Figure A. Correlation between pooled plasmid sizes and chromosome sizes of *Rickettsia* species. The coefficient of determination is $R^2 = 0.76$ and the coefficient of correlation of Pearson is $R = 0.91$, *P-value* < 0.05.

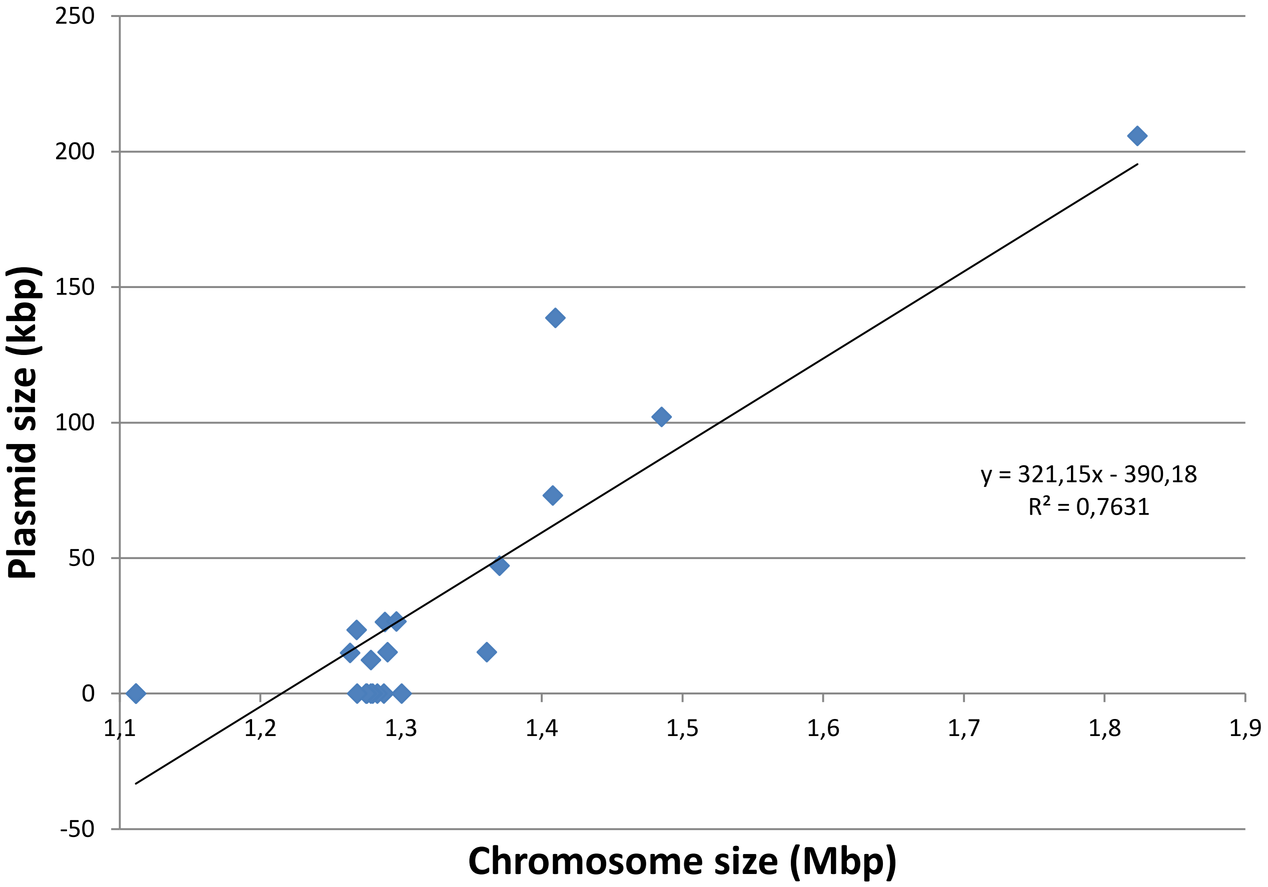
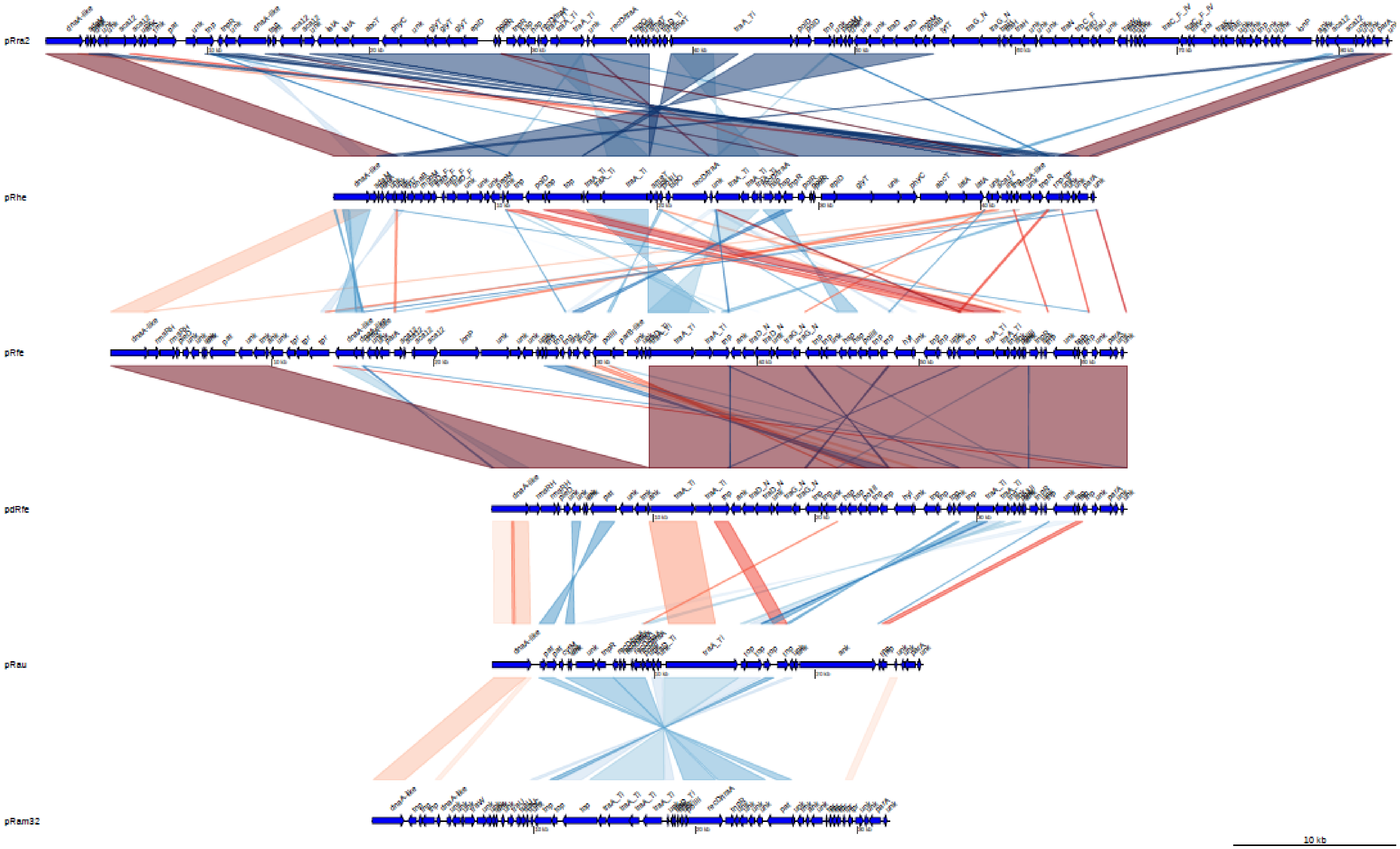
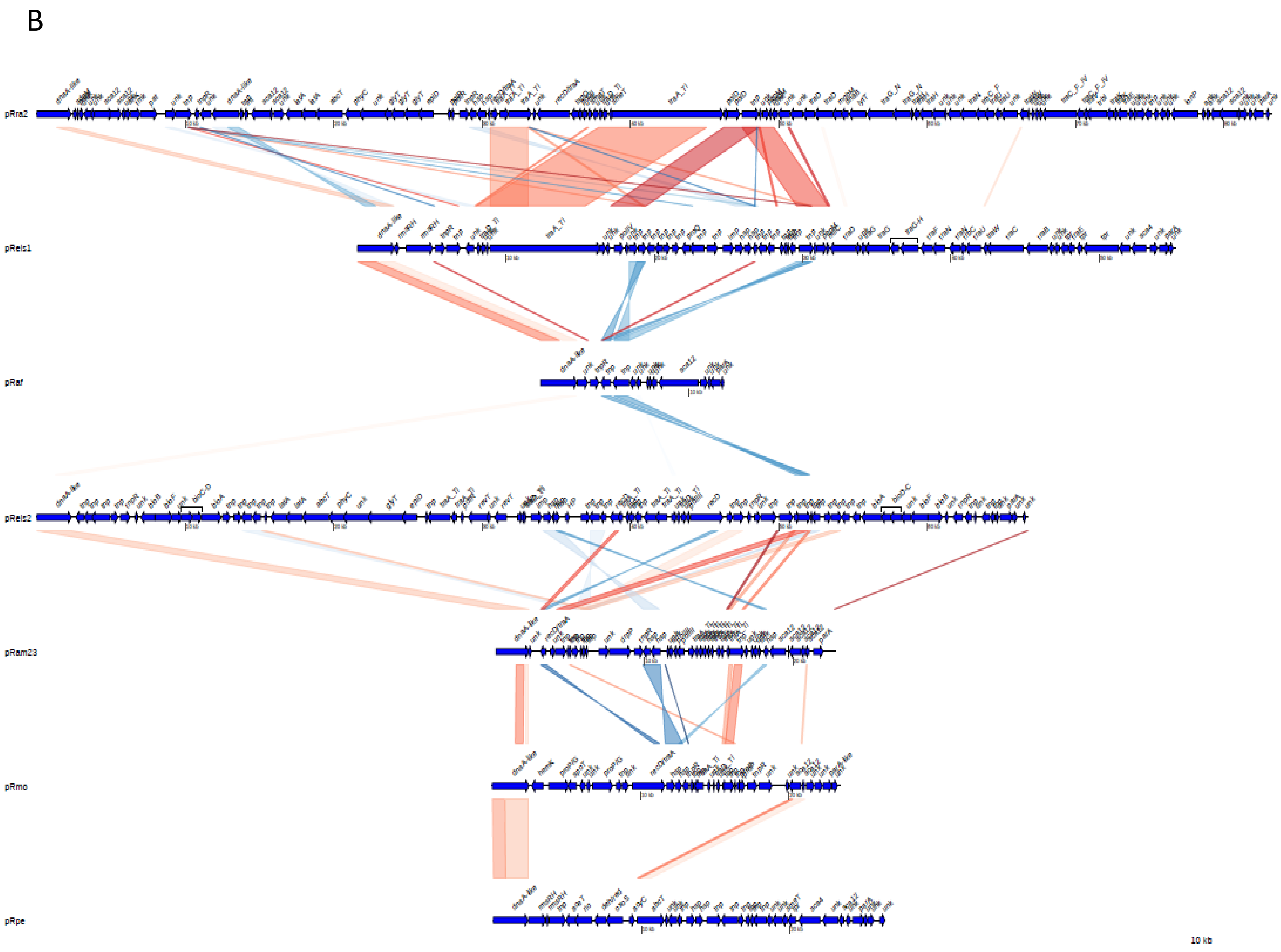


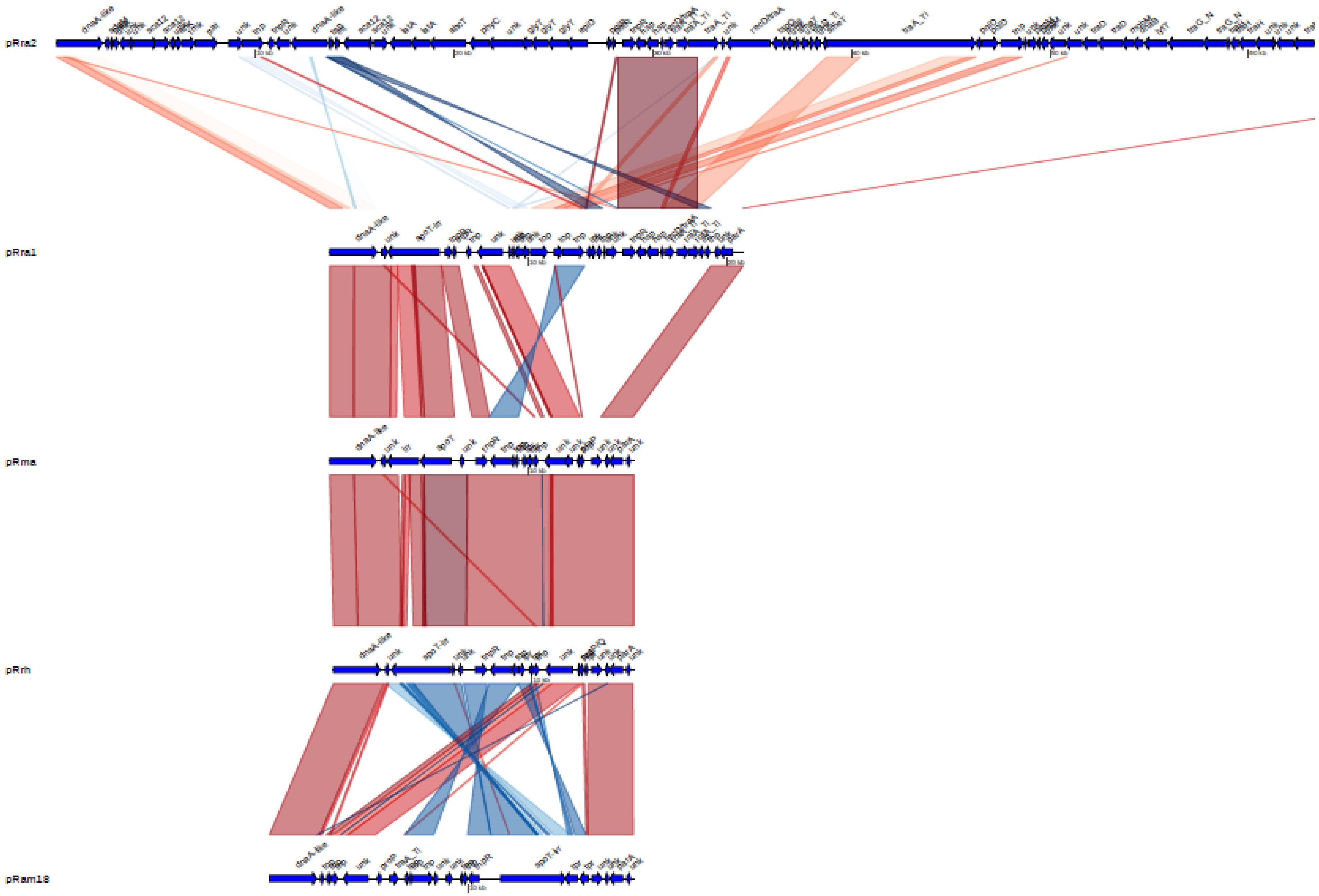
Figure B. Pairwise alignments of complete sequences of the four major groups I (A), II (B), III (C) and IV (D) of *Rickettsia* plasmids as well as of intra-cellular plasmid of *R. raoultii* (E), *R. endosymbionte of I. scapularis* (F) and *R. amblyomii* (G). The plasmid pRra2 was used as reference for all alignments. All sequences started with *dna*A-like gene and ended with *par*A and some unknown genes.

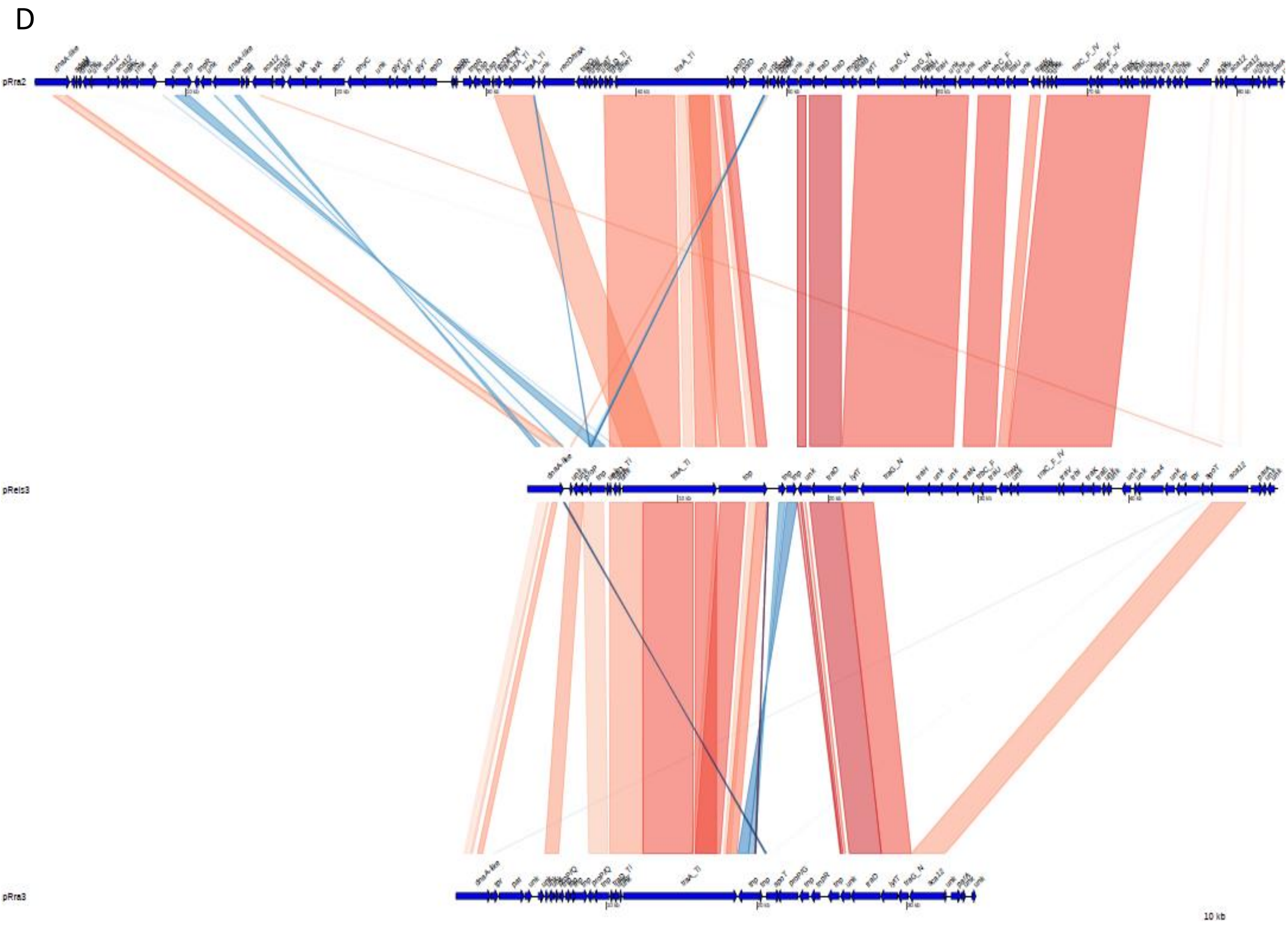
A

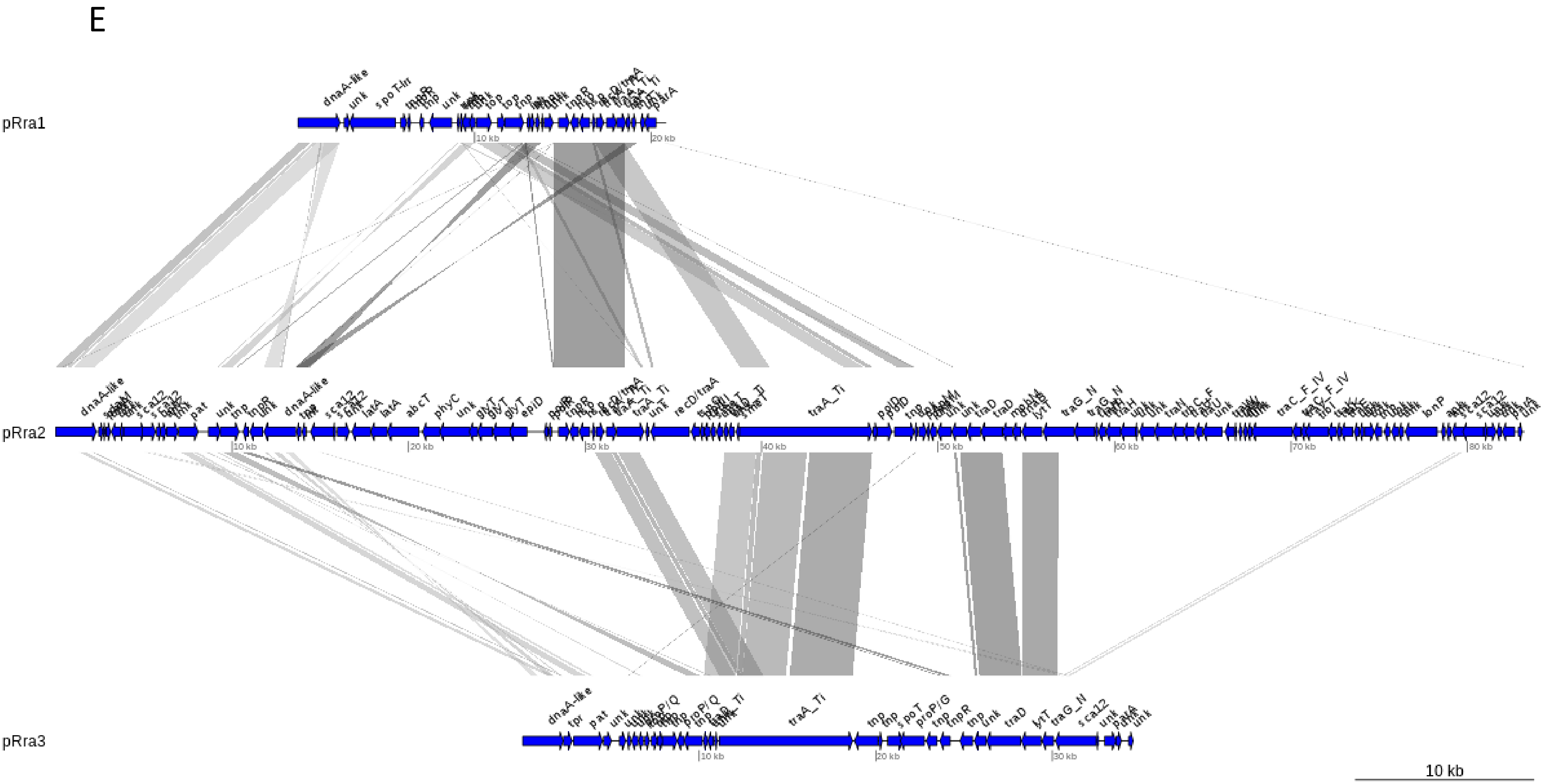


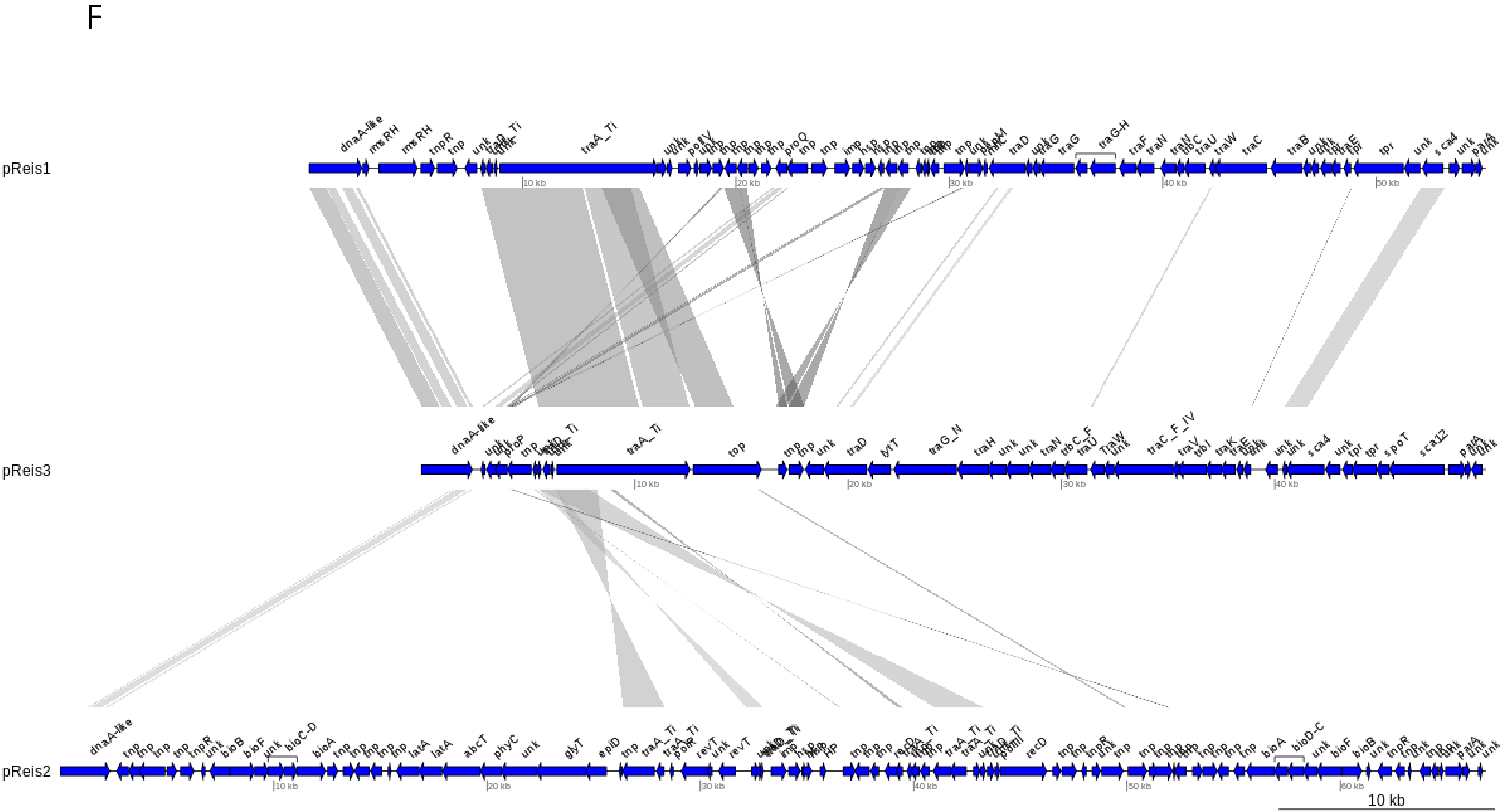

B
pRra2
pRels1
pRaf
pRels2
pRam23
pRmo
pRpe
10 kb

C




D
pRra2
pRels3
pRra3
dnaA-like
traA_Ti
traG_N
traC_F_IV
lytT
traD
tnp
unk
10 kb


E
pRra1
dnaA-like
unk
spoT-lir
tnp
unk
top
top
tnp
unk
tnpR
repC/traA
traA_Ti
parA
10 kb
20 kb
pRra2
dnaA-like
sca12
pat
unk
tnp
tnpR
dnaA-like
sca12
latA
latA
abcT
phyC
unk
glyT
glyT
epiD
polR
tnpR
repC/traA
traA_Ti
traA_Ti
unk
recD/traA
traA_Ti
polD
tnp
unk
traD
lytT
traG_N
traG_N
traH
traH
traC_F
traC_F_IV
traC_F_IV
lonP
sca12
parA
unk
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
pRra3
dnaA-like
tpr
pat
unk
proP/Q
proP/Q
tnp
traA_Ti
traA_Ti
tnp
tnp
spoT
proP/G
tnp
tnpR
tnp
unk
traD
lytT
traG_N
sca12
unk
parA
unk
10 kb
20 kb
30 kb
10 kb


F
pReis1
pReis3
pReis2
dnaA-like
rmsRH
rmsRH
tnpR
tnp
unk
traD_Ti
traA_Ti
pomV
proQ
traD
traG
traG-H
traF
traN
traW
traC
traB
tpr
sca4
parA
10 kb
20 kb
30 kb
40 kb
50 kb
dnaA-like
proP
traA_Ti
top
traD
tytT
traG_N
traH
traN
tbC_F
traU
TraW
traC_F_IV
traV
traK
sca4
tpr
spoT
sca12
parA
dnaA-like
tnpR
bioB
bioF
bioC-D
bioA
latA
latA
abcT
phyC
glyT
epiD
traA_Ti
polR
revT
revT
recD
bioA
bioD-C
bioF
bioB
60 kb
10 kb

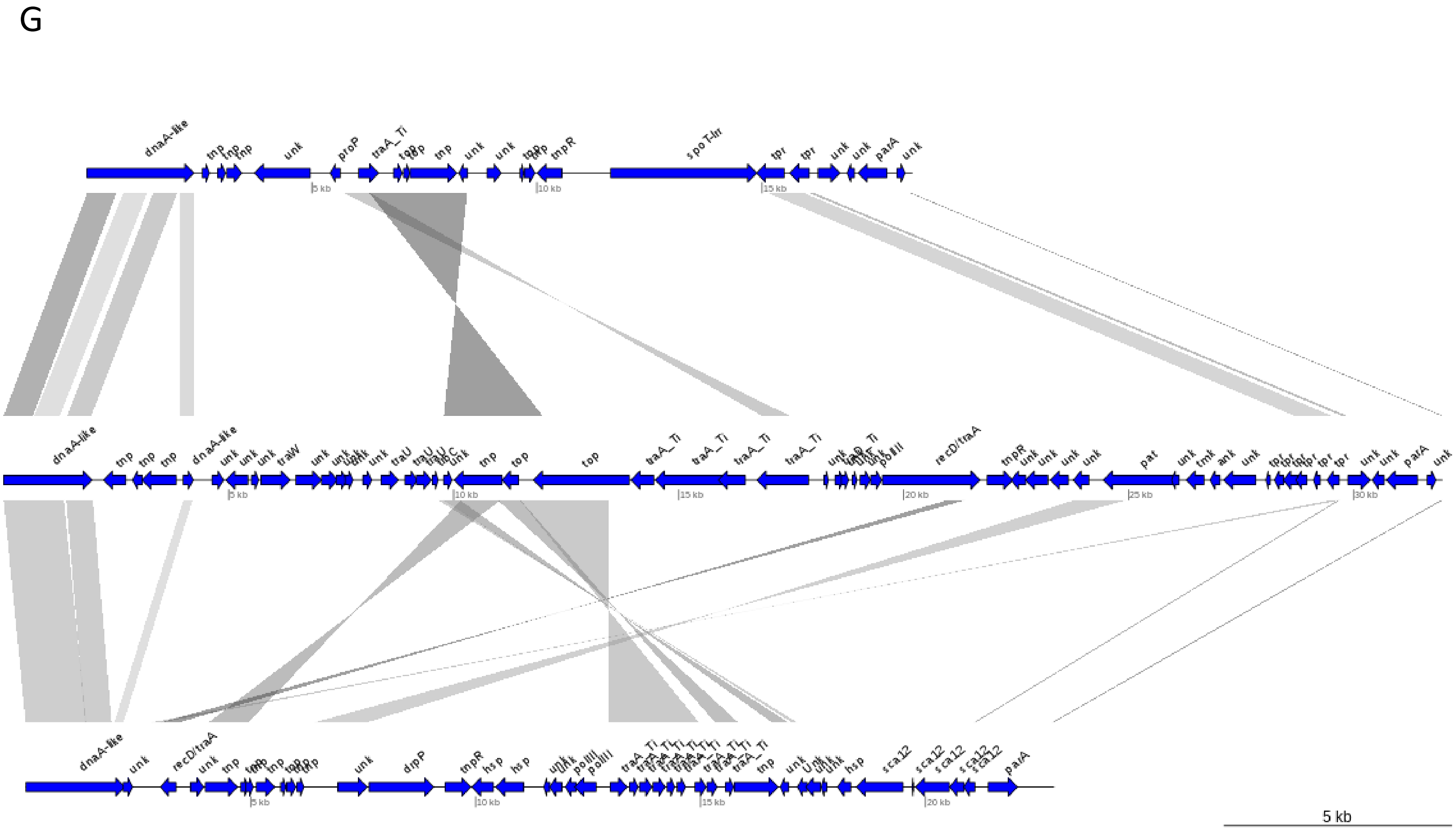

G
pRam18
dnaA-like
tnp
tnp
tnp
unk
proP
traA_Ti
top
top
tnp
unk
unk
top
tnp
tnpR
spoT-lr
tpr
tpr
unk
unk
parA
unk
5 kb
10 kb
15 kb
pRam32
dnaA-like
tnp
tnp
tnp
dnaA-like
unk
unk
unk
traW
unk
unk
unk
unk
traU
traU
traC
unk
tnp
top
top
traA_Ti
traA_Ti
traA_Ti
traA_Ti
unk
traA_Ti
unk
polIII
recD/traA
tnpR
unk
unk
unk
unk
pat
unk
tmk
ank
unk
tpr
tpr
tpr
tpr
tpr
unk
unk
parA
unk
5 kb
10 kb
15 kb
20 kb
25 kb
30 kb
pRam23
dnaA-like
unk
recD/traA
unk
tnp
tnp
tnp
tnp
top
tnp
unk
drpP
tnpR
hsp
hsp
unk
unk
polIII
polIII
traA_Ti
traA_Ti
traA_Ti
traA_Ti
traA_Ti
traA_Ti
traA_Ti
tnp
unk
unk
unk
hsp
sca12
sca12
sca12
sca12
sca12
parA
5 kb
10 kb
15 kb
20 kb
5 kb

Figure C. Horizontal gene transfers occurred between *R. raoultii* chromosome, *R. peacokii* plasmid and *Pseudomonas aeruginosa* chromosome.

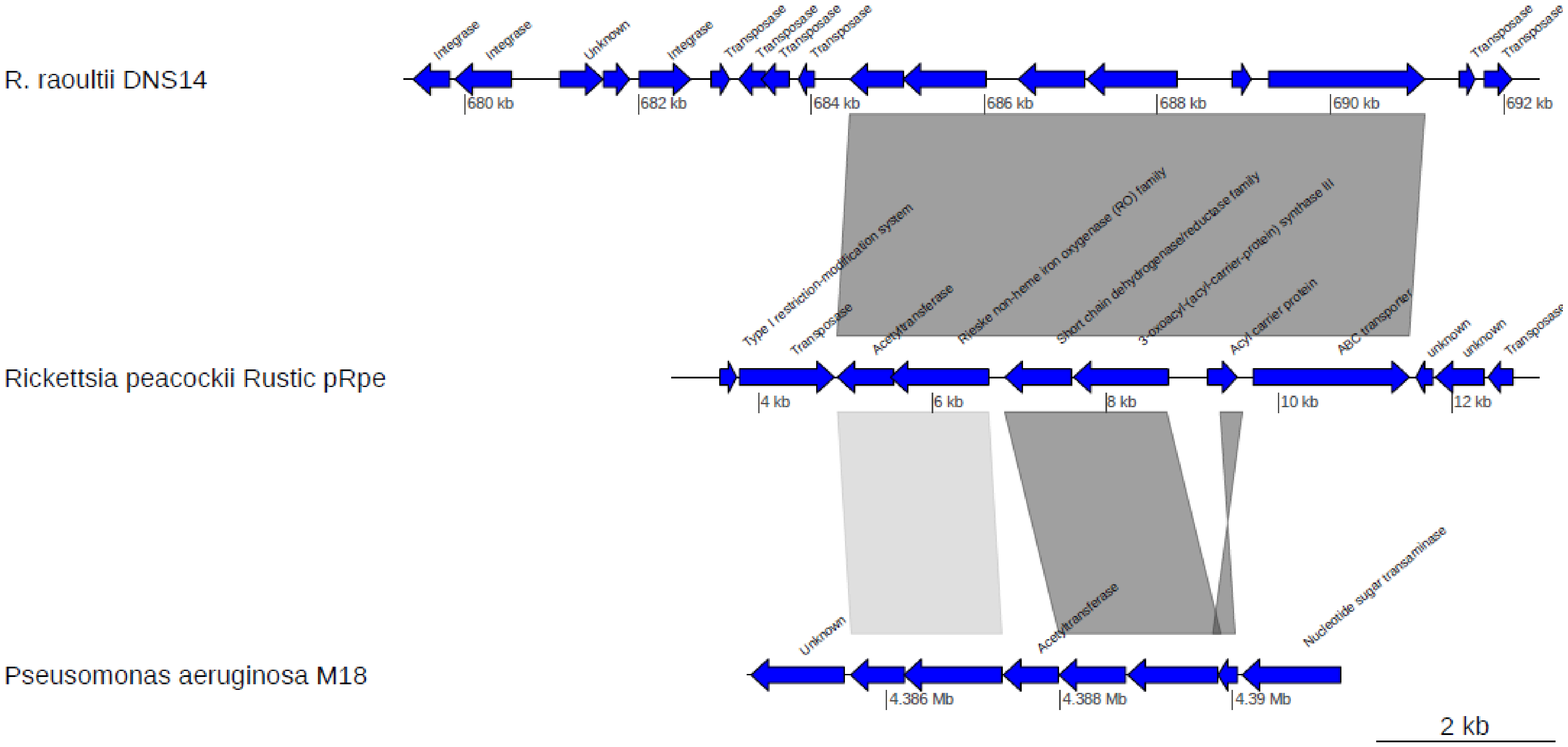


Figure D. Species details of evident HGT2 and 3 events occurred between rickettsial plasmids and non-*Rickettsia/Orientia* genomes, as inferred from best BLAST homology and phylogenetic relationships (50>=aa identity<=100 and BP>=60). Colors of species correspond to α-proteobacteria (blue), γ-proteobacteria (yellow), β-proteobacteria (cyan), δ-proteobacteria (beige), Bacteoidetes (red), Planctomycetes (green) and Other bacteria (white).

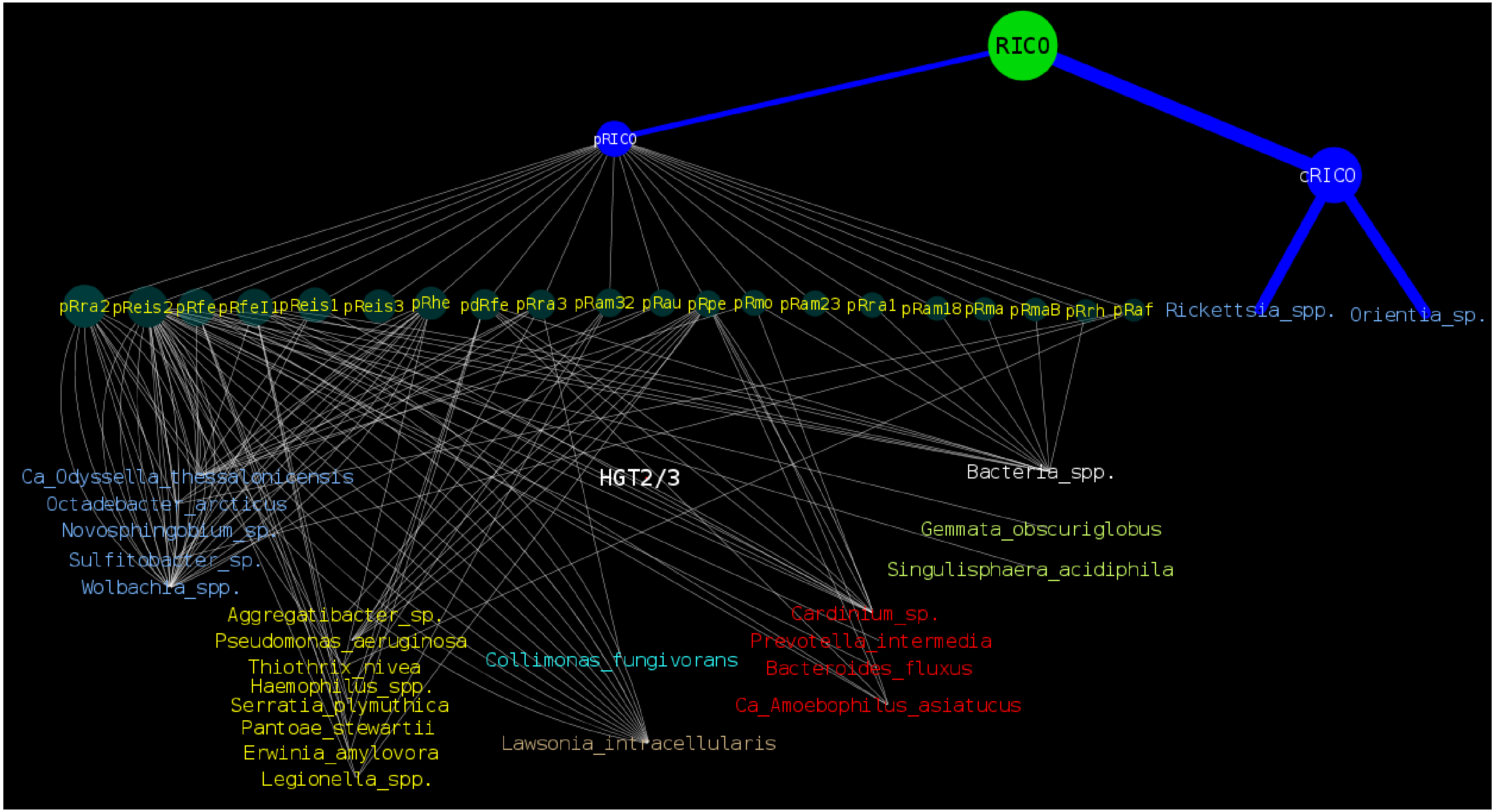


Figure E. Genus detail of putative HGT2 events occurred between rickettsial plasmids and unknown non-*Rickettsia/Orientia* genomes, as inferred from best BLAST homology (25>=aa identity<80). Colors of species correspond to α-proteobacteria (blue), γ-proteobacteria (yellow), β-proteobacteria (cyan), Bacteoidetes (red), Deferribacteres (yellow), Cyanobacteria (silver), Chlamydiae (white), Firmicutes (grey), Spirochaetes (white), Archaea (brown) and Eukaryota (turqoise).