

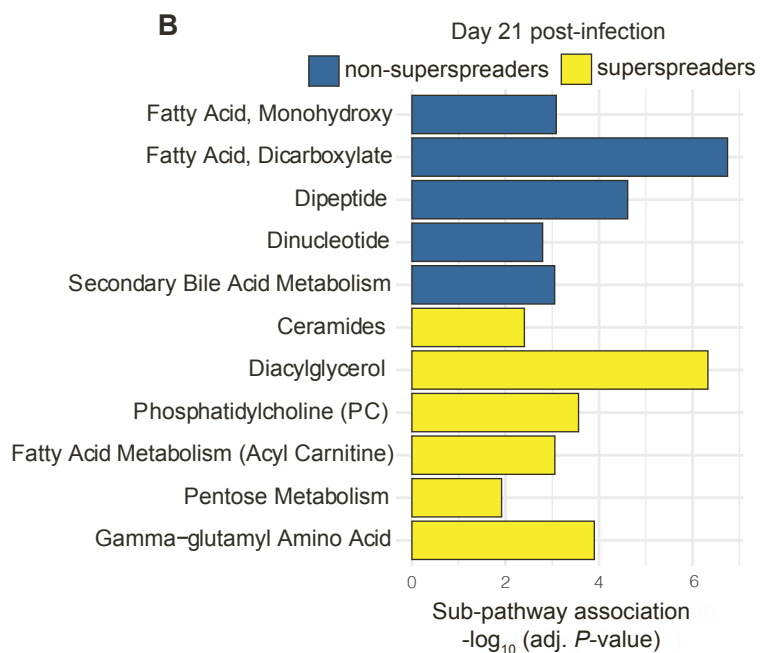
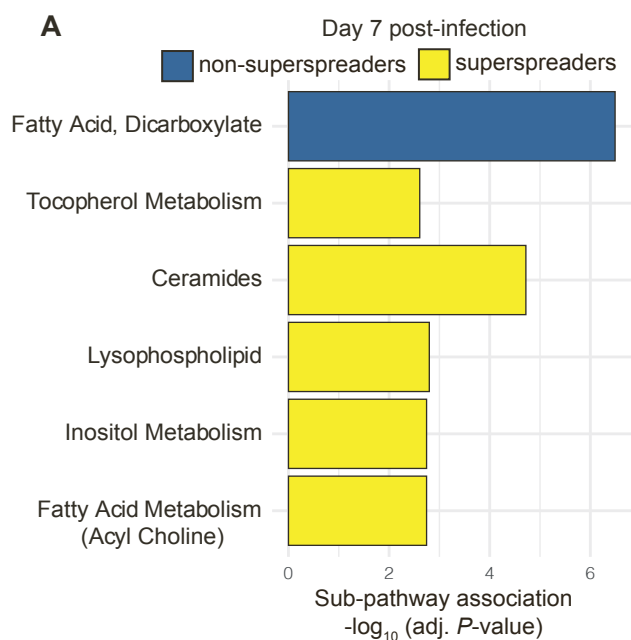
Cell Host & Microbe, Volume 31

Supplemental information

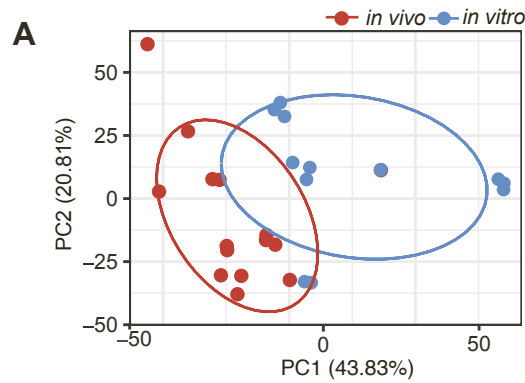
***Salmonella*-liberated dietary L-arabinose
promotes expansion in superspreaders**

Sarah J. Ruddle, Liliana M. Massis, Alyssa C. Cutter, and Denise M. Monack

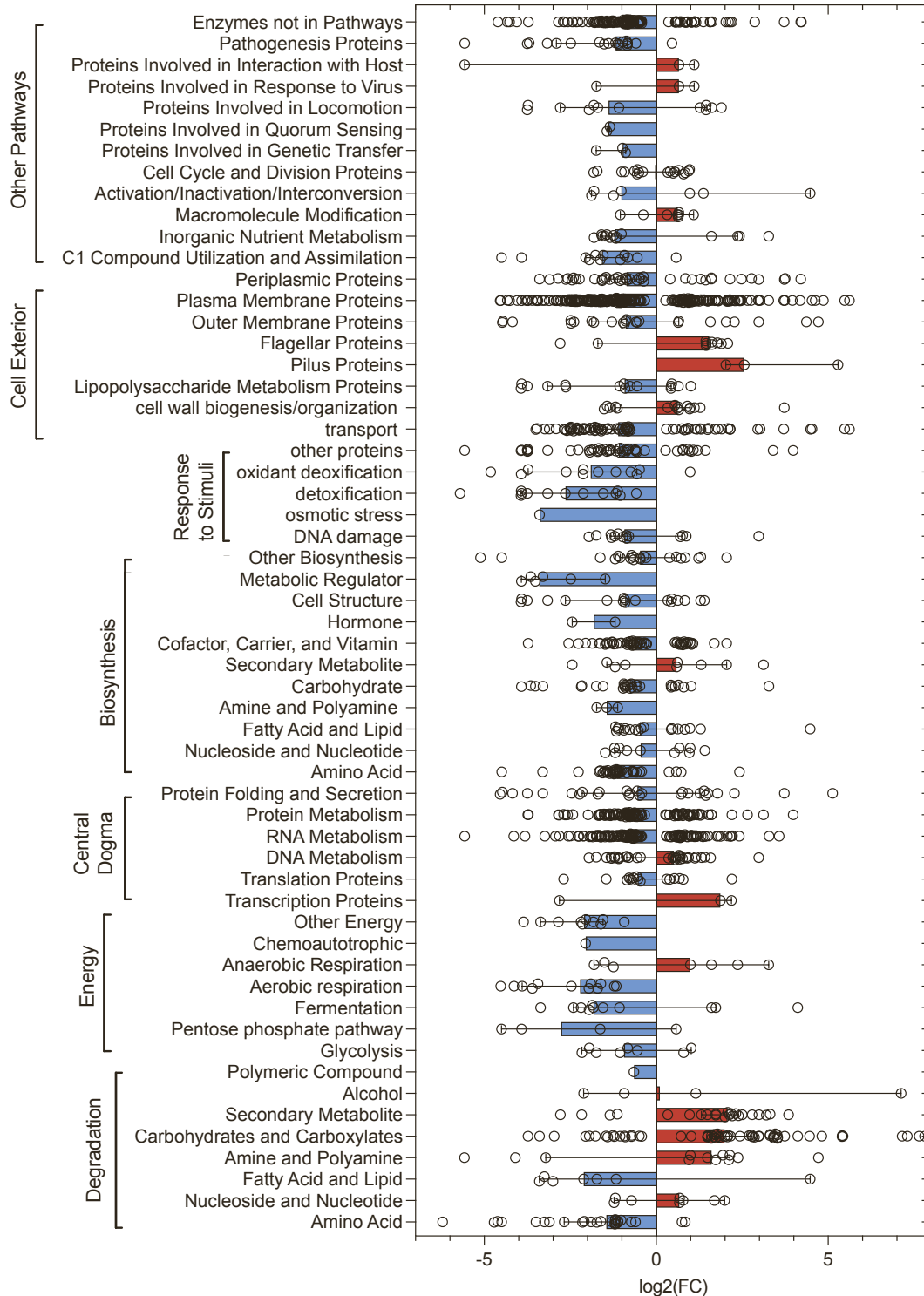
Supplemental figure 1



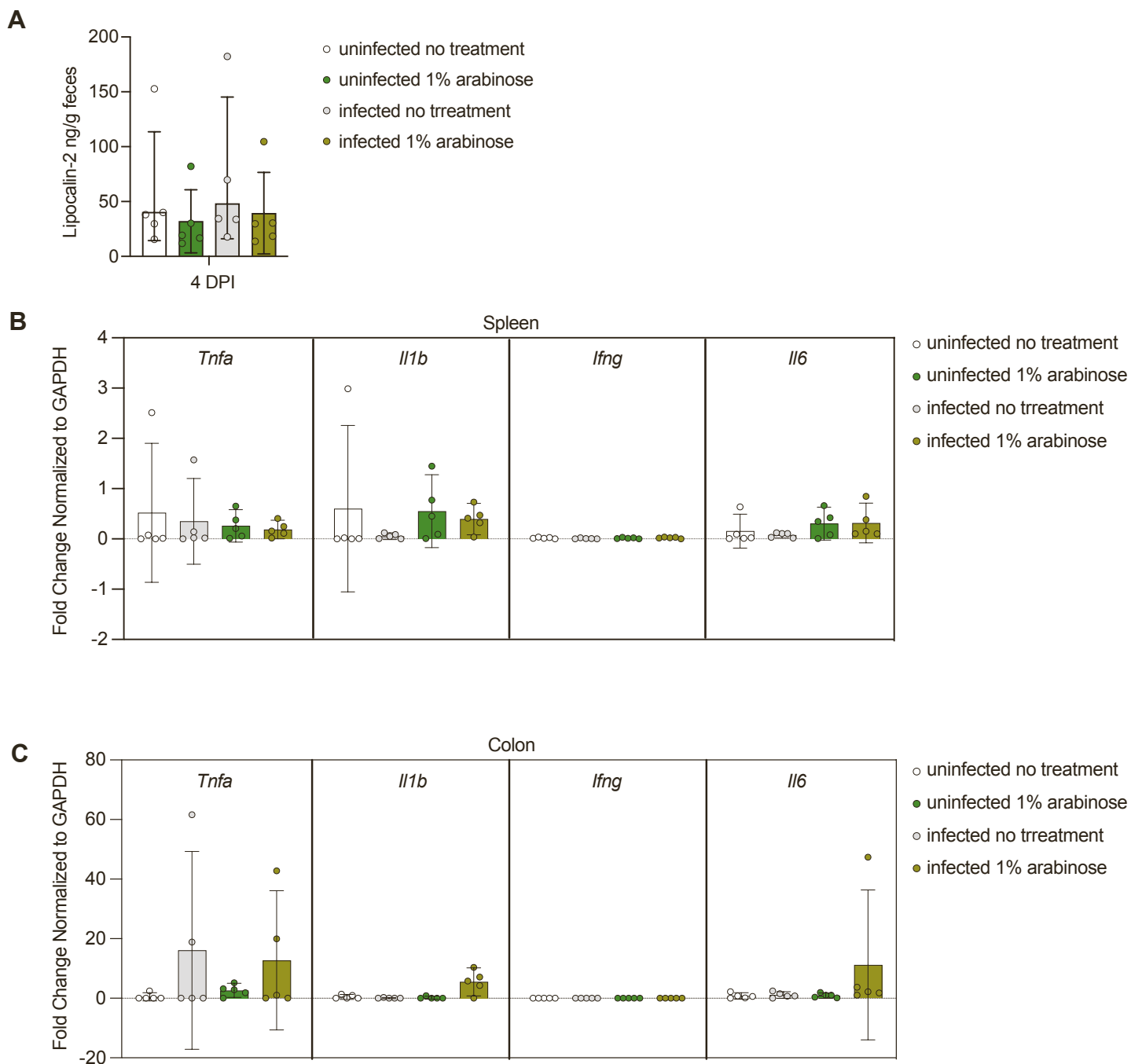
Supplemental figure 2



B

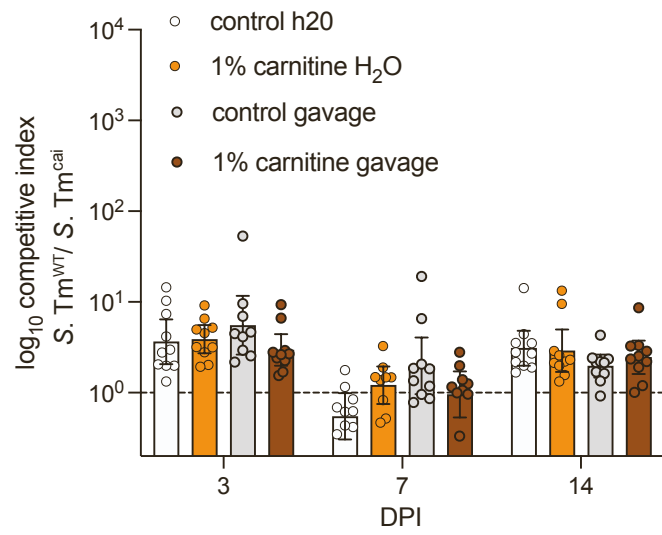


Supplemental figure 3

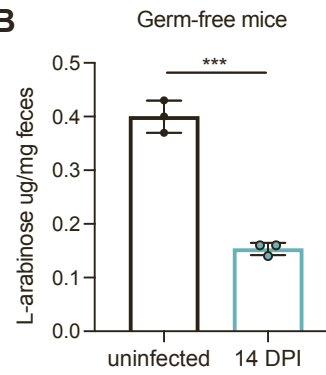


Supplemental figure 4

A



B



Supplemental figure 5

A

1	11	21	31	41	50	
MTTSLNSRRL	WLHRLCALLL	GTGSAL----	-----VQAE	NPIFTDVFTA	40	C. japonicus
MRKKC-SVCL	WILVLLSCL	SGKSAYAATS	TTIAKHIGNS	NPLIDHHLGA	49	B. subtilis
M-RRL-TVRL	FTAVLAALAL	LTMGTPAHAT	APASPSVFTT	NPLAEKR--A	46	S. avermitilis
M-----	-----	-----	-----ANWP	NPFIEQR--A	13	S. Typhimurium
DPAAALVH-KG	RVVLYAGRDE	APDNT-----	---TFFVMNEW	LVYSSDDMAN	82	C. japonicus
DPVALTY-NG	RVYIYMSSDD	YEYNSNGTIK	DNSFANLNRV	FVISSADMVN	98	B. subtilis
DPHIFKHTDG	Y--YYFATVP	-EYDRIVLRR	ATTLQGLA--	---TAPETTI	89	S. avermitilis
DPFILR--DG	SDYFYIASVP	-EYDRLEIRR	ANSLEGLR--	---AADPVVV	55	S. Typhimurium
WEAHPGLR--	-AKDFTWAKG	DA-----	WA SQVI--ERNG	--KFYWYVTV	120	C. japonicus
WTDHGAIPVA	GANGANGGRG	IAKWAGASWA	PSIAVKKING	KDKFFLYFA-	147	B. subtilis
WTKHASGVM-	-----	---GAH--WA	PEIH--FIDG	--KWYVYFAA	120	S. avermitilis
WRKPESGPM-	-----	---SQL--WA	PEMH--RING	--KWYVYFAA	86	S. Typhimurium
RHDD-----	---TKPGFAIG	VAVGDSPIGP	FKDALGKALI	TNDMTTDTPI	162	C. japonicus
-----D	---NSGGGIG	VLTADSPIGP	WTDPIGKPLV	TPSTPGMSGV	184	B. subtilis
GSTS-----	D WFAIRMYVLE	SGAANPLTGS	W-----	TEKGQIATPV	156	S. avermitilis
THTQALDKLG	WQHRMFALE	CADADPLTKG	W-----	TEKGQIKTPF	127	S. Typhimurium
DWDDIDPSVF	IDDDGQAYLF	WGNTRP----	-----	---RYAKL	193	C. japonicus
VW-LRDPAVF	VDDDGTGYLY	AGGGVPGVSN	PTQ---GQWA	NPKTARVIKL	230	B. subtilis
SSFSLDATTF	VVN-GVRHLA	WAQRNPAEDN	NTSLFIAKMA	NPWT-----	199	S. avermitilis
DTFALDATT	YHQ-GKQWYL	WAQKAPDIAG	NSNIYLAELE	NPWT-----	170	S. Typhimurium
KKNMVELDGP	IRAIEGLPEF	T-----	EAIWVHKYQD	NYLVS-----	230	C. japonicus
GPDMTSVVG	ASTIDA-PFM	F-----	EDSGLHKYNG	TYYSY-----	266	B. subtilis
-----ISGT	PTEISQ-PTL	SWETVGYKVN	EPPAVIQHGG	KVFLTYSASA	242	S. avermitilis
-----IKGE	PVRLSK-PEY	DWECRGFVWN	EPPAVVVHGD	KLFISYSASA	213	S. Typhimurium

B

SL1344	1	MANWPNPFI	EQRADPFI	LRDGSDDYF	IASVPEYDRLE	IRRAN	SLEGLRAAD	DPVVVWRKP	PESGPM	S	65					
S. Typhimurium	D23580	1	MANWPNPFI	EQRADPFI	LRDGSDDYF	IASVPEYDRLE	IRRAN	SLEGLRAAD	DPVVVWRKP	PESGPM	S	65				
S. Typhimurium	4,[5],12:i-	1	MANWPNPFI	EQRADPFI	LRDGSDDYF	IASVPEYDRLE	IRRAN	SLEGLRAAD	DPVVVWRKP	PESGPM	S	65				
S. Dublin	ATCC 39184	1	MANWPNPFI	EQRADPFI	LRDGSDDYF	IASVPEYDRLE	IRRAD	SLEGLRAAD	DPVVVWRKP	PESGPM	S	65				
S. Paratyphi	AATCC 9150	1	MANWPNPFI	EQRADPFI	LRDGSDDYF	IASVPEYDRLE	IRRAN	SLEGLRAAD	DPVVVWRKP	KTGPM	S	65				
S. Typhi	Ty2	1	MANWPNPFI	EQRADPFI	LRDGSDDYF	IASVPEYDRLE	IRRAD	SLEGLRAAD	DPVVVWRKP	PESGPM	S	65				
SL1344	66	QLIWAPEMHR	INGKWYI	YFAATHQAL	DKLGMFQHRM	FAL	LECADADP	LTGKWT	EKGQ	IKTPFDT	F	130				
S. Typhimurium	D23580	66	QLIWAPEMHR	INGKWYI	YFAATHQAL	DKLGMFQHRM	FAL	LECADADP	LTGKWT	EKGQ	IKTPFDT	F	130			
S. Typhimurium	4,[5],12:i-	66	QLIWAPEMHR	INGKWYI	YFAATHQAL	DKLGMFQHRM	FAL	LECADADP	LTGKWT	EKGQ	IKTPFDT	F	130			
S. Dublin	ATCC 39184	66	QLIWAPEMHR	INGKWYI	YFAATHQAL	DKLGMFQHRM	FAL	LECADADP	LTGKWT	EKGQ	IKTPFDT	F	130			
S. Paratyphi	AATCC 9150	66	QLIWAPEMHR	INGKWYI	YFAATHQAL	DKLGMFQHRM	FAL	LECADADP	LTGKWT	EKGQ	IKTPFDT	F	130			
S. Typhi	Ty2	66	QLIWAPEMHR	INGKWYI	YFAATHQAL	DKLGMFQHRM	FAL	LECADADP	LTGKWT	EKGQ	IKTPFDT	F	130			
SL1344	131	ALDATT	FYHQGKQY	LWAQKAPD	IAGNSNIYLA	ELENPWT	IKGEPVRLSKP	EYDWECR	GFVW	NEG	195					
S. Typhimurium	D23580	131	ALDATT	FYHQGKQY	LWAQKAPD	IAGNSNIYLA	ELENPWT	IKGEPVRLSKP	EYDWECR	GFVW	NEG	195				
S. Typhimurium	4,[5],12:i-	131	ALDATT	FYHQGKQY	LWAQKAPD	IAGNSNIYLA	ELENPWT	IKGEPVRLSKP	EYDWECR	GFVW	NEG	195				
S. Dublin	ATCC 39184	131	ALDATT	FYHQGKQY	LWAQKAPD	IAGNSNIYLA	ELENPWT	IKGEPVRLSKP	EYDWECR	GFVW	NEG	195				
S. Paratyphi	AATCC 9150	131	ALDATT	FYHQGKQY	LWAQKAPD	IAGNSNIYLA	ELENPWT	IKGEPVRLSKP	EYDWECR	GFVW	NEG	195				
S. Typhi	Ty2	131	SLDATT	FYHQGKQY	LWAQKAPD	IAGNSNIYLA	ELENPWT	LK	KGEPVRLSKP	EYDWECR	GFVW	NEG	195			
SL1344	196	PAVVVHGD	KLFI	SY SASATD	ENYCMGLLW	INVNDP	RDPA	NWHK	SPRPV	F	FTSYENRQY	GP	GHNS	260		
S. Typhimurium	D23580	196	PAVVVHGD	KLFI	SY SASATD	ENYCMGLLW	INVNDP	RDPA	NWHK	SPRPV	F	FTSYENRQY	GP	GHNS	260	
S. Typhimurium	4,[5],12:i-	196	PAVVVHGD	KLFI	SY SASATD	ENYCMGLLW	INVNDP	RDPA	NWHK	SPRPV	F	FTSYENRQY	GP	GHNS	260	
S. Dublin	ATCC 39184	196	PAVVVHGD	KLFI	SY SASATD	ENYCMGLLW	INVNDP	RDPA	NWHK	SPRPV	F	FTSYENRQY	GP	GHNS	260	
S. Paratyphi	AATCC 9150	196	PAVVVHGD	KLFI	SY SASATD	ENYCMGLLW	INVNDP	LD	PQ	NWHK	SPRPV	F	FTSYENRQY	GP	GHNS	260
S. Typhi	Ty2	196	PAVVVHGD	KLFI	SY SASATD	ENYCMGLLW	INVNDP	RDPA	NWHK	SPRPV	F	FTSYENRQY	GP	GHNS	260	
SL1344	261	FTQT	PEGENV	LVIYHARNY	TE	EGDPLYDP	NRHTRLKRV	RWD	EN	GMP	DFGV	P	PADT	I	316	
S. Typhimurium	D23580	261	FTQT	PEGENV	LVIYHARNY	TE	EGDPLYDP	NRHTRLKRV	RWD	EN	GMP	DFGV	P	PADT	I	316
S. Typhimurium	4,[5],12:i-	261	FTQT	PEGENV	LVIYHARNY	TE	EGDPLYDP	NRHTRLKRV	RWD	EN	GMP	DFGV	P	PADT	I	316
S. Dublin	ATCC 39184	261	FTQT	PEGEDV	LVIYHARNY	TE	EGDPLYDP	NRHTRLKRV	RWD	EN	GMP	DFGV	P	PADT	I	316
S. Paratyphi	AATCC 9150	261	FTQT	PEGEDV	LVIYHARNY	TE	EGDPLYDP	NRHTRLKRV	RWD	EN	GMP	DFGV	P	PADT	I	316
S. Typhi	Ty2	261	FTQT	SEGEDV	LVIYHARNY	TE	EGDPLYDP	NRHTRLKRV	RWD	EN	GMP	DFGV	P	PADT	I	316

Supplemental figure 1. *S. Tm* superspreaders and non-superspreaders have differentially enriched metabolic pathways at 7 and 14 DPI

Corresponds with figure 1

- A) Differential pathway enrichment of non-superspreaders and superspreaders at 7 DPI with multiple hypothesis correction (Likelihood ratio with Benjamini & Hochberg correction).
- B) Differential pathway enrichment of non-superspreaders and superspreaders at 21 DPI with multiple hypothesis correction (Likelihood ratio with Benjamini & Hochberg correction).

Supplemental figure 2. *S. Tm* genetic pathways enriched *in vivo* and *in vitro*

Corresponds with figure 2

- A) Log2 fold differences of differentially enriched genetic pathways (adjusted p-value < 0.05) *in vitro* (blue) and *in vivo* (red). Each data point represents single gene within each sub pathway (y-axis). Sub pathways are annotated with corresponding major pathways (brackets along y-axis)
- B) Principal component analysis of *in vivo* and *in vitro* transcriptomes. *In vivo* and *in vitro* transcriptomes separate along PC1.

Supplemental figure 3: Exogenous dietary L-arabinose does not induce inflammation

Corresponds with figure 4. The data in this figure are from a single mouse experiment.

- A) Lipocalin-2 levels detected in feces of the indicated groups 4-days post treatment (diet and/or infection) by Elisa. n=5 mice
- B) qRT-PCR of mRNA extracted from spleens from indicated groups 5 days post treatment. n=5 mice.
- C) qRT-PCR of mRNA extracted from colons from indicated groups 5 days post treatment. n=5 mice

Supplemental figure 4: Carnitine supplementation does not confer a competitive advantage to WT *S. Tm* and L-arabinose concentrations decrease during infection in germ-free mice

Corresponds with figure 4

- A) 129X1/SvJ mice were inoculated with an equal mixture of *S. Tm*^{WT} and *S. Tm*^{cai}. Each dot represents data from one animal (biological replicate). Bars represent +/- SEM. *p < 0.05, ** p < 0.01. Kruskal-Wallis. No difference across groups. N=10 per group.
- B) L-Arabinose concentration in the germ-free mouse feces was quantified by liquid LC/MS. Students T test, *** p < 0.001

Supplemental figure 5. *S. Tm* arabinofuranosidase has conserved functional residues with previously characterized arabinofuranosidases

Corresponds with figure 5

- A) Amino acid sequence alignment of STM0148 (grey highlight) against three characterized arabinofuranosidase amino acid sequences. Red rectangles show conserved critical residues for enzyme function.
- B) Amino acid sequence alignment of STM0148 against five other *Salmonella* serovars'' arabinofuranosidase amino acid sequences. Red rectangles show conserved critical residues for enzyme function. Pink highlight indicates amino acid differences compared to SL1344 (first strand).

Table S1: Related to Figure 5. SL1344 predicted glycoside hydrolases

Gene ID	Cazyme family	Reference accession
SL1344_0018	GH18	CBW16119.1
SL1344_3087	GH23	CBW19186.1
SL1344_0016	GH108	CBW16117.1
SL1344_0042	GH31	CBW16143.1
SL1344_0148	GH43	CAB89837.1
SL1344_0234	GH19	CBW16336.1
SL1344_0255 (MltD)	GH23	CBW16357.1
SL1344_0396	GH13	CBW16496.1
SL1344_0966 (NucD)	GH24	CBW17063.1
SL1344_1119 (FlgJ)	GH73	CBW17215.1
SL1344_1146 (NagZ)	GH3	CBW17242.1
SL1344_1188	GH33	CBW17283.1
SL1344_1251 (CelF)	GH4	CBW17347.1
SL1344_1488 (GlgX)	GH13	CBW17583.1
SL1344_1489	GH13	CBW17584.1
SL1344_1490	GH13	CBW17585.1
SL1344_1724 (TreA)	GH37	CBW17819.1
SL1344_1727 (MltE)	GH23	CBW17822.1
SL1344_1846	GH105	CBW17940.1
SL1344_1892 (AmyA)	GH13	CBW17987.1
SL1344_1956	GH19	CBW18053.1
SL1344_2144 (BglX)	GH3	CBW18240.1
SL1344_2529 (YfhD)	GH23	CBW18629.1
SL1344_2576	GH24	CBW18677.1
SL1344_2686 (Nucd2)	GH24	CBW18788.1
SL1344_2811 (MltB)	GH103	CBW18909.1
SL1344_2857 (IagB)	GH23	CBW18955.1
SL1344_2968 (MltA)	GH102	CBW19067.1
SL1344_3027 (BglA)	GH1	CBW19126.1
SL1344_3480 (MalQ)	GH77	CBW19575.1
SL1344_3504 (GlgX)	GH13	CBW19598.1
SL1344_3505 (GlgB)	GH13	CBW19599.1
SL1344_3568 (TreF)	GH37	CBW19662.1
SL1344_3570 (fragment)	GH24	CBW19664.1
SL1344_3582 (YhjM)	GH8	CBW19676.1
SL1344_3628 (BaX)	GH73	CBW19721.1
SL1344_3629 (MalS)	GH13	CBW19722.1
SL1344_3644	GH127	CBW19737.1
SL1344_3715	GH31	CBW19809.1
SL1344_3740	GH1	CBW19832.1

SL1344_3767	GHnc	CBW19857.1
SL1344_3965	GH31	CBW20055.1
SL1344_4153	GH23	CBW20241.1
SL1344_4235	GH4	CBW20321.1
SL1344_4358	GH30	CBW20445.1
SL1344_4384 (TreC)	GH13	CBW20472.1
SL1344_4509 (Sit)	GH23	CBW20598.1
SL1344_P2_0087 (PilT)	GH23	CCF76895.1

Table S2: Related to STAR Methods. Oligonucleotides used in this study

Primer name: description	Sequence 5'-3'	Source
SR114: caiTABCD forward lambda	AAATCGGGAATTGAACCGAAGGTTTTTTTTCCGCC ATTAAGTGTAGGCTGGAGCTGCTTC	IDT
SR115: caiTABCD reverse lambda	CGGATCGCGTTTTTCGGCAAATGCCTGCGGTCCTT CGAGCCATATGAATATCCTCCTTAG	IDT
SR116: caiTABCD forward verification	CTGGCTCAACAATATTGAACGC	IDT
SR117: caiTABCD reverse verification	GCGAGTGGGCCAATATAAACAC	IDT
SR118: caiTABCD reverse/internal verification	CGCGATGGTGTATACGCC	IDT
SR119: araBAD forward verification	GACCAGGACGACAGAGCTTCC	IDT
SR120: araBAD reverse verification	CAGATTCATCAACGCGCCC	IDT
SR121: araBAD reverse-internal verification	GCGTCAGGGTATAGCTGCTTTCATACTC	IDT
SR148: 0148 lamda forward	AAACCCGTTTATTGAACAACGTGCCGATCCGTTTA TTTTAGTGTAGGCTGGAGCTGCTTC	IDT
SR149: 0148 lamda reverse	TGGCGGCACGCCAAAATCAGGCATCCCGTTTTTCGT CCCAGCATATGAATATCCTCCTTAG	IDT
SR150: 0148 forward verification primer	CGGCGTTGGCTATCTGATTA	IDT
SR151: 0148 reverse verification primer	CAATATCAGGTGCTCACACGTCTG	IDT
SR150: 0148 reverse-internal verification primer	CTGGGAATGTTCCAGCATCG	IDT
Mouse IFN γ qPCR forward	AGCGGCTGACTGAACTCAGATTGTAG	IDT
Mouse IFN γ qPCR reverse	GTCACAGTTTTTCAGCTGTATAGGG	IDT
Mouse <i>GAPDH</i> qPCR F primer	ACAGTCCATGCCATCACTGCC	IDT
Mouse <i>GAPDH</i> qPCR R primer	GCCTGCTTCACCACCTTCTTG	IDT
Mouse TNF α qPCR F primer	GATCGGTCCCCAAAGGGATG	IDT
Mouse TNF α qPCR R primer	TGGTTTGTGAGTGTGAGGGTC	IDT
Mouse IL-6 qPCR F primer	TCCAGTTGCCTTCTTGGGAC	IDT

Mouse IL-6 qPCR R primer	AGTCTCCTCTCCGGACTTGT	IDT
Mouse IL-1 β qPCR F primer	AGCTTCCTTGTGCAAGTGTCT	IDT
Mouse IL-1 β qPCR R primer	GACAGCCCAGGTCAAAGGTT	IDT
Pfog forward	CGATTCTGAATTCTATCGATAAGCTTGATATCGCGA CAAG	IDT
Pfog reverse	CGATTCGGATCCCGCTCTAGAACTAGTGGATCGGA TAAATC	IDT
0148_up_forward	CGACAAGTGAATCCAATAT	IDT
0148_up_reverse	CTTTTGGATCGTTAGTGATCACGCCCTGGCATTAT CGTCTGTC	IDT
0148_insert_forward	CGTGATCACTAACGATCCAAAAG	IDT
0148_insert_reverse	CAGTTTGCGGGAAGACTTTCAC	IDT