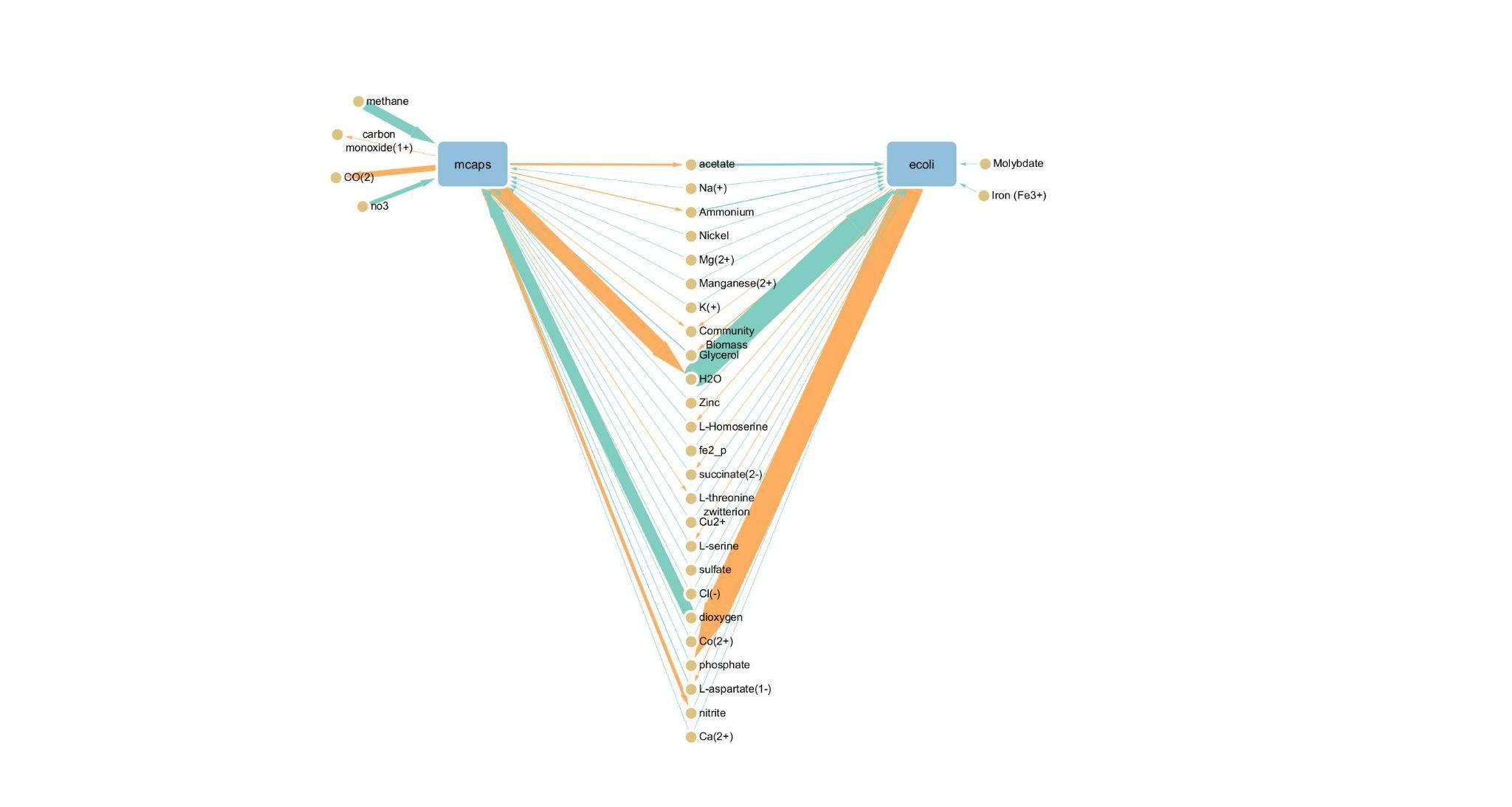
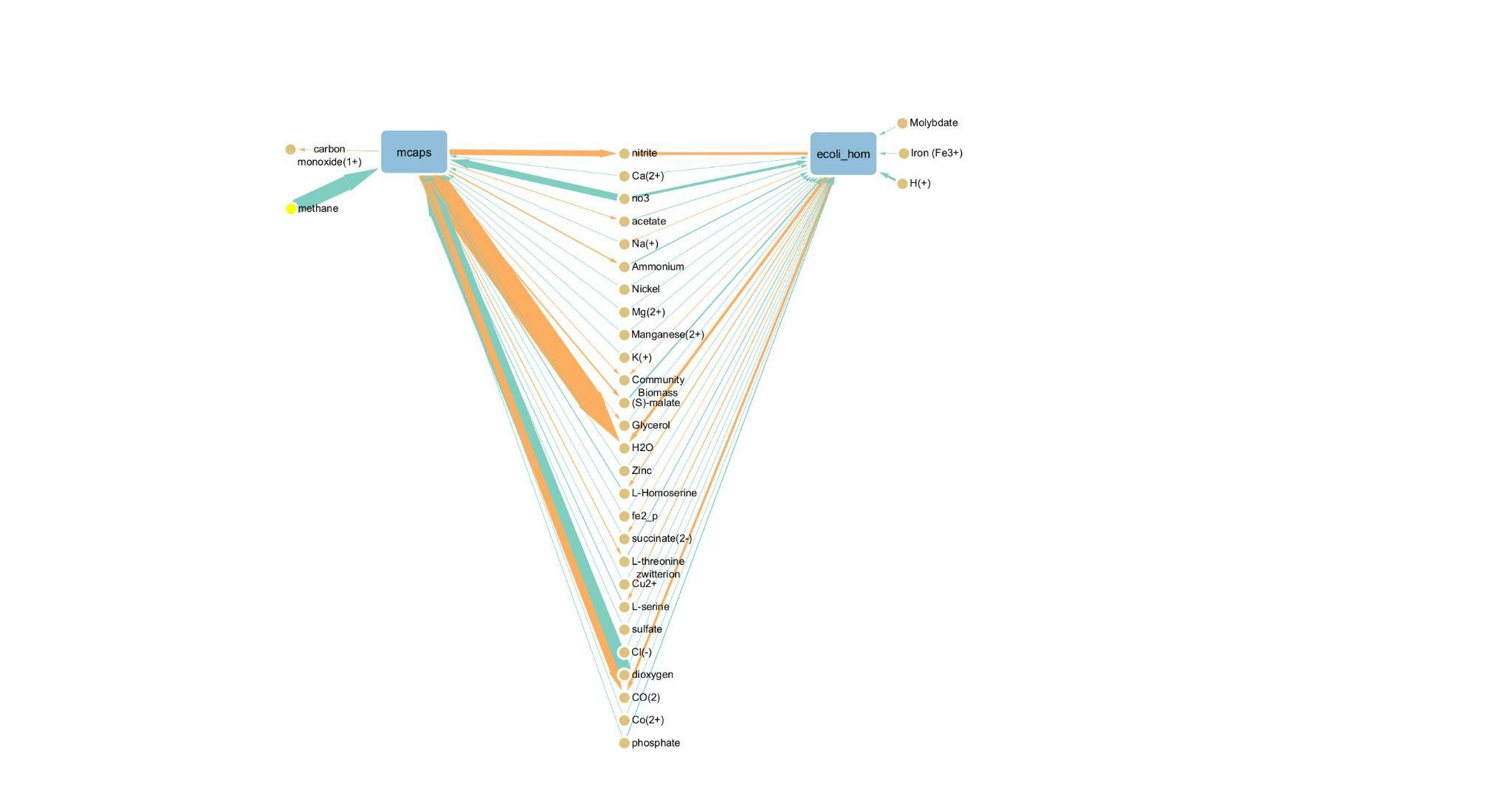
***Supplementary Material***

# Supplementary Figures and Tables

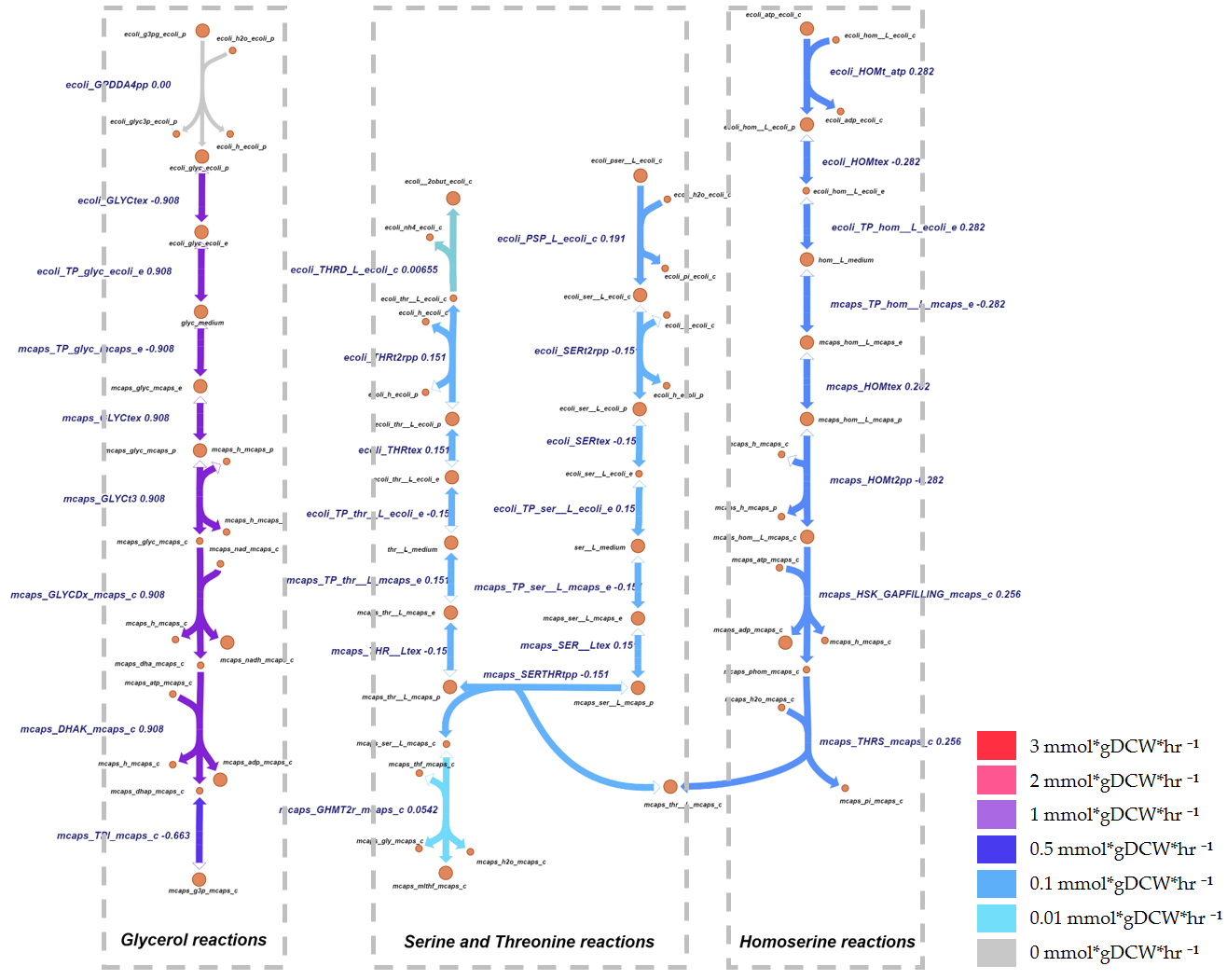
## Supplementary Figures



## Supplementary Figure 1. Visualization of cross-feeding metabolites in the *i*McBath and *i*EC1372\_W3110 communitу under oxygen-limited conditions using ScyNet. The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.

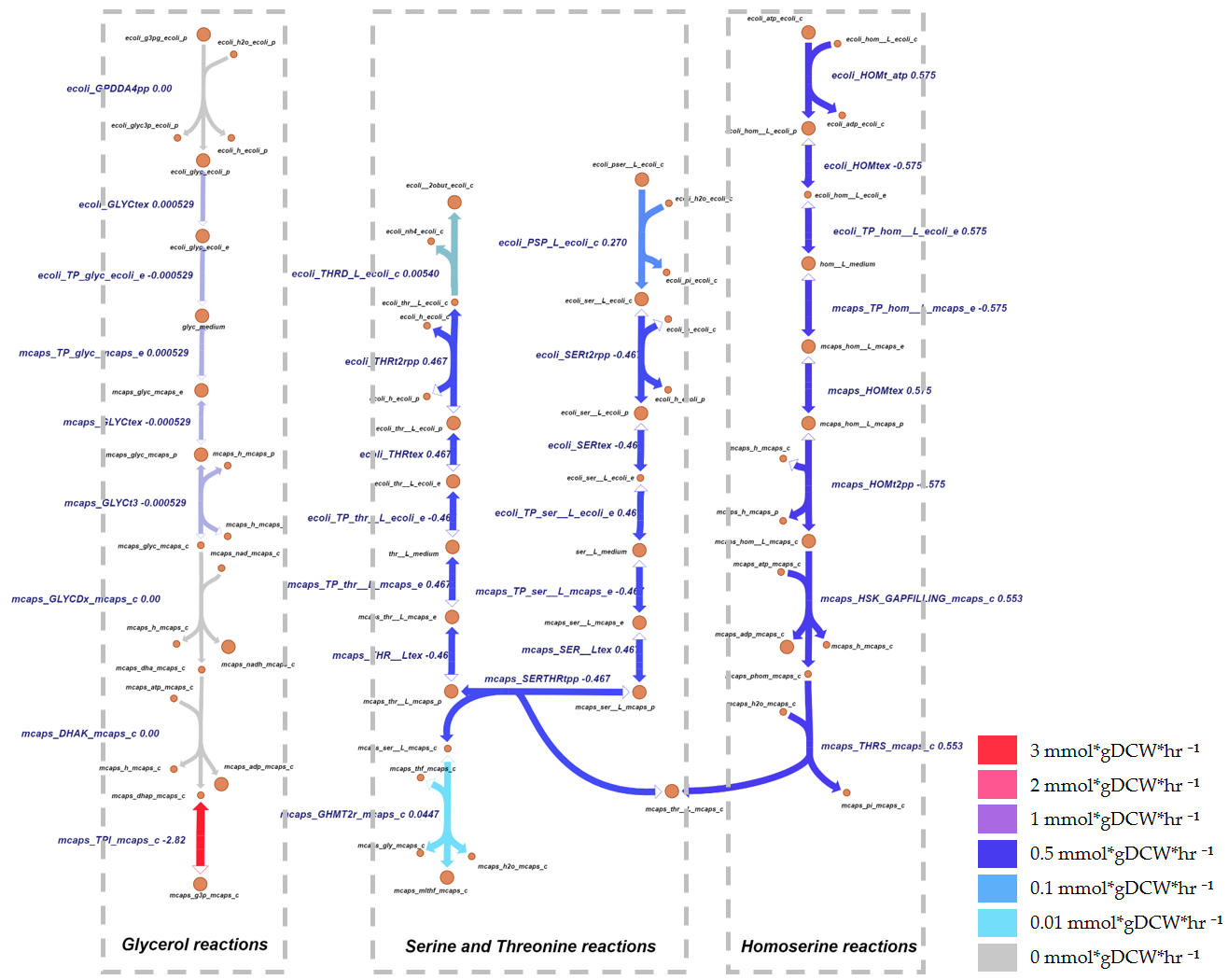


## Supplementary Figure 2. Visualization of cross-feeding metabolites in the *i*McBath and modified *i*EC1372\_W3110 communitу under oxygen-limited conditions using ScyNet.The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.



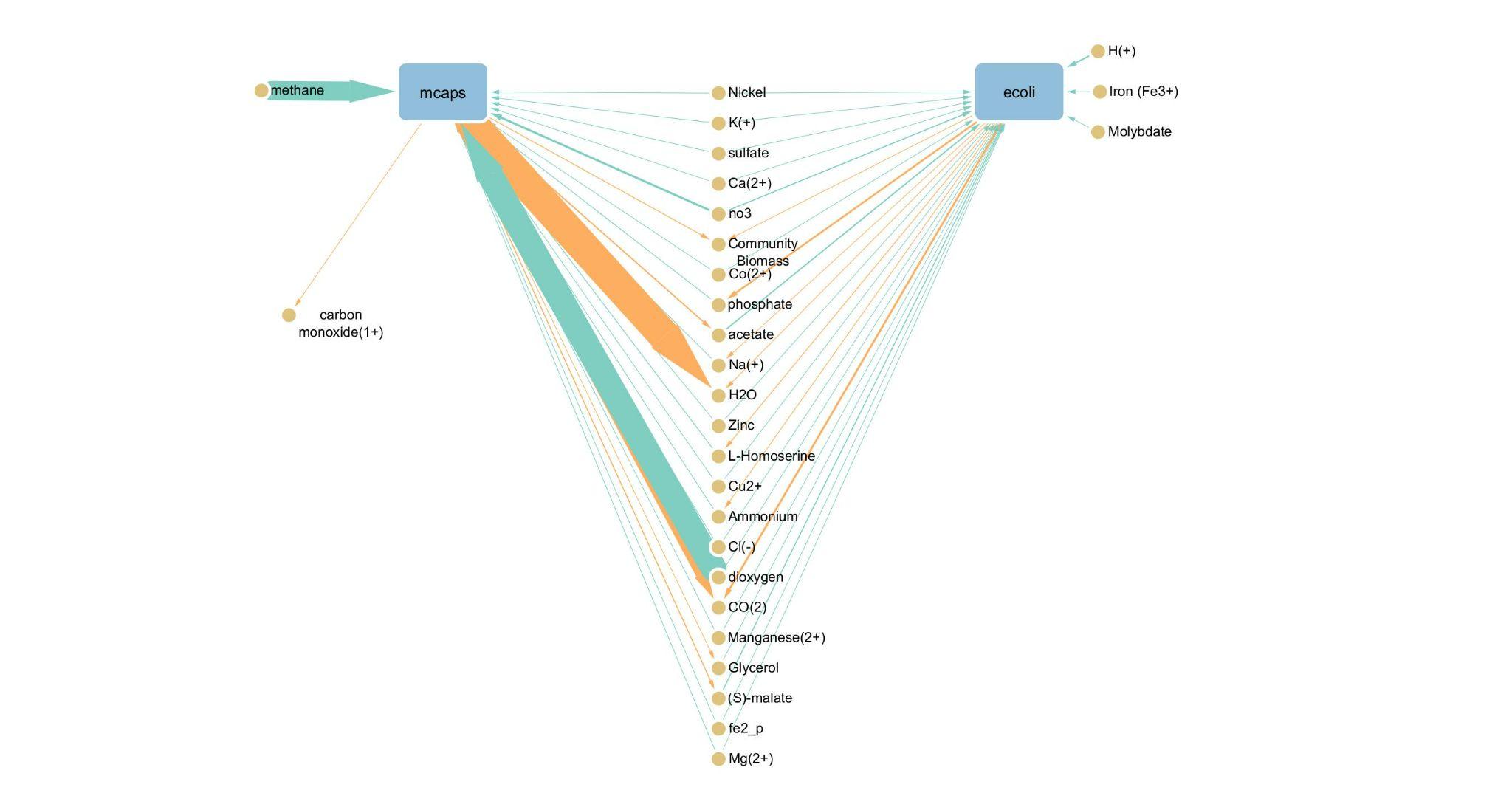
## Supplementary Figure 3. Visualization with Escher of cross-feeding of glycerol and amino acids in the community model of *i*McBath and *i*EC1372\_W3110 under oxygen-limited conditions. The legend in the figure indicates the flux intensity designations, and dashed lines represent reactions related to the production, exchange, and assimilation of glycerol, serine, threonine, and homoserine.

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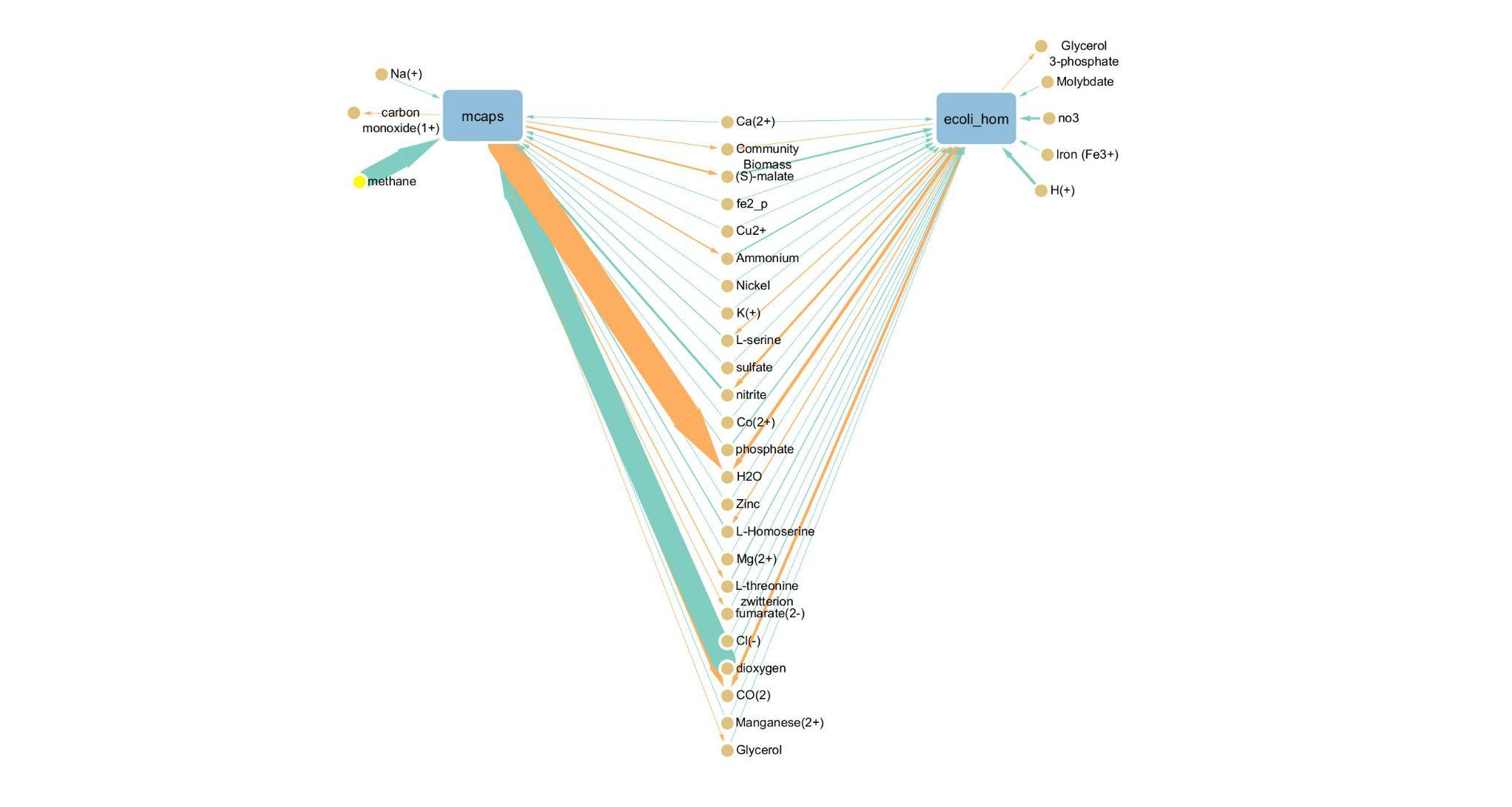


## Supplementary Figure 4. Visualization with Escher of cross-feeding of glycerol and amino acids in the community model of *i*McBath and modified *i*EC1372\_W3110 under oxygen-limited conditions. The legend in the figure indicates the flux intensity designations, and dashed lines represent reactions related to the production, exchange, and assimilation of glycerol, serine, threonine, and homoserine.

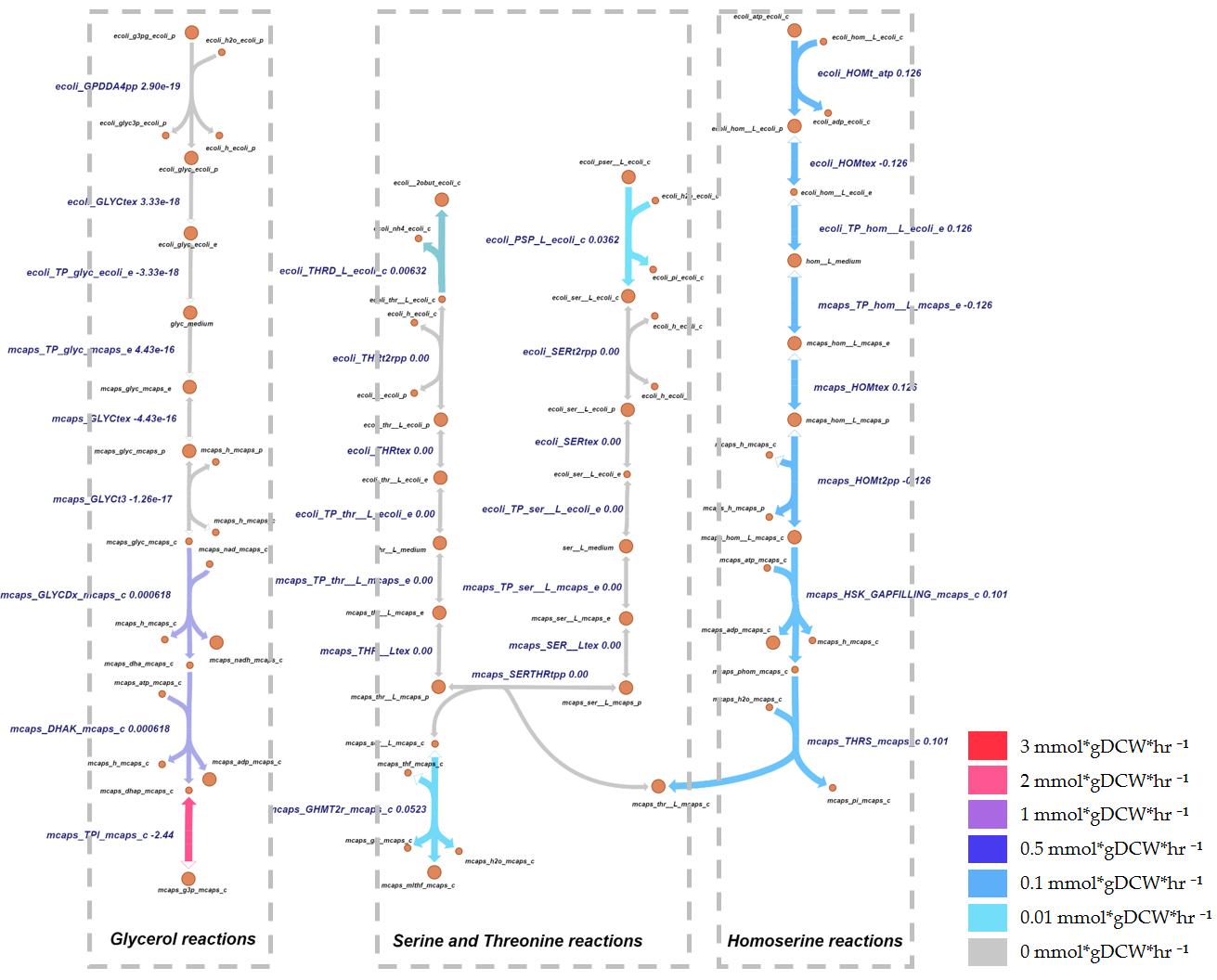
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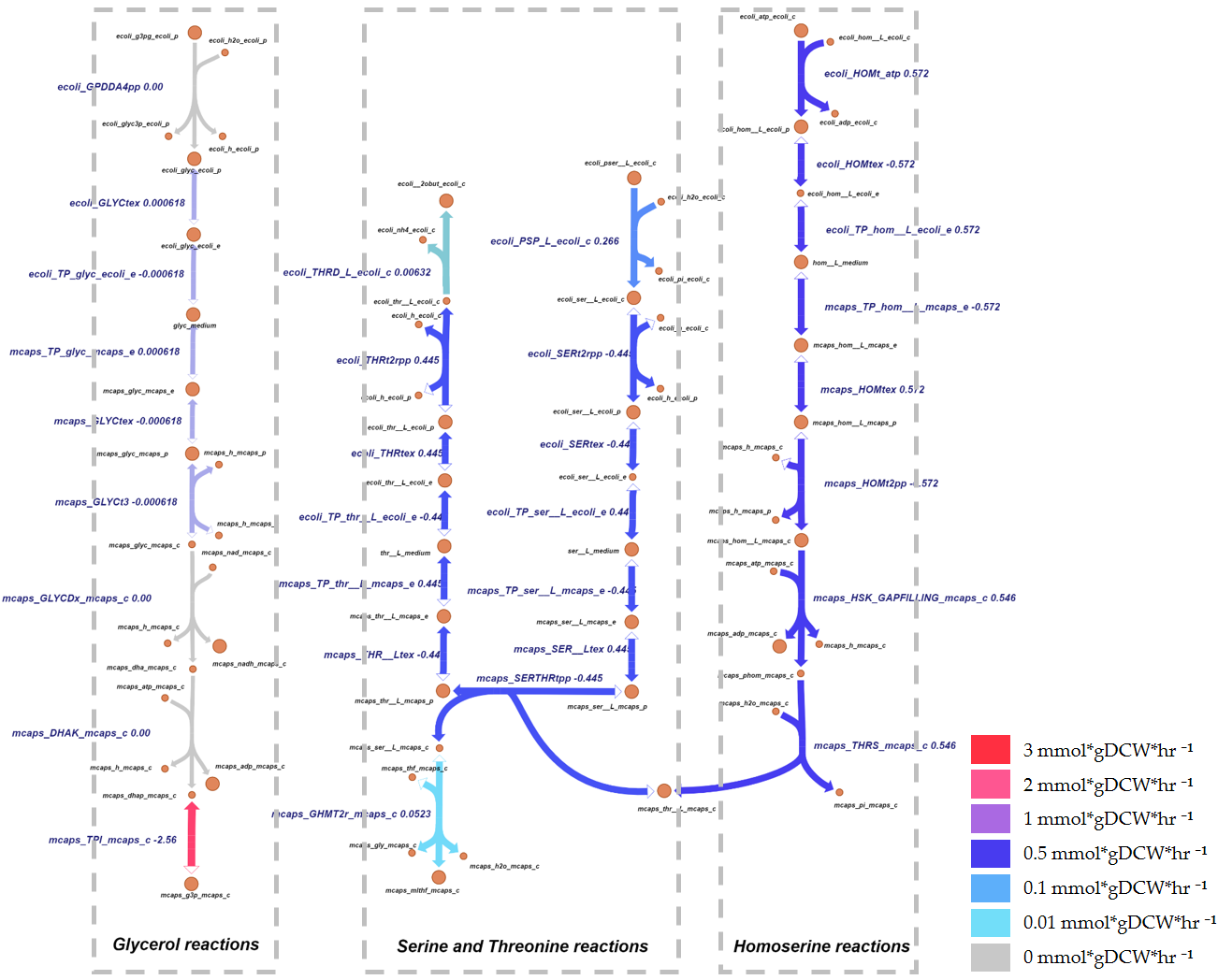
## Supplementary Figure 5. Visualization of cross-feeding metabolites in the *i*McBath and *i*EC1372\_W3110 community under nitrogen-limited conditions using ScyNet.The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.



## Supplementary Figure 6. Visualization of cross-feeding metabolites in the *i*McBath and modified *i*EC1372\_W3110 community under nitrogen-limited conditions using ScyNet.The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.



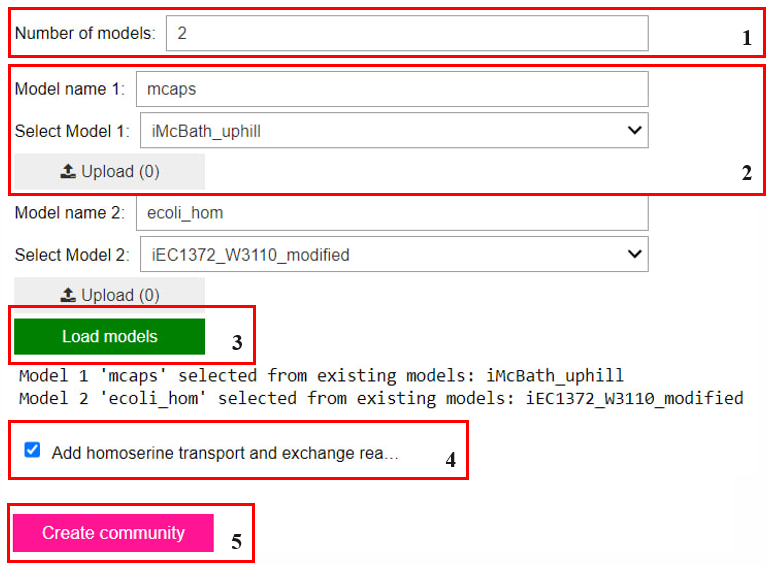
## Supplementary Figure 7. Visualization with Escher of cross-feeding of glycerol and amino acids in the community model of *i*McBath and *i*EC1372\_W3110 under nitrate-limited conditions. The legend in the figure indicates the flux intensity designations, and dashed lines represent reactions related to the production, exchange, and assimilation of glycerol, serine, threonine, and homoserine.



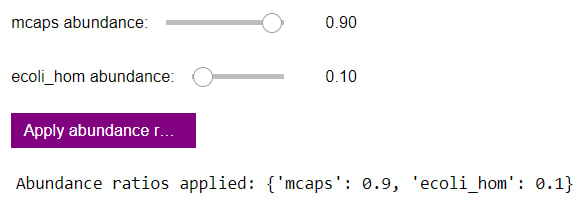
## Supplementary Figure 8. Visualization with Escher of cross-feeding of glycerol and amino acids in the community model of *i*McBath and modified *i*EC1372\_W3110 under nitrate-limited conditions. The legend in the figure indicates the flux intensity designations, and dashed lines represent reactions related to the production, exchange, and assimilation of glycerol, serine, threonine, and homoserine.

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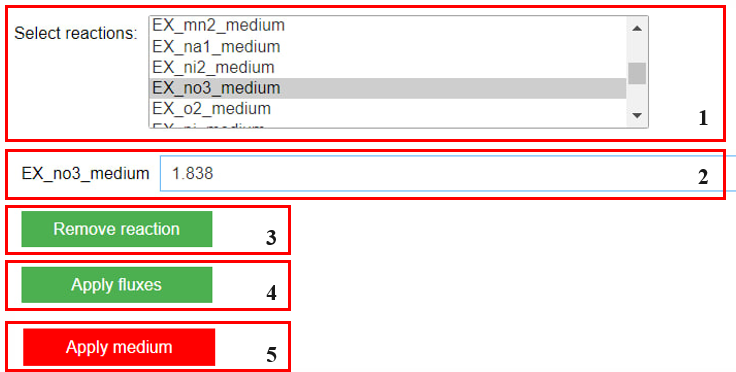
## 



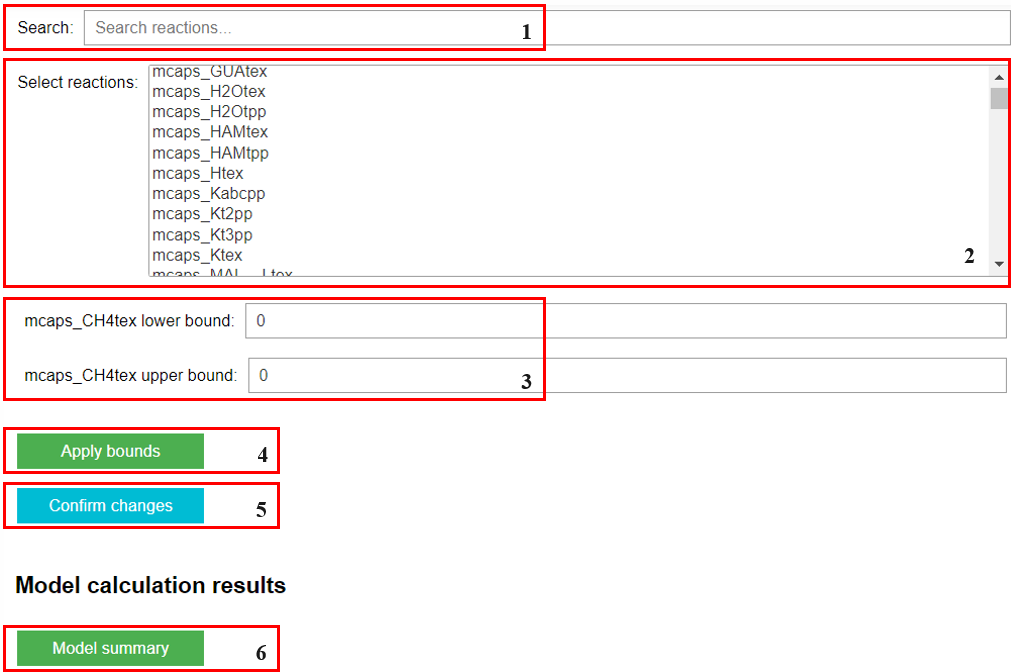
## Supplementary Figure 9. The model loading step includes: 1 Selection of the number of models to be used for community reconstruction; 2 Loading or selecting models used in the study; 3 A button for loading models; 4 Checkbox for adding transport and exchange reactions for homoserine in the *i*McBath\_uphill model; 5 A button for the community model reconstruction.



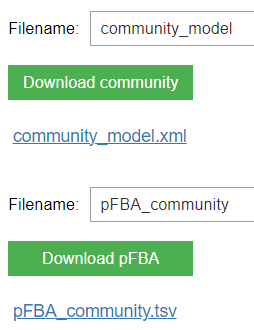
## Supplementary Figure 10. A slider for setting the abundance of microorganisms in the community, with the sum required to equal 1.



## Supplementary Figure 11. The step for set up the environment parameter for the community model consists of: 1 A selector for exchange reactions in the community; 2 A window for setting the boundaries for the chosen reactions; 3 A button to remove a metabolites from the environment; 4 A button for setting a boundary for reactions to continue the modification of metabolites in the environment; 5 A button for adding the configured environment to the community model.



## Supplementary Figure 12. The step for modifications of reactions in the community model includes: 1 A window for searching reactions in the community model; 2 A selector to choose a reaction; 3 Changing the upper and lower bounds of the reaction; 4 A button for setting the boundaries of the selected reaction; 5 A button to confirm and apply those modifications, and 6 - a button for displaying the model summary.



## Supplementary Figure 13. The step includes buttons for downloading the built community model in SBML format and pFBA results with all calculated fluxes for the community model.

## Supplementary Tables

## Supplementary Table 1: Solutions found by OptFlux for the *E. coli* model.

| **Reaction** | **Growth rate, h⁻¹** | **Homoserine production, mmol\*gDCW⁻¹\*hr⁻¹** |
| --- | --- | --- |
| R\_PItex = 8.0  R\_ICL = 0.5 | 0.355 | 5.378 |
| R\_PItex = 8.0  R\_FCLT = 32.0 | 0.361 | 5.372 |
| R\_PItex = 8.0  R\_CU2tpp = 16.0 | 0.369 | 5.365 |
| R\_PItex = 8.0 | 0.369 | 5.365 |

## Supplementary Table 2: Cross-metabolites of the *i*McBath and *i*EC1372\_W3110 community without homoserine production from *i*EC1372\_W3110 and with its production.

| **Metabolite** | **Producer** | **Сonsumer** | **o2\_lim** | **o2\_lim\_**  **homoserine** | **no3\_lim** | **no3\_lim\_**  **homoserine** |
| --- | --- | --- | --- | --- | --- | --- |
| Acetate | *M.capsulatus* | *E.coli* | 3.343 | 0.205 | 0.612 | - |
| Aspartate | *E.coli* | *M.capsulatus* | 0.515 | - | - | - |
| Fumarate | *E.coli* | *M.capsulatus* | - | - | - | 0.096 |
| Glycerol | *M.capsulatus* | *E.coli* | - | 5.3E-4 | 3.3E-18 | 6.2E-4 |
| Glycerol | *E.coli* | *M.capsulatus* | 0.908 | - | - | - |
| H2O | *M.capsulatus* | *E.coli* | 30.896 | - | - | - |
| Homoserine | *E.coli* | *M.capsulatus* | 0.282 | 0.575 | 0.126 | 0.572 |
| Malate | *M.capsulatus* | *E.coli* | - | 1.144 | 0.361 | 1.197 |
| Na+ | *E.coli* | *M.capsulatus* | - | 0.007 | 2.2E-20 | - |
| NH4 | *E.coli* | *M.capsulatus* | - | - | 0.071 | - |
| NH4 | *M.capsulatus* | *E.coli* | 0.981 | 0.775 | - | 0.777 |
| NO2 | *M.capsulatus* | *E.coli* | 0.059 | - | - | - |
| Pi | *E.coli* | *M.capsulatus* | 0.112 | - | 0.108 | - |
| Serine | *E.coli* | *M.capsulatus* | 0.151 | 0.467 | - | 0.445 |
| Succinate | *E.coli* | *M.capsulatus* | 4.06E-4 | 3.3E-4 | - | - |
| Threonine | *M.capsulatus* | *E.coli* | 0.151 | 0.467 | - | 0.445 |

## Supplementary Table 3: Reactions required for considered electron transfer mechanisms in the *i*McBath model.

| **Electron transfer mechanism/Reactions** | sMMOi | pMMODCipp | pMMOipp | CyLCyHORpp | NADH16pp | NADHNQR2ipp | NADH5ppi | CYOR\_q8ppi |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Redox-arm** | 0 | - | (0,1000) | - | 0 | 0 | - | - |
| **Direct** | 0 | (0,1000) | - | 0 | - | - | - | - |
| **Uphill** | 0 | - | (0,1000) | - | - | - | 0 | (-1000,0) |

## Supplementary Table 4: FBA results of the *i*McBath model under different electron transfer mechanisms.

| **Model** | **Original\_model** | **Uphill** | **Redox-arm** | **Direct** |
| --- | --- | --- | --- | --- |
| **Ratio О2/СН4** | 1,5  (27,81/18,46) | 1,24  (22,84/18,46) | 1,5  (27,81/18,46) | 1,13 (20,92/18,46) |
| **Biomass** | 0,178 | 0,275 | 0,178 | 0,313 |
| **Uptake** |  |  |  |  |
| EX\_ca2\_e | 0,01244 | 0,01921 | 0,01244 | 0,02184 |
| EX\_ch4\_e | 18,46 | 18,46 | 18,46 | 18,46 |
| EX\_cl\_e | 0,03816 | 0,05895 | 0,03816 | 0,067 |
| EX\_cobalt2\_e | 1,03E-05 | 1,59E-05 | 1,03E-05 | 1,80E-05 |
| EX\_cu2\_e | 0,0002689 | 0,0004154 | 0,0002689 | 0,0004721 |
| EX\_fe2\_e | 0,001089 | 0,001683 | 0,001089 | 0,001913 |
| EX\_h\_e | 1,458 | 2,253 | 1,458 | 2,561 |
| EX\_k\_e | 0,03141 | 0,04853 | 0,03141 | 0,05516 |
| EX\_mg2\_e | 0,02197 | 0,03394 | 0,02197 | 0,03858 |
| EX\_mn2\_e | 3,20E-06 | 4,95E-06 | 3,20E-06 | 5,63E-06 |
| EX\_na1\_e | 0,006968 | 0,01076 | 0,006968 | 0,01224 |
| EX\_ni2\_e | 6,05E-06 | 9,35E-06 | 6,05E-06 | 1,06E-05 |
| EX\_no3\_e | 1,459 | 2,253 | 1,459 | 2,561 |
| EX\_o2\_e | 27,81 | 22,84 | 27,81 | 20,92 |
| EX\_pi\_e | 0,09814 | 0,1516 | 0,09814 | 0,1723 |
| EX\_so4\_e | 0,03005 | 0,04641 | 0,03005 | 0,05276 |
| EX\_zn2\_e | 0,000178 | 0,000275 | 0,000178 | 0,0003126 |
| **Secretion** |  |  |  |  |
| DM\_4hba\_c | 5,10E-06 | 7,88E-06 | 5,10E-06 | 8,95E-06 |
| DM\_doxopa\_c | 0,0001895 | 0,0002928 | 0,0001895 | 0,0003328 |
| DM\_h2o2\_c | 0,05718 | 0,08834 | 0,05718 | 0,1004 |
| DM\_rdmbzi\_c | 0,0001895 | 0,0002928 | 0,0001895 | 0,0003327 |
| EX\_co2\_e | 12,47 | 9,204 | 12,47 | 7,94 |
| EX\_co\_e | 5,10E-06 | 7,88E-06 | 5,10E-06 | 8,95E-06 |
| EX\_h2o\_e | 32,96 | 30,8 | 32,96 | 29,97 |
| **EX\_ac\_e** | **-** | **-** | **-** | **-** |

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## Supplementary Table 5: Modified reactions with new boundaries in the *i*McBath model.

| **Metabolic pathway** | **Response ID in the model** | **Set boundaries** |
| --- | --- | --- |
| **TCA** | MDH | -1000,1000 |
|  | CITL | -1000,1000 |
|  | ACONTa | -1000,1000 |
|  | ACONTb | -1000,1000 |
|  | ACONT | -1000,1000 |
|  | SSALx | -1000,0 |
|  | SSALy | -1000,0 |
|  | SUCCt2\_2pp | -1000,1000 |
|  | FUM | -1000,1000 |
|  | ADSL1i | -1000,1000 |
|  | ARGSL | -1000,1000 |
|  | ME1 | -1000,1000 |
|  | FUMt2\_2pp | -1000,1000 |
|  | MALt2\_2pp | -1000,1000 |
| **EMP** | PFK\_ppi | 0,1000 |
|  | PYK | 0,1000 |
| **RuMP** | HPS | 0,1000 |
|  | AH6PI | 0,1000 |
|  | TKT2 | 0,1000 |
|  | RPI | 0,1000 |
|  | TKT1 | 0,1000 |
|  | TALA | 0,1000 |
|  | RPE | 0,1000 |
| **ED** | G6PDH2 | 0,1000 |
|  | PGI | -1000,1000 |
|  | PGL | 0,1000 |
|  | EDD | 0,1000 |
|  | EDA | 0,1000 |
|  | GND | 0,1000 |

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## Supplementary Table 6: Impact of changes in ED pathway flux on EMP reaction fluxes in the *i*McBath model (PFK—phosphofructokinase, PFK3—pyrophosphate-dependent 6-phosphofructokinase, PGM—phosphoglycerate mutase), methane and oxygen consumption, and acetate production.

| **ED** | **Biomass, h-1** | **ratio O2/CH4, mmol\***  **gDCW⁻¹\*hr⁻¹** | **PFK, mmol\***  **gDCW⁻¹\*hr⁻¹** | **PFK3, mmol\***  **gDCW⁻¹\*hr⁻¹** | **PGM, mmol\***  **gDCW⁻¹\*hr⁻¹** | **Acetate, mmol\***  **gDCW⁻¹\*hr⁻¹** |
| --- | --- | --- | --- | --- | --- | --- |
| 0 | 0 | (-12.515/-8.391) | 0 | 0 | 0 | 0 |
| 0.503 | 0.277 | (-22.744/-18.46) | 2.529 | 0 | 1.921 | 0 |
| 1.007 | 0.275 | (-22.824/-18.46) | 2.009 | 0 | 1.404 | 0 |
| 1.510 | 0.274 | (-22.904/-18.46) | 1.488 | 0 | 0.887 | 0 |
| 2.014 | 0.272 | (-22.983/-18.46) | 0.968 | 0 | 0.370 | 0 |
| 2.517 | 0.270 | (-23.089/-18.46) | 0.442 | 0 | -0.151 | 0 |
| 3.021 | 0.268 | (-23.224/-18.46) | 0 | -0.091 | -0.678 | 0 |
| 3.524 | 0.265 | (-23.359/-18.46) | 0 | -0.623 | -1.205 | 0 |
| 4.028 | 0.262 | (-23.494/-18.46) | 0 | -1.155 | -1.731 | 0 |
| 4.531 | 0.260 | (-23.630/-18.46) | 0 | -1.688 | -2.258 | 0 |
| 5.035 | 0.257 | (-23.765/-18.46) | 0 | -2.220 | -2.784 | 0 |
| 5.538 | 0.254 | (-23.9/-18.46) | 0 | -2.753 | -3.311 | 0 |
| 6.041 | 0.246 | (-23.95/-18.46) | 0 | -3.157 | -3.697 | 0.191 |
| 6.545 | 0.188 | (-25.082/1.111) | 0 | -3.377 | -3.789 | 1.111 |

## Supplementary Table 7: Additional modifications of the community model.

| **Reactions of the community model** | **Boundaries** |
| --- | --- |
| ecoli\_TP\_ecoli\_eca4colipa\_ecoli\_e | 0,0 |
| ecoli\_TP\_colipa\_ecoli\_e | 0,0 |
| ecoli\_TP\_colipap\_ecoli\_e | 0,0 |
| ecoli\_TP\_btn\_ecoli\_e | 0,0 |
| ecoli\_TP\_acolipa\_ecoli\_e | 0,0 |
| ecoli\_TP\_hacolipa\_ecoli\_e | 0,0 |
| ecoli\_TP\_o16a4colipa\_ecoli\_e | 0,0 |
| ecoli\_TP\_o6a4colipa\_ecoli\_e | 0,0 |
| ecoli\_TP\_lipa\_ecoli\_e | 0,0 |
| ecoli\_GPDDA1pp | 0,0 |
| ecoli\_TP\_lipa\_cold\_ecoli\_e | 0,0 |
| ecoli\_hom\_TP\_ecoli\_hom\_eca4colipa\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_colipa\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_colipap\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_btn\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_acolipa\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_hacolipa\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_o16a4colipa\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_o6a4colipa\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_lipa\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_GPDDA1pp | 0,0 |
| ecoli\_hom\_TP\_lipa\_cold\_ecoli\_hom\_e | 0,0 |
| ecoli\_TP\_h\_ecoli\_e | -1000,0 |
| mcaps\_TP\_h\_mcaps\_e | -1000,0 |
| ecoli\_hom\_TP\_h\_ecoli\_hom\_e | -1000,0 |
| ecoli\_TP\_co2\_ecoli\_e | 0,1000 |
| ecoli\_TP\_pser\_\_L\_ecoli\_e | 0,0 |
| ecoli\_hom\_TP\_pser\_\_L\_ecoli\_hom\_e | 0,0 |
| ecoli\_hom\_TP\_glyclt\_ecoli\_hom\_e | 0,0 |

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