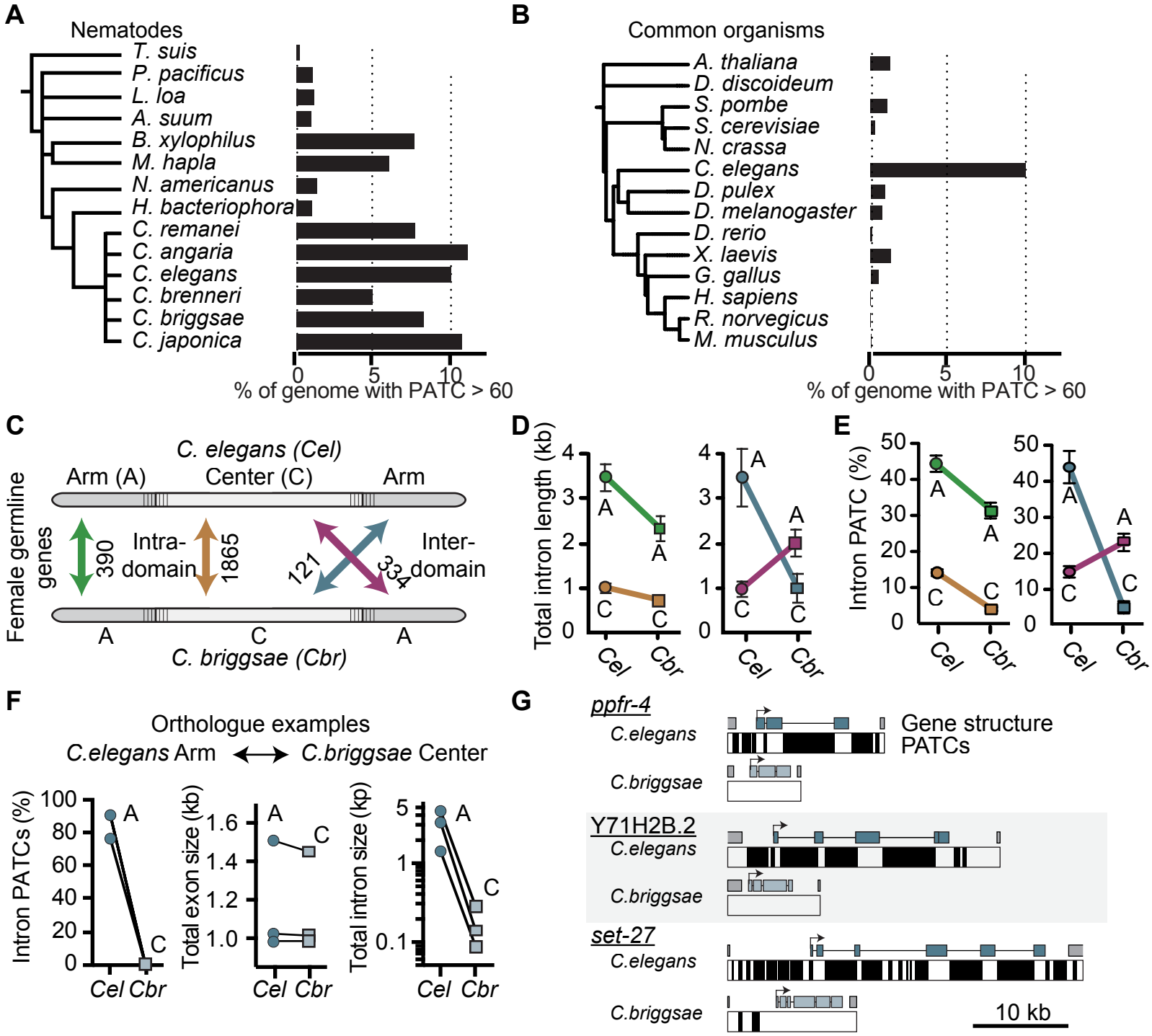
A
Nematodes
T. suis
P. pacificus
L. loa
A. suum
B. xylophilus
M. hapla
N. americanus
H. bacteriophora
C. remanei
C. angaria
C. elegans
C. brenneri
C. briggsae
C. japonica
0
5
10
% of genome with PATC > 60
B
Common organisms
A. thaliana
D. discoideum
S. pombe
S. cerevisiae
N. crassa
C. elegans
D. pulex
D. melanogaster
D. rerio
X. laevis
G. gallus
H. sapiens
R. norvegicus
M. musculus
0
5
10
% of genome with PATC > 60
C
C. elegans (Cel)
Arm (A)
Center (C)
Arm
Female germline genes
390
Intra-domain
1865
121
334
Inter-domain
A
C
A
C. briggsae (Cbr)
D
Total intron length (kb)
Cel
Cbr
E
Intron PATC (%)
Cel
Cbr
F
Orthologue examples
C.elegans Arm
C.briggsae Center
Intron PATCs (%)
Total exon size (kb)
Total intron size (kp)
Cel
Cbr
G
ppfr-4
C.elegans
C.briggsae
Gene structure
PATCs
Y71H2B.2
C.elegans
C.briggsae
set-27
C.elegans
C.briggsae
10 kb