

Table S1: Abundant proteins expressed by *S. enterica* 14028S at 24 h during growth in germinating alfalfa exudate

Protein name	GenBank accession	Gene name
METABOLIC		
Carbon		
Glycolysis/gluconeogenesis		
pyruvate dehydrogenase subunit E1	ACY86719.1	<i>aceE</i>
dihydrolipoamide dehydrogenase	ACY86721.1	<i>lpdA</i>
glucose-1-phosphatase/inositol phosphatase	ACY87762.1	<i>agp</i>
phosphopyruvate hydratase	ACY89970.1	<i>eno</i>
fructose-bisphosphate aldolase	ACY90115.1	<i>fba</i>
fructose-bisphosphate aldolase	ACY89085.1	<i>fbaB</i>
glyceraldehyde-3-phosphate dehydrogenase	ACY88044.1	<i>gapA</i>
phosphoglyceromutase	ACY87394.1	<i>gpmA</i>
glycogen synthase	ACY90644.1	<i>glgA</i>
glucose-1-phosphate adenylyltransferase	ACY90645.1	<i>glgC</i>
phosphoenolpyruvate carboxykinase	ACY90605.1	<i>pckA</i>
6-phosphofructokinase 2	ACY88089.1	<i>pfkB</i>
phosphoglycerate kinase	ACY90116.1	<i>pgk</i>
pyruvate kinase	ACY88754.1	<i>pykA</i>
pyruvate kinase	ACY88150.1	<i>pykF</i>
triosephosphate isomerase	ACY91263.1	<i>tpiA</i>
Pyruvate metabolism		
acetate kinase	ACY89321.1	<i>ackA</i>
acetyl-CoA synthetase	ACY91480.1	<i>acs</i>
bifunctional acetaldehyde-CoA/alcohol dehydrogenase	ACY88579.1	<i>adhE</i>
alcohol dehydrogenase	ACY88362.1	<i>adhP</i>
pyruvate formate lyase	ACY87593.1	<i>pfIB</i>
phosphate acetyltransferase	ACY89322.1	<i>pta</i>
Pentose phosphate pathway		
6-phosphogluconate dehydrogenase	ACY89020.1	<i>gnd</i>
ribose-5-phosphate isomerase A	ACY90108.1	<i>rpiA</i>
transaldolase A	ACY89465.1	<i>talA</i>
transaldolase B	ACY86544.1	<i>talB</i>
transketolase	ACY90124.1	<i>tktA</i>
transketolase	ACY89466.1	<i>tktB</i>
6-phosphogluconolactonase	ACY87409.1	<i>ybhE</i>
Tricarboxylic acid cycle/glyoxylate shunt		
isocitrate lyase	ACY91371.1	<i>aceA</i>
aconitate hydratase	ACY88538.1	<i>acnA</i>

bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	ACY86725.1	<i>acnB</i>
fumarase A	ACY88244.1	<i>fumA</i>
citrate synthase	ACY87353.1	<i>gltA</i>
isocitrate dehydrogenase	ACY87902.1	<i>icdA</i>
malate dehydrogenase	ACY90448.1	<i>mdh</i>
alpha-ketoglutarate decarboxylase	ACY87359.1	<i>sucA</i>
dihydrolipoamide acetyltransferase	ACY87360.1	<i>sucB</i>
succinyl-CoA synthetase subunit beta	ACY87361.1	<i>sucC</i>

Alternate carbon metabolism

aldehyde dehydrogenase B	ACY90822.1	<i>aldB</i>
phosphopentomutase	ACY91817.1	<i>deoB</i>
deoxyribose-phosphate aldolase	ACY91815.1	<i>deoC</i>
2,5-diketo-D-gluconate reductase A	ACY90235.1	<i>dkgA</i>
UDP-galactose-4-epimerase	ACY87399.1	<i>galE</i>
galactokinase	ACY87397.1	<i>galK</i>
aldose 1-epimerase	ACY87396.1	<i>galM</i>
galactose-1-phosphate uridylyltransferase	ACY87398.1	<i>galT</i>
alpha-galactosidase	ACY91510.1	<i>meIA</i>
glucosamine-6-phosphate deaminase	ACY87300.1	<i>nagB</i>
phosphoglucomutase	ACY87319.1	<i>pgm</i>
2-methylisocitrate lyase	ACY86951.1	<i>prpB</i>
2-methylisocitrate dehydratase	ACY86953.1	<i>prpD</i>
putative D-mannonate oxidoreductase	ACY90199.1	<i>STM14_3796</i>
putative dehydrogenase	ACY91652.1	<i>STM14_5317</i>
trehalase	ACY88635.1	<i>treA</i>

Energy

F0F1 ATP synthase subunit epsilon	ACY91036.1	<i>atpC</i>
F0F1 ATP synthase subunit beta	ACY91037.1	<i>atpD</i>
F0F1 ATP synthase subunit gamma	ACY91038.1	<i>atpG</i>
F0F1 ATP synthase subunit alpha	ACY91039.1	<i>atpA</i>
F0F1 ATP synthase subunit delta	ACY91040.1	<i>atpH</i>
bifunctional NADH:ubiquinone oxidoreductase subunit C/D	ACY89306.1	<i>nuoC</i>
succinate dehydrogenase flavoprotein subunit	ACY87357.1	<i>sdhA</i>

Amino acid

argininosuccinate synthase	ACY90371.1	<i>argG</i>
L-asparaginase II	ACY90156.1	<i>ansB</i>
phospho-2-dehydro-3-deoxyheptonate aldolase	ACY87383.1	<i>aroG</i>
aromatic amino acid aminotransferase	ACY87622.1	<i>aspC</i>
cysteine synthase A	ACY89417.1	<i>cysK</i>
2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	ACY86787.1	<i>dapD</i>

succinate-semialdehyde dehydrogenase I	ACY89786.1	<i>gabD</i>
glycine cleavage system protein H	ACY90095.1	<i>gcvH</i>
glutamate dehydrogenase	ACY88056.1	<i>gdhA</i>
glutamine synthetase	ACY91177.1	<i>glnA</i>
serine hydroxymethyltransferase	ACY89564.1	<i>glyA</i>
ketol-acid reductoisomerase	ACY91075.1	<i>ilvC</i>
dihydroxy-acid dehydratase	ACY91070.1	<i>ilvD</i>
branched-chain amino acid aminotransferase	ACY91069.1	<i>ilvE</i>
isopropylmalate isomerase large subunit	ACY86669.1	<i>leuC</i>
S-ribosylhomocysteinase	ACY89821.1	<i>luxS</i>
5-methyltetrahydropteroyltriglutamate— homocysteine methyltransferase	ACY91132.1	<i>metE</i>
methionine sulfoxide reductase A	ACY91629.1	<i>msrA</i>
D-3-phosphoglycerate dehydrogenase	ACY90106.1	<i>serA</i>
phosphoserine aminotransferase	ACY87599.1	<i>serC</i>
agmatinase	ACY90127.1	<i>speB</i>
threonine synthase	ACY86541.1	<i>thrC</i>
tRNA		
glutamyl-tRNA synthetase	ACY87303.1	<i>glnS</i>
lysyl-tRNA synthetase	ACY90079.1	<i>lysS</i>
prolyl-tRNA synthetase	ACY86817.1	<i>proS</i>
seryl-tRNA synthetase	ACY87582.1	<i>serS</i>
tyrosyl-tRNA synthetase	ACY88223.1	<i>tyrS</i>
Nucleotide		
adenylate kinase	ACY87091.1	<i>adk</i>
bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/ 3'-nucleotidase	ACY91622.1	<i>cpdB</i>
inositol-5-monophosphate dehydrogenase	ACY89508.1	<i>guaB</i>
nucleoside diphosphate kinase	ACY89529.1	<i>ndk</i>
adenylosuccinate synthetase	ACY91583.1	<i>purA</i>
uridine phosphorylase	ACY91137.1	<i>udp</i>
Cofactors		
putative uroporphyrinogen III C-methyltransferase	ACY91099.1	<i>hemX</i>
cysteine desulfurase	ACY89549.1	<i>nifS</i>
riboflavin synthase subunit beta	ACY87013.1	<i>ribH</i>
Fatty acid/lipid		
3-ketoacyl-CoA thiolase	ACY91151.1	<i>fadA</i>
3-oxoacyl-(acyl carrier protein) synthase I	ACY89366.1	<i>fabB</i>
3-ketoacyl-(acyl-carrier-protein) reductase	ACY87855.1	<i>fabG</i>
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	ACY89525.1	<i>ispG</i>

Transport

lysine/arginine/ornithine transport protein	ACY89340.1	<i>argT</i>
arginine transport system	ACY87537.1	<i>artI</i>
cystine transporter subunit	ACY88825.1	<i>fliY</i>
glutamine ABC transporter periplasmic protein	ACY87461.1	<i>glnH</i>
glutamate and aspartate transporter subunit	ACY87284.1	<i>gltI</i>
histidine transport protein	ACY89339.1	<i>hisJ</i>
high-affinity branched-chain amino acid transporter	ACY90682.1	<i>livJ</i>
dipeptide transport protein	ACY90762.1	<i>dppA</i>
vitamin B12/cobalamin outer membrane transporter	ACY91321.1	<i>btuB</i>
glucose-specific PTS system component	ACY89423.1	<i>crr</i>
bifunctional fructose-specific PTS IIA/HPr protein	ACY89166.1	<i>fruF</i>
maltoporin	ACY91426.1	<i>lamB</i>
maltose ABC transporter periplasmic protein	ACY91424.1	<i>malE</i>
mannose-specific enzyme IIAB	ACY88675.1	<i>manX</i>
galactose transport protein	ACY89141.1	<i>mgIB</i>
outer membrane porin protein C	ACY89238.1	<i>ompC</i>
outer membrane protein F	ACY87624.1	<i>ompF</i>
PTS system phosphohistidinoprotein-hexose phosphotransferase	ACY89421.1	<i>ptsH</i>
phosphoenolpyruvate-protein phosphotransferase	ACY89422.1	<i>ptsI</i>
D-ribose transporter subunit	ACY91057.1	<i>rbsB</i>
tricarboxylic transport	ACY89780.1	STM14_3361
glycerol-3-phosphate transporter periplasmic binding protein	ACY90671.1	<i>ugpB</i>
nucleoside channel	ACY87008.1	<i>tsx</i>
long-chain fatty acid outer membrane transporter	ACY89381.1	<i>fadL</i>
thiosulfate transporter subunit	ACY89434.1	<i>cysP</i>
phosphate transporter subunit	ACY91028.1	<i>pstS</i>
outer membrane channel protein	ACY90262.1	<i>tolC</i>
ferrichrome outer membrane transporter	ACY86763.1	<i>fhuA</i>
putative transport protein	ACY89112.1	<i>yehZ</i>

Cell envelope

acetyl-CoA carboxylase carboxyltransferase subunit alpha	ACY86808.1	<i>accA</i>
acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	ACY90472.1	<i>accB</i>
acetyl-CoA carboxylase biotin carboxylase subunit	ACY90473.1	<i>accC</i>
UTP--glucose-1-phosphate uridylyltransferase subunit GalF	ACY89037.1	<i>galF</i>
UTP--glucose-1-phosphate uridylyltransferase subunit GalU	ACY88584.1	<i>galU</i>
2-dehydro-3-deoxyphosphooctonate aldolase	ACY88605.1	<i>kdsA</i>
murein lipoprotein	ACY88149.1	<i>lpp</i>
periplasmic murein tripeptide transport protein	ACY88495.1	<i>mppA</i>
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	ACY90390.1	<i>murA</i>
oligopeptide transport protein	ACY88576.1	<i>oppA</i>

aminoacyl-histidine dipeptidase	ACY86894.1	<i>pepD</i>
ADP-L-glycero-D-mannoheptose-6-epimerase	ACY90855.1	<i>rfaD</i>
bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase	ACY90279.1	<i>rfaE</i>
CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	ACY89029.1	<i>rfbH</i>

Oxidative stress response

glutathione peroxidase	ACY88107.1	<i>btuE</i>
gamma-glutamyltranspeptidase	ACY90664.1	<i>ggt</i>
glutathione reductase	ACY90715.1	<i>gor</i>
glutaredoxin 2	ACY87822.1	<i>grxB</i>
glutaredoxin 3	ACY91028.1	<i>grxC</i>
hypothetical protein	ACY88207.1	<i>ydhD</i>
putative catalase	ACY88561.1	<i>STM14_2094</i>
superoxide dismutase	ACY88214.1	<i>sodC</i>
alkyl hydroperoxide reductase subunit C	ACY87219.1	<i>ahpC</i>
hydroperoxidase II	ACY88079.1	<i>katE</i>
putative thiol-alkyl hydroperoxide reductase	ACY86996.1	<i>STM14_0476</i>
thioredoxin	ACY91082.1	<i>trxA</i>
thioredoxin reductase	ACY87574.1	<i>trxB</i>

Other

inorganic pyrophosphatase	ACY91636.1	<i>ppa</i>
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NON-METABOLIC

“Unknown metabolic”, no associated reaction

Amino acid

putative glutamic dehydrogenase-like protein	ACY88633.1	<i>STM14_2170</i>
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Sugar

maltose regulon periplasmic protein	ACY91428.1	<i>malM</i>
putative glycosyl hydrolase	ACY88352.1	<i>STM14_1881</i>
putative glycosyl hydrolase	ACY88353.1	<i>STM14_1882</i>
putative nucleoside-diphosphate-sugar epimerase	ACY89929.1	<i>STM14_3516</i>
putative oxidoreductase	ACY87018.1	<i>yajO</i>

Iron

bacterioferritin, iron storage and detoxification protein	ACY90537.1	<i>bfr</i>
ferric uptake regulator	ACY87312.1	<i>fur</i>
putative ferripyochelin-binding protein	ACY90493.1	<i>yrdA</i>

Transport

putrescine ABC transporter periplasmic substrate-binding protein ACY87523.1 *potF*

Genetic information processing**DNA replication**

DNA gyrase subunit B ACY91005.1 *gyrB*

single-strand DNA-binding protein ACY91453.1 *ssb*

Homologous recombination

Recombinase A ACY89831.1 *recA*

Transcription

transcription elongation factor GreA ACY90381.1 *greA*

transcriptional regulator HU subunit alpha ACY91356.1 *hupA*

transcription elongation factor NusA ACY90369.1 *nusA*

DNA-binding transcriptional activator OsmE ACY88071.1 *osmE*

transcription termination factor Rho ACY91083.1 *rho*

nucleoside diphosphate kinase regulator ACY87229.1 *rnk*

DNA-directed RNA polymerase subunit alpha ACY90509.1 *rpoA*

DNA-directed RNA polymerase subunit beta ACY91336.1 *rpoB*

DNA-directed RNA polymerase subunit beta' ACY91337.1 *rpoC*

TrpR binding protein WrbA ACY87764.1 *wrbA*

RNA degradation

polynucleotide phosphorylase/polyadenylase ACY90363.1 *pnp*

ribonuclease E ACY87845.1 *rne*

Translation

translation initiation factor IF-3 ACY88099.1 *infC*

putative translation initiation inhibitor ACY91684.1 *yjhF*

elongation factor G ACY90541.1 *fusA*

elongation factor P ACY89175.1 *yeiP*

elongation factor Ts ACY86792.1 *tsf*

elongation factor Tu ACY90540.1 *tuf*

ribosome recycling factor ACY86794.1 *frr*

translation-associated GTPase ACY88620.1 *ychF*

Ribosomal

50S ribosomal protein L1 ACY91333.1 *rplA*

50S ribosomal protein L2 ACY90531.1 *rplB*

50S ribosomal protein L3 ACY90534.1 *rplC*

50S ribosomal protein L4 ACY90533.1 *rplD*

50S ribosomal protein L5	ACY90522.1	<i>rplE</i>
50S ribosomal protein L6	ACY90519.1	<i>rplF</i>
50S ribosomal protein L9	ACY91613.1	<i>rplI</i>
50S ribosomal protein L10	ACY91334.1	<i>rplJ</i>
50S ribosomal protein L11	ACY91332.1	<i>rplK</i>
50S ribosomal protein L13	ACY90433.1	<i>rplM</i>
50S ribosomal protein L14	ACY90524.1	<i>rplN</i>
50S ribosomal protein L15	ACY90515.1	<i>rplO</i>
50S ribosomal protein L17	ACY90508.1	<i>rplQ</i>
50S ribosomal protein L18	ACY90518.1	<i>rplR</i>
50S ribosomal protein L19	ACY89700.1	<i>rplS</i>
30S ribosomal protein S1	ACY87604.1	<i>rpsA</i>
30S ribosomal protein S2	ACY86791.1	<i>rpsB</i>
30S ribosomal protein S3	ACY90528.1	<i>rpsC</i>
30S ribosomal protein S4	ACY90510.1	<i>rpsD</i>
30S ribosomal protein S5	ACY90517.1	<i>rpsE</i>
30S ribosomal protein S6	ACY91610.1	<i>rpsF</i>
30S ribosomal protein S7	ACY90542.1	<i>rpsG</i>
30S ribosomal protein S10	ACY90535.1	<i>rpsJ</i>
30S ribosomal protein S11	ACY90511.1	<i>rpsK</i>
30S ribosomal protein S13	ACY90512.1	<i>rpsM</i>

tRNA

putative tRNA synthase	ACY89932.1	<i>ygbK</i>
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Post-translational processing

methionine aminopeptidase	ACY86789.1	<i>map</i>
trigger factor	ACY87047.1	<i>tig</i>

Proteases

serine endoprotease	ACY90436.1	<i>degQ</i>
oligopeptidase A	ACY90711.1	<i>priC</i>
putative Zn-dependent peptidase	ACY90737.1	<i>yhjJ</i>

Environmental information processing

Biofilm formation

cellulose synthase subunit BcsC	ACY90743.1	<i>bcsC</i>
putative curli operon transcriptional regulator	ACY87791.1	<i>csgG</i>

Osmotic homeostasis

molecular chaperone DnaK	ACY86550.1	<i>dnaK</i>
putative envelope protein	ACY88357.1	<i>osmC</i>

Quorum sensing

putative sugar transport protein	ACY91259.1	<i>IsrB</i>
aldolase	ACY91260.1	<i>IsrF</i>
autoinducer-2 (AI-2) modifying protein	ACY91261.1	<i>IsrG</i>

Signal transduction

two-component response regulator	ACY91847.1	<i>arcA</i>
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Stress response

ATP-dependent Clp protease proteolytic subunit	ACY87048.1	<i>clpP</i>
chaperonin GroEL	ACY91545.1	<i>groEL</i>
co-chaperonin GroES	ACY91544.1	<i>groES</i>
ATP-dependent protease ATP-binding subunit	ACY91276.1	<i>hslU</i>
serine endoprotease	ACY86784.1	<i>htrA</i>
periplasmic chaperone	ACY86801.1	<i>skp</i>
FKBP-type peptidyl-prolyl cis-trans isomerase	ACY90550.1	<i>slyD</i>
peptidyl-prolyl cis-trans isomerase B (rotamase B)	ACY87143.1	<i>STM14_0626</i>
peptidyl-prolyl cis-trans isomerase SurA	ACY86648.1	<i>surA</i>
thioredoxin-dependent thiol peroxidase	ACY89486.1	<i>bcp</i>
DNA starvation/stationary phase protection protein Dps	ACY87463.1	<i>dps</i>
organic solvent tolerance protein	ACY86649.1	<i>imp</i>
thiol peroxidase	ACY88498.1	<i>tpx</i>
exonuclease III	ACY88059.1	<i>xthA</i>
cytochrome d ubiquinol oxidase subunit III	ACY90435.1	<i>yhcb</i>

Transport

putative outer membrane porin precursor	ACY88369.1	<i>nmpC</i>
preprotein translocase subunit SecB	ACY90845.1	<i>secB</i>
putative outer membrane efflux protein	ACY89720.1	<i>STM14_3298</i>
conjugative transfer protein	ACY91438.1	<i>STM14_5099</i>
translocation protein TolB	ACY87374.1	<i>tolB</i>
putative DNA uptake protein	ACY90618.1	<i>yhgl</i>
putative ABC transporter ATP-binding protein	ACY91830.1	<i>yjjK</i>

Cellular processes**Cell cycle/division**

cold shock-like protein CspC	ACY88683.1	<i>cspC</i>
cell division protein FtsZ	ACY86696.1	<i>ftsZ</i>
cell division inhibitor MinD	ACY88657.1	<i>minD</i>

rod shape-determining protein	ACY90464.1	<i>mreB</i>
peptidase PmbA	ACY91663.1	<i>pmbA</i>

Cell envelope

outer-membrane lipoprotein carrier protein	ACY87579.1	<i>lolA</i>
lipoprotein	ACY89483.1	<i>nlpB</i>
outer membrane protein A	ACY87707.1	<i>ompA</i>
outer membrane protein X	ACY87468.1	<i>ompX</i>
peptidoglycan-associated outer membrane lipoprotein	ACY87375.1	<i>pal</i>
carboxy-terminal protease	ACY88695.1	<i>prc</i>
rare lipoprotein A	ACY87258.1	<i>rlpA</i>
LPS-assembly lipoprotein RplB	ACY87267.1	<i>rlpB</i>
putative outer membrane lipoprotein	ACY88219.1	<i>slyB</i>
putative outer membrane lipoprotein	ACY88416.1	<i>STM14_1945</i>
outer membrane protein assembly factor YaeT	ACY86800.1	<i>yaeT</i>
putative outer membrane lipoprotein	ACY87868.1	<i>ycfM</i>
putative outer membrane lipoprotein	ACY90779.1	<i>yiaD</i>

Unknown function

Cytoplasm

putative cytoplasmic protein	ACY87716.1	<i>STM14_1223</i>
putative cytoplasmic protein	ACY88435.1	<i>STM14_1964</i>
putative cytoplasmic protein	ACY88483.1	<i>STM14_2012</i>
putative cytoplasmic protein	ACY88702.1	<i>STM14_2239</i>
putative cytoplasmic protein	ACY88560.1	<i>yciE</i>
putative cytoplasmic protein	ACY88559.1	<i>yciF</i>
putative intracellular proteinase	ACY90350.1	<i>yhbO</i>

Periplasm

periplasmic protein	ACY91808.1	<i>ybiS</i>
putative periplasmic protein	ACY88242.1	<i>ydgA</i>
putative periplasmic protein	ACY88258.1	<i>ydgH</i>

Hypothetical proteins

hypothetical protein	ACY86786.1	<i>STM14_0251</i>
hypothetical protein	ACY87067.1	<i>STM14_0549</i>
hypothetical protein	ACY89526.1	<i>STM14_3095</i>
hypothetical protein	ACY89790.1	<i>STM14_3371</i>
hypothetical protein	ACY90112.1	<i>STM14_3705</i>
hypothetical protein	ACY90348.1	<i>STM14_3949</i>
hypothetical protein	ACY87474.1	<i>ybiS</i>
hypothetical protein	ACY90882.1	<i>yicC</i>

Unassigned

electron carrier protein	ACY89544.1	<i>fds</i>
global DNA-binding transcriptional dual regulator H-NS	ACY88582.1	<i>hns</i>
N-ethylmaleimide reductase	ACY88210.1	<i>nemA</i>
quinone oxidoreductase, NADPH-dependent	ACY91442.1	<i>qor</i>
putative NAD-dependent aldehyde dehydrogenase	ACY91761.1	<i>STM14_5430</i>
GTP-binding protein	ACY91179.1	<i>typA</i>
iron-sulfur cluster insertion protein ErpA	ACY86779.1	<i>yadR</i>
nucleotide-binding protein	ACY87033.1	<i>yajQ</i>
putative dehydrogenase	ACY87228.1	<i>ybdR</i>
purine nucleoside phosphoramidase	ACY87866.1	<i>ycfF</i>
putative serine protein kinase	ACY88037.1	<i>yeaG</i>
putative methyltransferase	ACY89674.1	<i>yfiF</i>
putative lipoprotein	ACY90008.1	<i>ygdI</i>
oxidoreductase	ACY90226.1	<i>yghA</i>
putative oxidoreductase	ACY91021.1	<i>yieF</i>
putative NADP-dependent oxidoreductase	ACY88395.1	<i>yncB</i>

Table S2: Amino acid supplementation complements the growth defects of amino acid auxotrophs

Mutant	Auxotrophy	n	48h		72h	
			Treatment	Relative growth	Treatment	Relative growth
<i>ΔasnA::Kan ΔasnB::Cm</i>	Asn	4	-	-0.36 ± 0.15	-	-0.36 ± 0.05
			+1mM Asn	-0.28 ± 0.18	+1mM Asn	-0.09 ± 0.14
<i>glnA::Cm</i>	Gln	3	-	-0.16 ± 0.13	-	WT
			+1mM Gly	+0.24 ± 0.05	+1mM Gln	WT
<i>glyA::Tn10</i>	Gly	3	-	-0.40 ± 0.10	-	-0.36 ± 0.10
			+1mM Gly	-0.23 ± 0.11	+1mM Gly	WT
<i>ΔhisB::Kan</i>	His	3	-	WT	-	WT
			+1mM His	WT	+1mM His	+0.13 ± 0.02
<i>ΔlysA::Kan</i>	Lys	3	-	-0.58 ± 0.04	-	-0.54 ± 0.11
			+1mM Lys	-0.65 ± 0.15	+1mM Lys	-0.33 ± 0.13
<i>ΔmetC::Kan</i>	Met	3	-	-0.84 ± 0.10	-	-0.83 ± 0.18
			+1mM Met	-0.22 ± 0.04	+1mM Met	-0.21 ± 0.01
<i>proC693::MudA</i>	Pro	3	-	-0.27 ± 0.07	-	WT
			+1mM Pro	WT	+1mM Pro	WT
<i>ΔtrpB::Kan</i>	Trp	3	-	-0.63 ± 0.13	-	-1.01 ± 0.12
			+1mM Trp	-0.55 ± 0.17	+1mM Trp	-0.34 ± 0.12

* indicates statistically significant differences between treatments (p<0.05).

Table S3: Amino acid auxotrophs are reduced in fitness in the alfalfa spermosphere/rhizosphere compared to *S. enterica* wild-type

Mutant	Auxotrophy	n	Percent total population of mutant		
			24h	48h	72h
<i>ΔasnA::Kan ΔasnB::Cm</i>	Asn	4	43.3 ± 16.0	19.0 ± 3.4 *	ND
<i>ΔglnA::Kan</i>	Gln	4	66.4 ± 10.6 *	16.5 ± 5.9 *	19.2 ± 8.7 *
<i>ΔgdhA::Kan ΔgltB::Cm</i>	Glu	4	43.3 ± 23.3	40.7 ± 4.9 *	ND
<i>glyA::Tn10d</i>	Gly	3	39.2 ± 11.8	17.2 ± 4.8 *	18.7 ± 8.9 *
<i>ΔhisB::Kan</i>	His	4	52.7 ± 22.5	68.9 ± 9.2 *	ND
<i>ΔilvE::Cm</i>	Ilv, Leu, Val	3	67.6 ± 13.2	43.2 ± 12.6	ND
<i>ΔleuB::Kan</i>	Leu	5	31.0 ± 10.7 *	11.3 ± 2.1 *	ND
<i>ΔlysA::Kan</i>	Lys	3	44.8 ± 15.5	20.7 ± 9.0 *	15.7 ± 4.4 *
<i>ΔmetC::Kan</i>	Met	4	34.6 ± 8.9 *	17.1 ± 6.3 *	ND
<i>ΔpheA::Kan</i>	Phe	4	33.4 ± 4.9 *	20.5 ± 4.5 *	ND
<i>pro693C::MudA</i>	Pro	4	32.5 ± 7.7 *	16.3 ± 2.8 *	16.4 ± 5.3 *
<i>thr557::Tn10</i>	Thr	4	72.4 ± 9.6*	64.4 ± 5.2 *	70.3 ± 7.0 *
<i>ΔtrpB::Kan</i>	Trp	5	24.2 ± 6.2 *	13.7 ± 2.8 *	ND
<i>ΔtyrA::Kan</i>	Tyr	4	34.6 ± 4.9 *	29.7 ± 11.6 *	ND
<i>ΔpheASTM2668tyrA::Cm</i>	Phe, Tyr	3	32.7 ± 5.8 *	19.8 ± 0.2 *	12.9 ± 3.7 *
<i>ΔpheASTM2668tyrA::Cm ΔtrpB::Kan</i>	Phe, Trp, Tyr	3	46.6 ± 3.4	13.0 ± 4.6 *	11.3 ± 2.5 *

* indicates statistically different from 50%

ND = not determined

Table S4: Concentrations (μM) of amino acids and their derivatives released by alfalfa seeds during germination and early plant development

Metabolite	Concentration (μM)				
	0 h *	8 h	24 h	48 h	72 h
Alanine	4.59 \pm 4.84	25.82 \pm 1.55	61.27 \pm 0.91	86.27 \pm 10.18	93.66 \pm 11.90
Arginine	0.86 \pm 0.13	44.61 \pm 4.18	79.82 \pm 1.96	76.20 \pm 9.07	23.54 \pm 16.25
Asparagine	1.17 \pm 0.13	35.38 \pm 0.26	48.73 \pm 0.94	80.74 \pm 4.82	45.08 \pm 17.36
Aspartate	1.07 \pm 0.08	22.45 \pm 1.72	47.08 \pm 5.93	100.51 \pm 1.30	52.96 \pm 12.79
Glutamate	0.74 \pm 0.04	30.90 \pm 2.83	52.99 \pm 2.59	92.04 \pm 12.95	66.21 \pm 16.64
Glutamine	0.10 \pm 0.00	9.23 \pm 0.04	30.70 \pm 2.26	46.02 \pm 1.82	32.87 \pm 10.60
Glycine	6.14 \pm 3.22	3.15 \pm 1.31	1.63 \pm 1.19	1.86 \pm 1.06	2.97 \pm 1.03
Histidine	0.34 \pm 0.02	8.40 \pm 0.47	19.50 \pm 4.12	16.89 \pm 0.07	7.80 \pm 3.50
Leucine/Isoleucine	2.79 \pm 0.21	18.88 \pm 2.11	60.21 \pm 2.24	117.41 \pm 16.81	54.64 \pm 22.76
Lysine	0.20 \pm 0.01	15.15 \pm 1.71	62.03 \pm 1.54	69.01 \pm 1.40	38.46 \pm 27.62
Methionine	0.24 \pm 0.05	2.35 \pm 0.11	8.97 \pm 0.37	7.88 \pm 0.25	3.62 \pm 2.33
Phenylalanine	0.45 \pm 0.00	13.49 \pm 0.12	30.61 \pm 1.27	50.93 \pm 0.34	24.70 \pm 8.44
Proline	3.92 \pm 1.92	11.67 \pm 0.47	29.76 \pm 0.15	38.38 \pm 0.24	24.80 \pm 7.33
Serine	0.76 \pm 0.51	14.68 \pm 1.91	56.15 \pm 6.84	82.45 \pm 4.63	53.14 \pm 31.89
Threonine	4.73 \pm 0.90	111.55 \pm 9.89	212.53 \pm 10.41	302.80 \pm 43.81	278.17 \pm 117.07
Tryptophan	0.02 \pm 0.02	1.88 \pm 0.07	4.79 \pm 0.03	6.04 \pm 0.24	4.77 \pm 1.71
Tyrosine	0.48 \pm 0.10	38.39 \pm 6.77	61.99 \pm 9.33	81.19 \pm 1.33	48.32 \pm 18.20
Valine	0.42 \pm 0.00	11.06 \pm 0.12	30.38 \pm 0.98	46.44 \pm 1.10	26.38 \pm 6.88
Acetyllysine	0.00 \pm 0.00	0.03 \pm 0.01	0.06 \pm 0.01	0.10 \pm 0.02	0.09 \pm 0.02
GABA	0.00 \pm 0.00	23.32 \pm 0.79	38.27 \pm 6.91	70.35 \pm 2.92	28.62 \pm 4.35
Hydroxyproline	0.38 \pm 0.02	2.26 \pm 0.20	3.22 \pm 0.17	3.33 \pm 0.08	2.11 \pm 0.022
Methionine sulfoxide	0.13 \pm 0.09	1.75 \pm 0.15	6.10 \pm 1.47	9.17 \pm 0.83	5.93 \pm 1.94
Ornithine	0.51 \pm 0.61	5.88 \pm 0.41	17.46 \pm 1.59	16.12 \pm 0.07	4.14 \pm 4.30
Pyroglutamate	0.79 \pm 0.70	10.36 \pm 1.37	19.04 \pm 4.23	15.88 \pm 0.16	6.88 \pm 2.17

* Values at 0h indicate concentrations present immediately after addition of water to seeds and likely indicate unbound amino acids present on the seed surface.

** Cysteine/Cystine could not be reliably detected by our system and was not included in the analysis.

Table S5: Relative depletion of amino acids and their derivatives in alfalfa seedling exudate in the presence of *S. enterica*

Metabolite	Average ratio of nutrient concentration with Se : no Se		
	24 h	48 h	72 h
Alanine	1.02 ± 0.13	0.04 ± 0.01 *	0.04 ± 0.02 *
Arginine	1.16 ± 0.42	0.00 ± 0.00 *	0.00 ± 0.00 *
Asparagine	0.93 ± 0.19	0.01 ± 0.00 *	0.01 ± 0.00 *
Aspartate	0.65 ± 0.18 †	0.01 ± 0.00 *	0.01 ± 0.00 *
Glutamate	0.87 ± 0.10	0.00 ± 0.00 *	0.00 ± 0.00 *
Glutamine	0.93 ± 0.08	0.02 ± 0.00 *	0.02 ± 0.00 *
Histidine	0.70 ± 0.45	0.11 ± 0.01 *	0.08 ± 0.09 *
Leucine/isoleucine	0.92 ± 0.13	0.00 ± 0.00 *	0.00 ± 0.00 *
Lysine	1.18 ± 0.54	0.01 ± 0.00 *	0.03 ± 0.01 *
Methionine	0.78 ± 0.16	0.00 ± 0.00 *	0.00 ± 0.02 *
Phenylalanine	0.95 ± 0.09	0.14 ± 0.14 *	0.19 ± 0.10 *
Proline	0.87 ± 0.02 †	0.01 ± 0.00 *	0.01 ± 0.00 *
Serine	0.36 ± 0.29 †	0.02 ± 0.00 *	0.03 ± 0.01 *
Threonine	1.06 ± 0.10	0.07 ± 0.01 *	0.06 ± 0.02 *
Tryptophan	0.79 ± 0.09 †	0.00 ± 0.01 *	0.03 ± 0.03 *
Tyrosine	1.07 ± 0.13	0.29 ± 0.32 †	0.46 ± 0.23 *
Valine	0.73 ± 0.22	0.00 ± 0.00 *	0.01 ± 0.00 *
Acetyllysine	0.41 ± 0.32 †	0.07 ± 0.01 *	0.11 ± 0.07 *
Hydroxyproline	1.02 ± 0.05	1.03 ± 0.10	1.06 ± 0.16
Methionine sulfoxide	0.91 ± 0.08	0.04 ± 0.01 *	0.05 ± 0.04 *
Ornithine	1.29 ± 0.71	0.02 ± 0.01 *	0.02 ± 0.01 *
Pyroglutamic acid	0.96 ± 0.07	0.84 ± 0.07 *	1.06 ± 0.53

* indicates p<0.05.

† indicates 0.05<p<0.1.

Table S6: Comparison of amino acid availability and *S. enterica* requirements for growth at 24 h in germinating alfalfa exudate

Metabolite	Concentration (μM)		Ratio required:available
	Exudate availability	Biomass requirement	
Gly	0.002	8.08	4954.24
Trp	0.005	0.47	98.94
Ala	0.061	4.03	65.83
Met	0.009	0.56	62.91
Val	0.030	1.53	50.49
Pro	0.030	1.39	46.55
Asp	0.047	2.02	42.82
Gln	0.030	1.08	35.15
Asn	0.048	1.47	30.34
Ser	0.056	0.04	30.16
Lys	0.062	1.68	27.06
Ile/Leu	0.060	1.58	26.31
Glu	0.053	1.38	26.05
Phe	0.031	0.75	24.43
His	0.019	0.36	18.56
Thr	0.213	1.89	8.87
Arg	0.080	0.71	9.93
Tyr	0.062	0.22	3.50



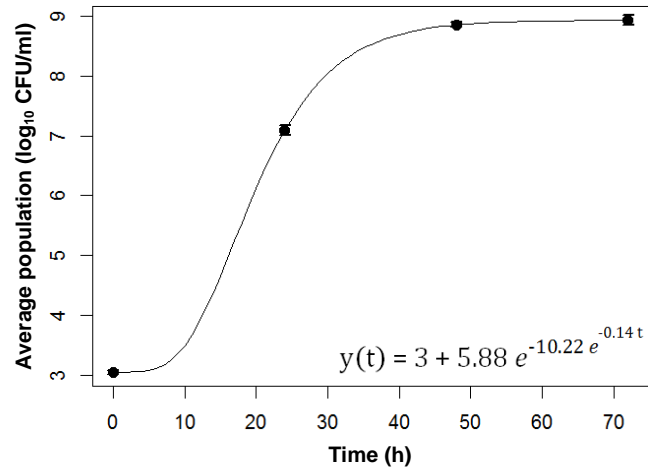


Figure S1: Growth of *S. enterica* in alfalfa exudates over time. Data shown are the WT population averages at each time point from a representative experiment (n=3). Error bars indicate the standard deviations of the means.