

Abs – BD vs Li+

NA	NA	NA	NA	NA	NA	NA	NA	NA	Lanz
1.0e+00	NA	NA	NA	NA	NA	NA	NA	NA	Rivera
3.9e−30	2.4e−02	NA	NA	NA	NA	NA	NA	NA	Akkouh
3.0e−03	1.0e+00	7.3e−01	NA	NA	NA	NA	NA	NA	FVA_BD
5.0e−01	1.0e+00	7.3e−01	5.0e−01	NA	NA	NA	NA	NA	FVA_BD_R
1.0e+00	9.4e−01	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA	FVA_BD_NR
2.7e−02	1.0e+00	1.0e+00	7.3e−01	4.3e−01	1.0e+00	NA	NA	NA	MTA_BD
1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e−09	1.0e+00	NA	NA	MTA_BD_R
5.0e−01	1.0e+00	1.0e+00	1.0e+00	9.4e−01	7.3e−01	2.3e−53	1.0e+00	NA	MTA_BD_NR
Lanz	Rivera	Akkouh	FVA_BD	FVA_BD_R	FVA_BD_NR	MTA_BD	MTA_BD_R	MTA_BD_NR	

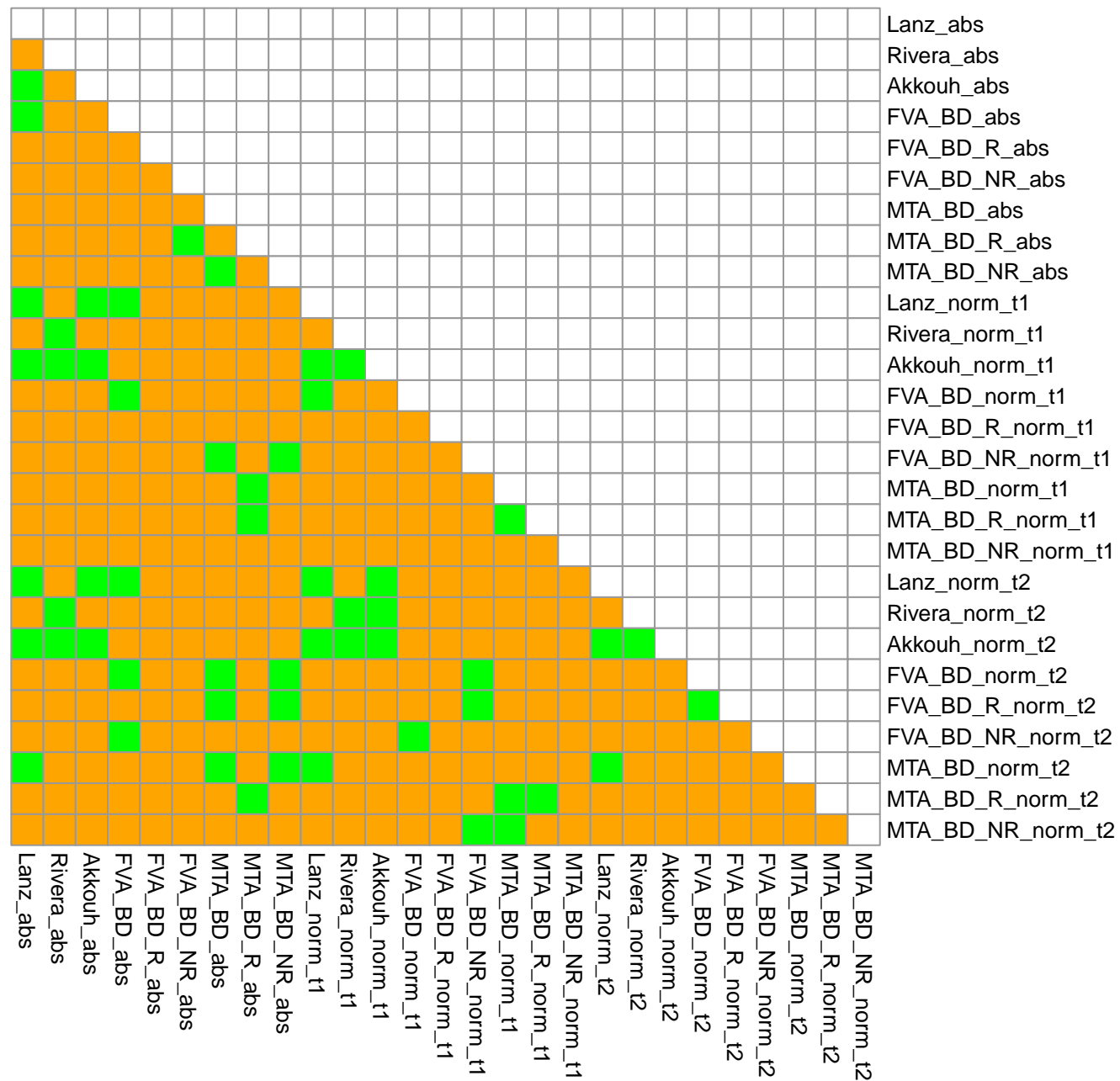
Norm_T1 – BD vs Li+

NA	NA	NA	NA	NA	NA	NA	NA	NA	Lanz
1.0e+00	NA	NA	NA	NA	NA	NA	NA	NA	Rivera
2.1e-18	1.0e-02	NA	NA	NA	NA	NA	NA	NA	Akkouh
1.1e-02	1.0e+00	1.0e+00	NA	NA	NA	NA	NA	NA	FVA_BD
1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA	NA	FVA_BD_R
1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA	FVA_BD_NR
1.0e+00	1.9e-01	8.1e-01	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	MTA_BD
1.0e+00	2.3e-01	1.0e+00	1.0e+00	1.0e+00	1.0e+00	4.0e-42	NA	NA	MTA_BD_R
1.0e+00	5.5e-01	1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	MTA_BD_NR
Lanz	Rivera	Akkouh	FVA_BD	FVA_BD_R	FVA_BD_NR	MTA_BD	MTA_BD_R	MTA_BD_NR	

Norm_T2 – BD vs Li+

NA	NA	NA	NA	NA	NA	NA	NA	NA	Lanz
1.0e+00	NA	NA	NA	NA	NA	NA	NA	NA	Rivera
1.4e-40	1.6e-02	NA	NA	NA	NA	NA	NA	NA	Akkouh
1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA	NA	NA	FVA_BD
1.0e+00	1.0e+00	1.0e+00	1.4e-54	NA	NA	NA	NA	NA	FVA_BD_R
1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA	FVA_BD_NR
1.9e-03	1.0e+00	6.4e-01	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	MTA_BD
1.0e+00	9.3e-02	5.7e-01	1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	NA	MTA_BD_R
1.0e+00	1.0e+00	1.0e+00	9.2e-02	5.3e-02	1.0e+00	1.0e+00	1.0e+00	NA	MTA_BD_NR
Lanz	Rivera	Akkouh	FVA_BD	FVA_BD_R	FVA_BD_NR	MTA_BD	MTA_BD_R	MTA_BD_NR	

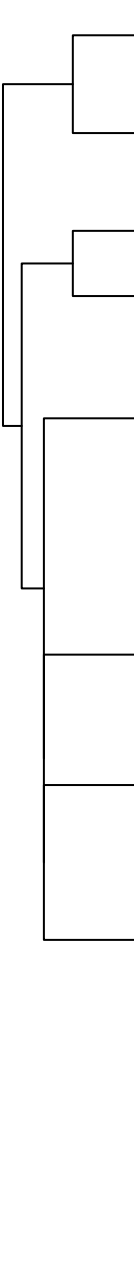
All – BD vs Li+



Abs

	0	0	0	1	0	1	Tyrosine metabolism
	0	0	0	1	0	1	Keratan sulfate degradation
	0	0	0	1	0	1	Chondroitin sulfate degradation
	0	0	0	1	0	1	Heparan sulfate degradation
	0	0	0	1	0	0	Chondroitin synthesis
	0	0	0	1	0	0	Sink
	1	1	0	1	0	1	Fatty acid oxidation
	0	1	0	0	0	0	Transport, endoplasmic reticular
	0	0	0	0	0	1	Keratan sulfate synthesis
	0	0	0	0	1	0	Transport, extracellular
	0	0	0	0	1	0	ROS detoxification
	0	0	0	0	1	0	Starch and sucrose metabolism
	1	0	0	0	1	0	Fructose and mannose metabolism
	1	0	0	0	0	0	Valine, leucine, and isoleucine metabolism
	1	0	0	0	0	0	Miscellaneous
	1	0	0	0	0	0	Lysine metabolism
	1	0	0	0	0	0	Methionine and cysteine metabolism
	0	0	1	0	1	1	Cholesterol metabolism
	0	0	1	0	1	0	Fatty acid synthesis
	0	0	1	0	0	0	Vitamin B6 metabolism
	0	0	1	0	0	0	Pyrimidine catabolism
	0	0	1	0	0	0	Propanoate metabolism
	0	0	1	0	0	0	Inositol phosphate metabolism
	0	0	1	0	0	0	Glycolysis/gluconeogenesis
	0	0	1	0	0	0	Biotin metabolism
	0	0	1	0	0	0	Glutamate metabolism
FVA_BD							
FVA_BD_R							
FVA_BD_NR							
MTA_BD							
MTA_BD_R							
MTA_BD_NR							

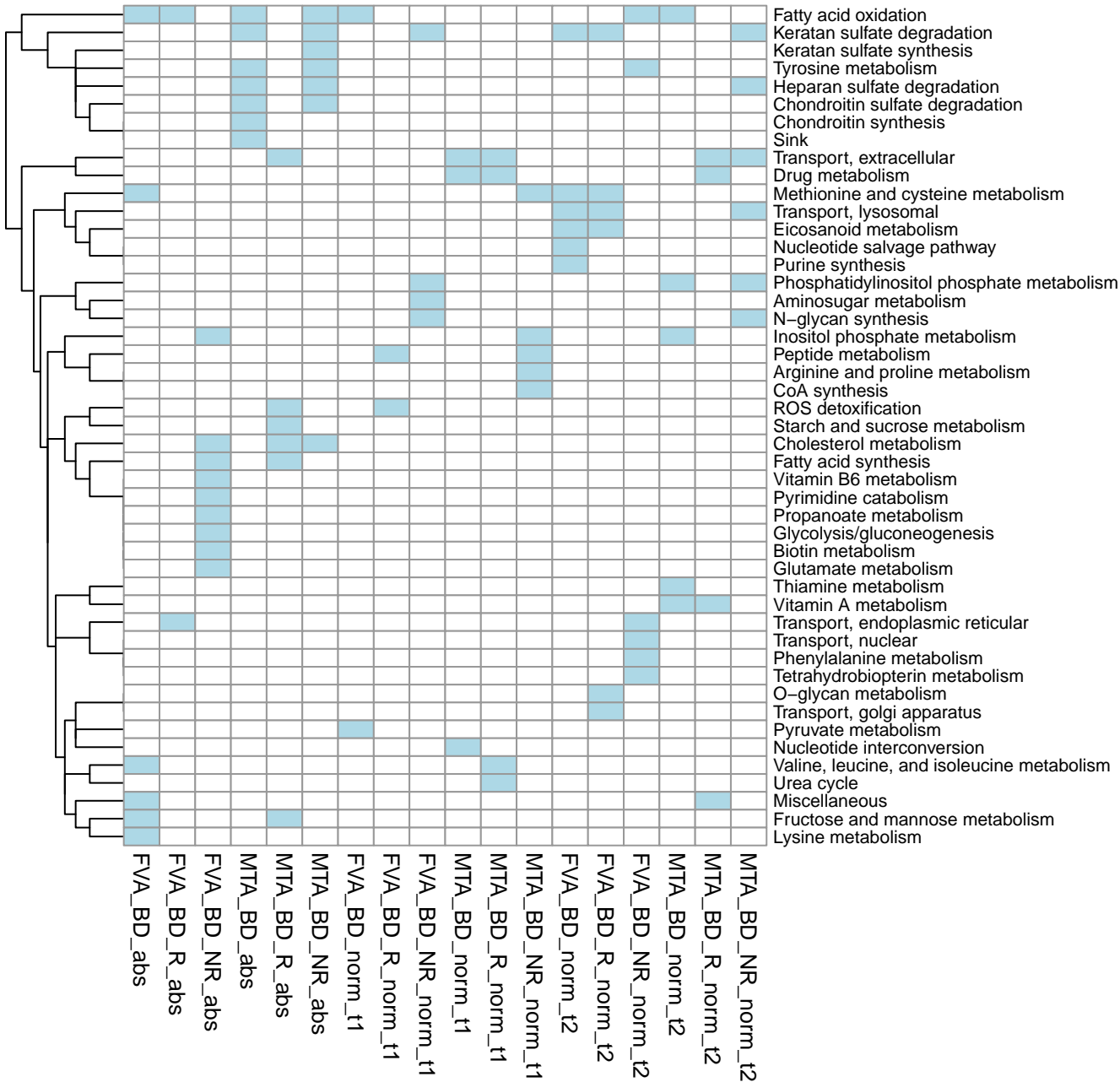
Norm_T1

	0	0	0	1	0	0	Nucleotide interconversion
	0	0	0	1	1	0	Drug metabolism
	0	0	0	1	1	0	Transport, extracellular
	0	1	0	0	0	1	Peptide metabolism
	0	1	0	0	0	0	ROS detoxification
	0	0	0	0	0	1	Methionine and cysteine metabolism
	0	0	0	0	0	1	Inositol phosphate metabolism
	0	0	0	0	0	1	Arginine and proline metabolism
	0	0	0	0	0	1	CoA synthesis
	0	0	0	0	1	0	Urea cycle
	0	0	0	0	1	0	Valine, leucine, and isoleucine metabolism
	1	0	0	0	0	0	Fatty acid oxidation
	1	0	0	0	0	0	Pyruvate metabolism
	0	0	1	0	0	0	Phosphatidylinositol phosphate metabolism
	0	0	1	0	0	0	N-glycan synthesis
	0	0	1	0	0	0	Aminosugar metabolism
0	0	1	0	0	0	Keratan sulfate degradation	
FVA_BD	FVA_BD_R	FVA_BD_NR	MTA_BD	MTA_BD_R	MTA_BD_NR		

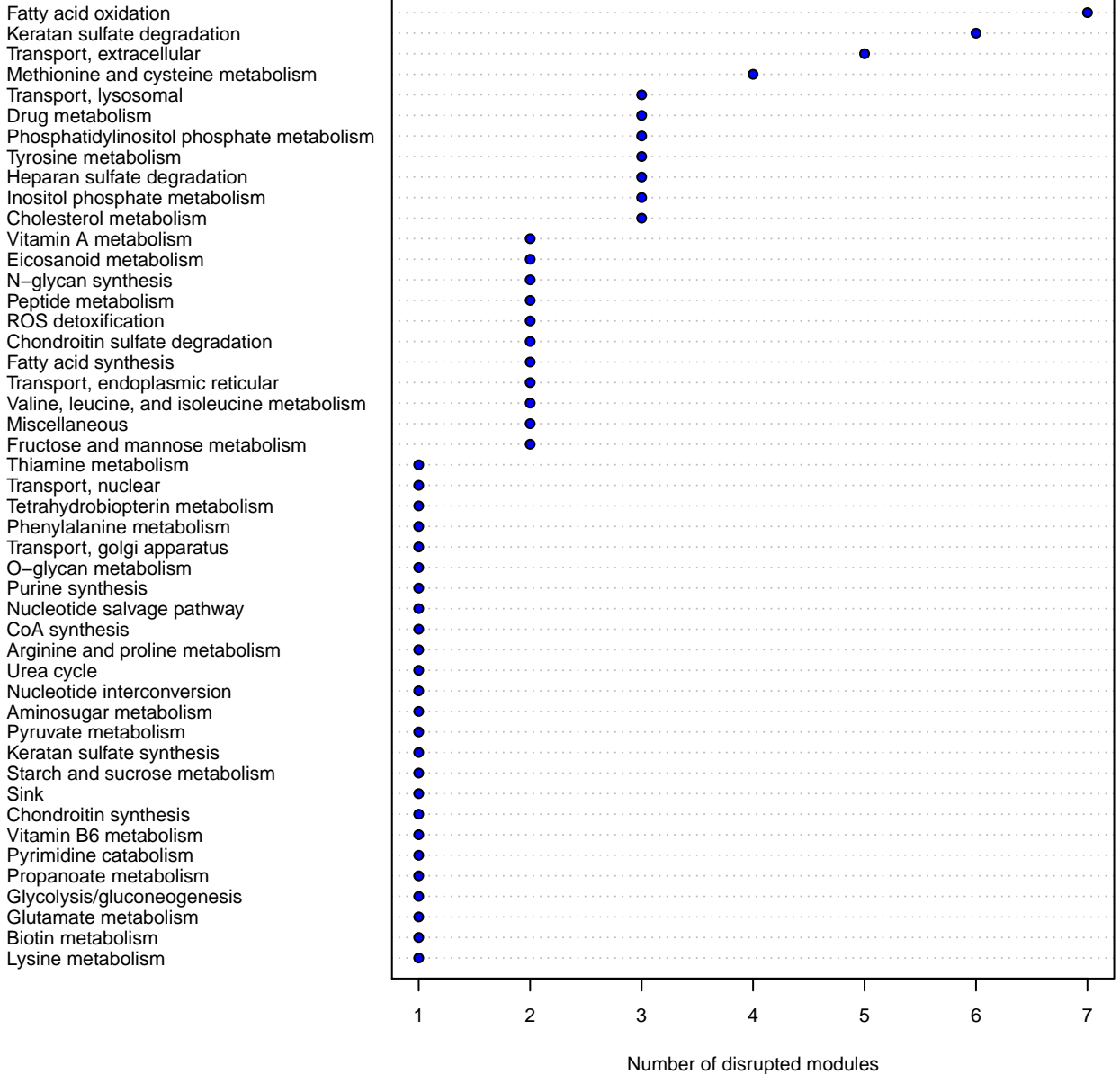
Norm_T2

	0	0	0	1	1	0	Vitamin A metabolism
	0	0	0	0	1	0	Drug metabolism
	0	0	0	0	1	0	Miscellaneous
	0	0	1	1	0	0	Fatty acid oxidation
	0	0	1	0	0	0	Tyrosine metabolism
	0	0	1	0	0	0	Transport, nuclear
	0	0	1	0	0	0	Transport, endoplasmic reticular
	0	0	1	0	0	0	Phenylalanine metabolism
	0	0	1	0	0	0	Tetrahydrobiopterin metabolism
	0	0	0	1	0	1	Phosphatidylinositol phosphate metabolism
	0	0	0	1	0	0	Inositol phosphate metabolism
	0	0	0	1	0	0	Thiamine metabolism
	0	0	0	0	1	1	Transport, extracellular
	0	0	0	0	0	1	Heparan sulfate degradation
	0	0	0	0	0	1	N-glycan synthesis
	0	1	0	0	0	0	O-glycan metabolism
	0	1	0	0	0	0	Transport, golgi apparatus
	1	0	0	0	0	0	Nucleotide salvage pathway
	1	0	0	0	0	0	Purine synthesis
	1	1	0	0	0	0	Eicosanoid metabolism
	1	1	0	0	0	0	Methionine and cysteine metabolism
	1	1	0	0	0	1	Keratan sulfate degradation
	1	1	0	0	0	1	Transport, lysosomal
	FVA_BD	FVA_BD_R	FVA_BD_NR	MTA_BD	MTA_BD_R	MTA_BD_NR	

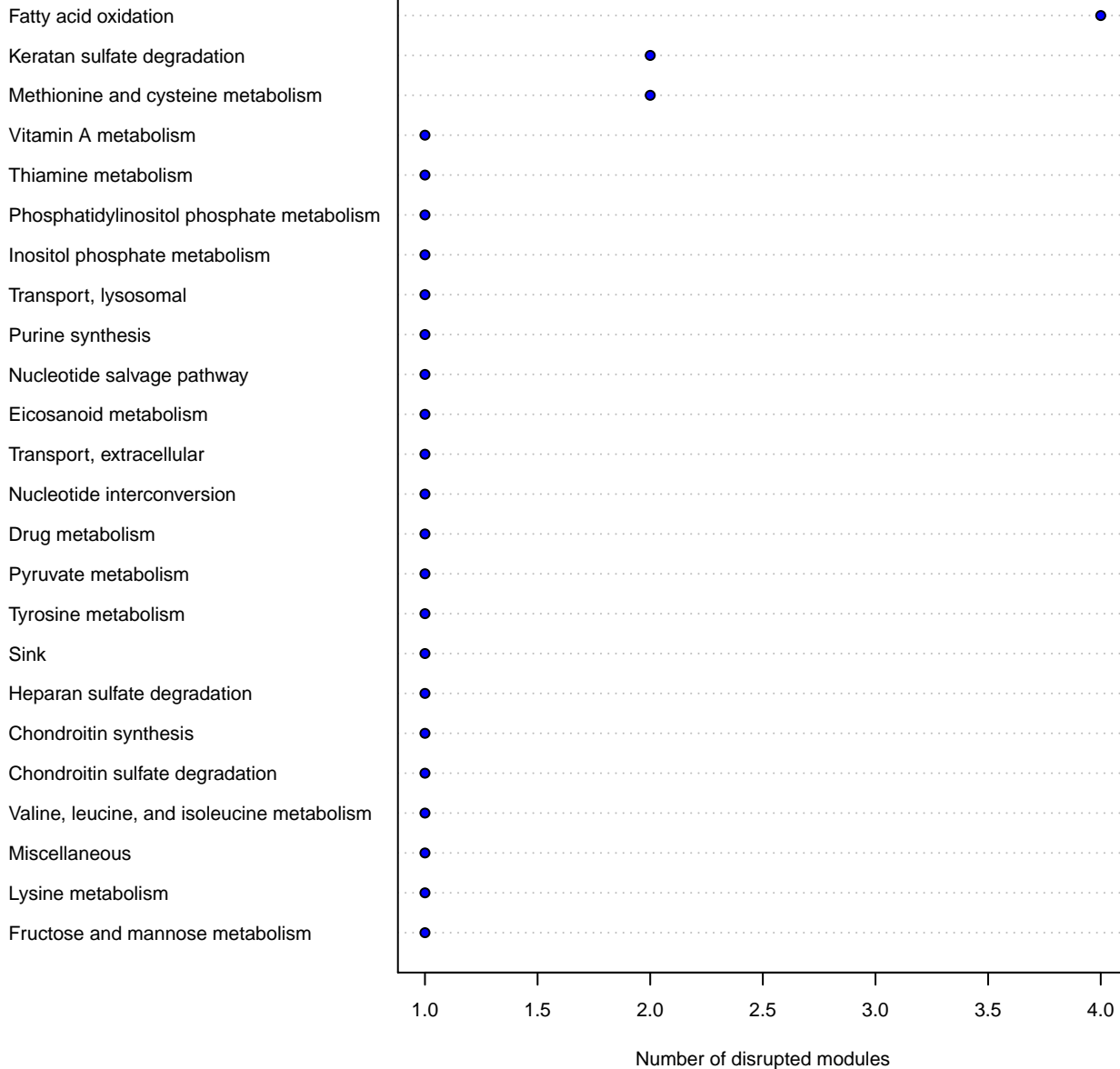
All



AII



BD_Lumped



BD_R

Transport, extracellular

Drug metabolism

ROS detoxification

Vitamin A metabolism

Miscellaneous

Transport, lysosomal

Transport, golgi apparatus

O-glycan metabolism

Methionine and cysteine metabolism

Keratan sulfate degradation

Eicosanoid metabolism

Valine, leucine, and isoleucine metabolism

Urea cycle

Peptide metabolism

Starch and sucrose metabolism

Fructose and mannose metabolism

Fatty acid synthesis

Cholesterol metabolism

Transport, endoplasmic reticular

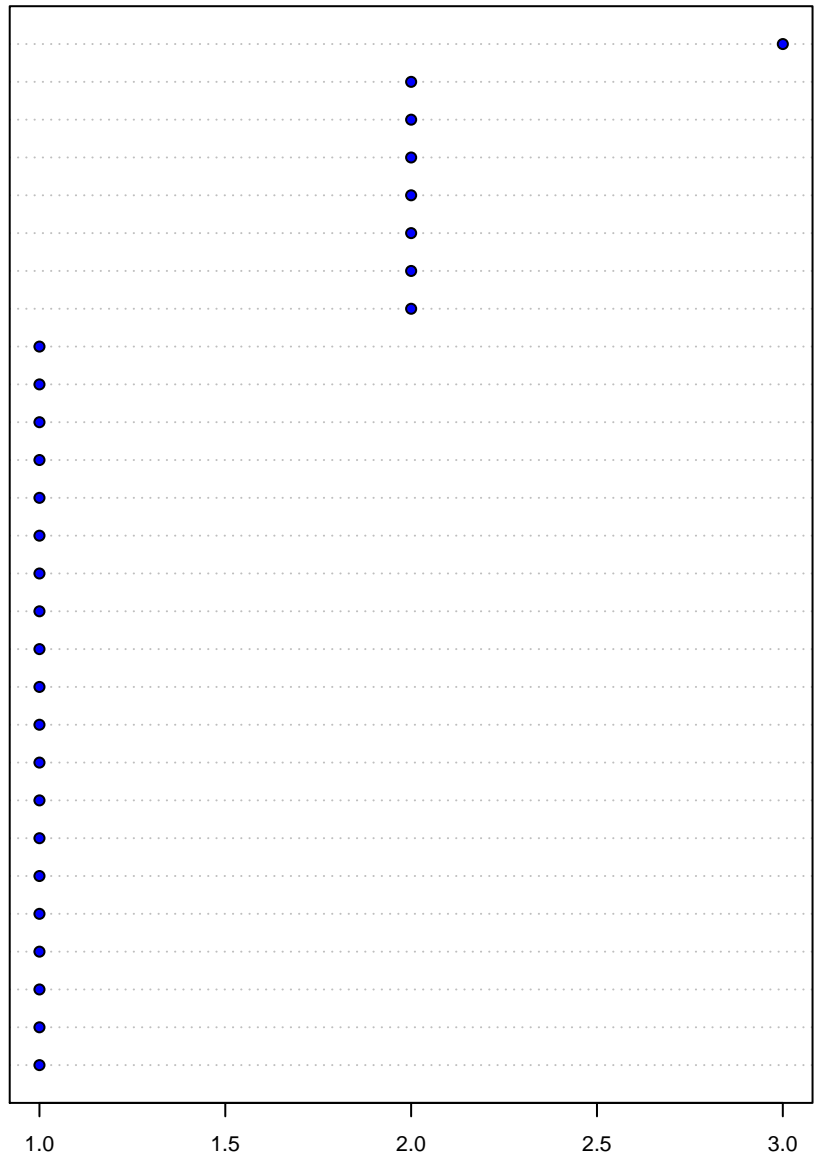
Fatty acid oxidation



Number of disrupted modules

BD_NR

Keratan sulfate degradation
Phosphatidylinositol phosphate metabolism
N-glycan synthesis
Tyrosine metabolism
Heparan sulfate degradation
Fatty acid oxidation
Inositol phosphate metabolism
Cholesterol metabolism
Transport, lysosomal
Transport, extracellular
Transport, nuclear
Transport, endoplasmic reticular
Tetrahydrobiopterin metabolism
Phenylalanine metabolism
Peptide metabolism
Methionine and cysteine metabolism
CoA synthesis
Arginine and proline metabolism
Aminosugar metabolism
Keratan sulfate synthesis
Chondroitin sulfate degradation
Vitamin B6 metabolism
Pyrimidine catabolism
Propanoate metabolism
Glycolysis/gluconeogenesis
Glutamate metabolism
Fatty acid synthesis
Biotin metabolism



Number of disrupted modules

