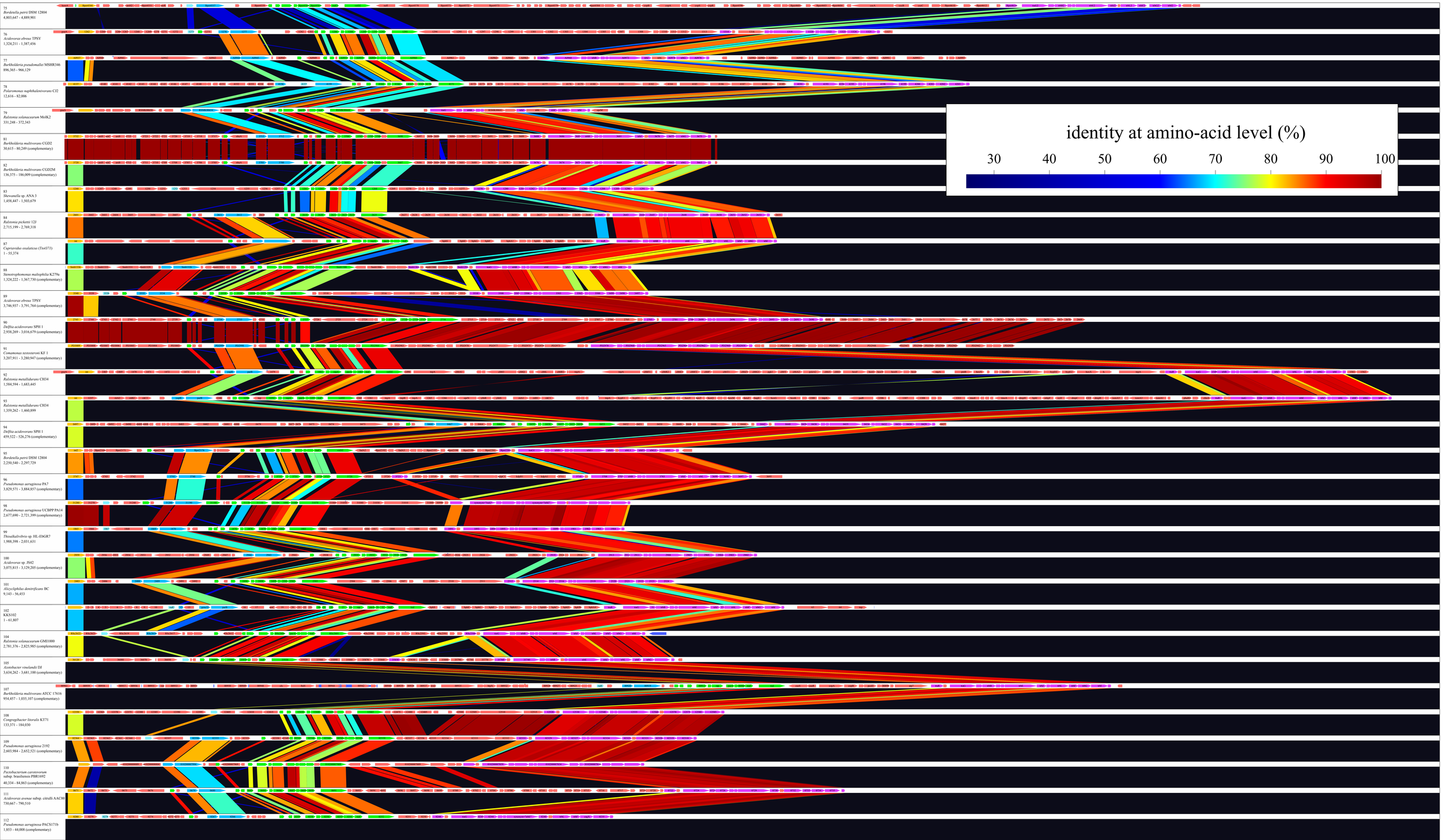
identity at amino-acid level (%)
30
40
50
60
70
80
90
100
75
Bordetella petrii DSM 12804
4,803,647 - 4,889,901
76
Acidovorax ebreus TPSY
1,324,211 - 1,387,456
77
Burkholderia pseudomallei MSHR346
896,365 - 966,129
78
Polaromonas naphthalenivorans CJ2
12,616 - 82,006
79
Ralstonia solanacearum MolK2
331,248 - 372,343
81
Burkholderia multivorans CGD2
30,615 - 80,249 (complementary)
82
Burkholderia multivorans CGD2M
136,375 - 186,009 (complementary)
83
Shewanella sp. ANA 3
1,458,447 - 1,503,679
84
Ralstonia pickettii 12J
2,715,199 - 2,769,318
87
Caprivirdus oxalaticus (Tn4371)
1 - 55,374
88
Stenotrophomonas maltophilia K279a
1,324,222 - 1,367,730 (complementary)
89
Acidovorax ebreus TPSY
3,746,937 - 3,791,764 (complementary)
90
Delftia acidovorans SPH 1
2,938,269 - 3,016,679 (complementary)
91
Comamonas testosteroni KF 1
3,207,911 - 3,280,947 (complementary)
92
Ralstonia metallidurans CH34
1,584,594 - 1,683,445
93
Ralstonia metallidurans CH34
1,359,262 - 1,460,899
94
Delftia acidovorans SPH 1
459,522 - 526,276 (complementary)
95
Bordetella petrii DSM 12804
2,550,540 - 2,597,729
96
Pseudomonas aeruginosa PA7
3,829,571 - 3,884,857 (complementary)
98
Pseudomonas aeruginosa UCBPP PA14
2,677,690 - 2,721,399 (complementary)
99
Thiosalivibrio sp. HL-EbGR7
1,988,398 - 2,031,631
100
Acidovorax sp. JS42
3,075,813 - 3,129,205 (complementary)
101
Alicycliphilus denitrificans BC
9,143 - 56,453
102
KKS102
1 - 61,807
104
Ralstonia solanacearum GMI1000
2,781,376 - 2,825,985 (complementary)
105
Azotobacter vinelandii DJ
3,634,282 - 3,681,100 (complementary)
107
Burkholderia multivorans ATCC 17616
954,457 - 1,035,107 (complementary)
108
Cupriavidus taiwanensis KT71
133,371 - 184,030
109
Pseudomonas aeruginosa 2192
2,603,984 - 2,652,521 (complementary)
110
Pectobacterium carotovorum
subsp. brasiliensis PBR1692
40,334 - 84,863 (complementary)
111
Acidovorax avenae subsp. citrulli AAC00
730,667 - 790,510
112
Pseudomonas aeruginosa PACS171b
1,853 - 44,008 (complementary)

Fig. S1 Comparative analysis of ICEs with *traG* that belonged to β and γ clusters. Coding sequences (CDSs) present in a range of genomic sequences from one organism were blastp-compared to those in another. Detected similarities with query coverage greater than 50% and identity score greater than 30% are depicted with colored lines. The relationships between colors and identity scores are shown in the top-right area. CDSs in the int, *parB*, *parI*, and *mpf* blocks are shown in orange, cyan, green, and purple, respectively. *radC* is shown in pale cyan and *traR* is shown in purple. At the left of each panel, the sequence number and exact sequence range used for the analysis are indicated. See Supplementary Table S4 for sequence numbers, source organisms, and accession numbers. This figure was drawn by using a computational tool, CompareSequences, which is available at: http://www.ige.tohoku.ac.jp/joho/gmProject/gmhome.html.

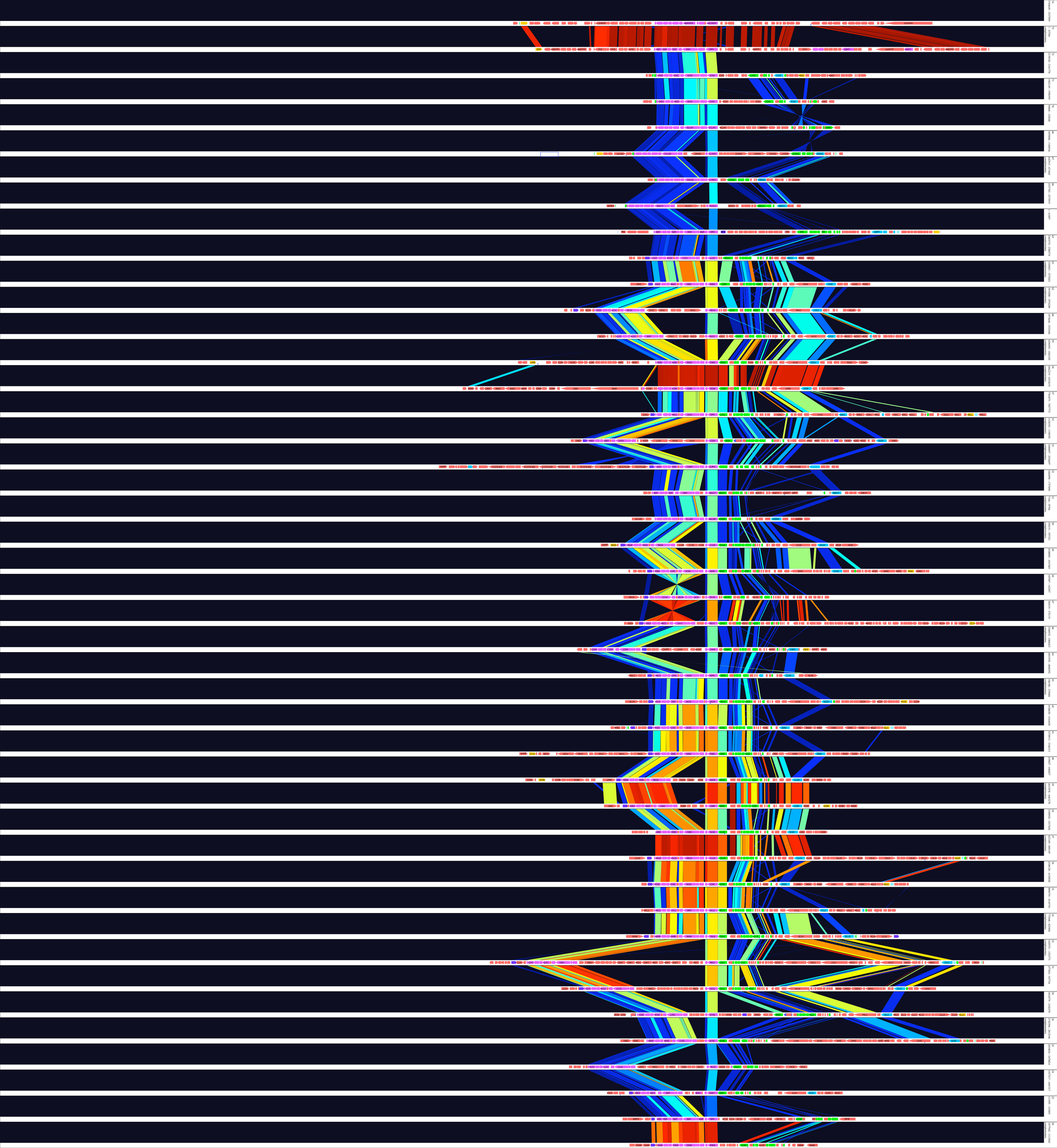

Fig. S2 Comparative analysis of putative ICEs carrying traG belonging to α clusters I and II. See the legend to Fig. S1. TraG sequences not surrounded by typical ICE genes were omitted from the figure.

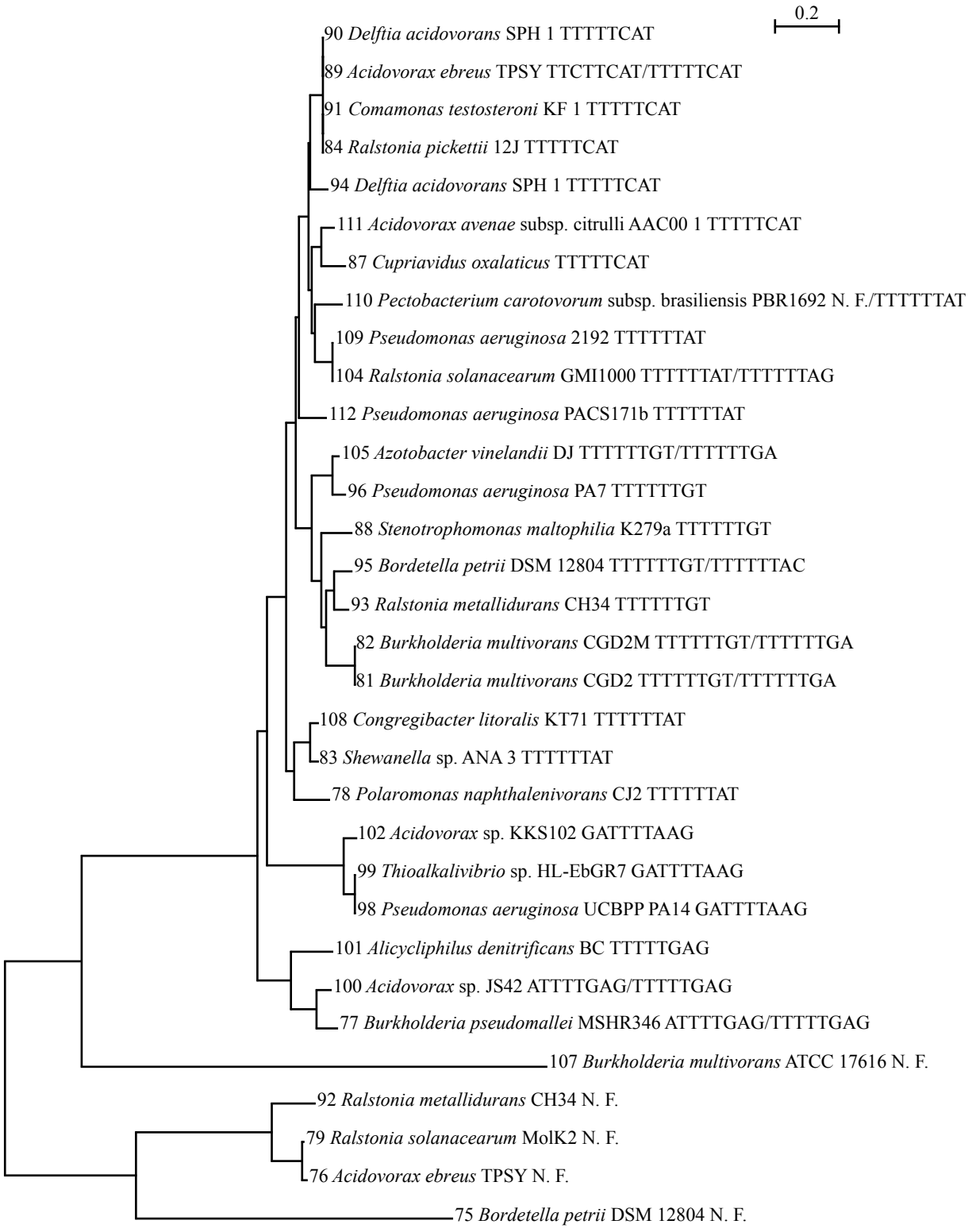

Fig. S3 Phylogenetic tree of Int proteins of Tn*4371*-like elements from β- and γ-proteobacteria Int protein sequences were aligned and a neighbor-joining tree was depicted by MAFFT (7). The strain names are followed by nucleotide sequences of att sites. In cases where the two sites are not identical, both sites are shown. N. F.: not found.