**Supplemental Figures and Tables.**

*Timeline

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**Figure S1.** **Biolog Results from Nitrogen (left two columns), Phosphorus (third column) and Sulfur (last column) sources.** Growth was classified into categories based on the maximum OD750 value achieved on each substrate as compared to the negative control for each nutrient source and plate.

**Calendar

Description automatically generated**

**Figure S2. First set of the Biolog Growth Data for carbon sources as measured at 750 nm.** Black dashed line represents the threshold for growth/no growth set based on the negative control value.

**Calendar

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**Figure S3. Second set of the Biolog Growth Data for carbon sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value (as displayed in Figure S1).

Calendar

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**Figure S4. Third set of the Biolog Growth Data for carbon sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value.

**Table, calendar

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**Figure S5. Fourth set of the Biolog Growth Data for carbon sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value (as displayed in Figure S3).

**Letter

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**Figure S6. First half of the Biolog Growth Data for nitrogen sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value.

A picture containing shape

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**Figure S7. Second half of the Biolog Growth Data for nitrogen sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value (as displayed in Figure S5).

**Chart, line chart

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**Figure S8. First set of Biolog growth data for phosphorus sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value.

Chart, line chart

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**Figure S9. Second set of Biolog growth data for phosphorus sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value.

Table

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**Figure S10. Biolog Growth Data for sulfur sources as measured at 750 nm.** Blue lines are OD measured at 750 nm.Black dashed line represents the threshold for growth/no growth set based on the negative control value (as displayed in Figure S1).

Diagram

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**Figure S11. Predicted metabolic flux map predicted from model iLst996 when redox cycles are blocked.** The central carbon predicted flux values using parsimonious flux balance analysis and with an uptake of 1 mmol/gDCW/h of glucose. Flux values were normalized to a percentage of carbon source uptake. Colors correspond to different metabolic pathways. Blue – glycolysis, Green – pentose phosphate pathway, yellow – citric acid cycle, purple – anaplerotic reactions, brown – transport reactions. Hollow arrows represent biomass drainage reactions.

Chart, bar chart

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**Figure S12. Pathways of Essential Genes.**

Chart, bar chart

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**Figure S13. Protein counts of the orthoMCL analyzed species.**

**Chart, bar chart

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**Figure S14. Percent presence of species’ genes in groups with a *L. starekeyi* NRRL Y-11557 gene (top) and those without (bottom).**

**Chart

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**Figure 15. Precent of conserved GSM reactions in each organism.** The percentage represents the number of reactions in the GSM for which there is an ortholog gene present in the specified organism.

**Tables.**

**Table S1. Updated *L. starkeyi* Biomass Equation**

|  |  |
| --- | --- |
| Reaction ID |  |
| BIOMASS\_Ls | '0.6542899047921068 13BDglcn\_c + 0.12116467064111869 16BDglcn\_c + 0.0008767124745935498 5mthf\_c + 0.45552 alatrna\_c + 0.141799 argtrna\_c + 0.132431 asntrna\_c + 0.204341 asptrna\_c + 96.233892 atp\_c + 0.0016522920994288411 btn\_m + 0.0005685306148572357 ca2\_c + 0.001224527478154046 camp\_c + 0.021186648694289174 chitin\_c + 1.1e-05 clpn\_LS\_m + 0.0005261641507693166 coa\_c + 0.045479 ctp\_c + 0.0003587482846154432 cu2\_c + 0.040268 cystrna\_c + 0.003483 datp\_c + 0.003166 dctp\_c + 0.00278 dgtp\_c + 0.003587 dttp\_c + 0.005033 ergst\_r + 1e-05 ergstest\_LS\_r + 0.0005131808795165673 fad\_c + 0.00040794804936270397 fe2\_c + 0.00040794804936270397 fe3\_c + 0.115471 glntrna\_c + 0.199788 glutrna\_c + 0.3540121239284534 glycogen\_c + 0.442117 glytrna\_c + 0.0013119937265936208 gthrd\_c + 0.050529 gtp\_c + 92.341901 h2o\_c + 0.0004721810755605166 hemeA\_m + 0.060743 histrna\_c + 0.201923 iletrna\_c + 0.4002284696078455 k\_c + 0.293113 leutrna\_c + 0.0021231065148574896 lipopb\_m + 0.16701 lystrna\_c + 0.5520903768009253 mannan\_r + 0.065101 mettrna\_c + 0.0421723983491937 mg2\_c + 0.0008828624451869573 mlthf\_c + 0.00041478135002204577 mn2\_c + 0.017834231390816097 na1\_c + 0.0006067970985495497 nad\_c + 0.0005432474024176711 nadp\_c + 6e-06 pa\_LS\_r + 0.000172 pc\_LS\_r + 0.000107 pe\_LS\_r + 0.108322 phetrna\_c + 0.20874 protrna\_c + 4.3e-05 ps\_LS\_r + 0.010348 psphings\_r + 4.2e-05 ptd1ino\_LS\_r + 0.0044580453501545745 ptrc\_c + 0.0016399921582420259 pydx5p\_c + 0.0005056642487912913 q9\_m + 0.0006764967652748358 ribflv\_c + 0.40151 sertrna\_c + 0.0027107703715608823 spmd\_c + 0.0009067789974946536 thf\_c + 0.0009518787818463092 thmpp\_c + 0.226918 thrtrna\_c + 0.015970790301013598 tre\_c + 0.00182 triglyc\_LS\_r + 0.025613 trptrna\_c + 0.077745 tyrtrna\_c + 0.050281 utp\_c + 0.273459 valtrna\_c + 0.00034849833362643056 zn2\_c + 0.005191 zymst\_r + 1e-05 zymstest\_LS\_d --> 96.183832 adp\_c + 96.183832 h\_c + 96.183832 pi\_c + 2.000000000002e-06 ppi\_c' |

**Table S2. Lipid yields on different carbon sources (uptake set at 1 mmol/gDCW/h), at 10% biomass yields.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | Maximum predicted growth rate (h-1) | Maximum theoretical lipid yield (g TAG/g substrate) | Maximum theoretical lipid yield (Cmol TAG/ Cmol substrate) |
| Glucose | 0.0889 | 0.30 | 0.57 |
| Xylose | 0.0731 | 0.29 | 0.55 |
| Sucrose | 0.1786 | 0.31 | 0.57 |
| Gluconate | 0.0814 | 0.25 | 0.52 |
| Maltose | 0.1786 | 0.31 | 0.57 |
| Glycerol | 0.0511 | 0.33 | 0.65 |
| Acetate | 0.0227 | 0.25 | 0.47 |
| Palmitic acid | 0.2691 | 0.83 | 0.84 |