Additional File 1: Microarray results for WT and Δ*rpoN S.* Typhimurium LT2 strains expressing DctD250

Locus Tag[a]	Gene Symbol	Function	WT/Δ*rpoN*[b]
Known σ^{54}-dependent operons and sRNA genes:			
STM0368	*prpB*	Proprionate catabolism (putative)	**45**
STM0369	*prpC*		**25**
STM0370	*prpD*		**72**
STM0371	*prpE*		**21**[c]
STM0830	*glnH*	Glutamine high-affinity transporter	**7.1**
STM0829	*glnP*		**2.4**
STM0828	*glnQ*		**2.9**
STM2355	*argT*	Lysine/arginine/ornithine transport	**3.5**
STM_R0152	*tke1*	GlmY sRNA	**0.9**
STM_R0167	*sraJ*	GlmZ sRNA	**1.1**
STM4007	*glnA*	Glutamine synthetase	**48**
STM4006	*glnL*		**3.5**
STM4005	*glnG*		**3.6**
Predicted σ^{54}-dependent operons:			
STM0462	*glnK*	Nitrogen regulatory protein pII	**3.6**
STM0463	*amtB*	Ammonium transport (putative)	**190**
STM0577		PTS system (putative)	**67**
STM0576			**3.8**
STM0575			**3.5**
STM0574			**59**
STM0573			**18**
STM0572			**23**
STM0649.S		Hydrolase (putative)	**11**
STM0650			**42**
STM0651			**8.8**
STM0652			**1.2**
STM0653	*ybeL*		**1.2**
STM0665	*gltI*	Glutamate/aspartate transporter	**1.8**
STM_R0126	*sroC*		**0.81**
STM0664	*gltJ*		**1.3**
STM0663	*gltK*		**1**
STM0662	*gltL*		**1.9**
STM1285	*yeaG*	Serine protein kinase (putative)	**2.5**
STM1284	*yeaH*		**2.5**
STM1303	*astC*	Arginine/ornithine/glutamine metabolism	**2.4**

Locus Tag[a]	Gene Symbol	Function	WT/Δ*rpoN*[b]
STM1304	*astA*		2.4
STM1305	*astD*		2.6
STM1306	*astB*		**3.3**
STM1307	*astE*		2.4
STM1690	*pspA*	Phage shock proteins	**17**
STM1689	*pspB*		0.9
STM1688	*pspC*		**4**
STM1687	*pspD*		1.3
STM1686	*pspE*		1.5
STM2360		Amino acid transport (putative)	**100**
STM2359			**11**
STM2358			**18**
STM2357			**3.3**
STM2356	*ubiX*		1.2
STM2840		Nitric oxide reductase	**16**
STM2841	*ygbD*		**7.1**
STM2842	*hypF*	Hydrogenase maturation proteins	**13**
STM2843	*hydN*		**14**
STM2853	*hycA*	Hydrogenase 3	**26**
STM2852	*hycB*		**12**
STM2851	*hycC*		**170**
STM2850	*hycD*		1.9
STM2849	*hycE*		**96**
STM2848	*hycF*		**25**
STM2847	*hycG*		**30**
STM2846	*hycH*		**6.4**
STM2845	*hycI*		**12**
STM2844			**9.4**
STM2854	*hypA*	Formate-hydrogen lyase system	**5.6**
STM2855	*hypB*		**39**
STM2856	*hypC*		**6.3**
STM2857	*hypD*		**25**
STM2858	*hypE*		**31**
STM3521		RNA repair system (putative)	**71**
STM3519	*rtcB*		**27**
STM3518	*rtcA*		**4.3**
STM3568	*rpoH*	Heat shock sigma factor (σ^{32})	1.7
STM3772		PTS system (putative)	**39**
STM3771			**37**
STM3770			**60**

Locus Tag[a]	Gene Symbol	Function	WT/Δ*rpoN*[b]
STM3769.S			**31**
STM3768			**24**
STM3767			**41**
STM3766			1.4
STM4172	*zraP*	Zinc resistance-associated protein	**16**
STM4173	*hydH*	Zinc resistance two-component system	**3.7**
STM4174	*hydG*		2.8
STM4244	*pspG*	Phage shock protein	1.4
STM4285	*fdhF*	Formate dehydrogenase	**29**
STM4535		PTS system (putative)	**16**
STM4536			1.7
STM4537			**66**
STM4538			**13**
STM4539			**43**
STM4540.S			**25**
Novel σ^{54}-dependent operon:			
STM2944	*ygcB*	CRISPR-associated proteins	1.6
STM2943			1.2
STM2942			1.3
STM2941	*yghJ*		1.2
STM2940			1.4
STM2939	*ygcH*		2.8
STM2938			**4.1**
STM2937	*ygbF*		0.8
Possible indirectly regulated σ^{54}-dependent operons:			
STM0144	*ppdD*	Pilin biogenesis (putative)	0.78
STM0143	*hofB*		**3.3**
STM0142	*hofC*		2.2
STM0515	*allA*	Allantoin utilization	1.1
STM0516	*allR*		1
STM0517	*gcl*		2
STM0518	*gip*		1.6
STM0519	*glxR*		2
STM0520			1.8
STM0521	*ybbV*		1.3
STM0523	*allB*		**3.2**
STM0524	*ybbY*		1.4
STM0525	*glxK*		0.99
STM0791	*hutH*	Histidine-ammonia lyase	**3.8**

Locus Tag[a]	Gene Symbol	Function	WT/Δ*rpoN*[b]
STM1252		Cytoplasmic protein (putative)	**3.1**
STM2038	*pduA*	Propanediol utilization	**0.75**
STM2039	*pudB*		**1.1**
STM2040	*pduC*		**2**
STM2041	*pduD*		**1.5**
STM2042	*pduE*		**0.46**
STM2043	*pduG*		**3.3**
STM2044	*pduH*		**0.46**
STM2045	*pduJ*		**0.58**
STM2046	*pduK*		**0.7**
STM2047	*pduL*		**4.3**[c]
STM2048	*pduM*		**2.5**
STM2049	*pduN*		**0.87**
STM2050	*pduO*		**1.4**
STM2051	*pduP*		**1.4**
STM2052	*pduQ*		**1.5**
STM2053	*pduS*		**1.7**
STM2054	*pduT*		**1.8**
STM2055	*pduU*		**0.94**
STM2056	*pduV*		**0.61**
STM2057	*pduW*		**2.1**
STM2058	*pduX*		**1.6**
STM2149	*stcD*	Chaperone-usher fimbriae (putative)	**1.5**
STM2150	*stcC*		**3.2**
STM2151	*stcB*		**1.9**
STM2152	*stcA*		**0.82**
STM2572	*yfhH*	Membrane transport protein (putative)	**3.1**
STM2773	*iroB*	Siderophore production	**2.1**
STM2774	*iroC*		**0.95**
STM2775	*iroD*		**4**
STM2776	*iroE*		**1.2**
STM2839	*ygaA*	EBP activator for STM2840 operon (putative)	**3.2**
STM2859	*fhlA*	EBP activator for *fdhF/hyc/hyp* operons	**3.5**
STM2899	*invF*	Cell invasion proteins	**2**
STM2898	*invG*		**5.9**
STM2897	*invE*		**1.7**
STM2896	*invA*		**1.8**
STM2895	*invB*		**1**
STM2894	*invC*		**1.9**
STM2893	*invI*		**0.9**
STM2892	*invJ*		**2**
STM2891	*spaO*		**1.9**

Locus Tag[a]	Gene Symbol	Function	WT/Δ*rpoN*[b]
STM2890	*spaP*		**1.6**
STM2889	*spaQ*		**0.69**
STM2888	*spaR*		**2.7**
STM2887	*spaS*		**1.4**
STM2886	*sicA*		**0.71**
STM2885	*sipB*		**1.1**
STM2884	*sipC*		**1.1**
STM2883	*sipD*		**1.2**
STM2882	*sipA*		**1.7**
STM3253		PTS system/sugar metabolism (putative)	**1.5**
STM3254			**1.8**
STM3255			**1**
STM3256			**3.7**
STM3257			**2.9**
STM3258			**1.4**
STM3259			**1.1**
STM3260			**2**
STM3261			**1.3**
STM3262			**1**

[a] Locus tags for all genes within operons in which at least one gene was up-regulated ≥3-fold (p-value <0.02) by RpoN in the microarray analysis; up-regulated genes are in **black** type and genes below the 3-fold cut off are in **grey** type). The up-regulated operons are grouped as known, predicted, novel, or possible indirectly regulated, as defined in Results.

[b] Both WT and Δ*rpoN* strains contain pPBHP92 expressing DctD250. Signal ratios below the 3-fold cutoff for up-regulation are displayed in **grey**.

[c] above 3-fold cutoff, but p-value >0.02