

bin	Distance	Novelty	P Values	Quality	Genes	Assembly	16S
2	The closest relatives found by MiGA in the database were <i>Thermoanaerobacter kivui</i> NZ CP009170T (47.17% AAI) and <i>Thermoanaerobacter italicus</i> Ab9 NC 013921T (47.12% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.015), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to an order not represented in the database (p-value: 0.29), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.97, domain 0.964, phylum 0.844, class 0.589, order 0.286, family 0.122, genus 0.015, species 0, subspecies 0.	Essential genes found: 106/111. Completeness: 95.5%. Contamination: 2.7%.	Predicted proteins: 2,050. Average length: 304.8166 aa. Coding density: 87.9272 %	Contigs: 103. N50: 29,922 bp. Total length: 2,132,015 bp. G+C content: 48.1346 %	No
4	The closest relative found by MiGA in the database was <i>Aminobacterium colombiense</i> DSM 12261 NC 014011T (99.39% ANI).	The dataset most likely belongs to a subspecies not represented in the database (p-value: 0.00084), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a species not represented in the database (p-value: 0.038), highest taxonomic rank with p-value $\leq$ 0.1.	P-values: root 0.998, domain 0.998, phylum 0.992, class 0.978, order 0.924, family 0.841, genus 0.671, species 0.0385, subspecies 0.000842.	Essential genes found: 101/111. Completeness: 91.0%. Contamination: 2.7%.	Predicted proteins: 1,830. Average length: 313.1459 aa. Coding density: 91.8879 %	Contigs: 59. N50: 99,008 bp. Total length: 1,870,943 bp. G+C content: 45.3507 %	No
8	The closest relatives found by MiGA in the database were <i>Sphaerochaeta globosa</i> str. Buddy NC 015152T (49.24% AAI) and <i>Sphaerochaeta pleomorpha</i> str. Grapes NC 016633T (49.0% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.00077), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.044), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to an order not represented in the database (p-value: 0.42), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.981, domain 0.977, phylum 0.903, class 0.742, order 0.419, family 0.18, genus 0.0442, species 0.00077, subspecies 0.	Essential genes found: 88/111. Completeness: 79.3%. Contamination: 1.8%.	Predicted proteins: 1,635. Average length: 284.0807 aa. Coding density: 94.0684 %	Contigs: 275. N50: 6,978 bp. Total length: 1,481,279 bp. G+C content: 36.7963 %	No
9	The closest relatives found by MiGA in the database were <i>Sulfurospirillum</i> sp. UCH001 NZ AP014723 (52.6% AAI) and <i>Sulfurospirillum deleyianum</i> DSM 6946 NC 013512T (52.5% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0015), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.09), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a family not represented in the database (p-value: 0.25), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.989, domain 0.986, phylum 0.94, class 0.843, order 0.601, family 0.255, genus 0.0898, species 0.00154, subspecies 0.	Essential genes found: 103/111. Completeness: 92.8%. Contamination: 1.8%.	Predicted proteins: 1,817. Average length: 309.1976 aa. Coding density: 95.0327 %	Contigs: 15. N50: 202,403 bp. Total length: 1,773,532 bp. G+C content: 33.5153 %	No
10	The closest relatives found by MiGA in the database were <i>Moorella thermoacetica</i> NZ CP012370 (44.26% AAI) and <i>Thermanaeromonas toyohensis</i> ToBe NZ LT838272 (44.04% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0029), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.059), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.29), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.945, domain 0.932, phylum 0.712, class 0.294, order 0.158, family 0.0592, genus 0.0029, species 0, subspecies 0.	Essential genes found: 87/111. Completeness: 78.4%. Contamination: 3.6%.	Predicted proteins: 2,114. Average length: 311.6698 aa. Coding density: 87.2072 %	Contigs: 189. N50: 22,496 bp. Total length: 2,266,567 bp. G+C content: 49.4937 %	No
12	The closest relatives found by MiGA in the database were <i>Parvimonas micra</i> NZ CP009761 (45.37% AAI) and <i>Gottschalkia acidurici</i> 9a NC 018664T (45.07% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0045), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.075), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.43), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.958, domain 0.949, phylum 0.782, class 0.432, order 0.197, family 0.0748, genus 0.00448, species 0, subspecies 0.	Essential genes found: 105/111. Completeness: 94.6%. Contamination: 0.9%.	Predicted proteins: 1,862. Average length: 310.4753 aa. Coding density: 92.086 %	Contigs: 53. N50: 61,314 bp. Total length: 1,883,364 bp. G+C content: 51.5252 %	No
13	The closest relatives found by MiGA in the database were <i>Salinicoccus</i> sp. BAB 3246 CP020916 (44.27% AAI) and <i>Finegoldia magna</i> ATCC 29328 NC 010376 (43.86% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0029), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.059), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.29), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.945, domain 0.932, phylum 0.712, class 0.294, order 0.158, family 0.0592, genus 0.0029, species 0, subspecies 0.	Essential genes found: 92/111. Completeness: 82.9%. Contamination: 2.7%.	Predicted proteins: 1,961. Average length: 315.1137 aa. Coding density: 91.4539 %	Contigs: 150. N50: 23,816 bp. Total length: 2,027,047 bp. G+C content: 32.0372 %	No
16	The closest relatives found by MiGA in the database were <i>Sphaerochaeta globosa</i> str. Buddy NC 015152T (56.63% AAI) and <i>Sphaerochaeta pleomorpha</i> str. Grapes NC 016633T (54.91% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.39), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.994, domain 0.992, phylum 0.966, class 0.911, order 0.698, family 0.387, genus 0.193, species 0.00385, subspecies 0.	Essential genes found: 79/111. Completeness: 71.2%. Contamination: 1.8%.	Predicted proteins: 2,021. Average length: 281.76 aa. Coding density: 93.0283 %	Contigs: 442. N50: 4,992 bp. Total length: 1,836,334 bp. G+C content: 53.2744 %	No
18	The closest relatives found by MiGA in the database were <i>Thermanaeromonas toyohensis</i> ToBe NZ LT838272 (43.24% AAI) and <i>Moorella thermoacetica</i> NZ CP012370 (43.18% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0021), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.05), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.2), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.93, domain 0.914, phylum 0.634, class 0.202, order 0.131, family 0.0504, genus 0.00211, species 0, subspecies 0.	Essential genes found: 104/111. Completeness: 93.7%. Contamination: 3.6%.	Predicted proteins: 2,447. Average length: 314.0699 aa. Coding density: 87.6683 %	Contigs: 202. N50: 22,058 bp. Total length: 2,629,898 bp. G+C content: 55.4388 %	No
19	The closest relatives found by MiGA in the database were <i>Virgibacillus</i> sp. SK37 NZ CP007161 (56.82% AAI) and <i>Virgibacillus halodenitrificans</i> NZ CP017962 (56.82% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.39), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.994, domain 0.992, phylum 0.967, class 0.912, order 0.702, family 0.393, genus 0.197, species 0.00385, subspecies 0.	Essential genes found: 106/111. Completeness: 95.5%. Contamination: 3.6%.	Predicted proteins: 2,767. Average length: 298.0683 aa. Coding density: 83.7693 %	Contigs: 92. N50: 55,314 bp. Total length: 2,953,667 bp. G+C content: 38.4214 %	No
21	The closest relatives found by MiGA in the database were <i>Sphaerochaeta globosa</i> str. Buddy NC 015152T (50.16% AAI) and <i>Sphaerochaeta coccoides</i> DSM 17374 NC 015436T (49.84% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.00077), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.058), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to an order not represented in the database (p-value: 0.49), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.984, domain 0.98, phylum 0.917, class 0.779, order 0.49, family 0.195, genus 0.0579, species 0.00077, subspecies 0.	Essential genes found: 101/111. Completeness: 91.0%. Contamination: 1.8%.	Predicted proteins: 1,716. Average length: 320.0542 aa. Coding density: 94.2819 %	Contigs: 145. N50: 18,141 bp. Total length: 1,747,566 bp. G+C content: 48.4637 %	No
22	The closest relatives found by MiGA in the database were <i>Brevifilum fermentans</i> NZ LT859958 (46.91% AAI) and <i>Anaerolinea thermophila</i> UNI 1 NC 014960T (45.84% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.013), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to an order not represented in the database (p-value: 0.27), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.969, domain 0.962, phylum 0.838, class 0.573, order 0.273, family 0.113, genus 0.0132, species 0, subspecies 0.	Essential genes found: 102/111. Completeness: 91.9%. Contamination: 2.7%.	Predicted proteins: 1,625. Average length: 347.1292 aa. Coding density: 90.8538 %	Contigs: 47. N50: 76,036 bp. Total length: 1,862,613 bp. G+C content: 46.9394 %	Yes

23	The closest relatives found by MiGA in the database were <i>Alkaliphilus oremlandii</i> OHLAs NC 009922T (57.32% AAI) and <i>Clostridium acetium</i> NZ CP009687T (52.77% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.41), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.994, domain 0.992, phylum 0.968, class 0.915, order 0.711, family 0.407, genus 0.213, species 0.00385, subspecies 0.	Essential genes found: 97/111. Completeness: 87.4%. Contamination: 6.3%.	Predicted proteins: 1,920. Average length: 294.8438 aa. Coding density: 85.1223 %.	Contigs: 238. N50: 12,320 bp. Total length: 1,995,130 bp. G+C content: 38.2884 %.	No
24	The closest relatives found by MiGA in the database were <i>Solitalea canadensis</i> DSM 3403 NC 017770T (46.7% AAI) and <i>Pseudopedobacter saltans</i> DSM 12145 NC 015177T (46.54% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.012), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to an order not represented in the database (p-value: 0.26), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.967, domain 0.96, phylum 0.83, class 0.553, order 0.259, family 0.1, genus 0.0119, species 0, subspecies 0.	Essential genes found: 105/111. Completeness: 94.6%. Contamination: 0.9%.	Predicted proteins: 2,027. Average length: 380.9773 aa. Coding density: 88.9874 %.	Contigs: 20. N50: 240,955 bp. Total length: 2,603,427 bp. G+C content: 37.6098 %.	Yes
25	The closest relatives found by MiGA in the database were <i>Thermanaeromonas toyohensis</i> ToBE NZ LT838272 (45.5% AAI) and <i>Moorella thermoacetica</i> NZ CP012370 (45.29% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0045), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.076), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.45), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.96, domain 0.951, phylum 0.791, class 0.453, order 0.209, family 0.0765, genus 0.00448, species 0, subspecies 0.	Essential genes found: 103/111. Completeness: 92.8%. Contamination: 2.7%.	Predicted proteins: 2,311. Average length: 301.5448 aa. Coding density: 88.8285 %.	Contigs: 186. N50: 21,438 bp. Total length: 2,353,534 bp. G+C content: 51.4071 %.	No
27	The closest relatives found by MiGA in the database were <i>Mageeibacillus indolicus</i> UPII9 5 NC 013895 (42.57% AAI) and <i>Salinicoccus</i> sp. BAB 3246 CP020916 (42.33% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0011), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.035), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.16), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.922, domain 0.905, phylum 0.593, class 0.162, order 0.102, family 0.035, genus 0.00105, species 0, subspecies 0.	Essential genes found: 85/111. Completeness: 76.6%. Contamination: 1.8%.	Predicted proteins: 1,250. Average length: 346.9384 aa. Coding density: 91.6381 %.	Contigs: 53. N50: 47,751 bp. Total length: 1,419,736 bp. G+C content: 58.5643 %.	No
33	The closest relatives found by MiGA in the database were <i>Bacteroidales bacterium</i> CF NZ CP006772 (52.6% AAI) and <i>Alistipes finegoldii</i> DSM 17242 NC 018011T (47.47% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0015), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.087), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a family not represented in the database (p-value: 0.25), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.988, domain 0.986, phylum 0.94, class 0.84, order 0.597, family 0.252, genus 0.0874, species 0.00154, subspecies 0.	Essential genes found: 104/111. Completeness: 93.7%. Contamination: 1.8%.	Predicted proteins: 1,576. Average length: 350.0425 aa. Coding density: 95.5335 %.	Contigs: 58. N50: 15,157 bp. Total length: 1,776,920 bp. G+C content: 44.8581 %.	No
34	The closest relatives found by MiGA in the database were <i>Thermanaeromonas toyohensis</i> ToBE NZ LT838272 (42.65% AAI) and <i>Moorella thermoacetica</i> NZ CP012370 (42.63% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0013), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.037), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.17), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.923, domain 0.906, phylum 0.599, class 0.166, order 0.107, family 0.0373, genus 0.00132, species 0, subspecies 0.	Essential genes found: 105/111. Completeness: 94.6%. Contamination: 3.6%.	Predicted proteins: 2,257. Average length: 306.8157 aa. Coding density: 86.017 %.	Contigs: 65. N50: 76,006 bp. Total length: 2,415,161 bp. G+C content: 38.8996 %.	No
38	The closest relatives found by MiGA in the database were <i>Salinicoccus</i> sp. BAB 3246 CP020916 (43.38% AAI) and <i>Candidatus</i> <i>Izimaplasma</i> sp. HR1 NZ CP009415 (43.23% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.0021), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a family not represented in the database (p-value: 0.051), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.21), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.931, domain 0.916, phylum 0.641, class 0.208, order 0.134, family 0.0513, genus 0.00211, species 0, subspecies 0.	Essential genes found: 105/111. Completeness: 94.6%. Contamination: 2.7%.	Predicted proteins: 1,551. Average length: 342.4223 aa. Coding density: 90.9214 %.	Contigs: 31. N50: 90,230 bp. Total length: 1,752,382 bp. G+C content: 46.9533 %.	No
40	The closest relatives found by MiGA in the database were <i>Clostridium clariflavum</i> DSM 19732 NC 016627T (42.46% AAI) and <i>Ruminiclostridium thermocellum</i> DSM 1313 NC 017304 (42.26% AAI).	The dataset most likely belongs to a genus not represented in the database (p-value: 0.00053), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to an order not represented in the database (p-value: 0.096), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a class not represented in the database (p-value: 0.16), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.921, domain 0.903, phylum 0.588, class 0.157, order 0.0963, family 0.0318, genus 0.000527, species 0, subspecies 0.	Essential genes found: 104/111. Completeness: 93.7%. Contamination: 4.5%.	Predicted proteins: 1,479. Average length: 346.288 aa. Coding density: 90.0911 %.	Contigs: 91. N50: 37,261 bp. Total length: 1,705,474 bp. G+C content: 50.7564 %.	No
45	The closest relatives found by MiGA in the database were <i>Desulfobulbus</i> sp. ORNL NZ CP021255 (57.99% AAI) and <i>Desulfobulbus propionicus</i> DSM 2032 CP002364T (55.28% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.43), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.994, domain 0.993, phylum 0.969, class 0.919, order 0.723, family 0.428, genus 0.229, species 0.00385, subspecies 0.	Essential genes found: 103/111. Completeness: 92.8%. Contamination: 2.7%.	Predicted proteins: 2,341. Average length: 310.8637 aa. Coding density: 88.8263 %.	Contigs: 185. N50: 21,010 bp. Total length: 2,457,827 bp. G+C content: 54.3237 %.	No
48	The closest relatives found by MiGA in the database were <i>Petrimonas</i> sp. IBARAKI AP018040 (47.85% AAI) and <i>Proteiniphilum saccharofermentans</i> NZ LT605205T (47.84% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.00077), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.023), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to an order not represented in the database (p-value: 0.33), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.975, domain 0.969, phylum 0.869, class 0.654, order 0.333, family 0.145, genus 0.0229, species 0.00077, subspecies 0.	Essential genes found: 105/111. Completeness: 94.6%. Contamination: 0.9%.	Predicted proteins: 2,566. Average length: 353.334 aa. Coding density: 90.9924 %.	Contigs: 188. N50: 29,590 bp. Total length: 2,989,223 bp. G+C content: 41.8863 %.	No
54	The closest relative found by MiGA in the database was <i>Methanoculleus</i> sp. MAB1 NZ LT158599 (98.36% ANI).	The dataset most likely belongs to a subspecies not represented in the database (p-value: 0.00084), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a species not represented in the database (p-value: 0.038), highest taxonomic rank with p-value $\leq$ 0.1.	P-values: root 0.998, domain 0.998, phylum 0.992, class 0.978, order 0.924, family 0.841, genus 0.67, species 0.0377, subspecies 0.000842.	Essential genes found: 21/26. Completeness: 80.8%. Contamination: 3.8%.	Predicted proteins: 2,397. Average length: 278.3146 aa. Coding density: 86.1405 %.	Contigs: 319. N50: 10,831 bp. Total length: 2,323,366 bp. G+C content: 61.9191 %.	No
55	The closest relatives found by MiGA in the database were <i>Mycoplasma parvum</i> str. Indiana NC 022575 (38.6% AAI) and <i>Mycoplasma haemofelis</i> str. Langford 1 NC 014970 (37.82% AAI).	The dataset most likely belongs to a family not represented in the database (p-value: 0.0087), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a class not represented in the database (p-value: 0.054), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to a phylum not represented in the database (p-value: 0.33), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.837, domain 0.802, phylum 0.33, class 0.0537, order 0.0223, family 0.00865, genus 0, species 0, subspecies 0.	Essential genes found: 88/111. Completeness: 79.3%. Contamination: 0.0%.	Predicted proteins: 583. Average length: 284.3156 aa. Coding density: 93.5634 %.	Contigs: 54. N50: 16,519 bp. Total length: 531,477 bp. G+C content: 32.3147 %.	Yes

57	The closest relatives found by MiGA in the database were <i>Sphaerochaeta globosa</i> str. Buddy NC 015152T (49.64% AAI) and <i>Sphaerochaeta pleomorpha</i> str. Grapes NC 016633T (49.44% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.00077), highest taxonomic rank with p-value $\leq$ 0.01. It probably belongs to a genus not represented in the database (p-value: 0.053), highest taxonomic rank with p-value $\leq$ 0.1. It possibly even belongs to an order not represented in the database (p-value: 0.45), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.983, domain 0.979, phylum 0.909, class 0.761, order 0.452, family 0.188, genus 0.0529, species 0.00077, subspecies 0.	Essential genes found: 103/111. Completeness: 92.8%. Contamination: 1.8%.	Predicted proteins: 1,639. Average length: 332.7132 aa. Coding density: 92.3977 %.	Contigs: 19. N50: 152,839 bp. Total length: 1,770,553 bp. G+C content: 40.6247 %.	No
59	The closest relatives found by MiGA in the database were <i>Petrimonas mucosa</i> NZ LT608328T (58.95% AAI) and <i>Proteiniphilum saccharofermentans</i> NZ LT605205T (58.86% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.46), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.994, domain 0.993, phylum 0.971, class 0.924, order 0.739, family 0.457, genus 0.257, species 0.00385, subspecies 0.	Essential genes found: 106/111. Completeness: 95.5%. Contamination: 0.9%.	Predicted proteins: 1,737. Average length: 370.2619 aa. Coding density: 91.4291 %.	Contigs: 74. N50: 50,989 bp. Total length: 2,110,307 bp. G+C content: 41.4571 %.	No
62	The closest relatives found by MiGA in the database were <i>Pelotomaculum thermopropionicum</i> SI AP009389T (56.61% AAI) and <i>Desulfofundulus kuznetsovii</i> DSM 6115 CP002770T (51.9% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.39), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.994, domain 0.992, phylum 0.966, class 0.911, order 0.698, family 0.387, genus 0.193, species 0.00385, subspecies 0.	Essential genes found: 106/111. Completeness: 95.5%. Contamination: 2.7%.	Predicted proteins: 2,347. Average length: 289.2015 aa. Coding density: 86.1534 %.	Contigs: 87. N50: 62,504 bp. Total length: 2,363,537 bp. G+C content: 47.0953 %.	Yes
63	The closest relatives found by MiGA in the database were <i>Pseudomonas stutzeri</i> NZ CP027543 (59.64% AAI) and <i>Pseudomonas</i> sp. R2A2 NZ CP029772 (59.62% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.48), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.995, domain 0.993, phylum 0.972, class 0.927, order 0.748, family 0.475, genus 0.27, species 0.00385, subspecies 0.	Essential genes found: 104/111. Completeness: 93.7%. Contamination: 0.9%.	Predicted proteins: 2,236. Average length: 317.3135 aa. Coding density: 87.9526 %.	Contigs: 35. N50: 83,678 bp. Total length: 2,420,099 bp. G+C content: 56.6054 %.	Yes
64	The closest relatives found by MiGA in the database were <i>Alkaliphilus oremlandii</i> OHILAs NC 009922T (58.02% AAI) and <i>Clostridium aceticum</i> NZ CP009687T (53.25% AAI).	The dataset most likely belongs to a species not represented in the database (p-value: 0.0038), highest taxonomic rank with p-value $\leq$ 0.01. It possibly even belongs to a family not represented in the database (p-value: 0.43), highest taxonomic rank with p-value $\leq$ 0.5.	P-values: root 0.994, domain 0.993, phylum 0.97, class 0.92, order 0.725, family 0.431, genus 0.233, species 0.00385, subspecies 0.	Essential genes found: 101/111. Completeness: 91.0%. Contamination: 4.5%.	Predicted proteins: 1,649. Average length: 296.6434 aa. Coding density: 85.895 %.	Contigs: 90. N50: 33,808 bp. Total length: 1,708,476 bp. G+C content: 38.5952 %.	No