

1403-1402-1401-1400-1399-1398-1397-1396-1395-1394-1393-1392	CM-M-M-O-M-M-M-N-O-O	1542621	1542653	-	I/C	-59	20.4	5.8	55.4	T3SS components HrpJ - HrcV - HrpQ - HrcN - HrpO - HrpP - HrcQa - HrcQb - HrcR - HrcS - HrcT - HrcU
5617*	NR	939413	939445	-	E/N	-96	20.2	6.8	45.7	conserved hypothetical protein (pseudogene)
5053	O	5751475	5751507	+	E/C	-487	19.8	5.5	56.5	hypothetical protein
2678-2679	FCM-N	2973825	2973857	+	I/C	-121	19.6	6.9	47.8	HopP1 - hypothetical protein
834-(835-836-837-838)	CR-CO-CO-O-O	905339	905371	+	I/C	-236	19.2	6.3	50.0	alcohol dehydrogenase, zinc-containing - ribD C-terminal domain protein - conserved domain protein - hypothetical protein - major facilitator family transporter
873	O	941100	941132	+	I/C	-919	19.2	5.9	44.6	amidinotransferase family protein
503-(502-501)	M-FCO-O	550602	550634	-	I/C	-65	18.8	6.3	39.1	T3SS chaperone ShcF - HopF2 - HopU1
4718	OR	5344375	5344407	-	I/C	-196	18.8	5.9	51.1	HopAA1-2
1372	FCM	1507652	1507684	+	I/C	-194	18.7	5.9	55.4	HopAA1-1
4589-4588	CO-CN	5186123	5186155	-	I/C	-61	18.7	5.3	57.6	T3SS chaperone ShcS2 - HopS2
A0005	FM	6595	6627	-	I/C	-66	18.4	5.8	48.9	HopAM1-2
1022	FCM	1116378	1116410	-	I/C	-66	18.4	5.8	48.9	HopAM1-1
1369-1370	FM-FCM	1504886	1504918	+	I/C	-63	18.4	6.1	41.3	conserved effector locus protein - HopN1
524	OR	572473	572505	+	I/C	-101	18.3	6.3	52.2	peptidase, M20 - M25 - M40 family
A0012	FM	16103	16135	-	I/C	-67	18.1	5.8	40.2	HopX1
1374-1375-(1376)	CM	1510881	1510913	+	I/C	-89	17.9	5.0	45.7	T3SS chaperone ShcM - HopM1 - T3SS chaperone ShcE
5353-5354	CM-FCM	6085756	6085788	+	I/C	-59	17.5	6.0	53.3	T3SS chaperone ShcA - HopA1

5620*-1568	O-CR	1731421	1731453	-	E/N	-288	17.0	5.8	43.5	hypothetic protein identified by sequence similarity - HopAF1
2856	O	3212151	3212183	-	I/C	-1634	16.8	5.1	48.9	site-specific recombinase, phage integrase family
4699	O	5328019	5328051	-	I/C	-854	16.8	5.6	35.9	non-ribosomal peptide synthetase, terminal component
4776	FCR	5418197	5418229	-	I/C	-56	16.5	6.0	52.2	HopI1
A0017-A0018-A0019	M-M-M	19658	19690	+	I/C	-61	16.4	5.7	56.5	T3SS chaperone ShcO1 - HopO1-1 - HopT1-1
1405-1406	CM	1543416	1543448	+	I/C	-64	16.4	6.3	51.1	HrpK1 - HopB1
61	FCM	82447	82479	+	I/C	-54	16.3	5.4	53.3	HopY1
5622*-1408-1409	O-FN-M(i)	1548389	1548421	+	I/C	-531	16.1	5.5	47.8	hypothetical protein - hypothetical protein - hypothetical protein
B00078*-B0005	P-MR	6894	6926	-	I/C	-820	16.0	6.4	45.7	unannotated protein - phosphoesterase family protein
4724-4725-4726#	N	5350034	5350066	+	I/C	-655	16.0	5.7	47.8	HopD (interruption-N) - IS52, transposase - Hop D (interruption-C)
[4579]	O	5176133	5176165	+	E/C	681	15.9	5.4	57.6	peptide chain release factor 3
852	FCM	921879	921911	-	I/C	-219	15.5	6.1	47.8	HopAJ1
1373	FCM	1510785	1510817	-	I/C	-153	15.4	6.1	55.4	HrpW1
1377	C0	1519570	1519602	-	I/C	-99	15.2	5.7	50.0	AvrE1
4101	FCM	4621129	4621161	+	I/C	-95	15.1	5.9	54.4	HopAK1
5616*-474-473	FOR-O	522444	522476	-	I/C	-309	14.7	6.2	50.0	conserved hypothetical protein - Hop AS1' (interruption-N) - HopAS1 (interruption-C)
4344	O	4905189	4905221	+	E/C	-1456	14.6	5.0	64.1	insecticidal toxin protein, putative
4727	CM	5355224	5355256	-	I/C	-90	14.4	5.7	45.7	HopG1
4464	O	5024215	5024247	+	E/N	-1316	14.3	5.3	57.6	conserved hypothetical protein
4276	O	4820136	4820168	-	E/N	-2127	13.9	4.7	56.5	transcriptional regulator, LysR

										family
4722 – (4721 – 4720)	FCO	5348578	5348610	-	I/C	-86	13.8	5.1	47.8	HopAO1 – T3SS chaperone ShcV – HopV1
437	O	488341	488373	-	E/N	-6645	13.3	5.3	48.9	dihydrofolate reductase
44	CR	61504	61536	-	E/N	-113	13.2	5.4	51.1	HopK1
370-(371)	O-FCO	404752	404784	+	I/C	-114	13.2	5.5	52.2	MATE efflux family protein - indoleacetate-lysine ligase (iaaL)
4703	CN	5330688	5330720	+	I/C	-114	13.2	5.4	52.2	HopAQ1
1398-1397- 1396-1395- 1394-1393- 1392	M-M- M-M- M-N- O-O	1536874	1536906	-	E/C	-870	13.1	5.4	57.6	T3SS components HrpP - HrcQa - HrcQb - HrcR - HrcS - HrcT - HrcU
[1707]	O	1876880	1876912	-	E/C	1104	12.9	5.3	60.9	L-sorbose dehydrogenase
1841	O	2008405	2008437	+	E/N	-887	12.9	4.4	53.3	threonine aldolase, low-specificity
1996-1995- 1994	O-O-N- O	2182088	2182120	-	E/C	-120	12.9	NA	66.3	copper-translocating P-type ATPase - cytochrome oxidase maturation protein, cbb3-type - membrane protein, putative
1370	FCM	1505219	1505251	+	E/C	-222	12.8	4.4	57.6	HopN1
2346	O	2600072	2600104	+	E/N	-1061	12.7	4.4	68.5	4-hydroxyphenylpyruvate dioxygenase, putative
1869	O	2044553	2044585	-	E/C	-1243	12.5	5.1	55.4	conserved hypothetical protein
5200	O	5908418	5908450	+	E/N	-9545	12.5	4.9	65.2	autotransporter, putative
1645	O	1802304	1802336	+	E/C	-722	12.3	4.8	62.0	transcriptional regulator, SlyA/MarR family
3019	O	3393410	3393442	+	E/C	-579	12.3	4.8	56.5	oxidoreductase, Gfo - Idh - MocA family
5522	O	6289194	6289226	+	E/N	-249	12.3	5.0	55.4	conserved hypothetical protein
[1268]	O	1391965	1391997	-	E/C	224	12.2	4.6	67.4	valyl-tRNA synthetase
4721	O	5346758	5346790	-	I/C	-60	12.2	5.6	43.5	hypothetical protein
4205	O	4733222	4733254	+	E/N	-3960	12.0	4.8	68.5	transcriptional regulator, GntR

										family
[B0069]	N	59060	59092	+	E/C	602	11.8	4.7	59.8	traY protein
5089	0	5790510	5790542	+	E/N	-977	11.8	4.8	55.4	conserved hypothetical protein
5619* - 901	C0	981177	981209	+	I/C	-324	11.7	5.2	39.1	putative T3SS chaperone - candidate HopAG1::ISPssy
[4248]	0	4786717	4786749	+	E/C	765	11.7	5.0	50.0	3-hydroxyacyl-CoA-acyl carrier protein transferase
2696	0	2990246	2990278	-	I/C	-241	11.6	4.4	48.9	mutT - nudix family protein
3489-3488	M(i)-M	3939658	3939690	-	E/C	-317	11.6	4.4	59.8	sugar ABC transporter, ATP-binding protein - sugar ABC transporter, permease protein
932	0	1014826	1014858	-	E/N	-3955	11.5	4.9	55.4	sugar ABC transporter, permease protein
5057	0	5761609	5761641	-	I/C	-316	11.5	4.6	64.1	dihydroxy-acid dehydratase
4920	0	5569089	5569121	+	I/C	-269	11.4	5.1	51.1	transcriptional regulator, LysR family
119	0	142796	142828	+	E/C	-179	11.3	4.9	51.1	peptidase, M16 family
224-223-222-221	0	247050	247082	-	E/C	-681	11.3	4.9	62.0	diaminopimelate epimerase - conserved hypothetical protein - integrase - recombinase XerC - HAD-superfamily hydrolase
2130	0	2304328	2304360	-	E/C	-220	11.3	4.8	51.1	DNA-binding response regulator, LuxR family
3984	0	4489552	4489584	+	I/N	-1436	11.3	5.2	62.0	cold shock domain family protein
[4005]	0	4519000	4519032	+	E/C	418	11.3	4.7	55.4	hypothetical protein
1213	0	1329860	1329892	-	E/N	-783	11.2	4.5	54.4	transcriptional regulator, AraC family
[1842]	0	2012107	2012139	+	E/C	1667	11.2	4.5	54.4	alanyl-tRNA synthetase

2145-2144-2143-2142-2141-2140-2139-2138	0	2354845	2354877	-	E/N	-25784	11.2	5.1	51.1	iron-regulated membrane protein, putative - conserved hypothetical protein - conserved hypothetical protein - conserved hypothetical protein - cation ABC transporter, periplasmic cation-binding protein - cation ABC transporter, ATP-binding protein - cation ABC transporter, permease protein - ABC transporter, periplasmic substrate-binding protein, putative
3721	0	4199603	4199635	+	E/C	-1220	11.0	4.6	62.0	enoyl-(acyl-carrier-protein) reductase
[2362]	0	2615952	2615984	+	E/C	513	10.9	4.8	60.9	methionine aminopeptidase, type I
3270	N	3693598	3693630	+	E/N	-2442	10.9	4.2	57.6	conserved hypothetical protein
5623* - 4732	MR	5355530	5355562	+	I/N	-4324	10.9	4.5	55.4	HopH:: IsPsy4 - HopQ1-2
665	0	714155	714187	+	E/N	-4377	10.7	4.4	68.5	ROK family protein
300	0	325510	325542	+	I/C	-255	10.6	4.2	53.3	succinate-semialdehyde dehydrogenase
2107	0	2287258	2287290	-	E/N	-3931	10.6	4.1	56.5	glycerophosphoryl diester phosphodiesterase, putative
4157-4158	0	4684462	4684494	+	E/N	-264	10.6	5.1	59.8	dihydroorotase, homodimeric type - ribonuclease T
4976	0	5649753	5649785	-	E/N	-1312	10.6	5.1	62.0	thiamin biosynthesis protein ThiC
[4996]	0	5673452	5673484	+	E/C	163	10.6	4.9	62.0	conserved domain protein
2431	0	2683181	2683213	+	E/C	-969	10.5	4.8	44.6	conserved hypothetical protein
3641	0	4099725	4099757	+	E/C	-639	10.5	4.0	64.1	endoribonuclease L-PSP family protein
4516.1	0	5085928	5085960	+	E/C	-255	10.5	4.6	54.4	tmRNA, putative [1]
[2151]	0	2358286	2358318	-	E/C	1194	10.4	4.4	60.9	TonB-dependent siderophore receptor, putative
4381	0	4943533	4943565	-	E/N	-353	10.4	4.8	65.2	conserved hypothetical protein

5045	0	5752184	5752216	-	E/N	-6388	10.4	4.9	66.3	twitching motility protein
2162	0	2377712	2377744	-	E/C	-533	10.3	4.3	55.4	hypothetical protein
4294-4295	0	4839209	4839241	+	I/C	-107	10.3	4.3	56.5	chaperone protein HscC - DnaJ domain protein
[4955]	0	5616670	5616702	+	E/C	881	10.3	4.3	57.6	rhodanese domain protein - phosphatidylserine decarboxylase
5396	0	6125242	6125274	+	I/N	-3202	10.3	4.2	66.3	dTDP-glucose 4,6-dehydratase
4507	0	5074481	5074513	+	E/N	-4119	10.2	4.9	64.1	DNA repair protein RecN
1621-1620-1619	0	1779969	1780001	-	E/N	-1902	10.1	5.0	63.0	conserved hypothetical protein - conserved hypothetical protein - hypothetical protein
[2014]	N	2201776	2201808	-	E/C	135	10.1	4.3	63.0	aerotaxis receptor
5150-5151-5152	0	5859272	5859304	+	E/N	-1729	10.1	4.6	68.5	ubiquinone - menaquinone biosynthesis methyltransferase UbiE - conserved hypothetical protein - ubiquinone biosynthesis protein UbiB
5353-5354	CM	6085463	6085495	+	E/C	-352	10.1	4.5	57.6	T3SS chaperone ShcA – HopA1
371	FCO	406209	406241	+	E/C	-114	10.0	4.8	54.4	indoleacetate-lysine ligase (iaaL)
675	0	731309	731341	-	I/C	-10	9.6	4.4/ 4.5	53.3	arylesterase
1209-1208	0	1325953	1325985	-	I/C	-177	9.1	3.8/ 4.3	47.8	RNA polymerase sigma-70 factor – regulatory protein, putative
4691	CO	5305220	5305252	+	I/C	-583	8.7	3.8/ 4.4	47.8	HopAD1
1278	0	1405112	1405144	-	I/C	-44	7.7	4.2/ 4.9	56.5	sensory box protein/response regulator
1708-1709-1710-1711-1712-1713-1714-1715-1716-1717	0	1878314	1878346	+	I/C	-127	7.1	3.9/ 3.8	64.1	cobO operon: cob(I)yrinic acid a,c-diamide adenosyltransferase – nitroreductase family protein – cobD – cobC – cobQ – cobP – cobT - alpha-ribazole-5'-phosphate

										phosphatase, putative - cobS
2497-2498	N	2762679	2762711	-	I/C	-54	6.9	4.1/ 4.6	46.7	hypothetical protein – hypothetical protein
4071	O	4577328	4577360	-	I/C	-39	6.4	3.9/ 4.2	52.2	hypothetical protein
2936	O	3300862	3300894	-	I/C	-52	6.1	4.5/ 3.8	46.7	LamB/YscF family protein
2525	O	2787908	2787940	+	E/N	-341	<6.0	4.7/ 4.1	59.8	peptide ABC transporter, permease protein
2790	O	3108233	3108265	+	E/C		<6.0	4.0/ 4.2	38.0	hypothetical protein
4964	O	5630188	5630220	-	I/C	-41	<6.0	4.1/ 4.0	53.3	conserved hypothetical protein
401	O	445291	445323	-	I/C	-233	<6.0	3.9/ 3.9	60.9	iron-sulfur cluster-binding protein, Rieske family
1672	O	1843567	1843599	+	I/C	-47	<6.0	4.0/ 3.9	63.0	DNA-binding response regulator
5618*	N	922923	922955	-	I/C		<6.0	4.1/ 4.5	46.7	HopAT1 (frameshift)
1407	CN	NO HRP PROMOTER								pseudogene not annotated as CDS
4680	CO	NO HRP PROMOTER								coronafacic acid synthetase, ligase component (cfl)
4681-4682- 4683-4684- 4685-4686- 4687-4688- 4689-4690	F-N- N-N- N-F- N-N- N-N	NO HRP PROMOTER								coronafacic acid (cfa) synthetase components cfa1 through cfa7 - hypothetical protein - cfa8- cfa9

Entries are color coded as follows:

BLUE: experimental evidence for HrpL-dependent expression both under conditions of *hrpL* deletion in Hrp minimal medium as examined here, and *hrpL* overexpression in rich medium, as previously reported (Chang *et al.*, 2005; Fouts *et al.*, 2002).

GREEN: experimental evidence for HrpL-dependent expression under conditions of *hrpL* deletion in Hrp minimal medium as examined here, but not under *hrpL* overexpression in rich medium, as previously reported (Chang *et al.*, 2005; Fouts *et al.*, 2002).

ORANGE: experimental evidence for HrpL-dependent expression under *hrpL* overexpression in rich medium, as reported (Chang *et al.*, 2005; Fouts *et al.*, 2002), but not under conditions of *hrpL* deletion in Hrp minimal medium as examined here.

GRAY: no experimental evidence for HrpL-dependent expression

For each Hrp promoter, the following items are identified:

- OPERON: the predicted downstream target(s) of the promoter. Operon members enclosed in parentheses are assumed to be part of the stated operon because of experimental evidence, but which were not identified so by our computational operon prediction method. Operon members enclosed in square brackets are not considered to be actual downstream targets but are included for the sake of completeness; these represent genes in which the predicted Hrp promoter is embedded, with no plausible downstream target that can be identified (i.e., no subsequent genes in a predicted operon which could be controlled by the promoter).
 - NOTES:
 - * PSPTO numbers annotated with an asterisk refer to new gene calls that we are making based on this work. These new PSPTO identifiers are included in the updated GenBank file we are submitting in conjunction with this paper.
 - # entry 4724-4725-4726 is presumed vestigial, although the promoter may indeed be functional; 4725 is a transposase which appears to have inserted into, and disrupted, a copy of HopD1, which is composed of the fragments in 4724 and 4726.
- EVID: summary of experimental evidence for HrpL-dependent expression, listing an entry for each member of the predicted operon, respectively; if only one entry is listed for a polycistronic operon, that evidence label applies to every member of the operon
 - M = exhibited differential expression (up-regulation) on our Microarray
 - M(i) = exhibited differential expression (up-regulation) on our Microarray, but just missed our spot intensity cutoff of 4000 units; reducing that cutoff to 3900 units included two extra spots, associated with PSPTO1409 and PSPTO3489. For further evidence of expression of PSPTO1409, see Petnicki-Ocwiega *et al.* (2005).
 - R = exhibited differential expression (up-regulation) in our RT-PCR assays
 - C = listed in Chang *et al.* (2005) Table 2 with nonzero reads in functional screen for DC3000

- F = listed in Fouts et al. (2002), Table 2
- O = on our Microarray, but did not exhibit differential expression
- N = not on our Microarray
- P = evidence for existence of peptide fragment via proteomics
- START: start coordinate of Hrp promoter
- STOP: stop coordinate of Hrp promoter
- S: strand of Hrp promoter
- GEO: geometry of the Hrp promoter hit with respect to the local genome
 - I = Intergenic (start of Hrp promoter is located between two predicted genes)
 - E = Embedded (start of Hrp promoter is located within a predicted coding region)
 - C = Coding: if hit is Embedded, then Hrp promoter is oriented in the coding direction of the gene in which it is embedded; if hit is Intergenic, then next downstream gene is on the same strand as the Hrp promoter
 - N = Noncoding: if hit is Embedded, then Hrp promoter is oriented oppositely to the coding direction of the gene in which it is embedded; if hit is Intergenic, then next downstream gene is on the opposite strand of the Hrp promoter\
- DIST: distance from the start of the Hrp promoter to the start of the predicted operon (NOTE: distance is calculated on the same strand as the Hrp promoter, even if the next downstream gene is on the opposite strand (e.g., Intergenic/Noncoding)); negative distances indicate the start of the Hrp promoter is upstream of the start of the target operon; positive distances indicate the start of the Hrp promoter is downstream of the start of the gene; in this case, the Hrp promoter is embedded
- HMM2: score of Hrp promoter within the Hidden Markov Model level 2 model
- WM2: score of Hrp promoter within the Weight Matrix level 2 model (number of standard deviations above the mean)
- GC: percentage of G+C nucleotides in a window around and including the Hrp promoter, extending 40 bases upstream of the start of the Hrp promoter and 20 bases downstream of the stop
- PROTEIN ANNOTATIONS: GenBank annotations of the protein corresponding to each member of the predicted operon. Abbreviations in annotations: TT = Type III; prot = protein. T3SS substrate names are updated to reflect the new Hop nomenclature conventions (Lindeberg et al. 2005).