

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	

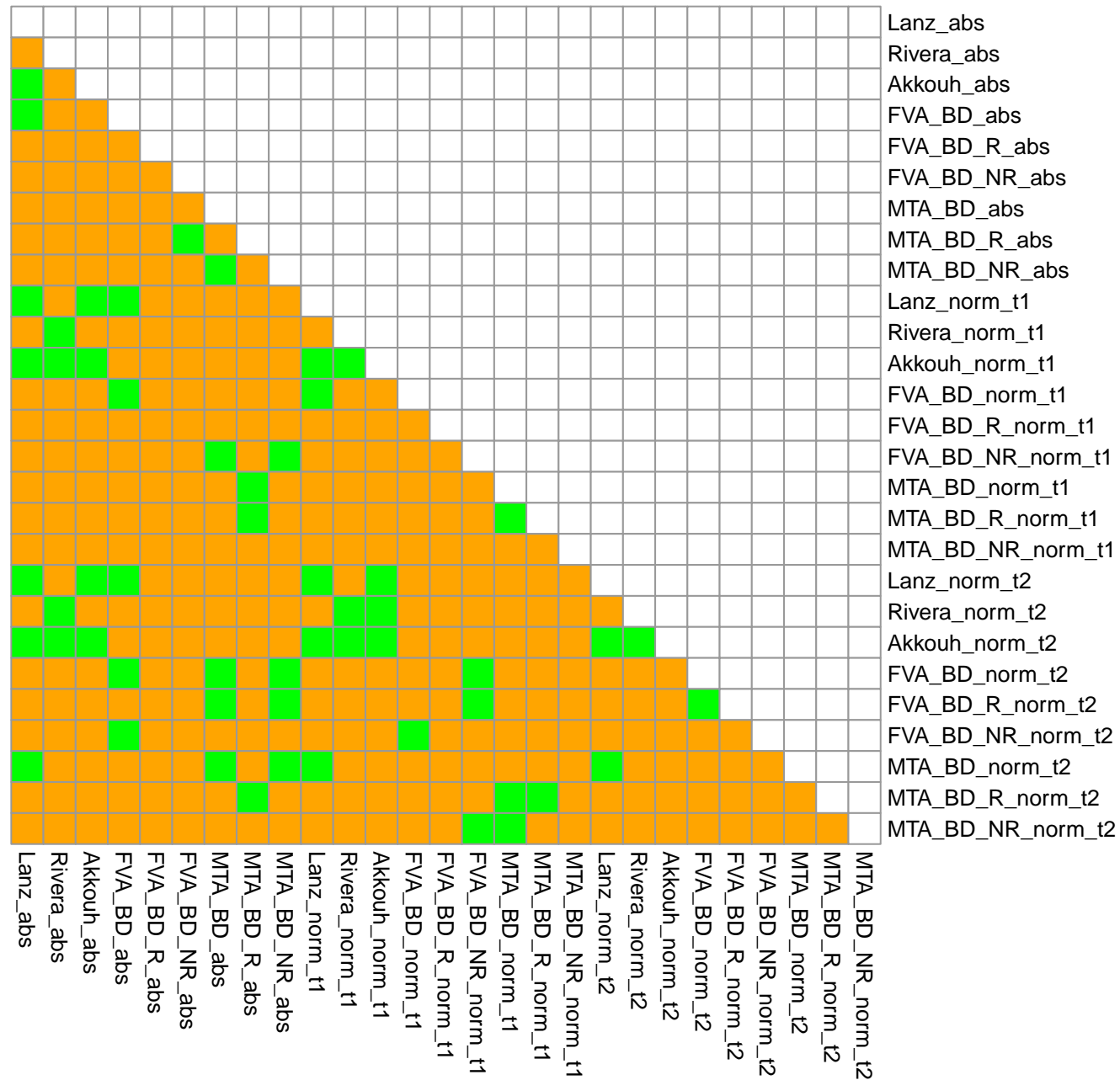
Norm_T1 – BD vs Li+

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	

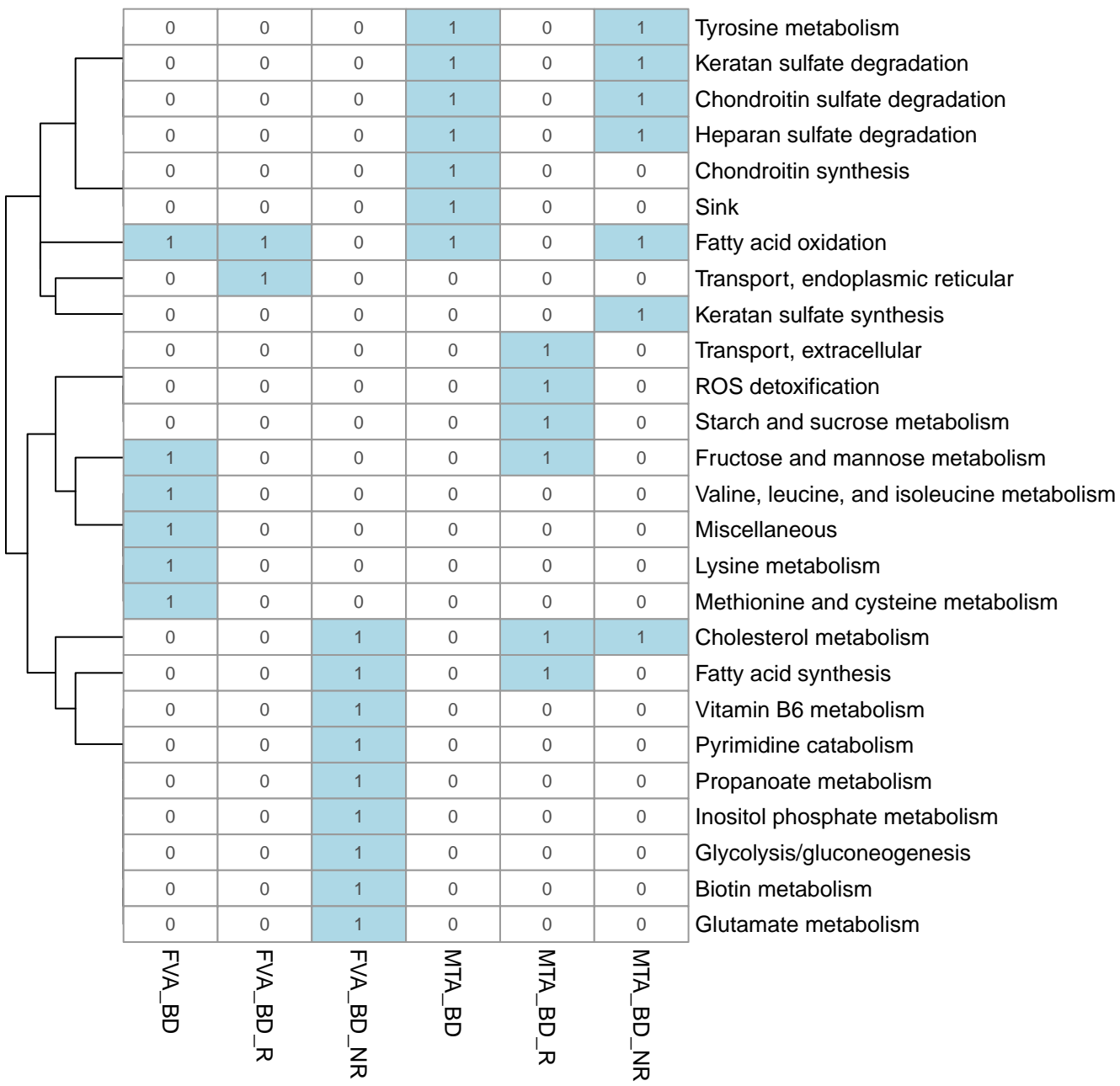
Norm_T2 – BD vs Li+

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



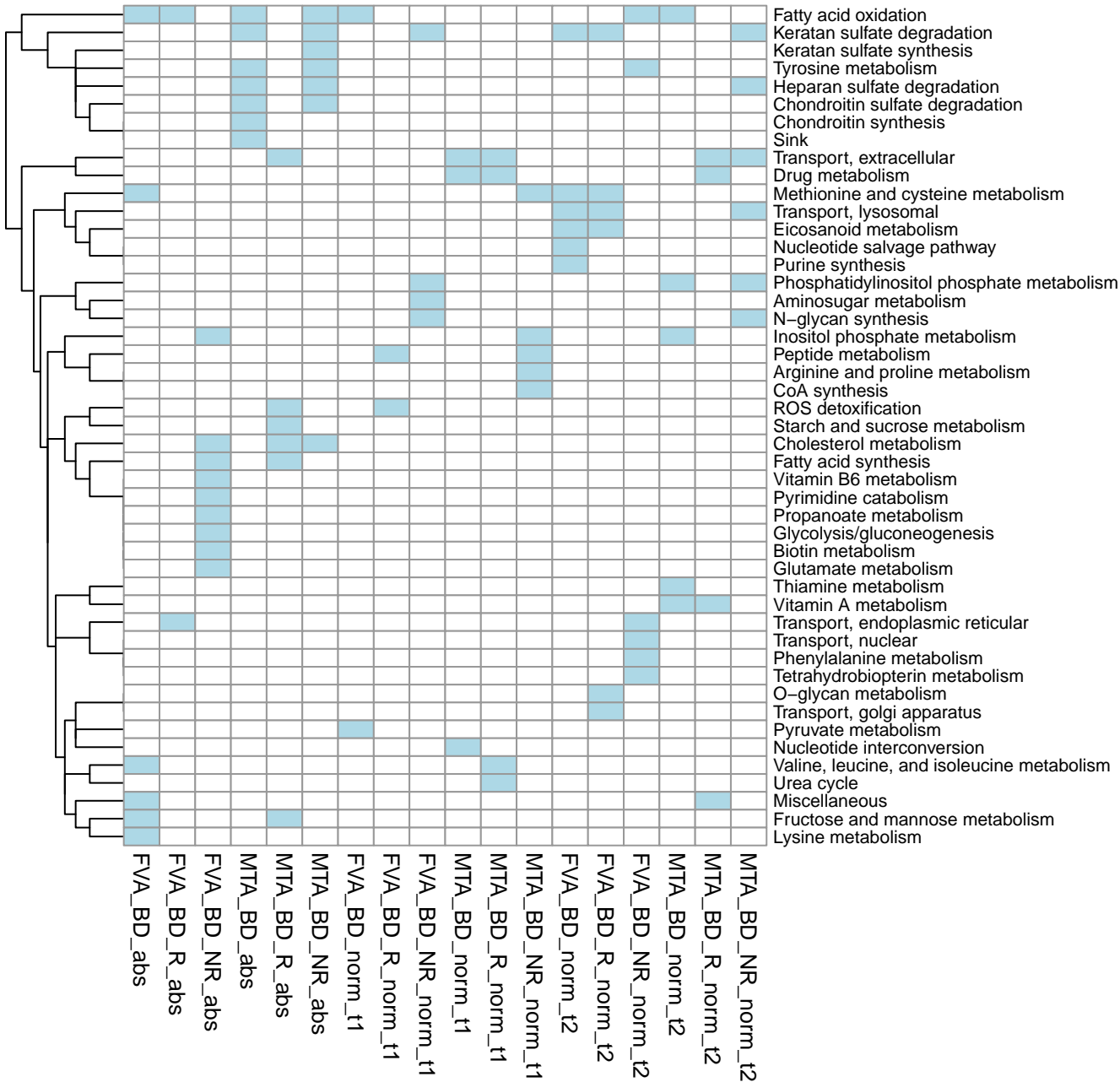
Norm_T1

	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

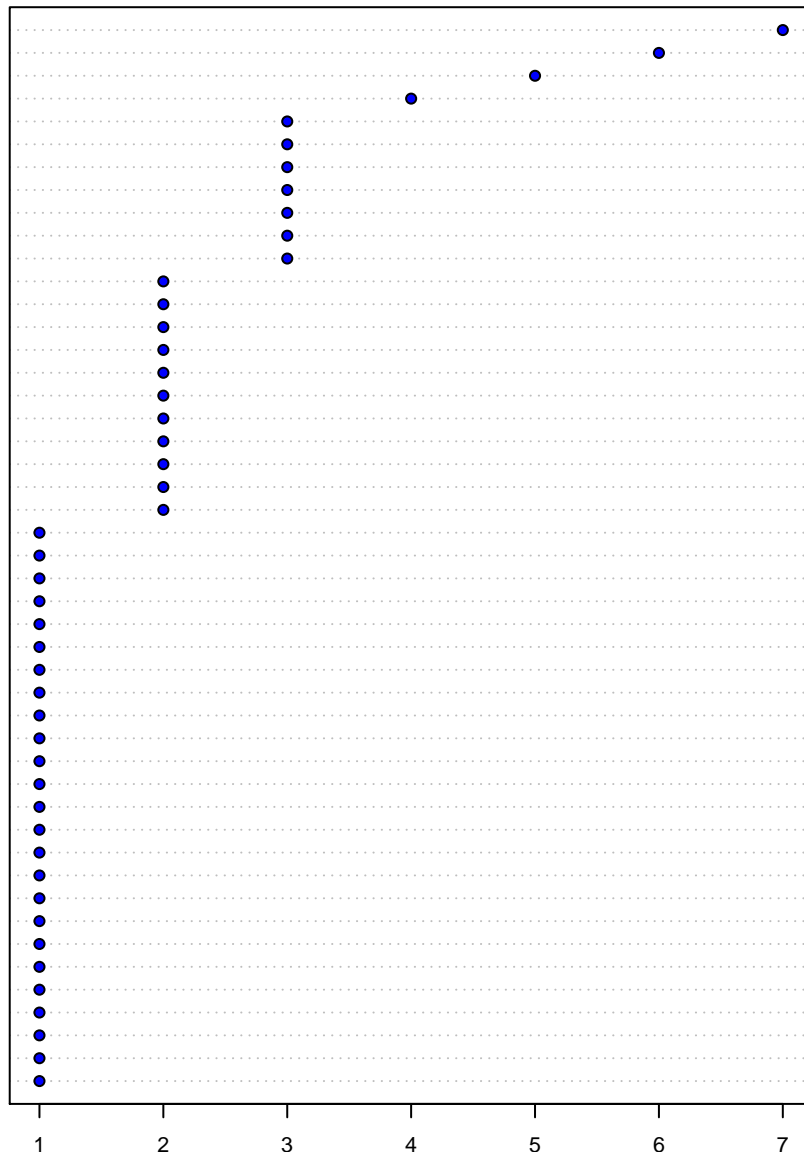
	0	0	0	1	1	0	Vitamin A metabolism
	0	0	0	0	1	0	Drug metabolism
	0	0	0	0	1	0	Miscellaneous
	0	0	1	1	0	0	Fatty acid oxidation
	0	0	1	0	0	0	Tyrosine metabolism
	0	0	1	0	0	0	Transport, nuclear
	0	0	1	0	0	0	Transport, endoplasmic reticular
	0	0	1	0	0	0	Phenylalanine metabolism
	0	0	1	0	0	0	Tetrahydrobiopterin 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



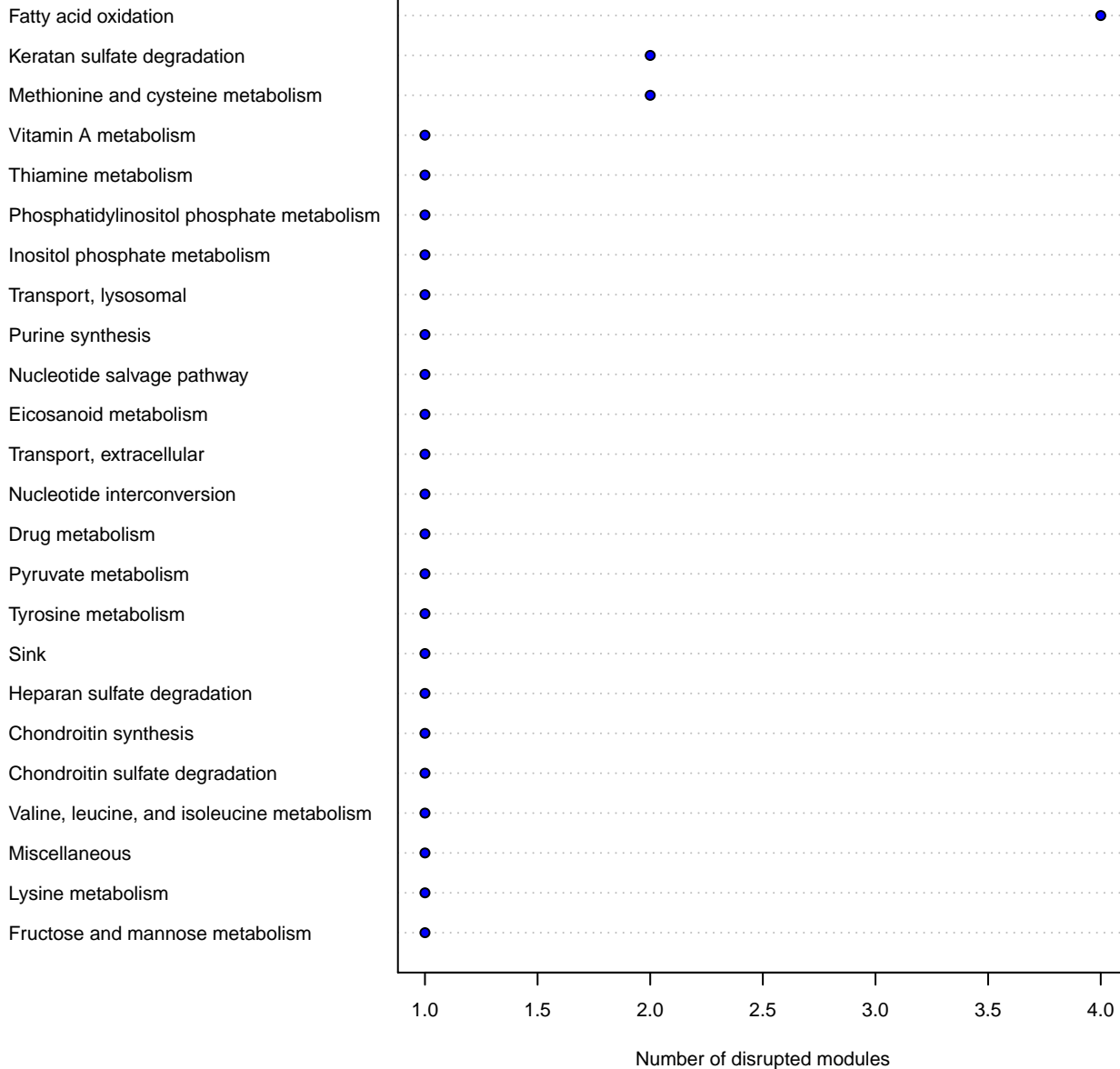
AII

Fatty acid oxidation
 Keratan sulfate degradation
 Transport, extracellular
 Methionine and cysteine metabolism
 Transport, lysosomal
 Drug metabolism
 Phosphatidylinositol phosphate metabolism
 Tyrosine metabolism
 Heparan sulfate degradation
 Inositol phosphate metabolism
 Cholesterol metabolism
 Vitamin A metabolism
 Eicosanoid metabolism
 N-glycan synthesis
 Peptide metabolism
 ROS detoxification
 Chondroitin sulfate degradation
 Fatty acid synthesis
 Transport, endoplasmic reticular
 Valine, leucine, and isoleucine metabolism
 Miscellaneous
 Fructose and mannose metabolism
 Thiamine metabolism
 Transport, nuclear
 Tetrahydrobiopterin metabolism
 Phenylalanine metabolism
 Transport, golgi apparatus
 O-glycan metabolism
 Purine synthesis
 Nucleotide salvage pathway
 CoA synthesis
 Arginine and proline metabolism
 Urea cycle
 Nucleotide interconversion
 Aminosugar metabolism
 Pyruvate metabolism
 Keratan sulfate synthesis
 Starch and sucrose metabolism
 Sink
 Chondroitin synthesis
 Vitamin B6 metabolism
 Pyrimidine catabolism
 Propanoate metabolism
 Glycolysis/gluconeogenesis
 Glutamate metabolism
 Biotin metabolism
 Lysine metabolism



Number of disrupted modules

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

1.0

1.5

2.0

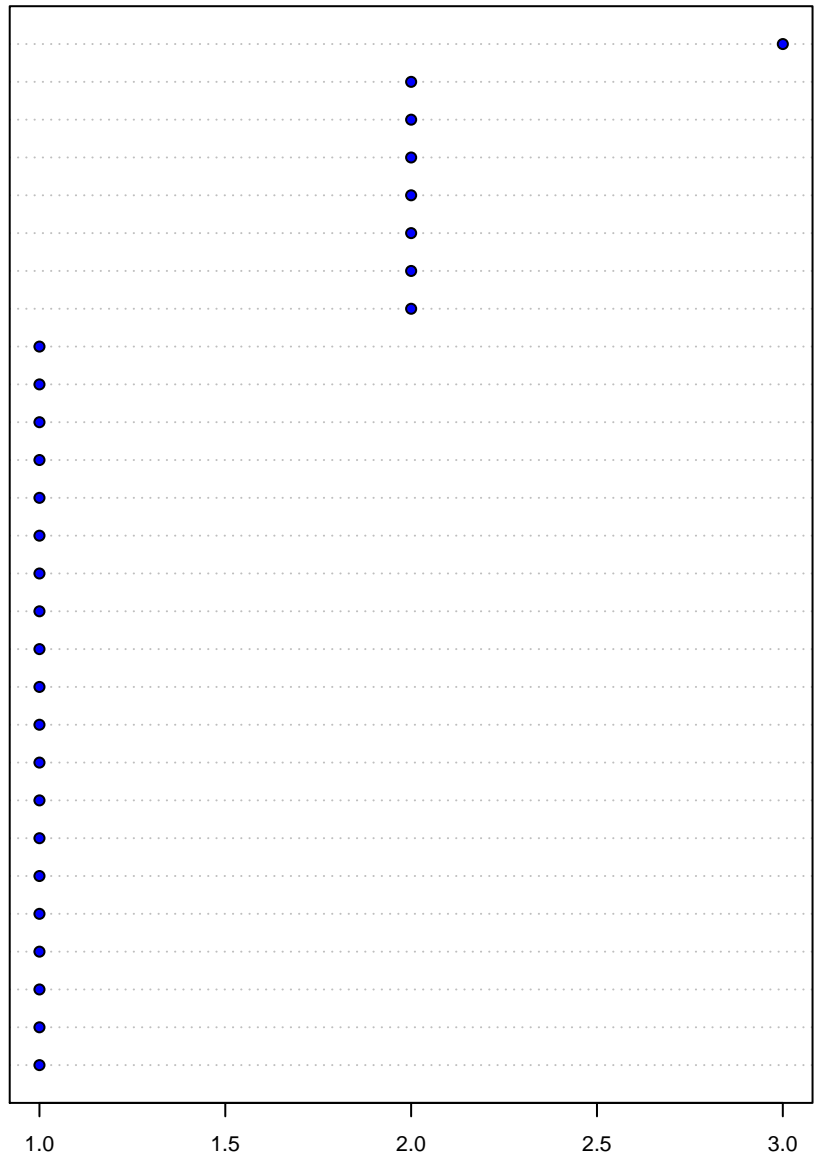
2.5

3.0

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

