	FFET PNLA	ALAAHLVE
psyPPbinding ctg1 12(12233-12313AA)		RRVQVYVQEK	LSALLRL	PLEDMDITLS	TLAMGMOSLV	GLEFROLISD			ALAADVLKRL
Consensus			LAEVLKL				AFG-ELSPTL		
Consensus 1007		LLEL	LAEVLNL	CUTUVUUP	FFETGGDSTL	AVELAEKLNÄ	AFG-ELSPIL	LECHPILA	ALAANLAA
Conservation									
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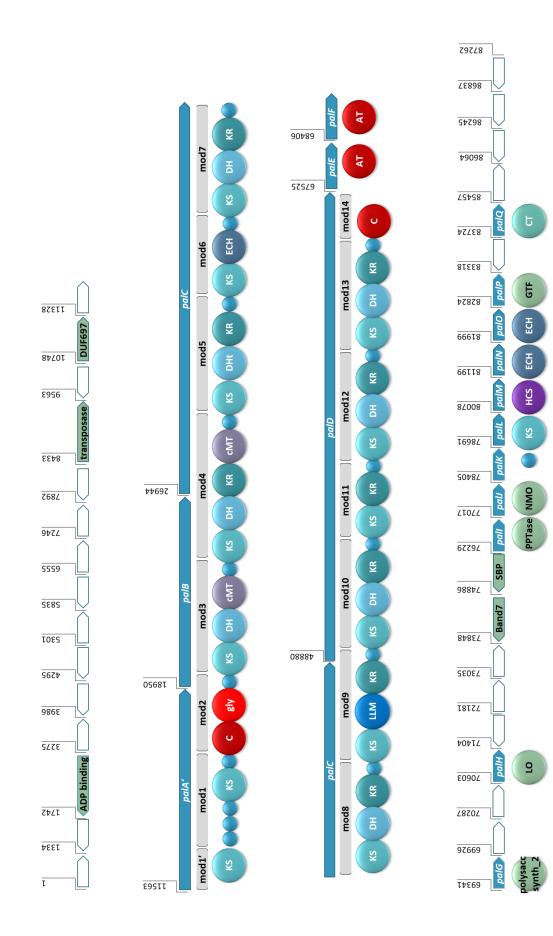
Supplementary Figure 2. Alignment of select carrier proteins in the *pal* BGC with acyl-carrier proteins (ACPs) and peptidyl-carrier proteins (PCPs) from other hybrid PKS-NRPS systems. The fifth carrier protein possess the (D/E)xGxDSL motif expected for a phosphopantetheine attachment site, though an isoleucine is present, rather than a leucine. This amino acid difference is not uncommon in other carrier proteins within PKS-NRPS BGCs.

		40		60		80	
(A) phormidolide mandelalide myxoviricin onnamide oocydin	YAE YRE YRE YRE YAE YRE YRE YRE YRE YRE YRE YRE	ADHSGEACC ADREGEAVY ADREGEAVY ADQEGTAIY ADQGETAIY ADQAGESVC ADRHGEAVW ADANGESAVW ADANGESAVW ADANGESAVW ADANGESAVW ADQNGAAWW ADQNGAAWW ADQHGTAWW	P RH H G G P RH H G G G G P RH H G G G G G P RH H G <t< td=""><td>60 SIYANSAYMA AIYANNAYYA SIHANSAYYA SIYANNAYA SIYANNAYA GIYSPATIM GIYPPAYG GIYPPAYG GIPPPAYG GIPPPAYG GIPNPSYSS GIPNPSYSS GIPNPSYSS</td><td>AYLIPOTOO AYFAPLINHY ASLIPOTOR AYFAPLINHY SYLIPOTOR AYFAPLIKNY AAAATYKR GAAATYTQR GAAATYTQR GAAATYTQR GAAATYTQR GAAATTRN GAAATTRN AAYAAYTKRY AAYAAYTKRY</td><td>80 R F T A G V S P R F T A G V S V T R F T A G V S P R F T A G V S P R F T A G V V P G T A G S V V P G T A G S V V P G T A G S V V P R F G S V V P A T A A A A A A A A A A A A A A A A A A</td><td>L HHPAEVYEW HHPAEVYEW HHPAEVYEW HPTIKIAED HHPAEVYEW LHPPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIKAE HHPYKAE HHPYKAE</td></t<>	60 SIYANSAYMA AIYANNAYYA SIHANSAYYA SIYANNAYA SIYANNAYA GIYSPATIM GIYPPAYG GIYPPAYG GIPPPAYG GIPPPAYG GIPNPSYSS GIPNPSYSS GIPNPSYSS	AYLIPOTOO AYFAPLINHY ASLIPOTOR AYFAPLINHY SYLIPOTOR AYFAPLIKNY AAAATYKR GAAATYTQR GAAATYTQR GAAATYTQR GAAATYTQR GAAATTRN GAAATTRN AAYAAYTKRY AAYAAYTKRY	80 R F T A G V S P R F T A G V S V T R F T A G V S P R F T A G V S P R F T A G V V P G T A G S V V P G T A G S V V P G T A G S V V P R F G S V V P A T A A A A A A A A A A A A A A A A A A	L HHPAEVYEW HHPAEVYEW HHPAEVYEW HPTIKIAED HHPAEVYEW LHPPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIVAE HOPIKAE HHPYKAE HHPYKAE
gi 108760219/801-1150 gi 149145382/740-1091 gi 149145382/740-1091 gi 115368201/1689-2029 gi 17548662/2342-2682 gi 227254159/1833-2173 gi 2272577272/1739-2079 gi 225872800/3-343 gi 67857341/3-342 gi 17230145/3-342 gi 17230145/3-342 gi 186683276/592-926 gi 111025435/7-353 gi 29827385/79-418 gi 108761496/21-362	Y Y	AD T N G C A W AD T N G C A W AD E N G E A W AD A G G S A W AD A G G S A W AD A G G S A W AD A G G F S A W AD A G G F S A W AD A G G F A W AD A G G F A W AD A G G F A W AD A G G S A W AD A G S G A AD A G C A AD C A W AD C C A	P RH HA G R R H H H G G G G G G G G G G G G G G G G G G G R	G F PNPAVTS G PYPNPSVIG G SYPNPSVIC G SPNPSVIC G SPNPSVIA A F PNPSVIA A F PNPSVIA G YPNPAVH G YPNPTTS G YPNPSVIA G YPNPSVIA A PYPSVIA S YANSAWA	AA AA A TRNY AA AA A TUNY SA AA TINY SA AR TKH AA AR TKH AA AR TKH AA AR TSH AA AR TROR AA ATSTHY AA AM TERY AA AM TERY AA AM TERY AA AM TKR AA AG TIKR AA AG TIKR SY AQ TKR	Q R AGS Y P Y R AGS Y P H R AGS Y P Q R AGS Y P R AGS Y P R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q R AGS Y P Q	$ \begin{array}{c} \textbf{H} \textbf{P} \textbf{T} \textbf{U} \textbf{R} \textbf{I} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{A} \textbf{R} \textbf{I} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{I} \textbf{R} \textbf{V} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{I} \textbf{R} \textbf{V} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{R} \textbf{R} \textbf{V} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{R} \textbf{A} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{R} \textbf{A} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{R} \textbf{A} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{R} \textbf{V} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{R} \textbf{V} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{R} \textbf{A} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{H} \textbf{P} \textbf{A} \textbf{R} \textbf{A} \textbf{E} \\ \textbf{H} \textbf{R} \textbf{A} \textbf{E} \textbf{R} \textbf{A} \\ \textbf{R} \textbf{E} \\ \textbf{H} \textbf{R} \textbf{A} \textbf{A} \textbf{K} \textbf{W} \textbf{W} \end{array} $
Consensus ^{100%} Conservation	YRLLLEGAXF	ADANGFXAVW	TPERHFHAFG	GLYPNPSVVA	AALAAVTKRV	RLRAGSVVLP	
		20)		40		
 (B) basiliskamide oxazolamycir phormidolide palmerolideA PPSB_BACSU/1052-1487 PPSA_BACSU/1052-1487 PPSA_BACSU/1052-1497 ACVS_EMENI/2018-2466 ACVS_EMENI/2018-2566 ENTF_ECOLI/1442 ACVS_EMENI/3105-3533 SRFAB_BACSU/3121-3576 PPSB_BACSU/308-2546 PPSA_BACSU/2089-2547 PPSA_BACSU/2444 SRFAA_BACSU/2447 PRSA_BACSU/2447 PRSA_BACSU/2447 PRSA_BACSU/2097-2531 SRFAB_BACSU/1054-1148 Consensus 	1 GTASGLRYAL 2 HELMINKA 3 SGAPLERACI 3 SGAPLERACI 4 AKAPLERACI 3 SGAPLERACI 4 AKAPLERACI 3 SGAPLERACI 4 AKAPLERACI 3 SGAPLERACI 4 AKAPLERACI 3 SGAPLERACI 4 AGSLERACI 4 AGSLERACI 5 SGPLERACI 6 SGPLERACI 7 RGGLEKACI 7 RGPLEKACI 8 GGLEKACI 9 KGPLERACI	A D A - T V R S - D Y C V T MGN - N R R V T MGN - N R R V T HK - G R R N G E N R N R R N R R V T HK T G N N N Y Y R R R N Y Y R R X Y Y R R R R R R X R Y Y R	V V S L V F C V V V F C H L V D M H L V D M H L F D M H L F D M H C V S H A V V S H V V S H L F C H V V S H V V S V H L V S V H H L V S V H L V S V H H L V S V H H L V S V H H L V S V H H V S V H H V S V H H V S V H H V S V H H V S V H H V S V H H V S V H H V S V H H V S V S	G G S F H G G S S H N A G Z S M N A G Z S M N B G Z S M N C G Z S M N C G G S M N D G V C G M D G V C G M D G V C G M D G V C G M Q G S M M M Q G S M M M Q G S M M M Q G S M M M Q G S	Image: Constraint of the second state of the second sta		
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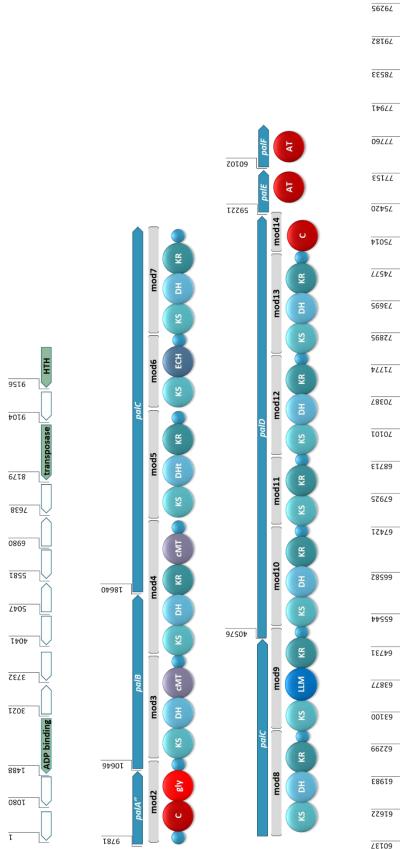
Supplementary Figure 3. (A) Alignment of the proposed palmerolide hydroxylase luciferase-like monooxygenase (LLM) with sequences from the TIGR subfamily 04020. **(B)** Alignment of the proposed termination condensation domain of the *pal* BGC_4 with that of basiliskamide and phormidolide as well as the HMM seed sequences for PF00668 (condensation domains); conservation of the HHXXXDG motif can be seen.

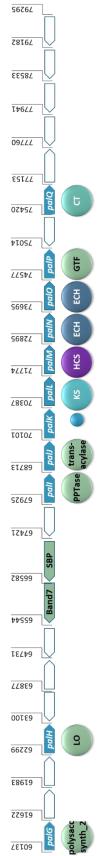


Supplementary Figure 4. Phylogenetic comparison of the amino acid sequences of the KS Pfam domains from the pal BGCs compared to those from the BGCs for bryostatin, onnamide, pederin, psymberin, and sorangicin. The KS domains are numbered based on their order for proposed biosynthesis. Though many of the PalKSs are within their own subclades, they show homology with enzymes of similar substrate affinity. PalKS1 and PalKS1' (from pal BGCs 1 and 3) fall within the same clade, though do not clade with the KSs accepting the starter unit in the BGCs for sorangicin, onnamide, and psymberin, and instead demonstrate more homology with KSs receiving methylated subunits. A trans-acting ER has been hypothesized to fully reduce the subunits containing C4-5 and C12-13 (module 12 and module 8), but interestingly, the phylogeny did not prove informative regarding the differentiation between KS modules receiving upstream olefins versus fully reduced subunits (PalKS8 and PalKS12). Additionally, PalKS9 is in a subclade that is distinct from those receiving reduced subunits with β -hydroxy groups and instead has greater homology to the KSs responsible for accepting β -functionalized subunits such as an β -exo double bond, β -branch, and β branch with endo-double bond (PalKS6). This supports the mechanism of the LLM acting as an αhydroxylase while the elongating polyketide chain is online the biosynthetic megaenzyme and prior to the activity of the downstream module. Interestingly, PalKS13 which associated with the HCS cassette, is in a clade of its own. Note, the KS domain from the type III PKS BGC responsible for 3-(2'-hydroxy-3'-oxo-4'-methylpentyl)-indole biosynthesis from Xenorhabdus bovienii SS-2004 was used for an outgroup.

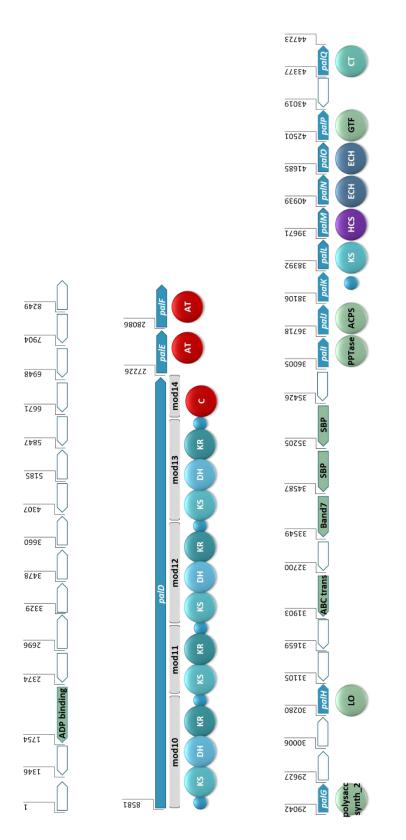


Supplementary Figure 5. The proposed BGC for *pal* BGC 1 which contains the same biosynthetic genes as *pal* BGC 3. The hybrid PKS-NRPS system has an additional elongation unit in *palA'* when compared to *palA*, seen at the beginning of the core biosynthetic genes. An ADP binding domain, a transposase, and a domain of unknown function (DUF697) are seen upstream of the core biosynthetic genes. KS: ketosynthase domain, C: condensation domain, gly: adenylation domain for glycine incorporation, DH: dehydratase domain, cMT: carbon methyl transferase domain, KR: ketoreductase domain, DH: dehydratase variant, ECH: enoyl-CoA hydratase, LLM: luciferase-like monooxygenase, AT: acyltransferase; polysacc synt_2: polysaccharide biosynthesis protein, LO: lactone oxidase, ABC trans: ATP-binding cassette transporter, Band7: stomatin-like integral membrane protein, SBP: bacterial extracellular solute-binding protein, PPTase: phosphopantetheinyl transferase, NMO: nitronante monooxygenase, HCS: hydroxymethylglutaryl-CoA synthase, GTF: glycosyl transferase, CT: carbamoyl transferase, small blue circles represent acyl- or peptidyl-carrier proteins. Blue arrows indicate biosynthetic genes. Green arrows indicate genes that encode for non-biosynthetic proteins. White arrows reflect genes that encode for hypothetical proteins. The BGC is displayed in reverse compliment.





Supplementary Figure 6. The proposed BGC for *pal* BGC 5, showing the hybrid PKS-NRPS system lacking the PKS portion of *palA* and designated here as *palA''* with the preservation of the enzymes responsible for incorporation of the glycine subunit. An ADP binding domain, a transposase, and a domain of unknown function (DUF697) are seen upstream of the core biosynthetic genes. KS: ketosynthase domain, C: condensation domain, gly: adenylation domain for glycine incorporation, DH: dehydratase domain, cMT: carbon methyl transferase domain, KR: ketoreductase domain, DHt: dehydratase variant; ECH: enoyl-CoA hydratase, LLM: luciferase-like monooxygenase, AT: acyl transferase; polysacc synt_2: polysaccharide biosynthesis protein, LO: lactone oxidase, ABC trans: ATP-binding cassette transporter, Band7: stomatin-like integral membrane, SBP: bacterial extracellular solute-binding protein, PPTase: phosphopantetheinyl transferase, CT: carbamoyl transferase, small blue circles represent acyl- or peptidyl-carrier proteins. Blue arrows indicate biosynthetic genes. Green arrows indicate genes that encode for non-biosynthetic proteins. White arrows reflect genes that encode for hypothetical proteins. The BGC is displayed in reverse compliment.



Supplementary Figure 7. The proposed BGC for *pal* BGC 2, showing the shortened BGC with no NRPS portion, seen at the beginning of the core biosynthetic genes. An ADP binding domain is

upstream of the core biosynthetic genes. The downstream tailoring enzymes are present, despite this cluster having the biosynthetic capability to only form an 8-carbon polyketide chain. KS: ketosynthase domain, C: condensation domain, DH: dehydratase domain, KR: ketoreductase domain, ECH: enoyl-CoA hydratase, AT: acyl transferase; polysacc synt_2: polysaccharide biosynthesis protein, LO: lactone oxidase, ABC trans: ATP-binding cassette transporter, SBP: bacterial extracellular solute-binding protein, PPTase: phosphopantetheinyl transferase, ACPS: acyl carrier protein synthase; HCS: hydroxymethylglutaryl-CoA synthase, GTF: glycosyl transferase, CT: carbamoyl transferase, small blue circles represent acyl- or peptidyl-carrier proteins. Blue arrows indicate biosynthetic genes. Green arrows indicate genes that encode for non-biosynthetic proteins. White arrows reflect genes that encode for hypothetical proteins. The BGC is displayed in reverse compliment.

Supplementary Table 1. GenBank Accession Numbers and versions for the genomes including the BGCs used in Figure 3 and Figure 4.

Compound	BGC name	GenBank Accession	Version
basiliskamide	bas	NZ_AXBT01000013	NZ_AXBT01000013.1
bryostatin 1	bry	EF032014	EF032014.1
calyculin	cal	AB933566	AB933566.1
corallopyronin	cor	HM071004	HM071004.1
mandelalide	mnd	NJAL01000001	NJAL01000001.1
onnamide	onn	AY688304	AY688304.2
oocydin	00C	JX315604	JX315604.1
oxazolamycin	ozm	EF552687	EF552687.1
pederin	ped	AH013687	AH013687.2
phormidolide	phm	KT727016	KT727016.1
psymberin	psy	FJ823461	FJ823461.1
sorangicin	sor	HM584908	HM584908.1
myxoviricin	ta	NC_008095	NC_008095.1

Supplementary Table 2. KS specificity predictions from *Trans*ATor. KS number designation is based on position in the pal BGC.

	Predicted specificity	<i>Trans</i> ATor Clade	<i>Trans</i> ATor Clade specificity	e-value	score
KS_1	β-branch with Double Bond	104	β-O-Me or β-Me double bond	1.10E-140	462
KS_2	Gly_Single Bond	96	various specificities	5.00E-171	562
KS_3	Double Bond with -Me	2	α-Me shifted double bond or OH	3.20E-189	622
KS_4	Double Bond with -Me	2	α-Me shifted double bond or OH	6.50E-191	627
KS_5	Secondary _D -OH	53	β-д-ОН	1.50E-192	633
KS_6	B-carb, β -meth with Double Bond	2	α-Me shifted double bond or OH	9.70E-192	630
KS_7	Double Bond	101	double bonds	4.20E-212	697
KS_8	Single Bond	101	double bonds	4.40E-214	704
KS_9	Secondary -OH	104	β-O-Me or β-Me double bond	9.50E-192	630
KS_10	Double Bond	127	double bonds (E-config)	1.40E-209	689
KS_11	Secondary _D -OH	53	β-д-ОН	8.90E-198	650
KS_12	Single Bond	96	various specificities	1.20E-197	650
KS_13	HCS Cassette	79	starters or β -OH	6.30E-36	117