Supplemental Figure

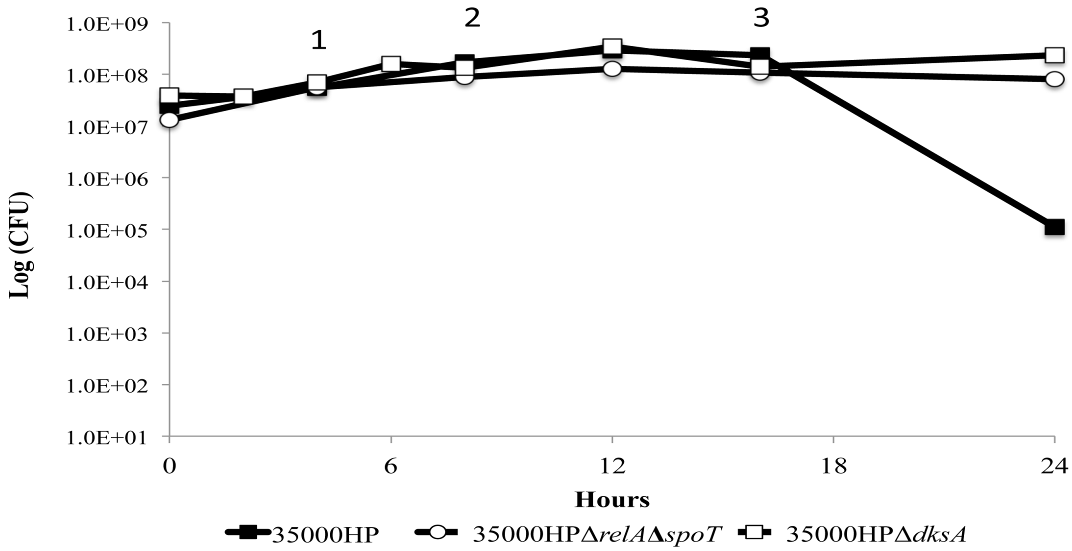

Fig. S1. Growth kinetics of 35000HP, 35000HPΔ*relA*Δ*spoT*, and 35000HPΔ*dksA* in GC broth. Growth kinetics were determined by measuring the colony forming units (CFU) at different time points following inoculation from overnight cultures. 1, 2, and 3 indicate the time points at which bacteria were harvested for transcriptome analysis in the mid-log, transition, and stationary growth phases, respectively.

TABLE S1. Bacterial strains and plasmids used in this study

Strain(s) or plasmid	Description[a]	Source or reference(s)
***E. coli* strains**		
DH5α, Top10, and HB101	Strains used for general cloning procedures	Invitrogen
DY380	DH10B derivative containing a defective λ prophage in which the *red, bet,* and *gam* genes are controlled by the temp-sensitive λ*cI857* repressor	(1)
***H. ducreyi* strains**		
35000HP	Human-passaged variant of strain 35000	(2)
35000HPΔ*dksA*	Unmarked, in-frame *dksA* deletion mutant	This study
FX517	35000HPΔ*dsrA::cat* insertion mutant	(3)
35000HPΔ*flp1-3*	Unmarked, in-frame *flp1-2-3* deletion mutant	(4)
35000HP.400	35000HPΔ*tadA::cat* insertion mutant	(5)
35000HPΔ*relA*Δ*spoT*	Unmarked, in-frame *relA* and *spoT* double deletion mutant	(6)
Plasmids		
pCH21	pCR-XL-TOPO containing the *dksA*-coding region along with 0.5- kb flanking regions	This study
pRSM2832	Plasmid containing spectinomycin resistance cassette flanked by the FRT sites	(7)
pRSM2072	*H. ducreyi* suicide vector	(8)
pRSM2975	Plasmid containing the origin of replication and kanamycin-resistance gene from pLS88, FLP recombinase gene from pFT-A and a point mutation conferring a temp-sensitive phenotype in *H. ducreyi*	(9)
pACYC177	Cloning vector, Kan^r Amp^r for complementation	New England Biolabs
pACYC184	Cloning vector, Cm^r Tet^r	New England Biolabs
pCH24	pACYC177 containing the 35000HP *dksA* gene with the *cat* promoter from pACYC184	This study
pCH30	pACYC177 containing the 35000HP *relA* and *spoT* gene with the *cat* promoter from pACYC184	(6)

[a] Kan^r, kanamycin; Amp^r, ampicillin; Cm^r and *cat,* chloramphenicol; and Tet^r, tetracycline.

TABLE S2. Oligonucleotides used in this study

Primer (gene)	Purpose	5' to 3' sequence[a]
P1 (*tbpA*-*dksA*, 5')	RT-PCR	ACGGAAGTGGATCCAGCATTTGTC
P2 *(tbpA*-*dksA*, 3')	RT-PCR	TAGCACGATCAGGATCAGCAA
P3 (*dksA*-*pcnB*, 5')	RT-PCR	TCGTCCGACTGCGGATATGTGTAT
P4 (*dksA*-*pcnB*, 3')	RT-PCR	TTCGCTTTGCTAAGGCTTCACTGC
P5 (*pcnB*- *folK*, 5')	RT-PCR	GTTGAATTATCGGCGTGGTGGCAT
P6 (*pcnB*- *folK*, 3')	RT-PCR	TGTGGCCCTATTGGCTGACTACAA
P7 (*dksA a*mplification, F)	*dksA* ORF and 500bp upstream	ATATATACTAGTGGCTGCTGAATTTGAAGAAGGCCA
P8 (*dksA* amplification, R)	*dksA* ORF and 500bp downstream	ATATATACTAGTCAGGTTTAGCATTAGTGGCAATATCC
P9 (Homology 1)	*dksA* and mutagenic cassette homology primer, Forward	AGTTATATTCAAAGATCAGGCTGACTTATCCAACAAGGAGTGCAATTATGA**TTCCGGGGATCCGTCGACC**
P10 (Homology 2)	*dksA* and mutagenic cassette homology primer, Reverse	CATTGTCCATTCCTATGTACCTATACTAACTAAAGCCCCATTTGTTTCTC**TGTAGGCTGGAGCTGCTTCG**
P11 (*dksA*, 5')	qRT-PCR	GTGCATGGCACGTGCAAATTATGG
P12 (*dksA*, 3')	qRT-PCR	TCTTCTTGGGTAGCACGATCAGCA
P13 (*pcnB*, 5')	qRT-PCR	AGTGGGTGGGTGTATCCGTGATTT
P14 (*pcnB*, 3')	qRT-PCR	TAAATCGCACCGCGCGTAACATTC
P15 (*dksA* ORF, F)	*dksA* fragment (#2) for complement, upstream	ATATATTCTAGACAAAGATCAGGCTGACTTATCATG
P16 (*dksA* ORF, R)	*dksA* fragment (#2) for complement, downstream	ATATATTCTAGAATTCCTATGTACCTATACTAACTA
P17 (*cat* promoter, R)	*cat* promoter of pACYC184 for complement (#1), upstream	CATATGATATCTAGAATATTTAGCTTCCTTAGCTCCTG
P18 (*cat* promoter, F)	*cat* promoter of pACYC184 for complement (#1), downstream	ATCCTGTCGGCTGTGGCACAGGCTGAACGCCGGAGGATCCGTTGATACCGGGAAGCCCTGGGCCAAC
P19 (*dnaE,* 5')	qRT-PCR, colony hybridization	AACGTTACCTTCAGCAAGCGGTTC
P20 (*dnaE,* 3')	qRT-PCR, colony hybridization	GGCGTTTGGGATCGTCGAGTGTAT
P21 (*dksA* int*,* 5')	mutagenesis, colony hybridization	TGCTGATCCTGCTGATCGTGCT
P22 (*dksA* int*,* 3')	mutagenesis, colony hybridization	TCCGCAGTCGGACGAGCTTCT
P23 (*lspB*, 5’)	qRT-PCR	AGCTAGAGCGGCTGACCCATTAAA
P24 (*lspB,* 3’)	qRT-PCR	GTGAGAAATTGCTCCGCTTTGGCT
P25 (*flp1, 5’)*	qRT-PCR	GGCTTAATTGCAGTCGCAGTTGCT
P26 (*flp1*, 3’)	qRT-PCR	GTGCCATTAGCGCTACTTATACCAG
P27 (*tadA,* 5’)	qRT-PCR	AATCAATGCCTTGCGTATGCGTCC
P28 (*tadA*, 3’)	qRT-PCR	TGTATTGGCGTGCAGGGTAGACAT
P29 (*ccmD,* 5’)	qRT-PCR	CGCAGATTTCTTTGCGATGGGA
P30 (*ccmD*, 3’)	qRT-PCR	CTCGGTAAGACAACCAAATTAGCCC
P31 (*HD1577,* 5’)	qRT-PCR	TAAATCAAGCGCTCGCACCGAAAC
P32 (*HD1577*, 3’)	qRT-PCR	AAACACACATTGTGGCGTGCCTTC
P33 (*sapF,* 5’)	qRT-PCR	TATTGGGCAGATTCTTGATGCGCC

P34 (*sapF*, 3')	qRT-PCR	CCCTTGCAAGTGCAATCCGTTGTT
P35 (*HD1904,* 5')	qRT-PCR	AGCTAACTATTCATTAGACGACCT
P36 (*HD1904*, 3')	qRT-PCR	AAGGCAATTTGTGGGAAATACT
P37 (*tadB,* 5')	qRT-PCR	GCAACCTCTTCAGGTGTTAGT
P38 (*tadB*, 3')	qRT-PCR	GCTTCTGCTGTCATTGCTTTC
P39 (*rfaD,* 5')	qRT-PCR	TATATGCTTCTAGCGCGGCCACTT
P40 (*rfaD*, 3')	qRT-PCR	CGCTTGCCATCGACCCTTTATGTT
P41 (*HD0457,* 5')	qRT-PCR	GCGTAATGATGGAAATGTCTCAAA
P42 (*HD0457*, 3')	qRT-PCR	TCCGCTAACTCTTTAGCTTTCTT
P43 (*lspA1,* 5')	qRT-PCR	CCGGAATTAAGTGGCTATGGT
P44 (*lspA1*, 3')	qRT-PCR	GCGATAAGCGCGGTCAATA
P45 (*glpF,* 5')	qRT-PCR	CGCCTGTATCGCAGAATGTAT
P46 (*glpF*, 3')	qRT-PCR	ACAAGTGCCGCAGCTAAA
P47 (*degP,* 5')	qRT-PCR	AGGGCAAACGGTGACATCTGGTAT
P48 (*degP*, 3')	qRT-PCR	AACTCACCGCCTTTAATGCCCAAC
P49 (*HD1218,* 5')	qRT-PCR	GCTCAGAGAATGAAATCACCAAAG
P50 (*HD1218*, 3')	qRT-PCR	TTATCGTTGGCTAGGAGTGTTG
P51 (*hfq,* 5')	qRT-PCR	TCGAGAGCGTATTCCCGTCTCAAT
P52 (*hfq*, 3')	qRT-PCR	TGTACGGCTTGTTGAGGAGCTTGT

[a] Boldfaced text represents sequences with homology to the mutagenic cassette. Underlined text indicates regions corresponding to restriction enzyme sites as mentioned in the text. *H. ducreyi* sequences are from GenBank accession no. AE017143.

Table S3: Summary of the RNA-seq read statistics

Bacterial Strain	Growth Phase	Biological Replicate	Total Reads	Aligned Reads	% Aligned Reads	% Unaligned Reads
35000HP	Mid-Log	R1	10,301,365	9,429,934	91.54%	8.46%
		R2	8,402,713	7,676,013	91.35%	8.65%
		R3	10,090,817	9,247,646	91.64%	8.36%
		R4	10,093,183	8,918,683	88.36%	11.64%
	Transition	R1	17,841,534	14,788,825	82.89%	17.11%
		R2	12,594,439	11,279,753	89.56%	10.44%
		R3	14,468,362	13,087,351	90.45%	9.55%
		R4	12,585,911	11,724,490	93.16%	6.84%
	Stationary	R1	12,250,624	10,667,706	87.08%	12.92%
		R2	13,022,098	11,743,715	90.18%	9.82%
		R3	11,638,354	10,314,179	88.62%	11.38%
		R4	11,745,737	10,479,877	89.22%	10.78%
35000HPΔ*relAspoT*	Mid-Log	R1	10,222,017	9,800,254	95.87%	4.13%
		R2	9,464,896	8,611,107	90.98%	9.02%
		R3	10,980,962	9,854,192	89.74%	10.26%
		R4	10,483,047	9,585,534	91.44%	8.56%
	Transition	R1	15,068,994	13,809,711	91.64%	8.36%
		R2	10,800,119	9,994,775	92.54%	7.46%
		R3	12,098,519	10,852,532	89.70%	10.30%
		R4	10,443,013	9,406,044	90.07%	9.93%
	Stationary	R1	15,008,374	13,617,319	90.73%	9.27%
		R2	10,355,069	9,240,150	89.23%	10.77%
		R3	11,335,796	10,479,164	92.44%	7.56%
		R4	8,205,523	7,542,286	91.92%	8.08%
35000HPΔ*dksA*	Mid-Log	R1	13,075,344	11,631,470	88.96%	11.04%
		R2	11,369,827	10,089,573	88.74%	11.26%
		R3	15,429,356	14,230,161	92.23%	7.77%
		R4	15,350,792	13,965,504	90.98%	9.02%
	Transition	R1	13,698,233	12,967,727	94.67%	5.33%
		R2	12,114,949	11,048,993	91.20%	8.80%
		R3	10,500,995	9,431,736	89.82%	10.18%
		R4	11,307,711	10,317,164	91.24%	8.76%
	Stationary	R1	13,934,290	12,469,947	89.49%	10.51%
		R2	13,181,478	12,347,374	93.67%	6.33%
		R3	12,793,798	11,909,717	93.09%	6.91%
		R4	13,875,693	12,545,996	90.42%	9.58%

SUPPLEMENTAL REFERENCES

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Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			35000HPΔ*dksA*/ 35000HP[c]		
			Fold-Change			Fold-Change		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
Amino acid biosynthesis								
	arcB1	Ornithine carbamoyltransferase	-2.67	-2.61				
	argB	Acetylglutamate kinase			-2.07			-2.24
	asd	Aspartate-semialdehyde dehydrogenase				2.79	3.49	3.53
	cysZ	Sulfate transporter, CysZ-type						3.26
	dapD	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase						2.06
	glnA	Glutamine synthetase type I					2.32	3.44
	HD1666	Probable phosphatase			-2.35			
	lysC	Aspartokinase			2.40			
	pheA	Chorismate mutase I / Prephenate dehydratase			2.99			3.02
	pyrD	Dihydroorotate dehydrogenase	-2.03	-2.38				
	pyrE	Orotate phosphoribosyltransferase			-3.76			
	pyrF	Orotidine 5`-phosphate decarboxylase			-3.46			
Amino acid Transport and Metabolism								
	aspA	Aspartate ammonia-lyase	3.06				-2.90	
	brnQ	Branched-chain amino acid carrier protein			-2.40			-2.65
	carA	Carbamoyl-phosphate synthase, small subunit	-4.29	-5.68				
	carB	Carbamoyl-phosphate synthase, large subunit	-3.97	-4.05				
	cysK	Cysteine synthase	-3.04					
	dat	Diaminobutyrate--2-oxoglutarate aminotransferase				3.80	4.90	2.81
	ddc	L-2,4-diaminobutyrate decarboxylase				3.06	3.16	
	HD1348	Nucleoside 5-triphosphatase RdgB (dHAPTP, dITP, XTP-specific)			-2.16			
	mazG	Nucleoside triphosphate pyrophosphohydrolase MazG			3.68			3.44
	nrdB	Ribonucleotide reductase of class Ia (aerobic), beta subunit			2.04			
	nudE	ADP compounds hydrolase			3.52			2.88
	pntA	NAD(P) transhydrogenase alpha subunit	-2.39		-2.53			
	pntB	NAD(P) transhydrogenase subunit beta	-2.50		-2.04		-2.44	
	potD1	Spermidine/putrescine-binding periplasmic protein (SPBP)	2.45			2.58	3.01	6.12
	potD2	ABC transporter, periplasmic spermidine putrescine-binding protein			7.01			5.06
	purA	Adenylosuccinate synthetase	-2.52		-2.24			
	purM	Phosphoribosylformylglycinamidine cyclo-ligase			2.58			2.36
	sdaC	Serine transporter	2.22					
	sucA	2-oxoglutarate dehydrogenase E1 component	-4.38					
	sucB	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex	-5.83					
	upp	Uracil phosphoribosyltransferase	-2.26		-6.29			-3.76
	uraA	Uracil permease		-2.17	5.77			5.07

Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			35000HPΔ*dksA*/ 35000HP[c]		
			Fold-Change			Fold-Change		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
Amino Sugar and nucleotide metabolism								
	apt	Adenine phosphoribosyltransferase			4.56			3.87
	apbE	Thiamin biosynthesis lipoprotein			-2.29			
	dxs	1-deoxy-D-xylulose 5-phosphate synthase			-2.09			
	glmU	Glucosamine-1-phosphate N-acetyltransferase	-2.60					
	kdsA	2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase			-2.60			-2.16
	manA	Mannose-6-phosphate isomerase		2.30				
	manX	Mannose-specific phosphotransferase IIAB component			-8.60			-5.21
	manY	Mannose-specific phosphotransferase system IIC component		2.35	-8.36			-6.35
	manZ	Mannose-specific phosphotransferase system IID component		2.56	-4.18			-3.27
	moaC	Molybdenum cofactor biosynthesis protein						-2.05
	moaD	Molybdenum cofactor biosynthesis protein			-2.81			-2.52
	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	-2.95		2.71			
	nagA	N-acetylglucosamine-6-phosphate deacetylase			-2.12			
	nanE	N-acetylmannosamine-6-phosphate 2-epimerase			-2.73			-2.96
	pta	Phosphate acetyltransferase			-2.34			
	ribH	6,7-dimethyl-8-ribityllumazine synthase			-2.54			
	thiL	Thiamine-monophosphate kinase	-2.59	-2.19	-2.31			
	thyA	Thymidylate synthase			4.53			2.24
	uppS	Undecaprenyl pyrophosphate synthetase			3.58			
	wecC	UDP-glucose dehydrogenase	-2.16					
Cellular Carbohydrate Biosynthetic Process								
	alr	Alanine racemase			2.23			
	araD	L-ribulose-5-phosphate 4-epimerase		2.27				
	eno	Phosphopyruvate hydratase			3.42		-2.16	3.48
	fbp	Fructose-1,6-bisphosphatase, type I		2.09				
	frdC	Fumarate reductase subunit C			-10.48			-5.81
	frdD	Fumarate reductase subunit D		3.01	-2.59			
	gmhA	Phosphoheptose isomerase 1			2.09			
	HD0112	Negative regulator of beta-lactamase expression					3.22	
	HD0297	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase			2.36			
	HD0746	Hypothetical protein				2.50	2.28	4.93
	HD0922	Tfp pilus assembly protein, pilus retraction ATPase PilT					3.04	
	kdkA	3-deoxy-D-manno-octulosonic acid kinase			2.09			
	lsgD	Lipopolysaccharide core biosynthesis glycosyltransferase WadA					2.04	
	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase			-2.74			
	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase			-2.47			
	neuA	N-Acetylneuraminate cytidylyltransferase			2.74			
	pckA	Phosphoenolpyruvate carboxykinase [ATP]			-2.60			
	rpiA	Ribose 5-phosphate isomerase A					2.92	2.22

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			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			35000HPΔ*dksA*/ 35000HP[c]		
			Fold-Change			Fold-Change		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	sgbU	L-xylulose 5-phosphate 3-epimerase		2.07				
	tpiA	Triosephosphate isomerase			2.13			
Carbohydrate Metabolism								
	aceF	Dihydrolipoamide acetyltransferase			-2.27			
	ampD	N-acetylmuramoyl-L-alanine amidase			5.80			2.24
	csrA	Carbon storage regulator			-2.34			
	rfaD	ADP-L-glycero-D-manno-heptose-6-epimerase						2.06
	suhB	Inositol-1-monophosphatase						2.44
Cell Division								
	ftsI	Peptidoglycan synthetase			-2.48			
	ftsL	Cell division protein			-5.21			-3.14
	ftsW	Cell division protein			-3.95			-2.11
	HD1001	Z-ring-associated protein ZapA			2.47			2.02
	HD1472	Conserved hypothetical protein			2.01			
	ispZ	Intracellular septation protein IspA			-2.01			
	mreC	Rod shape-determining protein			-2.41			
Cell Membrane								
	cdsA	Phosphatidate cytidylyltransferase			2.48			
	cdtA	Cytolethal distending toxin protein A	-2.49					
	cdtB	Cytolethal distending toxin protein B	-2.79		-2.59			-2.62
	cdtC	Cytolethal distending toxin protein C	-3.25		-2.93			-2.47
	crcB	putative fluoride ion transporter			-2.15			
	dppB	Dipeptide transport system permease protein			-2.22			
	dppC	Dipeptide transport system permease protein			-2.21			
	dsbB	Periplasmic thiol:disulfide oxidoreductase			2.14			
	dsrA	serum resistance protein					-2.06	
	fimA	Possible fimbrial major pilin protein	3.00	3.30	2.79	3.55		2.44
	fimB	Possible fimbrial structural subunit	2.38	2.15	3.04	2.61		2.48
	flp1	*flp* operon protein Flp1		-3.22	-3.72			
	flp2	*flp* operon protein Flp2		-3.39	-3.81			
	flp3	*flp* operon protein Flp3		-3.08	-8.91			-2.33
	glpT	Glycerol 3-phosphate transporter			-3.02		-2.11	-2.43
	HD0196	Putative membrane protein					-2.71	2.74
	HD0470	Probable component of the lipoprotein assembly complex with YaeT, YfgL, and NlpB)			3.27		2.13	4.80
	HD0587	LptA, protein essential for LPS transport across the periplasm			3.21			
	HD0665	Hypothetical protein	-2.73		4.15			
	HD1071	Putative membrane protein		3.92	4.59			
	HD1123	Type IV pilin PilA						-4.76
	hgbA	Outer membrane receptor proteins, mostly Fe transport	-2.35	-2.13	-2.54			

Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			**35000HPΔ*dksA*/ 35000HP[c]**		
			Fold-Change			**Fold-Change**		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	kefB	putative Glutathione-regulated potassium-efflux system protein		2.12				2.04
	lolC	Lipoprotein releasing system transmembrane protein			-2.19			
	momp	Major outer membrane protein			2.81			
	mrdA	Penicillin-binding protein 2 (PBP-2)			-2.31			-2.07
	oapB	opacity associated protein B	-2.92					
	ompA2	Outer membrane protein A precursor		-2.06		-2.67		
	ompP2A	Outer membrane protein P2 homolog	-3.05	-2.47		-2.71		
	ompP2B	Outer membrane protein P2 homolog	2.02		10.28	2.06		3.93
	ompP4	Outer membrane lipoprotein e (P4)						2.32
	pal	18K peptidoglycan-associated outer membrane lipoprotein					-2.15	
	rnfD	Putative Na-translocating NADH-quinone reductase			-2.21			
	smpA	Outer membrane lipoprotein SmpA, a component of the essential YaeT outer-membrane protein assembly complex	-2.34		9.96			5.06
	tadB	Flp pilus assembly protein			-12.05			-3.68
	tadC	Type II/IV secretion system protein TadC, associated with Flp pilus assembly			-2.19			
	yidC	Inner membrane protein translocase component YidC, long form						2.22
Cellular Homeostasis								
	citD	Citrate lyase, gamma subunit					2.00	
	citE	Citrate lyase, beta chain		2.36				
	cydA	Cytochrome d ubiquinol oxidase subunit I					-2.32	
	cydB	Cytochrome d ubiquinol oxidase subunit II					-2.11	
	dsbA	Periplasmic thiol:disulfide interchange protein			4.97			2.93
	dsbE1	Cytochrome c-type biogenesis protein			-2.12			-2.27
	ftpA	Fine tangled pili major subunit	-2.15		7.79			3.03
	ftsH	Cell division protein		4.41				
	HD0697	thioredoxin-like protein			3.74			
	HD0700	Peroxiredoxin family protein/glutaredoxin			2.66		-2.24	
	lpdA	Dihydrolipoamide dehydrogenase			-2.02			
Cellular Response to Stress								
	cpxR	Transcriptional regulatory protein CpxR			7.19			5.89
	HD0357	Probable carbon starvation protein A			-2.23		-2.02	
	hfq	RNA-binding protein			11.67			2.64
	spoT	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	NA	NA	NA			2.09
DNA Binding								
	HD0292	Hypothetical protein			5.41			4.00
	HD0509	Hypothetical protein				2.17	4.63	2.18
	HD1613	Hypothetical protein			3.84			2.37
	hupA	DNA-binding protein HU-alpha			3.04		-2.18	2.19

Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			35000HPΔ*dksA*/ 35000HP[c]		
			Fold-Change			Fold-Change		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	ner	possible DNA-binding protein						-2.77
	uspA	Universal stress protein A			-4.57			-3.20
DNA Metabolic Process								
	dnaA	Chromosomal replication initiator protein			2.82			2.88
	dnaJ	Chaperone protein		7.55				
	gam	putative host-nuclease inhibitor protein					2.24	
	HD0095	Mu phage DNA transposition protein B			-2.06		2.02	
	HD1444	Hypothetical protein					2.80	2.61
	HD1452	Hypothetical protein					2.85	2.86
	HD1686	methylates LSU ribosomal protein L3p					-2.12	2.15
	ihfA	Integration host factor alpha subunit			-2.13			-2.26
	ihfB	Integration host factor, beta subunit			-3.68			
	lexA	Probable LexA repressor			2.05			
	mutM	Formamidopyrimidine-DNA glycosylase		2.15		-2.09		
	mutT	Mutator MutT protein			2.16			
	mutY	A/G-specific adenine glycosylase					2.23	2.33
	nrdA	Ribonucleotide reductase of class Ia (aerobic), alpha subunit			-3.17			
	parC	Topoisomerase IV subunit A	2.01					
	rdgC	DNA recombination-dependent growth factor C			2.17			
	recN	DNA repair protein RecN			2.42			
	recR	Recombination protein RecR			2.99			2.07
	rep	ATP-dependent DNA helicase Rep			2.46			2.17
	ssb2	Single-stranded DNA-binding protein in PFGI-1-like cluster	-2.09					
	topB1	DNA topoisomerase III in PFGI-1-like cluster						6.19
	uvrA	Excinuclease ABC subunit A		2.02				
	xseB	Exodeoxyribonuclease VII small subunit			2.16			
Fatty Acid Biosynthesis and Metabolism								
	accA	Acetyl-coenzyme A carboxyl transferase alpha chain			-2.97			-2.83
	acpP	Acyl carrier protein			3.08			3.12
	fabA	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase		2.53	2.61			
	fabB	3-oxoacyl-[acyl-carrier-protein] synthase	3.02	6.02	2.86			
	fabH	3-oxoacyl-[acyl-carrier-protein] synthase			-2.47			
	fabI	Enoyl-[acyl-carrier-protein] reductase			4.80			3.18
	HD1711	Acyl-CoA thioesterase YciA, involved in membrane biogenesis			-3.59			-2.38
	ispB	Octaprenyl diphosphate synthase			2.27			2.56
	lst	N-acetylneuraminic acid synthase-like protein			2.83			
	waaF	ADP-heptose--lipooligosaccharide heptosyltransferase II	-2.95		2.28			2.03
Intracellular Trafficking and Secretion								
	HD0974	Chromosome partitioning ATPase in PFGI-1-like cluster, ParA-like	2.61					

Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			35000HPΔ*dksA*/ 35000HP[c]		
			Fold-Change			Fold-Change		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	HD1305	Type II/IV secretion system ATPase TadZ/CpaE, associated with Flp pilus assembly			-3.47			
	HD1528	Eha					2.25	
	hhdA	Hemolysin			-3.99			-2.09
	hhdB	Channel-forming transporter/cytolysins activator of TpsB family	-2.08	-2.19				
	hofB	Type IV fimbrial assembly, ATPase PilB						-2.25
	lspA1	Large supernatant protein 1	-2.22		-2.75			
	lspA2	Large supernatant protein 2	-3.28		-5.07			
	lspB	Large supernatant protein exporter			-5.36			
	rcpA	Type II/IV secretion system secretin RcpA/CpaC, associated with Flp pilus assembly			-4.89			
	rcpB	Flp pilus assembly protein RcpB			-5.80			-2.18
	secG	Preprotein translocase subunit			2.28			2.27
	secY	Preprotein translocase SecY subunit			-2.45			
	tadD	Flp pilus assembly protein TadD, contains TPR repeat			-2.31			
	tadF	Flp pilus assembly surface protein TadF, ATP/GTP-binding motif			-3.21			
	tatA	Twin-arginine translocation protein						-2.00
	yajC	Preprotein translocase subunit			-3.25			-2.34
Ion Transport								
	corA	Magnesium and cobalt transport protein CorA	4.29	2.90				
	HD0003	ATP synthase protein I2			-3.77			-2.03
	HD0810	Conserved hypothetical protein	2.27		2.08			2.67
	HD0866	Anion permease ArsB/NhaD-like	2.47					
	HD1227	Putative Na+/H+ antiporter			3.48			
	HD1621	Conserved hypothetical protein	2.13					
	nqrA	Na+-translocating NADH-ubiquinone oxidoreductase, subunit A			-10.26			
	nqrB	NADH dehydrogenase			-8.72			-2.32
	nqrC	Na+-translocating NADH-ubiquinone oxidoreductase, subunit C			-6.16			
	nqrD	Na+-translocating NADH-ubiquinone oxidoreductase, subunit D		2.00	-5.39			-2.22
	nqrE	Na+-translocating NADH-ubiquinone oxidoreductase, subunit E		2.15	-3.63			
	nqrF	Na+-translocating NADH-ubiquinone oxidoreductase, subunit F		2.85	-2.03			
	oadB	Oxaloacetate decarboxylase beta chain		2.04				-2.21
	yfeB	Manganese ABC transporter, ATP-binding protein SitB			4.97			
	znuA	Zinc ABC transporter, periplasmic-binding protein						2.89
Iron Sulfur Cluster Binding								
	bioA	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase			2.05			
	bioB	Biotin synthetase		2.10				
	bioD	Dethiobiotin synthetase		-2.04				
	chuW	Putative heme iron utilization protein			-3.14			-2.01
	fdx2	Ferredoxin, 2Fe-2S			-2.37			

Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			**35000HPΔ*dksA*/ 35000HP[c]**		
			Fold-Change			**Fold-Change**		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	HD0319	Ribosomal RNA large subunit methyltransferase N			-2.85	2.40	2.63	
	HD0684	Probable iron binding protein from the HesB_IscA_SufA family			2.38			
	HD1084	HesB family protein			-5.34			-3.16
	iscU	Iron-sulfur cluster assembly scaffold protein		2.51	-2.67			-2.05
	ykgF	Putative iron-sulfur electron transport protein			-2.39			
Lipid Biosynthesis and Metabolism								
	glpB	Anaerobic glycerol-3-phosphate dehydrogenase subunit B			-3.95			-2.58
	hlp	putative lipoprotein			2.17			2.48
	hlpB	lipoprotein			3.35			3.12
	lgtB	diadenosine tetraphosphatase						3.13
	lipB	Lipoate-protein ligase B			-2.40			
	lpxB	Lipid-A-disaccharide synthase				2.13	2.83	
	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase						2.16
	menB	Naphthoate synthase			-2.05			
	pgpA	Phosphatidylglycerophosphatase A	-2.06					
	pgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase			2.49			2.16
	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase			-3.94			-2.73
Metal Ion Binding								
	cysQ	3'(2'),5'-bisphosphate nucleotidase			3.17			2.79
	ftnA	Ferritin-like protein 2		-2.08	2.42		-2.26	4.17
	ftnB	Ferritin-like protein 2		-2.05	3.17		-2.38	5.26
	glmM	Phosphoglucosamine mutase					2.78	2.56
	gpt	Xanthine-guanine phosphoribosyltransferase)			2.58			3.33
	HD0117	hypothetical protein					3.91	
	HD0457	Soluble cytochrome b562			5.44			5.49
	HD1365	Carbonic anhydrase			2.33			
	HD1915	Membrane protein YedZ			2.56			
	msrB							
	napA	Periplasmic nitrate reductase precursor			-2.19		-2.09	-2.07
	napB	Nitrate reductase cytochrome c550-type subunit			-7.27	-2.05	-2.26	-5.53
	napC	Cytochrome c-type protein			-3.32		-2.24	-2.71
	napD	Possible protein		-2.48	-2.01		-2.02	
	napF	Ferredoxin-type protein		-3.04				
	napG	Ferredoxin-type protein NapG (periplasmic nitrate reductase)		-2.12	-5.26	-2.16		-4.01
	napH	Polyferredoxin NapH (periplasmic nitrate reductase)			-8.44	-2.22	-2.00	-5.89
	nrfA	Cytochrome c552 precursor					-2.27	
	nrfB	Cytochrome c-type protein NrfB precursor					-2.43	
	ppa	Inorganic pyrophosphatase			5.08			3.76
	rimO	Ribosomal protein methylthiotransferase			-2.50			

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			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			35000HPΔ*dksA*/ 35000HP[c]		
			Fold-Change			Fold-Change		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	sodA	Manganese superoxide dismutase			2.02			
	sodC	Superoxide dismutase [Cu-Zn] precursor		-2.06	2.40		-2.21	
	torZ	Trimethylamine-N-oxide reductase			-2.50			
Nucelotide Binding								
	atpA	ATP synthase alpha chain			-2.74			
	atpC	ATP synthase epsilon chain			-7.96			-3.16
	atpD	ATP synthase beta chain			-6.57			-2.09
	atpE	ATP synthase C chain			-9.69			-2.83
	atpF	ATP synthase B chain			-8.29			-2.65
	atpG	ATP synthase gamma chain			-4.20			
	atpH	ATP synthase delta chain			-4.63			
	coaD	Phosphopantetheine adenylyltransferase			-2.40			-2.38
	deaD	Cold-shock DEAD box protein-A	2.36					
	era	GTP-binding protein era homolog			-2.89			
	frdA	Fumarate reductase flavoprotein subunit			-6.76			-3.75
	frdB	Fumarate reductase iron-sulfur subunit			-6.61			-3.81
	guaA	GMP synthase [glutamine-hydrolyzing]	-2.40		2.13			
	guaB	Inosine-5-monophosphate dehydrogenase	-2.52	-2.16	3.02			
	HD0584	Hypothetical protein	-2.00		3.01			2.03
	HD0586	Lipopolysaccharide ABC transporter, ATP-binding protein LptB			2.89			
	HD0905	Mobile element protein	-2.60		-5.45			-3.04
	hflX	GTP-binding protein			11.32			2.98
	lldD	L-lactate dehydrogenase			-2.95			
	lolD	Lipoprotein releasing system ATP-binding protein			-3.10			-2.33
	ndk	Nucleoside diphosphate kinase			2.45			
	obgE	GTP-binding protein			-2.22			
	rnfG	Electron transport complex protein RnfG			-2.72			
	sapF	Peptide transport system ATP-binding protein SapF			3.77			3.47
	selD	Selenide, water dikinase						-2.21
	surE	5-nucleotidase / Exopolyphosphatase			-2.08		2.28	
	tadA	Type II/IV secretion system ATP hydrolase TadA/VirB11/CpaF, TadA subfamily			-6.86			-2.37
	tmk	Thymidylate kinase			2.05			
	typA	GTP-binding protein TypA/BipA						2.41
	uup	ABC-type transport protein Uup			-3.04			
	visC	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	-2.26					
Protein Fate								
	ccmA	ABC transporter involved in cytochrome c biogenesis, ATPase component			-3.08			-2.25
	clpB	Chaperone protein	-2.41	8.36				
	degP	Outer membrane stress sensor protease DegQ			2.50			

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			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			**35000HPΔ*dksA*/ 35000HP**[c]		
			Fold-Change			**Fold-Change**		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	dnaK	Chaperone protein	-2.09	7.70			2.00	
	fkpA	FKBP-type peptidyl-prolyl cis-trans isomerase			2.71			
	gcp							
	groEL	60 kDa chaperonin	-3.99	4.78	2.05			
	groES	10 kDa chaperonin	-3.47	5.10				
	grpE	Heat shock protein	-2.00	7.32				-7.21
	HD1278	Possible serine protease			-2.02		-2.39	
	HD1280	Possible serine protease homolog			-2.72		-2.21	
	HD1339	Cell wall endopeptidase, family M23/M37					2.07	
	HD1436	Hypothetical protein					2.11	
	HD1513	Putative RND efflux membrane fusion protein		2.81				
	HD1895	putative accessory processing protein			-3.53			-2.16
	hemK	Protein-N(5)-glutamine methyltransferase PrmC			-2.07			-2.08
	hscA	Chaperone protein		2.22	-2.69			
	hscB	Chaperone protein		2.06				
	hslU	ATP-dependent hsl protease ATP-binding subunit		15.78				
	hslV	ATP-dependent protease \		13.12				
	htpX	putative protease		14.26				
	icc	3',5'-cyclic-nucleotide phosphodiesterase			-2.78			-2.57
	iscS	Cysteine desulfurase		2.12				
	lepB	Signal peptidase I			-2.67			
	lon	ATP-dependent protease La, Type I		3.30				
	map	Methionine aminopeptidase						2.73
	pepB	Peptidase B	-2.51					
	pepD	Peptidase D			2.41			2.23
	ppiD	Peptidyl-prolyl cis-trans isomerase			2.42			
	prlC	Oligopeptidase A	-2.29	6.38				
	prmA	Ribosomal protein L11 methyltransferase			-2.02			
	proQ	ProQ: influences osmotic activation of compatible solute ProP			5.81			2.49
	slyD	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD		-2.12		2.01		2.05
	SohB	Possible secreted protease sohB						
	surA	Survival protein SurA homolog			4.13			2.21
RNA Binding								
	HD0356	Putative deoxyribonuclease YjjV			2.06			
	HD1200	RNA binding protein			3.97			2.98
	rsuA	Ribosomal small subunit pseudouridine synthase A			3.31			
	vacB	3'-to-5' exoribonuclease RNase R			2.04			
RNA Processing								
	HD0270	Putative tRNA/rRNA methyltransferase			-2.10			
	HD0448	tRNA dihydrouridine synthase B	2.23		-4.61			

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			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			**35000HPΔ*dksA*/ 35000HP[c]**		
			Fold-Change			**Fold-Change**		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	HD0478	23S rRNA (Uracil-5-) -methyltransferase rumB			2.75			2.52
	HD1138	tRNA pseudouridine synthase C			2.10			2.08
	HD1664	tRNA:Cm32/Um32 methyltransferase	-2.55		-2.68			
	ksgA	Dimethyladenosine transferase			2.03			
	miaA	tRNA dimethylallyltransferase			7.64			
	mnmC	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	-2.51	-2.77				
	pcnB	Poly A polymerase						2.14
	rbfA	Ribosome binding factor A	2.19	2.41	-8.10			-4.14
	rimM	16S rRNA processing protein RimM			-2.80			
	rnc	Ribonuclease III			-2.86			
	rnpA	Ribonuclease P protein component			3.80			3.54
	rrmJ	Cell division protein FtsJ / Ribosomal RNA large subunit methyltransferase E		2.32				
	rumA	23S rRNA (Uracil-5-) -methyltransferase RumA	2.21					
	sun	16S rRNA (cytosine(967)-C(5))-methyltransferase			-4.35			-3.63
	trmB	tRNA (guanine46-N7-)-methyltransferase			-2.91			-2.44
	trmD	tRNA (Guanine37-N1) -methyltransferase	2.02				-2.06	
	truA	tRNA pseudouridine synthase A						2.00
	truB	tRNA pseudouridine synthase B		2.00				
Transcription								
	argR	Arginine pathway regulatory protein, repressor of arg regulon			2.38			
	crp	Cyclic AMP receptor protein			2.78			
	cspC	Cold shock protein CspA	2.23		9.40		-2.84	7.48
	cspD	Cold shock protein CspD			-4.06			-2.63
	fis	DNA-binding protein			-4.63			
	greA	Transcription elongation factor			2.33			
	greB	Transcription elongation factor			-2.31			-2.21
	HD0089	Transcriptional regulatory protein			-3.15			
	HD0698	Unsaturated fatty acid biosythesis repressor FabR, TetR family			3.15			
	HD1533	Transcriptional regulator, IclR family		2.07		2.15	3.34	
	HD2030	Hypothetical protein	-2.36					
	hlyX	Catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases			2.14			2.35
	lrp	Leucine-responsive regulatory protein			-2.04			
	purR	Purine nucleotide synthesis repressor			2.08			
	rpoB	DNA-directed RNA polymerase beta subunit		2.25	-2.48			
	rpoC	DNA-directed RNA polymerase beta' subunit		2.92	-4.07			
	rpoE	RNA polymerase sigma-E factor			3.59			
	rpoZ	RNA polymerase omega subunit			2.88			
	rseA	Sigma factor RpoE negative regulatory protein			2.02			
	rseC	Sigma factor RpoE regulatory protein			-2.09			

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			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			35000HPΔ*dksA*/ 35000HP[c]		
			Fold-Change			Fold-Change		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	tldD	TldD protein, part of TldE/TldD proteolytic complex			-2.21			-2.07
Translation								
	asnA	Aspartate--ammonia ligase			4.83			
	def	Peptide deformylase			3.40		-2.08	2.21
	efp	Translation elongation factor P	2.01					4.27
	fusA	Translation elongation factor G			-2.85			
	HD1357	Conserved possible translation initiation factor	-2.38					
	hisS	Histidyl-tRNA synthetase			-3.50			
	infB	Translation initiation factor IF-2	2.03		-2.78			-2.22
	prfB	Peptide chain release factor 2; programmed frameshift-containing			2.42			
	prfC	Peptide chain release factor 3			-2.40			
	pth	Peptidyl-tRNA hydrolase			2.32			3.18
	rplA	LSU ribosomal protein L1p (L10Ae)	2.31					2.46
	rplB	LSU ribosomal protein L2p (L8e)			-2.36			
	rplC	LSU ribosomal protein L3p (L3e)	2.40		-2.44			
	rplD	LSU ribosomal protein L4p (L1e)	2.30		-3.03			
	rplE	LSU ribosomal protein L5p (L11e)	2.17					
	rplF	LSU ribosomal protein L6p (L9e)			-2.24			
	rplI	LSU ribosomal protein L9p	2.39		3.11			
	rplJ	LSU ribosomal protein L10p (P0)	4.69					
	rplK	LSU ribosomal protein L11p (L12e)	2.27		-2.01			
	rplL	LSU ribosomal protein L7/L12 (P1/P2)	5.31		2.19			3.25
	rplN	LSU ribosomal protein L14p (L23e)	2.10					
	rplO	LSU ribosomal protein L15p (L27Ae)			-4.03			-2.06
	rplP	LSU ribosomal protein L16p (L10e)			-2.06			
	rplX	LSU ribosomal protein L19p	2.41					
	rplY	LSU ribosomal protein L20p			-2.75			2.19
	rplS	LSU ribosomal protein L22p (L17e)	2.03		-3.43			
	rplT	LSU ribosomal protein L23p (L23Ae)	2.16		-3.49			
	rplV	LSU ribosomal protein L24p (L26e)	2.23					-2.13
	rplW	LSU ribosomal protein L25p	3.71		3.25			
	rpmB	LSU ribosomal protein L28p			2.35			2.58
	rpmC	LSU ribosomal protein L29p (L35e)			-2.04			
	rpmD	LSU ribosomal protein L30p (L7e)			-4.01			-2.00
	rpmE	LSU ribosomal protein L31p, zinc-dependent		-2.14	2.05			2.17
	rpmE2	50S ribosomal protein L31		2.31		2.90		
	rpmG	LSU ribosomal protein L33p, zinc-independent			3.00			3.00
	rpmH	LSU ribosomal protein L34p			2.68			2.35
	rpmI	LSU ribosomal protein L35p			-2.73			
	rpmJ	LSU ribosomal protein L36p		2.27	-3.14	2.81		
	rpsB	SSU ribosomal protein S2p (SAe)			2.19			

Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			**35000HPΔ*dksA*/ 35000HP[c]**		
			Fold-Change			**Fold-Change**		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	rpsE	SSU ribosomal protein S5p (S2e)			-2.12			
	rpsH	SSU ribosomal protein S8p (S15Ae)			-2.02			
	rpsI	SSU ribosomal protein S9p (S16e)			2.60			
	rpsJ	SSU ribosomal protein S10p (S20e)	2.58		-2.13			
	rpsM	SSU ribosomal protein S13p (S18e)			-2.28			
	rpsN	SSU ribosomal protein S14p (S29e), zinc-independent	2.08		-2.17			
	rpsO	SSU ribosomal protein S15p (S13e)	2.18		3.54			2.47
	rpsP	SSU ribosomal protein S16p	2.00		-2.69			
	rpsQ	SSU ribosomal protein S17p (S11e)			-2.14			
	rpsR	SSU ribosomal protein S18p, zinc-independent	2.13		2.07			
	rpsS	SSU ribosomal protein S19p (S15e)			-3.91			-2.07
	rpsT	SSU ribosomal protein S20p	3.23				-2.17	2.69
	selA	L-seryl-tRNA(Sec) selenium transferase						-2.05
	valS	Valyl-tRNA synthetase			-2.09			
Transport of Proteins and Carbohydrates								
	ampG	AmpG permease		2.02				
	ccmB	ABC transporter involved in cytochrome c biogenesis subunit			-3.68			-2.79
	ccmC	putative heme lyase for CcmE			-5.33			-3.32
	ccmD	Cytochrome C maturation protein D			-4.46			-2.57
	ccmF	Cytochrome c heme lyase subunit			-2.16			
	comE	Type IV pilus biogenesis protein PilQ			2.08			
	crr	PTS system, glucose-specific IIA component		2.06	5.85			4.64
	dcuB1	Anaerobic C4-dicarboxylate transporter	-2.25		3.59			
	dppD	Dipeptide transport ATP-binding protein			-2.19			
	glpF	Glycerol uptake facilitator protein	4.56		-46.33			-27.32
	HD0665	Hypothetical protein	-2.73		4.15			
	HD0800	21 kDa hemolysin precursor			2.61			
	HD1859	Ascorbate-specific PTS system, EIIA component			-5.34			-2.34
	ptsH	Phosphotransferase system, phosphocarrier protein HPr			4.12			3.08
	ptsN	PTS system nitrogen-specific IIA component, PtsN			2.05			
	thiQ	Thiamin ABC transporter, ATPase component / Thiamine transport ATP-binding protein thiQ			-2.73			
	tolB	Colicin tolerance protein			-2.96			
	tolR	Tol biopolymer transport system			-2.69			
	ulaA	Ascorbate-specific PTS system, EIIC component	2.00		-6.40			-4.41
Uncharacterized Conserved Protein								
	HD0105	Hypothetical protein	-2.21		-2.87		2.23	
	HD0123	Hypothetical protein					2.76	
	HD0134	Mu-like prophage protein GP36				3.71	5.03	
	HD0135	hypothetical protein				3.18	4.50	2.64

Table S4: Functional Classification of Genes differentially expressed by deletion of either (p)ppGpp or DksA In Mid-Log, Transition, or Stationary Phase.

			35000HPΔ*relA*Δ*spoT* / 35000HP[b]			**35000HPΔ*dksA*/ 35000HP**[c]		
			Fold-Change			**Fold-Change**		
Functional Category[a]	**Gene**	**Description or homolog**	**Mid- Log**	**Transition**	**Stationary**	**Mid- Log**	**Transition**	**Stationary**
	HD0136	hypothetical protein				3.77	4.99	
	HD0150	Phage FAD/FMN-containing dehydrogenase			-2.66		2.84	
	HD0250	Putative preQ0 transporter				2.11		3.69
	HD0326	Hypothetical protein co-occurring with RecR			2.27			
	HD0412	Tex			-2.52			
	HD0534	Phage FAD/FMN-containing dehydrogenase		2.55	-2.37		3.67	
	HD0588	Uncharacterized protein YrbK clustered with lipopolysaccharide transporters			2.25			
	HD0778	UPF0235 protein VC0458	-2.73	-2.42	-2.21			
	HD1218	Periplasmic lysozyme inhibitor of c-type lysozyme	-2.53		5.62			
	HD1377	Protein YeeX	-2.26	-2.46				
	HD1379	Hypothetical protein			-2.87			
	HD1386	Predicted P-loop ATPase fused to an acetyltransferase	-2.00		-2.00			
	HD1555	Phage terminase, large subunit					2.99	
	HD1556	Mu-like prophage FluMu protein gp29					2.28	
	HD1576	Phage FAD/FMN-containing dehydrogenase					2.72	
	HD1622	Conserved hypothetical protein						2.89
	HD1756	Putative xanthine/uracil permease			-5.78	3.11	2.42	6.18
	phnA	Alkylphosphonate utilization operon protein PhnA			2.05			3.87
	plpR1	RstR-like phage repressor protein			3.81			3.91
	plpR2	RstR-like phage repressor protein			3.93			4.00
	sanA	SanA protein			-3.86			-4.44
	slyX	SlyX-like protein					-2.68	
	ykgE	Conserved putative dehydrogenase subunit			-2.78			

[a] Does not include genes that encode hypothetical proteins.

[b] Genes or operons differentially regulated in 35000HPΔ*relAspoT* versus 35000HP.

[c] Genes or operons differentially regulated in 35000HPΔ*dksA* versus 35000HP.