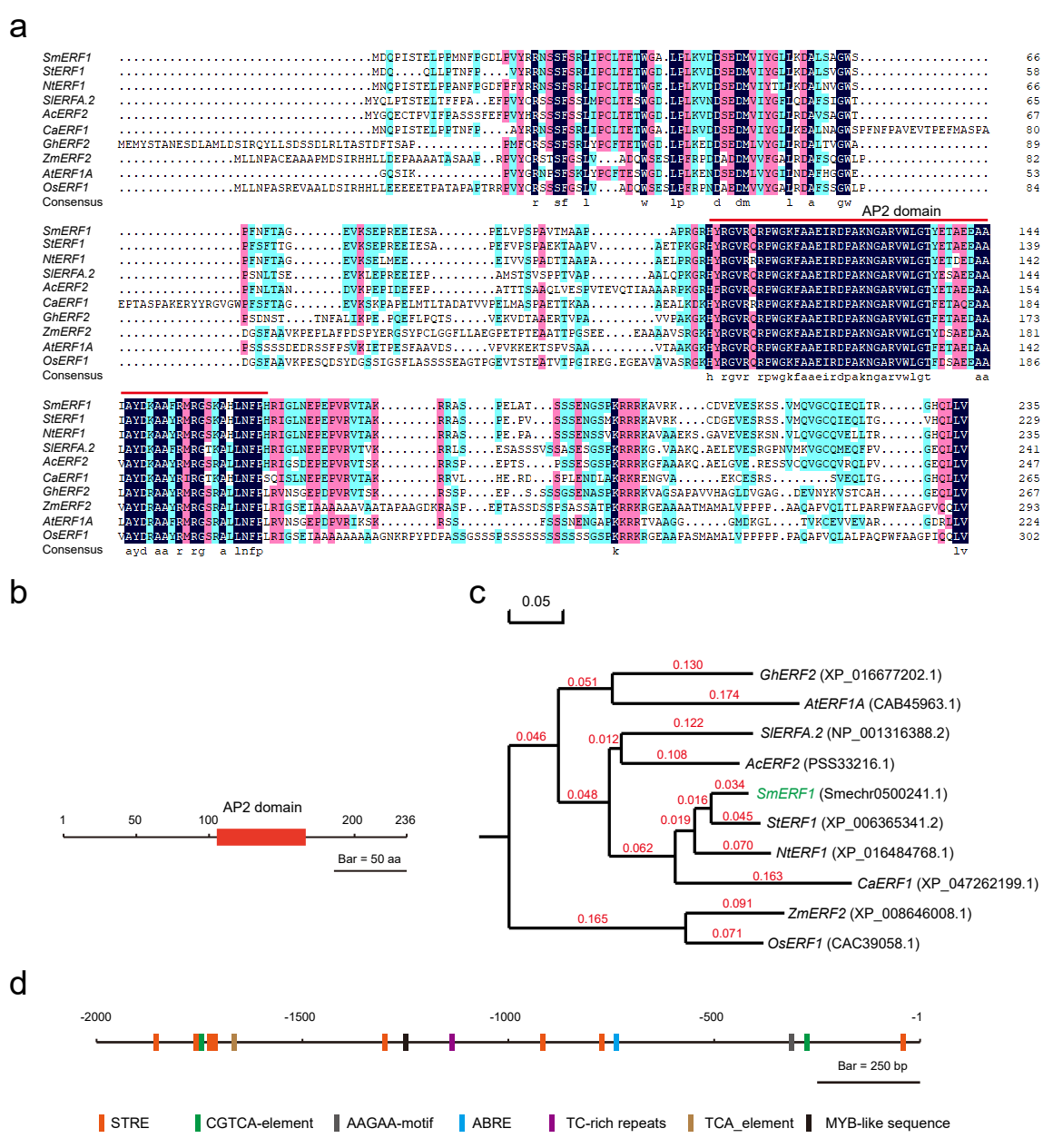
a
SmERF1
StERF1
NtERF1
SlERFA.2
AcERF2
CaERF1
GhERF2
ZmERF2
AtERF1A
OsERF1
Consensus
AP2 domain
b
AP2 domain
1
50
100
200
236
Bar = 50 aa
c
0.05
0.130
GhERF2 (XP_016677202.1)
0.051
0.174
AtERF1A (CAB45963.1)
0.122
SlERFA.2 (NP_001316388.2)
0.046
0.012
0.108
AcERF2 (PSS33216.1)
0.034
SmERF1 (Smechr0500241.1)
0.048
0.016
0.045
StERF1 (XP_006365341.2)
0.019
0.070
NtERF1 (XP_016484768.1)
0.062
0.163
CaERF1 (XP_047262199.1)
0.091
ZmERF2 (XP_008646008.1)
0.165
0.071
OsERF1 (CAC39058.1)
d
-2000
-1500
-1000
-500
-1
Bar = 250 bp
STRE
CGTCA-element
AAGAA-motif
ABRE
TC-rich repeats
TCA_element
MYB-like sequence