Expanded View Figures

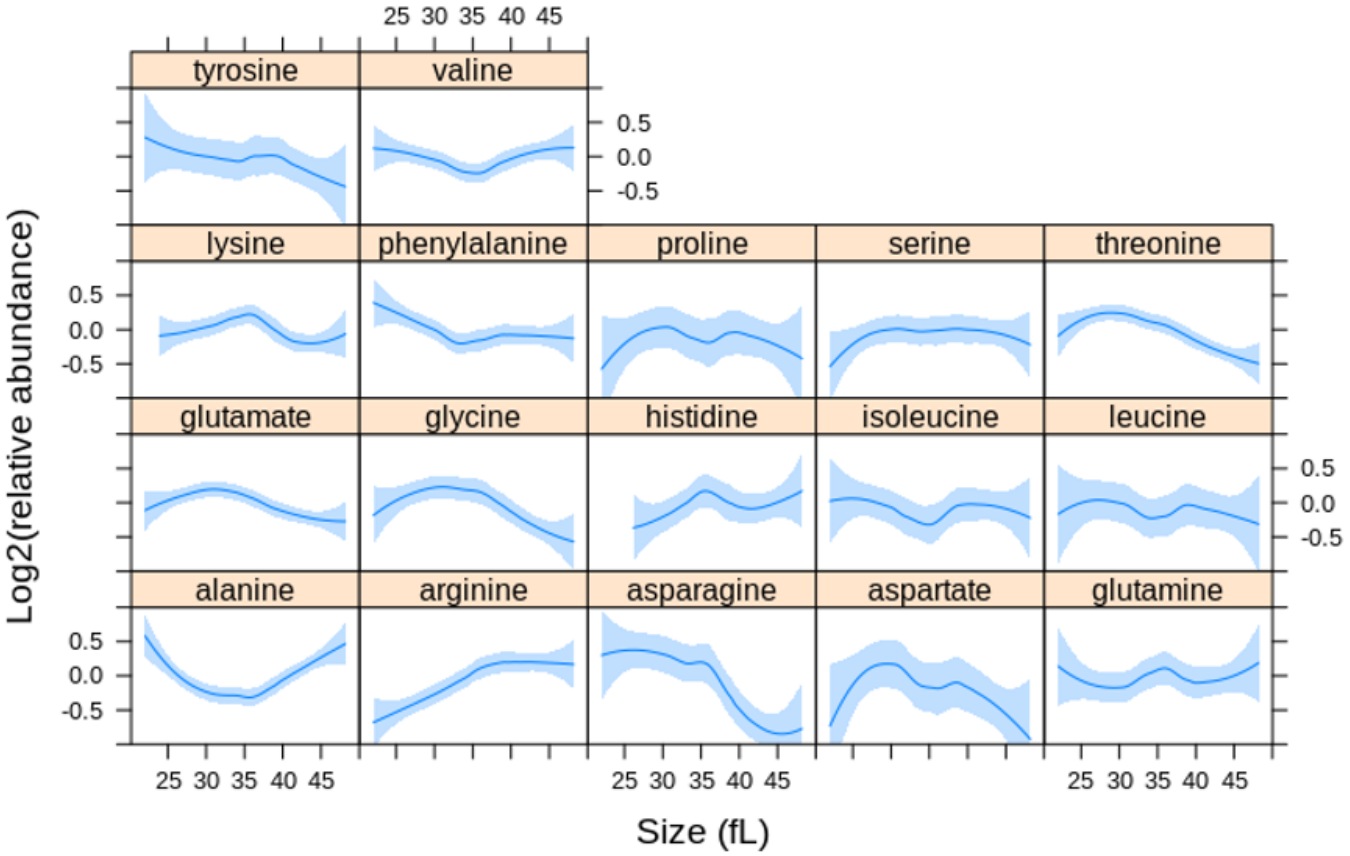

Figure EV1. Steady-state amino acid levels in the cell cycle.

Intracellular amino acid levels were measured as described in Materials and Methods from synchronous, elutriated cultures in SMM media. The relative abundance of each amino acid is on the *y*-axis.

Source data are available online for this figure.

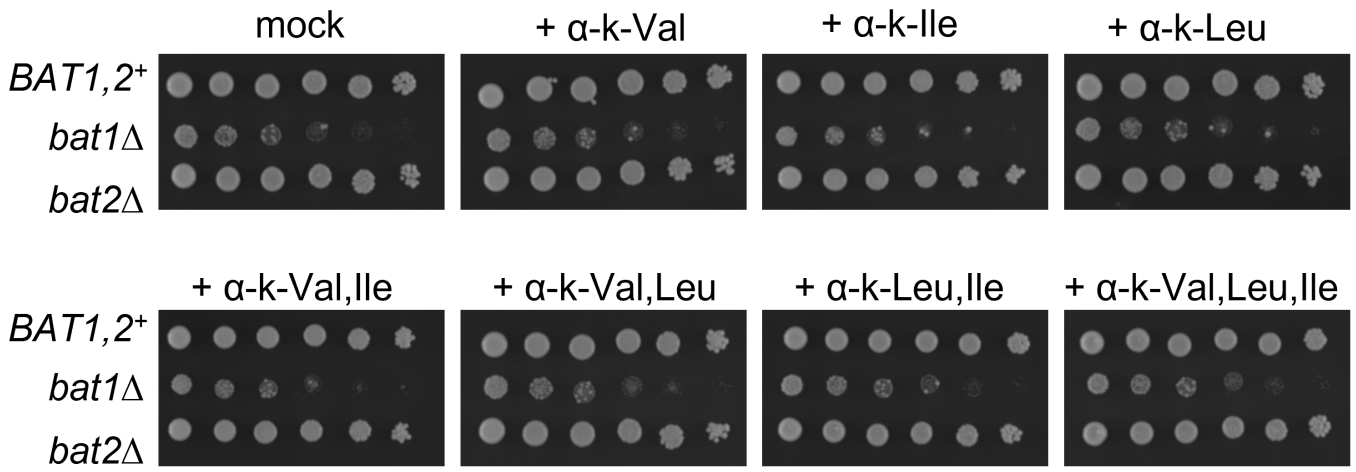

Figure EV2. Alpha-keto acid supplementation does not suppress the growth defect of bat1Δ mutants.

The experiment was done as in Fig 3. Exogenous alpha-keto acids were added at 1 mM final concentration, as indicated in each case.

Source data are available online for this figure.

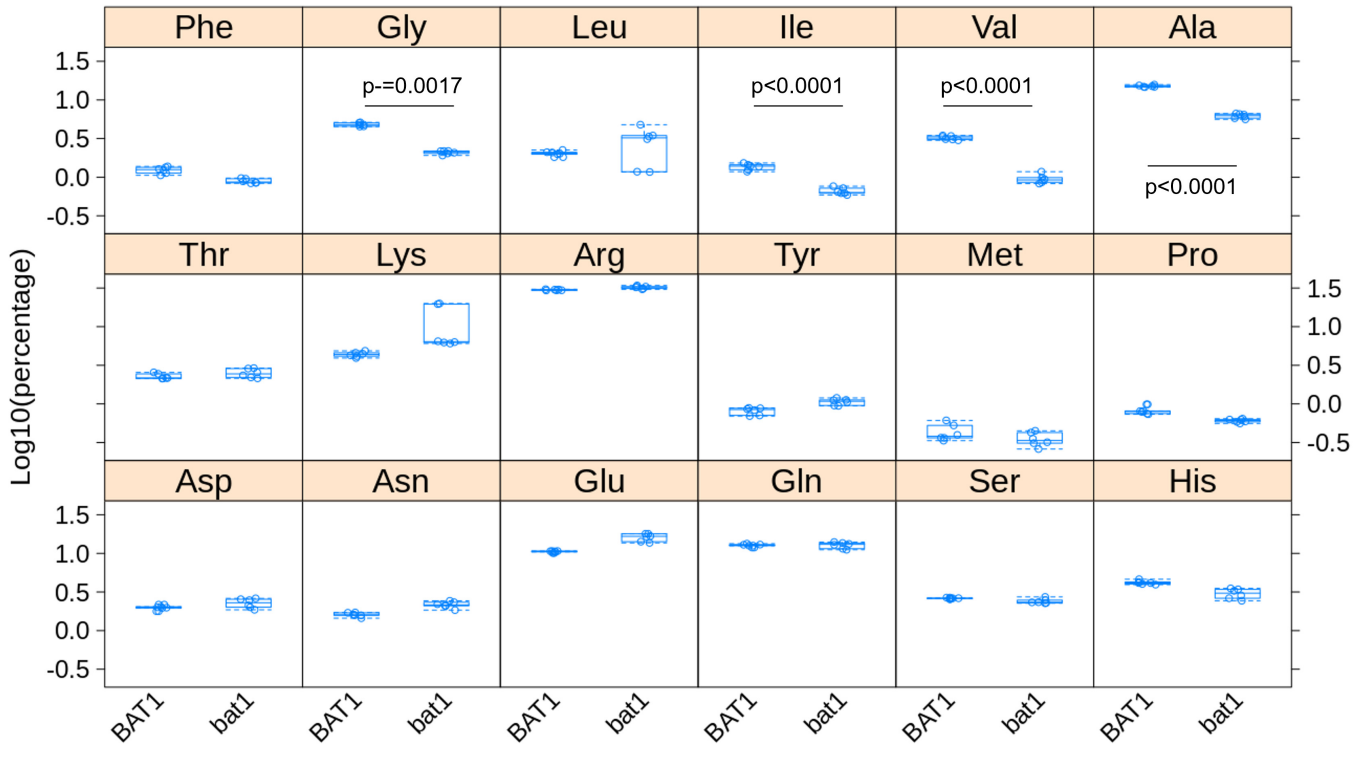

Figure EV3. Amino acid levels in *BAT1*$^+$ and *bat1Δ* cells.

Intracellular amino acid levels were measured as described in Materials and Methods and Fig EV1, from exponentially growing cultures in SMM media. The fraction of each amino acid is on the y-axis. The four amino acids (Gly, Ile, Val, Ala) with significantly altered fractional abundance (> 2-fold, $P < 0.05$; from six independent samples in each case) are indicated. The boxplot graphs were generated with R language functions. Each box is drawn from the first to the third quartile, with a horizontal line drawn in the middle to denote the median. The whiskers show the interquartile range (IQR), and they were drawn at 1.5xIQR. The replicates were all biological ones.

Source data are available online for this figure.

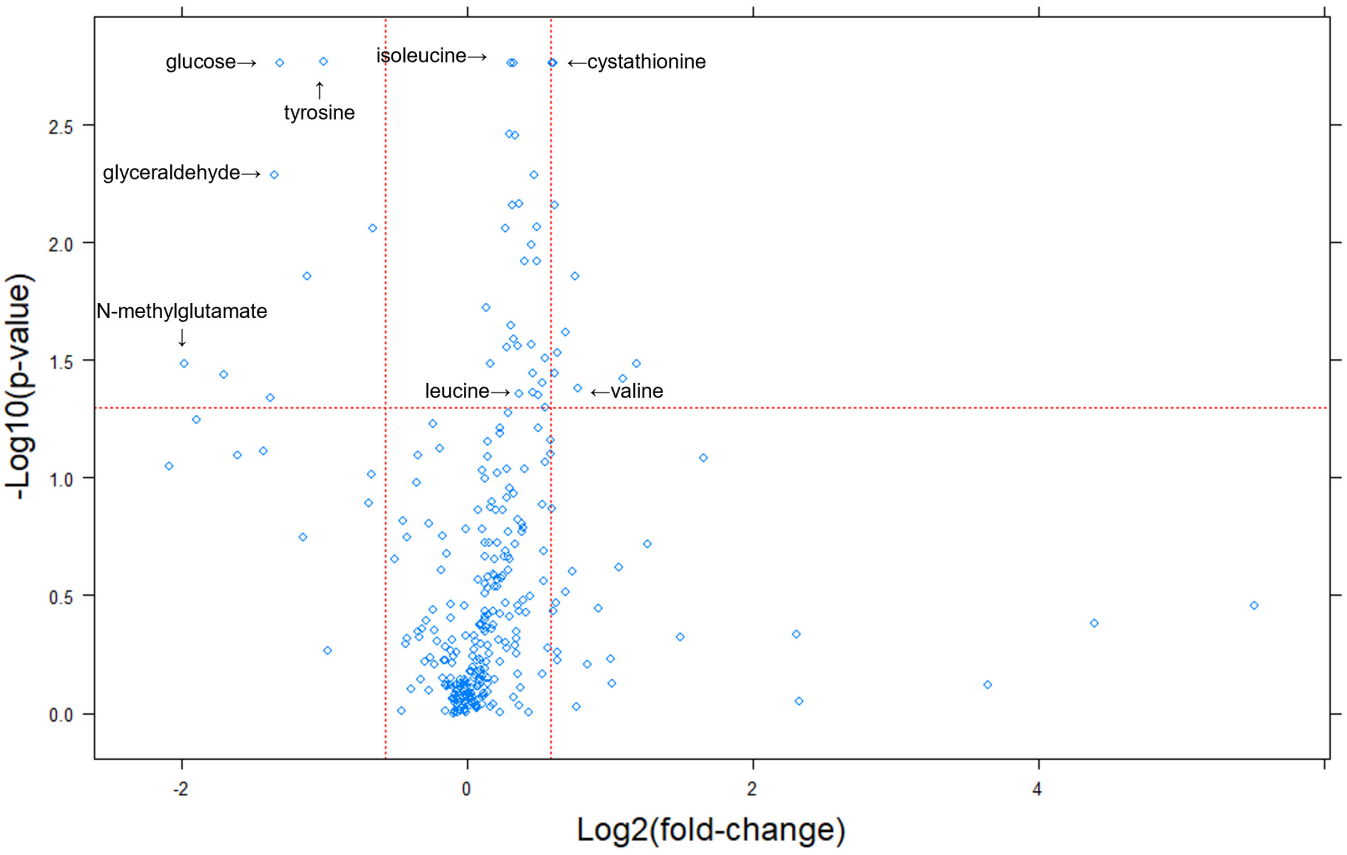

Figure EV4. Changes in primary and biogenic amine metabolites in cells lacking Bat1.

Metabolites whose levels changed were identified from the magnitude of the difference (*x*-axis; Log2-fold change in $BAT1^{+}$: bat1Δ cells) and statistical significance (y-axis), indicated by the red lines. The analytical and statistical approaches are described in Materials and Methods. The labels indicate selected metabolites.

Source data are available online for this figure.

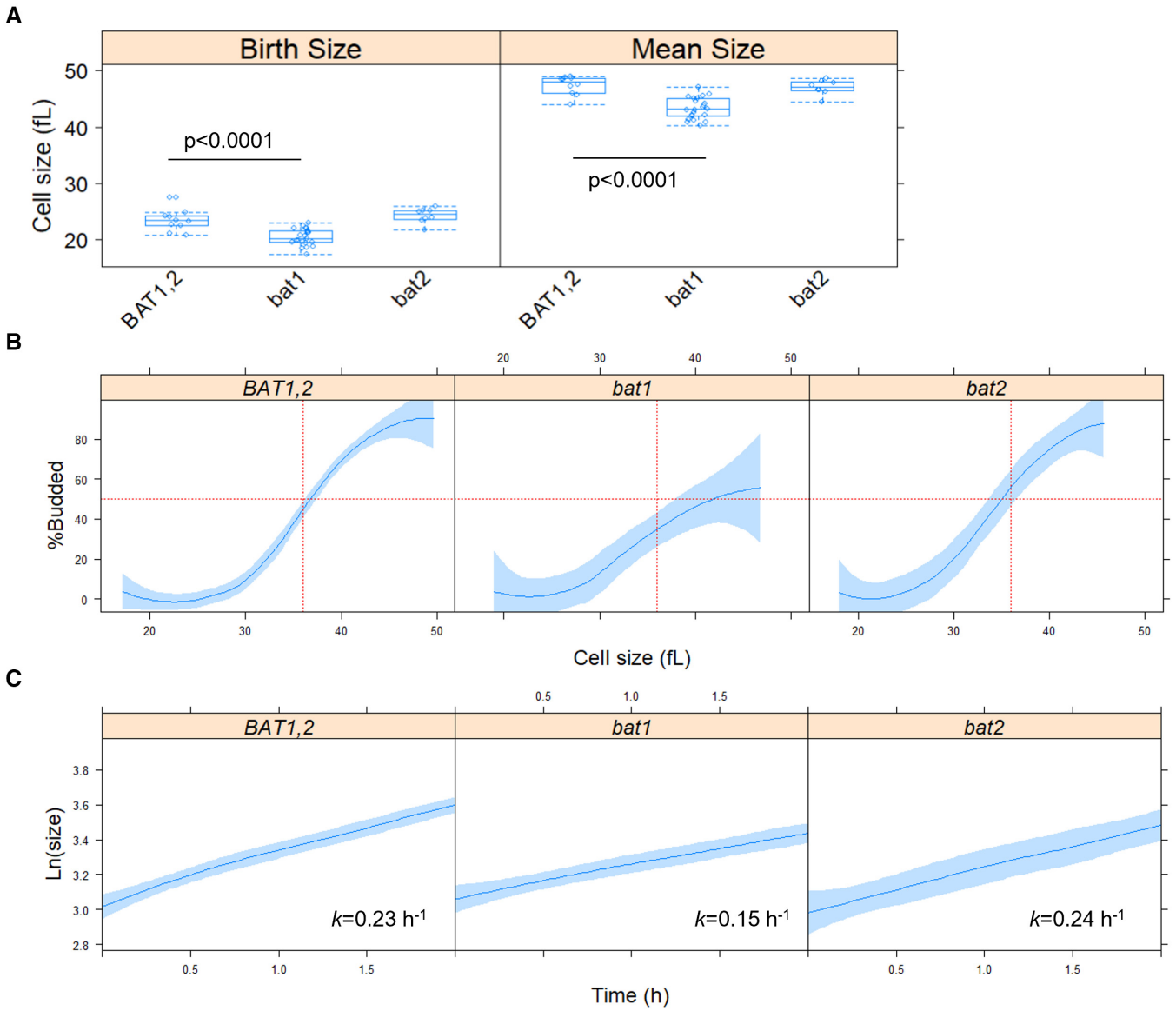

Figure EV5. Cells lacking Bat1 are smaller, increase in size slower, and are delayed in the G1 phase of the cell cycle.

A Boxplots showing the size of the cells (in fL). The measurements were taken from asynchronous cultures in synthetic minimal media (SMM) without amino acid supplementation. The boxplot graphs were generated with R language functions. Each box is drawn from the first to the third quartile, with a horizontal line drawn in the middle to denote the median. The whiskers show the interquartile range (IQR), and they were drawn at 1.5xIQR. The replicates were all biological ones.

B Plots of the percentage of budded cells (*y*-axis) as a function of size (*x*-axis). The measurements were from daughter cells of the indicated strains, obtained by centrifugal elutriation, progressing in the cell cycle in SMM medium. Loess curves and the std errors at a 0.95 level are shown.

C From the same experiments as in (B), the specific rate of the increase in size (*k*) was calculated, from the slope of the regression lines plotting the Ln-transformed cell size values (*y*-axis) against time (*x*-axis).

Source data are available online for this figure.