

Behaviour tracking platforms



A

Metadata

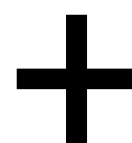
id	machine_name	date	...	condition	sex	...	p
xxx...xx x	machine_001	2016-09-01	...	A	M	...	p ₁
xxx...xx y	machine_001	2016-09-01	...	B	M	...	p ₂
xxx...xx z	machine_002	2016-09-03	...	A	F	...	p ₃
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
n	machine _n	date _n	...	condition _n	sex _n	...	p _n

Platform fields
(mandatory)

Experiment fields
(arbitrary & optional)

Data


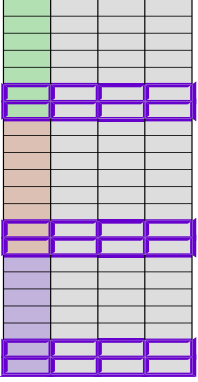
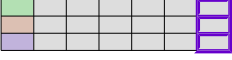
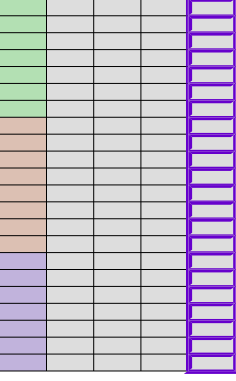
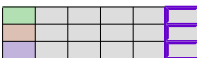
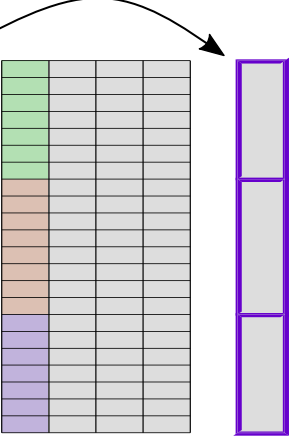
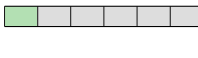
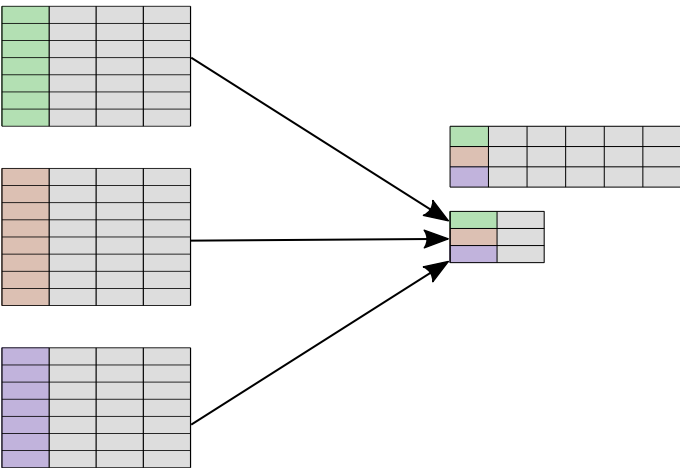
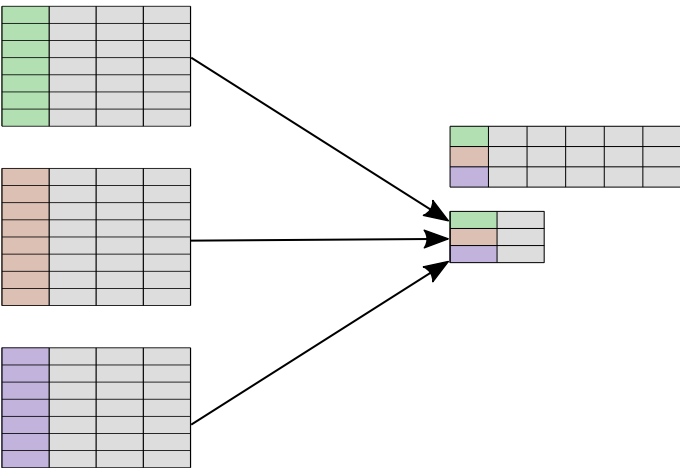
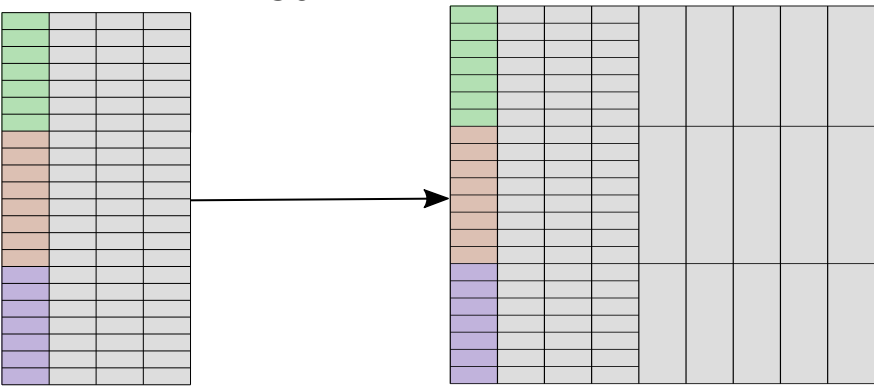
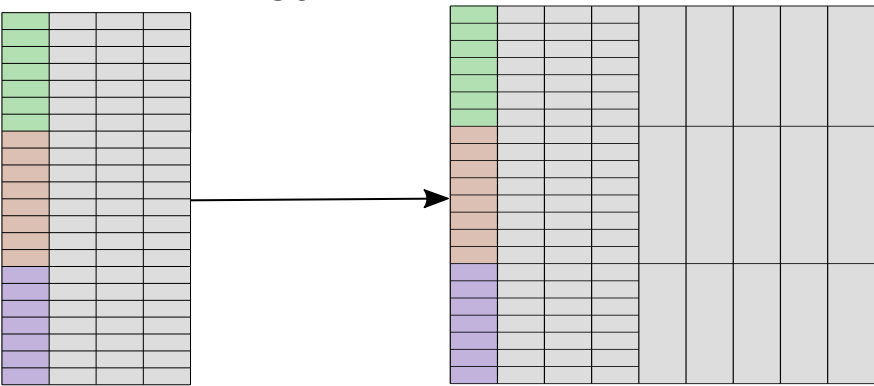
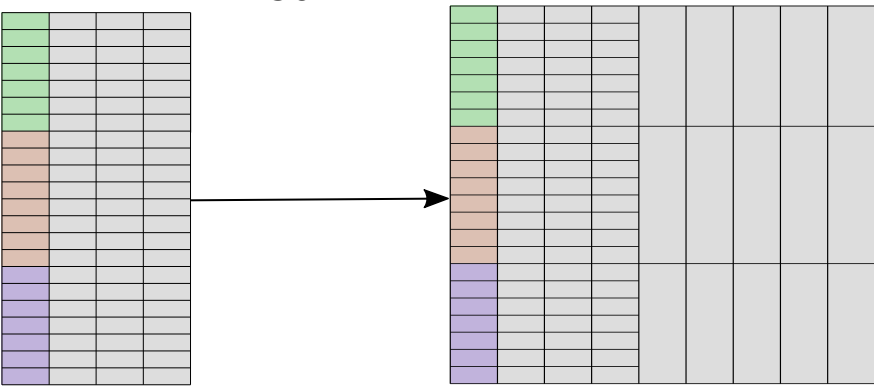
id	t	activity	...	q
xxx...xx x	1	1	⋮	q _{1,1}
xxx...xx x	2	0	⋮	q _{1,2}
xxx...xx x	3	0	⋮	q _{1,3}
xxx...xx x	⋮	⋮	⋮	⋮
xxx...xx y	⋮	⋮	⋮	⋮
xxx...xx z	1	0	⋮	q _{3,1}
xxx...xx z	2	2	⋮	q _{3,2}
xxx...xx z	3	0	⋮	q _{3,3}
xxx...xx z	⋮	⋮	⋮	⋮
⋮	⋮	⋮	⋮	⋮
n	⋮	⋮	⋮	q _{n,k_n}



B

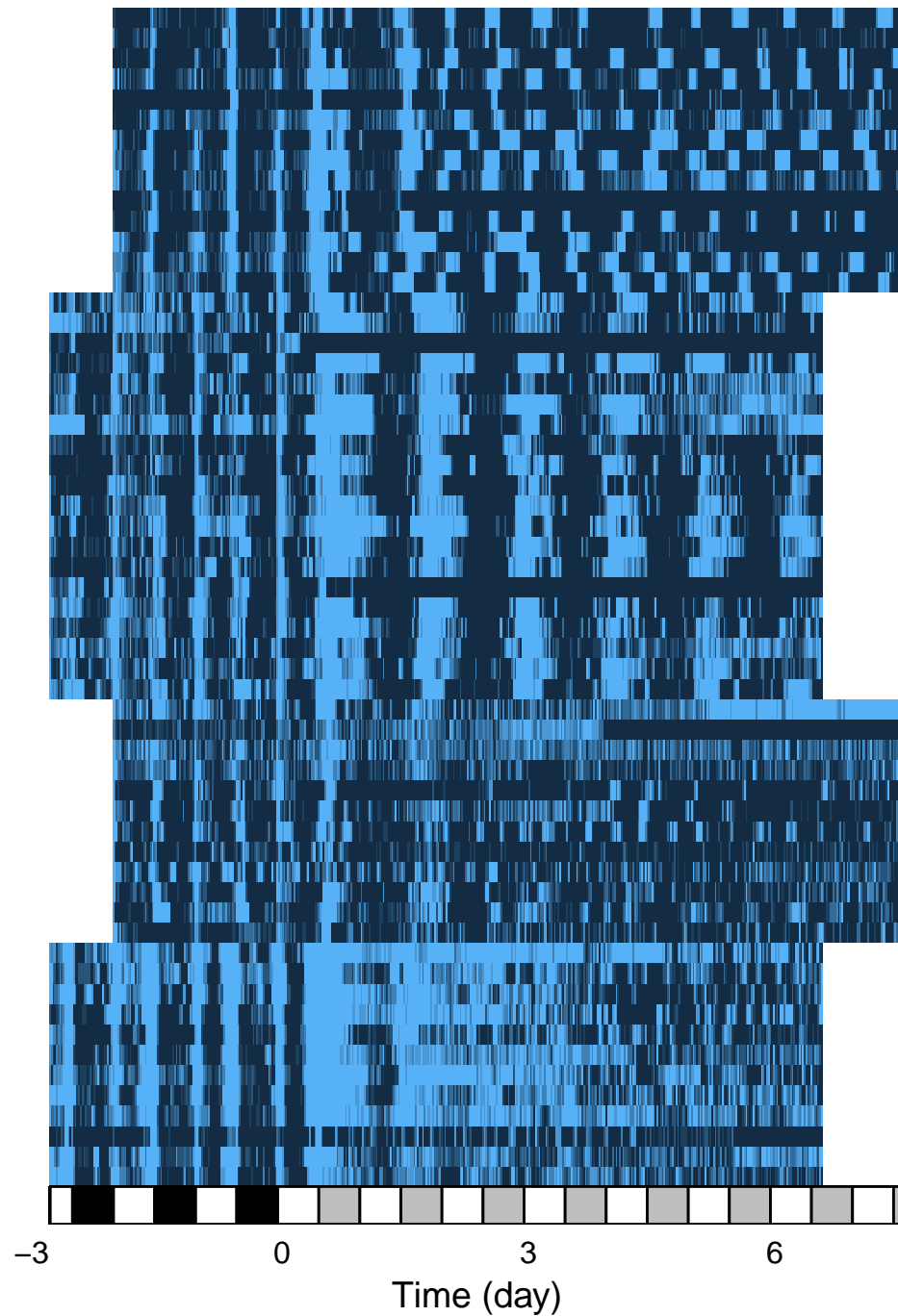
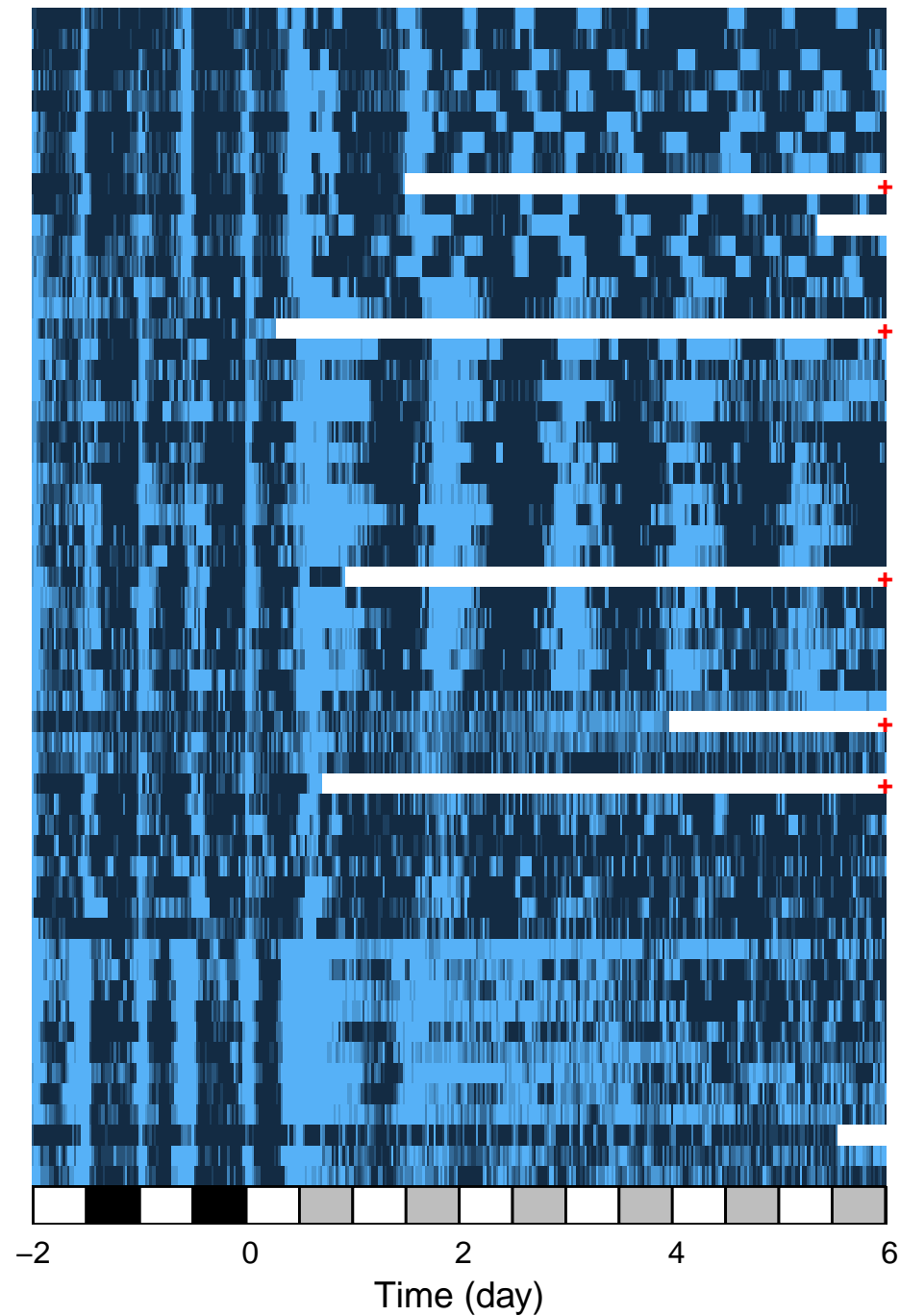
Metadata

Data

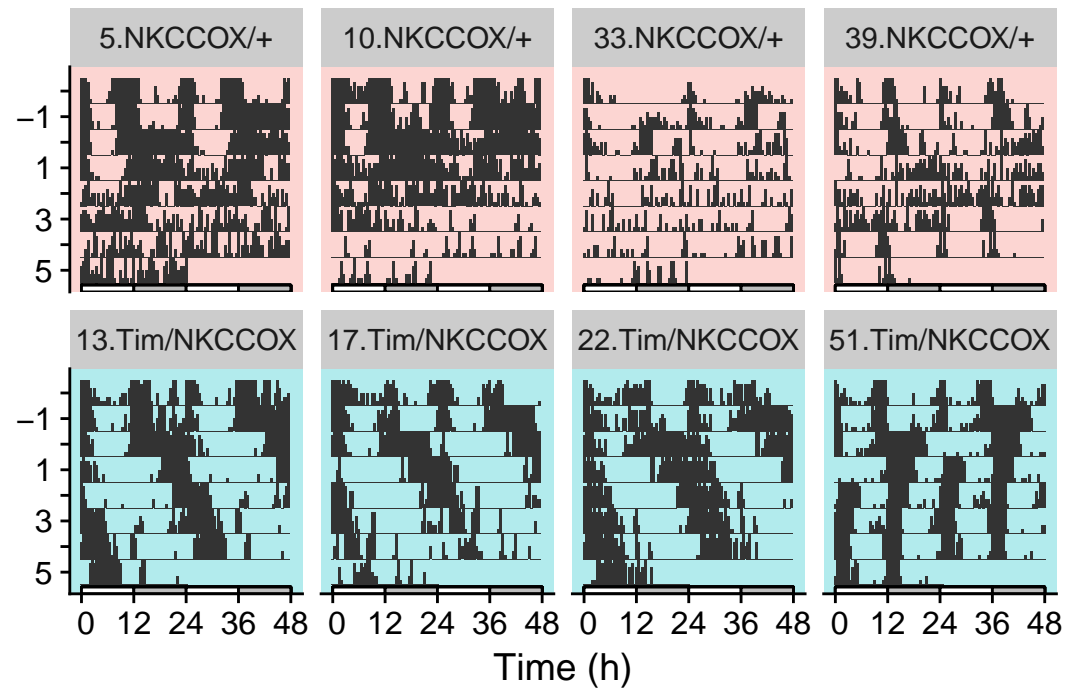
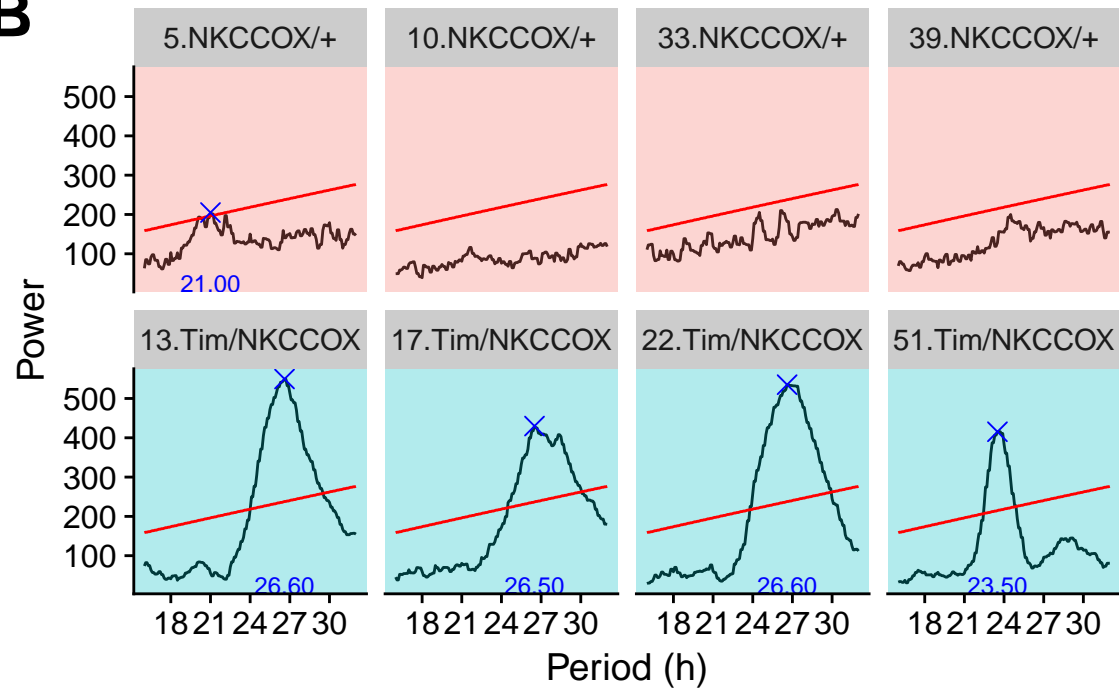
Select	dt[CRITERIA, meta = TRUE]  <pre># to subset the metadata only for males > male_meta <- dt[sex == "M", meta = TRUE]</pre>	dt[CRITERIA]  <pre># to keep only data > 5s > late_dt <- dt[t > 5]</pre> <p>Note: metadata is updated when selection removes all data from one id.</p>
Alter, create & delete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

A

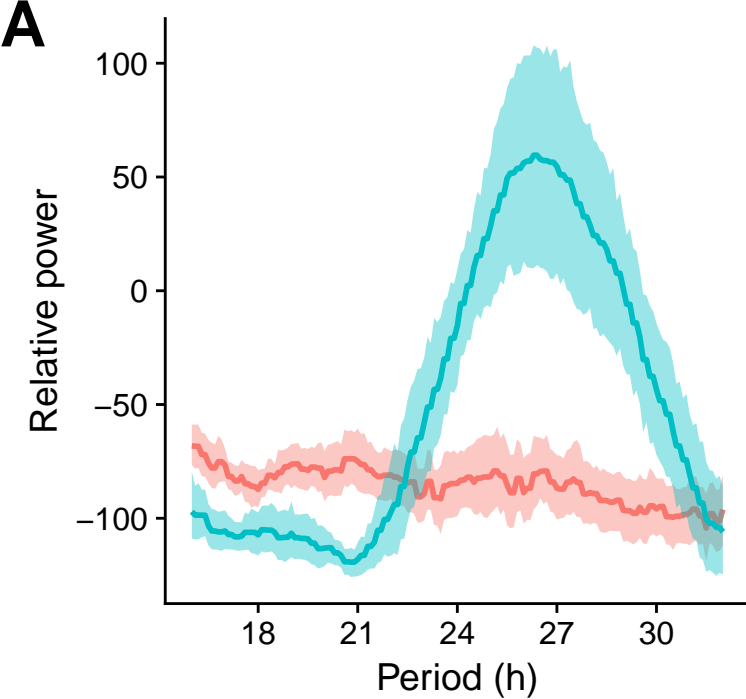
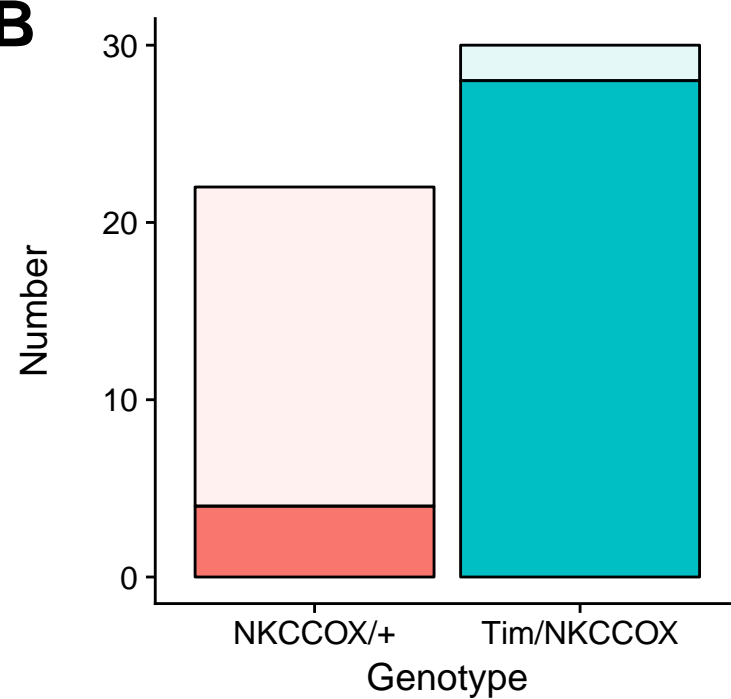
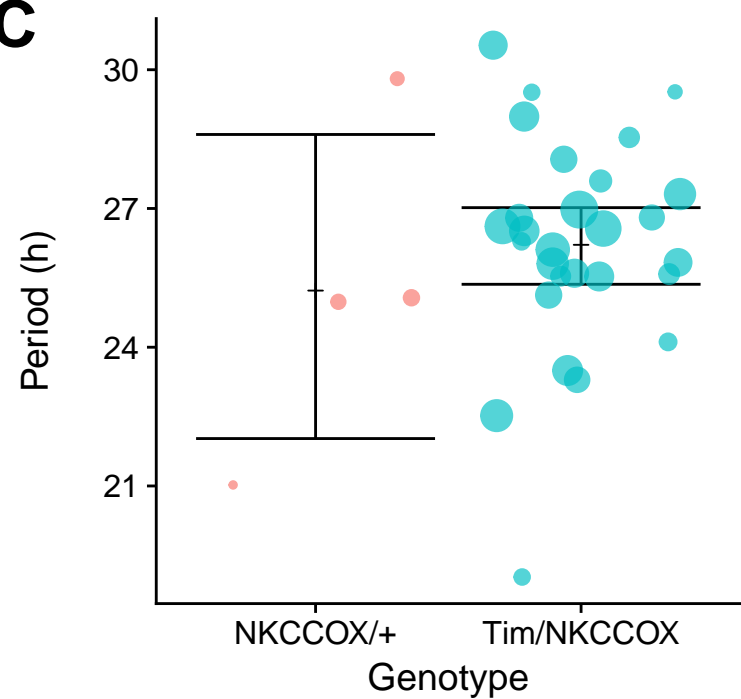
58.Tim/NKCCOX
57.Tim/NKCCOX
56.Tim/NKCCOX
55.Tim/NKCCOX
54.Tim/NKCCOX
53.Tim/NKCCOX
52.Tim/NKCCOX
51.Tim/NKCCOX
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30.Tim/NKCCOX
29.Tim/NKCCOX
28.Tim/NKCCOX
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16.Tim/NKCCOX
15.Tim/NKCCOX
14.Tim/NKCCOX
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**

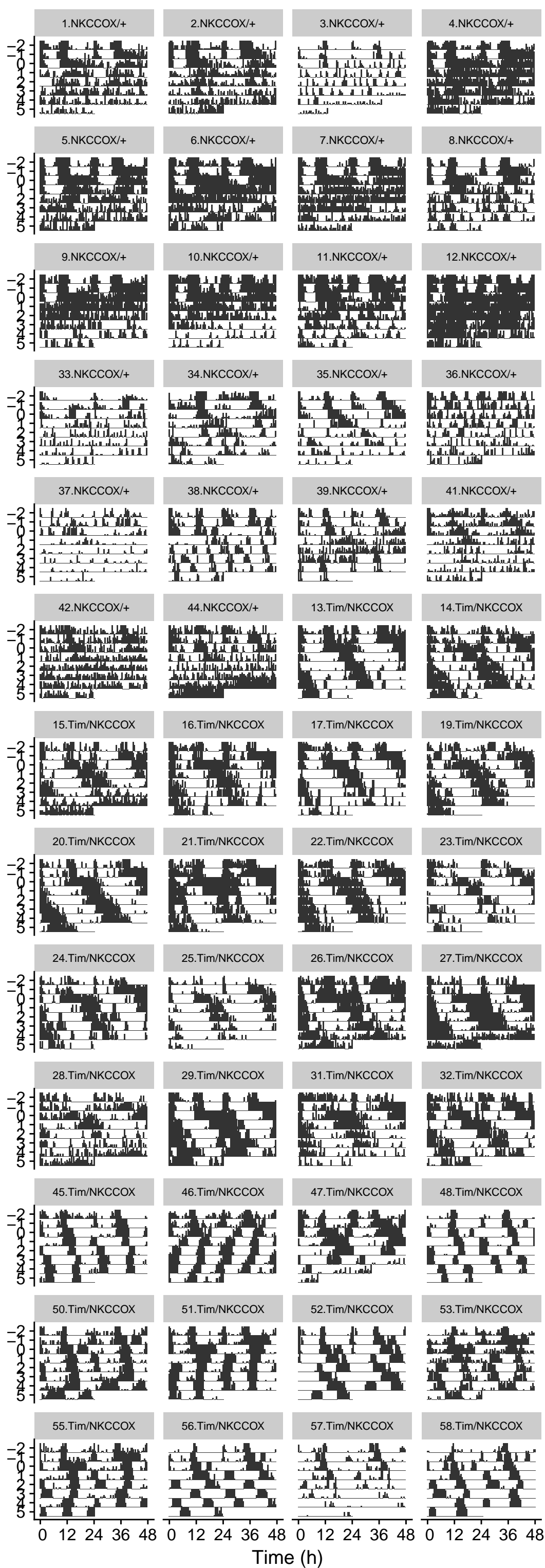
Genotype ■ *NKCCOX/+* ■ *Tim/NKCCOX*

A**B****C**

Genotype ■ NKCCOX/+ ■ Tim/NKCCOX

■ Arhythmic ■ Rhythmic

Peak relative power ● 100 ● 200 ● 300

A**B**