Insoluble/soluble fraction ratio determines effects of dietary fiber on gut microbiota and serum metabolites in healthy mice

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Table S1 The composition of nine dietary fiber recipes used in this study

Groups / Ingredients	AIN93G diet	IxSyDF_CF
Casein, 30mech	20.00%	20.00%
L-cystine	0.30%	0.30%
Corn starch	39.75%	39.75%
Maltodextrin	13.20%	13.20%
Sucrose	10.00%	10.00%
Cellulose	5.00%	-
Soybean oil	7.00%	7.00%
T-butylhydroquinone	0.0014%	0.0014%
Mineral mix s10022G	3.50%	3.50%
Vitamin mix V10037	1.00%	1.00%
Choline bitartrate	0.25%	0.25%
IxSyDF	-	5.00%

Note: IxSyDF represents I1S9DF, I2S8DF, I3S7DF, I4S6DF, I5S5DF, I6S4DF, I7S3DF, I8S2DF, and I9S1DF.

Figures legends:

Figure S1. Animal experiment design.

Figure S2. HPGPC chromatograms of (A) ASDF; (B) CSDF; (C) KSDF; (D) BSDF; (E) OSDF; (F) SSDF.

Figure S3. PCA score plots (A) between I1S9DF and Control groups; (B) between I2S8DF and Control groups; (C) between I3S7DF and Control groups; (D) between I4S6DF and Control groups; (E) between I5S5DF and Control groups; (F) between I6S4DF and Control groups; (G) between I7S3DF and Control groups; (H) between I8S2DF and Control groups; (I) between I9S1DF and Control groups.

Figure S4. The chemRICH enrichment analysis illustrates the markedly affected metabolites clusters ($p < 0.05$) (A) between I1S9DF and Control groups, (B) between I2S8DF and Control groups, (C) between I3S7DF and Control groups, (D) between I4S6DF and Control groups, (E) between I5S5DF and Control groups, (F) between I6S4DF and Control groups, (G) between I7S3DF and Control groups, (H) between I8S2DF and Control groups, (I) between I9S1DF and Control groups. The plot y-axis represents the remarkably changed clusters. The total of metabolites was represented by the sizes of node. The colors of the cluster indicate the trend of increased or decreased metabolites (red = totally increased, blue = totally reduced, fuchsia = both but major increased, dark orchid = both but major decreased).

Figure S5. Pathway analysis of markedly affected metabolites (A) between I1S9DF and Control groups; (B) between I2S8DF and Control groups; (C) between I3S7DF and Control groups, (D) between I4S6DF and Control groups, (E) between I5S5DF and Control groups, (F) between I6S4DF and Control groups, (G) between I7S3DF and Control groups, (H) between I8S2DF and Control groups, (I) between I9S1DF and Control groups by using MetaboAnalyst 5.0 (based on $p<0.05$, impact factor>0.1).

Figure S1

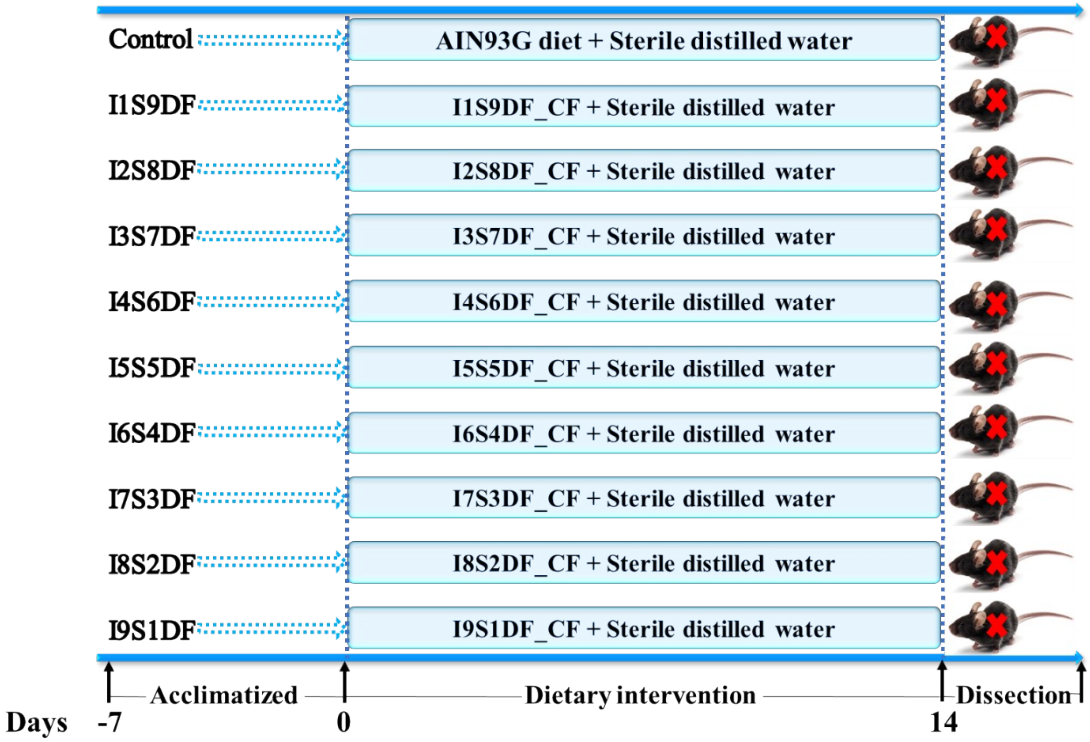

Control
AIN93G diet + Sterile distilled water
I1S9DF
I1S9DF_CF + Sterile distilled water
I2S8DF
I2S8DF_CF + Sterile distilled water
I3S7DF
I3S7DF_CF + Sterile distilled water
I4S6DF
I4S6DF_CF + Sterile distilled water
I5S5DF
I5S5DF_CF + Sterile distilled water
I6S4DF
I6S4DF_CF + Sterile distilled water
I7S3DF
I7S3DF_CF + Sterile distilled water
I8S2DF
I8S2DF_CF + Sterile distilled water
I9S1DF
I9S1DF_CF + Sterile distilled water
Acclimatized
Dietary intervention
Dissection
Days
-7
0
14

Figure S2

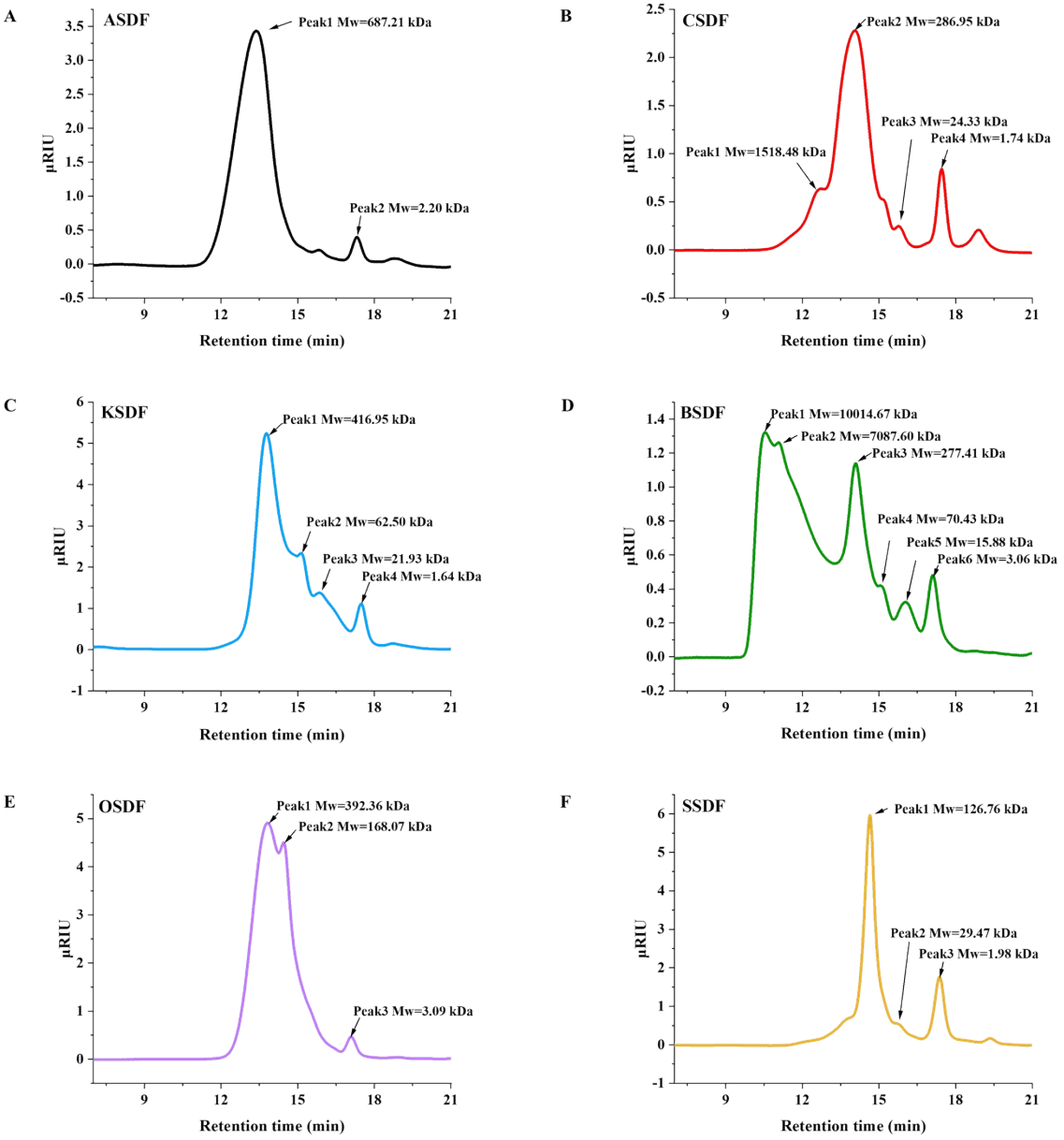

A
ASDF
Peak1 Mw=687.21 kDa
Peak2 Mw=2.20 kDa
μRIU
Retention time (min)
B
CSDF
Peak2 Mw=286.95 kDa
Peak3 Mw=24.33 kDa
Peak4 Mw=1.74 kDa
Peak1 Mw=1518.48 kDa
μRIU
Retention time (min)
C
KSDF
Peak1 Mw=416.95 kDa
Peak2 Mw=62.50 kDa
Peak3 Mw=21.93 kDa
Peak4 Mw=1.64 kDa
μRIU
Retention time (min)
D
BSDF
Peak1 Mw=10014.67 kDa
Peak2 Mw=7087.60 kDa
Peak3 Mw=277.41 kDa
Peak4 Mw=70.43 kDa
Peak5 Mw=15.88 kDa
Peak6 Mw=3.06 kDa
μRIU
Retention time (min)
E
OSDF
Peak1 Mw=392.36 kDa
Peak2 Mw=168.07 kDa
Peak3 Mw=3.09 kDa
μRIU
Retention time (min)
F
SSDF
Peak1 Mw=126.76 kDa
Peak2 Mw=29.47 kDa
Peak3 Mw=1.98 kDa
μRIU
Retention time (min)

Figure S3

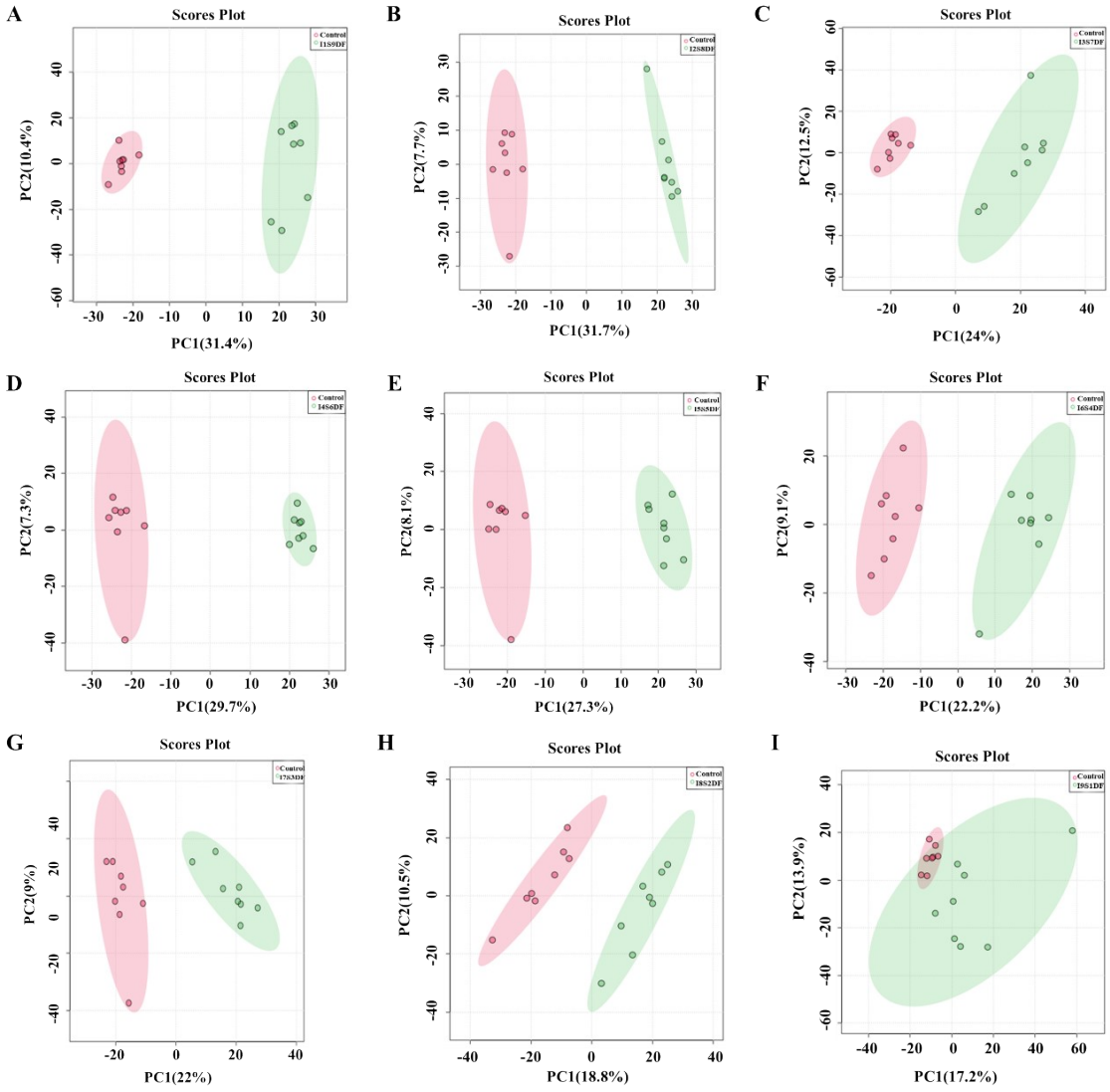

A
Scores Plot
PC2(10.4%)
PC1(31.4%)
B
Scores Plot
PC2(7.7%)
PC1(31.7%)
C
Scores Plot
PC2(12.5%)
PC1(24%)
D
Scores Plot
PC2(7.3%)
PC1(29.7%)
E
Scores Plot
PC2(8.1%)
PC1(27.3%)
F
Scores Plot
PC2(9.1%)
PC1(22.2%)
G
Scores Plot
PC2(9%)
PC1(22%)
H
Scores Plot
PC2(10.5%)
PC1(18.8%)
I
Scores Plot
PC2(13.9%)
PC1(17.2%)

Figure S4

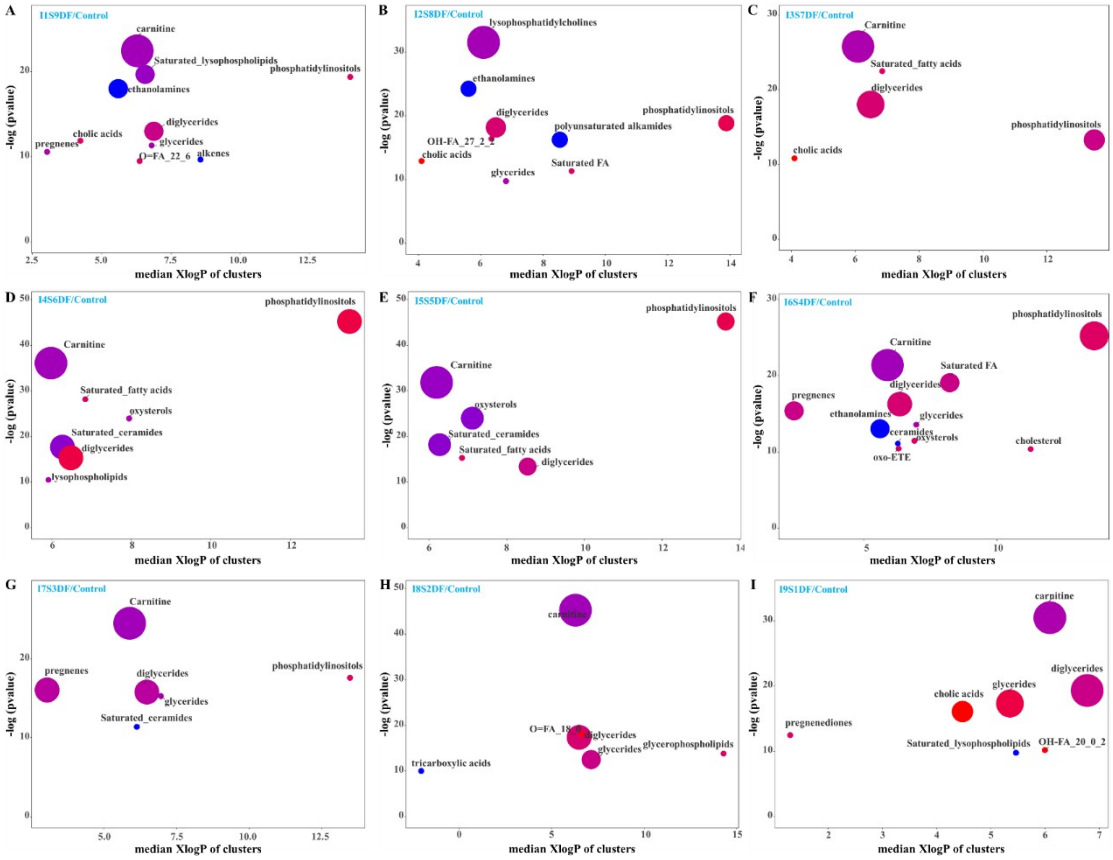
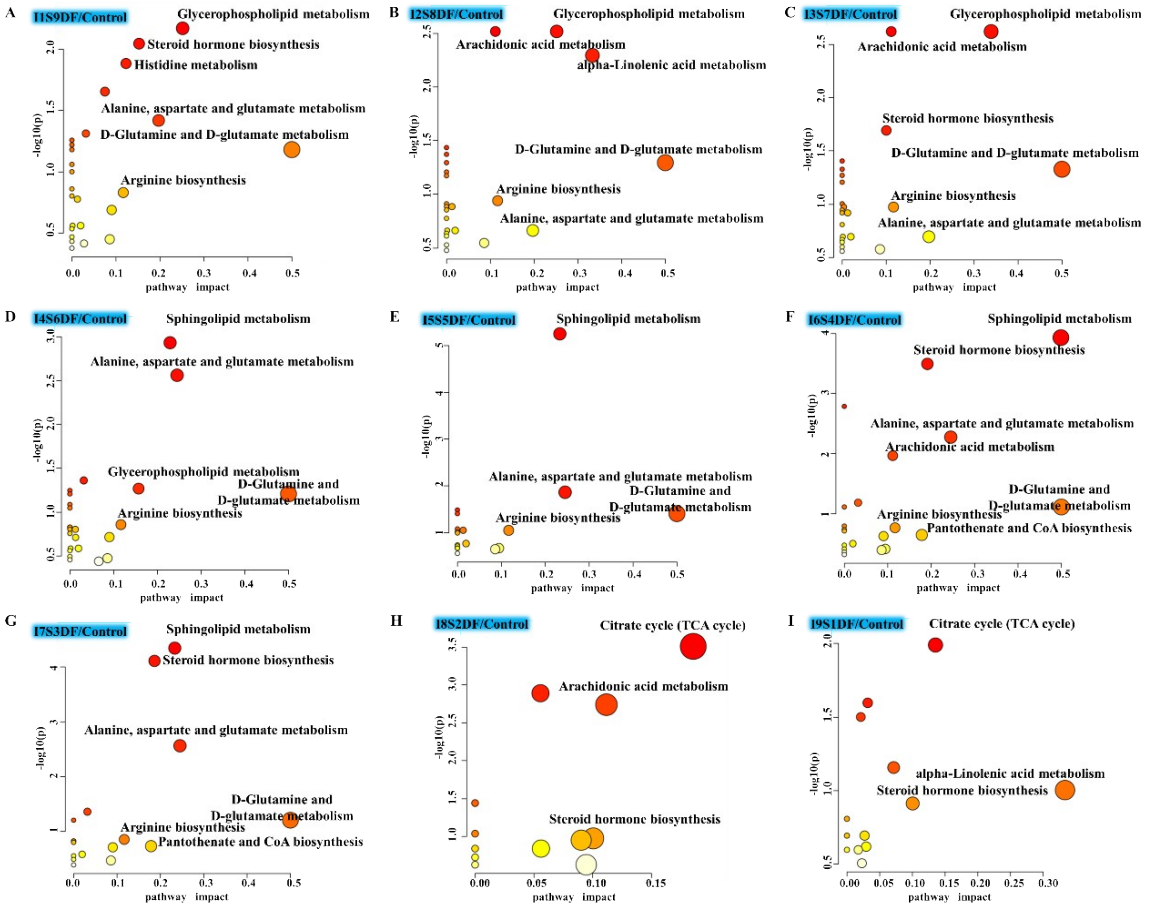

A
11S9DF/Control
carnitine
Saturated_lysophospholipids
phosphatidylinositols
ethanolamines
diglycerides
cholic acids
glycerides
pregnenes
O=FA_22_6
alkenes
B
12S8DF/Control
lysophosphatidylcholines
ethanolamines
diglycerides
phosphatidylinositols
polyunsaturated alkamides
OH-FA_27_2_2
cholic acids
Saturated FA
glycerides
C
13S7DF/Control
Carnitine
Saturated_fatty acids
diglycerides
phosphatidylinositols
cholic acids
D
14S6DF/Control
phosphatidylinositols
Carnitine
Saturated_fatty acids
oxysterols
Saturated_ceramides
diglycerides
lysophospholipids
E
15S5DF/Control
phosphatidylinositols
Carnitine
oxysterols
Saturated_ceramides
Saturated_fatty acids
diglycerides
F
16S4DF/Control
phosphatidylinositols
Carnitine
Saturated FA
diglycerides
pregnenes
ethanolamines
glycerides
ceramides
oxysterols
cholesterol
oxo-ETE
G
17S3DF/Control
Carnitine
pregnenes
diglycerides
phosphatidylinositols
glycerides
Saturated_ceramides
H
18S2DF/Control
carnitine
O=FA_18_3
diglycerides
glycerides
glycerophospholipids
tricarboxylic acids
I
19S1DF/Control
carnitine
diglycerides
glycerides
cholic acids
pregnenediones
Saturated_lysophospholipids
OH-FA_20_0_2
-log (pvalue)
median XlogP of clusters

Figure S5


A
I1S9DF/Control
Glycerophospholipid metabolism
Steroid hormone biosynthesis
Histidine metabolism
Alanine, aspartate and glutamate metabolism
D-Glutamine and D-glutamate metabolism
Arginine biosynthesis
B
I2S8DF/Control
Glycerophospholipid metabolism
Arachidonic acid metabolism
alpha-Linolenic acid metabolism
D-Glutamine and D-glutamate metabolism
Arginine biosynthesis
Alanine, aspartate and glutamate metabolism
C
I3S7DF/Control
Glycerophospholipid metabolism
Arachidonic acid metabolism
Steroid hormone biosynthesis
D-Glutamine and D-glutamate metabolism
Arginine biosynthesis
Alanine, aspartate and glutamate metabolism
D
I4S6DF/Control
Sphingolipid metabolism
Alanine, aspartate and glutamate metabolism
Glycerophospholipid metabolism
D-Glutamine and
D-glutamate metabolism
Arginine biosynthesis
E
I5S5DF/Control
Sphingolipid metabolism
Alanine, aspartate and glutamate metabolism
D-Glutamine and
D-glutamate metabolism
Arginine biosynthesis
F
I6S4DF/Control
Sphingolipid metabolism
Steroid hormone biosynthesis
Alanine, aspartate and glutamate metabolism
Arachidonic acid metabolism
D-Glutamine and
D-glutamate metabolism
Arginine biosynthesis
Pantothenate and CoA biosynthesis
G
I7S3DF/Control
Sphingolipid metabolism
Steroid hormone biosynthesis
Alanine, aspartate and glutamate metabolism
D-Glutamine and
D-glutamate metabolism
Arginine biosynthesis
Pantothenate and CoA biosynthesis
H
I8S2DF/Control
Citrate cycle (TCA cycle)
Arachidonic acid metabolism
Steroid hormone biosynthesis
I
I9S1DF/Control
Citrate cycle (TCA cycle)
alpha-Linolenic acid metabolism
Steroid hormone biosynthesis
-log10(p)
pathway impact