

Supplementary Table S2 of Amrine *et al.* (2014)

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This document presents Supplementary Table S2 of Amrine et al. (2014) “tRNA signatures reveal polyphyletic origins of streamlined SAR11 genomes among the Alphaproteobacteria” published in *PLoS Computational Biology*.

1 PDF attachments and how to regenerate this PDF file

The original org-mode file that generated this PDF is attached to this PDF. To generate the PDF from the org-mode document attachment, extract the attachment, open it in an Emacs with org-mode and export the org-mode document to PDF with *e.g.* `⌘ E d`. The data table presented below is also attached to this PDF in comma-separated-values (CSV) format. Attachments may be added or extracted in Adobe Acrobat Pro or the open-source pdftk toolkit.

2 Description

The table presents the number of times out of 100 bootstrap replicates that specific alphaproteobacterial test genomes classified into one among seven alphaproteobacterial clades.

Genome	CIFs[1]	C[2]	H[3]	B[4]	Z[5]	S[6]	D[7]	K[8]
LABRENZIA ALEXANDRII DFL-11	all	0	0	1	53	37	9	0
LABRENZIA ALEXANDRII DFL-11	>0.5[9]	0	1	0	43	28	28	0
STAPPPIA AGGREGATA IAM 12614	all	0	0	1	48	23	26	2
STAPPPIA AGGREGATA IAM 12614	>0.5	0	4	0	45	14	36	1
PSEUDOVIBRIO SP- JE062	all	0	0	37	61	2	0	0
PSEUDOVIBRIO SP- JE062	>0.5	0	0	29	57	12	2	0
PELAGIBACTER UBIQUE HIMB5	all	13	3	3	48	9	6	18
PELAGIBACTER UBIQUE HIMB5	>0.5	0	13	3	59	5	12	8
PELAGIBACTER UBIQUE HTCC7211	all	7	2	2	54	13	9	13
PELAGIBACTER UBIQUE HTCC7211	>0.5	0	15	5	56	3	10	11
PELAGIBACTER UBIQUE HIMB114	all	1	0	0	70	3	11	15
PELAGIBACTER UBIQUE HIMB114	>0.5	0	9	1	66	2	12	10
PELAGIBACTER UBIQUE IMCC9063	all	2	1	3	80	12	2	0
PELAGIBACTER UBIQUE IMCC9063	>0.5	0	9	1	79	11	0	0
PELAGIBACTER UBIQUE HTCC1062	all	2	0	1	85	4	3	5
PELAGIBACTER UBIQUE HTCC1062	>0.5	0	9	3	80	2	5	1
PELAGIBACTER UBIQUE HTCC1002	all	4	1	2	81	4	3	5
PELAGIBACTER UBIQUE HTCC1002	>0.5	0	9	3	80	2	5	1
PELAGIBACTER UBIQUE HTCC9565	all	0	2	1	86	4	5	2
PELAGIBACTER UBIQUE HTCC9565	>0.5	0	9	3	79	4	5	0
PELAGIBACTER UBIQUE HIMB59	all	0	0	0	1	4	87	8
PELAGIBACTER UBIQUE HIMB59	>0.5	0	0	0	16	3	75	6

¹ Which CIFs were bootstrapped.

² Caulobacteriales

³ Hyphomonadaceae

⁴ Rhodobacteraceae

⁵ Rhizobiales

⁶ Sphingomonadales

⁷ Rhodospirillales

⁸ Rickettsiales

⁹ Only CIFs with Gorodkin heights > 0.5 bits were retained and bootstrapped.