Supplementary

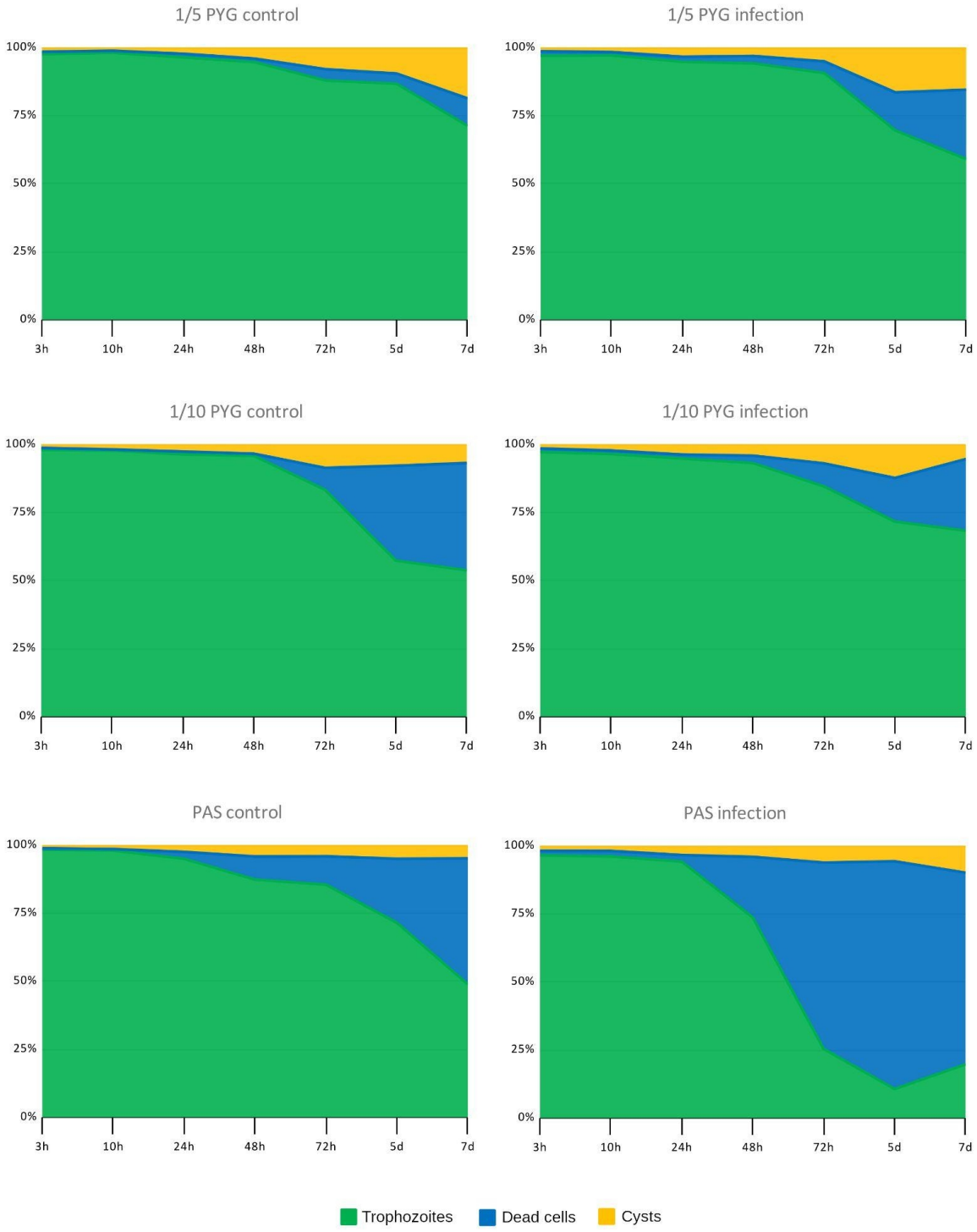
Table S1. List of primers used in this study. All primers were designed using the Vector NTI program (Invitrogen, USA).

	Primer sequence (5` – 3`)	Gene function
	katG	catalase-peroxidase
F	ATTCCAACCGTTCTAACCCGCTG	
R	GCCATACGAATAAACAAACCGACATAGC	
	grxA	Glutaredoxin I. Cell redox homeostasis.
F	GCCCTTATTGCGTGCGTGC	
R	CTGCGGTACGGTTTCTACAGGTTTAC	
	sitA (SPI-1)	manganese/iron transport system, iron uptake
F	CGCCGATCAACAGGGGACG	
R	CGACATACAGCACGCCGCC	
	entS	enterobactin exporter, iron uptake
F	ATGAATCGACAATCCTGGCTGCTC	
R	AGGTGGAGTGCGTCATCATTTGG	
	aceB	Malate synthase
F	TACGCCAAAACGCAATAAACTCCTG	
R	CGGAATACCACGAATCTGCCAATTAC	
	agp	glucose-1-phosphatase/inositol phosphatase
F	GCTGTTTTGTTGTCATCCGCCG	
R	CGCCTTTCGTCGTCAGTTGCC	
	fliL	flagellar basal body-associated protein FliL
F	GTTGATTACCCTCGCCGCCTG	
R	GGTCACGCCGATATACAACACGC	
	cheA	chemotaxis family, sensor kinase
F	GAGAGCGTAGCCGAAACCGAATC	
R	TCCGTCAGAGTAGCCAGATTGCC	
	yjdE	arginine:agmatine antiporter
F	GTCAAAAACCCGAAACGCAATGTG	
R	CCGCACAGAAGGAAACAATAGCCC	
	cadB	lysine/cadaverine antiporter
F	GTTTCCGCCTTTACCGCTTTCG	
R	TTTCACCGCAGCCAACAGCAG	
	rfaZ	lipopolysaccharide core biosynthesis protein
F	GGGCGACTGGCTGGATTTTG	
R	TGGCATAGGGCTGGTAGATTCGTC	
	mliC	lysozyme inhibitor
F	GGAATACCAGTGTGATGAGAAGCCG	
R	GCCTTGCGACCAGAAAACATAAATC	
	pliC	lysozyme inhibitor
F	CGTCAACACCGAGGCTGGAAAC	
R	CGTCAACACCGAGGCTGGAAAC GTCTATGGCTTCGTAATTTGCTCCG	
	hilA (SPI-1)	main transcriptional regulator of SPI1
F	TGCCGTTCTGGTCATCCTGCTC	
R	ACCGATAGCCCTGTCCGTACAGTG	
	sipC (SPI-1)	Actin-binding protein that interferes with host cell actin cytoskeleton
F	GCGAAGGGATGAATGCGTTGTC	
R	TGTGGCTTTCAGTGGTCAGTTTATCG	
	invF (SPI-1)	invasion regulatory protein, SPI-1
F	TGGGTTTTGCTGAGTCCTGAGTTTC	
R	CATTCTCATCGTGTTGCCGCTG	
	phoP (SPI-2)	DNA-binding transcriptional regulator SPI-2
F	CATCCCGCCGTTCCAGGTG	

R	CGAATCTTTGCTGACCACTTTACCG	
	sseC (SPI-2)	translocation machinery component
F	AATGTCAGTTGCGTTTCCTCGGG	
R	CGGGTACGGCATCAAGCAGTTG	
	gyrA	DNA gyrase subunit A
F	TGAGCGACCTTGCGAGAGAAATTAC	
R	TGTTCCAGTCATTGCCCAATACG	
	glnA	glutamine synthetase
F	CTGAACGAGCACGAAGTGAAGTTTG	
R	CCGCCGATAGAGGAGCCGTC	

Table S2. qPCR results showing relative expression of *Salmonella* Typhimurium 14028S genes during infection of *Acanthamoeba castellanii*. Statistically significant differences ($p \leq 0.05$) between experimental and control cultures are marked with an asterisk (*).

Gene	Function	SA (2 h)	SA (8 h)	SA (15 h)
Carbon metabolism				
agp	Glycolysis	-1.20	-1.27	-5.81*
aceB	Glyoxylate cycle	1.55	1.92	-1.87
Intracellular stress adaptation				
grxA	oxidative stress	13.59*	5.52*	1.73
katG	oxidative stress	3.80*	2.94*	-5.26*
sitA	Iron uptake	5.47*	6.90*	2.99*
entS	Iron uptake	28.76*	883*	54.16*
Virulence				
hilA	SPI-1	3.50*	6.48*	4.5*
invF	SPI-1	1.72*	1.25	-1.02
sipC	SPI-1	-1.16	-1.34	-1.33
phoP	SPI-2	-1.37	25.77*	5.46*
sseC	SPI-2	-4.98*	3.45*	1.05
mgtC	SPI-3	35.59*	11439*	1108*
Persistence				
cheA	chemotaxis	26.79*	36.68*	1.46
mliC	Lysozyme inhibitor	11.18*	30.76*	5.01*
pliC	Lysozyme inhibitor	5.47*	8.92*	2.01*



Supplementary Fig, 1. The dynamics of trophozoites, dead cells and cysts of *Acanthamoeba castellanii* in control cultures (A, C, E) and cultures infected with *Salmonella* Typhimurium 14028S (B, D, F) in media with different concentration of organic compounds (1/5 PYG, 1/10-PYG, and PAS).