Supplementary materials

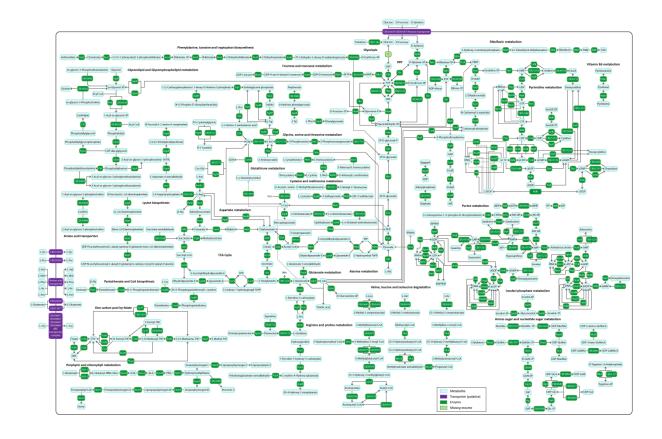
Figure S1. Complete metabolic pathway map of *C. burnetii*. Pale blue boxes indicate metabolites. Dark green boxes indicate existing enzymes while pale green boxes indicate missing enzymes based on genome annotation data in KEGG. Purple denotes putative transporters. Metabolite abbreviations are listed in Table S1.

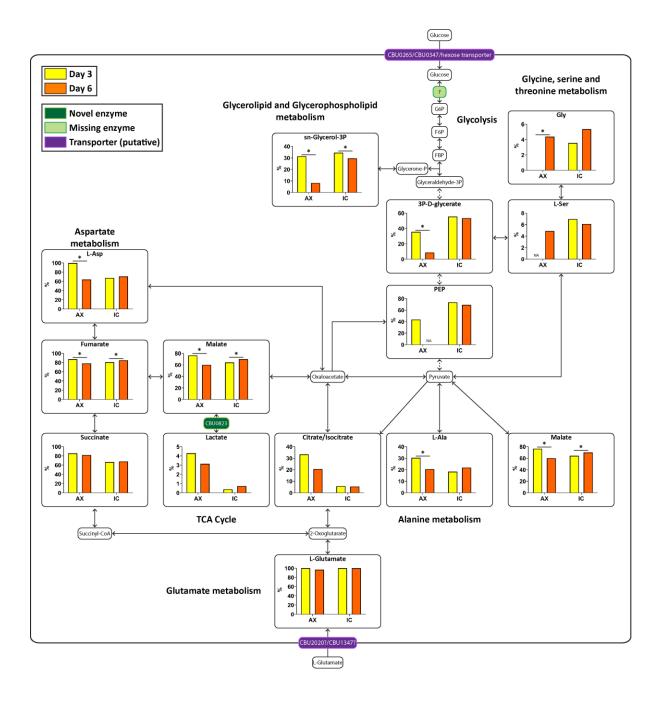
Figure S2. Day 3 vs day 6 comparisons of [13 C]glutamate labeled *C. burnetii*. Metabolic pathway map of *C. burnetii* comparing 13 C-label incorporation at day 3 and day 6 within the same culture condition after 10 minute incubation with [13 C]glutamate. Metabolites detected on the GC/MS as having incorporated 13 C-label are shown in larger boxes, with percentage labeling in bar graphs. Yellow bars indicate day 3 samples while orange bars indicate day 6 samples. Pale green boxes indicate missing enzymes based on genome annotation data in KEGG. Dotted arrows indicate pathways which have been abbreviated. * = p<0.05. NA indicates metabolites which were unable to be detected in a given condition. Metabolite abbreviations are listed in Table S1.

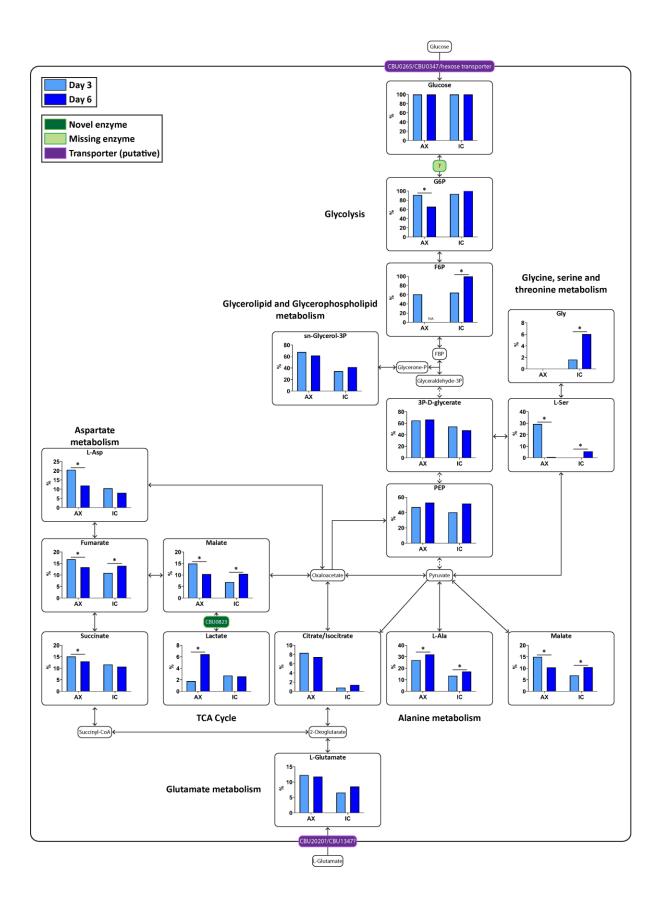
Figure S3. Day 3 vs day 6 comparisons of [13 C]glucose labeled *C. burnetii*. Metabolic pathway map of *C. burnetii* comparing 13 C-label incorporation at day 3 and day 6 within the same culture condition after 10 minute incubation with [13 C]glucose. Metabolites detected on the GC/MS as having incorporated 13 C label are shown in larger boxes, with percentage labeling in bar graphs. Light blue bars indicate day 3 samples while dark blue bars indicate day 6 samples. Pale green boxes indicate missing enzymes based on genome annotation data in KEGG. Dotted arrows indicate pathways which have been abbreviated. * = p<0.05. NA

indicates metabolites which were unable to be detected in a given condition. Metabolite abbreviations are listed in Table S1.

Figure S4. Transposon insertion sites and confirmation of transposon mutant complementation. Schematic of transposon insertions sites in 0265::Tn and 0347::Tn mutants (A). Red arrows indicate insertion sites for *cbu0265* (light blue) and *cbu0347* (yellow). Direction of internal arrows indicate direction of open reading frame. Numbers indicate base pairs within *C. burnetii* RSA 439 Phase II genome. Western blot showing expression of 3xFLAG-0265 or 3xFLAG-0347 in *C. burnetii* strains (B). RpoA used as loading control.







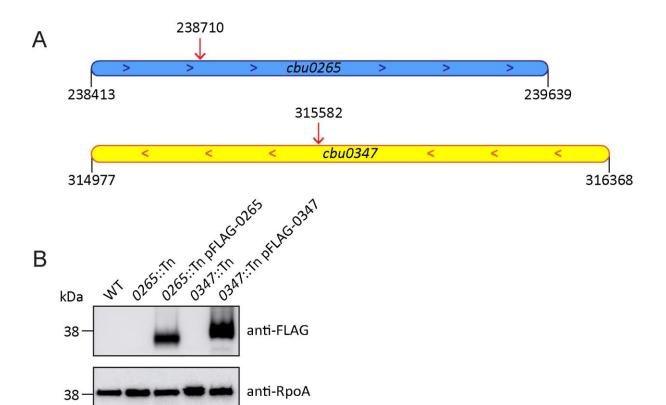


Table S1. Metabolite abbreviations.

Abbroriotion	Matabalita
Abbreviation P	Metabolite
	Phosphate
1P	1-phosphate
2P	2-phosphate
3P	3-phosphate
4P	4-phosphate
5P	5-phosphate
6P	6-phosphate
G6P	D-Glucose 6-phoshate
F6P	D-Fructose 6-phosphate
FBP	D-Fructose 1,6-bisphosphate
PEP	Phophoenolpyruvate
TPP	Thiamin diphosphate
ThPP	Thiamin diphosphate
R5P	D-Ribose 5-phosphate
PRPP	5-phospho-D-ribose 1-diphosphate
M1P	D-Mannose 1-phosphate
M6P	D-Mannose 6-phosphate
UMP	Uridine 5'-monophosphate
UDP	Uridine 5'-diphosphate
UTP	Uridine 5'-triphosphate
CMP	Cytidine 5'-monophosphate
CDP	Cytidine 5'-diphosphate
CTP	Cytidine 5'-triphosphate
dCMP	Deoxycytidine 5'-monophosphate
dCDP	Deoxycytidine 5'-diphosphate
dCTP	Deoxycytidine 5'-triphosphate
dUMP	Deoxyuridine 5'-monophosphate
dUDP	Deoxyuridine 5'-diphosphate
dUTP	Deoxyuridine 5'-triphosphate
dTMP	Deoxythymidine 5'-monophosphate
dTDP	Deoxythymidine 5'-diphosphate
hm5dCDP	2'-Deoxy-5-hydroxymethylcytidine-5'-diphosphate
hm5dCTP	2'-Deoxy-5-hydroxymethylcytidine-5'-triphosphate
GAR	5'-Phosphoribosylgycinamide
FGAR	5'-Phosphoribosyl-N-formylglycinamide
FGAM	5'-Phosphoribosylformylglycinamidine
AIR	Aminoimidazole ribotide
AppppA	P1,P4-Bis(5'-adenosyl)tetraphosphate
AppppA AMP	Adenosine 5'-monophosphate
ADP	Adenosine 5'-diphosphate
ATP	
	Adenosine 5'-triphosphate
IMP	Inosine 5'-monophosphate
IDP	Inosine 5'-diphosphate
ITP	Inosine 5'-triphosphate
XMP	Xanthosine 5'-monophosphate
XTP	Xanthosine 5'-triphosphate
GMP	Guanosine 5'-monophosphate

GDP Guanosine 5'-diphosphate GTP Guanosine 5'-triphosphate

dAMP Deoxydenosine 5'-monophosphate
dADP Deoxyadenosine 5'-diphosphate
dIMP Deoxyinosine 5'-monophosphate
dIDP Deoxyinosine 5'-diphosphate
dITP Deoxyinosine 5'-triphosphate

dGMP Deoxyguanosine 5'-monophosphate dGDP Deoxyguanosine 5'-diphosphate dGTP Deoxyguanosine 5'-triphosphate

FAICAR 5'-Phosphoribosyl-5-formamido-4-imidazolecarboxamide AICAR 5'-Phosphoribosyl-5-amino-4-imidazolecarboxamide

SAICAR 5'-Phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole CAIR 1-(5-Phospho-D-ribosyl)-5-amino-4-imidazolecarboxylate

ppGpp Guanosine 3',5'-bis(diphosphate)

pppGpp Guanosine 3'-diphosphate 5'-triphosphate

L-Ala L-Alanine L-Aspartate L-Asp L-Asparagine L-Asn L-Cysteine L-Cys L-Glu L-Glutamine L-Ile L-Isoleucine L-Leu L-Leucine L-Methionine L-Met L-Phe L-Phenylalanine

 $\begin{array}{cccc} L\text{-Pro} & & L\text{-Proline} \\ L\text{-Ser} & & L\text{-Serine} \\ L\text{-Thr} & & L\text{-Threonine} \\ L\text{-Trp} & & L\text{-Tryptophan} \\ L\text{-Tyr} & & L\text{-Tyrosine} \\ L\text{-Val} & & L\text{-Valine} \\ \beta\text{-Ala} & & \text{Beta-Alanine} \end{array}$

HTPA (2S,4S)-4-Hydroxy-2,3,4,5-tetrahydrodipicolinate

Gly Glycine

Cys-Gly L-Cysteinylglycine

GSH Glutathione

MurNAc N-Acetylmuramate
GlcNAc N-Acetyl-D-glucosamine
GlcNAcA N-Acetyl-D-glucosaminuronate

GlcN D-Glucosamine
Glc D-Glucose
GlcA D-Glucuronate
Gal D-Galactose
GalA D-Galacturonate

GalNAc N-Acetyl-D-galactosamine
GalNAcA N-Acetyl-D-galactosaminuronate

ManNAc N-Acetyl-D-mannosamine FMN Riboflavin-5-phosphate FAD Flavin adenine dinucleotide

DHF Dihydrofolate

THF	Tetrahydrofolate	
GSA	Glutamate-1-semialdehyde	
ALA	5-Aminolevulinate	
PBG	Porphobilinogen	

Table S2. ¹³C-label incorporation values in mock or uninfected THP-1 cell samples.

Metabolite	Percentage label incorporation	
[¹³ C]glutamate		
Succinate	18.53%	
Lactate	0.92%	
[¹³ C]glucose		
Succinate	12.43%	
Lactate	0.53%	

Metabolites not listed did not have detectable label incorporation on GC/MS