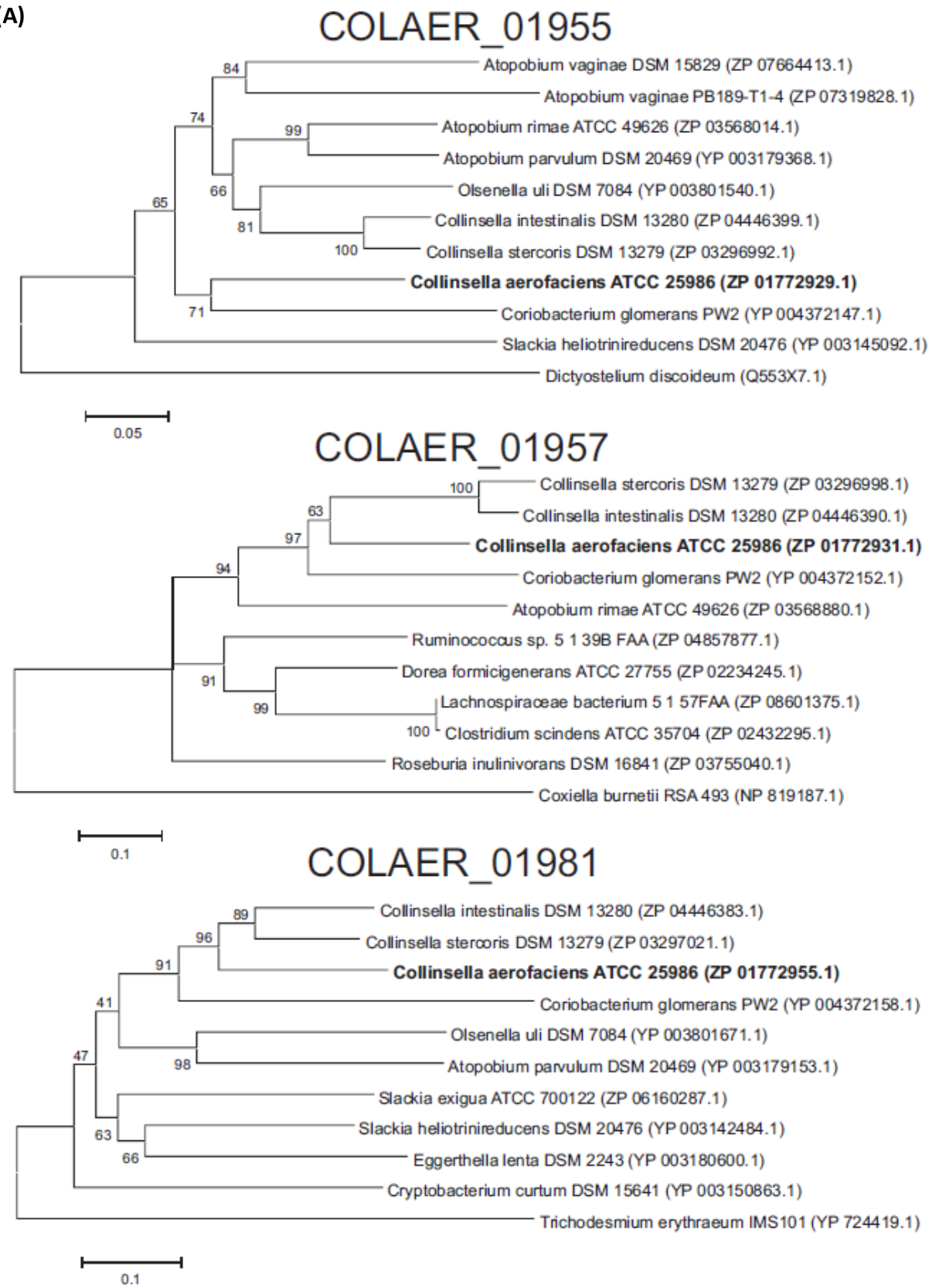
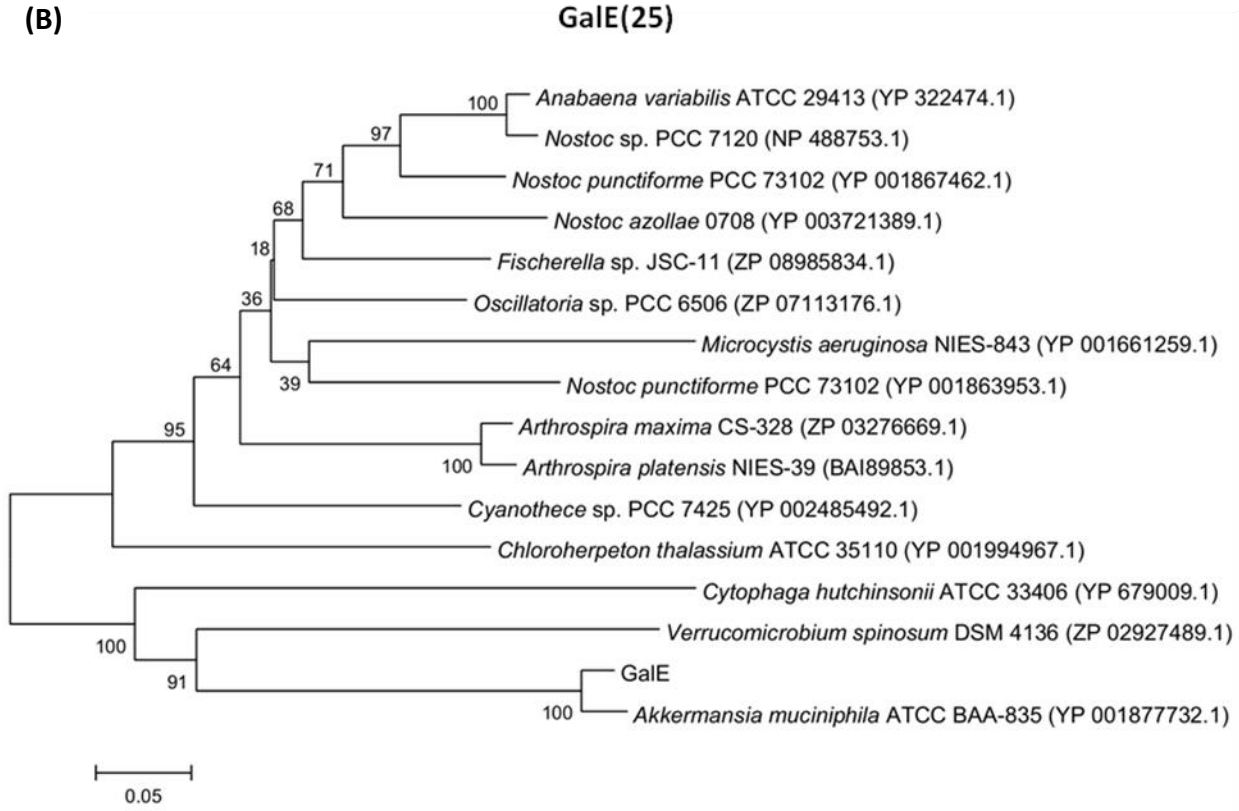
(A)


COLAER_01955
Atopobium vaginae DSM 15829 (ZP 07664413.1)
Atopobium vaginae PB189-T1-4 (ZP 07319828.1)
Atopobium rimae ATCC 49626 (ZP 03568014.1)
Atopobium parvulum DSM 20469 (YP 003179368.1)
Olsenella uli DSM 7084 (YP 003801540.1)
Collinsella intestinalis DSM 13280 (ZP 04446399.1)
Collinsella stercoris DSM 13279 (ZP 03296992.1)
Collinsella aerofaciens ATCC 25986 (ZP 01772929.1)
Coriobacterium glomerans PW2 (YP 004372147.1)
Slackia heliotrinireducens DSM 20476 (YP 003145092.1)
Dictyostelium discoideum (Q553X7.1)
84
74
99
66
65
81
100
71
0.05
COLAER_01957
Collinsella stercoris DSM 13279 (ZP 03296998.1)
Collinsella intestinalis DSM 13280 (ZP 04446390.1)
Collinsella aerofaciens ATCC 25986 (ZP 01772931.1)
Coriobacterium glomerans PW2 (YP 004372152.1)
Atopobium rimae ATCC 49626 (ZP 03568880.1)
Ruminococcus sp. 5 1 39B FAA (ZP 04857877.1)
Dorea formicigenerans ATCC 27755 (ZP 02234245.1)
Lachnospiraceae bacterium 5 1 57FAA (ZP 08601375.1)
Clostridium scindens ATCC 35704 (ZP 02432295.1)
Roseburia inulinivorans DSM 16841 (ZP 03755040.1)
Coxiella burnetii RSA 493 (NP 819187.1)
100
63
97
94
91
99
100
0.1
COLAER_01981
Collinsella intestinalis DSM 13280 (ZP 04446383.1)
Collinsella stercoris DSM 13279 (ZP 03297021.1)
Collinsella aerofaciens ATCC 25986 (ZP 01772955.1)
Coriobacterium glomerans PW2 (YP 004372158.1)
Olsenella uli DSM 7084 (YP 003801671.1)
Atopobium parvulum DSM 20469 (YP 003179153.1)
Slackia exigua ATCC 700122 (ZP 06160287.1)
Slackia heliotrinireducens DSM 20476 (YP 003142484.1)
Eggerthella lenta DSM 2243 (YP 003180600.1)
Cryptobacterium curtum DSM 15641 (YP 003150863.1)
Trichodesmium erythraeum IMS101 (YP 724419.1)
89
96
91
41
47
98
63
66
0.1

(B)


GalE(25)
100
Anabaena variabilis ATCC 29413 (YP 322474.1)
97
Nostoc sp. PCC 7120 (NP 488753.1)
71
Nostoc punctiforme PCC 73102 (YP 001867462.1)
68
Nostoc azollae 0708 (YP 003721389.1)
18
Fischerella sp. JSC-11 (ZP 08985834.1)
36
Oscillatoria sp. PCC 6506 (ZP 07113176.1)
Microcystis aeruginosa NIES-843 (YP 001661259.1)
64
39
Nostoc punctiforme PCC 73102 (YP 001863953.1)
95
Arthrospira maxima CS-328 (ZP 03276669.1)
100
Arthrospira platensis NIES-39 (BAI89853.1)
Cyanothece sp. PCC 7425 (YP 002485492.1)
Chloroherpeton thalassium ATCC 35110 (YP 001994967.1)
Cytophaga hutchinsonii ATCC 33406 (YP 679009.1)
100
Verrucomicrobium spinosum DSM 4136 (ZP 02927489.1)
91
GalE
100
Akkermansia muciniphila ATCC BAA-835 (YP 001877732.1)
0.05

(C)

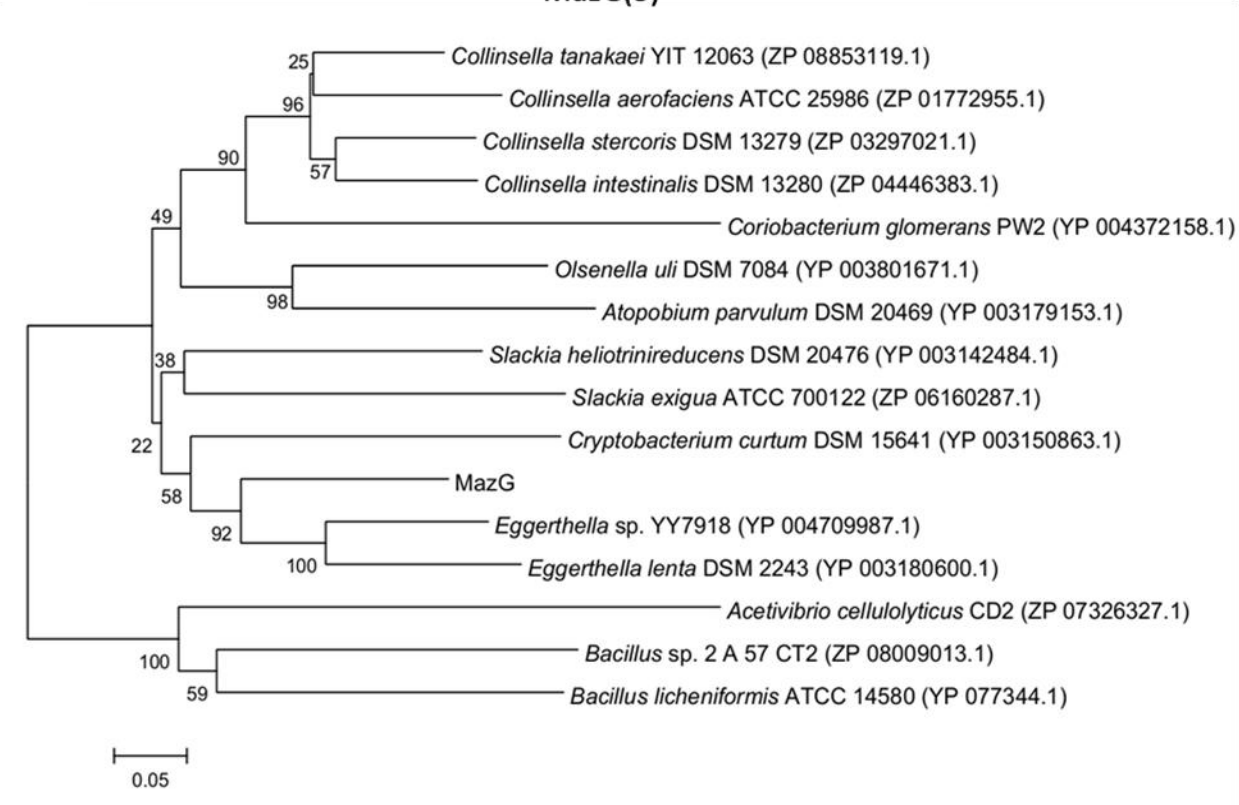

MazG(5)
25
Collinsella tanakaei YIT 12063 (ZP 08853119.1)
96
Collinsella aerofaciens ATCC 25986 (ZP 01772955.1)
Collinsella stercoris DSM 13279 (ZP 03297021.1)
90
57
Collinsella intestinalis DSM 13280 (ZP 04446383.1)
49
Coriobacterium glomerans PW2 (YP 004372158.1)
Olsenella uli DSM 7084 (YP 003801671.1)
98
Atopobium parvulum DSM 20469 (YP 003179153.1)
38
Slackia heliotrinireducens DSM 20476 (YP 003142484.1)
Slackia exigua ATCC 700122 (ZP 06160287.1)
22
Cryptobacterium curtum DSM 15641 (YP 003150863.1)
58
MazG
92
Eggerthella sp. YY7918 (YP 004709987.1)
100
Eggerthella lenta DSM 2243 (YP 003180600.1)
Acetivibrio cellulolyticus CD2 (ZP 07326327.1)
100
Bacillus sp. 2 A 57 CT2 (ZP 08009013.1)
59
Bacillus licheniformis ATCC 14580 (YP 077344.1)
0.05

Fig. S3: Phylogenetic analysis of **(A)** GalE(3) (COLAER_01955), MurB(3) (COLAER_01957), MazG(3) (COLAER_01981), **(B)** GalE(25) (Amuc_1125) and **(C)** MazG(5) (EGYY_03530) and related proteins. Phylogenetic analysis was performed using the program MEGA 5.0 (Tamura *et al.*, 2011). The bootstrap method (500 replicates) was used to test the percentage of replicate trees in which the associated taxa clustered together