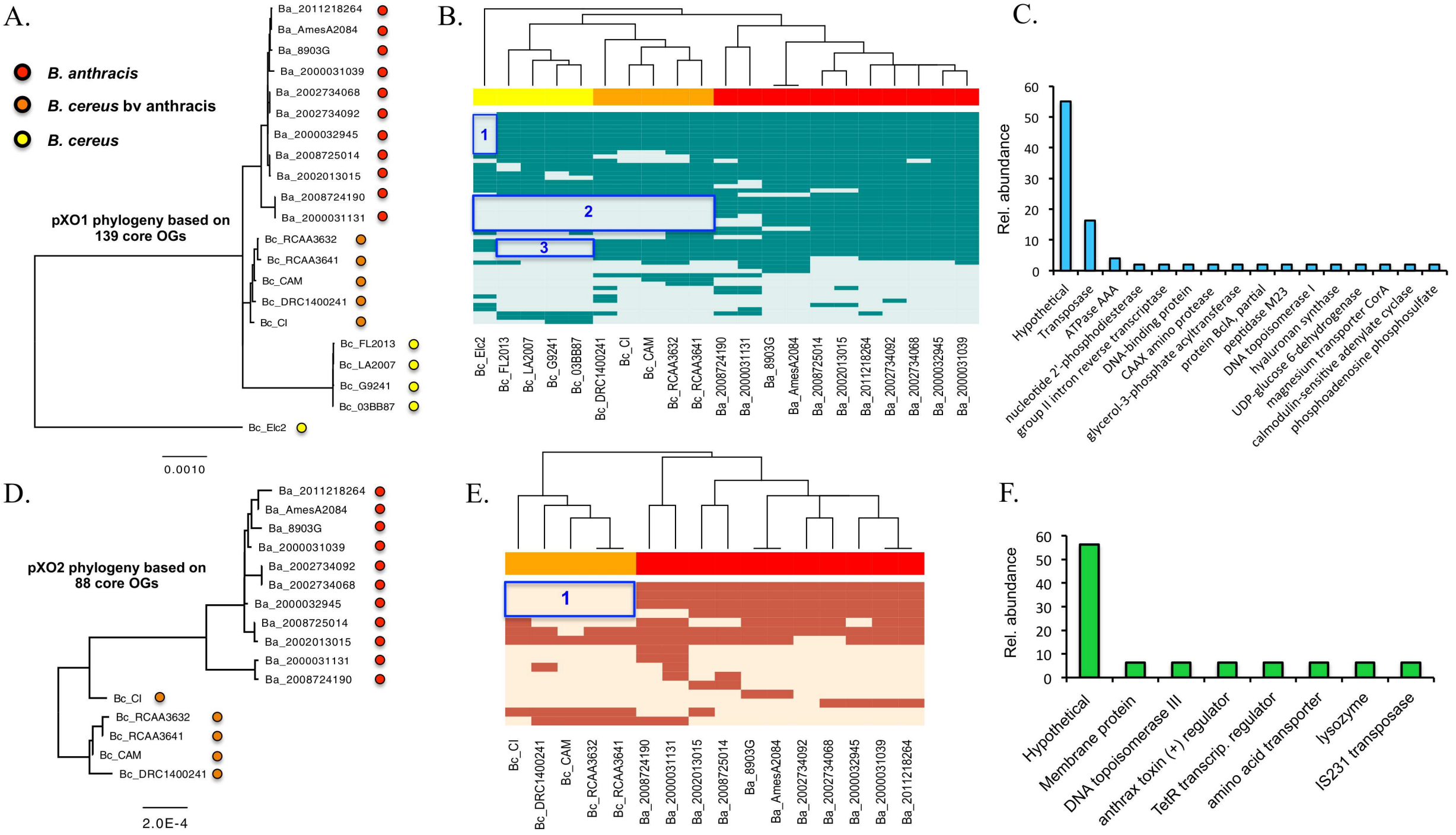
A.
B. anthracis
B. cereus bv anthracis
B. cereus
Ba_2011218264
Ba_AmesA2084
Ba_8903G
Ba_2000031039
Ba_2002734068
Ba_2002734092
Ba_2000032945
Ba_2008725014
Ba_2002013015
Ba_2008724190
Ba_2000031131
pXO1 phylogeny based on 139 core OGs
Bc_RCAA3632
Bc_RCAA3641
Bc_CAM
Bc_DRC1400241
Bc_Cl
Bc_FL2013
Bc_LA2007
Bc_G9241
Bc_03BB87
Bc_Elc2
0.0010
B.
1
2
3
Bc_Elc2
Bc_FL2013
Bc_LA2007
Bc_G9241
Bc_03BB87
Bc_DRC1400241
Bc_Cl
Bc_CAM
Bc_RCAA3632
Bc_RCAA3641
Ba_2008724190
Ba_2000031131
Ba_8903G
Ba_AmesA2084
Ba_2008725014
Ba_2002013015
Ba_2011218264
Ba_2002734092
Ba_2002734068
Ba_2000032945
Ba_2000031039
C.
Rel. abundance
60
50
40
30
20
10
0
Hypothetical
Transposase
ATPase AAA
nucleotide 2'-phosphodiesterase
group II intron reverse transcriptase
DNA-binding protein
CAAX amino protease
glycerol-3-phosphate acyltransferase
protein BclA, partial
peptidase M23
DNA topoisomerase I
hyaluronan synthase
UDP-glucose 6-dehydrogenase
magnesium transporter CorA
calmodulin-sensitive adenylate cyclase
phosphoadenosine phosphosulfate
D.
pXO2 phylogeny based on 88 core OGs
Ba_2011218264
Ba_AmesA2084
Ba_8903G
Ba_2000031039
Ba_2002734092
Ba_2002734068
Ba_2000032945
Ba_2008725014
Ba_2002013015
Ba_2000031131
Ba_2008724190
Bc_Cl
Bc_RCAA3632
Bc_RCAA3641
Bc_CAM
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2.0E-4
E.
1
Bc_Cl
Bc_DRC1400241
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Bc_RCAA3641
Ba_2008724190
Ba_2000031131
Ba_2002013015
Ba_2008725014
Ba_8903G
Ba_AmesA2084
Ba_2002734092
Ba_2002734068
Ba_2000032945
Ba_2000031039
Ba_2011218264
F.
Rel. abundance
60
50
40
30
20
10
0
Hypothetical
Membrane protein
DNA topoisomerase III
anthrax toxin (+) regulator
TetR transcrip. regulator
amino acid transporter
lysozyme
IS231 transposase