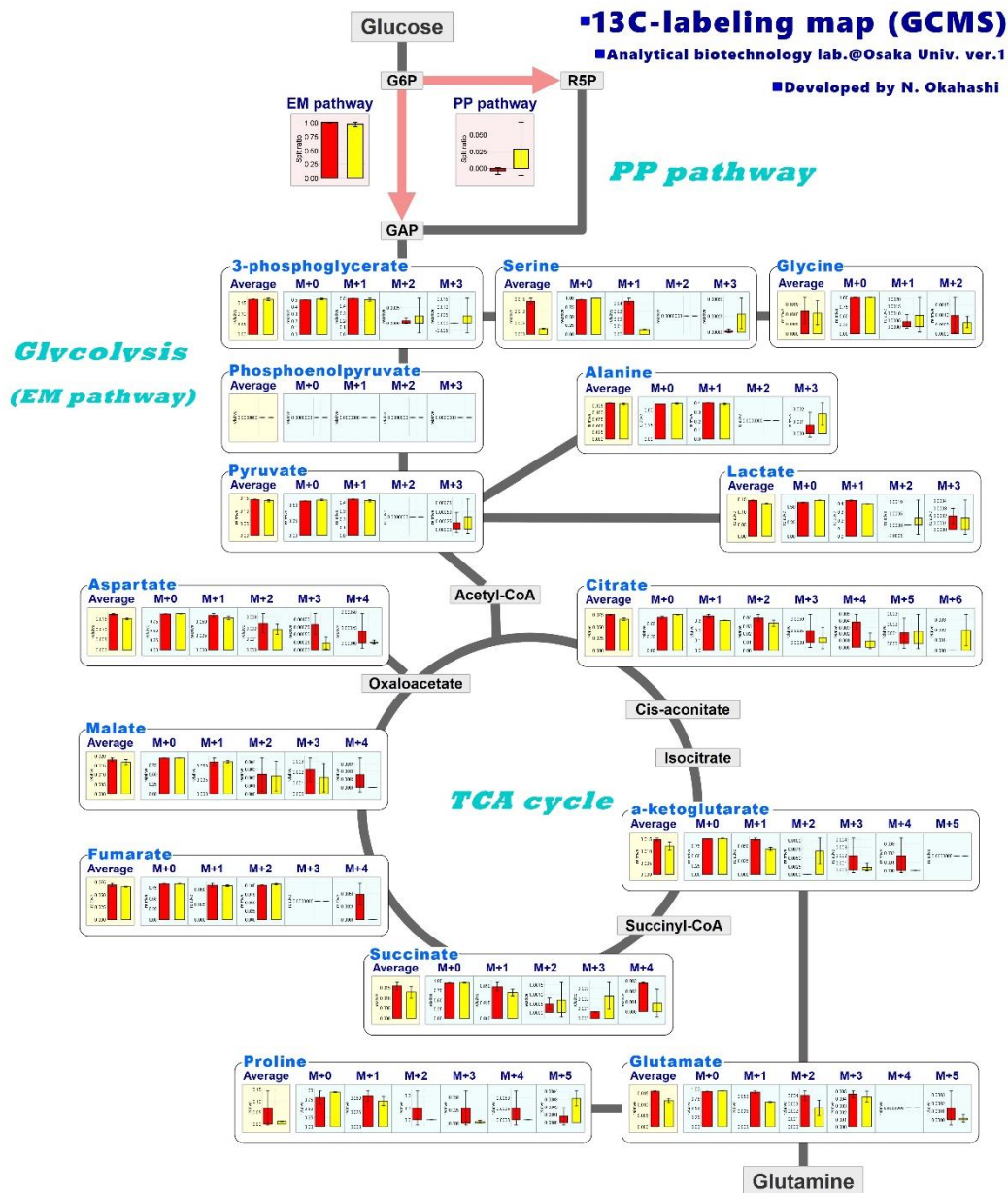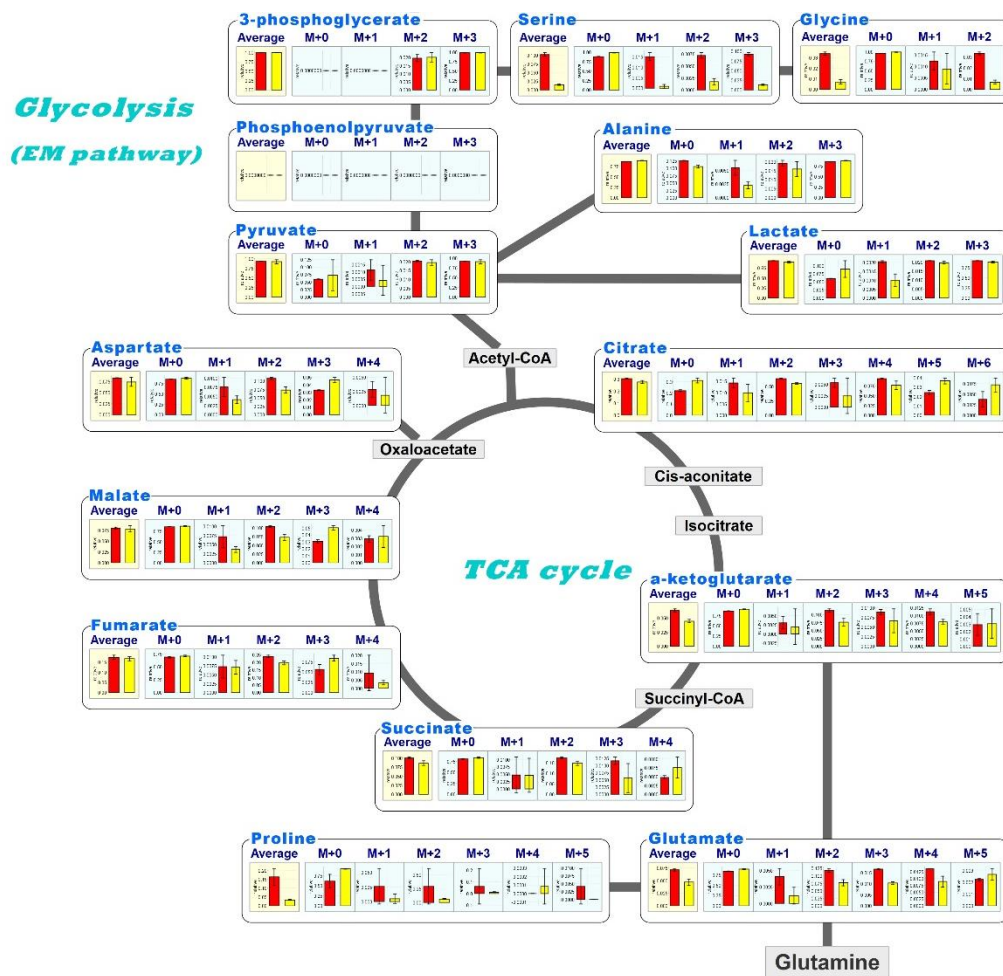## Supplementary information
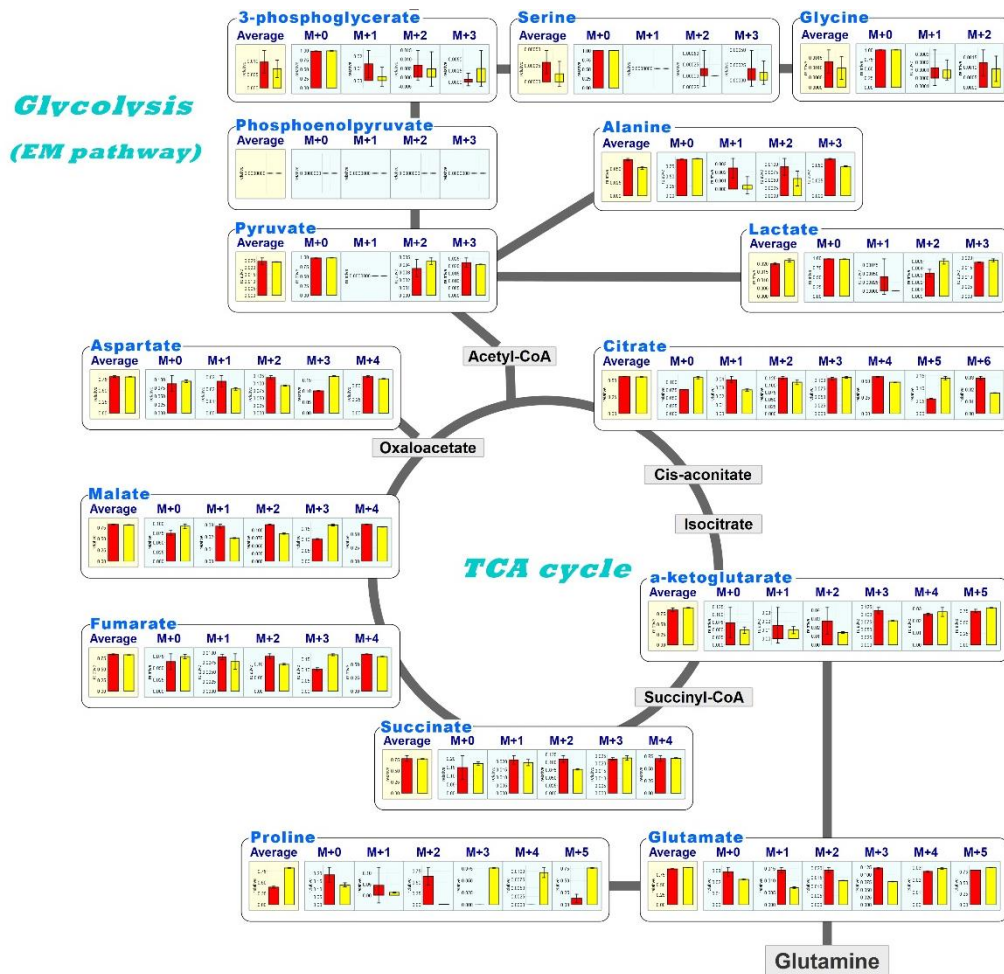


**Figure S1. Labeling data visualization on a metabolic map ([1-$^{13}$C]glucose and unlabeled glutamine).**
HCT116 (red) and WiDr (yellow) were cultured in medium containing [1-$^{13}$C]glucose and unlabeled glutamine. Blue, yellow, and pink boxes represent mass isotopologue distribution, fractional labeling, and split ratio, respectively.
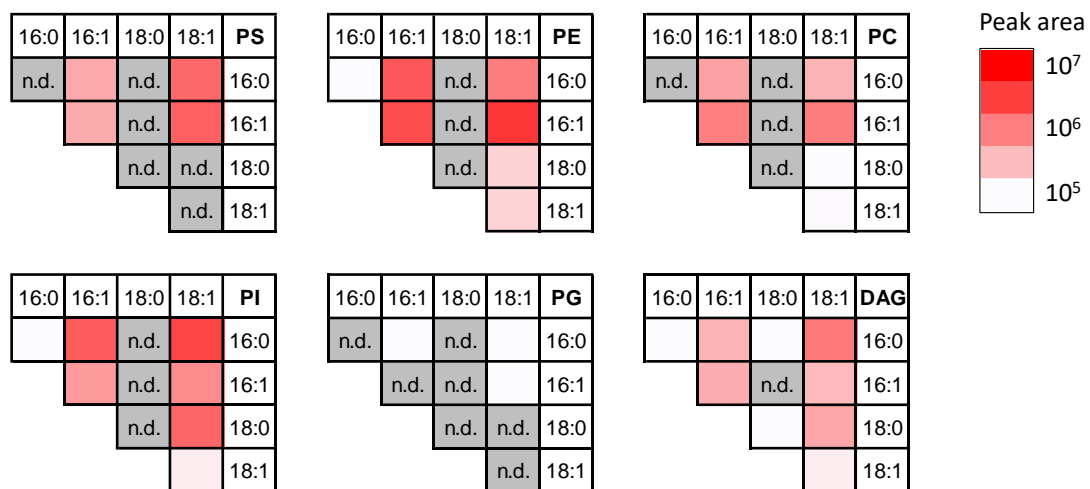
**Figure S2. Labeling data visualization on a metabolic map ([U-¹³C]glucose and unlabeled glutamine).**

HCT116 (red) and WiDr (yellow) were cultured in medium containing [U-¹³C]glucose and unlabeled glutamine. Blue and yellow boxes represent mass isotopologue distribution and fractional labeling, respectively.

**Figure S3. Labeling data visualization on a metabolic map (unlabeled glucose and [U-¹³C]glutamine).**

HCT116 (red) and WiDr (yellow) were cultured in medium containing unlabeled glucose and [U-¹³C]glutamine. Blue and yellow boxes represent mass isotopologue distribution and fractional labeling, respectively.

**Figure S4. Heatmaps of glycerolipid abundance.**

Peak areas of glycerolipids obtained from unlabeled yeasts were shown on the heatmaps. The columns and rows represent combinations of acyl chains.