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meta_2_contig00239_6_NewType -----RLALEVAYEVLMOA----R
meta_1_contig00008_3_FASlike -----QQRLLLEVAHEALS DANINPD
meta_2_contig00087_6_TRANS -----AMDPQQRVFLENCWRCIEDSGLNPF
meta_2_contig00009_1_NRPS_PKS -----AMDPQQRVLECAWTALEDAGYAPQ
meta_2_contig00158_1_CIS SSGLTVPNQQAQKALIREALENAGVKPAELSYVEGAMDPQQRVVLEVGWEALEYAGLAPD
meta_2_contig00196_1_Sup -----MLETSWEALEDAGIDPE
YP_001102988_EryKS2_Actinobact LMASDAAGTRAHGNFMAGAGDFDAAFFGISPREALAMPDPQQRQALETTWAEALSAGIPPE
ABK01326_Sup_Fieseler -----AMDPQQRVMVETSWRALEDAGIDPL
ABK01383_CIS_Fieseler -----AMEPQQRLLLELSWQALEDGAFDPS
ABK01395_NRPS_PKS_Fieseler -----AMDPQQRIFLETALTALEDAGYNPD
AAW84182_Sup_Schirmer -----AMDPQQRVMLEVSWEALAHAGIDPD
AAW84222_CIS_Schirmer -----AMDPQQRLLLEVSWEALAHAGQDVS
AAW84203_NRPS_PKS_Schirmer -----AMDPQQRVFLCECWHALEHAGYPPS

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meta_2_contig00239_6_NewType ALDQNAVGVFGALMVSNDLQRRVA-----SPF-----SAAGGSPAILSNRVSYALGLW
meta_1_contig00008_3_FASlike QLAGQKVGVFVGSgiaEYQAMAFG-----DPLNITQHTMSGNSLAVIANRLSYFLNLD
meta_2_contig00087_6_TRANS LLSGSTCGVFVGCATGNYGQLMNG-----DVLNAQGLMGGSPILSARIYFFLNK
meta_2_contig00009_1_NRPS_PKS GEA-LAVGWAGSSISTYLLFHLFNRRGGVG-TLPG-GFRFLMHNDDKYLATRVAYKLNK
meta_2_contig00158_1_CIS SLVGSRTGVFVGITASDYLHESLN-----DLDNADPHMTTGNVLFNFAAGRLSYLLGLQ
meta_2_contig00196_1_Sup GLRESRTGVYTGISNDEYRMLVVDSD---SKPAEAGCLYALSGTNLNGASGRVSVLGLLE
YP_001102988_EryKS2_Actinobact TLRGSDTGVFVGMHQGY-ATGRPR-----PEDGVDGYLLTGN TASVASGRIAYVLGLE
ABK01326_Sup_Fieseler GLKGSALTGVYTGVSNEYRMRIVESN--HKPVDAASSLYAMSGTSMGPNRVSFFLGLR
ABK01383_CIS_Fieseler GLGGSRTAVYVGMGASEYDARFQRR-----TGEVIDAYSGTGNDTFAAGRVAYTLGLR
ABK01395_NRPS_PKS_Fieseler QTE-EYIGVYATASMNLYLVRNLSSN--PERLESMDVSVVWGNKDFLATRTSFKLGLR
AAW84182_Sup_Schirmer RLRESRTGVYSGISNDEYRMLVVDSD---AKPAAAAACLYALSGTNLNGTAGRVSVLGLT
AAW84222_CIS_Schirmer HLRGSRGGIFVGMNDWYDTQLSLDA----GERHHIDEYTSGLAPSTAGRLSYFFDLT
AAW84203_NRPS_PKS_Schirmer QHG-ARTGVFAGSFLPSYLLHCLHGGGFMEFNNPGLGHLEIGNDKDYLTTRVSHLLNLR

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#
meta_2_contig00239_6_NewType GPSMTVDTA#SSSLVAIDAASKAIN-NRDCEIAVVGVNLLQSMEAYAAKCAAGMLSRKG
meta_1_contig00008_3_FASlike GPSMTVDTA#SAGLTAFLACQSLM-SGECDAAI VAAVNVLLGSPFVGFSGQAKMLSPRG
meta_2_contig00087_6_TRANS GPCLAITDA#SSSLVAIAEACNSLTFQRTSDLALAGGVGVLGSPSMHIMTSKAGMLSKDG
meta_2_contig00009_1_NRPS_PKS GPAMTVQTA#STSLVAVHEACQSL-AGECAMLAGGVSNLPQVSGTYVEGDILSPDG
meta_2_contig00158_1_CIS GPCMAVDA#SSSLVTVHLACQALR-NREADLALAGGVNLI LSPYGTVLVSKTRTLAPDG
meta_2_contig00196_1_Sup GAAKAVDA#SSSMVSHVDAVADLQ-QGKADLAIAGGVQAILNGRIYELRADSMMLSPDG
YP_001102988_EryKS2_Actinobact GPALTVDTA#SSSLVALHTACGSLR-DGDCGLAVAGGVSMAGPEVFTEFSRQALS PDG
ABK01326_Sup_Fieseler GPSKAIDAA#SSSLVAVNDAVSDLQ-RGKTDMAIVGGVQNILSGHVFKIRADAGILSPDG
ABK01383_CIS_Fieseler GPALTVNTA#SSSLVTLHLACEALR-SGRTDALAGGVNLMVSDSTVRLAQLRALSPDG
ABK01395_NRPS_PKS_Fieseler GPSMALGTG#SSSFTAMHTAIKLNK-TYDCDVAVVGGANVKLPQKSGYLYRRGINS PDG
AAW84182_Sup_Schirmer GPAKAVDA#SSSAMVAINDAVADLQ-QGRANLAIAGGVQAILNGRIYELRADAMMLSDAG
AAW84222_CIS_Schirmer GPSMVIDTA#SSSLVALHLAVGSLR-SGESDLTIAGGVDLMLTPESYIALSKLRALSDVG
AAW84203_NRPS_PKS_Schirmer GPSLSVQTS#STGLVAIATACQALL-AGQCDVALAGASSLTFPQG-GYQYLEGFVNSHDG

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meta_2_contig00239_6_NewType RCATFSDQADGYSPEGCAIIVLKPLQNALEDDDG-VWGILHGSAVNQDGR-TATLTAPN
meta_1_contig00008_3_FASlike ILAPFDESADGFFVRAEGCGALVLSRKNCSFI PSLRRVYAEVLGWGINVAGK-TESLTMP
meta_2_contig00087_6_TRANS RCFTFDQADGFFVPEGVGVVLLKRHSDAKRQDQH-IYGVIRGWGINQDGA-TNGITAPS
meta_2_contig00009_1_NRPS_PKS HCRPFDFHKAQGTYSSEGVGMVVLKPRAAAVHDGDH-IYAVIKGTAINNDGREKIGY TAPS
meta_2_contig00158_1_CIS RCKTFDAAAADGMRGEGCGMVVLRKLSDALAAKDP-VLAVLRGS AVQQDGR-SSGLTVPN
meta_2_contig00196_1_Sup QCKAFDASANGYVRGEGCGVVVLRKLSAEADGDR-IWAVIRGAAVNHGGA-SVGLTVPN
YP_001102988_EryKS2_Actinobact RCKPFSDEADGFLGEGSAFVVLQRLSDARREGRR-VLGVVAGSAVNQDGA-SNGLSAPS
ABK01326_Sup_Fieseler QCKVFDASANGYVRGEGCGVVVLRKLEAEADGDK-IWAVIKGS AVNHGGD-SVGMTVPH
ABK01383_CIS_Fieseler RCRAF DASADG YVRGEGGFV LQRLSDAQAQRPP-ILAVIRGSAMNHGGA-ASALT VPS
ABK01395_NRPS_PKS_Fieseler LCRAFDADASGTIFGNGVAAVVLKRMADAVEDGDD-IYAVIRASAINNDGDKVAY TAPS
AAW84182_Sup_Schirmer QCKTFDASANGYVRAEGCGVVVLRKLSDAEADGDR-IWAVIRGS VVNHHGT-GVGLTVPN
AAW84222_CIS_Schirmer RCHTFDEAANGFAKGECCLLVLRKLADAEERDGR-ILAVIKGS AVNHGDE-SNGLTAPN
AAW84203_NRPS_PKS_Schirmer QSRAFDADASGTVLGDGVVVALKRLDEAEAGDH-ILAVIKGF AVNNDGNLKYDAPS

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#
meta_2_contig00239_6_NewType GPA#EQVIRRAMERAGIEAEVEVGYVEAHGTG-----
meta_1_contig00008_3_FASlike ENR#CQLLQQLIQNAEILGEDVVYVEAHGTG-----
meta_2_contig00087_6_TRANS VDS#IRLEKDVYQRFGINPETISLVEGHGTG-----
meta_2_contig00009_1_NRPS_PKS QDG#AEVIAAAHRQASVHPDISISYVEAHGTG-----
meta_2_contig00158_1_CIS QQA#KALIREALENAGVKPAELSYVEG-----
meta_2_contig00196_1_Sup TPAL#EVMATALADAGVSPLEMDYVEG?-----
YP_001102988_EryKS2_Actinobact GVA#QQRVIRRAWARAGITGADVAVVEAHGTG#RLGDPVEASALLATY GKS RGS SGPVLLG
ABK01326_Sup_Fieseler IPAL#EQVMGQALRDAGVTA#EVDYVEAHGTG-----
ABK01383_CIS_Fieseler GPA#TALLREAWHAAGITADDLGYVEAHGTG-----
ABK01395_NRPS_PKS_Fieseler VKG#EEVIAMALELAKATPDDIGYVEAHGTG-----
AAW84182_Sup_Schirmer TPAL#EQVMEDALFQAGVD#LEVYVEAHGTG-----
AAW84222_CIS_Schirmer ALA#KRVIEQALQDA#VEPGHVGYVEAHGTG-----
AAW84203_NRPS_PKS_Schirmer VQG#VEVVAQAAMAVNAETISYVEV#HGTG-----

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; end;

**Supplementary Figure S2: Active Site and Conserved Domains.** In yellow are the conserved motifs where the primers attach. Two of three amino acids that compose the active site are marked with #.