

16S

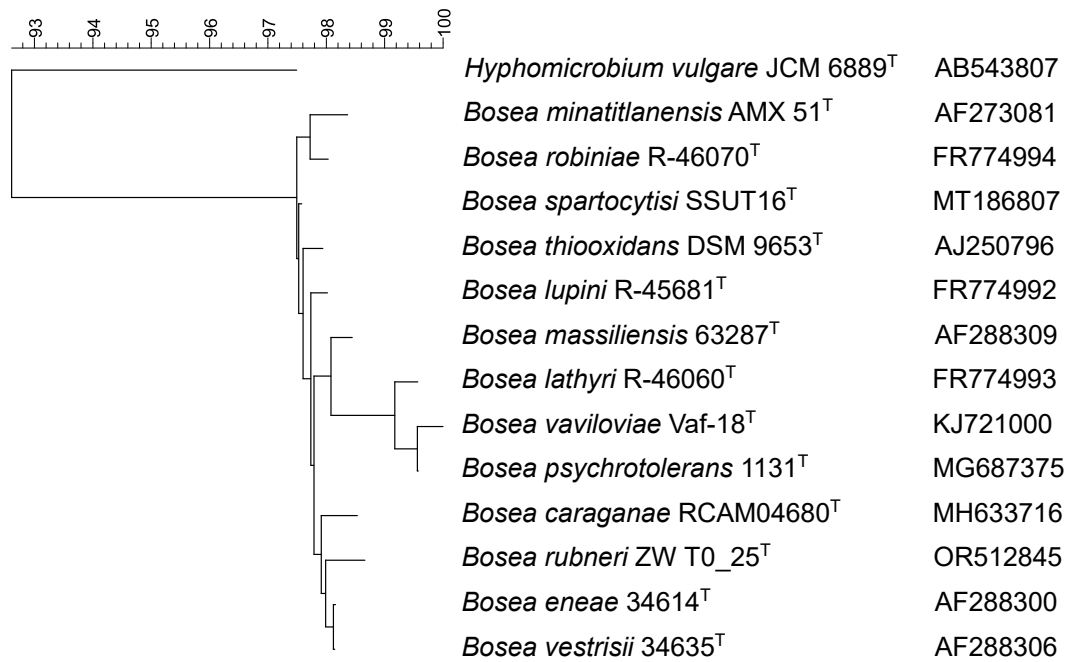


Fig. S1. Analysis of 16S rRNA gene sequences of strain ZW T0_25^T and all 12 type strains of *Bosea*. *Hyphomicrobium vulgare* JCM 6889^T was used as an outgroup. Clustering was performed using fast algorithm and neighbour joining (BioNumerics, version 8.1; Applied Maths).

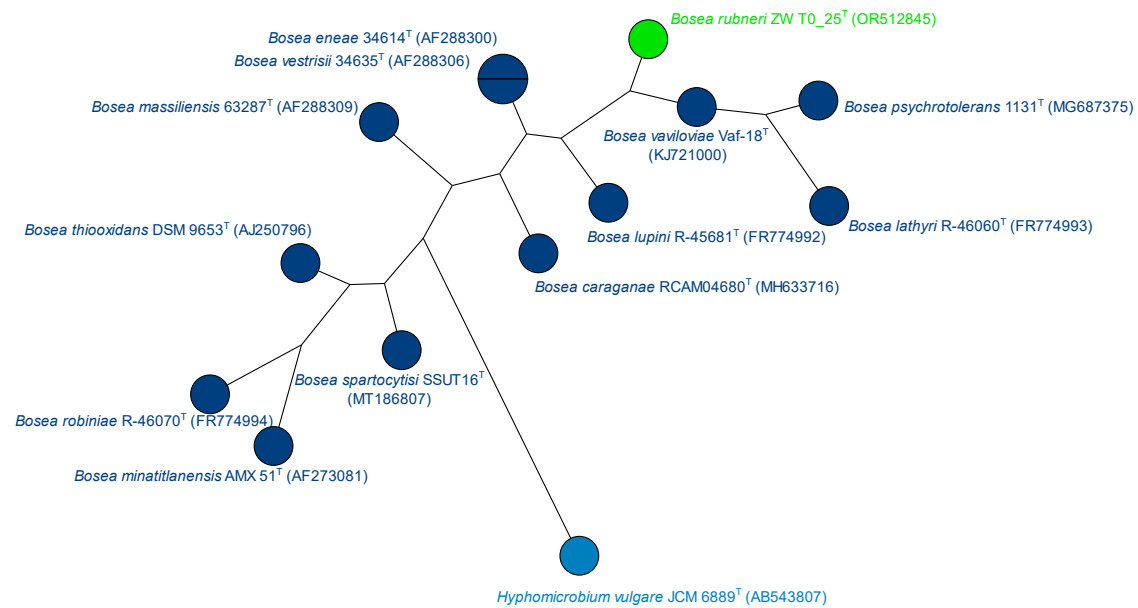


Fig. S2. Analysis of 16S rRNA gene sequences (length ca. 1500 bp) of strain ZW T0_25^T and all 12 type strains of *Bosea*. *Hyphomicrobium vulgare* JCM 6889^T was used as an outgroup. The tree was built using maximum parsimony (BioNumerics, version 8.1; Applied Maths). Square root scaling was used to display branch length.

Table S1. Pairwise nucleotide similarities of the 16S rRNA gene sequences of ZW T0_25^T versus type strains of the genus *Bosea.**

Strain: 1, *B. rubneri* sp. nov. ZW T0_25^T (OR512845); 2, *B. caraganae* RCAM04680^T (MH633716); 3, *B. eneeae* 34614^T (AF288300); 4, *B. lathyri* R-46060^T (FR774993); 5, *B. lupini* R-45681^T (FR774992); 6, *B. massiliensis* 63287^T (AF288309); 7, *B. minatitlanensis* AMX51^T (AF273081); 8, *B. psychrotolerans* 1131^T (MG687375); 9, *B. robiniae* R-46070^T (FR774994); 10, *B. spartocytisi* SSUT16^T (MT186807); 11, *B. thiooxidans* DSM 9653^T (AJ250796); 12, *B. vaviloviae* Vaf-18^T (KJ721000); 13, *B. vestrisii* 34635^T (AF288306)

Pairwise Nucleotide Similarity [%]*	1	2	3	4	5	6	7	8	9	10	11	12	13
1	100	98.68	99.15	98.77	99.05	98.49	97.45	99.34	98.02	98.75	98.58	99.62	99.15
2	-	100	99.07	98.93	98.86	98.85	98.07	98.74	98.21	98.76	98.43	98.64	99.07
3	-	-	100	98.25	99.58	98.88	97.99	98.39	98.81	99.20	99.03	98.43	99.93
4	-	-	-	100	98.12	98.23	97.57	99.12	97.71	97.96	97.78	98.86	98.18
5	-	-	-	-	100	99.01	98.54	98.32	99.03	99.56	99.45	98.36	99.58
6	-	-	-	-	-	100	98.32	98.32	98.44	98.90	98.67	98.35	98.88
7	-	-	-	-	-	-	100	97.51	99.03	98.98	98.84	97.43	98.07
8	-	-	-	-	-	-	-	100	97.80	98.18	97.95	99.56	98.39
9	-	-	-	-	-	-	-	-	100	99.42	98.96	97.72	98.81
10	-	-	-	-	-	-	-	-	-	100	99.49	98.47	99.27
11	-	-	-	-	-	-	-	-	-	-	100	97.93	99.03
12	-	-	-	-	-	-	-	-	-	-	-	100	98.43
13	-	-	-	-	-	-	-	-	-	-	-	-	100

Values were obtained using EZBioCloud [27].

*Pairwise nucleotide similarities above the threshold value of 98.7% [39] are coloured in grey.

Table S2. Phenotypes predicted by TraitAr (<https://galaxy.bifo.helmholtz-hzi.de/>) for strain ZW T0_25^T and of other nine type strains of the genus *Bosea*, for which genome sequences were available. 0, no predictor positive; 1, one predictor positive and labelled in light blue; 2, two predictors positive and labelled in dark blue.

Category	Phenotype	<i>Bosea rubneri</i> sp. nov. ZW T0_25 ^T	<i>B. thiooxidans</i> DSM 9653 ^T	<i>B. robiniae</i> DSM 26672 ^T	<i>B. minatitlanensis</i> LMG 26207 ^T	<i>B. lupini</i> DSM 26673 ^T	<i>B. caraganae</i> RCAM04680 ^T	<i>B. spartocytisi</i> SSUT 16 ^T	<i>B. lathyri</i> DSM 26656 ^T	<i>B. vaviloviae</i> VAF_18 ^T	<i>B. psychrotolerans</i> 1131 ^T
enzyme	Pyrrolidonyl–naphthylamide	0	0	0	0	0	1	1	2	0	0
enzyme	Beta-hemolysis	0	0	0	0	0	0	0	0	0	0
enzyme	Nitrite to gas	0	0	0	0	0	0	0	0	0	0
enzyme	Coagulase production	1	1	1	1	0	1	0	1	0	0
enzyme	Nitrate-to-nitrite conversion	2	2	1	1	2	2	1	2	2	2
enzyme	Alkaline phosphatase	2	2	2	2	2	2	2	2	2	2
enzyme	Lipase	2	2	2	2	1	2	2	2	2	2
growth	Growth at 42°C	0	0	0	1	0	0	0	0	0	1
growth	DNase	0	0	0	0	0	0	0	0	0	0
growth	Growth in 6.5% NaCl	0	0	0	0	0	0	0	0	0	0
growth	Mucate utilization	1	1	1	1	1	1	1	1	1	1
growth	Growth on MacConkey agar	1	2	1	2	1	2	2	1	1	1
growth	Bile susceptible	2	2	2	2	2	2	2	2	2	2
growth	Growth in KCN	2	2	2	2	2	2	2	2	2	2
growth	Colistin-polymyxin susceptible	2	2	2	2	2	2	2	2	2	2
growth	Growth on ordinary blood agar	2	2	2	2	2	2	2	2	2	2
growth amino acid	Indole	0	0	0	0	0	0	0	0	0	0
growth amino acid	Ornithine decarboxylase	0	0	0	0	0	0	0	0	0	0
growth amino acid	Lysine decarboxylase	0	0	0	0	0	0	0	0	0	0
growth amino acid	Arginine dihydrolase	2	0	0	2	0	0	0	2	0	2
growth carboxylic acid	Citrate	0	0	0	0	0	0	0	0	0	0
growth carboxylic acid	Tartrate utilization	0	0	0	1	1	1	1	1	1	1
growth carboxylic acid	acetate utilization	2	1	1	0	2	1	1	2	0	2

morphology	Coccus—pairs or chains predominate	0	0	0	0	0	0	0	0	0	0
morphology	Bacillus or coccobacillus	2	2	2	2	2	2	2	2	2	2
morphology	Gram negative	2	2	2	2	2	2	2	2	2	2
morphology	Motile	2	2	2	2	2	2	2	2	2	2
oxygen	Anaerobe	0	0	0	0	0	0	0	0	0	0
oxygen	Facultative	0	0	0	0	0	0	0	0	0	0
oxygen	Capnophilic	0	1	1	1	1	1	1	1	0	1
oxygen	aerobe	2	2	2	1	2	2	2	2	2	2
oxygen enzyme	Oxidase	2	2	2	2	2	2	0	0	0	2
oxygen enzyme	Catalase	2	2	2	2	2	2	2	2	2	2
product	Hydrogen sulfide	0	0	0	0	0	0	0	0	0	0
proteolysis	Gelatin hydrolysis	0	0	0	0	0	0	0	0	0	0
proteolysis	Casein hydrolysis	0	0	0	0	1	2	1	1	2	2

DSMZ Identification Services polar lipid report



PE = Phosphatidylethanolamine
PG = Phosphatidylglycerol

APL = Aminophospholipid
AL = Aminolipid
GL = Glycolipid
PL = Phospholipid

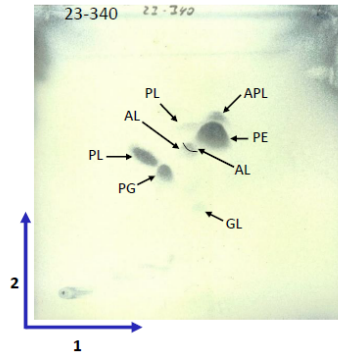


Fig. S3. Polar lipid report as provided by DSMZ Identification Services for strain ZW T0_25^T.

Table S3. Fatty acid composition of *B. rubneri* sp. nov. ZW T0_25^T.

Fatty acids*	Percent
C _{14:0}	0.2
C _{14:0} DMA	0.1
C _{15:0}	0.3
C _{16:0}	7.1
C _{16:0} 3OH	3.5
C _{16:1} w5c	2.7
C _{16:1} w7c	19.5
C _{17:0}	0.4
C _{17:1} w6c	0.2
C _{17:1} w8c	0.6
C _{18:0}	0.3
C _{18:1} w7c	63.3
C _{18:1} w7c 11-methyl	1.4
C _{18:1} w9c	0.5

* Analyses were carried out by the Identification Service of the DSMZ (German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany).