

Behaviour tracking platforms



A

Metadata

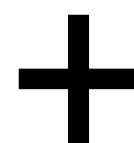
| id | machine_name | date | ... | condition | sex | ... | p |
|------------|----------------------|-------------------|-----|------------------------|------------------|-----|----------------|
| xxx...xx x | machine_001 | 2016-09-01 | ... | A | M | ... | p ₁ |
| xxx...xx y | machine_001 | 2016-09-01 | ... | 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


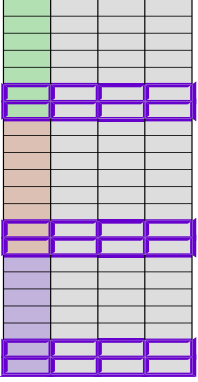
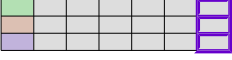
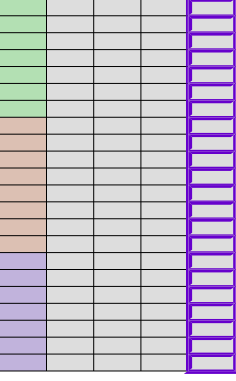
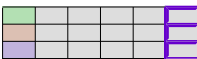
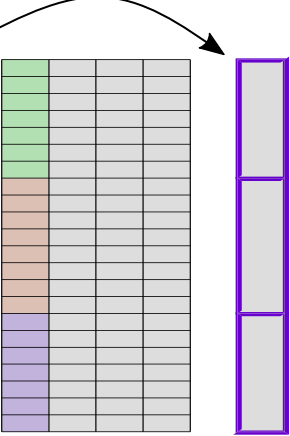

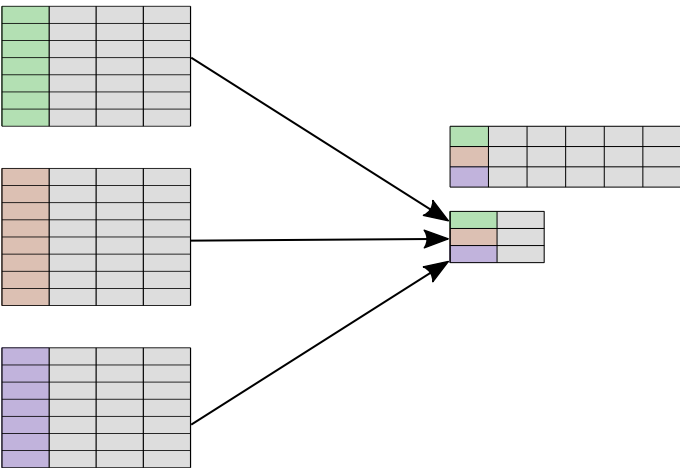
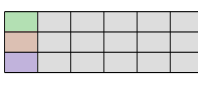
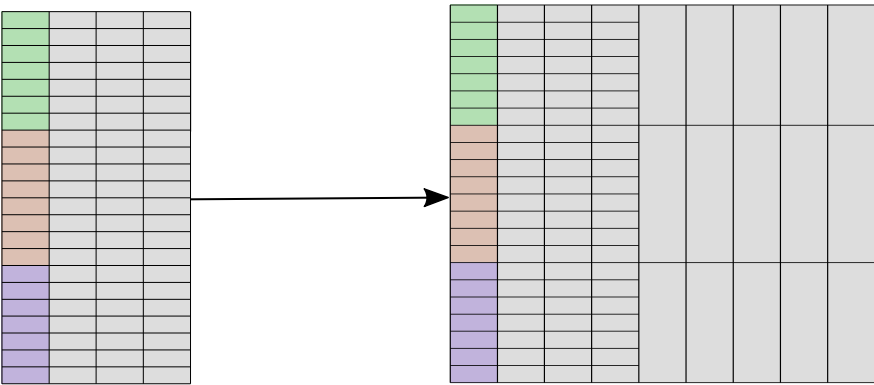
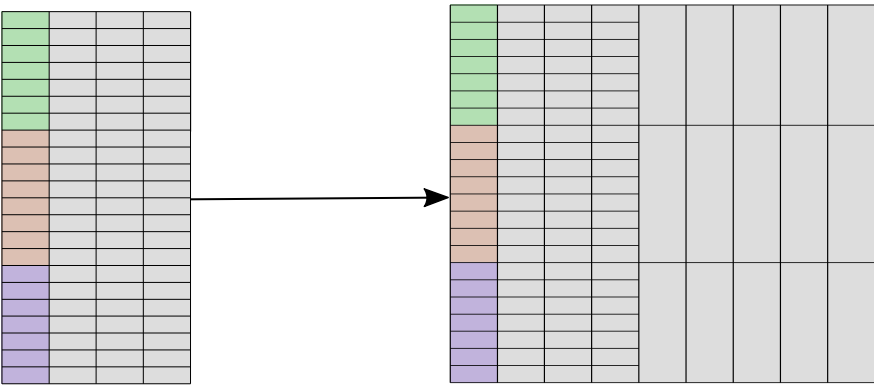
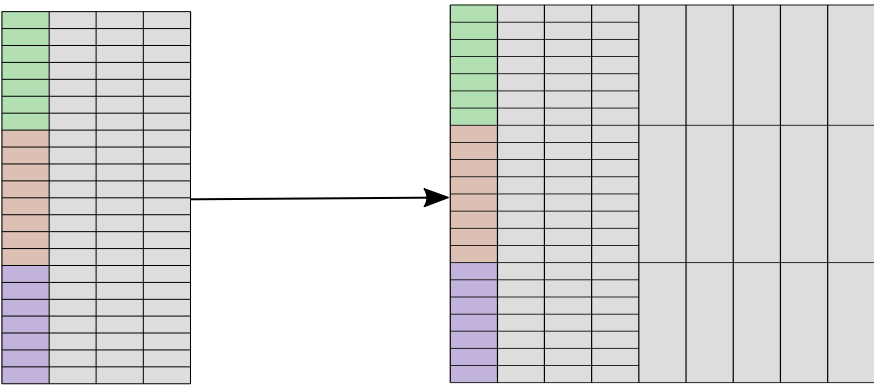
| id | t | activity | ... | q |
|------------|---|----------|-----|------------------------------|
| xxx...xx x | 1 | 1 | ⋮ | q _{1,1} |
| xxx...xx x | 2 | 0 | ⋮ | q _{1,2} |
| xxx...xx x | 3 | 0 | ⋮ | q _{1,3} |
| xxx...xx x | ⋮ | ⋮ | ⋮ | ⋮ |
| xxx...xx y | ⋮ | ⋮ | ⋮ | ⋮ |
| xxx...xx z | 1 | 0 | ⋮ |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

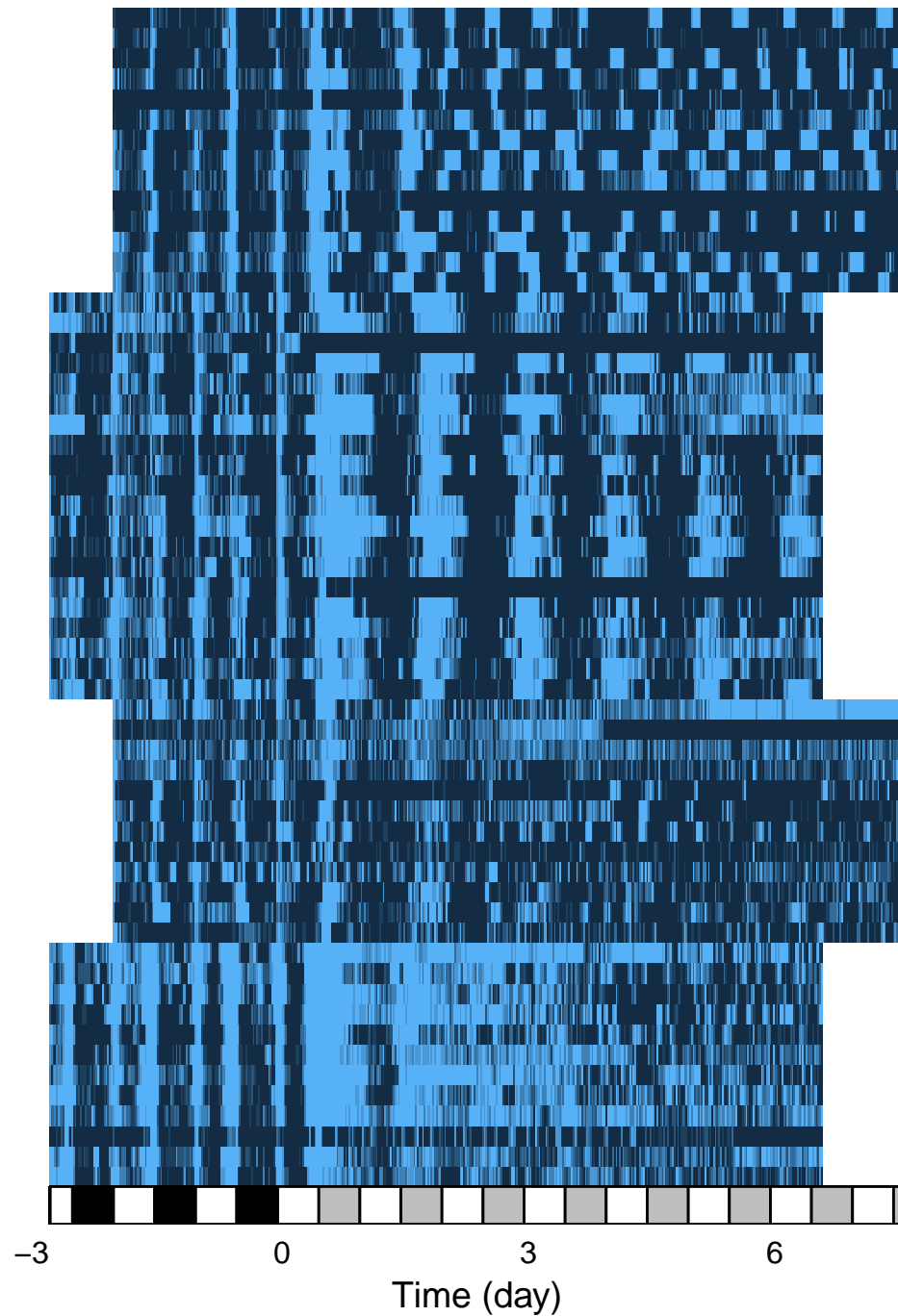
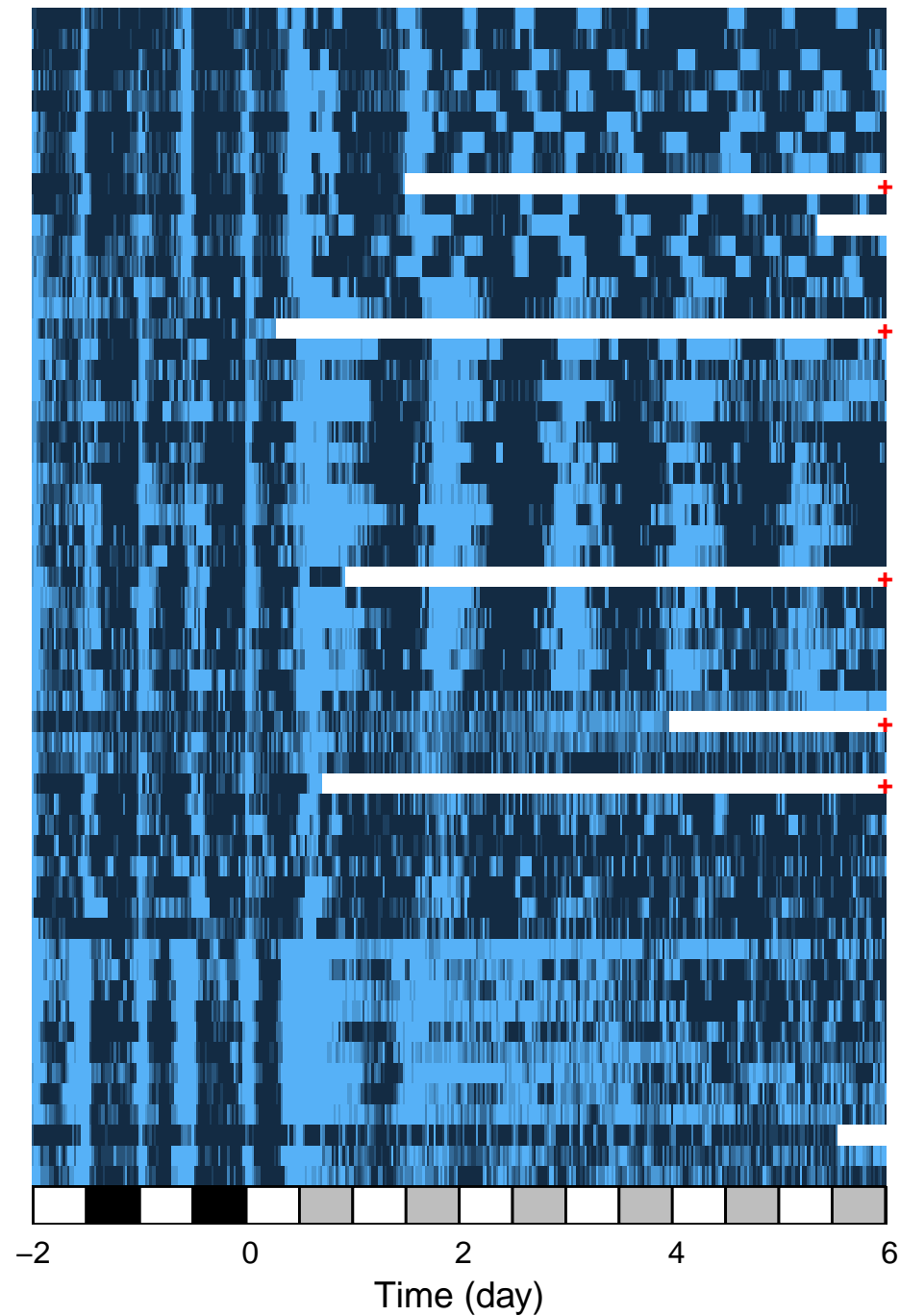
Metadata

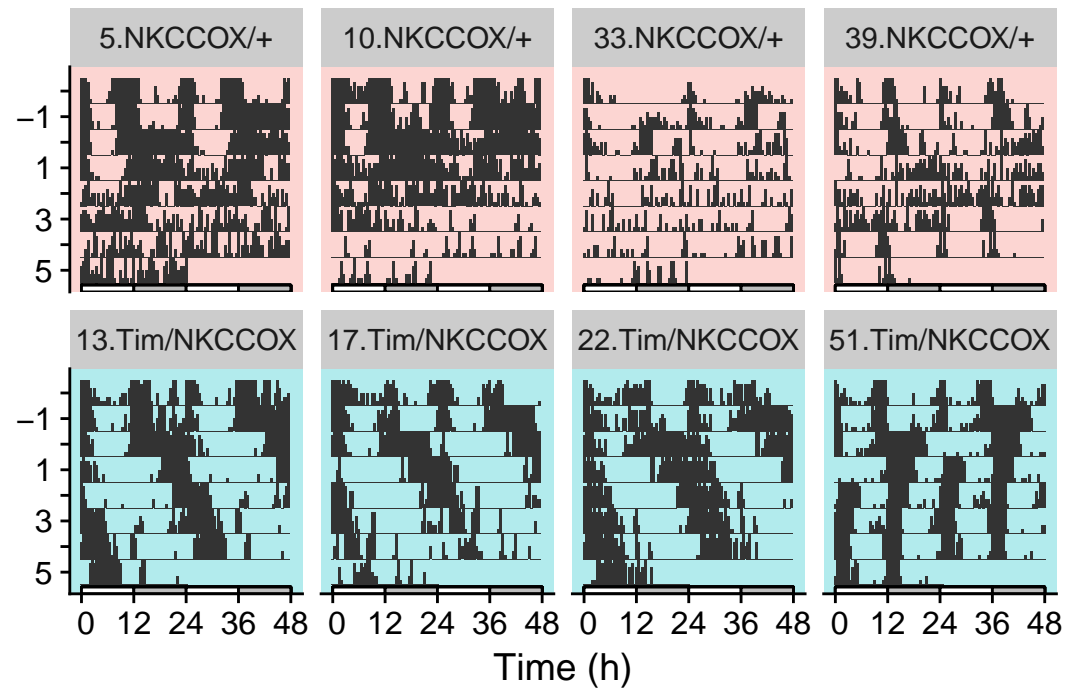
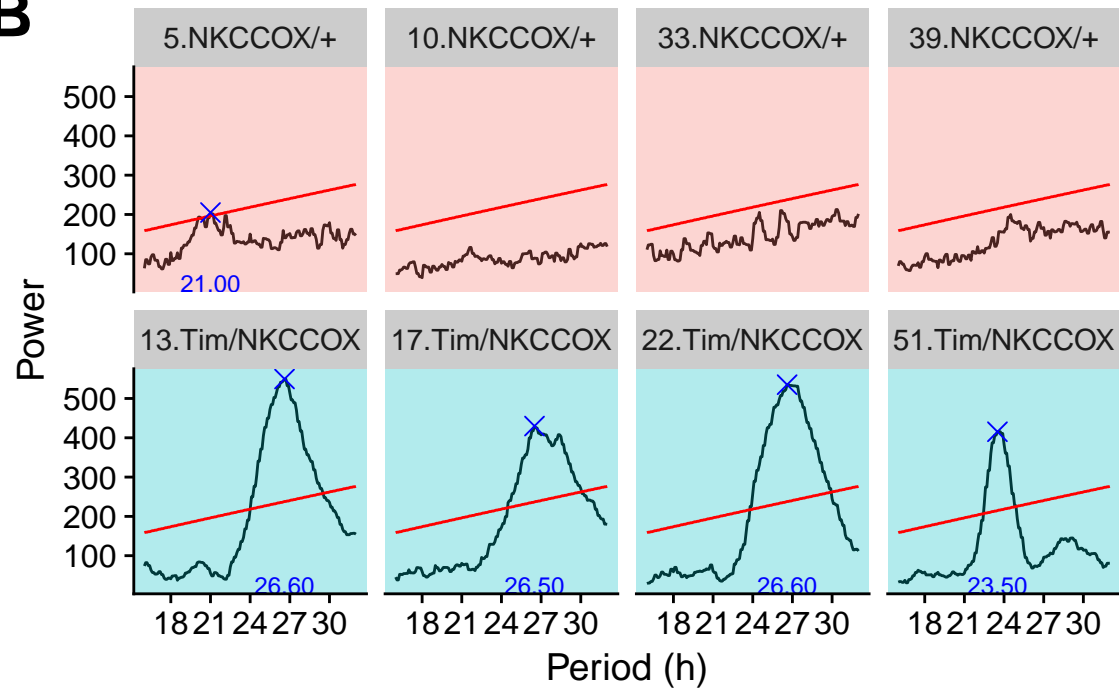
Data

| | | |
|---|--|---|
| Select | dt[CRITERIA, meta = TRUE]  <pre># to subet 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  |

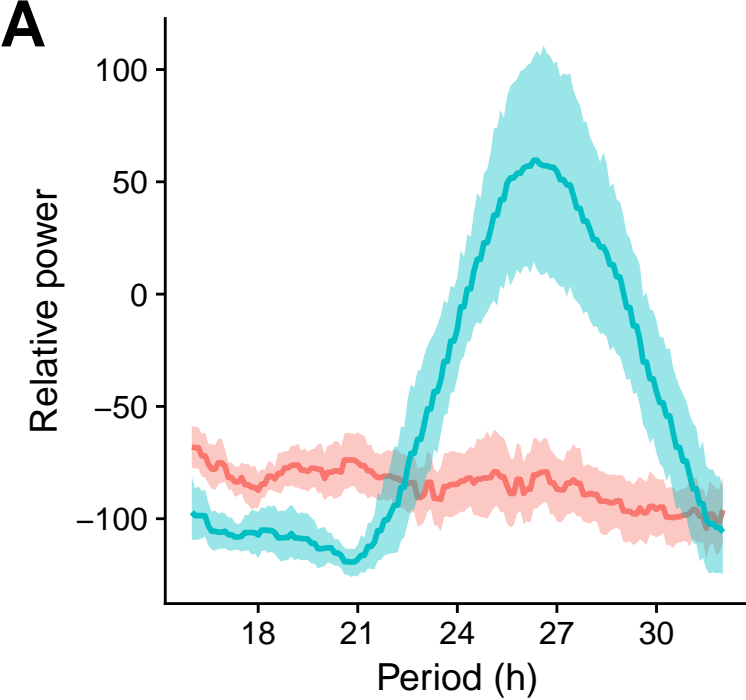
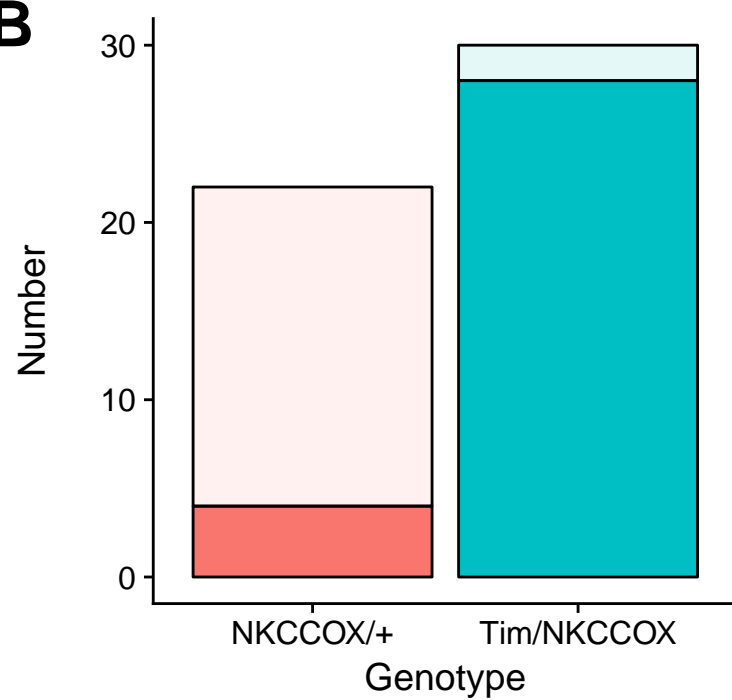
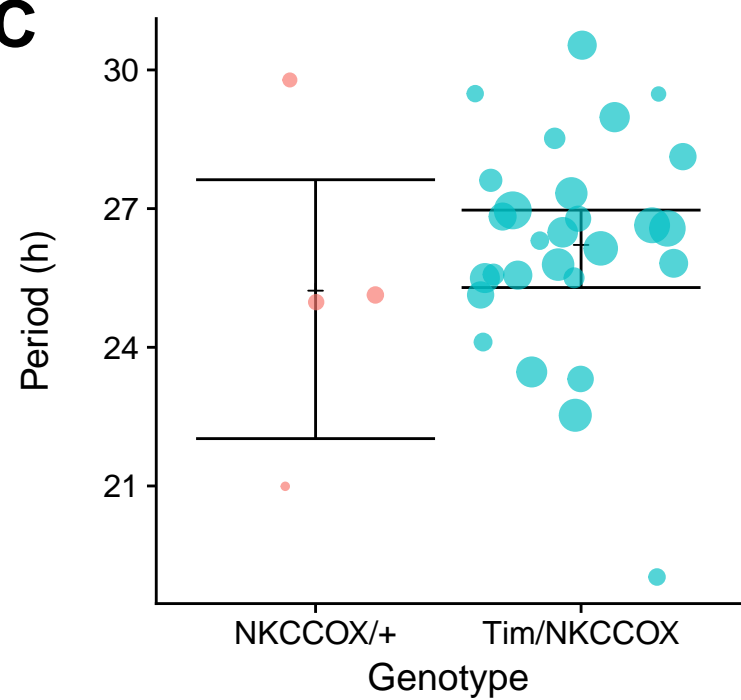
A

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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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**

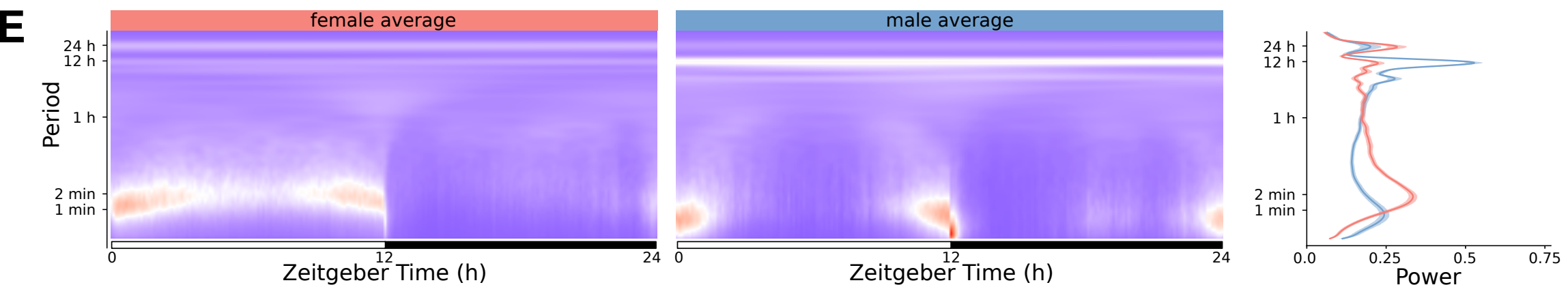
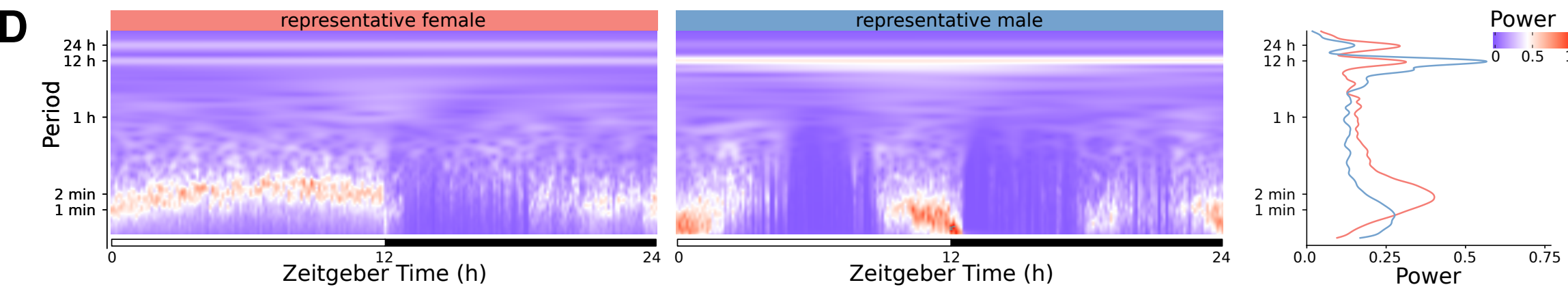
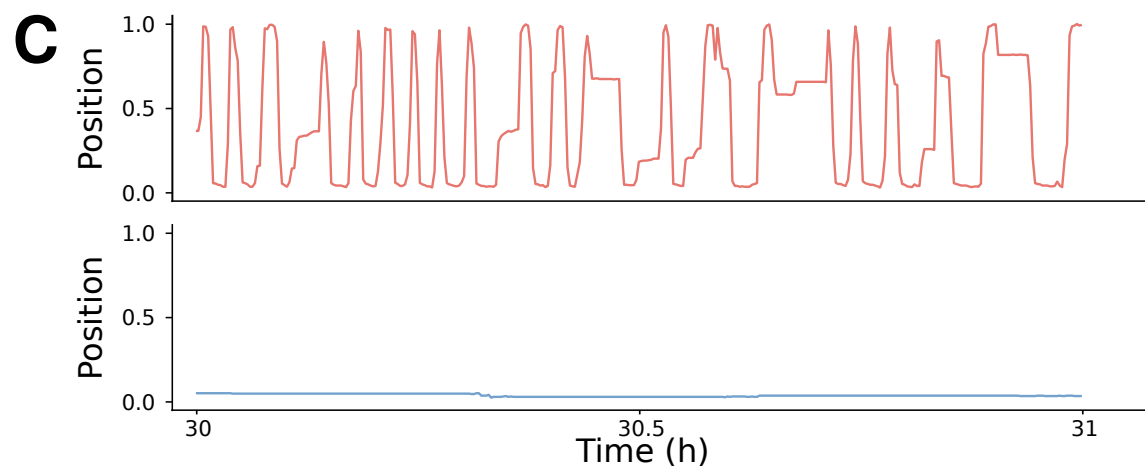
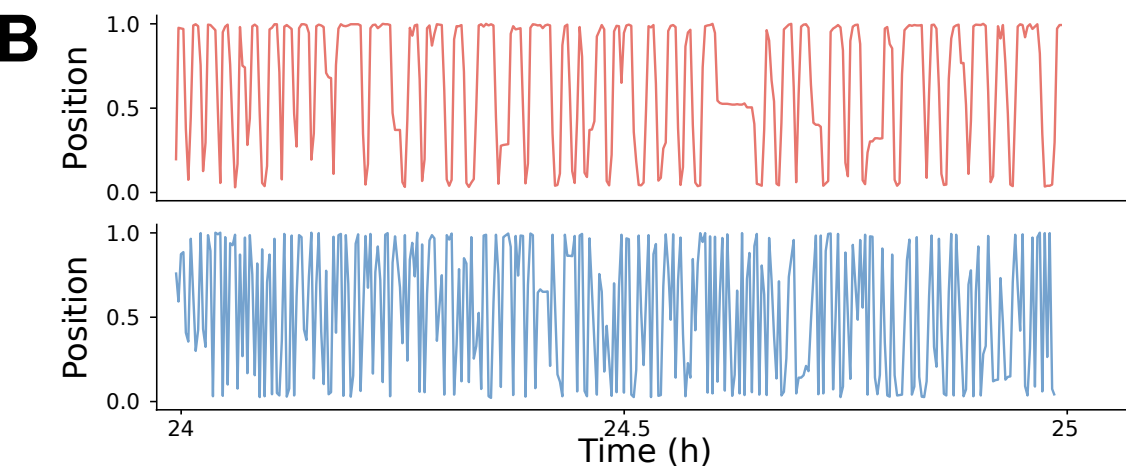
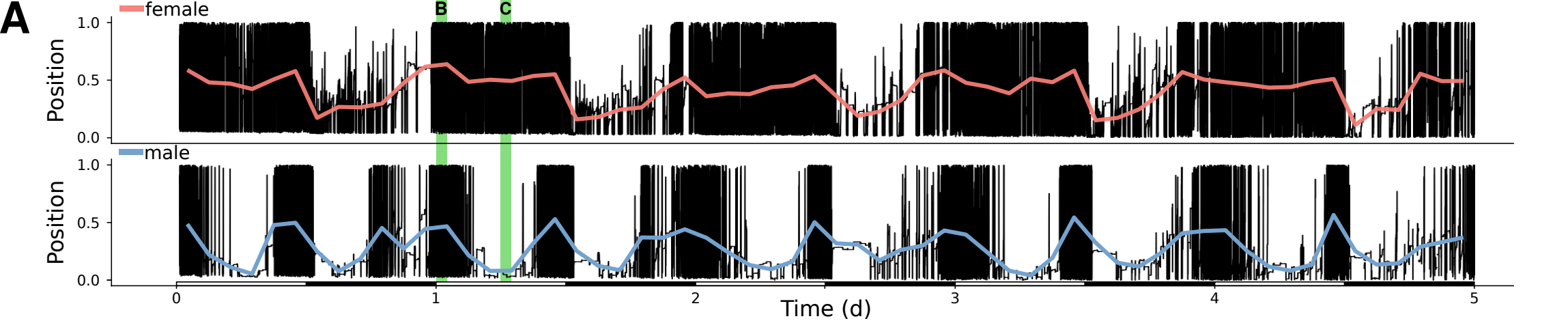
Genotype ■ *NKCCOX/+* ■ *Tim/NKCCOX*

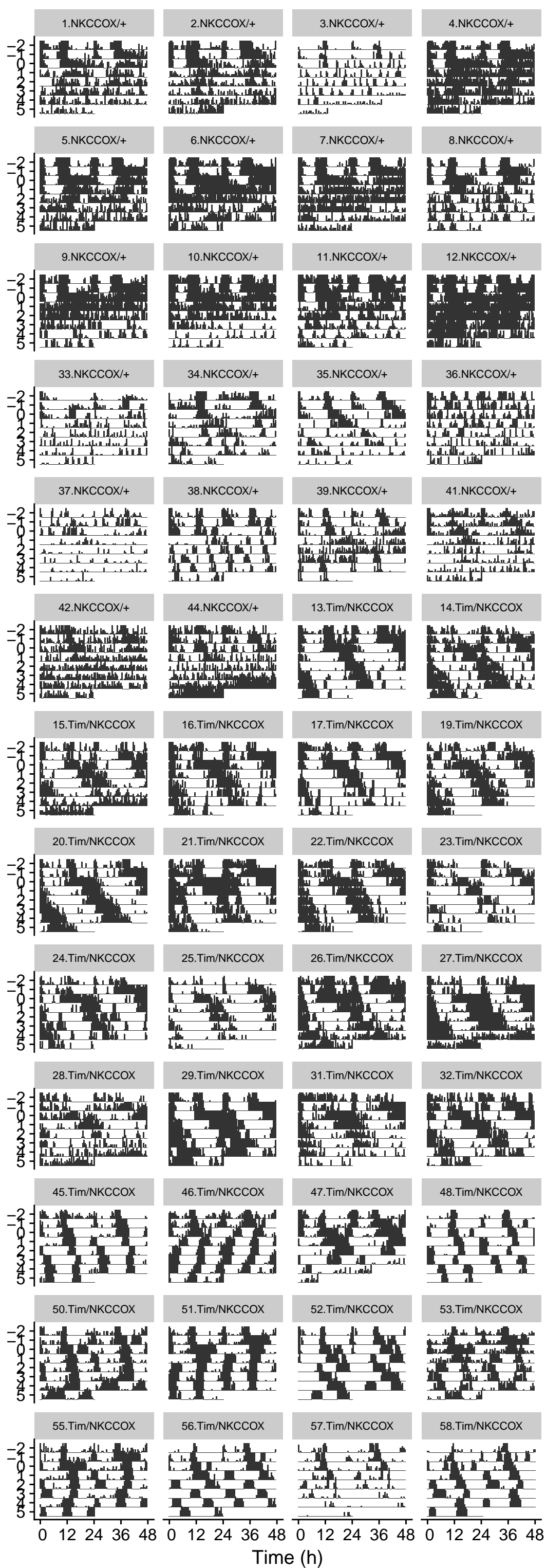
A**B****C**

Genotype ■ NKCCOX/+ ■ Tim/NKCCOX

■ Arhythmic ■ Rhythmic

Peak relative power ● 100 ● 200 ● 300



A**B**