

Table	SILAC-L	SILAC-M	SILAC-H	Total sites	Decoy sites	FDR
S2	BY4742 Lys ⁰ EP		BY4742 Lys ⁸ SP	2,784	10	0.36%
S3	BY4742 Lys ⁰ EP		BY4742 Lys ⁸ SP	3,327 Proteins	1	0.03%
S4	BY4742 Lys ⁰ EP		BY4742 Lys ⁸ SP	6,260 Phospho.	7	0.11%
S5	BY4742 Lys ⁰ EP	BY4742 Lys ⁴ GA + glucose	BY4742 Lys ⁸ GA + 2DG	1,484	5	0.34%
S6	BY4742 Lys ⁰ EP		<i>pda1</i> Δ Lys ⁸ EP	1,254	3	0.24%
S6	BY4742 Lys ⁰ EP		<i>cit1</i> Δ Lys ⁸ EP	1,254	3	0.24%
S7	BY4742 Lys ⁰ EP	BY4742 Lys ⁴ GA	<i>pda1</i> Δ Lys ⁸ GA	1,988	8	0.40%
S7	BY4742 Lys ⁰ EP	BY4742 Lys ⁴ GA	<i>cit1</i> Δ Lys ⁸ GA	1,988	8	0.40%
S8	BY4742 Lys ⁰ EP		BY4742 Lys ⁸ GA + 2% Glu. or 2% Ace.	2,139	8	0.37%
S9	BY4742 Lys ⁰ EP		BY4742 Lys ⁸ EP	9,666	29	0.30%

Table S1. Quantitative MS experiments performed in this study. The yeast strain used and growth phase (exponential phase (EP), stationary phase (SP), or growth-arrested (GA)), SILAC labeling scheme (L=light, M=medium, H=heavy), total sites identified, and the number of sites identified from a reversed sequence, decoy database is shown. The estimated false discovery rate (FDR) is calculated from the frequency of decoy sites identified in the data set (Elias & Gygi, 2007).