



Supporting Online Material for

**Multiple High-Throughput Analyses Monitor  
the Response of *E. coli* to Perturbations**

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## Materials and Methods

**Strains and culture.** *E. coli* K-12 strain BW25113 (*lacI<sup>q</sup> rrnB<sub>T14</sub> ΔlacZ<sub>WJ16</sub> hsdR514 ΔaraBAD<sub>AH33</sub> ΔrhaBAD<sub>LD78</sub>*) (1) (wild-type) and single open reading frame (ORF) knockout strains from the Keio collection (2) were used in this study. Glucose-limited chemostat cultures were grown using a synthetic medium (48 mM Na<sub>2</sub>HPO<sub>4</sub>, 22 mM KH<sub>2</sub>PO<sub>4</sub>, 10 mM NaCl, 45 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 4 g/l glucose), supplemented with 1 mM MgSO<sub>4</sub>, 1 mg/l thiamin·HCl, 5.6 mg/l CaCl<sub>2</sub>, 8 mg/l FeCl<sub>3</sub>, 1 mg/l MnCl<sub>2</sub>·4H<sub>2</sub>O, 1.7 mg/l ZnCl<sub>2</sub>, 0.43 mg/l CuCl<sub>2</sub>·2H<sub>2</sub>O, 0.6 mg/l CoCl<sub>2</sub>·2H<sub>2</sub>O and 0.6 mg/l Na<sub>2</sub>MoO<sub>4</sub>·2H<sub>2</sub>O. Cultures were grown aerobically at 37 °C in a total working volume of 1 l, in a 2-l jar fermentor (BMJ-PI; Able, Tokyo, Japan) equipped with pH, dissolved oxygen concentration and temperature sensors and a turbidity meter. The O<sub>2</sub> and CO<sub>2</sub> concentration in exhaust gas was monitored using Offgas Jar Jr. DEX-2562 (Able). The airflow rate was kept at 1 l/min and pH was maintained at 7.0 by automatic addition of HCl or NaOH for the duration of the culture. The dilution rate of the chemostat culture was set at 0.1, 0.2, 0.4, 0.5 or 0.7 h<sup>-1</sup> depending on the experiment. Samples for transcriptome, proteome and metabolome analysis were taken at the same time after five complete medium volume changes had taken place.

**Measurement of dry cell weight.** *E. coli* cells from 100 ml of culture were harvested by centrifugation and dried at 105 °C for 1-2 days. After confirming that the weight of the dried material was constant, the dry cell weight per liter of culture was calculated from the measured weight (Table S3).

**Transcriptome analysis.**

After collection, the culture sample was immediately mixed with RNAprotect Bacteria reagent (Qiagen) and stored at -80 °C until RNA extraction. Total RNA was extracted using the RNAeasy Midi kit (Qiagen) and treated with RNase free DNase I (Takara, Japan). For qRT-PCR, cDNA was synthesised using the ExScript RT reagent kit (Takara) using random hexamers as primers. qRT-PCR was performed using the SYBR Premix Taq (Takara) reagent mix and Opticon System (Bio-Rad). For each amplification, using a 96-well microtiter plate, standard DNA (a linearized plasmid DNA clone of the target gene (3)) and at least two independent reference samples (cDNAs from independent cultures of the wild-type at a dilution rate of 0.2 h<sup>-1</sup>) were amplified. Triplicate analysis of two independently synthesised cDNAs was performed for each analyzed sample. For data processing, the Ct value was transformed to copy number using standard DNA, and the average of six values was then normalized against the average value from the reference samples. To correct for the efficiency of cDNA synthesis, the relative value was then normalized against the median of all of the 85 transcript values for the sample. A specific amount of 16S rRNA was also examined as a control for total measurement and correction, and less than 2-fold changes were observed in all samples. To evaluate the absolute RNA amount, the average of the absolute copy number per microgram of total RNA was calculated from a total of 14 replicate measurements for the reference samples. Because more than half of the total cellular RNA is rRNA, the absolute copy number of 16S rRNA determined by qRT-PCR was compared with that calculated from the total RNA amount (determined by cellular component analysis), and this ratio was used to correct the amount of all the other RNAs. For this, we assumed that RNA extraction and cDNA conversion

efficiency were not significantly different between different RNAs. This was at least partially confirmed using spiked RNA and different primers for amplification.

For the microarray experiment, we followed the labelling, hybridization and detection method of Oshima *et al.* (4). Duplicate two-colour experiments were performed using Filgen array *E. coli* (Filgen, Aichi, Japan). cDNA from cultures of the wild-type at a dilution rate of  $0.2 \text{ h}^{-1}$  was used for control channel of all experiments. Data were normalized in accordance with the locally weighted scatterplot smoothing (LOWESS) method (5) using GeneSpring software (Agilent Technologies). Genes classified in bacterial chemotaxis and flagellar assembly in KEGG (6) pathways were omitted from further analysis, since highly frequent insertion of insertion sequence (IS) to the regulatory region of *fliD* causes unregulated expression of these genes (7), and we confirmed the occurrence of such a phenomenon at least in *rpiB*, *talB* and *gapC* disruptants and probably in some of the other disruptants.

### **Proteome analysis.**

**Absolute protein quantification.** To obtain absolute measurements of protein concentrations in complex samples we used a liquid chromatography / tandem mass spectrometry (LC-MS/MS) method that is a modification of previous work in absolute quantification making use of either external or internal standards with or without isotopically labelled synthetic peptides as standard (8-10). The main characteristics of the current approach are that it combines mass spectrometric analysis in the multiple reaction monitoring mode (MRM), for specific and sensitive quantification of target proteins, with the use of peptides derived from purified recombinant proteins as external calibrants.

To first optimize the MS settings and select MRM parameters, LC-MS/MS analysis of Lys-C (Wako, Osaka, Japan) digests of each purified recombinant target protein was performed essentially as previously described (11). Completion of digestion of both purified proteins and crude *E. coli* extracts was confirmed by measuring peptide yields with time and using different concentrations of Lys-C. LC-MS/MS analysis of peptides was performed on a QSTAR XL hybrid quadrupole time-of-flight instrument (AB/MDS-Sciex, Toronto, Canada) as previously described (11). Different fragmentation voltage settings were tested to optimize marker peptide detection. Peptides that were readily observable (excluding N-terminal and C-terminal peptides which contain extra amino acids originating from the recombinant protein expression vector) and whose precursor and product ion pair was computationally found to be unique in the *E. coli* proteome were used as protein-specific signals to quantify the corresponding endogenous protein target.

*E. coli* samples were cooled immediately on ice, washed twice by centrifugation with wash buffer (50 mM Tris-HCl, 50 mM NaCl, 1 mM EDTA, pH 7.0) and split into 1 ml aliquots. These were then centrifuged for 5 min at 5,000 g to collect cells, and pellets were stored at -80 °C. To quantify target proteins in experimental *E. coli* samples, two tubes of frozen cell pellets collected from a single sampling of a continuous culture were used. Peptide mixtures derived from Lys-C digestion of recombinant standard proteins or from total *E. coli* cell extracts were similarly separated by LC-MS/MS on a 1.5 mm × 50 mm C18 reversed-phase column at a flow rate of 0.2 ml/min. Peptides were eluted with a two-step gradient combination (1% to 40% acetonitrile over 50 min and up to 50% over the next 5 min) and the column eluent electrosprayed into the API 3000 (AB/MDS-Sciex) triple-quadrupole instrument for simultaneous monitoring of specific marker peptides for 68 different protein targets. MRM analysis was performed in positive mode with an ion-spray voltage of 5.5 kV and a monitoring time of 10 ms per peptide. To quantify proteins

accurately, the peak areas in extracted ion current chromatograms corresponding to target specific peptides were integrated automatically using the Analyst software (ver.1.4.1, AB/MDS-Sciex), followed by manual verification, and the results were used to calculate the absolute amount of protein in the cell extracts. Absolute intracellular concentrations of proteins were calculated using the measured dry cell weight per 1 ml of culture.

In order to validate the quantitation method, the reproducibility, linearity, and detection limit were investigated by MRM analysis of digests of 12 purified recombinant enzymes of the TCA cycle. The coefficient of variance (CV) values of repeatability ( $n = 6$ ) obtained with different preparations varied between 5.3 and 13.2% for peak areas. The calibration curves for all proteins were linear at 1, 5, 10, 50, 100, and 500 mg/l with correlation coefficients between 0.995 and 0.999 and the detection limit ranged from 0.6 to 112 nmol/l. We also validated this method using total *E. coli* cell extracts spiked with known amounts of purified recombinant enzymes to confirm the repeatability and the linearity. It is thus possible to quantify each target protein in an unknown sample by comparing the peak area with that of a known amount of the standard protein. In addition, for most targets the average of measurements derived from at least three different peptides per target protein was used for quantification, thus limiting the possibility of erroneous quantification due to peptide-specific suppression effects. Finally, the reliability of this quantitative method was verified and validated for 28 target proteins using conventional Western blot analysis or isotope-coded affinity tag (ICAT) method and the results were found to usually differ by less than 2-3 fold with these other methods, which can be considered reasonable since none of these methods can guarantee accurate results equally for all targets.

**Proteome analysis by 2D-DIGE.** Usually, two different samples of the same culture were collected from the steady-state culture, respectively 5 h before, and immediately before the addition of labelled glucose. Samples were processed as for absolute protein quantification. Analysis of protein samples by 2D-DIGE (GE Healthcare) was performed essentially in accordance with the manufacturer's instructions or as previously described (12). Briefly, frozen sample pellets were directly solubilised in isoelectrofocusing sample buffer containing urea and thio-urea and the protein concentration was measured using the Bio-Rad reagent. Solubilised protein samples (50 µg) were labelled with either cy3 (GE Healthcare) or cy5 (GE Healthcare) (200 pmol) and a pooled sample made up of an equal amount (25 µg each) of wild-type at a dilution rate of 0.2 h<sup>-1</sup> and test sample was labelled with cy2 (GE Healthcare) for use as an internal standard for accurate relative concentration measurements.

After two-dimensional electrophoresis, gels were scanned with a Typhoon scanner (GE Healthcare). Image analysis and protein spot selection were performed using Decyder software (GE Healthcare) using both the DIA and BVA modules. For all samples and reference gels (wild-type strain at 0.2 h<sup>-1</sup>), the internal standard spots were matched, and the relative signal intensities were used for calculating the average expression index. The automatic spot matching was manually verified to eliminate common false matches across images. A total of 2325 spots were thus matched (though their identity is unknown in most cases) and assumed to originate from the same protein. The relative spot intensities calculated using RF02 (see Table S2) as reference were exported using the XML export feature of the software.

For protein identification, a separate gel containing the same non-labeled samples (500  $\mu$ g) as used for DIGE was stained with SyproRuby (PerkinElmer). Spots displaying a greater than 2-fold intensity change and a Student t-test P-value smaller than 0.01 were selected for further analysis. The selected spots were picked using a robotic workstation and in-gel digested using a Millipore kit in accordance with the manufacturer's instructions. Recovered peptides were plated on a MALDI target plate and analyzed by mass spectrometry using an Agilent XCT MALDI-ion trap (Agilent Technologies, Inc.) or a Voyager-DE Pro MALDI-TOF mass spectrometer (ABI) operated in the positive mode. Raw data files were used to search an *E. coli* K-12 W3110-specific protein sequence database using MASCOT (Matrix Science) to identify proteins present in the sample. Additional technical details and notes and the results of the protein global expression analysis are available at the project web site <http://ecoli.iab.keio.ac.jp/>.

### **Metabolome analysis.**

**Sample preparation.** Sample preparation was performed in accordance with a previously published method (13).

**CE-TOFMS conditions for cationic metabolite analysis.** Separations were carried out in a fused silica capillary (50  $\mu$ m i.d.  $\times$  100 cm total length) filled with 1 M formic acid as the electrolyte (14). Approximately 3 nl of sample solution was injected at 50 mbar for 3 s and 30 kV of voltage was applied. The capillary temperature was maintained at 20°C and the sample tray was cooled below 5°C. A methanol-water mixture (50% v/v) containing 0.5



$\mu\text{M}$  reserpine was delivered as the sheath liquid at  $10\ \mu\text{l}/\text{min}$ . Electrospray ionization (ESI)-TOFMS was conducted in the positive ion mode and the capillary voltage was set at  $4,000\ \text{V}$ . A flow rate of heated dry nitrogen gas (heater temperature  $300^\circ\text{C}$ ) was maintained at  $10\ \text{psig}$ . The fragmentor, skimmer, and Oct RFV voltages were set at  $75\ \text{V}$ ,  $50\ \text{V}$ , and  $130\ \text{V}$ , respectively. Automatic recalibration of each acquired spectrum was performed using reference masses of reference standards. The methanol adduct ion ( $[\text{2MeOH}+\text{H}^2\text{O}+\text{H}]^+$ ,  $m/z\ 83.0703$ ) and reserpine ( $[\text{M}+\text{H}]^+$ ,  $m/z\ 609.2806$ ) provided the lock mass for exact mass measurements. Exact mass data were acquired at a rate of  $10\ \text{spectra/s}$  over a  $50\text{--}1,000\ m/z$  range.

**CE-TOFMS conditions for anionic metabolite analysis.** A cationic polymer-coated SMILE (+) capillary (15) (Nacalai Tesque, Kyoto, Japan) was used as the separation capillary (13). A  $50\ \text{mM}$  ammonium acetate solution ( $\text{pH}\ 8.5$ ) was used as the electrolyte solution for CE separation. Sample solution ( $30\ \text{nl}$ ) was injected at  $50\ \text{mbar}$  for  $30\ \text{s}$  and  $-30\ \text{kV}$  of voltage was applied. Ammonium acetate ( $5\ \text{mM}$ ) in a  $50\%$  methanol-water mixture ( $\text{v}/\text{v}$ ) containing  $20\ \mu\text{M}$  piperazine-1,4-bis(2-ethansulfonate) (PIPES) and  $1\ \mu\text{M}$  reserpine was delivered as the sheath liquid at  $10\ \mu\text{l}/\text{min}$ . ESI-TOFMS was conducted in the negative ion mode; the capillary voltage was set at  $3,500\ \text{V}$ . The fragmentor, skimmer, and Oct RFV voltages were set at  $100\ \text{V}$ ,  $50\ \text{V}$ , and  $200\ \text{V}$ , respectively. Automatic recalibration of each acquired spectrum was performed using the reference masses of standards, that is, divalent PIPES ( $[\text{M}-2\text{H}]^{2-}$ ,  $m/z\ 150.0230$ ), monovalent PIPES ( $[\text{M}-\text{H}]^-$ ,  $m/z\ 301.0534$ ), and reserpine ( $[\text{M}-\text{H}]^-$ ,  $m/z\ 607.2661$ ). Other conditions were identical to those used in cationic metabolite analysis.

**CE-MS conditions for nucleotide and CoA compound analysis.** Separations were carried out on a fused-silica capillary with 50  $\mu\text{m}$  i.d.  $\times$  100 cm total length. The electrolyte for the CE separation was 50 mM ammonium acetate solution (pH 7.5). Prior to first use, a new capillary was pre-treated for 20 min with preconditioning buffer: a 25 mM ammonium acetate–75 mM phosphate solution (pH 7.5). Before each injection, the capillary was equilibrated for 10 min by flushing with the preconditioning buffer, then for 6 min by flushing with the run electrolyte, which was replenished every run using a buffer replenishment system supplied with the Agilent CE. The sample was injected with a pressure injection of 50 mbar for 30 s (approximately 30 nl). The applied voltage was set at 30 kV and a pressure of 50 mbar was added to the inlet capillary during the run. The capillary temperature was thermostatted to 20°C and the sample tray was cooled below 5°C. The Agilent 1100 series pump equipped with a 1:100 splitter was used to deliver 10  $\mu\text{L}/\text{min}$  of 5 mM ammonium acetate in a 50 % (v/v) methanol-water mixture to the CE interface, where it was used as a sheath liquid around the outside of the CE capillary to provide a stable electrical connection between the tip of the capillary and the grounded electrospray needle. ESI-MS was conducted in the negative ion mode and the capillary voltage was set at 3500 V. The timetable of the pressure of heated dry nitrogen gas (heater temperature 300°C) was set to 0 psi at 0 min (sample injection time) and 10 psi after 0.1 min. Monovalent deprotonated  $[\text{M-H}]^-$  ions for nucleotides and nicotinamide-adenine dinucleotides and divalent deprotonated  $[\text{M-2H}]^{2-}$  ions for CoA compounds were monitored using the selective ion monitoring mode.

**Calculation of intracellular metabolite concentrations.** Metabolites were quantified using integrated peak areas obtained from measurements of chemical standards mixtures that were analyzed in parallel with experimental samples. The relative peak areas were used

to derive absolute concentration for compounds for which chemical standards were available after global normalization of signal intensities using internal standards spiked into both the chemical mixtures and the *E. coli* samples. The intracellular concentrations of metabolites were calculated using the measured dry cell weight per 1 ml of culture, the estimated weight of a single cell ( $2.80 \times 10^{-13}$  g) (16) and the estimated volume of a single cell ( $4.96 \times 10^{-16}$  l) (16).

### **Metabolic flux analysis.**

**$^{13}\text{C}$ -labeling experiment.** For metabolic flux analysis,  $^{13}\text{C}$ -labeling experiments were initiated after taking samples for transcriptome, proteome and metabolome analysis. For experiments with gene disruptants, the feed medium containing 4 g/l of natural glucose was replaced by an identical medium containing 0.4 g/l of [ $1\text{-}^{13}\text{C}$ ] glucose, 0.4 g/l of uniformly labeled [ $\text{U-}^{13}\text{C}$ ] glucose and 3.2 g/l of natural glucose. For experiments examining the effect of changes in dilution rate on flux distributions, the composition of glucose in the feed medium was changed to 0.8 g/l of [ $1\text{-}^{13}\text{C}$ ] glucose, 0.8 g/l of [ $\text{U-}^{13}\text{C}$ ] glucose and 2.4 g/l of natural glucose. After two residence times, for gas chromatography-mass spectrometry (GC-MS) analysis, *E. coli* cells were harvested by centrifugation.

**GC-MS analysis.** The cells obtained from about 250 ml of culture were suspended in 4 ml of 6 M HCl and then hydrolyzed at 105 °C for 16 h. After cooling, HCl was evaporated with a centrifugal evaporator (CVE-3100, Tokyo Rikakikai Co., Ltd., Japan). The dried hydrolysate was resuspended in water and then filtrated through a 0.22- $\mu\text{m}$  pore size filter (Millipore Co., USA). The filtrate was dried again and redissolved in 1.5 ml of acetonitrile.

For derivatization, the resulting 80  $\mu$ l of biomass hydrolysate dissolved in acetonitrile was mixed with an equal volume of *N*-methyl-*N*-(*tert*-butyldimethylsilyl)-trifluoroacetamide and then incubated at 110 °C for 30 min. After cooling, the derivatized sample was used for the GC-MS analysis using a TurboMass Gold mass spectrometer (Perkin Elmer, USA). In the present study, two fragment ions,  $[M-57]^+$  and  $[M-159]^+$ , of *tert*-butyldimethylsilylated (TBDMS-) amino acids (Ala, Gly, Val, Ile, Pro, Ser, Met, Phe, Asp, Glu and Tyr) were monitored. The analytical conditions for GC-MS were as described by Zhao et al (17).

**Measurement of extracellular metabolites concentration.** To determine the extracellular fluxes, the extracellular concentration of ethanol, lactate, acetate, formate, succinate, pyruvate, and glucose was measured using an enzymatic assay kit (F-kit, Roche Diagnostics).

**Estimation of metabolic flux distribution.** For metabolic flux analysis, we constructed a basic stoichiometric reaction model for the main metabolic pathways including glycolysis, the pentose phosphate pathway, the tricarboxylic acid (TCA) cycle, the glyoxylate shunt and the anaplerotic pathway (Fig. S2 and Table S4). For flux estimation in *pgi* and *gnd* mutants, the Entner-Doudoroff pathway was added to the above reaction model, according to a previous report demonstrating its activity in these mutants (18, 19). For flux estimation in *pgl*, *rpe*, *rpiA* and *tktA* mutants, the Entner-Doudoroff pathway was also added because large variations in expression data of *edd* and *eda* genes were observed for these strains (Table S7A) that may result in changes of activity of this pathway. Note that for flux estimation in the wild-type strain at dilution rates of 0.4, 0.5 and 0.7 h<sup>-1</sup>, the glyoxylate

shunt was omitted from above reaction model as its activity was previously shown to be negligible at such higher growth rates (20). The biomass content reported by Li et al. (21) was used for calculations.

The mass distributions of the measured proteinogenic amino acids were corrected, taking into account the natural isotope abundances of C, H, O, N, P, S, and Si atoms, according to the method reported by van Winden et al. (22). Additionally, to achieve isotopomeric steady state, further corrections in mass distributions was performed according to the method reported by Dauner et al. (23). For estimation of fluxes for reversible reactions, the concept of exchange coefficient (24) was adopted. For the mutants that do not have any known isozyme(s) corresponding to the disrupted enzyme, the flux for the reaction catalyzed by the disrupted enzyme was set to zero in advance. Note that *E. coli* does not have any isozymes for the Pgl protein that catalyzes the conversion of 6-phosphogluconolactone to 6-phosphogluconate, corresponding to reaction  $r_{11}$ , but this reaction is known to also proceed non-enzymatically (25). Therefore, the flux for  $r_{11}$  was defined as an induced variable for *pgl* disruptant. The free fluxes ( $r_8$ ,  $r_{26}$  and  $r_{28}$  for flux estimation in *pgi*, *gnd* and *rpe* disruptants,  $r_2$ ,  $r_8$ ,  $r_{26}$  and  $r_{28}$  for *pgl*, *rpiA* and *tktA* disruptants,  $r_8$  and  $r_{26}$  for *zwf* disruptant,  $r_2$  and  $r_8$  for wild-type cultured at 0.4, 0.5 and 0.7  $\text{h}^{-1}$ , and  $r_2$ ,  $r_8$  and  $r_{26}$  for wild-type cultured at 0.1 and 0.2  $\text{h}^{-1}$  and other disruptants) and seven exchange coefficients for  $r_2$ ,  $r_7$ ,  $r_{14}$ ,  $r_{15}$ ,  $r_{16}$ ,  $r_{23}$  and  $r_{24}$  were optimized by determining the mass distributions iteratively computed from the assumed flux as a best fit to the measured mass distributions of proteinogenic amino acids. The optimizing function ( $F$ ) to be minimized was defined as

$$F = \sum_{i=1}^N (MDV_i^{\text{measured}} - MDV_i^{\text{simulated}})^2$$

where  $MDV_i^{\text{measured}}$  represents the mass distribution vector of the measured  $i$ th amino acid,  $MDV_i^{\text{simulated}}$ , the mass distribution vector of the corresponding amino acid simulated from the estimated flux distribution and  $N$ , the number of measured proteinogenic amino acids. In the present study, a two-step optimization was implemented: the first step is a global search using a genetic algorithm (26) whereas the second step is a local search using sequential quadratic programming method (27). The overall flux distributions were calculated from the estimated free fluxes and exchange coefficients (Table S5A). For each flux or exchange coefficient of the reference sample (wild-type cells cultured at a specific growth rate of  $0.2 \text{ h}^{-1}$ ), the 90% confidence boundaries were calculated based on the average and standard deviation of the four samples (RF03, RF04, RF05 and RF06, see Table S2) (Table S5B).

All calculations were carried out using Matlab 7.1 (Mathworks Inc., USA) using the provided genetic algorithm and direct search toolbox 2.0 modules.

**Evaluation of calculated flux.** Scatter plots to compare mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (28) are shown in Fig. S7. The corresponding correlation coefficients between the calculated and measured mass distributions are shown in Table S6. For Fig. S7 and Table S6, the calculated mass distributions were corrected for the presence of naturally labeled H, C, N, O, Si, P and S elements in the derivatized amino acid fragments.

## Data analysis.

**EI and AEI calculation.** The expression index (EI) of a component is defined as follows:

$$M_{ij} = \log_2(v_{ij} / v_{j,control})$$

$$MAD_j = median_j \left\{ M_{ij} - median_j(M_{ij}) \right\}$$

$$EI_{ij} = \frac{M_{ij} - median_j}{MAD_j}$$

where  $M_{ij}$  is the normalized measurement value of the  $j$ th component in the  $i$ th sample,  $v_{ij}$  is the measured value of the  $j$ th component in the  $i$ th sample, and  $v_{j,control}$  is the measured value of the  $j$ th component for the reference value. For targeted quantitative measurements, the reference value corresponds to the median value of compounds in samples that were analyzed on the same day or for a specific series (qRT-PCR; see Table S2 for definition of the series of qRT-PCR). We used this as a more robust reference value due to sometimes large variations occurring between different days of analysis. For semi-quantitative global measurements, the reference value control corresponds to the value of the  $j$ th component in the control sample (parent cell type BW2511 cultured at a specific growth rate of  $0.2 \text{ h}^{-1}$ ).  $MAD_j$  is the median absolute deviation (29) of the  $j$ th component, and  $EI_{ij}$  is the expression ratio of the  $j$ th component in the  $i$ th sample.

The average expression index (AEI) is defined here as the average of the expression indexes of all types of measured components (for either mRNAs, proteins or metabolites). Using the EI, AEI of the  $i$ th sample is calculated as follows:

$$AEI_i = \frac{\sum_{j=1}^n |EI_{ij}|}{n}$$

where  $n$  is the number of components measured with a specific method. For AEI calculation of mRNAs and proteins in single gene disruptants, the value of the product of the deleted gene was excluded to avoid undesirable distortion of the average ratio by this single zero expression value.

**Statistical analyses for AEIs.** The SPSS statistical software version 14.0 for Windows (SPSS Inc., Chicago, IL) was used for all statistical calculations. For each type of analytical method, Levene's test (30) was first used to test whether all examined samples had equal variances. Second, to detect significant differences among the AEIs obtained for each analytical method, one-way analysis of variance (one-way ANOVA) (31) and Welch-ANOVA test (32), which is an expansion of ANOVA for cases in which variances are not equal between groups, were applied. Finally, post hoc tests were performed to identify which sample pairs were significantly different. The Games-Howell test (33) was employed. In all statistical evaluations,  $P < 0.05$  was considered as statistically significant.

For measurements performed by qRT-PCR, LC-MS/MS absolute quantitative proteomics, CE-(TOF)MS metabolomics, and DNA microarray, a single sample per condition was used, with the exception of the reference sample (wild-type, specific growth rate  $0.2 \text{ h}^{-1}$ ), for which multiple replications were performed. For most 2D-DIGE analyses, usually two samples were taken for each chemostat culture (see Proteome analysis by 2D-DIGE on page 5). However, for both the reference and test samples in 2D-DIGE



measurements we did not use the averages of multiple measurements or of merged data from multiple samples for the statistic analysis, to avoid comparisons in a non-uniform way with cases where only a single sample was available. To choose the most suitable reference sample for qRT-PCR and most suitable sample (including both reference and test) for 2D-DIGE, the median of the AEIs among the samples was calculated, and the sample with the AEI closest to or matched to the median was employed for the analysis (for qRT-PCR, RF05-Series5). For LC-MS/MS absolute quantitative proteomics and CE-(TOF)MS metabolomics, the reference sample that was analyzed on the same date as the other samples for growth rate change was chosen (RF02-Series4 for LC-MS/MS absolute quantitative proteomic, RF06-Series6 for CE-(TOF)MS metabolomics. See Table S2 for series details). For DNA microarray analyses, the reference sample was analyzed twice and a randomly selected sample was taken for the analysis.

## Supporting text

**Noise in quantitative measurement data.** We performed exhaustive analyses of the variability in measurement of the various quantitative data. Although biological replications were not performed for the disruptant and growth rate change analysis, for each measurement method employed in this study we performed multiple biological measurements of the reference sample, defined here as wild-type *E. coli* growing at a specific growth rate of  $0.2 \text{ h}^{-1}$ . The average coefficient of variance (CV) of all components measured by qRT-PCR (85 genes, a total of 15 measurement replicates including 7 biological replicates), LC-MS/MS absolute quantification of proteins (57 proteins, a total of 6 measurement replicates including 2 biological replicates), and CE-(TOF)MS metabolomics (139 metabolites, a total of 5 measurement replicates including 5 biological replicates) was 21.4%, 56.6% and 50.3%, respectively. The distributions of frequencies in the CV ranges of the raw data are shown in Fig. S4.

While analyzing the data, we observed that day-to-day variability in LC-MS/MS absolute quantification of proteins and CE-(TOF)MS metabolomics, or the variance between series of qRT-PCR, was a major cause of these broad variances. In order to make inferences across samples more effective, we thus decided to calculate the relative value of each component by dividing the raw value of the component by the median of the same component for all samples (including those from disruptant strains and wild-type or reference samples showing altered specific growth rates) analyzed on the same day (in the case of LC-MS/MS, absolute quantification of proteins, and CE-(TOF)MS metabolomics) or within the same series (Table S7). Since some outliers may be present in the raw data because of large changes in the phenotype of the included samples or because of errors in

measurement, the median of all samples is less sensitive to outliers and is thus a better parameter than the average for normalizations.

After this normalization, the average CVs of the reference samples in qRT-PCR, LC-MS/MS quantification of proteins, and CE-(TOF)MS metabolomics were 14.2%, 25.2% and 29.9%, respectively. The frequency distributions of CVs for the normalized values are shown in Fig. S4. Comparison with the CVs of the raw data reveals that extreme CVs have been removed and the CV distribution has shifted to smaller values for each type of component analyzed, showing the effectiveness of this method.

Next, we scaled the expression index (EI) using the median absolute variances method described above to minimize the sensitivity of the average to components that showed large variations, and we calculated the average expression index (AEI) as an index of global change for each type of cellular component (mRNA, proteins, metabolites). Use of these indexes can considerably reduce the effects of observation errors and variance.

**Statistical analyses.** The average expression index (AEI) was used as an index of global change within a specific type of cellular component (mRNAs, proteins or metabolites) measured by 5 different methods (qRT-PCR, LC-MS/MS absolute quantitative proteomics, CE-(TOF)MS metabolomics, DNA microarray, and 2D-DIGE). To support any conclusions derived from the data, the significance of differences among AEIs in all examined samples should be estimated. By definition, the AEI represents an average calculated from the EIs of all components measured by one of the analytical methods. Thus the statistical analysis can involve common statistical tests for significant differences between averages among multiple independent groups. However, we analyzed 29 groups (samples) (24 disruptant

samples cultured at the same specific growth rate, and 5 wild-type samples grown at variable specific growth rates) by each analytical method, with the exception of DNA microarray, where five disruptants and three specific growth rates of wild-type cells were analyzed. Such multi-group comparisons may considerably lower the power of the statistical test to detect significant differences (34). Furthermore, our hypothesis includes the stability of cellular component levels under different perturbations, meaning that there should be no significant differences among the various groups examined. However, general statistical tests cannot prove the validity of such hypotheses where a test fails to detect a difference when there actually is one. The observed absence of difference may originate from type II errors (false negative results) (35). However, if statistically significant differences are detected but the relative magnitudes of the differences are adequately small, then the tested groups can be considered more or less similar in terms of global expression.

According to these criteria, to evaluate the significance of observed changes in AEIs, we performed statistical tests between the AEIs of all 29 samples (8 samples in the case of DNA microarray) for each measurement method.

For each type of analytical method, the  $P$  values of Levene's test were below the 5% significance level; thus the variances between the samples were unequal (Table S10). For this reason, both ANOVA and Welch-ANOVA were employed. ANOVA and Welch-ANOVA detected significant differences ( $P < 0.05$ ) among the included samples for all types of measurements (Table S10). The results of the Games-Howell test are shown in Table S10, and the pairs displaying significant differences ( $P < 0.05$ ) are shown in Table S11.

From the statistical analysis using AEI the following results emerged:

- (1) The AEIs for mRNAs (qRT-PCR and DNA microarray) and proteins (absolute quantitative proteomics and 2D-DIGE) appeared larger at higher growth rates.
- (2) The AEIs for metabolites did not show significant differences at different growth rates.
- (3) The AEI values of mRNAs and proteins of 23 disruptants were smaller than the AEI observed in wild-type cells at a specific growth rate of  $0.7 \text{ h}^{-1}$ , and this difference was significant for all disruptants (mRNAs) and 15 disruptants (proteins), respectively.
- (4) Results similar to (3) were obtained for the AEI values representing the global analysis of mRNA (DNA microarray) and protein expression (2D-DIGE).
- (5) The AEIs for metabolites in 3 disruptants (*pgm*, *pgi* and *rpe*) were higher than in wild-type cells at high specific growth rates ( $0.5 \text{ h}^{-1}$  and  $0.7 \text{ h}^{-1}$ ). The same result was obtained even when nucleotides were excluded from the AEI calculations.
- (6) With the exception of a few strains, overall metabolite levels remained stable in most disruptants.

The following discussion provides more detail on points (1) to (6) above:

- (1) For mRNAs (qRT-PCR) in the variable specific growth rate experiments, all pairs ( $0.2 \text{ h}^{-1}$  vs. other growth rates) showed significant differences. This suggests that the AEIs of metabolic gene transcripts (qRT-PCR) in the  $0.1$ ,  $0.4$ ,  $0.5$  and  $0.7 \text{ h}^{-1}$  samples were different from that of the  $0.2 \text{ h}^{-1}$  sample. Furthermore, significant differences were detected for most other pairs except for  $0.1 \text{ h}^{-1} - 0.4 \text{ h}^{-1}$ ,  $0.1 \text{ h}^{-1} - 0.5 \text{ h}^{-1}$  and  $0.5 \text{ h}^{-1} - 0.7 \text{ h}^{-1}$ . Similarly, for the AEIs of mRNAs measured using DNA microarray, all pairs included in the specific growth rate change samples showed significant differences. From these results,

the changes in AEI of mRNAs for the experiment involving change in specific growth rate (shown in Fig. 2C and Fig. 2D) can be considered meaningful.

On the other hand, for proteins analyzed by quantitative LC-MS/MS, no pair of AEIs in the growth rate change experiment displayed a significant difference. However, as discussed below, the protein AEI for  $0.7 \text{ h}^{-1}$  showed significant differences against 15 of the 24 knockout samples showing low protein AEI values, which suggests a difference between the  $0.7 \text{ h}^{-1}$  sample and the  $0.2 \text{ h}^{-1}$  sample. The difference in growth rates may have been missed because of the larger variance in these samples. However, for proteins measured by 2D-DIGE, the AEIs of the  $0.5 \text{ h}^{-1}$  and  $0.7 \text{ h}^{-1}$  samples were significantly different from those of all other specific growth rate samples. Thus, at least in Fig. 2D, the increase in protein AEI that accompanied the increase in specific growth rate can also be considered meaningful.

(2) The difficulty in detecting significant differences in metabolite AEIs among samples in the specific growth rate experiments presumably reflects both the larger variance observed in the metabolite data and also the limited magnitude of changes in metabolite levels at different growth rates, as explained in the main text of the manuscript. However, when we used the AEIs without the nucleotide data, some pairs ( $0.1 \text{ h}^{-1} - 0.2 \text{ h}^{-1}$ ,  $0.2 \text{ h}^{-1} - 0.4 \text{ h}^{-1}$ ,  $0.2 \text{ h}^{-1} - 0.7 \text{ h}^{-1}$ ) showed significant differences. Since the differences among these pairs were all relatively small, we can at least regard the group of metabolite (without nucleotides) AEIs as an ensemble of very similar sub-groups. This suggests the robust maintenance of metabolite concentrations at all growth rates.

(3) For mRNAs (qRT-PCR), the AEIs of most disruptants except for *pgm*, *pgi*, *pfkA*, *gapC*, *rpe* and *tktA* were significantly different from that of the wild-type at  $0.5\text{ h}^{-1}$ . These six disruptants displayed the highest mRNA AEIs among all the disruptants. In addition, the AEIs of all disruptants except *rpe* were significantly different from that of the wild-type at  $0.7\text{ h}^{-1}$ . Figure 2C shows that the mRNA AEIs of the wild-type samples cultured at  $0.5\text{ h}^{-1}$  and  $0.7\text{ h}^{-1}$  were higher than those of the disruptants displaying lower AEIs (*i.e.*, the remaining 18 disruptants). For proteins (absolute quantitative proteomics), the differences between the two higher growth rate groups (wild-type,  $0.5\text{ h}^{-1}$ , and  $0.7\text{ h}^{-1}$ ) and the disruptants were not as clear. However, during comparisons between the wild-type cultured at the highest growth rate ( $0.7\text{ h}^{-1}$ ) and the different disruptants, 15 strains included in the lower AEI group showed significant differences. This indirectly supports the fact that the protein AEIs of the wild-type at higher specific growth rates were higher than those of many disruptants.

(4) In the AEIs obtained by DNA microarray, only *rpe*, which showed the highest AEI of the disruptants, showed no significant difference from the wild-type at either  $0.5\text{ h}^{-1}$  or  $0.7\text{ h}^{-1}$ . Thus the AEIs of the higher growth rate group (wild-type,  $0.5\text{ h}^{-1}$  and  $0.7\text{ h}^{-1}$ ) were higher than those of most of the disruptants examined (*pgm*, *pgi*, *gapC*, and *zwf*). In the AEIs obtained from the 2D-DIGE measurements, the AEI of the wild-type at  $0.7\text{ h}^{-1}$  was significantly different from those of all the disruptants. These results suggest that the differences in AEIs for global analyses, shown in Figure 2D, between the wild-type higher growth rate group and most of the disruptants are meaningful, similarly to the targeted mRNA and protein results shown in Figure 2C.

(5) This specific conclusion is not directly or strongly supported by the statistical analysis. For metabolite AEIs, the three strains *pgm*, *pgi* and *rpe* were significantly different from the wild-type at  $0.5 \text{ h}^{-1}$ , whereas none of them showed significant differences from the wild-type at  $0.7 \text{ h}^{-1}$ . If nucleotides were excluded from the AEI calculations, then only the pair of *rpe* – wild-type at  $0.5 \text{ h}^{-1}$  showed a significant difference. However, the situation for metabolite AEIs was different from that of mRNA and protein AEIs, because at least some disruptant strains showed significantly larger AEIs than that of the wild-type at a high specific growth rate ( $0.5 \text{ h}^{-1}$ ).

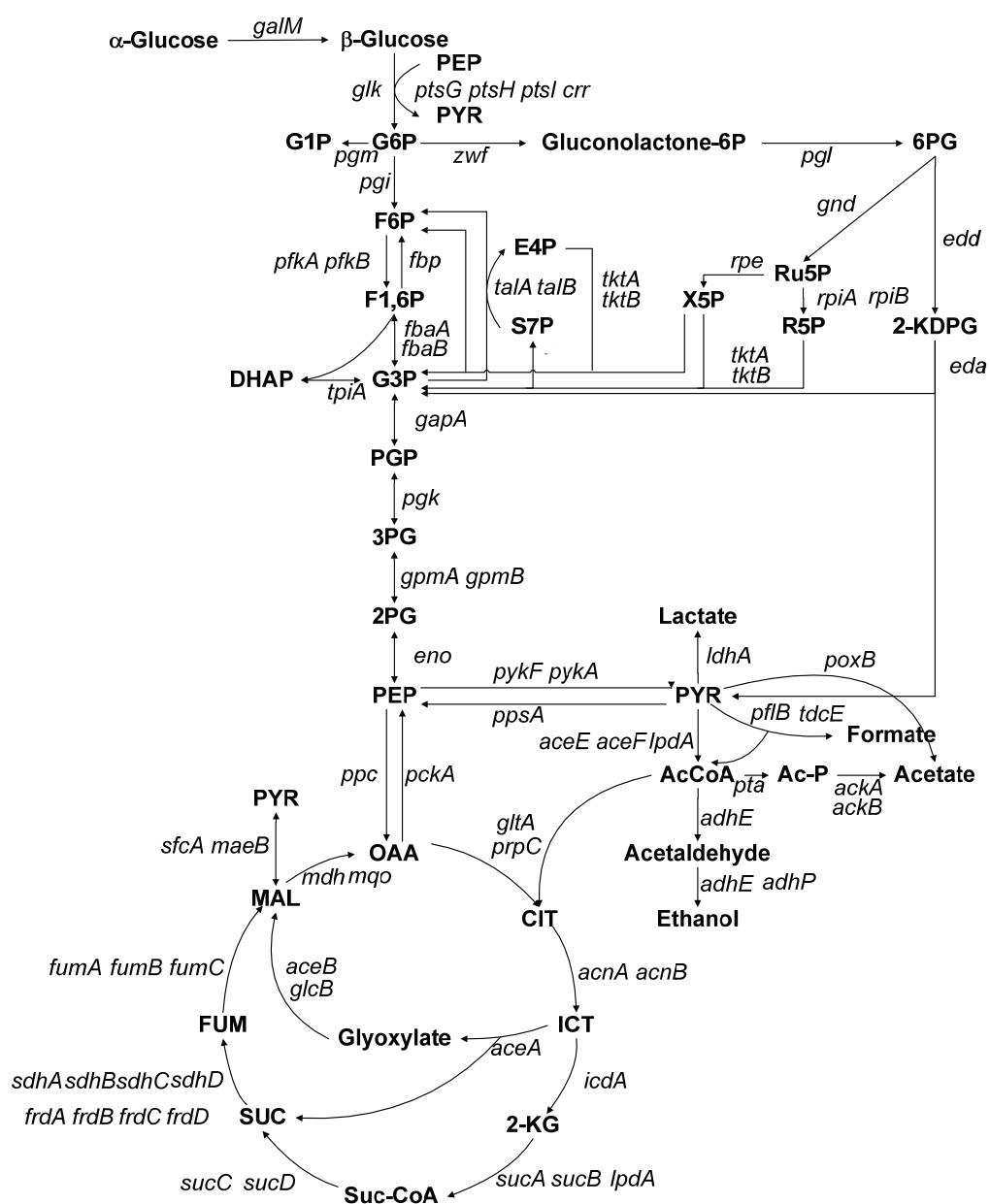
(6) The provision of unambiguous evidence for this conclusion carries the same difficulty as in (2). However, for metabolite AEIs, 61 pairs showed significant differences among a possible total of 210 pairs in the 21 disruptants, excluding *pgm*, *pgi* and *rpe*. Since the metabolite AEIs of disruptants were distributed over a relatively narrow range (Fig. 2C), at least the size of the differences among the 61 pairs can be estimated as very small. Thus, as in (2), the metabolite AEI group of all gene disruptants can be considered to include similar sub-groups. This similarity in metabolite AEIs also suggests stability in metabolite concentration levels among most of the tested disruptants.

**On the nature of the observed response to certain gene disruptions.** We believe our data likely captures the immediate response of *E. coli* to genetic perturbations. This early response may be somewhat different from the more optimised response that *E. coli* eventually displays following a longer period of adaptive evolution, as previously

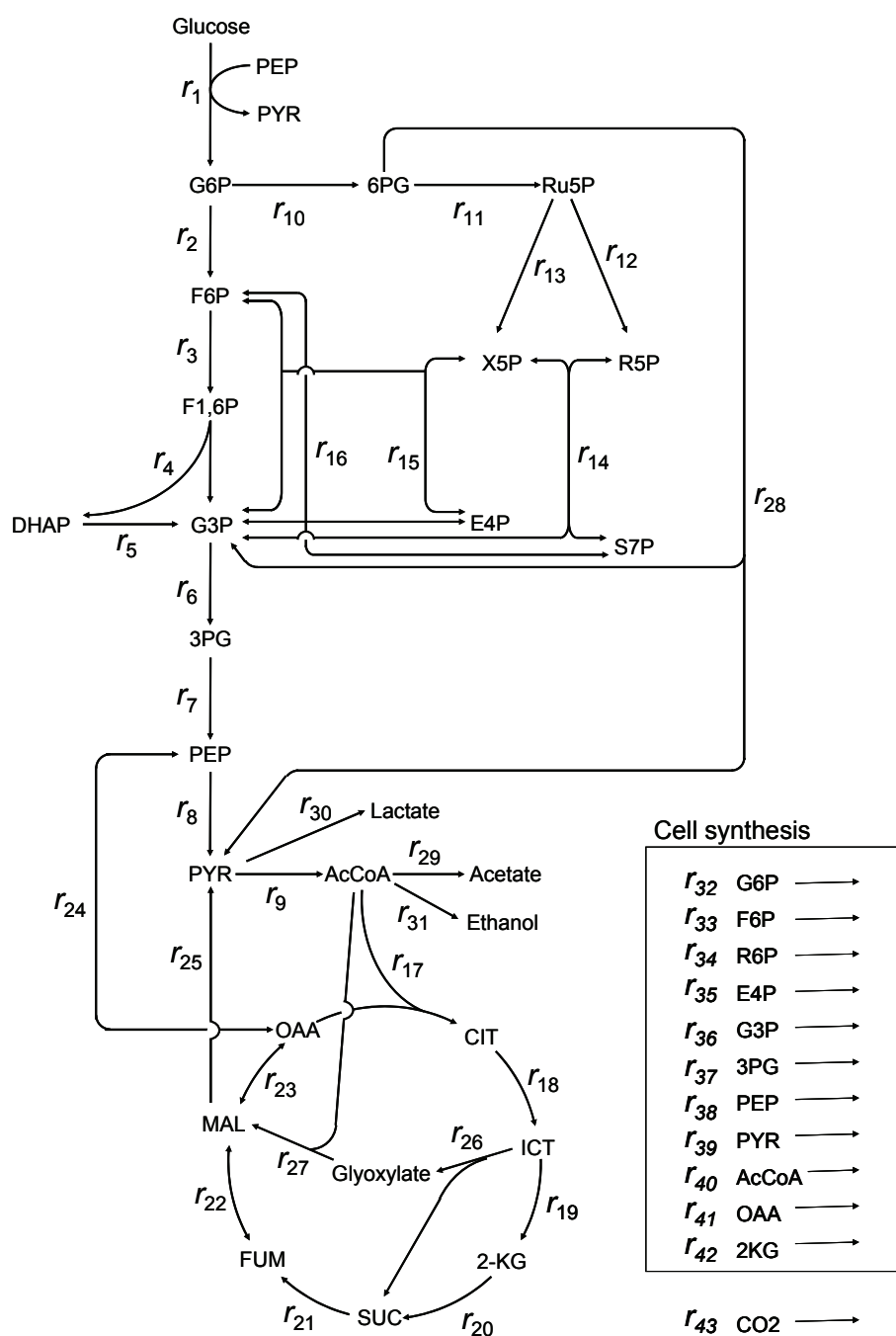


demonstrated (36, 37). However, we found that some of the disruptants examined in the present study rapidly accumulated mutations during the relatively short continuous culture period. To monitor and try to avoid using data from cultures with such adaptive mutations, an aliquot of some of the cultured bacteria was collected at sampling times for phenotypic analysis. Serially diluted cultures were plated and the resulting colonies were checked for size and shape. If the colony phenotype was significantly different from the original bacterial stock, the whole experiment was repeated. As a result, we repeated the culture of the *pfkA* disruptant three times, but faster-growing colonies emerged in all cases. We examined the genotypes of these colonies and found that they had accumulated a mutation in the -10 region of the *pfkB* promoter, which is described as *pfkB1*, a mutation activating *pfkB* transcription (38). The results shown in the present report are from one of the three different cultures, which contained about 70% evolved cells at the time of sampling. Similarly, we observed that most (if not all) of the colonies from the *rpiA* disruptants accumulated mutations in the *rpiR* gene, which result in derepression of *rpiB* expression (39). The observed mutations included insertions of IS1 or IS5 and a frameshift mutation caused by a single base insertion at position 521 from the *rpiR* initiation codon. Data collection for the *rpiA* disruptant was not repeated, because accumulation of this type of mutation was inevitable during pre-culture. It is thus likely that for these specific disruptants, the metabolic network is compromised to such an extent that a strong selective pressure exists that strongly favours cells that have accumulated other beneficial mutations. This secondary response appears to be the main factor explaining the large increase in expression seen in Fig. S5.

**Detected metabolite candidates not previously reported in *E. coli*.** The large amount of quantitative data collected in the present study revealed additional valuable information. For instance, we detected some candidate metabolites that have not yet been registered in EcoCyc (40) Ver 10.0 (Table S12). While confirmation of their identity may require further structural analyses in addition to a more detailed investigation of their functions, these candidates support the idea that there remains many unreported metabolic reactions or even possibly whole pathways in *E. coli* (41). The list is not necessarily exhaustive since only metabolites for which chemical standards are available were examined.



**Figure S1 Map of *Escherichia coli* K-12 central carbon metabolism.** This map, showing metabolites (bold font) and genes (italics) is derived from Shimizu (2004) (42), but is slightly modified with information obtained from KEGG (6) maps (<http://www.genome.jp/kegg/>) and EcoCyc (40) (<http://ecocyc.org/>). Abbreviations for metabolites are shown in Table S1.



**Figure S2 Main metabolic pathways of *E. coli* K-12 used for metabolic flux analysis.**

The  $r_x$  values represent the various net reactions used for flux calculations and further details are provided in Table S4. Abbreviations for metabolites are provided in Table S1.

**Figure S3 A mRNAs detected in more than half of samples.**

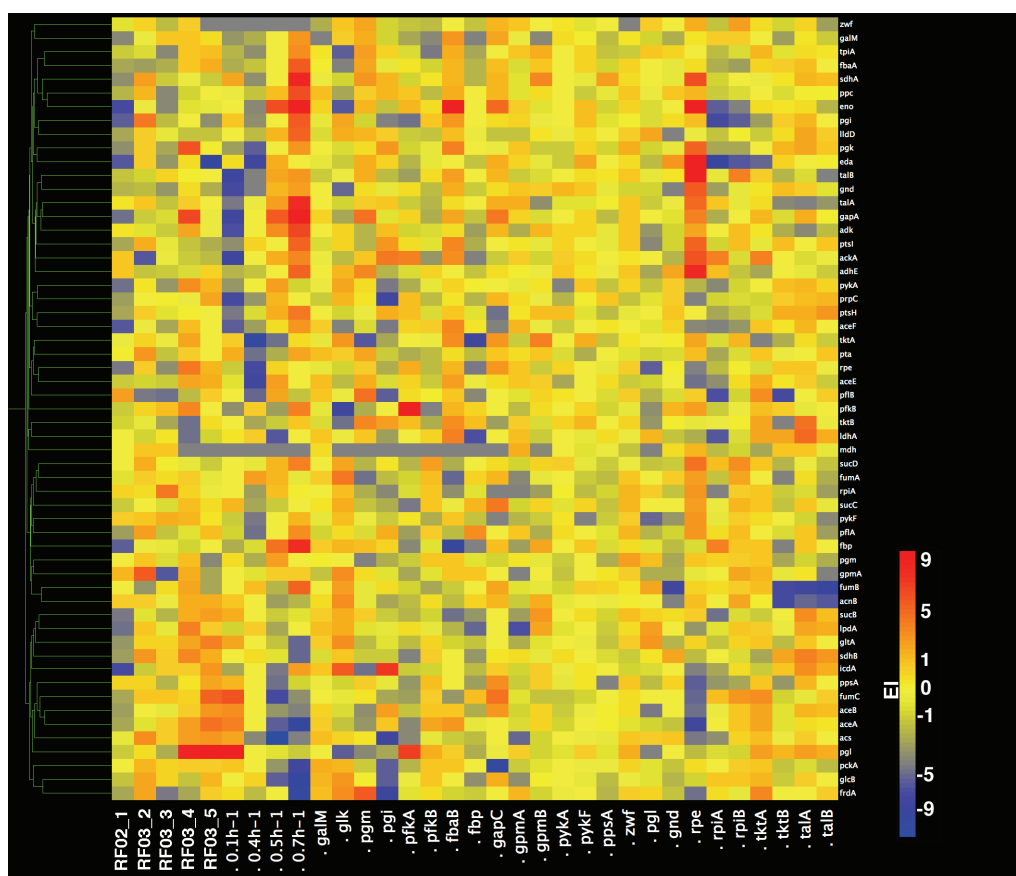
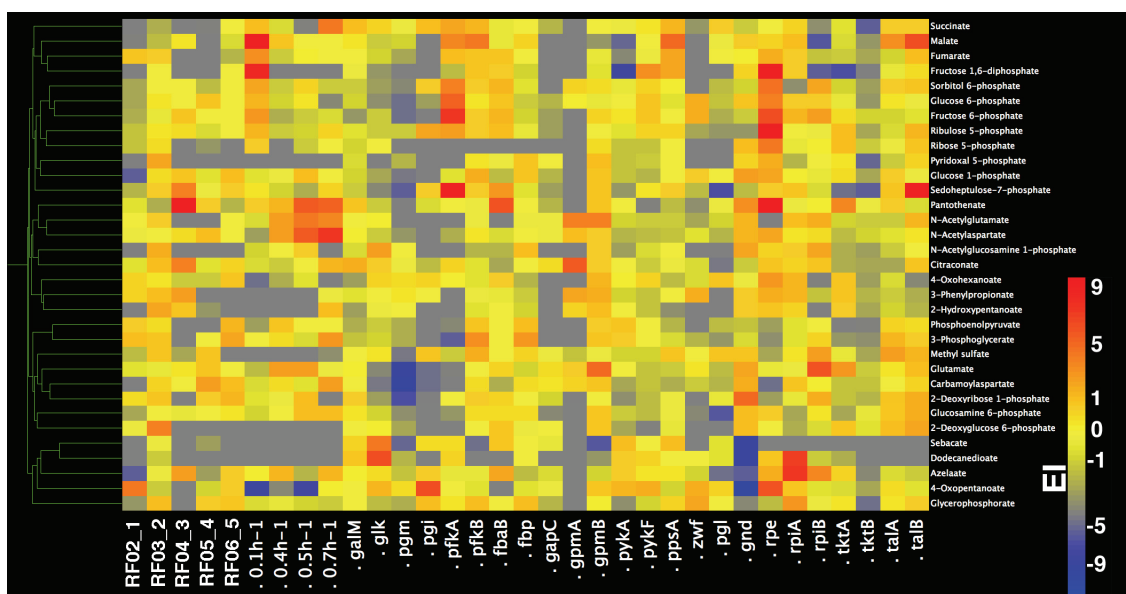


Figure S3 B Proteins detected in more than half of samples.



**Figure S3 C Metabolites (Anions) detected in more than half of samples.**

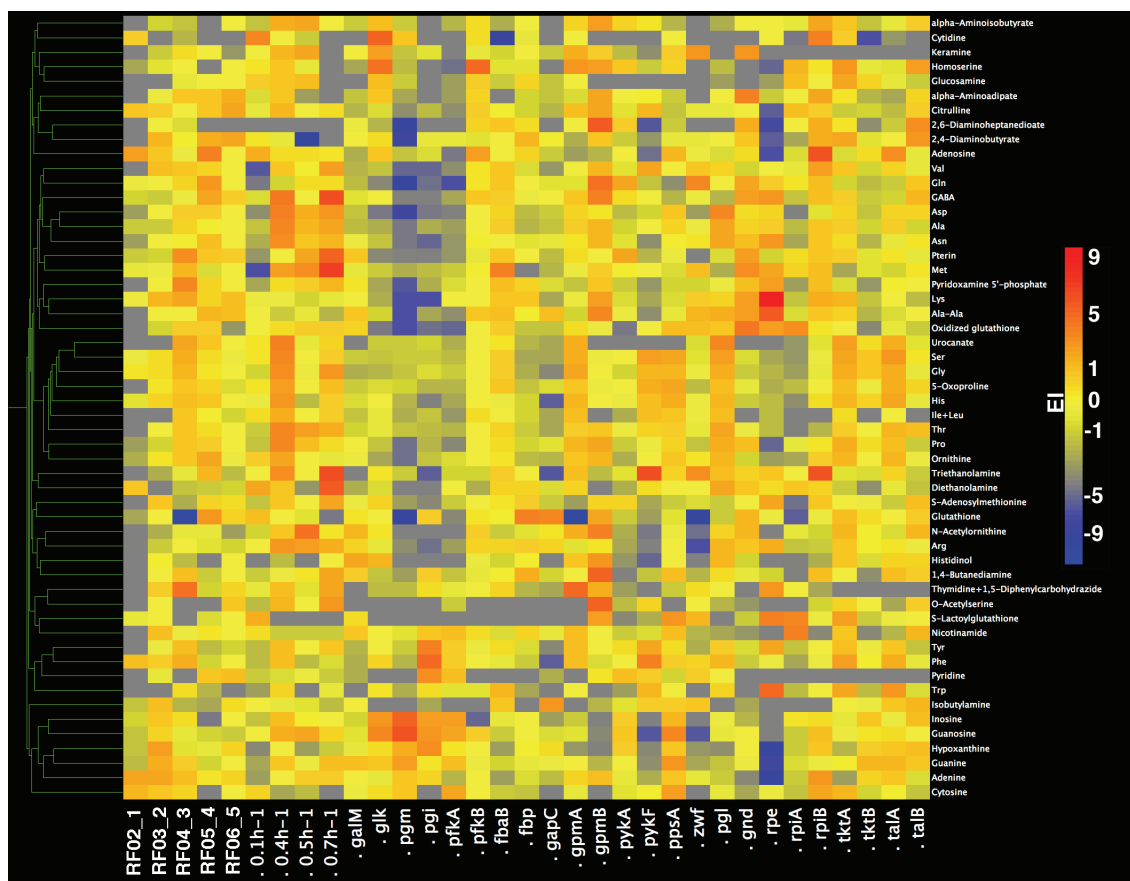
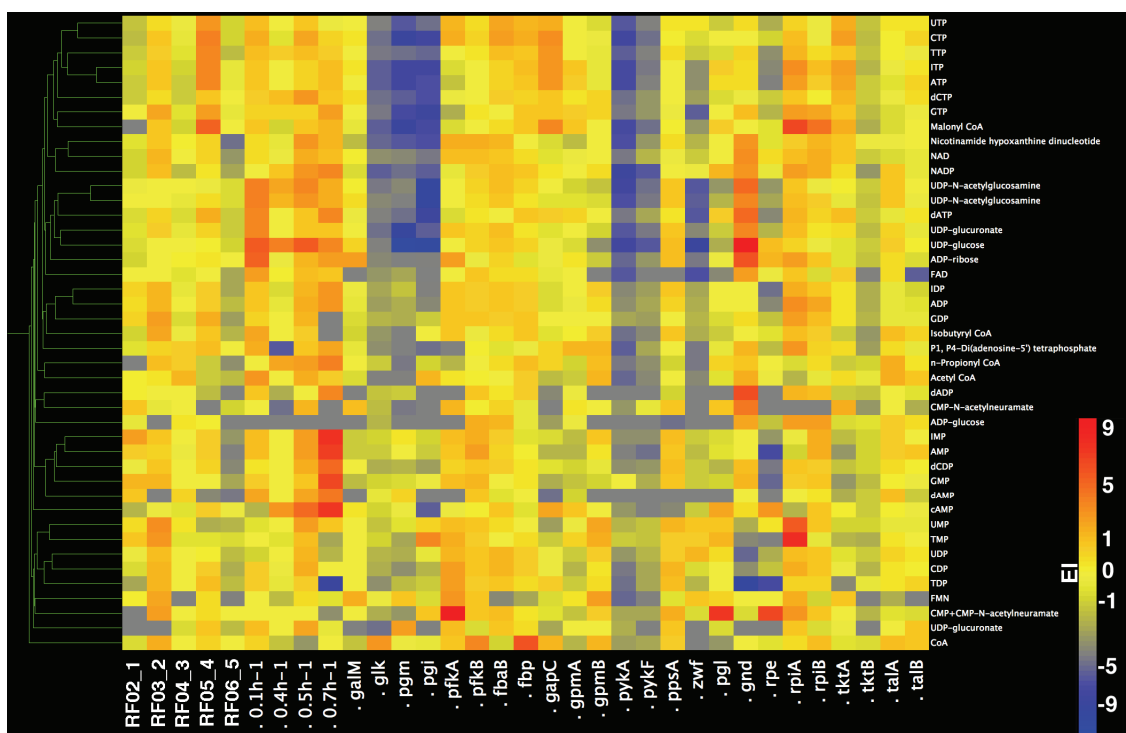


Figure S3 D Metabolites (Cations) detected in more than half of samples.

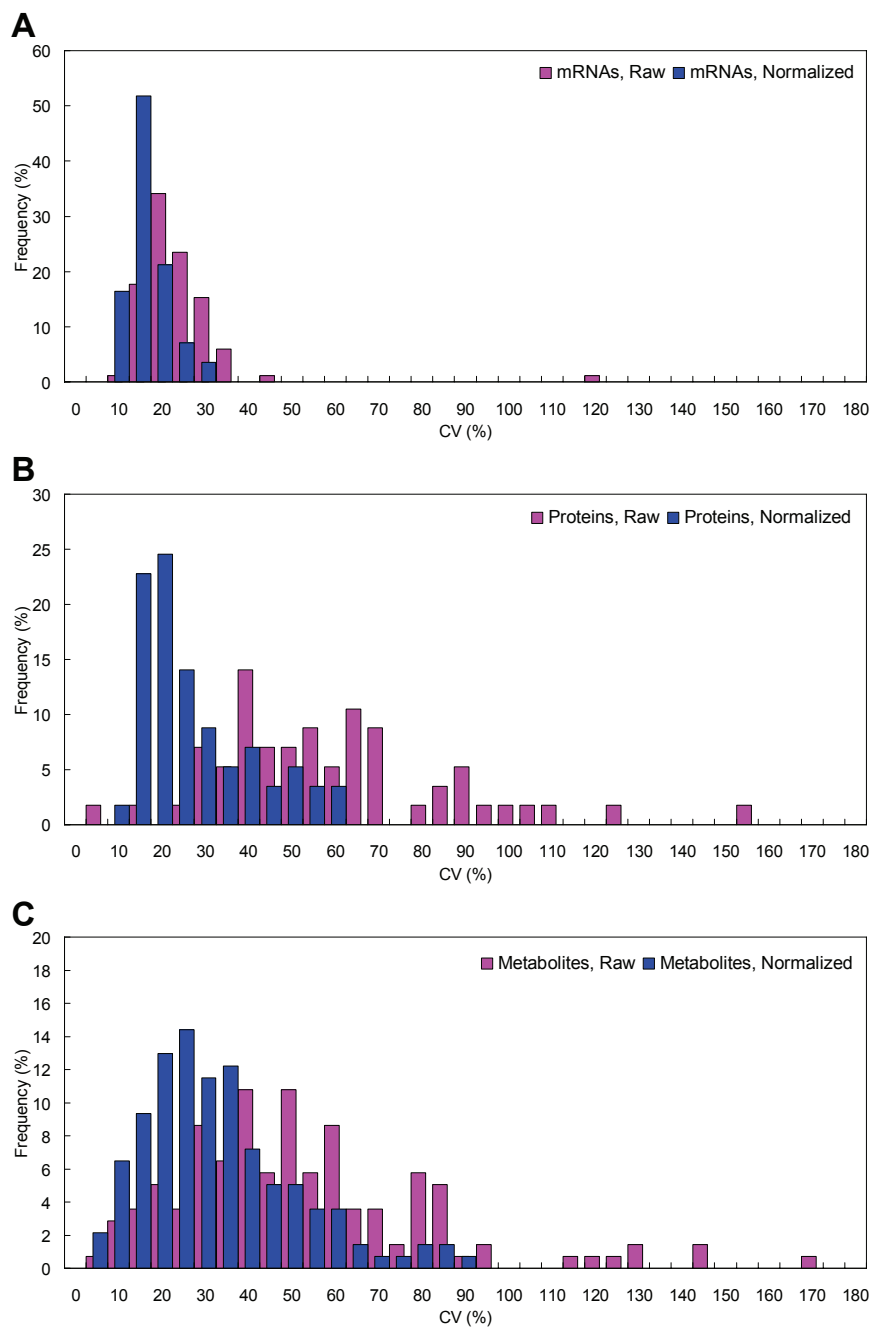




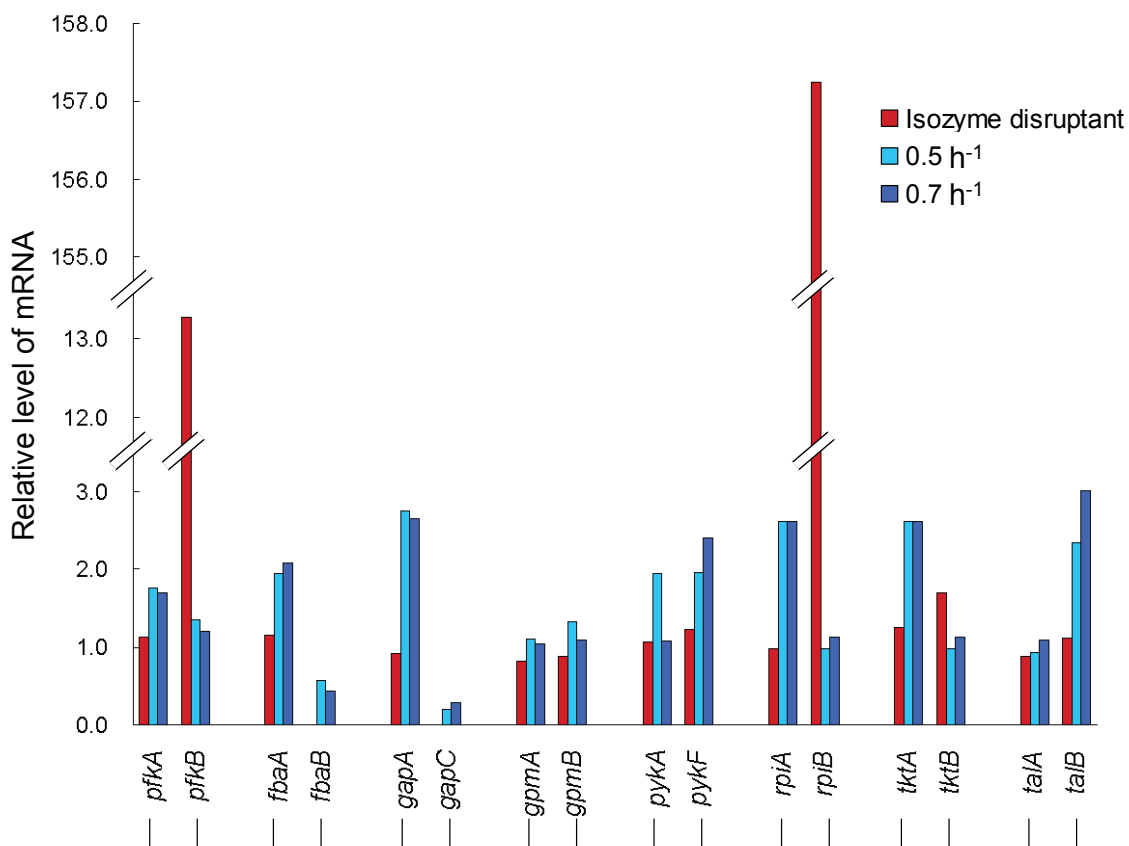
**Figure S3 E Metabolites (Nucleotides) detected in more than half of samples.**

### Figure S3

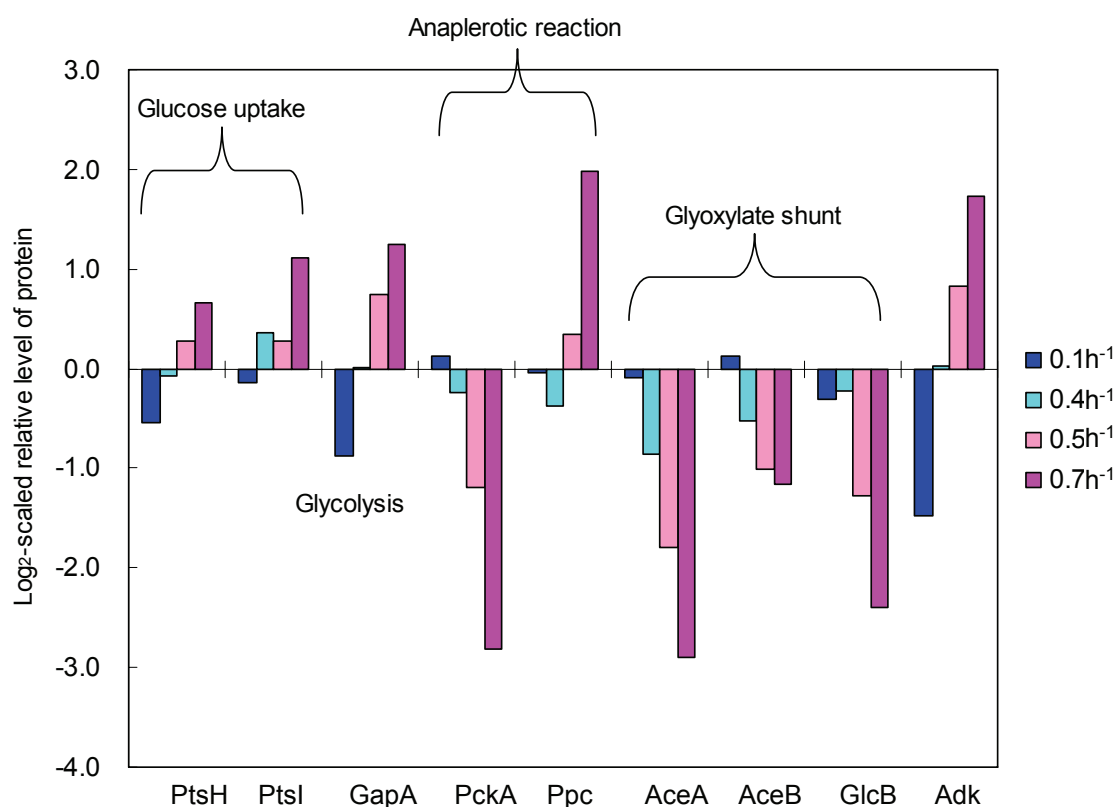
The heatmaps shown in Fig. 1 are individually enlarged here for each independent type of analysis and the names of the components are indicated to the right. The colours of tiles correspond to the EI value, and hierarchical clusters shown to the left were obtained from average linkage analysis using Pearson correlation coefficient as a measure of similarity. A; RNA measured by qRT-PCR. B; protein measured by LC-MS/MS. C, D, E; metabolite measured by CE-(TOF)MS for anions, cations and nucleotides, respectively. RF; reference sample (wild-type cells cultured at a specific growth rate of  $0.2 \text{ h}^{-1}$ ). RFs are denoted by Sample ID and Series ID shown in Table S2.



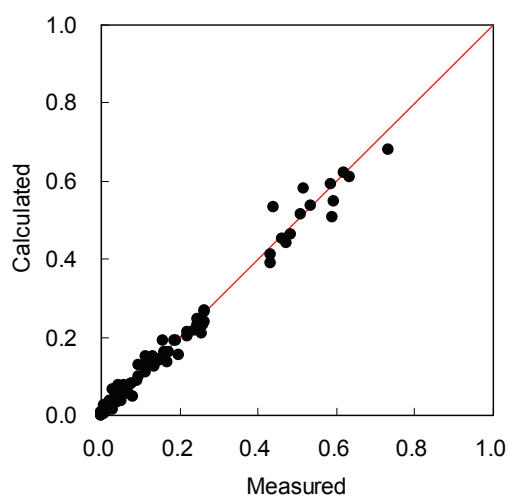
**Figure S4 Distributions of CV frequencies for raw and normalized obtained using the various targeted quantitative methods. A; mRNAs measured by qRT-PCR. B; proteins measured by LC-MS/MS. C; metabolites measured by CE-(TOF)MS.**



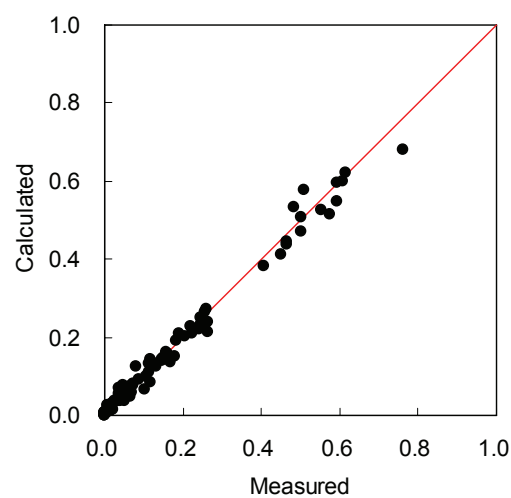
**Figure S5 Effect of growth rate change or enzyme disruption on mRNA transcript levels for specific pairs of isozymes.** The values correspond to the relative level of mRNA compared to wild-type at a specific growth rate of 0.2 h<sup>-1</sup>, upon either an increase in specific growth rate (0.5 h<sup>-1</sup> and 0.7 h<sup>-1</sup>; light and dark blue bars, respectively) or upon disruption of the corresponding isozyme gene (red bars). No data is shown for the isozyme disruptants of *fbaB* and *gapC*, because disruptions in these genes are lethal.



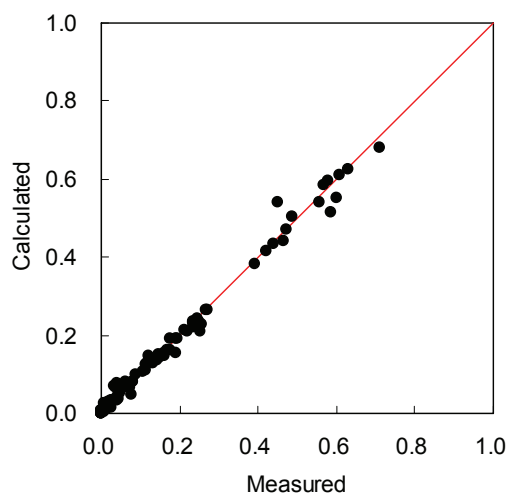
**Figure S6 Proteins showing some of the largest relative level changes during culture at various growth rates.** The y-axis represents the log<sub>2</sub> relative level compared to the wild-type strain at a specific growth rate of 0.2 h<sup>-1</sup>. PtsH and PtsI are proteins involved in the extracellular glucose uptake system, PTS. GapA is one of the enzymes of glycolysis. PckA converts oxaloacetate to phosphoenol pyruvate and Ppc catalyzes the reverse reaction. AceA, AceB and GlcB together form the glyoxylate shunt. Adk catalyzes the interconversion reaction between ATP, ADP, and AMP.



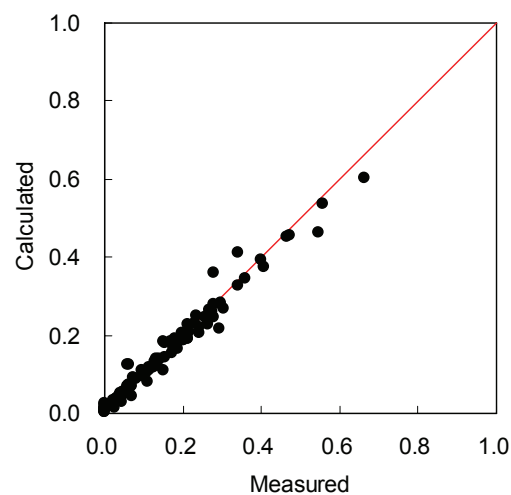
**RF03 (WT, 0.2 h<sup>-1</sup>)**



**RF04 (WT, 0.2 h<sup>-1</sup>)**

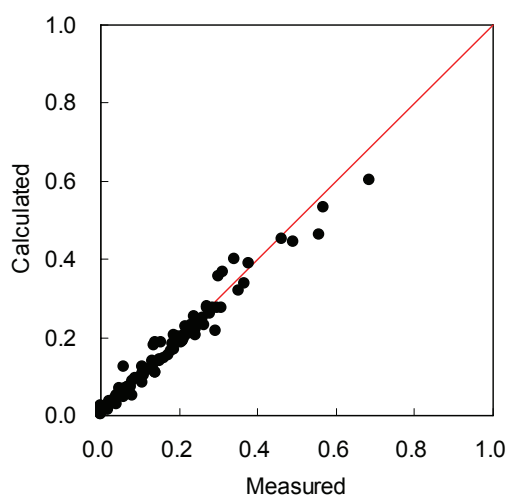


**RF05 (WT, 0.2 h<sup>-1</sup>)**

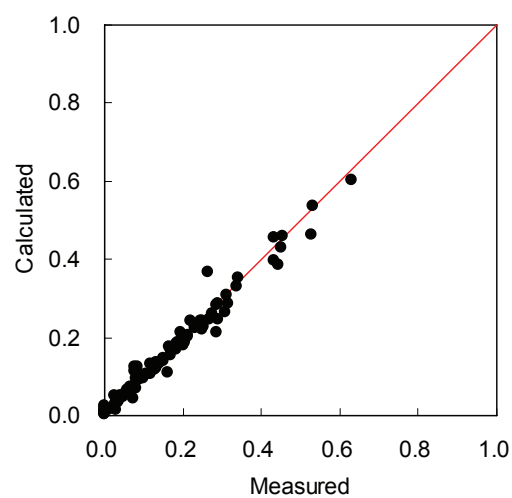


**RF06 (WT, 0.2 h<sup>-1</sup>)**

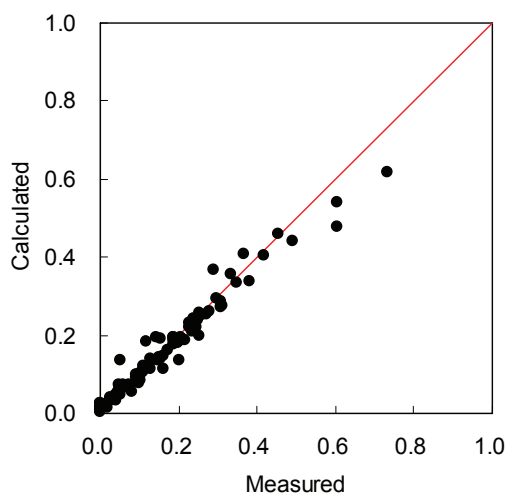
**Figure S7 A Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (RF03, RF04, RF05, RF06).**



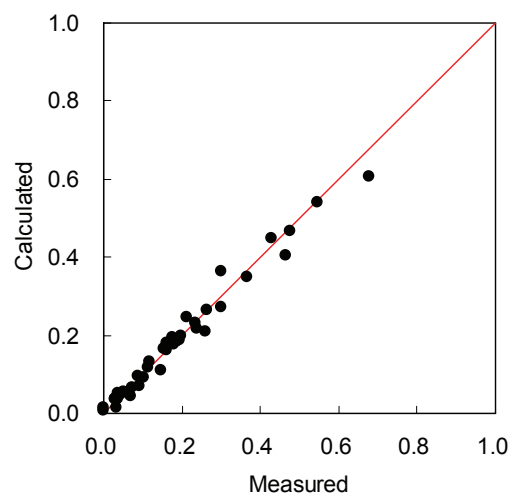
**GR01 (WT, 0.1 h<sup>-1</sup>)**



**GR02 (WT, 0.4 h<sup>-1</sup>)**

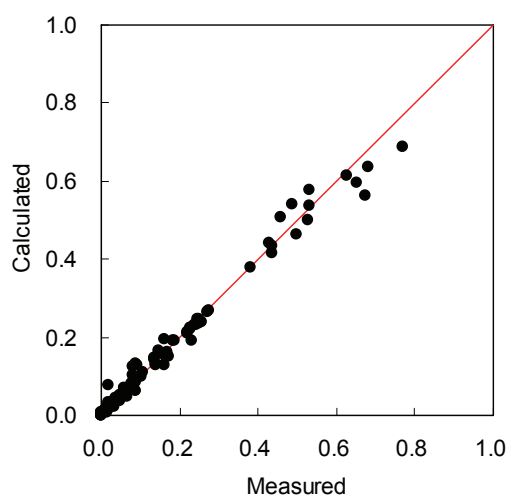


**GR03 (WT, 0.5 h<sup>-1</sup>)**

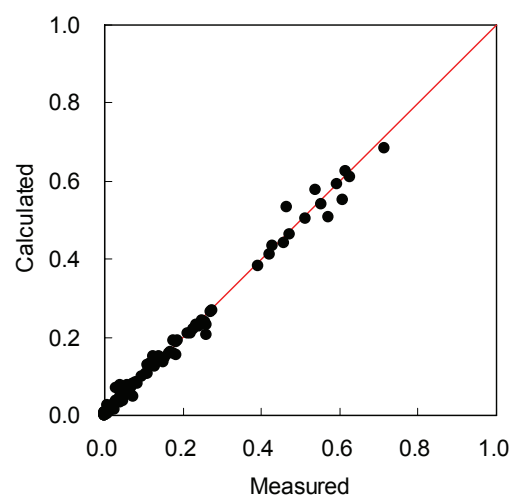


**GR04 (WT, 0.7 h<sup>-1</sup>)**

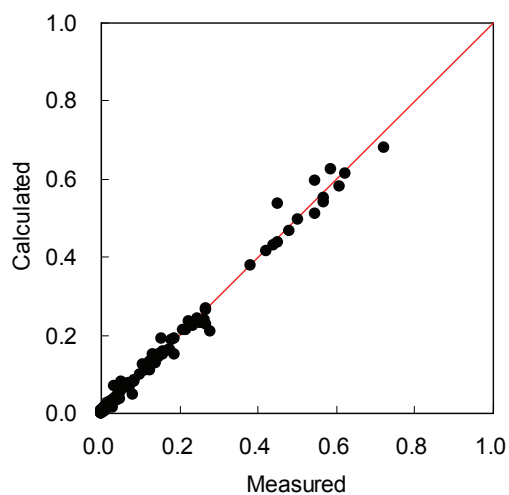
**Figure S7 B Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (GR01, GR02, GR03, GR04).**



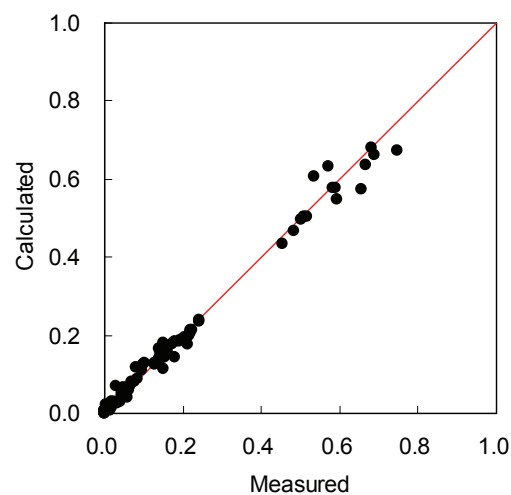
**KO01 (*galM*)**



**KO02 (*glk*)**

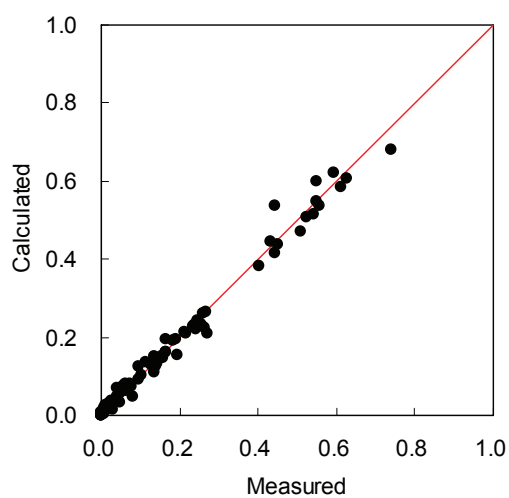


**KO03 (*pgm*)**

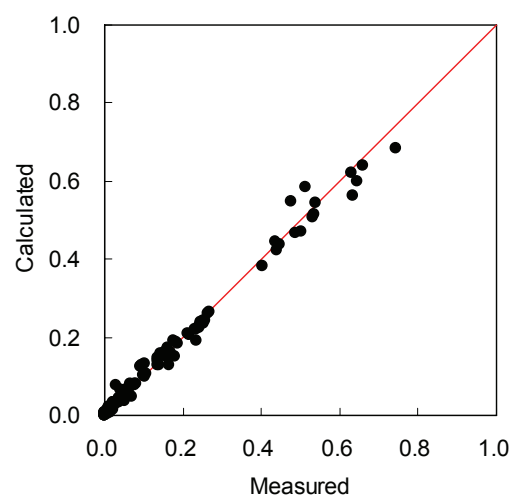


**KO04 (*pgi*)**

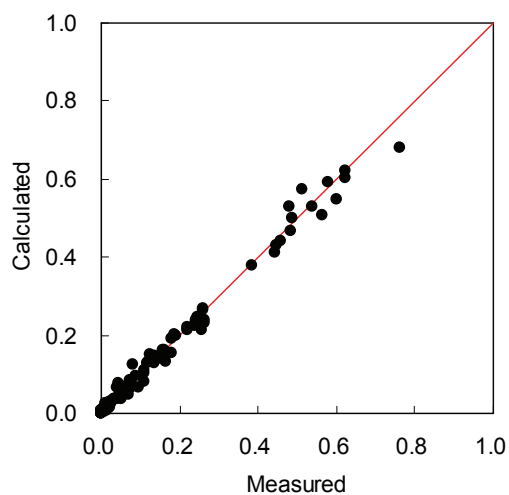
**Figure S7 C Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO01, KO02, KO03, KO04).**



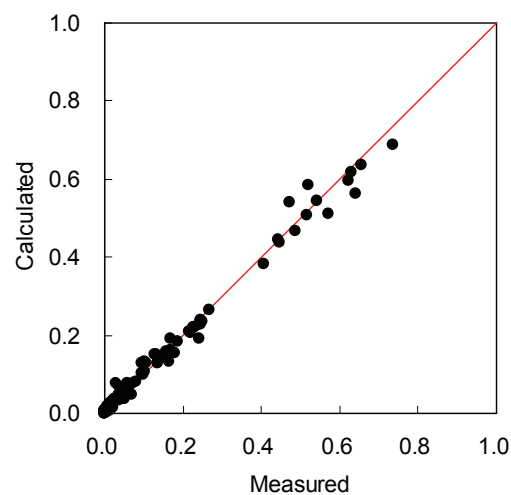
**KO05 (*pfkA*)**



**KO06 (*pfkB*)**



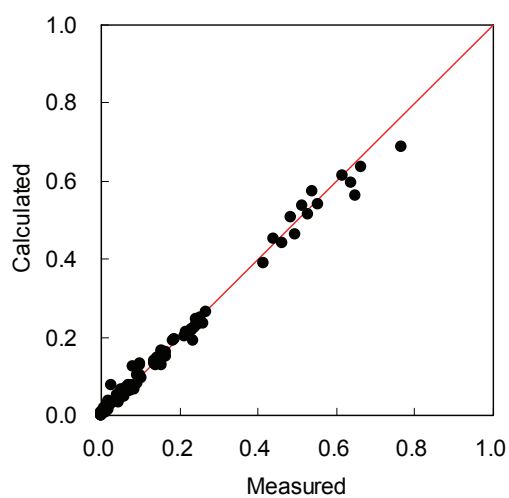
**KO07 (*fbp*)**



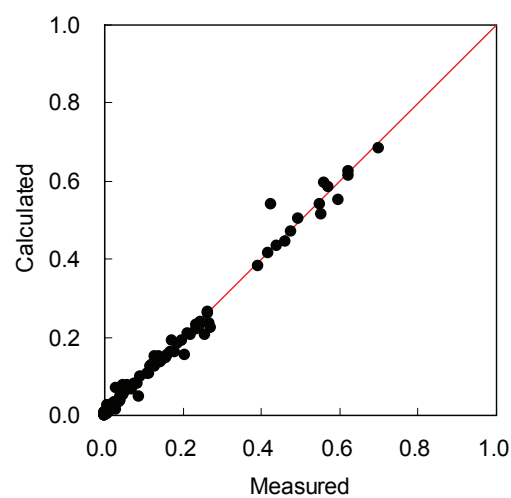
**KO08 (*fbaB*)**

**Figure S7 D Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO05, KO06, KO07, KO08).**

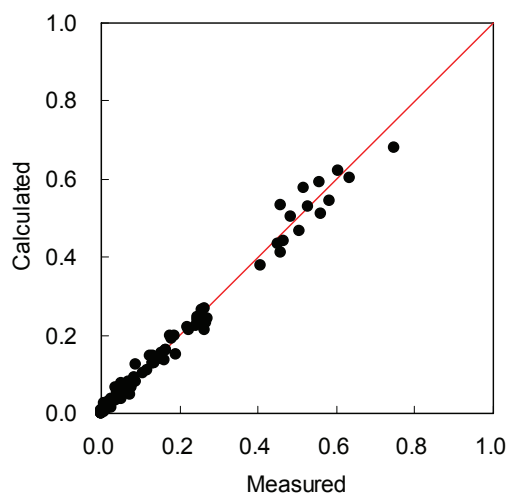




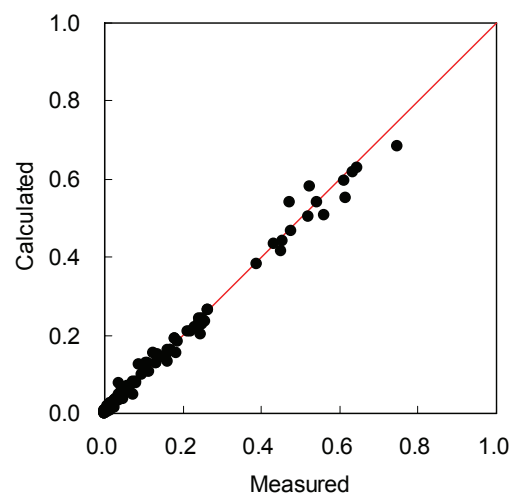
**KO09 (*gapC*)**



**KO10 (*gpmA*)**

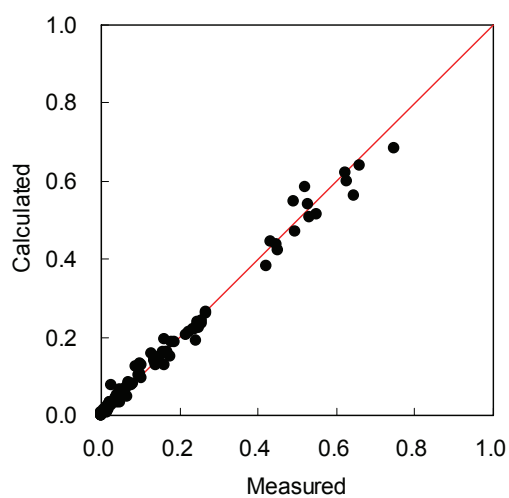


**KO11 (*gpmB*)**

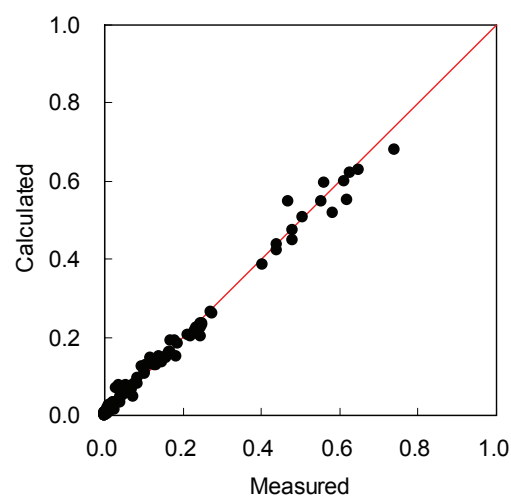


**KO12 (*pykA*)**

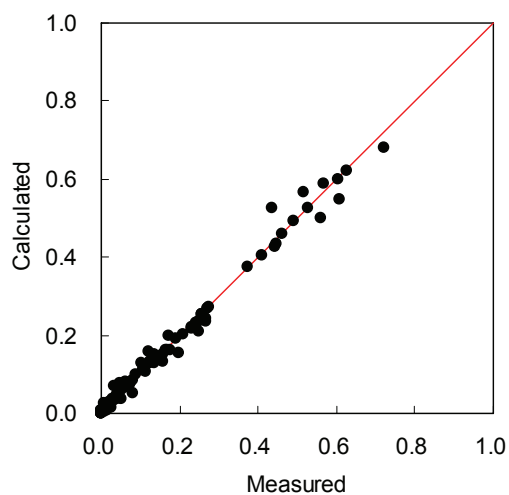
**Figure S7 E Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO09, KO10, KO11, KO12).**



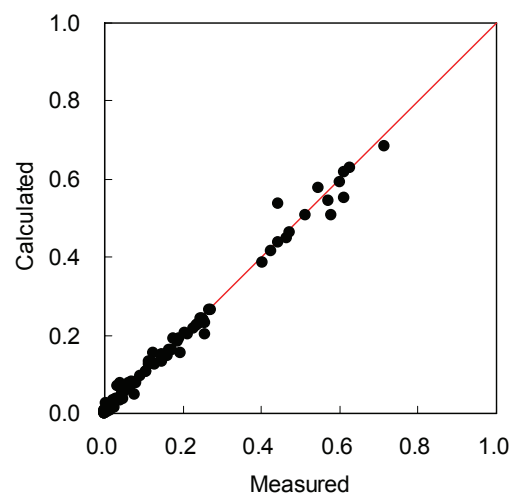
**KO13 (*pykF*)**



**KO14 (*ppsA*)**

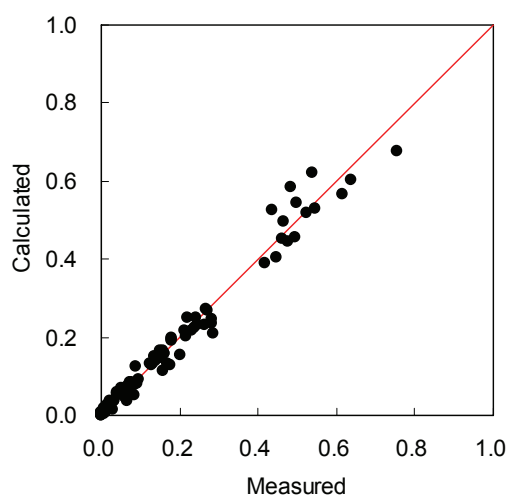


**KO15 (*zwf*)**

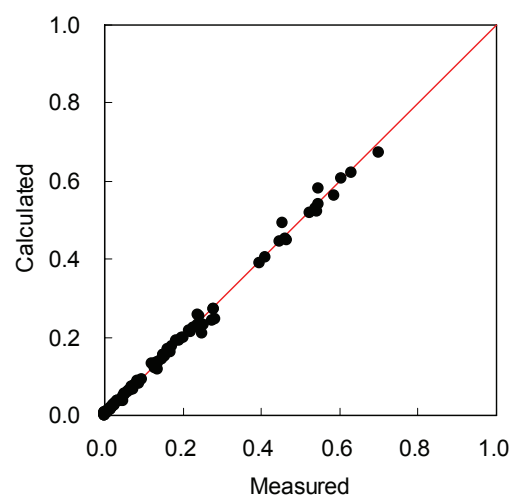


**KO16 (*pgl*)**

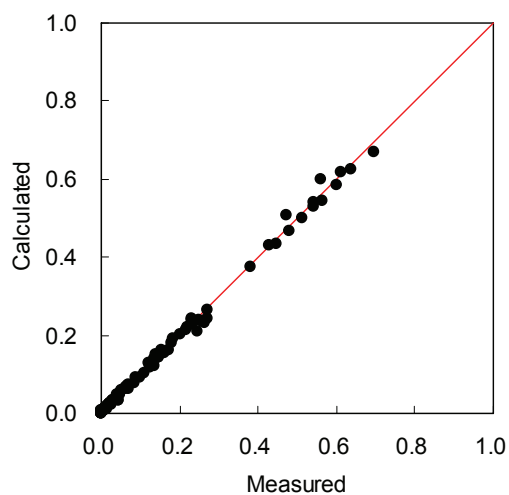
**Figure S7 F Comparison of mass distributions of proteinogenic amino acids between value calculated from the estimated flux distributions and those measured by GC-MS (KO13, KO14, KO15, KO16).**



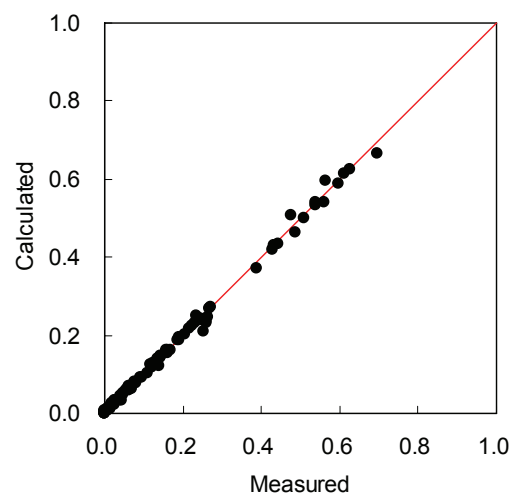
**KO17 (*gnd*)**



**KO18 (*rpe*)**

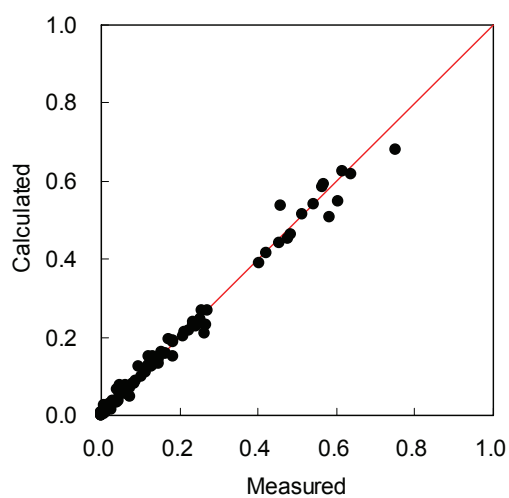


**KO19 (*rpiA*)**

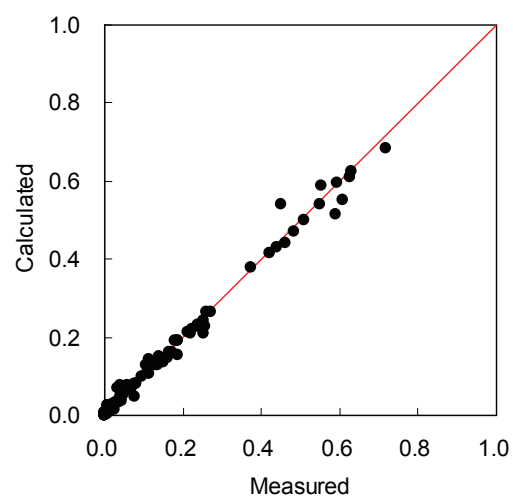


**KO20 (*rpiB*)**

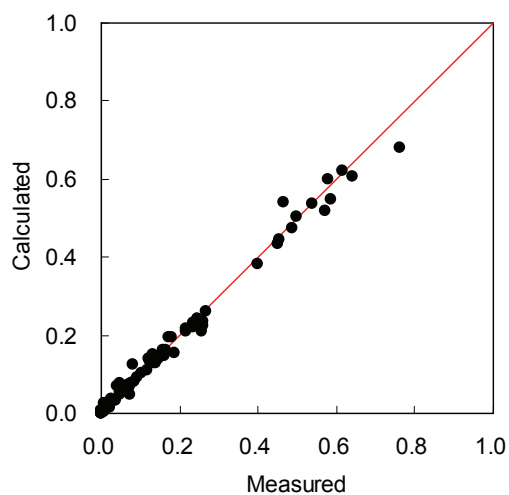
**Figure S7 G Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO17, KO18, KO19, KO20).**



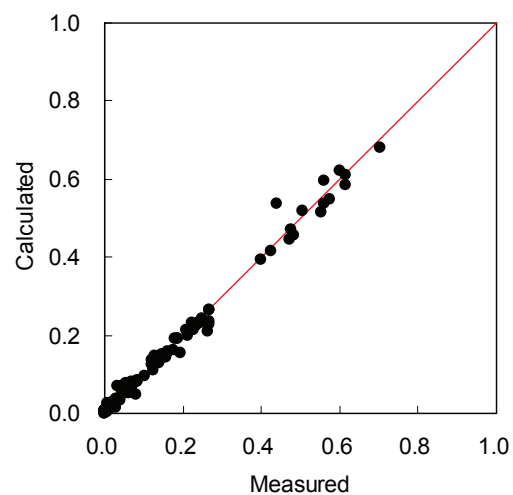
**KO21 (*tktA*)**



**KO22 (*tktB*)**



**KO23 (*talA*)**



**KO24 (*talB*)**

**Figure S7 H Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO21, KO22, KO23, KO24).**

RF, reference sample (wild-type cells cultured at a specific growth rate of  $0.2 \text{ h}^{-1}$ ); GR, wild-type cells cultured at the indicated specific growth rates; KO, single-gene knockout mutants cultured at a specific growth rate of  $0.2 \text{ h}^{-1}$ ; WT, wild-type. X-axis, measured mass distribution; Y-axis, calculated mass distribution; red line, guide line that indicates “ $Y = X$ ”.

**Table S1 Abbreviations for metabolites.**

Abbreviation	Compound name
2-KDPG	2-keto-3-deoxy-6-phospho-gluconate
2-KG	2-keto-glutarate
2PG	2-phosphoglycerate
3PG	3-phosphoglycerate
6PG	6-phosphogluconate
Ac-P	acetylphosphate
AcCoA	acetyl-CoA
ADP	adenosine diphosphate
AMP	adenosine monophosphate
ATP	adenosine triphosphate
CIT	citrate
DHAP	dihydroxyacetone phosphate
E4P	erythrose 4-phosphate
EtOH	ethanol
F6P	fructose 6-phosphate
F1,6P	fructose 1,6-bisphosphate
FUM	fumarate
G1P	glucose 1-phosphate
G3P	glyceraldehyde 3-phosphate
G6P	glucose 6-phosphate
Gcl6P	gluconolactone 6-phosphate
ICT	isocitrate
MAL	malate
NAD	nicotinamide adenine dinucleotide, oxidized
NADH	nicotinamide adenine dinucleotide, reduced
NADP	nicotinamide adenine dinucleotide phosphate, oxidized
NADPH	nicotinamide adenine dinucleotide phosphate, reduced
OAA	oxaloacetate
PEP	phosphoenolpyruvate
PGP	1,3-bisphospho glycerate
PYR	pyruvate
R5P	ribose 5-phosphate
Ru5P	ribulose 5-phosphate
S7P	sedoheptulose 7-phosphate
SUC	succinate
Suc-CoA	succinate-CoA
X5P	xylulose 5-phosphate

**Table S2 Sample ID, sample name, culture date and series ID for quantitative measurements.**

Sample ID	Sample Name	Culture Date	Series ID		
			mRNAs (qRT-PCR)	Proteins (LC-MS/MS)	Metabolites
KO01	galM	9-Jun-05	2	2	2
KO02	glk	4-Aug-05	4	5	3
KO03	pgm	11-Aug-05	4	5	3
KO04	pgi	15-Sep-05	5	5	4
KO05	pfkA	27-Oct-05	6	5	5
KO06	pfkB	11-Aug-05	4	5	3
KO07	fbp	4-Aug-05	4	6	3
KO08	fbaB	25-Aug-05	5	6	3
KO09	gapC	29-Sep-05	5	6	4
KO10	gpmA	21-Jul-05	4	3	3
KO11	gpmB	23-Jun-05	3	3	2
KO12	pykA	16-Jun-05	3	2	2
KO13	pykF	16-Jun-05	3	2	2
KO14	ppsA	9-Jun-05	2	2	2
KO15	zwf	30-Jun-05	3	3	4
KO16	pgl	10-Nov-05	6	6	5
KO17	gnd	2-Jun-05	2	1	2
KO18	rpe	8-Apr-05	1	1	1*
KO19	rpiA	13-Apr-05	1	1	1*
KO20	rpiB	21-Apr-05	1	1	1*
KO21	tktA	27-Apr-05	2	1	1
KO22	tktB	12-May-05	2	1	1
KO23	talA	19-May-05	2	1	1
KO24	talB	26-May-05	2	1	1
GR01	WT, 0.1h <sup>-1</sup>	20-Oct-05	5	4	5
GR02	WT, 0.4h <sup>-1</sup>	20-Oct-05	7	4	5
GR03	WT, 0.5h <sup>-1</sup>	13-Oct-05	6	4	5
GR04	WT, 0.7h <sup>-1</sup>	6-Oct-05	5	4	4
RF01	WT, 0.2h <sup>-1</sup>	11-Feb-05	1, 2, 3		
RF02	WT, 0.2h <sup>-1</sup>	31-Mar-05	1, 2, 3, 5	1	1
RF03	WT, 0.2h <sup>-1</sup>	23-Jun-05	3, 4	2, 3, 4, 5, 6	2
RF04	WT, 0.2h <sup>-1</sup>	21-Jul-05	4		3
RF05	WT, 0.2h <sup>-1</sup>	1-Sep-05	5, 6, 7		4
RF06	WT, 0.2h <sup>-1</sup>	27-Oct-05			5
RF07	WT, 0.2h <sup>-1</sup>	15-Dec-05	6		
RF08	WT, 0.2h <sup>-1</sup>	2-Mar-06	7		

By definition, samples that were analyzed on the same day are given the same series ID number. However, for mRNAs, even though performing all 87 target gene qRT-PCR reactions may have taken more than one day, the samples analyzed together were given the same series ID number.

\* The cations and nucleotides in this series were measured on a day that differed from the measurement of anions.

**Table S3 Dry cell weight measurements.**

Sample ID	Sample Name	Dry cell weight (g/l)
RF01	WT, 0.2h <sup>-1</sup>	-
RF02	WT, 0.2h <sup>-1</sup>	1.621
RF03	WT, 0.2h <sup>-1</sup>	1.409
RF04	WT, 0.2h <sup>-1</sup>	1.609
RF05	WT, 0.2h <sup>-1</sup>	1.556
RF06	WT, 0.2h <sup>-1</sup>	1.510
RF07	WT, 0.2h <sup>-1</sup>	1.604
RF08	WT, 0.2h <sup>-1</sup>	1.622
GR01	WT, 0.1h <sup>-1</sup>	1.615
GR02	WT, 0.4h <sup>-1</sup>	1.720
GR03	WT, 0.5h <sup>-1</sup>	1.640
GR04	WT, 0.7h <sup>-1</sup>	1.060
KO01	galM	1.497
KO02	glk	1.380
KO03	pgm	1.380
KO04	pgi	1.615
KO05	pfkA	1.651
KO06	pfkB	1.430
KO07	fbp	1.580
KO08	fbaB	1.435
KO09	gapC	1.469
KO10	gpmA	1.636
KO11	gpmB	1.439
KO12	pykA	1.591
KO13	pykF	1.541
KO14	ppsA	1.583
KO15	zwf	1.359
KO16	pgl	1.537
KO17	gnd	1.430
KO18	rpe	1.126
KO19	rpiA	1.364
KO20	rpiB	1.171
KO21	tktA	1.189
KO22	tktB	1.585
KO23	talA	1.442
KO24	talB	1.483

-- denotes not measured. RF, reference sample (wild-type cells cultured at a specific growth rate of 0.2 h<sup>-1</sup>); GR, wild-type cells cultured at the indicated specific growth rates; KO, single-gene knockout mutants cultured at a specific growth rate of 0.2 h<sup>-1</sup>; WT, wild-type. See Table S2 for definition of the Sample ID.



**Table S4 Metabolic reactions of *E. coli* K-12 used for metabolic flux analysis.**

Reaction name	Enzymes catalyzing	Reaction
$r_1$	PtsG	Glucose + PEP $\rightarrow$ G6P + PYR
$r_2$	Pgi	G6P $\leftrightarrow$ F6P
$r_3$	PfkA, PfkB	F6P $\rightarrow$ F1,6P
$r_4$	FbaA, FbaB	F1,6P $\rightarrow$ DHAP + G3P
$r_5$	TpiA	DHAP $\rightarrow$ G3P
$r_6$	GapA; Pgk	G3P $\rightarrow$ 3PG
$r_7$	GpmA, GpmB; Eno	3PG $\leftrightarrow$ PEP
$r_8$	PykA, PykF	PEP $\rightarrow$ PYR
$r_9$	AceEF LpdA	PYR $\rightarrow$ AcCoA + CO <sub>2</sub>
$r_{10}$	Zwf	G6P $\rightarrow$ 6PG
$r_{11}$	Pgl; Gnd	6PG $\rightarrow$ Ru5P + CO <sub>2</sub>
$r_{12}$	Rpe	Ru5P $\rightarrow$ X5P
$r_{13}$	RpiA, RpiB	Ru5P $\rightarrow$ R5P
$r_{14}$	TktA, TktB	R5P + X5P $\leftrightarrow$ S7P + G3P
$r_{15}$	TalA, TalB	S7P + G3P $\leftrightarrow$ E4P + F6P
$r_{16}$	TktA, TktB	X5P + E4P $\leftrightarrow$ F6P + G3P
$r_{17}$	GltA, PrpC	AcCoA + OAA $\rightarrow$ CIT
$r_{18}$	AcnA, AcnB	CIT $\rightarrow$ ICT
$r_{19}$	IcdA	ICT $\rightarrow$ 2-KG + CO <sub>2</sub>
$r_{20}$	SucAB LpdA; SucCD	2-KG $\rightarrow$ SUC + CO <sub>2</sub>
$r_{21}$	SdhABCD	SUC $\rightarrow$ FUM
$r_{22}$	FumA, FumB, FumC	FUM $\rightarrow$ MAL
$r_{23}$	Mdh, Mqo	MAL $\leftrightarrow$ OAA
$r_{24}$	Ppc; PckA	PEP + CO <sub>2</sub> $\leftrightarrow$ OAA
$r_{25}$	SfcA, MaeB	MAL $\rightarrow$ PYR + CO <sub>2</sub>
$r_{26}$	AceA	ICT $\rightarrow$ Glyoxylate + SUC
$r_{27}$	AceB	Glyoxylate + AcCoA $\rightarrow$ MAL
$r_{28}$	Edd; Eda	6-PG $\rightarrow$ G3P + PYR
$r_{29}$	Pta; AckA, AckB	AcCoA $\rightarrow$ Acetate
$r_{30}$	LdhA	PYR $\rightarrow$ Lactate
$r_{31}$	AdhE, AdhP	AcCoA $\rightarrow$ Ethanol
$r_{32}$	(Cell synthesis)	G6P $\rightarrow$
$r_{33}$	(Cell synthesis)	F6P $\rightarrow$
$r_{34}$	(Cell synthesis)	R5P $\rightarrow$
$r_{35}$	(Cell synthesis)	E4P $\rightarrow$
$r_{36}$	(Cell synthesis)	G3P $\rightarrow$
$r_{37}$	(Cell synthesis)	3PG $\rightarrow$
$r_{38}$	(Cell synthesis)	PEP $\rightarrow$
$r_{39}$	(Cell synthesis)	PYR $\rightarrow$
$r_{40}$	(Cell synthesis)	AcCoA $\rightarrow$
$r_{41}$	(Cell synthesis)	OAA $\rightarrow$
$r_{42}$	(Cell synthesis)	2KG $\rightarrow$
$r_{43}$	(Evolution)	CO <sub>2</sub> $\rightarrow$

Abbreviations for metabolites are provided in Table S1. Reaction names are shown on a metabolic map in Fig. S2. The enzymes separated by a comma represent isozymes catalyzing the same reaction. Semi columns are used to separate the two individual reactions that are merged into one in the metabolic reaction model.

Table S5 A Metabolic flux analysis results.

Reaction name	RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR			KO			RF			GR		
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**Table S5 B Metabolic flux analysis results (error estimation of reference sample).**

Reaction name	Reaction	Ave	SD	SE	LB	UB
$r_1$	Glucose + PEP → G6P + PYR	100	0	0	NA	NA
$r_2$	G6P ↔ F6P	78	13	6	68	88
$r_3$	F6P → F1,6P	85	5	2	81	89
$r_4$	F1,6P → DHAP + G3P	85	5	2	81	89
$r_5$	DHAP → G3P	85	5	2	81	89
$r_6$	G3P → 3PG	172	6	3	167	177
$r_7$	3PG ↔ PEP	162	6	3	156	167
$r_8$	PEP → PYR	47	1	1	46	49
$r_9$	PYR → AcCoA + CO <sub>2</sub>	129	6	3	125	134
$r_{10}$	G6P → 6PG	21	12	6	10	31
$r_{11}$	6PG → Ru5P + CO <sub>2</sub>	21	12	6	10	31
$r_{12}$	Ru5P → X5P	8	8	4	1	15
$r_{13}$	Ru5P → R5P	12	5	2	9	16
$r_{14}$	R5P + X5P ↔ S7P + G3P	6	4	2	2	9
$r_{15}$	S7P + G3P ↔ E4P + F6P	6	4	2	2	9
$r_{16}$	X5P + E4P ↔ F6P + G3P	2	4	2	-1	6
$r_{17}$	AcCoA + OAA → CIT	86	13	6	76	96
$r_{18}$	CIT → ICT	86	13	6	76	96
$r_{19}$	ICT → 2-KG + CO <sub>2</sub>	71	23	11	52	89
$r_{20}$	2-KG → SUC + CO <sub>2</sub>	62	23	12	43	82
$r_{21}$	SUC → FUM	77	13	7	67	88
$r_{22}$	FUM → MAL	77	13	7	67	88
$r_{23}$	MAL ↔ OAA	89	6	3	84	94
$r_{24}$	PEP + CO <sub>2</sub> ↔ OAA	11	7	4	5	16
$r_{25}$	MAL → PYR + CO <sub>2</sub>	3	7	3	-2	9
$r_{26}$	ICT → Glyoxylate + SUC	15	11	5	6	24
$r_{27}$	Glyoxylate + AcCoA → MAL	15	11	5	6	24
$r_{28}$	6-PG → G3P + PYR	-	-	-	-	-
$r_{29}$	AcCoA → Acetate	0	0	0	NA	NA
$r_{30}$	PYR → Lactate	0	0	0	NA	NA
$r_{31}$	AcCoA → Ethanol	0	0	0	0	0
$r_{32}$	G6P → (Cell synthesis)	2	0	0	1	2
$r_{33}$	F6P → (Cell synthesis)	1	0	0	1	1
$r_{34}$	R5P → (Cell synthesis)	7	1	0	6	7
$r_{35}$	E4P → (Cell synthesis)	3	0	0	3	3
$r_{36}$	G3P → (Cell synthesis)	1	0	0	1	1
$r_{37}$	3PG → (Cell synthesis)	10	1	0	10	11
$r_{38}$	PEP → (Cell synthesis)	4	0	0	3	4
$r_{39}$	PYR → (Cell synthesis)	21	2	1	20	23
$r_{40}$	AcCoA → (Cell synthesis)	29	2	1	26	31
$r_{41}$	OAA → (Cell synthesis)	14	1	1	13	15
$r_{42}$	2KG → (Cell synthesis)	8	1	0	8	9
$r_{43}$	CO <sub>2</sub> → (Evolution)	276	28	14	253	299
$r_2$ <i>exch</i>	G6P ↔ F6P	0.72	0.19	0.09	0.57	0.88
$r_7$ <i>exch</i>	3PG ↔ PEP	0.95	0.00	0.00	0.95	0.95
$r_{14}$ <i>exch</i>	R5P + X5P ↔ S7P + G3P	0.00	0.00	0.00	0.00	0.00
$r_{15}$ <i>exch</i>	S7P + G3P ↔ E4P + F6P	0.65	0.14	0.07	0.54	0.76
$r_{16}$ <i>exch</i>	X5P + E4P ↔ F6P + G3P	0.00	0.00	0.00	0.00	0.00
$r_{23}$ <i>exch</i>	MAL ↔ OAA	0.69	0.39	0.20	0.36	0.95
$r_{24}$ <i>exch</i>	PEP + CO <sub>2</sub> ↔ OAA	0.38	0.05	0.03	0.34	0.42

Error estimations calculated from four reference samples (RF03, RF04, RF05 and RF06).

Ave, average; SD, standard deviation; SE, standard error; LB, lower bound of 90%

confidence interval; UB, upper bound of 90% confidence interval; NA, not applicable

(fluxes are fixed). ”-“ denotes reaction excluded from the model.

**Table S6 Correlation coefficient of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS.**

Sample ID	Sample Name	Correlation coefficient	Number of measurements	P-value
RF03	WT, 0.2h <sup>-1</sup>	0.992	94	< 0.01
RF04	WT, 0.2h <sup>-1</sup>	0.993	94	< 0.01
RF05	WT, 0.2h <sup>-1</sup>	0.995	94	< 0.01
RF06	WT, 0.2h <sup>-1</sup>	0.985	94	< 0.01
GR01	WT, 0.1h <sup>-1</sup>	0.985	94	< 0.01
GR02	WT, 0.4h <sup>-1</sup>	0.987	94	< 0.01
GR03	WT, 0.5h <sup>-1</sup>	0.982	94	< 0.01
GR04	WT, 0.7h <sup>-1</sup>	0.988	41	< 0.01
KO01	galM	0.993	94	< 0.01
KO02	glk	0.995	94	< 0.01
KO03	pgm	0.993	94	< 0.01
KO04	pgi	0.995	94	< 0.01
KO05	pfkA	0.994	94	< 0.01
KO06	pfkB	0.995	94	< 0.01
KO07	fbp	0.995	94	< 0.01
KO08	fbaB	0.994	88	< 0.01
KO09	gapC	0.996	88	< 0.01
KO10	gpmA	0.993	94	< 0.01
KO11	gpmB	0.994	94	< 0.01
KO12	pykA	0.995	94	< 0.01
KO13	pykF	0.994	94	< 0.01
KO14	ppsA	0.995	94	< 0.01
KO15	zwf	0.993	94	< 0.01
KO16	pgl	0.994	94	< 0.01
KO17	gnd	0.989	94	< 0.01
KO18	rpe	0.998	94	< 0.01
KO19	rpiA	0.998	88	< 0.01
KO20	rpiB	0.999	94	< 0.01
KO21	tktA	0.995	94	< 0.01
KO22	tktB	0.994	94	< 0.01
KO23	talA	0.995	83	< 0.01
KO24	talB	0.995	94	< 0.01

RF, reference sample (wild-type cells cultured at a specific growth rate of 0.2 h<sup>-1</sup>); GR, wild-type cells cultured at the indicated specific growth rates; KO, single-gene knockout mutants cultured at a specific growth rate of 0.2 h<sup>-1</sup>; WT, wild-type. See Table S2 for definition of the Sample ID.



Table S7 B Expression ratio values for all measured components (Protein, LC-MS/MS).

RF	GR										KO										RF													
	0.5h <sup>1</sup>	0.4h <sup>1</sup>	0.5h <sup>1</sup>	0.7h <sup>1</sup>	gallM	gik	gpm	pil	pikA	pikB	fbp	fbxB	gapC	gpmA	gpmB	pXA	pXK	pXA	zwf	pil	gnd	ppe	pilA	pilB	tkaA	tkaB	laaB							
RF02-1	0.57	0.99	1.22	1.18	1.00	1.05	1.09	0.66	1.82	1.00	1.01	1.00	0.64	0.79	1.12	0.90	1.24	0.84	1.05	0.95	0.82	1.00	0.65	1.77	1.37	0.63	1.24	1.11	1.17	1.25	0.62	0.85	0.67	
RF03-2	0.56	1.69	0.84	1.00	0.77	0.71	1.12	0.72	1.00	1.97	0.97	1.32	0.91	0.60	1.12	0.90	1.41	0.85	1.07	1.00	1.18	0.95	1.00	0.65	1.77	1.37	0.63	1.24	1.11	1.17	1.25	0.62	0.85	0.67
RF03-3	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-4	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-5	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-6	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-7	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-8	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-9	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-10	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-11	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-12	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-13	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-14	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-15	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-16	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-17	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-18	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-19	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-20	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-21	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-22	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-23	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-24	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-25	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-26	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-27	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56	2.73	0.93	0.19	0.64	1.00	10.87	1.14	1.52	1.00	0.89	1.06	1.00	1.11	0.82	0.94	0.51	1.47	1.92	0.80	0.98	1.40	1.23	0.96	1.00	
RF03-28	0.77	1.16	1.32	2.43	0.68	1.00	0.49	1.17	0.56																									



Table S7 D Expression ratio values for all measured components (Metabolite, Cation(1)).

	RF				GR				KO																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
	RF02	RF03	RF04	RF05	RF06	0.1h	0.4h	0.6h	0.7h	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM



Table S7 E Expression ratio values for all measured components (Metabolite, Cation(2)).

	RF			GR			KO																												
	RF02	RF03	RF04	RF05	RF06	0.1h <sup>+</sup>	0.4h <sup>+</sup>	0.6h <sup>+</sup>	0.7h <sup>+</sup>	gM	gK	gM	gK	pH	pH	pH	pH	pH	pH	pH	pH														
N-Acetylserine	0.84	0.94	0.94	0.96	0.97	0.82	1.33	3.42	1.07	1.48	1.06	1.20	0.89	1.12	1.14	1.12	1.09	0.92	1.03	0.66	0.47	1.00	0.36	1.18	1.60	0.86	0.84	1.53	1.04	0.85	1.52				
N-Ethylglycine	0.47	0.80	1.00	0.91	0.86	1.00	1.85	1.75	1.51	1.11	0.84	0.54	0.43	0.80	1.12	1.14	1.12	1.09	0.92	1.03	0.66	0.47	1.00	0.29	1.38	1.23	1.49	0.79	0.82	1.22	1.02	1.03	0.98		
2-Guanidinobenzimidazole	1.26	1.16	1.00	1.00	1.24	1.05	0.93	1.41	1.00	1.08	0.89	0.86	0.51	0.74	0.51	1.16	0.83	1.01	0.88	1.34	1.70	0.92	1.45	0.76	0.94	0.95	1.00	0.32	1.36	1.21	0.79	0.83	1.18		
Citronellol																																			
Glucosamine																																			
Tyrosine	0.99	1.48	0.64	0.75		1.14	1.19	1.30		0.60	1.27	0.81	0.65	1.16	1.10	0.83	0.78	1.00	0.63	1.20	1.13	2.09	1.14	0.55	1.27	0.84	2.12	0.69	1.00	1.51	0.97	1.39	0.65		
N-Acetylserine																																			
N8-Acetylserine																																			
N8-Acetylserine																																			
Gly-Leu																																			
N8-Acetylserine																																			
2,6-Diaminohexanedioate																																			
5-Methoxytryptamine-2,6-Diaminohexanedioate																																			
2,6-Diaminohexanedioate	1.00	0.93				0.98	0.81	0.30		0.98	0.81	0.30																							
N-Acetylserine																																			
Hydroxylamine																																			
Arginine ethyl ester	0.95					2.69	1.00	0.97		0.92	2.04	1.08	0.72	0.86																					
Tryptophanamide-O-Acetylserine	0.52					1.37	0.63			1.91	0.89	1.43	0.76																						
5-Methoxy-3-Indoleacetaldehyde	1.04	0.76				0.88	1.08	0.96		1.13	0.74	1.04	0.92	0.93	0.72	1.32																			
N-Acetylglucosamine						0.82	1.20	1.10		1.03	0.74	1.04	0.92	0.93	0.72	1.32																			
Carnitine						0.83	1.17			1.00	1.05	1.10	1.25																						
N-Acetylserine						1.00	1.31	1.41		1.00	1.05	1.10	1.25																						
Thymidine-1,5-Diphosphoribitol						0.95	1.27	0.92	1.58	1.00	0.75	0.76	1.06	0.86	1.03	0.68	0.43																		
Cytidine	1.07	0.85				1.43	1.00	0.91		1.67	1.08	1.06	1.03	0.68	0.43																				
N-Acetylserine						1.00	1.05	1.10	1.25	1.02	0.72	0.45	0.75	0.91	1.00	1.00	1.21	0.82	0.84	1.16	0.86	0.68	0.88	0.88	0.88	1.20	1.49	0.89	1.21	0.91	0.66	1.01	1.00		
2-Deoxyadenosine-5'-Oxoadenosine						1.26	0.74			1.00	1.05	1.10	1.25																						
N6-Methyl-2'-deoxyadenosine						1.00	1.03	1.04	1.02	0.78	1.13	0.87	0.92	0.81	1.40	1.05	1.00	0.88	0.74	0.82	1.00	0.58	1.23	0.98	0.91	1.03	0.48	0.93	0.25	0.92	1.04	1.53	0.96		
Adenosine	1.39	1.14	0.88			1.29	1.31	1.01	1.30	0.83	1.78	3.13	1.75	1.68	1.06	1.00	0.86	0.44	0.87	0.50	1.14	1.37	1.37	1.37	0.97	0.71	0.50	1.03	1.06	1.74	1.00	0.94			
Adenosine	0.85	1.21	1.13			1.13	0.87			1.00	1.05	1.10	1.25																						
1-Methyladenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Carnitine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1.00	1.01	1.05	1.00		
Adenosine						1.00	1.23	1.28	1.07	0.95	1.58	2.05	1.44	1.32	1.08	1.00	0.90	0.93	0.94	0.88	1.14	0.54	1.57	0.53	0.96	1.00	0.67	0.89	1.17	1					

Table S7 F Expression ratio values for all measured components (Metabolite, Nucleotide).

	GR										KO																									
	RF02	RF03	RF04	RF05	RF06	0.1h <sup>-1</sup>	0.4h <sup>-1</sup>	0.6h <sup>-1</sup>	0.7h <sup>-1</sup>	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK															
Cratite	1.00	1.00	0.83	1.11	0.71	1.36	1.67	1.80	0.93	0.63	1.07	0.39	2.02	0.05	1.00	0.43	1.00	0.38	0.81	1.32	0.59	1.00	0.59	1.26	1.39	0.87	0.63	0.23	0.83	3.20	0.53	1.51	1.22	0.95	1.00	0.78
Divalent ion from UDP-glucuronate	1.00	1.00	0.83	1.11	0.81	3.32	1.67	2.82	1.76	1.07	0.39	2.02	0.05	1.00	0.43	1.00	0.38	0.81	1.32	0.59	1.00	0.59	1.26	1.39	0.87	0.63	0.23	0.83	3.20	0.53	1.51	1.22	0.95	1.00	0.78	
Divalent ion from UDP-N-acetylglucosamine	1.00	1.00	0.83	1.11	0.81	3.32	1.67	2.82	1.76	1.07	0.39	2.02	0.05	1.00	0.43	1.00	0.38	0.81	1.32	0.59	1.00	0.59	1.26	1.39	0.87	0.63	0.23	0.83	3.20	0.53	1.51	1.22	0.95	1.00	0.78	
dCMP	1.49	2.90	0.84	0.94	0.76	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
dCMP-N-acetylneuramate	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
UMP	1.08	2.32	0.94	0.62	0.85	0.89	1.00	1.08	1.33	1.00	0.72	0.88	1.11	0.40	1.26	1.00	1.09	0.56	0.99	1.81	0.68	0.73	1.47	1.32	1.26	0.63	0.44	4.39	1.27	0.83	0.62	0.94	0.86	1.00	0.90	
cAMP	0.73	0.99	1.04	1.17	1.00	0.74	1.00	2.60	4.06	1.00	1.04	0.86	1.00	0.41	1.00	0.92	1.20	1.53	1.23	1.01	0.62	0.56	0.83	1.26	1.08	0.71	0.75	1.21	1.01	0.84	1.02	0.99	1.00	0.96	1.00	
UMP	1.25	1.15	1.15	1.31	0.91	1.65	1.02	1.14	2.95	1.00	0.82	1.15	0.69	0.94	1.00	0.92	1.20	1.53	1.23	1.01	0.62	0.56	0.83	1.26	1.08	0.71	0.75	1.21	1.01	0.84	1.02	0.99	1.00	0.96	1.00	
GMP	1.11	1.10	0.99	1.13	0.59	1.24	1.00	1.51	3.04	1.00	0.86	0.86	1.00	0.87	1.19	1.01	1.07	0.78	0.77	1.02	0.57	0.52	1.16	0.82	0.93	1.00	0.38	0.88	1.33	0.67	0.89	1.14	1.15	1.00	0.98	
NMP	1.60	1.18	1.00	1.12	0.62	1.28	1.00	1.57	4.30	1.00	0.84	0.85	1.04	0.88	1.29	1.40	0.92	1.13	0.88	0.77	1.19	0.80	0.57	1.30	0.83	0.91	1.00	0.62	1.00	1.45	0.77	0.86	1.17	1.00	0.99	
GMP-N-acetylneuramate	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from NADPH	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from CoA	0.76	2.28	1.00	1.30	1.00	1.32	0.57	0.28	1.00	1.00	0.98	0.48	0.98	0.87	1.59	5.46	0.69	0.69	2.18	0.49	2.04	0.32	0.36	1.45	0.26	1.00	0.62	1.18	1.90	0.79	0.76	1.78	1.50	1.00	0.98	
dCDP	0.98	1.28	1.00	1.10	0.48	1.05	1.00	1.62	3.30	1.00	1.00	0.64	0.69	0.59	1.12	1.25	1.04	1.20	0.90	0.83	0.93	0.52	0.54	1.34	0.78	0.67	1.31	0.41	1.27	1.18	0.77	0.82	1.07	1.02	1.00	
dUDP	0.98	1.28	1.00	1.10	0.48	1.05	1.00	1.62	3.30	1.00	1.00	0.64	0.69	0.59	1.12	1.25	1.04	1.20	0.90	0.83	0.93	0.52	0.54	1.34	0.78	0.67	1.31	0.41	1.27	1.18	0.77	0.82	1.07	1.02	1.00	
CDP	0.87	1.42	1.00	1.02	0.63	1.21	0.99	1.66	1.00	1.00	0.66	0.52	0.69	0.77	1.24	1.18	1.50	0.98	0.72	1.04	0.41	0.60	1.42	0.87	1.00	0.51	0.75	1.33	1.24	0.99	0.89	1.04	1.01	0.98	1.00	
UDP	0.97	1.47	1.00	1.02	0.63	0.79	1.00	1.69	0.59	1.00	0.60	0.58	0.91	1.59	1.34	1.29	1.59	0.98	0.72	1.04	0.46	0.59	1.26	1.60	1.00	0.59	0.75	1.33	1.24	0.99	0.89	1.04	1.01	0.98	1.00	
Divalent ion from Acetyl CoA	1.01	1.09	1.88	0.64	0.96	3.82	1.00	2.36	1.36	1.00	0.76	0.23	0.23	2.01	1.07	1.03	1.30	1.00	0.57	0.68	2.04	0.14	0.26	1.00	0.25	0.84	2.25	0.99	0.48	0.93	1.16	0.90	2.26	1.49	1.00	
Divalent ion from Lauryl CoA	1.02	1.00	1.00	0.68		1.36	0.58	1.00	2.86	1.00	0.70	0.76	0.23	0.23	2.01	1.07	1.03	1.30	1.00	0.57	0.68	2.04	0.14	0.26	1.00	0.25	0.84	2.25	0.99	0.48	0.93	1.16	0.90	2.26	1.49	1.00
Divalent ion from n-Propionyl CoA	0.89	1.15	1.22	0.67	0.28	1.00	2.51	3.31	6.15	1.00	0.63	0.20	0.73	0.51	1.00	1.07	1.16	1.27	0.71	1.66	0.18	0.29	0.72	0.20	1.26	1.03	0.40	0.93	1.48	0.69	2.08	1.13	1.06	0.55	1.08	0.94
Divalent ion from D11 <sup>+</sup>	0.89	1.15	1.22	0.67	0.28	1.00	2.51	3.31	6.15	1.00	0.63	0.20	0.73	0.51	1.00	1.07	1.16	1.27	0.71	1.66	0.18	0.29	0.72	0.20	1.26	1.03	0.40	0.93	1.48	0.69	2.08	1.13	1.06	0.55	1.08	0.94
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
ADP-N-acetylneuramate	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Malonyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.73	0.45	1.16	0.35	1.00	0.78
Divalent ion from Succinyl CoA	1.00	1.00	0.83	1.11	0.81	1.00	0.88	1.63	1.00	1.00	0.73	0.45	1.16	0.35																						

Table S8 A Expression index values for all measured components (mRNA, qRT-PCR).

REF	RG1-1	RF02-2	RF01-1	RF02-3	RF01-3	RF03-4	RF03-5	RF05-5	RF07-6	RF05-7	GH	0.5h	0.4h	0.5h	0.7h	0.9h	1h	1.5h	2h	3h	4h	6h	8h	12h	18h	24h	36h	48h	60h	72h	84h	96h	108h	120h	144h	168h	192h	216h	240h	264h	288h	312h	336h	360h	384h	408h	432h	456h	480h	504h	528h	552h	576h	600h	624h	648h	672h	696h	720h	744h	768h	792h	816h	840h	864h	888h	912h	936h	960h	984h	1008h	1032h	1056h	1080h	1104h	1128h	1152h	1176h	1200h	1224h	1248h	1272h	1296h	1320h	1344h	1368h	1392h	1416h	1440h	1464h	1488h	1512h	1536h	1560h	1584h	1608h	1632h	1656h	1680h	1704h	1728h	1752h	1776h	1800h	1824h	1848h	1872h	1896h	1920h	1944h	1968h	1992h	2016h	2040h	2064h	2088h	2112h	2136h	2160h	2184h	2208h	2232h	2256h	2280h	2304h	2328h	2352h	2376h	2400h	2424h	2448h	2472h	2496h	2520h	2544h	2568h	2592h	2616h	2640h	2664h	2688h	2712h	2736h	2760h	2784h	2808h	2832h	2856h	2880h	2904h	2928h	2952h	2976h	3000h	3024h	3048h	3072h	3096h	3120h	3144h	3168h	3192h	3216h	3240h	3264h	3288h	3312h	3336h	3360h	3384h	3408h	3432h	3456h	3480h	3504h	3528h	3552h	3576h	3600h	3624h	3648h	3672h	3696h	3720h	3744h	3768h	3792h	3816h	3840h	3864h	3888h	3912h	3936h	3960h	3984h	4008h	4032h	4056h	4080h	4104h	4128h	4152h	4176h	4200h	4224h	4248h	4272h	4296h	4320h	4344h	4368h	4392h	4416h	4440h	4464h	4488h	4512h	4536h	4560h	4584h	4608h	4632h	4656h	4680h	4704h	4728h	4752h	4776h	4800h	4824h	4848h	4872h	4896h	4920h	4944h	4968h	4992h	5016h	5040h	5064h	5088h	5112h	5136h	5160h	5184h	5208h	5232h	5256h	5280h	5304h	5328h	5352h	5376h	5400h	5424h	5448h	5472h	5496h	5520h	5544h	5568h	5592h	5616h	5640h	5664h	5688h	5712h	5736h	5760h	5784h	5808h	5832h	5856h	5880h	5904h	5928h	5952h	5976h	6000h	6024h	6048h	6072h	6096h	6120h	6144h	6168h	6192h	6216h	6240h	6264h	6288h	6312h	6336h	6360h	6384h	6408h	6432h	6456h	6480h	6504h	6528h	6552h	6576h	6600h	6624h	6648h	6672h	6696h	6720h	6744h	6768h	6792h	6816h	6840h	6864h	6888h	6912h	6936h	6960h	6984h	7008h	7032h	7056h	7080h	7104h	7128h	7152h	7176h	7200h	7224h	7248h	7272h	7296h	7320h	7344h	7368h	7392h	7416h	7440h	7464h	7488h	7512h	7536h	7560h	7584h	7608h	7632h	7656h	7680h	7704h	7728h	7752h	7776h	7800h	7824h	7848h	7872h	7896h	7920h	7944h	7968h	7992h	8016h	8040h	8064h	8088h	8112h	8136h	8160h	8184h	8208h	8232h	8256h	8280h	8304h	8328h	8352h	8376h	8400h	8424h	8448h	8472h	8496h	8520h	8544h	8568h	8592h	8616h	8640h	8664h	8688h	8712h	8736h	8760h	8784h	8808h	8832h	8856h	8880h	8904h	8928h	8952h	8976h	9000h	9024h	9048h	9072h	9096h	9120h	9144h	9168h	9192h	9216h	9240h	9264h	9288h	9312h	9336h	9360h	9384h	9408h	9432h	9456h	9480h	9504h	9528h	9552h	9576h	9600h	9624h	9648h	9672h	9696h	9720h	9744h	9768h	9792h	9816h	9840h	9864h	9888h	9912h	9936h	9960h	9984h	10008h	10032h	10056h	10080h	10104h	10128h	10152h	10176h	10200h	10224h	10248h	10272h	10296h	10320h	10344h	10368h	10392h	10416h	10440h	10464h	10488h	10512h	10536h	10560h	10584h	10608h	10632h	10656h	10680h	10704h	10728h	10752h	10776h	10800h	10824h	10848h	10872h	10896h	10920h	10944h	10968h	10992h	11016h	11040h	11064h	11088h	11112h	11136h	11160h	11184h	11208h	11232h	11256h	11280h	11304h	11328h	11352h	11376h	11400h	11424h	11448h	11472h	11496h	11520h	11544h	11568h	11592h	11616h	11640h	11664h	11688h	11712h	11736h	11760h	11784h	11808h	11832h	11856h	11880h	11904h	11928h	11952h	11976h	12000h	12024h	12048h	12072h	12096h	12120h	12144h	12168h	12192h	12216h	12240h	12264h	12288h	12312h	12336h	12360h	12384h	12408h	12432h	12456h	12480h	12504h	12528h	12552h	12576h	12600h	12624h	12648h	12672h	12696h	12720h	12744h	12768h	12792h	12816h	12840h	12864h	12888h	12912h	12936h	12960h	12984h	13008h	13032h	13056h	13080h	13104h	13128h	13152h	13176h	13200h	13224h	13248h	13272h	13296h	13320h	13344h	13368h	13392h	13416h	13440h	13464h	13488h	13512h	13536h	13560h	13584h	13608h	13632h	13656h	13680h	13704h	13728h	13752h	13776h	13800h	13824h	13848h	13872h	13896h	13920h	13944h	13968h	13992h	14016h	14040h	14064h	14088h	14112h	14136h	14160h	14184h	14208h	14232h	14256h	14280h	14304h	14328h	14352h	14376h	14400h	14424h	14448h	14472h	14496h	14520h	14544h	14568h	14592h	14616h	14640h	14664h	14688h	14712h	14736h	14760h	14784h	14808h	14832h	14856h	14880h	14904h	14928h	14952h	14976h	15000h	15024h	15048h	15072h	15096h	15120h	15144h	15168h	15192h	15216h	15240h	15264h	15288h	15312h	15336h	15360h	15384h	15408h	15432h	15456h	15480h	15504h	15528h	15552h	15576h	15600h	15624h	15648h	15672h	15696h	15720h	15744h	15768h	15792h	15816h	15840h	15864h	15888h	15912h	15936h	15960h	15984h	16008h	16032h	16056h	16080h	16104h	16128h	16152h	16176h	16200h	16224h	16248h	16272h	16296h	16320h	16344h	16368h	16392h	16416h	16440h	16464h	16488h	16512h	16536h	16560h	16584h	16608h	16632h	16656h	16680h	16704h	16728h	16752h	16776h	16800h	16824h	16848h	16872h	16896h	16920h	16944h	16968h	16992h	17016h	17040h	17064h	17088h	17112h	17136h	17160h	17184h	17208h	17232h	17256h	17280h	17304h	17328h	17352h	17376h	17400h	17424h	17448h	17472h	17496h	17520h	17544h	17568h	17592h	17616h	17640h	17664h	17688h	17712h	17736h	17760h	17784h	17808h	17832h	17856h	17880h	17904h	17928h	17952h	17976h	18000h	18024h	18048h	18072h	18096h	18120h	18144h	18168h	18192h	18216h	18240h	18264h	18288h	18312h	18336h	18360h	18384h	18408h	18432h	18456h	18480h	18504h	18528h	18552h	18576h	18600h	18624h	18648h	18672h	18696h	18720h	18744h	18768h	18792h	18816h	18840h	18864h	18888h	18912h	18936h	18960h	18984h	19008h	19032h	19056h	19080h	19104h	19128h	19152h	19176h	19200h	19224h	19248h	19272h	19296h	19320h	19344h	19368h	19392h	19416h	19440h	19464h	19488h	19512h	19536h	19560h	19584h	19608h	19632h	19656h	19680h	19704h	19728h	19752h	19776h	19800h	19824h	19848h	19872h	19896h	19920h	19944h	19968h	19992h	20016h	20040h	20064h	20088h	20112h	20136h	20160h	20184h	20208h	20232h	20256h	20280h	20304h	20328h	20352h	20376h	20400h	20424h	20448h	20472h	20496h	20520h	20544h	20568h	20592h	20616h	20640h	20664h	20688h	20712h	20736h	20760h	20784h	20808h	20832h	20856h	20880h	20904h	20928h	20952h	20976h	21000h	21024h	21048h	21072h	21096h	21120h	21144h	21168h	21192h	21216h	21240h	21264h	21288h	21312h	21336h	21360h	21384h	21408h	21432h	21456h	21480h	21504h	21528h	21552h	21576h	21600h	21624h	21648h	21672h	21696h	21720h	21744h	21768h	21792h	21816h	21840h	21864h	21888h	21912h	21936h	21960h	21984h	22008h	22032h	22056h	22080h	22104h	22128h	22152h	22176h	22200h	22224h	22248h	22272h	22296h	22320h	22344h	22368h	22392h	22416h	22440h	22464h	22488h	22512h	22536h	22560h	22584h	22608h	22632h	22656h	22680h	22704h	22728h	22752h	22776h	22800h	22824h	22848h	22872h	22896h	22920h	22944h	22968h	22992h	23016h	23040h	23064h	23088h	23112h	23136h	23160h	23184h	23208h	23232h	23256h	23280h	23304h	23328h	23352h	23376h	23400h	23424h	23448h	23472h	23496h	23520h	23544h	23568h	23592h	23616h	23640h	23664h	23688h	23712h	23736h	23760h	23784h	23808h	23832h	23856h	23880h	23904h	23928h	23952h	23976h	24000h	24024h	24048h	24072h	24096h	24120h	24144h	24168h	24192h	24216h	24240h	24264h	24288h	24312h	24336h	24360h	24384h	24408h	24432h	24456h	24480h	24504h	24528h	24552h	24576h	24600h	24624h	24648h	24672h	24696h	24720h	24744h	24768h	24792h	24816h	24840h	24864h	24888h	24912h	24936h	24960h	24984h	25008h	25032h	25056h	25080h	25104h	25128h	25152h	25176h	25200h	25224h	25248h	25272h	25296h	25320h	25344h	25368h	25392h	25416h	25440h	25464h	25488h	25512h	25536h	25560h	25584h	25608h	25632h	25656h	25680h	25704h	25728h	25752h	25776h	25800h	25824h	25848h	25872h	25896h	25920h	25944h	25968h	25992h	26016h	26040h	26064h	26088h	26112h	26136h	26160h	26184h	26208h	26232h	26256h	26280h	26304h	26328h	26352h	26376h	26400h	26424h	26448h	26472h	26496h	26520h	26544h	26568h	26592h	26616h	26640h	26664h	26688h	26712h	26736h	26760h	26784h	26808h	26832h	26856h	26880h	26904h	26928h	26952h	26976h	27000h	27024h	27048h	27072h	27096h	27120h	27144h	27168h	27192h	27216h</
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Table S8 D Expression index values for all measured components (Metabolite, Cation(1)).

	GR										KO										MB													
	RF02	RF03	RF04	RF05	RF06	0.1h <sup>+</sup>	0.4h <sup>+</sup>	0.6h <sup>+</sup>	0.7h <sup>+</sup>	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	gM	gK	
Gly	0.21	0.32				-0.80	0.375	-0.11	3.20	0.00	-1.86	-1.75	-1.17	-0.65	-0.98	0.00	-1.91	0.77	-3.40	2.39	0.00	-0.80	1.82	1.60	-0.13	2.13	-1.00	-1.79	-2.45	-0.22	1.95	0.94	2.18	-0.27
Isopropylamine						0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Trimethylamine N-oxide						0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Pyridine	-0.25			1.00	1.37	-1.00	-0.74	0.00	-1.10	-2.02	3.65	0.17	3.63	1.24	-0.11	-3.94		-1.90	0.11														0.00	
Pyridine				-5.07		1.83	-2.23	0.00			0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Isopropylamine				-0.96	-1.15	0.15	2.33			0.82	-1.22	-2.42	0.68	-1.21	-0.32	2.07	0.04	-0.79	0.00	5.90	-3.84	-1.37	1.22	-1.64	0.27	-0.33	-0.88	-3.72	1.43	0.00	-3.00	1.23	0.75	
Trimethylamine				-1.30	3.95	1.58	2.40			-1.46	-2.03	-3.05	-2.61	-0.20	-1.64	0.90	-1.25	0.69	1.71	-0.80	0.00	0.44	-0.10	2.54	0.54	0.88	-1.51	1.06	0.75	-0.78	0.76	-0.84	0.58	
beta-Ala				-2.86	-0.12					1.82	0.73		-5.44	0.12	-0.75				1.07														0.68	
3-Amino-1,2-propanediol	-1.00			-2.21		0.00				0.00	2.72	1.60	1.04																					
1,5-Diaminopropane						-0.60	4.62	0.00	6.89	-0.38	0.00	-3.61		2.30	0.10	-0.11	0.90	0.00	1.07	4.39	0.36	0.00	-1.78	-0.01	-1.64	2.66	3.06	-1.37	1.36	0.73	-1.00	-0.87	1.59	
GABA				-0.95	-1.24	-1.23	1.93	2.37	0.00	-1.03	1.36	-1.11		-1.62	0.32	0.00	-1.96		0.54	2.89	0.65	0.13	-1.62	-2.02	0.00	-0.36	2.34	0.97	-1.31	-0.30	0.67			
alpha-Aminoisobutyrate						0.00				0.00	1.00							1.00																
N,N-Dimethylglycine	0.00			-8.57		0.21	3.92	0.00	0.76	-0.95	-1.27	-1.15	-1.01	-1.53	0.00	-2.19	0.68	-2.24	2.03	-0.04	0.00	2.62	2.61	-0.43	2.89	-0.61	-2.21	-2.75	-0.16	2.31	1.00	3.02	0.12	
Ser	-0.12	0.37	1.98	0.37	-0.13	0.00	-0.96	-1.15	2.33	0.82	-1.22	-2.42	0.68	-1.21	-0.32	2.07	0.04	-0.79	0.00	5.90	-3.84	-1.37	1.22	-1.64	0.27	-0.33	-0.88	-3.72	1.43	0.00	-3.00	1.23	0.75	
Dihydroxyacetone	1.65	1.00	0.56			2.42	1.15	-2.80	6.10	-1.89	-0.58	0.98	-0.60	0.52	-1.91	0.34	0.00	0.00	2.89	1.20	0.26	1.20	0.50	-1.16	-3.07	-0.26	1.25	0.00	-0.26	1.25	0.00	-0.26	1.25	
Histamine				0.00		0.57	-2.17	-1.55		-0.07	0.34	1.09		2.26	0.00	-1.28	-1.15	-0.20	-0.48	0.07	2.81												-1.18	
Creatine						0.00			1.89		2.92	1.41	-5.52		-0.48	-0.04	-0.59	-2.53	0.56															
2-Mercapto-1-methylimidazole						0.00				0.00	-1.33	-4.26	-1.73	-3.36	0.00	-0.87	0.40	-0.39	1.58	2.58	-0.99	-0.13	0.60	-1.18	2.12	1.46	-4.52	-0.21	2.05	0.35	1.31	-1.00		
Guanidoxalate	-2.51	-0.84	1.00	0.74	0.00	-1.18	3.84	1.28	0.37	0.00	-1.33	-4.26	-1.73	-3.36	0.00	-0.87	0.40	-0.39	1.58	2.58	-0.99	-0.13	0.60	-1.18	2.12	1.46	-4.52	-0.21	2.05	0.35	1.31	-1.00		
Val						0.00			2.34	-1.67	-1.22	-4.93	-4.94	-3.09	0.21	-0.66	1.03	-2.65	0.00	1.69	-0.50	2.32	0.00	0.97	0.46	-0.86	0.00	-0.24	2.89	1.20	-0.88	0.64	-0.19	
Val						-5.94	1.12	0.03	2.68	0.00	0.29	-0.84	-0.28	-0.30	-0.55	1.74	0.00	0.08	-2.05	1.11	-1.03	-2.75	-0.30	-0.32	0.00	1.00	-5.58	-2.13	1.94	2.44	-0.49	0.00	3.22	
2,4-Diaminobutyrate						0.00	0.29	-0.84	-0.28	0.00	0.29	-0.84	-0.28	-0.30	-0.55	1.74	0.00	0.08	-2.05	1.11	-1.03	-2.75	-0.30	-0.32	0.00	1.00	-5.58	-2.13	1.94	2.44	-0.49	0.00	3.22	
2,4-Diaminobutyrate						0.00	0.29	-0.84	-0.28	0.00	0.29	-0.84	-0.28	-0.30	-0.55	1.74	0.00	0.08	-2.05	1.11	-1.03	-2.75	-0.30	-0.32	0.00	1.00	-5.58	-2.13	1.94	2.44	-0.49	0.00	3.22	
Homoserine						0.12	0.93	-0.25		-2.35	0.44	-1.52		-4.38	5.33	-0.48		0.00	0.78	1.00	-0.99	0.52	-1.51	-4.75	0.20	3.33	-0.29	3.39	2.71	0.00	1.79	1.30		
Thr						-1.07	3.81	2.65	1.98	-0.85	-0.18	-1.22	-1.53	-1.72	0.00	-1.14	0.63	-2.20	0.90	1.11	-0.16	0.50	0.86	-0.29	2.34	-0.04	-1.43	-3.88	-1.63	0.90	0.00	1.79	1.30	
Pro						0.00				0.00	2.02	1.41	-5.52		-0.48	-0.04	-0.59	-2.53	0.56															
Cys						0.00				0.00	-1.33	-4.26	-1.73	-3.36	0.00	-0.87	0.40	-0.39	1.58	2.58	-0.99	-0.13	0.60	-1.18	2.12	1.46	-4.52	-0.21	2.05	0.35	1.31	-1.00</		



Table S8 F Expression index values for all measured components (Metabolite, Nucleotide).

RF02	GR					KO										wild-type																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
	RF02	RF03	RF04	RF05	RF06	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk	gk



Table S9 A, B AEI values for all experimental conditions tested.

## A. mRNAs, qRT-PCR

		mRNAs (qRT-PCR)					
	N	Ave (AEI)	SD	SE	LB	UB	
RF	RF02-1	85	1.120	1.050	0.114	0.894	1.346
	RF01-1	85	0.886	1.084	0.118	0.652	1.119
	RF02-2	85	1.579	1.375	0.149	1.282	1.875
	RF01-1	85	0.873	1.077	0.117	0.641	1.105
	RF02-3	85	1.647	1.338	0.145	1.359	1.936
	RF01-3	85	0.679	0.668	0.072	0.535	0.823
	RF03-3	85	0.945	0.864	0.094	0.759	1.132
	RF04-4	85	1.003	0.894	0.097	0.810	1.196
	RF03-4	85	0.865	0.966	0.105	0.656	1.073
	RF02-5	85	1.404	1.161	0.126	1.154	1.654
	RF05-5	85	1.152	1.027	0.111	0.930	1.373
	RF05-6	85	1.746	1.342	0.146	1.456	2.035
	RF07-6	85	2.050	1.817	0.197	1.658	2.442
	RF05-7	85	1.192	1.120	0.121	0.950	1.433
	RF08-7	85	1.170	1.277	0.138	0.895	1.445
GR	0.1h-1	85	2.086	1.654	0.179	1.730	2.443
	0.4h-1	85	1.996	1.659	0.180	1.638	2.353
	0.5h-1	85	4.369	5.407	0.586	3.202	5.535
	0.7h-1	85	6.727	6.426	0.697	5.341	8.113
KO	galM	84	0.724	0.883	0.096	0.532	0.915
	glk	84	1.499	1.476	0.161	1.179	1.819
	pgm	84	2.467	1.866	0.204	2.062	2.872
	pgi	84	3.161	3.344	0.365	2.435	3.887
	pfkA	84	3.283	3.612	0.394	2.499	4.067
	pfkB	84	0.643	0.582	0.064	0.516	0.769
	fbp	84	1.014	0.896	0.098	0.820	1.208
	fbaB	84	1.382	1.296	0.141	1.101	1.664
	gapC	83	2.143	2.247	0.247	1.653	2.634
	gpmA	84	0.904	0.997	0.109	0.687	1.120
	gpmB	84	0.944	0.800	0.087	0.770	1.117
	pykA	84	0.648	0.661	0.072	0.505	0.791
	pykF	84	0.569	0.599	0.065	0.439	0.699
	ppsA	84	0.636	0.573	0.063	0.512	0.761
	zwf	84	1.117	1.123	0.123	0.874	1.361
	pgl	84	1.737	1.696	0.185	1.369	2.105
	gnd	84	1.666	1.541	0.168	1.332	2.000
	rpe	84	5.162	4.995	0.545	4.078	6.246
	rpiA	84	1.584	3.280	0.358	0.872	2.296
	rpiB	84	1.012	1.217	0.133	0.747	1.276
	tktA	84	2.680	2.073	0.226	2.230	3.130
	tktB	84	0.912	0.863	0.094	0.725	1.099
	talA	84	0.962	0.998	0.109	0.746	1.179
	talB	84	1.154	0.974	0.106	0.942	1.365

## B. Proteins, LC-MS/MS

		Proteins (LC-MS/MS)					
	N	Ave (AEI)	SD	SE	LB	UB	
RF	RF02-1	57	2.070	1.853	0.245	1.578	2.562
	RF03-2	57	1.379	1.422	0.188	1.002	1.756
	RF03-3	58	1.443	1.321	0.174	1.095	1.790
	RF03-4	56	1.875	1.901	0.254	1.366	2.384
	RF03-5	56	1.082	1.046	0.140	0.802	1.362
	RF03-6	56	1.729	2.299	0.307	1.113	2.344
GR	0.1h-1	56	2.437	2.837	0.379	1.678	3.197
	0.4h-1	55	2.033	2.554	0.344	1.343	2.724
	0.5h-1	56	2.558	3.597	0.481	1.595	3.521
	0.7h-1	55	4.031	3.970	0.535	2.958	5.105
KO	galM	56	0.595	0.544	0.073	0.449	0.740
	glk	56	2.163	1.758	0.235	1.692	2.634
	pgm	55	1.831	1.591	0.215	1.401	2.261
	pgi	55	2.257	2.189	0.295	1.665	2.849
	pfkA	56	1.771	1.836	0.245	1.279	2.262
	pfkB	55	1.121	0.866	0.117	0.887	1.355
	fbp	55	1.593	1.624	0.219	1.154	2.031
	fbaB	56	2.058	2.144	0.286	1.484	2.632
	gapC	54	1.706	2.231	0.304	1.097	2.316
	gpmA	57	1.237	1.150	0.152	0.932	1.542
	gpmB	58	1.070	1.066	0.140	0.790	1.351
	pykA	56	0.475	0.547	0.073	0.328	0.621
	pykF	56	0.500	0.570	0.076	0.347	0.652
	ppsA	56	0.653	0.615	0.082	0.488	0.817
	zwf	57	0.801	0.589	0.078	0.644	0.957
	pgl	55	1.243	1.269	0.171	0.900	1.586
	gnd	55	1.049	1.254	0.169	0.710	1.388
	rpe	55	3.333	3.116	0.420	2.490	4.175
	rpiA	56	1.864	2.034	0.272	1.319	2.409
	rpiB	57	1.358	1.288	0.171	1.016	1.700
	tktA	56	1.339	1.172	0.157	1.025	1.653
	tktB	56	1.434	1.636	0.219	0.996	1.872
	talA	56	1.480	1.615	0.216	1.048	1.913
	talB	56	1.369	1.685	0.225	0.918	1.821

Table S9 C, D AEI values for all experimental conditions tested.

## C. Metabolites\*

		Metabolites					
		N	Ave (AEI)	SD	SE	LB	UB
RF	RF02-1	103	1.228	1.187	0.117	0.996	1.460
	RF03-2	129	0.925	0.903	0.079	0.768	1.083
	RF04-3	156	1.257	1.827	0.146	0.968	1.545
	RF05-4	119	1.220	1.181	0.108	1.006	1.434
	RF06-5	125	0.951	1.052	0.094	0.764	1.137

## D. Metabolites (excluding nucleotides)\*

		Metabolites (excluding nucleotides)					
	N	Ave (AEI)	SD	SE	LB	UB	
RF	RF02-1	64	1.530	1.345	0.168	1.194	1.866
	RF03-2	89	0.816	0.870	0.092	0.633	0.999
	RF04-3	112	1.570	2.032	0.192	1.190	1.950
	RF05-4	75	1.157	1.032	0.119	0.920	1.395
	RF06-5	82	0.662	0.811	0.090	0.483	0.840

GR	0.1h-1	170	1.560	1.854	0.142	1.279	1.841
	0.4h-1	154	1.336	1.295	0.104	1.130	1.543
	0.5h-1	132	1.590	1.726	0.150	1.292	1.887
	0.7h-1	122	2.046	2.170	0.196	1.657	2.435

GR	0.1h-1	125	1.550	1.960	0.175	1.203	1.897
	0.4h-1	109	1.517	1.204	0.115	1.288	1.745
	0.5h-1	88	1.417	1.886	0.201	1.017	1.816
	0.7h-1	82	1.681	1.951	0.215	1.253	2.110

KO	galM	127	0.732	0.756	0.067	0.600	0.865
	glk	183	2.322	3.362	0.249	1.832	2.813
	pgm	157	2.762	2.976	0.238	2.292	3.231
	pgi	100	2.946	2.752	0.275	2.400	3.492
	pfkA	122	1.972	1.940	0.176	1.624	2.319
	pfkB	171	0.861	1.122	0.086	0.692	1.031
	fbp	184	0.925	1.112	0.082	0.763	1.087
	fbaB	145	1.065	1.216	0.101	0.866	1.265
	gapC	114	1.411	1.280	0.120	1.174	1.649
	gpmA	151	1.091	1.501	0.122	0.850	1.332
	gpmB	128	1.497	1.783	0.158	1.186	1.809
	pykA	130	2.223	2.089	0.183	1.860	2.585
	pykF	124	2.045	1.540	0.138	1.771	2.318
	ppsA	133	0.960	0.979	0.085	0.792	1.128
	zwf	105	1.889	1.923	0.188	1.516	2.261
	pgl	124	1.429	1.577	0.142	1.149	1.709
	gnd	132	1.997	2.344	0.204	1.593	2.400
	rpe	131	2.797	2.863	0.250	2.303	3.292
	rpiA	144	1.749	1.776	0.148	1.457	2.042
	rpiB	138	1.333	1.500	0.128	1.081	1.586
	tktA	168	1.211	1.356	0.105	1.005	1.418
	tktB	134	1.535	1.273	0.110	1.318	1.753
	talA	142	0.978	1.375	0.115	0.750	1.206
	talB	141	1.238	2.932	0.247	0.750	1.726

KO	galM	89	0.842	0.773	0.082	0.679	1.005
	glk	138	2.174	3.768	0.321	1.540	2.809
	pgm	118	2.436	2.576	0.237	1.966	2.906
	pgi	60	2.205	1.773	0.229	1.747	2.663
	pfkA	80	2.300	2.005	0.224	1.854	2.746
	pfkB	124	0.876	1.222	0.110	0.659	1.093
	fbp	135	0.977	1.146	0.099	0.782	1.172
	fbaB	97	1.131	1.395	0.142	0.850	1.412
	gapC	70	1.450	1.316	0.157	1.136	1.764
	gpmA	106	1.288	1.716	0.167	0.957	1.618
	gpmB	89	1.817	1.989	0.211	1.398	2.236
	pykA	90	1.248	1.243	0.131	0.987	1.508
	pykF	87	1.623	1.489	0.160	1.305	1.940
	ppsA	92	1.005	1.020	0.106	0.793	1.216
	zwf	67	1.550	1.806	0.221	1.110	1.991
	pgl	82	1.620	1.632	0.180	1.261	1.978
	gnd	90	1.823	2.095	0.221	1.384	2.261
	rpe	91	3.064	3.163	0.332	2.406	3.723
	rpiA	98	1.648	1.783	0.180	1.291	2.006
	rpiB	91	1.379	1.585	0.166	1.049	1.709
	tktA	124	1.250	1.482	0.133	0.986	1.513
	tktB	90	1.601	1.446	0.152	1.298	1.904
	talA	97	1.165	1.587	0.161	0.845	1.485
	talB	96	1.563	3.463	0.353	0.862	2.265

\* For calculation of AEIs of metabolites, the following compounds were excluded because they included extreme outliers values that were considered unreliable: 2-mercapto-1-methylimidazol, phenaceturate and 2,4-dihydroxypyrimidine-5-carboxylate.

**Table S9 E, F AEI values for all experimental conditions tested.****E. mRNAs, DNA microarray**

mRNAs (Microarray)						
	N	Ave (AEI)	SD	SE	LB	UB
RF	3757	1.268	1.553	0.025	1.218	1.317
(WT, 0.2 h <sup>-1</sup> )	3633	1.341	2.227	0.037	1.269	1.414

**F. Proteins, 2D-DIGE**

Proteins (2D-DIGE)						
	N	Ave (AEI)	SD	SE	LB	UB
RF	1311	1.384	1.471	0.041	1.304	1.463
(WT, 0.2 h <sup>-1</sup> )	1311	0.981	0.909	0.025	0.932	1.030
	1013	0.952	0.905	0.028	0.896	1.007
	1013	1.346	1.356	0.043	1.262	1.430

GR	0.1h-1					
	0.4h-1					
	0.5h-1	3964	2.245	3.426	0.054	2.138 2.352
	0.7h-1	4063	3.137	4.360	0.068	3.003 3.271
KO	galM					
	glk					
	pgm	4122	1.125	1.757	0.027	1.071 1.178
	pgi	4141	1.445	2.698	0.042	1.363 1.528
	pfkA					
	pfkB					
	fbp					
	fbaB					
	gapC	4128	1.327	2.223	0.035	1.259 1.395
	gpmA					
	gpmB					
	pykA					
	pykF					
	ppsA					
	zwf	4126	0.912	1.116	0.017	0.878 0.947
	pgl					
	gnd					
	rpe	4049	2.065	3.619	0.057	1.953 2.176
	rpiA					
	rpiB					
	tktA					
	tktB					
	talA					
	talB					

GR	0.1h-1	1042	1.372	1.252	0.039	1.296 1.448
	0.4h-1	1102	1.420	1.377	0.041	1.339 1.502
	0.5h-1	1067	2.127	2.679	0.082	1.966 2.288
	0.7h-1	1086	3.319	3.563	0.108	3.107 3.531
KO	galM	1120	1.035	1.125	0.034	0.969 1.101
	glk	1543	1.029	1.303	0.033	0.964 1.094
	pgm	1213	1.758	1.772	0.051	1.658 1.858
	pgi	1392	2.483	2.555	0.068	2.349 2.617
	pfkA	1082	1.802	1.990	0.060	1.684 1.921
	pfkB	1121	0.973	1.136	0.034	0.907 1.040
	fbp	1234	1.495	5.926	0.169	1.164 1.826
	fbaB	1330	1.299	1.364	0.037	1.226 1.373
	gapC	1386	1.071	1.271	0.034	1.004 1.138
	gpmA	1271	1.161	1.779	0.050	1.063 1.259
	gpmB	1069	1.300	1.192	0.036	1.228 1.371
	pykA	1087	1.144	1.147	0.035	1.075 1.212
	pykF	1091	1.286	1.650	0.050	1.188 1.384
	ppsA	995	1.155	1.430	0.045	1.066 1.244
	zwf	1148	1.283	1.153	0.034	1.216 1.349
	pgl	1250	2.380	3.805	0.108	2.169 2.591
	gnd	1219	1.166	1.906	0.055	1.059 1.273
	rpe	1038	2.506	2.700	0.084	2.342 2.671
	rpiA	1098	1.323	3.246	0.098	1.131 1.516
	rpiB	1367	1.131	1.309	0.035	1.061 1.200
	tktA	1006	1.101	1.187	0.037	1.028 1.175
	tktB	1053	1.104	1.241	0.038	1.029 1.179
	talA	1049	0.988	0.995	0.031	0.928 1.048
	talB	1096	1.501	1.446	0.044	1.416 1.587

RF, reference sample (wild-type cells cultured at a specific growth rate of 0.2 h<sup>-1</sup>); GR, wild-type cells cultured at the indicated specific growth rates; KO, single-gene knockout mutants cultured at a specific growth rate of 0.2 h<sup>-1</sup>; WT, wild-type. The components marked by blank cells were not examined. N, number of components; Ave, average of EIs (AEI); SD, standard deviation of EIs; SE, standard error; LB, lower bound of 95% confidence interval; UB, upper bound of 95% confidence interval.

**Table S10 A Statistical tests for AEIs (mRNAs, qRT-PCR)****Test of Homogeneity of Variances**

mRNA(qRT-PCR)

Levene Statistic	df1	df2	Sig.
30.604	28	2,411	3.44E-137

**ANOVA**

mRNA(qRT-PCR)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	5,080.689	28	181.453	31.018	5.46E-139
Within Groups	14,104.142	2,411	5.850		
Total	19,184.831	2,439			

**Robust Tests of Equality of Means**

mRNA(qRT-PCR)

	Statistic(a)	df1	df2	Sig.
Welch	21.700	28	860.026	5.81E-81

a. Asymptotically F distributed.

Multiple Comparisons											Multiple Comparisons										
Dependent Variable: mRNA(qRT-PCR)											Dependent Variable: mRNA(qRT-PCR)										
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval		(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval							
						Lower Bound	Upper Bound							Lower Bound	Upper Bound						
gpm	gk	-0.775	S	0.188	1.77E-02	-1.401	-0.060	pkb	gsm	0.081	S	0.115	1.00E+00	-0.521	0.359						
	pgm	-1.743	S	0.229	1.56E-09	-2.605	-0.881	pkb	gk	-0.856	S	0.173	9.96E-04	-1.520	-0.190						
	pgl	-2.437	S	0.377	1.77E-06	-3.890	-0.985	pgm	-1.824	S	0.213	1.13E-10	-2.644	-1.004							
	pkA	-2.560	S	0.292	3.65E-06	-4.122	-0.997	pkB	-2.517	S	0.369	1.12E-06	-3.947	-1.089							
	pkB	0.081	S	0.115	1.00E+00	-0.359	0.521	pkB	-2.640	S	0.369	1.11E-06	-4.181	-1.100							
	fbp	-0.282	S	0.137	9.46E-01	-0.812	0.231	fbp	-0.371	ns	0.171	2.65E-01	-0.815	0.073							
	ftaB	-0.659	S	0.171	4.39E-02	-1.311	-0.007	ftaB	-0.748	S	0.205	1.45E-02	-1.152	-0.344							
	gapC	-1.420	S	0.265	1.76E-04	-2.435	-0.404	gapC	-1.500	S	0.255	2.30E-05	-2.481	-0.519							
	gpmA	-0.183	S	0.145	1.00E+00	-0.732	0.372	gpmA	-0.261	ns	0.126	9.95E-01	-0.723	0.220							
	gpmB	-0.220	S	0.130	9.97E-01	-0.714	0.274	gpmB	-0.133	ns	0.106	5.45E-01	-0.712	0.445							
	pykA	0.076	S	0.102	1.00E+00	-0.382	0.534	pykA	-0.005	ns	0.096	1.00E+00	-0.370	0.360							
	pykF	0.154	S	0.116	1.00E+00	-0.289	0.598	pykF	0.074	ns	0.109	1.00E+00	-0.273	0.420							
	ppsA	0.087	S	0.115	1.00E+00	-0.350	0.525	ppsA	0.036	ns	0.105	1.00E+00	-0.332	0.404							
	zwf	-0.394	S	0.156	7.42E-01	-0.998	0.199	zwf	-0.473	ns	0.138	1.46E-01	-1.002	0.053							
	gnd	-1.013	S	0.209	1.20E-03	-1.810	-0.216	gnd	-1.094	S	0.198	9.96E-05	-1.845	-0.343							
	rpe	-4.438	S	0.554	1.73E-09	-6.574	-2.303	rpe	-4.103	S	0.581	9.75E-10	-6.139	-2.067							
	rpA	-0.860	S	0.371	8.61E-01	-2.287	0.566	rpA	-0.941	ns	0.363	9.64E-01	-2.243	0.461							
	rpB	-0.288	S	0.166	9.95E-01	-0.912	0.337	rpB	-0.369	ns	0.147	7.55E-01	-0.932	0.194							
	tdA	-1.956	S	0.246	6.80E-10	-2.898	-1.014	tdA	-2.035	S	0.235	1.34E-11	-2.941	-1.133							
	tdB	-0.188	S	0.135	1.00E+00	-0.700	0.324	tdB	-0.269	ns	0.114	8.40E-01	-0.800	0.261							
	tdB	-0.238	S	0.145	9.99E-01	-0.791	0.314	tdB	-0.319	ns	0.126	7.36E-01	-0.800	0.162							
	0.1h-1	-1.363	S	0.204	2.43E-07	-2.140	-0.585	0.1h-1	-1.443	S	0.194	1.79E-05	-2.174	-0.712							
	0.2h-1	-0.428	S	0.147	4.52E-01	-0.988	0.132	0.2h-1	-0.509	ns	0.128	0.96E-02	-0.998	-0.010							
	0.4h-1	-1.272	S	0.204	2.39E-06	-2.150	-0.493	0.4h-1	-1.353	S	0.191	6.95E-02	-2.029	-0.621							
	0.5h-1	-3.645	S	0.594	8.98E-06	-5.937	-1.352	0.5h-1	-3.722	S	0.591	8.44E-06	-6.003	-1.340							
	0.7h-1	-6.003	S	0.704	2.12E-10	-8.718	-3.288	0.7h-1	-6.084	S	0.700	1.38E-10	-8.787	-3.381							
	gk	gsm	0.081	S	0.188	1.77E-02	0.060	1.491	gsm	0.296	ns	0.137	9.46E-01	-0.231	0.817						
		pgm	-0.968	S	0.260	6.30E-02	-1.955	0.019	pgm	-1.488	S	0.408	1.05E-01	-2.303	-0.673						
		pgl	-1.662	S	0.399	1.68E-02	-3.190	-0.135	pgl	-2.145	S	0.522	0.07E-02	-3.217	-0.889						
		pkA	-1.794	S	0.429	1.57E-02	-3.416	-0.153	pkA	-2.147	S	0.378	5.36E-05	-3.601	-0.693						
pkB		0.081	S	0.173	8.99E-04	-0.192	1.320	pkB	-0.260	ns	0.146	8.26E-05	-0.799	0.439							
fbp		0.485	S	0.188	7.06E-01	-0.233	1.203	fbp	0.371	ns	0.171	2.65E-01	-0.073	0.819							
ftaB		0.116	S	0.214	1.00E+00	-0.698	0.931	ftaB	-0.369	ns	0.172	9.37E-01	-1.023	0.288							
gapC		-0.644	S	0.295	9.22E-01	-1.757	0.478	gapC	-1.129	S	0.265	1.27E-02	-2.147	-0.111							
gpmA		0.595	S	0.194	3.41E-01	-0.145	1.335	gpmA	0.116	ns	0.111	1.00E+00	-0.466	0.700							
gpmB		0.555	S	0.183	3.63E-01	-0.144	1.255	gpmB	0.070	ns	0.131	1.00E+00	-0.428	0.588							
pykA		0.651	S	0.176	1.47E-03	0.175	1.527	pykA	0.369	ns	0.121	3.73E-01	-0.096	0.829							
pykF		0.930	S	0.174	1.78E-04	0.263	1.596	pykF	0.448	S	0.146	5.43E-02	0.150	0.746							
ppsA		0.662	S	0.173	7.98E-04	0.200	1.525	ppsA	0.377	ns	0.116	2.27E-01	-0.606	0.819							
zwf		0.381	S	0.202	9.86E-01	-0.398	1.151	zwf	-0.104	ns	0.157	1.00E+00	-0.699	0.492							
gnd		-0.238	S	0.245	1.00E+00	-1.171	0.694	gnd	-0.320	ns	0.172	9.61E-01	-1.522	0.400							
rpe		-3.603	S	0.233	1.00E+00	-1.051	0.717	rpe	-0.652	ns	0.194	1.80E-01	-1.394	0.096							
rpA		-0.065	S	0.568	1.72E-06	-5.649	-1.477	rpA	-4.148	S	0.554	1.96E-08	-6.284	-2.012							
rpB		0.497	S	0.362	1.00E+00	-1.187	1.417	rpB	-0.576	ns	0.371	9.96E-01	-1.998	0.860							
tdA		-1.181	S	0.209	8.59E-01	-2.306	1.281	tdA	-1.002	ns	0.202	1.00E+00	-1.625	0.630							
tdB		-0.897	S	0.278	1.10E-02	-2.238	-0.124	tdB	-0.588	S	0.248	2.51E-07	-2.610	-0.722							
tdB		-0.537	S	0.187	2.89E-01	-1.125	1.298	tdB	0.102	ns	0.136	1.00E+00	-0.414	0.610							
tdB		0.537	S	0.194	5.64E-01	-0.204	1.277	tdB	0.686	S	0.177	1.05E-05	0.324	1.048							
tdB		0.345	S	0.193	9.93E-01	-0.389	1.080	tdB	-0.140	ns	0.144	1.00E+00	-0.688	0.400							
0.1h-1		-0.587	S	0.241	8.02E-01	-1.503	0.328	0.1h-1	-1.072	S	0.204	2.20E-04	-1.852	-0.290							
0.2h-1		-0.347	S	0.198	9.94E-01	-0.796	0.103	0.2h-1	-0.136	ns	0.137	1.00E+00	-0.620	0.448							
0.4h-1		-0.497	S	0.241	9.60E-01	-1.414	0.421	0.4h-1	-0.982	S	0.205	1.49E-03	-1.763	-0.220							
0.5h-1		-2.870	S	0.608	2.58E-03	-5.209	-0.530	0.5h-1	-3.393	S	0.595	7.29E-05	-5.648	-1.081							
0.7h-1		-5.125	S	0.718	3.67E-06	-7.265	-2.473	0.7h-1	-5.719	S	0.717	3.67E-06	-7.869	-2.569							
pgm		gsm	1.743	S	0.225	1.56E-06	0.881	2.605	gsm	0.659	ns	0.171	4.39E-02	0.007	1.311						
		pgl	0.968	S	0.260	6.30E-02	-0.019	1.955	pgl	-0.116	ns	0.214	1.00E+00	-0.931	0.699						
	pkA	-0.694	S	0.419	9.98E-01	-2.290	0.901	pgm	-1.084	S	0.248	7.12E-03	-2.028	-0.140							
	pkB	-0.817	S	0.444	9.98E-01	-2.511	0.876	pkA	-1.777	S	0.435	3.39E-03	-3.267	-0.287							
	fbp	1.824	S	0.213	1.13E-10	1.004	2.644	pkB	-1.901	S	0.419	4.72E-03	-3.508	-0.298							
	ftaB	1.453	S	0.226	1.07E-06	0.589	2.317	fbp	0.740	ns	0.155	1.81E-01	0.146	1.333							
	gapC	1.084	S	0.246	7.10E-03	0.140	2.028	ftaB	-0.369	ns	0.177	9.37E-01	-1.023	0.288							
	gpmA	0.323	S	0.320	1.00E+00	-0.893	1.539	gapC	-0.761	ns	0.284	6.31E-01	-1.846	0.324							
	gpmB	1.563	S	0.231	1.72E-07	0.881	2.445	gpmA	0.479	ns	0.178	2.61E-01	-0.200	1.151							
	pykA	1.523	S	0.242	1.49E-07	0.794	2.372	gpmB	0.436	ns	0.176	6.58E-01	-0								

Multiple Comparisons									
Dependent Variable: mRNA(qRT-PCR)									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound		
gpmB	galM	0.220		0.130	0.97E-01	-0.274	0.714		
	gk	-0.555		0.125	3.03E-01	-1.256	0.144		
	pgm	-1.523	S	0.222	1.46E-07	-2.372	-0.674		
	pgl	-2.218	S	0.375	2.13E-05	-3.663	-0.772		
	pKbA	-2.340	S	0.404	3.58E-05	-3.895	-0.784		
	pKbB	0.301		0.105	5.45E-01	-0.110	0.712		
	fbp	-0.070		0.131	1.00E+00	-0.568	0.428		
	flaB	-0.439		0.166	6.58E-01	-1.073	0.195		
	gspC	-1.203		0.262	4.05E-03	-2.205	-0.195		
	gpmA	0.040		0.140	1.00E+00	-0.491	0.570		
	pykA	0.296		0.113	6.81E-01	-0.135	0.726		
	pykF	0.374		0.109	1.46E-01	-0.041	0.785		
	ppaA	0.307		0.107	4.87E-01	-0.102	0.716		
	zwf	-0.174		0.150	1.00E+00	-0.746	0.399		
	pgl	-0.793	S	0.209	4.27E-02	-1.576	-0.010		
	gnd	-0.722	S	0.186	5.11E-02	-1.444	0.001		
	rpe	-4.218	S	0.552	1.04E-08	-6.349	-2.088		
	rpiA	-0.640		0.368	9.95E-01	-2.059	0.779		
	rpiB	-0.968		0.159	1.00E+00	-0.974	0.535		
	ksA	-1.735	S	0.242	4.23E-08	-2.666	-0.806		
pykA	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
	ksB	0.032		0.128	1.00E+00	-0.458	0.520		
pykF	0.1h-1	-1.143	S	0.199	2.85E-05	-1.905	-0.380		
	0.2h-1	-0.208		0.142	1.00E+00	-0.746	0.330		
	0.4h-1	-1.052	S	0.202	2.27E-04	-1.816	-0.287		
	0.5h-1	-3.425	S	0.593	4.23E-05	-5.713	-1.137		
	0.7h-1	-5.783	S	0.702	7.34E-10	-8.494	-3.072		
	galM	-0.078		0.157	1.00E+00	-1.341	0.334		
	gk	-0.851	S	0.176	1.47E-03	-1.527	-0.175		
	pgm	-1.819	S	0.216	1.42E-10	-2.648	-0.989		
	pgl	-2.513	S	0.372	5.43E-07	-3.948	-1.079		
	pKbA	-2.635	S	0.401	1.25E-06	-4.160	-1.086		
	pKbB	0.005		0.096	1.00E+00	-0.360	0.370		
	fbp	-0.366		0.121	3.73E-01	-0.628	0.096		
	flaB	-1.735	S	0.159	3.01E-03	-2.341	-1.129		
	gspC	-1.495	S	0.257	2.93E-05	-2.484	-0.507		
	gpmA	-0.258		0.131	9.77E-01	-0.753	0.241		
	gpmB	-0.295		0.115	6.81E-01	-0.726	0.135		
	pykF	0.079		0.097	1.00E+00	-0.291	0.446		
	ppaA	0.011		0.095	1.00E+00	-0.351	0.374		
	zwf	-0.470		0.142	2.03E-01	-1.012	0.073		
	pgl	-1.088	S	0.199	1.03E-04	-1.597	-0.549		
	gnd	-1.018	S	0.183	6.67E-05	-1.719	-0.317		
ppaA	rpe	-4.514	S	0.593	8.51E-10	-6.637	-2.391		
	rpiA	-0.968		0.368	7.12E-01	-2.344	0.472		
	rpiB	-0.364		0.151	8.18E-01	-0.941	0.213		
	ksA	-0.032		0.237	1.08E-10	-2.944	-1.119		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		
	ksB	-0.364		0.159	9.08E-01	-0.715	0.197		

\*, S\* The mean difference is significant at the .05 level.

Multiple Comparisons									
Dependent Variable: mRNA(qRT-PCR)									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound		
pgl	galM	1.013	S	0.209	1.20E-03	0.216	1.810		
	gk	0.236		0.245	1.00E+00	-0.694	1.170		
	pgm	-0.730	S	0.275	6.49E-01	-1.775	0.316		
	pgl	-1.424	S	0.409	1.32E-01	-2.988	0.139		
	pKbA	-1.546	S	0.435	1.10E-01	-3.212	0.119		
	pKbB	1.094	S	0.196	6.96E-05	0.343	1.845		
	fbp	0.723		0.209	1.41E-01	-0.078	1.522		
	flaB	0.354		0.233	9.99E-01	-0.531	1.240		
	gspC	-0.405		0.308	1.00E+00	-1.580	0.769		
	gpmA	0.833	S	0.215	4.07E-02	0.014	1.652		
	gpmB	0.793	S	0.205	4.27E-02	0.010	1.576		
	pykF	1.089	S	0.199	1.03E-04	0.327	1.851		
	ppaA	1.168	S	0.196	1.41E-05	0.414	1.921		
	zwf	1.100	S	0.195	5.86E-05	0.350	1.851		
	pgl	0.619		0.222	5.41E-01	-0.228	1.469		
	gnd	0.071		0.255	1.00E+00	-0.879	1.021		
	rpe	-3.425	S	0.576	1.45E-05	-5.638	-1.214		
	rpiA	0.153		0.403	1.00E+00	-1.386	1.692		
	rpiB	0.725		0.228	2.84E-01	-0.142	1.592		
	ksA	-0.943	S	0.262	2.39E-01	-2.054	0.168		
gnd	ksB	0.825	S	0.208	3.11E-02	0.031	1.618		
	ksB	0.825	S	0.215	9.21E-02	-0.044	1.594		
	ksB	0.825	S	0.215	9.21E-02	-0.044	1.594		
	0.1h-1	-0.349		0.258	1.00E+00	-1.328	0.629		
	0.2h-1	0.585		0.216	6.05E-01	-0.238	1.409		
	0.4h-1	-0.259		0.258	1.00E+00	-1.239	0.722		
	0.5h-1	-2.932	S	0.615	1.22E-02	-4.995	-0.269		
	0.7h-1	-4.660	S	0.721	2.02E-07	-7.765	-2.215		
	galM	-0.942	S	0.194	1.11E-03	-1.203	-0.681		
	gk	0.167		0.233	1.00E+00	-0.717	1.051		
	pgm	-0.801		0.264	3.60E-01	-1.804	0.203		
	pgl	-1.495	S	0.402	6.89E-02	-3.033	0.043		
	pKbA	-1.617	S	0.435	5.91E-02	-3.248	0.024		
	pKbB	1.023	S	0.190	4.18E-05	0.334	1.713		
	pKb	0.652		0.194	1.80E-01	-0.059	1.194		
	fbp	0.284		0.223	9.99E-01	-0.551	1.119		
	gspC	-0.477		0.299	9.99E-01	-1.674	0.720		
	gpmA	0.762		0.200	5.00E-02	-0.001	1.525		
	gpmB	0.722		0.189	5.11E-02	-0.001	1.446		
	pykF	1.093	S	0.196	6.67E-05	0.347	1.719		
ppaA	1.037	S	0.180	7.16E-05	0.404	1.785			
ksA	0.543	S	0.179	3.44E-05	0.341	1.748			
ksB	-0.071	S	0.250	1.00E+00	-1.021	0.879			
rpe	-3.496	S	0.570	7.00E-06	-5.689	-1.303			
rpe	rpiA	0.082		0.395	1.00E+00	-1.433	1.595		
	rpiB	0.654		0.191	3.44E-01	-1.051	2.360		
	ksA	-1.014	S	0.282	9.29E-02	-2.088	0.055		
	ksB	0.754	S	0.193	3.70E-02	0.019	1.490		
	ksB	0.754	S	0.207	1.18E-01	-0.214	1.467		
	0.1h-1	-0.512		0.199	7.05E-01	-0.245	1.272		
	0.1h-1	-0.425		0.246	9.97E-01	-1.354	0.514		
	0.2h-1	-2.703	S	0.246	7.24E-01	-3.193	-0.213		
	0.5h-1	-5.003	S	0.246	1.00E+00	-1.265	0.556		
	0.7h-1	-7.601	S	0.610	7.35E-03	-5.049	-3.356		
	galM	-2.503	S	0.717	1.14E-07	-7.821	-0.201		
	gk	0.514		0.176	2.30E-02	-0.274	1.302		
	pgm	3.863	S	0.586	1.72E-06	1.477	5.848		
	pgl	2.699	S	0.582	3.30E-03	0.463	4.935		
	pKbA	2.101	S	0.601	3.48E-01	-2.001	6.681		
	pKbB	1.879	S	0.673	5.39E-01	-0.680	4.438		
	fbp	1.414	S	0.549	7.97E-04	2.400	6.638		
	gspC	3.780	S	0.551	1.99E-08	2.681	4.879		
	gpmA	3.019	S	0.563	5.62E-07	1.612	5.947		
	gpmB	4.258	S	0.598	5.94E-04	2.716	5.306		
pykF	4.593	S	0.559	8.31E-09	2.463	6.401			
ppaA	4.514	S	0.559	8.31E-09	2.463	6.401			
ksA	2.426	S	0.550	8.15E-01	-2.391	6.837			
ksB	2.426	S	0.550	8.15E-01	-2.391	6.837			
0.1h-1	-0.329		0.246	1.00E+00	-1.265	0.516			
0.2h-1	-2.703	S	0.610	7.35E-03	-5.049	-3.356			
0.5h-1	-5.003	S	0.717	1.14E-07	-7.821	-0.201			
0.7h-1	-7.601	S	0.717	1.14E-07	-7.821	-0.201			
galM	-2.503	S	0.586	1.72E-06	1.477	5.848			
gk	2.699	S	0.582	3.30E-03	0.463	4.935			
pgm	3.863	S	0.601	3.48E-01	-2.001	6.681			
pgl	4.258	S	0.550	8.15E-01	-2.391	6.837			
pKbA	4.593	S	0.549	7.97E-04	2.400	6.638			
pKbB	4.514	S	0.551	7.97E-04	2.400	6.638			
fbp	3.019	S	0.563	5.62E-07	1.612	5.947			
gspC	3.019	S	0.598	5.94E-04	2.716	5.306			
gpmA	4.258	S	0.559	8.31E-09	2.463	6.401			
gpmB	4.514	S	0.559	8.31E-09	2.463	6.401			
pykF	4.593	S	0.550	8.15E-01	-2.391	6.837			
ppaA	4.514	S	0.550	8.15E-01	-2.391	6.837			
ksA	2.426	S	0.550	8.15E-01	-2.391	6.837			
ksB	2.426	S	0.550	8.15E-01	-2.391	6.837			
0.1h-1	-0.425		0.246	1.00E+00	-1.265	0.516			
0.2h-1	-2.703	S	0.610	7.35E-03	-5.049	-3.356			
0.5h-1	-5.003	S	0.717	1.14E-07	-7.821	-0.201			
0.7h-1	-7.601	S	0.717	1.14E-07	-7.821	-0.201			
galM	-2.503	S	0.586	1.72E-06	1.477	5.848			
gk	2.699	S	0.582	3.30E-03	0.463	4.935			
pgm	3.863	S	0.601	3.48E-01	-2.001	6.681			
pgl	4.258	S	0.550	8.15E-01	-2.391	6.837			
pKbA	4.593	S	0.549	7.97E-04	2.400	6.638			
pKbB	4.514	S	0.551	7.97E-04	2.400	6.638			
fbp	3.019	S	0.563	5.62E-07	1.612	5.947			
gspC	3.019	S	0.598	5.94E-04	2.716	5.306			
gpmA	4.258	S	0.559	8.31E-09	2.463	6.401			
gpmB	4.514	S	0.559	8.31E-09	2.463	6.401			
pykF	4.593	S	0.550	8.15E-01	-2.391	6.837			
ppaA	4.514	S	0.550	8.15E-01	-2.391	6.837			
ksA	2.426	S	0.550	8.15E-01	-2.391	6.837			
ksB	2.426	S	0.550	8.15E-01	-2.391	6.837			
0.1h-1	-0.329		0.246	1.00E+00	-1.265	0.516			
0.2h-1	-2.703	S	0.610	7.35E-03	-5.049	-3.356			
0.5h-1	-5.003	S	0.717	1.14E-07	-7.821	-0.201			
0.7h-1	-7.601	S	0.717	1.14E-07	-7.821	-0.201			
galM	-2.503	S	0.586	1.72E-06	1.477	5.848			
gk	2.699	S	0.582	3.30E-03	0.463	4.935			
pgm	3.863	S	0.601	3.48E-01	-2.001	6.681			
pgl	4.258	S	0.550	8.15E-01	-2.391	6.837			
pKbA	4.593	S	0.549	7.97E-04	2.400	6.638			
pKbB	4.514	S	0.551	7.97E-04	2.400	6.638			
fbp	3.019	S	0.563	5.62E-07	1.612	5.947			
gspC	3.019	S	0.598	5.94E-04	2.716	5.306			
gpmA	4.258	S	0.559	8.31E-09	2.463	6.401			
gpmB	4.514	S	0.559	8.31E-09	2.463	6.401			
pykF	4.593	S	0.550	8.15E-01	-2.391	6.837			

Multiple Comparisons										Multiple Comparisons									
Dependent Variable: mRNA(qRT-PCR)										Dependent Variable: mRNA(qRT-PCR)									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval		(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval					
						Lower Bound	Upper Bound							Lower Bound	Upper Bound				
rSA	gaIM	1.956	S	0.246	6.80E-10	1.014	2.898	0.1h-1	gaIM	1.363	S	0.204	2.43E-07	0.585	2.140				
	gk	1.181	S	0.276	1.10E-02	-0.124	2.236		gk	0.587	S	0.241	8.02E-01	-0.328	1.503				
	pgm	0.213	S	0.304	1.00E+00	-0.943	1.370		pgm	-0.380	S	0.271	1.00E+00	-1.411	0.651				
	pgl	-0.481	S	0.429	1.00E+00	-2.118	1.155		pgl	-1.075	S	0.407	6.55E-01	-2.630	0.489				
	pKA	-0.603	S	0.454	1.00E+00	-2.337	1.130		pKA	-1.197	S	0.433	5.62E-01	-2.854	0.463				
	pKB	2.037	S	0.235	9.34E-11	1.133	2.941		pKB	1.443	S	0.190	5.71E-08	0.713	2.174				
	fbp	1.666	S	0.246	2.51E-07	0.722	2.610		fbp	1.072	S	0.204	2.20E-04	0.293	1.852				
	ftaB	1.297	S	0.287	1.07E-03	0.280	2.314		ftaB	0.704	S	0.228	3.27E-01	-0.165	1.572				
	gspC	0.537	S	0.335	9.99E-01	-0.735	1.808		gspC	-0.057	S	0.305	1.00E+00	-1.218	1.104				
	gpmA	1.776	S	0.251	4.40E-08	0.816	2.736		gpmA	1.182	S	0.210	3.57E-05	0.383	1.982				
	gpmB	1.736	S	0.242	4.23E-08	0.808	2.666		gpmB	1.143	S	0.199	2.85E-05	0.380	1.905				
	pyKA	2.032	S	0.237	1.08E-10	1.119	2.944		pyKA	1.438	S	0.193	9.36E-08	0.698	2.178				
	pyKF	2.111	S	0.235	5.99E-11	1.205	3.016		pyKF	1.517	S	0.191	9.31E-10	0.785	2.250				
	ppsA	2.043	S	0.235	8.72E-11	1.140	2.946		ppsA	1.450	S	0.190	4.66E-08	0.721	2.179				
	zwf	1.562	S	0.257	5.19E-06	0.588	2.545		zwf	0.869	S	0.217	5.11E-03	0.142	1.796				
	ggl	0.943	S	0.292	2.39E-01	-0.168	2.054		ggl	0.349	S	0.298	1.00E+00	-0.629	1.329				
	gnd	1.014	S	0.282	9.29E-02	-0.058	2.086		gnd	0.420	S	0.246	9.97E-01	-0.514	1.354				
	rpe	-2.482	S	0.590	1.49E-02	-4.744	-0.221		rpe	-3.078	S	0.574	1.91E-04	-5.280	-0.871				
	rpiA	1.068	S	0.423	6.97E-01	-0.517	2.705		rpiA	0.502	S	0.460	1.00E+00	-1.028	2.033				
	rpiB	1.698	S	0.262	1.16E-06	0.668	2.669		rpiB	1.075	S	0.223	1.20E-03	0.226	1.924				
	rtbB	1.768	S	0.248	2.85E-08	0.829	2.707		rtbB	-0.594	S	0.289	9.80E-01	-1.891	0.504				
	talA	1.716	S	0.251	1.42E-07	0.757	2.678		talA	1.174	S	0.203	1.46E-04	0.401	1.944				
	talB	1.526	S	0.250	5.20E-06	0.570	2.482		talB	1.124	S	0.204	1.26E-04	0.324	1.924				
	0.1h-1	0.594	S	0.289	9.60E-01	-0.504	1.691		0.1h-1	0.933	S	0.208	5.06E-03	0.138	1.728				
	0.2h-1	1.528	S	0.252	6.14E-06	0.564	2.492		0.2h-1	0.935	S	0.211	5.66E-03	0.134	1.731				
	0.4h-1	0.684	S	0.286	8.42E-01	-0.415	1.783		0.4h-1	0.989	S	0.254	1.00E+00	-0.870	2.843				
	0.5h-1	-1.686	S	0.629	6.23E-01	-4.099	0.721		0.5h-1	-2.282	S	0.613	7.14E-02	-4.639	-0.077				
	0.7h-1	-0.407	S	0.733	9.48E-05	-6.862	-1.232		0.7h-1	-4.640	S	0.720	1.82E-06	-7.410	-1.871				
	rAB	0.1h-1	0.188	S	0.138	1.00E+00	-0.462	0.839	0.2h-1	0.422	S	0.147	4.52E-01	-0.889	1.738				
		gk	-0.597	S	0.187	2.88E-01	-1.299	0.125		gk	-0.347	S	0.196	9.94E-01	-1.093	0.399			
pgm		-1.555	S	0.224	8.80E-08	-2.413	-0.696		pgm	-1.315	S	0.232	3.47E-05	-2.201	-0.429				
pgl		-2.249	S	0.377	1.80E-05	-3.700	-0.798		pgl	-2.015	S	0.382	2.91E-04	-3.477	-0.543				
pKA		-2.371	S	0.402	2.73E-05	-3.832	-0.811		pKA	-2.133	S	0.417	3.49E-05	-4.000	-0.666				
pKB		0.269	S	0.114	8.40E-01	-0.163	0.702		pKB	0.509	S	0.128	3.96E-02	0.019	0.998				
fbp		-0.102	S	0.136	1.00E+00	-0.617	0.414		fbp	0.138	S	0.148	1.00E+00	-0.425	0.701				
ftaB		-0.470	S	0.170	5.59E-01	-1.118	0.177		ftaB	0.231	S	0.172	1.00E+00	-0.519	0.981				
gspC		-1.231	S	0.264	2.95E-03	-2.244	-0.218		gspC	-0.992	S	0.271	8.12E-02	-2.028	0.040				
gpmA		0.008	S	0.144	1.00E+00	-0.538	0.555		gpmA	0.248	S	0.156	9.99E-01	-0.344	0.838				
gpmB		-0.028	S	0.128	1.00E+00	-0.628	0.456		gpmB	0.268	S	0.147	1.00E+00	-0.230	0.744				
pyKA		0.264	S	0.119	9.08E-01	-0.187	0.715		pyKA	0.504	S	0.133	5.23E-02	-0.002	1.000				
pyKF		0.343	S	0.115	3.90E-01	-0.094	0.779		pyKF	0.582	S	0.128	4.48E-03	0.090	1.071				
ppsA		0.276	S	0.113	8.00E-01	-0.155	0.706		ppsA	0.519	S	0.126	5.20E-02	0.028	1.003				
zwf		-0.205	S	0.195	1.00E+00	-0.763	0.353		zwf	0.385	S	0.209	1.00E+00	-0.595	1.369				
ggl		-0.825	S	0.208	3.11E-02	-1.618	-0.031		ggl	-0.588	S	0.216	6.05E-01	-1.409	0.233				
gnd		-0.754	S	0.193	3.70E-02	-1.490	-0.019		gnd	-0.519	S	0.202	7.47E-01	-1.283	0.254				
rpe		-4.252	S	0.563	8.22E-08	-6.364	-2.116		rpe	-4.015	S	0.566	6.70E-08	-6.150	-1.867				
rpiA		-0.672	S	0.370	9.90E-01	-2.096	0.753		rpiA	-0.432	S	0.375	1.00E+00	-1.873	1.000				
rpiB		-0.100	S	0.163	1.00E+00	-0.719	0.520		rpiB	0.140	S	0.173	1.00E+00	-0.595	0.799				
rtbB		-1.768	S	0.165	2.85E-06	-2.707	-0.829		rtbB	-1.526	S	0.165	6.14E-06	-2.462	-0.570				
talA		-0.050	S	0.144	1.00E+00	-0.597	0.497		talA	0.240	S	0.148	9.98E-01	-0.315	0.794				
talB		-0.242	S	0.142	9.97E-01	-0.781	0.298		talB	0.189	S	0.156	1.00E+00	-0.402	0.778				
0.1h-1		-1.174	S	0.203	1.54E-05	-1.948	-0.401		0.1h-1	-0.002	S	0.154	1.00E+00	-0.587	0.583				
0.2h-1		-0.242	S	0.146	9.98E-01	-0.794	-0.315		0.2h-1	0.211	S	0.158	9.86E-03	-0.139	1.178				
0.4h-1		-1.084	S	0.203	1.56E-04	-1.859	-0.308		0.4h-1	-0.844	S	0.212	2.83E-04	-1.506	-0.033				
0.5h-1		-3.457	S	0.594	3.47E-05	-5.748	-1.165		0.5h-1	-3.217	S	0.597	2.01E-04	-5.518	-0.919				
0.7h-1		-5.815	S	0.745	6.14E-10	-8.328	-3.302		0.7h-1	-5.076	S	0.745	9.86E-09	-8.298	-1.855				
rAB		gaIM	0.238	S	0.145	9.98E-01	-0.314	0.791	0.4h-1	gaIM	1.272	S	0.204	2.36E-06	0.493	2.051			
		gk	-0.537	S	0.194	5.64E-01	-1.277	0.204		gk	0.497	S	0.241	9.60E-04	-0.421	1.414			
	pgm	-1.504	S	0.231	6.11E-07	-2.386	-0.623		pgm	-1.477	S	0.272	9.96E-01	-1.603	0.561				
	pgl	-2.186	S	0.381	3.43E-05	-3.863	-0.735		pgl	-1.168	S	0.407	4.85E-01	-2.721	0.390				
	pKA	-2.321	S	0.409	5.43E-05	-3.894	-0.748		pKA	-1.288	S	0.433	4.06E-01	-2.946	0.370				
	pKB	0.319	S	0.126	7.36E-01	-0.162	0.800		pKB	0.383	S	0.191	6.50E-06	0.621	2.085				
	fbp	-0.052	S	0.146	1.00E+00	-0.608	0.504		fbp	0.980	S	0.167	1.00E+00	-0.460	1.401				
	ftaB	-0.420	S	0.179	8.49E-01	-1.099	0.259		ftaB	0.613	S	0.228	6.28E-01	-0.257	1.481				
	gspC	-1.181	S	0.270	8.00E-03	-2.214	-0												

**Table S10 B Statistical tests for AEIs (Proteins, LC-MS/MS)****Test of Homogeneity of Variances**

Protein(LC-MS/MS)

Levene Statistic	df1	df2	Sig.
11.552	28	1,589	1.07E-46

**ANOVA**

Protein(LC-MS/MS)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	1,008.400	28	36.014	9.753	2.75E-38
Within Groups	5,867.635	1,589	3.693		
Total	6,876.035	1,617			

**Robust Tests of Equality of Means**

Protein(LC-MS/MS)

	Statistic(a)	df1	df2	Sig.
Welch	13.048	28	566.097	5.64E-45

a. Asymptotically F distributed.



Multiple Comparisons										Multiple Comparisons										
Dependent Variable: Protein(LC-MS)										Dependent Variable: Protein(LC-MS)										
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval				(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval				
						Lower Bound	Upper Bound									Lower Bound	Upper Bound			
gpm	gk	-1.568	S	0.246	7.89E-06	-2.528	-0.608			pkB	gkM	0.528	S	0.138	4.54E-02	-0.004	1.056			
	gpm	-1.238	S	0.227	2.67E-04	-2.120	-0.353					gpm	-0.802	S	0.262	3.71E-02	-2.057	-0.027		
	pgl	-1.662	S	0.304	3.09E-04	-2.852	-0.472					gpmB	-1.136	S	0.244	4.58E-01	-1.654	-0.234		
	pkA	-1.176	S	0.256	5.94E-03	-2.175	-0.177					gpmA	-0.750	S	0.272	8.75E-01	-2.300	0.801		
	pkB	-0.528	S	0.138	5.45E-02	-1.058	0.004					fbp	-0.670	S	0.272	8.75E-01	-1.702	0.403		
	fbp	-0.998	S	0.231	1.40E-02	-1.898	-0.098					ftaB	-0.428	S	0.245	9.82E-01	-1.431	0.489		
	ftaB	-1.464	S	0.296	1.85E-03	-2.620	-0.308					gapC	-0.957	S	0.308	3.74E-01	-2.138	0.264		
	gapC	-1.112	S	0.312	1.27E-01	-2.338	0.112					gpmC	-0.582	S	0.325	9.90E-01	-1.853	0.681		
	gpmA	-0.642	S	0.169	6.00E-02	-1.295	0.011					gpmA	-0.118	S	0.192	1.00E+00	-0.853	0.620		
	gpmB	-0.476	S	0.158	3.81E-01	-1.085	0.134					pyKA	0.065	S	0.152	1.00E+00	-0.753	0.881		
	pyKA	0.120	S	0.103	1.00E+00	-0.276	0.515					pyKF	0.646	S	0.168	3.06E-03	0.115	1.177		
	pyKF	0.095	S	0.105	1.00E+00	-0.309	0.499					ppaA	0.821	S	0.139	6.97E-03	0.084	1.158		
	ppaA	-0.058	S	0.110	1.00E+00	-0.479	0.362					zwf	0.468	S	0.143	6.01E-01	-0.071	0.981		
	zwf	-0.206	S	0.107	9.80E-01	-0.615	0.203					gnd	-0.206	S	0.140	8.81E-01	-0.220	0.861		
	gnd	-0.848	S	0.186	1.43E-01	-1.371	0.074					gnd	-0.072	S	0.207	1.00E+00	-0.920	0.875		
	gnd	-0.454	S	0.184	7.76E-01	-1.169	0.261					gnd	0.122	S	0.206	1.00E+00	-0.719	0.863		
	rpe	-2.738	S	0.426	1.05E-05	-4.412	-1.064					rpe	-2.438	S	0.411	1.21E-02	-3.272	-1.507		
	rpA	-1.269	S	0.281	8.05E-03	-2.369	-0.169					rpA	-0.734	S	0.296	7.46E-01	-1.891	0.406		
	rpB	-0.764	S	0.186	2.45E-02	-1.483	-0.044					rpB	-0.237	S	0.207	1.00E+00	-1.032	0.558		
	ksA	-0.744	S	0.173	1.30E-02	-1.413	-0.075					ksA	-0.198	S	0.207	1.00E+00	-0.968	0.631		
	ksB	-0.840	S	0.230	9.94E-02	-1.738	0.059					ksB	-0.313	S	0.248	1.00E+00	-1.271	0.645		
	ksA	-0.886	S	0.226	5.12E-02	-1.773	0.002					ksB	-0.360	S	0.245	1.00E+00	-1.308	0.589		
	0.1h-1	-1.843	S	0.386	3.63E-03	-3.356	-0.330					0.1h-1	-1.317	S	0.397	2.15E-01	-2.664	0.231		
	0.2h-1	-1.134	S	0.316	1.16E-01	-2.370	0.102					0.2h-1	-0.608	S	0.329	9.87E-01	-1.886	0.671		
	0.4h-1	-1.438	S	0.352	3.13E-02	-2.819	-0.058					0.4h-1	-0.911	S	0.364	7.47E-01	-2.331	0.506		
	0.5h-1	-1.963	S	0.486	3.64E-02	-3.871	-0.055					0.5h-1	-1.538	S	0.548	5.94E-01	-3.572	-0.488		
	0.7h-1	-3.437	S	0.540	1.41E-05	-5.560	-1.314					0.7h-1	-2.912	S	0.568	5.94E-04	-5.058	-0.767		
gk	gkM	1.568	S	0.246	7.89E-06	0.608	2.528			fbp	gkM	0.998	S	0.231	1.40E-02	0.098	1.898			
	gpm	1.238	S	0.338	1.00E+00	-0.898	1.552					gpm	-0.327	S	0.377	1.00E+00	-1.414	0.937		
	pgl	-0.094	S	0.377	1.00E+00	-1.542	1.354					gpmB	-0.238	S	0.307	1.00E+00	-1.414	0.937		
	pkA	0.392	S	0.340	1.00E+00	-0.910	1.694					gpmA	-0.674	S	0.368	9.91E-01	-2.077	0.748		
	pkB	1.042	S	0.262	3.71E-02	0.520	1.564					fbp	-0.178	S	0.328	1.00E+00	-1.438	1.082		
	fbp	0.570	S	0.321	9.93E-01	-0.661	1.801					ftaB	-0.466	S	0.248	9.82E-01	-1.488	0.414		
	ftaB	0.104	S	0.370	1.00E+00	-1.317	1.526					gapC	-0.118	S	0.361	1.00E+00	-1.850	0.919		
	gapC	0.458	S	0.384	1.00E+00	-1.019	1.931					gpmC	-0.444	S	0.374	1.00E+00	-1.554	1.326		
	gpmA	0.926	S	0.280	2.09E-01	-0.152	2.003					gpmA	0.356	S	0.262	1.00E+00	-0.381	1.093		
	gpmB	1.092	S	0.274	3.29E-02	0.038	2.147					gpmB	1.522	S	0.260	9.60E-01	-0.479	1.523		
	pyKA	1.658	S	0.266	1.13E-05	0.726	2.648					pyKA	0.118	S	0.231	2.50E-03	0.217	2.018		
	pyKF	1.693	S	0.247	1.79E-06	0.700	2.626					pyKF	0.233	S	0.260	1.00E+00	-0.961	1.427		
	ppaA	1.510	S	0.249	2.37E-05	0.540	2.479					ppaA	0.940	S	0.234	3.46E-02	0.029	1.850		
	zwf	1.362	S	0.248	2.20E-04	0.397	2.327					zwf	0.792	S	0.232	1.79E-01	-0.114	1.698		
	gnd	0.920	S	0.291	2.84E-01	-0.107	1.037					gnd	0.278	S	0.277	1.00E+00	-1.178	1.417		
	rpe	1.114	S	0.289	4.92E-02	0.001	2.227					gnd	0.544	S	0.277	9.74E-01	-0.519	1.607		
	rpA	-1.170	S	0.481	7.99E-01	-3.028	0.899					rpe	-1.740	S	0.474	8.84E-02	-3.573	-0.027		
	rpB	0.269	S	0.359	1.00E+00	-1.078	1.677					rpA	-0.340	S	0.340	1.00E+00	-1.811	1.006		
	ksA	0.804	S	0.290	5.58E-01	-0.311	1.920					rpB	0.234	S	0.279	1.00E+00	-0.832	1.300		
	ksA	0.824	S	0.282	4.48E-01	-0.263	1.910					ksA	0.254	S	0.269	1.00E+00	-0.781	1.289		
	ksB	0.725	S	0.321	8.87E-01	-0.502	1.959					ksB	0.198	S	0.309	1.00E+00	-1.026	1.345		
	ksA	0.682	S	0.313	9.36E-01	-0.541	1.905					0.1h-1	-0.843	S	0.438	9.79E-01	-2.534	0.844		
	ksB	0.793	S	0.325	7.98E-01	-0.454	2.041					0.2h-1	-1.051	S	0.407	1.00E+00	-2.177	1.074		
	0.1h-1	-0.275	S	0.446	1.00E+00	-1.993	1.444					0.4h-1	-0.481	S	0.408	1.00E+00	-2.013	1.132		
	0.2h-1	-0.434	S	0.407	1.00E+00	-2.247	1.310					0.5h-1	-0.965	S	0.528	9.89E-01	-3.013	1.082		
	0.4h-1	0.128	S	0.417	1.00E+00	-1.475	1.734					0.7h-1	-2.470	S	0.571	1.35E-02	-4.002	-0.938		
	0.5h-1	-0.395	S	0.535	1.00E+00	-2.468	1.678					0.7h-1	-1.983	S	0.596	1.00E+00	-3.680	0.602		
0.7h-1	-1.865	S	0.585	2.73E-01	-3.138	-0.400				fbtA	0.296	S	0.296	1.00E+00	-0.308	2.620				
gpm	1.238	S	0.227	2.67E-04	0.353	-2.120				gk	-1.040	S	0.370	1.00E+00	-1.526	1.131				
gk	-0.332	S	0.318	1.00E+00	-1.552	0.888				gpm	-0.228	S	0.368	1.00E+00	-1.147	1.602				
pgl	-0.426	S	0.365	1.00E+00	-1.826	0.977				pkA	-0.118	S	0.371	1.00E+00	-1.378	0.941				
pkA	0.065	S	0.385	1.00E+00	-1.160	1.310				pkB	0.298	S	0.377	1.00E+00	-1.159	1.734				
pkB	0.710	S	0.244	4.58E-01	-0.234	1.654				fbp	0.931	S	0.309	3.74E-01	-0.264	2.139				
fbp	0.238	S	0.307	1.00E+00	-0.807	1.414				ftaB	0.267	S	0.347	1.00E+00	-1.019	1.518				
ftaB	0.228	S	0.364	1.00E+00	-1.147	1.477				gapC	0.062	S	0.417	1.00E+00	-1.249	1.953				
gapC	0.124	S	0.372	1.00E+00	-1.306	1.555				gpmA	0.384	S	0.324	7.34E-01	-0.432	2.075				
gpmA	0.594	S	0.263	8.91E-01	-0.418	1.605				gpmB	0.765	S	0.315	2.22E-01	-0.246	2.246				
gpmB	0.765	S	0.265	4.12E-01	-0.225	1.747				pyKA	1.356	S	0.226	4.40E-04	0.427	2.740				
pyKA	1.356	S	0.227	3.56E-05	0.472	2.240				pyKF	1.583	S	0.296	6.16E-04	0.400	2.717				
pyKF	1.331	S	0.228	5.80E-05	0.444	2.218				ppaA	1.178	S	0.296	4.00E-03	0.242	2.689				
ppaA	1.178	S	0.230	8.35E-04	0.284	2.072				zwf	1.038	S	0.226	7.40E-03	0.141	1.915				
zwf	1.038	S	0.226	7.40E-03	0.141	1.915				gnd	0.588	S	0.274	9.35E-01	-0.471	2.102				
gnd	0.588	S	0.274	9.35E-01	-0.468	1.642				rpe	0.782	S	0.273	4.88E-01	-0.267	1.831				
rpA	-1.502	S	0.472	2.77E-01	-3.326	1.324				rpA	-1.502	S	0.472	2.77E-01	-3.326	1.324				
rpB	-0.033	S	0.346	1.00E+00	-1.362	1.296				rpB	-0.033	S	0.346	1.00E+00	-1.319	1.708				
ksA	0.473	S	0.274	9.96E-01	-0.580	1.525				ksA	0.473	S	0.274	9.96E-01	-0.580	1.525				
ksB	0.492	S	0.266	9.88E-01	-0.502	1.515				ksB	0.492	S	0.266	9.88E-01	-0.502	1.515				
ksA	0.397	S	0.306	1.00E+00	-0.778	1.571				0.1h-1	-0.378	S	0.363	9.95E-01	-1.760	2.008				

Multiple Comparisons										Multiple Comparisons									
Dependent Variable: Protein(LC-MS)										Dependent Variable: Protein(LC-MS)									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval	Lower Bound	Upper Bound		(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval	Lower Bound	Upper Bound	
gpmB	gpmA	0.476		0.158	3.81E-01	-0.134	-0.134	1.085		pgl	gpmA	0.648		0.186	1.43E-01	-0.074	-0.074	1.371	
	gk	-1.092	S	0.274	3.29E-02	-2.147	-2.147	-0.038			gk	-0.648		0.291	2.84E-01	-2.037	-2.037	0.197	
	pgm	-0.765		0.256	4.12E-01	-1.247	-1.247	0.226			pgm	-0.588		0.274	9.35E-01	-1.842	-1.842	0.466	
	pgl	-1.186		0.327	9.81E-02	-2.453	-2.453	0.080			pgl	-1.014		0.341	4.12E-01	-2.331	-2.331	0.303	
	pKRA	-0.700		0.283	7.70E-01	-1.261	-1.261	0.380			pKRA	-0.528		0.299	9.94E-01	-1.678	-1.678	0.823	
	pKRB	-0.050		0.182	1.00E+00	-0.700	-0.700	0.640			pKRB	0.122		0.207	1.00E+00	-0.875	-0.875	0.920	
	fbp	-0.522		0.260	6.66E-01	-1.523	-1.523	0.479			fbp	-0.349		0.278	1.00E+00	-1.417	-1.417	0.718	
	fbtA	-0.898		0.319	3.28E-01	-2.222	-2.222	0.246			fbtA	-0.815		0.334	7.92E-01	-2.102	-2.102	0.471	
	gspC	-0.638		0.334	9.81E-01	-1.304	-1.304	0.661			gspC	-0.463		0.349	1.00E+00	-1.810	-1.810	0.884	
	gpmA	-0.167		0.207	1.00E+00	-0.959	-0.959	0.626			gpmA	0.008		0.229	1.00E+00	-0.872	-0.872	0.884	
	pykA	0.595		0.158	6.53E-02	-0.015	-0.015	1.205			gpmB	0.173		0.221	1.00E+00	-0.676	-0.676	1.021	
	pykF	0.571		0.159	1.09E-01	-0.045	-0.045	1.186			pykA	0.768	S	0.186	2.42E-02	0.045	0.045	1.491	
	ppaA	0.417		0.162	7.07E-01	-0.208	-0.208	1.043			pykF	0.743	S	0.187	3.88E-02	0.016	0.016	1.470	
	zwf	0.270		0.160	9.97E-01	-0.348	-0.348	0.888			ppaA	0.590		0.190	3.23E-01	-0.145	-0.145	1.328	
	pgl	-0.173		0.221	1.00E+00	-1.621	-1.621	0.676			zwf	0.443		0.188	8.42E-01	-0.287	-0.287	1.172	
	gnd	0.022		0.225	1.00E+00	-0.821	-0.821	0.864			rpe	-0.090	S	0.454	5.15E-03	-3.853	-3.853	-0.328	
	rpe	-2.262	S	0.443	9.70E-04	-3.990	-3.990	-0.535			rpe	-0.290		0.454	5.15E-03	-3.853	-3.853	-0.328	
	rpIA	-0.794		0.306	6.90E-01	-1.978	-1.978	0.389			rpIA	-0.621		0.321	9.79E-01	-1.858	-1.858	0.618	
	rpIB	-0.288		0.221	1.00E+00	-1.134	-1.134	0.555			rpIB	-0.115		0.242	1.00E+00	-1.041	-1.041	0.811	
	rpIA	-0.288		0.210	1.00E+00	-1.074	-1.074	0.537			rpIB	-0.096		0.232	1.00E+00	-0.985	-0.985	0.794	
	rpIB	-0.364		0.280	1.00E+00	-1.363	-1.363	0.636			rpIB	-0.191		0.278	1.00E+00	-1.257	-1.257	0.875	
	rpIB	-0.410		0.257	9.99E-01	-1.400	-1.400	0.580			rpIB	-0.237		0.275	1.00E+00	-1.295	-1.295	0.828	
	rpIB	-0.298		0.255	1.00E+00	-1.321	-1.321	0.723			rpIB	-0.125		0.283	1.00E+00	-1.213	-1.213	0.960	
pykA	0.1h-1	-1.367		0.404	1.85E-01	-2.938	-2.938	0.205		gnd	0.1h-1	-1.194		0.416	4.85E-01	-2.807	-2.807	0.418	
	0.2h-1	-0.658		0.338	9.75E-01	-1.967	-1.967	0.650			0.2h-1	-0.486		0.352	1.00E+00	-1.844	-1.844	0.872	
	0.4h-1	-0.963		0.372	6.92E-01	-2.408	-2.408	0.482			0.4h-1	-0.790		0.385	9.55E-01	-2.278	-2.278	0.689	
	0.5h-1	-1.488		0.501	4.17E-01	-3.442	-3.442	0.467			0.5h-1	-1.315		0.510	7.01E-01	-3.301	-3.301	0.672	
	0.7h-1	-2.961	S	0.553	4.56E-04	-5.128	-5.128	-0.796			0.7h-1	-0.796	S	0.562	1.68E-03	-4.982	-4.982	-0.599	
	gpmA	-0.120		0.296	4.40E-04	-0.718	-0.718	0.276			gpmA	-0.154		0.164	7.95E-01	-1.169	-1.169	0.761	
	gk	-1.698	S	0.246	1.13E-06	-2.648	-2.648	-0.728			gk	-1.114	S	0.289	4.92E-02	-2.227	-2.227	-0.001	
	pgm	-1.356	S	0.227	3.56E-05	-2.240	-2.240	-0.472			pgm	-0.782		0.273	4.88E-01	-1.831	-1.831	0.267	
	pgl	-1.762		0.304	7.25E-05	-2.972	-2.972	-0.591			pgl	-1.208		0.340	1.18E-01	-2.522	-2.522	0.105	
	pKRA	-1.296		0.255	1.19E-03	-2.295	-2.295	-0.296			pKRA	-0.722		0.298	9.05E-01	-1.888	-1.888	0.424	
	pKRB	-0.646	S	0.138	3.06E-03	-1.177	-1.177	-0.115			pKRB	-0.072		0.206	1.00E+00	-0.863	-0.863	0.719	
	fbp	-1.118		0.231	2.50E-03	-2.018	-2.018	-0.217			fbp	-0.544		0.277	9.74E-01	-1.807	-1.807	0.519	
	fbtA	-1.583	S	0.295	4.40E-04	-2.740	-2.740	-0.427			fbtA	-1.010		0.333	5.67E-01	-2.023	-2.023	0.271	
	gspC	-1.232	S	0.312	4.69E-02	-2.456	-2.456	-0.007			gspC	-0.658		0.348	9.83E-01	-2.001	-2.001	0.686	
	gpmA	-0.762		0.169	6.40E-03	-1.416	-1.416	-0.108			gpmA	-0.188		0.228	1.00E+00	-1.061	-1.061	0.684	
	gpmB	-0.595		0.169	6.35E-03	-1.250	-1.250	-0.340			gpmB	-0.228		0.228	1.00E+00	-1.061	-1.061	0.684	
	pykF	-0.025		0.106	1.00E+00	-0.430	-0.430	0.380			pykA	0.574		0.194	3.21E-01	-0.142	-0.142	1.289	
	ppaA	-0.178		0.110	9.98E-01	-0.600	-0.600	0.244			pykF	0.549		0.185	4.23E-01	-0.171	-0.171	1.268	
	zwf	-0.326		0.107	3.56E-01	-0.735	-0.735	0.084			ppaA	0.396		0.188	9.43E-01	-0.333	-0.333	1.124	
	gnd	-0.768	S	0.186	2.62E-02	-1.040	-1.040	-0.495			zwf	0.248		0.186	1.00E+00	-0.474	-0.474	0.970	
	rpIA	-0.574		0.184	3.21E-01	-1.289	-1.289	0.142			rpIA	-0.194		0.241	1.00E+00	-1.117	-1.117	0.728	
	rpe	-2.858	S	0.426	3.64E-06	-4.532	-4.532	-1.184			rpe	-2.284	S	0.453	1.10E-03	-4.045	-4.045	-0.523	
pykF	rpIB	-1.389	S	0.281	1.93E-03	-2.408	-2.408	-0.370			rpIB	-0.815		0.320	7.24E-01	-1.468	-1.468	0.418	
	rpIB	-0.893	S	0.186	2.85E-03	-1.603	-1.603	-0.163			rpIB	-0.310		0.240	1.00E+00	-1.230	-1.230	0.611	
	rpIB	-0.864	S	0.173	1.15E-03	-1.534	-1.534	-0.194			rpIB	-0.290		0.231	1.00E+00	-1.174	-1.174	0.594	
	rpIB	-0.858	S	0.201	2.19E-03	-1.858	-1.858	-0.858			rpIB	-0.389		0.276	1.00E+00	-1.447	-1.447	0.678	
	rpIB	-1.005	S	0.223	1.04E-02	-2.189	-2.189	-0.117			rpIB	-0.432		0.274	9.99E-01	-1.485	-1.485	0.621	
	rpIB	-0.894	S	0.237	7.00E-02	-1.818	-1.818	0.029			rpIB	-0.321		0.282	1.00E+00	-1.403	-1.403	0.761	
	0.1h-1	-1.962		0.389	1.27E-03	-3.476	-3.476	-0.448			0.1h-1	-1.389		0.415	1.98E-01	-2.999	-2.999	0.221	
	0.2h-1	-1.254		0.312	4.27E-02	-2.269	-2.269	-0.880			0.2h-1	-0.880		0.351	7.72E-01	-2.035	-2.035	0.674	
	0.4h-1	-1.558	S	0.352	1.12E-02	-2.938	-2.938	-0.178			0.4h-1	-0.985		0.384	7.10E-01	-2.471	-2.471	0.501	
	0.5h-1	-2.083	S	0.486	1.77E-02	-3.991	-3.991	-0.175			0.5h-1	-1.509		0.510	4.22E-01	-3.494	-3.494	0.475	
	0.7h-1	-3.552	S	0.553	6.25E-06	-5.589	-5.589	-1.433			0.7h-1	-2.983	S	0.561	7.55E-04	-4.174	-4.174	-0.792	
	gpmA	-0.095		0.105	1.00E+00	-0.499	-0.499	0.309		rpe	gpmA	2.738		0.426	1.05E-05	1.064	1.064	4.412	
	gk	-1.663	S	0.247	1.79E-06	-2.626	-2.626	-0.700			gk	1.170		0.481	7.99E-01	-0.689	-0.689	3.029	
	pgm	-1.331	S	0.229	5.80E-05	-2.216	-2.216	-0.440			pgm	1.602		0.472	2.77E-01	-0.324	-0.324	3.328	
	pgl	-1.767	S	0.305	1.01E-04	-2.850	-2.850	-0.684			pgl	1.076		0.513	9.47E-01	-1.888	-1.888	3.051	
	pKRA	-1.271	S	0.257	1.75E-03	-2.273	-2.273	-0.268			pKRA	1.562		0.487	2.60E-01	-0.316	-0.316	3.448	
	pKRB	-0.621	S	0.139	6.97E-03	-1.158	-1.158	-0.084			pKRB	2.212	S	0.436	1.21E-03	0.507	0.507	3.917	
	fbp	-1.093	S	0.232	3.82E-03	-2.559	-2.559	-0.189			fbp	1.740		0.474	6.84E-02	0.092	0.092	3.571	
	fbtA	-1.558	S	0.296	6.16E-04	-2.717	-2.717	-0.400			fbtA	1.274		0.508	7.52E-01	-0.682	-0.682	3.231	
	gspC	-1.207		0.313	5.96E-02	-2.433	-2.433	0.020			gspC	1.628		0.518	3.00E-01	-0.367	-0.367	3.620	
gpmA	-0.731		0.173	1.17E-02	-1.289	-1.289	-0.749		gpmA	2.099		0.406	4.07E-01	0.365	0.365	3.883			
gpmB	-0.571		0.159	1.09E-01	-1.186	-1.186	0.045		gpmB	2.262	S	0.443	9.70E-04	0.535	0.535	3.998			
pykA	0.029		0.106	1.00E+00	-0.380	-0.380	0.430		pykA	2.858	S	0.429	3.46E-04	1.184	1.184	4.532			
ppaA	-0.153		0.121	1.00E+00	-0.583	-0.583	0.276		ppaA	2.689	S	0.427	4.58E-04	1.075	1.075	4.508			
gnd	-0.301		0.108	6.68E-01	-0.517	-0.517	0.117		gnd	2.833	S	0.428	3.71E-04	1.089	1.089	4.389			
pgl	-0.743		0.187	3.88E-02	-1.470	-1.470	-0.016		pgl	2.552	S	0.427	4.65E-04	0.855	0.855	4.209			
gnd	-0.549		0.185	4.23E-01	-1.268	-1.268	0.171		gnd	2.243	S	0.454	5.15E-03	0.326	0.326	3.863			
rpIA	-0.831		0.427	4.59E-02	-1.697	-1.697	-0.167		rpIA	1.404		0.453	1.04E-01	-0.443	-0.443	2.448			
rpIB	-1.364	S	0.282	2.71E-03	-2.467	-2.467	-0.281		rpIB	1.409		0.500	4.35E-01	-0.458	-0.458	3.396			
rpIB	-0.858	S	0.187	4.99E-03	-1.583	-1.583	-0.134		rpIB	1.897		0.453	1.20E-02						

Multiple Comparisons										Multiple Comparisons											
Dependent Variable: Protein(LC-MS)										Dependent Variable: Protein(LC-MS)											
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval				(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval					
						Lower Bound	Upper Bound									Lower Bound	Upper Bound				
r5A	gaIM	0.744	S	0.173	1.30E-02	0.075	1.413			0.1h-1	gaIM	0.843	S	0.389	3.63E-03	0.330	3.359				
	gk	-0.824		0.282	4.48E-01	-1.910	0.263				gk	0.275		0.446	1.00E+00	-1.444	1.993				
	pgm	-0.492		0.266	9.88E-01	-1.513	0.529				pgm	0.607		0.436	1.00E+00	-1.075	2.288				
	pgl	-0.918		0.334	5.77E-01	-2.210	0.374				pgl	0.181		0.480	1.00E+00	-1.664	2.025				
	pkA	-0.432		0.291	1.00E+00	-1.553	0.689				pkA	0.867		0.452	1.00E+00	-1.072	2.405				
	pkB	0.218		0.155	1.00E+00	-0.533	0.969				pkB	1.317		0.397	2.15E-01	-0.231	2.864				
	fbp	-0.254		0.269	1.00E+00	-1.289	0.781				fbp	0.845		0.438	9.79E-01	-0.844	2.534				
	fbab	-0.719		0.326	9.11E-01	-1.880	0.542				fbab	0.379		0.475	1.00E+00	-1.448	2.204				
	gspC	-0.368		0.342	1.00E+00	-1.690	0.955				gspC	0.731		0.486	9.99E-01	-1.134	2.595				
	gpmA	0.102		0.218	1.00E+00	-0.735	0.939				gpmA	1.200		0.409	4.38E-01	-0.387	2.788				
	gpmB	0.268		0.210	1.00E+00	-0.537	1.074				gpmB	1.367		0.404	1.85E-01	-0.205	2.939				
	pykA	0.864	S	0.173	1.15E-03	0.194	1.534				pykA	1.962	S	0.386	1.27E-03	0.449	3.478				
	pykF	0.839	S	0.174	2.18E-03	0.165	1.513				pykF	1.938	S	0.387	1.61E-03	0.422	3.453				
	ppsA	0.686	S	0.177	4.82E-02	0.002	1.370				ppsA	1.784	S	0.388	6.29E-03	0.265	3.304				
	zwf	0.538		0.175	3.43E-01	-0.139	1.215				zwf	1.637	S	0.387	2.03E-02	0.120	3.153				
	ggl	0.096		0.232	1.00E+00	-0.794	0.985				ggl	1.194		0.416	4.85E-01	-0.418	2.807				
	gnd	0.290		0.231	1.00E+00	-0.594	1.174				gnd	1.389		0.415	1.98E-01	-0.221	2.999				
	rpe	-1.994	S	0.448	9.11E-03	-3.740	-0.248				rpe	-0.895		0.566	9.99E-01	-3.066	1.275				
	rpiA	-0.525		0.314	9.97E-01	-1.735	0.685				rpiA	0.573		0.466	1.00E+00	-1.219	2.369				
	rpiB	-0.019		0.232	1.00E+00	-0.907	0.868				rpiB	1.079		0.416	6.89E-01	-0.533	2.691				
	ktB	-0.095		0.269	1.00E+00	-1.129	0.939				ktA	1.099		0.410	6.29E-01	-0.494	2.691				
	ktA	-0.142		0.267	1.00E+00	-1.166	0.883				ktB	1.003		0.429	8.74E-01	-0.695	2.992				
	talB	-0.031		0.274	1.00E+00	-1.085	1.024				talA	0.999		0.436	9.15E-01	-0.727	2.644				
	talA	-0.099		0.410	6.29E-01	-2.691	0.944				talB	1.068		0.441	8.05E-01	-0.635	2.761				
	0.2h-1	-0.390		0.345	1.00E+00	-1.724	0.944				0.2h-1	0.709		0.488	1.00E+00	-1.164	2.585				
	0.4h-1	-0.694		0.378	9.88E-01	-2.162	0.773				0.4h-1	-0.404		0.512	1.00E+00	-1.563	2.366				
	0.5h-1	-1.216		0.506	8.08E-01	-3.190	0.752				0.5h-1	-0.949		0.617	9.99E-01	-2.422	0.747				
	0.7h-1	-2.693	S	0.558	2.77E-03	-4.872	-0.513				0.7h-1	-1.894		0.656	8.01E-01	-4.116	0.921				
	r5B	gaIM	0.840		0.323	9.94E-02	-0.059	1.738				0.2h-1	gaIM	1.134		0.316	1.16E-01	-0.102	2.376		
		gk	-0.728		0.321	8.87E-01	-1.999	0.550					gk	-0.620		0.389	1.00E+00	-1.705	0.455		
pgm		-0.397		0.306	1.00E+00	-1.571	0.778			pgm	-0.102			0.375	1.00E+00	-1.543	1.335				
pgl		-0.823		0.367	8.99E-01	-2.234	0.589			pgl	-0.628			0.428	1.00E+00	-2.162	1.101				
pkA		-0.337		0.325	1.00E+00	-1.597	0.924			pkA	-0.529			0.399	1.00E+00	-1.551	0.844				
pkB		0.313		0.248	1.00E+00	-0.645	1.271			pkB	0.936			0.329	9.87E-01	-0.671	1.889				
fbp		-0.158		0.309	1.00E+00	-1.345	1.028			fbp	0.336			0.437	1.00E+00	-1.314	1.588				
fbab		-0.624		0.362	9.95E-01	-2.008	0.763			fbab	-0.138			0.422	1.00E+00	-1.340	1.281				
gspC		-0.272		0.374	1.00E+00	-1.712	1.167			gspC	0.727			0.487	1.00E+00	-1.174	2.627				
gpmA		0.197		0.266	1.00E+00	-0.827	1.222			gpmA	0.462			0.343	1.00E+00	-0.835	1.811				
gpmB		0.364		0.266	1.00E+00	-0.636	1.363			gpmB	0.698			0.338	9.75E-01	-0.655	1.967				
pykA		0.955	S	0.231	2.31E-02	0.061	1.859			pykA	1.254		S	0.232	5.92E-02	-0.002	1.911				
pykF		0.934	S	0.232	3.33E-02	0.032	1.836			pykF	1.228		S	0.231	3.31E	4.48E-02	-0.009	2.467			
ppsA		0.781	S	0.234	2.01E-01	-0.127	1.690			ppsA	1.079		S	0.231	3.31E	1.83E-01	-0.167	2.311			
zwf		0.634		0.232	5.92E-01	-0.770	1.538			zwf	0.538			0.232	5.92E-01	-0.770	1.538				
ggl		0.191		0.278	1.00E+00	-0.875	1.257			ggl	0.486			0.352	1.00E+00	-0.872	1.841				
gnd		0.386		0.276	1.00E+00	-0.678	1.447			gnd	0.680			0.351	9.77E-01	-0.674	2.033				
rpe		-1.898	S	0.474	3.29E-02	-3.731	-0.067			rpe	-1.804		S	0.528	3.34E-01	-3.605	0.998				
rpiA		-0.430		0.348	1.00E+00	-1.768	0.909			rpiA	-0.430			0.348	1.00E+00	-1.768	0.909				
rpiB		0.076		0.277	1.00E+00	-0.988	1.141			rpiB	0.370			0.351	1.00E+00	-0.988	1.728				
ktA		0.056		0.269	1.00E+00	-0.839	1.128			ktA	0.396			0.349	1.00E+00	-0.844	1.728				
ktB		-0.046		0.307	1.00E+00	-1.224	1.131			ktB	-0.046			0.376	1.00E+00	-1.195	1.682				
talB		0.065		0.314	1.00E+00	-1.138	1.268			talA	0.248			0.376	1.00E+00	-1.195	1.682				
0.1h-1		-1.003		0.428	8.74E-01	-2.692	0.686			talB	-0.359			0.381	1.00E+00	-1.104	1.821				
0.2h-1		-0.295		0.377	1.00E+00	-1.714	1.155			0.2h-1	-0.458			0.469	1.00E+00	-1.744	0.837				
0.4h-1		-0.599		0.408	1.00E+00	-2.171	0.973			0.4h-1	-0.305			0.462	1.00E+00	-2.075	1.468				
0.5h-1		-1.124		0.528	9.96E-01	-3.171	0.923			0.5h-1	-0.828			0.570	1.00E+00	-3.026	1.361				
0.7h-1		-2.697	S	0.558	2.77E-03	-4.872	-0.513			0.7h-1	-1.894		S	0.617	9.99E-01	-3.088	0.686				
r5C		gaIM	0.886		0.228	5.12E-02	-0.002	1.773			0.4h-1		gaIM	1.432		0.332	3.13E-02	0.058	2.811		
		gk	-0.682		0.319	9.36E-01	-1.905	0.541					gk	-0.122		0.417	1.00E+00	-1.734	1.471		
	pgm	-0.359		0.304	1.00E+00	-1.517	0.816			pgm		-0.208		0.406	1.00E+00	-1.362	1.761				
	pgl	-0.776		0.366	9.40E-01	-2.162	0.620			pgl		-0.222		0.452	1.00E+00	-1.922	1.411				
	pkA	-0.290		0.327	1.00E+00	-1.543	0.963			pkA		0.263		0.423	1.00E+00	-1.364	1.881				
	pkB	0.360		0.245	1.00E+00	-0.589	1.308			pkB		0.912		0.364	7.47E-01	-0.508	2.333				
	fbp	-0.112		0.307	1.00E+00	-1.321	0.941			fbp		0.191		0.421	1.00E+00	-1.132	1.514				
	fbab	-0.624		0.359	9.98E-01	-1.995	0.800			fbab		-0.025		0.448	1.00E+00	-1.744	1.691				
	gspC	-0.226		0.373	1.00E+00	-1.659	1.207			gspC		-0.327		0.459	1.00E+00	-1.435	2.089				
	gpmA	0.243		0.266	1.00E+00	-0.772	1.259			gpmA		0.596		0.377	9.39E-01	-0.655	2.259				
	gpmB	0.410		0.257	9.99E-01	-0.569	1.400			gpmB		0.698		0.362	9.62E-01	-0.612	2.381				
	pykA	1.005	S	0.228	1.04E-02	0.117	1.894			pykA		1.558	S	0.352	1.12E-02	0.178	2.939				
	pykF	0.981	S	0.229	1.55E-02	0.089	1.872			pykF		1.533	S	0.353	1.43E-02	0.151	2.916				
	ppsA	0.827	S	0.231	1.14E-01	-0.071	1.726			ppsA		1.084	S	0.230	5.92E-02	-0.151	2.611				
	zwf	0.680		0.230	4.22E-01	-0.214	1.573			zwf		0.533		0.353	1.49E-01	-0.151	2.611				
	ggl	0.237		0.275	1.00E+00	-0.620	1.295			ggl		0.790		0.385	9.95E-01	-0.699	2.278				
	gnd	0.432		0.274	9.99E-01	-0.621	1.485			gnd		0.686		0.385	7.10E-01	-0.477	2.851				
	rpe	-1.852	S	0.472	4.29E-02	-3.680	-0.025			rpe		-1.700	S	0.543	8.24E-01	-3.385	0.780				
	rpiA	-0.383		0.347	1.00E+00	-1.716	0.949			rpiA		0.169		0.439	1.00E+00	-1.515	1.845				
	rpiB	0.122		0.275	1.00E+00	-0.934	1.178			rpiB		0.387		0.387	1.00E+00	-0.934	1.178				
	ktA	0.142		0.267	1.00E+00	-0.883	1.166			ktA		0.099		0.378	9.98E-01	-0.773	2.162				
	ktB	0.046		0.307	1.00E+00	-1.131	1.224			ktB		0.598		0.308	1.00E+00	-0.573	2.171				
	talB	0.111		0.312	1.00E+00	-1.															

**Table S10 C Statistical tests for AEs (Metabolites)****Test of Homogeneity of Variances**

Metabolite

Levene Statistic	df1	df2	Sig.
	28	4,002	2.88E-62

**ANOVA**

Metabolite

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	1,412.815	28	50.458	13.985	2.50E-62
Within Groups	14,439.104	4,002	3.608		
Total	15,851.919	4,030			

**Robust Tests of Equality of Means**

Metabolite

	Statistic(a)	df1	df2	Sig.
Welch	14.737	28	1,394.173	2.68E-60

a. Asymptotically F distributed.

Multiple Comparisons										Multiple Comparisons											
Dependent Variable: Metabolite										Dependent Variable: Metabolite											
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval				(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval					
						Lower Bound	Upper Bound									Lower Bound	Upper Bound				
gpm	gik	-1.590	S	0.257	1.35E-06	-2.564	-0.616			pkfb	galm	-1.129	S	0.109	1.00E+00	-0.281	0.543				
	gpm	-2.029	S	0.247	6.57E-11	-2.966	-1.093					gik	-0.486	S	0.263	3.00E-05	-2.495	-0.467			
	pgl	-2.214	S	0.283	1.42E-09	-3.299	-1.129					gpm	-0.905	S	0.288	2.04E-08	-1.898	-0.982			
	pka	-1.239	S	0.188	2.54E-07	-1.954	-0.524					pkA	-1.110	S	0.195	2.09E-05	-1.852	-0.368			
	pfb	-0.129	S	0.109	1.00E+00	-0.540	0.281					fbp	-0.050	S	0.119	1.00E+00	-0.510	0.383			
	fbp	-0.193	S	0.108	9.92E-01	-0.552	0.206					ftab	-0.204	S	0.121	5.73E-01	-0.743	0.235			
	ftab	-0.333	S	0.121	5.73E-01	-0.791	0.125					gapC	-0.564	S	0.147	5.87E-02	-1.108	0.007			
	gapC	-0.679	S	0.137	6.24E-04	-1.200	-0.158					gpmA	-0.236	S	0.144	9.99E-01	-0.793	0.333			
	gpmA	-0.359	S	0.139	7.08E-01	-0.888	0.168					gpmB	-0.765	S	0.171	4.62E-03	-1.313	-0.048			
	gpmB	-0.765	S	0.171	4.62E-03	-1.415	-0.115					pykA	-1.490	S	0.202	8.35E-08	-2.128	-0.954			
	pykA	-1.490	S	0.195	7.65E-10	-2.232	-0.749					pykF	-1.132	S	0.163	2.74E-09	-1.795	-0.568			
	pykF	-1.312	S	0.158	5.26E-11	-1.895	-0.729					ppsA	-0.228	S	0.121	1.00E+00	-0.855	0.357			
	ppsA	-0.228	S	0.108	9.51E-01	-0.836	0.181					zwf	-1.167	S	0.206	6.27E-04	-1.813	-0.242			
	zwf	-1.156	S	0.199	1.81E-05	-1.917	-0.396					gnd	-0.897	S	0.157	4.93E-03	-1.194	-0.059			
	pgl	-0.897	S	0.157	4.93E-03	-1.291	-0.102					gnd	-1.264	S	0.215	8.79E-06	-2.001	-0.446			
	gnd	-1.264	S	0.215	8.79E-06	-2.081	-0.446					rpe	-2.065	S	0.259	2.03E-10	-3.051	-1.079			
	rpe	-2.065	S	0.259	2.03E-10	-3.051	-1.079					rpIA	-1.017	S	0.162	9.33E-07	-1.632	-0.402			
	rpIA	-1.017	S	0.162	9.33E-07	-1.632	-0.402					rpIB	-0.882	S	0.171	1.71E-04	-1.534	-0.241			
	rpIB	-0.882	S	0.171	1.71E-04	-1.447	-0.317					tkIA	-0.479	S	0.154	3.31E-01	-1.053	0.109			
	tkIA	-0.479	S	0.154	3.31E-01	-1.053	0.109					tkIB	-0.803	S	0.139	9.18E-04	-1.200	-0.418			
	tkIB	-0.803	S	0.129	9.18E-07	-1.290	-0.316					talA	-0.245	S	0.144	1.00E+00	-0.659	0.428			
	talA	-0.245	S	0.133	9.91E-01	-0.750	0.259					talB	-0.505	S	0.259	9.75E-01	-1.369	0.816			
	talB	-0.505	S	0.259	9.75E-01	-1.478	0.467					0.1h-1	-0.828	S	0.166	1.09E-02	-1.325	-0.277			
	0.1h-1	-0.828	S	0.157	1.20E-04	-1.422	-0.233					0.2h-1	-0.218	S	0.127	1.00E+00	-0.570	0.391			
	0.2h-1	-0.218	S	0.116	9.87E-01	-0.655	0.219					0.4h-1	-0.604	S	0.123	1.08E-01	-0.984	0.034			
	0.4h-1	-0.604	S	0.124	7.05E-04	-0.781	-0.136					0.5h-1	-0.857	S	0.165	1.89E-04	-1.474	-0.240			
	0.5h-1	-0.857	S	0.165	1.89E-04	-1.481	-0.233					0.7h-1	-1.314	S	0.214	4.88E-06	-1.999	-0.371			
	0.7h-1	-1.314	S	0.208	1.08E-06	-2.104	-0.524					fbp	galm	1.590	S	0.257	1.35E-06	-0.616	2.800		
gpm	gik	0.439	S	0.344	1.00E+00	-0.855	1.734				gpm		-0.439	S	0.344	1.00E+00	-1.734	0.855			
	pgl	-0.624	S	0.371	9.98E-01	-2.025	0.777				pka		0.351	S	0.263	3.00E-05	-2.495	-0.467			
	pka	0.351	S	0.304	1.00E+00	-0.796	1.498				pfb		1.481	S	0.258	1.55E-07	0.673	2.723			
	pfb	1.481	S	0.263	3.00E-05	0.947	2.015				fbp		1.397	S	0.262	8.79E-05	0.407	2.387			
	ftab	1.257	S	0.288	1.63E-03	0.243	2.270				ftab		1.257	S	0.288	1.63E-03	0.243	2.270			
	gapC	0.931	S	0.276	1.95E-01	-0.131	1.953				gapC		0.931	S	0.248	1.44E-01	-0.149	1.036			
	gpmA	1.671	S	0.287	7.56E-07	0.661	2.680				gpmA		1.671	S	0.277	4.26E-03	0.186	2.276			
	gpmB	1.264	S	0.294	5.29E-01	-0.285	1.934				gpmB		1.264	S	0.294	5.29E-01	-0.285	1.934			
	pykA	0.109	S	0.309	1.00E+00	-1.054	1.263				pykA		0.109	S	0.329	1.00E+00	-1.264	1.263			
	pykF	0.278	S	0.284	1.00E+00	-0.795	1.350				pykF		0.278	S	0.277	4.26E-03	0.186	2.276			
	ppsA	1.362	S	0.263	1.78E-04	0.369	2.356				ppsA		1.362	S	0.263	1.78E-04	0.369	2.356			
	zwf	0.434	S	0.311	1.00E+00	-0.741	1.608				zwf		0.434	S	0.311	1.00E+00	-0.741	1.608			
	pgl	0.897	S	0.286	2.93E-01	-0.192	1.972				pgl		0.897	S	0.286	2.93E-01	-0.192	1.972			
	gnd	0.326	S	0.322	1.00E+00	-0.888	1.537				gnd		0.326	S	0.322	1.00E+00	-0.888	1.537			
	rpe	0.475	S	0.353	1.00E+00	-1.804	0.854				rpe		0.475	S	0.353	1.00E+00	-1.804	0.854			
	rpIA	0.573	S	0.289	9.76E-01	-0.116	1.664				rpIA		0.573	S	0.289	9.76E-01	-0.116	1.664			
	rpIB	0.989	S	0.279	1.02E-01	-0.095	2.043				rpIB		0.989	S	0.279	1.02E-01	-0.095	2.043			
	tkIA	1.111	S	0.270	1.53E-02	0.093	2.130				tkIA		1.111	S	0.270	1.53E-02	0.093	2.130			
	tkIB	0.797	S	0.272	4.56E-01	-0.238	1.813				tkIB		0.797	S	0.272	4.56E-01	-0.238	1.813			
	talA	1.345	S	0.274	6.00E-04	0.310	2.379				talA		1.345	S	0.274	6.00E-04	0.310	2.379			
	talB	1.084	S	0.350	3.10E-01	-0.235	2.404				talB		1.084	S	0.350	3.10E-01	-0.235	2.404			
	0.1h-1	0.753	S	0.286	6.41E-01	-0.317	1.842				0.1h-1		0.753	S	0.286	6.41E-01	-0.317	1.842			
	0.2h-1	1.372	S	0.295	1.97E-04	0.780	2.024				0.2h-1		1.372	S	0.295	1.97E-04	0.780	2.024			
	0.4h-1	0.986	S	0.270	7.28E-02	-0.032	2.004				0.4h-1		0.986	S	0.270	7.28E-02	-0.032	2.004			
	0.5h-1	0.733	S	0.290	7.46E-01	-0.362	1.828				0.5h-1		0.733	S	0.290	7.46E-01	-0.362	1.828			
	0.7h-1	1.717	S	0.317	1.00E+00	-0.918	3.352				0.7h-1		1.717	S	0.317	1.00E+00	-0.918	3.352			
	gpm	galm	2.028	S	0.247	6.57E-11	1.093	2.966					gpm	galm	2.028	S	0.247	6.57E-11	1.093	2.966	
	gik	0.439	S	0.344	1.00E+00	-0.855	1.734				gik	0.439	S	0.344	1.00E+00	-0.855	1.734				
	pgl	-0.184	S	0.364	1.00E+00	-1.559	1.190				pgl	-0.184	S	0.364	1.00E+00	-1.559	1.190				
	pka	0.765	S	0.295	6.32E-01	-0.334	1.865				pka	0.765	S	0.295	6.32E-01	-0.334	1.865				
	pfb	1.900	S	0.253	8.05E-10	0.943	2.857				pfb	1.900	S	0.253	8.05E-10	0.943	2.857				
	fbp	1.836	S	0.251	2.87E-09	0.884	2.789				fbp	1.836	S	0.251	2.87E-09	0.884	2.789				
	ftab	1.698	S	0.258	1.55E-07	0.673	2.723				ftab	1.698	S	0.258	1.55E-07	0.673	2.723				
	gapC	1.350	S	0.266	2.99E-04	0.344	2.356				gapC	1.350	S	0.266	2.99E-04	0.344	2.356				
	gpmA	1.671	S	0.287	7.56E-07	0.661	2.680				gpmA	1.671	S	0.287	7.56E-07	0.661	2.680				
	gpmB	1.264	S	0.295	4.47E-03	0.680	1.848				gpmB	1.264	S	0.295	4.47E-03	0.680	1.848				
	pykA	0.539	S	0.300	9.94E-01	-0.592	1.671				pykA	0.539	S	0.300	9.94E-01	-0.592	1.671				
	pykF	0.717	S	0.275	6.83E-01	-0.321	1.755				pykF	0.717	S	0.275	6.83E-01	-0.321	1.755				
	ppsA	1.802	S	0.252	7.23E-05	0.846	2.758				ppsA	1.802	S	0.252	7.23E-05	0.846	2.758				
	zwf	0.873	S	0.303	4.65E-01	-0.270	1.946				zwf	0.873	S	0.303	4.65E-01	-0.270	1.946				
	pgl	1.333	S	0.277	8.99E-04	0.288	2.377				pgl	1.333	S	0.277	8.99E-04	0.288	2.377				
	gnd	0.755	S	0.313	8.00E-01	-0.415	1.946				gnd	0.755	S	0.313	8.00E-01	-0.415	1.946				
	rpe	-0.038	S	0.302	1.00E+00	-1.337	1.265				rpe	-0.038	S	0.302	1.00E+00	-1.337	1.265				
	rpIA	1.012	S	0.280	8.17E-02	-0.044	2.069				rpIA	1.012	S	0.280	8.17E-02	-0.044	2.069				
	rpIB	1.428	S	0.270	1.02E-04	0.409	2.447				rpIB	1.428	S	0.270	1.02E-04	0.409	2.447				
	tkIA	1.654	S	0.269	3.74E-05	0.699	2.533				tkIA	1.654	S	0.269	3.74E-05	0.699	2.5				

Multiple Comparisons									
Dependent Variable: Metabolite									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound		
gpmB	galM	0.765	S	0.171	4.62E-03	0.115	1.415		
	gk	-0.825	S	0.294	2.59E-01	-1.934	0.285		
	pgm	-1.264	S	0.285	4.47E-03	-2.340	-0.188		
	pgl	-1.440	S	0.317	3.21E-03	-2.654	-0.243		
	pKbA	-0.474	S	0.236	9.71E-01	-1.365	0.417		
	pKbB	0.536	S	0.175	1.04E-01	-0.044	1.316		
	fbp	0.572	S	0.178	2.39E-01	-0.101	1.245		
	fbtB	0.432	S	0.187	8.75E-01	-0.276	1.140		
	gapC	0.088	S	0.266	1.00E+00	-0.662	0.834		
	gpmA	0.406	S	0.199	9.66E-01	-0.347	1.159		
	pykA	-0.725	S	0.242	3.77E-01	-1.638	0.187		
	pykF	-0.547	S	0.216	6.82E-01	-1.338	0.245		
	ppsA	0.538	S	0.179	3.77E-01	-0.141	1.216		
	zwf	-0.391	S	0.245	9.99E-01	-1.319	0.536		
	pgl	0.068	S	0.212	1.00E+00	-0.732	0.868		
	gnd	-0.498	S	0.258	9.83E-01	-1.473	0.475		
	rpe	-1.300	S	0.296	5.52E-03	-2.418	-0.182		
	rpiA	-0.252	S	0.216	1.00E+00	-1.068	0.564		
	rpiB	0.164	S	0.203	1.00E+00	-0.602	0.930		
	pKbA	tkiA	0.286	S	0.189	1.00E+00	-0.429	1.001	
tkiB		-0.038	S	0.192	1.00E+00	-0.764	0.689		
talB		0.520	S	0.195	6.43E-01	-0.216	1.255		
talB		0.255	S	0.235	1.00E+00	-0.848	1.356		
0.1h-1		0.047	S	0.212	1.00E+00	-0.863	0.748		
0.2h-1		-0.561	S	0.184	3.95E-01	-0.148	1.242		
0.4h-1		0.161	S	0.189	1.00E+00	-0.554	0.876		
0.5h-1		-0.092	S	0.218	1.00E+00	-0.914	0.730		
0.7h-1		-0.549	S	0.252	9.28E-01	-1.500	0.403		
galM		-1.450	S	0.148	7.65E-04	-1.746	-1.154		
gk		-0.100	S	0.309	1.00E+00	-1.263	1.064		
pgm		-0.539	S	0.300	9.94E-01	-1.671	0.592		
pgl		-0.723	S	0.331	9.24E-01	-1.978	0.531		
pKbA		0.251	S	0.254	1.00E+00	-0.707	1.209		
pKbB		1.361	S	0.202	8.35E-08	0.954	2.128		
fbp		1.297	S	0.201	3.68E-07	0.538	2.059		
fbtB		1.157	S	0.209	3.74E-05	0.365	1.949		
gapC		0.811	S	0.219	6.39E-02	-0.017	1.639		
gpmA		1.132	S	0.220	2.19E-04	0.299	1.964		
gpmB		0.725	S	0.232	3.77E-01	-0.187	1.639		
pKbB	pykF	0.178	S	0.230	1.00E+00	-0.689	1.045		
	zwf	1.263	S	0.202	1.10E-06	0.497	2.029		
	pgl	0.794	S	0.232	1.41E-01	-0.391	1.668		
	gnd	0.226	S	0.274	1.00E+00	-0.809	1.261		
	rpe	-0.575	S	0.310	9.90E-01	-1.746	0.597		
	rpiA	-0.473	S	0.286	9.71E-01	-1.416	1.363		
	rpiB	0.899	S	0.223	2.53E-02	0.045	1.733		
	tkiA	1.012	S	0.211	1.08E-03	0.213	1.810		
	tkiB	0.897	S	0.214	2.41E-01	-0.121	1.496		
	talA	1.245	S	0.217	1.16E-02	0.426	2.064		
	talB	0.985	S	0.307	2.47E-01	-0.176	2.145		
	0.1h-1	0.653	S	0.232	4.86E-01	-0.213	1.538		
	0.2h-1	1.272	S	0.262	1.53E-02	0.754	1.790		
	0.4h-1	0.886	S	0.211	1.18E-02	0.088	1.684		
	0.5h-1	0.633	S	0.237	6.34E-01	-0.262	1.528		
	0.7h-1	1.177	S	0.297	1.00E+00	-0.538	1.911		
	galM	1.312	S	0.154	5.26E-11	0.729	1.895		
	gk	-0.278	S	0.284	1.00E+00	-1.350	0.795		
	pgm	-0.717	S	0.275	6.83E-01	-1.755	0.321		
	pgl	-0.901	S	0.308	4.36E-01	-2.074	0.271		
pKbC	pKbA	0.073	S	0.224	1.00E+00	-0.772	0.918		
	pKbB	1.183	S	0.183	2.74E-09	0.568	1.799		
	fbp	1.120	S	0.161	1.73E-08	0.811	1.728		
	fbtB	0.979	S	0.171	1.27E-05	0.332	1.626		
	gapC	0.633	S	0.183	1.29E-01	-0.059	1.325		
	gpmA	0.954	S	0.194	1.70E-04	0.561	1.650		
	gpmB	0.547	S	0.210	6.82E-01	-0.245	1.339		
	pykA	-0.178	S	0.230	1.00E+00	-1.045	0.689		
	pykF	1.095	S	0.162	8.45E-08	0.471	1.699		
	zwf	0.158	S	0.232	1.00E+00	-0.727	1.137		
	pgl	0.616	S	0.198	3.02E-01	-0.132	1.363		
	gnd	0.048	S	0.246	1.00E+00	-0.883	0.980		
	rpe	-0.753	S	0.286	6.84E-01	-1.836	0.330		
	rpiA	0.295	S	0.203	1.00E+00	-0.469	1.060		
	rpiB	0.508	S	0.188	4.91E-02	0.001	1.422		
	tkiA	0.834	S	0.173	9.41E-04	0.178	1.490		
	tkiB	0.507	S	0.177	4.66E-01	-0.158	1.177		
	talA	1.067	S	0.180	4.10E-06	0.367	1.747		
	talB	0.807	S	0.283	4.92E-01	-0.264	1.877		
	0.1h-1	0.485	S	0.198	7.59E-01	-0.501	1.233		
ppsA	0.2h-1	1.094	S	0.167	1.73E-07	0.461	1.727		
	0.4h-1	0.708	S	0.173	1.72E-02	0.054	1.363		
	0.5h-1	-0.042	S	0.246	9.15E-01	-1.016	1.226		
	0.7h-1	-0.001	S	0.240	1.00E+00	-0.910	0.907		
	galM	0.228	S	0.108	9.51E-01	-0.181	0.636		
	gk	-1.362	S	0.263	1.78E-04	-2.356	-0.369		
	pgm	-1.802	S	0.352	7.23E-02	-2.758	-0.846		
	pgl	-1.886	S	0.288	1.12E-07	-3.088	-0.884		
	pKbA	-1.012	S	0.195	2.17E-04	-1.752	-0.271		
	pKbB	0.068	S	0.121	1.00E+00	-0.357	0.553		
	fbp	0.035	S	0.118	1.00E+00	-0.410	0.479		
	fbtB	-0.106	S	0.132	1.00E+00	-0.603	0.392		
	gapC	-0.452	S	0.147	3.27E-01	-1.008	0.104		
	gpmA	-0.131	S	0.149	1.00E+00	-0.693	0.430		
	gpmB	-0.538	S	0.179	3.77E-01	-1.216	0.141		
	pykA	-1.263	S	0.202	1.10E-06	-2.028	-0.497		
	pykF	-1.065	S	0.162	8.45E-08	-0.698	-0.471		
	zwf	-0.929	S	0.206	4.27E-03	-1.713	-0.144		
	pgl	-0.469	S	0.185	4.98E-01	-1.094	0.158		
	gnd	-1.037	S	0.221	1.89E-03	-1.875	-0.198		
zwf	rpe	-1.838	S	0.264	3.43E-08	-2.842	-0.833		
	rpiA	-0.789	S	0.171	2.13E-03	-1.435	-0.144		
	rpiB	-0.373	S	0.153	8.04E-01	-0.953	0.206		
	tkiA	-0.251	S	0.135	9.89E-01	-0.759	0.257		
	tkiB	-0.576	S	0.139	1.40E-02	-1.100	-0.051		
	talA	-0.018	S	0.143	1.00E+00	-0.559	0.523		
	talB	-0.278	S	0.261	1.00E+00	-1.269	0.713		
	0.1h-1	-0.600	S	0.166	8.02E-02	-1.225	0.025		
	0.2h-1	0.009	S	0.127	1.00E+00	-0.469	0.488		
	0.4h-1	-0.377	S	0.136	5.31E-01	-0.994	0.131		
	0.5h-1	-0.630	S	0.173	7.61E-02	-1.283	0.023		
	0.7h-1	-1.086	S	0.214	3.73E-04	-1.899	-0.273		
	galM	1.156	S	0.199	1.81E-05	0.396	1.917		
	gk	-0.434	S	0.311	1.00E+00	-1.608	0.741		
	pgm	-0.873	S	0.303	4.65E-01	-2.016	0.270		
	pgl	-1.057	S	0.333	2.67E-01	-2.322	0.207		
	pKbA	-0.083	S	0.257	1.00E+00	-1.055	0.885		
	pKbB	1.027	S	0.206	6.27E-04	0.242	1.813		
	fbp	0.864	S	0.205	1.99E-03	0.183	1.744		
	fbtB	0.823	S	0.213	4.10E-02	0.133	1.633		
gapC	0.477	S	0.223	3.38E-01	-0.368	1.322			
gpmA	0.788	S	0.224	9.98E-02	-0.051	1.647			
gpmB	0.391	S	0.245	9.99E-01	-0.538	1.319			
pykA	-0.334	S	0.262	1.00E+00	-1.326	0.658			
pykF	-1.156	S	0.233	1.00E+00	-1.039	0.727			
ppsA	0.929	S	0.206	4.27E-03	0.144	1.713			
pgl	-0.468	S	0.235	9.79E-01	-1.431	0.537			
gnd	-1.108	S	0.277	1.00E+00	-1.155	0.940			
rpe	-0.909	S	0.313	4.49E-01	-2.091	0.274			
rpiA	0.138	S	0.236	1.00E+00	-0.765	1.044			
rpiB	0.556	S	0.227	7.95E-01	-0.305	1.416			
tkiA	0.678	S	0.215	2.80E-01	-0.138	1.494			
tkiB	0.353	S	0.218	9.99E-01	-0.473	1.179			
talA	0.911	S	0.222	1.59E-02	0.075	1.747			
talB	0.619	S	0.310	9.52E-01	-0.521	1.822			
0.1h-1	0.329	S	0.236	1.00E+00	-0.562	1.220			
0.2h-1	0.931	S	0.210	4.86E-03	0.139	1.737			
0.4h-1	0.557	S	0.215	7.10E-01	-0.263	1.368			
0.5h-1	-0.299	S	0.245	1.00E+00	-1.051	0.451			
0.7h-1	-1.052	S	0.272	1.00E+00	-1.185	0.078			

Multiple Comparisons										Multiple Comparisons									
Dependent Variable: Metabolite										Dependent Variable: Metabolite									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval				(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound									Lower Bound	Upper Bound		
kIA	galM	0.479	S	0.124	3.84E-02	0.070	0.948			0.1h-1	galM	0.828	S	0.157	1.20E-04	0.233	1.422		
	gik	-1.111	S	0.270	1.53E-02	-2.130	-0.093				gik	-0.763	S	0.286	6.41E-01	-1.842	0.317		
	pgm	-1.591	S	0.260	3.74E-06	-2.533	-0.569				pgm	-1.202	S	0.277	6.52E-03	-2.247	-0.157		
	pgl	-1.735	S	0.294	1.21E-05	-2.859	-0.611				pgl	-1.386	S	0.310	4.75E-03	-2.565	-0.200		
	pkA	-0.761	S	0.204	6.15E-02	-1.533	0.013				pkA	-0.412	S	0.226	9.92E-01	-1.265	0.444		
	pkB	0.350	S	0.135	7.02E-01	-0.160	0.859				pkB	0.686	S	0.166	1.09E-02	0.072	1.325		
	fbp	0.286	S	0.133	9.39E-01	-0.215	0.786				fbp	0.635	S	0.164	3.68E-02	0.015	1.254		
	ftaB	0.146	S	0.145	1.00E+00	-0.402	0.693				ftaB	0.494	S	0.174	5.04E-01	-0.163	1.151		
	gapC	-0.203	S	0.159	1.00E+00	-0.801	0.400				gapC	0.148	S	0.186	1.00E+00	-0.553	0.859		
	gpmA	0.120	S	0.161	1.00E+00	-0.486	0.726				gpmA	0.469	S	0.187	7.63E-01	-0.237	1.175		
	gpmB	-0.286	S	0.189	1.00E+00	-1.001	0.429				gpmB	0.062	S	0.212	1.00E+00	-0.738	0.863		
	pyrA	-1.012	S	0.211	1.08E-03	-1.810	-0.213				pyrA	-0.603	S	0.232	4.89E-01	-1.538	0.213		
	pyrF	-0.834	S	0.173	9.44E-04	-1.489	-0.170				pyrF	-0.485	S	0.197	7.99E-01	-1.233	0.263		
	ppsA	0.251	S	0.135	8.99E-01	-0.257	0.759				ppsA	0.600	S	0.166	8.02E-02	-0.025	1.229		
	zwf	-0.878	S	0.215	2.80E-01	-1.494	0.138				zwf	-0.329	S	0.236	1.00E+00	-1.224	0.563		
	pgl	-0.718	S	0.176	1.00E+00	-0.883	0.447				pgl	0.131	S	0.201	1.00E+00	-0.626	0.887		
	gnd	-0.785	S	0.229	1.44E-01	-1.654	0.083				gnd	-0.437	S	0.249	9.95E-01	-1.378	0.503		
	rpe	-1.586	S	0.271	9.17E-06	-2.615	-0.557				rpe	-1.238	S	0.288	8.11E-03	-2.327	-0.149		
	rpiA	-0.538	S	0.181	3.59E-01	-1.222	0.146				rpiA	-0.189	S	0.205	1.00E+00	-0.963	0.584		
	rpiB	-0.122	S	0.165	1.00E+00	-0.745	0.500				rpiB	0.229	S	0.191	1.00E+00	-0.639	1.071		
	tkiB	-0.324	S	0.152	9.42E-01	-0.896	0.248				tkiA	0.349	S	0.177	9.77E-01	-0.316	1.014		
	talA	0.233	S	0.156	1.00E+00	-0.354	0.820				tkiB	0.024	S	0.180	1.00E+00	-0.653	0.702		
	talB	-0.260	S	0.255	1.00E+00	-1.043	0.889				talA	0.583	S	0.256	2.59E-01	-0.108	1.277		
	0.1h-1	-0.349	S	0.177	9.77E-01	-1.014	0.316				talB	0.322	S	0.289	1.00E+00	-0.756	1.399		
	0.2h-1	0.260	S	0.141	9.90E-01	-0.270	0.791				0.2h-1	0.609	S	0.171	9.29E-02	-0.034	1.251		
	0.4h-1	-0.125	S	0.148	1.00E+00	-0.862	0.431				0.4h-1	0.223	S	0.176	1.00E+00	-0.441	0.888		
	0.5h-1	-0.379	S	0.183	9.59E-01	-1.070	0.313				0.5h-1	0.030	S	0.212	1.00E+00	-0.810	0.755		
	0.7h-1	-0.835	S	0.223	5.64E-02	-1.679	0.008				0.7h-1	-0.486	S	0.243	9.72E-01	-1.403	0.433		
kIB	galM	0.803	S	0.129	9.18E-07	0.316	1.290			0.7h-1	0.218	S	0.116	9.87E-01	-0.219	0.655			
	gik	-0.787	S	0.272	4.56E-01	-1.813	0.239			gik	-1.372	S	0.295	6.84E-01	-2.362	-0.382			
	pgm	-1.226	S	0.262	1.70E-03	-2.216	-0.236			pgm	-1.811	S	0.255	8.89E-09	-2.776	-0.844			
	pgl	-1.411	S	0.296	1.70E-03	-2.542	-0.280			pgl	-1.995	S	0.291	1.21E-07	-3.107	-0.878			
	pkA	-0.436	S	0.207	9.50E-01	-1.221	0.349			pkA	-1.022	S	0.242	2.75E-02	-1.509	-0.535			
	pkB	0.674	S	0.139	8.18E-04	0.148	1.200			pkB	0.089	S	0.127	1.00E+00	-0.391	0.570			
	fbp	0.610	S	0.137	4.22E-03	0.093	1.128			fbp	0.026	S	0.125	1.00E+00	-0.445	0.498			
	ftaB	0.470	S	0.146	2.78E-01	-0.053	1.033			ftaB	-0.115	S	0.138	1.00E+00	-0.638	0.404			
	gapC	0.124	S	0.163	1.00E+00	-0.491	0.738			gapC	0.463	S	0.162	3.62E-01	-0.139	1.065			
	gpmA	0.444	S	0.164	6.09E-01	-0.175	1.064			gpmA	-0.140	S	0.154	1.00E+00	-0.722	0.441			
	gpmB	0.038	S	0.192	1.00E+00	-0.689	0.764			gpmB	-0.547	S	0.194	3.95E-01	-1.242	0.144			
	pyrA	-0.887	S	0.214	2.41E-01	-1.496	0.121			pyrA	-1.272	S	0.217	1.53E-02	-2.054	-0.490			
	pyrF	-0.509	S	0.177	4.68E-01	-1.177	0.158			pyrF	-1.094	S	0.167	1.73E-07	-1.727	-0.461			
	ppsA	0.576	S	0.139	1.40E-02	0.051	1.100			ppsA	-0.009	S	0.127	1.00E+00	-0.488	0.469			
	zwf	-0.353	S	0.218	9.88E-01	-1.176	0.473			zwf	0.910	S	0.232	4.69E-03	-1.137	0.739			
	pgl	0.106	S	0.179	1.00E+00	-0.571	0.784			pgl	-0.478	S	0.170	5.21E-01	-1.122	0.169			
	gnd	-0.461	S	0.232	9.74E-01	-1.339	0.416			gnd	-1.046	S	0.225	2.10E-01	-1.898	-0.194			
	rpe	-1.262	S	0.273	2.44E-03	-2.066	-0.225			rpe	-1.847	S	0.287	3.92E-06	-2.862	-0.833			
	rpiA	-0.214	S	0.184	1.00E+00	-0.910	0.482			rpiA	0.779	S	0.172	9.13E-03	-0.161	1.681			
	rpiB	0.202	S	0.168	1.00E+00	-0.434	0.838			rpiB	-0.382	S	0.159	8.19E-01	-0.981	0.217			
	tkiA	0.024	S	0.152	9.42E-01	-0.248	0.886			tkiA	-0.260	S	0.141	9.90E-01	-0.779	0.270			
	talA	0.558	S	0.158	1.55E-01	-0.044	1.159			talA	-0.586	S	0.245	2.03E-02	-1.086	0.534			
	talB	0.287	S	0.270	1.00E+00	-0.727	1.322			talA	-0.027	S	0.149	1.00E+00	-0.589	0.513			
	0.1h-1	-0.024	S	0.180	1.00E+00	-0.702	0.653			talB	-0.287	S	0.292	2.09E-02	-1.290	0.718			
	0.2h-1	0.585	S	0.165	2.03E-02	0.038	1.131			0.1h-1	0.671	S	0.160	9.29E-02	-0.034	1.251			
	0.4h-1	0.198	S	0.152	1.00E+00	-0.373	0.771			0.4h-1	-0.386	S	0.140	5.75E-01	-0.916	0.144			
	0.5h-1	-0.054	S	0.186	1.00E+00	-0.758	0.649			0.5h-1	-0.639	S	0.177	8.65E-02	-1.309	0.033			
	0.7h-1	-0.511	S	0.215	8.92E-01	-1.327	0.104			0.7h-1	-1.098	S	0.242	4.02E-02	-1.586	-0.610			
talA	galM	0.246	S	0.133	9.91E-01	-0.299	0.750			0.4h-1	0.604	S	0.124	7.05E-04	0.136	1.077			
	gik	-1.345	S	0.274	6.00E-04	-2.378	-0.310			gik	-0.986	S	0.270	7.28E-02	-2.004	-0.034			
	pgm	-1.764	S	0.264	4.88E-06	-2.762	-0.785			pgm	-1.425	S	0.259	4.28E-05	-2.407	-0.444			
	pgl	-1.968	S	0.298	3.57E-07	-3.107	-0.830			pgl	-1.819	S	0.290	5.84E-05	-3.045	-0.593			
	pkA	-0.994	S	0.210	1.43E-03	-1.789	-0.199			pkA	-0.632	S	0.204	3.06E-01	-1.049	0.138			
	pkB	0.116	S	0.144	1.00E+00	-0.428	0.659			pkB	0.475	S	0.135	1.00E+00	-0.434	0.986			
	fbp	0.053	S	0.142	1.00E+00	-0.587	0.691			fbp	0.413	S	0.133	3.84E-01	-0.204	1.039			
	ftaB	-0.088	S	0.153	1.00E+00	-0.666	0.491			ftaB	0.271	S	0.145	9.89E-01	-0.276	0.819			
	gapC	-0.434	S	0.166	6.85E-01	-1.062	0.195			gapC	-0.075	S	0.159	1.00E+00	-0.678	0.528			
	gpmA	-0.113	S	0.197	1.00E+00	-0.713	0.520			gpmA	0.245	S	0.161	1.00E+00	-0.363	0.854			
	gpmB	-0.520	S	0.195	6.43E-01	-1.258	0.218			gpmB	-0.161	S	0.189	1.00E+00	-0.876	0.556			
	pyrA	-1.245	S	0.217	1.18E-05	-2.064	-0.426			pyrA	0.886	S	0.211	1.18E-02	-1.874	-0.088			
	pyrF	-1.067	S	0.180	4.10E-06	-1.747	-0.387			pyrF	-0.708	S	0.173	1.72E-02	-1.363	-0.054			
	ppsA	0.018	S	0.143	1.00E+00	-0.528	0.556			ppsA	0.377	S	0.137	3.31E-01	-0.610	1.164			
	zwf	-0.911	S	0.220	1.59E-02	-1.747	-0.075			zwf	-0.552	S	0.215	7.07E-01	-1.368	0.263			
	pgl	-0.451	S	0.183	7.82E-01	-1.141	0.239			pgl	-0.093	S	0.176	1.00E+00	-0.757	0.574			
	gnd	-1.018	S	0.234	6.83E-03	-1.596	-0.132			gnd	-1.662	S	0.246	4.69E-01	-2.200	-0.925			
	rpe	-1.820	S	0.275	1.67E-07	-2.864	-0.775			rpe	-1.461	S	0.271	8.52E-05	-2.490	-0.430			
	rpiA	-0.771	S	0.188	1.55E-02	-1.480	-0.063			rpiA	-0.413	S	0.181	8.89E-01	-1.096	0.271			
	rpiB	-0.355	S	0.172	9.40E-01	-1.005	0.294			rpiB	-0.006	S	0.160	1.00E+00	-0.616	0.504			
	tkiA	-0.233	S	0.156	1.00E+00	-0.820	0.354			tkiA	0.125	S	0.148	1.00E+00	-0.431	0.682			
	tkiB	-0.558	S	0.159	1.15E-01	-1.159	0.044			tkiB	-0.199	S	0.152	1.00E+00	-0.771	0.373			
	talB	-0.260	S	0.273	1.00E+00	-1.293	0.772			talB	-0.356	S							



**Table S10 D Statistical tests for AEIs (Metabolites, excluding nucleotides)****Test of Homogeneity of Variances**

Metabolite(excluding nucleotides)

Levene Statistic	df1	df2	Sig.
6.737	28	2,758	9.38E-25

**ANOVA**

Metabolite(excluding nucleotides)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	742.188	28	26.507	7.015	4.00E-26
Within Groups	10,420.876	2,758	3.778		
Total	11,163.065	2,786			

**Robust Tests of Equality of Means**

Metabolite(excluding nucleotides)

	Statistic(a)	df1	df2	Sig.
Welch	8.683	28	944.616	1.47E-31

a. Asymptotically F distributed.



Multiple Comparisons											Multiple Comparisons										
Dependent Variable: Metabolite(nucleotides removed)											Dependent Variable: Metabolite(nucleotides removed)										
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval		(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval							
						Lower Bound	Upper Bound							Lower Bound	Upper Bound						
gaM	gk	-1.333	S	0.331	2.43E-02	-2.562	-0.073	pkB	gaM	0.334	S	0.137	1.00E+00	-0.484	0.951						
	pgm	-1.594	S	0.251	1.04E-06	-2.550	-0.636	pkB	gk	-1.268	S	0.339	4.02E-02	-2.586	-0.010						
	pgl	-1.363	S	0.243	1.19E-04	-2.307	-0.419	pkB	pgm	-1.584	S	0.281	5.55E-06	-2.553	-0.603						
	pkA	-1.458	S	0.239	7.41E-08	-2.375	-0.541	pkB	pgl	-1.309	S	0.243	1.34E-04	-2.309	-0.309						
	pkB	-0.104	S	0.137	1.00E+00	-0.553	0.484	pkB	pkA	-1.424	S	0.250	3.36E-05	-2.379	-0.469						
	fbp	-0.155	S	0.125	1.00E+00	-0.520	0.350	pkB	gk	-1.071	S	0.148	1.00E+00	-0.658	0.456						
	ftaB	-0.289	S	0.164	9.94E-01	-0.912	0.333	pkB	pgm	-1.175	S	0.175	1.00E+00	-0.825	0.475						
	gapC	-0.808	S	0.177	1.54E-01	-1.289	0.072	pkB	pgl	-0.549	S	0.192	3.96E-01	-1.306	0.151						
	gpmA	-0.448	S	0.185	8.23E-01	-1.152	0.261	pkB	pkA	-0.412	S	0.200	9.60E-01	-1.168	0.349						
	gpmB	-0.975	S	0.226	1.03E-02	-1.841	-0.098	pkB	pyKA	-0.948	S	0.315	5.52E-01	-1.847	0.243						
	pyKA	-0.408	S	0.155	6.89E-01	-0.994	0.182	pkB	pyKF	-0.372	S	0.171	9.27E-01	-1.019	0.276						
	pyKF	-0.781	S	0.179	8.29E-02	-1.466	-0.096	pkB	ppsA	-0.746	S	0.194	4.23E-02	-1.483	0.017						
	ppsA	-0.183	S	0.134	1.00E+00	-0.673	0.347	pkB	zwf	-0.347	S	0.191	1.00E+00	-1.107	0.413						
	zwf	-0.709	S	0.235	3.85E-01	-1.618	0.201	pkB	gnd	-0.674	S	0.246	5.84E-01	-1.621	-0.277						
	gnd	-0.778	S	0.198	3.68E-02	-1.538	-0.020	pkB	rpe	-0.744	S	0.211	1.15E-01	-1.548	0.066						
	rpe	-0.981	S	0.236	1.70E-02	-1.883	-0.079	pkB	rpiA	-0.947	S	0.247	4.65E-02	-1.887	-0.006						
	rpiA	-2.222	S	0.341	1.17E-08	-3.534	-0.910	pkB	rpiB	-0.947	S	0.252	9.86E-02	-1.843	-0.051						
	rpiB	-0.808	S	0.198	2.15E-02	-1.561	-0.052	pkB	tkA	-0.772	S	0.211	7.63E-02	-1.573	0.029						
	tkA	-0.337	S	0.185	4.60E-01	-1.244	0.170	pkB	tkB	-0.503	S	0.199	7.44E-01	-1.259	0.252						
	tkB	-0.408	S	0.156	6.84E-01	-1.000	0.185	pkB	talA	-0.373	S	0.173	9.33E-01	-1.025	0.274						
	talA	-0.759	S	0.173	7.06E-03	-1.419	-0.098	pkB	talB	-0.725	S	0.188	4.09E-02	-1.438	-0.012						
	talB	-0.325	S	0.101	9.93E-01	-1.012	0.365	pkB	0.1h-1	-0.289	S	0.195	1.00E+00	-1.029	0.445						
	0.1h-1	-0.721	S	0.363	9.71E-01	-2.114	0.671	pkB	0.2h-1	-0.673	S	0.207	9.86E-01	-1.457	0.109						
	0.2h-1	-0.708	S	0.194	7.63E-02	-1.442	0.027	pkB	0.4h-1	-0.214	S	0.142	1.00E+00	-0.322	0.751						
	0.4h-1	0.193	S	0.121	1.00E+00	-0.281	0.641	pkB	0.5h-1	-0.844	S	0.156	2.21E-02	-1.242	-0.030						
	0.5h-1	-0.875	S	0.141	1.30E-03	-1.221	-0.048	pkB	0.7h-1	-0.541	S	0.204	1.00E+00	-1.414	0.322						
	0.7h-1	-0.575	S	0.217	6.53E-01	-1.406	0.256	pkB	0.1h-1	-0.805	S	0.242	1.92E-01	-1.728	0.119						
	gk	gaM	1.333	S	0.331	2.43E-02	0.073	2.562	fbp	gaM	0.139	S	0.126	1.00E+00	-0.350	0.629					
		pgm	-0.261	S	0.369	1.00E+00	-1.768	1.246	fbp	gk	-1.179	S	0.340	1.00E+00	-2.413	0.964					
		pgl	-0.031	S	0.394	1.00E+00	-1.524	1.462	fbp	pgm	-1.459	S	0.257	2.46E-05	-2.435	-0.482					
		pkA	-0.126	S	0.391	1.00E+00	-1.808	1.355	fbp	pgl	-1.228	S	0.249	1.41E-03	-2.192	-0.264					
		pkB	1.288	S	0.338	4.52E-02	0.011	2.566	fbp	pkA	-1.324	S	0.245	1.41E-04	-2.349	-0.301					
		fbp	1.197	S	0.336	1.00E-01	-0.078	2.473	fbp	pkB	0.101	S	0.148	1.00E+00	-0.456	0.655					
ftaB		1.043	S	0.351	3.98E-01	-0.288	2.373	fbp	ftaB	-0.154	S	0.173	1.00E+00	-0.809	0.500						
gapC		1.724	S	0.357	9.97E-01	-0.533	2.978	fbp	gapC	-0.473	S	0.198	7.26E-01	-1.163	0.487						
gpmA		0.887	S	0.362	7.92E-01	-0.482	2.256	fbp	gpmA	-0.807	S	0.370	9.96E-02	-1.640	0.425						
gpmB		0.358	S	0.384	1.00E+00	-1.094	1.810	fbp	gpmB	-0.839	S	0.233	9.35E-02	-1.728	0.055						
pyKA		0.827	S	0.347	6.32E-01	-0.388	2.241	fbp	pyKA	-0.270	S	0.164	9.98E-01	-0.893	0.350						
pyKF		0.552	S	0.358	8.99E-01	-0.808	1.910	fbp	pyKF	-0.645	S	0.184	4.34E-01	-1.286	0.000						
ppsA		1.170	S	0.338	1.33E-01	-0.114	2.454	fbp	ppsA	-0.027	S	0.145	1.00E+00	-0.577	0.522						
zwf		0.624	S	0.389	9.99E-01	-0.850	2.098	fbp	zwf	-0.573	S	0.242	8.34E-01	-1.504	0.357						
gnd		0.658	S	0.368	1.00E+00	-0.838	1.944	fbp	gnd	-0.645	S	0.308	1.00E+00	-1.676	0.723						
rpe		-0.890	S	0.389	1.00E+00	-1.121	1.825	fbp	rpe	-0.845	S	0.242	1.27E-01	-1.769	0.077						
rpiA		0.526	S	0.461	9.82E-01	-2.635	0.856	fbp	rpiA	-0.671	S	0.346	9.12E-05	-3.414	-0.769						
rpiB		0.796	S	0.361	9.19E-01	-0.573	2.164	fbp	rpiB	-0.871	S	0.295	2.18E-01	-1.954	0.202						
tkA		0.925	S	0.347	6.41E-01	-0.392	2.242	fbp	tkA	-0.461	S	0.307	9.55E-01	-1.334	0.137						
tkB		0.574	S	0.355	9.99E-01	-0.773	1.920	fbp	tkB	-0.272	S	0.166	9.98E-01	-0.899	0.354						
talA		1.008	S	0.359	5.24E-01	-0.351	2.369	fbp	tkB	-0.624	S	0.182	1.43E-01	-1.314	0.068						
talB		0.611	S	0.477	1.00E+00	-1.195	2.417	fbp	talA	-0.188	S	0.188	1.00E+00	-0.533	0.500						
0.1h-1		0.625	S	0.369	9.97E-01	-0.759	2.008	fbp	talB	-0.586	S	0.367	9.96E-01	-1.993	0.829						
0.2h-1		1.513	S	0.353	3.59E-03	0.348	2.778	fbp	0.1h-1	-0.573	S	0.201	4.96E-01	-1.335	0.189						
0.4h-1		0.658	S	0.341	9.82E-01	-0.636	1.952	fbp	0.2h-1	-0.313	S	0.139	1.00E+00	-0.261	0.740						
0.5h-1		0.758	S	0.379	9.72E-01	-0.674	2.190	fbp	0.4h-1	-0.539	S	0.152	9.92E-02	-1.113	0.034						
0.7h-1		0.463	S	0.405	1.00E+00	-0.935	1.955	fbp	0.5h-1	-0.439	S	0.224	9.76E-01	-1.294	0.414						
gaM		1.594	S	0.251	1.04E-06	0.638	2.550	fbp	0.7h-1	-0.703	S	0.245	4.07E-01	-1.601	0.194						
gk		0.261	S	0.399	1.00E+00	-1.248	1.768	fbp	gaM	0.268	S	0.164	9.94E-01	-0.333	0.912						
pgl		0.231	S	0.330	1.00E+00	-1.022	1.484	fbp	gk	-1.043	S	0.351	3.98E-01	-2.373	0.285						
pkA		0.136	S	0.326	1.00E+00	-1.101	1.373	fbp	pgm	-1.309	S	0.276	1.57E-03	-2.352	-0.251						
pkB		1.560	S	0.261	5.55E-06	0.967	2.553	fbp	pgl	-1.070	S	0.282	9.14E-02	-2.107	0.740						
fbp		1.459	S	0.257	2.46E-05	0.482	2.435	fbp	pkA	-1.169	S	0.265	6.48E-03	-2.180	-0.158						
ftaB	1.305	S	0.276	1.97E-05	0.352	2.257	fbp	pkB	0.295	S	0.179	1.00E+00	-0.424	0.934							
gapC	0.986	S	0.289	1.31E-01	-0.094	2.065	fbp	ftaB	-0.169	S	0.179	1.00E+00	-0.848	0.510							
gpmA	1.148	S	0.290	2.80E-02	0.051	2.246	fbp	gapC	-0.319	S	0.212	1.00E+00	-1.124	0.488							
gpmB	0.618	S	0.317	9.79E-01	-0.582	1.821	fbp	gpmA	-0.186	S	0.219	1.00E+00	-0.985	0.672							
pyKA	1.188	S	0.271	6.25E-03	0.165	2.215	fbp	gpmB	-0.655	S	0.266	6.15E-02	-1.651	0.289							
pyKF	0.813	S	0.286	4.97E-01	-0.270	1.897	fbp	pyKA	-0.118	S	0.193	1.00E+00	-0.848	0.619							
ppsA	1.431	S	0.260	5.42E-05	0.443	2.419	fbp	pyKF	-0.491	S	0.213	8.76E-01	-1.301	0.319							
zwf	0.885	S	0.324	8.89E-01	-0.344	2.115	fbp	ppsA	0.127	S	0.177	1.00E+00	-0.545	0.798							
gnd	0.816	S	0.298	5.80E-01	-0.312	1.945	fbp	zwf	-0.492	S	0.292	9.95E-01	-1.284	0.296							
rpe	0.613	S	0.324	9.88E-01	-0.614	1.840	fbp	gnd	-0.488	S	0.229	9.41E-01	-1.359	0.383							
rpiA	-0.628	S	0.408	9.99E-01	-2.176	0.915	fbp	rpe	-0.691	S	0.282	6.62E-01	-1.689	0.300							
rpiB	0.788	S	0.298	6.55E-01	-0.340	1.915	fbp	rpiA	-0.918	S	0.319	1.00E+00	-2.041	0.704							
tkA	1.057	S	0.290	7.63E-02	-0.040	2.154	fbp	rpiB	-0.517	S	0.229	8.97E-01	-1.381	0.352							
tkB	1.168	S	0.272	6.72E-03	0.234	2.216	fbp	tkA	-0.247	S	0.218	1.00E+00	-1.076	0.581							
talA	0.835	S	0.282	4.08E-01	-0.234	1.903	fbp	tkB	-0.119	S											

Multiple Comparisons										Multiple Comparisons									
Dependent Variable: Metabolite(nucleotides removed)										Dependent Variable: Metabolite(nucleotides removed)									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval				(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound									Lower Bound	Upper Bound		
gpmB	galM	0.975		0.226	1.03E-02	0.109	1.841			pgl	galM	0.775		0.198	3.68E-02	0.020	1.536		
	gk	-0.358		0.156	1.00E+00	-1.810	1.094				gpmA	-0.589		0.368	1.00E+00	-1.948	0.838		
	pgm	-0.619		0.317	9.79E-01	-1.821	0.582				gpmB	-0.819		0.368	5.80E-01	-1.948	0.310		
	pgl	-0.389		0.311	1.00E+00	-1.576	0.798				pKbA	-0.291		0.291	9.68E-01	-1.770	0.528		
	pKbA	-0.483		0.308	9.99E-01	-1.652	0.686				pKbB	-0.680		0.288	8.42E-01	-1.775	0.414		
	pKbB	-0.341	S	0.238	3.17E-02	-0.534	0.847				fbp	0.744		0.211	1.15E-01	-0.061	1.548		
	fbp	0.839		0.233	9.35E-02	-0.050	1.728				flaB	0.642		0.203	3.00E-01	-0.142	1.427		
	flaB	0.885		0.254	6.13E-01	-0.280	1.651				flaB	0.488		0.229	9.41E-01	-0.383	1.359		
	gapC	0.368		0.263	1.00E+00	-0.634	1.367				gapC	0.169		0.239	1.00E+00	-0.741	1.080		
	gpmA	0.529		0.269	9.77E-01	-0.491	1.549				gpmB	0.243		0.243	1.00E+00	-0.752	1.238		
	pykA	0.569		0.248	8.80E-01	-0.376	1.514				gpmB	-0.197		0.277	1.00E+00	-1.250	0.856		
	pykF	0.194		0.264	1.00E+00	-0.811	1.199				pykA	0.372		0.223	9.98E-01	-0.476	1.220		
	pykF	0.812		0.236	1.46E-01	-0.089	1.713				pykF	0.056		0.241	1.00E+00	-1.063	0.813		
	zwf	0.266		0.305	1.00E+00	-0.895	1.428				ppaA	0.615		0.209	4.28E-01	-0.183	1.413		
	pgl	0.197		0.277	1.00E+00	-0.858	1.250				zwf	0.060		0.285	1.00E+00	-1.017	1.156		
	gnd	-0.008		0.305	1.00E+00	-1.160	1.152				gnd	0.210		0.210	1.00E+00	-0.293	0.713		
	rpe	-1.248		0.393	2.68E-01	-2.743	0.247				rpe	-1.446	S	0.377	4.75E-02	-2.683	-0.006		
	rpIA	0.168		0.277	1.00E+00	-0.884	1.220				rpIA	0.029		0.255	1.00E+00	-0.998	0.903		
	rpIB	0.438		0.288	9.98E-01	-0.362	1.457				rpIB	-0.224		0.245	1.00E+00	-0.898	0.172		
	ktA	0.567		0.249	8.88E-01	-0.381	1.515				ktA	0.378		0.224	9.98E-01	-0.121	1.222		
	ktB	0.216		0.280	1.00E+00	-0.773	1.204				ktB	0.019		0.238	1.00E+00	-0.878	0.916		
	talA	0.551		0.265	7.90E-01	-0.350	1.659				talA	0.454		0.242	8.87E-01	-0.464	1.372		
	talB	0.253		0.412	1.00E+00	-1.312	1.819				talB	0.056		0.305	1.00E+00	-1.456	1.568		
	0.1h-1	0.267		0.274	1.00E+00	-0.773	1.306				0.1h-1	0.070		0.251	1.00E+00	-0.883	1.022		
	0.2h-1	1.155	S	0.229	5.88E-04	0.279	2.031				0.2h-1	0.986	S	0.201	1.83E-03	0.188	1.728		
	0.4h-1	0.303		0.242	1.00E+00	-0.616	1.216				0.4h-1	1.033	S	0.210	1.00E+00	-0.918	1.956		
	0.5h-1	0.400		0.291	1.00E+00	-0.706	1.506				0.5h-1	0.202		0.270	1.00E+00	-0.822	1.228		
	0.7h-1	0.135		0.301	1.00E+00	-1.009	1.280				0.7h-1	-0.063		0.281	1.00E+00	-1.128	1.006		
pykA	galM	0.406		0.155	6.69E-01	-0.182	0.994			gnd	galM	0.598		0.236	1.70E-02	0.079	1.863		
	gk	-0.927		0.347	6.32E-01	-2.241	0.388				gpmA	-0.389		0.368	1.00E+00	-1.948	0.181		
	pgm	-1.188	S	0.271	6.25E-03	-2.216	-0.160				pgm	-0.913		0.324	9.88E-01	-1.840	0.014		
	pgl	-0.958		0.264	9.27E-02	-1.972	0.057				pgl	-0.383		0.318	1.00E+00	-1.595	0.803		
	pKbA	-1.052	S	0.282	2.34E-02	-2.044	-0.061				pKbA	-1.077	S	0.317	2.04E-02	-2.477	-0.677		
	pKbB	0.372		0.171	9.29E-01	-0.276	1.019				pKbB	0.247		0.247	4.65E-02	0.006	1.887		
	fbp	0.270		0.164	9.98E-01	-0.352	0.893				fbp	0.845		0.242	1.27E-01	0.079	1.769		
	flaB	0.116		0.183	1.00E+00	-0.815	0.846				flaB	0.361		0.262	1.00E+00	-0.708	0.686		
	gapC	-0.203		0.205	1.00E+00	-0.982	0.577				gapC	0.372		0.271	1.00E+00	-0.659	1.404		
	gpmA	-0.040		0.212	1.00E+00	-0.844	0.764				gpmA	0.039		0.277	9.81E-01	-0.515	1.585		
	gpmB	-0.559		0.206	8.80E-01	-1.514	0.370				gpmB	0.558		0.305	1.00E+00	-1.152	1.169		
	pykF	-0.375		0.206	9.92E-01	-1.159	0.405				pykF	0.903		0.206	9.03E-01	-0.501	2.308		
	ppaA	0.243		0.169	1.00E+00	-0.398	0.884				ppaA	0.200		0.272	1.00E+00	-0.835	1.236		
	zwf	-0.303		0.257	1.00E+00	-1.286	0.680				zwf	0.812		0.245	1.88E-01	-0.118	1.754		
	pgl	-0.372		0.222	9.98E-01	-0.810	0.476				pgl	0.212		0.212	1.00E+00	-0.987	0.800		
	gnd	-0.575		0.257	9.03E-01	-1.553	0.403				gnd	0.285		0.285	1.00E+00	-0.980	1.268		
	rpe	-1.817	S	0.356	4.74E-04	-3.181	-0.453				rpe	-1.243		0.398	3.04E-01	-2.756	0.273		
	rpIA	-1.401		0.223	9.93E-01	-2.346	0.445				rpIA	0.174		0.216	1.00E+00	-0.987	0.568		
	rpIB	-0.131		0.212	1.00E+00	-0.934	0.672				rpIB	0.474		0.276	9.99E-01	-0.606	1.944		
	ktA	-0.002		0.187	1.00E+00	-0.709	0.705				ktA	0.553		0.258	9.09E-01	-0.408	1.554		
	ktB	-0.353		0.291	9.95E-01	-1.116	0.410				ktB	0.222		0.262	1.00E+00	-0.798	0.798		
	talA	0.082		0.208	1.00E+00	-0.705	0.870				talA	0.056		0.273	8.21E-01	-0.581	1.696		
	talB	-0.316		0.377	1.00E+00	-1.757	1.126				talB	0.259		0.417	1.00E+00	-1.325	1.844		
	0.1h-1	-0.302		0.219	1.00E+00	-1.130	0.526				0.1h-1	0.273		0.282	1.00E+00	-0.796	1.342		
	0.2h-1	0.586		0.266	7.01E-02	-0.018	1.216				0.2h-1	1.231	S	0.211	1.00E+00	-0.923	2.073		
	0.4h-1	-0.269		0.175	9.99E-01	-0.931	0.393				0.4h-1	0.036		0.249	1.00E+00	-0.644	1.256		
	0.5h-1	-0.169		0.240	1.00E+00	-1.082	0.744				0.5h-1	0.400		0.299	1.00E+00	-0.727	1.333		
	0.7h-1	-0.432		0.173	9.99E-01	-1.035	0.528				0.7h-1	-0.105		0.308	1.00E+00	-1.143	0.733		
pykF	galM	0.781	S	0.179	8.28E-03	0.096	1.466			ppeA	galM	2.422	S	0.341	1.17E-06	0.910	3.534		
	gk	-0.552		0.358	9.99E-01	-1.910	0.806				gk	0.890		0.461	9.82E-01	-0.856	2.635		
	pgm	-0.813		0.286	4.97E-01	-1.897	0.270				pgm	0.628		0.409	9.99E-01	-0.408	1.986		
	pgl	-0.953		0.279	9.50E-01	-1.652	0.486				pgl	0.896		0.303	4.03E-01	-0.675	2.303		
	pKbA	-0.678		0.279	7.84E-01	-1.725	0.370				pKbA	0.764		0.400	9.84E-01	-0.788	2.288		
	pKbB	0.748	S	0.194	4.23E-02	0.010	1.483				pKbB	2.188	S	0.349	2.89E-06	0.850	3.527		
	fbp	0.645		0.188	1.43E-01	-0.359	1.399				fbp	2.061	S	0.287	8.13E-02	0.414	3.706		
	flaB	0.491		0.213	8.76E-01	-0.316	1.301				flaB	1.933	S	0.360	1.46E-04	0.555	3.311		
	gapC	0.172		0.224	1.00E+00	-0.880	1.025				gapC	1.817	S	0.367	1.07E-03	0.212	3.016		
	gpmA	0.355		0.241	1.00E+00	-0.610	1.311				gpmA	1.777	S	0.377	1.48E-03	0.383	3.162		
	gpmB	-0.194		0.264	1.00E+00	-1.199	0.811				gpmB	1.248	S	0.363	2.68E-01	-0.247	2.743		
	pykA	0.375		0.206	9.92E-01	-0.409	1.159				pykA	1.817	S	0.356	4.74E-04	0.453	3.181		
	ppaA	0.818		0.192	2.43E-01	-0.112	1.348				ppaA	1.463	S	0.317	3.64E-02	0.267	2.639		
	zwf	0.072		0.272	1.00E+00	-0.958	1.112				zwf	2.054	S	0.348	1.50E-05	0.725	3.395		
	pgl	0.003		0.241	1.00E+00	-0.912	0.918				pgl	1.416		0.398	5.08E-02	-0.002	3.030		
	gnd	-0.200		0.272	1.00E+00	-1.238	0.835				gnd	1.445		0					

Multiple Comparisons									
Dependent Variable: Metabolite(nucleotides removed)									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound		
r5A	galM	0.408		0.156	8.84E-01	-0.185	1.000		
	gik	-0.325		0.347	6.41E-01	-2.242	0.392		
	pgm	-1.196	S	0.272	6.72E-02	-2.216	-0.155		
	pgl	-0.956		0.265	9.75E-02	-1.973	0.062		
	pK8A	-1.150	S	0.261	2.50E-02	-2.045	-0.056		
	pK8B	0.373		0.173	8.33E-01	-0.276	1.025		
	fbp	0.272		0.166	9.98E-01	-0.354	0.899		
	flaB8	0.118		0.194	1.00E+00	-0.617	0.854		
	gspC	-0.201		0.205	1.00E+00	-0.984	0.583		
	gpmA	-0.038		0.213	1.00E+00	-0.845	0.769		
	gpmB	-0.567		0.249	8.88E-01	-1.515	0.381		
	pykA	0.002		0.189	1.00E+00	-0.705	0.709		
	pykF	-0.373		0.208	9.93E-01	-1.161	0.415		
	ppsA	0.245		0.170	1.00E+00	-0.400	0.890		
	zwf	-0.301		0.259	1.00E+00	-1.287	0.686		
	pgl	-0.370		0.224	9.98E-01	-1.222	0.481		
	gnd	-0.573		0.258	9.09E-01	-1.554	0.408		
	rpe	-1.815	S	0.357	5.00E-04	-3.181	-0.448		
	rpiA	-0.358		0.224	9.94E-01	-1.248	0.450		
	rpiB	-0.125		0.213	1.00E+00	-0.936	0.678		
r5B	galM	-0.351		0.202	9.99E-01	-1.118	0.415		
	gik	0.044		0.209	1.00E+00	-0.707	0.876		
	pgm	-0.314		0.373	1.00E+00	-1.755	1.130		
	pgl	-0.300		0.220	1.00E+00	-1.132	0.532		
	0.2h-1	0.588		0.160	7.33E-02	-0.020	1.196		
	0.4h-1	-0.267		0.175	1.00E+00	-0.833	0.399		
	0.5h-1	-0.167		0.241	1.00E+00	-1.084	0.750		
	0.7h-1	-0.432		0.253	9.97E-01	-1.398	0.533		
	galM	0.758	S	0.206	7.00E-03	0.346	1.414		
	gik	-0.574		0.355	9.99E-01	-1.920	0.773		
	pgm	-0.635		0.282	4.08E-01	-1.903	0.234		
	pgl	-0.604		0.275	9.16E-01	-1.858	0.450		
	pK8A	-0.698		0.271	7.04E-01	-1.732	0.334		
	pK8B	0.725	S	0.188	4.09E-02	0.012	1.438		
	fbp	0.624		0.182	1.43E-01	-0.068	1.314		
	flaB8	-0.470		0.268	8.97E-01	-1.470	0.256		
	gspC	0.151		0.219	1.00E+00	-0.683	0.984		
	gpmA	0.313		0.226	1.00E+00	-0.542	1.169		
	gpmB	-0.216		0.202	1.00E+00	-1.204	0.773		
	pykA	0.353		0.201	9.95E-01	-0.410	1.116		
r5A	pykF	-0.022		0.221	1.00E+00	-0.859	0.816		
	ppsA	0.186		0.186	2.49E-01	-0.110	1.303		
	zwf	0.058		0.268	1.00E+00	-0.974	0.075		
	pgl	-0.019		0.236	1.00E+00	-0.916	0.878		
	gnd	-0.222		0.268	1.00E+00	-1.242	0.798		
	rpe	-1.463	S	0.365	2.72E-02	-2.487	-0.070		
	rpiA	-0.047		0.236	1.00E+00	-0.942	0.848		
	rpiB	0.222		0.225	1.00E+00	-0.833	1.078		
	r5A	0.351		0.352	9.99E-01	-0.945	1.116		
	galM	0.436		0.222	9.77E-01	-0.405	1.277		
	gik	0.038		0.385	1.00E+00	-1.432	1.507		
	0.1h-1	0.051		0.232	1.00E+00	-0.828	0.930		
	0.2h-1	0.638	S	0.157	1.50E-04	0.324	1.011		
	0.4h-1	0.084		0.191	1.00E+00	-0.641	0.810		
	0.5h-1	0.184		0.252	1.00E+00	-0.774	1.143		
	0.7h-1	-0.064		0.244	1.00E+00	-1.064	0.924		
	galM	0.323		0.181	9.93E-01	-0.365	1.012		
	gik	-1.009		0.359	5.24E-01	-2.369	0.351		
	pgm	-1.271	S	0.287	4.99E-03	-2.357	-0.185		
	pgl	-1.044		0.282	7.01E-02	-2.112	0.032		
r5B	pK8A	-1.135	S	0.276	1.83E-02	-2.135	-0.084		
	pK8B	0.289		0.195	1.00E+00	-0.451	1.028		
	fbp	0.188		0.168	1.00E+00	-0.356	0.956		
	flaB8	0.034		0.215	1.00E+00	-0.779	0.847		
	gspC	-0.285		0.225	1.00E+00	-1.141	0.571		
	gpmA	-0.122		0.228	1.00E+00	-1.204	0.756		
	gpmB	-0.551		0.265	7.90E-01	-1.859	0.356		
	pykA	-0.082		0.208	1.00E+00	-0.870	0.705		
	pykF	-0.457		0.227	9.95E-01	-1.317	0.403		
	ppsA	0.161		0.193	1.00E+00	-0.573	0.894		
	zwf	-0.385		0.273	1.00E+00	-1.428	0.658		
	pgl	-0.454		0.242	9.97E-01	-1.372	0.464		
	gnd	-0.657		0.273	8.21E-01	-1.694	0.381		
	rpe	-1.899	S	0.369	3.34E-04	-3.306	-0.492		
	rpiA	-0.483		0.242	9.72E-01	-1.398	0.433		
	rpiB	-0.213		0.231	1.00E+00	-1.091	0.684		
	r5A	-0.084		0.209	1.00E+00	-0.879	0.707		
	galM	-0.436		0.222	9.77E-01	-1.277	0.405		
	gik	-0.398		0.389	1.00E+00	-1.880	1.084		
	0.1h-1	-0.385		0.238	9.99E-01	-1.395	0.516		
r5B	0.2h-1	0.504		0.184	5.87E-01	-0.198	1.205		
	0.4h-1	-0.351		0.198	9.94E-01	-1.103	0.400		
	0.5h-1	-0.251		0.258	1.00E+00	-1.228	0.727		
	0.7h-1	-0.516		0.268	9.83E-01	-1.539	0.507		
	galM	0.721		0.363	9.71E-01	-0.671	2.114		
	gik	-0.611		0.477	1.00E+00	-2.417	1.135		
	pgm	-0.872		0.425	9.62E-01	-2.488	0.743		
	pgl	-0.642		0.421	9.99E-01	-2.245	0.961		
	pK8A	-0.737		0.419	9.95E-01	-2.328	0.855		
	pK8B	0.867		0.370	9.88E-01	-0.730	2.105		
	fbp	0.586		0.367	9.99E-01	-0.820	1.993		
	flaB8	0.432		0.381	1.00E+00	-1.023	1.887		
	gspC	0.113		0.387	1.00E+00	-1.364	1.593		
	gpmA	0.276		0.391	1.00E+00	-1.214	1.766		
	gpmB	-0.253		0.412	1.00E+00	-1.819	1.312		
	pykA	0.316		0.377	1.00E+00	-1.128	1.757		
	pykF	-0.058		0.388	1.00E+00	-1.838	1.421		
	ppsA	0.559		0.369	9.99E-01	-0.855	1.973		
	zwf	0.013		0.417	1.00E+00	-1.573	1.598		
	pgl	-0.058		0.397	1.00E+00	-1.568	1.456		
r5B	gnd	-0.299		0.417	1.00E+00	-1.844	1.325		
	rpe	-1.501		0.485	3.14E-01	-3.338	0.337		
	rpiA	-0.065		0.397	1.00E+00	-1.599	1.427		
	rpiB	0.185		0.391	1.00E+00	-1.305	1.674		
	r5A	0.314		0.378	1.00E+00	-1.130	1.758		
	galM	-0.038		0.389	1.00E+00	-1.507	1.432		
	gik	0.398		0.388	1.00E+00	-1.084	1.880		
	0.1h-1	0.014		0.396	1.00E+00	-1.400	1.517		
	0.2h-1	0.802		0.365	7.75E-01	-0.497	2.300		
	0.4h-1	0.047		0.372	1.00E+00	-1.378	1.470		
	0.5h-1	0.147		0.407	1.00E+00	-1.401	1.694		
	0.7h-1	-0.118		0.414	1.00E+00	-1.892	1.457		

\*, S\* The mean difference is significant at the .05 level.

Multiple Comparisons									
Dependent Variable: Metabolite(nucleotides removed)									
(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval			
						Lower Bound	Upper Bound		
0.1h-1	galM	0.708		0.194	7.83E-02	-0.027	1.442		
	gik	-0.625		0.356	9.97E-01	-2.008	0.758		
	pgm	-0.886		0.295	3.76E-01	-2.002	0.229		
	pgl	-0.655		0.288	8.87E-01	-1.757	0.448		
	pK8A	-0.750		0.285	6.61E-01	-1.831	0.331		
	pK8B	0.874	S	0.207	2.19E-01	-0.109	1.451		
	fbp	0.573		0.201	4.96E-01	-0.189	1.335		
	flaB8	0.418		0.225	9.89E-01	-0.434	1.271		
	gspC	0.099		0.236	1.00E+00	-0.794	0.992		
	gpmA	0.262		0.242	1.00E+00	-0.652	1.177		
	gpmB	-0.267		0.274	1.00E+00	-1.308	0.773		
	pykA	-0.302		0.302	1.00E+00	-0.928	1.138		
	pykF	-0.073		0.237	1.00E+00	-0.970	0.825		
	ppsA	0.545		0.209	6.44E-01	-0.232	1.322		
	zwf	-0.001		0.282	1.00E+00	-1.074	1.072		
	pgl	-0.070		0.251	1.00E+00	-1.022	0.883		
	gnd	-0.273		0.282	1.00E+00	-1.342	0.796		
	rpe	-1.515	S	0.375	2.40E-02	-2.944	-0.085		
	rpiA	-0.098		0.251	1.00E+00	-1.048	0.853		
	rpiB	0.171		0.242	1.00E+00	-0.743	1.085		

**Table S10 E Statistical tests for AEIs (mRNAs, DNA microarray)****Test of Homogeneity of Variances**

mRNA(DNA array)

Levene Statistic	df1	df2	Sig.
355.083	7	32,342	0.00E+00

**ANOVA**

mRNA(DNA array)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	15,567	7	2,223.787	282.918	0.00E+00
Within Groups	254,214	32,342	7.860		
Total	269,780	32,349			

**Robust Tests of Equality of Means**

mRNA(DNA array)

	Statistic(a)	df1	df2	Sig.
Welch	246.321	7	13,616.001	0.00E+00

a. Asymptotically F distributed.

## Multiple Comparisons

Dependent Variable: mRNA(DNA array)

(I)	(J)	Mean Difference (I-J)	*	Std. Error	Sig.	95% Confidence Interval	
						Lower Bound	Upper Bound
pgm	pgi	-0.321	S	0.050	4.53E-09	-0.472	-0.169
	gapC	-0.202	S	0.044	1.23E-04	-0.336	-0.069
	zwf	0.212	S	0.032	1.71E-09	0.114	0.311
	rpe	-0.940	S	0.063	0.00E+00	-1.131	-0.748
	0.2h-1	-0.143	S	0.037	3.26E-03	-0.256	-0.030
	0.5h-1	-1.120	S	0.061	3.20E-13	-1.305	-0.935
pgi	0.7h-1	-2.012	S	0.074	1.84E-12	-2.235	-1.789
	pgm	0.321	S	0.050	4.53E-09	0.169	0.472
	gapC	0.118		0.054	3.68E-01	-0.047	0.283
	zwf	0.533	S	0.045	0.00E+00	0.395	0.671
	rpe	-0.619	S	0.071	1.49E-12	-0.833	-0.405
	0.2h-1	0.178	S	0.049	6.94E-03	0.029	0.326
gapC	0.5h-1	-0.799	S	0.069	5.09E-13	-1.008	-0.591
	0.7h-1	-1.691	S	0.080	1.95E-12	-1.935	-1.448
	pgm	0.202	S	0.044	1.23E-04	0.069	0.336
	pgi	-0.118		0.054	3.68E-01	-0.283	0.047
	zwf	0.415	S	0.039	4.45E-13	0.297	0.532
	rpe	-0.737	S	0.067	1.89E-12	-0.939	-0.536
zwf	0.2h-1	0.060		0.043	8.62E-01	-0.070	0.190
	0.5h-1	-0.918	S	0.064	1.92E-12	-1.113	-0.722
	0.7h-1	-1.810	S	0.077	0.00E+00	-2.042	-1.577
	pgm	-0.212	S	0.032	1.71E-09	-0.311	-0.114
	pgi	-0.533	S	0.045	0.00E+00	-0.671	-0.395
	gapC	-0.415	S	0.039	4.45E-13	-0.532	-0.297
rpe	rpe	-1.152	S	0.059	1.13E-12	-1.333	-0.972
	0.2h-1	-0.355	S	0.031	0.00E+00	-0.448	-0.262
	0.5h-1	-1.332	S	0.057	3.68E-13	-1.506	-1.159
	0.7h-1	-2.224	S	0.071	7.32E-13	-2.438	-2.010
	pgm	0.940	S	0.063	0.00E+00	0.748	1.131
	pgi	0.619	S	0.071	1.49E-12	0.405	0.833
0.2h-1	gapC	0.737	S	0.067	1.89E-12	0.536	0.939
	zwf	1.152	S	0.059	1.13E-12	0.972	1.333
	0.2h-1	0.797	S	0.062	6.06E-13	0.608	0.986
	0.5h-1	-0.180		0.079	2.99E-01	-0.419	0.058
	0.7h-1	-1.072	S	0.089	0.00E+00	-1.342	-0.803
	pgm	0.143	S	0.037	3.26E-03	0.030	0.256
0.5h-1	pgi	-0.178	S	0.049	6.94E-03	-0.326	-0.029
	gapC	-0.060		0.043	8.62E-01	-0.190	0.070
	zwf	0.355	S	0.031	0.00E+00	0.262	0.448
	rpe	-0.797	S	0.062	6.06E-13	-0.986	-0.608
	0.5h-1	-0.977	S	0.060	1.77E-12	-1.159	-0.795
	0.7h-1	-1.869	S	0.073	0.00E+00	-2.090	-1.648
0.7h-1	pgm	1.120	S	0.061	3.20E-13	0.935	1.305
	pgi	0.799	S	0.069	5.09E-13	0.591	1.008
	gapC	0.918	S	0.064	1.92E-12	0.722	1.113
	zwf	1.332	S	0.057	3.68E-13	1.159	1.506
	rpe	0.180		0.079	2.99E-01	-0.058	0.419
	0.2h-1	0.977	S	0.060	1.77E-12	0.795	1.159
0.7h-1	0.7h-1	-0.892	S	0.087	2.31E-12	-1.157	-0.627
	pgm	2.012	S	0.074	1.84E-12	1.789	2.235
	pgi	1.691	S	0.080	1.95E-12	1.448	1.935
	gapC	1.810	S	0.077	0.00E+00	1.577	2.042
	zwf	2.224	S	0.071	7.32E-13	2.010	2.438
	rpe	1.072	S	0.089	0.00E+00	0.803	1.342
0.7h-1	0.2h-1	1.869	S	0.073	0.00E+00	1.648	2.090
	0.5h-1	0.892	S	0.087	2.31E-12	0.627	1.157

\*. "S" The mean difference is significant at the .05 level.

**Table S10 F Statistical tests for AEIs (Proteins, 2D-DIGE)****Test of Homogeneity of Variances**

Protein(2D-DIGE)

Levene Statistic	df1	df2	Sig.
59.674	28	33,539	0.00E+00

**ANOVA**

Protein(2D-DIGE)

	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	10,302	28	367.921	76.419	0.00E+00
Within Groups	161,475	33,539	4.815		
Total	171,777	33,567			

**Robust Tests of Equality of Means**

Protein(2D-DIGE)

	Statistic(a)	df1	df2	Sig.
Welch	60.866	28	11,822.861	0.00E+00

a. Asymptotically F distributed.

Multiple Comparisons										Multiple Comparisons									
Dependent Variable: Protein(2D-DIGE)										Dependent Variable: Protein(2D-DIGE)									
(I)	(J)	Mean Difference	Std. Error	Sig.	95% Confidence Interval		(I)	(J)	Mean Difference	Std. Error	Sig.	95% Confidence Interval							
					Bound	Bound						Bound	Bound						
gpmM	gk	0.008	0.047	1.00E+00	-0.170	0.183	pKb	gM	-0.047	0.048	1.00E+00	-0.240	0.145						
	pgm	-0.723S	0.061	5.01E-11	-0.951	-0.495		pgm	-0.765S	0.061	1.00E+00	-1.023	-0.512						
	pgj	-1.448S	0.076	5.02E-11	-1.733	-1.163		pgm	-0.058	0.048	5.05E-11	-0.175	0.059						
	pKa	-0.767S	0.068	4.98E-11	-1.026	-0.508		pgj	-1.509S	0.076	5.03E-11	-1.795	-1.224						
	pKb	0.062	0.048	1.00E+00	-0.117	0.240		pKa	-0.826S	0.069	5.00E-11	-1.088	-0.570						
	fbp	-0.458	0.172	6.35E-01	-1.103	0.184		fbp	-0.521S	0.172	3.51E-01	-1.165	0.123						
	fbab	-0.264S	0.050	6.50E-05	-0.452	-0.076		fbab	-0.328S	0.051	5.46E-08	-0.514	-0.137						
	gapC	-0.038	0.048	1.00E+00	-0.215	0.143		gapC	-0.067	0.047	9.71E-01	-0.261	0.186						
	gpmA	-0.128	0.060	9.57E-01	-0.351	0.099		gpmA	-0.188	0.060	2.92E-01	-0.413	0.037						
	gpmB	-0.265S	0.050	4.15E-05	-0.450	-0.079		gpmB	-0.312S	0.050	2.87E-08	-0.512	-0.140						
	pykA	-0.108	0.048	9.10E-01	-0.289	0.072		pykA	-0.175	0.048	1.05E-01	-0.345	0.011						
	pykF	-0.250S	0.060	1.05E-02	-0.475	-0.025		pykF	-0.326S	0.060	9.90E-05	-0.538	-0.087						
	ppsA	-0.128	0.056	9.48E-01	-0.331	0.091		ppsA	-0.182	0.057	2.31E-01	-0.394	0.030						
	zwf	-0.247S	0.048	9.59E-05	-0.426	-0.069		zwf	-0.309S	0.048	1.00E-06	-0.469	-0.149						
	pgl	-1.345S	0.113	5.04E-11	-1.766	-0.923		pgl	-1.407S	0.113	5.00E-11	-1.828	-1.009						
	gnd	-0.131	0.064	9.68E-01	-0.370	0.109		gnd	-0.193	0.064	3.72E-01	-0.433	0.047						
	rpe	-1.471S	0.090	5.03E-11	-1.809	-1.133		rpe	-1.553S	0.090	5.03E-11	-1.871	-1.195						
	rpiA	-0.288	0.064	5.44E-01	-0.675	0.099		rpiA	-0.352	0.064	1.53E-01	-0.611	0.191						
	rpiB	-0.098	0.048	9.81E-01	-0.278	0.087		rpiB	-0.157	0.049	2.32E-01	-0.341	0.026						
	tkA	-0.068	0.050	1.00E+00	-0.254	0.122		tkA	-0.128	0.051	7.41E-01	-0.317	0.061						
	tkB	-0.069	0.051	1.00E+00	-0.259	0.121		tkB	-0.131	0.051	7.24E-01	-0.322	0.040						
	talA	0.047	0.046	1.00E+00	-0.123	0.217		talA	-0.015	0.046	1.00E+00	-0.186	0.156						
	talB	-0.468S	0.055	5.02E-11	-0.672	-0.260		talB	-0.528S	0.055	4.98E-11	-0.735	-0.321						
	0.1h-1	-0.338S	0.051	2.84E-08	-0.526	-0.145		0.1h-1	-0.349	0.052	2.99E-11	-0.591	-0.206						
	0.2h-1	-0.311S	0.054	4.68E-06	-0.514	-0.108		0.2h-1	-0.378	0.055	4.08E-09	-0.576	-0.165						
	0.4h-1	-0.385S	0.053	3.81E-10	-0.584	-0.185		0.4h-1	-0.447S	0.054	5.01E-11	-0.647	-0.246						
	0.5h-1	-1.092S	0.055	5.02E-11	-1.423	-0.761		0.5h-1	-1.153S	0.059	5.04E-11	-1.485	-0.822						
	0.7h-1	-2.284S	0.113	5.04E-11	-2.707	-1.860		0.7h-1	-2.701S	0.113	5.03E-11	-3.211	-2.249						
	gk	galM	-0.008	0.047	1.00E+00	-0.183	0.170	fbp	galM	0.045	0.047	1.00E+00	-0.184	0.101					
		pgm	-0.728S	0.061	5.04E-11	-0.989	-0.502		pgm	-0.768S	0.062	6.08E-01	-1.108	-0.308					
		pgj	-1.454S	0.076	5.02E-11	-1.738	-1.169		pgj	-1.509S	0.076	5.02E-11	-1.795	-1.122					
		pKa	-0.773S	0.069	5.02E-11	-1.031	-0.515		pKj	-0.885S	0.072	2.57E-05	-1.069	-0.500					
pKb		0.058	0.047	1.00E+00	-0.122	0.233		pKa	-0.308	0.078	9.97E-01	-0.978	-0.362						
fbp		-0.465	0.172	6.06E-01	-1.098	0.178		pKb	-0.521	0.172	3.51E-01	-1.123	0.165						
fbab		-0.270S	0.050	2.86E-05	-0.457	-0.083		fbab	-0.170	0.049	2.92E-01	-0.342	0.037						
gapC		-0.042	0.048	1.00E+00	-0.220	0.136		gapC	-0.034	0.048	1.79E-01	-0.220	0.167						
gpmA		-0.132	0.060	9.24E-01	-0.356	0.092		gpmA	-0.223	0.062	1.76E-08	-0.325	0.091						
gpmB		-0.271S	0.048	1.77E-05	-0.455	-0.086		gpmB	-0.319	0.048	1.99E-08	-0.490	-0.148						
pykA		-0.114	0.048	8.42E-01	-0.294	0.065		pykA	-0.201	0.051	1.76E-09	-0.293	0.095						
pykF		-0.256S	0.060	6.52E-03	-0.481	-0.032		pykF	-0.357S	0.060	1.00E+00	-0.448	-0.067						
ppsA		-0.128	0.056	9.08E-01	-0.336	0.084		ppsA	-0.178	0.056	9.30E-01	-0.385	0.041						
zwf		-0.254S	0.048	4.06E-05	-0.431	-0.076		zwf	-0.372	0.048	1.00E+00	-0.432	0.055						
pgl		-1.351S	0.113	5.04E-11	-1.772	-0.930		pgl	-1.888S	0.113	5.00E+00	-2.363	-1.413						
gnd		-0.137	0.064	9.43E-01	-0.376	0.102		gnd	-0.238	0.062	1.77E-01	-0.411	0.111						
rpe		-1.477S	0.090	5.05E-11	-1.814	-1.140		rpe	-1.583S	0.090	5.03E-11	-1.901	-1.261						
rpiA		-0.294	0.103	4.93E-01	-0.681	0.093		rpiA	-0.371	0.103	1.99E-01	-0.558	-0.008						
rpiB		-0.102	0.048	9.56E-01	-0.283	0.080		rpiB	-0.364	0.049	1.93E-01	-0.531	-0.197						
tkA		-0.072	0.050	1.00E+00	-0.256	0.134		tkA	-0.178	0.050	8.56E-01	-0.371	0.095						
tkB		-0.075	0.051	1.00E+00	-0.264	0.114		tkB	-0.300	0.051	9.03E-01	-0.497	-0.103						
talA		0.041	0.045	1.00E+00	-0.128	0.210		talA	-0.007	0.045	1.00E+00	-0.135	0.145						
talB		-0.472S	0.055	5.00E-11	-0.687	-0.257		talB	-0.506	0.055	4.97E-11	-0.705	-0.305						
0.1h-1		-0.342S	0.051	1.00E-08	-0.533	-0.152		0.1h-1	-0.370	0.052	1.00E+00	-0.541	-0.199						
0.2h-1		-0.317S	0.054	2.05E-06	-0.519	-0.115		0.2h-1	-0.349	0.054	1.00E+00	-0.502	-0.196						
0.4h-1		-0.391S	0.053	1.52E-10	-0.589	-0.192		0.4h-1	-0.474	0.054	1.00E+00	-0.675	-0.274						
0.5h-1		-1.088S	0.058	6.02E-11	-1.429	-0.747		0.5h-1	-1.181S	0.058	5.04E-11	-1.492	-0.871						
0.7h-1		-2.290S	0.113	5.03E-11	-2.713	-1.867		0.7h-1	-2.824S	0.113	5.02E-11	-3.273	-2.075						
pgm		galM	0.723S	0.061	5.01E-11	0.495	0.951	fbab	galM	0.264S	0.050	6.50E-05	0.076	0.452					
		gk	0.728S	0.075	5.04E-11	0.931	0.525		gk	0.728S	0.075	5.04E-11	0.931	0.525					
		pgj	-0.725S	0.085	5.04E-11	-1.044	-0.406		pgm	-0.459S	0.063	2.52E-10	-0.695	-0.223					
		pKa	-0.044	0.079	1.00E+00	-0.340	0.251		pgl	-1.184S	0.078	5.00E-11	-1.475	-0.892					
	pKb	0.768S	0.051	5.05E-11	1.015	0.501		pKb	-0.503	0.071	8.96E-01	-0.708	-0.237						
	fbp	0.264	0.176	1.00E+00	-0.395	0.922		pKa	0.302	0.176	1.00E+00	-0.342	0.914						
	fbab	0.459S	0.063	2.52E-10	0.223	0.695		fbp	-0.195	0.173	1.00E+00	-0.842	-0.451						
	gapC	0.687S	0.061	5.01E-11	0.428	0.916		gapC	0.222S	0.051	2.41E-03	0.036	0.417						
	gpmA	0.597S	0.071	5.03E-11	0.331	0.863		gpmA	0.163S	0.069	5.01E-11	0.371	0.008						
	gpmB	0.458S	0.063	1.90E-10	0.234	0.692		gpmB	-0.001	0.052	1.00E+00	-0.186	0.195						
	pykA	0.614S	0.062	5.00E-11	0.384	0.845		pykA	0.155	0.051	3.39E-01	-0.035	0.346						
	pykF	0.472S	0.061	1.74E-08	0.260	0.684		pykF	0.138	0.051	3.00E-01	-0.247	0.161						
	ppsA	0.603S	0.068	5.02E-11	0.348	0.857		ppsA	0.144	0.059	8.03E-01	-0.075	0.363						
	zwf	0.475S	0.061	5.53E-11	0.247	0.704		zwf	0.106	0.051	1.00E+00	-0.173	0.205						
	pgl	-0.622S	0.119	7.47E-05	-1.067	-0.177		pgl	-1.081S	0.114	4.98E-11	-1.507	-0.655						
	gnd	0.592S	0.075	5.10E-11	0.313	0.871		gnd	-0.186	0.075	1.00E+00	-0.362	0.190						
	rpe	-0.438S	0.098	6.51E-11	-1.115	-0.382		rpe	-1.207S	0.092	5.03E-11	-1.550	-0.864						
	rpiA	0.439S	0.110	2.48E-02	0.022	0.847		rpiA	-0.204	0.109	1.00E+00	-0.416	0.368						
	rpiB	0.627S	0.062	5.04E-11	0.396	0.859		rpiB	-0.352	0.062	1.00E+00	-0.516	-0.188						
	tkA	0.657S	0.063	5.01E-11	0.421	0.893		tkA</											

Multiple Comparisons								
Dependent Variable: Protein(2D-DIGE)								
(I)	(J)	Mean Difference	Std. Error	Sig.	95% Confidence Interval	Lower Bound	Upper Bound	
gpmB	galM	0.265 S	0.050	4.15E-02	0.079	0.450		
	gk	0.271 S	0.049	1.77E-02	0.086	0.445		
	pgm	-0.488 S	0.063	1.90E-02	0.002	0.222		
	pgl	-1.183 S	0.078	5.07E-11	-1.473	-0.893		
	pkA	-0.503 S	0.071	6.88E-02	-0.767	-0.239		
	pkB	0.326 S	0.050	2.87E-02	0.140	0.512		
	ftb	-0.195	0.173	1.00E+00	-0.840	0.451		
	ftaB	0.001	0.102	1.00E+00	-0.195	0.196		
	gapC	0.229 S	0.050	1.73E-03	0.042	0.416		
	gpmA	0.135	0.062	9.10E-01	-0.092	0.369		
	galM	0.156	0.050	3.02E-01	-0.032	0.344		
	gk	0.014	0.062	1.00E+00	-0.217	0.245		
	pgm	0.144	0.056	7.79E-01	-0.073	0.362		
	pgl	-0.017	0.050	1.00E+00	-0.169	0.203		
	pkA	-1.080 S	0.114	4.99E-11	-1.505	-0.656		
	pkB	0.134	0.066	9.69E-01	-0.112	0.379		
	ftb	-1.208 S	0.091	5.03E-11	-1.548	-0.865		
	ftaB	-0.024	0.105	1.00E+00	-0.414	0.367		
	gapC	0.169	0.051	1.75E-01	-0.021	0.359		
	pykA	gkA	0.198 S	0.052	4.09E-02	0.003	0.394	
galM		0.196	0.053	5.64E-02	-0.002	0.393		
gk		0.312 S	0.048	3.20E-08	0.134	0.490		
pgm		-0.202	0.057	9.31E-02	-0.414	0.111		
pgl		-0.072	0.053	1.00E+00	-0.271	0.127		
pkA		-0.046	0.056	1.00E+00	-0.256	0.163		
pkB		0.129	0.055	9.32E-01	-0.327	0.086		
ftb		-0.827 S	0.057	4.99E-11	-1.153	-0.492		
ftaB		-0.711 S	0.114	5.04E-11	-2.446	-1.592		
gapC		0.108	0.048	9.10E-01	-0.072	0.289		
gpmA		0.114	0.064	8.42E-01	-0.062	0.246		
galM		-0.614 S	0.062	5.00E-11	-0.845	-0.384		
gk		-1.339 S	0.077	5.05E-11	-1.626	-1.052		
pgm		-0.659 S	0.070	4.99E-11	-0.920	-0.398		
pgl		-0.178	0.067	1.25E-01	-0.111	0.352		
pkA		-0.351	0.172	9.69E-01	-0.995	0.293		
pkB		-0.159	0.051	3.39E-01	-0.346	0.035		
ftb		0.073	0.056	1.00E+00	-0.295	0.255		
pykF		ftaB	-0.018	0.061	1.00E+00	-0.245	0.210	
		gapB	-0.156	0.050	3.02E-01	-0.344	0.032	
	pykF	-0.142	0.061	8.87E-01	-0.370	0.085		
	galM	-0.012	0.057	1.00E+00	-0.225	0.157		
	gk	-0.139	0.049	4.82E-01	-0.321	0.043		
	pgm	-1.237 S	0.113	5.07E-11	-1.659	-0.814		
	pgl	-0.022	0.065	1.00E+00	-0.264	0.219		
	pkA	-1.362 S	0.091	5.02E-11	-1.702	-1.023		
	pkB	-0.180	0.104	9.97E-01	-0.568	0.209		
	ftb	0.013	0.050	1.00E+00	-0.173	0.196		
	ftaB	0.042	0.061	1.00E+00	-0.149	0.253		
	gapB	0.039	0.052	1.00E+00	-0.154	0.233		
	gpmA	0.156	0.046	1.62E-01	-0.018	0.329		
	galM	-0.358 S	0.057	7.40E-08	-0.569	-0.148		
	gk	-0.228 S	0.052	4.31E-03	-0.423	-0.033		
	pgm	-0.202	0.055	6.07E-02	-0.408	0.003		
	pgl	-0.276 S	0.054	1.36E-04	-0.479	-0.074		
	pkA	-0.883 S	0.089	6.05E-11	-1.316	-0.450		
	pssA	pkB	-0.711 S	0.114	5.02E-11	-2.600	-1.750	
		ftb	0.259 S	0.060	1.05E-02	0.025	0.475	
ftaB		0.256 S	0.061	6.52E-03	0.032	0.481		
gapB		-0.472 S	0.071	1.74E-08	-0.739	-0.206		
gpmA		-1.197 S	0.085	5.06E-11	-1.514	-0.880		
pkA		-0.517 S	0.076	2.28E-08	-0.801	-0.244		
gk		-0.312 S	0.078	9.90E-02	-0.567	0.009		
pgm		-0.209	0.176	1.00E+00	-0.867	0.449		
pgl		-0.013	0.062	1.00E+00	-0.247	0.220		
pkA		0.215	0.061	9.14E-02	-0.111	0.441		
pkB		0.124	0.071	9.96E-01	-0.139	0.388		
ftb		-0.014	0.062	1.00E+00	-0.245	0.217		
ftaB		-0.142	0.061	8.87E-01	-0.370	0.085		
gapB		0.130	0.067	9.84E-01	-0.122	0.382		
gpmA		-0.003	0.060	1.00E+00	-0.223	0.229		
galM		-1.094 S	0.119	5.01E-11	-1.538	-0.651		
gk		-0.121	0.074	9.99E-01	-0.157	0.392		
pgm		-1.220 S	0.098	5.04E-11	-1.585	-0.856		
zwf		pkA	-0.153	0.110	1.00E+00	-0.449	0.373	
		pkB	0.181	0.061	7.48E-01	-0.384	0.166	
	ftb	0.184	0.062	4.07E-01	-0.049	0.417		
	ftaB	0.208 S	0.059	1.63E-04	0.078	0.517		
	gapB	-0.216	0.066	2.10E-01	-0.464	0.192		
	gpmA	-0.086	0.063	1.00E+00	-0.322	0.150		
	galM	-0.261	0.066	1.00E+00	-0.308	0.185		
	gk	-0.134	0.065	9.62E-01	-0.377	0.167		
	pgm	-0.841 S	0.096	5.04E-11	-1.200	-0.482		
	pgl	-0.711 S	0.119	5.02E-11	-2.478	-1.588		
	pkA	-0.120	0.062	9.45E-01	-0.091	0.311		
	pkB	0.126	0.056	9.08E-01	-0.084	0.336		
	ftb	-0.603 S	0.068	5.02E-11	-0.857	-0.348		
	ftaB	-1.327 S	0.082	4.99E-11	-1.634	-1.021		
	gapC	-0.947 S	0.076	5.04E-11	-1.030	-0.864		
	gpmA	-0.182	0.057	2.31E-01	-0.030	0.394		
	galM	0.336	0.175	9.83E-01	-0.992	0.314		
	gk	-0.144	0.059	8.03E-01	-0.363	0.076		
	pgm	0.085	0.057	1.00E+00	-0.128	0.297		
	pgl	-0.008	0.067	1.00E+00	-0.258	0.246		
pkA	-0.144	0.058	7.79E-01	-0.362	0.073			
pkB	0.012	0.067	1.00E+00	-0.202	0.225			
ftb	-0.130	0.067	9.84E-01	-0.382	0.122			
ftaB	-0.127	0.057	9.08E-01	-0.339	0.085			
gapC	-1.225 S	0.117	5.02E-11	-1.661	-0.789			
gpmB	-0.011	0.071	1.00E+00	-0.276	0.254			
galM	-1.351 S	0.095	4.99E-11	-1.707	-0.995			
gk	-0.168	0.106	9.99E-01	-0.572	0.236			
pgm	-0.024	0.058	1.00E+00	-0.191	0.239			
pgl	0.054	0.059	1.00E+00	-0.166	0.274			
pkA	0.051	0.059	1.00E+00	-0.170	0.273			
pkB	0.167	0.056	3.31E-01	-0.037	0.372			
ftb	-0.348 S	0.063	1.72E-02	-0.581	-0.111			
ftaB	-0.216	0.060	7.26E-02	-0.439	0.007			
gapC	-0.191	0.062	3.25E-01	-0.423	0.049			
gpmA	-0.411	0.061	5.74E-03	-0.494	-0.035			
galM	-0.972 S	0.094	5.04E-11	-1.322	-0.621			
gk	-0.711 S	0.117	5.04E-11	-2.462	-1.729			
pgm	-0.247 S	0.048	9.59E-05	-0.069	0.426			
pgl	0.254 S	0.048	4.06E-05	0.076	0.431			
pkA	-0.478 S	0.061	5.53E-11	-0.704	-0.247			
pkB	-1.208 S	0.076	5.03E-11	-1.496	-0.914			
ftb	-0.520 S	0.069	9.49E-11	-0.779	-0.260			
ftaB	-0.309 S	0.048	6.00E-08	0.130	0.489			
gapC	-0.212	0.172	1.00E+00	-0.855	0.432			
gpmB	-0.016	0.051	1.00E+00	-0.205	0.173			
galM	0.212 S	0.048	3.94E-03	0.032	0.392			
gk	0.121	0.060	9.73E-01	-0.104	0.347			
pgm	-0.017	0.061	1.00E+00	-0.203	0.186			
pgl	-0.136	0.049	4.82E-01	-0.043	0.321			
pkA	-0.003	0.060	1.00E+00	-0.229	0.223			
pkB	0.127	0.057	9.08E-01	-0.085	0.339			
ftb	-1.007 S	0.113	5.03E-11	-1.519	-0.675			
ftaB	0.117	0.064	9.84E-01	-0.124	0.357			
gapC	-1.223 S	0.090	5.03E-11	-1.562	-0.885			
gpmA	-0.041	0.064	1.00E+00	-0.426	0.347			
galM	0.152	0.049	3.06E-01	-0.032	0.335			
gk	0.181	0.051	8.20E-02	-0.008	0.370			
pgm	-0.179	0.051	1.10E-01	-0.173	0.370			
pgl	-0.295 S	0.046	6.40E-08	-0.123	0.466			
pkA	-0.219 S	0.055	2.35E-02	-0.426	-0.012			
pkB	-0.111	0.052	9.97E-01	-0.282	0.104			
ftb	-0.063	0.056	1.00E+00	-0.267	0.140			
ftaB	-0.411	0.054	7.21E-01	-0.338	0.063			
gapC	-0.844 S	0.089	5.02E-11	-1.176	-0.512			
gpmB	-0.711 S	0.113	5.01E-11	-2.460	-1.612			

\*. S\* The mean difference is significant at the .05 level.

Multiple Comparisons								
Dependent Variable: Protein(2D-DIGE)								
(I)	(J)	Mean Difference	Std. Error	Sig.	95% Confidence Interval	Lower Bound	Upper Bound	
gpmB	galM	1.343 S	0.113	5.04E-11	0.923	1.769		
	gk	1.351 S	0.113	5.04E-11	0.930	1.772		
	pgm	0.622 S	0.119	1.47E-08	0.177	1.067		
	pgl	-0.103	0.128	1.00E+00	-0.579	0.374		
	pkA	0.578 S	0.123	1.11E-03	0.116	1.039		
	pkB	1.407 S	0.113	5.04E-11	0.965	1.829		
	ftb	0.895 S	0.200	3.46E-03	0.138	1.633		
	ftaB	1.081 S	0.114	4.98E-11	0.655	1.507		
	gapC	1.309 S	0.113	5.02E-11	0.887	1.731		
	gpmA	1.215 S	0.119	5.03E-11	0.776	1.662		
	gpmA	galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmB	1.215 S	0.119	5.03E-11	0.776	1.662	
gpmB		galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmA	1.215 S	0.119	5.03E-11	0.776	1.662	
	gpmA	galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmB	1.215 S	0.119	5.03E-11	0.776	1.662	
gpmB		galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmA	1.215 S	0.119	5.03E-11	0.776	1.662	
	gpmA	galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmB	1.215 S	0.119	5.03E-11	0.776	1.662	
gpmB		galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmA	1.215 S	0.119	5.03E-11	0.776	1.662	
	gpmA	galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmB	1.215 S	0.119	5.03E-11	0.776	1.662	
gpmB		galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmA	1.215 S	0.119	5.03E-11	0.776	1.662	
	gpmA	galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmB	1.215 S	0.119	5.03E-11	0.776	1.662	
gpmB		galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmA	1.215 S	0.119	5.03E-11	0.776	1.662	
	gpmA	galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmB	1.215 S	0.119	5.03E-11	0.776	1.662	
gpmB		galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmA	1.215 S	0.119	5.03E-11	0.776	1.662	
	gpmA	galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmB	1.215 S	0.119	5.03E-11	0.776	1.662	
gpmB		galM	1.083 S	0.114	4.99E-11	0.656	1.509	
		gk	1.237 S	0.113	5.07E-11	0.814	1.659	
		pgm	1.094 S	0.119	5.01E-11	0.651	1.538	
		pgl	1.223 S	0.117	5.02E-11	0.788	1.681	
		pkA	1.007 S	0.113	5.03E-11	0.675	1.519	
		pkB	1.214 S	0.121	5.03E-11	0.763	1.666	
		ftb	0.128	0.136	1.00E+00	-0.636	0.394	
		ftaB	1.057 S	0.146	2.58E-10	0.513	1.601	
		gapC	1.309 S	0.113	5.02E-11	0.887	1.731	
		gpmA	1.215 S	0.119	5.03E-11	0.776	1.662	
	gpmA	galM	1.083 S	0.114				



Multiple Comparisons										Multiple Comparisons									
Dependent Variable: Protein(2D-DIGE)										Dependent Variable: Protein(2D-DIGE)									
(I)	(J)	Mean Difference	Std. Error	Sig.	95% Confidence Interval	(I)	(J)	Mean Difference	Std. Error	Sig.	95% Confidence Interval								
					Bound						Bound								
gla	glaM	0.069	0.052	1.00E+00	-0.122 0.254	glaM	0.069	0.051	0.04E+00	0.258	-0.143 0.268								
	gk	0.072	0.055	1.00E+00	-0.115 0.259	gk	0.342S	0.051	1.00E+00	0.152	0.533								
	gpm	-0.657S	0.063	5.01E-11	-0.893 -0.421	gpm	-0.386S	0.054	7.26E-07	-0.625	-0.147								
	pgl	-1.381S	0.079	4.98E-11	-1.673 -1.090	pgl	-1.111S	0.079	4.99E-11	-1.405	-0.817								
	pkA	-0.701S	0.071	5.04E-11	-0.967 -0.435	pkA	-0.431S	0.072	9.85E-07	-0.699	-0.162								
	pkB	0.128	0.051	7.41E-01	-0.061 0.317	pkB	0.396S	0.052	5.69E-11	0.206	0.591								
	ftb	-0.383	0.173	8.95E-01	-1.039 0.253	ftb	-0.123	0.173	1.00E+00	-0.770	0.525								
	ftaB	-0.198S	0.053	5.00E-02	-0.395 0.000	ftaB	0.073	0.054	1.00E+00	-0.129	0.274								
	gapC	0.031	0.051	1.00E+00	-0.159 0.220	gapC	0.301S	0.052	2.69E-08	0.108	0.494								
	gpmA	-0.063	0.062	1.00E+00	-0.293 0.173	gpmA	0.213	0.063	1.72E-01	-0.026	0.447								
	gpmB	-0.198S	0.052	4.09E-02	-0.394 -0.003	gpmB	0.072	0.053	1.00E+00	-0.127	0.271								
	pykA	-0.042	0.051	1.00E+00	-0.233 0.149	pykA	0.228S	0.052	4.31E-03	0.033	0.423								
	pykF	-0.184	0.062	4.07E-01	-0.417 0.049	pykF	0.086	0.063	1.00E+00	-0.159	0.322								
	ppsA	-0.054	0.059	1.00E+00	-0.274 0.169	ppsA	0.218	0.060	7.26E-02	-0.007	0.439								
	zwf	-0.181	0.051	8.20E-02	-0.370 0.008	zwf	0.088	0.052	9.97E-01	-0.104	0.282								
	pgl	-1.278S	0.114	5.01E-11	-1.705 -0.853	pgl	-1.008S	0.114	5.03E-11	-1.436	-0.588								
	gnd	-0.065	0.066	1.00E+00	-0.312 0.183	gnd	0.208	0.087	3.21E-01	-0.045	0.458								
	rpe	-1.405S	0.092	5.03E-11	-1.748 -1.062	rpe	-1.134S	0.092	5.02E-11	-1.480	-0.789								
	rpA	-0.222	0.105	9.51E-01	-0.614 0.170	rpA	0.048	0.105	1.00E+00	-0.346	0.442								
	rpB	-0.029	0.052	1.00E+00	-0.222 0.163	rpB	0.241S	0.053	1.71E-03	0.045	0.437								
	tkB	-0.003	0.054	1.00E+00	-0.203 0.197	tkB	0.270S	0.054	2.20E-04	0.069	0.472								
	tkA	0.113	0.048	8.63E-01	-0.068 0.294	tkB	0.287S	0.054	3.68E-04	0.064	0.471								
	taB	-0.400S	0.058	1.95E-09	-0.615 -0.185	taA	0.384S	0.049	5.98E-11	0.199	0.589								
	0.1h-1	-0.273S	0.054	2.20E-04	-0.472 -0.059	0.1h-1	-0.273S	0.054	2.20E-04	-0.472	-0.059								
	0.2h-1	-0.245S	0.057	5.60E-03	-0.456 -0.033	0.2h-1	-0.245S	0.057	5.60E-03	-0.456	-0.033								
	0.4h-1	-0.319S	0.056	5.25E-06	-0.527 -0.110	0.4h-1	-0.319S	0.056	5.25E-06	-0.527	-0.110								
	0.5h-1	-1.028S	0.090	5.08E-11	-1.363 -0.688	0.5h-1	-1.028S	0.090	5.08E-11	-1.363	-0.688								
	0.7h-1	-2.217S	0.114	5.02E-11	-2.645 -1.789	0.7h-1	-2.217S	0.114	5.02E-11	-2.645	-1.789								
	tkB	glaM	0.069	0.051	1.00E+00	-0.121 0.259	glaM	0.311S	0.054	4.68E-08	0.108	0.514							
		gk	0.073	0.051	1.00E+00	-0.114 0.254	gk	0.317S	0.054	2.06E-08	0.115	0.511							
		gpm	-0.654S	0.064	5.06E-11	-0.892 -0.416	gpm	-0.387S	0.055	7.05E-07	-0.665	-0.109							
		pgl	-1.379S	0.078	5.05E-11	-1.672 -1.086	pgl	-1.137S	0.081	5.06E-11	-1.438	-0.833							
		pkA	-0.698S	0.072	5.05E-11	-0.966 -0.431	pkA	-0.478S	0.074	3.37E-07	-0.733	-0.181							
		pkB	0.131	0.071	7.24E-01	-0.060 0.322	pkB	0.373S	0.054	4.26E-09	0.169	0.570							
		ftb	-0.390	0.173	9.03E-01	-1.037 0.257	ftb	-0.146	0.173	1.00E+00	-0.746	0.525							
		ftaB	-0.198	0.054	6.79E-02	-0.395 0.005	ftaB	0.047	0.057	1.00E+00	-0.165	0.291							
		gapC	0.033	0.051	1.00E+00	-0.159 0.225	gapC	0.275S	0.052	1.93E-04	0.071	0.474							
		gpmA	-0.057	0.063	1.00E+00	-0.291 0.178	gpmA	0.213	0.064	1.00E+00	-0.026	0.447							
		gpmB	-0.196	0.053	5.64E-02	-0.393 0.002	gpmB	0.046	0.056	1.00E+00	-0.163	0.250							
		pykA	-0.039	0.052	1.00E+00	-0.233 0.154	pykA	0.202	0.063	6.07E-02	-0.003	0.404							
pykF		-0.181	0.063	4.00E-01	-0.417 0.056	pykF	0.086	0.056	1.00E+00	-0.159	0.320								
ppsA		-0.051	0.059	1.00E+00	-0.273 0.170	ppsA	0.219	0.062	3.25E-01	-0.042	0.423								
zwf		-0.179	0.051	1.10E-01	-0.370 0.013	zwf	0.093	0.055	1.00E+00	-0.140	0.261								
pgl		-1.278S	0.114	5.02E-11	-1.703 -0.849	pgl	-1.103S	0.116	5.08E-11	-1.407	-0.800								
gnd		-0.062	0.067	1.00E+00	-0.311 0.187	gnd	0.208	0.087	3.00E-01	-0.071	0.471								
rpe		-1.402S	0.092	5.05E-11	-1.746 -1.058	rpe	-1.164S	0.094	5.06E-11	-1.512	-0.809								
rpA		-0.219	0.105	9.59E-01	-0.612 0.174	rpA	0.043	0.107	1.00E+00	-0.377	0.422								
rpB		-0.022	0.052	1.00E+00	-0.221 0.163	rpB	0.241S	0.053	1.70E-03	0.045	0.437								
tkA		0.003	0.054	1.00E+00	-0.197 0.203	tkA	0.292S	0.055	5.60E-03	0.033	0.458								
tkB		0.116	0.049	8.49E-01	-0.067 0.299	tkB	0.285S	0.057	8.11E-03	0.028	0.459								
taB		-0.397S	0.059	4.16E-08	-0.614 -0.180	taB	0.384S	0.049	5.75E-09	0.192	0.585								
0.1h-1		-0.267S	0.054	3.68E-04	-0.471 -0.064	0.1h-1	-0.267S	0.054	3.68E-04	-0.471	-0.064								
0.2h-1		-0.242S	0.057	8.11E-03	-0.456 -0.028	0.2h-1	-0.242S	0.057	8.11E-03	-0.456	-0.028								
0.4h-1		-0.316S	0.056	9.56E-06	-0.527 -0.105	0.4h-1	-0.316S	0.056	9.56E-06	-0.527	-0.105								
0.5h-1		-1.023S	0.090	4.89E-11	-1.361 -0.684	0.5h-1	-1.023S	0.090	4.89E-11	-1.361	-0.684								
0.7h-1		-2.215S	0.115	5.02E-11	-2.644 -1.786	0.7h-1	-1.973S	0.116	5.02E-11	-2.407	-1.531								
taA		glaM	-0.047	0.046	1.00E+00	-0.217 0.123	glaM	0.383S	0.053	3.61E-10	0.185	0.584							
		gk	-0.041	0.045	1.00E+00	-0.210 0.128	gk	0.328	0.052	1.00E+00	-0.126	0.271							
		gpm	-0.770S	0.059	5.05E-11	-0.992 -0.548	gpm	-0.338S	0.056	1.10E-04	-0.583	-0.091							
		pgl	-1.495S	0.075	5.04E-11	-1.775 -1.214	pgl	-1.063S	0.080	5.07E-11	-1.362	-0.766							
		pkA	-0.814S	0.068	5.06E-11	-0.968 -0.661	pkA	-0.481S	0.069	7.07E-09	-0.739	-0.223							
		pkB	0.019	0.046	1.00E+00	-0.156 0.188	pkB	0.447S	0.054	5.01E-11	0.246	0.641							
		ftb	-0.508	0.171	4.06E-01	-1.148 0.135	ftb	-0.074	0.174	1.00E+00	-0.724	0.575							
		ftaB	-0.311S	0.048	6.38E-08	-0.492 -0.130	ftaB	0.121	0.056	9.37E-01	-0.088	0.330							
		gapC	-0.083	0.046	9.94E-01	-0.254 0.086	gapC	0.258	0.056	3.05E-08	0.086	0.441							
		gpmA	-0.173	0.059	4.04E-01	-0.392 0.046	gpmA	0.225S	0.056	2.02E-02	0.016	0.501							
		gpmB	-0.312S	0.048	3.20E-08	-0.490 -0.134	gpmB	0.123	0.055	9.32E-01	-0.086	0.327							
		pykA	-0.158	0.046	1.62E-01	-0.329 0.016	pykA	0.275	0.056	1.36E-04	0.074	0.474							
	pykF	-0.298S	0.059	1.63E-04	-0.517 -0.078	pykF	0.086	0.056	9.62E-01	-0.108	0.371								
	ppsA	-0.167	0.055	3.31E-01	-0.372 0.037	ppsA	0.263S	0.061	5.74E-03	0.035	0.499								
	zwf	-0.295S	0.046	6.40E-08	-0.468 -0.123	zwf	0.137	0.055	7.23E-03	0.033	0.433								
	pgl	-1.392S	0.112	5.02E-11	-1.811 -0.974	pgl	-0.966S	0.115	4.96E-11	-1.391	-0.529								
	gnd	-0.178	0.063	4.94E-01	-0.412 0.056	gnd	-0.258	0.069	5.96E-02	-0.002	0.510								
	rpe	-1.518S	0.089	5.01E-11	-1.852 -1.184	rpe	-1.068S	0.093	4.99E-11	-1.438	-0.730								
	rpA	-0.335	0.103	2.04E-01	-0.719 0.049	rpA	0.048	0.107	1.00E+00	-0.346	0.442								
	rpB	-0.143	0.047	3.36E-01	-0.318 0.032	rpB	0.289S	0.055	4.82E-09	0.085	0.491								
	tkA	-0.113	0.048	8.63E-01	-0.294 0.068	tkA	0.319S	0.056	5.26E-01	0.101	0.621								
	tkB	-0.114	0.049	8.49E-01	-0.299 0.087	tkB	0.316S	0.056	5.06E-08	0.108	0.527								
	taB	-0.513S	0.053	5.05E-11	-0.713 -0.314	taA	0.432S	0.052	4.99E-11	0.239	0.621								
	0.1h-1	-0.384S	0.049	5.59E-11	-0.569 -0.199	0.1h-1	-0.381	0.060	1.00E+00	-0.306	0.144								
	0.2h-1	-0.358S	0.053	5.17E-09	-0.554 -0.162	0.2h-1	-0.348	0.057	1.00E+00	-0.164	0.261								
	0.4h-1	-0.432S	0.052	4.99E-11	-0.625 -0.239	0.4h-1	-0.428	0.059	1.00E+00	-0.291	0.258								
	0.5h-1	-1.138S	0.088	5.03E-11	-1.466 -0.811	0.5h-1	-1.077S	0.092	6.03E-11	-1.050	-0.363								
	0.7h-1	-2.333S	0.112	5.03E-11	-2.751 -1.910	0.7h-1	-1.899S	0.116	5.01E-11	-2.332	-1.481								
	taB	glaM	0.468S	0.055	5.02E-11	0.260 0.672	glaM	0.062	0.055	1.00E+00	-0.126	0.271							
		gk	0.472S	0.055	5.00E-11	0.267 0.677	gk	1.098S	0.058	5.02E-11	0.767	1.421							
		gpm	-0.257S	0.067	3.65E-02	-0.507 -0.006	gpm	0.369S	0.056	3.74E-02	0.008	0.739							
		pgl	-0.981S	0.081	5.05E-11	-1.285 -0.678	pgl	-0.737	0.081	1.71E-01	-0.016	0.431							
		pkA	-0.301S	0.075	1.72E-02	-0.580 -0.022	pkA	0.325	0.072	2.47E-01	-0.056	0.705							
		pkB	0.528S	0.055	4.98E-11	0.321 0.735	pkB	1.153S	0.088	5.04E-11	0.822	1.481							
		ftb	0.007	0.174	1.00E+00	-0.645 0.659	ftb	0.832	0.188	1.54E-01	-0.069	1.334							
		ftaB	0.202	0.058	1.01E-01	-0.013 0.417	ftaB	0.068S	0.056	9.37E-01	-0.088	0.330							
		gapC	0.431S	0.055	5.48E-11	0.223 0.638	gapC	0.106S	0.062	4.09E-01	0.071	0.724							
		gpmA	0.340S	0.066	1.20E-04	0.092 0.588	gpmA	0.066S	0.066	5.02E-11	0.007	1.382							
		gpmB	0.202	0.057	9.31E-02	-0.011 0.414	gpmB	0.027	0.056	4.09E-11	0.042	0.474							
		pykA	0.358S	0.066	7.40E-08	0.149 0.569	pykA	0.083S	0.068	5.05E-11	0.050	0.314							
pykF		0.216	0.066	2.10E-01	-0.032														

Table S11 A Significant differences in tested pairs (mRNAs, qRT-PCR)

	galM	gjk	pgm	pgl	pykA	pykB	fbp	ftsAB	gapC	gpmA	gpmB	pykA	pykF	ppsA	zwf	pgl	gnd	rpe	pyA	pyB	hka	hkB	talA	talB	0.1h-1	0.2h-1	0.4h-1	0.5h-1	0.7h-1
galM																													
gjk																													
pgm																													
pgl																													
pykA																													
pykB																													
fbp																													
ftsAB																													
gapC																													
gpmA																													
gpmB																													
pykA																													
pykF																													
ppsA																													
zwf																													
gnd																													
rpe																													
pyA																													
pyB																													
hka																													
hkB																													
talA																													
talB																													
0.1h-1																													
0.2h-1																													
0.4h-1																													
0.5h-1																													
0.7h-1																													

Table S11 B Significant differences in tested pairs (Proteins, LC-MS/MS)

	galM	gjk	pgm	pgl	pykA	pykB	fbp	ftsAB	gapC	gpmA	gpmB	pykA	pykF	ppsA	zwf	pgl	gnd	rpe	pyA	pyB	hka	hkB	talA	talB	0.1h-1	0.2h-1	0.4h-1	0.5h-1	0.7h-1
galM																													
gjk																													
pgm																													
pgl																													
pykA																													
pykB																													
fbp																													
ftsAB																													
gapC																													
gpmA																													
gpmB																													
pykA																													
pykF																													
ppsA																													
zwf																													
pgl																													
gnd																													
rpe																													
pyA																													
pyB																													
hka																													
hkB																													
talA																													
talB																													
0.1h-1																													
0.2h-1																													
0.4h-1																													
0.5h-1																													
0.7h-1																													

○ The mean difference is significant at the .05 level.

Table S11 C Significant differences in tested pairs (Metabolites)

	galM	gik	pgm	pgl	pykA	pykB	fbp	ftsAB	gapC	gpmA	gpmB	pykA	pykF	ppsA	zwf	pgl	gnd	rpe	pyA	pyB	hka	hkB	talA	talB	0.1h-1	0.2h-1	0.4h-1	0.5h-1	0.7h-1
galM																													
gik																													
pgm																													
pgl																													
pykA																													
pykB																													
fbp																													
ftsAB																													
gapC																													
gpmA																													
gpmB																													
pykA																													
pykF																													
ppsA																													
zwf																													
gnd																													
rpe																													
pyA																													
pyB																													
hka																													
hkB																													
talA																													
talB																													
0.1h-1																													
0.2h-1																													
0.4h-1																													
0.5h-1																													
0.7h-1																													

Table S11 D Significant differences in tested pairs (Metabolites, excluding nucleotides)

	galM	gik	pgm	pgl	pykA	pykB	fbp	ftsAB	gapC	gpmA	gpmB	pykA	pykF	ppsA	zwf	pgl	gnd	rpe	pyA	pyB	hka	hkB	talA	talB	0.1h-1	0.2h-1	0.4h-1	0.5h-1	0.7h-1
galM																													
gik																													
pgm																													
pgl																													
pykA																													
pykB																													
fbp																													
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gapC																													
gpmA																													
gpmB																													
pykA																													
pykF																													
ppsA																													
zwf																													
pgl																													
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pyA																													
pyB																													
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hkB																													
talA																													
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0.1h-1																													
0.2h-1																													
0.4h-1																													
0.5h-1																													
0.7h-1																													

○ The mean difference is significant at the .05 level.

Table S11 E Significant differences in tested pairs (mRNAs, DNA microarray)

	galM	gik	pgm	pgl	pkA	pkB	fbp	ftsB	gapC	gpmA	gpmB	pyKA	pyKF	ppsA	zwf	pgl	gnd	rpe	rpA	rpB	hka	hkB	tsiA	tsiB	0.1h-1	0.2h-1	0.4h-1	0.5h-1	0.7h-1
galM																													
gik																													
pgm																													
pgl																													
pkA																													
pkB																													
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gapC																													
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gpmB																													
pyKA																													
pyKF																													
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0.2h-1																													
0.4h-1																													
0.5h-1																													
0.7h-1																													

Table S11 F Significant differences in tested pairs (Proteins, 2D-DIGE)

	galM	gik	pgm	pgl	pkA	pkB	fbp	ftsB	gapC	gpmA	gpmB	pyKA	pyKF	ppsA	zwf	pgl	gnd	rpe	rpA	rpB	hka	hkB	tsiA	tsiB	0.1h-1	0.2h-1	0.4h-1	0.5h-1	0.7h-1
galM																													
gik																													
pgm																													
pgl																													
pkA																													
pkB																													
fbp																													
ftsB																													
gapC																													
gpmA																													
gpmB																													
pyKA																													
pyKF																													
ppsA																													
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rpA																													
rpB																													
hka																													
hkB																													
tsiA																													
tsiB																													
0.1h-1																													
0.2h-1																													
0.4h-1																													
0.5h-1																													
0.7h-1																													

○ The mean difference is significant at the .05 level.

**Table S12 Metabolites detected in this work that have not been previously reported in *E. coli*.**

Compound name	Average concentration (mM)	Number of samples detected
Citraconate	$1.96 \times 10^{-2}$	34
N-Acetylaspartate	$1.41 \times 10^{-1}$	33
Azelaate	$1.98 \times 10^{-2}$	33
5-Oxoproline	$1.97 \times 10^{-1}$	33
Nicotinamide hypoxanthine dinucleotide	$1.46 \times 10^{-1}$	33
2,4-Diaminobutyrate	$3.30 \times 10^{-2}$	32
Triethanolamine	$6.08 \times 10^{-2}$	32
Pterin	$2.41 \times 10^{-2}$	32
Isobutyryl CoA	$8.37 \times 10^{-3}$	32
4-Oxopentanoate	1.26	31
4-Oxohexanoate	$3.22 \times 10^{-2}$	31
Methyl sulfate	$1.30 \times 10^{-1}$	30
trans-Cinnamate	$9.02 \times 10^{-2}$	30
Diethanolamine	$2.00 \times 10^{-2}$	30
$\alpha$ -Aminoisobutyrate	$1.08 \times 10^{-2}$	28
2-Mercapto-1-methylimidazole	$1.86 \times 10^1$	28
Urocanate	$6.89 \times 10^{-2}$	25
Isobutylamine	$2.56 \times 10^{-2}$	24

The metabolites listed were detected in at least 70% of all experimental samples (the total number of samples was 34). Their migration times and m/z values in CE-TOFMS (43) analysis were identical to those of commercially available chemicals, but they have not yet been registered in EcoCyc (40) Ver 10.0. The listed concentration corresponds to the average concentration in all samples where the metabolite was detected.

### Supporting References and Notes

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### Author Contributions

T.H., M.N., K.H., A.H., Y.K., K.Su., S.I., S.H., T.M., N.S., T.T., M.H., Y.Ta. and K.N. performed the experimental work. P.Y.H., K.Y., K.A., N.Iw., Y.To., and Y.N. contributed to the data analysis and K.A. developed the database and web site. N.Is., K.N., T.B., M.R., T.S., A.K. and T.H. managed and supervised the efforts of the different experimental groups, performed data analysis and conceptualised the manuscript. N.Is., K.N., M.R., and T.H. co-wrote the manuscript with feedback from the other authors. T.N., K.Sh., H.M. and M.T. headed the various research groups and provided the research environment and support.