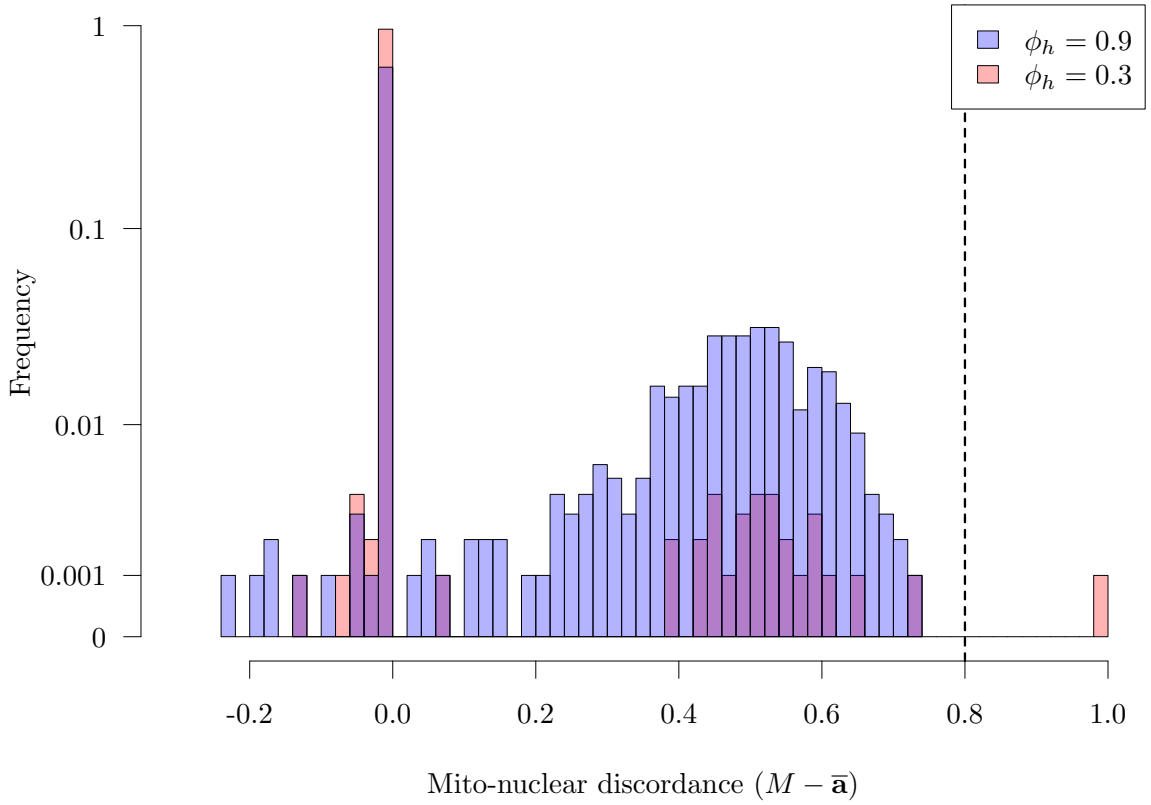
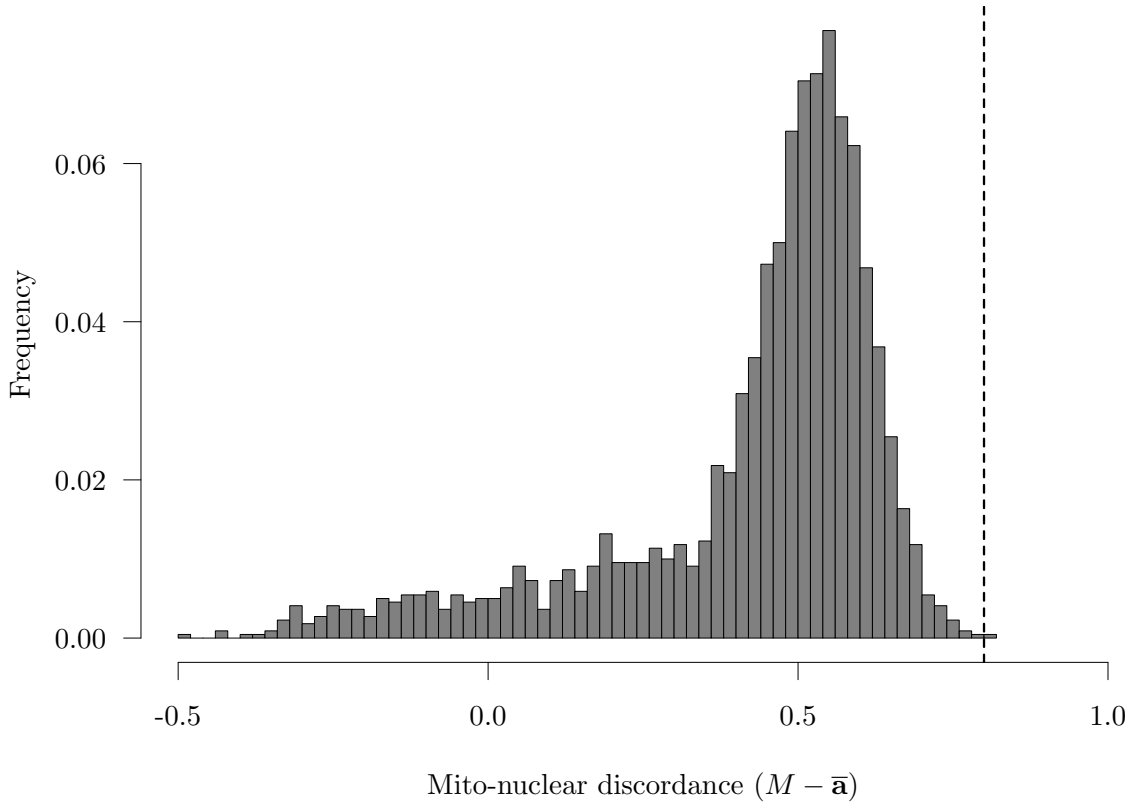
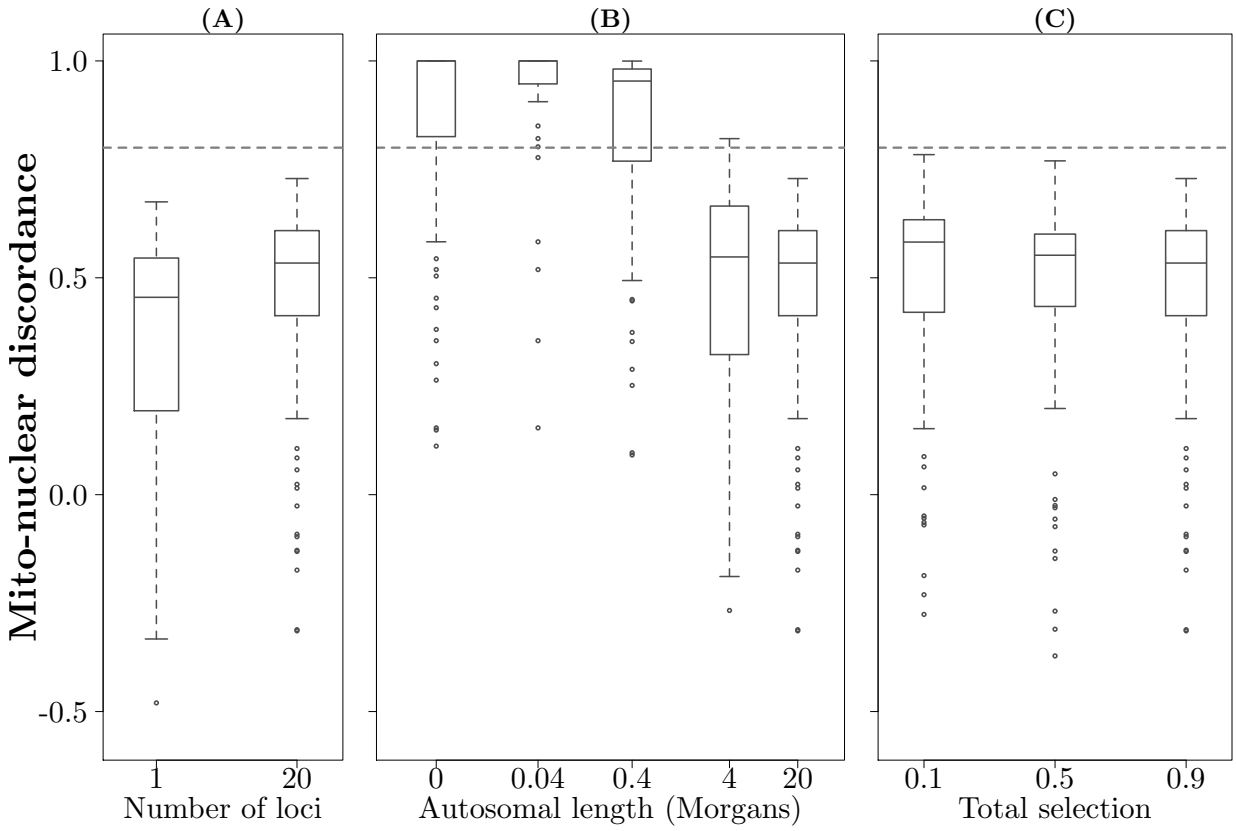
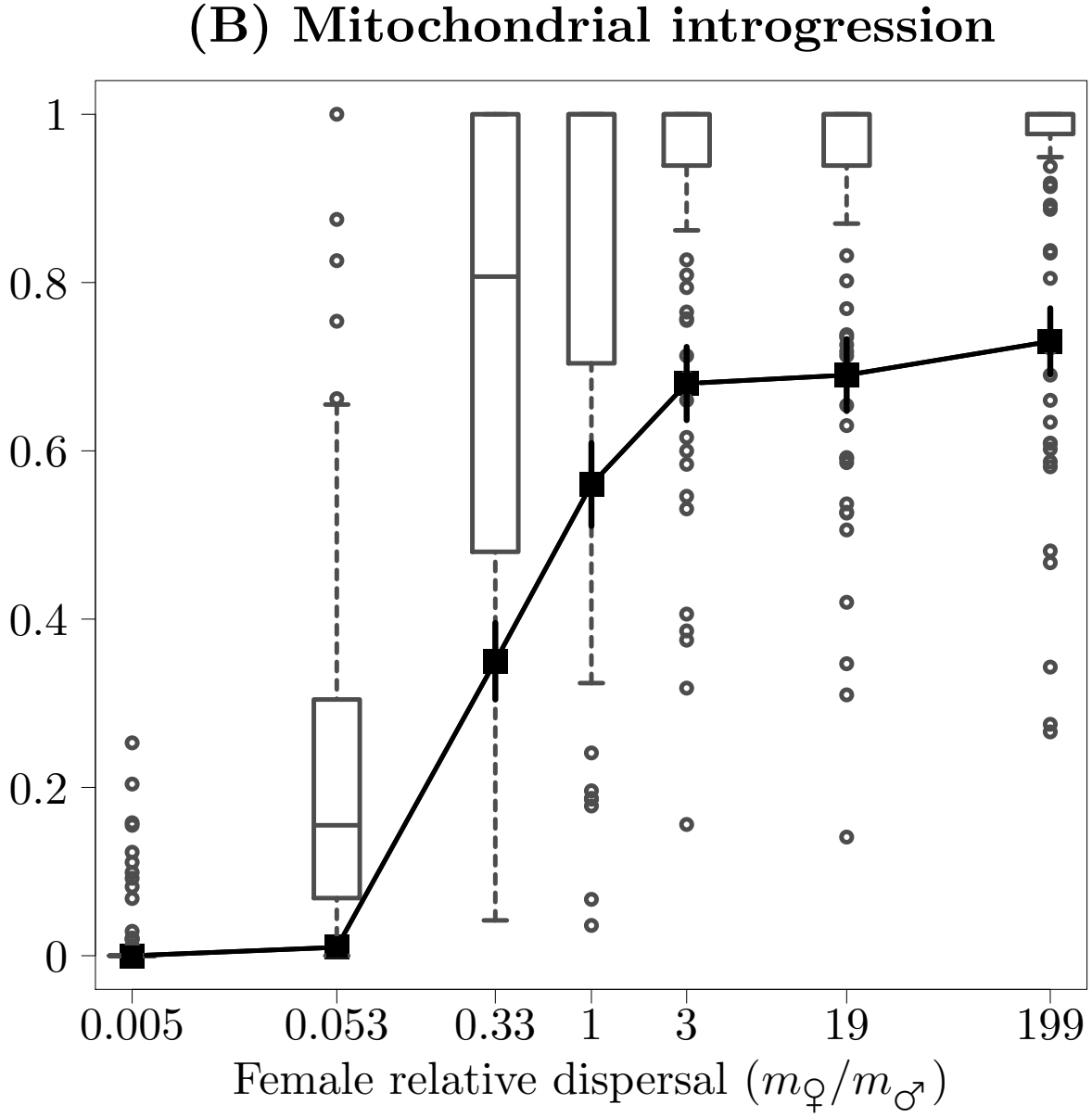
```
## Warning in RecdistriMt$DistriMtMax[(RecdistriMt$Simul == "wRmAmHMt0" | RecdistriMt$Simul
== :  le nombre d'objets  remplacer n'est pas multiple de la taille du remplacement

##  [1] 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 0.795 1.000 0.802
## [12] 1.000 1.000 1.000 1.000 0.583 1.000 0.947 0.821 1.000 0.519 0.355
## [23] 0.934 0.850 1.000 1.000 1.000 1.000 1.000 0.906 1.000 1.000 0.154
## [34] 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000
##   [1] 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 0.795 1.000 0.802
##  [12] 1.000 1.000 1.000 1.000 0.583 1.000 0.947 0.821 1.000 0.519 0.355
##  [23] 0.934 0.850 1.000 1.000 1.000 1.000 1.000 0.906 1.000 1.000 0.154
##  [34] 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 0.786 0.711 0.302
##  [45] 1.000 0.989 0.149 0.544 1.000 1.000 0.453 0.990 1.000 0.908 0.381
##  [56] 1.000 1.000 0.112 0.621 1.000 0.605 0.770 1.000 1.000 1.000 1.000
##  [67] 1.000 1.000 1.000 1.000 0.993 0.264 1.000 1.000 0.864 1.000 1.000
##  [78] 1.000 1.000 0.830 1.000 1.000 0.990 0.734 0.619 1.000 1.000 1.000
##  [89] 0.971 0.431 0.950 0.743 0.760 0.504 1.000 1.000 1.000 1.000 1.000
## [100] 1.000
## [1] 0.78367
## [1] 0.81763
## [1] 0.76742
## [1] 0.3268576
## [1] 0.2793721
## [1] 0.3183194
```

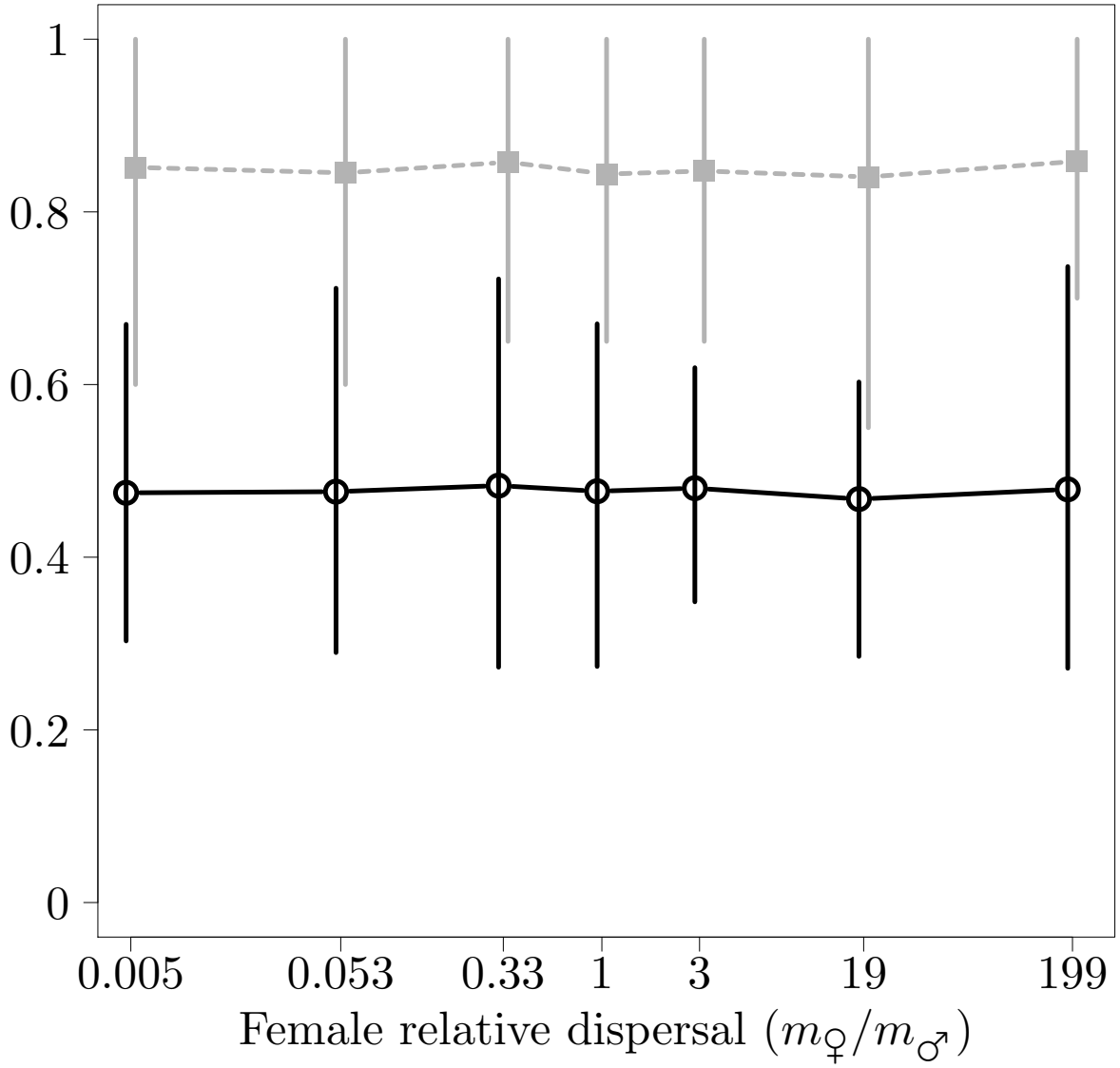


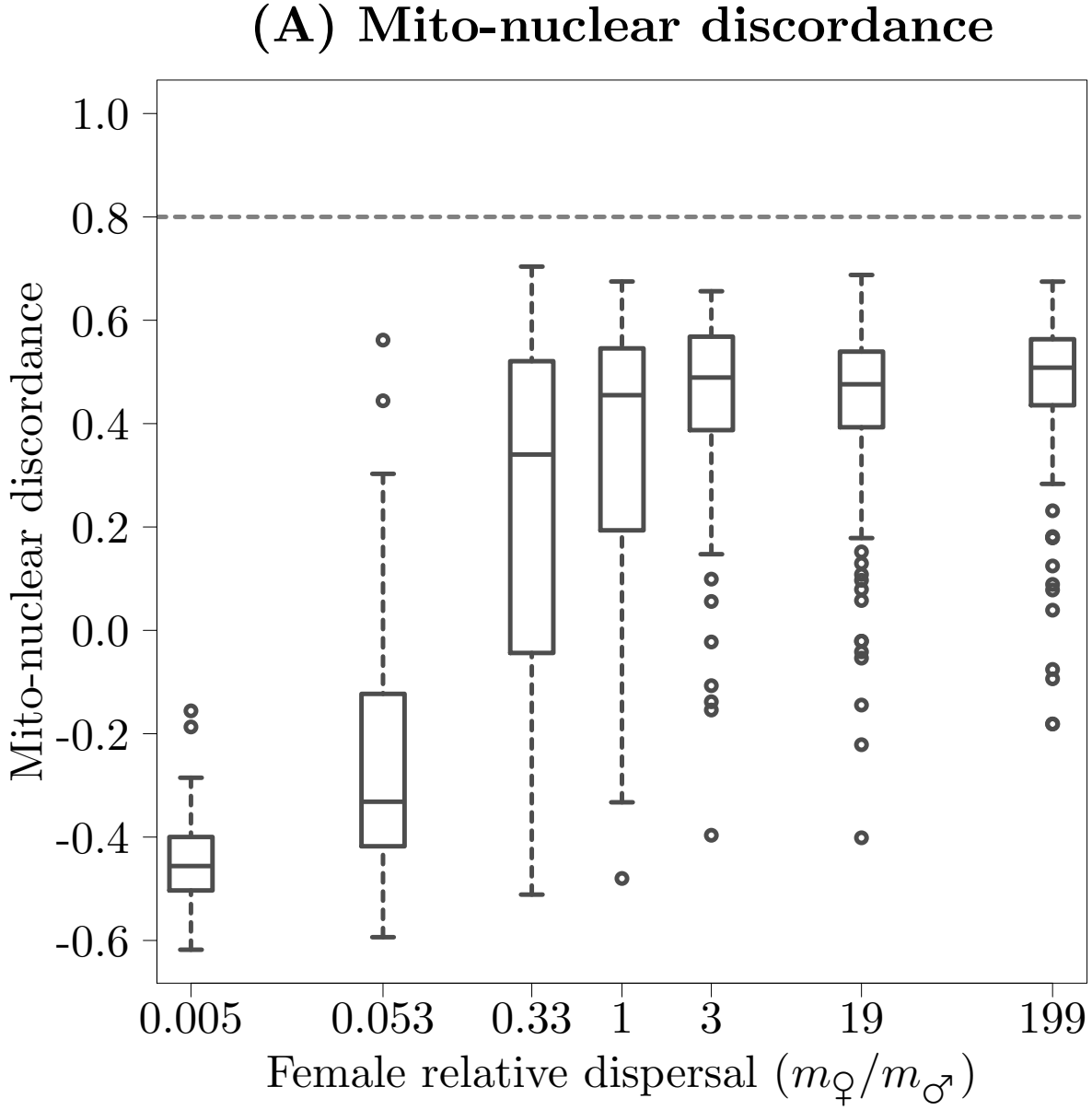


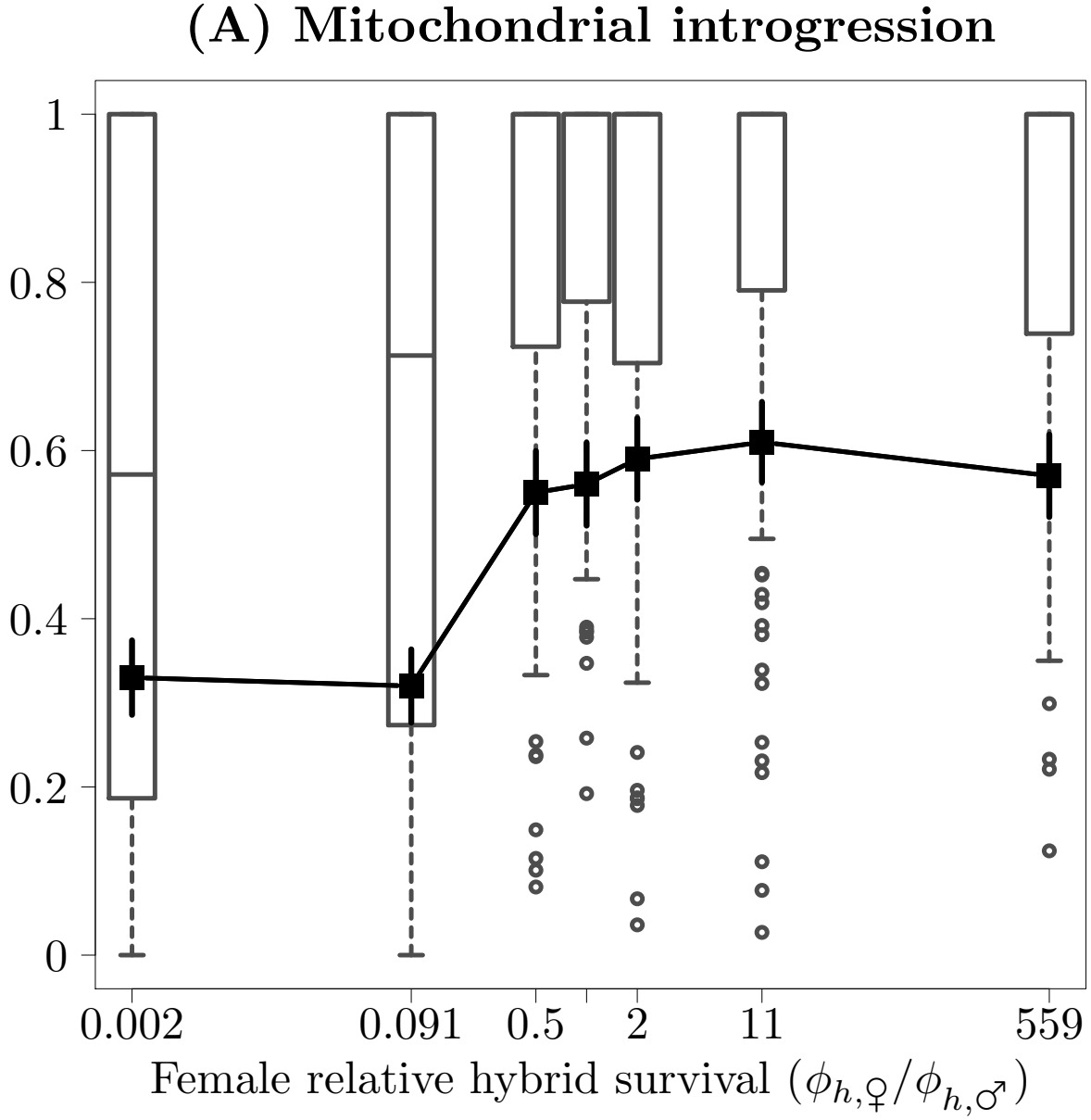
All nuclear selection together:

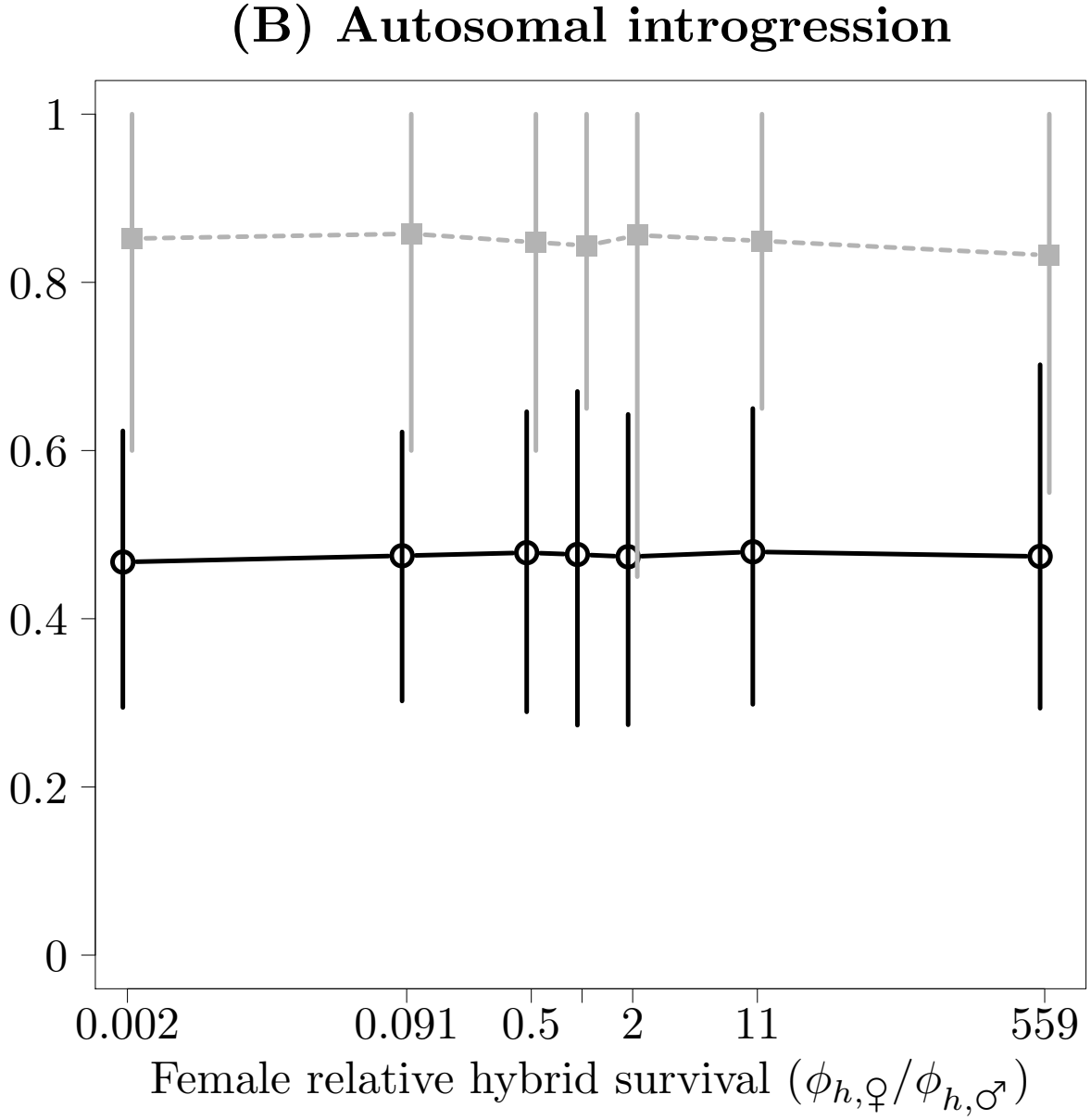

(A)
(B)
(C)
Mito-nuclear discordance
1.0
0.5
0.0
-0.5
1
20
Number of loci
0
0.04
0.4
4
20
Autosomal length (Morgans)
0.1
0.5
0.9
Total selection

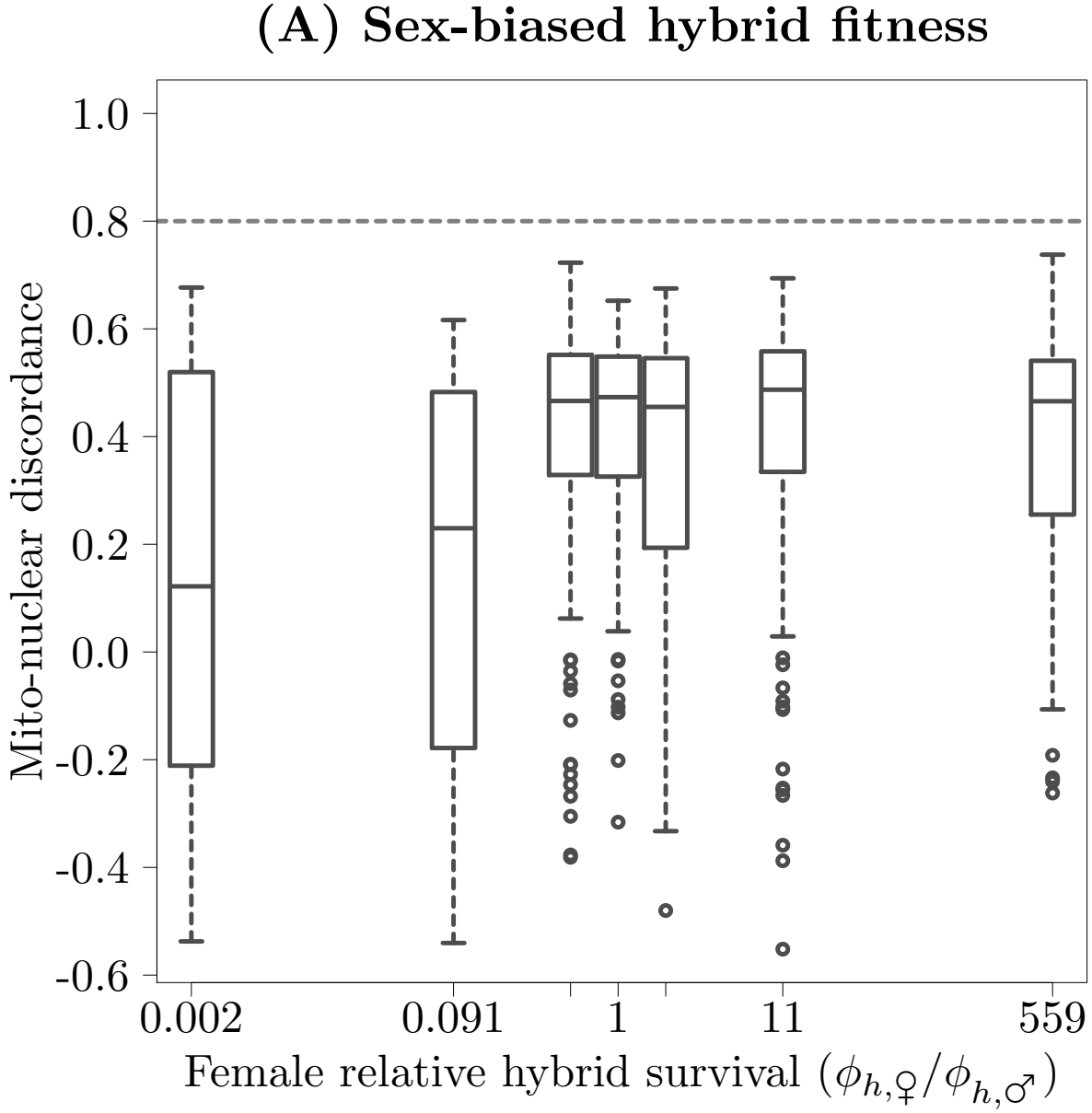

(B) Mitochondrial introgression
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

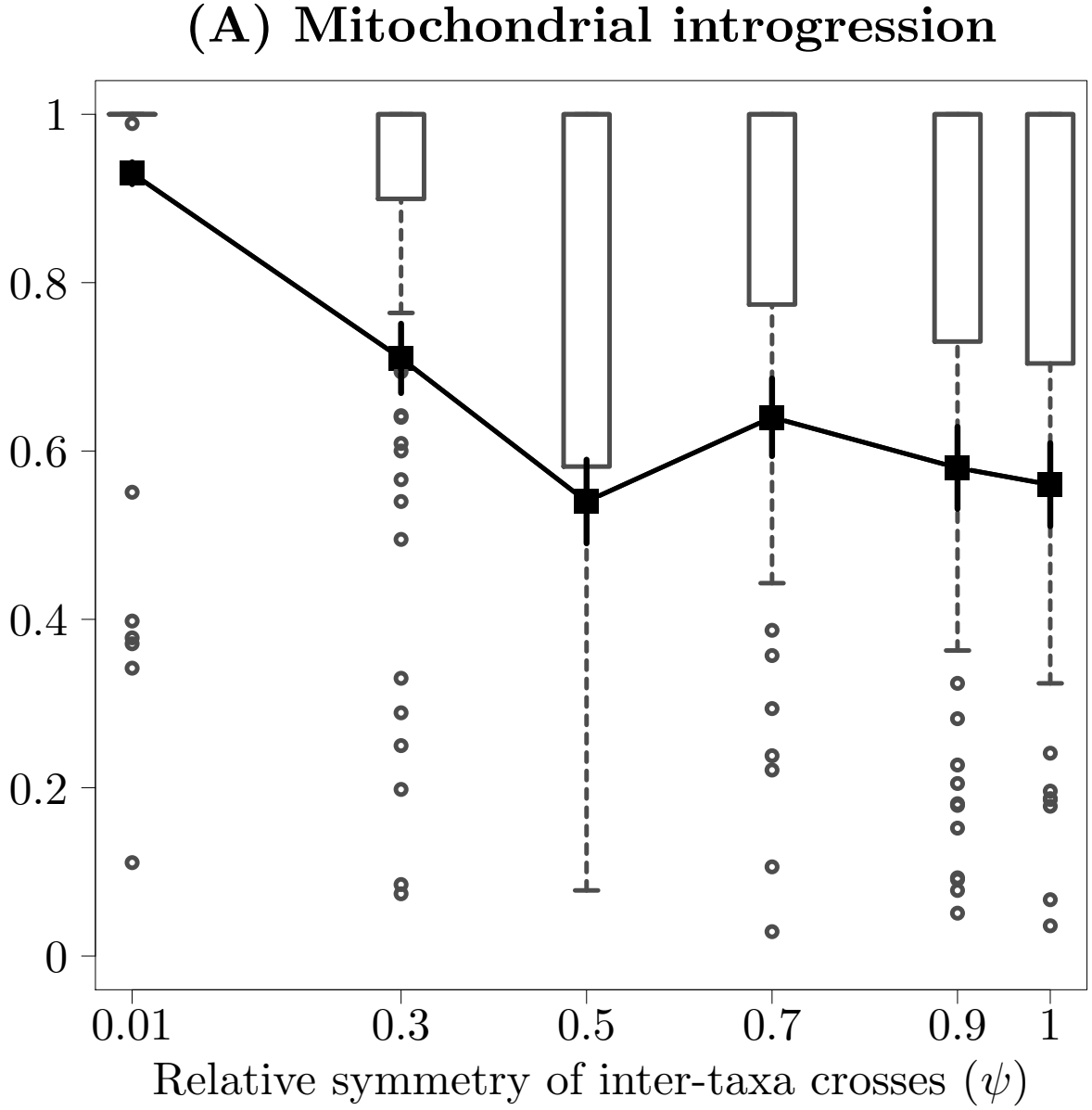

(C) Autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

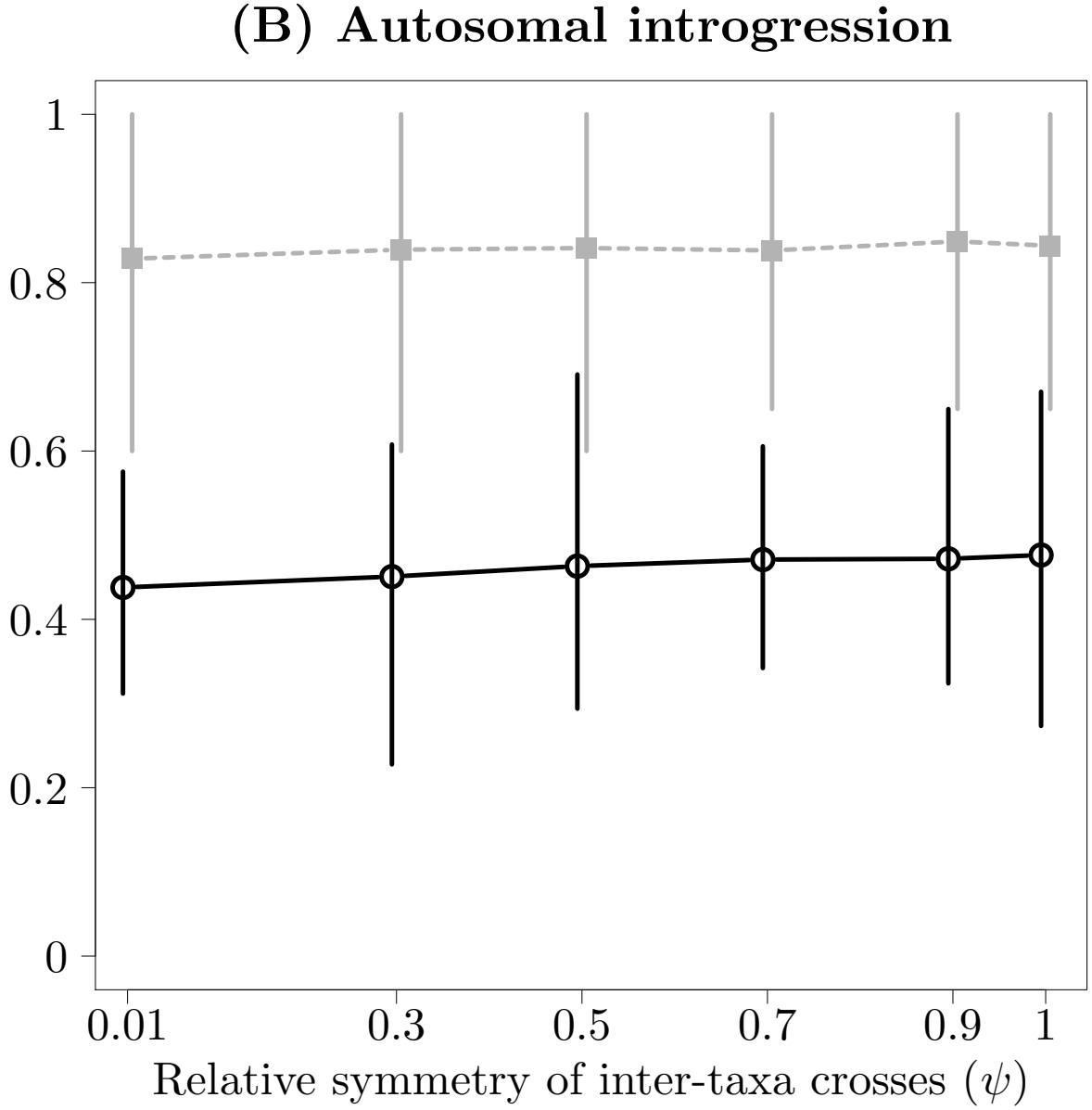

(A) Mito-nuclear discordance
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

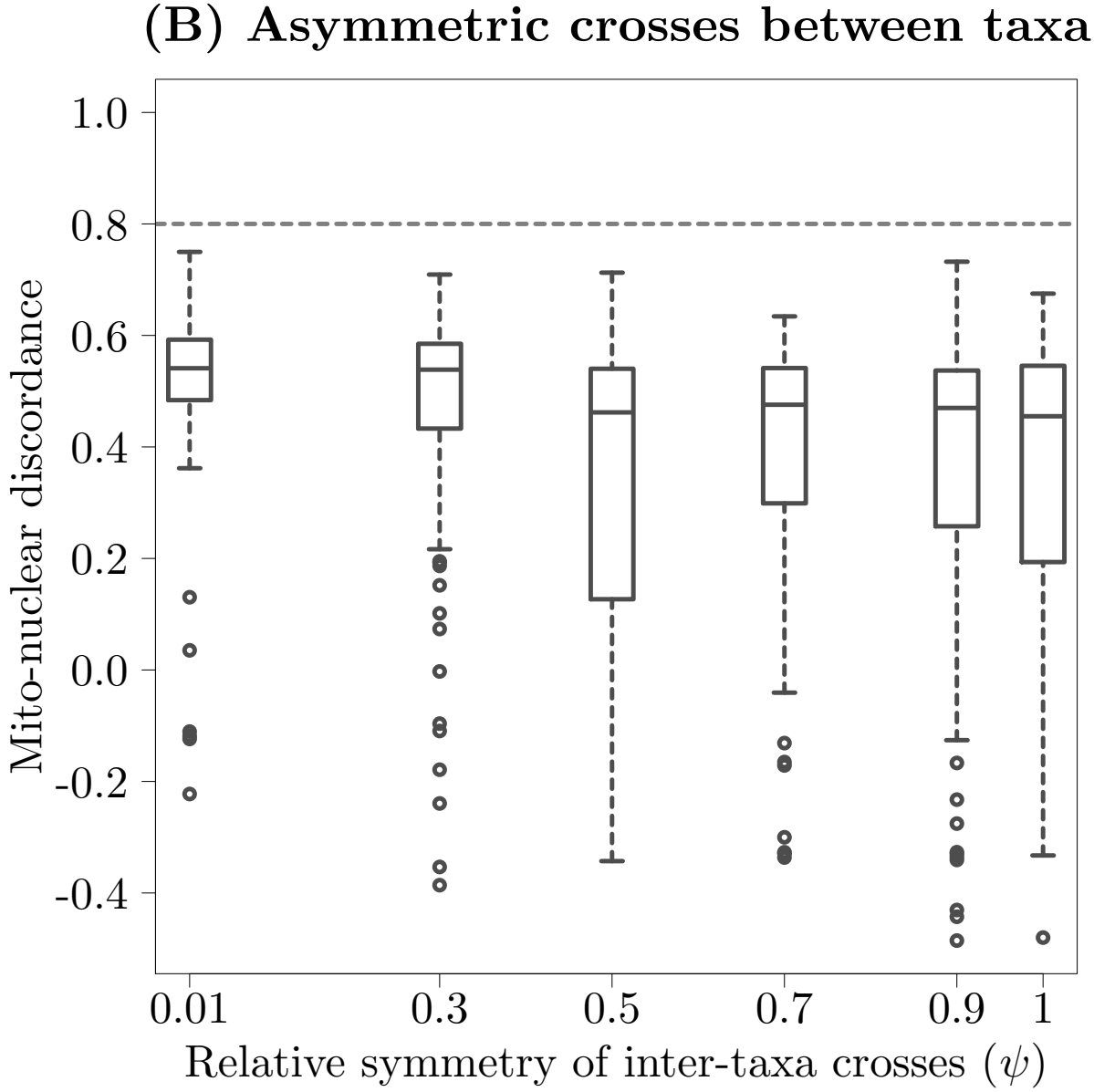

(A) Mitochondrial introgression
1
0.8
0.6
0.4
0.2
0
0.002
0.091
0.5
2
11
559
Female relative hybrid survival ($\phi_{h,♀}/\phi_{h,♂}$)


(B) Autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.002
0.091
0.5
2
11
559
Female relative hybrid survival ($\phi_{h,♀}/\phi_{h,♂}$)

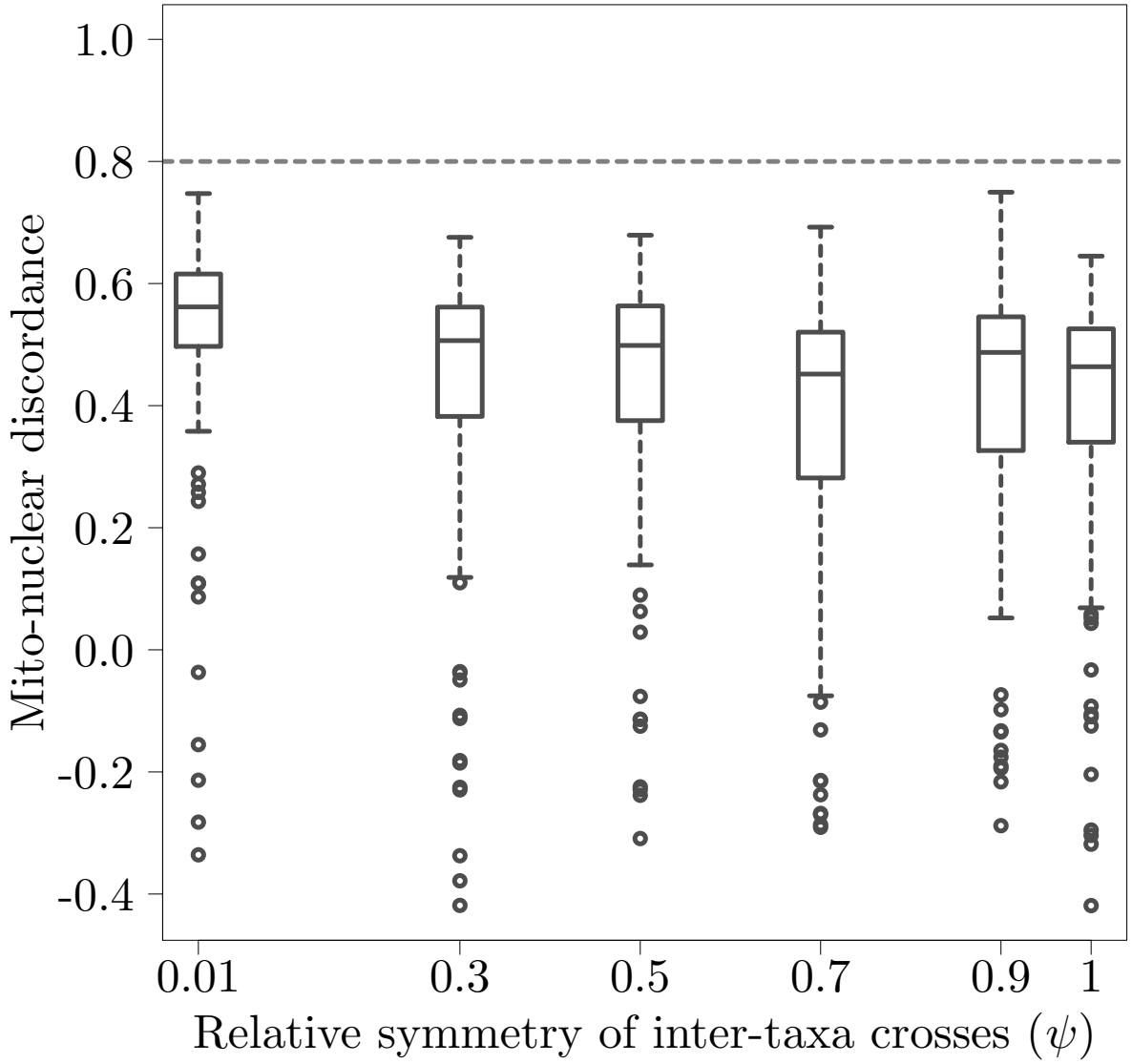

(A) Sex-biased hybrid fitness
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
0.002
0.091
1
11
559
Female relative hybrid survival ($\phi_{h,♀}/\phi_{h,♂}$)

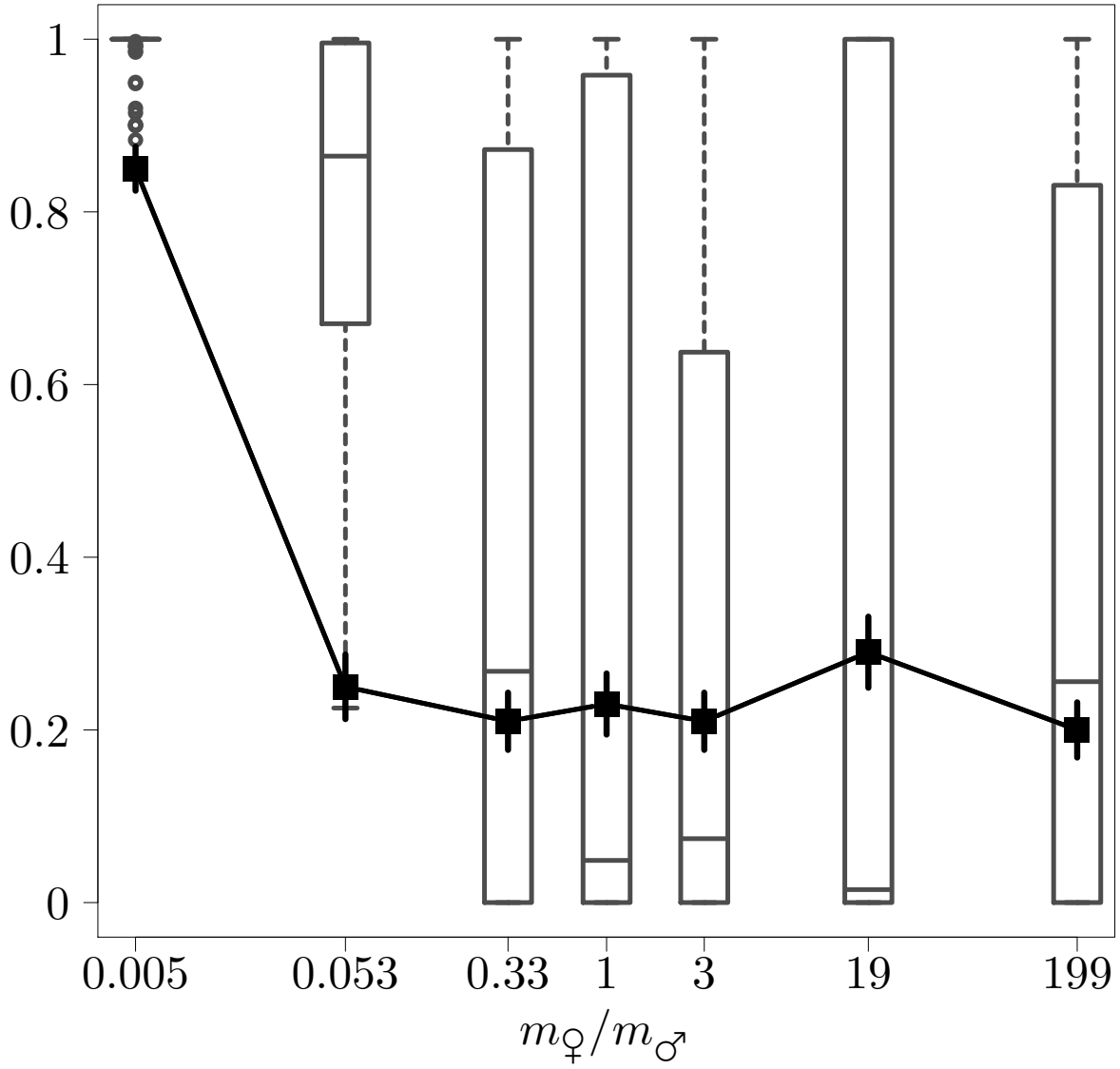

(A) Mitochondrial introgression
1
0.8
0.6
0.4
0.2
0
0.01
0.3
0.5
0.7
0.9
1
Relative symmetry of inter-taxa crosses (ψ)

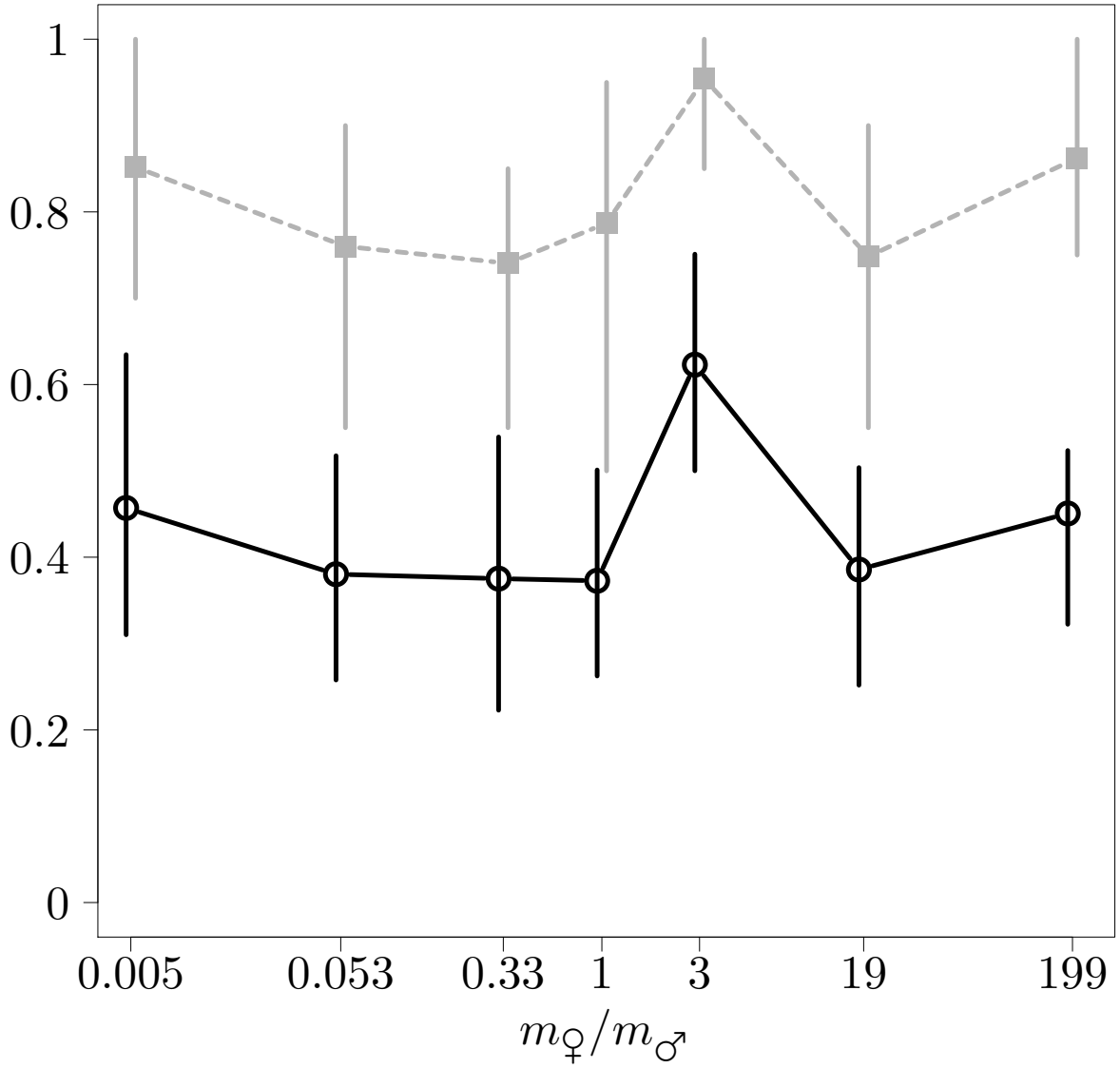

(B) Autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.01
0.3
0.5
0.7
0.9
1
Relative symmetry of inter-taxa crosses (ψ)

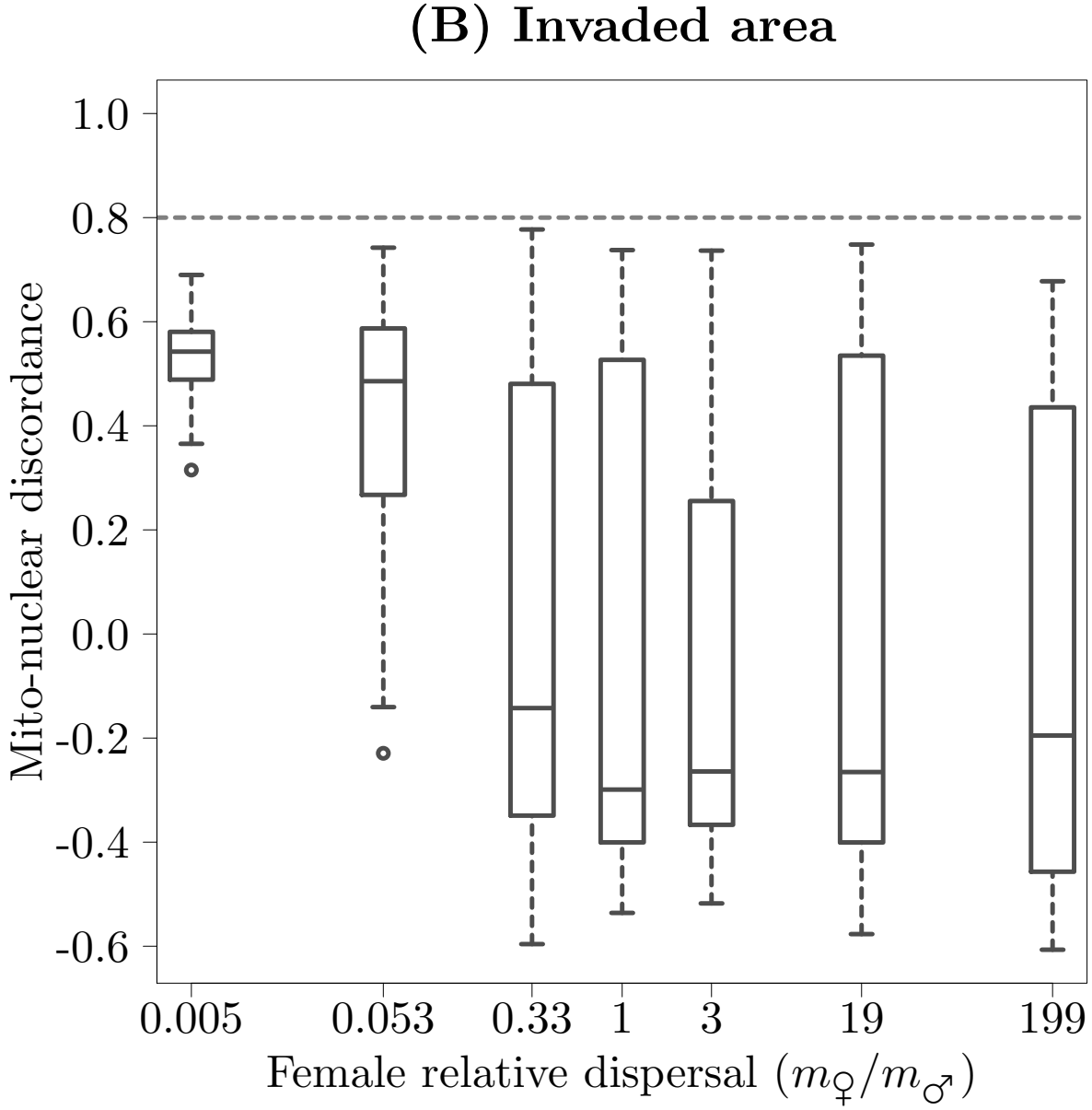

(B) Asymmetric crosses between taxa
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
0.01
0.3
0.5
0.7
0.9
1
Relative symmetry of inter-taxa crosses (ψ)

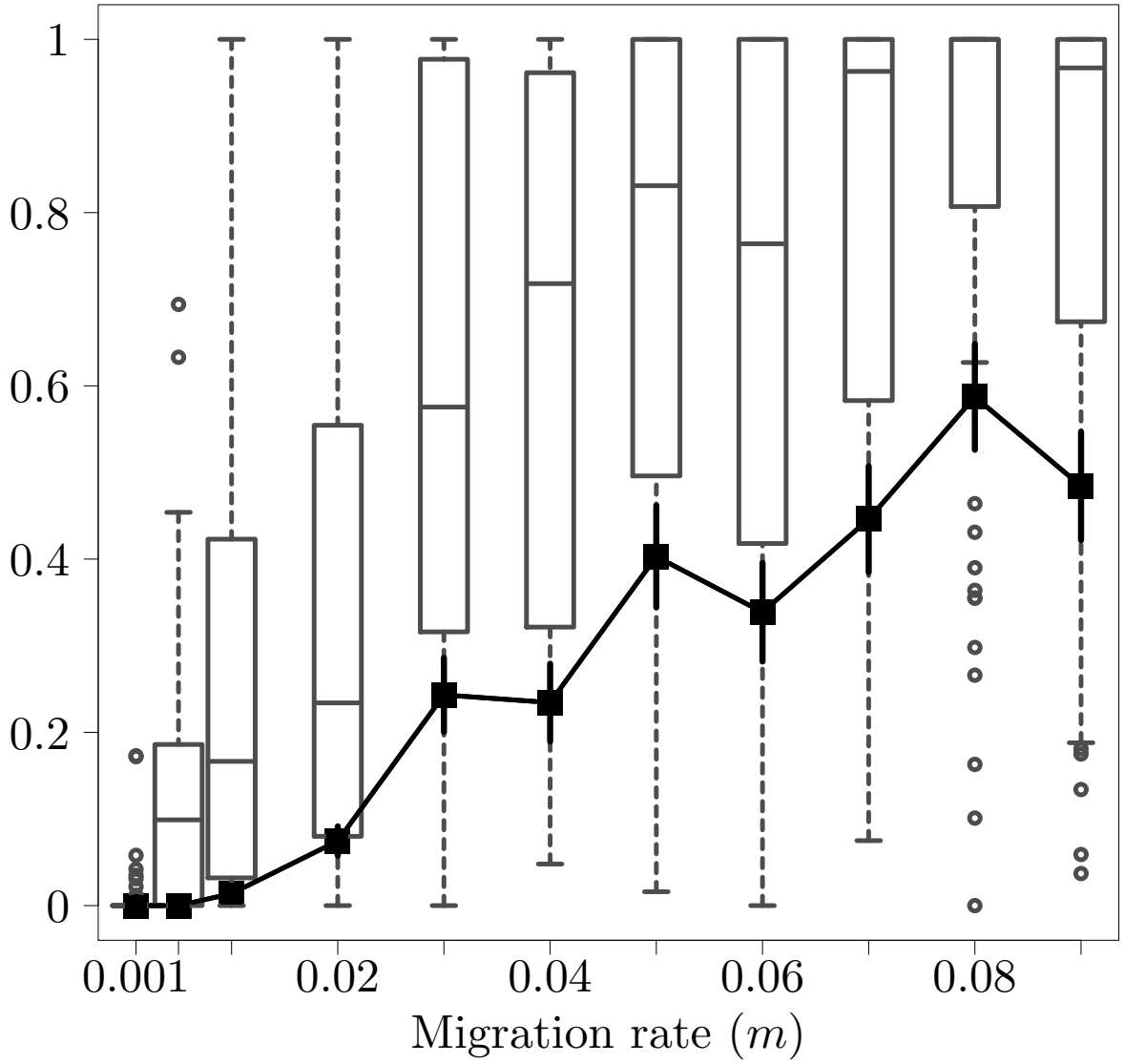
nmetric crosses between taxa (20 loci for mat

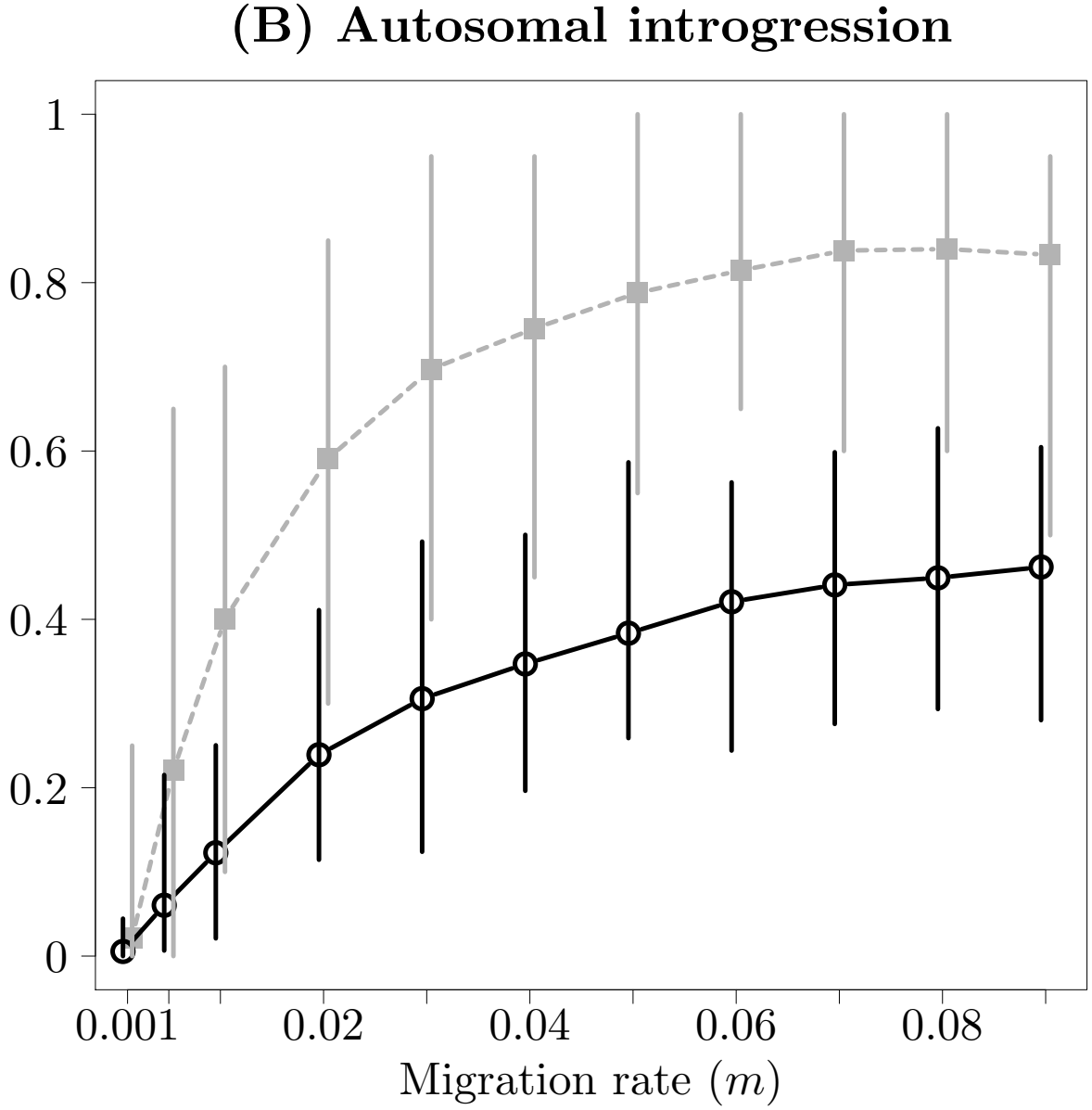


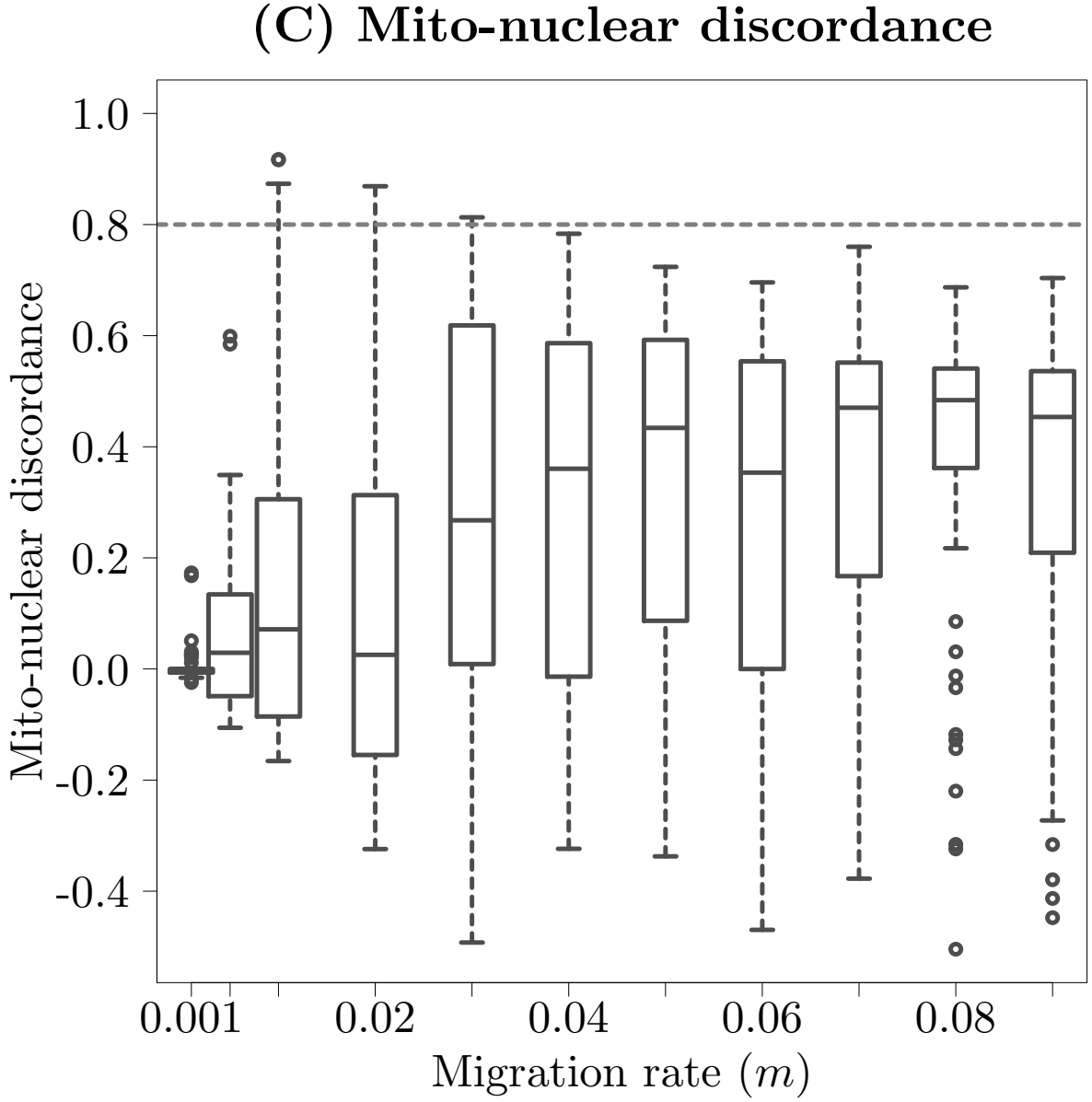

1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
$m_♀/m_♂$

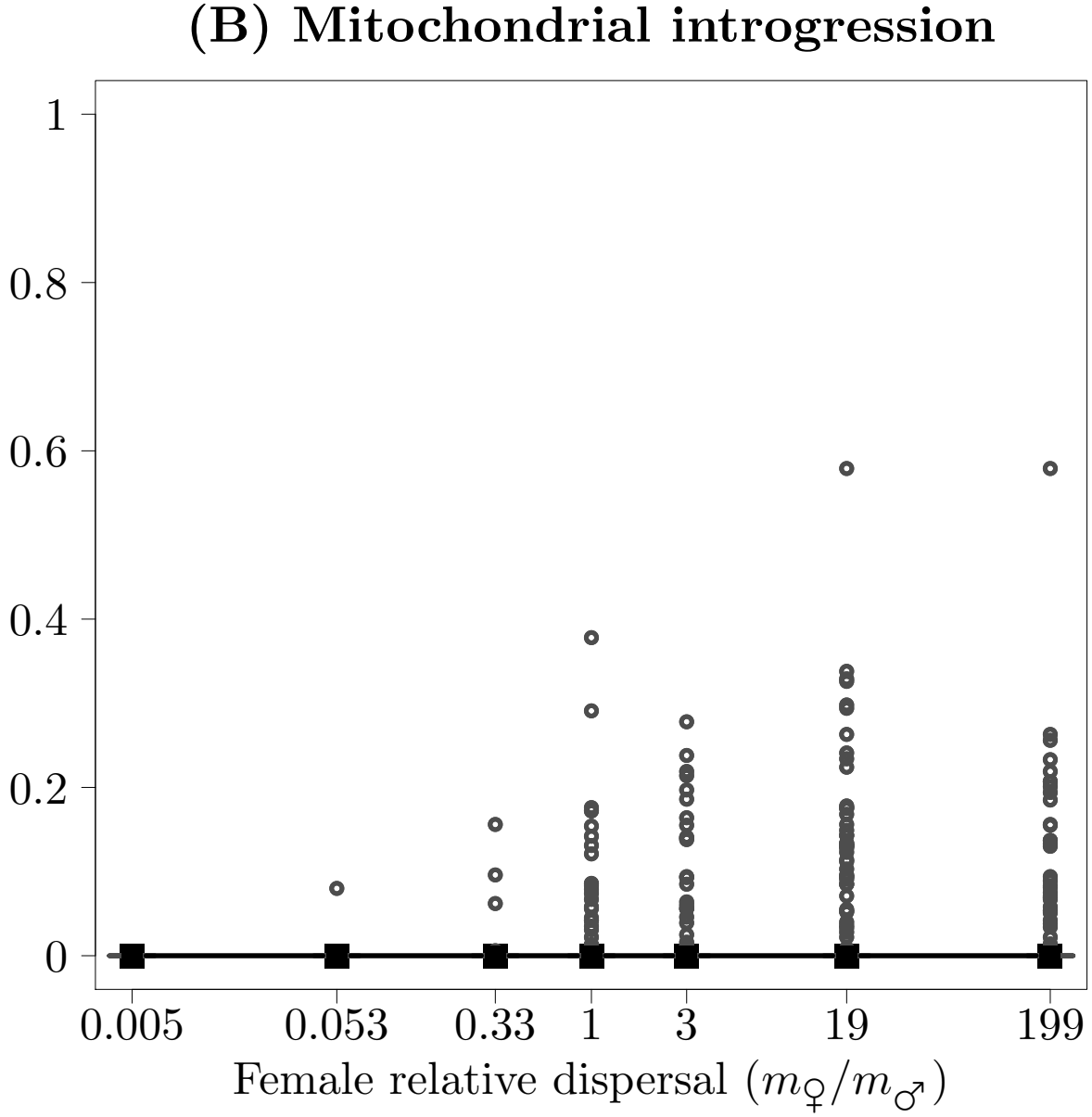

1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
$m_♀/m_♂$

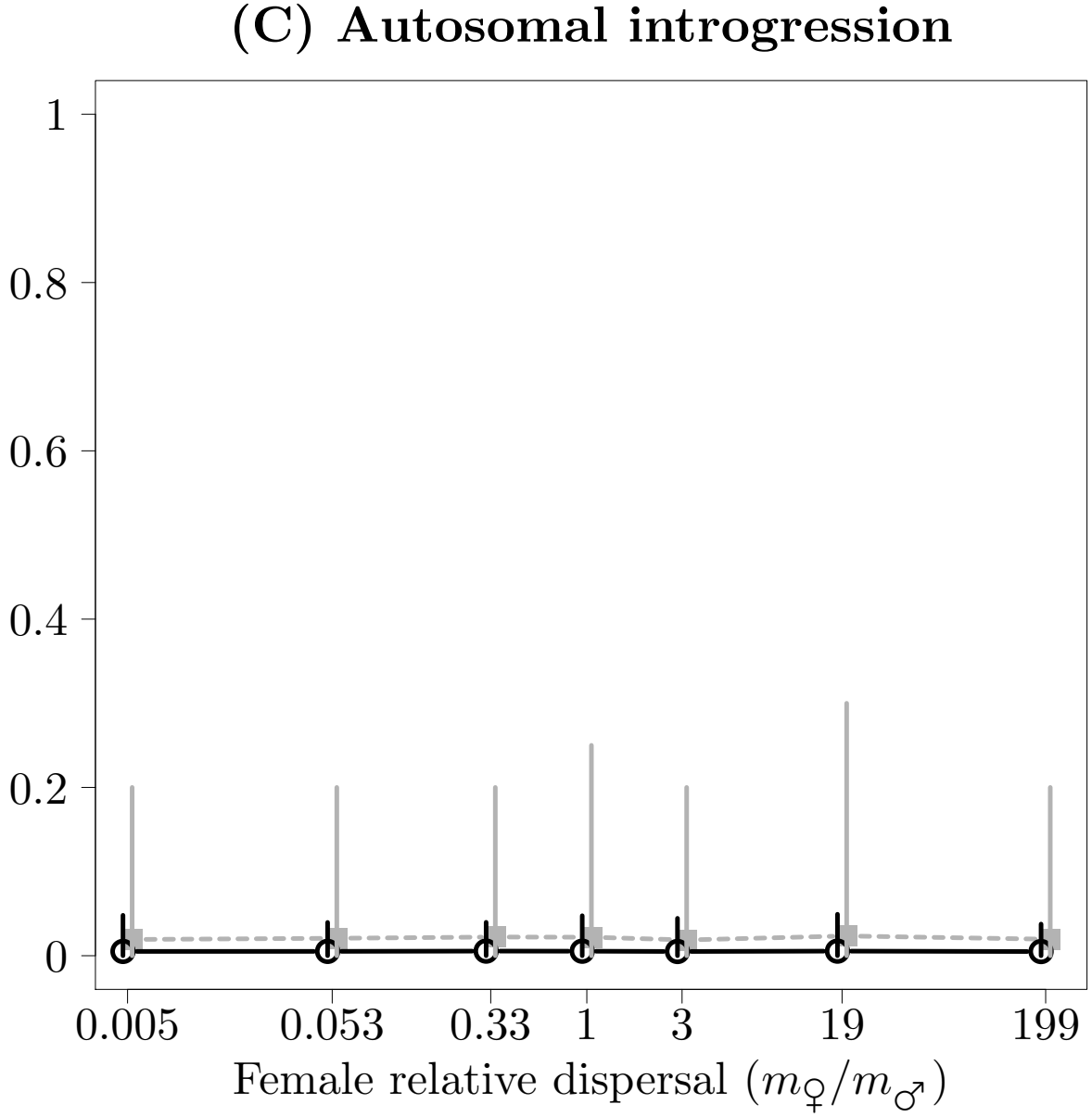

(B) Invaded area
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

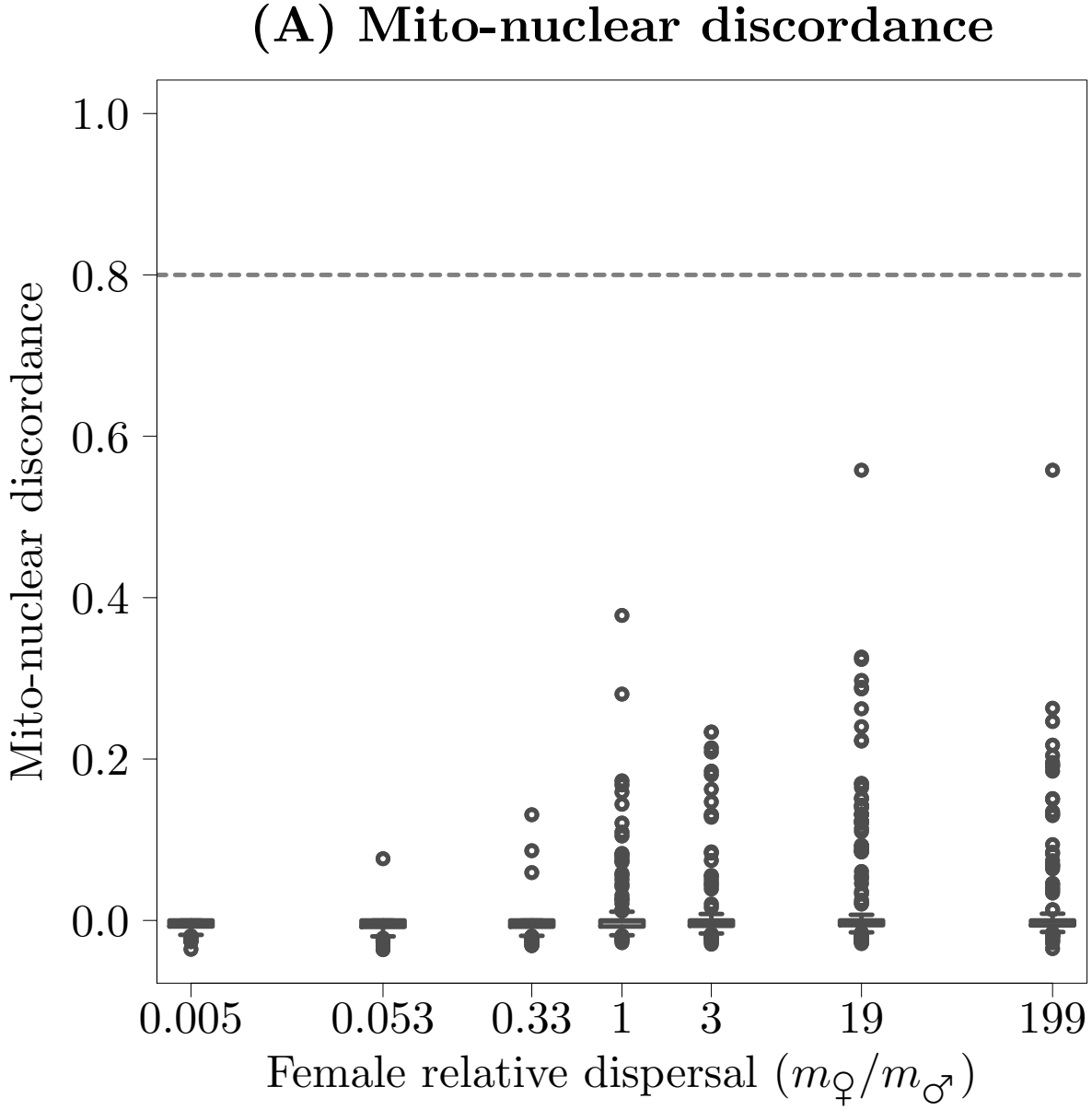

(A) Mitochondrial introgression
1
0.8
0.6
0.4
0.2
0
0.001
0.02
0.04
0.06
0.08
Migration rate (m)

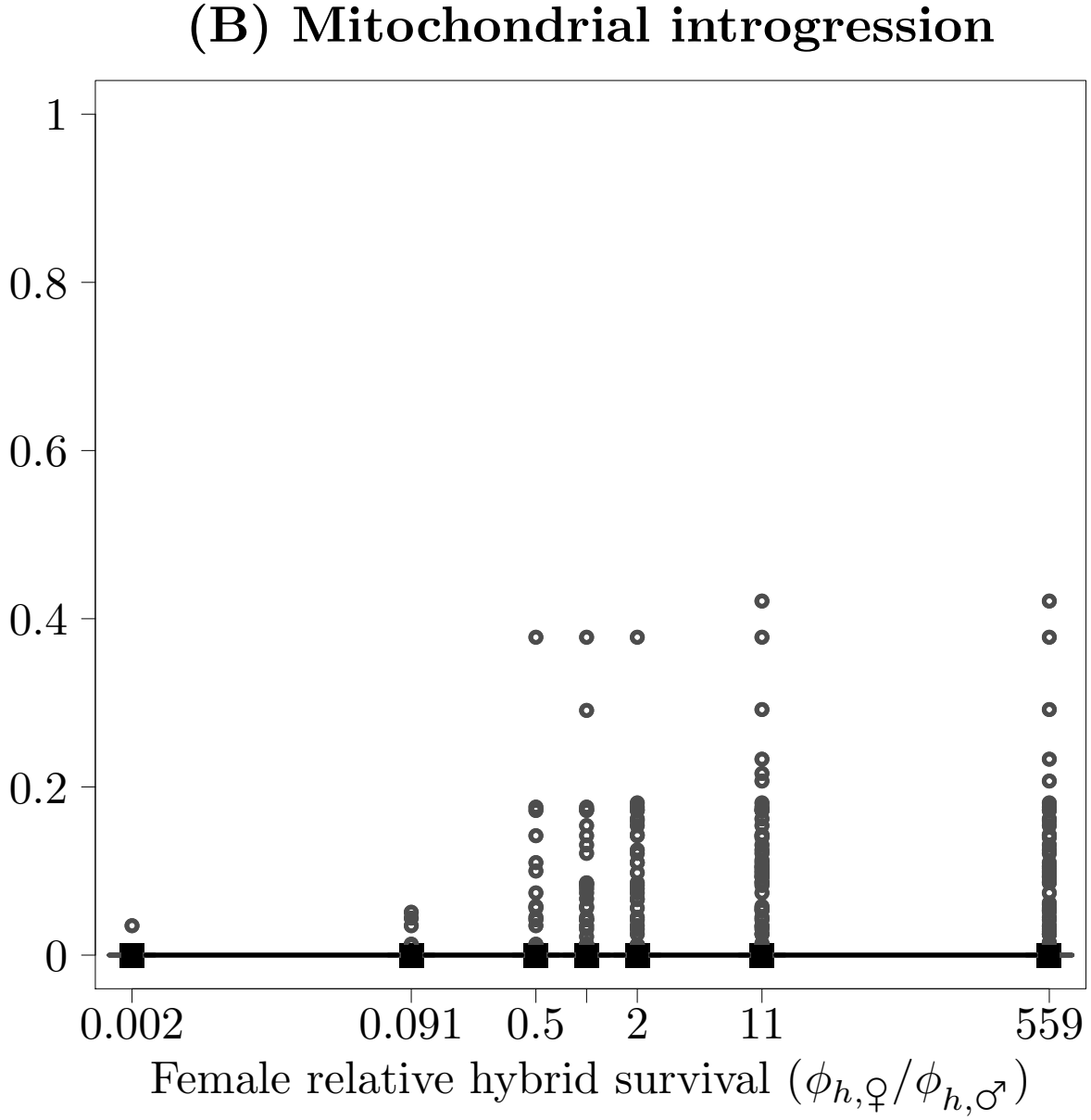

(B) Autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.001
0.02
0.04
0.06
0.08
Migration rate (m)

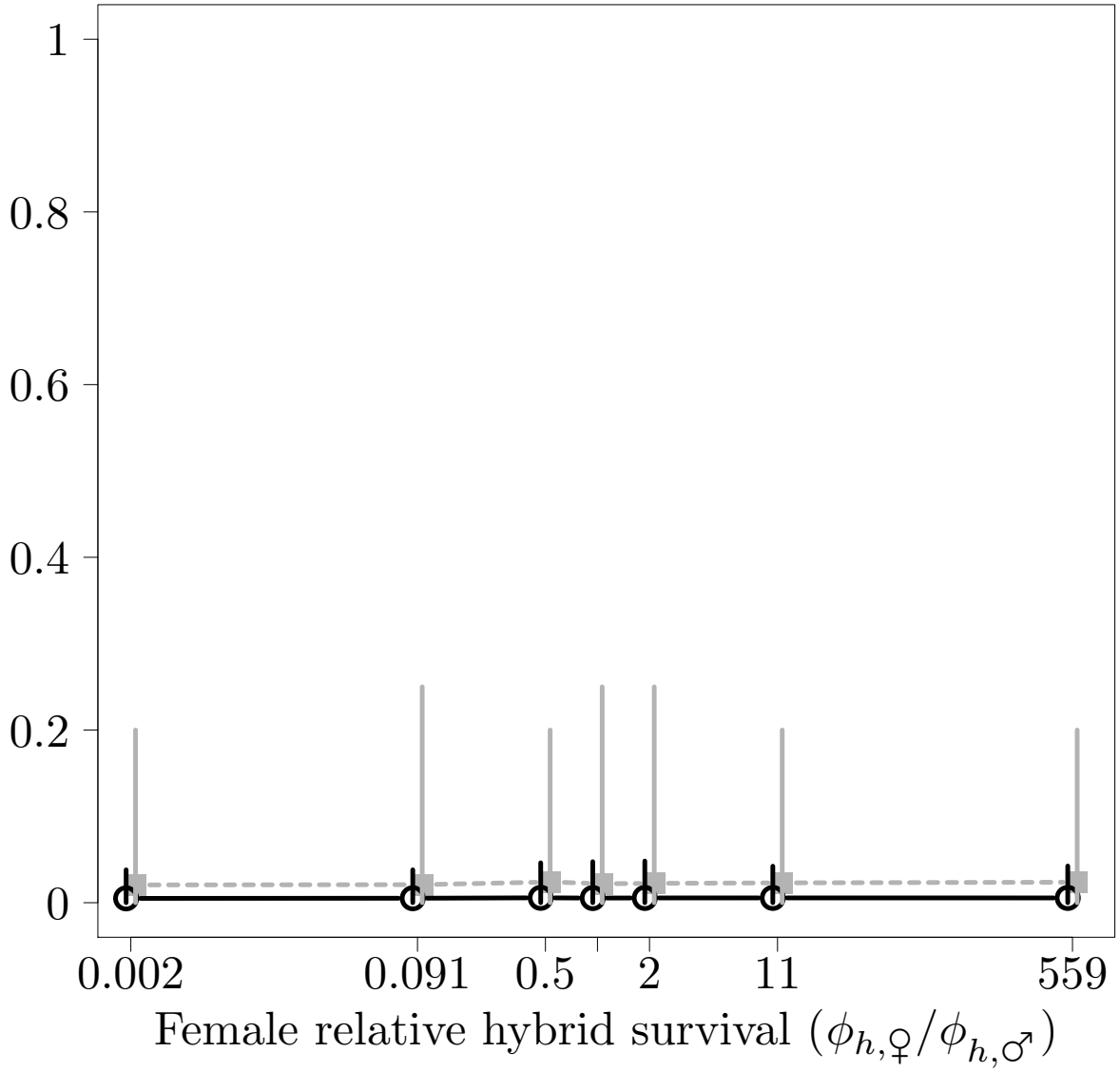

(C) Mito-nuclear discordance
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
0.001
0.02
0.04
0.06
0.08
Migration rate (m)

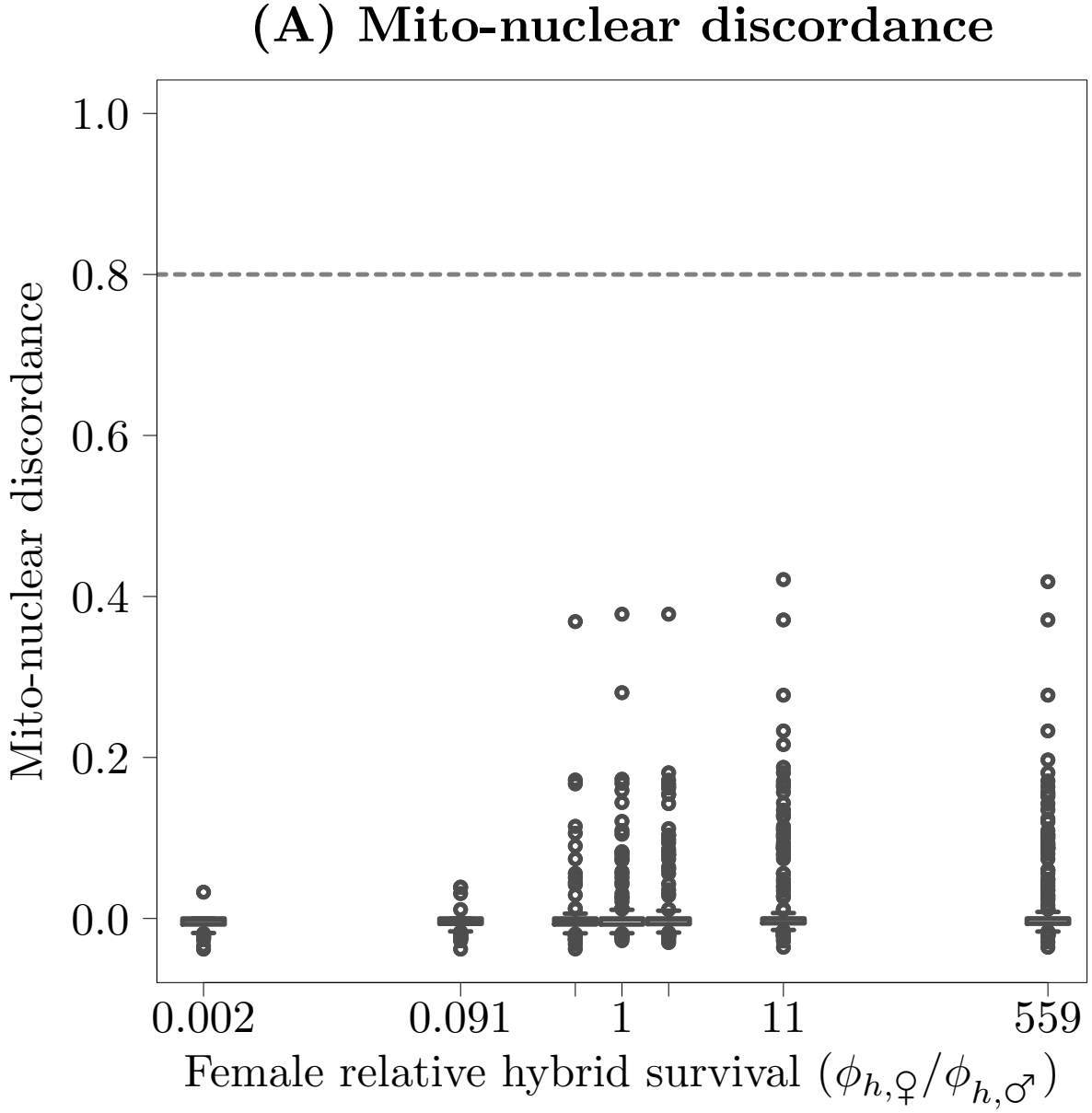

(B) Mitochondrial introgression
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

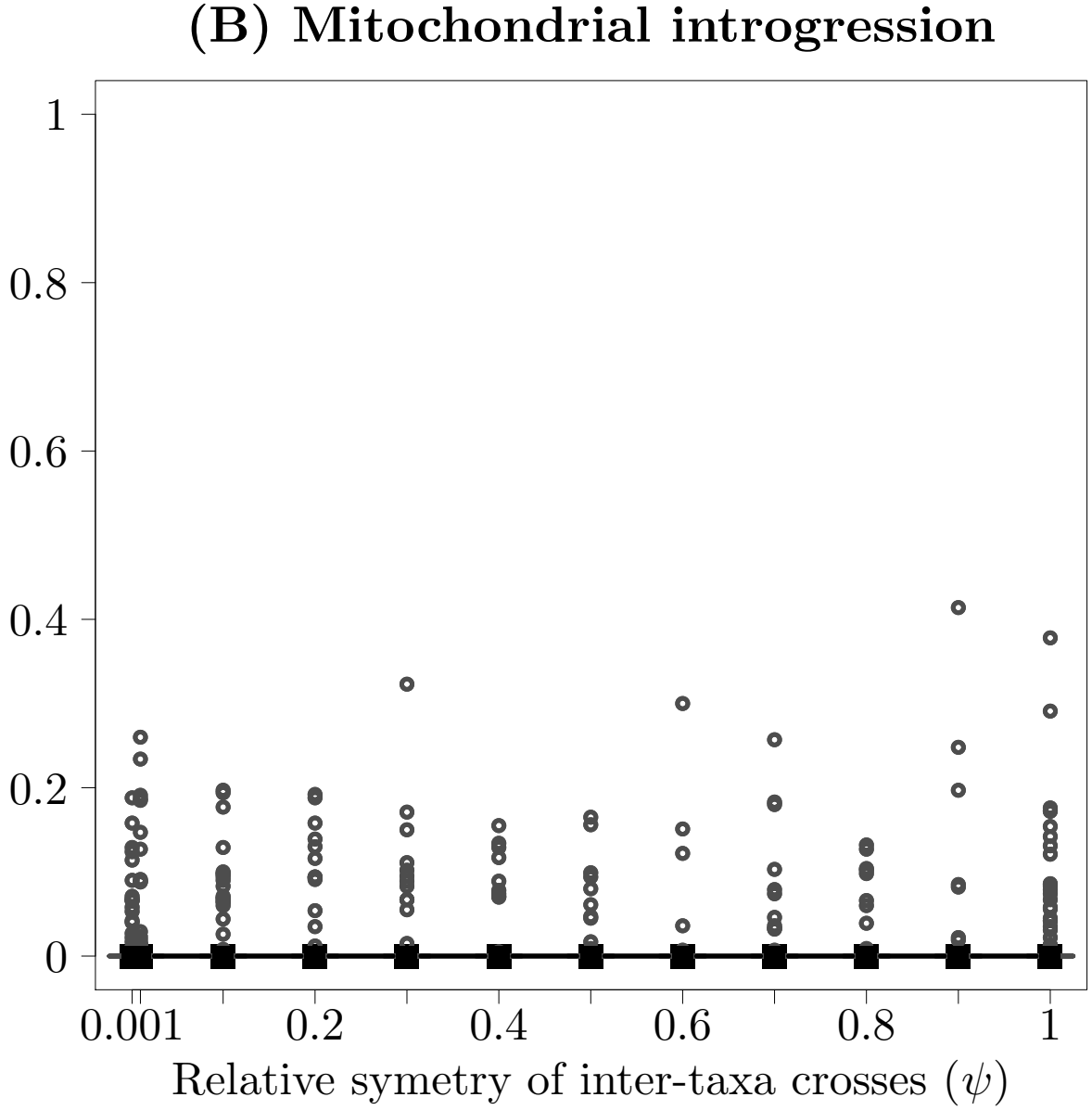

(C) Autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

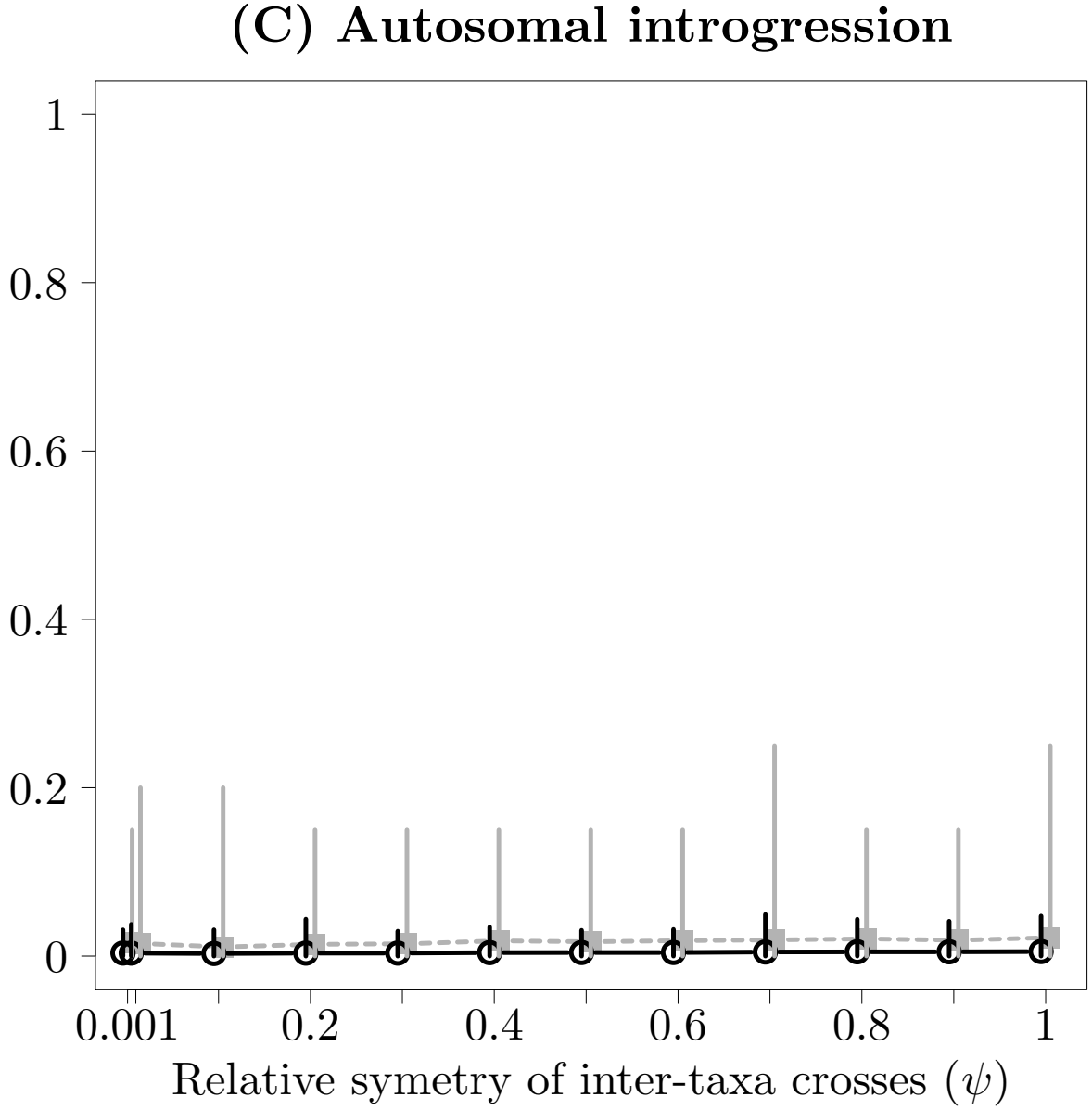

(A) Mito-nuclear discordance
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

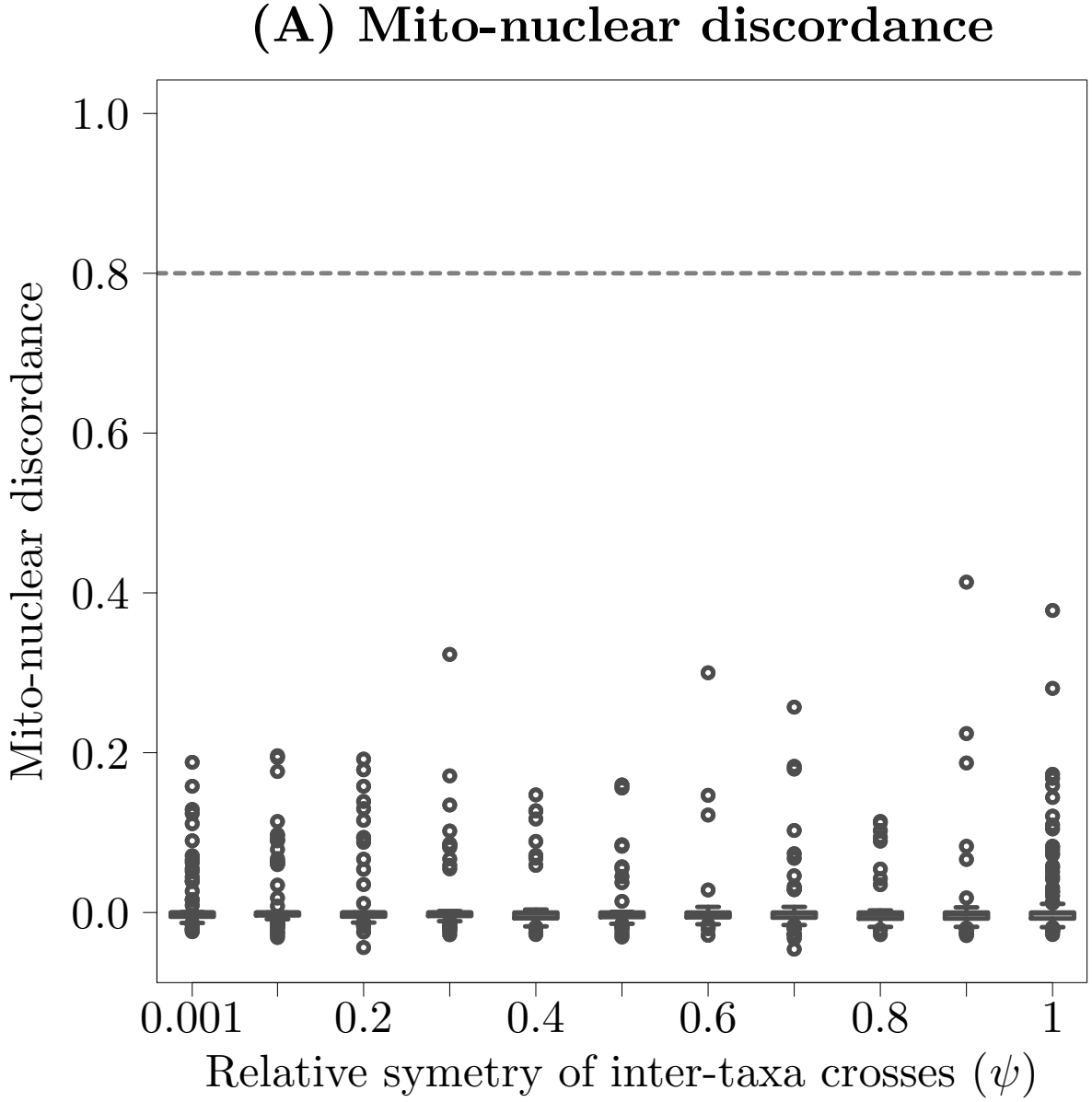

(B) Mitochondrial introgression
1
0.8
0.6
0.4
0.2
0
0.002
0.091
0.5
2
11
559
Female relative hybrid survival ($\phi_{h,♀}/\phi_{h,♂}$)


(C) Autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.002
0.091
0.5
2
11
559
Female relative hybrid survival ($\phi_{h,♀}/\phi_{h,♂}$)

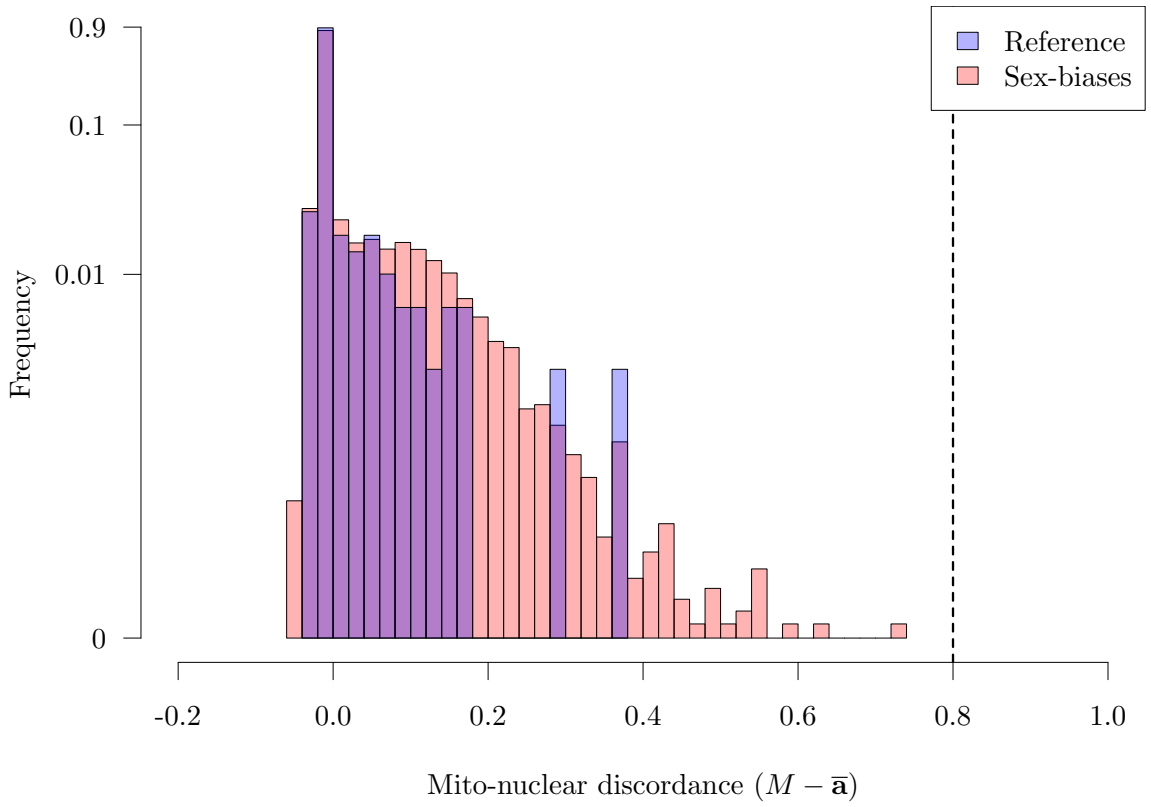

(A) Mito-nuclear discordance
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
0.002
0.091
1
11
559
Female relative hybrid survival ($\phi_{h,♀}/\phi_{h,♂}$)

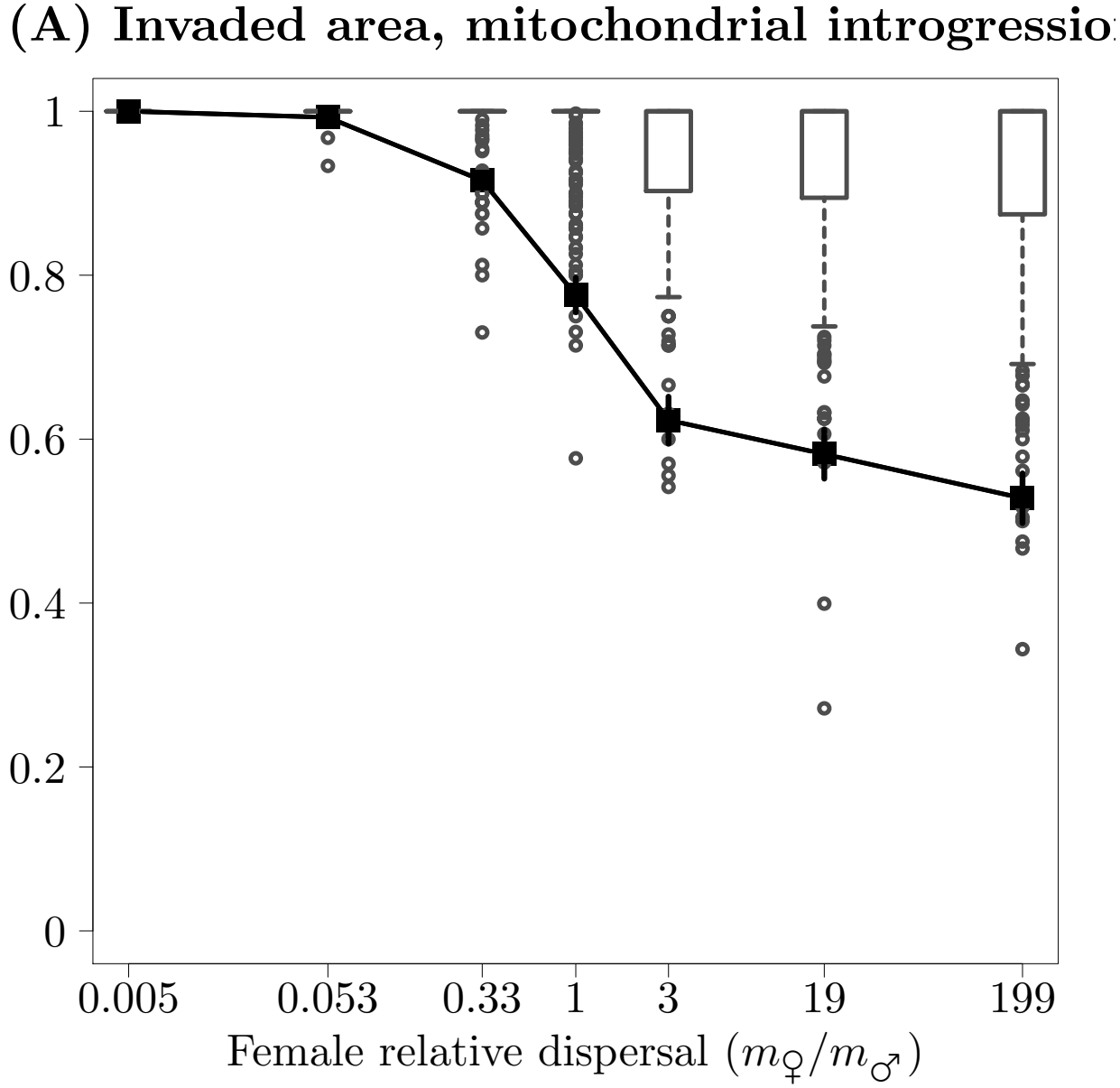

(B) Mitochondrial introgression
1
0.8
0.6
0.4
0.2
0
0.001
0.2
0.4
0.6
0.8
1
Relative symetry of inter-taxa crosses (ψ)

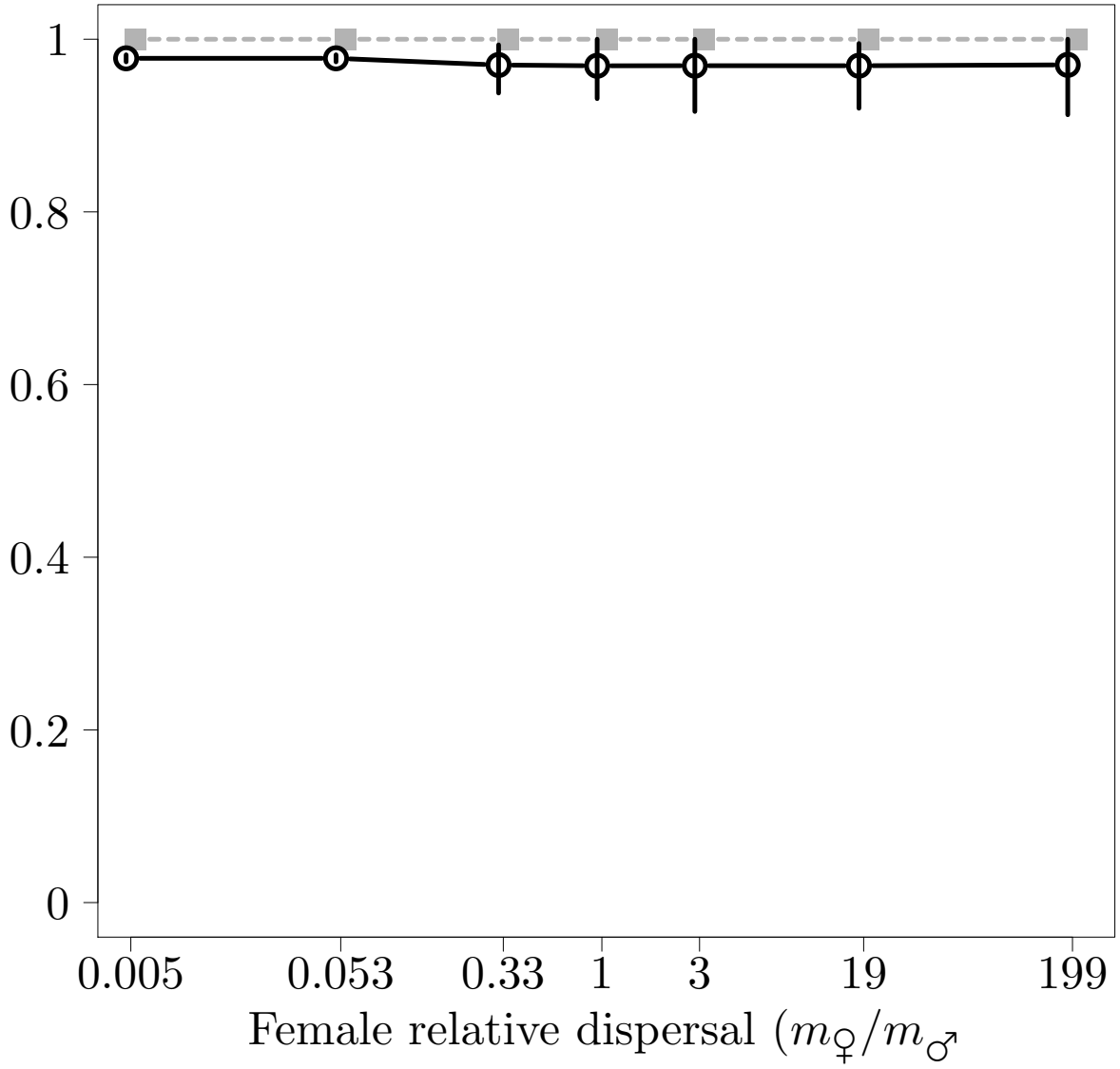

(C) Autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.001
0.2
0.4
0.6
0.8
1
Relative symetry of inter-taxa crosses (ψ)




```
## [1] 0.001994615
## [1] 0.736
```


Reference
Sex-biases
0.9
0.1
0.01
0
Frequency
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
Mito-nuclear discordance ($M - \bar{\mathbf{a}}$)


(A) Invaded area, mitochondrial introgressio
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)


(B) Invaded area, autosomal introgression
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.33
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

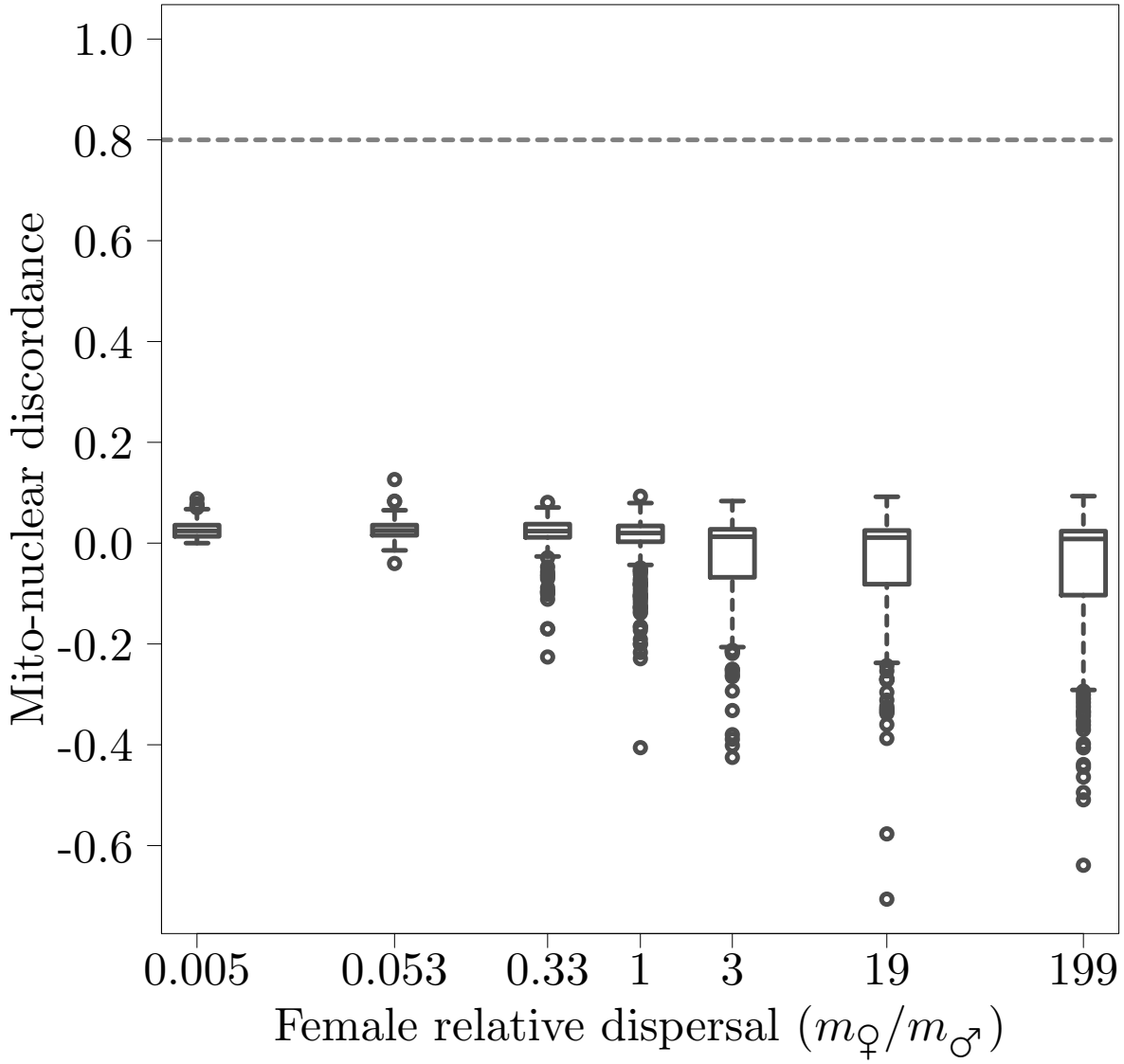


Table 1:

	ϕ_M	f($M = 1$)	$\overline{M}$	$\bar{D}$	f($p_D < 0.05$)	$\bar{F}_s$	f($p_{F_s} < 0.05$)		
1	1.000	0.000	0.009	-0.112	0.037	8.521	0	0.004	0.005
2	0.998	0.000	0.011	-0.086	0.036	8.592	0	0.006	0.005
3	0.995	0.000	0.011	-0.092	0.045	9.059	0	0.005	0.005
4	0.993	0.000	0.014	0.077	0.057	10.437	0	0.008	0.005
5	0.990	0.000	0.015	0.803	0.062	12.274	0	0.009	0.005
6	0.975	0.000	0.058	2.194	0.035	17.906	0	0.052	0.006
7	0.950	0.003	0.261	2.375	0.049	19.797	0	0.254	0.006
8	0.925	0.061	0.575	2.143	0.036	15.982	0	0.568	0.007
9	0.900	0.424	0.873	0.413	0.098	10.065	0	0.865	0.007
10	0.800	1.000	1.000	-0.167	0.000	2.454	0	0.992	0.008
11	0.700	1.000	1.000	-0.184	0.006	2.826	0	0.993	0.007