

Figure S1: Minimal medium PAH plate screening for marine strains. (A) Pyrene top agar screening plates after 7 days of incubation. Colonies have been scraped from plates to score for clearing zones. (B) Phenanthrene top agar screening plates after 7 days of incubation. Colonies have been scraped from plates to score for clearing zones. 1) *R. pomeroyi* DSS-3, 2) *Citricella* sp. SE45, 3) *S. stellata* E-37, 4) *Bacillus-Clostridium* strain SE165, 5) *Bacillus-Clostridium* strain SE98, 6) *M. georgiense* DSM 11526, 7) *V. natriegens* ATCC 14048, 8) *Rhodospirillaceae* strain EZ35, 9) *Alcanivorax* sp. strain EZ46, 10) *A. macleodii* strain EZ55, 11) *Flavobacteriaceae* strain EZ40, and 12) *E. coli* DH5 α . Clearing zones appear as dark circles on the media.

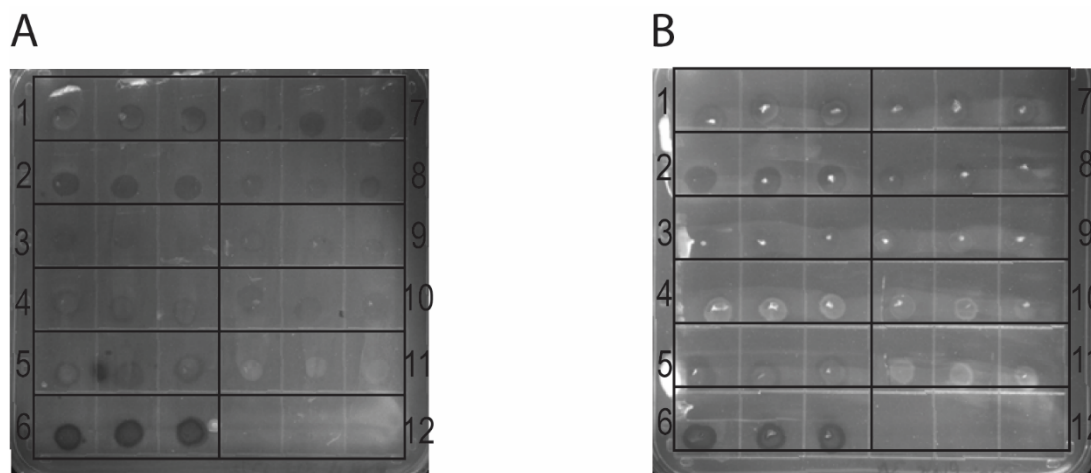


Figure S2: Complex medium PAH plate screening for *Roseobacteraceae* strains. A) *Roseobacteraceae* strains in pyrene top agar screening plates after 4 days of incubation. Colonies have been scraped from plates to score for clearing zones. B) *Roseobacteraceae* strains on phenanthrene top agar screening plates after 3 days of incubation. Colonies have been scraped from plates to score for clearing zones. 1) *R. pomeroyi* DSS-3, 2) *S. stellata* E-37, 3) *R. nubinihibens* ISM, 4) *Sulfitobacter* sp. EE-36, 5) *Citricella* sp. SE45, 6) Rhodobacterales strain Y4I, 7) *Ruegeria* sp. TM1040, 8) *Roseovarius* sp. 217, 9) *Sulfitobacter* sp. NAS-14.1, 10) *S. pontiacus* CB-D, 11) *E. coli* DH5 α , and 12) None. Clearing zones appear as dark circles on the media.

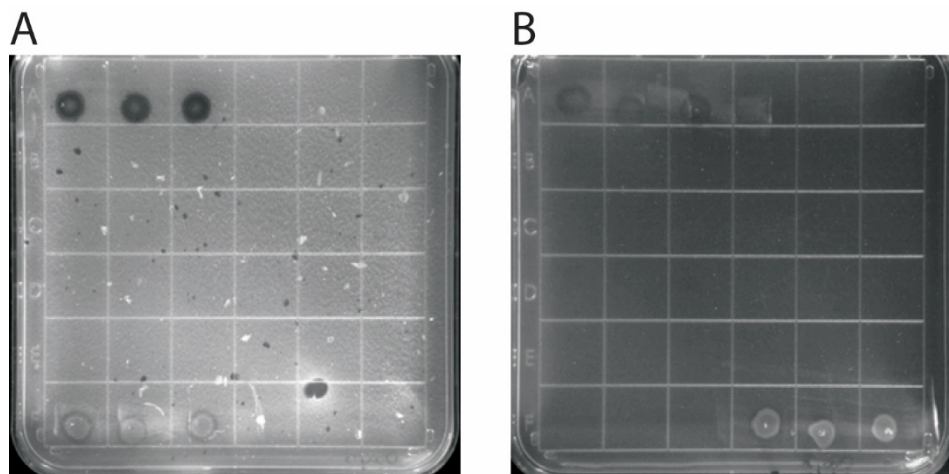


Figure S3: Rhodobacterales strain Y4I and *igiD* pyrene and phenanthrene screening. Wild type Y4I is shown on the top of the plate and the *igiD* mutant strain is shown on the bottom of the plate. A) Pyrene top agar screening plate and B) Phenanthrene top agar screening plate after 5 days of incubation.

Rhodobacterales strain Y41
Roseovarius sp. 217
Roseovarius nubinihibens ISM
Ruegeria pomeroyi DSS-3
Sagittula stellata E-37
Roseovarius sp. 217
Sulfitobacter pontiacus CB-D
Sulfitobacter sp. EE-36
Sulfitobacter sp. NAS-14.1
Citricella sp. SE45
Ruegeria sp. TM1040
Citricella sp. SE45
Ruegeria pomeroyi DSS-3
Roseovarius nubinihibens ISM
Roseovarius nubinihibens ISM
Roseovarius sp. 217
Ruegeria pomeroyi DSS-3
Pseudomonas aeruginosa PaK1
Clustal Consensus

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      10      20      30      40      50      60      70
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-----MFKGSM PALVTPFS-----NGELDL DALKRIV EWQIA-EGSNALV PVGTTSES
-----MRTAMTPIFRFDGIYTPVITPYNA-----DGSVNH DALS DVI EHLIA-AGVBGIIISGSGSTGEN
-----MTNRFDRBAQGVYIIAATPFPAE-----DGSLDLESTDRMVD FYLD-CGVTGM IILGIMSEA
-----MFKGSM PALVTPFS-----NGELDL EALKRIV EWQIG-EGSTGIV PVGTTSES
-----MFKGSM PALVTPFK-----DGAVDFE TLKQLVD WHDV-QGSHGLV PVGTTSES
-----MKKDVFHGTIPALLTPCTP-----DRKPDF DALVRKQ QEMIA-AGMSGV VYVCGSCGDW
-----MLQGS L PALVTPFT-----DGALDLATLKKLV EWHIA-EGSNGI V PVGTTSES
-----MLQGS L PALVTPFT-----DGALDLATLKKLV EWHIA-EGSNGI V PVGTTSES
-----MLQGS L PALVTPFT-----DGALDLATLKKLV EWHIA-EGSNGI V PVGTTSES
-----MKTPLTGILPVAPTPFHD-----DGRIDPEGM CRVLD CMID-QGVD AICILIANSEQ
-----MKT TNWSVPMFKGSM PALVTPFR-----NGELDL TLKHLV EWHIA-EGSTGIV PVGTTSES
-----MLKGS MPALVTPFK-----DGAVDFD TLKRLV EWHVA-EGSHGIV PVGTTSES
-----MSTRYTG IWPVAPTPFHD-----DGSLDL DGMKRVLD CLID-QGADGICILIANSEQ
-----MLKGS L PALVTPFK-----NGALD VDTLKH LV EWHIN-QGSHGIV PVGTTSES
-----MT-----LEGIYTPVVTPLHD-----DPSVDY DALAD VVDHLVA-SGVHGLISGSGSTGEN
-----MDVETLKKLV EWHIG-EGSHGIV PVGTTSES
-----MRGIWAAALNPFPAE-----DLSFDEAGFRNRIRHWVDD LGIEGLFTICGKQSEF
MSNKIMKTSRLTAEDINGAWTITMPTPSTPDASDWRSTATVDLEETARIVEELIA-AGVNGI L SMGTFSEC
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Rhodobacterales strain Y41
Roseovarius sp. 217
Roseovarius nubinihibens ISM
Ruegeria pomeroyi DSS-3
Sagittula stellata E-37
Roseovarius sp. 217
Sulfitobacter pontiacus CB-D
Sulfitobacter sp. EE-36
Sulfitobacter sp. NAS-14.1
Citricella sp. SE45
Ruegeria sp. TM1040
Citricella sp. SE45
Ruegeria pomeroyi DSS-3
Roseovarius nubinihibens ISM
Roseovarius nubinihibens ISM
Roseovarius sp. 217
Ruegeria pomeroyi DSS-3
Pseudomonas aeruginosa PaK1
Clustal Consensus

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      80      90      100     110     120     130     14
.....|.....|.....|.....|.....|.....|.....|
P T L T H E E H E T V I A E V V K A A A G R V P V I A G A G S N N T V E M I R F V E F A E K V G A D A A L V V T P Y Y N ---KPTQRGM
Y A Q T V Q E R V D L A R F A H A C I K G R V P L V I G T G A M L D D S I A L A Q A A R D I G A D V I L L S P P Y A ---VPTDR EN
P K L S G E E S A Q F A T R V L D R V A G R V P V I V G S G A G L D P M K A L T D R V M A A G A G V M V A P M S I Q ---TDAQKQK
P T L S H E E H E T V V A E V V K A A A G R V P V I A G A G S N N T T E A I R F V Q F A Q R I G A D A A L V V T P Y Y N ---RPTQRGL
P T L T H D E H E E V I R C V V E A A A G R I P V I A G A G S N N T D E A V R F M V Y A Q T V G A D G A L V V T P Y Y N ---KPTQAGM
P L L T D D E R ---M E G V A R L T K A G V P V V G T G A I N T K S A V A H A A H A Q K V G A A G L M V I F R V L S R G ---LSVAQR
P T L T H A E H E T V V A E V V K A A A G R I P V V A G A G S N N T T E S I R L A K H A E S V G A D A V L V V T P Y Y N ---KPTQAGL
P T L T H A E H E T V V A E V V K A A A G R I P V V A G A G S N N T T E S I R L A K H A E S V G A D A V L V V T P Y Y N ---KPTQAGL
P L L S D E E R A T L T R V S L E H V A G R V P V I V T I S A F A T A I V T A R A R E A E S L G A A M L M M P P Y H G V G L V P A E A G I
P T L T H E E H E L V I K V V V E T A A G R V P V I A G A G S N N T V E A I R F V E Y A H R V G A D A A L V V T P Y Y N ---KPTQRGM
P T L T H K E H E A V I A C V V E A V A G R I P V I A G A G S N N T D E A M R F V Q F A K T V G A D A A L V V T P Y Y N ---KPTQAGL
F L I S D A E R E T L T R L C L E H V A G R V P M I V T I S H F A T Q I A V E R A R F A K G L G A D I V M M P P Y H G A L L K G T A Q Q T
P T L S H E E H E A V V E I V V K A V N G R I P V V A G A G S N N T A E S L R F M E H A K K V G A D A A L V V T P Y Y N ---KPTQRGL
Y T Q T V E E R L E I A R F T Q R L K R L P L F V G T G M M R T E D S L A M A T G A R E M G A D G I L H G T P P Y S ---VPTREH
P T L T H Q E H E M V V E E V V R A A A G R I P V I A G A G S N N T L E G I R L M Q H A H K V G A D A A L V V T P Y Y N ---KPTQAGL
F S M S L E E R K R N L E V A V E E C A G R A G T M M S V S D Q N F D T V L E L A R H A Q D V G A N I V V H A P V L E ---FVHDRDALL
A T L T W D E K R D Y V S T I V E T I R G R V P Y P C G T T A L N T R E V I R Q T R E L I D I G A N T M L G V P M V V K ---MDLPTAV
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Roseovarius sp. 217
Roseovarius nubinihibens ISM
Ruegeria pomeroyi DSS-3
Sagittula stellata E-37
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Sulfitobacter pontiacus CB-D
Sulfitobacter sp. EE-36
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Citricella sp. SE45
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Roseovarius nubinihibens ISM
Roseovarius nubinihibens ISM
Roseovarius sp. 217
Ruegeria pomeroyi DSS-3
Pseudomonas aeruginosa PaK1
Clustal Consensus

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      150     160     170     180     190     200     21
.....|.....|.....|.....|.....|.....|.....|
V Q H F T A A H D C A G I P I I I Y N I P G R S - V V D M P A T M G E L A K L P R I V G V K - D A T G D L A R V S Q Q R A S C G A D F I Q
A L N A L A I D R A A N L P V M I Y N Y P G R T - G T M M G E E F L D R V G R S R N F C G I K - E S S G D I N R V H L L A R D Y - P H I Q L
Y F A Q V C Q T L G P D V P I C I Q D Y P M T T K V N F S T E T L L D I F R D N P Q I I M L K H E D W P G L N K L D R M R A E T G S D Q I D
I A H F T A L H D C A E I P I V I Y N I P G R S - V V D M P A T M G A L A K L P R I V G V K - D A T G D L A R V S Q Q R A S C G A D F I Q
I A H F K A V H D A D L P I I I Y N I P G R S - A V D M S P E T M G E L A K L P R I V G V K - D A T G D L A R V C Q R I T C G K D F T Q
N H F K A I L D A A P D V P A I T Y N S P Y Y G - Y S T K A D L F F A L R G E H K N L I G F K E F G G K N D L S Y A A E H I T S Q D D N V I
I A H F T A I H E A C G L P I I I Y N I P G R S - V V D M L P E T M A E L A K L P R I I G V K - D A T G D L A R V C D Q R M L C G P D F V Q
F E H F Q A V S D A V A I P I M V Q A P L S G - V T L T V P L L A R M A R E I G N V S Y F K - M E T P F A A D K L A A L I E A G G E H I V
I A H F S A L H D C A D I P I I I Y N I P P R S - V V D M S P A T M G E L A K L P R I I G V K - D A T G K L E R V S Q Q R A S C G A D F T Q
Y A H F K A L H D C A E I P I V I Y N I P G R S - A V D M L P A T M G E L A K L P R V I G V K - D A T G D L A R V C A Q R I T C G P D F I Q
F D Q F K A V G - E V G I P I M V Q A P L S G - V D L P V P L L V R M A Q E I D M V R L F K - I E C F R A N K L R A L I E Q G G A A I E
I A H F K T L H D A C D L P I V I Y N I P G R S - V V D M L P A T M G E L A K L P R I I G V K - D A T G D L A R V C Q Q R I T C G T D F L Q
A L N T L A V D R A A D L P M I I Y N Y P G R M - G V N M G E E F L D R V G R S R N V I G I K - E S S G D I N R V H L L A R D Y - P H I Q L
I A H F T A L H D C C D L P I I I Y N I P G R S - V V D M A P D T M K L A Q L P R I V G V K - D A T G D L A R V S A Q R I T C G K D F T Q
Y E Y Y K A I S E A V D I G I A M S H P D S G - Y L M S P E L C T R I A D L P N V V A I K ---Y S V P R E M Y A R L T E L A G D R I Q
Q Y R D V A D A V P E A A I A I Y A N P E A F - K F D F R P F W A E M S K I P Q V V T A K ---Y L G I G M L D L D I R L A P N I R F
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Residue; : indicates Strong Similarity; · Weak Similarity). Active and catalytic sites were derived from the CHBPH_aldolase subfamily using the NCBI Conserved Domains Database (<https://www.ncbi.nlm.nih.gov/cdd>).

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