Comparative genomics reveals low levels of inter- and intraspecies diversity in the causal agents of dwarf and common bunt of wheat and hint at conspecificity of *Tilletia caries* and *T. laevis*

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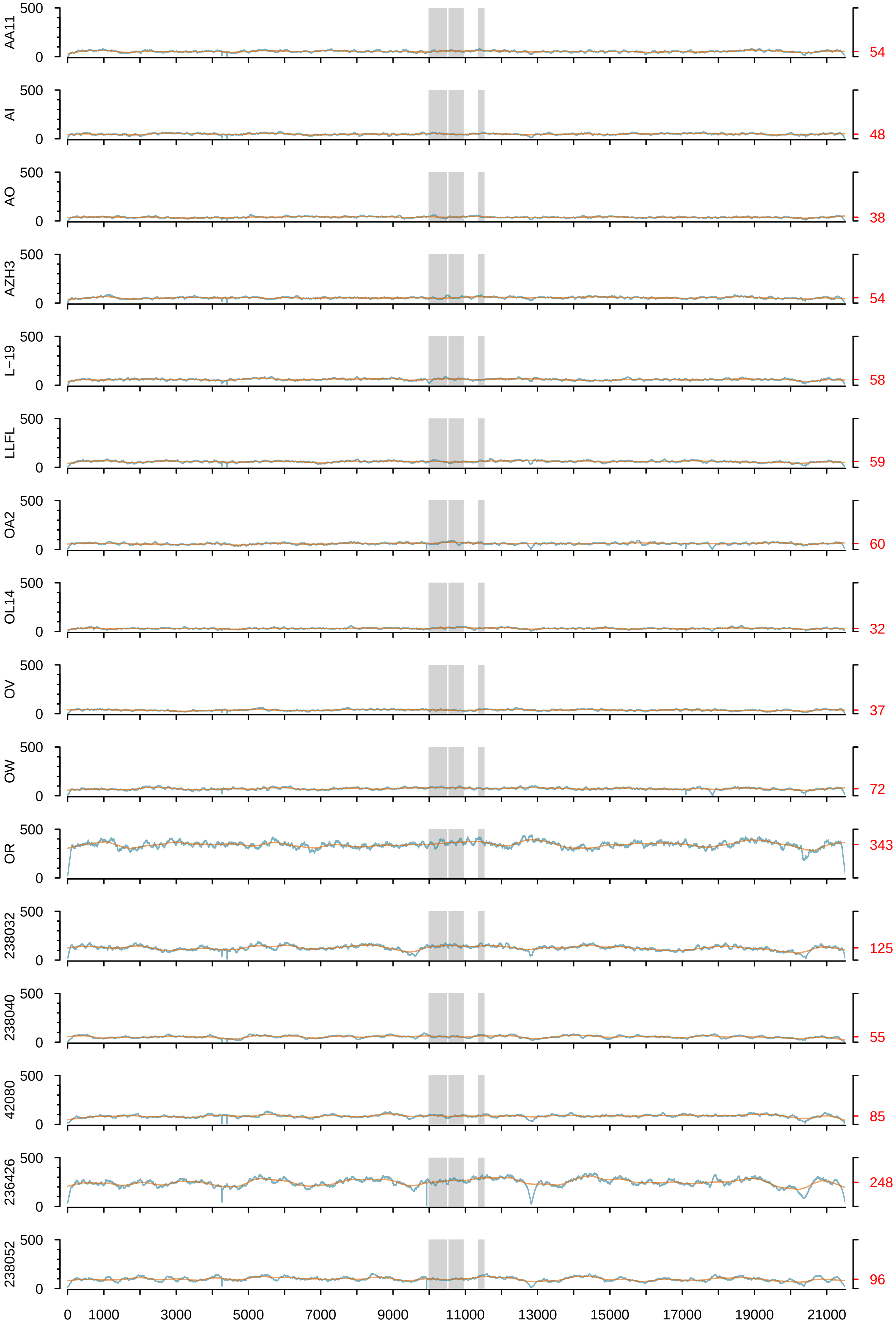

Indole

AA11
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AO
AZH3
L−19
LLFL
OA2
OL14
OV
OW
OR
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42080
236426
238052
500
0
54
48
38
54
58
59
60
32
37
72
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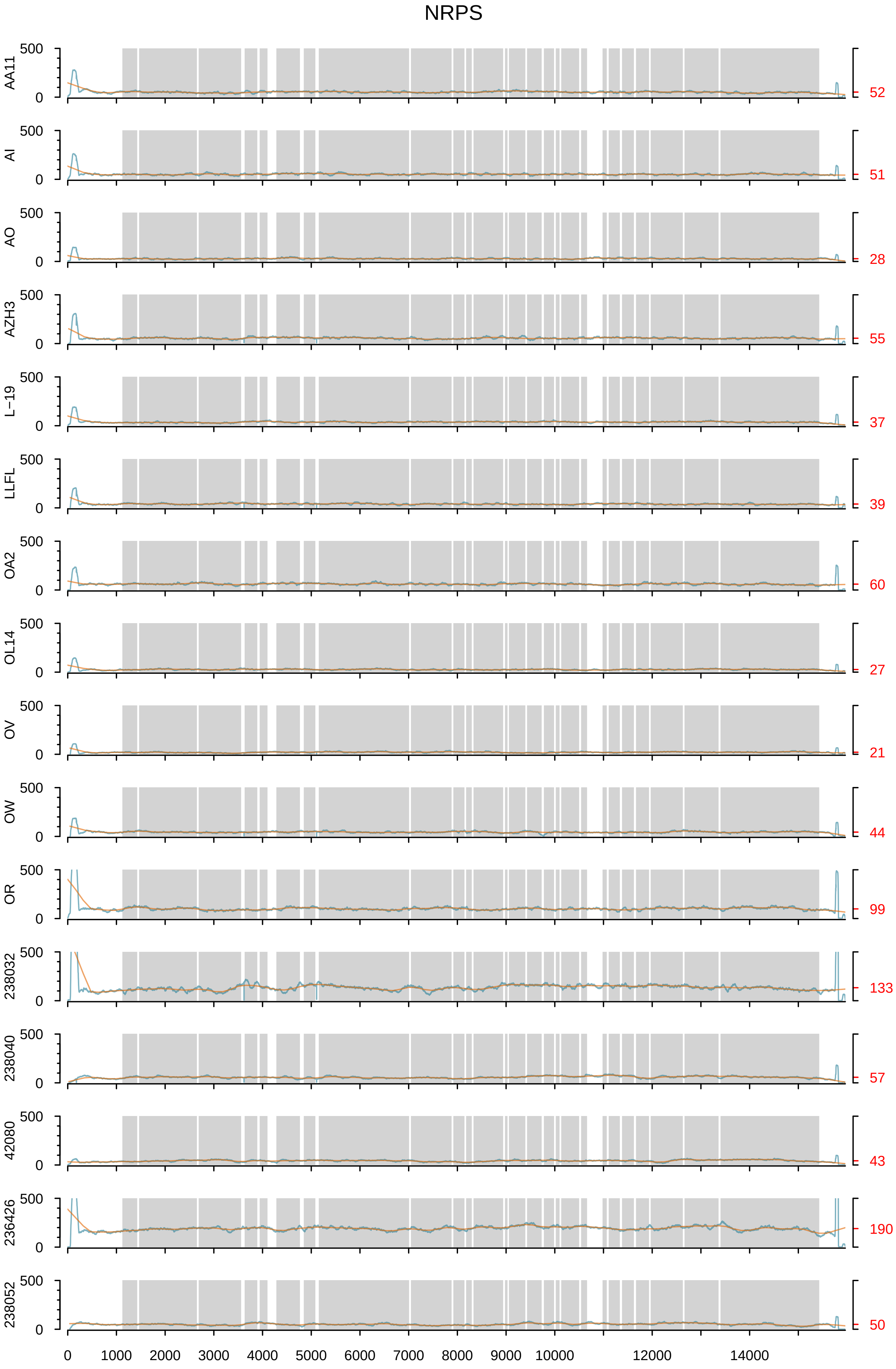
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238052
500
0
52
51
28
55
37
39
60
27
21
44
99
133
57
43
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50
0
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2000
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4000
5000
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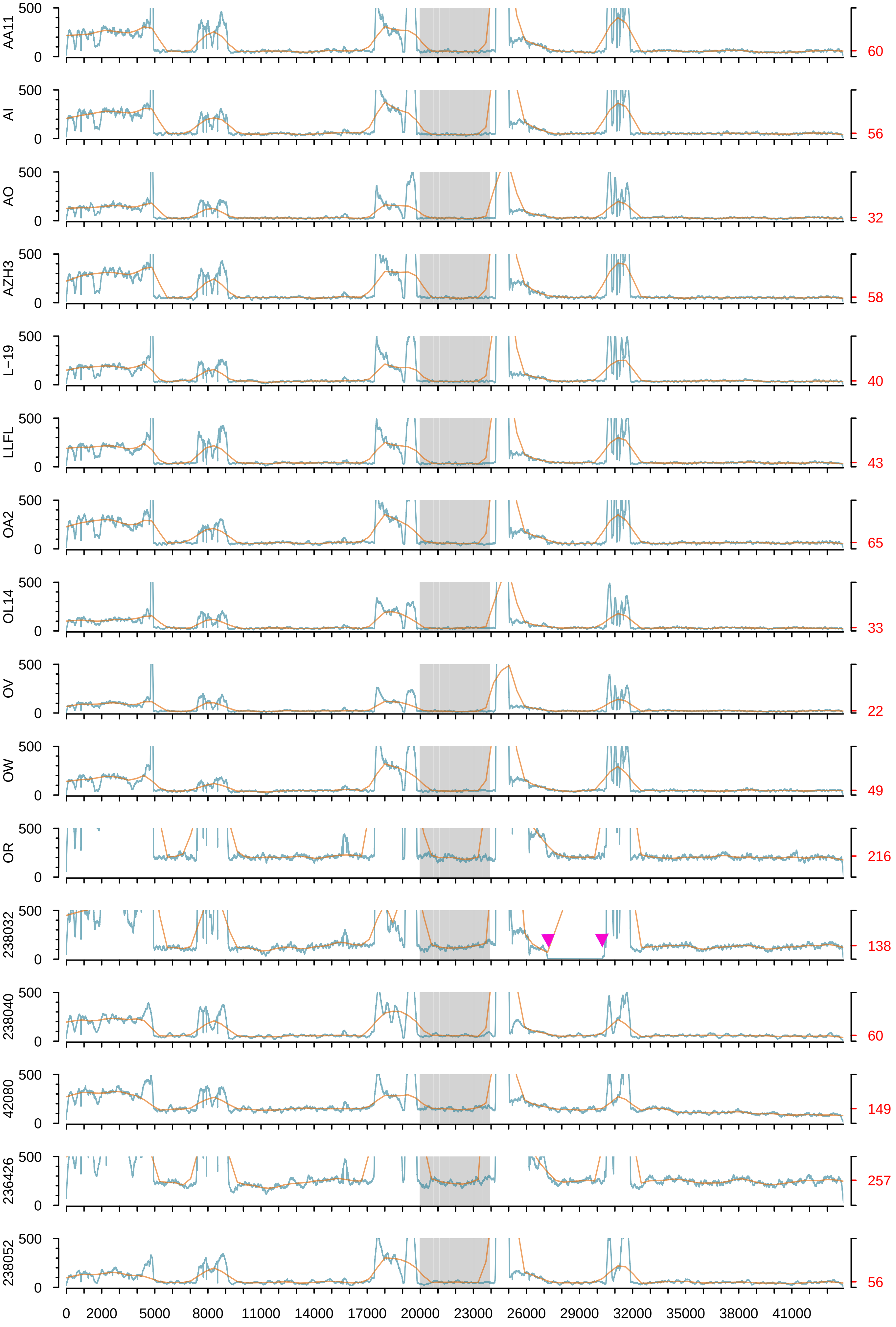
8000
9000
10000
12000
14000

NRPS−like I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500
0
60
56
32
58
40
43
65
33
22
49
216
138
60
149
257
56
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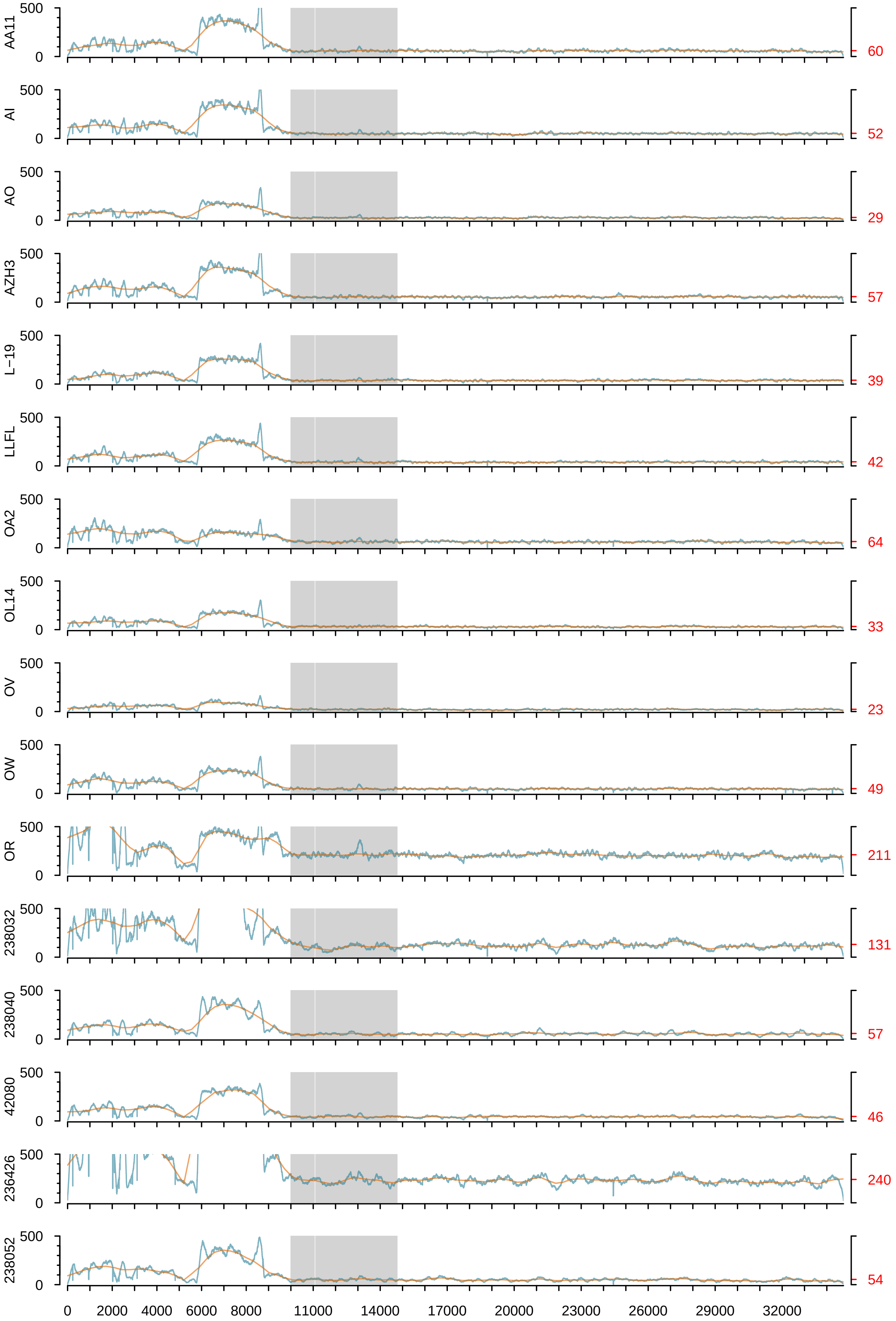
41000

NRPS−like II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0
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52
29
57
39
42
64
33
23
49
211
131
57
46
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6000
8000
11000
14000
17000
20000
23000
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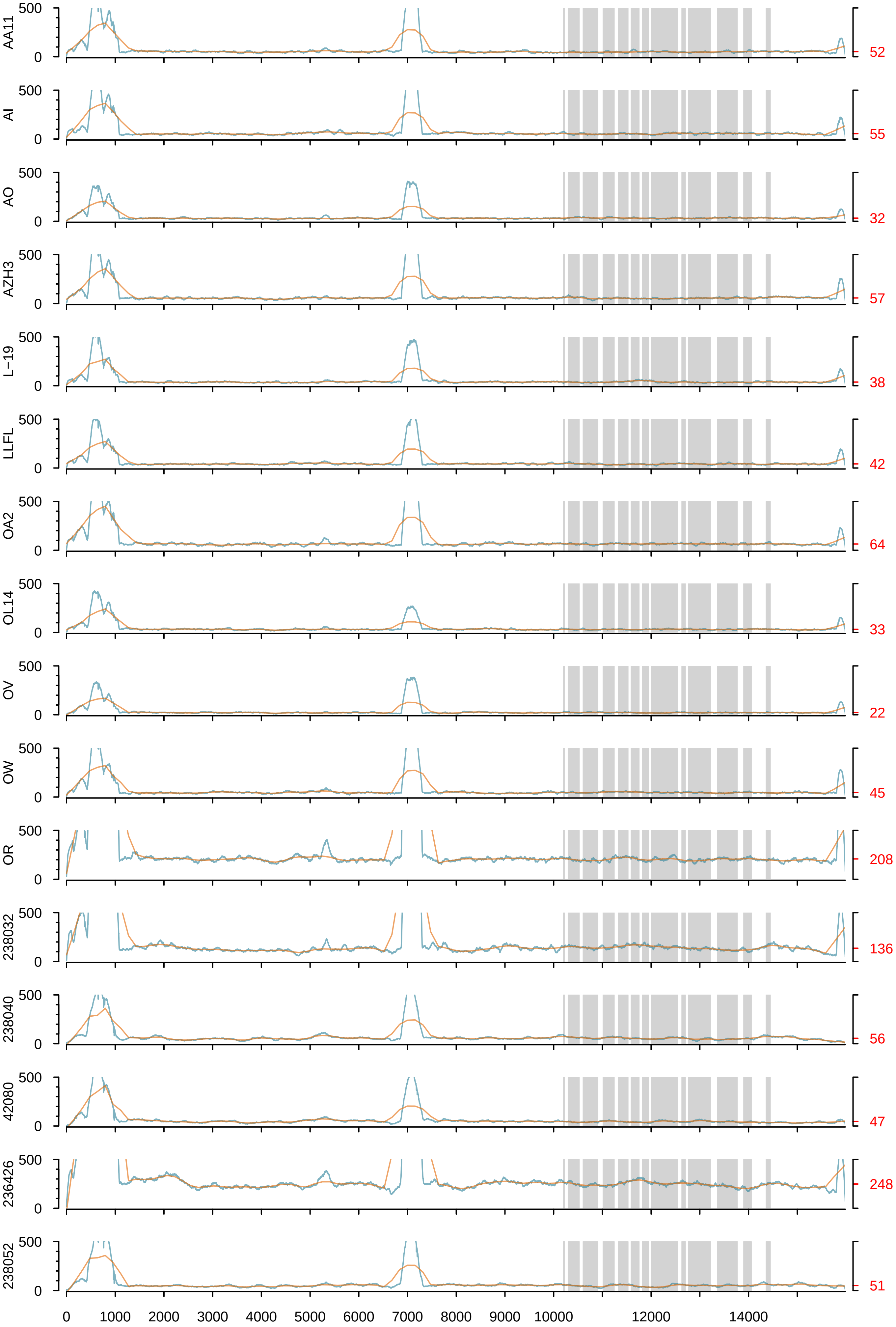
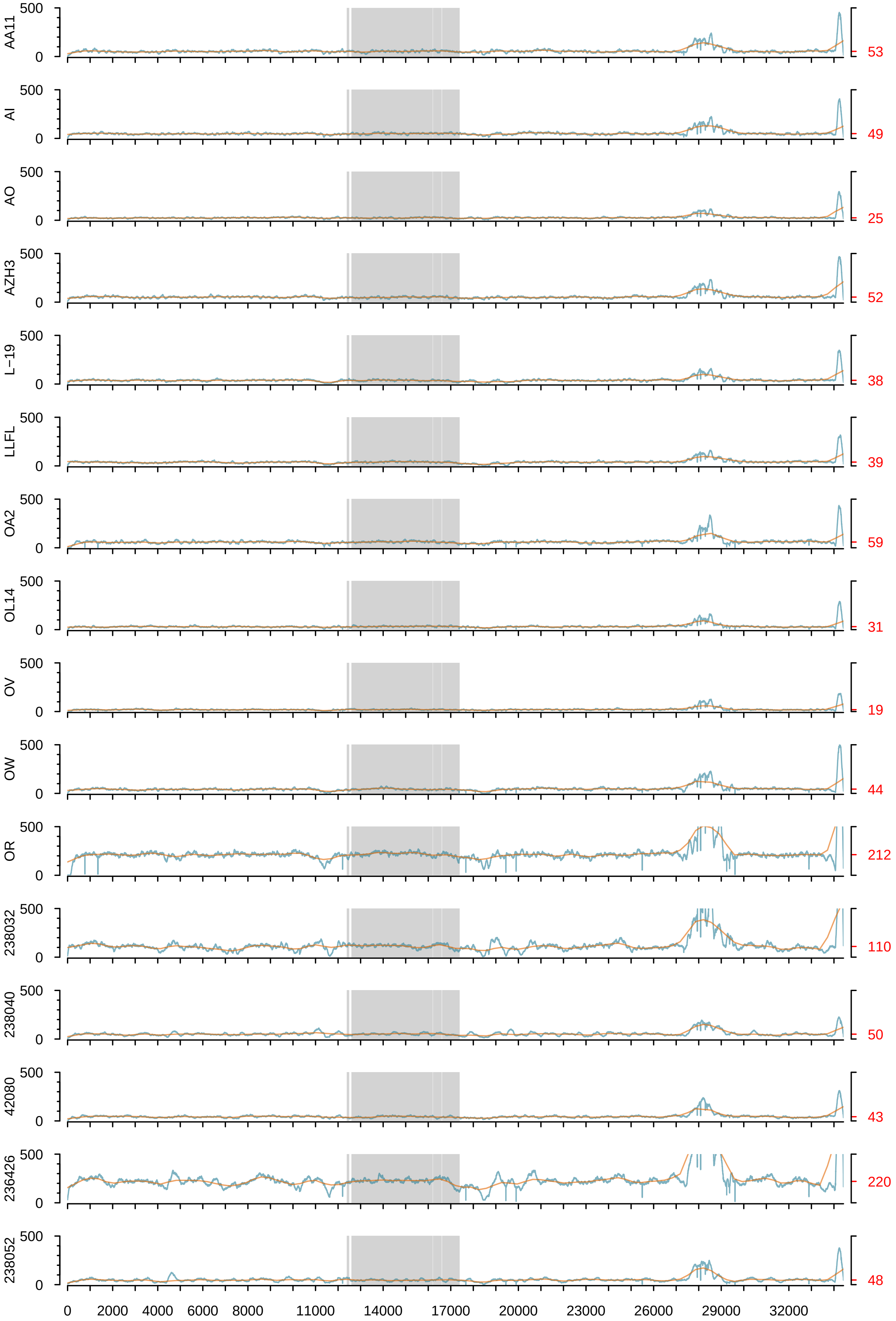
29000
32000

NRPS−like III



NRPS−like IV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500
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AZH3
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L−19
500
0
38
LLFL
500
0
39
OA2
500
0
59
OL14
500
0
31
OV
500
0
19
OW
500
0
44
OR
500
0
212
238032
500
0
110
238040
500
0
50
42080
500
0
43
236426
500
0
220
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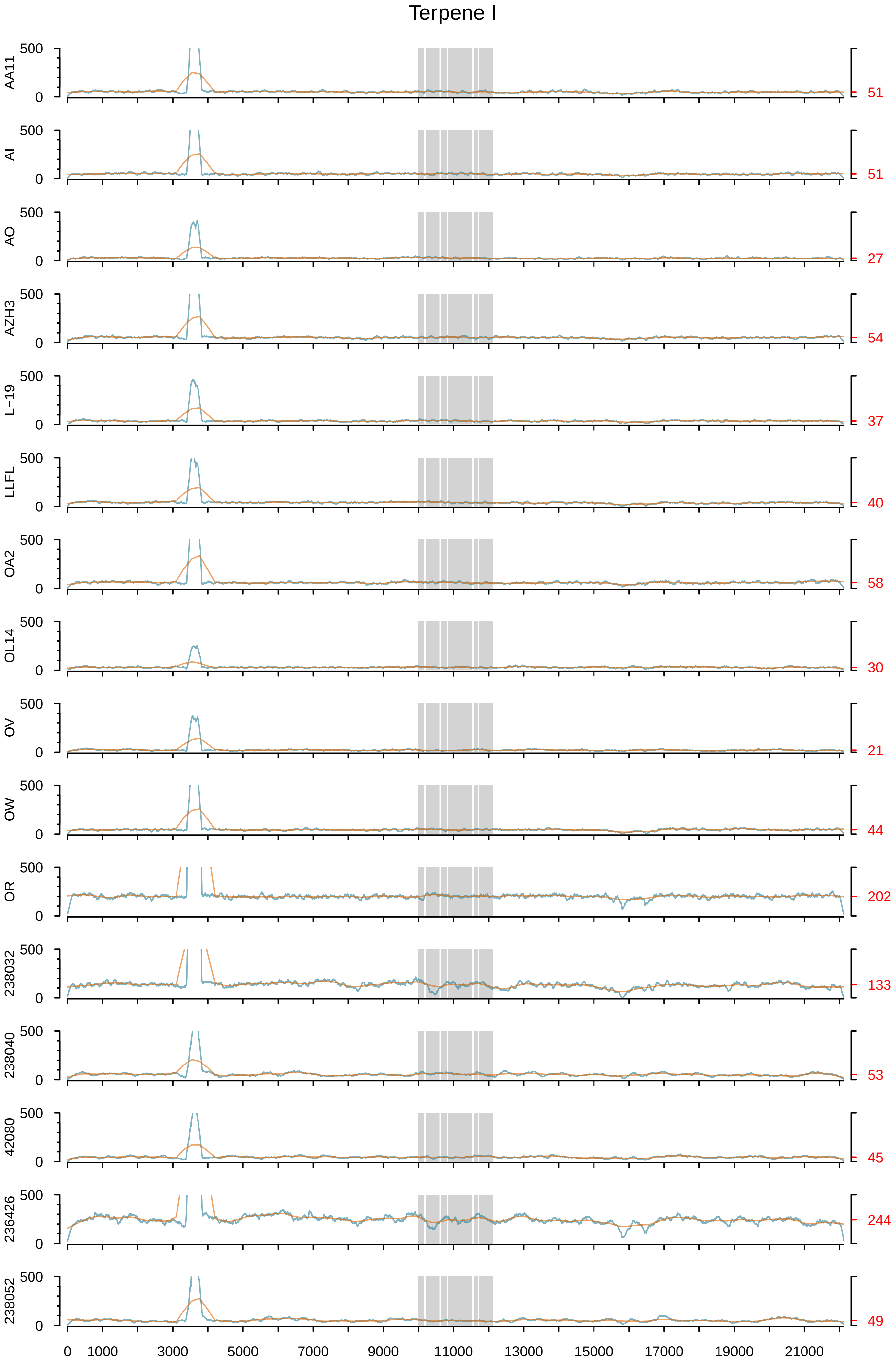
Terpene I
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AO
AZH3
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LLFL
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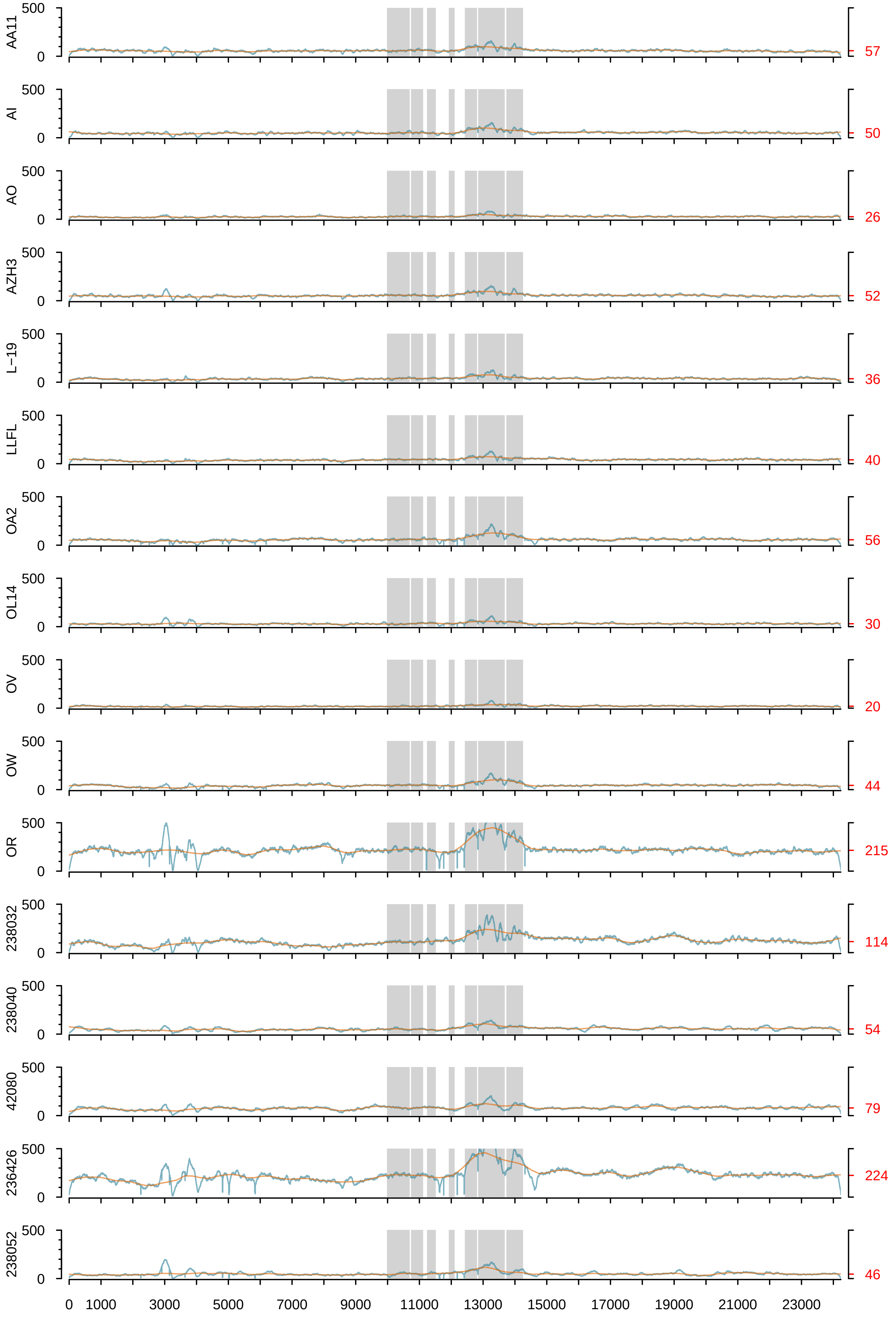
OL14
OV
OW
OR
238032
238040
42080
236426
238052
500
0
51
51
27
54
37
40
58
30
21
44
202
133
53
45
244
49
0
1000
3000
5000
7000
9000
11000
13000
15000
17000
19000
21000

Terpene II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AO
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0
26
AZH3
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0
52
L−19
500
0
36
LLFL
500
0
40
OA2
500
0
56
OL14
500
0
30
OV
500
0
20
OW
500
0
44
OR
500
0
215
238032
500
0
114
238040
500
0
54
42080
500
0
79
236426
500
0
224
238052
500
0
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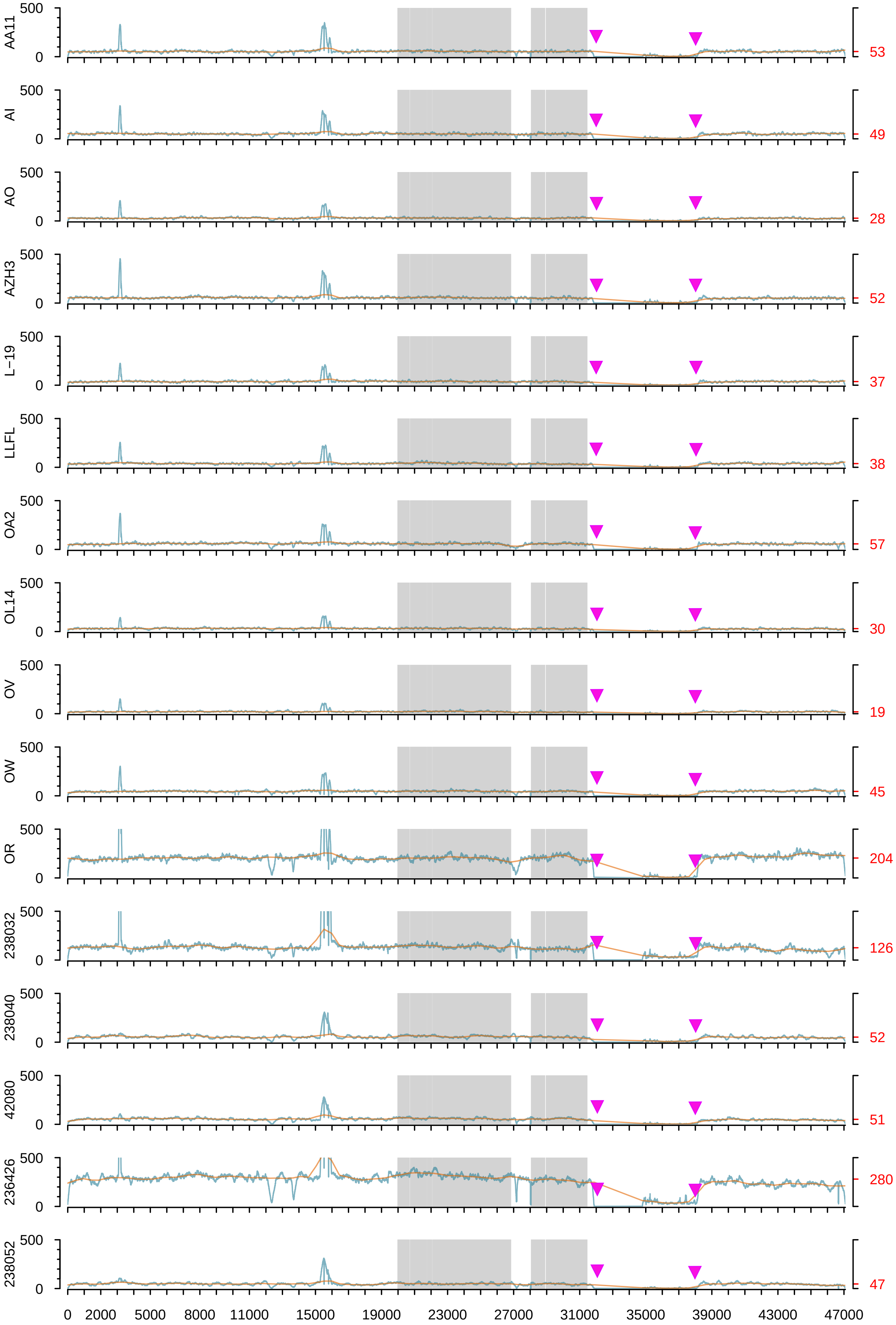
9000
11000
13000
15000
17000
19000
21000
23000

T1PKS/NRPS−like



Additional Figure 1 Coverage of putative secondary metabolites and biosynthetic gene clusters. Trimmed Illumina reads of each isolate were aligned to the selected reference gene cluster sequence using default mapping parameters. The plot shows the read depth up to 500 (blue line) and the lowest regression (filter: 1/25; orange line). The median coverage is indicated on the right y-axis in red and the x-axes shows length of the predicted secondary metabolite gene cluster in bp. Regions which were annotated as core genes by antiSMASH are shaded in gray. The reference secondary metabolite gene clusters used for mappings are as follow: The predicted gene cluster of *T. controversa* strain OR for, Indole, NRPS-like I, NRPS-like II, T1PKS/NRPS-like, *T. caries* isolate AA11 for NRPS, Terpene I, Terpene II, *T. laevis* isolate ATCC 42080 for NRPS-like IV, and *T. controversa* isolate DAOMC 236426 for NRPS-like III. The region marked with arrow represent non-covered regions by reads. While the present and the order of nearly all gene clusters were also supported by Illumina reads, the observed drop in reads coverage in T1PKS/NRPS-like synthases was probably due to the present of long stretches of Ts and Ns nucleotides within this gene cluster in our selected reference. Part of the NRPS-like I gene cluster in the *T. caries* isolate DOAMC 238032 could not be recovered by mapping.