

Supplementary data

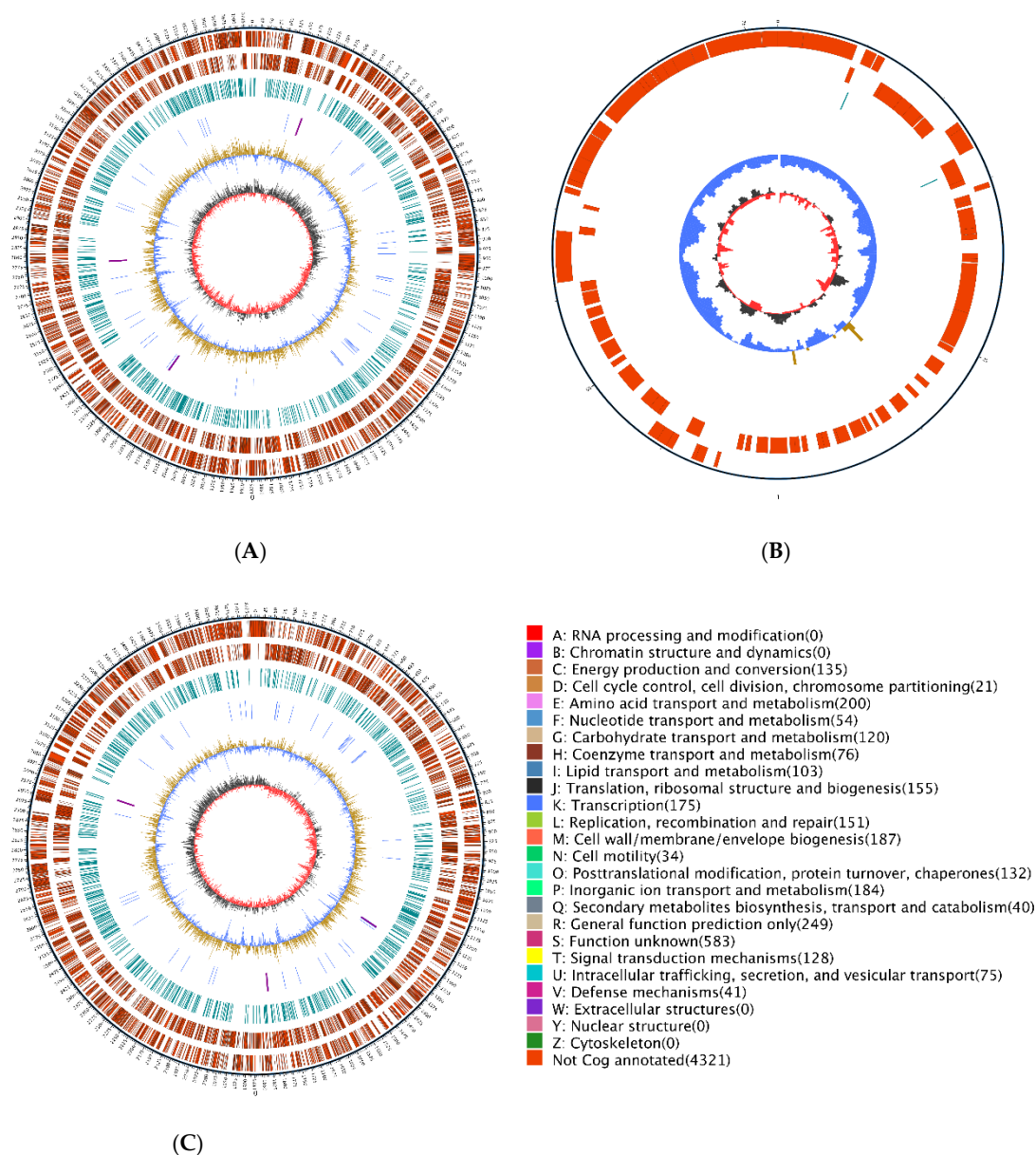
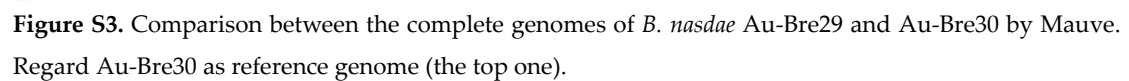
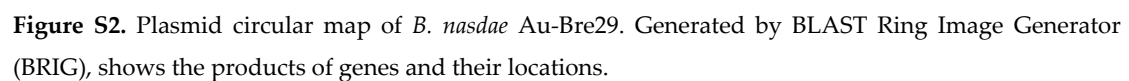


Figure S1. Circular map of the complete genome of *B. nasdae* Au-Bre29 and Au-Bre30. (A) Chromosome of Au-Bre29, (B) Plasmid of Au-Bre29 and (C) Chromosome of Au-Bre30. Circles from the outwards to inwards, ring 1: genome size (Kb); ring 2 and 3: genes existing on the Forward strand and Reverse strand, with different color indicate genes with different COG function; ring 4: repetitive sequence; ring 5: tRNA(blue) and rRNA(purple); ring 6: GC-content, with blue indicating the region with GC-content higher than average, light yellow indicate the region with GC-content lower than average; ring 7: GC-skew.

Table S1. General genomic feature of *B. nasdae* Au-Bre29 and Au-Bre30

Genomic contents	<i>B. nasdae</i> Au-Bre29	<i>B. nasdae</i> Au-Bre30
Bio Project Number	PRJNA744386	PRJNA744387
NCBI Accession	NZ_CP080034.1 NZ_CP080035.1	NZ_CP080036.1
Chromosome	1 (3.747438 Mb)	1 (3.746705 Mb)
Plasmid	1 (0.076784 Mb)	0
G+C content (%)	65.69%	65.8%
Genome size (Mp)	3.8251164	3.746705
Total CDS	3665	3577
Total tRNAs	53	53
Total Genes	3731	3643
Protein coding genes	3618	3531
Genes with function prediction	3531	3474
Genes assigned to KEGGs	1772	1751
Genes with signal peptides	531	523
Genes assigned to VFDB (Virulence)	670	668
Clustered gene	8	9
Gene encoding transport protein	888	882
Gene encoding secreted protein	531	523
Genes assigned to CARD (Antibiotic)	8	6
Genes assigned to TCDB (Transport	888	875

Genes assigned to CAZy (EPS)	139	138
CRISPR	3	2
GIs	9	9
Prophage	5	4
Phage	3(1/3 intact)	3(1/3 intact)



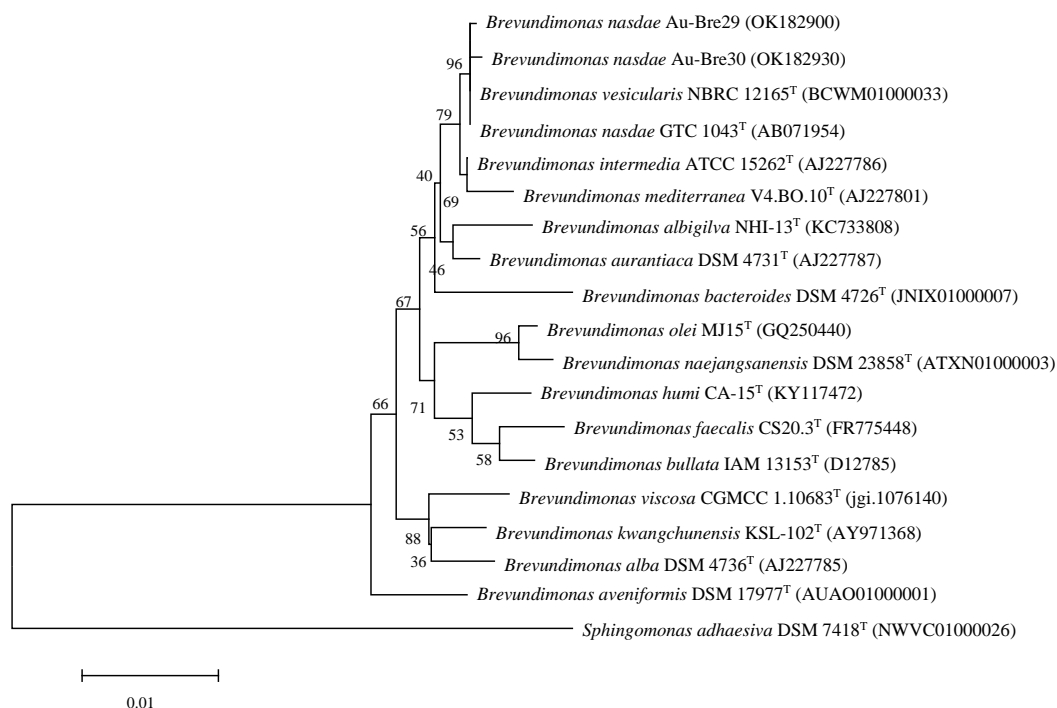


Figure S4. Neighbor-joining phylogenetic tree constructed based on the 16S rRNA gene sequences. Showing the phylogenetic relationships between strains *Brevundimonas nasdae* Au-Bre29 and Au-Bre30 and other species in the genus *Brevundimonas*. Values indicate percentages of identical branching in 1000 bootstrap replications. The sequence of *Sphingomonas adhaesiva* DSM 7418^T was used as an out-group. Bar, 0.01 substitutions per nucleotide position.