Supplementary Figure Legends

Supplementary Figure S1: Phenolic inhibitors hindered anaerobic xylose consumption. *E. coli* RL3000 was grown in M9 minimal medium, 0.25% (w/v) xylose until the culture reached an early exponential phase (OD_{600}~0.2-0.3) before it was exposed to 2.75 mM or 5.5 mM feruloyl amide, coumaroyl amide, or ferulic acid. Concentrations of xylose remained in the culture over time were quantified using LC-MS. Growth rates (/hour) and xylose uptake rates (mM/hour/OD) were obtained from nonlinear least-squares (curve-fitting). The extrapolated rates were normalized to those of the controls. Bars represent means of two biological replicates ± SEM.

Supplementary Figure S2: Feruloyl amide and coumaroyl amide are major contributors to anaerobic growth inhibition of *E. coli*.

(A) Cells were grown in an absence of phenolic inhibitors until early exponential phase (OD_{600} ~ 0.2) The cultures were then treated with either of lignin-derived phenolic inhibitor (LDPI) cocktail or feruloyl amide combined with coumaroyl amide. 1X concentrations of LDPI cocktail (see also Figure 1 and Table S1) led to strong anaerobic growth inhibition. 0.5X concentration (2.75 mM) of feruloyl amide and coumaroyl amide (each) was sufficient to account for the same degree of inhibition observed in LDPI cocktail treatment.

(B) Inhibitory effects of LDPIs are pronounced in cells grown in xylose. Anaerobic exponential cultures (OD_{600} ~ 0.2-0.3) in LDPI-free media with either xylose or glucose were introduced to 1.375 mM, 2.75 mM, or 5.5 mM of feruloyl amide, coumaroyl amide, or ferulic acid.

Supplementary Figure S3: Anaerobic growth inhibition by ferulic acid.

(A) Ferulic acid treatment leads to different alterations in intracellular metabolite levels compared to those in feruloyl amide and coumaroyl amide-treated cells.

Exponential *E. coli* cultures grown anaerobically on xylose were treated with 5.5 mM ferulic acid. Intracellular metabolites were extracted at 10, 30, 60, 120, 180, and 240 min after exposure to ferulic acid and measured by LC-MS. Metabolite levels of treated samples were normalized against those of controls at each corresponding time points. Metabolites whose level increases upon phenolic amide treatment are shown in shades of yellow and those that decreases are shown in shades of blue. The data represents the averages of two biological replicates.

(B) Ferulic acid leads to anaerobic growth inhibition of *E. coli.* Anaerobic *E. coli* was grown in an absence of inhibitor before it was introduced to 5.5 mM ferulic acid at early exponential growth (arrow).

(C) PRPP accumulation in the presence of ferulic acid. While PRPP sharply accumulates (at 10 min after treatment) in the presence of feruloyl amide and coumaroyl amide (Figures 1C, 3), the accumulation is not drastic in the presence of ferulic acid. Bars represent means of four biological replicates ± SEM.

(D) Impeded biosynthesis of deoxynucleotide in the presence of ferulic acid. Anaerobic, exponential culture of *E. coli* was exposed to 5.5 mM ferulic acid for 5 min before switched into a medium containing ^{13}C-xylose. ^{13}C incorporation was allowed for 0, 0.5, 1, 2, 4, 7, 10, and 15 min before quenching. While synthesis of ribose-5-phospate (ribose-5-P), glutamate, and ATP was comparable between the control and ferulic acid-treated samples, biosynthesis of dCTP was impeded in the presence of ferulic acid.

Supplementary Figure S4: Feruloyl amide inhibits nucleotide biosynthesis at both 5 minutes (short-term) and 2 hours (long-term). Anaerobic *E. coli* culture in minimal medium with non-labeled xylose was exposed to 5.5 mM feruloyl amide for either 5 minutes (short-term) or 2 hours (long-term) before it was switched to 1, 2 ^{13}C-xylose-containing medium. Samples for intracellular metabolite analysis were the taken at 0.5, 1, 2, 4, 7, 10, and 15 min thereafter. The blue-to-red gradient represents the amount of ^{13}C-label incorporation (sum of all ^{13}C-labeled forms) into each metabolite as a fraction of its total pool; for each metabolite, the lowest value (non-labeled) was set to blue while the highest ^{13}C-label fraction value in control samples was set to red. The data represent the average of two biological replicates.

Supplementary Figure S5: Complete inhibition of nucleotide *de novo* biosynthesis in the presence of phenolic amide inhibitors. Fragmentation (LC-MS/MS) analysis from the ^{13}C isotopic tracer experiments described in Fig. 2 showed no ^{13}C incorporation into nucleobases (adenine of ATP and uracil of UTP) in the presence of feruloyl amide while ^{13}C-carbon was incorporated into both phospho-ribose sugar and nucleobases in the control. The same pattern was observed in coumaroyl amide-treated cells. The data represent identical results from two biological replicates.

Supplementary Figure S6: Nucleoside supplementation rescued growth inhibition by phenolic inhibitors. (Top) Feruloyl amide. **(Middle)** Coumaroyl amide. **(Bottom)** Ferulic acid. *E. coli* was grown anaerobically with xylose and supplemented with 0, 0.25, or 0.75 mM of nucleosides (adenosine, guanosine, cytidine, thymidine, and uridine). Exponential culture (OD_{600} 0.2-0.3) was then divided into individual flasks containing 2.75 mM feruloyl amide, coumaroyl

amide, or ferulic acid. Cell growth was measured using OD_{600}. This graph is a representation of 2 independent experiments that gave identical results.

Figure S1

Xylose uptake rates (mM/hour/OD)		
	2.75 mM treatment	**5.5 mM treatment**
Control	4.593 ± 0.171	
Feruloyl amide	2.196 ± 0.152	1.548 ± 0.248
Coumaroyl amide	3.119 ± 0.116	1.747 ± 0.110

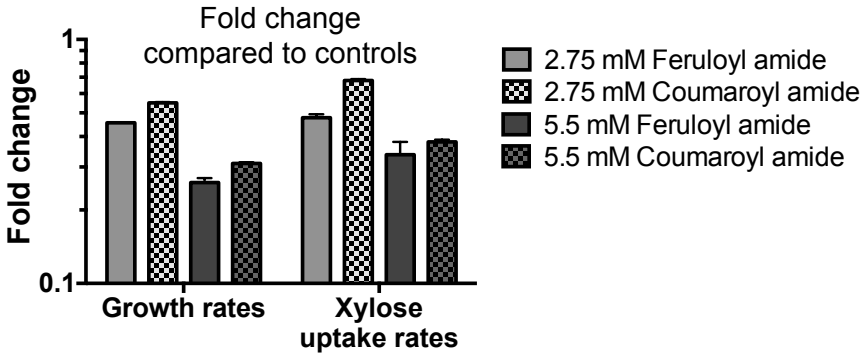


Figure S2

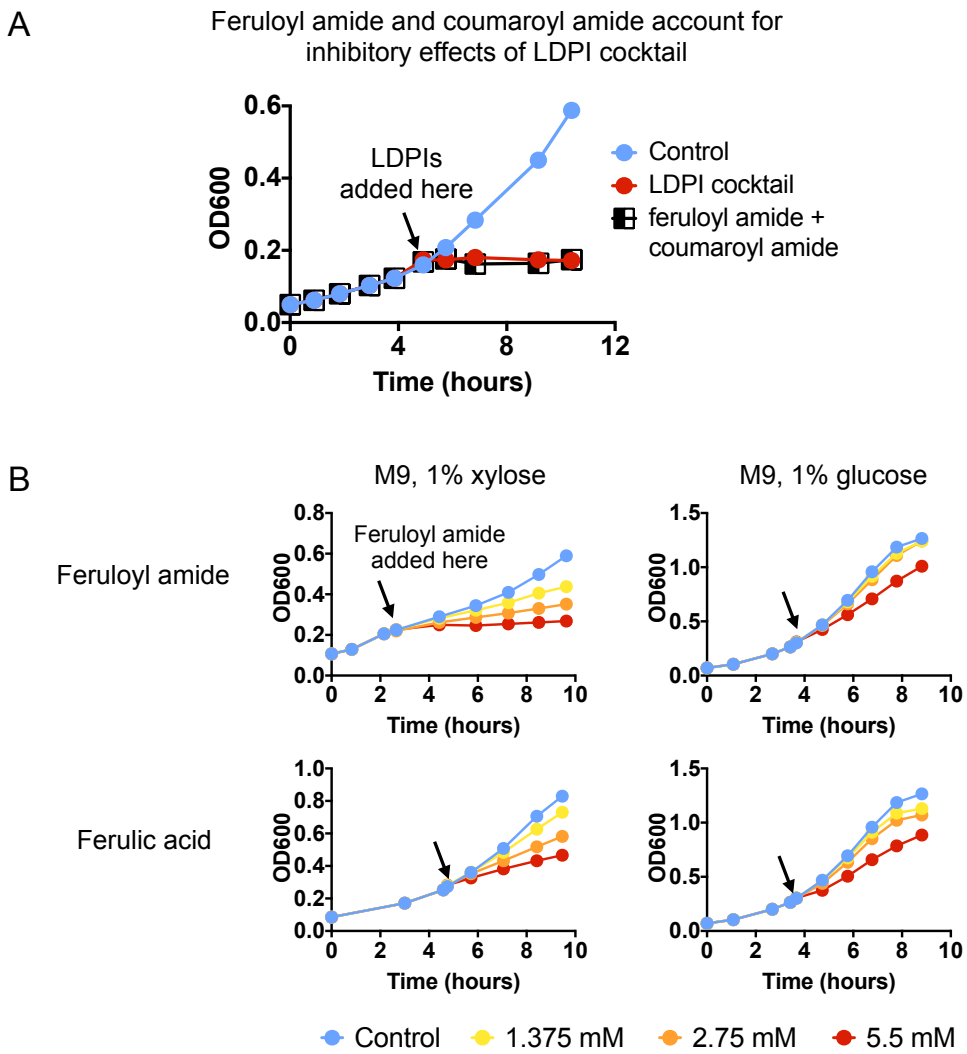

A
Feruloyl amide and coumaroyl amide account for inhibitory effects of LDPI cocktail
OD600
0.6
0.4
0.2
0.0
LDPIs added here
0
4
8
12
Time (hours)
Control
LDPI cocktail
feruloyl amide + coumaroyl amide
B
M9, 1% xylose
M9, 1% glucose
Feruloyl amide
Ferulic acid
Feruloyl amide added here
OD600
Time (hours)
Control
1.375 mM
2.75 mM
5.5 mM

Figure S3

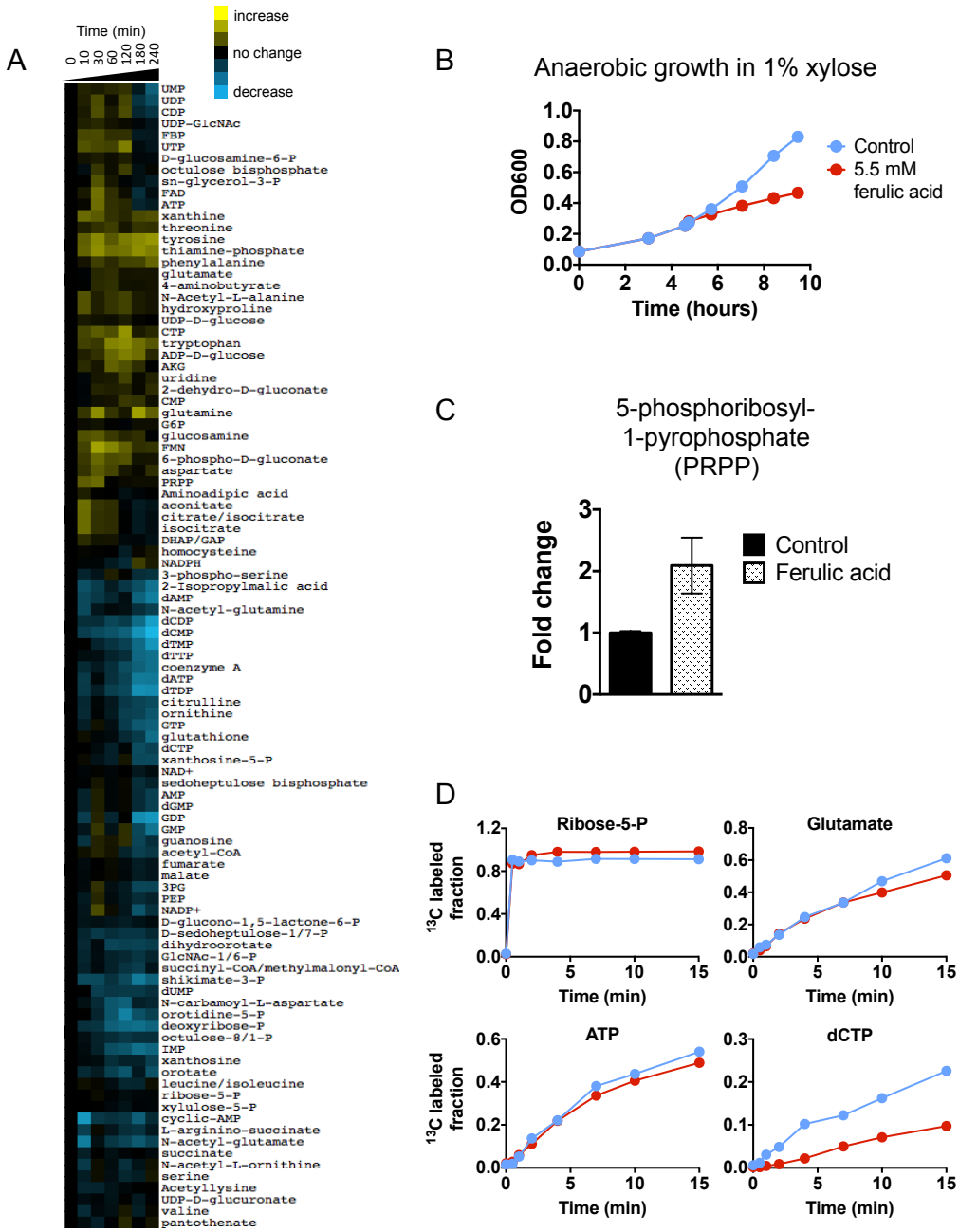

A
Time (min)
0
10
30
60
120
180
240
increase
no change
decrease
UMP
UDP
CDP
UDP-GlcNAc
FBP
UTP
D-glucosamine-6-P
octulose bisphosphate
sn-glycerol-3-P
FAD
ATP
xanthine
threonine
tyrosine
thiamine-phosphate
phenylalanine
glutamate
4-aminobutyrate
N-Acetyl-L-alanine
hydroxyproline
UDP-D-glucose
CTP
tryptophan
ADP-D-glucose
AKG
uridine
2-dehydro-D-gluconate
CMP
glutamine
G6P
glucosamine
FMN
6-phospho-D-gluconate
aspartate
PRPP
Aminoadipic acid
aconitate
citrate/isocitrate
isocitrate
DHAP/GAP
homocysteine
NADPH
3-phospho-serine
2-Isopropylmalic acid
dAMP
N-acetyl-glutamine
dCDP
dCMP
dTMP
dTTP
coenzyme A
dATP
dTDP
citrulline
ornithine
GTP
glutathione
dCTP
xanthosine-5-P
NAD+
sedoheptulose bisphosphate
AMP
dGMP
GDP
GMP
guanosine
acetyl-CoA
fumarate
malate
3PG
PEP
NADP+
D-glucono-1,5-lactone-6-P
D-sedoheptulose-1/7-P
dihydroorotate
GlcNAc-1/6-P
succinyl-CoA/methylmalonyl-CoA
shikimate-3-P
dUMP
N-carbamoyl-L-aspartate
orotidine-5-P
deoxyribose-P
octulose-8/1-P
IMP
xanthosine
orotate
leucine/isoleucine
ribose-5-P
xylulose-5-P
cyclic-AMP
L-arginino-succinate
N-acetyl-glutamate
succinate
N-acetyl-L-ornithine
serine
Acetyllysine
UDP-D-glucuronate
valine
pantothenate
B
Anaerobic growth in 1% xylose
OD600
1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
10
Time (hours)
Control
5.5 mM
ferulic acid
C
5-phosphoribosyl-
1-pyrophosphate
(PRPP)
Fold change
3
2
1
0
Control
Ferulic acid
D
Ribose-5-P
Glutamate
ATP
dCTP
13C labeled
fraction
Time (min)
0
5
10
15

Figure S4

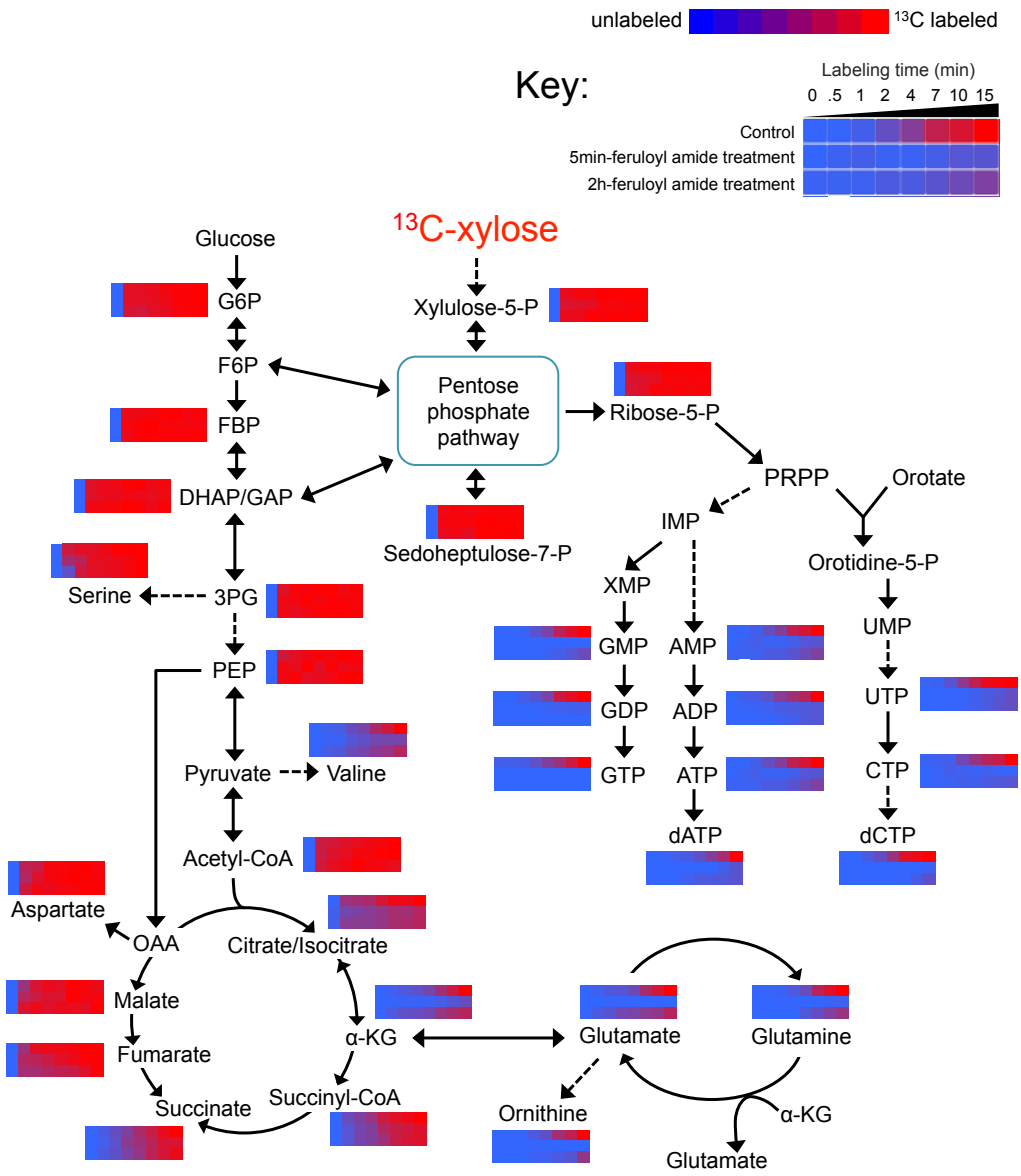

unlabeled
13C labeled
Key:
Labeling time (min)
0 .5 1 2 4 7 10 15
Control
5min-feruloyl amide treatment
2h-feruloyl amide treatment
13C-xylose
Glucose
G6P
F6P
FBP
DHAP/GAP
Serine
3PG
PEP
Pyruvate
Valine
Acetyl-CoA
Aspartate
OAA
Citrate/Isocitrate
Malate
Fumarate
Succinate
Succinyl-CoA
α-KG
Xylulose-5-P
Pentose phosphate pathway
Sedoheptulose-7-P
Ribose-5-P
PRPP
Orotate
IMP
XMP
GMP
GDP
GTP
AMP
ADP
ATP
dATP
Orotidine-5-P
UMP
UTP
CTP
dCTP
Glutamate
Glutamine
Ornithine
α-KG
Glutamate

Figure S5

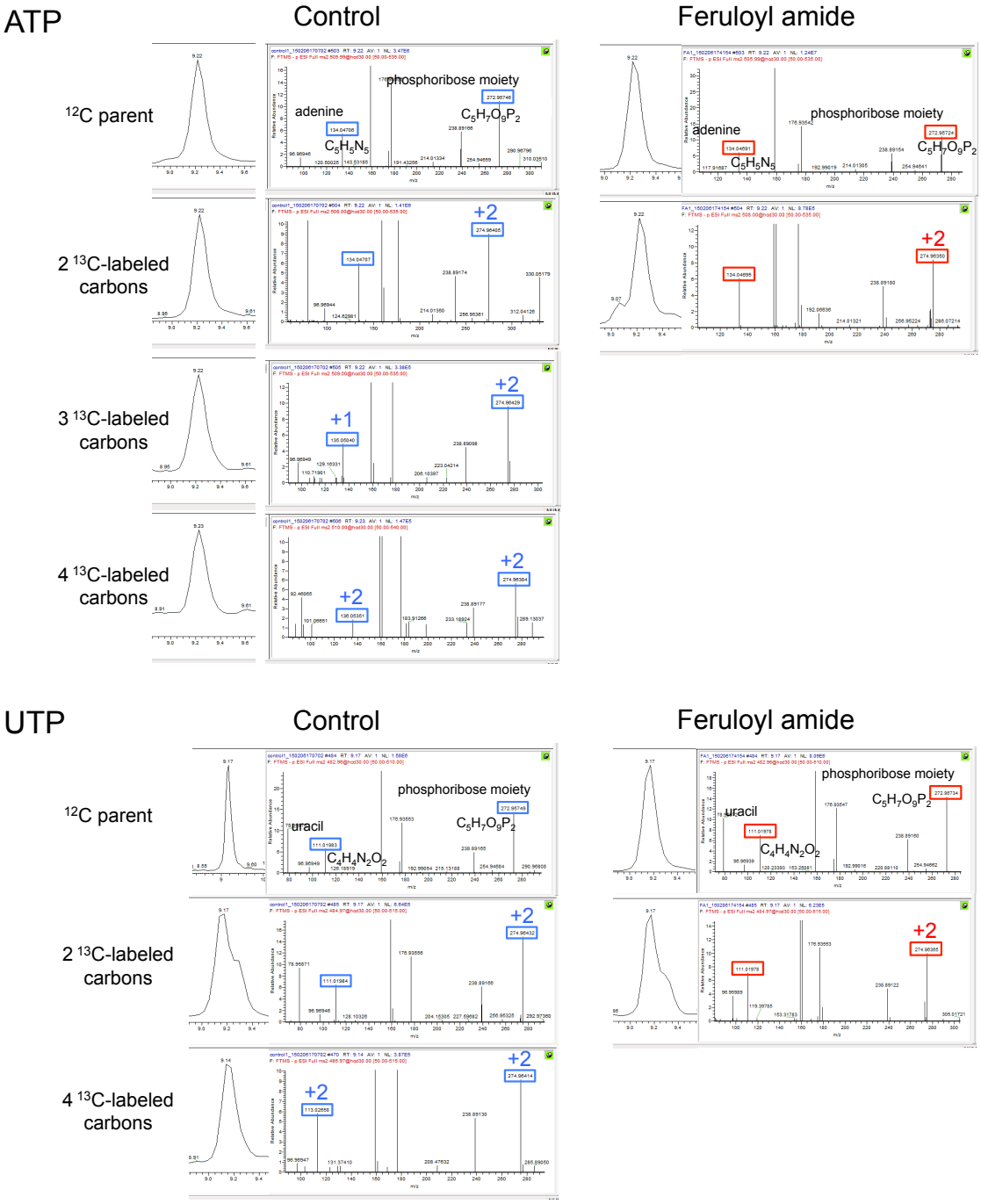
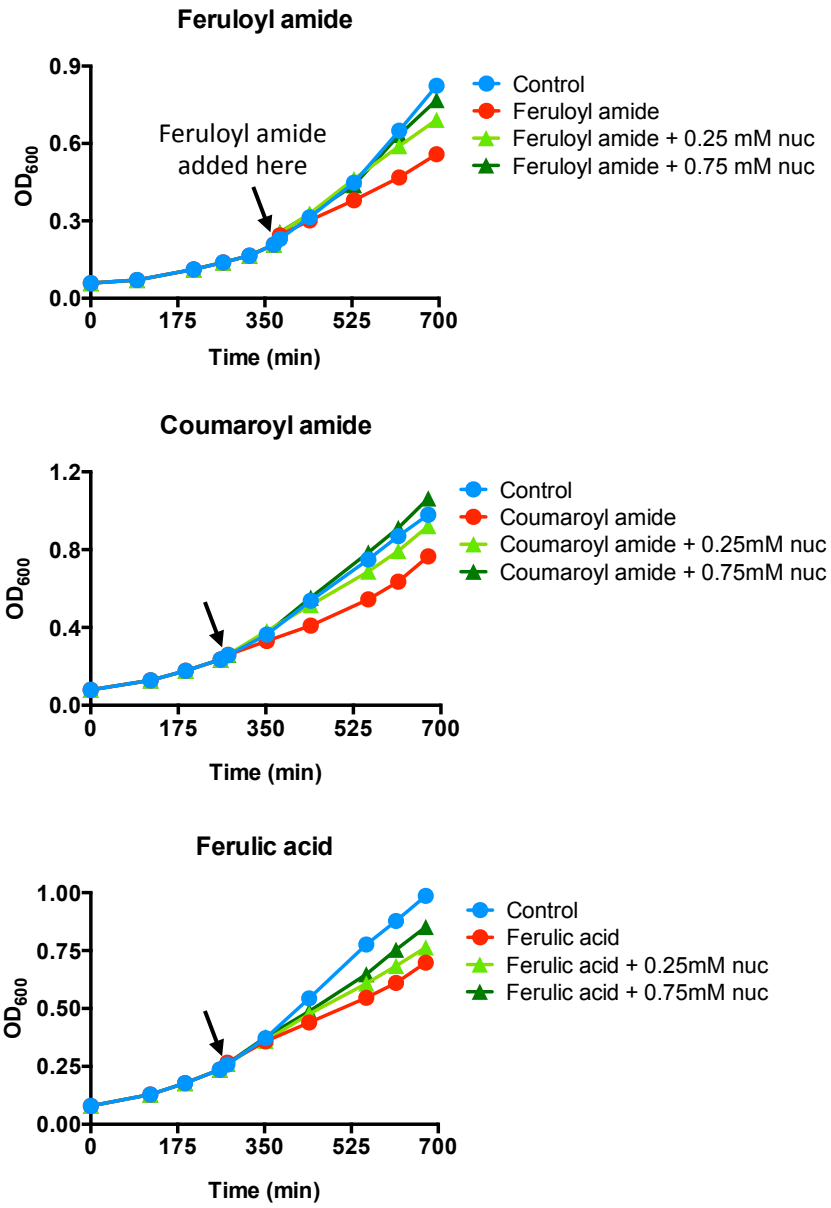
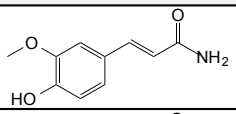
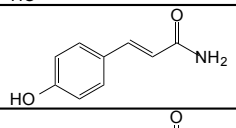
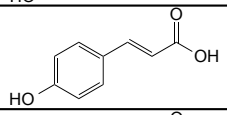
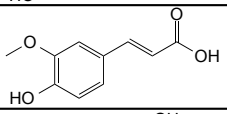
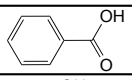
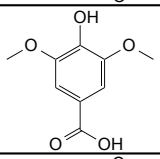
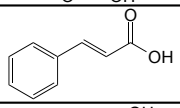
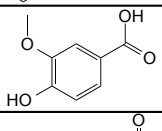
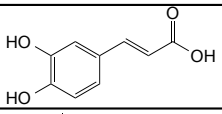
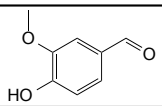
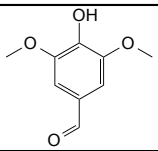
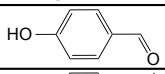
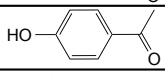

ATP
Control
Feruloyl amide
12C parent
2 13C-labeled carbons
3 13C-labeled carbons
4 13C-labeled carbons
adenine
phosphoribose moiety
C5H5N5
C5H7O9P2
+1
+2
UTP
Control
Feruloyl amide
12C parent
2 13C-labeled carbons
4 13C-labeled carbons
uracil
phosphoribose moiety
C4H4N2O2
C5H7O9P2
+2

Figure S6


Feruloyl amide
0.9
0.6
0.3
0.0
OD600
Feruloyl amide
added here
0
175
350
525
700
Time (min)
Control
Feruloyl amide
Feruloyl amide + 0.25 mM nuc
Feruloyl amide + 0.75 mM nuc
Coumaroyl amide
1.2
0.8
0.4
0.0
OD600
0
175
350
525
700
Time (min)
Control
Coumaroyl amide
Coumaroyl amide + 0.25mM nuc
Coumaroyl amide + 0.75mM nuc
Ferulic acid
1.00
0.75
0.50
0.25
0.00
OD600
0
175
350
525
700
Time (min)
Control
Ferulic acid
Ferulic acid + 0.25mM nuc
Ferulic acid + 0.75mM nuc

Supplementary Table S1: Lignocellulose-derived phenolic inhibitors identified in AFEX-pretreated corn stover hydrolysates (Keating, D. H. et al. Front Microbiol 5, 402 (2014))

Lignotoxins	Structures	Concentrations (mM)
Feruloyl amide		5.5
Coumaroyl amide		5.5
p-Coumaric acid		1.05
Ferulic acid		0.36
Benzoic acid		0.48
Syringic acid		0.08
Cinnamic acid		0.09
Vanillic acid		0.09
Caffeic acid		0.01
Vanillin		0.13
Syringaldehyde		0.16
4-Hydroxybenzeldehyde		0.2
4-Hydroxyacetophenone		0.02

5-Hydroxymethylfurfural (HMF) was not included in this study

Supplementary Table S2: Target MS/MS parameters used to obtain ^{13}C labeling patterns of ATP and UTP

Metabolites	Collision energy	Labeled forms	Mass (m/z)	Fragment mass (m/z) of interest	Molecular formula (neutral)	Names of fragments
ATP	30	non-labeled	505.98846	134.047 272.957	$C_5H_5N_5$ $C_5H_7O_9P_2$	Adenine phosphoribosyl moiety
		2 ^{13}C-labeled carbons	507.99518	134.047 274.964	$C_5H_5N_5$ $C_5H_7O_9P_2$	Adenine phosphoribosyl moiety
		3 ^{13}C-labeled carbons	508.99854	135.050 274.964	$C_5H_5N_5$ $C_5H_7O_9P_2$	Adenine phosphoribosyl moiety
		4 ^{13}C-labeled carbons	510.00189	136.054 274.964	$C_5H_5N_5$ $C_5H_7O_9P_2$	Adenine phosphoribosyl moiety
UTP	30	non-labeled	482.96124	111.020 272.957	$C_4H_4N_2O_2$ $C_5H_7O_9P_2$	Uracil phosphoribosyl moiety
		2 ^{13}C-labeled carbons	484.96796	111.020 272.957	$C_4H_4N_2O_2$ $C_5H_7O_9P_2$	Uracil phosphoribosyl moiety
		4 ^{13}C-labeled carbons	486.97467	111.020 272.957	$C_4H_4N_2O_2$ $C_5H_7O_9P_2$	Uracil phosphoribosyl moiety

Other parameters for targeted MS/MS
Resolution: 35,000
AGC target: 5E5
Isolation width: 1.4 (m/z)
Default charge: 1
Polarity: negative

Supplementary Table 3: Intracellular metabolite levels after exposure to feruloyl amide and coumaroyl amide

	Feruloyl amide							Coumaroyl amide						
Metabolites\Exposure time	0_min	10_min	30_min	60_min	120_min	180_min	240_min	0_min	10_min	30_min	60_min	120_min	180_min	240_min
3PG	0	-0.59898782	-0.506917429	-0.070448779	-0.953475782	-0.553614415	-1.09574809	0	-0.386337578	-0.70499683	-1.380296819	-0.456253057	-1.043775617	-2.087450862
3-phospho-serine	0	-1.886182023	-2.880006452	-1.769996236	-2.918024288	-2.742565151	-4.321431897	0	-2.252407572	-1.447773206	-4.852652033	-1.453334767	-2.32227962	-3.811537489
acetyl-CoA	0	-0.671685291	-0.981932281	-0.143037379	-1.005443628	-0.955475561	-0.963870413	0	-0.835240966	-0.440193926	-0.781857382	-0.079382381	-0.370139467	-0.67161571
AKG	0	-0.608070824	-0.67652452	-0.026542189	-0.403627659	-0.797574028	-0.663304666	0	-0.98693902	-0.607038758	-1.015102282	-0.061688026	-0.369530951	-0.96354267
aspartate	0	-0.879699073	-1.17081422	-0.593656448	-1.202421564	-0.917891735	-1.137405649	0	-0.803416045	0.134044406	-1.016579667	-0.994883509	-1.358962221	-1.472981282
ATP	0	-0.630375586	-0.177057855	0.378582281	-0.917786245	-1.247771673	-0.502931479	0	0.146880651	-0.235440204	-0.151838751	0.795169863	0.488753576	-0.359039922
citrate/isocitrate	0	-0.181960469	0.305849193	0.442980239	0.100969747	0.38047117	0.278132073	0	0.524859953	-0.353442286	-2.84437926	-1.217884693	-2.476358451	-3.937436739
citrulline	0	-0.726735885	-0.388898822	-0.198126774	-1.144461879	-0.949436546	-1.345600193	0	-0.178079281	-0.612614603	-0.279480868	-0.163213957	-0.180714083	-0.345277727
CMP	0	0.760649528	-0.931421482	-0.387138595	-0.073951871	0.346488492	0.759488889	0	1.349386675	0.502267031	1.199810162	1.46464053	1.604473667	1.499065364
coenzyme A	0	0.096423214	-1.627843093	-0.92488701	-1.566858342	-0.51891144	-1.271203731	0	0.331769156	-0.355755175	-0.778401042	0.417920465	0.125650036	-0.629324214
CTP	0	1.004377262	-0.502424797	0.100400591	-0.898973301	-0.479296314	-0.333801304	0	2.002477591	-0.18528667	0.82382117	1.43728845	1.10542505	0.452006923
dATP	0	-2.750964161	-1.523913384	-1.47904151	-2.550318023	-3.466489929	-2.303691177	0	-0.451113806	-0.878320656	-0.983877978	-0.053529612	-0.950421308	-2.101970885
dCTP	0	0.295027293	-0.383065441	-0.397343375	-1.869116106	-0.902919769	-1.078428322	0	1.052347072	-0.613740726	-0.167239864	0.025069682	-0.564370052	-1.329084623
deoxyribose-P	0	-2.268392832	-1.909604973	-1.618258642	-1.683541653	-0.896709714	-0.928174275	0	-1.696114704	-1.019439184	-2.292484096	-1.665740483	-1.832161553	-2.182202075
DHAP/GAP	0	-0.590864623	-0.984414423	-0.446651256	-0.547102958	-0.481484363	-0.259955814	0	0.221133863	0.255269517	0.410127188	0.423848504	0.390738094	0.33527536
D-sedoheptulose-1/7-P	0	-0.201353484	-0.590743541	-0.283720223	-0.294913895	-0.277207715	0.158099108	0	-0.507531552	-0.487295986	-1.037788745	-0.648223574	-0.575139619	-0.658830361
dTDP	0	-1.363613946	-1.402745097	-1.230765214	-2.507755722	-1.690524191	-2.155881472	0	-0.333467771	-0.542750318	-0.396657032	-0.18104534	-0.573395518	-0.846452523
dTMP	0	0.087212842	0.137126342	0.465019444	-0.786650702	-1.105302894	-0.881428071	0	0.460430789	-0.315563696	-0.925433316	-1.025652222	-1.638361108	-1.59899078
dTTP	0	0.302550241	0.015338095	-0.337562881	-1.5749491	-1.607474017	-1.709458458	0	1.184571099	-0.197544801	-0.250215408	-0.310575024	-0.347484366	-1.041501427
FAD	0	-0.552688529	-0.142851531	0.529475703	-0.98894527	-0.371564817	-0.520356472	0	-0.345629392	-0.322829806	-0.50327442	0.378506967	-0.208110692	-0.784457264
FBP	0	-1.328195186	-1.231283845	-0.593885733	-1.442785594	-1.911695137	-1.055011642	0	0.339367009	0.40838806	0.52592838	0.832938285	0.722803728	0.171994578
fumarate	0	-0.108946317	-0.136968325	0.20553425	-0.095477238	-0.07828425	-0.381673658	0	-0.309740119	-0.00138323	-0.689577837	-0.138902505	-0.535057976	-1.066432701
G6P	0	-0.619381603	-1.504236824	-1.368150081	-1.209058054	-1.276995488	-0.517781147	0	-0.273863666	-0.322908413	-0.404451792	-0.30878653	-0.303606669	-0.236091409
glutamate	0	-1.58278072	-1.631342259	-1.427897451	-1.77740545	-1.586558198	-1.764924219	0	-1.922932823	-1.173687038	-2.199621829	-1.722504732	-1.733632979	-2.040599336
glutamine	0	-0.411709916	-1.231352228	-0.492941262	-0.559099872	0.258839172	0.38687285	0	-1.283211895	-0.905820394	-1.78997159	-2.318148271	-1.811942167	-2.027331316
glutathione disulfide	0	0.847329152	1.319080432	1.199321026	0.717623721	0.05020459	0.719031693	0	1.713181917	1.298859219	1.456549648	1.196887569	1.419693257	1.205004332
glycerate	0	0.001587054	0.318851428	0.576069586	0.491940767	0.855369544	0.937971302	0	1.17415091	0.590720598	1.822196234	1.146584361	1.211007909	0.59012599
GTP	0	-0.8296316	-1.149349761	-0.425022447	-1.552155094	-1.255786571	-1.188814834	0	0.378621127	-0.907223901	-0.577178118	0.866977681	0.136142279	-1.240683589
IMP	0	-0.124985003	0.207152416	0.601735597	0.281674797	-0.110090473	-0.2968092	0	-1.59300979	-1.510950438	-2.136314067	-0.265936959	-0.530459349	-1.211754177
L-arginino-succinate	0	-1.110828995	-1.25583887	-0.789644256	-1.391582226	-1.644317823	-1.365141863	0	-1.377661222	-1.324126136	-1.312928279	-1.057152506	-1.190493245	-1.462441823
leucine/isoleucine	0	-1.247016795	-0.00808449	0.475659657	-0.31077895	0.035220232	-0.026791378	0	0.352590431	-0.016307185	-0.561765912	-0.057783246	-0.755327457	-0.911540365
malate	0	-0.417328509	-0.325550448	-0.299165606	-0.900431014	-1.066002318	-1.331475793	0	-0.281553566	-0.022739485	-0.673862578	-0.147224288	-0.621207676	-1.12970998
methionine	0	-2.741134793	-0.111378123	1.044394279	0.036862039	1.151601816	-0.287660819	0	-1.017595696	-0.302993552	-0.384447473	0.281411236	-0.014550454	0.44965592
N-acetyl-glutamate	0	-2.72652703	0.013579674	-0.205291666	-1.123468862	-1.273583284	-1.735675108	0	-1.77909959	-0.685583331	-2.204569913	-1.949320594	-2.386895923	-2.610614382
N-acetyl-L-ornithine	0	-2.433716247	-0.799444301	-1.133174175	-1.891107356	-1.862247123	-1.681617934	0	-1.447784372	-0.373840484	-1.012010834	-0.924897073	-1.245271593	-1.16496231
NAD+	0	-0.088173424	-0.056098815	0.327999561	-0.34158218	-0.350443739	0.100232055	0	-0.09655746	-0.392732052	-0.668778546	-0.062691412	-0.351307439	-0.621026955
NADP+	0	-0.234174699	-0.251911551	0.380129084	-1.577859806	-1.620806708	-1.342102099	0	-0.726018544	-0.950876194	-1.110845296	-0.341037848	-0.970036735	-1.582543035
octoluse 8/1P	0	-0.359133323	-1.050850117	-0.599830634	-0.969681838	-0.609689943	-0.098854055	0	-0.45113663	-0.494267921	-1.075844045	-0.891367706	-0.738583735	-0.642534062
octulose bisphosphate	0	-1.460247341	-1.227749914	-0.689986123	-1.691935336	-1.274621975	-1.361383503	0	-0.686615845	-0.819836081	-0.77099249	-0.164320051	-0.112801837	-0.752652087
ornithine	0	-1.052629975	-0.598442733	-0.084625475	-1.407413624	-1.236849648	-1.31454358	0	-0.16741834	-0.750290967	-0.349581496	-0.235711224	-0.223347669	-0.265830449
pantothenate	0	2.162674766	1.584593187	1.73373355	1.012083916	1.476944513	0.794280203	0	3.648657839	1.426293304	1.09290469	1.29614786	1.152768614	0.618542457
phenylalanine	0	0.1517583	0.038015922	0.496243924	0.382173908	0.715383116	0.514596314	0	-0.000387084	0.290141044	0.12243114	0.5261247	0.518895207	0.440650905
phenylpyruvate	0	-0.374063883	-0.460245839	-0.179928494	-1.285206965	1.092136504	-0.206152414	0	-0.041088999	0.026756265	-0.124082659	0.312042654	0.270467373	0.082631698
PEP	0	-0.888481	-0.66648388	0.038257718	-0.6698149	0.256971825	-0.375101126	0	-0.284888605	-1.879636608	-1.864951794	-1.474259148	-1.865490388	-1.89863543
PRPP	0	7.017897051	5.644413204	6.332452458	3.753766632	6.106137053	3.285572094	0	4.794875634	2.225095911	3.23156321	3.075182961	2.76046013	0.90092252
ribose-P	0	-0.251446527	-0.448780732	-0.110143177	-0.213372299	-0.45375126	0.042770316	0	-0.162205468	0.232547759	-0.398240973	0.034281189	0.264889317	0.270929395
sedoheptulose bisphosphate	0	-1.351586396	-0.633731364	-0.20615956	-1.543036769	-1.676847691	-1.621704693	0	-0.160618689	-0.403137914	-0.31961957	0.293054667	0.344956092	-0.240608048
serine	0	-0.835660035	-0.911403166	0.236451618	-1.052017194	-0.611056178	-1.028469129	0	-0.105262832	0.208365341	0.072349243	0.732789528	0.020936917	-0.284208377
sn-glycerol-3-P	0	0.022127214	-0.111305817	0.795885903	0.44695891	1.40898792	0.143261761	0	0.623267429	0.481469616	-0.628126597	-0.236056669	-0.284502103	-0.690220484
succinate	0	0.022193028	0.173666377	0.499748737	0.739158709	1.769458625	0.236102435	0	0.656716453	0.462621199	0.46125054	0.718288347	0.631420086	0.270725807
succinyl-CoA	0	-0.742500942	-0.540808312	0.205807582	-0.244229327	0.134137816	0.05224166	0	0.758846438	-0.176658911	-0.273732406	0.661221845	0.34890373	0.068404428
threonine	0	-0.454134752	-0.270000523	0.14550092	-0.343914234	0.076008231	-0.256057998	0	-0.661194056	-0.079121592	-0.345873598	-0.684471628	-0.42733106	-0.487272369
tyrosine	0	-0.097476926	0.043300662	1.027242489	1.232624659	2.052910106	1.724867844	0	0.905270572	1.301224514	1.848772525	2.178774314	2.403833449	2.366164864
UDP	0	1.09208944	-0.563345022	0.035323736	-0.848777964	-0.240420334	-0.326596064	0	1.083876129	-1.416166721	-0.998075833	-0.05967842	-0.312449574	-0.785988889
UDP-D-glucose	0	-0.163827418	-1.848858216	-1.319152344	-0.910690031	-0.934371692	-0.701054141	0	-0.020637705	-0.982156006	-0.924450597	-0.700052117	-0.675709648	-0.713097783
UDP-D-glucuronate	0	0.024490082	-0.42408877	-0.000790609	-0.609952893	-0.80417099	-0.783280392	0	0.002347726	-0.731001714	-0.975024289	-0.483432052	-0.735924872	-1.243135271
UDP-GlcNAc	0	-0.034140501	-1.08156606	-0.527603109	-0.658604825	-0.643073283	-0.461703633	0	0.423880357	-0.167109358	-0.476092189	-0.333673398	-0.517019342	-0.461819487
UMP	0	0.299822539	-1.209811403	-0.211828042	-0.253250766	0.124025798	0.288859886	0	-0.402789996	-1.260042905	-1.282986427	-0.892692538	-0.586679995	-0.654970541
UTP	0	0.610055734	-1.565124407	-0.985968338	-1.614126678	-1.428872757	-1.09759562	0	1.214543407	-1.934901301	-1.002903426	-0.139767237	-0.589344135	-1.238561338
valine	0	-0.582214316	-0.51300558	0.200495424	-0.531002783	-0.220833367	-0.682997891	0	-0.438480289	-0.319568966	-0.781201847	-0.699645107	-1.284656438	-1.361043049
xylulose-5-P	0	-0.414002322	-0.480563199	0.031081124	-0.24513169	-0.377882451	0.218505749	0	0.046513569	0.010417967	-0.20180348	0.147688608	0.306142019	0.28925022

For each metabotlie, peak intensity was normalized to a "0 min" control. Numbers shown here are log2 of the normalized values.