

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

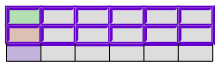
Data

| 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} |

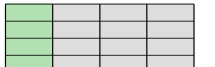
+

B

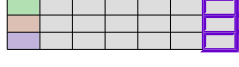
Metadata

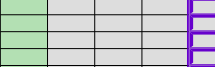
| | |
|--------|--|
| Select | dt[CRITERIA, meta = TRUE]  <pre>> male_meta <- dt[sex == "M", meta = TRUE]</pre> |
|--------|--|

Data

| |
|--|
| dt[CRITERIA]  <pre>> late_dt <- dt[t > 5]</pre> <p>Note: metadata is updated when selection removes all data from one id.</p> |
|--|

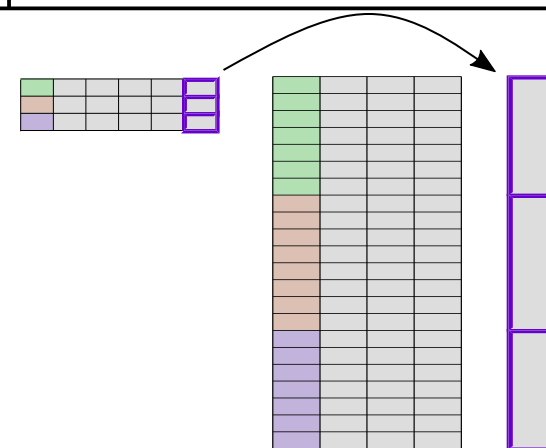
Alter, create & delete
(meta)variables

| |
|---|
| dt[, X := value, meta = TRUE]  <pre>> dt[, genotype := "wt", meta = TRUE] > dt[, sex := NULL] #delete sex</pre> |
|---|

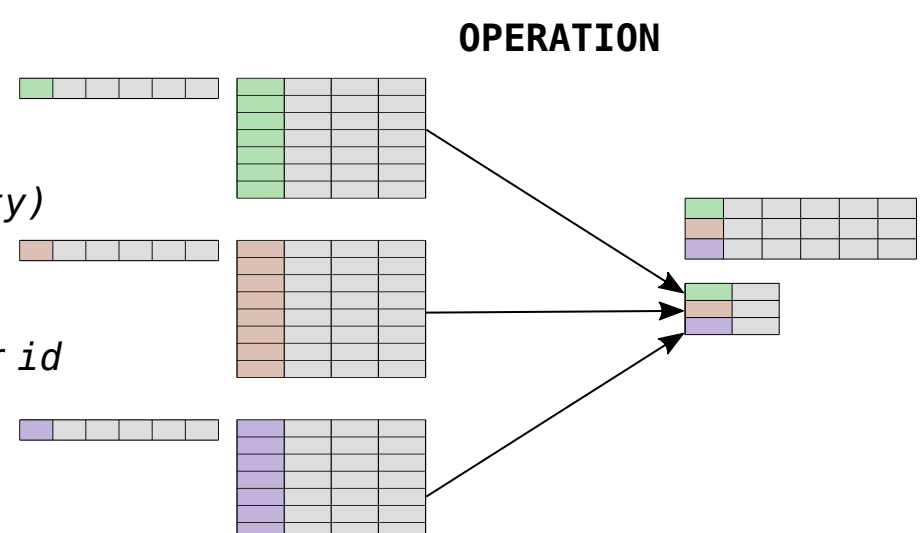
| |
|---|
| dt[, Y := value]  <pre>> dt[, t_2 := t-1] > dt[, t := NULL] #delete t</pre> <p>Note: update data in place. No copy of dt in memory.</p> |
|---|

Expand
metavariables
as variables

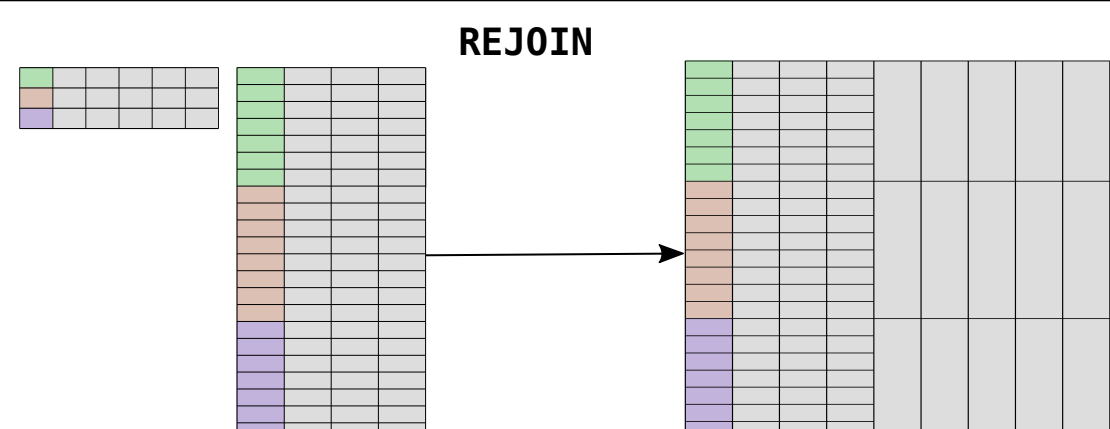
| |
|---|
| dt[xmv(X)] <pre>> dt <- dt[xmv(sex) == "M"] > dt[, s := xmv(sex)]</pre> |
|---|

Aggregate &
summary

| |
|--|
| dt[, OPERATION, by = id] <pre>> dt <- dt[,.(mean_act = mean(activity)), by = id] > dt[, .N, by = id] # count reads per id</pre> |
|--|

Join data &
metadata

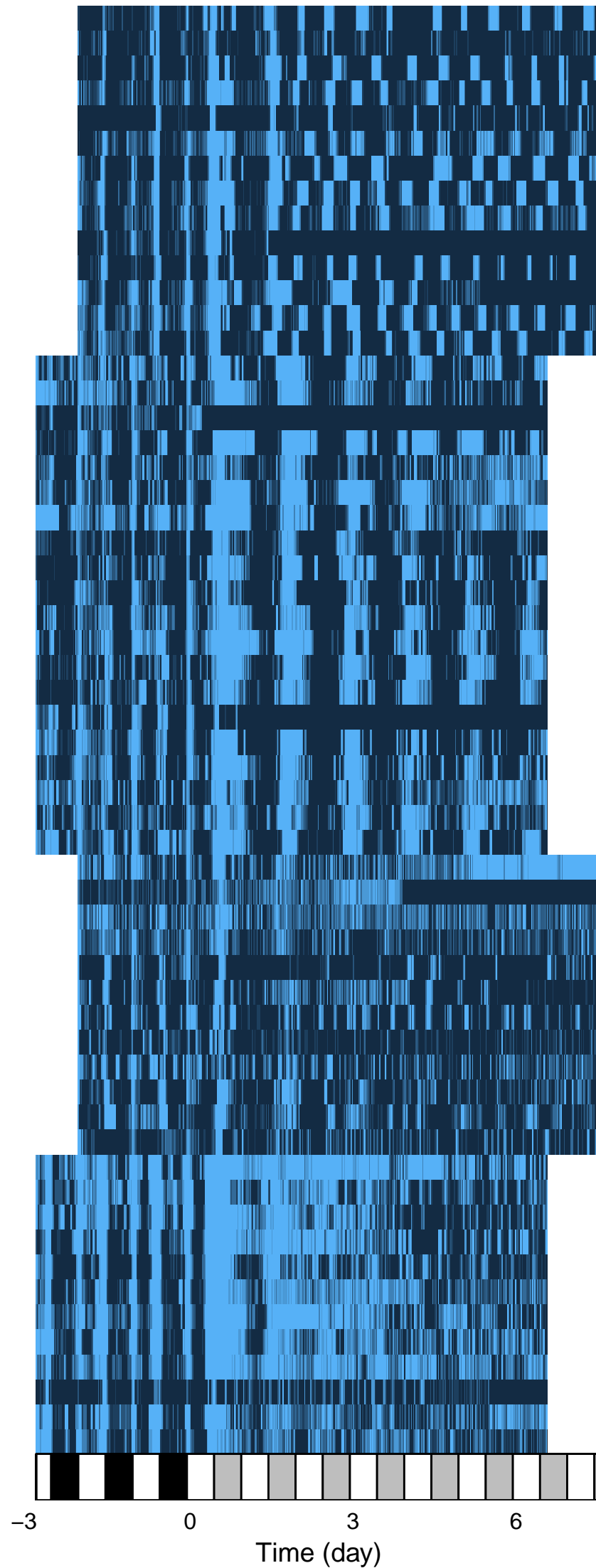
| |
|---|
| rejoin(dt) <pre>> full_table <- rejoin(dt)</pre> <p>Note: used mostly after aggregate or preprocessing</p> |
|---|



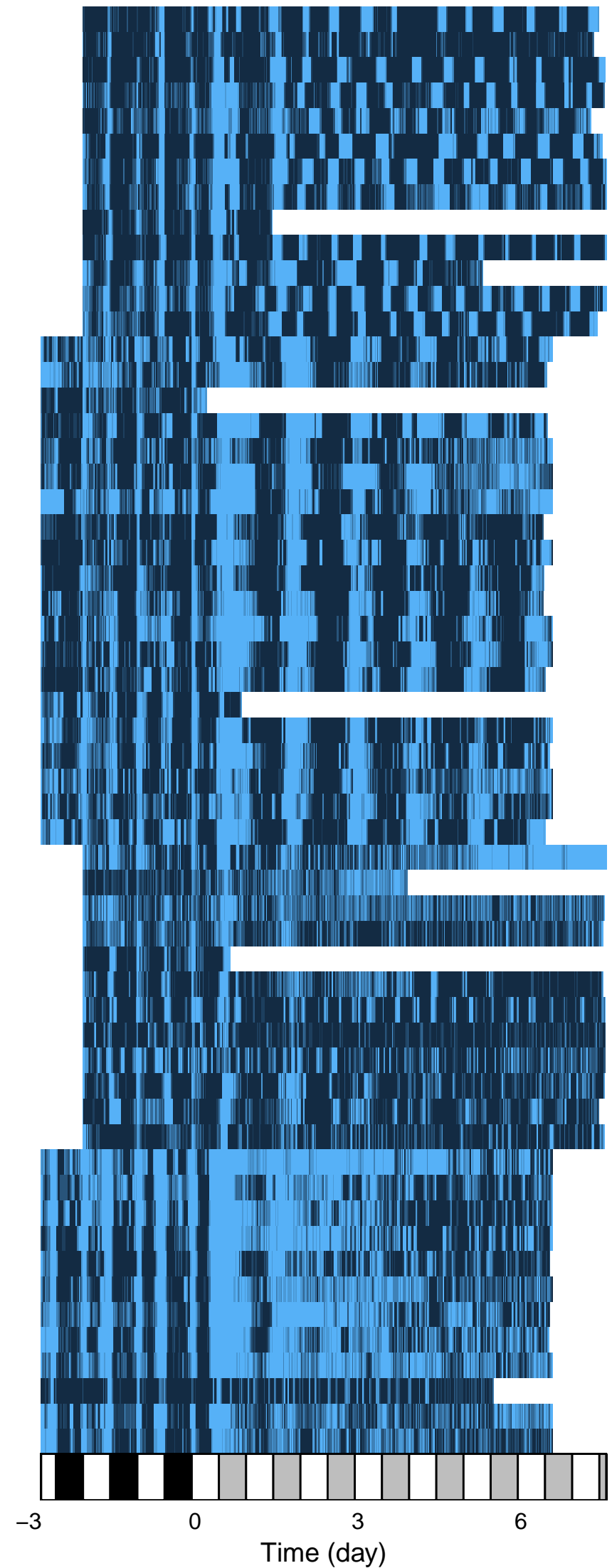
A

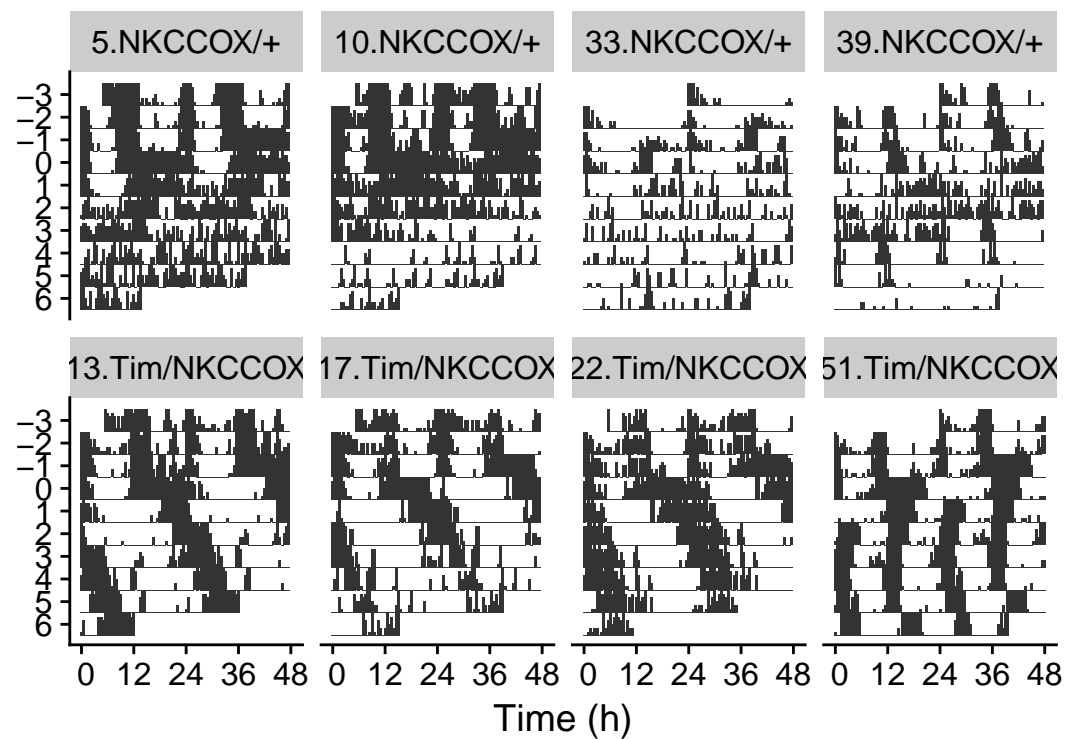
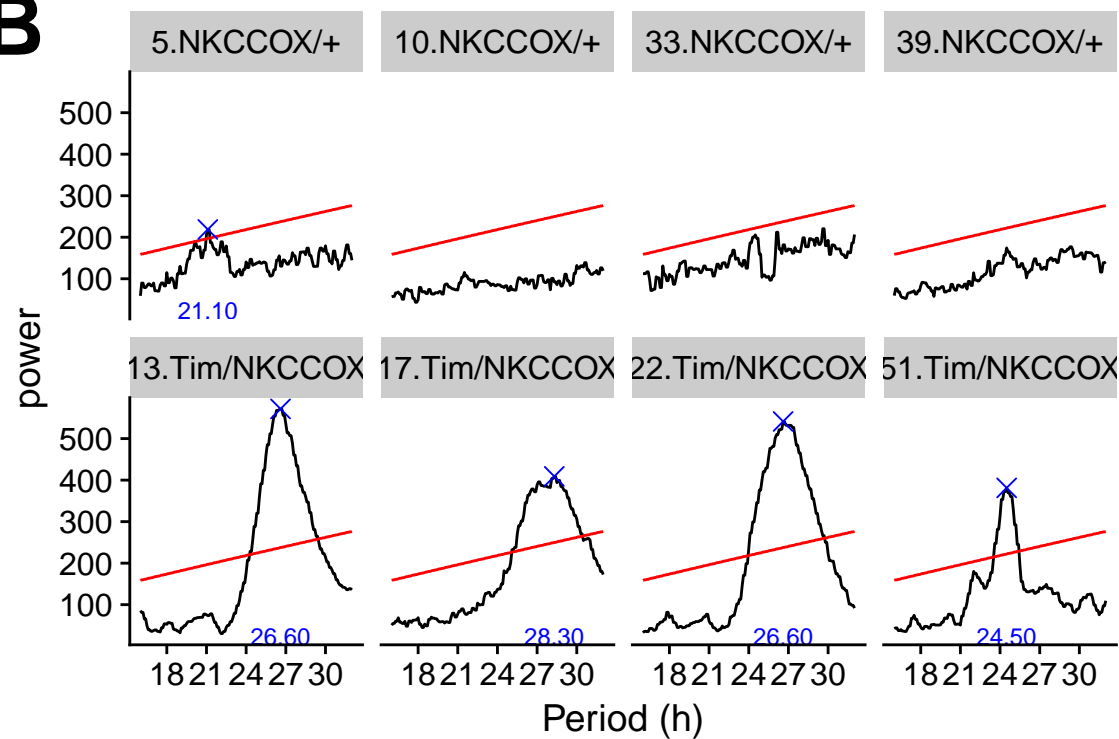
58.Tim/NKCCOX
 57.Tim/NKCCOX
 56.Tim/NKCCOX
 55.Tim/NKCCOX
 54.Tim/NKCCOX
 53.Tim/NKCCOX
 52.Tim/NKCCOX
 51.Tim/NKCCOX
 50.Tim/NKCCOX
 49.Tim/NKCCOX
 48.Tim/NKCCOX
 47.Tim/NKCCOX
 46.Tim/NKCCOX
 45.Tim/NKCCOX
 32.Tim/NKCCOX
 31.Tim/NKCCOX
 30.Tim/NKCCOX
 29.Tim/NKCCOX
 28.Tim/NKCCOX
 27.Tim/NKCCOX
 26.Tim/NKCCOX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

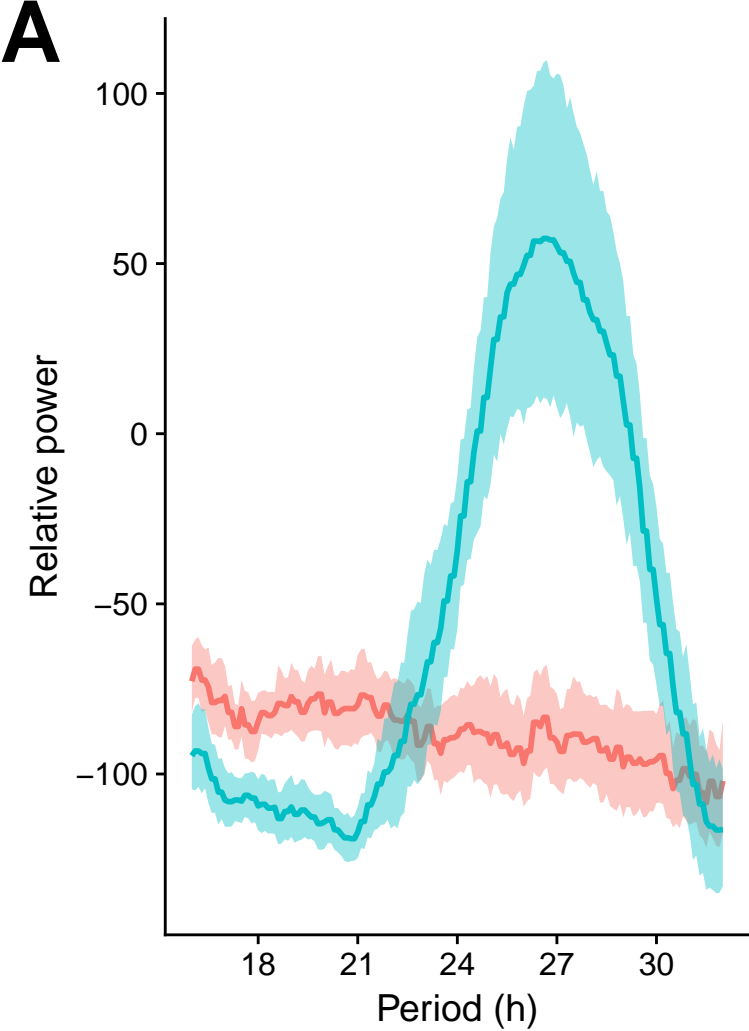
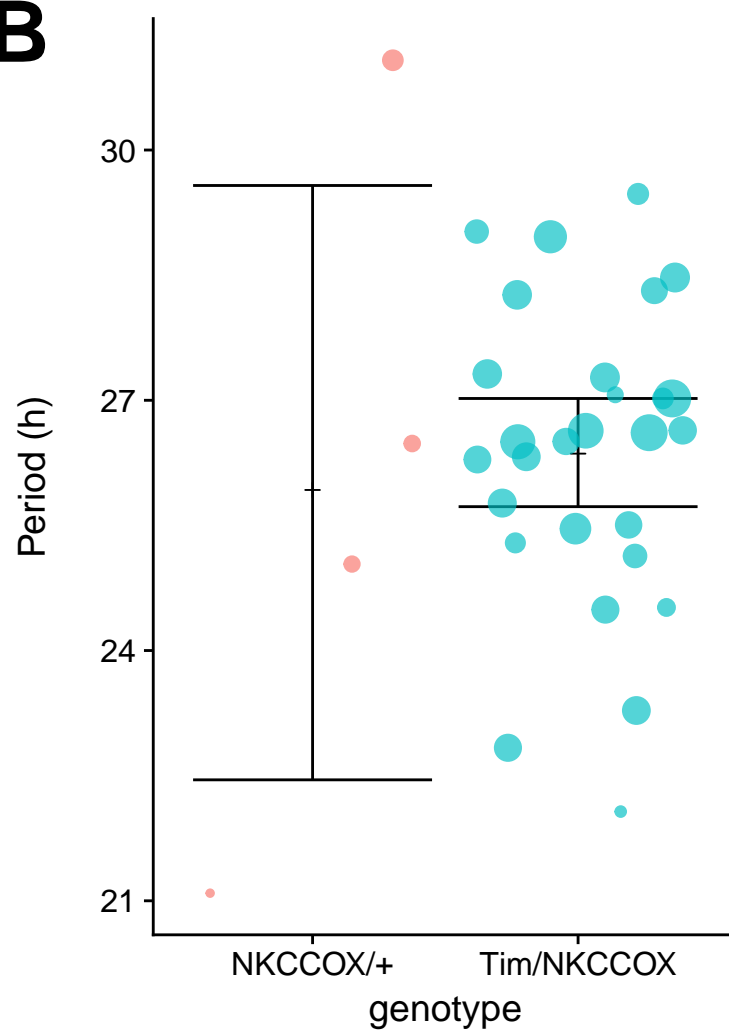
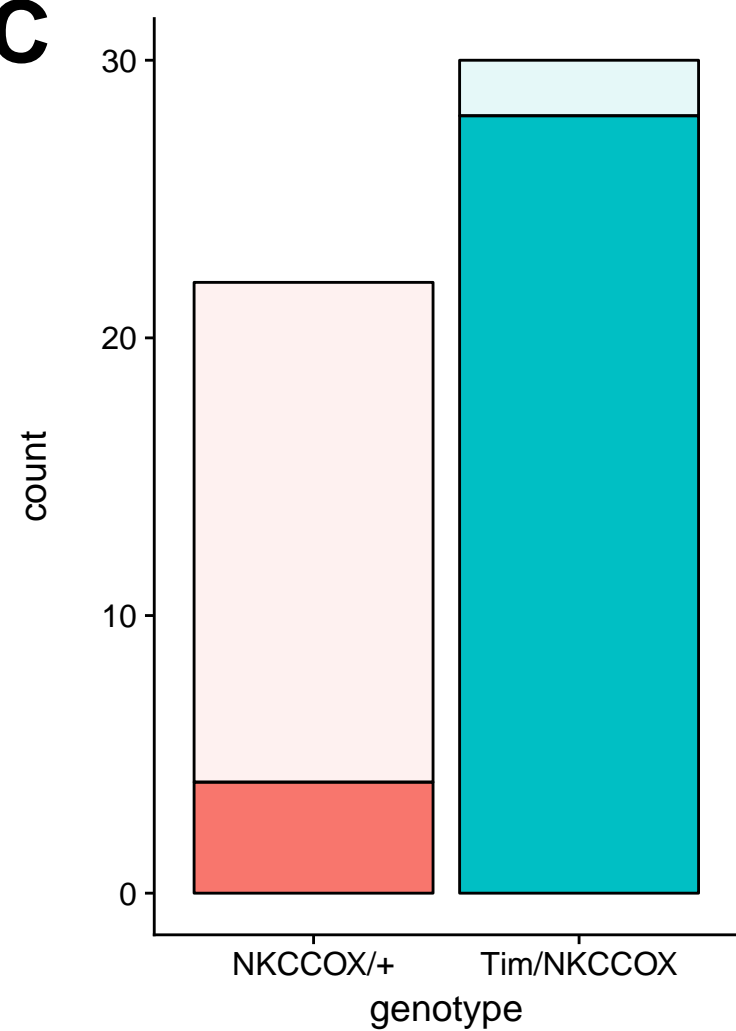
value
 1.00
 0.75
 0.50
 0.25
 0.00



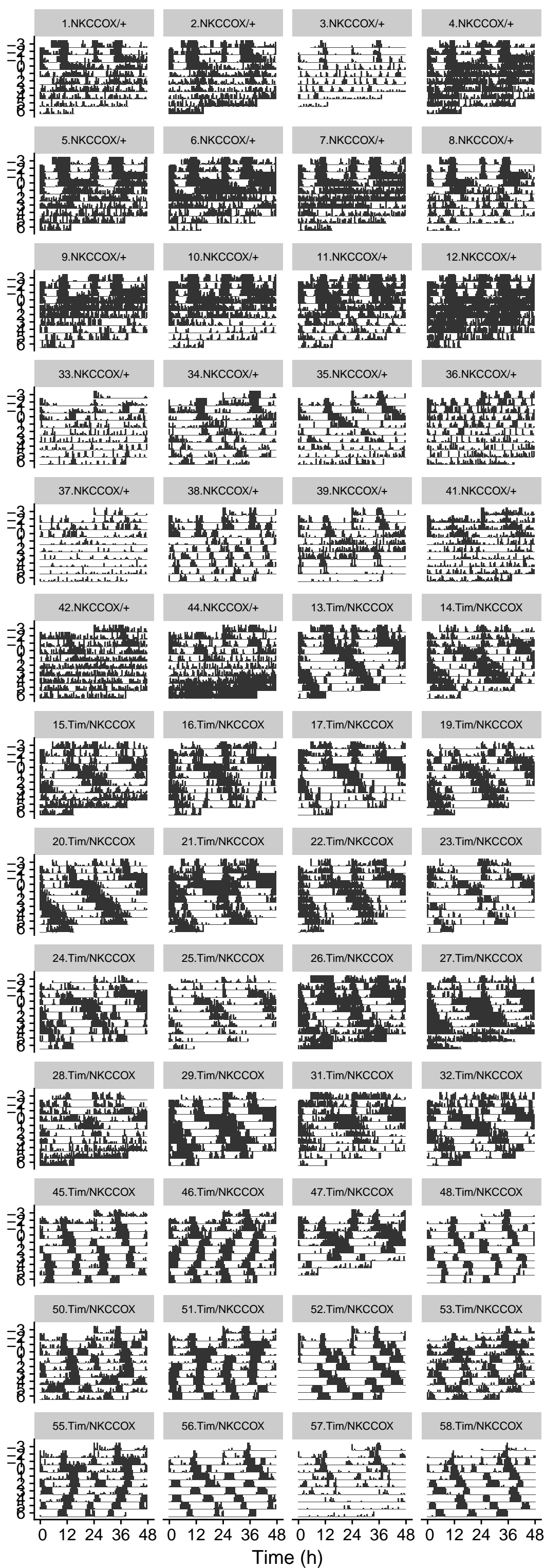
B



A**B**

A**B****C**

genotype • NKCCOX/+ • Tim/NKCCOX first_peak_power ● 300 ● 400 ● 500

A**B**