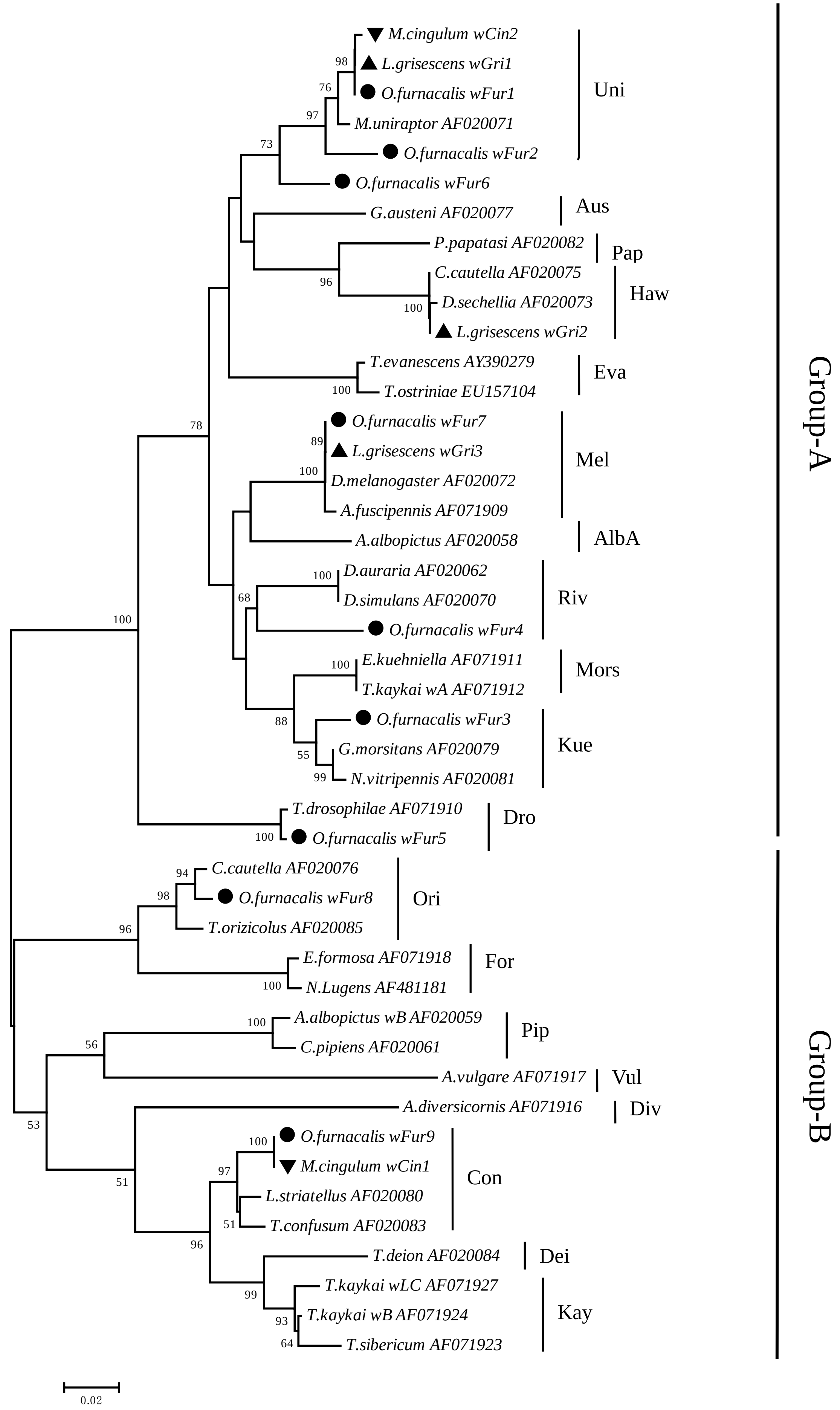
M.cingulum wCin2
L.grisescens wGri1
O.furnacalis wFur1
M.uniraptor AF020071
O.furnacalis wFur2
O.furnacalis wFur6
G.austeni AF020077
P.papatasi AF020082
C.cautella AF020075
D.sechellia AF020073
L.grisescens wGri2
T.evanescens AY390279
T.ostriniae EU157104
O.furnacalis wFur7
L.grisescens wGri3
D.melanogaster AF020072
A.fuscipennis AF071909
A.albopictus AF020058
D.auraria AF020062
D.simulans AF020070
O.furnacalis wFur4
E.kuehniella AF071911
T.kaykai wA AF071912
O.furnacalis wFur3
G.morsitans AF020079
N.vitripennis AF020081
T.drosophilae AF071910
O.furnacalis wFur5
C.cautella AF020076
O.furnacalis wFur8
T.orizicolus AF020085
E.formosa AF071918
N.Lugens AF481181
A.albopictus wB AF020059
C.pipiens AF020061
A.vulgare AF071917
A.diversicornis AF071916
O.furnacalis wFur9
M.cingulum wCin1
L.striatellus AF020080
T.confusum AF020083
T.deion AF020084
T.kaykai wLC AF071927
T.kaykai wB AF071924
T.sibericum AF071923
Uni
Aus
Pap
Haw
Eva
Mel
AlbA
Riv
Mors
Kue
Dro
Ori
For
Pip
Vul
Div
Con
Dei
Kay
Group-A
Group-B
98
76
97
73
96
100
100
78
89
100
100
68
100
88
55
99
100
100
94
98
96
100
100
56
53
100
97
51
51
96
99
93
64
0.02

Fig. S1. Phylogenetic tree based on *wsp* gene sequence data generated by minimum evolution algorithm under nucleotide maximum composite likelihood model in MEGA 4.1. Each *wsp* sequence is labeled with the host species from which the *Wolbachia* strain was isolated (GenBank Accession No. is indicated in parentheses). Bootstrap values detected above 50% for 1000 replicates are shown before the branch. Size bar reflects phylogenetic divergence in genetic distance units. The *wsp* sequences isolated from *O. furnacalis*, *M. cingulum* and *L. grisescens* were labeled with "●", "▼" and "▲" respectively.