Supplementary material

Alteriqipengyuania abyssalis sp. nov., a novel member of the class *Alphaproteobacteria* isolated from sponge, and emended description of the genus *Alteriqipengyuania*

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Table S1. Physiological and biochemical characteristics of NZ-12B^T and reference strains on API ZYM strip system.

No.	Enzymes	NZ-12B^T	***A. lutimaris* strain S-5^T**	***Q. pelagi* strain UST081027-248^T**	***Q. citreus* strain RE35F/1^T**	****A. halimionae* CPA5^T**
1.	Alkaline phosphatase	+	ND	+	+	+
2.	Esterase (C 4)	w+	_	w+	+	+
3.	Esterase lipase (C 8)	w+	ND	+	+	+
4.	Lipase (C 14)	w+	ND	w+	w+	+
5.	Leucine arylamidase	+	ND	+	+	+
6.	Valine arylamidase	+	ND	+	+	+
7.	Cystine arylamidase	+	w+	w+	w+	w+
8.	Trypsin	+	ND	w+	+	w+
9.	α- chmotrypsin	+	+	+	-	+
10.	Acid phosphatase	+	+	+	+	+
11.	Naphthol-AS-BI-phosphohy-drolase	+	+	w+	+	+
12.	α- galactosidase	-	ND	-	-	-
13.	β- galactosidase	-	-	-	-	-
14.	β- glucuronidase	-	ND	-	-	-
15.	α- glucosidase	+	-	+	-	-
16.	β- glucosidase	-	ND	-	-	-
17.	N- acetyl- β- glucosaminidase	-	+	-	-	-
18.	α- mannosidase	-	ND	-	-	-
19.	α- fucosidase	-	ND	-	-	-

+ Positive; - Negative; w+ Weakly positive; ND not determined. * Data from [40]; ** Data from [5].

NZ-12B^T was positive for alkaline phosphotase, leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase and α- glucosidase whereas negative for β- glucosidase, N-acetyl-β- glucosaminidase, α- mannosidase, α- fucosidase, α- galactosidase, β- galactosidase and β- glucuronidase and displayed weak growth for Esterase (C 4), Esterase lipase (C 8) and Lipase (C 14).

Table S2. Physiological and biochemical characteristics of NZ-12B^T and reference strains on API 20E strip system.

No.	Enzymes	NZ-12B^T	***A. lutimaris* strain S-5^T**	***Q. pelagi* strain UST081027-248^T**	***Q. citreus* strain RE35F/1^T**	****A. halimionae* CPA5^T**
1.	β-galactosidase (ONPG)	_	ND	_	_	ND
2.	Arginine dihydrolase	+	ND	_	_	ND
3.	lysine decarboxylase	w+	ND	_	_	ND
4.	Ornithine decarboxylase	_	ND	_	_	ND
5.	Citrate utilization	w+	ND	_	_	ND
6.	Hydrogen sulfide production	_	ND	W+	+	ND
7.	Urease	_	ND	_	_	ND
8.	Tryptophan deaminase	w+	ND	+	+	ND
9.	Indole production	-	ND	_	_	ND
10.	Voges proskauer (acetoin produc-tion)	-	ND	_	_	ND
11.	Gelatinase	+	ND	W+	_	ND
12.	Glucose fermentation	_	ND	_	_	ND
13.	Mannitol fermentation	_	ND	_	_	ND
14.	Inositol fermentation	_	ND	_	_	ND
15.	Sorbitol fermentation	_	ND	_	_	ND
16.	Rhamnose fermentation	_	ND	_	_	ND
17.	Saccharose fermentation	_	ND	_	+	ND
18.	Melibiose fermentation	_	ND	_	_	ND
19.	Amygdalin fermentation	_	ND	+	_	ND
20.	Arabinose fermentation	_	ND	_	_	ND

+ Positive; - Negative; w+ weakly positive; ND not determined. * Data from [40]; ** Data from [5].

NZ-12B^T was positive for arginine dihydrolase and gelatinase whereas negative for Glucose fermentation, mannitol fermentation, Inositol fermentation, sorbitol fermentation, rhamnose fermentation, saccharose fermentation, melibiose fermentation, amygdalin fermentation, arabinose fermentation and displayed weak growth for tryptophan deaminase, citrate utilization and lysine decarboxylase.

Table S3. Physiological and biochemical characteristics of NZ-12B^T and reference strains on API 20NE strip system.

No.	Enzymes	NZ-12B^T	***A. lutimaris strain S-5^T*	*Q. pelagi* strain UST081027-248^T	*Q. citreus* strain RE35F/1^T	**A. halimionae* CPA5^T
1.	Nitrate reduction	_	ND	_	_	_
2.	Indole production	_	ND	_	_	_
3.	Arginine Dihydrolase	+	ND	_	_	_
4.	Urease	_	ND	_	_	_
5.	Esculin hydrolysis	+	ND	+	+	+
6.	Gelatin hydrolysis	_	ND	_	_	_
7.	β-galactosidase (PNPG)	_	ND	_	W+	_
8.	Glucose assimilation	_	ND	_	_	_
9.	Arabinose assimilation	_	ND	_	_	_
10.	Mannose assimilation	–	ND	+	_	_
11.	Mannitol assimilation	_	ND	_	_	_
12.	N-acetyl- Glucosamine assimilation	–	ND	_	–	–
13.	Maltose assimilation	_	ND	_	+	_
14.	Potassium gluconate assimilation	–	ND	–	–	–
15.	Capric acid assimilation	_	ND	_	_	_
16.	Adipic acid assimilation	_	ND	_	_	_
17.	Malate assimilation	_	ND	_	_	_
18.	Trisodium citrate assimilation	–	ND	–	–	–
19.	Phenylacetic acid assimilation	–	ND	–	–	–

+ Positive; - Negative; w+ weakly positive; ND not determined.* Data from [40]; ** Data from [5].

NZ-12B^T was positive for esculin hydrolysis and arginine dihydrolase whereas negative for mannose assimilation, mannitol assimilation, N-acetyl-Glucosamine assimilation, maltose assimilation and potassium gluconate assimilation and remaining substrates in the API 20NE strip system.

Table S4. Physiological and biochemical characteristics of NZ-12B^T on Biolog Gen III Microplate.

A1	Dextrin	D-Maltose	D-Trehalose	D-cellobiose	Gentiobiose	Sucrose	D-Turanose	stachyose
	+	+	_	-	-	-	+	_
D-Raffinose	α-D-lactose	D-Melibiose	β-Methyl-D-Glucoside	D-Salicin	N-Acetyl-D-Glucoasamine	N-Acetyl-βD-Mannosamine	N-Acetyl-D-Galactosamine	N-Acetyl Neuraminic acid
-	+	-	+	+	+	+	+	+
α-D-Glucose	D-Mannose	D-Fructose	D-Galactose	3-Methyl Glucose	D-Fucose	L-Fucose	L-Rhamnose	Inosine
-	-	+	+	-	+	+	-	
D-Sorbitol	D-Mannitol	D-Arabitol	myo-Inositol	Glycerol	D-Glucose-6-PO4	D-Fructose-6-PO4	D-Aspartic acid	D-Serine
-	-	+	-	+	-	+		+
Gelatin	Glycyl-L-Proline	L-Alanine	L-Arginine	L-Aspartic acid	L-Glutamic acid	L-Histidine	L-Pyroglutamic acid	L-Serine
-	+	-	+	+	+	-	+	+
Pectin	D-Galacturonic acid	L-Galactonic Acid lactone	D-Gluconic acid	D-Glucuronic acid	Glucuronamide	Mucic acid	Quinic acid	D-Saccharic acid
+	+	+	+	+	+	+	+	+
p-Hydroxy-phenylacetic acid	Methyl Pyruvate	D-Lactic acid Methyl ester	L-Lactic acid	Citric acid	α–keto-Glutaric acid	D-Malic acid	L-Malic acid	Bromo-succinic acid
-		+	+	+	+	+	+	
Tween 40	γ-Amino-Butyric Acid	α-hydroxy-Butyric acid	β-hydroxy-D,LButyriacid	α–keto-Butyric acid	Acetoacetic acid	Propionic acid	Acetic acid	Formic acid
+		-	+		+	-	+	-

+ Positive; - Negative

NZ-12B^T was positive for acetoacetic acid, L-Galactonic Acid lactone, glycyl-L-proline, L-Glutamic acid, α-D-lactose, L-Fucose and negative for L-Histidine, myo-Inositol, L-Rhamnose and Sucrose, β-Methyl-D-Glucoside, D-Salicin, N-Acetyl-D-Glucoasamine, N-Acetyl-βD-Mannosamine, N-Acetyl Neuraminic acid, D-Fructose, L-Aspartic acid, α–keto-Glutaric acid, L-Malic acid, Citric acid, D-Malic acid.

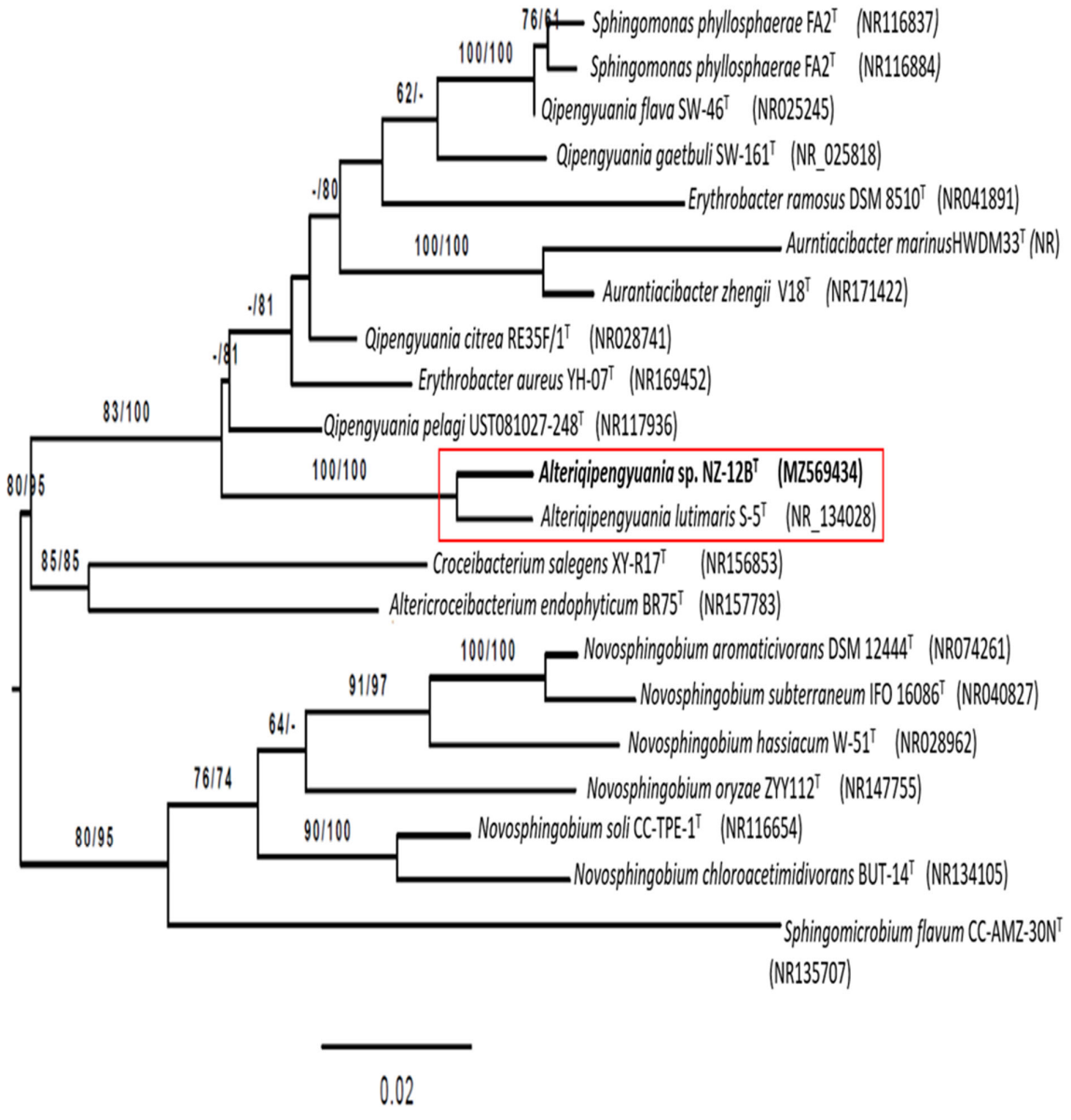

Figure S1. Maximum-likelihood phylogenetic tree based on almost complete 16S rRNA gene sequence of strain NZ-12B^T and its most closely related species using the GTR+GAMMA model of GGDC. The numbers above the branches are bootstrap support values greater than 60% for maximum likelihood (left) and maximum-parsimony (right). Bar, 0.02 substitution per nucleotide position.

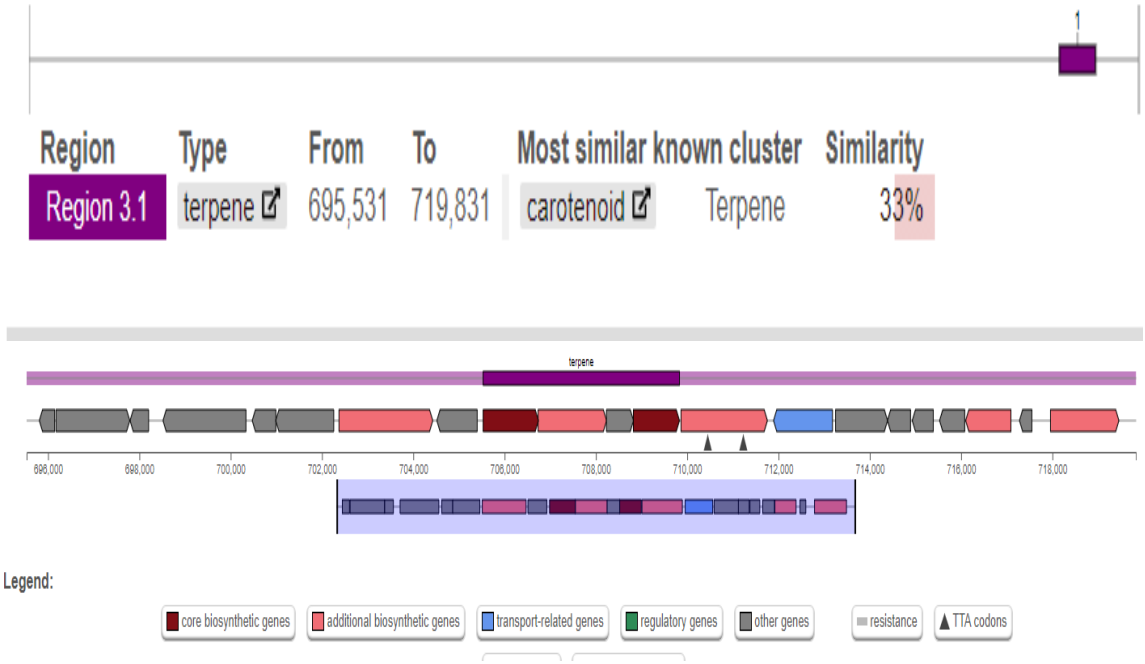

Figure S2. Predicted secondary metabolite gene cluster for strain NZ-12B^T identified by analysis of the NZ-12B^T genome sequence with the bioinformatic tool antiSMASH 5.0.