TABLE S2 Differentially expressed genes in *lysR1*-Tn*5* vs wild type as determined by RNA-Seq analysis[a]

NC_013961.1 gene symbol/ locus tag	old locus tag FN434113.1	Locus position Min - Max	Differential Expression Adjusted p-value	Differential Expression Log2 Ratio	gene description
budA/ EAMY_RS17335	EAMY_0013	29382 - 30164	8.68E-31	-1.6261825	acetolactate decarboxylase
alsS/ EAMY_RS17340	EAMY_0014	30183 - 31862	9.28E-48	-1.5095395	acetolactate synthase AlsS
cpxP/ EAMY_RS17805	EAMY_0106	129538 – 130047	2.59E-25	1.1038690	Cell-envelope stress modulator CpxP
metE/ EAMY_RS18320	EAMY_0208	242743 - 245016	9.90E-25	1.28405867	5-methyltetrahydropteroyl triglutamate--homocysteine S-methyltransferase
argF/ EAMY_RS19145	EAMY_0367	427139 - 428149	2.25E-20	1.26159241	ornithine carbamoyltransferase
exbB/ EAMY_RS19610	EAMY_0469	549624 - 550358	2.27E-44	-1.4035499	tol-pal system-associated acyl-CoA thioesterase
exbD/ EAMY_RS19615	EAMY_0470	550364 - 550786	7.65E-22	-1.1577103	TonB system transport protein ExbD
ftnA/ EAMY_RS19690	EAMY_0487	567256 - 567771	1.25E-109	1.72997827	non-heme ferritin
EAMY_RS20500	EAMY_0663/ lysR1	736613 - 737533	3.35E-16	1.24839465	LysR family transcriptional regulator
lysA/ EAMY_RS20505	EAMY_0664	737660 - 738913	1.27E-32	-1.5251502	diaminopimelate decarboxylase
ssuB/ EAMY_RS23805	EAMY_1369	1447291 - 1448079	2.86E-17	-1.2804098	aliphatic sulfonates ABC transporter ATP-binding protein
ssuC/ EAMY_RS23810	EAMY_1370	1448076 - 1448867	7.99E-20	-1.5615225	aliphatic sulfonate ABC transporter permease SsuC
ssuD/ EAMY_RS23815	EAMY_1371	1448878 - 1450023	2.59E-08	-1.2842988	FMNH2-dependent alkanesulfonate monooxygenase
ssuE/ EAMY_RS23825	EAMY_1373	1451012 - 1451563	1.73E-33	-1.8082901	NADPH-dependent FMN reductase (FM = flavin mononucleotide)

spy / EAMY_RS25005	EAMY_1633	1701423 - 1701911	1.47E-33	-1.6465003	ATP-independent periplasmic protein-refolding chaperone
cho/ EAMY_RS25010	EAMY_1634	1702039 - 1702908	3.27E-13	-1.0090262	excinuclease Cho
pspF (check) / EAMY_RS25750	EAMY_1804	1867056 - 1868945	1.11E-10	-1.1111577	sigma-54-dependent Fis family transcriptional regulator CDS Putative phage shock protein pspF)
pspB/ EAMY_RS26055	EAMY_1876	1941956 - 1942183	1.94E-12	-1.1315087	envelope stress response membrane protein PspB
pspA/ EAMY_RS26060	EAMY_1877	1942246 - 1942917	8.20E-24	-1.4341551	phage shock protein PspA
phoA/ EAMY_RS27095	EAMY_2120	2164215 – 2165618	3.13E-13	-1.0285378	alkaline phosphatase
EAMY_RS27445	adhB; EAMY_2196	2235033 - 2236088	1.49E-60	-1.6072554	2,3-butanediol dehydrogenase
EAMY_RS28245	EAMY_2359	2427468 - 2428826	1.19E-10	-1.1684954	hypothetical protein
EAMY_RS28935	none given	2573310 - 2573585	8.64E-31	-1.5933057	DUF1471 domain-containing protein CDS
recN/ EAMY_RS29535	EAMY_2641	2725846 - 2727507	6.57E-20	1.04683248	DNA repair protein RecN
EAMY_RS32010	EAMY_3190	3278158 - 3279747	3.06E-26	-1.012391	asparagine synthetase B
EAMY_RS32015	panC3; EAMY_3191	3279809 - 3280732	1.96E-25	-1.1268426	pantoate--beta-alanine ligase (vitamin B5 biosynth pathway)
EAMY_RS32035	EAMY_3195	3284375 - 3285640	8.77E-30	-1.2689572	ATP phosphoribosyltransferase regulatory subunit
EAMY_RS32040	EAMY_3196	3285681 - 3286736	2.61E-46	-1.4098597	class I SAM-dependent methyltransferase
EAMY_RS32045	none given	3286833 - 3287414	8.99E-23	-1.1672617	hypothetical protein CDS
sosX/ EAMY_RS32460	EAMY_3287	3394429 - 3394854	1.57E-26	-1.5676232	superoxide response transcriptional regulator SoxS

glpD/ EAMY_RS33305	EAMY_3460	3554448 - 3555953	6.26E-18	-1.1364015	glycerol-3-phosphate dehydrogenase
ugpB/ EAMY_RS33405	EAMY_3484	3579894 - 3581210	5.01E-13	-1.2228179	sn-glycerol-3-phosphate ABC transporter substrate-binding protein UgpB
EAMY_RS33720	sidE; EAMY_3562	3649912 - 3650814	1.38E-14	-1.1302889	siderophore-interacting protein
mgtA/ EAMY_RS33845	EAMY_3590	3678765 - 3681446	1.85E-40	1.35328662	magnesium-translocating P-type ATPase

[a] Gene and genomic position information is in the *Erwinia amylovora* CFBP1430 annotated genome (Smits et al., 2010).

Literature Cited

Smits, T.H., Rezzonico, F., Kamber, T., Blom, J., Goesmann, A., Frey, J.E. et al. (2010) Complete genome sequence of the fire blight pathogen *Erwinia amylovora* CFBP 1430 and comparison to other *Erwinia* spp. Molecular Plant-Microbe Interactions, 23:384–393. https://doi.org/10.1094/mpmi-23-4-0384