

## Supporting Online Material for

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

Nobuyoshi Ishii, Kenji Nakahigashi, Tomoya Baba, Martin Robert, Tomoyoshi Soga, Akio Kanai, Takashi Hirasawa, Miki Naba, Kenta Hirai, Aminul Hoque, Pei Yee Ho, Yuji Kakazu, Kaori Sugawara, Saori Igarashi, Satoshi Harada, Takeshi Masuda, Naoyuki Sugiyama, Takashi Togashi, Miki Hasegawa, Yuki Takai, Katsuyuki Yugi, Kazuharu Arakawa, Nayuta Iwata, Yoshihiro Toya, Yoichi Nakayama, Takaaki Nishioka, Kazuyuki Shimizu, Hirotada Mori, Masaru Tomita\*

\*To whom correspondence should be addressed. E-mail: mt@sfc.keio.ac.jp

Published 22 March 2007 on *Science* Express DOI: 10.1126/science.1132067

#### This PDF file includes:

Materials and Methods SOM Text Figs. S1 to S7 Tables S1 to S12 References

#### **Materials and Methods**

Strains and culture. E. coli K-12 strain BW25113 (lacl<sup>q</sup> rrnB<sub>T14</sub> \(\Delta\lac{LacZ}{WJ16}\) hsdR514  $\triangle araBAD_{AH33} \triangle rhaBAD_{LD78}$ ) (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 regent (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 h<sup>-1</sup> 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 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 μg) 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 <a href="http://ecoli.iab.keio.ac.jp/">http://ecoli.iab.keio.ac.jp/</a>.

#### 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. × 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

μM reserpine was delivered as the sheath liquid at 10 μl/min. Electrospray ionization (ESI)-TOFMS was conducted in the positive ion mode and the capillary voltage was set at 4,000 V. A flow rate of heated dry nitrogen gas (heater temperature 300°C) was maintained at 10 psig. The fragmentor, skimmer, and Oct RFV voltages were set at 75 V, 50 V, and 130 V, respectively. Automatic recalibration of each acquired spectrum was performed using reference masses of reference standards. The methanol adduct ion ([2MeOH+H<sup>2</sup>O +H]<sup>+</sup>, m/z 83.0703) and reserpine ([M+H]<sup>+</sup>, m/z 609.2806) provided the lock mass for exact mass measurements. Exact mass data were acquired at a rate of 10 spectra/s over a 50–1,000 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 mM ammonium acetate solution (pH 8.5) was used as the electrolyte solution for CE separation. Sample solution (30 nl) was injected at 50 mbar for 30 s and – 30kV of voltage was applied. Ammonium acetate (5 mM) in a 50% methanol-water mixture (v/v) containing 20 μM piperazine-1,4-bis(2-ethansulfonate) (PIPES) and 1 μM reserpine was delivered as the sheath liquid at 10 μl/min. ESI-TOFMS was conducted in the negative ion mode; the capillary voltage was set at 3,500 V. The fragmentor, skimmer, and Oct RFV voltages were set at 100 V, 50 V, and 200 V, respectively. Automatic recalibration of each acquired spectrum was performed using the reference masses of standards, that is, divalent PIPES ([M-2H]<sup>2-</sup>, m/z 150.0230), monovalent PIPES ([M-H]<sup>-</sup>, m/z 301.0534), and reserpine ([M-H]<sup>-</sup>, 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 µm i.d. × 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 μL/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 [M-H] ions for nucleotides and nicotinamide-adenine dinucleotides and divalent deprotonated [M-2H]<sup>2-</sup> 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  $(2.80 \times 10^{-13} \text{ g})$  (16) and the estimated volume of a single cell  $(4.96 \times 10^{-16} \text{ l})$  (16).

#### Metabolic flux analysis.

<sup>13</sup>C-labeling experiment. For metabolic flux analysis, <sup>13</sup>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-<sup>13</sup>C] glucose, 0.4 g/l of uniformly labeled [U-<sup>13</sup>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-<sup>13</sup>C] glucose, 0.8 g/l of [U-<sup>13</sup>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-μm pore size filter (Millipore Co., USA). The filtrate was dried again and redissolved in 1.5 ml of acetonitrile.

For derivatization, the resulting 80 μl 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]<sup>+</sup> and [M-159]<sup>+</sup>, 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 6phosphogluconolactone 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 tktAdisruptants,  $r_8$  and  $r_{26}$  for zwf disruptant,  $r_2$  and  $r_8$  for wild-type cultured at 0.4, 0.5 and 0.7  $h^{-1}$ , and  $r_2$ ,  $r_8$  and  $r_{26}$  for wild-type cultured at 0.1 and 0.2  $h^{-1}$  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

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:

$$\begin{aligned} M_{ij} &= \log_2 \left( v_{ij} / v_{j,control} \right) \\ MAD_j &= median_j \left\{ M_{ij} - median_j \left( M_{ij} \right) \right\} \\ EI_{ij} &= \frac{M_{ij} - median_j}{MAD_j} \end{aligned}$$

where  $M_{ij}$  is the normalized measurement value of the jth component in the ith sample,  $v_{ij}$  is the measured value of the jth component in the ith sample, and  $v_{j,control}$  is the measured value of the jth 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 jth component in the control sample (parent cell type BW2511 cultured at a specific growth rate of  $0.2 \, h^{-1}$ ). MAD $_j$  is the median absolute deviation (29) of the jth component, and EI $_{ij}$  is the expression ratio of the jth component in the ith 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:

$$AEI_{i} = \frac{\sum_{j=1}^{n} \left| EI_{ij} \right|}{n}$$

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 h<sup>-1</sup>), 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 h<sup>-1</sup>. 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 h<sup>-1</sup>, 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  $h^{-1}$  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  $h^{-1}$  samples were different from that of the 0.2  $h^{-1}$  sample. Furthermore, significant differences were detected for most other pairs except for 0.1  $h^{-1}$  – 0.4  $h^{-1}$ , 0.1  $h^{-1}$  – 0.5  $h^{-1}$  and 0.5  $h^{-1}$  – 0.7  $h^{-1}$ . 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 h<sup>-1</sup> showed significant differences against 15 of the 24 knockout samples showing low protein AEI values, which suggests a difference between the 0.7 h<sup>-1</sup> sample and the 0.2 h<sup>-1</sup> 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 h<sup>-1</sup> and 0.7 h<sup>-1</sup> 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 h<sup>-1</sup>. 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 h<sup>-1</sup>. Figure 2C shows that the mRNA AEIs of the wild-type samples cultured at 0.5 h<sup>-1</sup> and 0.7 h<sup>-1</sup> 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 h<sup>-1</sup>, and 0.7 h<sup>-1</sup>) and the disruptants were not as clear. However, during comparisons between the wild-type cultured at the highest growth rate (0.7 h<sup>-1</sup>) 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 h<sup>-1</sup> or 0.7 h<sup>-1</sup>. Thus the AEIs of the higher growth rate group (wild-type, 0.5 h<sup>-1</sup> and 0.7 h<sup>-1</sup>) 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 h<sup>-1</sup> 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  $0.5 \, h^{-1}$ , whereas none of them showed significant differences from the wild-type at  $0.7 \, h^{-1}$ . If nucleotides were excluded from the AEI calculations, then only the pair of rpe wild-type at  $0.5 \, h^{-1}$  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  $(0.5 \, h^{-1})$ .
- (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.

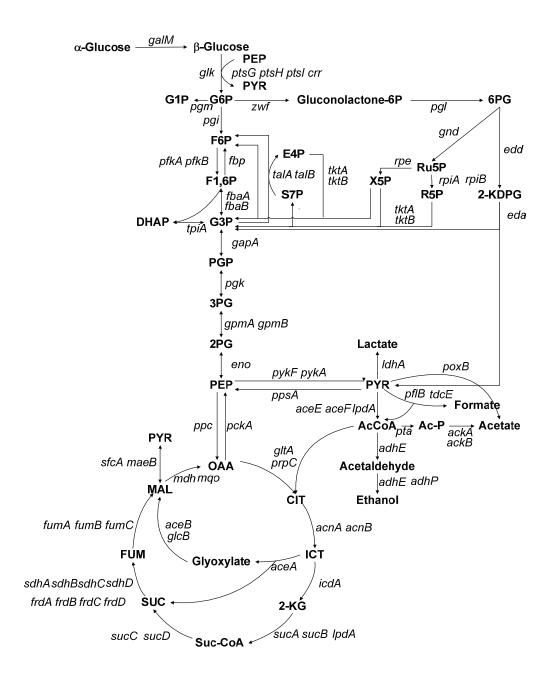


Figure S1 Map of *Escherichia coli* K-12 central carbon metabolism. This map, showing metabolites (bold font) and genes (italics) is derived from Shimizu (2004) (42), but is slightly modified with information obtained from KEGG (6) maps (http://www.genome.jp/kegg/) and EcoCyc (40) (http://ecocyc.org/).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

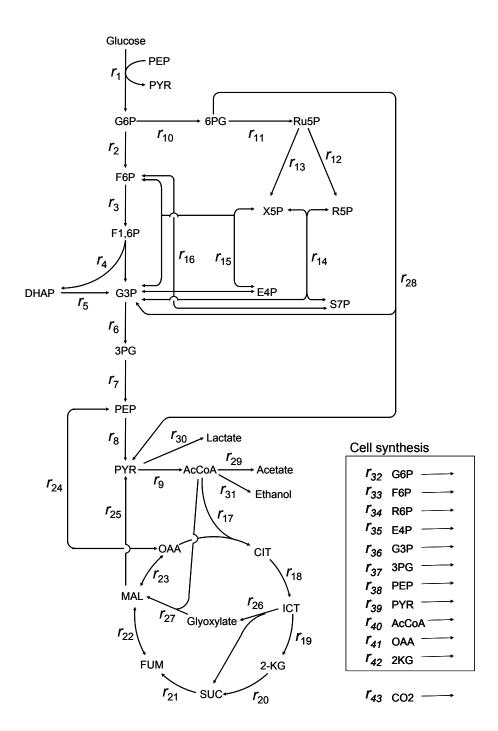


Figure S2 Main metabolic pathways of E. coli K-12 used for metabolic flux analysis.

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.

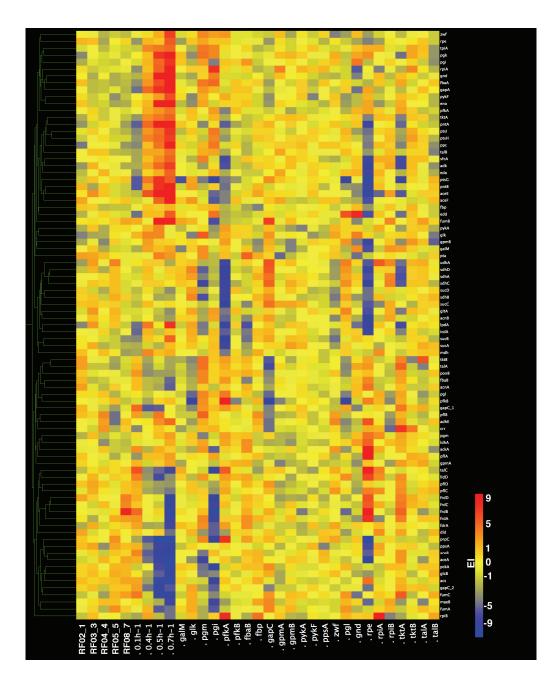


Figure S3 A mRNAs detected in more than half of samples.

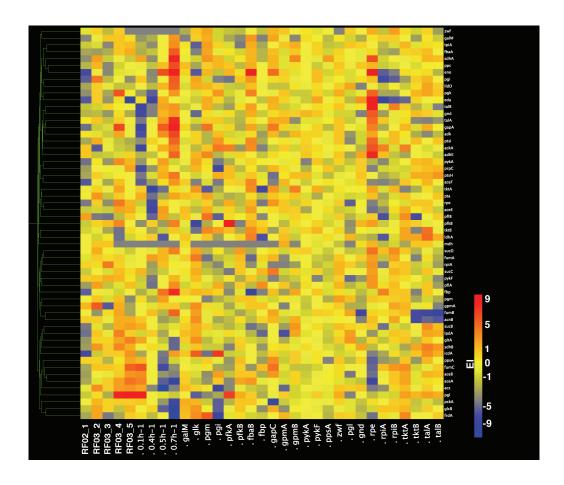


Figure S3 B Proteins detected in more than half of samples.

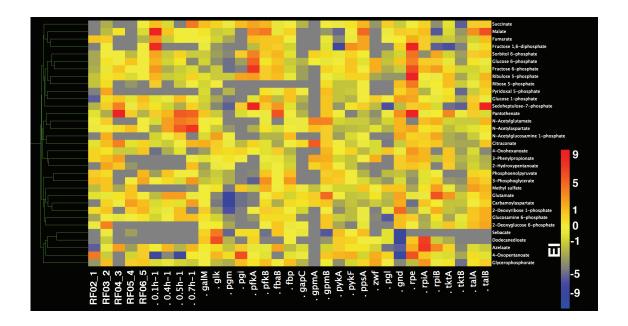


Figure S3 C Metabolites (Anions) detected in more than half of samples.

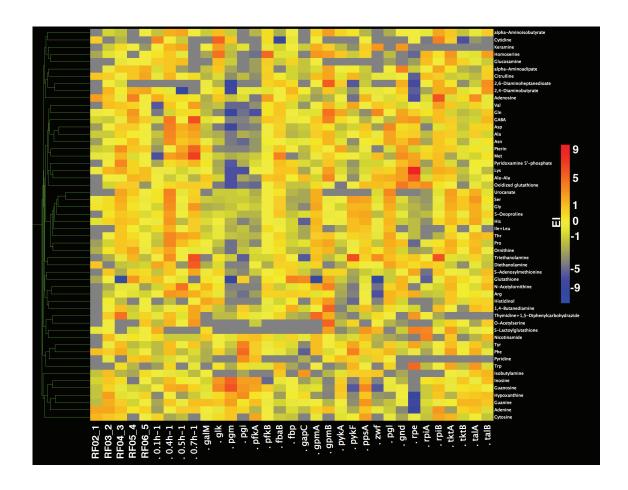


Figure S3 D Metabolites (Cations) detected in more than half of samples.

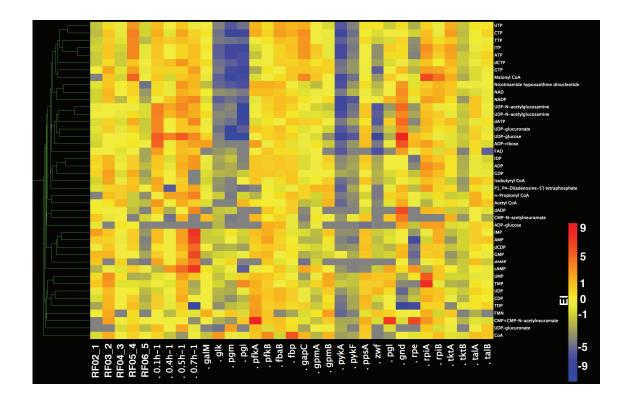


Figure S3 E Metabolites (Nucleotides) detected in more than half of samples.

### 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 h<sup>-1</sup>). RFs are denoted by Sample ID and Series ID shown in Table S2.

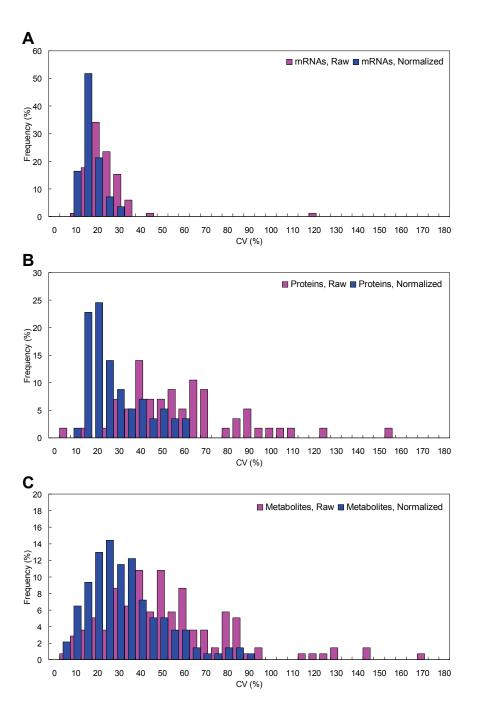


Figure S4 Distributions of CV frequencies for raw and normalized obtained using the various targeted quantitative methods. A; mRNAs measured by qRT-PCR. B; proteins measured by LC-MS/MS. C; metabolites measured by CE-(TOF)MS.

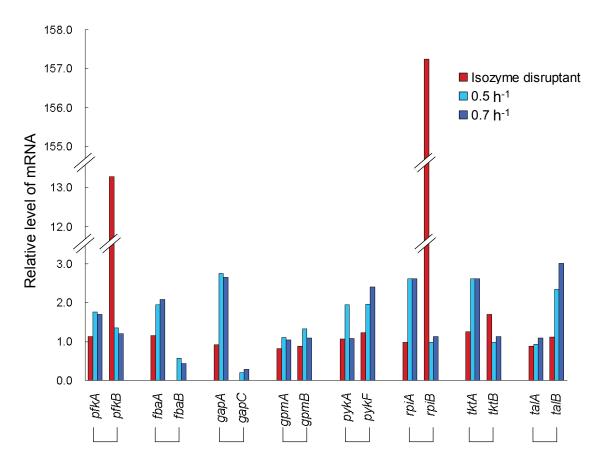
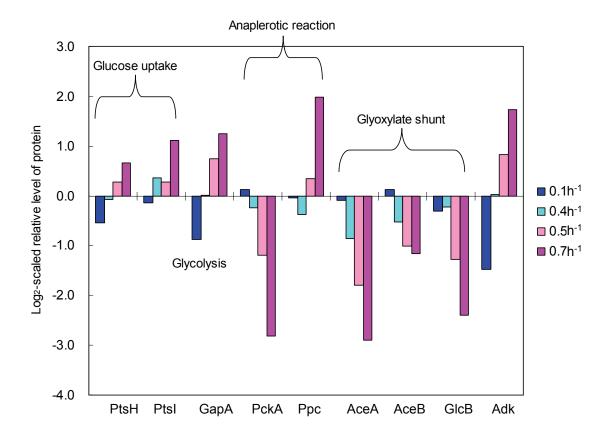


Figure S5 Effect of growth rate change or enzyme disruption on mRNA transcript levels for specific pairs of isozymes. The values correspond to the relative level of mRNA compared to wild-type at a specific growth rate of  $0.2 \, h^{-1}$ , upon either an increase in specific growth rate  $(0.5 \, h^{-1})$  and  $0.7 \, h^{-1}$ ; 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 log2 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.

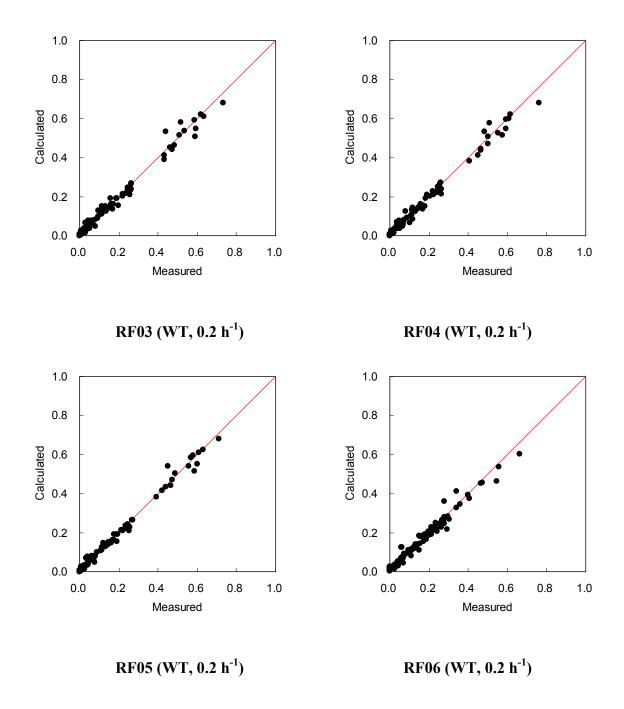


Figure S7 A Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (RF03, RF04, RF05, RF06).

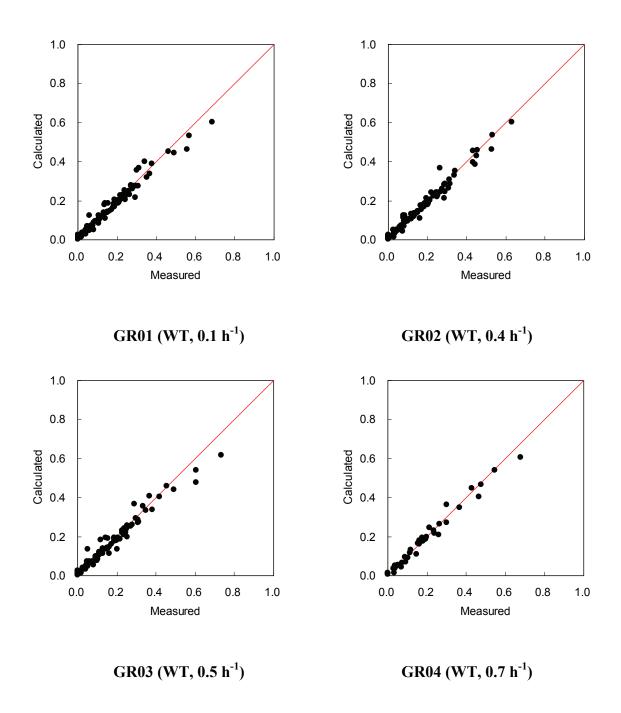


Figure S7 B Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (GR01, GR02, GR03, GR04).

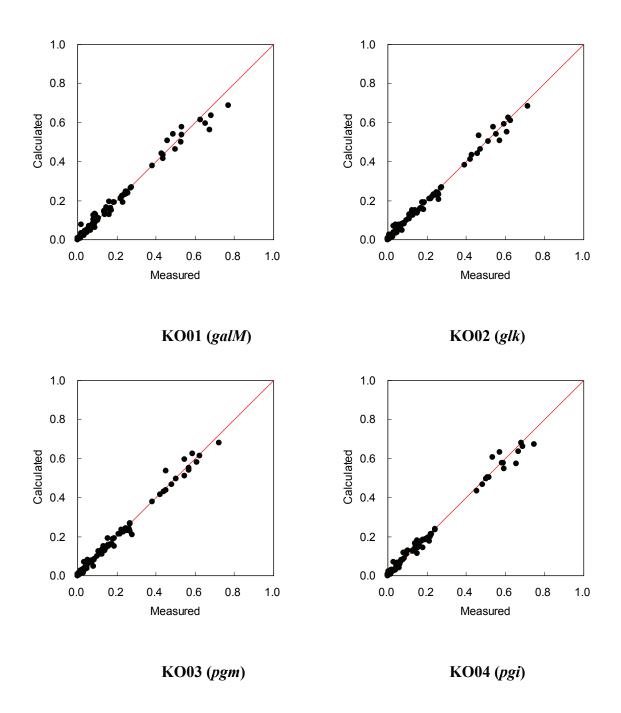


Figure S7 C Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO01, KO02, KO03, KO04).

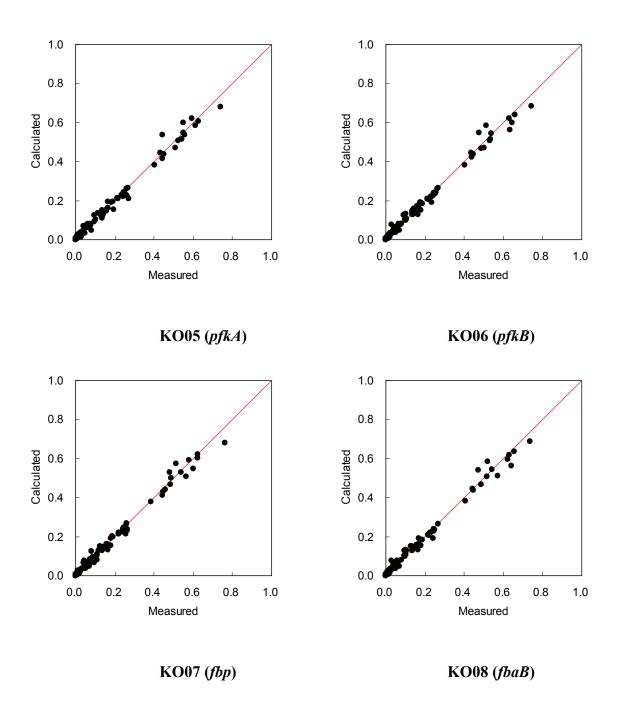


Figure S7 D Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO05, KO06, KO07, KO08).

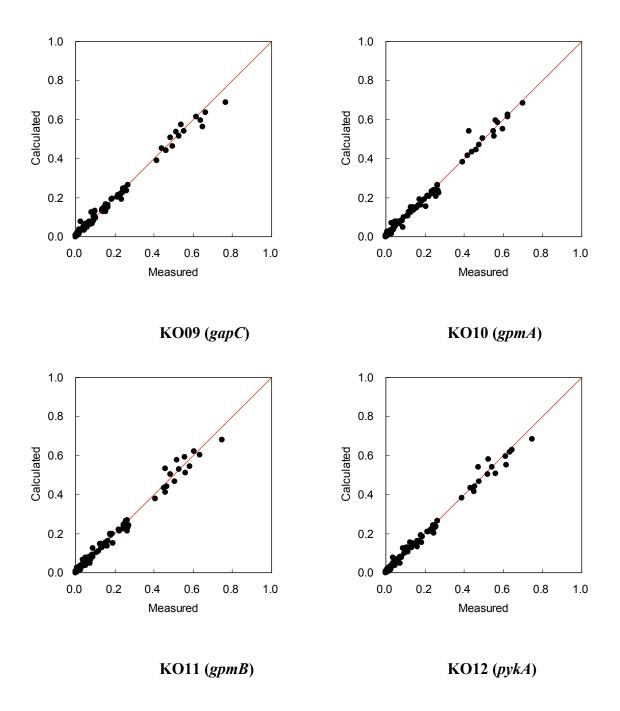


Figure S7 E Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO09, KO10, KO11, KO12).

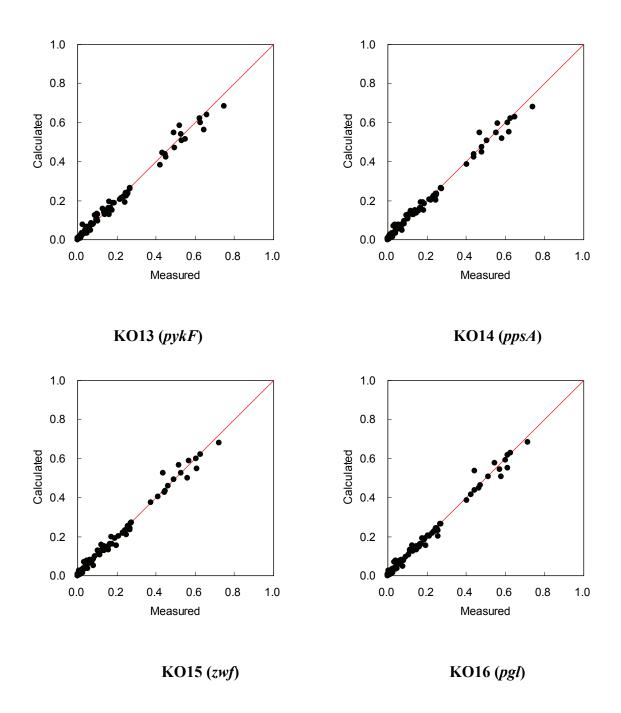


Figure S7 F Comparison of mass distributions of proteinogenic amino acids between value scalculated from the estimated flux distributions and those measured by GC-MS (KO13, KO14, KO15, KO16).

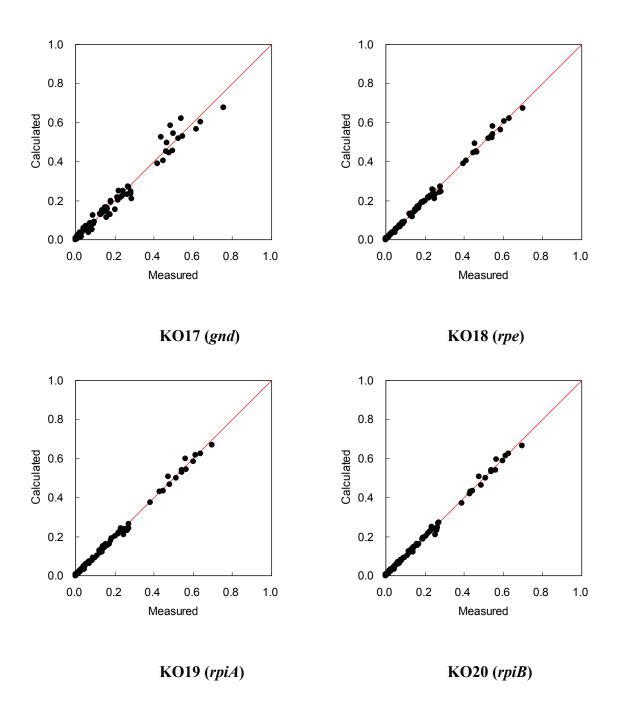


Figure S7 G Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO17, KO18, KO19, KO20).

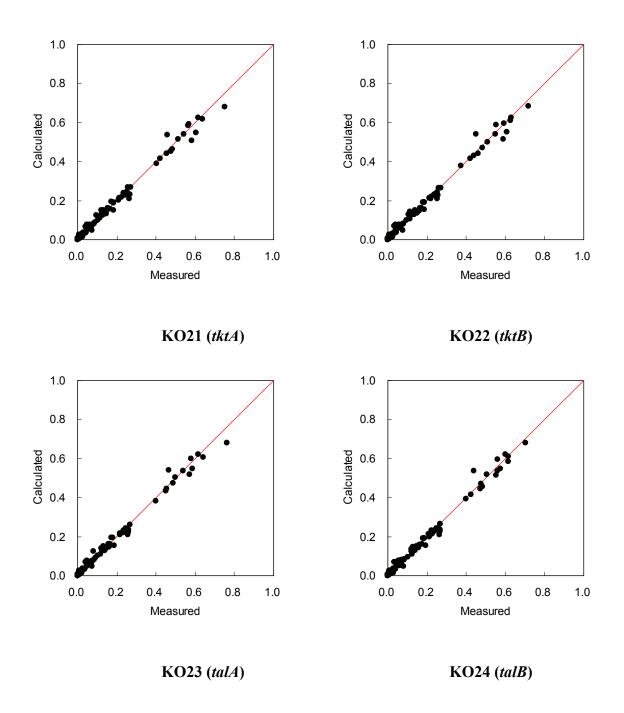


Figure S7 H Comparison of mass distributions of proteinogenic amino acids between values calculated from the estimated flux distributions and those measured by GC-MS (KO21, KO22, KO23, KO24).

RF, reference sample (wild-type cells cultured at a specific growth rate of  $0.2 \, h^{-1}$ ); GR, wild-type cells cultured at the indicated specific growth rates; KO, single-gene knockout mutants cultured at a specific growth rate of  $0.2 \, h^{-1}$ ; 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.** 

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

				Series ID	
01- 15	OI- N	Outhing Data	mRNAs	Proteins	NA-4-1114
Sample IL	) Sample Name	Culture Date	(qRT-PCR)	(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	3	2 2
KO12 KO13	pykA	16-Jun-05 16-Jun-05	3	2 2	2
KO13 KO14	pykF ppsA	9-Jun-05	2	2	2
KO14 KO15	zwf	30-Jun-05	3	3	4
KO15 KO16	pgl	10-Nov-05	6	6	5
KO10 KO17	gnd	2-Jun-05	2	1	2
KO17	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
0.10.	VV 1, 0.711	0 00.00	· ·	•	•
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		J
RF08	, -	2-Mar-06	7		
KFU8	WT, 0.2h <sup>-1</sup>	Z-IVIAI-U6	1		

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.

<sup>\*</sup> 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
141 00	VV 1, O.ZII	1.022
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 KO08	fbp fbaB	1.580 1.435
KO08 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	Enzymes catalyzing	Reaction
<u>name</u>	PtsG	Chicago I DED > CCD I DVD
r <sub>1</sub>		Glucose + PEP -> G6P + PYR
r <sub>2</sub>	Pgi	G6P <-> F6P
r <sub>3</sub>	PfkA, PfkB	F6P -> F1,6P
r <sub>4</sub>	FbaA, FbaB	F1,6P -> DHAP + G3P
r <sub>5</sub>	TpiA	DHAP -> G3P
<i>r</i> <sub>6</sub>	GapA; Pgk	G3P -> 3PG 3PG <-> PEP
r <sub>7</sub>	GpmA, GpmB; Eno	PEP -> PYR
r <sub>8</sub>	PykA, PykF	. —
r <sub>9</sub>	AceEF LpdA	PYR -> AcCoA + CO <sub>2</sub>
r <sub>10</sub>	Zwf	G6P -> 6PG
r <sub>11</sub>	Pgl; Gnd	6PG -> Ru5P + CO <sub>2</sub>
r <sub>12</sub>	Rpe	Ru5P -> X5P
r <sub>13</sub>	RpiA, RpiB	Ru5P -> R5P
r <sub>14</sub>	TktA, TktB	R5P + X5P <-> S7P + G3P
r <sub>15</sub>	TalA, TalB	S7P + G3P <-> E4P + F6P
r <sub>16</sub>	TktA, TktB	X5P + E4P <-> F6P + G3P
r <sub>17</sub>	GltA, PrpC	AcCoA + OAA -> CIT
r <sub>18</sub>	AcnA, AcnB	CIT -> ICT
r <sub>19</sub>	IcdA	ICT -> 2-KG + CO <sub>2</sub>
$r_{20}$	SucAB LpdA; SucCD	2-KG -> SUC + CO <sub>2</sub>
r <sub>21</sub>	SdhABCD	SUC -> FUM
$r_{22}$	FumA, FumB, FumC	FUM -> MAL
$r_{23}$	Mdh, Mqo	MAL <-> OAA
$r_{24}$	Ppc; PckA	PEP + CO <sub>2</sub> <-> OAA
r <sub>25</sub>	SfcA, MaeB	MAL -> PYR + CO <sub>2</sub>
r <sub>26</sub>	AceA	ICT -> Glyoxylate + SUC
r <sub>27</sub>	AceB	Glyoxylate + AcCoA -> MAL
r <sub>28</sub>	Edd; Eda	6-PG -> G3P + PYR
r <sub>29</sub>	Pta; AckA, AckB	AcCoA -> Acetate
r <sub>30</sub>	LdhA	PYR -> Lactate
r <sub>31</sub>	AdhE, AdhP	AcCoA -> Ethanol
r <sub>32</sub>	(Cell synthesis)	G6P ->
r <sub>33</sub>	(Cell synthesis)	F6P ->
r <sub>34</sub>	(Cell synthesis)	R5P ->
r <sub>35</sub>	(Cell synthesis)	E4P ->
r <sub>36</sub>	(Cell synthesis)	G3P ->
r <sub>37</sub>	(Cell synthesis)	3PG ->
r <sub>38</sub>	(Cell synthesis)	PEP ->
r <sub>39</sub>	(Cell synthesis)	PYR ->
r <sub>40</sub>	(Cell synthesis)	AcCoA ->
r <sub>41</sub>	(Cell synthesis)	OAA ->
r <sub>42</sub>	(Cell synthesis)	2KG ->
r <sub>43</sub>	(Evolution)	CO2 ->

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.

	C	RF.		ì	Ì	89					0																							
Reaction Hallie Reaction	IIE REACTOIL	RF03	RF04	RF04 RF05	RF06	0.1 h <sup>-1</sup>	0.4	0.5	ll	h.1	galM				pfkA pf	kB fb	ã	g	g	б	g	ğ	d	Š	g	Б	6	2	ď	¥	꿏	ta	tal	
1,	Glucose + PEP -> G6P + PYR	_	9	_	_	5	_	•	_	00 1	100	100	100	100	100	100						•			_			_						
2 .	G6P <-> F6P	8/8	1 3	2 80	9 60	6 6				9 8	64 6	× 6	80 8	, ?	4 6	25.																		
	F1.6P -> DHAP + G3P	68				5 80				8 8	<u> </u>	6 8	8 8	, ¥	87	: 1																		
. 5	DHAP -> G3P	88	8			8				80	. 18	88	88	34	87	12																		
r <sub>6</sub>	G3P -> 3PG	178				167	-	•		02	168	177	173	120	173	163						•												
1,	3PG <-> PEP	169	_	_	_	15.	-	•		62	159	167	164	109	162	153						•												
8,	PEP-> PYR	4 4			49	, or	m (			£ 15	22	51	20	υ ç	5 4	49											2 5	_						
6 ,	G6P-> 6PG	130	13/	7 7 7		5 8	2 "	36 15		12/	747	132	130	22 86	120	47	747 7	55	36	218	13/	24	22.2	31 - 12	96 .	20 02			31 48	747	120	711 0	7 7 7	_ ~
2 ==	6PG -> Ru5P + CO,	= =	. 7	. 4	36	ੰ ਲੋ				i 4	32	1 2	. 5	61	. 4	4											,							
, ta	Ru5P -> X5P	6	,	3 7	20	=				54	18	က	80	35	က	25									ιģ		- 2							
r 13	Ru5P -> R5P	6	9	0 12	19	=		18 1	-	18	17	6	12	56	=	21											2	7						_
F 14	R5P + X5P <-> S7P + G3P	9	.,	3	12	+	_			13	10	က	9	19	3	4																		~
F 15	S7P + G3P <-> E4P + F6P	9	.,	3	12	+	_			13	10	က	9	19	ဗ	4																		~
F 16	X5P + E4P <-> F6P + G3P	0				-	m	_	0	7	7	0	က	16	0	=																		_
r 17	AcCoA + OAA -> CIT	102				80	2			88	87	86	93	29	82	9/																		_
F 18	CIT -> ICT	102				80	7			88	87	86	93	29	82	9/																		_
r 19	ICT -> 2-KG + CO <sub>2</sub>	100				ũ	(0			88	61	91	82	4	73	21																		•
r <sub>20</sub>	2-KG -> SUC + CO <sub>2</sub>	92				4 1	m ·			8 1	23	83	44	83	<b>4</b> 1	6 1																		
121	SUC -> FUM	95				r 1				8 8	4	9	8	28	1 3	89																		m /
<sup>2</sup> 2	FUM -> MAL	95				-	4			æ :	19	9	82	28	23	89																		m 1
23	MAL <-> OAA	97	8 8	5 87	98 9	ō '	· ·			g !	100	86 9	96	۶ %	£ ;	90																		
× ,	MAI - DVB - CO	,		2 .	0 0		· ·			۲ ،	0 1	<u></u>	5 0	0 (	32	0 (																		
8.	IMAL -> PTR + CO <sub>2</sub>	0 (		4 4 O 6		7 6	+ 0			0	n e	1 0	> 7	7 5	o •	מ מ																		
. 38	Chambra Accord	ν (	7 6		2 6	₹ 7					9 8	- 1	= ;	0 10	ю о	62 2																		
7.27	6-PG -> G3P + PVP	7				Ψ,					97	٠,	Ξ,	6 6	o ,	67																		N.
8 8	AcCoA -> Acetate	0		0	0			0		4	0	C	0	5 0	0	0			0	0										٠				
, s	PYR -> Lactate	0		. 0	0			0	. 0	. 0	0	0	0	0	0	0			0	0	0						0 0		. 0	. 0	0			
r <sub>31</sub>	AcCoA -> Ethanol	0	J	0	0		0	0	2	_	0	0	0	0	0	0			0	0									0	0		0	0	_
F 32	G6P -> (Cell synthesis)	_	. 4	2 2	2		~	2	2	-	-	-	~	7	5	7			7	7									_	<del>-</del>		2		01
r <sub>333</sub>	F6P -> (Cell synthesis)	_	,-	,	_		_	<del>-</del>	_	-	~	-	~	-	<del>-</del>	-			-	_									_	_	_	_	_	_
F 34	R5P -> (Cell synthesis)	9		7 7	7		_	00	7	2	7	9	9	7	7	7			7	7					9	7	9	2	9	2	4	_	_	
r 35	E4P -> (Cell synthesis)	က		3	3		m	3	က	2	က	က	က	က	က	က		က	က	က									က	2	7	8	e	~
, 36	G3P -> (Cell synthesis)		. ;		- ;			- ;	<b>.</b> .		- :		- ;	- ;	- ;	- ;	- ;	- ;	- ;	- ;		- ;	- :							<del>-</del> 1				
7.37	SPG -> (Cell synthesis)	יי מ	- `	= =	= 5	= '	- <del>-</del>	= -		ω «	2 4	יה מ	2 7	= 5	= 5	= =	= <		2 4	= 5	ים מ	= <		2 4	י מ	01.		" a	י מ	- 0	01 ~			
8 8 	PYR -> (Cell synthesis)	9	22	2 21	53	. 2		24		16	50	9 6	50	52	23	52	. 23		50	23	. 6													
r 40	AcCoA -> (Cell synthesis)	25				1 73	m	31 3	30 8	5	27	56	27	30	30	58	30	30	27	8	52	_	58							20 1		8 .	_	
F 41	OAA -> (Cell synthesis)	12	7	4 14	15	4	-	15 1		10	13	13	13	15	15	4	15		13	15	12									_				
r 42	2KG -> (Cell synthesis)	7	٠,	3 6	6		m	6		9	00	80	80	6	6	6		_					_		_		7	7				_	_	~
r <sub>43</sub>	CO <sub>2</sub> -> (Evolution)	316	261	1 275	252	28	75	43 23	38	55	295	305	296	259	256	273	257	263		255	322 2	270 2	268 2	290 307		12 324	34		376	93	13 287	7 268		m
r <sub>2</sub> exch	G6P <-> F6P	0.50				0.95	_	0.95 0.93		0.95	0.91	0.95	0.93		0.94	0.83	0.74 0	0.95 0	0.90	0.94 0	0.82 0.	0.89	0.87 0.	0.92 0.10	0 0.92	0.00	00.00	0 0.33	33 0.94	4 0.87	7 0.94	4 0.57	7 0.38	_
r, exch	3PG <-> PEP	0.95				0.9	_			92	0.00	0.95	0.95					_			_													10
r 14 exch	R5P + X5P <-> S7P + G3P	0.00				0.0	_			0	0.00	0.00	0.00					_			_													_
r 15 exch	S7P + G3P <-> E4P + F6P	0.68				0.6	_			34	0.70	0.59	0.68	0.53							_													
r 16 exch	X5P + E4P <-> F6P + G3P	0.00				0.0				8 7	0.0	0.00	0.00																					SI (
r 23 exch	MAL <-> UAA	0.95		0.93	0.73	46.0				4 6	0.93	9.0	0.90																					~ ~
24 exci	TET + CO <sub>2</sub> <-> OAA	0.35	0.40	- 1	- 1	0.3	1	- 1		53	0.30	0.31	0.35	- 1	- 1				- 1	- 1	1		- 1			- 1	- 1	0.4	0.0	- 1	- 1		- 1	٠,

cultured at a specific growth rate of 0.2 h<sup>-1</sup>; WT, wild-type; exch r<sub>n</sub>, exchange coefficient of reaction r<sub>n</sub>. Reaction names are All fluxes are normalized to specific glucose uptake rate. 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 shown on a metabolic map in Fig. S2. "-" denotes reaction excluded from the model.

Table S5 B Metabolic flux analysis results (error estimation of reference sample).

Reaction name	Reaction	Ave	SD	SE	LB	UB
r <sub>1</sub>	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 <sub>8</sub>	PEP -> PYR	47	1	1	46	49
r <sub>g</sub>	PYR -> AcCoA + CO <sub>2</sub>	129	6	3	125	134
r <sub>10</sub>	G6P -> 6PG	21	12	6	10	31
r <sub>11</sub>	6PG -> Ru5P + CO <sub>2</sub>	21	12	6	10	31
r <sub>12</sub>	Ru5P -> X5P	8	8	4	1	15
r <sub>13</sub>	Ru5P -> R5P	12	5	2	9	16
r <sub>14</sub>	R5P + X5P <-> S7P + G3P	6	4	2	2	9
r <sub>15</sub>	S7P + G3P <-> E4P + F6P	6	4	2	2	9
r <sub>16</sub>	X5P + E4P <-> F6P + G3P	2	4	2	-1	6
r <sub>17</sub>	AcCoA + OAA -> CIT	86	13	6	76	96
r <sub>18</sub>	CIT -> ICT	86	13	6	76	96
r <sub>19</sub>	ICT -> 2-KG + CO <sub>2</sub>	71	23	11	52	89
r <sub>20</sub>	2-KG -> SUC + CO <sub>2</sub>	62	23	12	43	82
r <sub>21</sub>	SUC -> FUM	77	13	7	67	88
r <sub>22</sub>	FUM -> MAL	77	13	7	67	88
r <sub>23</sub>	MAL <-> OAA	89	6	3	84	94
r <sub>24</sub>	PEP + CO <sub>2</sub> <-> OAA	11	7	4	5	16
r <sub>25</sub>	MAL -> PYR + CO <sub>2</sub>	3	7	3	-2	9
r <sub>26</sub>	ICT -> Glyoxylate + SUC	15	11	5	6	24
r <sub>27</sub>	Glyoxylate + AcCoA -> MAL	15	11	5	6	24
r <sub>28</sub>	6-PG -> G3P + PYR	-	-	-	-	-
r <sub>29</sub>	AcCoA -> Acetate	0	0	0	NA	NA
r <sub>30</sub>	PYR -> Lactate	0	0	0	NA	NA
r <sub>31</sub>	AcCoA -> Ethanol	0	0	0	0	0
r <sub>32</sub>	G6P -> (Cell synthesis)	2	0	0	1	2
r <sub>33</sub>	F6P -> (Cell synthesis)	1	0	0	1	1
r <sub>34</sub>	R5P -> (Cell synthesis)	7	1	0	6	7
r <sub>35</sub>	E4P -> (Cell synthesis)	3	0	0	3	3
r <sub>36</sub>	G3P -> (Cell synthesis)	1	0	0	1	1
r <sub>37</sub>	3PG -> (Cell synthesis)	10	1	0	10	11
r <sub>38</sub>	PEP -> (Cell synthesis)	4	0	0	3	4
r <sub>39</sub>	PYR -> (Cell synthesis)	21	2	1	20	23
r <sub>40</sub>	AcCoA -> (Cell synthesis)	29	2	1	26	31
r <sub>41</sub>	OAA -> (Cell synthesis)	14	1	1	13	15
r <sub>42</sub>	2KG -> (Cell synthesis)	8	1	0	8	9
r <sub>43</sub>	CO <sub>2</sub> -> (Evolution)	276	28	14	253	299
	000 500	0.70	0.40	0.00	0.55	0.00
r <sub>2</sub> exch	G6P <-> F6P	0.72	0.19	0.09	0.57	0.88
r <sub>7</sub> exch	3PG <-> PEP	0.95	0.00	0.00	0.95	0.95
r <sub>14</sub> exch	R5P + X5P <-> S7P + G3P	0.00	0.00	0.00	0.00	0.00
r <sub>15</sub> exch	S7P + G3P <-> E4P + F6P	0.65	0.14	0.07	0.54	0.76
r <sub>16</sub> exch	X5P + E4P <-> F6P + G3P	0.00	0.00	0.00	0.00	0.00
r <sub>23</sub> exch	MAL <-> OAA	0.69	0.39	0.20	0.36	0.95
r <sub>24</sub> exch	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 I	D Sample Name	Correlation Nu coefficient me		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
111 00	VV 1, U.ZII	0.000	01	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
01101	VV 1, 0.711	0.000		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 KO17	pgl	0.994	94 94	< 0.01
KO17 KO18	gnd	0.989 0.998	94 94	< 0.01 < 0.01
KO18 KO19	rpe	0.998	9 <del>4</del> 88	< 0.01
KO20	rpiA rpiB	0.999	94	< 0.01
KO20 KO21	tktA	0.995	9 <del>4</del> 94	< 0.01
KO21	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 A Expression ratio values for all measured components (mRNA, qRT-PCR)

1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 1985 | 19 See a see a

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

1.00	1.00 1.00 1.02 1.02 1.12 0.73	0.91 1.08 0.47 1.00 0.74 1.17 0.94 0.99	0.89	1.01 0.90 1.00 0.71 1.01	1.00	0.44	1.13 0.96 0.83 1.09 1.10 0.77 0.06	0.94 1.02 1.00 1.00 1.31 1.17	0.55	0.80 1.19 0.99 0.80 1.35
0.85	0.96 1.08 1.15 1.19 1.10 1.01	1.02 0.83 0.83 1.23 1.13 1.13 0.88	1.05 2.32 0.95	1.06 1.10 1.23 1.02 1.02	1.12	0.50	1.46 0.98 1.13 2.51 1.05 0.12 0.96	451 451 451 451 451 451 451 451	1.28	0.96 1.00 0.97 0.59 1.21
0.62	1.23 0.78 0.93 0.94 1.15 0.98	1.01 1.20 1.00 0.69 0.90 1.15 1.18	0.80 0.72 0.86	1.04 1.01 1.01 0.99 0.73	0.84	0.35	1.00 0.84 0.80 1.01 1.70 0.61 0.61 0.88	1.24 0.95 0.94 0.88 0.11 1.11 1.21	0.88	1.00 0.97 1.00 0.73 1.21
1.25	1.08 1.05 1.12 1.00 1.16	1.01 1.08 1.08 1.124 1.02 0.90 0.90	1.03	0.66 1.19 1.07 1.08 1.26 1.00	1.14	1.01	0.91 1.16 1.15 1.00 0.64 1.52 1.00 1.40	0.64 1.33 1.23 1.23 0.88 0.88	1.00	0.62 1.17 1.04 0.93 0.98
1.17	0.98 1.06 0.78 0.93 1.00 1.21	0.82 0.88 1.17 0.74 1.40 0.93 0.98 1.02	1.2.0 1.0.0	0.61 1.04 0.84 1.10 0.87	1.08	1.45	0.94 1.59 1.00 0.87 0.98 1.39 1.25 1.55	0.85 1.16 1.13 1.05 0.89 0.94	0.94	0.76 0.91 1.28 0.88 0.88
1.11	0.80 0.82 0.82 0.82 0.86 0.81	0.76 0.95 0.95 0.85 0.95 0.70 0.70	0.92 0.92 0.97 1.12 0.98	0.43 0.76 0.96 0.96 0.81	0.85	1.00	0.65 0.94 0.94 0.98 0.84 0.84 1.10	0.73 1.00 0.98 0.72 0.87 0.62	1.10	1.37 0.72 1.24 0.81 0.92
1.24	1.92 0.96 1.04 1.43 1.74 0.98	1.83 0.81 0.48 0.89 2.34 2.01	1.34 0.95 1.67 2.34	3.50 0.68 0.82 0.79 1.08	1.07	1.19	1.08 1.47 1.95 1.55 0.75 0.63 1.48 1.19 0.49	1.37 0.58 0.90 0.90 0.95 0.99	2.17	7.32 1.23 1.45 1.00 1.75
0.63	1.47 0.90 0.97 1.06 0.96 0.97 0.85	1.00 0.56 1.06 1.00 1.00 1.01	1.01 0.98 1.02	1.33 1.00 1.00 0.73 1.20	0.81	0.58	1.04 1.00 0.87 0.98 1.67 0.87 1.12 0.13	1.07 0.87 0.80 0.80 1.11 0.90	0.84	0.92 0.92 0.91 1.11 0.91
1.37	0.51 1.00 1.100 0.93 0.93	0.96 0.34 0.34 0.81 1.11 0.89 0.40	1.00 0.63 0.91 0.98	0.88 0.92 0.97 1.26 0.92 0.97	1.46	1.00	0.1 0.84 0.1 0.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	0.91 0.93 0.93 1.15 1.15	0.67	0.63 0.89 1.00 1.00 0.71
1.77	0.94 1.02 1.07 0.87 1.08 1.06	1.03 1.06 1.14 1.18 0.90 0.90 1.17	1.02 1.12 1.09	1.02 0.91 1.03 1.12 1.22	1.12	1.01	1.16 0.99 0.80 1.08 1.15 1.06	0.79 0.94 0.99 0.82 0.99 0.99	1.53	0.93 0.93 1.16 0.98 1.11
0.65	0.82 0.95 0.93 0.89 0.93	0.96 0.85 0.80 1.00 0.97 0.94 0.93	0.87 1.00 1.01	1.00 1.03 1.01 0.91 0.95	0.86	1.00	0.92 0.86 0.86 0.88 0.83 0.83 0.00 1.00	0.99 1.00 0.97 1.02 1.02 1.00	0.92	0.96 1.00 0.96 0.97
1.00	1.01 1.06 1.08 1.05 1.05 1.05	1.06 1.14 1.02 0.95 1.06 1.14 1.00 0.73	1.25 0.96 1.03	1.22 1.00 1.00 0.98 0.82	1.00	1.00	1.08 0.96 0.98 0.08 0.08 0.88 0.88	0.92 0.99 0.99 0.99 0.99 0.97	1.00	1.03 0.74 1.09 0.96 1.00
0.82	00.1.1.00	1.00 1.05 0.96 0.96 0.96 1.27 1.09	1.00 1.10 0.96 1.00	0.92 0.94 0.96 1.00	1.00	96.0	0.93 1.00 1.00 1.00 0.99 0.83	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	1.08	0.92 1.04 1.10 1.15
0.95	1.06 1.10 1.31 0.95 0.90 1.00	0.97 0.79 0.79 1.10 0.93 0.83 0.61	1.62 0.90 0.74 0.95	0.98 1.09 1.23 0.89 1.07	0.94	1.38	1.10 1.10 1.28 1.28 0.92 0.96 0.96 0.96	0.49 0.00 0.92 0.93 0.93 0.93	0.62	0.99 1.16 0.96 1.31 1.15
1.05	0.69 0.85 0.93 1.13 1.10	1.03 0.97 0.69 0.87 1.16 1.15 1.15 0.45	0.89 1.12 1.22 0.91	1.05 1.09 1.11 0.59 0.79 0.93	0.80	0.96	0.78 0.87 0.97 1.20 0.64 0.87	1.51 0.92 0.60 0.60 1.12 0.80	1.25	1.07
0.84	0.1.1.00.1.00.0.1.00.0.1.00.0.1.00.0.1.00.0.1.0	1.32 1.00 1.23 0.99 1.06 1.76	1.43 0.66 1.24 1.17	1.20 1.03 1.00 1.38	1.00	1.26	2,202 2,202 2,035	1.32 1.32 1.32 1.32 1.32 1.32	1.00	1.10 0.95 0.65 0.65 1.00
1.24	1.52 1.28 1.33 1.51 1.51 1.51	1.24 1.00 1.00 1.32 1.32 0.54	1.73 1.03 1.28	0.1. 7.2. 1.30 1.30 4.1	0.90	0.80	0.64 0.76 0.76 1.00 0.92 0.53 0.74 0.67	24.1.100 0.90 1.4.5 23.1.03	0.72	1.05 1.05 1.05 1.09 1.09
0.90	1.14 0.85 0.90 1.00 1.08	1.00 0.77 0.77 0.85 0.86 0.87 0.98	0.1. 1.00 1.00 1.00	0.89 1.00 1.01 1.00 1.00	0.86	1.08	0.76 0.89 0.56 0.58 0.10 0.10 0.10 0.10 0.10 0.10 0.10 0.1	0.98 0.68 0.75 0.59 0.97	2.27	0.75 0.78 0.83 0.68 0.96 0.96
1.27	0.97 0.91 0.60 0.85 0.97	1.02 0.96 0.64 1.22 0.83 1.16 0.78 1.22	1.00 0.72 0.85 1.03	0.98 0.91 1.05 0.98 1.28 0.74	1.06	1.05	0.9 1.16 1.01 1.01 1.21 0.56 0.56	1.14 0.098 0.79 0.80	1.21	0.79 0.87 0.89 0.95 0.96
0.79	10.87 0.81 1.02 0.93 0.93 0.83	0.79 0.70 0.70 0.86 1.79 1.45 0.86	1.00 0.91 0.81	0.87 1.05 1.04 1.02 0.67	0.82	0.79	0.85 0.79 0.94 0.96 0.96 0.90 0.70	0.67 0.85 0.99 0.69 1.00 0.84	0.55	0.88 0.73 1.25 0.87 1.13
0.64	1.00 1.03 0.98 1.07 1.34 0.96	0.94 0.58 0.78 0.90 0.90 0.96 0.36	0.77 1.55 1.12 0.87	1.05 0.95 0.79 0.98 0.28 1.40	0.94	0.71	0.90 0.75 1.02 1.12 0.79 0.38 0.83 1.07	1.14 1.39 0.50 0.30 0.81 1.16	1.61	0.69 0.85 1.26 1.24 1.37
0.91	0.64 1.10 1.53 1.03 1.03	1.10 1.04 1.11 1.13 1.04 1.12 0.68	0.52 1.87 1.08 1.21	1.20 1.20 0.96 0.97 0.77	0.83	0.95	0.84 0.79 0.73 0.81 1.96 0.93 0.93	0.72 0.68 1.02 1.02 1.09 1.32	0.86	2.38 1.50 1.05 0.75 0.84
1.00	0.19 1.11 0.70 0.62 0.83 0.94 1.32	0.74 1.35 1.33 0.89 0.68 0.52 0.88 1.35	1.44 0.48 0.92 0.99	0.92 0.87 0.81 1.17 1.51 0.64	1.53	1.72	1.22 1.32 1.40 0.94 1.23 1.89 2.09 0.97	0.86 0.92 1.54 1.05 1.00 1.41	1.08	1.45 1.15 0.93 0.92 1.05
1.01	0.93 1.04 1.03 1.04 1.00 0.91	1.03 0.99 0.98 0.79 0.79 1.00 1.00 1.00	0.97 0.91 0.91 0.91	0.98 1.15 1.05 1.12 1.55 1.29	1.10	1.04	1.09 1.09 0.10 0.88 0.88 1.11 1.10 1.00	1.09 1.10 1.22 1.15 0.85 0.90	0.82	0.170 0.99 0.100 0.93
1.00	2.73 1.78 1.84 1.55 2.35 1.36	2.59 0.90 0.90 0.93 0.93 1.00	1.04 1.18 2.32 1.30	1.00 1.20 1.00 0.17 3.96	0.55	0.78	0.95 0.95 1.76 1.79 0.38 0.24 0.97 0.63	0.24 0.64 0.23 1.00 2.71	2.33	3.67 1.22 3.26 1.58
1.82	0.56 1.39 1.00 1.00 1.00	1.42 1.00 0.56 0.56 1.23 1.37	0.60 0.85 1.29	1.19 1.29 1.02 0.83 0.52	0.85	0.69	0.89 0.85 0.92 0.63 0.63 0.63	0.52 0.71 0.07 1.34 0.62	1.00	1.00 0.74 1.11 1.75 1.21
0.66	1.17 0.95 0.88 0.67 1.00 0.61	0.84 1.00 0.42 1.00 1.00 0.31 0.58	0.21 0.70 0.98 0.73	0.52 0.51 0.87 1.06 1.00 0.77	1.00	1.00	0.95 0.72 0.96 0.85 1.09 1.50	1.00 1.00 1.06 0.69 0.64 1.07	0.35	0.75 0.51 1.00 0.95 1.06
1.09	0.49 0.87 0.82 0.82 0.54 0.79	1.00 0.71 0.79 1.24 2.97 0.82 1.00	1.09 1.00 0.67 0.49	1.03 0.97 0.93 1.29 0.93	45.	1.16	2.51 1.00 1.00 2.51 2.51 2.51 2.51	1.69 1.57 1.00 1.31 1.02 1.00 1.00	0.83	0.69 1.37 0.65 0.36 0.68
).49 ).71		2.98 1.25 1.38 1.38 2.44 1.32 0.97	00100	7.41 1.00 1.06 1.18 1.18	69.1	1.34		81 23 38 45 93	1.36	1.11 1.00 0.93 0.99 1.00 0.82
	_			_						400.1.1.00.1.1.00.1.1.1.00.1.1.1.1.1.1.1
1.34				1.02 1.05 1.09 1.23 1.23 1.84	1.34	1.34 0		_		0.86 1.15 1.15 1.45 1.00 1.00 1.00 1.00
1.87					•					0.81 0.82 0.99 0.99 1.095 1.095
69 0	0.78 0.92 0.92 0.92 0.92 0.93 0.93	1.00 1.24 1.07 1.07 1.08 0.81 0.81 0.81 0.81 0.81 0.81 0.81	1.07 0.97 0.1.10 0.92	0.94 0.99 0.99 0.1.10 1.48 1.39		0.95	0.96 0.100 0.1131 1.19 0.17 1.09 1.09 1.71		0.76	0.77 1.67 0.75 0.93 0.108 0.124
		0	. 5 - 5		-	٠.٠	2		٠,٧	2.00++
	7 134 100 049 1.09 066 182 1.00 1.01 1.00 064 0.79 1.27 0.90 1.24 0.84 1.05 0.95 082 1.00 0.65 1.77 1.37 0.63 1.24 1.11 1.17 1.25 0.62 0.85 1.10 0.77 0.71 1.12 0.72 1.00 1.71 1.05 0.87 0.97 0.71 0.71 0.71 0.71 0.71 0.71 0.71 0.7	134 100 049 112 026 182 100 160 183 120 113 0 10 10 10 10 10 10 10 10 10 10 10 10 1	134 100 649 1109 066 182 100 101 101 101 101 101 101 101 101 10	143 100 0449 162 162 162 162 163 143 140 140 140 140 140 140 140 140 140 140	1.0   1.0	1.0. 1.0. 0.49 11.2 0.56 11.2 1.0. 1.0. 1.0. 1.0. 1.0. 1.0. 1.0.	14   10   0.44   110   0.64	1,	1	1

Table S7 C Expression ratio values for all measured components (Metabolite, Anion).

	RF					GR			1	KO																							ı
	RF02-1 RF03-2 RF04-3 RF0	03-2 RF	04-3 RF	-05-4 RF06-	2	1h.1 0.4h	_	0.5h <sup>-1</sup> 0.7	0.7h <sup>-1</sup>	galM	JK F	d mb	gip	pfkA p	pfkB f	bp f		gapC	gpmA g	gpmB p	pykA p	pykF pg	ppsA zwt	vf pgl	l gnd	di p	e rpiA	ď	tktA	tktB	tal	talB	1
Pyruvate	0.54								1.00		0.88	1.68			99.1	0.1	0.74									1.00	2.00	0.93 (	0.80	07 0.55		1.08	2
D-Hydroxybutanoate Methyl sulfate			0.74	1,5					0.66	100	50	0.0	1 17	0.85	134	90.1	100	100	0.83	00 0	0.88	0.88	114	1 00	7,	16	0.74						u
Fumarate		1.25		0	93		0.77	1.02	00.1	8	0.80	0.57	-	24.	8	9	133	3	3	0.95	0.45	0.99	194	3	8	5 5	1.72	_	_		_		, 0
4-Oxopentanoate	3.37	0.75			1.22	0.14	0.42	0.14	1.02	1.00	1.55	Ξ:	5.55	1.00	0.89	0.88		0.98		1.3	1.57	1.65	0.79	1.63	4.1	0.05	5.11		0.90	0.85 0.	0.56	1.09 0.91	_
2-Oxopentanoate Hexanoate	1.92	.,	2.85								1.15	100			989	0.69							100			9.	122	_				-	9
Succinate				0.59 1.	00:	1.20	06.0	0.61	1.94	1.23	1.07	0.99	1.22	1.38	1.24	1.00	0.98	0.78		1.00	0.98	1.03	1.29	69.0	1.13	98.0	100.	1.09	0.66 0	0.95 0.	0.48 1.	1.13 1.1	1.12
2-Hydroxypentanoate Benzoate		1.01	1.58	-	99:	0.81	0.89	1.1	1.68	0.36	1.71	1.26		0.83	0.81	0.72	9 9		1.29	2 8 9 9 9	1.00	0.60	0.27			1.33	1.58	1.31	-			_	6
Isethionate				•	9					,	1.00		i	,			0		0	,	8	0		0	9	8							,
Unaconate 4-Oxohexanoate	1.14	1.04	0.77	0.76	2. 29. 12	0.36	0.61	0.91	1.30	0.56	5 4	1.09	1.15	8 6	0.91	0.68	1.21	20,	3.28	1.16	3 8	1.11	0.69	0.89	1.25	0.99	2.14	1.47	0.41	1.28 0.	0.55	0.86 0.45	- 40
4-Acetylbulanoate Hartanoata	2.10		114								1.37	1.04			9.0	0.93	1.00									1.00	1.00	-		-	**	0	9
Malate	0.61	0.81	1.03	0	06:0	5.60	1.15	1.00	1.00	1.02	0.87	0.88		1.73	8.5	1.08	0.97			0.67	0.51	1.00	2.17		1.00	1.13	1.09	1.21	0.43 0	0.91 0.	0.68 1.	1.67 2.69	6
o-Hydroxybenzoate Octanoate		_	0.52								1.42	2.88			88	0.39	1.11																
2-Oxoglutarate						1.00				0.77	0.99				1.01	0.79	1.12			1.05			1.00			2.31					_		4
Glutamate	0.94	0.94	1.03	1.22	8 8	0.75	1.63	1.62	0.97	2.5	0.52	0.19	0.43	0.50	9 5	0.85	1.12	1.06	1.15	2.71	9.0	0.78	0.83	1.03	0.75	1.61	0.96	0.97	3.36	77.	7.82	1.03	9 0
3-Phenylpropionate					3	2	3	9	0.95	0.73	1.00	1.1	1.00	5	0.91	0.50	0.83	5	4.74	3.74	0.54	0.44	0.00	4.29	3	1.67	3.76	3.07	_	Ī	0.31	_	, 0
Phosphoenolpyruvate		1.10			88, 88	0.38	1.46	9 5	00.1	0.50	0.70	0.48		0.27	1.56	1.68	1.00			.38	1.45	1.00	0.52		0.56	0.64	0.38	0.83		_		1.13	e 0
Diriyu oxyacetorie prospirate Grycerophosphorate	0.58	1.30		1.18	8 25	0.88	0.95	0.85	0.81	1.00	0.72	0.65	1.31	8.5	1.37	1.31	1.00	0.68		1.01	0.53	0.84	1.12	1.69	9.6	0.50	0.72		1 76.0	1.04	0.41 1.	1.03	0 0
Decanoale											1.00	1.04			0.60	0.27	1.61																
Phenyl phosphate cis-Aconitate											2.13	0.97			0.62	1.03																	
Shikimate	į												96.0							!		!			:	;	1.00						
N-Acetylaspartate Carbamoylaspartate	0.91	0.1.1	1.0	2.24	8 8	0.87	1.11 2	0.89	2.30	9.0	0.31	0.22	0.28	9,3	1.13	1.0	0.68	1.07	1.19	4. K.	0.50	0.68	0.54	0.76	0.60	1.91	3.87	33	0 0	0.444	0.60	184	£ £ :
p-Hydroxyphenylpyruvate 4-Pyridoxate		1.04							1.49	0.73	2.40	0.79	1.00		0.24	121				8	0.67	0.82	01.1			8.	1.83			_		_	0
3-Phosphoglycerate Azelaate	1.53	1.35	1.38		2.10	0.01	1.12	0.82	2.68	0.68	0.76	0.55	1.08	0.21	2.84	2.55	1.00	0.92		0.88	1.27	1.02	0.80	0.59	0.42	0.82	0.39	2.70	115 0	0.43	0.40	1.68 1.24	4 1-
N-Acetylglutamate					8	0.82	2.68	4.85	4.17	1.00	1.03		o o		96'0	0.97		100	4.83	4.45	0.75	0.67	69.0	0.48	0.73	1.7		1.56	_	_	-		80
Phenaceturate				2					5				7.89					0.99						9.0				3			5	3	
Dodecanoate Sebacate		98		0.74						1 07	1.00	1.88	104	105	25 E	0.34	113	0.97		0.48	8	00	10		98	0.33		00.					
Benzylsuccinate		1.24								1.42										1.28	0.86	1.00	0.79										
2-Deoxyribose 1-phosphate Pantothenate	1.06	1.26		1.17	4.8	0.89	0.99	1.35	1.85	1.16	0.90	0.28	0.93	8 8	1.20	0 0	1.14	0.83		8 =	0.52	0.74	0.99	0.72	96.0		3.00			-		1.28	1.52
Ribulose 5-phosphate			1.08		8	1.58	0.72	0.76	1.19	0.88	0.73	0.72	2.11	2.37	1.28	0.92	1.46	0.50		9: 5	0.89	1.15	1.16	0.50	4.0	_	7.68			-			0 0
Dodecanedioate		0.88		5		5		3	9	1.13	2.32	0.81		1.05		1.00				0.72	1.09	1.07	8 8	1.00	96.0		1.12	-	_				,
2-Deoxyglucose 6-phosphate Pvridoxal 5-phosphate	0.99	1.40								0.90	1.04	0.49			8 2	1.18	1.38	8 8		8 8	0.51	0.30	0.90			1.61	135	0.53	1.00	0.0	0.50	1.55 2.17	~ !
Glucosamine 6-phosphate	0.68			_	93	98'0	1.00	1.28	1.27	1.04	0.87	0.59		0.62	1.05	1.05	1.06	0.58		1.22	0.85	0.77	0.98	0.58	0.38		1.12		Ĭ	-			0
Glucose 1-phosphate Fundose 6-phosphate	0.21		1.39	0.86	8 S	0.86	0.96	1.47	1.00	0.78	0.50	0.31		9.85	1.90	1.35	0.65	0.58		8 5	0.7	0.58	8 8	1.32	9.6		2.20					-	
Glucose 6-phosphate	0.54			_	88	171	0.77	1.06	0.37	0.77	0.41	0.27	0.49	5.18	1.07	0.75	1.33	0.63	1.01	0.91	8 6	1.38	0.89	1.76	0.68		3.40		_	_			
Sorbitol 6-phosphate	0.44	1.00		_	8	2.36	69.0	1.19	0.70	0.70	0.43	0.30	1.30	4.50	1,33	0.83	1.74		1.18	1.15	0.91	1.25	4 5		0.59		6.17		_	_			9
Galacturonale 1-phosphate	1.00									3					3					3													
6-Phosphogluconate Sedobartubes-7-phosphate	0.20		205	0 05	Ę	0.33	0.85	0,60	105	83	0.75	0.42	-	4 78	-	125	1.67	0.64		0.04	0 63	100	00	0 77	797		0.98	1.02		0 47 0	-	15 5.59	α
Argininosuccinate					2	2		3	2	1.00	0.87	0.25		2	1.24	1.00	1.55	5		8	0.80	0.65	1.18	-	5		=	0.89			8		,
N-Acety/glucosamine 1-phosphate Fructose 1,6-diphosphate		1.00		÷	00'	7.04	1.00	1.18		0.98	1.61	1.00		0.71	1.28	1.29	1.16			0.90	0.63	2.10	1.00			1.55	1.09	1.15	.53	0.71 0.		0.94	0.9
Bis (p-nitrophenyl) phosphate Isobut/lamine	0.65	1.61	0.53	0.45	=	100	0.91	0.87	0.58	100	1.39		0.45			0.61	1.47	3.17		0.52	0.85	133	138	1.42		0.45			-	00	0.98	1.44	6
	L	L	ı			ı		ı		3			2								9	2	2							ı	l	l	ı

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

	L		5			S																				1
ē	RF02 RF03 RF04	RF05 RF06	0.1h <sup>-1</sup> 0.4h	0	0.7h <sup>-1</sup>	galM glk	glk pgm	pgi	J. J.	pfkB fbp	fbaB	gapC	6	gbmB	pykA p	pykF pp	ppsA zwf	zwf pgl s	bug	ф	hid	rpiB	ktA	tktB ta	talA tall	talB
lsopropanolamine	1.05	50.		_	1.00	8.0	90.70	0.80	87.0	3	# #	9	0.72	3			94.	Ä.	8	0.00		0.80	1.00	ē.	2.64	82 4
Trimethylamine N-oxide	0.94	1.29 1.42			0.76	0.60		2.53	1.37			0.62		1.06	1.39	1.19	0.82	1.20 1.	1.00							
Piperidine Poamylamine 1,4-Butandamine	0.61 0.82 1.00 1.30	0.80	1.19 0 1.35 0 0.81 0	0.81 0.65 0.97 1.03	1.65	1.19	1.41 1.02 1.83 1.19 0.77 0.59	1.16		0.63 0.0	0.73 1.56 1.01	1 0.84	2 4 8	3.55	4.0	0.75	0 021	0.70	0.93	3 0.83	0.45	1.36	888	0.52	1.30	17
Ala Ata-Ala 3-Amino-1,2-propanediol				.06 1.34 .50 1.31	1.55										98:0	1:00			1.59 1.1			1.21	1.15 0.82 1.37	0.87	_	1.18
Aniline 1.5-John Inopentane		,			6									•	5							6	1.00	3	8	ä
GABA Alpha-Aminoisobutyrate Natarivalanina	0.90 0.87 0.99	1.40		1.54 1.69	1.00	8.0	1.35 0.78		5.0		1.00 0.65	2 1.00		96.1	1.15	1.03	0.70	30	0.64 1.00	100.	0.92	1.68	1.24	0.75	9.6	1.16
NVerlygalarine NVimetryglycine Ser	1.00 0.56 0.96 1.13 1.94	1.13	1.00		1.29	_	1.00	0.71		220.0	0.91	5 0.47	1.97	0.99	0.1	2.40		0.87 2.			_	0.95	2.16	1.40		9
Dethandamine Cytosine Hietamine	1.18	0		0.70 0.77	3.21	0.39	1.06 1.20		84:	_	12 1.12 B1 0.83				0.69	1.07	1.59	_	0.95 0.69	9 0.98	0.82	1.10	1.33	0.56		0.79
Creating Creation 2-Mercanto-1-methylimidazole	1.00		100		1.55	-			0		_									1.41			1.00		0.72	
Pro Guanidoacetate	0.64 0.86 1.20	1.14 1.00		2.00 1.26	1.07	1.00	0.79 0.46	0.73	0.54	0 00.1	0.85 1.08	8 0.93	1.33	1.59	0.84	0.98	1.11	0.81	1.47 1.30		_	1.04	1.45	1.07		0.83
Betaine Val	1.20 1.17	1.08	1.00	1.16 1.00	1.16	_		0.52	0.66	_				1.25	0.93	1.07	.00	1.14	68.0 90.1	9 1.00	1.24	1.47	1.17	0.89	99.1	96.0
Benzimnazoe 2.4-Deminazoe Thomoserine Thr	0.80 0.94 1.00	1.41 1.44 1.00 1.00 1.00	1.03 0	0.97 0.16 1.10 0.97 2.53 1.91	1.62	0.78	1.05 0.29 1.68 0.85 1.96 0.74	0.96	0.95	1.75	1.31 1.00 1.95 0.95 1.76 1.17	1.01	0.73	5.4.5	1.11	0.90	0.95 0	0.95 1.0	1.00 1.17 0.85 1.77 0.99	0.61	1.20	1.35	1.46	0.93	0.96	1.65
Benzamidine Cys																						1.00	0.97	0.95	1.16	34
2-Amino-2-(hydrox ymethyl)-1,3-propanediol alpha-Methylbenzylamine				0.57	;																0.41		1.00		į	:
Nootinamide 5-Methykoyosine 1-Makahistamina	1.64 0.94	1.07		0.68 0.69	69:0	94.	1.00 0.83 1.47	1.48	1.7	- 5 - 0 -	0.77	7 0.93		1:00	0.65	0.80	0 09:1	0.51 0.44	4 29	••	5.38	0.29	1.00	0.29	. 52.	06:1
Melanine 5-Oxoprdine	1.00 1.01 1.14 1.05 1.48	1.22 0.79	1.08	1.53 3.06 1.00	1.65	0.65	0.76 0.72	0.52	0.43	60	82 58 1.55	5 0.78	0.93	0.63	1.00	2.17	1.00 0	0.74 1.	1.13	0.45	0.52	1.00	1.77	96.0	2.28	1.20
1-Amino-1-cyclopentanecarboxylate Pipecolate Metronomia	1.10		1.00										06:0										8 8 8			
Mettornin Octyamine N-Acatyloufrascine	0.92		1.00	0.76		-			0	0.96	26		1.08										388			
Agmatine Hydroxyproline	0.48					-			-		10		0.78													
beta-Guanidinopropionate Creatine Itaal au	0.78	2	1.89	1.00 0.54	4	8	1.23 0.94	80	940	0.78 0.	0.87	0.67	1.06		02.0	23	5	9	8	0.78			995		8	
Fen 		2			2										3	3			B	,			3		3	
Bis (3-aminopropyl) amine	0.65 1.00 1.01	1.26	0.70		1.32				0.60					1.33	0.91	0.58	10.1					1.19	1.05	0.74	0.97	.03
Orntrine Orntrine 2-Aminobenzimidazole	30	13.0		1.83 1.37	1.52			-						1.03	0.82	0.89						0.93	0.09	9.8		60.
Adenine Acetanliide	1.71	1.05			1.20	0.1	0.94 1.25				88 0.58 00 1.83			1.31	0.93	99.0						1.97	0.57	1.12		0.88
Hypoxanthine 1-Metrylnicotinamide	0.80 1.59 0.93	0.95 1.10	0.56	1.00 0.66	0.85		1.05 1.39	1.81	1.03		1.01 0.6	4 1.05	_	0.52	1.12	0.56	1.19 0	0.61	0.57 1.00	_		1.18	1.00	1.16	1.18	125
Anthraniate p-Aminobenzoate	0.91										5 50		1.00		1.00					1.37	0.86	1.00				
l yramine beta-hdroxyphenethylamine I monoreda	0.68	30	200	000	4.00	N C	233 1.34	0 24	2 6	68 6	1.06	070						3 60	g		2	0 0	240	5	20	200
Hexamethyene tetramine Histidinol	1.02 0.68				1.00	, 1.99			_		_			2.37	0.46	0.27	, 01	, –	.58 0.77		0.35	0.59	1.32	0.83		1.20
Ectoine gamma-Guanidinobutyrate	77.0				1.00		1.				89 0.69	6	1.25										1.00			
Acetylcholine Spermidine Gin	0.92 0.93	~	1.71 0	0.91 1.00	1.08		3.33	0.38	0.53	0.89	1.00	7 092		90	1.71	0.75	0.52	3.	3.05	122	103	35	2.82	0.73	98	25
5.6-Dimethylbenzimidazol Lys		1.07			0.97	1.00	.50 1.00 80 0.50							1.35	0.92					4	_	1.25	1.00	0.87		0.84
Carbachol Glu-Abizzilne C. A.carbacina					4.	-			_	_	92		1.25	98	0 74	4	•			~		0 83	0.1	Ę		á
Met Triethanolamine	0.97 1.00 1.27	0.92 1.00	1.00	1.49 1.69 2.79 1.01	2.98	0.95	.86 0.75 .06 0.75	0.81	0.87	1.00	1.86	6 0.77 7 0.18	1.50	1.18	0.87	1.00	1.15 2	271	0.75 1.65	144	1.09	1.24	0.73	0.92	1.88	1.03
Guanine 1-Adamantanamine	1.47	0.84			1.28		1.20 1.61			•	0.94 0.8			0.72	1.00	0.58				_	_	0.99	1.01	1.39		22
Mesalamine Nomega-Acetyhistamine	1.00			.63							1.30		1.02										1.00			
Pseudopelletierine His Indias 2 control to the	0.92 1.12 1.34	1.28	0.96 1	1.93 0.71	1.16	0.88	07.0	0.44	0.63	1.00	86 0.98	8 0.33	1.26	1.00	96:0	1.34		.1 76.0	1.47 0.81	1 0.72	0.52	1.05	1.48	1.10	1.63	96.0
induce of acceptance by the Ala-Ala-Ala-Ala-Ala-Ala-Ala-Ala-Ala-Ala-	1.00 1.00	1.29	1.00	0.86 0.96	0.77	_		0.70			1.02 1.26		1.31	1.80	1.00			1.27 1.			_	1.17	1.07	0.78		00
alpha-Aminoadipate N-Methyglutamate	0.98 1.14	1.15		_		0.83	_				0.89	0.85		1.39	1.00	1.01	98.0	÷	1.80	0.88	1.00	1.37	1.02	0.79		.05
Camitine Prenin Pre	0.85 0.89 1.74 1.17 1.10 1.31	1.20 1.12 0.90 1.00	0.06	1.27 0.64 1.00 1.47 1.21 0.83	1.19 2.49 0.92	1.18	1.60 1.59 0.60 0.57 1.06 0.81	2.05	0.05	0.96	1.05 1.00 1.17 3.88 0.97	0.81 7 0.80 7 0.52	1.06	0.92	1.46	0.78	0.98	- 6 -	1.17 0.92 1.57 1.24 0.87	7 0.87	1.04	1.16	4 1 1 3 4	20.0	8.8	0.66
Pyridoxal Synephrine			_																			1.01	1.49	0.94		
Pyridoxine 3-Metryfilistidine	0.47		1.00			(4 (	2.68 1.51		-	9.	;		0.95										66			
1-Methyl-4-phenyl-1,2,3,6-tetrahydropyridine	0.96					.4	2.35			-	00												1.00			1

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

	L					5				5																						1
	RF02 RF	RF03 RF	RF04 RF0	2	RF06	0.1h <sup>-1</sup> 0	0.4h <sup>-1</sup> 0.	0.56 0	0.7h	dalM	ak	od mbd	pa iba	pfkA pfi	ofkB fbo		fbaB qapC	OC GDMA	A apmB	B pvkA	DVKF	Asda	Zwf	lpd	dnd	me	Mig	roiB	tktA	tktB	talA	talB
N-Acetylomithine		0.64	0.94 0	0.95		0,0	_	١	1.07	1.48	1.06	l				89		١.,	1_		m	۱.	0 0.36		9 1.60	Ι.	0.96		1.53	1.04	0.85	1.52
n-Emyguiamine Arg	0.47	0.80		0.91	0.86	86	1.85	1.75	1.51	1.1	0.94	0.54	0.43	09:0	1.12	1.14	1.12	1.09 0.		99.0 0.0	36 0.47	1.00	0 0.29	9 1.38	8 1.23	1.49	0.79	0.82	1.22	1.02	1.03	96.0
2-Guanidinobenzimidazole	1 26	4	9.5		485	1.00	7	5	90	080	0.88	6	0.73	52	9	, ,	5	1.	1.29	000	145	0.78	0 0	0 05	100	0 33	1 36	5	1.00	0	5	4
Cys-Gly						0.35	ŧ	3	90:	60.0	0.00	0.0	t		9														0.73	0.89	1.00	09.9
Glucosamine Tyr		66'0	0.96 1	0.64	1.00	1.14	1.19	1.30	1.36	09.0	1.27	0.81	4.03	1.23	1.16	0.83	0.83	0.78 1.	1.00	1.00	1.13 2.09	1.14	4 0.55	0.63	3 0.84	0.64	1.26	1.00	1.57	1.10	0.96	0.81
Epinephrine Nalpha-Dimettry/histdine																													9.0			
N8-Acetylspermidine Gly-Leu			0.63			2.36	1.12	0.88			1.31	1.00		0.41	0.85	1.00			4 0										9 8			
Nepsilon-Acetyllysine			66			5												•	9										1.00			
Castalrospermine 5-Methoxytryptamine+2.6-Diaminoheptanedioate			5			99:												-	5													
2,6-Diaminoheptanedioate		1.00	0.93			6				96.0	0.81	0.30			1.05	1.04	1.12	₩.		2.00 1.11	11 0.53	3 0.88	80		1.28	0.46	1.00	1.28	1.02	0.71	0.89	1.50
n-Acetynisudire Hydroxyatrazine		_	0.92			2.69	1.00	0.97			2.04	1.08			0.67	0.86		o ←	300										1.49			0.51
Arginine ethyl ester		_	0.95			1,39	0.61				1.91	0.99			1.43	92'0		-	10										1.00			
Tryptophanamide+O-Acetylcarnitine Tm			0.52	0.76		1.37	0.63		96.0		1.13	0.74	1.04	0.92	0.93	0.72	1.32		00.0	0		1.00	0	1.10	_	2.36	0.81	1.00	1.00	0.78	63	0.91
5-Methoxy-3-indoleacetate										0.82						!	1.01	0	66	÷	1.18											
N-Acetylglucosamine						0.83	1.17				1.20	1.10			06.0	0.85		•	1													
Keramine		0.86		1.00	0.67	86	1.31	1.4		1.00	1.50	0.84	0.94		0.97					1.14 0.8	30 0.65		_	0	1.61							
Thymidine+1,5-Diphenylcarbohydrazide	107		2.56 0		1.11	0.95	1.27	0.92	1.58		0.75	0.76	1.06	96.0	8.5	0.72	0.43	0.66 2.	2.73 1.		0.62	0.83	3 1.05	5 1.00		1.87	1.00	0.66	1 07	0.58	07.0	
N1-Acety/spermine	2					00.	2				2	2			3															3		
Pyridoxamine 5'-phosphate 2'-Deoxyadenosine+5'-Deoxyadenosine		0.1		1.08	1.00	1.26	1.05	1.10	1.25	1.02	0.72	0.45	0.75	0.91	1.00	. 001	1.21	0.92 0.	1.33	1.16 0.8	0.86 0.68	88.0.88	8 0.88	8 0.98	1.20	1.49	1.00	1.21	0.91	99.0	1.0	1.00
N6-Methyl-2-deoxyadenosine	6	;	0.0	•	8	00.0	5	3	9	0 10		1	5	9	5						9		000						0.0	3	5	90
Notine	0.86			0.46	8.8	0.79	1.29	5 6	20.0	0.89	1.78	3.13	1.75	1.68	0.39	1.00	0.96	0.64	0.83 0.	0.50	3 4	1.37		0.97	7 0.7	0.50	1.03	1.06	0.97	2 2	0.97	1.27
Glu-Glu 1. Motheledenoeine			1.13			1.13	0.87				214					08.0		0	87										1.74		1.00	0.94
Guanosine	0.88	1.05		0.91	06.0	001	1.23	1.28	1.07	0.95	1.58	2.05	1,44	1.32	1.08	1.00		0.93 0.		0.68	1.14 0.54	1.57	7 0.53	3 0.96	00.1				8 8	1.01	1.05	1.00
5'-Deoxy-5'-Methylthioadenosine	0.61		1.35				1.00				0.82				96.0		0.87		1.33							128	6.04	1.00	2.50	0.54	0.64	
Scopolamine Molaka Bearmelessisies ethelestes			0.80			90	000				000	6			03	90 0			20													
Nathria-Derizerolarginine en grester Glutathione	0.56	1.00			1.18	1.48	1.00	0.88	0.34	40.1	1.00	0.07	1.18	0.41	1.06	2.98	1.03 2	2.83 0.		72.0 08.1	77 0.52	2 0.87	7 0.06	6 0.78	1.51	96'0	0.25	1.00	1.38	1.07	1.00	1.24
5-Aminoimidazole-4-carboxamide-1-ribofuranosyl 5'-monophosphate	90	9	٥ ر	0.71	8				1.29	5									•						8			,	4	8	8	5
S-Lacroyglutatrilone S-Adenosylpomocysteine	080	8			8.	200				9									-	00.0	0.0	00'	0	0	0.0	74.7	1.00	3	8/-	0.02	3	3
S-Adenosylmethionine		1.27 (	0.65	1.13	1.07	0.78	1.21	1.00	1.63	0.97	1.12	0.60	0.49	0.79	1.00		1.02	0.81 0.		1.11 1.12	12 0.64	14 0.79	9 0.87	7 0.80	0 1.00	1.66		1.28	1.00	0.99	0.81	1.36
Leu-Leu- lyr Oxidized alutathione		0.73	1.43	1.36	0.33	1.00	1.15	1.32	1.43	121	2.07	0.09	0.17	0.14	1.00	0.80	1.35	0.59	1.15	0.99	0.19 1.00	0 1.69	9 1.81	1.54	4 6.56	2.88	3.89	1.09	8 8	0.27	0.89	0.63
		ı		ı									ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı	ı			١

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

	i d					g				2																						
	RF02 RF	RF03 RF	RF04 RF	F05 RF06	1	0.1h <sup>-1</sup> 0.4	0.4h <sup>-1</sup> 0.5	0.5h <sup>-1</sup> 0.7h <sup>-1</sup>	- <u>-</u>	galM	ş	d mbx	d ibd	pfkA pf	ofkB ft	fbp ft	baB ga	gapC gp	gp Amgp	gpmB pykA	A pykF	F ppsA	A zwf	lbd	bug	be	hid	15	tktA	tktB	talA	talB
Citrate Divalent ion from UDP-glucuronate			0.85		0.71	1.36		۰	0.93		0.63	1.00	0.43	1.00	1.19	1.10	1.32	_		1	_		_		0.87			1.09 0.91	13 0.99		1.00	0.78
Divalent ion from UDP-N-acety/glucosamine dCMP	8.6	0.1	0.93		18:	3.32	1.67		1.76	1.07	0.39		0.05	1.00	5.6	1.07	1.35		68.0			_					0.53			_	-	1:00
dWL				-	78	1.00	0.88	Ī	0.48	1.00	0.73	0.46	3.86	2.05	1.30	1.12	1.00	0.69	1.18		_						-	Ĭ	-	_		1.00
CMP+CMP-N-acetyneuramate UMP		2.32	8 4	0.62 0.6	0.65	0.89	8 8	1.98	1.33	8 6.	0.69	0.62	<del>2</del> -	6.13	1.24	9 6	1.28	0.93	0.80	5. 26.	0.67	0.73	1.47	1.32 4	129	0.63	1.04 4.3	1.75 1.22 4.39 1.27	7 0.83	3 0.74	9.9	0.89
CAMP	0.73		0.94		00	0.74	1.80		4.06	40.	0.86	1.00	0.41	1.00	20.	0.92	1.20	1.53	1.23			_	Ī									0.99
CGMP	1.25		£		9.6	1.64	3 2		2.95		0.92	£.	0.69	0.94	5	90	0.92	1.51	787							3	2			_	_	0.78
AMP	1.1	1.10	66.0	-	29	124	1.00		3.04	0.86	0.86	1.00	0.87	1.19	1.49	1.01	1.07	0.79	7.0		_			_		-	_		-	-		1.15
dWI dW	1.60		9.6		25.25	128	8 8		4.30	20.0	0.85	1.04	0.88	2 2	6 4	1.05	1.13	0.88	0.77	1.19	990	1.57	1.30	0.83	. 1.	8.6	0.62	1.00 1.45	5 0.77	7 0.86 8 0.76		0.00
Divalent ion from NADPH			2.88		5	1.70	0.30		2	2	0.83	8	3	1	1.46	0.80	1.17	200	0.76							_						9
Divalent ion from CoA	97.0	2.28	1.00		00.1	1.32	0.57	0.28 1	1.00	0.58	4.08	0.98	0.87	1.59	5.46	18.87	0.69	2.18	0.49	2.04	0.32	1.36	1.45	٠.	1.29	0.1			0.79	9 0.76	2.7	1.50
ACCE.	0.98		88	_	¥ £2	1.17	0.93		3.30	8.8	0.52	0.75	0.59	2 8	6 6	40.0	123	1.19	58.0		_			20.70	_					_		1.14
CDP	0.87		1.00	_	49	121	0.99		1.00	1.00	99.0	0.52	69.0	1.77	1.24	1.18	1.50	1.00	0.70		_	_	-		-	_			-	_		1.01
UDP Disabation from Acadel CoA	0.97		98	-	8 4	0.79	9.9	-	0.59	1.00	0.60	0.58	0.9	9.5	8 5	1.29	1.59	0.98	0.72		-								-	-		1.03
Maloryl CoA	2		9		3	20.0	3		3	2	0.43	24.0	0.4	5	0.67	1.12	1.39	5	. 88.0													t.
dADP	1.02	1.00	0.1		;	1.36	0.58		2.86		0.70	0.76	į	i	1.35	1.25	1.05	0.41	66.0											-		0.88
Divalent ion from n-Propionyl CoA	0.80		1.42		8,8	1.00	2.51		1.72	00.0	0.63	0.20	0.73	0.51	9.6	87.1	1.16	1.27	1.45	_										_		1.08
Divalent ion from Isobutyryl CoA	0.80		96.0	Ĭ	88	2.00	1.00		4	0.80	0.46		1.00	1.40	0.98	1.39	1.08	0.89	102	_						_			_	_		1.1
ADP	1.08		0.1	_	2.5	1.30	0.95		1.94	0.95	0.58	99.0	0.48	1.30	1.19	1.20	1.25	0.87	98.0	_	_					_				_	_	0.92
Divalent ion from Malonyl CoA	1.10	2.4	68.0		95.00	1.17	0.88	1.16	8 5	0.95	0.42	0.23	0.33	1.24	8 8	1.19	1.06	1.88	1.1	8 9	0.35	1.58	1.01	0.64	5.6	88	0.93	3.23 2.25	1.38	5 0.73	0.00	0.84
Divalent ion from succinyl CoA				_	92	1.32	1.06		1.70				98.0	0.1				0.59						_						_		1.79
GDP	1.10		0.88	_	09	1.10	1.00			0.90	0.71	0.68	0.80	1.26	27	1.22	1.16	1.00	1.00	-	_			_						_	_	96'0
FMN	1.02	1.56	0 77		8,8	1.00	1.41		0.92	4 8	0.97	1.19	0.87	4 8 8	8.8	0.66	120	0.90	5 5	£ 5	0.40	0.50 0.	1.00			98.0	78 1.00	30 0.8	1.24			109
Divalent ion from Lauroyl CoA																1.26	0.74															
TTP	0.80	121	0.92	-	57.0	1,3	1.21	1.35	1.17	8.5	0.40	0.36	0.36	0.1	2.8	125	1.40	2.00	88	0.95	0.31	1.43	0 001	0.78 0	986	1.10	1,1	1.43 1.06				0.99
- ATD	0.75		0.97		8.8	138	1.00	_	0.97	3 8	0.44	0.26	0.36	1.50	9.1	44	1,75	1.65	8.8					_								1.03
dATP	0.85		0.86		8.28	2.65	1.00	.,	2.65	96:0	0.40	0.33	0.13	0.84	1.06	128	1.00	1.19	4:			_										1.05
AIP	0.82		0.84	-	8.8	91.19	9.6		1.26	8.6	0.39	0.25	0.30	18.0	8.8	123	90.0	1.75	- 0		-					-						1.09
GTP	1.00		0.91		. 96		1.13		1,20	8	0.45	0.24	0.20	0.68	8.5	126	00.1	1.22	1.15												_	100
ADP-ribose	0.82		1.02		88	4.48	1.00		1.98	5.04	0.41	3	0.39	2.10	96.0	0.87	1.12	0.97	90.1						. '					_		0.86
UDP-glucuse	0.87		000		3,8	3.23	100	•	1.34	. 6	0.40	0.0	0.02	3 8	1 4	104	5.1	0.90	100						-	_						0 0
ADP-glucose	0.94		1.02								0.74				4	0.95	1.32	0.64	96.0			Ĭ				_			_	_		1.06
UDP-N-acetylglucosamine		1.00	00.1	-	26.0	3.44	1.89	2.95	1.78	1.03	0.34	0.40	0.04	0.1	1.13	1.16	1.51	1.00	18.0	99.0	0.12	1.31	_	0.22 0	0.46	_		_				1.00
CMP-N-acetylneuramate			9.6		68	9.5	- 00		110	, t	0.03	0.18	0 20	2.5	3 5	5.5	7.5	0.05	9.6							•			•			96.0
Nicotinamide hypoxanthine dinucleotide			1.00		67	1.02	0.98		1.15	0.87	0.65	0.60	0.58	12	120	1.00	1.16	0.95	0.87					187		_	10.97					1.00
NADH	980	130	0.78		89 0	100	18	1 77 1	1 90	08.0	0.40	0.48	0.39	0 95	1,	117	125	103	8	90	0.25	138 1	00	0 97	28	175 0	0.7	0.75 0.18	8 1.65	5 0.89	2. 5. 52. 5	1.11
NADPH			1.19		3	2				3	i	2		3	00.	1.00	0.95											-				2
FAD	1.00	1.00	0.91	1.00 0.1	0.59	1.91	1.01	1.38	1.32		0.52	0.58		1.00	1.32	1.08	1.07	0.95	1.00	0	0.25		0	0.23 0	0.44	1.93 1.0	1.00		1.21	1 0.42	1.06	0.30

Normalized expression ratio values are shown, and were calculated by dividing the measured value by the median of the simultaneously measured samples. RF, reference sample (wild-type cells cultured at a specific growth rate of 0.2 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 h<sup>-1</sup>; WT, wild-type. RFs are denoted by Sample ID and Series ID shown in Table S2. The components marked by blank cells were either not detected or the product of the deleted gene.

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

Table S8 B Expression index values for all measured components (Protein, LC-MS/MS).

-1.89	0.00 0.00 0.00 0.15 0.03 -3.89	-1.79 0.63 -2.39 -2.39 -0.49 -0.66 -2.50	-1.07 -0.06 -2.82	0.06 -1.11 0.00 2.15 -1.49 0.05	0.00	2.07	0.30 -0.30 -1.37 -1.37 0.86 0.86 -1.94	-10.1 0.86 0.28 6.28	24.0	1.69 1.88 0.78	-2.53	1.03 1.10 3.10 3.10
1.75	0.18 0.42 0.42 0.15 0.16	0.40 0.83 0.51 0.51 0.08 0.08 0.08 0.08 0.08	0.40 5.22 -0.60	0.00 0.67 1.70 2.46 -0.63 0.09	0.92	3.68	3.75 -0.15 1.86 0.02 0.34	1.06	0.75	1.38 5.39 2.30	1.05	0.00 3.24 2.00 65
-2.24	0.90 0.74 0.54 0.54 0.31	0.140 0.00 0.00 0.89 1.26 1.26 1.26	-1.92 -3.45 -1.79	0.48 0.14 0.22 -0.12 -0.63	-1.41	0.99	0.00 -1.77 -1.77 0.16 0.00 -3.75	1.07 1.07	0.51	0.65 0.26 0.26	-0.56	0.00 -0.17 -1.97
1.04	1.47 1.21 0.50 1.62 0.00 1.82	0.27 0.03 0.33 0.34 0.07 0.07 1.13	2.38 0.33 0.82	4.93 1.92 1.11 0.88 0.98 0.00	1.08	-1.01	0.98 0.09 0.02 0.02 0.00 0.00	3.61 2.18 2.18	2.27 1.62	-0.84 -1.13	3.68	0.99 0.99 0.73 0.73
0.72	0.00 0.03 0.05 0.05 1.25 1.25 1.25 1.25 1.25 1.25 1.25 1.2	3.83 2.2.27 2.2.27 2.2.27 2.0.09 2.009 3.009 3.009	1.69 0.06 0.21 4.18	5.94 0.40 1.16 0.82 0.74	0.64	2.55 0.36	0.06 0.07 0.09 0.09 0.09 0.09 0.09 0.09 0.09	3.06.4	10.0	0.03	1.41	0.64 0.64 1.26 1.26
0.51	0.54.1.1.88 8.1.1.2.2.0 0.00	5.5.3 5.2.2 5.2.2 5.2.2 5.2.2 7.2.0 7.0.0	0.73 0.17 0.25	-10.09 -3.01 -0.43 -0.00 -1.06	-1.31	0.00	4.0.0.0.1. 8.0.00.0.1. 8.0.00.0.1.	2 + + 5 2 × 3 × 5	8.00 c 8.00 c	- 6.88 - 1.88 - 1.38	0.39	4.24.00.94
1.03	2.86 -0.64 0.00 0.00 -0.19 -0.19	11.81 -1.62 3.16 -5.46 2.01 -1.51 6.37 3.33	2.56 -0.34 5.34 9.81	44.88 4.35 4.35 0.34 1.80	0.53	1.22 -3.75	0.79 2.63 6.84 1.39 2.24 2.24 3.44 3.44 3.44 3.44 3.44 3.44	-5.05 -1.55	4.04	-2.03	3.31	9.02 1.34 0.00
-2.20	1.69 -1.56 -0.32 0.50 -0.48 -0.31 -1.96	0.00 0.73 -2.66 0.45 0.00 0.00 0.00 -1.37	0.07 0.08 -0.17 0.24	3.37 0.00 0.46 0.00 -1.38 0.93	-1.70	-3.80	0.39 -0.33 -0.33 -1.32 -1.32 -0.84	0.00	0.00	-1.32	-0.76 -0.56	2.39 -0.55 -0.88 -0.88
1.49	-2.93 -0.43 -0.00 -0.82 -1.88	0.70 -1.33 -1.51 0.84 0.89 0.65	0.00 -2.89 -1.01 -0.26	-1.49 -0.94 -0.49 -0.38 -0.38	3.10	0.00	0.63 -1.33 0.00 0.16 0.59	0.00	6.53	-0.43 1.73 2.33	-1.71	-2.12 -0.76 -2.86 0.00
2.70	-0.28 0.29 0.65 -1.08 0.97 0.75	0.52 0.43 0.98 0.98 0.98 -0.81 0.86	0.14 0.59 1.14 1.00	0.27 -1.02 0.02 0.32 0.50 1.01	1.71	0.09	1.03 0.70 0.70 0.70 0.70	0.42 -1.16	0.26	-1.24 -0.16 0.73	1.82	0.92 0.92 0.18
-2.01	0.88 0.77 1.25 1.46 0.24	0.77 0.00 0.00 0.31 0.36 0.92	-1.24 0.00 0.07 0.23	0.00 0.31 0.17 -1.12 -0.11	-1.21	0.00	0.80 -1.21 -1.15 -1.71 -1.71 -1.71	80.00	0.09	1.04	-0.38	0.00 0.00 0.27 -1.41
0.00	0.45 0.54 0.54 0.61 0.50 0.00	1.23 1.00 0.14 0.75 0.09 0.00 1.51	1.94 -0.41 0.39	2.38 0.00 0.00 0.00 0.10 0.99	-0.02	0.00	0.34 0.55 0.00 0.00 0.00	4 8 9 9	0 0 0 0	0.04	0.00	0.15 0.33 0.56 0.56
0.00	0.00 0.00 1.1.1.00 1.31	0.00 0.23 0.19 0.19 1.81 0.49	0.00 0.58 0.00 0.00	-1.01 -2.25 -1.09 -0.50 0.00	0.00	0.30	0.00 0.	0.00	96.0	-1.71 0.00 -0.10	0.34	1.10 -0.55 0.80 0.57 1.47
-0.25	0.26 2.51 0.94 -0.69 -1.09 0.00	0.54 0.20 -1.10 0.88 0.00 -0.95 0.73 -1.02 -2.36	4.24 -0.65 -3.11 -0.64	0.28 0.91 0.02 2.43 0.36	0.51	2.23	3.31 0.64 0.60 3.83 0.28 0.76 0.76	5.50 4.50 5.50 5.50 5.50	0.45	-0.07 -1.13 0.18	-2.01 0.47	0.06 0.92 0.75 1.69
0.24	-1.61 -2.50 -0.69 0.59 0.99	0.66 -0.20 -1.71 -1.00 -1.20 0.88 0.98 0.98 -3.81	-1.00 0.69 2.06 -1.09	0.57 1.00 1.83 -6.15 -0.39	-1.86	-0.98	0.94 0.95 0.26 0.26 0.26 3.32	2.03	2.97 2.97	0.42 1.40 1.26	0.95	0.06 0.41 0.77 -2.05 0.18
0.80	0.00 1.42 0.00 0.00 0.03 0.03	5.42 0.00 3.45 1.67 -0.18 0.42 3.18	3.15 -2.58 2.23 1.81	2.21 0.34 -3.56 0.00 -13.43 1.65	0.00	0.87	0.00 4.74 0.40 1.61 0.03 0.00	5.03	8 6 8 8	1.75 0.00 1.18	0.00	0.41 0.95 1.60 1.60
3.09	2.42 2.42 2.43 1.21 1.21	11.19 0.04 0.00 0.00 0.72 2.04 2.04 2.24 2.24 2.24 2.24	3.48 3.38 0.30 2.87	0.00 2.90 1.82 1.82 1.89	-0.85	0.00	4.0.0.1. 2.0.4. 2.0.00.4. 3.0.00.4.	-2.78	8 6 6 6	22.4.1	1.12	0.00 3.41 0.28 0.93
-0.49	0.59 -1.62 -2.25 -1.35 0.00 1.00	0.00 0.07 -1.19 -2.49 -1.30 -1.05 -1.05 -0.37	-7.71 1.27 0.00 0.00	1.36 0.02 0.11 7.4.7 0.00	-1.24	0.52	-2.76 1.73 -1.84 -2.79 -1.14 0.47	1.29	2.	6.33	3.50	-1.32 -3.82 -0.46
1.13	-0.45 -0.94 -4.14 -1.98 -0.32	0.37 -0.32 -2.01 1.46 -1.46 -1.54 -1.54 -1.38 0.96	-0.02 -2.04 -1.75 0.31	-0.27 -1.01 0.76 -0.28 1.07 -1.54	0.50	0.34	0.92 1.01 2.75 0.12 0.83 0.41 1.46	0.70	0.94	-1.48 -1.29	0.80	0.51 -2.70 -0.71 -0.56
-1.13 4.64	10.44 -3.28 -0.57 -0.57 -0.79 -2.25	1.64 -1.86 0.14 -1.18 7.67 0.30 0.30 0.74	0.02 1.53 -0.97 -2.37	-1.70 0.52 0.63 0.26 -1.76	-1.59	-1.60	-1.64 -1.73 -0.90 -0.42 -0.42	-0.88	0.10	0.00	-2.55 0.32	-2.05 -2.05 -0.85 -0.85
-2.08	0.00 0.44 -0.21 0.53 -0.53 -0.53	-1.29 -1.15 -0.23 -0.87 -0.30 -1.96 -3.25	-2.26 2.73 1.17 -1.55	0.53 0.55 4.05 0.27 -5.50 1.73	-0.54	-2.35 8.08	1.02 1.194 1.79 1.15 -8.98 1.40	-2.31	5.30	-7.55 -2.52 0.85	2.03	1.68 1.01 1.44 1.63
-0.90	-1.94 2.61 2.83 5.21 0.31 0.36	1.78 0.31 0.79 0.79 2.38 -3.45 0.29 0.66	-5.74 3.86 0.77 2.22	2.15 2.04 -0.65 -0.42 -1.11 0.76	-1.56	-0.36 -4.59	0.84 -1.18 -1.73 3.27 -1.01 -4.44	0.18	3.22 0.10	0.12 1.01 1.62	-0.66 5.15	3.93 2.59 0.92 -0.04
0.00	-7.37 -3.60 -5.27 -0.64 3.48	5.83 2.33 1.20 1.20 5.20 5.20 1.44 1.44	3.23 0.83 0.06	-0.99 -1.54 -3.73 1.88 1.77 -2.30	3.50	3.75	1.98 1.98 1.98 1.57 1.98 1.98 1.98 1.98 1.98 1.98	0.18	3.31	0.00	0.34	1.70 0.87 -1.38 0.64 -0.82
0.04	-0.33 0.66 0.09 0.50 0.50 1.18	0.56 0.05 0.00 0.00 0.00 0.00 0.00	-0.28 -0.57 0.00 -1.11	0.20 1.52 0.91 1.31 1.33	0.81	0.26	0.87 0.00 0.00 0.06 0.16 0.05 0.00	0.00 0.02 0.41	0.50 4.51 4.55 4.55 4.55 4.55 4.55	0.99	1.07	0.00
0.00	4.39 8.74 6.10 3.50 10.53 0.86	18.58 -0.82 -0.79 -1.00 -2.66 0.00	0.34 1.00 8.73 3.04	0.00 0.00 3.10 0.00 -7.74 7.09	4.91	-1.75 2.61	0.00 0.04 0.00 0.09 0.09 0.09 0.09 0.09	-3.22 -1.76	-3.73	0.00 0.00 5.77	3.60	5.90 2.27 4.00 7.28 4.73
2.83	2.54 0.00 0.00 0.00 0.81	6.81 2.88 2.88 4.33 1.54 1.54	4.55 1.02 2.63 2.49	2.09 2.84 0.31 -2.24 1.22	-1.30	4.03 3.05	21.1.1.09 0.00 0.00 1.69 1.69	7.09	-2.83	1.84	0.00	0.00 2.05 3.44 1.95
-1.94	-0.69 -1.22 -3.18 -5.31 -0.39	-3.38 0.00 0.00 0.00 0.00	13.64 -2.18 -0.17	-7.75 -7.49 -2.36 0.73 0.00	0.00	0.00	2.1.0.3.0.4.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0				4.49	4.29 0.00 0.00 0.57
1.00	3.10 2.05 2.01 1.63 7.753 2.552 0.00	0.00 -2.66 -1.07 1.62 14.39 -6.58 -1.11	0.04.8 6.32.8 -	0.32 0.38 0.45 0.15 0.15 0.15	2.39	1.02 -2.13 -2.16	2.52 0.00 0.00 0.03 0.03	0.00 9.46	3.74 0.00 74	0.00 0.00 0.00	0.00	68.2.69 46.89 46.39
3.37	0.00 0.00 2.05 1.53 0.06 2.35	0.33 0.12 2.38 1.81 1.94 0.16	0.00 0.00 0.00	0.68 0.00 0.00 0.71 0.00	4.33	3.18 0.00	2.28 0.98 0.98 1.12 0.77 0.23	5.86	3.01	2.35 0.84 1.24	1.32	0.46 0.00 -1.53 0.00
0.00			0.53 0.00 3.75	0.50 -1 0.00 0.00 1.53 2.12							0.14	0.16 0.00 0.00 2.67
0.00				0.26 2.51 1.47 4.30 0.88							0.37	0.71 0.90 2.28 0.04
-0.63	2.03 2.03 2.03 2.03 2.23 5.61	2.2.72 2.72 2.14 1.67 1.53 1.97 2.65 3.11	-0.14 -2.27 -1.28 0.61	2.77 2.33 0.44 0.44							-1.22	-0.97 -0.124 -1.08 -0.53
	0.64 -2.51 -0.64 -1.03 -1.03 -0.78	0.07 0.01 0.51 0.51 0.27 1.59 0.71	0.59	0.73 -0.75 -0.15 1.13 1.71		0.72	0.00 0.00 2.70 2.35 0.67				3.93	3.29 5.82 0.42
1.05 4.72	00000		1 7	1.1				. 7		, -	70	
	63 1.39 0.00 -3.37 0.41 -1.94 2.88 0.00 0.04 0.00 -2.08 -1.13 1.13 -0.49 1.00 -0.80 0.24 -0.25 -0.96 0.00 -2.01 2.70 1.49 -2.20 1.03 0.51 0.72 1.04 -2.24 1.05 0.59 0.00 6.14 -0.23 2.52 -0.99 4.64 0.99 0.00 3.09 0.40 0.60 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 1.52 0.45 0.04 0.00 0.27 1.46 0.48 0.50 2.24 0.66 1.75	138 0.00 3.37 0.41 1.94 2.83 0.00 0.04 0.04 0.00 0.04 0.	138 0.00 3.37 0.44 1.94 2.85 0.00 0.04 0.04 0.00 0.04 0.04 0.00 0.04 0.04 0.00 0.04 0.	143 0 000 3.37 0 044 1 194 0 289 0 000 0 044 0 000 0 044 0 000 0 044 0 000 0 044 0 0	14. 1 1. 1 1. 1 1. 1 1. 1 1. 1 1. 1 1.	1.0   1.0	1.0   1.0	10	10   10   10   10   10   10   10   10	1.0   1.0	1	1

Table S8 C Expression index values for all measured components (Metabolite, Anion).

													I
	RF		KO			- 1				-			
	RF02-1 RF03-2 RF04-3 RF05-4 RF06-5	0.1h" 0.4h" 0.5h" 0.7h"	gk	ogi pfkA pl	4	gpmA gpmB	pykA pykF ppsA	zwf pgl	rpe rr	rpiA rpiB	tktA tktB	talA	alB
Pyruvate	-4.80	0.00							0.00 5.39	-0.53 -1.73	0.49 4.6	68 0.63	0.85
D-Hydroxybutanoate		0 00	2.06	100	0.46 -1.81	1 24 0 40	000	9					4 10
Firmprate	3	100		137	5 5	5.5	3.35	256	210	0.73 -1.34	100	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	30
4-Oxonentanoate		-7.97 -3.51 -7.80 0.08	1.76	6.86 0.00		1.18	200	1.96					-0.38
2-Oxopentanoate			0.36						ď				-134
Hexanoate	3.33							00	0.62	-0.77			
Succinate		1.33 -0.74 -3.61 4.81		1.47 2.36	Ċ	-	-0.14 0.18	1.84 -2.68 0.90		0.63 -3.02	-0.40 -5.28	8 0.88	0.80
2-Hydroxypentanoate			-2.47 -0.01 0.00		-0.81 0.01	0.62 1.46	0.00 -1.23	20	0.69 1.11	0.65			-1.75
Benzoate	0.04	-1.17 -0.63 0.56		00.1-		0.00			90.1-				
Citraconate	1.35 4.22 -0.39	-1.04	0.74	-1.55 0.51		6.23 0.76	-1.00	-0.64					1.02
4-Oxohexanoate	0.59 0.18 -1.06 -1.13 1.02	-433 -2.04 -0.37		0.61 0.03	0.85	198	0.03 0.46	-1.53 -0.59 0.98	-0.03 3.25	167 -3.77	1.07 -2.50	0.61	-3.40
4-Acetylbulanoate			1.74						-				-5.80
Heptanoate	1.02		-0.45										
Malate	-3.55 -1.53 0.23 -0.72	12.34 0.97 0.00 0.00		3.92		-2.84	-4.88 0.00	5.55 -0.03	0.85 0.65	1.34 -6.01	-0.71 -2.72	2 3.67	7.10
O-Hydroxybenzoate	90												
Octahoate	2001-	000	99			0.45		90	00 0			1 20	00 1
2-Conglutation	-0.34 0.17 1.07	263	0.08 -351 -915	4 53	-0.90 0.59 0.30	0.75 5.42	-137					0 17	125
trans-Cinnamate		1.39 1.52	-2.20	-3.15		-	-0.46 -1.42 -0	61 0,23 -1.79		0.68 1.02	1.13		000
3-Phenylpropionate	1.26 2.86		0.00	0.00	-0.28	2.38 2.01	-1.24	2.22					-1.86
Phosphoenolpyruvate		1.00 0.00	-0.96	-3.47		0.82	0.00						0.32
Dihydroxyacetone phosphate	0.48	6.84 -4.48 0.00 0.00		0.89		000	200	90.9	0.00 16.54	0.94	9.23	0	-1.06
Olycanophol ate Decanopho	0.77	-0.20 -0.70	0.00		-273 100 -1.02		-0.03	7.30					70.0
Phenyl phosphate				8									
cis-Aconitate			2.97 -0.11	-1.89	0.11								
Shikimate				-1.00									
N-Acetylaspartate	-0.17 0.00 0.30 1.51 0.00	-2.46 2.63 6.13 8.11	0.10 -1.06 -2.86	-2.00 0.22	0.00 -0.72 -0.13	1.30 0.71	-1.65 -1.41	1.25 -0.52 -1.68	1.77 2.53	0.16 0.34	-1.52 -0.94	4 0.48	0.22
Carbamoylaspartate ptk/drox/oben/lawrin/ate	0.00	0.36 -0.41	-3.80	87.4 4	-1.80	0.58	. 0.78	-1.00		7			1.20
4-Puridoxate		200	3.71	0.00	0.81	0.0	9	5					2
3-Phosphoglycerate	1.00	0.38 -0.65	-1.25 -0.92 -2.00		3.09 0.00	0.95	0.00		-0.66 -3.12				0.71
Azelaate	-5.38 -0.05 2.63 -2.55 0.81	-1.73	0.38	0.66 -0.36	2.59	95.0	0.82 0.23 (		-5.20 2.11	8.08 3.80	0.65 -3.43		-1.06
N-Acety/glutamate	0.85	2.83		-0.11	-0.09	4.53 4.27	4.1.	-2.11	1.55	1.28 1.90		9 	1.8.1
Phenaceturate	04:1-	20.02		or or	0,00			90.0		8		ţ.	
Dodecanoate			0.00 1.56		-2.68 2.23					00:00			
Sebacate	-0.13 -2.40		4.60	0.35 0.42		-5.82	0.00	39 -0.44	8.79				
Benzylsuccinate	1.00	900			000	1.15	0.00						000
Z-Deuxyilbose I-priospriate Paniothenate	0.73	171 639	1.45	223	8.50	90.0	3 40	-3.20					-0.86
Ribulose 5-phosphate		1.54 -1.10 -0.93 0.60	-1.07	2.54 2.92 0.84	-0.26 1.29 -2.37	00:0	0.46	50 -2.33 -2.77			1.32 -2.19	99.0- 6	1.57
Ribose 5-phosphate		-1.07	0.00			0.27	-1.33	:					1.18
Dodecanedioate	-1.06		6.88	0.43	9	100	9.69	00 0.00 -0.45					2 30
Pyridoxal 5-phosphate			5		-0.13	18	1.00	8 8					0.47
Glucosamine 6-phosphate	0.00 -0.30 0.00	0.00 1.51	-0.86	-2.90	0.34	1.21	-1.60	-3.30					2.03
Glucose 1-phosphate	0.29 1.10 -0.50	-0.14 1.27	-2.27	-0.53		1.06	-1.78	0.91		Ċ			-0.05
Fructose 6-phosphate	-0.26 1.00 0.00	-1.88 -0.95	-0.96	7.81	1.64		1.20	2.06					-0.43
Glucose o-phosphate Sorbitol 6-phosphate	-2.33 0.00 0.00 -1.54 0.00	2.45 -1.08 0.19 -3.48	-100 -238 -3.12	0.76 4.29 0.24	-1.02 1.00 -1.52 -0.55 1.59	0.03	41.1 0.00	0.39 1.97 -1.30	1.09	-2 93 2 29 -2 93 2 29	0.34 -2.85	0.12	10.13
2.3-Diphosphodycerate	1.00	1:00	-2.30	0.70		_	0.00						40.
Galacturonate 1-phosphate	!												
6-Phosphogluconate			-0.72			-12.64			Ċ				
Sedoheptulose-7-phosphate Arginipositocipate	-1.80 0.65 4.45 -0.15 0.73	0.15 -0.85 -2.08 0.43	0.98 -3.52 -5.13	0.79 9.56 0.75	0.52 3.23 -2.56	0.94	-2.65 0.15 (	3.69 -1.39 -6.38	1.42 0.81	1.02 0.59	4.34 -5.22	2 0.97	10.48
N-Acetylalicosamine 1-phosphate	2.01	-0.76 0.00 0.90	2.61	•		0.85	-0.74	2 8					000
Fructose 1,6-diphosphate	0.00		-2.77	-1.58		0.46	3.45	28	_		60.9	-0.27	0.26
Bis (p-nitrophenyl) phosphate	400	0	1.00	000		2	9	200					1 1
Isobutylamine	-1.19 1.30 -1.74 -2.17 0.28	0.00 -0.26 -0.37 -1.47	0.00	-2.20	1.06 3.17	 1.8.	-0.45 0.78 (	0.89 0.95	.7.7-		0.00	00.1	1./5

Table S8 D Expression index values for all measured components (Metabolite, Cation(1)).

		1													1
	RE04 RE05	GR 04h1 04h1 05h1 0	Zh-1	muu	nfkA		Janc	annB	Ason Hybrid		bus	miA	tktΔ	talA	ı
Gly	0.32	-0.80 3.75 -0.11	3.20 -1.86	-1.75 -1.17	-0.65 -0.98 0.00	-1.91	-3.40	0.00 -0.80	1.82 1.60	-0.13 2.13	-1.00 -1.79	-2.45 -0.22		2.18 -0.27	l~
Isopropanolamine Trimethylamine N-oxide	-0.68	-1.56	0	1.00									0.00		20
Pyridine	-0.25 1.00 1.37		-1.10 -2.02	6	3.63 1.24		-1.90	0.23 1.29	0.68 -0.78	0.72 0.00			0		
Pipendine		1,83		2.03 0.60		-1.05									
1,4-Butanediamine	0.00 1.22 -1.04 0.00	-0.96 -0.15 0.15	2.33 0.82	-1.22 -2.42	0.68 -1.21 -0.5	0.32 2.07 0	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	E 4
beta-Ala	-2.86	2.72 1.60		1.82 0.73	4.4	-0.75			8					2	+ 00
3-Amino-1,Z-propanediol Aniine	1.22-	0.00					0.1						99:0		
1,5-Diaminopentane GABA	-0.07 2.48	-0.60 4.62		000		-0.11	0.00	4.39	0.00	-0.01				-0.87	G
alpha-Aminoisobutyrate	-0.95 -1.24		0.00 -1.03	1.36	-1.62 0.3	0.32 0.00 -1.		4 2.89 0.65	0.13 -1.62	-2.02	0.00 0.00	-0.36 2.34	0.97 -1.31	-0.30 0.67	_
N-N-Dimethylglygine	-8.57	00:0		0.00		-1,45									
Ser Diethanolamine	1.00 -1.29 -0.96 -0.89	2.42 1.15 -2.80	0.76 -0.95 6.10 -1.89	-1.27 -1.15	-1.01 -1.53 0.0	0.00 -2.19 0.	0.68 -2.24 2.03 0.59 -0.60 0.52	0.04 0.00	0.34 0.00	0.00 2.58	1.20 0.26	1.20 0.50	-1.16 -3.07	3.02 0.12 -0.28 -1.25	21.0
Cytosine Histamine	1.00 0.56	0.57 -2.17		0.34 1.09	2.28	-128			0.07	-0.29			1.72	0.09	80
Creatinine 2-Mercanto-1-methylimidazole	00'0	00:0	1.89	1.41		-0.04	-2.53	ro.			1.47		0.00	-1.45	
Pro Guanidacatata	-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	3 2.58 -0.99		-1.18 2.12	1.45 -4.92	-0.21 0.21	2.05 0.35		
Betaine Betaine Val	135 118 055 000	-5 94 112 0.03	2.34		4 94 -3 09 0 21	-0.66	-265		1.00	0.97 0.46	000	3.35	120 -0.88		a
Benzimidazole				5.00	8	-5.02	8	3						5	
2.4-Diaminobulyrate Homoserine Thr	-2.10 -0.54 0.00 0.00 -2.10 -0.54 0.00 0.00	0.20 -0.21 -11.67 0.12 0.93 -0.25 -107 3.81 2.65	198 -0.85	4.94 -1.52 -0.18 -1.22	4.38 55	5.33 -0.51 -0.00	0.00 0.08 -2.05 -0.48 3.00	2.78 1.00	-0.99 0.52	0.32 0.00	1.00 -5.38	-2.13 1.94 1.75 0.20	3.33 -0.21	0.00 322	N F C
Benzamidine		5							8					2 3	, ,
2-Amino-2-(hydroxymethyl)-1,3-propanediol	0.63	-0.63										-1.37	1.67	\$	_
alpha-wetrylibenzylamine Nicotinamide	1.30 -0.17 0.19 0.00	0.33 -1.02 -0.99	6:0 86:0-		1.03 1.41 0.30	0.46	-0.70 -0.20 1.4	5 0.00 -1.14	-0.58 1.24	-1.76 -2.15	-2.84	4.42 -3.25	1.00 -3.27	-1.63 1.69	6
5-Mettry/cytosine 1-Metyfristamine	-1.06	0000		3.48 14.40		0.00	-2.00						0.00		
Melamine 5-Oxoproline	0.00 0.09 1.04 0.00 0.11 0.97 0.49 -0.57	-1.08 3.42 0.18 2.75 0.00	1.23 -1.04	-0.67 -0.82	-6.69 0.4 -1.61 -1.73 0.0		-0.5 1.07 -0.62 1.0	3 -3.72	1.90 2.42	-2.46 0.96 -1.54 1.38	-0.25 -1.93	-1.60 0.00	1.40 -0.12	2.02 0.44	4
1-Amino-1-cyclopentanecarboxylate Pipecolate							·	_							
Metformin	6.00	000					0.0	-					000		
Nocetyputrescine Anmarine	0000	1.47 -1.87			9	0.29 -3.94	99.0						0.00		
Hydroxyroline Hoto Compilation	-3.73				0.0	0.00 0.52	-2.0						8		
Deta-tuanionopropionale Creatine Creatine		3.26 0.00 -3.13		2.31 0.65	7	1.29 -0.71			•		4		800	8	
ell elle	1.17 60.0 71.1	2.04	0.90	-0.27	\$	-0.82	-2.14	\$	1.53	-0.05 -0.05	-1.46		0.26	0.00	
Leu Bis(3-aminopropyl)amine															
Asn Ornthine	-2.36 0.00 0.04 1.27 0.00 -1.86 0.13 1.10 2.54 -0.05	-2.00 3.86 1.00 0.70 2.58 0.00	0.24 -0.15	-1.20 -4.16	-1.31 -0.59 0.7	0.00 -1.50 0.00	0.13 -1.65 0.93	1.58 -0.53	0.00 1.00	0.22 2.49	-0.85 -2.54	-2.23 0.95 -2.10 0.73	1.67 0.01	1.87 -0.01	m ← c
Asp 2-Aminobenzimidazole	0.00 0.78 0.86	1.00 -1.56		-3.97 -6.30	8 1	201	-0.98	0.23	-0.87				0.00	0.40	N 1
Adenine Acetanlide	2.51 1.43 0.24	0.00		-0.27	-1.78	0.00		. 25	-1.92					7	_
Hypoxanthine 1-Methylnicotinamide	-1.28 2.70 -0.41 -0.28 0.56	-3.40 0.00 -2.43	-0.98 -0.34		3.45 0.20 0.0		0.27	9 -3.82 0.65	-3.32 1.00	-2.88 -3.22	0.00 -9.82		-1.82 0.86	0.94 1.28	00
Anthraniate n-Aminohanzoate	-0.77			6.85	-0.71	71 1,44	0.00	0			2.50	-1.23 0.00			
Tyraminocariosass	-2.29	0.00		5.06 1.77	1.5	1.00 0.36	-0.38								
Urocanate	2.24 1.03 0.00	0.22 4.30 -0.22	0.47	-1.07 -0.97	-0.92 -1.92 0.00	-1.65	0.12 -2.19 2.03			-0.56 4.04		-2.79 -0.42	2.72 0.37	2.11 -0.52	2
Hexameniyere equamire Histolinol Factorio	0.06 -1.38 0.00	-1.51	0.00 2.46	1.54	-0.07	0.07	0.75 1.13	3 3.09 -2.75	-4.71 0.00	29.1	6.94	-3.80 -1.90	1.00 -0.68	0.57 0.65	2
gamma-Guanidinobutyrate	97.1-	0.93	00:00	0.74	22.	-0.83	2.49 1.54						0.00		
Acetyationite Spermidine Gla	0.40 0.00 0.54	4.58 -0.79 0.00	0.00	10.26	5.48 -1.0	7. 00.0	040	2 2 2	133 .206	9.52	980	1 20	4.02	90.00	
5,6-Dimethylbenzimidazol	4:0	9		00.00	5	8	P	5	3					8	
Lys Carachol Chirthrening	-0.02 1.85 2.52 0.60 1.22 -1.00	-0.04 -0.11 -0.82 1.64 -2.39	-0.26 0.00	2.43 0.56	6.38 0.00	0.00 0.94 1.	1.00 -2.23 -0.15	5 2.66 -0.71	-2.21 -0.59	0.77 0.63	2.64 13.68	-1.18 1.99	1.69 -1.24 0.00	0.02	_
O-Acetylserine	0.00	1.84		;	40.1			5.70	0.53				0.60	-2.11	6.
Wet Trifthanolamine Cristian	-0.22 -0.01 1.64 -0.59 0.01 -1.86 -0.22 1.61 -1.53	0.00 3.54 0.02	7.09	0.19 -1.01	5.22 0.76 0.1	0.00	0.83 -5.85 1.39	4.57 -0.50	7.03 0.49	3.44	0.44 1.18	0.00 6.56	0.41 -0.51	0.58 -1.00	+00
Guarine 1-damantanamine Mandamantanamine	2.14 0.74 -0.94	# 8:0		0.00	8	2.00	<u>*</u>	<u> </u>	-3.08				90:0	8	N
mesaanime Nomga-Acetyhistamine Pseudopelletkerine	-0.99	120 -1.78 1.16 -1.65		1.77 -0.07		-1.69 1.00 -0.36 -0.54							0.00		
His Indole-3-acetaldehyde	0.51 1.50 1.14 (	3.06	7	0.00 -1.65		-0.81	-0.10 -5.19 1.8	0.00	1.36			-3.04 0.24	1.84 0.43	2.26	ω.
Ala-Ala Tolazoline	0.00 1.67	0.00 -0.97 -0.28	1.06 1.01	-0.90 -6.54		0.10	1.47 1.32 -0.94	3.79	-3.09	1.57 2.08				-0.67	0
alpha-Aminoadipate N-Memoplitamate	-0.14 0.99 1.01 1.93	-0.67	45.1-	0.94			-1.17 -0.6	2 2.43 0.00	0.08 -1.07	0.00	4.34 -0.98	0.00 2.30	0.17 -1.69	-2.16	o u
Camithe Pterin	-1.69 -2.26 -1.07 -0.74 3.66 1.17 0.74	0.14 0.97 -2.13 -2.73 0.00 2.52	0.66 1.11	2.01 1.96	-0.11 -0.33 -2.75 -0.24	0.00	-1.03 -0.34 1.01 -1.43 0.39	9 0.00 2.47	-1.61 -0.13	0.61	2.96 -0.91		1.21		<b>~</b> 8
Phe Pyridoxal	0.74 2.12 -0.83	0.96 -1.04		0.47		-1.00	-5.12	98	4.52	0.56 1.68	-1.06 -0.13	-2.11 -0.08		6. 4 6. 24	m
Syndphine	-3.21			4.24 1.78	0.0	0:00	-0.22	2					00:00		
3-Methylhistidine 1-Methyl-4-phenyl-1,2,3,6-letrahydropyridine	-2.00			39.34		0.00							0.00		1
						ĺ				ĺ					i

Table S8 E Expression index values for all measured components (Metabolite, Cation(2)).

	#					5																										
	RF02 R	RF03 R	RF04	RF05	RF06	0.1h	1 0.4h <sup>-1</sup>	1 0.5h <sup>-1</sup>	11 0.7h <sup>-1</sup>	galM	glk	mbd	pgi	pfkA	pfkB	dqJ	fbaB	gapC	gpmA	gmdg	pykA	pykF	Asdd	zwf	lbd	pub	ube	rpiA	rpiB	tktA 1	tktB t	talA talB
N-Acetylomithine		-1.92	-0.33	-0.28	١.	-0.89	6	L	m	1.55	0.17				0.70	-0.54	-1.15		1.96	3 4.46	1.97	-3.90	-0.07	4.36		1.87		-0.23	-0.78	1.70	0.07	-0.73
N-Euryglutanine	-381	1,1	000	A 47	24	00	000	3 14 2	285 210	0.53	-033	.3 16	4 32	.2 RD	0.50	0.66	0.57	0.43	.0.42	0 18	-5 13	-381	000	8 36	188	9	20.5	101-	-102	1 00	80.0	0 13
2-Guanidinobenzimidazole			9			Š				5																				8	3	2
Citrulline	1.05	0.67	0.00	1.00		-0.34		1.56 0.	0.00 0.36	-1.67	-0.68	-3.05	-1.39	-3.10	0.69	-0.84	90.0	-1.77	1.33	3 2.43	36.0	1.71	-1.24	-0.26	-0.24	0.00	-5.27	1.39	0.85	-1.08	-0.90	-1.49
Cys-Gly											9									,					0			,	0		-2.00	0.00
Glucosamine		000	-0.24	0.00	00.0	0.73	-	0.96	1.42	4	1.28	-1.13	90 8	-2.37	0.83	0.51	-1.04	-1.35	0.00	9	0 07	000	0	9	2.55	92 0	-2.41	1.24	0.00	2.45	0.52	9.53
Epinephrine		t0:0-	2			-				0																			90.0	67	9	3
Nalpha, Nalpha-Dimethy/histidine																																
N8-Acetylspermidine			-3.47			6.39		0.86 -0.	96:0		8.10	-0.01		-6.65	-1.22	0.01			1.00	_										0.00		
Gly-Leu			-2.05			-1,6		93			2.06								0.0	_										0.00		
Nepsilon-Acetyllysine			9			0	,												,	,												
Castanospermine 5. Mathov doutemine + 2.6. Disminohantanedinste			8			0.00	3												ne: 1-	_												
2-indundryuptamine 2, 2-paminoneptanedioate		000	A 64							J 17		-			0.45	0.31	0.07		0	6 11	0.88	.566	-100			2 18	6.01	000	215	0 14	30.6	00
N-Acetylhistidine			5			0.0	00			5		-107			0.93				4.							1		9	į	000	3	3
Hydroxyatrazine			-0.31			3.7			-0.11		2.71				-1.53				10											1.51		
Arainine ethyl ester			-0.20			1,7					2.41				1,33	-100			0.0											000		
Tryptophanamide+O-Acetylcarnitine			-2.96			4.1	1.42 -2.0	-2.09			0.58								0.00	_										0.00		
Tp.			0.28	-1.78		-2.5		49	-0.29			-1.99	0.27	-0.53	-0.46	-2.12	1.80		0.0	0	-2.44	1.58	00'0		0.61		5.61	-1.39	0.00	2.35	-1.61	3.21
5-Methoxy-3-indoleacetate										-2.24								_	9	~	1.8											
N-Acety/glucosamine						-13		1.01			1.16				99.0		_															
Camosine						0,0																										
Keramine		-1.03	0.40	0.00	-2.78	7.0				00:00			0.45					-0.97		0.91	58	-3.04		3.30		3.33			0			
I nymidine+1,5-Dipnenyicarbonydrazide	0.40	0.84	5.09			-0.28		1.28	107 2.49		-1.59	-1.46		9.19	0.00	18.1	0.49		5.43				00.1-		0.00		338	0.00	-2.23	2 40	000	27.
N1-Acetylenermine	0.70		70.1-			Ť			· 0		0.0				0.30			_	5	,			5				0.00	-4.00	ŧ	77.0	3	7.7
Pyridoxamine 5'-phosphate		0.00	4.08	0.55	00.00	-2.1			0.68 1.61	0.17			-2.02	-0.65	000	_	1.38	-0.60		1.06	-1.07	-2.76	-0.92	-0.94	-0.15	1.28	2.84	-2.60	1.38	-0.68	-2.92	0.05
2'-Deoxyadenosine+5'-Deoxyadenosine			-0.70			1.30		1.68			3.04	-0.13				0.00			1.63									00'0				
N6-Methyl-2-deoxyadenosine	į	:																											1		i	1
Adenosine	2.74	90.0	9.75	4.40	0.00	2.13		0.24	0.34 0.17	-2.04	00.1	-1.20	99.0	4.6	2.79	0.45	0.00	-1.06	-2.54	9.0	0.00	-4.47	1.73	9.18	9.7	9.5	90.9	-0.64	9.76	79.0	4 6	3.52
Inosine On Oh	-0.80	0.99	0.35			71.				-0.7															9				0.3	9 9	3	2 6
1-Methyladenosine			3			Ď		4																						9		3
Guanosine	-1.18	0.43	-0.36	-0.86	-1.00	0.00			2.24 0.62	-0.48		6.52	3.32	2.50				99.0-		3 -3.53	1.19	-5.59	4.11	-5.82	-0.33	0.00	-3.58		1.43	00.0	0.13	0.41
5'-Deoxy-5'-Methylthioadenosine	-1.86		1.13				-	00.0			-0.74				0.14	0.13	-0.53		1.07								0.93	6.79	0.00	3.47	-2.36	-1.69
Scopolamine			-1.00																1.0	0												
Naipha-Benzenolarginine ethylester			-0.65			₹!	1.35 -1.8	-1.88		!	3.02	0.56			92.0	-0.59													:			:
Glutathione	-2.25	000	-14.65	3.21	0.64	₹			0.51 4.16	0.17			99.0	ώ. 4			0.11	4.05		2.29	-1.00	-2.58	-0.53	-10.96	96.0	1.60	-0.15	-5.40	0.00	1.25	0.26	0.00
5-Aminoimidaz ole-4-carboxamide-1-riboturanosyl 5-monophosphate	100	000		00.1	8	0.40	9		00.1	90.0										0.74	07 70	000	0 10	1 0 1		8	4 63	4.4	6	000	8	8
S-Eactoyyjutatiinoine S-Adenosylhomocysteine	-0.5	99		90.00			2			0.20																3			è	7.30	3	90.02
S-Adenosylmethionine		1.14	-2.05	0.58	0.34	-1.1			0.00 2.35	-0.14			-3.40	-1.1	0.00	0.84	0.11	-1.00	-2.57	7 0.48	3 0.56	-2.14	-1.12	99:0-	-1.10	0.00	2.44	-4.29	1.18	00:00	-0.03	-1.00
Leu-Leu-Tyr			-0.08			2.25		-3.81		:	4.10	0.00			-		_							-						0.00		
Oxidized alutathione		-0.79	06.0	0 77	á	ć				4																						

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

	L				1				1																							
	RF02 RF03	3 RF04	04 RF0	35 RF06		0.1h <sup>-1</sup> 0.4h <sup>-1</sup>	h' 0.5h'	h1 0.7h1	1	galM gik	200	m pgi		A pfk	3 fbp		B gapC	C gpmA	A gpmB	B pykA	pykF	Asdd	zwf	lbd	bub	be	hiq	rpiB	tktA	tktB	talA	talB
Citrate Divalention from UDP-glucuronate Divalention from UDP-N-acelyglucosamine	0.01	0.00	-0.64 1.0	34				2.35 -0.31 3.29 2.01		ιΩ	-2.20 -4.48 -3.31	0.00 2.82 -10	4.07 0 1 -10.95 0	0.00	0.83 -1 -0.60 0.34 0	-1.00 0.38 1. 0.22	1.34 1.04 -2 1.07 -0						~ ~			428	8 0.42 0.98 8 1.47	2 -0.46 8 -0.74 7 0.72	6 4 -0.02 2 -0.19			-1.22 1.02 -0.01
dCMP TMP	1.15 3.		9	52					22		_									_												00:0
CMP+CMP-N-acetylneuramate		2.76 0.	0.00	940					210			-2.66	0.93 10	0.18					28 0.76	79 -2.21	-2.28	1.95	5 -0.72	2 8.02	20.77	7.18	8 3.13	1.11	0.00	1.77	9.4	-0.67
DAMP.	1.78		- 0	84 9					2 5		_																					0 0
dAMP			0.60	48 4.06		2.54	0.00	2.44 4.75	2	?	-0.34				1.20	0.00	0.38 -4	4.53 -0	0.90			5										-1.07
GGMP AMP			- 0	5.5							_	000	2.08	1.42					84 0 12					90.09								0.95
IMP	2.71 0.	0.95	0	92																			-1.05		0.00						06:0	0.03
GMP			0								_																		1 -2.76			-0.04
Divalention from NADPH			•	4																												000
Divalention from CoA	0.05	1.69	000	- 64			٠.			9 9									0.84	25.50	2.23	135	5 -1.13	1.80	2.00	3 -0.43	3 0.37	0.77	1.18	9 6	30	0.03
TDP			~	31																												0.63
CDP			0	85																												90'0
UDP Displantion from Acadel Co.A			0 +	8 6																												0.12
Mahand CoA			-	2																												3
dADP	0.05 0.		7																92													-0.47
Divalent ion from n-Propionyl CoA			9	66		_														_							Ĺ					0.18
Divalention from D111*	-0.52	0.61	0.87			· 					-3.09									79 -5.27	27 -2.21				2.69							-0.26
ADP			- c																			_										-0.39
Divalent ion from Malonyl CoA			9	05		_														_	ď					ď				ď		0.00
IDP	0.47 1.		0																	_	ı	_				ı	_			ı		-0.84
Divalent ion from succinyl CoA			0																													2.09
100			-0.63																													-0.23
4CTP	-1.11	0.33 -1.	-1.14	14 0.00		0.90	1.49 3	3.37 1.19		0.32	4.36	5.51	4.6	_	900				0.20	44 430	30 -2.79	6.000	-2.49	69.0	900	-1.10	0 1.13	3 0.10	1.58	-1.15	5.4	0.39
Divalent ion from Lauroyl CoA																																
TTP	-0.99		ω.						0.0																	Ċ						-0.06
a E			4 (1)		•				5 2																							0.0
dATP			0		.,				9																							0.19
ATP			4	90			-		8:										Ċ							Ċ						0.45
ITP GTS	-0.95	1.17	-0.88 3.9	97 -0.19		0.00	0.00	0.56 1.34	<b>4</b> 5	9.0	-5.23	7.70	-7.39 -0	0.69	0.00			3.25	0.99 -0.21	21 -7.06	96 -4.14	4 0.00	7 -2.95	95 0.88	98 0.28	326						0.13
ADP-ribose			4 C	t =					4 6																							-0.00
UDP-glucose			0	90					4																							0.04
UDP-glucuronate			0		•				00																	Ċ						-0.24
ADP-glucose	-0.35		0.13															Ċ														0.41
ODF-IN-acetyglucosamine CMP-N-acetylne iramate		0.00	?						2			٠.																				1.95
NAD			0.00	.61 -2.77		0.31 -0	0.17	2.21 1.30	0,		ď	3.25 -3	-3.89					ď			38 -1.75											-0.28
Nicotinamide hypoxanthine dinucleotide	-0.43 1.	_	0	.56					0,									Ċ				_				Ċ	_					0.03
NADH	-0.86	151	41 0.21	21 -2.25		0.00	0.96	3.28 3.96	ç	0.60	-5.27	-4.26 -5	-5.40	0.29	_			0.16	0.00 0.31	31 -8.00	-5.65	0.00	0 -0.17	1.69	3.21	-0.35	-1.14	4 -7.02	2 2.10	2.86	1.00	-0.31
NADPH			1.56												0.01	0.01	0.44															
FAD	0.02 0.	0.00	o	.00 -2.26		2.74 0	0.03	1.36 1.7	8	1	-2.74	-2.31	٦	0.00				-0.22 0.	0.00	-2.90	8		9	3.53	53 2.81	31 -0.02			5 0.82	-3.72	0.25	-5.19

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. RFs are denoted by Sample ID and Series ID shown in table S2. The components marked by blank EI values are shown. RF, reference sample (wild-type cells cultured at a specific growth rate of 0.2 h<sup>-1</sup>); GR, wild-type cells were either not detected or the product of the deleted gene.

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

# A. mRNAs, qRT-PCR

B. Proteins, LC-MS/MS

			ı	mRNAs	(qRT-PC	R)						Р	roteins	(LC-MS/N	MS)	
		N	Ave (AEI)	SD	SE	LB	UB			N		Ave (AEI)	SD	SE	LB	UB
RF	RF02-1	85	1.120	1.050	0.114	0.894	1.346	RF	RF02-1		57	2.070	1.853	0.245	1.578	2.562
	RF01-1	85	0.886						RF03-2		57	1.379				
	RF02-2	85		1.375					RF03-3		58				1.095	
	RF01-1		0.873						RF03-4			1.875				
	RF02-3	85		1.338					RF03-5			1.082				
	RF01-3	85		0.668					RF03-6		56	1.729	2.299	0.307	1.113	2.344
	RF03-3	85		0.864												
	RF04-4	85		0.894												
	RF03-4	85		0.966												
	RF02-5	85		1.161												
	RF05-5	85		1.027												
	RF05-6	85		1.342												
	RF07-6		2.050													
	RF05-7		1.192													
	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	GR	0.1h-1		56	2.437	2.837	0.379	1.678	3.197
	0.4h-1	85	1.996	1.659	0.180	1.638	2.353		0.4h-1		55	2.033	2.554	0.344	1.343	2.724
	0.5h-1	85	4.369	5.407	0.586	3.202	5.535		0.5h-1		56	2.558	3.597	0.481	1.595	3.521
	0.7h-1	85	6.727	6.426	0.697	5.341	8.113		0.7h-1		55	4.031	3.970	0.535	2.958	5.105
KO	galM	84	0.724	0.883	0.096	0.532	0.915	КО	galM		56	0.595	0.544	0.073	0.449	0.740
	glk	84	1.499	1.476	0.161	1.179	1.819		glk		56	2.163	1.758	0.235	1.692	2.634
	pgm	84	2.467	1.866	0.204	2.062	2.872		pgm		55	1.831	1.591	0.215	1.401	2.261
	pgi	84	3.161	3.344	0.365	2.435	3.887		pgi			2.257				
	pfkA		3.283						pfkA		56	1.771	1.836	0.245	1.279	2.262
	pfkB		0.643						pfkB			1.121				
	fbp	84	1.014						fbp			1.593				
	fbaB	84		1.296					fbaB			2.058				
	gapC		2.143						gapC			1.706				
	gpmA		0.904						gpmA			1.237				
	gpmB		0.944						gpmB			1.070				
	pykA		0.648						pykA			0.475				
	pykF		0.569						pykF			0.500				
	ppsA		0.636						ppsA			0.653				
	zwf		1.117						zwf			0.801				
	pgl	84		1.696					pgl			1.243				
	gnd	84		1.541					gnd			1.049				
	rpe		5.162						rpe			3.333				
	rpiA rpiB	84		3.280					rpiA			1.864				
	rpiB		1.012						rpiB			1.358				
	tktA		2.680 0.912						tktA			1.339 1.434				
	tktB talA								tktB							
			0.962						talA			1.480 1.369				
	talB	04	1.154	0.974	U. 1U0	0.942	1.303		talB		00	1.309	1.000	0.225	บ.ฮาช	1.021

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

### C. Metabolites\*

## D. Metabolites (excluding nucleotides)\*

		A					_								
DE 00 1	N	Ave (AEI)	SD	SE	LB	UB				N	Ave (AEI)	SD	SE	LB	UB
RF RF02-1 RF03-2 RF04-3 RF05-4 RF06-5	119		0.903 1.827 1.181	0.108	0.768 0.968 1.006	1.083 1.545 1.434	R	lF.	RF02-1 RF03-2 RF04-3 RF05-4 RF06-5	112 75	1.530 0.816 1.570 1.157 0.662	0.870 2.032 1.032	0.192 0.119	0.633 1.190 0.920	0.999 1.950 1.395
GR 0.1h-1 0.4h-1 0.5h-1 0.7h-1	154 132	1.560 1.336 1.590 2.046	1.295 1.726	0.104 0.150	1.130 1.292	1.543 1.887	G	SR	0.1h-1 0.4h-1 0.5h-1 0.7h-1	109 88	1.550 1.517 1.417 1.681	1.204 1.886	0.115 0.201	1.288 1.017	1.745 1.816
KO galM glk pgm pgi pfkA pfkB fbp fbaB gapC gpmA gpmB pykA pykF ppsA zwf pgl gnd rpe rpiA rpiB tktA tktB talA	183 157 100 122 171 184 145 114 151 128 130 124 133 105 124 132 131 144 138 168	0.732 2.322 2.762 2.946 1.972 0.861 0.925 1.065 1.411 1.091 1.497 2.223 2.045 0.960 1.889 1.429 1.977 1.749 1.333 1.211 1.535 0.978	3.362 2.976 2.752 1.940 1.122 1.112 1.216 1.280 1.540 0.979 1.923 1.577 2.344 2.863 1.776 1.500 1.356 1.273	0.249 0.238 0.275 0.176 0.086 0.082 0.101 0.120 0.158 0.183 0.138 0.142 0.204 0.250 0.148 0.142 0.204 0.250 0.148	1.832 2.292 2.400 1.624 0.692 0.763 0.866 1.174 0.850 1.771 0.792 1.516 1.149 1.593 2.303 1.457 1.081	2.813 3.231 3.492 2.319 1.031 1.087 1.265 1.649 1.332 2.585 2.318 1.128 2.261 1.709 2.400 3.292 2.042 1.586 1.418 1.753	К	co.	galM glk pgm pgi pfkA pfkB fbp fbaB gapC gpmA gpmB pykA pykF ppsA zwf pgl gnd rpe rpiA rpiB tktA tktB talA	118 60 80 124 135 97 70 106 89 90 87 92 67 82 90 91 98 91 124	1.288 1.817 1.248 1.623 1.005 1.550 1.620 1.823 3.064 1.648	3.768 2.576 1.773 2.005 1.222 1.146 1.395 1.316 1.716 1.989 1.243 1.489 1.020 1.803 2.095 3.163 1.783 1.585 1.482 1.446	0.321 0.237 0.229 0.229 0.110 0.099 0.142 0.157 0.160 0.211 0.180 0.221 0.332 0.180 0.163 0.133 0.152	1.540 1.966 1.747 1.854 0.659 0.782 0.850 1.136 0.957 1.305 0.987 1.305 0.793 1.110 1.261 1.384 2.406 1.291 1.049 0.986 1.298	2.809 2.906 2.663 2.746 1.093 1.172 1.412 1.764 1.618 2.236 1.940 1.216 1.991 1.978 2.261 3.723 2.006 1.709 1.513 1.904

<sup>\*</sup> 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

F. Proteins, 2D-DIGE

			n	nRNAs	(Microarra	ay)						roteins	(2D-DIG	E)	
		N	Ave (AEI)	SD	SE	LB	UB			N	Ave (AEI)	SD	SE	ĹB	UB
RF (WT, 0	.2 h-1)	3757 3633	1.268 1.341	1.553 2.227			1.317 1.414	RF (WT,	0.2 h-1)	1013	1.384 0.981 0.952 1.346	0.905	0.025 0.028	0.896	1.030 1.007
GR	0.1h-1 0.4h-1 0.5h-1 0.7h-1			3.426 4.360				GR	0.1h-1 0.4h-1 0.5h-1 0.7h-1	1102 1067	1.372 1.420 2.127 3.319	1.377 2.679	0.041 0.082	1.339 1.966	1.502 2.288
КО	galM glk pgm pgi pfkA pfkB fbp fbaB gapC gpmA gpmB pykA	4122 4141	1.125 1.445	1.757 2.698 2.223	0.027 0.042	1.071 1.363	1.178 1.528	ко	galM glk pgm pgi pfkA pfkB fbp fbaB gapC gpmA gpmB pykA	1120 1543 1213 1392 1082 1121 1234 1330 1386 1271 1069	1.035 1.029 1.758 2.483 1.802 0.973 1.495 1.299 1.071 1.161 1.300	1.125 1.303 1.772 2.555 1.990 1.136 5.926 1.364 1.271 1.779 1.192	0.034 0.033 0.051 0.068 0.060 0.034 0.169 0.037 0.034 0.050 0.036	0.969 0.964 1.658 2.349 1.684 0.907 1.164 1.226 1.004 1.063 1.228	1.101 1.094 1.858 2.617 1.921 1.040 1.826 1.373 1.138 1.259 1.371
	pykF ppsA zwf pgl gnd rpe rpiA rpiB tktA tktB talA talB			1.116 3.619					pykF ppsA zwf pgl gnd rpe rpiA rpiB tktA tktB talA	995 1148 1250 1219 1038 1098 1367 1006 1053 1049	1.286 1.155 1.283 2.380 1.166 2.506 1.323 1.131 1.101 1.104 0.988	1.430 1.153 3.805 1.906 2.700 3.246 1.309 1.187 1.241 0.995	0.045 0.034 0.108 0.055 0.084 0.098 0.035 0.037 0.038 0.031	1.066 1.216 2.169 1.059 2.342 1.131 1.061 1.028 1.029 0.928	1.244 1.349 2.591 1.273 2.671 1.516 1.200 1.175 1.179

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.

Depende	nt Variable: mRN	IA(qRT-PCR)	multiple Co	omparisons					Dependen	t Variable: mRN	IA(qRT-PCR)	Multiple Co	mparisons			
m	(J)	Mean Difference (I-J)		Std. Error	Sia.	95% Confide Lower Bound	Upper Bound		Th.	(J)	Mean Difference (I-J)		Std Error	Sia.	95% Confide Lower Bound	Upper
galM	glk pgm	-0.775 -1.743	S	0.188 0.225	1.77E-02 1.56E-09	-1.491 -2.605	-0.060 -0.881	P	ofkB	galM olk	-0.081 -0.856	s	0.115 0.173	1.00E+00 9.59E-04	-0.521 -1.520	0.359 -0.192
	pgi pfkA	-2.437 -2.560	s s	0.377 0.406	1.77E-06 3.63E-06	-3.890 -4.122	-0.985 -0.997			pgm pgi	-1.824 -2.518	s	0.213 0.370	1.13E-10 4.74E-07	-2.644 -3.947	-1.004 -1.089
	pfkB fbp fbaB	0.081 -0.290 -0.659		0.115 0.137 0.171	1.00E+00 9.46E-01 4.39E-02	-0.359 -0.812 -1.311	0.521 0.231 -0.007			pfkA fbp fbaB	-2.640 -0.371 -0.740	S	0.399 0.117 0.155	1.11E-06 2.65E-01 1.81E-03	-4.181 -0.815 -1.333	-1.100 0.073 -0.146
	gapC gpmA	-1.420 -0.180	s	0.265 0.145	1.76E-04 1.00E+00	-2.435 -0.732	-0.404 0.372			gapC gpmA	-1.500 -0.261	S	0.255 0.126	2.30E-05 9.56E-01	-2.481 -0.742	-0.519 0.220
	gpmB pykA	-0.220 0.076		0.130 0.120	9.97E-01 1.00E+00	-0.714 -0.382	0.274 0.534			gpmB pykA	-0.301 -0.005		0.108 0.096	5.45E-01 1.00E+00	-0.712 -0.370	0.110 0.360
	pykF ppsA zwf	0.154 0.087 -0.394		0.116 0.115 0.156	1.00E+00 1.00E+00 7.42E-01	-0.289 -0.350 -0.986	0.598 0.525 0.199			pykF ppsA zwf	0.074 0.006 -0.475		0.091 0.089 0.138	1.00E+00 1.00E+00 1.46E-01	-0.273 -0.332 -1.002	0.420 0.345 0.053
	pgl gnd	-1.013 -0.942	s	0.209 0.194	1.20E-03 1.11E-03	-1.810 -1.682	-0.216 -0.203			pgl gnd	-1.094 -1.023	S	0.196 0.180	6.96E-05 4.18E-05	-1.845 -1.713	-0.343 -0.334
	rpe rpiA	-4.438 -0.860	S	0.554 0.371	1.73E-09 8.61E-01	-6.574 -2.287	-2.303 0.566			rpe rpiA	-4.519 -0.941	S	0.549 0.363	7.97E-10 6.94E-01	-6.639 -2.343	-2.400 0.461
	rpiB tktA tktB	-0.288 -1.956 -0.188	s	0.164 0.246 0.135	9.95E-01 6.80E-10 1.00E+00	-0.912 -2.898 -0.700	0.337 -1.014 0.324			rpiB tktA tktB	-0.369 -2.037 -0.269	s	0.147 0.235 0.114	7.55E-01 9.34E-11 8.40E-01	-0.932 -2.941 -0.702	0.194 -1.133 0.163
	talA talB	-0.188 -0.239 -0.430		0.145 0.143	9.98E-01 3.84E-01	-0.791 -0.975	0.314			talA talB	-0.205 -0.319 -0.511	s	0.126 0.124	7.36E-01 1.79E-02	-0.800 -0.983	0.162
	0.1h-1 0.2h-1	-1.363 -0.428	s	0.204 0.147	2.43E-07 4.52E-01	-2.140 -0.988	-0.585 0.132			0.1h-1 0.2h-1	-1.443 -0.509	s s	0.190 0.128	5.71E-09 3.09E-02	-2.174 -0.998	-0.713 -0.019
	0.4h-1 0.5h-1 0.7h-1	-1.272 -3.645 -6.003	s s	0.204 0.594 0.704	2.39E-06 8.98E-06 2.12E-10	-2.051 -5.937 -8.718	-0.493 -1.352 -3.288			0.4h-1 0.5h-1 0.7h-1	-1.353 -3.726 -6.084	S	0.191 0.590 0.700	6.50E-08 4.37E-06 1.38E-10	-2.085 -6.003 -8.787	-0.621 -1.448 -3.381
glk	galM pgm	0.775 -0.968	S	0.704 0.188 0.260	1.77E-02 6.30E-02	0.060	1.491 0.019	f	, dq	galM glk	0.290 -0.485	3	0.137 0.188	9.46E-01 7.06E-01	-0.707 -0.231 -1.203	0.812 0.233
	pgi nfkA	-1.662 -1.784	S S	0.399 0.426	1.68E-02 1.57E-02	-3.190 -3.416	-0.135 -0.153			pgm pgi	-1.453 -2.147	S S	0.226 0.378	1.07E-06 5.36E-05	-2.317 -3.601	-0.589 -0.693
	pfkB fbp fbaB	0.856 0.485 0.116	S	0.173 0.188 0.214	9.59E-04 7.06E-01 1.00E+00	0.192 -0.233 -0.698	1.520 1.203 0.931			pfkA pfkB fbaB	-2.269 0.371 -0.369	S	0.406 0.117 0.172	8.26E-05 2.65E-01 9.37E-01	-3.833 -0.073 -1.023	-0.706 0.815 0.286
	gapC gpmA	-0.644 0.595		0.214 0.295 0.194	9.22E-01 3.41E-01	-1.767 -0.145	0.478 1.335			gapC gpmA	-1.129 0.110	s	0.172 0.265 0.146	1.27E-02 1.00E+00	-2.147 -0.446	-0.112 0.666
	gpmB pykA	0.555 0.851	s	0.183 0.176	3.63E-01 1.47E-03	-0.144 0.175	1.255 1.527			gpmB pykA	0.070 0.366		0.131 0.121	1.00E+00 3.73E-01	-0.428 -0.096	0.568 0.828
	pykF ppsA zwf	0.930 0.862	s s	0.174 0.173	1.78E-04 7.98E-04	0.263	1.596 1.525			pykF ppsA zwf	0.445		0.118 0.116	5.43E-02 2.27E-01	-0.003 -0.065	0.892
	pgl gnd	0.381 -0.238 -0.167		0.202 0.245 0.233	9.86E-01 1.00E+00 1.00E+00	-0.388 -1.170 -1.051	1.151 0.694 0.717			pgl gnd	-0.104 -0.723 -0.652		0.157 0.209 0.194	1.00E+00 1.41E-01 1.80E-01	-0.699 -1.522 -1.394	0.492 0.076 0.090
	rpe rpiA	-3.663 -0.085	s	0.568 0.392	1.72E-06 1.00E+00	-5.849 -1.587	-1.477 1.417			rpe rpiA	-4.148 -0.570	S	0.554 0.371	1.96E-08 9.99E-01	-6.284 -1.998	-2.012 0.858
	rpiB tktA tktB	0.487 -1.181 0.587	s	0.209 0.278 0.187	8.59E-01 1.10E-02 2.88E-01	-0.306 -2.238 -0.125	1.281 -0.124 1.299			rpiB tktA tktB	0.002 -1.666 0.102	s	0.165 0.246 0.136	1.00E+00 2.51E-07 1.00E+00	-0.625 -2.610 -0.414	0.630 -0.722 0.617
	talA talB	0.587 0.537 0.345		0.187 0.194 0.193	5.64E-01 9.93E-01	-0.125 -0.204 -0.389	1.299 1.277 1.080			talA talB	0.102 0.052 -0.140		0.136 0.146 0.144	1.00E+00 1.00E+00	-0.414 -0.504 -0.688	0.608 0.409
	0.1h-1 0.2h-1	-0.587 0.347		0.241 0.196	8.02E-01 9.94E-01	-1.503 -0.398	0.328 1.093			0.1h-1 0.2h-1	-1.072 -0.138	S	0.204 0.148	2.20E-04 1.00E+00	-1.852 -0.701	-0.293 0.425
	0.4h-1 0.5h-1	-0.497 -2.870	S	0.241 0.608	9.60E-01 2.58E-03	-1.414 -5.209	0.421 -0.530			0.4h-1 0.5h-1	-0.982 -3.355	S	0.205 0.595	1.49E-03 7.26E-05	-1.763 -5.648	-0.200 -1.061
pgm	0.7h-1 galM glk	-5.228 1.743 0.968	S	0.715 0.225 0.260	3.67E-08 1.56E-09 6.30E-02	-7.983 0.881 -0.019	-2.473 2.605 1.955	f	baB	0.7h-1 galM glk	-5.713 0.659 -0.116	S	0.704 0.171 0.214	1.17E-09 4.39E-02 1.00E+00	-8.429 0.007 -0.931	-2.997 1.311 0.698
	pgi pfkA	-0.694 -0.817		0.418 0.444	9.98E-01 9.89E-01	-2.290 -2.511	0.901 0.878			pgm pgi	-1.084 -1.779	S S	0.248 0.391	7.12E-03 4.53E-03	-2.028 -3.280	-0.140 -0.278
	pfkB fbp	1.824 1.453	S	0.213 0.226	1.13E-10 1.07E-06	1.004 0.589	2.644 2.317			pfkA pfkB	-1.901 0.740	S S	0.419 0.155	4.72E-03 1.81E-03	-3.508 0.146	-0.294 1.333
	fbaB gapC gpmA	1.084 0.323 1.563	S	0.248 0.320 0.231	7.12E-03 1.00E+00 1.72E-07	0.140 -0.893 0.681	2.028 1.539 2.445			fbp gapC gpmA	0.369 -0.761 0.479		0.172 0.284 0.178	9.37E-01 6.31E-01 6.26E-01	-0.286 -1.846 -0.200	1.023 0.324 1.157
	gpmB pykA	1.523	S	0.222 0.216	1.46E-07 1.42E-10	0.674 0.989	2.372 2.648			gpmB pykA	0.439 0.735	s	0.166 0.159	6.58E-01 3.01E-03	-0.195 0.128	1.073 1.341
	pykF ppsA	1.897 1.830	s	0.214 0.213	6.21E-11 1.03E-10	1.076 1.011	2.719 2.649			pykF ppsA	0.813 0.746	S S	0.156 0.155	2.84E-04 1.48E-03	0.217 0.154	1.410 1.338
	zwf pgl gnd	1.349 0.730 0.801	S	0.238 0.275 0.264	3.02E-05 6.49E-01 3.60E-01	0.443 -0.316 -0.203	2.255 1.775 1.804			zwf pgl gnd	0.265 -0.354 -0.284		0.187 0.233 0.220	1.00E+00 9.99E-01 1.00E+00	-0.446 -1.240 -1.119	0.976 0.531 0.551
	rpe rpiA	-2.695 0.883	s	0.582 0.412	3.30E-03 9.36E-01	-4.928 -0.688	-0.463 2.454			rpe rpiA	-3.780 -0.201	s	0.563 0.385	5.62E-07 1.00E+00	-5.947 -1.677	-1.612 1.274
	rpiB tktA	1.455 -0.213	S	0.243 0.304	6.48E-06 1.00E+00	0.529 -1.370	2.381 0.943			rpiB tktA	0.371 -1.297	s	0.194 0.267	9.84E-01 1.07E-03	-0.366 -2.314	1.108 -0.280
	tktB talA talB	1.555 1.504 1.313	S	0.224 0.231 0.230	9.80E-08 6.11E-07 2.86E-05	0.696 0.623 0.436	2.413 2.386 2.191			tktB talA talB	0.470 0.420 0.229		0.170 0.179 0.177	5.59E-01 8.49E-01 1.00E+00	-0.177 -0.259 -0.444	1.118 1.099 0.902
	0.1h-1 0.2h-1	0.380	s	0.271 0.232	1.00E+00 3.47E-05	-0.651 0.429	1.411			0.1h-1 0.2h-1	-0.704 0.231		0.228	3.27E-01 1.00E+00	-1.572 -0.454	0.165 0.916
	0.4h-1 0.5h-1	0.471 -1.902		0.272 0.621	9.96E-01 3.45E-01	-0.561 -4.285	1.503 0.481			0.4h-1 0.5h-1	-0.613 -2.986	s	0.229 0.603	6.28E-01 1.10E-03	-1.483 -5.309	0.257 -0.663
pgi	0.7h-1 galM glk	-4.260 2.437 1.662	S	0.726 0.377 0.399	2.26E-05 1.77E-06 1.68E-02	-7.052 0.985 0.135	-1.468 3.890 3.190	9	gapC	0.7h-1 galM glk	-5.344 1.420 0.644	S	0.711 0.265 0.295	1.54E-08 1.76E-04 9.22E-01	-8.085 0.404 -0.478	-2.603 2.435 1.767
	pgm pfkA	0.694	3	0.418 0.537	9.98E-01 1.00E+00	-0.901 -2.162	2.290			pgm pgi	-0.323 -1.018		0.320	1.00E+00 8.70E-01	-1.539 -2.695	0.893
	pfkB fbp	2.518 2.147	s s	0.370 0.378	4.74E-07 5.36E-05	1.089 0.693	3.947 3.601			pfkA pfkB	-1.140 1.500	s	0.465 0.255	7.91E-01 2.30E-05	-2.912 0.519	0.632 2.481
	fbaB gapC	1.779 1.018 2.257	S	0.391 0.440 0.381	4.53E-03 8.70E-01 1.75E-05	0.278 -0.659 0.793	3.280 2.695 3.722			fbp fbaB	1.129 0.761 1.239	S	0.265 0.284 0.270	1.27E-02 6.31E-01 3.59E-03	0.112 -0.324 0.207	2.147 1.846 2.272
	gpmA gpmB pykA	2.218 2.513	S	0.375 0.372	2.13E-05 5.43E-07	0.772 1.079	3.663 3.948			gpmA gpmB pykA	1.200 1.495	S	0.262 0.257	4.05E-03 2.93E-05	0.195 0.507	2.205 2.484
	pykF ppsA	2.592 2.525	s s	0.371 0.370	1.95E-07 4.36E-07	1.162 1.096	4.022 3.953			pykF ppsA	1.574 1.507	s s	0.255 0.254	6.70E-06 2.03E-05	0.591 0.527	2.557 2.487
	zwf pgl and	2.044 1.424 1.495	s	0.385 0.409 0.402	2.34E-04 1.32E-01 6.85E-02	0.565 -0.139 -0.042	3.522 2.988 3.033			zwf pgl and	1.026 0.406		0.275 0.308 0.299	6.74E-02 1.00E+00	-0.027 -0.767 -0.660	2.079 1.580 1.614
	rpe rpiA	-2.001 1.577		0.656 0.511	3.48E-01 3.23E-01	-4.499 -0.364	0.497 3.519			rpe rpiA	-3.019 0.559	s	0.598 0.435	5.94E-04 1.00E+00	-5.309 -1.095	-0.729 2.214
	rpiB tktA	2.150 0.481	S	0.388 0.429	8.56E-05 1.00E+00	0.659 -1.155	3.640 2.118			rpiB tktA	1.132 -0.537	s	0.280 0.335	2.48E-02 9.99E-01	0.062 -1.808	2.202 0.735
	tktB talA talB	2.249 2.199 2.008	S	0.377 0.381 0.380	1.60E-05 3.43E-05 2.79E-04	0.798 0.735 0.546	3.700 3.663 3.469			tktB talA talB	1.231 1.181 0.990	S	0.264 0.270 0.269	2.95E-03 8.00E-03 7.69E-02	0.218 0.148 -0.039	2.244 2.214 2.019
	0.1h-1 0.2h-1	1.075 2.010	s	0.407 0.382	6.55E-01 2.91E-04	-0.480 0.543	2.630 3.477			0.1h-1 0.2h-1	0.057 0.992		0.305 0.271	1.00E+00 8.12E-02	-1.104 -0.045	1.218 2.028
	0.4h-1 0.5h-1	1.166		0.407 0.691	4.85E-01 9.95E-01	-0.390 -3.840	2.721 1.425			0.4h-1 0.5h-1	0.148 -2.225		0.305 0.636	1.00E+00 1.28E-01	-1.014 -4.662	1.309 0.212
pfkA	0.7h-1 galM	-3.566 2.560 1.784	S	0.787 0.406 0.426	4.24E-03 3.63E-06 1.57E-02	-6.570 0.997 0.153	-0.561 4.122 3.416	9	gpmA	0.7h-1 galM	-4.583 0.180 -0.595	S	0.739 0.145 0.194	4.42E-06 1.00E+00 3.41E-01	-7.421 -0.372 -1.335	-1.746 0.732 0.145
	glk pgm pgi	0.817 0.122	"	0.444 0.537	9.89E-01 1.00E+00	-0.878 -1.918	2.511 2.162			glk pgm pgi	-1.563 -2.257	S	0.231 0.381	1.72E-07 1.75E-05	-2.445 -3.722	-0.681 -0.793
	pfkB fbp	2.640 2.269	s s	0.399 0.406	1.11E-06 8.26E-05	1.100 0.706	4.181 3.833			pfkA pfkB	-2.379 0.261	s	0.409 0.126	2.93E-05 9.56E-01	-3.952 -0.220	-0.806 0.742
	fbaB gapC	1.901	s	0.419 0.465	4.72E-03 7.91E-01	0.294 -0.632	3.508 2.912			fbp fbaB gapC	-0.110 -0.479		0.146 0.178	1.00E+00 6.26E-01	-0.666 -1.157	0.446
	gpmA gpmB pykA	2.379 2.340 2.635	s s	0.409 0.404 0.401	2.93E-05 3.58E-05 1.25E-06	0.806 0.784 1.090	3.952 3.895 4.180			gapC gpmB pykA	-1.239 -0.040 0.256	S	0.270 0.140 0.131	3.59E-03 1.00E+00 9.77E-01	-2.272 -0.570 -0.241	-0.207 0.491 0.753
	pykF ppsA	2.714 2.647	s	0.399 0.399	4.93E-07 1.03E-06	1.173 1.107	4.255 4.186			pykF ppsA	0.335 0.267		0.127 0.125	6.61E-01 9.40E-01	-0.149 -0.211	0.819 0.746
	zwf pgl	2.166 1.546	s	0.413 0.435	3.12E-04 1.10E-01	0.579 -0.119	3.752 3.212			zwf pgl	-0.214 -0.833	s	0.164	1.00E+00 4.07E-02	-0.836 -1.652	0.409 -0.014
	gnd rpe rpiA	1.617 -1.879 1.699		0.428 0.673 0.532	5.91E-02 5.39E-01 2.58E-01	-0.024 -4.438 -0.323	3.258 0.680 3.722			gnd rpe rpiA	-0.762 -4.258 -0.680	s	0.200 0.556 0.374	5.06E-02 8.31E-09 9.90E-01	-1.525 -6.401 -2.118	0.001 -2.115 0.758
	rpiB tktA	2.272 0.603	s	0.416 0.454	1.22E-04 1.00E+00	0.674 -1.130	3.869 2.337			rpiB tktA	-0.108 -1.776	s	0.172 0.251	1.00E+00 4.40E-08	-0.760 -2.736	0.545 -0.816
	tktB talA	2.371 2.321	S S	0.405 0.409	2.73E-05 5.43E-05	0.811 0.748	3.932 3.894			tktB talA	-0.008 -0.058		0.144 0.154	1.00E+00 1.00E+00	-0.555 -0.643	0.539 0.526
	talB 0.1h-1 0.2h-1	2.130 1.197 2.132	S	0.408 0.433 0.410	3.72E-04 5.62E-01 3.85E-04	0.559 -0.460 0.556	3.700 2.854 3.707			talB 0.1h-1 0.2h-1	-0.250 -1.182 -0.248	s	0.152 0.210 0.156	9.98E-01 3.57E-05 9.99E-01	-0.827 -1.982 -0.839	0.328 -0.383 0.344
	0.4h-1 0.5h-1	1.288 -1.085	"	0.433 0.707	4.06E-01 9.99E-01	-0.370 -3.776	2.946 1.605			0.4h-1 0.5h-1	-1.092 -3.465	S	0.210 0.596	2.64E-04 3.51E-05	-1.893 -5.765	-0.290 -1.165
*. *S* The	0.7h-1 e mean difference	-3.444	at the .05 lev	0.801	9.77E-03	-6.498	-0.389	Ļ	". "S" The	0.7h-1 mean difference	-5.823	S at the .05 lev	0.705	6.08E-10	-8.544	-3.101

Dependen	t Variable: mRN	A(qRT-PCR)	Multiple Co	omparisons				D	Dependen	t Variable: mRt	NA(qRT-PCR)	Multiple Co	mparisons			
m	(J)	Mean Difference (I-J)		Std. Error	Sia.	95% Confide Lower Bound	Upper Bound	a	n	(J)	Mean Difference (I-J)		Std. Error	Sia.	95% Confide Lower Bound	Upper Bound
gpmB	galM glk	0.220 -0.555		0.130 0.183	9.97E-01 3.63E-01	-0.274 -1.255	0.714 0.144	PI	gl	galM glk	1.013	S	0.209 0.245	1.20E-03 1.00E+00	0.216 -0.694	1.810 1.170
	pgm pgi pfkA	-1.523 -2.218 -2.340	s	0.222 0.375 0.404	1.46E-07 2.13E-05 3.58E-05	-2.372 -3.663 -3.895	-0.674 -0.772 -0.784			pgm pgi pfkA	-0.730 -1.424 -1.546		0.275 0.409 0.435	6.49E-01 1.32E-01 1.10E-01	-1.775 -2.988 -3.212	0.316 0.139 0.119
	pfkB fbp	-2.340 0.301 -0.070	5	0.404 0.108 0.131	5.45E-01 1.00E+00	-0.110 -0.568	0.712 0.428			pfkB fbp	1.094 0.723	s	0.435 0.196 0.209	6.96E-05 1.41E-01	-3.212 0.343 -0.076	1.845
	fbaB gapC	-0.439 -1.200	s	0.166 0.262	6.58E-01 4.05E-03	-1.073 -2.205	0.195 -0.195			fbaB gapC	0.354 -0.406		0.233 0.308	9.99E-01 1.00E+00	-0.531 -1.580	1.240 0.767
	gpmA pykA	0.040 0.296 0.374		0.140 0.113 0.109	1.00E+00 6.81E-01 1.46E-01	-0.491 -0.135 -0.041	0.570 0.726 0.789			gpmA gpmB	0.833 0.793 1.089	S	0.215 0.205 0.199	4.07E-02 4.27E-02 1.03E-04	0.014 0.010 0.327	1.652 1.576 1.851
	pykF ppsA zwf	0.374 0.307 -0.174		0.109 0.107 0.150	1.46E-01 4.87E-01 1.00E+00	-0.041 -0.102 -0.746	0.789 0.716 0.399			pykA pykF ppsA	1.089 1.168 1.100	S	0.199 0.196 0.195	1.41E-05 5.86E-05	0.327 0.414 0.350	1.851 1.921 1.851
	pgl gnd	-0.793 -0.722	s	0.205 0.189	4.27E-02 5.11E-02	-1.576 -1.446	-0.010 0.001			zwf gnd	0.619 0.071		0.222 0.250	5.41E-01 1.00E+00	-0.226 -0.879	1.465 1.021
	rpe rpiA rpiB	-4.218 -0.640 -0.068	S	0.552 0.368 0.159	1.04E-08 9.95E-01 1.00E+00	-6.349 -2.059 -0.674	-2.088 0.779 0.538			rpe rpiA rpiB	-3.425 0.153 0.725	S	0.576 0.403 0.228	1.45E-05 1.00E+00 2.64E-01	-5.636 -1.386 -0.142	-1.214 1.692 1.592
	tktA tktB	-1.736 0.032	s	0.242 0.128	4.23E-08 1.00E+00	-2.666 -0.456	-0.806 0.520			tktA tktB	-0.943 0.825	s	0.292 0.208	2.39E-01 3.11E-02	-2.054 0.031	0.168 1.618
	talA talB 0.1h-1	-0.019 -0.210 -1.143		0.140 0.138 0.199	1.00E+00 9.99E-01 2.85E-05	-0.549 -0.733 -1.905	0.512 0.313 -0.380			talA talB 0.1h-1	0.775 0.583 -0.349		0.215 0.213 0.258	9.21E-02 5.86E-01 1.00E+00	-0.044 -0.231 -1.328	1.594 1.397 0.629
	0.2h-1 0.4h-1	-0.208 -1.052	s	0.142 0.200	1.00E+00 2.27E-04	-0.746 -1.816	0.330			0.2h-1 0.4h-1	0.585 -0.259		0.216 0.258	6.05E-01 1.00E+00	-0.238 -1.239	1.409
pykA	0.5h-1 0.7h-1 galM	-3.425 -5.783 -0.076	s s	0.593 0.702 0.120	4.23E-05 7.34E-10 1.00E+00	-5.713 -8.494 -0.534	-1.137 -3.072 0.382		ind	0.5h-1 0.7h-1 galM	-2.632 -4.990 0.942	S	0.615 0.721 0.194	1.22E-02 2.02E-07 1.11E-03	-4.995 -7.765 0.203	-0.269 -2.215 1.682
pykk	glk pgm	-0.851 -1.819	s	0.126 0.176 0.216	1.47E-03 1.42E-10	-1.527 -2.648	-0.175 -0.989	91	inu	glk pgm	0.167	3	0.233 0.264	1.00E+00 3.60E-01	-0.717 -1.804	1.051
	pgi pfkA	-2.513 -2.635	S S	0.372 0.401	5.43E-07 1.25E-06	-3.948 -4.180	-1.079 -1.090			pgi pfkA	-1.495 -1.617		0.402 0.428	6.85E-02 5.91E-02	-3.033 -3.258	0.042 0.024
	pfkB fbp fbaB	0.005 -0.366 -0.735	s	0.096 0.121 0.159	1.00E+00 3.73E-01 3.01E-03	-0.360 -0.828 -1.341	0.370 0.096 -0.128			pfkB fbp fbaB	1.023 0.652 0.284	S	0.180 0.194 0.220	4.18E-05 1.80E-01 1.00E+00	0.334 -0.090 -0.551	1.713 1.394 1.119
	gapC gpmA	-1.495 -0.256	s	0.257 0.131	2.93E-05 9.77E-01	-2.484 -0.753	-0.507 0.241			gapC gpmA	-0.477 0.762		0.299 0.200	9.99E-01 5.06E-02	-1.614 -0.001	0.660 1.525
	gpmB pykF ppsA	-0.296 0.079 0.011		0.113 0.097 0.095	6.81E-01 1.00E+00 1.00E+00	-0.726 -0.291 -0.351	0.135 0.449 0.374			gpmB pykA pykF	0.722 1.018 1.097	S	0.189 0.183 0.180	5.11E-02 6.67E-05 7.16E-06	-0.001 0.317 0.405	1.446 1.719 1.789
	zwf pgl	-0.470 -1.089	s	0.142 0.199	2.03E-01 1.03E-04	-1.012 -1.851	0.073 -0.327			ppsA zwf	1.030 0.549	s	0.179 0.208	3.44E-05 6.61E-01	0.341 -0.243	1.718 1.340
	gnd rpe rpiA	-1.018 -4.514	S	0.183 0.550	6.67E-05 8.51E-10	-1.719 -6.637	-0.317 -2.391			pgl rpe rpiA	-0.071 -3.496	s	0.250 0.570	1.00E+00 7.00E-06 1.00E+00	-1.021 -5.689	0.879 -1.303
	rpiB tktA	-0.936 -0.364 -2.032	s	0.365 0.151 0.237	7.12E-01 8.18E-01 1.08E-10	-2.343 -0.941 -2.944	0.472 0.213 -1.119			rpiB tktA	0.082 0.654 -1.014		0.395 0.214 0.282	3.44E-01 9.29E-02	-1.430 -0.160 -2.086	1.595 1.469 0.058
	tktB talA	-0.264 -0.314		0.119 0.131	9.08E-01 8.19E-01	-0.715 -0.812	0.187 0.183			tktB talA	0.754 0.704	s	0.193 0.200	3.70E-02 1.18E-01	0.019 -0.059	1.490 1.467
	talB 0.1h-1 0.2h-1	-0.506 -1.438 -0.504	s	0.128 0.193 0.133	3.30E-02 9.36E-09 5.23E-02	-0.995 -2.179 -1.009	-0.017 -0.698 0.002			talB 0.1h-1 0.2h-1	0.512 -0.420 0.515		0.199 0.246 0.202	7.05E-01 9.97E-01 7.24E-01	-0.245 -1.354 -0.254	1.270 0.514 1.283
	0.4h-1 0.5h-1	-1.348 -3.721	s s	0.194 0.591	1.05E-07 4.67E-06	-2.090 -6.002	-0.605 -1.440			0.4h-1 0.5h-1	-0.329 -2.703	s	0.246 0.610	1.00E+00 7.35E-03	-1.265 -5.049	0.606 -0.356
pykF	0.7h-1 galM glk	-6.079 -0.154 -0.930	S	0.701 0.116 0.174	1.42E-10 1.00E+00 1.78E-04	-8.784 -0.598 -1.596	-3.373 0.289 -0.263	rp	pe	0.7h-1 galM glk	-5.061 4.438 3.663	S	0.717 0.554 0.568	1.14E-07 1.73E-09 1.72E-06	-7.821 2.303 1.477	-2.300 6.574 5.849
	pgm pgi	-1.897 -2.592	S	0.214 0.371	6.21E-11 1.95E-07	-2.719 -4.022	-1.076 -1.162			pgm pgi	2.695 2.001	S	0.582 0.656	3.30E-03 3.48E-01	0.463 -0.497	4.928 4.499
	pfkA pfkB	-2.714 -0.074 -0.445	s	0.399 0.091 0.118	4.93E-07 1.00E+00 5.43E-02	-4.255 -0.420 -0.892	-1.173 0.273 0.003			pfkA pfkB	1.879 4.519 4.148	s	0.673 0.549 0.554	5.39E-01 7.97E-10 1.96E-08	-0.680 2.400 2.012	4.438 6.639 6.284
	fbp fbaB gapC	-0.445 -0.813 -1.574	s	0.118 0.156 0.255	5.43E-02 2.84E-04 6.70E-06	-0.892 -1.410 -2.557	-0.217 -0.591			fbp fbaB gapC	4.148 3.780 3.019	S	0.563 0.598	5.62E-07 5.94E-04	1.612 0.729	5.947 5.309
	gpmA gpmB	-0.335 -0.374		0.127 0.109	6.61E-01 1.46E-01	-0.819 -0.789	0.149 0.041			gpmA gpmB	4.258 4.218	S	0.556 0.552	8.31E-09 1.04E-08	2.115 2.088	6.401 6.349
	pykA ppsA zwf	-0.079 -0.067 -0.548	s	0.097 0.090 0.139	1.00E+00 1.00E+00 3.33E-02	-0.449 -0.411 -1.079	0.291 0.276 -0.018			pykA pykF ppsA	4.514 4.593 4.526	S	0.550 0.549 0.549	8.51E-10 4.53E-10 7.56E-10	2.391 2.473 2.407	6.637 6.713 6.644
	pgl gnd	-1.168 -1.097	s	0.196 0.180	1.41E-05 7.16E-06	-1.921 -1.789	-0.414 -0.405			zwf pgl	4.045 3.425	S	0.559 0.576	5.43E-08 1.45E-05	1.892 1.214	6.197 5.636
	rpe rpiA rpiB	-4.593 -1.015 -0.442	S	0.549 0.364 0.148	4.53E-10 5.45E-01 3.94E-01	-6.713 -2.418 -1.008	-2.473 0.389 0.124			gnd rpiA rpiB	3.496 3.578 4.150	S	0.570 0.652 0.561	7.00E-06 6.76E-05 2.41E-08	1.303 1.094 1.990	5.689 6.062 6.311
	tktA tktB	-2.111 -0.343	s	0.235 0.115	5.99E-11 3.90E-01	-3.016 -0.779	-1.205 0.094			tktA tktB	2.482 4.250	S	0.590 0.553	1.49E-02 8.22E-09	0.221 2.116	4.744 6.384
	talA talB 0.1h-1	-0.393 -0.584 -1.517	s	0.127 0.125 0.191	3.21E-01 2.22E-03 9.31E-10	-0.877 -1.060 -2.250	0.091 -0.109 -0.785			talA talB 0.1h-1	4.200 4.008 3.076	S	0.556 0.555 0.574	1.36E-08 6.60E-08 1.91E-04	2.057 1.867 0.871	6.343 6.150 5.280
	0.1h-1 0.2h-1 0.4h-1	-0.582 -1.426	S	0.129 0.191	4.48E-03 1.06E-08	-2.250 -1.075 -2.161	-0.785 -0.090 -0.692			0.1h-1 0.2h-1 0.4h-1	4.010 3.167	S	0.574 0.556 0.574	6.70E-08 9.82E-05	1.866	6.155 5.372
	0.5h-1 0.7h-1	-3.799 -6.158	S	0.590 0.700	2.55E-06 1.04E-10	-6.078 -8.861	-1.521 -3.454			0.5h-1 0.7h-1	0.793 -1.565		0.801 0.885	1.00E+00 9.94E-01	-2.248 -4.929	3.835 1.799
ppsA	galM glk pgm	-0.087 -0.862 -1.830	s	0.115 0.173 0.213	1.00E+00 7.98E-04 1.03E-10	-0.525 -1.525 -2.649	0.350 -0.200 -1.011	rp	piA	galM glk pgm	0.860 0.085 -0.883		0.371 0.392 0.412	8.61E-01 1.00E+00 9.36E-01	-0.566 -1.417 -2.454	2.287 1.587 0.688
	pgi pfkA	-2.525 -2.647	S	0.370 0.399	4.36E-07 1.03E-06	-3.953 -4.186	-1.096 -1.107			pgi pfkA	-1.577 -1.699		0.511 0.532	3.23E-01 2.58E-01	-3.519 -3.722	0.364 0.323
	pfkB fbp fbaB	-0.006 -0.377 -0.746	9	0.089 0.116 0.155	1.00E+00 2.27E-01 1.48E-03	-0.345 -0.819 -1.338	0.332 0.065 -0.154			pfkB fbp fbaB	0.941 0.570 0.201		0.363 0.371 0.385	6.94E-01 9.99E-01 1.00E+00	-0.461 -0.858 -1.274	2.343 1.998 1.677
	gapC gpmA	-1.507 -0.267	S	0.254 0.125	2.03E-05 9.40E-01	-2.487 -0.746	-0.527 0.211			gapC gpmA	-0.559 0.680		0.435 0.374	1.00E+00 9.90E-01	-2.214 -0.758	1.095 2.118
	gpmB pykA pykF	-0.307 -0.011 0.067		0.107 0.095 0.090	4.87E-01 1.00E+00 1.00E+00	-0.716 -0.374 -0.276	0.102 0.351 0.411			gpmB pykA pykF	0.640 0.936 1.015		0.368 0.365 0.364	9.95E-01 7.12E-01 5.45E-01	-0.779 -0.472 -0.389	2.059 2.343 2.418
	zwf pgl	-0.481 -1.100	s	0.138 0.195	1.26E-01 5.86E-05	-1.007 -1.851	0.045			ppsA zwf	0.947 0.466		0.363 0.378	6.81E-01 1.00E+00	-0.369 -0.454 -0.986	2.349 1.919
	gnd rpe rpiA	-1.030 -4.526 -0.947	s s	0.179 0.549 0.363	3.44E-05 7.56E-10 6.81E-01	-1.718 -6.644 -2.349	-0.341 -2.407 0.454			pgl gnd rpe	-0.153 -0.082 -3.578		0.403 0.395 0.652	1.00E+00 1.00E+00 6.76E-05	-1.692 -1.595 -6.062	1.386 1.430 -1.094
	rpiB tktA	-0.947 -0.375 -2.043	s	0.363 0.147 0.235	7.20E-01 8.72E-11	-2.349 -0.937 -2.946	0.454 0.187 -1.140			rpiB tktA	-3.576 0.572 -1.096	5	0.382 0.423	1.00E+00 6.97E-01	-0.002 -0.892 -2.709	2.037
	tktB talA	-0.276 -0.326		0.113 0.126	8.00E-01 6.92E-01	-0.706 -0.805	0.155 0.153			tktB talA	0.672 0.622		0.370 0.374	9.90E-01 9.97E-01	-0.753 -0.817	2.096 2.060
	talB 0.1h-1 0.2h-1	-0.517 -1.450 -0.515	S	0.123 0.190 0.128	1.42E-02 4.66E-09 2.50F-02	-0.987 -2.179 -1.003	-0.047 -0.721 -0.028			talB 0.1h-1 0.2h-1	0.430 -0.502 0.432		0.373 0.400 0.375	1.00E+00 1.00E+00 1.00E+00	-1.005 -2.033 -1.009	1.866 1.028 1.873
	0.4h-1 0.5h-1	-1.359 -3.732	S	0.190 0.590	5.32E-08 4.16E-06	-2.090 -6.009	-0.628 -1.455			0.4h-1 0.5h-1	-0.412 -2.785	s	0.401 0.687	1.00E+00 2.28E-02	-1.943 -5.404	1.119 -0.166
zwf	0.7h-1 galM glk	-6.090 0.394 -0.381	S	0.700 0.156 0.202	1.34E-10 7.42E-01 9.86E-01	-8.793 -0.199 -1.151	-3.388 0.986 0.388	rp	piB	0.7h-1 galM glk	-5.143 0.288 -0.487	S	0.783 0.164 0.209	4.95E-07 9.95E-01 8.59E-01	-8.136 -0.337 -1.281	-2.150 0.912 0.306
	pgm pgi	-1.349 -2.044	s	0.238 0.385	3.02E-05 2.34E-04	-2.255 -3.522	-0.443 -0.565			pgm pgi	-1.455 -2.150	S	0.243 0.388	6.48E-06 8.56E-05	-2.381 -3.640	-0.529 -0.659
	pfkA pfkB fbp	-2.166 0.475 0.104	S	0.413 0.138 0.157	3.12E-04 1.46E-01 1.00E+00	-3.752 -0.053 -0.492	-0.579 1.002 0.699			pfkA pfkB fbp	-2.272 0.369 -0.002	S	0.416 0.147 0.165	1.22E-04 7.55E-01 1.00E+00	-3.869 -0.194 -0.630	-0.674 0.932 0.625
	fbaB gapC	-0.265 -1.026		0.187 0.187 0.275	1.00E+00 6.74E-02	-0.492 -0.976 -2.079	0.446 0.027			fbaB gapC	-0.002 -0.371 -1.132	s	0.194 0.280	9.84E-01 2.48E-02	-1.108 -2.202	0.366 -0.062
	gpmA gpmB	0.214 0.174		0.164 0.150	1.00E+00 1.00E+00	-0.409 -0.399	0.836 0.746			gpmA gpmB	0.108 0.068	Ī	0.172 0.159	1.00E+00 1.00E+00	-0.545 -0.538	0.760 0.674
	pykA pykF ppsA	0.470 0.548 0.481	s	0.142 0.139 0.138	2.03E-01 3.33E-02 1.26E-01	-0.073 0.018 -0.045	1.012 1.079 1.007			pykA pykF ppsA	0.364 0.442 0.375		0.151 0.148 0.147	8.18E-01 3.94E-01 7.20E-01	-0.213 -0.124 -0.187	0.941 1.008 0.937
	pgl gnd	-0.619 -0.549		0.222 0.208	5.41E-01 6.61E-01	-1.465 -1.340	0.226 0.243			zwf pgl	-0.106 -0.725		0.181 0.228	1.00E+00 2.64E-01	-0.792 -1.592	0.581 0.142
	rpe rpiA miB	-4.045 -0.466 0.106	S	0.559 0.378 0.181	5.43E-08 1.00E+00 1.00E+00	-6.197 -1.919 -0.581	-1.892 0.986 0.792			gnd rpe rpiA	-0.654 -4.150 -0.572	s	0.214 0.561 0.382	3.44E-01 2.41E-08 1.00E+00	-1.469 -6.311 -2.037	0.160 -1.990 0.892
	rpiB tktA tktB	-1.562 0.205	s	0.257 0.155	5.19E-06 1.00E+00	-2.545 -0.382	-0.580 0.793			tktA tktB	-1.668 0.100	s	0.262 0.163	1.16E-06 1.00E+00	-2.669 -0.520	-0.668 0.719
	talA talB 0.1h-1	0.155 -0.036		0.164 0.162	1.00E+00 1.00E+00	-0.468 -0.652	0.778 0.580			talA talB	0.049 -0.142		0.172 0.170 0.223	1.00E+00 1.00E+00 1.20F-03	-0.604 -0.789	0.702 0.505
	0.1h-1 0.2h-1 0.4h-1	-0.969 -0.034 -0.878	s	0.217 0.166 0.218	5.11E-03 1.00E+00 2.38E-02	-1.796 -0.663 -1.707	-0.142 0.595 -0.050			0.1h-1 0.2h-1 0.4h-1	-1.075 -0.140 -0.984	S	0.223 0.173 0.224	1.20E-03 1.00E+00 6.29E-03	-1.924 -0.799 -1.835	-0.226 0.519 -0.133
	0.5h-1 0.7h-1	-3.251 -5.609	9 9	0.599 0.708	1.69E-04 2.48E-09	-5.560 -8.338	-0.942 -2.880			0.5h-1 0.7h-1	-3.357 -5.715	S	0.601 0.710	8.61E-05 1.30E-09	-5.673 -8.450	-1.041 -2.980
*. *S* The	mean difference	is significant	at the .05 lev	rel.				•	"S" The	mean differenc	e is significant	at the .05 lev	el.			

		Mean Difference			7	95% Confide Lower	nce Intervi
1)	(J)	(I-J)		Std. Error	Sig.	Bound	Bound
ktA	galM glk	1.956	S	0.246 0.278	6.80E-10 1.10F-02	1.014 0.124	2.89
	pgm	0.213	3	0.304	1.00E+00	-0.943	1.33
	pgi pfkA	-0.481		0.429	1.00E+00	-2.118 -2.337	1.15
	pfkA pfkB	-0.603 2.037	s	0.454 0.235	1.00E+00 9.34E-11	-2.337 1.133	1.13
	fbp	1.666	S	0.235	2.51E-07	0.722	2.6
	fbaB	1 297	s	0.267	1.07E-03	0.280	2.3
	gapC gpmA	0.537 1.776	s	0.335 0.251	9.99E-01 4.40E-08	-0.735 0.816	1.8
	gpmB	1.776	S	0.251	4.40E-08	0.806	2.6
	pykA pykF	2.032	S	0.237	1.08E-10	1 110	20
	pykF	2.111 2.043	s s	0.235 0.235	5.99E-11	1.205 1.140	3.0
	ppsA zwf	1.562	S	0.235	8.72E-11 5.19E-06	0.580	2.9
	pgl	0.943	3	0.292	2.39E-01	-0.168	2.5
	gnd	1.014		0.282	9.29E-02	-0.058	2.0
	rpe rpiA	-2.482 1.006	s	0.590	1.49E-02 6.97E-01	-4.744 -0.517	-0.2 2.7
	rpiB	1.668	s	0.262	1.16E-06	0.668	2.6
	tktB	1 768	s	0.245	2.85E-08	0.829	2.7
	talA talB	1.718 1.526	S	0.251	1.42E-07 5.20E-06	0.757	2.6
	0.1h-1	0.594	s	0.250	9.60E-01	0.504	1.6
	0.2h_1	1.528	s	0.252	6 14F-06	0.564	2.4
	0.4h-1 0.5h-1	0.684		0.289	8.42E-01	-0.415	1.7
	0.5h-1 0.7h-1	-1.689 -4.047	s	0.629 0.733	6.23E-01 9.48E-05	-4.099 -6.862	0.7
ktB	galM	0.188	ŭ	0.135	1.00E+00	-6.862 -0.324	-1.2 0.7
	glk	-0.587		0.187	2.88E-01	-1.299	0.1
	pgm pgi	-1.555 -2.249	S	0.224 0.377	9.80E-08 1.60F-05	-2.413 -3.700	-0.6 -0.7
	pfkA	-2.371	s s	0.405	1.60E-05 2.73E-05	-3.932	-0.8
	pfkB	0.260		0.114	8 40F-01	-0.163	0.7
	fbp fbaB	-0.102 -0.470		0.136 0.170	1.00E+00 5.59E-01	-0.617 -1.118	0.4
	ganC	-1.231	s	0.264	2.95E-03	-2.244	-0.2
	gpmA	0.008		0.144 0.128	1.00E+00	-0.539	0.5
	gpmB	-0.032 0.264		0.128 0.119	1.00E+00 9.08E-01	-0.520 -0.187	0.4
	pykA pykF	0.264		0.119	9.08E-01 3.90E-01	-0.187 -0.094	0.7
	ppsA	0.276		0.113	8.00E-01	-0.155	0.7
	zwf	-0.205 -0.825	s	0.155 0.208	1.00E+00 3.11E-02	-0.793 -1.618	-0.0
	pgl gnd	-0.825	S	0.208	3.11E-02 3.70E-02	-1.618 -1.490	-0.0
	me	-4 250	s	0.553	8.22E-09	-6 384	-21
	rpiA	-0.672 -0.100		0.370 0.163	9.90E-01	-2.096 -0.719	0.7
	rpiB tktA	-0.100 -1.768	s	0.163	1.00E+00 2.85F-08	-0.719 -2.707	-0.5
	talA	-0.050	ŭ	0.144	1.00E+00	-0.597	0.4
	talB	-0.242		0.142	9.97E-01	-0.781	0.2
	0.1h-1 0.2h-1	-1.174 -0.240	s	0.203 0.146	1.94E-05 9.98E-01	-1.948 -0.794	-0.4 0.3
	0.4h-1	-1.084	s	0.203	1.56E-04	-1.859	-0.3
	0.5h-1	-3.457	S	0.594	3 47F-05	-5 748	-1.1 -3.1
nIA.	0.7h-1 galM	-5.815 0.239	s	0.703 0.145	6.14E-10 9.98E-01	-8.529 -0.314	-3.1
BIA	gaiwi	-0.537		0.145	9.98E-01 5.64E-01	-0.314 -1.277	0.7
	pam	-1.504	s	0.231	6 11F-07	-2.386	-0.6
	pgi pfkA	-2.199 -2.321	S	0.381 0.409	3.43E-05 5.43E-05	-3.663 -3.894	-0.7
	pfkB	0.319	s	0.409	7.36F-01	-3.894 -0.162	0.8
	fbp	-0.052		0.146	1.00E+00	-0.608	0.5
	fbaB gapC	-0.420 -1.181	s	0.179 0.270	8.49E-01 8.00E-03	-1.099 -2.214	0.2 -0.1
	gapC gpmA	-1.181 0.058	s	0.270	1.00E+00	-2.214 -0.526	-0.1
	gpmB	0.019		0.154 0.140	1.00E+00	-0.512	0.5
	pykA	0.314		0.131	8.19E-01	-0.183	0.8
	pykF nnsA	0.393		0.127 0.126	3.21E-01 6.92F-01	-0.091 -0.153	0.8
	ppsA zwf	-0.155		0.126 0.164	1.00E+00	-0.778	0.4
	pgl gnd	-0.775		0.215	9.21E-02	-1.594	0.0
		-0.704 -4.200	s	0.200 0.556	1.18E-01 1.36E-08	-1.467 -6.343	0.0 -2.0
	rpiA	-0.622	3	0.374	9.97E-01	-2.060	0.8
	rpiB	-0.049		0.172	1.00E+00	-0.702	0.6
	tktA tktB	-1.718 0.050	s	0.251 0.144	1.42E-07 1.00E+00	-2.678 -0.497	-0.7 0.5
	talB	-0.191		0.152	1.00E+00	-0.769	0.3
	0.1h-1	-1.124	S	0.210	1.28E-04	-1.924	-0.3
	0.2h-1 0.4h-1	-0.189 -1.033	s	0.156 0.210	1.00E+00 8.69E-04	-0.781 -1.835	-0.2
	0.5h-1	-3.406	s	0.210	5.32E-05	-1.835 -5.706	-1.1
	0.7h-1	-5.765	s	0.705	8.73E-10	-8.486	-3.0
alB	galM glk	0.430 -0.345		0.143 0.193	3.84E-01 9.93E-01	-0.115 -1.080	0.9
		-1.313	s	0.230	2 86F-05	-1.080 -2.191	-0.4
	pgm pgi	-2.008	s	0.380	2.79E-04 3.72E-04	-3.469	-0.5
	pfkA pfkB	-2.130	S	0.408	3.72E-04	-3.700	-0.5
	fbp	0.511 0.140	S	0.124 0.144	1.79E-02 1.00E+00	0.039 -0.409	0.9
	fbaB	-0.229		0.177	1.00E+00	-0.902	0.4
	gapC	_n oon		0.269	7.69E-02	-2.019	0.0
	gpmA gpmB	0.250 0.210		0.152 0.138	9.98E-01 9.99E-01	-0.328 -0.313	0.8
	pykA	0.506	s	0.138	3.30E-02 2.22E-03	0.017	0.9
	nvkF	0.584	s	0 125	2.22E-03	0.017 0.109	1.0
	ppsA zwf	0.517 0.036	s	0.123 0.162	1.42E-02 1.00E+00	0.047 -0.580	0.9 0.6
	zwr pgl	-0.583		0.213	5.86E-01	-1.397	0.5
	gnd	-0.512		0.199	5.86E-01 7.05E-01	-1.270	0.2
	rpe	-4.008 -0.430	s	0.555 0.373	6.60E-08 1.00E+00	-6.150	-1.8 1.0
	rpiA rpiB	-0.430 0.142		0.373	1.00E+00	-1.866 -0.505	0.7
	tktA	-1.526	s	0.250	5.20E-06	-2.482	-0.5
	tktB	0.242	Ī	0.142	9.97E-01	-0.298	0.7
	talA 0.1h-1	0.191		0.152	1.00E+00	-0.387	0.7
	0.1h-1 0.2h-1	-0.933 0.002	S	0.208 0.154	5.06E-03 1.00E+00	-1.728 -0.583	-0.1 0.5
	0.4h-1	-0.842	s	0.209	2.49E-02 1.99E-04	-1.639	-0.0
	0.5h-1	-3.215	s	0.596		-5.513	-0.9

	nt Variable: mRh	Mean Difference	•			95% Confide Lower	ence Interv Upper
1)	(J)	(I-J)		Std. Error	Sig.	Bound	Bound
.1h-1	galM glk	1.363 0.587	s	0.204 0.241	2.43E-07 8.02E-01	0.585 -0.328	2.1 1.5
	pgm	-0.380 -1.075		0.271 0.407	1.00E+00 6.55E-01	-1.411 -2.630	0.6
	pgi pfkA	-1.197		0.433	5.62E-01	-2.854	0.4
	pfkB fbp	1.443	S	0.190 0.204	5.71E-09 2.20E-04	0.713 0.293	2.1
	fbaB	0.704	5	0.228	3.27E-01	-0.165	1.5
	gapC gpmA	-0.057 1.182	s	0.305 0.210	1.00E+00 3.57E-05	-1.218 0.383	1.1
	gpmB	1.143	S	0.199	2.85E-05	0.380	1.9
	pykA pykF	1.438 1.517	S	0.193 0.191	9.36E-09 9.31E-10	0.698 0.785	2.1
	ppsA zwf	1.450 0.969	S	0.190 0.217	4.66E-09 5.11E-03	0.721 0.142	2.1
	pgl	0.349	5	0.258	1.00E+00	-0.629	1.3
	gnd rpe	0.420 -3.076	s	0.246 0.574	9.97E-01 1.91E-04	-0.514 -5.280	1.3 -0.8
	rpiA	0.502		0.400	1.00E+00	-1.028	2.0
	rpiB tktA	1.075 -0.594	S	0.223 0.289	1.20E-03 9.60E-01	0.226 -1.691	1.9 0.5
	tktB talA	1.174	S	0.203	1.94E-05 1.28F-04	0.401 0.324	1.9
	talB	0.933	S	0.208	5.06E-03	0.138	1.7
	0.2h-1 0.4h-1	0.935 0.091	S	0.211 0.254	5.96E-03 1.00E+00	0.130 -0.874	1.7
	0.5h-1 0.7h-1	-2.282 -4.640	s	0.613 0.720	7.14E-02 1.82E-06	-4.639 -7.410	0.0 -1.8
.2h-1	galM	0.428	3	0.147	4.52E-01	-0.132	0.9
	glk pgm	-0.347 -1.315	s	0.196 0.232	9.94E-01 3.47E-05	-1.093 -2.201	0.3 -0.4
	pgi	-2.010	S	0.382	2.91E-04	-3.477	-0.5
	pfkA pfkB	-2.132 0.509	S	0.410 0.128	3.85E-04 3.09E-02	-3.707 0.019	-0.5 0.9
	fbp	0.138	Ü	0.148	1.00E+00	-0.425	0.7
	fbaB gapC	-0.231 -0.992		0.180 0.271	1.00E+00 8.12E-02	-0.916 -2.028	0.4
	gpmA gpmB	0.248 0.208		0.156 0.142	9.99E-01 1.00E+00	-0.344 -0.330	0.8
	pvkA	0.504		0.133	5.23E-02	-0.002	1.0
	pykF ppsA	0.582 0.515	S	0.129 0.128	4.48E-03 2.50E-02	0.090 0.028	1.0
	zwf	0.034	3	0.166	1.00E+00	-0.595	0.6
	pgl gnd	-0.585 -0.515		0.216 0.202	6.05E-01 7.24E-01	-1.409 -1.283	0.2
	rpe rpiA	-4.010 -0.432	S	0.556 0.375	6.70E-08 1.00E+00	-6.155 -1.873	-1.8 1.0
	rpiB	0.140		0.173	1.00E+00	-0.519	0.7
	tktA tktB	-1.528 0.240	S	0.252 0.146	6.14E-06 9.98E-01	-2.492 -0.315	-0.5 0.7
	talA	0.189		0.156	1.00E+00	-0.402	0.7
	talB 0.1h-1	-0.002 -0.935	s	0.154 0.211	1.00E+00 5.96E-03	-0.587 -1.739	0.5 -0.1
	0.4h-1 0.5h-1	-0.844 -3.217	s s	0.212 0.597	2.83E-02 2.01E-04	-1.650 -5.518	-0.0 -0.9
	0.7h-1	-5.575	S	0.706	2.98E-09	-8.298	-2.8
.4h-1	galM glk	1.272 0.497	S	0.204 0.241	2.39E-06 9.60E-01	0.493 -0.421	2.0
	pgm	-0.471		0.272	9.96E-01	-1.503	0.5
	pgi pfkA	-1.166 -1.288		0.407	4.85E-01 4.06E-01	-2.721 -2.946	0.3
	pfkB fbp	1.353 0.982	S	0.191 0.205	6.50E-08 1.49E-03	0.621 0.200	2.0
	fbaB	0.613	3	0.229	6.28E-01	-0.257	1.4
	gapC gpmA	-0.148 1.092	s	0.305 0.210	1.00E+00 2.64E-04	-1.309 0.290	1.0
	gpmB	1.052	s	0.200	2.27E-04	0.287	1.8
	pykA pykF	1.348 1.426	S	0.194 0.191	1.05E-07 1.06E-08	0.605 0.692	2.0
	ppsA	1.359	S	0.190	5.32E-08	0.628	2.0
	zwf pgl	0.878 0.259	S	0.218 0.258	2.38E-02 1.00E+00	0.050 -0.722	1.3
	gnd rpe	0.329 -3.167	s	0.246 0.574	1.00E+00 9.82E-05	-0.606 -5.372	1.2 -0.9
	rpiA	0.412		0.401	1.00E+00	-1.119	1.9
	rpiB tktA	0.984 -0.684	S	0.224	6.29E-03 8.42E-01	0.133 -1.783	1.8
	tktB	1.084	S	0.203	1.56E-04	0.308	1.8
	talA talB	1.033 0.842	S	0.210 0.209	8.69E-04 2.49E-02	0.232 0.045	1.8
	0.1h-1 0.2h-1	-0.091 0.844	s	0.254 0.212	1.00E+00 2.83E-02	-1.056 0.038	0.8
	0.5h-1	-2.373	s	0.613	4.64E-02	-4.731	-0.0
.5h-1	0.7h-1 galM	-4.731 3.645	S	0.720 0.594	1.03E-06 8.98E-06	-7.501 1.352	-1.9 5.9
	glk	2.870	s	0.608	2.58E-03	0.530	5.2
	pgm pgi	1.902		0.621	3.45E-01 9.95E-01	-0.481 -1.425	4.2
	pfkA	1.085 3.726	s	0.707 0.590	9.99E-01 4.37E-06	-1.605 1.448	3.7 6.0
	pfkB fbp	3.355	S	0.595	7.26E-05	1.061	5.6
	fbaB gapC	2.986 2.225	S	0.603 0.636	1.10E-03 1.28E-01	0.663 -0.212	5.3 4.6
	gpmA	3.465	s	0.596	3.51E-05	1.165	5.7
	gpmB pykA	3.425 3.721	S	0.593 0.591	4.23E-05 4.67E-06	1.137 1.440	5.7
	pykF ppsA	3.799 3.732	S	0.590 0.590	2.55E-06 4.16E-06	1.521	6.0
	zwf	3.251	S	0.599	1.69E-04	0.942	5.5
	pgl gnd	2.632 2.703	S	0.615 0.610	1.22E-02 7.35E-03	0.269 0.356	4.9 5.0
	rpe	-0.793	-	0.801	1.00E+00	-3.835	2.2
	rpiA rpiB	2.785 3.357	s s	0.687 0.601	2.28E-02 8.61E-05	0.166 1.041	5.4 5.6
	tktA tktB	1.689 3.457	s	0.629 0.594	6.23E-01 3.47E-05	-0.721 1.165	4.0
	talA	3.406	S	0.597	5.32E-05	1.107	5.7
	talB 0.1h-1	3.215 2.282	S	0.596 0.613	1.99E-04 7.14E-02	0.917 -0.075	5.5 4.6
	0.2h-1	3.217	S	0.597	2.01E-04	0.916	5.5
	0.4h-1 0.7h-1	2.373 -2.358	s	0.613 0.911	4.64E-02 6.97E-01	0.015 -5.819	4.5
.7h-1	galM	6.003 5.228	s	0.704	2.12E-10 3.67E-08	3.288	8.7
	glk pgm	4.260	s	0.726	2.26E-05	1.468	7.0
	pgi pfkA	3.566 3.444	S	0.787 0.801	4.24E-03 9.77E-03	0.561 0.389	6.6
	pfkB	6.084	S	0.700	1.38E-10	3.381	8.7
	fbp fbaB	5.713 5.344	S S S	0.704 0.711	1.17E-09 1.54E-08	2.997 2.603	8.4
	gapC	4.583 5.823	S	0.739 0.705	4.42E-06	1.746	7.4
	gpmA gpmB	5.783	S	0.702	6.08E-10 7.34E-10	3.101 3.072	8.5 8.4
	pykA pykF	6.079 6.158	S	0.701	1.42E-10 1.04E-10	3.373 3.454	8.7
	ppsA	6.090	S	0.700	1.34E-10	3.388	8.7
	zwf pgl	5.609 4.990	S	0.708 0.721	2.48E-09 2.02E-07	2.880 2.215	8.3 7.7
	gnd	5.061	S	0.717	1.14E-07	2.300	7.8
	rpe rpiA	1.565 5.143	s	0.885 0.783	9.94E-01 4.95E-07	-1.799 2.150	4.9
	rpiB	5.715	s	0.710	1.30E-09	2.980	8.4
	tktA tktB	4.047 5.815	S	0.733 0.703	9.48E-05 6.14E-10	1.232 3.100	6.8 8.5
	talA talB	5.765	S	0.705	8.73E-10	3.043	8.4
	0.1h-1	5.573 4.640	S	0.705 0.720	2.97E-09 1.82E-06	2.853 1.871	8.2 7.4
	0.2h-1	5.575	S	0.706 0.720	2.98E-09 1.03E-06	2.852 1.961	8.2 7.5
	0.4h-1	4.731					

## **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.

Depende	ent Variable: Prote	ein(LC-MS)	Multiple Co	omparisons				Depender	nt Variable: Prote	ein(LC-MS)	Multiple Co	mparisons			
m	(J)	Mean Difference (I-J)		Std Error	Sia.	95% Confide Lower Bound	Upper Bound	m.	(J)	Mean Difference (I-J)		Std. Error	Sia.	95% Confide Lower Bound	Upper Bound
galM	glk pgm	-1.568 -1.236	s	0.246 0.227	7.89E-06 2.67E-04	-2.528 -2.120	-0.608 -0.353	pfkB	galM glk	0.526 -1.042	s	0.138 0.262	5.45E-02 3.71E-02	-0.004 -2.057	1.056
	pgi pfkA pfkB	-1.662 -1.176 -0.526	s s	0.304 0.256 0.138	3.09E-04 5.94E-03 5.45E-02	-2.852 -2.175 -1.056	-0.472 -0.177 0.004		pgm pgi pfkA	-0.710 -1.136 -0.650		0.244 0.317 0.272	4.58E-01 1.15E-01 8.21E-01	-1.654 -2.371 -1.702	0.234 0.099 0.403
	fbp fbaB	-0.998 -1.464	s	0.231 0.296	1.40E-02 1.85E-03	-1.898 -2.620	-0.098 -0.308		fbp fbaB	-0.472 -0.937		0.272 0.248 0.309	9.82E-01 3.74E-01	-1.702 -1.431 -2.139	0.488 0.264
	gapC gpmA	-1.112 -0.642		0.312 0.169	1.27E-01 6.00E-02	-2.336 -1.295	0.112 0.011		gapC gpmA	-0.586 -0.116		0.325 0.192	9.90E-01 1.00E+00	-1.853 -0.853	0.681 0.620
	gpmB pykA	-0.476 0.120		0.158 0.103	3.81E-01 1.00E+00	-1.085 -0.276	0.134 0.515		gpmB pykA	0.050 0.646	S	0.182 0.138	1.00E+00 3.06E-03	-0.649 0.115	0.750 1.177
	pykF ppsA zwf	0.095 -0.058 -0.206		0.105 0.110 0.107	1.00E+00 1.00E+00 9.80E-01	-0.309 -0.479 -0.615	0.499 0.362 0.203		pykF ppsA zwf	0.621 0.468 0.320	S	0.139 0.143 0.140	6.97E-03 2.23E-01 8.81E-01	0.084 -0.081 -0.220	1.158 1.017 0.861
	pgl gnd	-0.648 -0.454		0.186 0.184	1.43E-01 7.76E-01	-1.371 -1.169	0.074 0.261		pgl gnd	-0.122 0.072		0.207 0.206	1.00E+00 1.00E+00	-0.920 -0.719	0.675 0.863
	rpe rpiA rpiB	-2.738 -1.269	S	0.426 0.281	1.05E-05 8.05E-03	-4.412 -2.369	-1.064 -0.169		rpe rpiA rpiB	-2.212 -0.743	S	0.436	1.21E-03 7.46E-01	-3.917 -1.891	-0.507 0.405
	tktA tktB	-0.764 -0.744 -0.840	S	0.186 0.173 0.230	2.45E-02 1.30E-02 9.94E-02	-1.483 -1.413 -1.738	-0.044 -0.075 0.059		tktA tktB	-0.237 -0.218 -0.313		0.207 0.195 0.248	1.00E+00 1.00E+00 1.00E+00	-1.032 -0.969 -1.271	0.558 0.533 0.645
	talA talB	-0.886 -0.775		0.228 0.237	5.12E-02 2.36E-01	-1.773 -1.698	0.002 0.148		talA talB	-0.360 -0.249		0.245 0.254	1.00E+00 1.00E+00	-1.308 -1.229	0.589 0.732
	0.1h-1 0.2h-1 0.4h-1	-1.843 -1.134 -1.439	S	0.386 0.316 0.352	3.63E-03 1.16E-01 3.13E-02	-3.356 -2.370 -2.819	-0.330 0.102 -0.058		0.1h-1 0.2h-1 0.4h-1	-1.317 -0.608 -0.912		0.397 0.329 0.364	2.15E-01 9.87E-01 7.47E-01	-2.864 -1.886 -2.331	0.231 0.671 0.506
	0.5h-1 0.7h-1	-1.963 -3.437	S	0.486 0.540	3.64E-02 1.41E-05	-3.871 -5.560	-0.055 -1.314		0.5h-1 0.7h-1	-1.437 -2.911	s	0.495 0.548	4.64E-01 5.64E-04	-3.372 -5.058	0.498 -0.763
glk	galM pgm	1.568 0.332	s	0.246 0.318	7.89E-06 1.00E+00	0.608 -0.888	2.528 1.552	fbp	galM glk	0.998 -0.570	S	0.231 0.321	1.40E-02 9.93E-01	0.098 -1.801	1.898 0.661
	pgi pfkA pfkB	-0.094 0.392 1.042		0.377 0.340 0.262	1.00E+00 1.00E+00 3.71E-02	-1.542 -0.910 0.027	1.354 1.694 2.057		pgm pgi pfkA	-0.238 -0.664 -0.178		0.307 0.368 0.329	1.00E+00 9.91E-01 1.00E+00	-1.414 -2.077 -1.439	0.937 0.748 1.083
	fbp fbaB	0.570	3	0.321 0.370	9.93E-01 1.00E+00	-0.661 -1.317	1.801 1.526		pfkB fbaB	0.472		0.248 0.361	9.82E-01 1.00E+00	-0.488 -1.850	1.431
	gapC gpmA	0.456 0.926		0.384 0.280	1.00E+00 2.09E-01	-1.019 -0.152	1.931 2.003		gapC gpmA	-0.114 0.356		0.374 0.267	1.00E+00 1.00E+00	-1.554 -0.670	1.326 1.381
	gpmB pykA	1.092 1.688 1.663	SSS	0.274 0.246 0.247	3.29E-02 1.13E-06 1.79E-06	0.038 0.728 0.700	2.147 2.648 2.626		gpmB pykA pykF	0.522 1.118 1.093	S	0.260 0.231 0.232	9.66E-01 2.50E-03 3.82E-03	-0.479 0.217 0.189	1.523 2.018 1.996
	pykF ppsA zwf	1.510	S	0.249 0.248	2.37E-05 2.20E-04	0.540 0.397	2.479		ppsA zwf	0.940	S	0.234 0.232	3.48E-02 1.75E-01	0.029	1.850
	pgl gnd	0.920 1.114	s	0.291 0.289	2.84E-01 4.92E-02	-0.197 0.001	2.037 2.227		pgl gnd	0.349 0.544		0.278 0.277	1.00E+00 9.74E-01	-0.718 -0.519	1.417 1.607
	rpe rpiA rpiB	-1.170 0.299 0.804		0.481 0.359 0.290	7.99E-01 1.00E+00 5.58E-01	-3.029 -1.079 -0.311	0.689 1.677 1.920		rpe rpiA rpiB	-1.740 -0.271 0.234		0.474 0.349 0.278	8.64E-02 1.00E+00 1.00E+00	-3.573 -1.611 -0.832	0.092 1.068 1.300
	tktA tktB	0.824 0.729		0.282 0.321	4.48E-01 8.87E-01	-0.263 -0.502	1.910		tktA tktB	0.254 0.158		0.269	1.00E+00 1.00E+00	-0.781 -1.028	1.289
	talA talB	0.682 0.793		0.319 0.325	9.36E-01 7.98E-01	-0.541 -0.454	1.905 2.041		talA talB	0.112 0.223		0.307 0.314	1.00E+00 1.00E+00	-1.067 -0.981	1.291 1.427
	0.1h-1 0.2h-1 0.4h-1	-0.275 0.434 0.129		0.446 0.387 0.417	1.00E+00 1.00E+00 1.00E+00	-1.993 -1.051 -1.475	1.444 1.919 1.734		0.1h-1 0.2h-1 0.4h-1	-0.845 -0.136 -0.441		0.438 0.377 0.408	9.79E-01 1.00E+00 1.00E+00	-2.534 -1.586 -2.013	0.844 1.314 1.132
	0.5h-1 0.7h-1	-0.395 -1.869		0.417 0.535 0.585	1.00E+00 2.73E-01	-1.475 -2.466 -4.138	1.676		0.5h-1 0.7h-1	-0.965 -2.439	s	0.528 0.578	9.89E-01 1.85E-02	-2.013 -3.013 -4.687	1.082
pgm	galM glk	1.236 -0.332	s	0.227 0.318	2.67E-04 1.00E+00	0.353 -1.552	2.120 0.888	fbaB	galM glk	1.464 -0.104	s	0.296 0.370	1.85E-03 1.00E+00	0.308 -1.526	2.620 1.317
	pgi pfkA pfkB	-0.426 0.060 0.710		0.365 0.326 0.244	1.00E+00 1.00E+00 4.58E-01	-1.829 -1.190 -0.234	0.977 1.310 1.654		pgm pgi pfkA	0.228 -0.198 0.288		0.358 0.411 0.377	1.00E+00 1.00E+00 1.00E+00	-1.147 -1.775 -1.159	1.602 1.379 1.734
	fbp fbaB	0.238		0.244 0.307 0.358	1.00E+00 1.00E+00	-0.234 -0.937 -1.602	1.414		pfkB fbp	0.288 0.937 0.466		0.309 0.361	3.74E-01 1.00E+00	-0.264 -0.919	2.139 1.850
	gapC gpmA	0.124 0.594		0.372 0.263	1.00E+00 8.91E-01	-1.306 -0.418	1.555 1.605		gapC gpmA	0.352 0.821		0.417 0.324	1.00E+00 7.34E-01	-1.249 -0.432	1.953 2.075
	gpmB pykA pykF	0.760 1.356 1.331	S	0.256 0.227 0.228	4.12E-01 3.56E-05 5.80E-05	-0.226 0.472 0.444	1.747 2.240 2.218		gpmB pykA pykF	0.988 1.583 1.558	S	0.319 0.296 0.296	3.28E-01 4.40E-04 6.16E-04	-0.246 0.427 0.400	2.222 2.740 2.717
	ppsA zwf	1.178	S	0.220 0.230 0.228	8.35E-04 7.40E-03	0.284	2.072		ppsA zwf	1.405 1.258	S	0.298 0.297	4.00E-03 1.91E-02	0.242 0.097	2.569 2.418
	pgl gnd	0.588 0.782		0.274 0.273	9.35E-01 4.88E-01	-0.466 -0.267	1.642 1.831		pgl gnd	0.815 1.010		0.334 0.333	7.92E-01 3.67E-01	-0.471 -0.273	2.102 2.293
	rpe rpiA rpiB	-1.502 -0.033 0.473		0.472 0.346 0.274	2.77E-01 1.00E+00 9.96E-01	-3.328 -1.362 -0.580	0.324 1.296 1.525		rpe rpiA rpiB	-1.274 0.194 0.700		0.508 0.395 0.333	7.52E-01 1.00E+00 9.45E-01	-3.231 -1.319 -0.585	0.682 1.708 1.986
	tktA tktB	0.492		0.266	9.88E-01 1.00E+00	-0.529 -0.778	1.513		tktA tktB	0.719		0.326	9.11E-01 9.95E-01	-0.542 -0.760	1.980
	talA talB	0.350 0.461		0.304 0.311	1.00E+00 1.00E+00	-0.816 -0.731	1.517 1.654		talA talB	0.578 0.689		0.359 0.364	9.98E-01 9.84E-01	-0.800 -0.710	1.955 2.088
	0.1h-1 0.2h-1 0.4h-1	-0.607 0.102 -0.202		0.436 0.375 0.406	1.00E+00 1.00E+00 1.00E+00	-2.288 -1.339 -1.767	1.075 1.543 1.362		0.1h-1 0.2h-1 0.4h-1	-0.379 0.330 0.025		0.475 0.420 0.448	1.00E+00 1.00E+00 1.00E+00	-2.204 -1.281 -1.694	1.446 1.940 1.744
	0.5h-1 0.7h-1	-0.202 -0.727 -2.201		0.406 0.526 0.577	1.00E+00 1.00E+00 6.13E-02	-1.767 -2.768 -4.443	1.314		0.5h-1 0.7h-1	-0.500 -1.973		0.560	1.00E+00 1.00E+00 2.41E-01	-2.657 -4.320	1.658
pgi	galM glk	1.662 0.094	s	0.304 0.377	3.09E-04 1.00E+00	0.472 -1.354	2.852 1.542	gapC	galM glk	1.112 -0.456		0.312 0.384	1.27E-01 1.00E+00	-0.112 -1.931	2.336 1.019
	pgm pfkA pfkB	0.426 0.486 1.136		0.365 0.384 0.317	1.00E+00 1.00E+00 1.15E-01	-0.977 -0.987 -0.099	1.829 1.959 2.371		pgm pgi pfkA	-0.124 -0.550 -0.064		0.372 0.423 0.390	1.00E+00 1.00E+00 1.00E+00	-1.555 -2.175 -1.563	1.306 1.074 1.435
	fbp fbaB	0.664 0.198		0.368 0.411	9.91E-01 1.00E+00	-0.748 -1.379	2.077		pfkB fbp	0.586 0.114		0.325 0.374	9.90E-01 1.00E+00	-0.681 -1.326	1.853 1.554
	gapC gpmA	0.550 1.020		0.423 0.332	1.00E+00 3.46E-01	-1.074 -0.265	2.175 2.305		fbaB gpmA	-0.352 0.469		0.417 0.340	1.00E+00 1.00E+00	-1.953 -0.846	1.249 1.785
	gpmB pykA pykF	1.186 1.782 1.757	S	0.327 0.304 0.305	9.81E-02 7.25E-05 1.01F-04	-0.080 0.591 0.564	2.453 2.972 2.950		gpmB pykA pykF	0.636 1.232 1.207	s	0.334 0.312 0.313	9.81E-01 4.69E-02 5.96E-02	-0.661 0.007 -0.020	1.934 2.456 2.433
	ppsA zwf	1.604 1.456	S	0.306 0.305	6.78E-04 3.50E-03	0.406 0.262	2.802 2.651		ppsA zwf	1.054 0.906		0.315 0.314	2.04E-01 4.76E-01	-0.178 -0.322	2.285 2.134
	pgl gnd	1.014		0.341 0.340	4.12E-01 1.18E-01	-0.303 -0.105	2.331		pgl gnd	0.463 0.658		0.349 0.348	1.00E+00 9.83E-01	-0.884 -0.686	1.810 2.001
	rpe rpiA rpiB	-1.076 0.393 0.899		0.513 0.401 0.341	9.47E-01 1.00E+00 6.61E-01	-3.051 -1.146 -0.418	0.899 1.932 2.215		rpe rpiA rpiB	-1.626 -0.157 0.348		0.518 0.408 0.348	3.00E-01 1.00E+00 1.00E+00	-3.620 -1.721 -0.998	0.367 1.406 1.694
	tktA tktB	0.918 0.823		0.334 0.367	5.77E-01 8.99E-01	-0.374 -0.589	2.210 2.234		tktA tktB	0.368 0.272		0.342 0.374	1.00E+00 1.00E+00	-0.955 -1.167	1.690 1.712
	talA talB 0.1h-1	0.776 0.887		0.366 0.371	9.40E-01 8.25E-01	-0.629 -0.539	2.182 2.314		talA talB	0.226 0.337		0.373 0.378	1.00E+00 1.00E+00	-1.207 -1.116	1.659 1.791
	0.1h-1 0.2h-1 0.4h-1	-0.181 0.528 0.223		0.480 0.426 0.454	1.00E+00 1.00E+00 1.00E+00	-2.025 -1.105 -1.517	1.664 2.162 1.964		0.1h-1 0.2h-1 0.4h-1	-0.731 -0.022 -0.327		0.486 0.432 0.459	9.99E-01 1.00E+00 1.00E+00	-2.595 -1.679 -2.089	1.134 1.634 1.435
	0.5h-1 0.7h-1	-0.301 -1.775		0.564 0.611	1.00E+00 4.60E-01	-2.475 -4.137	1.873 0.587		0.5h-1 0.7h-1	-0.851 -2.325		0.569 0.615	9.99E-01 6.37E-02	-3.042 -4.702	1.339 0.052
pfkA	galM glk	1.176 -0.392	s	0.256 0.340	5.94E-03 1.00E+00	0.177 -1.694	2.175 0.910	gpmA	galM glk	0.642 -0.926		0.169 0.280	6.00E-02 2.09E-01	-0.011 -2.003	1.295 0.152
	pgm pgi pfkB	-0.060 -0.486 0.650		0.326 0.384 0.272	1.00E+00 1.00E+00 8.21E-01	-1.310 -1.959 -0.403	1.190 0.987 1.702		pgm pgi pfkA	-0.594 -1.020 -0.534		0.263 0.332 0.289	8.91E-01 3.46E-01 9.88E-01	-1.605 -2.305 -1.646	0.418 0.265 0.579
	fbp fbaB	0.178		0.329	1.00E+00 1.00E+00	-1.083 -1.734	1.439		pfkB fbp	0.116		0.192	1.00E+00 1.00E+00	-0.620 -1.381	0.853
	gapC gpmA	0.064 0.534		0.390 0.289	1.00E+00 9.88E-01	-1.435 -0.579	1.563 1.646		fbaB gapC	-0.821 -0.469		0.324 0.340	7.34E-01 1.00E+00	-2.075 -1.785	0.432 0.846
	gpmB pykA pykF	0.700 1.296 1.271	S	0.283 0.256 0.257	7.70E-01 1.19E-03 1.75E-03	-0.390 0.296 0.268	1.791 2.295 2.273		gpmB pykA pykF	0.167 0.762 0.737	S	0.207 0.169 0.170	1.00E+00 6.40E-03 1.17E-02	-0.626 0.108 0.079	0.959 1.416 1.396
	ppsA zwf	1.2/1 1.118 0.970	S	0.257 0.259 0.258	1.40E-02 7.21E-02	0.268 0.109 -0.034	2.273 2.126 1.974		ppsA zwf	0.737 0.584 0.436	S	0.170 0.173 0.171	1.17E-02 1.81E-01 7.21E-01	-0.084 -0.225	1.252 1.098
	pgl gnd	0.528 0.722		0.299 0.298	9.94E-01 8.06E-01	-0.623 -0.424	1.678 1.868		pgl gnd	-0.006 0.188		0.229 0.228	1.00E+00 1.00E+00	-0.884 -0.684	0.872 1.061
	rpe rpiA miB	-1.562 -0.093 0.412		0.487 0.366 0.299	2.60E-01 1.00E+00 1.00E+00	-3.440 -1.497 -0.737	0.316 1.311 1.562		rpe rpiA rpiB	-2.096 -0.627 -0.121	S	0.447 0.312 0.229	4.07E-03 9.65E-01 1.00F+00	-3.836 -1.830 -0.998	-0.355 0.576 0.755
	rpiB tktA tktB	0.432 0.337		0.291 0.329	1.00E+00 1.00E+00	-0.689 -0.924	1.553 1.597		tktA tktB	-0.102 -0.197		0.218 0.266	1.00E+00 1.00E+00	-0.939 -1.222	0.735 0.827
	talA talB	0.290 0.401		0.327 0.333	1.00E+00 1.00E+00	-0.963 -0.876	1.543		talA talB	-0.243 -0.132		0.264 0.272	1.00E+00 1.00E+00	-1.259 -1.178	0.772 0.913
	0.1h-1 0.2h-1 0.4h-1	-0.667 0.042		0.452 0.393	1.00E+00 1.00E+00	-2.405 -1.467 -1.889	1.072 1.551		0.1h-1 0.2h-1 0.4h-1	-1.200 -0.492 -0.796		0.409 0.343	4.38E-01 1.00E+00 9.39E-01	-2.788 -1.819	0.387 0.835 0.665
	0.4h-1 0.5h-1 0.7h-1	-0.263 -0.787 -2.261		0.423 0.540 0.589	1.00E+00 1.00E+00 5.59E-02	-1.889 -2.875 -4.544	1.364 1.300 0.023		0.4n-1 0.5h-1 0.7h-1	-0.796 -1.321 -2.794	9	0.377 0.504 0.556	9.39E-01 6.71E-01 1.43E-03	-2.258 -3.287 -4.970	0.665 0.646 -0.619
*. *S* Th	e mean difference		at the .05 lev					*, *S* The	mean difference		at the .05 lev		30		

Dependen	nt Variable: Prot		Multiple Co	omparisons					Depende	nt Variable: Pro		Multiple C	omparisons			
m	(P	Mean Difference		Std. Error	Sia.	95% Confide Lower	Upper		m	(D	Mean Difference		Std. Error	Oin.	95% Confide Lower	Upper
(I) gpmB	(J) galM glk	(I-J) 0.476 -1.092		0.158 0.274	Sig. 3.81E-01 3.29E-02	-0.134 -2.147	Bound 1.085 -0.038	ŀ	(I) pgl	(J) galM glk	(I-J) 0.648 -0.920	_	0.186 0.291	Sig. 1.43E-01 2.84E-01	-0.074 -2.037	1.37 0.19
	pgm	-0.760	5	0.256	4.12E-01	-1.747	0.226			pgm	-0.588		0.274	9.35E-01	-1.642	0.46
	pgi pfkA	-1.186 -0.700		0.327 0.283	9.81E-02 7.70E-01	-2.453 -1.791	0.080			pgi pfkA pfkB	-1.014 -0.528		0.341	4.12E-01 9.94E-01	-2.331 -1.678	0.30
	pfkB fbp	-0.050 -0.522		0.182 0.260	1.00E+00 9.66E-01	-0.750 -1.523	0.649			fbp	0.122 -0.349		0.207	1.00E+00 1.00E+00	-0.675 -1.417	0.92
	fbaB gapC	-0.988 -0.636		0.319 0.334	3.28E-01 9.81E-01	-2.222 -1.934	0.246 0.661			fbaB gapC	-0.815 -0.463		0.334 0.349	7.92E-01 1.00E+00	-2.102 -1.810	0.47
	gpmA pykA	-0.167 0.595		0.207 0.158	1.00E+00 6.53E-02	-0.959 -0.015	0.626 1.205			gpmA gpmB	0.006 0.173		0.229 0.221	1.00E+00 1.00E+00	-0.872 -0.676	0.88
	pykF ppsA	0.571 0.417		0.159 0.162	1.09E-01 7.07E-01	-0.045 -0.208	1.186 1.043			pykA pykF	0.768 0.743	5	0.186 0.187	2.42E-02 3.88E-02	0.045 0.016	1.49
	zwf pgl	0.270 -0.173		0.160 0.221	9.97E-01 1.00E+00	-0.348 -1.021	0.888 0.676			ppsA zwf	0.590 0.443		0.190 0.188	3.23E-01 8.42E-01	-0.145 -0.287	1.32
	gnd rpe	0.022 -2.262	s	0.220 0.443	1.00E+00 9.70E-04	-0.821 -3.990	0.864 -0.535			gnd rpe	0.194 -2.090	s	0.241 0.454	1.00E+00 5.15E-03	-0.728 -3.853	1.11 -0.32
	rpiA rpiB	-0.794 -0.288		0.306 0.221	6.90E-01 1.00E+00	-1.976 -1.134	0.389 0.559			rpiA rpiB	-0.621 -0.115		0.321 0.242	9.79E-01 1.00E+00	-1.858 -1.041	0.61
	tktA tktB	-0.268 -0.364		0.210 0.260	1.00E+00 1.00E+00	-1.074 -1.363	0.537 0.636			tktA tktB	-0.096 -0.191		0.232 0.278	1.00E+00 1.00E+00	-0.985 -1.257	0.79
	talA talB	-0.410 -0.299		0.257 0.265	9.99E-01 1.00E+00	-1.400 -1.321	0.580			talA talB	-0.237 -0.126		0.275 0.283	1.00E+00 1.00E+00	-1.295 -1.213	0.82
	0.1h-1 0.2h-1	-1.367 -0.658		0.404 0.338	1.85E-01 9.75E-01	-2.939 -1.967	0.205 0.650			0.1h-1 0.2h-1	-1.194 -0.486		0.416 0.352	4.85E-01 1.00E+00	-2.807 -1.844	0.4
	0.4h-1 0.5h-1	-0.963 -1.488		0.372 0.501	6.92E-01 4.17E-01	-2.408 -3.442	0.482			0.4h-1 0.5h-1	-0.790 -1.315		0.385	9.55E-01 7.01E-01	-2.279 -3.301	0.69
	0.7h-1	-1.466 -2.961 -0.120	s	0.553 0.103	4.56E-04 1.00E+00	-5.126 -0.515	-0.796 0.276			0.7h-1	-2.788 0.454	s	0.510 0.562 0.184	1.68E-03 7.76E-01	-4.982 -0.261	-0.59 1.16
pykA	galM glk	-1.688	s	0.246	1.13E-06	-2.648	-0.728		gnd	galM glk	-1.114	5	0.289	4.92E-02	-2.227	-0.00
	pgm pgi	-1.356 -1.782	S	0.227 0.304	3.56E-05 7.25E-05	-2.240 -2.972	-0.472 -0.591			pgm pgi pfkA	-0.782 -1.208		0.273 0.340	4.88E-01 1.18E-01	-1.831 -2.522	0.20
	pfkA pfkB	-1.296 -0.646	S	0.256 0.138	1.19E-03 3.06E-03	-2.295 -1.177	-0.296 -0.115			pfkB	-0.722 -0.072		0.298 0.206	8.06E-01 1.00E+00	-1.868 -0.863	0.42
	fbp fbaB	-1.118 -1.583	S	0.231 0.296	2.50E-03 4.40E-04	-2.018 -2.740	-0.217 -0.427			fbp fbaB	-0.544 -1.010		0.277 0.333	9.74E-01 3.67E-01	-1.607 -2.293	0.51
	gapC gpmA	-1.232 -0.762	S	0.312 0.169	4.69E-02 6.40E-03	-2.456 -1.416	-0.007 -0.108			gapC gpmA	-0.658 -0.188		0.348 0.228	9.83E-01 1.00E+00	-2.001 -1.061	0.68
	gpmB pykF	-0.595 -0.025		0.158 0.106	6.53E-02 1.00E+00	-1.205 -0.430	0.015 0.380			gpmB pykA	-0.022 0.574		0.220 0.184	1.00E+00 3.21E-01	-0.864 -0.142	0.82
	ppsA zwf	-0.178 -0.326		0.110 0.107	9.98E-01 3.56E-01	-0.600 -0.735	0.244			pykF ppsA	0.549 0.396		0.185 0.188	4.23E-01 9.43E-01	-0.171 -0.333	1.26
	pgl gnd	-0.768 -0.574	s	0.186 0.184	2.42E-02 3.21E-01	-0.735 -1.491 -1.289	-0.045 0.142			zwf pgl	0.248 -0.194		0.186 0.241	1.00E+00 1.00E+00	-0.333 -0.474 -1.117	0.97
	rpe rpiA	-2.858 -1.389	s	0.426	3.64E-06 1.93E-03	-4.532 -2.489	-1.184 -0.289			rpe rpiA	-2.284 -0.815	5	0.241 0.453 0.320	1.10E-03 7.24E-01	-4.045 -2.049	-0.52 0.41
	rpiB tktA	-1.389 -0.883 -0.864	S	0.281 0.186 0.173	1.93E-03 2.85E-03 1.15E-03	-2.489 -1.603 -1.534	-0.289 -0.163 -0.194			rpiB tktA	-0.815 -0.310 -0.290		0.320 0.240 0.231	1.00E+00 1.00E+00	-2.049 -1.230 -1.174	0.41 0.61 0.59
	tktB talA	-0.864 -0.959 -1.005	S	0.173 0.231 0.228	1.15E-03 2.31E-02 1.04E-02	-1.858	-0.194 -0.061 -0.117			tktB talA	-0.290 -0.386 -0.432		0.231 0.276 0.274	1.00E+00 1.00E+00 9.99E-01	-1.447	0.67
	talB	-1.005 -0.894 -1.962	S	0.228 0.237 0.386	1.04E-02 7.00E-02 1.27E-03	-1.894 -1.818 -3.476	-0.117 0.029 -0.449			talB	-0.432 -0.321 -1.389		0.274 0.282 0.415	9.99E-01 1.00E+00 1.98E-01	-1.485 -1.403 -2.999	0.62 0.76 0.22
	0.1h-1 0.2h-1 0.4h-1	-1.962 -1.254 -1.558	S	0.386 0.316 0.352	1.27E-03 4.27E-02 1.12E-02	-3.476 -2.490 -2.939	-0.449 -0.018 -0.178			0.1h-1 0.2h-1 0.4h-1	-1.389 -0.680 -0.985		0.415 0.351 0.384	1.98E-01 9.77E-01 7.10E-01	-2.999 -2.035 -2.471	0.22 0.67 0.50
	0.5h-1	-2.083	S	0.486	1.77E-02	-3.991	-0.175			0.5h-1	-1.509		0.510	4.22E-01	-3.494	0.47
pykF	0.7h-1 galM	-3.556 -0.095	s	0.540 0.105	6.20E-06 1.00E+00	-5.680 -0.499	-1.433 0.309		rpe	0.7h-1 galM	-2.983 2.738	5	0.561 0.426	4.75E-04 1.05E-05	-5.174 1.064	-0.79 4.41
	glk pgm	-1.663 -1.331	S S	0.247 0.228	1.79E-06 5.80E-05	-2.626 -2.218	-0.700 -0.444			glk pgm	1.170 1.502		0.481 0.472	7.99E-01 2.77E-01	-0.689 -0.324	3.02
	pgi pfkA	-1.757 -1.271	S	0.305 0.257	1.01E-04 1.75E-03	-2.950 -2.273	-0.564 -0.268			pgi pfkA	1.076 1.562		0.513 0.487	9.47E-01 2.60E-01	-0.899 -0.316	3.05
	pfkB fbp	-0.621 -1.093	S	0.139 0.232	6.97E-03 3.82E-03	-1.158 -1.996	-0.084 -0.189			pfkB fbp	2.212 1.740	S	0.436 0.474	1.21E-03 8.64E-02	0.507 -0.092	3.91 3.57
	fbaB gapC	-1.558 -1.207	s	0.296 0.313	6.16E-04 5.96E-02	-2.717 -2.433	-0.400 0.020			fbaB gapC	1.274 1.626		0.508 0.518	7.52E-01 3.00E-01	-0.682 -0.367	3.23
	gpmA gpmB	-0.737 -0.571	s	0.170 0.159	1.17E-02 1.09E-01	-1.396 -1.186	-0.079 0.045			gpmA gpmB	2.096 2.262	8	0.447 0.443	4.07E-03 9.70E-04	0.355 0.535	3.83
	pykA ppsA	0.025		0.106 0.112	1.00E+00 1.00E+00	-0.380 -0.583	0.430			pykA pykF	2.858 2.833	8	0.426	3.64E-06 4.59E-06	1.184	4.53
	zwf	-0.301 -0.743		0.109 0.187	5.68E-01	-0.719 -1.470	0.117 -0.016			ppsA zwf	2.680 2.532	S	0.428	1.82E-05 6.45E-05	1.000	4.35
	pgl gnd	-0.549	3	0.185	4.23E-01	-1.268	0.171			pgl gnd	2.090	8	0.454	5.15E-03	0.326	3.85
	rpe rpiA	-2.833 -1.364	S	0.427 0.282	4.59E-06 2.71E-03	-4.509 -2.467	-1.157 -0.261			rpiA	2.284 1.469		0.453 0.500	1.10E-03 4.35E-01	0.523 -0.458	4.04 3.39
	rpiB tktA	-0.858 -0.839	S	0.187 0.174	4.99E-03 2.18E-03	-1.583 -1.513	-0.134 -0.165			rpiB tktA	1.975 1.994	8	0.453 0.448	1.20E-02 9.11E-03	0.212 0.248	3.73 3.74
	tktB talA	-0.934 -0.981	S S	0.232 0.229	3.33E-02 1.55E-02	-1.836 -1.872	-0.032 -0.089			tktB talA	1.899 1.852	8	0.474 0.472	3.29E-02 4.29E-02	0.067 0.025	3.73 3.68
	talB 0.1h-1	-0.870 -1.938	s	0.238 0.387	9.56E-02 1.61E-03	-1.796 -3.453	0.057 -0.422			talB 0.1h-1	1.963 0.895	8	0.477 0.566	2.31E-02 9.99E-01	0.121 -1.275	3.80 3.06
	0.2h-1 0.4h-1	-1.229 -1.533	s	0.317 0.353	5.43E-02 1.43E-02	-2.467 -2.916	0.009 -0.151			0.2h-1 0.4h-1	1.604 1.300		0.520 0.543	3.34E-01 8.24E-01	-0.396 -0.786	3.60
	0.5h-1 0.7h-1	-2.058 -3.532	S	0.487	2.09E-02 7.41E-06	-3.968 -5.656	-0.148 -1.407			0.5h-1 0.7h-1	0.775		0.638	1.00E+00 1.00E+00	-1.674 -3.312	3.22
psA	galM glk	0.058	9	0.110 0.249	1.00E+00 2.37E-05	-0.362 -2.479	0.479		rpiA	galM glk	1.269	s	0.281 0.359	8.05E-03 1.00E+00	0.169	2.36
	pgm pgi	-1.178 -1.604	S	0.230 0.306	8.35E-04 6.78E-04	-2.072 -2.802	-0.284 -0.406			pgm pgi	0.033		0.346	1.00E+00 1.00E+00	-1.296 -1.932	1.36
	pfkA pfkB	-1.604 -1.118 -0.468	s	0.306 0.259 0.143	1.40E-02 2.23E-01	-2.802 -2.126 -1.017	-0.406 -0.109 0.081			pfkA pfkB	-0.393 0.093 0.743		0.401 0.366 0.296	1.00E+00 1.00E+00 7.46E-01	-1.932 -1.311 -0.405	1.14 1.49 1.89
	fbp fbaB	-0.940	s	0.234	3.48E-02	-1.850	-0.029			fbp fbaB	0.271		0.349	1.00E+00	-1.068	1.61
	gapC	-1.405 -1.054	s	0.298 0.315	4.00E-03 2.04E-01	-2.569 -2.285	-0.242 0.178			gapC	-0.194 0.157		0.395	1.00E+00 1.00E+00	-1.708 -1.406	1.31
	gpmA gpmB	-0.584 -0.417		0.173 0.162	1.81E-01 7.07E-01	-1.252 -1.043	0.084 0.208			gpmA gpmB	0.627 0.794		0.312 0.306	9.65E-01 6.90E-01	-0.576 -0.389	1.83
	pykA pykF	0.178 0.153		0.110 0.112	9.98E-01 1.00E+00	-0.244 -0.276	0.600 0.583			pykA pykF	1.389 1.364	8	0.281 0.282	1.93E-03 2.71E-03	0.289 0.261	2.48 2.46
	zwf pgl	-0.148 -0.590		0.113 0.190	1.00E+00 3.23E-01	-0.582 -1.326	0.287 0.145			ppsA zwf	1.211 1.063	S	0.284 0.283	1.71E-02 7.44E-02	0.103 -0.041	2.31
	gnd rpe	-0.396 -2.680	s	0.188 0.428	9.43E-01 1.82E-05	-1.124 -4.359	0.333 -1.000			pgl gnd	0.621 0.815		0.321 0.320	9.79E-01 7.24E-01	-0.616 -0.418	1.85
	rpiA rpiB	-1.211 -0.705	s	0.284 0.189	1.71E-02 7.55E-02	-2.319 -1.438	-0.103 0.028			rpe rpiB	-1.469 0.506		0.500 0.321	4.35E-01 9.99E-01	-3.396 -0.730	0.45 1.74
	tktA tktB	-0.686 -0.781	s	0.177 0.234	4.82E-02 2.01E-01	-1.370 -1.690	-0.002 0.127			tktA tktB	0.525 0.430		0.314 0.349	9.97E-01 1.00E+00	-0.685 -0.909	1.73
	talA talB	-0.827 -0.716		0.231 0.240	1.14E-01 4.04E-01	-1.726 -1.649	0.071			talA talB	0.383 0.495		0.347 0.353	1.00E+00 1.00E+00	-0.949 -0.860	1.71
	0.1h-1 0.2h-1	-1.784 -1.076	s	0.388 0.318	6.29E-03 1.88E-01	-3.304 -2.319	-0.265 0.167			0.1h-1 0.2h-1	-0.573 0.135		0.466 0.410	1.00E+00 1.00E+00	-2.366 -1.438	1.21
	0.4h-1 0.5h-1	-1.380 -1.905		0.354 0.488	5.26E-02 5.23E-02	-2.767 -3.818	0.006			0.4h-1 0.5h-1	-0.169 -0.694		0.439	1.00E+00 1.00E+00	-1.854 -2.825	1.51
cwf	0.7h-1 galM	-1.905 -3.379 0.206	s	0.488 0.542 0.107	2.16E-05 9.80E-01	-3.818 -5.506 -0.203	-1.251 0.615		rpiB	0.7h-1	-0.694 -2.168 0.764		0.552 0.600 0.186	1.00E+00 1.03E-01 2.45E-02	-2.825 -4.491 0.044	1.43 0.15 1.48
***	glk	-1.362	s	0.248	9.80E-01 2.20E-04 7.40F-03	-2.327	-0.397		נוועי	galM glk	0.764 -0.804 -0.473	*	0.290	2.45E-02 5.58E-01 9.96F-01	-1.920	1.48 0.31 0.58
	pgm pgi	-1.030 -1.456	s s	0.228 0.305	3.50E-03	-1.919 -2.651	-0.141 -0.262			pgm pgi	-0.899		0.274	6.61E-01	-1.525 -2.215	0.41
	pfkA pfkB	-0.970 -0.320		0.258 0.140	7.21E-02 8.81E-01	-1.974 -0.861	0.034 0.220			pfkA pfkB	-0.412 0.237		0.299 0.207	1.00E+00 1.00E+00	-1.562 -0.558	0.73 1.03
	fbp fbaB	-0.792 -1.258	s	0.232 0.297	1.75E-01 1.91E-02	-1.698 -2.418	0.114 -0.097			fbp fbaB	-0.234 -0.700		0.278 0.333	1.00E+00 9.45E-01	-1.300 -1.986	0.83 0.58
	gapC gpmA	-0.906 -0.436		0.314 0.171	4.76E-01 7.21E-01	-2.134 -1.098	0.322 0.225			gapC gpmA	-0.348 0.121		0.348 0.229	1.00E+00 1.00E+00	-1.694 -0.755	0.99
	gpmB pykA	-0.270 0.326		0.160 0.107	9.97E-01 3.56E-01	-0.888 -0.084	0.348 0.735			gpmB pykA	0.288 0.883	5	0.221 0.186	1.00E+00 2.85E-03	-0.559 0.163	1.13
	pykF ppsA	0.301		0.109 0.113	5.68E-01 1.00E+00	-0.117 -0.287	0.719 0.582			pykF ppsA	0.858 0.705	Š	0.187	4.99E-03 7.55E-02	0.134	1.58
	pgl gnd	-0.443 -0.248		0.188 0.186	8.42E-01 1.00E+00	-1.172 -0.970	0.287 0.474			zwf pgl	0.558 0.115		0.188 0.242	4.13E-01 1.00F+00	-0.169 -0.811	1.28
	rpe	-0.248 -2.532 -1.063	s	0.186 0.427 0.283	6.45E-05 7.44E-02	-0.970 -4.209 -2.168	-0.855 0.041			gnd	0.115 0.310 -1.975		0.242 0.240 0.453	1.00E+00 1.00E+00 1.20E-02	-0.811 -0.611 -3.737	1.04 1.23 -0.21
	rpiA rpiB	-0.558		0.188	4.13E-01	-1.284	0.169			rpe rpiA	-0.506	*	0.321	9.99E-01	-1.742	0.73
	tktA tktB	-0.538 -0.634		0.175 0.232	3.43E-01 5.92E-01	-1.215 -1.538	0.139			tktA tktB	0.019 -0.076		0.232	1.00E+00 1.00E+00	-0.868 -1.141	0.90
	talA talB	-0.680 -0.569		0.230 0.238	4.22E-01 8.22E-01	-1.573 -1.497	0.214 0.360			talA talB	-0.122 -0.011		0.275 0.283	1.00E+00 1.00E+00	-1.178 -1.096	0.93 1.07
	0.1h-1 0.2h-1	-1.637 -0.928	S	0.387 0.317	2.03E-02 4.48E-01	-3.153 -2.168	-0.120 0.312			0.1h-1 0.2h-1	-1.079 -0.370		0.416 0.351	6.89E-01 1.00E+00	-2.691 -1.727	0.53 0.98
	0.4h-1 0.5h-1	-1.233 -1.757		0.353 0.487	1.49E-01 1.13E-01	-2.616 -3.668	0.151 0.153			0.4h-1 0.5h-1	-0.675 -1.200		0.384 0.510	9.94E-01 8.41E-01	-2.163 -3.186	0.81 0.78
	0.7h-1	-3.231		0.541	5.83E-05	-5.356	-1.105			0.7h-1	-2.673		0.562	3.40E-03	-4.866	-0.48

		Mean Difference				95% Confide Lower	nce Interva Upper
1)	(J)	(I-J)		Std. Error	Sig.	Bound	Bound
ktA	galM glk	0.744	S	0.173 0.282	1.30E-02 4.48F-01	0.075 -1.910	1.41
	pgm	-0.492		0.266	9.88E-01	-1.513	0.52
	pgi pfkA	-0.918 -0.432		0.334	5.77E-01	-2.210	0.37
	pfkB	0.218		0.291 0.195	1.00E+00 1.00E+00	-1.553 -0.533	0.68
	fbp	-0.254		0.269	1.00E+00	-1.289	0.78
	fbaB gapC	-0.719 -0.368		0.326 0.342	9.11E-01 1.00E+00	-1.980 -1.690	0.54 0.95
	nnmA	0.102		0.218	1.00E+00	-0.735	0.93
	gpmB	0.268 0.864	s	0.210 0.173	1.00E+00	-0.537 0.194	1.07
	pykA pykF	0.839	S	0.173 0.174 0.177	1.15E-03 2.18E-03 4.82E-02	0.194	1.51
	ppsA zwf	0.686 0.538	S	0.177	4.82E-02	0.002	1.37
	nol	0.538		0.175 0.232	3.43E-01 1.00E+00	-0.139 -0.794	1.21
	gnd rpe	0.290		0.231	1.00E+00	-0.594	1.17
	rpe rpiA	-1.994 -0.525	s	0.448 0.314	9.11E-03	-3.740 -1.735	-0.24 0.68
	rpiB	-0.019		0.232	9.97E-01 1.00E+00	-0.907	0.86
	tktB talA	-0.095 -0.142		0.269 0.267	1.00E+00 1.00E+00	-1.129 -1.166	0.93
	talB	-0.031		0.274	1.00E+00	-1.085	1.02
	0.1h-1	-1.099		0.410	1.00E+00 6.29E-01	-2.691	0.49
	0.2h-1 0.4h-1	-0.390 -0.694		0.345 0.378	1.00E+00 9.88E-01	-1.724 -2.162	0.94 0.77
	0.4h-1 0.5h-1	-1 210		0.506	8 08F-01	-3.190	0.75
ktB	0.7h-1 galM	-2.693 0.840	s	0.558 0.230	2.77E-03 9.94E-02	-4.872 -0.059	-0.51 1.73
, and	glk	-0.729		0.321	8.87E-01	-1.959	0.50
	pgm	-0.397 -0.823		0.306 0.367	1 00E+00	-1.571 -2.234	0.77
	pgi pfkA	-0.337		0.367	8.99E-01 1.00E+00	-1 597	0.58
	pfkB	0.313 -0.158		0.248	1.00E+00 1.00E+00	-0.645 -1.345	1.27
	fbp fbaB	-0.158 -0.624		0.309	1.00E+00	-1.345 -2 008	1.02
	gapC	-0.272		0.374	9.95E-01 1.00E+00	-1.712	0.76
	gpmA gpmB	0.197 0.364		0.266 0.260	1.00E+00 1.00E+00	-0.827 -0.636	1.22
	pykA	0.959	s	0.231	2.31E-02	0.061	1.85
	pykF	0.934	S	0.232	3.33E-02 2.01F-01	0.032	1.83
	ppsA zwf	0.781		0.234	5.92E-01	-0.127 -0.270	1.69
	pal	0.191		0.278	1.00E+00	-0.875	1.25
	gnd rpe	0.386 -1.899	s	0.276 0.474	1.00E+00	-0.676 -3.731	-0.06
	rpiA	-0.430	ŭ	0.349	3.29E-02 1.00E+00 1.00E+00	-1.768	0.90
	rpiB tktA	0.076		0.277	1.00E+00 1.00E+00	-0.989 -0.939	1.14
	talA	-0.046		0.307	1.00E+00	-1.224	1.13
	talB 0.1h-1	0.065 -1.003		0.314	1.00E+00 8.74E-01	-1.138	1.26
	0.1n-1 0.2h-1	-1.003		0.438 0.377	8.74E-01 1.00E+00	-2.692 -1.744	0.68
	0.4h-1	-0.599		0.408	1.00E+00	-2.171	0.97
	0.5h-1 0.7h-1	-1.124 -2.597	s	0.528 0.578	9.36E-01 7.58E-03	-3.171 -4.845	0.92 -0.35
alA	galM	0.886	ŭ	0.228	5 12F-02	-0.002	1.77
	glk pgm	-0.682 -0.350		0.319 0.304	9.36E-01 1.00E+00	-1.905 -1.517	0.54
	pgi	-0.350		0.366	9.40E-01	-2.182	0.62
	pfkA	-0.290		0.327	1.00E+00	-1 543	0.96
	pfkB fbp	0.360 -0.112		0.245 0.307	1.00E+00 1.00E+00	-0.589 -1.291	1.30
	fbaB	-0.578		0.359	9.98E-01	-1.955	0.80
	gapC gpmA	-0.226		0.373	1.00E+00 1.00E+00	-1.659 -0.772	1.20
	gpmB	0.410		0.257	9.99E-01	-0.580	1.40
	pykA pykF	1.005	S	0.228	1.04E-02 1.55E-02	0.117	1.89
	ppsA zwf	0.981 0.827	S	0.229 0.231	1.55E-02 1.14E-01	0.089 -0.071	1.72
	zwf	0.680		0.230	1.14E-01 4.22E-01	-0.214	1.57
	pgl gnd	0.237 0.432		0.275 0.274	1.00E+00 9.99E-01	-0.820 -0.621	1.29
	me	-1.852	s	0.472	4 20F-02	-3.680	-0.02
	rpiA rpiB	-0.383 0.122		0.347 0.275	1.00E+00 1.00E+00	-1.716 -0.934	0.94
	tktA	0.142		0.267	1.00E+00	-0.883	1.16
	tktB telB	0.046		0.307	1 00E+00	-1.131 -1.085	1.22
	0.1h-1	0.111 -0.957		0.436	1.00E+00 9.15E-01	-2 640	0.72
	0.2h-1 0.4h-1	-0.248 -0.553		0.376	1.00E+00 1.00E+00	-1.692 -2.119	1.19
	0.5h-1	-0.553		0.406 0.527	9.57E-01	-2.119 -3.121	1.01
	0.7h-1	-2.551	s	0.577	9.67E-03	-4.795	-0.30
alB	galM glk	0.775 -0.793		0.237 0.325	2.36E-01 7.98E-01	-0.148 -2.041	1.69 0.45
	pgm	-0.461		0.311	1.00E+00	-1.654	0.73
	pgi pfkA	-0.887 -0.401		0.371	8.25E-01	-2.314 -1.678	0.53
	pfkB	0.249		0.353	1.00E+00 1.00E+00	-0.732	1.22
	fbp fbaB	-0.223		0.314		-1.427	0.98
	fbaB gapC	-0.689 -0.337		0.364 0.378	9.84E-01 1.00E+00	-2.088 -1.791	0.71
	gpmA	0.132 0.299		0.272 0.265	1.00E+00 1.00E+00	-0.913	1.17
	anmB	0.299 0.894		0.265 0.237	1.00E+00	-0.723 -0.029	1.32
	pykA pykF	0.870		0.238	7.00E-02 9.56E-02	-0.057	1.79
	ppsA zwf	0.716 0.569		0.240 0.238	4.04E-01 8.22E-01	-0.217 -0.360	1.64
	zwf pgl	0.126		0.238	0.22E-U1 1.00E+00	-0.360 -0.960	1.21
	and	0.321		0.282	1.00E+00 1.00E+00	-0.761	1.40
	rpe rpiA	-1.963 -0.495	S	0.477 0.353	2.31E-02 1.00E+00	-3.806 -1.849	-0.12 0.86
	rpiB	0.011		0.283	1.00E+00	-1.074	1.09
	tktA	0.031		0.274	1.00E+00 1.00E+00	-1.024	1.08
	tktB talA	-0.065 -0.111		0.314 0.312	1.00E+00 1.00E+00	-1.268 -1.307	1.13
	0.1h-1	-1.068		0.441	8.05E-01	-2.768	0.63
	0.2h-1 0.4h-1	-0.359 -0.664		0.381 0.412	1.00E+00 9.98E-01	-1.823 -2.249	1.10
	0.4h-1 0.5h-1	-0.664 -1.189		0.412	9.98E-01 8.96E-01	-2.249 -3.245	0.92
	0.7h-1	-2.662					

		Mean Difference				95% Confide Lower	ence Interv Upper
(I) 0.1h-1	(J) galM	(I-J) 1 843		Std. Error 0.386	Sig. 3.63F-03	Bound	Bound 3.3
.1n-1	glk	0.275	S	0.446	1.00E+00	0.330 -1.444	1.9
	pgm pgi	0.607 0.181		0.436 0.480	1.00E+00 1.00E+00	-1.075 -1.664	2.2
	pfkA pfkB	0.667		0.452 0.397	1.00E+00 2.15E-01	-1.072 -0.231	2.4
	fbp	0.845		0.438	9.79E-01	-0.844	2.5
	fbaB gapC	0.379 0.731		0.475 0.486	1.00E+00 9.99E-01	-1.446 -1.134	2.2
	apmA	1.200		0.409	4.38E-01	-0.387	2.7
	gpmB pykA	1.367 1.962	s	0.404 0.386	1.85E-01 1.27E-03	-0.205 0.449	2.9
	pykF	1.938 1.784	s s	0.387 0.388	1.61E-03 6.29E-03	0.422 0.265	3.4 3.3
	ppsA zwf	1.637	S	0.387	2.03E-02	0.120	3.1
	pgl gnd	1.194 1.389		0.416 0.415	4.85E-01 1.98F-01	-0.418 -0.221	2.8
	rpe	-0.895		0.566	9.99E-01	-3.066	1.2
	rpiA rpiB	0.573 1.079		0.466 0.416	1.00E+00 6.89E-01	-1.219 -0.533	2.3 2.6
	tktA tktB	1.099		0.410	6.29E-01 8.74F-01	-0.494 -0.685	2.6
	talA	0.957		0.436	9.15E-01	-0.005	2.6
	talB 0.2h-1	1.068 0.709		0.441 0.488	8.05E-01 1.00E+00	-0.632 -1.164	2.7 2.5
	0.4h-1	0.404		0.512	1.00E+00	-1.560	2.3
	0.5h-1 0.7h-1	-0.121 -1.594		0.612 0.656	1.00E+00 8.01E-01	-2.470 -4.116	2.2 0.9
.2h-1	galM glk	1.134		0.316 0.387	1.16E-01 1.00E+00	-0.102	2.3
	pgm	-0.102		0.375	1.00E+00	-1.919 -1.543	1.3
	pgi pfkA	-0.528 -0.042		0.426	1.00E+00 1.00E+00	-2.162 -1.551	1.1
	pfkB	0.608		0.329	9.87E-01	-0.671	1.8
	fbp fbaB	0.136 -0.330		0.377 0.420	1.00E+00 1.00E+00	-1.314 -1.940	1.5
	gapC gpmA	0.022 0.492		0.432 0.343	1.00E+00 1.00E+00	-1.634 -0.835	1.6 1.8
	gpmB	0.658		0.338	9.75E-01	-0.650	1.9
	pykA pykF	1.254 1.229	S	0.316 0.317	4.27E-02 5.43E-02	0.018 -0.009	2.4 2.4
	ppsA	1.076		0.318	1.88E-01	-0.167	2.3
	zwf pgl	0.928 0.486		0.317 0.352	4.48E-01 1.00E+00	-0.312 -0.872	2.1
	gnd rpe	0.680		0.351 0.520	9.77E-01 3.34E-01	-0.674 -3.605	2.0
	miA	-0.135		0.410	1.00E+00	-1.708	1.4
	rpiB tktA	0.370		0.351 0.345	1.00E+00 1.00E+00	-0.986 -0.944	1.7
	tktB	0.295		0.377	1.00E+00	-1.155 -1.195	1.7
	talA talB	0.248 0.359		0.376 0.381	1.00E+00 1.00E+00	-1.104	1.6
	0.1h-1 0.4h-1	-0.709 -0.305		0.488 0.462	1.00E+00 1.00E+00	-2.581 -2.075	1.1
	0.5h-1	-0.829		0.570	1.00E+00	-3.026	1.3
.4h-1	0.7h-1 galM	-2.303 1.439	s	0.617 0.352	7.25E-02 3.13E-02	-4.685 0.058	0.0
	glk	-0.129	Ü	0.417	1.00E+00	-1.734	1.4
	pgm pgi	0.202 -0.223		0.406 0.454	1.00E+00 1.00E+00	-1.362 -1.964	1.7
	pfkA pfkB	0.263 0.912		0.423	1.00E+00 7.47E-01	-1.364 -0.506	1.8
	fbp	0.441		0.408	1.00E+00	-1.132	2.0
	fbaB gapC	-0.025 0.327		0.448 0.459	1.00E+00 1.00E+00	-1.744 -1.435	1.6
	gpmA	0.796		0.377	9.39E-01 6.92E-01	-0.665	2.2
	gpmB pykA	0.963 1.558	s	0.372 0.352	1.12E-02	-0.482 0.178	2.4
	pykF ppsA	1.533 1.380	S	0.353 0.354	1.43E-02 5.26E-02	0.151 -0.006	2.9
	zwf	1.233		0.353	1.49E-01	-0.151	2.6
	pgl gnd	0.790 0.985		0.385 0.384	9.55E-01 7.10E-01	-0.699 -0.501	2.2
	rpe	-1.300		0.543	8.24E-01	-3.385	0.7
	rpiA rpiB	0.169 0.675		0.439 0.384	1.00E+00 9.94E-01	-1.515 -0.813	1.8
	tktA tktB	0.694		0.378 0.408	9.88E-01 1.00E+00	-0.773 -0.973	2.1
	talA	0.553		0.406	1.00E+00	-1.014	2.1
	talB 0.1h-1	0.664 -0.404		0.412 0.512	9.98E-01 1.00E+00	-0.921 -2.368	2.2
	0.2h-1	0.305		0.462	1.00E+00	-1.466	2.0
	0.5h-1 0.7h-1	-0.525 -1.998		0.591 0.636	1.00E+00 3.00E-01	-2.797 -4.450	1.7
.5h-1	galM glk	1.963 0.395	s	0.486 0.535	3.64E-02 1.00E+00	0.055 -1.676	3.8 2.4
	pgm	0.727		0.526	1.00E+00	-1.314	2.7
	pgi pfkA	0.301 0.787		0.564 0.540	1.00E+00	-1.873 -1.300	2.4
	pfkB	1.437		0.495 0.528	4.64E-01	-0.498 -1.082	3.3
	fbp fbaB	0.965 0.500		0.560	9.89E-01 1.00E+00	-1.658	3.0 2.6
	gapC gpmA	0.851 1.321		0.569 0.504	9.99E-01 6.71E-01	-1.339 -0.646	3.0
	gpmB	1.488		0.501	4.17E-01	-0.467	3.4
	pykA pykF	2.083 2.058	S	0.486 0.487	1.77E-02 2.09E-02	0.175 0.148	3.9 3.9
	ppsA zwf	1.905		0.488 0.487	5.23E-02 1.13E-01	-0.008 -0.153	3.8
	pgl	1.315		0.510	7.01E-01	-0.672	3.3
	gnd rpe	1.509 -0.775		0.510 0.638	4.22E-01 1.00E+00	-0.475 -3.223	3.4 1.6
	rpiA	0.694		0.552	1.00E+00	-1.437	2.8
	rpiB tktA	1.200 1.219		0.510 0.506	8.41E-01 8.08E-01	-0.786 -0.752	3.1 3.1
	tktB talA	1.124		0.528 0.527	9.36E-01 9.57E-01	-0.923 -0.966	3.1
	talB	1.189		0.531	8.96E-01	-0.868	3.2
	0.1h-1 0.2h-1	0.121 0.829		0.612 0.570	1.00E+00 1.00E+00	-2.229 -1.367	2.4
	0.4h-1	0.525		0.591	1.00E+00	-1.748	2.7
.7h-1	0.7h-1 galM	-1.473 3.437	s	0.719 0.540	9.60E-01 1.41E-05	-4.232 1.314	1.2 5.5
	glk	1.869		0.585	2.73E-01 6.13E-02	-0.400	4.1
	pgm pgi	1.775		0.577 0.611	4.60E-01	-0.042 -0.587	4.1
	pfkA pfkB	2.261 2.911	s	0.589 0.548	5.59E-02 5.64E-04	-0.023 0.763	4.5 5.0
	fbp	2.439	S	0.578	1.85E-02	0.191	4.6
	fbaB gapC	1.973		0.607 0.615	2.41E-01 6.37E-02	-0.374 -0.052	4.3 4.7
	apmA	2.794	s	0.556	1.43E-03	0.619	4.9
	gpmB pykA	2.961 3.556	S	0.553 0.540	4.56E-04 6.20E-06	0.796 1.433	5.1 5.6
	pykF ppsA	3.532 3.379	S	0.541 0.542	7.41E-06 2.16E-05	1.407 1.251	5.6
	ppsA zwf	3.231	s	0.541	5.83E-05	1.105	5.3
	pgl gnd	2.788 2.983	S	0.562 0.561	1.68E-03 4.75E-04	0.595 0.792	4.9
	rpe	0.699	S	0.680	1.00E+00	-1.915	3.3
	rpiA rpiB	2.168 2.673	s	0.600 0.562	1.03E-01 3.40E-03	-0.156 0.480	4.4
	tktA	2.693	s	0.558	2.77E-03	0.513	4.8
	tktB talA	2.597 2.551	S	0.578 0.577	7.58E-03 9.67E-03	0.350 0.307	4.8
	talB	2.662	s	0.581	5.47E-03	0.406	4.9
	0.1h-1 0.2h-1	1.594		0.656 0.617	8.01E-01 7.25E-02	-0.928 -0.080	4.1
	0.4h-1	1.998		0.636	3.00E-01	-0.454	4.4

# **Table S10 C Statistical tests for AEIs (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.

-									Depender	nt Variable: Meta	bolite					
(I) (	(J)	Mean Difference (I-J)		Std. Error	Sig.	95% Confide Lower Bound	Upper Bound	•	(1)	(J)	Mean Difference (I-J)		Std. Error	Sig.	95% Confide Lower Bound	Upper Bound
galM g	glk pgm	-1.590 -2.029	s	0.257 0.247	1.35E-06 6.57E-11	-2.564 -2.966	-0.616 -1.093	•	pfkB	galM glk	0.129 -1.461	s	0.109 0.263	1.00E+00 3.00E-05	-0.281 -2.455	0.540 -0.467
F	pgi pfkA pfkB	-2.214 -1.239 -0.129	s s	0.283 0.188 0.109	1.42E-09 2.54E-07 1.00E+00	-3.299 -1.954 -0.540	-1.128 -0.524 0.281			pgm pgi pfkA	-1.900 -2.085 -1.110	S	0.253 0.288 0.195	8.05E-10 2.04E-08 2.09E-05	-2.857 -3.188 -1.852	-0.943 -0.982 -0.369
f	fbp fbaB	-0.123 -0.333		0.106 0.121	9.92E-01 5.73E-01	-0.592 -0.791	0.206 0.125			fbp fbaB	-0.064 -0.204	3	0.119 0.133	1.00E+00 9.99E-01	-0.510 -0.704	0.383 0.295
	gapC gpmA	-0.679 -0.359	s	0.137 0.139	6.24E-04 7.08E-01	-1.200 -0.886	-0.158 0.168			gapC gpmA	-0.550 -0.230		0.147 0.149	5.87E-02 9.99E-01	-1.108 -0.793	0.007 0.333
9	gpmB pykA	-0.765 -1.490	s s	0.171 0.195	4.62E-03 7.65E-10	-1.415 -2.232	-0.115 -0.749			gpmB pykA	-0.636 -1.361	s	0.179 0.202	1.04E-01 8.35E-08	-1.316 -2.128	0.044 -0.594
F	pykF ppsA	-1.312 -0.228		0.154 0.108	5.26E-11 9.51E-01	-1.895 -0.636	-0.729 0.181			pykF ppsA	-1.183 -0.098	s	0.163 0.121	2.74E-09 1.00E+00	-1.799 -0.553	-0.568 0.357
F	zwf pgl gnd	-1.156 -0.697 -1.264	S	0.199 0.157 0.215	1.81E-05 4.93E-03 8.79E-06	-1.917 -1.291 -2.081	-0.396 -0.102 -0.448			zwf pgl gnd	-1.027 -0.568 -1.135	8	0.206 0.166 0.221	6.27E-04 1.42E-01 2.78E-04	-1.813 -1.194 -1.975	-0.242 0.059 -0.295
r	rpe rpiA	-2.065 -1.017	S	0.259 0.162	2.03E-10 9.33E-07	-3.051 -1.632	-1.079 -0.402			rpe rpiA	-1.936 -0.888	S	0.264	4.56E-09 1.71E-04	-2.941 -1.534	-0.931 -0.241
t	rpiB tktA	-0.601 -0.479	8 8 8 8 8	0.144 0.124	1.35E-02 3.84E-02	-1.147 -0.948	-0.055 -0.010			rpiB tktA	-0.472 -0.350		0.154 0.135	3.31E-01 7.02E-01	-1.053 -0.859	0.109 0.160
t	tktB talA talB	-0.803 -0.246	s	0.129 0.133	9.18E-07 9.91E-01	-1.290 -0.750	-0.316 0.259			tktB talA talB	-0.674 -0.116	S	0.139 0.144	8.18E-04 1.00E+00 1.00E+00	-1.200 -0.659	-0.148 0.426
c	0.1h-1 0.2h-1	-0.506 -0.828 -0.218	s	0.256 0.157 0.116	9.75E-01 1.20E-04 9.87E-01	-1.478 -1.422 -0.655	0.467 -0.233 0.219			0.1h-1 0.2h-1	-0.377 -0.698 -0.089	s	0.261 0.166 0.127	1.00E+00 1.09E-02 1.00E+00	-1.369 -1.325 -0.570	0.616 -0.072 0.391
C	0.4h-1 0.5h-1	-0.604 -0.857	s	0.124	7.05E-04 1.89E-04	-1.073 -1.481	-0.136 -0.233			0.4h-1 0.5h-1	-0.475 -0.728	s	0.135	1.08E-01	-0.984 -1.383	0.034
glk g	0.7h-1 galM	-1.314 1.590	s s	0.208 0.257	1.08E-06 1.35E-06	-2.104 0.616	-0.524 2.564		fbp	0.7h-1 galM	-1.185 0.193	S	0.214 0.106	4.68E-05 9.92E-01	-1.999 -0.206	-0.371 0.592
F	pgm pgi pfkA	-0.439 -0.624 0.351		0.344 0.371 0.304	1.00E+00 9.98E-01 1.00E+00	-1.734 -2.025 -0.796	0.855 0.777 1.498			glk pgm	-1.397 -1.836 -2.021	S	0.262 0.251 0.287	8.79E-05 2.87E-09 5.72E-08	-2.387 -2.789 -3.120	-0.407 -0.884 -0.922
F	pfkB fbp	1.461	s	0.263 0.262	3.00E-05 8.79E-05	0.467	2.455 2.387			pgi pfkA pfkB	-1.046 0.064	S	0.194 0.119	8.22E-05 1.00E+00	-1.782 -0.383	-0.311 0.510
f	fbaB gapC	1.257 0.911	S	0.268 0.276	1.63E-03 1.95E-01	0.243 -0.131	2.270 1.953			fbaB gapC	-0.140 -0.486		0.130 0.145	1.00E+00 1.75E-01	-0.631 -1.036	0.350 0.063
9	gpmA gpmB	1.231 0.825	s	0.277 0.294	4.26E-03 5.29E-01	0.186 -0.285	2.276 1.934			gpmA gpmB	-0.166 -0.572		0.147 0.178	1.00E+00 2.39E-01	-0.721 -1.245	0.389 0.101
F	pykA pykF ppsA	0.100 0.278 1.362	s	0.309 0.284 0.263	1.00E+00 1.00E+00 1.78E-04	-1.064 -0.795 0.369	1.263 1.350 2.356			pykA pykF ppsA	-1.297 -1.120 -0.035	S	0.201 0.161 0.118	3.68E-07 1.73E-08 1.00E+00	-2.059 -1.728 -0.479	-0.536 -0.511 0.410
Z F	zwf pgl	0.434 0.893	3	0.311 0.286	1.00E+00 2.93E-01	-0.741 -0.186	1.608 1.972			zwf pgl	-0.964 -0.504	s	0.205 0.164	1.99E-03 3.24E-01	-1.744 -1.123	-0.183 0.116
9	gnd rpe	0.326 -0.475		0.322 0.353	1.00E+00 1.00E+00	-0.885 -1.804	1.537 0.854			gnd rpe	-1.071 -1.872	s	0.220 0.263	8.70E-04 1.51E-08	-1.906 -2.873	-0.237 -0.871
r	rpiA rpiB tktA	0.573 0.989 1.111	_	0.289 0.279 0.270	9.76E-01 1.02E-01 1.53E-02	-0.518 -0.065 0.093	1.664 2.043 2.130			rpiA rpiB tktA	-0.824 -0.408 -0.286	s	0.169 0.152 0.133	7.45E-04 6.21E-01 9.39E-01	-1.464 -0.981 -0.786	-0.184 0.165 0.215
t	tktA tktB talA	1.111 0.787 1.345	S	0.270 0.272 0.274	1.53E-02 4.56E-01 6.00E-04	0.093 -0.239 0.310	2.130 1.813 2.379			tktA tktB talA	-0.286 -0.610 -0.053	s	0.133 0.137 0.142	9.39E-01 4.22E-03 1.00E+00	-0.786 -1.128 -0.587	0.215 -0.093 0.482
t	talB 0.1h-1	1.084 0.763	3	0.350 0.286	3.10E-01 6.41E-01	-0.235 -0.317	2.404 1.842			talB 0.1h-1	-0.313 -0.635	s	0.260 0.164	1.00E+00 3.68E-02	-1.301 -1.254	0.675 -0.015
0	0.2h-1 0.4h-1	1.372 0.986	S	0.266 0.270	1.97E-04 7.28E-02	0.367 -0.032	2.376 2.004			0.2h-1 0.4h-1	-0.026 -0.411		0.125 0.133	1.00E+00 3.08E-01	-0.496 -0.911	0.445 0.089
c	0.5h-1 0.7h-1 galM	0.733 0.276 2.029		0.290 0.317 0.247	7.46E-01 1.00E+00 6.57E-11	-0.362 -0.918 1.093	1.828 1.470 2.966		fbaB	0.5h-1 0.7h-1 galM	-0.664 -1.121 0.333	S	0.171 0.213 0.121	3.65E-02 1.61E-04 5.73E-01	-1.312 -1.930 -0.125	-0.017 -0.312 0.791
g	gaim glk pgi	0.439 -0.184	3	0.344	1.00E+00 1.00E+00	-0.855 -1.559	1.734 1.190		ibab	glk pgm	-1.257 -1.696	s	0.268	1.63E-03 1.55E-07	-2.270 -2.673	-0.243 -0.719
F	pfkA pfkB	0.790 1.900	s	0.295 0.253	6.32E-01 8.05E-10	-0.324 0.943	1.905 2.857			pgi pfkA	-1.881 -0.906	S	0.293 0.203	1.02E-06 4.26E-03	-3.000 -1.674	-0.761 -0.139
f	fbp fbaB	1.836 1.696	S	0.251 0.258	2.87E-09 1.55E-07	0.884 0.719 0.344	2.789 2.673			pfkB fbp	0.204 0.140		0.133 0.130	9.99E-01 1.00E+00	-0.295 -0.350	0.704 0.631
	gapC gpmA gpmB	1.350 1.671 1.264	s s s	0.266 0.267 0.285	2.99E-04 7.56E-07 4.47E-03	0.344 0.661 0.188	2.356 2.680 2.340			gapC gpmA gpmB	-0.346 -0.026 -0.432		0.157 0.158 0.187	9.18E-01 1.00E+00 8.75E-01	-0.938 -0.623 -1.140	0.246 0.572 0.276
F	pykA pykF	0.539 0.717	3	0.300 0.275	9.94E-01 6.83E-01	-0.592 -0.321	1.671 1.755			pykA pykF	-1.157 -0.979	s	0.209	3.74E-05 1.27E-05	-1.949 -1.626	-0.365 -0.332
F 2	ppsA zwf	1.802 0.873	s	0.252 0.303	7.23E-09 4.65E-01	0.846 -0.270	2.758 2.016			ppsA zwf	0.106 -0.823	s	0.132 0.213	1.00E+00 4.10E-02	-0.392 -1.633	0.603 -0.013
g	pgl gnd rpe	1.333 0.765 -0.036	S	0.277 0.313 0.345	8.99E-04 8.00E-01 1.00E+00	0.288 -0.415 -1.337	2.377 1.946 1.265			pgl gnd rpe	-0.364 -0.931 -1.732	S	0.174 0.228 0.270	9.54E-01 1.81E-02 5.11E-07	-1.021 -1.794 -2.756	0.294 -0.069 -0.708
r	rpiA rpiB	1.012 1.428	s	0.280 0.270	8.17E-02 1.02E-04	-0.044 0.409	2.069 2.447			rpiA rpiB	-0.684 -0.268	S	0.179 0.163	4.37E-02 9.98E-01	-2.756 -1.360 -0.882	-0.700 -0.007 0.347
t	tktA tktB	1.551 1.226	8 8 8 8 8	0.260 0.262	3.74E-06 1.70E-03	0.569 0.236	2.533 2.216			tktA tktB	-0.146 -0.470		0.145 0.149	1.00E+00 2.78E-01	-0.693 -1.033	0.402 0.093
t	talA talB	1.784 1.524	S	0.264 0.343	4.88E-08 4.10E-03	0.785 0.232	2.782 2.815			talA talB	0.088 -0.173		0.153 0.267	1.00E+00 1.00E+00	-0.491 -1.184	0.666 0.839
C	0.1h-1 0.2h-1 0.4h-1	1.202 1.811 1.425	s s	0.277 0.255 0.259	6.52E-03 8.98E-09 4.28E-05	0.157 0.844 0.444	2.247 2.778 2.407			0.1h-1 0.2h-1 0.4h-1	-0.494 0.115 -0.271		0.174 0.138 0.145	5.04E-01 1.00E+00 9.89E-01	-1.152 -0.406 -0.818	0.163 0.636 0.276
c	0.5h-1 0.7h-1	1.172 0.716	s	0.281	1.26E-02 8.69E-01	0.111	2.233			0.5h-1 0.7h-1	-0.524 -0.981	s	0.181 0.221	4.57E-01 4.99E-03	-1.208 -1.818	0.160 -0.143
pgi g	galM glk	2.214 0.624	s	0.283 0.371	1.42E-09 9.98E-01	1.128 -0.777	3.299 2.025		gapC	galM glk	0.679 -0.911	S	0.137 0.276	6.24E-04 1.95E-01	0.158 -1.953	1.200 0.131
F	pgm pfkA	0.184		0.364	1.00E+00 3.92E-01	-1.190 -0.265	1.559 2.214			pgm pgi	-1.350 -1.535	S S	0.266	2.99E-04 3.81E-04	-2.356 -2.679	-0.344 -0.390
f	pfkB fbp fbaB	2.085 2.021 1.881	S	0.288 0.287 0.293	2.04E-08 5.72E-08 1.02E-06	0.982 0.922 0.761	3.188 3.120 3.000			pfkA pfkB fbp	-0.560 0.550 0.486		0.213 0.147 0.145	6.63E-01 5.87E-02 1.75E-01	-1.365 -0.007 -0.063	0.245 1.108 1.036
9	gapC gpmA	1.535 1.855	s	0.300 0.301	3.81E-04 2.91E-06	0.390 0.707	2.679 3.003			fbaB gpmA	0.346 0.320		0.157 0.171	9.18E-01 9.88E-01	-0.246 -0.326	0.938 0.966
9	gpmB pykA	1.449 0.723	s	0.317 0.331	3.21E-03 9.24E-01	0.243 -0.531	2.654 1.978			gpmB pykA	-0.086 -0.811		0.198 0.219	1.00E+00 6.39E-02	-0.834 -1.639	0.662
F	pykF ppsA zwf	0.901 1.986 1.057	s	0.308 0.288 0.333	4.36E-01 1.12E-07 2.67E-01	-0.271 0.884 -0.207	2.074 3.088 2.322			pykF ppsA zwf	-0.633 0.452 -0.477		0.183 0.147 0.223	1.29E-01 3.27E-01 9.38E-01	-1.325 -0.104 -1.322	0.058 1.008 0.368
F	pgl gnd	1.517 0.950	s	0.309 0.343	8.57E-04 5.55E-01	0.339	2.695 2.248			pgl gnd	-0.018 -0.585		0.185 0.237	1.00E+00 7.80E-01	-0.719 -1.481	0.683 0.310
r	rpe rpiA	0.149 1.197	s	0.372 0.312	1.00E+00 4.59E-02	-1.258 0.008	1.556 2.385			rpe rpiA	-1.386 -0.338	S	0.277 0.190	4.86E-04 9.95E-01	-2.438 -1.057	-0.334 0.381
t	rpiB tktA tktB	1.613 1.735 1.411	s s	0.303 0.294 0.296	1.49E-04 1.21E-05 1.70E-03	0.457 0.611 0.280	2.769 2.859 2.542			rpiB tktA tktB	0.078 0.200 -0.124		0.175 0.159 0.163	1.00E+00 1.00E+00 1.00E+00	-0.583 -0.400 -0.738	0.740 0.801 0.491
t	talA talB	1.411 1.968 1.708	S	0.298 0.370	1.70E-03 3.57E-07 2.22E-03	0.280 0.830 0.310	3.107 3.106			talA talB	-0.124 0.434 0.173		0.163 0.166 0.274	6.85E-01 1.00E+00	-0.738 -0.195 -0.866	1.062 1.213
C	0.1h-1 0.2h-1	1.386 1.995	S	0.310 0.291	4.75E-03 1.21E-07	0.208 0.884	2.565 3.107			0.1h-1 0.2h-1	-0.148 0.461		0.186 0.152	1.00E+00 3.62E-01	-0.850 -0.116	0.553 1.037
C	0.4h-1 0.5h-1	1.610 1.357	s	0.294 0.314	8.54E-05 8.25E-03	0.486 0.164	2.734 2.549			0.4h-1 0.5h-1	0.075 -0.178		0.159 0.192	1.00E+00 1.00E+00	-0.525 -0.904	0.675 0.548
pfkA g	0.7h-1 galM glk	0.900 1.239 -0.351	s	0.338 0.188 0.304	6.42E-01 2.54E-07 1.00E+00	-0.382 0.524 -1.498	2.182 1.954 0.796		gpmA	0.7h-1 galM glk	-0.635 0.359 -1.231	q	0.230 0.139 0.277	5.66E-01 7.08E-01 4.26E-03	-1.506 -0.168 -2.276	0.237 0.886 -0.186
Ē	pgm pgi	-0.790 -0.975		0.295 0.326	6.32E-01 3.92E-01	-1.905 -2.214	0.324 0.265			pgm pgi	-1.671 -1.855	S	0.267 0.301	7.56E-07 2.91E-06	-2.680 -3.003	-0.661 -0.707
F	pfkB fbp	1.110 1.046	S	0.195 0.194	2.09E-05 8.22E-05	0.369 0.311	1.852 1.782			pfkA pfkB	-0.880 0.230	s	0.214 0.149	1.59E-02 9.99E-01	-1.689 -0.333	-0.072 0.793
g	fbaB gapC gamA	0.906 0.560 0.880	s	0.203 0.213 0.214	4.26E-03 6.63E-01 1.59E-02	0.139 -0.245 0.072	1.674 1.365 1.689			fbp fbaB	0.166 0.026 -0.320		0.147 0.158 0.171	1.00E+00 1.00E+00 9.88E-01	-0.389 -0.572 -0.966	0.721 0.623 0.326
9	gpmA gpmB pykA	0.880 0.474 -0.251	S	0.214 0.236 0.254	1.59E-02 9.71E-01 1.00E+00	-0.417 -1.209	1.689 1.365 0.707			gapC gpmB pykA	-0.320 -0.406 -1.132	q	0.171 0.199 0.220	9.88E-01 9.66E-01 2.19E-04	-0.966 -1.159 -1.964	0.326 0.347 -0.299
F	pykF ppsA	-0.073 1.012	s	0.224 0.195	1.00E+00 2.17E-04	-0.918 0.271	0.772 1.752			pykF ppsA	-0.954 0.131	s	0.184 0.149	1.76E-04 1.00E+00	-1.650 -0.430	-0.257 0.693
z F	zwf pgl	0.083 0.542		0.257 0.226	1.00E+00 8.23E-01	-0.889 -0.310	1.055 1.395			zwf pgl	-0.798 -0.338		0.224 0.187	9.98E-02 9.93E-01	-1.647 -1.044	0.051 0.368
r	gnd rpe rpiA	-0.025 -0.826 0.222		0.269 0.306 0.230	1.00E+00 6.10E-01 1.00E+00	-1.041 -1.981 -0.645	0.992 0.330 1.090			gnd rpe rpiA	-0.905 -1.706 -0.658	s s	0.238 0.278 0.192	4.61E-02 1.97E-06 1.38E-01	-1.805 -2.762 -1.382	-0.006 -0.651 0.065
r	rpiB tktA	0.638 0.761		0.217 0.204	4.23E-01 6.15E-02	-0.183 -0.013	1.459 1.535			rpiB tktA	-0.050 -0.242 -0.120		0.192 0.177 0.161	1.00E+00 1.00E+00	-0.908 -0.726	0.424 0.486
t	tktB talA	0.436 0.994	s	0.207 0.210	9.50E-01 1.43E-03	-0.348 0.199	1.221 1.789			tktB talA	-0.444 0.113		0.164 0.168	6.09E-01 1.00E+00	-1.064 -0.520	0.175 0.747
Ċ	talB 0.1h-1	0.734 0.412		0.303 0.226	8.13E-01 9.92E-01	-0.411 -0.442	1.878 1.265			talB 0.1h-1	-0.147 -0.469		0.275 0.187	1.00E+00 7.63E-01	-1.190 -1.175	0.896 0.237
C	0.2h-1 0.4h-1 0.5h-1	1.021 0.635 0.382	s	0.199 0.204 0.231	2.75E-04 3.06E-01 9.98E-01	0.265 -0.139 -0.491	1.776 1.409 1.255			0.2h-1 0.4h-1 0.5h-1	0.140 -0.245 -0.498		0.154 0.161 0.194	1.00E+00 1.00E+00 7.09E-01	-0.441 -0.851 -1.229	0.722 0.360 0.232
C	0.7h-1 an difference	-0.075	at the .05 leve	0.263	1.00E+00	-1.070	0.921		*. "S" The	0.7h-1 mean difference	-0.955	S at the .05 lev	0.231	1.55E-02	-1.831	-0.079

Dependen	nt Variable: Meta	bolite	Multiple Co	omparisons				Depender	nt Variable: Meta	abolite	Multiple Co	omparisons			
(I)	(J)	Mean Difference (I-J)		Std. Error	Sig.	95% Confide Lower Bound	Upper Bound	(1)	(J)	Mean Difference (I-J)		Std. Error	Sig.	95% Confide Lower Bound	Upper Bound
gpmB	galM glk	0.765 -0.825	S	0.171 0.294	4.62E-03 5.29E-01	0.115 -1.934	1.415 0.285	pgl	galM glk	0.697 -0.893	S	0.157 0.286	4.93E-03 2.93E-01 8.99E-04	0.102 -1.972	1.291 0.186
	pgm pgi pfkA	-1.264 -1.449 -0.474	s	0.285 0.317 0.236	4.47E-03 3.21E-03 9.71E-01	-2.340 -2.654 -1.365	-0.188 -0.243 0.417		pgm pgi pfkA	-1.333 -1.517 -0.542	s s	0.277 0.309 0.226	8.57E-04 8.23E-01	-2.377 -2.695 -1.395	-0.288 -0.339 0.310
	pfkB fbp	0.636 0.572		0.179 0.178	1.04E-01 2.39E-01	-0.044 -0.101	1.316 1.245		pfkB fbp	0.568 0.504		0.166 0.164	1.42E-01 3.24E-01	-0.059 -0.116	1.194 1.123
	fbaB gapC gpmA	0.432 0.086 0.406		0.187 0.198 0.199	8.75E-01 1.00E+00 9.66E-01	-0.276 -0.662 -0.347	1.140 0.834 1.159		fbaB gapC gpmA	0.364 0.018 0.338		0.174 0.185 0.187	9.54E-01 1.00E+00 9.93E-01	-0.294 -0.683 -0.368	1.021 0.719 1.044
	pykA pykF	-0.725 -0.547		0.242 0.210	3.77E-01 6.82E-01	-0.347 -1.638 -1.339	0.187 0.245		gpmB pykA	-0.068 -0.794		0.212	1.00E+00 1.41E-01	-0.868 -1.668	0.732
	ppsA zwf	0.538 -0.391		0.179 0.245	3.77E-01 9.99E-01	-0.141 -1.319	1.216 0.536		pykF ppsA	-0.616 0.469		0.198 0.165	3.02E-01 4.98E-01	-1.363 -0.156	0.132 1.094
	pgl gnd rpe	0.068 -0.499 -1.300	9	0.212 0.258 0.296	1.00E+00 9.82E-01 5.52E-03	-0.732 -1.473 -2.418	0.868 0.475 -0.182		zwf gnd rpe	-0.460 -0.567 -1.368	9	0.235 0.248 0.287	9.79E-01 8.86E-01 1.28E-03	-1.350 -1.506 -2.457	0.431 0.371 -0.280
	rpiA rpiB	-0.252 0.164		0.216 0.203	1.00E+00 1.00E+00	-1.068 -0.602	0.564 0.930		rpiA rpiB	-0.320 0.096		0.205 0.191	9.99E-01 1.00E+00	-1.093 -0.624	0.453 0.816
	tktA tktB talA	0.286 -0.038 0.520		0.189 0.192 0.195	1.00E+00 1.00E+00 6.43E-01	-0.429 -0.764 -0.218	1.001 0.689 1.258		tktA tktB talA	0.218 -0.106 0.451		0.176 0.179 0.183	1.00E+00 1.00E+00 7.82E-01	-0.447 -0.784 -0.239	0.883 0.571 1.141
	talB 0.1h-1	0.259 -0.062		0.293 0.212	1.00E+00 1.00E+00	-0.848 -0.863	1.366 0.738		talB 0.1h-1	0.191 -0.131		0.285 0.201	1.00E+00 1.00E+00	-0.885 -0.887	1.268 0.626
	0.2h-1 0.4h-1 0.5h-1	0.547 0.161 -0.092		0.184 0.189 0.218	3.95E-01 1.00E+00 1.00E+00	-0.148 -0.554 -0.914	1.242 0.876 0.730		0.2h-1 0.4h-1 0.5h-1	0.478 0.093 -0.160		0.170 0.176 0.206	5.21E-01 1.00E+00 1.00E+00	-0.165 -0.572 -0.940	1.122 0.757 0.619
pykA	0.7h-1 galM	-0.549 1.490	s	0.218 0.252 0.195	9.28E-01 7.65E-10	-1.500 0.749	0.403 2.232	gnd	0.7h-1 galM	-0.617 1.264	s	0.242 0.215	7.28E-01 8.79E-06	-1.533 0.448	0.299 2.081
	glk pgm	-0.100 -0.539 -0.723		0.309 0.300 0.331	1.00E+00 9.94E-01 9.24E-01	-1.263 -1.671 -1.978	1.064 0.592 0.531		glk pgm	-0.326 -0.765 -0.950		0.322 0.313 0.343	1.00E+00 8.00E-01 5.55E-01	-1.537 -1.946 -2.248	0.885 0.415 0.348
	pgi pfkA pfkB	0.251 1.361	s	0.254 0.202	1.00E+00 8.35E-08	-0.707 0.594	1.209		pgi pfkA pfkB	0.025 1.135	s	0.269 0.221	1.00E+00 2.78E-04	-2.240 -0.992 0.295	1.041 1.975
	fbp fbaB	1.297 1.157	S	0.201 0.209	3.68E-07 3.74E-05	0.536 0.365	2.059 1.949		fbp fbaB	1.071 0.931	S	0.220 0.228	8.70E-04 1.81E-02	0.237	1.906
	gapC gpmA gpmB	0.811 1.132 0.725	s	0.219 0.220 0.242	6.39E-02 2.19E-04 3.77E-01	-0.017 0.299 -0.187	1.639 1.964 1.638		gapC gpmA gpmB	0.585 0.905 0.499	s	0.237 0.238 0.258	7.80E-01 4.61E-02 9.82E-01	-0.310 0.006 -0.475	1.481 1.805 1.473
	pykF ppsA	0.178 1.263	s	0.230 0.202	1.00E+00 1.10E-06	-0.689 0.497	1.045 2.029		pykA pykF	-0.226 -0.048		0.274 0.246	1.00E+00 1.00E+00	-1.261 -0.980	0.809 0.883
	zwf pgl gnd	0.334 0.794 0.226		0.262 0.232 0.274	1.00E+00 1.41E-01 1.00E+00	-0.658 -0.081 -0.809	1.326 1.668 1.261		ppsA zwf pgl	1.037 0.108 0.567	S	0.221 0.277 0.248	1.85E-03 1.00E+00 8.86E-01	0.198 -0.940 -0.371	1.875 1.155 1.506
	rpe rpiA	-0.575 0.473		0.310 0.236	9.90E-01 9.71E-01	-1.746 -0.416	0.597 1.363		rpe rpiA	-0.801 0.247		0.323 0.252	7.75E-01 1.00E+00	-2.020 -0.705	0.418 1.199
	rpiB tktA tktB	0.889 1.012 0.687	s	0.223 0.211 0.214	2.53E-02 1.08E-03 2.41E-01	0.045 0.213 -0.121	1.733 1.810 1.496		rpiB tktA tktB	0.663 0.785 0.461		0.241 0.229 0.232	5.67E-01 1.44E-01 9.74E-01	-0.247 -0.083 -0.416	1.573 1.654 1.339
	tktB talA talB	1.245 0.985	s	0.217 0.307	1.16E-05 2.47E-01	0.426 -0.176	2.064 2.145		tktB talA talB	1.019 0.758	s	0.234 0.320	6.83E-03 8.44E-01	0.132 -0.450	1.906 1.967
	0.1h-1 0.2h-1 0.4h-1	0.663 1.272	s	0.232 0.206	4.86E-01 1.53E-06	-0.213 0.491	1.538 2.052		0.1h-1 0.2h-1 0.4h-1	0.437 1.046	s	0.249 0.225	9.95E-01 2.10E-03	-0.503 0.194	1.376 1.898
	0.4h-1 0.5h-1 0.7h-1	0.886 0.633 0.177	s	0.211 0.237 0.269	1.18E-02 6.34E-01 1.00E+00	0.088 -0.262 -0.838	1.684 1.528 1.191		0.4h-1 0.5h-1 0.7h-1	0.660 0.407 -0.050		0.229 0.253 0.283	4.69E-01 9.99E-01 1.00E+00	-0.208 -0.550 -1.119	1.528 1.364 1.020
pykF	galM glk	1.312 -0.278	s	0.154 0.284	5.26E-11 1.00E+00	0.729 -1.350	1.895 0.795	rpe	galM glk	2.065 0.475	s	0.259 0.353	2.03E-10 1.00E+00	1.079 -0.854	3.051 1.804
	pgm pgi pfkA	-0.717 -0.901 0.073		0.275 0.308 0.224	6.83E-01 4.36E-01 1.00E+00	-1.755 -2.074 -0.772	0.321 0.271 0.918		pgm pgi pfkA	0.036 -0.149 0.826		0.345 0.372 0.306	1.00E+00 1.00E+00 6.10E-01	-1.265 -1.556 -0.330	1.337 1.258 1.981
	pfkB fbp	1.183 1.120	s s	0.163 0.161	2.74E-09 1.73E-08	0.568 0.511	1.799 1.728		pfkB fbp	1.936 1.872	S	0.264 0.263	4.56E-09 1.51E-08	0.931 0.871	2.941 2.873
	fbaB gapC gpmA	0.979 0.633 0.954	S	0.171 0.183 0.184	1.27E-05 1.29E-01 1.76E-04	0.332 -0.058 0.257	1.626 1.325 1.650		fbaB gapC gpmA	1.732 1.386 1.706	S	0.270 0.277 0.278	5.11E-07 4.86E-04 1.97E-06	0.708 0.334 0.651	2.756 2.438 2.762
	gpmB pykA	0.547 -0.178	3	0.210 0.230	6.82E-01	-0.245 -1.045	1.339 0.689		gpmB pykA	1.300 0.575	S	0.296 0.310	5.52E-03 9.90E-01	0.182 -0.597	2.418 1.746
	ppsA zwf pgl	1.085 0.156 0.616	s	0.162 0.233 0.198	8.45E-08 1.00E+00 3.02E-01	0.471 -0.727 -0.132	1.699 1.039 1.363		pykF ppsA zwf	0.753 1.838 0.909	s	0.286 0.264 0.313	6.64E-01 3.43E-08 4.49E-01	-0.330 0.833 -0.274	1.835 2.842 2.091
	gnd rpe	0.048 -0.753		0.196 0.246 0.286	1.00E+00 6.64E-01	-0.883 -1.835	0.980 0.330		pgl gnd	1.368 0.801	s	0.287 0.323	1.28E-03 7.75E-01	-0.274 0.280 -0.418	2.457 2.020
	rpiA rpiB tktA	0.295 0.712 0.834	s	0.203 0.188 0.173	1.00E+00 4.91E-02 9.44E-04	-0.469 0.001 0.179	1.060 1.422 1.489		rpiA rpiB tktA	1.048 1.464 1.586	s	0.291 0.281 0.271	8.63E-02 1.76E-04 9.17E-06	-0.052 0.400 0.557	2.148 2.528 2.615
	tktB talA	0.834 0.509 1.067	s	0.173 0.177 0.180	9.44E-04 4.66E-01 4.10E-06	-0.179 -0.158 0.387	1.489 1.177 1.747		tktB talA	1.586 1.262 1.820	S S	0.271 0.273 0.275	9.17E-06 2.48E-03 1.67E-07	0.557 0.225 0.775	2.815 2.299 2.864
	talB 0.1h-1	0.807 0.485		0.283 0.198	4.92E-01 7.99E-01	-0.264 -0.263	1.877 1.233		talB 0.1h-1	1.559 1.238	S	0.351 0.288	4.39E-03 8.11E-03	0.233 0.149	2.886 2.327
	0.2h-1 0.4h-1 0.5h-1	1.094 0.708 0.455	s	0.167 0.173 0.204	1.73E-07 1.72E-02 9.10E-01	0.461 0.054 -0.316	1.727 1.363 1.226		0.2h-1 0.4h-1 0.5h-1	1.847 1.461 1.208	S S	0.267 0.271 0.292	3.99E-08 8.52E-05 1.48E-02	0.831 0.432 0.104	2.862 2.490 2.312
ppsA	0.7h-1 galM	-0.001 0.228		0.240 0.108	1.00E+00 9.51E-01	-0.910 -0.181	0.907 0.636	rpiA	0.7h-1 galM	0.751 1.017	s	0.318 0.162	8.47E-01 9.33E-07	-0.450 0.402	1.953 1.632
	glk pgm pgi	-1.362 -1.802 -1.986	S	0.263 0.252 0.288	1.78E-04 7.23E-09 1.12E-07	-2.356 -2.758 -3.088	-0.369 -0.846 -0.884		glk pgm pgi	-0.573 -1.012 -1.197		0.289 0.280 0.312	9.76E-01 8.17E-02 4.59E-02	-1.664 -2.069 -2.385	0.518 0.044 -0.008
	pfkA pfkB	-1.012 0.098	S	0.195 0.121	2.17E-04 1.00E+00	-1.752 -0.357	-0.271 0.553		pfkA pfkB	-0.222 0.888	s	0.230 0.171	1.00E+00 1.71E-04	-1.090 0.241	0.645 1.534
	fbp fbaB gapC	0.035 -0.106 -0.452		0.118 0.132 0.147	1.00E+00 1.00E+00 3.27E-01	-0.410 -0.603 -1.008	0.479 0.392 0.104		fbp fbaB gapC	0.824 0.684 0.338	S S	0.169 0.179 0.190	7.45E-04 4.37E-02 9.95E-01	0.184 0.007 -0.381	1.464 1.360 1.057
	gpmA gpmB	-0.131 -0.538		0.149 0.179	1.00E+00 3.77E-01	-0.693 -1.216	0.430 0.141		gpmA gpmB	0.658 0.252		0.192 0.216	1.38E-01 1.00E+00	-0.065 -0.564	1.382 1.068
	pykA pykF zwf	-1.263 -1.085 -0.929	S	0.202 0.162 0.206	1.10E-06 8.45E-08 4.27E-03	-2.029 -1.699 -1.713	-0.497 -0.471 -0.144		pykA pykF ppsA	-0.473 -0.295 0.789	_	0.236 0.203 0.171	9.71E-01 1.00E+00 2.13E-03	-1.363 -1.060 0.144	0.416 0.469 1.435
	pgl gnd	-0.469 -1.037	s	0.165 0.221	4.98E-01 1.85E-03	-1.094 -1.875	0.156 -0.198		zwf pgl	-0.139 0.320	S	0.239 0.205	1.00E+00 9.99E-01	-1.044 -0.453	0.765 1.093
	rpe rpiA	-1.838 -0.789 -0.373	s	0.264 0.171 0.153	3.43E-08 2.13E-03 8.04E-01	-2.842 -1.435 -0.953	-0.833 -0.144 0.206		gnd rpe rplB	-0.247 -1.048 0.416		0.252 0.291 0.195	1.00E+00 8.63E-02 9.44E-01	-1.199 -2.148 -0.321	0.705 0.052 1.153
	rpiB tktA tktB	-0.251 -0.576	s	0.135 0.139	9.89E-01 1.40E-02	-0.759 -1.100	0.257 -0.051		tktA tktB	0.538 0.214		0.181 0.184	3.99E-01 1.00E+00	-0.146 -0.482	1.222 0.910
	talA talB	-0.018 -0.278		0.143 0.261	1.00E+00 1.00E+00	-0.559 -1.269	0.523 0.713		talA talB 0.1h-1	0.771 0.511	S	0.188 0.288	1.55E-02 9.94E-01	0.063 -0.577	1.480 1.599
	0.1h-1 0.2h-1 0.4h-1	-0.600 0.009 -0.377		0.166 0.127 0.135	8.02E-02 1.00E+00 5.31E-01	-1.225 -0.469 -0.884	0.025 0.488 0.131		0.1h-1 0.2h-1 0.4h-1	0.189 0.799 0.413	s	0.205 0.175 0.181	1.00E+00 2.84E-03 8.89E-01	-0.584 0.136 -0.271	0.963 1.461 1.096
١.	0.5h-1 0.7h-1	-0.630 -1.086	s	0.173 0.214	7.61E-02 3.73E-04	-1.283 -1.899	0.023 -0.273		0.5h-1 0.7h-1	0.160 -0.297		0.211 0.246	1.00E+00 1.00E+00	-0.636 -1.226	0.955 0.633
zwf	galM glk pgm	1.156 -0.434 -0.873	s	0.199 0.311 0.303	1.81E-05 1.00E+00 4.65E-01	0.396 -1.608 -2.016	1.917 0.741 0.270	rpiB	galM glk pgm	0.601 -0.989 -1.428	S	0.144 0.279 0.270	1.35E-02 1.02E-01 1.02E-04	0.055 -2.043 -2.447	1.147 0.065 -0.409
	pgi pfkA	-1.057 -0.083		0.333 0.257	2.67E-01 1.00E+00	-2.322 -1.055	0.207 0.889		pgi pfkA	-1.613 -0.638	S	0.303 0.217	1.49E-04 4.23E-01	-2.769 -1.459	-0.457 0.183
	pfkB fbp fbaB	1.027 0.964 0.823	S	0.206 0.205 0.213	6.27E-04 1.99E-03 4.10E-02	0.242 0.183 0.013	1.813 1.744 1.633		pfkB fbp fbaB	0.472 0.408 0.268		0.154 0.152 0.163	3.31E-01 6.21E-01 9.98F-01	-0.109 -0.165 -0.347	1.053 0.981 0.882
	gapC gpmA	0.477 0.798	8	0.223 0.224	9.38E-01 9.98E-02	-0.368 -0.051	1.322 1.647		gapC gpmA	-0.078 0.242		0.175 0.177	1.00E+00 1.00E+00	-0.740 -0.424	0.583 0.908
	gpmB pykA	0.391 -0.334 -0.156		0.245 0.262 0.233	9.99E-01 1.00E+00 1.00E+00	-0.536 -1.326 -1.039	1.319 0.658 0.727		gpmB pykA pykF	-0.164 -0.889 -0.712	s	0.203 0.223 0.188	1.00E+00 2.53E-02 4.91E-02	-0.930 -1.733 -1.422	0.602 -0.045 -0.001
	pykF ppsA pgl	0.929 0.460	s	0.206 0.235	4.27E-03 9.79E-01	0.144 -0.431	1.713 1.350		pykF ppsA zwf	0.373 -0.556	S	0.153 0.227	8.04E-01 7.96E-01	-0.206 -1.416	0.953 0.305
	gnd rpe	-0.108 -0.909		0.277 0.313	1.00E+00 4.49E-01	-1.155 -2.091	0.940 0.274		pgl gnd	-0.096 -0.663		0.191 0.241	1.00E+00 5.67E-01	-0.816 -1.573	0.624 0.247
	rpiA rpiB tktA	0.139 0.556 0.678		0.239 0.227 0.215	1.00E+00 7.96E-01 2.80E-01	-0.765 -0.305 -0.138	1.044 1.416 1.494		rpe rpiA tktA	-1.464 -0.416 0.122	S	0.281 0.195 0.165	1.76E-04 9.44E-01 1.00E+00	-2.528 -1.153 -0.500	-0.400 0.321 0.745
	tktB talA	0.353 0.911	s	0.218 0.220	9.98E-01 1.59E-02	-0.473 0.075	1.179 1.747		tktB talA	-0.202 0.355		0.168 0.172	1.00E+00 9.60E-01	-0.838 -0.294	0.434 1.005
	talB 0.1h-1 0.2h-1	0.651 0.329 0.938	6	0.310 0.236 0.210	9.52E-01 1.00E+00 4.86E-03	-0.521 -0.562 0.139	1.822 1.220 1.737		talB 0.1h-1 0.2h-1	0.095 -0.227 0.382		0.278 0.191 0.159	1.00E+00 1.00E+00 8.19E-01	-0.957 -0.947 -0.216	1.147 0.494 0.981
	0.4h-1 0.5h-1	0.552 0.299	5	0.215 0.240	7.10E-01 1.00E+00	-0.263 -0.611	1.368 1.209		0.4h-1 0.5h-1	-0.003 -0.256		0.165 0.197	1.00E+00 1.00E+00	-0.625 -1.000	0.619 0.488
*. "S" The	0.7h-1 mean difference	-0.157 is significant	at the .05 lev	0.272 rel.	1.00E+00	-1.185	0.870	*. *S* The	0.7h-1 mean difference	-0.713 e is significant	at the .05 lev	0.234 el.	3.49E-01	-1.599	0.174

	nt Variable: Meta	bolite					
		Mean Difference				95% Confide Lower	nce Interval
)	(J)	(I-J)	•	Std. Error	Sig.	Bound	Bound
κtΑ	galM glk	0.479 -1.111	S	0.124 0.270	3.84E-02 1.53E-02	0.010 -2.130	-0.94
	pgm	-1.551	S S	0.260	3.74E-06	-2.533	-0.56
	pgi pfkA	-1.735 -0.761	s	0.294 0.204	1.21E-05	-2.859 -1.535	-0.61 0.01
	pfkB	0.350		0.135	6.15E-02 7.02E-01 9.39E-01	-0.160	0.85
	fbp fbaB	0.286 0.146		0.133 0.145	9.39E-01 1.00E+00	-0.215 -0.402	0.78
	gapC	-0.200			1.00E+00	-0.801	0.40
	gpmA gpmB	0.120 -0.286		0.161 0.189	1.00E+00 1.00E+00	-0.486 -1.001	0.72
	pykA	-1.012 -0.834	s	0.211 0.173	1.08E-03	-1.810	-0.21
	pykF	-0.834 0.251	S S	0.173	9.44E-04 9.89E-01	-1.489 -0.257	-0.21 -0.17
	ppsA zwf	-0.678		0.135 0.215	9.89E-01 2.80E-01	-0.257	0.75 0.13
	pgl	-0.218		0.176 0.229	1.00E+00	-0.883	0.44
	gnd	-0.785 -1.586	s	0.271	1.44E-01 9.17E-06	-1.654 -2.615	0.08
	rpe rpiA	-0.538		0.181	3.99E-01	-1.222	0.14
	rpiB tktB	-0.122 -0.324		0.165 0.152	1.00E+00 9.42E-01	-0.745 -0.896	0.50
	talA	0.233		0.156	1.00E+00	-0.354	0.82
	talB 0.1h-1	-0.027 -0.349		0.268 0.177	1.00E+00 9.77E-01	-1.043 -1.014	0.98
	0.1h-1 0.2h-1	0.260		0.141	9.77E-01 9.90E-01	-0.270	0.79
	0.4h-1 0.5h-1	-0.125		0.148	1.00E+00	-0.682	0.43
	0.7h-1	-0.379 -0.835		0.183 0.223	9.59E-01 5.64F-02	-1.070 -1.679	0.31
tB	galM	0.803	s	0.129 0.272	5.64E-02 9.18E-07 4.56E-01	0.316	1.29
	glk pgm	-0.787 -1.226	s	0.272	4.56E-01	-1.813 -2.216	0.23
		-1.411	S	0.262 0.296	1.70E-03 1.70E-03	-2.216 -2.542	-0.23 -0.28
	pfkA pfkB	-0.436 0.674	s	0.207 0.139	9.50E-01 8.18E-04	-1.221 0.148	0.34
	fbp	0.610 0.470	S	0.137	4 22F-03	0.093	1.12
	fbaB	0.470		0.149 0.163	2.78E-01	-0.093 -0.491	1.03
	gapC gpmA	0.124 0.444		0.164	1.00E+00 6.09E-01	-0.491	1.06
	gpmB	0.038		0.192 0.214 0.177	1.00E+00 2.41E-01	-0.689	0.76 0.12
	pykA pykF	-0.687 -0.509		0.214	4.66E-01	-1.496 -1.177	0.12
	ppsA	0.576	s	0.139	1.40E-02	0.051	1.10
	zwf pgl	-0.353 0.106		0.218 0.179	9.98E-01 1.00E+00	-1.179 -0.571	0.47
	gnd	-0.461		0.232	9.74E-01	-1.339	0.41
	rpe rpiA	-1.262 -0.214	S	0.273 0.184	2.48E-03 1.00E+00	-2.299 -0.910	-0.22 0.48
	rpiB	0.202 0.324		0.168	1.00E+00	-0.434 -0.248	0.83
	tktA talA	0.324		0.152	9 42F-01	-0.248	0.89
	taiA talB	0.558 0.297		0.159 0.270	1.15E-01 1.00E+00	-0.044 -0.727	1.15
	0.1h-1	-0.024		0.180 0.145	1.00F+00	-0.702	0.65
	0.2h-1 0.4h-1	0.585 0.199	s	0.145 0.152	2.03E-02	0.038	1.13
	0.5h-1	-0.054		0.186	1.00E+00 1.00E+00	-0.373 -0.758	0.77
	0.7h-1 galM	-0.511 0.246		0.225 0.133	8.92E-01 9.91E-01	-1.364 -0.259	0.34
	glk	-1.345	s	0.274	6.00E-04	-2.379	-0.31
	pgm	-1.784 -1.968	S	0.264	4.88E-08 3.57E-07	-2.782 -3.107	-0.78
	pgi pfkA	-0.994	S	0.290	1.43E-03	-1.789	-0.63
	pfkB	0.116		0.144	1.00E+00 1.00E+00	-0.426 -0.482	0.65
	fbp fbaB	0.053 -0.088		0.142 0.153	1.00E+00	-0.666	0.58
	gapC	-0.434		0.166	6.85E-01	-1.062	0.19
	gpmA gpmB	-0.113 -0.520		0.168 0.195	1.00E+00 6.43E-01	-0.747 -1.258	0.52
	pykA	-1.245	s	0.217	6.43E-01 1.16E-05	-2.064	-0.42
	pykF	-1.067 0.018	S	0.180 0.143	4.10E-06 1.00E+00	-1.747 -0.523	-0.38 0.55
	ppsA zwf	-0.911 -0.451	s	0.220 0.183	1.59E-02 7.82E-01	-1.747 -1.141	-0.07 0.23
	pgl	-0.451		0.183	7.82E-01 6.83E-03	-1.141	0.23
	gnd rpe	-1.019 -1.820	S S	0.234 0.275	1 67F-07	-1.906 -2.864	-0.13 -0.77
	rpiA	-0.771 -0.355	S	0.188 0.172	1.55E-02 9.60E-01	-1.480	-0.06
	rpiB tktA	-0.233		0.156	1.00E+00	-1.005 -0.820	0.29
	tktB	-0.558		0.159	1 15F-01	-1.159	0.04
	talB 0.1h-1	-0.260 -0.582		0.273 0.183	1.00E+00 2.59E-01	-1.293 -1.272	0.77
	0.2h-1	0.027		0.149 0.156	1.00E+00 8.77E-01	-0.535	0.58
	0.4h-1 0.5h-1	-0.359 -0.612		0.156 0.189	2 32F-01	-0.945 -1.327	0.22
	0.7h-1	-1.068	s	0.228	1.75E-03 9.75E-01	-1.931	-0.20
iΒ	galM	0.506		0.256 0.350	9.75E-01	-0.467	1.47
	glk pgm	-1.084 -1.524	s	0.343	3.10E-01 4.10E-03	-2.404 -2.815	0.23 -0.23
	pgi	-1.708	s	0.370	2.22E-03 8.13E-01	-3.106	-0.31
	pfkA pfkB	-0.734 0.377		0.303 0.261	8.13E-01 1.00F+00	-1.878 -0.616	0.41
	fbp	0.377 0.313		0.260	1.00E+00 1.00E+00	-0.616 -0.675	1.30
	fbaB gapC	0.173 -0.173		0.267 0.274	1.00E+00 1.00E+00	-0.839 -1.213	1.18
	gpmA	0.147		0.275	1.00F+00	-0.896	1.19
	gpmB pykA	-0.259 -0.985		0.293	1.00E+00	-1.366 -2.145	0.84
	nvkF	-0.807		0.283	2.47E-01 4.92E-01	-1.877	0.17
	ppsA zwf	0.278		0.261	1.00E+00 9.52E-01	-0.713	1 26
	zwf pgl	-0.651 -0.191		0.310	9.52E-01	-1.822 -1.268	0.52
	gnd	-0.758		0.320	1.00E+00 8.44E-01 4.39E-03	-1.967	0.45
	rpe rpiA	-1.559 -0.511	S	0.351 0.288	4.39E-03 9.94E-01	-2.886 -1.599	-0.23 0.57
	rpiB	-0.095		0.278	1.00E+00	-1.147	0.95
	tktA tktB	0.027 -0.297		0.268 0.270	1.00E+00 1.00E+00 1.00E+00	-0.989 -1.322	1.04
	talA	-0.297 0.260		0.270 0.273	1.00E+00 1.00E+00	-1.322 -0.772	1.29
	0.1h-1	-0.322		0.285	1.00E+00	-1.399	0.75
	0.2h-1	0.287	1	0.264	1.00E+00	-0.715	1.29
	0.4h-1	-0.098		0.268	1.00E+00 1.00E+00	-1.115	0.91

		Mean Difference				95% Confide Lower	ence Interv Upper
1)	(J)	(I-J)	٠	Std. Error	Sig.	Bound	Bound
).1h-1	galM glk	0.828 -0.763	S	0.157 0.286	1.20E-04 6.41E-01	0.233 -1.842	1.4
	pgm	-1.202	S	0.277	6.52E-03	-2.247	-0.1
	pgi pfkA	-1.386 -0.412	s	0.310 0.226	4.75E-03 9.92E-01	-2.565 -1.265	-0.2 0.4
	pfkB fbp	0.698 0.635	s s	0.166 0.164	1.09E-02 3.68E-02	0.072 0.015	1.3
	fbaB	0.494	3	0.174	5.04E-01	-0.163	1.1
	gapC gpmA	0.148 0.469		0.186 0.187	1.00E+00 7.63E-01	-0.553 -0.237	0.8
	gpmB	0.062		0.212	1.00E+00	-0.738	0.8
	pykA pykF	-0.663 -0.485		0.232 0.198	4.86E-01 7.99E-01	-1.538 -1.233	0.2
	ppsA zwf	0.600 -0.329		0.166 0.236	8.02E-02 1.00E+00	-0.025 -1.220	1.2
	pgl	0.131		0.236	1.00E+00	-0.626	0.8
	gnd rpe	-0.437 -1.238	s	0.249 0.288	9.95E-01 8.11E-03	-1.376 -2.327	0.5 -0.1
	rpiA	-0.189	3	0.205	1.00E+00	-0.963	0.5
	rpiB tktA	0.227		0.191 0.177	1.00E+00 9.77F-01	-0.494 -0.316	0.9
	tktB	0.024		0.180	1.00E+00	-0.653	0.7
	talA talB	0.582 0.322		0.183 0.285	2.59E-01 1.00E+00	-0.108 -0.756	1.2
	0.2h-1	0.609		0.171	9.29E-02	-0.034	1.2
	0.4h-1 0.5h-1	0.223 -0.030		0.176 0.207	1.00E+00 1.00E+00	-0.441 -0.810	0.8
	0.7h-1	-0.486		0.243	9.72E-01	-1.403	0.4
.2h-1	galM glk	0.218 -1.372	s	0.116 0.266	9.87E-01 1.97E-04	-0.219 -2.376	0.6 -0.3
	pgm	-1.811	S	0.255	8.98E-09	-2.778	-0.8
	pgi pfkA	-1.995 -1.021	S	0.291 0.199	1.21E-07 2.75E-04	-3.107 -1.776	-0.8 -0.2
	pfkB	0.089		0.127	1.00E+00	-0.391	0.5
	fbp fbaB	0.026 -0.115		0.125 0.138	1.00E+00 1.00E+00	-0.445 -0.636	0.4
	gapC	-0.461		0.152	3.62E-01	-1.037	0.1
	gpmA gpmB	-0.140 -0.547		0.154 0.184	1.00E+00 3.95E-01	-0.722 -1.242	0.4
	pykA	-1.272	S	0.206	1.53E-06	-2.052	-0.4
	pykF ppsA	-1.094 -0.009	s	0.167 0.127	1.73E-07 1.00E+00	-1.727 -0.488	-0.4 0.4
	zwf	-0.938	s	0.210	4.86E-03	-1.737 -1.122	-0.1
	pgl gnd	-0.478 -1.046	s	0.170 0.225	5.21E-01 2.10E-03	-1.122 -1.898	0.1 -0.1
	rpe	-1.847	S	0.267	3.99E-08	-2.862	-0.8
	rpiA rpiB	-0.799 -0.382	s	0.175 0.159	2.84E-03 8.19E-01	-1.461 -0.981	-0.1 0.2
	tktA tktB	-0.260		0.141	9.90E-01	-0.791 -1.131	0.2
	talA	-0.585 -0.027	S	0.149	2.03E-02 1.00E+00	-1.131 -0.589	0.5
	talB 0.1h-1	-0.287 -0.609		0.264 0.171	1.00E+00 9.29E-02	-1.290 -1.252	0.7
	0.1h-1	-0.886		0.171	5.75E-01	-0.916	0.0
	0.5h-1 0.7h-1	-0.639 -1.095	s	0.177 0.218	8.65E-02 4.40E-04	-1.309 -1.922	-0.2
.4h-1	nalM	0.604	S	0.216	7.05E-04	0.136	1.0
	glk	-0.986 -1.425		0.270 0.259	7.28E-02 4.28E-05	-2.004 -2.407	-0.4
	pgm pgi	-1.610	S S	0.294	4.26E-05 8.54E-05	-2.734	-0.4
	pfkA pfkB	-0.635 0.475		0.204 0.135	3.06E-01 1.08E-01	-1.409 -0.034	0.1
	fbp	0.411		0.133	3.08E-01	-0.089	0.9
	fbaB gapC	0.271 -0.075		0.145 0.159	9.89E-01 1.00E+00	-0.276 -0.675	0.8
	gpmA	0.245		0.161	1.00E+00	-0.360	0.6
	gpmB pykA	-0.161 -0.886	s	0.189 0.211	1.00E+00 1.18E-02	-0.876 -1.684	-0.6
	pykF	-0.708	s	0.173	1.72E-02	-1.363	-0.0
	ppsA zwf	0.377 -0.552		0.135 0.215	5.31E-01 7.10E-01	-0.131 -1.368	0.8
	pgl	-0.093		0.176	1.00E+00	-0.757	0.5
	gnd rpe	-0.660 -1.461	s	0.229 0.271	4.69E-01 8.52E-05	-1.528 -2.490	0.2
	rpiA	-0.413	ŭ	0.181	8.89E-01	-1.096	0.2
	rpiB tktA	0.003 0.125		0.165 0.148	1.00E+00 1.00E+00	-0.619 -0.431	0.6
	tktB	-0.199		0.152	1.00E+00	-0.771	0.3
	talA talB	0.359		0.156 0.268	8.77E-01 1.00E+00	-0.228 -0.918	0.9
	0.1h-1	-0.223		0.176	1.00E+00	-0.888	0.4
	0.2h-1 0.5h-1	0.386 -0.253		0.140 0.183	5.75E-01 1.00E+00	-0.144 -0.944	0.9
	0.7h-1	-0.710		0.222	2.57E-01	-1.553	0.1
.5h-1	galM glk	0.857 -0.733	S	0.165 0.290	1.89E-04 7.46E-01	0.233 -1.828	1.4
	pgm	-1.172	s	0.281	1.26E-02	-2.233	-0.1
	pgi pfkA	-1.357 -0.382	S	0.314 0.231	8.25E-03 9.98E-01	-2.549 -1.255	-0.1 0.4
	pfkB	0.728	s	0.173	1.14E-02	0.074	1.3
	fbp fbaB	0.664	S	0.171 0.181	3.65E-02 4.57E-01	0.017 -0.160	1.3
	gapC	0.178		0.192	1.00E+00	-0.548	0.9
	gpmA gpmB	0.498 0.092		0.194 0.218	7.09E-01 1.00E+00	-0.232 -0.730	1.2
	pykA	-0.633		0.237	6.34E-01 9.10E-01	-1.528 -1.226	0.2
	pykF ppsA	-0.455 0.630		0.204 0.173	7.61E-02	-0.023	0.3
	zwf	-0.299 0.160		0.240	1.00E+00	-1.209	0.6
	pgl gnd	-0.407		0.206 0.253	1.00E+00 9.99E-01	-0.619 -1.364	0.9
	rpe	-1.208 -0.160	S	0.292 0.211	1.48E-02 1.00E+00	-2.312 -0.955	-0.1 0.6
	rpiA rpiB	0.256		0.197	1.00E+00	-0.488	1.0
	tktA tktB	0.379 0.054		0.183 0.186	9.59E-01 1.00E+00	-0.313 -0.649	1.0
	talA	0.612		0.189	2.32E-01	-0.104	1.3
	talB 0.1h-1	0.352 0.030		0.289 0.207	1.00E+00	-0.741 -0.750	1.4
	0.2h-1	0.639		0.177	8.65E-02	-0.032	1.3
	0.4h-1 0.7h-1	0.253 -0.457		0.183 0.247	1.00E+00 9.90E-01	-0.438 -1.391	0.9
.7h-1	galM	1.314	s	0.208	1.08E-06	0.524	2.1
	glk pgm	-0.276 -0.716		0.317 0.308	1.00E+00 8.69E-01	-1.470 -1.878	0.9
	pgi	-0.900		0.338	6.42E-01	-2.182	0.3
	pfkA pfkB	0.075 1.185	s	0.263 0.214	1.00E+00 4.68F-05	-0.921 0.371	1.0
	fbp	1.121	S	0.213	1.61E-04	0.312	1.9
	fbaB gapC	0.981 0.635	s	0.221 0.230	4.99E-03 5.66E-01	0.143 -0.237	1.8
	gpmA	0.955	s	0.231	1.55E-02	0.079	1.8
	gpmB pykA	0.549 -0.177		0.252	9.28E-01 1.00E+00	-0.403 -1 191	1.5
	pvkF	0.001		0.240	1.00E+00	-0.907	0.9
	ppsA zwf	1.086 0.157	s	0.214 0.272	3.73E-04 1.00E+00	0.273 -0.870	1.8
	pgl	0.617		0.242	7.28E-01	-0.299	1.5
	gnd rpe	0.050		0.283 0.318	1.00E+00 8.47E-01	-1.020 -1.953	1.1
	rpiA	0.297		0.246	1.00E+00	-0.633	1.2
	rpiB	0.713		0.234	3.49E-01	-0.174	1.5
	tktA tktB	0.835 0.511		0.223 0.225	5.64E-02 8.92E-01	-0.008 -0.342	1.6
	talA	1.068	s	0.228	1.75E-03	0.205	1.9
	talB 0.1h-1	0.808 0.486		0.316 0.243	7.19E-01 9.72E-01	-0.383 -0.430	1.9
		1.095	s	0.218	4.40E-04	0.269	1.9
	0.2h-1 0.4h-1	0.710	3	0.222	2.57E-01	-0.134	1.5

# 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.

Depender	nt Variable: Meta	bolite(nucleoti	Multiple Co					Depender	nt Variable: Meta	bolite(nucleot	Multiple Co				
m.	(J)	Mean Difference (I-J)		Std. Error	Sia.	95% Confide Lower Bound	Upper Bound	m	(J)	Mean Difference (I-J)		Std. Error	Sia.	95% Confide Lower Bound	Upper Bound
galM	glk pgm	-1.333 -1.594	S	0.331 0.251	2.43E-02 1.04E-06	-2.592 -2.550	-0.073 -0.638	pfkB	galM glk	0.034	s	0.137 0.339	1.00E+00 4.52E-02	-0.484 -2.586	0.553 -0.011
	pgi pfkA pfkB	-1.363 -1.458 -0.034	s s	0.243 0.239 0.137	1.19E-04 7.41E-06 1.00E+00	-2.307 -2.375 -0.553	-0.419 -0.541 0.484		pgm pgi pfkA	-1.560 -1.329 -1.424	S	0.261 0.254 0.250	5.55E-06 3.94E-04 3.36E-05	-2.553 -2.309 -2.379	-0.567 -0.349 -0.469
	fbp fbaB	-0.034 -0.135 -0.289		0.137 0.128 0.164	1.00E+00 9.94E-01	-0.620 -0.912	0.350		fbp fbaB	-0.101 -0.255	3	0.148 0.179	1.00E+00 1.00E+00	-0.658 -0.934	0.456 0.424
	gapC gpmA	-0.608 -0.446		0.177 0.186	1.54E-01 8.23E-01	-1.289 -1.152	0.072 0.261		gapC gpmA	-0.574 -0.412		0.192 0.200	3.89E-01 9.60E-01	-1.306 -1.168	0.157 0.345
	gpmB pykA pykF	-0.975 -0.406 -0.781	S	0.226 0.155 0.179	1.03E-02 6.69E-01 8.28E-03	-1.841 -0.994 -1.466	-0.109 0.182 -0.096		gpmB pykA pykF	-0.941 -0.372 -0.746	S	0.238 0.171 0.194	3.17E-02 9.29E-01 4.23E-02	-1.847 -1.019 -1.483	-0.034 0.276 -0.010
	ppsA zwf	-0.163 -0.709	3	0.175 0.134 0.235	1.00E+00 3.85E-01	-0.673 -1.618	0.347		ppsA zwf	-0.129 -0.674	3	0.153 0.246	1.00E+00 5.84E-01	-0.707 -1.621	0.450
	pgl gnd	-0.778 -0.981	S	0.198 0.236	3.68E-02 1.70E-02	-1.536 -1.883	-0.020 -0.079		pgl gnd	-0.744 -0.947	s	0.211 0.247	1.15E-01 4.65E-02	-1.548 -1.887	0.061 -0.006
	rpe rpiA rpiB	-2.222 -0.806 -0.537	S	0.341 0.198 0.185	1.17E-06 2.15E-02 4.60E-01	-3.534 -1.561 -1.244	-0.910 -0.052 0.170		rpe rpiA rpiB	-2.188 -0.772 -0.503	S	0.349 0.211 0.199	2.89E-06 7.63E-02 7.44E-01	-3.527 -1.573 -1.259	-0.850 0.029 0.254
	tktA tktB	-0.408 -0.759	s	0.156 0.173	6.84E-01 7.06E-03	-1.000 -1.419	0.185 -0.099		tktA tktB	-0.373 -0.725	s	0.173 0.188	9.33E-01 4.09E-02	-1.025 -1.438	0.278 -0.012
	talA talB 0.1h-1	-0.323 -0.721 -0.708		0.181 0.363 0.194	9.93E-01 9.71E-01 7.63E-02	-1.012 -2.114 -1.442	0.365 0.671 0.027		talA talB 0.1h-1	-0.289 -0.687 -0.674		0.195 0.370 0.207	1.00E+00 9.88E-01 2.19E-01	-1.029 -2.105 -1.457	0.451 0.730 0.109
	0.2h-1 0.4h-1	0.180 -0.675	s	0.121 0.141	1.00E+00 1.30E-03	-0.281 -1.211	0.641 -0.138		0.1h-1 0.2h-1 0.4h-1	0.214 -0.640	s	0.142 0.159	1.00E+00 2.21E-02	-0.322 -1.242	0.751 -0.039
_	0.5h-1 0.7h-1	-0.575 -0.839		0.217	6.53E-01 8.84E-02	-1.406 -1.724	0.256 0.045		0.5h-1 0.7h-1	-0.540 -0.805		0.229	8.45E-01 1.92E-01	-1.414 -1.729	0.333 0.119
glk	galM pgm pgi	1.333 -0.261 -0.031	S	0.331 0.399 0.394	2.43E-02 1.00E+00 1.00E+00	0.073 -1.768 -1.524	2.592 1.246 1.462	fbp	galM glk pgm	0.135 -1.197 -1.459	q	0.128 0.336 0.257	1.00E+00 1.00E-01 2.46E-05	-0.350 -2.473 -2.435	0.620 0.078 -0.482
	pfkA pfkB	-0.126 1.298	s	0.391	1.00E+00 4.52E-02	-1.606 0.011	1.355		pgi pfkA	-1.228 -1.323	S S	0.249 0.245	1.41E-03 1.41E-04	-2.192 -2.261	-0.264 -0.384
	fbp fbaB	1.197 1.043		0.336 0.351	1.00E-01 3.98E-01	-0.078 -0.286	2.473 2.373		pfkB fbaB	0.101 -0.154		0.148 0.173	1.00E+00 1.00E+00	-0.456 -0.809	0.658 0.500
	gapC gpmA gpmB	0.724 0.887 0.358		0.357 0.362 0.384	9.67E-01 7.92E-01 1.00E+00	-0.630 -0.482 -1.094	2.078 2.256 1.810		gapC gpmA gpmB	-0.473 -0.310 -0.839		0.186 0.194 0.233	7.26E-01 9.99E-01 9.35E-02	-1.183 -1.046 -1.728	0.236 0.425 0.050
	pykA pykF	0.927 0.552		0.347 0.358	6.32E-01 9.99E-01	-0.388 -0.806	2.241 1.910		pykA pykF	-0.270 -0.645		0.164 0.188	9.98E-01 1.43E-01	-0.893 -1.359	0.352 0.069
	ppsA zwf	1.170 0.624		0.338	1.33E-01 9.99E-01 1.00E+00	-0.114 -0.850	2.454		ppsA zwf	-0.027 -0.573		0.145 0.242	1.00E+00 8.34E-01 3.00E-01	-0.577 -1.504	0.522
	pgl gnd rpe	0.555 0.352 -0.890		0.368 0.389 0.461	1.00E+00 1.00E+00 9.82E-01	-0.838 -1.121 -2.635	1.948 1.825 0.856		pgl gnd rpe	-0.642 -0.845 -2.087	s	0.205 0.242 0.346	1.27E-01 9.13F-06	-1.427 -1.769 -3.414	0.142 0.079 -0.760
	rpiA rpiB	0.526 0.796		0.368 0.361	1.00E+00 9.19E-01	-0.866 -0.573	1.919 2.164		rpiA rpiB	-0.671 -0.401		0.205 0.193	2.18E-01 9.55E-01	-1.452 -1.137	0.110 0.334
	tktA tktB talA	0.925 0.574 1.009		0.347 0.355 0.359	6.41E-01 9.99E-01 5.24E-01	-0.392 -0.773 -0.351	2.242 1.920 2.369		tktA tktB talA	-0.272 -0.624 -0.188		0.166 0.182 0.189	9.98E-01 1.43E-01 1.00E+00	-0.899 -1.314 -0.906	0.354 0.066 0.530
	talB 0.1h-1	0.611 0.625		0.477 0.366	1.00E+00 9.97E-01	-0.351 -1.195 -0.759	2.417 2.008		talB 0.1h-1	-0.186 -0.586 -0.573		0.367 0.201	9.99E-01 4.96E-01	-1.993 -1.335	0.820 0.189
	0.2h-1 0.4h-1	1.513 0.658	s	0.333 0.341	3.59E-03 9.82E-01	0.246 -0.636	2.779 1.952		0.2h-1 0.4h-1	0.316 -0.539		0.133 0.152	8.43E-01 9.97E-02	-0.189 -1.113	0.820 0.034
pgm	0.5h-1 0.7h-1 galM	0.758 0.493 1.594	s	0.379 0.386 0.251	9.72E-01 1.00E+00 1.04E-06	-0.674 -0.969 0.638	2.190 1.955 2.550	fbaB	0.5h-1 0.7h-1 galM	-0.439 -0.704 0.289		0.224 0.237 0.164	9.76E-01 4.07E-01 9.94E-01	-1.294 -1.611 -0.333	0.416 0.203 0.912
pym	glk pgi	0.261 0.231	5	0.399	1.00E+00 1.00E+00	-1.246 -1.022	1.768 1.484	ibab	glk pgm	-1.043 -1.305	s	0.351 0.276	3.98E-01 1.57E-03	-0.333 -2.373 -2.352	0.286 -0.257
	pfkA pfkB	0.136 1.560	s	0.326 0.261	1.00E+00 5.55E-06	-1.101 0.567	1.373 2.553		pgi pfkA	-1.074 -1.169	S	0.269 0.265	3.14E-02 6.48E-03	-2.107 -2.180	-0.041 -0.158
	fbp fbaB gapC	1.459 1.305 0.986	8 8 8	0.257 0.276 0.285	2.46E-05 1.57E-03 1.31E-01	0.482 0.257 -0.094	2.435 2.352 2.065		pfkB fbp gapC	0.255 0.154 -0.319		0.179 0.173 0.212	1.00E+00 1.00E+00 1.00E+00	-0.424 -0.500 -1.124	0.934 0.809 0.486
	gpmA gpmB	1.148 0.619	s	0.290 0.317	2.80E-02 9.79E-01	0.051	2.246 1.821		gpmA apmB	-0.156 -0.685		0.219 0.254	1.00E+00 6.13E-01	-0.985 -1.651	0.672 0.280
	pykA pykF	1.188 0.813	S	0.271 0.286	6.25E-03 4.97E-01	0.160 -0.270	2.216 1.897		pykA pykF	-0.116 -0.491		0.193 0.213	1.00E+00 8.76E-01	-0.848 -1.301	0.615 0.318
	ppsA zwf pgl	1.431 0.885 0.816	S	0.260 0.324 0.298	5.42E-05 5.86E-01 5.80E-01	0.443 -0.344 -0.312	2.419 2.115 1.945		ppsA zwf pgl	0.127 -0.419 -0.488		0.177 0.262 0.229	1.00E+00 9.99E-01 9.41E-01	-0.545 -1.422 -1.359	0.799 0.584 0.383
	gnd rpe	0.613 -0.628		0.324 0.408	9.86E-01 9.99E-01	-0.614 -2.176	1.840 0.919		gnd rpe	-0.691 -1.933	s	0.262 0.360	6.62E-01 1.46E-04	-1.689 -3.311	0.306 -0.555
	rpiA rpiB tktA	0.788 1.057 1.186		0.298 0.290 0.272	6.55E-01 7.63E-02 6.72E-03	-0.340 -0.040 0.155	1.915 2.154 2.218		rpiA rpiB tktA	-0.517 -0.247 -0.118		0.229 0.218 0.194	8.97E-01 1.00E+00 1.00E+00	-1.386 -1.076 -0.854	0.352 0.581 0.617
	tktB talA	0.835 1.271	s	0.272 0.282 0.287	4.08E-01 4.99E-03	-0.234 0.185	1.903		tktB talA	-0.116 -0.470 -0.034		0.208 0.215	8.97E-01 1.00E+00	-0.654 -1.259 -0.847	0.319 0.779
	talB 0.1h-1	0.873 0.886		0.426 0.295	9.62E-01 3.76E-01	-0.743 -0.229	2.488 2.002		talB 0.1h-1	-0.432 -0.418		0.381 0.225	1.00E+00 9.89E-01	-1.887 -1.271	1.023 0.434
	0.2h-1 0.4h-1 0.5h-1	1.774 0.919 1.019	S	0.254 0.264 0.311	3.33E-08 1.25E-01 2.08E-01	0.809 -0.082 -0.158	2.739 1.921 2.196		0.2h-1 0.4h-1 0.5h-1	0.470 -0.385 -0.285		0.168 0.183 0.246	5.31E-01 9.48E-01 1.00E+00	-0.167 -1.077 -1.220	1.107 0.307 0.649
pgi	0.7h-1 galM	0.755	s	0.320	8.50E-01 1.19E-04	-0.459 0.419	1.968	gapC	0.7h-1 galM	-0.550 0.608		0.258 0.177	9.40E-01 1.54E-01	-1.532 -0.072	0.432
	glk pgm pfkA	0.031 -0.231		0.394 0.330	1.00E+00 1.00E+00	-1.462 -1.484	1.524 1.022		glk pgm	-0.724 -0.986		0.357 0.285	9.67E-01 1.31E-01	-2.078 -2.065	0.630 0.094
	pfkB fbp	-0.095 1.329 1.228	S	0.320 0.254 0.249	1.00E+00 3.94E-04 1.41E-03	-1.317 0.349 0.264	1.127 2.309 2.192		pgi pfkA pfkB	-0.755 -0.850 0.574		0.278 0.274 0.192	5.99E-01 3.15E-01 3.89E-01	-1.820 -1.894 -0.157	0.310 0.194 1.306
	fbaB gapC	1.074 0.755	s	0.269 0.278	3.14E-02 5.99E-01	0.041 -0.310	2.107 1.820		fbp fbaB	0.473 0.319		0.186 0.212	7.26E-01 1.00E+00	-0.236 -0.486	1.183 1.124
	gpmA gpmB pykA	0.918 0.389 0.958		0.283 0.311 0.264	2.37E-01 1.00E+00 9.27E-02	-0.166 -0.798 -0.057	2.001 1.576 1.972		gpmA gpmB pykA	0.163 -0.366 0.203		0.229 0.263 0.205	1.00E+00 1.00E+00 1.00E+00	-0.708 -1.367 -0.577	1.033 0.634 0.982
	pykF ppsA	0.583 1.201	s	0.279	9.50E-01 2.55E-03	-0.486 0.225	1.652 2.176		pykF ppsA	-0.172 0.446		0.224	1.00E+00 8.51E-01	-1.025 -0.280	0.680
	zwf pgl	0.655 0.586		0.318 0.291	9.58E-01 9.68E-01	-0.560 -0.528	1.870 1.700		zwf pgl	-0.100 -0.169		0.271 0.239	1.00E+00 1.00E+00	-1.136 -1.080	0.936 0.741
	gnd rpe rpiA	0.383 -0.859 0.557		0.318 0.403 0.291	1.00E+00 9.40E-01 9.83E-01	-0.830 -2.393 -0.556	1.595 0.675 1.670		gnd rpe rpiA	-0.372 -1.614 -0.198	s	0.271 0.367 0.239	1.00E+00 7.01E-03 1.00E+00	-1.404 -3.016 -1.106	0.659 -0.212 0.711
	rpiB tktA	0.827 0.956		0.283 0.265	4.42E-01 9.75E-02	-0.256 -0.062	1.909 1.973		rpiB tktA	0.072 0.201		0.229 0.206	1.00E+00 1.00E+00	-0.798 -0.583	0.942 0.984
	tktB talA talB	0.604 1.040 0.642		0.275 0.280 0.421	9.16E-01 7.01E-02 9.99E-01	-0.450 -0.032 -0.961	1.659 2.112 2.245		tktB talA talB	-0.151 0.285 -0.113		0.219 0.225 0.387	1.00E+00 1.00E+00 1.00E+00	-0.984 -0.571 -1.590	0.683 1.141 1.364
	0.1h-1 0.2h-1	0.655 1.544	s	0.288 0.246	8.87E-01 6.99E-06	-0.446 0.591	1.757 2.497		0.1h-1 0.2h-1	-0.099 0.789	s	0.236 0.181	1.00E+00 8.77E-03	-0.992 0.095	0.794 1.482
	0.4h-1 0.5h-1	0.689 0.789		0.256 0.305	6.23E-01 6.96E-01	-0.300 -0.374	1.677 1.951		0.4h-1 0.5h-1	-0.066 0.034		0.195 0.255	1.00E+00 1.00E+00	-0.810 -0.937	0.677 1.005
pfkA	0.7h-1 galM glk	0.524 1.458 0.126	s	0.314 0.239 0.391	9.98E-01 7.41E-06 1.00E+00	-0.675 0.541 -1.355	1.723 2.375 1.606	gpmA	0.7h-1 galM glk	-0.231 0.446 -0.887		0.267 0.186 0.362	1.00E+00 8.23E-01 7.92E-01	-1.247 -0.261 -2.256	0.785 1.152 0.482
	pgm pgi	-0.136 0.095		0.326 0.320	1.00E+00 1.00E+00	-1.373 -1.127	1.101 1.317		pgm pgi	-1.148 -0.918	S	0.290 0.283	2.80E-02 2.37E-01	-2.246 -2.001	-0.051 0.166
	pfkB fbp fbaB	1.424	S	0.250 0.245	3.36E-05 1.41E-04	0.469 0.384	2.379 2.261		pfkA pfkB	-1.012 0.412		0.279	8.57E-02 9.60E-01	-2.075 -0.345	0.050 1.168
	gapC gpmA	1.169 0.850 1.012	S	0.265 0.274 0.279	6.48E-03 3.15E-01 8.57E-02	0.158 -0.194 -0.050	2.180 1.894 2.075		fbp fbaB gapC	0.310 0.156 -0.163		0.194 0.219 0.229	9.99E-01 1.00E+00 1.00E+00	-0.425 -0.672 -1.033	1.046 0.985 0.708
	gpmB pykA	0.483 1.052	s	0.308 0.260	9.99E-01 2.34E-02	-0.686 0.061	1.652 2.044		gpmB pykA	-0.529 0.040		0.269 0.212	9.77E-01 1.00E+00	-1.549 -0.764	0.491 0.844
	pykF ppsA	0.678 1.295	s	0.275 0.248	7.84E-01 2.92E-04	-0.370 0.345	1.725 2.245		pykF ppsA	-0.335 0.283		0.231 0.198	1.00E+00 1.00E+00	-1.209 -0.467	0.540 1.033
	zwf pgl gnd	0.750 0.680 0.477		0.314 0.288 0.315	8.32E-01 8.42E-01 1.00E+00	-0.448 -0.414 -0.718	1.947 1.775 1.672		zwf pgl gnd	-0.263 -0.332 -0.535		0.276 0.245 0.277	1.00E+00 1.00E+00 9.81E-01	-1.317 -1.263 -1.585	0.792 0.599 0.515
	rpe rpiA	-0.764 0.652		0.400 0.288	9.84E-01 8.92E-01	-2.286 -0.441	0.758 1.745		rpe rpiA	-1.777 -0.361	s	0.371 0.245	1.49E-03 1.00E+00	-3.192 -1.290	-0.361 0.569
	rpiB tktA	0.921 1.050	s	0.279 0.261	2.01E-01 2.50E-02	-0.141 0.056	1.983 2.045		rpiB tktA	-0.091 0.038		0.235 0.213	1.00E+00 1.00E+00	-0.983 -0.769	0.801 0.845
	tktB talA talB	0.699 1.135 0.737	s	0.271 0.276 0.419	7.04E-01 1.83E-02 9.95E-01	-0.334 0.084 -0.855	1.732 2.185 2.328		tktB talA talB	-0.313 0.122 -0.276		0.226 0.232 0.391	1.00E+00 1.00E+00 1.00E+00	-1.169 -0.756 -1.766	0.542 1.000 1.214
	0.1h-1 0.2h-1	0.750 1.638	s	0.285 0.241	6.61E-01 2.88E-07	-0.331 0.712	1.831 2.565		0.1h-1 0.2h-1	-0.262 0.626		0.242 0.189	1.00E+00 1.97E-01	-1.177 -0.093	0.652 1.345
	0.4h-1 0.5h-1 0.7h-1	0.783 0.883 0.619		0.252 0.301 0.311	3.14E-01 4.30E-01 9.73E-01	-0.180 -0.261 -0.563	1.747 2.028 1.801		0.4h-1 0.5h-1 0.7h-1	-0.229 -0.129 -0.393		0.203 0.261 0.272	1.00E+00 1.00E+00 1.00E+00	-0.997 -1.120 -1.429	0.539 0.862 0.642
*. *S* The	0.7h-1 mean difference	u.619 is significant	at the .05 lev	u.311 el.	9./3E-01	-u.563	1.801	*. "S" The	0.7h-1 mean difference		at the .05 lev		1.UUE+00	-1.429	U.642

		Mean Difference				95% Confide Lower	ence Interval Upper
I) gpmB	(J) galM	(I-J)	٠ .	Std. Error	Sig.	Bound 0.109	Bound 1.841
Jpmb	glk	-0.358	3	0.384	1.00E+00	-1.810	1.094
	pgm pgi	-0.619 -0.389		0.317 0.311	9.79E-01 1.00E+00	-1.821 -1.576	0.582
	pfkA pfkB	-0.483 0.941	s	0.308 0.238	9.99E-01 3.17E-02	-1.652 0.034	0.686
	fbp	0.839	3	0.233	9.35E-02	-0.050	1.728
	fbaB gapC	0.685 0.366		0.254 0.263	6.13E-01 1.00E+00	-0.280 -0.634	1.651
	gpmA	0.529 0.569		0.269	9.77E-01 8.80E-01	-0.491	1.549
	pykA pykF	0.194		0.248 0.264	8.80E-01 1.00E+00	-0.376 -0.811	1.514
	ppsA zwf	0.812 0.266		0.236 0.305	1.46E-01 1.00E+00	-0.089 -0.895	1.713
	pgl	0.197		0.277	1.00E+00	-0.856	1.250
	gnd rpe	-0.006 -1.248		0.305 0.393	1.00E+00 2.68E-01	-1.165 -2.743	1.152
	rpiA rpiB	0.168		0.277	1.00E+00	-0.884 -0.582	1.220
	tktA	0.438 0.567		0.268 0.249	9.98E-01 8.88E-01	-0.381	1.45
	tktB talA	0.216 0.651		0.260 0.265	1.00E+00 7.90E-01	-0.773 -0.356	1.204
	talB	0.253		0.412	1.00E+00	-1.312	1.819
	0.1h-1 0.2h-1	0.267 1.155	s	0.274 0.229	1.00E+00 5.88E-04	-0.773 0.279	1.306
	0.4h-1 0.5h-1	0.300		0.240 0.291	1.00E+00 1.00E+00	-0.616 -0.706	1.216
	0.7h-1	0.135		0.301	1.00E+00	-1.009	1.280
ykA	galM glk	0.406 -0.927		0.155 0.347	6.69E-01 6.32E-01	-0.182 -2.241	0.994
	pgm	-1.188	s	0.271	6.25E-03	-2.216	-0.160
	pgi pfkA	-0.958 -1.052	s	0.264 0.260	9.27E-02 2.34E-02	-1.972 -2.044	-0.05
	pfkB fbp	0.372 0.270		0.171 0.164	9.29E-01 9.98E-01	-0.276 -0.352	1.019
	fbaB	0.116		0.193	1.00E+00	-0.615	0.848
	gapC gpmA	-0.203 -0.040		0.205 0.212	1.00E+00 1.00E+00	-0.982 -0.844	0.57
	gpmB	-0.569 -0.375		0.248	8.80E-01 9.92E-01	-1.514 -1.159	0.376
	pykF ppsA	0.243		0.169	1.00E+00	-0.398	0.884
	zwf pgl	-0.303 -0.372		0.257 0.223	1.00E+00 9.98E-01	-1.286 -1.220	0.680
	gnd rpe	-0.575 -1.817	s	0.257	9.03E-01 4.74E-04	-1.553 -3.181	0.470
	rpiA	-0.401	3	0.223	9.93E-01	-1.246	0.445
	rpiB tktA	-0.131 -0.002		0.212 0.187	1.00E+00 1.00E+00	-0.934 -0.709	0.672
	tktB	-0.353		0.201	9.95E-01	-1.116	0.410
	talA talB	0.082 -0.316		0.208 0.377	1.00E+00 1.00E+00	-0.705 -1.757	0.870
	0.1h-1 0.2h-1	-0.302 0.586		0.219 0.159	1.00E+00 7.01E-02	-1.130 -0.018	0.526
	0.4h-1	-0.269		0.175	9.99E-01	-0.931	0.393
	0.5h-1 0.7h-1	-0.169 -0.433		0.240 0.252	1.00E+00 9.96E-01	-1.082 -1.395	0.744
ykF	galM	0.781	s	0.179	8.28E-03	0.096	1.466
	glk pgm	-0.552 -0.813		0.358 0.286	9.99E-01 4.97E-01	-1.910 -1.897	0.800
	pgi pfkA	-0.583 -0.678		0.279	9.50E-01 7.84F-01	-1.652 -1.725	0.486
	pfkB	0.746	s	0.194	4.23E-02	0.010	1.483
	fbp fbaB	0.645 0.491		0.188 0.213	1.43E-01 8.76E-01	-0.069 -0.318	1.359
	gapC gpmA	0.172 0.335		0.224 0.231	1.00E+00 1.00E+00	-0.680 -0.540	1.025
	gpmB	-0.194		0.264	1.00E+00	-1.199	0.81
	pykA ppsA	0.375 0.618		0.206 0.192	9.92E-01 2.43E-01	-0.409 -0.112	1.159
	zwf pgl	0.072		0.272 0.241	1.00E+00 1.00E+00	-0.968 -0.912	1.112
	gnd	-0.200		0.272	1.00E+00	-1.236	0.835
	rpe rpiA	-1.442 -0.026	s	0.368 0.241	3.64E-02 1.00E+00	-2.846 -0.938	-0.037 0.887
	rpiB tktA	0.244 0.373		0.230 0.208	1.00E+00 9.93E-01	-0.630 -0.415	1.118
	tktB	0.022		0.221	1.00E+00	-0.816	0.859
	talA talB	0.457		0.227 0.388	9.69E-01 1.00E+00	-0.403 -1.421	1.317
	0.1h-1 0.2h-1	0.073 0.961	s	0.237 0.183	1.00E+00 2.11E-04	-0.825 0.263	0.970
	0.4h-1	0.106	S	0.197	1.00E+00	-0.642	0.854
	0.5h-1 0.7h-1	0.206 -0.059		0.257 0.268	1.00E+00 1.00E+00	-0.769 -1.079	1.18
psA	galM	0.163		0.134	1.00E+00 1.33E-01	-0.347 -2.454	0.673
	glk pgm	-1.170 -1.431	s	0.338 0.260	5.42E-05	-2.419	-0.443
	pgi pfkA	-1.201 -1.295	S	0.252 0.248	2.55E-03 2.92E-04	-2.176 -2.245	-0.225 -0.345
	pfkB	0.129	J	0.153	1.00E+00	-0.450	0.707
	fbp fbaB	0.027 -0.127		0.145 0.177	1.00E+00 1.00E+00	-0.522 -0.799	0.57
	gapC gpmA	-0.446 -0.283		0.190 0.198	8.51E-01 1.00E+00	-1.171 -1.033	0.280
	apmB	-0.812		0.236	1.46E-01	-1.713	0.089
	pykA pykF	-0.243 -0.618		0.169 0.192	1.00E+00 2.43E-01	-0.884 -1.348	0.398
	zwf	-0.546 -0.615		0.245 0.209	9.03E-01 4.28F-01	-1.488 -1.413	0.396
	pgl gnd	-0.818		0.245	1.88E-01	-1.754	0.118
	rpe rpiA	-2.060 -0.644	S	0.348 0.209	1.50E-05 3.30E-01	-3.395 -1.439	-0.725 0.152
	rpiB	-0.374		0.197	9.85E-01	-1.125	0.377
	tktA tktB	-0.245 -0.596		0.170 0.186	1.00E+00 2.49E-01	-0.890 -1.303	0.400
	talA talB	-0.161 -0.559		0.193	1.00E+00 9.99E-01	-0.894 -1.973	0.573
	0.1h-1	-0.545		0.205	6.44E-01	-1.322	0.232
	0.2h-1 0.4h-1	0.343 -0.512		0.139 0.157	7.82E-01 2.17E-01	-0.185 -1.106	0.87
	0.5h-1	-0.412		0.227	9.92E-01	-1.280	0.456
wf	0.7h-1 galM	-0.676 0.709		0.240 0.235	5.22E-01 3.85E-01	-1.595 -0.201	0.242 1.618
	glk pgm	-0.624 -0.885		0.389	9.99E-01 5.86E-01	-2.098 -2.115	0.850
	pgi	-0.655		0.318	9.58E-01	-1.870	0.560
	pfkA pfkB	-0.750 0.674		0.314 0.246	8.32E-01 5.84E-01	-1.947 -0.273	0.448 1.62
	fbp fbaB	0.573		0.242	8.34F-01	-0.357	1.504
	gapC	0.419 0.100		0.262 0.271	9.99E-01 1.00E+00	-0.584 -0.936	1.422
	gpmA gpmB	0.263 -0.266		0.276 0.305	1.00E+00	-0.792 -1.428	1.317
	pvkA	0.303		0.257	1.00E+00	-0.680	1.286
	pykF ppsA	-0.072 0.546		0.272 0.245	1.00E+00 9.03E-01	-1.112 -0.396	0.968
	pgl	-0.069		0.285	1.00E+00	-1.156	1.017
	gnd rpe	-0.272 -1.514		0.312 0.398	1.00E+00 5.08E-02	-1.460 -3.030	0.915
	rpiA	-0.098 0.172		0.285	1.00E+00 1.00E+00	-1.183 -0.882	0.988
	rpiB tktA	0.301		0.258	1.00E+00	-0.686	1.287
	tktB talA	-0.050 0.385		0.268 0.273	1.00E+00 1.00E+00	-1.075 -0.658	0.974
	talB	-0.013 0.001		0.417	1.00E+00 1.00E+00	-1.598	1.573
	0.1h-1 0.2h-1	0.889		0.238	7.17E-02	-1.072 -0.030	1.074
	0.4h-1 0.5h-1	0.034 0.134		0.249 0.298	1.00E+00 1.00E+00	-0.922 -1.003	0.990
				0.250	1.00E+00	-1.305	1.04

	ent Variable: Meta	Mean Difference				95% Confide	ence Interva
(1)	(J)	(I-J)		Std. Error	Sig.	Lower Bound	Upper Bound
gl	galM glk	0.778 -0.555	S	0.198 0.368	3.68E-02 1.00E+00	0.020 -1.948	1.53 0.83
	pgm pgi	-0.816 -0.586		0.298 0.291	5.80E-01 9.68E-01	-1.945 -1.700	0.31 0.52
	pfkA pfkB	-0.680 0.744		0.288 0.211	8.42E-01 1.15E-01	-1.775 -0.061	0.41
	fbp	0.642		0.205	3.00E-01	-0.142	1.42
	fbaB gapC	0.488 0.169		0.229 0.239	9.41E-01 1.00E+00	-0.383 -0.741	1.35 1.08
	gpmA gpmB	0.332 -0.197		0.245 0.277	1.00E+00 1.00E+00	-0.599 -1.250	1.26
	pykA pykF	0.372 -0.003		0.223 0.241	9.98E-01 1.00E+00	-0.476 -0.918	1.22
	ppsA zwf	0.615		0.209	4.28E-01 1.00E+00	-0.183 -1.017	1.41
	gnd	-0.203		0.285	1.00E+00	-1.286 -2.883	0.88
	rpe rpiA	-1.445 -0.029	S	0.377 0.255	4.75E-02 1.00E+00	-0.995	-0.00 0.93
	rpiB tktA	0.241 0.370		0.245 0.224	1.00E+00 9.98E-01	-0.690 -0.481	1.17
	tktB talA	0.019 0.454		0.236 0.242	1.00E+00 9.87E-01	-0.878 -0.464	0.91
	talB 0.1h-1	0.056 0.070		0.397	1.00E+00 1.00E+00	-1.456 -0.883	1.56
	0.2h-1	0.958	s	0.201	1.83E-03 1.00E+00	0.188	1.72
	0.4h-1 0.5h-1	0.103 0.203		0.214 0.270	1.00E+00	-0.712 -0.822	0.91 1.22
gnd	0.7h-1 galM	-0.062 0.981	s	0.281 0.236	1.00E+00 1.70E-02	-1.129 0.079	1.00
	glk pgm	-0.352 -0.613		0.389 0.324	1.00E+00 9.86E-01	-1.825 -1.840	1.12
	pgi pfkA	-0.383 -0.477		0.318 0.315	1.00E+00 1.00E+00	-1.595 -1.672	0.83
	pfkB fbp	0.947 0.845	s	0.247	4.65E-02 1.27E-01	0.006	1.88
	fbaB	0.691		0.262	6.62E-01	-0.306	1.68
	gapC gpmA	0.372 0.535		0.271 0.277	1.00E+00 9.81E-01	-0.659 -0.515	1.40
	gpmB pykA	0.006 0.575		0.305 0.257	1.00E+00 9.03E-01	-1.152 -0.403	1.16 1.55
	pykF ppsA	0.200 0.818		0.272 0.245	1.00E+00 1.88E-01	-0.835 -0.118	1.23
	zwf pgl	0.272		0.312	1.00E+00 1.00E+00	-0.915 -0.880	1.46
	rpe rpiA	-1.242		0.398	3.04E-01	-2.756	0.27
	rpiB	0.174 0.444		0.285 0.276	1.00E+00 9.99E-01	-0.907 -0.606	1.25 1.49
	tktA tktB	0.573 0.222		0.258 0.268	9.09E-01 1.00E+00	-0.408 -0.798	1.55 1.24
	talA talB	0.657		0.273 0.417	8.21E-01 1.00E+00	-0.381 -1.325	1.69
	0.1h-1 0.2h-1	0.273 1.161	s	0.282 0.238	1.00E+00 1.19E-03	-0.796 0.249	1.34
	0.4h-1 0.5h-1	0.306	Ü	0.249	1.00E+00	-0.644	1.25
	0.7h-1	0.142		0.308	1.00E+00	-0.727 -1.030	1.31
pe	galM glk	2.222 0.890	S	0.341 0.461	1.17E-06 9.82E-01	0.910 -0.856	3.53 2.63
	pgm pgi	0.628 0.859		0.408 0.403	9.99E-01 9.40E-01	-0.919 -0.675	2.17
	pfkA pfkB	0.764 2.188	s	0.400	9.84E-01 2.89E-06	-0.758 0.850	2.28 3.52
	fbp fbaB	2.087 1.933	S	0.346	9.13E-06 1.46E-04	0.760 0.555	3.41 3.31
	gapC	1.614	S	0.367	7.01E-03 1.49E-03	0.212 0.361	3.01
	gpmA gpmB	1.777 1.248		0.371 0.393	2.68E-01	-0.247	3.19 2.74
	pykA pykF	1.817 1.442	S	0.356 0.368	4.74E-04 3.64E-02	0.453 0.037	3.18 2.84
	ppsA zwf	2.060 1.514	S	0.348 0.398	1.50E-05 5.08E-02	0.725 -0.002	3.39
	pgl gnd	1.445 1.242	S	0.377	4.75E-02 3.04E-01	0.006 -0.273	2.88
	rpiA rpiB	1.416		0.377 0.371	5.97E-02 3.92E-03	-0.022 0.271	2.85
	tktA	1.815	S	0.357	5.00E-04	0.448	3.18
	tktB talA	1.463 1.899	S S	0.365 0.369	2.72E-02 3.34E-04	0.070 0.492	2.85 3.30
	talB 0.1h-1	1.501 1.515	s	0.485 0.375	3.14E-01 2.40E-02	-0.337 0.085	3.33 2.94
	0.2h-1 0.4h-1	2.403 1.548	S S	0.343 0.351	1.08E-07 7.24E-03	1.084 0.203	3.72 2.89
	0.5h-1 0.7h-1	1.648 1.383	s	0.388	1.12E-02 1.22E-01	0.172 -0.121	3.12 2.88
piA	galM	0.806 -0.526	s	0.198 0.368	2.15E-02 1.00E+00	0.052	1.56
	glk pgm	-0.788		0.298	6.55E-01	-1.915	0.34
	pgi pfkA	-0.557 -0.652		0.291 0.288	9.83E-01 8.92E-01	-1.670 -1.745	0.55 0.44
	pfkB fbp	0.772 0.671		0.211 0.205	7.63E-02 2.18E-01	-0.029 -0.110	1.57 1.45
	fbaB gapC	0.517 0.198		0.229	8.97E-01 1.00E+00	-0.352 -0.711	1.38
	gpmA gpmB	0.361		0.245 0.277	1.00E+00 1.00E+00	-0.569 -1.220	1.29
	pykA	0.401		0.223	9.93E-01 1.00E+00	-0.445	1.24 0.93
	pykF ppsA	0.026 0.644		0.241	1.00E+00 3.30E-01 1.00E+00	-0.887 -0.152	1.43
	zwf pgl	0.098 0.029		0.285 0.255	1.00E+00	-0.988 -0.938	1.18
	gnd rpe	-0.174 -1.416		0.285 0.377	1.00E+00 5.97E-02	-1.256 -2.854	0.90
	rpiB tktA	0.270 0.399		0.245	1.00E+00 9.94E-01	-0.660 -0.450	1.19
	tktB talA	0.047		0.236	1.00E+00	-0.848	0.94
	talB	0.483 0.085		0.242 0.397	9.72E-01 1.00E+00	-0.433 -1.427	1.59
	0.1h-1 0.2h-1	0.098 0.987	s	0.251 0.201	1.00E+00 8.89E-04	-0.852 0.220	1.04 1.75
	0.4h-1 0.5h-1	0.132 0.232		0.214 0.270	1.00E+00 1.00E+00	-0.681 -0.792	0.94 1.25
piB	0.7h-1	-0.033 0.537		0.281	1.00E+00 4.60E-01	-1.100 -0.170	1.03
	glk	-0.796 -1.057		0.361	9.19E-01 7.63E-02	-0.170 -2.164	0.57
	pgm pgi	-0.827		0.283	4.42E-01	-1.909	0.04
	pfkA pfkB	-0.921 0.503		0.279 0.199	2.01E-01 7.44E-01	-1.983 -0.254	0.14 1.25
	fbp fbaB	0.401 0.247		0.193 0.218	9.55E-01 1.00E+00	-0.334 -0.581	1.13 1.07
	gapC gpmA	-0.072 0.091		0.229 0.235	1.00E+00 1.00E+00	-0.942 -0.801	0.79
	gpmB	-0.438		0.268 0.212	9.98E-01	-1.457	0.58
	pykA pykF	0.131 -0.244		0.230	1.00E+00 1.00E+00	-0.672 -1.118	0.93 0.63
	ppsA zwf	0.374 -0.172		0.197 0.276	9.85E-01 1.00E+00	-0.377 -1.226	1.12 0.88
	pgl gnd	-0.241 -0.444		0.245 0.276	1.00E+00 9.99E-01	-1.172 -1.494	0.69
	rpe rpiA	-1.686 -0.270	s	0.371	3.92E-03 1.00E+00	-3.101 -1.199	-0.27 0.66
	tktA	0.129		0.213	1.00E+00	-0.678	0.93
	tktB talA	-0.222 0.213		0.225 0.231	1.00E+00 1.00E+00	-1.078 -0.664	0.63 1.09
	talB 0.1h-1	-0.185 -0.171		0.391 0.242	1.00E+00 1.00E+00	-1.674 -1.085	1.30 0.74
	0.2h-1 0.4h-1	0.717 -0.138		0.189	5.22E-02 1.00E+00	-0.003 -0.906	1.43
	0.5h-1 0.7h-1	-0.138 -0.302		0.261 0.272	1.00E+00 1.00E+00	-1.028 -1.337	0.95 0.73
". "S" Th	0.7n-1 ne mean difference		at the .05 lev		002*00	-1.33/	0.73

		Mean Difference				95% Confide Lower	nce Interva Upper
I)	(J)	(I-J)		Std. Error	Sig.	Bound	Bound
ktA	galM glk	0.408		0.156 0.347	6.84E-01 6.41E-01	-0.185 -2.242	1.00
	pgm	-1.186	s	0.272	6.72E-03	-2.218	-0.15
	pgi pfkA	-0.956	s	0.265	9.75E-02	-1.973	0.06
	pfkB	-1.050 0.373	8	0.261 0.173	2.50E-02 9.33E-01	-2.045 -0.278	1.02
	fbp	0.272		0.166	9.98E-01	-0.354	0.89
	fbaB gapC	0.118 -0.201		0.194 0.206	1.00E+00 1.00E+00	-0.617 -0.984	0.85
	apmA	-0.038		0.213	1.00E+00	-0.845	0.76
	gpmB	-0.567 0.002		0.249 0.187	8.88E-01 1.00E+00	-1.515 -0.705	0.38
	pykA pykF	-0.373 0.245		0.107 0.208 0.170	9.93E-01	-1.161	0.41
	ppsA zwf	0.245		0.170	1.00E+00	-0.400	0.89
	pal	-0.301 -0.370		0.258 0.224	1.00E+00 9.98E-01	-1.287 -1.222	0.68
	gnd	-0.573		0.258	9.09E-01	-1.554	0.40
	rpe rpiA	-1.815 -0.399	S	0.357	5.00E-04	-3.181 -1.248	-0.44
	rpiB	-0.129		0.213	1.00E+00	-0.936	0.67
	tktB talA	-0.351 0.084		0.202 0.209	9.96E-01 1.00E+00	-1.118 -0.707	0.41
	talB	-0.314		0.378	1.00E+00	-0.707	1.13
	0.1h-1	-0.300		0.220	1.00E+00	-1.758 -1.132	0.53
	0.2h-1 0.4h-1	0.588 -0.267		0.160 0.176	7.33E-02 1.00E+00	-0.020 -0.933	1.19 0.39
	0.4h-1 0.5h-1	-0.167		0.241	1.00E+00	-1.084	0.75
dВ	0.7h-1 galM	-0.432 0.759	S	0.253 0.173	9.97E-01 7.06E-03	-1.396 0.099	0.53
NID.	glk	-0.574	3	0.175	9.99E-01	-1.920	0.77
	pgm	-0.835 -0.604		0.282 0.275	4.08E-01	-1.903 -1.659	0.23
	pgi pfkA	-0.699		0.275	9.16E-01 7.04E-01	-1.659 -1.732	0.45
	pfkB	0.725 0.624	S	0.188	4.09E-02	0.012	1.43
	fbp fbaR	0.624		0.182 0.208	1.43E-01 8.97E-01	-0.066 -0.319	1.31
	gapC	0.151		0.219	1.00E+00	-0.683	0.98
	gpmA gpmB	0.313 -0.216		0.226 0.260	1.00E+00 1.00E+00	-0.542 -1.204	1.16
	pykA	0.353		0.201	9.95E-01	-0.410	1.11
	pykF	-0.022 0.596		0.221	1.00E+00 2.49F-01	-0.859 -0.110	0.81
	ppsA zwf	0.596		0.186	1.00E+00	-0.110 -0.974	1.07
	pgl	-0.019 -0.222		0.236 0.268	1.00E+00	-0.916 -1.242	0.87
	gnd rpe	-1.463	s	0.268 0.365	1.00E+00 2.72E-02	-1.242 -2.857	-0.07
	rpiA	-0.047 0.222		0.236	1.00E+00 1.00E+00	-0.942	0.84
	rpiB tktA	0.222		0.225	1.00E+00 9.96F-01	-0.633 -0.415	1.07
	talA	0.436		0.222	9.77E-01	-0.405	1.27
	talB 0.1h-1	0.038 0.051		0.385	1.00E+00	-1.432	1.50
	0.1n-1 0.2h-1	0.051	s	0.232 0.177	1.00E+00 1.50E-04	-0.828 0.266	0.93
	0.4h-1	0.084		0.191	1.00E+00	-0.641	0.81
	0.5h-1 0.7h-1	0.184 -0.080		0.252 0.264	1.00E+00 1.00E+00	-0.774 -1.085	1.14 0.92
alA	galM	0.323		0.181	0.03F_01	-0.365	1.01
	glk	-1.009 -1.271	s	0.359 0.287	5.24E-01 4.99E-03	-2.369 -2.357	0.35
	pgm pgi pfkA	-1.040	5	0.280	7.01E-02	-2.357	0.03
	pfkA	-1.135	S	0.276	1.83E-02	-2.185	-0.08
	pfkB fbp	0.289 0.188		0.195 0.189	1.00E+00 1.00E+00	-0.451 -0.530	1.02
	fbaB	0.034		0.215	1.00E+00	-0.779	0.84
	gapC gpmA	-0.285 -0.122		0.225 0.232	1.00E+00 1.00E+00	-1.141 -1.000	0.57
	gpmB	-0.651		0.265	7.90E-01	-1.659	0.35
	pykA pykF	-0.082 -0.457		0.208 0.227	1.00E+00 9.69E-01	-0.870 -1.317	0.70
	ppsA zwf	0.161		0.193	1.00E+00	-0.573	0.80
	zwf	-0.385		0.273	1.00E+00	-1.428	0.65
	pgl gnd	-0.454 -0.657		0.242 0.273	9.87E-01 8.21E-01	-1.372 -1.696	0.46
	rne	-1.899	s	0.369	3.34E-04	-3.306	-0.49
	rpiA rpiB	-0.483 -0.213		0.242 0.231	9.72E-01 1.00E+00	-1.399 -1.091	0.43
	tktA	-0.084		0.209	1.00E+00 9.77E-01	-0.876	0.70
	tktB telB	-0.436 -0.398		0.222 0.388	9.77E-01 1.00F+00	-1.277 -1.880	0.40
	0.1h-1	-0.385		0.238	9.99E-01	-1.285	0.51
	0.2h-1	0.504 -0.351		0.184	5.87E-01	-0.198	1.20
	0.4h-1 0.5h-1	-0.351 -0.251		0.198 0.258	9.94E-01 1.00E+00	-1.103 -1.229	0.40
	0.7h-1	-0.516		0.269	9.83E-01	-1 539	0.50
alB	galM glk	0.721 -0.611		0.363 0.477	9.71E-01 1.00E+00	-0.671 -2.417	2.11
	pgm	-0.873		0.426	9.62E-01	-2.488	0.74
	pgi pfkA	-0.642 -0.737		0.421	9.99E-01 9.95E-01	-2.245 -2.328	0.96
	pfkB	0.687		0.370	9.88E-01	-0.730	2.10
	fbp fbaB	0.586		0.367	9.99E-01	-0.820	1.99
	fbaB gapC	0.432 0.113		0.381 0.387	1.00E+00 1.00E+00	-1.023 -1.364	1.88
	gpmA	0.276		0.391	1.00E+00 1.00E+00	-1.214	1.76
	gpmB pykA	-0.253 0.316		0.412 0.377	1.00E+00 1.00E+00	-1.819	1.31
	nvkF	-0.059		0.388	1.00E+00	-1.126 -1.539	1.45
	ppsA zwf	0.559		0.369	9.99E-01	-0.855	1.97
	zwf pgl	0.013 -0.056		0.417 0.397	1.00E+00 1.00E+00	-1.573 -1.568	1.59
	gnd	-0.259		0.417	1.00E+00	-1.844	1.32
	rpe rpiA	-1.501 -0.085		0.485 0.397	3.14E-01 1.00E+00	-3.338 -1.596	0.33
	miB	0.185		0.391	1.00E+00	-1.305	1.67
	tktA	0.314		0.378	1.00E+00	-1.130	1.75
	tktB talA	-0.038 0.398		0.385 0.388	1.00E+00 1.00E+00	-1.507 -1.084	1.43
	0.1h-1	0.014		0.395	1.00E+00	-1 490	1.51
	0.2h-1	0.902		0.365	7.75E-01 1.00E+00	-0.497 -1.376	2.30
	0.4h-1 0.5h-1	0.047 0.147		0.372 0.407	1.00E+00 1.00E+00	-1.376 -1.401	1.47
	0.7h-1						

		Mean Difference				95% Confide Lower	ence Interv Upper
(I) 0.1h-1	(J) galM	(I-J) 0.708		Std. Error 0.194	Sig. 7.63E-02	Bound -0.027	Bound 1.4
D. 111-1	glk pgm	-0.625 -0.886		0.366	9.97E-01 3.76E-01	-2.008 -2.002	0.7
	pgi	-0.655		0.288	8.87E-01	-1.757	0.4
	pfkA pfkB	-0.750 0.674		0.285 0.207	6.61E-01 2.19E-01	-1.831 -0.109	0.3 1.4
	fbp fbaB	0.573 0.418		0.201	4.96E-01 9.89E-01	-0.189 -0.434	1.3
	gapC	0.099		0.236	1.00E+00	-0.794	0.9
	gpmA gpmB	0.262		0.242 0.274	1.00E+00 1.00E+00	-0.652 -1.306	1.1
	pykA	0.302		0.219	1.00E+00	-0.526 -0.970	1.1
	pykF ppsA	-0.073 0.545		0.237 0.205	1.00E+00 6.44E-01	-0.232	0.8 1.3
	zwf pgl	-0.001 -0.070		0.282 0.251	1.00E+00 1.00E+00	-1.074 -1.022	1.0
	gnd	-0.273		0.282	1.00E+00	-1.342	0.7
	rpe rpiA	-1.515 -0.098	s	0.375 0.251	2.40E-02 1.00E+00	-2.944 -1.049	-0.0 0.8
	rpiB tktA	0.171 0.300		0.242 0.220	1.00E+00 1.00E+00	-0.743 -0.532	1.0
	tktB	-0.051		0.232	1.00E+00	-0.930	0.8
	talA talB	0.385		0.238 0.395	9.99E-01 1.00E+00	-0.516 -1.517	1.2
	0.2h-1 0.4h-1	0.888 0.033	S	0.197 0.210	3.80E-03 1.00E+00	0.141 -0.761	1.6
	0.5h-1	0.133		0.267	1.00E+00	-0.877	1.1
0.2h-1	0.7h-1 galM	-0.131 -0.180		0.278 0.121	1.00E+00 1.00E+00	-1.185 -0.641	0.9
	glk	-1.513	s	0.333	3.59E-03	-2.779	-0.2
	pgm pgi	-1.774 -1.544	S	0.254 0.246	3.33E-08 6.99E-06	-2.739 -2.497	-0.8 -0.5
	pfkA pfkB	-1.638 -0.214	s	0.241 0.142	2.88E-07 1.00E+00	-2.565 -0.751	-0.7 0.3
	fbp	-0.316		0.133	8.43E-01	-0.820	0.1
	fbaB gapC	-0.470 -0.789	s	0.168 0.181	5.31E-01 8.77E-03	-1.107 -1.482	0.1 -0.0
	apmA	-0.626 -1.155		0.189 0.229	1.97E-01 5.88E-04	-1.345	0.0
	gpmB pykA	-0.586	s	0.159	7.01E-02	-2.031 -1.190	0.0
	pykF ppsA	-0.961 -0.343	S	0.183 0.139	2.11E-04 7.82E-01	-1.659 -0.871	-0.2 0.1
	zwf	-0.889	s	0.238	7.17E-02	-1.808	0.0
	pgl gnd	-0.958 -1.161	S	0.201 0.238	1.83E-03 1.19E-03	-1.728 -2.073	-0.1 -0.2
	rpe rpiA	-2.403 -0.987	S	0.343 0.201	1.08E-07 8.89E-04	-3.721 -1.753	-1.0 -0.2
	rpiB	-0.717	3	0.189	5.22E-02	-1.437	0.0
	tktA tktB	-0.588 -0.939	s	0.160 0.177	7.33E-02 1.50E-04	-1.196 -1.613	-0.2
	talA talB	-0.504 -0.902		0.184 0.365	5.87E-01 7.75E-01	-1.205 -2.300	0.1
	0.1h-1	-0.888	S	0.197	3.80E-03	-1.635	0.4 -0.1
	0.4h-1 0.5h-1	-0.855 -0.755	S	0.146 0.220	8.22E-06 1.51F-01	-1.409 -1.597	-0.3 0.0
	0.7h-1	-1.020	s	0.233	8.49E-03	-1.914	-0.1
0.4h-1	galM glk	0.675 -0.658	S	0.141 0.341	1.30E-03 9.82E-01	0.138 -1.952	1.2
	pgm pgi	-0.919 -0.689		0.264 0.256	1.25E-01 6.23E-01	-1.921 -1.677	0.0
	pfkA	-0.783		0.252	3.14E-01	-1.747	0.1
	pfkB fbp	0.640	S	0.159 0.152	2.21E-02 9.97E-02	0.039 -0.034	1.2
	fbaB gapC	0.385 0.066		0.183 0.195	9.48E-01 1.00E+00	-0.307 -0.677	1.0
	gpmA	0.229		0.203	1.00E+00	-0.539	0.9
	gpmB pykA	-0.300 0.269		0.240 0.175	1.00E+00 9.99E-01	-1.216 -0.393	0.6
	pykF	-0.106 0.512		0.197 0.157	1.00E+00 2.17E-01	-0.854 -0.082	0.6
	ppsA zwf	-0.034		0.249	1.00E+00	-0.990	0.9
	pgl gnd	-0.103 -0.306		0.214 0.249	1.00E+00 1.00E+00	-0.918 -1.256	0.7
	rpe	-1.548	s	0.351	7.24E-03	-2.893	-0.2
	rpiA rpiB	-0.132 0.138		0.214 0.202	1.00E+00 1.00E+00	-0.944 -0.630	0.6
	tktA tktB	0.267		0.176 0.191	1.00E+00 1.00E+00	-0.399 -0.810	0.9
	talA	0.351		0.198	9.94E-01	-0.400	1.1
	talB 0.1h-1	-0.047 -0.033		0.372 0.210	1.00E+00 1.00E+00	-1.470 -0.827	1.3
	0.2h-1 0.5h-1	0.855 0.100	S	0.146 0.232	8.22E-06 1.00E+00	0.301 -0.783	1.4
	0.7h-1	-0.165		0.244	1.00E+00	-1.098	0.7
0.5h-1	galM glk	0.575 -0.758		0.217 0.379	6.53E-01 9.72E-01	-0.256 -2.190	1.4
	pgm	-1.019		0.311	2.08E-01	-2.196	0.1
	pgi pfkA	-0.789 -0.883		0.305 0.301	6.96E-01 4.30E-01	-1.951 -2.028	0.3
	pfkB	0.540		0.229	8.45E-01	-0.333	1.4
	fbp fbaB	0.439 0.285		0.224 0.246	9.76E-01 1.00E+00	-0.416 -0.649	1.2 1.2
	gapC gpmA	-0.034 0.129		0.255 0.261	1.00E+00 1.00E+00	-1.005 -0.862	0.9
	gpmB	-0.400		0.291	1.00E+00	-1.506	0.7
	pykA pykF	0.169 -0.206		0.240 0.257	1.00E+00 1.00E+00	-0.744 -1.181	1.0
	ppsA zwf	0.412		0.227 0.298	9.92E-01 1.00F+00	-0.456 -1.270	1.2
	pgl	-0.203		0.270	1.00E+00	-1.228	0.8
	gnd rpe	-0.406 -1.648	s	0.299 0.388	1.00E+00 1.12E-02	-1.539 -3.124	0.7 -0.1
	rpiA	-0.232		0.270 0.261	1.00E+00 1.00E+00	-1.256 -0.952	0.7
	rpiB tktA	0.167		0.241	1.00E+00	-0.750	1.0
	tktB talA	-0.184 0.251		0.252 0.258	1.00E+00 1.00E+00	-1.143 -0.727	0.7
	talB	-0.147		0.407	1.00E+00	-1.694	1.4
	0.1h-1 0.2h-1	-0.133 0.755		0.267 0.220	1.00E+00 1.51E-01	-1.144 -0.087	0.8
	0.4h-1 0.7h-1	-0.100 -0.265		0.232 0.295	1.00E+00 1.00E+00	-0.983 -1.384	0.7
0.7h-1	galM	0.839		0.230	8.84E-02	-0.045	1.7
	glk pgm	-0.493 -0.755		0.386	1.00E+00 8.50E-01	-1.955 -1.968	0.9
	pgi	-0.524		0.314	9.98E-01	-1.723	0.6
	pfkA pfkB	-0.619 0.805		0.311 0.242	9.73E-01 1.92E-01	-1.801 -0.119	0.5 1.7
	fbp fbaB	0.704		0.237 0.258	4.07E-01 9.40E-01	-0.203 -0.432	1.6
	gapC	0.231		0.267	1.00E+00	-0.785	1.2
	gpmA gpmB	0.393		0.272 0.301	1.00E+00 1.00E+00	-0.642 -1.280	1.4
	pvkA	0.433		0.252	9.96E-01	-0.528 -0.961	1.3
	pykF ppsA	0.059 0.676		0.268 0.240	1.00E+00 5.22E-01	-0.242	1.0
	zwf	0.131		0.308 0.281	1.00E+00 1.00E+00	-1.044 -1.006	1.3
	pgl gnd	-0.142		0.308	1.00E+00	-1.313	1.0
	rpe rpiA	-1.383 0.033		0.395 0.281	1.22E-01 1.00E+00	-2.887 -1.034	0.1
	rpiB	0.302		0.272	1.00E+00	-0.732	1.3
	tktA tktB	0.432 0.080		0.253 0.264	9.97E-01 1.00E+00	-0.533 -0.924	1.3
	talA talB	0.516 0.118		0.269	9.83E-01 1.00E+00	-0.507 -1.457	1.5
	talB 0.1h-1	0.118		0.414 0.278	1.00E+00	-0.923	1.1
	0.2h-1	1.020	S	0.233	8.49E-03	0.125	1.9

# Table S10 E Statistical tests for AEIs (mRNAs, DNA microarray)

## **Test of Homogeneity of Variances**

mRNA(DNA array)

- 1				
	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)

	nt Variable: mRN	Mean				95% Confide	ence Interval
		Difference				Lower	Upper
(I)	(J)	(I-J)	*	Std. Error	Sig.	Bound	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
	0.7h-1	-2.012	S	0.074	1.84E-12	-2.235	-1.789
pgi	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		0.671
	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
	0.5h-1 0.7h-1	-0.799	S	0.069	5.09E-13 1.95E-12	-1.008	-0.591
aanC		-1.691 0.202	S S	0.080 0.044	1.95E-12 1.23E-04	-1.935 0.069	-1.448 0.336
gapC	pgm	-0.118	5	0.044	3.68E-01	-0.283	0.336
	pgi zwf	0.116	S	0.034	4.45E-13	-0.263 0.297	0.532
	rpe	-0.737	S	0.039	4.45E-13 1.89E-12	-0.939	-0.532
	0.2h-1	0.060	3	0.007	8.62E-01	-0.939	0.190
	0.5h-1	-0.918	S	0.043	1.92E-12	-1.113	-0.722
	0.7h-1	-1.810	S	0.004	0.00E+00	-2.042	-1.577
zwf	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	-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
rpe	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
	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
0.2h-1	pgm	0.143	S	0.037	3.26E-03	0.030	0.256
	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
0.55.4	0.7h-1	-1.869	8	0.073	0.00E+00	-2.090	-1.648
0.5h-1	pgm	1.120	S	0.061	3.20E-13		1.305
	pgi	0.799	S S	0.069 0.064	5.09E-13		1.008
	gapC zwf	0.918 1.332	S	0.064	1.92E-12 3.68E-13	0.722 1.159	1.113 1.506
		0.180		0.057	2.99E-01	-0.058	0.419
	rpe 0.2h-1	0.100	S	0.079	1.77E-12	0.795	1.159
	0.7h-1	-0.892	S	0.087	2.31E-12	-1.157	-0.627
0.7h-1	pgm	2.012	S	0.087	1.84E-12	1.789	2.235
	pgi	1.691	S	0.080	1.95E-12	1.448	1.935
	gapC	1.810		0.000	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
	0.2h-1	1.869		0.073	0.00E+00		2.090
	0.5h-1	0.892	S	0.087	2.31E-12	0.627	1.157

<sup>\*. &</sup>quot;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-DIDE)

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

#### ANOVA

## Protein(2D-DIDE)

	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-DIDE)

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

a. Asymptotically F distributed.

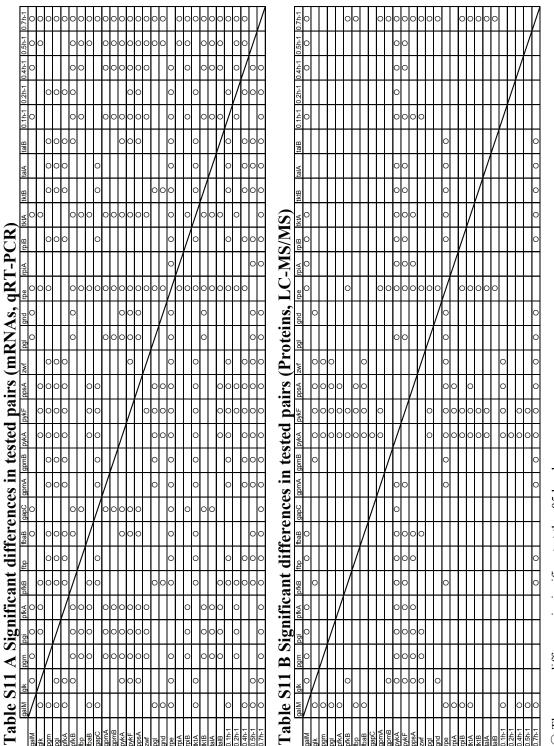
Depende (I)	ent Variable: Prote	Mean Difference	* Std. Error	Sig.	95% Confid Bound	ence Interval	De	ependent Variable: Prote (J)	Mean Differen
galM	glk pgm	0.006 -0.723 S	0.047 0.061	1.00E+00 5.01E-11	-0.170 -0.951	0.183 -0.495	pfk		-0.0 -0.0
	pgi pfkA	-1.448 S -0.767 S	0.076	5.02E-11 4.98E-11	-1.733	-1.163 -0.508		pgm pgi	-0.1
	pfkB fbp	0.062 -0.459	0.048 0.172	1.00E+00 6.36E-01	-0.117 -1.103	0.240 0.184		pfkA fbp	-0.8 -0.5
	fbaB gapC	-0.264 S -0.036	0.050 0.048	6.50E-05		-0.076 0.143		fbaB gapC	-0.3 -0.0
	gpmA gpmB	-0.126 -0.265 S	0.060	9.57E-01 4.15E-05	-0.351 -0.450	0.099 -0.079		gpmA gpmB	-0.1 -0.3
	pykA pykF	-0.108 -0.250 S	0.048 0.060	9.10E-01 1.05E-02	-0.289	0.072 -0.025		pykA pykF	-0.: -0.:
	ppsA zwf	-0.120 -0.247 S	0.056 0.048	9.48E-01 9.59E-05	-0.331 -0.426	0.091 -0.069		ppsA zwf	-0.°
	pgl gnd	-1.345 S -0.131	0.113 0.064	5.04E-11 9.68E-01	-1.766 -0.370	-0.923 0.109		pgl gnd	-1.4 -0.1
	rpe rpiA	-1.471 S -0.288	0.090 0.104	5.03E-11 5.44E-01	-1.809 -0.675	-1.133 0.099		rpe rpiA	-1.5 -0.3
	rpiB tktA	-0.096 -0.066	0.049 0.050	9.81E-01 1.00E+00	-0.278 -0.254	0.087 0.122		rpiB tktA	-0.1 -0.1
	tktB talA	-0.069 0.047	0.051 0.046	1.00E+00	-0.123	0.121 0.217		tktB talA	-0.1 -0.0
	talB 0.1h-1	-0.466 S -0.336 S	0.055 0.051	5.02E-11 2.84E-08	-0.672	-0.260 -0.145		talB 0.1h-1	-0.5 -0.3
	0.2h-1 0.4h-1	-0.311 S -0.385 S	0.054 0.053	4.68E-06 3.61E-10	-0.514 -0.584	-0.108 -0.185		0.2h-1 0.4h-1	-0.3 -0.4
	0.5h-1 0.7h-1	-1.092 S -2.284 S	0.089 0.113	5.02E-11 5.04E-11	-1.423 -2.707	-0.760 -1.860		0.5h-1 0.7h-1	-1.1 -2.3
glk	galM pgm	-0.006 -0.729 S	0.047 0.061	1.00E+00 5.04E-11	-0.183 -0.956	0.170 -0.502	fbp	p galM glk	0.4
	pgi pfkA	-1.454 S -0.773 S	0.076 0.069	5.02E-11 5.02E-11	-1.738 -1.031	-1.169 -0.515		pgm	-0.1 -0.1
	pfkB fbp	0.056 -0.465	0.047 0.172	1.00E+00 6.06E-01	-0.122 -1.108	0.233 0.178		pgi pfkA pfkB	-0.: 0.:
	fbaB gapC	-0.270 S -0.042	0.050	2.86E-05	-0.457 -0.220	-0.083 0.136		fbaB gapC	0.1
	gpmA gpmB	-0.132 -0.271 S	0.060 0.049	9.24E-01 1.77E-05	-0.356 -0.455	0.092 -0.086		gpmA gpmB	0.3 0.1
	pykA pykF	-0.114 -0.256 S	0.048 0.060	8.42E-01 6.52E-03	-0.294 -0.481	0.065 -0.032		pykA pykF	0.3
	ppsA zwf	-0.126 -0.254 S	0.056 0.048	9.08E-01 4.06E-05	-0.336 -0.431	0.084 -0.076		ppsA zwf	0.3
	pgl gnd	-1.351 S -0.137	0.113 0.064	5.04E-11 9.43E-01	-1.772 -0.376	-0.930 0.102		pgl gnd	-0.8 0.3
	rpe rpiA	-1.477 S -0.294	0.090 0.103	5.05E-11 4.93E-01	-1.814 -0.681	-1.140 0.093		rpe rpiA	-1.0 0.1
	rpiB tktA	-0.102 -0.072	0.049 0.050	9.56E-01 1.00E+00		0.080 0.115		rpiB tktA	0.3
	tktB talA	-0.075 0.041	0.051 0.045	1.00E+00 1.00E+00		0.114 0.210		tktB talA	0.3
	talB 0.1h-1	-0.472 S -0.342 S	0.055 0.051	5.00E-11 1.00E-08	-0.677 -0.533	-0.267 -0.152		talB 0.1h-1	-0.0 0.1
	0.2h-1 0.4h-1	-0.317 S -0.391 S	0.054 0.053	2.05E-06 1.52E-10	-0.589	-0.115 -0.192		0.2h-1 0.4h-1	0.1
	0.5h-1 0.7h-1	-1.098 S -2.290 S	0.088 0.113	5.02E-11 5.03E-11	-2.713	-0.767 -1.867		0.5h-1 0.7h-1	-0.6 -1.8
pgm	galM glk	0.723 S 0.729 S	0.061 0.061	5.01E-11 5.04E-11	0.502	0.951 0.956	fba	glk	0.2
	pgi pfkA	-0.725 S -0.044	0.085 0.079	5.04E-11 1.00E+00	-1.044 -0.340	-0.406 0.251		pgm pgi	-0.4 -1.1
	pfkB fbp	0.785 S 0.264	0.061 0.176	5.05E-11 1.00E+00		1.013 0.922		pfkA pfkB	-0.5 0.3
	fbaB gapC	0.459 S 0.687 S	0.063 0.061	2.52E-10 5.01E-11	0.458	0.695 0.916		fbp gapC	-0.1 0.2
	gpmA gpmB	0.597 S 0.458 S	0.071 0.063	5.03E-11 1.90E-10	0.224	0.863 0.692		gpmA gpmB	0.1 -0.0
	pykA pykF	0.614 S 0.472 S	0.062 0.071	5.00E-11 1.74E-08	0.206	0.845 0.739		pykA pykF	0.1
	ppsA zwf	0.603 S 0.475 S	0.068 0.061	5.02E-11 5.53E-11	0.348 0.247	0.857 0.704		ppsA zwf	0.1
	pgl gnd	-0.622 S 0.592 S	0.119 0.075	7.47E-05 5.10E-11	-1.067 0.313	-0.177 0.871		pgl gnd	-1.0 0.1
	rpe rpiA	-0.748 S 0.435 S	0.098 0.110	6.51E-11 2.48E-02		-0.382 0.847		rpe rpiA	-1.2 -0.0
	rpiB tktA	0.627 S 0.657 S	0.062 0.063	5.04E-11 5.01E-11	0.396 0.421	0.859 0.893		rpiB tktA	0.1
	tktB talA	0.654 S 0.770 S	0.064 0.059	5.06E-11 5.05E-11	0.416 0.548	0.892 0.992		tktB talA	0.1 0.3
	talB 0.1h-1	0.257 S 0.386 S	0.067 0.064	3.65E-02 7.28E-07	0.147	0.507 0.625		talB 0.1h-1	-0.2 -0.0
	0.2h-1 0.4h-1	0.412 S 0.338 S	0.066 0.066	2.55E-07 1.10E-04	0.093	0.660 0.583		0.2h-1 0.4h-1	-0.0 -0.1
	0.5h-1 0.7h-1	-0.369 S -1.561 S	0.096 0.119	3.74E-02 4.98E-11	-0.730 -2.008	-0.008 -1.114		0.5h-1 0.7h-1	-0.8 -2.0
pgi	galM glk	1.448 S 1.454 S	0.076 0.076	5.02E-11 5.02E-11		1.733 1.738	ga	ipC galM glk	0.0
	pgm pfkA	0.725 S 0.680 S	0.085 0.091	5.04E-11 1.03E-10		1.044 1.022		pgm pgi	-0.6 -1.4
	pfkB fbp	1.509 S 0.988 S	0.076 0.182	5.03E-11 2.57E-05	1.224 0.308	1.795 1.669		pfkA pfkB	-0.7 0.0
	fbaB gapC	1.184 S 1.412 S	0.078 0.077	5.04E-11 4.99E-11	1.126	1.475 1.698		fbp fbaB	-0.4 -0.2
	gpmA gpmB	1.322 S 1.183 S	0.085 0.078	5.01E-11 5.07E-11	1.005 0.893	1.638 1.473		gpmA gpmB	-0.0 -0.2
	pykA pykF	1.339 S 1.197 S	0.077 0.085	5.05E-11 5.06E-11	1.052 0.880	1.626 1.514		pykA pykF	-0.0 -0.2
	ppsA zwf	1.327 S 1.200 S	0.082 0.076	4.99E-11 5.03E-11		1.634 1.486		ppsA zwf	-0.0 -0.2
	pgl gnd	0.103 1.317 S	0.128 0.088	1.00E+00 5.02E-11	0.990	0.579 1.644		pgl gnd	-1.3 -0.0
	rpe rpiA	-0.023 1.160 S	0.108 0.120	1.00E+00 5.02E-11	0.713	0.381 1.606		rpe rpiA	-1.4 -0.2
	rpiB tktA	1.352 S 1.381 S	0.077 0.078	4.99E-11 4.98E-11	1.090	1.640 1.673		rpiB tktA	-0.0 -0.0
	tktB talA	1.379 S 1.495 S	0.078 0.075	5.05E-11 5.04E-11	1.214	1.672 1.775		tktB talA	-0.0 0.0
	talB 0.1h-1	0.981 S 1.111 S	0.081 0.079	5.05E-11 4.99E-11	0.817	1.285 1.405		talB 0.1h-1	-0.4 -0.3
	0.2h-1 0.4h-1	1.137 S 1.063 S	0.081 0.080	5.06E-11 5.07E-11	0.764	1.438 1.362		0.2h-1 0.4h-1	-0.2 -0.3
	0.5h-1 0.7h-1	0.356 -0.836 S	0.107 0.128	1.71E-01 3.38E-08		0.755 -0.358		0.5h-1 0.7h-1	-1.0 -2.2
pfkA	galM glk	0.767 S 0.773 S	0.069 0.069	4.98E-11 5.02E-11	0.515	1.026 1.031	gpi	mA galM glk	0.1 0.1
	pgm pgi	0.044 -0.680 S	0.079 0.091	1.00E+00	-1.022	0.340 -0.339		pgm pgi	-0.5 -1.3
	pfkB fbp fboB	0.829 S 0.308	0.069 0.179	5.04E-11 9.97E-01		1.088 0.978		pfkA pfkB	-0.6 0.1
	fbaB gapC	0.503 S 0.732 S	0.071 0.069	8.96E-10 5.05E-11	0.472	0.769 0.991		fbp fbaB	-0.3 -0.1
	gpmA gpmB	0.641 S 0.503 S	0.078 0.071	5.02E-11 6.98E-10	0.239	0.934		gapC gpmB	0.0 -0.1
	pykA pykF	0.659 S 0.517 S	0.070 0.078	4.99E-11 2.28E-08		0.920 0.810		pykA pykF	-0.1
	ppsA zwf	0.647 S 0.520 S	0.076 0.069	5.04E-11 9.49E-11	0.364	0.930 0.779		ppsA zwf	0.0 -0.1
	pgl gnd	-0.578 S 0.636 S	0.123 0.081	1.11E-03 5.39E-11	0.332	-0.116 0.941		pgl gnd	-1.2 -0.0
	rpe rpiA	-0.704 S 0.479 S	0.103 0.115	5.33E-09 1.05E-02	0.049	-0.317 0.909		rpe rpiA	-1.3 -0.1
	rpiB tktA	0.671 S 0.701 S	0.070 0.071	5.01E-11 5.04E-11	0.435	0.933 0.967		rpiB tktA	0.0
	tktB talA	0.698 S 0.814 S	0.072 0.068	5.05E-11 5.06E-11	0.561	0.966 1.068		tktB talA	0.0
	talB 0.1h-1	0.301 S 0.431 S	0.075 0.072	1.72E-02 9.85E-07	0.162	0.580		talB 0.1h-1	-0.3 -0.2
	0.2h-1 0.4h-1 0.5h-1	0.456 S 0.382 S	0.074 0.073	3.37E-07 7.97E-05 2.47E-01	0.180 0.108	0.733 0.656		0.2h-1 0.4h-1	-0.1 -0.2
	0.5h-1 0.7h-1	-0.325 -1.516 S	0.102 0.124	2.47E-01 5.07E-11	-0.705 -1.980	0.056 -1.053	Ļ	0.5h-1 0.7h-1	-0.1 -2.1

(I)	ent Variable: Pro	Mean		Std. Error	Sig.	95% Confid Bound	ence Interv
pfkB	(J) galM	Difference -0.062		0.048	1.00E+00	-0.240	0.1
	glk pgm	-0.056 -0.785	S	0.047 0.061	1.00E+00 5.05E-11	-0.233 -1.013	0.1 -0.5
	pgi pfkA fbp	-1.509 -0.829 -0.521	s s	0.076 0.069 0.172	5.03E-11 5.04E-11 3.51E-01	-1.795 -1.088 -1.165	-1.2 -0.5 0.1
	fbaB gapC	-0.326 -0.097	s	0.051 0.048	5.46E-08 9.71E-01	-0.514 -0.277	-0.1 0.0
	gpmA gpmB	-0.188 -0.326	s	0.060	2.92E-01 2.87E-08	-0.413 -0.512	0.0
	pykA pykF	-0.320 -0.170 -0.312	s	0.049	1.05E-01 9.90F-05	-0.512 -0.352 -0.538	-0.1 0.0 -0.0
	ppsA zwf	-0.182 -0.309	s	0.057 0.048	2.31E-01 6.00E-08	-0.394 -0.489	0.0 -0.1
	pgl	-0.309 -1.407 -0.193	s	0.113 0.064	5.04E-11 3.72E-01	-0.469 -1.829 -0.433	-0.9
	gnd rpe	-0.193 -1.533 -0.350	s	0.090	5.03E-11 1.53E-01	-0.433 -1.871 -0.738	0.0 -1.1 0.0
	rpiA rpiB tktA	-0.350 -0.157 -0.128		0.049 0.051	2.32E-01 7.41E-01	-0.736 -0.341 -0.317	0.0
	tktB	-0.131		0.051	7.24E-01	-0.322	0.0
	talA talB 0.1h-1	-0.015 -0.528 -0.398	s s	0.046 0.055 0.052	1.00E+00 4.98E-11 5.69E-11	-0.186 -0.735 -0.591	0.1 -0.3 -0.2
	0.2h-1 0.4h-1	-0.373 -0.447	s s	0.054 0.054	4.26E-09 5.01E-11	-0.576 -0.647	-0.2 -0.1
	0.5h-1	-1.153	s s	0.089	5.04E-11	-1.485	-0.8
fbp	0.7h-1 galM	-2.345 0.459 0.465	8	0.113 0.172 0.172	5.03E-11 6.36E-01 6.06E-01	-2.769 -0.184 -0.178	-1.9 1.1 1.1
	glk pgm	-0.264	s	0.176	1.00E+00	-0.922	0.3
	pgi pfkA	-0.988 -0.308	8	0.182 0.179	2.57E-05 9.97E-01	-1.669 -0.978	-0.3 0.3
	pfkB fbaB	0.521 0.195		0.172 0.173	3.51E-01 1.00E+00	-0.123 -0.451	1.1 0.8
	gapC gpmA	0.424 0.333		0.172 0.176	7.92E-01 9.88E-01	-0.220 -0.325	1.0
	gpmB pykA	0.195 0.351		0.173 0.172	1.00E+00 9.69E-01	-0.451 -0.293	0.8 0.9
	pykF ppsA	0.209		0.176 0.175	1.00E+00 9.83E-01	-0.449 -0.314	0.8
	zwf pgl	0.212 -0.886	s	0.172 0.200	1.00E+00 3.46E-03	-0.432 -1.633	0.8 -0.1
	gnd rpe	0.328 -1.012	s	0.177 0.188	9.91E-01 3.47E-05	-0.335 -1.716	0.9 -0.3
	rpiA rpiB	0.171 0.364		0.195 0.172	1.00E+00 9.53E-01	-0.558 -0.281	0.9 1.0
	tktA tktB	0.393 0.390		0.173 0.173	8.95E-01 9.03E-01	-0.253 -0.257	1.0
	talA talB	0.506 -0.007		0.171 0.174	4.06E-01 1.00E+00	-0.135 -0.659	1.1 0.6
	0.1h-1 0.2h-1	0.123 0.149		0.173 0.174	1.00E+00 1.00E+00	-0.525 -0.502	0.7 0.7
	0.4h-1 0.5h-1	0.074 -0.632		0.174 0.188	1.00E+00 1.54E-01	-0.575 -1.334	0.7 0.0
fbaB	0.7h-1 galM	-1.824 0.264	S S	0.200 0.050	5.02E-11 6.50E-05	-2.573 0.076	-1.0 0.4
	glk pgm	0.270 -0.459	s s	0.050 0.063	2.86E-05 2.52E-10	0.083 -0.695	0.4 -0.2
	pgi pfkA	-1.184 -0.503	s s	0.078 0.071	5.04E-11 8.96E-10	-1.475 -0.769	-0.8 -0.2
	pfkB fbp	0.326 -0.195	S	0.051 0.173	5.46E-08 1.00E+00	0.137 -0.842	0.5 0.4
	gapC gpmA	0.228 0.138	S	0.051 0.062	2.41E-03 9.21E-01	0.039 -0.095	0.4 0.3
	gpmB pykA	-0.001 0.155		0.052 0.051	1.00E+00 3.39E-01	-0.196 -0.035	0.1 0.3
	pykF ppsA	0.013 0.144		0.062 0.059	1.00E+00 8.03E-01	-0.220 -0.076	0.2 0.3
	zwf pgl	0.016 -1.081	s	0.051 0.114	1.00E+00 4.98E-11	-0.173 -1.507	0.2 -0.6
	gnd rpe	0.133 -1.207	s	0.066 0.092	9.74E-01 5.03E-11	-0.114 -1.550	0.3 -0.8
	rpiA rpiB	-0.024 0.168		0.105 0.052	1.00E+00 2.02E-01	-0.416 -0.024	0.3 0.3
	tktA tktB	0.198 0.195	S	0.053 0.054	5.00E-02 6.79E-02	0.000 -0.005	0.3 0.3
	talA talB	0.311 -0.202	S	0.048 0.058	6.38E-08 1.01E-01	0.130 -0.417	0.4
	0.1h-1 0.2h-1	-0.073 -0.047		0.054 0.057	1.00E+00 1.00E+00	-0.274 -0.259	0.1 0.1
	0.4h-1 0.5h-1	-0.121 -0.828	s	0.056 0.090	9.37E-01 5.00E-11	-0.330 -1.165	0.0 -0.4
gapC	0.7h-1 galM	-2.020 0.036	s	0.114 0.048	5.02E-11 1.00E+00	-2.448 -0.143	-1.5 0.2
	glk pgm	0.042 -0.687	s	0.048 0.061	1.00E+00 5.01E-11	-0.136 -0.916	0.2 -0.4
	pgi pfkA	-1.412 -0.732	s s	0.077 0.069	4.99E-11 5.05E-11	-1.698 -0.991	-1.1 -0.4
	pfkB fbp	0.097 -0.424		0.048 0.172	9.71E-01 7.92E-01	-0.082 -1.067	0.2 0.2
	fbaB gpmA	-0.228 -0.090	s	0.051 0.060	2.41E-03 1.00E+00	-0.417 -0.316	-0.0 0.1
	gpmB pykA	-0.229 -0.073	S	0.050 0.049	1.73E-03 1.00E+00	-0.416 -0.255	-0.0 0.1
	pykF ppsA	-0.215 -0.085		0.061 0.057	9.14E-02 1.00E+00	-0.441 -0.297	0.0 0.1
	zwf pgl	-0.212 -1.309	s s	0.048 0.113	3.94E-03 5.02E-11	-0.392 -1.731	-0.0 3.0-
	gnd rpe	-0.095 -1.435	s	0.064 0.090	1.00E+00 5.01E-11	-0.336 -1.774	0.1 -1.0
	rpiA rpiB	-0.252 -0.060		0.104 0.049	8.10E-01 1.00E+00	-0.640 -0.244	0.1 0.1
	tktA tktB	-0.031 -0.033		0.051 0.051	1.00E+00 1.00E+00	-0.220 -0.225	0.1 0.1
	talA talB	0.083 -0.431	s	0.046 0.055	9.94E-01 5.48E-11	-0.089 -0.638	0.2 -0.2
	0.1h-1 0.2h-1	-0.301 -0.275	s s	0.052 0.055	2.69E-06 1.93E-04	-0.494 -0.479	-0.1 -0.0
	0.4h-1 0.5h-1	-0.349 -1.056	s s	0.054 0.089	3.95E-08 5.01E-11	-0.550 -1.388	-0.1 -0.7
gpmA	0.7h-1 galM	-2.248 0.126	s	0.113 0.060	5.01E-11 9.57E-01	-2.672 -0.099	-1.8 0.3
	glk pgm	0.132 -0.597	s	0.060 0.071	9.24E-01 5.03E-11	-0.092 -0.863	0.3 -0.3
	pgi pfkA	-1.322 -0.641	s s	0.085 0.078	5.01E-11 5.02E-11	-1.638 -0.934	-1.0 -0.3
	pfkB fbp	0.188 -0.333		0.060 0.176	2.92E-01 9.88E-01	-0.038 -0.991	0.4
	fbaB gapC	-0.138 0.090		0.062 0.060	9.21E-01 1.00E+00	-0.371 -0.136	0.0 0.3
	gpmB nvkA	-0.139 0.018		0.062 0.061	9.10E-01 1.00E+00	-0.369 -0.210	0.0 0.2
	pykF ppsA	-0.124 0.006		0.071 0.067	9.96E-01 1.00E+00	-0.388 -0.246	0.1 0.2
	zwf pgl	-0.121 -1.219	s	0.060 0.119	9.73E-01 5.03E-11	-0.347 -1.662	0.1 -0.7
	gnd rpe	-0.005 -1.345	s	0.074 0.098	1.00E+00 4.98E-11	-0.281 -1.709	0.2 -0.9
	rpiA rpiB	-0.162 0.030		0.110 0.061	1.00E+00 1.00E+00	-0.573 -0.198	0.2
	tktA tktB	0.060		0.062 0.063	1.00E+00 1.00E+00	-0.173 -0.178	0.2
	talA talB	0.173 -0.340	s	0.059 0.066	4.04E-01 1.20E-04	-0.046 -0.588	0.3 -0.0
	0.1h-1 0.2h-1	-0.210 -0.185		0.063 0.066	1.72E-01 5.15E-01	-0.447 -0.430	0.0
	0.4h-1 0.5h-1	-0.259 -0.966	s s	0.065 0.096	2.02E-02 5.02E-11	-0.501 -1.324	-0.0 -0.6
	0.7h-1	-2 158	S	0.119	5 04F-11	-2 603	-17

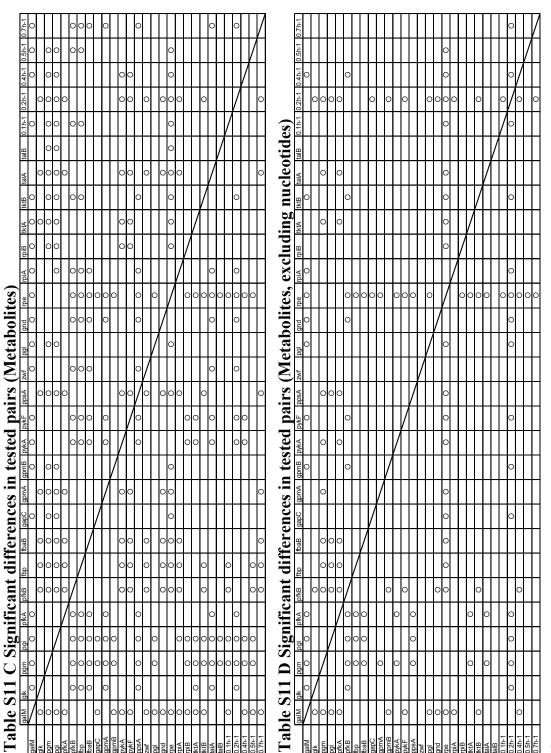
Denendent	t Variable: Prote	in(2D-DIDE)	Multiple Compari	sons				Denenden	t Variable: Prote	in(2D-DIDE)	Multiple Co	omparisons			
(I)	(J)	Mean Difference	* Std.	Error Sig	T	95% Confidenc Bound	e Interval Bound	(I)	(J)	Mean Difference	*	Std. Error	Sig.	95% Confider Bound	Bound
gpmB	galM glk	0.265 0.271	S S	0.050 4.15 0.049 1.77		0.079 0.086	0.450 0.455	pgl	galM glk	1.345 1.351	S S	0.113 0.113	5.04E-11 5.04E-11	0.923 0.930	1.766 1.772
	pgm pgi	-0.458 -1.183	s s	0.063 1.90 0.078 5.07	E-11	-0.692 -1.473	-0.224 -0.893		pgm pgi	0.622 -0.103	S	0.119 0.128	7.47E-05 1.00E+00	0.177 -0.579	1.067 0.374
	pfkA pfkB	-0.503 0.326	S S	0.071 6.98 0.050 2.87	E-08	-0.767 0.140	-0.239 0.512		pfkA pfkB	0.578 1.407	s s	0.123 0.113	1.11E-03 5.04E-11	0.116 0.985	1.039 1.829
	fbp fbaB	-0.195 0.001		0.173 1.00I 0.052 1.00I	+00	-0.840 -0.195	0.451 0.196		fbp fbaB	0.886 1.081	S S	0.200 0.114	3.46E-03 4.98E-11	0.138 0.655	1.633
	gapC gpmA	0.229 0.139 0.156	8	0.050 1.73 0.062 9.10 0.050 3.02	E-01	0.042 -0.092 -0.032	0.416 0.369 0.344		gapC gpmA gpmB	1.309 1.219 1.080	S	0.113 0.119 0.114	5.02E-11 5.03E-11 4.99E-11	0.887 0.776 0.656	1.731 1.662 1.505
	pykA pykF ppsA	0.156 0.014 0.144		0.050 3.02 0.062 1.000 0.058 7.79	+00	-0.032 -0.217 -0.073	0.245		pykA pykF	1.237	s s	0.114 0.113 0.119	5.07E-11 5.01E-11	0.814 0.651	1.659
	zwf pgl	0.017	s	0.050 1.00i 0.114 4.99	+00	-0.169 -1.505	0.203		ppsA zwf	1.225	s s	0.117 0.113	5.02E-11 5.03E-11	0.788 0.675	1.661
	gnd rpe	0.134 -1.206	s	0.066 9.69 0.091 5.03	E-01 E-11	-0.112 -1.548	0.379 -0.865		gnd rpe	1.214 -0.126	S	0.121 0.136	5.03E-11 1.00E+00	0.763	1.665 0.384
	rpiA rpiB	-0.024 0.169		0.105 1.00i 0.051 1.75	E-01	-0.414 -0.021	0.367 0.359		rpiA rpiB	1.057 1.249	s s	0.146 0.113	2.58E-10 4.98E-11	0.826	1.601 1.673
	tktA tktB	0.196	S	0.052 4.09 0.053 5.64	E-02	0.003 -0.002	0.394		tktA tktB	1.279	S S	0.114 0.114	5.01E-11 5.02E-11	0.853	1.705
	talA talB 0.1h-1	0.312 -0.202 -0.072	S	0.048 3.20 0.057 9.31 0.053 1.000	E-02	0.134 -0.414 -0.271	0.490 0.011 0.127		talA talB 0.1h-1	1.392 0.879 1.008	S S S	0.112 0.116 0.114	5.02E-11 7.55E-11 5.03E-11	0.974 0.445 0.581	1.811 1.313 1.436
	0.2h-1 0.4h-1	-0.046 -0.120		0.056 1.00i 0.055 9.32	+00	-0.256 -0.327	0.163		0.2h-1 0.4h-1		S S	0.116 0.115	5.06E-11 4.99E-11	0.601 0.529	1.467
	0.5h-1 0.7h-1	-0.827 -2.019	s s	0.090 4.99 0.114 5.04	E-11	-1.163 -2.446	-0.492 -1.592		0.5h-1 0.7h-1	0.253	s	0.135 0.153	9.90E-01 3.60E-07	-0.252 -1.509	0.759 -0.369
pykA	galM glk	0.108 0.114		0.048 9.10 0.048 8.42	E-01	-0.072 -0.065	0.289 0.294	gnd	galM glk	0.131 0.137		0.064 0.064	9.68E-01 9.43E-01	-0.109 -0.102	0.370 0.376
	pgm pgi		S S	0.062 5.00 0.077 5.05	E-11	-0.845 -1.626	-0.384 -1.052		pgm pgi	-0.592 -1.317	S S	0.075 0.088	5.10E-11 5.02E-11	-0.871 -1.644	-0.313 -0.990
	pfkA pfkB fbp	-0.659 0.170 -0.351	S	0.070 4.99 0.049 1.05 0.172 9.69	E-01	-0.920 -0.011 -0.995	-0.398 0.352 0.293		pfkA pfkB fbp	-0.636 0.193 -0.328	S	0.081 0.064 0.177	5.39E-11 3.72E-01 9.91E-01	-0.941 -0.047 -0.991	-0.332 0.433 0.335
	fbaB gapC	-0.155 0.073		0.051 3.39 0.049 1.00	E-01	-0.346 -0.109	0.035 0.255		fbaB gapC	-0.133 0.095		0.066	9.74E-01 1.00E+00	-0.380 -0.145	0.114 0.336
	gpmA gpmB	-0.018 -0.156		0.061 1.001	+00	-0.245 -0.344	0.210		gpmA gpmB	0.005		0.074	1.00E+00 9.69E-01	-0.271	0.281
	pykF ppsA	-0.142 -0.012		0.061 8.67 0.057 1.000		-0.370 -0.225	0.085		pykA pykF	0.022 -0.120		0.065 0.074	1.00E+00 9.99E-01	-0.219 -0.396	0.264 0.157
	zwf pgl	-0.139 -1.237	s	0.049 4.82 0.113 5.07	E-11	-0.321 -1.659	0.043 -0.814		ppsA zwf	0.011 -0.117		0.071 0.064	1.00E+00 9.94E-01	-0.254 -0.357	0.276 0.124
	gnd rpe	-0.022 -1.362	s	0.065 1.00E 0.091 5.02	E-11	-0.264 -1.702	0.219 -1.023		pgl rpe	-1.214 -1.340	s s	0.121 0.100	5.03E-11 5.05E-11	-1.665 -1.714	-0.763 -0.966
	rpiA rpiB tktA	-0.180 0.013 0.042		0.104 9.97 0.050 1.000 0.051 1.000	+00	-0.568 -0.173 -0.149	0.209 0.198 0.233		rpiA rpiB tktA	-0.157 0.035 0.065		0.112 0.065 0.066	1.00E+00 1.00E+00	-0.576 -0.208 -0.183	0.262 0.278 0.312
	tktB talA	0.039		0.052 1.00I 0.046 1.62	+00	-0.154 -0.018	0.233		tktB talA	0.062 0.178		0.067 0.063	1.00E+00 4.94E-01	-0.187 -0.056	0.311 0.412
	talB 0.1h-1	-0.358 -0.228	S S	0.056 7.40 0.052 4.31	E-03	-0.566 -0.423	-0.149 -0.033		talB 0.1h-1	-0.335 -0.206	S	0.070 0.067	6.37E-04 3.21E-01	-0.596 -0.456	-0.074 0.045
	0.2h-1 0.4h-1	-0.202 -0.276	s	0.055 6.07 0.054 1.36 0.089 5.05	E-04	-0.408 -0.479	0.003 -0.074		0.2h-1 0.4h-1	-0.180 -0.254		0.069 0.069	6.93E-01 5.56E-02	-0.439 -0.510	0.079 0.002
pykF	0.5h-1 0.7h-1 galM	-0.983 -2.175 0.250	s s	0.089 5.05 0.114 5.02 0.060 1.05	E-11	-1.316 -2.600 0.025	-0.650 -1.750 0.475	rpe	0.5h-1 0.7h-1 galM	-0.961 -2.153 1.471	S S	0.099 0.121 0.090	4.99E-11 5.02E-11 5.03E-11	-1.329 -2.605 1.133	-0.593 -1.700 1.809
рукі	glk pgm	0.256 -0.472	S S	0.060 1.05 0.060 6.52 0.071 1.74	E-03	0.032 -0.739	0.475 0.481 -0.206	ipe	glk pgm	1.477	s s	0.090	5.05E-11 6.51E-11	1.140 0.382	1.814
	pgi pfkA	-1.197	s s	0.085 5.06 0.078 2.28	E-11	-1.514 -0.810	-0.880 -0.224		pgi pfkA	0.023	s	0.108 0.103	1.00E+00 5.33E-09	-0.381 0.317	0.428 1.090
	pfkB fbp	0.312 -0.209	S	0.060 9.90 0.176 1.00i	+00	0.087 -0.867	0.538 0.449		pfkB fbp	1.533 1.012	s s	0.090 0.188	5.03E-11 3.47E-05	1.195	1.871 1.716
	fbaB gapC	-0.013 0.215		0.062 1.00I 0.061 9.14	E-02	-0.247 -0.011	0.220		fbaB gapC	1.207	S S S	0.092	5.03E-11 5.01E-11	0.864 1.097	1.550
	gpmA gpmB pykA	0.124 -0.014 0.142		0.071 9.96 0.062 1.000 0.061 8.67	+00	-0.139 -0.245 -0.085	0.388 0.217 0.370		gpmA gpmB pykA	1.345 1.206 1.362	S S S	0.098 0.091 0.091	4.98E-11 5.03E-11 5.02E-11	0.980 0.865 1.023	1.709 1.548 1.702
	ppsA zwf	0.130		0.067 9.84 0.060 1.000	E-01	-0.122 -0.223	0.382		pykF ppsA	1.220	s s	0.098 0.095	5.04E-11 4.99E-11	0.856 0.995	1.585 1.707
	pgl gnd	-1.094 0.120	S	0.119 5.01 0.074 9.99	E-11 E-01	-1.538 -0.157	-0.651 0.396		zwf pgl	1.223 0.126	S	0.090 0.136	5.03E-11 1.00E+00	0.885	1.562 0.636
	rpe rpiA	-1.220 -0.038	S	0.098 5.04 0.110 1.000	+00	-1.585 -0.449	-0.856 0.373		gnd rpiA	1.340 1.183	S S	0.100 0.129	5.05E-11 4.98E-11	0.966 0.701	1.714 1.665
	rpiB tktA tktB	0.155 0.184 0.181		0.061 7.46 0.062 4.07 0.063 4.60	E-01	-0.074 -0.049 -0.054	0.384 0.417 0.417		rpiB tktA tktB	1.375 1.405 1.402	S S	0.091 0.092 0.092	5.03E-11 5.03E-11 5.05E-11	1.035 1.062 1.058	1.715 1.748 1.746
	talA talB	0.298	s	0.059 1.63 0.066 2.10	E-04	0.078	0.517		talA talB	1.518	s s	0.089	5.01E-11 4.99E-11	1.184	1.852
	0.1h-1 0.2h-1	-0.086 -0.060		0.063 1.00E 0.066 1.00E	+00	-0.322 -0.306	0.150 0.185		0.1h-1 0.2h-1	1.134 1.160	s s	0.092 0.094	5.02E-11 5.06E-11	0.789	1.480 1.512
	0.4h-1 0.5h-1	-0.134 -0.841	s	0.065 9.62 0.096 5.04	E-11	-0.377 -1.200	0.108 -0.482		0.4h-1 0.5h-1 0.7h-1	1.086 0.379	S	0.093 0.117	4.99E-11 2.19E-01	0.736	1.436 0.817
ррѕА	0.7h-1 galM glk	-2.033 0.120 0.126	S	0.119 5.02 0.056 9.48 0.056 9.08	E-01	-2.478 -0.091 -0.084	-1.588 0.331 0.336	rpiA	galM glk	-0.813 0.288 0.294	S	0.137 0.104 0.103	1.34E-06 5.44E-01 4.93E-01	-1.324 -0.099 -0.093	-0.301 0.675 0.681
	pgm pgi		s s	0.068 5.02 0.082 4.99	E-11	-0.064 -0.857 -1.634	-0.348 -1.021		pgm pgi	-0.435 -1.160	s s	0.110 0.110 0.120	2.48E-02 5.02E-11	-0.093 -0.847 -1.606	-0.022 -0.713
	pfkA pfkB	-0.647 0.182	s	0.076 5.04 0.057 2.31	E-11 E-01	-0.930 -0.030	-0.364 0.394		pfkA pfkB	-0.479 0.350	S	0.115 0.104	1.05E-02 1.53E-01	-0.909 -0.038	-0.049 0.738
	fbp fbaB	-0.339 -0.144		0.175 9.83 0.059 8.03	E-01	-0.992 -0.363	0.314 0.076		fbp fbaB	-0.171 0.024		0.195 0.105	1.00E+00	-0.900 -0.368	0.558 0.416
	gapC gpmA gpmB	0.085 -0.006 -0.144		0.057 1.000 0.067 1.000 0.058 7.79	+00	-0.128 -0.258 -0.362	0.297 0.246 0.073		gapC gpmA gpmB	0.252 0.162 0.024		0.104 0.110 0.105	8.10E-01 1.00E+00 1.00E+00	-0.136 -0.249 -0.367	0.640 0.573 0.414
	pykA pykF	0.012		0.057 1.00I 0.067 9.84	+00	-0.202 -0.382	0.225 0.122		pykA pykF	0.180		0.103 0.104 0.110	9.97E-01	-0.209 -0.373	0.568
	zwf pgl	-0.127 -1.225	s	0.057 9.08 0.117 5.02	E-01 E-11	-0.339 -1.661	0.085 -0.788		ppsA zwf	0.168 0.041		0.108 0.104	9.99E-01 1.00E+00	-0.236 -0.347	0.572 0.428
	gnd rpe	-0.011 -1.351	s	0.071 1.00I 0.095 4.99	E-11	-0.276 -1.707	0.254 -0.995		pgl gnd	-1.057 0.157	s	0.146 0.112	2.58E-10 1.00E+00	-1.601 -0.262	-0.513 0.576
	rpiA rpiB tktA	-0.168 0.024 0.054		0.108 9.99 0.058 1.000 0.059 1.000	+00	-0.572 -0.191 -0.166	0.236 0.239 0.274		rpe rpiB tktA	-1.183 0.192 0.222	8	0.129 0.104 0.105	4.98E-11 9.91E-01 9.51E-01	-1.665 -0.197 -0.170	-0.701 0.582 0.614
	tktB talA	0.054 0.051 0.167		0.059 1.00I 0.059 1.00I 0.055 3.31	+00	-0.170 -0.037	0.273 0.372		tktB talA	0.219 0.335		0.105 0.105 0.103	9.59E-01 2.04E-01	-0.170 -0.174 -0.049	0.612 0.719
	talB 0.1h-1	-0.346 -0.216	s	0.063 1.72 0.060 7.26	E-05 E-02	-0.581 -0.439	-0.111 0.007		talB 0.1h-1	-0.178 -0.048		0.107 0.105	9.98E-01 1.00E+00	-0.579 -0.442	0.223 0.346
	0.2h-1 0.4h-1	-0.191 -0.265	s	0.062 3.25 0.061 5.74	E-03	-0.423 -0.494	0.042 -0.035		0.2h-1 0.4h-1	-0.023 -0.097		0.107 0.106	1.00E+00 1.00E+00	-0.422 -0.495	0.377 0.301
zwf	0.5h-1 0.7h-1 galM	-0.972 -2.163 0.247	s s	0.094 5.04 0.117 5.04 0.048 9.59	E-11	-1.322 -2.602 0.069	-0.621 -1.725 0.426	rpiB	0.5h-1 0.7h-1 galM	-0.804 -1.995 0.096	s s	0.128 0.146 0.049	1.55E-07 5.00E-11 9.81E-01	-1.281 -2.541 -0.087	-0.326 -1.450 0.278
ZWI	glk pgm		s s	0.048 4.06 0.061 5.53	E-05	0.009 0.076 -0.704	0.426 0.431 -0.247	грію	glik pgm	0.102	s	0.049 0.062	9.56E-01 5.04E-11	-0.080 -0.859	0.283 -0.396
	pgi pfkA	-1.200 -0.520		0.076 5.03 0.069 9.49	E-11 E-11	-1.486 -0.779	-0.914 -0.260		pgi pfkA		s s	0.077 0.070	4.99E-11 5.01E-11	-1.640 -0.933	-1.064 -0.410
	pfkB fbp	0.309	s	0.048 6.00 0.172 1.000	E-08 +00	0.130 -0.855	0.489 0.432		pfkB fbp	0.157 -0.364		0.049 0.172	2.32E-01 9.53E-01	-0.026 -1.008	0.341 0.281
	fbaB gapC	-0.016 0.212	s	0.051 1.00I 0.048 3.94	E-03	-0.205 0.032	0.173 0.392		fbaB gapC	-0.168 0.060		0.052 0.049	2.02E-01 1.00E+00	-0.361 -0.124	0.024 0.244
	gpmA gpmB pykA	0.121 -0.017 0.139		0.060 9.73 0.050 1.000 0.049 4.82	+00	-0.104 -0.203 -0.043	0.347 0.169 0.321		gpmA gpmB pykA	-0.030 -0.169 -0.013		0.061 0.051 0.050	1.00E+00 1.75E-01 1.00E+00	-0.259 -0.359 -0.198	0.198 0.021 0.173
	pykA pykF ppsA	-0.003 0.127		0.049 4.82 0.060 1.000 0.057 9.08	+00	-0.043 -0.229 -0.085	0.321 0.223 0.339		pykA pykF ppsA	-0.013 -0.155 -0.024		0.050 0.061 0.058	7.46E-01 1.00E+00	-0.198 -0.384 0 -0.239	0.173 0.074 0.191
	pgl gnd	-1.097 0.117	s	0.113 5.03 0.064 9.94	E-11 E-01	-1.519 -0.124	-0.675 0.357		zwf pgl	-0.152 -1.249	s	0.049 0.113	3.06E-01 4.98E-11	-0.335 -1.673	0.032 -0.826
	rpe rpiA	-1.223 -0.041	s	0.090 5.03 0.104 1.000	+00	-1.562 -0.428	-0.885 0.347		gnd rpe	-0.035 -1.375	s	0.065 0.091	1.00E+00 5.03E-11	-0.278 -1.715	0.208 -1.035
	rpiB tktA tktB	0.152 0.181		0.049 3.06 0.051 8.20 0.051 1.10	E-02	-0.032 -0.008	0.335 0.370 0.370		rpiA tktA tktB	-0.192 0.029 0.027		0.104 0.052	9.91E-01 1.00E+00	-0.582 -0.163	0.197 0.222 0.221
	tktB talA talB	0.179 0.295 -0.219	s s	0.051 1.10 0.046 6.40 0.055 2.35	E-08	-0.013 0.123 -0.426	0.370 0.466 -0.012		tktB talA talB	0.027 0.143 -0.370	s	0.052 0.047 0.056	1.00E+00 3.36E-01 2.21E-08	-0.168 -0.032 -0.581	0.221 0.318 -0.160
	0.1h-1 0.2h-1	-0.089 -0.063	-	0.052 9.97 0.055 1.000	E-01 +00	-0.282 -0.267	0.104 0.140		0.1h-1 0.2h-1	-0.241 -0.215	s s	0.053 0.055	1.71E-03 3.00E-02	-0.437 -0.422	-0.045 -0.008
	0.4h-1 0.5h-1	-0.137 -0.844	s	0.054 7.21 0.089 5.02	E-01 E-11	-0.338 -1.176	0.063 -0.512		0.4h-1 0.5h-1	-0.289 -0.996	s s	0.055 0.089	4.82E-05 5.04E-11	-0.493 -1.330	-0.085 -0.662
*. *S* The I	0.7h-1 mean difference	-2.036 is significant	S at the .05 level.	0.113 5.01	E-11	-2.460	-1.612	*. *S* The	0.7h-1 mean difference	-2.188 is significant	S at the .05 le	0.114 /el.	5.01E-11	-2.613	-1.762

I)	(J)	Mean * Difference	Std. Error	Sig.	Bound	Bound
ktA	galM glk	0.066	0.050	1.00E+00	-0.122 -0.115	0.25
	pam	0.072 -0.657 S	0.050 0.063	1.00E+00 5.01E-11	-0.115	-0.42
	pgi pfkA	-1.381 S	0.078	4.98E-11	-1.673	-1.09
	pfkA pfkB	-0.701 S 0.128	0.071 0.051	5.04E-11 7.41E-01	-0.967 -0.061	-0.43 0.3
	fbp	-0.128	0.173	7.41E-01 8.95E-01	-0.061	0.3
	fbaB	-0.198 S	0.053	5.00E-02	-0.395	0.00
	gapC	0.031	0.051	1.00E+00	-0.159	0.22
	gpmA	-0.060 -0.198.S	0.062	1.00E+00 4.09E-02	-0.293 -0.394	0.17
	gpmB pykA	-0.198 S -0.042	0.052	1.00E+00	-0.394	0.14
	nvkF	-0.184	0.062	4.07E-01 1.00E+00	-0.417	0.04
	ppsA zwf	-0.054	0.059	1.00E+00	-0.274	0.16
	zwf pgl	-0.181 -1.279 S	0.051 0.114	8.20E-02 5.01E-11	-0.370 -1.705	0.00
	gnd	-0.065	0.066	1.00E+00 5.03E-11	-0.312 -1.748	0.18
	rpe	-1.405 S	0.092	5.03E-11	-1.748	-1.06
	rpiA rpiB	-0.222 -0.029	0.105 0.052	9.51E-01 1.00E+00	-0.614 -0.222	0.17
	rpiB tktB	-0.029	0.052	1.00E+00 1.00E+00	-0.222	0.19
	talA	0.113 -0.400 S	0.048	8.63E-01	-0.068	0.29
	talB	-0.400 S	0.058	1.95E-09	-0.615	-0.18
	0.1h-1 0.2h-1	-0.270 S -0.245 S	0.054 0.057	2.20E-04 5.60E-03	-0.472 -0.456	-0.00
	0.4h-1	-0.245 S -0.319 S	0.057	5.25E-06	-0.430	-0.0
	0.5h-1	-1.026 S	0.090	5.06E-11	-1.363	-0.68
	0.7h-1	-2.217 S 0.069	0.114	5.02E-11 1.00E+00	-2.645 -0.121	-1.78 0.25
κtΒ	galM glk	0.069	0.051 0.051	1.00E+00 1.00E+00	-0.121 -0.114	0.28
	pgm	-0.654 S	0.064	5.06E-11	-0.892	-0.4
	pgi	-1.379 S	0.078	5.05E-11	-1.672	-1.08
	pfkA pfkB	-0.698 S 0.131	0.072 0.051	5.05E-11 7.24E-01	-0.966 -0.060	-0.43 0.32
	fbp	-0.390	0.173	9.03E-01	-1.037	0.25
	fbaB	-0.195	0.054	6.79E-02	-0.395	0.00
	gapC gpmA	0.033 -0.057	0.051	1.00E+00 1.00E+00	-0.158 -0.292	0.22
	gpmA gpmB	-0.057 -0.196	0.063	1.00E+00 5.64E-02	-0.292	0.17
	pykA	-0.039	0.052	5.64E-02 1.00E+00	-0.233	0.00
	pykF	-0.181	0.063	4.60E-01	-0.417	0.08
	ppsA zwf	-0.051	0.059 0.051	1.00E+00	-0.273 -0.370	0.17
	pal	-0.179 -1.276 S	0.051	1.10E-01 5.02E-11	-1.703	-0.84
	gnd	-0.062	0.067	1.00E+00	-0.311	0.18
	rpe rpiA	-1.402 S -0.219	0.092 0.105	5.05E-11 9.59E-01	-1.746 -0.612	-1.05 0.17
	rpiA rpiB	-0.219	0.105	1.00E+00	-0.612	0.16
	tktA	0.003	0.054	1.00E+00	-0.197	0.16
	talA talB	0.116	0.049	8.49E-01	-0.067	0.29
	0.1h-1	-0.397 S -0.267 S	0.058 0.054	4.16E-09 3.68E-04	-0.614 -0.471	-0.18 -0.06
	0.2h-1	-0.242 S	0.057	8 11F-03	-0.456	-0.02
	0.4h-1	-0.316 S	0.056	9.56E-06 4.99E-11	-0.527	-0.10
	0.5h-1 0.7h-1	-1.023 S -2.215 S	0.090 0.115	4.99E-11 5.02E-11	-1.361 -2.644	-0.68 -1.78
alA	galM	-0.047	0.046	1.00E+00	-0.217	0.12
	glk	-0.041 -0.770 S	0.045	1.00E+00 5.05E-11	-0.210	0.12
	pgm pgi	-0.770 S -1.495 S	0.059	5.05E-11	-0.992	-0.54 -1.21
	pfkA	-1.495 S -0.814 S	0.075 0.068	5.04E-11 5.06E-11	-1.775 -1.068	-0.56
	pfkB	0.015	0.046	1.00E+00	-0.156	0.18
	fbp	-0.506	0.171	4.06E-01	-1.148 -0.492	0.13 -0.13
	fbaB gapC	-0.311 S -0.083	0.048	6.38E-08 9.94F-01	-0.492 -0.254	-0.13
	apmA	-0.173	0.059	4.04E-01	-0.392	0.0
	apmB	-0.312 S	0.048	3.20E-08	-0.490	-0.13 0.0
	pykA	-0.156 -0.298 S	0.046 0.059	1.62E-01 1.63E-04	-0.329 -0.517	-0.07
	pykF nnsA	-0.298 S -0.167	0.059	1.63E-04 3.31E-01	-0.517	0.03
	ppsA zwf	-0.295 S	0.046	6.40E-08	-0.466	-0.12
	pgl	-1.392 S	0.112	5.02E-11	-1.811	-0.97
	gnd rpe	-0.178 -1.518 S	0.063 0.089	4.94E-01 5.01E-11	-0.412 -1.852	0.05
	rpiA	-0.335	0.103	2.04E-01	-0.719	0.04
	rpiB	-0.143	0.047	3.36E-01	-0.318	0.03
	tktA tktB	-0.113	0.048	8.63E-01	-0.294 -0.299	0.00
	talB	-0.116 -0.513 S	0.049	8.49E-01 5.05E-11	-0.299 -0.713	0.06
	0.1h-1	-0.384 S	0.049	5.59E-11	-0.569	-0.19
	0.2h-1	-0.358 S	0.053	5.17E-09	-0.554	-0.16
	0.4h-1 0.5h-1	-0.432 S -1.139 S	0.052 0.088	4.99E-11 5.03E-11	-0.625 -1.466	-0.23 -0.8
	0.5h-1	-2.331 S 0.466 S	0.112	5.03E-11	-2.751	-1.9
alB	galM	0.466 S	0.112 0.055	5.03E-11 5.02E-11	0.260	0.67
	glk	0.472 S -0.257 S	0.055	5.00E-11	0.267	0.67
	pgm pgi	-0.257 S -0.981 S	0.067 0.081	3.65E-02 5.05E-11	-0.507 -1.285	-0.00 -0.67
	pfkA	-0.301 S	0.075	1.72E-02	-0.580	-0.02
	pfkB	0.528 S	0.055	4.98E-11	0.321	0.73
	fbp fbaB	0.007	0.174 0.058	1.00E+00 1.01E-01	-0.645 -0.013	0.65
	nanC	0.202 0.431 S	0.055	5 48F-11	0.223	0.41
	gpmA	0.340 S	0.066	1.20E-04	0.092	0.60
	gpmB	0.202	0.057	9.31E-02	-0.011	0.4
	pykA	0.358 S 0.216	0.056 0.066	7.40E-08 2.10E-01	0.149 -0.032	0.56
	pykF ppsA	0.346.5	0.068	1.72E-05	0.111	0.46
	zwf	0.219 S	0.055	2.35E-02	0.012 -1.313	0.42
	pal	-0.879 S	0.116	7.55E-11	-1.313	-0.44
	gnd rpe	0.335 S -1.005 S	0.070 0.094	6.37E-04 4.99E-11	0.074 -1.358	0.59
	rpiA	0.178	0.107	9.98E-01	-0.223	0.57
	rpiB	0.370 S	0.056	2 21F-08	0.160 0.185	0.58
	tktA tktB	0.400 S 0.397 S	0.058	1.95E-09 4.16E-09	0.185	0.6
	tktB talA	0.397 S 0.513 S	0.058	4.16E-09 5.05E-11	0.180 0.314	0.6
	0.1h-1 0.2h-1	0.513 S 0.130 0.155	0.058	9.18E-01 7.32E-01	-0.089	0.34
		0.455	0.061	7 32F-01	-0.073	0.38
	0.2h-1	0.155				0.00
	0.2h-1 0.4h-1 0.5h-1	0.081 -0.626IS	0.060	1.00E+00 9.35E-09	-0.144 -0.973	0.30

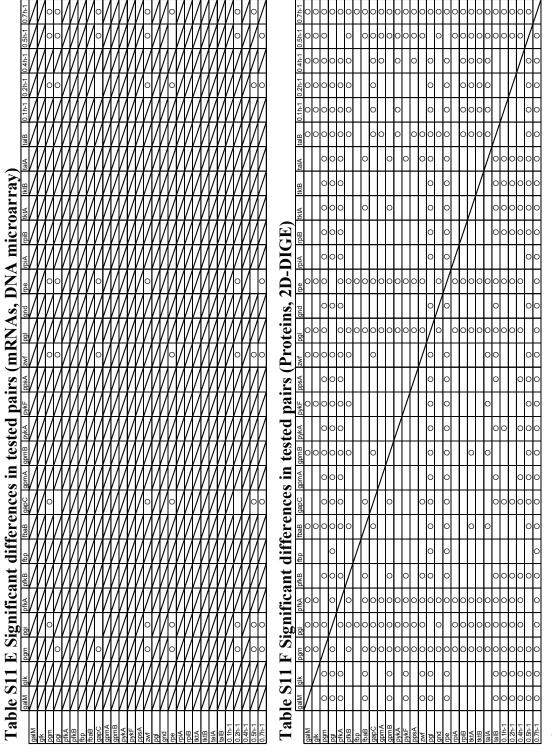
	nt Variable: Pro	Mean		e			ence Interva
(I) 0.1h-1	(J) galM	Difference 0.336	s	Std. Error 0.051	Sig. 2.84E-08	Bound 0.145	Bound 0.52
III* I	glk	0.342	S	0.051	1.00E-08	0.152	0.53
	pgm pgi	-0.386 -1.111	s s	0.064 0.079	7.28E-07 4.99E-11	-0.625 -1.405	-0.14 -0.8
	pfkA	-0.431	s	0.072	9.85E-07	-0.699	-0.16
	pfkB fbp	-0.123	S	0.052	5.69E-11 1.00E+00	0.206 -0.770	0.59
	fbaB	0.073		0.054	1.00E+00	-0.129	0.27
	gapC gpmA	0.301	s	0.052 0.063	2.69E-06 1.72E-01	0.108 -0.026	0.49
	gpmB	0.072		0.053	1.00E+00	-0.127	0.27
	pykA pykF	0.228	s	0.052 0.063	4.31E-03 1.00E+00	0.033 -0.150	0.33
	ppsA	0.216		0.060	7.26E-02	-0.007	0.43
	zwf pgl	0.089	s	0.052 0.114	9.97E-01 5.03E-11	-0.104 -1.436	-0.58
	gnd	0.206		0.067	3.21E-01	-0.045	0.45 -0.78
	rpe rpiA	-1.134 0.048	s	0.092 0.105	5.02E-11 1.00E+00	-1.480 -0.346	0.44
	rpiB	0.241	s	0.053	1.71E-03	0.045	0.43
	tktA tktB	0.270	s s	0.054 0.054	2.20E-04 3.68E-04	0.069 0.064	0.47
	talA talB	0.384	S	0.049 0.058	5.59E-11 9.18E-01	0.199 -0.348	0.56
	0.2h-1	0.026		0.058	1.00E+00	-0.190	0.24
	0.4h-1 0.5h-1	-0.048 -0.755	s	0.057 0.091	1.00E+00 5.02E-11	-0.261 -1.094	-0.4
	0.7h-1	-1.947	s	0.115	5.02E-11	-2.377	-1.5
0.2h-1	galM glk	0.311	s s	0.054 0.054	4.68E-06 2.05E-06	0.108 0.115	0.5
	pgm	-0.412	S	0.066	2.55E-07	-0.660	-0.16
	pgi pfkA	-1.137 -0.456	s s	0.081 0.074	5.06E-11 3.37E-07	-1.438 -0.733	-0.83 -0.18
	pfkB	0.373	S	0.054	4.26E-09	0.169	0.57
	fbp fbaB	-0.149		0.174 0.057	1.00E+00 1.00E+00	-0.799 -0.165	0.50
	gapC	0.047 0.275	s	0.055	1.93E-04	0.071	0.25
	gpmA gpmB	0.185	l	0.066 0.056	5.15E-01 1.00E+00	-0.060 -0.163	0.43
	pvkA	0.202		0.055	6.07E-02	-0.003	0.40
	pykF ppsA	0.060	l	0.066 0.062	1.00E+00 3.25E-01	-0.185 -0.042	0.30
	zwf	0.063		0.055	1.00E+00	-0.140	0.42
	pgl gnd	-1.034 0.180	s	0.116 0.069	5.06E-11 6.93E-01	-1.467 -0.079	-0.60 0.43
	rpe	-1.160 0.023	s	0.094	5.06E-11 1.00E+00	-1.512 -0.377	-0.80
	rpiA rpiB	0.023	s	0.107 0.055	1.00E+00 3.00E-02	-0.377 0.008	0.42
	tktA	0.245	S	0.057	5.60E-03	0.033	0.45
	tktB talA	0.242	s s	0.057 0.053	8.11E-03 5.17E-09	0.028 0.162	0.45
	talB	-0.155	_	0.061	7.32E-01 1.00F+00	-0.383 -0.241	0.07
	0.1h-1 0.4h-1	-0.026 -0.074		0.058	1.00E+00 1.00E+00	-0.241	0.19
	0.5h-1	-0.781	s s	0.092	5.02E-11	-1.126	0.14 -0.43 -1.53
0.4h-1	0.7h-1 galM	-1.973 0.385	S	0.116 0.053	5.02E-11 3.61E-10	-2.407 0.185	-1.53 0.58
	glk	0.391	s	0.053 0.066	1.52E-10 1.10E-04	0.192 -0.583	0.58
	pgm pgi	-0.336	s s	0.080	5.07E-11	-1.362	-0.76
	pfkA pfkB	-0.382 0.447	s s	0.073 0.054	7.97E-05 5.01E-11	-0.656 0.246	-0.10 0.64
	fbp	-0.074	3	0.174	1.00E+00	-0.724	0.57
	fbaB gapC	0.121	s	0.056 0.054	9.37E-01 3.95E-08	-0.088 0.149	0.33
	gpmA	0.259	s	0.065	2.02E-02	0.016	0.50
	gpmB pykA	0.120	s	0.055 0.054	9.32E-01 1.36E-04	-0.086 0.074	0.32
	pvkF	0.134		0.065	9.62E-01	-0.108	0.37
	ppsA zwf	0.265	s	0.061 0.054	5.74E-03 7.21E-01	0.035 -0.063	0.49
	pgl	-0.960	s	0.115	4.99E-11	-1.391	-0.52 0.5
	gnd rpe	0.254 -1.086	s	0.069 0.093	5.56E-02 4.99E-11	-0.002 -1.436	-0.73
	rniA	0.097		0.106	1.00E+00	-0.301	0.49
	rpiB tktA	0.289	s s	0.055 0.056	4.82E-05 5.25E-06	0.085 0.110	0.49
	tktB	0.316	s	0.056	9.56E-06	0.105	0.50
	talA talB	0.432 -0.081	s	0.052 0.060	4.99E-11 1.00E+00	0.239 -0.306	0.62
	0.1h-1	0.048		0.057	1.00E+00	-0.164	0.26
	0.2h-1 0.5h-1	0.074 -0.707	s	0.059 0.092	1.00E+00 6.03E-11	-0.148 -1.050	-0.36
).5h-1	0.7h-1 galM	-1.899 1.092	s s	0.116 0.089	5.01E-11 5.02E-11	-2.332 0.760	-1.46 1.42
U.5N-1	gaim glk	1.098	S	0.089	5.02E-11 5.02E-11	0.760	1.42
	pgm	0.369	S	0.096 0.107	3.74E-02	0.008	0.73
	pgi pfkA	-0.356 0.325	l	0.102	1.71E-01 2.47E-01	-0.755 -0.056	0.70
	pfkB fbp	1.153	s	0.089 0.188	5.04E-11 1.54F-01	0.822 -0.069	1.48
	fbaB	0.828	s	0.090	5.00E-11	0.491	1.16
	gapC	1.056	s	0.089 0.096	5.01E-11 5.02E-11	0.724 0.607	1.38
	gpmB	0.827	S	0.090	4.99E-11	0.492	1.16
	pykA pykF	0.983 0.841	s s	0.089 0.096	5.05E-11 5.04E-11	0.650 0.482	1.3
	ppsA	0.972	S	0.094	5.04E-11	0.621	1.32
	zwf pgl	0.844 -0.253	s	0.089 0.135	5.02E-11 9.90E-01	0.512 -0.759	1.17
	gnd	0.961	s	0.099	4.99E-11	0.593	1.32
	rpe rpiA	-0.379 0.804	s	0.117 0.128	2.19E-01 1.55E-07	-0.817 0.326	0.08
	rpiB	0.996	s	0.089	5.04E-11	0.662	1.33
	tktA tktB	1.026	s s	0.090	5.06E-11 4.99E-11	0.688 0.684	1.36
	talA talB	1.139	s s	0.088	5.03E-11 9.35E-09	0.811 0.278	1.46
	0.1h-1	0.626	S	0.093	9.35E-09 5.02E-11	0.278	0.97
	0.2h-1 0.4h-1	0.781	s s	0.092	5.02E-11 6.03E-11	0.435	1.12
	0.7h-1	0.707 -1.192	S	0.092 0.136	5.02E-11	0.363 -1.699	-0.68
0.7h-1	galM	2.284	s	0.113 0.113	5.04E-11 5.03E-11	1.860 1.867	2.70
	glk pgm	1.561	S	0.119	4.98E-11	1.114	2.00
	pgi pfkA	0.836 1.516	s s	0.128 0.124	3.38E-08 5.07E-11	0.358 1.053	1.3
	pfkB	2.345	s	0.113	5.03E-11	1.921	2.76
	fbp fbaB	1.824	s	0.200 0.114	5 02F-11	1.075	2.57
	gapC	2.248	S	0.113	5.02E-11 5.01E-11	1.824	2.67
	gpmA gpmB	2.158 2.019	s s	0.119 0.114	5.04E-11 5.04E-11	1.712 1.592	2.60
	pvkA	2.175	s	0.114	5.02E-11	1.750	2.60
	pykF ppsA	2.033	s s	0.119 0.117	5.02E-11 5.04E-11	1.588 1.725	2.47
	zwf	2.036	S	0.113	5.01E-11	1.612	2.46
	pgl gnd	0.939 2.153	s s	0.153 0.121	3.60E-07 5.02E-11	0.369 1.700	1.50
	rpe	0.813	s	0.137	1.34E-06	0.301	1.32
	rpiA rpiB	1.995	s s	0.146 0.114	5.00E-11 5.01E-11	1.450 1.762	2.54 2.61
	tktA	2.217	S	0.114	5.02E-11	1.789	2.64
	tktB talA	2.215 2.331	s s	0.115 0.112	5.02E-11 5.03E-11	1.786 1.910	2.64
	talB 0.1h-1	1.817	s s	0.117 0.115	5.02E-11 5.02E-11	1.381 1.518	2.25
	0.2h-1	1.973	s	0.116	5.02E-11	1.538	2.40
	0.4h-1	1.899	S	0.116	5.01E-11	1.466	2.3



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



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



○ 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	1.96×10 <sup>-2</sup>	34
N-Acetylaspartate	1.41×10 <sup>-1</sup>	33
Azelaate	1.98×10 <sup>-2</sup>	33
5-Oxoproline	1.97×10 <sup>-1</sup>	33
Nicotinamide hypoxanthine dinucleotide	1.46×10 <sup>-1</sup>	33
2,4-Diaminobutyrate	3.30×10 <sup>-2</sup>	32
Triethanolamine	6.08×10 <sup>-2</sup>	32
Pterin	2.41×10 <sup>-2</sup>	32
Isobutyryl CoA	8.37×10 <sup>-3</sup>	32
4-Oxopentanoate	1.26	31
4-Oxohexanoate	3.22×10 <sup>-2</sup>	31
Methyl sulfate	1.30×10 <sup>-1</sup>	30
trans-Cinnamate	9.02×10 <sup>-2</sup>	30
Diethanolamine	2.00×10 <sup>-2</sup>	30
$\alpha$ -Aminoisobutyrate	1.08×10 <sup>-2</sup>	28
2-Mercapto-1-methylimidazole	1.86×10 <sup>1</sup>	28
Urocanate	6.89×10 <sup>-2</sup>	25
Isobutylamine	2.56×10 <sup>-2</sup>	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**

- 1. K. A. Datsenko, B. L. Wanner, *Proc. Natl. Acad. Sci. U. S. A.* **97**, 6640 (2000).
- 2. T. Baba *et al.*, *Mol. Syst. Biol.* **2**, published online 21 February 2006 (10.1038/msb4100050).
- 3. M. Kitagawa *et al.*, *DNA Res.* **12**, 291 (2005).
- 4. T. Oshima et al., Mol. Microbiol. 45, 673 (2002).
- 5. W. S. Cleveland, J. Am. Stat. Assoc. 74, 829 (1979).
- 6. M. Kanehisa et al., Nucleic Acids Res. **34**, D354 (2006).
- 7. C. S. Barker, B. M. Pruss, P. Matsumura, *J. Bacteriol.* **186**, 7529 (2004).
- 8. S. A. Gerber, J. Rush, O. Stemman, M. W. Kirschner, S. P. Gygi, *Proc. Natl. Acad. Sci. U. S. A.* **100**, 6940 (2003).
- 9. W. Wang et al., Anal. Chem. 75, 4818 (2003).
- 10. L. Anderson, C. L. Hunter, Mol. Cell Proteomics 5, 573 (2006).
- 11. K. Shinoda et al., J. Proteome Res. 5, 3312 (2006).
- 12. J. X. Yan et al., Proteomics 2, 1682 (2002).
- 13. T. Soga et al., Anal. Chem. 74, 2233 (2002).
- 14. T. Soga, D. N. Heiger, Anal. Chem. 72, 1236 (2000).
- 15. H. Katayama, Y. Ishihama, N. Asakawa, *Anal. Chem.* **70**, 5272 (1998).
- F. C. Neidhardt, R. Curtiss, in *Escherichia coli and Salmonella 2nd Ed.* F. C.
   Neidhardt *et al.*, Eds. (ASM press, Washington, D.C, 1996) pp. 13-16.
- 17. J. Zhao, K. Shimizu, J. Biotechnol. **101**, 101 (2003).
- 18. Q. Hua, C. Yang, T. Baba, H. Mori, K. Shimizu, *J. Bacteriol.* **185**, 7053 (2003).

- 19. J. Zhao, T. Baba, H. Mori, K. Shimizu, Appl. Microbiol. Biotechnol. 64, 91 (2004).
- 20. A. Nanchen, A. Schicker, U. Sauer, Appl. Environ. Microbiol. 72, 1164 (2006).
- 21. M. Li, P. Y. Ho, S. Yao, K. Shimizu, *J. Biotechnol.* **122**, 254 (2006).
- 22. W. A. van Winden, C. Wittmann, E. Heinzle, J. J. Heijnen, *Biotechnol. Bioeng.* **80**, 477 (2002).
- 23. M. Dauner, J. E. Bailey, U. Sauer, *Biotechnol. Bioeng.* **76**, 144 (2001).
- 24. W. Wiechert, A. A. de Graaf, Biotechnol. Bioeng. 55, 101 (1997).
- 25. S. R. Kupor, D. G. Fraenkel, *J. Biol. Chem.* **247**, 1904 (1972).
- 26. D. E. Goldberg, *Genetic algorithms in search, optimization and machine learning* (Addison-Wesley, Boston, MA, 1989).
- R. Fletcher, *Practical Methods of Optimization* (John Wiley & Sons Inc, Hoboken, NJ, 2000).
- 28. J. Zhu, S. Shalel-Levanon, G. Bennett, K. Y. San, *Metab. Eng.* **8**, 619 (2006).
- 29. Y. H. Yang et al., Nucleic Acids Res. **30**, e15 (2002).
- 30. H. Levene, in *Contributions to Probability and Statistics:Essays in Honor of Harold Hotelling* I. Olkin *et al.* Eds. (Stanford Univ. Press, Palo Alto, CA, 1960) pp. 278-292.
- 31. V. Bewick, L. Cheek, J. Ball, Crit. Care 8, 130 (2004).
- 32. J. F. Reed, 3rd, D. B. Stark, Comput. Methods Programs Biomed. 26, 233 (1988).
- 33. P. A. Games, J. F. Howell, J. Educ. Stat. 1, 113 (1976).
- 34. J. Ludbrook, Clin. Exp. Pharmacol. Physiol. 28, 488 (2001).
- 35. H. Matsuda, Int. J. Occup. Med. Environ. Health 17, 137 (2004).
- 36. S. S. Fong, A. Nanchen, B. O. Palsson, U. Sauer, J. Biol. Chem. 281, 8024 (2006).

- 37. R. U. Ibarra, J. S. Edwards, B. O. Palsson, *Nature* **420**, 186 (2002).
- 38. F. Daldal, *J. Mol. Biol.* **168**, 285 (1983).
- 39. K. I. Sorensen, B. Hove-Jensen, *J. Bacteriol.* **178**, 1003 (1996).
- 40. I. M. Keseler et al., Nucleic Acids Res. 33, D334 (2005).
- 41. K. D. Loh et al., Proc. Natl. Acad. Sci. U. S. A. 103, 5114 (2006).
- 42. K. Shimizu, Adv. Biochem. Eng. Biotechnol. 91, 1 (2004).
- 43. T. Soga et al., J. Biol. Chem. 281, 16768 (2006).

#### **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.