Standardizing LSC Proliferation for Precise Metabolic Normalization

Stem Cell; Leukemic SC, Metabolic Normalization	
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Standardization	X
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Viability	
Volume	

Zarou et al. (2024). Inhibition of mitochondrial folate metabolism drives differentiation through mTORC1 mediated purine sensing; Nature Communications, 15:1931. DOI: 10.1038/s41467-024-46141-8.

The Challenge:

Investigating the complex role of mitochondrial folate metabolism in leukemic stem cells (LSCs) required exceptionally precise and reliable cell counts to monitor proliferation, standardize experiments, and normalize data for metabolomic analysis.

CASY's Contribution:

The CASY automated cell counter was a foundational tool, providing the precise and reliable cell counts essential for accurate proliferation monitoring (e.g., generating growth curves over 24-hour intervals). It also enabled the standardization of initial cell counts for accurate comparison of treatment effects and facilitated normalization for subsequent metabolomic analysis.

Key Benefits to Researchers:

- **Accurate Proliferation Monitoring:** Generate precise growth curves and calculate proliferation rates with confidence.
- **Experiment Standardization:** Ensure consistent initial cell counts, enabling direct and reliable comparisons between different treatment conditions.
- **Enhanced Metabolomic Analysis:** Obtain accurate cell counts and total cell volume for robust normalization of metabolomic samples.
- **Underpins Data Reliability:** Even without generating novel biological data, CASY's precise measurements fundamentally strengthen the credibility and reproducibility of your functional data.

Utilizing CASY for Normalized Assessment of SHIN1-Induced Growth Retardation

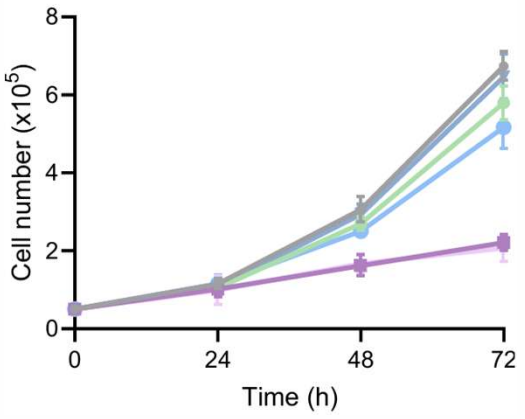

Fig.1 Folate metabolism is deregulated in LSCs and necessary for tumour formation in vivo. Growth (d) and proliferation rate (e) of *K562* untreated(UT)or cultured with 2.5 µM SHIN1 with or without 1 mM formate.