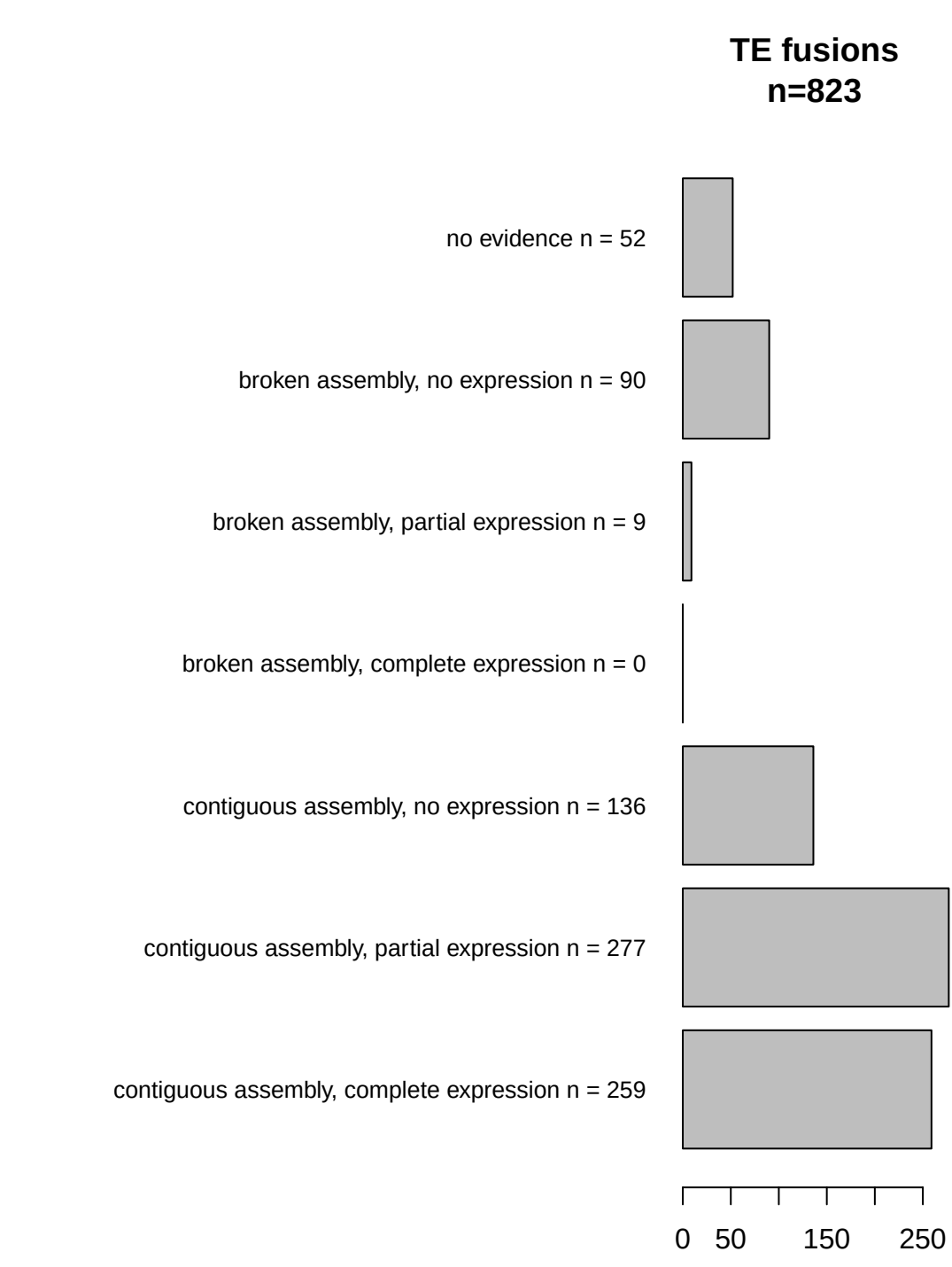
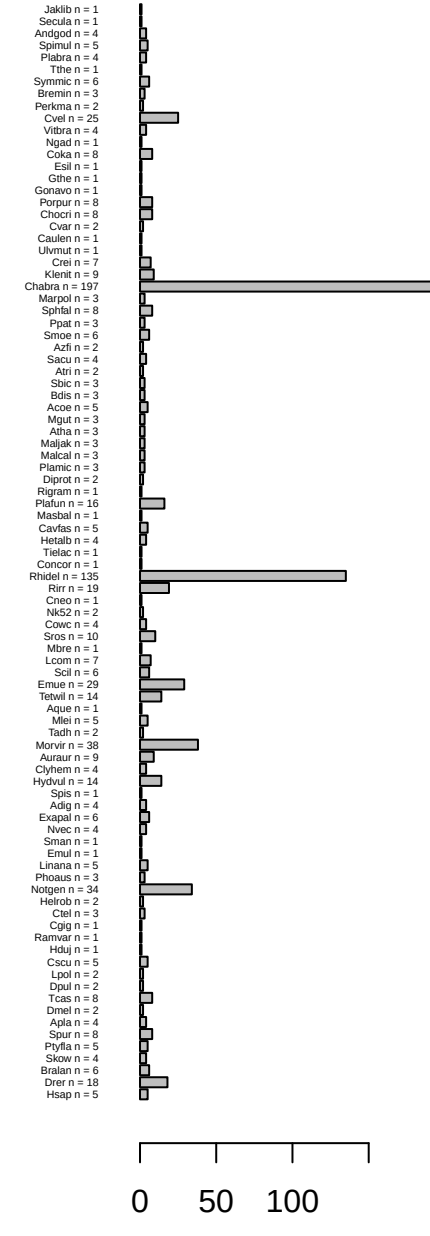
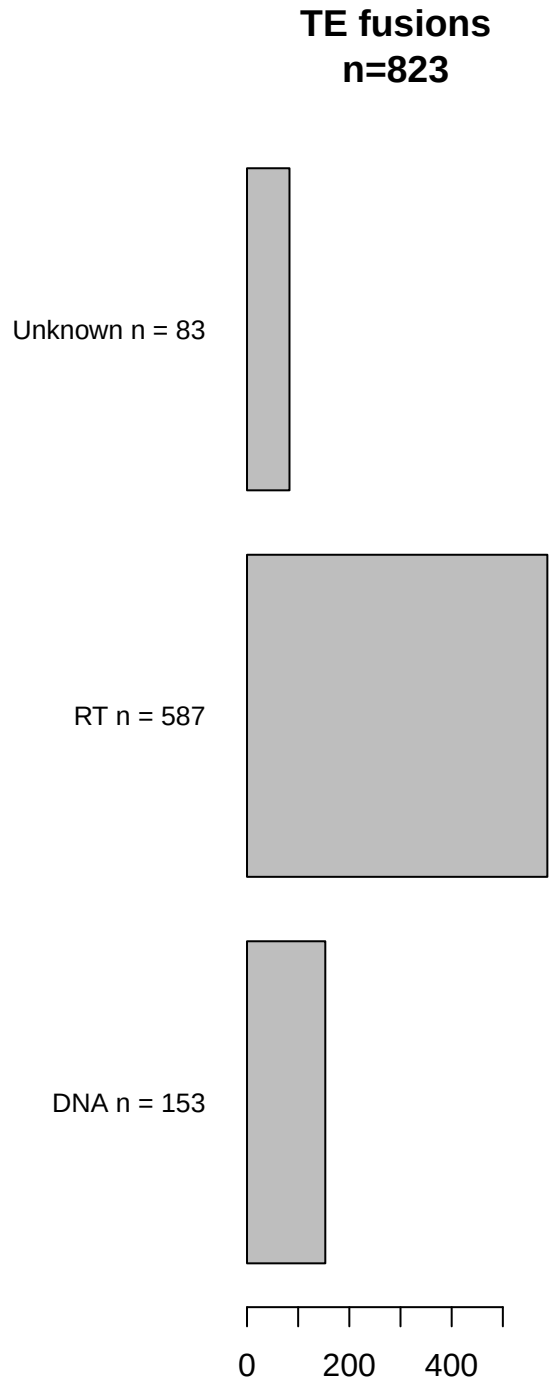
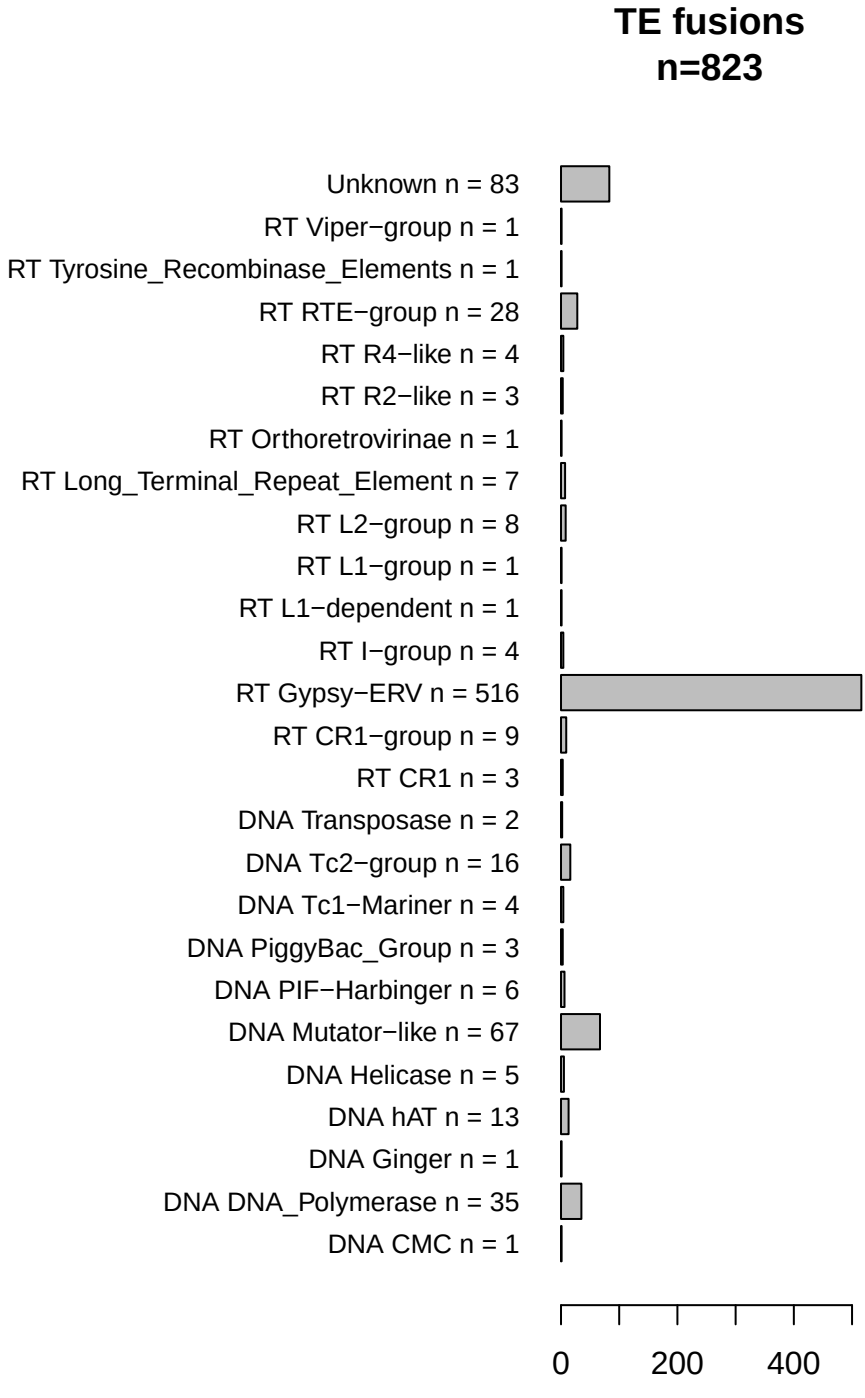
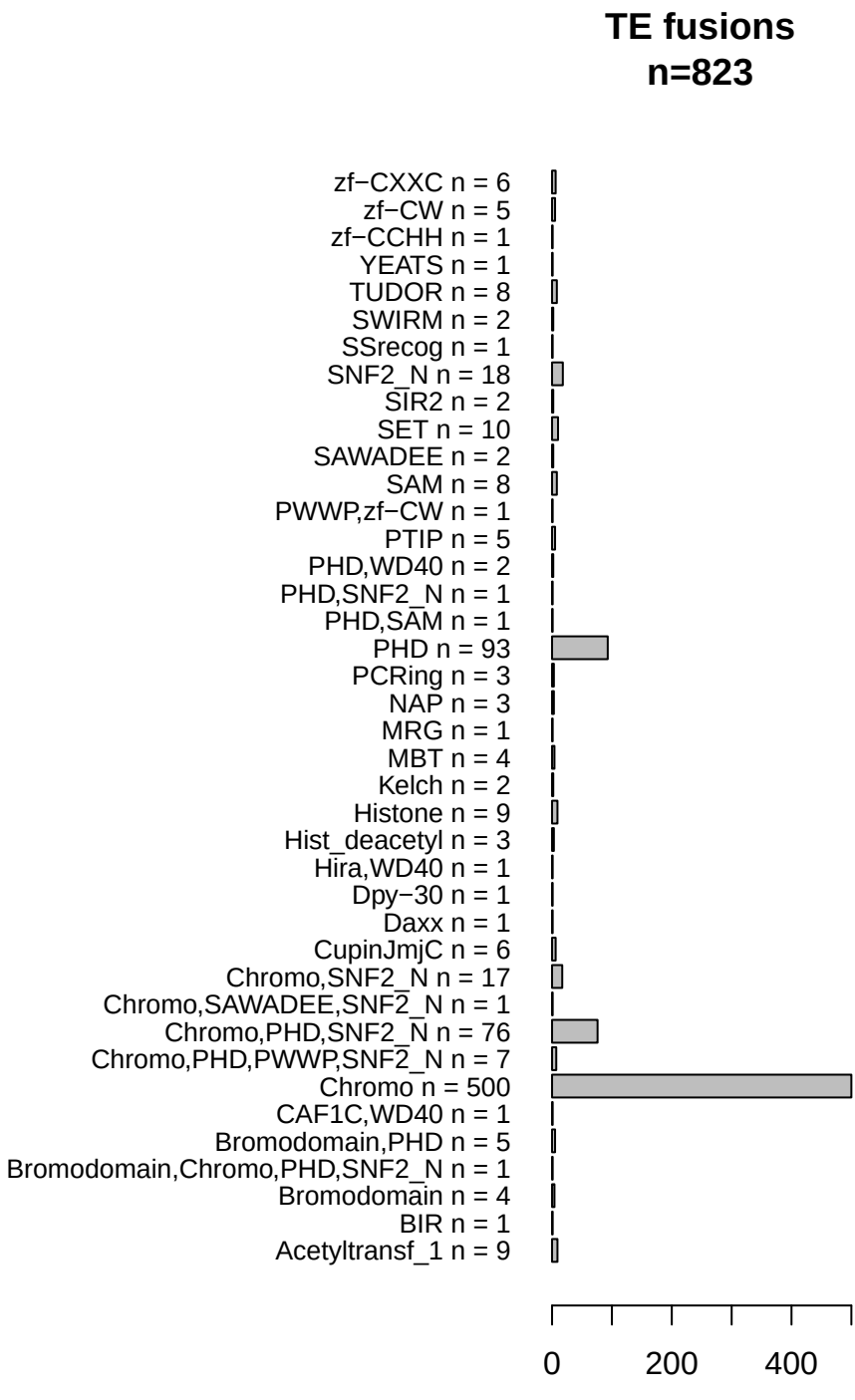

TE fusions
n=823
no evidence n = 52
broken assembly, no expression n = 90
broken assembly, partial expression n = 9
broken assembly, complete expression n = 0
contiguous assembly, no expression n = 136
contiguous assembly, partial expression n = 277
contiguous assembly, complete expression n = 259
0
50
150
250

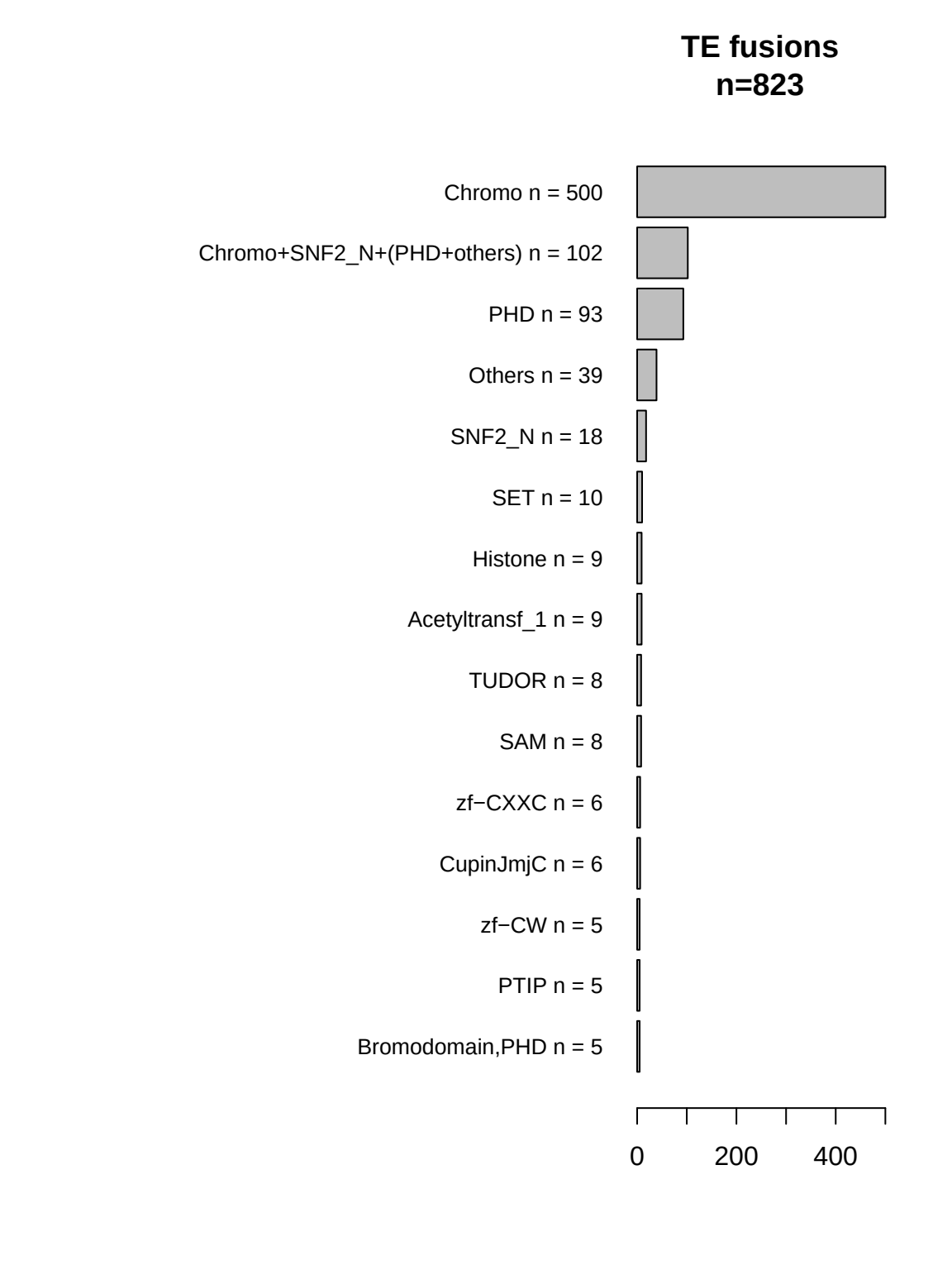
TE fusions
n=823

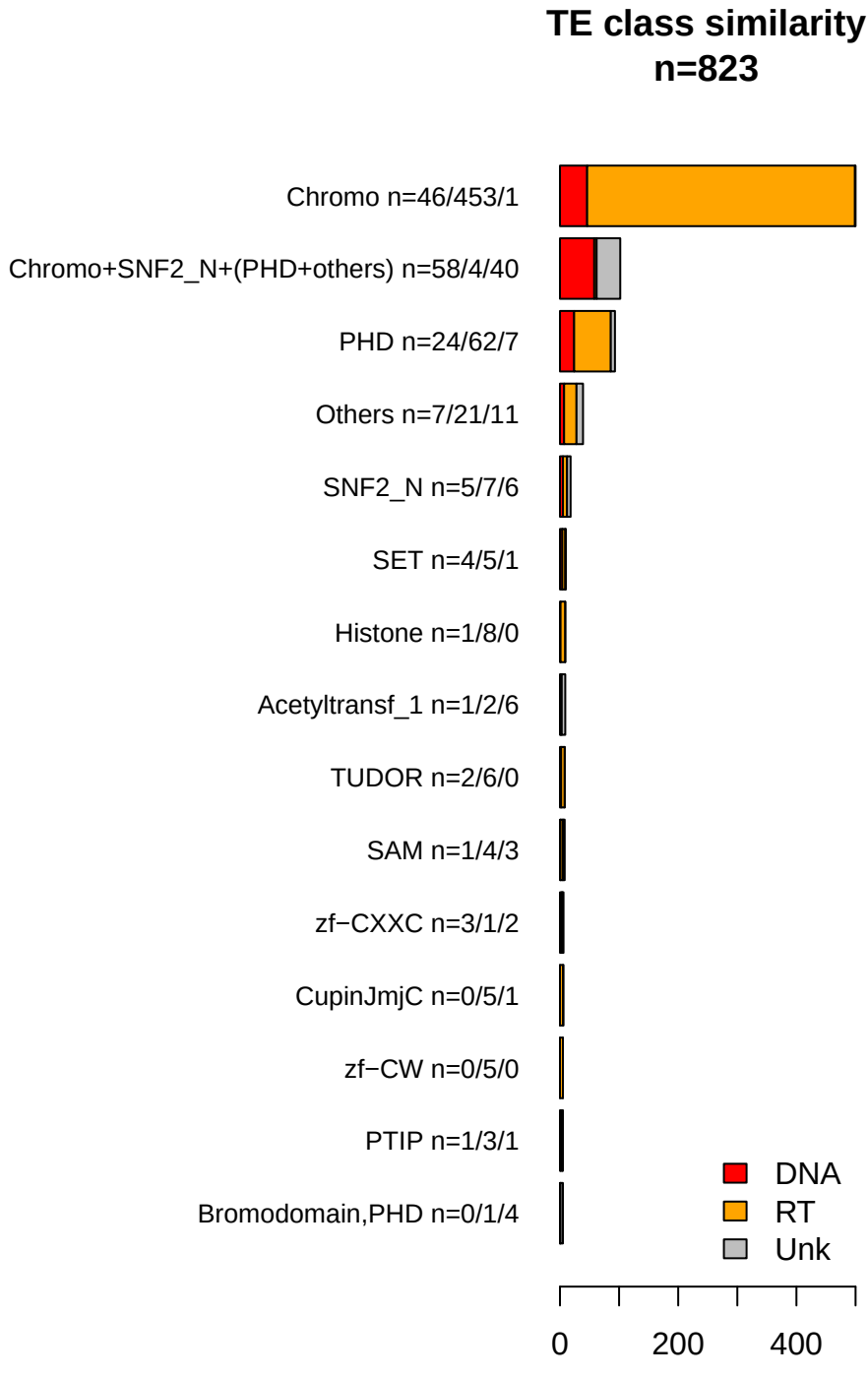


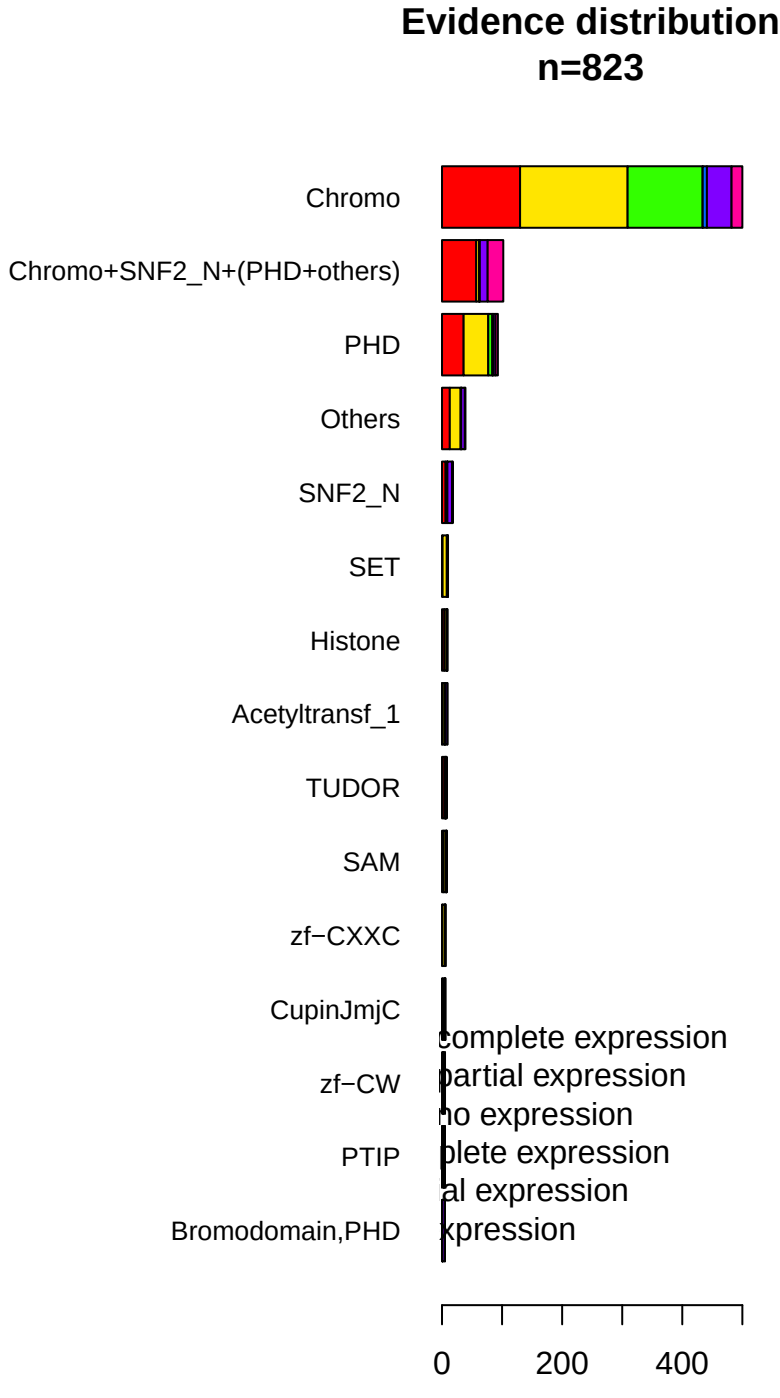

TE fusions
n=823
Unknown n = 83
RT n = 587
DNA n = 153
0
200
400

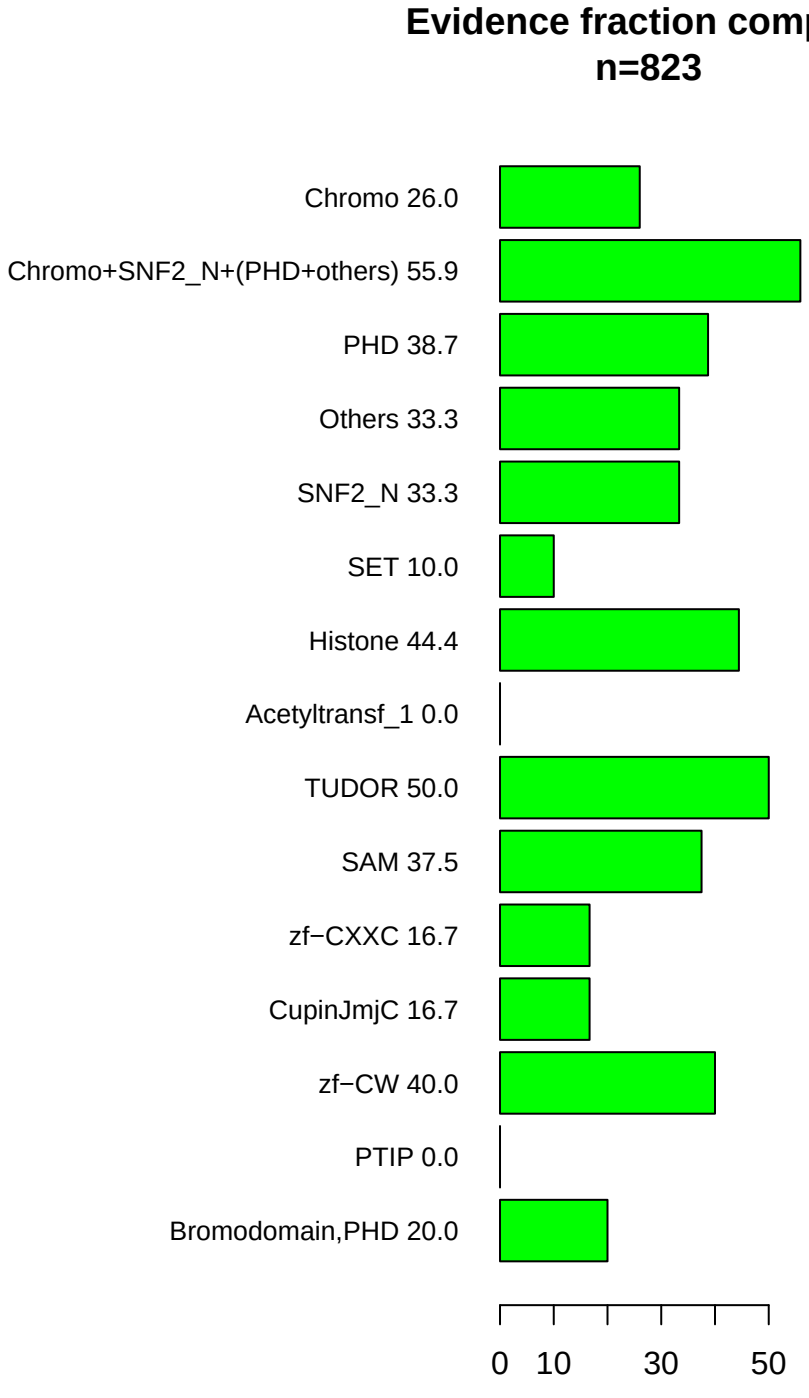

TE fusions
n=823
Unknown n = 83
RT Viper−group n = 1
RT Tyrosine_Recombinase_Elements n = 1
RT RTE−group n = 28
RT R4−like n = 4
RT R2−like n = 3
RT Orthoretrovirinae n = 1
RT Long_Terminal_Repeat_Element n = 7
RT L2−group n = 8
RT L1−group n = 1
RT L1−dependent n = 1
RT I−group n = 4
RT Gypsy−ERV n = 516
RT CR1−group n = 9
RT CR1 n = 3
DNA Transposase n = 2
DNA Tc2−group n = 16
DNA Tc1−Mariner n = 4
DNA PiggyBac_Group n = 3
DNA PIF−Harbinger n = 6
DNA Mutator−like n = 67
DNA Helicase n = 5
DNA hAT n = 13
DNA Ginger n = 1
DNA DNA_Polymerase n = 35
DNA CMC n = 1
0
200
400

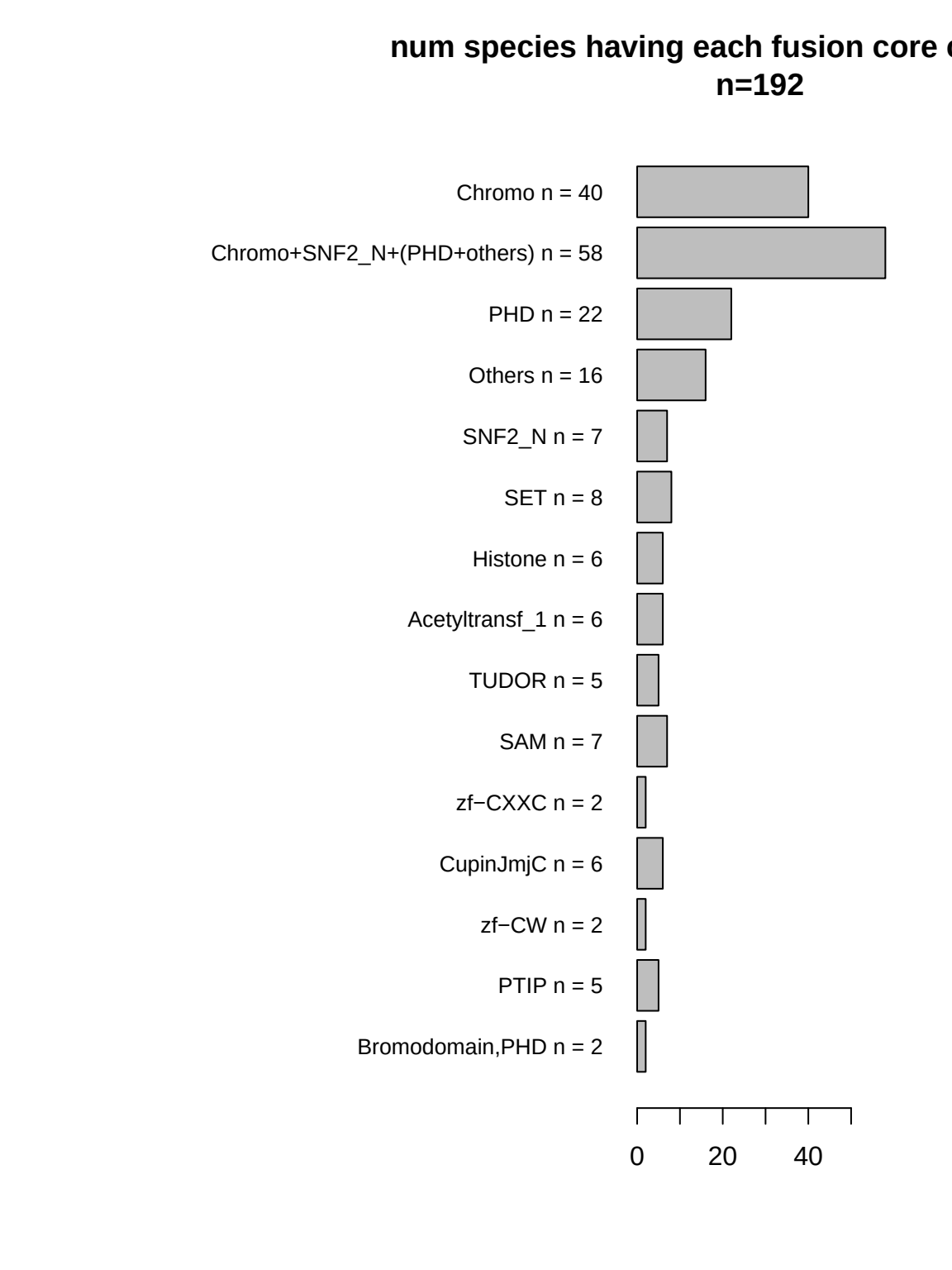

TE fusions
n=823
zf−CXXC n = 6
zf−CW n = 5
zf−CCHH n = 1
YEATS n = 1
TUDOR n = 8
SWIRM n = 2
SSrecog n = 1
SNF2_N n = 18
SIR2 n = 2
SET n = 10
SAWADEE n = 2
SAM n = 8
PWWP,zf−CW n = 1
PTIP n = 5
PHD,WD40 n = 2
PHD,SNF2_N n = 1
PHD,SAM n = 1
PHD n = 93
PCRing n = 3
NAP n = 3
MRG n = 1
MBT n = 4
Kelch n = 2
Histone n = 9
Hist_deacetyl n = 3
Hira,WD40 n = 1
Dpy−30 n = 1
Daxx n = 1
CupinJmjC n = 6
Chromo,SNF2_N n = 17
Chromo,SAWADEE,SNF2_N n = 1
Chromo,PHD,SNF2_N n = 76
Chromo,PHD,PWWP,SNF2_N n = 7
Chromo n = 500
CAF1C,WD40 n = 1
Bromodomain,PHD n = 5
Bromodomain,Chromo,PHD,SNF2_N n = 1
Bromodomain n = 4
BIR n = 1
Acetyltransf_1 n = 9
0
200
400

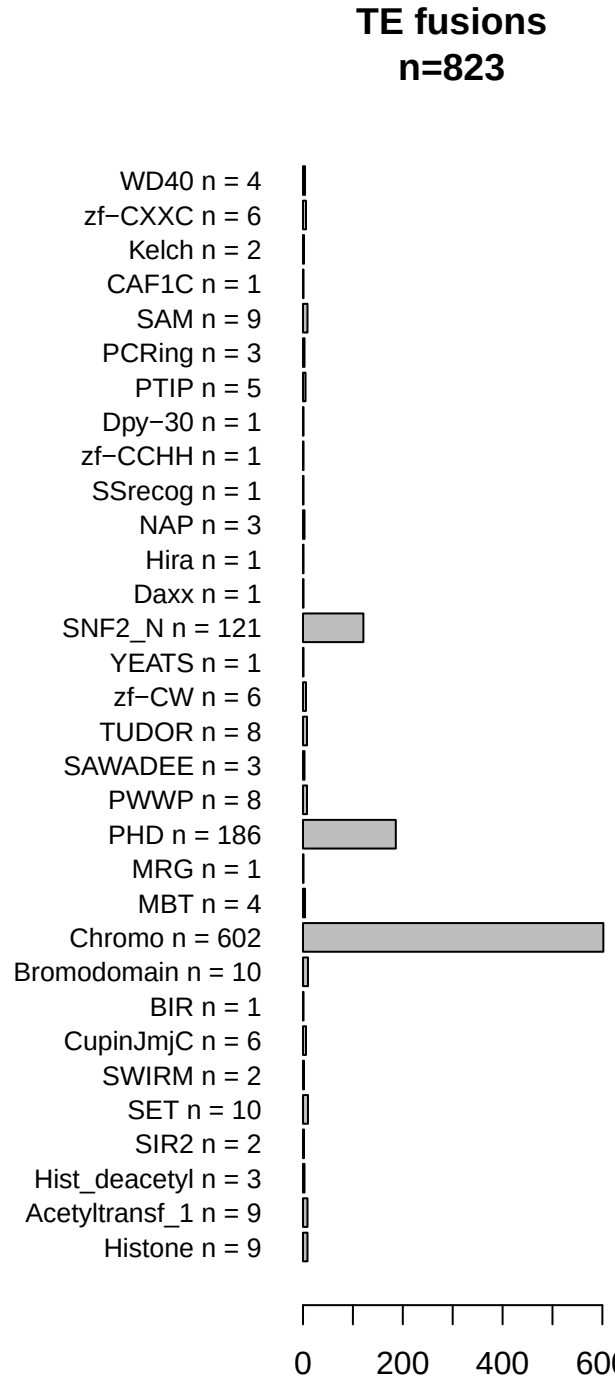

TE fusions
n=823
Chromo n = 500
Chromo+SNF2_N+(PHD+others) n = 102
PHD n = 93
Others n = 39
SNF2_N n = 18
SET n = 10
Histone n = 9
Acetyltransf_1 n = 9
TUDOR n = 8
SAM n = 8
zf−CXXC n = 6
CupinJmjC n = 6
zf−CW n = 5
PTIP n = 5
Bromodomain,PHD n = 5
0
200
400


TE class similarity
n=823
Chromo n=46/453/1
Chromo+SNF2_N+(PHD+others) n=58/4/40
PHD n=24/62/7
Others n=7/21/11
SNF2_N n=5/7/6
SET n=4/5/1
Histone n=1/8/0
Acetyltransf_1 n=1/2/6
TUDOR n=2/6/0
SAM n=1/4/3
zf−CXXC n=3/1/2
CupinJmjC n=0/5/1
zf−CW n=0/5/0
PTIP n=1/3/1
Bromodomain,PHD n=0/1/4
DNA
RT
Unk
0
200
400


Evidence distribution
n=823
Chromo
Chromo+SNF2_N+(PHD+others)
PHD
Others
SNF2_N
SET
Histone
Acetyltransf_1
TUDOR
SAM
zf−CXXC
CupinJmjC
zf−CW
PTIP
Bromodomain,PHD
complete expression
partial expression
no expression
plete expression
al expression
xpression
0
200
400


Evidence fraction complete
n=823
Chromo 26.0
Chromo+SNF2_N+(PHD+others) 55.9
PHD 38.7
Others 33.3
SNF2_N 33.3
SET 10.0
Histone 44.4
Acetyltransf_1 0.0
TUDOR 50.0
SAM 37.5
zf−CXXC 16.7
CupinJmjC 16.7
zf−CW 40.0
PTIP 0.0
Bromodomain,PHD 20.0
0
10
30
50


num species having each fusion core d
n=192
Chromo n = 40
Chromo+SNF2_N+(PHD+others) n = 58
PHD n = 22
Others n = 16
SNF2_N n = 7
SET n = 8
Histone n = 6
Acetyltransf_1 n = 6
TUDOR n = 5
SAM n = 7
zf−CXXC n = 2
CupinJmjC n = 6
zf−CW n = 2
PTIP n = 5
Bromodomain,PHD n = 2
0
20
40


TE fusions
n=823
WD40 n = 4
zf−CXXC n = 6
Kelch n = 2
CAF1C n = 1
SAM n = 9
PCRing n = 3
PTIP n = 5
Dpy−30 n = 1
zf−CCHH n = 1
SSrecog n = 1
NAP n = 3
Hira n = 1
Daxx n = 1
SNF2_N n = 121
YEATS n = 1
zf−CW n = 6
TUDOR n = 8
SAWADEE n = 3
PWWP n = 8
PHD n = 186
MRG n = 1
MBT n = 4
Chromo n = 602
Bromodomain n = 10
BIR n = 1
CupinJmjC n = 6
SWIRM n = 2
SET n = 10
SIR2 n = 2
Hist_deacetyl n = 3
Acetyltransf_1 n = 9
Histone n = 9
0
200
400
600