# Supplemental tables

Table S1: Description of variables

| symbol | description |
|--------|-------------|
| $\sigma$ | translational activity |
| $\chi_{Rb}$ | regulation function of ribosomal protein allocation |
| $\chi_C$ | regulation function of catabolic protein allocation |
| $\phi_{Rb}$ | fraction of ribosomal protein over total protein |
| $\phi_C$ | fraction of catabolic protein over total protein |
| $\nu_{aa}$ | protein synthesis flux |
| $\nu_C$ | carbon uptake rate |
| $\lambda$ | cell growth rate |

Table S2: Description of parameters. Default values were used unless otherwise stated.

| symbol | description | value | source |
|--------|-------------|-------|--------|
| $\gamma$ | Inverse slope of growth laws | 13.52 h$^{-1}$ | [2] |
| $\lambda_C$ | Strain specific constant of growth laws | 1.17 h$^{-1}$ | [2] |
| $\phi_{Rb,0}$ | A growth rate-independent offset of R sector | 0.049 | [2] |
| $\phi_Q$ | Fraction of house-keeping protein | 0.45 | [14] |
| $\phi_{C,max}$ | Maximum of proteome attainable to C, E and R sectors | 0.44 | [15] |
| $\beta$ | conversion factor between moles and gram | 0.1968 g/mmol | |
| $h_{1,2}$ | carbon-specific allocation | | |
| $\omega_E$ | enzyme cost per unit metabolic influx | 8.3×10$^{-4}$ gh/mmol | [31] |
| $\omega_C$ | enzyme cost per unit carbon influx | See Table S3 | |

Table S3: The constants of the substrates used in the simulation of dCAFBA.

| Substrate1 | Substrate2 | $\lambda_1$ (h$^{-1}$) | $\lambda_2$ (h$^{-1}$) | $\lambda_{12}$ (h$^{-1}$) | $\omega_{C1}$ | $\omega_{C2}$ | $h_1$ | $h_2$ |
|------------|------------|---------------|---------------|----------------|---------------|---------------|-------|-------|
| succinate | glucose | 0.45 | 0.91 | 0.92 | 1.96×10$^{-2}$ | 4.3×10$^{-3}$ | 0.64 | 1 |
| | gluconate | 0.45 | 0.91 | 0.94 | 1.96×10$^{-2}$ | 2.29×10$^{-3}$ | 0.63 | 1 |
| pyruvate | gluconate | 0.60 | 0.91 | 0.97 | 5.17×10$^{-3}$ | 2.39×10$^{-3}$ | 0.77 | 1 |

Table S4: The parameters used in the dCAFBA simulations with the *E.coli i*ML1515 metabolic model.

| | Substrate1 | Substrate2 | $\omega_{C1}$(gh/mmol) | $\omega_{C2}$(gh/mmol) | $\omega_E$(gh/mmol) | $\beta$(g/mmol) | $h_1$ | $h_2$ |
|--|-----------|------------|-----------------|-----------------|----------------|----------------|-------|-------|
| Up-shift | succinate | gluconate | 1.96×10$^{-2}$ | 2.1×10$^{-3}$ | 3.3×10$^{-4}$ | 0.1870 | 0.63 | 1 |
| Down-shift | succinate | glucose | 1.6×10$^{-2}$ | 2.9×10$^{-3}$ | 5.15×10$^{-4}$ | 0.1870 | 0.6 | 1 |

Table S5: The parameters used in the simulations of lycopene production by dCAFBA.

| Substrate | $\lambda_1$ (h$^{-1}$) | $\omega_C$(gh/mmol) | $\omega_E$(gh/mmol) | $\phi_{Cmax}$ | $k_{eff}$ | $t_C$ (h) |
|-----------|---------------|----------------|----------------|--------------|-----------|-----------|
| glucose | 0.85 | 1.0×10$^{-3}$ | 4.1×10$^{-4}$ | 0.24 | 0.05 | 0.6 |