Abs − BD vs Li+

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

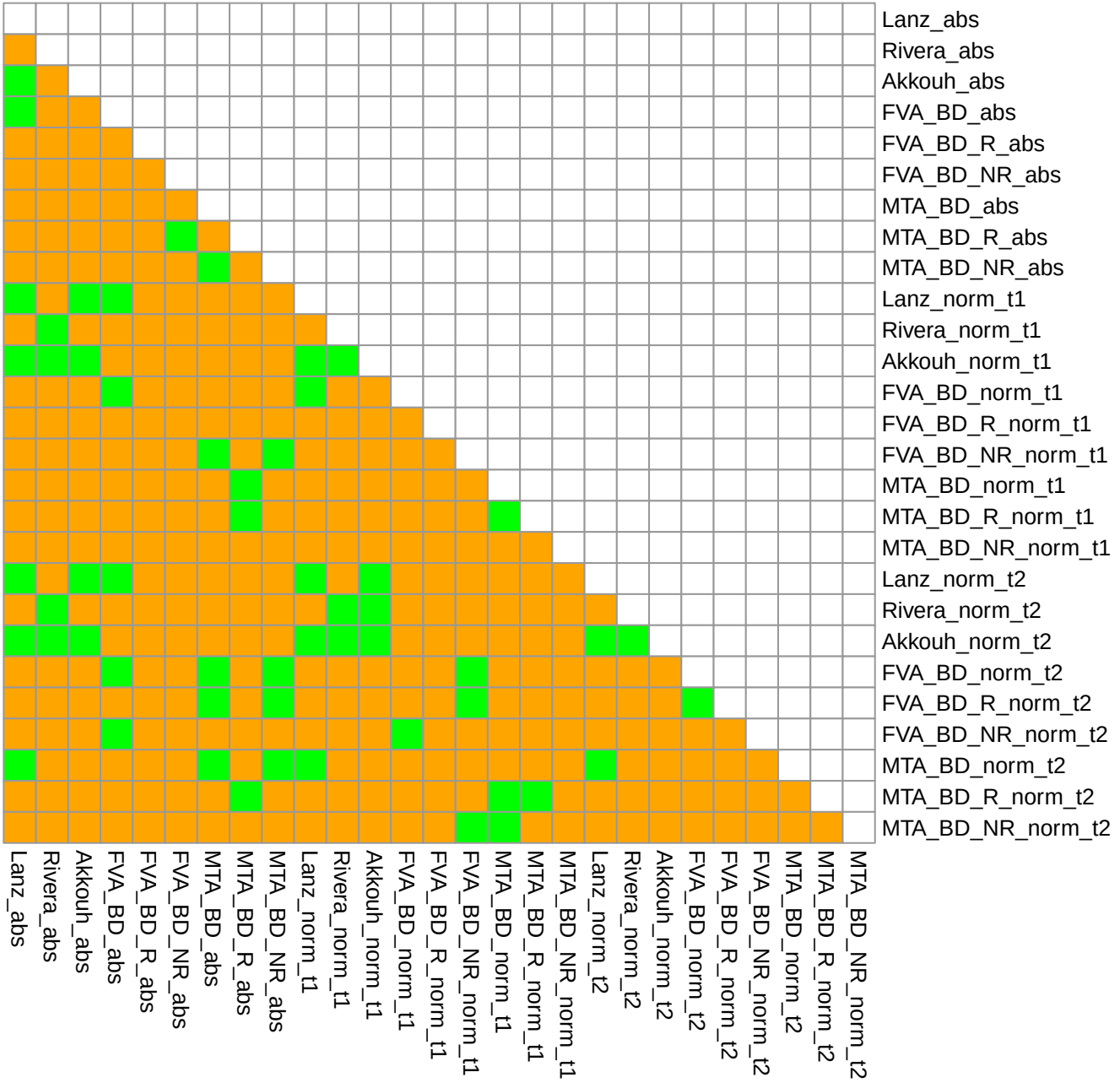
Norm_T1 − BD vs Li+

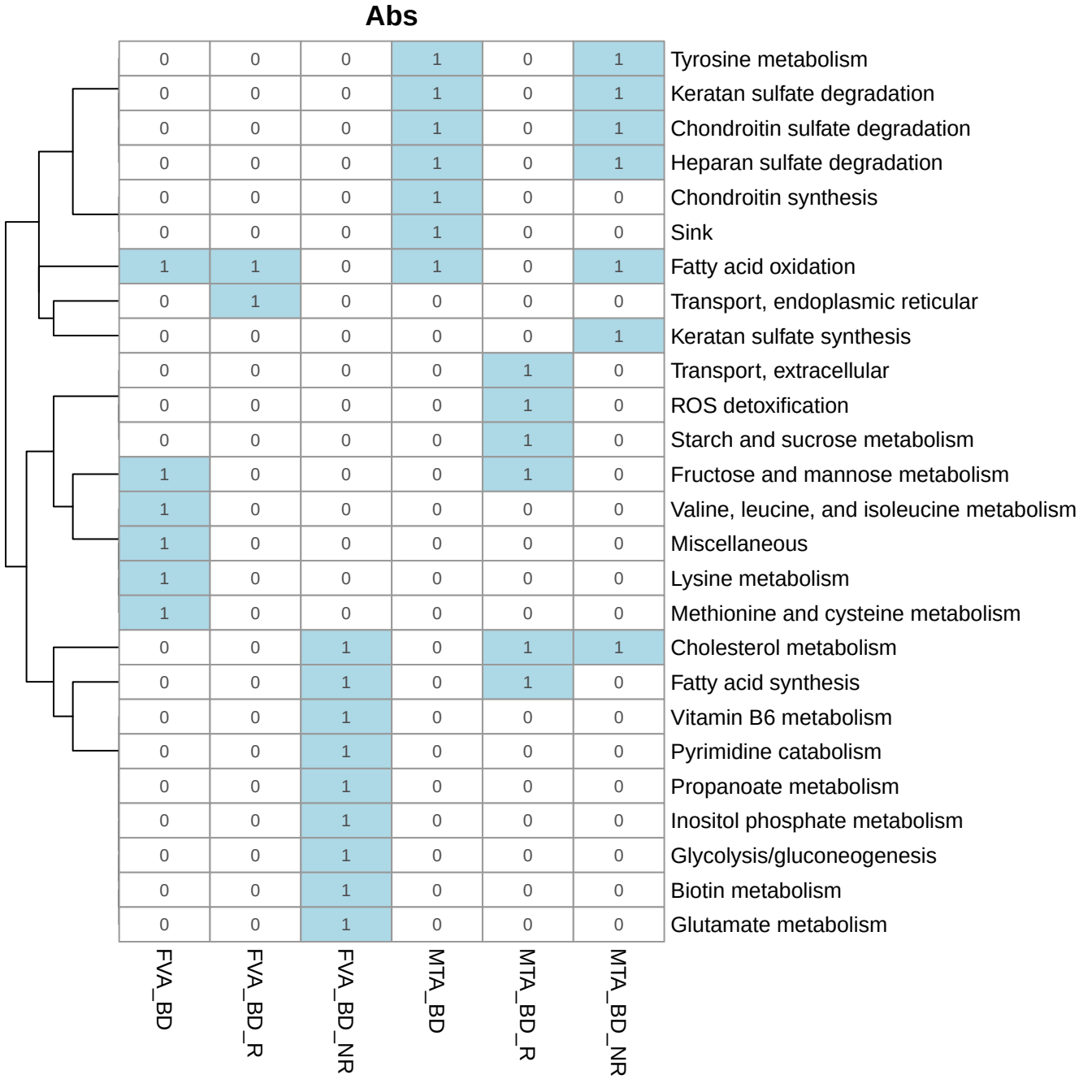
	Lanz	Rivera	Akkouh	FVA_BD	FVA_BD_R	FVA_BD_NR	MTA_BD	MTA_BD_R	MTA_BD_NR
Lanz	NA	NA	NA	NA	NA	NA	NA	NA	NA
Rivera	1.0e+00	NA	NA	NA	NA	NA	NA	NA	NA
Akkouh	2.1e−18	1.0e−02	NA	NA	NA	NA	NA	NA	NA
FVA_BD	1.1e−02	1.0e+00	1.0e+00	NA	NA	NA	NA	NA	NA
FVA_BD_R	1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA	NA
FVA_BD_NR	1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA
MTA_BD	1.0e+00	1.9e−01	8.1e−01	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA
MTA_BD_R	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_NR	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

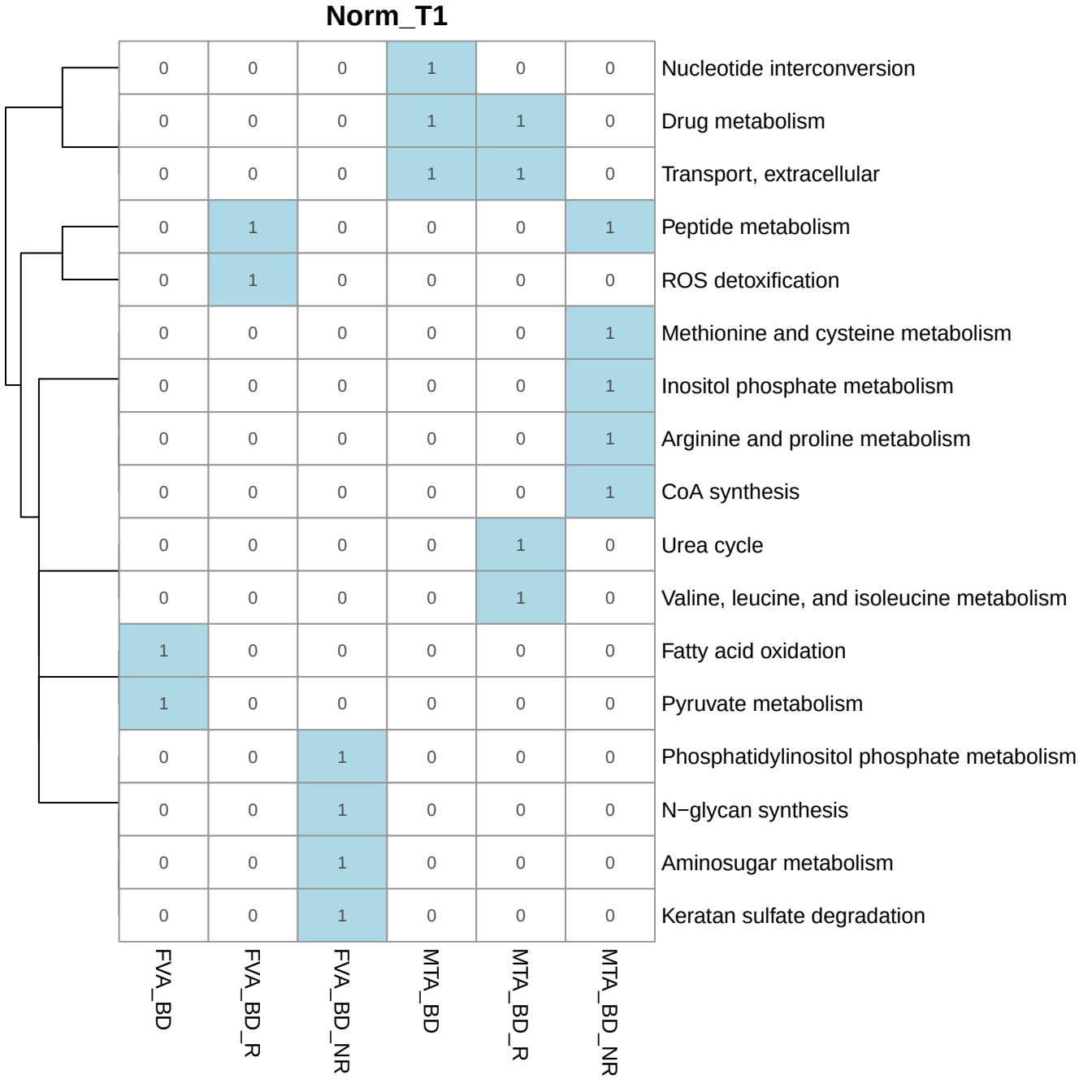
Norm_T2 − BD vs Li+

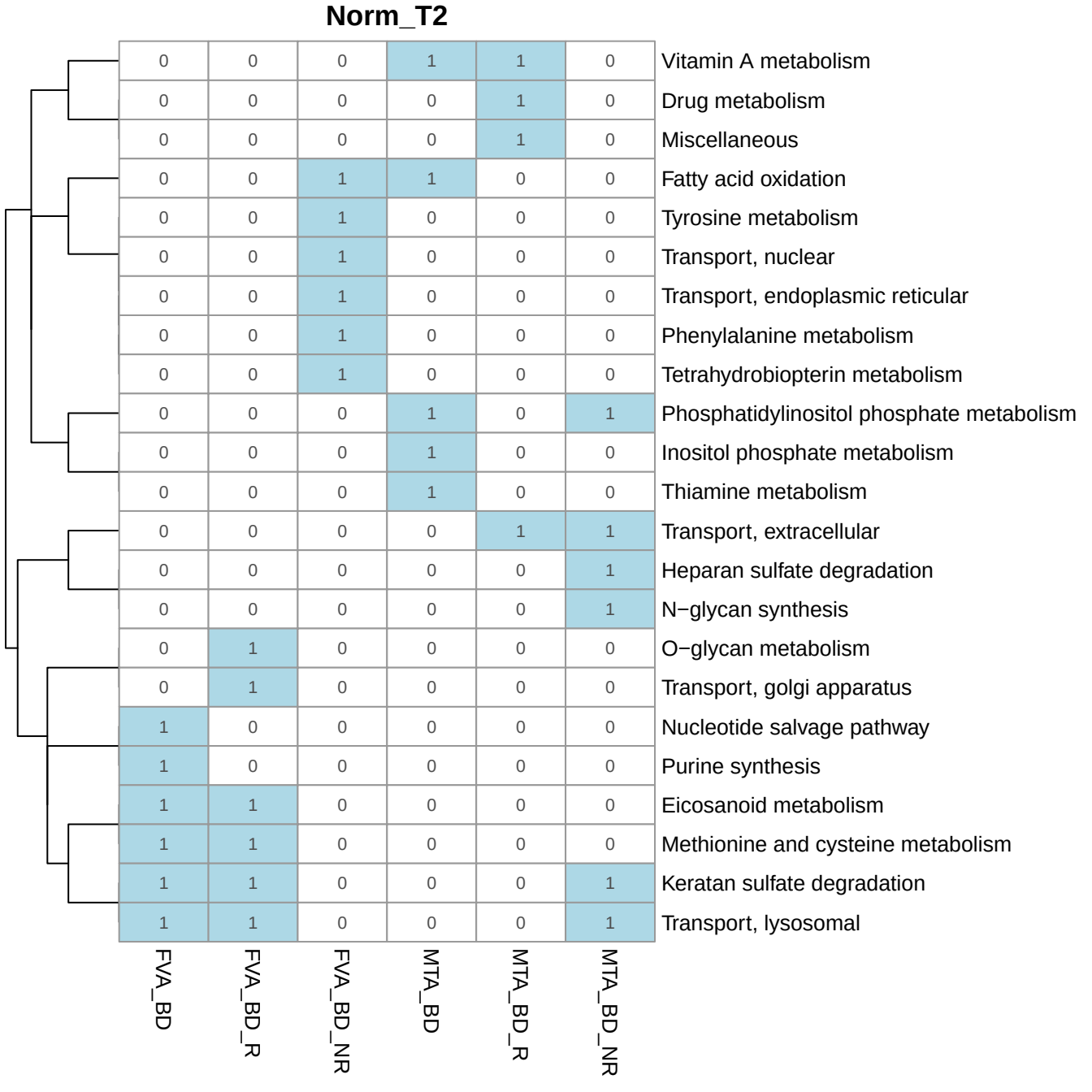
	Lanz	Rivera	Akkouh	FVA_BD	FVA_BD_R	FVA_BD_NR	MTA_BD	MTA_BD_R	MTA_BD_NR
Lanz	NA	NA	NA	NA	NA	NA	NA	NA	NA
Rivera	1.0e+00	NA	NA	NA	NA	NA	NA	NA	NA
Akkouh	1.4e−40	1.6e−02	NA	NA	NA	NA	NA	NA	NA
FVA_BD	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA	NA	NA
FVA_BD_R	1.0e+00	1.0e+00	1.0e+00	1.4e−54	NA	NA	NA	NA	NA
FVA_BD_NR	1.0e+00	1.0e+00	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA	NA
MTA_BD	1.9e−03	1.0e+00	6.4e−01	1.0e+00	1.0e+00	1.0e+00	NA	NA	NA
MTA_BD_R	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_NR	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

All − BD vs Li+

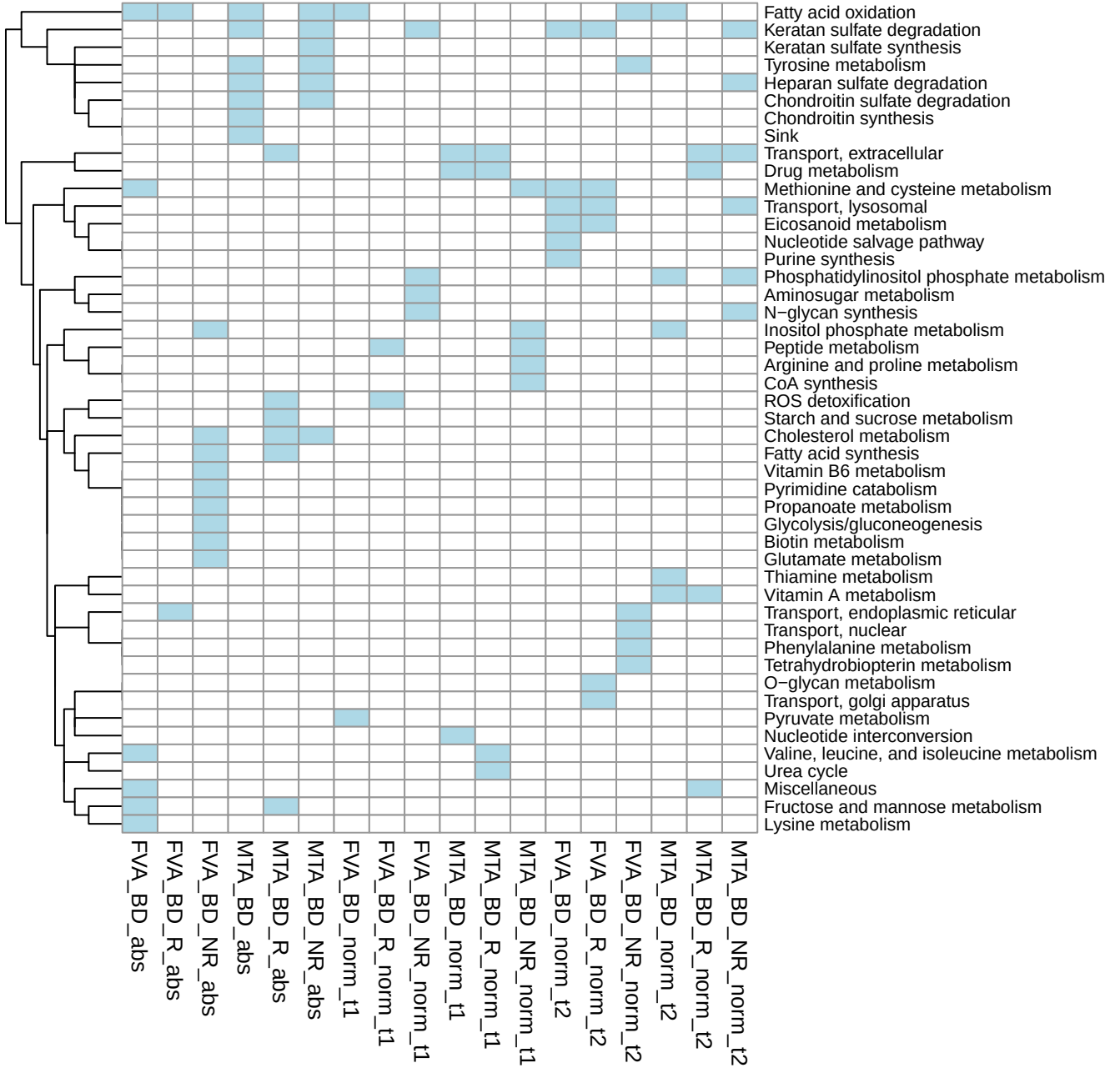

Lanz_abs
Rivera_abs
Akkouh_abs
FVA_BD_abs
FVA_BD_R_abs
FVA_BD_NR_abs
MTA_BD_abs
MTA_BD_R_abs
MTA_BD_NR_abs
Lanz_norm_t1
Rivera_norm_t1
Akkouh_norm_t1
FVA_BD_norm_t1
FVA_BD_R_norm_t1
FVA_BD_NR_norm_t1
MTA_BD_norm_t1
MTA_BD_R_norm_t1
MTA_BD_NR_norm_t1
Lanz_norm_t2
Rivera_norm_t2
Akkouh_norm_t2
FVA_BD_norm_t2
FVA_BD_R_norm_t2
FVA_BD_NR_norm_t2
MTA_BD_norm_t2
MTA_BD_R_norm_t2
MTA_BD_NR_norm_t2

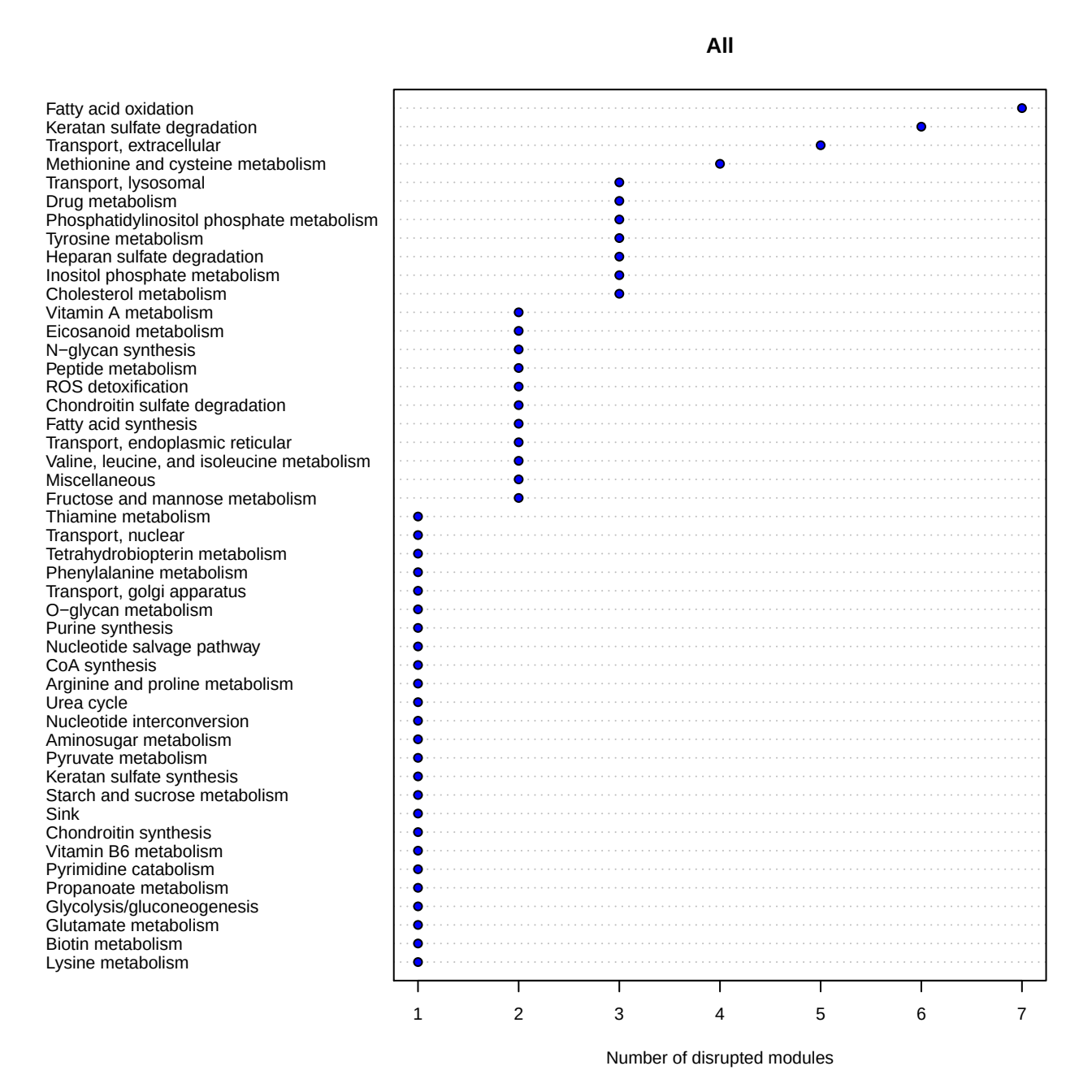

Abs
0 0 0 1 0 1 Tyrosine metabolism
0 0 0 1 0 1 Keratan sulfate degradation
0 0 0 1 0 1 Chondroitin sulfate degradation
0 0 0 1 0 1 Heparan sulfate degradation
0 0 0 1 0 0 Chondroitin synthesis
0 0 0 1 0 0 Sink
1 1 0 1 0 1 Fatty acid oxidation
0 1 0 0 0 0 Transport, endoplasmic reticular
0 0 0 0 0 1 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

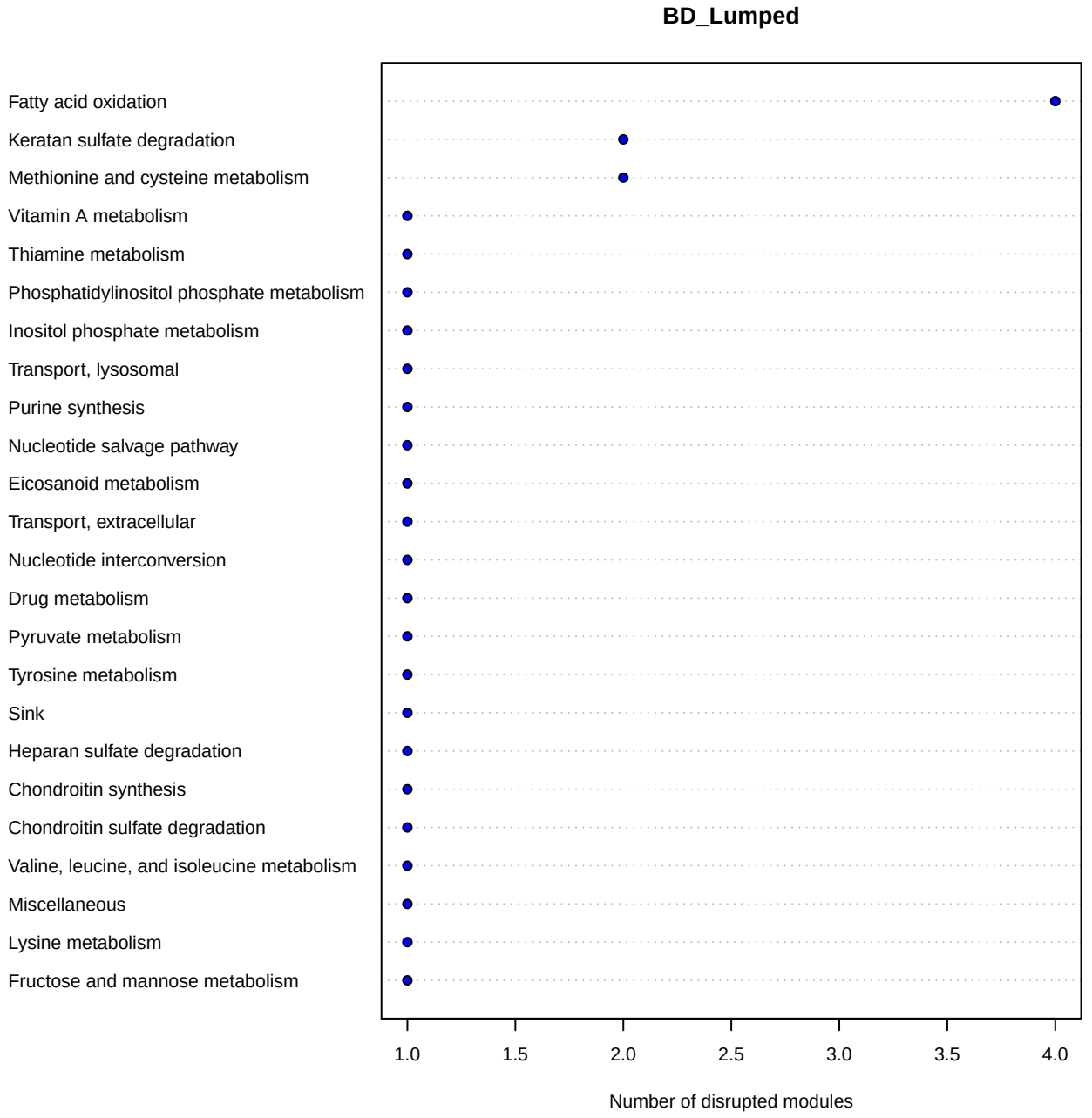

Norm_T1
0 0 0 1 0 0 Nucleotide interconversion
0 0 0 1 1 0 Drug metabolism
0 0 0 1 1 0 Transport, extracellular
0 1 0 0 0 1 Peptide metabolism
0 1 0 0 0 0 ROS detoxification
0 0 0 0 0 1 Methionine and cysteine metabolism
0 0 0 0 0 1 Inositol phosphate metabolism
0 0 0 0 0 1 Arginine and proline metabolism
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

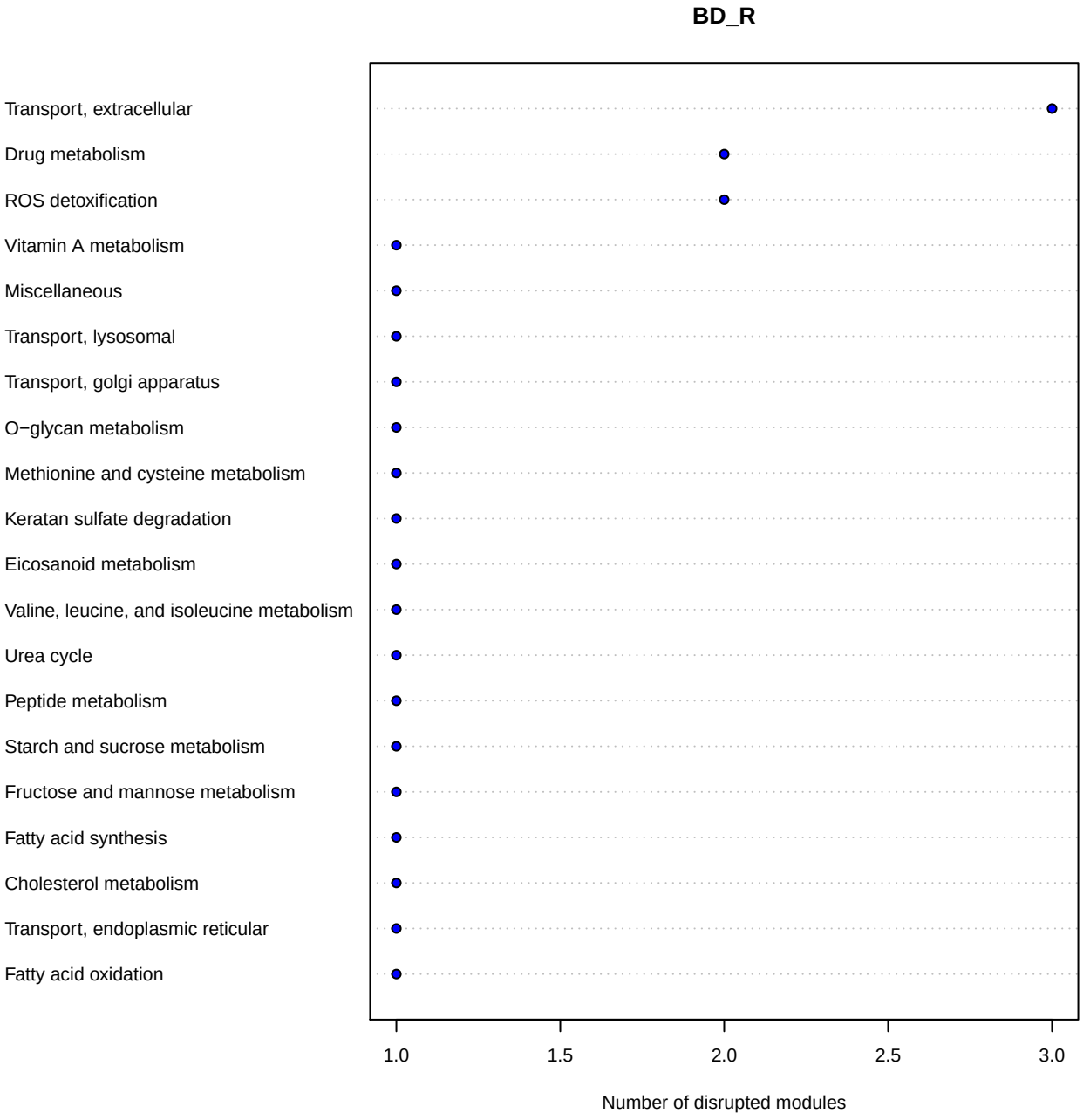

Norm_T2
0 0 0 1 1 0 Vitamin A metabolism
0 0 0 0 1 0 Drug metabolism
0 0 0 0 1 0 Miscellaneous
0 0 1 1 0 0 Fatty acid oxidation
0 0 1 0 0 0 Tyrosine metabolism
0 0 1 0 0 0 Transport, nuclear
0 0 1 0 0 0 Transport, endoplasmic reticular
0 0 1 0 0 0 Phenylalanine metabolism
0 0 1 0 0 0 Tetrahydrobiopterin 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

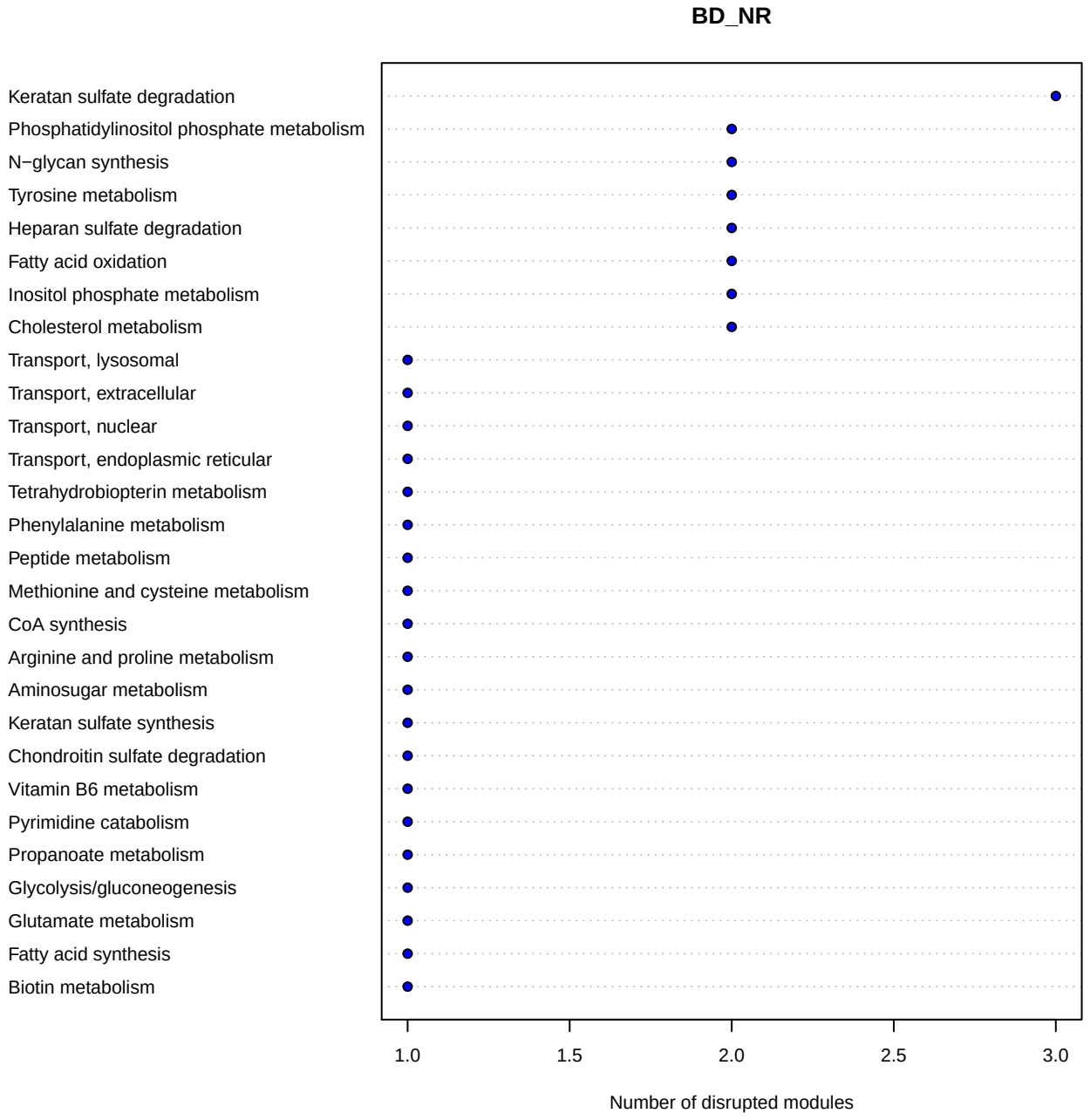
All

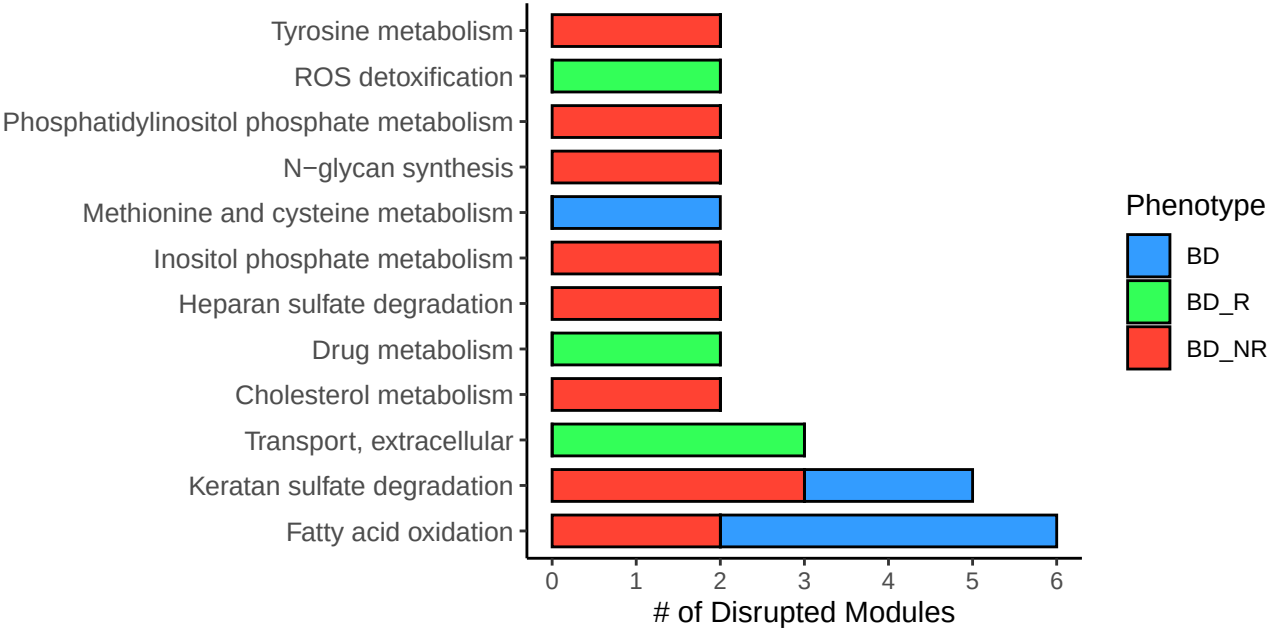

Fatty acid oxidation
Keratan sulfate degradation
Keratan sulfate synthesis
Tyrosine metabolism
Heparan sulfate degradation
Chondroitin sulfate degradation
Chondroitin synthesis
Sink
Transport, extracellular
Drug metabolism
Methionine and cysteine metabolism
Transport, lysosomal
Eicosanoid metabolism
Nucleotide salvage pathway
Purine synthesis
Phosphatidylinositol phosphate metabolism
Aminosugar metabolism
N−glycan synthesis
Inositol phosphate metabolism
Peptide metabolism
Arginine and proline metabolism
CoA synthesis
ROS detoxification
Starch and sucrose metabolism
Cholesterol metabolism
Fatty acid synthesis
Vitamin B6 metabolism
Pyrimidine catabolism
Propanoate metabolism
Glycolysis/gluconeogenesis
Biotin metabolism
Glutamate metabolism
Thiamine metabolism
Vitamin A metabolism
Transport, endoplasmic reticular
Transport, nuclear
Phenylalanine metabolism
Tetrahydrobiopterin metabolism
O−glycan metabolism
Transport, golgi apparatus
Pyruvate metabolism
Nucleotide interconversion
Valine, leucine, and isoleucine metabolism
Urea cycle
Miscellaneous
Fructose and mannose metabolism
Lysine metabolism
FVA_BD_abs
FVA_BD_R_abs
FVA_BD_NR_abs
MTA_BD_abs
MTA_BD_R_abs
MTA_BD_NR_abs
FVA_BD_norm_t1
FVA_BD_R_norm_t1
FVA_BD_NR_norm_t1
MTA_BD_norm_t1
MTA_BD_R_norm_t1
MTA_BD_NR_norm_t1
FVA_BD_norm_t2
FVA_BD_R_norm_t2
FVA_BD_NR_norm_t2
MTA_BD_norm_t2
MTA_BD_R_norm_t2
MTA_BD_NR_norm_t2


All
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
1
2
3
4
5
6
7
Number of disrupted modules


BD_Lumped
Fatty acid oxidation
Keratan sulfate degradation
Methionine and cysteine metabolism
Vitamin A metabolism
Thiamine metabolism
Phosphatidylinositol phosphate metabolism
Inositol phosphate metabolism
Transport, lysosomal
Purine synthesis
Nucleotide salvage pathway
Eicosanoid metabolism
Transport, extracellular
Nucleotide interconversion
Drug metabolism
Pyruvate metabolism
Tyrosine metabolism
Sink
Heparan sulfate degradation
Chondroitin synthesis
Chondroitin sulfate degradation
Valine, leucine, and isoleucine metabolism
Miscellaneous
Lysine metabolism
Fructose and mannose metabolism
1.0
1.5
2.0
2.5
3.0
3.5
4.0
Number of disrupted modules


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
1.0
1.5
2.0
2.5
3.0
Number of disrupted modules


Tyrosine metabolism
ROS detoxification
Phosphatidylinositol phosphate metabolism
N−glycan synthesis
Methionine and cysteine metabolism
Inositol phosphate metabolism
Heparan sulfate degradation
Drug metabolism
Cholesterol metabolism
Transport, extracellular
Keratan sulfate degradation
Fatty acid oxidation
0
1
2
3
4
5
6
# of Disrupted Modules
Phenotype
BD
BD_R
BD_NR