

BD_Lumped

subsystem

Pyruvate metabolism

Fatty acid oxidation

0

20

40

60

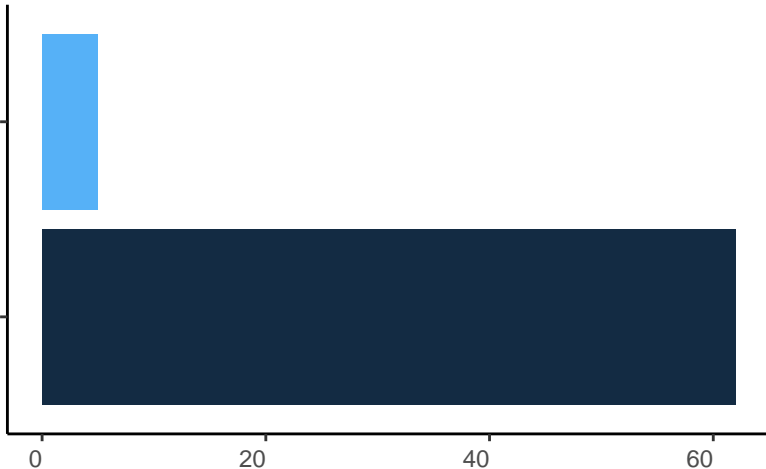
of disrupted reactions

p.val.fdr (≤ 0.05)

0.006

0.004

0.002



BD_Lumped

subsystem

Pyruvate metabolism

5

Fatty acid oxidation

27

35

Flux



H

L

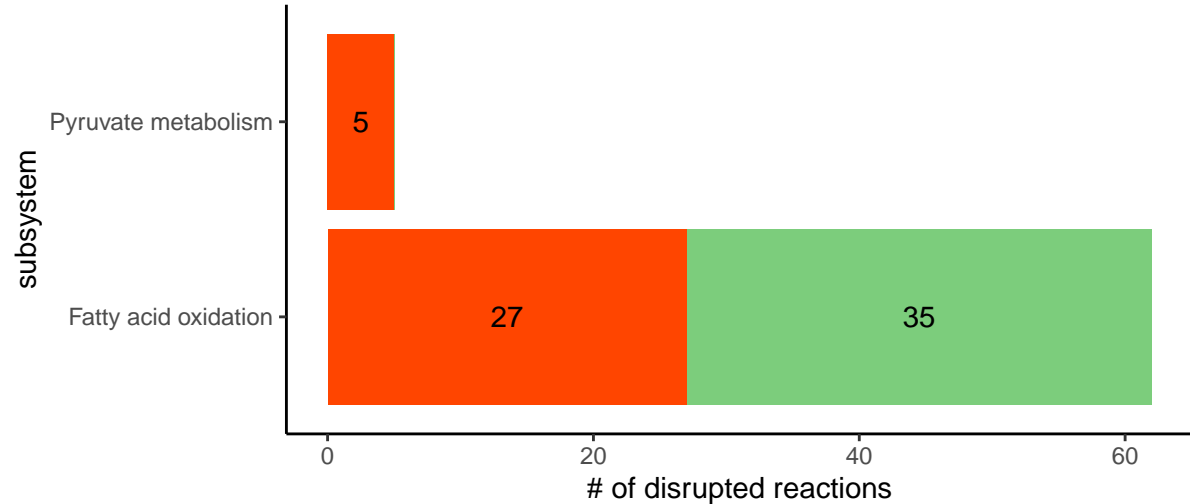
0

20

40

60

of disrupted reactions



BD_Responder

subsystem

ROS detoxification

Peptide metabolism

0

10

20

of disrupted reactions

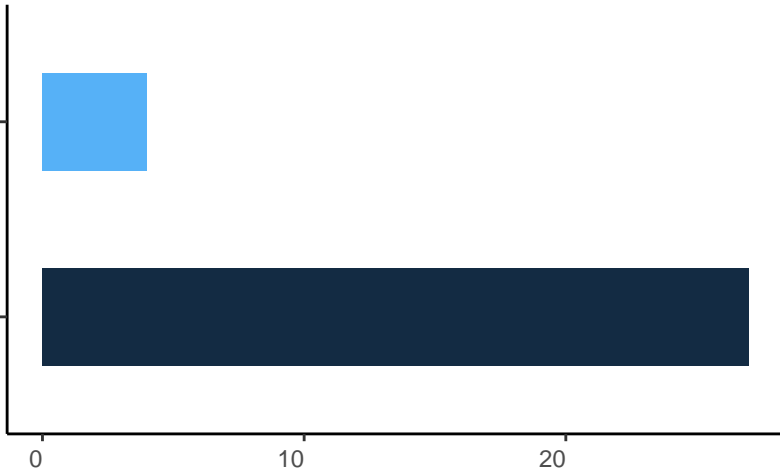
p.val.fdr (≤ 0.05)

$8e-05$

$6e-05$

$4e-05$

$2e-05$



BD_Responder

subsystem

ROS detoxification

4

Peptide metabolism

26

1

Flux



H



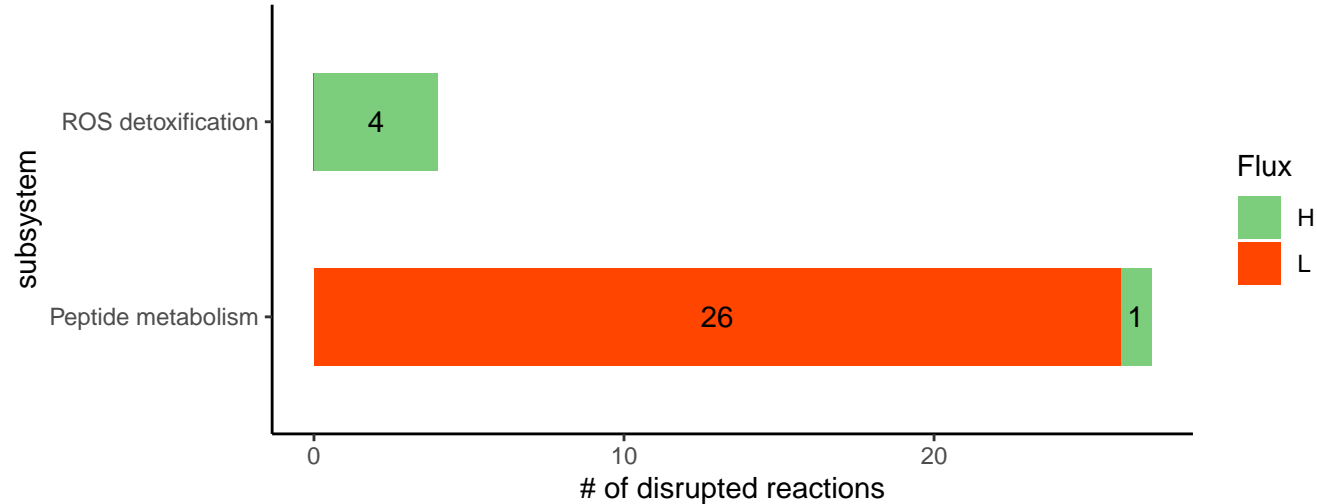
L

0

10

20

of disrupted reactions



BD_NonResponder

subsystem

N-glycan synthesis

Aminosugar metabolism

Phosphatidylinositol phosphate metabolism

Keratan sulfate degradation

0

5

10

15

of disrupted reactions

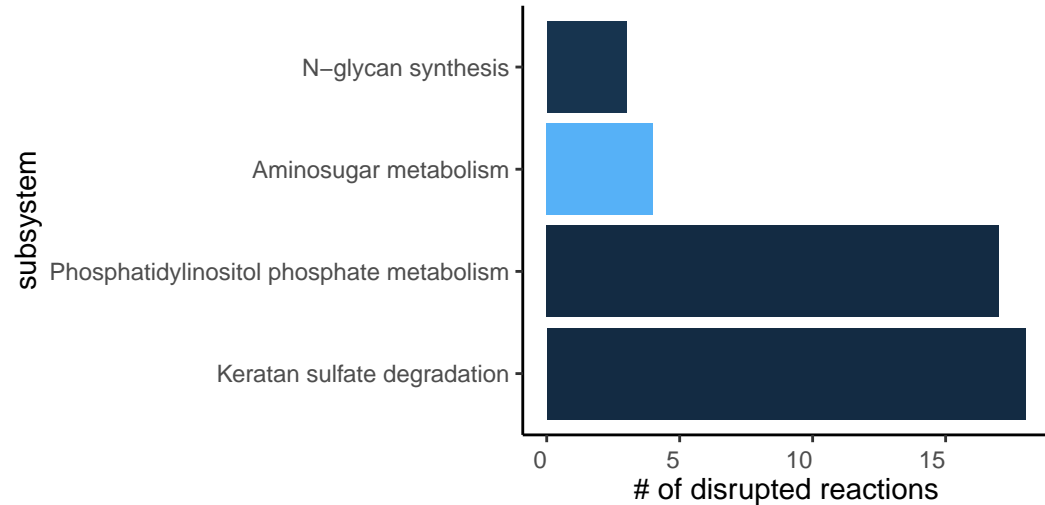
p.val.fdr (≤ 0.05)

0.020

0.015

0.010

0.005



BD_NonResponder

subsystem

N-glycan synthesis

3

Aminosugar metabolism

4

Phosphatidylinositol phosphate metabolism

17

Keratan sulfate degradation

18

Flux



H

0

5

10

15

of disrupted reactions



BD_Lumped

compartment

peroxisome

endoplasmic reticulum

mitochondrion

cytoplasm

Flux



0

10

20

30

of disrupted reactions

17

4

1

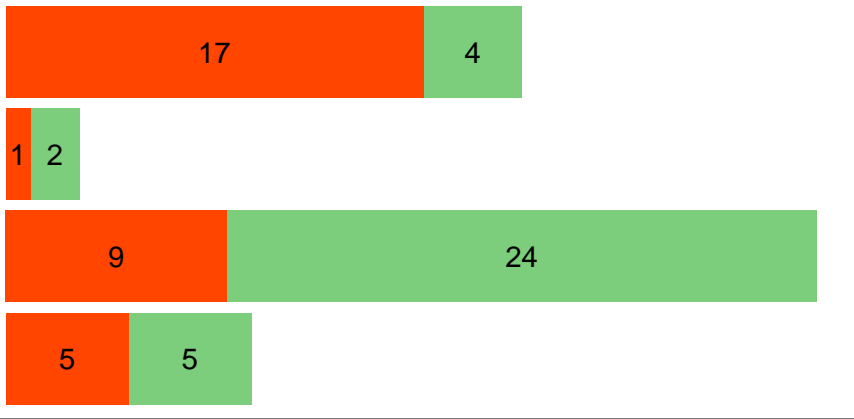
2

9

24

5

5



BD_Responder

compartment

peroxisome

nucleus

mitochondrion

cytoplasm

Flux



0

10

20

of disrupted reactions

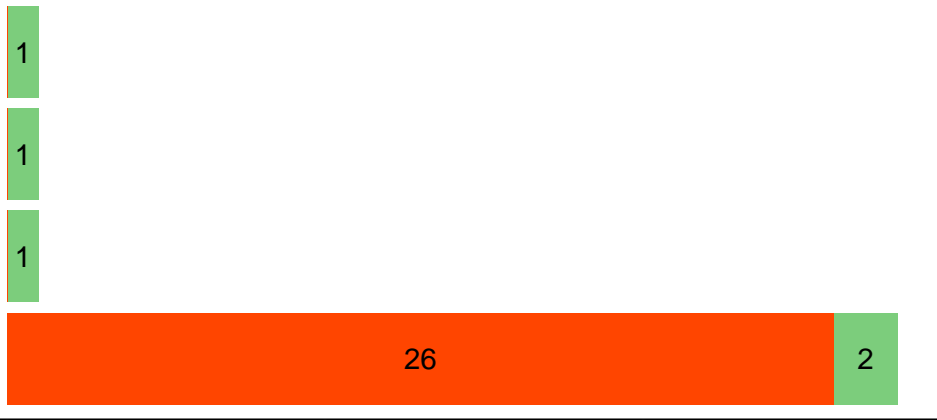
1

1

1

26

2



BD_NonResponder

compartment

intercompartmental

2

endoplasmic reticulum

14

lysosome

18

cytoplasm

8

Flux



H

of disrupted reactions

0

5

10

15