

Supplementary Materials

Description and genome analysis of *Luteimonas viscosa* sp. nov., a novel bacterium isolated from soil of a sunflower field

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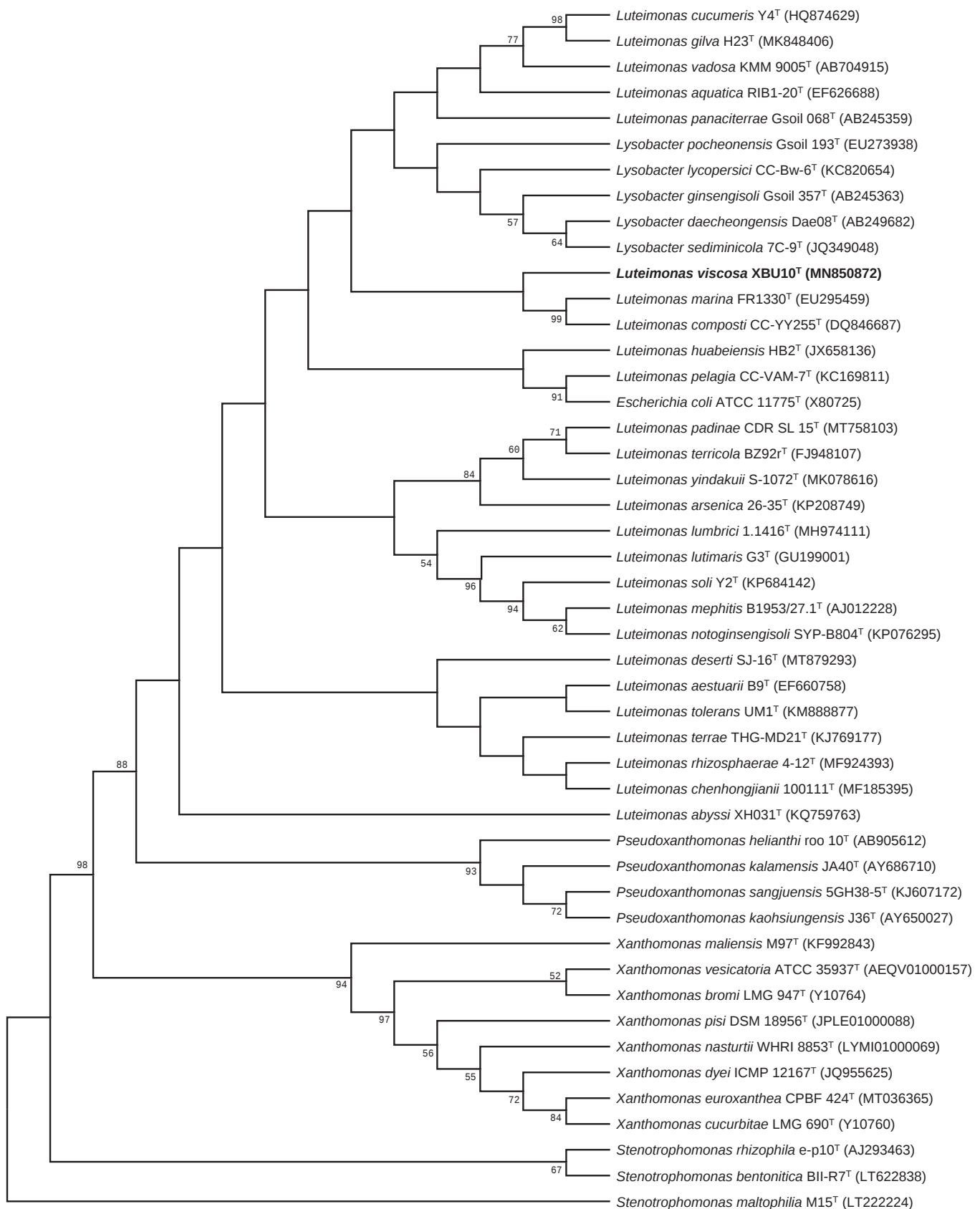
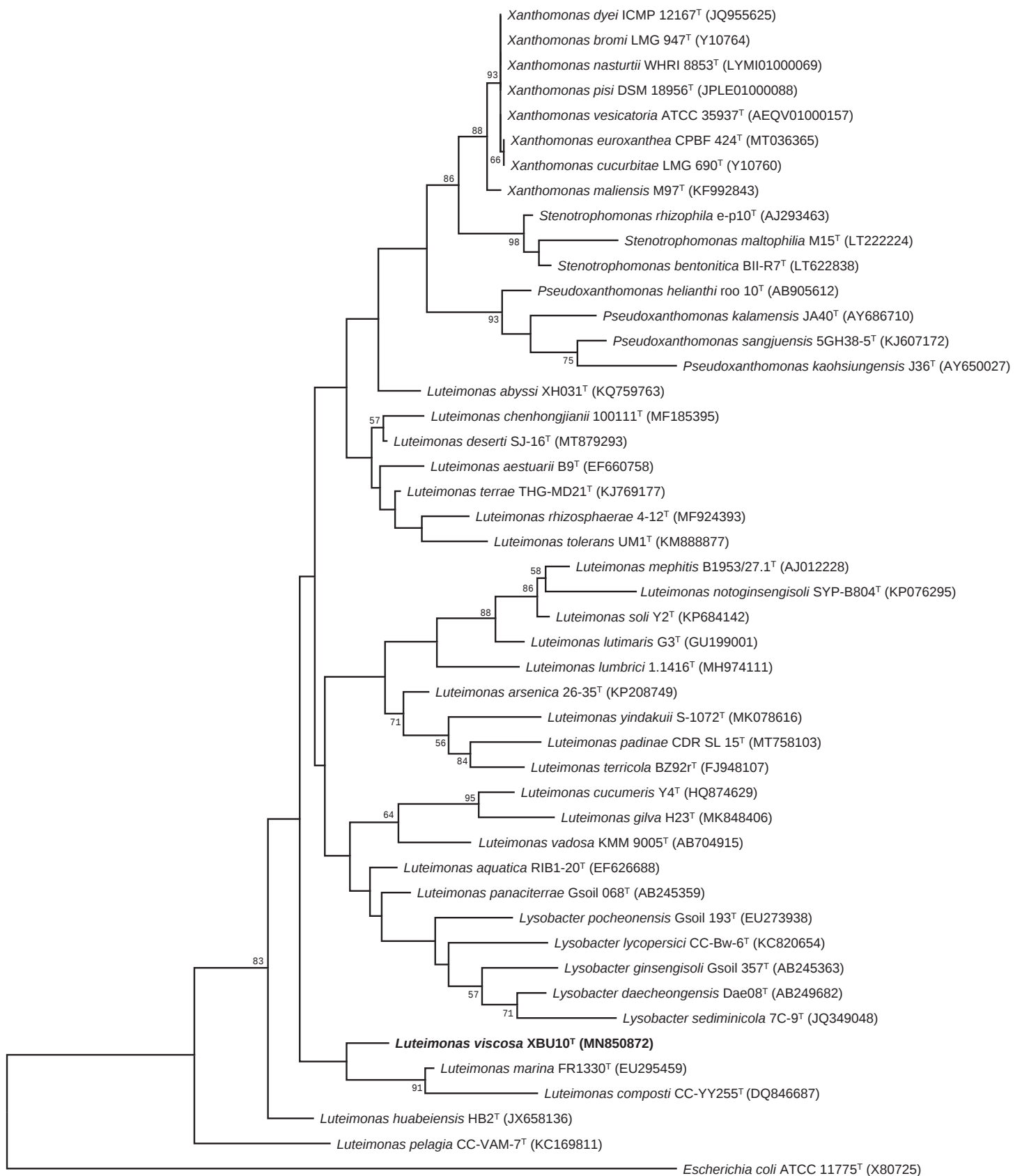


Fig. S1. The maximum-parsimony tree based on 16S rRNA gene sequences of strain XBU10^T and phylogenetically related type strains in the family *Lysobacteraceae*. Bootstrap values of above 50% based on 1000 replications are shown at branch nodes. GenBank accession numbers are given in parentheses. The sequence of *Escherichia coli* ATCC 11775^T is included as an outgroup.



0.01

Fig. S2. The maximum-likelihood tree based on 16S rRNA gene sequences of strain XBU10^T and phylogenetically related type strains in the family *Lysobacteraceae*. Bootstrap values of above 50% based on 1000 replications are shown at branch nodes. GenBank accession numbers are given in parentheses. The sequence of *Escherichia coli* ATCC 11775^T is included as an outgroup. Bar represents 0.01 substitutions per nucleotide position.

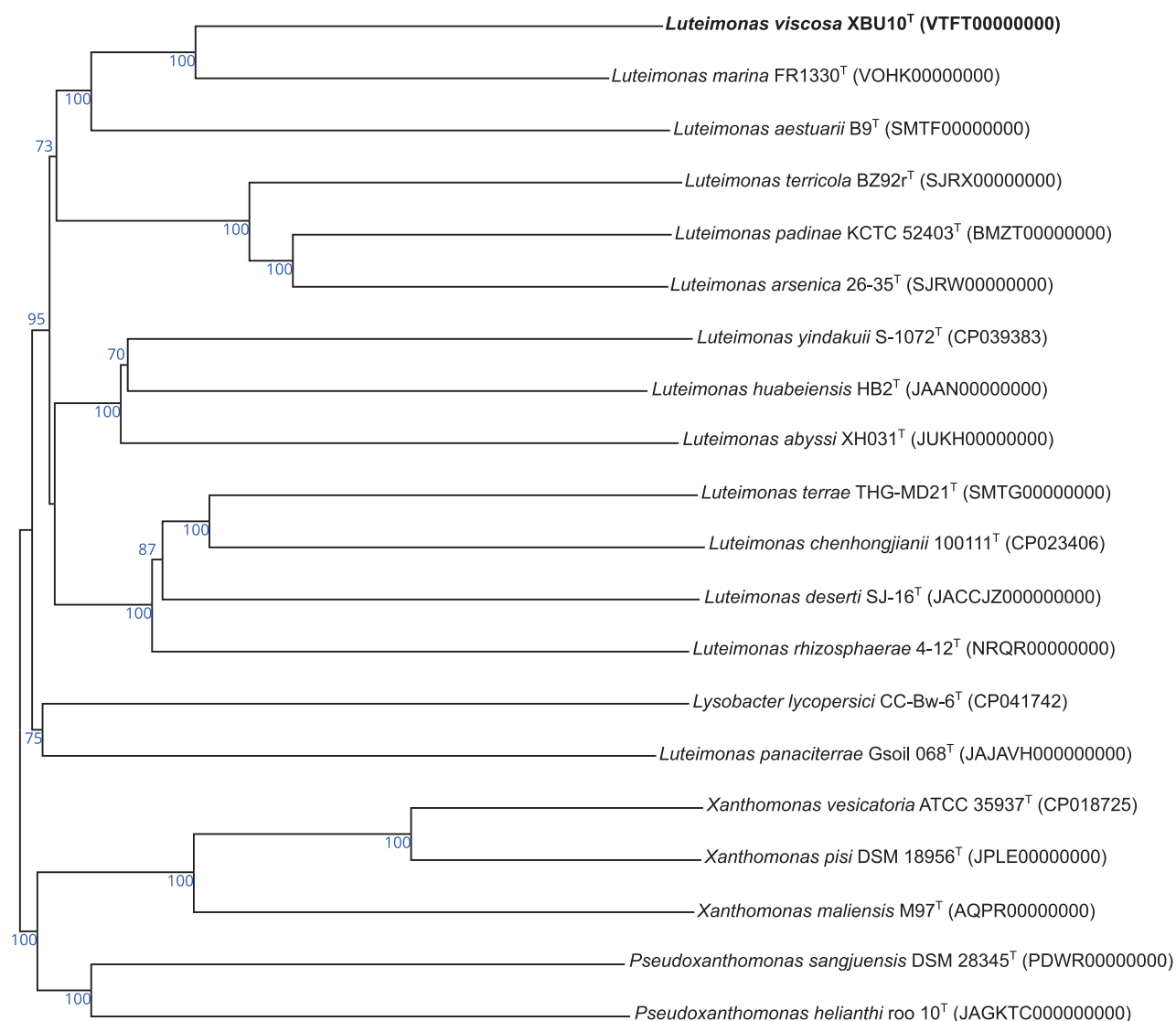


Fig. S3. Whole-genome sequence tree generated with TYGS for strain XBU10^T and phylogenetically related type strains in the family *Lysobacteraceae*. Tree inferred with FastME from GBDP distances calculated from genome sequences. Branch lengths are scaled in terms of GBDP distance formula d5. The numbers above branches are GBDP pseudo-bootstrap support values > 60% from 100 replications, with an average branch support of 91.2%.

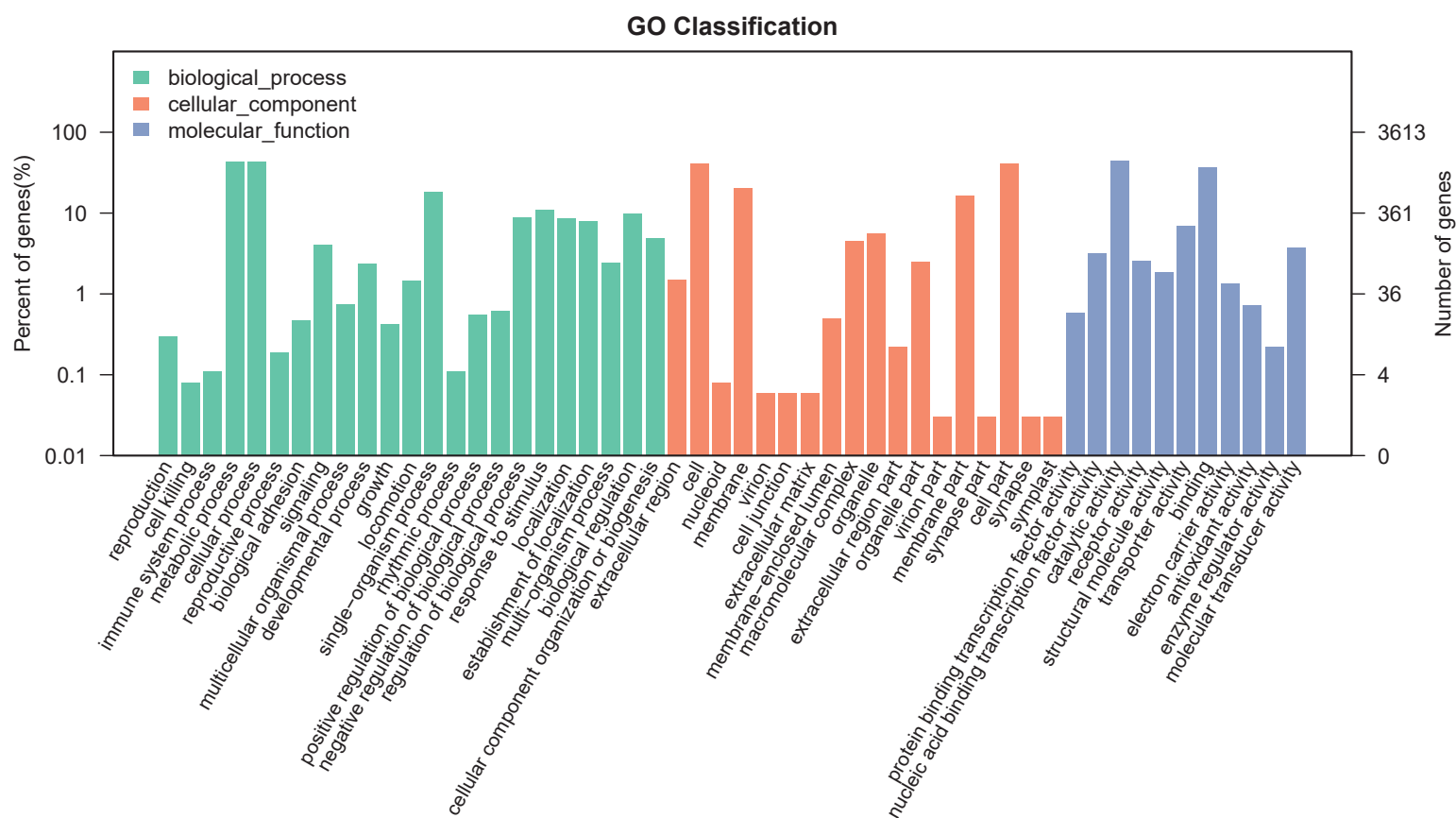


Fig. S4. Distribution of the predicted genes of strain XBU10^T to different GO functional categories

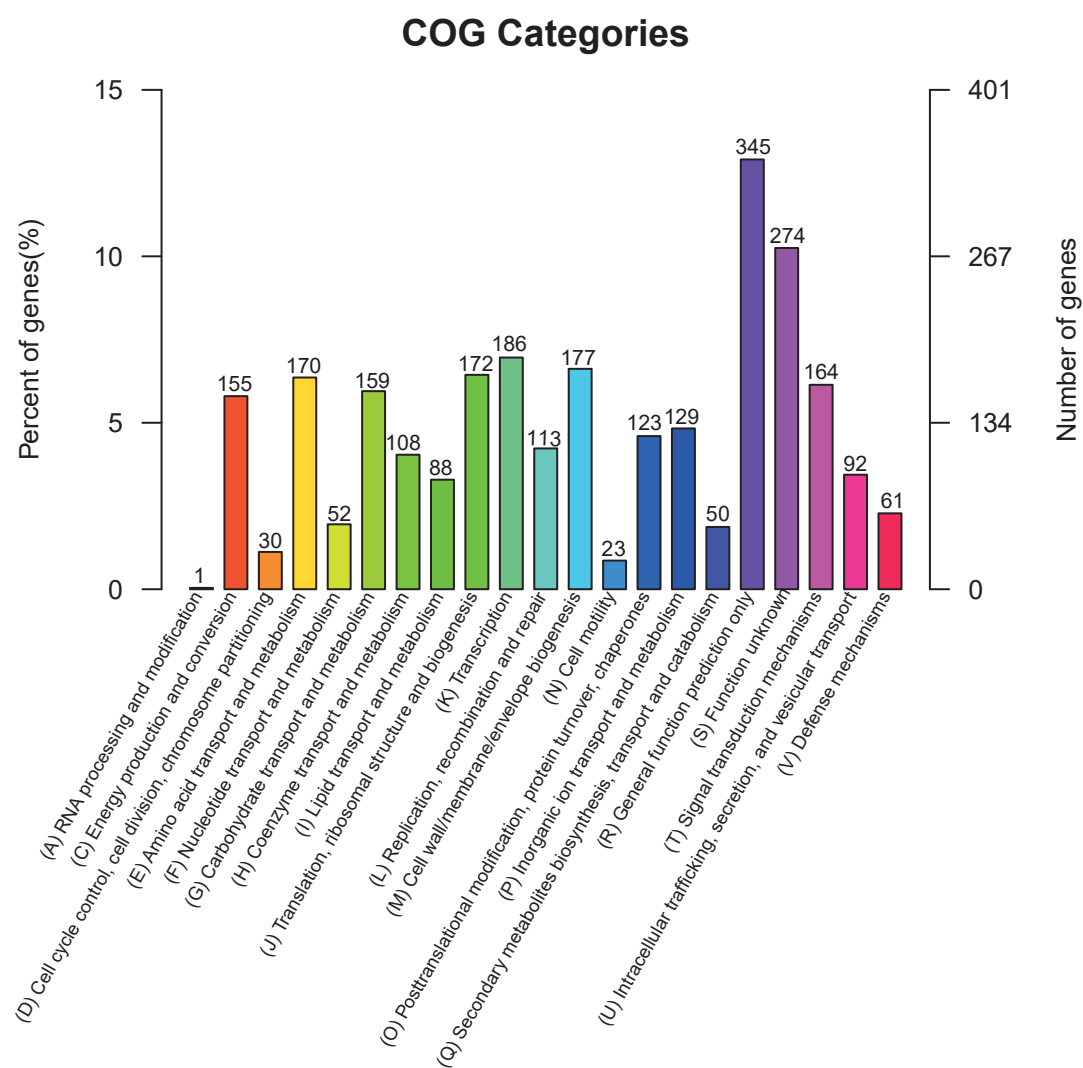


Fig. S5. Genes associated with general COG functional category prediction of strain XBU10^T

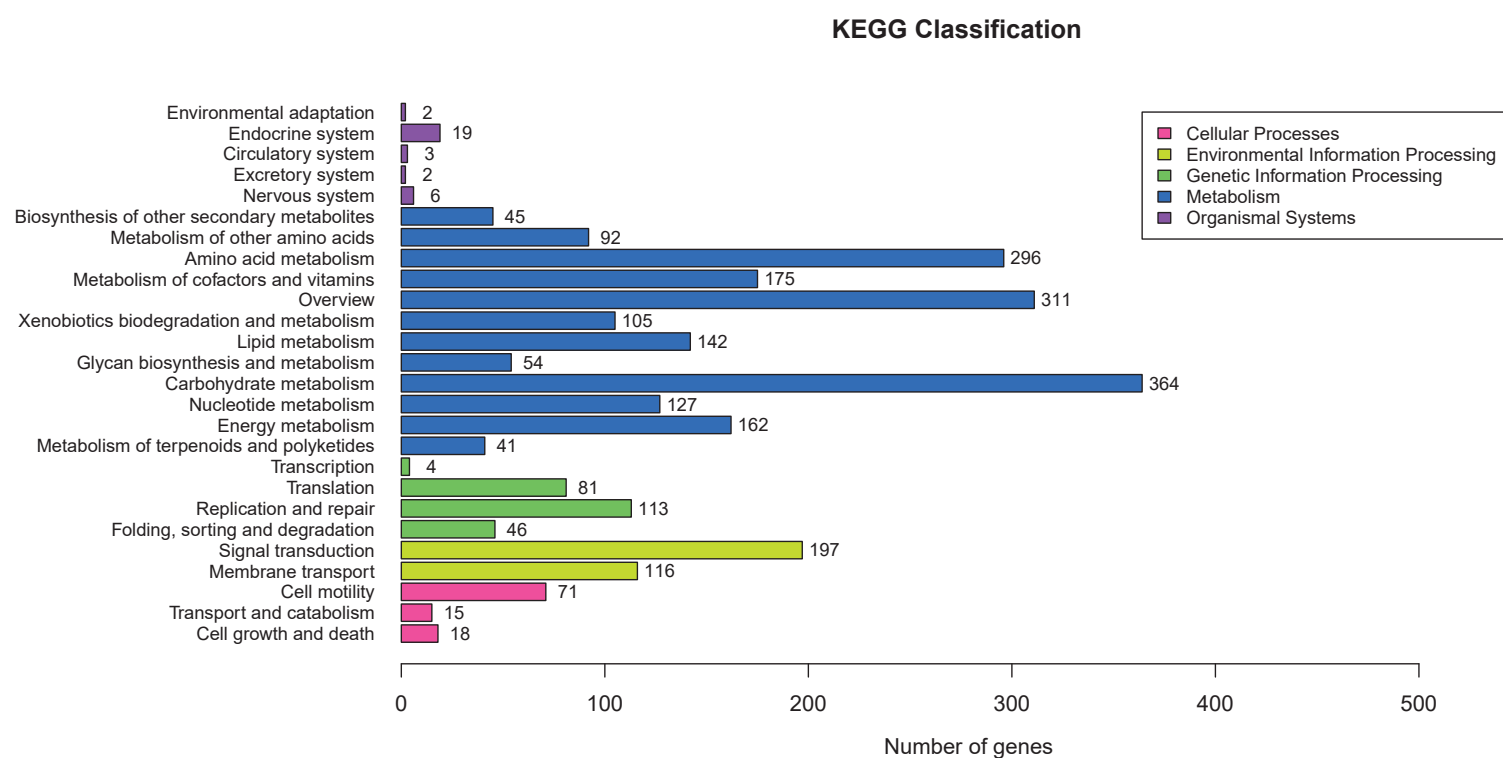


Fig. S6. Genes associated with general KEGG functional category prediction of strain XBU10^T

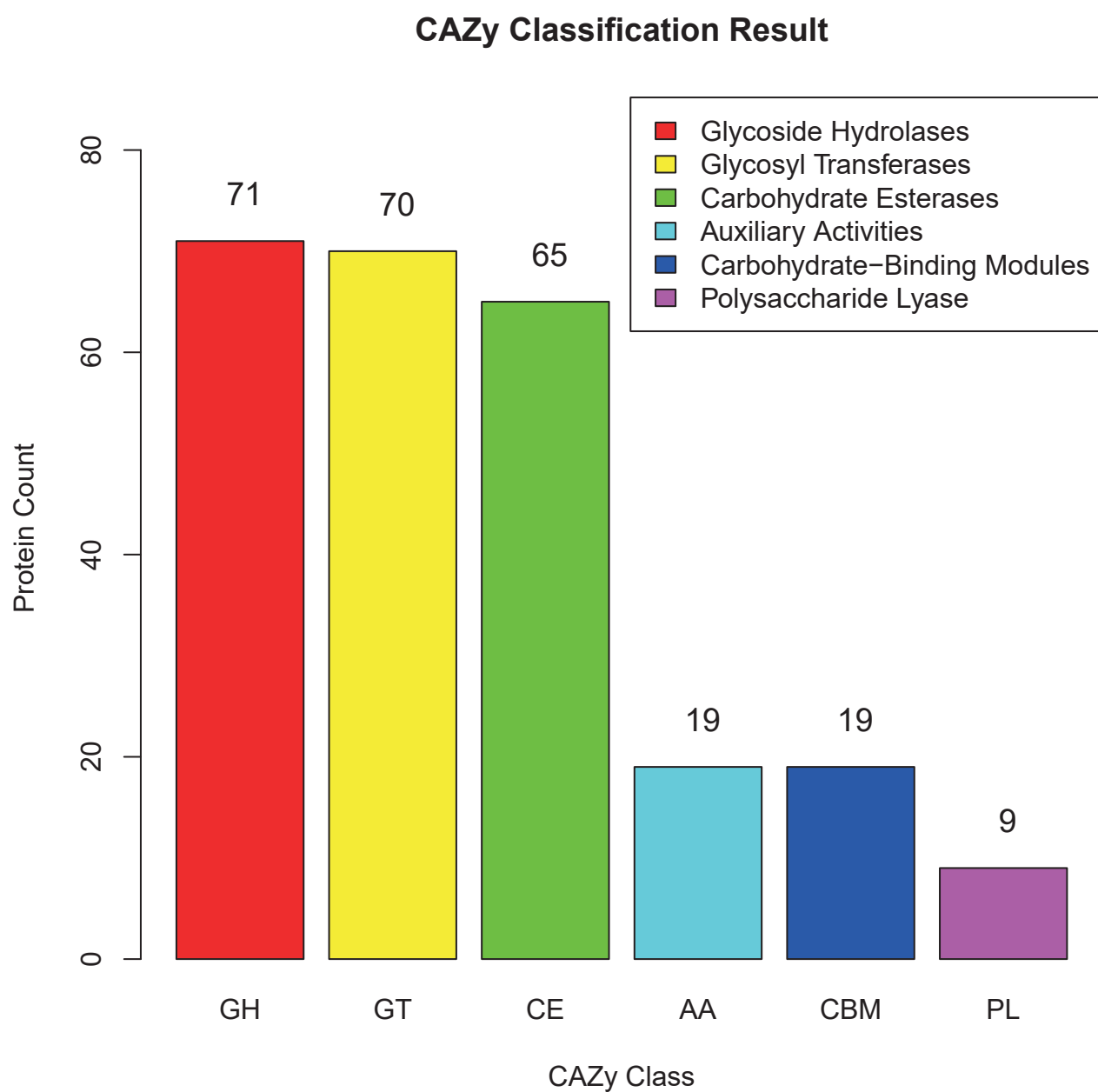


Fig. S7. Predicted gene modules for carbohydrate-active enzymes (CAZymes) families in the genome of strain XBU10^T

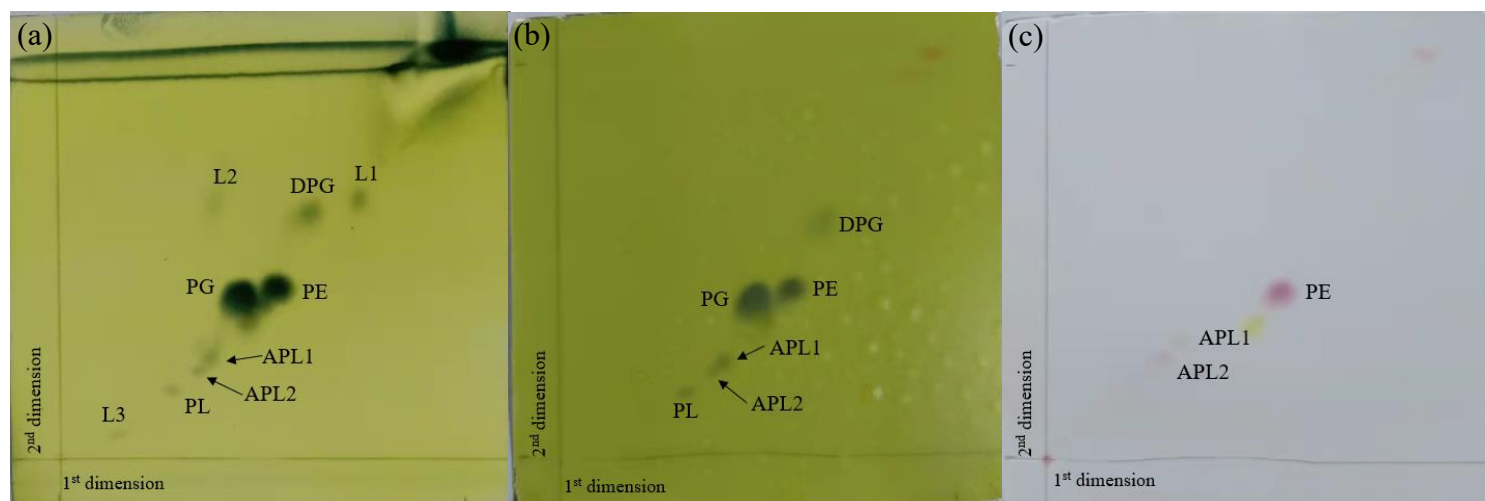


Fig. S8. Polar lipid profiles of strain XBU10^T after separation by two-dimensional TLC. Spots were revealed by spraying with (a) 10% ethanolic phosphomolybdic acid hydrate reagent, (b) molybdenum blue reagent and (c) 0.4% ninhydrin reagent on the plate, respectively. Abbreviations: PG, phosphatidylglycerol; DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PL, unidentified phospholipid; APL1–APL2, unidentified aminophospholipids; L1–L3, unidentified lipids.

Table S1. General features of the genome of strain XBU10^T.

Genome features	Value
Genome size (bp)	4169055
G+C content (%)	69.9
No. of contigs	9
Contig N50 (bp)	3026340
Scaffold N50 (bp)	3315587
No. of proteins	3579
Total genes	3681
CDSs (total)	3626
Protein-coding genes	3579
Genes (RNAs)	55
rRNAs (5S, 16S, 23S)	3 (1, 1, 1)
Complete rRNAs (5S, 16S, 23S)	3 (1, 1, 1)
tRNAs	47
ncRNA	5
Pseudo Genes (total)	47
Genome coverage	283×

Table S2. Average nucleotide identity (ANIm, ANIb and OrthoANIu), digital DNA-DNA hybridization (dDDH) and average amino acid identity (AAI) values (%) between strain XBU10^T (VTFT000000000) and related strains of the genus *Luteimonas*.

Strain	Accession number	ANIm (%)	ANIb (%)	OrthoANIu (%)	dDDH (%)	AAI (%)
<i>L. panaciterrae</i> Gsoil 068 ^T	JAJAVH010000000	84.7	76.2	76.6	21.4	67.1
<i>L. marina</i> FR1330 ^T	VOHK000000000	87.3	84.4	84.7	28.9	82.3
<i>L. huabeiensis</i> HB2 ^T	JAAN000000000	85.1	77.5	78.2	21.8	68.4
<i>L. abyssi</i> XH031 ^T	JUKH000000000	84.7	76.0	76.5	21.4	68.0
<i>L. aestuarii</i> B9 ^T	SMTF000000000	85.5	78.9	79.6	22.9	74.1
<i>L. terrae</i> THG-MD21 ^T	SMTG000000000	84.6	76.9	77.5	21.3	69.1
<i>L. arsenica</i> 26-35 ^T	SJRW000000000	85.0	77.8	78.4	21.9	69.7
<i>L. rhizosphaerae</i> 4-12 ^T	NRQR000000000	84.7	77.0	77.7	21.2	69.4
<i>L. chenhongjianii</i> 100111 ^T	CP023406	84.6	76.6	77.3	21.3	69.4
<i>L. yindakuii</i> S-1072 ^T	CP039383	84.8	76.7	77.2	21.2	69.2
<i>L. tolerans</i> UM1 ^T	FTLW000000000	84.0	72.4	73.1	20.3	64.2
<i>L. terricola</i> BZ92r ^T	SJRX000000000	84.8	77.3	78.0	21.5	69.4
<i>L. padinae</i> KCTC 52403 ^T	BMZT000000000	85.0	77.6	78.3	21.7	69.4
<i>L. mephitis</i> DSM 12574 ^T	AULN000000000	85.0	77.5	77.9	21.9	69.1
<i>L. lumbrici</i> 1.1416 ^T	SRZZ000000000	84.6	76.8	77.4	21.8	68.1
<i>L. gilva</i> H23 ^T	SZUA000000000	84.4	75.7	76.3	21.1	66.9
<i>L. cucumeris</i> CGMCC 1.10821 ^T	VLKN000000000	84.4	76.0	76.5	20.8	67.7
<i>L. deserti</i> SJ-16 ^T	JACCJZ000000000	84.8	76.4	77.2	21.1	68.7

Table S3. Cellular fatty acid compositions (%) of strain XBU10^T and closely related species

Strains: 1, Strain XBU10^T; 2, *Luteimonas panaciterrae* Gsoil 068^T; 3, *Luteimonas marina* FR1330^T; 4, *Luteimonas aquatica* RIB1-20^T; 5, *Luteimonas huabeiensis* HB2^T; 6, *Luteimonas composti* CC-YY255^T. Values are percentages of total fatty acids. All tests were carried out using similar methods. Bold face indicated the major fatty acids (> 10%); tr, trace amount, <1%; –, not detected.

Fatty acid (%)	1	2	3	4	5	6
Saturated straight-chain						
C _{14:0}	tr	tr	tr	tr	1.4	–
C _{16:0}	2.0	2.8	5.9	2.4	2.7	4.7
C _{18:0}	tr	tr	2.8	tr	–	–
Saturated branched						
iso-C _{11:0}	5.2	4.0	6.4	4.0	12.4	6.5
iso-C _{14:0}	tr	1.1	tr	tr	4.9	1.9
iso-C _{15:0}	21.0	25.2	26.2	25.3	38.7	26.2
anteiso-C _{15:0}	tr	4.9	4.5	6.2	tr	3.2
iso-C _{16:0}	10.3	14.9	1.7	4.4	9.7	13.8
iso-C _{17:0}	11.9	3.5	14.5	21.5	3.3	6.3
anteiso-C _{17:0}	tr	1.7	tr	1.9	–	–
Unsaturated						
iso-C _{17:1} <i>ω</i> 9 <i>c</i>	34.7	24.8	26.0	23.3	15.6	25.5
Hydroxy						
iso-C _{11:0} 3-OH	5.4	7.3	5.6	6.7	4.6	5.5
Cyclopropane acids						
C _{17:0} cyclo	–	tr	–	–	–	–
Summed feature*						
1	4.8	–	tr	tr	tr	–
2	–	4.5	3.4	2.0	4.0	–
3	4.3	4.8	2.2	1.7	–	5.7
4	tr	–	tr	tr	tr	–

*Summed features are fatty acids that cannot be resolved reliably from another fatty acid using the chromatographic conditions chosen. The MIDI system groups these fatty acids together as one feature with a single percentage of the total. Summed feature 1 comprised iso-C_{15:1} H and/or C_{13:0} 3-OH; summed feature 2 comprised C_{16:1} *ω*7*c* and/or iso-C_{15:0} 2-OH; summed feature 3 comprised C_{16:1} *ω*7*c* and/or C_{16:1} *ω*6*c*; summed feature 4 comprised iso-C_{17:1} I and/or anteiso-C_{17:1} B.