Table S3. Sequence similarity values of the complete 16S rRNA gene sequence (1,552 bp) of strain CCUG 66741^{T} with type strains, using the 'Identify' engine of EzBioCloud and ANIb and *in silico* DNA-DNA hybridization (DDH) values between the genome sequence of strain CCUG 66741^{T} and the genome sequences of the type strains showing 16S rRNA gene sequence similarity values $\geq$ 98.7% (shaded in green). Species with 16S rRNA gene sequence similarity $<$ 98.7% are shaded in red.

Type strain	**16S rRNA gene sequence similarity (%)**	***In silico* DDH (%)**	**ANIb (%)**	**GenBank accession number**
Leclercia adecarboxylata NBRC 102595^{T}	98.8	22.2	78.31	JMPM00000000
Enterobacter ludwigii EN-119^{T}	98.8	22.0	78.20	CP017279
Enterobacter roggenkampii EN-117^{T}	98.8	22.5	78.66	CP017184
Pantoea rodasii LMG 26273^{T}	98.8	19.8	72.57	PIQI00000000
Buttiauxella izardii DSM 9397^{T}	98.7	20.5	75.61	QZWH00000000
Citrobacter freundii DSM 30039^{T}	98.6	n/a	n/a	n/a
Buttiauxella agrestis ATCC 33320^{T}	98.6	n/a	n/a	n/a
Enterobacter cancerogenus ATCC 33241^{T}	98.6	n/a	n/a	n/a
Buttiauxella noackiae ATCC 51607^{T}	98.6	n/a	n/a	n/a
Buttiauxella ferragutiae ATCC 51602^{T}	98.6	n/a	n/a	n/a
Buttiauxella gaviniae ATCC 51604^{T}	98.6	n/a	n/a	n/a
Klebsiella aerogenes KCTC 2190^{T}	98.6	n/a	n/a	n/a
Enterobacter asburiae JCM 6051^{T}	98.6	n/a	n/a	n/a
Lelliottia amnigena NBRC 105700^{T}	98.6	n/a	n/a	n/a
Enterobacter chuandaensis 090028	98.6	n/a	n/a	n/a
Enterobacter huaxiensis 090008^{T}	98.5	n/a	n/a	n/a
Kluyvera cryocrescens ATCC 33435^{T}	98.5	n/a	n/a	n/a
Erwinia aphidicola DSM 19347^{T}	98.5	n/a	n/a	n/a
Citrobacter werkmanii NBRC 105721^{T}	98.5	n/a	n/a	n/a
Kluyvera intermedia NBRC 102594^{T}	98.5	n/a	n/a	n/a
Enterobacter bugandensis EB-247^{T}	98.5	n/a	n/a	n/a
Lelliottia aquatilis 6331-17^{T}	98.5	n/a	n/a	n/a
Enterobacter sichuanensis WCHECl1597^{T}	98.5	n/a	n/a	n/a

Lelliottia jeotgali PFL01^{T}	98.4	n/a	n/a	n/a
Citrobacter braakii ATCC 51113^{T}	98.4	n/a	n/a	n/a
Citrobacter portucalensis A60^{T}	98.4	n/a	n/a	n/a
Citrobacter murliniae CDC 2970-59^{T}	98.3	n/a	n/a	n/a
Kluyvera ascorbata ATCC 33433^{T}	98.3	n/a	n/a	n/a
Buttiauxella warmboldiae DSM 9404^{T}	98.3	n/a	n/a	n/a
Lelliottia nimipressuralis LMG 10245^{T}	98.3	n/a	n/a	n/a
Buttiauxella brennerae DSM 9396^{T}	98.2	n/a	n/a	n/a
Pseudescherichia vulneris NBRC 102420^{T}	98.2	n/a	n/a	n/a
Citrobacter pasteurii CIP 55.13^{T}	98.2	n/a	n/a	n/a
Yokenella regensburgei ATCC 49455^{T}	98.2	n/a	n/a	n/a