

| Pathway                              | CC<br>activity<br>(tran-<br>scriptome<br>data) | CC<br>activity<br>(model) |
|--------------------------------------|--|---------------------------|
| Glutamine biosynthesis III           | higher   | higher*                   |
| Arginine biosynthesis I and IV       | higher   | higher                    |
| Alanine degradation II (to lactate)  | higher   | lower                     |
| Aerobic respiration (AOX)            | higher   | no flux in model          |
| PRPP biosynthesis I                  | higher   | higher                    |
| PPP (non-oxidative)                  | higher   | lower (l) higher (d)      |
| Sulphate reduction II (assimilatory) | higher   | lower                     |
| Rubisco shunt                        | higher   | lower (l) higher (d)      |
| Glycolysis                           | higher   | lower (l) higher (d)      |
| Glyoxylate cycle                     | higher   | higher                    |
| TCA cycle                            | higher   | lower (l) higher (d)      |
| Aerobic respiration                  | higher   | lower (l) higher (d)      |
| Leucine biosynthesis                 | lower  | lower                     |
| Methionine biosynthesis              | lower  | lower                     |
| Lysine biosynthesis                  | lower  | higher                    |
| Valine biosynthesis                  | lower  | lower                     |
| Glycine biosynthesis                 | lower  | lower*                    |
| Isoleucine biosynthesis              | lower  | lower                     |
| Histidine biosynthesis               | lower  | higher                    |
| Phenylalanine biosynthesis II        | lower  | lower                     |
| Homoserine biosynthesis              | lower  | lower                     |
| Photorespiration                     | lower  | lower                     |
| Citrulline nitric acid cycle         | lower  | higher                    |
| Photosynthesis light reactions       | lower  | lower                     |

Table ST2: Comparison of pathway activity predictions based off only transcriptome data and the transcriptome-weighted model solution. CC (Companion Cell) activity (model) takes into account reaction fluxes in companion cells, sieve elements and petiole sieve elements because companion cells produce mRNA for all three. \* indicates that flux variability analysis indicates this pathway could be either higher or lower without changing how well the solution matches the transcriptome data. (l) indicates light phase only. (d) indicates dark phase only.