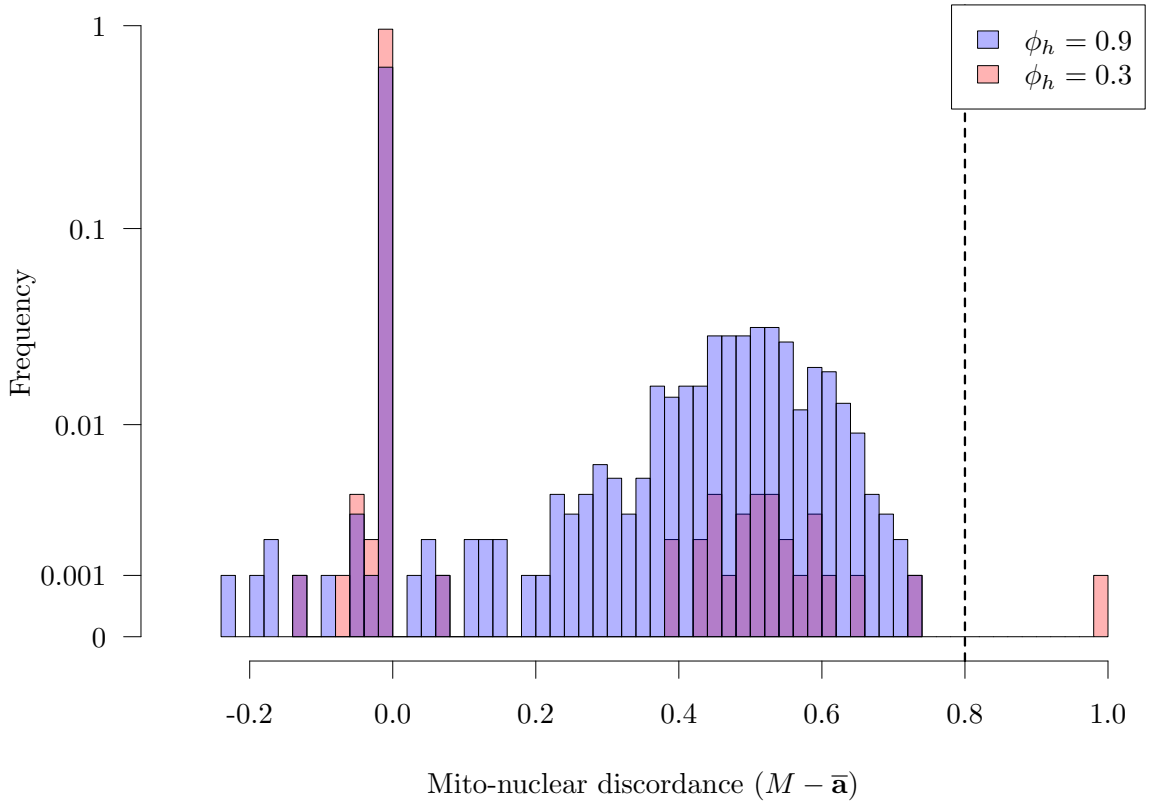
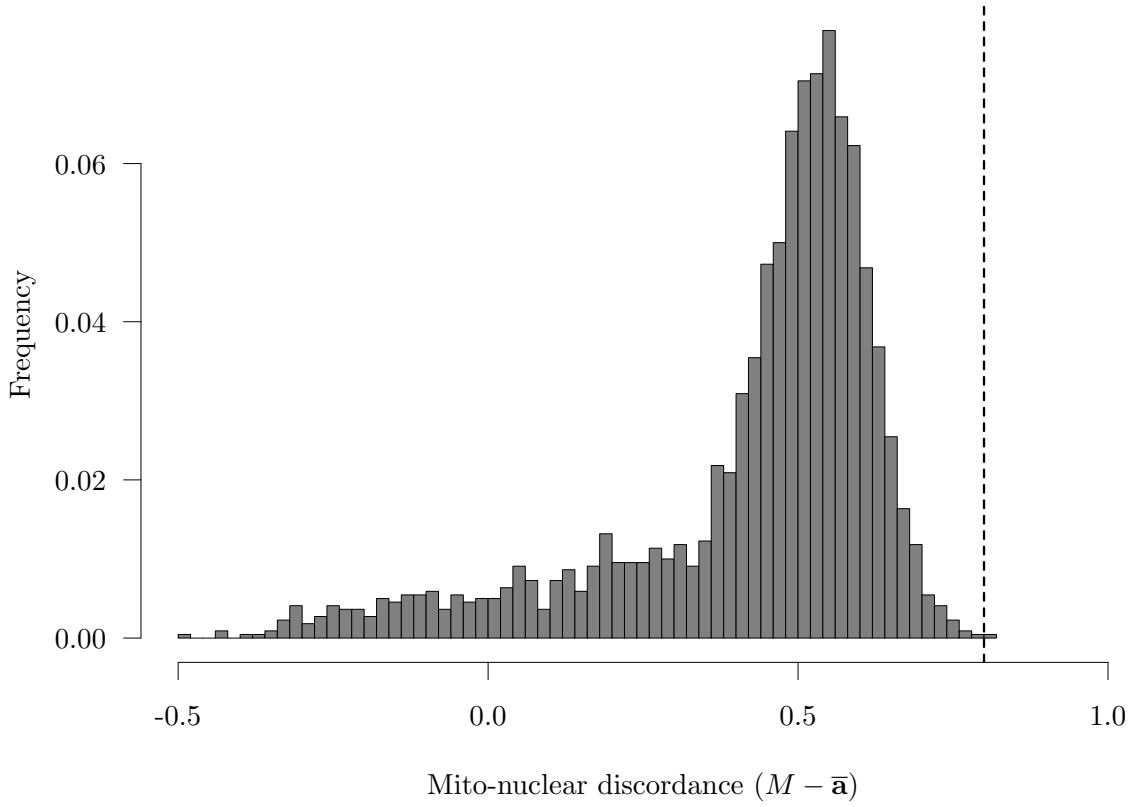
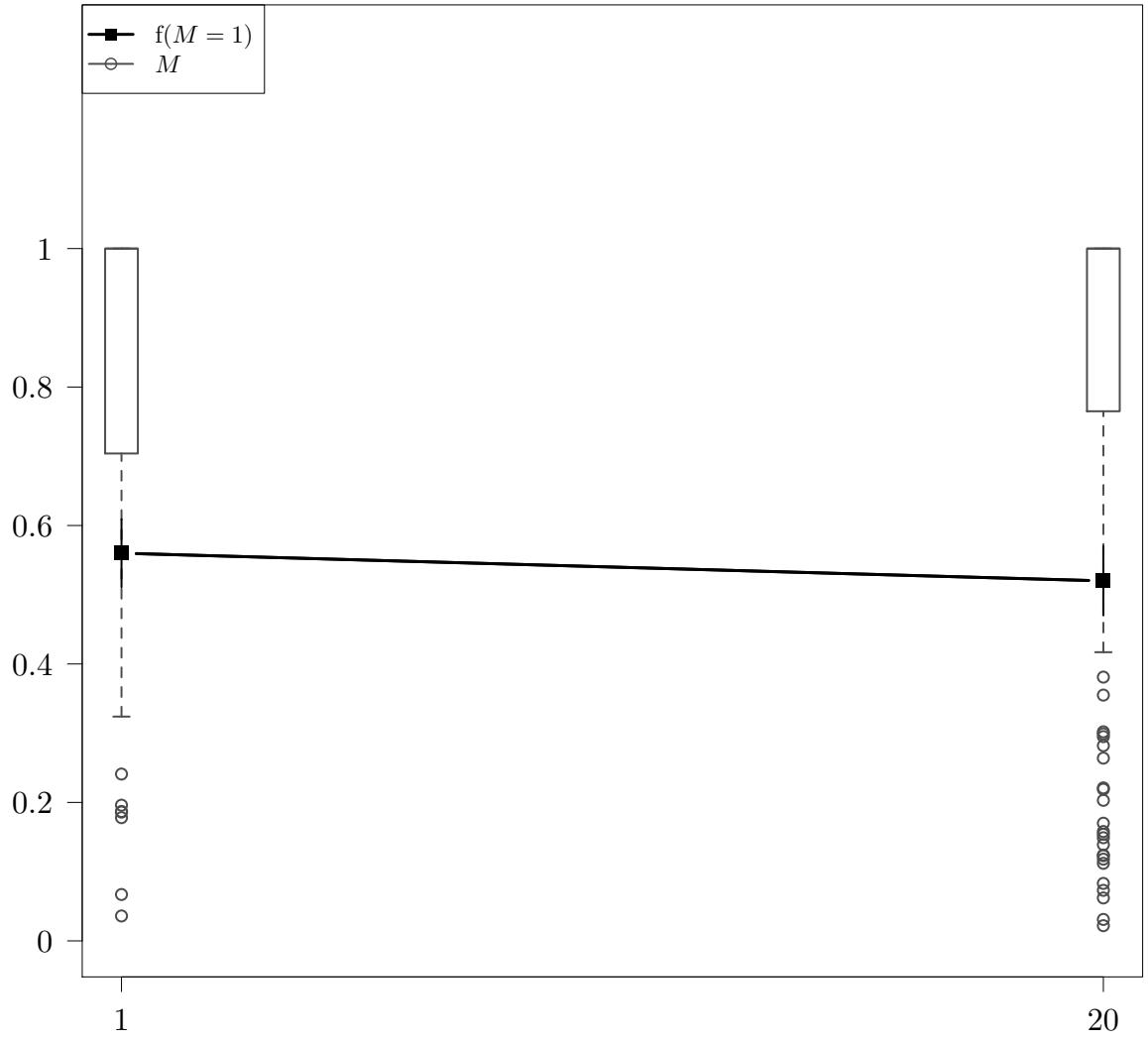
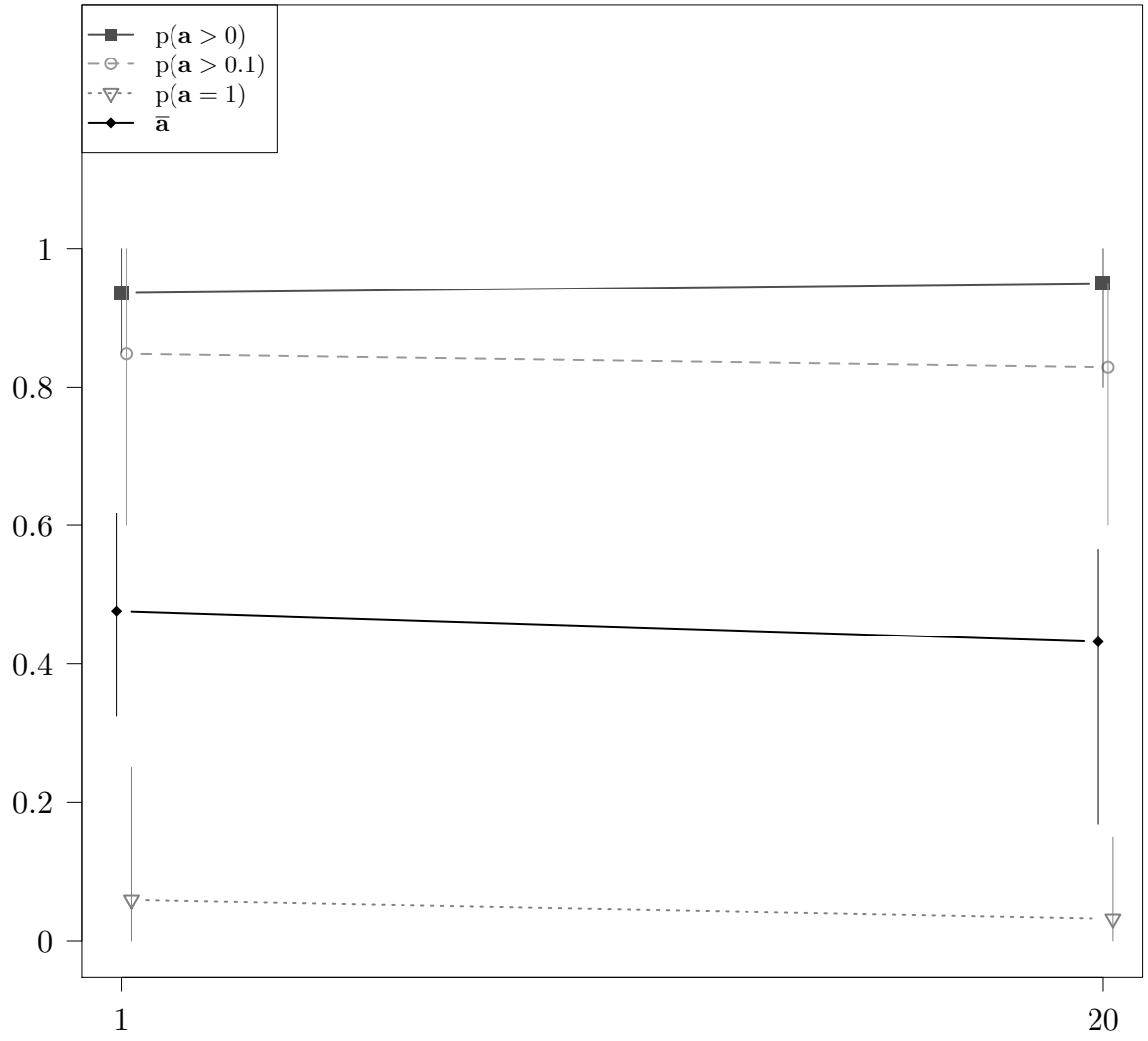
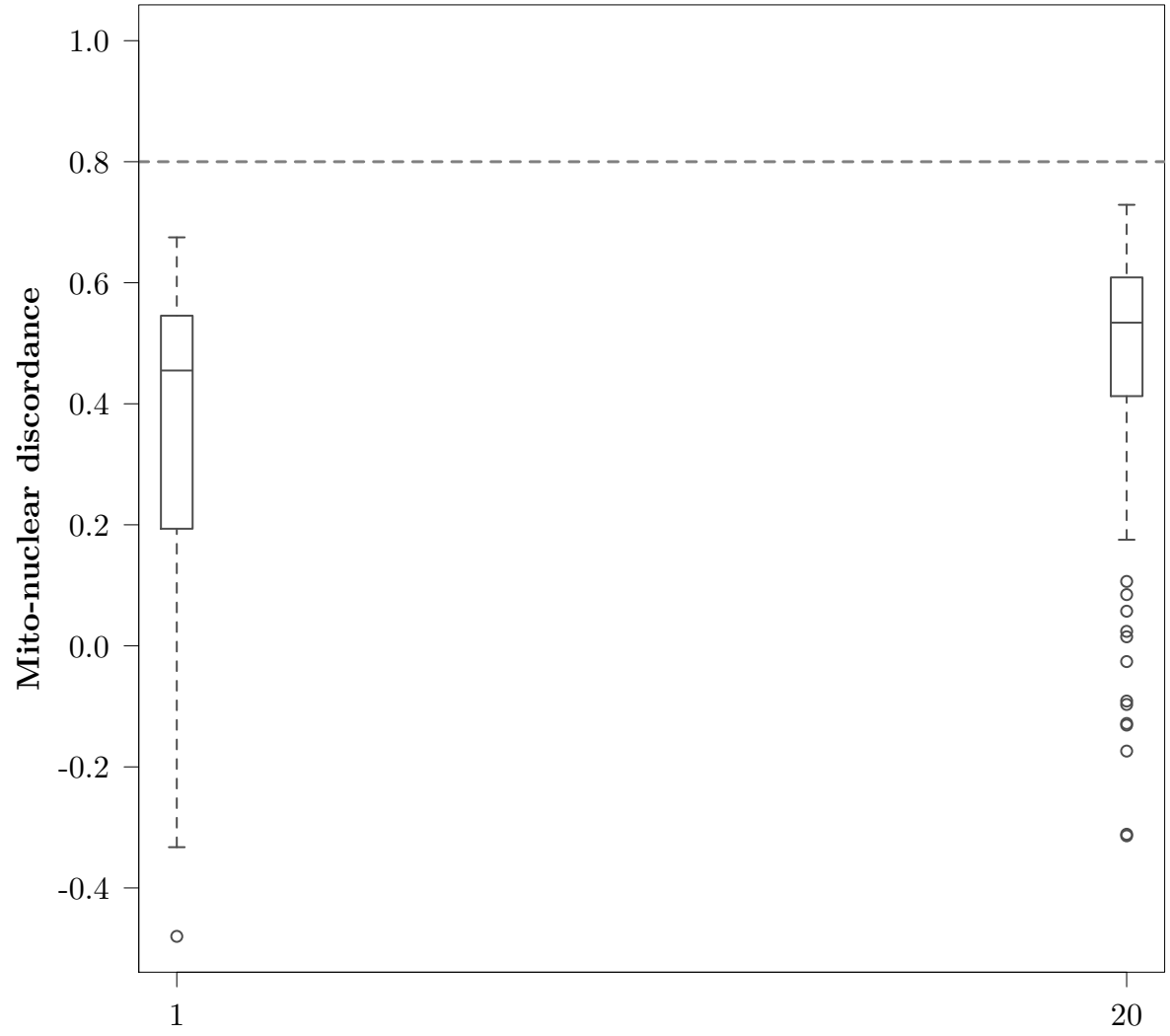
```
## Warning in RecdistriMt$DistriMtMax[(RecdistriMt$Simul == "wRmAmHMt0" | RecdistriMt$Simul
== :  le nombre d'objets  remplacer n'est pas multiple de la taille du remplacement

##  [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
```




0.06
0.04
0.02
0.00
Frequency
-0.5
0.0
0.5
1.0
Mito-nuclear discordance ($M - \overline{\mathbf{a}}$)

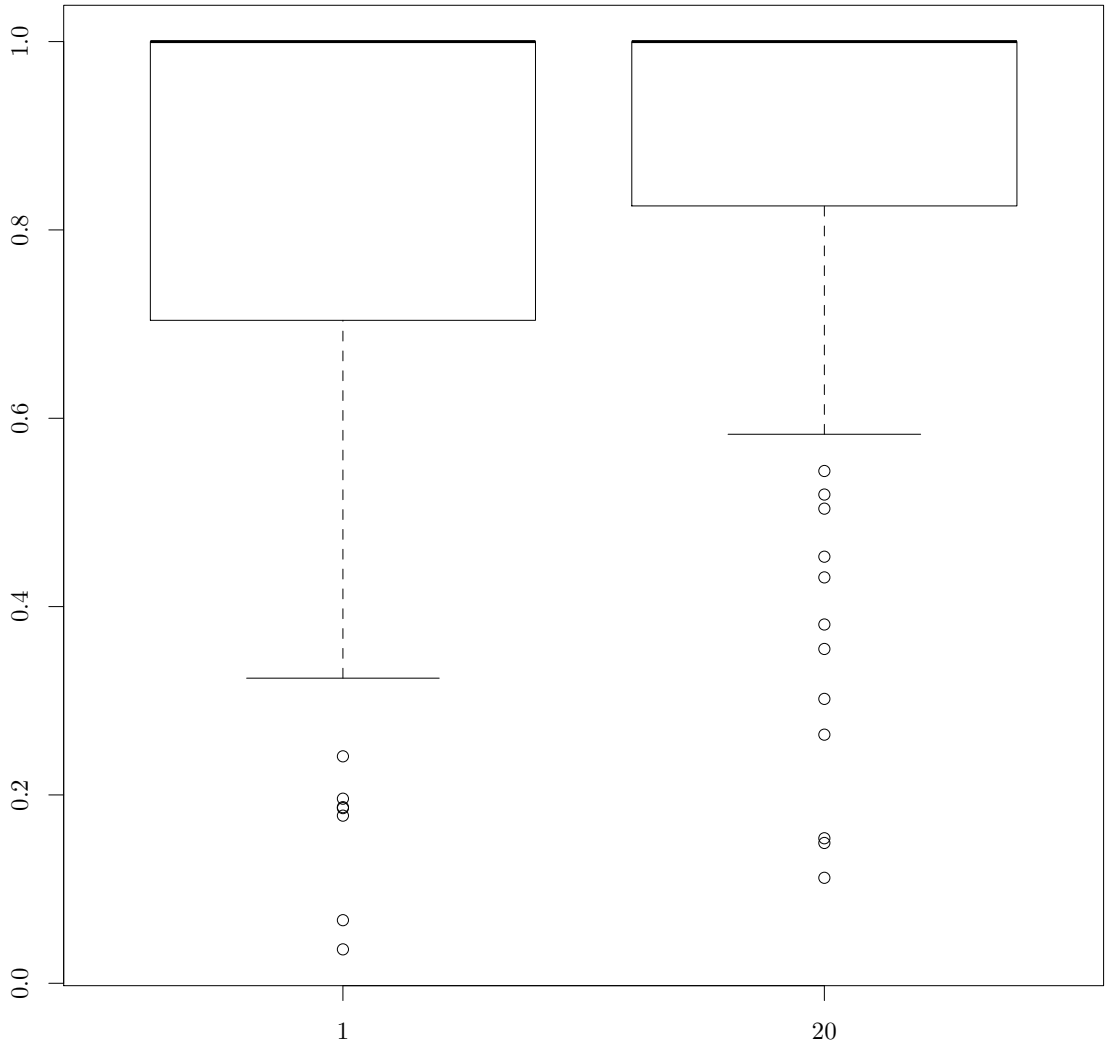

f($M = 1$)
M
1
0.8
0.6
0.4
0.2
0
1
20
Number of local adaptation loci

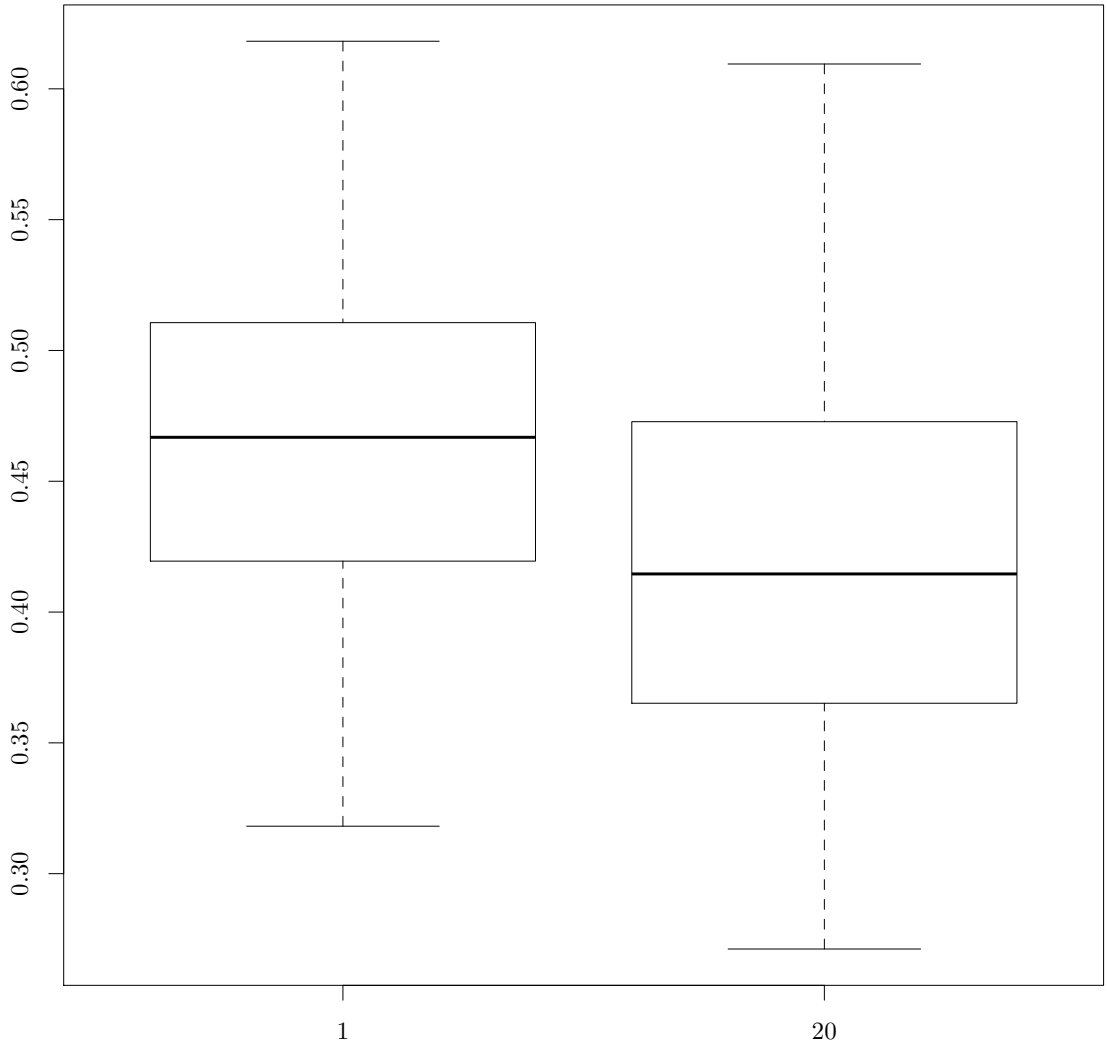

p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
1
20
Number of local adaptation loci

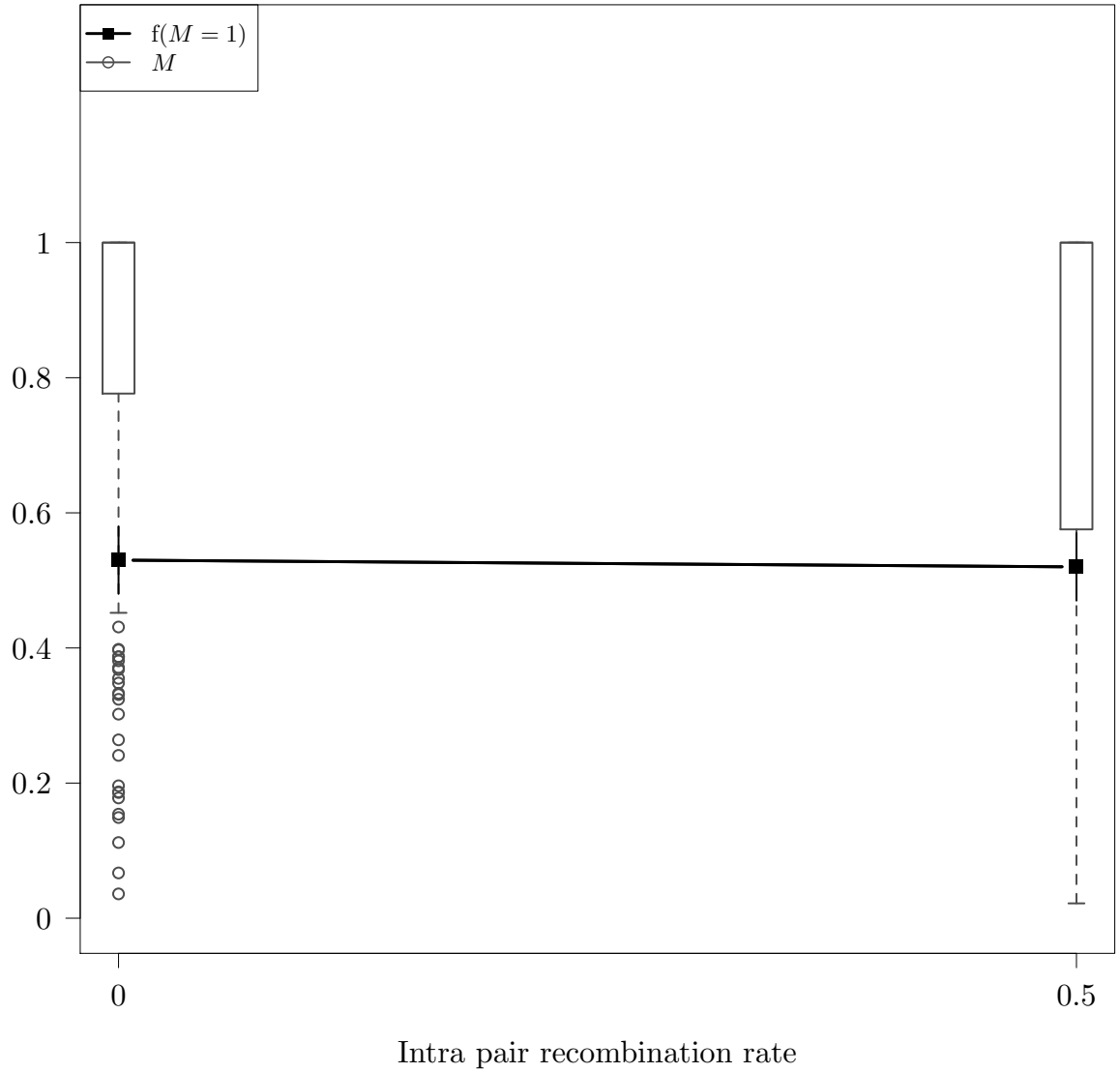


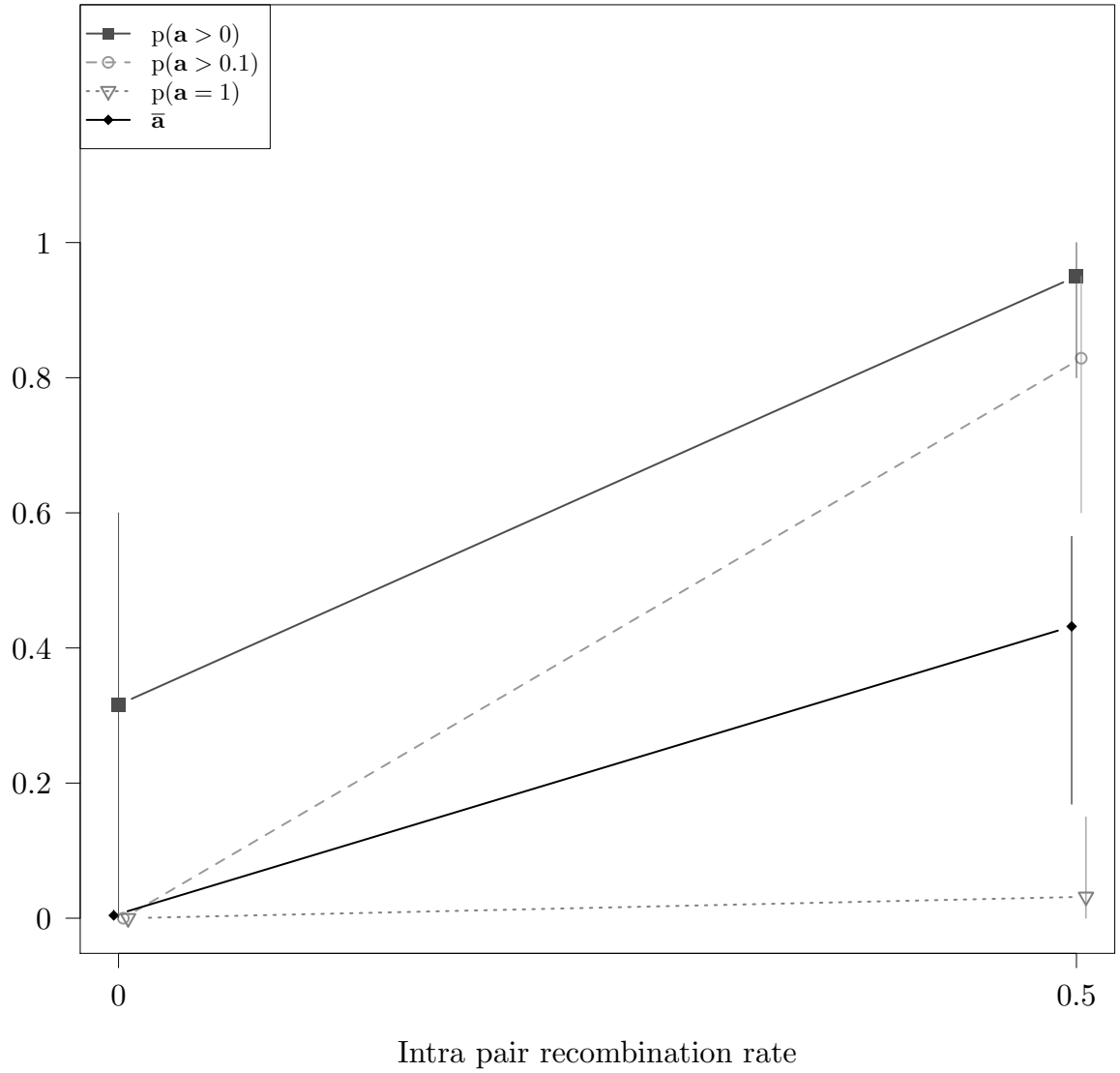

```
##       NbRun FixMt IntMt   MtExo    IntAut  IntAut10     FixAut MeanExoAut
## BDb0    100  0.56     1 0.46378 0.9357143 0.8482143 0.05892857  0.4766393
## BDDS0   100  0.52     1 0.42324 0.9500000 0.8288462 0.03173077  0.4318587
##        SDExoAut     FstAut       FstZ      FstW     FstMt Introgq0
## BDb0  0.3142080 0.09511372 0.09078571 0.2305357 0.2157143     0.85
## BDDS0 0.2964481 0.10215486 0.11173077 0.2477115 0.2313077     0.80
##       Introgq025 Introgq50 Introgq975 Introgq100 Introg10q0 Introg10q025
## BDb0        0.85      0.95          1          1        0.6      0.66875
## BDDS0       0.85      0.95          1          1        0.6      0.60000
##       Introg10q50 Introg10q975 Introg10q100 Fixq0 Fixq025 Fixq50 Fixq975
## BDb0         0.85         0.95         1.00     0       0   0.05 0.15000
## BDDS0        0.85         0.95         0.95     0       0   0.00 0.13625
##       Fixq100 MeanExoq0 MeanExoq025 MeanExoq50 MeanExoq975 MeanExoq100
## BDb0     0.25   0.32500   0.3508938   0.469225   0.6064812     0.61820
```

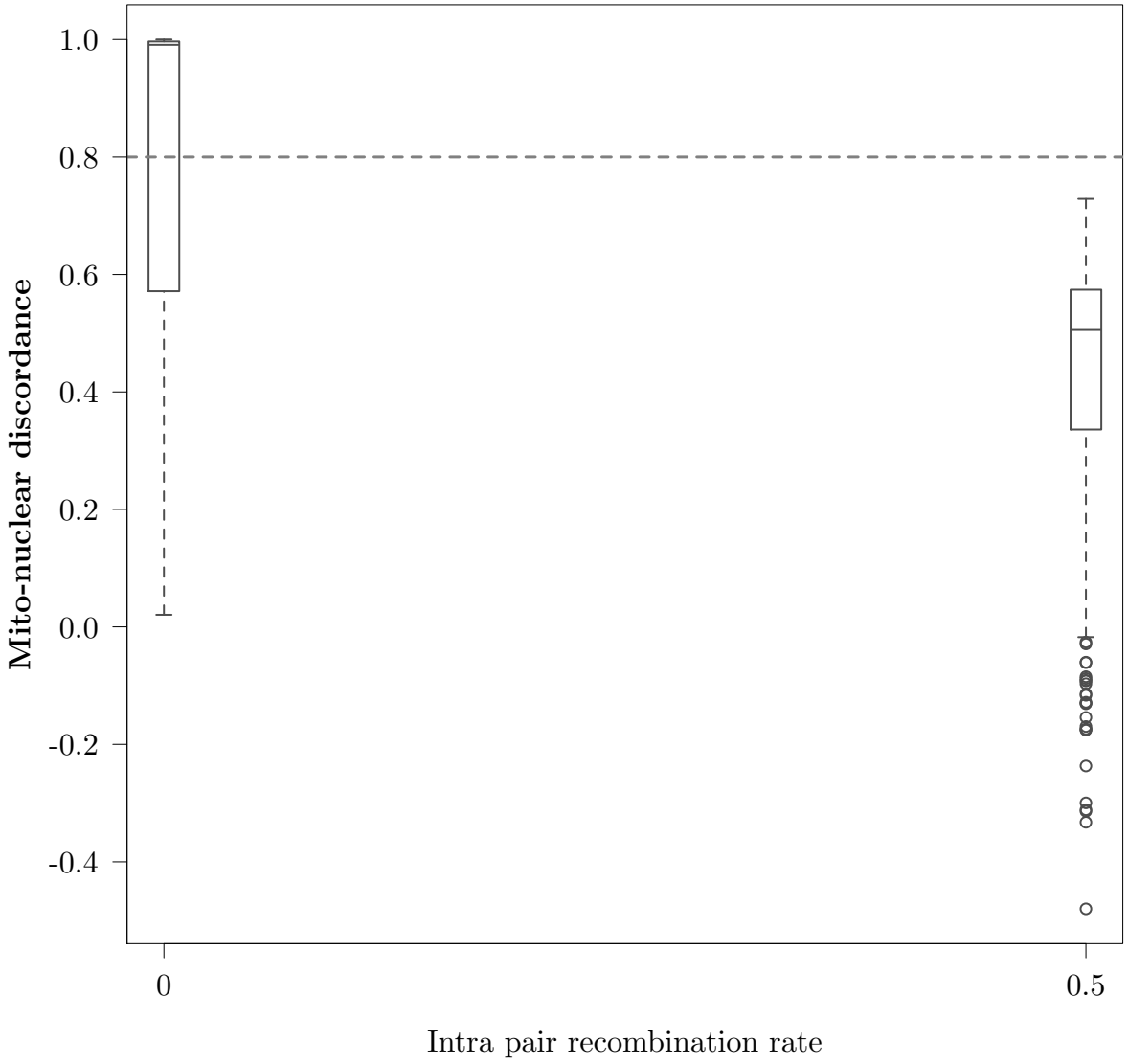
```
## BDDS0    0.15   0.16875   0.2933812   0.436150   0.5518550     0.56515
##       Param NbL Neu   R  TS
## BDb0      1   1 0.5 0.5 0.9
## BDDS0     1  20 0.5 0.5 0.9
```

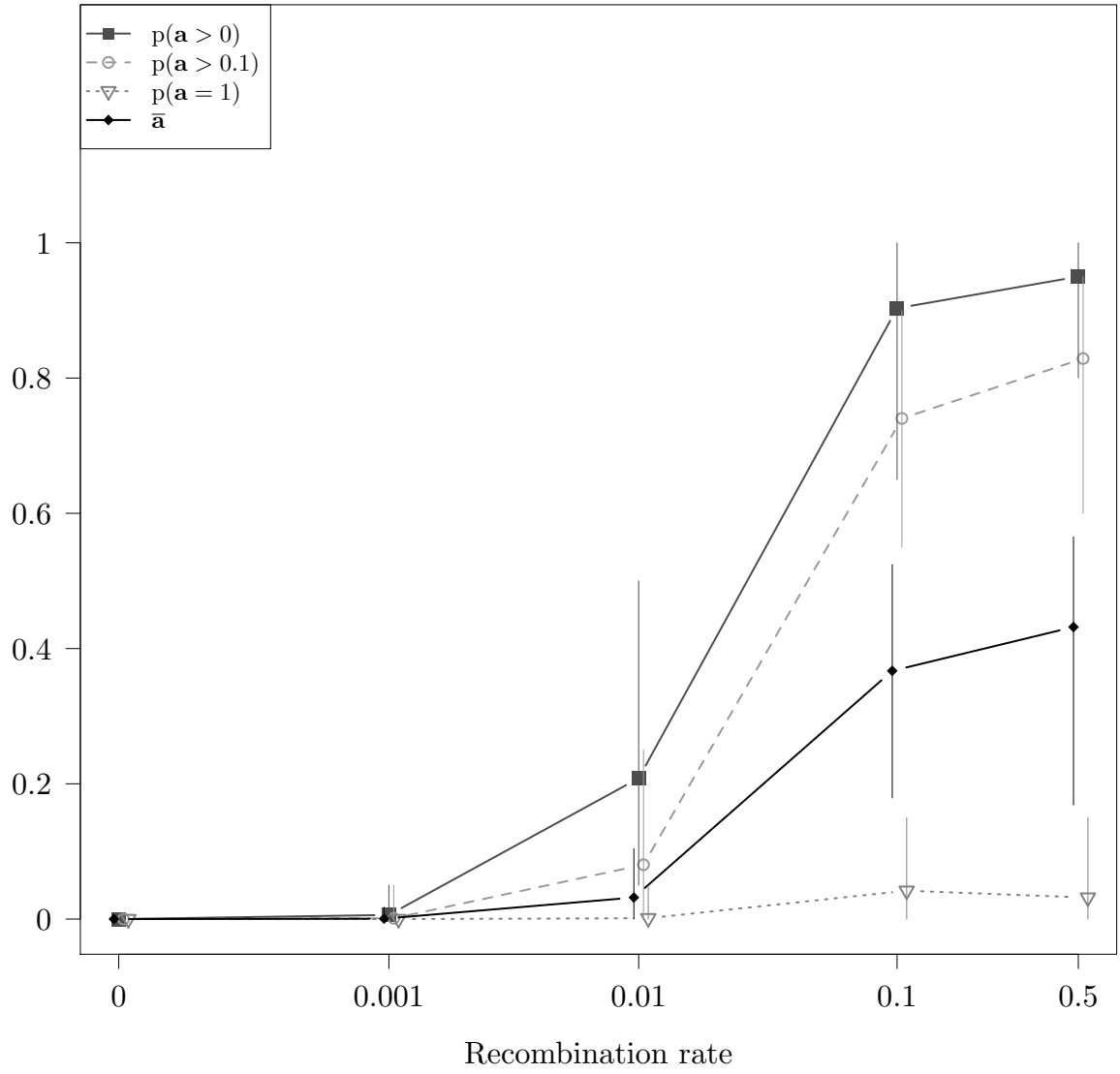


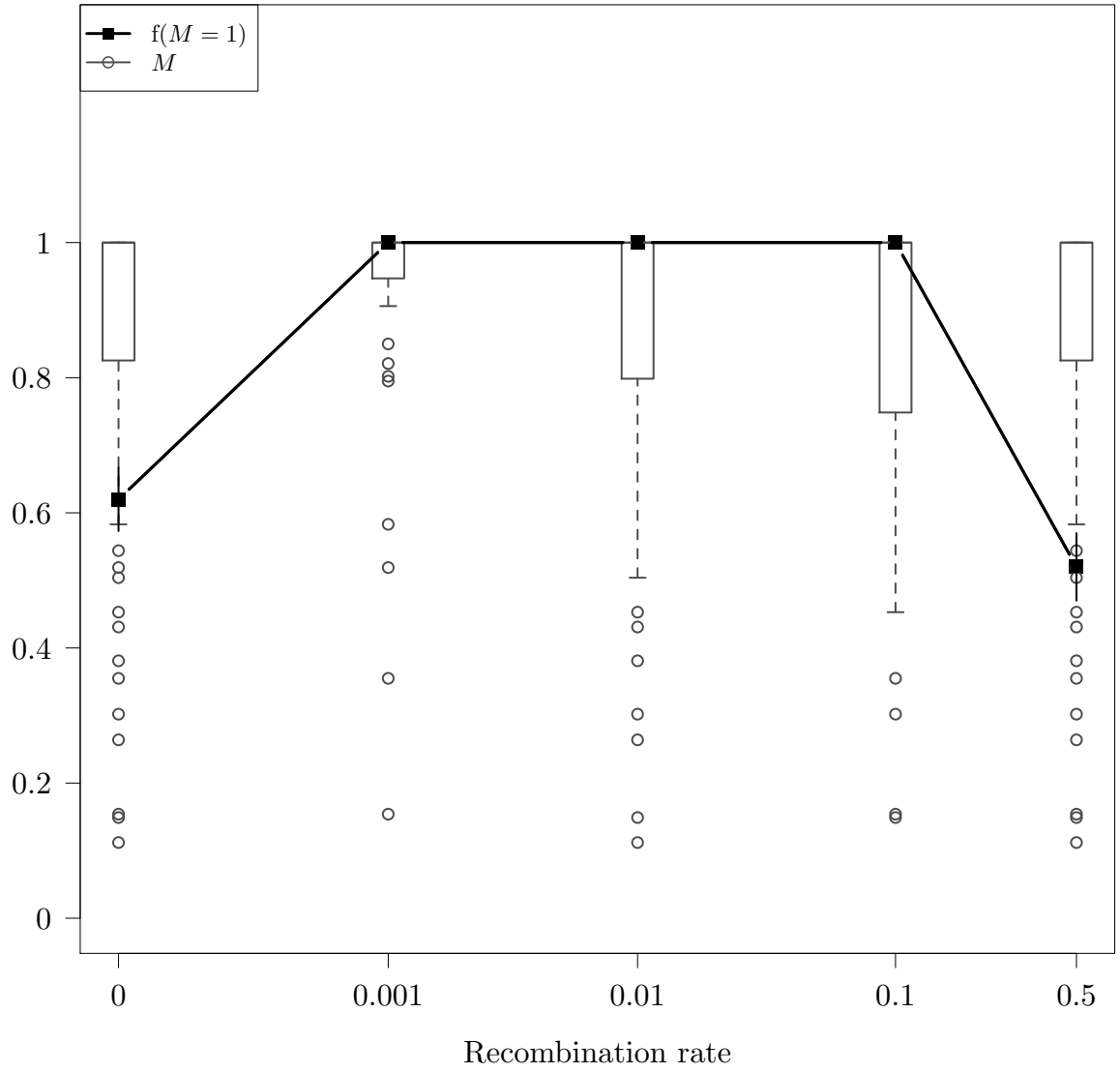

0.30
0.35
0.40
0.45
0.50
0.55
0.60
1
20

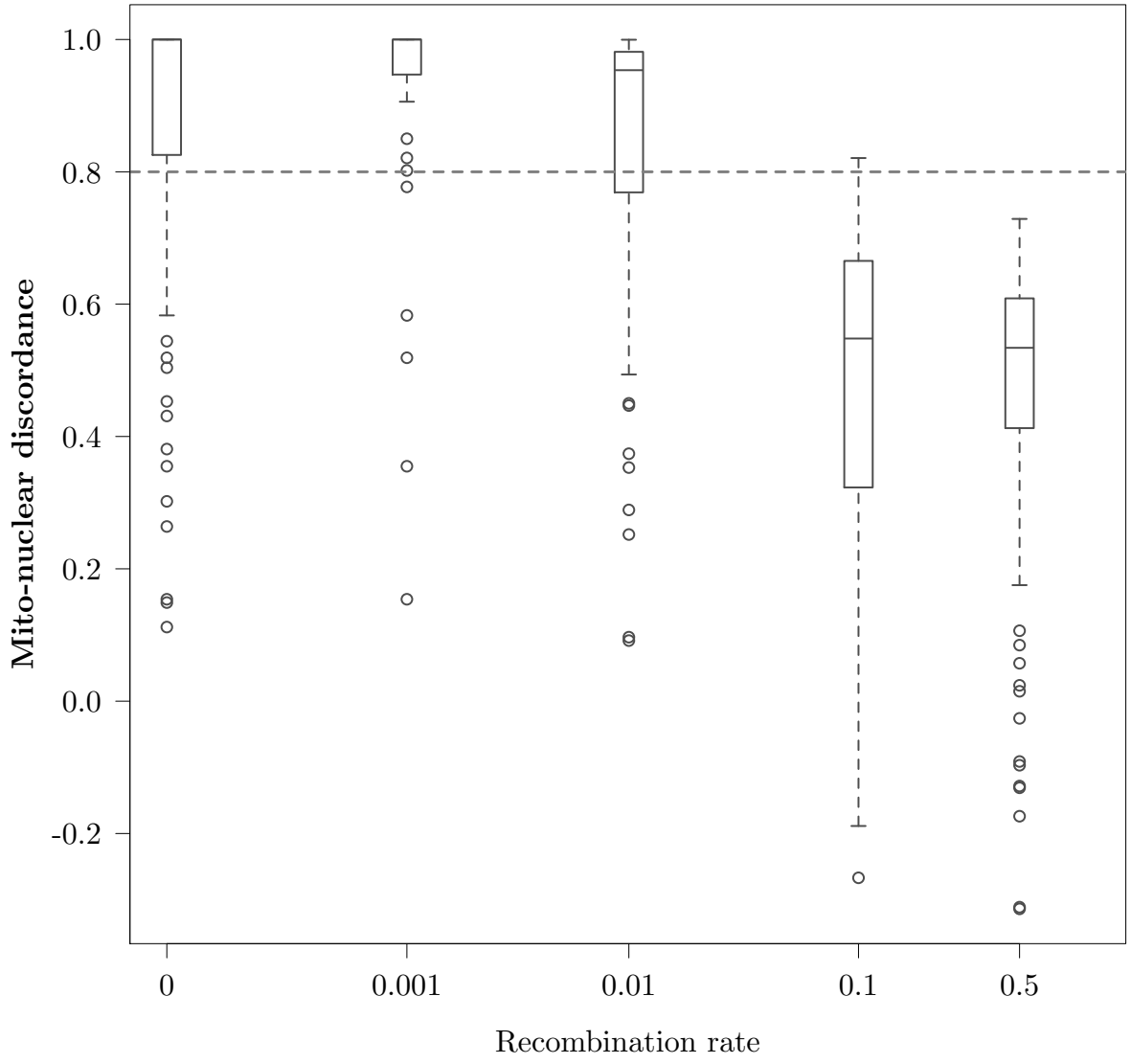

f($M = 1$)
M
1
0.8
0.6
0.4
0.2
0
0
0.5
Intra pair recombination rate

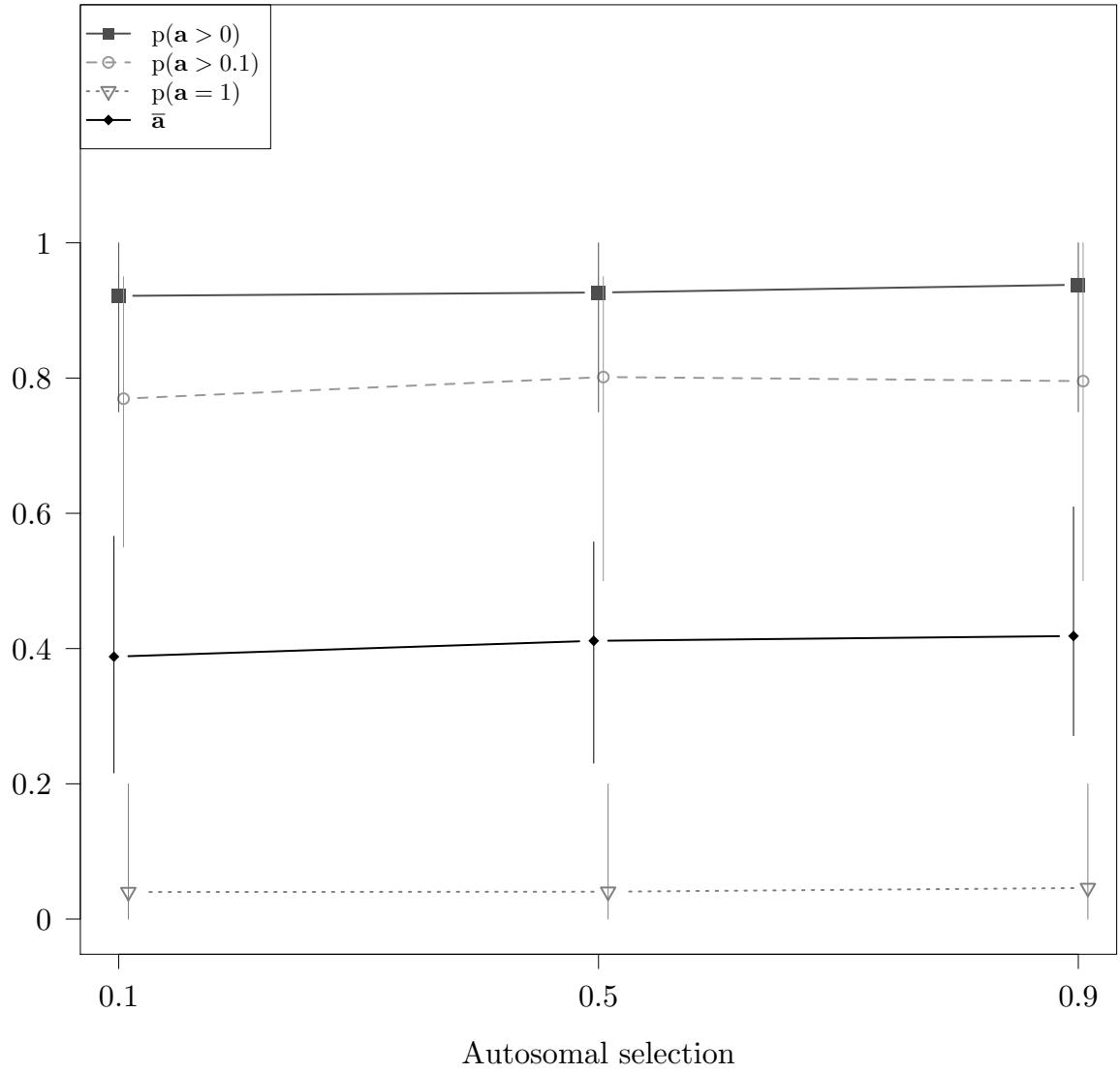

p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
0
0.5
Intra pair recombination rate

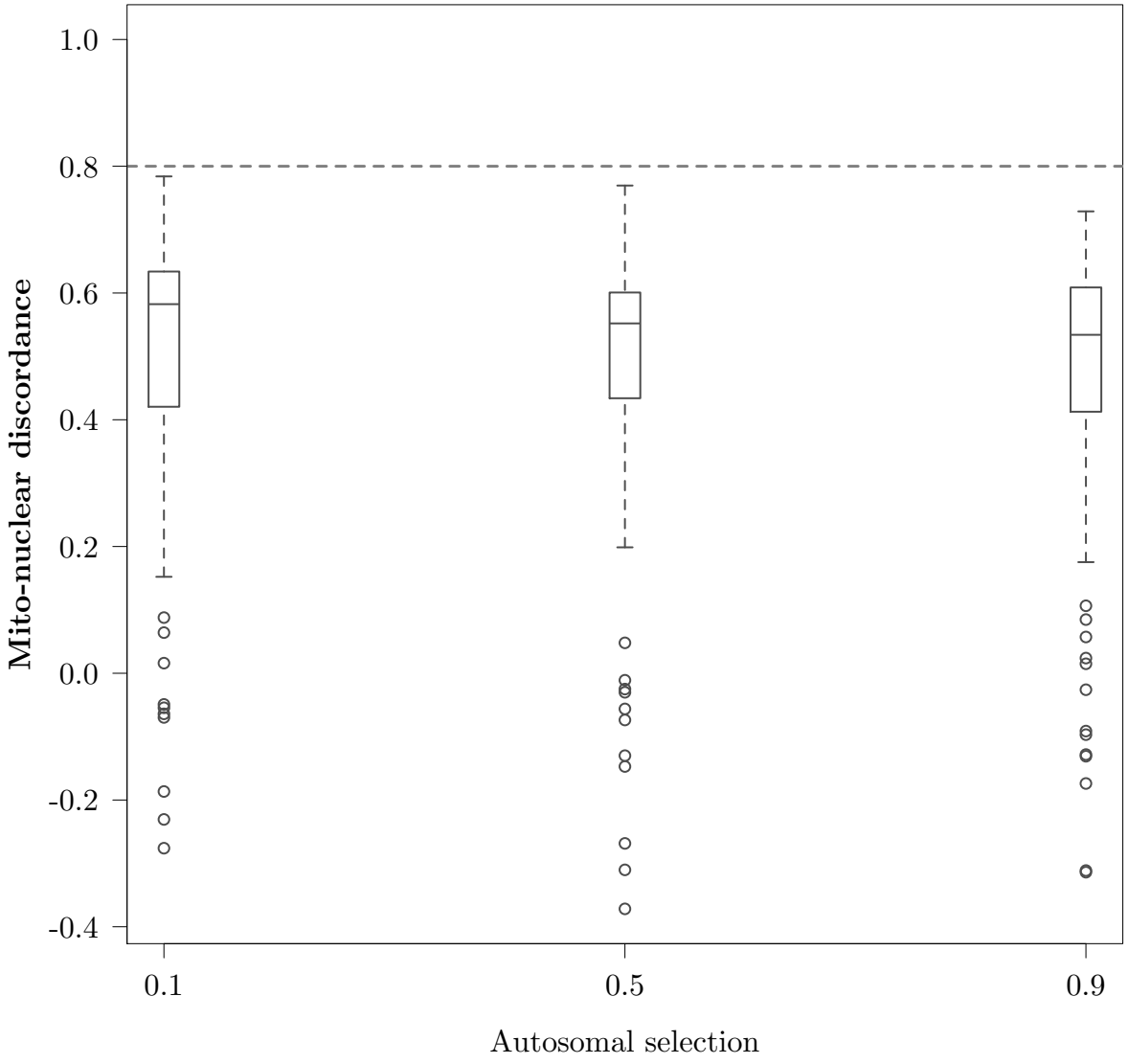

1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
Mito-nuclear discordance
0
0.5
Intra pair recombination rate


p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
0
0.001
0.01
0.1
0.5
Recombination rate

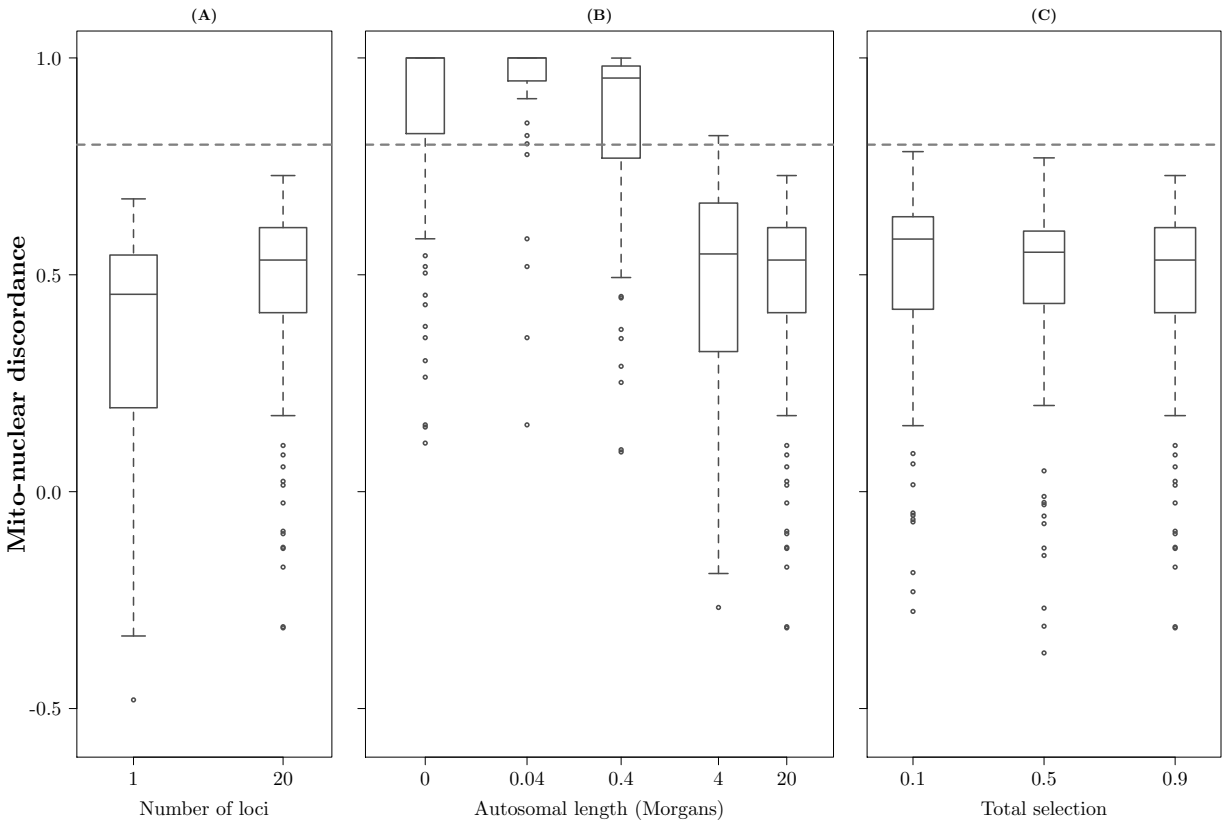

f(M = 1)
M
1
0.8
0.6
0.4
0.2
0
0
0.001
0.01
0.1
0.5
Recombination rate


1.0
0.8
0.6
0.4
0.2
0.0
-0.2
Mito-nuclear discordance
0
0.001
0.01
0.1
0.5
Recombination rate

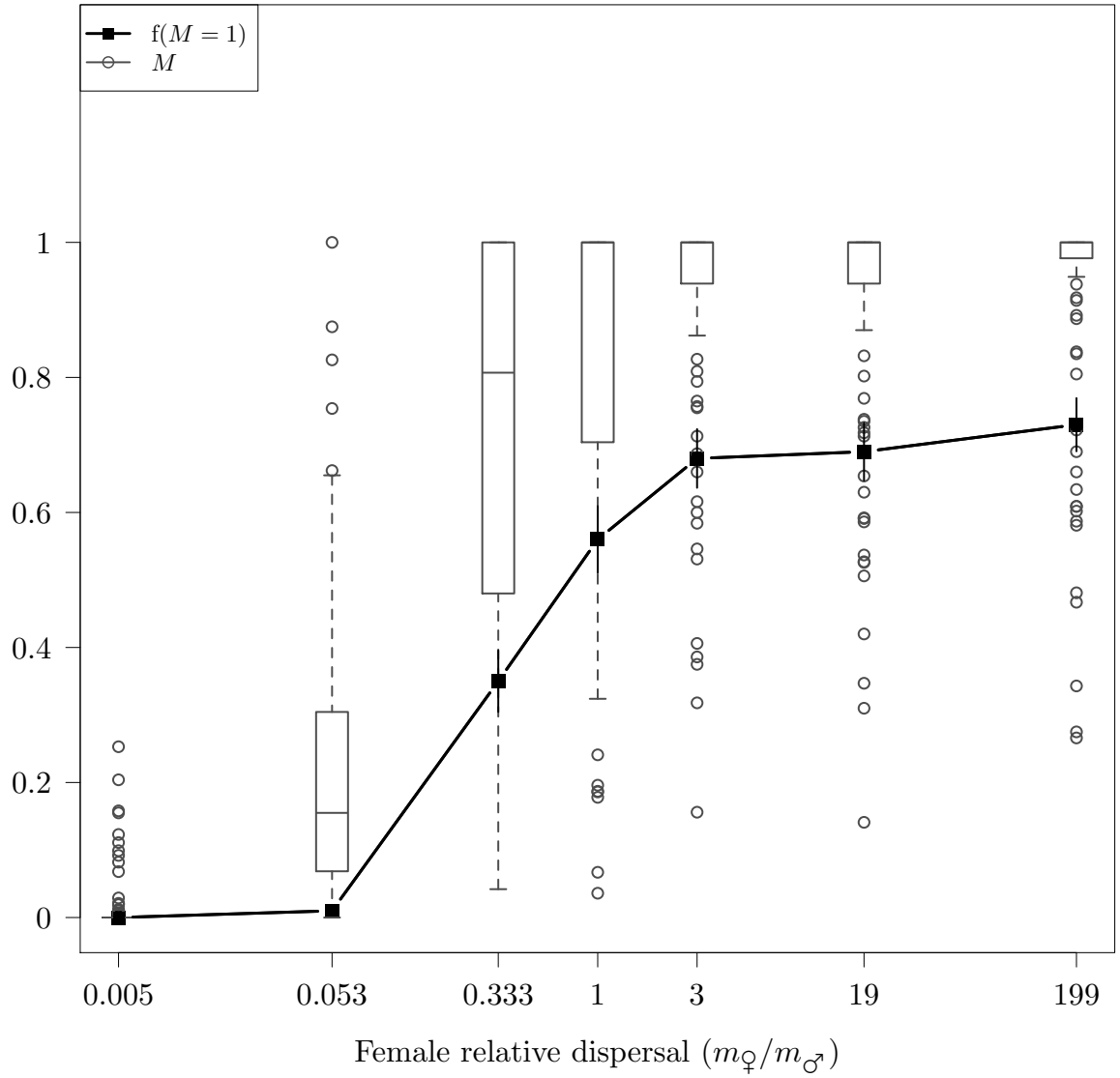

p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
0.1
0.5
0.9
Autosomal selection



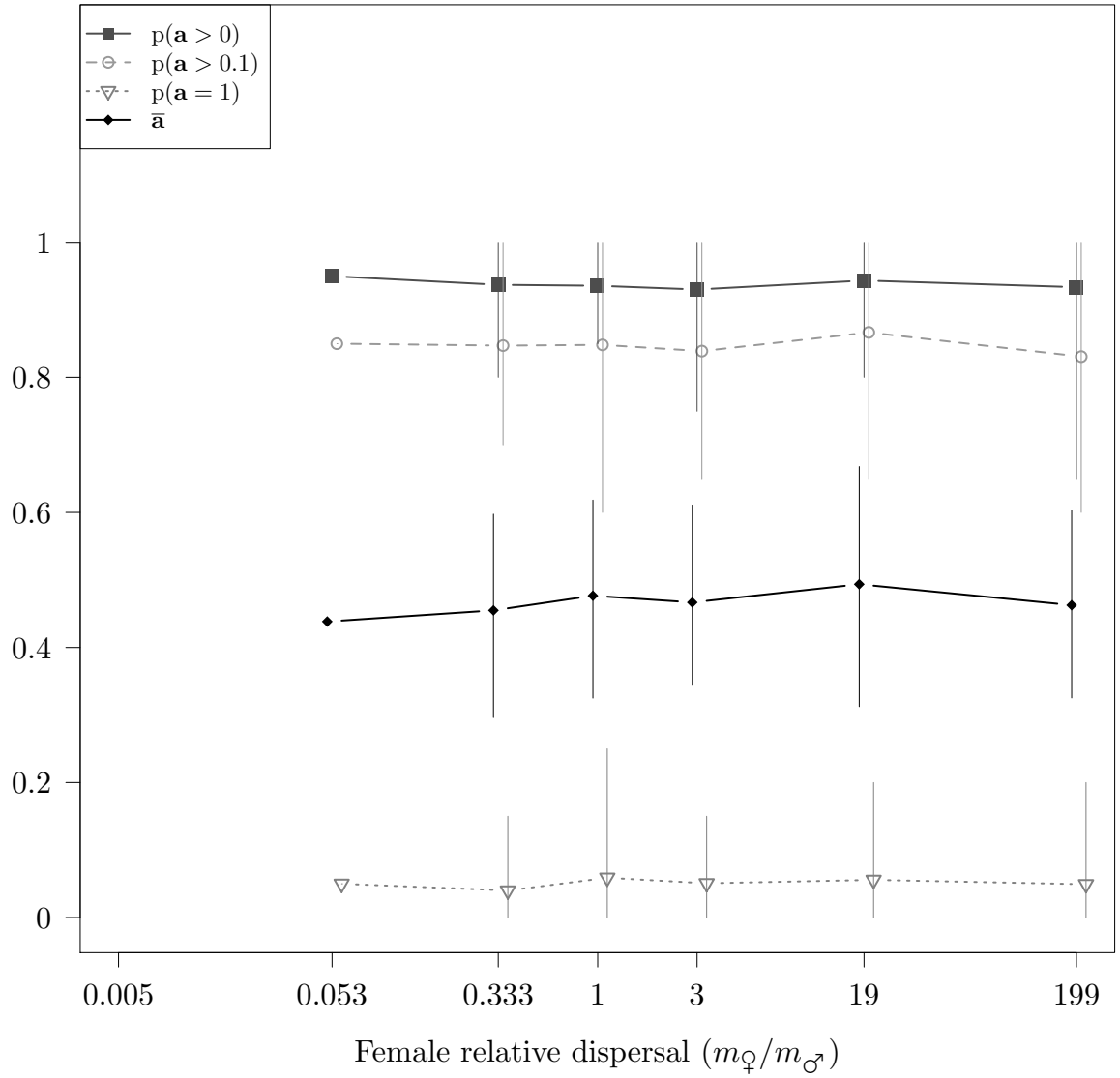
All nuclear selection together:


(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

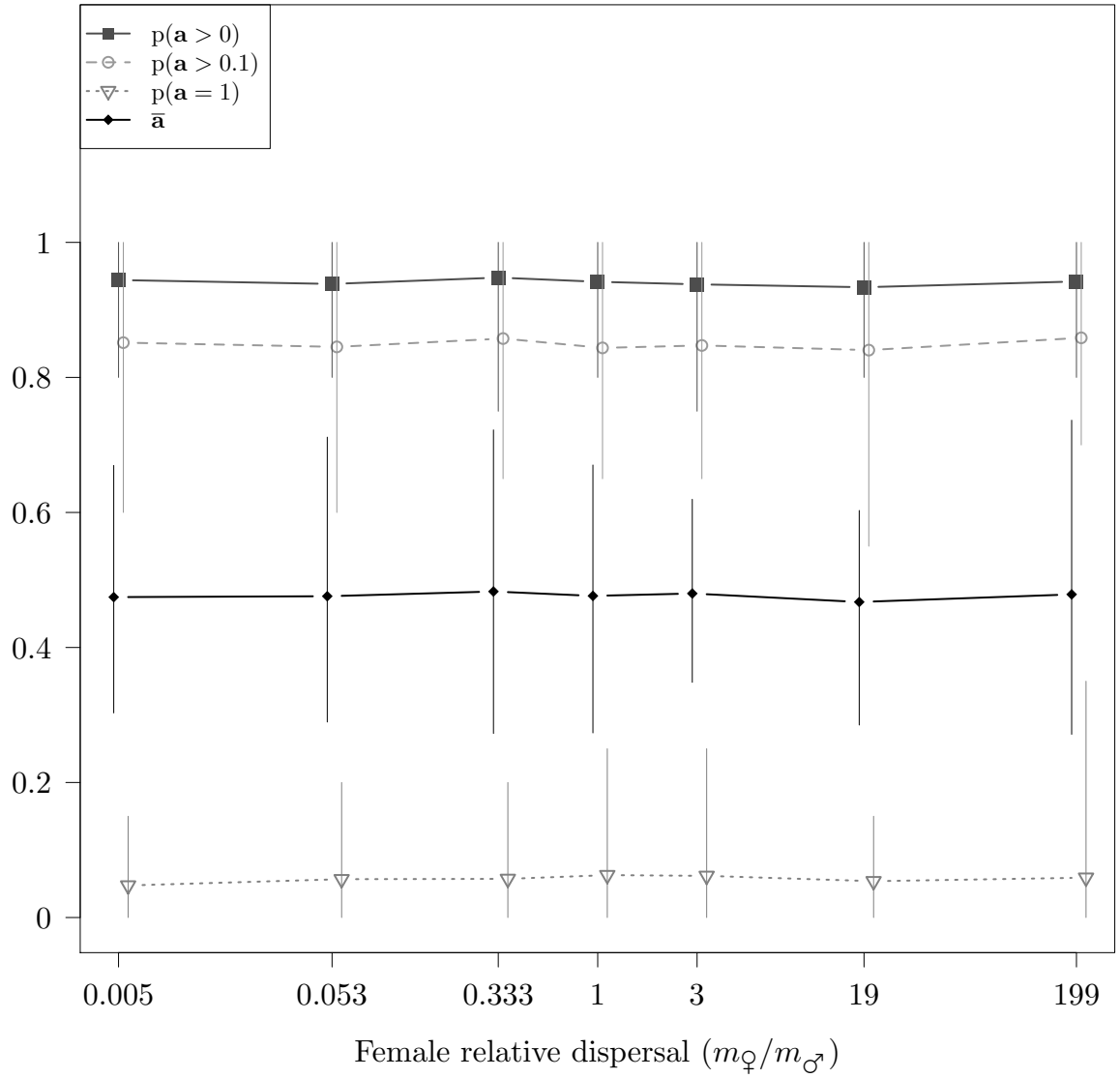
(B) Mitochondrial introgression



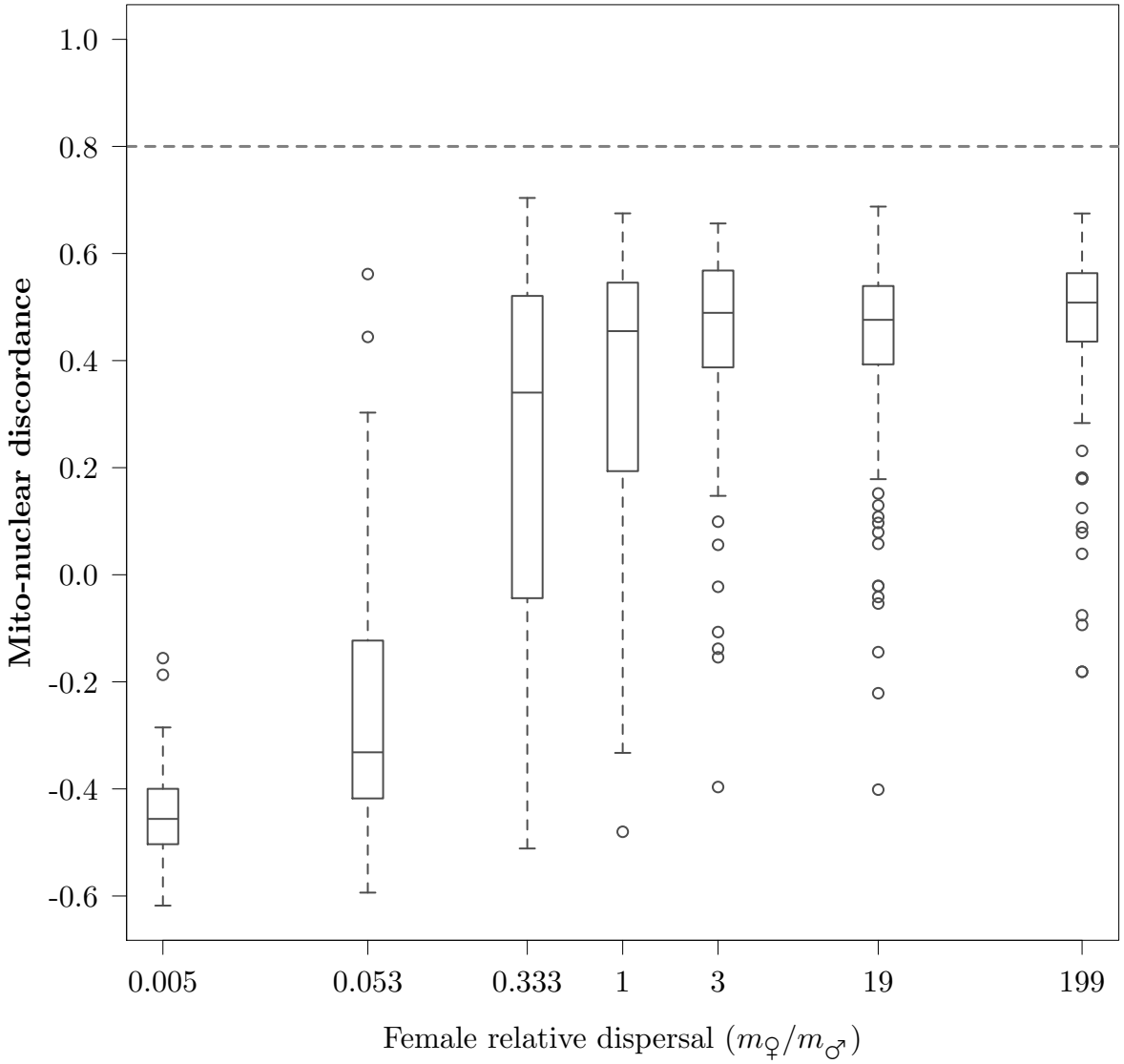
(C) Autosomal introgression



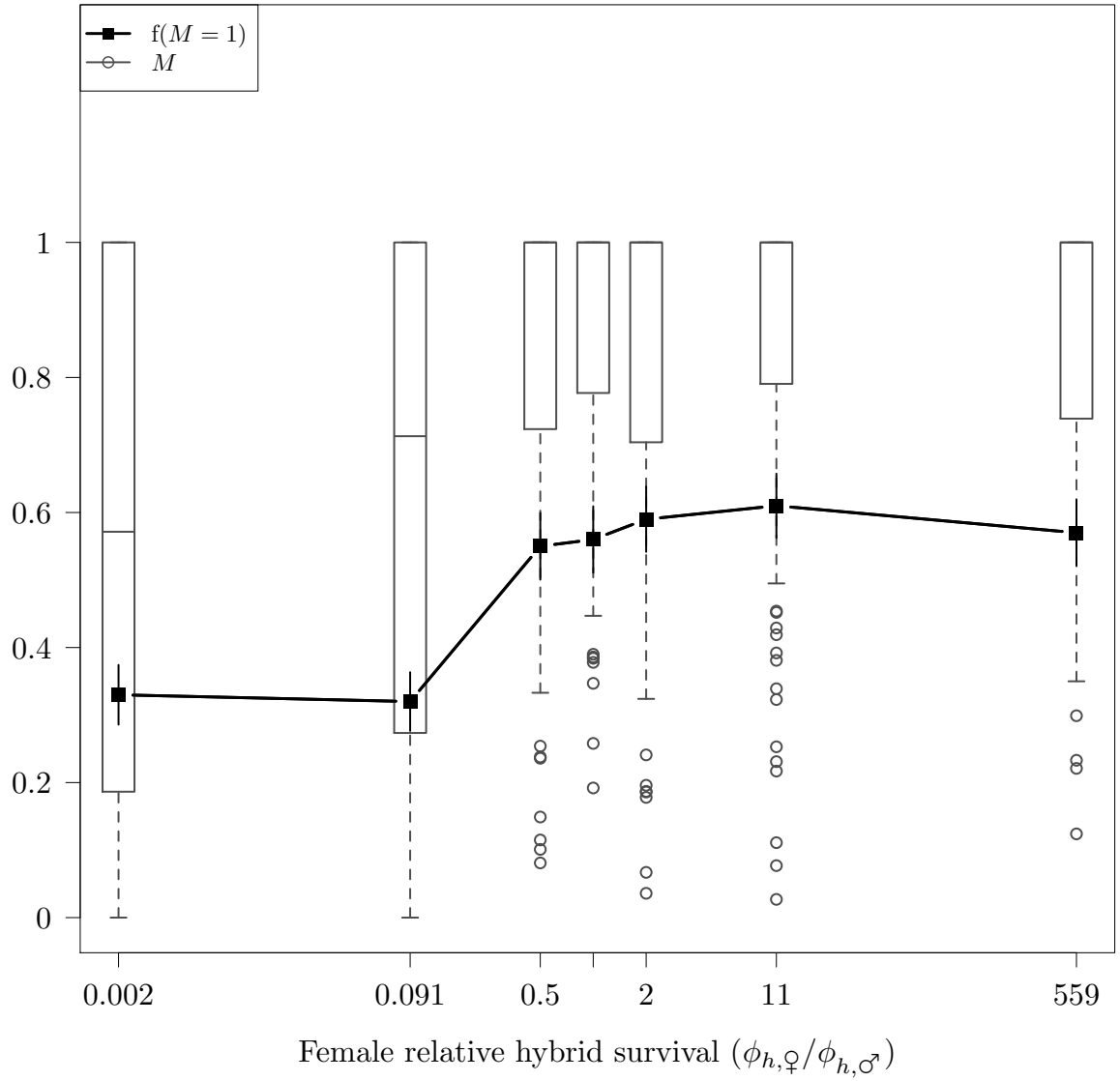
(C) Autosomal introgression

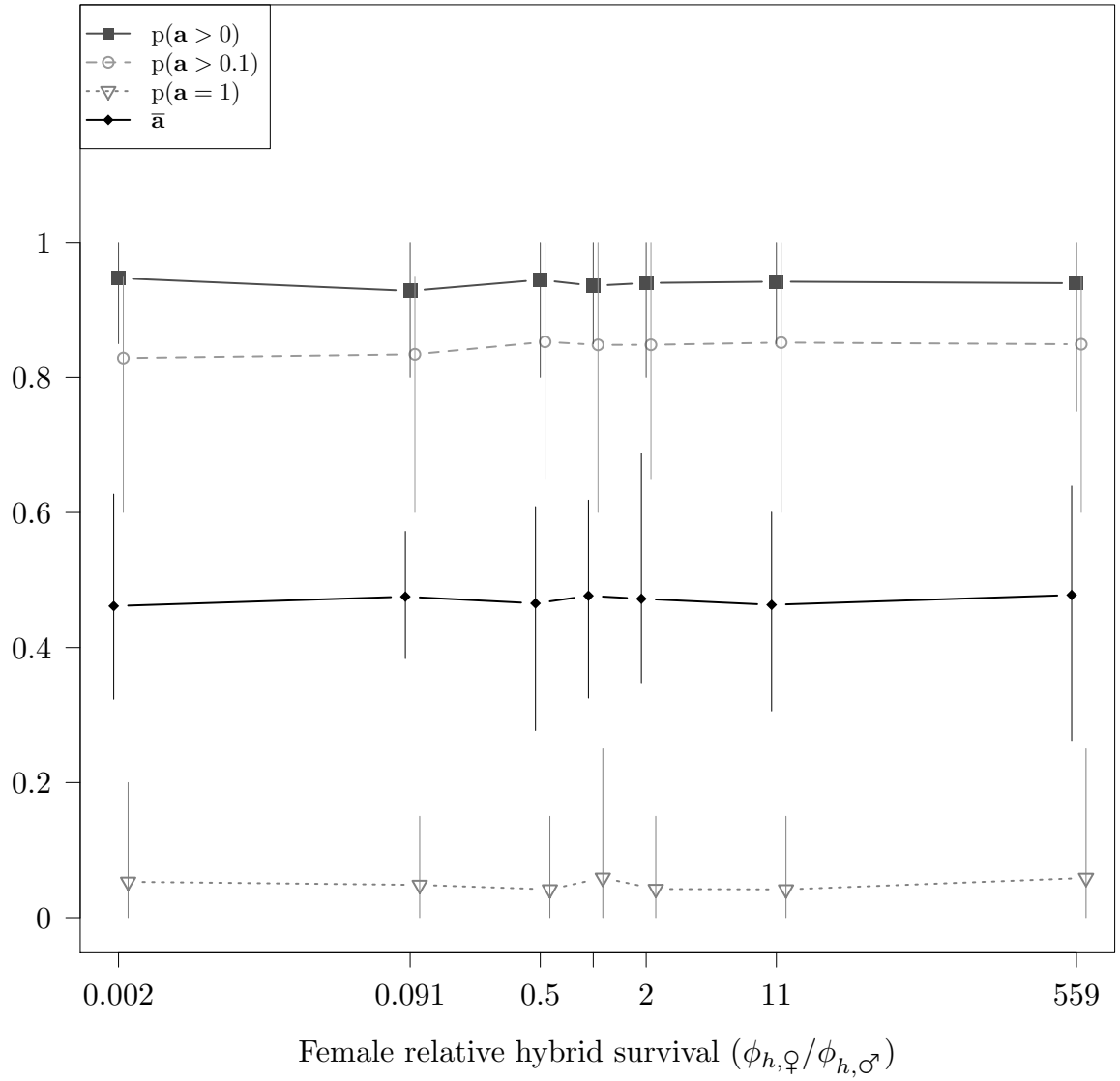


(A) Mito-nuclear discordance

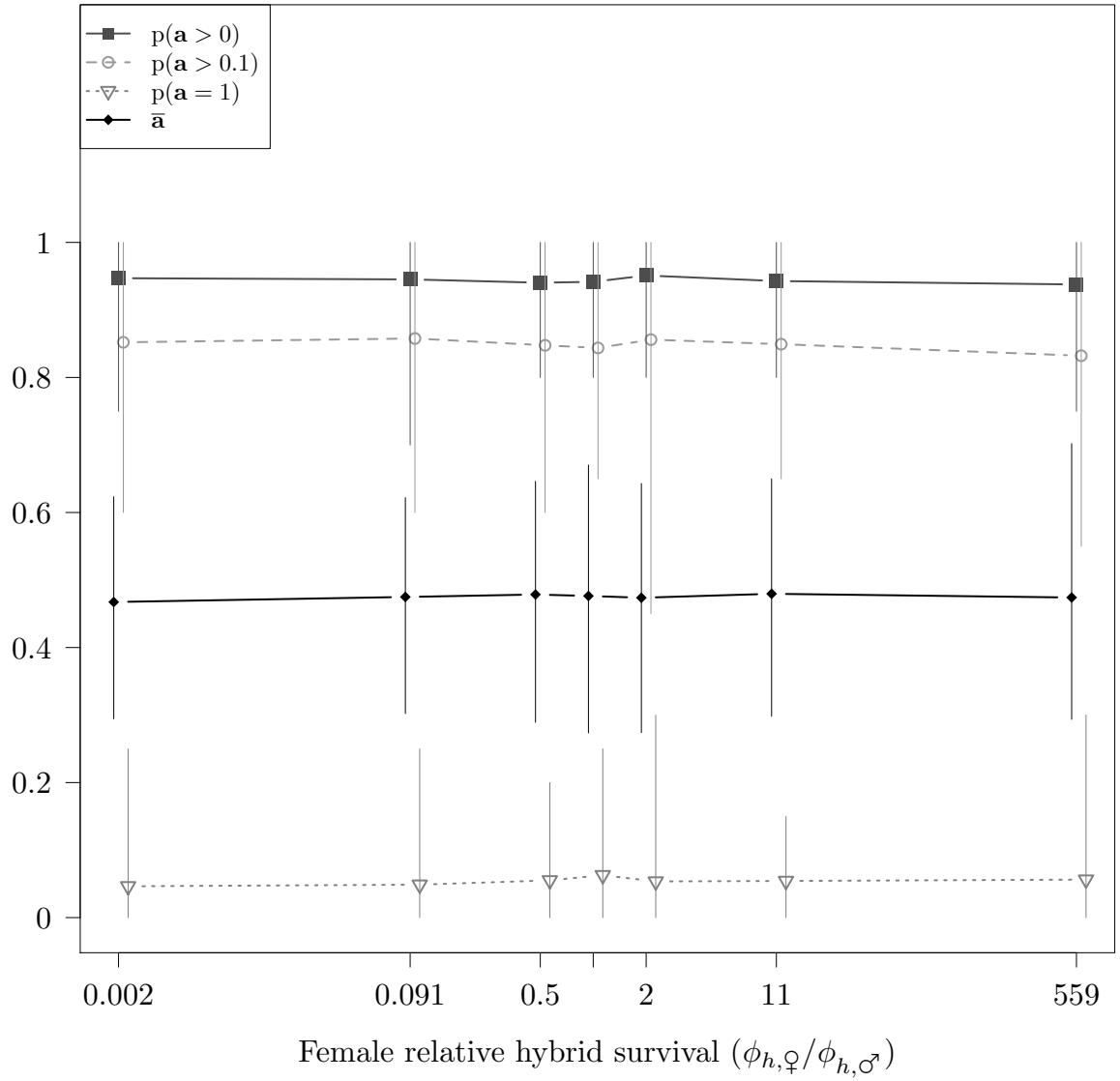


(A) Mitochondrial introgression

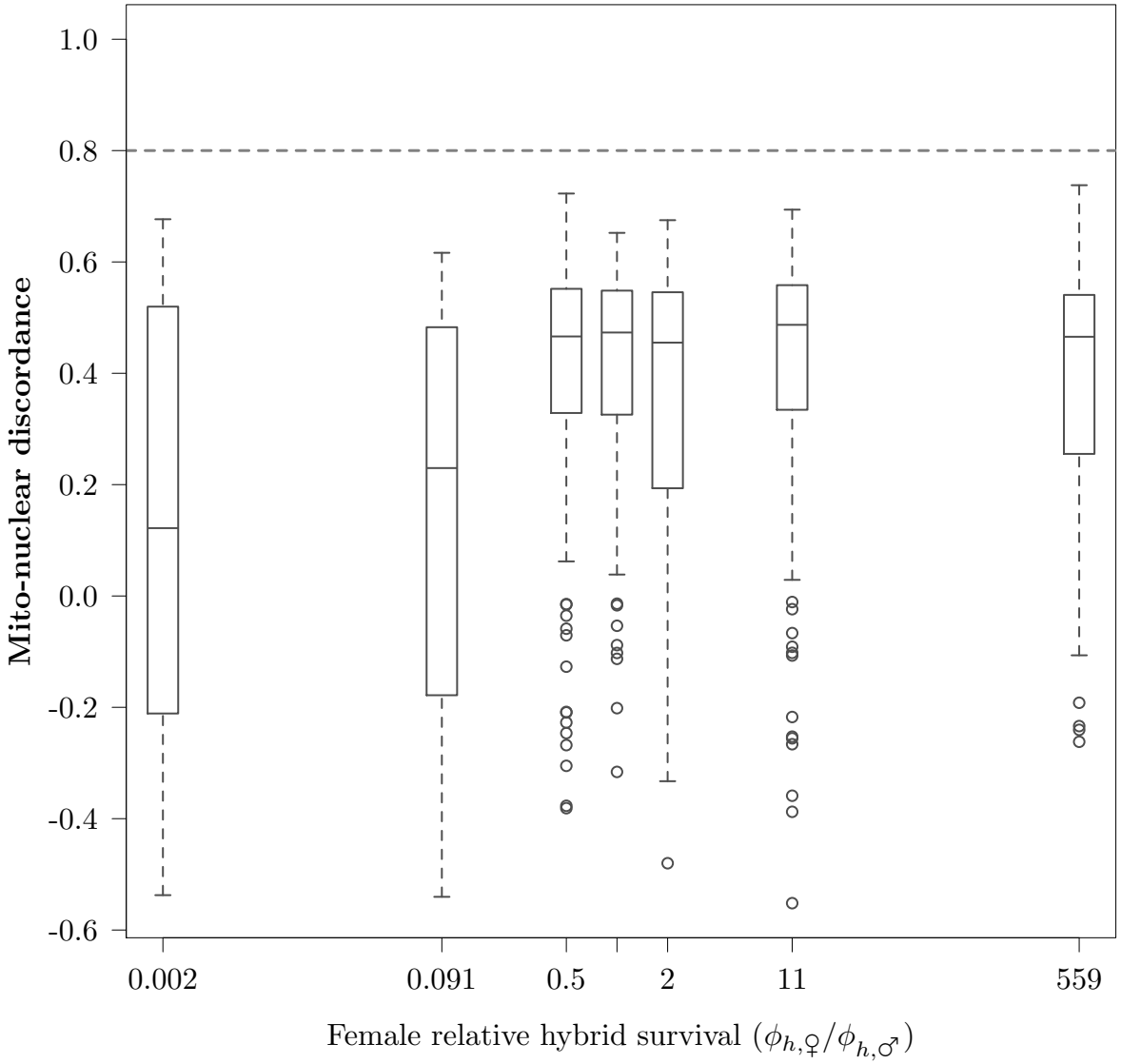



p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
0.002
0.091
0.5
2
11
559
Female relative hybrid survival ($\phi_{h,♀}/\phi_{h,♂}$)

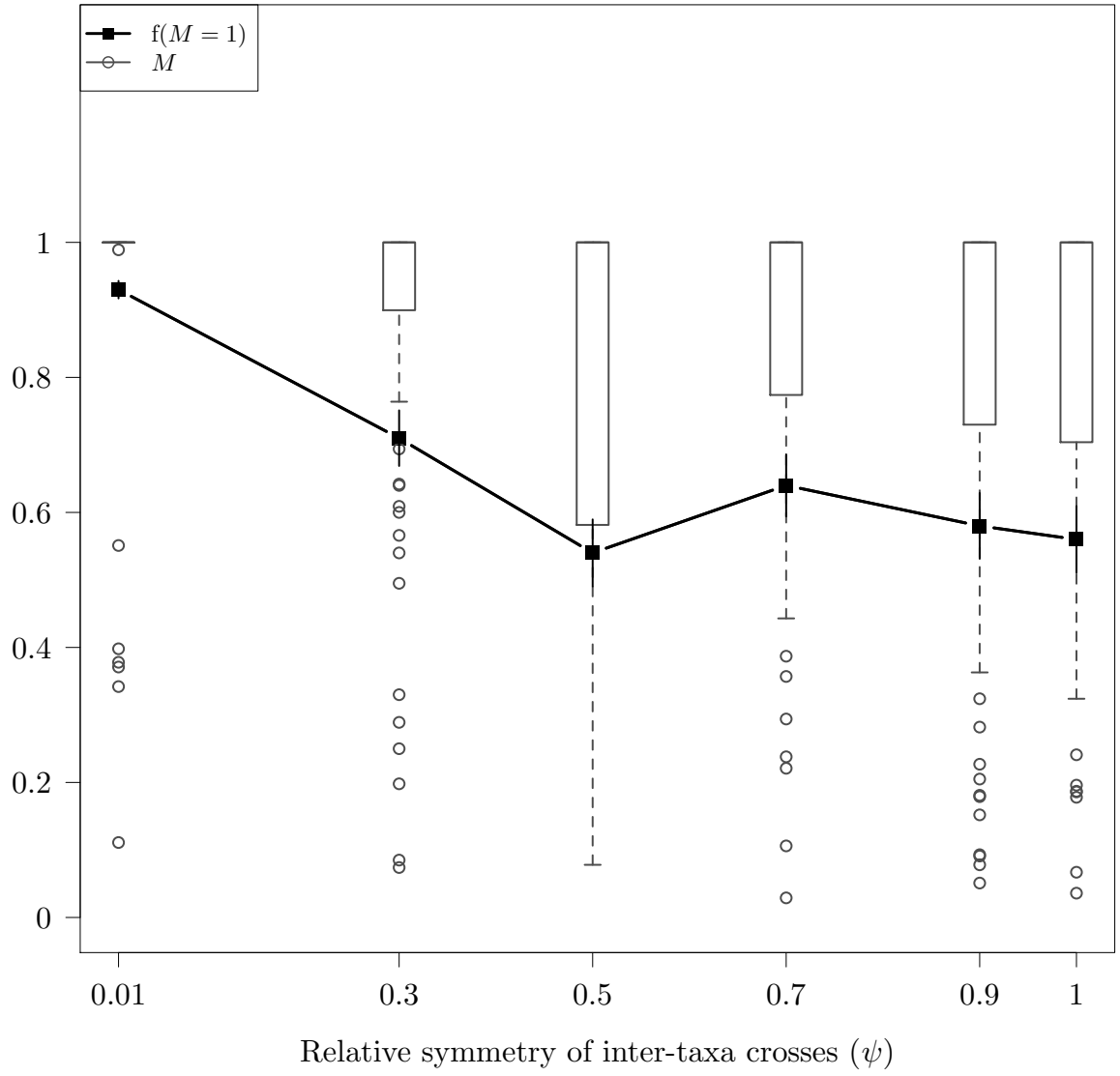
(B) Autosomal introgression



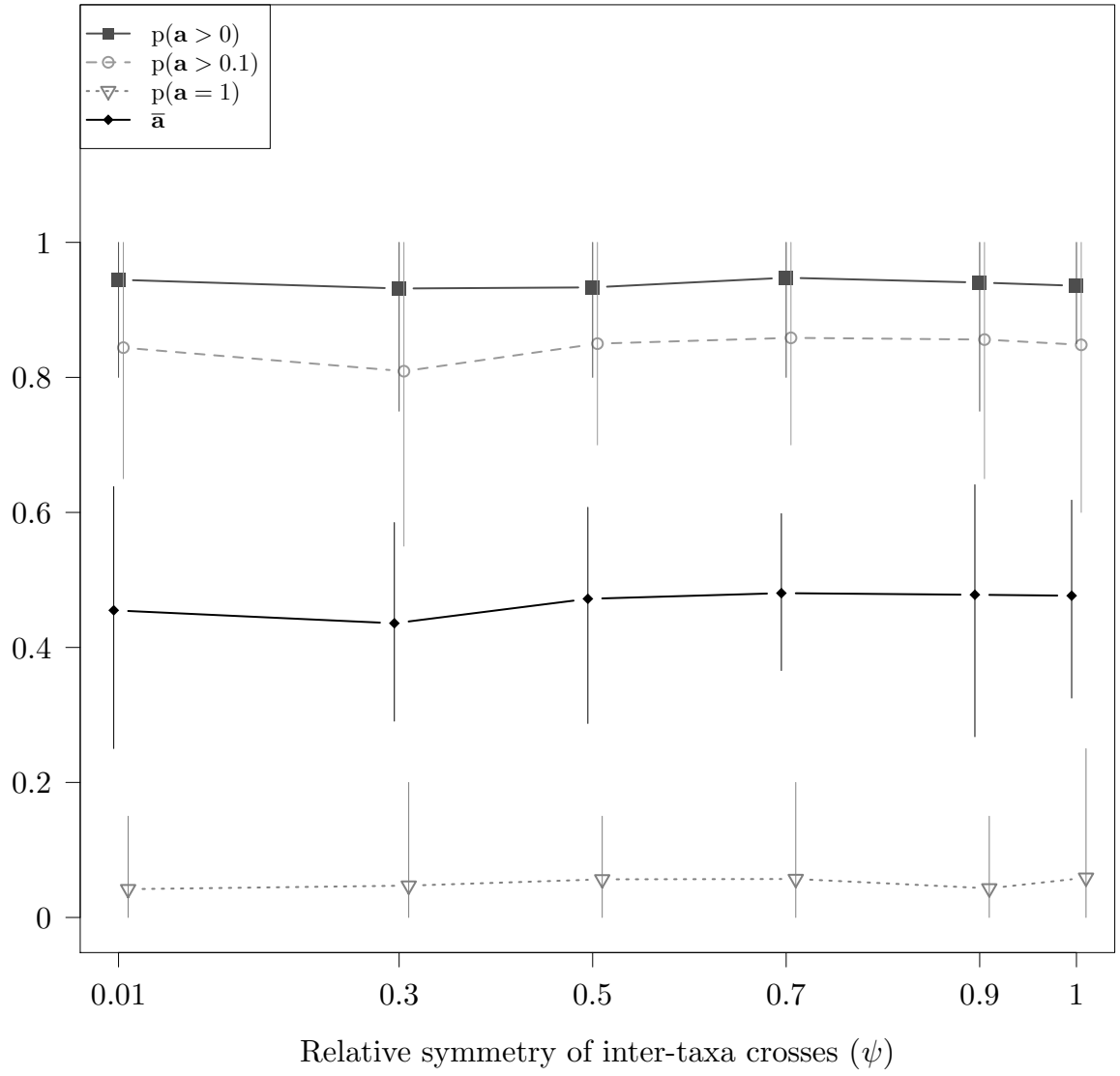
(A) Sex-biased hybrid fitness



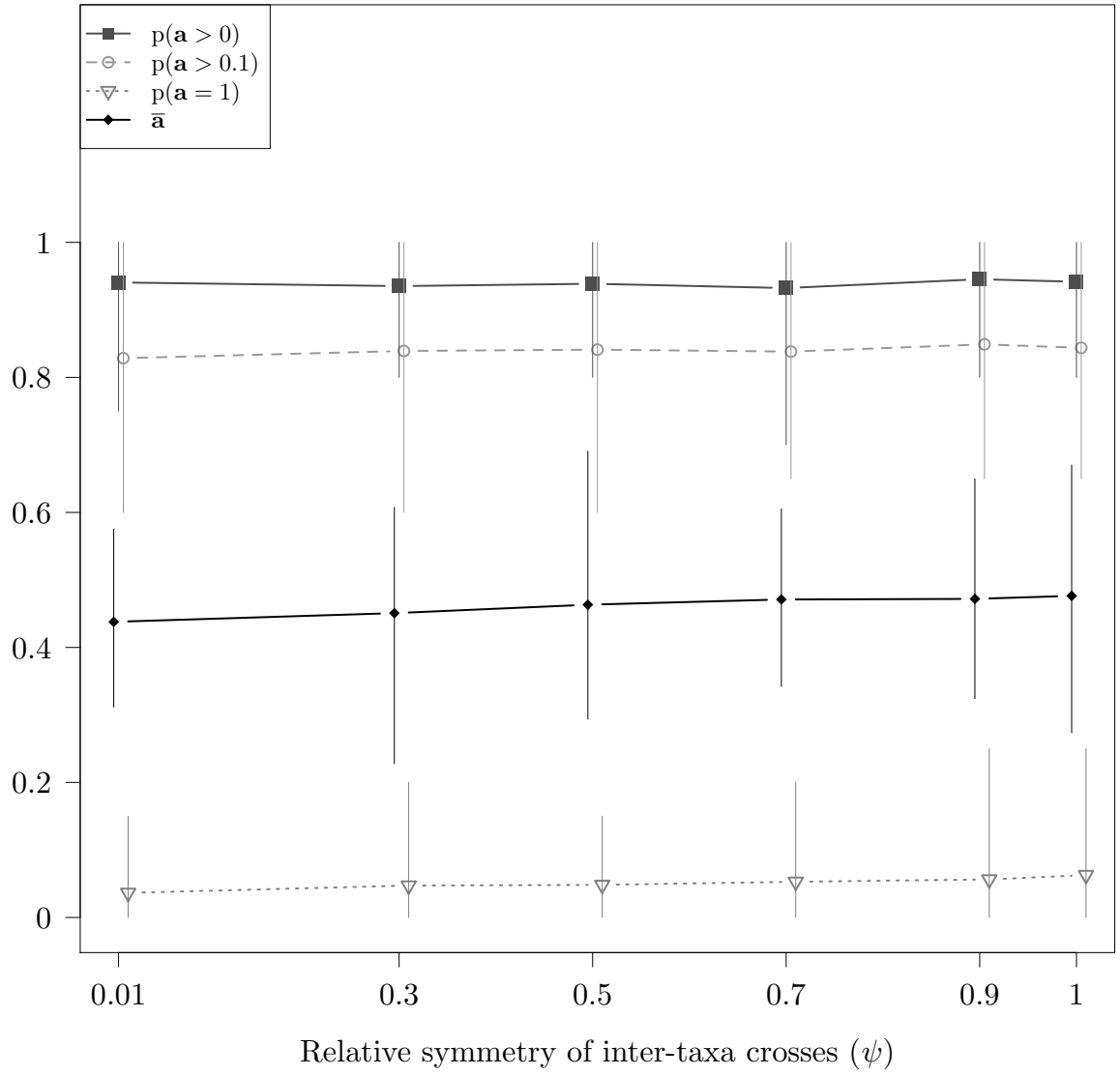
(A) Mitochondrial introgression

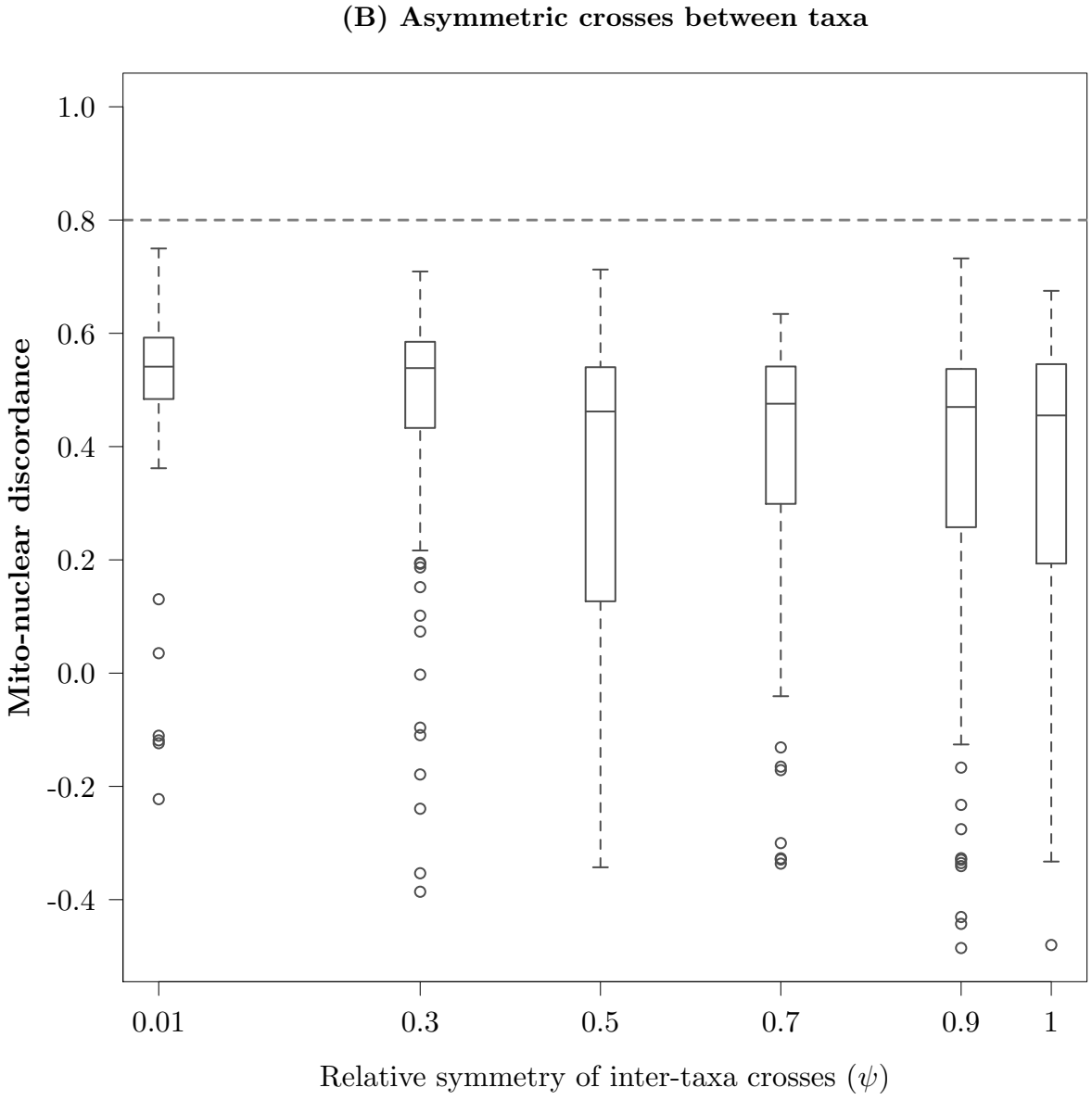


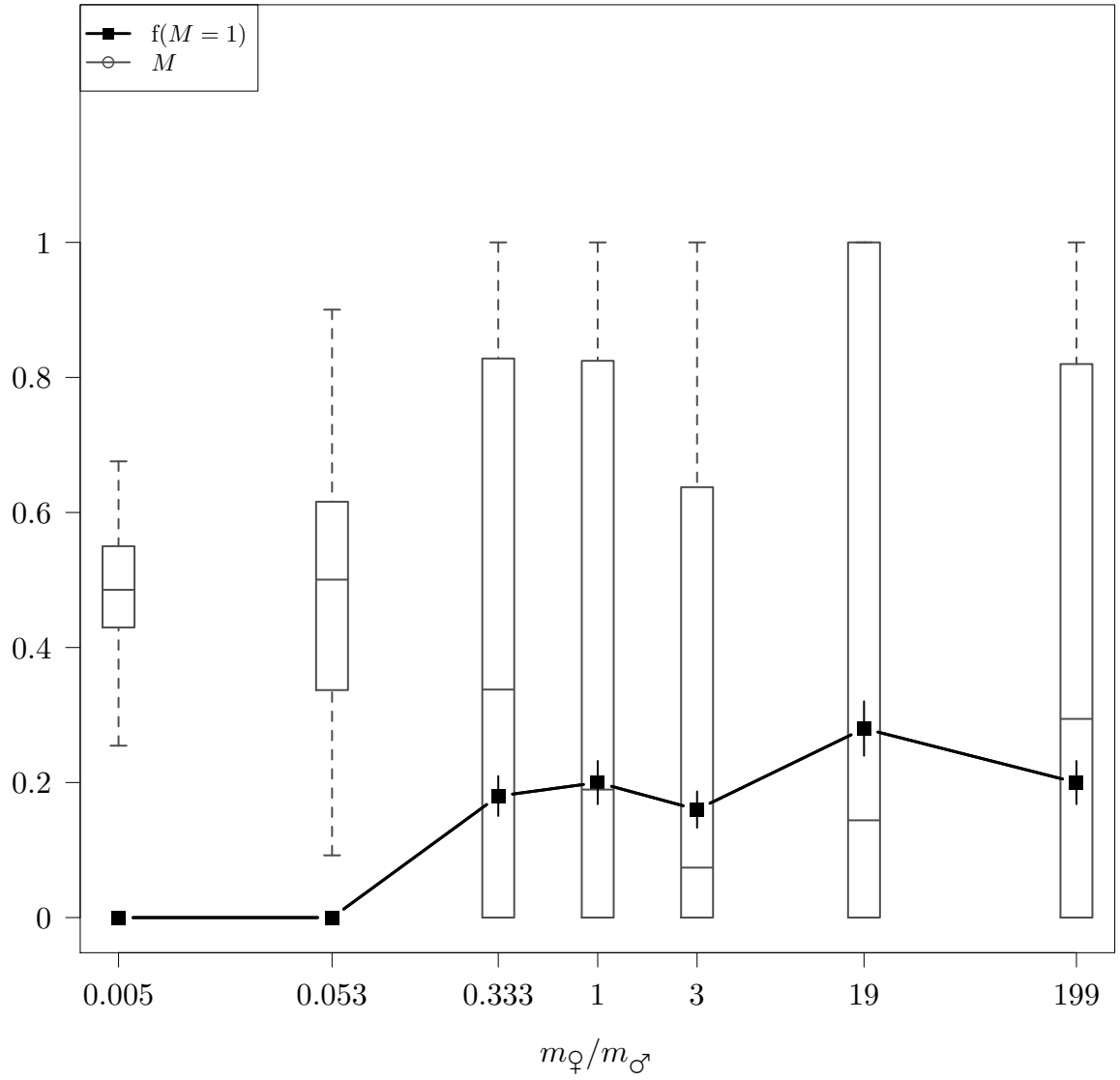
(B) Autosomal introgression

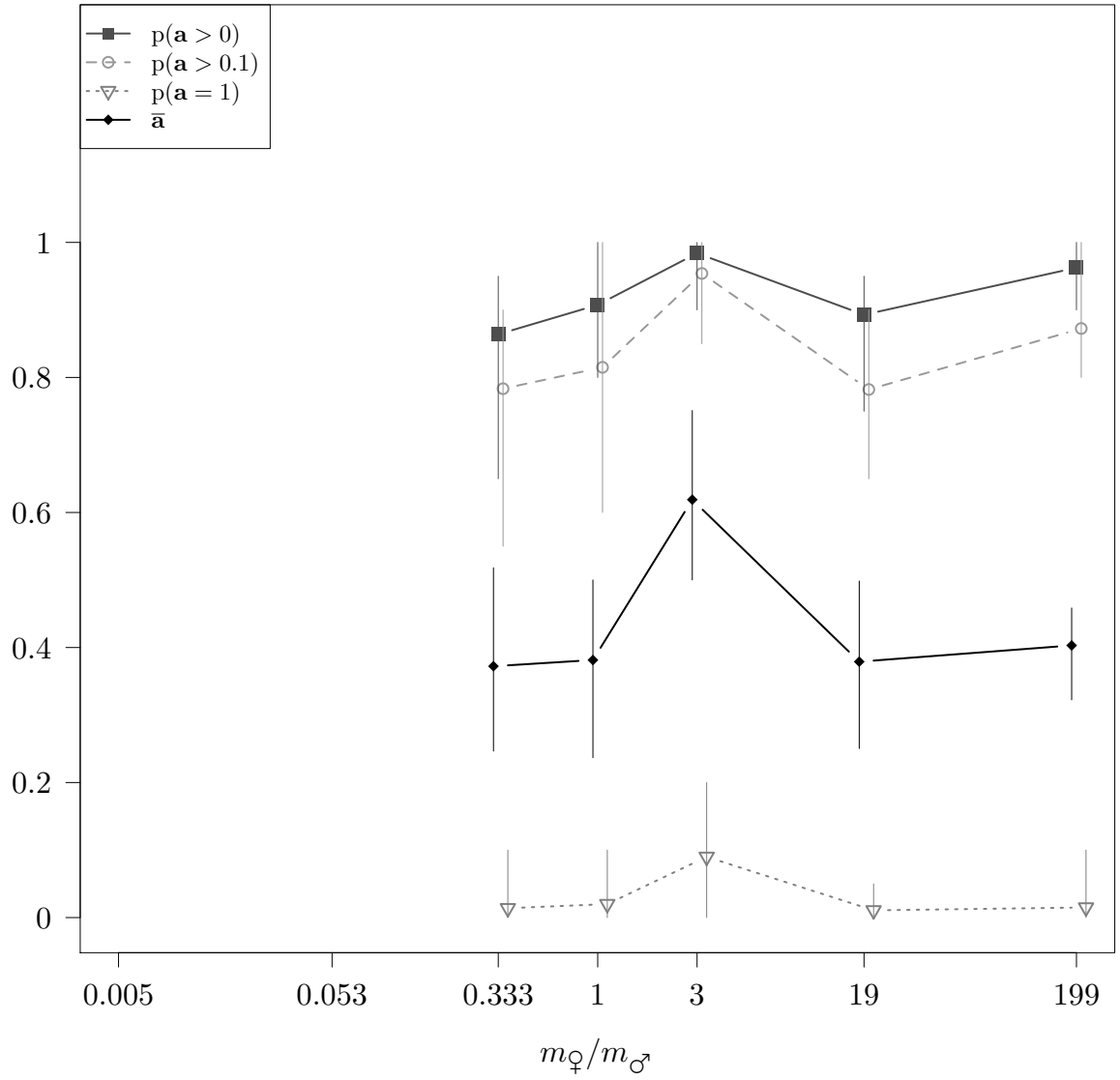


(B) Autosomal introgression

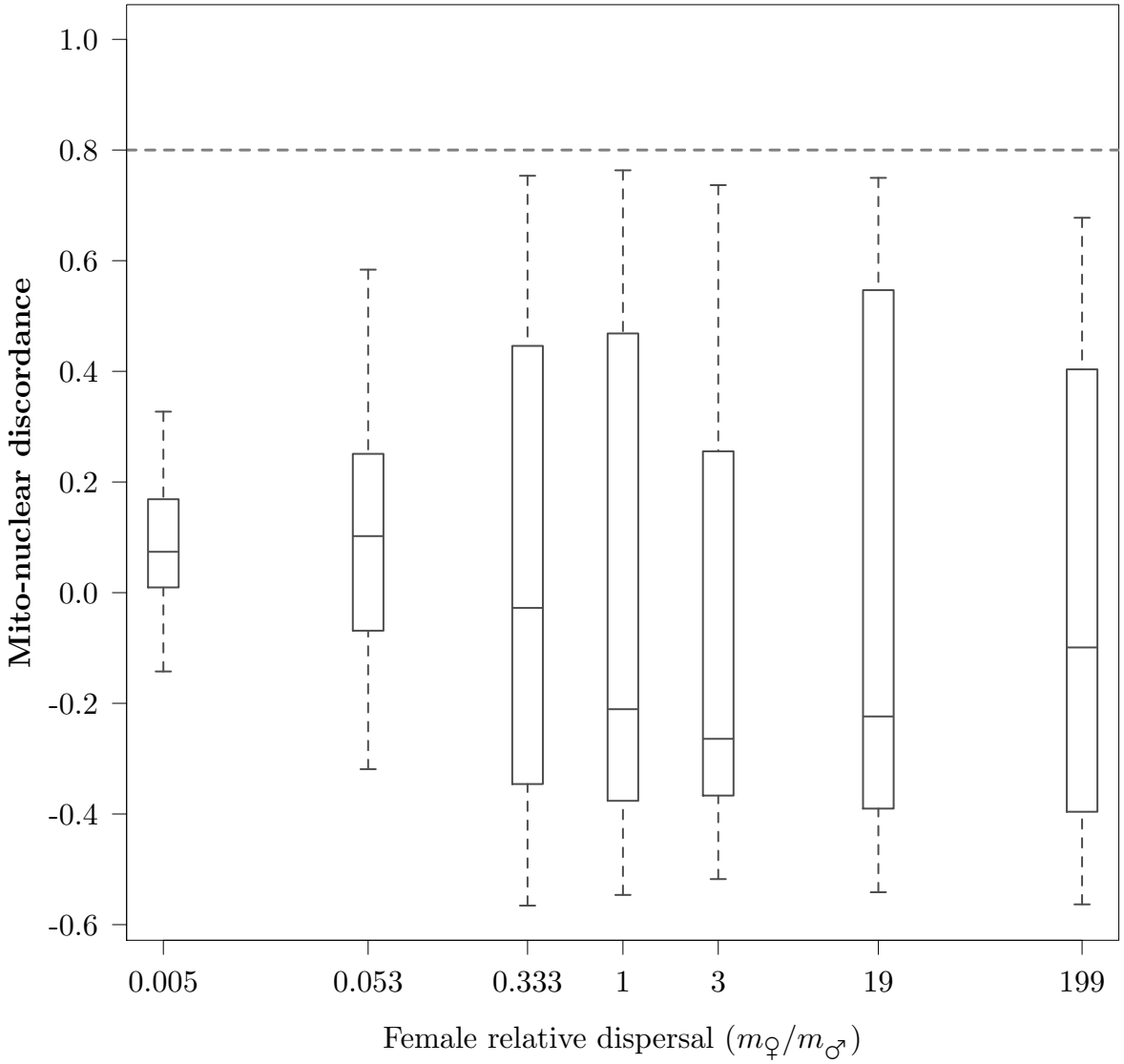


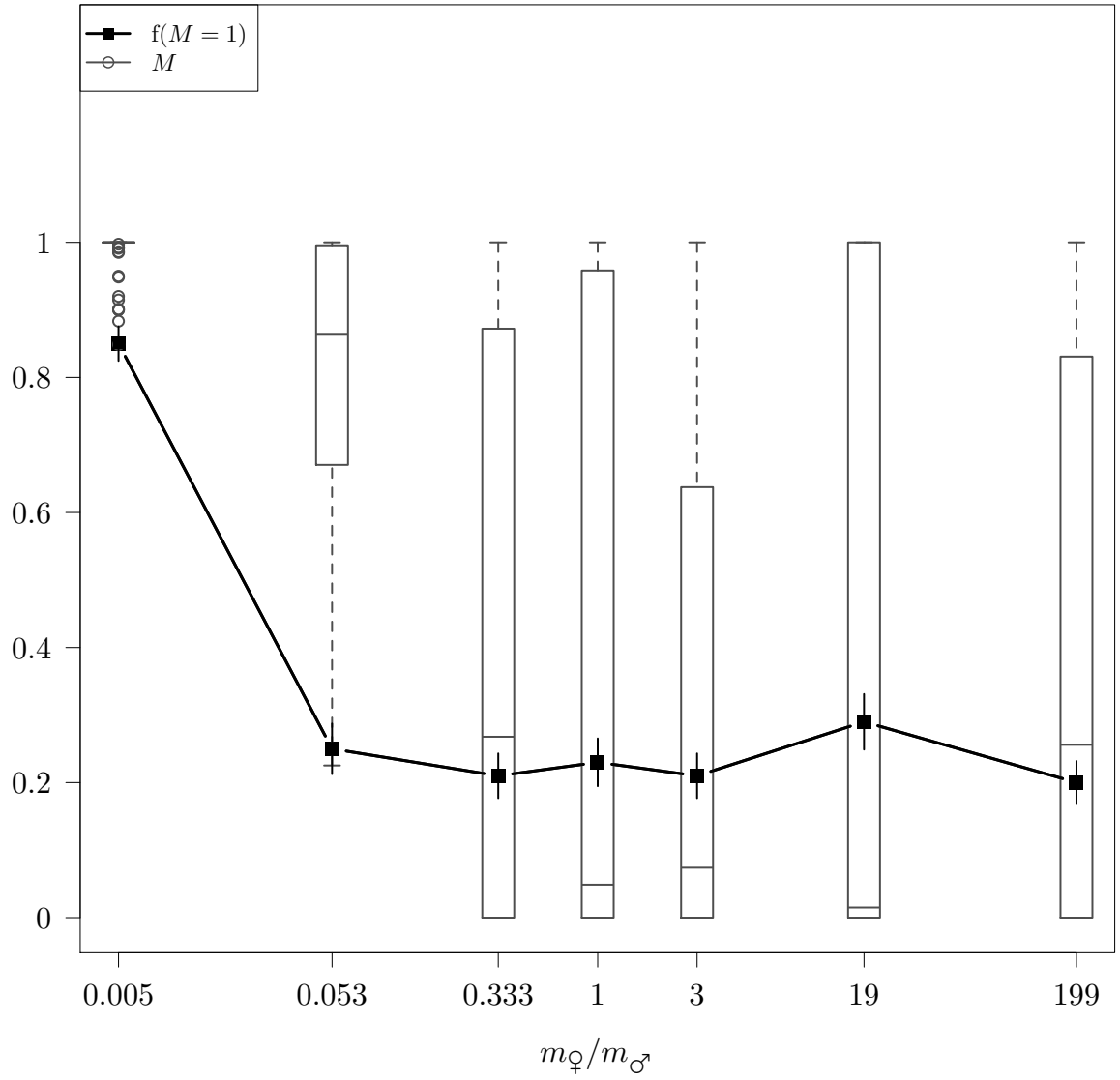

(B) Asymmetric crosses between taxa
Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
0.01
0.3
0.5
0.7
0.9
1
Relative symmetry of inter-taxa crosses (ψ)

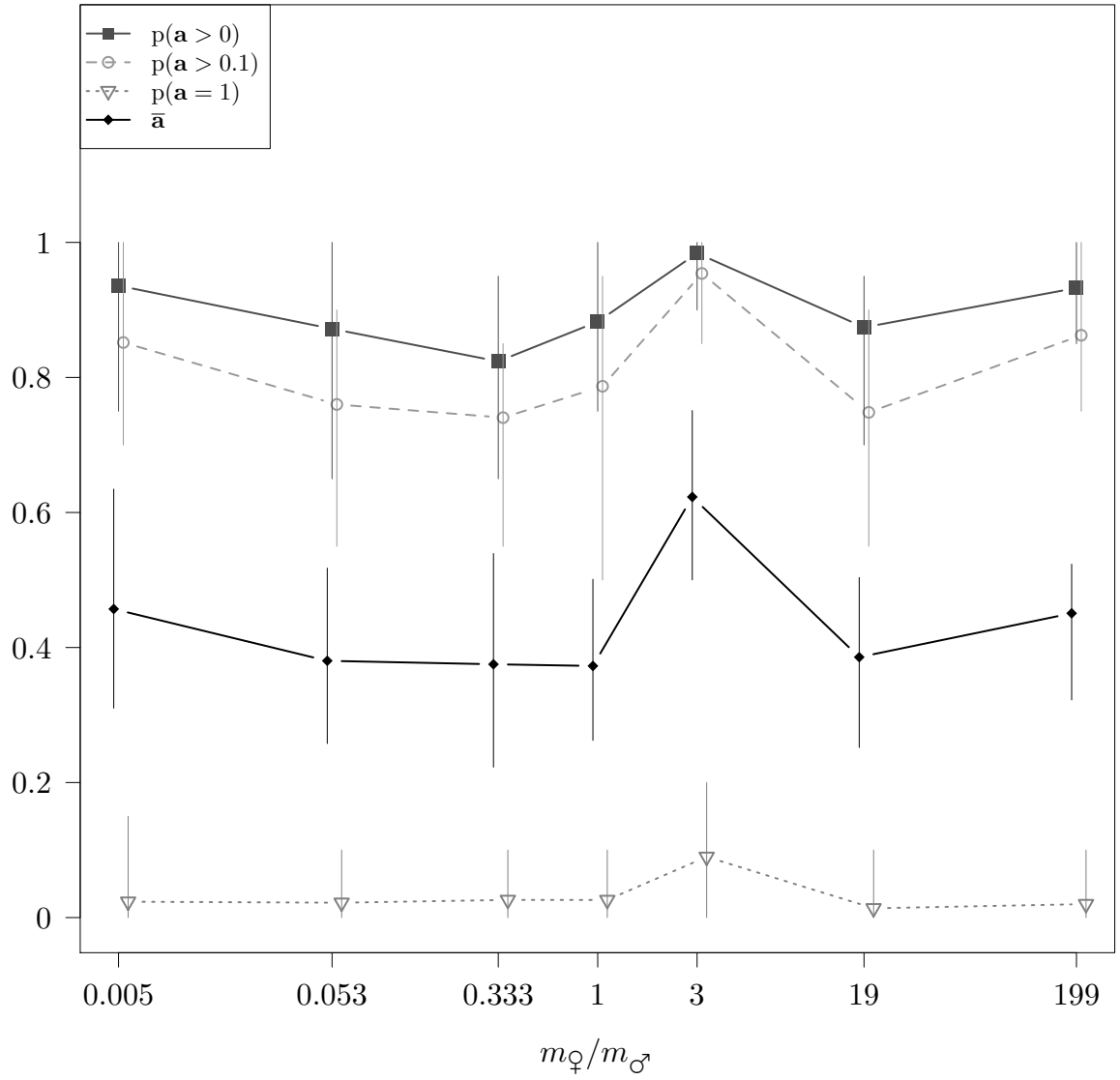

f(M = 1)
M
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.333
1
3
19
199
m♀/m♂


p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.333
1
3
19
199
m♀/m♂

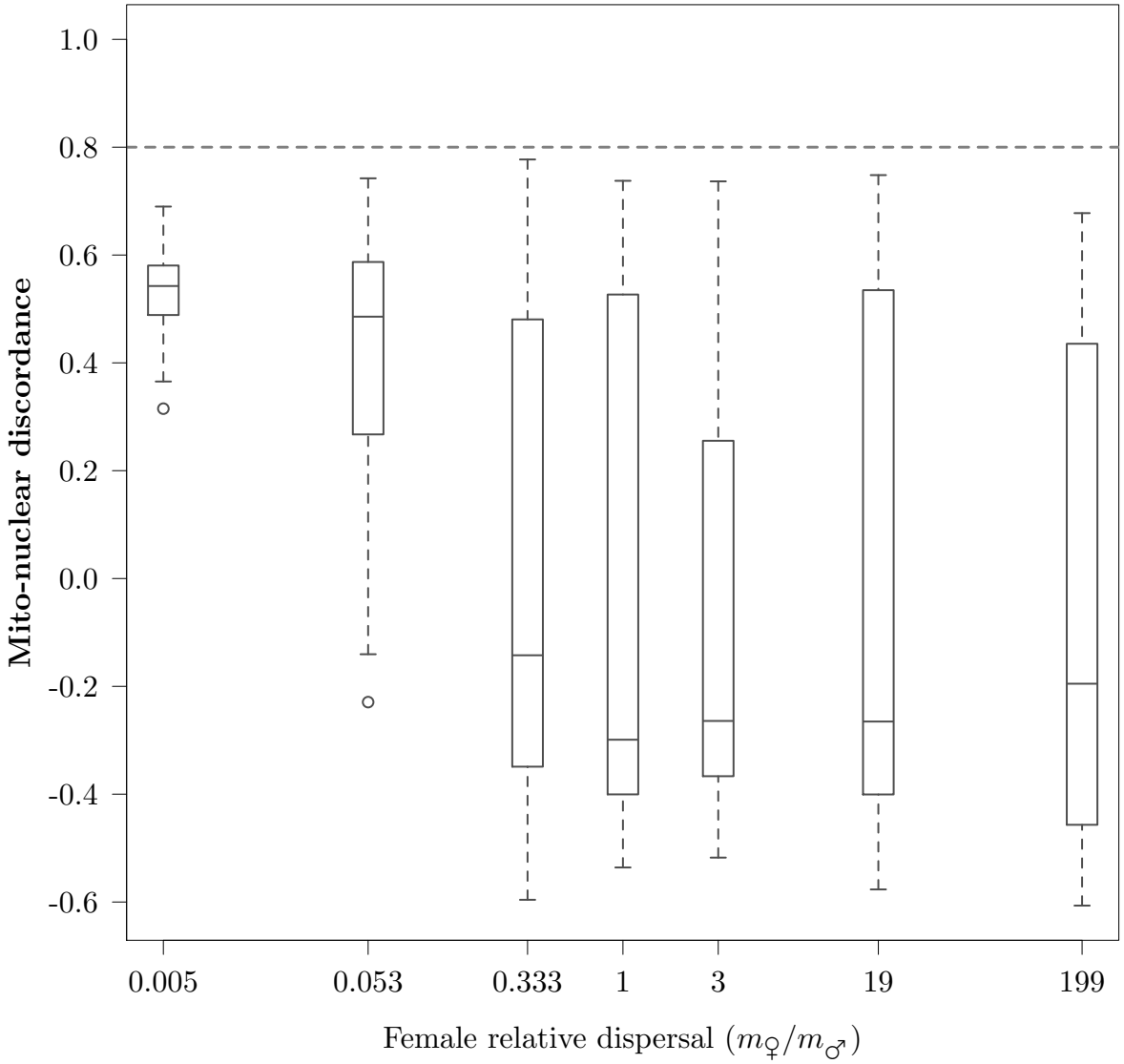
(A) Whole area

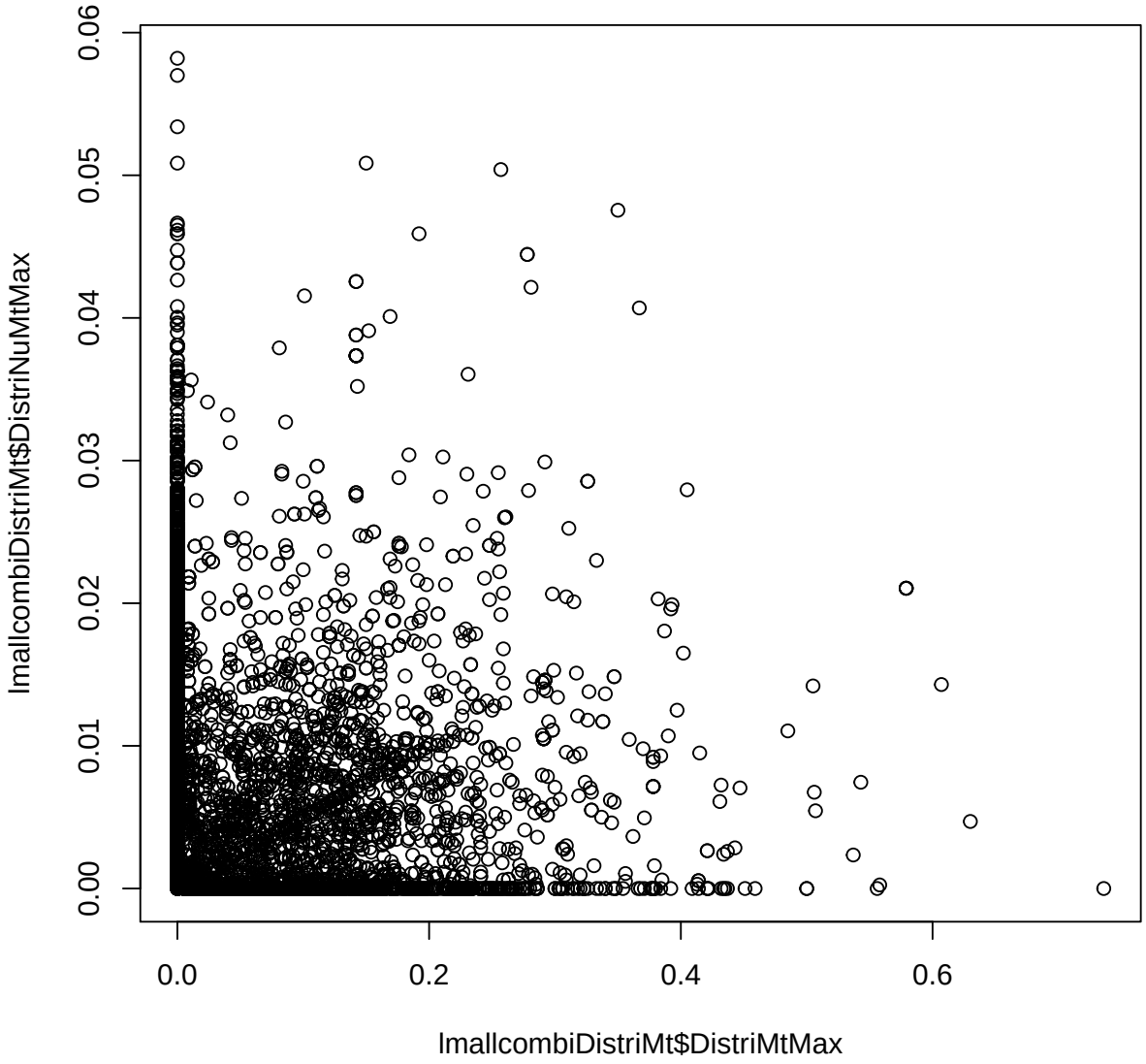

Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
0.005
0.053
0.333
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)


f($M = 1$)
M
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.333
1
3
19
199
$m_♀/m_♂$


p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.333
1
3
19
199
m♀/m♂

(B) Invaded area



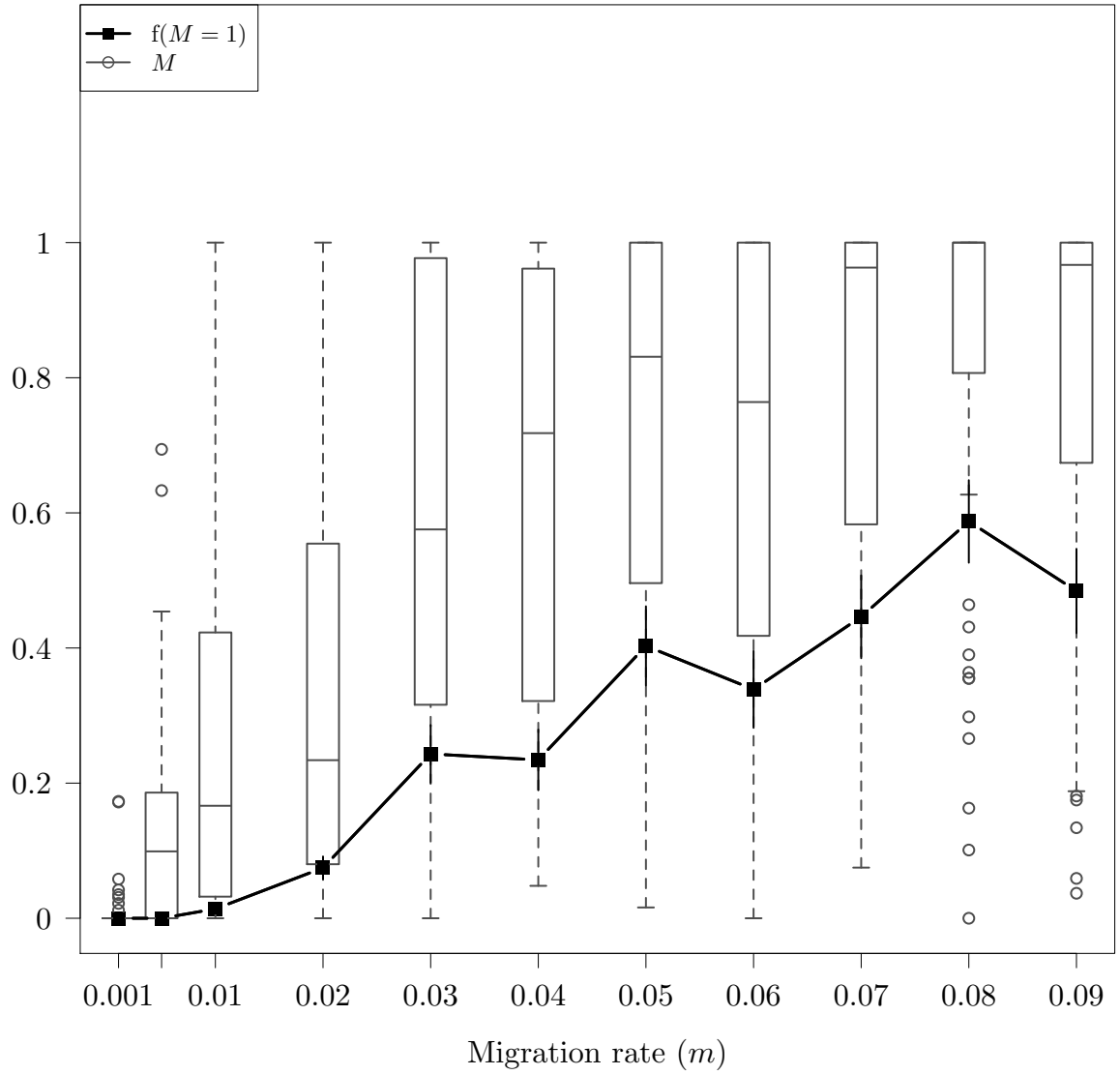


[1] 0.08150453

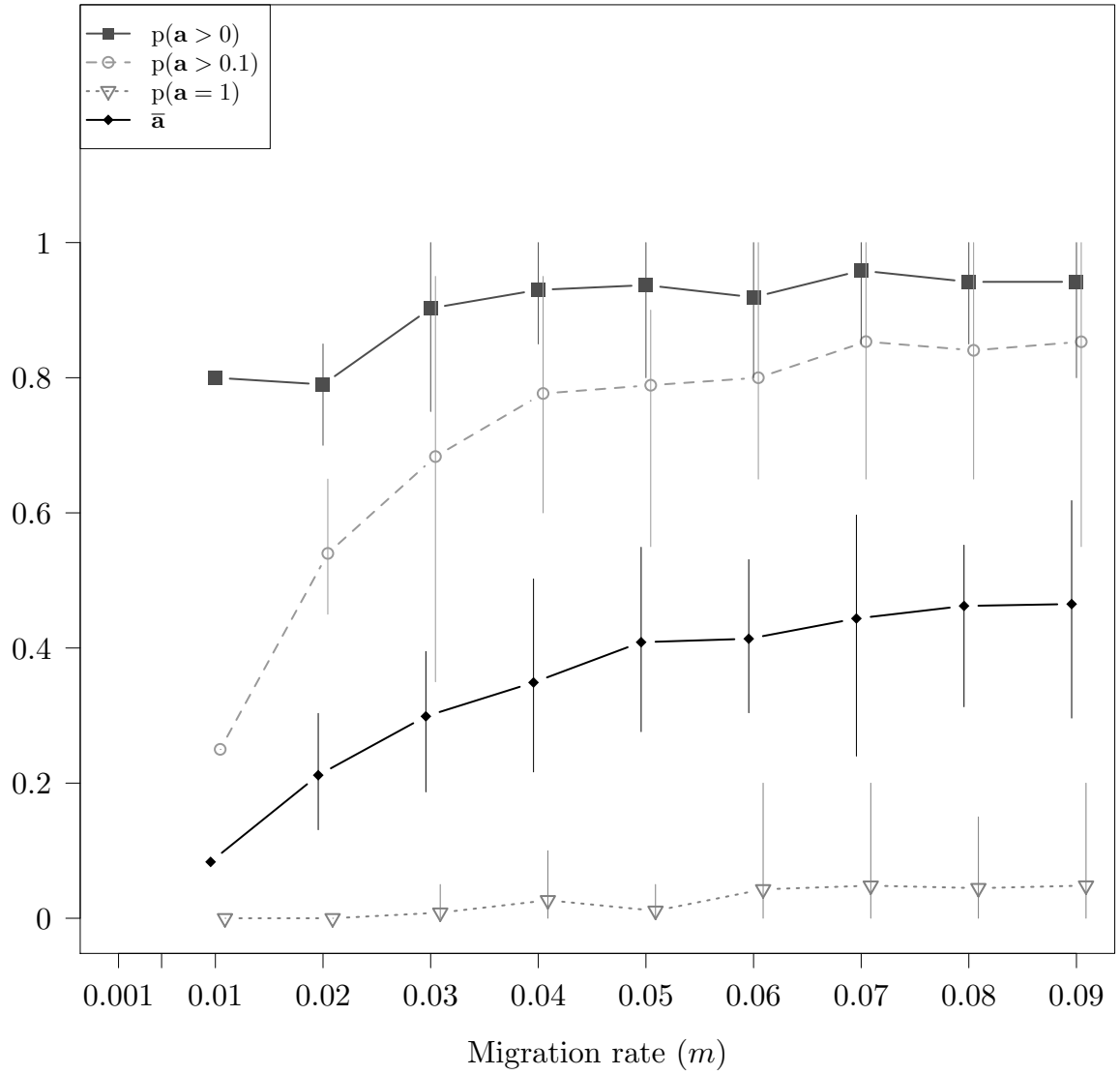
Pearson's product-moment correlation

data: lmallcombiDistriMt*DistriMtMax*and*lmallcombiDistriMt*DistriNuMtMax t = 11.58, df = 20052, p-value ¡ 2.2e-16 alternative hypothesis: true correlation is not equal to 0 95 percent confidence interval: 0.06774042 0.09523761 sample estimates: cor 0.08150453

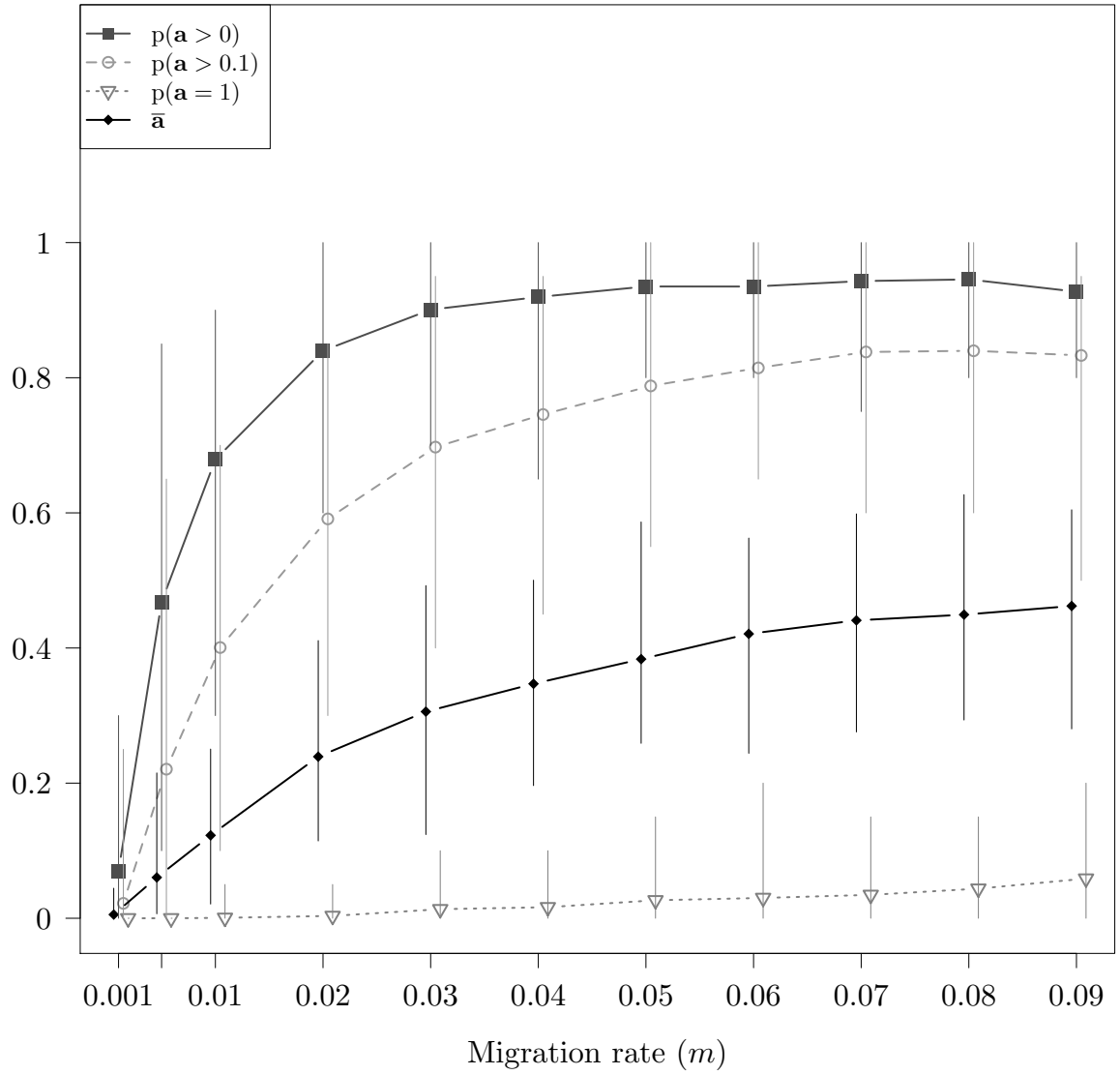
(A) Mitochondrial introgression



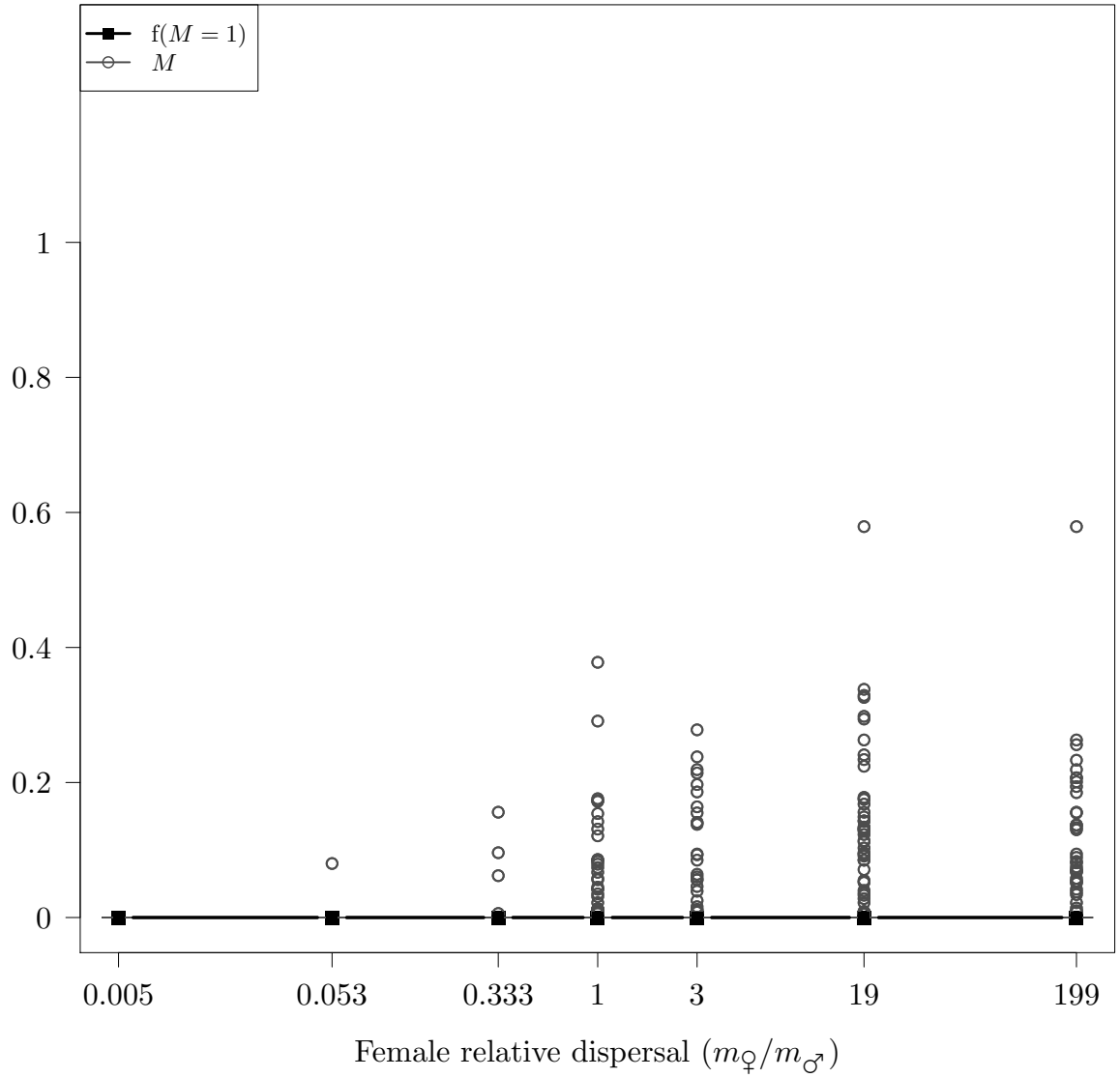
(B) Autosomal introgression



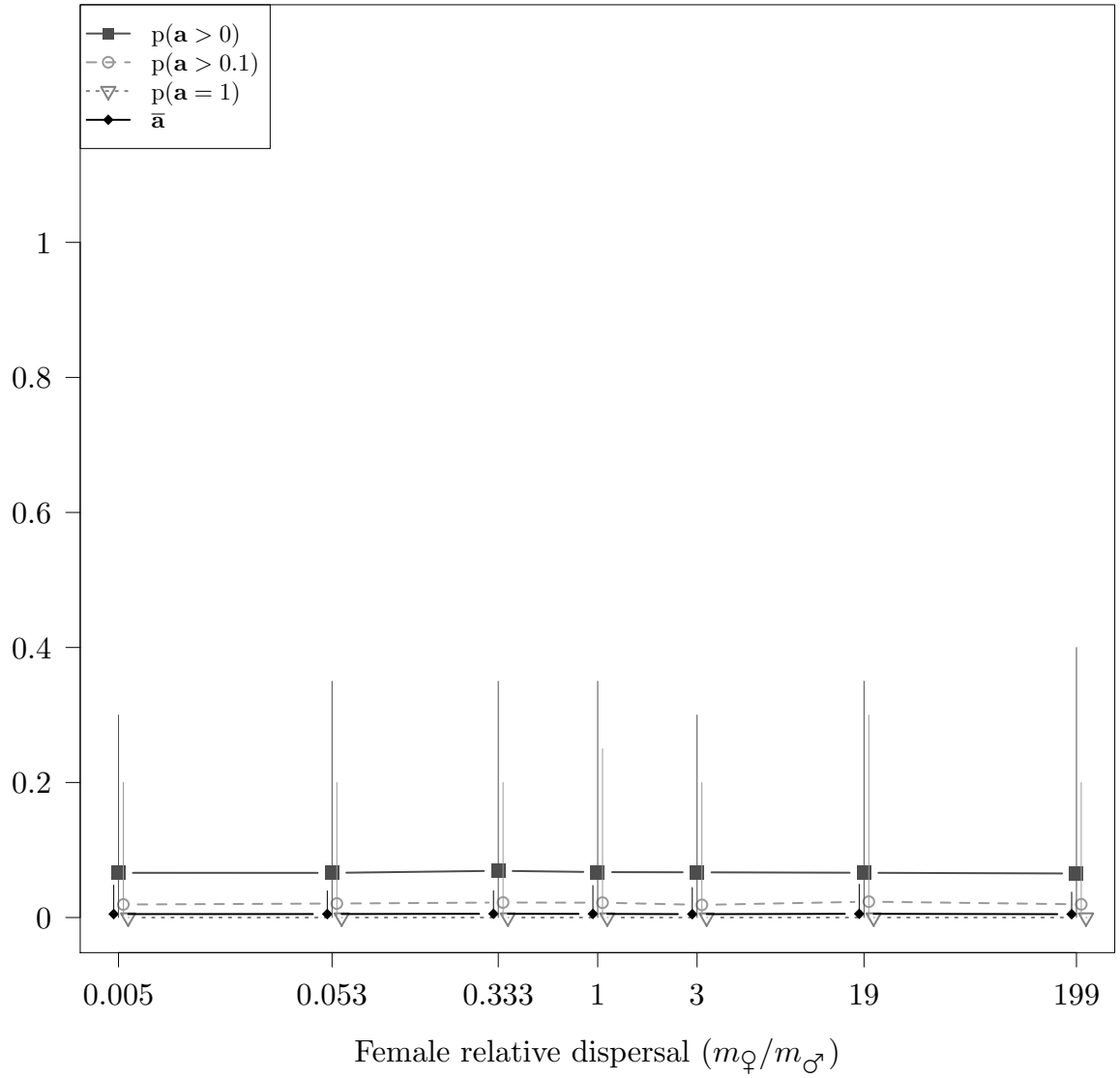
(B) Autosomal introgression



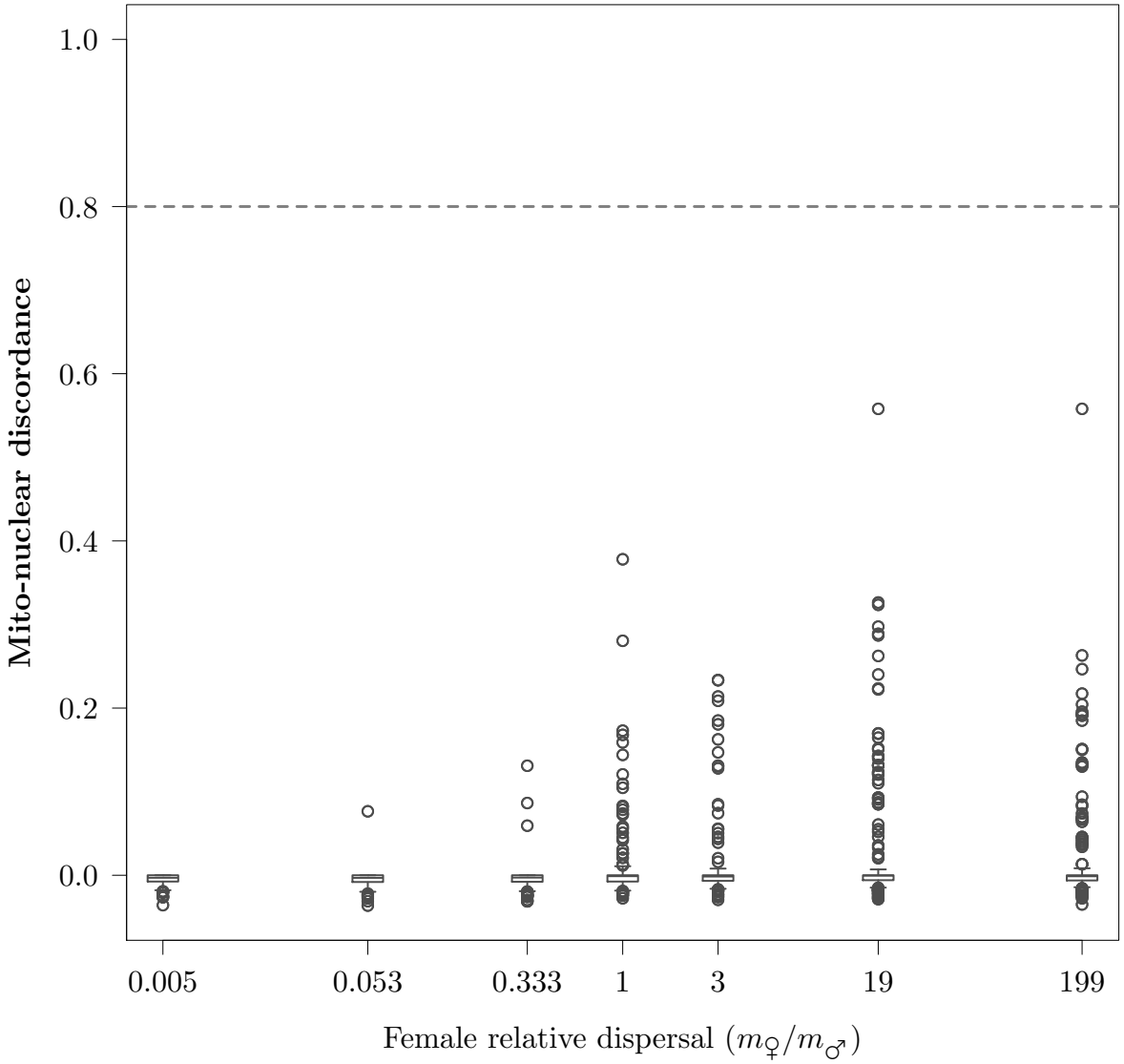
(B) Mitochondrial introgression



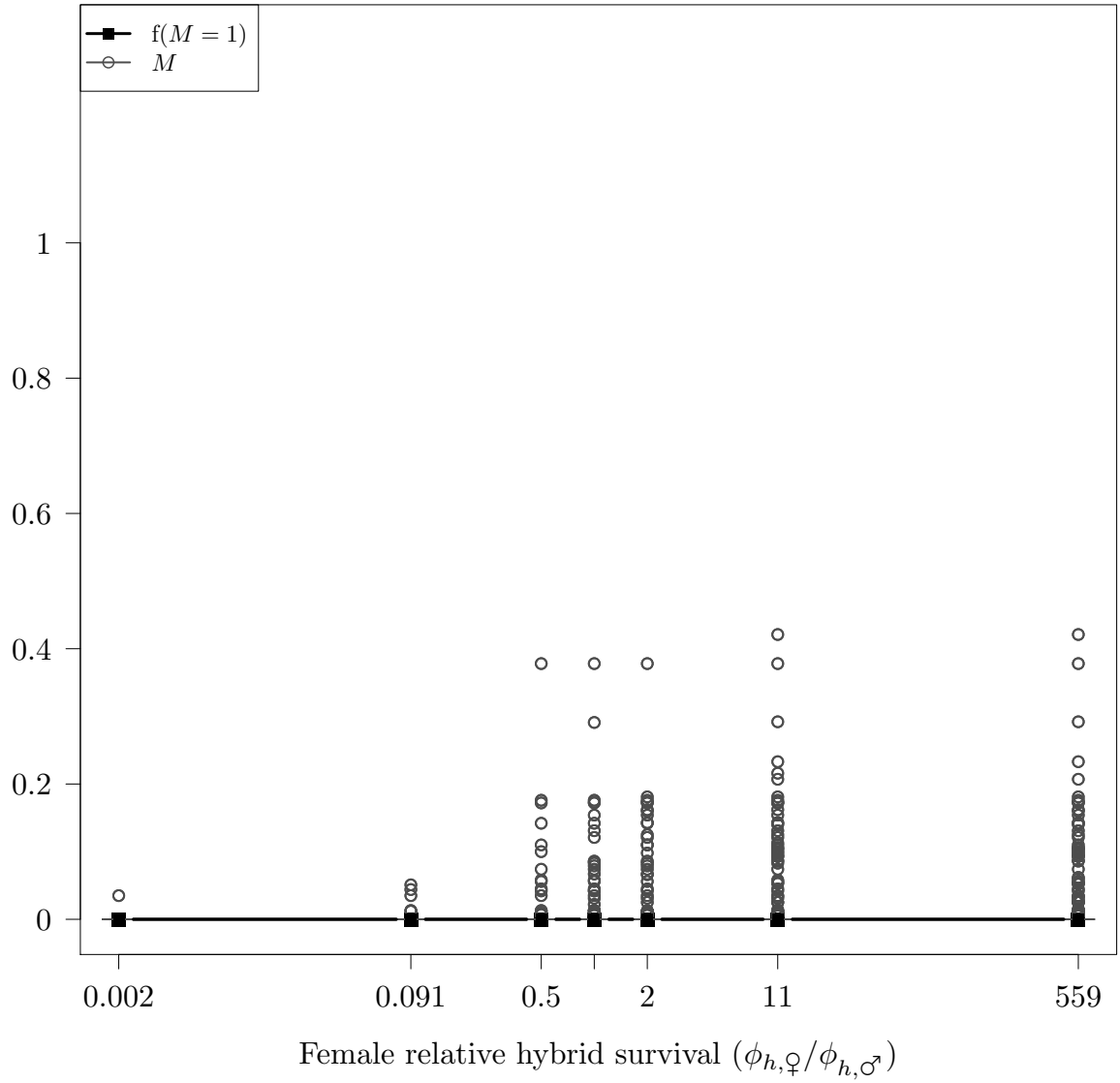
(C) Autosomal introgression



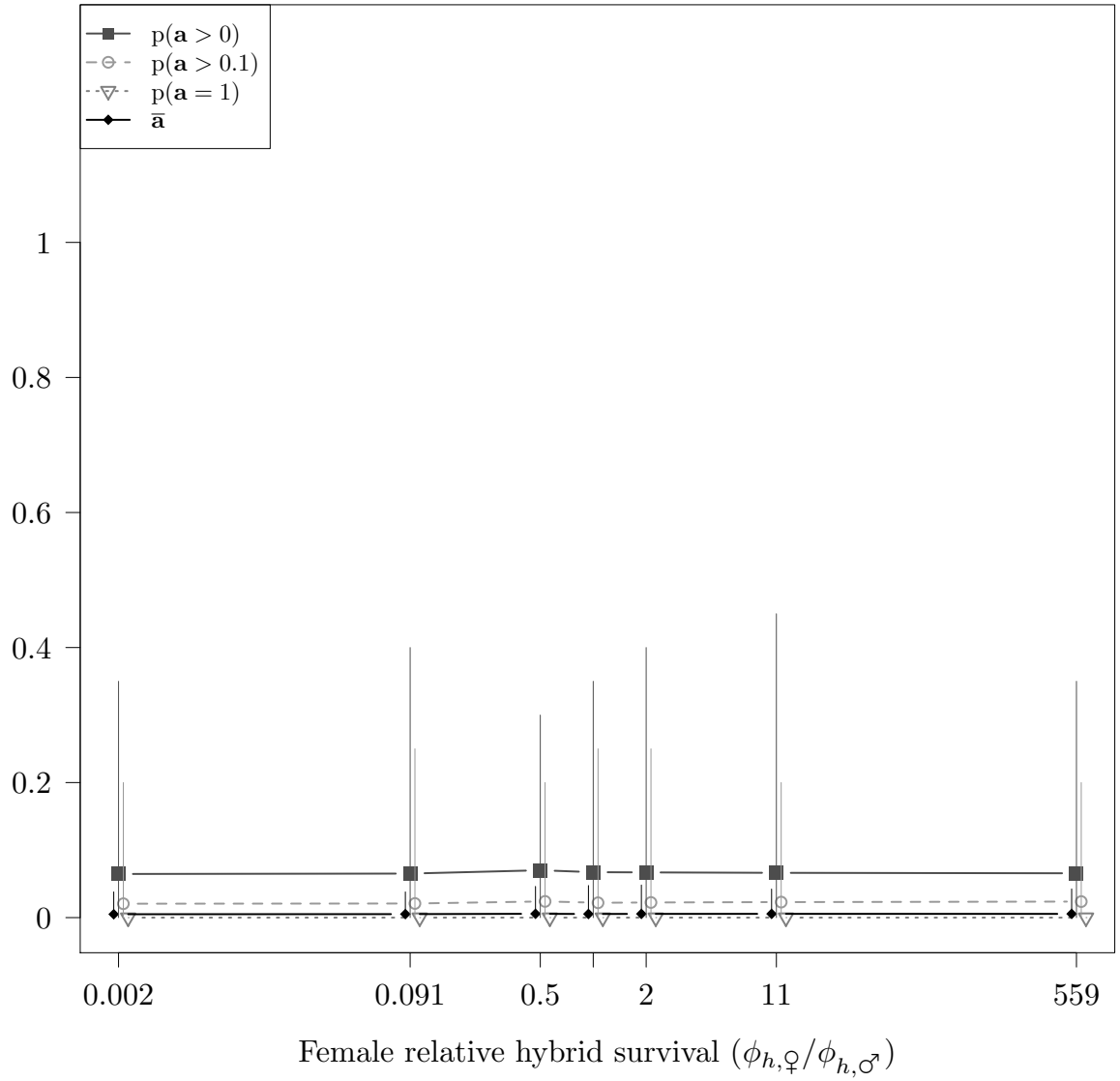
(A) Mito-nuclear discordance



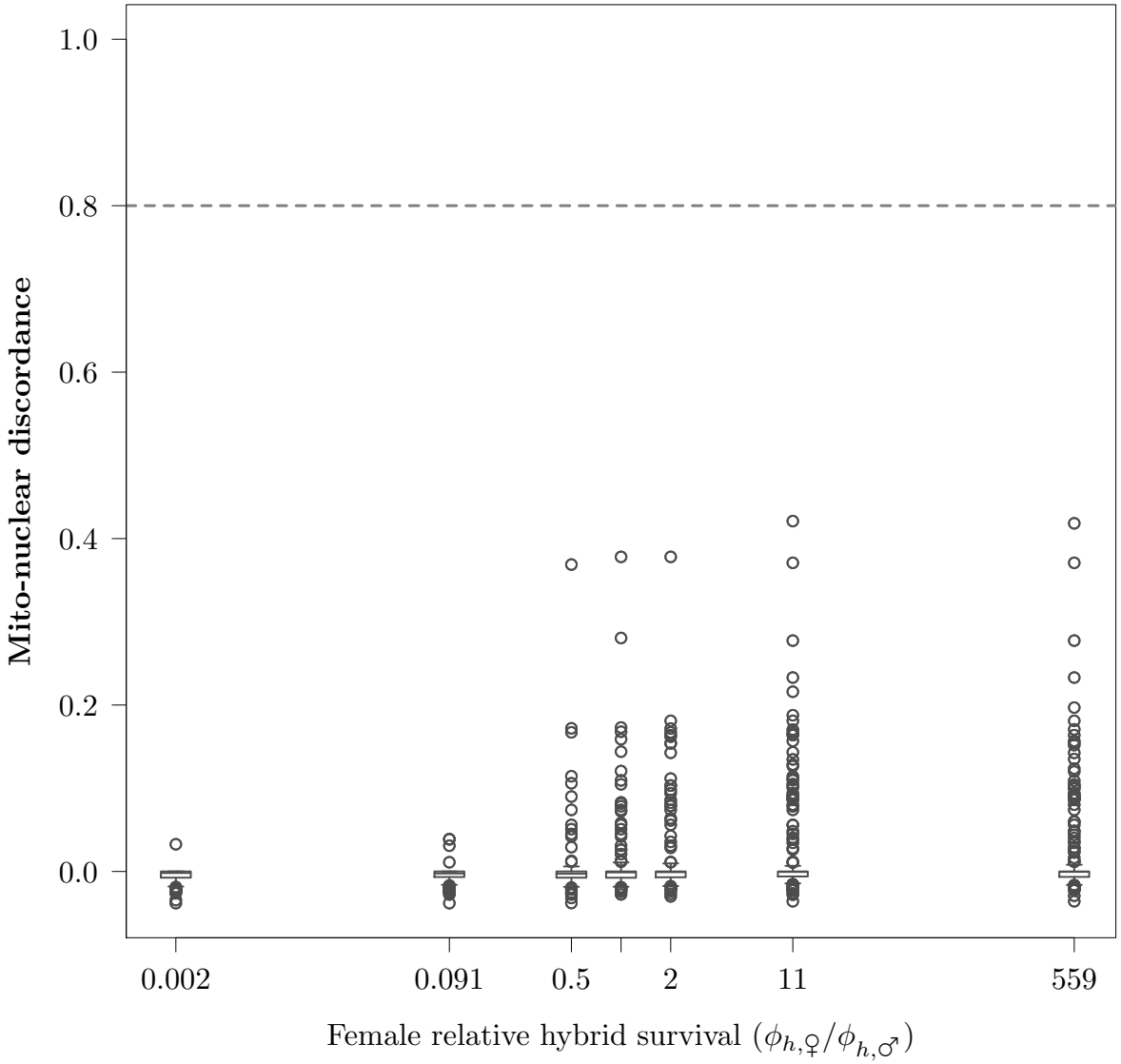
(B) Mitochondrial introgression



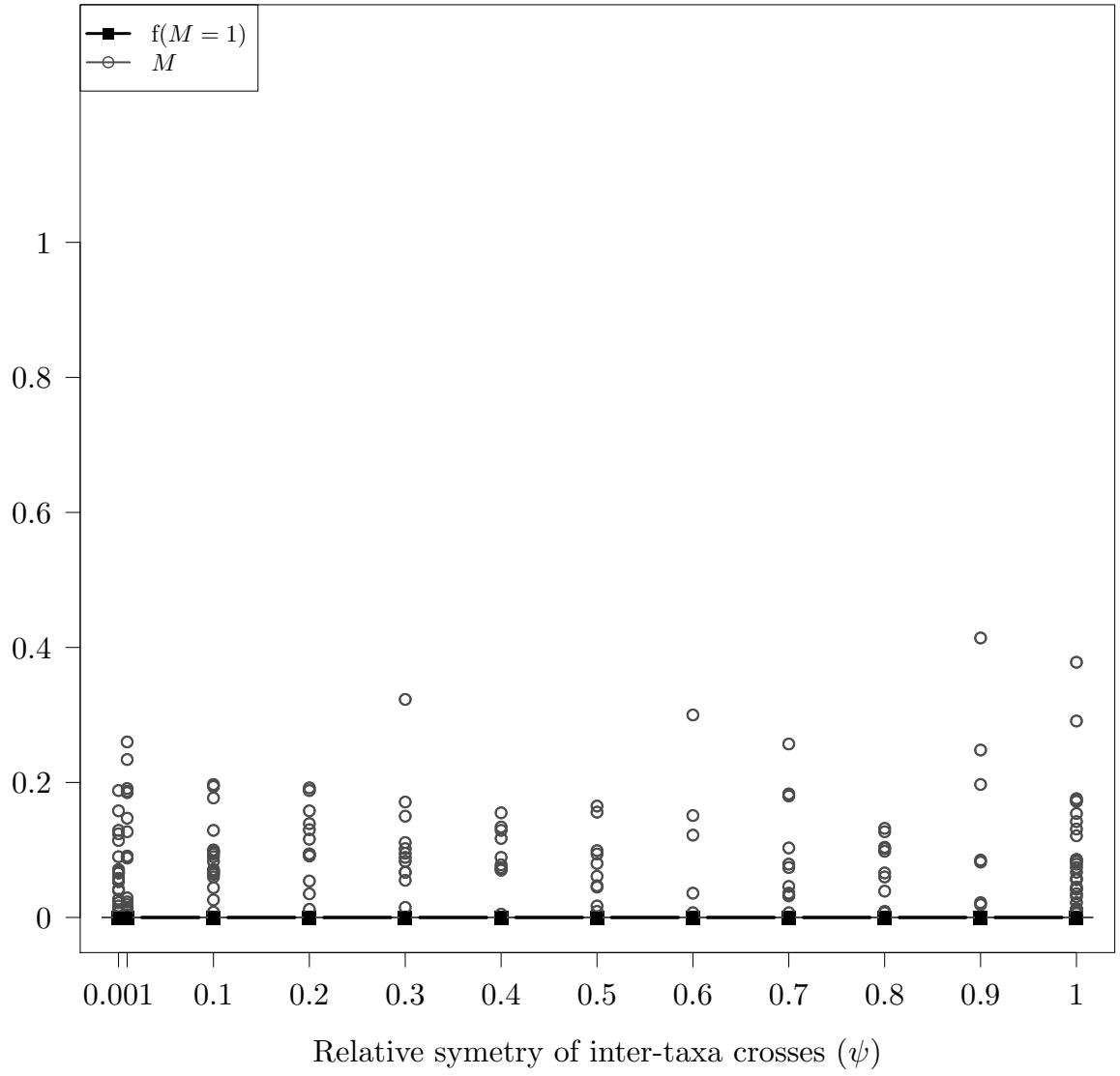
(C) Autosomal introgression



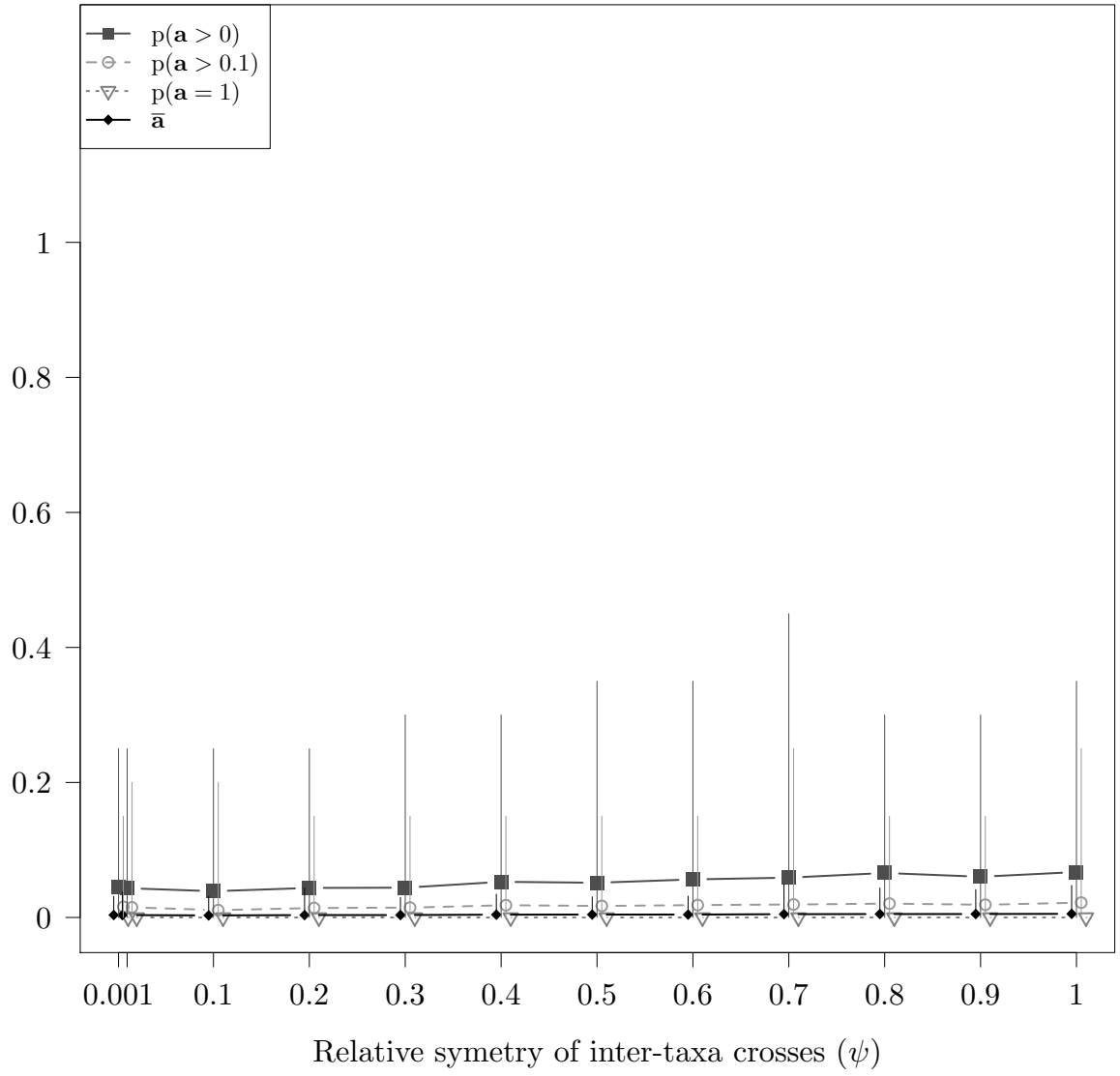
(A) Mito-nuclear discordance

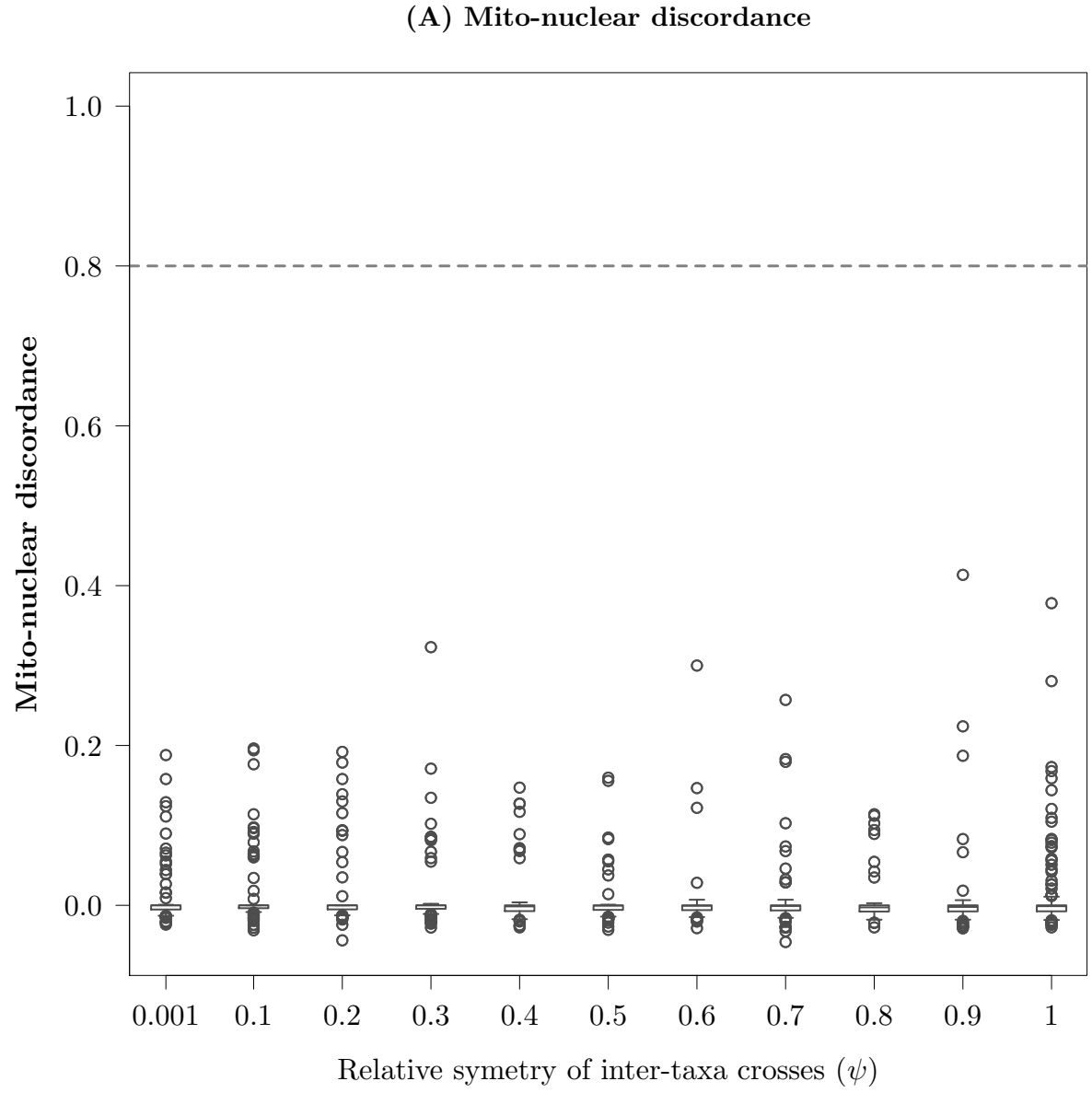


(B) Mitochondrial introgression

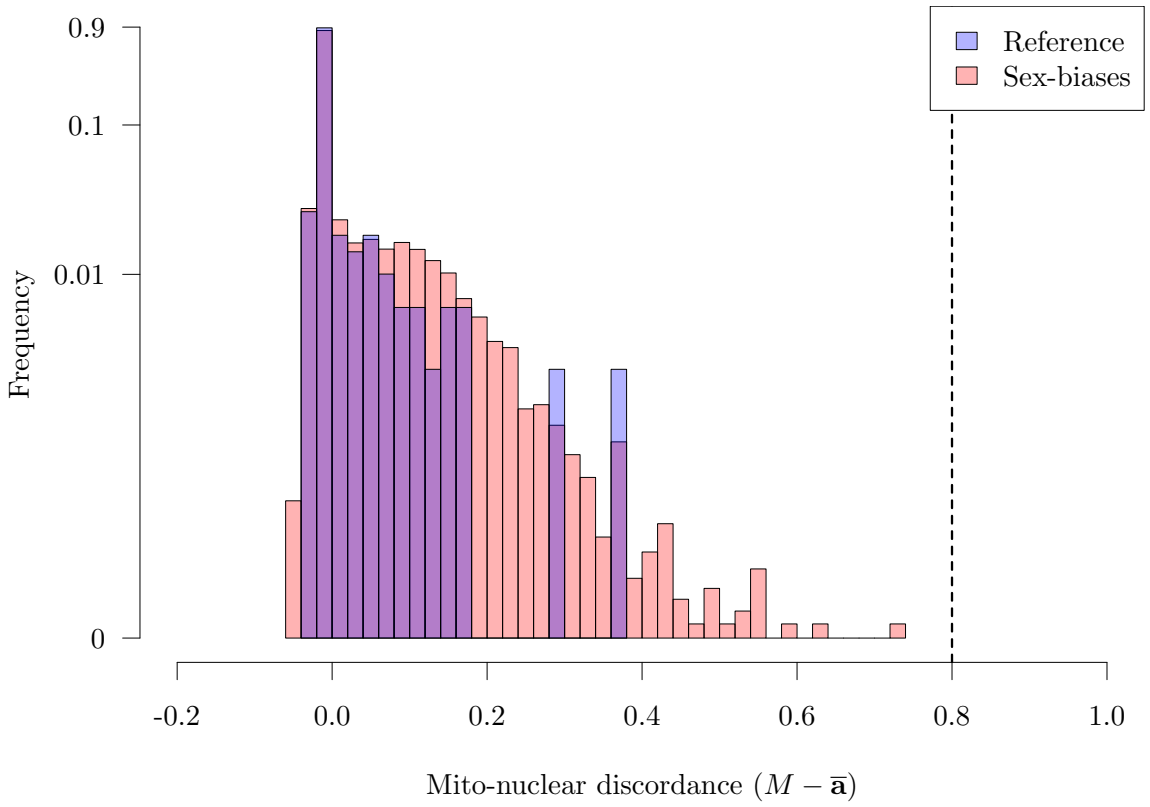


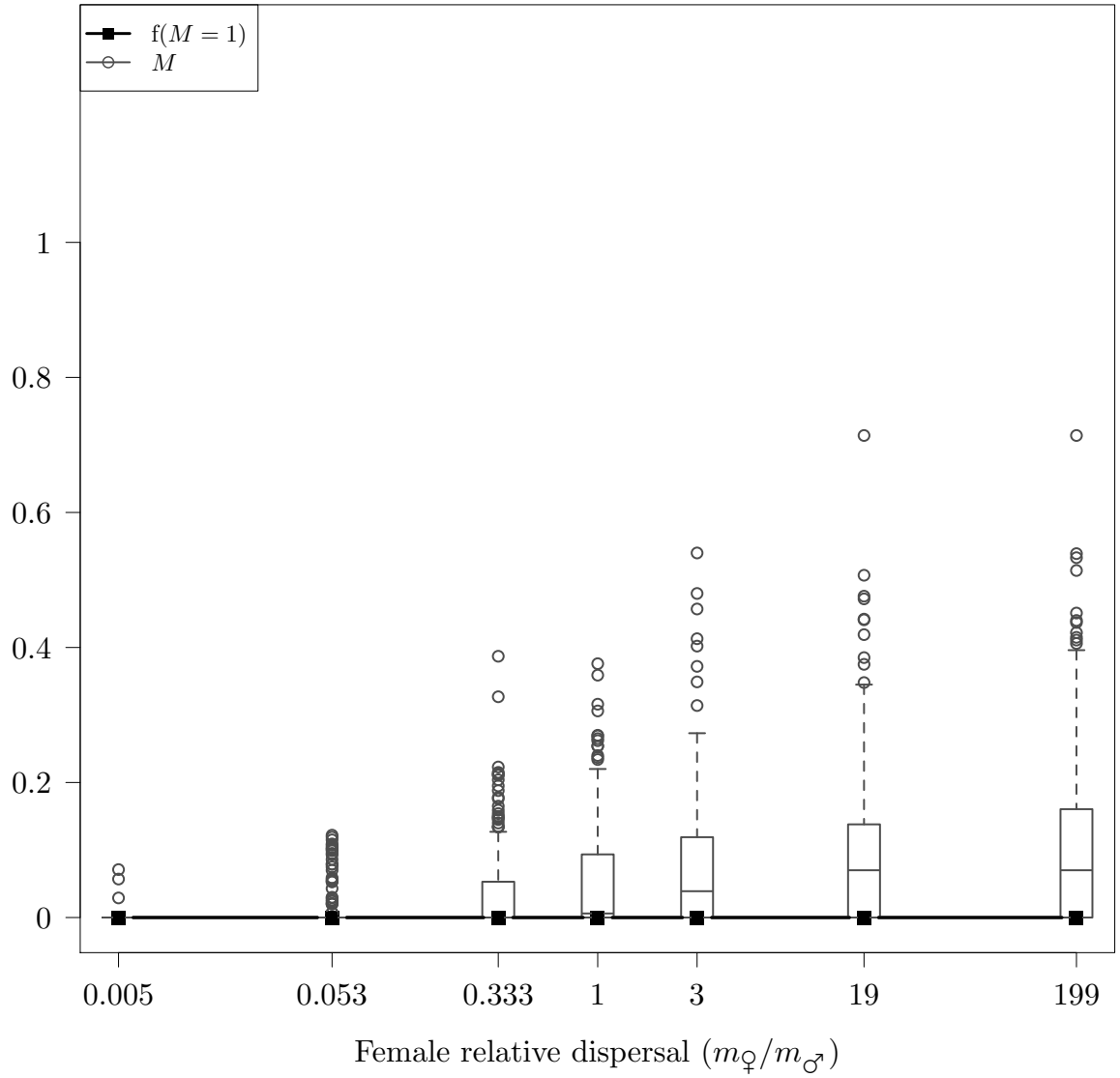
(C) Autosomal introgression

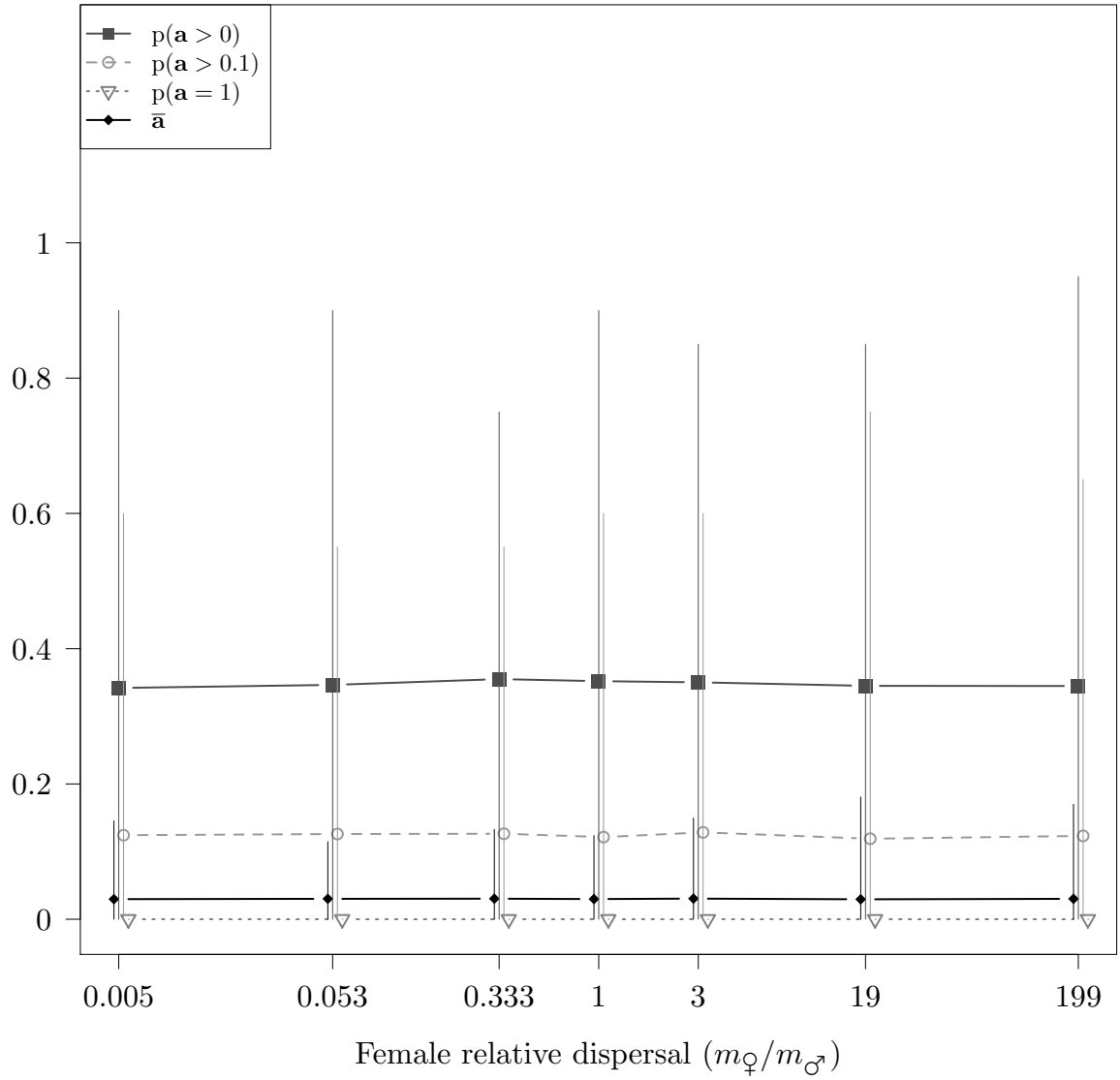




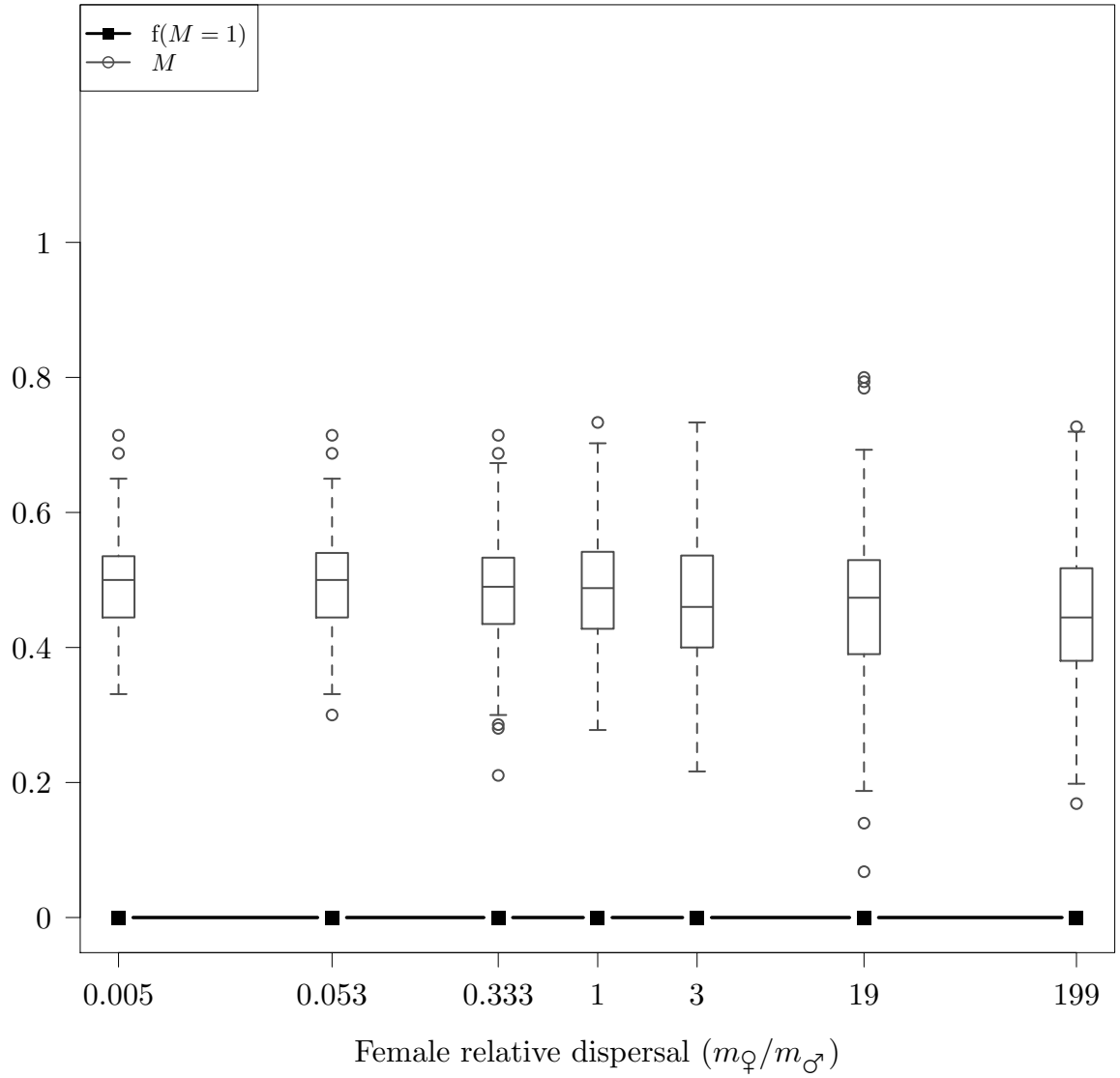

```
## [1] 0.001994615
## [1] 0.736
```


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 ($M - \bar{\mathbf{a}}$)

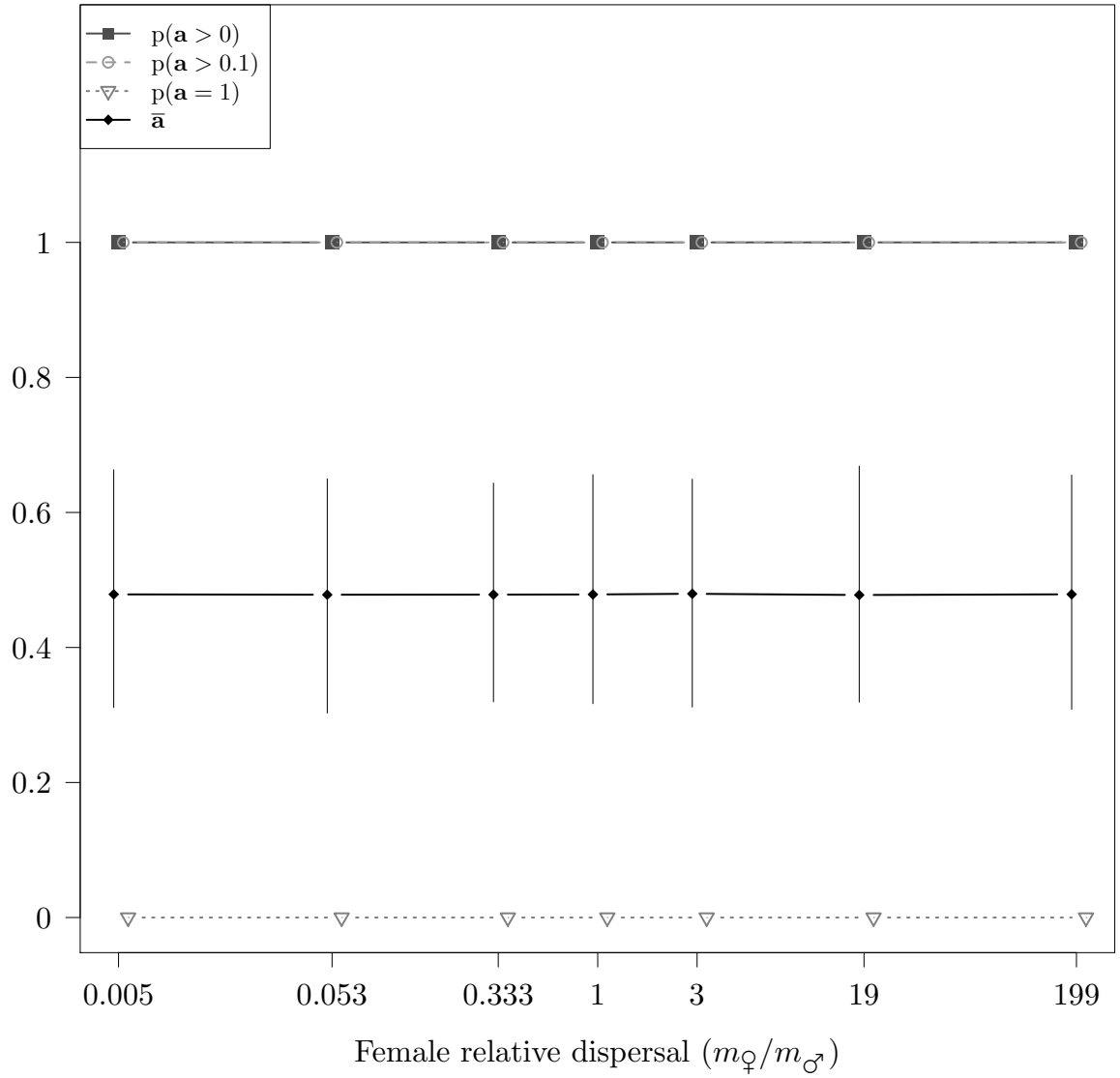

f(M = 1)
M
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.333
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)


p(a > 0)
p(a > 0.1)
p(a = 1)
ā
1
0.8
0.6
0.4
0.2
0
0.005
0.053
0.333
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

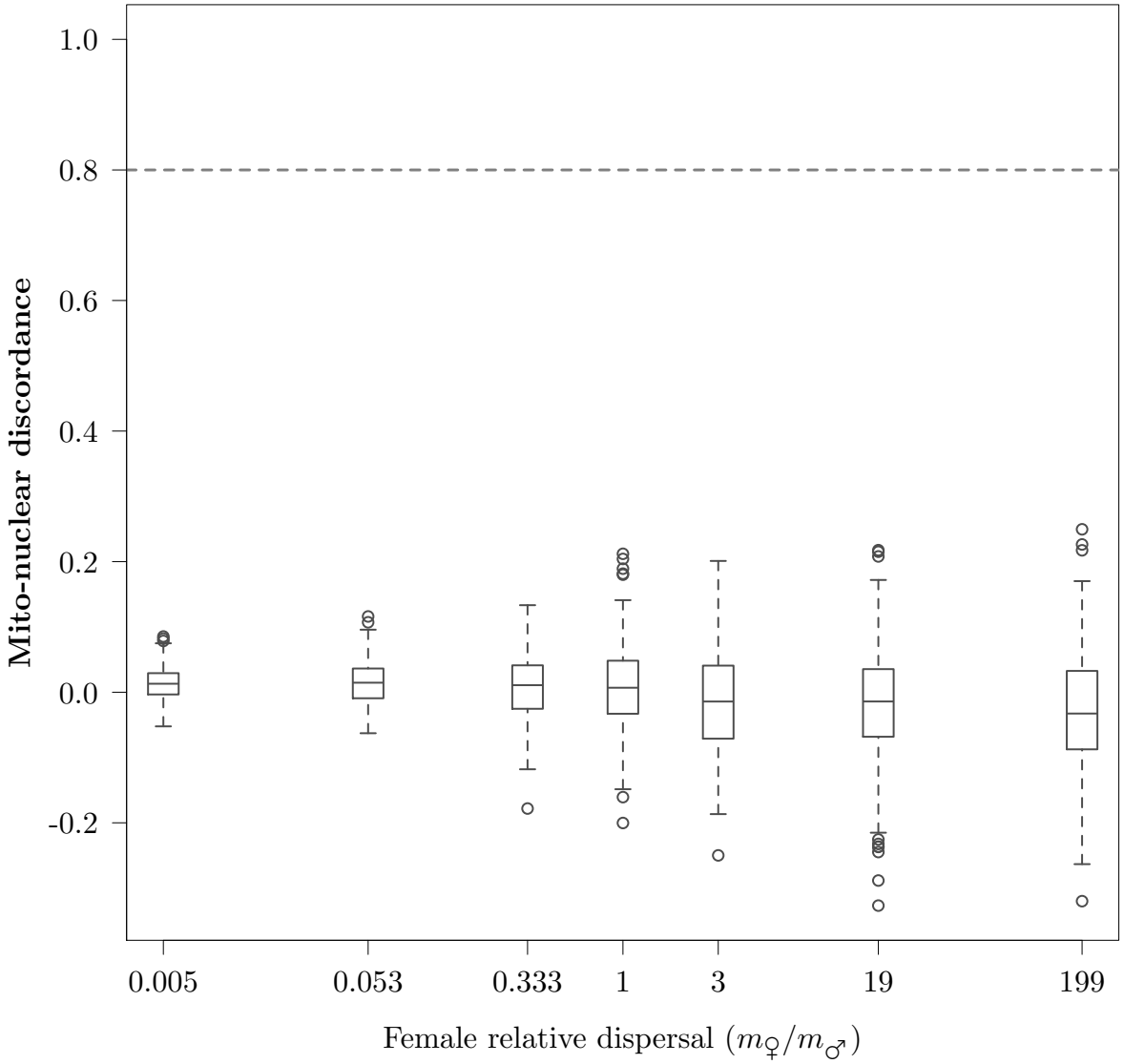
(A) Whole area, mitochondrial introgression



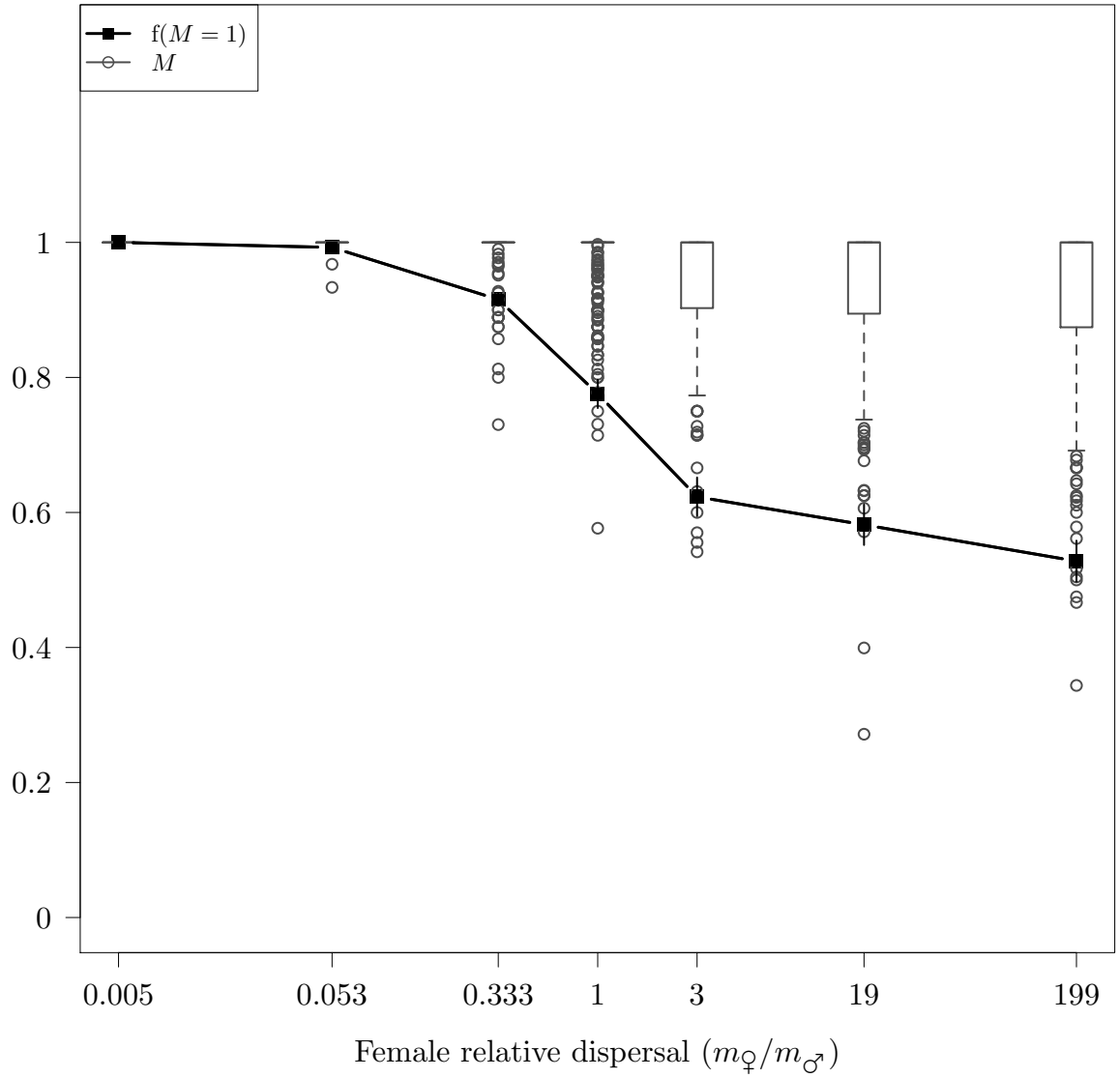
(B) Whole area, autosomal introgression



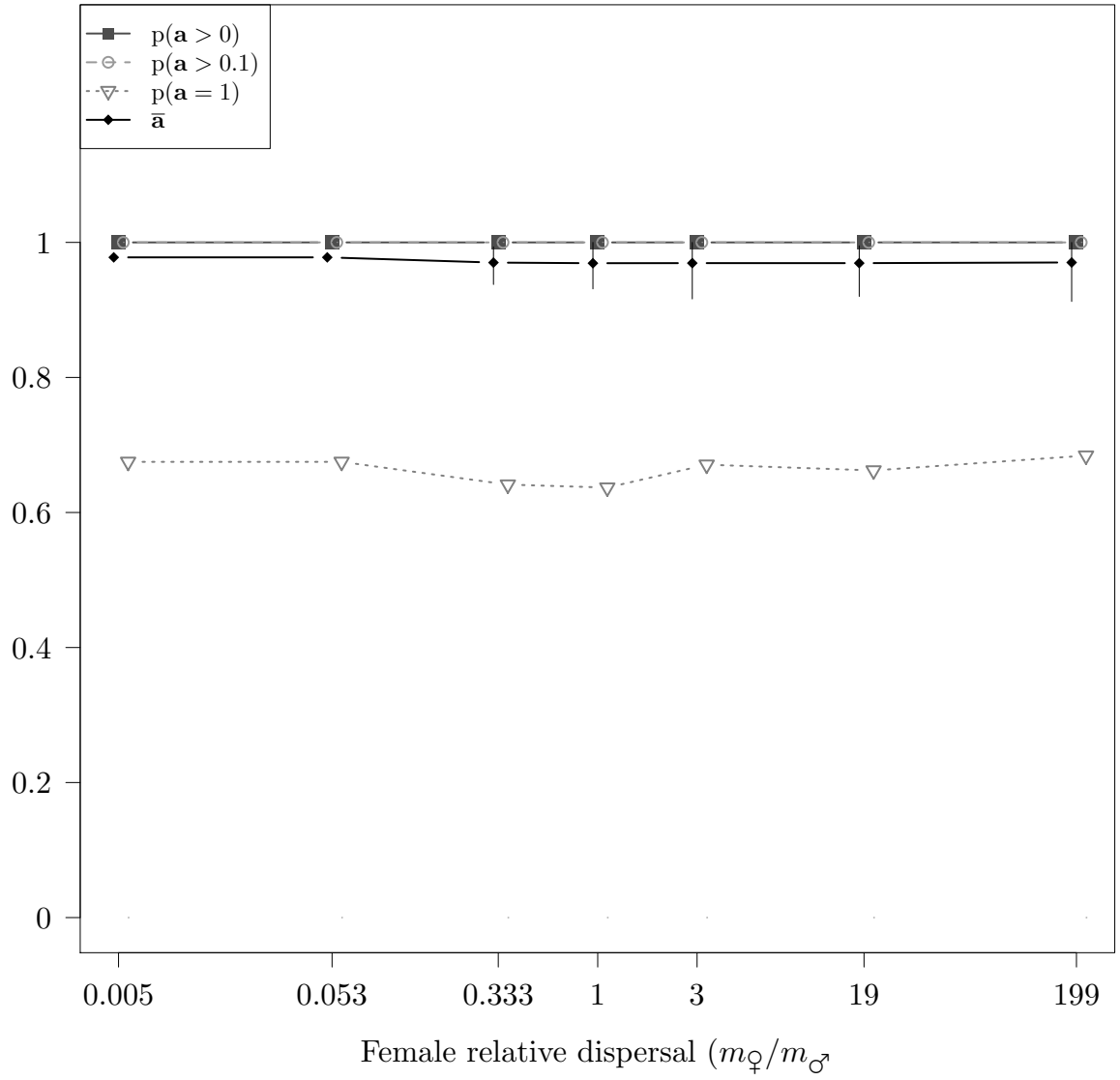
(A) Whole area


Mito-nuclear discordance
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
0.005
0.053
0.333
1
3
19
199
Female relative dispersal ($m_♀/m_♂$)

(C) Invaded area, mitochondrial introgression



(D) Invaded area, autosomal introgression



(B) Invaded area

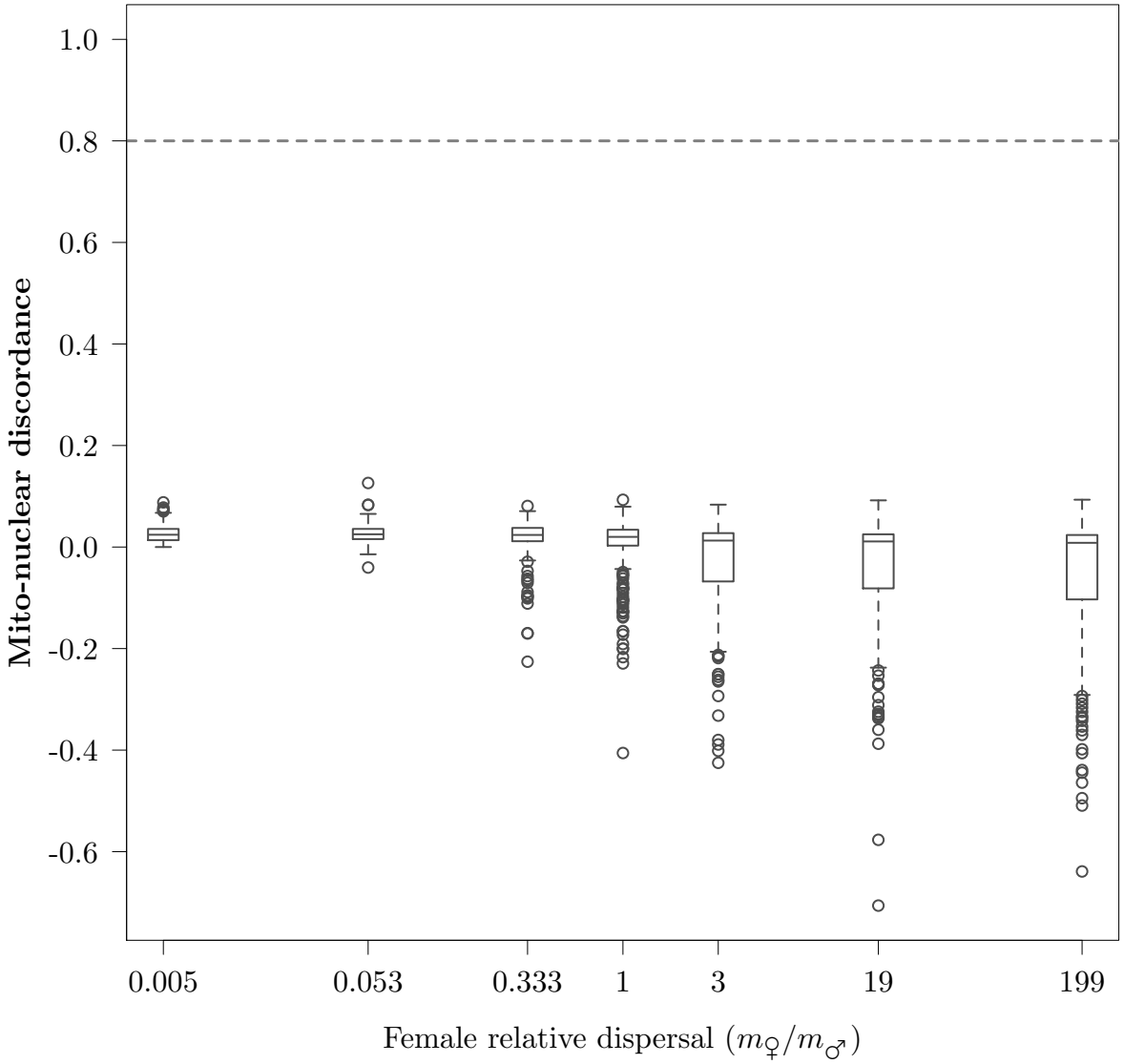


Table 1:

	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