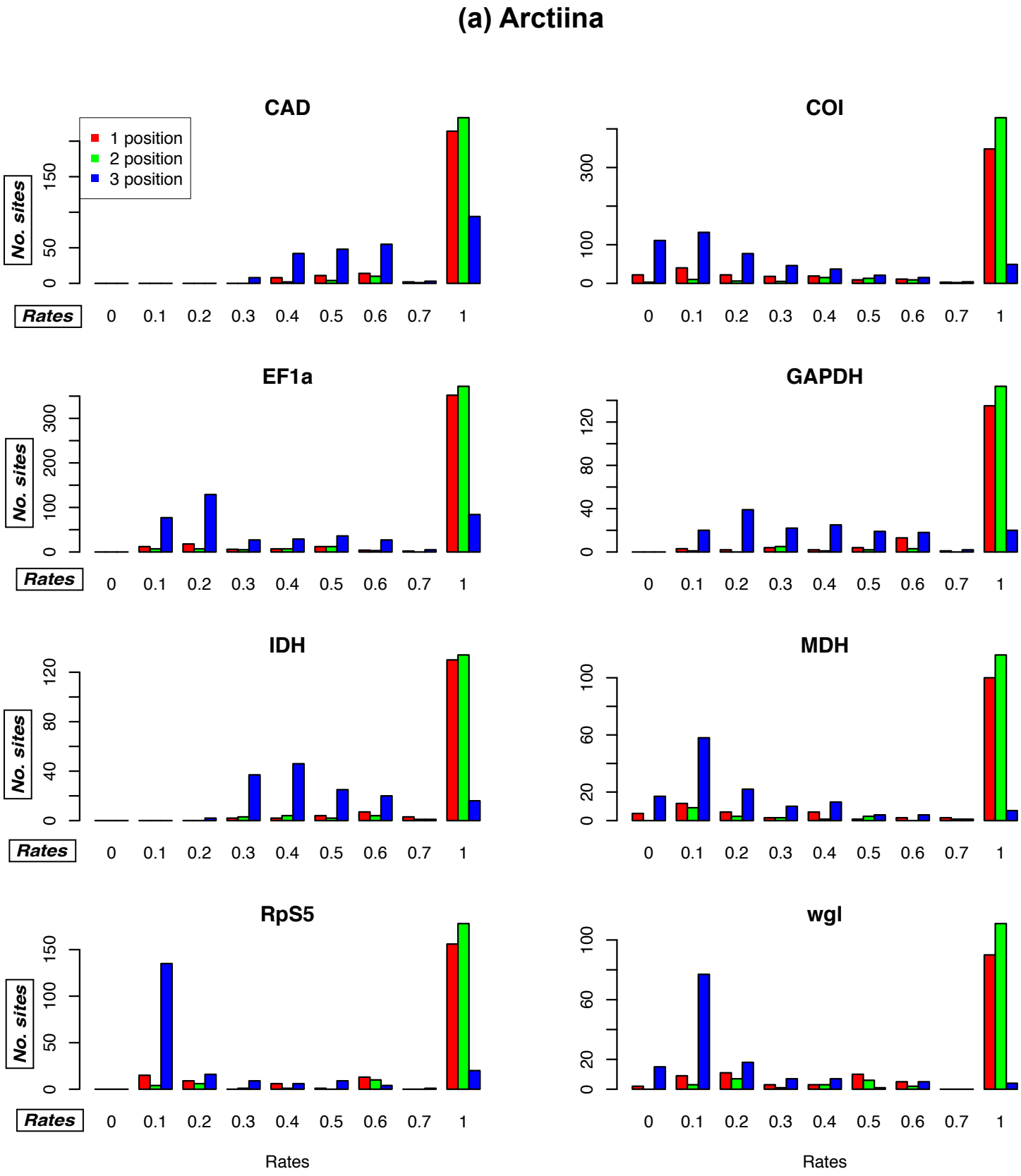
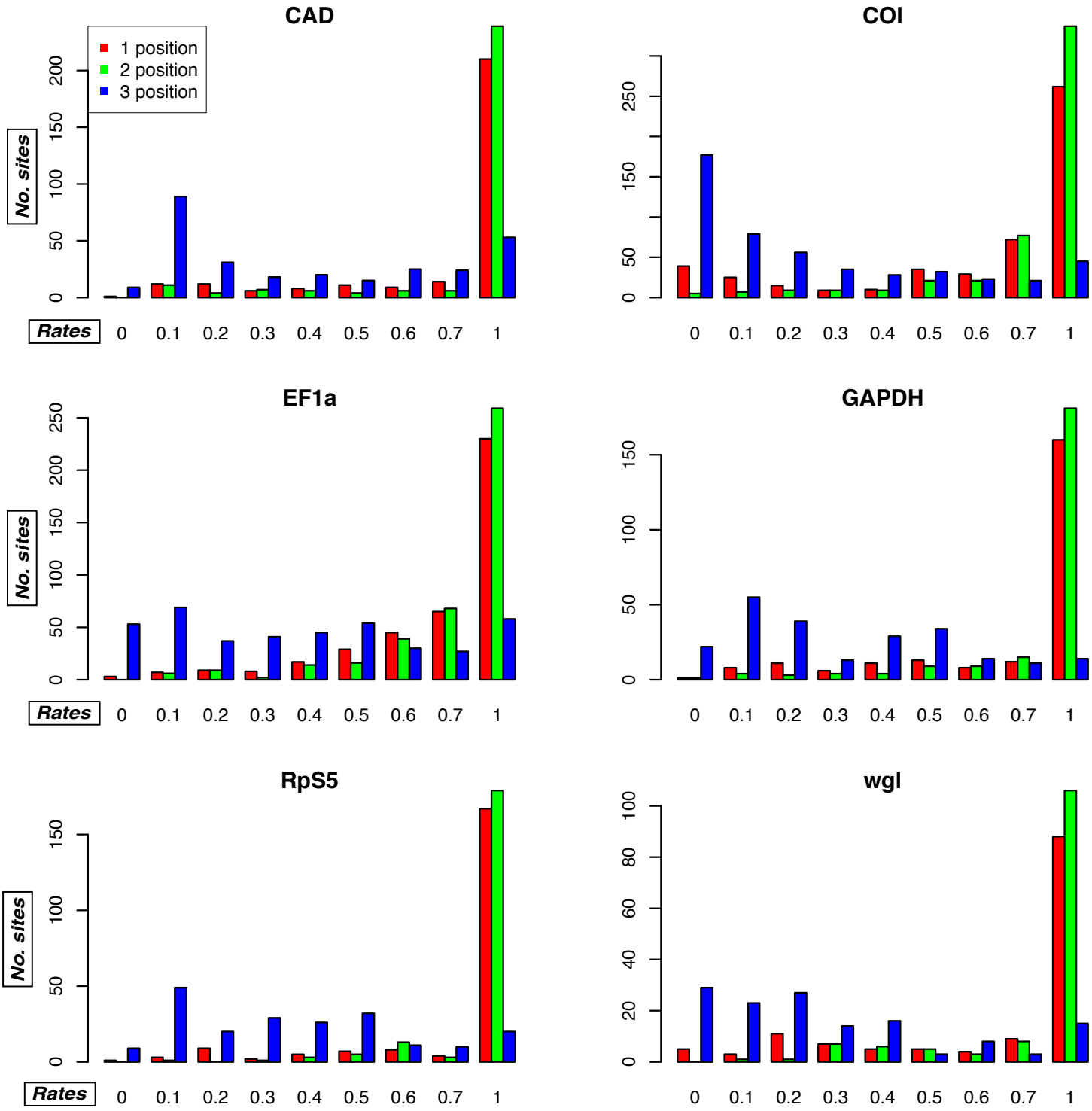
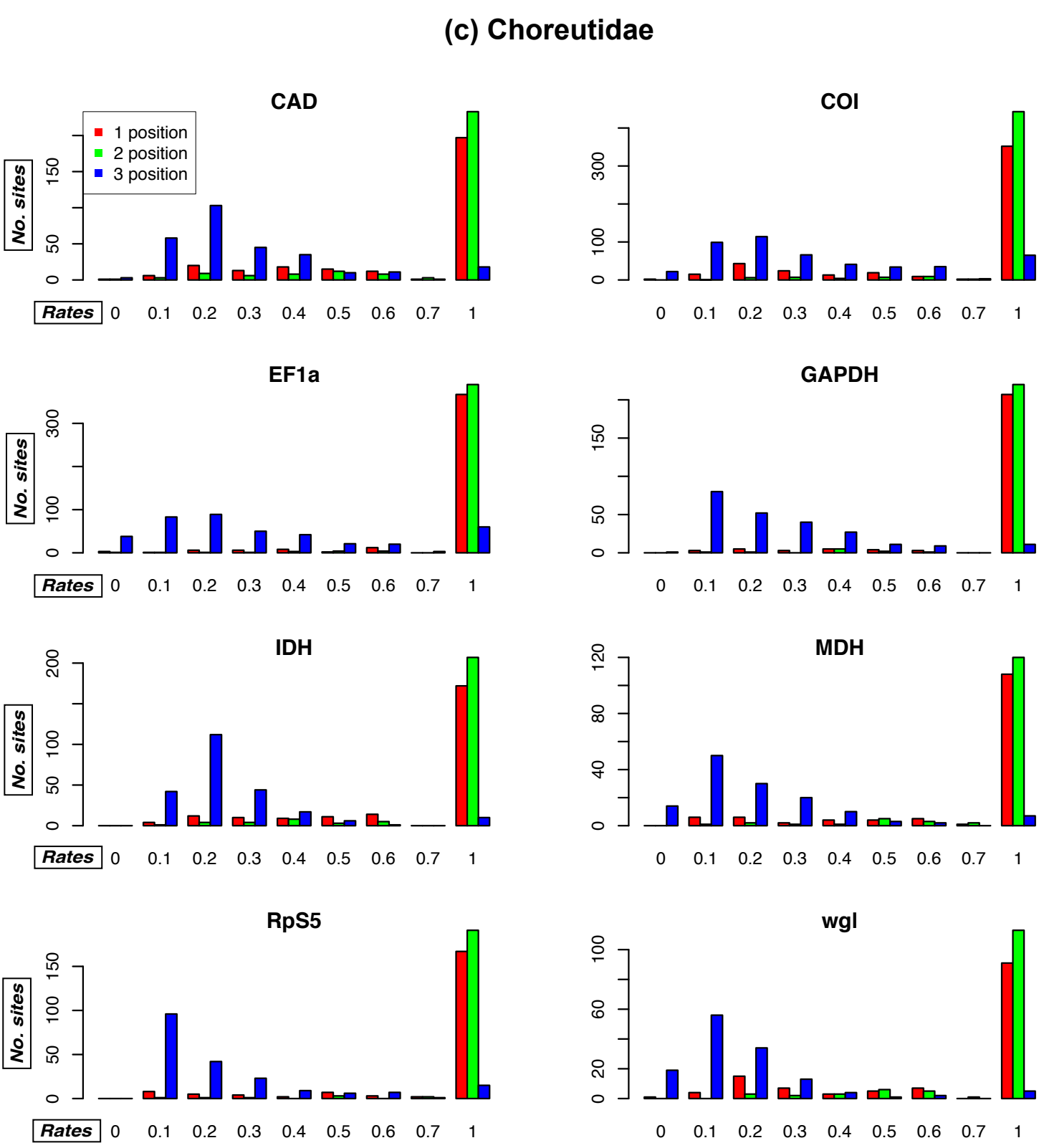


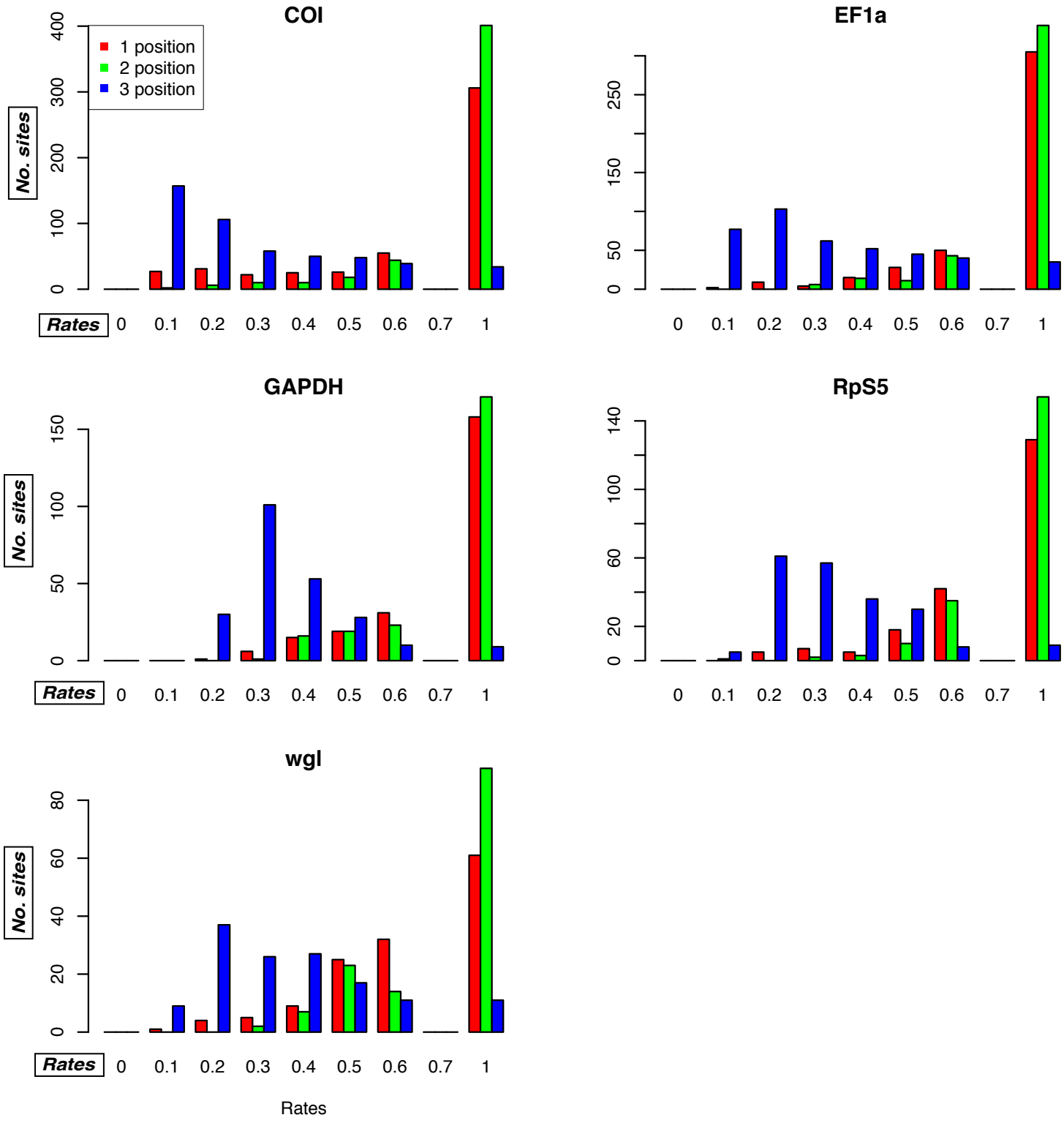
Figure S1. Plots showing the assigned TIGER rates to codon positions of each of the genes in datasets Arctiina (a), *Calisto* (b), Choreutidae (c), Coenonymphina (d), Geometridae (e), *Morpho* (f), and Pieridae (g).

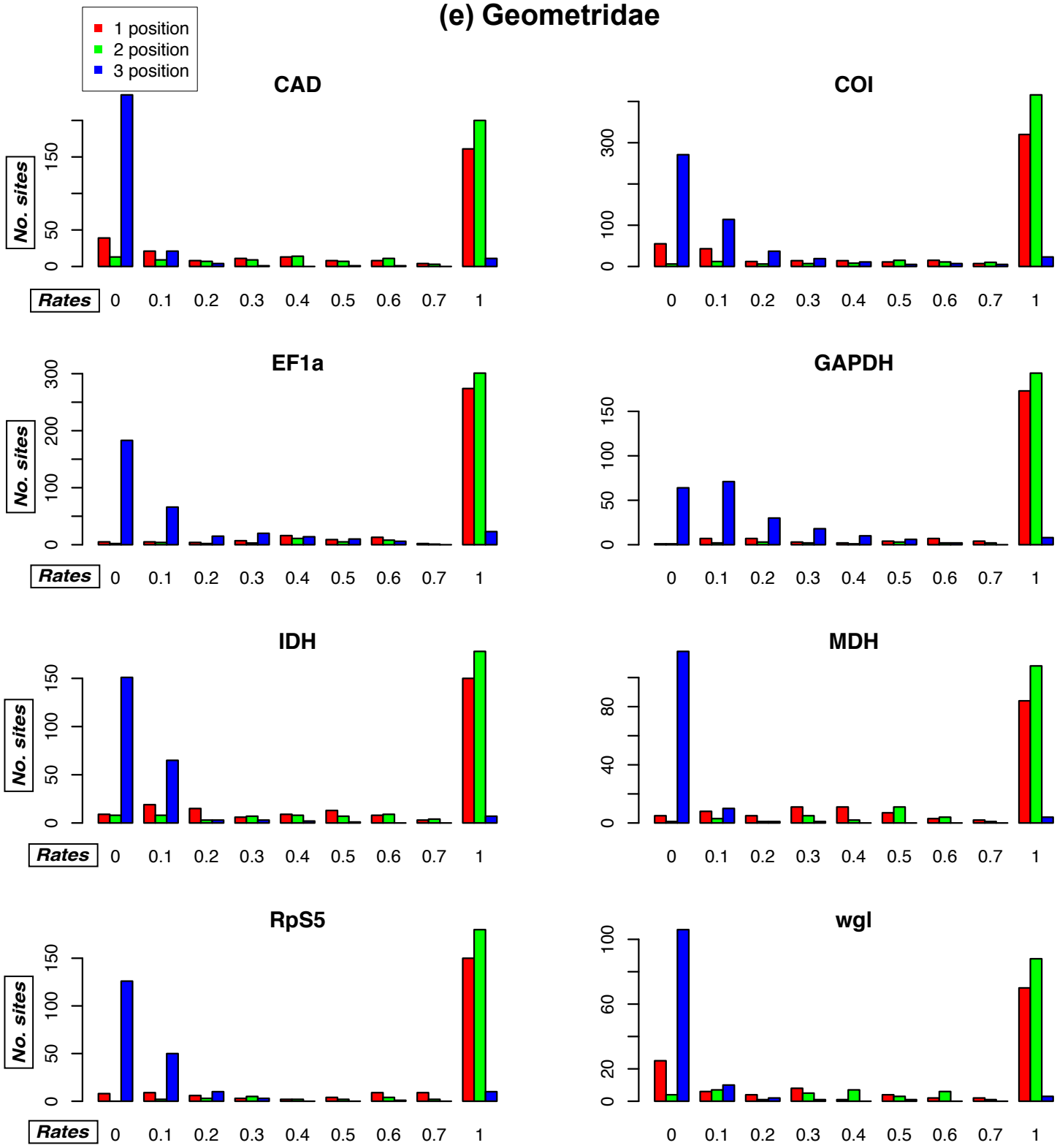
(b) *Calisto*


CAD
COI
EF1a
GAPDH
RpS5
wgl
1 position
2 position
3 position
No. sites
Rates
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
1

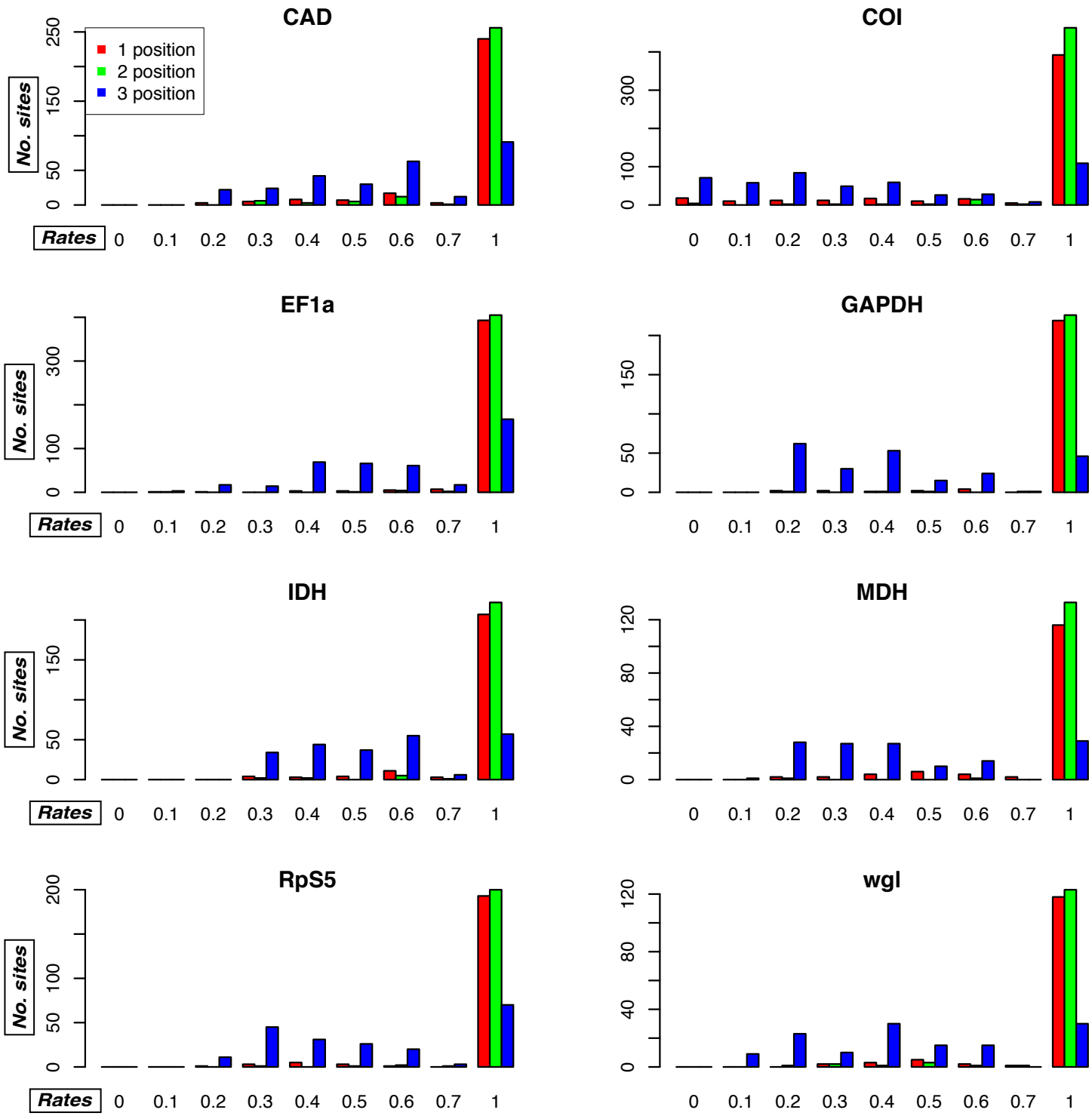

(c) Choreutidae
CAD
COI
EF1a
GAPDH
IDH
MDH
RpS5
wgl
1 position
2 position
3 position
No. sites
Rates
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
1

(d) Coenonymphina

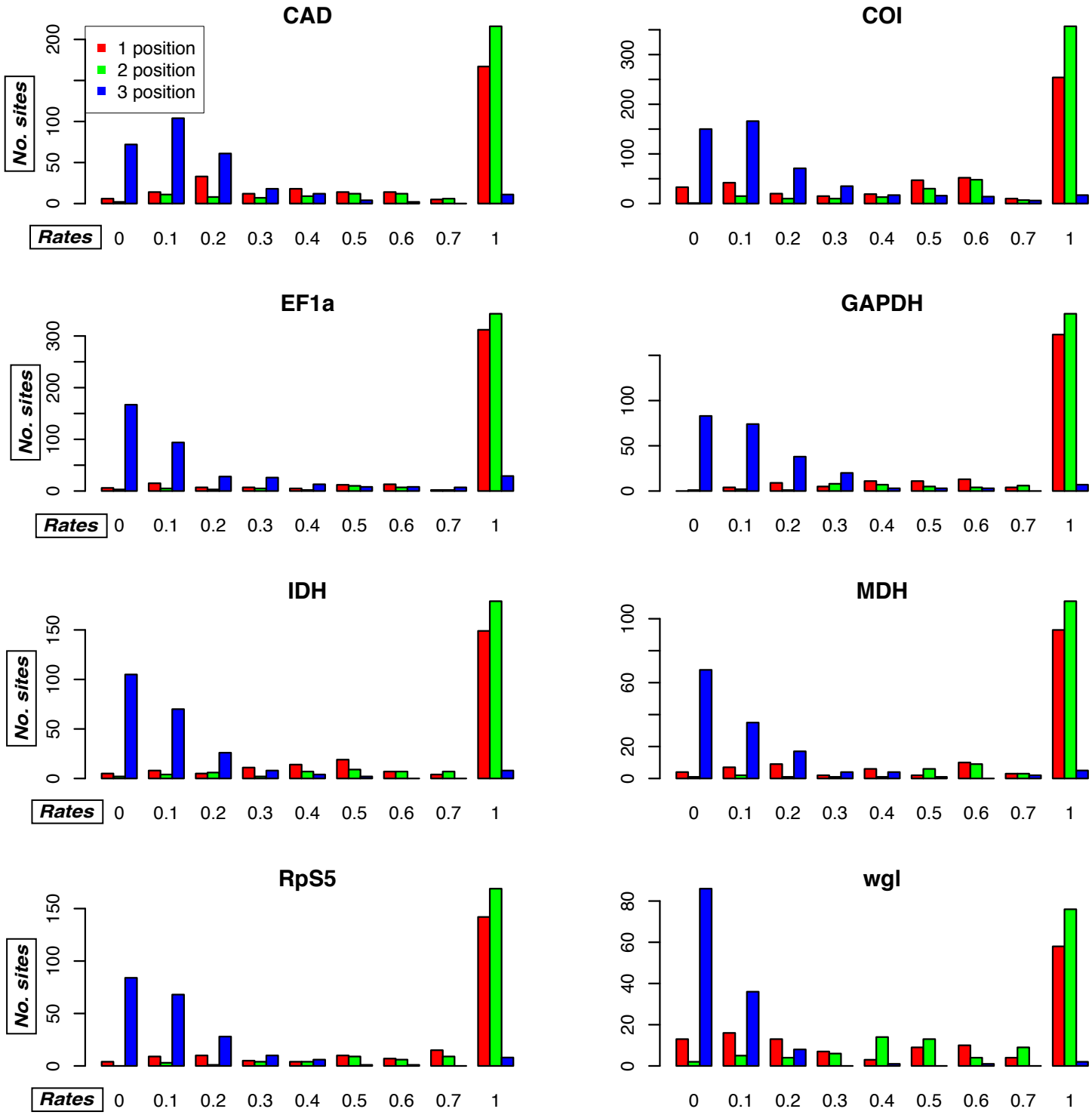



(e) Geometridae
1 position
2 position
3 position
CAD
COI
EF1a
GAPDH
IDH
MDH
RpS5
wgl
No. sites
Rates
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
1

(f) *Morpho*


CAD
COI
EF1a
GAPDH
IDH
MDH
RpS5
wgl
1 position
2 position
3 position
No. sites
Rates
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
1

(g) Pieridae


CAD
COI
EF1a
GAPDH
IDH
MDH
RpS5
wgl
1 position
2 position
3 position
No. sites
Rates
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
1