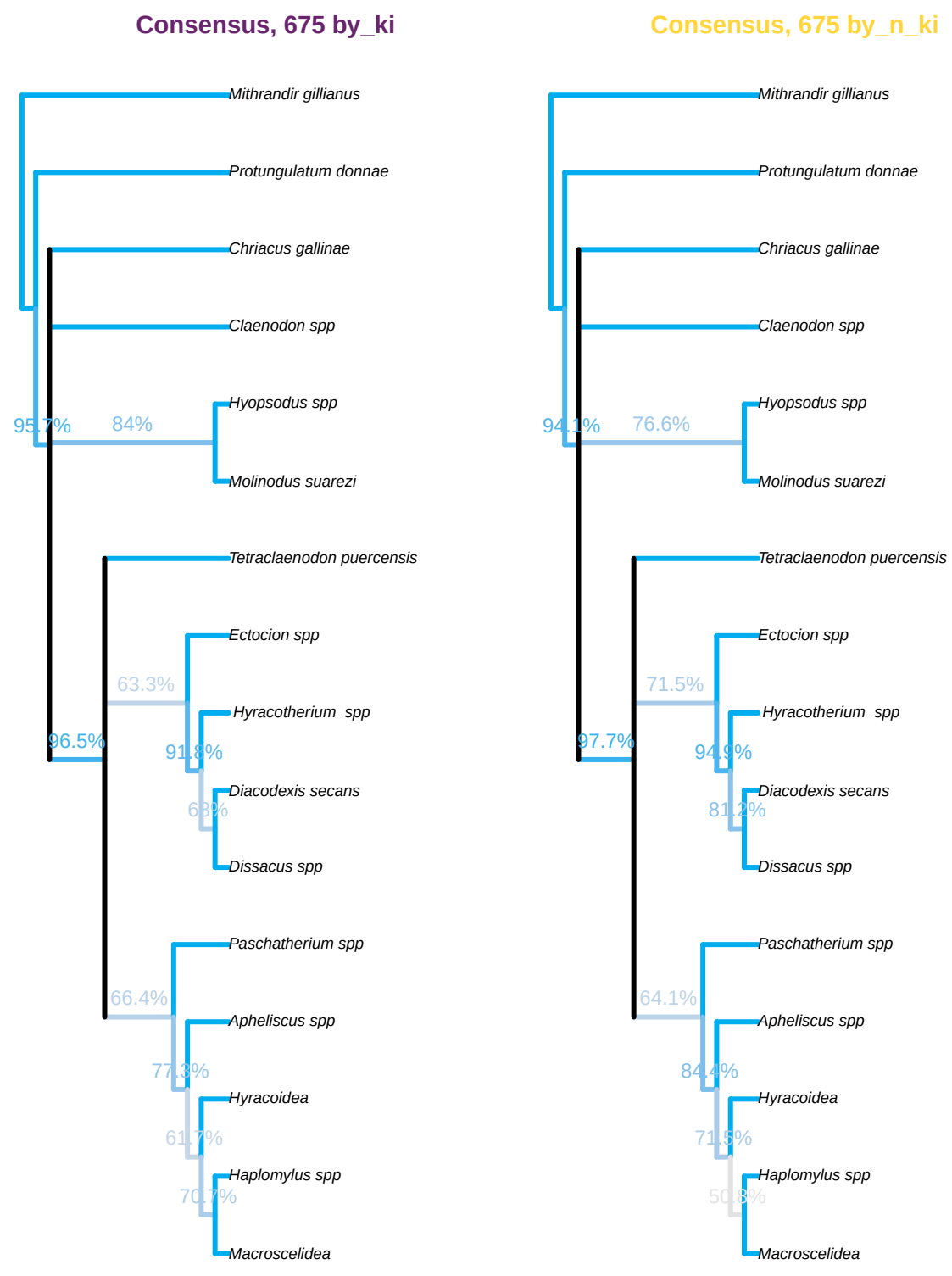
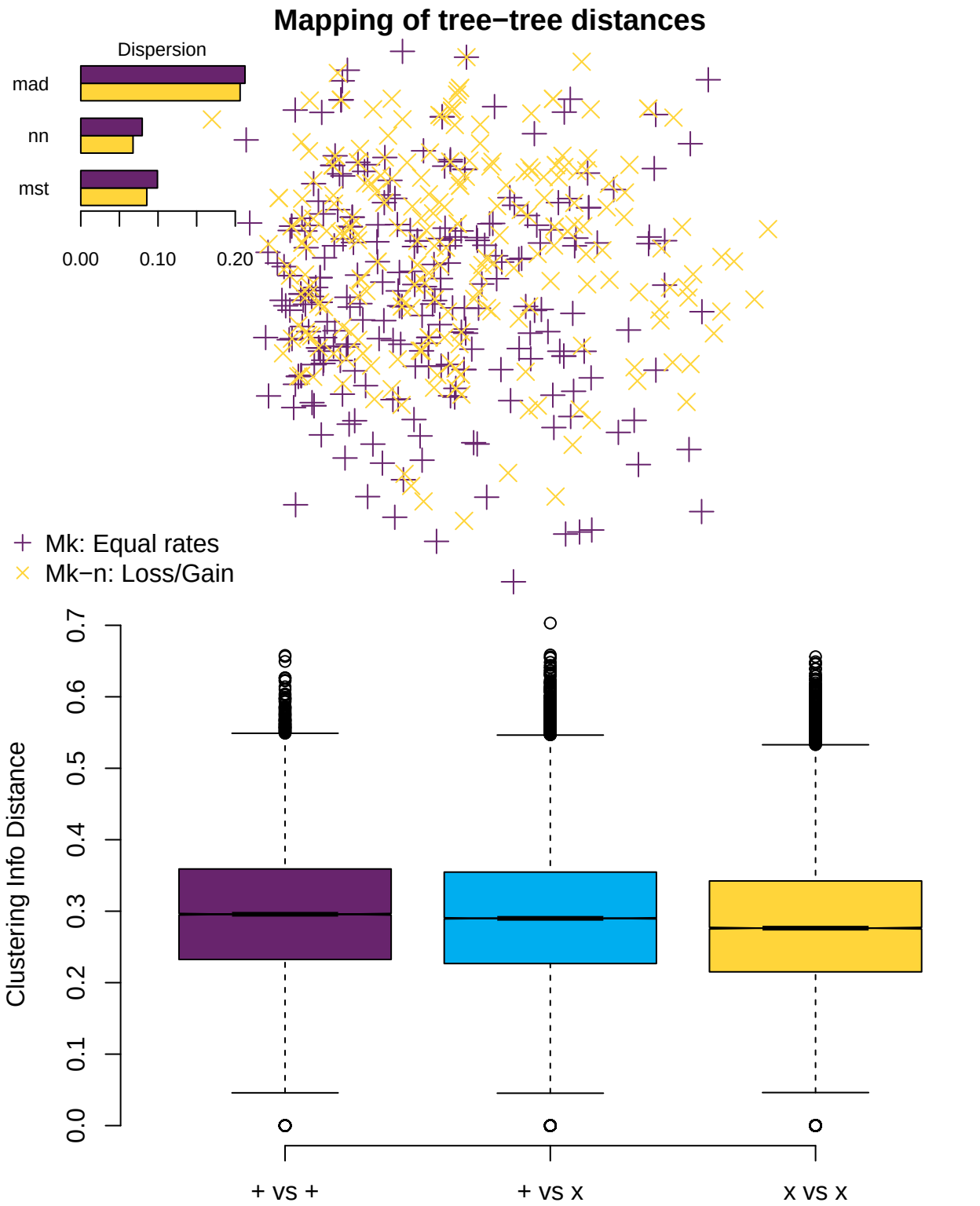

Consensus, 675 by_ki
Mithrandir gillianus
Protungulatum donnae
Chriacus gallinae
Claenodon spp
95.7%
84%
Hyopsodus spp
Molinodus suarezi
Tetraclaenodon puercensis
Ectocion spp
63.3%
Hyracotherium spp
96.5%
91.8%
Diacodexis secans
63%
Dissacus spp
Paschatherium spp
66.4%
Apheliscus spp
77.3%
Hyracoidea
61.7%
Haplomylus spp
70.7%
Macroscelidea
Consensus, 675 by_n_ki
Mithrandir gillianus
Protungulatum donnae
Chriacus gallinae
Claenodon spp
94.1%
76.6%
Hyopsodus spp
Molinodus suarezi
Tetraclaenodon puercensis
Ectocion spp
71.5%
Hyracotherium spp
97.7%
94.9%
Diacodexis secans
81.2%
Dissacus spp
Paschatherium spp
64.1%
Apheliscus spp
84.4%
Hyracoidea
71.5%
Haplomylus spp
50.8%
Macroscelidea


Mapping of tree−tree distances
Dispersion
mad
nn
mst
0.00
0.10
0.20
Mk: Equal rates
Mk−n: Loss/Gain
Clustering Info Distance
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
+ vs +
+ vs x
x vs x

Silhouette plot
n = 512
2 clusters C_j
j : n_j | $ave_{i \in Cj}$ s_i
1 : 256 | −0.01
2 : 256 | 0.04
0.0
0.2
0.4
0.6
0.8
1.0
Silhouette width s_i
Average silhouette width : 0.01

	Burnin	PSRF	ESS	FrechESS	mdPsESS	steppingStn	pathSmpl
Mk: Equal rates	0.1	1.00074	566.306	455.299	422.791	−613.729	−613.395
Mk−n: Loss/Gain	0.1	1.00157	268.727	297.689	325.901	−610.492	−610.373