**Table S5. Key metabolites per pathway used for calculating fluxSum of pathways of interest**. Abbreviations as used in Recon3D and full names are given for all used metabolites. Letters in brackets indicate the cellular compartment: c, cytoplasm; m, mitochondria.

|  |  |  |
| --- | --- | --- |
| Pathway | Key metabolite abbreviation | Key metabolite  full name |
| Glycolysis | 'glc\_D[c]' | 'D-Glucose' |
| 'g6p[c]' | 'D-Glucose 6-Phosphate' |
| 'f6p[c]' | 'D-Fructose 6-Phosphate' |
| 'fdp[c]' | 'D-Fructose 1,6-Bisphosphate' |
| 'dhap[c]' | 'Dihydroxyacetone Phosphate' |
| 'g3p[c]' | 'Glyceraldehyde 3-Phosphate' |
| '13dpg[c]' | '3-Phospho-D-Glyceroyl Phosphate' |
| '3pg[c]' | '3-Phospho-D-Glycerate' |
| '2pg[c]' | '2-Phospho-D-Glycerate' |
| 'pep[c]' | 'Phosphoenolpyruvate' |
| 'pyr[c]' | 'Pyruvate' |
|  |  |  |
| Tricarboxylic acid cycle  (TCA) | 'cit[m]' | 'Citrate' |
| 'icit[m]' | 'Isocitric Acid' |
| 'akg[m]' | '2-Oxoglutarate' |
| 'succoa[m]' | 'Succinyl Coenzyme A' |
| 'succ[m]' | 'Succinate' |
| 'fum[m]' | 'Fumarate' |
| 'mal\_L[m]' | '(S)-Malate' |
| 'oaa[m]' | 'Oxaloacetate' |
|  |  |  |
| Oxidative phosphorylation  (OXPHOS) | nadh[m]' | 'Nicotinamide Adenine Dinucleotide - Reduced' |
| 'fadh2[m]' | 'Flavin Adenine Dinucleotide Reduced' |
| 'focytC[m]' | 'Ferrocytochrome C' |
| 'q10h2[m]' | 'Ubiquinol-10' |
| 'atp[m]' | 'Adenosine Triphosphate' |
|  |  |  |
| Fatty acid oxidation  (FAO) | 'accoa[c]' | 'Acetyl Coenzyme A' |
| 'accoa[m]' | 'Acetyl Coenzyme A' |
| 'coa[c]' | 'Coenzyme A' |
| 'coa[m]' | 'Coenzyme A' |