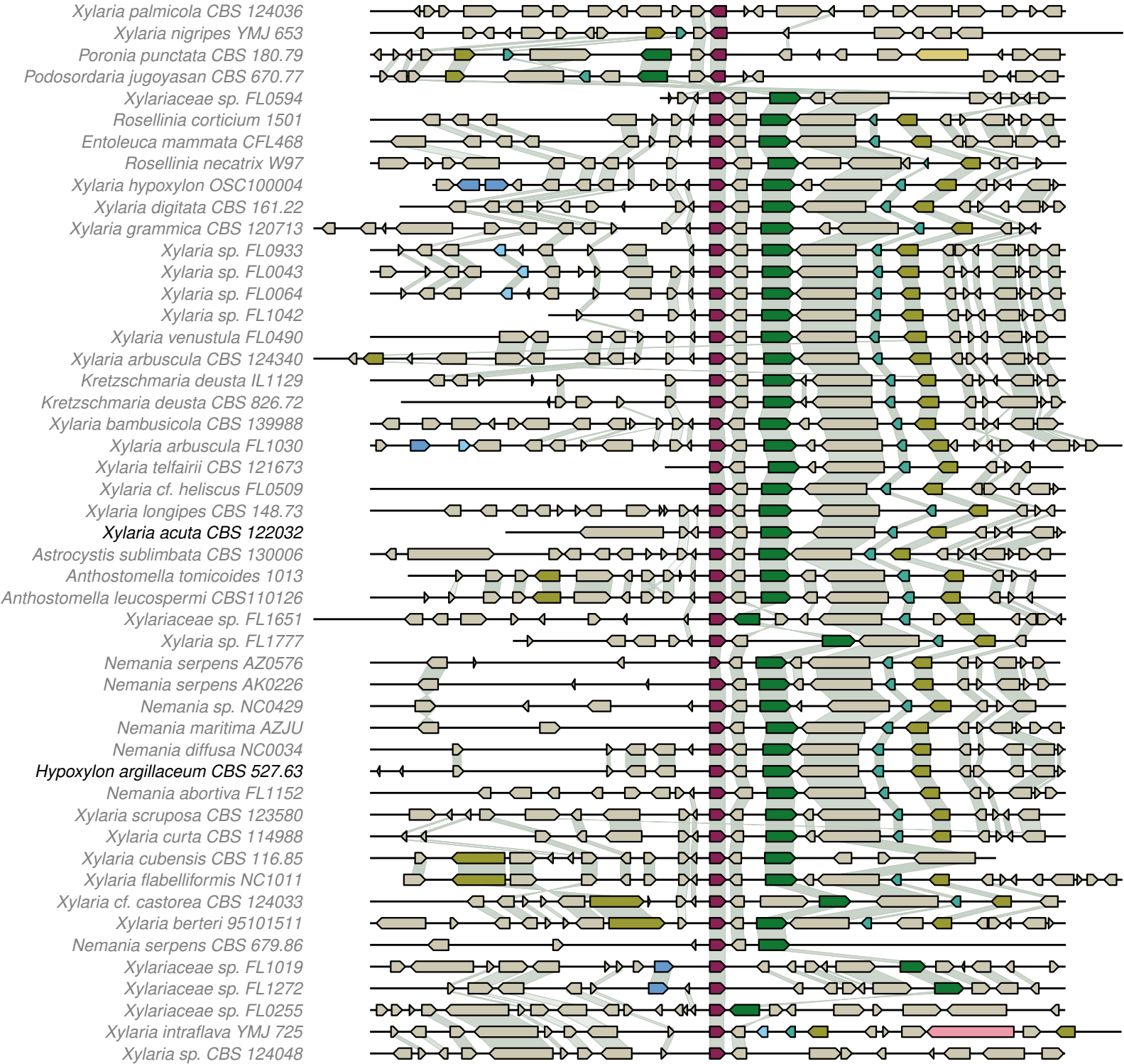


a



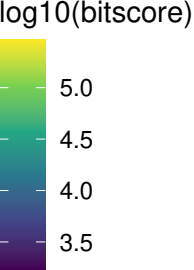
b

Gene functions

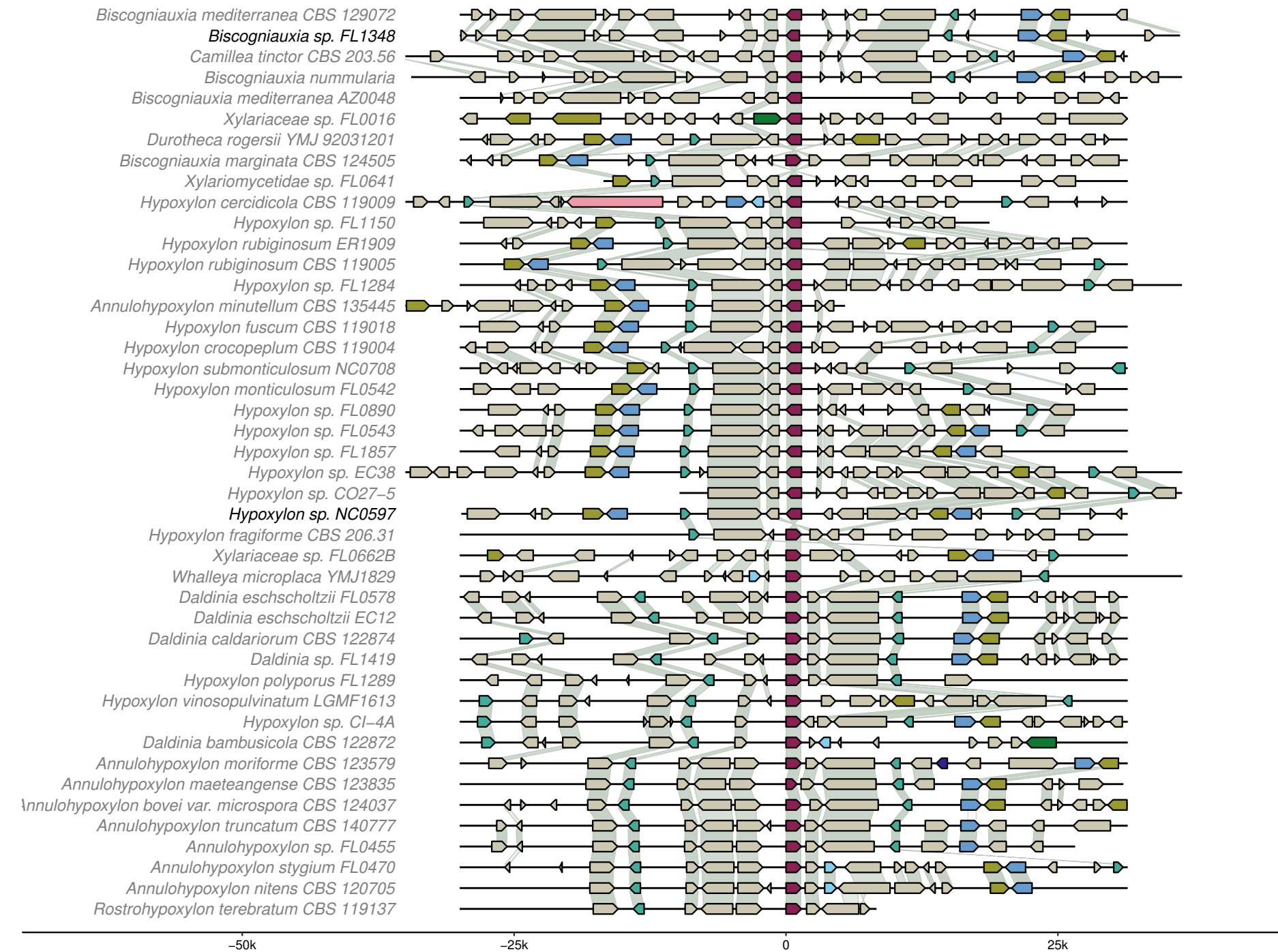
- T3PKS
- T1PKS
- p450
- short-chain dehydrogenase
- pectate lyase
- glycosyl hydrolase
- regulatory
- transport

Amino acid identity

- 0.4
- 0.6
- 0.8
- 1.0

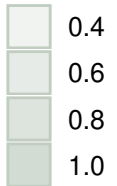


a

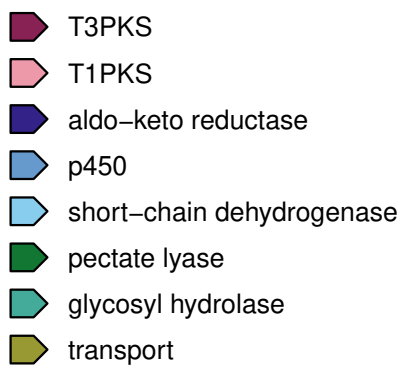


b

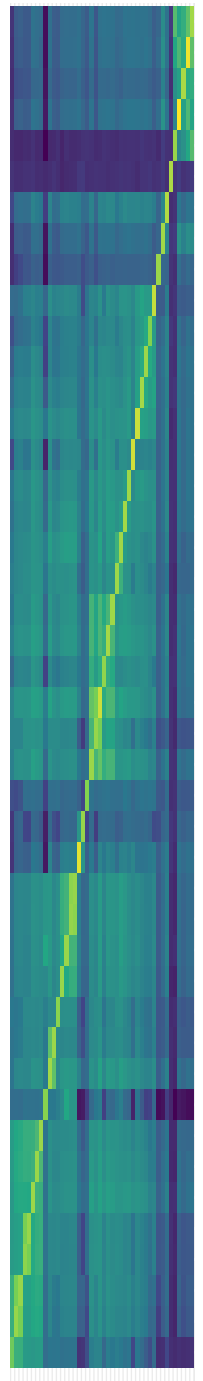
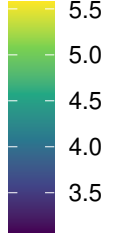
Amino acid identity



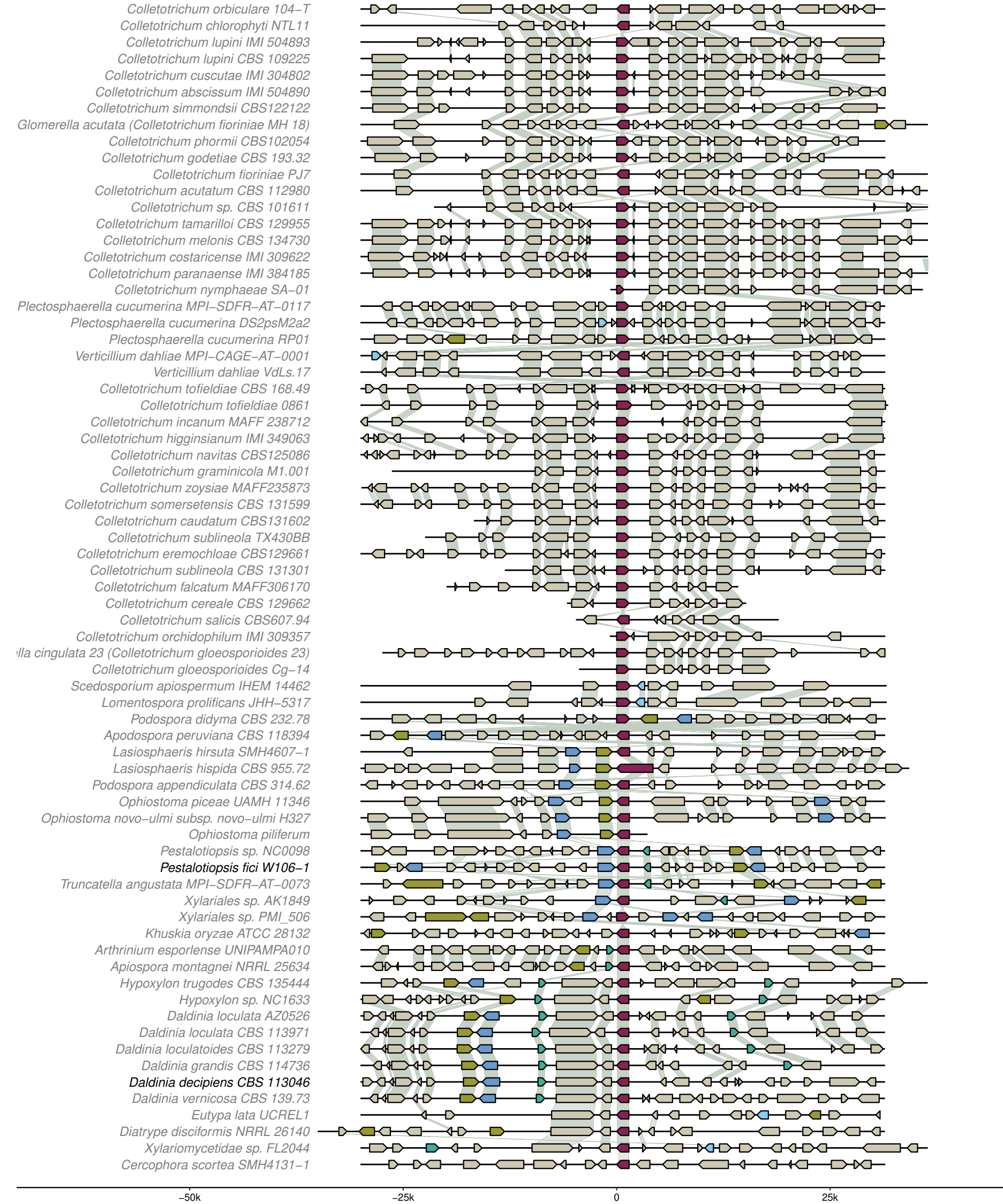
Gene functions



log10(bitscore)

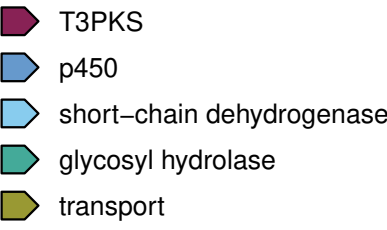


a

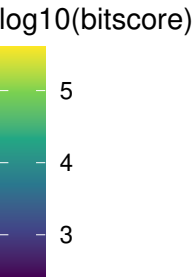
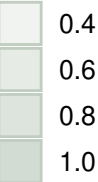


b

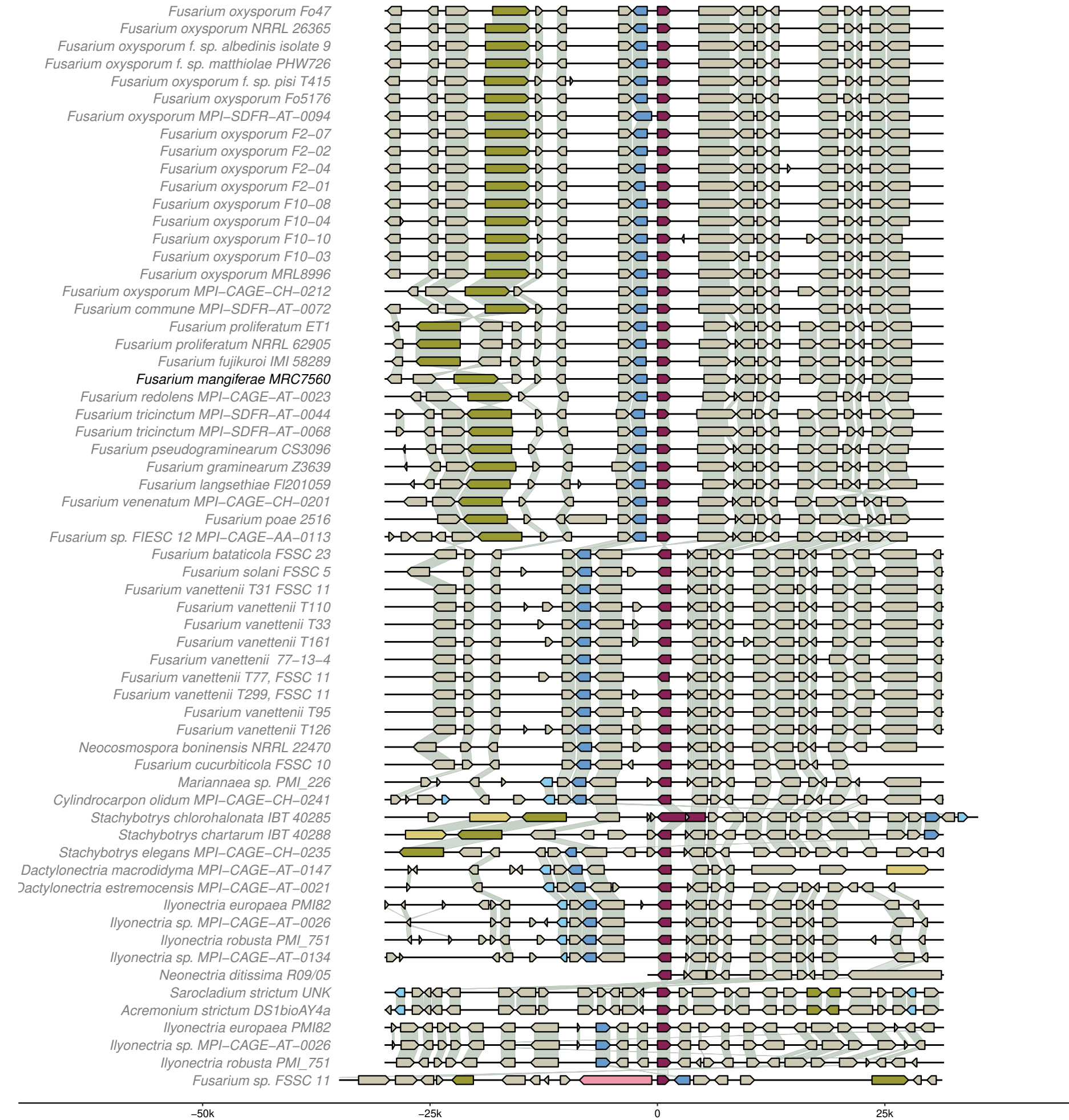
Gene functions



Amino acid identity



a

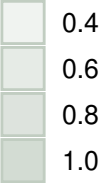


b

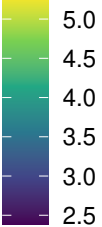
Gene functions



Amino acid identity



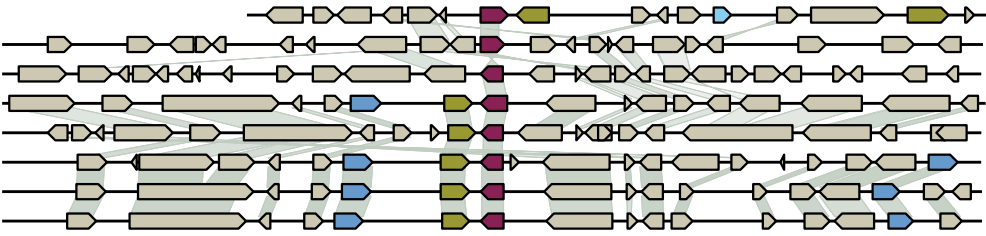
log10(bitscore)



Cluster 1–5

a

Calosphaeria pulchella
Acremonium alcalophilum
Emericellopsis sp. TS7
***Sporothrix insectorum* RCEF 264**
Grosmannia clavigera kw1407
Sporothrix schenckii 1099–18
Sporothrix brasiliensis 5110
Ophiostoma sp. PMI_507



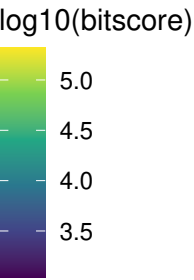
b

Gene functions

- T3PKS
- p450
- short-chain dehydrogenase
- transport

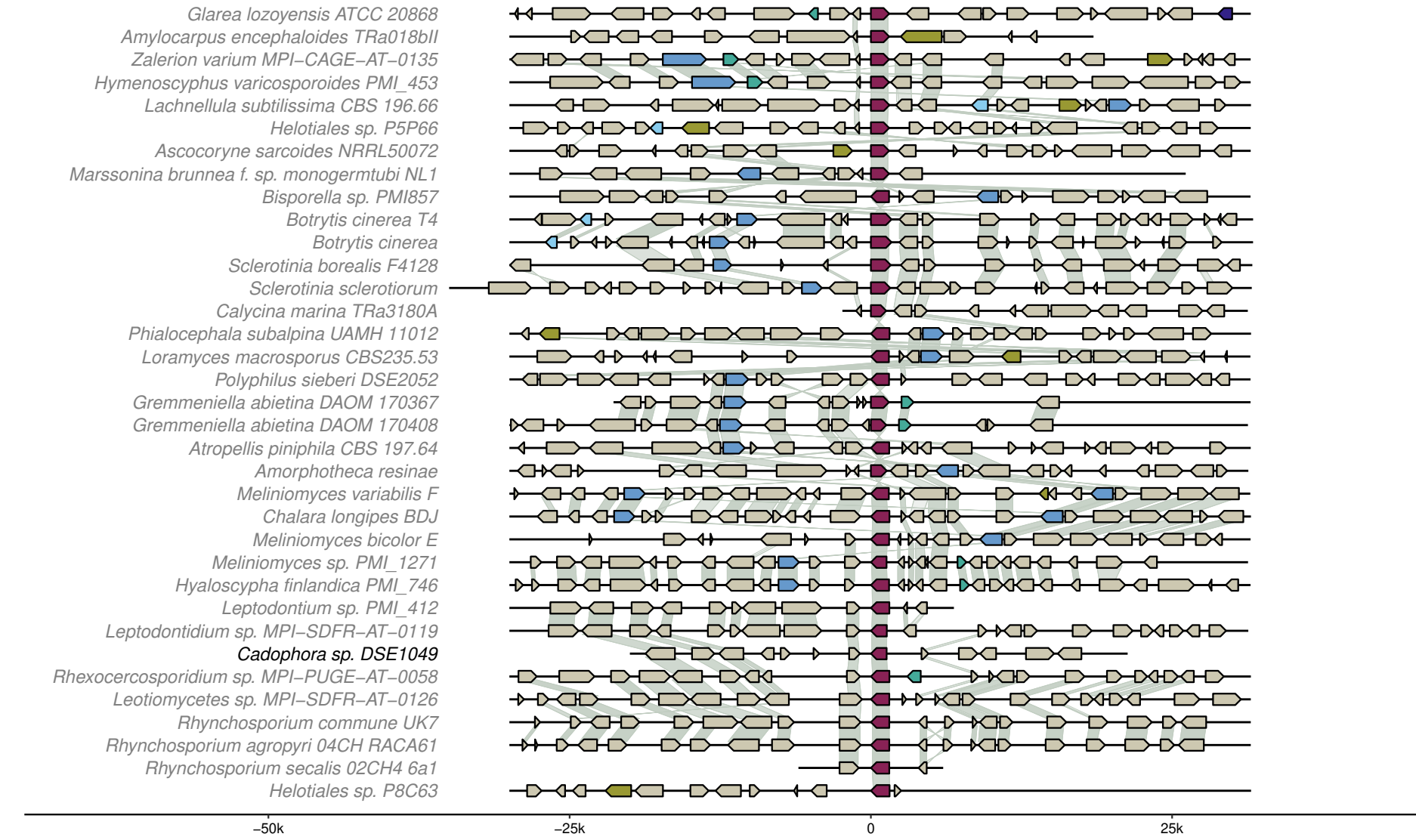
Amino acid identity

- 0.4
- 0.6
- 0.8
- 1.0



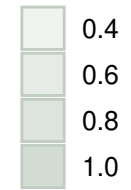
Cluster 2

a

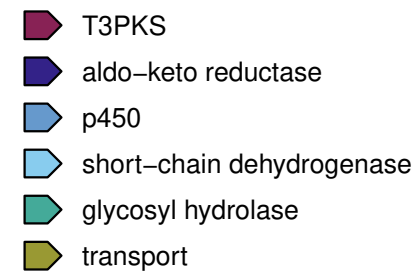


b

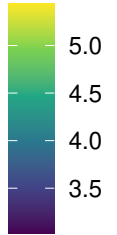
Amino acid identity



Gene functions

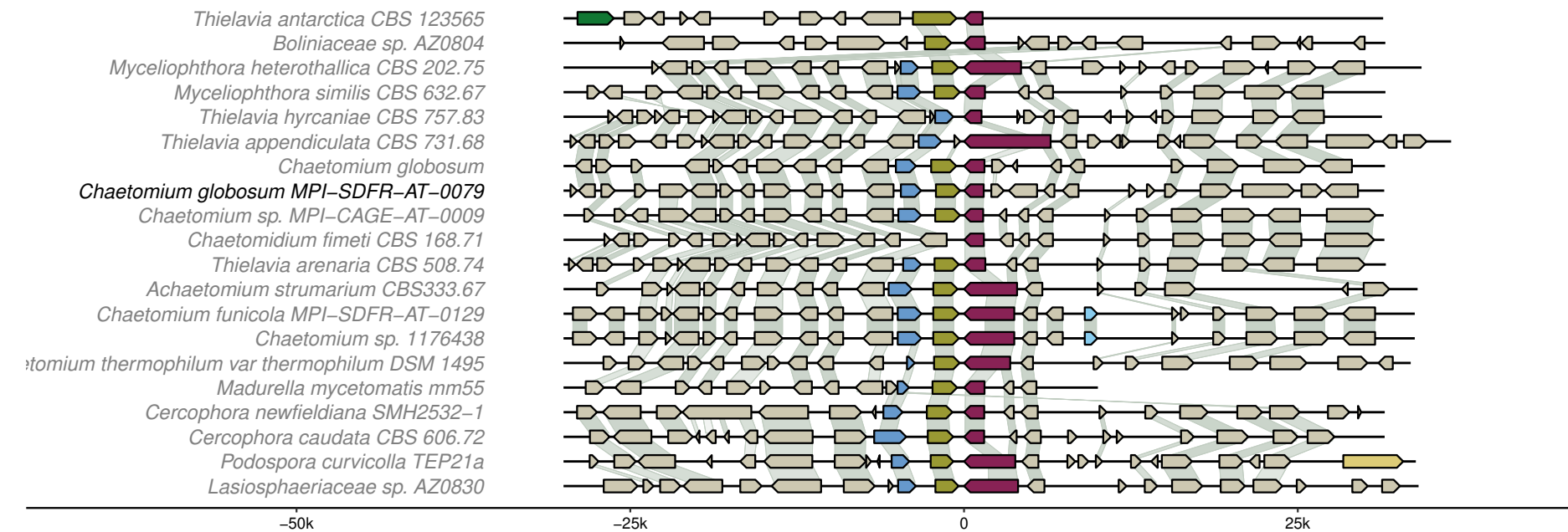


log10(bitscore)

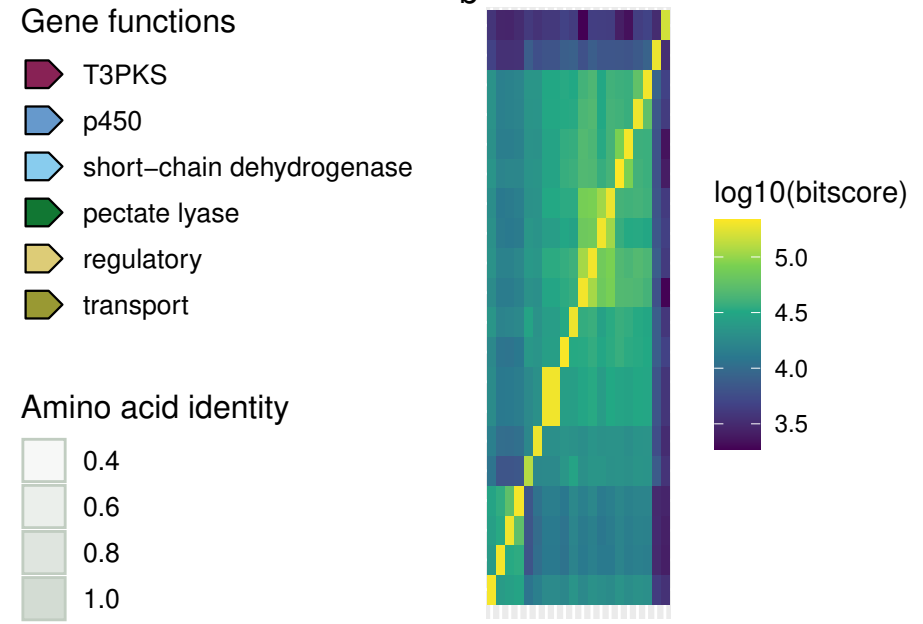


Cluster 3

a

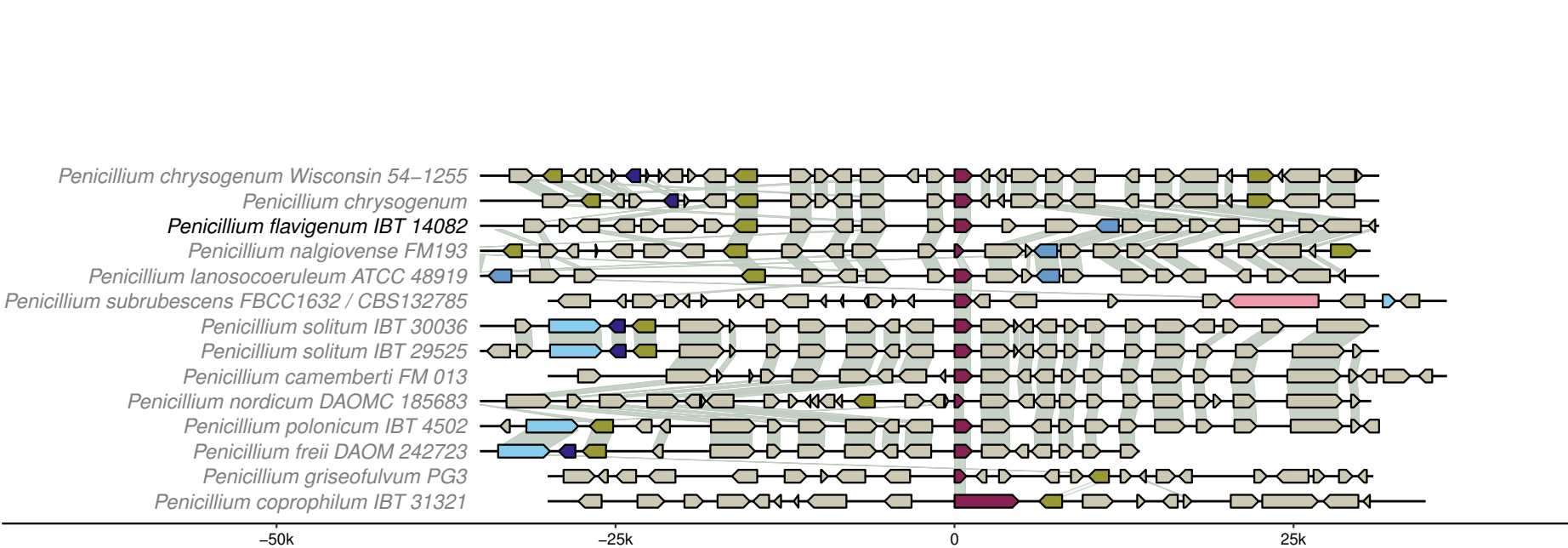


b

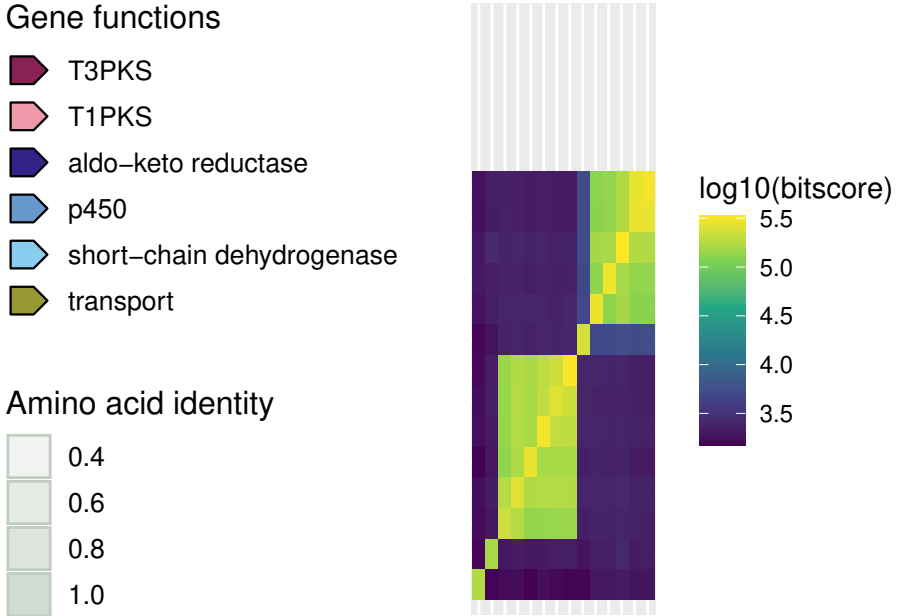


Cluster 4

a

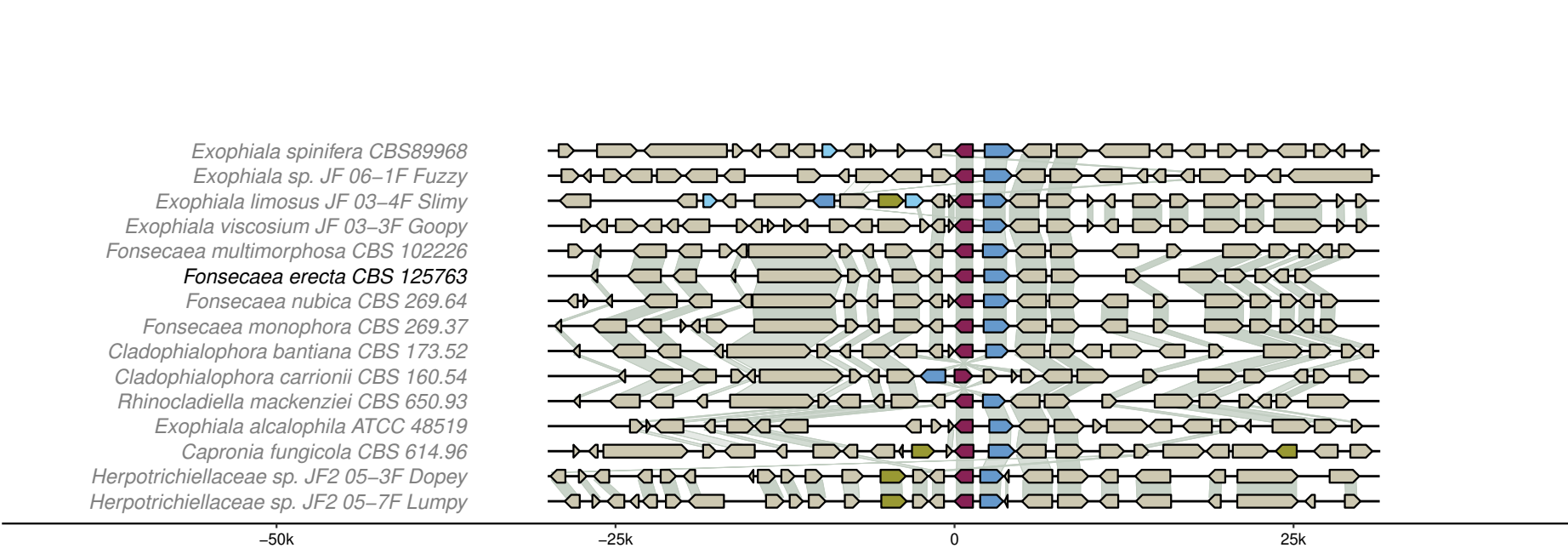


b

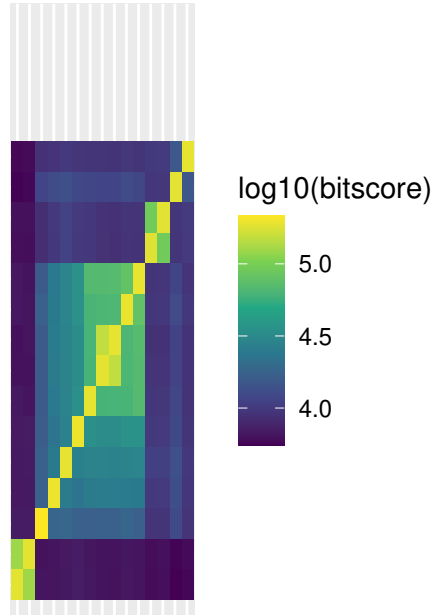


Cluster 5

a

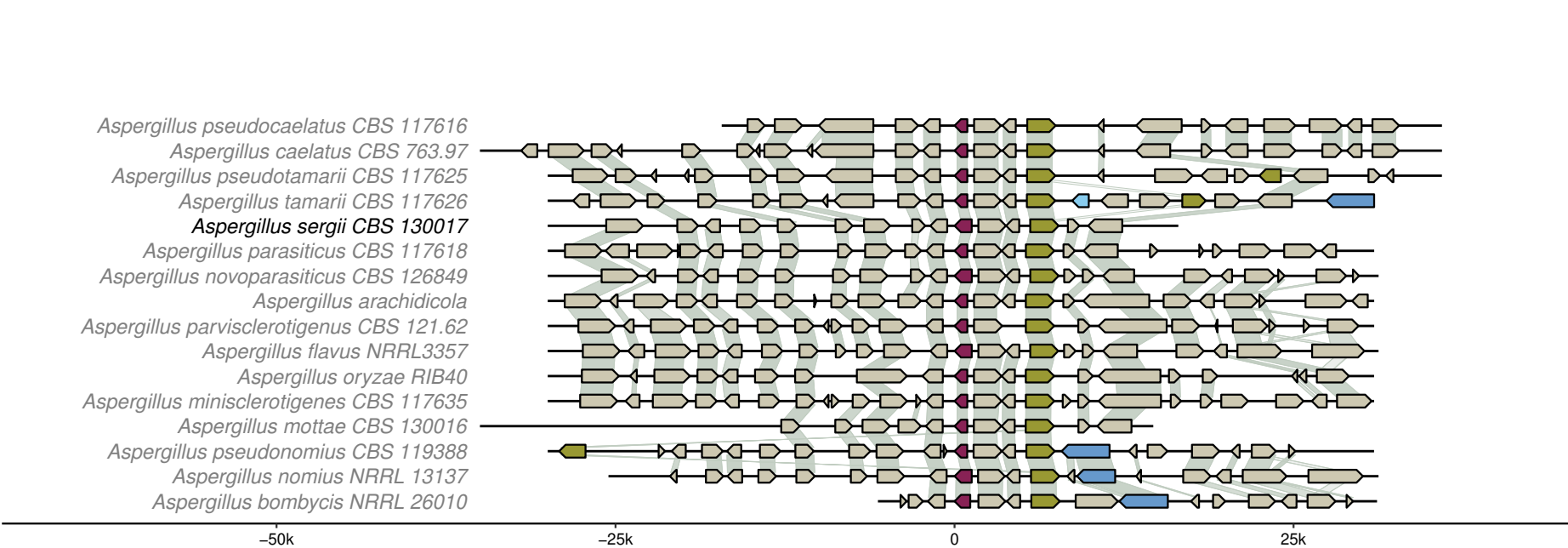


b

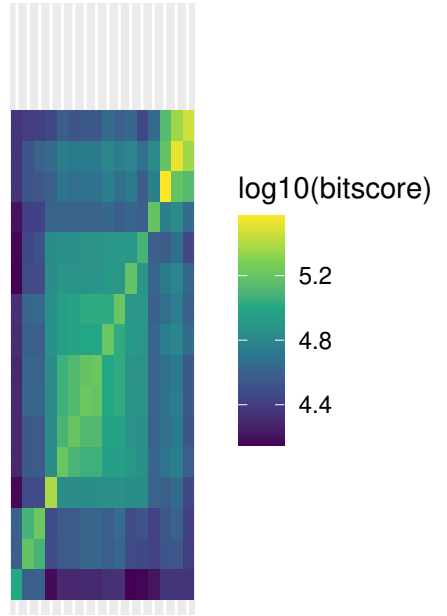


Cluster 6

a

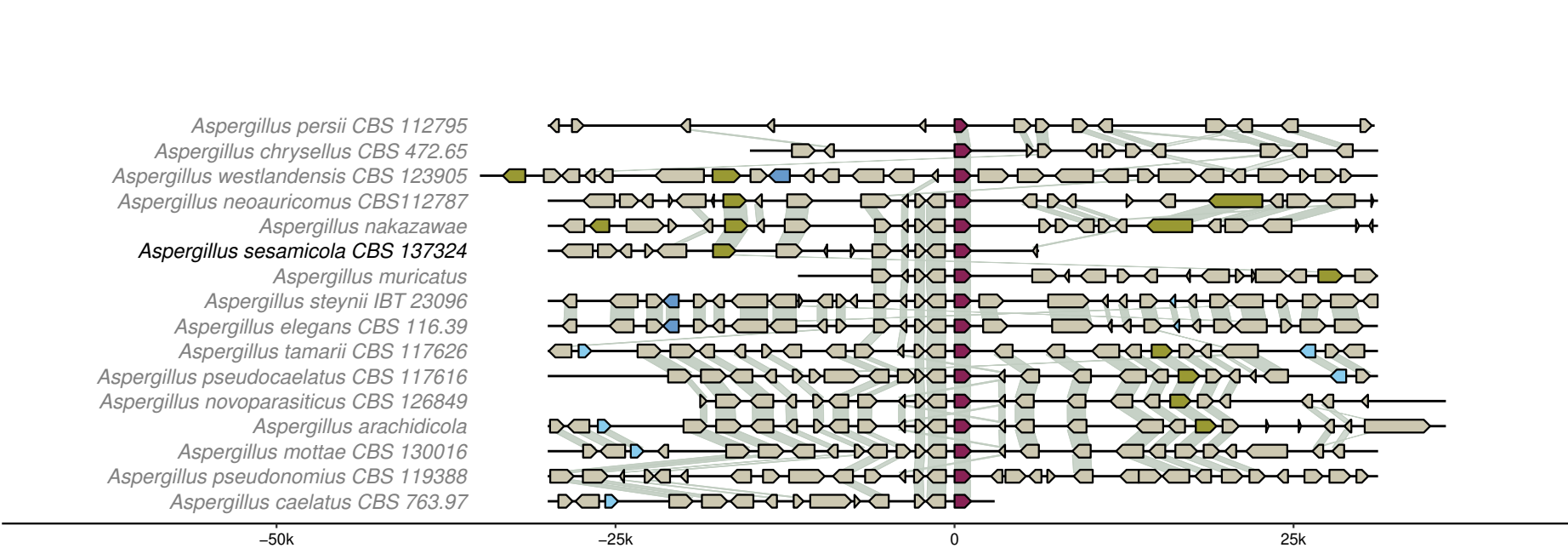


b

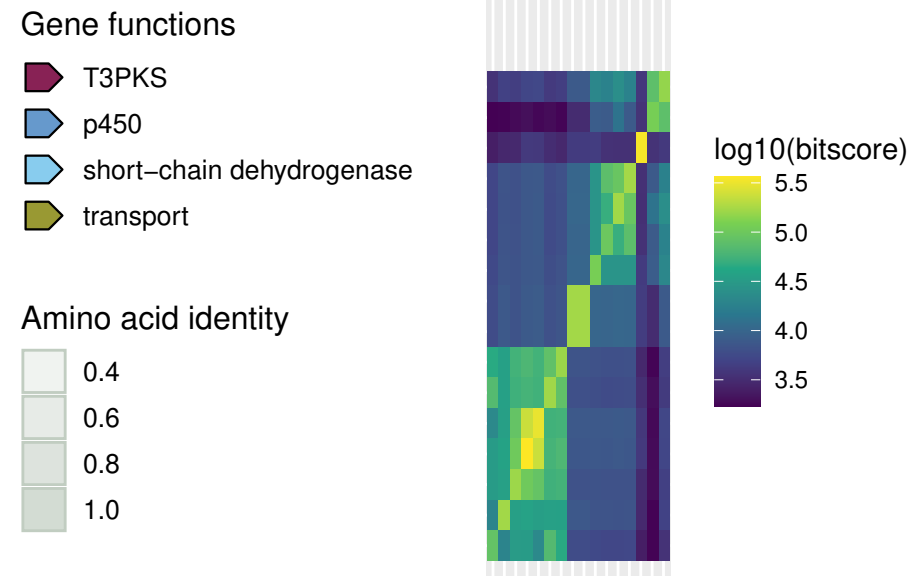


Cluster 7

a

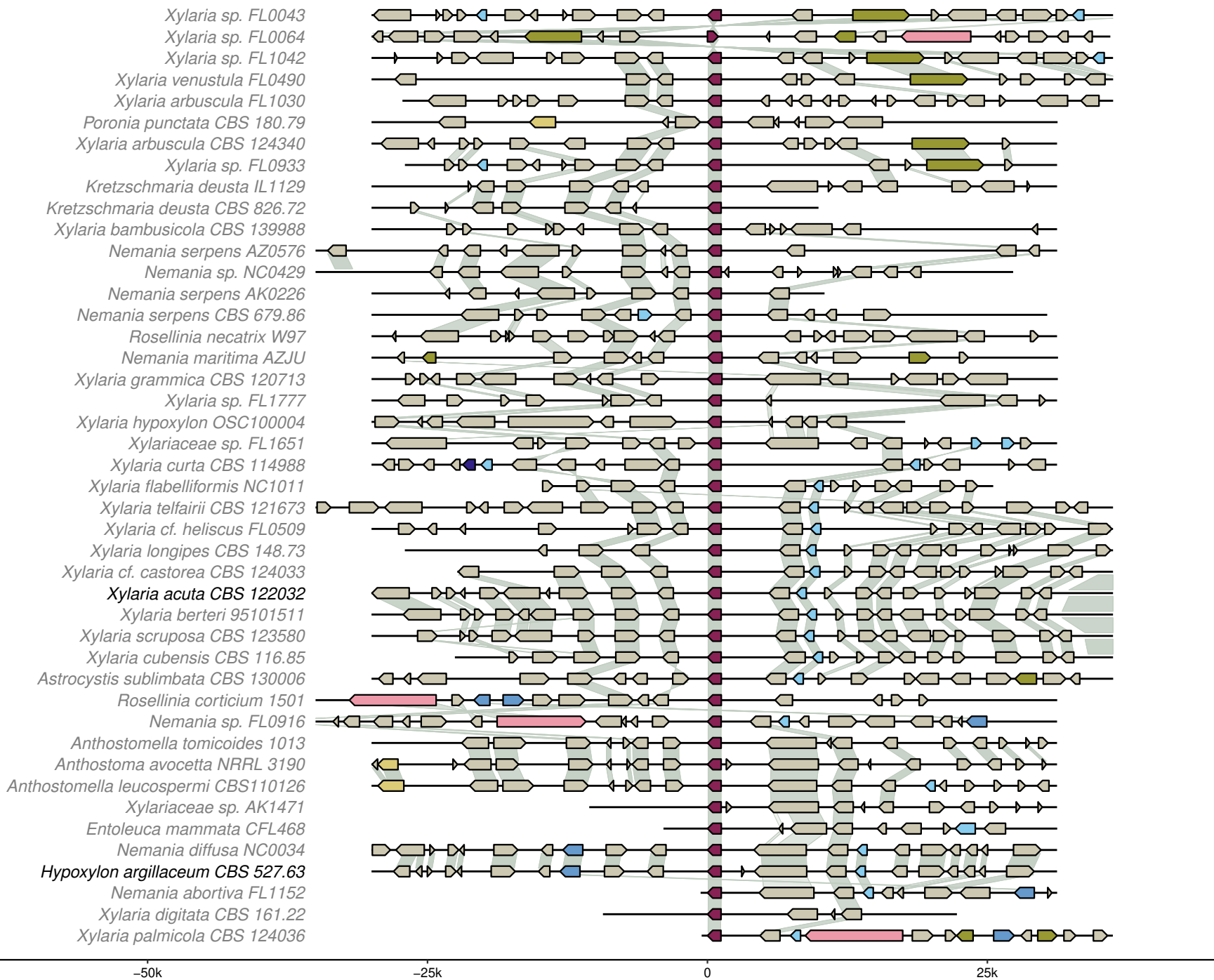


b



Cluster 8

a



b

Gene functions

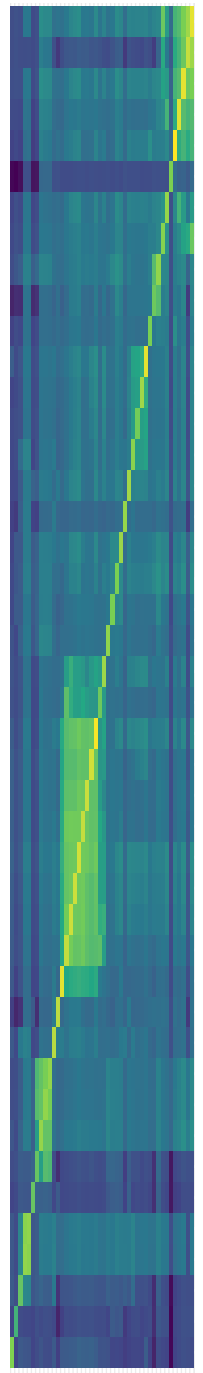
- T3PKS
- T1PKS
- aldo-keto reductase
- p450
- short-chain dehydrogenase
- regulatory
- transport

Amino acid identity

- 0.4
- 0.6
- 0.8
- 1.0

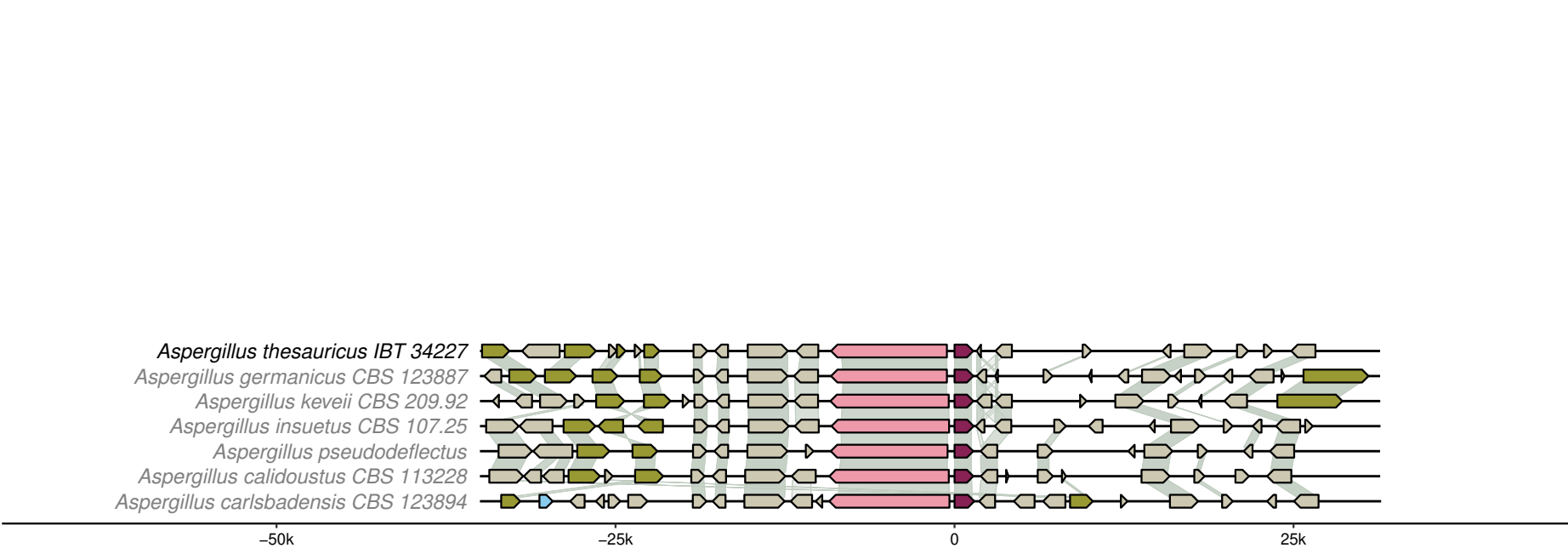
log10(bitscore)

- 5.5
- 5.0
- 4.5
- 4.0
- 3.5
- 3.0

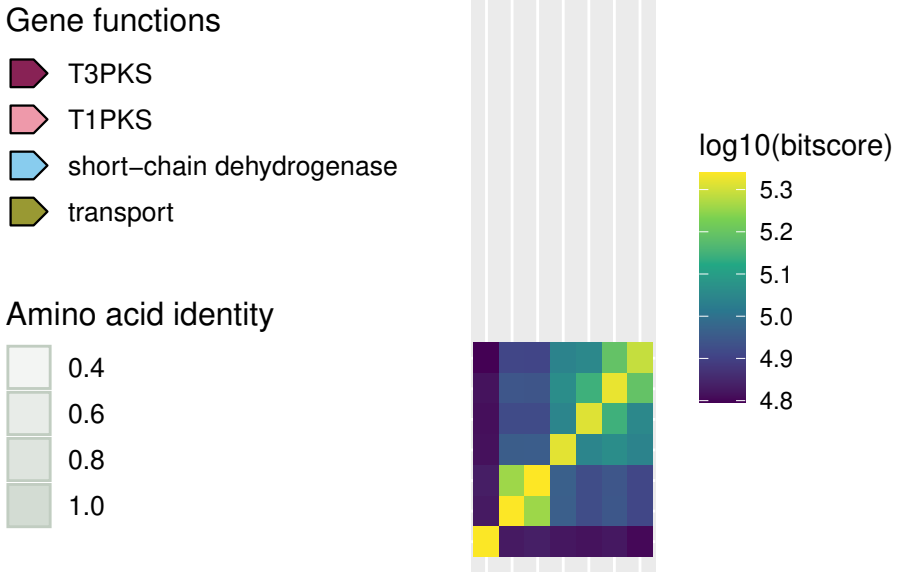


Cluster 9

a

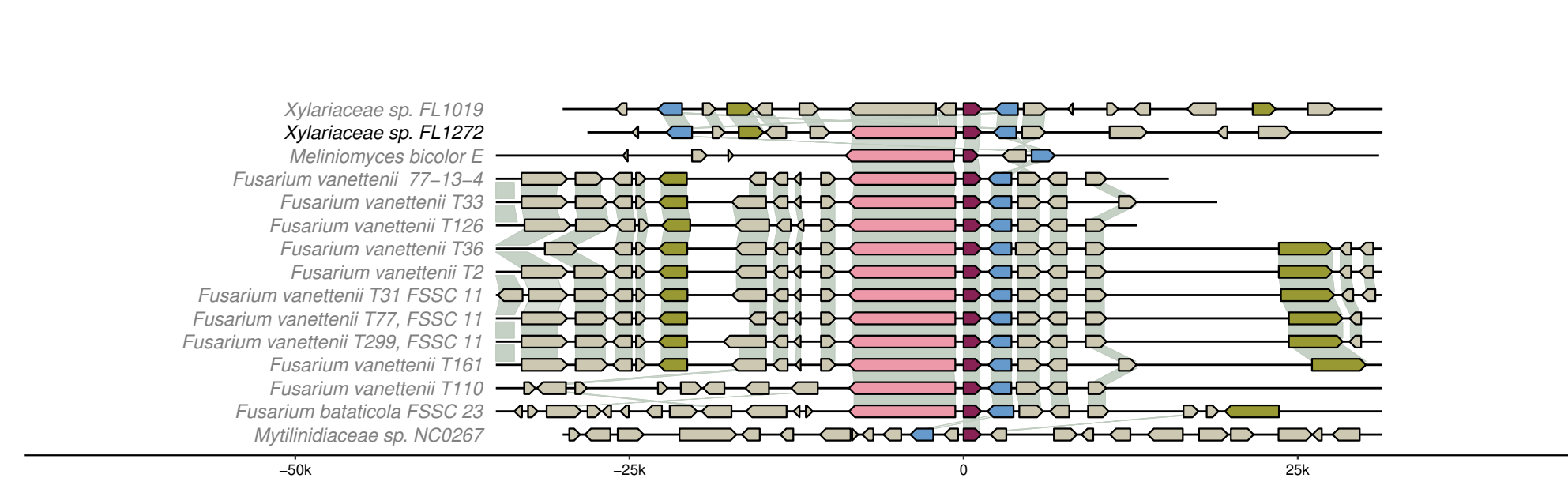


b

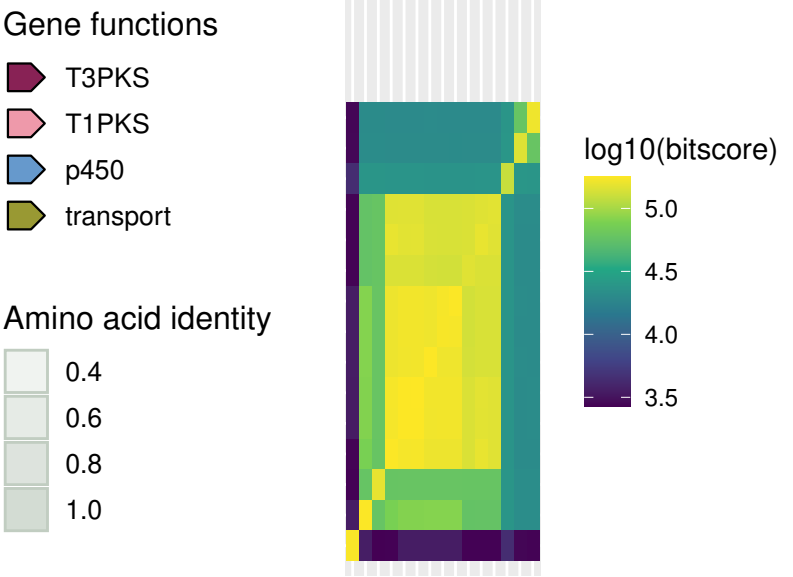


Cluster 10

a

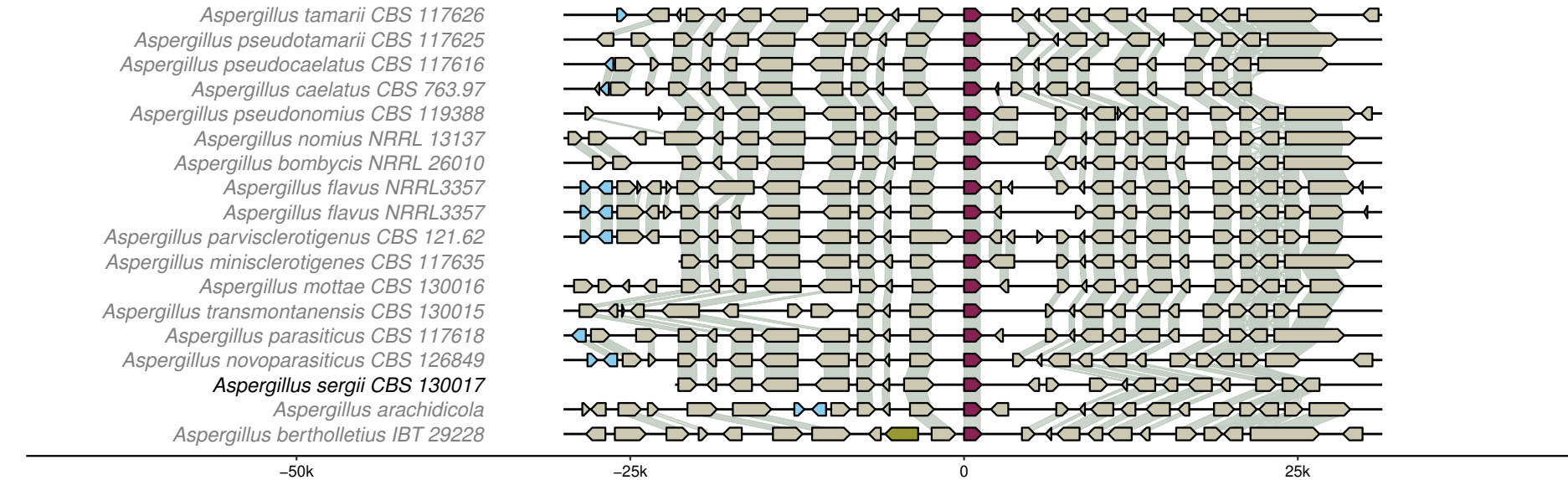


b

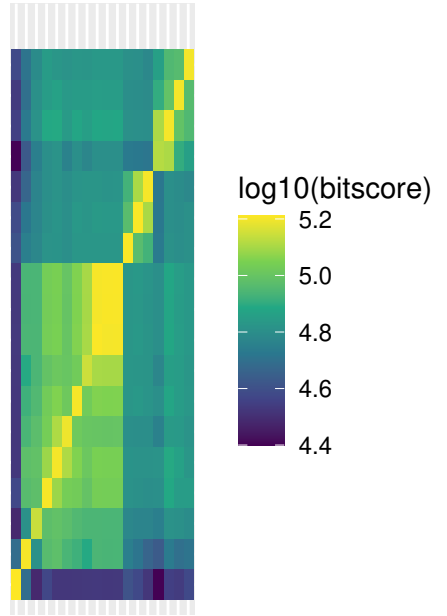


Cluster 11

a

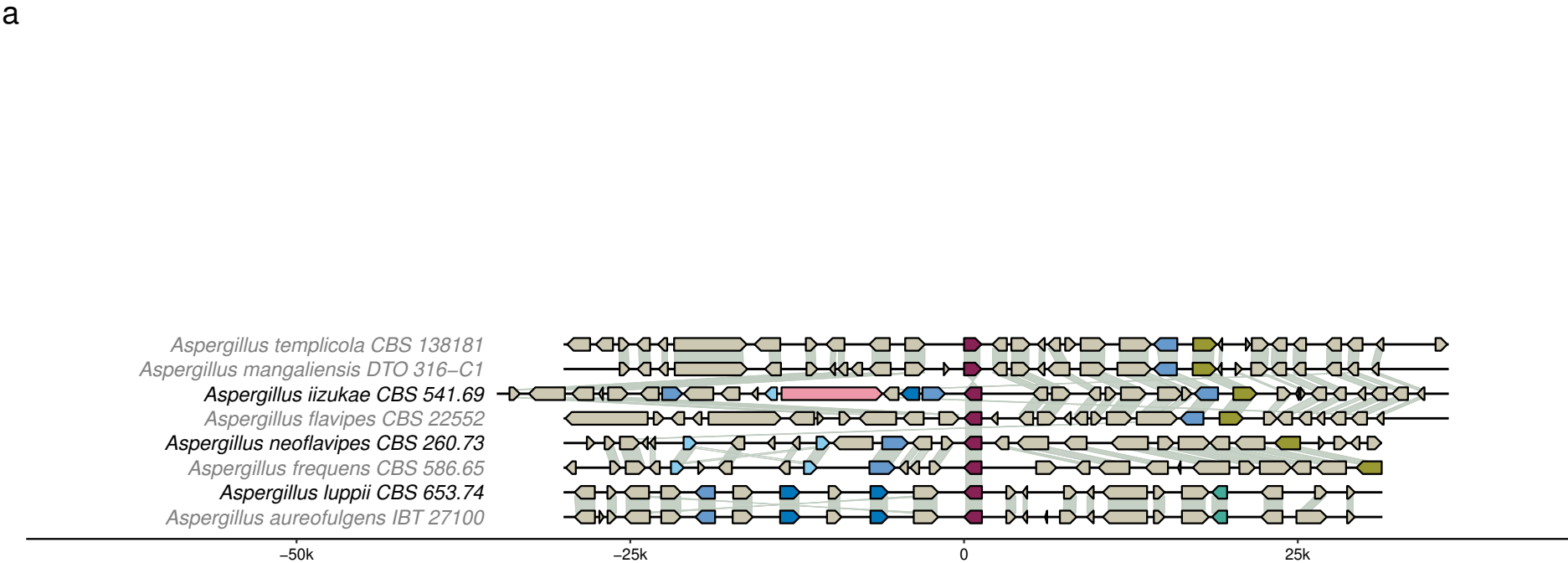


b

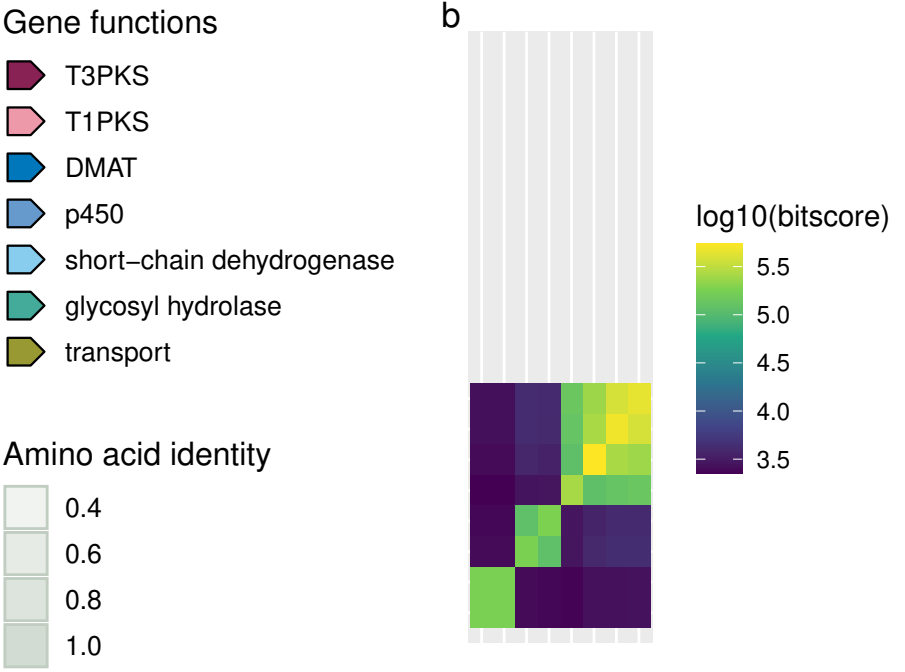


Cluster 12

a

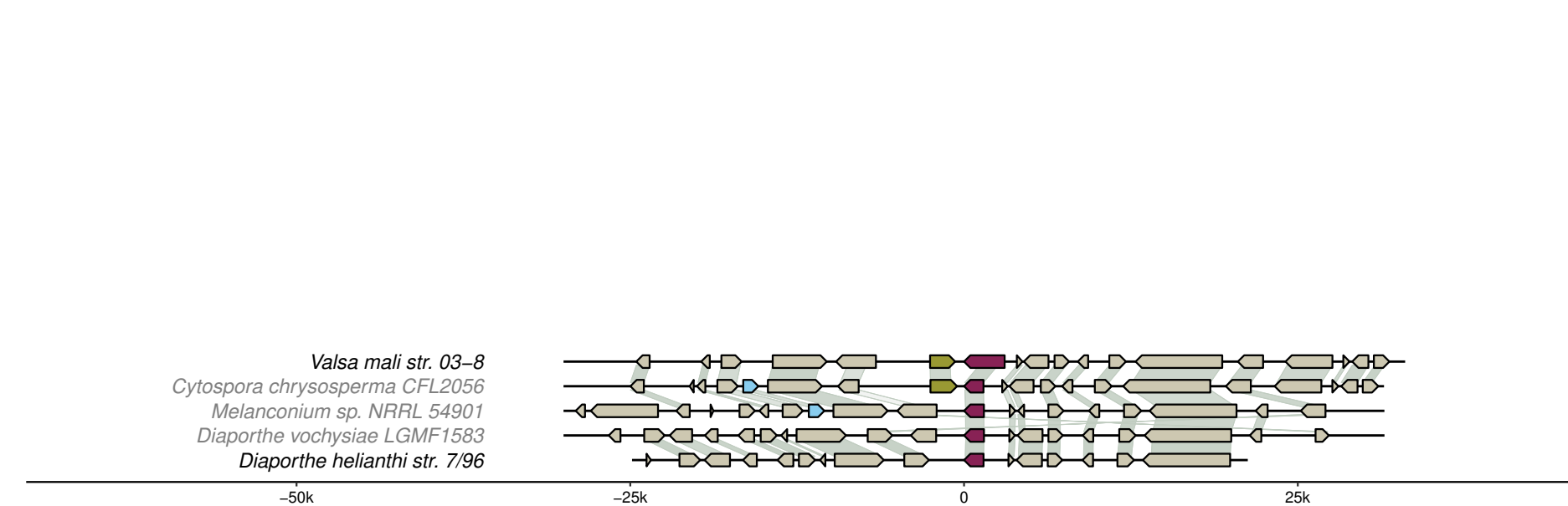


b

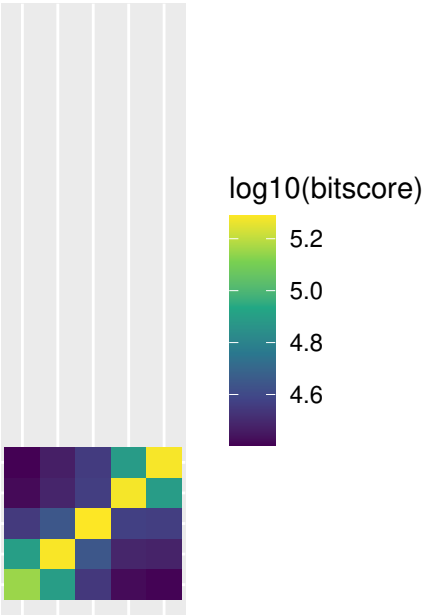


Cluster 13

a

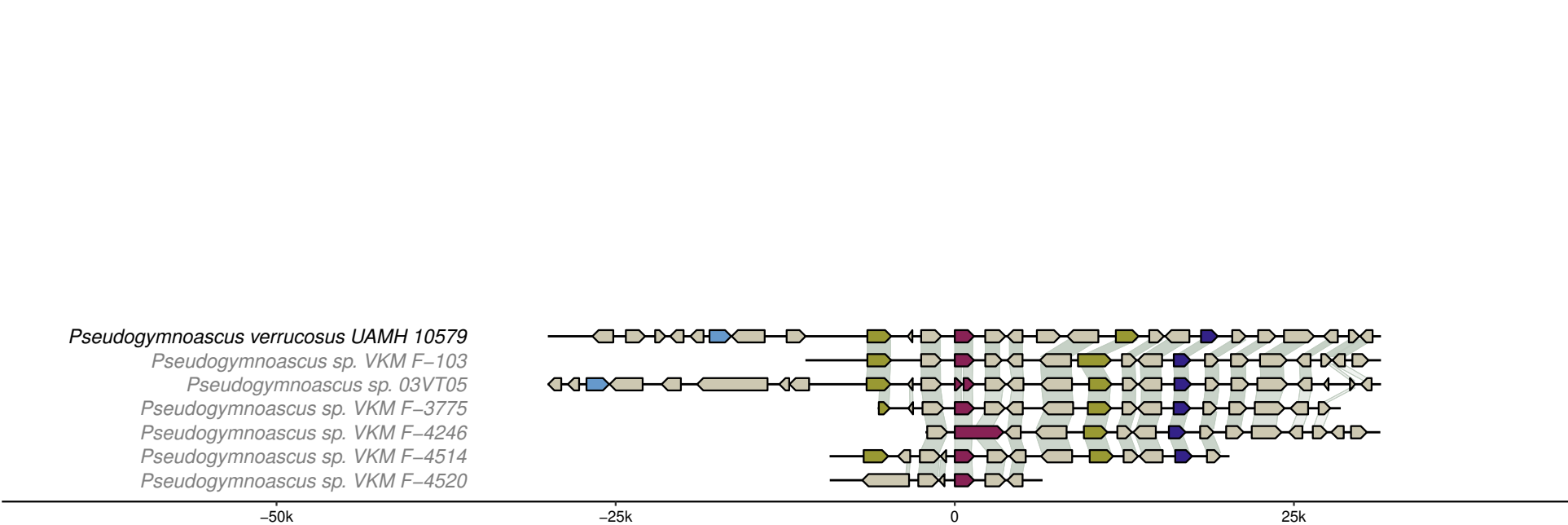


b

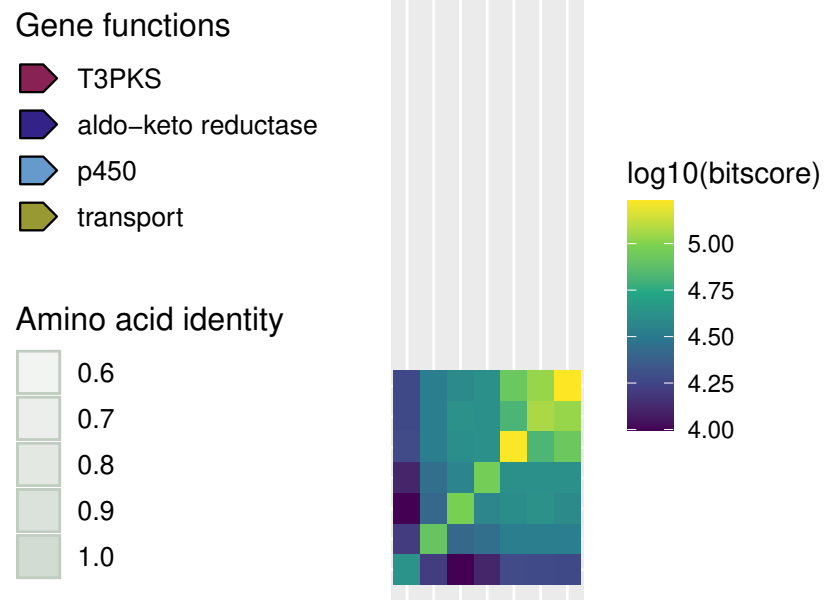


Cluster 14

a

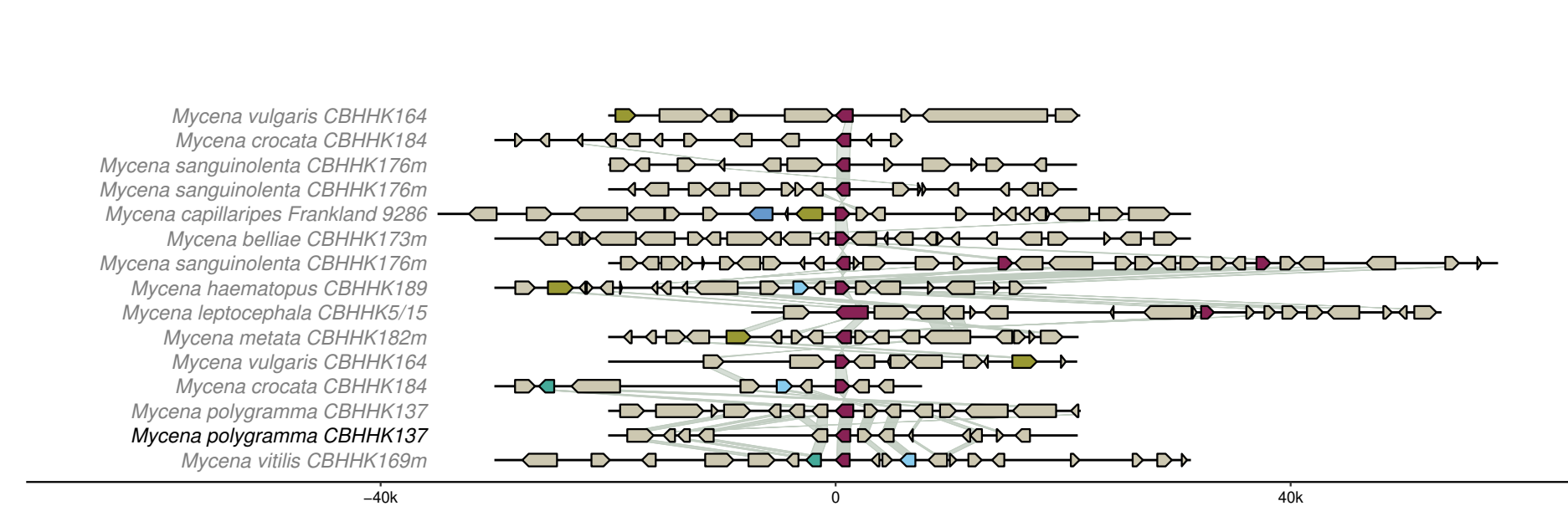


b

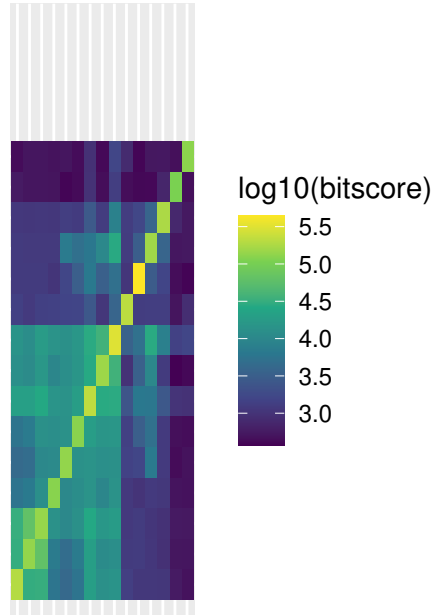


Cluster 15

a

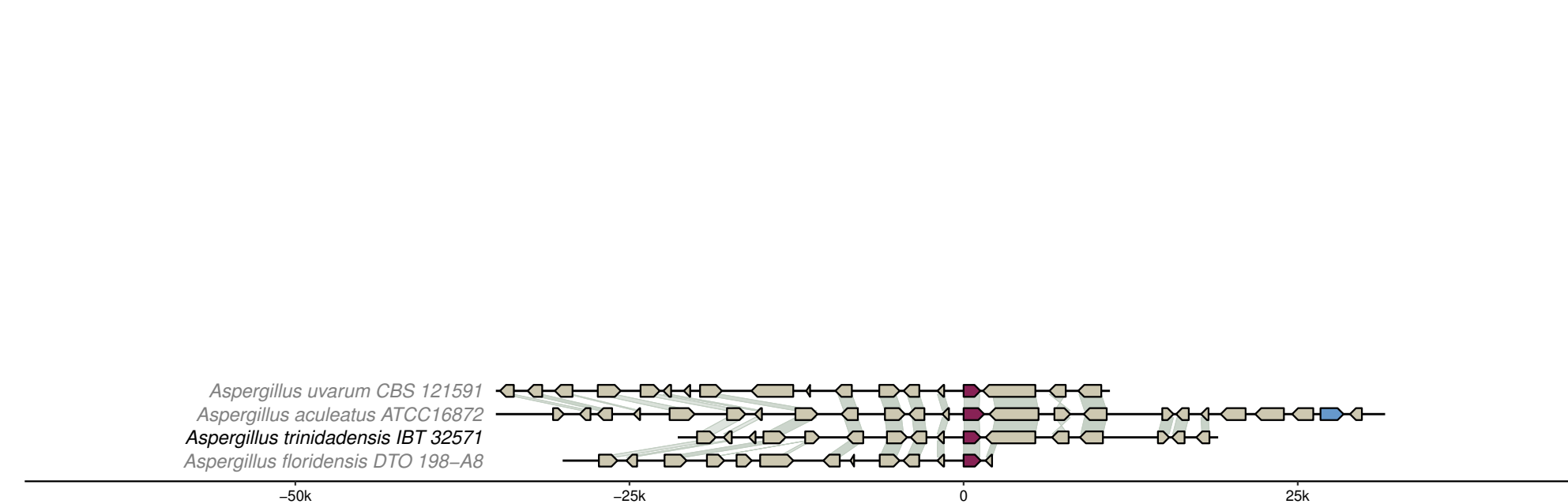


b

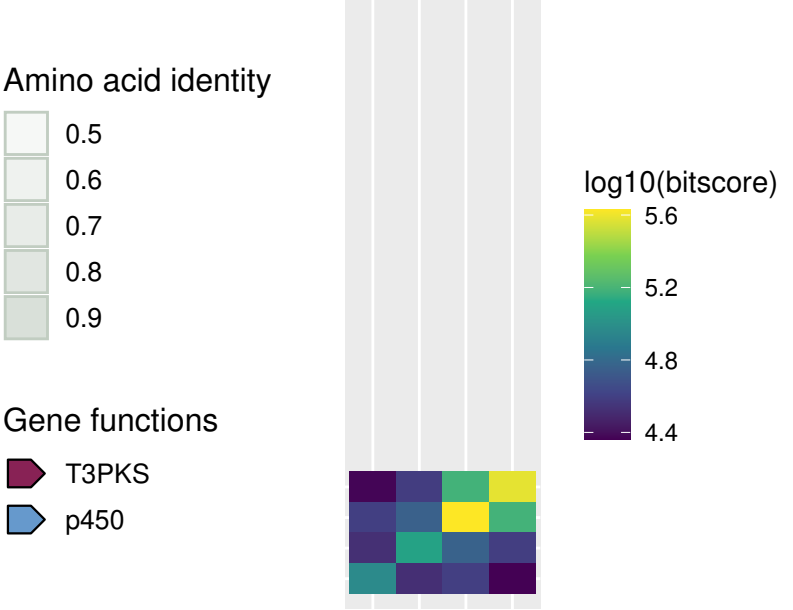


Cluster 16

a

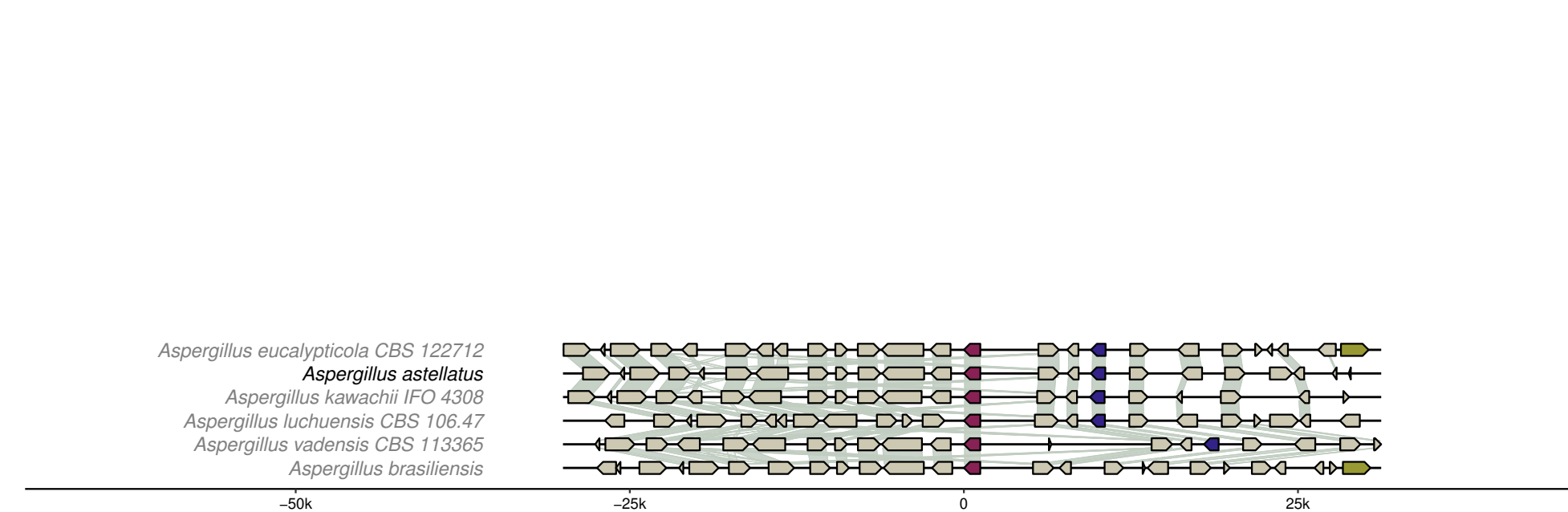


b

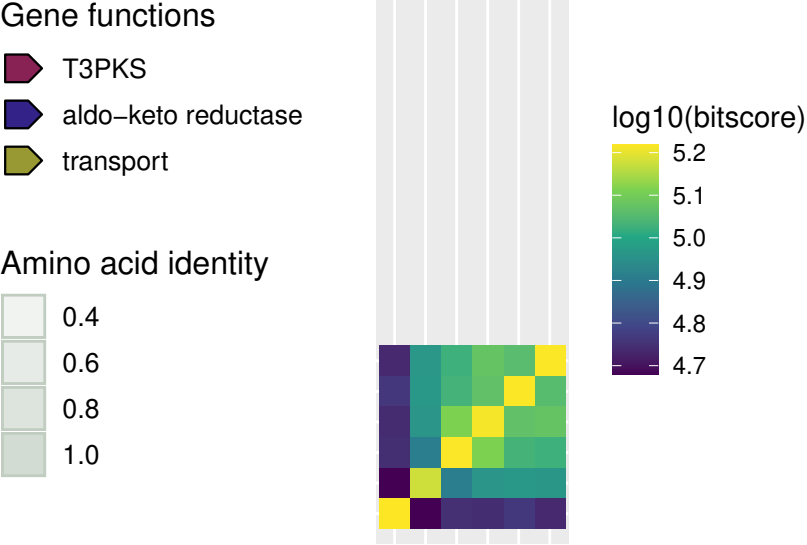


Cluster 17

a

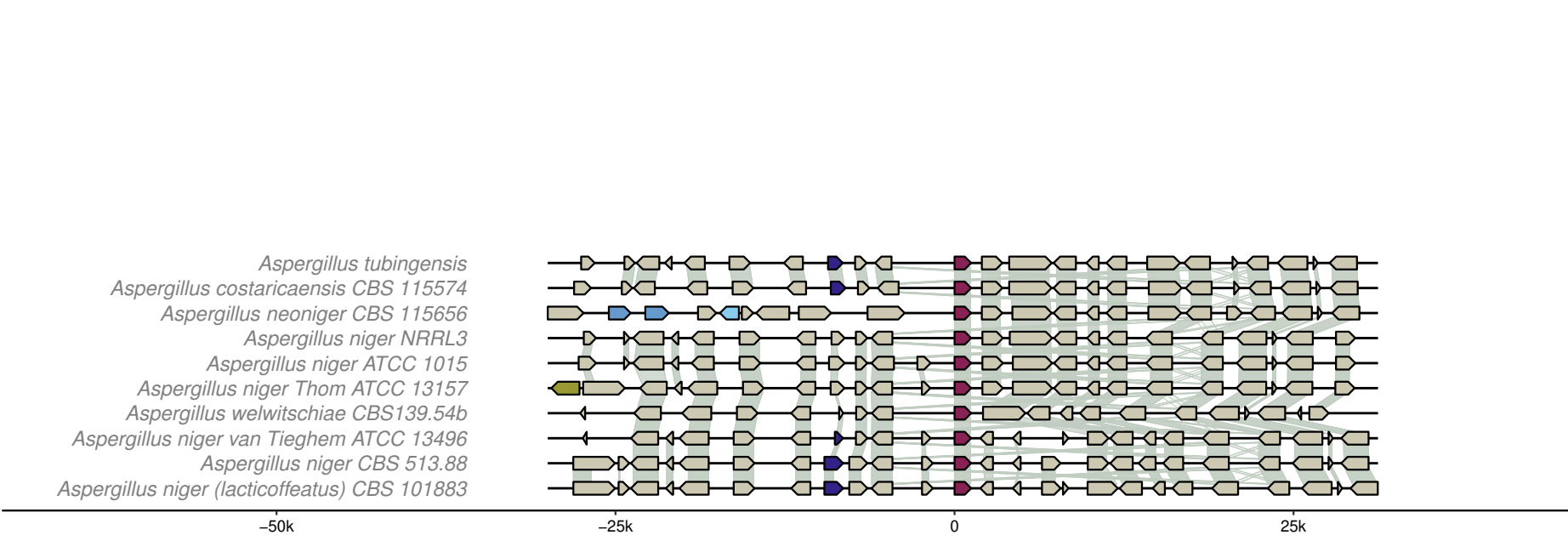


b

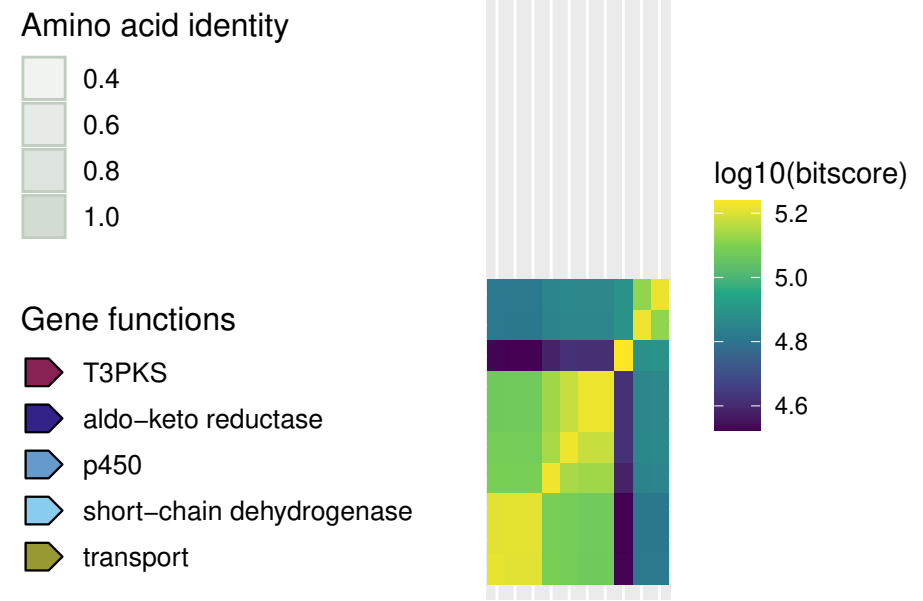


Cluster 18

a



b



Cluster 19

a

Pyricularia oryzae TH0003
Pyricularia oryzae GY0011
Pyricularia oryzae FR0013
Pyricularia oryzae 70-15

-50k

-25k

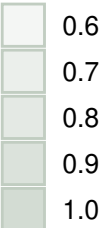
0

25k

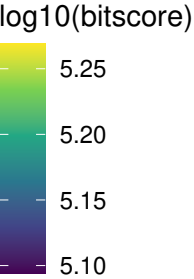
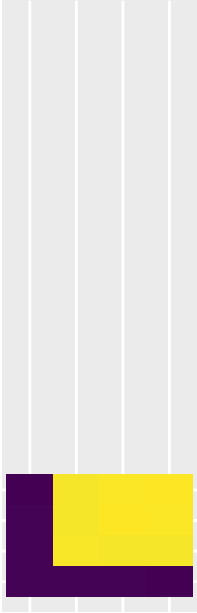
Gene functions

T3PKS

Amino acid identity

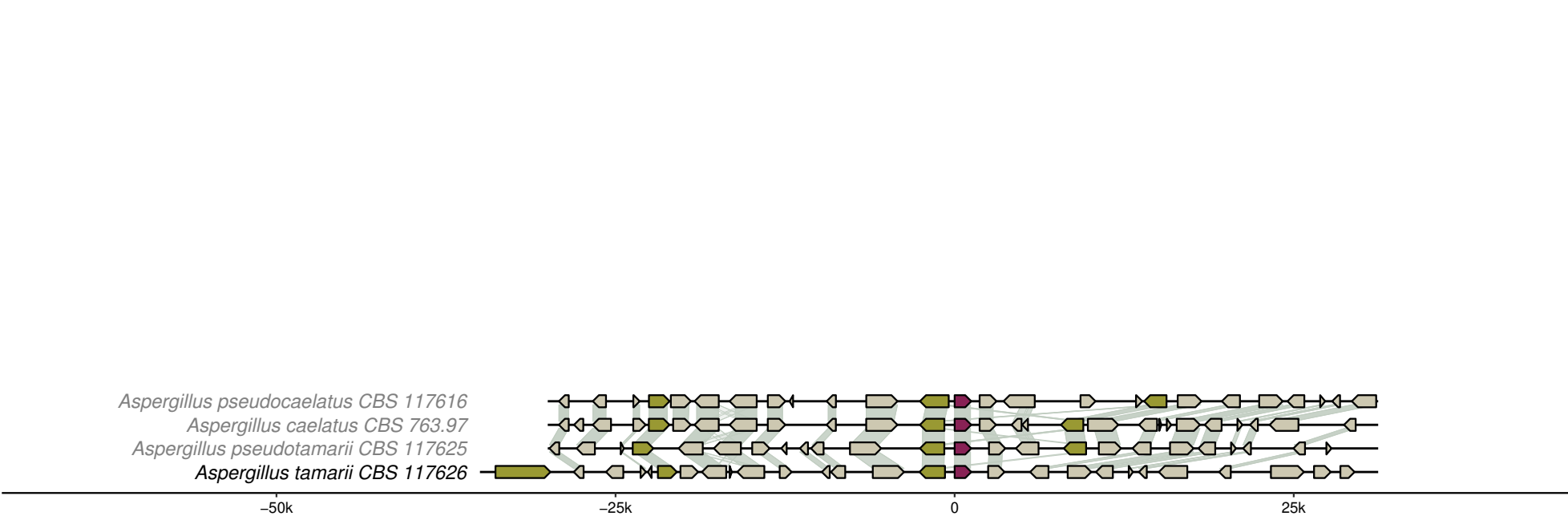


b

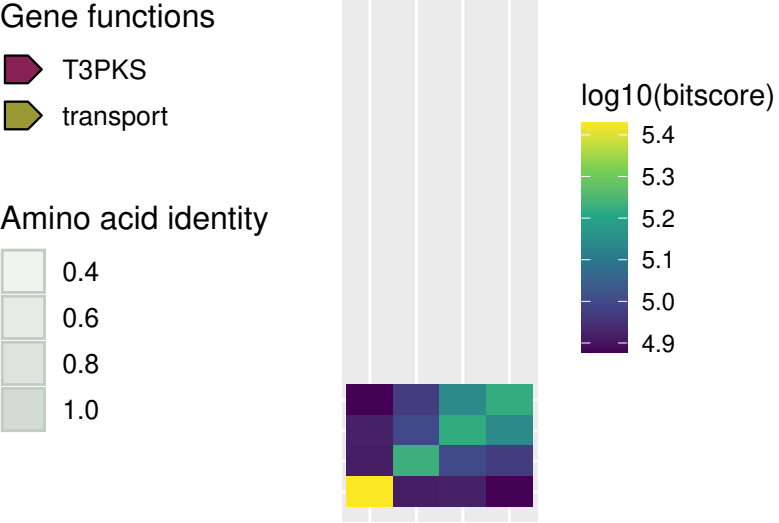


Cluster 20

a

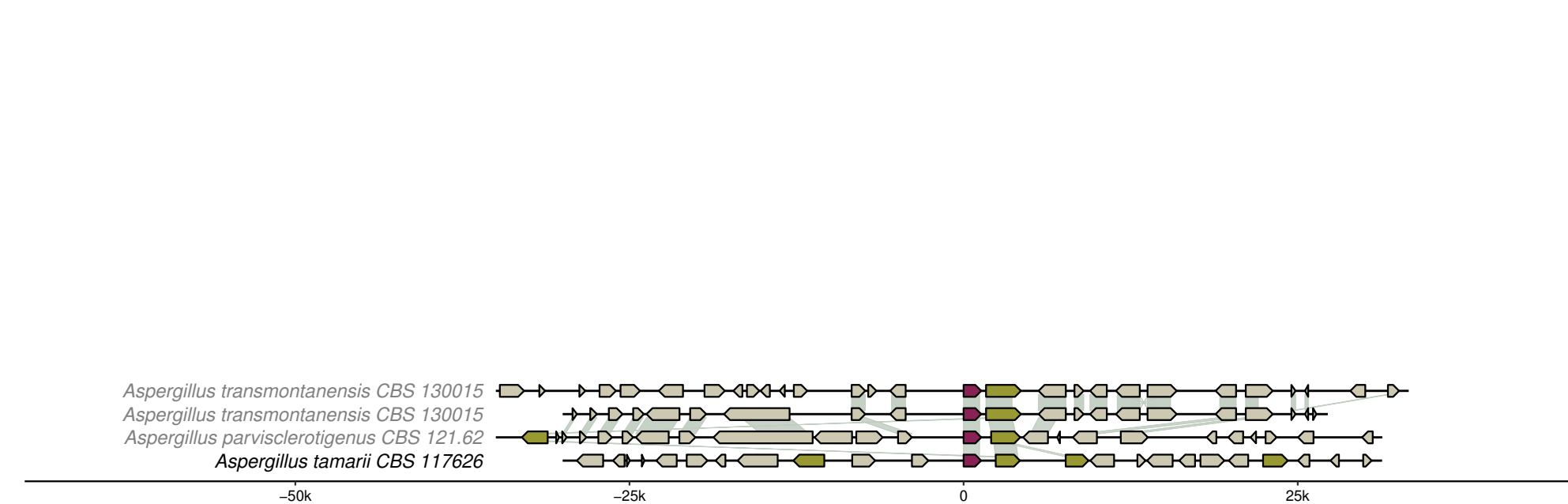


b



Cluster 21

a

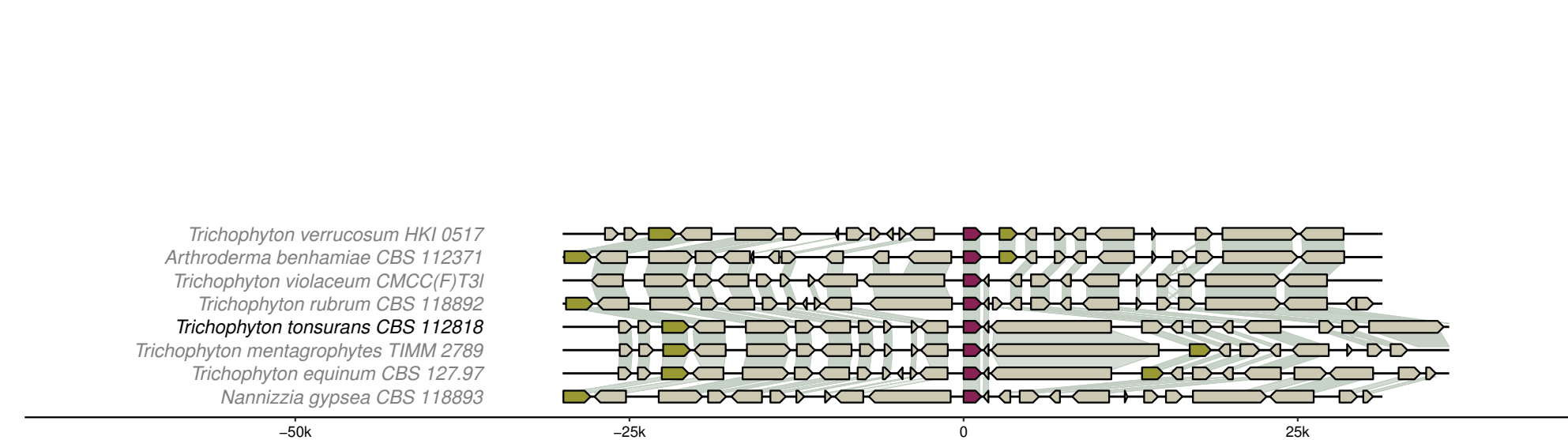


b

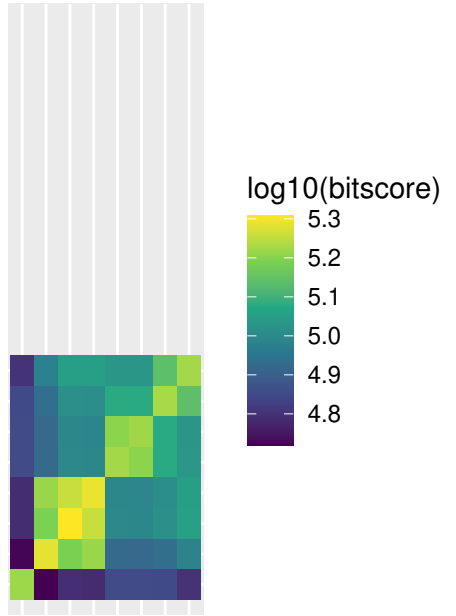


Cluster 22

a

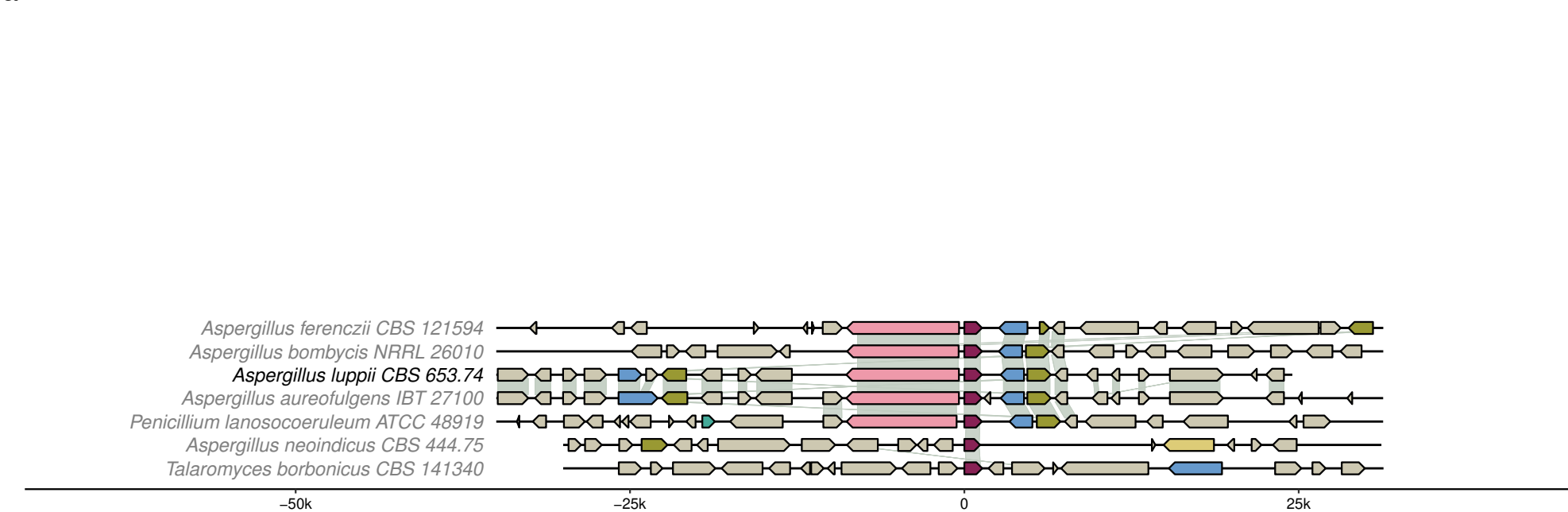


b

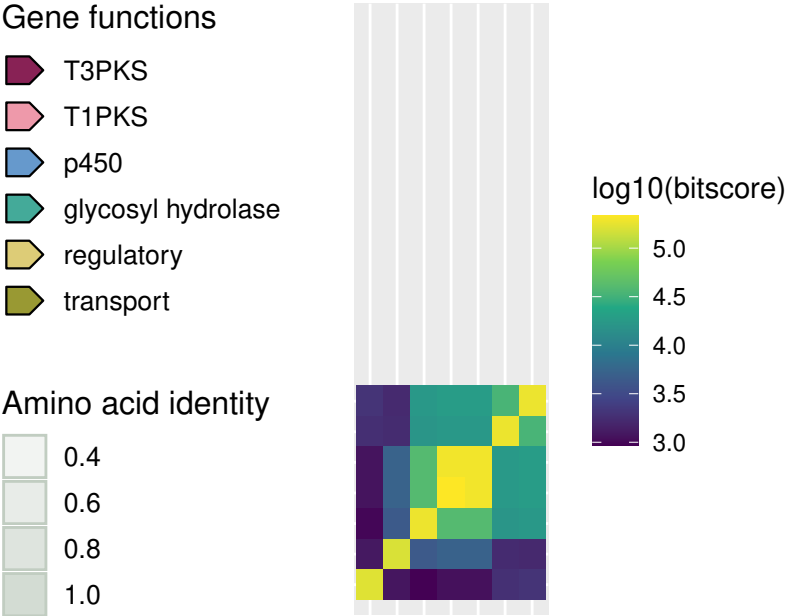


Cluster 23

a



b



Cluster 24

