

**S1 Table.** Results of Mash, the *in silico* method for estimating genome distance, for genomic sequencing of the novel *Cupriavidus* species.

Identity	Shared-hashes	Median-multiplicity	P-value	Accession No.	Taxon name
0.979767	651/1000	1	0	GCA_001281465.1	<i>Cupriavidus gilardii</i>
0.882821	73/1000	1	2.59E-318	GCA_900249755.1	<i>Cupriavidus taiwanensis</i>
0.873204	58/1000	1	2.74E-247	GCA_001598055.1	<i>Cupriavidus oxalaticus</i>
0.871746	56/1000	1	6.06E-238	GCA_000069785.1	<i>Cupriavidus taiwanensis</i>
0.860849	43/1000	1	4.68E-178	GCA_900249985.1	<i>Cupriavidus taiwanensis</i>
0.853596	36/1000	1	1.63E-146	GCA_000876015.1	<i>Cupriavidus basilensis</i>
0.852452	35/1000	1	4.69E-142	GCA_003854935.1	<i>Cupriavidus pauculus</i>
0.851276	34/1000	1	1.31E-137	GCA_001592245.1	<i>Cupriavidus oxalaticus</i>
0.850067	33/1000	1	3.56E-133	GCA_004217045.1	<i>Cupriavidus</i> sp. ASC-9842