Table S1. Physiological and biochemical characteristics of NZ-96^T and reference strains on API ZYM strip system.

S.No	Enzymes	NZ-96^T	*Qipengyuania pelagi* strain UST081027-248^T	*Qipengyuania citreus* strain RE35F/1^T	*Erythrobacter aureus* strain YH-07^T
1.	Alkaline phosphatase	+	+	+	+
2.	Esterase (C 4)	w+	w+	+	+
3.	Esterase lipase (C 8)	w+	+	+	+
4.	Lipase (C 14)	w+	w+	w+	w+
5.	Leucine arylamidase	+	+	+	+
6.	Valine arylamidase	+	+	+	+
7.	Cystine arylamidase	+	w+	w+	w+
8.	Trypsin	+	w+	+	+
9.	α- chmotrypsin	w+	+	-	+
10.	Acid phosphatase	+	+	+	+
11.	Naphthol-AS-BI-phosphohydrolase	+	w+	+	+
12.	α- galactosidase	-	-	-	-
13.	β- galactosidase	-	-	-	-
14.	β- glucuronidase	-	-	-	-
15.	α- glucosidase	+	+	-	-
16.	β- glucosidase	-	-	-	-
17.	N- acetyl- β-glucosaminidase	-	-	-	-
18.	α- mannosidase	-	-	-	-
19.	α- fucosidase	-	-	-	-

Note: + Positive; - Negative; w+ weakly positive. NZ-96^T was positive for alkaline phosphotase, leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, 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-96^T and reference strains on API 20E strip system.

S.No	Enzymes	NZ-96^T	*Qipengyuania pelagi* strain UST081027-248^T	*Qipengyuania citreus* strain RE35F/1^T	*Erythrobacter aureus* strain YH-07^T
1.	β-galactosidase (ONPG)	-	-	-	-
2.	Arginine dihydrolase	+	+	+	+
3.	Lysine decarboxylase	w+	-	-	-
4.	ornithine decarboxylase	-	-	-	-
5.	Citrate utilization	w+	-	-	-
6.	Hydrogen sulfide production	-	-	-	-
7.	Urease	-	-	-	-
8.	Tryptophan deaminase	w+	+	+	+
9.	Indole production	-	-	-	-
10.	Voges proskauer (acetoin production)	-	–	-	-
11.	Gelatinase	-	w+	-	-

12.	Glucose fermentation	-	-	-	-
13.	Mannitol fermentation	-	-	-	-
14.	Inositol fermentation	+	-	-	-
15.	Sorbitol fermentation	-	-	-	-
16.	Rhamnose fermentation	+	-	-	-
17.	Saccharose fermentation	-	-	-	-
18.	Melibiose fermentation	-	-	-	-
19.	Amygdalin fermentation	-	-	-	-
20.	Arabinose fermentation	-	-	-	-

Note: + Positive; - Negative; w+ weakly positive. NZ-96T was positive for arginine dihydrolase, inositol fermentation and rhamnose fermentation whereas negative for Glucose fermentation, mannitol fermentation, sorbitol 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-96^T and reference strains on API 20NE strip system.

S.No	**Enzymes**	**NZ-96^T**	***Qipengyuania pelagi* strain UST081027-248^T**	***Qipengyuania citreus* strain RE35F/1^T**	***Erythrobacter aureus* strain YH-07^T**
1.	Nitrate reduction	-	+	+	+
2.	Indole production	-	-	-	-
3.	Glucose fermentation	-	-	-	-
4.	Arginine Dihydrolase	+	-	-	-
5.	Urease	-	-	-	-
6.	Esculin hydrolysis	+	+	+	+
7.	Gelatin hydrolysis	-	-	-	-
8.	β-galactosidase (PNPG)	-	-	-	-
9.	Glucose assimilation	-	-	-	-
10.	Arabinose assimilation	-	-	-	-
11.	Mannose assimilation	-	-	-	-
12.	Mannitol assimilation	-	-	-	-
13.	N-acetyl- Glucosamine assimilation	-	-	-	-
14.	Maltose assimilation	-	-	+	-
15.	Potassium gluconate assimilation	-	-	-	-
16.	Capric acid assimilation	-	-	-	-
17.	Adipic acid assimilation	-	-	-	-
18.	Malate assimilation	-	-	-	+
19.	Trisodium citrate assimilation	-	-	-	-
20.	Phenylacetic acid assimilation	-	-	-	W+

Note: + Positive; - Negative; w+ weakly positive.NZ-96T 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-96^{T} on Biolog Gen III Microplate.

A1	**Dextrin**	**D-Maltose**	**D-Trehalose**	**D-cellobiose**	**Gentiobiose**	**Sucrose**	**D-Turanose**	**stachyose**	**1% sodium lactate**	**Niaproof 4**
	+	**-**	**+**	**+**	**+**	**+**	**+**	**_**	**+**	**-**
D-Raffinose	α-D-lactose	D-Melibiose	β-Methyl-D-Glucoside	D-Salicin	N-Acetyl-D-Glucoasamine -	N-Acetyl-β-D-Mannosamine	N-Acetyl-D-Galactosamine	N-Acetyl Neuraminic acid	Guanidine HCL	
+	+	-	+	+		+	+	+	-	
α-D-Glucose	D-Mannose	D-Fructose	D-Galactose	3-Methyl Glucose	D-Fucose	L-Fucose	L-Rhamnose	Inosine	Nalidixic acid	
-	-	+	+	+	+	+	+	_	+	
D-Sorbitol	D-Mannitol	D-Arabitol	myo-Inositol	Glycerol	D-Glucose-6-PO4	D-Fructose-6-PO4	D-Aspartic acid	D-Serine	Tetrazolium violet	
-	-	+	+	+	+	+	_	_	-	
Gelatin	Glycyl-L-Proline	L-Alanine	L-Arginine	L-Aspartic acid	L-Glutamic acid	L-Histidine	L-Pyroglutamic acid	L-Serine	Lithium Chloride	
-	+	-	+	+	+	-	+	+	+	
Pectin	D-Galacturonic acid	L-Galactonic Acid lactone	D-Gluconic acid	D-Glucuronic acid	Glucuronamide	Mucic acid	Quinic acid	D-Saccharic acid	Sodium butyrate	
+	+	+	+	+	+	+	+	+	-	
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	Tetrazolium Blue	
-	_	+	+	_	+	+	+	_	-	

Tween 40	γ-Amino-	α-hydroxy-	β-hydroxy-	α–keto-Butyric	Acetoacetic	Propionic acid	Acetic acid	Formic acid	Potassium
+	Butyric Acid	Butyric acid	D,L-	acid	acid	+	+	W+	Tellurite
	_	W+	Butyriacid	_	+				+
			+						

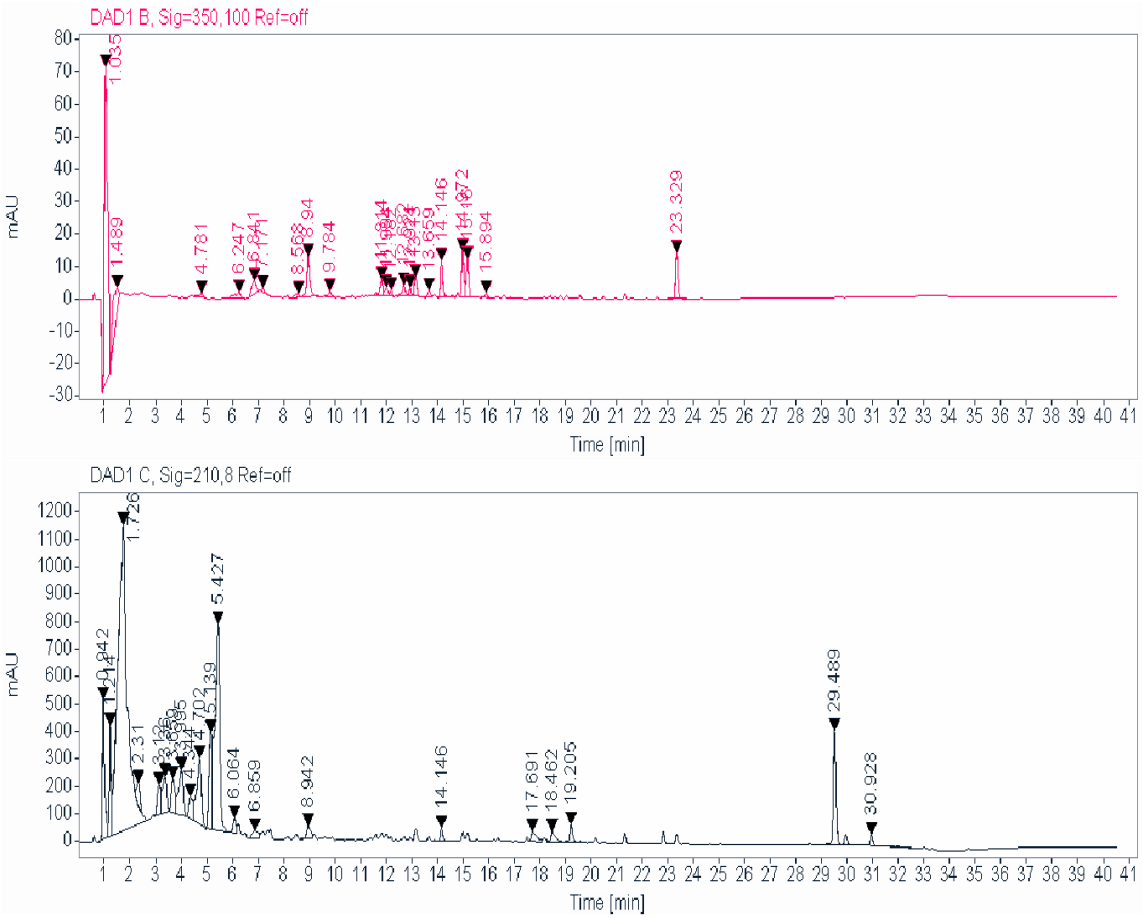
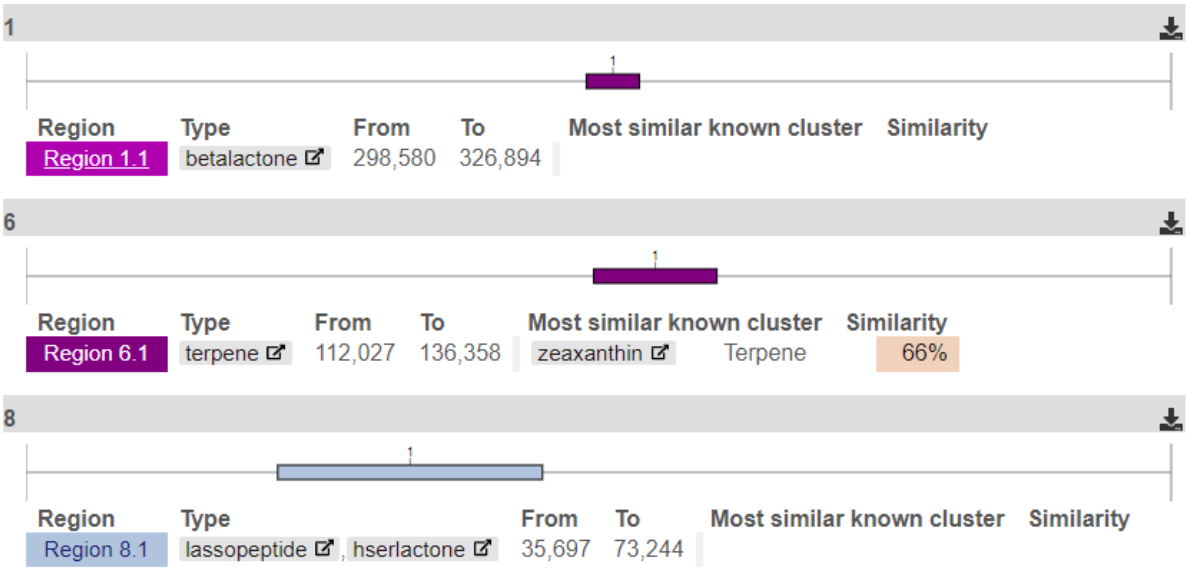


Figure S1. HPLC FRACTIONATION CHROMATOGRAM OF NZ-96 vs Staphylococcus aureus Newman.



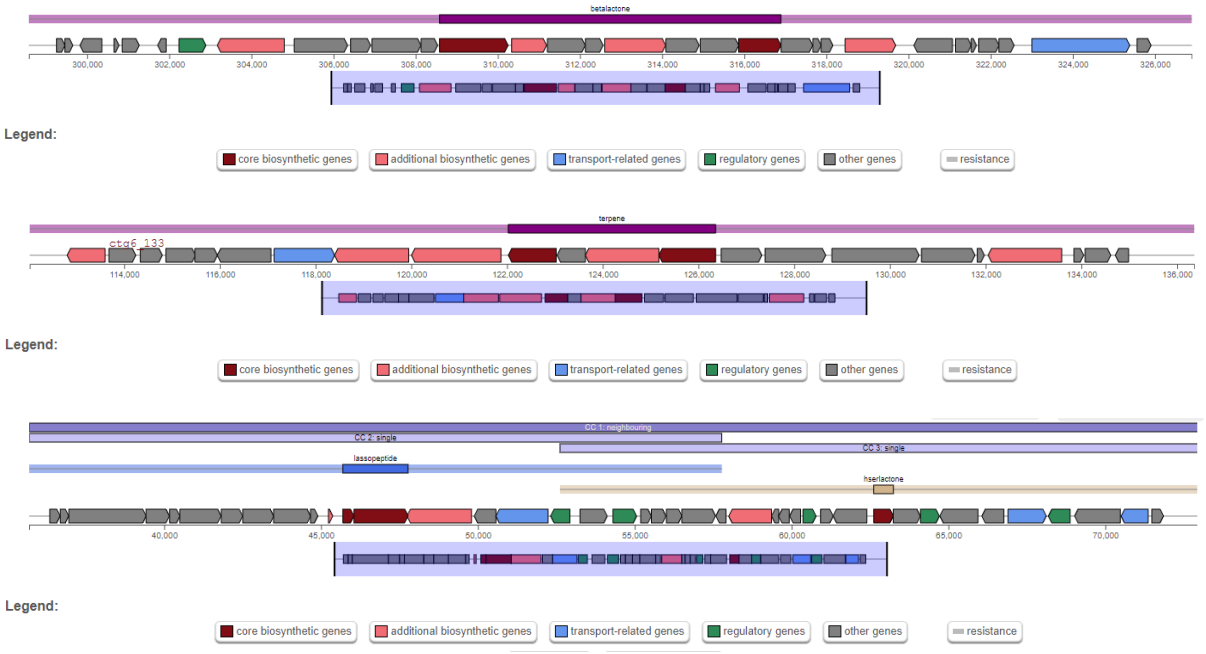


Figure S2. Predicted secondary metabolite gene clusters for strain NZ-96^{T} identified by analysis of the NZ-96^{T} genome sequence with the bioinformatic tool antiSMASH 5.0.

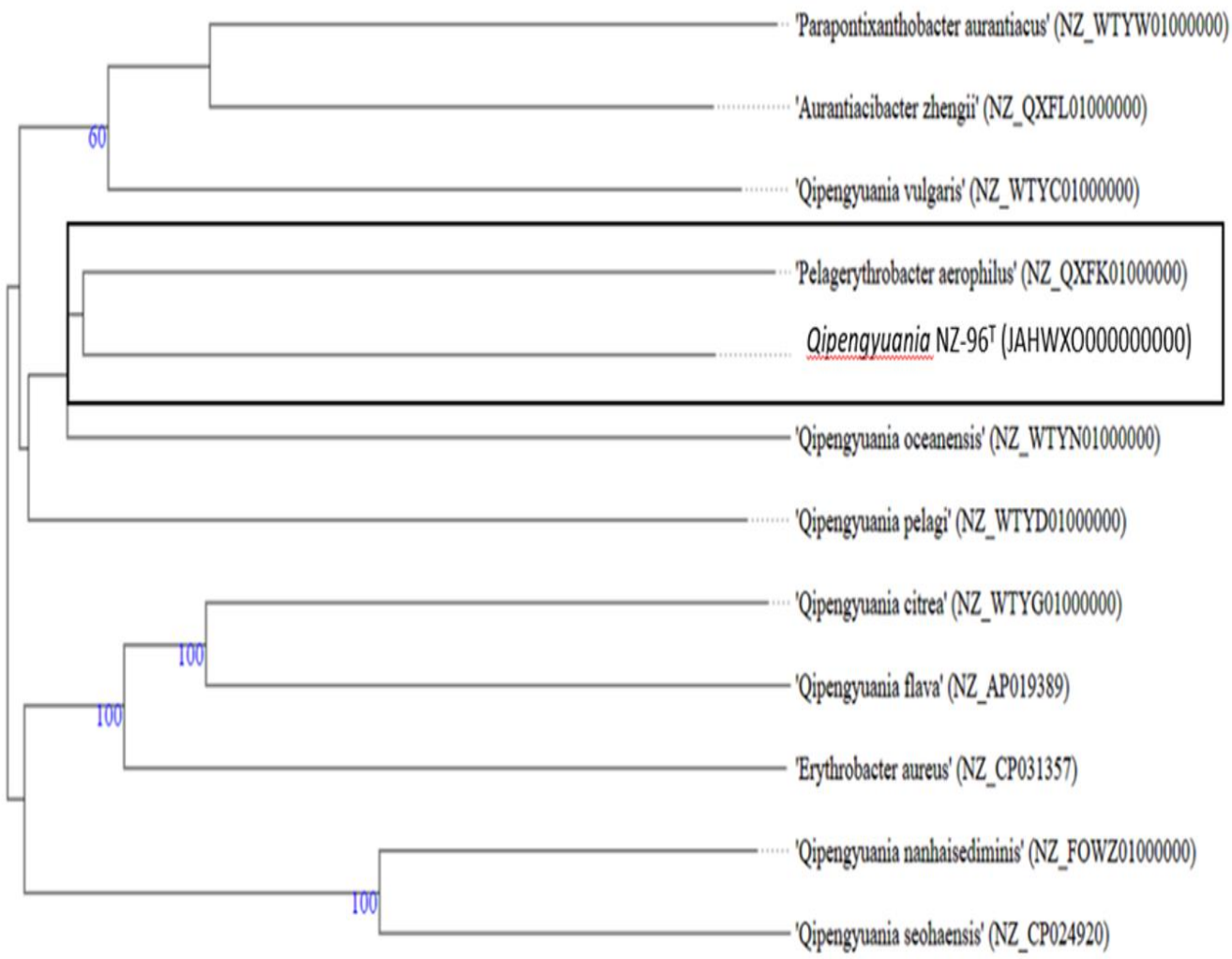


Figure S3. Tree inferred with FastME 2.1.6.1 from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d5. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 61.8 %.