

Table 6. Genes with significantly altered expression in *ntrA* and *rpoS* mutants relative to WT (regulatory group 3).

ORF	Name	Description	<i>ntrA</i> /WT			<i>rpoS</i> /WT			Main role	Subrole	Potential to cross-hybridize [‡]	Putative prom. [§]	Paralog. family no.	Rank [¶]	Taqman <i>ntrA</i> /WT	Taqman <i>rpoS</i> /WT
			Ratio	SE*	<i>P</i> [†]	Ratio	SE*	<i>P</i> [†]								
BB0015	udk	Uridine kinase	1.59	0.20	0.01	1.66	0.20	0.004	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides		Y		34,44		
BB0044		Hypothetical protein	1.59	0.14	9E-04	1.74	0.18	3E-04	Hypothetical proteins			Y		35,47		
BB0084	nifS	NifS protein	1.61	0.17	0.002	1.70	0.22	0.005	Biosynthesis of cofactors, prosthetic groups, and carriers	Other		N		37,45		
BB0204	hflC	Lambda CII stability-governing protein	1.98	0.11	1E-06	1.64	0.26	0.019	Protein fate	Degradation of proteins, peptides, and glycopeptides		Y		50,42		
BB0232		HbbU protein	1.33	0.04	2E-06	1.75	0.24	0.008	Protein synthesis	Nucleoproteins		N		26,49		
BB0265		Hypothetical protein	0.70	0.06	0.006	0.68	0.07	0.007	Hypothetical proteins			N		21,17		
BB0279	fliL	Flagellar protein	1.68	0.13	2E-04	1.80	0.13	5E-06	Cellular processes	Chemotaxis and motility		Y		43,50		
BB0287	flbA	Flagellar protein	1.40	0.07	2E-04	1.62	0.26	0.023	Cellular processes	Chemotaxis and motility		N		28,39		
BB0295	hslU	Heat shock protein	0.57	0.06	0.002	0.66	0.03	3E-05	Protein fate	Protein folding and stabilization		Y	127	11,16		
BB0320		Hypothetical protein	1.68	0.10	5E-05	1.70	0.24	0.005	Hypothetical proteins			Y		42,46		
BB0321		Hypothetical protein	1.73	0.11	3E-05	1.46	0.13	0.004	Hypothetical proteins			N		45,33		
BB0334	oppD	Oligopeptide ABC transporter, ATP-binding protein	1.55	0.05	4E-08	1.48	0.17	0.013	Transport and binding proteins	Amino acids, peptides and amines		Y	4	32,34		
BB0337	eno	Enolase	1.42	0.06	9E-05	1.37	0.13	0.016	Energy metabolism	Glycolysis/ gluconeogenesis		N		29,29		
BB0428		Hypothetical protein	1.64	0.16	0.001	1.64	0.12	2E-04	Hypothetical proteins			Y		39,41		
BB0548	polA	DNA polymerase I	0.69	0.05	0.002	0.74	0.06	0.014	DNA metabolism	DNA replication, recombination, and repair		N		19,21		
BB0593		Long-chain-fatty-acid CoA ligase	1.48	0.11	0.002	1.63	0.15	7E-04	Fatty acid and phospholipid metabolism	Degradation		Y	25	31,40		
BB0597	mcp-3	Methyl-accepting chemotaxis protein	1.88	0.09	1E-07	1.45	0.10	4E-04	Cellular processes	Chemotaxis and motility		N	13	46,31		
BB0601	glyA	Serine hydroxymethyl-transferase	1.42	0.07	1E-05	1.62	0.15	9E-04	Amino acid biosynthesis	Serine family		Y		30,38		

BB0617		Hypothetical protein	1.93	0.25	0.003	1.56	0.11	2E-04	Hypothetical proteins		N		48,37		
BB0625		<i>N</i> -acetylmuramoyl-L-alanine amidase, putative	1.60	0.14	0.002	2.02	0.26	9E-04	Cell envelope	Biosynthesis of murein sacculus and peptidoglycan	Y		36,51		
BB0645	ptsG	PTS system, glucose-specific IIBC component	1.64	0.16	0.003	1.42	0.13	0.004	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	Y	16	40,30		
BB0681	mcp-5	Methyl-accepting chemotaxis protein	0.59	0.07	0.006	0.52	0.04	8E-05	Cellular processes	Chemotaxis and motility	Y	13	12,8		
BB0816		Hypothetical protein	2.13	0.37	0.005	1.52	0.15	0.002	Hypothetical proteins		N		51,36		
BB0825		Hypothetical protein	1.93	0.25	0.002	1.30	0.07	5E-04	Hypothetical proteins		N		49,28		
BB0828	topA	DNA topoisomerase I	1.89	0.22	0.002	0.76	0.05	0.005	DNA metabolism	DNA replication, recombination, and repair	N		47,23		
BB0836	uvrB	Excinuclease ABC, subunit B	0.75	0.04	2E-04	0.62	0.05	6E-04	DNA metabolism	DNA replication, recombination, and repair	N		25,12		
BB0844		Hypothetical protein	0.73	0.04	0.002	0.75	0.06	0.008	Hypothetical proteins		N	12	24,22		
BBA08		Conserved hypothetical protein	1.71	0.18	0.002	1.65	0.14	2E-04	Hypothetical proteins - Conserved	Conserved	N	139	44,43		
BBA25	dbpB	Decorin binding protein B	0.24	0.04	4E-04	0.34	0.08	0.004	Cell envelope	Other	N	74	1,2	0.07	0.13
BBA36		Lipoprotein	0.34	0.01	2E-07	0.43	0.06	0.001	Cell envelope	Other	N		4,5	0.05	0.09
BBA38		Hypothetical protein	0.63	0.05	4E-04	1.45	0.18	0.022	Hypothetical proteins		Y	146	13,32		
BBA60		Surface lipoprotein P27	1.58	0.20	0.012	0.74	0.03	1E-04	Cell envelope	Other	N		33,20		
BBA64		Antigen, P35	0.27	0.04	3E-04	0.35	0.11	0.010	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Y	54	3,3		
BBA65		Hypothetical protein	0.39	0.03	8E-07	0.49	0.06	0.002	Hypothetical proteins		Y	54	5,7		
BBA66		Antigen, P35, putative	0.26	0.02	8E-08	0.25	0.03	8E-05	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	Y	54	2,1		
BBA71		Hypothetical protein	0.66	0.06	0.004	0.65	0.08	0.013	Hypothetical proteins		Y	54	15,14		
BBA72		Hypothetical protein	0.43	0.05	3E-04	0.47	0.03	2E-05	Hypothetical proteins		N		6,6		
BBB19	ospC	Outer surface protein C	0.44	0.13	0.026	0.40	0.16	0.042	Cell envelope	Other	Y		7,4	0.02	0.01
BBB21		Hypothetical protein	0.52	0.05	5E-04	0.54	0.14	0.05	Hypothetical proteins		N		8,9		
BBF28		Hypothetical protein	1.66	0.20	0.008	1.75	0.15	2E-04	Hypothetical proteins		N		41,48		
BBI17		Hypothetical protein	1.63	0.17	0.003	1.48	0.18	0.02	Hypothetical proteins		Y		38,35		

BBM01		Hypothetical protein	0.55	0.06	0.001	0.78	0.05	0.007	Hypothetical proteins		Y	146	10,25
BBM21		Conserved hypothetical protein	0.55	0.05	2E-04	0.71	0.04	0.001	Hypothetical proteins - Conserved	+	N	141	9,18
BBM31		Conserved hypothetical protein	1.37	0.07	2E-04	1.26	0.04	5E-04	Hypothetical proteins - Conserved	+	N	50	27,27
BBO39	erpL	ErpL protein	0.64	0.02	2E-07	0.56	0.07	0.006	Cell envelope		Y	164	14,10
BBP33		Conserved hypothetical protein	0.68	0.02	5E-07	0.61	0.04	6E-05	Hypothetical proteins - Conserved		N	49	16,11
BBP41		Hypothetical protein	0.71	0.03	8E-05	0.74	0.02	5E-07	Hypothetical proteins	+	N	115	22,19
BBR06		Conserved hypothetical protein	0.70	0.05	0.003	0.84	0.02	1E-04	Hypothetical proteins - Conserved		N	149	20,26
BBR26		Conserved hypothetical protein	0.69	0.03	2E-06	0.64	0.08	0.007	Hypothetical proteins - Conserved	+	N	143	18,13
BBS44		Hypothetical protein	0.72	0.03	8E-05	0.66	0.08	0.015	Hypothetical proteins		N	115	23,15
BBS45		Conserved hypothetical protein	0.69	0.04	0.001	0.77	0.05	0.003	Hypothetical proteins - Conserved	+	Y	145	17,24

*Standard Error.

† *t*-test *P*-value indicating significant difference from ratio of 1.0.

‡ Probe for this ORF has ≥ 80% identity to another probe on the array.

§ Putative σ^{54} -dependent promoter upstream of this ORF. Y, putative promoter is present. N, no promoter found.

¶ Rank order, from lowest to highest, of *ntrA* mutant/WT, *rpoS* mutant/WT ratios.

|| Taqman ratio of indicated mutant/WT.