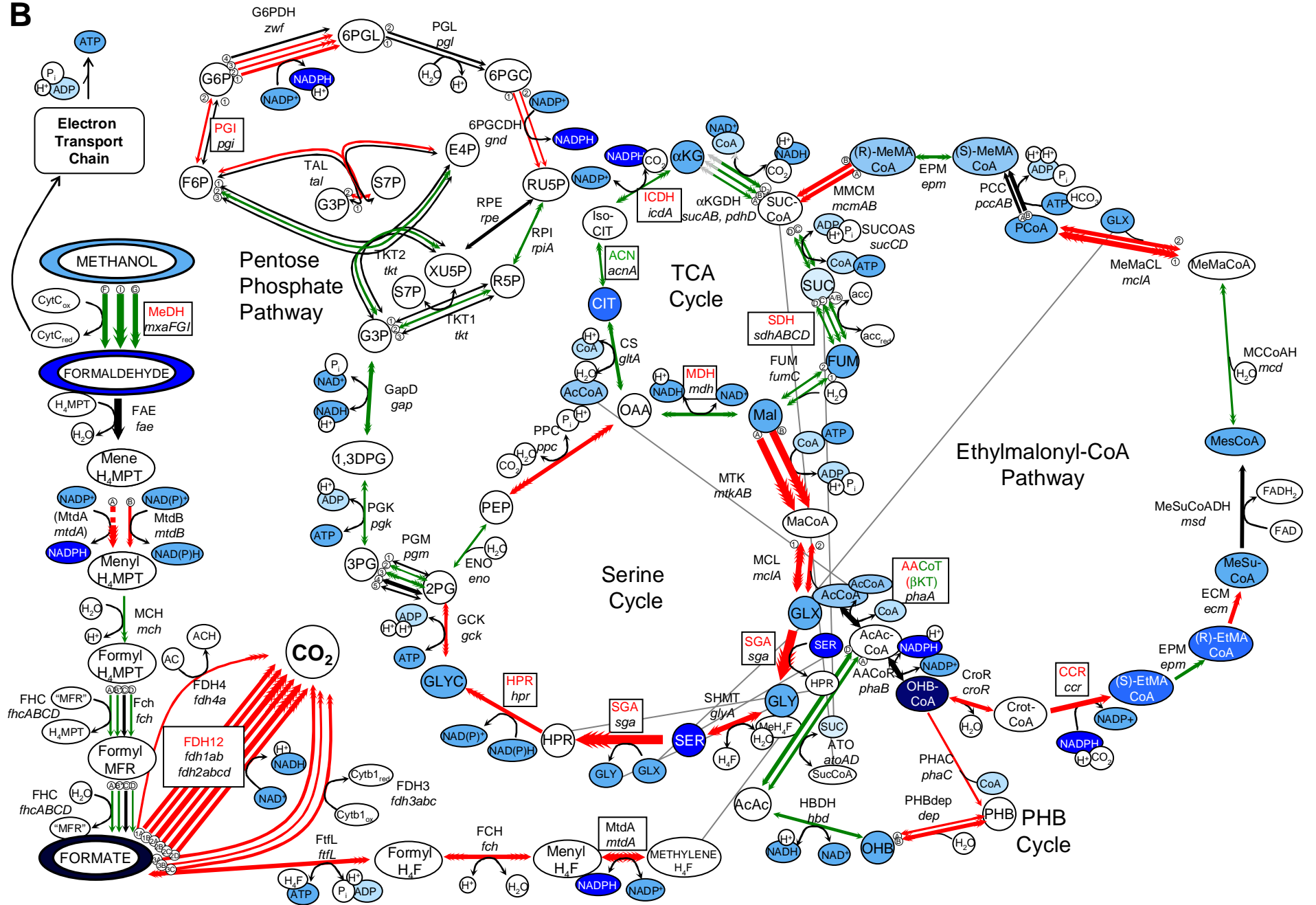
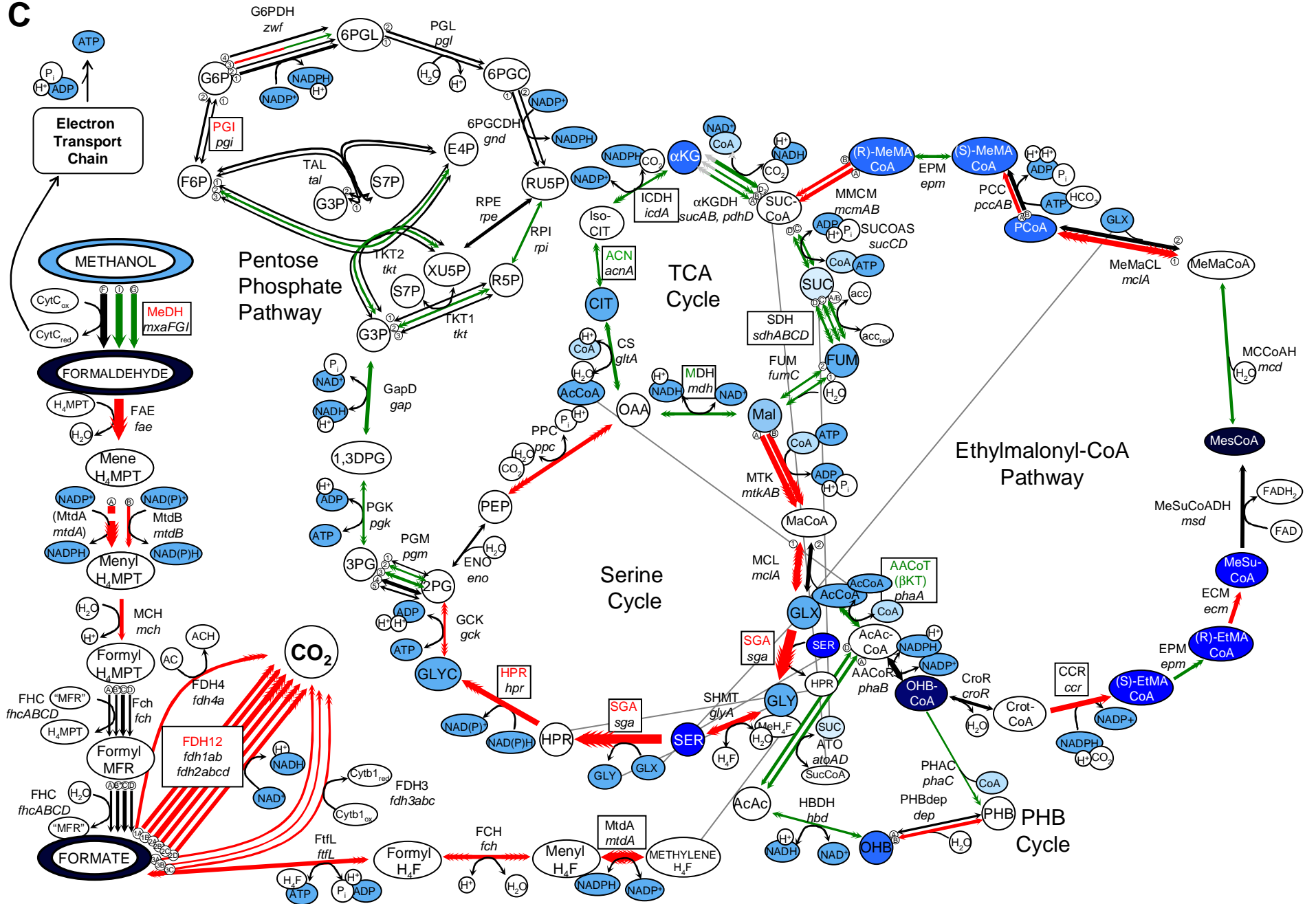
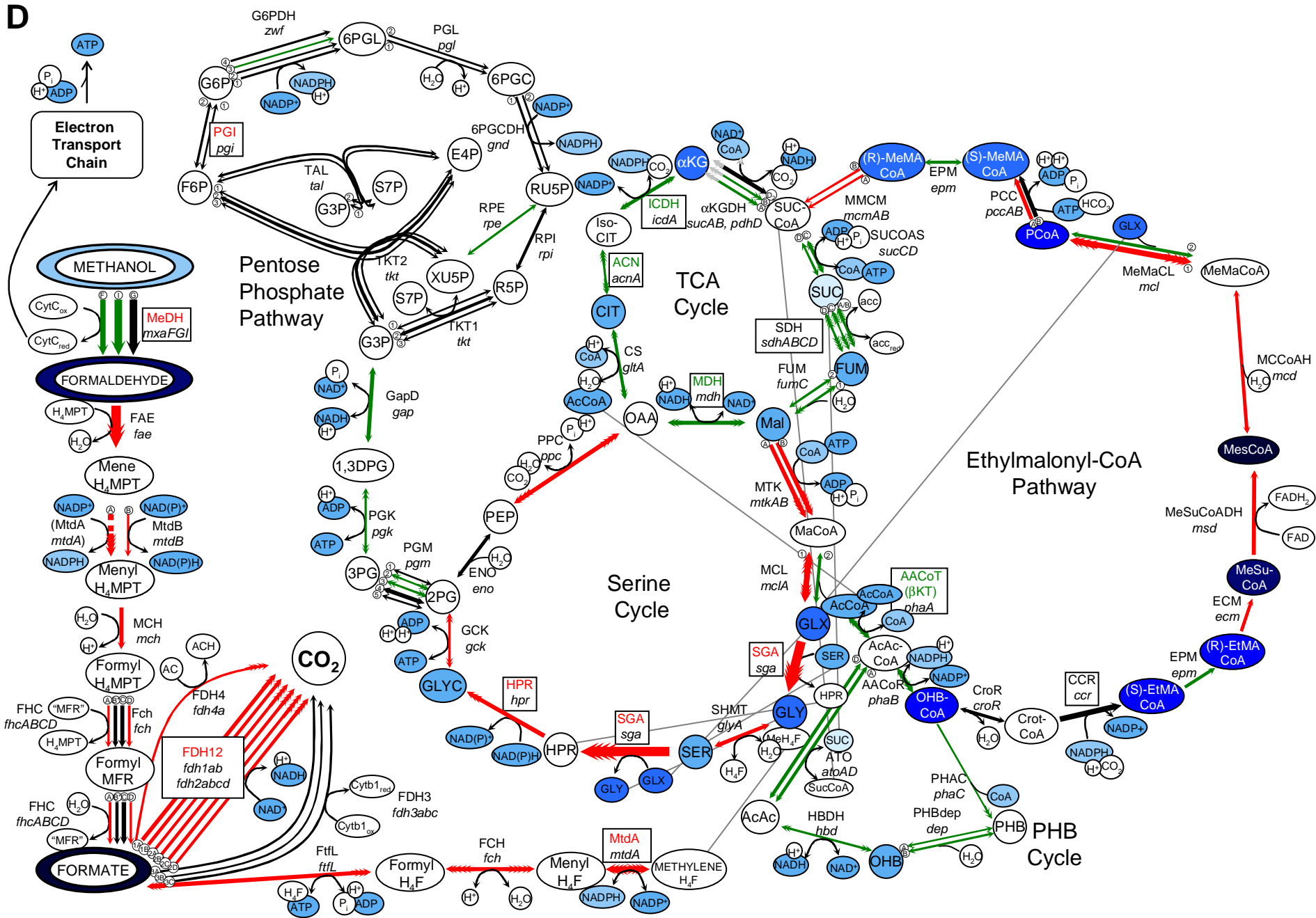


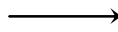







B

C

D

E ARROWS:




Thickness **Processed Signal Intensity**

| | |
|---|-----------------|
|  | 0-500 |
|  | 501-1000 |
|  | 1001-5000 |
|  | 5001-10,000 |
|  | 10,001-50,000 |
|  | 50,01-100,000 |
|  | 100,001-200,000 |
|  | >200,000 |

Arrowhead No. **Fold Change**










| | |
|---|---------|
| 1 | 1.5-1.9 |
| 2 | 2-4.9 |
| 3 | 5-9.9 |
| 4 | 10-19.9 |
| 5 | 20-49.9 |
| 6 | 50-99.9 |
| 7 | ≥100 |



Arrow Color **Description**

| | |
|---|-------------------------|
|  | Increase in expression |
|  | Decrease in expression |
|  | No change in expression |

METABOLITES:

Color **Fold Change/Description**

| | |
|---|------------------------|
|  | >10x increase |
|  | 5.1-10x increase |
|  | 2.1-5x increase |
|  | 1.5-2x increase |
|  | Concentration at T=0** |
|  | 1.5-2x decrease |
|  | 2.1-5x decrease |
|  | >5x decrease |
|  | Was not measured |

| | |
|---|---------------------------|
| Pattern | Measurement Type |
|  | Intracellular |
|  | Extracellular/supernatant |

Symbols:

- ① Number designates gene number if multiple genes per reaction
- Ⓐ Letter designates gene name or subunit label

**PATHWAY
KEY**

Supplementary figure S1. Pathway schematics depicting changes that occurred in measured metabolites, gene expression, and enzymatic activities for central metabolism after cells were transitioned from succinate to methanol growth. A boxed gene/protein name indicates the activity of this enzyme was measured. Red lettering for the protein designation indicates an increase in activity; green, decrease; black, no change. Metabolites appearing more than once are connected by gray lines. Diagrams are shown for the following time periods: (A) pre-methanol addition, time = 0 min; (B) initial response, time = 10-30 min post methanol addition; (C) just prior to/at the start of cell growth, time = 1-2 h post methanol addition; and (D) exponential cell growth, time = 3-6 h post methanol addition with (E) serving as a legend. Gene expression intensities are represented by arrow thickness while gene expression fold changes are depicted by arrowhead number. Abbreviations and reaction descriptions are included in Supplementary Table II along with gene expression intensities, LogRatios, fold changes and p-values. Mesoconyl-CoA, ethylmalonyl-CoA, methylsuccinyl-CoA were measured as free acids. **Color at T=0 represents the concentration before methanol was added for all metabolites except for methanol which was calculated as 50 mM for the initial T=0 value.