

Table S1. Project information.

MIGS ID	PROPERTY	TERM
MIGS 31	Finishing quality	Improved-high-quality-draft
MIGS-28	Libraries used	Illumina paired-end library
MIGS 29	Sequencing platforms	Illumina MiSeq
MIGS 31.2	Fold coverage	114x
MIGS 30	Assemblers	CLC Genomics workbench v 7.5.1
MIGS 32	Gene calling method	RAST/PGAP
	Locus Tag	BLD48
	Genbank ID	MOLV000000000.1
	GenBank Date of Release	07-Nov-2016
	GOLD ID	NOT REGISTERED
	BIOPROJECT	PRJNA350615
MIGS 13	Source Material Identifier	
	Project relevance	Pharmaceutical

Table S2. Peaks list of FAMES from GC-MS analysis with relative abundance indicated.

<i>Peak #</i>	<i>Start RT</i>	<i>End RT</i>	<i>Area</i>	<i>%Area</i>
1	7.65	7.87	3.051.800.287	2.39
2	9.28	9.44	2.478.062.528	1.94
3	9.50	9.60	2.076.911.907	1.62
4	9.62	9.73	7.944.850.288	6.21
5	9.96	10.10	7.515.367.087	5.88
6	10.59	10.75	4.260.692.434	3.33
7	11.07	11.22	24.307.015.339	19.00
8	11.24	11.33	2.889.259.050	2.26
9	11.34	11.44	2.398.989.121	1.88
10	13.04	13.16	50.216.135.074	39.26
11	13.17	13.25	2.487.499.744	1.94
12	13.51	13.62	8.038.254.542	6.28
13	13.85	13.96	637.560.014	0.50
14	14.60	14.69	627.607.671	0.49
15	16.36	16.50	1.995.372.092	1.56
16	16.54	16.70	2.862.982.667	2.24
17	23.30	23.42	4.123.673.734	3.22

Table S3. Number of genes protein coding genes of *Exiguobacterium sp.* KRL4 associated with general COG functional categories.

CODE	VALUE	%AGE	DESCRIPTION
J	150	4.6	Translation, ribosomal structure and biogenesis
A	0	0	RNA processing and modification
K	162	5	Transcription
L	162	5	Replication, recombination and repair
B	0	0	Chromatin structure and dynamics
D	23	0.7	Cell cycle control, Cell division, chromosome partitioning
V	0	0	Defense mechanisms
T	127	3.7	Signal transduction mechanisms
M	120	3.9	Cell wall/membrane biogenesis
N	58	1.8	Cell motility
U	0	0	Intracellular trafficking and secretion
O	81	2.5	Posttranslational modification, protein turnover, chaperones
C	124	3.8	Energy production and conversion
G	162	5	Carbohydrate transport and metabolism
E	179	5.5	Amino acid transport and metabolism
F	71	2.2	Nucleotide transport and metabolism
H	78	2.4	Coenzyme transport and metabolism
I	84	2.6	Lipid transport and metabolism
P	117	3.6	Inorganic ion transport and metabolism
Q	26	0.8	Secondary metabolites biosynthesis, transport and catabolism
R	250	7.7	General function prediction only
S	165	5.1	Function unknown
-	1008	31.8	Not in COGs

The total is based on the total number of protein coding genes in the genome.

Table S4. List of genes identified in the terpenes and siderophore pathways.

GENE	PUTATIVE FUNCTION
CLUSTER 1: TERPENE	
CTG1_41	Class I SAM-dependent methyltransferase
CTG1_42	Phytoene desaturase
CTG1_43	Phytoene desaturase
CTG1_44	Phytoene synthase
CTG1_45	Phytoene desaturase
CTG1_46	Glycosyl transferase
CTG1_47	Glycerol acyltransferase
CTG1_52	enol-CoA hydratase
CTG1_54	alpha glycosidase
CLUSTER 2: TERPENE	
CTG1_1452	Phytoene synthase
CTG1_1453	alpha-beta hydrolases
CTG1_1455	diguanylate cyclase
CTG1_1460	N-acetyltransferase
CLUSTER 3: SIDEROPHORE	
CTG1_1637	iucA/iucC siderophore synthesis
CTG1_1638	iucA/iucC siderophore synthesis
CTG1_1639	acyl-CoA synthase
CTG1_1640	putative acyl carrier protein
CTG1_1643	glycerol dehydrogenase

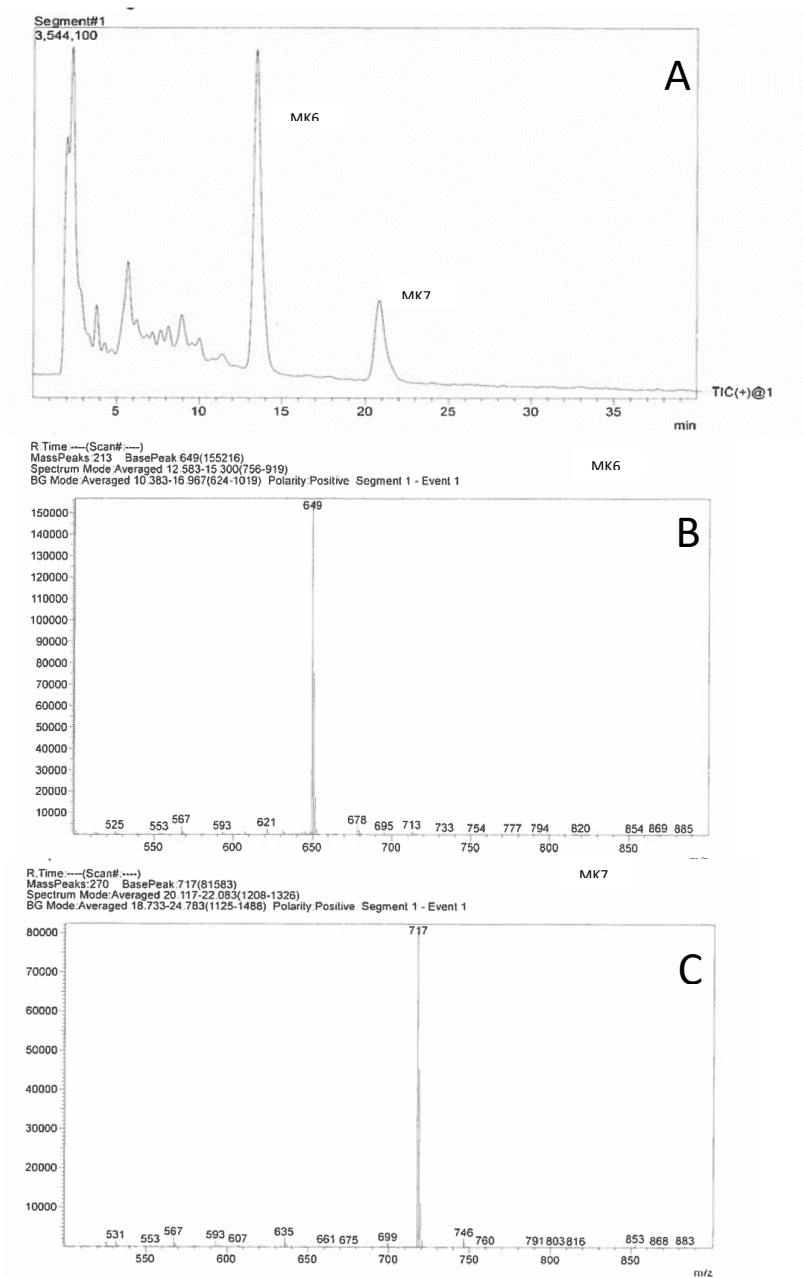


Figure S1. LC-MS analysis of quinones. A) Chromatogram of extracted quinones analysed on a reverse-phase RP-18 Lichrospher column eluted with n-hexane/ethylacetate (99:1, by vol.) with a flow rate of 1.0 mL min⁻¹. Identification by ESI/MS of quinone MK6 (B) and quinone MK7 (C).

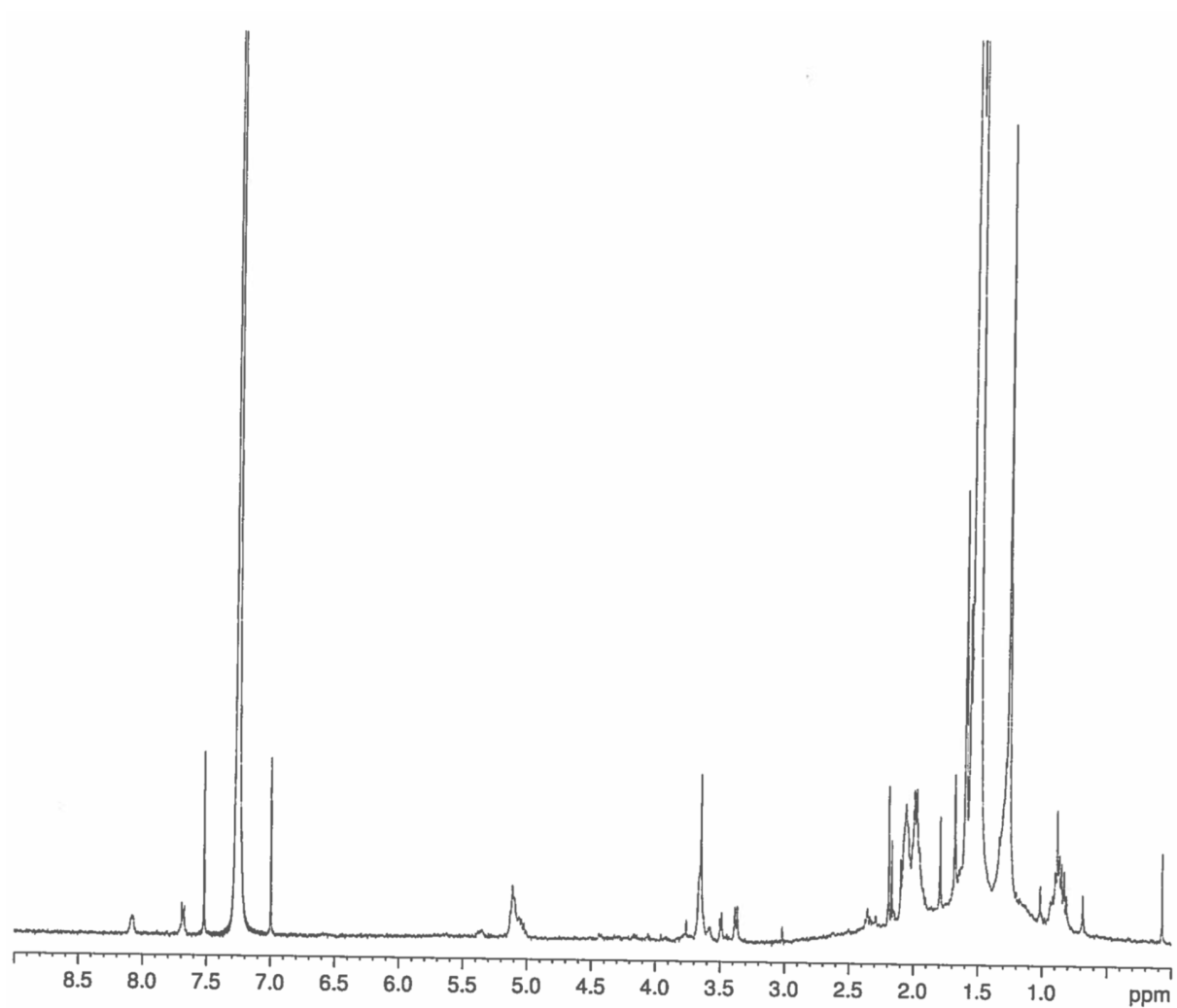


Figure S2. ^1H -NMR spectrum of extracted quinones.

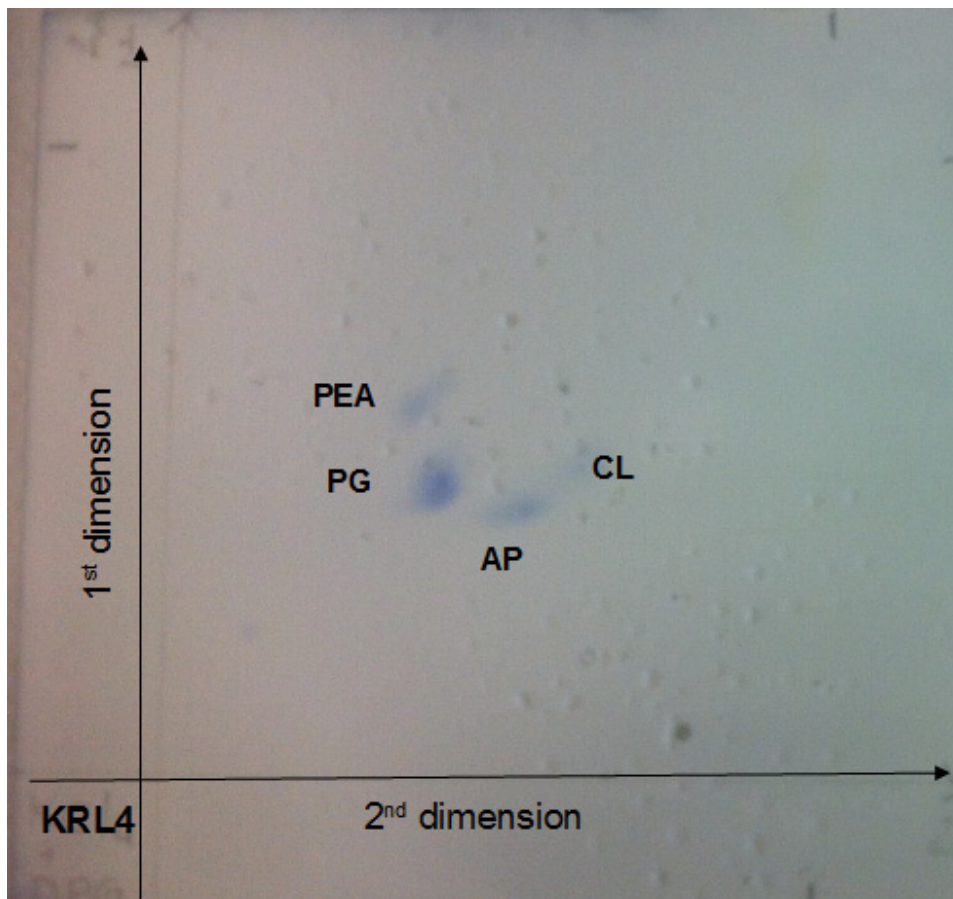


Figure S3. Bi-dimensional Thin Layer Chromatography (TLC) showing the phospholipids of strain KRL4. First dimension: $\text{CHCl}_3/\text{MeOH}/\text{H}_2\text{O}$ (65:25:4, by vol.); second dimension: $\text{CHCl}_3/\text{MeOH}/\text{Acetic acid}/\text{H}_2\text{O}$ (80:12:15:4, by vol.). Phospholipids were detected by spraying TLC with the Dittmer- Lester reagent. 1,2 diacylglycerol-3-phosphorylethanolamine (PEA), 1,2 dipalmitoyl-3-glycerol-phosphatidic acid (AP), 1-(3-sn-phosphatidyl)-sn-glycerol disodium salt (PG), 1,3-di(3-sn-phosphatidyl)-sn-glycerol disodium salt (cardiolipin, CL).

RT: 7.51 - 15.31

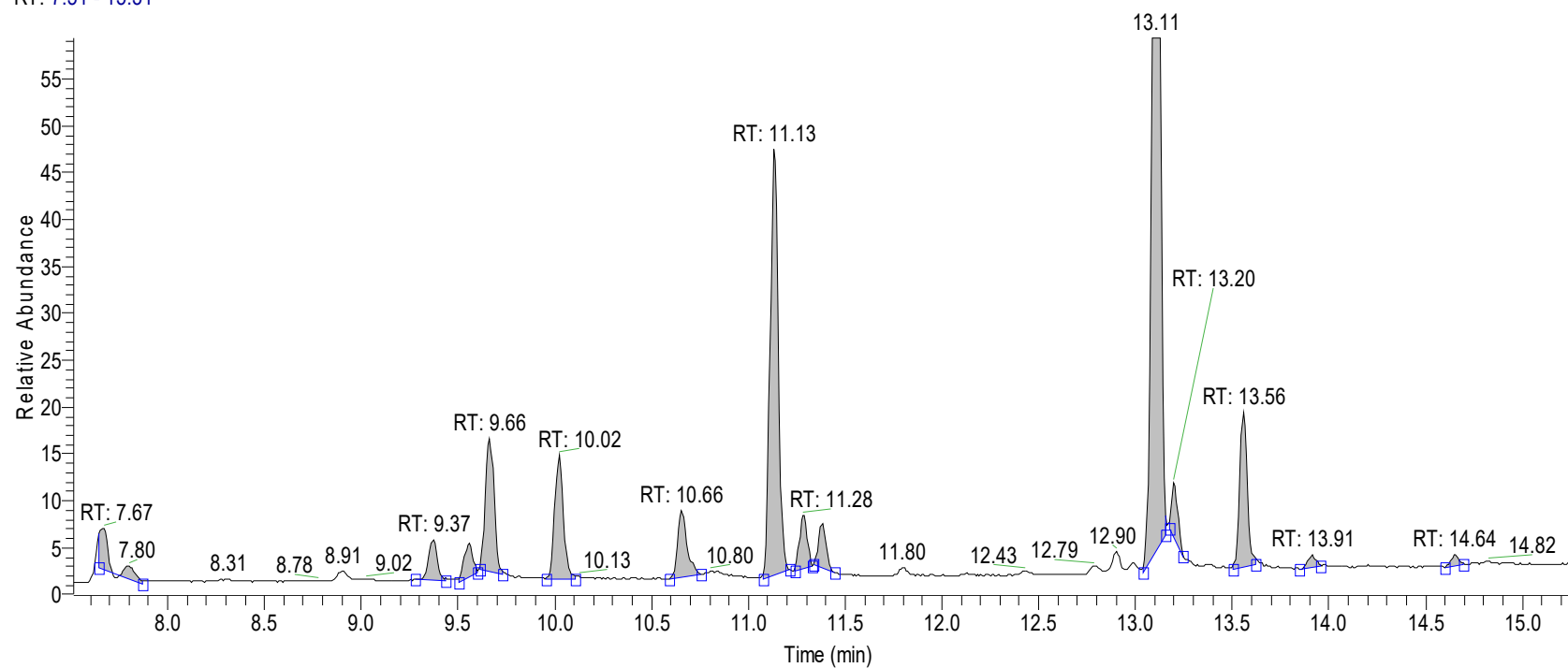


Figure S4. Total Ion Chromatogram of FAMES obtained by GC-MS analysis.

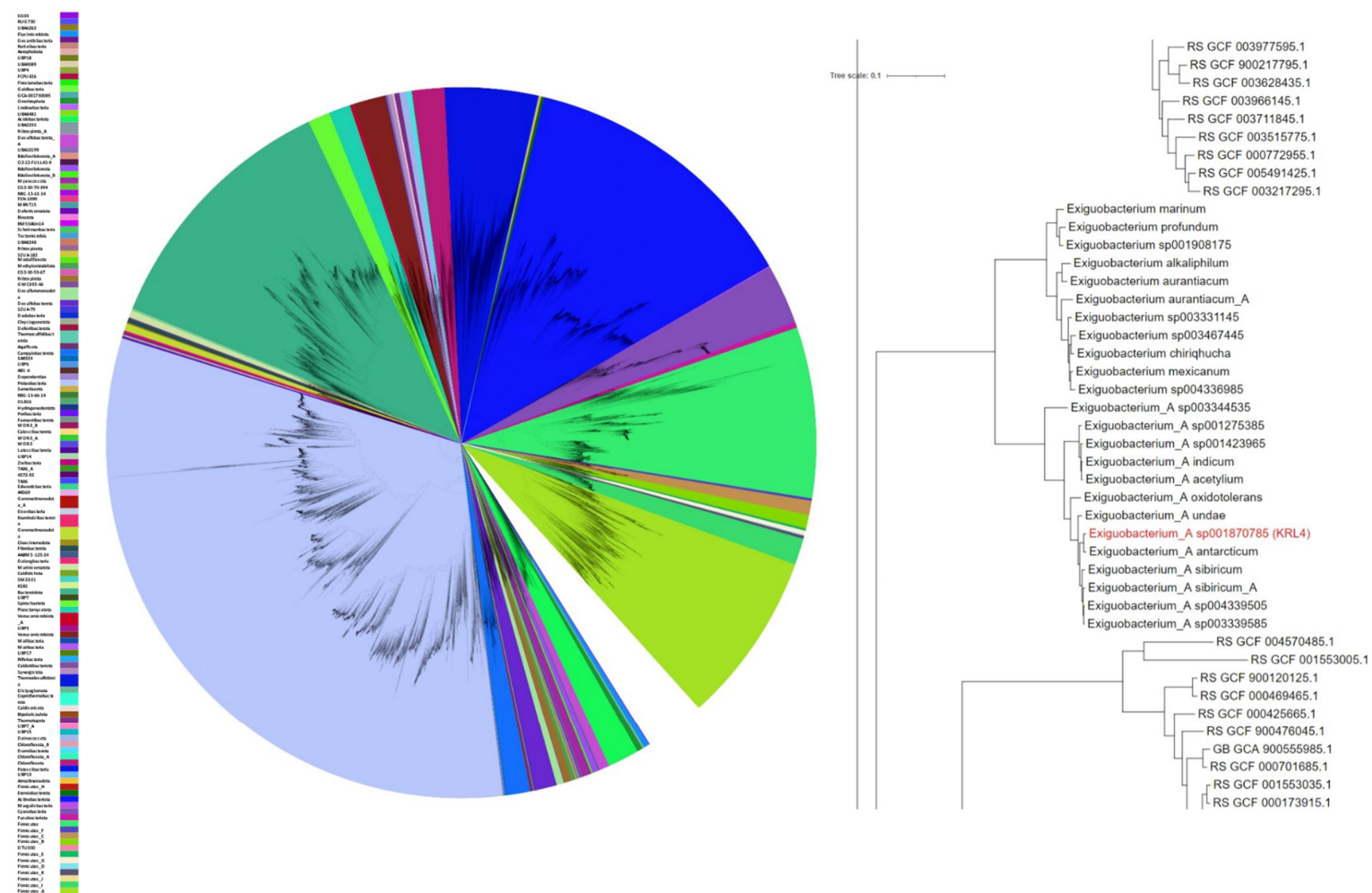


Figure S5. Whole genome-based classification of strain KRL4 according to the GTDB bacterial phylogeny