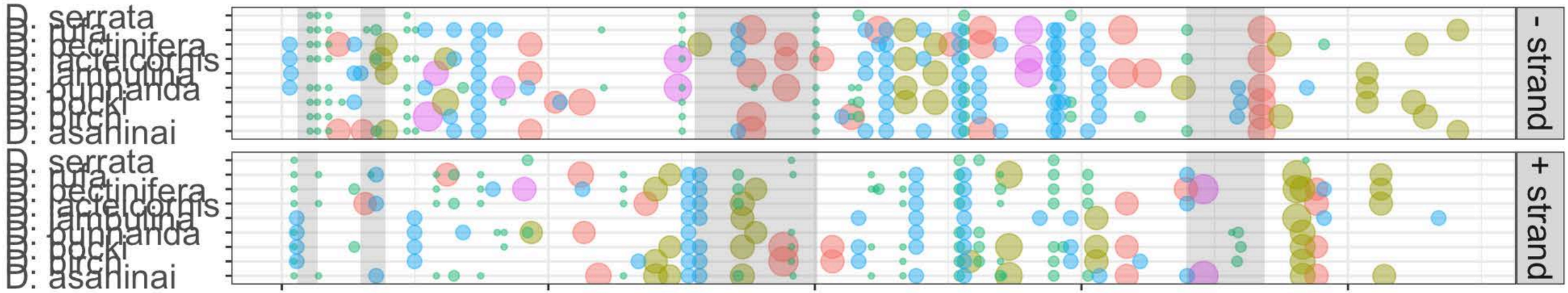
A

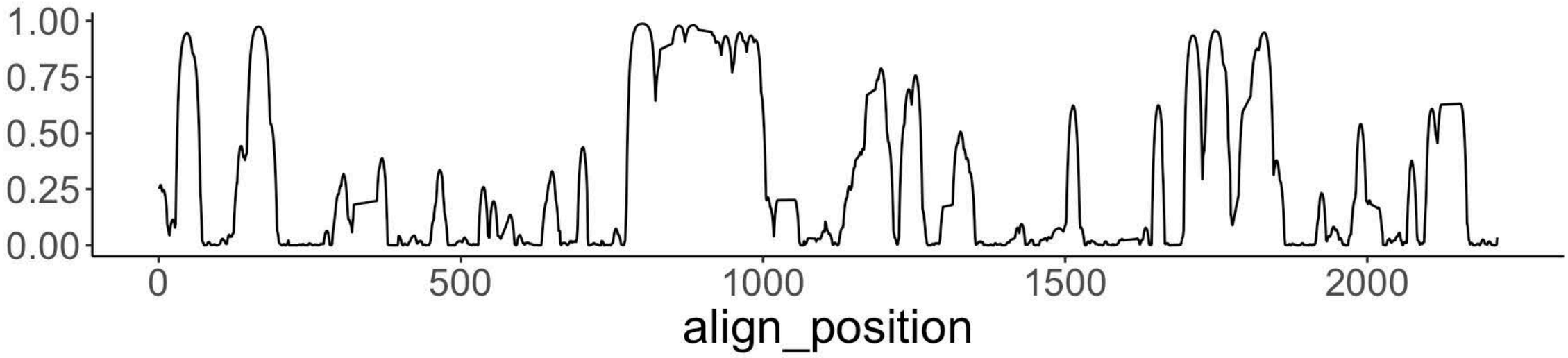
ID:VT46222
GAL4 expression: yes
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_



B



A

ID:VT17374
GAL4 expression: no
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_

species

D. serrata
D. rufa
D. pectinifera
D. lacteicornis
D. jambulina
D. bunnanda
D. bocki
D. birch
D. asahinai

- strand

+ strand

B

post.prob

1.00
0.75
0.50
0.25
0.00

0
1000
2000
3000

align_position

A

ID:VT49336
GAL4 expression: yes
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_

species

D. serrata
D. rufa
D. pectinifera
D. lacteicornis
D. jambulina
D. bunnanda
D. bocki
D. birch
D. asahinai

- strand

+ strand

B

post.prob

1.00
0.75
0.50
0.25
0.00

0
500
1000
1500
2000

align_position

A

ID:VT14983
GAL4 expression: no
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_

species

D. serrata
D. rufa
D. pectinifera
D. lacteicornis
D. jambulina
D. bunnanda
D. bocki
D. birch
D. asahinai

- strand

+ strand

B

post.prob

1.00
0.75
0.50
0.25
0.00

0 500 1000 1500 2000 2500

align_position

A

ID:VT17872
GAL4 expression: no
DNAse Peaks: 0

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_

score 4 6 8

Are these conserved?

When all are conserved? How often is the motif conserved?

species

D. serrata
D. rufa
D. pectinifera
D. lacteicornis
D. bunnanda
D. bocki
D. birch
D. asahinai

negative strand

positive strand

B

Can we programmatically define co-occurance?

post.prob

1.00
0.75
0.50
0.25
0.00

0
200
400
600

align_position

A

ID:VT10262
GAL4 expression: no
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_

species

D. serrata
D. rufa
D. pectinifera
D. lacteicornis
D. jambulina
D. bunnanda
D. bocki
D. birch
D. asahinai

negative strand

positive strand

This is a great example of conservation wobble

Is this offsetting a visual artifact error or really how phastcons is defining conservation?

B

post.prob

1.00
0.75
0.50
0.25
0.00

Why are there so many regions that begin with two spikes of conservation?

I have to fix these connecting regions.

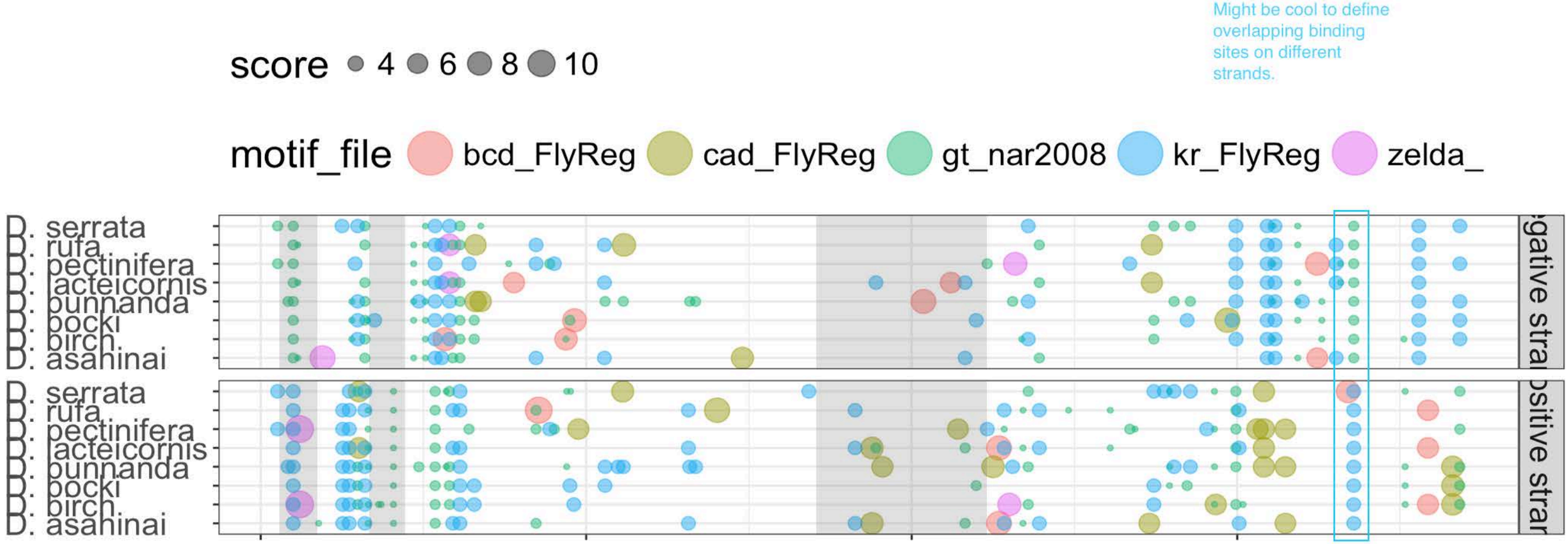
0
1000
2000
3000
4000

align_position

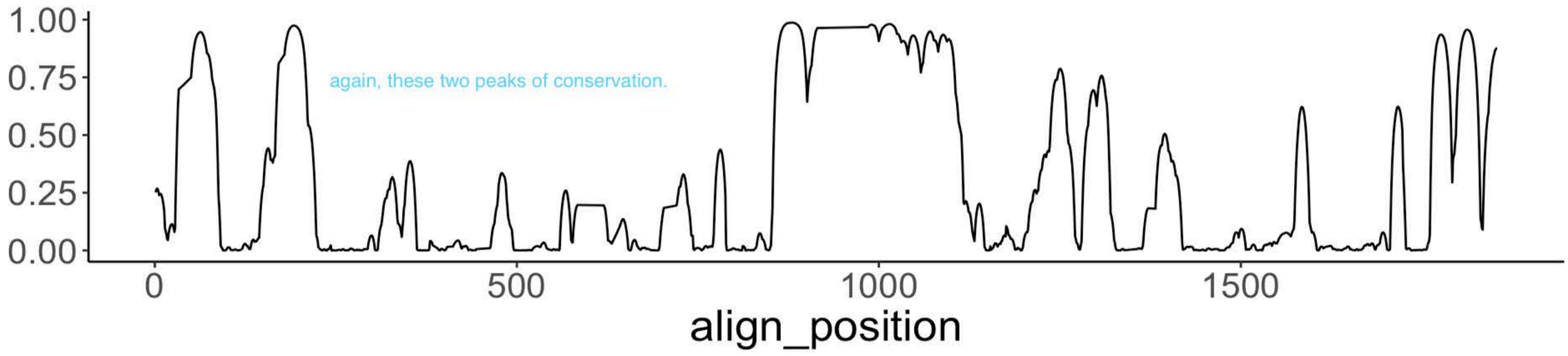
A

ID:VT22281
GAL4 expression: no
DNAse Peaks: 0

Might be cool to define overlapping binding sites on different strands.



B

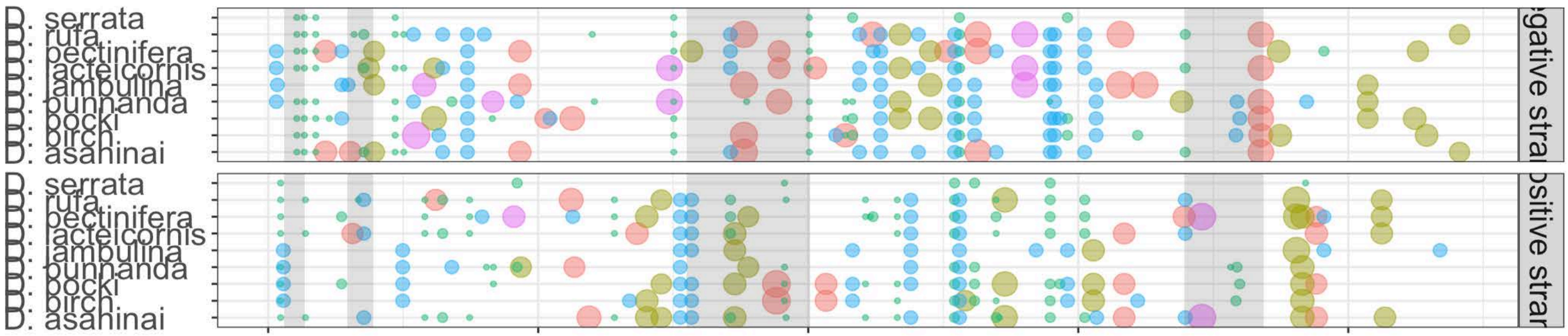


A

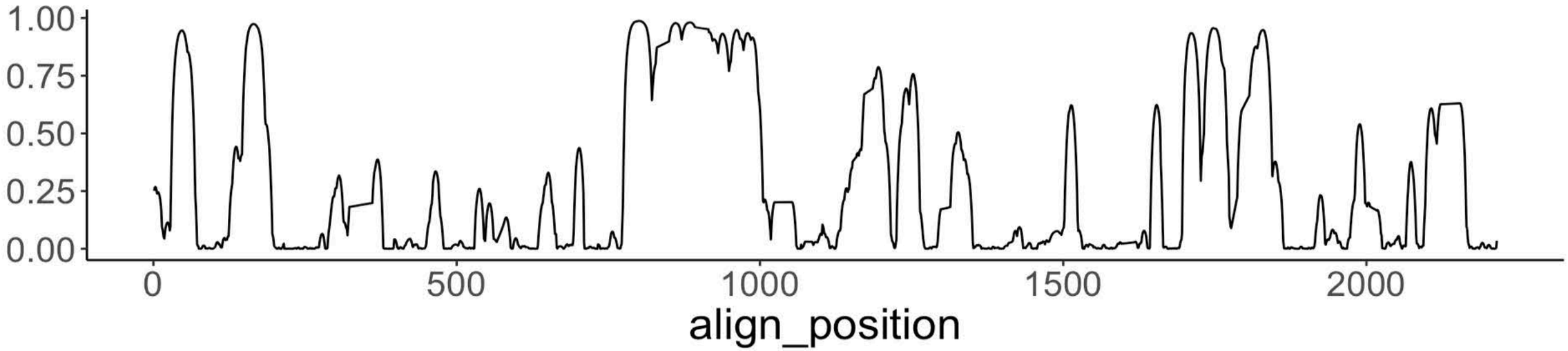
ID:VT46222
GAL4 expression: yes
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_



B

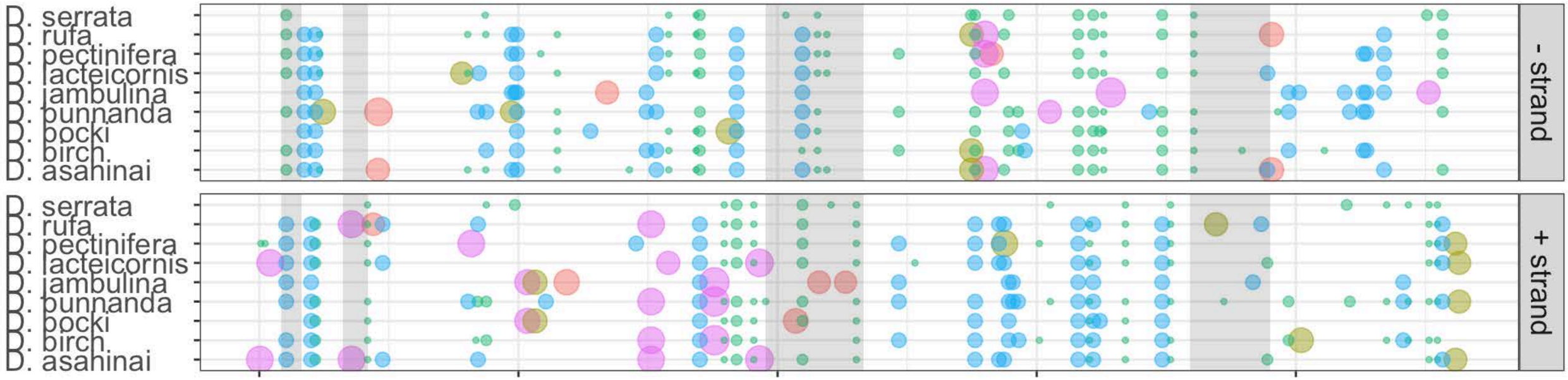


A

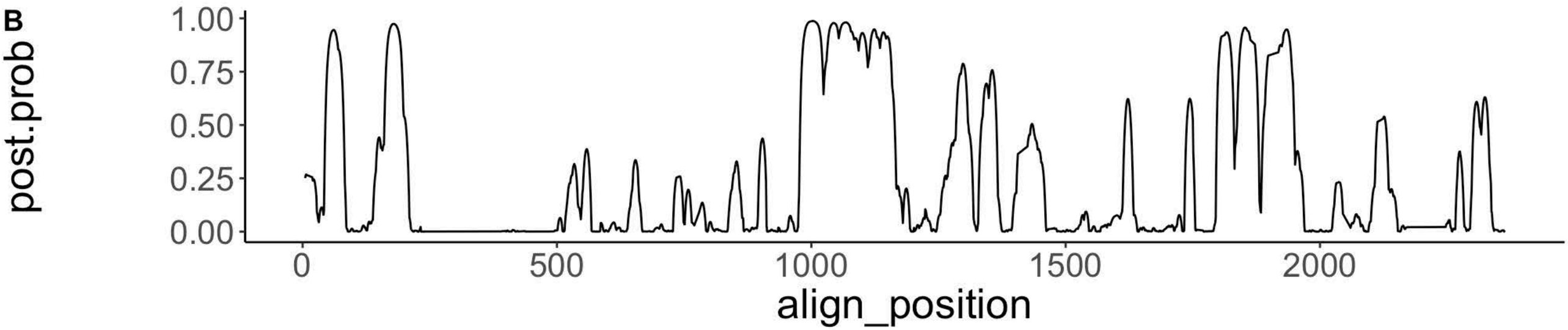
ID:VT58684
GAL4 expression: no
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_



B



A

ID:VT0849
GAL4 expression: yes
DNAse Peaks: 0

score 4 6 8 10

motif_file bcd_FlyReg cad_FlyReg gt_nar2008 kr_FlyReg zelda_

species

D. serrata
D. rufa
D. pectinifera
D. lacteicornis
D. bunnanda
D. bocki
D. birch
D. asahinai

- strand

D. serrata
D. rufa
D. pectinifera
D. lacteicornis
D. bunnanda
D. bocki
D. birch
D. asahinai

+ strand

B

post.prob

1.00
0.75
0.50
0.25
0.00

0
1000
2000
3000

align_position