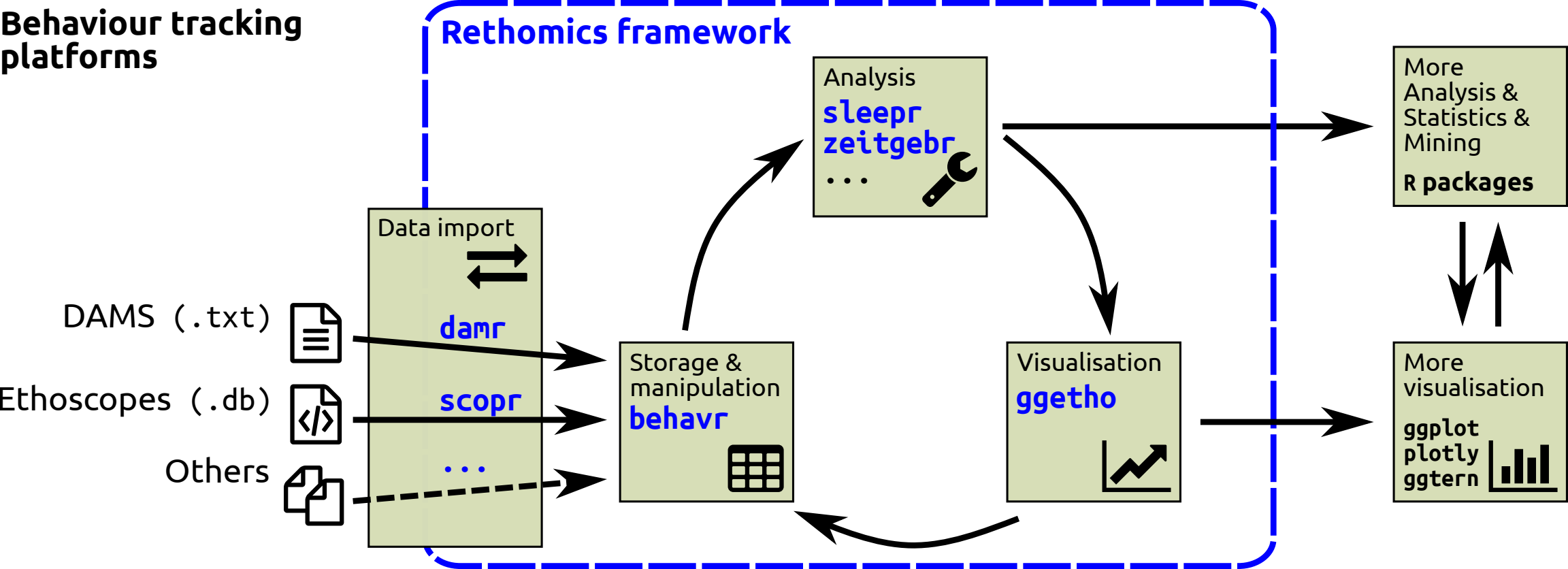


Behaviour tracking platforms

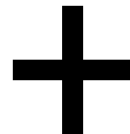


Metadata

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)

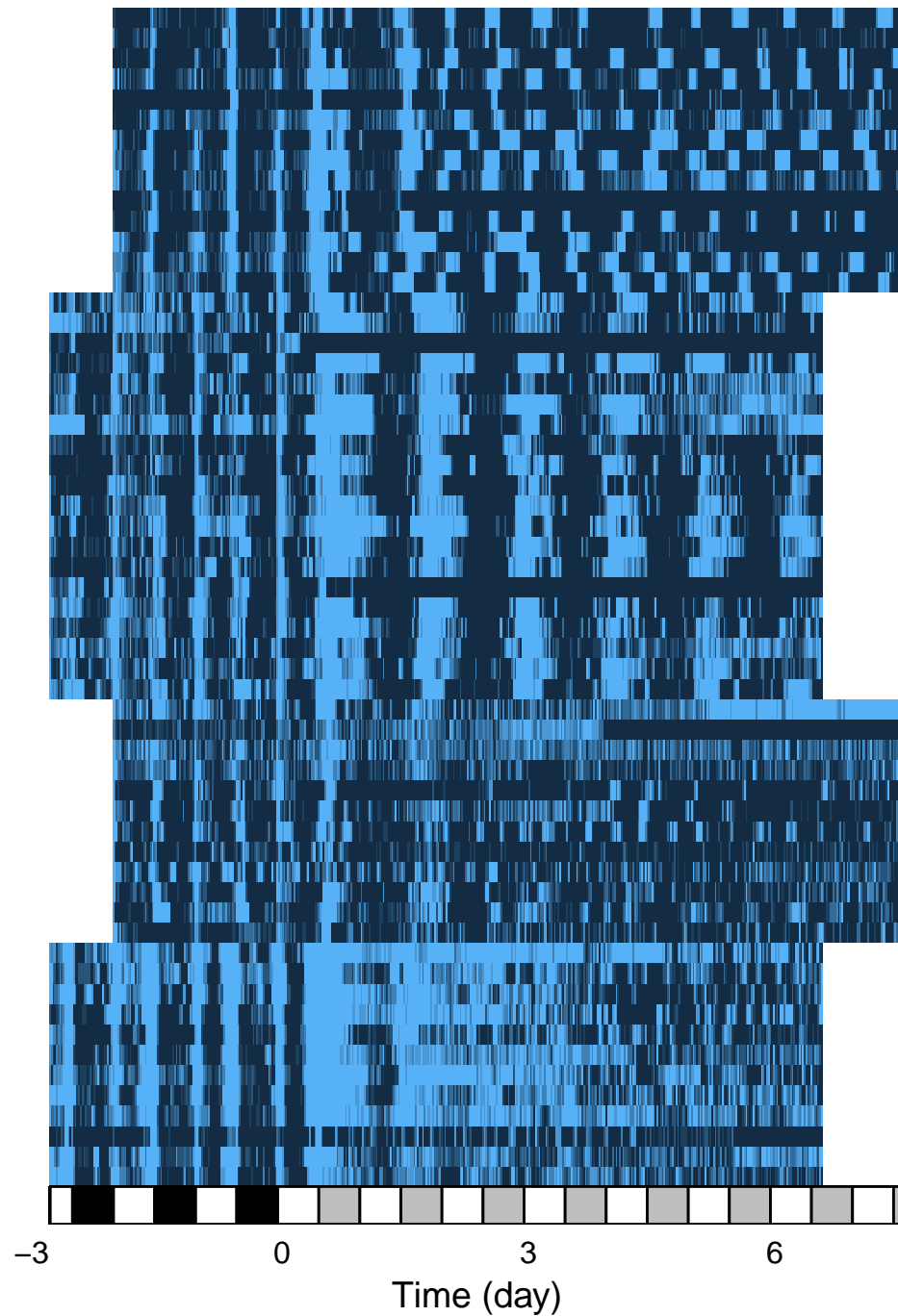
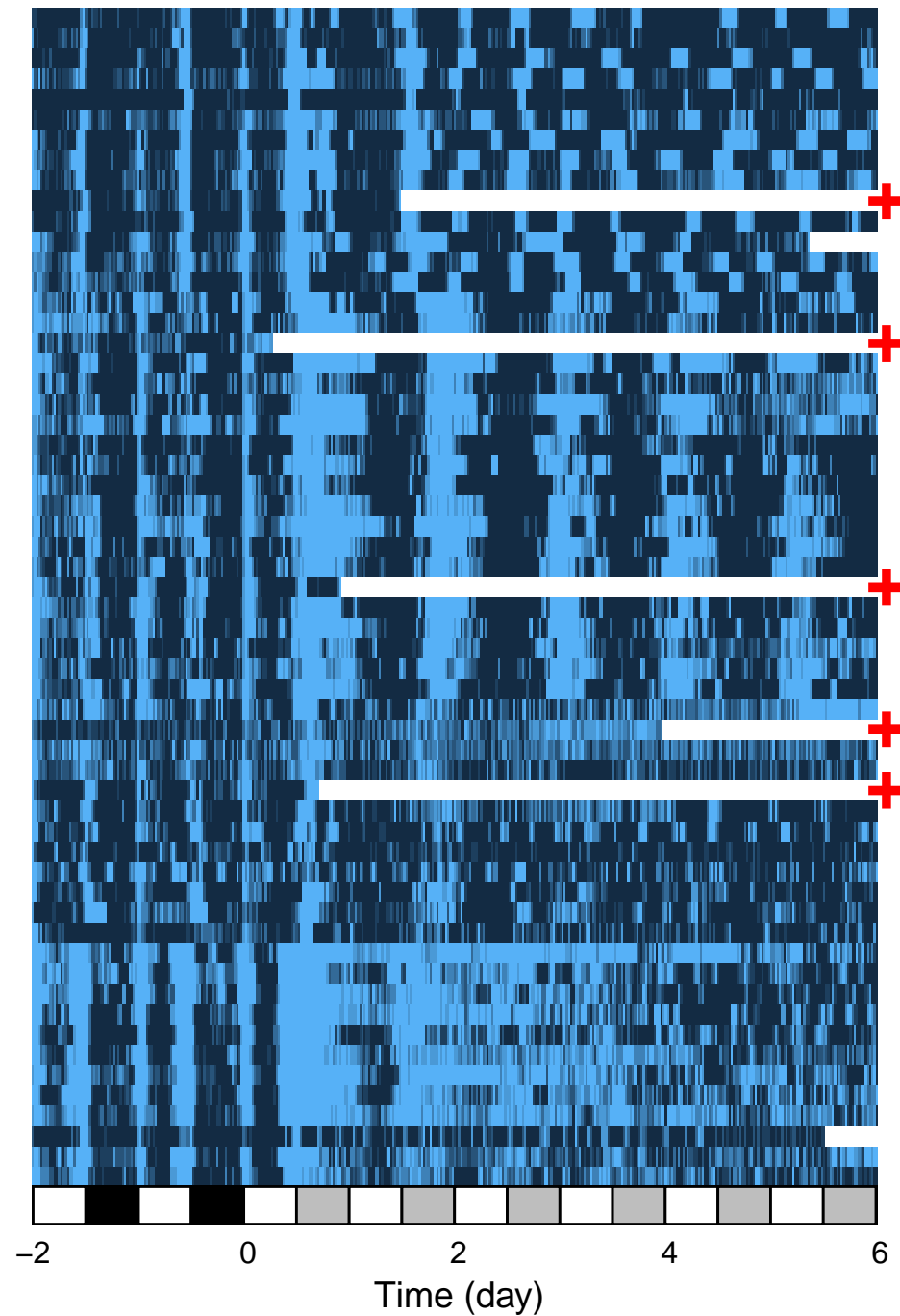


Data

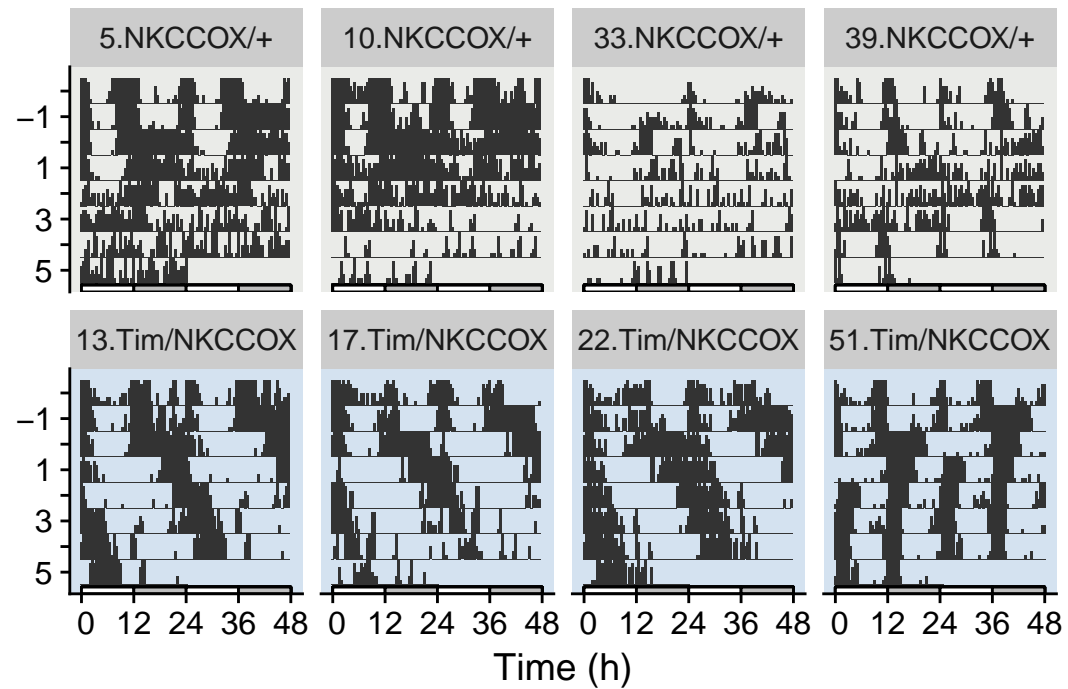
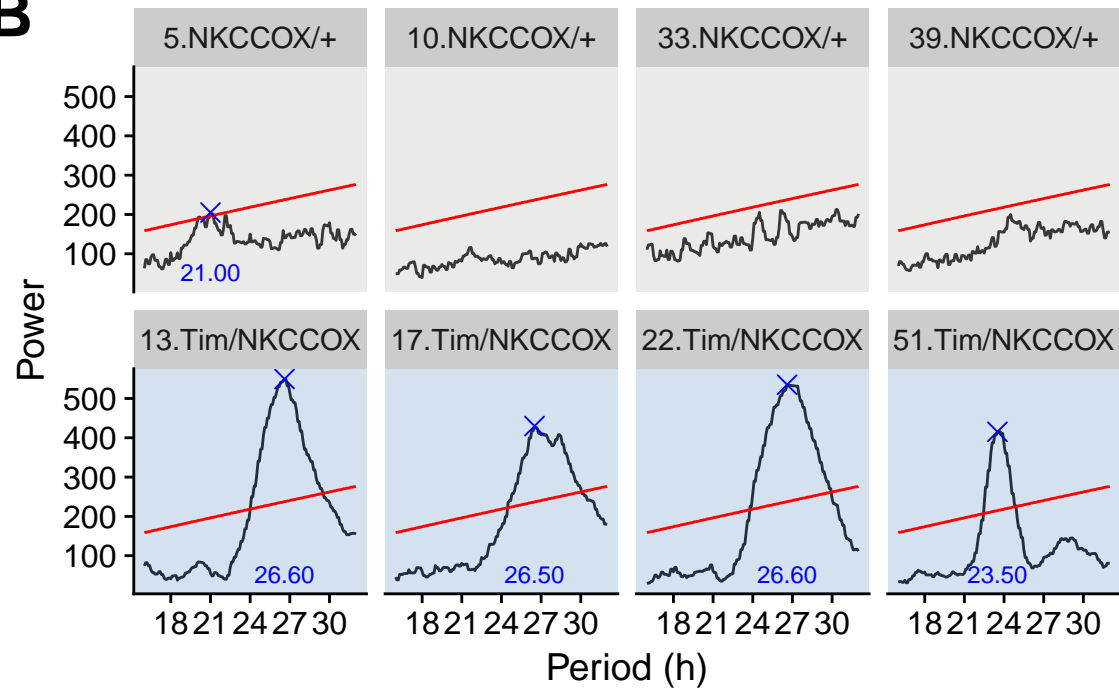
id	t	activity	...	q
xxx...xx x	1	1	⋱	$q_{1,1}$
xxx...xx x	2	0	⋱	$q_{1,2}$
xxx...xx x	3	0	⋱	$q_{1,3}$
xxx...xx x	⋮	⋮	⋱	⋮
xxx...xx y	⋮	⋮	⋱	⋮
xxx...xx z	1	0	⋱	$q_{3,1}$
xxx...xx z	2	2	⋱	$q_{3,2}$
xxx...xx z	3	0	⋱	$q_{3,3}$
xxx...xx z	⋮	⋮	⋱	⋮
⋮	⋮	⋮	⋱	⋮
n	⋮	⋮	⋱	q_{n,k_n}

A

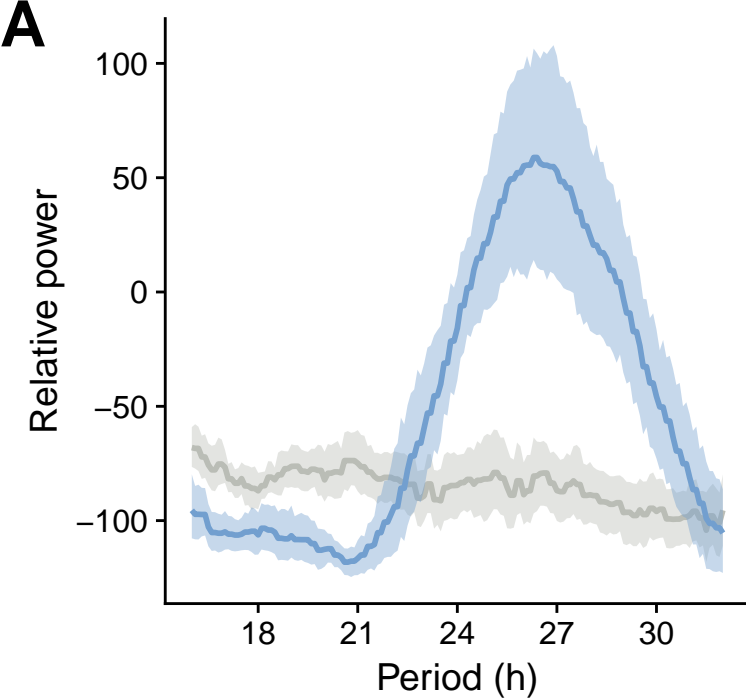
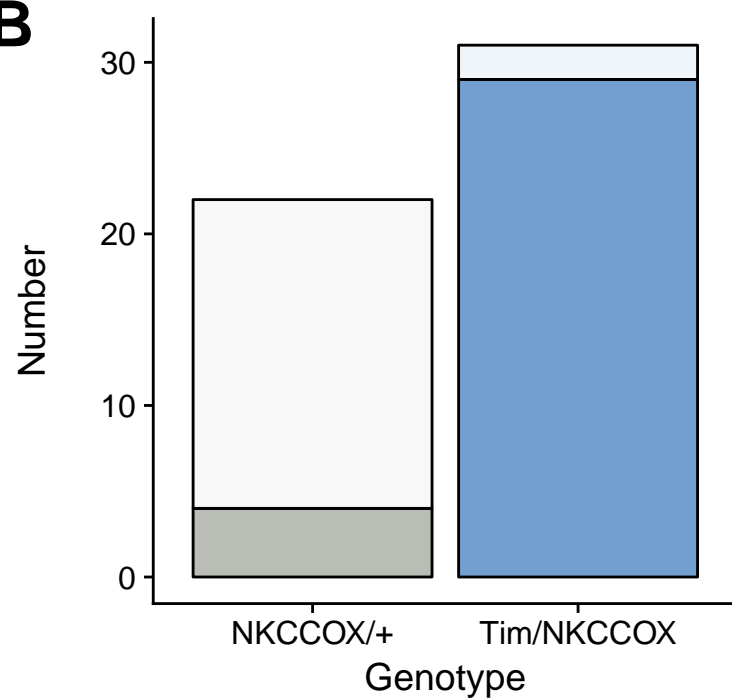
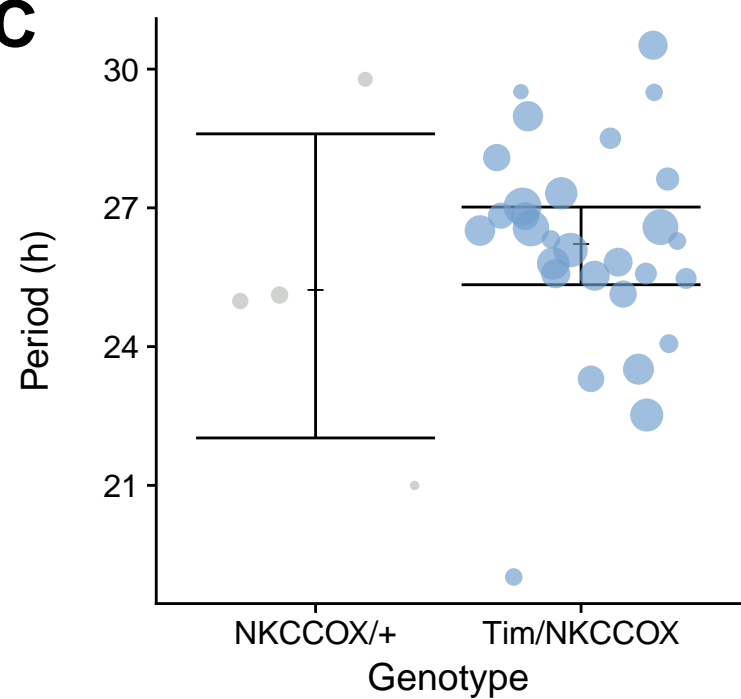
58.Tim/NKCCOX
57.Tim/NKCCOX
56.Tim/NKCCOX
55.Tim/NKCCOX
54.Tim/NKCCOX
53.Tim/NKCCOX
52.Tim/NKCCOX
51.Tim/NKCCOX
50.Tim/NKCCOX
49.Tim/NKCCOX
48.Tim/NKCCOX
47.Tim/NKCCOX
46.Tim/NKCCOX
45.Tim/NKCCOX
32.Tim/NKCCOX
31.Tim/NKCCOX
30.Tim/NKCCOX
29.Tim/NKCCOX
28.Tim/NKCCOX
27.Tim/NKCCOX
26.Tim/NKCCOX
25.Tim/NKCCOX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

**B**

Moving
0% 50% 100%

A**B**

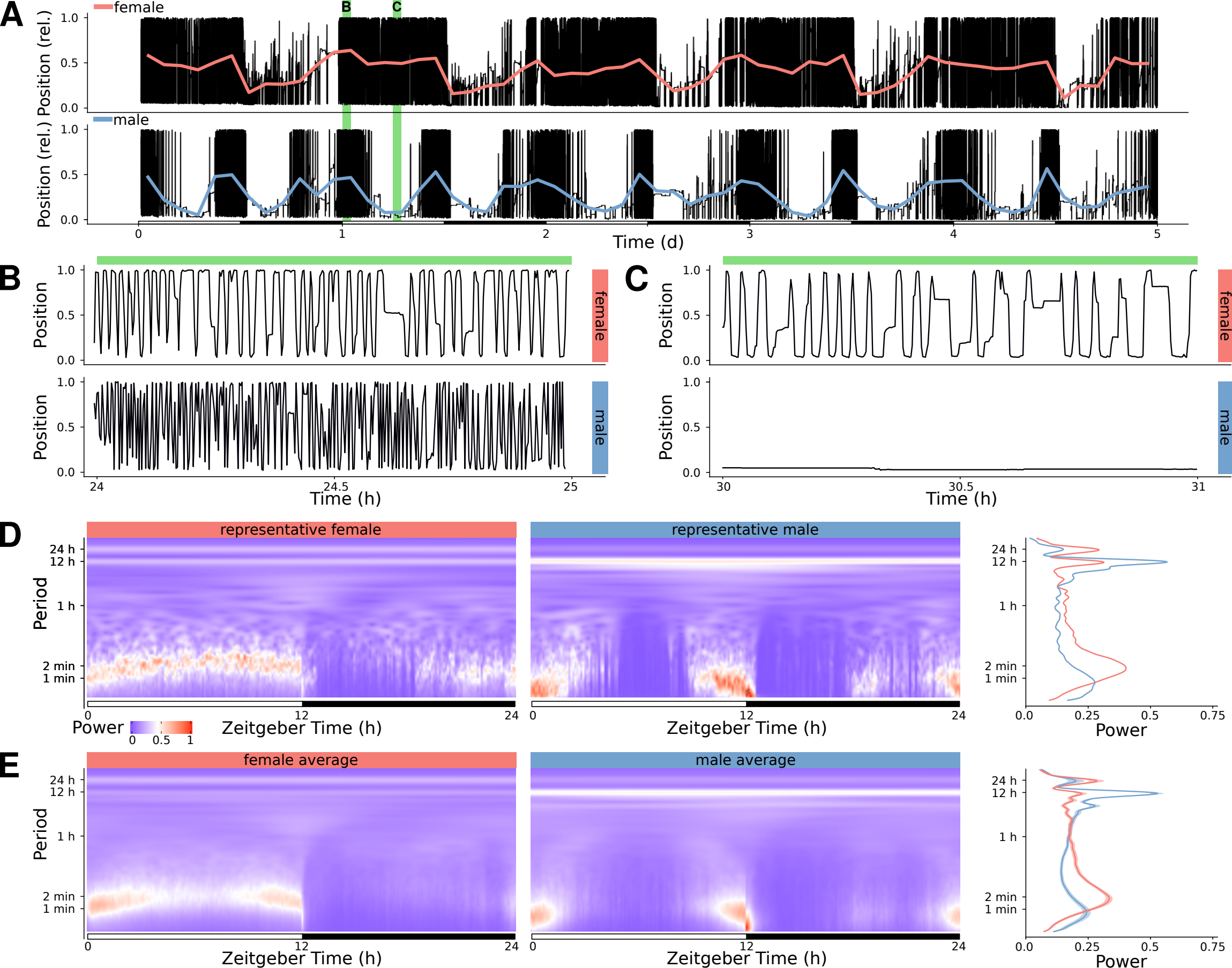
Genotype NKCCOX/+ Tim/NKCCOX

A**B****C**

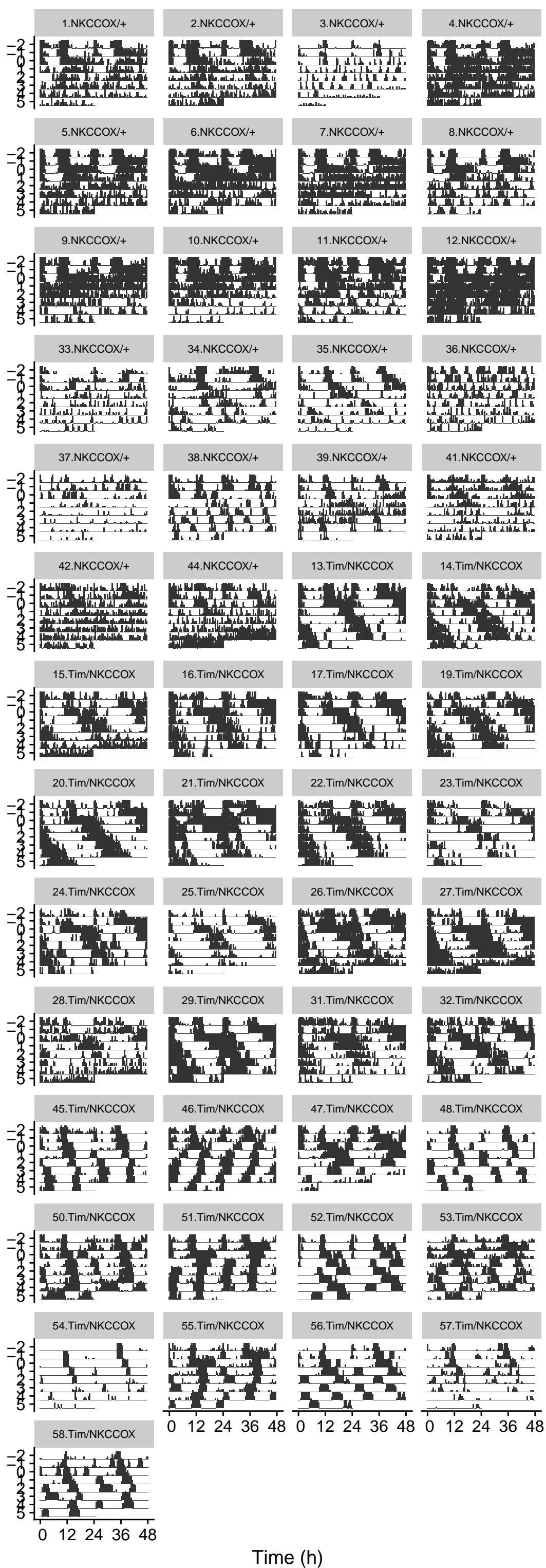
Genotype NKCCOX/+ Tim/NKCCOX

Arhythmic Rhythmic

Peak relative power 100 200 300



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

A**B**