

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	

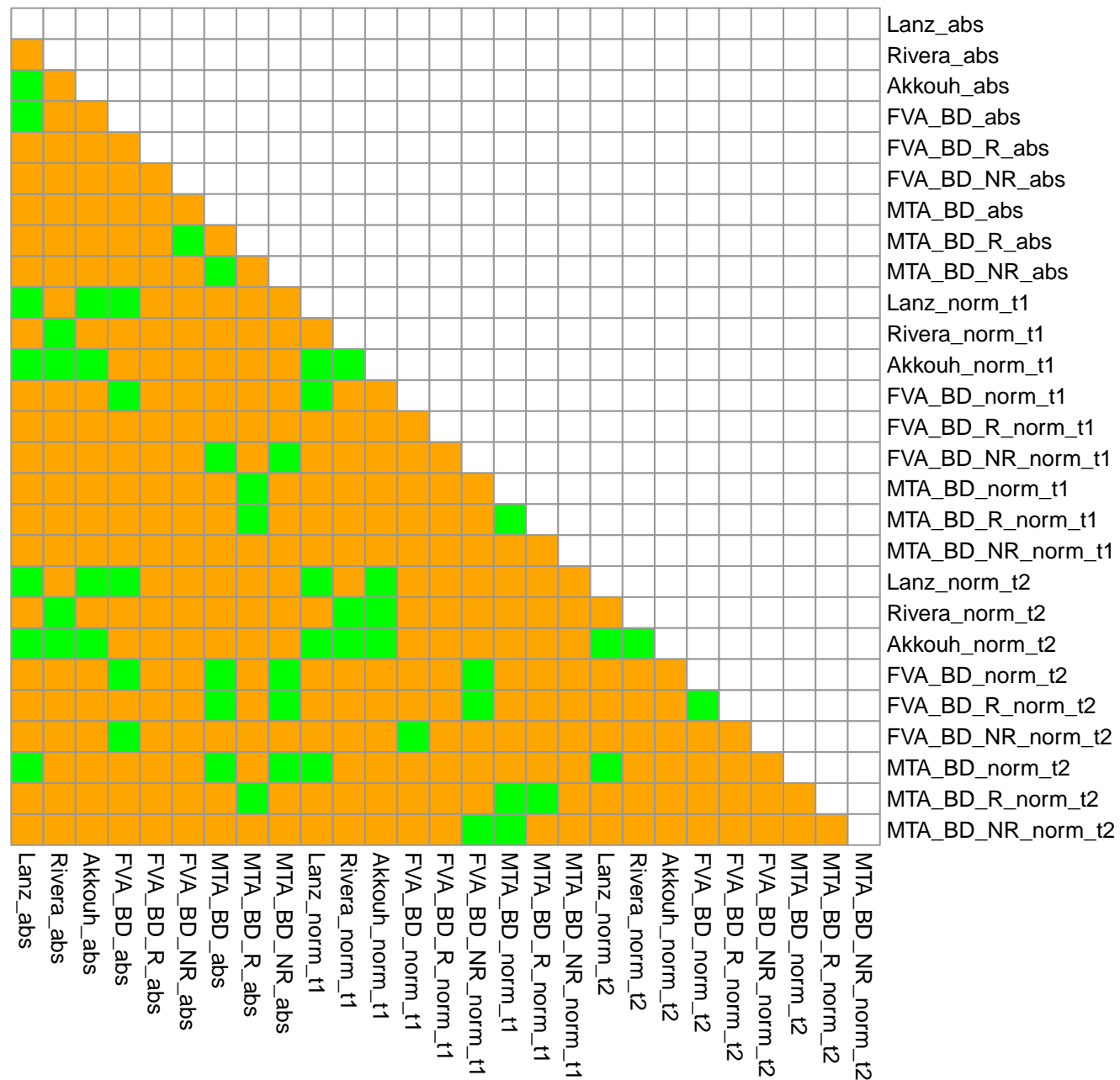
Norm\_T1 – BD vs Li+

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							

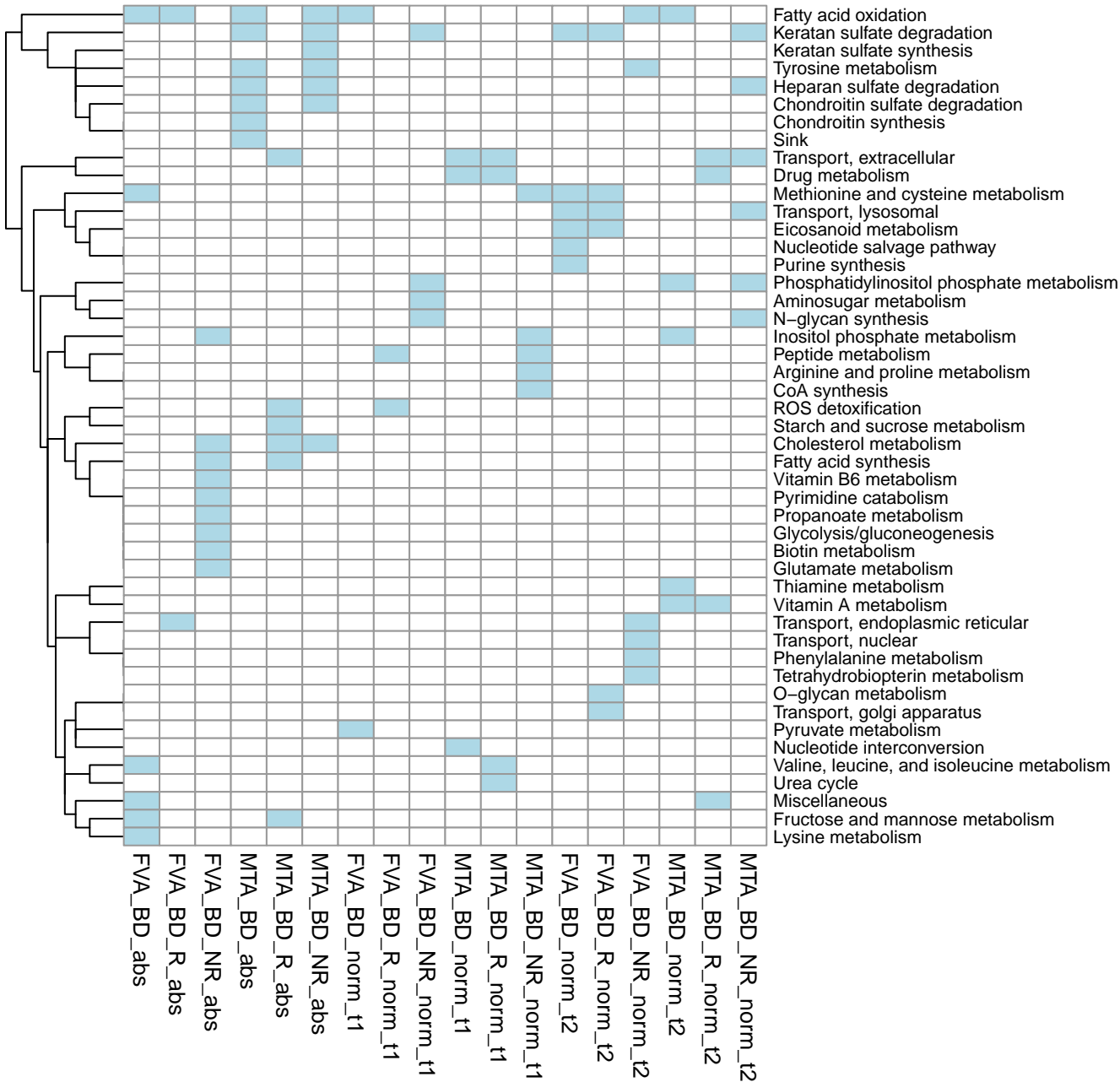
# Norm\_T1

	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

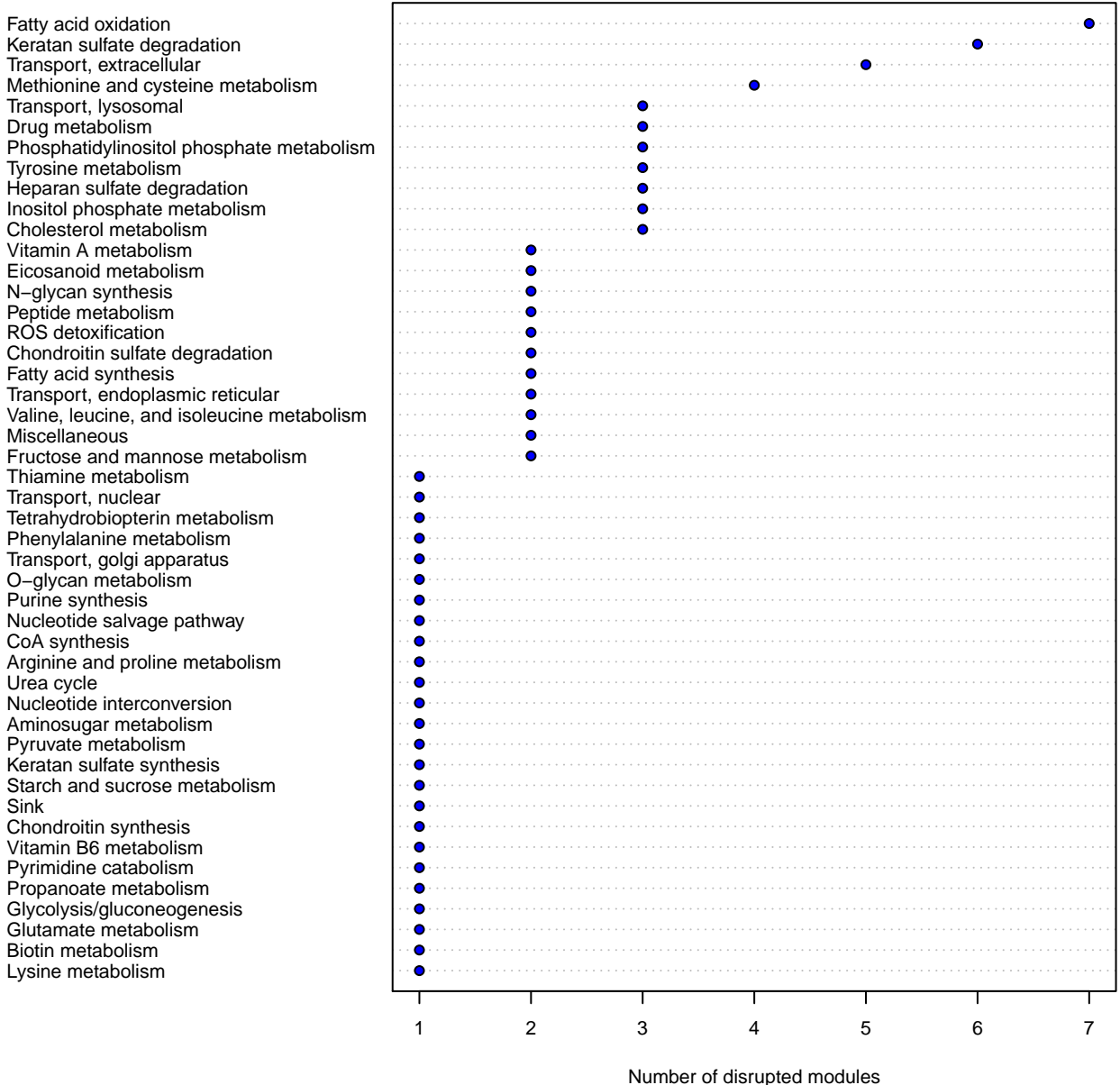
		0	0	0	1	1	0	Vitamin A metabolism
		0	0	0	0	1	0	Drug metabolism
		0	0	0	0	1	0	Miscellaneous
		0	0	1	1	0	0	Fatty acid oxidation
		0	0	1	0	0	0	Tyrosine metabolism
		0	0	1	0	0	0	Transport, nuclear
		0	0	1	0	0	0	Transport, endoplasmic reticular
		0	0	1	0	0	0	Phenylalanine metabolism
		0	0	1	0	0	0	Tetrahydrobiopterin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

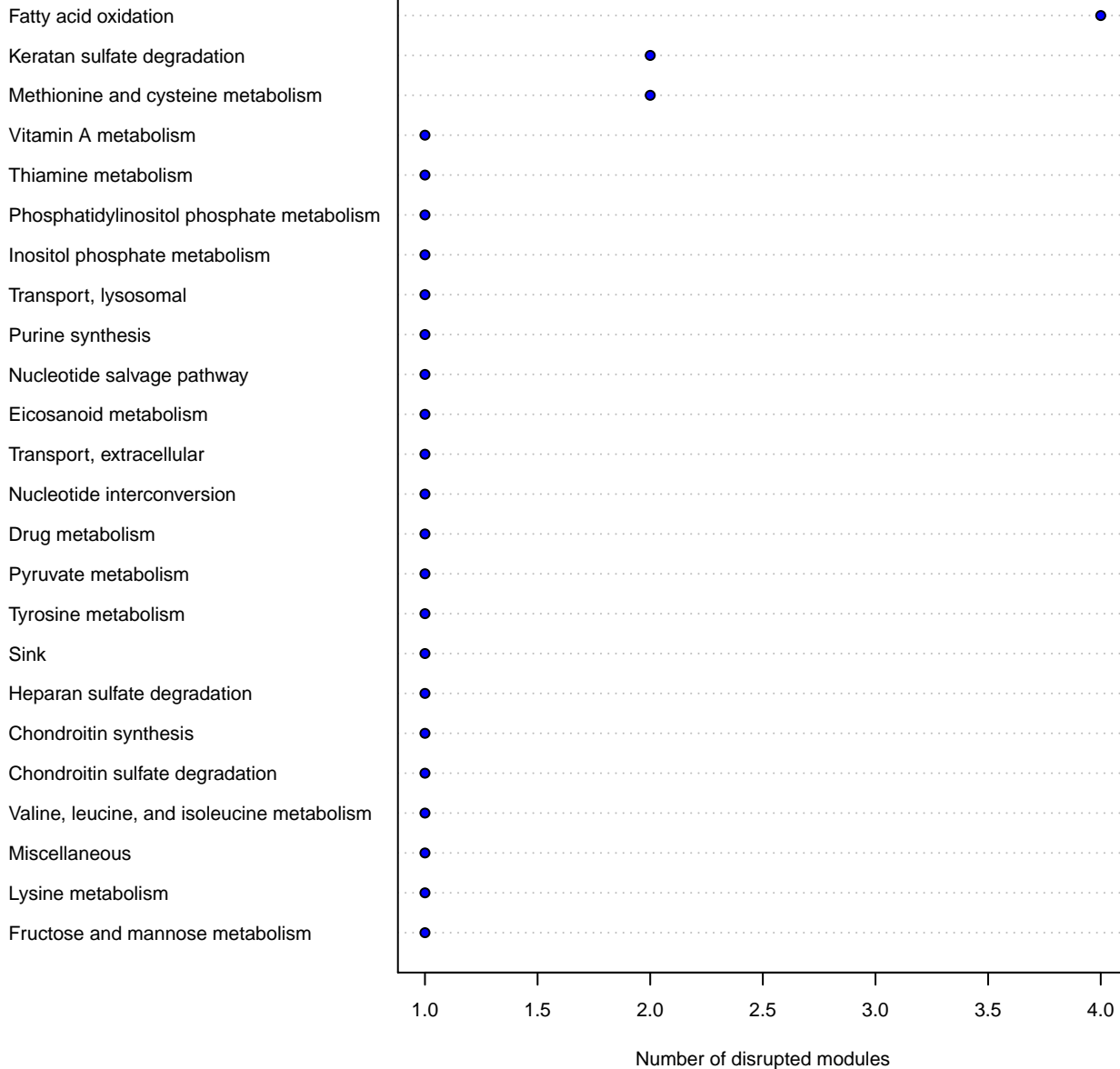




# AII



## 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

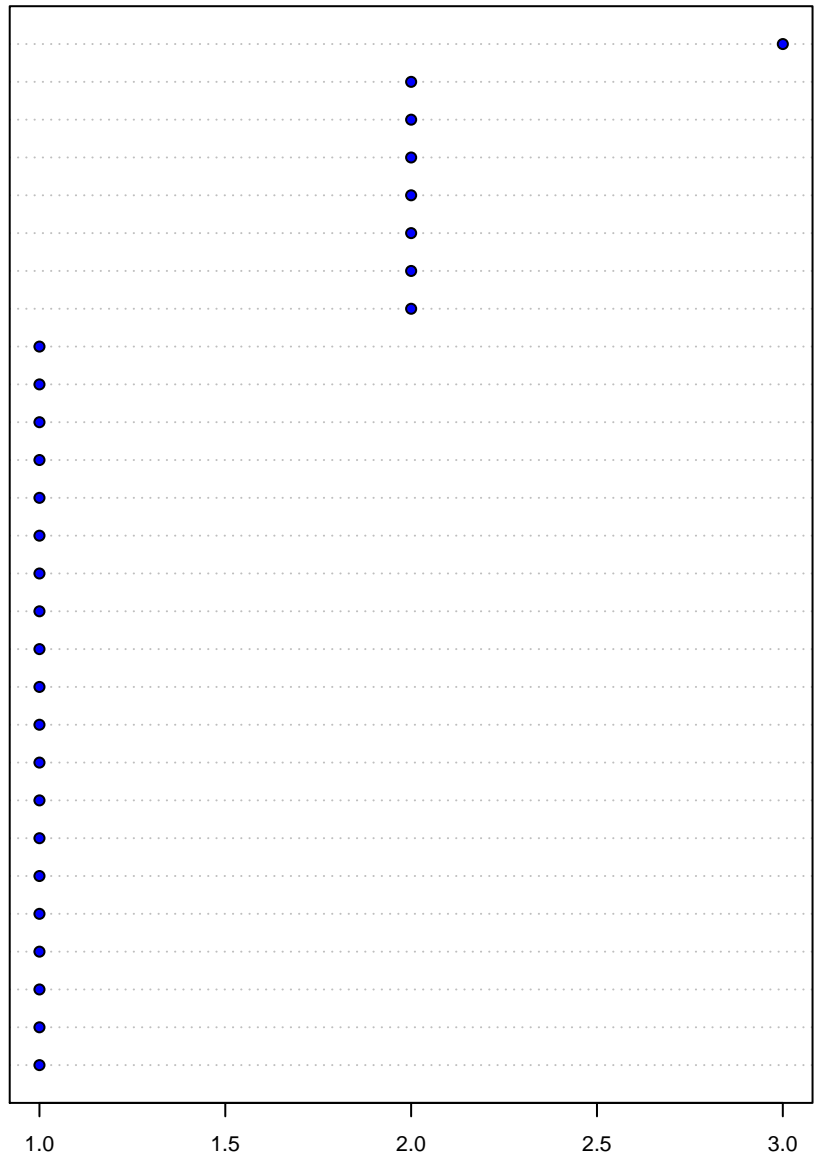
Fatty acid oxidation



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

