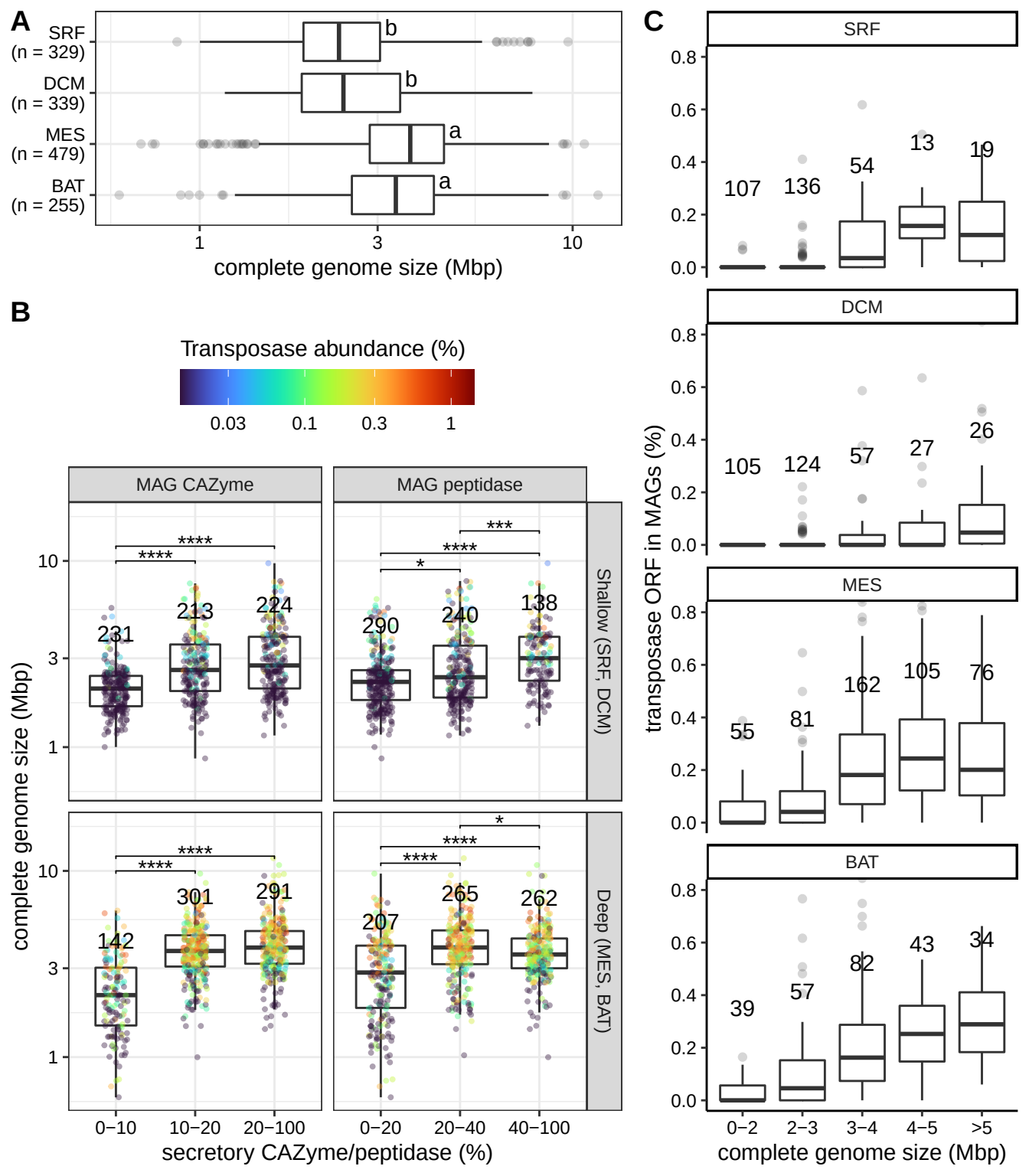
A
SRF (n = 329)
DCM (n = 339)
MES (n = 479)
BAT (n = 255)
b
b
a
a
1
3
10
complete genome size (Mbp)
B
Transposase abundance (%)
0.03
0.1
0.3
1
MAG CAZyme
MAG peptidase
Shallow (SRF, DCM)
Deep (MES, BAT)
complete genome size (Mbp)
231
213
224
290
240
138
142
301
291
207
265
262
****
***
*
0–10
10–20
20–100
0–20
20–40
40–100
secretory CAZyme/peptidase (%)
C
SRF
DCM
MES
BAT
107
136
54
13
19
105
124
57
27
26
55
81
162
105
76
39
57
82
43
34
transposase ORF in MAGs (%)
0–2
2–3
3–4
4–5
>5
complete genome size (Mbp)