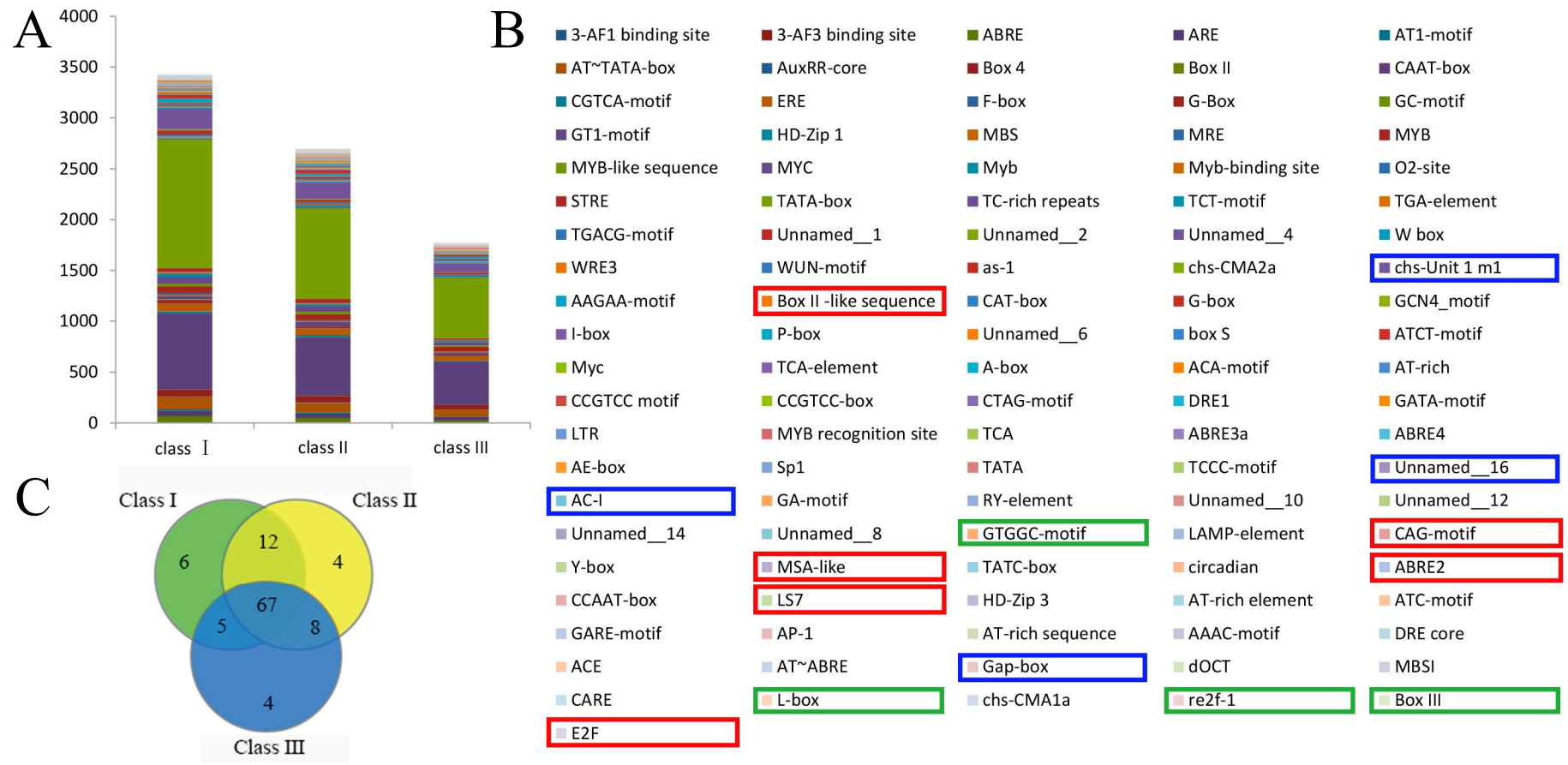
A
4000
3500
3000
2500
2000
1500
1000
500
0
class Ⅰ
class II
class III
B
3-AF1 binding site
3-AF3 binding site
ABRE
ARE
AT1-motif
AT~TATA-box
AuxRR-core
Box 4
Box II
CAAT-box
CGTCA-motif
ERE
F-box
G-Box
GC-motif
GT1-motif
HD-Zip 1
MBS
MRE
MYB
MYB-like sequence
MYC
Myb
Myb-binding site
O2-site
STRE
TATA-box
TC-rich repeats
TCT-motif
TGA-element
TGACG-motif
Unnamed__1
Unnamed__2
Unnamed__4
W box
WRE3
WUN-motif
as-1
chs-CMA2a
chs-Unit 1 m1
AAGAA-motif
Box II -like sequence
CAT-box
G-box
GCN4_motif
I-box
P-box
Unnamed__6
box S
ATCT-motif
Myc
TCA-element
A-box
ACA-motif
AT-rich
CCGTCC motif
CCGTCC-box
CTAG-motif
DRE1
GATA-motif
LTR
MYB recognition site
TCA
ABRE3a
ABRE4
AE-box
Sp1
TATA
TCCC-motif
Unnamed__16
AC-I
GA-motif
RY-element
Unnamed__10
Unnamed__12
Unnamed__14
Unnamed__8
GTGGC-motif
LAMP-element
CAG-motif
Y-box
MSA-like
TATC-box
circadian
ABRE2
CCAAT-box
LS7
HD-Zip 3
AT-rich element
ATC-motif
GARE-motif
AP-1
AT-rich sequence
AAAC-motif
DRE core
ACE
AT~ABRE
Gap-box
dOCT
MBSI
CARE
L-box
chs-CMA1a
re2f-1
Box III
E2F
C
Class I
Class II
Class III
6
12
4
67
5
8
4