

Table S1. Comparison of transcript levels relative to wild type between *P. aeruginosa* *retS* and *retSgacS* double mutants. Transcriptomes of the *retS* and the wt strains have been published previously (Goodman *et al.*, 2004) Only those genes whose transcript levels changed >2-fold in the *retS* mutant relative to wt are shown.

Gene Name	<i>retS</i> /wt	<i>retSgacS</i> /wt	Description
PA1695_pscP_at	0.01	1.27	translocation protein in type III secretion
PA1707_pcrH_at	0.01	1.15	regulatory protein PcrH
PA0044_exoT_at	0.01	1.29	exoenzyme T
PA3843_at	0.01	1.28	hypothetical protein
PA2191_exoY_at	0.01	1.02	adenylate cyclase ExoY
PA3841_exoS_at	0.01	0.91	exoenzyme S
PA1706_pcrV_at	0.01	1.29	type III secretion protein PcrV
PA3842_at	0.01	1.31	probable chaperone
PA2783_at	0.01	1.50	hypothetical protein
PA1708_popB_at	0.01	1.47	translocator protein PopB
PA1699_at	0.01	1.72	conserved hypothetical protein in type III secretion
PA1709_popD_at	0.01	1.65	Translocator outer membrane protein PopD precursor
PA1693_pscR_at	0.02	1.29	translocation protein in type III secretion
PA1700_at	0.02	1.80	conserved hypothetical protein in type III secretion
PA1702_i_at	0.02	1.83	conserved hypothetical protein in type III secretion
PA1701_at	0.02	1.69	conserved hypothetical protein in type III secretion
PA1703_pcrD_at	0.02	1.54	type III secretory apparatus protein PcrD
PA2782_at	0.02	1.20	hypothetical protein
PA1715_pscB_at	0.03	1.52	type III export apparatus protein
PA1696_pscO_at	0.03	1.53	translocation protein in type III secretion
PA1704_pcrR_at	0.03	1.81	transcriptional regulator protein PcrR
PA1705_pcrG_i_at	0.03	1.25	regulator in type III secretion
PA1712_exsB_at	0.03	1.54	exoenzyme S synthesis protein B
PA1719_pscF_at	0.03	1.12	type III export protein PscF
PA1698_popN_at	0.03	1.85	Type III secretion outer membrane protein PopN precursor
PA1721_pscH_at	0.03	1.29	type III export protein PscH
PA1716_pscC_at	0.03	1.21	Type III secretion outer membrane protein PscC precursor
PA1692_at	0.04	0.98	probable translocation protein in type III secretion
PA2258_ptxR_at	0.04	1.80	transcriptional regulator PtxR
PA1691_pscT_at	0.04	1.08	translocation protein in type III secretion
PA1720_pscG_at	0.04	1.24	type III export protein PscG
PA1722_pscI_at	0.04	1.83	type III export protein PscI
PA1717_pscD_at	0.04	1.23	type III export protein PscD
PA1723_pscJ_at	0.04	1.18	type III export protein PscJ
PA1694_pscQ_at	0.04	1.17	translocation protein in type III secretion
PA1718_pscE_at	0.04	1.29	type III export protein PscE
PA1711_at	0.04	1.73	hypothetical protein
PA0852_cpbD_at	0.05	1.45	chitin-binding protein CbpD precursor
PA1710_exsC_at	0.05	1.18	exoenzyme S synthesis protein C precursor
PA2189_at	0.05	3.55	hypothetical protein
PA1714_at	0.05	1.37	hypothetical protein
PA1867_at	0.06	0.87	hypothetical protein
PA1183_dctA_at	0.06	0.97	C4-dicarboxylate transport protein
PA1725_pscL_at	0.06	1.57	type III export protein PscL
PA1697_at	0.06	1.78	ATP synthase in type III secretion system
PA4553_pilX_at	0.07	1.20	type 4 fimbrial biogenesis protein PilX
PA1724_pscK_at	0.07	1.46	type III export protein PscK
PA1713_exsA_at	0.07	1.63	transcriptional regulator ExsA

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA2255_pvcB_at	0.07	0.63	pyoverdine biosynthesis protein PvcB
PA1690_pscU_at	0.07	1.40	translocation protein in type III secretion
PA1868_xqhA_at	0.08	1.03	secretion protein XqhA
PA4555_pilY2_at	0.08	0.78	type 4 fimbrial biogenesis protein PilY2
PA0952_at	0.09	1.44	hypothetical protein
PA4554_pilY1_at	0.09	1.24	type 4 fimbrial biogenesis protein PilY1
PA4552_pilW_at	0.09	1.15	type 4 fimbrial biogenesis protein PilW
PA4556_pilE_at	0.09	0.75	type 4 fimbrial biogenesis protein PilE
PA4550_fimU_at	0.09	1.16	type 4 fimbrial biogenesis protein FimU
PA3091_at	0.10	1.52	hypothetical protein
PA1869_at	0.10	0.94	probable acyl carrier protein
PA3840_at	0.11	2.21	conserved hypothetical protein
PA4551_pilV_at	0.11	0.98	type 4 fimbrial biogenesis protein PilV
PA2784_at	0.12	1.75	hypothetical protein
PA0713_at	0.12	0.29	hypothetical protein
PA3278_at	0.14	0.78	hypothetical protein
PA4523_at	0.15	1.49	hypothetical protein
PA0396_pilU_at	0.17	0.97	twitching motility protein PilU
PA4704_at	0.18	1.12	hypothetical protein
PA0359_at	0.18	1.38	hypothetical protein
PA4528_pilD_at	0.19	0.91	type 4 prepilin peptidase PilD
PA0758_at	0.19	0.99	hypothetical protein
PA5043_pilN_at	0.19	1.69	type 4 fimbrial biogenesis protein PilN
PA5042_pilO_at	0.19	1.63	type 4 fimbrial biogenesis protein PilO
PA2179_at	0.19	0.31	hypothetical protein
PA0834_at	0.19	1.25	conserved hypothetical protein
PA5041_pilP_at	0.19	1.25	type 4 fimbrial biogenesis protein PilP
PA0714_at	0.19	0.88	hypothetical protein
PA5122_at	0.20	1.43	hypothetical protein
PA5040_pilQ_at	0.21	1.10	Type 4 fimbrial biogenesis outer membrane protein PilQ
ig_4326394_4327696_at	0.21	1.02	
PA1934_at	0.21	0.77	hypothetical protein
PA4771_lldD_at	0.22	0.56	L-lactate dehydrogenase
PA4404_at	0.22	1.17	hypothetical protein
PA1525_at	0.22	1.06	alkane-1-monooxygenase 2
PA0027_at	0.23	1.26	hypothetical protein
PA2785_at	0.23	1.30	conserved hypothetical protein
PA0391_at	0.23	1.23	hypothetical protein
PA4979_at	0.23	1.23	probable acyl-CoA dehydrogenase
PA5405_i_at	0.24	1.18	hypothetical protein
PA2873_at	0.24	0.79	hypothetical protein
PA5044_pilM_at	0.24	1.04	type 4 fimbrial biogenesis protein PilM
PA0602_at	0.24	0.80	probable binding protein component of ABC transporter
PA2436_at	0.24	0.88	hypothetical protein
PA2187_at	0.24	1.85	hypothetical protein
PA5404_at	0.25	1.46	hypothetical protein
PA3149_wbpH_at	0.25	1.27	probable glycosyltransferase WbpH
PA2841_at	0.25	1.54	probable enoyl-CoA hydratase/isomerase
PA1562_acnA_at	0.25	1.54	aconitate hydratase 1
PA4770_lldP_at	0.26	0.49	L-lactate permease

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA5139_at	0.27	1.17	hypothetical protein
PA0395_pilT_at	0.27	1.29	twitching motility protein PilT
PA1143_at	0.27	0.93	hypothetical protein
PA4682_at	0.28	1.07	hypothetical protein
PA3762_at	0.28	0.83	hypothetical protein
ig_5820909_5820113_at	0.28	0.98	
PA4369_at	0.29	1.13	hypothetical protein
PA3066_at	0.29	1.48	hypothetical protein
PA2178_at	0.29	0.73	hypothetical protein
PA3090_at	0.29	1.99	hypothetical protein
PA0026_at	0.30	1.25	phospholipase C, PlcB
PA3845_at	0.30	1.17	probable transcriptional regulator
PA0028_at	0.30	1.09	hypothetical protein
PA4772_at	0.30	0.48	probable ferredoxin
PA2054_cynR_at	0.30	1.21	transcriptional regulator CynR
PA4390_at	0.30	1.89	hypothetical protein
PA2874_at	0.30	0.93	hypothetical protein
PA2350_at	0.30	1.65	probable ATP-binding component of ABC transporter
PA0135_at	0.30	0.97	hypothetical protein
PA1036_at	0.30	0.81	hypothetical protein
PA5543_at	0.31	0.67	hypothetical protein
PA5210_at	0.31	1.79	probable secretion pathway ATPase
PA0020_at	0.31	1.11	hypothetical protein
PA5262_algZ_at	0.31	1.04	alginate biosynthesis protein AlgZ/FimS
PA3097_xcpX_at	0.31	0.82	general secretion pathway protein K
PA2346_at	0.31	1.71	conserved hypothetical protein
PA4616_at	0.32	1.68	probable c4-dicarboxylate-binding protein
PA2559_at	0.32	1.21	hypothetical protein
PA2761_at	0.32	0.67	hypothetical protein
PA5472_at	0.32	0.90	hypothetical protein
PA3956_at	0.32	0.93	hypothetical protein
PA3844_at	0.32	1.58	hypothetical protein
PA0645_at	0.32	0.34	hypothetical protein
PA1825_at	0.33	0.69	hypothetical protein
PA3100_xcpU_at	0.33	1.75	General secretion pathway outer membrane protein H
ig_5774806_5775619_at	0.33	1.24	
ig_3129728_3129070_at	0.33	0.84	
PA2824_at	0.33	1.27	probable sensor/response regulator hybrid
PA5167_at	0.33	0.50	probable c4-dicarboxylate-binding protein
PA0410_pilI_at	0.34	1.74	twitching motility protein PilI
PA0882_at	0.34	1.39	hypothetical protein
PA0413_at	0.34	0.97	probable component of chemotactic signal transduction system
PA2412_at	0.35	9.95	conserved hypothetical protein
PA1133_at	0.35	1.02	hypothetical protein
PA2044_at	0.35	1.23	hypothetical protein
PA3578_at	0.36	1.45	conserved hypothetical protein
PA1894_at	0.36	0.95	hypothetical protein
PA0720_at	0.36	1.46	helix destabilizing protein of bacteriophage Pf1
PA0406_at	0.36	1.12	hypothetical protein
PA3099_xcpV_at	0.36	1.12	general secretion pathway protein I

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA4697_at	0.36	0.63	hypothetical protein
PA5363_at	0.37	1.46	hypothetical protein
PA4546_pilS_at	0.37	0.82	two-component sensor PilS
PA4179_at	0.37	1.25	probable porin
PA5123_at	0.37	1.36	hypothetical protein
PA4856_at	0.37	0.36	RtsM
PA2990_at	0.37	1.80	probable phosphodiesterase
PA2676_at	0.37	0.55	probable type II secretion system protein
PA0414_at	0.37	1.16	probable methyltransferase
ig_2281578_2282480_at	0.37	2.15	probable transcriptional regulator
PA5545_at	0.37	0.67	conserved hypothetical protein
PA4108_at	0.38	1.12	hypothetical protein
PA1216_at	0.38	1.89	hypothetical protein
PA4526_pilB_at	0.38	1.25	type 4 fimbrial biogenesis protein PilB
PA5402_at	0.38	2.05	hypothetical protein
PA2458_at	0.38	0.89	hypothetical protein
PA2875_at	0.38	1.25	conserved hypothetical protein
PA2181_at	0.38	2.29	hypothetical protein
PA5295_at	0.38	1.10	hypothetical protein
PA4092_hpaC_at	0.39	1.94	4-hydroxyphenylacetate 3-monooxygenase small chain
PA2002_at	0.39	0.27	conserved hypothetical protein
PA5116_at	0.39	1.16	probable transcriptional regulator
PA2983_at	0.39	0.91	probable tolQ-type transport protein
PA3546_algX_at	0.40	1.34	alginate biosynthesis protein AlgX
PA1506_at	0.40	0.82	hypothetical protein
PA0449_at	0.40	1.21	hypothetical protein
PA4547_pilR_at	0.41	1.54	two-component response regulator PilR
PA4396_at	0.41	1.32	probable two-component response regulator
PA0664_at	0.41	0.80	hypothetical protein
PA2937_at	0.42	0.70	hypothetical protein
PA0572_at	0.42	1.58	hypothetical protein
PA5039_aroK_at	0.42	1.67	shikimate kinase
PA3098_xcpW_at	0.42	1.45	general secretion pathway protein J
PA2453_at	0.42	0.68	hypothetical protein
PA0411_pilJ_at	0.43	1.12	twitching motility protein PilJ
PA4073_at	0.43	1.33	probable aldehyde dehydrogenase
PA1595_at	0.43	1.59	hypothetical protein
PA0346_at	0.43	1.36	hypothetical protein
PA0408_pilG_at	0.43	1.11	twitching motility protein PilG
PA2981_lpxK_at	0.44	1.05	tetraacyldisaccharide 4*-kinase
PA2959_at	0.44	1.14	conserved hypothetical protein
PA2434_at	0.44	1.27	hypothetical protein
PA4397_panE_at	0.45	1.28	ketopantoate reductase
ig_5992382_5991130_at	0.45	1.24	
PA3102_xcpS_at	0.45	1.56	general secretion pathway protein F
PA1148_toxA_at	0.45	1.46	exotoxin A precursor
ig_5563964_5563286_at	0.45	1.36	
PA2872_at	0.45	0.84	hypothetical protein
PA2960_pilZ_at	0.46	0.95	type 4 fimbrial biogenesis protein PilZ
PA0538_dsbB_at	0.46	1.02	disulfide bond formation protein

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA4677_at	0.46	2.07	hypothetical protein
PA5530_at	0.46	0.42	probable MFS dicarboxylate transporter
PA3115_at	0.46	1.59	Motility protein FimV
PA2786_at	0.46	2.23	hypothetical protein
PA3101_xcpT_at	0.46	1.16	general secretion pathway protein G
PA0663_at	0.46	1.39	hypothetical protein
PA3096_xcpY_at	0.46	0.93	general secretion pathway protein L
PA4837_at	0.47	1.26	probable outer membrane protein precursor
PA0295_at	0.47	1.20	probable periplasmic polyamine binding protein
PA4325_at	0.48	1.00	hypothetical protein
PA5261_algR_at	0.48	1.21	alginate biosynthesis regulatory protein AlgR
PA0415_at	0.48	0.99	probable chemotaxis protein
PA4530_at	0.49	0.99	conserved hypothetical protein
PA2028_at	0.49	0.77	probable transcriptional regulator
PA1191_at	0.49	0.62	hypothetical protein
PA1419_at	0.49	0.85	probable transporter
PA2674_at	0.50	1.08	probable type II secretion system protein
PA0416_at	0.50	1.12	probable transcriptional regulator
PA0409_pilH_at	0.50	1.08	twitching motility protein PilH
PA2386_pvdA_at	0.50	2.58	L-ornithine N5-oxygenase
PA4166_at	2.02	0.89	probable acetyltransferase
PA3496_at	2.02	1.65	hypothetical protein
PA0869_pbpG_at	2.03	0.62	D-alanyl-D-alanine-endopeptidase
PA4331_at	2.03	0.98	probable ferredoxin reductase
PA4614_mscl_at	2.03	0.46	conductance mechanosensitive channel
PA0855_at	2.04	0.89	hypothetical protein
PA3427_at	2.05	0.11	probable short-chain dehydrogenases
PA2432_at	2.07	0.88	probable transcriptional regulator
PA1197_at	2.07	1.25	hypothetical protein
PA3334_at	2.09	1.23	probable acyl carrier protein
PA2917_at	2.09	0.87	probable transcriptional regulator
PA3919_at	2.10	0.91	conserved hypothetical protein
PA2062_at	2.10	0.69	probable pyridoxal-phosphate dependent enzyme
PA3189_at	2.12	0.17	probable permease of ABC sugar transporter
PA5390_at	2.13	3.01	probable peptidic bond hydrolase
PA3293_at	2.13	1.50	hypothetical protein
PA0938_at	2.13	2.03	hypothetical protein
PA0333_at	2.14	1.29	hypothetical protein
PA2867_at	2.16	0.62	probable chemotaxis transducer
PA0013_at	2.17	1.99	conserved hypothetical protein
PA5369_at	2.18	1.30	hypothetical protein
PA4201_ddIA_at	2.19	1.89	D-alanine-D-alanine ligase A
ig_517462_518083_at	2.19	0.11	probable ClpA/B protease ATP binding subunit
PA1806_fabI_at	2.19	0.80	NADH-dependent enoyl-ACP reductase
PA3939_at	2.19	0.35	hypothetical protein
PA1567_at	2.19	5.52	conserved hypothetical protein
PA3662_at	2.20	0.57	hypothetical protein
PA2355_at	2.21	1.10	probable FMNH2-dependent monooxygenase
PA4375_at	2.22	2.82	Resistance-Nodulation-Cell Division (RND) efflux transporter
PA4632_at	2.24	1.05	hypothetical protein

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA0537_at	2.26	0.86	conserved hypothetical protein
PA4352_at	2.28	0.76	conserved hypothetical protein
PA2358_at	2.28	0.41	hypothetical protein
PA0284_at	2.28	0.58	hypothetical protein
PA0211_mdcD_at	2.29	1.62	malonate decarboxylase beta subunit
PA1544_anr_at	2.29	0.93	transcriptional regulator Anr
PA5381_at	2.30	3.17	hypothetical protein
PA0659_at	2.31	0.85	hypothetical protein
PA3450_at	2.31	0.37	probable antioxidant protein
PA2916_at	2.32	0.50	hypothetical protein
PA2503_at	2.33	1.15	hypothetical protein
PA1746_at	2.34	1.30	hypothetical protein
PA2370_at	2.35	5.11	hypothetical protein
PA3536_at	2.36	1.20	hypothetical protein
PA1789_at	2.41	0.09	hypothetical protein
PA5461_at	2.41	0.56	hypothetical protein
PA2753_at	2.42	0.55	hypothetical protein
PA0064_at	2.42	1.36	hypothetical protein
PA2772_at	2.43	1.40	hypothetical protein
PA5412_at	2.44	0.73	hypothetical protein
ig_2894451_2893827_at	2.44	0.73	hypothetical protein
PA2723_at	2.45	0.64	hypothetical protein
PA0039_at	2.46	0.97	hypothetical protein
PA5171_arcA_at	2.46	0.36	arginine deiminase
PA3141_wbpM_g_at	2.47	1.36	nucleotide sugar epimerase/dehydratase WbpM
PA3793_at	2.49	0.85	hypothetical protein
PA0829_at	2.50	3.83	probable hydrolase
PA2727_at	2.51	0.82	hypothetical protein
PA2592_at	2.51	0.87	periplasmic spermidine/putrescine-binding protein
PA3317_at	2.51	1.16	hypothetical protein
PA2720_at	2.51	0.82	hypothetical protein
PA2380_at	2.52	0.71	hypothetical protein
PA1940_at	2.53	0.87	hypothetical protein
PA5375_betT1_at	2.54	5.00	choline transporter BetT
PA3911_at	2.55	1.34	conserved hypothetical protein
PA1659_at	2.57	0.33	hypothetical protein
PA1557_at	2.57	0.31	probable cytochrome oxidase subunit (cbb3-type)
PA1494_at	2.59	1.01	conserved hypothetical protein
PA2238_at	2.59	0.68	hypothetical protein
PA5290_at	2.59	1.16	conserved hypothetical protein
PA3933_at	2.60	3.78	probable choline transporter
PA5120_at	2.61	1.41	hypothetical protein
PA1414_at	2.62	0.16	hypothetical protein
PA1555_at	2.62	0.41	probable cytochrome c
PA4059_at	2.63	1.10	hypothetical protein
PA0806_i_at	2.64	1.04	hypothetical protein
PA1171_at	2.66	1.16	probable transglycolase
PA0050_r_at	2.66	0.99	hypothetical protein
PA3294_s_at	2.68	1.73	hypothetical protein ; conserved hypothetical protein
PA5475_at	2.72	0.57	hypothetical protein

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA4995_at	2.73	0.58	probable acyl-CoA dehydrogenase
PA4032_at	2.74	1.28	probable two-component response regulator
PA3922_at	2.76	1.11	conserved hypothetical protein
PA3058_at	2.77	1.46	hypothetical protein
PA0527_dnr_at	2.77	0.68	transcriptional regulator Dnr
PA2496_at	2.82	1.22	hypothetical protein
PA3483_at	2.83	1.08	hypothetical protein
PA4323_at	2.84	0.85	hypothetical protein
PA4321_at	2.84	0.74	hypothetical protein
PA0749_at	2.84	0.94	hypothetical protein
PA3446_at	2.85	0.27	conserved hypothetical protein
PA2501_at	2.85	0.55	hypothetical protein
PA4111_i_at	2.87	1.11	hypothetical protein
PA1377_at	2.87	1.11	conserved hypothetical protein
PA4119_aph_at	2.88	1.68	aminoglycoside 3'-phosphotransferase type IIb
PA5025_metY_at	2.90	1.21	homocysteine synthase
PA1913_at	2.91	0.93	hypothetical protein
PA3931_at	2.96	0.41	conserved hypothetical protein
PA1451_at	2.96	1.52	conserved hypothetical protein
PA1378_at	2.97	1.24	hypothetical protein
PA0092_at	2.97	1.16	hypothetical protein
PA0081_at	2.99	1.32	hypothetical protein
PA5033_at	2.99	1.65	hypothetical protein
PA0052_at	3.04	0.64	hypothetical protein
PA3063_at	3.05	1.28	hypothetical protein
PA0867_at	3.10	0.87	hypothetical protein
PA4611_at	3.13	0.79	hypothetical protein
PA1556_at	3.16	0.43	probable cytochrome c oxidase subunit
PA1941_at	3.17	1.31	hypothetical protein
PA3732_at	3.19	1.12	conserved hypothetical protein
PA4495_at	3.21	0.75	hypothetical protein
PA2204_at	3.21	0.41	probable binding protein component of ABC transporter
PA2567_at	3.22	0.77	hypothetical protein
PA0201_at	3.24	0.20	hypothetical protein
PA0706_cat_at	3.26	0.98	chloramphenicol acetyltransferase
PA4034_aqpZ_at	3.27	0.36	aquaporin Z
PA0320_at	3.28	0.70	conserved hypothetical protein
PA2425_at	3.28	3.15	PvdG
PA5427_adhA_at	3.31	0.34	alcohol dehydrogenase
PA4320_at	3.34	1.21	hypothetical protein
PA4328_at	3.37	1.54	hypothetical protein
PA3572_at	3.38	0.39	hypothetical protein
PA3731_at	3.46	1.55	conserved hypothetical protein
PA1196_at	3.48	0.65	probable transcriptional regulator
PA1727_at	3.49	1.40	conserved hypothetical protein
PA1202_at	3.50	0.66	probable hydrolase
PA2683_at	3.51	0.60	probable serine/threonine dehydratase, degradative
PA2833_i_at	3.52	0.45	conserved hypothetical protein
PA5170_arcD_at	3.52	0.09	arginine/ornithine antiporter
PA2440_at	3.59	1.18	hypothetical protein

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA4518_at	3.60	0.89	hypothetical protein
PA3794_at	3.62	0.86	hypothetical protein
PA1432_lasl_at	3.66	1.12	autoinducer synthesis protein LasI
PA1657_at	3.70	0.70	conserved hypothetical protein
PA2560_at	3.73	1.24	hypothetical protein
PA1645_at	3.73	1.18	hypothetical protein
PA1673_at	3.75	0.85	hypothetical protein
PA5112_estA_at	3.81	0.78	esterase EstA
PA0736_at	3.86	1.36	hypothetical protein
PA4571_at	3.87	1.11	probable cytochrome c
PA0095_at	3.93	1.40	conserved hypothetical protein
PA2240_at	3.95	1.22	hypothetical protein
PA3188_at	3.96	0.17	probable permease of ABC sugar transporter
PA4651_at	3.97	1.03	probable pili assembly chaperone
PA4577_at	3.97	0.59	hypothetical protein
PA3309_at	3.99	0.25	conserved hypothetical protein
PA3337_rfaD_at	4.00	0.40	ADP-L-glycero-D-mannoheptose 6-epimerase
PA4319_at	4.03	1.06	conserved hypothetical protein
PA1126_at	4.05	0.81	hypothetical protein
PA0730_at	4.05	0.93	probable transferase
PA1068_at	4.06	1.23	probable heat shock protein (hsp90 family)
PA0042_at	4.16	1.09	hypothetical protein
ig_1348401_1349416_at	4.17	9.17	hypothetical protein
PA0200_i_at	4.17	0.09	hypothetical protein
PA2517_xylY_at	4.20	4.04	toluate 1,2-dioxygenase beta subunit
PA0735_at	4.23	1.04	hypothetical protein
PA2231_at	4.30	1.14	probable glycosyl transferase
PA0040_s_at	4.31	1.67	conserved hypothetical protein ; hypothetical protein
PA1132_at	4.41	0.64	hypothetical protein
PA4830_at	4.42	4.59	hypothetical protein
PA2242_at	4.49	0.90	hypothetical protein
PA1450_at	4.50	1.18	conserved hypothetical protein
PA2239_at	4.51	1.24	probable transferase
PA4800_at	4.55	1.26	hypothetical protein
PA4801_at	4.55	0.84	hypothetical protein
PA2685_at	4.56	1.14	conserved hypothetical protein
PA3340_at	4.57	0.77	hypothetical protein
PA4058_at	4.73	2.26	hypothetical protein
PA2541_at	4.78	0.78	probable CDP-alcohol phosphatidyltransferase
PA1791_at	4.80	1.76	hypothetical protein
PA2775_at	4.82	0.99	hypothetical protein ; tRNA-Val
PA2450_at	4.84	1.55	hypothetical protein
PA4322_at	4.84	1.24	conserved hypothetical protein
PA4318_at	4.87	0.99	hypothetical protein
PA3730_at	4.90	1.17	hypothetical protein
PA0172_at	4.91	1.15	hypothetical protein
PA1667_at	4.94	0.51	hypothetical protein
PA4492_at	5.32	1.09	conserved hypothetical protein
PA4488_at	5.47	0.70	conserved hypothetical protein
PA2789_at	5.50	1.47	hypothetical protein

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA4487_at	5.59	0.83	conserved hypothetical protein
ig_2918211_2918966_at	5.64	1.95	
PA4491_at	5.74	0.70	conserved hypothetical protein
PA2536_at	5.76	1.10	probable phosphatidate cytidyltransferase
PA0886_at	5.78	3.07	probable C4-dicarboxylate transporter
PA2441_at	5.79	1.54	hypothetical protein
PA1236_at	5.85	2.64	probable major facilitator superfamily (MFS) transporter
PA2232_at	5.95	0.99	P-mannose isomerase/GDP-mannose pyrophosphorylase
PA2423_at	5.96	1.21	hypothetical protein
PA5136_at	6.13	1.44	hypothetical protein
ig_3545880_3545073_at	6.32	1.88	O-antigen chain length regulator
PA4489_at	6.38	1.22	conserved hypothetical protein
PA4490_at	6.39	1.11	conserved hypothetical protein
PA0097_at	6.50	1.25	hypothetical protein
PA2774_at	6.50	1.09	hypothetical protein
PA2237_at	6.55	0.85	probable glycosyl hydrolase
PA2537_at	6.68	0.61	probable acyltransferase
PA3715_at	6.73	2.20	hypothetical protein
PA2233_at	6.77	1.69	probable glycosyl transferase
PA2236_at	6.92	1.22	hypothetical protein
PA4317_at	6.99	0.91	hypothetical protein
PA3727_at	7.03	1.65	hypothetical protein
PA2684_at	7.10	1.01	conserved hypothetical protein
PA1396_at	7.16	0.64	probable two-component sensor
PA0170_at	7.18	0.88	hypothetical protein
PA2235_at	7.27	0.82	hypothetical protein
PA2464_at	7.27	0.82	hypothetical protein
PA0072_at	7.39	1.13	hypothetical protein
PA3729_at	7.48	0.95	conserved hypothetical protein
PA4033_at	7.70	0.93	hypothetical protein
PA2538_at	7.76	0.95	hypothetical protein
PA3061_at	7.88	0.75	hypothetical protein
PA3484_at	8.28	0.90	hypothetical protein
PA3728_at	8.39	1.15	hypothetical protein
PA0820_at	8.46	1.73	hypothetical protein
PA1069_at	8.58	1.03	hypothetical protein
PA2234_at	8.61	1.11	probable exopolysaccharide transporter
PA5113_at	8.72	0.74	hypothetical protein
PA0094_at	8.77	0.73	hypothetical protein
PA0074_ppkA_at	8.86	1.22	serine/threonine protein kinase PpkA
PA5361_phoR_at	8.88	2.89	two-component sensor PhoR
ig_6125795_6125079_at	9.13	1.09	hypothetical protein
PA5441_at	9.16	1.45	hypothetical protein
PA0093_at	9.31	1.73	hypothetical protein
PA3850_at	9.34	1.17	hypothetical protein
PA0073_at	9.38	0.77	probable ATP-binding component of ABC transporter
PA2581_at	9.65	1.72	hypothetical protein ; tRNA-Cys
PA2702_at	9.78	0.96	hypothetical protein
PA3021_at	10.00	1.07	hypothetical protein
PA2703_at	10.26	0.74	hypothetical protein

Table S1. (continued)

Gene Name	retS/wt	retSgacS/wt	Description
PA0076_at	10.26	0.98	hypothetical protein
PA3716_at	10.66	1.02	hypothetical protein
PA3064_at	10.96	3.55	hypothetical protein
PA3619_at	11.01	1.57	hypothetical protein
PA4624_at	11.20	1.19	hypothetical protein
PA3722_at	11.20	1.06	hypothetical protein
PA0071_at	11.27	1.33	hypothetical protein
PA4625_at	11.70	1.73	hypothetical protein
PA0563_at	12.05	0.78	conserved hypothetical protein
PA0079_at	12.22	0.95	hypothetical protein
PA2793_at	12.56	1.69	hypothetical protein
PA0171_at	12.79	1.42	hypothetical protein
PA1844_at	13.39	2.21	hypothetical protein
PA0169_at	14.13	1.32	hypothetical protein
PA2540_at	14.46	1.09	conserved hypothetical protein
PA0080_at	14.69	1.01	hypothetical protein
PA1672_at	14.74	5.56	hypothetical protein
PA2792_at	14.81	1.76	hypothetical protein
PA0070_at	15.01	1.05	hypothetical protein
PA0077_at	15.15	0.91	hypothetical protein
PA1845_at	15.36	1.30	hypothetical protein
PA1394_at	15.42	0.74	hypothetical protein
PA0075_at	15.60	1.30	probable phosphoprotein phosphatase
PA3485_r_at	16.09	1.48	hypothetical protein
PA0088_at	16.39	1.05	hypothetical protein
PA0989_at	20.01	1.33	hypothetical protein
PA0082_at	20.44	0.96	hypothetical protein
ig_6125079_6125795_at	22.48	1.64	
PA0078_at	22.92	1.63	hypothetical protein
PA5114_at	22.93	0.76	hypothetical protein
PA2539_at	22.99	1.67	conserved hypothetical protein
PA2205_at	23.11	0.62	hypothetical protein
PA3060_at	23.39	1.21	hypothetical protein
PA1395_at	27.56	0.57	hypothetical protein
PA0126_at	28.38	1.35	hypothetical protein
PA0091_at	31.64	2.32	conserved hypothetical protein
PA0086_at	36.83	1.22	hypothetical protein
PA0084_at	39.13	0.98	conserved hypothetical protein
PA0087_at	39.26	1.05	hypothetical protein
PA0083_at	49.62	1.00	conserved hypothetical protein
PA0090_at	57.20	1.61	probable ClpA/B-type chaperone
PA0277_at	59.87	2.08	conserved hypothetical protein
PA0089_at	72.35	0.62	hypothetical protein
PA0085_at	113.80	1.76	conserved hypothetical protein
PA3661_at	444.40	0.40	hypothetical protein

Table S2. Genes whose expression changed >2x relative to wild type in at least one of the mutant strains.

Gene name	<i>gacA</i>/wt	<i>rsmYZ</i>/wt	Description
ig_2164548_2165213_at	10.0	9.1	
ig_2918211_2918966_at	0.5	0.3	
PA0007_at	0.5	0.2	hypothetical protein
PA0044_exoT_at	4.2	4.5	exoenzyme T
PA0046_at	0.4	0.3	hypothetical protein
PA0047_at	0.3	0.4	hypothetical protein
PA0050_r_at	0.5	0.5	hypothetical protein
PA0070_at	0.2	0.2	hypothetical protein
PA0075_at	0.5	0.5	probable phosphoprotein phosphatase
PA0076_at	0.6	0.5	hypothetical protein
PA0079_at	0.5	0.3	hypothetical protein
PA0082_at	0.4	0.4	hypothetical protein
PA0083_at	0.1	0.1	conserved hypothetical protein
PA0084_at	0.2	0.2	conserved hypothetical protein
PA0085_at	0.1	0.1	conserved hypothetical protein
PA0090_at	0.2	0.4	probable ClpA/B-type chaperone
PA0092_at	0.5	0.6	hypothetical protein
PA0093_at	0.3	0.6	hypothetical protein
PA0094_at	0.5	0.5	hypothetical protein
PA0122_at	0.5	0.5	conserved hypothetical protein
PA0169_at	0.3	0.2	hypothetical protein
PA0170_at	0.3	0.3	hypothetical protein
PA0171_at	0.2	0.2	hypothetical protein
PA0208_mdcA_at	0.7	0.5	malonate decarboxylase alpha subunit
PA0209_at	0.8	0.4	conserved hypothetical protein
PA0211_mdcD_at	0.8	0.5	malonate decarboxylase beta subunit
PA0333_at	0.4	0.6	hypothetical protein
PA0347_glpQ_at	1.2	2.5	glycerophosphoryl diester phosphodiesterase, periplasmic
PA0563_at	0.2	0.2	conserved hypothetical protein
PA0566_at	3.1	3.0	hypothetical protein
PA0651_trpC_at	4.7	0.8	indole-3-glycerol-phosphate synthase
PA0672_at	0.3	0.3	heme oxygenase
PA0675_at	0.6	0.5	probable sigma-70 factor, ECF subfamily
PA0706_cat_at	0.5	0.5	chloramphenicol acetyltransferase
PA0736_at	0.4	0.5	hypothetical protein
PA0805_at	0.4	0.6	hypothetical protein
PA0807_at	1.6	2.4	conserved hypothetical protein
PA0817_at	1.6	2.0	probable ring-cleaving dioxygenase
PA0884_at	2.6	3.1	probable C4-dicarboxylate-binding periplasmic protein
PA0931_at	0.3	0.5	siderophore receptor protein
PA0938_at	0.2	0.4	hypothetical protein
PA1012_at	0.4	0.7	conserved hypothetical protein
PA1132_at	0.4	0.3	hypothetical protein
PA1300_at	0.5	0.4	probable sigma-70 factor, ECF subfamily
PA1301_at	0.7	0.4	probable transmembrane sensor
PA1302_at	0.3	0.4	probable heme utilization protein precursor
PA1325_at	0.4	0.2	conserved hypothetical protein
PA1361_at	0.4	0.5	probable transporter

Table S2. (continued)

Gene name	<i>gacA</i>/wt	<i>rsmYZ</i>/wt	Description
PA1363_at	0.5	0.4	probable sigma-70 factor, ECF subfamily
PA1432_lasl_at	0.6	0.5	autoinducer synthesis protein LasI
PA1657_at	0.4	0.7	conserved hypothetical protein
PA1688_at	1.1	0.4	hypothetical protein
PA1692_at	1.9	2.5	probable translocation protein in type III secretion
PA1693_pscR_at	2.8	3.7	translocation protein in type III secretion
PA1694_pscQ_at	2.8	3.3	translocation protein in type III secretion
PA1695_pscP_at	2.5	2.7	translocation protein in type III secretion
PA1697_at	2.2	2.0	ATP synthase in type III secretion system
PA1698_popN_at	2.6	2.4	Type III secretion outer membrane protein PopN precursor
PA1700_at	2.7	2.3	conserved hypothetical protein in type III secretion
PA1705_pcrG_i_at	2.8	2.4	regulator in type III secretion
PA1706_pcrV_at	3.9	3.9	type III secretion protein PcrV
PA1707_pcrH_at	4.5	4.7	regulatory protein PcrH
PA1708_popB_at	4.2	4.2	translocator protein PopB
PA1709_popD_at	4.5	4.4	Translocator outer membrane protein PopD precursor
PA1710_exsC_at	2.5	2.1	exoenzyme S synthesis protein C precursor
PA1711_at	3.0	2.5	hypothetical protein
PA1712_exsB_at	2.8	2.7	exoenzyme S synthesis protein B
PA1714_at	2.5	2.2	hypothetical protein
PA1715_pscB_at	5.4	3.9	type III export apparatus protein
PA1716_pscC_at	3.4	3.2	Type III secretion outer membrane protein PscC precursor
PA1717_pscD_at	2.3	2.3	type III export protein PscD
PA1718_pscE_at	3.5	4.2	type III export protein PscE
PA1719_pscF_at	3.5	4.4	type III export protein PscF
PA1720_pscG_at	3.1	3.9	type III export protein PscG
PA1721_pscH_at	3.1	4.0	type III export protein PscH
PA1722_pscI_at	3.2	4.1	type III export protein PscI
PA1723_pscJ_at	2.5	3.1	type III export protein PscJ
PA1724_pscK_at	1.6	2.3	type III export protein PscK
PA1725_pscL_at	1.8	2.8	type III export protein PscL
PA1842_at	0.6	0.5	hypothetical protein
PA1887_at	0.9	0.5	hypothetical protein
PA1894_at	0.3	0.5	hypothetical protein
PA1897_at	0.5	0.4	hypothetical protein
PA1913_at	0.4	0.4	hypothetical protein
PA1941_at	0.4	0.4	hypothetical protein
PA1974_at	3.7	4.4	hypothetical protein
PA1976_at	6.9	7.8	probable two-component sensor
PA1977_at	2.5	2.3	hypothetical protein
PA1978_at	12.1	11.2	probable transcriptional regulator
PA1979_at	27.0	27.6	probable two-component sensor
PA1980_at	11.6	12.5	probable two-component response regulator
PA1981_at	7.6	7.6	hypothetical protein
PA1982_exaA_at	5.7	6.2	quinoprotein alcohol dehydrogenase
PA1983_exaB_at	109.8	97.7	cytochrome c550
PA1984_s_at	7.8	7.3	probable aldehyde dehydrogenase
PA1985_pqqA_at	6.2	5.9	pyrroloquinoline quinone biosynthesis protein A
PA1986_pqqB_at	9.6	9.4	pyrroloquinoline quinone biosynthesis protein B

Table S2. (continued)

Gene name	<i>gacA</i>/wt	<i>rsmYZ</i>/wt	Description
PA1987_pqqC_at	8.0	6.4	pyrroloquinoline quinone biosynthesis protein C
PA1988_pqqD_at	9.7	8.8	pyrroloquinoline quinone biosynthesis protein D
PA1989_pqqE_at	4.8	5.4	pyrroloquinoline quinone biosynthesis protein E
PA1990_at	4.8	5.5	probable peptidase
PA2033_at	0.4	0.4	hypothetical protein
PA2034_at	0.4	0.4	hypothetical protein
PA2189_at	2.5	2.7	hypothetical protein
PA2191_exoY_at	4.3	4.3	adenylate cyclase ExoY
PA2193_hcnA_at	0.2	0.2	hydrogen cyanide synthase HcnA
PA2361_at	0.4	0.5	hypothetical protein
PA2362_at	0.5	0.2	hypothetical protein
PA2363_at	0.5	0.5	hypothetical protein
PA2365_at	0.2	0.2	conserved hypothetical protein
PA2366_at	0.2	0.2	conserved hypothetical protein
PA2367_at	0.2	0.2	hypothetical protein
PA2368_i_at	0.2	0.1	hypothetical protein
PA2423_at	0.6	0.1	hypothetical protein
PA2426_pvdS_at	0.4	0.4	sigma factor PvdS
PA2441_at	0.3	0.3	hypothetical protein
PA2454_at	0.5	0.4	hypothetical protein
PA2464_at	0.5	0.5	hypothetical protein
PA2468_at	0.6	0.4	probable sigma-70 factor, ECF subfamily
PA2496_at	0.9	0.4	hypothetical protein
PA2516_xylZ_at	0.7	0.2	toluate 1,2-dioxygenase electron transfer component
PA2537_at	0.3	0.3	probable acyltransferase
PA2539_at	0.5	0.2	conserved hypothetical protein
PA2540_at	0.3	0.4	conserved hypothetical protein
PA2541_at	0.5	0.5	probable CDP-alcohol phosphatidyltransferase
PA2560_at	1.5	0.5	hypothetical protein
PA2581_at	0.6	0.5	hypothetical protein ; tRNA-Cys
PA2684_at	0.6	0.4	conserved hypothetical protein
PA2686_pfeR_at	0.4	0.6	two-component response regulator PfeR
PA2703_at	0.4	0.4	hypothetical protein
PA2725_at	0.6	0.3	probable chaperone
PA2726_at	0.4	0.7	probable radical activating enzyme
PA2727_at	0.3	0.3	hypothetical protein
PA2780_at	0.4	0.6	hypothetical protein
PA2782_at	1.9	2.1	hypothetical protein
PA2793_at	0.5	0.3	hypothetical protein
PA2924_hisQ_at	2.4	2.7	histidine transport system permease HisQ
PA2976_rne_at	0.6	0.5	ribonuclease E
PA3015_at	0.6	0.3	hypothetical protein
PA3021_at	0.4	0.4	hypothetical protein
PA3062_at	0.4	0.5	hypothetical protein
PA3186_oprB_s_at	0.7	0.4	Glucose/carbohydrate outer membrane porin OprB
PA3189_at	0.4	0.4	probable permease of ABC sugar transporter
PA3273_at	3.0	2.4	hypothetical protein
PA3280_oprO_at	1.0	2.2	Pyrophosphate-specific outer membrane porin OprO
PA3374_at	1.2	4.2	conserved hypothetical protein

Table S2. (continued)

Gene name	<i>gacA</i>/wt	<i>rsmYZ</i>/wt	Description
PA3375_at	0.9	3.5	probable ATP-binding component of ABC transporter
PA3377_at	1.1	2.8	conserved hypothetical protein
PA3378_at	0.9	2.3	conserved hypothetical protein
PA3379_at	1.0	2.7	conserved hypothetical protein
PA3380_at	1.6	3.3	conserved hypothetical protein
PA3407_hasAp_at	0.4	0.4	heme acquisition protein HasAp
PA3461_at	1.2	2.1	conserved hypothetical protein
PA3484_at	0.5	0.4	hypothetical protein
PA3715_at	0.9	0.3	hypothetical protein
PA3716_at	0.5	0.4	hypothetical protein
PA3722_at	0.4	0.3	hypothetical protein
PA3729_at	0.4	0.4	conserved hypothetical protein
PA3730_at	0.4	0.4	hypothetical protein
PA3742_rplS_at	0.6	0.5	50S ribosomal protein L19
PA3743_trmD_at	0.5	0.4	tRNA (guanine-N1)-methyltransferase
PA3744_rimM_at	0.7	0.5	16S rRNA processing protein
PA3745_rpsP_at	0.7	0.5	30S ribosomal protein S16
PA3779_at	0.5	0.6	hypothetical protein
PA3789_at	2.1	2.1	hypothetical protein
PA3840_at	2.6	2.4	conserved hypothetical protein
PA3841_exoS_at	4.8	4.7	exoenzyme S
PA3842_at	4.0	3.7	probable chaperone
PA3899_at	0.5	0.5	probable sigma-70 factor, ECF subfamily
PA3904_i_at	0.3	0.5	hypothetical protein
PA3919_at	1.7	3.0	conserved hypothetical protein
PA4034_aqpZ_at	0.4	0.6	aquaporin Z
PA4139_at	0.5	0.4	hypothetical protein
PA4140_at	0.8	0.4	hypothetical protein
PA4156_at	0.5	0.6	probable TonB-dependent receptor
PA4160_fepD_at	1.0	0.4	ferric enterobactin transport protein FepD
PA4168_at	0.2	0.1	probable TonB-dependent receptor
PA4196_at	2.1	1.8	probable two-component response regulator
PA4198_at	7.4	6.4	probable AMP-binding enzyme
PA4199_at	3.0	2.5	probable acyl-CoA dehydrogenase
PA4220_i_at	0.5	0.5	hypothetical protein
PA4223_at	0.4	0.6	probable ATP-binding component of ABC transporter
PA4259_rpsS_at	0.7	0.5	30S ribosomal protein S19
PA4317_at	0.4	0.3	hypothetical protein
PA4375_at	0.5	0.3	Resistance-Nodulation-Cell Division (RND) efflux transporter
PA4421_at	0.8	0.5	conserved hypothetical protein
PA4432_rpsL_at	0.5	0.4	30S ribosomal protein S9
PA4467_at	0.3	0.4	hypothetical protein
PA4468_sodM_at	0.4	0.5	superoxide dismutase
PA4469_at	0.4	0.5	hypothetical protein
PA4470_fumC1_at	0.3	0.4	fumarate hydratase
PA4471_at	0.4	0.3	hypothetical protein
PA4489_at	0.5	0.6	conserved hypothetical protein
PA4514_at	0.4	0.3	probable outer membrane receptor for iron transport
PA4550_fimU_at	1.7	2.0	type 4 fimbrial biogenesis protein FimU

Table S2. (continued)

Gene name	<i>gacA</i>/wt	<i>rsmYZ</i>/wt	Description
PA4551_pilV_at	1.6	2.2	type 4 fimbrial biogenesis protein PilV
PA4552_pilW_at	1.7	2.4	type 4 fimbrial biogenesis protein PilW
PA4555_pilY2_at	1.6	2.1	type 4 fimbrial biogenesis protein PilY2
PA4563_rpsT_at	0.5	0.4	30S ribosomal protein S20
PA4567_rpmA_at	0.6	0.5	50S ribosomal protein L27
PA4583_at	0.5	0.5	conserved hypothetical protein
PA4624_at	0.4	0.6	hypothetical protein
PA4671_at	0.4	0.4	probable ribosomal protein L25
PA4706_at	0.5	0.5	probable ATP-binding component of ABC transporter
PA4707_at	0.5	0.5	probable permease of ABC transporter
PA4709_at	0.5	0.5	probable hemin degrading factor
PA4710_at	0.3	0.3	Haem/Haemoglobin uptake outer membrane receptor PhuR
PA4741_rpsO_at	0.8	0.5	30S ribosomal protein S15
PA4742_truB_at	0.7	0.3	tRNA pseudouridine 55 synthase
PA4746_at	0.8	0.5	conserved hypothetical protein ; tRNA-Met ; tRNA-Leu
PA4747_secG_at	0.5	0.5	secretion protein SecG
PA4774_at	0.4	0.5	hypothetical protein
PA4775_at	0.3	0.3	hypothetical protein
PA4777_at	0.5	0.4	two-component regulator system signal sensor kinase PmrB
PA4782_at	0.4	0.3	hypothetical protein
PA4811_fdhH_at	2.4	2.0	nitrate-inducible formate dehydrogenase, beta subunit
PA4822_at	0.4	0.5	hypothetical protein
PA4823_at	0.1	0.0	hypothetical protein
PA4825_mgtA_at	0.1	0.1	Mg(2+) transport ATPase, P-type 2
PA4826_at	0.1	0.0	hypothetical protein
PA4896_at	0.6	0.4	probable sigma-70 factor, ECF subfamily
PA4929_at	0.8	0.5	hypothetical protein
PA4932_rplI_at	0.5	0.4	50S ribosomal protein L9
PA4934_rpsR_at	0.5	0.4	30S ribosomal protein S18
PA4935_rpsF_at	0.5	0.4	30S ribosomal protein S6
PA4968_at	0.6	0.5	conserved hypothetical protein
PA5114_at	0.4	0.4	hypothetical protein
PA5120_at	0.2	0.2	hypothetical protein
PA5136_at	0.7	0.5	hypothetical protein
PA5137_at	0.6	0.5	hypothetical protein
PA5316_rpmB_at	0.6	0.4	50S ribosomal protein L28
PA5357_at	0.5	0.7	hypothetical protein
PA5441_at	0.5	0.3	hypothetical protein
PA5479_gltP_at	0.6	0.4	proton-glutamate symporter
PA5502_at	0.7	0.4	hypothetical protein
Pae_AF241171cds21_at	0.7	0.5	
Pae_AF241171cds22_at	2.0	2.0	
Pae_AF241171cds7_at	2.0	2.4	
Pae_tRNA_Arg_s_at	0.4	0.7	
Pae_tRNA_Gly_s_at	0.6	0.4	
Pae_tRNA_Ile_f_at	0.4	0.4	

Table S3. Results of the microarray analysis of the *P. aeruginosa* wt, *gacA* and *rsmYZ* mutant. Only those genes whose expression changed >2x relative to wild type in only one of the two mutants are listed.

<i>Change in gacA only</i>	<i>gacA/wt</i>	<i>rsmYZ/wt</i>	Description
PA0651_trpC_at	4.7	0.8	indole-3-glycerol-phosphate synthase
<i>Change in rsmYZ only</i>	<i>gacA/wt</i>	<i>rsmYZ/wt</i>	Description
PA1688_at	1.1	0.4	hypothetical protein
PA1887_at	0.9	0.5	hypothetical protein
PA2496_at	0.9	0.4	hypothetical protein
PA3715_at	0.9	0.3	hypothetical protein
PA4160_fepD_at	1.0	0.4	ferric enterobactin transport protein FepD
PA3280_oprO_at	1.0	2.2	Pyrophosphate-specific outer membrane porin
PA3374_at	1.2	4.2	conserved hypothetical protein
PA3375_at	0.9	3.5	ATP-binding component of ABC transporter
PA3377_at	1.1	2.8	conserved hypothetical protein
PA3378_at	0.9	2.3	conserved hypothetical protein
PA3379_at	1.0	2.7	conserved hypothetical protein
PA3380_at	1.6	3.3	conserved hypothetical protein
PA3461_at	1.2	2.1	conserved hypothetical protein

Table S4. Position of the conserved Upstream Activating Sequence (UAS) relative to the sRNA transcription start site in various bacterial species.

Bacterial Species	sRNA	Distance from the 3' of the UAS to +1 of the RNA (nt)*
<i>Pseudomonas aeruginosa</i>	<i>rsmY</i>	57
	<i>rsmZ</i>	174
<i>Pseudomonas fluorescens Pf-5</i>	<i>rsmX</i>	52
	<i>rsmY</i>	57
	<i>rsmZ</i>	171
<i>Pseudomonas putida KT2440</i>	<i>rsmY</i>	58
	<i>rsmZ</i>	172
<i>Pseudomonas syringae</i>	<i>rsmX</i>	57
	<i>rsmY</i>	57
	<i>rsmZ</i>	173
<i>Legionella pneumophila Paris</i>	<i>rsmY</i>	64
	<i>rsmZ</i>	173
<i>Acinetobacter sp ADP1</i>	<i>rsmX</i>	59
	<i>rsmY</i>	72
	<i>rsmZ</i>	59
<i>Escherichia coli K12</i>	<i>csrB</i>	182
	<i>csrC</i>	150
<i>Salmonella typhimurium LT2</i>	<i>csrB</i>	172
	<i>csrC</i>	150
<i>Vibrio cholerae</i>	<i>csrB1/csrC</i>	158
	<i>csrB2/csrB</i>	159
	<i>csrB3/csrD</i>	159
<i>Yersinia pestis C092</i>	<i>csrB</i>	211
	<i>csrC</i>	207

* Distances were calculated based on the described or predicted UAS and sRNA genomic locations (Kulkarni *et al.*, Nucleic Acid Research, 2006).

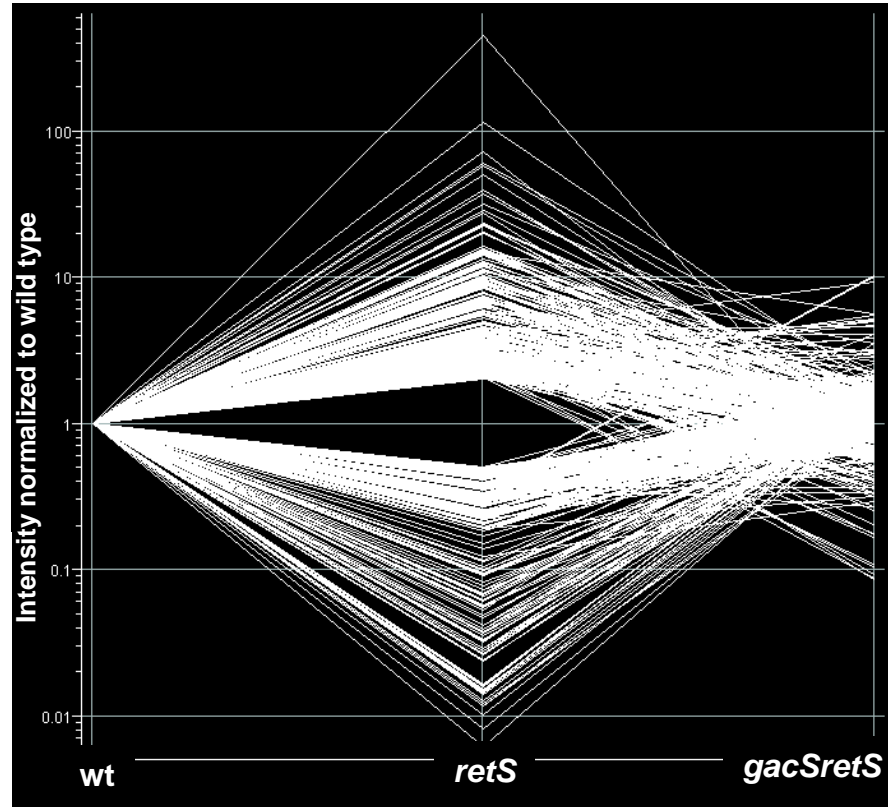


Figure S1. Comparison of transcript levels in *P. aeruginosa* wild type, *retS* mutant and *retS gacS* double mutant. Transcriptome of the *P. aeruginosa retS gacS* strain was compared to the previously published transcriptomes of the *P. aeruginosa* wild type and *retS* mutant strains (Goodman *et al.*, 2004). RNA used for the microarray analysis of the *P. aeruginosa retS gacS* double mutant was isolated from cultures in the exponential phase of growth (OD₆₀₀=0.5) exactly following the procedure used in the analysis of the wild type and the *retS* mutant strain. Only those genes whose transcript levels changed more than two fold in the *retS* mutant relative to wild type are shown.

SUPPORTING EXPERIMENTAL PROCEDURES

Construction of in-frame deletion mutants using pEXG2

Deletion strains were constructed by SOE-PCR of deletion alleles, ligation into plasmid pEXG2 (Rietsch *et al.*, 2005), and allelic exchange by sucrose selection on LB agar containing 6% sucrose as described (Hoang *et al.*, 1998). Plasmids were introduced into recipient cells by conjugation. All mutations were verified by PCR and sequencing. See supporting tables below for more detail.

VSV-G tagging of GacA

The GacA-V integration vector, pP30 Δ FRT-GacA-V, was constructed by subcloning a *NotI/HindIII* fragment of approximately 600 bp from pP30 Δ FRT-GacA-TAP, corresponding to a 3' portion of the *gacA* gene, which was amplified by using primers 5' GacA-TAP1 and 3' GacA TAP. This fragment was ligated into *NotI/HindIII*-cut pP30 Δ FRT-MvaT-V (Castang *et al.*, 2008), such that the *gacA* coding region was in frame with the DNA specifying the VSV-G tag. Plasmid pP30 Δ FRT-GacA-V and recipient strains PAO1, PAO1 Δ *retS*, and PAK, PAK *rsmY-lacZ*, and PAK *rsmZ-lacZ* were used to make PAO1 GacA-V, PAO1 Δ *retS* GacA-V, and PAK GacA-V, PAK GacA-V *rsmY-lacZ*, and PAK GacA-V *rsmZ-lacZ* respectively, by integration of the plasmid into the chromosome (See Supporting Tables below for additional information.). Production of the GacA-V protein was confirmed by Western blot analysis with an anti-VSV-G antibody (Sigma-Aldrich).

Construction of lacZ-reporter fusions using mini-CTX-lacZ

For each gene, regions directly upstream of the coding sequences were PCR-amplified using pairs of primers as indicated in the Supporting Tables below. The resulting fragments were cloned using the indicated restriction sites (Table S4) into mini-CTX-*lacZ*. The resulting plasmids were introduced into *Pseudomonas* wild type and mutant strains by conjugation. In those strains where vector backbones were removed the procedure described by Hoang and colleagues was used (Hoang *et al.*, 1998). See Supporting Tables below for additional information.

Construction of pMMB67-PlacUV5-rsmYZ

PlacUV5 promoter was fused to the +1 position (transcription start site) of *rsmZ* and *rsmY* genes by SOE-PCR using primers 5' *PlacUV5* (SOE1), 3' *PlacUV5 rsmY* (SOE2), 5' *rsmY* (SOE3), 3' *rsmY* for the construction of the *rsmY* clone, and primers 5' *PlacUV5* (SOE1), 3' *PlacUV5 rsmZ* (SOE2), 5' *rsmZ* (SOE3), 3' *rsmZ* (SOE4) for the construction of the *rsmZ* clone (Table S4). Vector pPSV35 and *P. aeruginosa* genomic DNA were used as templates for amplification of the *PlacUV5* promoter and of the *rsmY* and *rsmZ* genes, respectively. The resulting hybrid fragments were cloned into pMMB67(EH) using *HpaI* and *HindIII* sites, which effectively eliminated the *P_{tac}* promoter of the pMMB67 plasmid. The resulting plasmids, of pMMB67-*PlacUV5-rsmY* and pMMB67-*PlacUV5-rsmZ* were introduced to *P. aeruginosa* strains by conjugation.

Construction of pPSV40-rsmYZ

Fragments containing upstream regulatory sequences and coding regions of *rsmZ* and *rsmY* were PCR-amplified using primers described in Table S4. The resulting fragments were cloned into a promoterless pPSV40 vector using restriction sites indicated in Table S4. The resulting plasmids, pPSV40-*rsmY*, and pPSV40-*rsmZ* were introduced to *P. aeruginosa* strains by conjugation.

SUPPORTING EXPERIMENTAL PROCEDURES - TABLES:

Primers used in the study

Gene/Construct	Primer Name	Sequence*
Construction of <i>rsmY</i> and <i>rsmZ</i> in frame deletions		
<i>rsmY</i> deletion	rsmY-SOE1	TTT gga tcc CCTTGTTGGAGAAACGGAACAGCTGG
	rsmY-SOE2	GCGGTTTTCTCGGGCAATAAAAGTCCTGACGGTTTGAAGATTACG
	rsmY-SOE3	CGTAATCTTCAAACCGTCAGGACTTTTATTGCCCGAGGAAAACCGC
	rsmY-SOE4	TTT aag ctt GCAGACGGTCAACGCCAGCCTGGTG
<i>rsmZ</i> deletion	rsmZ-SOE1	CCT ggt acc CATGCTCGGCCTGAACGAACGGGTG
	rsmZ-SOE2	CGACGAGTAAAACGGCAGGCAAAACGCAGGAGTGATATTAGCGATTC
	rsmZ-SOE3	GAATCGCTAATATCACTCCTGCGTTTTGCCTGCCGTTTTACTCGTCCG
	rsmZ-SOE4	GGG gtc gac GCACGAGATGCCGAGCCAGCAGAG
Construction of <i>rsmY</i> and <i>rsmZ</i> overexpression clones - pPSV40		
pPSV40- <i>rsmZ</i>	5' <i>rsmZ</i> -1	TCC gaa ttc ATC TCA GCG AAA GCA TCG ACC AGT G
	3' <i>rsmZ</i> -NEW	GGT tct aga CTT TGG CGA CGA GTA AAA CGG CAG
pPSV40- <i>rsmY</i>	5' <i>rsmY</i> CTX	GGTT ctc gag CGG AAA TCA GGT AGT AGA AGG CGT G
	3' <i>rsmY</i>	AAT aag ctt AAG GCG TGG TCT GAG CGA C
Construction of <i>rsmY</i> and <i>rsmZ</i> overexpression clones - pMMB67-PlacUV5		
pMMB67-PlacUV5- <i>rsmYZ</i>	5' PlacUV5 (SOE1)	TTT CAC gtt aac TTC GAC ATT CCT TGT GTA TAA GGG GAC AC
	3' PlacUV5 <i>rsmZ</i> (SOE2)	GGT TGC GTG TTC CCT GTA CG CCA CAC ATT ATA CGA GCC GGA AGC
	5' <i>rsmZ</i> (SOE3)	GCT TCC GGC TCG TAT AAT GTG TGG CGT ACA GGG AAC ACG CAA CC
	3' <i>rsmZ</i> (SOE4)	GCC aag ctt CCG AAC ATC ACC GAG AAG AAG GA
	3' PlacUV5 <i>rsmY</i> (SOE2)	CTT CCT GCG CAA TGT CCT GAC CCA CAC ATT ATA CGA GCC GGA AGC
	5' <i>rsmY</i> (SOE3)	GCT TCC GGC TCG TAT AAT GTG TGG GTC AGG ACA TTG CGC AGG AAG
3' <i>rsmY</i>	AAT aag ctt AAG GCG TGG TCT GAG CGA C	
Construction of <i>lacZ</i>-fusions		
<i>exoS</i>	5' <i>exoS</i>	GGTTt aag ctt GGC TGA ACA GGT TCT GCT CGT TG
	3' <i>exoS</i> PR	AACA gaa ttc GGG CCT CAA TCT GTC CCA AAC G
<i>rsmY</i>	5' <i>rsmY</i> CTX	GGTT ctc gag CGG AAA TCA GGT AGT AGA AGG CGT G
	5' <i>rsmY</i> -2	CCC gaa ttc GCG AGC GGA ACT ATT ACA GCG
	5' <i>rsmY</i> -3	CTT gaa ttc GGT GGT TTT GGC TGC TTT CTC C
<i>rsmZ</i>	3' <i>rsmY</i> CTX	AACA aag ctt CAG ACC TCT ATC CTG ACA TCC GTG
	5' <i>rsmZ</i> -1	TCC gaa ttc ATC TCA GCG AAA GCA TCG ACC AGT G
	5' <i>rsmZ</i>	GAT gaa ttc CAG TGA CGG AAA ACC TTA GAC CCA
	5' <i>rsmZ</i> NEW	GGT gaa ttc CAC TGA AGA CCC GGC GTT CG
	5' <i>rsmZ</i> -3	TCT gaa ttc GTG AGC CTA AGT AGA TAA ATG CCC GG
PA2004/2005	3' <i>rsmZ</i> -1	CCT gga tcc GAT CCT TCG GGG TTG CGT GTT C
	PA2004-01	TTT aag ctt CGC TCT GCG AGT CGA TCC TCG
<i>trpGC</i>	PA2004-03	TTT aag ctt CGA ACA GGA TGA CGC TGT AGC
	5' <i>trpG</i> -1	CTT aag ctt GGA TCA GGT TTC CAG AGA GCG GG
	3' <i>trpG</i> -1	TAT gaa ttc CAC CAG GTT GTA GGT GAA GGA GTC GTA G
	5' <i>trpC</i> -2	TTT gaa ttc TCG GCG ATG CCT TCT TGA TCT CG
3' <i>trpC</i> -4	TAT aag ctt CAC ATT GCC GAG TTG AAG GAC GG	
Construction of <i>GacA</i>-VSV-G		
pP30ΔFRT- <i>Gac</i> -VSV-G	5' <i>GacA</i> TAP 1	CCT aag ctt GAC TGC GGT GAA GAC TGT CTG AAA CTG
	3' <i>GacA</i> TAP	TAGA gcgccgc GCT GGC GGC ATC GAC CAT G

*small caps are used to indicate the restriction sites

Plasmids used in the study

Plasmid	Characteristics / Primers used in construction	Reference
Constructions of in frame deletions*		
pEXG2	ColE1 <i>mob+</i> <i>sacB+</i> suicide vector (Gm ^r)	(Rietsch <i>et al.</i> , 2005)
pEXG2- Δ <i>rsmY</i>	<i>rsmY</i> -SOE1, SOE2, SOE3, SOE4	This study
pEXG2- Δ <i>rsmZ</i>	<i>rsmZ</i> -SOE1, SOE2, SOE3, SOE4	This study
Construction of <i>lacZ</i>-fusions*		
mini-CTX- <i>lacZ</i>	integrative gene reporter vector (Tc ^r)	(Becher and Schweizer, 2000)
pCTX- <i>exoS-lacZ</i>	5' <i>exoS</i> PR, 3' <i>exoS</i>	This study
pCTX- <i>rsmY-lacZ</i>	5' <i>rsmY</i> CTX, 3' <i>rsmY</i> CTX	(Brencic and Lory, 2009)
pCTX- <i>rsmZ-lacZ</i>	5' <i>rsmZ</i> -1, 3' <i>rsmZ</i> -1	This study
pCTX- <i>rsmY-lacZ</i> -2	5' <i>rsmY</i> -2, 3' <i>rsmY</i> CTX	This study
pCTX- <i>rsmY-lacZ</i> -3	5' <i>rsmY</i> -3, 3' <i>rsmY</i> CTX	This study
pCTX- <i>rsmZ-lacZ</i> -2	5' <i>rsmZ</i> , 3' <i>rsmZ</i> -1	This study
pCTX- <i>rsmZ-lacZ</i> -3	5' <i>rsmZ</i> -NEW, 3' <i>rsmZ</i> -1	This study
pCTX- <i>rsmZ-lacZ</i> -4	5' <i>rsmZ</i> -3, 3' <i>rsmZ</i> -1	This study
pCTX- <i>trpG-lacZ</i>	5' <i>trpG</i> -1, 3' <i>trpG</i> -1	This study
pCTX- <i>trpC-lacZ</i>	5' <i>trpC</i> -2, 3' <i>trpC</i> -4	This study
pCTX-PA2004/2005- <i>lacZ</i>	PA2004-01, PA2004-03	This study
pCTX-PA2005/2004- <i>lacZ</i>	PA2004-01, PA2004-03	This study
Construction of GacA-VSV-G*		
pP30 Δ FRT-MvaT-V		(Castang <i>et al.</i> , 2008)
pP30 Δ FRT-GacA-TAP	5' GacA TAP 1, 3' GacA TAP	(Vallet-Gely <i>et al.</i> , 2005)
pP30 Δ FRT-GacA-V	see supporting text	This study
<i>rsmZ</i> and <i>rsmY</i> overexpression*		
pPSV40	<i>P. aeruginosa oriV</i> , <i>mob+</i> pUC18 MCS cloning vector (Gm ^r)	(Rietsch <i>et al.</i> , 2005)
pPSV40- <i>rsmY</i>	5' <i>rsmY</i> CTX, 3' <i>rsmY</i>	This study
pPSV40- <i>rsmZ</i>	5' <i>rsmZ</i> -1, 3' <i>rsmZ</i> NEW	This study
pPSV35	<i>P. aeruginosa oriV</i> , <i>lacI^f</i> <i>mob+</i> P _{<i>lacUV5</i>} pUC18 MCS expression vector (Gm ^r)	(Rietsch <i>et al.</i> , 2005)
pMMB67(EH)	IncQ, RSF1010, <i>lacI^f</i> P _{<i>tac</i>} expression vector (Ap ^r)	(Furste <i>et al.</i> , 1986)
pMMB67-PlacUV5- <i>rsmY</i>	5' PlacUV5 (SOE1), 3' PlacUV5 <i>rsmY</i> (SOE2), 5' <i>rsmY</i> (SOE3), 3' <i>rsmY</i>	This study
pMMB67-PlacUV5- <i>rsmZ</i>	5' PlacUV5 (SOE1), 3' PlacUV5 <i>rsmZ</i> (SOE2), 5' <i>rsmZ</i> (SOE3), 3' <i>rsmZ</i> (SOE4)	This study

* For more detail, see supporting experimental procedures - text.

P. aeruginosa* strains used in the study

Strain	Characteristics	Reference
Figure 1		
PAK	wild type, laboratory collection	-
PAK $\Delta retS$	deletion mutant;	(Goodman <i>et al.</i> , 2004)
PAK $\Delta gacS$	deletion mutant	(Ventre <i>et al.</i> , 2006)
PAK $\Delta gacA$	deletion mutant	(Goodman <i>et al.</i> , 2009)
PAK $\Delta rsmY$	deletion mutant	This study
PAK $\Delta rsmZ$	deletion mutant	This study
PAK $\Delta rsmY \Delta rsmZ$	double deletion mutant	This study
PAK $\Delta rsmA$	deletion mutant	(Ventre <i>et al.</i> , 2006)
PAK <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the wt strain, vector backbone was removed	This study
PAK $\Delta retS$ <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the $\Delta retS$ strain, vector backbone was removed	This study
PAK $\Delta gacS$ <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the $\Delta gacS$ strain, vector backbone was removed	This study
PAK $\Delta gacA$ <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the $\Delta gacA$ strain, vector backbone was removed	This study
PAK $\Delta rsmZ$ <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the $\Delta rsmZ$ strain, vector backbone was removed	This study
PAK $\Delta rsmY$ <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the $\Delta rsmY$ strain, vector backbone was removed	This study
PAK $\Delta rsmYZ$ <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the $\Delta rsmYZ$ strain, vector backbone was removed	This study
PAK $\Delta rsmA$ <i>exoS-lacZ</i>	pCTX- <i>exoS-lacZ</i> was conjugated into the $\Delta rsmA$ strain, vector backbone was removed	This study
Figure 2		
PAK <i>exoS-lacZ</i> (pPSV40) Gm^R	pPSV40 plasmid was introduced into PAK <i>exoS-lacZ</i> strain by conjugation	This study
PAK <i>exoS-lacZ</i> (pPSV40- <i>rsmY</i>) Gm^R	pPSV40- <i>rsmY</i> was introduced into PAK <i>exoS-lacZ</i> strain by conjugation	This study
PAK <i>exoS-lacZ</i> (pPSV40- <i>rsmZ</i>) Gm^R	pPSV40- <i>rsmZ</i> was introduced into PAK <i>exoS-lacZ</i> strain by conjugation	This study
PAK <i>exoS-lacZ</i> (pMMB67) Gm^R	pMMB67 plasmid was introduced into PAK <i>exoS-lacZ</i> strain by conjugation	This study
PAK <i>exoS-lacZ</i> (pMMB67-PlacUV5- <i>rsmY</i>) Gm^R	pMMB67-PlacUV5- <i>rsmY</i> was introduced into PAK <i>exoS-lacZ</i> strain by conjugation	This study
PAK <i>exoS-lacZ</i> (pMMB67-PlacUV5- <i>rsmZ</i>) Gm^R	pMMB67-PlacUV5- <i>rsmZ</i> was introduced into PAK <i>exoS-lacZ</i> strain by conjugation	This study
Figure 3		
PAK ::pCTX- <i>trpG-lacZ</i> Tc^R	pCTX- <i>trpG-lacZ</i> plasmid was introduced into the wt strain by conjugation	This study
PAK $\Delta gacA$::pCTX- <i>trpG-lacZ</i> Tc^R	pCTX- <i>trpG-lacZ</i> plasmid was introduced into the $\Delta gacA$ strain by conjugation	This study
PAK $\Delta rsmYZ$::pCTX- <i>trpG-lacZ</i> Tc^R	pCTX- <i>trpG-lacZ</i> plasmid was introduced into the $\Delta rsmYZ$ strain by conjugation	This study
PAK ::pCTX- <i>trpC-lacZ</i> Tc^R	pCTX- <i>trpC-lacZ</i> plasmid was introduced into the wt strain by conjugation	This study
PAK $\Delta gacA$::pCTX- <i>trpC-lacZ</i> Tc^R	pCTX- <i>trpC-lacZ</i> plasmid was introduced into the $\Delta gacA$ strain by conjugation	This study
PAK $\Delta rsmYZ$::pCTX- <i>trpC-lacZ</i> Tc^R	pCTX- <i>trpC-lacZ</i> plasmid was introduced into the $\Delta rsmYZ$ strain by conjugation	This study
Figure 4		
PAO1	wild type, laboratory collection	-
PAO1 $\Delta retS$	deletion mutant; provided by Josh Sharp, Children's Hospital Boston	This study
PAO1 <i>gacA-V</i> Gm^R	pP30 Δ FRT-GacA-V was introduced into the wt strain by conjugation	This study
PAO1 $\Delta retS$ <i>gacA-V</i> Gm^R	pP30 Δ FRT-GacA-V was introduced into the $\Delta retS$ strain by conjugation	This study
PAK <i>rsmY-lacZ</i>	pCTX- <i>rsmY-lacZ</i> was conjugated into the wt strain, vector backbone was removed	(Brencic and Lory, 2009)
PAK $\Delta retS$ <i>rsmY-lacZ</i>	pCTX- <i>rsmY-lacZ</i> was conjugated into the $\Delta retS$ strain, vector backbone was removed	This study
PAK $\Delta gacS$ <i>rsmY-lacZ</i>	pCTX- <i>rsmY-lacZ</i> was conjugated into the $\Delta gacS$ strain, vector backbone was removed	This study
PAK $\Delta gacA$ <i>rsmY-lacZ</i>	pCTX- <i>rsmY-lacZ</i> was conjugated into the $\Delta gacA$ strain, vector backbone was removed	This study
PAK <i>gacA-V</i> <i>rsmY-lacZ</i> Gm^R	pP30 Δ FRT-GacA-V was introduced into the PAK <i>rsmY-lacZ</i> strain by conjugation	This study
PAK <i>rsmZ-lacZ</i>		(Ventre <i>et al.</i> , 2006)
PAK $\Delta retS$ <i>rsmZ-lacZ</i>		(Ventre <i>et al.</i> , 2006)
PAK $\Delta gacS$ <i>rsmZ-lacZ</i>		(Ventre <i>et al.</i> , 2006)
PAK $\Delta gacA$ <i>rsmZ-lacZ</i>		(Ventre <i>et al.</i> , 2006)
PAK <i>gacA-V</i> <i>rsmZ-lacZ</i> Gm^R	pP30 Δ FRT-GacA-V was introduced into the PAK <i>rsmZ-lacZ</i> strain by conjugation	This study
PAK ::pCTX-PA2004/05- <i>lacZ</i> Tc^R	pCTX-PA2004/05- <i>lacZ</i> was introduced into the wt strain by conjugation	This study
PAK $\Delta retS$::pCTX-PA2004/05- <i>lacZ</i> Tc^R	pCTX-PA2004/05- <i>lacZ</i> was introduced into the $\Delta retS$ strain by conjugation	This study
PAK $\Delta gacS$::pCTX-PA2004/05- <i>lacZ</i> Tc^R	pCTX-PA2004/05- <i>lacZ</i> was introduced into the $\Delta gacS$ strain by conjugation	This study
PAK $\Delta gacA$::pCTX-PA2004/05- <i>lacZ</i> Tc^R	pCTX-PA2004/05- <i>lacZ</i> was introduced into the $\Delta gacA$ strain by conjugation	This study
PAK ::pCTX-PA2005/04- <i>lacZ</i> Tc^R	pCTX-PA2005/04- <i>lacZ</i> was introduced into the wt strain by conjugation	This study
PAK $\Delta retS$::pCTX-PA2005/04- <i>lacZ</i> Tc^R	pCTX-PA2005/04- <i>lacZ</i> was introduced into the $\Delta retS$ strain by conjugation	This study
PAK $\Delta gacS$::pCTX-PA2005/04- <i>lacZ</i> Tc^R	pCTX-PA2005/04- <i>lacZ</i> was introduced into the $\Delta gacS$ strain by conjugation	This study
PAK $\Delta gacA$::pCTX-PA2005/04- <i>lacZ</i> Tc^R	pCTX-PA2005/04- <i>lacZ</i> was introduced into the $\Delta gacA$ strain by conjugation	This study

P. aeruginosa* strains used in the study – continued

Strain	Characteristics	Reference
Figure 5		
PAK ::pCTX- <i>rsmY-lacZ</i> (1)	pCTX- <i>rsmY-lacZ</i> plasmid was introduced into the wt strain by conjugation	This study
PAK ::pCTX- <i>rsmY-lacZ</i> (2)	pCTX- <i>rsmY-lacZ-2</i> plasmid was introduced into the wt strain by conjugation	This study
PAK ::pCTX- <i>rsmY-lacZ</i> (3)	pCTX- <i>rsmY-lacZ-3</i> plasmid was introduced into the wt strain by conjugation	This study
PAK ::pCTX- <i>rsmZ-lacZ</i> (1)	pCTX- <i>rsmZ-lacZ-1</i> plasmid was introduced into the wt strain by conjugation	This study
PAK ::pCTX- <i>rsmZ-lacZ</i> (2)	pCTX- <i>rsmZ-lacZ-2</i> plasmid was introduced into the wt strain by conjugation	This study
PAK ::pCTX- <i>rsmZ-lacZ</i> (3)	pCTX- <i>rsmZ-lacZ-3</i> plasmid was introduced into the wt strain by conjugation	This study
PAK ::pCTX- <i>rsmZ-lacZ</i> (4)	pCTX- <i>rsmZ-lacZ-4</i> plasmid was introduced into the wt strain by conjugation	This study
PAK Δ <i>gacA</i> ::pCTX- <i>rsmY-lacZ</i> (1)	pCTX- <i>rsmY-lacZ</i> plasmid was introduced into the Δ <i>gacA</i> strain by conjugation	This study
PAK Δ <i>gacA</i> ::pCTX- <i>rsmY-lacZ</i> (2)	pCTX- <i>rsmY-lacZ-2</i> plasmid was introduced into the Δ <i>gacA</i> strain by conjugation	This study
PAK Δ <i>gacA</i> ::pCTX- <i>rsmY-lacZ</i> (3)	pCTX- <i>rsmY-lacZ-3</i> plasmid was introduced into the Δ <i>gacA</i> strain by conjugation	This study
PAK Δ <i>gacA</i> ::pCTX- <i>rsmZ-lacZ</i> (1)	pCTX- <i>rsmZ-lacZ-1</i> plasmid was introduced into the Δ <i>gacA</i> strain by conjugation	This study
PAK Δ <i>gacA</i> ::pCTX- <i>rsmZ-lacZ</i> (2)	pCTX- <i>rsmZ-lacZ-2</i> plasmid was introduced into the Δ <i>gacA</i> strain by conjugation	This study
PAK Δ <i>gacA</i> ::pCTX- <i>rsmZ-lacZ</i> (3)	pCTX- <i>rsmZ-lacZ-3</i> plasmid was introduced into the Δ <i>gacA</i> strain by conjugation	This study
PAK Δ <i>gacA</i> ::pCTX- <i>rsmZ-lacZ</i> (4)	pCTX- <i>rsmZ-lacZ-4</i> plasmid was introduced into the Δ <i>gacA</i> strain by conjugation	This study
Figure 6		
PAO1 Δ <i>mvaT</i>	deletion mutant	(Diggle <i>et al.</i> , 2002)
PAO1 Δ <i>mvaU</i>	deletion mutant	(Vallet-Gely <i>et al.</i> , 2005)
PAO1 Δ <i>mvaT</i> ::pCTX- <i>rsmY-lacZ</i>	pCTX- <i>rsmY-lacZ</i> plasmid was introduced into the Δ <i>mvaT</i> strain by conjugation	This study
PAO1 Δ <i>mvaU</i> ::pCTX- <i>rsmY-lacZ</i>	pCTX- <i>rsmY-lacZ</i> plasmid was introduced into the Δ <i>mvaU</i> strain by conjugation	This study
PAO1 Δ <i>mvaT</i> ::pCTX- <i>rsmZ-lacZ</i>	pCTX- <i>rsmZ-lacZ-1</i> plasmid was introduced into the Δ <i>mvaT</i> strain by conjugation	This study
PAO1 Δ <i>mvaU</i> ::pCTX- <i>rsmZ-lacZ</i>	pCTX- <i>rsmZ-lacZ-1</i> plasmid was introduced into the Δ <i>mvaU</i> strain by conjugation	This study
Figure S1		
PAK Δ <i>retS</i> Δ <i>gacS</i>	double deletion mutant	This study

* For more detail, see supporting experimental procedures - text.

SUPPORTING EXPERIMENTAL PROCEDURES – REFERENCES:

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