

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

Experiment fields

+

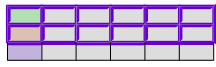
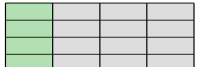
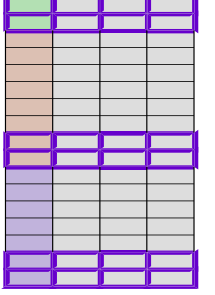
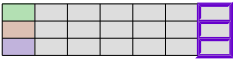
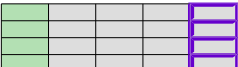
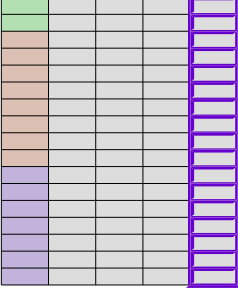
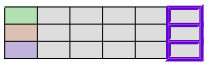
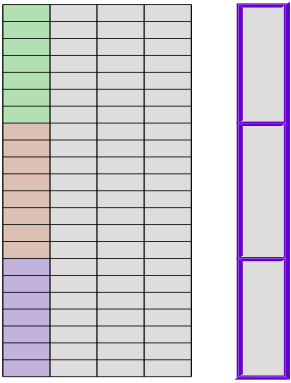

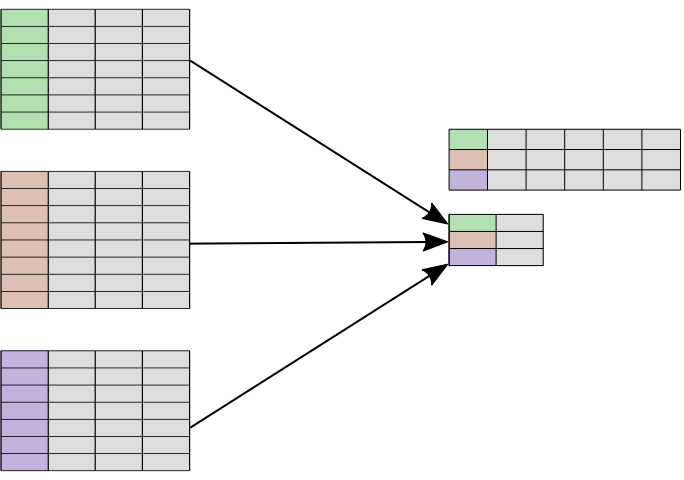
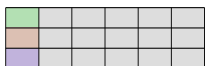
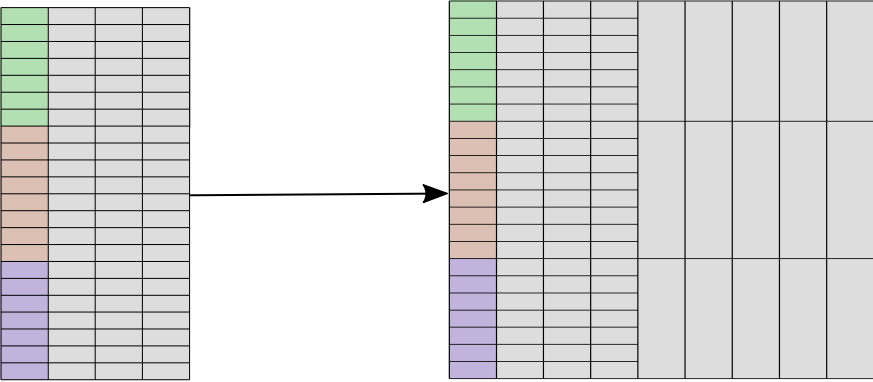
Data

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

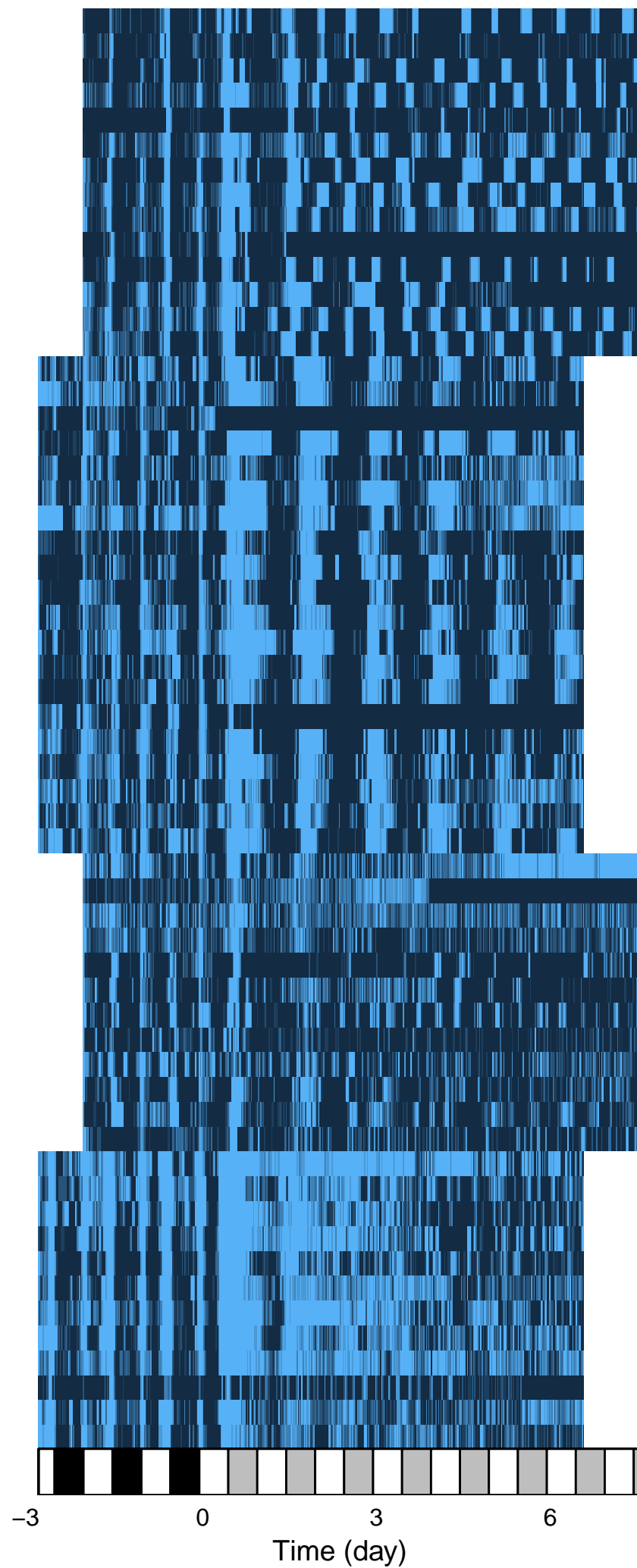
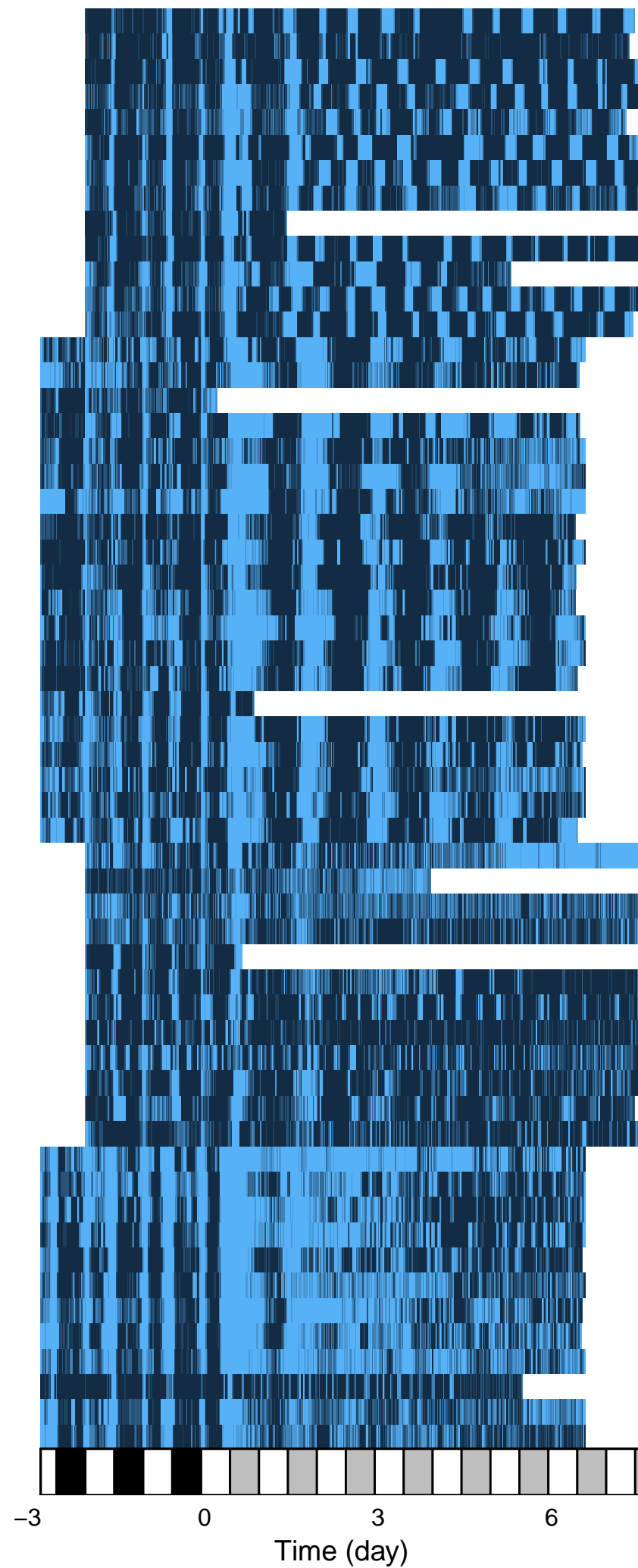
Metadata

Data

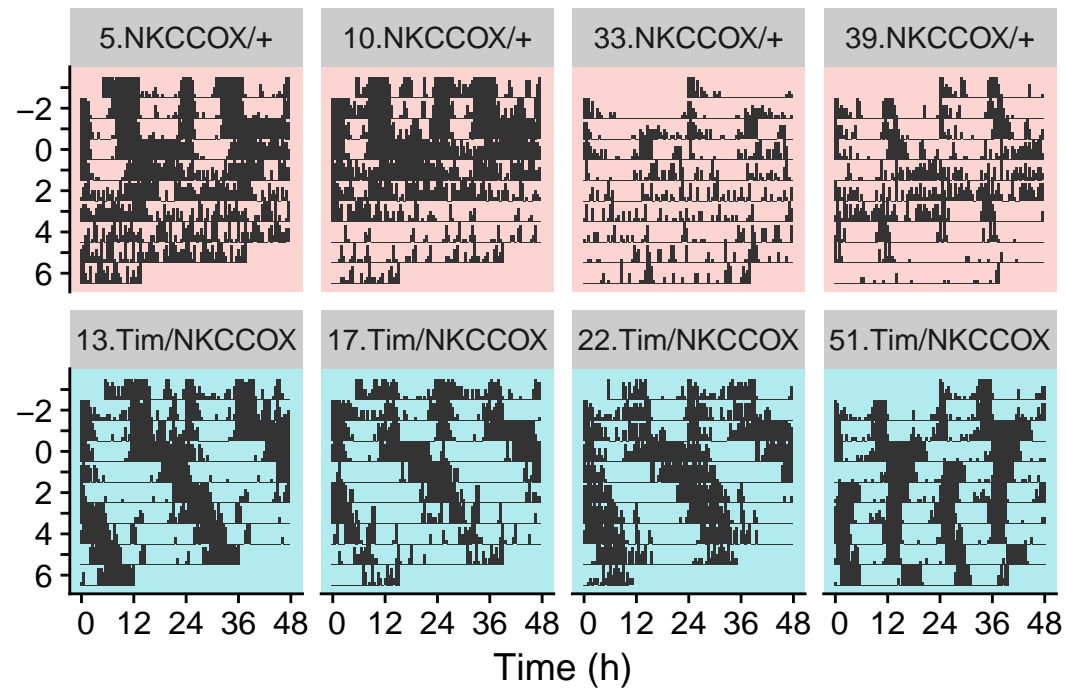
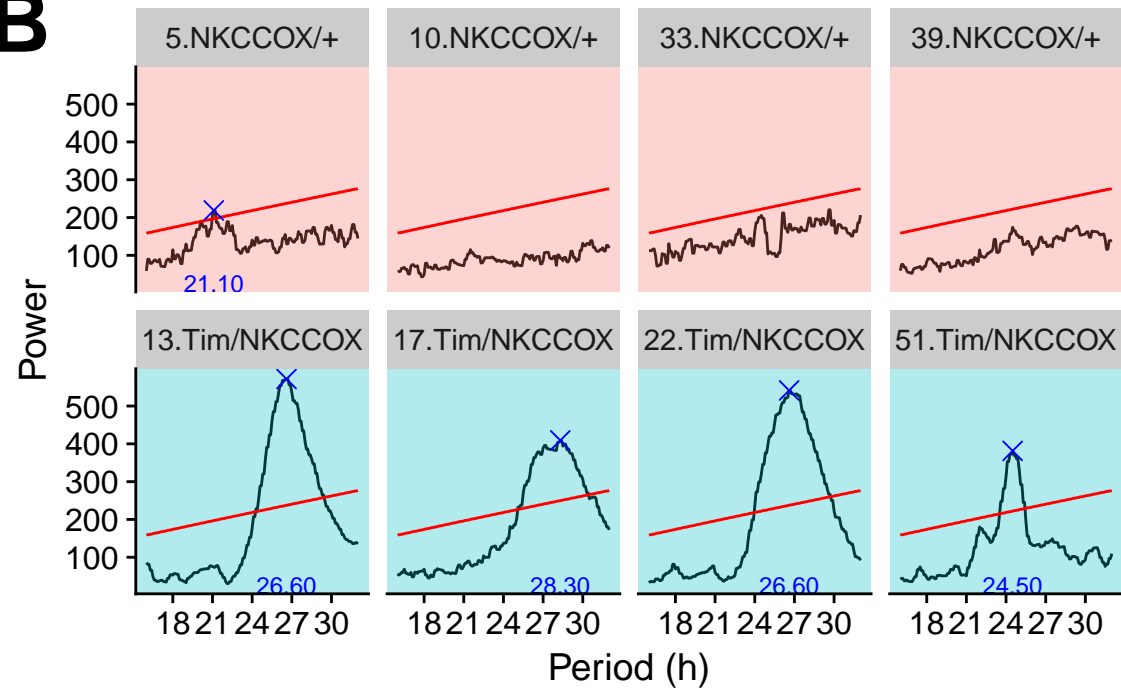
Select	dt[CRITERIA, meta = TRUE]  <pre>> male_meta <- dt[sex == "M", meta = TRUE]</pre>	dt[CRITERIA]  <pre>> late_dt <- dt[t > 5]</pre> <p>Note: metadata is updated when selection removes all data from one id.</p> 
Alter, create & delete (meta)variables	dt[, X := value, meta = TRUE]  <pre>> dt[, genotype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

A

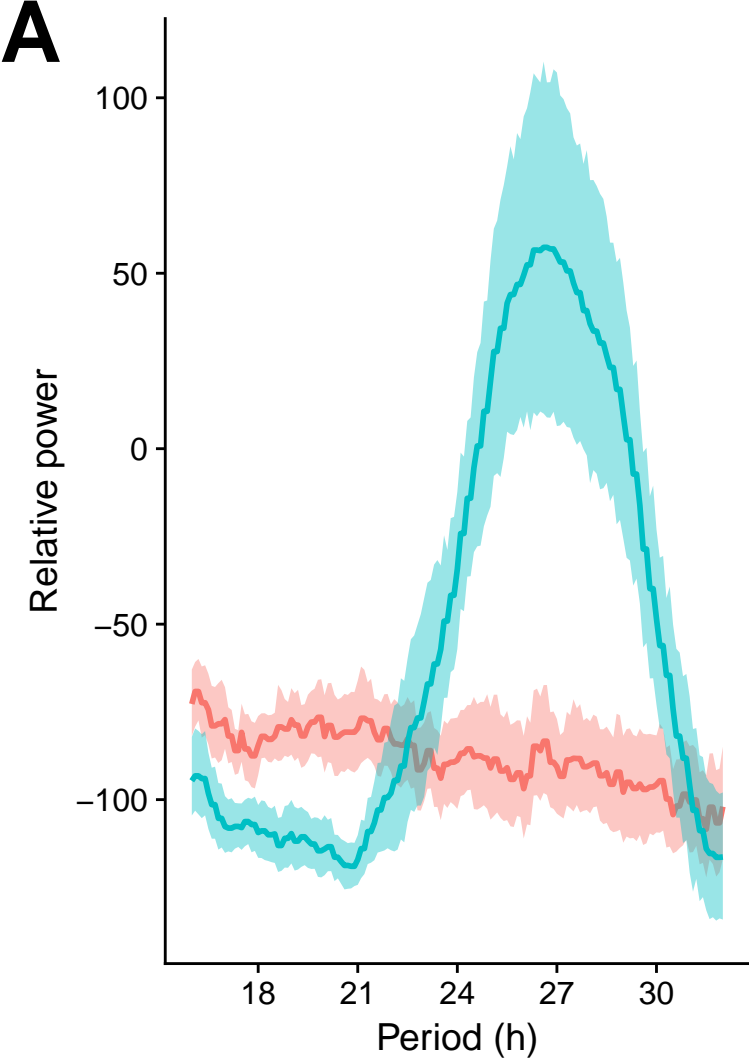
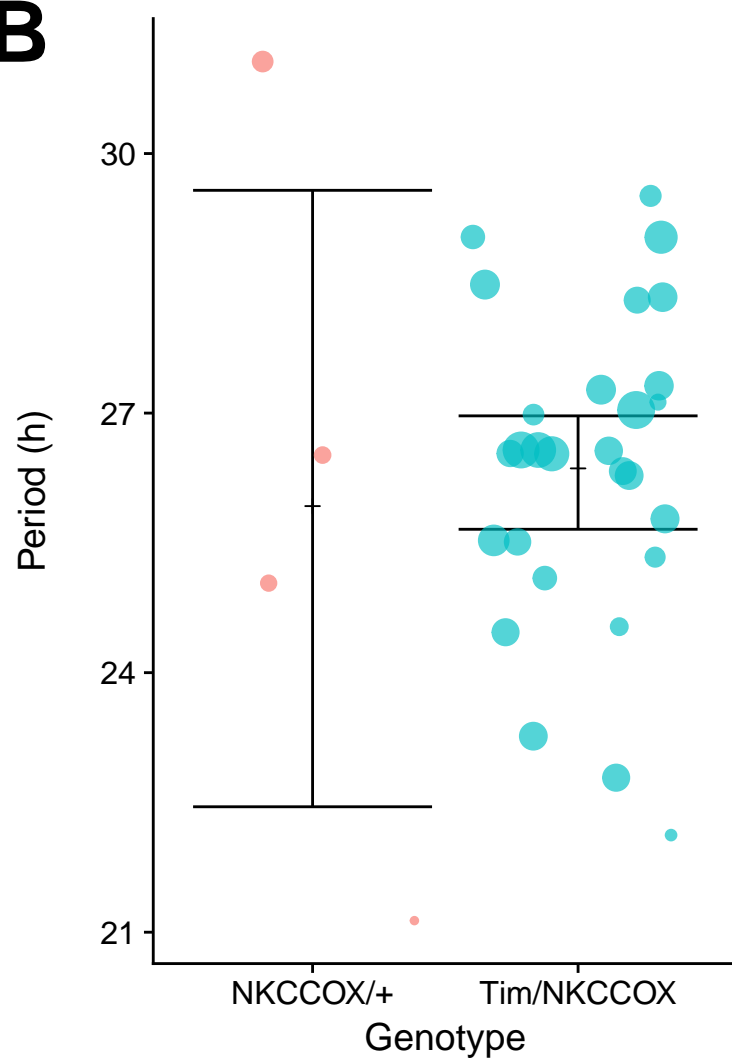
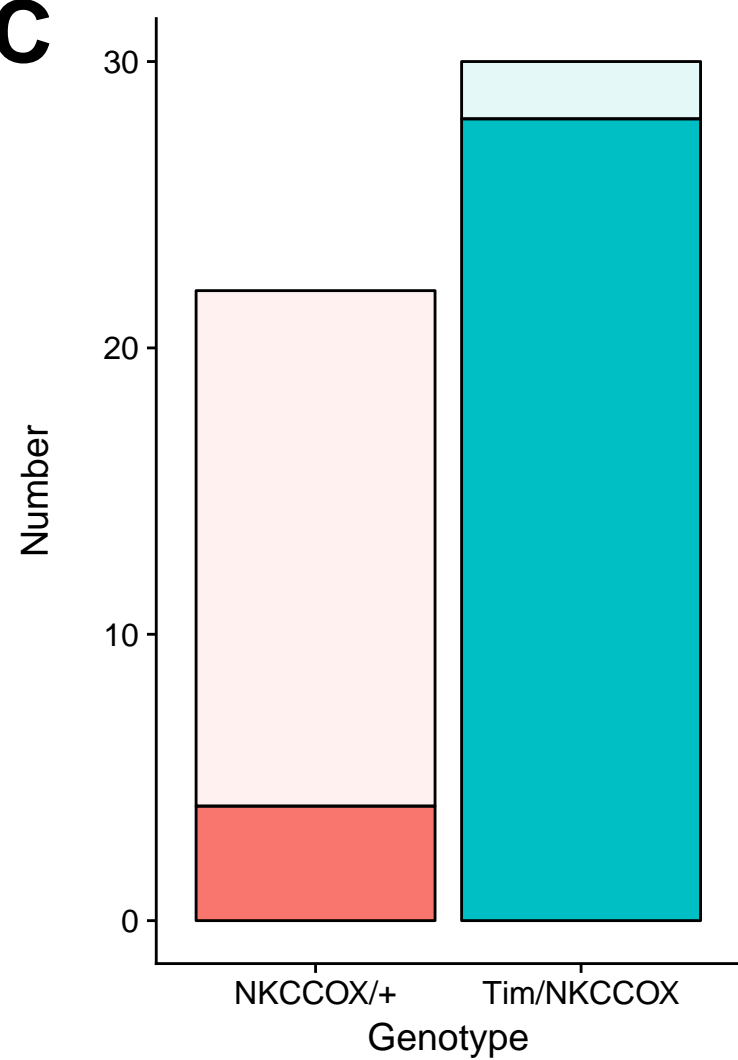
58.Tim/NKCCOX
57.Tim/NKCCOX
56.Tim/NKCCOX
55.Tim/NKCCOX
54.Tim/NKCCOX
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44.NKCCOX/+
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39.NKCCOX/+
38.NKCCOX/+
37.NKCCOX/+
36.NKCCOX/+
35.NKCCOX/+
34.NKCCOX/+
33.NKCCOX/+
12.NKCCOX/+
11.NKCCOX/+
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9.NKCCOX/+
8.NKCCOX/+
7.NKCCOX/+
6.NKCCOX/+
5.NKCCOX/+
4.NKCCOX/+
3.NKCCOX/+
2.NKCCOX/+
1.NKCCOX/+

**B**

Moving 0% 50% 100%

A**B**

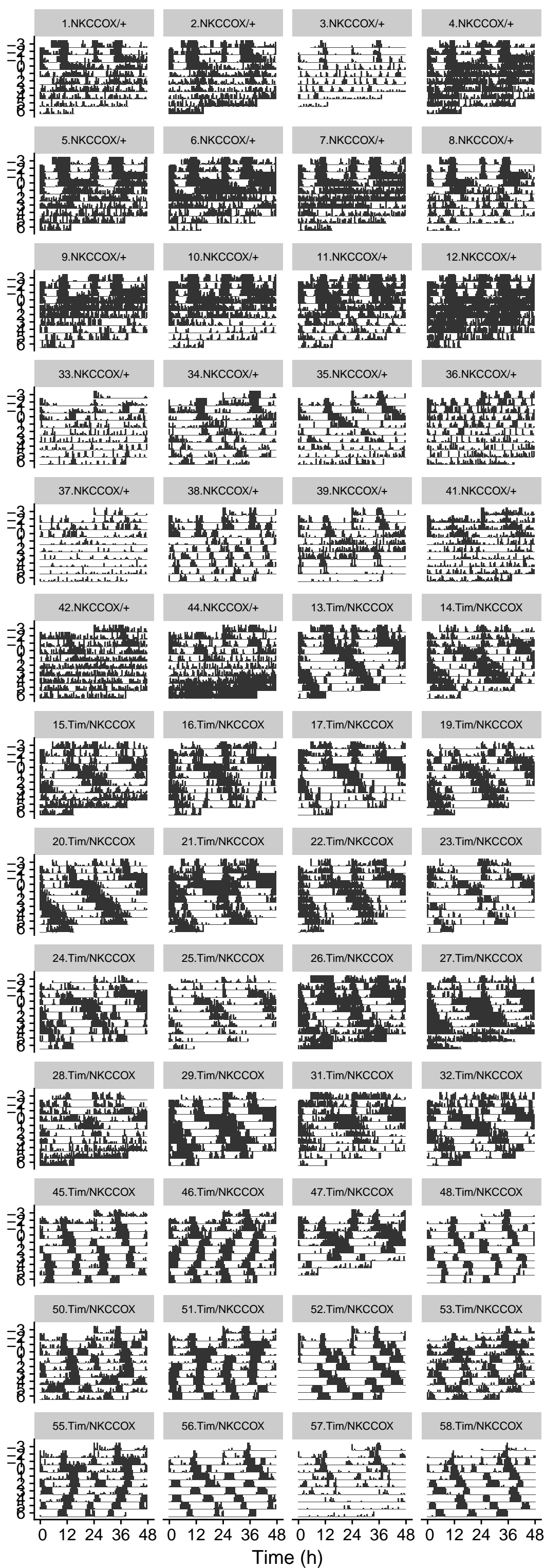
Genotype ■ NKCCOX/+ ■ Tim/NKCCOX

A**B****C**

Genotype ■ NKCCOX/+ ■ Tim/NKCCOX

Peak power ● 300 ● 400 ● 500

■ Arhythmic ■ Rhythmic

A**B**