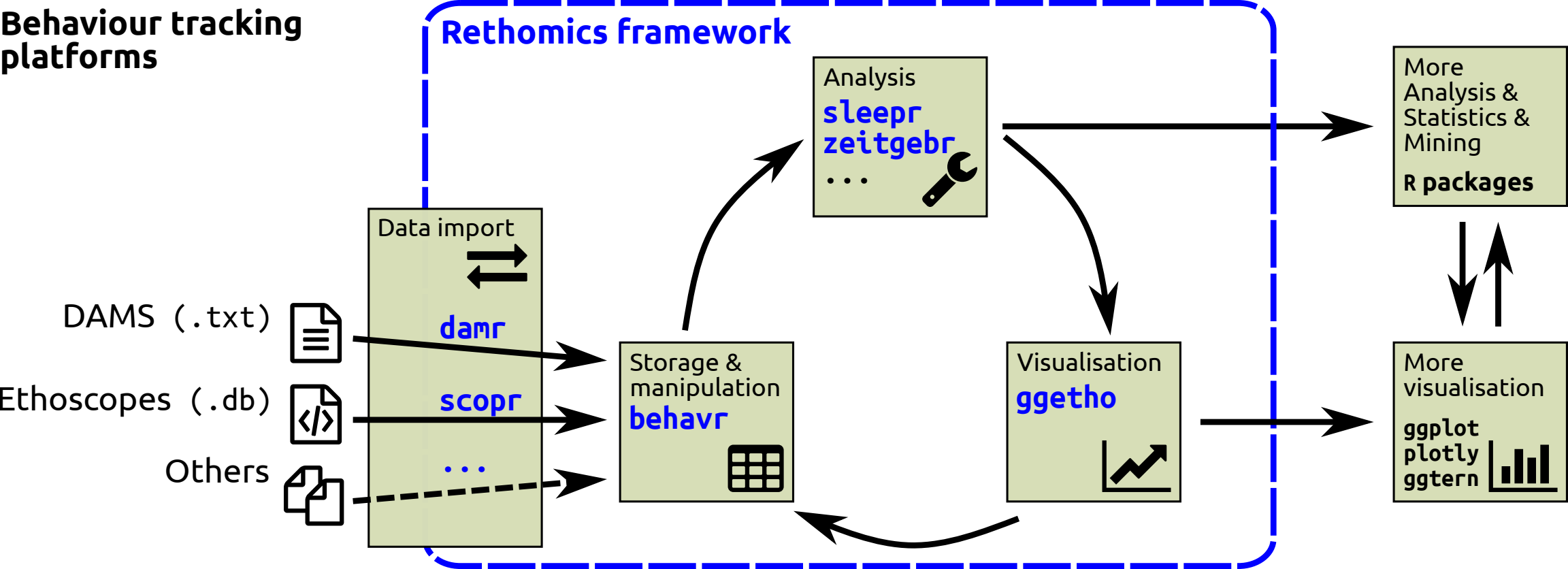


# Behaviour tracking platforms



A

## Metadata

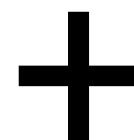
id	machine_name	date	...	condition	sex	...	p
xxx...xx x	machine_001	2016-09-01	...	A	M	...	p <sub>1</sub>
xxx...xx y	machine_001	2016-09-01	...	B	M	...	p <sub>2</sub>
xxx...xx z	machine_002	2016-09-03	...	A	F	...	p <sub>3</sub>
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
n	machine <sub>n</sub>	date <sub>n</sub>	...	condition <sub>n</sub>	sex <sub>n</sub>	...	p <sub>n</sub>

Platform fields  
(mandatory)

Experiment fields  
(arbitrary & optional)

## Data


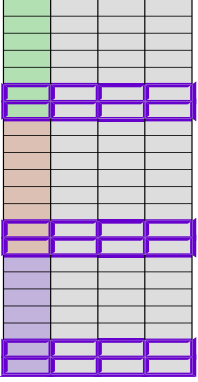
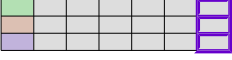
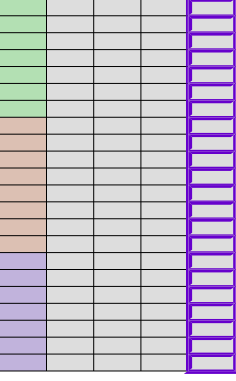
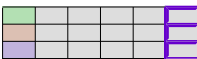
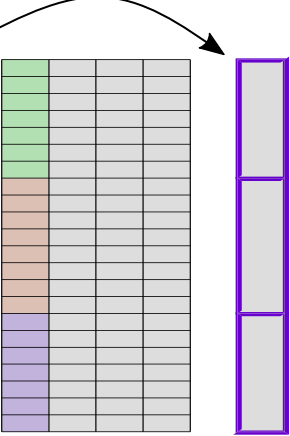

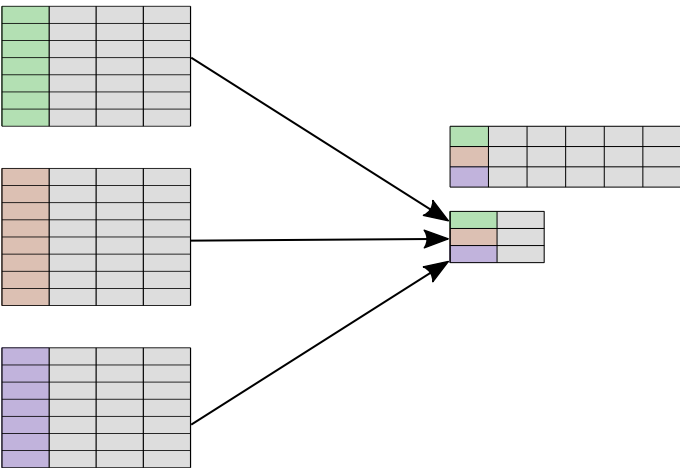
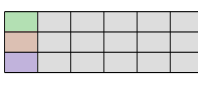
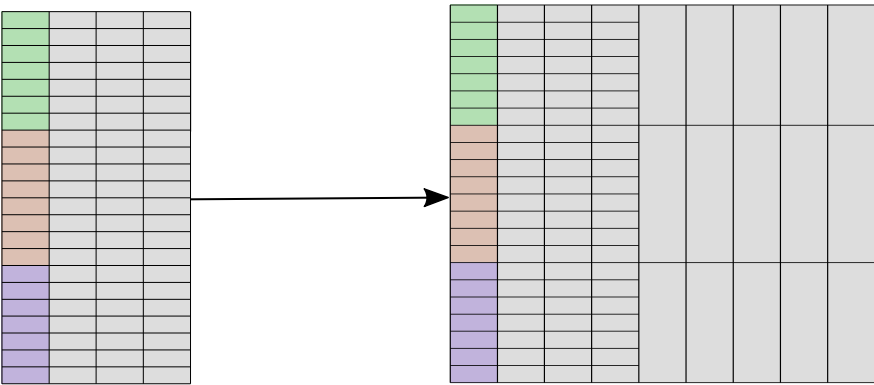
id	t	activity	...	q
xxx...xx x	1	1	⋮	q <sub>1,1</sub>
xxx...xx x	2	0	⋮	q <sub>1,2</sub>
xxx...xx x	3	0	⋮	q <sub>1,3</sub>
xxx...xx x	⋮	⋮	⋮	⋮
xxx...xx y	⋮	⋮	⋮	⋮
xxx...xx z	1	0	⋮	q <sub>3,1</sub>
xxx...xx z	2	2	⋮	q <sub>3,2</sub>
xxx...xx z	3	0	⋮	q <sub>3,3</sub>
xxx...xx z	⋮	⋮	⋮	⋮
⋮	⋮	⋮	⋮	⋮
n	⋮	⋮	⋮	q <sub>n,k<sub>n</sub></sub>



B

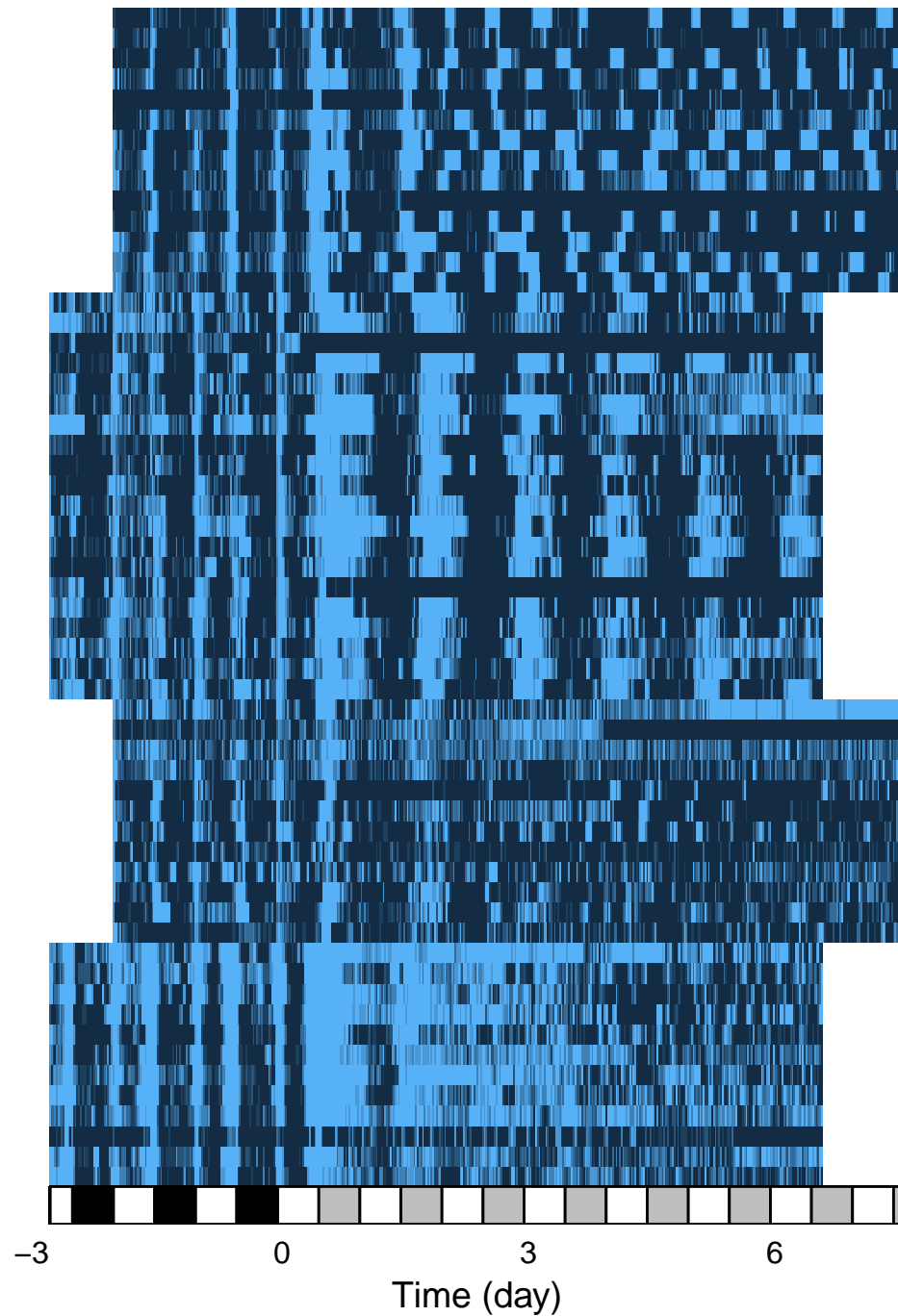
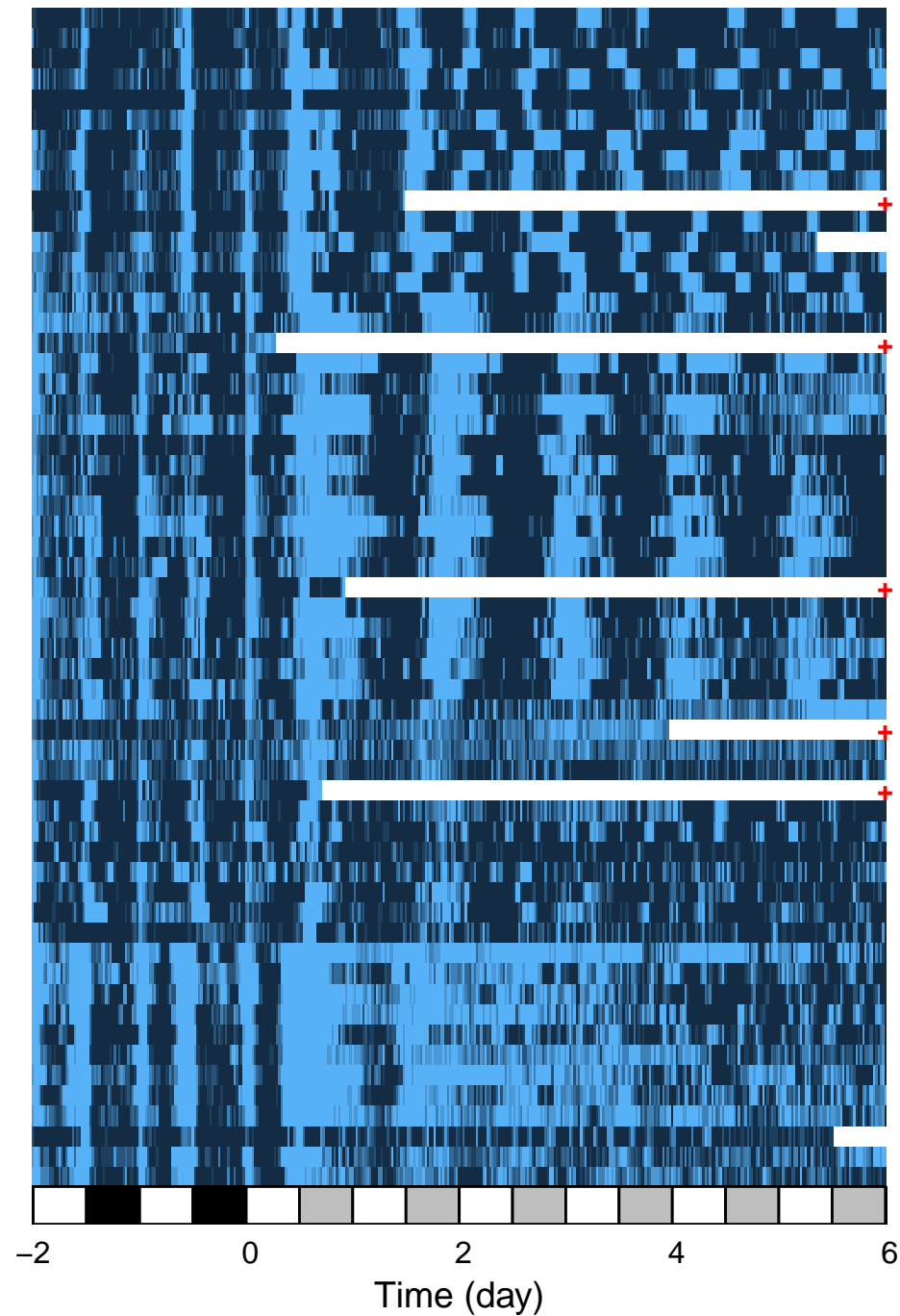
## Metadata

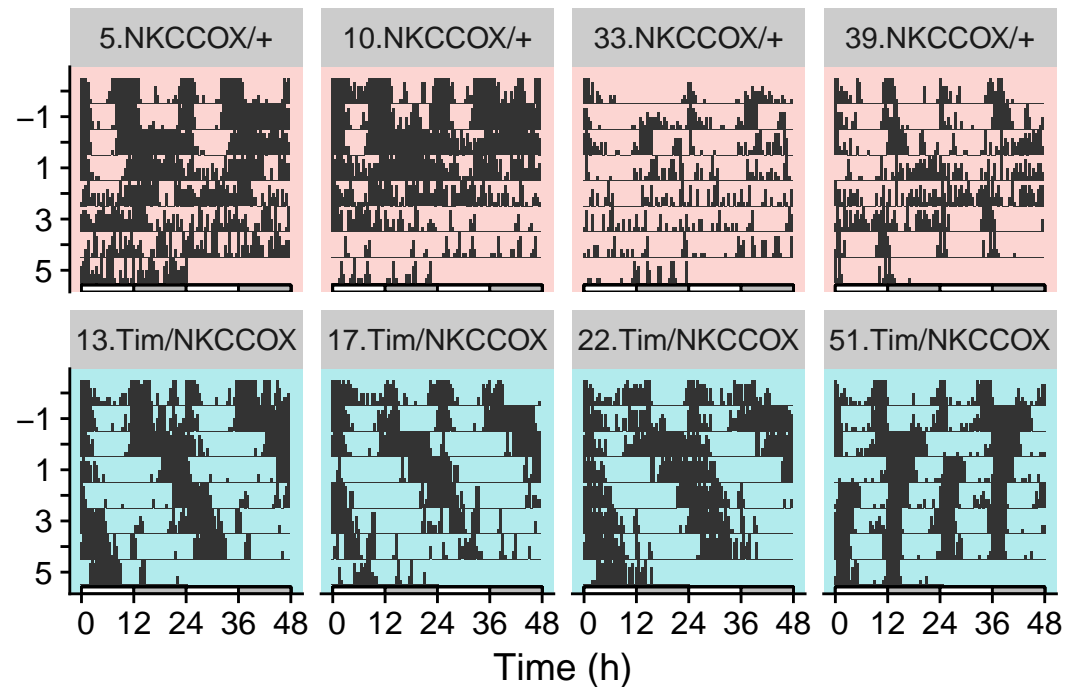
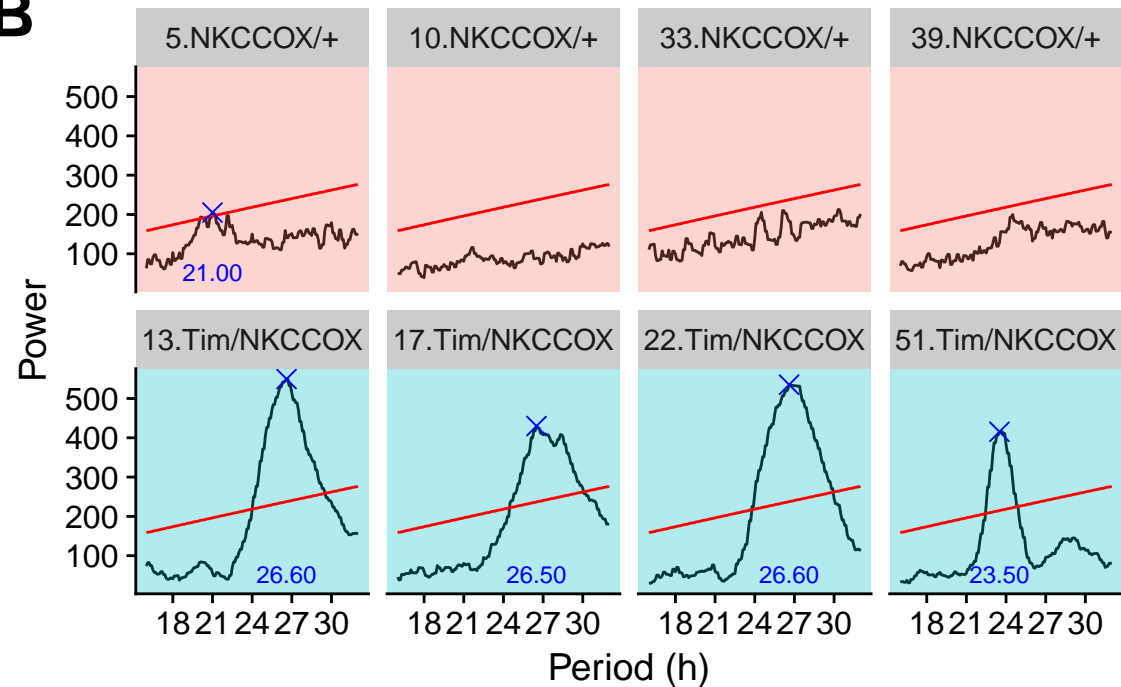
## Data

Select	<b>dt[CRITERIA, meta = TRUE]</b>  <pre># to subet the metadata only for males &gt; male_meta &lt;- dt[sex == "M",   meta = TRUE]</pre>	<b>dt[CRITERIA]</b>  <pre># to keep only data &gt; 5s &gt; late_dt &lt;- dt[t &gt; 5]</pre> <p>Note: metadata is updated when selection removes all data from one id.</p>
Alter, create & delete (meta)variables	<b>dt[, X := value, meta = TRUE]</b>  <pre># to create a metavariable set to "wt" &gt; dt[, genotype := "wt", meta = TRUE] # delete &gt; dt[, sex := NULL, meta = TRUE]</pre>	<b>dt[, Y := value]</b>  <pre># to create t_2 (t - 1) &gt; dt[, t_2 := t - 1] # to delete t &gt; dt[, t := NULL]</pre> <p>Note: update data in place. No copy of dt in memory.</p>
Expand metavariables as variables	<b>dt[xmv(X)]</b>  <pre># to select data with sex &gt; dt &lt;- dt[xmv(sex) == "M"]  # to copy a metavariable as a variable &gt; dt[, s := xmv(sex)]</pre> 	
Aggregate & summary	<b>dt[, OPERATION, by = id]</b>  <pre># to compute mean activity, per individual &gt; dt &lt;- dt[,.(   mean_act = mean(activity) ), by = id]  # to count reads per id &gt; dt[, .N, by = id]</pre> 	
Join data & metadata	<b>rejoin(dt)</b>  <pre># to reunite data and metadata &gt; full_table &lt;- rejoin(dt)</pre> <p>Note: used mostly after aggregation or preprocessing</p> 	

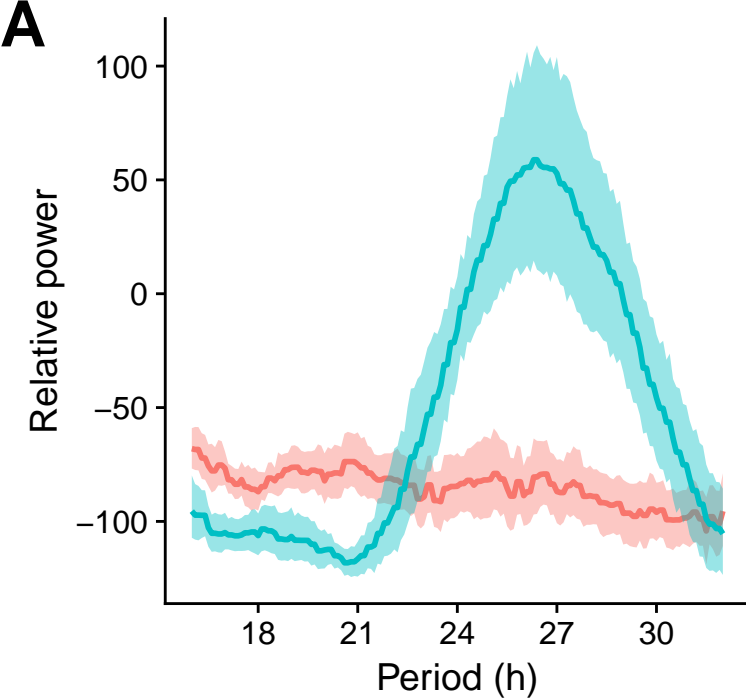
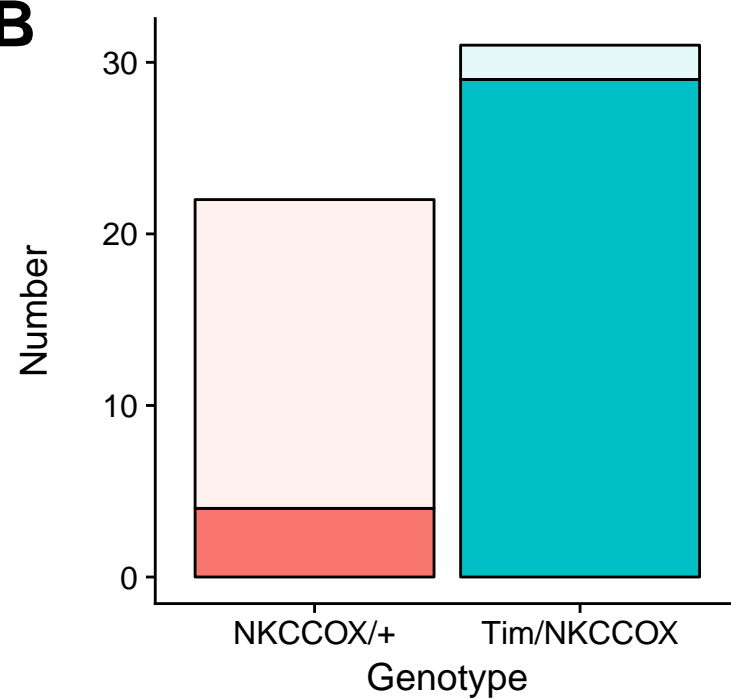
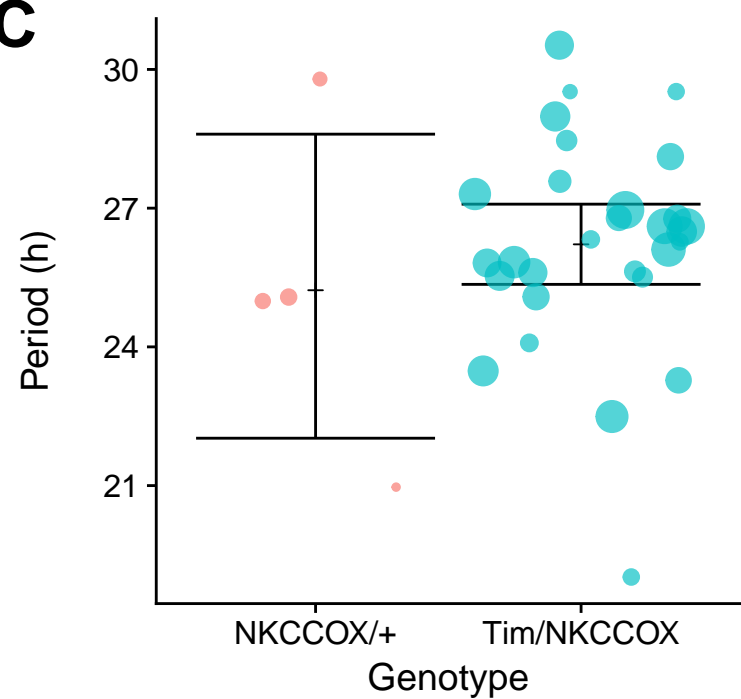
**A**

58.Tim/NKCCOX  
57.Tim/NKCCOX  
56.Tim/NKCCOX  
55.Tim/NKCCOX  
54.Tim/NKCCOX  
53.Tim/NKCCOX  
52.Tim/NKCCOX  
51.Tim/NKCCOX  
50.Tim/NKCCOX  
49.Tim/NKCCOX  
48.Tim/NKCCOX  
47.Tim/NKCCOX  
46.Tim/NKCCOX  
45.Tim/NKCCOX  
32.Tim/NKCCOX  
31.Tim/NKCCOX  
30.Tim/NKCCOX  
29.Tim/NKCCOX  
28.Tim/NKCCOX  
27.Tim/NKCCOX  
26.Tim/NKCCOX  
25.Tim/NKCCOX  
24.Tim/NKCCOX  
23.Tim/NKCCOX  
22.Tim/NKCCOX  
21.Tim/NKCCOX  
20.Tim/NKCCOX  
19.Tim/NKCCOX  
18.Tim/NKCCOX  
17.Tim/NKCCOX  
16.Tim/NKCCOX  
15.Tim/NKCCOX  
14.Tim/NKCCOX  
13.Tim/NKCCOX  
44.NKCCOX/+  
43.NKCCOX/+  
42.NKCCOX/+  
41.NKCCOX/+  
40.NKCCOX/+  
39.NKCCOX/+  
38.NKCCOX/+  
37.NKCCOX/+  
36.NKCCOX/+  
35.NKCCOX/+  
34.NKCCOX/+  
33.NKCCOX/+  
12.NKCCOX/+  
11.NKCCOX/+  
10.NKCCOX/+  
9.NKCCOX/+  
8.NKCCOX/+  
7.NKCCOX/+  
6.NKCCOX/+  
5.NKCCOX/+  
4.NKCCOX/+  
3.NKCCOX/+  
2.NKCCOX/+  
1.NKCCOX/+

**B**

**A****B**

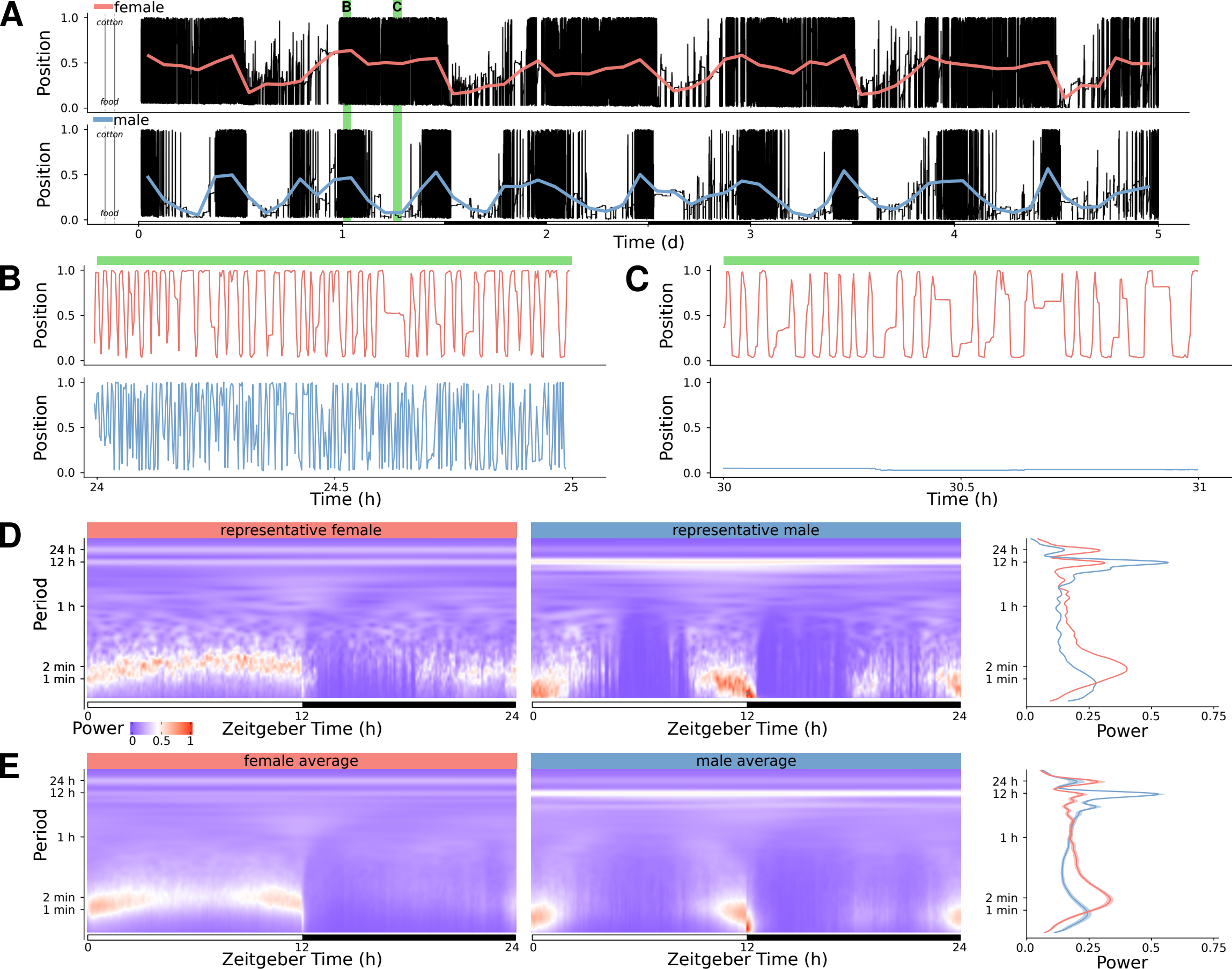
Genotype ■ NKCCOX/+ ■ Tim/NKCCOX

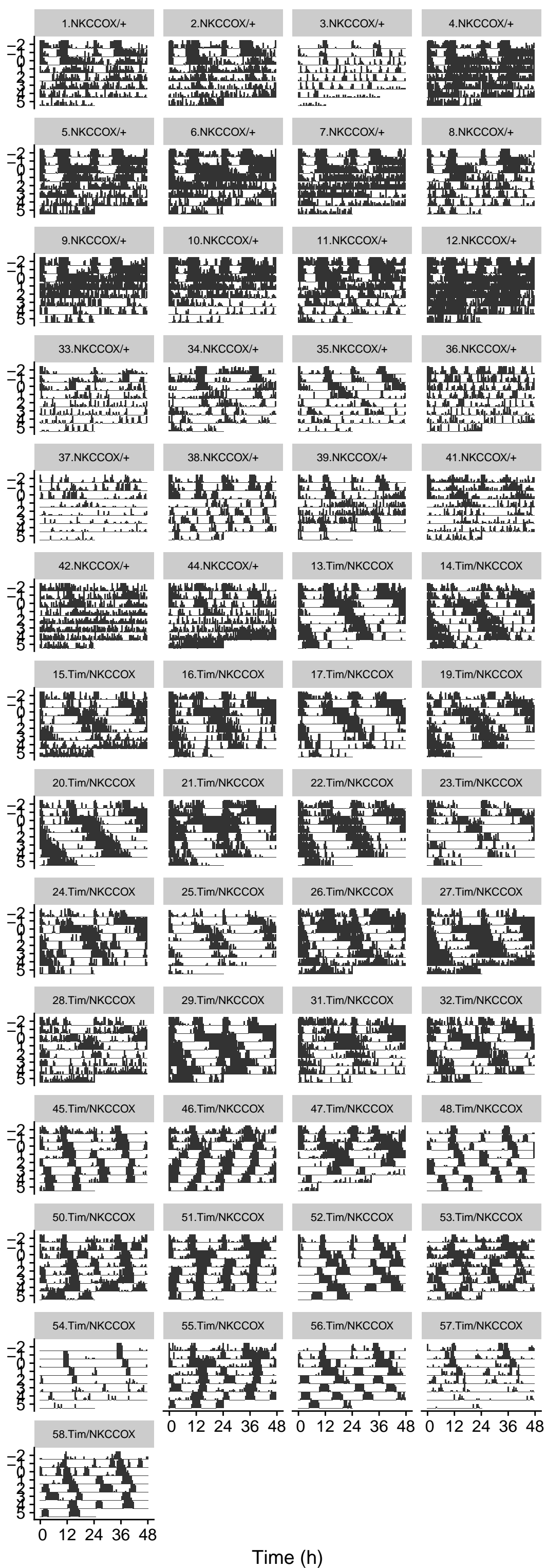
**A****B****C**

Genotype ■ NKCCOX/+ ■ Tim/NKCCOX

■ Arhythmic ■ Rhythmic

Peak relative power ● 100 ● 200 ● 300



**A****B**