

The influence of phosphate supply on the metabolic flux phenotype of heterotrophic *Arabidopsis* cells

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SUPPORTING INFORMATION

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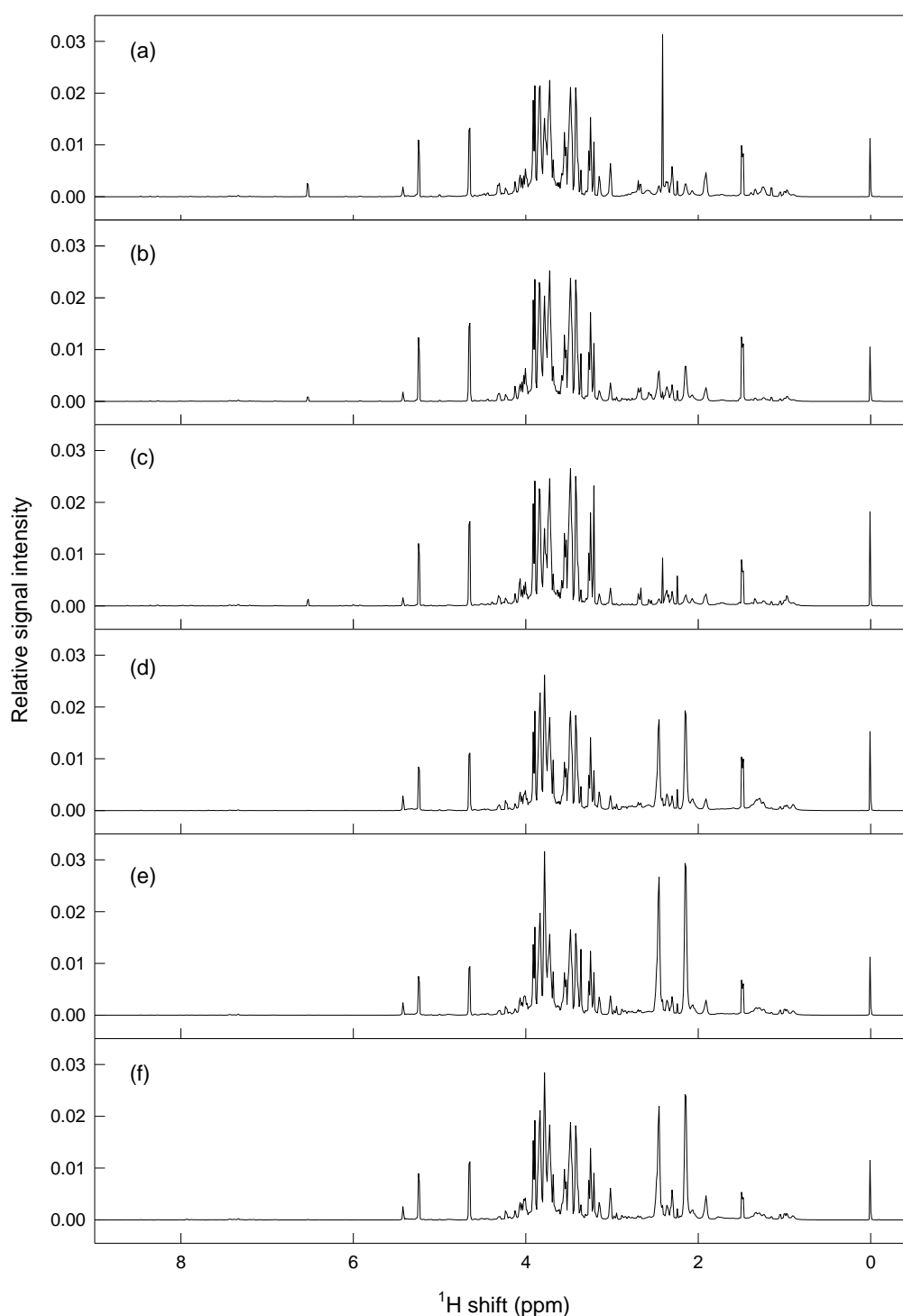


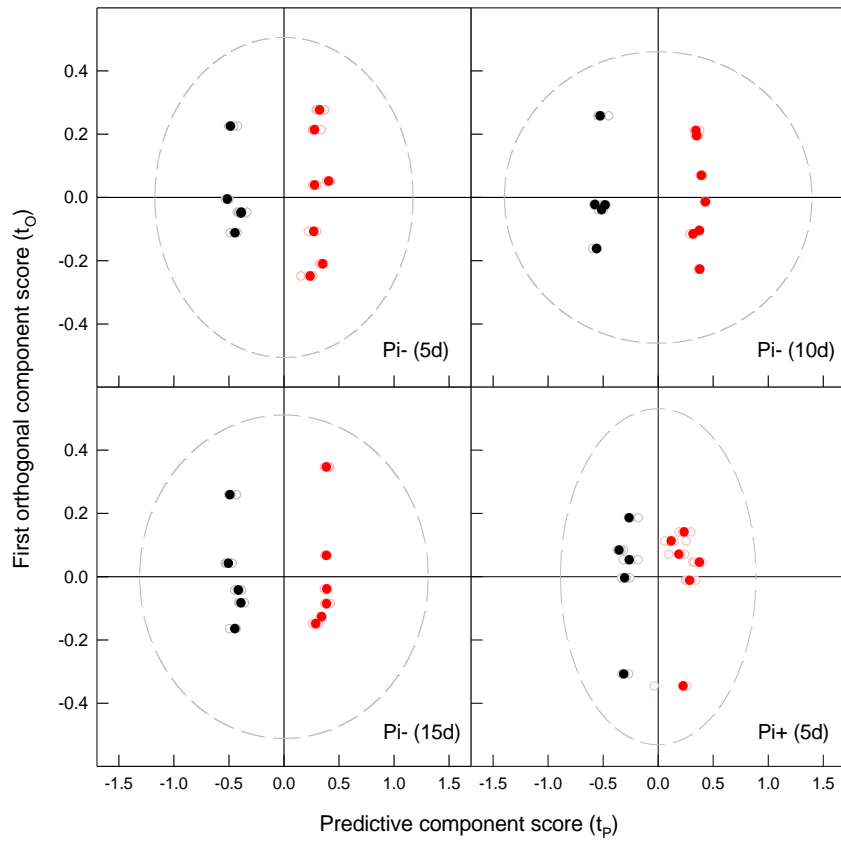
Figure S1. Influence of Pi supply on NMR metabolite profiles of Arabidopsis cultures

^1H -NMR spectra were obtained from methanolic extracts of heterotrophic cell samples harvested immediately prior to subculture (a); 5 d after transfer to either MS medium (b) or Pi^+ medium (c); and 5 d (d), 10 d (e) and 15 d (f) after transfer to Pi^- medium. Each profile is the average of spectra acquired from 4-6 independent cell cultures grown under the specified conditions. Spectra were referenced to the TSP signal at 0.00 ppm.

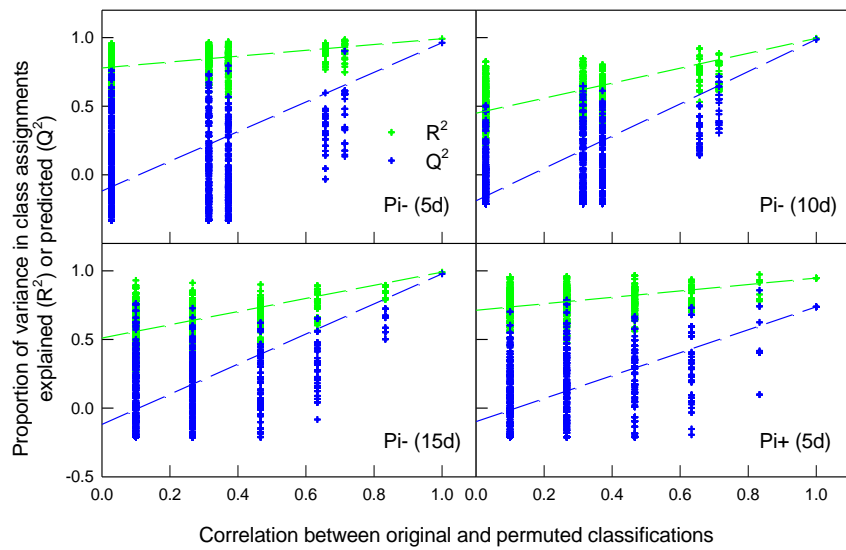
(a)

Cell culture compared with MS	Statistical parameter of OPLS-DA model		
	$R^2(X)$	$R^2(Y)$	$Q^2(Y)$
Pi- (5d)	0.736	0.980	0.952
Pi- (10d)	0.763	0.994	0.987
Pi- (15d)	0.811	0.990	0.978
Pi+ (5d)	0.600	0.947	0.751

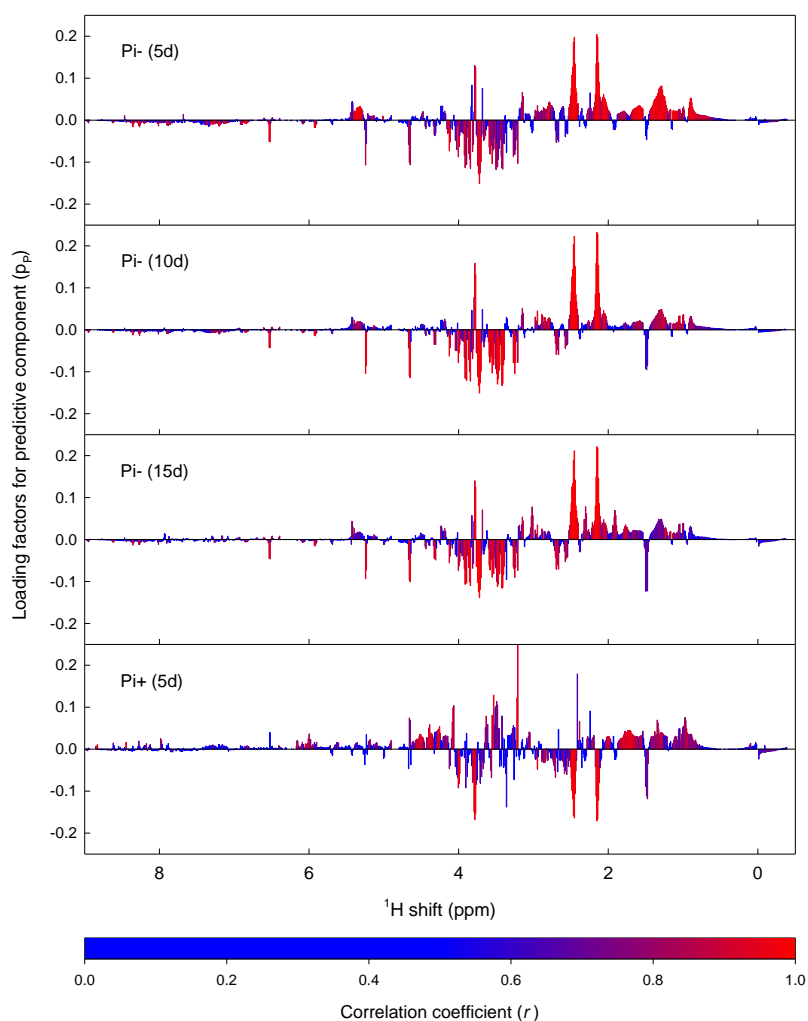
(b)



(c)



(d)



(e)

Metabolite	Chemical shift (ppm)	Correlation coefficient of spectral intensity and class assignment (r)				95% jackknife confidence interval of loading factor (p_p)			
		Pi- (d5)	Pi- (d10)	Pi- (d15)	Pi+ (d5)	Pi- (d5)	Pi- (d10)	Pi- (d15)	Pi+ (d5)
Glutamine	2.15	0.96	0.99	0.96	-0.89	0.195 - 0.213	0.206 - 0.260	0.194 - 0.249	-0.221 - -0.112
	2.45	0.96	0.99	0.96	-0.90	0.188 - 0.206	0.202 - 0.244	0.185 - 0.239	-0.140 - -0.069
	3.77	0.95	0.99	0.94	-0.93	0.101 - 0.143	0.117 - 0.146	0.101 - 0.149	-0.180 - -0.119
Glucose	4.64	-0.84	-0.96	-0.91	0.52	-0.133 - -0.080	-0.133 - -0.097	-0.128 - -0.076	-0.026 - 0.155
	5.24	-0.87	-0.93	-0.92	-0.12	-0.135 - -0.081	-0.131 - -0.077	-0.124 - -0.067	-0.053 - 0.026
Fumarate	6.52	-0.93	-0.94	-0.93	0.45	-0.066 - -0.034	-0.056 - -0.030	-0.064 - -0.027	-0.026 - 0.095

Figure S2. Multivariate analysis of cellular metabolite profiles of Arabidopsis cultures grown in differing Pi supplies

^1H -NMR spectra of methanolic extracts of cell were compared by orthogonal partial least squares-discriminant analysis (OPLS-DA). Signal intensities across each spectrum were combined to generate a series of discrete fractions (data binning) to a resolution of 0.01 ppm/fraction and normalised relative to the total signal intensity (excluding TSP and water). The binned spectral data were then mean-centred and Pareto scaled across samples prior to analysis.

(a) Summary statistics of OPLS-DA models in which $R^2(\text{X})$ is the proportion of the variance in spectral data contributing to the discrimination achieved by the predictive component (t_p), $R^2(\text{Y})$ is the proportion of class assignments explained by the model, and $Q^2(\text{Y})$ is the proportion of class assignments predicted by the model.

(b) Scores plots obtained by comparison of cells grown in MS medium for 5 d (●) with others grown in Pi- medium for 5 d, 10 d or 15 d, or 5 d in Pi+ medium (●). Open symbols (○ and ○) indicate the distribution of scores obtained during 7-fold cross-validation of OPLS-DA models and demonstrate the robustness of the discrimination. The elliptical dashed line indicates the 95% confidence limit defined by Hotelling's T^2

(c) Permutation analysis of OPLS-DA models defining the differences between the spectral profiles of cells grown in MS medium for 5 d with those grown in Pi- medium for 5 d, 10 d or 15 d, and those grown for 5 d in Pi+ medium. Variation in $R^2(\text{Y})$ (+) and $Q^2(\text{Y})$ (+) of the models obtained by OPLS were compared after 999 random permutations of the class assignments for each spectral profile. For each comparison, linear regression analysis yielded a line with a positive gradient and, additionally, each comparison involving $Q^2(\text{Y})$ yielded a line with a y-intercept below zero. The superior goodness of fit of the original (actual) classification of spectra suggests that the analysis is not generating a spurious discrimination between designated groups of spectra.

(d) Loadings plots identifying the relative contributions of each spectral region to the OPLS-DA models differentiating between the spectral profiles of cells grown in MS medium for 5 d with those grown in Pi- medium for 5 d, 10 d or 15 d, or 5 d in Pi+ medium. The coloured scale shows the correlation coefficient between the spectral intensity and class assignment for each spectral region.

(e) Characterisation of metabolic differences between cultures grown on differing Pi supplies. Metabolites contributing to the spectral difference between extracts of cultures grown on different media, as specified, relative to MS medium were identified from OPLS-DA by three criteria: (i) strong correlation between spectral intensity and class assignment; (ii) reliably non-zero loading factor for the predictive component (p_p) as determined from the 95% jackknife confidence interval; (iii) consistent response across multiple spectral signals associated with the same metabolite. Negative values (shown in red) indicate a decrease in signal intensity in the metabolite profile of cells relative to those grown in MS medium. Values indicating a metabolite signal differing significantly between cells grown on different media relative to MS are highlighted in bold. Here only three of the most prominent metabolite differences are presented.

(a)

Model parameter	Flux solution for cells grown in:		
	Pi- medium	MS medium	Pi+ medium
Number of isotopomer measurements	2318	2790	2605
Number of metabolite fragments/groups	551	659	603
Number of free fluxes	38	37	37
Degrees of freedom	1729	2094	1965
Total residuum	1570.88	1653.02	1796.40
Critical χ^2 value ($p = 0.10$)	1804.78	2177.35	2045.76
Critical χ^2 value ($p = 0.05$)	1826.85	2201.57	2069.23
Model test status (Residuum < χ^2)	Passed	Passed	Passed

(b)

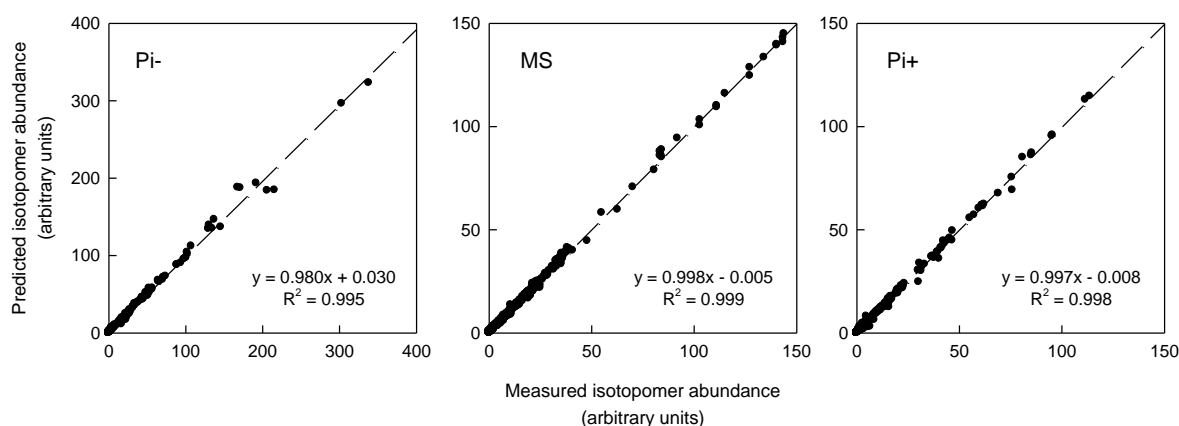


Figure S3. Statistical characteristics of best-fit models of central carbon metabolism in *Arabidopsis* cultures grown with differing Pi supply

(a) Summary of characteristics of best-fit flux models containing three replicate subnetworks each supplied with a different positionally labelled [^{13}C]glucose using data derived from cultures supplied with 99% [$1\text{-}^{13}\text{C}$]glucose, 99% [$2\text{-}^{13}\text{C}$]glucose or 20% [$^{13}\text{C}_6$]glucose. Each feeding experiment was conducted in triplicate, yielding a total of nine independently labelled cultures for each model. Degrees of freedom were calculated as described in Masakapalli *et al.* (2013, Supplemental Table S13).

(b) Comparison of predicted and measured isotopomer abundances. The analysis is based on the measured relative isotopomer values taken from Tables S6 and S7, and the predicted relative isotopomer values derived from the global best fit flux maps for cultures grown in Pi-, MS and Pi+ media, as indicated. Data from cell cultures labelled separately with [$1\text{-}^{13}\text{C}$]glucose, [$2\text{-}^{13}\text{C}$]glucose, and [$^{13}\text{C}_6$]glucose were combined for these evaluations. The line of best fit was determined by linear regression analysis and the equation of the line is reported together with the coefficient of determination (R^2). Values used in this comparison are presented in Data S1.

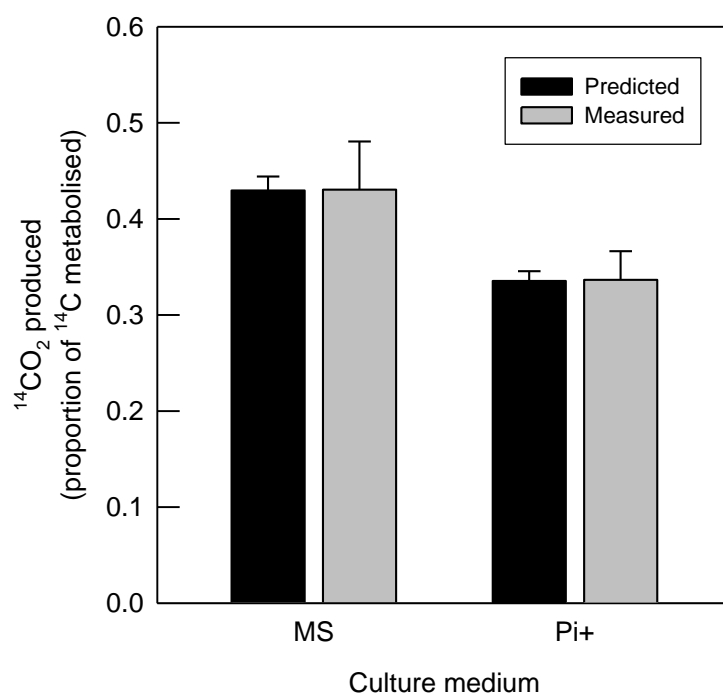


Figure S4. Validation of estimates of CO_2 release obtained by MFA

The proportion of carbon released as CO_2 predicted by MFA was compared with that determined from $[\text{U-}^{14}\text{C}]$ glucose radiolabelling studies for cultures grown in MS and Pi+ media. The measured values were obtained from data presented in Table 1. The predicted values were deduced from isotopomer data presented in Tables S3-7 by MFA using a model in which the relative proportions of biomass components were fixed and the absolute yield of biomass was unconstrained by allowing the rate of glucose uptake to be varied. Error bars are the SE of the best fit estimate for predicted values and the mean for measured values ($n = 3$).

Table S1. Fractional ^{13}C abundance of metabolites extracted from Arabidopsis cell cultures grown on 20% [$^{13}\text{C}_6$]glucose

Cell cultures were grown in Pi+ and MS media for 5.5 d and Pi- medium for 15 d. The average ^{13}C abundance of each metabolite fragment was calculated from the relative abundance of mass isotopomer fractions for each metabolite fragment derived by GC-MS analysis and assigned as described in Masakapalli *et al.* (2013). Data are presented as the mean \pm SD from three replicate cell cultures.

Metabolite	Carbon atoms	Fragment ion	Fractional ¹³ C abundance of metabolite in cells cultured in:								
			Pi- medium			MS medium			Pi+ medium		
<i>Soluble amino acids</i>											
Alanine	1-3	M-57	0.197	±	0.001	0.196	±	0.003	0.196	±	0.001
Aspartate	1-4	M-57	0.153	±	0.007	0.178	±	0.003	0.185	±	0.001
GABA	1-4	M-57	0.182	±	0.003	0.189	±	0.003	0.189	±	0.002
Glutamate	1-5	M-57	0.188	±	0.001	0.189	±	0.001	0.190	±	0.001
Glycine	1-2	M-57	0.170	±	0.001	0.181	±	0.003	0.187	±	0.001
Histidine	1-6	M-57	0.129	±	0.009	0.191	±	0.008	0.173	±	0.005
Phenylalanine	1-9	M-57	0.170	±	0.004	0.184	±	0.005	0.184	±	0.007
Pyroglutamate	1-5	M-57	0.181	±	0.001	0.190	±	0.001	0.191	±	0.002
Serine	1-3	M-57	0.175	±	0.001	0.186	±	0.001	0.188	±	0.001
Threonine	1-4	M-57	0.109	±	0.030	0.159	±	0.01	0.182	±	0.004
Valine	1-5	M-57	0.138	±	0.010	0.173	±	0.002	0.173	±	0.006
<i>Organic acids</i>											
Citrate	1-6	M-57	0.186	±	0.001	0.191	±	0.005	0.185	±	0.003
Malate	1-4	M-57	0.187	±	0.001	0.190	±	0.002	0.189	±	0.001
Maleate	1-4	M-57	0.169	±	0.003	0.176	±	0.010	0.181	±	0.007
Succinate	1-4	M-57	0.163	±	0.008	0.189	±	0.003	0.195	±	0.004
<i>Soluble sugars</i>											
Fructose	4-6	M-262	0.182	±	0.003	0.182	±	0.003	0.182	±	0.001
	1-4	M-205	0.189	±	0.002	0.186	±	0.003	0.189	±	0.004
Glucose	1-2	M-409	0.207	±	0.001	0.208	±	0.001	0.201	±	0.001
	3-6	M-250	0.200	±	0.001	0.199	±	0.002	0.196	±	0.001
<i>Protein hydrolysate</i>											
Alanine	1-3	M-57	0.157	±	0.002	0.173	±	0.003	0.176	±	0.002
Arginine	1-6	M-57	0.082	±	0.003	0.151	±	0.003	0.159	±	0.004
Aspartate	1-4	M-57	0.142	±	0.001	0.163	±	0.003	0.169	±	0.005
Glutamate	1-5	M-57	0.148	±	0.001	0.168	±	0.003	0.174	±	0.004
Glycine	1-2	M-57	0.130	±	0.001	0.162	±	0.002	0.167	±	0.003
Histidine	1-6	M-57	0.092	±	0.001	0.151	±	0.003	0.157	±	0.003
Isoleucine	2-6	M-159	0.076	±	0.001	0.145	±	0.004	0.154	±	0.004
Leucine	2-6	M-85	0.081	±	0.002	0.148	±	0.003	0.155	±	0.004
Lysine	1-6	M-57	0.081	±	0.003	0.149	±	0.005	0.160	±	0.006
Methionine	1-5	M-57	0.100	±	0.001	0.150	±	0.003	0.159	±	0.003
Phenylalanine	1-9	M-57	0.106	±	0.004	0.157	±	0.001	0.158	±	0.003
Proline	2-5	M-85	0.114	±	0.002	0.153	±	0.003	0.159	±	0.004

Serine	1-3	M-57	0.136	±	0.001	0.167	±	0.003	0.172	±	0.003
Threonine	1-4	M-57	0.104	±	0.002	0.154	±	0.003	0.161	±	0.003
Tyrosine	2-9	M-85	0.110	±	0.002	0.162	±	0.004	0.171	±	0.004
Valine	1-5	M-57	0.101	±	0.002	0.152	±	0.004	0.158	±	0.004
<i>Cell wall hydrolysate</i>											
Arabinose	5	M-364	0.107	±	0.005	0.118	±	0.003	0.137	±	0.003
	3-5	M-160	0.097	±	0.005	0.108	±	0.003	0.131	±	0.004
Galactose	3-6	M-250	0.122	±	0.005	0.160	±	0.003	0.170	±	0.001
Glucose	1-2	M-409	0.092	±	0.007	0.136	±	0.005	0.151	±	0.003
	3-6	M-250	0.097	±	0.007	0.139	±	0.003	0.152	±	0.004
Mannose	3-6	M-250	0.099	±	0.012	0.145	±	0.001	0.155	±	0.006
Xylose	5	M-364	0.080	±	0.005	0.121	±	0.004	0.139	±	0.001
	3-5	M-160	0.066	±	0.005	0.109	±	0.005	0.129	±	0.001
<i>Starch hydrolysate</i>											
Glucose	1-2	M-409	0.125	±	0.023	0.129	±	0.015	0.151	±	0.005
	3-6	M-250	0.131	±	0.023	0.132	±	0.015	0.155	±	0.004

Table S2. Reporter metabolites used in the scaling correction for incomplete isotopic equilibration of biosynthetic products

Where possible, scaling corrections for amino acids derived from hydrolysis of protein were based on the average isotopic abundance of the corresponding soluble amino acid. For tissues in which the average ^{13}C abundance of the soluble amino acid or immediate precursor metabolite of other biosynthetic polymers could not be reliably estimated, the isotopic composition of each end-product was corrected for the presence of pre-existing material using the average isotopic abundance of the specified reporter metabolite derived from the same metabolic pool as the biosynthetic precursor. Compounds for which no suitable reporter metabolites were available were corrected using proxy reactions as defined in Table S8.

Compound	Reporter metabolite
Protein hydrolysate	
Alanine	Soluble alanine
Arginine	<i>None – proxy reaction used</i>
Aspartate/asparagine	Malate/oxaloacetate
Glutamate/glutamine	Malate/oxaloacetate and citrate
Glycine	<i>None – proxy reaction used</i>
Histidine	<i>None – proxy reaction used</i>
Isoleucine	Soluble alanine and malate/oxaloacetate
Leucine	Soluble alanine
Lysine	Soluble alanine and malate/oxaloacetate
Methionine	<i>None – proxy reaction used</i>
Phenylalanine	Soluble alanine
Proline	Malate/oxaloacetate and citrate
Serine	<i>None – proxy reaction used</i>
Threonine	Malate/oxaloacetate
Tyrosine	Soluble alanine
Valine	Soluble alanine
Soluble	
Alanine	<i>None</i>
Glycine	<i>None</i>
Serine	<i>None</i>
GABA	Malate/oxaloacetate and citrate
Fructose	Soluble alanine
Succinate	<i>None</i>
Citrate	<i>None</i>
Malate/oxaloacetate	<i>None</i>
Cell wall	
Hexose and pentose units	Soluble alanine representing supplied glucose
Starch	
Glucosyl units	Soluble alanine representing supplied glucose

Table S3. Influence of Pi supply on glucose metabolism by heterotrophic Arabidopsis suspension cultures

Cells grown on either Pi-, MS or Pi+ media were supplied with 74 kBq [U-¹⁴C]glucose for 120 h (Pi- medium) or 24 h (MS and Pi+ media) beginning 10 d or 4.5 d after subculture, respectively. Cells were then extracted and the distribution of radioactivity determined by chemical fractionation. Ethanol was separated from the cell culture filtrate by distillation. Specific sugars were resolved by TLC, and partitioning amongst individual amino acids and organic acids was estimated from their relative C atom abundance (Table S4). Total ¹⁴C metabolised and the recovery of ¹⁴C during fractionation are also presented. Each value is the mean ± SD from three separate cell cultures. nd, not determined.

Fraction	Metabolite	Distribution of radioactivity (dpm) in cultures grown in:								
		Pi- medium			MS medium		Pi+ medium			
Alkali trap										
	Carbon dioxide	377071.1	±	3102.3*	278137.8	±	92557.2	658616.3	±	147076.3
Chloroform extract										
	Lipid	5773.6	±	1389.0	16030.9	±	1599.4	71818.1	±	13287.9
Cell culture filtrate										
Distillate										
	Ethanol	896.3	±	206.1	949.5	±	380.7	3527.2	±	656.7
Cationic fraction		28240.6	±	5277.8		-			-	
	Ala	1124.7	±	210.2		-			-	
	GABA	7309.6	±	1366.1		-			-	
	Gln	12727.2	±	2378.5		-			-	
	Thr	253.1	±	47.3		-			-	
	Tyr	6260.6	±	1170.0		-			-	
	Val	565.4	±	105.7		-			-	
Anionic fraction		13502.9	±	1035.6		-			-	
	Citrate	1584.4	±	121.5		-			-	
	Glycolate	57.8	±	4.4		-			-	
	Isocitrate	164.1	±	12.6		-			-	
	Malate	4004.3	±	307.1		-			-	
	Maleate	773.0	±	59.3		-			-	

	Oxoglutarate	3221.6	±	247.1	-	-
	Succinate	900.7	±	69.1	-	-
	Urea	2797.0	±	214.5	-	-
Aqueous methanol extract						
<i>Cationic fraction</i>		48321.9	±	3747.5	102774.3 ± 16821.4	283507.2 ± 82538.9
	Ala	4741.5	±	833.6	28152.9 ± 2452.1	70712.2 ± 27775.9
	Arg	749.4	±	405.4	349.4 ± 75.7	899.1 ± 292.0
	Asn	0.0	±	0.0	0.0 ± 0.0	0.0 ± 0.0
	Asp	968.0	±	147.1	1148.5 ± 308.4	3338.4 ± 978.9
	Cys	0.0	±	0.0	0.0 ± 0.0	0.0 ± 0.0
	Glu	6877.4	±	830.7	14140.7 ± 2853.5	48581.2 ± 16077.6
	Gln	18208.3	±	2649.3	30972.8 ± 7396.6	71365.3 ± 34158.5
	Gly	1174.6	±	245.5	2060.0 ± 231.9	7901.5 ± 3227.4
	His	225.1	±	86.0	54.6 ± 18.3	1934.3 ± 795.7
	Iso	44.2	±	15.2	76.8 ± 9.6	1433.2 ± 402.2
	Leu	161.5	±	55.3	151.1 ± 18.9	3695.2 ± 1073.5
	Lys	222.5	±	67.4	66.8 ± 18.2	1948.0 ± 435.7
	Met	7.7	±	2.5	13.7 ± 3.9	66.5 ± 27.6
	Phe	473.7	±	104.7	2722.7 ± 1457.5	9028.9 ± 2992.5
	Pro	1631.3	±	429.2	2132.8 ± 572.5	6008.4 ± 2480.6
	Ser	3106.6	±	350.3	10689.8 ± 1516.1	23556.2 ± 7556.6
	Thr	306.4	±	104.6	313.1 ± 76.5	2861.4 ± 675.6
	Trp	0.0	±	0.0	0.0 ± 0.0	0.0 ± 0.0
	Tyr	96.6	±	25.6	134.9 ± 45.4	1248.4 ± 424.8
	Val	556.5	±	139.5	648.1 ± 92.1	7282.5 ± 2010.8
	Pyroglu	2991.6	±	1371.7	1607.7 ± 499.3	3960.2 ± 1218.5
	GABA	5778.9	±	1632.5	7338.1 ± 2272.8	17686.4 ± 7918.1
<i>Anionic fraction</i>		12013.0	±	780.4	38652.5 ± 7359.7	135043.5 ± 10863.5
	Citrate	4173.4	±	1068.4	16689.9 ± 3524.6	29627.0 ± 14576.8
	Glycolate	36.4	±	23.5	59.3 ± 10.0	88.2 ± 69.4

	Isocitrate	516.2	±	608.0	1844.4	±	1017.9	627.3	±	197.7
	Malate	2988.2	±	1012.7	14884.9	±	5301.6	44557.6	±	17275.3
	Maleate	68.1	±	17.1	184.8	±	75.6	456.1	±	308.1
	Pyroglu	2474.7	±	725.7	573.5	±	124.4	613.9	±	514.3
	Succinate	421.8	±	164.9	4155.5	±	1924.8	58878.0	±	20274.0
	Urea	1334.3	±	496.7	260.2	±	167.8	195.4	±	280.8
Neutral fraction		39522.3	±	3609.8	79808.3	±	15578.6	443733.3	±	187463.0
	Fructose	9927.1	±	1318.6	24163.6	±	5224.6	124166.3	±	57502.1
	Glucose	9927.1	±	1318.6	24163.6	±	5224.6	124166.3	±	57502.1
	Sucrose	19668.0	±	990.1	31481.1	±	5189.3	195400.7	±	76464.9
Methanol insoluble residue										
Cationic fraction		19445.0	±	1492.4	50273.8	±	2636.1	108315.1	±	23664.4
	Ala	1282.4	±	160.6	2745.8	±	161.5	4784.3	±	1329.8
	Arg	394.6	±	103.3	1743.2	±	120.9	4070.0	±	1032.4
	Asx	1582.5	±	106.1	3212.6	±	151.6	5256.8	±	1922.3
	Cys	319.5	±	38.8	935.6	±	51.9	1795.6	±	467.8
	Glx	2123.3	±	132.1	4331.6	±	158.6	7455.0	±	2521.7
	Gly	1007.7	±	158.9	2545.6	±	174.9	4388.6	±	1259.6
	His	300.8	±	49.9	942.1	±	65.5	1813.3	±	465.5
	Iso	299.1	±	48.3	1116.2	±	228.2	2353.2	±	465.9
	Leu	1059.3	±	62.8	3426.2	±	222.2	6169.2	±	1791.8
	Lys	2007.4	±	298.4	7033.9	±	511.1	12413.6	±	4186.8
	Met	319.5	±	38.8	935.6	±	51.9	1795.6	±	467.8
	Phe	1080.6	±	153.0	2881.1	±	104.8	5282.0	±	1338.2
	Pro	1958.5	±	277.3	5433.7	±	245.9	10205.8	±	2468.1
	Ser	1316.2	±	131.2	3117.9	±	101.6	5328.5	±	1595.5
	Thr	1852.2	±	352.9	3356.4	±	751.8	22836.0	±	4582.5
	Trp	1080.6	±	153.0	2881.1	±	104.8	5282.0	±	1338.2
	Tyr	829.2	±	88.9	2229.0	±	136.2	4175.7	±	1163.0
	Val	631.6	±	25.5	1406.3	±	222.3	2910.2	±	596.3

<i>Anionic fraction and insoluble residue</i>								
Cell wall	18660.7	±	3835.4	24091.7	±	1622.5	140422.1	± 39118.3
<i>Neutral fraction</i>								
Starch	21885.2	±	3544.9	42731.3	±	4684.9	117835.6	± 13667.2
Metabolism and recovery								
¹⁴ C absorbed	585333.1	±	34145.3	622810.6	±	17727.6	1960666.0	± 419201.4
¹⁴ C in cell culture filtrate	3777259.0	±	52088.1	3027786.0	±	652546.1	1524855.0	± 590480.1
Total ¹⁴ C recovered	4362592.1	±	19837.6	3650597.0	±	666175.2	3485521.0	± 187231.4
¹⁴ C supplied	4612724.0	±	18332.2	4612724.0	±	18332.2	4612724.0	± 18332.2
Recovery (%)	94.6	±	0.4	79.1	±	14.4	75.6	± 4.1

* As discussed in the Results section of the paper, this value is likely to be an underestimate of the true value; subsequent flux analysis predicted this value to be 648202.9 ± 25842.4 dpm

Table S4. Composition of metabolite fractions of Arabidopsis cell cultures grown in media with differing Pi supply

The relative abundance of metabolites from each fraction was quantified from the standard curves of commercial metabolites using quantifier ions obtained from GC-MS, except for the metabolite composition of the cationic fraction of the culture filtrate from cells grown in Pi- medium which was determined by ¹H NMR. The relative abundance of metabolites produced de novo was used to estimate the proportion of radioactivity in each metabolite (Table S3) from which relative carbon fluxes are calculated (Table S5). Data are presented as the mean ± SE from measurements on three separate cell cultures.

Metabolite	Mass abundance (ng/μl sample in GC-MS)						Mr	No of C	Proportion of metabolite pool synthesized de novo ^a (%)			Relative abundance of metabolite produced de novo ^b (% C atom)											
	Pi- medium		MS medium		Pi+ medium				Pi-	MS	Pi+	Pi- medium		MS medium		Pi+ medium							
Soluble cationic fraction																							
Ala	69.5	±	9.8	191.5	±	14.7	131.2	±	16.8	89.1	3	100.0	100.0	100.0	9.8	±	0.9	27.7	±	1.5	25.2	±	4.8
Arg	16.0	±	5.4	3.0	±	0.3	2.0	±	0.1	210.7	6	81.5	92.1	99.9	1.5	±	0.5	0.3	±	0.0	0.3	±	0.0
Asn	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0	132.1	4	-	-	-	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0
Asp	20.2	±	0.4	9.4	±	0.7	7.5	±	0.9	133.1	4	77.4	90.8	94.5	2.0	±	0.1	1.1	±	0.1	1.2	±	0.0
Cys	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0	121.2	3	-	-	-	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0
Glu	103.4	±	5.2	97.0	±	2.7	93.3	±	8.9	147.1	5	95.5	96.7	96.9	14.2	±	0.4	13.8	±	1.2	17.0	±	0.4
Gln	270.8	±	2.6	211.3	±	22.4	140.8	±	44.8	146.1	5	95.5	96.7	96.9	37.6	±	2.1	29.9	±	1.5	24.9	±	6.3
Gly	24.7	±	1.5	19.2	±	1.5	19.3	±	2.2	75.1	2	86.2	92.3	95.7	2.4	±	0.3	2.0	±	0.1	2.8	±	0.4
His	5.8	±	1.0	0.4	±	0.0	5.1	±	1.6	209.6	6	65.2	97.7	88.5	0.5	±	0.1	0.1	±	0.0	0.7	±	0.2
Iso	2.0	±	0.4	0.6	±	0.1	3.2	±	0.4	131.2	6	23.3	62.4	63.4	0.1	±	0.0	0.1	±	0.0	0.5	±	0.0
Leu	3.8	±	0.7	1.0	±	0.1	6.4	±	1.2	131.2	6	45.2	78.0	81.4	0.3	±	0.1	0.1	±	0.0	1.3	±	0.1
Lys	4.1	±	0.5	0.6	±	0.0	4.8	±	0.8	182.6	6	80.2	80.2	80.2	0.5	±	0.1	0.1	±	0.0	0.7	±	0.1
Met	0.1	±	0.0	0.1	±	0.0	0.1	±	0.0	149.2	5	77.4	90.8	94.5	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0
Phe	4.9	±	0.3	12.3	±	4.0	11.8	±	3.4	165.2	9	86.1	94.0	94.3	1.0	±	0.1	2.6	±	0.7	3.3	±	0.7
Pro	20.2	±	3.6	11.6	±	1.7	8.9	±	1.3	115.1	5	91.3	96.4	96.7	3.4	±	0.4	2.1	±	0.2	2.1	±	0.4
Ser	60.0	±	4.5	89.2	±	1.0	54.0	±	2.6	105.1	3	88.7	95.2	96.3	6.4	±	0.2	10.5	±	0.6	8.3	±	0.7
Thr	5.7	±	1.1	2.3	±	0.1	5.8	±	0.2	119.1	4	77.4	90.8	94.5	0.6	±	0.1	0.3	±	0.0	1.0	±	0.1
Trp	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0	204.2	11	-	-	-	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0

Tyr	1.1	±	0.1	0.7	±	0.1	1.7	±	0.1	181.2	9	86.1	94.0	94.3	0.2	±	0.0	0.1	±	0.0	0.4	±	0.1
Val	9.0	±	0.9	3.9	±	0.2	12.4	±	1.7	117.1	5	69.9	88.5	88.3	1.2	±	0.2	0.6	±	0.0	2.6	±	0.1
Pyroglu	42.2	±	12.9	9.6	±	1.3	6.8	±	1.4	129.1	5	91.9	97.1	97.8	6.4	±	2.0	1.6	±	0.3	1.4	±	0.2
GABA	79.6	±	15.6	44.4	±	7.3	29.2	±	3.7	103.1	4	92.4	96.5	96.4	11.9	±	1.7	7.0	±	0.7	6.2	±	1.0
Soluble anionic fraction																							
Citrate	47.6	±	29.3	99.5	±	3.2	53.3	±	17.9	192.0	6	94.2	97.7	94.6	35.2	±	6.5	44.0	±	6.9	21.5	±	5.5
Glycolate	0.7	±	0.5	0.7	±	0.0	0.3	±	0.1	76.1	2	46.0	60.0	46.5	0.3	±	0.1	0.2	±	0.0	0.1	±	0.0
Isocitrate	12.3	±	11.3	10.6	±	3.0	1.2	±	0.4	192.1	6	94.2	97.7	94.6	4.3	±	2.9	4.7	±	1.4	0.5	±	0.1
Malate	48.6	±	40.1	106.6	±	27.2	81.7	±	13.2	134.1	4	85.7	89.8	92.4	24.7	±	4.5	37.9	±	5.4	32.5	±	5.9
Maleate	0.9	±	0.6	1.3	±	0.3	1.0	±	0.5	138.1	4	85.7	89.8	92.4	0.6	±	0.1	0.5	±	0.2	0.3	±	0.1
Pyroglu	20.6	±	14.1	3.0	±	0.5	0.8	±	0.3	129.1	5	91.5	95.0	95.0	20.4	±	2.8	1.5	±	0.1	0.4	±	0.2
Succinate	3.8	±	2.1	24.8	±	8.0	93.9	±	24.2	118.1	4	82.6	96.4	99.5	3.5	±	0.7	10.6	±	2.5	44.6	±	10.8
Urea	36.7	±	25.3	5.0	±	1.9	0.8	±	0.6	60.1	1	61.4	61.4	61.4	11.0	±	2.0	0.6	±	0.2	0.1	±	0.1
Protein hydrolysate																							
Ala	50.2	±	9.7	68.3	±	1.3	86.4	±	8.3	89.1	3	79.5	88.5	90.2	6.6	±	0.2	5.5	±	0.2	4.4	±	0.2
Arg	35.6	±	8.9	58.9	±	1.4	96.7	±	9.2	210.7	6	41.6	77.0	81.5	2.0	±	0.2	3.5	±	0.0	3.7	±	0.1
Asn	nd			nd			nd			132.1	4	-	-	-	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0
Asp	75.5	±	10.3	95.0	±	0.2	108.6	±	1.8	133.1	4	72.0	83.3	86.3	8.2	±	0.3	6.4	±	0.1	4.8	±	0.5
Cys	nd			nd			nd			121.2	3	-	-	-	1.6	±	0.0	1.9	±	0.0	1.6	±	0.0
Glu	86.2	±	13.2	110.1	±	0.8	132.9	±	4.3	147.1	5	75.1	85.8	89.0	10.9	±	0.2	8.6	±	0.1	6.8	±	0.6
Gln	nd			nd			nd			146.1	5	-	-	-	0.0	±	0.0	0.0	±	0.0	0.0	±	0.0
Gly	60.5	±	12.6	85.7	±	2.6	105.6	±	10.0	75.1	2	65.8	82.6	85.4	5.2	±	0.3	5.1	±	0.3	4.0	±	0.2
His	23.9	±	5.5	31.6	±	0.4	43.7	±	5.0	209.6	6	46.6	77.1	80.0	1.5	±	0.1	1.9	±	0.0	1.7	±	0.0
Iso	24.6	±	4.3	25.2	±	2.1	39.1	±	5.5	131.2	6	27.9	71.4	73.8	1.6	±	0.2	2.2	±	0.2	2.2	±	0.1
Leu	62.0	±	11.2	78.1	±	1.2	98.0	±	7.3	131.2	6	39.1	71.1	75.2	5.5	±	0.1	6.8	±	0.1	5.6	±	0.3
Lys	157.4	±	35.1	207.8	±	2.1	249.7	±	9.6	182.6	6	41.2	76.3	81.7	10.3	±	0.5	14.0	±	0.2	11.3	±	1.0
Met	19.8	±	4.0	26.9	±	0.2	36.5	±	4.0	149.2	5	50.5	76.8	81.0	1.6	±	0.0	1.9	±	0.0	1.6	±	0.0
Phe	38.6	±	7.6	48.8	±	0.6	66.2	±	7.1	165.2	9	53.7	80.3	80.9	5.5	±	0.2	5.7	±	0.1	4.9	±	0.1
Pro	82.4	±	18.9	118.6	±	1.3	160.3	±	21.3	115.1	5	57.9	78.2	81.5	10.1	±	0.6	10.8	±	0.1	9.4	±	0.3
Ser	69.3	±	11.3	95.0	±	1.9	116.0	±	7.4	105.1	3	69.1	85.2	87.7	6.8	±	0.2	6.2	±	0.2	4.9	±	0.3

Thr	105.2 ± 4.5	94.4 ± 13.2	487.5 ± 118.9	119.1	4	52.6	78.7	82.3	9.6 ± 1.4	6.7 ± 0.8	21.7 ± 3.2
Trp	nd	nd	nd	204.2	11	-	-	-	5.5 ± 0.2	5.7 ± 0.1	4.9 ± 0.1
Tyr	31.3 ± 6.1	40.3 ± 0.4	52.7 ± 4.9	181.2	9	56.0	82.5	87.5	4.3 ± 0.1	4.4 ± 0.1	3.8 ± 0.1
Val	30.2 ± 5.2	31.4 ± 2.2	47.1 ± 6.0	117.1	5	51.1	77.6	80.9	3.3 ± 0.1	2.8 ± 0.2	2.7 ± 0.0
Culture filtrate - cationic fraction											
Ala	10.1 ± 1.9	-	-	-	3	-	-	-	4.0 ± 0.7	-	-
GABA	49.3 ± 0.3	-	-	-	4	-	-	-	25.9 ± 0.2	-	-
Gln	68.6 ± 17.4	-	-	-	5	-	-	-	45.1 ± 11.4	-	-
Thr	1.7 ± 0.5	-	-	-	4	-	-	-	0.9 ± 0.3	-	-
Tyr	18.8 ± 1.4	-	-	-	9	-	-	-	22.2 ± 1.6	-	-
Val	3.0 ± 0.5	-	-	-	5	-	-	-	2.0 ± 0.4	-	-
Culture filtrate - anionic fraction											
Citrate	34.5	-	-	192.0	6	94.5		11.7		-	-
Glycolate	3.2	-	-	76.1	2	43.9		0.4		-	-
Isocitrate	3.6	-	-	192.1	6	94.5		1.2		-	-
Malate	98.4	-	-	134.1	4	87.8		29.7		-	-
Maleate	19.6	-	-	138.1	4	87.8		5.7		-	-
Succinate	19.7	-	-	118.1	4	86.9		6.7		-	-
Urea	175.9	-	-	60.1	1	61.4		20.7		-	-
Oxoglutarate	64.0	-	-	146.1	5	94.5		23.9		-	-

Footnotes

^a The proportion of metabolite pool produced during the ¹⁴C labeling period was estimated from the average ¹³C abundance of the metabolite in cells grown in 20% [¹³C₆]glucose.

^b The relative amount of each metabolite produced during the period of labeling was calculated as (Mass abundance/Mr) x (No of C) x (proportion of metabolite pool produced de novo) and is expressed as a percentage of the total C atom abundance in the relevant chemical fraction (soluble cationic, soluble anionic, protein hydrolysate and culture filtrate - anionic fraction). For the cationic fraction of culture filtrate, the amount of metabolite produced

during the labeling period was estimated from the difference between the concentrations determined from NMR spectra of samples analysed 10 d and 15 d after subculture into Pi- medium.

nd - not determined. Cys and Trp are lost during acid hydrolysis of protein, while Gln and Asn are converted to Glu and Asp, respectively. The relative C atom abundances of Trp and Cys are assumed to be equal to Phe and Met, respectively.

Table S5. Flux to metabolic products in Arabidopsis cultures grown with differing Pi supply

Flux was determined relative to the rate of glucose consumption and is expressed both as a proportion of total carbon atom abundance and as a molar output flux. The proportional carbon atom flux was obtained from the relative distribution of radioactivity after metabolism of [U-¹⁴C]glucose (Table S3). The C atom composition of each metabolite was used to calculate molar output fluxes and these were used as constraints in parameter fitting during MFA using 13C-FLUX. For MS and Pi+ cultures the rate of glucose consumption was set to unity, whereas fluxes to biomass outputs in Pi- cells are expressed relative to a rate of glucose consumption of 1.44 as deduced from the subsequent best-fit solution of the labelling patterns. Data are presented as mean \pm SD from measurements on three separate cell cultures.

Metabolite	Relative carbon atom flux									No of C atoms	Output flux	Relative molar output flux								
	Pi- medium			MS medium			Pi+ medium					Pi- medium			MS medium			Pi+ medium		
CO ₂	0.644	±	0.009	0.430	±	0.087	0.337	±	0.052	1	CO ₂ ‡	3.865	±	0.055	2.582	±	0.520	2.019	±	0.310
Fructose	0.017	±	0.002	0.039	±	0.014	0.061	±	0.019	6	fruOUT	*			*			*		
Glucose	0.017	±	0.002	0.039	±	0.014	0.061	±	0.019	6	glcOUT	*			*			*		
Sucrose-glucosyl	0.017	±	0.001	0.026	±	0.008	0.048	±	0.012	6	suc(g)OUT	0.034	±	0.003	0.065	±	0.022	0.110	±	0.030
Sucrose-fructosyl	0.017	±	0.001	0.026	±	0.008	0.048	±	0.012	6	suc(f)OUT	0.034	±	0.003	0.065	±	0.022	0.110	±	0.030
Cellwall C6	0.026	±	0.005	0.031	±	0.003	0.058	±	0.007	6	cellwall(h)OUT	0.026	±	0.005	0.031	±	0.003	0.058	±	0.007
Cellwall C5	0.006	±	0.001	0.007	±	0.001	0.013	±	0.002	5	cellwall(p)OUT	0.007	±	0.001	0.008	±	0.001	0.015	±	0.002
Starch	0.037	±	0.006	0.069	±	0.015	0.062	±	0.018	6	starchOUT	0.037	±	0.006	0.069	±	0.015	0.062	±	0.018
Lipid-glycerol†	0.001	±	0.000	0.002	±	0.001	0.003	±	0.001	3	glycerolOUT	0.002	±	0.000	0.004	±	0.001	0.006	±	0.002
Lipid-FA†	0.009	±	0.002	0.024	±	0.006	0.035	±	0.014	2	lipidOUT	0.027	±	0.007	0.072	±	0.018	0.106	±	0.041
Ethanol	0.002	±	0.000	0.002	±	0.001	0.002	±	0.000	2	ethanolOUT	0.005	±	0.001	0.005	±	0.002	0.005	±	0.001
Citrate	0.010	±	0.002	0.026	±	0.002	0.015	±	0.006	6	citOUT	0.011	±	0.002	0.029	±	0.002	0.015	±	0.006
Isocitrate	0.001	±	0.001	0.003	±	0.001	0.000	±	0.000	6		*			*			*		
Malate	0.013	±	0.002	0.024	±	0.009	0.023	±	0.007	4	malOUT	0.020	±	0.002	0.036	±	0.013	0.034	±	0.011
Oxoglutarate	0.006	±	0.000	0.000	±	0.000	0.000	±	0.000	5		*			*			*		
Succinate	0.002	±	0.000	0.007	±	0.004	0.032	±	0.016	4	succOUT	0.003	±	0.001	0.010	±	0.005	0.048	±	0.025
Urea	0.007	±	0.001	0.000	±	0.000	0.000	±	0.000	1	Urea [#]	0.042	±	0.007	0.003	±	0.002	0.001	±	0.001

Glycolate	0.000	±	0.000	0.000	±	0.000	0.000	±	0.000	2	Glycolate ^{##}	0.000	±	0.000	0.000	±	0.000	0.000	±	0.000
Ala	0.012	±	0.002	0.049	±	0.005	0.039	±	0.015	3	alaOUT	0.024	±	0.004	0.098	±	0.009	0.078	±	0.030
Arg	0.002	±	0.001	0.003	±	0.001	0.003	±	0.001	6	argOUT	0.002	±	0.001	0.003	±	0.001	0.003	±	0.001
Asx	0.004	±	0.000	0.007	±	0.001	0.005	±	0.002	4	aspOUT	0.007	±	0.001	0.010	±	0.001	0.007	±	0.002
Cys	0.001	±	0.000	0.002	±	0.000	0.001	±	0.000	3	cysOUT	0.001	±	0.000	0.003	±	0.001	0.002	±	0.001
Glx	0.078	±	0.001	0.081	±	0.003	0.066	±	0.012	5	gluOUT	0.093	±	0.001	0.097	±	0.003	0.079	±	0.014
Gly	0.004	±	0.001	0.007	±	0.001	0.006	±	0.002	2	glyOUT	0.011	±	0.002	0.022	±	0.002	0.019	±	0.007
His	0.001	±	0.000	0.002	±	0.000	0.002	±	0.000	6	hisOUT	0.001	±	0.000	0.002	±	0.000	0.002	±	0.000
Iso	0.001	±	0.000	0.002	±	0.001	0.002	±	0.000	6	ileOUT	0.001	±	0.000	0.002	±	0.001	0.002	±	0.000
Leu	0.002	±	0.000	0.006	±	0.001	0.005	±	0.001	6	leuOUT	0.002	±	0.000	0.006	±	0.001	0.005	±	0.001
Lys	0.004	±	0.000	0.011	±	0.003	0.008	±	0.004	6	lysOUT	0.004	±	0.000	0.011	±	0.003	0.008	±	0.004
Met	0.001	±	0.000	0.002	±	0.000	0.001	±	0.000	5	metOUT	0.001	±	0.000	0.002	±	0.000	0.001	±	0.001
Phe	0.003	±	0.000	0.009	±	0.002	0.007	±	0.001	9	pheOUT	0.002	±	0.000	0.006	±	0.001	0.005	±	0.001
Pro	0.006	±	0.001	0.012	±	0.002	0.009	±	0.003	5	proOUT	0.007	±	0.001	0.015	±	0.002	0.010	±	0.004
Ser	0.008	±	0.001	0.022	±	0.002	0.015	±	0.004	3	serOUT	0.015	±	0.001	0.044	±	0.003	0.030	±	0.007
Thr	0.004	±	0.001	0.006	±	0.002	0.013	±	0.002	4	thrOUT	0.006	±	0.001	0.009	±	0.003	0.020	±	0.003
Trp	0.002	±	0.000	0.005	±	0.001	0.003	±	0.001	11	trpOUT	0.001	±	0.000	0.003	±	0.001	0.002	±	0.001
Tyr	0.012	±	0.002	0.004	±	0.001	0.003	±	0.001	9	tyrOUT	0.008	±	0.001	0.003	±	0.001	0.002	±	0.001
Val	0.003	±	0.000	0.003	±	0.001	0.005	±	0.001	5	valOUT	0.004	±	0.000	0.004	±	0.001	0.006	±	0.001
GABA	0.022	±	0.004	0.011	±	0.003	0.009	±	0.003	4	gabaOUT	0.034	±	0.007	0.017	±	0.004	0.014	±	0.005

Footnotes

† Assumes that the bulk of lipid is phospholipid containing 35 C atom in fatty acids per glycerol backbone. The total radioactivity in lipid was thus partitioned between glycerol (C = 3) and fatty acid (FA, C = 35).

‡ CO₂ efflux was not used as a constraint during 13C-FLUX analysis, but was determined by the other output fluxes defined in the model. The long incubation time for Pi- cultures compromised quantitative recovery of the ¹⁴CO₂ released, resulting in an under-estimate of the proportion of substrate oxidised to CO₂.

* Production of glucose and fructose by the network was incorporated into sucrose output fluxes (suc(g)OUT and suc(f)OUT, respectively) since they are assumed to be produced via sucrose degradation and are thus derived indirectly from the same metabolite pool as the respective hexosyl moiety of sucrose. Similarly isocitrate is assigned as output with citrate (citrateOUT) and oxoglutarate assigned as output along with glx (gluOUT)

Urea is assumed to be synthesized exclusively from CO₂ and is not considered as an output of glucose metabolism in the model.

Flux to glycolate is negligible in all three culture conditions and is not included in subsequent metabolic modelling.

Table S6. Positional isotopomer abundance of metabolites derived from Arabidopsis cultures in Pi- MS and Pi+ media containing [¹³C]glucose

Cultures were grown in either 99% [1-¹³C]glucose, 99% [2-¹³C]glucose or 20% [¹³C₆]glucose and the relative abundance of cumomer groups was determined by NMR. Triplicate cultures were analysed for each labelled substrate.

Pi- cultures					
Metabolite	Network metabolite	Carbon atom subgroups	Peak area	SD	Cumomer
[1-¹³C]glucose: Replicate 1					
Alanine	ALA	C12aala	8.343	0.733	#10x
			2.260	0.614	#010
		C3aala	71.481	2.694	#x01
			0.166	2.694	#x11
Aspartate	ASP	C4aasn	2.375	0.385	#xx11
			7.142	0.680	#xx01
		C2aasp	5.326	0.576	#010x
			3.080	0.602	#110x+#011x
		C4aasp	6.724	0.818	#xx11
			23.898	1.972	#xx01
Citrate	CIT	C3aasp	1.987	0.314	#x011+#x110
			4.952	0.485	#x010
		C15acit	16.225	0.679	#10xxxx+#xxx01x
			6.225	0.496	#11xxxx+#xxx11x
		C24acit	38.346	2.314	#010xxx+#xx010x
			20.765	1.086	#110xxx+#xx011x+#011xxx+#xx110x
GABA	GABA	C3acit	2.992	0.472	#x111x0
			17.303	1.120	#x110x0+#x011x0
		C6acit	2.400	0.430	#x010x1
			17.450	1.805	#x010x0+#x111x0
		C2agaba	3.780	0.353	#xx1xx1
			10.960	0.690	#xx0xx1
Glutamate/glutamine	GLU	C3agaba	38.391	1.679	#010x
			20.889	1.167	#110x+#011x
		C3agaba	28.196	1.562	#x010
			31.976	1.680	#x110+#x011+#x111
Glycine	GLY	C3aglu	21.434	1.269	#x010x
			20.964	1.248	#x110x+#x011x
		C4aglu	34.405	1.678	#xx010
			16.730	1.123	#xx110
		C1agln	57.085	5.020	#11xxx
			134.820	5.538	#10xxx
		C3agln	206.330	6.940	#x010x
			171.277	5.823	#x110x+#x011x
Lysine	LYS	C4agln	303.199	9.710	#xx010
			129.936	4.962	#xx110
Malate	OAA	C1gly	2.591	0.391	#10
			0	0.391	#11
Lysine	LYS	C3alys	7.058	0.715	#x010xx
			3.645	0.608	#x110xx+#x011xx
Malate	OAA	C1amal	3.712	0.418	#10xx

			1.644	0.336	#11xx
		C2amal	6.340	0.630	#010x
			2.980	0.512	#110x+#111x
			3.044	0.916	#011x
		C3amal	6.162	0.553	#x010
			1.848	0.277	#x110
Valine	VAL	C45aval	3.465	0.437	#xx01x
			3.342	0.404	#xx0x1
Sucrose	FSUC	C16afsuc	48.755	2.341	#10xxxx
			18.085	1.216	#xxxxx01
Sucrose	GSUC	C6agsuc	17.733	1.317	#10xxxx
			0.001	1.317	#11xxxx
Starch	STA	StaA	0.087	0.009	#10xxxx
			0.060	0.012	#xxxxx01
[1-¹³C]glucose: Replica 2					
Alanine	ALA	C12bala	3.668	0.387	#10x
			1.196	0.412	#010
		C3bala	45.742	1.912	#x01
			0.251	0.139	#x11
Aspartate	ASP	C4basn	2.471	0.382	#xx11
			5.946	0.574	#xx01
		C2basp	4.792	0.543	#010x
			2.908	0.525	#110x+#011x
		C4basp	4.224	0.603	#xx11
			14.577	1.176	#xx01
Citrate	CIT	C3bcit	1.780	0.689	#x111x0
			13.694	3.118	#x110x0+#x011x0
			1.296	0.814	#x010x1
			17.146	3.444	#x010x0
		C6bcit	7.298	0.661	#xx1xx1
			15.150	0.939	#xx0xx1
GABA	GABA	C2bgaba	27.357	1.274	#010x
			15.433	0.996	#110x+#011x
		C3bgaba	18.260	1.146	#x010
			17.704	1.150	#x110+#x011
Glutamate/glutamine	GLU	C3bglu	18.242	1.082	#x010x
			17.732	1.115	#x110x+#x011x
		C4bglu	13.954	0.935	#xx110
			28.685	1.382	#xx010
		C1bgln	51.520	4.828	#11xxx
			107.636	7.838	#10xxx
		C3bgln	146.058	4.966	#x010x
			130.891	4.591	#x110x+#x011x
		C4bgln	192.150	6.116	#xx010
			88.667	4.571	#xx110
Glycine	GLY	C1bgly	2.045	0.414	#10
			0.001	0.414	#11
Lysine	LYS	C3blys	3.421	0.431	#x010xx
			2.412	0.530	#x110xx+#x011xx
Malate	OAA	C1bmal	4.537	0.459	#10xx
			1.762	0.299	#11xx
		C2bmal	9.218	0.696	#010x
			1.741	0.320	#110x+#111x
			3.369	0.433	#011x

		C3bmal	8.475	0.632	#x010
			2.949	0.412	#x110
			1.256	0.269	#x011
		C4bmal	2.233	0.384	#xx11
			7.508	0.815	#xx01
Valine	VAL	C35bval	2.754	0.350	#xx01x
			2.776	0.347	#xx0x1
Sucrose	FSUC	C16afsuc	48.807	2.256	#10xxxx
			16.913	1.138	#xxxxx01
Sucrose	GSUC	C6agsuc	15.696	1.122	#10xxxx
			0.001	1.122	#11xxxx
Starch	STA	StaB	0.156	0.012	#10xxxx
			0.051	0.009	#xxxxx01
[1-¹³C]glucose: Replica 3					
Alanine	ALA	C12cala	5.520	0.571	#10x
			3.191	0.880	#010
		C3cala	70.593	2.909	#x01
			0.720	0.199	#x11
Aspartate	ASP	C2casn	14.283	1.174	#010x
			7.842	0.933	#110x+#011x
		C2casp	8.381	0.822	#010x
			4.642	0.687	#110x+#011x
Citrate	CIT	C15ccit	31.565	1.758	#10xxxx+#xxx01x
			13.387	1.169	#11xxxx+#xxx11x
		C24ccit	97.934	3.694	#010xxx+#xx010x
			7.896	0.790	#110xxx+#xx011x
			41.506	2.054	#011xxx+#xx110x
		C3ccit	3.493	1.266	#x111x0
			26.138	2.324	#x110x0+#x011x0
			5.081	1.076	#x010x1
			28.584	2.269	#x010x0
		C6ccit	11.629	0.873	#xx1xx1
			23.240	1.223	#xx0xx1
GABA	GABA	C2cgaba	7.560	0.675	#010x
			3.056	0.400	#011x
		C3cgaba	25.119	1.451	#x010
			4.408	0.708	#x111
			23.100	1.427	#x110+#x011
Glutamate/glutamine	GLU	C3cglu	27.298	1.689	#x010x
			22.290	1.411	#x110x+#x011x
		C4cglu	19.926	1.341	#xx110
			42.435	1.993	#xx010
		C3cgln	215.947	8.092	#x010x
			167.907	6.438	#x110x+#x011x
		C4cgln	338.322	11.005	#xx010
			137.409	5.561	#xx110
Glycine	GLY	C1cgly	2.222	0.323	#10
			0.001	0.323	#11
Lysine	LYS	C3clys	7.020	0.594	#x010xx
			3.840	1.073	#x110xx+#x011xx
Malate	OAA	C1cmal	8.315	0.676	#10xx
			5.199	0.724	#11xx
		C2cmal	16.613	1.150	#010x
			5.859	0.716	#011x

		C3cmal	15.760	1.014	#x010
			5.752	0.650	#x110
			1.359	0.221	#x011
		C4cmal	4.248	0.651	#xx11
			9.366	0.831	#xx01
Valine	VAL	C3cmal	4.584	0.553	#xx01x
			5.064	0.603	#xx0x1
Sucrose	FSUC	C16afsuc	89.193	3.701	#10xxxx
			25.488	1.689	#xxxx01
Sucrose	GSUC	C6agsuc	28.358	1.818	#10xxxx
			0.001	1.818	#11xxxx
Starch	STA	StaC	0.156	0.012	#10xxxx
			0.051	0.009	#xxxx01
[2-¹³C]glucose: Replica 1					
Alanine	ALA_2	C2dala	74.216	2.879	#010
			4.668	0.601	#011+#110+#111
		C1dala	3.061	0.784	#11x
			3.395	0.362	#10x
		C3dala	7.820	0.626	#x01
			1.297	0.289	#x11
Aspartate	ASP_2	C23das	1.776	0.269	#010x
			1.558	0.250	#x010
Citrate	CIT_2	C15dcit	65.457	2.584	#10xxxx+#xxx01x
			1.912	0.363	#11xxxx+#xxx11x
		C24dcit	15.505	1.045	#010xxx+#xx010x
			1.604	0.329	#110xxx+#xx011x+#011xxx+#xx110x
GABA	GABA_2	C3dgaba	6.462	0.492	#x010
			0.536	0.174	#x110+#x011
Glutamate/glutamine	GLU_2	C4dglu	3.946	0.375	#xx010
			1.078	0.415	#xx110
			0.493	0.147	#xx011
		C2dgln	100.827	3.845	#010xx
			6.044	0.641	#110xx
			4.257	0.539	#011xx
		C3dglu	100.912	3.689	#x010x
			8.378	0.776	#x110x+#x011x
		C4dglu	44.486	2.036	#xx010
			4.972	0.604	#xx011
			4.549	0.559	#xx110
Glycine	GLY_2	C2dgly	27.538	1.471	#01
			0.890	1.471	#11
Malate	OAA_2	C1dmal	6.832	0.612	#10xx
			1.857	0.376	#11xx
		C14dmal	6.550	0.586	#xx01
			6.832	0.612	#10xx
Sucrose	GSUC_2	C25dgsuc	52.432	2.385	#010xxx
			17.266	1.071	#xxx010
Sucrose	FSUC_2	C25dfsuc	33.96	2.952	#010xxx
			16.691	2.062	#xxx010
Starch	STA_2	StaA_beta	0.029	0.006	#xxx010+#x010xx
			0.072	0.008	#010xxx
[2-¹³C]glucose: Replica 2					

Alanine	ALA_2	C2eala	53.597	2.161	#010	
			3.112	0.362	#011+#110+#111	
		C3eala	5.485	0.474	#x01	
			0.522	0.385	#x11	
Citrate	CIT_2	C24ecit	15.088	0.944	#010xxx+#xx010x	
			0.843	0.232	#110xxx+#xx011x	
			1.139	0.230	#011xxx+#xx110x	
GABA	GABA_2	C14egaba	20.162	1.097	#10xx	
			5.660	0.513	#xx01	
		C3egaba	5.489	0.446	#x010	
			1.546	0.406	#x110+#x011	
Glutamate/glutamine	GLU_2	C4eglu	6.007	0.557	#xx010	
			0.556	0.169	#xx110	
			0.467	0.146	#xx011	
		C2eglu	94.222	3.798	#010xx	
			5.473	0.696	#110xx	
			3.867	0.510	#011xx	
		C4egl n	49.789	2.358	#xx010	
			5.342	0.736	#xx011	
			5.172	0.625	#xx110	
Glycine	GLY_2	C2egly	18.855	1.107	#01	
			0.512	1.107	#11	
Malate	OAA_2	C3emal	4.065	0.399	#x010	
			0.211	0.065	#x011+#x110	
		C14emal	7.038	0.587	#xx01	
			8.181	0.649	#10xx	
Sucrose	FSUC_2	C25dfsuc	52.767	4.020	#010xxx	
			22.860	2.488	#xxx010	
Starch	STA_2	StaB_beta	0.055	0.008	#xxx010+#x010xx	
			0.110	0.009	#010xxx	
[2- ¹³ C]glucose: Replica 3						
Alanine	ALA_2	C2fala	66.32	2.567	#010	
			4.642	0.496	#011+#110+#111	
		C3fala	8.494	0.609	#x01	
			1.165	0.468	#x11	
Aspartate	ASP_2	C23	1.995	0.308	#010x	
			1.751	0.263	#x010	
Citrate	CIT_2	C15	56.891	2.246	#10xxxx+#xxx01x	
			0.691	0.247	#11xxxx+#xxx11x	
			14.707	0.964	#010xxx+#xx010x	
		C24fcit	1.061	0.204	#110xxx+#xx011x+#011xxx+#xx110x	
			C36fcit	1.760	0.319	#x010x0
				3.597	0.426	#xx0xx1
GABA	GABA_2	C3fgaba	7.497	0.624	#x010	
			1.524	0.481	#x110+#x011	
Glutamate/glutamine	GLU_2	C2fglu	102.910	3.840	#010xx	
			7.637	0.711	#110xx	
			4.680	0.489	#011xx	
		C3fgln	102.376	3.668	#x010x	
			12.660	1.437	#x110x+#x011x	
			44.844	1.968	#xx010	
		C4fglu	5.699	0.653	#xx011	
			6.225	0.646	#xx110	

Glycine	GLY_2	C2fgly	22.435 0.782	1.245 1.245	#01 #11
Malate	OAA_2	C1fmal	1.419 6.156	0.320 0.527	#11xx #10xx
		C14fmal	6.423 6.156	0.570 0.527	#xx01 #10xx
Sucrose	GSUC_2	C25dgsuc	64.833 20.120	2.733 1.142	#010xxx #xxx010
Sucrose	FSUC_2	C25dfsuc	64.768 21.891	2.589 1.264	#010xxx #xxx010
Starch	STA_2	StaC_beta	0.042 0.107	0.008 0.011	#xxx010+#x010xx #010xxx
20% [¹³C₆]glucose: Replica 1					
Alanine	ALA_3	C2gala	21.315 43.763	0.951 1.752	#010+#011+#110 #111
		C1gala	15.030 5.216	0.801 0.373	#11x #10x
Glycine	GLY_3	C1ggly	2.748 6.159	0.418 0.638	#10 #11
20% [¹³C₆]glucose: Replica 2					
Alanine	ALA_3	C2hala	14.469 27.653	0.780 1.370	#010+#011+#110 #111
		C1hala	8.983 4.197	0.566 0.329	#11x #10x
		C3hala	4.428 32.990	0.300 1.320	#x01 #x11
20% [¹³C₆]glucose: Replica 3					
Alanine	ALA_3	C2iala	11.594 23.491	0.606 1.174	#010+#011+#110 #111
		C1iala	7.943 3.680	0.568 0.329	#11x #10x
		C3iala	3.335 25.627	0.241 1.073	#x01 #x11
Malate	OAA_3	C1imal	1.274 1.628	0.139 0.171	#10xx #11xx

MS cultures					
Metabolite	Network metabolite	Carbon atom subgroups	Peak area	SD	Cumomer
[1- ¹³ C]glucose: Replica 1					
Starch	STA	StaA	0.454	0.027	#10xxxx
			0.132	0.017	#xxxx01
Alanine	ALA	C1a	0.437	0.126	#11x
			11.174	0.806	#10x
		C2a	5.452	0.644	#010
			1.559	0.336	#011
		C3a	134.185	4.513	#x01
			1.300	0.469	#x11
Citrate	CIT	C1C5a	24.858	1.606	#10xxxx+#xxx01x
			9.926	1.057	#11xxxx+#xxx11x
		C6a	6.769	0.616	#xx1xx1
			20.328	1.289	#xx0xx1
		nosubCITa	24.858	1.606	#10xxxx+#xxx01x
			21.332	1.445	#x010x0
			20.328	1.289	#xx0xx1
GABA	GABA	C24a	6.158	0.547	#010x
			7.365	0.747	#xx01
		C3a	7.248	0.636	#x010
			4.934	0.498	#x110+#x011
Glutamate/glutamine	GLU	C1a	6.097	0.632	#11xxx
			14.299	0.938	#10xxx
		C3a	14.733	0.820	#x010x
			10.641	2.735	#x110x+#x011x
		C1a	36.226	1.732	#10xxx
			14.023	1.037	#11xxx
		C2a	62.831	2.617	#010xx
			7.233	0.659	#110xx
			20.212	1.240	#011xx
		C3a	48.067	2.088	#x010x
			38.288	1.803	#x110x+#x011x
Glycine	GLY	C1a	0.492	0.169	#10
			0.010	0.169	#11
Malate	OAA	C1a	13.493	0.830	#10xx
			4.463	0.460	#11xx
		C2a	24.597	1.237	#010x
			2.645	0.316	#110x
			8.316	0.661	#011x
		C3a	26.000	1.332	#x010
			9.198	0.752	#x110
			3.613	0.456	#x011
		C4a	17.143	1.152	#xx01
			5.885	0.644	#xx11
		nonsubOAA	13.493	0.830	#10xx
			24.597	1.237	#010x
			24.000	1.233	#x010
Serine	SER	C3a	24.492	1.213	#x01
			0.010	0.853	#x11
Succinate	SUCC	C1C4a	2.904	0.510	#10xx+#xx01
			1.008	0.226	#11xx+#xx11
Sucrose	GSUC	Ca	0.464	0.080	#xxx010

Sucrose	FSUC	C16a1	7.546	0.687	#xxxx01
			38.328	1.930	#10xxxx
			10.068	0.884	#xxxx01
		C16a2	80.710	3.124	#10xxxx
			17.604	1.034	#xxxx01
		C16a3	23.947	1.303	#10xxxx
			5.223	0.763	#xxxx01
			1.290	0.300	#xx010x
[1- ¹³ C]glucose: Replica 2					
Starch	STA	StaB	0.302	0.021	#10xxxx
			0.094	0.013	#xxxx01
Alanine	ALA	C1b	0.316	0.070	#11x
			8.567	0.680	#10x
		C2b	3.197	0.491	#011
			7.053	0.637	#010
		C3b	115.249	3.913	#x01
			1.841	0.254	#x11
		Citrate	CIT	C1C5b	24.969
9.168	0.810				#11xxxx+#xxx11x
C2C4b	84.365			3.158	#010xxx+#xx010x
	6.361			0.664	#110xxx+#xx011x
C6b	31.554			1.600	#011xxx+#xx110x
	5.336			0.451	#xx1xx1
	12.811			0.695	#xx0xx1
no subCITb	24.969			1.363	#10xxxx+#xxx01x
	84.365			3.158	#010xxx+#xx010x
	23.394			1.198	#x010x0
GABA	GABA			C2b	3.607
		1.363	0.244		#011x
		C3b	8.470	0.676	#x010
			8.112	0.740	#x110+#x011
		C4b	12.89	0.924	#xx01
			4.631	0.566	#xx11
		nosubGAGAb	8.470	0.676	#x010
			12.89	0.924	#xx01
Glutamate/glutamine	GLU	C2b	21.534	1.197	#010xx
			2.980	0.435	#110xx
			8.595	0.805	#011xx
		C3b	15.976	0.985	#x010x
			15.074	1.027	#x110x+#x011x
		C4b	28.098	1.374	#xx010
			11.917	0.883	#xx110
		C1b	19.389	1.183	#10xxx
			8.218	0.791	#11xxx
		C2b	35.007	1.643	#010xx
			6.001	0.647	#110xx
			13.661	1.024	#011xx
		C3b	23.708	1.216	#x010x
			25.197	1.497	#x110x+#x011x
		C4b	35.829	1.702	#xx010
			14.460	1.143	#xx110
		Glycine	GLY	C1b	3.156
0.010	0.464				#11
Malate	OAA	C1b	11.138	0.626	#10xx

			4.523	0.411	#11xx
		C2b	33.471	1.601	#010x
			4.531	0.500	#110x
			12.555	0.934	#011x
		C3b	34.126	1.552	#x010
			12.311	0.863	#x110
			5.023	0.525	#x011
		C4b	17.683	1.040	#xx01
			6.768	0.634	#xx11
		NosubOAAb	33.471	1.601	#010x
			34.126	1.552	#x010
Serine	SER	C3b	22.156	1.132	#x01
			0.010	0.893	#x11
Succinate	SUCC	C1C4b	4.455	0.371	#10xx+#xx01
			1.257	0.221	#11xx+#xx11
Valine	VAL	C4b	1.304	0.250	#xx01x
			1.367	0.249	#xx0x1
Sucrose	GSUC	Cb	1.068	0.279	#x010xx
			10.203	0.908	#xxxx01
Sucrose	FSUC	C16b1	35.269	1.794	#10xxxx
			10.955	1.027	#xxxx01
			0.880	0.230	#xx010x
		C16b2	84.178	3.173	#10xxxx
			21.348	1.226	#xxxx01
		C16b3	27.030	1.419	#10xxxx
			6.855	0.924	#xxxx01
[1-¹³C]glucose: Replica 3					
Starch	STA	StaC	0.426	0.028	#10xxxx
			0.126	0.016	#xxxx01
Alanine	ALA	C1c	1.605	0.396	#11x
			12.499	0.944	#10x
		C2c	8.184	0.668	#010
			3.436	0.479	#011
			0.682	0.145	#110
		C3c	143.979	4.707	#x01
			2.566	0.431	#x11
Citrate	CIT	C1C5c	25.103	1.377	#10xxxx+#xxx01x
			9.697	0.850	#11xxxx+#xxx11x
		C2C4c	83.552	3.145	#010xxx+#xx010x
			6.272	0.648	#110xxx+#xx011x
			33.153	1.663	#011xxx+#xx110x
		C6c	8.377	0.679	#xx1xx1
			18.697	1.000	#xx0xx1
		nosubCITc	25.103	1.377	#10xxxx+#xxx01x
			83.552	3.145	#010xxx+#xx010x
			23.273	1.187	#x010x0
			18.697	1.000	#xx0xx1
GABA	GABA	C2c	15.447	0.871	#010x
			6.809	0.600	#011x
		C3c	9.350	0.712	#x010
			9.070	0.774	#x110+#x011
		C4c	13.933	0.974	#xx01
			5.425	0.664	#xx11
		nosubGABAc	9.350	0.712	#x010

			13.933	0.974	#xx01
Glutamate/glutamine	GLU	C2c	23.377	1.258	#010xx
			3.449	0.428	#110xx
			10.027	0.850	#011xx
		C3c	17.363	0.996	#x010x
			15.594	0.965	#x110x+#x011x
		C4c	31.002	1.473	#xx010
			13.672	0.951	#xx110
		C1c	29.441	1.501	#10xxx
			11.961	0.888	#11xxx
		C2c	55.010	2.261	#010xx
			9.559	0.826	#110xx
			21.721	1.344	#011xx
		C3c	40.968	1.873	#x010x
			35.833	1.751	#x110x+#x011x
Glycine	GLY	C1c	3.412	0.467	#10
			0.010	0.467	#11
Malate	OAA	C1c	13.516	0.796	#10xx
			6.316	0.593	#11xx
		C2c	19.097	0.960	#010x
			2.382	0.284	#110x
			7.484	0.580	#011x
		C3c	28.276	1.362	#x010
			10.101	0.734	#x110
			4.326	0.472	#x011
		C4c	14.856	0.932	#xx01
			6.281	0.661	#xx11
		NosubOAAc	13.516	0.796	#10xx
			28.276	1.362	#x010
Serine	SER	C3c	27.683	1.309	#x01
			0.010	0.862	#x11
Succinate	SUCC	C1C4c	2.978	0.369	#10xx+#xx01
			1.351	0.296	#11xx+#xx11
Valine	VAL	C4c	1.645	0.307	#xx01x
			1.627	0.274	#xx0x1
Sucrose	GSUC	Cc	0.517	0.139	#x010xx
			10.868	0.995	#xxxx01
Sucrose	FSUC	C16c1	37.759	1.932	#10xxxx
			11.102	1.044	#xxxx01
		C16c2	91.964	3.413	#10xxxx
			23.589	1.305	#xxxx01
		C16c3	29.165	1.500	#10xxxx
			7.481	0.953	#xxxx01
[2-¹³C]glucose: Replica 1					
Starch	STA_2	StaA_beta	0.0466	0.008	#10xxxx
			0.0626	0.008	#xxx010+#x010xx
			0.2086	0.016	#010xxx
		StaA_alpha	0.1726	0.017	#010xxx+#xxx010
			0.0353	0.008	#10xxxx
Alanine	ALA_2	C2d	140.469	4.708	#010
			3.997	0.468	#110
		C1d	5.437	0.628	#11x
			14.498	0.945	#10x
		C3d	22.549	1.225	#x01

		NosubALAd	1.922	0.693	#x11
			140.469	4.708	#010
			14.498	0.945	#10x
			22.549	1.225	#x01
Citrate	CIT_2	C1C5d	111.188	3.803	#10xxxx+#xxx01x
			2.988	0.410	#11xxxx+#xxx11x
		C2C4d	35.402	1.741	#010xxx+#xx010x
			2.443	0.435	#110xxx+#xx011x
		C3d	2.488	0.385	#011xxx+#xx110x
			23.002	1.204	#x010x0
			3.622	0.376	#x110x0+#x011x0
			1.468	0.197	#x010x1
		C6d	2.118	0.322	#xx1xx1
			34.567	1.567	#xx0xx1
		NoSubCITd	111.188	3.803	#10xxxx+#xxx01x
			35.402	1.741	#010xxx+#xx010x
			23.002	1.204	#x010x0
			35.567	1.567	#xx0xx1
GABA	GABA_2	C2d	3.923	0.420	#010x
			8.323	0.832	#xx01
		C3d	7.738	0.637	#x010
			1.030	0.259	#x110+#x011
Glutamate/glutamine	GLU_2	C2d	11.864	0.914	#010xx
			6.078	0.542	#xx010
		C3d	11.831	0.806	#x010x
			2.298	0.509	#x110x+#x011x
		C2d	23.393	1.414	#010xx
			1.648	0.393	#110xx
			0.928	0.239	#011xx
		C3d	23.566	1.428	#x010x
			3.970	0.768	#x110x+#x011x
		C4d	10.746	0.916	#xx010
			0.927	0.267	#xx110
			1.768	0.406	#xx110
		Cdglu	11.864	0.914	#010xx
			11.831	0.806	#x010x
		Cdglu	23.393	1.414	#010xx
			23.566	1.428	#x010x
			10.746	0.916	#xx010
Glycine	GLY_2	C2d	16.005	1.058	#01
			1.025	0.168	#11
		C1d	1.460	0.390	#10
			0.010	0.390	#11
Malate	OAA_2	C1d	32.977	1.487	#10xx
			1.218	0.313	#11xx
		C3d	19.395	1.069	#x010
			0.658	0.154	#x110
			0.760	0.163	#x011
		C4d	34.053	1.563	#xx01
			1.410	0.275	#xx11
		NosubMALd	32.977	1.487	#10xx
			19.395	1.069	#x010
			34.053	1.563	#xx01
Succinate	SUCC_2	C1C4d	10.361	0.646	#10xx+#xx01

			5.952	0.537	#01xx+#xx10
Sucrose	GSUC_2	Cd	10.100	0.773	#xxx010
			39.174	1.916	#010xxx
			1.629	0.330	#xxxx01
Sucrose	FSUC_2	Cd	1.695	0.317	#10xxxx
			24.227	1.137	#010xxx
			0.755	0.192	#110xxx+#011xxx
[2-¹³C]glucose: Replica 2					
Starch	STA_2	StaB_beta	0.059	0.010	#10xxxx
			0.102	0.014	#xxx010+#x010xx
			0.257	0.021	#010xxx
		StaB_alpha	0.223	0.021	#010xxx+#xxx010
			0.045	0.010	#10xxxx
Alanine	ALA_2	C2e	127.347	4.225	#010
			3.265	0.360	#110
		C3e	13.583	0.763	#x01
			1.41	0.304	#x11
		NosubALAE	127.347	4.225	#010
			12.726	0.920	#10x
Citrate	CIT_2	C1C5e	102.983	3.508	#10xxxx+#xxx01x
			4.118	1.850	#11xxxx+#xxx11x
		C2C4e	21.446	1.028	#010xxx+#xx010x
			1.410	0.225	#110xxx+#xx011x
			1.562	0.219	#011xxx+#xx110x
		C3e	21.193	1.120	#x010x0
			3.841	0.388	#x110x0+#x011x0
			1.985	0.294	#x010x1
		C6e	2.577	0.345	#xx1xx1
			33.313	1.505	#xx0xx1
		NoSubCITe	102.983	3.508	#10xxxx+#xxx01x
			21.193	1.120	#x010x0
			33.313	1.505	#xx0xx1
GABA	GABA_2	C3e	7.254	0.614	#x010
			1.005	0.263	#x110+#x011
Glutamate/glutamine	GLU_2	C4e	3.852	0.354	#xx010
			0.434	0.139	#xx110
			0.395	0.120	#xx011
		C2e	19.361	1.265	#010xx
			1.035	0.248	#110xx
			0.940	0.250	#011xx
		C4e	9.251	0.798	#xx010
			0.880	0.226	#xx110
			1.755	0.616	#xx110
		Ceglu	10.760	0.832	#010xx
			3.852	0.354	#xx010
		Cegln	19.361	1.265	#010xx
			9.251	0.798	#xx010
Glycine	GLY_2	C2e	10.758	0.769	#01
			0.745	0.250	#11
Malate	OAA_2	C1e	25.769	1.194	#10xx
			1.420	0.282	#11xx
		C3e	15.123	0.816	#x010
			0.706	0.136	#x110
			1.026	0.194	#x011

		C4e	26.275	1.247	#xx01
			0.964	0.182	#xx11
		NosubMALe	25.769	1.194	#10xx
			15.123	0.816	#x010
			26.275	1.247	#xx01
Succinate	SUCC_2	C1C4e	10.077	0.604	#10xx+#xx01
			3.719	0.324	#01xx+#xx10
Sucrose	GSUC_2	Ce	8.539	0.637	#xxx010
			35.811	1.726	#010xxx
			1.053	0.199	#xxxx01
Sucrose	FSUC_2	Ce	2.112	0.358	#10xxxx
			23.071	1.079	#010xxx
			1.243	0.287	#110xxx+#011xxx
[2-¹³C]glucose: Replica 3					
Starch	STA_2	StaC_beta	0.0749	0.014	#10xxxx
			0.0889	0.012	#xxx010+#x010xx
			0.2413	0.020	#010xxx
		StaC_alpha	0.2083	0.020	#010xxx+#xxx010
			0.0385	0.010	#10xxxx
Alanine	ALA_2	C2f	143.533	4.644	#010
			3.779	0.404	#110
		C1f	6.707	0.828	#11x
			15.231	0.970	#10x
		C3f	22.987	1.164	#x01
			1.981	0.312	#x11
		NosubALAf	143.533	4.644	#010
			15.231	0.970	#10x
			22.987	1.164	#x01
Citrate	CIT_2	C1C5f	70.310	2.385	#10xxxx+#xxx01x
			2.301	0.296	#11xxxx+#xxx11x
		C2C4f	31.715	1.508	#010xxx+#xx010x
			2.232	0.338	#110xxx+#xx011x
		C3f	21.302	1.099	#x010x0
			3.220	0.330	#x110x0+#x011x0
		C6f	2.304	0.353	#xx1xx1
			32.729	1.467	#xx0xx1
		NoSubCITf	31.715	1.508	#010xxx+#xx010x
			21.302	1.099	#x010x0
			32.729	1.467	#xx0xx1
GABA	GABA_2	C2f	3.569	0.350	#010x
			0.235	0.155	#011x
			7.012	0.679	#xx01
		C3f	6.914	0.564	#x010
			0.866	0.254	#x110+#x011
Glutamate/glutamine	GLU_2	C2f	11.458	0.820	#010xx
			0.767	0.213	#011xx
		C3f	12.111	0.810	#x010x
			1.610	0.325	#x110x+#x011x
		C4f	6.029	0.503	#xx010
			0.878	0.278	#xx110
			0.535	0.170	#xx011
		C2f	22.632	1.325	#010xx
			2.182	0.446	#110xx
			1.001	0.211	#011xx

		C3f	22.531	1.395	#x010x
			4.523	0.779	#x110x+#x011x
		C4f	10.988	0.886	#xx010
			2.555	1.105	#xx110
		Cfglu	11.458	0.820	#010xx
			12.111	0.810	#x010x
			6.029	0.503	#xx010
		Cfgln	22.632	1.325	#010xx
			22.531	1.395	#x010x
			10.988	0.886	#xx010
Glycine	GLY_2	C2f	14.448	0.894	#01
			0.896	0.234	#11
Malate	OAA_2	C1f	27.601	1.247	#10xx
			1.427	0.392	#11xx
		C3f	16.526	0.878	#x010
			1.353	0.260	#x110+#x011
		C4f	28.857	1.331	#xx01
			0.917	0.191	#xx11
		NosubMALf	27.601	1.247	#10xx
			20.523	1.128	#010x
			16.526	0.878	#x010
			28.857	1.331	#xx01
Succinate	SUCC_2	C1C4f	8.850	0.558	#10xx+#xx01
			4.551	0.413	#01xx+#xx10
Sucrose	GSUC_2	Cf	9.451	0.689	#xxx010
			37.034	1.730	#010xxx
			1.731	0.302	#xxxx01
Sucrose	FSUC_2	Cf	1.756	0.541	#10xxxx
			35.914	1.643	#010xxx
			0.986	0.238	#110xxx+#011xxx

Pi+ cultures					
Metabolite	Network metabolite	Carbon atom subgroups	Peak area	SD	Cumomer
[1- ¹³ C]glucose: Replica 1					
Alanine	ALA	C2	3.792	0.438	#010
			0.839	0.390	#011
		C1	0.905	0.467	#11x
			5.645	0.498	#10x
		C3	62.222	2.367	#x01
			0.814	0.310	#x11
Citrate	CIT	C1C5	17.498	1.042	#10xxxx+#xxx01x
			5.986	0.640	#11xxxx+#xxx11x
					#011xxx+#xx110x+#1
		C2C4	19.858	1.960	10xxx+#xx011x
			57.328	2.288	#010xxx+#xx010x
		C3	15.475	0.856	#x010x0
			12.280	0.820	#x110x0+#x011x0
		GABA	GABA	C3	4.597
2.918	0.367				#x110+#x011
C4	2.163			0.789	#xx11
	7.468			0.659	#xx01
Glutamate/glutamine	GLU	C5	4.981	0.507	#xxx11
			14.118	0.809	#xxx01
		C2	10.621	0.746	#010xx
			0.908	0.186	#110xx
			2.762	0.408	#011xx
		C3	7.247	0.591	#x010x
			5.546	0.560	#x110x+#x011x
			4.859	0.568	#xx110
		C4	14.034	0.858	#xx010
			7.881	0.623	#010xx
			0.760	0.167	#110xx
		C2	1.650	0.279	#011xx
			3.930	0.422	#x010x
			3.370	0.436	#x110x+#x011x
		C3	10.308	0.853	#xx010
			3.489	0.610	#xx110
Malate	OAA	C1	20.198	1.010	#10xx
			5.407	0.479	#11xx
		C2	37.156	1.727	#010x
			4.383	0.514	#110x
			10.768	0.854	#011x
		C3	39.842	1.702	#x010
			10.157	0.746	#x110
			5.018	0.500	#x011
		C4	6.825	0.602	#xx11
			22.237	1.134	#xx01
Valine	VAL	C45	2.709	0.397	#xx01x
			2.212	0.335	#xx0x1
Sucrose	FSUC	C16	32.583	1.683	#10xxxx
			5.200	0.634	#xxxx01
Starch	STA	StaA	0.160	0.015	#10xxxx
			0.057	0.012	#xxxx01

[1- ¹³ C]glucose: Replica 2					
Alanine	ALA	C2	5.654	0.852	#010
			1.884	1.026	#011
			8.305	0.736	#10x
		C23	85.549	3.436	#x01
			5.654	0.852	#010
Citrate	CIT	C24	22.427	2.193	#011xxx+#xx110x+#10xxx+#xx011x
			59.716	3.168	#010xxx+#xx010x
GABA	GABA	C3	6.812	0.768	#x010
			5.881	0.832	#x110+#x011
Glutamate/glutamine	GLU	C1	5.150	0.850	#11xxx
			9.374	0.773	#10xxx
		C2	13.918	1.064	#010xx
			2.039	0.711	#110xx
		C3	3.319	1.011	#011xx
			9.257	0.703	#x010x
		C1	6.835	0.622	#x110x+#x011x
			1.238	0.344	#11xxx
		C2	6.636	0.615	#10xxx
			12.798	1.074	#010xx
		C3	4.620	0.711	#110xx+#011xx
			8.746	0.775	#x010x
		C4	1.603	0.747	#x111x
			7.416	0.758	#x110x+#x011x
		C4	12.663	0.815	#xx010
			5.386	1.347	#xx110
Malate	OAA	C2	37.795	1.677	#010x
			4.105	0.412	#110x
			9.863	0.743	#011x
		C3	41.078	2.593	#x010
			10.843	0.839	#x110
			5.548	0.584	#x011
		C4	7.600	0.706	#xx11
			22.943	1.268	#xx01
Threonine	THR	C3	0.553	0.103	#x110
			1.494	0.172	#x010
			0.461	0.093	#x110
Valine	VAL	C25	3.348	0.392	#xx01x
			3.697	0.417	#xx0x1
Starch	STA	StaB	0.214	0.018	#10xxxx
			0.049	0.009	#xxxx01
[1- ¹³ C]glucose: Replica 3					
Alanine	ALA	C2	6.247	0.666	#010
			2.049	0.870	#011
		C1	0.646	0.388	#11x
			9.636	0.703	#10x
		C3	95.260	3.375	#x01
			1.345	0.435	#x11
Citrate	CIT	C15	19.656	1.154	#10xxxx+#xxx01x
			5.918	0.633	#11xxxx+#xxx11x
		C24	22.879	2.179	#011xxx+#xx110x+#10xxx+#xx011x
			61.125	3.287	#010xxx+#xx010x

		C3	16.738 13.406 1.364	2.017 1.268 0.307	#x010x0 #x110x0+#x011x0 #x010x1
GABA	GABA	C3	6.391 5.099	0.621 1.295	#x010 #x110+#x011
		C4	2.482 10.656	1.006 1.167	#xx11 #xx01
Glutamate/glutamine	GLU	C5	4.861 15.895	0.448 0.899	#xxx11 #xxx01
		C1	3.504 9.776	0.463 0.718	#11xxx #10xxx
		C2	16.612 1.975 5.217	1.052 0.386 0.608	#010xx #110xx #011xx
		C3	11.327 9.034	0.736 0.699	#x010x #x110x+#x011x
		C2	14.334 1.553 2.659	0.929 0.297 0.321	#010xx #110xx #011xx
		C3	9.794 0.858 7.469	0.734 0.195 0.680	#x010x #x111x #x110x+#x011x
Malate	OAA	C1	21.089 6.134	0.998 0.506	#10xx #11xx
		C2	41.942 5.134 11.911	1.716 0.471 0.772	#010x #110x #011x
		C3	45.207 11.798 6.011	1.803 0.765 0.519	#x010 #x110 #x011
Threonine	THR	C3	0.278 1.990 0.278	0.056 0.237 0.077	#x110 #x010 #x110
Valine	VAL	C45	3.981 4.292	0.400 0.435	#xx01x #xx0x1
Sucrose	FSUC	C16	81.044 15.856	3.166 1.146	#10xxxx #xxxx01
Starch	STA	StaC	0.207 0.076	0.018 0.013	#10xxxx #xxxx01
[2-¹³C]glucose: Replica 1					
Alanine	ALA_2	C2	69.139 3.549	2.665 0.493	#010 #011+#110
		C1	2.849 9.281	0.346 0.693	#11x #10x
		C3	14.167 1.050	0.900 0.232	#x01 #x11
Aspartate	ASP_2	C23	0.599 0.593	0.162 0.161	#010x #x010
Citrate	CIT_2	C15	61.736 1.994	2.410 0.350	#10xxxx+#xxx01x #11xxxx+#xxx11x
		C24	22.612 2.802	1.276 0.663	#010xxx+#xx010x #110xxx+#xx011x+#011xxx+#xx110x
		C3	15.494	0.948	#x010x0

			4.366	0.400	#x110x0+#x011x0+#x010x1
GABA	GABA_2	C24	1.343	0.215	#010x
			3.441	0.480	#xx01
		C34	4.423	0.499	#x010
			3.441	0.480	#xx01
			0.195	0.056	#x110+#x011
Glutamate/glutamine	GLU_2	C3	8.238	0.657	#x010x
			1.247	0.324	#x110x+#x011x
		C3	6.596	0.655	#x010x
			1.007	0.280	#x110x+#x011x
		C24	2.522	0.455	#xx010
			0.987	0.264	#xx110+#xx011
			5.554	0.632	#010xx
Malate	OAA_2	C1	31.838	1.483	#10xx
			1.318	0.497	#11xx
		C2	19.330	1.009	#010x
			1.176	0.229	#110x
			1.196	0.191	#011x
		C3	15.398	0.801	#x010
			2.469	0.563	#x110
			1.184	0.214	#x011
		C4	33.263	1.566	#xx01
			1.798	0.306	#xx11
Succinate	SUCC_2	C14	75.779	3.481	#10xx+#xx01
			2.505	0.636	#11xx+#xx11
Sucrose	FSUC_2	C25	8.619	0.808	#xxx010
			42.370	1.932	#010xxx
			1.480	0.382	#110xxx+#011xxx
	GSUC_2	C25	46.843	2.213	#010xxx
			8.126	0.654	#xxx010
Starch	STA_2	StaA_beta	0.032	0.008	#10xxxx
			0.038	0.009	#xxx010+#x010xx
			0.075	0.009	#010xxx
		StaA_alpha	0.070	0.010	#010xxx+#xxx010
			0.013	0.004	#10xxxx
[2-¹³C]glucose: Replica 2					
Alanine	ALA_2	C2	46.567	2.063	#010
			1.527	0.463	#011+#110
		C1	7.773	0.814	#10x
			2.528	1.228	#11x
		C3	9.690	0.863	#x01
			1.166	0.325	#x11
Citrate	CIT_2	C15	95.569	3.545	#10xxxx+#xxx01x
			4.123	1.400	#11xxxx+#xxx11x
		C24	23.313	1.218	#010xxx+#xx010x
			2.815	0.500	#110xxx+#xx011x
			2.668	0.386	#011xxx+#xx110x
		C3	16.556	0.978	#x010x0
			5.080	0.529	#x110x0+#x011x0+#x010x1
		C6	3.674	1.246	#xx1xx1
			30.064	1.554	#xx0xx1
GABA	GABA_2	C24	1.544	0.276	#010x

		C3	3.854	0.572	#xx01
			3.626	0.473	#x010
			0.626	0.293	#x110+#x011
Glutamate/glutamine	GLU_2	C4	3.881	0.487	#xx010
			0.718	0.280	#xx110
			0.315	0.199	#xx011
		C14	3.289	0.536	#10xxx
			1.148	0.333	#xx010
Malate	OAA_2	C1	41.428	1.848	#10xx
			1.544	0.548	#11xx
		C23	40.293	1.895	#010x
			30.731	1.490	#x010
		C4	44.138	2.022	#xx01
			3.064	0.639	#xx11
Succinate	SUCC_2	C14	85.218	3.067	#10xx+#xx01
			3.986	0.544	#11xx+#xx11
Sucrose	FSUC_2	C25	20.191	1.130	#010xxx
			6.687	0.939	#xxx010
Sucrose	GSUC_2	C25	21.805	1.268	#010xxx
			4.436	0.605	#xxx010
Starch	STA_2	StaB_beta	0.032	0.008	#xxx010+#x010xx
			0.046	0.007	#010xxx
[2-¹³C]glucose: Replica 3					
Alanine	ALA_2	C2	75.978	2.829	#010
			2.986	0.345	#011+#110
		C1	30.295	2.582	#10x
			4.791	1.100	#11x
		C3	19.439	1.129	#x01
			2.251	0.675	#x11
Citrate	CIT_2	C15	3.542	1.118	#11xxxx+#xxx11x
			55.297	2.197	#10xxxx+#xxx01x
		C24	20.328	1.149	#010xxx+#xx010x
			2.443	0.534	#110xxx+#xx011x+#011xxx+#xx110x
		C3	15.281	0.956	#x010x0
			6.098	1.095	#x110x0+#x011x0+#x010x1
GABA	GABA_2	C24	2.399	0.294	#010x
			5.67	0.687	#xx01
		C3	5.575	0.586	#x010
			0.797	0.205	#x110+#x011
Glutamate/glutamine	GLU_2	C3	12.304	0.831	#x010x
			1.694	0.459	#x110x+#x011x
		C4	11.842	0.957	#xx010
			2.330	0.480	#xx011+#xx110
Malate	OAA_2	C1	43.050	1.763	#10xx
			3.058	0.729	#11xx
		C2	39.331	1.712	#010x
			5.134	0.629	#110x+#011x
		C3	31.542	1.384	#x010
			3.582	0.392	#x110+#x011
		C4	45.525	1.906	#xx01
			3.277	0.824	#xx11
Succinate	SUCC_2	C14	36.584	1.493	#10xx+#xx01

			1.620	0.309	#11xx+#xx11
Sucrose	FSUC_2	C25	17.336	1.692	#xxx010
			113.666	4.054	#010xxx
	GSUC_2	C25	111.540	4.091	#010xxx
			15.221	0.882	#xxx010
Starch	STA_2	StaC_beta	0.072	0.011	#10xxxx
			0.089	0.011	#xxx010+#x010xx
			0.268	0.019	#010xxx
			0.037	0.010	#xxxx01
	STA_2	StaC_alpha	0.238	0.020	#010xxx+#xxx010
			0.041	0.008	#10xxxx

Table S7. Mass isotopomer abundance of metabolites derived from Arabidopsis cultures in Pi-, MS and Pi+ media containing [¹³C]glucose

Cultures were grown in either 99% [1-¹³C]glucose, 99% [2-¹³C]glucose or 20% [¹³C₆]glucose and the relative mass isotopomer abundance of metabolites was determined by GC-MS. Triplicate cultures were analysed for each labelled substrate. For flux analysis these values were corrected for any pre-existing pools of unlabelled metabolites using a scaling adjustment as described in Masakapalli *et al.* (2013) and assigned the SD values indicated in Data S1.

Pi- cultures												
Metabolite	Network Metabolite	Carbon Atoms	Mass (m+)	[1- ¹³ C]glucose			[2- ¹³ C]glucose			[¹³ C ₆]glucose		
				Replica 1	Replica 2	Replica 3	Replica 1	Replica 2	Replica 3	Replica 1	Replica 2	Replica 3
Alanine (soluble)	ALA	1-3	0	0.568	0.567	0.582	0.535	0.545	0.542	0.734	0.720	0.717
			1	0.411	0.407	0.400	0.437	0.419	0.422	0.082	0.097	0.100
			2	0.021	0.025	0.023	0.028	0.036	0.035	0.046	0.054	0.054
			3	0	0	-0.004	0	0	0	0.139	0.128	0.129
		2-3	0	0.589	0.590	0.598	0.560	0.572	0.565	0.780	0.774	0.772
			1	0.406	0.403	0.394	0.435	0.422	0.43	0.044	0.054	0.056
			2	0.005	0.007	0.008	0.005	0.005	0.006	0.176	0.172	0.173
			3	0.001	0.001	0.001	0.001	0.001	0.001	0.118	0.111	0.112
Glycine (soluble)	GLY	1-2	0	0.936	0.937	0.941	0.637	0.652	0.648	0.777	0.773	0.772
			1	0.063	0.064	0.061	0.345	0.328	0.331	0.105	0.116	0.116
			2	0.001	-0.001	-0.002	0.017	0.02	0.021	0.118	0.111	0.112
			3	0.972	0.972	0.973	0.675	0.692	0.685	0.829	0.829	0.828
		2	0	0.972	0.972	0.973	0.675	0.692	0.685	0.829	0.829	0.828
			1	0.028	0.028	0.027	0.325	0.308	0.315	0.171	0.171	0.172
			2	0.028	0.028	0.027	0.325	0.308	0.315	0.171	0.171	0.172
			3	0.028	0.028	0.027	0.325	0.308	0.315	0.171	0.171	0.172
Serine (soluble)	SER	1-3	0	0.647	0.658	0.668	0.583	0.587	0.584	0.658	0.651	0.648
			1	0.337	0.325	0.317	0.375	0.367	0.369	0.200	0.211	0.211
			2	0.017	0.016	0.016	0.042	0.046	0.047	0.104	0.103	0.105
			3	-0.001	0	-0.001	0.001	0	0.001	0.038	0.036	0.036
		2-3	0	0.670	0.680	0.690	0.615	0.620	0.619	0.704	0.697	0.697
			1	0.325	0.315	0.306	0.363	0.355	0.358	0.245	0.253	0.251
			2	0.005	0.005	0.003	0.022	0.025	0.023	0.052	0.050	0.052
			3	0.005	0.005	0.003	0.022	0.025	0.023	0.052	0.050	0.052
		2-3	0	0.669	0.681	0.692	0.616	0.623	0.620	0.703	0.699	0.699
			1	0.324	0.314	0.300	0.360	0.353	0.355	0.243	0.252	0.250
			2	0.324	0.314	0.300	0.360	0.353	0.355	0.243	0.252	0.250
			3	0.324	0.314	0.300	0.360	0.353	0.355	0.243	0.252	0.250

GABA	GABA	1-4	2	0.007	0.005	0.007	0.024	0.024	0.025	0.053	0.049	0.051
			0	0.236	0.256	0.270	0.470	0.493	0.451	0.526	0.531	0.536
			1	0.415	0.432	0.424	0.429	0.42	0.398	0.250	0.256	0.257
			2	0.284	0.259	0.259	0.090	0.079	0.125	0.166	0.159	0.155
			3	0.063	0.053	0.051	0.012	0.008	0.025	0.050	0.047	0.045
Fructose	F6P	4-6	4	0.001	0	-0.002	0	0.001	0.001	0.008	0.007	0.007
			0	0.767	0.779	0.792	0.750	0.771	0.759	0.763	0.757	0.756
			1	0.233	0.224	0.210	0.246	0.225	0.237	0.051	0.054	0.054
			2	0.007	0.003	0.005	0.011	0.011	0.012	0.027	0.026	0.025
			3	-0.007	-0.006	-0.007	-0.007	-0.007	-0.007	0.159	0.163	0.165
		1-4	0	0.306	0.289	0.275	0.247	0.220	0.238	0.653	0.658	0.670
			1	0.658	0.687	0.693	0.705	0.723	0.715	0.144	0.143	0.133
			2	0.039	0.032	0.043	0.049	0.061	0.048	0.043	0.043	0.043
			3	0.001	-0.006	-0.010	0	0	0.001	0.077	0.058	0.055
			4	-0.004	-0.003	-0.002	-0.002	-0.004	-0.002	0.083	0.097	0.099
Starch	STA	3-6	0	0.775	0.762	0.758		0.688	0.697		0.670	0.659
			1	0.219	0.231	0.234		0.275	0.270		0.140	0.141
			2	0.012	0.013	0.015		0.041	0.038		0.029	0.029
			3	-0.003	-0.003	-0.004		0	-0.001		0.072	0.074
			4	-0.004	-0.004	-0.004		-0.003	-0.004		0.089	0.096
		3-6	0	0.768	0.755	0.757		0.690	0.692		0.667	0.659
			1	0.221	0.235	0.231		0.269	0.271		0.140	0.142
			2	0.015	0.015	0.016		0.044	0.040		0.031	0.032
			3	-0.001	-0.002	-0.001		0	0		0.073	0.072
			4	-0.003	-0.003	-0.003		-0.003	-0.003		0.088	0.095
	OAA	1-4	0	0.321	0.336	0.351	0.440	0.460	0.458	0.549	0.553	0.551
			1	0.433	0.434	0.435	0.434	0.439	0.441	0.237	0.230	0.234
			2	0.209	0.197	0.186	0.099	0.096	0.096	0.146	0.144	0.145
			3	0.037	0.033	0.029	0.022	0.004	0.004	0.056	0.060	0.058
			4	0.001	0.001	0	0.004	0	0	0.011	0.014	0.012
Citrate	CIT	1-6	0	0.202	0.211	0.211		0.292	0.290	0.424	0.430	0.427
			1	0.371	0.379	0.390		0.438	0.438	0.228	0.222	0.225
			2	0.294	0.286	0.285		0.226	0.228	0.213	0.210	0.211
			3	0.115	0.106	0.100		0.041	0.041	0.090	0.092	0.091
			4	0.018	0.018	0.014		0.004	0.002	0.033	0.034	0.034

Cell Wall	G6P	3-6	5	0	0	0		0	0	0.010	0.009	0.010
			6	0	0	0		0	0	0.001	0.002	0.002
			0	0.769	0.774	0.788	0.736	0.755	0.773	0.680	0.688	0.674
			1	0.238	0.230	0.213	0.257	0.239	0.218	0.125	0.116	0.129
			2	0.007	0.008	0.009	0.019	0.020	0.021	0.016	0.02	0.027
			3	0.01	0.005	0.004	0.005	0.006	0.006	0.074	0.062	0.063
			4	0.01	0.006	0.007	0.008	0.007	0.006	0.105	0.114	0.106
	G6P	3-6	0							0.667	0.674	
			1							0.136	0.129	
			2							0.023	0.027	
			3							0.077	0.064	
			4							0.096	0.106	
Alanine	ALA	1-3	0	0.578	0.578	0.581	0.532	0.532	0.534	0.739	0.719	0.715
			1	0.401	0.399	0.395	0.438	0.433	0.430	0.079	0.099	0.103
			2	0.020	0.023	0.023	0.030	0.035	0.035	0.044	0.055	0.058
			3	0	0.001	0.001	0.001	0	0	0.138	0.127	0.124
		2-3	0	0.594	0.596	0.603	0.552	0.554	0.556	0.782	0.773	0.773
			1	0.401	0.398	0.392	0.443	0.440	0.437	0.044	0.054	0.057
			2	0.005	0.005	0.005	0.006	0.006	0.006	0.173	0.172	0.170
	GLYeff	1-2	0	0.950	0.948	0.948	0.729	0.732	0.733	0.831	0.825	0.825
			1	0.049	0.051	0.052	0.260	0.254	0.254	0.079	0.090	0.090
			2	0.001	0.001	0	0.011	0.014	0.013	0.090	0.085	0.085
		2	0	0.977	0.977	0.977	0.762	0.766	0.768	0.871	0.870	0.870
			1	0.023	0.023	0.023	0.238	0.234	0.232	0.129	0.130	0.130
Valine	VAL	1-5	0	0.350	0.357	0.356	0.292	0.283	0.297	0.569	0.566	0.553
			1	0.471	0.468	0.471	0.490	0.497	0.494	0.098	0.108	0.114
			2	0.167	0.167	0.161	0.202	0.207	0.201	0.170	0.175	0.173
			3	0.012	0.008	0.011	0.016	0.014	0.013	0.129	0.118	0.121
			4	0	-0.001	0.001	0	0	-0.002	0.013	0.013	0.017
		2-5	5	0	0	0	0	-0.001	-0.003	0.023	0.020	0.021
			0	0.358	0.366	0.361	0.299	0.292	0.303	0.601	0.598	0.596
			1	0.478	0.476	0.482	0.509	0.518	0.509	0.079	0.089	0.090
			2	0.158	0.153	0.151	0.191	0.185	0.184	0.275	0.268	0.269
			3	0.006	0.006	0.006	0.002	0.005	0.004	0.015	0.018	0.020
			4	0	0	0	0	0	0	0.029	0.026	0.025

Proline	GLU	2-5	0	0.295	0.289	0.291	0.468	0.444	0.451	0.545	0.533	0.529
			1	0.441	0.449	0.457	0.450	0.464	0.455	0.242	0.247	0.246
			2	0.224	0.222	0.215	0.080	0.091	0.089	0.161	0.169	0.172
			3	0.041	0.040	0.036	0.003	0.002	0.005	0.043	0.044	0.044
			4	0	0.001	0	0	-0.001	0	0.008	0.008	0.009
		2-5	0	0.291	0.281	0.280	0.465	0.439	0.447	0.546	0.531	0.528
			1	0.446	0.456	0.466	0.454	0.468	0.462	0.238	0.244	0.244
			2	0.226	0.226	0.222	0.082	0.091	0.091	0.166	0.174	0.178
			3	0.039	0.038	0.035	0.001	0.003	0.003	0.044	0.043	0.043
			4	-0.002	-0.001	-0.002	-0.002	-0.002	-0.002	0.007	0.007	0.007
Methionine	METeff	1-5	0	0.574	0.581	0.581	0.686	0.673	0.679	0.684	0.684	0.688
			1	0.273	0.272	0.274	0.261	0.267	0.262	0.193	0.192	0.188
			2	0.118	0.115	0.114	0.049	0.056	0.054	0.080	0.079	0.078
			3	0.030	0.028	0.026	0.003	0.003	0.004	0.034	0.033	0.033
			4	0.002	0.002	0.002	0	-0.001	0	0.008	0.008	0.008
		2-5	5	0.002	0.002	0.002	0.002	0.002	0.001	0.002	0.003	0.005
			0	0.607	0.615	0.615	0.767	0.753	0.755	0.715	0.716	0.721
			1	0.273	0.271	0.274	0.208	0.216	0.216	0.197	0.195	0.193
			2	0.099	0.095	0.092	0.023	0.027	0.027	0.065	0.064	0.063
			3	0.018	0.017	0.016	0	0.001	0.001	0.019	0.020	0.020
		2-5	4	0.003	0.003	0.003	0.002	0.003	0.002	0.004	0.004	0.004
			0	0.610	0.616	0.618	0.764	0.754	0.755	0.717	0.718	0.723
			1	0.273	0.270	0.272	0.209	0.218	0.215	0.197	0.196	0.192
			2	0.099	0.095	0.093	0.026	0.028	0.029	0.065	0.065	0.064
			3	0.018	0.017	0.016	0.001	0.001	0.002	0.019	0.020	0.020
Serine	SEReff	1-3	4	0	0.001	0	0	-0.001	0	0.001	0.002	0.002
			0	0.723	0.728	0.732	0.675	0.673	0.676	0.733	0.728	0.726
			1	0.266	0.260	0.257	0.299	0.297	0.294	0.156	0.166	0.167
			2	0.011	0.011	0.011	0.026	0.030	0.030	0.078	0.077	0.077
			3	0	0	0	0	0	0	0.033	0.029	0.029
		2-3	0	0.742	0.747	0.753	0.701	0.705	0.705	0.768	0.765	0.765
			1	0.255	0.250	0.245	0.286	0.282	0.281	0.190	0.195	0.195
			2	0.003	0.003	0.003	0.013	0.014	0.014	0.042	0.040	0.039
		2-3	0	0.741	0.746	0.753	0.703	0.705	0.706	0.768	0.766	0.767
			1	0.255	0.250	0.243	0.282	0.280	0.279	0.190	0.194	0.193

Threonine	THR	1-4	2	0.004	0.005	0.004	0.014	0.015	0.015	0.043	0.040	0.040
			0	0.322	0.329	0.345	0.461	0.457	0.467	0.538	0.549	0.557
			1	0.445	0.445	0.451	0.458	0.457	0.451	0.243	0.238	0.229
			2	0.203	0.197	0.182	0.081	0.086	0.083	0.153	0.148	0.149
			3	0.032	0.031	0.027	-0.001	0.002	0.002	0.056	0.054	0.056
		2-4	4	-0.002	-0.002	-0.005	0.001	-0.002	-0.003	0.010	0.012	0.009
			0	0.391	0.402	0.413	0.623	0.603	0.614	0.598	0.615	0.621
			1	0.446	0.441	0.439	0.347	0.364	0.353	0.257	0.245	0.238
			2	0.148	0.146	0.134	0.031	0.032	0.033	0.119	0.111	0.113
			3	0.015	0.011	0.013	0	0	0	0.027	0.028	0.028
Phenylalanine	PHE_TYR	1-9	0	0.295	0.292	0.271	0.186	0.152	0.158	0.410	0.366	0.354
			1	0.396	0.401	0.415	0.375	0.389	0.386	0.139	0.153	0.154
			2	0.240	0.238	0.244	0.303	0.315	0.312	0.137	0.152	0.156
			3	0.062	0.062	0.062	0.113	0.118	0.118	0.162	0.166	0.167
			4	0.006	0.007	0.007	0.020	0.023	0.023	0.074	0.082	0.084
			5	0.001	0.001	0.001	0.002	0.003	0.003	0.040	0.041	0.043
			6	0	0	0	0.001	0.001	0	0.024	0.025	0.026
			7	0	0	0	0	-0.001	-0.001	0.009	0.010	0.010
			8	0	0	0	0	0	0	0.003	0.003	0.003
			9	0	0	0	0	0	0	0.001	0.001	0.002
		2-9	0	0.300	0.298	0.275	0.192	0.155	0.164	0.423	0.388	0.379
			1	0.403	0.407	0.426	0.388	0.407	0.406	0.137	0.145	0.147
			2	0.234	0.234	0.236	0.300	0.311	0.307	0.202	0.217	0.218
			3	0.056	0.055	0.057	0.104	0.107	0.105	0.111	0.114	0.116
			4	0.005	0.005	0.005	0.015	0.017	0.017	0.071	0.078	0.080
			5	0	0	0	0.001	0.002	0.002	0.033	0.034	0.034
			6	0	0	0.001	0	0	0	0.017	0.019	0.020
			7	0	0	0	-0.001	0	0	0.004	0.004	0.003
			8	0	0	0	0	0	0	0.002	0.002	0.003
			9									
		2-9	0			0.278	0.191			0.425	0.387	0.380
			1			0.418	0.387			0.134	0.144	0.144
			2			0.239	0.3			0.204	0.217	0.221
			3			0.058	0.104			0.112	0.116	0.116
			4			0.006	0.017			0.070	0.077	0.080
			5			0.001	0.001			0.033	0.034	0.034

Aspartate	ASP	1-2	6			0	0			0.017	0.019	0.019			
			7			0	0			0.003	0.004	0.004			
			8			0	0			0.002	0.002	0.002			
		0	0.961	0.957	0.954	0.586	0.576	0.580	0.771	0.747	0.739				
		1	0.040	0.043	0.049	0.397	0.404	0.400	0.091	0.117	0.123				
		2	-0.002	0	-0.002	0.017	0.020	0.021	0.137	0.137	0.138				
		1-4	0	0.300	0.301	0.312	0.467	0.462	0.464	0.544	0.542	0.544			
			1	0.442	0.448	0.449	0.453	0.452	0.450	0.242	0.244	0.243			
			2	0.217	0.212	0.205	0.077	0.083	0.082	0.149	0.150	0.148			
			3	0.041	0.039	0.035	0.003	0.004	0.004	0.056	0.054	0.055			
			4	0.001	0	0	0	0	0	0.010	0.009	0.010			
			2-4	0	0.367	0.369	0.378	0.629	0.617	0.618	0.606	0.605	0.609		
		1		0.449	0.451	0.451	0.341	0.348	0.348	0.254	0.255	0.252			
		2		0.165	0.162	0.155	0.030	0.034	0.033	0.115	0.114	0.112			
			3	0.019	0.018	0.016	0	0	0.001	0.025	0.025	0.027			
			2-4	0	0.386	0.387	0.398	0.637	0.624	0.626	0.615	0.615	0.617		
				1	0.432	0.434	0.433	0.325	0.334	0.332	0.243	0.242	0.241		
		2		0.158	0.154	0.147	0.030	0.034	0.034	0.110	0.111	0.110			
		Glutamate	GLU		3	0.024	0.024	0.022	0.008	0.008	0.008	0.031	0.032	0.032	
					1-5	0	0.226	0.229	0.236	0.356	0.353	0.355	0.480	0.478	0.480
						1	0.418	0.420	0.429	0.469	0.470	0.466	0.225	0.229	0.228
				2		0.269	0.267	0.258	0.160	0.161	0.163	0.204	0.204	0.203	
					3	0.078	0.076	0.069	0.015	0.016	0.016	0.067	0.066	0.067	
					4	0.009	0.008	0.007	0	0.001	0	0.020	0.019	0.019	
5	0				0	0	0	0	0	0.004	0.004	0.004			
2-5	0			0.276	0.279	0.286	0.466	0.464	0.462	0.536	0.533	0.535			
	1			0.443	0.445	0.450	0.452	0.451	0.451	0.247	0.248	0.246			
	2			0.234	0.234	0.225	0.079	0.082	0.085	0.161	0.164	0.168			
	3			0.046	0.043	0.039	0.002	0.003	0.003	0.049	0.045	0.046			
	4			0.001	-0.001	-0.001	0	-0.001	-0.001	0.007	0.009	0.006			
	2-5			0	0.274	0.277	0.287	0.466	0.461	0.464	0.537	0.534	0.536		
1				0.443	0.447	0.451	0.453	0.451	0.448	0.244	0.246	0.244			
2				0.237	0.233	0.223	0.078	0.085	0.084	0.165	0.167	0.168			
	3			0.046	0.043	0.039	0.003	0.003	0.004	0.047	0.045	0.044			
	4			0.001	0	0	0	0	0	0.008	0.008	0.008			

Lysine	LYS	1-6	0	0.213	0.230		0.299	0.288	0.306	0.413	0.436	0.452
			1	0.409	0.410		0.474	0.476	0.467	0.224	0.219	0.215
			2	0.276	0.270		0.208	0.212	0.199	0.190	0.186	0.180
			3	0.093	0.084		0.025	0.028	0.030	0.121	0.114	0.107
			4	0.011	0.009		0.001	0.005	-0.001	0.038	0.034	0.038
			5	-0.002	0.008		-0.003	-0.005	-0.002	0.013	0.011	0.006
			6	0	-0.011		-0.003	-0.004	0.002	0	-0.001	0.002
Histidine	HISeff	1-6	0	0.649	0.654	0.651	0.603	0.587	0.595	0.725	0.725	0.723
			1	0.231	0.227	0.232	0.264	0.267	0.263	0.123	0.126	0.128
			2	0.100	0.100	0.098	0.120	0.126	0.121	0.068	0.068	0.067
			3	0.021	0.018	0.017	0.014	0.020	0.019	0.056	0.052	0.054
			4	0	0.001	0.001	0.001	0	0	0.015	0.016	0.016
			5	0	0	0	0	0	0.001	0.011	0.011	0.011
			6	0	0	0	-0.002	0.001	0	0.002	0.002	0.002
		2-6	0	0.713	0.714	0.714	0.607	0.595	0.602	0.724	0.723	0.724
			1	0.219	0.219	0.223	0.259	0.267	0.264	0.127	0.133	0.131
			2	0.054	0.054	0.049	0.110	0.115	0.107	0.098	0.095	0.096
			3	0.011	0.010	0.011	0.019	0.019	0.022	0.034	0.032	0.033
			4	0.002	0.002	0.003	0.004	0.003	0.003	0.014	0.014	0.013
			5	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.003	0.003
			6	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.003	0.003
		1-2	0	0.833	0.832	0.834	0.806	0.806	0.809	0.888	0.884	0.887
			1	0.167	0.167	0.165	0.194	0.190	0.189	0.031	0.037	0.038
			2	0	0.001	0.001	0	0.004	0.003	0.081	0.079	0.075
Tyrosine	PHE_TYR	2-9	0	0.252	0.273	0.280				0.371	0.390	0.392
			1	0.432	0.429	0.433				0.139	0.141	0.139
			2	0.262	0.256	0.249				0.232	0.228	0.225
			3	0.063	0.061	0.057				0.127	0.117	0.118
			4	0.005	0.004	0.003				0.079	0.079	0.078
			5	-0.002	-0.003	-0.003				0.034	0.032	0.033
			6	-0.004	-0.008	-0.005				0.017	0.015	0.017
			7	-0.004	-0.005	-0.007				0	0.001	0.001
			8	-0.005	-0.006	-0.007				-0.001	-0.003	-0.002
			9	0.001	0.001	0.001				0.001	0.001	0.001
			10	0.001	0.001	0.001				0.001	0.001	0.001
Arginine	ARGeff	1-6	0	0.616	0.624	0.622	0.660	0.651	0.662	0.694	0.701	0.709
			1	0.222	0.219	0.227	0.238	0.244	0.240	0.156	0.158	0.155
			2	0.116	0.115	0.115	0.091	0.090	0.087	0.101	0.090	0.090

		3	0.040	0.039	0.034	0.013	0.019	0.018	0.037	0.039	0.037
		4	0.009	0.006	0.006	0.002	0.004	0.002	0.014	0.015	0.013
		5	0	0.001	-0.002	-0.002	-0.010	-0.009	0.003	0.003	0.001
		6	-0.004	-0.004	-0.003	-0.001	0.001	0.001	-0.005	-0.005	-0.005
	2-6	0	0.627	0.640	0.64	0.684	0.676	0.688	0.698	0.707	0.708
		1	0.213	0.214	0.218	0.230	0.229	0.229	0.162	0.158	0.157
		2	0.112	0.105	0.101	0.064	0.065	0.064	0.088	0.084	0.085
		3	0.036	0.031	0.031	0.012	0.017	0.010	0.034	0.035	0.031
		4	0.006	0.005	0.005	0.005	0.005	0.004	0.010	0.009	0.012
		5	0.006	0.004	0.005	0.006	0.007	0.005	0.007	0.006	0.006

MS cultures												
Metabolite	Network Metabolite	Carbon Atoms	Mass (m+)	[1- ¹³ C]glucose			[2- ¹³ C]glucose			[¹³ C ₆]glucose		
				Replica 1	Replica 2	Replica 3	Replica 1	Replica 2	Replica 3	Replica 1	Replica 2	Replica 3
Alanine (soluble)	ALA	1-3	0	0.593	0.590	0.588	0.539	0.541	0.538	0.744	0.751	0.743
			1	0.387	0.391	0.391	0.429	0.428	0.431	0.072	0.068	0.070
			2	0.020	0.018	0.019	0.031	0.031	0.031	0.036	0.034	0.034
		2-3	3	0.001	0.001	0.001	0	0	0	0.149	0.147	0.153
			0	0.610	0.606	0.606	0.565	0.568	0.565	0.776	0.783	0.776
			1	0.382	0.386	0.386	0.431	0.428	0.430	0.052	0.047	0.051
Glycine (soluble)	GLY	1-2	2	0.008	0.008	0.008	0.004	0.004	0.004	0.172	0.169	0.174
			0	0.943	0.942	0.946	0.627	0.627	0.630	0.766	0.773	0.767
			1	0.055	0.059	0.055	0.358	0.358	0.354	0.103	0.099	0.103
		2	2	0.002	-0.001	-0.001	0.015	0.016	0.016	0.131	0.128	0.130
			0	0.981	0.980	0.979	0.678	0.677	0.684	0.817	0.817	0.818
			1	0.019	0.020	0.021	0.322	0.323	0.316	0.183	0.183	0.182
Serine (soluble)	SER	1-3	0	0.667	0.655	0.660	0.552	0.556	0.553	0.664	0.669	0.662
			1	0.324	0.331	0.328	0.400	0.396	0.398	0.176	0.171	0.178
			2	0.010	0.014	0.013	0.047	0.048	0.048	0.098	0.095	0.098
		2-3	3	-0.001	-0.001	-0.001	0.001	0.001	0.001	0.062	0.065	0.062
			0	0.693	0.679	0.681	0.593	0.593	0.590	0.701	0.706	0.701

GABA	GABA	2-3	1	0.304	0.319	0.317	0.382	0.382	0.386	0.225	0.216	0.225	
			2	0.003	0.002	0.002	0.025	0.025	0.023	0.075	0.079	0.074	
			0	0.689	0.679	0.680	0.592	0.595	0.592	0.702	0.708	0.702	
		1-4	1	0.308	0.318	0.316	0.382	0.379	0.383	0.224	0.214	0.224	
			2	0.003	0.003	0.004	0.026	0.025	0.025	0.073	0.078	0.074	
			0	0.299	0.290	0.300	0.429	0.419	0.435	0.521	0.535	0.536	
			1	0.443	0.452	0.442	0.447	0.454	0.456	0.245	0.232	0.233	
			2	0.224	0.222	0.219	0.115	0.115	0.107	0.173	0.178	0.174	
			3	0.038	0.033	0.039	0.008	0.012	0.004	0.050	0.044	0.048	
			4	-0.004	0.002	-0.001	0	0.001	-0.001	0.010	0.011	0.009	
		1-4	0	0.305	0.297	0.305	0.435	0.430	0.436	0.535	0.534	0.537	
			1	0.440	0.443	0.437	0.449	0.449	0.448	0.234	0.233	0.233	
			2	0.216	0.222	0.220	0.109	0.113	0.111	0.174	0.178	0.174	
			3	0.037	0.037	0.038	0.006	0.008	0.006	0.047	0.045	0.046	
4	0.001		0	0	0	0	0	0.010	0.011	0.010			
Fructose	F6P		4-6	0	0.830	0.813	0.812	0.785	0.788	0.788	0.780	0.775	0.776
				1	0.179	0.194	0.196	0.215	0.212	0.211	0.036	0.036	0.035
		2		-0.002	0	-0.001	0.007	0.007	0.008	0.011	0.011	0.011	
		3		-0.007	-0.007	-0.006	-0.008	-0.007	-0.007	0.173	0.178	0.178	
		1-4		0	0.273	0.258	0.258	0.207	0.202	0.198	0.689	0.701	0.701
				1	0.703	0.719	0.714	0.755	0.755	0.766	0.119	0.105	0.109
				2	0.027	0.027	0.032	0.044	0.045	0.041	0.019	0.019	0.020
			3	0	-0.003	-0.002	-0.003	0.001	-0.001	0.058	0.061	0.056	
		4-6	4	-0.003	-0.001	-0.001	-0.004	-0.003	-0.004	0.115	0.115	0.113	
			0	0.832	0.817	0.813	0.786	0.788	0.787	0.776	0.776	0.776	
			1	0.181	0.194	0.195	0.215	0.213	0.214	0.037	0.037	0.038	
			2	-0.004	-0.004	0	0.009	0.007	0.007	0.013	0.010	0.010	
			3	-0.009	-0.008	-0.008	-0.009	-0.008	-0.008	0.174	0.178	0.177	
			Succinate	SUCC		0	0.324	0.318	0.315	0.439	0.439	0.437	0.540
1-4	1			0.429	0.439	0.434	0.448	0.448	0.451	0.233	0.227	0.233	
	2	0.209		0.209	0.213	0.107	0.108	0.108	0.171	0.173	0.174		
	3	0.036		0.034	0.037	0.005	0.005	0.005	0.045	0.044	0.046		
	4	0.001		0	0.001	0	0	0	0.010	0.011	0.010		
1-4	0	0.355		0.356	0.345	0.447	0.447	0.446	0.543	0.554	0.540		
	1	0.434		0.433	0.435	0.443	0.442	0.443	0.237	0.228	0.238		

Citrate	CIT	1-6	2	0.182	0.182	0.190	0.105	0.106	0.105	0.148	0.145	0.149
			3	0.029	0.027	0.030	0.005	0.005	0.005	0.058	0.060	0.060
			4	0	0.002	0.001	0	0	0	0.013	0.014	0.014
			0	0.224	0.225	0.215	0.268	0.268	0.265	0.413	0.424	0.405
			1	0.399	0.399	0.396	0.438	0.437	0.439	0.230	0.227	0.229
			2	0.275	0.274	0.279	0.242	0.241	0.244	0.215	0.212	0.216
			3	0.089	0.088	0.096	0.049	0.052	0.049	0.095	0.092	0.099
			4	0.013	0.013	0.012	0.004	0.003	0.003	0.036	0.035	0.038
			5	-0.001	0.001	0	0	0	-0.001	0.010	0.008	0.010
			6	0	0	0	0	0	0	0.002	0.002	0.002
Cell Wall	G6P	3-6	0	0.838	0.834	0.828	0.786	0.789	0.787	0.72	0.715	0.010
			1	0.172	0.172	0.177	0.201	0.198	0.202	0.092	0.091	0.010
			2	0	0.003	0.003	0.019	0.020	0.018	0.009	0.007	0.010
			3	-0.005	-0.004	-0.004	-0.002	-0.002	-0.003	0.053	0.053	0.010
			4	-0.006	-0.004	-0.004	-0.004	-0.004	-0.004	0.127	0.134	0.010
Alanine	ALA	1-3	0	0.609	0.605	0.602	0.545	0.539	0.537	0.748	0.740	0.744
			1	0.373	0.377	0.380	0.418	0.422	0.425	0.069	0.071	0.071
			2	0.017	0.017	0.017	0.037	0.038	0.038	0.035	0.035	0.035
			3	0.001	0.001	0.001	0	0.001	0.001	0.148	0.153	0.150
			0	0.626	0.621	0.619	0.572	0.567	0.566	0.779	0.773	0.776
		2-3	1	0.366	0.371	0.373	0.424	0.428	0.429	0.051	0.051	0.052
			2	0.008	0.008	0.008	0.005	0.005	0.005	0.170	0.175	0.172
		1-2	0	0.952	0.947	0.950	0.679	0.677	0.676	0.791	0.789	0.790
			1	0.047	0.053	0.050	0.306	0.308	0.308	0.098	0.095	0.096
			2	0	0	0	0.015	0.015	0.016	0.111	0.116	0.113
Glycine	GLYeff	2	0	0.985	0.985	0.985	0.730	0.729	0.727	0.841	0.838	0.840
			1	0.015	0.015	0.015	0.270	0.271	0.273	0.159	0.162	0.160
			0	0.377	0.363	0.367	0.313	0.302	0.294	0.576	0.555	0.572
			1	0.460	0.472	0.464	0.478	0.486	0.487	0.105	0.112	0.105
			2	0.151	0.154	0.156	0.190	0.194	0.200	0.159	0.164	0.160
		1-5	3	0.012	0.012	0.013	0.019	0.017	0.019	0.126	0.132	0.128
			4	0.001	0	0	0	0	0	0.013	0.014	0.014
			5	-0.001	-0.001	0	0	0	0	0.021	0.022	0.022
			0	0.392	0.380	0.383	0.340	0.330	0.324	0.604	0.584	0.596
			1	0.460	0.469	0.464	0.487	0.493	0.498	0.096	0.103	0.099
Valine	VAL	1-5	0	0.377	0.363	0.367	0.313	0.302	0.294	0.576	0.555	0.572
			1	0.460	0.472	0.464	0.478	0.486	0.487	0.105	0.112	0.105
			2	0.151	0.154	0.156	0.190	0.194	0.200	0.159	0.164	0.160
			3	0.012	0.012	0.013	0.019	0.017	0.019	0.126	0.132	0.128
			4	0.001	0	0	0	0	0	0.013	0.014	0.014
		2-5	5	-0.001	-0.001	0	0	0	0	0.021	0.022	0.022
			0	0.392	0.380	0.383	0.340	0.330	0.324	0.604	0.584	0.596
			1	0.460	0.469	0.464	0.487	0.493	0.498	0.096	0.103	0.099

Leucine	LEU	2-5	2	0.140	0.144	0.144	0.169	0.172	0.173	0.254	0.265	0.259
			3	0.008	0.008	0.009	0.005	0.005	0.004	0.020	0.022	0.020
			4	0	0	0	0	0	0	0.025	0.026	0.026
			0	0.408	0.396	0.40	0.362	0.349	0.343	0.612	0.594	0.606
		2-6	1	0.433	0.444	0.438	0.458	0.467	0.469	0.089	0.094	0.089
			2	0.137	0.140	0.141	0.162	0.165	0.169	0.245	0.256	0.250
			3	0.019	0.019	0.020	0.017	0.017	0.017	0.030	0.030	0.030
			4	0.001	0.001	0.002	0.002	0.002	0.002	0.025	0.026	0.026
			0	0.272	0.253	0.259	0.319	0.305	0.297	0.494	0.469	0.485
			1	0.437	0.446	0.440	0.460	0.469	0.473	0.183	0.191	0.186
			2	0.236	0.243	0.242	0.196	0.199	0.203	0.231	0.242	0.235
			3	0.051	0.053	0.054	0.023	0.024	0.024	0.062	0.065	0.063
			4	0.004	0.004	0.004	0.002	0.002	0.003	0.026	0.027	0.026
			5	0	0	0	0	0	0	0.005	0.005	0.005
		2-6	0	0.288	0.264	0.275	0.319	0.304	0.295	0.485	0.461	0.478
			1	0.451	0.460	0.455	0.474	0.483	0.487	0.206	0.214	0.207
			2	0.209	0.219	0.216	0.179	0.185	0.190	0.213	0.223	0.216
			3	0.044	0.047	0.047	0.023	0.023	0.024	0.068	0.073	0.069
Isoleucine	ILE	2-5	4	0.004	0.005	0.005	0.001	0.001	0.001	0.020	0.021	0.020
			5	0.004	0.004	0.003	0.003	0.003	0.003	0.009	0.009	0.009
			0	0.334	0.322	0.323	0.427	0.412	0.407	0.538	0.522	0.535
			1	0.457	0.465	0.461	0.457	0.466	0.471	0.229	0.232	0.228
		2-6	2	0.183	0.188	0.189	0.112	0.117	0.118	0.181	0.192	0.184
			3	0.025	0.025	0.026	0.005	0.005	0.005	0.041	0.043	0.042
			4	0.001	0	0	-0.001	0	-0.001	0.010	0.011	0.011
			0	0.330	0.318	0.319	0.424	0.410	0.403	0.540	0.522	0.535
			1	0.463	0.469	0.466	0.461	0.472	0.476	0.224	0.230	0.226
			2	0.185	0.188	0.190	0.112	0.116	0.118	0.184	0.194	0.187
			3	0.024	0.025	0.025	0.004	0.004	0.004	0.041	0.043	0.042
			4	-0.001	-0.001	-0.001	-0.001	-0.002	-0.002	0.010	0.011	0.010
			0	0.426	0.411	0.416	0.522	0.510	0.506	0.559	0.546	0.557
		1-5	1	0.362	0.368	0.368	0.362	0.369	0.371	0.243	0.247	0.244
			2	0.169	0.175	0.172	0.105	0.110	0.111	0.119	0.125	0.120
			3	0.038	0.041	0.040	0.011	0.011	0.011	0.058	0.061	0.059
			4	0.003	0.004	0.003	0	0	0.001	0.018	0.019	0.018
Methionine	METeff	1-5	0	0.426	0.411	0.416	0.522	0.510	0.506	0.559	0.546	0.557
			1	0.362	0.368	0.368	0.362	0.369	0.371	0.243	0.247	0.244
			2	0.169	0.175	0.172	0.105	0.110	0.111	0.119	0.125	0.120
			3	0.038	0.041	0.040	0.011	0.011	0.011	0.058	0.061	0.059
			4	0.003	0.004	0.003	0	0	0.001	0.018	0.019	0.018
			0	0.426	0.411	0.416	0.522	0.510	0.506	0.559	0.546	0.557
			1	0.362	0.368	0.368	0.362	0.369	0.371	0.243	0.247	0.244
			2	0.169	0.175	0.172	0.105	0.110	0.111	0.119	0.125	0.120

Serine	Sereff	2-5	5	0.001	0.001	0.001	0.001	0	0.001	0.003	0.003	0.003
			0	0.462	0.448	0.454	0.610	0.602	0.596	0.598	0.589	0.596
			1	0.368	0.371	0.371	0.324	0.330	0.333	0.254	0.257	0.255
			2	0.143	0.149	0.147	0.061	0.062	0.064	0.101	0.104	0.103
			3	0.023	0.027	0.025	0.002	0.002	0.003	0.039	0.040	0.037
		2-5	4	0.004	0.004	0.004	0.003	0.003	0.004	0.008	0.009	0.009
			0	0.469	0.453	0.459	0.612	0.605	0.599	0.601	0.592	0.599
			1	0.367	0.373	0.369	0.323	0.329	0.332	0.255	0.258	0.255
			2	0.140	0.147	0.146	0.061	0.062	0.064	0.103	0.107	0.105
			3	0.024	0.026	0.026	0.004	0.004	0.004	0.037	0.039	0.037
		1-3	4	0	0.001	0.001	0	0	0	0.004	0.005	0.004
			0	0.716	0.710	0.711	0.612	0.608	0.607	0.703	0.703	0.703
			1	0.276	0.281	0.280	0.345	0.348	0.350	0.157	0.151	0.156
			2	0.009	0.010	0.009	0.043	0.043	0.043	0.082	0.081	0.082
			3	-0.001	-0.001	0	0.001	0.001	0.001	0.058	0.065	0.059
Threonine	THR	2-3	0	0.739	0.733	0.731	0.649	0.646	0.645	0.740	0.738	0.739
			1	0.261	0.267	0.268	0.331	0.334	0.336	0.191	0.186	0.190
			2	0	0	0.001	0.020	0.020	0.019	0.069	0.076	0.071
		2-3	0	0.736	0.731	0.731	0.649	0.646	0.644	0.742	0.741	0.739
			1	0.261	0.268	0.267	0.330	0.332	0.335	0.190	0.184	0.190
			2	0.002	0.002	0.002	0.021	0.021	0.021	0.068	0.076	0.071
		1-4	0	0.382	0.375	0.379	0.441	0.426	0.429	0.551	0.539	0.553
			1	0.449	0.456	0.451	0.451	0.462	0.464	0.228	0.231	0.222
			2	0.153	0.154	0.157	0.104	0.106	0.107	0.148	0.148	0.146
			3	0.015	0.018	0.017	0.005	0.006	0.003	0.059	0.066	0.065
			4	0	-0.003	-0.004	-0.001	0	-0.003	0.014	0.015	0.014
		2-4	0	0.448	0.432	0.437	0.564	0.556	0.556	0.614	0.602	0.613
			1	0.439	0.444	0.439	0.389	0.395	0.397	0.237	0.239	0.235
			2	0.105	0.115	0.116	0.049	0.048	0.048	0.114	0.121	0.116
Phenylalanine	PHE_TYR	1-9	3	0.007	0.009	0.008	-0.002	0	-0.002	0.035	0.038	0.035
			0	0.318	0.303	0.305	0.207	0.192	0.182	0.377	0.384	0.383
			1	0.430	0.437	0.434	0.381	0.39	0.391	0.141	0.139	0.141
			2	0.207	0.214	0.213	0.283	0.286	0.293	0.135	0.135	0.134
			3	0.041	0.042	0.043	0.104	0.107	0.108	0.180	0.175	0.177
			4	0.003	0.003	0.003	0.022	0.022	0.022	0.080	0.082	0.081

Aspartate	ASP	2-9	5	0	0	0	0.003	0.003	0.003	0.043	0.042	0.043
			6	0.001	0	0	0	0	0	0.028	0.027	0.027
			7	0	0	0	0	0	0	0.010	0.010	0.011
			8	0	0	0	0	0	0	0.004	0.003	0.003
			9	0	0	0	0	0	0	0.002	0.002	0.002
			0	0.325	0.311	0.312	0.216	0.202	0.193	0.394	0.399	0.399
			1	0.431	0.438	0.436	0.396	0.403	0.405	0.136	0.133	0.136
			2	0.204	0.208	0.210	0.278	0.285	0.289	0.214	0.214	0.210
			3	0.038	0.040	0.040	0.093	0.093	0.096	0.117	0.113	0.115
			4	0.002	0.003	0.003	0.016	0.016	0.017	0.077	0.079	0.078
			5	0	0	0	0.001	0.001	0.001	0.036	0.035	0.036
			6	0	0	0	0	0	0	0.020	0.021	0.020
			7	0	0	0	0	0	-0.001	0.004	0.004	0.004
			8	0	0	0	0	0	0	0.002	0.002	0.002
		2-9	0	0.325	0.312	0.313	0.218	0.204	0.196	0.396	0.401	0.397
			1	0.428	0.434	0.433	0.392	0.400	0.402	0.136	0.133	0.135
			2	0.204	0.209	0.210	0.278	0.283	0.287	0.212	0.212	0.211
			3	0.039	0.041	0.041	0.094	0.094	0.096	0.117	0.112	0.117
			4	0.003	0.003	0.003	0.017	0.017	0.017	0.077	0.080	0.078
			5	0	0	0	0.002	0.002	0.002	0.036	0.035	0.036
			6	0	0	0	0	0	0	0.020	0.021	0.020
			7	0	0	0	0	0	0	0.004	0.004	0.004
			8	0	0	0	0	0	0	0.002	0.002	0.002
		1-2	0	0.969	0.968	0.968	0.611	0.604	0.598	0.763	0.769	0.772
			1	0.032	0.034	0.032	0.378	0.385	0.391	0.075	0.072	0.070
			2	-0.001	-0.002	0	0.011	0.012	0.011	0.162	0.159	0.158
		1-4	0	0.384	0.374	0.370	0.444	0.437	0.432	0.550	0.541	0.552
			1	0.438	0.443	0.443	0.445	0.451	0.452	0.227	0.227	0.226
			2	0.157	0.160	0.165	0.105	0.106	0.109	0.145	0.148	0.144
			3	0.021	0.022	0.022	0.006	0.005	0.006	0.063	0.068	0.064
		2-4	4	0	0.001	0	0	0	0	0.014	0.016	0.014
			0	0.447	0.438	0.438	0.572	0.566	0.563	0.613	0.604	0.612
			1	0.431	0.436	0.435	0.380	0.385	0.388	0.237	0.237	0.237
			2	0.113	0.117	0.117	0.047	0.048	0.049	0.116	0.120	0.117
			3	0.008	0.009	0.009	0	0.001	0.001	0.034	0.039	0.034

Glutamate	GLU	2-4	0	0.463	0.455	0.452	0.582	0.576	0.572	0.620	0.612	0.620		
			1	0.412	0.416	0.418	0.364	0.370	0.373	0.228	0.229	0.227		
			2	0.110	0.113	0.115	0.047	0.047	0.048	0.113	0.117	0.114		
			3	0.015	0.015	0.016	0.007	0.007	0.007	0.039	0.042	0.040		
		1-2	0	0.634	0.630	0.626	0.665	0.661	0.658	0.732	0.718	0.730		
			1	0.332	0.335	0.337	0.325	0.329	0.331	0.156	0.164	0.157		
			2	0.034	0.035	0.037	0.010	0.010	0.011	0.112	0.118	0.113		
		1-5	0	0.285	0.272	0.275	0.332	0.325	0.321	0.481	0.469	0.479		
			1	0.435	0.441	0.437	0.462	0.467	0.467	0.216	0.217	0.216		
			2	0.225	0.231	0.230	0.183	0.185	0.188	0.207	0.213	0.207		
			3	0.051	0.052	0.053	0.022	0.023	0.023	0.071	0.074	0.072		
			4	0.004	0.004	0.005	0.001	0	0.001	0.020	0.021	0.021		
			5	0	0	0	0	0	0	0.005	0.006	0.006		
			2-5	0	0.336	0.325	0.324	0.431	0.423	0.419	0.539	0.529	0.536	
		Lysine	LYS	2-5	1	0.444	0.453	0.450	0.452	0.459	0.460	0.228	0.229	0.227
					2	0.192	0.195	0.197	0.113	0.113	0.115	0.179	0.187	0.182
					3	0.028	0.028	0.030	0.004	0.005	0.006	0.043	0.044	0.044
					4	0	0	0	0.001	0	0	0.011	0.012	0.011
					2-5	0	0.334	0.326	0.323	0.430	0.422	0.419	0.540	0.529
				1-6	1	0.447	0.452	0.451	0.453	0.458	0.461	0.227	0.228	0.228
2	0.191				0.192	0.196	0.112	0.114	0.114	0.178	0.187	0.182		
3	0.028				0.029	0.030	0.006	0.006	0.006	0.044	0.044	0.044		
4	0.001				0.001	0.001	0	0	0	0.011	0.012	0.011		
0	0.252				0.230	0.238	0.270	0.257	0.245	0.443	0.410	0.435		
Histidine	HISeff	1-6	1	0.436	0.452	0.444	0.457	0.468	0.472	0.211	0.223	0.214		
			2	0.238	0.247	0.247	0.226	0.235	0.237	0.172	0.185	0.181		
			3	0.063	0.062	0.062	0.043	0.043	0.043	0.119	0.122	0.115		
			4	0.006	0.009	0.008	0.003	0.001	0.003	0.038	0.039	0.039		
			5	0.008	0	0.001	0.001	0	0.001	0.014	0.014	0.014		
6	-0.002	0	0	-0.001	-0.004	0	0.003	0.006	0.003					
			0	0.560	0.553	0.556	0.355	0.343	0.333	0.591	0.583	0.591		
			1	0.324	0.332	0.328	0.409	0.418	0.421	0.169	0.172	0.171		
			2	0.100	0.100	0.102	0.196	0.199	0.205	0.093	0.092	0.092		
			3	0.015	0.013	0.014	0.037	0.037	0.037	0.087	0.087	0.086		
			4	0.002	0.001	0	0.003	0.003	0.004	0.027	0.028	0.028		

Tyrosine	PHE_TYR	2-6	5	-0.001	0	0	-0.001	0	0	0.028	0.032	0.028
			6	0	0	0	0	0	0	0.005	0.006	0.005
			0	0.664	0.667	0.664	0.368	0.351	0.345	0.596	0.580	0.590
			1	0.275	0.274	0.279	0.417	0.428	0.427	0.171	0.181	0.175
			2	0.047	0.044	0.046	0.180	0.185	0.192	0.145	0.150	0.146
			3	0.010	0.011	0.008	0.030	0.030	0.030	0.050	0.048	0.050
		1-2	4	0.002	0.002	0.003	0.004	0.004	0.004	0.031	0.033	0.032
			5	0.001	0.001	0.001	0.001	0.002	0.002	0.008	0.008	0.007
			0	0.792	0.788	0.788	0.737	0.737	0.735	0.837	0.828	0.829
			1	0.207	0.213	0.210	0.261	0.262	0.265	0.039	0.040	0.044
			2	0.001	-0.001	0.002	0.002	0	0	0.124	0.132	0.127
		2-9	0	0.303	0.285	0.289	0.188	0.175	0.166	0.394	0.383	0.392
			1	0.446	0.458	0.454	0.411	0.419	0.419	0.134	0.133	0.134
			2	0.216	0.226	0.221	0.295	0.300	0.302	0.219	0.225	0.219
			3	0.042	0.044	0.044	0.100	0.100	0.102	0.117	0.118	0.116
			4	0.003	0.001	0.002	0.016	0.017	0.018	0.079	0.084	0.081
			5	-0.001	-0.002	-0.002	0	0	0	0.035	0.035	0.036
Arginine	ARGeff	1-6	6	-0.002	-0.003	-0.002	-0.002	-0.002	-0.001	0.020	0.021	0.020
			7	-0.002	-0.004	-0.004	-0.004	-0.004	-0.002	0.002	0.002	0.002
			8	-0.003	-0.004	-0.003	-0.004	-0.004	-0.003	0	0	0
			0	0.401	0.390	0.397	0.431	0.418	0.413	0.516	0.502	0.513
			1	0.348	0.349	0.344	0.367	0.372	0.368	0.223	0.225	0.221
			2	0.187	0.194	0.196	0.161	0.171	0.178	0.154	0.164	0.162
		2-6	3	0.054	0.056	0.051	0.034	0.035	0.036	0.074	0.076	0.071
			4	0.007	0.008	0.009	0.004	0.002	0.003	0.024	0.023	0.022
			5	0.002	0.002	0.003	0.002	0.002	0.001	0.008	0.008	0.009
			6	0	0	-0.001	0	0	0	0.001	0.001	0.001
			0	0.427	0.415	0.418	0.485	0.473	0.470	0.555	0.529	0.540
			1	0.349	0.361	0.357	0.361	0.368	0.365	0.227	0.240	0.231
			2	0.169	0.175	0.171	0.123	0.128	0.129	0.144	0.151	0.151
			3	0.040	0.038	0.040	0.019	0.018	0.024	0.054	0.057	0.053
			4	0.008	0.005	0.007	0.005	0.005	0.004	0.013	0.015	0.018
			5	0.007	0.006	0.007	0.007	0.007	0.007	0.007	0.007	0.007

Pi+ cultures												
Metabolite	Network Metabolite	Carbon Atoms	Mass (m+)	[1- ¹³ C]glucose			[2- ¹³ C]glucose			[¹³ C ₆]glucose		
				Replica 1	Replica 2	Replica 3	Replica 1	Replica 2	Replica 3	Replica 1	Replica 2	Replica 3
Alanine (Soluble)	ALA	1-3	0	0.628	0.624	0.624	0.557	0.548	0.563	0.737	0.737	0.734
			1	0.356	0.359	0.357	0.401	0.407	0.391	0.084	0.081	0.084
			2	0.015	0.018	0.018	0.041	0.044	0.045	0.040	0.038	0.041
			3	0	0	0.001	0.001	0.002	0.001	0.140	0.144	0.142
		2-3	0	0.646	0.645	0.646	0.585	0.578	0.600	0.774	0.774	0.771
			1	0.347	0.349	0.348	0.408	0.412	0.394	0.064	0.061	0.065
			2	0.006	0.006	0.007	0.007	0.010	0.007	0.162	0.166	0.164
			0	0.912	0.909	0.913	0.634	0.627	0.650	0.745	0.738	0.744
		1-2	1	0.088	0.089	0.084	0.343	0.348	0.328	0.139	0.148	0.137
			2	-0.001	0.002	0.003	0.023	0.025	0.022	0.117	0.114	0.119
			0	0.976	0.976	0.976	0.697	0.699	0.717	0.810	0.815	0.814
			1	0.024	0.024	0.024	0.303	0.301	0.283	0.190	0.185	0.186
Serine (Soluble)	SER	1-3	0	0.685	0.678	0.678	0.571	0.569	0.581	0.667	0.663	0.669
			1	0.302	0.307	0.308	0.376	0.375	0.367	0.174	0.181	0.171
			2	0.014	0.016	0.014	0.051	0.053	0.053	0.084	0.087	0.085
			3	-0.001	-0.001	0	0.001	0.002	-0.001	0.075	0.070	0.074
		2-3	0	0.718	0.707	0.712	0.616	0.619	0.620	0.713	0.709	0.715
			1	0.281	0.290	0.288	0.364	0.358	0.358	0.195	0.203	0.194
			2	0.001	0.003	0.001	0.021	0.023	0.022	0.092	0.088	0.091
			0	0.716	0.709	0.711	0.618	0.621	0.623	0.715	0.713	0.715
		2-3	1	0.281	0.288	0.285	0.359	0.357	0.353	0.194	0.199	0.193
			2	0.003	0.003	0.003	0.023	0.022	0.024	0.091	0.088	0.092
			0	0.362	0.353	0.356	0.415	0.429	0.428	0.533	0.538	0.544
			1	0.438	0.445	0.435	0.405	0.450	0.438	0.232	0.235	0.228
GABA	GABA	1-4	2	0.178	0.182	0.187	0.146	0.122	0.126	0.183	0.176	0.171
			3	0.022	0.020	0.022	0.030	0.002	0.010	0.043	0.040	0.044
			4	0	-0.001	0	0.005	-0.003	-0.002	0.009	0.010	0.012
			0	0.360	0.356	0.353	0.436	0.434	0.433	0.535	0.537	0.541
		1-4	1	0.438	0.441	0.443	0.444	0.443	0.434	0.234	0.233	0.225

Fructose	F6P	4-6	2	0.178	0.179	0.180	0.115	0.118	0.123	0.177	0.176	0.181
			3	0.024	0.023	0.024	0.006	0.007	0.010	0.043	0.044	0.041
			4	0	0	0	-0.001	-0.001	0	0.011	0.010	0.012
			0	0.886	0.869	0.865	0.856	0.874	0.838	0.777	0.777	0.778
			1	0.126	0.142	0.144	0.147	0.129	0.161	0.036	0.036	0.035
			2	-0.005	-0.003	-0.002	0.006	0.005	0.009	0.010	0.010	0.010
		4-6	3	-0.007	-0.007	-0.007	-0.009	-0.008	-0.008	0.177	0.177	0.177
			0	0.890	0.871	0.866	0.855	0.877	0.840	0.775	0.778	0.781
			1	0.124	0.140	0.144	0.148	0.128	0.161	0.036	0.035	0.034
			2	-0.005	-0.003	-0.002	0.005	0.004	0.007	0.010	0.009	0.008
			3	-0.009	-0.008	-0.008	-0.008	-0.009	-0.008	0.179	0.177	0.177
			0	0.829	0.808	0.806	0.754	0.773	0.727	0.685	0.692	0.697
Starch	STA	3-6	1	0.173	0.193	0.195	0.212	0.196	0.232	0.118	0.122	0.112
			2	0.004	0.005	0.006	0.037	0.033	0.042	0.016	0.016	0.013
			3	-0.003	-0.003	-0.002	0.001	0.001	0.001	0.071	0.072	0.068
			4	-0.003	-0.004	-0.004	-0.003	-0.003	-0.003	0.110	0.098	0.109
			0	0.825	0.805	0.797	0.747	0.771	0.720	0.682	0.689	0.700
			1	0.172	0.191	0.198	0.214	0.194	0.233	0.121	0.122	0.111
		3-6	2	0.009	0.010	0.010	0.042	0.033	0.047	0.016	0.018	0.013
			3	-0.003	-0.003	-0.002	-0.001	0.005	0.002	0.072	0.072	0.067
			4	-0.003	-0.003	-0.003	-0.002	-0.003	-0.002	0.109	0.099	0.108
			0	0.379	0.371	0.364	0.431	0.438	0.439	0.530	0.527	0.541
			1	0.434	0.436	0.439	0.444	0.442	0.436	0.230	0.230	0.223
			2	0.166	0.170	0.173	0.119	0.115	0.117	0.185	0.186	0.183
Succinate	SUCC	1-4	3	0.020	0.022	0.023	0.006	0.006	0.007	0.042	0.045	0.040
			4	0	0.001	0.001	0	0	0	0.012	0.013	0.012
			0	0.427	0.423	0.418	0.459	0.462	0.457	0.552	0.551	0.557
			1	0.419	0.422	0.423	0.429	0.427	0.427	0.233	0.234	0.226
			2	0.138	0.138	0.141	0.106	0.106	0.108	0.138	0.139	0.137
			3	0.016	0.017	0.017	0.006	0.005	0.008	0.062	0.062	0.064
		1-4	4	0.001	0.001	0.001	0	0	0	0.015	0.014	0.016
			0	0.279	0.278	0.274	0.289	0.289	0.295	0.423	0.419	0.431
			1	0.412	0.414	0.416	0.437	0.432	0.428	0.240	0.231	0.226
			2	0.236	0.238	0.237	0.223	0.230	0.222	0.204	0.211	0.209
			3	0.065	0.063	0.065	0.047	0.046	0.051	0.090	0.095	0.089

Cell wall	G6P	3-6	4	0.007	0.006	0.007	0.004	0.003	0.006	0.033	0.032	0.034
			5	0	0	0	0	0	-0.002	0.008	0.010	0.008
			6	0	0	0	0	0	0.001	0.002	0.002	0.003
			0	0.882	0.870	0.876	0.836	0.850	0.814	0.722	0.727	0.728
			1	0.124	0.136	0.132	0.153	0.142	0.168	0.083	0.084	0.082
			2	0.001	0	-0.001	0.015	0.013	0.023	0.007	0.008	0.008
			3	-0.004	-0.004	-0.004	-0.001	-0.001	-0.002	0.048	0.048	0.046
			4	-0.004	-0.003	-0.004	-0.003	-0.004	-0.003	0.140	0.133	0.137
			0	0.877	0.871	0.871	0.837	0.848	0.820	0.724		0.728
			1	0.130	0.135	0.136	0.152	0.142	0.165	0.084		0.082
Alanine	G6P	3-6	2	0	0.001	0.001	0.016	0.015	0.019	0.008		0.007
			3	-0.004	-0.003	-0.004				0.047		0.047
			4	-0.004	-0.004	-0.004				0.138		0.136
	ALA	1-3	0	0.633	0.635	0.635	0.556	0.555	0.554	0.743	0.747	0.743
			1	0.352	0.349	0.350	0.401	0.400	0.401	0.073	0.072	0.072
			2	0.014	0.015	0.015	0.042	0.044	0.044	0.035	0.034	0.035
			3	0.001	0	0	0.001	0.001	0.001	0.149	0.146	0.149
		2-3	0	0.650	0.652	0.652	0.585	0.586	0.586	0.777	0.781	0.777
			1	0.344	0.341	0.342	0.410	0.409	0.408	0.053	0.052	0.053
			2	0.006	0.006	0.006	0.005	0.005	0.006	0.170	0.167	0.170
	GLYeff	1-2	0	0.928	0.928	0.929	0.673	0.670	0.678	0.769	0.770	0.773
			1	0.071	0.072	0.071	0.307	0.309	0.303	0.125	0.131	0.118
			2	0.001	0.001	0.001	0.020	0.020	0.019	0.106	0.098	0.110
		2	0	0.986	0.986	0.987	0.738	0.736	0.737	0.833	0.837	0.833
			1	0.014	0.014	0.013	0.262	0.264	0.263	0.167	0.163	0.167
Valine	VAL	1-5	0	0.393	0.402	0.403	0.318	0.314	0.320	0.571	0.588	0.568
			1	0.460	0.455	0.452	0.474	0.475	0.471	0.104	0.099	0.109
			2	0.137	0.136	0.136	0.188	0.190	0.189	0.158	0.154	0.159
			3	0.010	0.008	0.009	0.019	0.021	0.020	0.130	0.125	0.128
			4	0	0	0	0	0	0	0.014	0.012	0.014
			5	0	0	0	0	0	0	0.023	0.022	0.022
		2-5	0	0.408	0.416	0.421	0.343	0.341	0.349	0.596	0.611	0.595
			1	0.456	0.450	0.447	0.486	0.488	0.483	0.097	0.092	0.100
			2	0.129	0.127	0.128	0.166	0.167	0.162	0.260	0.253	0.258
			3	0.007	0.006	0.004	0.005	0.005	0.005	0.020	0.019	0.021

Leucine	LEU	2-5	4	0	0	0	0	0	0.026	0.025	0.026			
			0	0.422	0.430	0.434	0.362	0.359	0.366	0.604	0.618	0.604		
			1	0.433	0.428	0.425	0.461	0.464	0.458	0.089	0.083	0.092		
			2	0.126	0.125	0.125	0.159	0.159	0.157	0.252	0.245	0.249		
			3	0.017	0.017	0.017	0.016	0.016	0.017	0.029	0.028	0.030		
		2-6	4	0.002	0	0	0.001	0.002	0.002	0.026	0.025	0.026		
			0	0.273	0.284	0.291	0.315	0.311	0.322	0.484	0.504	0.480		
			1	0.443	0.438	0.433	0.464	0.467	0.459	0.189	0.178	0.190		
			2	0.232	0.227	0.226	0.194	0.196	0.193	0.233	0.226	0.234		
			3	0.048	0.047	0.047	0.024	0.023	0.024	0.063	0.061	0.065		
Isoleucine	ILE	2-6	4	0.003	0.003	0.003	0.002	0.002	0.002	0.026	0.025	0.026		
			5	0	0	0	0	0	0	0.005	0.005	0.005		
			0	0.291	0.303	0.311	0.327	0.323	0.333	0.480	0.501	0.481		
			1	0.447	0.440	0.434	0.465	0.468	0.461	0.210	0.203	0.210		
			2	0.211	0.207	0.205	0.180	0.181	0.179	0.211	0.204	0.212		
		2-5	3	0.044	0.043	0.043	0.023	0.024	0.023	0.070	0.066	0.070		
			4	0.004	0.004	0.004	0.001	0.001	0.001	0.020	0.019	0.021		
			5	0.002	0.003	0.003	0.003	0.002	0.002	0.008	0.008	0.007		
			0	0.367	0.378	0.380	0.442	0.442	0.438	0.547	0.567	0.548		
			1	0.443	0.436	0.434	0.442	0.443	0.444	0.221	0.212	0.220		
Proline	GLU	2-5	2	0.170	0.167	0.166	0.111	0.111	0.114	0.180	0.170	0.180		
			3	0.021	0.020	0.020	0.005	0.004	0.005	0.040	0.039	0.040		
			4	-0.001	-0.001	0	0	-0.001	0	0.012	0.011	0.011		
			2-5	0	0.361	0.372	0.375	0.439	0.437	0.435	0.550	0.567	0.547	
				1	0.447	0.441	0.437	0.447	0.449	0.448	0.218	0.211	0.218	
		2		0.172	0.168	0.167	0.111	0.111	0.113	0.182	0.173	0.183		
		3		0.021	0.020	0.021	0.004	0.004	0.005	0.040	0.038	0.040		
		4		-0.001	-0.001	0	-0.001	-0.001	-0.001	0.011	0.010	0.011		
		Methionine	METeff	1-5	0	0.396	0.405	0.409	0.486	0.485	0.486	0.530	0.541	0.531
					1	0.382	0.376	0.375	0.383	0.383	0.382	0.254	0.251	0.252
2	0.179				0.176	0.174	0.118	0.117	0.118	0.128	0.123	0.129		
3	0.039				0.039	0.039	0.013	0.013	0.013	0.065	0.062	0.064		
4	0.004				0.004	0.003	0	0	0	0.020	0.019	0.020		
2-5	5			0.001	0.001	0	0.001	0	0.001	0.003	0.004	0.004		
	0			0.437	0.444	0.448	0.578	0.577	0.578	0.571	0.583	0.575		

Serine	SEReff	2-5	1	0.384	0.380	0.377	0.345	0.347	0.344	0.267	0.261	0.264
			2	0.149	0.148	0.145	0.070	0.070	0.070	0.111	0.106	0.110
			3	0.024	0.024	0.024	0.004	0.004	0.004	0.042	0.039	0.042
			4	0.005	0.004	0.006	0.003	0.003	0.004	0.010	0.010	0.009
		1-3	0	0.440	0.448	0.452	0.579	0.579	0.578	0.575	0.588	0.575
			1	0.382	0.380	0.377	0.345	0.345	0.344	0.268	0.261	0.265
			2	0.151	0.148	0.146	0.072	0.071	0.072	0.113	0.108	0.112
			3	0.026	0.024	0.024	0.005	0.005	0.005	0.040	0.038	0.042
		2-3	4	0.001	0	0.001	0	0	0	0.004	0.004	0.006
			0	0.723	0.722	0.722	0.605	0.602	0.609	0.693	0.693	0.694
			1	0.266	0.267	0.266	0.344	0.345	0.341	0.163	0.169	0.160
			2	0.011	0.011	0.012	0.049	0.051	0.049	0.078	0.077	0.078
		2-3	3	0	0	0	0.002	0.001	0.001	0.067	0.061	0.068
			0	0.755	0.753	0.754	0.650	0.649	0.650	0.736	0.738	0.736
			1	0.244	0.246	0.246	0.329	0.330	0.330	0.184	0.188	0.183
			2	0.001	0	0	0.021	0.021	0.020	0.080	0.074	0.081
Threonine	THR	2-3	0	0.752	0.752	0.752	0.651	0.649	0.649	0.736	0.738	0.736
			1	0.245	0.245	0.246	0.328	0.329	0.330	0.183	0.188	0.183
			2	0.002	0.003	0.002	0.022	0.022	0.021	0.081	0.075	0.081
		1-4	0	0.412	0.419	0.423	0.458	0.457	0.456	0.563	0.574	0.563
			1	0.434	0.427	0.423	0.436	0.436	0.434	0.222	0.217	0.218
			2	0.140	0.140	0.139	0.103	0.103	0.105	0.137	0.133	0.139
			3	0.015	0.014	0.016	0.004	0.005	0.004	0.064	0.061	0.064
		2-4	4	-0.001	-0.001	0	-0.001	-0.001	0	0.014	0.014	0.015
			0	0.477	0.487	0.488	0.578	0.580	0.575	0.622	0.634	0.626
			1	0.417	0.409	0.408	0.373	0.372	0.377	0.229	0.224	0.225
			2	0.101	0.098	0.097	0.049	0.048	0.047	0.114	0.109	0.113
		1-9	3	0.006	0.006	0.007	0	0	0.001	0.035	0.033	0.036
			0	0.316	0.320	0.326	0.188	0.186	0.190	0.384	0.403	0.386
			1	0.447	0.442	0.439	0.402	0.401	0.400	0.140	0.139	0.137
			2	0.200	0.199	0.197	0.283	0.283	0.282	0.133	0.129	0.133
Phenylalanine	PHE_TYR	1-9	3	0.036	0.037	0.035	0.102	0.103	0.102	0.172	0.166	0.172
			4	0.003	0.003	0.003	0.023	0.022	0.023	0.084	0.082	0.085
			5	0	0	0	0.003	0.003	0.003	0.043	0.040	0.042
			6	-0.001	0	0	0	0.001	0	0.028	0.026	0.028

Aspartate	ASP	2-9	7	0	0	0	0	0	0	0.011	0.011	0.011
			8	0	0	0	0	0	0	0.003	0.003	0.003
			9	0	0	0	0	0	0	0.002	0.002	0.002
			0	0.322	0.328	0.335	0.202	0.199	0.203	0.400	0.419	0.403
			1	0.447	0.443	0.438	0.415	0.417	0.416	0.134	0.134	0.132
			2	0.195	0.193	0.191	0.276	0.276	0.275	0.211	0.203	0.211
			3	0.034	0.033	0.034	0.089	0.089	0.088	0.110	0.105	0.110
			4	0.002	0.002	0.002	0.016	0.017	0.017	0.083	0.079	0.083
		2-9	5	0	0	0	0.001	0.002	0.001	0.034	0.033	0.034
			6	0	0	0	0	0	0	0.023	0.021	0.022
			7	0	0	0	0	0	0	0.004	0.003	0.004
			8	0	0	0	0	0	0	0.002	0.002	0.002
			0	0.323	0.329	0.334	0.203	0.200	0.204	0.401	0.419	0.402
			1	0.443	0.440	0.435	0.413	0.415	0.413	0.133	0.133	0.132
			2	0.195	0.193	0.192	0.275	0.276	0.275	0.211	0.203	0.211
			3	0.035	0.035	0.034	0.089	0.090	0.089	0.110	0.106	0.109
		1-2	4	0.003	0.003	0.003	0.017	0.017	0.017	0.082	0.078	0.082
			5	0.001	0.001	0.002	0.002	0.002	0.002	0.034	0.033	0.035
			6	0	0	0	0	0	0	0.022	0.022	0.023
			7	0	0	0	0	0	0	0.004	0.004	0.004
			8	0	0	0	0	0	0	0.002	0.002	0.002
			0	0.966	0.965	0.966	0.602	0.600	0.602	0.769	0.776	0.769
			1	0.035	0.036	0.035	0.385	0.386	0.385	0.070	0.072	0.071
		1-4	2	-0.001	-0.001	-0.001	0.013	0.014	0.013	0.161	0.153	0.160
			0	0.425	0.437	0.433	0.467	0.464	0.469	0.569	0.581	0.563
			1	0.417	0.412	0.412	0.422	0.424	0.422	0.217	0.215	0.216
			2	0.140	0.134	0.138	0.105	0.105	0.103	0.136	0.130	0.139
			3	0.018	0.016	0.017	0.007	0.007	0.006	0.063	0.061	0.066
			4	0.001	0	0.001	0	0	0	0.015	0.014	0.016
		2-4	0	0.486	0.498	0.494	0.584	0.582	0.585	0.629	0.638	0.620
			1	0.404	0.398	0.400	0.366	0.366	0.365	0.225	0.222	0.227
			2	0.101	0.096	0.100	0.050	0.051	0.049	0.111	0.108	0.116
			3	0.009	0.007	0.007	0	0.001	0.001	0.034	0.032	0.037
		2-4	0	0.497	0.508	0.504	0.590	0.588	0.590	0.633	0.644	0.628
			1	0.392	0.386	0.386	0.354	0.356	0.356	0.219	0.214	0.219

Glutamate	GLU	1-2	2	0.099	0.094	0.097	0.049	0.049	0.048	0.110	0.105	0.112
			3	0.013	0.012	0.013	0.007	0.007	0.006	0.038	0.037	0.042
			0	0.671	0.681	0.676	0.677	0.675	0.681	0.741	0.749	0.734
		1-5	1	0.299	0.292	0.295	0.312	0.314	0.309	0.149	0.146	0.154
			2	0.030	0.027	0.030	0.011	0.011	0.010	0.110	0.105	0.113
			0	0.329	0.339	0.339	0.359	0.356	0.363	0.498	0.506	0.491
			1	0.421	0.419	0.417	0.441	0.442	0.438	0.209	0.208	0.206
			2	0.203	0.199	0.200	0.176	0.177	0.176	0.198	0.193	0.202
			3	0.043	0.040	0.042	0.023	0.024	0.022	0.069	0.067	0.073
			4	0.003	0.003	0.003	0.001	0.001	0.001	0.020	0.020	0.021
			5	0	0	0	0	0	0	0.006	0.005	0.006
		2-5	0	0.383	0.393	0.392	0.451	0.449	0.454	0.556	0.564	0.548
			1	0.427	0.425	0.421	0.431	0.434	0.429	0.215	0.213	0.216
			2	0.167	0.161	0.166	0.112	0.111	0.112	0.176	0.173	0.180
			3	0.023	0.020	0.021	0.006	0.007	0.005	0.042	0.039	0.043
Lysine	LYS	2-5	4	0	0.001	0	0	0	0	0.012	0.011	0.013
			0	0.380	0.389	0.387	0.449	0.446	0.451	0.555	0.564	0.548
			1	0.430	0.427	0.425	0.433	0.435	0.431	0.215	0.212	0.215
			2	0.168	0.163	0.165	0.112	0.113	0.112	0.178	0.172	0.181
		1-6	3	0.022	0.021	0.022	0.006	0.006	0.006	0.041	0.041	0.043
			4	0.001	0	0.001	0	0	0	0.011	0.011	0.012
			0	0.274	0.298	0.296	0.294	0.287	0.303	0.451	0.472	0.436
			1	0.428	0.427	0.418	0.438	0.444	0.435	0.209	0.205	0.213
			2	0.233	0.221	0.224	0.219	0.218	0.215	0.170	0.161	0.175
			3	0.058	0.055	0.055	0.046	0.047	0.044	0.113	0.108	0.116
			4	0.007	0.005	0.007	0.002	0.004	0.003	0.039	0.037	0.042
Histidine	HISeff	1-6	5	0	0.001	0	0.001	0	0	0.013	0.014	0.015
			6	-0.001	-0.006	0	0	0	0	0.005	0.004	0.004
			0	0.575	0.576	0.582	0.315	0.312	0.316	0.572	0.582	0.571
			1	0.331	0.331	0.326	0.448	0.450	0.445	0.186	0.182	0.185
			2	0.085	0.084	0.083	0.196	0.198	0.197	0.089	0.088	0.089
			3	0.010	0.009	0.008	0.038	0.038	0.039	0.082	0.079	0.081
			4	-0.001	0	0.001	0.002	0.002	0.004	0.029	0.029	0.031
			5	0	0	0	0	0	-0.001	0.036	0.033	0.036
			6	0	0	0	0	0	0	0.007	0.007	0.007

Arginine	ARGeff	2-6	0	0.679	0.678	0.682	0.325	0.321	0.327	0.568	0.584	0.570
			1	0.273	0.272	0.270	0.456	0.460	0.454	0.189	0.186	0.188
			2	0.036	0.037	0.035	0.181	0.181	0.181	0.143	0.137	0.141
			3	0.008	0.009	0.008	0.032	0.030	0.032	0.054	0.048	0.054
			4	0.003	0.003	0.003	0.004	0.005	0.005	0.037	0.036	0.038
		1-2	5	0	0.001	0.001	0.002	0.003	0.001	0.009	0.008	0.010
			0	0.811	0.814	0.818	0.761	0.756	0.751	0.816	0.827	0.818
			1	0.188	0.187	0.185	0.236	0.244	0.250	0.046	0.042	0.042
			2	0.001	-0.001	-0.003	0.002	0	-0.001	0.138	0.131	0.141
		1-6	0	0.364	0.369	0.377	0.390	0.391	0.392	0.482	0.503	0.479
			1	0.360	0.361	0.357	0.382	0.379	0.381	0.230	0.222	0.232
			2	0.208	0.205	0.197	0.184	0.187	0.185	0.173	0.165	0.174
			3	0.057	0.054	0.059	0.038	0.039	0.035	0.080	0.075	0.079
			4	0.008	0.008	0.007	0.003	0.002	0.004	0.025	0.026	0.025
		2-6	5	0.003	0.003	0.002	0.002	0.001	0.002	0.009	0.008	0.009
			6	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001
			0	0.396	0.394	0.409	0.452	0.449	0.456	0.514	0.534	0.514
			1	0.369	0.371	0.363	0.377	0.380	0.376	0.247	0.236	0.241
			2	0.182	0.177	0.176	0.137	0.138	0.134	0.154	0.156	0.160
			3	0.041	0.042	0.040	0.022	0.021	0.022	0.060	0.054	0.060
			4	0.005	0.009	0.006	0.004	0.004	0.004	0.016	0.014	0.017
			5	0.006	0.007	0.006	0.008	0.007	0.007	0.007	0.006	0.008

Table S8. Definition of reaction network used to model heterotrophic carbon metabolism in *Arabidopsis* cell cultures

FLUX_NAME	EDUCT_1	EDUCT_2	PRODUCT_1	PRODUCT_2	Comment
//Subnetwork 1					
// Metabolic Input					
Vupt1	GLC_1 #ABCDEF		GLCext #ABCDEF		Uptake of [1- ¹³ C]glucose
Vupt0	GLC_0 #ABCDEF		GLCext #ABCDEF		Uptake of natural abundance glucose
// Uptake					
Vupt	GLCext #ABCDEF		G6P #ABCDEF		Net glucose uptake
Vco2in	CO2ex #A		CO2 #A		Utilisation of atmospheric CO ₂ at natural abundance
Vcxin	Cxex #A		CX #A		MTHF (1-carbon) utilization at natural abundance
//Cytosol					
Vchex1	G6P #ABCDEF		F6P #ABCDEF		Cytosolic phosphoglucose isomerase
Vchex2	F6P #ABCDEF		TP #CBA	TP #DEF	Cytosolic Fru-6-P → triose-P /PEP interconversion
Vchex3	TP #ABC		PYRc #ABC		Cytosolic pyruvate kinase
//Plastid					
Vphex1	G6Pp #ABCDEF		F6Pp #ABCDEF		Plastidic phosphoglucose isomerase
Vphex2	F6Pp #ABCDEF		TPp #CBA	TPp #DEF	Plastidic Fru-6-P → triose-P/ PEP interconversion
Vphex3	TPp #ABC		PYRp #ABC		Plastidic pyruvate kinase
//Cytosolic pentose-P pathway					
VcPPP1	G6P #ABCDEF		CO2 #A	P5Pp #BCDEF	Cytosolic pentose-P pathway - oxidative steps
//Plastidic pentose-P pathway					
Vpppp1	G6Pp #ABCDEF		CO2 #A	P5Pp #BCDEF	Plastidic pentose phosphate pathway - oxidative steps
Vpppp2a	P5Pp #abcde	TKC2p #AB	S7Pp #ABabcde		Plastidic transketolase - C7/C5 conversion
Vpppp2b	E4Pp #abcd	TKC2p #AB	F6Pp #ABabcd		Plastidic transketolase - C6/C4 conversion
Vpppp2c	P5Pp #ABCDE		TPp #CDE	TKC2p #AB	Plastidic transketolase - C5/C3 conversion
Vpppp3a	S7Pp		E4Pp	TAC3p	Plastidic transaldolase -

	#ABCDEFGF		#DEFG	#ABC	C7/C4 conversion
<i>Vpppp3b</i>	TPp	TAC3p	F6Pp		Plastidic transaldolase -
	#abc	#ABC	#ABCabc		C6/C3 conversion
//Cytosol-plastid exchange					
<i>Vcmex</i>	PYRc		PYRm		Pyruvate uptake by mitochondria
	#ABC		#ABC		
<i>Vcpex</i>	PYRc		PYRp		Pyruvate uptake by plastids
	#ABC		#ABC		
<i>Vgpt</i>	G6P		G6Pp		Plastidic Glc-6-P/Pi translocator
	#ABCDEF		#ABCDEF		
<i>Vtpt</i>	TP		TPp		Plastidic triose-P/Pi & PEP/Pi translocators
	#ABC		#ABC		
// TCA cycle					
<i>Vtca1</i>	PYRm		CO2	AcCoA	Mitochondrial pyruvate dehydrogenase
	#ABC		#A	#BC	
<i>Vtca2</i>	AcCoA	OAA	CIT		Citrate synthase
	#AB	#abcd	#dcbBAa		
<i>Vtca3</i>	CIT		CO2	AKG	Aconitase/isocitrate dehydrogenase
	#ABCDEF		#F	#ABCDE	
<i>Vtca4</i>	AKG		CO2	SUCC	2-Oxoglutarate → succinate
	#ABCDE		#A	#BCDE	
<i>Vtca5</i>	SUCC		FUM		Succinate → fumarate conversion
	#ABCD		#ABCD		
<i>Vtca6a</i>	FUM		OAA		Malate and OAA considered as a single pool,
	#ABCD		#ABCD		randomisation by fumarase
<i>Vtca6b</i>	FUM		OAA		
	#ABCD		#DCBA		
//Anaplerotic reactions					
<i>Vana1</i>	TP	CO2	OAA		PEP carboxylase
	#ABC	#a	#ABCa		
<i>Vana2</i>	OAA		CO2	PYRm	Mitochondrial malic enzyme
	#ABCD		#D	#ABC	
<i>Vana3</i>	OAA		PYRp	CO2	Plastidic malic enzyme
	#ABCD		#ABC	#D	
//Other intermediary reactions					
<i>Vpdhp</i>	PYRp		CO2	AcCoAp	Plastidic pyruvate dehydrogenase
	#ABC		#A	#BC	
<i>Vthrox</i>	THR		GLY	AcCoA	Threonine aldolase
	#ABCD		#AB	#CD	
<i>Vgly</i>	SER		GLY	CX	Serine to glycine
	#ABC		#AB	#C	
<i>Vgly1</i>	GLY		CO2	CX	Glycine decarboxylase
	#AB		#A	#B	
// Fatty acid, glycerol and ethanol synthesis					
<i>Vfas1</i>	AcCoAp		AcCoAeff		Fatty acid OUT
	#AB		#AB		

Vfas2	TP #ABC	G3P #ABC		Glycerol OUT
Vadh	PYRc #ABC	EtOH #BC	CO2 #A	
Vadheff	EtOH #AB	EtOH_out #AB		Ethanol OUT
//Carbohydrate accumulation				
Vgsuc	G6P #ABCDEF	GSUC #ABCDEF		Sucrose_glucosyl OUT
Vgsuceff	GSUC #ABCDEF	G6Peff #ABCDEF		Sucrose_fructosyl OUT
Vfsuc	F6P #ABCDEF	FSUC #ABCDEF		
Vfsuceff	FSUC #ABCDEF	F6Peff #ABCDEF		
Vstsp	G6Pp #ABCDEF	STA #ABCDEF		Starch OUT
Vsta	STA #ABCDEF	STAEff #ABCDEF		
Vwall	G6P #ABCDEF	WALL #ABCDEF		Cell wall OUT
Vpentan	G6P #ABCDEF	PENTAN #ABCDE	CO2 #F	
Vpentaneff	PENTAN #ABCDE	PENTANeff #ABCDE		
//CO ₂ and MTHF outputs				
Vco2out	CO2 #A	CO2eff #A		CO ₂ OUT
Vcxout	CX #A	CXeff #A		Methylene tetrahydrofolate OUT
//TCA cycle efflux				
VcitOUT	CIT #ABCDEF	CITeff #ABCDEF		Citrate OUT
VsuccOUT	SUCC #ABCD	SUCCeff #ABCD		Succinate OUT
VmalOUT	OAA #ABCD	MALeff #ABCD		Malate OUT
Vgabaeff	AKG #ABCDE	GABA #EDCB	CO2 #A	
VgabaOUT	GABA #ABCD	GABAEff #ABCD		GABA OUT
//Amino acid metabolism and outputs				
Vglu	AKG #ABCDE	GLU #ABCDE		
Vglueff	GLU #ABCDE	GLUEff #ABCDE		Glutamate+Glutamine +Proline OUT

Vasp	OAA		ASP		
	#ABCD		#ABCD		
Vaspeff	ASP		ASPeff		Aspartate OUT
	#ABCD		#ABCD		
Varg	AKG	CO2	ARG		
	#ABCDE	#a	#ABCDEa		
Vargeff	ARG		ARGeff		Arginine OUT
	#ABCDEF		#ABCDEF		
Vasp_arg	ASP		FUM		
	#ABCD		#ABCD		
Vser	TPp		SER		
	#ABC		#ABC		
Vcys	SER		CYS		
	#ABC		#ABC		
Vcyseff	CYS		CYSeff		Cystine OUT
	#ABC		#ABC		
Vglyeff	GLY		GLYeff		Glycine OUT
	#AB		#AB		
Vala	PYRc		ALA		
	#ABC		#ABC		
Valaeff	ALA		ALAEff		Alanine OUT
	#ABC		#ABC		
Varo1	E4Pp	TPp	ARO		
	#ABCD	#abc	#abcABCD		
Varo2	E4Pp	TPp	ARO		
	#ABCD	#abc	#abDCBAC		
Vleu1	PYRp	PYRp	ISOVAL	CO2	
	#ABC	#abc	#abBCc	#A	
Vleu	ISOVAL	AcCoAp	LEU	CO2	
	#ABCDE	#ab	#abBCDE	#A	
Vleueff	LEU		LEUeff		Leucine OUT
	#ABCDEF		#ABCDEF		
Vval	ISOVAL		VAL		
	#ABCDE		#ABCDE		
Vvaleff	VAL		VALeff		Valine OUT
	#ABCDE		#ABCDE		
Vmet	ASP	CX	MET		
	#ABCD	#a	#ABCDa		
Vmeteff	MET		METeff		Methionine OUT
	#ABCDE		#ABCDE		
Vthr	ASP		THR		
	#ABCD		#ABCD		
Vthreff	THR		THReff		Threonine OUT
	#ABCD		#ABCD		
Vile	PYRp	THR	ILE	CO2	
	#ABC	#abcd	#abBcdC	#A	

Vileff	ILE		ILEeff		Isoleucine OUT
	#ABCDEF		#ABCDEF		
Vphe_tyr	ARO	TPp	PHE_TYR	CO2	
	#ABCDEFG	#abc	#abcBCDEFG	#A	
Vphe_tyreff	PHE_TYR		PHE_TYReff		Phenylalanine and Tyrosine OUT
	#ABCDEFGHI		#ABCDEFGHI		
Vlys	OAA	PYRp	LYS	CO2	
	#ABCD	#abc	#ABCDcb	#a	
Vlys1	OAA	PYRp	LYS	CO2	
	#ABCD	#abc	#abcDCB	#A	
Vlyseff	LYS		LYSeff		Lysine OUT
	#ABCDEF		#ABCDEF		
Vhis	P5Pp	CX	HIS		
	#ABCDE	#a	#EDCBAA		
Vhiseff	HIS		HISeff		Histidine OUT
	#ABCDEF		#ABCDEF		
// Tryptophan synthesis: fragments are considered separately to minimize the number of cumomer groups used in calculations					
Vtrp2ca	P5Pp		TPp	CCa	
	#ABCDE		#CDE	#AB	
Vtrp2caeff	CCa		CCaeff		Tryptophan 2C OUT
	#AB		#AB		
Vtrp2cb	TPp		CO2	CCb	
	#ABC		#A	#BC	
Vtrp2cbef	CCb		CCbeff		Tryptophan 2C OUT
	#AB		#AB		
Vtrp3c_sereff	SER		SEReff		Tryptophan + serine OUT
	#ABC		#ABC		
Vtrp4c	E4Pp		E4Ppeff		Tryptophan 4C OUT
	#ABCD		#ABCD		
//Additional proxy reactions (See text for explanation)					
Vserin	AA3Cex		SEReff		Pre-existing serine at natural abundance
	#ABC		#ABC		
Vserprotout	SEReff		SERProt		
	#ABC		#ABC		
Vglyin	AA2Cex		GLYeff		Pre-existing glycine at natural abundance
	#AB		#AB		
Vglyprotout	GLYeff		GLYProt		
	#AB		#AB		
Vargin	AA6Cex		ARGeff		Pre-existing arginine at natural abundance
	#ABCDEF		#ABCDEF		
Vargprotout	ARGeff		ARGProt		
	#ABCDEF		#ABCDEF		
Vmetin	AA5Cex		METeff		Pre-existing methionine at natural abundance
	#ABCDE		#ABCDE		
Vmetprotout	METeff		METProt		

	#ABCDE	#ABCDE	
Vhisin	AA6Cex	HISeff	Pre-existing histidine at
	#ABCDE	#ABCDE	natural abundance
Vhisprotout	HISeff	HISProt	
	#ABCDE	#ABCDE	

Subnetwork 2

// Metabolic Input

V2upt2	GLC_2	GLCext_2	Uptake of [2- ¹³ C]glucose
	#ABCDE	#ABCDE	
V2upt0	GLC_0	GLCext_2	Uptake of natural
	#ABCDE	#ABCDE	abundance glucose
V2upt	GLCext_2	G6P_2	
	#ABCDE	#ABCDE	

The remainder of reactions in subnetwork 2 are the same as those defined in subnetwork 1, with the exception that all fluxes begin with the prefix V2 and all metabolites end with suffix _2

Subnetwork 3

// Metabolic Input

V3uptU	GLC_U	GLCext_3	Uptake of [¹³ C ₆]glucose
	#ABCDE	#ABCDE	
V3upt0	GLC_0	GLCext_3	Uptake of natural
	#ABCDE	#ABCDE	abundance glucose
V3upt	GLCext_3	G6P_3	
	#ABCDE	#ABCDE	

The remainder of reactions in subnetwork 3 are the same as those defined in subnetwork 1, with the exception that all fluxes begin with the prefix V3 and all metabolites end with suffix _3

Table S9. Summary of flux constraints used in modelling the redistribution of label through the reaction network of heterotrophic carbon metabolism in Arabidopsis cultures

The reactions are defined in Table S8. The flux constraints are: F, free flux – varied during the optimisation to provide the best fit to the experimental isotopomer values; C, constrained flux – a net flux set to the value determined from measurement of output fluxes or an exchange flux (indicated by *) set to zero by the thermodynamic constraints of the reaction; D, dependent flux – fixed by the values of free and constrained fluxes, the stoichiometric relationships of the network and defined reaction equality relationships. All input and output fluxes in the network are irreversible by definition and the exchange flux of each (indicated by †) is set to zero. Fluxes indicated D‡ in subnetworks 2 and 3 are set to be equal to the flux of the corresponding reaction in subnetwork 1. In the model of Pi- cells, net flux through *Vupt* was set as F in subnetwork 1 and D‡ in the other two subnetworks to allow the proportion of glucose converted to biosynthetic products to be varied.

Reaction	Flux constraint					
	Subnetwork 1		Subnetwork 2		Subnetwork 3	
	Net	Exchange	Net	Exchange	Net	Exchange
<i>Vupt1</i>	F	D†	F	D†	F	D†
<i>Vupt0</i>	D	D†	D	D†	D	D†
<i>Vupt</i>	C	C*	C	C*	C	C*
<i>Vco2in</i>	F	D†	D‡	D†	D‡	D†
<i>Vcxin</i>	F	D†	D‡	D†	D‡	D†
<i>Vchex1</i>	F	F	D‡	D‡	D‡	D‡
<i>Vchex2</i>	D	F	D	D‡	D	D‡
<i>Vchex3</i>	D	C*	D	C*	D	C*
<i>Vphex1</i>	D	F	D	D‡	D	D‡
<i>Vphex2</i>	D	C*	D	C*	D	C*
<i>Vphex3</i>	F	C*	D‡	C*	D‡	C*
<i>VcPPP1</i>	F	C*	D‡	C*	D‡	C*
<i>Vpppp1</i>	F	C*	D‡	C*	D‡	C*
<i>Vpppp2a</i>	D	F	D	D‡	D	D‡
<i>Vpppp2b</i>	D	F	D	D‡	D	D‡
<i>Vpppp2c</i>	D	F	D	D‡	D	D‡
<i>Vpppp3a</i>	D	F	D	D‡	D	D‡
<i>Vpppp3b</i>	D	F	D	D‡	D	D‡
<i>Vcmex</i>	D	C*	D	C*	D	C*
<i>Vcpex</i>	F	C*	D‡	C*	D‡	C*
<i>Vgpt</i>	D	F	D	D‡	D	D‡
<i>Vtpt</i>	D	F	D	D‡	D	D‡
<i>Vtca1</i>	D	C*	D	C*	D	C*
<i>Vtca2</i>	D	C*	D	C*	D	C*
<i>Vtca3</i>	D	C*	D	C*	D	C*
<i>Vtca4</i>	D	C*	D	C*	D	C*
<i>Vtca5</i>	D	C*	D	C*	D	C*

<i>Vtca6a</i>	D	F	D	D‡	D	D‡
<i>Vtca6b</i>	D	D	D	D	D	D
<i>Vana1</i>	D	F	D	D‡	D	D‡
<i>Vana2</i>	F	C*	D‡	C*	D‡	C*
<i>Vana3</i>	D	C*	D	C*	D	C*
<i>Vpdhp</i>	D	C*	D	C*	D	C*
<i>Vthrox</i>	F	F	D‡	D‡	D‡	D‡
<i>Vgly</i>	D	F	D	D‡	D	D‡
<i>Vgly1</i>	F	F	D‡	D‡	D‡	D‡
<i>Vfas1</i>	C	D†	C	D†	C	D†
<i>Vfas2</i>	C	D†	C	D†	C	D†
<i>Vadh</i>	D	C*	D	C*	D	C*
<i>Vadheff</i>	C	D†	C	D†	C	D†
<i>Vgsuc</i>	C	C*	C	C*	C	C*
<i>Vgsuceff</i>	D	D†	D	D†	D	D†
<i>Vfsuc</i>	D	C*	D	C*	D	C*
<i>Vfsuceff</i>	D	D†	D	D†	D	D†
<i>Vstsp</i>	D	C*	D	C*	D	C*
<i>Vsta</i>	C	D†	C	D†	C	D†
<i>Vwall</i>	C	D†	C	D†	C	D†
<i>Vpentan</i>	D	C*	D	C*	D	C*
<i>Vpentaneff</i>	C	D†	C	D†	C	D†
<i>Vco2out</i>	D	D†	D	D†	D	D†
<i>Vcxout</i>	D	D†	D	D†	D	D†
<i>VcitOUT</i>	C	D†	C	D†	C	D†
<i>VsuccOUT</i>	C	D†	C	D†	C	D†
<i>VmalOUT</i>	C	D†	C	D†	C	D†
<i>Vgabaeff</i>	D	C*	D	C*	D	C*
<i>VgabaOUT</i>	C	D†	C	D†	C	D†
<i>Vglu</i>	D	F	D	D‡	D	D‡
<i>Vglueff</i>	C	D†	C	D†	C	D†
<i>Vasp</i>	D	C*	D	C*	D	C*
<i>Vaspeff</i>	C	D†	C	D†	C	D†
<i>Varg</i>	D	C*	D	C*	D	C*
<i>Vargeff</i>	D	C*	D	C*	D	C*
<i>Vasp_arg</i>	D	C*	D	C*	D	C*
<i>Vser</i>	D	C*	D	C*	D	C*
<i>Vcys</i>	D	C*	D	C*	D	C*
<i>Vcyseff</i>	C	D†	C	D†	C	D†
<i>Vglyeff</i>	D	C*	D	C*	D	C*
<i>Vala</i>	D	F	D	D‡	D	D‡
<i>Valaeff</i>	C	D†	C	D†	C	D†
<i>Varol</i>	D	C*	D	C*	D	C*

<i>Varo2</i>	D	C*	D	C*	D	C*
<i>Vleu1</i>	D	C*	D	C*	D	C*
<i>Vleu</i>	D	C*	D	C*	D	C*
<i>Vleueff</i>	C	D†	C	D†	C	D†
<i>Vval</i>	D	C*	D	C*	D	C*
<i>Vvaleff</i>	C	D†	C	D†	C	D†
<i>Vmet</i>	D	C*	D	C*	D	C*
<i>Vmeteff</i>	D	C*	D	C*	D	C*
<i>Vthr</i>	D	F	D	D‡	D	D‡
<i>Vthreff</i>	C	D†	C	D†	C	D†
<i>Vile</i>	D	C*	D	C*	D	C*
<i>Vileeff</i>	C	D†	C	D†	C	D†
<i>Vphe_tyr</i>	D	C*	D	C*	D	C*
<i>Vphe_tyreff</i>	C	D†	C	D†	C	D†
<i>Vlys</i>	D	C*	D	C*	D	C*
<i>Vlys1</i>	F	C*	D‡	C*	D‡	C*
<i>Vlyseff</i>	C	D†	C	D†	C	D†
<i>Vhis</i>	D	C*	D	C*	D	C*
<i>Vhiseff</i>	D	C*	D	C*	D	C*
<i>Vtrp2ca</i>	D	C*	D	C*	D	C*
<i>Vtrp2caeff</i>	C	D†	C	D†	C	D†
<i>Vtrp2cb</i>	D	C*	D	C*	D	C*
<i>Vtrp2cbef</i>	C	D†	C	D†	C	D†
<i>Vtrp3c_sereff</i>	D	C*	D	C*	D	C*
<i>Vtrp4c</i>	C	D†	C	D†	C	D†
<i>Vserin</i>	F	D†	D‡	D†	D‡	D†
<i>Vserprotout</i>	D	D†	D	D†	D	D†
<i>Vglyin</i>	F	D†	D‡	D†	D‡	D†
<i>Vglyprotout</i>	D	D†	D	D†	D	D†
<i>Vargin</i>	F	D†	D‡	D†	D‡	D†
<i>Vargprotout</i>	D	D†	D	D†	D	D†
<i>Vmetin</i>	F	D†	D‡	D†	D‡	D†
<i>Vmetprotout</i>	D	D†	D	D†	D	D†
<i>Vhisin</i>	F	D†	D‡	D†	D‡	D†
<i>Vhisprotout</i>	D	D†	D	D†	D	D†

Network summary

Flux category	Number of reactions		
	Net	Exchange	Total
Free	19	18	37
Constrained	75	135	210
Dependent	221	162	383

Table S10. Fluxes through the central network of heterotrophic carbon metabolism in Arabidopsis cell suspension cultures grown with differing Pi supply

Absolute fluxes are calculated from the best fit estimates (Table 2) and the measured rate of glucose uptake. Net fluxes are the best fit flux estimates \pm SD as determined by the *EstimateStat* tool in 13C-FLUX. Exchange fluxes are the best fit flux estimates (and asymmetric 68% confidence limits) obtained from the optimum normalized exchange flux \pm SD determined after hyperbolic transformation. Italicised values in parentheses are the 95% confidence limits of free fluxes obtained by non-linearised statistical analysis after appropriate transformation. “Ind” indicates an indeterminable exchange flux for which the confidence interval spans the range 0 to ∞ , and for which the non-linear confidence interval was not determined (*nd*).

Reaction step(s)	Symbol	Absolute molar flux ($\mu\text{mol h}^{-1} \text{g}^{-1}$ fresh weight)								
		Pi- medium			MS medium			Pi+ medium		
Net fluxes										
Hexose/triose phosphate metabolism										
Glucose uptake	<i>upt</i>	1.23	±	0.19	3.85	±	0.36	7.27	±	0.36
Cytosolic phosphoglucose isomerase	<i>chex1</i>	-0.03	±	0.59	0.72	±	0.27	1.32	±	0.21
		(-0.09, 0.03)			(0.45, 1.00)			(0.76, 1.53)		
Cytosolic Fru-6-P → triose-P/PEP interconversion	<i>chex2</i>	-0.06	±	0.59	0.47	±	0.27	0.52	±	0.21
Cytosolic PEP → pyruvate	<i>chex3</i>	1.75	±	0.08	3.89	±	0.09	5.73	±	0.17
Plastidic phosphoglucose isomerase	<i>phex1</i>	1.03	±	0.60	1.37	±	0.23	2.41	±	0.15
Plastidic Fru-6-P → triose-P/PEP interconversion	<i>phex2</i>	1.12	±	0.59	2.07	±	0.25	3.54	±	0.19
Plastidic PEP → pyruvate	<i>phex3</i>	0.00	±	0.02	0.18	±	0.07	0.65	±	0.12
		(0, 0)			(0.10, 0.26)			(0.47, 0.65)		
Pentose phosphate pathway										
Cytosolic pentose phosphate pathway - oxidative steps	<i>cppp1</i>	0.00	±	0.12	0.50	±	0.25	1.76	±	0.11
		(0, 0.15)			(0.22, 0.85)			(1.31, 1.78)		

Plastidic pentose phosphate pathway - oxidative steps	<i>pppp1</i>	0.15 ± 0.05 (0.11, 0.15)	0.60 ± 0.32 (0.20, 0.92)	0.00 ± 0.15 (0, 0.51)
Plastidic transketolase - C7/C5 conversion	<i>pppp2a</i>	0.05 ± 0.02	0.37 ± 0.03	0.60 ± 0.04
Plastidic transketolase - C6/C4 conversion	<i>pppp2b</i>	0.04 ± 0.02	0.33 ± 0.03	0.54 ± 0.04
Plastidic transketolase - C5/C3 conversion	<i>pppp2c</i>	0.09 ± 0.03	0.70 ± 0.05	1.13 ± 0.07
Plastidic transaldolase - C7/C4 conversion	<i>pppp3a</i>	0.05 ± 0.02	0.37 ± 0.03	0.60 ± 0.04
Plastidic transaldolase - C6/C3 conversion	<i>pppp3b</i>	0.05 ± 0.02	0.37 ± 0.03	0.60 ± 0.04
Transporters/exchanges				
Pyruvate uptake by mitochondria	<i>cmex</i>	1.69 ± 0.07	3.28 ± 0.05	4.78 ± 0.12
Pyruvate uptake by plastids	<i>cpex</i>	0.04 ± 0.02 (0.04, 0.04)	0.21 ± 0.08 (0.15, 0.29)	0.34 ± 0.12 (0.19, 0.38)
Plastidic Glc-6-P/Pi translocator	<i>gpt</i>	1.20 ± 0.61	2.23 ± 0.43	2.86 ± 0.17
Plastidic triose-P/Pi & PEP/Pi translocators	<i>tpt</i>	-2.24 ± 1.18	-3.97 ± 0.54	-6.51 ± 0.39
Tricarboxylic acid cycle				
Mitochondrial pyruvate dehydrogenase	<i>tca1</i>	1.89 ± 0.03	3.31 ± 0.03	4.78 ± 0.04
Citrate synthase	<i>tca2</i>	1.89 ± 0.03	3.31 ± 0.03	4.78 ± 0.04
Aconitase/isocitrate dehydrogenase	<i>tca3</i>	1.88 ± 0.03	3.20 ± 0.03	4.67 ± 0.04
2-oxoglutarate → Succinate	<i>tca4</i>	1.76 ± 0.03	2.69 ± 0.03	3.90 ± 0.04
Succinate → fumarate conversion	<i>tca5</i>	1.75 ± 0.03	2.65 ± 0.03	3.55 ± 0.04
Fumarase	<i>tca6a+b</i>	1.76 ± 0.03	2.66 ± 0.03	3.58 ± 0.04
Anaplerotic fluxes				
PEP carboxylase	<i>ana1</i>	0.37 ± 0.07	1.00 ± 0.06	1.79 ± 0.12
Mitochondrial malic enzyme	<i>ana2</i>	0.20 ± 0.07 (0.17, 0.24)	0.03 ± 0.06 (0, 0.08)	0.00 ± 0.12 (0, 0.19)
Plastidic malic enzyme	<i>ana3</i>	0.00 ± 0.00	0.03 ± 0.01	0.05 ± 0.01
Net CO ₂ respired		5.58 ± 0.23	9.91 ± 0.64	14.62 ± 0.44

Normalised exchange fluxes					
Cytosolic phosphoglucose isomerase	<i>chex1</i>	121.69 (39.74, ∞) (19.26, 121.60)	46.75 (36.21, 64.82) (31.11, 92.28)	77.25 (54.85, 124.88) (41.19, 719.56)	
Cytosolic Fru-6-P \rightarrow triose-P/PEP interconversion	<i>chex2</i>	0.80 (0.49, 1.24) (0.66, 0.98)	2.74 (2.67, 2.81) (2.60, 2.84)	3.07 (2.88, 3.27) (2.55, 3.27)	
Plastidic phosphoglucose isomerase	<i>phex1</i>	2.67 (2.35, 3.05) (2.28, 2.87)	7.14 (5.01, 10.61) (4.51, 16.39)	6.04 (4.27, 8.46) (0, 10.03)	
Plastidic transketolase - C7/C5 conversion	<i>pppp2a</i>	Ind (nd)	Ind (nd)	Ind (nd)	
Plastidic transketolase - C6/C4 conversion	<i>pppp2b</i>	2.13 (1.91, 2.38) (1.92, 2.29)	0.57 (0.51, 0.64) (0.38, 0.70)	0.00 (0, 0.07) (0, 0)	
Plastidic transketolase - C5/C3 conversion	<i>pppp2c</i>	0.59 (0.52, 0.66) (0.49, 0.70)	1.31 (1.23, 1.39) (1.15, 1.42)	1.62 (1.50, 1.74) (1.49, 1.70)	
Plastidic transaldolase - C7/C4 conversion	<i>pppp3a</i>	Ind (nd)	Ind (nd)	Ind (nd)	
Plastidic transaldolase - C6/C3 conversion	<i>pppp3b</i>	4.28 (3.52, 5.34) (3.69, 5.24)	0.04 (0, 0.09) (0, 0.12)	1.18 (1.03, 1.34) (0.81, 1.82)	
Plastidic Glc-6-P/Pi translocator	<i>gpt</i>	12.13 (9.46, 16.58) (8.23, 26.09)	1.23 (0.96, 1.53) (0.79, 1.89)	1.86 (1.21, 2.62) (0, 2.49)	
Plastidic triose-P/Pi & PEP/Pi translocators	<i>tpt</i>	0.00 (0, 32.91) (0, 0.36)	0.32 (0, 1.34) (0, 1.65)	0.63 (0, 2.28) (0, 16.96)	
Fumarase	<i>tca6</i>	63.46 (19.96, ∞) (9.95, 121.69)	56.23 (31.76, 188.41) (21.79, 380.66)	28.71 (20.37, 44.28) (11.86, 719.56)	
PEP carboxylase/carboxykinase	<i>ana1</i>	0.10 (0.08, 0.12) (0.07, 0.13)	0.10 (0.08, 0.11) (0.07, 0.14)	0.16 (0.10, 0.22) (0.08, 0.33)	

Table S11. Influence of Pi supply on adenylate and coenzyme balance of metabolism in Arabidopsis cultures expressed as absolute flux values

ATP, NADH and NADPH requirements for biosynthesis, expressed as mean values \pm SE, and the rates of ATP and coenzyme generation by the metabolic network were determined from net fluxes between network intermediates in the best-fit flux solutions as detailed in the paper (Table 4). Separate estimates assume conversion of isocitrate to 2-oxoglutarate via either NAD- or NADP-dependent isocitrate dehydrogenase (ICDH). Values for ATP generation: ^a based on production via substrate level phosphorylation only; ^b calculated assuming that NADH not required for biosynthesis generates 2.5 ATP/NADH. In these calculations FADH₂ is taken to be equivalent to 0.6 NADH. All values are absolute molar fluxes expressed per unit fresh mass of cell culture.

Metabolite	Absolute flux ($\mu\text{mol h}^{-1} \text{g}^{-1}$ fresh weight)			
	Requirement for biomass production		Generated by network including:	
			NAD-ICDH	NADP-ICDH
Pi- medium				
ATP	0.75	\pm 0.01	3.30 ^a /33.76 ^b	3.30 ^a /29.11 ^b
NADH	0.10	\pm 0.01	12.38	10.42
NADPH	0.56	\pm 0.01	0.29	2.15
MS medium				
ATP	4.26	\pm 0.26	5.45 ^a /59.69 ^b	5.45 ^a /51.69 ^b
NADH	0.94	\pm 0.07	22.63	19.43
NADPH	4.53	\pm 0.26	2.21	5.41
Pi+ medium				
ATP	8.54	\pm 0.52	7.312 ^a /89.49 ^b	7.312 ^a /77.45 ^b
NADH	1.77	\pm 0.26	34.64	29.82
NADPH	7.78	\pm 0.89	3.68	8.50

Method S1. Metabolomic analysis of cell culture extracts by ^1H -NMR

Cells were harvested from the cultures by filtration, then frozen in liquid nitrogen and extracted in chloroform:methanol as described by Masakapalli *et al.* (2010). The aqueous methanol fraction obtained following phase separation was evaporated to dryness and reconstituted in 0.9 ml of 25 mM sodium phosphate buffer (pH 7.5) in D_2O containing of 1 μmol TSP (sodium 3-(trimethylsilyl)propionate-2,2,3,3- d_4 (Sigma-Aldrich)) as a spectroscopic reference.

^1H -NMR spectra of the cell extracts were recorded at 20°C on a Varian Unity Inova 600 spectrometer (Varian Inc., Palo Alto, USA) using a 5-mm diameter $^1\text{H}\{^{13}\text{C}/^{15}\text{N}\}$ triple resonance probe, a 90° pulse angle, a 6000 Hz spectral width, a 2 s relaxation delay (including a 1.98 s water suppression pulse), a 4 s acquisition time, and 256 transients per sample. Free induction decays were processed with a 1 Hz line broadening using Nuts for Windows (Acorn NMR Inc., Livermore, CA, USA). ^1H NMR chemical shifts in the spectra were referenced to the TSP signal at 0.00 ppm.

NMR spectra were converted to numerical values and stored as ASCII files using the histogram routine in Nuts. The -0.39 to 9 ppm region of each spectrum was reduced to a set of bins at 0.01 ppm resolution, each bin corresponding to 16 data points. The bins for TSP (-0.01 – 0.01 ppm) and water (4.61 – 4.96 ppm) signals were removed, and the values for the remaining 902 bins were normalised relative to their summed value.

Multivariate analysis of binned spectral data was conducted as described by Kruger *et al.* (2008) using Simca-P 11.5 (Umetrics, Umeå, Sweden). All data were mean-centred and Pareto scaled prior to analysis (van den Berg *et al.*, 2006; Craig *et al.*, 2006). No anomalous samples were identified in an initial comparison of the dataset by principal component analysis (Fig. 2 in paper). The contributions of spectral signals to discrimination between cell cultures grown in different amounts of Pi were determined by orthogonal partial least squares projection of latent structures-discriminant analysis (OPLS-DA) using the procedures described by Eriksson *et al.* (2006). The potential for over-fitting the data (Broadhurst and Kell, 2006) was assessed by jackknife cross-validation testing (Wiklund *et al.*, 2008) and response permutation analysis (Lindgren *et al.*, 1996). The significance of the contribution of spectral signals to prediction of class assignment was assessed by considering both the covariance and the correlation loading profiles (Wiklund *et al.*, 2008) which were visualised graphically as described in Kruger *et al.* (2008). The covariance loading, which provides an estimate of the magnitude of the contribution of the spectral signal to class assignment, was provided by the loading value for the first (predictive) component of the OPLS-DA and its robustness was indicated by the standard error determined from cross-validation analysis. The latter was used to calculate the jackknifed 95% confidence interval, and only signals for which this interval excludes zero were considered significant. The correlation loading provides an indication of the reliability of the particular spectral signal in classification and is defined by the Pearson correlation coefficient (r) between spectral bin intensity and class assignment. Spectral regions with r values greater than ± 0.8 were considered highly reliable.

Appendix S1. References for Supporting Information

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