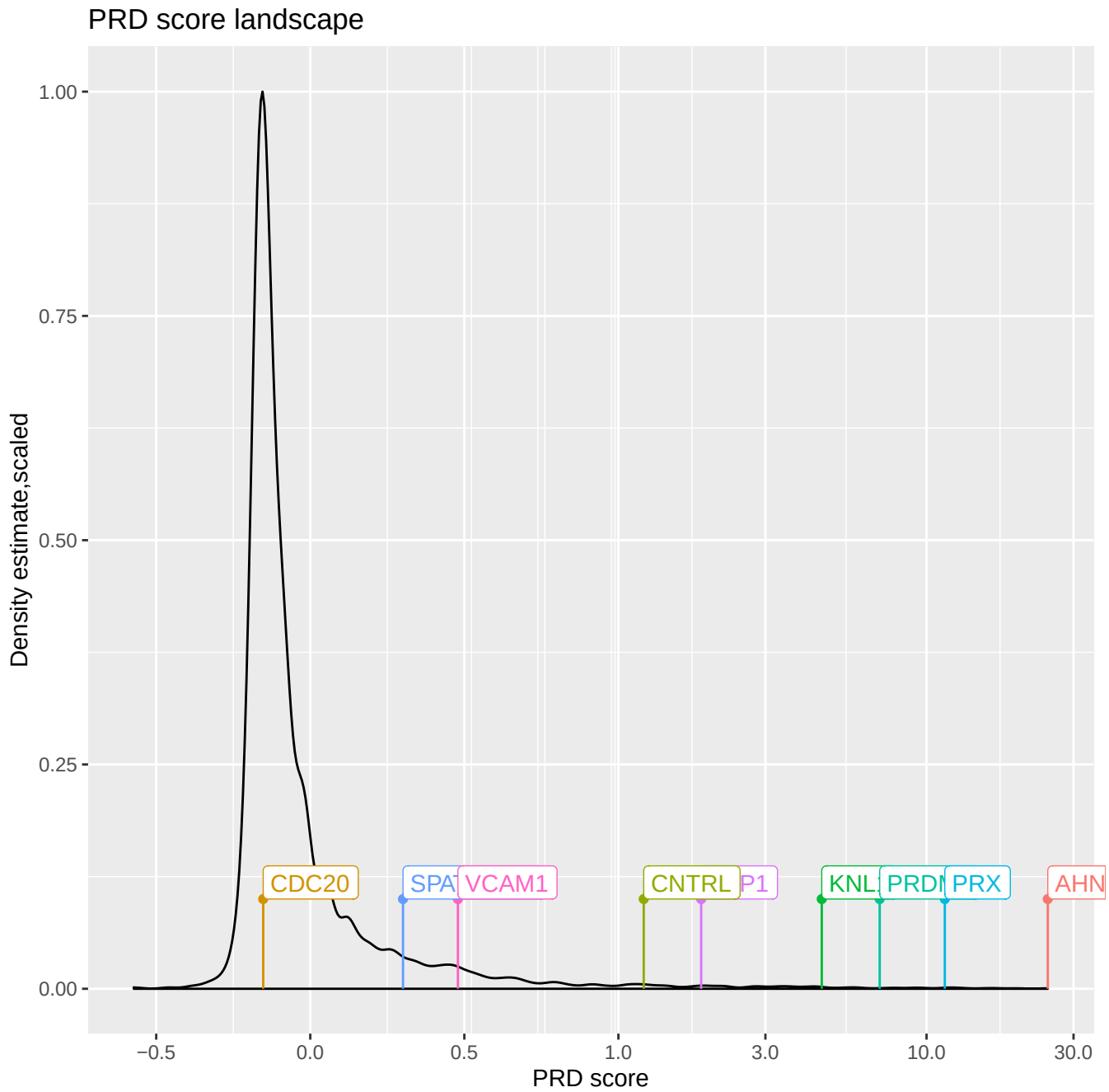
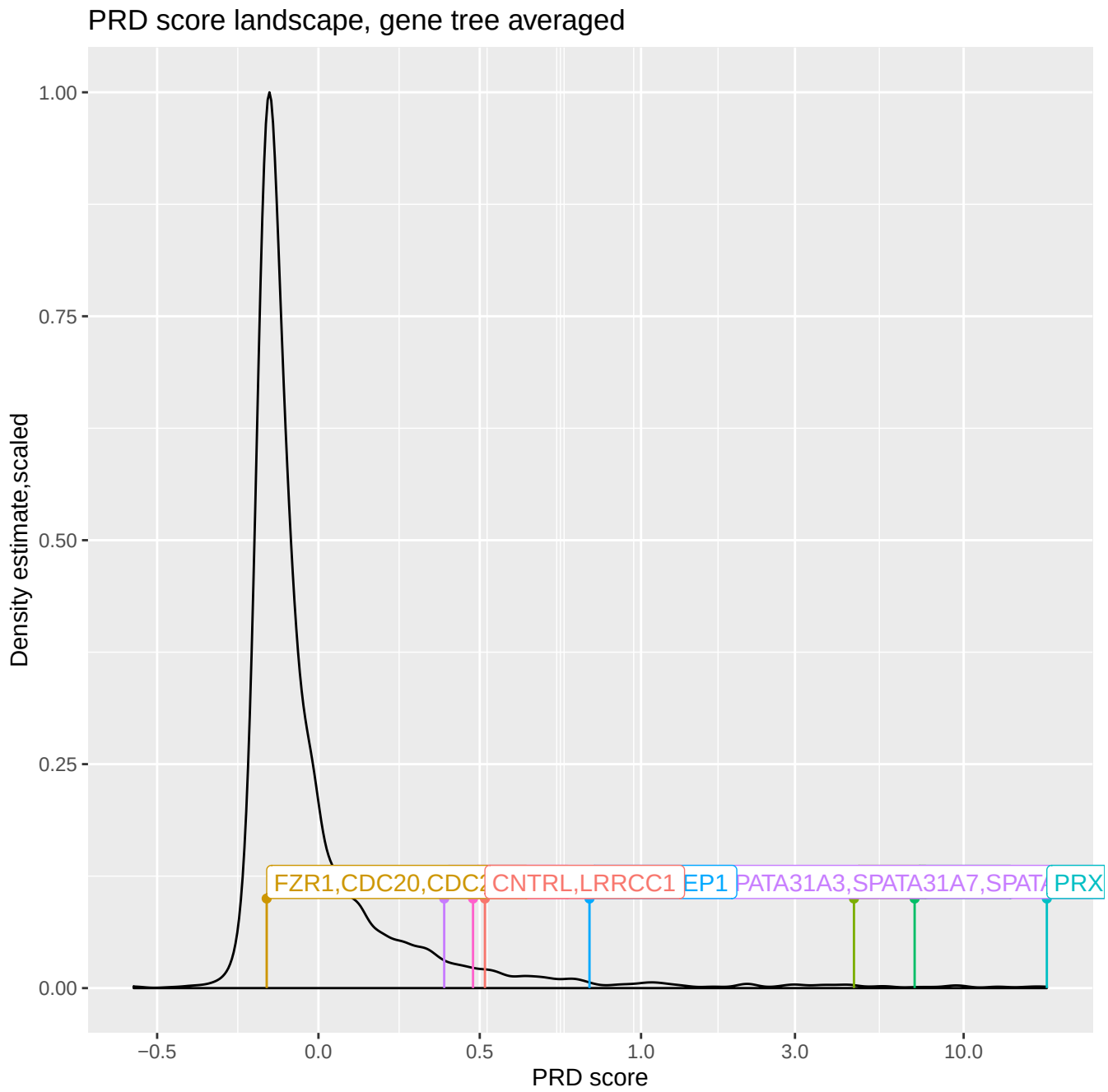
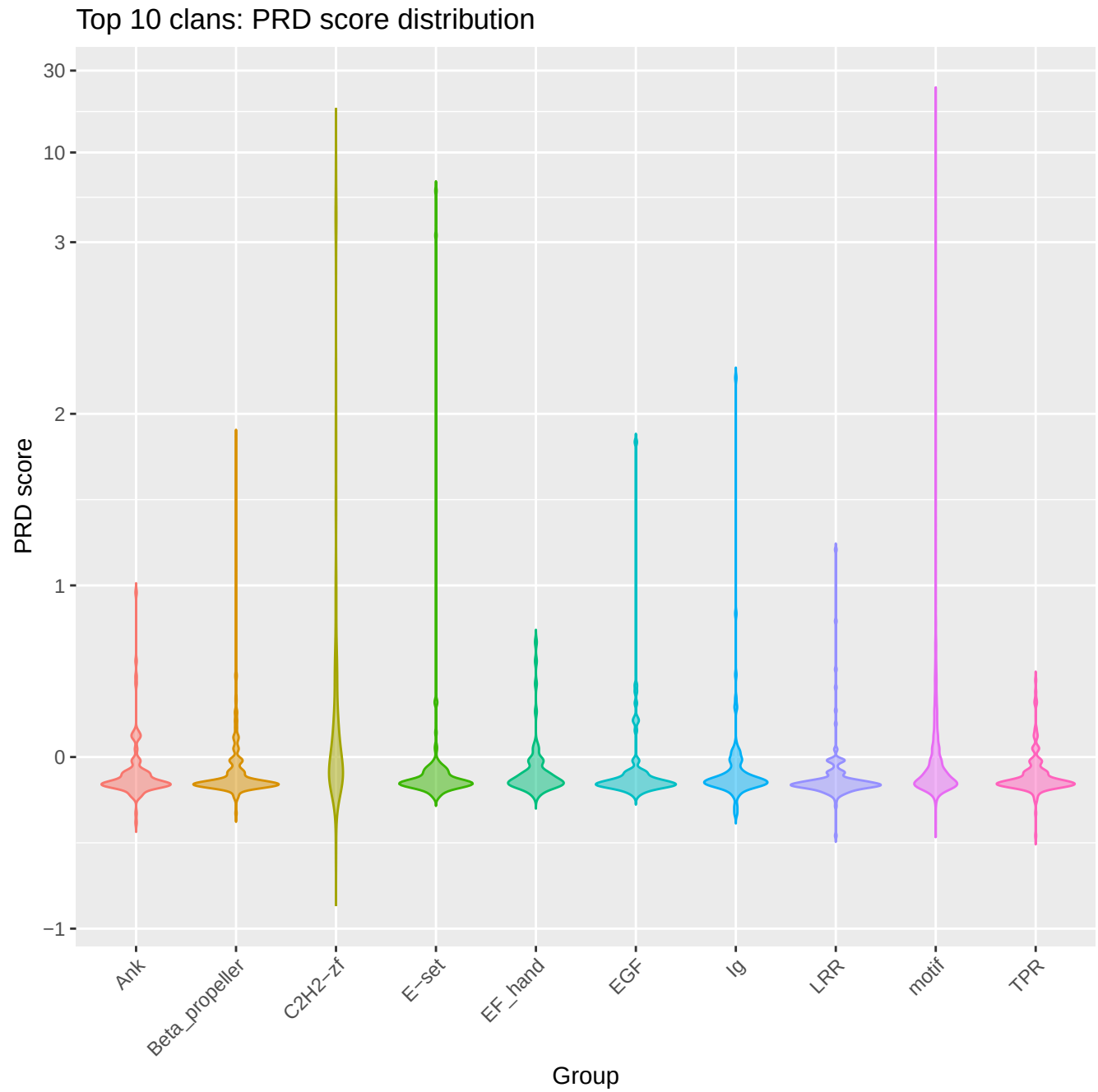
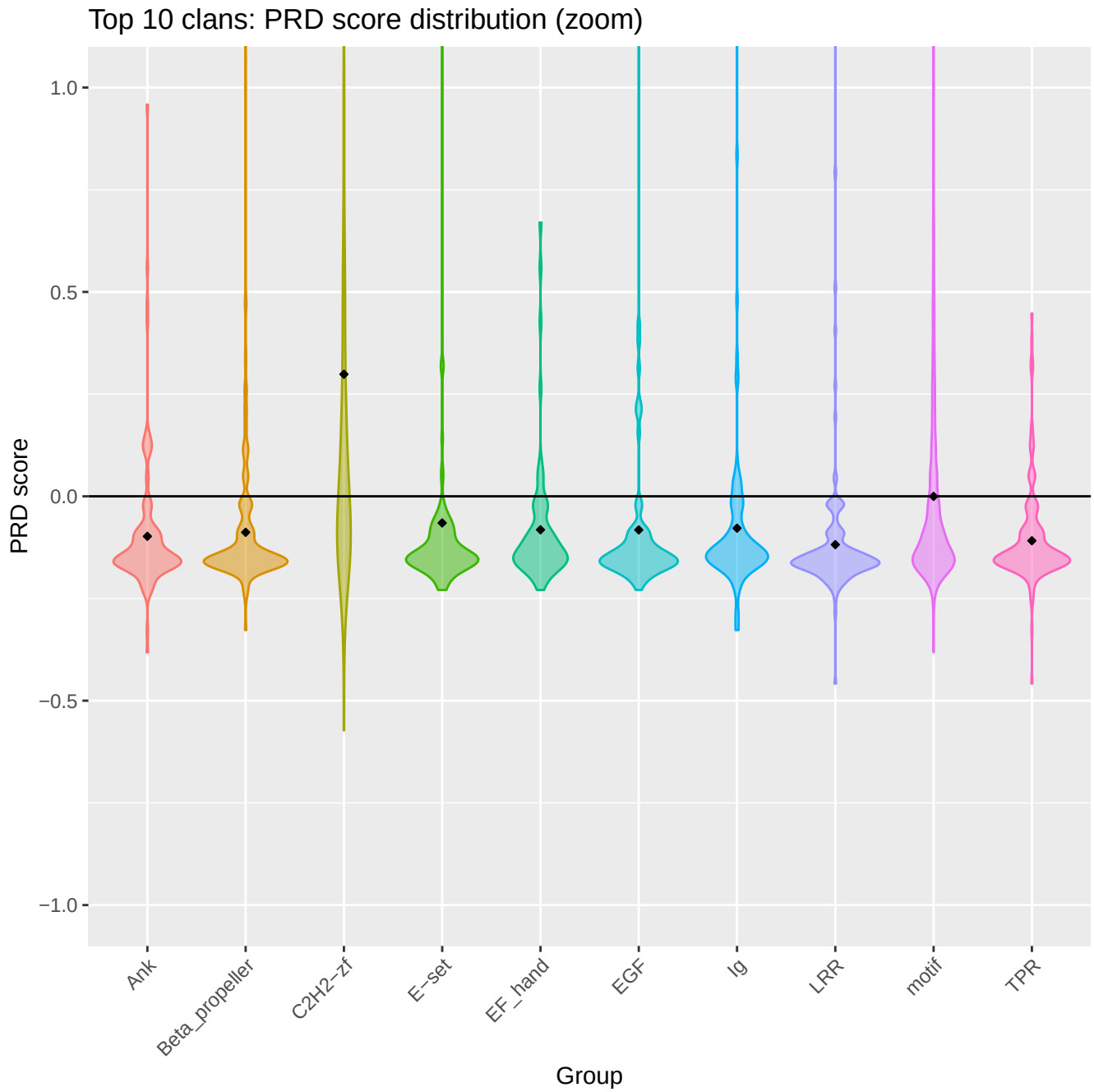
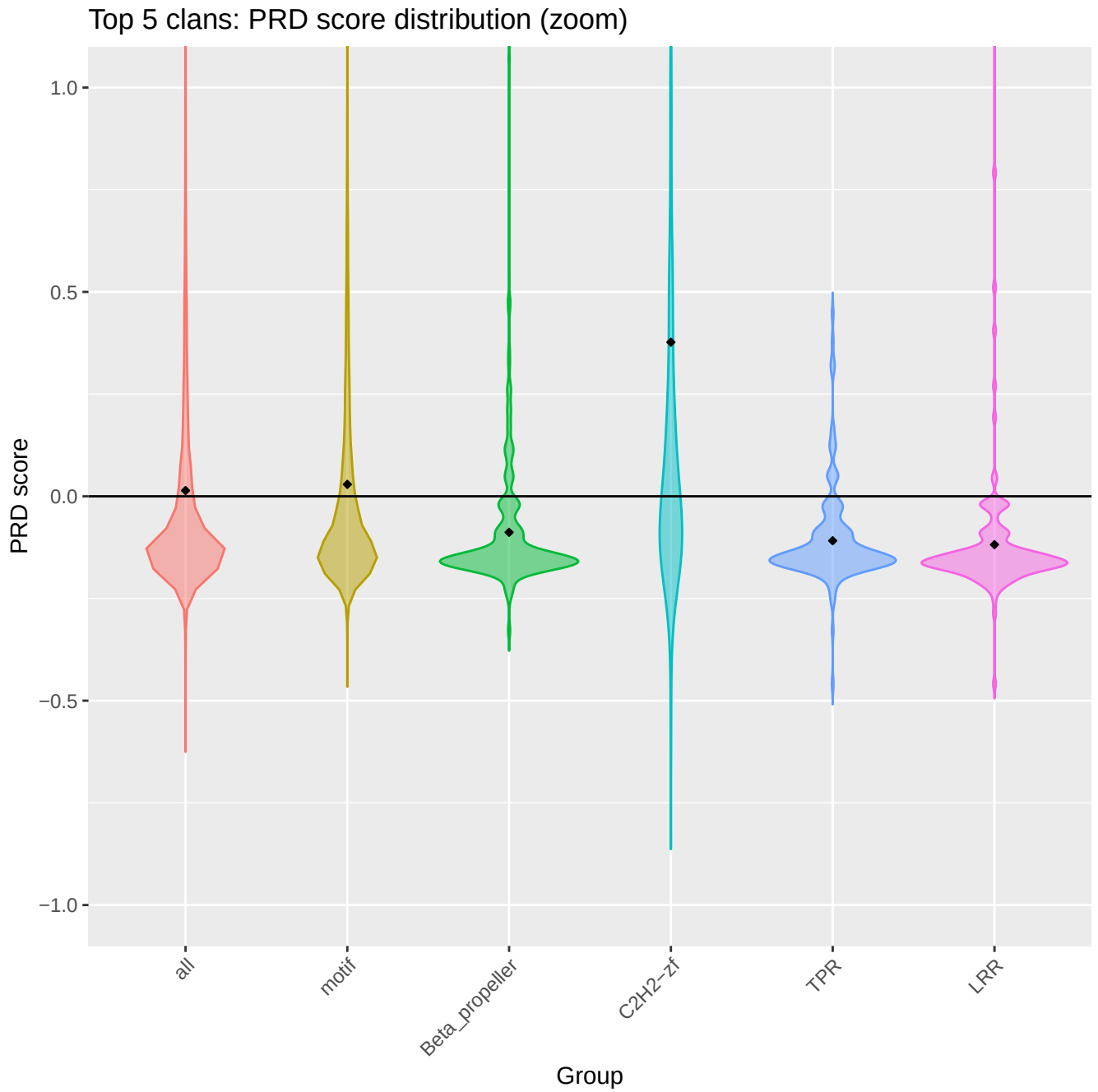
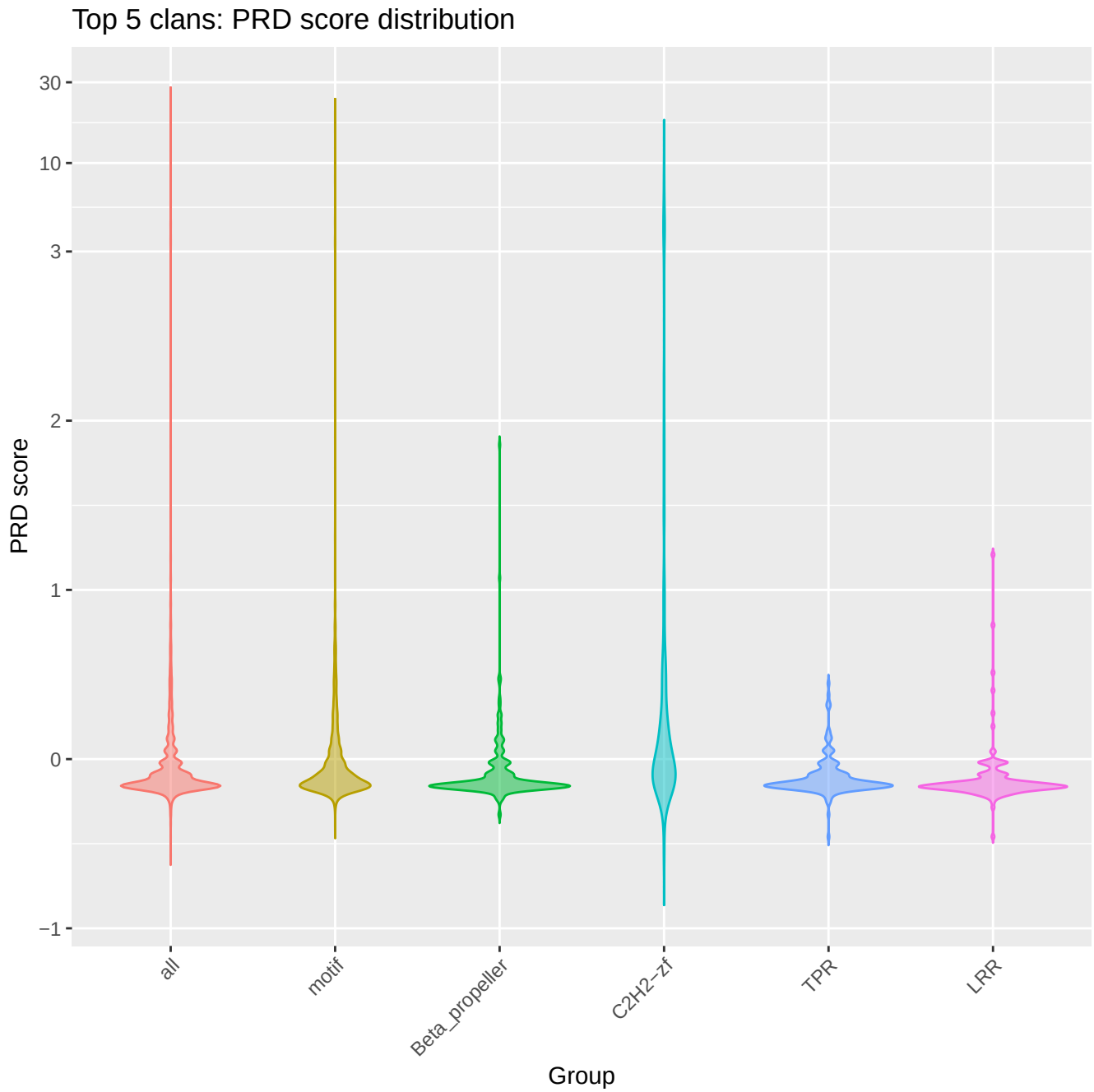

PRD score landscape
1.00
0.75
0.50
0.25
0.00
Density estimate,scaled
CDC20
SPA
VCAM1
CNTRL
P1
KNL
PRDI
PRX
AHN
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score

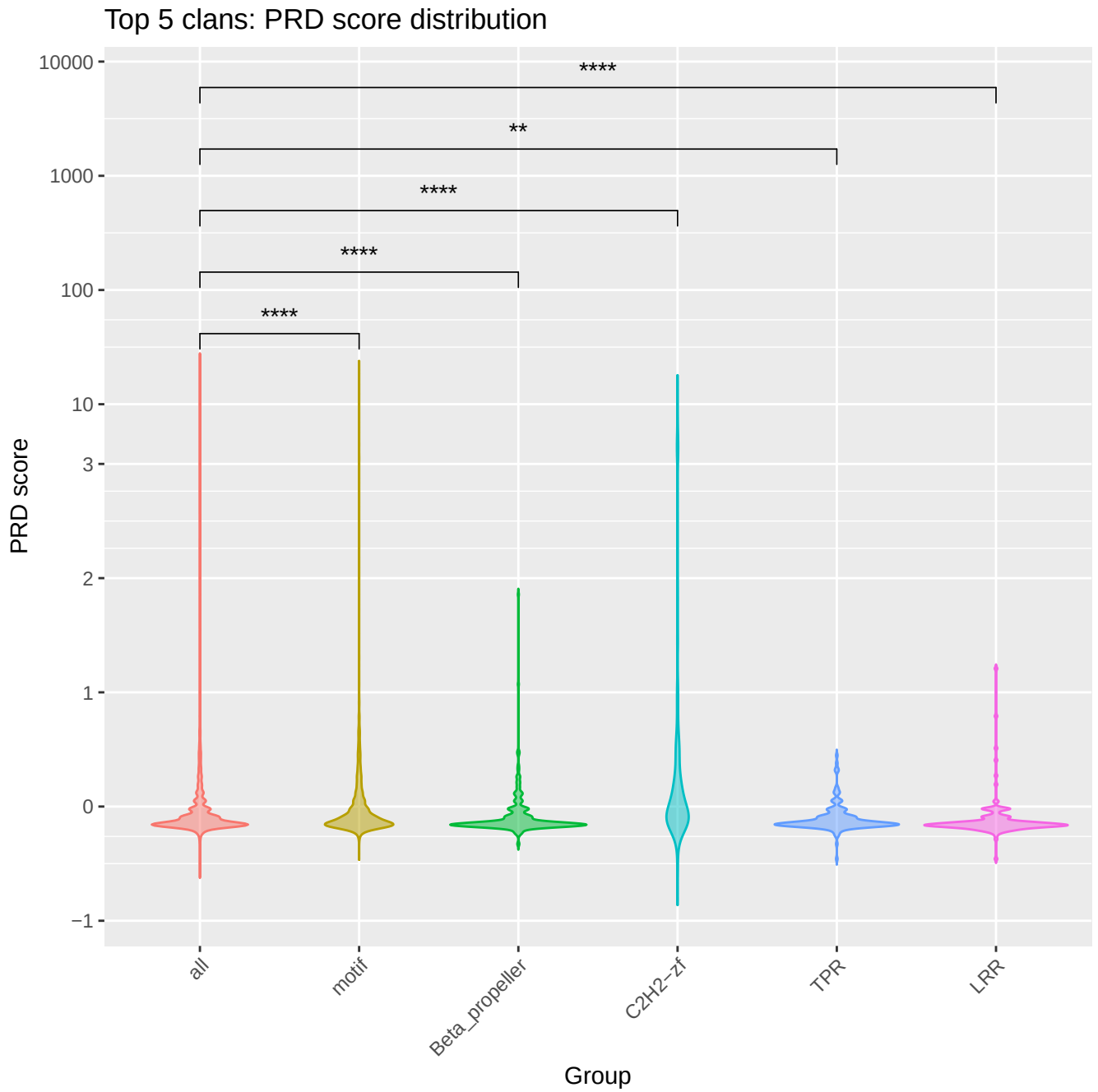

PRD score landscape, gene tree averaged
Density estimate,scaled
1.00
0.75
0.50
0.25
0.00
FZR1,CDC20,CDC2
CNTRL,LRRCC1
EP1
PATA31A3,SPATA31A7,SPAT
PRX
−0.5
0.0
0.5
1.0
3.0
10.0
PRD score

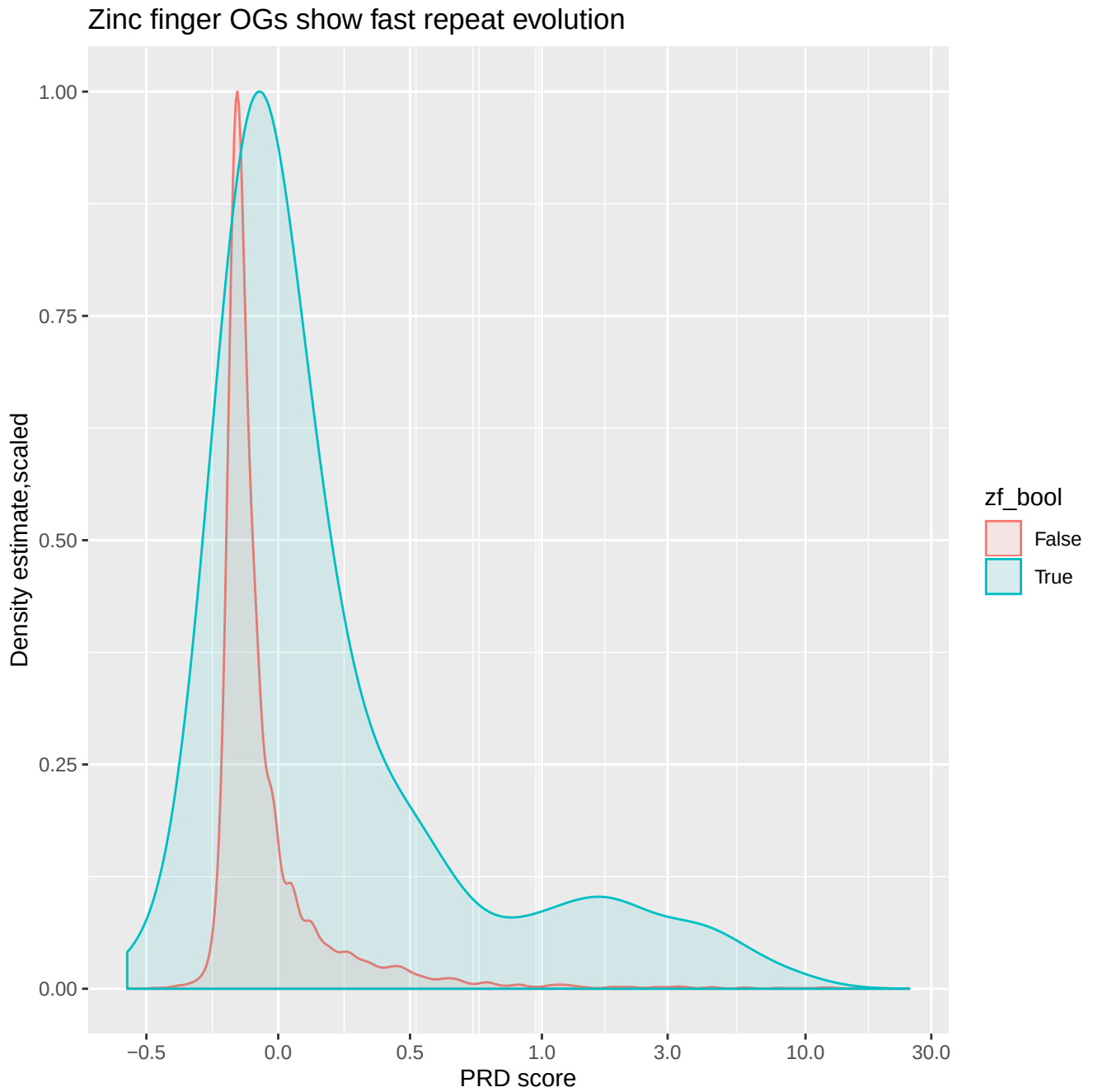

Top 10 clans: PRD score distribution
PRD score
30
10
3
2
1
0
−1
Ank
Beta_propeller
C2H2−zf
E−set
EF_hand
EGF
Ig
LRR
motif
TPR
Group

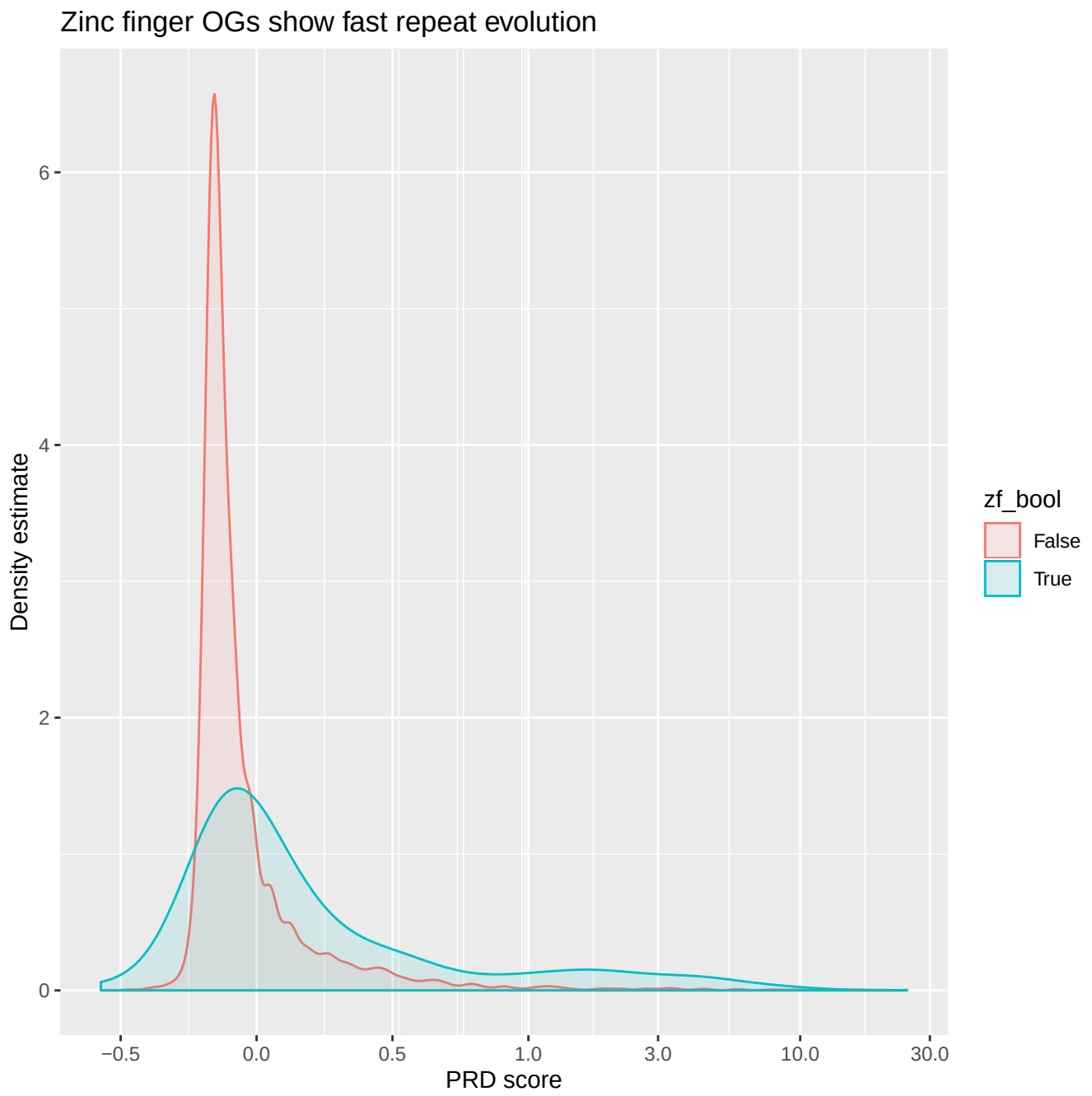

Top 10 clans: PRD score distribution (zoom)
PRD score
1.0
0.5
0.0
−0.5
−1.0
Ank
Beta_propeller
C2H2−zf
E−set
EF_hand
EGF
Ig
LRR
motif
TPR
Group

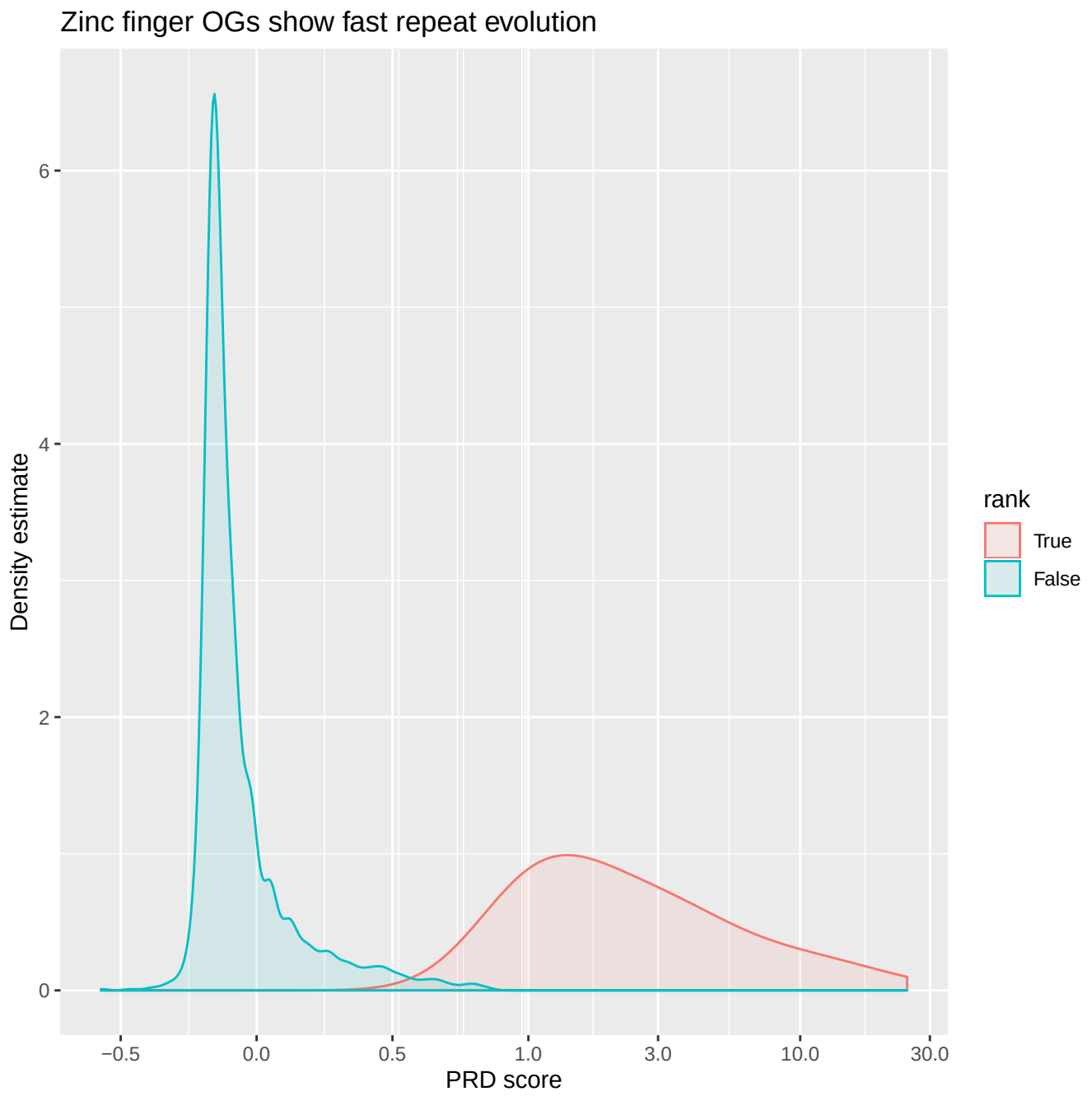

Top 5 clans: PRD score distribution (zoom)
PRD score
1.0
0.5
0.0
−0.5
−1.0
all
motif
Beta_propeller
C2H2−zf
TPR
LRR
Group

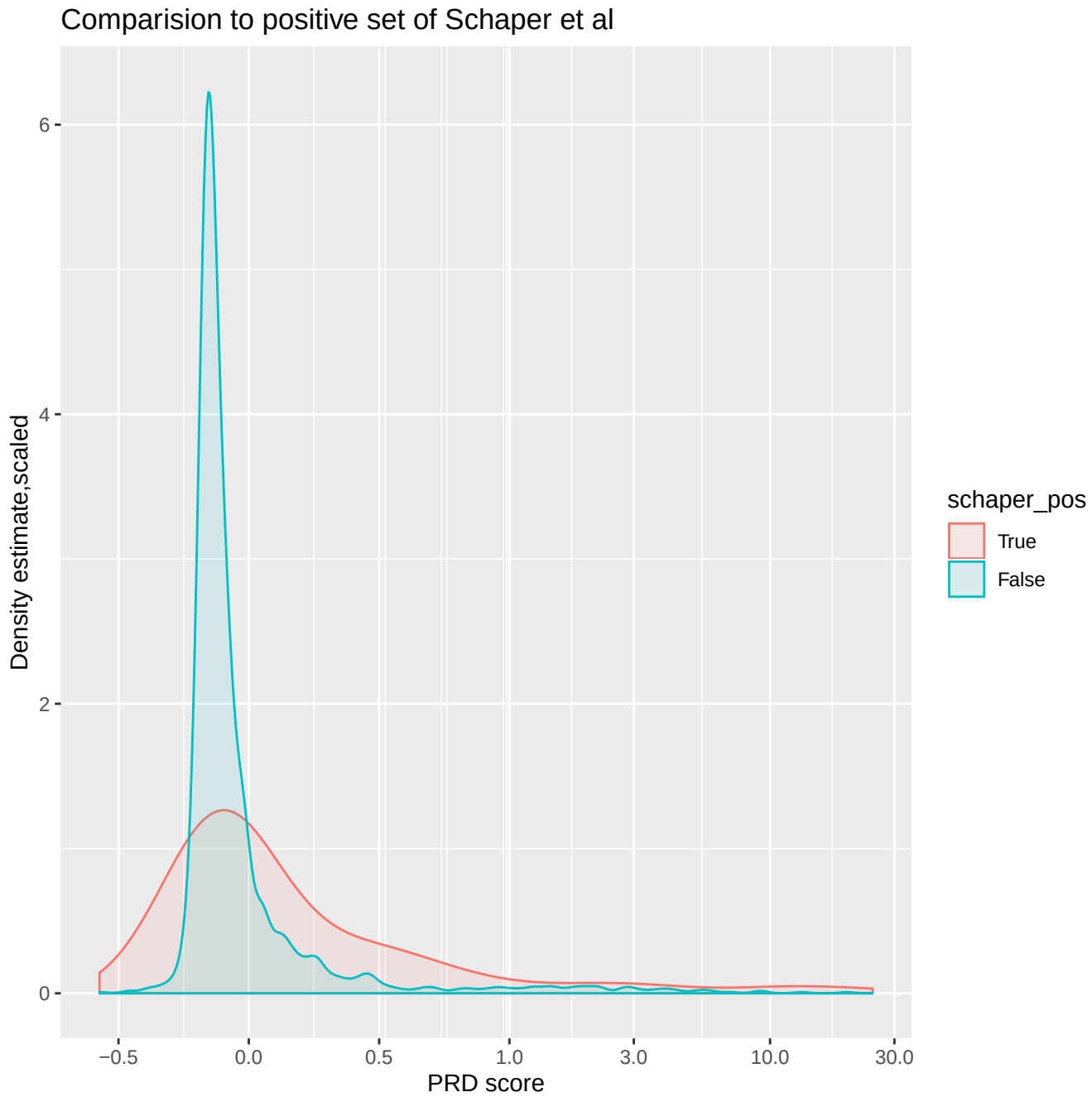

Top 5 clans: PRD score distribution
PRD score
30
10
3
2
1
0
−1
all
motif
Beta_propeller
C2H2−zf
TPR
LRR
Group

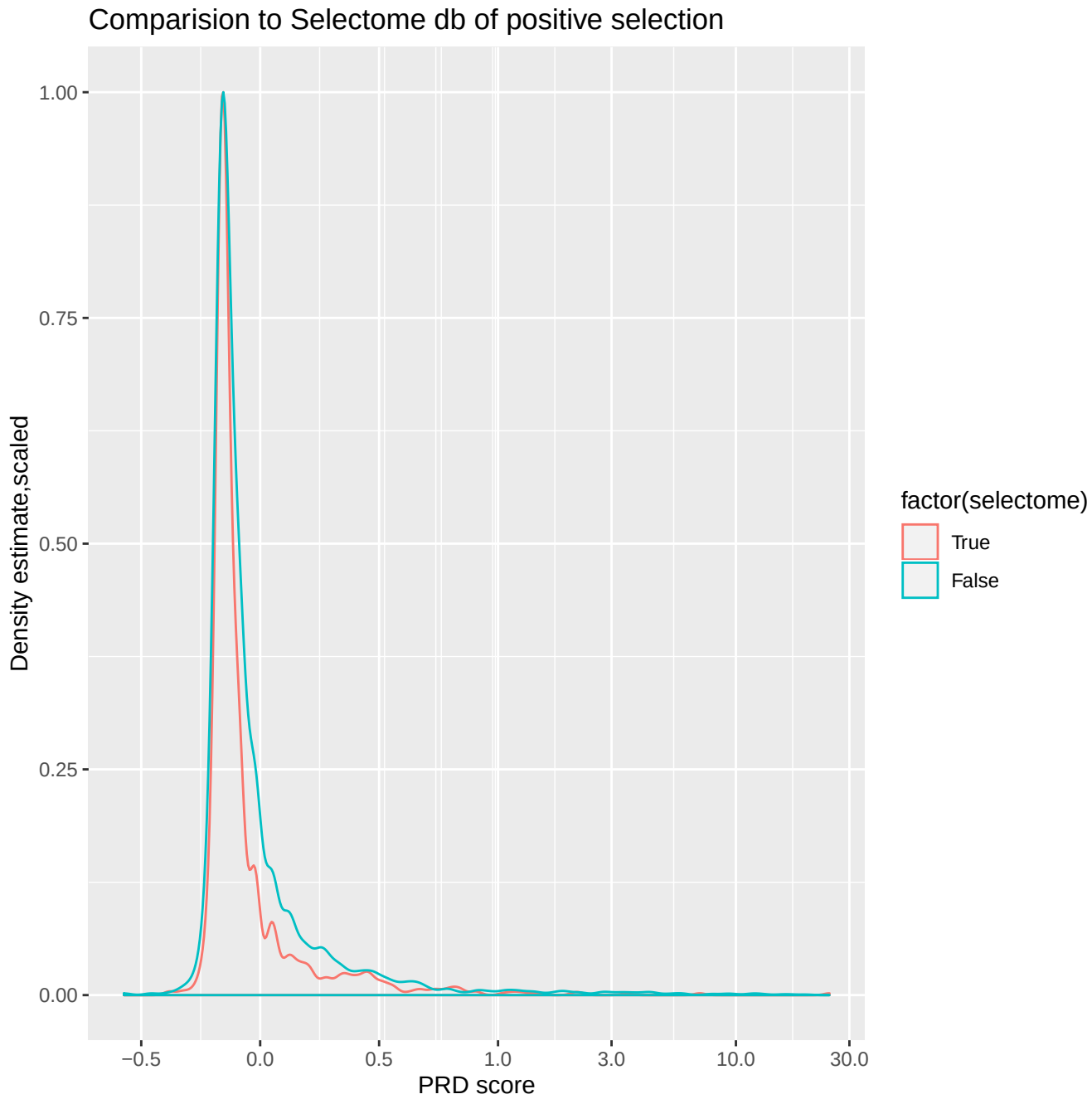

Top 5 clans: PRD score distribution
PRD score
10000
1000
100
10
3
2
1
0
−1
****
**
****
****
****
all
motif
Beta_propeller
C2H2−zf
TPR
LRR
Group

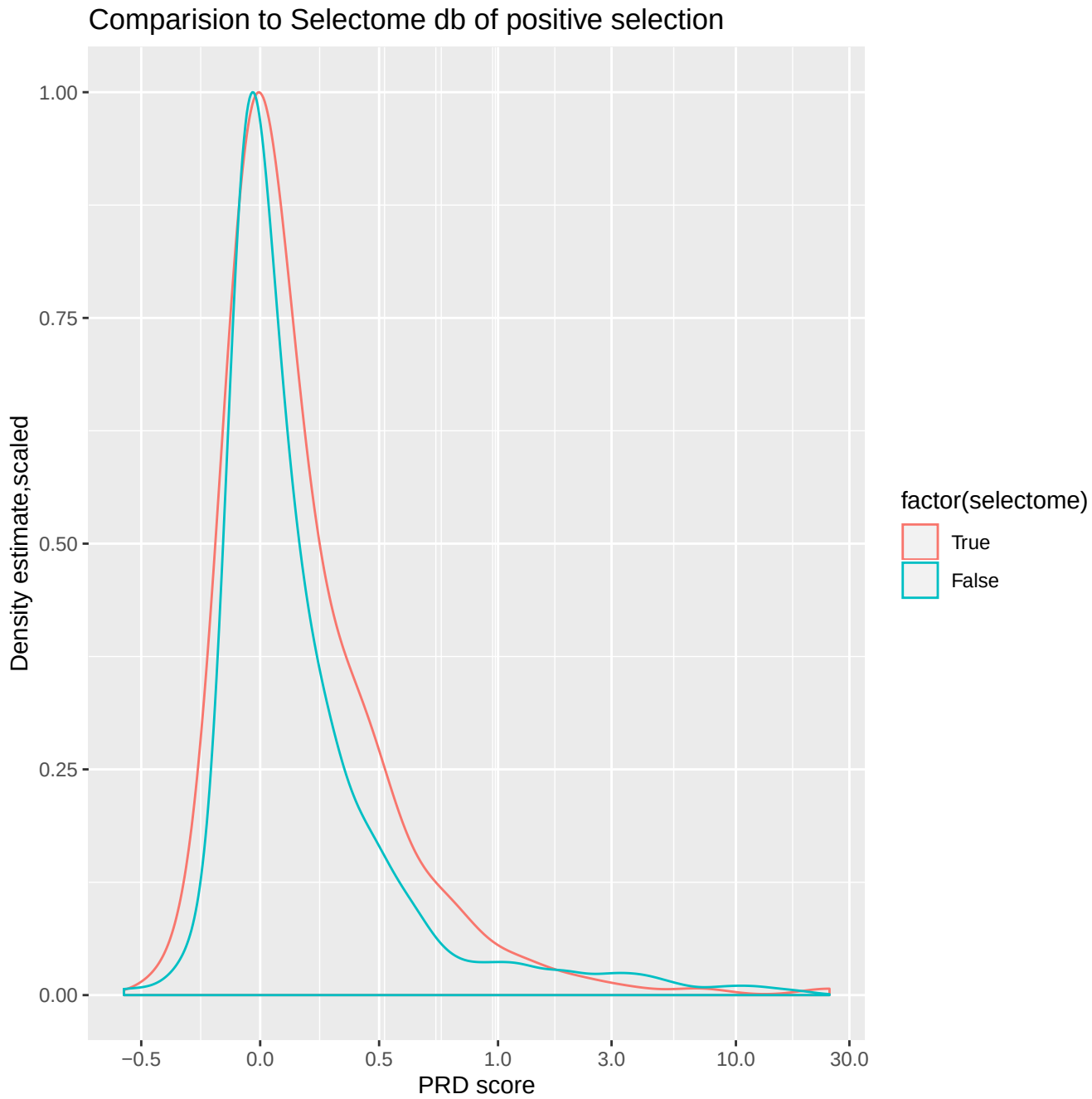

Zinc finger OGs show fast repeat evolution
Density estimate,scaled
1.00
0.75
0.50
0.25
0.00
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
zf_bool
False
True

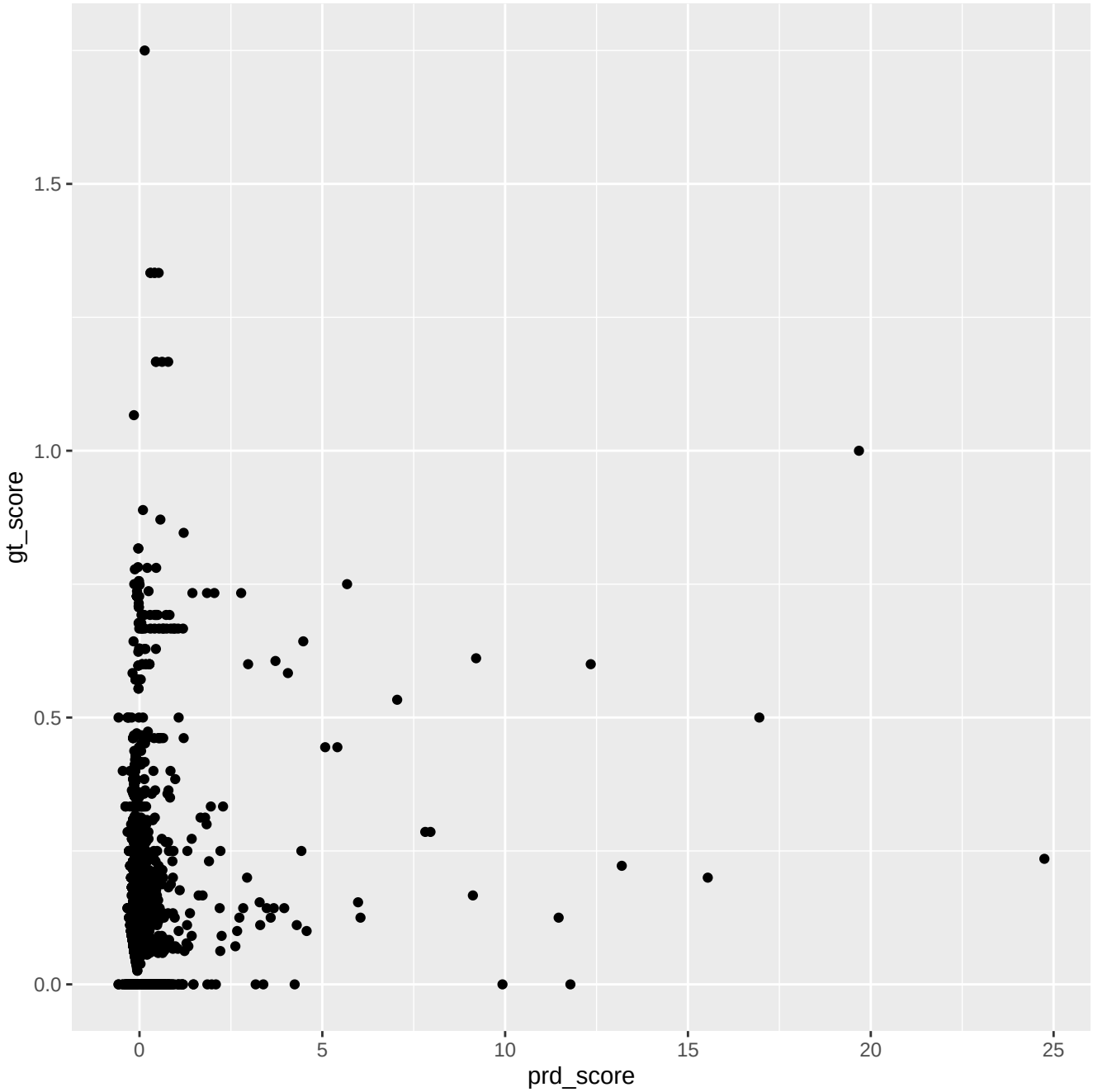

Zinc finger OGs show fast repeat evolution
Density estimate
6
4
2
0
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
zf_bool
False
True

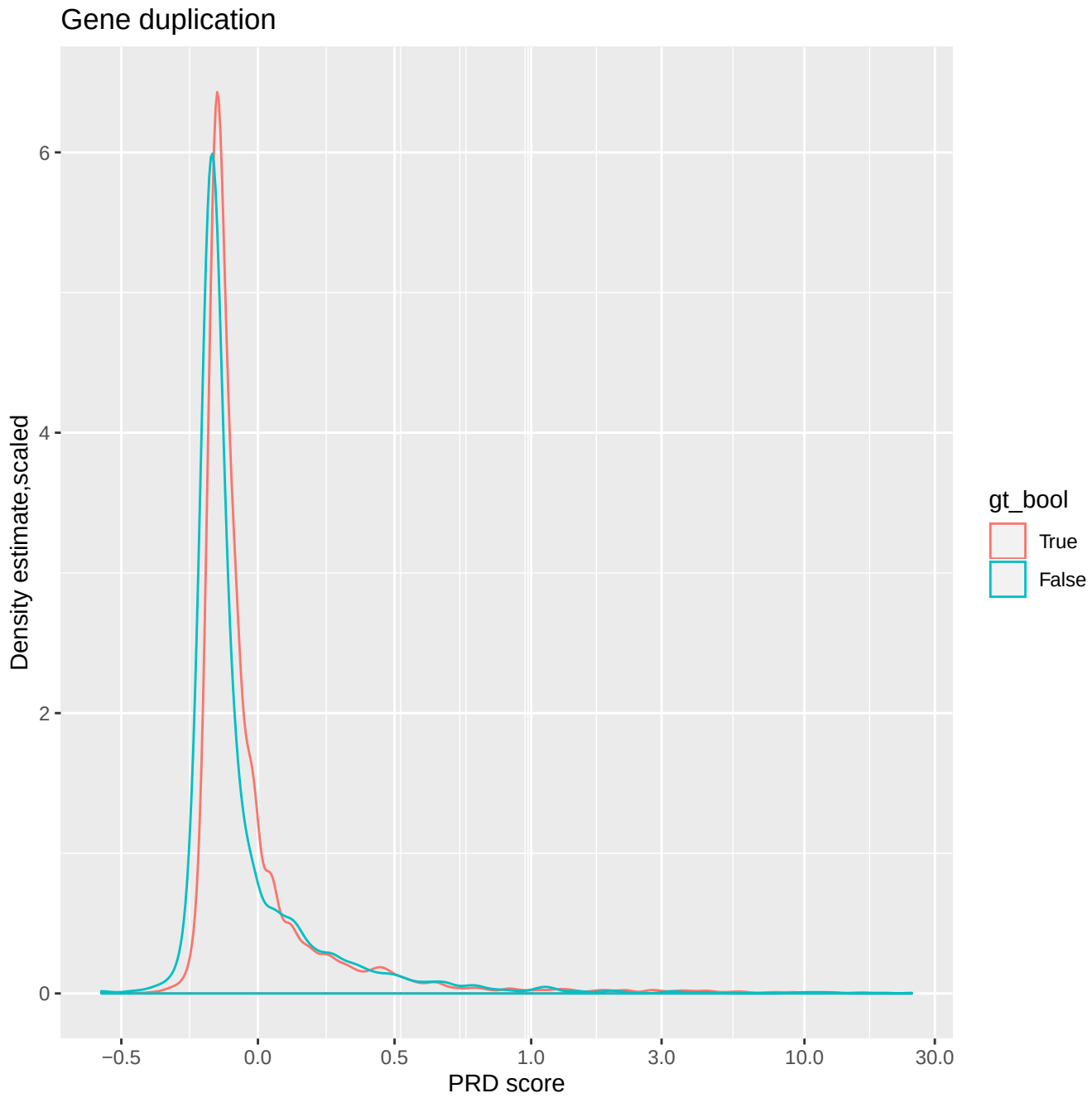

Zinc finger OGs show fast repeat evolution
Density estimate
6
4
2
0
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
rank
True
False

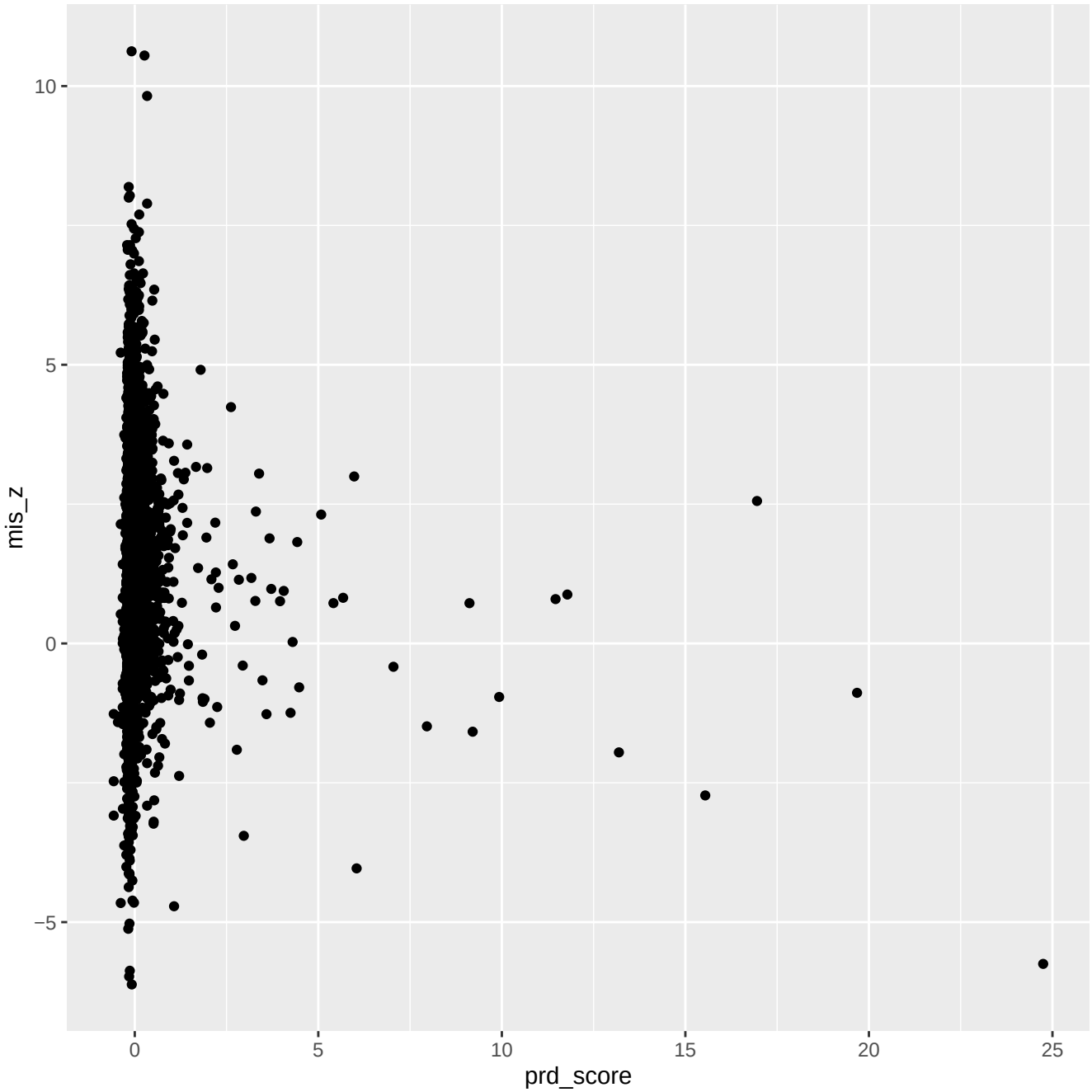

Comparision to positive set of Schaper et al
Density estimate,scaled
6
4
2
0
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
schaper_pos
True
False

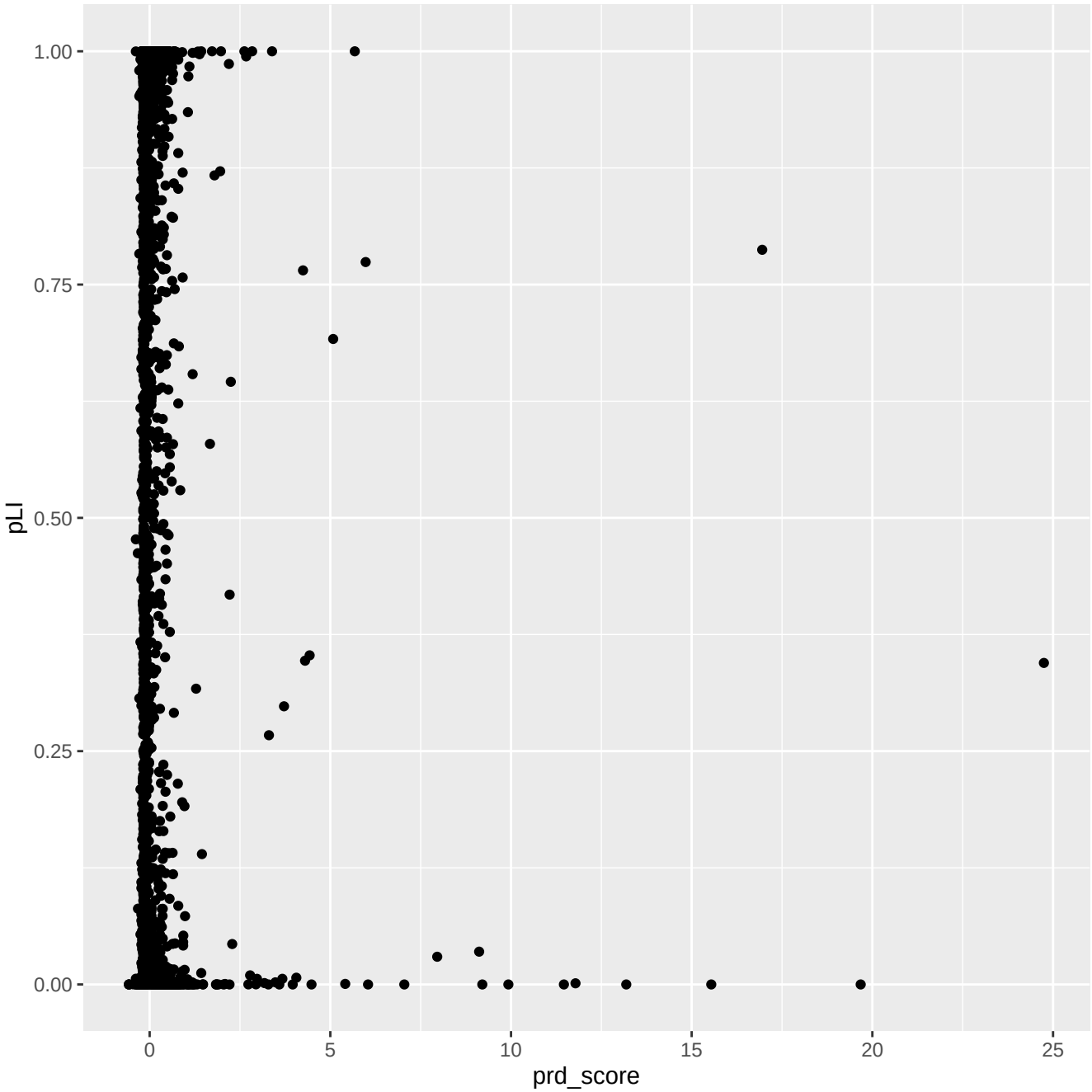

Comparision to Selectome db of positive selection
Density estimate,scaled
1.00
0.75
0.50
0.25
0.00
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
factor(selectome)
True
False

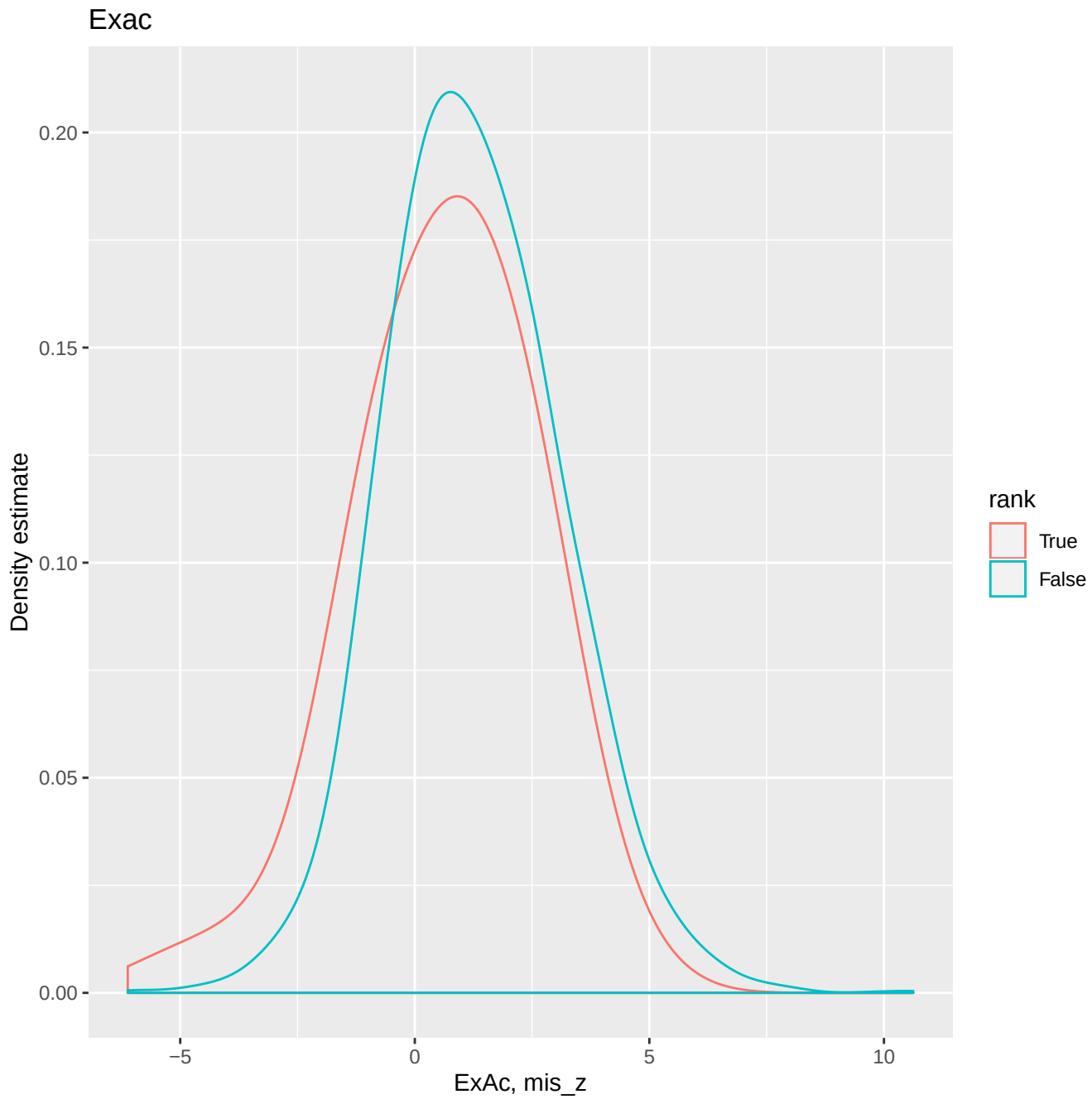

Comparision to Selectome db of positive selection
1.00
0.75
0.50
0.25
0.00
Density estimate,scaled
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
factor(selectome)
True
False

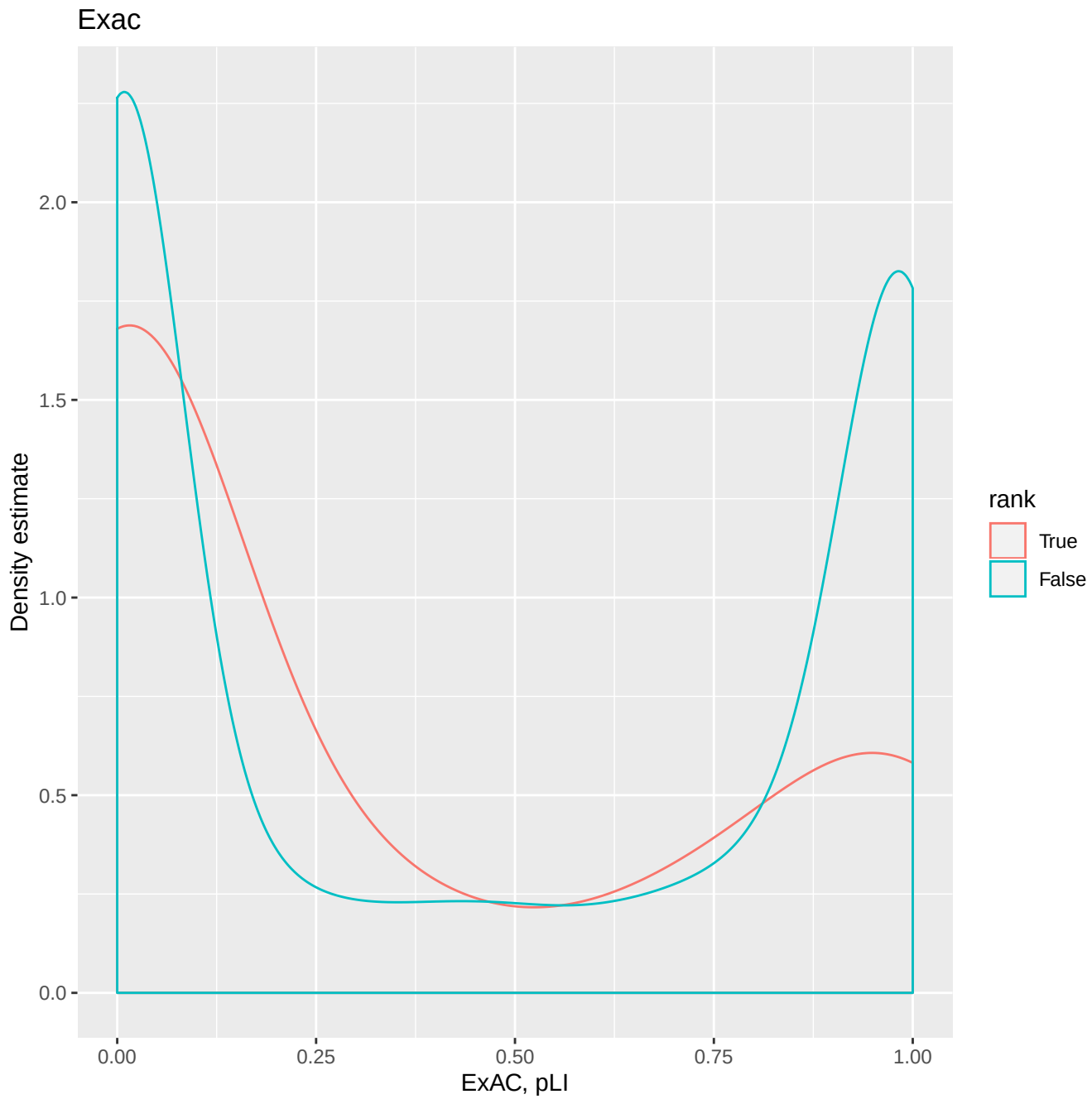

gt_score
1.5
1.0
0.5
0.0
0
5
10
15
20
25
prd_score

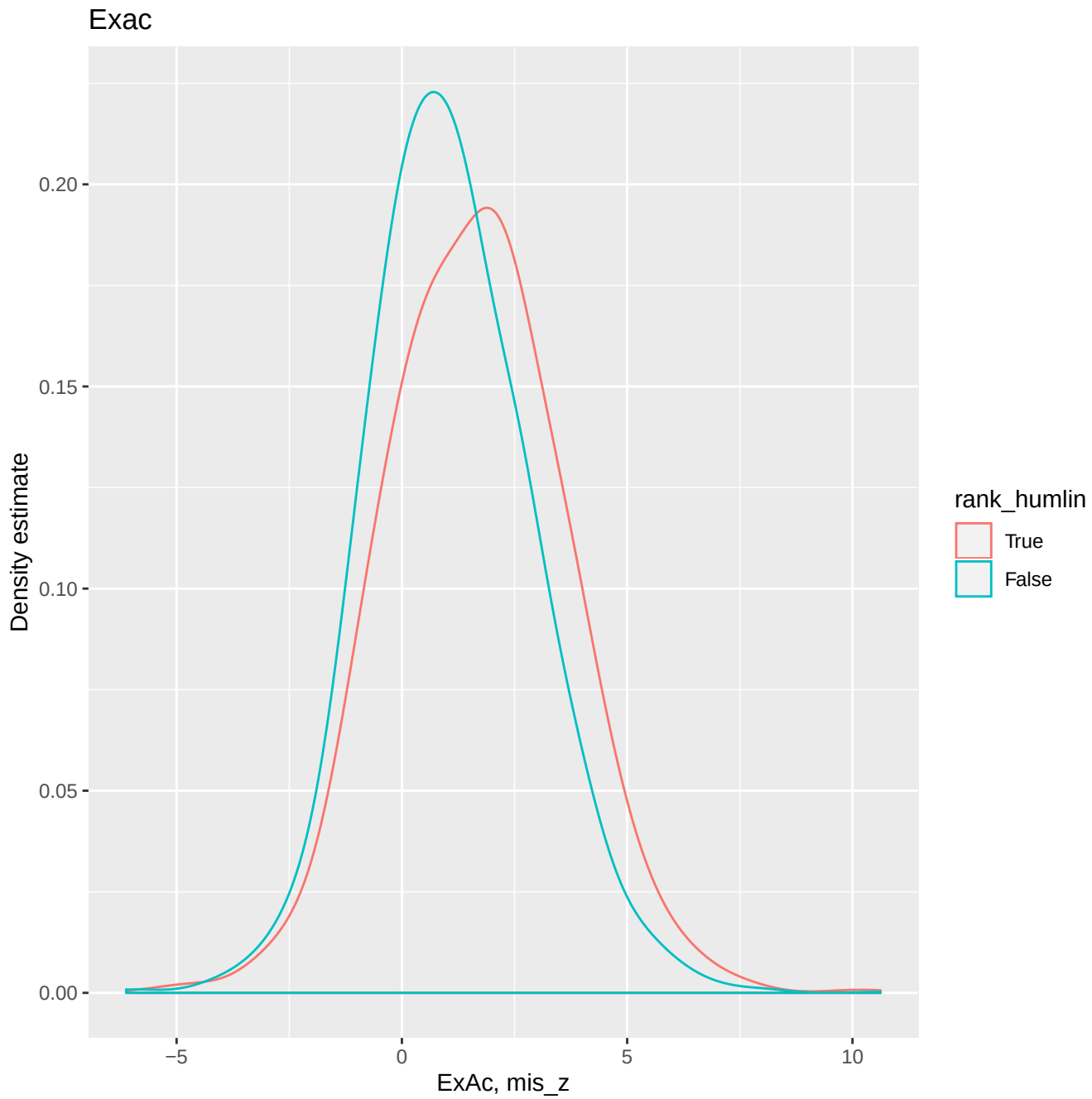

Gene duplication
Density estimate,scaled
6
4
2
0
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
gt_bool
True
False

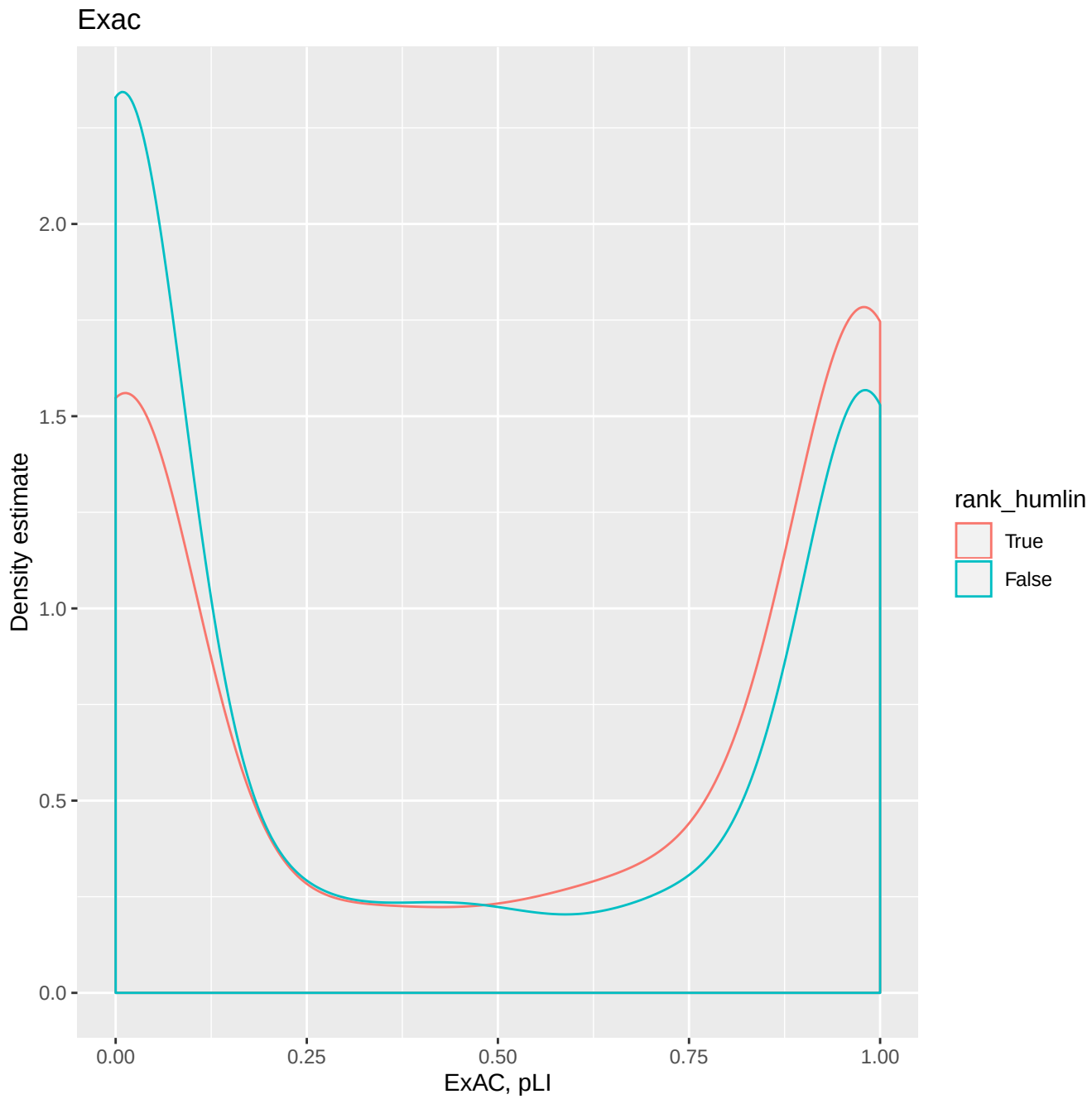

10
5
0
−5
mis_z
0
5
10
15
20
25
prd_score

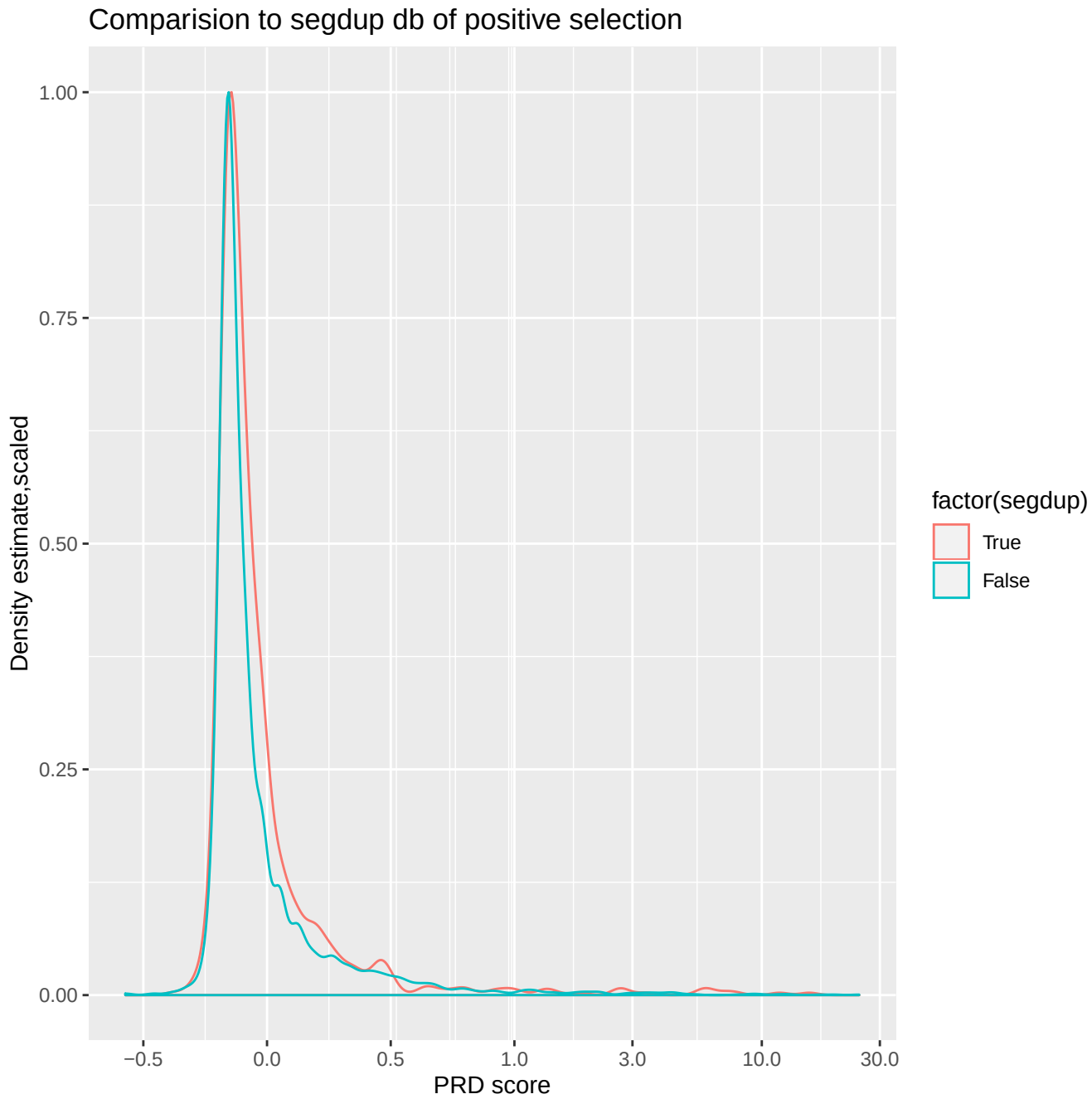

1.00
0.75
0.50
0.25
0.00
pLI
0
5
10
15
20
25
prd_score

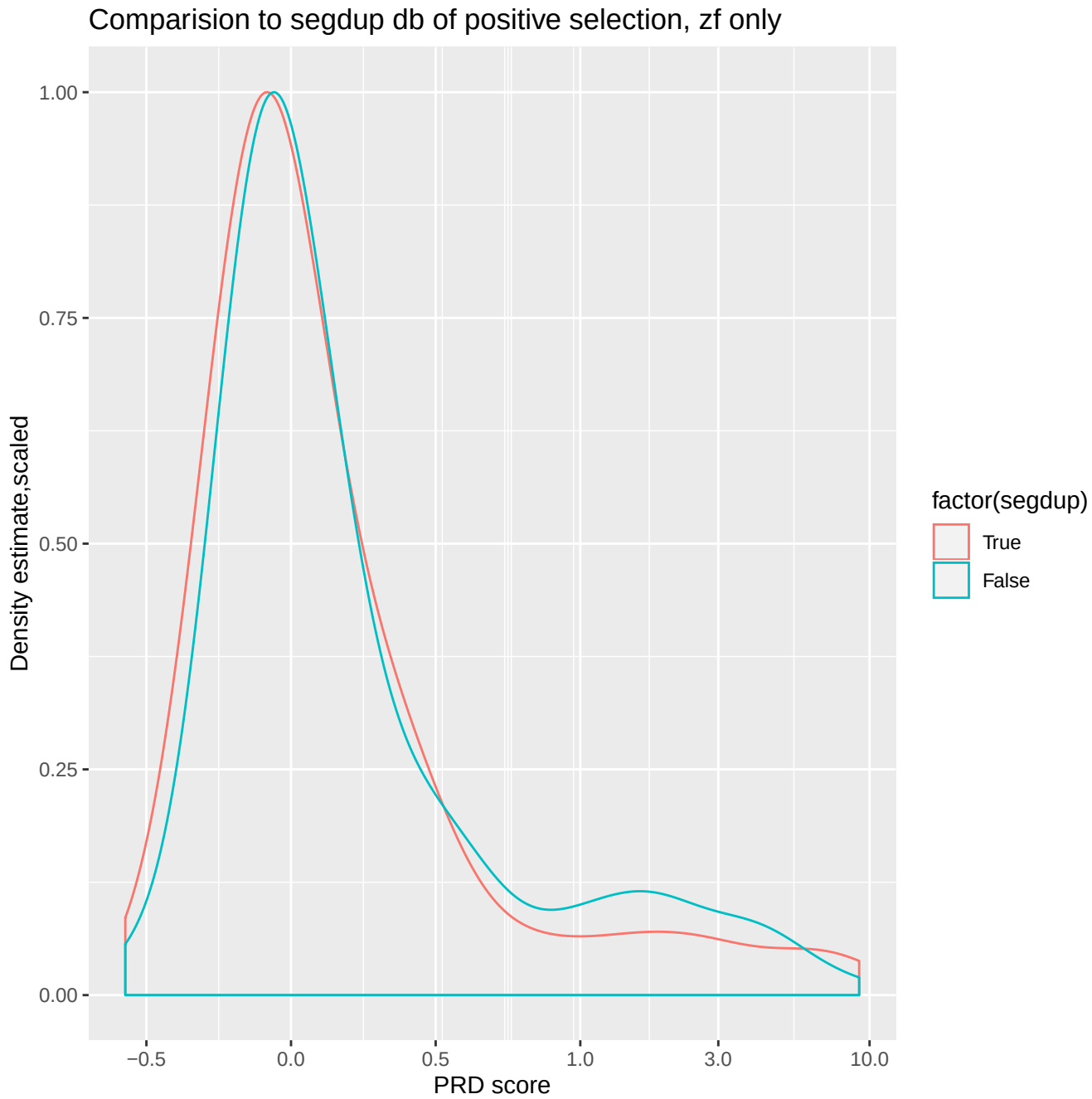

Exac
0.20
0.15
0.10
0.05
0.00
Density estimate
−5
0
5
10
ExAc, mis_z
rank
True
False

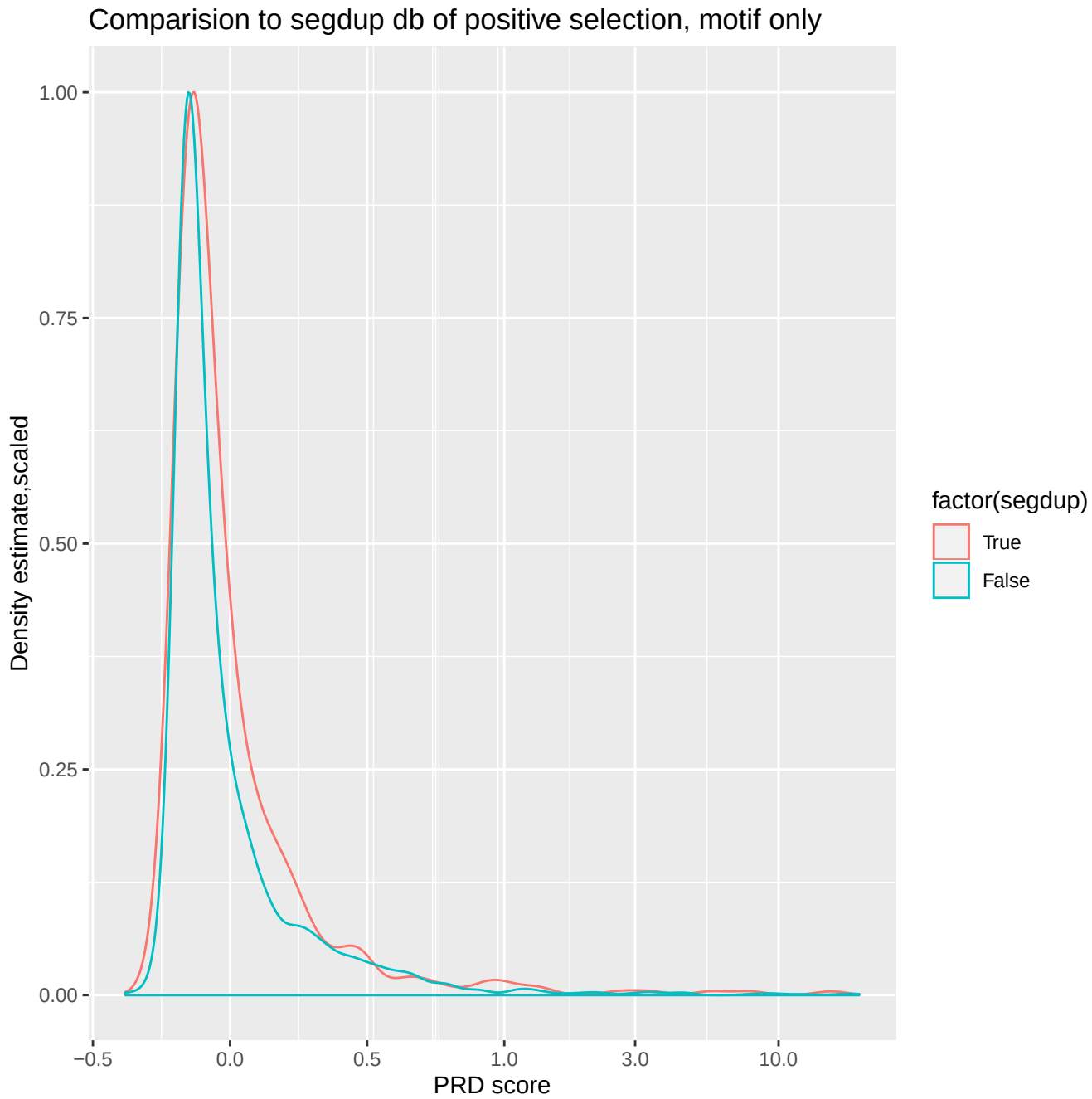

Exac
Density estimate
2.0
1.5
1.0
0.5
0.0
0.00
0.25
0.50
0.75
1.00
ExAC, pLI
rank
True
False


Exac
0.20
0.15
0.10
0.05
0.00
Density estimate
−5
0
5
10
ExAc, mis_z
rank_humlin
True
False


Exac
Density estimate
2.0
1.5
1.0
0.5
0.0
0.00
0.25
0.50
0.75
1.00
ExAC, pLI
rank_humlin
True
False


Comparision to segdup db of positive selection
1.00
0.75
0.50
0.25
0.00
Density estimate,scaled
−0.5
0.0
0.5
1.0
3.0
10.0
30.0
PRD score
factor(segdup)
True
False


Comparision to segdup db of positive selection, zf only
1.00
0.75
0.50
0.25
0.00
Density estimate,scaled
−0.5
0.0
0.5
1.0
3.0
10.0
PRD score
factor(segdup)
True
False


Comparision to segdup db of positive selection, motif only
Density estimate,scaled
1.00
0.75
0.50
0.25
0.00
−0.5
0.0
0.5
1.0
3.0
10.0
PRD score
factor(segdup)
True
False