

Supplementary material

Diversity of the tryptophanase gene and its evolutionary implications in living organisms

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Table S1. % GC content of all the species sequences

Organism	%GC content	Organism	%GC content
1162092-1165253 <i>Acropora digitifera</i>	42	<i>Histophilus somni</i> strain USDA-ARS-USMARC-63368	38
121674-126752 <i>Acropora digitifera</i>	44	<i>Klebsiella michiganensis</i> strain 4928STDY7071129	57
39236-46093 <i>Stylophora pistillata</i> isolate CSM Monaco	41	<i>Klebsiella oxytoca</i> 10-5243 strain Oct-43	56
46873-52854 <i>Stylophora pistillata</i> isolate CSM Monaco	39	<i>Leclercia adecarboxylata</i> strain USDA-ARS-USMARC-60222	51
682667-687350 <i>Pocillopora damicornis</i>	42	<i>Limulus polyphemus</i>	38
<i>Acropora digitifera</i>	41	<i>Metarhizium acridum</i> CQMa 102	53
<i>Acropora millepora</i> isolate SF001	39	<i>Metarhizium brunneum</i> ARSEF 3297	52
<i>Acropora millepora</i> isolate SF001	43	<i>Metarhizium robertsii</i> ARSEF 23	53
<i>Actinia tenebrosa</i>	39	<i>Monoraphidium neglectum</i> strain SAG 48.87	65
<i>Aeromonas caviae</i> strain NCTC12244	64	<i>Moritella viscosa</i>	40
<i>Aeromonas dhakensis</i> strain KOR1	65	<i>Naegleria gruberi</i> strain NEG-M	36
<i>Aeromonas hydrophila</i> strain ZYAH75	64	<i>Natrarchaeobaculum sulfurreducens</i> strain AArc1	67
<i>Aeromonas media</i> strain BAQ071013-115	64	<i>Natrarchaeobaculum sulfurreducens</i> strain AArc-Mg	67
<i>Aeromonas salmonicida</i> strain O23A	62	<i>Natrialba magadii</i> ATCC 43099	66
<i>Aeromonas veronii</i> B565	64	<i>Natrinema pallidum</i> strain BOL6-1	66
<i>Aeropyrum pernix</i> K1	56	<i>Natrinema pellirubrum</i> DSM 15624	68
<i>Aggregatibacter actinomycetemcomitans</i> strain VT1169	46	<i>Natrinema</i> sp. J7-2	66
<i>Akkermansia muciniphila</i> strain YL44	59	<i>Natrinema versiforme</i> strain BOL5-4	69

<i>Aliivibrio wodanis</i> AWOD1	41	<i>Natronobacterium gregoryi</i> SP2	65
<i>Anaerotruncus colihominis</i> DSM 17241	54	<i>Natronococcus occultus</i> SP4	68
<i>Aspergillus aculeatinus</i> CBS 121060	65	<i>Natronorubrum aibiense</i> strain 7-3	66
<i>Aspergillus aculeatus</i> ATCC 16872	63	<i>Natronorubrum bangense</i> strain JCM 10635	65
<i>Aspergillus brunneoviolaceus</i> CBS 621.78	65	<i>Nematostella vectensis</i> strain CH2xCH6	44
<i>Aspergillus japonicus</i> CBS 114.51	62	<i>Octopus bimaculoides</i> isolate UCB-OBI-ISO-001	38
<i>Aspergillus saccharolyticus</i> JOP 1030-1	65	<i>Octopus vulgaris</i> isolate Ov201803	40
<i>Aspergillus uvarum</i> CBS 121591	64	<i>Odoribacter splanchnicus</i> strain An45	43
<i>Bacteroides cellulosilyticus</i> strain WH2	46	<i>Orbicella faveolata</i>	41
<i>Bacteroides eggerthii</i> strain NCTC11155	45	<i>Orbicella faveolata</i>	41
<i>Bacteroides faecis</i> MAJ27	46	<i>Orbicella faveolata</i> isolate FL	40
<i>Bacteroides intestinalis</i> DSM 17393	46	<i>Paeniclostridium sordellii</i> strain AM370	32
<i>Bacteroides ovatus</i> strain BSD2780061688st1_C6	47	<i>Pantoea ananatis</i> PA13	48
<i>Bacteroides salyersiae</i> CL02T12C01	46	<i>Pantoea stewartii</i> strain A206	50
<i>Bacteroides stercoris</i> ATCC 43183	44	<i>Paraclostridium bifermentans</i> ATCC638	33
<i>Bacteroides thetaiotaomicron</i> strain 7330	48	<i>Penicillium chrysogenum</i> Wisconsin	51
<i>Bacteroides uniformis</i> strain 2789STDY5834847	53	<i>Phaeodactylum tricornutum</i> CCAP	48
<i>Blastocystis hominis</i> , Singapore isolate B	56	<i>Photorhabdus laumondii</i> subsp. laumondii strain DJC	40
<i>Blastocystis</i> sp. subtype 4 strain WR1	57	<i>Photorhabdus luminescens</i> strain HIM3	40
<i>Brachyspira hyodysenteriae</i> ATCC 27164 strain B-78	32	<i>Plesiomonas shigelloides</i> strain FDAARGOS_725	53
<i>Brachyspira hyodysenteriae</i> WA1	32	<i>Pocillopora damicornis</i>	43
c138856-133320 <i>Exaiptasia pallida</i> isolate CC7	38	<i>Podospora anserina</i> S mat+	56
c33648-26504 <i>Exaiptasia pallida</i> isolate CC7	39	<i>Porphyromonas gingivalis</i> ATCC33277	48
c692470-687622 <i>Pocillopora damicornis</i>	41	<i>Porphyromonas gulae</i> strain COT-052	49
<i>Chromobacterium violaceum</i> strain 16-419A	68	<i>Prevotella intermedia</i> strain KCOM 1949	48
<i>Chryseobacterium indologenes</i> strain NCTC10796	39	<i>Priapulus caudatus</i>	46

<i>Citrobacter amalonaticus</i> strain FDAARGOS_122	48	<i>Proteus vulgaris</i> strain ATCC 49132	37
<i>Citrobacter koseri</i> ATCC BAA-895	55	<i>Providencia alcalifaciens</i> strain FDAARGOS_408	41
<i>Citrobacter portucalensis</i> strain FDAARGOS_738	50	<i>Providencia rettgeri</i> strain YPR31	38
<i>Clostridium novyi</i> NT	31	<i>Providencia stuartii</i> MRSN 2154	40
<i>Clostridium tetani</i> E88	34	<i>Raoultella ornithinolytica</i> strain 172117885	56
<i>Colletotrichum graminicola</i> M1.001	56	<i>Rhodobacter capsulatus</i> strain DSM 1710	64
<i>Cronobacter dublinensis</i> subsp. dublinensis LMG 23823	56	<i>Rhodopseudomonas palustris</i> strain CGMCC 1.2180	64
<i>Cutibacterium acnes</i> KPA171202	59	<i>Rodentibacter pneumotropicus</i> strain Ln316_4	41
<i>Dickeya dadantii</i> 3937	59	<i>Saccharopolyspora erythraea</i> NRRL2338	71
<i>Dickeya dianthicola</i> strain ME23	59	<i>Saccoglossus kowalevskii</i>	45
<i>Dickeya solani</i> IPO 2222	59	<i>Salinibacter ruber</i> DSM 13855	67
<i>Dickeya zeae</i> EC1	57	<i>Shigella boydii</i> strain 600384	50
<i>Dictyostelium purpureum</i>	32	<i>Shigella dysenteriae</i> strain BCW_4872	50
<i>Drosophila melanogaster</i> chromosome 3L	47	<i>Shigella flexneri</i> 2a str. 301	50
<i>Drosophila melanogaster</i> chromosome 3R	48	<i>Shigella sonnei</i> strain ECSW+14	51
<i>Edwardsiella piscicida</i> strain LADL99-462	57	<i>Streptomyces scabiei</i> 87.22	72
<i>Edwardsiella tarda</i> strain LADL88-209	55	<i>Stylophora pistillata</i> isolate CSM Monaco	43
<i>Elizabethkingia anophelis</i> R26	39	<i>Treponema denticola</i> ATCC 35405	41
<i>Elizabethkingia meningoseptica</i> strain NCTC10016	40	<i>Treponema phagedenis</i> 4A	45
<i>Elizabethkingia miricola</i> strain FL160902	39	<i>Treponema phagedenis</i> strain B43.1	45
<i>Entamoeba dispar</i> SAW760	34	<i>Trichoderma virens</i> Gv29-8	46
<i>Entamoeba histolytica</i> HM-1	33	<i>Trichomonas vaginalis</i> G3	48
<i>Entamoeba invadens</i> IP1	41	<i>Vibrio alginolyticus</i> strain FA2	47
<i>Entamoeba nuttalli</i> P19	33	<i>Vibrio anguillarum</i> 96F contig00051	47
<i>Enterocloster clostridioformis</i> strain FDAARGOS_739	44	<i>Vibrio campbellii</i> strain 1114GL	49

<i>Enterovibrio norvegicus</i> strain 10N.261.49.F5	52	<i>Vibrio cholerae</i> MS6	48
<i>Escherichia albertii</i> strain EC06-170	49	<i>Vibrio coralliilyticus</i> strain OfT6-21	48
<i>Escherichia coli</i> O157:H7 str. Sakai	51	<i>Vibrio crassostreae</i> strain 16BF1_28	47
<i>Escherichia coli</i> str. K-12 MG1655	51	<i>Vibrio cyclitrophicus</i> strain ECSMB14105	46
<i>Escherichia fergusonii</i> strain RHB18-C03	51	<i>Vibrio diabolicus</i> strain FA3	47
<i>Escherichia marmotae</i> strain UMB2500_14	50	<i>Vibrio fluvialis</i> strain FDAARGOS_104	54
<i>Folsomia candida</i> strain VU	42	<i>Vibrio furnissii</i> strain FDAARGOS_777	55
<i>Fusarium fujikuroi</i> IMI 58289	50	<i>Vibrio jasicida</i> 090810c	47
<i>Fusarium proliferatum</i> ET1	50	<i>Vibrio kanaloae</i> strain CCUG 56968	46
<i>Fusarium vanettenii</i>	58	<i>Vibrio lentus</i> strain 10N.286.45.C8	47
<i>Fusobacterium hwasookii</i> ChDC	34	<i>Vibrio metoecus</i> strain YB5B04	48
<i>Fusobacterium hwasookii</i> ChDC F300	31	<i>Vibrio mimicus</i> MB451	48
<i>Fusobacterium necrophorum</i> subsp. funduliforme strain 1_1_36S	40	<i>Vibrio nigripulchritudo</i>	50
<i>Fusobacterium nucleatum</i> subsp. nucleatum ATCC 25586	33	<i>Vibrio owensii</i> strain XSBZ03	48
<i>Fusobacterium nucleatum</i> subsp. polymorphum strain NCTC10562	33	<i>Vibrio rotiferianus</i> strain B64D1	48
<i>Grimontia hollisae</i> strain FDAARGOS_111	52	<i>Vibrio splendidus</i>	47
<i>Haemophilus haemolyticus</i> strain NCTC10839	40	<i>Vibrio tasmaniensis</i> strain UCD-FRSSP16_25	47
<i>Haemophilus influenzae</i> R2866	40	<i>Vibrio vulnificus</i> MO6-24/O	50
<i>Haemophilus influenzae</i> strain Hi375	40	<i>Xenorhabdus bovienii</i> str. puntauense	43
<i>Haemophilus influenzae</i> strain NML-Hia-1	40	<i>Yersinia enterocolitica</i> strain ERL053484	48
<i>Haemophilus parainfluenzae</i> T3T1	39	<i>Yersinia frederiksenii</i> ATCC 33641	48
<i>Halalkalicoccus jeotgali</i> B3	65	<i>Yersinia intermedia</i> strain CFSAN060537	49
<i>Halanaeroarchaeum sulfurreducens</i> strain HSR2	67	<i>Yersinia kristensenii</i> strain Y231	49
<i>Halanaeroarchaeum sulfurreducens</i> strain M27-SA2	67	<i>Yersinia massiliensis</i> strain SCPM-O-B-8025	49
<i>Haloarcula hispanica</i> ATCC 33960	64	<i>Yokenella regensburgei</i> strain NCTC11966	44

<i>Haloarcula hispanica</i> N601	64	<i>Halopiger xanaduensis</i> SH-6	69
<i>Haloarcula marismortui</i> ATCC 43049	63	<i>Haloprofundus sp.</i> MHR1	68
<i>Haloarcula sp.</i> CBA1115	64	<i>Halostagnicola larsenii</i> XH-48	65
<i>Haloarcula taiwanensis</i> strain Taiwanensis	64	<i>Halostella pelagica</i> strain DL-M4	67
<i>Halobacterium hubeiense</i> strain JI20-1	71	<i>Haloterrigena daqingensis</i> strain JX313	67
<i>Halobacterium salinarum</i> NRC-1	71	<i>Haloterrigena jeotgali</i> strain A29	68
<i>Halobacterium salinarum</i> R1	71	<i>Haloterrigena turkmenica</i> DSM 5511	69
<i>Halobacterium salinarum</i> strain 91-R6	71	<i>Haloferax gibbonsii</i> strain ARA6	68
<i>Halobacterium sp.</i> DL1	71	<i>Haloferax mediterranei</i> ATCC 33500	63
<i>Halobiforma lacisalsi</i> AJ5	69	<i>Haloferax volcanii</i> DS2	68
<i>Haloferax alexandrinus</i> strain wsp1	68	<i>Halogeometricum borinquense</i> DSM 11551	63

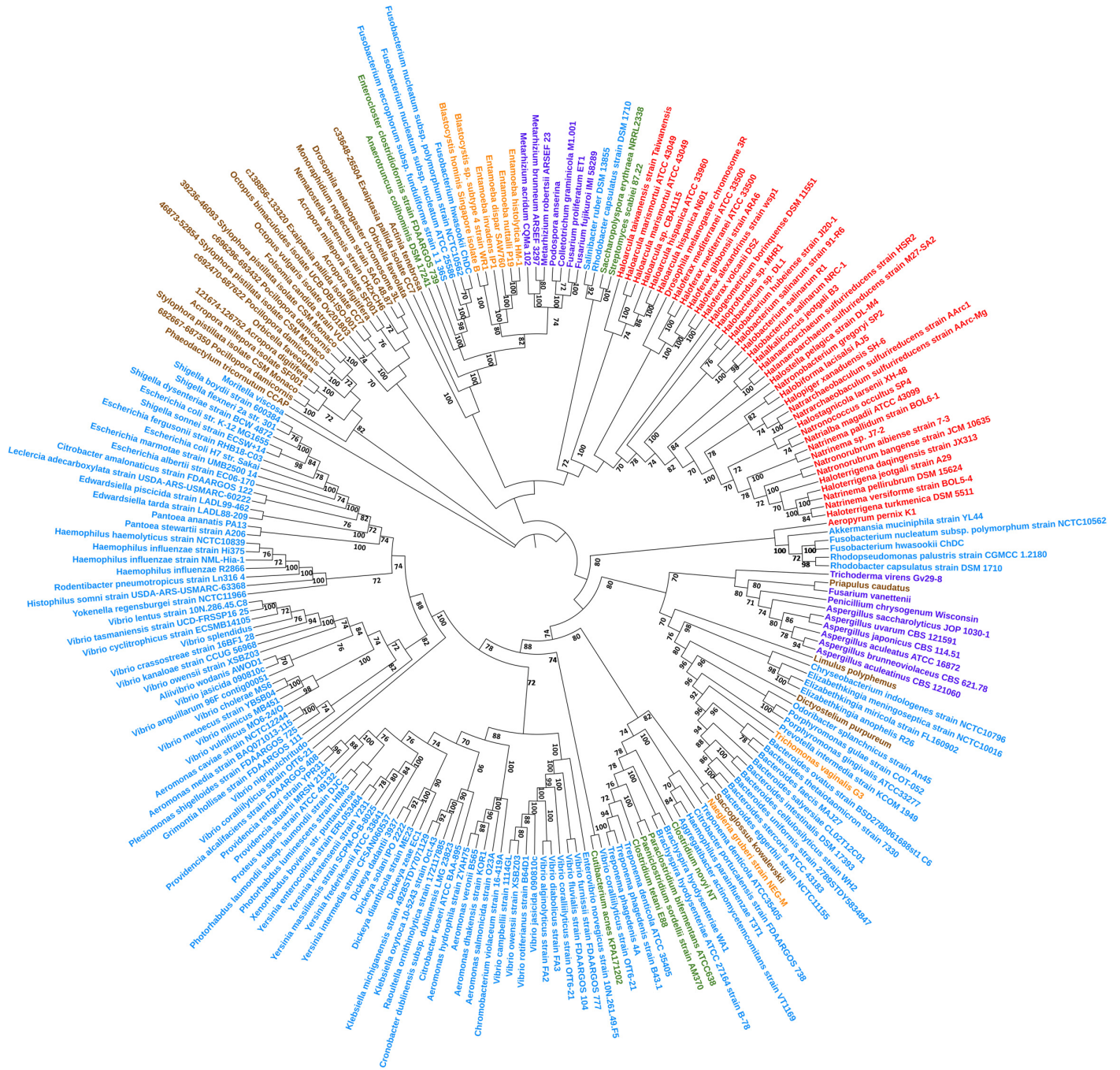


Figure S1. Nucleotide sequence phylogenetic tree (arbitrarily rooted maximum likelihood tree) of the *trnA* gene representing a total of 221 nucleotide sequences belonging to 95 genera of various taxonomic groups. All the nodes represent bootstrap values ≥ 70 (1000 replications). Details of the phylogenetic analysis are provided in Methods. A complete list of genera and species and their taxonomic classifications are provided in Table 1. Species names are labelled according to phylogenetic classifications by the following colour codes. Gram-negative bacteria (blue), Gram-positive bacteria (green), archaea (red), unicellular eukaryotes (orange), higher eukaryotes (brown).

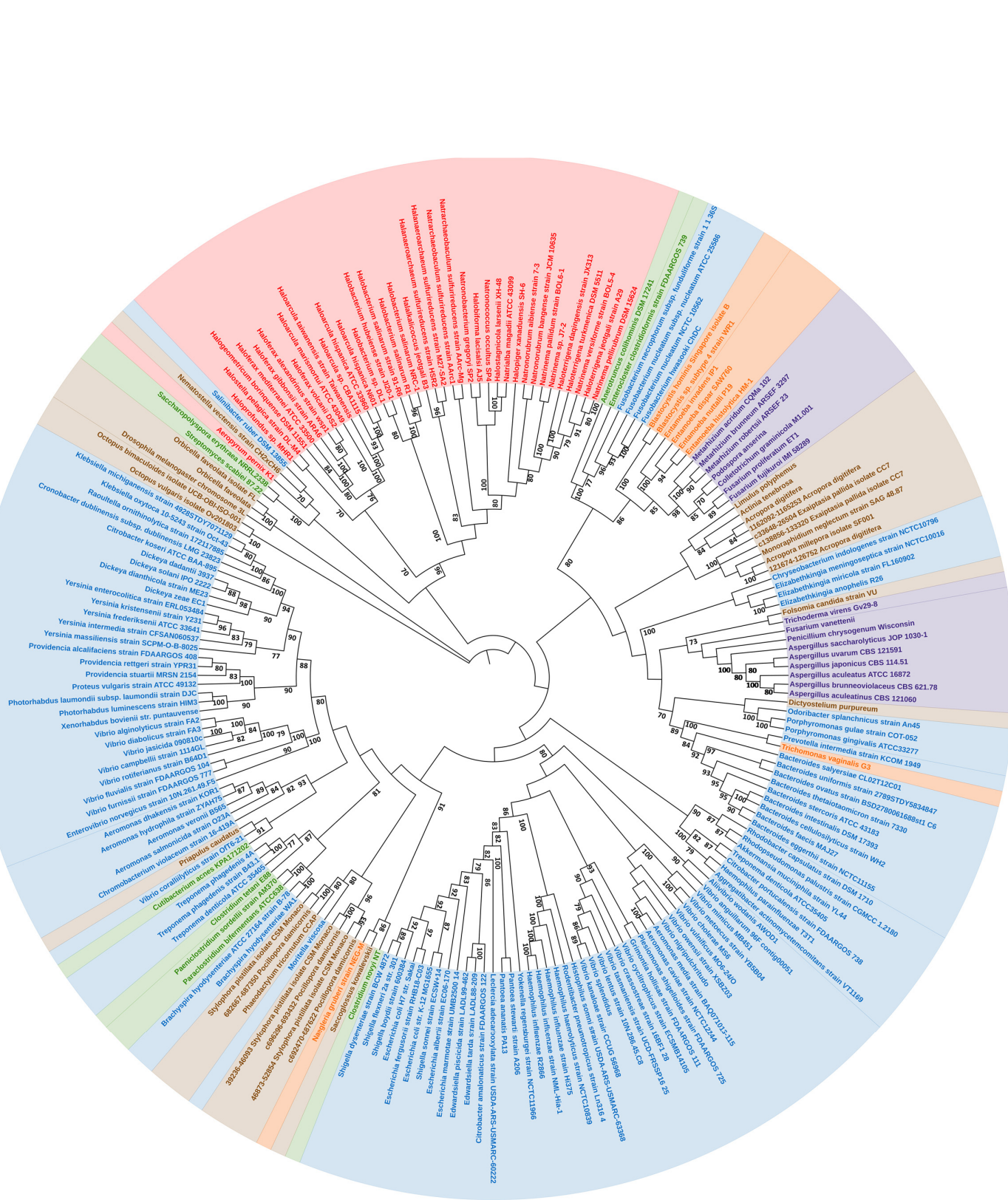


Figure S2. Amino acid sequence phylogenetic tree (arbitrarily rooted maximum likelihood tree) of the *tnaA* gene representing a total of 221 amino acid sequences belonging to 95 genera of various taxonomic groups. All the nodes represent bootstrap values ≥ 70 (1000 replications). Details of the phylogenetic analysis are provided in Methods. A complete list of genera and species and their taxonomic classifications are provided in Table 1. Species names are labelled according to phylogenetic classifications by the following colour codes. Gram-negative bacteria (blue), Gram-positive bacteria (green), archaea (red), fungi (purple), unicellular eukaryotes (orange), higher eukaryotes (brown).