

# 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

Experiment fields

+

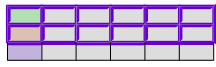
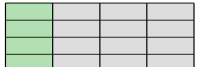
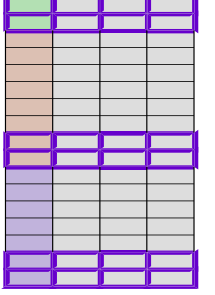
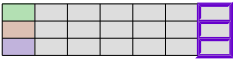
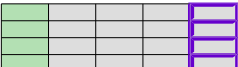
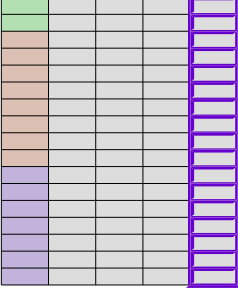
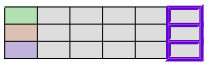
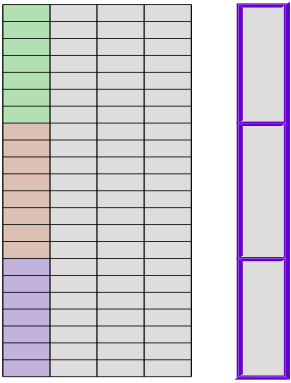

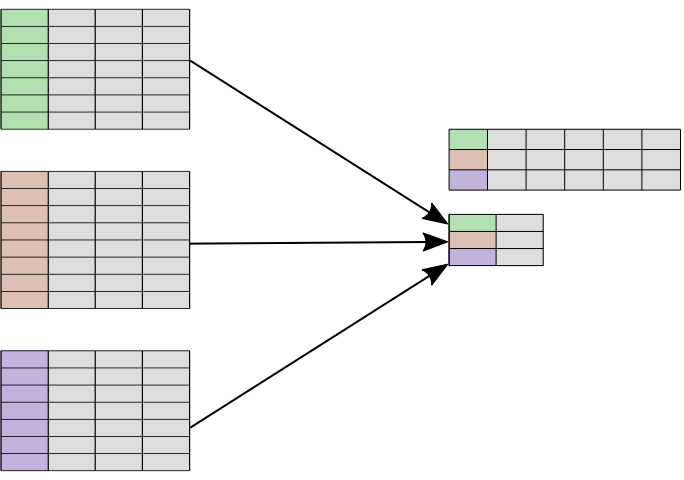
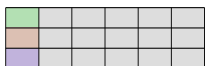
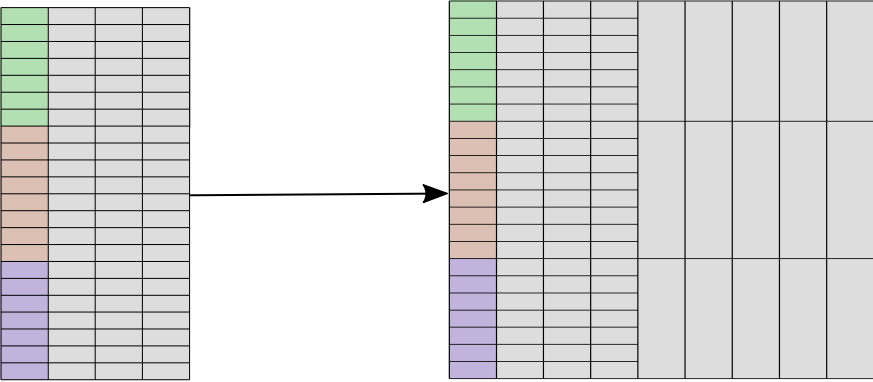
## Data

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

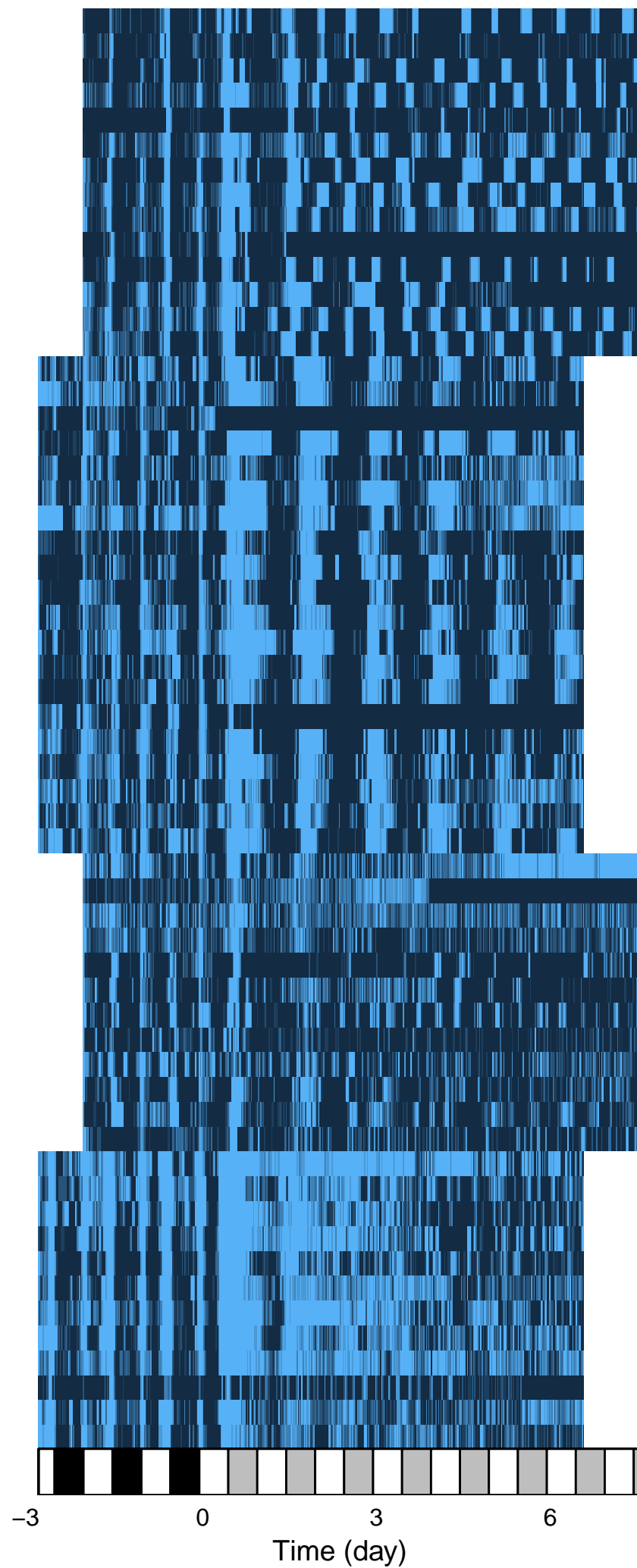
## Metadata

## Data

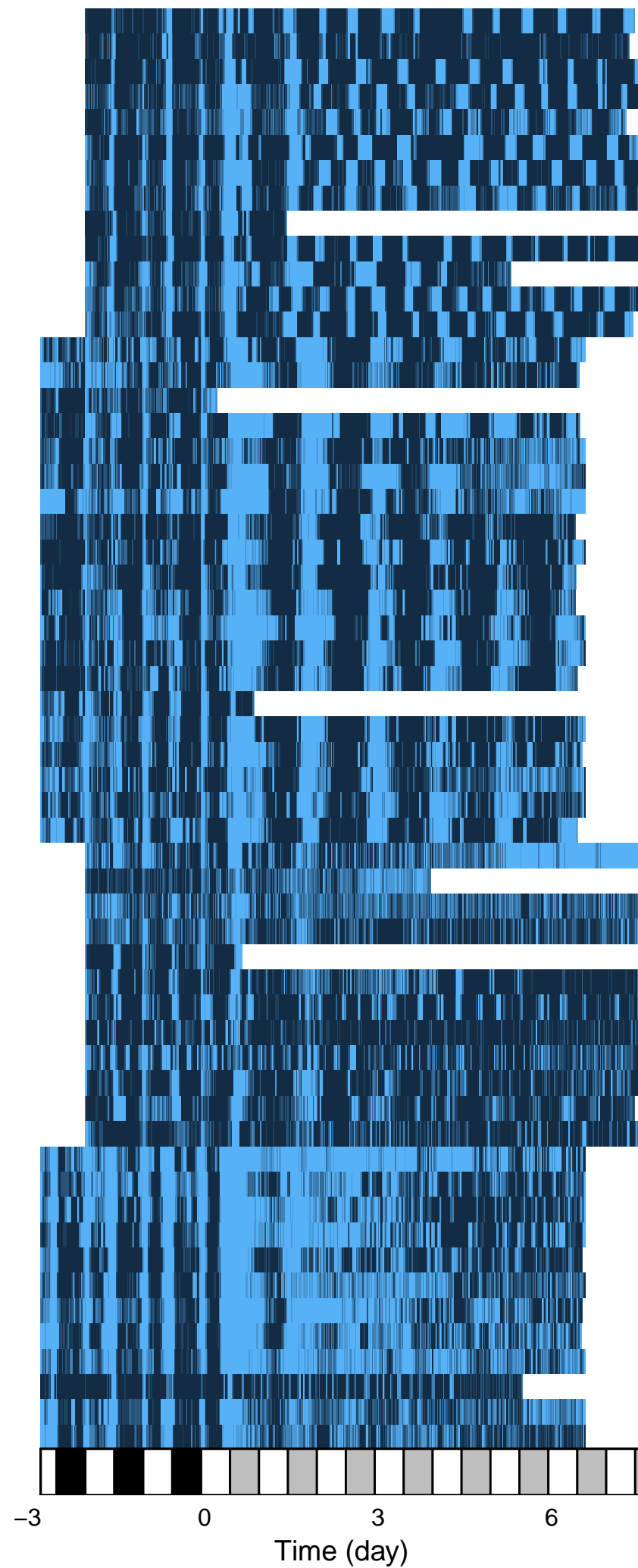
Select	<b>dt[CRITERIA, meta = TRUE]</b>  <pre>&gt; male_meta &lt;- dt[sex == "M",                     meta = TRUE]</pre>	<b>dt[CRITERIA]</b>  <pre>&gt; late_dt &lt;- dt[t &gt; 5]</pre> <p>Note: metadata is updated when selection removes all data from one id.</p> 
Alter, create & delete (meta)variables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

A

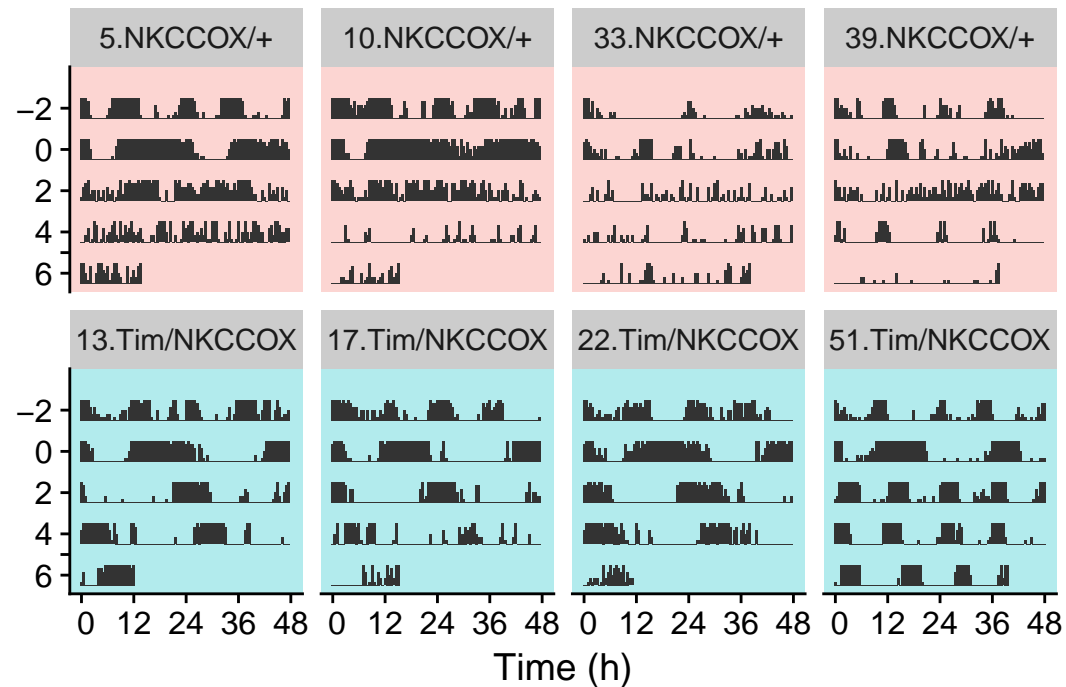
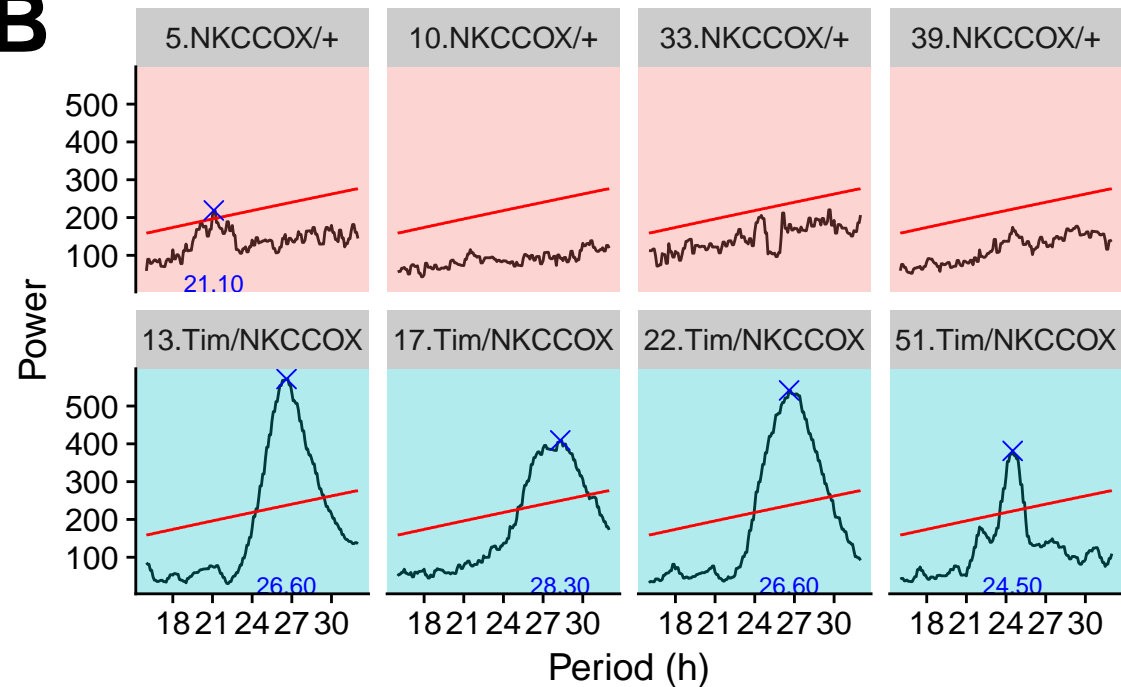
58.Tim/NKCCOX  
57.Tim/NKCCOX  
56.Tim/NKCCOX  
55.Tim/NKCCOX  
54.Tim/NKCCOX  
53.Tim/NKCCOX  
52.Tim/NKCCOX  
51.Tim/NKCCOX  
50.Tim/NKCCOX  
49.Tim/NKCCOX  
48.Tim/NKCCOX  
47.Tim/NKCCOX  
46.Tim/NKCCOX  
45.Tim/NKCCOX  
32.Tim/NKCCOX  
31.Tim/NKCCOX  
30.Tim/NKCCOX  
29.Tim/NKCCOX  
28.Tim/NKCCOX  
27.Tim/NKCCOX  
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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/+



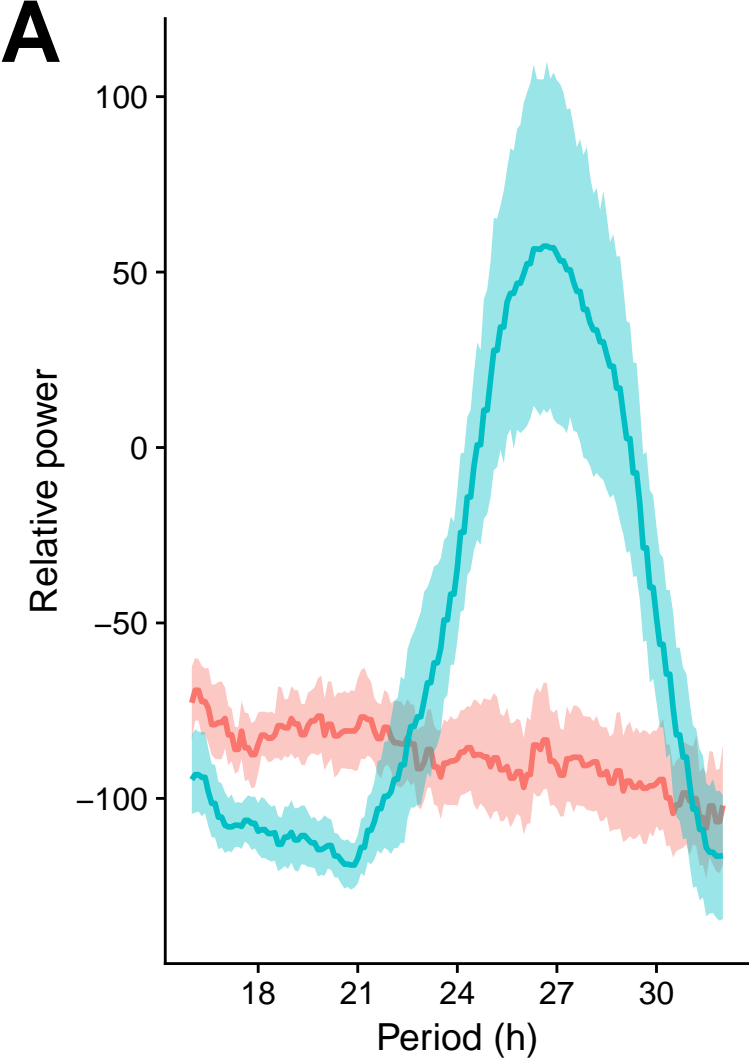
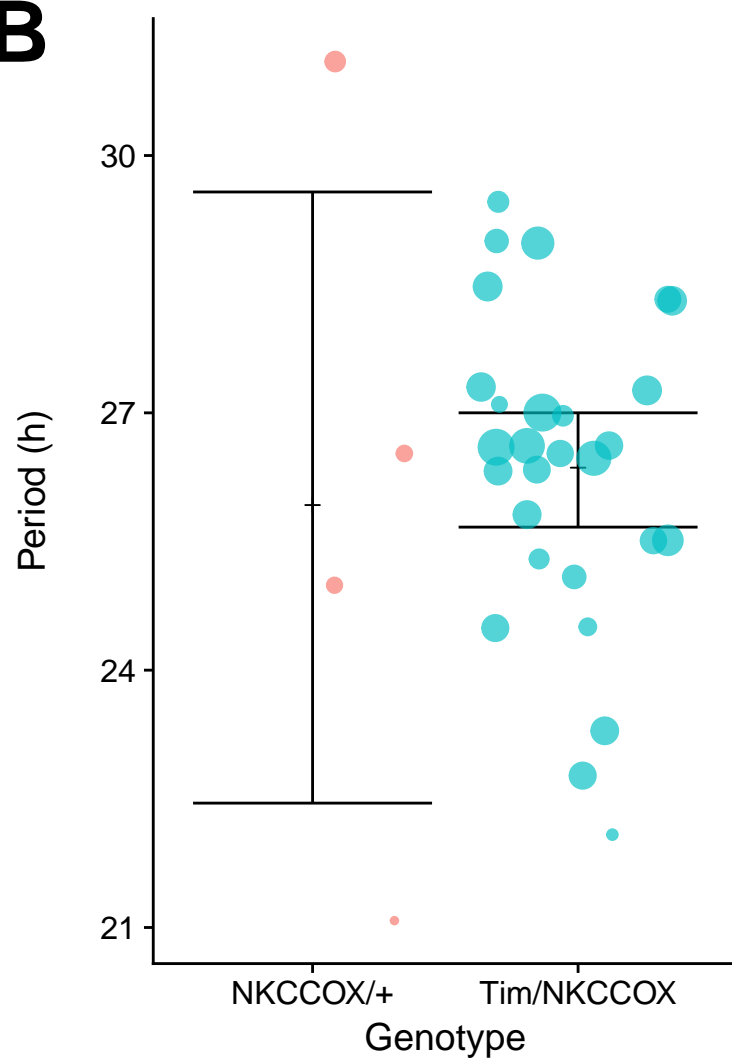
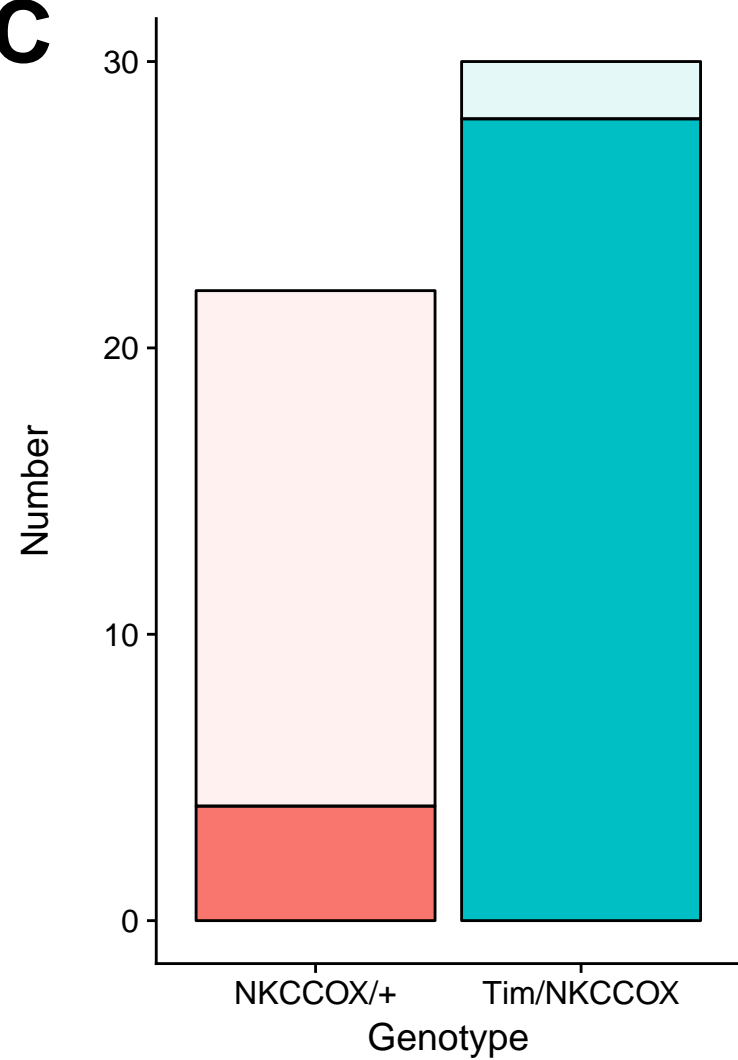
B



Moving 0% 50% 100%

**A****B**

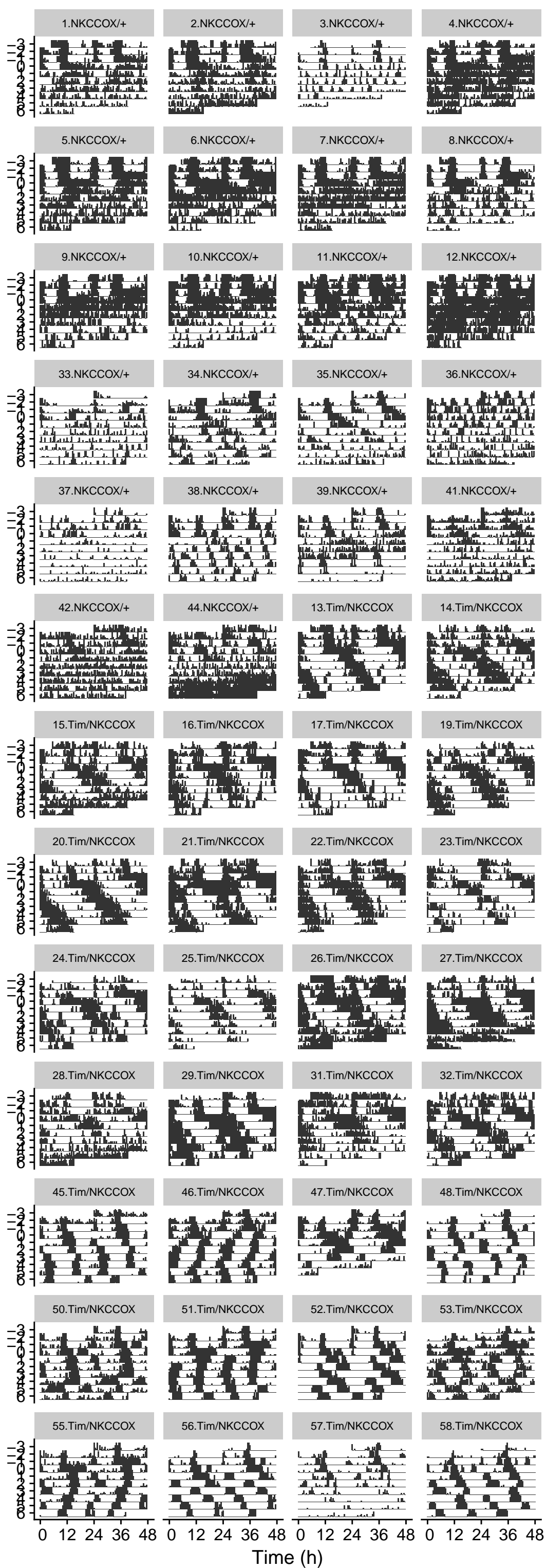
Genotype ■ *NKCCOX/+* ■ *Tim/NKCCOX*

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

Genotype ■ NKCCOX/+ ■ Tim/NKCCOX

Peak power ● 300 ● 400 ● 500

Arhythmic  Rhythmic

**A****B**