1	Supporting Information		
2	Comprehensive Isotopic Targeted Mass Spectrometry (CIT-MS): Reliable Metabolic Flux		
3	Analysis with Broad Coverage		
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- 30 Separate Excel Table S1. The in-house metabolite library containing 310 unlabeled chemical
- 31 standards and their LC-MS/MS parameters.
- 32 **Separate Excel Table S2.** All isotopic MRM transitions in CIT-MS.
- 33 **Page S-3: Table S3.** Linear regression analysis of the data in **Figure 2**.
- 34 **Page S-4: Figure S1**. Pathway view showing only 179 (red dots) of the 310 metabolites in the
- 35 detection panel.
- 36 **Page S-5: Figure S2.** Enriched carbohydrate metabolites from U-¹³C₆-glucose that were detected
- 37 by CIT-MS in a steady state study using Myc-On and Myc-Off Tet21N cells.

38 **Page S-6: Figure S3.** Enriched TCA cycle metabolites from U-¹³C₆-glucose that were detected

- 39 by CIT-MS in a steady state study using Myc-On and Myc-Off Tet21N cells.
- 40 **Page S-7: Figure S4.** Enriched amino acid metabolites from U-¹³C₆-glucose that were detected
- 41 by CIT-MS in a steady state study using Myc-On and Myc-Off Tet21N cells.
- 42 Page S-8: Figure S5. Exponential fitting of the time-course data of nucleotide metabolites for the
- 43 comparison of Myc-On and Myc-Off Tet21N cells under the pseudosteady state post U-¹³C₆-
- 44 glucose labeling.
- 45 **Page S-9: Figure S6.** Exponential fitting of the time-course data of carbohydrate metabolites for
- the comparison of Myc-On and Myc-Off Tet21N cells under the pseudosteady state post U-¹³C₆-
- 47 glucose labeling.
- 48 Page S-10: Figure S7. Exponential fitting of the time-course data of TCA cycle metabolites for
- 49 the comparison of Myc-On and Myc-Off Tet21N cells under the pseudosteady state post $U^{-13}C_{6^-}$
- 50 glucose labeling.
- 51 Page S-11: Figure S8. Exponential fitting of the time-course data of amino acid metabolites for
- 52 the comparison of Myc-On and Myc-Off Tet21N cells under the pseudosteady state post U-¹³C₆-
- 53 glucose labeling.

Compound	Linear Equation	R ²
G	Y=1.0025X-0.1388	0.9987
1- ¹³ C-G	Y=0.9915X-0.5353	0.9996
1,6- ¹³ C ₂ -G	Y=1.0014X-0.6499	0.9995
U- ¹³ C ₆ -G	Y=0.9378X+1.7373	0.9981

 Table S3. Linear regression analysis of the data in Figure 2.

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- 58 **Figure S1**. Pathway view showing only 179 (red dots) of the 310 metabolites in the detection
- 59 panel.
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Figure S2. Enriched carbohydrate metabolites from U-¹³C₆-glucose that were detected by CIT-

- 65 MS in a steady state study using Myc-On and Myc-Off Tet21N cells.



Figure S3. Enriched TCA cycle metabolites from U-¹³C₆-glucose that were detected by CIT-MS



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- 74 **Figure S4.** Enriched amino acid metabolites from U-¹³C₆-glucose that were detected by CIT-MS
- in a steady state study using Myc-On and Myc-Off Tet21N cells.

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Figure S5. Exponential fitting of the time-course data of nucleotide metabolites for the comparison





Figure S6. Exponential fitting of the time-course data of carbohydrate metabolites for the comparison of Myc-On and Myc-Off Tet21N cells under the pseudosteady state post $U^{-13}C_{6^-}$ glucose labeling.



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86 Figure S7. Exponential fitting of the time-course data of TCA cycle metabolites for the comparison

- 87 of Myc-On and Myc-Off Tet21N cells under the pseudosteady state post $U^{-13}C_6$ -glucose labeling.
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Figure S8. Exponential fitting of the time-course data of amino acid metabolites for the comparison of Myc-On and Myc-Off Tet21N cells under the pseudosteady state post $U^{-13}C_{6^{-1}}$ glucose labeling.